Table S2. Enrichment_all

Module	ID	Descriptior	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID
GO_BP_m1	GO:004345	regulation	5/2606	5/23843	1.55E-05	0.045515	0.04328	Bpgm/Hsd
GO_BP_m1	GO:007097	protein loc	5/2606	5/23843	1.55E-05	0.045515	0.04328	Bcap29/Bc
GO_BP_m1	GO:200019	negative re	5/2606	5/23843	1.55E-05	0.045515	0.04328	Amh/Hyal3
GO_BP_m1	GO:000963	response t	62/2606	337/23843	2.80E-05	0.061596	0.058572	Abat/Adh1
GO_BP_m1	GO:004578	negative re	75/2606	442/23843	7.48E-05	0.131424	0.12497	Atr/AY0748
GO_BP_m1	GO:000301	vascular pr	39/2606	194/23843	0.000123	0.179743	0.170916	Acta2/Adm
GO_BP_m1	GO:004748	regulation	6/2606	10/23843	0.000241	0.206138	0.196015	Abcb1a/Gy
GO_BP_m1	GO:005158	negative re	10/2606	26/23843	0.000243	0.206138	0.196015	Abat/Arl6ip
GO_BP_m1	GO:000945	RNA modif	28/2606	128/23843	0.00025	0.206138	0.196015	Virma/2210
GO_BP_m1	GO:190203	regulation	5/2606	7/23843	0.00027	0.206138	0.196015	Bpgm/Hsd
GO_BP_m1	GO:004311	receptor cl	16/2606	57/23843	0.000287	0.206138	0.196015	Cdh2/Cdk5
GO_BP_m1	GO:009775	negative re	24/2606	104/23843	0.000292	0.206138	0.196015	Acta2/Adm
GO_BP_m1	GO:004426	cellular car	48/2606	266/23843	0.000338	0.206138	0.196015	Abhd10/Ac
GO_BP_m1	GO:005088	regulation	34/2606	170/23843	0.000356	0.206138	0.196015	Acta2/Adm
GO_BP_m1	GO:003276	regulation	13/2606	42/23843	0.00037	0.206138	0.196015	Atp2b4/Ca
GO_BP_m1	GO:004427	cellular car	11/2606	32/23843	0.000377	0.206138	0.196015	Abhd10/Pg
GO_BP_m1	GO:003515	regulation	34/2606	171/23843	0.000399	0.206138	0.196015	Acta2/Adm
GO_BP_m1	GO:000166	ameboidal	63/2606	378/23843	0.000442	0.20835	0.198118	Acta2/Adar
GO_BP_m1	GO:004428	small mole	52/2606	298/23843	0.000452	0.20835	0.198118	Abat/Abcd
GO_BP_m1	GO:001585	organic hy	41/2606	221/23843	0.000495	0.20835	0.198118	Abat/Abca
GO_BP_m1	GO:005134	regulation	19/2606	77/23843	0.000498	0.20835	0.198118	Abl2/Aoc3/
GO_BP_m1	GO:000761	learning	32/2606	161/23843	0.000585	0.209255	0.198978	Abl2/Adam
GO_BP_m1	GO:005118	cofactor m	74/2606	465/23843	0.000603	0.209255	0.198978	Acot1/Aco
GO_BP_m1	GO:001482	vascular sm	9/2606	24/23843	0.000619	0.209255	0.198978	Acta2/Bbs2
GO_BP_m1	GO:006002	soft palate	4/2606	5/23843	0.00065	0.209255	0.198978	Col11a2/Fc
GO_BP_m1	GO:190594	negative re	5/2606	8/23843	0.000655	0.209255	0.198978	Amh/Hyal3
GO_BP_m1	GO:001569	ammonium	25/2606	116/23843	0.00066	0.209255	0.198978	Abat/Abcb
GO_BP_m1	GO:006032	cell chemo	48/2606	274/23843	0.00067	0.209255	0.198978	Adam8/Bc
GO_BP_m1	GO:007037	regulation	54/2606	318/23843	0.000695	0.209255	0.198978	Abl2/Acta2
GO_BP_m1	GO:190136	organic cyc	76/2606	483/23843	0.000716	0.209255	0.198978	Aifm1/Aldh
GO_BP_m1	GO:005166	localizatior	27/2606	130/23843	0.000754	0.209255	0.198978	Arhgap44/
GO_BP_m1	GO:004231	vasoconstr	22/2606	98/23843	0.000762	0.209255	0.198978	Acta2/Adm
GO_BP_m1	GO:007190	negative re	23/2606	105/23843	0.00084	0.223588	0.212608	Cav1/Cav3/
GO_BP_m1	GO:000803	tRNA proce	24/2606	112/23843	0.000912	0.223588	0.212608	2210016F1
GO_BP_m1	GO:003529	regulation	31/2606	159/23843	0.000986	0.223588	0.212608	Acta2/Adm
GO_BP_m1	GO:009774	regulation	31/2606	159/23843	0.000986	0.223588	0.212608	Acta2/Adm
GO_BP_m1	GO:001584	monoamin	21/2606	94/23843	0.001061	0.223588	0.212608	Abat/Adra1
GO_BP_m1	GO:001701	regulation	21/2606	94/23843	0.001061	0.223588	0.212608	Cav1/Cav3/
GO_BP_m1	GO:009875	detoxificati	12/2606	41/23843	0.001075	0.223588	0.212608	Adh5/Cd36
GO_BP_m1	GO:000801	blood circu	73/2606	467/23843	0.001082	0.223588	0.212608	Abat/Acta2
GO_BP_m1	GO:004662	regulation	23/2606	107/23843	0.001103	0.223588	0.212608	Akap6/Arx/
GO_BP_m1	GO:009917	postsynaps	24/2606	114/23843	0.001183	0.223588	0.212608	Abl2/Arhga
GO_BP_m1	GO:003592	rRNA impo	3/2606	3/23843	0.001304	0.223588	0.212608	Mrpl18/Pn
GO_BP_m1	GO:006030	regulation	3/2606	3/23843	0.001304	0.223588	0.212608	Grem2/Il10
GO_BP_m1	GO:190560	regulation	3/2606	3/23843	0.001304	0.223588	0.212608	Anxa2/Ldlr
GO_BP_m1	GO:001605	vesicle org	52/2606	312/23843	0.001324	0.223588	0.212608	Ankfy1/An

GO_BP_m1	GO:005195	negative re	7/2606	17/23843	0.001331	0.223588	0.212608	Abat/Adora
GO_BP_m1	GO:001083	regulation	5/2606	9/23843	0.00134	0.223588	0.212608	Pum3/Ifng/
GO_BP_m1	GO:001063	epithelial c	45/2606	261/23843	0.001351	0.223588	0.212608	Adam8/Ad
GO_BP_m1	GO:003033	positive reg	76/2606	494/23843	0.00136	0.223588	0.212608	Acta2/Adam
GO_BP_m1	GO:000301	circulatory	73/2606	471/23843	0.001368	0.223588	0.212608	Abat/Acta2
GO_BP_m1	GO:200123	positive reg	33/2606	176/23843	0.001382	0.223588	0.212608	Atf3/Bcap3
GO_BP_m1	GO:004354	endothelial	34/2606	183/23843	0.001389	0.223588	0.212608	Adam8/Ad
GO_BP_m1	GO:190384	regulation	21/2606	96/23843	0.001409	0.223588	0.212608	Cav1/Cav3/
GO_BP_m1	GO:005134	positive reg	76/2606	495/23843	0.001439	0.223588	0.212608	Abl2/Adcya
GO_BP_m1	GO:004347	regulation	6/2606	13/23843	0.001471	0.223588	0.212608	Bpgm/Hsd
GO_BP_m1	GO:200105	positive reg	26/2606	129/23843	0.001479	0.223588	0.212608	Aifm1/Alox
GO_BP_m1	GO:007037	ERK1 and E	55/2606	336/23843	0.001495	0.223588	0.212608	Abl2/Acta2
GO_BP_m1	GO:003367	negative re	42/2606	241/23843	0.001549	0.223588	0.212608	Rtraf/Camk
GO_BP_m1	GO:004427	cellular nitr	68/2606	435/23843	0.001567	0.223588	0.212608	Aifm1/Apo
GO_BP_m1	GO:009013	epithelium	45/2606	263/23843	0.001581	0.223588	0.212608	Adam8/Ad
GO_BP_m1	GO:000151	RNA methy	15/2606	60/23843	0.001631	0.223588	0.212608	Virma/Cmt
GO_BP_m1	GO:001063	positive reg	26/2606	130/23843	0.001661	0.223588	0.212608	Adgra2/Alc
GO_BP_m1	GO:007037	positive reg	42/2606	242/23843	0.001681	0.223588	0.212608	Abl2/Acta2
GO_BP_m1	GO:000663	neutral lipi	24/2606	117/23843	0.001719	0.223588	0.212608	Acsl1/Angp
GO_BP_m1	GO:001095	positive reg	29/2606	151/23843	0.001791	0.223588	0.212608	Aifm1/Alox
GO_BP_m1	GO:000761	learning or	46/2606	272/23843	0.0018	0.223588	0.212608	Abl2/Adam
GO_BP_m1	GO:000690	vesicle bud	13/2606	49/23843	0.001836	0.223588	0.212608	Anxa2/Dnm
GO_BP_m1	GO:009013	tissue migr	45/2606	265/23843	0.001845	0.223588	0.212608	Adam8/Ad
GO_BP_m1	GO:000663	fatty acid m	60/2606	377/23843	0.00187	0.223588	0.212608	Abcd3/Abh
GO_BP_m1	GO:000196	synaptic tra	11/2606	38/23843	0.001897	0.223588	0.212608	Adra1d/Cd
GO_BP_m1	GO:000697	response to	61/2606	385/23843	0.00192	0.223588	0.212608	Adnp2/Aifm
GO_BP_m1	GO:000150	regulation	51/2606	310/23843	0.001944	0.223588	0.212608	Abat/Ache/
GO_BP_m1	GO:200123	positive reg	15/2606	61/23843	0.001947	0.223588	0.212608	Atf3/Casp8
GO_BP_m1	GO:001968	glyceraldeh	7/2606	18/23843	0.001974	0.223588	0.212608	Bpgm/Hsd
GO_BP_m1	GO:001583	amine tran	22/2606	105/23843	0.001977	0.223588	0.212608	Abat/Adora
GO_BP_m1	GO:001404	glutamate	10/2606	33/23843	0.002071	0.223588	0.212608	Adora1/Av
GO_BP_m1	GO:001063	regulation	37/2606	209/23843	0.002151	0.223588	0.212608	Adamts9/A
GO_BP_m1	GO:003248	negative re	8/2606	23/23843	0.002179	0.223588	0.212608	Cactin/Dhx
GO_BP_m1	GO:009011	COPII-coat	8/2606	23/23843	0.002179	0.223588	0.212608	Mia3/Pdcd
GO_BP_m1	GO:199074	cellular det	9/2606	28/23843	0.002184	0.223588	0.212608	Adh5/Cd36
GO_BP_m1	GO:001922	cytokine-m	59/2606	372/23843	0.002199	0.223588	0.212608	Acsl1/Adip
GO_BP_m1	GO:009723	cellular res	29/2606	153/23843	0.002201	0.223588	0.212608	Adh5/Bnip3
GO_BP_m1	GO:000639	tRNA meta	31/2606	167/23843	0.00223	0.223588	0.212608	2210016F1
GO_BP_m1	GO:200024	negative re	15/2606	62/23843	0.002314	0.223588	0.212608	Amh/Arhg
GO_BP_m1	GO:005105	regulation	64/2606	411/23843	0.002318	0.223588	0.212608	Aifm1/Ank
GO_BP_m1	GO:001923	sensory pe	26/2606	133/23843	0.002323	0.223588	0.212608	Acpp/Ador
GO_BP_m1	GO:006054	regulation	6/2606	14/23843	0.002337	0.223588	0.212608	Bok/Casp8/
GO_BP_m1	GO:007088	positive reg	6/2606	14/23843	0.002337	0.223588	0.212608	Akap6/Cib1
GO_BP_m1	GO:010605	positive reg	6/2606	14/23843	0.002337	0.223588	0.212608	Akap6/Cib1
GO_BP_m1	GO:001605	organic aci	37/2606	210/23843	0.002342	0.223588	0.212608	Abat/Abcd
GO_BP_m1	GO:004639	carboxylic a	37/2606	210/23843	0.002342	0.223588	0.212608	Abat/Abcd
GO_BP_m1	GO:000007	DNA dama	22/2606	107/23843	0.002537	0.239667	0.227897	Atr/Blm/Ba
GO_BP_m1	GO:005080	synapse or	54/2606	337/23843	0.002634	0.246095	0.23401	Abl2/Ache/

GO_BP_m1	GO:001059	positive reg	19/2606	88/23843	0.002718	0.251312	0.23897	Adgra2/Al
GO_BP_m1	GO:004390	regulation	62/2606	399/23843	0.00282	0.251671	0.239312	Anxa2/Arg
GO_BP_m1	GO:003466	ncRNA me	69/2606	453/23843	0.002822	0.251671	0.239312	2210016F1
GO_BP_m1	GO:004348	regulation	18/2606	82/23843	0.002869	0.251671	0.239312	Apobec1/
GO_BP_m1	GO:004311	receptor m	32/2606	177/23843	0.002946	0.251671	0.239312	Ache/Adm/
GO_BP_m1	GO:000614	purine nuc	8/2606	24/23843	0.002959	0.251671	0.239312	Acpp/Aprt/
GO_BP_m1	GO:001093	regulation	8/2606	24/23843	0.002959	0.251671	0.239312	Bnip3/Bok/
GO_BP_m1	GO:003277	positive reg	8/2606	24/23843	0.002959	0.251671	0.239312	Gch1/Gdnf
GO_BP_m1	GO:001569	organic cat	11/2606	40/23843	0.00297	0.251671	0.239312	Abcb1a/Ac
GO_BP_m1	GO:000663	acylglycero	23/2606	115/23843	0.00298	0.251671	0.239312	Acsl1/Ang
GO_BP_m1	GO:000758	response t	19/2606	89/23843	0.003109	0.258472	0.245779	Arsb/Asph/
GO_BP_m1	GO:007252	purine-co	73/2606	486/23843	0.003119	0.258472	0.245779	Acpp/Adcy
GO_BP_m1	GO:000646	negative re	38/2606	221/23843	0.003193	0.260483	0.247691	Rtraf/Cam
GO_BP_m1	GO:002240	regulation	57/2606	363/23843	0.003226	0.260483	0.247691	Abat/Abl2/
GO_BP_m1	GO:005090	leukocyte	50/2606	310/23843	0.003232	0.260483	0.247691	Adam8/Ad
GO_BP_m1	GO:000664	triglyceride	20/2606	96/23843	0.003313	0.262326	0.249444	Acsl1/Ang
GO_BP_m1	GO:005134	negative re	45/2606	273/23843	0.00332	0.262326	0.249444	Rtraf/Cam
GO_BP_m1	GO:005089	cognition	49/2606	303/23843	0.003345	0.262326	0.249444	Abl2/Adam
GO_BP_m1	GO:004670	heterocycle	67/2606	441/23843	0.00342	0.265816	0.252762	Aifm1/Ald
GO_BP_m1	GO:005170	interaction	17/2606	77/23843	0.003476	0.267828	0.254676	Anxa2/Arg
GO_BP_m1	GO:000609	pentose-pl	6/2606	15/23843	0.003538	0.267914	0.254758	Bpgm/Hsd
GO_BP_m1	GO:200019	regulation	6/2606	15/23843	0.003538	0.267914	0.254758	Amh/Hyal3
GO_BP_m1	GO:003225	methylatio	52/2606	327/23843	0.003656	0.2732	0.259783	Virma/643
GO_BP_m1	GO:003465	nucleobase	61/2606	396/23843	0.0037	0.2732	0.259783	Aifm1/Apo
GO_BP_m1	GO:004820	vesicle targ	4/2606	7/23843	0.003794	0.2732	0.259783	Pdcd6/Pre
GO_BP_m1	GO:004820	COPII vesic	4/2606	7/23843	0.003794	0.2732	0.259783	Pdcd6/Pre
GO_BP_m1	GO:190185	regulation	4/2606	7/23843	0.003794	0.2732	0.259783	Flcn/Lig3/
GO_BP_m1	GO:200024	regulation	30/2606	166/23843	0.003923	0.2732	0.259783	Amh/Arhg
GO_BP_m1	GO:190403	negative re	8/2606	25/23843	0.003939	0.2732	0.259783	Camk2n1/
GO_BP_m1	GO:001059	regulation	27/2606	145/23843	0.003948	0.2732	0.259783	Adamts9/A
GO_BP_m1	GO:005115	glucose 6-	7/2606	20/23843	0.003951	0.2732	0.259783	Bpgm/G6p
GO_BP_m1	GO:000193	negative re	63/2606	413/23843	0.004036	0.2732	0.259783	Rtraf/Atf3/
GO_BP_m1	GO:000176	membrane	5/2606	11/23843	0.004071	0.2732	0.259783	Anxa2/Cav
GO_BP_m1	GO:000690	vesicle coa	5/2606	11/23843	0.004071	0.2732	0.259783	Gbf1/Pdcd
GO_BP_m1	GO:190116	regulation	5/2606	11/23843	0.004071	0.2732	0.259783	Arhgdib/C
GO_BP_m1	GO:190329	regulation	5/2606	11/23843	0.004071	0.2732	0.259783	Cox11/Fox
GO_BP_m1	GO:004648	glycerolipi	49/2606	306/23843	0.004074	0.2732	0.259783	Tmem269/
GO_BP_m1	GO:005068	regulation	16/2606	72/23843	0.004211	0.278313	0.264645	Ddx60/Dh
GO_BP_m1	GO:000152	angiogenes	73/2606	492/23843	0.004241	0.278313	0.264645	Adam8/Ad
GO_BP_m1	GO:004639	carboxylic	53/2606	337/23843	0.004246	0.278313	0.264645	Abat/Abcd
GO_BP_m1	GO:006101	regulation	21/2606	105/23843	0.004414	0.287192	0.273089	Apobec1/
GO_BP_m1	GO:001605	organic aci	53/2606	338/23843	0.004513	0.288197	0.274044	Abat/Abcd
GO_BP_m1	GO:190353	negative re	36/2606	211/23843	0.004578	0.288197	0.274044	Abat/Ador
GO_BP_m1	GO:000647	protein AD	9/2606	31/23843	0.004715	0.288197	0.274044	Art1/Art5/
GO_BP_m1	GO:001943	aromatic c	68/2606	455/23843	0.004751	0.288197	0.274044	Aifm1/Apo
GO_BP_m1	GO:000684	pyruvate tr	3/2606	4/23843	0.00479	0.288197	0.274044	Mpc2/Myc
GO_BP_m1	GO:001405	negative re	3/2606	4/23843	0.00479	0.288197	0.274044	Abat/Hrh3/
GO_BP_m1	GO:003111	positive re	3/2606	4/23843	0.00479	0.288197	0.274044	Htr1a/Stm

GO_BP_m1	GO:004241	epinephrin	3/2606	4/23843	0.00479	0.288197	0.274044	Pnmt/Rnls/
GO_BP_m1	GO:004362	cortical mi	3/2606	4/23843	0.00479	0.288197	0.274044	Ezr/Pafah1
GO_BP_m1	GO:006024	negative re	3/2606	4/23843	0.00479	0.288197	0.274044	Dach1/Pak
GO_BP_m1	GO:190390	regulation	3/2606	4/23843	0.00479	0.288197	0.274044	Dock8/Flot
GO_BP_m1	GO:000664	phospholip	52/2606	332/23843	0.004984	0.297841	0.283214	Tmem269/
GO_BP_m1	GO:000762	copulation	8/2606	26/23843	0.005153	0.302199	0.287359	Abat/Avpr
GO_BP_m1	GO:004345	regulation	8/2606	26/23843	0.005153	0.302199	0.287359	Bnip3/Cdk
GO_BP_m1	GO:004348	regulation	19/2606	93/23843	0.00517	0.302199	0.287359	Apobec1/C
GO_BP_m1	GO:000194	postsynapt	10/2606	37/23843	0.005195	0.302199	0.287359	Cdh2/Gdnf
GO_BP_m1	GO:003162	receptor in	20/2606	100/23843	0.005378	0.310804	0.295541	Ache/Adm/
GO_BP_m1	GO:001587	dopamine	12/2606	49/23843	0.005511	0.315962	0.300446	Abat/Adra
GO_BP_m1	GO:005158	regulation	21/2606	107/23843	0.005539	0.315962	0.300446	Abat/Arl6ip
GO_BP_m1	GO:003157	DNA integr	22/2606	114/23843	0.005658	0.320653	0.304907	Atr/Blm/Ba
GO_BP_m1	GO:009950	synaptic ve	25/2606	135/23843	0.005806	0.322011	0.306198	Ap1s2/Can
GO_BP_m1	GO:000015	rRNA modi	9/2606	32/23843	0.005934	0.322011	0.306198	Ftsj3/Gm18
GO_BP_m1	GO:005195	regulation	20/2606	101/23843	0.006033	0.322011	0.306198	Abat/Adora
GO_BP_m1	GO:000906	cellular am	18/2606	88/23843	0.006305	0.322011	0.306198	Abat/Aldh4
GO_BP_m1	GO:006053	muscle tiss	66/2606	445/23843	0.006353	0.322011	0.306198	Acta1/Adar
GO_BP_m1	GO:000008	regulation	5/2606	12/23843	0.006356	0.322011	0.306198	E2f1/E2f7/
GO_BP_m1	GO:006054	negative re	5/2606	12/23843	0.006356	0.322011	0.306198	Bok/Casp8
GO_BP_m1	GO:006117	negative re	5/2606	12/23843	0.006356	0.322011	0.306198	Fkbp1b/Jag
GO_BP_m1	GO:006145	trophoblas	5/2606	12/23843	0.006356	0.322011	0.306198	Arhgdib/Ca
GO_BP_m1	GO:009720	activation	5/2606	12/23843	0.006356	0.322011	0.306198	Asph/Casp
GO_BP_m1	GO:000727	synaptic tra	10/2606	38/23843	0.006373	0.322011	0.306198	Chrm1/Chr
GO_BP_m1	GO:000007	cell cycle c	31/2606	179/23843	0.006493	0.322011	0.306198	Atr/Blm/Ba
GO_BP_m1	GO:005135	positive reg	11/2606	44/23843	0.006552	0.322011	0.306198	Abl2/Gch1/
GO_BP_m1	GO:000673	coenzyme	48/2606	306/23843	0.006575	0.322011	0.306198	Acot1/Aco
GO_BP_m1	GO:004478	modulation	8/2606	27/23843	0.006633	0.322011	0.306198	Cfl1/Fmr1/
GO_BP_m1	GO:007170	membrane	8/2606	27/23843	0.006633	0.322011	0.306198	Anxa2/Cav
GO_BP_m1	GO:009907	regulation	8/2606	27/23843	0.006633	0.322011	0.306198	Arhgap44/
GO_BP_m1	GO:000628	DNA repair	65/2606	438/23843	0.006635	0.322011	0.306198	Aplf/Aptx/
GO_BP_m1	GO:003355	unsaturate	20/2606	102/23843	0.006752	0.322011	0.306198	Akr1c12/Al
GO_BP_m1	GO:000608	cellular ald	15/2606	69/23843	0.006793	0.322011	0.306198	Adh1/Adh5
GO_BP_m1	GO:000741	synapse as	28/2606	158/23843	0.006834	0.322011	0.306198	Ache/Cadn
GO_BP_m1	GO:000923	cobalamin	4/2606	8/23843	0.006933	0.322011	0.306198	Clybl/Gif/M
GO_BP_m1	GO:003237	regulation	4/2606	8/23843	0.006933	0.322011	0.306198	Anxa2/Ldlr
GO_BP_m1	GO:003238	regulation	4/2606	8/23843	0.006933	0.322011	0.306198	Anxa2/Ldlr
GO_BP_m1	GO:003238	regulation	4/2606	8/23843	0.006933	0.322011	0.306198	Anxa2/Ldlr
GO_BP_m1	GO:005177	response t	4/2606	8/23843	0.006933	0.322011	0.306198	Adh5/Arntl
GO_BP_m1	GO:006024	contact inh	4/2606	8/23843	0.006933	0.322011	0.306198	Dach1/Pak
GO_BP_m1	GO:200002	positive reg	4/2606	8/23843	0.006933	0.322011	0.306198	Dmrt1/Nr5
GO_BP_m1	GO:200054	positive reg	4/2606	8/23843	0.006933	0.322011	0.306198	Foxa2/Osr
GO_BP_m1	GO:190134	negative re	22/2606	116/23843	0.006983	0.322011	0.306198	Adamts1/A
GO_BP_m1	GO:001095	positive reg	26/2606	144/23843	0.006985	0.322011	0.306198	Aifm1/Alox
GO_BP_m1	GO:000726	neurotrans	25/2606	137/23843	0.007029	0.322011	0.306198	Camk2a/Fr
GO_BP_m1	GO:009964	signal relea	25/2606	137/23843	0.007029	0.322011	0.306198	Camk2a/Fr
GO_BP_m1	GO:004232	negative re	67/2606	455/23843	0.007061	0.322011	0.306198	Rtraf/Atf3/
GO_BP_m1	GO:007055	response t	18/2606	89/23843	0.007115	0.322011	0.306198	Ankrd1/Ca

GO_BP_m1	GO:005104	regulation	7/2606	22/23843	0.00715	0.322011	0.306198	Adam8/Ifn
GO_BP_m1	GO:00639	mitochond	6/2606	17/23843	0.007222	0.322011	0.306198	Gm1818/M
GO_BP_m1	GO:00331	response t	6/2606	17/23843	0.007222	0.322011	0.306198	Cd36/Dapk
GO_BP_m1	GO:006054	negative re	6/2606	17/23843	0.007222	0.322011	0.306198	Bok/Casp8
GO_BP_m1	GO:00147	striated mu	63/2606	424/23843	0.007238	0.322011	0.306198	Acta1/Ada
GO_BP_m1	GO:00068	receptor-m	33/2606	195/23843	0.007267	0.322011	0.306198	Ache/Adm
GO_BP_m1	GO:00068	dicarboxyli	16/2606	76/23843	0.007295	0.322011	0.306198	Abat/Ador
GO_BP_m1	GO:000697	response t	16/2606	76/23843	0.007295	0.322011	0.306198	Abcb1a/Ap
GO_BP_m1	GO:00519	catecholan	16/2606	76/23843	0.007295	0.322011	0.306198	Abat/Adra
GO_BP_m1	GO:00481	Golgi vesic	9/2606	33/23843	0.007383	0.322661	0.306816	Gbf1/Mia3
GO_BP_m1	GO:00519	negative re	9/2606	33/23843	0.007383	0.322661	0.306816	Abat/Ador
GO_BP_m1	GO:00158	acidic amir	13/2606	57/23843	0.007489	0.325646	0.309654	Abat/Ador
GO_BP_m1	GO:005144	regulation	12/2606	51/23843	0.007726	0.330015	0.313809	Calr/Cdc2
GO_BP_m1	GO:190352	negative re	10/2606	39/23843	0.007748	0.330015	0.313809	Adm/Ador
GO_BP_m1	GO:005087	brown fat	11/2606	45/23843	0.007834	0.330015	0.313809	Adig/Arl4a
GO_BP_m1	GO:00519	regulation	11/2606	45/23843	0.007834	0.330015	0.313809	Abat/Ador
GO_BP_m1	GO:00324	response t	55/2606	363/23843	0.007844	0.330015	0.313809	Adh5/Adm
GO_BP_m1	GO:00725	reactive ox	41/2606	256/23843	0.008031	0.330015	0.313809	5730559C1
GO_BP_m1	GO:00181	peptidyl-se	50/2606	325/23843	0.008168	0.330015	0.313809	Atp2b4/At
GO_BP_m1	GO:00352	organ grov	31/2606	182/23843	0.008261	0.330015	0.313809	Akap6/Arx
GO_BP_m1	GO:001094	negative re	36/2606	219/23843	0.008315	0.330015	0.313809	Blm/Baba
GO_BP_m1	GO:00995	presynapti	26/2606	146/23843	0.008363	0.330015	0.313809	Camk2a/Fr
GO_BP_m1	GO:00513	negative re	8/2606	28/23843	0.008412	0.330015	0.313809	Aoc3/Atp2
GO_BP_m1	GO:190304	meiotic cel	33/2606	197/23843	0.008461	0.330015	0.313809	Btbd18/Ca
GO_BP_m1	GO:000627	regulation	22/2606	118/23843	0.00855	0.330015	0.313809	Atr/Blm/Ca
GO_BP_m1	GO:190352	regulation	37/2606	227/23843	0.008632	0.330015	0.313809	Adm/Ador
GO_BP_m1	GO:19037	negative re	9/2606	34/23843	0.009087	0.330015	0.313809	Abat/Ador
GO_BP_m1	GO:00518	regulation	25/2606	140/23843	0.009254	0.330015	0.313809	Adam8/C1
GO_BP_m1	GO:003157	membrane	7/2606	23/23843	0.009326	0.330015	0.313809	Anxa2/Cav
GO_BP_m1	GO:003581	regulation	7/2606	23/23843	0.009326	0.330015	0.313809	Adora1/Av
GO_BP_m1	GO:00457	negative re	7/2606	23/23843	0.009326	0.330015	0.313809	Cdkn1a/He
GO_BP_m1	GO:00988	cellular oxi	7/2606	23/23843	0.009326	0.330015	0.313809	Cd36/Fbln
GO_BP_m1	GO:000911	nucleobase	10/2606	40/23843	0.00934	0.330015	0.313809	Acpp/Aprt
GO_BP_m1	GO:00070	spindle org	29/2606	169/23843	0.009378	0.330015	0.313809	Ankrd53/B
GO_BP_m1	GO:003134	positive re	48/2606	312/23843	0.009395	0.330015	0.313809	5730559C1
GO_BP_m1	GO:00712	cellular res	5/2606	13/23843	0.009409	0.330015	0.313809	Aoc1/Atp7
GO_BP_m1	GO:00026	regulation	31/2606	184/23843	0.009647	0.330015	0.313809	Adam8/Ad
GO_BP_m1	GO:00069	vesicle fusi	26/2606	148/23843	0.009957	0.330015	0.313809	Ankfy1/An
GO_BP_m1	GO:00457	regulation	45/2606	290/23843	0.010015	0.330015	0.313809	Adamts1/A
GO_BP_m1	GO:000167	long-chain	18/2606	92/23843	0.010062	0.330015	0.313809	Acot1/Aco
GO_BP_m1	GO:003051	negative re	13/2606	59/23843	0.010079	0.330015	0.313809	Cav1/Danc
GO_BP_m1	GO:009881	nuclear chr	40/2606	252/23843	0.010123	0.330015	0.313809	Ankrd53/T
GO_BP_m1	GO:00518	modificatic	15/2606	72/23843	0.010142	0.330015	0.313809	Anxa2/Arg
GO_BP_m1	GO:00182	peptidyl-se	54/2606	360/23843	0.010154	0.330015	0.313809	Atp2b4/At
GO_BP_m1	GO:00193	fatty acid c	19/2606	99/23843	0.010248	0.330015	0.313809	Abcd3/Aca
GO_BP_m1	GO:001652	negative re	20/2606	106/23843	0.010358	0.330015	0.313809	Adamts1/A
GO_BP_m1	GO:004887	homeostas	47/2606	306/23843	0.010374	0.330015	0.313809	Asxl1/Bcr/
GO_BP_m1	GO:00705	regulation	31/2606	185/23843	0.010408	0.330015	0.313809	Ankrd53/B

GO_BP_m1	GO:00690	vesicle targ	8/2606	29/23843	0.010526	0.330015	0.313809	Gbf1/Map4
GO_BP_m1	GO:00865	phospholip	27/2606	156/23843	0.010629	0.330015	0.313809	Tmem269/
GO_BP_m1	GO:00305	leukocyte	32/2606	193/23843	0.010886	0.330015	0.313809	Adam8/Ca
GO_BP_m1	GO:00511	regulation	11/2606	47/23843	0.010973	0.330015	0.313809	Bpgm/Coq
GO_BP_m1	GO:00192	transmissi	17/2606	86/23843	0.010987	0.330015	0.313809	Ahnak2/Av
GO_BP_m1	GO:00062	base-excisi	3/2606	5/23843	0.011001	0.330015	0.313809	Pcna/Pole/
GO_BP_m1	GO:00157	lactate tra	3/2606	5/23843	0.011001	0.330015	0.313809	Myc/Slc16
GO_BP_m1	GO:00161	synaptic ve	3/2606	5/23843	0.011001	0.330015	0.313809	Dnajc6/Sh
GO_BP_m1	GO:00217	amygdala	3/2606	5/23843	0.011001	0.330015	0.313809	Nf1/Pak1/
GO_BP_m1	GO:00331	negative re	3/2606	5/23843	0.011001	0.330015	0.313809	Cox11/Fox
GO_BP_m1	GO:00358	lactate tra	3/2606	5/23843	0.011001	0.330015	0.313809	Myc/Slc16
GO_BP_m1	GO:00358	plasma me	3/2606	5/23843	0.011001	0.330015	0.313809	Myc/Slc16
GO_BP_m1	GO:00359	RNA impor	3/2606	5/23843	0.011001	0.330015	0.313809	Mrpl18/Pn
GO_BP_m1	GO:00359	positive re	3/2606	5/23843	0.011001	0.330015	0.313809	Kat2a/Kat2
GO_BP_m1	GO:00458	negative re	3/2606	5/23843	0.011001	0.330015	0.313809	Naa10/Tnk
GO_BP_m1	GO:00714	cellular res	3/2606	5/23843	0.011001	0.330015	0.313809	Ei24/Polh/
GO_BP_m1	GO:00901	receptor-m	3/2606	5/23843	0.011001	0.330015	0.313809	Anxa2/Ldlr
GO_BP_m1	GO:19011	negative re	3/2606	5/23843	0.011001	0.330015	0.313809	Arhgdib/Ca
GO_BP_m1	GO:19033	negative re	3/2606	5/23843	0.011001	0.330015	0.313809	Cox11/Fox
GO_BP_m1	GO:19037	negative re	3/2606	5/23843	0.011001	0.330015	0.313809	Ezr/Hsph1/
GO_BP_m1	GO:00102	response t	23/2606	128/23843	0.011332	0.330015	0.313809	Apobec1/
GO_BP_m1	GO:00030	regulation	4/2606	9/23843	0.011408	0.330015	0.313809	Chrm1/Chr
GO_BP_m1	GO:00067	cholesterol	4/2606	9/23843	0.011408	0.330015	0.313809	Cyp46a1/H
GO_BP_m1	GO:00140	negative re	4/2606	9/23843	0.011408	0.330015	0.313809	Adora1/Hr
GO_BP_m1	GO:00161	sterol cata	4/2606	9/23843	0.011408	0.330015	0.313809	Cyp46a1/H
GO_BP_m1	GO:00340	endosomal	4/2606	9/23843	0.011408	0.330015	0.313809	Ankfy1/Rbs
GO_BP_m1	GO:00485	regulation	4/2606	9/23843	0.011408	0.330015	0.313809	Ankfy1/Cav
GO_BP_m1	GO:00512	spindle elo	4/2606	9/23843	0.011408	0.330015	0.313809	Kif23/Kif4/
GO_BP_m1	GO:00718	response t	4/2606	9/23843	0.011408	0.330015	0.313809	Akap6/Atp
GO_BP_m1	GO:00718	cellular res	4/2606	9/23843	0.011408	0.330015	0.313809	Akap6/Atp
GO_BP_m1	GO:00989	receptor di	4/2606	9/23843	0.011408	0.330015	0.313809	Cacng5/Ca
GO_BP_m1	GO:00989	postsynapt	4/2606	9/23843	0.011408	0.330015	0.313809	Cacng5/Ca
GO_BP_m1	GO:00996	neurotrans	4/2606	9/23843	0.011408	0.330015	0.313809	Cacng5/Ca
GO_BP_m1	GO:20001	regulation	4/2606	9/23843	0.011408	0.330015	0.313809	Cd36/Fbln
GO_BP_m1	GO:00510	negative re	38/2606	239/23843	0.011642	0.330015	0.313809	Abat/Ador
GO_BP_m1	GO:19013	regulation	48/2606	316/23843	0.011788	0.330015	0.313809	Adamts1/
GO_BP_m1	GO:00008	regulation	2/2606	2/23843	0.011942	0.330015	0.313809	Atp2b4/Slc
GO_BP_m1	GO:00062	uracil cata	2/2606	2/23843	0.011942	0.330015	0.313809	Dpyd/Dpy
GO_BP_m1	GO:00065	phosphage	2/2606	2/23843	0.011942	0.330015	0.313809	Ckm/Ckmt
GO_BP_m1	GO:00066	phosphocr	2/2606	2/23843	0.011942	0.330015	0.313809	Ckm/Ckmt
GO_BP_m1	GO:00072	osmosens	2/2606	2/23843	0.011942	0.330015	0.313809	Osr1/Trpv4
GO_BP_m1	GO:00096	response t	2/2606	2/23843	0.011942	0.330015	0.313809	Gpx1/Gpx2
GO_BP_m1	GO:00096	response t	2/2606	2/23843	0.011942	0.330015	0.313809	Gpx1/Gpx2
GO_BP_m1	GO:00157	myo-inosit	2/2606	2/23843	0.011942	0.330015	0.313809	Pgap1/Slc5
GO_BP_m1	GO:00171	N-terminal	2/2606	2/23843	0.011942	0.330015	0.313809	Naa10/Na
GO_BP_m1	GO:00180	N-terminal	2/2606	2/23843	0.011942	0.330015	0.313809	Naa10/Na
GO_BP_m1	GO:00192	glucose 1-	2/2606	2/23843	0.011942	0.330015	0.313809	Pgm3/Ugp
GO_BP_m1	GO:00309	peptidyl-s	2/2606	2/23843	0.011942	0.330015	0.313809	Naa10/Na

GO_BP_m1	GO:003224	negative re	2/2606	2/23843	0.011942	0.330015	0.313809	Nup153/Tp
GO_BP_m1	GO:003229	positive reg	2/2606	2/23843	0.011942	0.330015	0.313809	Cdk2/Ciz1
GO_BP_m1	GO:004241	epinephrin	2/2606	2/23843	0.011942	0.330015	0.313809	Pnmt/Th
GO_BP_m1	GO:004341	homocyste	2/2606	2/23843	0.011942	0.330015	0.313809	Blmh/Mtrr
GO_BP_m1	GO:004629	formaldehy	2/2606	2/23843	0.011942	0.330015	0.313809	Adh5/Esd
GO_BP_m1	GO:004683	negative re	2/2606	2/23843	0.011942	0.330015	0.313809	Nup153/Tp
GO_BP_m1	GO:004821	Golgi vesic	2/2606	2/23843	0.011942	0.330015	0.313809	Cog4/Dnaj
GO_BP_m1	GO:005141	response to	2/2606	2/23843	0.011942	0.330015	0.313809	Htr7/Npas4
GO_BP_m1	GO:005187	lateral elem	2/2606	2/23843	0.011942	0.330015	0.313809	Sycp1/Sycp
GO_BP_m1	GO:006030	negative re	2/2606	2/23843	0.011942	0.330015	0.313809	Il10/Nog
GO_BP_m1	GO:006153	gamma-am	2/2606	2/23843	0.011942	0.330015	0.313809	Nf1/Pak1
GO_BP_m1	GO:007016	positive reg	2/2606	2/23843	0.011942	0.330015	0.313809	C1qtnf3/Hc
GO_BP_m1	GO:007127	cellular resp	2/2606	2/23843	0.011942	0.330015	0.313809	Bnip3/Tiga
GO_BP_m1	GO:007216	posterior m	2/2606	2/23843	0.011942	0.330015	0.313809	Osr1/Wt1
GO_BP_m1	GO:007218	metanephr	2/2606	2/23843	0.011942	0.330015	0.313809	Myc/Osr1
GO_BP_m1	GO:007218	metanephr	2/2606	2/23843	0.011942	0.330015	0.313809	Myc/Osr1
GO_BP_m1	GO:007253	tumor necr	2/2606	2/23843	0.011942	0.330015	0.313809	Adam8/Ifng
GO_BP_m1	GO:009009	metanephr	2/2606	2/23843	0.011942	0.330015	0.313809	Myc/Osr1
GO_BP_m1	GO:190208	negative re	2/2606	2/23843	0.011942	0.330015	0.313809	Hrc/Mrln
GO_BP_m1	GO:190228	negative re	2/2606	2/23843	0.011942	0.330015	0.313809	Aoc3/Park2
GO_BP_m1	GO:190390	positive reg	2/2606	2/23843	0.011942	0.330015	0.313809	Dock8/Flot
GO_BP_m1	GO:190497	regulation	2/2606	2/23843	0.011942	0.330015	0.313809	Park2/Synj1
GO_BP_m1	GO:190559	regulation	2/2606	2/23843	0.011942	0.330015	0.313809	Anxa2/Pcsk
GO_BP_m1	GO:190560	positive reg	2/2606	2/23843	0.011942	0.330015	0.313809	Anxa2/Ldlr
GO_BP_m1	GO:200030	regulation	2/2606	2/23843	0.011942	0.330015	0.313809	Adam8/Ifng
GO_BP_m1	GO:200030	positive reg	2/2606	2/23843	0.011942	0.330015	0.313809	Adam8/Ifng
GO_BP_m1	GO:200035	negative re	2/2606	2/23843	0.011942	0.330015	0.313809	Amh/Hyal3
GO_BP_m1	GO:200062	regulation	2/2606	2/23843	0.011942	0.330015	0.313809	Pnpt1/Zc3h
GO_BP_m1	GO:200062	positive reg	2/2606	2/23843	0.011942	0.330015	0.313809	Pnpt1/Zc3h
GO_BP_m1	GO:001404	regulation	7/2606	24/23843	0.011947	0.330015	0.313809	Adora1/Av
GO_BP_m1	GO:003581	renal sodiu	7/2606	24/23843	0.011947	0.330015	0.313809	Adora1/Av
GO_BP_m1	GO:190593	regulation	7/2606	24/23843	0.011947	0.330015	0.313809	Amh/Dmrt
GO_BP_m1	GO:000652	cellular am	42/2606	270/23843	0.012004	0.330548	0.314315	Dglucy/Aba
GO_BP_m1	GO:004578	positive reg	56/2606	379/23843	0.012046	0.33065	0.314413	Adam8/Ad
GO_BP_m1	GO:000706	sister chron	12/2606	54/23843	0.012289	0.335242	0.318779	Cdc20/Esco
GO_BP_m1	GO:003646	synaptic ve	12/2606	54/23843	0.012289	0.335242	0.318779	Ap1s2/Can
GO_BP_m1	GO:000640	tRNA modi	14/2606	67/23843	0.012413	0.336518	0.319992	2210016F1
GO_BP_m1	GO:009917	regulation	14/2606	67/23843	0.012413	0.336518	0.319992	Arhgap44/
GO_BP_m1	GO:001076	regulation	48/2606	317/23843	0.012458	0.336719	0.320183	Aatk/Ache/
GO_BP_m1	GO:000716	negative re	41/2606	263/23843	0.012498	0.336753	0.320216	Abat/Abl2/
GO_BP_m1	GO:003444	lipid oxidat	19/2606	101/23843	0.012632	0.339324	0.322661	Abcd3/Aca
GO_BP_m1	GO:006201	regulation	59/2606	404/23843	0.012838	0.343459	0.326592	Adcyap1r1/
GO_BP_m1	GO:190002	regulation	11/2606	48/23843	0.012864	0.343459	0.326592	Bcar1/Calr/
GO_BP_m1	GO:003240	regulation	40/2606	256/23843	0.013009	0.344347	0.327437	Abcb1a/Ac
GO_BP_m1	GO:006102	membrane	35/2606	218/23843	0.013012	0.344347	0.327437	Adam8/An
GO_BP_m1	GO:004678	microtubul	15/2606	74/23843	0.013015	0.344347	0.327437	Ankrd53/C
GO_BP_m1	GO:005144	negative re	6/2606	19/23843	0.013082	0.344565	0.327644	Dmrt1/Fbxo
GO_BP_m1	GO:003592	cellular resp	10/2606	42/23843	0.01326	0.344565	0.327644	Adgra2/Cd

GO_BP_m1	GO:190384	negative re	13/2606	61/23843	0.01332	0.344565	0.327644	Cav1/Danc
GO_BP_m1	GO:00001	inactivatio	5/2606	14/23843	0.013337	0.344565	0.327644	Cav1/Dusp
GO_BP_m1	GO:00327	negative re	5/2606	14/23843	0.013337	0.344565	0.327644	Atp2b4/Ca
GO_BP_m1	GO:00434	regulation	5/2606	14/23843	0.013337	0.344565	0.327644	Bpgm/Hsd
GO_BP_m1	GO:00722	metanephr	5/2606	14/23843	0.013337	0.344565	0.327644	Lamb2/Lgr
GO_BP_m1	GO:19047	positive re	5/2606	14/23843	0.013337	0.344565	0.327644	Dock4/Doc
GO_BP_m1	GO:014001	meiotic nu	30/2606	181/23843	0.013408	0.345387	0.328426	Btbd18/Ca
GO_BP_m1	GO:00345	cellular res	39/2606	249/23843	0.013539	0.3469	0.329865	Adnp2/Arl
GO_BP_m1	GO:00104	proteasom	63/2606	437/23843	0.013576	0.3469	0.329865	1500015O
GO_BP_m1	GO:00347	regulation	64/2606	445/23843	0.013585	0.3469	0.329865	Abcb1a/Ac
GO_BP_m1	GO:00071	meiosis I	21/2606	116/23843	0.013881	0.353425	0.336069	Btbd18/Te
GO_BP_m1	GO:000177	leukocyte	20/2606	109/23843	0.013964	0.353486	0.336127	Dock10/Gp
GO_BP_m1	GO:20001	negative re	20/2606	109/23843	0.013964	0.353486	0.336127	Adamts1/A
GO_BP_m1	GO:00487	cardiac mu	38/2606	242/23843	0.014087	0.353899	0.33652	Adamts9/A
GO_BP_m1	GO:00676	vitamin me	14/2606	68/23843	0.014101	0.353899	0.33652	Acpp/Clyb
GO_BP_m1	GO:003241	negative re	14/2606	68/23843	0.014101	0.353899	0.33652	Adra1d/Ca
GO_BP_m1	GO:003447	ncRNA pro	50/2606	335/23843	0.014162	0.354222	0.336827	2210016F1
GO_BP_m1	GO:000801	regulation	28/2606	167/23843	0.014235	0.354222	0.336827	Adm/Ador
GO_BP_m1	GO:00971	ammonium	28/2606	167/23843	0.014235	0.354222	0.336827	Abat/Abhd
GO_BP_m1	GO:004341	macromole	42/2606	273/23843	0.014343	0.355902	0.338424	Virma/Ash
GO_BP_m1	GO:00068	neurotrans	39/2606	250/23843	0.014398	0.355902	0.338424	Abat/Arl6i
GO_BP_m1	GO:00439	negative re	30/2606	182/23843	0.014424	0.355902	0.338424	Anxa2/Arh
GO_BP_m1	GO:00458	positive re	47/2606	312/23843	0.014511	0.357049	0.339514	Adam8/Aif
GO_BP_m1	GO:007134	cellular res	15/2606	75/23843	0.014671	0.35996	0.342283	Ankrd1/Ca
GO_BP_m1	GO:00228	regulation	38/2606	243/23843	0.014989	0.363461	0.345612	Abcb1a/Ac
GO_BP_m1	GO:009017	organelle r	26/2606	153/23843	0.015036	0.363461	0.345612	Ankfy1/Anx
GO_BP_m1	GO:00070	mitotic sist	7/2606	25/23843	0.015061	0.363461	0.345612	Cdc20/H2a
GO_BP_m1	GO:00072	spermatid	7/2606	25/23843	0.015061	0.363461	0.345612	Dmrtc2/Ift
GO_BP_m1	GO:00328	negative re	7/2606	25/23843	0.015061	0.363461	0.345612	Abat/Ador
GO_BP_m1	GO:005077	RNA destal	7/2606	25/23843	0.015061	0.363461	0.345612	Cnot6l/Cpe
GO_BP_m1	GO:00311	cytoplasmi	13/2606	62/23843	0.015213	0.364422	0.346526	Cav3/Cib1/
GO_BP_m1	GO:00160	carbohydra	21/2606	117/23843	0.015226	0.364422	0.346526	Abhd10/Pg
GO_BP_m1	GO:00432	positive re	21/2606	117/23843	0.015226	0.364422	0.346526	Aifm1/Alox
GO_BP_m1	GO:00022	response t	56/2606	384/23843	0.015413	0.367891	0.349824	5730559C1
GO_BP_m1	GO:00712	cellular res	40/2606	259/23843	0.015589	0.371092	0.352868	Ankrd1/Bc
GO_BP_m1	GO:00485	lymph nod	8/2606	31/23843	0.015893	0.375883	0.357424	Cd248/Cxc
GO_BP_m1	GO:00509	regulation	8/2606	31/23843	0.015893	0.375883	0.357424	Atp2b4/Ca
GO_BP_m1	GO:00303	negative re	38/2606	244/23843	0.015937	0.375883	0.357424	Adamts9/A
GO_BP_m1	GO:00060	gluconeog	14/2606	69/23843	0.015961	0.375883	0.357424	Atf3/Bpgm
GO_BP_m1	GO:000081	sister chro	29/2606	176/23843	0.016019	0.376232	0.357755	Ankrd53/C
GO_BP_m1	GO:00072	spermatog	69/2606	489/23843	0.016083	0.37672	0.35822	1110017D1
GO_BP_m1	GO:00062	DNA replic	40/2606	260/23843	0.016536	0.385154	0.36624	Atr/Baz1a/
GO_BP_m1	GO:003241	regulation	37/2606	237/23843	0.016598	0.385154	0.36624	Abcb1a/Ac
GO_BP_m1	GO:00514	stress-acti	37/2606	237/23843	0.016598	0.385154	0.36624	5730559C1
GO_BP_m1	GO:00464	membrane	21/2606	118/23843	0.016671	0.385154	0.36624	Abo/Acer3
GO_BP_m1	GO:00619	meiosis I c	21/2606	118/23843	0.016671	0.385154	0.36624	Btbd18/Te
GO_BP_m1	GO:00075	cell aging	25/2606	147/23843	0.016706	0.385154	0.36624	1500015O
GO_BP_m1	GO:00468	positive re	16/2606	83/23843	0.01682	0.385675	0.366735	Avpr1a/Cc

GO_BP_m1	GO:00230	signal relea	66/2606	466/23843	0.016915	0.385675	0.366735	Abat/Adm
GO_BP_m1	GO:200011	regulation	6/2606	20/23843	0.016995	0.385675	0.366735	Bcas3/Cfl1/
GO_BP_m1	GO:001571	organic ani	58/2606	402/23843	0.017014	0.385675	0.366735	Abat/Abca
GO_BP_m1	GO:00719	regulation	60/2606	418/23843	0.017034	0.385675	0.366735	5730559C1
GO_BP_m1	GO:001584	organic aci	43/2606	284/23843	0.017262	0.385675	0.366735	Abat/Abcc
GO_BP_m1	GO:00063	tRNA splici	4/2606	10/23843	0.017387	0.385675	0.366735	Rtraf/Tsen
GO_BP_m1	GO:00331	regulation	4/2606	10/23843	0.017387	0.385675	0.366735	Cox11/Fox
GO_BP_m1	GO:003524	peptidyl-a	4/2606	10/23843	0.017387	0.385675	0.366735	Ndufaf7/Pr
GO_BP_m1	GO:003524	peptidyl-a	4/2606	10/23843	0.017387	0.385675	0.366735	Ndufaf7/Pr
GO_BP_m1	GO:00395	negative re	4/2606	10/23843	0.017387	0.385675	0.366735	Dhx58/Npl
GO_BP_m1	GO:00460	adenosine	4/2606	10/23843	0.017387	0.385675	0.366735	Acpp/Adk/
GO_BP_m1	GO:00515	positive re	4/2606	10/23843	0.017387	0.385675	0.366735	Bcap31/Bn
GO_BP_m1	GO:00620	secondary	4/2606	10/23843	0.017387	0.385675	0.366735	Col11a2/Fc
GO_BP_m1	GO:190251	regulation	4/2606	10/23843	0.017387	0.385675	0.366735	Aifm1/Dffa
GO_BP_m1	GO:000961	response t	40/2606	261/23843	0.017528	0.386261	0.367293	Abcf3/Apo
GO_BP_m1	GO:00062	DNA-depe	23/2606	133/23843	0.017528	0.386261	0.367293	Baz1a/Blm
GO_BP_m1	GO:003134	negative re	32/2606	200/23843	0.01776	0.386261	0.367293	Adora1/Ac
GO_BP_m1	GO:00605	skeletal mu	32/2606	200/23843	0.01776	0.386261	0.367293	Acta1/Ank
GO_BP_m1	GO:005067	epithelial c	58/2606	403/23843	0.017818	0.386261	0.367293	Slurp2/A4
GO_BP_m1	GO:00072	sperm axo	5/2606	15/23843	0.018236	0.386261	0.367293	Bbs2/Dnah
GO_BP_m1	GO:00429	lipoprotein	5/2606	15/23843	0.018236	0.386261	0.367293	Apobec1/C
GO_BP_m1	GO:004482	modulation	5/2606	15/23843	0.018236	0.386261	0.367293	Fmr1/Nuck
GO_BP_m1	GO:004487	lipoprotein	5/2606	15/23843	0.018236	0.386261	0.367293	Apobec1/C
GO_BP_m1	GO:190011	positive re	5/2606	15/23843	0.018236	0.386261	0.367293	Bok/Endog
GO_BP_m1	GO:190162	regulation	5/2606	15/23843	0.018236	0.386261	0.367293	Cdh2/Lrp4
GO_BP_m1	GO:005164	vesicle loc	33/2606	208/23843	0.01826	0.386261	0.367293	Bloc1s5/Cc
GO_BP_m1	GO:190382	positive re	50/2606	340/23843	0.018299	0.386261	0.367293	Abca12/Ar
GO_BP_m1	GO:00427	eating beh	10/2606	44/23843	0.0183	0.386261	0.367293	Aoc3/Cd36
GO_BP_m1	GO:00702	regulation	10/2606	44/23843	0.0183	0.386261	0.367293	Adam8/Bln
GO_BP_m1	GO:00902	regulation	10/2606	44/23843	0.0183	0.386261	0.367293	Apobec1/C
GO_BP_m1	GO:00064	mRNA cat	31/2606	193/23843	0.018434	0.386261	0.367293	Apobec1/E
GO_BP_m1	GO:00158	drug trans	31/2606	193/23843	0.018434	0.386261	0.367293	Abat/Abcb
GO_BP_m1	GO:003241	negative re	15/2606	77/23843	0.018465	0.386261	0.367293	Adra1d/Ca
GO_BP_m1	GO:19016	alpha-ami	15/2606	77/23843	0.018465	0.386261	0.367293	Aldh4a1/A
GO_BP_m1	GO:00028	regulation	24/2606	141/23843	0.018568	0.386261	0.367293	Arg1/Cacti
GO_BP_m1	GO:20012	regulation	57/2606	396/23843	0.018647	0.386261	0.367293	Atf3/Bcap3
GO_BP_m1	GO:00065	catecholan	12/2606	57/23843	0.018676	0.386261	0.367293	Abat/Gch1
GO_BP_m1	GO:000971	catechol-c	12/2606	57/23843	0.018676	0.386261	0.367293	Abat/Gch1
GO_BP_m1	GO:00480	platelet-de	12/2606	57/23843	0.018676	0.386261	0.367293	Abl2/Bcar1
GO_BP_m1	GO:004582	negative re	7/2606	26/23843	0.018712	0.386261	0.367293	Adora1/Ad
GO_BP_m1	GO:00513	negative re	7/2606	26/23843	0.018712	0.386261	0.367293	Adra1d/Ak
GO_BP_m1	GO:00516	defense re	34/2606	216/23843	0.018722	0.386261	0.367293	Abcf3/Apo
GO_BP_m1	GO:00508	negative re	16/2606	84/23843	0.018733	0.386261	0.367293	Adora1/Ad
GO_BP_m1	GO:190101	regulation	16/2606	84/23843	0.018733	0.386261	0.367293	Adra1d/Ak
GO_BP_m1	GO:00072	germ cell c	41/2606	270/23843	0.018824	0.386337	0.367365	Acrbp/Amh
GO_BP_m1	GO:00310	stress-acti	41/2606	270/23843	0.018824	0.386337	0.367365	5730559C1
GO_BP_m1	GO:00224	positive re	35/2606	224/23843	0.019147	0.392052	0.372799	Adam8/Ad
GO_BP_m1	GO:190161	organic hy	62/2606	437/23843	0.019425	0.392813	0.373523	Abat/Acer

GO_BP_m1	GO:003287	regulation	33/2606	209/23843	0.019478	0.392813	0.373523	5730559C1
GO_BP_m1	GO:000751	muscle org	58/2606	405/23843	0.01952	0.392813	0.373523	Acta1/Akap
GO_BP_m1	GO:000693	regulation	25/2606	149/23843	0.019536	0.392813	0.373523	Abat/Adora
GO_BP_m1	GO:000717	transformin	25/2606	149/23843	0.019536	0.392813	0.373523	Cav1/Cav3
GO_BP_m1	GO:004692	regulation	13/2606	64/23843	0.019608	0.392813	0.373523	Camk2a/Fr
GO_BP_m1	GO:000609	generation	50/2606	342/23843	0.020207	0.392813	0.373523	Adh1/Adh5
GO_BP_m1	GO:000629	nucleotide-	3/2606	6/23843	0.020221	0.392813	0.373523	Lig3/Pold3
GO_BP_m1	GO:000719	adenylate c	3/2606	6/23843	0.020221	0.392813	0.373523	Chrm1/Chr
GO_BP_m1	GO:000719	adenylate c	3/2606	6/23843	0.020221	0.392813	0.373523	Htr1a/Htr5
GO_BP_m1	GO:003323	negative re	3/2606	6/23843	0.020221	0.392813	0.373523	Atp2b4/Itg
GO_BP_m1	GO:003953	regulation	3/2606	6/23843	0.020221	0.392813	0.373523	Ddx60/Dhx
GO_BP_m1	GO:004521	neurotrans	3/2606	6/23843	0.020221	0.392813	0.373523	Ache/Fnta/
GO_BP_m1	GO:009016	Golgi disas	3/2606	6/23843	0.020221	0.392813	0.373523	Cdk1/Gbf1
GO_BP_m1	GO:009703	protein line	3/2606	6/23843	0.020221	0.392813	0.373523	Park2/Rbck
GO_BP_m1	GO:190162	negative re	3/2606	6/23843	0.020221	0.392813	0.373523	Prkacb/Tra
GO_BP_m1	GO:190162	positive reg	3/2606	6/23843	0.020221	0.392813	0.373523	Lrp4/Mesd
GO_BP_m1	GO:190172	negative re	3/2606	6/23843	0.020221	0.392813	0.373523	Flcn/Ifng/W
GO_BP_m1	GO:190391	positive reg	3/2606	6/23843	0.020221	0.392813	0.373523	Lrp4/Mesd
GO_BP_m1	GO:190479	positive reg	3/2606	6/23843	0.020221	0.392813	0.373523	Foxc1/Ifng/
GO_BP_m1	GO:200063	positive reg	3/2606	6/23843	0.020221	0.392813	0.373523	Nfkb1/Pnp
GO_BP_m1	GO:003289	regulation	14/2606	71/23843	0.020238	0.392813	0.373523	Abat/Adora
GO_BP_m1	GO:004273	embryonic	14/2606	71/23843	0.020238	0.392813	0.373523	B9d1/Frem
GO_BP_m1	GO:005092	regulation	32/2606	202/23843	0.020258	0.392813	0.373523	Adgra2/Ca
GO_BP_m1	GO:001714	negative re	35/2606	225/23843	0.020364	0.394	0.374651	Btg2/Calr/C
GO_BP_m1	GO:000694	regulation	15/2606	78/23843	0.020622	0.39781	0.378274	Adora1/Ak
GO_BP_m1	GO:007030	regulation	33/2606	210/23843	0.020759	0.39781	0.378274	5730559C1
GO_BP_m1	GO:003210	negative re	46/2606	311/23843	0.020824	0.39781	0.378274	Abat/Adora
GO_BP_m1	GO:005181	modificatio	17/2606	92/23843	0.020833	0.39781	0.378274	Anxa2/Arg
GO_BP_m1	GO:006002	roof of mo	17/2606	92/23843	0.020833	0.39781	0.378274	Asph/Col1
GO_BP_m1	GO:006035	response to	17/2606	92/23843	0.020833	0.39781	0.378274	Abat/Adra1
GO_BP_m1	GO:190160	alpha-amin	31/2606	195/23843	0.021061	0.40131	0.381602	Dglucy/Ads
GO_BP_m1	GO:003424	negative re	37/2606	241/23843	0.021107	0.401316	0.381608	Btg2/C330
GO_BP_m1	GO:003288	regulation	34/2606	218/23843	0.02122	0.402576	0.382806	Ankrd53/B
GO_BP_m1	GO:004887	multicellula	51/2606	351/23843	0.021279	0.402825	0.383043	5730559C1
GO_BP_m1	GO:007121	cellular res	43/2606	288/23843	0.021456	0.405319	0.385414	Ankrd1/Atg
GO_BP_m1	GO:001086	regulation	6/2606	21/23843	0.021644	0.406234	0.386284	Dgat1/Gpa
GO_BP_m1	GO:003116	rRNA meth	6/2606	21/23843	0.021644	0.406234	0.386284	Ftsj3/Gm18
GO_BP_m1	GO:004358	tongue dev	6/2606	21/23843	0.021644	0.406234	0.386284	Hdac1/Hda
GO_BP_m1	GO:001067	regulation	24/2606	143/23843	0.021731	0.407001	0.387014	Adcyap1r1
GO_BP_m1	GO:200011	regulation	36/2606	234/23843	0.022025	0.411637	0.391422	Aifm1/Alox
GO_BP_m1	GO:005511	regulation	13/2606	65/23843	0.022133	0.412772	0.392501	Adora1/Ak
GO_BP_m1	GO:006300	double-stra	9/2606	39/23843	0.022344	0.413973	0.393644	Dclre1a/De
GO_BP_m1	GO:003086	cortical act	9/2606	39/23843	0.022344	0.413973	0.393644	Calr/Cdk5/
GO_BP_m1	GO:001931	hexose bio	14/2606	72/23843	0.022675	0.413973	0.393644	Atf3/Bpgm
GO_BP_m1	GO:003808	vascular en	7/2606	27/23843	0.02294	0.413973	0.393644	Adgra2/Cd
GO_BP_m1	GO:004303	positive reg	7/2606	27/23843	0.02294	0.413973	0.393644	Il10/Il1rl1/I
GO_BP_m1	GO:009020	positive reg	7/2606	27/23843	0.02294	0.413973	0.393644	Cd36/Dgat
GO_BP_m1	GO:190011	regulation	7/2606	27/23843	0.02294	0.413973	0.393644	Aifm1/Bok/

GO_BP_m1	GO:000719	adenylate c	15/2606	79/23843	0.022964	0.413973	0.393644	Adora1/Ad
GO_BP_m1	GO:003051	negative re	11/2606	52/23843	0.022969	0.413973	0.393644	Cav1/Danc
GO_BP_m1	GO:003086	cortical cyt	11/2606	52/23843	0.022969	0.413973	0.393644	Calr/Cdk5/
GO_BP_m1	GO:005507	sodium ion	11/2606	52/23843	0.022969	0.413973	0.393644	Adora1/Atp
GO_BP_m1	GO:200014	negative re	39/2606	258/23843	0.022976	0.413973	0.393644	Adamts9/A
GO_BP_m1	GO:000275	cytoplasmi	8/2606	33/23843	0.022999	0.413973	0.393644	5730559C1
GO_BP_m1	GO:003111	positive reg	8/2606	33/23843	0.022999	0.413973	0.393644	Ankrd53/C
GO_BP_m1	GO:004801	ephrin rece	8/2606	33/23843	0.022999	0.413973	0.393644	Chn1/Epha
GO_BP_m1	GO:190002	positive reg	8/2606	33/23843	0.022999	0.413973	0.393644	Calr/Cib1/E
GO_BP_m1	GO:190074	regulation	8/2606	33/23843	0.022999	0.413973	0.393644	Cav3/Ezr/H
GO_BP_m1	GO:003591	skeletal mu	16/2606	86/23843	0.023052	0.414087	0.393752	Ankrd1/Arr
GO_BP_m1	GO:004677	protein aut	37/2606	243/23843	0.023701	0.424879	0.404014	Aatk/Abl2/
GO_BP_m1	GO:004239	regulation	61/2606	434/23843	0.024127	0.429232	0.408153	Abat/Abcb
GO_BP_m1	GO:003603	osteoclast	5/2606	16/23843	0.024188	0.429232	0.408153	Anxa2/Cldn
GO_BP_m1	GO:004501	negative re	5/2606	16/23843	0.024188	0.429232	0.408153	Atp2b4/Ca
GO_BP_m1	GO:007201	glomerular	5/2606	16/23843	0.024188	0.429232	0.408153	Basp1/Foxc
GO_BP_m1	GO:190440	negative re	5/2606	16/23843	0.024188	0.429232	0.408153	Atp2b4/Ca
GO_BP_m1	GO:000756	aging	35/2606	228/23843	0.024384	0.430971	0.409806	1500015O1
GO_BP_m1	GO:004544	fat cell diffe	35/2606	228/23843	0.024384	0.430971	0.409806	Adig/Ap1s
GO_BP_m1	GO:000610	regulation	27/2606	167/23843	0.024493	0.431673	0.410474	Adcyap1r1
GO_BP_m1	GO:005109	regulation	53/2606	370/23843	0.024536	0.431673	0.410474	Abl2/Anxa2
GO_BP_m1	GO:000698	response to	19/2606	108/23843	0.024573	0.431673	0.410474	Atf3/Bok/C
GO_BP_m1	GO:004347	regulation	10/2606	46/23843	0.024621	0.431673	0.410474	Bpgm/Esrrb
GO_BP_m1	GO:007250	cellular div	64/2606	459/23843	0.024828	0.432216	0.41099	Abl2/Adcya
GO_BP_m1	GO:000865	cellular am	13/2606	66/23843	0.024892	0.432216	0.41099	Abat/Apip/
GO_BP_m1	GO:004340	negative re	13/2606	66/23843	0.024892	0.432216	0.41099	Cav1/Cav3/
GO_BP_m1	GO:004694	carboxylic a	42/2606	283/23843	0.02494	0.432216	0.41099	Abat/Abcc
GO_BP_m1	GO:000721	G-protein c	4/2606	11/23843	0.024996	0.432216	0.41099	Chrm1/Chr
GO_BP_m1	GO:190291	positive reg	4/2606	11/23843	0.024996	0.432216	0.41099	Nmi/Park2/
GO_BP_m1	GO:190390	regulation	4/2606	11/23843	0.024996	0.432216	0.41099	Gsn/Lrp4/N
GO_BP_m1	GO:190406	regulation	46/2606	315/23843	0.025468	0.43921	0.417641	Adra1d/Ak
GO_BP_m1	GO:001491	regulation	15/2606	80/23843	0.025501	0.43921	0.417641	Dock4/Doc
GO_BP_m1	GO:007121	cellular res	40/2606	268/23843	0.025888	0.445016	0.423162	Ankrd1/Bcr
GO_BP_m1	GO:000268	positive reg	23/2606	138/23843	0.026118	0.447571	0.425591	Adam8/Ao
GO_BP_m1	GO:000910	coenzyme	27/2606	168/23843	0.026244	0.447571	0.425591	Bpgm/Coq
GO_BP_m1	GO:000673	oxidoreduc	25/2606	153/23843	0.026314	0.447571	0.425591	Bpgm/Coq
GO_BP_m1	GO:000693	smooth mu	19/2606	109/23843	0.026812	0.447571	0.425591	Abat/Acta2
GO_BP_m1	GO:007162	granulocyte	19/2606	109/23843	0.026812	0.447571	0.425591	Ccl20/Ccl2
GO_BP_m1	GO:000670	steroid cata	6/2606	22/23843	0.027079	0.447571	0.425591	Cyp46a1/H
GO_BP_m1	GO:000706	regulation	6/2606	22/23843	0.027079	0.447571	0.425591	Fen1/H2afy
GO_BP_m1	GO:001088	positive reg	6/2606	22/23843	0.027079	0.447571	0.425591	Cd36/Fitm
GO_BP_m1	GO:007024	thymocyte	6/2606	22/23843	0.027079	0.447571	0.425591	Adam8/Bln
GO_BP_m1	GO:000679	sulfur comp	39/2606	261/23843	0.027081	0.447571	0.425591	Acot1/Aco
GO_BP_m1	GO:003292	circadian re	12/2606	60/23843	0.027266	0.447571	0.425591	Arntl/Cartp
GO_BP_m1	GO:005119	regulation	12/2606	60/23843	0.027266	0.447571	0.425591	Bpgm/Clyb
GO_BP_m1	GO:001404	dopamine	8/2606	34/23843	0.027279	0.447571	0.425591	Abat/Adra1
GO_BP_m1	GO:001405	regulation	8/2606	34/23843	0.027279	0.447571	0.425591	Abat/Adra1
GO_BP_m1	GO:004409	membrane	8/2606	34/23843	0.027279	0.447571	0.425591	Anxa2/Cav

GO_BP_m1	GO:004500	DNA-depe	8/2606	34/23843	0.027279	0.447571	0.425591	Blm/Fbxo1
GO_BP_m1	GO:000182	kidney dev	40/2606	269/23843	0.027303	0.447571	0.425591	Adamts1/A
GO_BP_m1	GO:007058	calcium io	40/2606	269/23843	0.027303	0.447571	0.425591	Adra1d/Ak
GO_BP_m1	GO:200102	regulation	18/2606	102/23843	0.027337	0.447571	0.425591	Abat/Abcb
GO_BP_m1	GO:003164	regulation	17/2606	95/23843	0.02777	0.447571	0.425591	Acpp/Ador
GO_BP_m1	GO:000223	positive re	7/2606	28/23843	0.027782	0.447571	0.425591	Il12b/Mb2
GO_BP_m1	GO:005193	regulation	10/2606	47/23843	0.028309	0.447571	0.425591	Acpp/Ador
GO_BP_m1	GO:005193	regulation	10/2606	47/23843	0.028309	0.447571	0.425591	Acpp/Ador
GO_BP_m1	GO:004671	acid secret	20/2606	117/23843	0.028485	0.447571	0.425591	Abat/Abcc
GO_BP_m1	GO:200123	regulation	26/2606	162/23843	0.029191	0.447571	0.425591	Atf3/Casp
GO_BP_m1	GO:000007	mitotic sist	24/2606	147/23843	0.029295	0.447571	0.425591	Ankrd53/C
GO_BP_m1	GO:000720	positive re	44/2606	302/23843	0.029329	0.447571	0.425591	Abl2/Adcy
GO_BP_m1	GO:005080	positive re	47/2606	326/23843	0.029494	0.447571	0.425591	Abat/Ador
GO_BP_m1	GO:004816	regulation	49/2606	342/23843	0.029508	0.447571	0.425591	Adora1/Ca
GO_BP_m1	GO:007156	cellular res	29/2606	185/23843	0.029552	0.447571	0.425591	Ankrd1/Ca
GO_BP_m1	GO:001895	phenol-co	18/2606	103/23843	0.029857	0.447571	0.425591	Abat/Dct/
GO_BP_m1	GO:000758	digestion	21/2606	125/23843	0.030006	0.447571	0.425591	5730559C1
GO_BP_m1	GO:000614	regulation	27/2606	170/23843	0.030032	0.447571	0.425591	Adm/Adra
GO_BP_m1	GO:000640	RNA catab	34/2606	224/23843	0.030318	0.447571	0.425591	Apobec1/
GO_BP_m1	GO:005069	regulation	9/2606	41/23843	0.030324	0.447571	0.425591	Ifng/Il12b/
GO_BP_m1	GO:006101	positive re	9/2606	41/23843	0.030324	0.447571	0.425591	Btg2/Cnot
GO_BP_m1	GO:004501	glycerolipi	23/2606	140/23843	0.030338	0.447571	0.425591	Tmem269/
GO_BP_m1	GO:000830	associative	17/2606	96/23843	0.030427	0.447571	0.425591	Abl2/Ada
GO_BP_m1	GO:014005	mitochond	17/2606	96/23843	0.030427	0.447571	0.425591	Gfm1/Gm1
GO_BP_m1	GO:005127	negative r	42/2606	287/23843	0.030609	0.447571	0.425591	Adamts9/A
GO_BP_m1	GO:004316	proteasom	53/2606	375/23843	0.030658	0.447571	0.425591	1500015O
GO_BP_m1	GO:005043	catechola	12/2606	61/23843	0.030681	0.447571	0.425591	Abat/Adra
GO_BP_m1	GO:200124	positive re	12/2606	61/23843	0.030681	0.447571	0.425591	Bcap31/Bc
GO_BP_m1	GO:000607	glycerol m	5/2606	17/23843	0.031258	0.447571	0.425591	Angptl3/C
GO_BP_m1	GO:001086	positive re	5/2606	17/23843	0.031258	0.447571	0.425591	Dgat1/Gpa
GO_BP_m1	GO:001405	gamma-a	5/2606	17/23843	0.031258	0.447571	0.425591	Abat/Hrh3
GO_BP_m1	GO:003953	regulation	5/2606	17/23843	0.031258	0.447571	0.425591	Ddx60/Dh
GO_BP_m1	GO:004274	hydrogen	5/2606	17/23843	0.031258	0.447571	0.425591	Gpx1/Prdx
GO_BP_m1	GO:004819	vesicle tar	5/2606	17/23843	0.031258	0.447571	0.425591	Gbf1/Pdcd
GO_BP_m1	GO:005100	positive re	5/2606	17/23843	0.031258	0.447571	0.425591	Gch1/Nod
GO_BP_m1	GO:007024	regulation	5/2606	17/23843	0.031258	0.447571	0.425591	Adam8/Bl
GO_BP_m1	GO:000672	isoprenoid	14/2606	75/23843	0.031301	0.447571	0.425591	Adh1/Adh
GO_BP_m1	GO:009028	negative r	22/2606	133/23843	0.031386	0.447571	0.425591	Adgra2/Ca
GO_BP_m1	GO:000941	response t	33/2606	217/23843	0.031693	0.447571	0.425591	Abat/Acsl1
GO_BP_m1	GO:005105	negative r	68/2606	498/23843	0.031793	0.447571	0.425591	Abat/Ador
GO_BP_m1	GO:001700	antibiotic c	8/2606	35/23843	0.032081	0.447571	0.425591	Adh1/Adh
GO_BP_m1	GO:004662	negative r	8/2606	35/23843	0.032081	0.447571	0.425591	Cav3/Hdac
GO_BP_m1	GO:009031	positive re	30/2606	194/23843	0.032093	0.447571	0.425591	Arih2/Asp
GO_BP_m1	GO:007250	divalent in	66/2606	482/23843	0.032277	0.447571	0.425591	Abl2/Adcy
GO_BP_m1	GO:000687	cellular cal	60/2606	433/23843	0.03231	0.447571	0.425591	Abl2/Adcy
GO_BP_m1	GO:004651	ceramide	10/2606	48/23843	0.032374	0.447571	0.425591	B4galt3/Ce
GO_BP_m1	GO:003102	microtubul	21/2606	126/23843	0.032428	0.447571	0.425591	Bcas3/Deu
GO_BP_m1	GO:000728	spermatid	25/2606	156/23843	0.032485	0.447571	0.425591	Acrbp/Bbs

GO_BP_m1	GO:000236	CD4-positi	3/2606	7/23843	0.032541	0.447571	0.425591	Ifng/Il2rg/
GO_BP_m1	GO:000337	sphingosin	3/2606	7/23843	0.032541	0.447571	0.425591	Ezr/Spns2/
GO_BP_m1	GO:001608	synaptic ve	3/2606	7/23843	0.032541	0.447571	0.425591	Stx1b/Stx4
GO_BP_m1	GO:003408	establishm	3/2606	7/23843	0.032541	0.447571	0.425591	Hdac8/Naa
GO_BP_m1	GO:003558	sequesterin	3/2606	7/23843	0.032541	0.447571	0.425591	Dand5/Fbn
GO_BP_m1	GO:003562	ceramide t	3/2606	7/23843	0.032541	0.447571	0.425591	Abca12/Ab
GO_BP_m1	GO:003646	TRAIL-acti	3/2606	7/23843	0.032541	0.447571	0.425591	Atf3/Casp8
GO_BP_m1	GO:003953	MDA-5 sig	3/2606	7/23843	0.032541	0.447571	0.425591	Ddx60/Dhx
GO_BP_m1	GO:003953	negative re	3/2606	7/23843	0.032541	0.447571	0.425591	Dhx58/Npl
GO_BP_m1	GO:004482	negative re	3/2606	7/23843	0.032541	0.447571	0.425591	Park2/Vapb
GO_BP_m1	GO:005094	positive reg	3/2606	7/23843	0.032541	0.447571	0.425591	Adamts9/B
GO_BP_m1	GO:005102	rRNA trans	3/2606	7/23843	0.032541	0.447571	0.425591	Mrpl18/Pnp
GO_BP_m1	GO:005104	negative re	3/2606	7/23843	0.032541	0.447571	0.425591	Il10/Timp1
GO_BP_m1	GO:005125	mitotic spin	3/2606	7/23843	0.032541	0.447571	0.425591	Kif23/Kif4/
GO_BP_m1	GO:005135	positive reg	3/2606	7/23843	0.032541	0.447571	0.425591	Gclm/Ripk3
GO_BP_m1	GO:007231	clathrin coa	3/2606	7/23843	0.032541	0.447571	0.425591	Dnajc6/Sh3
GO_BP_m1	GO:190389	regulation	3/2606	7/23843	0.032541	0.447571	0.425591	Bok/Nck2/
GO_BP_m1	GO:190479	regulation	3/2606	7/23843	0.032541	0.447571	0.425591	Foxc1/Ifng/
GO_BP_m1	GO:190505	positive reg	3/2606	7/23843	0.032541	0.447571	0.425591	Antxr1/Ddr
GO_BP_m1	GO:199086	response to	3/2606	7/23843	0.032541	0.447571	0.425591	Dock8/Fox
GO_BP_m1	GO:199086	cellular res	3/2606	7/23843	0.032541	0.447571	0.425591	Dock8/Fox
GO_BP_m1	GO:200076	negative re	3/2606	7/23843	0.032541	0.447571	0.425591	Cpeb3/Cpe
GO_BP_m1	GO:004213	neurotrans	23/2606	141/23843	0.032632	0.447571	0.425591	Abat/Ache/
GO_BP_m1	GO:009900	vesicle-me	23/2606	141/23843	0.032632	0.447571	0.425591	Bloc1s5/Ca
GO_BP_m1	GO:004828	organelle f	64/2606	466/23843	0.032746	0.447571	0.425591	Ankrd53/B
GO_BP_m1	GO:000647	protein ace	28/2606	179/23843	0.032827	0.447571	0.425591	Arntl/Brpf3
GO_BP_m1	GO:009752	myeloid leu	28/2606	179/23843	0.032827	0.447571	0.425591	Adam8/Ccl
GO_BP_m1	GO:000030	retrograde	2/2606	3/23843	0.033217	0.447571	0.425591	Cog4/Dnaj
GO_BP_m1	GO:000037	tRNA-type	2/2606	3/23843	0.033217	0.447571	0.425591	Tsen2/Tsen
GO_BP_m1	GO:000212	maternal a	2/2606	3/23843	0.033217	0.447571	0.425591	Avpr1a/Crh
GO_BP_m1	GO:000620	pyrimidine	2/2606	3/23843	0.033217	0.447571	0.425591	Dpyd/Dpys
GO_BP_m1	GO:000621	thymine ca	2/2606	3/23843	0.033217	0.447571	0.425591	Dpyd/Dpys
GO_BP_m1	GO:000621	5-methylcy	2/2606	3/23843	0.033217	0.447571	0.425591	Tet2/Tet3
GO_BP_m1	GO:000653	aspartate c	2/2606	3/23843	0.033217	0.447571	0.425591	Ddo/Got1
GO_BP_m1	GO:001059	negative re	2/2606	3/23843	0.033217	0.447571	0.425591	Cfl1/Plxnb3
GO_BP_m1	GO:001985	5-methylcy	2/2606	3/23843	0.033217	0.447571	0.425591	Tet2/Tet3
GO_BP_m1	GO:001985	thymine m	2/2606	3/23843	0.033217	0.447571	0.425591	Dpyd/Dpys
GO_BP_m1	GO:001986	uracil meta	2/2606	3/23843	0.033217	0.447571	0.425591	Dpyd/Dpys
GO_BP_m1	GO:003202	response to	2/2606	3/23843	0.033217	0.447571	0.425591	Bnip3/Tiga
GO_BP_m1	GO:003283	positive reg	2/2606	3/23843	0.033217	0.447571	0.425591	Ifng/Il2rg
GO_BP_m1	GO:003409	negative re	2/2606	3/23843	0.033217	0.447571	0.425591	Naa10/Tnk
GO_BP_m1	GO:003415	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Ptpn22/Tre
GO_BP_m1	GO:003415	positive reg	2/2606	3/23843	0.033217	0.447571	0.425591	Ptpn22/Tre
GO_BP_m1	GO:003418	negative re	2/2606	3/23843	0.033217	0.447571	0.425591	Naa10/Tnk
GO_BP_m1	GO:003602	limb joint r	2/2606	3/23843	0.033217	0.447571	0.425591	Osr1/Osr2
GO_BP_m1	GO:003602	embryonic	2/2606	3/23843	0.033217	0.447571	0.425591	Osr1/Osr2
GO_BP_m1	GO:004483	modulation	2/2606	3/23843	0.033217	0.447571	0.425591	Fmr1/Vapb
GO_BP_m1	GO:004519	establishm	2/2606	3/23843	0.033217	0.447571	0.425591	Dock7/Fgf1

GO_BP_m1	GO:00452	establishm	2/2606	3/23843	0.033217	0.447571	0.425591	Dock7/Fgf
GO_BP_m1	GO:00469	sensitizatio	2/2606	3/23843	0.033217	0.447571	0.425591	Drd5/Grin
GO_BP_m1	GO:00719	negative re	2/2606	3/23843	0.033217	0.447571	0.425591	E2f1/E2f7
GO_BP_m1	GO:00903	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Apobec1/
GO_BP_m1	GO:009897	excitatory	2/2606	3/23843	0.033217	0.447571	0.425591	Pdlim4/Ssh
GO_BP_m1	GO:01100	cellular det	2/2606	3/23843	0.033217	0.447571	0.425591	Adh5/Esd
GO_BP_m1	GO:190024	positive re	2/2606	3/23843	0.033217	0.447571	0.425591	Ddx60/Dh
GO_BP_m1	GO:19004	negative re	2/2606	3/23843	0.033217	0.447571	0.425591	Adora1/Fm
GO_BP_m1	GO:190147	pyruvate tr	2/2606	3/23843	0.033217	0.447571	0.425591	Mpc2/Slc1
GO_BP_m1	GO:19015	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Cxcl10/Fgf
GO_BP_m1	GO:19016	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Lrp4/Lrrtm
GO_BP_m1	GO:19016	glycoside t	2/2606	3/23843	0.033217	0.447571	0.425591	Abcb1a/Ra
GO_BP_m1	GO:19020	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Hrc/Mrln
GO_BP_m1	GO:19028	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Nln/Tbx1
GO_BP_m1	GO:19028	terminal w	2/2606	3/23843	0.033217	0.447571	0.425591	Ezr/Pls1
GO_BP_m1	GO:19035	meiotic cel	2/2606	3/23843	0.033217	0.447571	0.425591	Ppp2r1a/Y
GO_BP_m1	GO:19035	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Ppp2r1a/Y
GO_BP_m1	GO:19038	negative re	2/2606	3/23843	0.033217	0.447571	0.425591	Nck2/Ptpn
GO_BP_m1	GO:190404	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Park2/Stx1
GO_BP_m1	GO:190421	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Serinc2/Se
GO_BP_m1	GO:190421	positive re	2/2606	3/23843	0.033217	0.447571	0.425591	Serinc2/Se
GO_BP_m1	GO:19042	positive re	2/2606	3/23843	0.033217	0.447571	0.425591	Serinc2/Se
GO_BP_m1	GO:20001	regulation	2/2606	3/23843	0.033217	0.447571	0.425591	Dgkq/Ppar
GO_BP_m1	GO:20002	receptor in	2/2606	3/23843	0.033217	0.447571	0.425591	Cav1/Rab5
GO_BP_m1	GO:00440	regulation	7/2606	29/23843	0.033273	0.447571	0.425591	Adora1/Av
GO_BP_m1	GO:00071	negative re	6/2606	23/23843	0.033344	0.447571	0.425591	Adra1d/Ak
GO_BP_m1	GO:00303	adrenal gla	6/2606	23/23843	0.033344	0.447571	0.425591	Cdkn1c/Ly
GO_BP_m1	GO:00611	mRNA des	6/2606	23/23843	0.033344	0.447571	0.425591	Cnot6l/Cp
GO_BP_m1	GO:00718	response t	6/2606	23/23843	0.033344	0.447571	0.425591	Akap6/Atp
GO_BP_m1	GO:00722	cell differe	6/2606	23/23843	0.033344	0.447571	0.425591	Gdnf/Lam
GO_BP_m1	GO:19029	positive re	6/2606	23/23843	0.033344	0.447571	0.425591	Adcyap1r1
GO_BP_m1	GO:00715	response t	29/2606	187/23843	0.033499	0.447571	0.425591	Ankrd1/Ca
GO_BP_m1	GO:00067	terpenoid	11/2606	55/23843	0.033669	0.447571	0.425591	Adh1/Adh
GO_BP_m1	GO:19031	regulation	24/2606	149/23843	0.033756	0.447571	0.425591	Adra1d/Ak
GO_BP_m1	GO:00003	RNA splici	4/2606	12/23843	0.034316	0.447571	0.425591	Rtraf/Tsen
GO_BP_m1	GO:00108	negative re	4/2606	12/23843	0.034316	0.447571	0.425591	Kat2a/Kat2
GO_BP_m1	GO:00108	regulation	4/2606	12/23843	0.034316	0.447571	0.425591	Fitm1/Osb
GO_BP_m1	GO:00199	cGMP-me	4/2606	12/23843	0.034316	0.447571	0.425591	Cd36/Ednr
GO_BP_m1	GO:003191	positive re	4/2606	12/23843	0.034316	0.447571	0.425591	Cdc20/Cfl1
GO_BP_m1	GO:004347	pigment a	4/2606	12/23843	0.034316	0.447571	0.425591	Bloc1s5/C
GO_BP_m1	GO:00469	negative re	4/2606	12/23843	0.034316	0.447571	0.425591	Fmr1/Htr6
GO_BP_m1	GO:00603	negative re	4/2606	12/23843	0.034316	0.447571	0.425591	Nog/Pbld1
GO_BP_m1	GO:00614	regulation	4/2606	12/23843	0.034316	0.447571	0.425591	Men1/Nr4
GO_BP_m1	GO:007097	interleukin	4/2606	12/23843	0.034316	0.447571	0.425591	Abl2/Btnl2
GO_BP_m1	GO:00904	catecholan	4/2606	12/23843	0.034316	0.447571	0.425591	Gdnf/Park
GO_BP_m1	GO:00904	dopamine	4/2606	12/23843	0.034316	0.447571	0.425591	Gdnf/Park
GO_BP_m1	GO:19036	regulation	4/2606	12/23843	0.034316	0.447571	0.425591	Aifm1/Dffa
GO_BP_m1	GO:200001	regulation	4/2606	12/23843	0.034316	0.447571	0.425591	Dmrt1/Nr5

GO_BP_m1	GO:200062	regulation	4/2606	12/23843	0.034316	0.447571	0.425591	Khsrp/Nfkb
GO_BP_m1	GO:003462	cellular res	15/2606	83/23843	0.03436	0.447571	0.425591	Atf3/Bok/C
GO_BP_m1	GO:000924	glycolipid b	12/2606	62/23843	0.034393	0.447571	0.425591	Abo/B4galt
GO_BP_m1	GO:004514	homologou	12/2606	62/23843	0.034393	0.447571	0.425591	Terb1/Ccne
GO_BP_m1	GO:200037	negative re	12/2606	62/23843	0.034393	0.447571	0.425591	Atp2b4/Bc
GO_BP_m1	GO:004864	animal org	13/2606	69/23843	0.034684	0.450501	0.428378	Fgf1/Gdnf/
GO_BP_m1	GO:000616	purine nuc	61/2606	443/23843	0.034747	0.450501	0.428378	Adcy4/Adk
GO_BP_m1	GO:004828	organelle f	28/2606	180/23843	0.034961	0.450501	0.428378	Ankfy1/Anx
GO_BP_m1	GO:003080	negative re	9/2606	42/23843	0.034977	0.450501	0.428378	Adra1d/Ak
GO_BP_m1	GO:004222	response t	9/2606	42/23843	0.034977	0.450501	0.428378	Abat/Adra1
GO_BP_m1	GO:004230	positive reg	9/2606	42/23843	0.034977	0.450501	0.428378	Cdk1/Hyal2
GO_BP_m1	GO:190037	negative re	9/2606	42/23843	0.034977	0.450501	0.428378	Adra1d/Ak
GO_BP_m1	GO:009010	negative re	18/2606	105/23843	0.035412	0.45484	0.432503	Cav1/Danc
GO_BP_m1	GO:005148	regulation	48/2606	338/23843	0.035418	0.45484	0.432503	Abl2/Adcy
GO_BP_m1	GO:001593	nucleobase	29/2606	188/23843	0.035617	0.456058	0.433662	Adora1/Ah
GO_BP_m1	GO:003461	response t	29/2606	188/23843	0.035617	0.456058	0.433662	Ankrd1/Ca
GO_BP_m1	GO:001969	ribose pho	62/2606	452/23843	0.035867	0.458592	0.436071	Adcy4/Adr
GO_BP_m1	GO:003313	positive reg	20/2606	120/23843	0.036172	0.461818	0.439139	Atp2b4/Bc
GO_BP_m1	GO:000301	renal syste	17/2606	98/23843	0.036301	0.462121	0.439427	Adm/Adora
GO_BP_m1	GO:000609	pyruvate m	17/2606	98/23843	0.036301	0.462121	0.439427	Bpgm/Eno3
GO_BP_m1	GO:001033	response t	10/2606	49/23843	0.036831	0.468192	0.445199	Apobec1/A
GO_BP_m1	GO:007200	renal syste	42/2606	291/23843	0.037231	0.472598	0.449389	Adamts1/A
GO_BP_m1	GO:003110	microtubul	19/2606	113/23843	0.037332	0.473052	0.449821	Ankrd53/C
GO_BP_m1	GO:000663	unsaturate	8/2606	36/23843	0.037428	0.473052	0.449821	Alox12/Avp
GO_BP_m1	GO:003022	macrophag	8/2606	36/23843	0.037428	0.473052	0.449821	Casp8/Ceb
GO_BP_m1	GO:000931	response t	54/2606	388/23843	0.037725	0.475159	0.451825	Abl2/Adam
GO_BP_m1	GO:009706	dendritic sp	15/2606	84/23843	0.037757	0.475159	0.451825	Abl2/Arhga
GO_BP_m1	GO:190595	positive reg	15/2606	84/23843	0.037757	0.475159	0.451825	Abca12/Ar
GO_BP_m1	GO:009719	extrinsic ap	34/2606	228/23843	0.037885	0.475716	0.452355	Atf3/Bok/C
GO_BP_m1	GO:009039	cellular sen	11/2606	56/23843	0.03791	0.475716	0.452355	1500015O1
GO_BP_m1	GO:007233	monocarbo	35/2606	236/23843	0.03817	0.478302	0.454813	Abat/Abcd
GO_BP_m1	GO:000300	regionaliza	51/2606	364/23843	0.03827	0.478621	0.455117	Abi1/Btg2/
GO_BP_m1	GO:003460	cellular res	12/2606	63/23843	0.038414	0.478621	0.455117	Ano1/Clpb
GO_BP_m1	GO:006099	dendritic sp	12/2606	63/23843	0.038414	0.478621	0.455117	Arhgap44/
GO_BP_m1	GO:190160	alpha-amin	12/2606	63/23843	0.038414	0.478621	0.455117	Apip/Atp2b
GO_BP_m1	GO:000742	peripheral	13/2606	70/23843	0.038489	0.478873	0.455356	Ahnak2/Cc
GO_BP_m1	GO:000686	amino acid	22/2606	136/23843	0.039077	0.479602	0.45605	Abat/Adora
GO_BP_m1	GO:003563	multicellula	22/2606	136/23843	0.039077	0.479602	0.45605	Ahnak2/Av
GO_BP_m1	GO:190331	regulation	32/2606	213/23843	0.039308	0.479602	0.45605	Apobec1/B
GO_BP_m1	GO:002160	cranial nerv	7/2606	30/23843	0.03944	0.479602	0.45605	Atp8b1/Ep
GO_BP_m1	GO:001054	negative re	5/2606	18/23843	0.039493	0.479602	0.45605	Abat/Alox1
GO_BP_m1	GO:001581	gamma-am	5/2606	18/23843	0.039493	0.479602	0.45605	Abat/Hrh3/
GO_BP_m1	GO:001890	ether meta	5/2606	18/23843	0.039493	0.479602	0.45605	Ephx2/Fasn
GO_BP_m1	GO:002203	corpus call	5/2606	18/23843	0.039493	0.479602	0.45605	Cdk5/Ephb
GO_BP_m1	GO:004241	norepineph	5/2606	18/23843	0.039493	0.479602	0.45605	Ly6e/Park2
GO_BP_m1	GO:005086	negative re	5/2606	18/23843	0.039493	0.479602	0.45605	Btnl2/Dusp
GO_BP_m1	GO:009002	positive reg	5/2606	18/23843	0.039493	0.479602	0.45605	Ccr1/Cxcl1
GO_BP_m1	GO:190204	positive reg	5/2606	18/23843	0.039493	0.479602	0.45605	Atf3/Nf1/S

GO_BP_m1	GO:00709	neuron dea	53/2606	381/23843	0.039518	0.479602	0.45605	Aatk/Ache/
GO_BP_m1	GO:001481	muscle cell	17/2606	99/23843	0.039529	0.479602	0.45605	Dock4/Doc
GO_BP_m1	GO:004213	neurotrans	17/2606	99/23843	0.039529	0.479602	0.45605	Abat/Aldh9
GO_BP_m1	GO:003053	adult beha	28/2606	182/23843	0.039541	0.479602	0.45605	Abat/Abl2/
GO_BP_m1	GO:005080	regulation	28/2606	182/23843	0.039541	0.479602	0.45605	Arhgap44/
GO_BP_m1	GO:200037	regulation	28/2606	182/23843	0.039541	0.479602	0.45605	Atp2b4/Bc
GO_BP_m1	GO:000915	purine ribo	59/2606	430/23843	0.039585	0.479602	0.45605	Adcy4/Adr
GO_BP_m1	GO:200125	regulation	25/2606	159/23843	0.039689	0.480206	0.456624	Adra1d/Ak
GO_BP_m1	GO:003053	male genit	6/2606	24/23843	0.040477	0.48308	0.459356	Asb1/Hsd1
GO_BP_m1	GO:003128	negative re	6/2606	24/23843	0.040477	0.48308	0.459356	Adra1d/Ak
GO_BP_m1	GO:004247	middle ear	6/2606	24/23843	0.040477	0.48308	0.459356	Myc/Nog/
GO_BP_m1	GO:004392	modulation	6/2606	24/23843	0.040477	0.48308	0.459356	Ccl4/Hdac1
GO_BP_m1	GO:004434	type B pan	6/2606	24/23843	0.040477	0.48308	0.459356	Adk/Igfbp3
GO_BP_m1	GO:005231	modulation	6/2606	24/23843	0.040477	0.48308	0.459356	Ccl4/Hdac1
GO_BP_m1	GO:005247	modulation	6/2606	24/23843	0.040477	0.48308	0.459356	Ccl4/Hdac1
GO_BP_m1	GO:005502	negative re	6/2606	24/23843	0.040477	0.48308	0.459356	Cav3/Hdac
GO_BP_m1	GO:006111	negative re	6/2606	24/23843	0.040477	0.48308	0.459356	Cav3/Hdac
GO_BP_m1	GO:007186	response to	6/2606	24/23843	0.040477	0.48308	0.459356	Akap6/Atp
GO_BP_m1	GO:009753	granulocyte	21/2606	129/23843	0.040572	0.483558	0.459811	Adam8/Ccl
GO_BP_m1	GO:004508	positive reg	30/2606	198/23843	0.040687	0.48428	0.460498	5730559C1
GO_BP_m1	GO:004547	response to	15/2606	85/23843	0.04139	0.49197	0.46781	Abat/Adh1
GO_BP_m1	GO:005133	regulation	10/2606	50/23843	0.041695	0.494925	0.47062	Adra1d/Ak
GO_BP_m1	GO:005507	calcium ior	61/2606	448/23843	0.042053	0.497019	0.472611	Abl2/Adcy
GO_BP_m1	GO:000663	acyl-CoA m	14/2606	78/23843	0.042097	0.497019	0.472611	Acot1/Aco
GO_BP_m1	GO:003538	thioester m	14/2606	78/23843	0.042097	0.497019	0.472611	Acot1/Aco
GO_BP_m1	GO:004636	monosacch	14/2606	78/23843	0.042097	0.497019	0.472611	Atf3/Bpgm
GO_BP_m1	GO:004327	negative re	25/2606	160/23843	0.042336	0.498025	0.473568	Abat/Adora
GO_BP_m1	GO:000925	ribonucleo	60/2606	440/23843	0.042395	0.498025	0.473568	Adcy4/Adr
GO_BP_m1	GO:000751	skeletal mu	29/2606	191/23843	0.042577	0.498025	0.473568	Acta1/Ank
GO_BP_m1	GO:003150	protein-co	29/2606	191/23843	0.042577	0.498025	0.473568	Akap6/Arh
GO_BP_m1	GO:001974	secondary	13/2606	71/23843	0.042579	0.498025	0.473568	Akr1c12/A
GO_BP_m1	GO:005188	regulation	13/2606	71/23843	0.042579	0.498025	0.473568	Alox12/Arl
GO_BP_m1	GO:190331	positive reg	13/2606	71/23843	0.042579	0.498025	0.473568	Apobec1/B
GO_BP_m1	GO:005178	negative re	12/2606	64/23843	0.042754	0.4994	0.474876	Dmrt1/Fbx
GO_BP_m1	GO:002260	digestive sy	17/2606	100/23843	0.042959	0.501137	0.476527	5730559C1
GO_BP_m1	GO:004349	protein kin	26/2606	168/23843	0.043177	0.502846	0.478152	Adam8/C1
GO_BP_m1	GO:000673	NADP meta	8/2606	37/23843	0.043342	0.502846	0.478152	Bpgm/Fmo
GO_BP_m1	GO:004616	alcohol cat	8/2606	37/23843	0.043342	0.502846	0.478152	Adh1/Adh5
GO_BP_m1	GO:190533	positive reg	8/2606	37/23843	0.043342	0.502846	0.478152	Gdnf/Lgr4/
GO_BP_m1	GO:000028	nuclear div	57/2606	416/23843	0.043392	0.502846	0.478152	Ankrd53/B
GO_BP_m1	GO:000688	ER to Golg	19/2606	115/23843	0.043602	0.504226	0.479464	Bcap29/Bc
GO_BP_m1	GO:004364	dicarboxyli	16/2606	93/23843	0.044162	0.504226	0.479464	Dglucy/Ads
GO_BP_m1	GO:190547	positive reg	16/2606	93/23843	0.044162	0.504226	0.479464	Cdk5/Cib1/
GO_BP_m1	GO:001598	energy der	36/2606	247/23843	0.044788	0.504226	0.479464	Bnip3/Cdk1
GO_BP_m1	GO:002241	cellular pro	51/2606	368/23843	0.045189	0.504226	0.479464	Acrbp/Amh
GO_BP_m1	GO:000165	metanephr	15/2606	86/23843	0.045264	0.504226	0.479464	Aph1a/Fbn
GO_BP_m1	GO:000626	DNA ligatio	4/2606	13/23843	0.045386	0.504226	0.479464	Aplf/Aptx/L
GO_BP_m1	GO:000732	inseminatio	4/2606	13/23843	0.045386	0.504226	0.479464	Avpr1a/Dd

GO_BP_m1	GO:001022	response t	4/2606	13/23843	0.045386	0.504226	0.479464	Ei24/Ercc5/
GO_BP_m1	GO:001821	peptidyl-a	4/2606	13/23843	0.045386	0.504226	0.479464	Ndufaf7/Pr
GO_BP_m1	GO:003581	positive re	4/2606	13/23843	0.045386	0.504226	0.479464	Avpr1a/Dr
GO_BP_m1	GO:00447	negative re	4/2606	13/23843	0.045386	0.504226	0.479464	Mptx2/Parl
GO_BP_m1	GO:00458	negative re	4/2606	13/23843	0.045386	0.504226	0.479464	Dmrt1/Fbx
GO_BP_m1	GO:00466	negative re	4/2606	13/23843	0.045386	0.504226	0.479464	Kat2a/Kat2
GO_BP_m1	GO:007221	positive re	4/2606	13/23843	0.045386	0.504226	0.479464	Gdnf/Myc/
GO_BP_m1	GO:00726	protein loc	4/2606	13/23843	0.045386	0.504226	0.479464	Epb41/Ezr/
GO_BP_m1	GO:00995	neurotrans	4/2606	13/23843	0.045386	0.504226	0.479464	Cacng5/Ca
GO_BP_m1	GO:190504	regulation	4/2606	13/23843	0.045386	0.504226	0.479464	Antxr1/Ddr
GO_BP_m1	GO:190594	positive re	4/2606	13/23843	0.045386	0.504226	0.479464	Dmrt1/Nr5
GO_BP_m1	GO:20001	positive re	4/2606	13/23843	0.045386	0.504226	0.479464	Cdc7/Cdk2
GO_BP_m1	GO:20006	negative re	4/2606	13/23843	0.045386	0.504226	0.479464	Drd3/Hecw
GO_BP_m1	GO:000072	non-recom	9/2606	44/23843	0.045704	0.504226	0.479464	Dclre1a/De
GO_BP_m1	GO:003304	negative re	9/2606	44/23843	0.045704	0.504226	0.479464	Klhl22/Mac
GO_BP_m1	GO:00430	regulation	9/2606	44/23843	0.045704	0.504226	0.479464	Cd200/Il10
GO_BP_m1	GO:00484	synaptic ve	9/2606	44/23843	0.045704	0.504226	0.479464	Canx/Cdk5
GO_BP_m1	GO:000721	Notch sign	26/2606	169/23843	0.04592	0.504226	0.479464	Aph1a/Ap
GO_BP_m1	GO:001571	monocarb	23/2606	146/23843	0.046096	0.504226	0.479464	Abat/Abcc
GO_BP_m1	GO:003304	regulation	14/2606	79/23843	0.046218	0.504226	0.479464	Cdc23/Fen
GO_BP_m1	GO:000202	regulation	7/2606	31/23843	0.046308	0.504226	0.479464	Adm/Atp2
GO_BP_m1	GO:00065	GPI anchor	7/2606	31/23843	0.046308	0.504226	0.479464	Pgap1/Pga
GO_BP_m1	GO:000697	hyperosm	7/2606	31/23843	0.046308	0.504226	0.479464	Mir7b/Mir
GO_BP_m1	GO:00106	positive re	7/2606	31/23843	0.046308	0.504226	0.479464	Bnip3/Cam
GO_BP_m1	GO:00708	regulation	7/2606	31/23843	0.046308	0.504226	0.479464	Akap6/Atp
GO_BP_m1	GO:01060	regulation	7/2606	31/23843	0.046308	0.504226	0.479464	Akap6/Atp
GO_BP_m1	GO:19018	positive re	7/2606	31/23843	0.046308	0.504226	0.479464	Cav1/Cfl1/
GO_BP_m1	GO:00511	cofactor bi	32/2606	216/23843	0.046313	0.504226	0.479464	Bdh2/Bpgr
GO_BP_m1	GO:006107	chaperone	13/2606	72/23843	0.046965	0.504226	0.479464	Calr/Canx/
GO_BP_m1	GO:000702	endoplasm	10/2606	51/23843	0.046979	0.504226	0.479464	Jagn1/Pex
GO_BP_m1	GO:001082	negative re	10/2606	51/23843	0.046979	0.504226	0.479464	Bnip3/Bok/
GO_BP_m1	GO:00515	histone H3	10/2606	51/23843	0.046979	0.504226	0.479464	Ash2l/H2af
GO_BP_m1	GO:00434	negative re	24/2606	154/23843	0.047122	0.504226	0.479464	Atf3/Camk
GO_BP_m1	GO:000914	purine nuc	37/2606	256/23843	0.047154	0.504226	0.479464	Adk/Atp5a
GO_BP_m1	GO:006024	anatomical	50/2606	361/23843	0.047352	0.504226	0.479464	5730559C1
GO_BP_m1	GO:000854	visual learn	12/2606	65/23843	0.047423	0.504226	0.479464	Abl2/Adam
GO_BP_m1	GO:004577	negative re	11/2606	58/23843	0.047479	0.504226	0.479464	Abat/Ador
GO_BP_m1	GO:00466	positive re	11/2606	58/23843	0.047479	0.504226	0.479464	Blm/Cd80/
GO_BP_m1	GO:00504	regulation	11/2606	58/23843	0.047479	0.504226	0.479464	Abat/Adra
GO_BP_m1	GO:00901	regulation	11/2606	58/23843	0.047479	0.504226	0.479464	Flcn/Gdnf/
GO_BP_m1	GO:00516	establishm	29/2606	193/23843	0.047747	0.504226	0.479464	Bloc1s5/Co
GO_BP_m1	GO:000002	mitotic spi	3/2606	8/23843	0.047906	0.504226	0.479464	Kif23/Kif4/
GO_BP_m1	GO:00107	negative re	3/2606	8/23843	0.047906	0.504226	0.479464	D1Ertd622
GO_BP_m1	GO:001991	peptidyl-a	3/2606	8/23843	0.047906	0.504226	0.479464	Prmt1/Prm
GO_BP_m1	GO:00341	regulation	3/2606	8/23843	0.047906	0.504226	0.479464	H2afy/Naa
GO_BP_m1	GO:00344	early endo	3/2606	8/23843	0.047906	0.504226	0.479464	Rbsn/Snx2/
GO_BP_m1	GO:003594	regulation	3/2606	8/23843	0.047906	0.504226	0.479464	Kat2a/Kat2
GO_BP_m1	GO:004482	meiotic tel	3/2606	8/23843	0.047906	0.504226	0.479464	Terb1/Lem

GO_BP_m1	GO:004808	positive reg	3/2606	8/23843	0.047906	0.504226	0.479464	Adamts9/B
GO_BP_m1	GO:005134	regulation	3/2606	8/23843	0.047906	0.504226	0.479464	Gclm/Ripk3
GO_BP_m1	GO:006090	positive reg	3/2606	8/23843	0.047906	0.504226	0.479464	Cd36/Gprc
GO_BP_m1	GO:006105	negative re	3/2606	8/23843	0.047906	0.504226	0.479464	Cav3/Pak1/
GO_BP_m1	GO:007019	meiotic att	3/2606	8/23843	0.047906	0.504226	0.479464	Terb1/Lem
GO_BP_m1	GO:007144	cellular res	3/2606	8/23843	0.047906	0.504226	0.479464	Cd36/Dapk
GO_BP_m1	GO:007149	cellular res	3/2606	8/23843	0.047906	0.504226	0.479464	Cdkn1a/Hy
GO_BP_m1	GO:007223	metanephr	3/2606	8/23843	0.047906	0.504226	0.479464	Osr1/Pdgfr
GO_BP_m1	GO:007231	vesicle unc	3/2606	8/23843	0.047906	0.504226	0.479464	Dnajc6/Sh3
GO_BP_m1	GO:009724	chromosom	3/2606	8/23843	0.047906	0.504226	0.479464	Terb1/Lem
GO_BP_m1	GO:009750	stress resp	3/2606	8/23843	0.047906	0.504226	0.479464	Mt2/Mt3/S
GO_BP_m1	GO:190011	extracellula	3/2606	8/23843	0.047906	0.504226	0.479464	Dand5/Fbn
GO_BP_m1	GO:190011	extracellula	3/2606	8/23843	0.047906	0.504226	0.479464	Dand5/Fbn
GO_BP_m1	GO:190162	regulation	3/2606	8/23843	0.047906	0.504226	0.479464	Prkacb/Tra
GO_BP_m1	GO:190185	positive reg	3/2606	8/23843	0.047906	0.504226	0.479464	Cdk1/Myc/
GO_BP_m1	GO:190223	positive reg	3/2606	8/23843	0.047906	0.504226	0.479464	Bok/Nck2/S
GO_BP_m1	GO:000906	fatty acid c	16/2606	94/23843	0.048034	0.504226	0.479464	Abcd3/Abh
GO_BP_m1	GO:003081	negative re	6/2606	25/23843	0.048502	0.504226	0.479464	Adra1d/Ak
GO_BP_m1	GO:003287	regulation	6/2606	25/23843	0.048502	0.504226	0.479464	Bcas3/Cfl1/
GO_BP_m1	GO:003327	response t	6/2606	25/23843	0.048502	0.504226	0.479464	Bche/Cyp2
GO_BP_m1	GO:003545	response t	6/2606	25/23843	0.048502	0.504226	0.479464	Eif2ak2/Ifit
GO_BP_m1	GO:006121	positive reg	6/2606	25/23843	0.048502	0.504226	0.479464	Gdnf/Lgr4/
GO_BP_m1	GO:000664	membrane	26/2606	170/23843	0.048789	0.504226	0.479464	Abo/Acer3
GO_BP_m1	GO:006900	pinocytosis	5/2606	19/23843	0.048926	0.504226	0.479464	Ankfy1/Cav
GO_BP_m1	GO:190473	vascular as	5/2606	19/23843	0.048926	0.504226	0.479464	Dock4/Doc
GO_BP_m1	GO:190475	regulation	5/2606	19/23843	0.048926	0.504226	0.479464	Dock4/Doc
GO_BP_m1	GO:190552	positive reg	5/2606	19/23843	0.048926	0.504226	0.479464	Cxcl17/Kars
GO_BP_m1	GO:004001	negative re	43/2606	305/23843	0.048992	0.504226	0.479464	Adamts9/A
GO_BP_m1	GO:004308	regulation	41/2606	289/23843	0.049278	0.504226	0.479464	Arhgap44/
GO_BP_m1	GO:004508	regulation	35/2606	241/23843	0.04938	0.504226	0.479464	5730559C1
GO_BP_m1	GO:001490	smooth mu	15/2606	87/23843	0.049386	0.504226	0.479464	Dock4/Doc
GO_BP_m1	GO:003444	substrate a	15/2606	87/23843	0.049386	0.504226	0.479464	Antxr1/Bca
GO_BP_m1	GO:010602	neuron pro	15/2606	87/23843	0.049386	0.504226	0.479464	Abl2/Arhga
GO_BP_m1	GO:004586	positive reg	59/2606	436/23843	0.049599	0.504226	0.479464	5730559C1
GO_BP_m1	GO:007221	metanephr	8/2606	38/23843	0.04984	0.504226	0.479464	Gdnf/Irx2/L
GO_BP_m1	GO:005080	regulation	29/2606	194/23843	0.050499	0.504226	0.479464	Arhgap44/
GO_BP_m1	GO:006099	dendritic sp	19/2606	117/23843	0.050597	0.504226	0.479464	Arhgap44/
GO_BP_m1	GO:009865	anion trans	30/2606	202/23843	0.050895	0.504226	0.479464	Abcb1a/Ar
GO_BP_m1	GO:003158	cell-substra	43/2606	306/23843	0.05119	0.504226	0.479464	Adam8/Ad
GO_BP_m1	GO:000221	activation o	22/2606	140/23843	0.051382	0.504226	0.479464	5730559C1
GO_BP_m1	GO:000718	G-protein c	32/2606	218/23843	0.051471	0.504226	0.479464	Adcy4/Adg
GO_BP_m1	GO:190402	regulation	13/2606	73/23843	0.051654	0.504226	0.479464	Blm/Camk2
GO_BP_m1	GO:000165	temperatur	9/2606	45/23843	0.051808	0.504226	0.479464	Abat/Adora
GO_BP_m1	GO:007124	cellular res	9/2606	45/23843	0.051808	0.504226	0.479464	Aoc1/Casp
GO_BP_m1	GO:009032	regulation	9/2606	45/23843	0.051808	0.504226	0.479464	Blm/Cdc7/
GO_BP_m1	GO:003569	cellular res	48/2606	347/23843	0.052013	0.504226	0.479464	Ankrd1/Bca
GO_BP_m1	GO:004513	meiotic chr	16/2606	95/23843	0.052138	0.504226	0.479464	Terb1/Ccne
GO_BP_m1	GO:005090	neuromusc	20/2606	125/23843	0.052222	0.504226	0.479464	Abl2/Aldh1

GO_BP_m1	GO:001633	morphoge	27/2606	179/23843	0.052408	0.504226	0.479464	Abl2/Adm/
GO_BP_m1	GO:003096	endoplasm	12/2606	66/23843	0.052429	0.504226	0.479464	Atf3/Bok/C
GO_BP_m1	GO:005129	centrosom	12/2606	66/23843	0.052429	0.504226	0.479464	Deup1/Cdk
GO_BP_m1	GO:004864	negative re	18/2606	110/23843	0.052554	0.504226	0.479464	Aatk/Bbs2/
GO_BP_m1	GO:000761	mating	10/2606	52/23843	0.052695	0.504226	0.479464	Abat/Avpr1
GO_BP_m1	GO:007009	chemokine	10/2606	52/23843	0.052695	0.504226	0.479464	Ccl20/Ccl2
GO_BP_m1	GO:001936	arachidoni	11/2606	59/23843	0.052829	0.504226	0.479464	Alox12/Alo
GO_BP_m1	GO:003133	regulation	11/2606	59/23843	0.052829	0.504226	0.479464	Anxa2/Sgs
GO_BP_m1	GO:007023	T cell apop	11/2606	59/23843	0.052829	0.504226	0.479464	Adam8/Bln
GO_BP_m1	GO:009700	regulation	11/2606	59/23843	0.052829	0.504226	0.479464	Anxa2/Cd3
GO_BP_m1	GO:004863	regulation	51/2606	372/23843	0.053013	0.504226	0.479464	Aatk/Akap
GO_BP_m1	GO:002176	limbic syste	15/2606	88/23843	0.053764	0.504226	0.479464	Aldh1a3/Bl
GO_BP_m1	GO:000630	DNA catab	7/2606	32/23843	0.053894	0.504226	0.479464	Aifm1/Dffa
GO_BP_m1	GO:000650	GPI anchor	7/2606	32/23843	0.053894	0.504226	0.479464	Pgap1/Pga
GO_BP_m1	GO:000676	water-solu	7/2606	32/23843	0.053894	0.504226	0.479464	Acpp/Clybl
GO_BP_m1	GO:000677	fat-soluble	7/2606	32/23843	0.053894	0.504226	0.479464	Crabp1/Cy
GO_BP_m1	GO:000693	muscle cor	40/2606	283/23843	0.054079	0.504226	0.479464	Abat/Acta2
GO_BP_m1	GO:003497	response t	32/2606	219/23843	0.054202	0.504226	0.479464	Aifm1/Atf3
GO_BP_m1	GO:005117	import intc	25/2606	164/23843	0.054229	0.504226	0.479464	1700123L1
GO_BP_m1	GO:004306	extracellula	38/2606	267/23843	0.05435	0.504226	0.479464	2300002M
GO_BP_m1	GO:000709	centrosom	19/2606	118/23843	0.054378	0.504226	0.479464	Deup1/Cdk
GO_BP_m1	GO:004347	pigmentati	17/2606	103/23843	0.054521	0.504226	0.479464	Adamts9/B
GO_BP_m1	GO:005067	regulation	47/2606	340/23843	0.054524	0.504226	0.479464	A4gnt/Arg
GO_BP_m1	GO:003514	tube forma	26/2606	172/23843	0.054913	0.504226	0.479464	Abl2/Adm/
GO_BP_m1	GO:007265	protein loc	63/2606	472/23843	0.054966	0.504226	0.479464	Abca12/Ac
GO_BP_m1	GO:000663	fatty acid b	20/2606	126/23843	0.055956	0.504226	0.479464	Abcd3/Abh
GO_BP_m1	GO:000709	mitotic cell	20/2606	126/23843	0.055956	0.504226	0.479464	Blm/Ccng1
GO_BP_m1	GO:002191	neural tube	28/2606	188/23843	0.055961	0.504226	0.479464	Abl2/Adm/
GO_BP_m1	GO:006034	bone devel	29/2606	196/23843	0.056345	0.504226	0.479464	Abi1/Alpl/
GO_BP_m1	GO:003031	flagellated	16/2606	96/23843	0.05648	0.504226	0.479464	Atp2b4/Bb
GO_BP_m1	GO:007232	monocarbc	18/2606	111/23843	0.05658	0.504226	0.479464	Abat/Abcd
GO_BP_m1	GO:001605	carbohydra	30/2606	204/23843	0.056647	0.504226	0.479464	Adcyap1r1
GO_BP_m1	GO:004328	regulation	30/2606	204/23843	0.056647	0.504226	0.479464	Aifm1/Alox
GO_BP_m1	GO:003320	tumor necr	13/2606	74/23843	0.056653	0.504226	0.479464	Ccdc3/Cldn
GO_BP_m1	GO:000268	negative re	60/2606	448/23843	0.05669	0.504226	0.479464	Adora1/Arg
GO_BP_m1	GO:007251	divalent inc	60/2606	448/23843	0.05669	0.504226	0.479464	Adcyap1r1
GO_BP_m1	GO:004576	regulation	8/2606	39/23843	0.056936	0.504226	0.479464	Adra1d/Ak
GO_BP_m1	GO:000165	urogenital	46/2606	333/23843	0.057164	0.504226	0.479464	Adamts1/A
GO_BP_m1	GO:005254	regulation	55/2606	407/23843	0.057421	0.504226	0.479464	Aifm1/Alox
GO_BP_m1	GO:002151	spinal cord	6/2606	26/23843	0.05744	0.504226	0.479464	Dbx1/Dll4/
GO_BP_m1	GO:003080	negative re	6/2606	26/23843	0.05744	0.504226	0.479464	Adra1d/Ak
GO_BP_m1	GO:003252	microvillus	6/2606	26/23843	0.05744	0.504226	0.479464	Atp8b1/Ezr
GO_BP_m1	GO:003292	regulation	6/2606	26/23843	0.05744	0.504226	0.479464	Dand5/Dm
GO_BP_m1	GO:004814	behavioral	6/2606	26/23843	0.05744	0.504226	0.479464	Abat/Adra1
GO_BP_m1	GO:004851	spermatid	25/2606	165/23843	0.057542	0.504226	0.479464	Acrbp/Bbs2
GO_BP_m1	GO:004814	positive reg	12/2606	67/23843	0.057782	0.504226	0.479464	Anxa2/Cdk
GO_BP_m1	GO:000681	calcium ior	54/2606	399/23843	0.057951	0.504226	0.479464	Adcyap1r1
GO_BP_m1	GO:000166	fever gene	4/2606	14/23843	0.058206	0.504226	0.479464	Ednrb/Il1rn

GO_BP_m1	GO:00066	glycerol et	4/2606	14/23843	0.058206	0.504226	0.479464	Fasn/Tme
GO_BP_m1	GO:00306	regulation	4/2606	14/23843	0.058206	0.504226	0.479464	Clybl/Dgat
GO_BP_m1	GO:00395	regulation	4/2606	14/23843	0.058206	0.504226	0.479464	Ddx60/Dh
GO_BP_m1	GO:006131	renal filtrat	4/2606	14/23843	0.058206	0.504226	0.479464	Basp1/Jag
GO_BP_m1	GO:007211	glomerular	4/2606	14/23843	0.058206	0.504226	0.479464	Basp1/Jag
GO_BP_m1	GO:007231	glomerular	4/2606	14/23843	0.058206	0.504226	0.479464	Basp1/Jag
GO_BP_m1	GO:007257	neurotrans	4/2606	14/23843	0.058206	0.504226	0.479464	Gphn/Htr1
GO_BP_m1	GO:19023	negative r	4/2606	14/23843	0.058206	0.504226	0.479464	Drd3/Hec
GO_BP_m1	GO:00485	spleen dev	9/2606	46/23843	0.058421	0.504226	0.479464	Cfc1/Onec
GO_BP_m1	GO:00519	negative r	9/2606	46/23843	0.058421	0.504226	0.479464	Klhl22/Ma
GO_BP_m1	GO:00027	negative r	22/2606	142/23843	0.058478	0.504226	0.479464	C1qtnf3/C
GO_BP_m1	GO:00071	leukocyte	42/2606	301/23843	0.058537	0.504226	0.479464	Adam8/Ad
GO_BP_m1	GO:004662	positive re	10/2606	53/23843	0.058854	0.504226	0.479464	Akap6/Arx
GO_BP_m1	GO:00063	double-str	28/2606	189/23843	0.059114	0.504226	0.479464	Aplf/Aptx/
GO_BP_m1	GO:19030	regulation	38/2606	269/23843	0.059547	0.504226	0.479464	Adam8/Ad
GO_BP_m1	GO:00002	nuclear-tr	5/2606	20/23843	0.059569	0.504226	0.479464	Btg2/Cpeb
GO_BP_m1	GO:00194	alditol met	5/2606	20/23843	0.059569	0.504226	0.479464	Angptl3/C
GO_BP_m1	GO:00194	removal of	5/2606	20/23843	0.059569	0.504226	0.479464	Cd36/Fbln
GO_BP_m1	GO:00224	cell cycle p	5/2606	20/23843	0.059569	0.504226	0.479464	Cdc20/Dek
GO_BP_m1	GO:00955	acetylcholi	5/2606	20/23843	0.059569	0.504226	0.479464	Chrm1/Ch
GO_BP_m1	GO:19013	negative r	5/2606	20/23843	0.059569	0.504226	0.479464	Adra1d/F
GO_BP_m1	GO:19038	signal tran	5/2606	20/23843	0.059569	0.504226	0.479464	Chrm1/Ch
GO_BP_m1	GO:190514	response t	5/2606	20/23843	0.059569	0.504226	0.479464	Chrm1/Ch
GO_BP_m1	GO:190514	cellular res	5/2606	20/23843	0.059569	0.504226	0.479464	Chrm1/Ch
GO_BP_m1	GO:200031	regulation	5/2606	20/23843	0.059569	0.504226	0.479464	Cfl1/Crhbp
GO_BP_m1	GO:000912	nucleoside	37/2606	261/23843	0.059724	0.504226	0.479464	Adss/Atp5
GO_BP_m1	GO:00460	ATP metab	32/2606	221/23843	0.059976	0.504226	0.479464	Atp5a1/At
GO_BP_m1	GO:003111	regulation	14/2606	82/23843	0.060249	0.504226	0.479464	Ankrd53/C
GO_BP_m1	GO:00066	icosanoid	18/2606	112/23843	0.060817	0.504226	0.479464	Akr1c12/A
GO_BP_m1	GO:004477	cell cycle p	52/2606	384/23843	0.061248	0.504226	0.479464	Abcb1a/At
GO_BP_m1	GO:000071	meiotic D	2/2606	4/23843	0.061645	0.504226	0.479464	Sycp1/Syc
GO_BP_m1	GO:00007	DNA catab	2/2606	4/23843	0.061645	0.504226	0.479464	Eri1/Xrn2
GO_BP_m1	GO:00019	intestinal	2/2606	4/23843	0.061645	0.504226	0.479464	Ezr/Pls1
GO_BP_m1	GO:00019	norepinep	2/2606	4/23843	0.061645	0.504226	0.479464	Adra1d/Dr
GO_BP_m1	GO:00025	arachidoni	2/2606	4/23843	0.061645	0.504226	0.479464	Alox5/Eph
GO_BP_m1	GO:00060	ethanol oxi	2/2606	4/23843	0.061645	0.504226	0.479464	Adh1/Adh
GO_BP_m1	GO:00061	purine ribo	2/2606	4/23843	0.061645	0.504226	0.479464	Adk/Aprt
GO_BP_m1	GO:000627	leading str	2/2606	4/23843	0.061645	0.504226	0.479464	Pcna/Pole
GO_BP_m1	GO:00069	negative r	2/2606	4/23843	0.061645	0.504226	0.479464	Itgb1bp1/
GO_BP_m1	GO:00072	phospholi	2/2606	4/23843	0.061645	0.504226	0.479464	Chrm1/Ch
GO_BP_m1	GO:000982	unidimensi	2/2606	4/23843	0.061645	0.504226	0.479464	Cadm1/Cfl
GO_BP_m1	GO:001584	aminergic	2/2606	4/23843	0.061645	0.504226	0.479464	Slc18a2/Th
GO_BP_m1	GO:001924	citrulline bi	2/2606	4/23843	0.061645	0.504226	0.479464	Atp2b4/Ot
GO_BP_m1	GO:00196	glucose ca	2/2606	4/23843	0.061645	0.504226	0.479464	Ldha/Tigar
GO_BP_m1	GO:00196	glycolytic	2/2606	4/23843	0.061645	0.504226	0.479464	Ldha/Tigar
GO_BP_m1	GO:00196	glucose ca	2/2606	4/23843	0.061645	0.504226	0.479464	Ldha/Tigar
GO_BP_m1	GO:00196	nitrogenou	2/2606	4/23843	0.061645	0.504226	0.479464	Ldha/Tigar
GO_BP_m1	GO:00308	negative r	2/2606	4/23843	0.061645	0.504226	0.479464	Il10/Tspan

GO_BP_m1	GO:003232	molybdopt	2/2606	4/23843	0.061645	0.504226	0.479464	Gphn/Moc
GO_BP_m1	GO:003237	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Anxa2/Ldlr
GO_BP_m1	GO:003238	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Anxa2/Ldlr
GO_BP_m1	GO:003238	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Anxa2/Ldlr
GO_BP_m1	GO:003282	regulation	2/2606	4/23843	0.061645	0.504226	0.479464	Ifng/Il2rg
GO_BP_m1	GO:003335	S-adenosy	2/2606	4/23843	0.061645	0.504226	0.479464	Ahcyl2/Mtr
GO_BP_m1	GO:003419	acylglycero	2/2606	4/23843	0.061645	0.504226	0.479464	Cd36/Mttp
GO_BP_m1	GO:003419	triglyceride	2/2606	4/23843	0.061645	0.504226	0.479464	Cd36/Mttp
GO_BP_m1	GO:003455	respiratory	2/2606	4/23843	0.061645	0.504226	0.479464	Sdhaf3/Sdh
GO_BP_m1	GO:003455	mitochond	2/2606	4/23843	0.061645	0.504226	0.479464	Sdhaf3/Sdh
GO_BP_m1	GO:003535	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Asxl1/Plin5
GO_BP_m1	GO:003558	sequesterin	2/2606	4/23843	0.061645	0.504226	0.479464	Dand5/Fbn
GO_BP_m1	GO:003953	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Dhx58/Tkfc
GO_BP_m1	GO:004477	meiotic cel	2/2606	4/23843	0.061645	0.504226	0.479464	Topaz1/Ttk
GO_BP_m1	GO:004533	farnesyl dip	2/2606	4/23843	0.061645	0.504226	0.479464	Fdft1/Hmg
GO_BP_m1	GO:004591	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Itgam/Snca
GO_BP_m1	GO:004596	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Itgam/Snca
GO_BP_m1	GO:004612	deoxyribon	2/2606	4/23843	0.061645	0.504226	0.479464	Dera/Dpyd
GO_BP_m1	GO:004629	formaldehy	2/2606	4/23843	0.061645	0.504226	0.479464	Adh5/Esd
GO_BP_m1	GO:004854	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Ankfy1/Ppt
GO_BP_m1	GO:005110	regulation	2/2606	4/23843	0.061645	0.504226	0.479464	Aplf/Xrcc1
GO_BP_m1	GO:005110	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Aplf/Xrcc1
GO_BP_m1	GO:005138	response to	2/2606	4/23843	0.061645	0.504226	0.479464	Htr7/Npas4
GO_BP_m1	GO:006006	oviduct dev	2/2606	4/23843	0.061645	0.504226	0.479464	Cdh1/Wnt7
GO_BP_m1	GO:006119	fungiform p	2/2606	4/23843	0.061645	0.504226	0.479464	Hdac1/Hda
GO_BP_m1	GO:007031	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Ctgf/Orc1
GO_BP_m1	GO:007083	caveola ass	2/2606	4/23843	0.061645	0.504226	0.479464	Cav1/Cav3
GO_BP_m1	GO:007104	nuclear pol	2/2606	4/23843	0.061645	0.504226	0.479464	Exosc9/Pnp
GO_BP_m1	GO:007104	polyadenyl	2/2606	4/23843	0.061645	0.504226	0.479464	Exosc9/Pnp
GO_BP_m1	GO:007164	regulation	2/2606	4/23843	0.061645	0.504226	0.479464	Mefv/Trpv4
GO_BP_m1	GO:007196	mitotic siste	2/2606	4/23843	0.061645	0.504226	0.479464	Naa10/Naa
GO_BP_m1	GO:007212	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Ifng/Wt1
GO_BP_m1	GO:007213	kidney mes	2/2606	4/23843	0.061645	0.504226	0.479464	Myc/Osr1
GO_BP_m1	GO:007213	metanephr	2/2606	4/23843	0.061645	0.504226	0.479464	Myc/Osr1
GO_BP_m1	GO:007226	pattern spe	2/2606	4/23843	0.061645	0.504226	0.479464	Irx2/Osr1
GO_BP_m1	GO:009019	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Ifng/Wt1
GO_BP_m1	GO:009898	NMDA sele	2/2606	4/23843	0.061645	0.504226	0.479464	Camk2a/Gr
GO_BP_m1	GO:010600	intestinal h	2/2606	4/23843	0.061645	0.504226	0.479464	Ezr/Pls1
GO_BP_m1	GO:011009	cellular resp	2/2606	4/23843	0.061645	0.504226	0.479464	Adh5/Esd
GO_BP_m1	GO:190074	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Adgra2/Dc
GO_BP_m1	GO:190149	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Epha2/Foxc
GO_BP_m1	GO:190185	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Flcn/Lig3
GO_BP_m1	GO:190199	regulation	2/2606	4/23843	0.061645	0.504226	0.479464	Topaz1/Ttk
GO_BP_m1	GO:190221	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Ptgs2/Ybx3
GO_BP_m1	GO:190251	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Endog/Igfb
GO_BP_m1	GO:190295	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Cfl1/Grin2b
GO_BP_m1	GO:190327	positive reg	2/2606	4/23843	0.061645	0.504226	0.479464	Atp1b2/Fxy
GO_BP_m1	GO:190393	cellular resp	2/2606	4/23843	0.061645	0.504226	0.479464	Mapk13/Zc

GO_BP_m1	GO:190422	regulation	2/2606	4/23843	0.061645	0.504226	0.479464	Serinc2/Se
GO_BP_m1	GO:190439	positive re	2/2606	4/23843	0.061645	0.504226	0.479464	Lrp4/Mesd
GO_BP_m1	GO:199003	calcium io	2/2606	4/23843	0.061645	0.504226	0.479464	Hrc/Mrln
GO_BP_m1	GO:199083	response t	2/2606	4/23843	0.061645	0.504226	0.479464	Bcar1/Edn
GO_BP_m1	GO:200120	negative re	2/2606	4/23843	0.061645	0.504226	0.479464	Cldn18/Fb
GO_BP_m1	GO:001922	regulation	13/2606	75/23843	0.061969	0.504226	0.479464	Adm/Adra
GO_BP_m1	GO:003247	regulation	13/2606	75/23843	0.061969	0.504226	0.479464	Cactin/Dhx
GO_BP_m1	GO:000627	DNA replic	7/2606	33/23843	0.062212	0.504226	0.479464	Ccne1/Ccn
GO_BP_m1	GO:000689	retrograde	7/2606	33/23843	0.062212	0.504226	0.479464	Arf5/Atp9b
GO_BP_m1	GO:001054	regulation	7/2606	33/23843	0.062212	0.504226	0.479464	Abat/Alox1
GO_BP_m1	GO:001943	triglyceride	7/2606	33/23843	0.062212	0.504226	0.479464	Dgat1/Gpa
GO_BP_m1	GO:009031	regulation	7/2606	33/23843	0.062212	0.504226	0.479464	Cdk5/Cib1/
GO_BP_m1	GO:005077	regulation	28/2606	190/23843	0.062391	0.504226	0.479464	Aatk/Ache/
GO_BP_m1	GO:000665	glyceropho	30/2606	206/23843	0.062853	0.504226	0.479464	Tmem269/
GO_BP_m1	GO:003019	extracellula	32/2606	222/23843	0.063023	0.504226	0.479464	2300002M
GO_BP_m1	GO:000183	embryonic	23/2606	151/23843	0.063197	0.504226	0.479464	Abl2/Adm/
GO_BP_m1	GO:005189	positive re	15/2606	90/23843	0.063305	0.504226	0.479464	Adam8/C1
GO_BP_m1	GO:190350	liposaccha	15/2606	90/23843	0.063305	0.504226	0.479464	Abo/Aoah/
GO_BP_m1	GO:003031	osteoclast	17/2606	105/23843	0.063336	0.504226	0.479464	Adam8/An
GO_BP_m1	GO:000663	fatty acid	12/2606	68/23843	0.063488	0.504226	0.479464	Abcd3/Aca
GO_BP_m1	GO:000763	visual beha	12/2606	68/23843	0.063488	0.504226	0.479464	Abl2/Adam
GO_BP_m1	GO:003248	Rab protei	12/2606	68/23843	0.063488	0.504226	0.479464	Aatk/Denn
GO_BP_m1	GO:004230	regulation	12/2606	68/23843	0.063488	0.504226	0.479464	Cdk1/Cdk
GO_BP_m1	GO:009732	response t	12/2606	68/23843	0.063488	0.504226	0.479464	Blm/Cdh1/
GO_BP_m1	GO:190121	regulation	47/2606	344/23843	0.063954	0.504226	0.479464	Adam8/Aif
GO_BP_m1	GO:003596	response t	20/2606	128/23843	0.063979	0.504226	0.479464	Atf3/Bok/C
GO_BP_m1	GO:001082	regulation	8/2606	40/23843	0.06464	0.504226	0.479464	Chmp1b/K
GO_BP_m1	GO:001088	regulation	8/2606	40/23843	0.06464	0.504226	0.479464	Cd36/Fitm
GO_BP_m1	GO:003273	positive re	8/2606	40/23843	0.06464	0.504226	0.479464	5730559C1
GO_BP_m1	GO:003806	p38MAPK	8/2606	40/23843	0.06464	0.504226	0.479464	Cav3/Ezr/H
GO_BP_m1	GO:004645	icosanoid	8/2606	40/23843	0.06464	0.504226	0.479464	Alox12/Alo
GO_BP_m1	GO:000758	excretion	10/2606	54/23843	0.065463	0.504226	0.479464	Adora1/Ad
GO_BP_m1	GO:009858	cellular res	9/2606	47/23843	0.065552	0.504226	0.479464	Ddx60/Dhx
GO_BP_m1	GO:190459	positive re	9/2606	47/23843	0.065552	0.504226	0.479464	Cdk1/Hyal
GO_BP_m1	GO:000920	purine ribo	35/2606	247/23843	0.065829	0.504226	0.479464	Atp5a1/At
GO_BP_m1	GO:000999	response t	52/2606	386/23843	0.065937	0.504226	0.479464	Aoc1/Arsb/
GO_BP_m1	GO:000176	establishm	3/2606	9/23843	0.066155	0.504226	0.479464	Dock8/Flot
GO_BP_m1	GO:000176	establishm	3/2606	9/23843	0.066155	0.504226	0.479464	Dock8/Flot
GO_BP_m1	GO:000721	serotonin	3/2606	9/23843	0.066155	0.504226	0.479464	Htr1a/Htr5
GO_BP_m1	GO:000911	purine nuc	3/2606	9/23843	0.066155	0.504226	0.479464	Aprt/Mthf
GO_BP_m1	GO:001633	calcium-in	3/2606	9/23843	0.066155	0.504226	0.479464	Cadm1/Cl
GO_BP_m1	GO:003022	neutrophil	3/2606	9/23843	0.066155	0.504226	0.479464	Csf3/Fasn/
GO_BP_m1	GO:003409	regulation	3/2606	9/23843	0.066155	0.504226	0.479464	H2afy/Naa
GO_BP_m1	GO:003439	telomere t	3/2606	9/23843	0.066155	0.504226	0.479464	Terb1/Lem
GO_BP_m1	GO:004358	tongue m	3/2606	9/23843	0.066155	0.504226	0.479464	Hdac1/Hd
GO_BP_m1	GO:004611	nucleobase	3/2606	9/23843	0.066155	0.504226	0.479464	Dpyd/Dpy
GO_BP_m1	GO:004651	sphingosin	3/2606	9/23843	0.066155	0.504226	0.479464	Acer3/Asa
GO_BP_m1	GO:004824	epinephrin	3/2606	9/23843	0.066155	0.504226	0.479464	Cartpt/Ly6

GO_BP_m1	GO:005093	regulation	3/2606	9/23843	0.066155	0.504226	0.479464	Adamts9/B
GO_BP_m1	GO:005102	chiasma as	3/2606	9/23843	0.066155	0.504226	0.479464	Msh4/Sycp
GO_BP_m1	GO:005125	spindle mic	3/2606	9/23843	0.066155	0.504226	0.479464	Kif23/Kif4/
GO_BP_m1	GO:00514	response t	3/2606	9/23843	0.066155	0.504226	0.479464	Adh5/Gclm
GO_BP_m1	GO:00604	positive re	3/2606	9/23843	0.066155	0.504226	0.479464	Ednrb/P2ry
GO_BP_m1	GO:007201	glomerular	3/2606	9/23843	0.066155	0.504226	0.479464	Jag1/Lamb
GO_BP_m1	GO:007231	glomerular	3/2606	9/23843	0.066155	0.504226	0.479464	Jag1/Lamb
GO_BP_m1	GO:007267	multinucle	3/2606	9/23843	0.066155	0.504226	0.479464	Adam8/Os
GO_BP_m1	GO:009052	sphingolipi	3/2606	9/23843	0.066155	0.504226	0.479464	Ezr/Spns2/
GO_BP_m1	GO:00971	postsynapt	3/2606	9/23843	0.066155	0.504226	0.479464	Cdh2/Lrp4/
GO_BP_m1	GO:00986	G-protein	3/2606	9/23843	0.066155	0.504226	0.479464	Htr1a/Htr5
GO_BP_m1	GO:190016	negative re	3/2606	9/23843	0.066155	0.504226	0.479464	C1qtnf3/Pt
GO_BP_m1	GO:190301	negative re	3/2606	9/23843	0.066155	0.504226	0.479464	Cldn18/Rfl
GO_BP_m1	GO:200064	regulation	3/2606	9/23843	0.066155	0.504226	0.479464	Anxa2/Pcsk
GO_BP_m1	GO:004583	positive re	22/2606	144/23843	0.066235	0.504226	0.479464	Angptl3/Av
GO_BP_m1	GO:003313	regulation	23/2606	152/23843	0.067087	0.504226	0.479464	Atp2b4/Bc
GO_BP_m1	GO:000692	cellular cor	6/2606	27/23843	0.067297	0.504226	0.479464	Aifm1/Bok/
GO_BP_m1	GO:003081	negative re	6/2606	27/23843	0.067297	0.504226	0.479464	Adra1d/Ak
GO_BP_m1	GO:003533	peptidyl-ty	6/2606	27/23843	0.067297	0.504226	0.479464	Dusp3/Dus
GO_BP_m1	GO:005112	RNA polym	6/2606	27/23843	0.067297	0.504226	0.479464	Cand1/Gtf2
GO_BP_m1	GO:007026	necroptotic	6/2606	27/23843	0.067297	0.504226	0.479464	Bok/Casp8/
GO_BP_m1	GO:009031	positive re	6/2606	27/23843	0.067297	0.504226	0.479464	Cdk5/Cib1/
GO_BP_m1	GO:005138	response t	13/2606	76/23843	0.067607	0.504226	0.479464	Alpl/Bche/
GO_BP_m1	GO:00066	protein im	24/2606	160/23843	0.067783	0.504226	0.479464	1700123L1
GO_BP_m1	GO:007083	divalent m	59/2606	445/23843	0.06804	0.504226	0.479464	Adcyap1r1/
GO_BP_m1	GO:000184	neural tube	20/2606	129/23843	0.068274	0.504226	0.479464	Abl2/Adm/
GO_BP_m1	GO:000912	purine nuc	35/2606	248/23843	0.06891	0.504226	0.479464	Adss/Atp5a
GO_BP_m1	GO:001936	pyridine nu	21/2606	137/23843	0.069421	0.504226	0.479464	Bpgm/Eno
GO_BP_m1	GO:190595	regulation	21/2606	137/23843	0.069421	0.504226	0.479464	Abca12/Ar
GO_BP_m1	GO:001081	positive re	18/2606	114/23843	0.069933	0.504226	0.479464	Calr/Ccl28/
GO_BP_m1	GO:004886	stem cell d	14/2606	84/23843	0.071051	0.504226	0.479464	Cfl1/Ednrb/
GO_BP_m1	GO:007189	DNA biosy	23/2606	153/23843	0.071139	0.504226	0.479464	Ankrd1/Atr
GO_BP_m1	GO:004542	regulation	11/2606	62/23843	0.071239	0.504226	0.479464	Atp2b4/Ca
GO_BP_m1	GO:009027	negative re	11/2606	62/23843	0.071239	0.504226	0.479464	Cartpt/Crh
GO_BP_m1	GO:190126	carbohydra	11/2606	62/23843	0.071239	0.504226	0.479464	Abcb1a/Ac
GO_BP_m1	GO:002184	cell prolifer	7/2606	34/23843	0.071269	0.504226	0.479464	Arx/Dct/Dc
GO_BP_m1	GO:003111	regulation	7/2606	34/23843	0.071269	0.504226	0.479464	Cib1/Fgf13
GO_BP_m1	GO:003323	regulation	7/2606	34/23843	0.071269	0.504226	0.479464	Abat/Atp2b
GO_BP_m1	GO:199008	response t	7/2606	34/23843	0.071269	0.504226	0.479464	Cib1/E2f1/
GO_BP_m1	GO:199009	cellular res	7/2606	34/23843	0.071269	0.504226	0.479464	Cib1/E2f1/
GO_BP_m1	GO:000046	maturation	5/2606	21/23843	0.071421	0.504226	0.479464	Eri1/Exosc9
GO_BP_m1	GO:000178	neutrophil	5/2606	21/23843	0.071421	0.504226	0.479464	Hcar2/Ifng/
GO_BP_m1	GO:001655	mRNA mod	5/2606	21/23843	0.071421	0.504226	0.479464	Virma/Apo
GO_BP_m1	GO:003204	mitochond	5/2606	21/23843	0.071421	0.504226	0.479464	Flcn/Lig3/P
GO_BP_m1	GO:003438	low-densit	5/2606	21/23843	0.071421	0.504226	0.479464	Anxa2/Cd3
GO_BP_m1	GO:003952	cytoplasmi	5/2606	21/23843	0.071421	0.504226	0.479464	Ddx60/Dhx
GO_BP_m1	GO:004205	regulation	5/2606	21/23843	0.071421	0.504226	0.479464	Abat/Htr1a
GO_BP_m1	GO:004664	positive re	5/2606	21/23843	0.071421	0.504226	0.479464	Blm/Cd80/

GO_BP_m1	GO:00707З	histone H3	5/2606	21/23843	0.071421	0.504226	0.479464	Ezh1/H2afy
GO_BP_m1	GO:007211	cell prolifer	5/2606	21/23843	0.071421	0.504226	0.479464	Flcn/Ifng/M
GO_BP_m1	GO:190012	regulation	5/2606	21/23843	0.071421	0.504226	0.479464	Anxa2/Gre
GO_BP_m1	GO:000628	nucleotide-	10/2606	55/23843	0.072529	0.504226	0.479464	Cul4a/Dclre
GO_BP_m1	GO:000021	meiotic spi	4/2606	15/23843	0.072741	0.504226	0.479464	Washc5/Fb
GO_BP_m1	GO:000286	negative re	4/2606	15/23843	0.072741	0.504226	0.479464	Gpx1/Gpx2
GO_BP_m1	GO:000737	segment sp	4/2606	15/23843	0.072741	0.504226	0.479464	Irx2/Meox2
GO_BP_m1	GO:000908	branched-	4/2606	15/23843	0.072741	0.504226	0.479464	Bcat2/Bckc
GO_BP_m1	GO:001569	quaternary	4/2606	15/23843	0.072741	0.504226	0.479464	Slc22a1/Slc
GO_BP_m1	GO:003073	sequesterin	4/2606	15/23843	0.072741	0.504226	0.479464	Fitm1/Osbp
GO_BP_m1	GO:003165	regulation	4/2606	15/23843	0.072741	0.504226	0.479464	Abat/Ednrb
GO_BP_m1	GO:003222	regulation	4/2606	15/23843	0.072741	0.504226	0.479464	Htr6/Ifng/T
GO_BP_m1	GO:003253	regulation	4/2606	15/23843	0.072741	0.504226	0.479464	Atp8b1/Ezr
GO_BP_m1	GO:003268	negative re	4/2606	15/23843	0.072741	0.504226	0.479464	Cactin/Nm
GO_BP_m1	GO:003644	neuronal st	4/2606	15/23843	0.072741	0.504226	0.479464	Dct/Dock7/
GO_BP_m1	GO:004398	histone H4	4/2606	15/23843	0.072741	0.504226	0.479464	Kansl1/Kan
GO_BP_m1	GO:004398	histone H4	4/2606	15/23843	0.072741	0.504226	0.479464	Kansl1/Kan
GO_BP_m1	GO:004479	positive reg	4/2606	15/23843	0.072741	0.504226	0.479464	Cfl1/Nucks
GO_BP_m1	GO:004654	saliva secre	4/2606	15/23843	0.072741	0.504226	0.479464	Chrm1/Chr
GO_BP_m1	GO:004830	organelle i	4/2606	15/23843	0.072741	0.504226	0.479464	Cdk1/Gbf1
GO_BP_m1	GO:005104	positive reg	4/2606	15/23843	0.072741	0.504226	0.479464	Adam8/Ifng
GO_BP_m1	GO:005505	neuroblast	4/2606	15/23843	0.072741	0.504226	0.479464	Dct/Dock7/
GO_BP_m1	GO:007252	pyrimidine-	4/2606	15/23843	0.072741	0.504226	0.479464	Dpyd/Dpys
GO_BP_m1	GO:190172	regulation	4/2606	15/23843	0.072741	0.504226	0.479464	Flcn/Ifng/M
GO_BP_m1	GO:190396	negative re	4/2606	15/23843	0.072741	0.504226	0.479464	Arl6ip5/Os
GO_BP_m1	GO:009747	synaptic ve	20/2606	130/23843	0.072762	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:000628	base-excisi	8/2606	41/23843	0.072959	0.504226	0.479464	Lig3/Mpg/
GO_BP_m1	GO:000650	membrane	8/2606	41/23843	0.072959	0.504226	0.479464	Adam8/Ap
GO_BP_m1	GO:004678	regulation	8/2606	41/23843	0.072959	0.504226	0.479464	Ccl4/Hdac1
GO_BP_m1	GO:007147	cellular resp	8/2606	41/23843	0.072959	0.504226	0.479464	Mir7b/Mir9
GO_BP_m1	GO:000257	myeloid leu	30/2606	209/23843	0.073042	0.504226	0.479464	Adam8/An
GO_BP_m1	GO:005122	spindle ass	17/2606	107/23843	0.073075	0.504226	0.479464	Cdc20/Chr
GO_BP_m1	GO:004340	regulation	40/2606	290/23843	0.073105	0.504226	0.479464	5730559C1
GO_BP_m1	GO:000276	negative re	9/2606	48/23843	0.073209	0.504226	0.479464	Cartpt/Cldr
GO_BP_m1	GO:000712	synapsis	9/2606	48/23843	0.073209	0.504226	0.479464	Terb1/Ccne
GO_BP_m1	GO:003127	regulation	9/2606	48/23843	0.073209	0.504226	0.479464	Adra1d/Ak
GO_BP_m1	GO:004512	regulation	9/2606	48/23843	0.073209	0.504226	0.479464	Adam8/Ca
GO_BP_m1	GO:004866	negative re	9/2606	48/23843	0.073209	0.504226	0.479464	Cav1/Ifng/
GO_BP_m1	GO:006100	cell differen	9/2606	48/23843	0.073209	0.504226	0.479464	Basp1/Gdn
GO_BP_m1	GO:001003	response to	58/2606	439/23843	0.073586	0.504226	0.479464	Abat/Aoc1/
GO_BP_m1	GO:004688	negative re	15/2606	92/23843	0.073925	0.504226	0.479464	Adora1/Ca
GO_BP_m1	GO:000609	glycolytic p	12/2606	70/23843	0.075978	0.504226	0.479464	Bpgm/Eno3
GO_BP_m1	GO:200024	positive reg	12/2606	70/23843	0.075978	0.504226	0.479464	Cib1/Dmrt1
GO_BP_m1	GO:009719	intrinsic ap	40/2606	291/23843	0.076166	0.504226	0.479464	Aifm1/Arl6
GO_BP_m1	GO:002240	negative re	25/2606	170/23843	0.076275	0.504226	0.479464	Abat/Abl2/
GO_BP_m1	GO:003209	positive reg	16/2606	100/23843	0.076317	0.504226	0.479464	Abl2/Anxa2
GO_BP_m1	GO:009772	sperm mot	16/2606	100/23843	0.076317	0.504226	0.479464	Atp2b4/Bb
GO_BP_m1	GO:000189	tissue hom	31/2606	218/23843	0.076525	0.504226	0.479464	5730559C1

GO_BP_m1	GO:000991	hormone t	48/2606	357/23843	0.076561	0.504226	0.479464	Abat/Abcb
GO_BP_m1	GO:000718	adenylate c	27/2606	186/23843	0.076711	0.504226	0.479464	Adcy4/Adc
GO_BP_m1	GO:004244	hormone n	29/2606	202/23843	0.076768	0.504226	0.479464	Ache/Adh1
GO_BP_m1	GO:006004	heart contr	29/2606	202/23843	0.076768	0.504226	0.479464	Adm/Adora
GO_BP_m1	GO:005109	positive reg	28/2606	194/23843	0.076782	0.504226	0.479464	Abl2/Anxa2
GO_BP_m1	GO:004247	odontogen	14/2606	85/23843	0.076899	0.504226	0.479464	Ambn/Foxc
GO_BP_m1	GO:000763	feeding be	20/2606	131/23843	0.077445	0.504226	0.479464	Aoc3/Cartp
GO_BP_m1	GO:190156	fatty acid d	20/2606	131/23843	0.077445	0.504226	0.479464	Akr1c12/Al
GO_BP_m1	GO:000606	alcohol me	37/2606	267/23843	0.077803	0.504226	0.479464	Acer3/Adcy
GO_BP_m1	GO:000073	DNA synth	6/2606	28/23843	0.078073	0.504226	0.479464	Pcna/Pole/
GO_BP_m1	GO:000692	substrate-d	6/2606	28/23843	0.078073	0.504226	0.479464	Abl2/Adam
GO_BP_m1	GO:002151	spinal cord	6/2606	28/23843	0.078073	0.504226	0.479464	Dbx1/Dll4/
GO_BP_m1	GO:003129	replication	6/2606	28/23843	0.078073	0.504226	0.479464	Blm/Fbxo1
GO_BP_m1	GO:004567	negative re	6/2606	28/23843	0.078073	0.504226	0.479464	Cartpt/Cldn
GO_BP_m1	GO:006121	regulation	6/2606	28/23843	0.078073	0.504226	0.479464	Gdnf/Lgr4/
GO_BP_m1	GO:004227	purine nuc	11/2606	63/23843	0.078183	0.504226	0.479464	Acpp/Adk/
GO_BP_m1	GO:001046	regulation	17/2606	108/23843	0.078298	0.504226	0.479464	Adora1/Ca
GO_BP_m1	GO:007200	nephron ep	17/2606	108/23843	0.078298	0.504226	0.479464	Basp1/Fgf1
GO_BP_m1	GO:000919	ribonucleos	35/2606	251/23843	0.078759	0.504226	0.479464	Atp5a1/Atp
GO_BP_m1	GO:002154	pallium dev	22/2606	147/23843	0.079156	0.504226	0.479464	Arx/Bbs2/B
GO_BP_m1	GO:003260	type I inter	13/2606	78/23843	0.079866	0.504226	0.479464	Cactin/Dhx
GO_BP_m1	GO:004603	ADP metab	13/2606	78/23843	0.079866	0.504226	0.479464	Bpgm/Eno3
GO_BP_m1	GO:007022	regulation	13/2606	78/23843	0.079866	0.504226	0.479464	Adam8/Blm
GO_BP_m1	GO:200105	reactive nit	13/2606	78/23843	0.079866	0.504226	0.479464	Atp2b4/Ca
GO_BP_m1	GO:001491	positive reg	10/2606	56/23843	0.080054	0.504226	0.479464	Dock4/Doc
GO_BP_m1	GO:190054	regulation	24/2606	163/23843	0.080171	0.504226	0.479464	Adm/Adra1
GO_BP_m1	GO:003025	lipid modif	29/2606	203/23843	0.08061	0.504226	0.479464	Abcd3/Abc
GO_BP_m1	GO:005087	positive reg	26/2606	179/23843	0.080648	0.504226	0.479464	Adam8/Ad
GO_BP_m1	GO:000600	glucose me	27/2606	187/23843	0.080724	0.504226	0.479464	Atf3/Bpgm
GO_BP_m1	GO:000009	sulfur amin	7/2606	35/23843	0.081066	0.504226	0.479464	Ahcyl2/Api
GO_BP_m1	GO:000761	long-term	7/2606	35/23843	0.081066	0.504226	0.479464	Cpeb3/Gria
GO_BP_m1	GO:200040	positive reg	7/2606	35/23843	0.081066	0.504226	0.479464	Adam8/Ccl
GO_BP_m1	GO:000602	aminoglyca	9/2606	49/23843	0.081394	0.504226	0.479464	B3gnt3/B3g
GO_BP_m1	GO:001657	histone ph	9/2606	49/23843	0.081394	0.504226	0.479464	Cdk1/Cdk2
GO_BP_m1	GO:001714	stem cell d	9/2606	49/23843	0.081394	0.504226	0.479464	Dct/Dock7/
GO_BP_m1	GO:004614	pigment bi	9/2606	49/23843	0.081394	0.504226	0.479464	Aprt/Cox15
GO_BP_m1	GO:003238	regulation	55/2606	417/23843	0.081463	0.504226	0.479464	Anxa2/Arih
GO_BP_m1	GO:000095	mitochond	8/2606	42/23843	0.081896	0.504226	0.479464	Fastkd1/Gr
GO_BP_m1	GO:003304	negative re	8/2606	42/23843	0.081896	0.504226	0.479464	Klhl22/Mac
GO_BP_m1	GO:004207	intraciliary	8/2606	42/23843	0.081896	0.504226	0.479464	Ift22/Ift27/
GO_BP_m1	GO:004241	dopamine	8/2606	42/23843	0.081896	0.504226	0.479464	Abat/Gch1
GO_BP_m1	GO:005189	negative re	8/2606	42/23843	0.081896	0.504226	0.479464	Cib1/Drd3/
GO_BP_m1	GO:009772	calcineurin	8/2606	42/23843	0.081896	0.504226	0.479464	Akap6/Atp
GO_BP_m1	GO:190138	regulation	8/2606	42/23843	0.081896	0.504226	0.479464	Adra1d/Ca
GO_BP_m1	GO:003596	cellular res	16/2606	101/23843	0.081911	0.504226	0.479464	Atf3/Bok/C
GO_BP_m1	GO:000761	memory	20/2606	132/23843	0.082324	0.504226	0.479464	Cpeb3/Fen
GO_BP_m1	GO:007188	leukocyte a	20/2606	132/23843	0.082324	0.504226	0.479464	Adam8/Blm
GO_BP_m1	GO:004592	positive reg	40/2606	293/23843	0.082554	0.504226	0.479464	Adnp2/Aka

GO_BP_m1	GO:00508	regulation	40/2606	293/23843	0.082554	0.504226	0.479464	Adam8/Ad
GO_BP_m1	GO:00675	ATP genera	12/2606	71/23843	0.082771	0.504226	0.479464	Bpgm/Eno
GO_BP_m1	GO:00099	dorsal/vent	17/2606	109/23843	0.083761	0.504226	0.479464	Dbx1/Dll4/
GO_BP_m1	GO:00440	regulation	17/2606	109/23843	0.083761	0.504226	0.479464	Abat/Abcb
GO_BP_m1	GO:19053	regulation	17/2606	109/23843	0.083761	0.504226	0.479464	Abl2/Cav3/
GO_BP_m1	GO:00513	regulation	22/2606	148/23843	0.083814	0.504226	0.479464	Ahctf1/Ank
GO_BP_m1	GO:00181	peptidyl-ty	42/2606	310/23843	0.084307	0.504226	0.479464	Aatk/Abi1/
GO_BP_m1	GO:00488	stem cell d	30/2606	212/23843	0.084325	0.504226	0.479464	Bche/Cfl1/
GO_BP_m1	GO:00068	serotonin t	5/2606	22/23843	0.084463	0.504226	0.479464	Hrh3/Htr1
GO_BP_m1	GO:00072	nitric oxide	5/2606	22/23843	0.084463	0.504226	0.479464	Atp2b4/Cd
GO_BP_m1	GO:00182	peptidyl-gl	5/2606	22/23843	0.084463	0.504226	0.479464	Naa10/Na
GO_BP_m1	GO:00328	negative re	5/2606	22/23843	0.084463	0.504226	0.479464	Ccl4/Hdac
GO_BP_m1	GO:00341	positive re	5/2606	22/23843	0.084463	0.504226	0.479464	Cav1/Ptpn
GO_BP_m1	GO:00420	regulation	5/2606	22/23843	0.084463	0.504226	0.479464	Abat/Htr1
GO_BP_m1	GO:00506	negative re	5/2606	22/23843	0.084463	0.504226	0.479464	Dhx58/Npl
GO_BP_m1	GO:00508	negative re	5/2606	22/23843	0.084463	0.504226	0.479464	Btnl2/Dus
GO_BP_m1	GO:00714	cellular res	5/2606	22/23843	0.084463	0.504226	0.479464	Cd36/Fbln
GO_BP_m1	GO:00714	cellular res	5/2606	22/23843	0.084463	0.504226	0.479464	Cd36/Fbln
GO_BP_m1	GO:00718	cellular res	5/2606	22/23843	0.084463	0.504226	0.479464	Akap6/Atp
GO_BP_m1	GO:00713	cellular res	25/2606	172/23843	0.084815	0.504226	0.479464	Ankrd1/Ca
GO_BP_m1	GO:00459	negative re	36/2606	261/23843	0.085232	0.504226	0.479464	Aatk/Adip
GO_BP_m1	GO:00075	embryo im	11/2606	64/23843	0.085536	0.504226	0.479464	Arhgdib/A
GO_BP_m1	GO:00090	glutamine	11/2606	64/23843	0.085536	0.504226	0.479464	Dglucy/Ald
GO_BP_m1	GO:00217	hippocam	11/2606	64/23843	0.085536	0.504226	0.479464	Bbs2/Btg2/
GO_BP_m1	GO:00313	negative re	11/2606	64/23843	0.085536	0.504226	0.479464	Cav1/Svbp
GO_BP_m1	GO:00468	positive re	11/2606	64/23843	0.085536	0.504226	0.479464	Cdk1/Hyal
GO_BP_m1	GO:199054	mitochond	11/2606	64/23843	0.085536	0.504226	0.479464	Atp5o/Grp
GO_BP_m1	GO:000157	microtubul	15/2606	94/23843	0.085652	0.504226	0.479464	Bbs2/Cc2d
GO_BP_m1	GO:00019	regulation	15/2606	94/23843	0.085652	0.504226	0.479464	Arg1/Cacti
GO_BP_m1	GO:00323	positive re	35/2606	253/23843	0.085842	0.504226	0.479464	Anxa2/Arih
GO_BP_m1	GO:00507	regulation	34/2606	245/23843	0.086421	0.504226	0.479464	Adora1/Ca
GO_BP_m1	GO:004327	response t	13/2606	79/23843	0.086494	0.504226	0.479464	Abat/Adra
GO_BP_m1	GO:000001	single stran	3/2606	10/23843	0.087056	0.504226	0.479464	Aplf/Aptx/
GO_BP_m1	GO:00065	aspartate	3/2606	10/23843	0.087056	0.504226	0.479464	Adss/Ddo/
GO_BP_m1	GO:00104	negative re	3/2606	10/23843	0.087056	0.504226	0.479464	Fkbp1b/Rn
GO_BP_m1	GO:00140	regulation	3/2606	10/23843	0.087056	0.504226	0.479464	Hrh3/Htr1
GO_BP_m1	GO:00158	amino-aci	3/2606	10/23843	0.087056	0.504226	0.479464	Slc22a5/Sl
GO_BP_m1	GO:00158	nucleoside	3/2606	10/23843	0.087056	0.504226	0.479464	Adora1/Slc
GO_BP_m1	GO:00162	gap junctic	3/2606	10/23843	0.087056	0.504226	0.479464	Cav1/Gjb2/
GO_BP_m1	GO:00303	fructose 1,	3/2606	10/23843	0.087056	0.504226	0.479464	Ifng/Pfkl/Ti
GO_BP_m1	GO:003162	regulation	3/2606	10/23843	0.087056	0.504226	0.479464	Ednrb/Ptgs
GO_BP_m1	GO:003222	positive re	3/2606	10/23843	0.087056	0.504226	0.479464	Ifng/Tac1/
GO_BP_m1	GO:00332	regulation	3/2606	10/23843	0.087056	0.504226	0.479464	Cdc7/Dach
GO_BP_m1	GO:003564	endosome	3/2606	10/23843	0.087056	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:00364	PERK-med	3/2606	10/23843	0.087056	0.504226	0.479464	Bok/Nck2/
GO_BP_m1	GO:00434	endosome	3/2606	10/23843	0.087056	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:00439	negative re	3/2606	10/23843	0.087056	0.504226	0.479464	Ccl4/Hdac
GO_BP_m1	GO:00465	sphingoid	3/2606	10/23843	0.087056	0.504226	0.479464	Acer3/Asa

GO_BP_m1	GO:004875	pigment gr	3/2606	10/23843	0.087056	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:005100	negative re	3/2606	10/23843	0.087056	0.504226	0.479464	Atp2b4/Ca
GO_BP_m1	GO:007024	negative re	3/2606	10/23843	0.087056	0.504226	0.479464	Blm/Jak3/P
GO_BP_m1	GO:007067	response tc	3/2606	10/23843	0.087056	0.504226	0.479464	Cldn1/Ifng/
GO_BP_m1	GO:007207	loop of He	3/2606	10/23843	0.087056	0.504226	0.479464	Irx2/Jag1/F
GO_BP_m1	GO:007220	cell prolifer	3/2606	10/23843	0.087056	0.504226	0.479464	Myc/Osr1/
GO_BP_m1	GO:190001	negative re	3/2606	10/23843	0.087056	0.504226	0.479464	D1Ertd622
GO_BP_m1	GO:190004	regulation	3/2606	10/23843	0.087056	0.504226	0.479464	Abl2/Btnl2/
GO_BP_m1	GO:190019	regulation	3/2606	10/23843	0.087056	0.504226	0.479464	Npr2/Ppp2
GO_BP_m1	GO:190207	response tc	3/2606	10/23843	0.087056	0.504226	0.479464	Mapk13/Rr
GO_BP_m1	GO:190344	protein loc	3/2606	10/23843	0.087056	0.504226	0.479464	Bbs2/Tulp1
GO_BP_m1	GO:005070	negative re	20/2606	133/23843	0.087403	0.504226	0.479464	C1qtnf3/Dr
GO_BP_m1	GO:005105	negative re	20/2606	133/23843	0.087403	0.504226	0.479464	Ankrd1/Ap
GO_BP_m1	GO:004560	positive reg	10/2606	57/23843	0.088043	0.504226	0.479464	Adig/Ccdc3
GO_BP_m1	GO:004354	positive reg	30/2606	213/23843	0.088334	0.504226	0.479464	Arhgef7/Bc
GO_BP_m1	GO:190547	regulation	22/2606	149/23843	0.088651	0.504226	0.479464	Appl1/Cam
GO_BP_m1	GO:000301	heart proce	29/2606	205/23843	0.088682	0.504226	0.479464	Adm/Adora
GO_BP_m1	GO:000627	DNA strand	4/2606	16/23843	0.088925	0.504226	0.479464	Fen1/Lig3/
GO_BP_m1	GO:000630	apoptotic [	4/2606	16/23843	0.088925	0.504226	0.479464	Aifm1/Dffa
GO_BP_m1	GO:000647	N-terminal	4/2606	16/23843	0.088925	0.504226	0.479464	Kat2b/Naa
GO_BP_m1	GO:000674	ubiquinone	4/2606	16/23843	0.088925	0.504226	0.479464	Coq10b/Co
GO_BP_m1	GO:001022	response tc	4/2606	16/23843	0.088925	0.504226	0.479464	Cdkn1a/Hy
GO_BP_m1	GO:003210	negative re	4/2606	16/23843	0.088925	0.504226	0.479464	Bbs2/Cartp
GO_BP_m1	GO:003210	negative re	4/2606	16/23843	0.088925	0.504226	0.479464	Bbs2/Cartp
GO_BP_m1	GO:003249	response tc	4/2606	16/23843	0.088925	0.504226	0.479464	5730559C1
GO_BP_m1	GO:003438	lipid particl	4/2606	16/23843	0.088925	0.504226	0.479464	Fitm1/Plin5
GO_BP_m1	GO:004308	penile erec	4/2606	16/23843	0.088925	0.504226	0.479464	Avpr1a/Edr
GO_BP_m1	GO:004693	pore comp	4/2606	16/23843	0.088925	0.504226	0.479464	Ahctf1/Cct3
GO_BP_m1	GO:004807	regulation	4/2606	16/23843	0.088925	0.504226	0.479464	Adamts9/B
GO_BP_m1	GO:006064	mammary	4/2606	16/23843	0.088925	0.504226	0.479464	Irf6/Lats1/S
GO_BP_m1	GO:007267	lamellipodi	4/2606	16/23843	0.088925	0.504226	0.479464	Abi1/Enpp2
GO_BP_m1	GO:009750	sialylation	4/2606	16/23843	0.088925	0.504226	0.479464	St3gal3/St6
GO_BP_m1	GO:190166	quinone bi	4/2606	16/23843	0.088925	0.504226	0.479464	Coq10b/Co
GO_BP_m1	GO:190188	positive reg	4/2606	16/23843	0.088925	0.504226	0.479464	Cfl1/Htr1a/
GO_BP_m1	GO:200124	positive reg	4/2606	16/23843	0.088925	0.504226	0.479464	Jak3/Nf1/P
GO_BP_m1	GO:001081	regulation	27/2606	189/23843	0.089171	0.504226	0.479464	Bcar1/Bcas
GO_BP_m1	GO:190303	positive reg	27/2606	189/23843	0.089171	0.504226	0.479464	Adam8/Ad
GO_BP_m1	GO:000645	protein fold	26/2606	181/23843	0.089292	0.504226	0.479464	Calr/Canx/
GO_BP_m1	GO:001936	pyridine nu	14/2606	87/23843	0.089507	0.504226	0.479464	Bpgm/Eno3
GO_BP_m1	GO:005192	regulation	35/2606	254/23843	0.089541	0.504226	0.479464	Adcyap1r1/
GO_BP_m1	GO:000047	maturation	6/2606	29/23843	0.089761	0.504226	0.479464	Ftsj3/Nop2
GO_BP_m1	GO:000155	oocyte mat	6/2606	29/23843	0.089761	0.504226	0.479464	Washc5/Fb
GO_BP_m1	GO:003080	negative re	6/2606	29/23843	0.089761	0.504226	0.479464	Adra1d/Ak
GO_BP_m1	GO:003243	negative re	6/2606	29/23843	0.089761	0.504226	0.479464	N4bp1/Og
GO_BP_m1	GO:003411	regulation	6/2606	29/23843	0.089761	0.504226	0.479464	Abat/Alox1
GO_BP_m1	GO:004311	regulation	6/2606	29/23843	0.089761	0.504226	0.479464	Adm/Bcr/C
GO_BP_m1	GO:004214	retrograde	12/2606	72/23843	0.089933	0.504226	0.479464	Ankfy1/Gb
GO_BP_m1	GO:005170	multi-orga	12/2606	72/23843	0.089933	0.504226	0.479464	Abl2/Avpr1

GO_BP_m1	GO:00701	chromoso	12/2606	72/23843	0.089933	0.504226	0.479464	Terb1/Ccn
GO_BP_m1	GO:00002	nuclear-tra	9/2606	50/23843	0.090108	0.504226	0.479464	Btg2/Noct
GO_BP_m1	GO:00336	cell adhesi	9/2606	50/23843	0.090108	0.504226	0.479464	Cib1/Epha
GO_BP_m1	GO:190161	organic hy	9/2606	50/23843	0.090108	0.504226	0.479464	Adh1/Adh
GO_BP_m1	GO:00169	antibiotic	18/2606	118/23843	0.09082	0.504226	0.479464	Adh1/Adh
GO_BP_m1	GO:00738	pattern sp	59/2606	454/23843	0.090999	0.504226	0.479464	Abi1/Alx3/
GO_BP_m1	GO:00706	regulation	32/2606	230/23843	0.091421	0.504226	0.479464	Adk/Arg1/
GO_BP_m1	GO:00019	negative re	8/2606	43/23843	0.091449	0.504226	0.479464	Arg1/Cacti
GO_BP_m1	GO:190311	regulation	8/2606	43/23843	0.091449	0.504226	0.479464	Acta2/Aka
GO_BP_m1	GO:190551	macropha	8/2606	43/23843	0.091449	0.504226	0.479464	Cklf/Cxcl17
GO_BP_m1	GO:00107	negative re	48/2606	362/23843	0.091503	0.504226	0.479464	Aatk/Bcar1
GO_BP_m1	GO:004001	positive re	7/2606	36/23843	0.0916	0.504226	0.479464	Foxa2/Gdn
GO_BP_m1	GO:00447	multi-orga	7/2606	36/23843	0.0916	0.504226	0.479464	Ddx60/Dh
GO_BP_m1	GO:00464	neutral lip	7/2606	36/23843	0.0916	0.504226	0.479464	Dgat1/Gpa
GO_BP_m1	GO:00464	acylglycer	7/2606	36/23843	0.0916	0.504226	0.479464	Dgat1/Gpa
GO_BP_m1	GO:00702	protein ho	7/2606	36/23843	0.0916	0.504226	0.479464	Arg1/Clybl
GO_BP_m1	GO:00027	regulation	19/2606	126/23843	0.091877	0.504226	0.479464	Aplf/Arg1/
GO_BP_m1	GO:00432	regulation	15/2606	95/23843	0.091936	0.504226	0.479464	Adcyap1r1
GO_BP_m1	GO:003294	regulation	31/2606	222/23843	0.091969	0.504226	0.479464	Adk/Arg1/
GO_BP_m1	GO:00902	regulation	31/2606	222/23843	0.091969	0.504226	0.479464	Abat/Adk/
GO_BP_m1	GO:000181	positive re	53/2606	404/23843	0.092153	0.504226	0.479464	5730559C1
GO_BP_m1	GO:00725	pyridine-c	21/2606	142/23843	0.093268	0.504226	0.479464	Bpgm/Eno
GO_BP_m1	GO:00319	response t	13/2606	80/23843	0.093456	0.504226	0.479464	Alpl/Bche/
GO_BP_m1	GO:003287	positive re	22/2606	150/23843	0.093666	0.504226	0.479464	5730559C1
GO_BP_m1	GO:004814	regulation	16/2606	103/23843	0.093878	0.504226	0.479464	Anxa2/Cdk
GO_BP_m1	GO:00607	regulation	16/2606	103/23843	0.093878	0.504226	0.479464	Arg1/Cacti
GO_BP_m1	GO:00453	cellular res	23/2606	158/23843	0.093903	0.504226	0.479464	Bnip3/Cdk
GO_BP_m1	GO:007217	epithelial t	23/2606	158/23843	0.093903	0.504226	0.479464	Abl2/Adm/
GO_BP_m1	GO:00091	purine ribo	34/2606	247/23843	0.094092	0.504226	0.479464	Adss/Atp5
GO_BP_m1	GO:001821	peptidyl-ty	42/2606	313/23843	0.094414	0.504226	0.479464	Aatk/Abi1/
GO_BP_m1	GO:00019	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Avpr1a/Dr
GO_BP_m1	GO:00029	positive re	2/2606	5/23843	0.095407	0.504226	0.479464	Il10/Myc
GO_BP_m1	GO:00060	fructose 2,	2/2606	5/23843	0.095407	0.504226	0.479464	Pfkfb1/Tiga
GO_BP_m1	GO:00060	ethanol ca	2/2606	5/23843	0.095407	0.504226	0.479464	Adh1/Adh
GO_BP_m1	GO:000611	fermentati	2/2606	5/23843	0.095407	0.504226	0.479464	Ldha/Tigar
GO_BP_m1	GO:00067	progestero	2/2606	5/23843	0.095407	0.504226	0.479464	Dgkq/Ppar
GO_BP_m1	GO:00072	spermatid	2/2606	5/23843	0.095407	0.504226	0.479464	Dmrtc2/Ift
GO_BP_m1	GO:00074	midgut de	2/2606	5/23843	0.095407	0.504226	0.479464	Ednrb/Smc
GO_BP_m1	GO:00108	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Osbpl8/Pn
GO_BP_m1	GO:00140	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Hrh3/Htr7
GO_BP_m1	GO:00147	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Myh7/Mylk
GO_BP_m1	GO:00158	folic acid tr	2/2606	5/23843	0.095407	0.504226	0.479464	Folr2/Slc46
GO_BP_m1	GO:00162	attachmen	2/2606	5/23843	0.095407	0.504226	0.479464	Pigs/Pigu
GO_BP_m1	GO:00190	transforma	2/2606	5/23843	0.095407	0.504226	0.479464	Hyal2/Myc
GO_BP_m1	GO:00195	L-methioni	2/2606	5/23843	0.095407	0.504226	0.479464	Apip/Enop
GO_BP_m1	GO:00302	dermatan	2/2606	5/23843	0.095407	0.504226	0.479464	Dse/Dsel
GO_BP_m1	GO:00322	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Ptgs2/Snca
GO_BP_m1	GO:00322	activation	2/2606	5/23843	0.095407	0.504226	0.479464	Asph/Stim

GO_BP_m1	GO:003280	low-densit	2/2606	5/23843	0.095407	0.504226	0.479464	Anxa2/Pcsk
GO_BP_m1	GO:003280	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Anxa2/Pcsk
GO_BP_m1	GO:003416	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Ptpn22/Tre
GO_BP_m1	GO:003502	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Arhgap44/
GO_BP_m1	GO:003543	copper ion	2/2606	5/23843	0.095407	0.504226	0.479464	Atp7b/Slc3
GO_BP_m1	GO:003643	maintenanc	2/2606	5/23843	0.095407	0.504226	0.479464	Foxc1/Gcnt
GO_BP_m1	GO:004212	nitrate met	2/2606	5/23843	0.095407	0.504226	0.479464	Por/Suox
GO_BP_m1	GO:004290	xenobiotic	2/2606	5/23843	0.095407	0.504226	0.479464	Abcc3/Slc2
GO_BP_m1	GO:004483	cell quiesce	2/2606	5/23843	0.095407	0.504226	0.479464	Dek/Nanos
GO_BP_m1	GO:004485	plasma me	2/2606	5/23843	0.095407	0.504226	0.479464	Cav1/Cav3
GO_BP_m1	GO:004485	plasma me	2/2606	5/23843	0.095407	0.504226	0.479464	Cav1/Cav3
GO_BP_m1	GO:004563	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Adamts9/K
GO_BP_m1	GO:004698	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Eif2ak1/Prr
GO_BP_m1	GO:004838	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Aldh1a3/As
GO_BP_m1	GO:004855	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Cav1/Nr1h
GO_BP_m1	GO:005166	establishm	2/2606	5/23843	0.095407	0.504226	0.479464	Ezr/Pafah1
GO_BP_m1	GO:005511	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Adora1/Zc3
GO_BP_m1	GO:006153	glutamate	2/2606	5/23843	0.095407	0.504226	0.479464	Nf1/Pak1
GO_BP_m1	GO:007042	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Peli3/Ptpn2
GO_BP_m1	GO:007043	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Peli3/Ptpn2
GO_BP_m1	GO:007122	cellular res	2/2606	5/23843	0.095407	0.504226	0.479464	Nod1/Ptpn
GO_BP_m1	GO:007160	macrophag	2/2606	5/23843	0.095407	0.504226	0.479464	Mefv/Trpv4
GO_BP_m1	GO:007165	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Ticam2/Trp
GO_BP_m1	GO:007169	maintenanc	2/2606	5/23843	0.095407	0.504226	0.479464	Dand5/Fbn
GO_BP_m1	GO:007184	TNFSF11-r	2/2606	5/23843	0.095407	0.504226	0.479464	Cldn18/Tnf
GO_BP_m1	GO:007192	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Hdac8/Wap
GO_BP_m1	GO:007204	proximal/d	2/2606	5/23843	0.095407	0.504226	0.479464	Irx2/Osr1
GO_BP_m1	GO:007208	specificatio	2/2606	5/23843	0.095407	0.504226	0.479464	Irx2/Osr1
GO_BP_m1	GO:007259	oxygen me	2/2606	5/23843	0.095407	0.504226	0.479464	Fmo2/Mt3
GO_BP_m1	GO:007271	response to	2/2606	5/23843	0.095407	0.504226	0.479464	Kdm3b/Slc
GO_BP_m1	GO:009750	receptor lo	2/2606	5/23843	0.095407	0.504226	0.479464	Tulp1/Tulp
GO_BP_m1	GO:009774	de novo ce	2/2606	5/23843	0.095407	0.504226	0.479464	Deup1/Plk4
GO_BP_m1	GO:009852	skeletal mu	2/2606	5/23843	0.095407	0.504226	0.479464	Nln/Tbx1
GO_BP_m1	GO:009853	de novo ce	2/2606	5/23843	0.095407	0.504226	0.479464	Deup1/Plk4
GO_BP_m1	GO:009888	postsynapt	2/2606	5/23843	0.095407	0.504226	0.479464	Dnm3/Synj
GO_BP_m1	GO:009890	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Cav3/Fgf13
GO_BP_m1	GO:009917	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Nlgn3/Snca
GO_BP_m1	GO:010604	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Ptgs2/Ybx3
GO_BP_m1	GO:015000	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Park2/Stx1
GO_BP_m1	GO:190012	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Has2/Nfkb
GO_BP_m1	GO:190221	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Ptgs2/Ybx3
GO_BP_m1	GO:190254	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Adgra2/Dc
GO_BP_m1	GO:190274	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Cfl1/Plxnb3
GO_BP_m1	GO:190327	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Atp1b2/Fxy
GO_BP_m1	GO:190362	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Endog/Igfb
GO_BP_m1	GO:190418	negative re	2/2606	5/23843	0.095407	0.504226	0.479464	Bok/Cav3
GO_BP_m1	GO:190439	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Lrp4/Mesd
GO_BP_m1	GO:190439	positive reg	2/2606	5/23843	0.095407	0.504226	0.479464	Lrp4/Mesd

GO_BP_m1	GO:190587	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Cdh2/Cfl1
GO_BP_m1	GO:199051	piRNA bios	2/2606	5/23843	0.095407	0.504226	0.479464	Btbd18/Dd
GO_BP_m1	GO:199074	protein sial	2/2606	5/23843	0.095407	0.504226	0.479464	St6gal1/St
GO_BP_m1	GO:20004	positive re	2/2606	5/23843	0.095407	0.504226	0.479464	Akap6/Atp
GO_BP_m1	GO:200064	positive re	2/2606	5/23843	0.095407	0.504226	0.479464	Pcsk9/Ptpr
GO_BP_m1	GO:20008	positive re	2/2606	5/23843	0.095407	0.504226	0.479464	Galr1/Tac1
GO_BP_m1	GO:20012	regulation	2/2606	5/23843	0.095407	0.504226	0.479464	Mir23a/Mi
GO_BP_m1	GO:190121	positive re	17/2606	111/23843	0.095413	0.504226	0.479464	Aifm1/Cas
GO_BP_m1	GO:00512	positive re	60/2606	464/23843	0.095477	0.504226	0.479464	Abat/Abl2/
GO_BP_m1	GO:00099	anterior/p	31/2606	223/23843	0.096133	0.504226	0.479464	Abi1/Btg2/
GO_BP_m1	GO:00305	neutrophil	14/2606	88/23843	0.096269	0.504226	0.479464	Ccl20/Ccl2
GO_BP_m1	GO:19034	regulation	14/2606	88/23843	0.096269	0.504226	0.479464	Atp2b4/Ca
GO_BP_m1	GO:00160	lipid catab	40/2606	297/23843	0.096418	0.504226	0.479464	Abcd3/Ab
GO_BP_m1	GO:00328	glomerulus	10/2606	58/23843	0.096493	0.504226	0.479464	Basp1/Fox
GO_BP_m1	GO:00457	positive re	10/2606	58/23843	0.096493	0.504226	0.479464	Calr/Cdc7/
GO_BP_m1	GO:19023	regulation	10/2606	58/23843	0.096493	0.504226	0.479464	Atp1b2/At
GO_BP_m1	GO:00703	Golgi orga	18/2606	119/23843	0.096606	0.504226	0.479464	Arhgef7/At
GO_BP_m1	GO:00170	protein im	30/2606	215/23843	0.096731	0.504226	0.479464	1700123L1
GO_BP_m1	GO:00439	regulation	30/2606	215/23843	0.096731	0.504226	0.479464	Anxa2/Arg
GO_BP_m1	GO:00700	glycosylati	29/2606	207/23843	0.097278	0.504226	0.479464	A4gnt/Abc
GO_BP_m1	GO:00462	nitric oxide	12/2606	73/23843	0.097463	0.504226	0.479464	Atp2b4/Ca
GO_BP_m1	GO:00604	regulation	12/2606	73/23843	0.097463	0.504226	0.479464	Akap6/Cav
GO_BP_m1	GO:006151	myeloid ce	12/2606	73/23843	0.097463	0.504226	0.479464	Abi1/Anxa
GO_BP_m1	GO:19045	regulation	12/2606	73/23843	0.097463	0.504226	0.479464	Cdk1/Cdk
GO_BP_m1	GO:00464	nicotinami	20/2606	135/23843	0.098161	0.504226	0.479464	Bpgm/Eno
GO_BP_m1	GO:19028	microtubul	20/2606	135/23843	0.098161	0.504226	0.479464	Ankrd53/B
GO_BP_m1	GO:00456	positive re	15/2606	96/23843	0.098502	0.504226	0.479464	Casp8/Ccr
GO_BP_m1	GO:006201	positive re	26/2606	183/23843	0.098528	0.504226	0.479464	Adcyap1r1
GO_BP_m1	GO:00007	DNA catab	5/2606	23/23843	0.098662	0.504226	0.479464	Aifm1/Dffa
GO_BP_m1	GO:001657	histone de	5/2606	23/23843	0.098662	0.504226	0.479464	Asxl1/Kat2
GO_BP_m1	GO:001904	modulatio	5/2606	23/23843	0.098662	0.504226	0.479464	Hyal2/Myc
GO_BP_m1	GO:002261	DNA stran	5/2606	23/23843	0.098662	0.504226	0.479464	Fen1/Lig3/
GO_BP_m1	GO:003164	heat gener	5/2606	23/23843	0.098662	0.504226	0.479464	Abat/Ednr
GO_BP_m1	GO:003237	positive re	5/2606	23/23843	0.098662	0.504226	0.479464	Abca12/Ar
GO_BP_m1	GO:003237	positive re	5/2606	23/23843	0.098662	0.504226	0.479464	Abca12/Ar
GO_BP_m1	GO:00328	receptor bi	5/2606	23/23843	0.098662	0.504226	0.479464	Ache/Hdac
GO_BP_m1	GO:00466	response t	5/2606	23/23843	0.098662	0.504226	0.479464	Aoc1/Atp7
GO_BP_m1	GO:007167	positive re	5/2606	23/23843	0.098662	0.504226	0.479464	Ccr1/Cxcl1
GO_BP_m1	GO:00718	cellular res	5/2606	23/23843	0.098662	0.504226	0.479464	Akap6/Atp
GO_BP_m1	GO:00901	positive re	5/2606	23/23843	0.098662	0.504226	0.479464	Gdnf/Lgr4/
GO_BP_m1	GO:200067	positive re	5/2606	23/23843	0.098662	0.504226	0.479464	Ddrgk1/Fo
GO_BP_m1	GO:20007	negative re	5/2606	23/23843	0.098662	0.504226	0.479464	Hdac1/Hd
GO_BP_m1	GO:00703	positive re	22/2606	151/23843	0.098863	0.504226	0.479464	5730559C1
GO_BP_m1	GO:00487	skeletal sys	33/2606	240/23843	0.098901	0.504226	0.479464	Alpl/Alx3/
GO_BP_m1	GO:003361	membrane	9/2606	51/23843	0.099351	0.504226	0.479464	Adam8/Ap
GO_BP_m1	GO:00487	embryonic	16/2606	104/23843	0.100253	0.504226	0.479464	Alx3/Dscar
GO_BP_m1	GO:19034	reactive ox	16/2606	104/23843	0.100253	0.504226	0.479464	5730559C1
GO_BP_m1	GO:00508	positive re	58/2606	449/23843	0.101069	0.504226	0.479464	Acta2/Ada

GO_BP_m1	GO:001991	lipid storag	11/2606	66/23843	0.101475	0.504226	0.479464	Angptl3/Ca
GO_BP_m1	GO:190357	regulation	11/2606	66/23843	0.101475	0.504226	0.479464	Cdk1/Esrrb
GO_BP_m1	GO:004247	odontogen	17/2606	112/23843	0.101604	0.504226	0.479464	Ambn/Fox
GO_BP_m1	GO:00190	viral transc	8/2606	44/23843	0.101615	0.504226	0.479464	Ccl4/Hdac
GO_BP_m1	GO:00508	positive re	8/2606	44/23843	0.101615	0.504226	0.479464	Akap6/Ccl
GO_BP_m1	GO:007167	regulation	8/2606	44/23843	0.101615	0.504226	0.479464	Ccr1/Cxcl1
GO_BP_m1	GO:00901	positive re	8/2606	44/23843	0.101615	0.504226	0.479464	Gdnf/Lgr4/
GO_BP_m1	GO:00070	centriole re	6/2606	30/23843	0.102341	0.504226	0.479464	Deup1/Cdk
GO_BP_m1	GO:000804	motor neu	6/2606	30/23843	0.102341	0.504226	0.479464	Cdk5/Chn1
GO_BP_m1	GO:00140	astrocyte d	6/2606	30/23843	0.102341	0.504226	0.479464	Fpr2/Lamb
GO_BP_m1	GO:00219	dorsal/ven	6/2606	30/23843	0.102341	0.504226	0.479464	Foxa2/Prka
GO_BP_m1	GO:190342	negative re	6/2606	30/23843	0.102341	0.504226	0.479464	Atp2b4/Ca
GO_BP_m1	GO:190552	regulation	6/2606	30/23843	0.102341	0.504226	0.479464	Cxcl17/Ddt
GO_BP_m1	GO:000282	negative re	7/2606	37/23843	0.10286	0.504226	0.479464	Arg1/Clec4
GO_BP_m1	GO:00358	epithelial c	7/2606	37/23843	0.10286	0.504226	0.479464	Basp1/Gdn
GO_BP_m1	GO:00458	positive re	7/2606	37/23843	0.10286	0.504226	0.479464	Foxa2/Ift17
GO_BP_m1	GO:00460	regulation	7/2606	37/23843	0.10286	0.504226	0.479464	Arg1/Gpan
GO_BP_m1	GO:00482	mRNA stab	7/2606	37/23843	0.10286	0.504226	0.479464	Apobec1/N
GO_BP_m1	GO:00610	positive re	7/2606	37/23843	0.10286	0.504226	0.479464	Adora1/Dc
GO_BP_m1	GO:190571	positive re	7/2606	37/23843	0.10286	0.504226	0.479464	Bnip3/Bok/
GO_BP_m1	GO:200102	negative re	7/2606	37/23843	0.10286	0.504226	0.479464	Abat/Arl6i
GO_BP_m1	GO:000914	nucleoside	37/2606	274/23843	0.103318	0.504226	0.479464	Adk/Atp5a
GO_BP_m1	GO:00066	glycolipid	14/2606	89/23843	0.103338	0.504226	0.479464	Abo/B4gal
GO_BP_m1	GO:00466	regulation	14/2606	89/23843	0.103338	0.504226	0.479464	Blm/Cd80/
GO_BP_m1	GO:004362	cellular prc	19/2606	128/23843	0.103352	0.504226	0.479464	Asph/Cfl1/
GO_BP_m1	GO:00550	cardiac mu	19/2606	128/23843	0.103352	0.504226	0.479464	Akap6/Cav
GO_BP_m1	GO:00723	signal trans	20/2606	136/23843	0.103843	0.504226	0.479464	Ankrd1/Atr
GO_BP_m1	GO:005254	regulation	46/2606	349/23843	0.103913	0.504226	0.479464	Aifm1/Alox
GO_BP_m1	GO:00313	positive re	43/2606	324/23843	0.104074	0.504226	0.479464	Adam8/Ari
GO_BP_m1	GO:007252	purine-cor	36/2606	266/23843	0.104369	0.504226	0.479464	Adcy4/Adk
GO_BP_m1	GO:00347	negative re	15/2606	97/23843	0.10535	0.504226	0.479464	Adra1d/Arl
GO_BP_m1	GO:00460	cAMP met	15/2606	97/23843	0.10535	0.504226	0.479464	Adcy4/Adr
GO_BP_m1	GO:003014	sphingolipi	12/2606	74/23843	0.105362	0.504226	0.479464	Acer3/Asa
GO_BP_m1	GO:00428	pyruvate b	12/2606	74/23843	0.105362	0.504226	0.479464	Bpgm/Eno
GO_BP_m1	GO:007167	mononucle	12/2606	74/23843	0.105362	0.504226	0.479464	Ccl20/Ccl2
GO_BP_m1	GO:004612	purine ribo	10/2606	59/23843	0.105404	0.504226	0.479464	Acpp/Adk/
GO_BP_m1	GO:00509	detection c	10/2606	59/23843	0.105404	0.504226	0.479464	Cav3/Denr
GO_BP_m1	GO:199077	protein loc	38/2606	283/23843	0.106216	0.504226	0.479464	Abca12/Ar
GO_BP_m1	GO:000182	serotonin s	4/2606	17/23843	0.106668	0.504226	0.479464	Hrh3/Htr1a
GO_BP_m1	GO:00019	suckling be	4/2606	17/23843	0.106668	0.504226	0.479464	Cntfr/Dach
GO_BP_m1	GO:000252	leukocyte r	4/2606	17/23843	0.106668	0.504226	0.479464	Adam8/Ao
GO_BP_m1	GO:000662	protein tar	4/2606	17/23843	0.106668	0.504226	0.479464	Lonp2/Pex
GO_BP_m1	GO:000674	ubiquinone	4/2606	17/23843	0.106668	0.504226	0.479464	Coq10b/Co
GO_BP_m1	GO:00107	negative re	4/2606	17/23843	0.106668	0.504226	0.479464	Drd3/Hecw
GO_BP_m1	GO:00300	microvillus	4/2606	17/23843	0.106668	0.504226	0.479464	Atp8b1/Fsc
GO_BP_m1	GO:00323	intracellula	4/2606	17/23843	0.106668	0.504226	0.479464	Anxa2/Ldlr
GO_BP_m1	GO:00323	intracellula	4/2606	17/23843	0.106668	0.504226	0.479464	Anxa2/Ldlr
GO_BP_m1	GO:003431	diol biosyn	4/2606	17/23843	0.106668	0.504226	0.479464	Acer3/Asa

GO_BP_m1	GO:003531	wound hea	4/2606	17/23843	0.106668	0.504226	0.479464	Col5a1/Mn
GO_BP_m1	GO:003952	RIG-I signa	4/2606	17/23843	0.106668	0.504226	0.479464	Ddx60/Dhx
GO_BP_m1	GO:004213	neurotrans	4/2606	17/23843	0.106668	0.504226	0.479464	Abat/Ache/
GO_BP_m1	GO:004244	hormone c	4/2606	17/23843	0.106668	0.504226	0.479464	Ache/Dio2/
GO_BP_m1	GO:004357	peroxisoma	4/2606	17/23843	0.106668	0.504226	0.479464	Lonp2/Pex
GO_BP_m1	GO:004659	regulation	4/2606	17/23843	0.106668	0.504226	0.479464	Kat2a/Kat2
GO_BP_m1	GO:004814	behavioral	4/2606	17/23843	0.106668	0.504226	0.479464	Adh1/Adra
GO_BP_m1	GO:004885	forebrain n	4/2606	17/23843	0.106668	0.504226	0.479464	Ift88/Nf1/S
GO_BP_m1	GO:006031	regulation	4/2606	17/23843	0.106668	0.504226	0.479464	Akap6/Fkb
GO_BP_m1	GO:007266	protein loc	4/2606	17/23843	0.106668	0.504226	0.479464	Lonp2/Pex
GO_BP_m1	GO:007266	establishm	4/2606	17/23843	0.106668	0.504226	0.479464	Lonp2/Pex
GO_BP_m1	GO:008018	histone H3	4/2606	17/23843	0.106668	0.504226	0.479464	Hist1h1c/C
GO_BP_m1	GO:190291	regulation	4/2606	17/23843	0.106668	0.504226	0.479464	Nmi/Park2/
GO_BP_m1	GO:002198	cerebral co	16/2606	105/23843	0.10689	0.504226	0.479464	Arx/Bbs2/C
GO_BP_m1	GO:004814	fibroblast p	16/2606	105/23843	0.10689	0.504226	0.479464	Anxa2/Cdk
GO_BP_m1	GO:004667	response to	40/2606	300/23843	0.107787	0.504226	0.479464	Abat/Adh1
GO_BP_m1	GO:000072	telomere m	18/2606	121/23843	0.108862	0.504226	0.479464	Atr/Blm/Cc
GO_BP_m1	GO:004848	synaptic ve	18/2606	121/23843	0.108862	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:009748	establishm	18/2606	121/23843	0.108862	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:190165	glycosyl co	18/2606	121/23843	0.108862	0.504226	0.479464	Abhd10/Ac
GO_BP_m1	GO:004577	positive reg	9/2606	52/23843	0.109116	0.504226	0.479464	Adh5/Ador
GO_BP_m1	GO:004583	negative re	9/2606	52/23843	0.109116	0.504226	0.479464	Klhl22/Mac
GO_BP_m1	GO:004667	negative re	9/2606	52/23843	0.109116	0.504226	0.479464	Fkbp1b/Hc
GO_BP_m1	GO:005087	multicellula	9/2606	52/23843	0.109116	0.504226	0.479464	Cav3/Chrn
GO_BP_m1	GO:005088	musculoske	9/2606	52/23843	0.109116	0.504226	0.479464	Cav3/Chrn
GO_BP_m1	GO:000705	chromosor	42/2606	317/23843	0.109116	0.504226	0.479464	Ankrd53/Tc
GO_BP_m1	GO:001077	positive reg	24/2606	169/23843	0.109294	0.504226	0.479464	Ache/Calr/
GO_BP_m1	GO:000001	vacuole inh	1/2606	1/23843	0.109298	0.504226	0.479464	Rbsn
GO_BP_m1	GO:000008	mitotic M p	1/2606	1/23843	0.109298	0.504226	0.479464	Cdc20
GO_BP_m1	GO:000008	mitotic me	1/2606	1/23843	0.109298	0.504226	0.479464	Cdc20
GO_BP_m1	GO:000198	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Adra1d
GO_BP_m1	GO:000201	vasoconstr	1/2606	1/23843	0.109298	0.504226	0.479464	Manf
GO_BP_m1	GO:000204	blood vess	1/2606	1/23843	0.109298	0.504226	0.479464	Lemd3
GO_BP_m1	GO:000229	CD4-positi	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:000229	alpha-beta	1/2606	1/23843	0.109298	0.504226	0.479464	Gpr18
GO_BP_m1	GO:000230	CD8-positi	1/2606	1/23843	0.109298	0.504226	0.479464	Gpr18
GO_BP_m1	GO:000239	MHC class	1/2606	1/23843	0.109298	0.504226	0.479464	Calr
GO_BP_m1	GO:000250	peptide an	1/2606	1/23843	0.109298	0.504226	0.479464	Calr
GO_BP_m1	GO:000253	prostaglan	1/2606	1/23843	0.109298	0.504226	0.479464	Ephx2
GO_BP_m1	GO:000273	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Jak3
GO_BP_m1	GO:000287	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Il10
GO_BP_m1	GO:000293	tendon she	1/2606	1/23843	0.109298	0.504226	0.479464	Mkx
GO_BP_m1	GO:000313	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:000340	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Preb
GO_BP_m1	GO:000599	trehalose c	1/2606	1/23843	0.109298	0.504226	0.479464	Pgghg
GO_BP_m1	GO:000611	acetaldehy	1/2606	1/23843	0.109298	0.504226	0.479464	Adh1
GO_BP_m1	GO:000614	guanine ca	1/2606	1/23843	0.109298	0.504226	0.479464	Gda
GO_BP_m1	GO:000616	adenosine	1/2606	1/23843	0.109298	0.504226	0.479464	Adk

GO_BP_m1	GO:000617	dATP biosy	1/2606	1/23843	0.109298	0.504226	0.479464	Adk
GO_BP_m1	GO:000621	thymidine	1/2606	1/23843	0.109298	0.504226	0.479464	Dpyd
GO_BP_m1	GO:000628	base-excisi	1/2606	1/23843	0.109298	0.504226	0.479464	Lig3
GO_BP_m1	GO:000643	lysyl-tRNA	1/2606	1/23843	0.109298	0.504226	0.479464	Kars
GO_BP_m1	GO:000658	acetylcholi	1/2606	1/23843	0.109298	0.504226	0.479464	Ache
GO_BP_m1	GO:000658	dopamine	1/2606	1/23843	0.109298	0.504226	0.479464	Th
GO_BP_m1	GO:000659	ornithine c	1/2606	1/23843	0.109298	0.504226	0.479464	Otc
GO_BP_m1	GO:000667	phytosphir	1/2606	1/23843	0.109298	0.504226	0.479464	Acer3
GO_BP_m1	GO:000719	adenylate	1/2606	1/23843	0.109298	0.504226	0.479464	Htr7
GO_BP_m1	GO:000729	sperm indi	1/2606	1/23843	0.109298	0.504226	0.479464	Spem1
GO_BP_m1	GO:000734	cellularizati	1/2606	1/23843	0.109298	0.504226	0.479464	Spem1
GO_BP_m1	GO:000737	ventral mic	1/2606	1/23843	0.109298	0.504226	0.479464	Smo
GO_BP_m1	GO:000740	ganglion m	1/2606	1/23843	0.109298	0.504226	0.479464	Ntf5
GO_BP_m1	GO:000749	posterior n	1/2606	1/23843	0.109298	0.504226	0.479464	Ednrb
GO_BP_m1	GO:000805	sensory org	1/2606	1/23843	0.109298	0.504226	0.479464	Ntf5
GO_BP_m1	GO:000865	lipopolysac	1/2606	1/23843	0.109298	0.504226	0.479464	Aoah
GO_BP_m1	GO:000923	cobalamin	1/2606	1/23843	0.109298	0.504226	0.479464	Mmachc
GO_BP_m1	GO:000923	siderophor	1/2606	1/23843	0.109298	0.504226	0.479464	Bdh2
GO_BP_m1	GO:000930	protein bio	1/2606	1/23843	0.109298	0.504226	0.479464	Hlcs
GO_BP_m1	GO:000937	quorum se	1/2606	1/23843	0.109298	0.504226	0.479464	Slc22a5
GO_BP_m1	GO:000981	stilbene me	1/2606	1/23843	0.109298	0.504226	0.479464	Ephx2
GO_BP_m1	GO:000999	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:001016	formation	1/2606	1/23843	0.109298	0.504226	0.479464	Ntf5
GO_BP_m1	GO:001018	vitamin E b	1/2606	1/23843	0.109298	0.504226	0.479464	Pltp
GO_BP_m1	GO:001031	detoxificati	1/2606	1/23843	0.109298	0.504226	0.479464	Slc30a3
GO_BP_m1	GO:001033	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Ptgs2
GO_BP_m1	GO:001079	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Coq3
GO_BP_m1	GO:001405	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Htr6
GO_BP_m1	GO:001568	molybdate	1/2606	1/23843	0.109298	0.504226	0.479464	Mfsd5
GO_BP_m1	GO:001578	UDP-gluc	1/2606	1/23843	0.109298	0.504226	0.479464	Slc35c2
GO_BP_m1	GO:001589	amiloride t	1/2606	1/23843	0.109298	0.504226	0.479464	Aoc1
GO_BP_m1	GO:001594	formate me	1/2606	1/23843	0.109298	0.504226	0.479464	Mthfd1l
GO_BP_m1	GO:001800	N-terminal	1/2606	1/23843	0.109298	0.504226	0.479464	Map6d1
GO_BP_m1	GO:001811	protein ade	1/2606	1/23843	0.109298	0.504226	0.479464	Ficd
GO_BP_m1	GO:001817	protein nu	1/2606	1/23843	0.109298	0.504226	0.479464	Ficd
GO_BP_m1	GO:001831	molybden	1/2606	1/23843	0.109298	0.504226	0.479464	Gphn
GO_BP_m1	GO:001887	arsonoacet	1/2606	1/23843	0.109298	0.504226	0.479464	As3mt
GO_BP_m1	GO:001896	4-nitrophe	1/2606	1/23843	0.109298	0.504226	0.479464	Sult1a1
GO_BP_m1	GO:001929	siderophor	1/2606	1/23843	0.109298	0.504226	0.479464	Bdh2
GO_BP_m1	GO:001939	glucuronos	1/2606	1/23843	0.109298	0.504226	0.479464	Abhd10
GO_BP_m1	GO:002168	cerebellar	1/2606	1/23843	0.109298	0.504226	0.479464	Cend1
GO_BP_m1	GO:002176	nucleus ac	1/2606	1/23843	0.109298	0.504226	0.479464	Aldh1a3
GO_BP_m1	GO:002199	initiation o	1/2606	1/23843	0.109298	0.504226	0.479464	Kdm2b
GO_BP_m1	GO:003045	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Susd4
GO_BP_m1	GO:003193	mitochond	1/2606	1/23843	0.109298	0.504226	0.479464	Slc25a33
GO_BP_m1	GO:003202	trypsinoge	1/2606	1/23843	0.109298	0.504226	0.479464	Cuzd1
GO_BP_m1	GO:003211	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:003222	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Htr6

GO_BP_m1	GO:003224	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Adora1
GO_BP_m1	GO:003224	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Adora1
GO_BP_m1	GO:003237	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Pcsk9
GO_BP_m1	GO:003238	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Pcsk9
GO_BP_m1	GO:003238	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Pcsk9
GO_BP_m1	GO:003281	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Cartpt
GO_BP_m1	GO:003283	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:003283	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:003290	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Adora1
GO_BP_m1	GO:003323	carbohydra	1/2606	1/23843	0.109298	0.504226	0.479464	Abcb1a
GO_BP_m1	GO:003324	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:003324	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:003331	meiotic spi	1/2606	1/23843	0.109298	0.504226	0.479464	Ttk
GO_BP_m1	GO:003417	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Treml4
GO_BP_m1	GO:003418	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Treml4
GO_BP_m1	GO:003512	post-embr	1/2606	1/23843	0.109298	0.504226	0.479464	Mir23a
GO_BP_m1	GO:003522	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Gclm
GO_BP_m1	GO:003522	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Gclm
GO_BP_m1	GO:003540	histone H3	1/2606	1/23843	0.109298	0.504226	0.479464	Pkn1
GO_BP_m1	GO:003564	phosphoar	1/2606	1/23843	0.109298	0.504226	0.479464	Ptpn22
GO_BP_m1	GO:003564	enteric sm	1/2606	1/23843	0.109298	0.504226	0.479464	Ednrb
GO_BP_m1	GO:003565	Wnt signali	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt7a
GO_BP_m1	GO:003585	chromoso	1/2606	1/23843	0.109298	0.504226	0.479464	Klhl21
GO_BP_m1	GO:003587	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Aoc1
GO_BP_m1	GO:003591	pore forma	1/2606	1/23843	0.109298	0.504226	0.479464	Gsdmd
GO_BP_m1	GO:003607	N-glycan f	1/2606	1/23843	0.109298	0.504226	0.479464	Fut8
GO_BP_m1	GO:003608	GDP-fucos	1/2606	1/23843	0.109298	0.504226	0.479464	Slc35c1
GO_BP_m1	GO:003611	very long-	1/2606	1/23843	0.109298	0.504226	0.479464	Hsd17b4
GO_BP_m1	GO:003633	intestinal s	1/2606	1/23843	0.109298	0.504226	0.479464	Lgr4
GO_BP_m1	GO:003800	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Cav3
GO_BP_m1	GO:003806	nitric oxide	1/2606	1/23843	0.109298	0.504226	0.479464	Kcnc2
GO_BP_m1	GO:003809	sequesteri	1/2606	1/23843	0.109298	0.504226	0.479464	Grem2
GO_BP_m1	GO:003810	sequesteri	1/2606	1/23843	0.109298	0.504226	0.479464	Dand5
GO_BP_m1	GO:004204	metal inco	1/2606	1/23843	0.109298	0.504226	0.479464	Gphn
GO_BP_m1	GO:004239	phosphage	1/2606	1/23843	0.109298	0.504226	0.479464	Ckm
GO_BP_m1	GO:004268	cardioblast	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:004268	cardioblast	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:004268	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:004321	daunorubi	1/2606	1/23843	0.109298	0.504226	0.479464	Abcb1a
GO_BP_m1	GO:004325	sodium-de	1/2606	1/23843	0.109298	0.504226	0.479464	Slc10a6
GO_BP_m1	GO:004337	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Nckap1l
GO_BP_m1	GO:004348	pigment a	1/2606	1/23843	0.109298	0.504226	0.479464	Krtap21-1
GO_BP_m1	GO:004360	nitrate cat	1/2606	1/23843	0.109298	0.504226	0.479464	Por
GO_BP_m1	GO:004393	ossification	1/2606	1/23843	0.109298	0.504226	0.479464	Cthrc1
GO_BP_m1	GO:004403	multi-orga	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:004403	multi-orga	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:004411	developme	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:004411	developme	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2

GO_BP_m1	GO:004414	modulatio	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:004414	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:004477	meiotic spi	1/2606	1/23843	0.109298	0.504226	0.479464	Ttk
GO_BP_m1	GO:004479	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Vapb
GO_BP_m1	GO:004485	plasma me	1/2606	1/23843	0.109298	0.504226	0.479464	Gsn
GO_BP_m1	GO:004485	plasma me	1/2606	1/23843	0.109298	0.504226	0.479464	Gsn
GO_BP_m1	GO:004485	plasma me	1/2606	1/23843	0.109298	0.504226	0.479464	Gsn
GO_BP_m1	GO:004508	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Nfkb1
GO_BP_m1	GO:004516	asymmetri	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt7a
GO_BP_m1	GO:004521	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Jak3
GO_BP_m1	GO:004522	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Jak3
GO_BP_m1	GO:004535	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Nmi
GO_BP_m1	GO:004579	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Slc12a2
GO_BP_m1	GO:004595	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Susd4
GO_BP_m1	GO:004595	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Susd4
GO_BP_m1	GO:004612	pyrimidine	1/2606	1/23843	0.109298	0.504226	0.479464	Dpyd
GO_BP_m1	GO:004618	acetaldehy	1/2606	1/23843	0.109298	0.504226	0.479464	Adh1
GO_BP_m1	GO:004621	nitric oxide	1/2606	1/23843	0.109298	0.504226	0.479464	Por
GO_BP_m1	GO:004627	stilbene ca	1/2606	1/23843	0.109298	0.504226	0.479464	Ephx2
GO_BP_m1	GO:004631	phosphocr	1/2606	1/23843	0.109298	0.504226	0.479464	Ckm
GO_BP_m1	GO:004635	disacchari	1/2606	1/23843	0.109298	0.504226	0.479464	Pgghg
GO_BP_m1	GO:004639	UDP-glucu	1/2606	1/23843	0.109298	0.504226	0.479464	Csgalnact1
GO_BP_m1	GO:004649	L-methylm	1/2606	1/23843	0.109298	0.504226	0.479464	Mcee
GO_BP_m1	GO:004658	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Kifap3
GO_BP_m1	GO:004658	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Kifap3
GO_BP_m1	GO:004667	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Casp6
GO_BP_m1	GO:004672	lactic acid	1/2606	1/23843	0.109298	0.504226	0.479464	Myc
GO_BP_m1	GO:004698	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Eif2ak1
GO_BP_m1	GO:004805	compound	1/2606	1/23843	0.109298	0.504226	0.479464	Abcb5
GO_BP_m1	GO:004813	spermatoc	1/2606	1/23843	0.109298	0.504226	0.479464	Topaz1
GO_BP_m1	GO:004833	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:004879	spontaneo	1/2606	1/23843	0.109298	0.504226	0.479464	Syt12
GO_BP_m1	GO:004887	homeostas	1/2606	1/23843	0.109298	0.504226	0.479464	Slc22a5
GO_BP_m1	GO:005065	chondroiti	1/2606	1/23843	0.109298	0.504226	0.479464	Csgalnact1
GO_BP_m1	GO:005071	interleukin	1/2606	1/23843	0.109298	0.504226	0.479464	Ccl20
GO_BP_m1	GO:005072	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ccl20
GO_BP_m1	GO:005072	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Ccl20
GO_BP_m1	GO:005103	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Zfp386
GO_BP_m1	GO:005106	dihydrobio	1/2606	1/23843	0.109298	0.504226	0.479464	Gch1
GO_BP_m1	GO:005123	meiotic spi	1/2606	1/23843	0.109298	0.504226	0.479464	Ppp2r1a
GO_BP_m1	GO:005132	metaphase	1/2606	1/23843	0.109298	0.504226	0.479464	Cdc20
GO_BP_m1	GO:005139	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Cav3
GO_BP_m1	GO:005146	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Crhbp
GO_BP_m1	GO:005151	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:005151	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:005158	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:005162	norepinep	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:005162	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Snca

GO_BP_m1	GO:005162	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:005178	behavioral	1/2606	1/23843	0.109298	0.504226	0.479464	Slc16a1
GO_BP_m1	GO:005194	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:005209	interspecie	1/2606	1/23843	0.109298	0.504226	0.479464	Slc22a5
GO_BP_m1	GO:005210	quorum se	1/2606	1/23843	0.109298	0.504226	0.479464	Slc22a5
GO_BP_m1	GO:005221	metabolisn	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005222	catabolism	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005222	metabolisn	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005236	catabolism	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005236	catabolism	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005236	catabolism	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005236	catabolism	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005236	catabolism	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005241	metabolisn	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005241	metabolisn	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005241	metabolisn	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:005241	metabolisn	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:006003	notochord	1/2606	1/23843	0.109298	0.504226	0.479464	Epha2
GO_BP_m1	GO:006003	notochord	1/2606	1/23843	0.109298	0.504226	0.479464	Epha2
GO_BP_m1	GO:006023	delaminati	1/2606	1/23843	0.109298	0.504226	0.479464	Trpv4
GO_BP_m1	GO:006024	detection c	1/2606	1/23843	0.109298	0.504226	0.479464	Smo
GO_BP_m1	GO:006024	detection c	1/2606	1/23843	0.109298	0.504226	0.479464	Smo
GO_BP_m1	GO:006024	detection c	1/2606	1/23843	0.109298	0.504226	0.479464	Smo
GO_BP_m1	GO:006029	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cav3
GO_BP_m1	GO:006034	spleen trab	1/2606	1/23843	0.109298	0.504226	0.479464	Slc40a1
GO_BP_m1	GO:006054	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:006055	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:006055	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:006055	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Ifng
GO_BP_m1	GO:006068	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Pdgfa
GO_BP_m1	GO:006073	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Slc22a5
GO_BP_m1	GO:006116	endoplasm	1/2606	1/23843	0.109298	0.504226	0.479464	Shtn1
GO_BP_m1	GO:006144	endocardia	1/2606	1/23843	0.109298	0.504226	0.479464	Jag1
GO_BP_m1	GO:006148	memory T	1/2606	1/23843	0.109298	0.504226	0.479464	Dock8
GO_BP_m1	GO:006152	aspartate s	1/2606	1/23843	0.109298	0.504226	0.479464	Abat
GO_BP_m1	GO:006157	actin filame	1/2606	1/23843	0.109298	0.504226	0.479464	Shtn1
GO_BP_m1	GO:006158	colon epith	1/2606	1/23843	0.109298	0.504226	0.479464	Arsb
GO_BP_m1	GO:006177	drug transp	1/2606	1/23843	0.109298	0.504226	0.479464	Cldn1
GO_BP_m1	GO:006186	hepatic ste	1/2606	1/23843	0.109298	0.504226	0.479464	Acta2
GO_BP_m1	GO:006186	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Acta2
GO_BP_m1	GO:006187	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Acta2
GO_BP_m1	GO:006187	hepatic ste	1/2606	1/23843	0.109298	0.504226	0.479464	Acta2
GO_BP_m1	GO:006187	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Acta2
GO_BP_m1	GO:006187	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Acta2
GO_BP_m1	GO:006190	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Fpr2
GO_BP_m1	GO:006190	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Fpr2
GO_BP_m1	GO:006198	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Foxa2
GO_BP_m1	GO:006198	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Foxa2

GO_BP_m1	GO:007034	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Fgf16
GO_BP_m1	GO:007054	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Cd36
GO_BP_m1	GO:007068	seminal clo	1/2606	1/23843	0.109298	0.504226	0.479464	Klk14
GO_BP_m1	GO:007071	sodium-de	1/2606	1/23843	0.109298	0.504226	0.479464	Slc22a5
GO_BP_m1	GO:007078	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Hlcs
GO_BP_m1	GO:007111	histone bic	1/2606	1/23843	0.109298	0.504226	0.479464	Hlcs
GO_BP_m1	GO:007138	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Npas4
GO_BP_m1	GO:007144	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Gng8
GO_BP_m1	GO:007144	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Mgst1
GO_BP_m1	GO:007147	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Ptgs2
GO_BP_m1	GO:007160	phytosphir	1/2606	1/23843	0.109298	0.504226	0.479464	Acer3
GO_BP_m1	GO:007196	maintenan	1/2606	1/23843	0.109298	0.504226	0.479464	Naa10
GO_BP_m1	GO:007196	establishm	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:007202	macula der	1/2606	1/23843	0.109298	0.504226	0.479464	Pou3f3
GO_BP_m1	GO:007203	mesenchyr	1/2606	1/23843	0.109298	0.504226	0.479464	Smo
GO_BP_m1	GO:007216	anterior m	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007216	specificatic	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007216	specificatic	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007216	specificatic	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007218	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007218	renal vesicl	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007220	metanephr	1/2606	1/23843	0.109298	0.504226	0.479464	Pou3f3
GO_BP_m1	GO:007220	metanephr	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007222	metanephr	1/2606	1/23843	0.109298	0.504226	0.479464	Pou3f3
GO_BP_m1	GO:007225	metanephr	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007225	metanephr	1/2606	1/23843	0.109298	0.504226	0.479464	Osr1
GO_BP_m1	GO:007227	metanephr	1/2606	1/23843	0.109298	0.504226	0.479464	Lamb2
GO_BP_m1	GO:007228	mesenchyr	1/2606	1/23843	0.109298	0.504226	0.479464	Smo
GO_BP_m1	GO:007229	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wt1
GO_BP_m1	GO:007230	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wt1
GO_BP_m1	GO:007257	glycine rec	1/2606	1/23843	0.109298	0.504226	0.479464	Gphn
GO_BP_m1	GO:007268	extracellula	1/2606	1/23843	0.109298	0.504226	0.479464	Adam8
GO_BP_m1	GO:007268	fibronectin	1/2606	1/23843	0.109298	0.504226	0.479464	Adam8
GO_BP_m1	GO:007270	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Mapk13
GO_BP_m1	GO:007274	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Mapk13
GO_BP_m1	GO:008610	endothelin	1/2606	1/23843	0.109298	0.504226	0.479464	Ednrb
GO_BP_m1	GO:009004	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Fnta
GO_BP_m1	GO:009009	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Myc
GO_BP_m1	GO:009009	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Myc
GO_BP_m1	GO:009010	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Nr1h2
GO_BP_m1	GO:009011	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Preb
GO_BP_m1	GO:009017	microtubul	1/2606	1/23843	0.109298	0.504226	0.479464	Pafah1b1
GO_BP_m1	GO:009028	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Esrrb
GO_BP_m1	GO:009034	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Nr1h2
GO_BP_m1	GO:009034	cellular org	1/2606	1/23843	0.109298	0.504226	0.479464	Por
GO_BP_m1	GO:009034	cellular org	1/2606	1/23843	0.109298	0.504226	0.479464	Por
GO_BP_m1	GO:009036	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Apobec1
GO_BP_m1	GO:009061	mitochond	1/2606	1/23843	0.109298	0.504226	0.479464	Pnpt1

GO_BP_m1	GO:00906	cell chemo	1/2606	1/23843	0.109298	0.504226	0.479464	Gab1
GO_BP_m1	GO:00906	endothelial	1/2606	1/23843	0.109298	0.504226	0.479464	Gab1
GO_BP_m1	GO:009067	calcium io	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:00970	selenocyst	1/2606	1/23843	0.109298	0.504226	0.479464	Sepsecs
GO_BP_m1	GO:00971	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Aoc1
GO_BP_m1	GO:00971	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Aoc1
GO_BP_m1	GO:00972	mitochond	1/2606	1/23843	0.109298	0.504226	0.479464	Pnpt1
GO_BP_m1	GO:009731	cap2 mRN	1/2606	1/23843	0.109298	0.504226	0.479464	Cmtr2
GO_BP_m1	GO:00974	blood vess	1/2606	1/23843	0.109298	0.504226	0.479464	Trpv4
GO_BP_m1	GO:009751	base-excisi	1/2606	1/23843	0.109298	0.504226	0.479464	Ung
GO_BP_m1	GO:00987	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:00987	meiotic pr	1/2606	1/23843	0.109298	0.504226	0.479464	Ttk
GO_BP_m1	GO:009904	ceramide t	1/2606	1/23843	0.109298	0.504226	0.479464	Abcb1a
GO_BP_m1	GO:00995	trans-syna	1/2606	1/23843	0.109298	0.504226	0.479464	Gucy1b1
GO_BP_m1	GO:00995	trans-syna	1/2606	1/23843	0.109298	0.504226	0.479464	Gucy1b1
GO_BP_m1	GO:01060	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Clybl
GO_BP_m1	GO:01401	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:015002	oxidised lo	1/2606	1/23843	0.109298	0.504226	0.479464	Cd36
GO_BP_m1	GO:190001	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Crhbp
GO_BP_m1	GO:190001	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Crhbp
GO_BP_m1	GO:190007	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Rapsn
GO_BP_m1	GO:190007	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Rapsn
GO_BP_m1	GO:19000	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:19000	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:19000	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cav1
GO_BP_m1	GO:190024	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cpeb3
GO_BP_m1	GO:19007	doxorubici	1/2606	1/23843	0.109298	0.504226	0.479464	Ralbp1
GO_BP_m1	GO:19008	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cav3
GO_BP_m1	GO:19010	ubiquinon	1/2606	1/23843	0.109298	0.504226	0.479464	Ndufa9
GO_BP_m1	GO:19010	ubiquinon	1/2606	1/23843	0.109298	0.504226	0.479464	Ndufa9
GO_BP_m1	GO:19012	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Antxr1
GO_BP_m1	GO:19012	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Fmr1
GO_BP_m1	GO:19013	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:19016	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Lrp4
GO_BP_m1	GO:19019	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Topaz1
GO_BP_m1	GO:19020	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Foxc1
GO_BP_m1	GO:190214	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Tigar
GO_BP_m1	GO:19021	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Tigar
GO_BP_m1	GO:19021	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Tigar
GO_BP_m1	GO:19026	carnitine tr	1/2606	1/23843	0.109298	0.504226	0.479464	Slc25a20
GO_BP_m1	GO:19030	protein loc	1/2606	1/23843	0.109298	0.504226	0.479464	Ttk
GO_BP_m1	GO:190321	glomerular	1/2606	1/23843	0.109298	0.504226	0.479464	Ppargc1a
GO_BP_m1	GO:190324	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:190324	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:19032	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:19032	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:19032	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:190341	iron cation	1/2606	1/23843	0.109298	0.504226	0.479464	Slc40a1

GO_BP_m1	GO:190342	protein loc	1/2606	1/23843	0.109298	0.504226	0.479464	Gbf1
GO_BP_m1	GO:190344	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Trpv4
GO_BP_m1	GO:190360	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cav1
GO_BP_m1	GO:190375	signal trans	1/2606	1/23843	0.109298	0.504226	0.479464	Trpv4
GO_BP_m1	GO:190390	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Gsn
GO_BP_m1	GO:190398	ferrous iro	1/2606	1/23843	0.109298	0.504226	0.479464	Slc40a1
GO_BP_m1	GO:190404	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Mtrr
GO_BP_m1	GO:190404	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Mtrr
GO_BP_m1	GO:190405	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Stx1b
GO_BP_m1	GO:190411	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Stox1
GO_BP_m1	GO:190412	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Stox1
GO_BP_m1	GO:190444	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Abat
GO_BP_m1	GO:190445	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Abat
GO_BP_m1	GO:190446	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Idh2
GO_BP_m1	GO:190448	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Shmt1
GO_BP_m1	GO:190448	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Shmt1
GO_BP_m1	GO:190462	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Nfkb1
GO_BP_m1	GO:190463	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Nfkb1
GO_BP_m1	GO:190463	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Nfkb1
GO_BP_m1	GO:190463	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Nfkb1
GO_BP_m1	GO:190463	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ppargc1a
GO_BP_m1	GO:190463	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Ppargc1a
GO_BP_m1	GO:190469	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wdr13
GO_BP_m1	GO:190471	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Ssh1
GO_BP_m1	GO:190487	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Xrcc1
GO_BP_m1	GO:190487	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Xrcc1
GO_BP_m1	GO:190497	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Park2
GO_BP_m1	GO:190498	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Synj1
GO_BP_m1	GO:190523	cellular res	1/2606	1/23843	0.109298	0.504226	0.479464	Park2
GO_BP_m1	GO:190525	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Nucks1
GO_BP_m1	GO:190535	protein loc	1/2606	1/23843	0.109298	0.504226	0.479464	Ttk
GO_BP_m1	GO:190536	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Park2
GO_BP_m1	GO:190536	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Park2
GO_BP_m1	GO:190558	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:190559	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Pcsk9
GO_BP_m1	GO:190559	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:190559	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Pcsk9
GO_BP_m1	GO:190559	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Anxa2
GO_BP_m1	GO:190560	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Pcsk9
GO_BP_m1	GO:190563	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Ddrgk1
GO_BP_m1	GO:190577	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:190587	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:190587	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:190590	positive re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:199035	stress resp	1/2606	1/23843	0.109298	0.504226	0.479464	Slc30a3
GO_BP_m1	GO:199064	response t	1/2606	1/23843	0.109298	0.504226	0.479464	Eif2ak1
GO_BP_m1	GO:199096	drug trans	1/2606	1/23843	0.109298	0.504226	0.479464	Abcb1a
GO_BP_m1	GO:199096	establishm	1/2606	1/23843	0.109298	0.504226	0.479464	Abcb1a

GO_BP_m1	GO:199096	modulation	1/2606	1/23843	0.109298	0.504226	0.479464	Nucks1
GO_BP_m1	GO:199096	modulation	1/2606	1/23843	0.109298	0.504226	0.479464	Nucks1
GO_BP_m1	GO:200004	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:200008	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Wnt3a
GO_BP_m1	GO:200018	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Ppargc1a
GO_BP_m1	GO:200028	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Atp2b4
GO_BP_m1	GO:200039	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Adam8
GO_BP_m1	GO:200039	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Adam8
GO_BP_m1	GO:200041	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Adam8
GO_BP_m1	GO:200041	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Adam8
GO_BP_m1	GO:200047	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Snca
GO_BP_m1	GO:200049	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Ticam2
GO_BP_m1	GO:200049	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Ticam2
GO_BP_m1	GO:200071	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Naa10
GO_BP_m1	GO:200071	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Naa10
GO_BP_m1	GO:200078	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:200078	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Cfl1
GO_BP_m1	GO:200084	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Igfbp3
GO_BP_m1	GO:200097	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Foxa2
GO_BP_m1	GO:200097	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Foxa2
GO_BP_m1	GO:200107	regulation	1/2606	1/23843	0.109298	0.504226	0.479464	Wt1
GO_BP_m1	GO:200107	positive reg	1/2606	1/23843	0.109298	0.504226	0.479464	Wt1
GO_BP_m1	GO:200122	negative re	1/2606	1/23843	0.109298	0.504226	0.479464	Prkdc
GO_BP_m1	GO:200130	lipoxin B4 r	1/2606	1/23843	0.109298	0.504226	0.479464	Alox12
GO_BP_m1	GO:200130	lipoxin B4 b	1/2606	1/23843	0.109298	0.504226	0.479464	Alox12
GO_BP_m1	GO:200131	lysobispho	1/2606	1/23843	0.109298	0.504226	0.479464	Acp6
GO_BP_m1	GO:000914	purine nuc	19/2606	129/23843	0.10941	0.504226	0.479464	Adk/Atp5a
GO_BP_m1	GO:003166	response to	47/2606	359/23843	0.109736	0.504226	0.479464	Aoc1/Arsb/
GO_BP_m1	GO:007066	positive reg	21/2606	145/23843	0.109847	0.504226	0.479464	Adk/Blm/B
GO_BP_m1	GO:000694	regulation	11/2606	67/23843	0.110057	0.504226	0.479464	Abat/Adora
GO_BP_m1	GO:003304	regulation	11/2606	67/23843	0.110057	0.504226	0.479464	Cdc23/H2a
GO_BP_m1	GO:005088	neuromusc	11/2606	67/23843	0.110057	0.504226	0.479464	Abl2/Aldh1
GO_BP_m1	GO:009719	execution p	11/2606	67/23843	0.110057	0.504226	0.479464	Aifm1/Bok/
GO_BP_m1	GO:000211	aggressive	3/2606	11/23843	0.110328	0.504226	0.479464	Abl2/Avpr1
GO_BP_m1	GO:000665	phosphatid	3/2606	11/23843	0.110328	0.504226	0.479464	Tmem269/
GO_BP_m1	GO:001088	regulation	3/2606	11/23843	0.110328	0.504226	0.479464	Cd36/Nr1h
GO_BP_m1	GO:001405	regulation	3/2606	11/23843	0.110328	0.504226	0.479464	Abat/Hrh3/
GO_BP_m1	GO:003545	cellular resp	3/2606	11/23843	0.110328	0.504226	0.479464	Ifit2/Myc/T
GO_BP_m1	GO:004348	cellular pig	3/2606	11/23843	0.110328	0.504226	0.479464	Bloc1s5/Cc
GO_BP_m1	GO:004660	positive reg	3/2606	11/23843	0.110328	0.504226	0.479464	Plk4/Poc1a
GO_BP_m1	GO:005158	dopamine	3/2606	11/23843	0.110328	0.504226	0.479464	Gdnf/Park2
GO_BP_m1	GO:005193	catecholam	3/2606	11/23843	0.110328	0.504226	0.479464	Gdnf/Park2
GO_BP_m1	GO:006040	regulation	3/2606	11/23843	0.110328	0.504226	0.479464	Ednrb/P2ry
GO_BP_m1	GO:006069	regulation	3/2606	11/23843	0.110328	0.504226	0.479464	Cdh1/Fgf7/
GO_BP_m1	GO:006108	positive reg	3/2606	11/23843	0.110328	0.504226	0.479464	Cd36/Gprc
GO_BP_m1	GO:007060	centromeri	3/2606	11/23843	0.110328	0.504226	0.479464	Naa10/Naa
GO_BP_m1	GO:007086	positive reg	3/2606	11/23843	0.110328	0.504226	0.479464	Bcap31/Se
GO_BP_m1	GO:007093	histone H4	3/2606	11/23843	0.110328	0.504226	0.479464	Hdac1/Hda

GO_BP_m1	GO:00712	cellular res	3/2606	11/23843	0.110328	0.504226	0.479464	Hvcn1/Mt2
GO_BP_m1	GO:007207	metanephr	3/2606	11/23843	0.110328	0.504226	0.479464	Myc/Osr1/
GO_BP_m1	GO:007217	mesoneph	3/2606	11/23843	0.110328	0.504226	0.479464	Gdnf/Nog/
GO_BP_m1	GO:20012	regulation	3/2606	11/23843	0.110328	0.504226	0.479464	Cldn18/Fbr
GO_BP_m1	GO:005084	regulation	14/2606	90/23843	0.110712	0.505692	0.480859	Akap6/Asp
GO_BP_m1	GO:00091	ribonucleo	34/2606	251/23843	0.110764	0.505692	0.480859	Adss/Atp5a
GO_BP_m1	GO:190161	organic hy	29/2606	210/23843	0.111166	0.507262	0.482351	Acer3/Adcy
GO_BP_m1	GO:000611	regulation	8/2606	45/23843	0.112384	0.511227	0.486122	C1qtnf3/Dg
GO_BP_m1	GO:001922	neuronal a	8/2606	45/23843	0.112384	0.511227	0.486122	Fmr1/Gria1
GO_BP_m1	GO:004484	biological	8/2606	45/23843	0.112384	0.511227	0.486122	Cdc20/Ctsl
GO_BP_m1	GO:00507	activated T	8/2606	45/23843	0.112384	0.511227	0.486122	Arg1/Gpam
GO_BP_m1	GO:00610	regulation	8/2606	45/23843	0.112384	0.511227	0.486122	Arhgap44/
GO_BP_m1	GO:190237	negative re	8/2606	45/23843	0.112384	0.511227	0.486122	Apobec1/N
GO_BP_m1	GO:007022	lymphocyt	15/2606	98/23843	0.11248	0.511398	0.486284	Adam8/Blm
GO_BP_m1	GO:00003	response t	27/2606	194/23843	0.112785	0.512523	0.487354	Aptx/Bcar1
GO_BP_m1	GO:003464	cellular res	12/2606	75/23843	0.113627	0.514787	0.489507	Atr/Cdc25a
GO_BP_m1	GO:00435	blood vess	16/2606	106/23843	0.113788	0.514787	0.489507	Adam8/Atp
GO_BP_m1	GO:004647	glyceropho	16/2606	106/23843	0.113788	0.514787	0.489507	Tmem269/
GO_BP_m1	GO:19902	neutrophil	16/2606	106/23843	0.113788	0.514787	0.489507	Adam8/Ccl
GO_BP_m1	GO:00029	response t	5/2606	24/23843	0.113974	0.514787	0.489507	Camk2a/Ca
GO_BP_m1	GO:00355	regulation	5/2606	24/23843	0.113974	0.514787	0.489507	Fbxo18/Hn
GO_BP_m1	GO:00518	positive re	5/2606	24/23843	0.113974	0.514787	0.489507	Cfl1/Enpp2
GO_BP_m1	GO:009002	regulation	5/2606	24/23843	0.113974	0.514787	0.489507	Ccr1/Cxcl1
GO_BP_m1	GO:19019	negative re	5/2606	24/23843	0.113974	0.514787	0.489507	Hdac1/Hda
GO_BP_m1	GO:190301	regulation	5/2606	24/23843	0.113974	0.514787	0.489507	Cldn18/Rfl
GO_BP_m1	GO:19058	negative re	5/2606	24/23843	0.113974	0.514787	0.489507	Cfl1/Dnm3
GO_BP_m1	GO:00760	sensory pe	35/2606	260/23843	0.113987	0.514787	0.489507	Atp8b1/Cd
GO_BP_m1	GO:000961	response t	24/2606	170/23843	0.114722	0.516479	0.491115	Abl2/Ankr
GO_BP_m1	GO:00068	drug trans	10/2606	60/23843	0.114772	0.516479	0.491115	Abcb1a/Ab
GO_BP_m1	GO:004477	mitotic DN	10/2606	60/23843	0.114772	0.516479	0.491115	Blm/Ccng1
GO_BP_m1	GO:00090	serine fami	7/2606	38/23843	0.114832	0.516479	0.491115	Ahcyl2/Gcl
GO_BP_m1	GO:003252	protein exi	7/2606	38/23843	0.114832	0.516479	0.491115	Bcap31/Hs
GO_BP_m1	GO:004502	plasma me	7/2606	38/23843	0.114832	0.516479	0.491115	Folr2/Mym
GO_BP_m1	GO:009712	receptor lo	7/2606	38/23843	0.114832	0.516479	0.491115	Arhgap44/
GO_BP_m1	GO:00988	regulation	7/2606	38/23843	0.114832	0.516479	0.491115	Adora1/Av
GO_BP_m1	GO:200124	regulation	23/2606	162/23843	0.115188	0.517817	0.492388	Bcap31/Bcl
GO_BP_m1	GO:00069	nucleus or	18/2606	122/23843	0.115332	0.517934	0.492499	Ahctf1/Chr
GO_BP_m1	GO:00095	detection	18/2606	122/23843	0.115332	0.517934	0.492499	Adora1/An
GO_BP_m1	GO:19019	negative re	22/2606	154/23843	0.11554	0.51824	0.49279	Blm/Baba
GO_BP_m1	GO:00106	negative re	48/2606	369/23843	0.115593	0.51824	0.49279	Apobec1/B
GO_BP_m1	GO:009032	regulation	6/2606	31/23843	0.115789	0.51824	0.49279	Cd36/Fbln
GO_BP_m1	GO:00985	centriole a	6/2606	31/23843	0.115789	0.51824	0.49279	Deup1/Cdk
GO_BP_m1	GO:190102	negative re	6/2606	31/23843	0.115789	0.51824	0.49279	Adra1d/Fk
GO_BP_m1	GO:007222	smoothene	20/2606	138/23843	0.115813	0.51824	0.49279	Ankmy2/B9
GO_BP_m1	GO:00072	female gan	20/2606	138/23843	0.115813	0.51824	0.49279	Adamts1/A
GO_BP_m1	GO:007222	integrin-m	13/2606	83/23843	0.116347	0.519833	0.494305	Bcar1/Cd6
GO_BP_m1	GO:00091	purine nuc	13/2606	83/23843	0.116347	0.519833	0.494305	Bpgm/Eno
GO_BP_m1	GO:000917	purine ribo	13/2606	83/23843	0.116347	0.519833	0.494305	Bpgm/Eno

GO_BP_m1	GO:00215	telencepha	32/2606	236/23843	0.117624	0.525003	0.499221	Aldh1a3/A
GO_BP_m1	GO:00510	positive re	32/2606	236/23843	0.117624	0.525003	0.499221	Anxa3/Aplf
GO_BP_m1	GO:00064	protein gly	27/2606	195/23843	0.117941	0.525884	0.500058	A4gnt/Alg
GO_BP_m1	GO:004341	macromole	27/2606	195/23843	0.117941	0.525884	0.500058	A4gnt/Alg
GO_BP_m1	GO:007252	pyridine-c	14/2606	91/23843	0.118391	0.527624	0.501713	Bpgm/Eno
GO_BP_m1	GO:00435	skin develo	38/2606	286/23843	0.118687	0.528675	0.502712	Abca12/Al
GO_BP_m1	GO:004424	cellular lipi	26/2606	187/23843	0.118801	0.528915	0.502941	Abcd3/Abh
GO_BP_m1	GO:00017	neural cres	9/2606	53/23843	0.119396	0.530221	0.504182	Cfl1/Ednrb
GO_BP_m1	GO:000254	monocyte	9/2606	53/23843	0.119396	0.530221	0.504182	Ccl20/Ccl2
GO_BP_m1	GO:00480	developme	9/2606	53/23843	0.119396	0.530221	0.504182	Adamts9/B
GO_BP_m1	GO:00709	demethyla	9/2606	53/23843	0.119396	0.530221	0.504182	Apobec1/K
GO_BP_m1	GO:190054	negative re	9/2606	53/23843	0.119396	0.530221	0.504182	Adra1d/Ak
GO_BP_m1	GO:002151	spinal cord	15/2606	99/23843	0.11989	0.531924	0.505802	Dbx1/Dll4/
GO_BP_m1	GO:00433	regulation	30/2606	220/23843	0.119961	0.531924	0.505802	Abl2/Anxa
GO_BP_m1	GO:005067	regulation	30/2606	220/23843	0.119961	0.531924	0.505802	Adk/Arg1/
GO_BP_m1	GO:00009	nuclear-tra	16/2606	107/23843	0.120947	0.536021	0.509698	Btg2/Noct/
GO_BP_m1	GO:000657	cellular mo	22/2606	155/23843	0.121462	0.538003	0.511583	Tmem269/
GO_BP_m1	GO:00704	response t	36/2606	270/23843	0.121561	0.538003	0.511583	Abat/Adam
GO_BP_m1	GO:00705	mitotic spi	17/2606	115/23843	0.121639	0.538003	0.511583	Ankrd53/B
GO_BP_m1	GO:001402	primary ne	17/2606	115/23843	0.121639	0.538003	0.511583	Abl2/Adm/
GO_BP_m1	GO:00095	detection c	18/2606	123/23843	0.12203	0.538562	0.512115	Adora1/An
GO_BP_m1	GO:00322	telomere o	18/2606	123/23843	0.12203	0.538562	0.512115	Atr/Blm/Co
GO_BP_m1	GO:00459	regulation	18/2606	123/23843	0.12203	0.538562	0.512115	Noct/Col5a
GO_BP_m1	GO:003294	positive re	20/2606	139/23843	0.122101	0.538562	0.512115	Adk/Blm/B
GO_BP_m1	GO:000667	ceramide n	12/2606	76/23843	0.122256	0.538562	0.512115	Acer3/Asah
GO_BP_m1	GO:000691	activation c	12/2606	76/23843	0.122256	0.538562	0.512115	Aifm1/Bok/
GO_BP_m1	GO:004591	positive re	12/2606	76/23843	0.122256	0.538562	0.512115	Adcyap1r1
GO_BP_m1	GO:190332	negative re	12/2606	76/23843	0.122256	0.538562	0.512115	Cav1/Svbp
GO_BP_m1	GO:00509	sensory pe	38/2606	287/23843	0.123043	0.541759	0.515154	Atp8b1/Cd
GO_BP_m1	GO:00605	epithelial t	48/2606	371/23843	0.12317	0.542045	0.515426	Abl2/Adm/
GO_BP_m1	GO:00485	oocyte dev	8/2606	46/23843	0.123745	0.542726	0.516073	Dmrt1/Wa
GO_BP_m1	GO:00986	regulation	8/2606	46/23843	0.123745	0.542726	0.516073	Cdh2/Dnm
GO_BP_m1	GO:20011	regulation	8/2606	46/23843	0.123745	0.542726	0.516073	Esrrb/Flcn/
GO_BP_m1	GO:19035	positive re	56/2606	439/23843	0.124031	0.542726	0.516073	Abat/Abl2/
GO_BP_m1	GO:00072	JNK cascad	26/2606	188/23843	0.124246	0.542726	0.516073	Cdc42ep5/
GO_BP_m1	GO:005067	positive re	26/2606	188/23843	0.124246	0.542726	0.516073	Arg1/Cav1
GO_BP_m1	GO:00316	zymogen a	10/2606	61/23843	0.12459	0.542726	0.516073	Asph/Casp
GO_BP_m1	GO:00193	nicotinami	13/2606	84/23843	0.124641	0.542726	0.516073	Bpgm/Eno
GO_BP_m1	GO:19035	positive re	13/2606	84/23843	0.124641	0.542726	0.516073	Adam8/Ccl
GO_BP_m1	GO:00313	negative re	30/2606	221/23843	0.124993	0.542726	0.516073	Anxa2/Apc
GO_BP_m1	GO:00507	positive re	25/2606	180/23843	0.125193	0.542726	0.516073	Adora1/Cd
GO_BP_m1	GO:000271	negative re	4/2606	18/23843	0.125861	0.542726	0.516073	Arg1/Clec4
GO_BP_m1	GO:00065	methionine	4/2606	18/23843	0.125861	0.542726	0.516073	Ahcyl2/Api
GO_BP_m1	GO:00107	positive re	4/2606	18/23843	0.125861	0.542726	0.516073	Cxcl17/Kar
GO_BP_m1	GO:00322	regulation	4/2606	18/23843	0.125861	0.542726	0.516073	Adora1/Nu
GO_BP_m1	GO:00326	negative re	4/2606	18/23843	0.125861	0.542726	0.516073	Il10/Jak3/
GO_BP_m1	GO:00331	positive re	4/2606	18/23843	0.125861	0.542726	0.516073	Cdk1/Ifng/
GO_BP_m1	GO:003411	negative re	4/2606	18/23843	0.125861	0.542726	0.516073	Abat/Alox1

GO_BP_m1	GO:00345٤	piRNA met	4/2606	18/23843	0.125861	0.542726	0.516073	Btbd18/Dd
GO_BP_m1	GO:003603	CD8-positi	4/2606	18/23843	0.125861	0.542726	0.516073	Gpr18/Ifng
GO_BP_m1	GO:00519	negative re	4/2606	18/23843	0.125861	0.542726	0.516073	Adora1/Ad
GO_BP_m1	GO:00602	mesenchyr	4/2606	18/23843	0.125861	0.542726	0.516073	Gdnf/Smo/
GO_BP_m1	GO:00901	negative re	4/2606	18/23843	0.125861	0.542726	0.516073	Flcn/Ifng/C
GO_BP_m1	GO:00028	negative re	7/2606	39/23843	0.127497	0.542726	0.516073	Cactin/Dhx
GO_BP_m1	GO:003157	G2 DNA da	7/2606	39/23843	0.127497	0.542726	0.516073	Blm/Baban
GO_BP_m1	GO:003287	negative re	7/2606	39/23843	0.127497	0.542726	0.516073	Dusp3/Ezr/
GO_BP_m1	GO:003317	calcineurin	7/2606	39/23843	0.127497	0.542726	0.516073	Akap6/Atp
GO_BP_m1	GO:004824	macrophag	7/2606	39/23843	0.127497	0.542726	0.516073	Cklf/Cxcl17
GO_BP_m1	GO:006032	face morpl	7/2606	39/23843	0.127497	0.542726	0.516073	Asph/Crisp
GO_BP_m1	GO:00703	negative re	7/2606	39/23843	0.127497	0.542726	0.516073	Dusp3/Ezr/
GO_BP_m1	GO:19029	regulation	7/2606	39/23843	0.127497	0.542726	0.516073	Adcyap1r1
GO_BP_m1	GO:00512	establishm	22/2606	156/23843	0.127564	0.542726	0.516073	Ahctf1/Atr/
GO_BP_m1	GO:00519	regulation	15/2606	100/23843	0.12758	0.542726	0.516073	Cdc23/Fen
GO_BP_m1	GO:000184	neural tub	16/2606	108/23843	0.128364	0.542726	0.516073	Abl2/Adm/
GO_BP_m1	GO:00444	symbiont p	45/2606	347/23843	0.128393	0.542726	0.516073	Anxa2/Arg
GO_BP_m1	GO:005072	negative re	20/2606	140/23843	0.128591	0.542726	0.516073	Adora1/Ao
GO_BP_m1	GO:00720	nephron d	20/2606	140/23843	0.128591	0.542726	0.516073	Basp1/Fgf1
GO_BP_m1	GO:000827	regulation	17/2606	116/23843	0.128801	0.542726	0.516073	Acpp/Adm
GO_BP_m1	GO:001802	peptidyl-ly	17/2606	116/23843	0.128801	0.542726	0.516073	Ash2l/Dmr
GO_BP_m1	GO:00448	cell cycle G	18/2606	124/23843	0.128954	0.542726	0.516073	Abcb1a/Bl
GO_BP_m1	GO:00902	regulation	34/2606	255/23843	0.129227	0.542726	0.516073	Adgra2/Ca
GO_BP_m1	GO:00071	cell-matrix	26/2606	189/23843	0.129841	0.542726	0.516073	Adam8/Ad
GO_BP_m1	GO:000244	neutrophil	6/2606	32/23843	0.130072	0.542726	0.516073	Anxa3/Arg
GO_BP_m1	GO:000301	respiratory	6/2606	32/23843	0.130072	0.542726	0.516073	Adh5/Ador
GO_BP_m1	GO:00070	peroxisom	6/2606	32/23843	0.130072	0.542726	0.516073	Abcd3/Lon
GO_BP_m1	GO:00335	mammary	6/2606	32/23843	0.130072	0.542726	0.516073	Epha2/Gpx
GO_BP_m1	GO:00602	long term	6/2606	32/23843	0.130072	0.542726	0.516073	Adora1/Dr
GO_BP_m1	GO:00708	DNA-temp	6/2606	32/23843	0.130072	0.542726	0.516073	Cand1/Gtf
GO_BP_m1	GO:00459	negative re	30/2606	222/23843	0.130153	0.542726	0.516073	Blm/Btg2/
GO_BP_m1	GO:00075	respiratory	9/2606	54/23843	0.130183	0.542726	0.516073	Adh5/Ador
GO_BP_m1	GO:00459	negative re	9/2606	54/23843	0.130183	0.542726	0.516073	Adra1d/Ak
GO_BP_m1	GO:00003	response t	5/2606	25/23843	0.130342	0.542726	0.516073	Cd36/Fbln
GO_BP_m1	GO:000151	prostaglan	5/2606	25/23843	0.130342	0.542726	0.516073	Avpr1a/Mg
GO_BP_m1	GO:00321	regulation	5/2606	25/23843	0.130342	0.542726	0.516073	Bbs2/Cartp
GO_BP_m1	GO:00321	regulation	5/2606	25/23843	0.130342	0.542726	0.516073	Bbs2/Cartp
GO_BP_m1	GO:00328	receptor ca	5/2606	25/23843	0.130342	0.542726	0.516073	Anxa2/Cdk
GO_BP_m1	GO:00464	prostanoid	5/2606	25/23843	0.130342	0.542726	0.516073	Avpr1a/Mg
GO_BP_m1	GO:004871	positive re	5/2606	25/23843	0.130342	0.542726	0.516073	Enpp2/Hda
GO_BP_m1	GO:007142	hematopoi	5/2606	25/23843	0.130342	0.542726	0.516073	Arih2/Eif2a
GO_BP_m1	GO:00718	podosome	5/2606	25/23843	0.130342	0.542726	0.516073	Dbnl/Fscn1
GO_BP_m1	GO:000001	regulation	12/2606	77/23843	0.131244	0.542726	0.516073	Aplf/Blm/F
GO_BP_m1	GO:005072	regulation	41/2606	314/23843	0.131267	0.542726	0.516073	Adam8/Ad
GO_BP_m1	GO:003424	regulation	56/2606	441/23843	0.131294	0.542726	0.516073	Bpgm/Btg
GO_BP_m1	GO:00613	neural pre	24/2606	173/23843	0.131991	0.542726	0.516073	Arx/Btg2/C
GO_BP_m1	GO:00422	ribosome b	38/2606	289/23843	0.132053	0.542726	0.516073	Bms1/Ddx
GO_BP_m1	GO:000631	DNA recon	32/2606	239/23843	0.13234	0.542726	0.516073	Aplf/Blm/C

GO_BP_m1	GO:004687	hormone s	45/2606	348/23843	0.132549	0.542726	0.516073	Abat/Adm
GO_BP_m1	GO:000082	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Atp2b4/Slc
GO_BP_m1	GO:000091	assembly c	2/2606	6/23843	0.133001	0.542726	0.516073	Kif23/Racg
GO_BP_m1	GO:000091	actomyosi	2/2606	6/23843	0.133001	0.542726	0.516073	Kif23/Racg
GO_BP_m1	GO:000282	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Il1rl1/Jak3
GO_BP_m1	GO:000606	ethanol me	2/2606	6/23843	0.133001	0.542726	0.516073	Adh1/Adh5
GO_BP_m1	GO:000610	isocitrate m	2/2606	6/23843	0.133001	0.542726	0.516073	Idh2/Idh3a
GO_BP_m1	GO:000677	Mo-molyb	2/2606	6/23843	0.133001	0.542726	0.516073	Gphn/Moc
GO_BP_m1	GO:001027	detoxificati	2/2606	6/23843	0.133001	0.542726	0.516073	Mt2/Mt3
GO_BP_m1	GO:001036	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Prkca/Tcaf
GO_BP_m1	GO:001058	miRNA cat	2/2606	6/23843	0.133001	0.542726	0.516073	Pnpt1/Zc3
GO_BP_m1	GO:001094	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Bnip3/Ripk
GO_BP_m1	GO:001405	acetylcholi	2/2606	6/23843	0.133001	0.542726	0.516073	Htr6/Tacr2
GO_BP_m1	GO:001405	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Htr6/Tacr2
GO_BP_m1	GO:001471	skeletal mu	2/2606	6/23843	0.133001	0.542726	0.516073	Ephb1/Wn
GO_BP_m1	GO:001969	choline me	2/2606	6/23843	0.133001	0.542726	0.516073	Ache/Bche
GO_BP_m1	GO:001972	Mo-molyb	2/2606	6/23843	0.133001	0.542726	0.516073	Gphn/Moc
GO_BP_m1	GO:002163	optic nerve	2/2606	6/23843	0.133001	0.542726	0.516073	Ephb1/Kcn
GO_BP_m1	GO:002186	forebrain v	2/2606	6/23843	0.133001	0.542726	0.516073	Dct/Pou3f
GO_BP_m1	GO:003017	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Cdk2/Ciz1
GO_BP_m1	GO:003088	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Il10/Tspan
GO_BP_m1	GO:003133	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Tbc1d4/Tri
GO_BP_m1	GO:003139	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Avpr1a/Ptg
GO_BP_m1	GO:003191	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Cdk5/Rgs1
GO_BP_m1	GO:003321	adiponecti	2/2606	6/23843	0.133001	0.542726	0.516073	Acsl1/Adip
GO_BP_m1	GO:003463	phosphatic	2/2606	6/23843	0.133001	0.542726	0.516073	Enpp2/Sca
GO_BP_m1	GO:003540	histone-th	2/2606	6/23843	0.133001	0.542726	0.516073	Pkn1/Prkca
GO_BP_m1	GO:003563	maintenan	2/2606	6/23843	0.133001	0.542726	0.516073	Abcb1a/Pt
GO_BP_m1	GO:003598	tendon de	2/2606	6/23843	0.133001	0.542726	0.516073	Col5a1/Mk
GO_BP_m1	GO:003800	paracrine s	2/2606	6/23843	0.133001	0.542726	0.516073	Mb21d1/T
GO_BP_m1	GO:004453	long-chain	2/2606	6/23843	0.133001	0.542726	0.516073	Acsl1/Cd36
GO_BP_m1	GO:004478	modulatio	2/2606	6/23843	0.133001	0.542726	0.516073	Pcx/Vapb
GO_BP_m1	GO:004479	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Pcx/Vapb
GO_BP_m1	GO:004483	actomyosi	2/2606	6/23843	0.133001	0.542726	0.516073	Kif23/Racg
GO_BP_m1	GO:004558	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Nckap1l/Pt
GO_BP_m1	GO:004664	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Nckap1l/Pt
GO_BP_m1	GO:004665	folic acid m	2/2606	6/23843	0.133001	0.542726	0.516073	Mtrr/Shmt
GO_BP_m1	GO:004679	transport c	2/2606	6/23843	0.133001	0.542726	0.516073	Cav1/Fmr1
GO_BP_m1	GO:004886	stem cell fa	2/2606	6/23843	0.133001	0.542726	0.516073	Ntf5/Sox18
GO_BP_m1	GO:005141	microtubul	2/2606	6/23843	0.133001	0.542726	0.516073	Tubgcp2/T
GO_BP_m1	GO:005157	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	H2afy/Prm
GO_BP_m1	GO:005158	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Arl6ip5/Sn
GO_BP_m1	GO:005158	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Gdnf/Snca
GO_BP_m1	GO:005194	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Gdnf/Snca
GO_BP_m1	GO:005505	asymmetri	2/2606	6/23843	0.133001	0.542726	0.516073	Dock7/Fgf
GO_BP_m1	GO:006043	lung growt	2/2606	6/23843	0.133001	0.542726	0.516073	Fgf7/Pdgfr
GO_BP_m1	GO:006072	intestinal e	2/2606	6/23843	0.133001	0.542726	0.516073	5730559C1
GO_BP_m1	GO:006090	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Dmrt1/Fbx

GO_BP_m1	GO:006119	fungiform	2/2606	6/23843	0.133001	0.542726	0.516073	Hdac1/Hda
GO_BP_m1	GO:006166	spontaneo	2/2606	6/23843	0.133001	0.542726	0.516073	Park2/Stx1
GO_BP_m1	GO:007016	adiponecti	2/2606	6/23843	0.133001	0.542726	0.516073	C1qtnf3/H
GO_BP_m1	GO:007016	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	C1qtnf3/H
GO_BP_m1	GO:007169	protein loc	2/2606	6/23843	0.133001	0.542726	0.516073	Dand5/Fbr
GO_BP_m1	GO:007192	cohesin loa	2/2606	6/23843	0.133001	0.542726	0.516073	Hdac8/Wa
GO_BP_m1	GO:007239	response t	2/2606	6/23843	0.133001	0.542726	0.516073	Fbxo18/Tig
GO_BP_m1	GO:007240	response t	2/2606	6/23843	0.133001	0.542726	0.516073	Fbxo18/Tig
GO_BP_m1	GO:007242	response t	2/2606	6/23843	0.133001	0.542726	0.516073	Fbxo18/Tig
GO_BP_m1	GO:007248	ammonium	2/2606	6/23843	0.133001	0.542726	0.516073	Rhd/Slc25a
GO_BP_m1	GO:007267	osteoclast	2/2606	6/23843	0.133001	0.542726	0.516073	Adam8/Sh
GO_BP_m1	GO:007267	thymocyte	2/2606	6/23843	0.133001	0.542726	0.516073	Adam8/Ccl
GO_BP_m1	GO:009025	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Park2/Ppar
GO_BP_m1	GO:009031	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Itgb1bp1/
GO_BP_m1	GO:009764	amylin rece	2/2606	6/23843	0.133001	0.542726	0.516073	Adm/Calcr
GO_BP_m1	GO:190207	cellular res	2/2606	6/23843	0.133001	0.542726	0.516073	Mapk13/Z
GO_BP_m1	GO:190393	response t	2/2606	6/23843	0.133001	0.542726	0.516073	Mapk13/Z
GO_BP_m1	GO:190423	pericyte ce	2/2606	6/23843	0.133001	0.542726	0.516073	Epha2/Osr
GO_BP_m1	GO:190477	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Epb41/Gna
GO_BP_m1	GO:190563	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Hdac8/Wa
GO_BP_m1	GO:199016	stress resp	2/2606	6/23843	0.133001	0.542726	0.516073	Mt2/Mt3
GO_BP_m1	GO:199041	replication	2/2606	6/23843	0.133001	0.542726	0.516073	Blm/Xrcc1
GO_BP_m1	GO:200007	regulation	2/2606	6/23843	0.133001	0.542726	0.516073	Arntl/Clock
GO_BP_m1	GO:200032	negative re	2/2606	6/23843	0.133001	0.542726	0.516073	Arntl/Clock
GO_BP_m1	GO:200039	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Enpp2/Rrel
GO_BP_m1	GO:200049	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Acta2/Dga
GO_BP_m1	GO:200067	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Hdac1/Spc
GO_BP_m1	GO:200080	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Cdh2/Nlgn
GO_BP_m1	GO:200101	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Arntl/Tbx1
GO_BP_m1	GO:200118	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Nckap1l/Pt
GO_BP_m1	GO:200128	positive re	2/2606	6/23843	0.133001	0.542726	0.516073	Avpr1a/Ptg
GO_BP_m1	GO:001403	neural cres	13/2606	85/23843	0.133261	0.542726	0.516073	Cfl1/Ednrb
GO_BP_m1	GO:001607	synaptic ve	13/2606	85/23843	0.133261	0.542726	0.516073	Fmr1/Rab5
GO_BP_m1	GO:200102	positive re	13/2606	85/23843	0.133261	0.542726	0.516073	Ankrd1/Atr
GO_BP_m1	GO:000854	epidermis	42/2606	323/23843	0.133841	0.542726	0.516073	Abca12/Ce
GO_BP_m1	GO:005077	negative re	22/2606	157/23843	0.133847	0.542726	0.516073	Arg1/Bcr/C
GO_BP_m1	GO:190495	positive re	60/2606	476/23843	0.13445	0.542726	0.516073	Abat/Abl2/
GO_BP_m1	GO:000224	hematopoi	21/2606	149/23843	0.134626	0.542726	0.516073	Acp6/Arhg
GO_BP_m1	GO:000157	vasculoger	14/2606	93/23843	0.134652	0.542726	0.516073	Adm/Cav1/
GO_BP_m1	GO:003475	cellular hor	14/2606	93/23843	0.134652	0.542726	0.516073	Adh1/Adm
GO_BP_m1	GO:001087	lipid localiz	46/2606	357/23843	0.134847	0.542726	0.516073	Abca12/Ab
GO_BP_m1	GO:001591	phospholip	10/2606	62/23843	0.134849	0.542726	0.516073	Abca12/Ab
GO_BP_m1	GO:005192	negative re	10/2606	62/23843	0.134849	0.542726	0.516073	Adra1d/Ca
GO_BP_m1	GO:003461	cellular res	20/2606	141/23843	0.135279	0.542726	0.516073	Bcar1/Bnip
GO_BP_m1	GO:004273	drug catab	20/2606	141/23843	0.135279	0.542726	0.516073	Ache/Adh1
GO_BP_m1	GO:007207	kidney epit	20/2606	141/23843	0.135279	0.542726	0.516073	Basp1/Eph
GO_BP_m1	GO:000602	aminoglyca	15/2606	101/23843	0.135545	0.542726	0.516073	B3gnt3/B3
GO_BP_m1	GO:003153	actin cytosl	15/2606	101/23843	0.135545	0.542726	0.516073	Antxr1/Arh

GO_BP_m1	GO:006041	heart grow	15/2606	101/23843	0.135545	0.542726	0.516073	Akap6/Cav
GO_BP_m1	GO:004484	cell cycle G	26/2606	190/23843	0.135585	0.542726	0.516073	Atp2b4/Ca
GO_BP_m1	GO:00017	neutrophil	3/2606	12/23843	0.135665	0.542726	0.516073	Hcar2/Ifng
GO_BP_m1	GO:000197	adenosine	3/2606	12/23843	0.135665	0.542726	0.516073	Acpp/Ador
GO_BP_m1	GO:000657	tyrosine m	3/2606	12/23843	0.135665	0.542726	0.516073	Dct/Hpdl/
GO_BP_m1	GO:000667	sphingosin	3/2606	12/23843	0.135665	0.542726	0.516073	Acer3/Asa
GO_BP_m1	GO:00094	carnitine m	3/2606	12/23843	0.135665	0.542726	0.516073	Aldh9a1/C
GO_BP_m1	GO:00157	nucleotide	3/2606	12/23843	0.135665	0.542726	0.516073	Slc35a5/Sl
GO_BP_m1	GO:00165	protein im	3/2606	12/23843	0.135665	0.542726	0.516073	Pex10/Pex
GO_BP_m1	GO:003114	anaphase-	3/2606	12/23843	0.135665	0.542726	0.516073	1500015O
GO_BP_m1	GO:00327	low-densit	3/2606	12/23843	0.135665	0.542726	0.516073	Anxa2/Pcs
GO_BP_m1	GO:00329	negative re	3/2606	12/23843	0.135665	0.542726	0.516073	Dand5/Len
GO_BP_m1	GO:00332	response t	3/2606	12/23843	0.135665	0.542726	0.516073	Cyp24a1/K
GO_BP_m1	GO:00340	maintenan	3/2606	12/23843	0.135665	0.542726	0.516073	H2afy/Naa
GO_BP_m1	GO:00341	toll-like re	3/2606	12/23843	0.135665	0.542726	0.516073	Ptpn22/Tn
GO_BP_m1	GO:00343	positive re	3/2606	12/23843	0.135665	0.542726	0.516073	E2f3/Ifng/I
GO_BP_m1	GO:00349	histone ar	3/2606	12/23843	0.135665	0.542726	0.516073	Prmt1/Prm
GO_BP_m1	GO:00423	fat-soluble	3/2606	12/23843	0.135665	0.542726	0.516073	Ifng/Nfkb1
GO_BP_m1	GO:00428	antibiotic t	3/2606	12/23843	0.135665	0.542726	0.516073	Abcb1a/Ra
GO_BP_m1	GO:004331	neutrophil	3/2606	12/23843	0.135665	0.542726	0.516073	Anxa3/Bcr
GO_BP_m1	GO:004337	CD8-positi	3/2606	12/23843	0.135665	0.542726	0.516073	Gpr18/Ifng
GO_BP_m1	GO:004814	astrocyte a	3/2606	12/23843	0.135665	0.542726	0.516073	Fpr2/Smo/
GO_BP_m1	GO:00514	myoblast n	3/2606	12/23843	0.135665	0.542726	0.516073	Itgb1bp1/
GO_BP_m1	GO:00605	multicellul	3/2606	12/23843	0.135665	0.542726	0.516073	Hyal2/Rhd
GO_BP_m1	GO:007034	fat cell pro	3/2606	12/23843	0.135665	0.542726	0.516073	E2f1/E2f3/
GO_BP_m1	GO:007034	regulation	3/2606	12/23843	0.135665	0.542726	0.516073	E2f1/E2f3/
GO_BP_m1	GO:00704	nucleotide	3/2606	12/23843	0.135665	0.542726	0.516073	5730559C1
GO_BP_m1	GO:00704	nucleotide	3/2606	12/23843	0.135665	0.542726	0.516073	5730559C1
GO_BP_m1	GO:00709	histone H3	3/2606	12/23843	0.135665	0.542726	0.516073	Elk4/Hdac1
GO_BP_m1	GO:007124	cellular res	3/2606	12/23843	0.135665	0.542726	0.516073	Mapk13/M
GO_BP_m1	GO:007134	skeletal m	3/2606	12/23843	0.135665	0.542726	0.516073	Lrp4/Mesd
GO_BP_m1	GO:19002	regulation	3/2606	12/23843	0.135665	0.542726	0.516073	Cd36/Eif2a
GO_BP_m1	GO:19004	regulation	3/2606	12/23843	0.135665	0.542726	0.516073	Kat2a/Kat2
GO_BP_m1	GO:190184	regulation	3/2606	12/23843	0.135665	0.542726	0.516073	Cacnb2/Pd
GO_BP_m1	GO:19022	semaphori	3/2606	12/23843	0.135665	0.542726	0.516073	Plxna2/Plx
GO_BP_m1	GO:00461	phenol-co	8/2606	47/23843	0.135681	0.542726	0.516073	Dct/Ddt/G
GO_BP_m1	GO:00607	negative re	8/2606	47/23843	0.135681	0.542726	0.516073	Arg1/Cacti
GO_BP_m1	GO:00702	necrotic ce	8/2606	47/23843	0.135681	0.542726	0.516073	Bnip3/Bok
GO_BP_m1	GO:00072	phospholi	16/2606	109/23843	0.136037	0.543328	0.516646	Adra1d/An
GO_BP_m1	GO:00606	tube closu	16/2606	109/23843	0.136037	0.543328	0.516646	Abl2/Adm
GO_BP_m1	GO:20001	regulation	16/2606	109/23843	0.136037	0.543328	0.516646	Adam8/Bl
GO_BP_m1	GO:00347	negative re	18/2606	125/23843	0.136102	0.543328	0.516646	Adra1d/Ar
GO_BP_m1	GO:00067	ATP biosyn	17/2606	117/23843	0.136203	0.543328	0.516646	Atp5a1/At
GO_BP_m1	GO:190037	regulation	17/2606	117/23843	0.136203	0.543328	0.516646	Adra1d/Ak
GO_BP_m1	GO:00068	nitric oxide	11/2606	70/23843	0.13821	0.550832	0.523782	Atp2b4/Ca
GO_BP_m1	GO:007217	mesoneph	11/2606	70/23843	0.13821	0.550832	0.523782	Fgf1/Gdnf/
GO_BP_m1	GO:00439	positive re	23/2606	166/23843	0.13923	0.554487	0.527257	Arg1/Cfl1/
GO_BP_m1	GO:000301	muscle sys	48/2606	375/23843	0.139253	0.554487	0.527257	Abat/Acta

GO_BP_m1	GO:003582	modificatic	22/2606	158/23843	0.140309	0.55802	0.530616	Anxa2/Arg
GO_BP_m1	GO:000226	lymphocyte	12/2606	78/23843	0.140585	0.55802	0.530616	Dock10/Gp
GO_BP_m1	GO:001403	neural cres	12/2606	78/23843	0.140585	0.55802	0.530616	Cfl1/Ednrb/
GO_BP_m1	GO:003016	platelet act	12/2606	78/23843	0.140585	0.55802	0.530616	Abat/Alox1
GO_BP_m1	GO:003019	regulation	12/2606	78/23843	0.140585	0.55802	0.530616	Abat/Alox1
GO_BP_m1	GO:007207	nephron tu	12/2606	78/23843	0.140585	0.55802	0.530616	Fgf1/Gdnf/
GO_BP_m1	GO:190004	regulation	12/2606	78/23843	0.140585	0.55802	0.530616	Abat/Alox1
GO_BP_m1	GO:000282	negative re	7/2606	40/23843	0.14083	0.558235	0.530821	Arg1/Clec4
GO_BP_m1	GO:000602	glycosamir	7/2606	40/23843	0.14083	0.558235	0.530821	Chst13/Csg
GO_BP_m1	GO:004337	regulation	7/2606	40/23843	0.14083	0.558235	0.530821	Ifng/Il2rg/J
GO_BP_m1	GO:004660	regulation	9/2606	55/23843	0.141463	0.560492	0.532967	Chmp1b/K
GO_BP_m1	GO:007146	cellular res	20/2606	142/23843	0.142167	0.562153	0.534547	Acsl1/Akr1
GO_BP_m1	GO:000611	oxidative p	13/2606	86/23843	0.142202	0.562153	0.534547	Atp5o/Cdk
GO_BP_m1	GO:000616	nucleoside	13/2606	86/23843	0.142202	0.562153	0.534547	Bpgm/Eno
GO_BP_m1	GO:000930	amine met	13/2606	86/23843	0.142202	0.562153	0.534547	Abat/Agma
GO_BP_m1	GO:004434	cellular res	13/2606	86/23843	0.142202	0.562153	0.534547	Ctgf/Dll4/F
GO_BP_m1	GO:190129	nucleoside	19/2606	134/23843	0.142903	0.564668	0.536938	Bpgm/Dera
GO_BP_m1	GO:005132	meiotic cel	44/2606	342/23843	0.143174	0.565232	0.537474	Btbd18/Ca
GO_BP_m1	GO:005196	negative re	44/2606	342/23843	0.143174	0.565232	0.537474	Aatk/Calr/C
GO_BP_m1	GO:003080	regulation	17/2606	118/23843	0.143842	0.567613	0.539738	Adra1d/Ak
GO_BP_m1	GO:000268	regulation	16/2606	110/23843	0.143964	0.56784	0.539955	Calr/Ccl4/C
GO_BP_m1	GO:000000	mitochond	6/2606	33/23843	0.145152	0.569433	0.541469	Flcn/Lig3/P
GO_BP_m1	GO:000046	maturation	6/2606	33/23843	0.145152	0.569433	0.541469	Eri1/Exosc9
GO_BP_m1	GO:000638	transcriptic	6/2606	33/23843	0.145152	0.569433	0.541469	Foxa2/Gtf3
GO_BP_m1	GO:003438	plasma lipc	6/2606	33/23843	0.145152	0.569433	0.541469	Anxa2/Cd3
GO_BP_m1	GO:190102	positive re	6/2606	33/23843	0.145152	0.569433	0.541469	Akap6/Asp
GO_BP_m1	GO:190166	quinone m	6/2606	33/23843	0.145152	0.569433	0.541469	Akr1c12/Cl
GO_BP_m1	GO:190305	regulation	6/2606	33/23843	0.145152	0.569433	0.541469	Abl2/Antxr
GO_BP_m1	GO:190395	regulation	6/2606	33/23843	0.145152	0.569433	0.541469	Abcb1a/Ar
GO_BP_m1	GO:007121	cellular res	36/2606	275/23843	0.145421	0.569433	0.541469	Ankrd1/Atr
GO_BP_m1	GO:010400	cellular res	36/2606	275/23843	0.145421	0.569433	0.541469	Ankrd1/Atr
GO_BP_m1	GO:000165	branching	10/2606	63/23843	0.145541	0.569433	0.541469	Fgf1/Gdnf/
GO_BP_m1	GO:004545	cell redox h	10/2606	63/23843	0.145541	0.569433	0.541469	Ero1l/Gpx1
GO_BP_m1	GO:000989	positive re	49/2606	385/23843	0.14557	0.569433	0.541469	Adam8/An
GO_BP_m1	GO:004352	regulation	33/2606	250/23843	0.146181	0.569433	0.541469	Adam8/Aif
GO_BP_m1	GO:004819	Golgi vesic	33/2606	250/23843	0.146181	0.569433	0.541469	Ankfy1/Arf
GO_BP_m1	GO:000197	response to	4/2606	19/23843	0.146377	0.569433	0.541469	Drd3/Drd5
GO_BP_m1	GO:000652	arginine m	4/2606	19/23843	0.146377	0.569433	0.541469	Arg1/Atp2l
GO_BP_m1	GO:000820	androgen r	4/2606	19/23843	0.146377	0.569433	0.541469	Adm/Hsd1
GO_BP_m1	GO:000908	branched-(	4/2606	19/23843	0.146377	0.569433	0.541469	Bcat2/Bckc
GO_BP_m1	GO:001066	positive re	4/2606	19/23843	0.146377	0.569433	0.541469	Bnip3/Cam
GO_BP_m1	GO:001066	positive re	4/2606	19/23843	0.146377	0.569433	0.541469	Bnip3/Cam
GO_BP_m1	GO:001622	iron-sulfur	4/2606	19/23843	0.146377	0.569433	0.541469	Ciao1/Iba5
GO_BP_m1	GO:003116	metallo-su	4/2606	19/23843	0.146377	0.569433	0.541469	Ciao1/Iba5
GO_BP_m1	GO:003209	regulation	4/2606	19/23843	0.146377	0.569433	0.541469	Bbs2/Cartp
GO_BP_m1	GO:003236	intracellula	4/2606	19/23843	0.146377	0.569433	0.541469	Anxa2/Ldlr
GO_BP_m1	GO:003549	SNARE cor	4/2606	19/23843	0.146377	0.569433	0.541469	Stx4a/Trim
GO_BP_m1	GO:003599	response to	4/2606	19/23843	0.146377	0.569433	0.541469	Ankrd1/Ca

GO_BP_m1	GO:005158	regulation	4/2606	19/23843	0.146377	0.569433	0.541469	Arl6ip5/Gd
GO_BP_m1	GO:005190	regulation	4/2606	19/23843	0.146377	0.569433	0.541469	Alox12/Bok
GO_BP_m1	GO:006045	positive reg	4/2606	19/23843	0.146377	0.569433	0.541469	Nr1h2/Opr
GO_BP_m1	GO:009720	renal filtrat	4/2606	19/23843	0.146377	0.569433	0.541469	Adora1/Itg
GO_BP_m1	GO:000708	regulation	22/2606	159/23843	0.146948	0.571038	0.542995	Bora/Cdc23
GO_BP_m1	GO:000636	rRNA proce	26/2606	192/23843	0.147519	0.571038	0.542995	Bms1/Ddx2
GO_BP_m1	GO:000688	cellular zinc	5/2606	26/23843	0.1477	0.571038	0.542995	Atp7b/Mt2
GO_BP_m1	GO:000906	glutamine	5/2606	26/23843	0.1477	0.571038	0.542995	Aldh4a1/Ar
GO_BP_m1	GO:000971	catechol-c	5/2606	26/23843	0.1477	0.571038	0.542995	Gch1/Hdc/
GO_BP_m1	GO:001049	proteasom	5/2606	26/23843	0.1477	0.571038	0.542995	Psma3/Psm
GO_BP_m1	GO:003026	apoptotic r	5/2606	26/23843	0.1477	0.571038	0.542995	Aifm1/Dffa
GO_BP_m1	GO:003136	N-terminal	5/2606	26/23843	0.1477	0.571038	0.542995	Kat2b/Map
GO_BP_m1	GO:004242	catecholam	5/2606	26/23843	0.1477	0.571038	0.542995	Gch1/Hdc/
GO_BP_m1	GO:004578	positive reg	5/2606	26/23843	0.1477	0.571038	0.542995	Adam8/Os
GO_BP_m1	GO:004685	positive reg	5/2606	26/23843	0.1477	0.571038	0.542995	Adam8/Os
GO_BP_m1	GO:007029	sarcoplasm	5/2606	26/23843	0.1477	0.571038	0.542995	Cacng1/Dh
GO_BP_m1	GO:009018	regulation	5/2606	26/23843	0.1477	0.571038	0.542995	Gdnf/Lgr4/
GO_BP_m1	GO:190339	positive reg	5/2606	26/23843	0.1477	0.571038	0.542995	Cfl1/Enpp2
GO_BP_m1	GO:001610	diterpenoic	8/2606	48/23843	0.148176	0.57158	0.54351	Adh1/Adh5
GO_BP_m1	GO:002154	cranial nerv	8/2606	48/23843	0.148176	0.57158	0.54351	Atp8b1/Ep
GO_BP_m1	GO:004366	regulation	8/2606	48/23843	0.148176	0.57158	0.54351	2810408A1
GO_BP_m1	GO:190157	fatty acid d	8/2606	48/23843	0.148176	0.57158	0.54351	Alox12/Alo
GO_BP_m1	GO:200040	regulation	8/2606	48/23843	0.148176	0.57158	0.54351	Adam8/Ccl
GO_BP_m1	GO:009009	regulation	29/2606	217/23843	0.148231	0.57158	0.54351	Bmp3/Cav1
GO_BP_m1	GO:000918	cyclic nucle	20/2606	143/23843	0.14925	0.575258	0.547008	Adcy4/Adr
GO_BP_m1	GO:007208	stem cell p	19/2606	135/23843	0.150231	0.576454	0.548145	Abcb1a/Ar
GO_BP_m1	GO:003450	protein loc	36/2606	276/23843	0.150507	0.576454	0.548145	1700123L1
GO_BP_m1	GO:000269	positive reg	13/2606	87/23843	0.151459	0.576454	0.548145	Calr/Ccl4/C
GO_BP_m1	GO:000918	ribonucleos	13/2606	87/23843	0.151459	0.576454	0.548145	Bpgm/Eno3
GO_BP_m1	GO:003243	regulation	17/2606	119/23843	0.151714	0.576454	0.548145	Arih2/Bcap
GO_BP_m1	GO:004863	positive reg	27/2606	201/23843	0.151889	0.576454	0.548145	Akap6/Arx/
GO_BP_m1	GO:000911	nucleoside	14/2606	95/23843	0.152092	0.576454	0.548145	Acpp/Adk/
GO_BP_m1	GO:000194	hair follicle	16/2606	111/23843	0.152141	0.576454	0.548145	Ctsl/Fgf7/F
GO_BP_m1	GO:000006	protein imp	9/2606	56/23843	0.153222	0.576454	0.548145	Abra/Arntl/
GO_BP_m1	GO:001081	negative re	9/2606	56/23843	0.153222	0.576454	0.548145	Bcar1/Bcas
GO_BP_m1	GO:007234	response to	9/2606	56/23843	0.153222	0.576454	0.548145	Abat/Adra1
GO_BP_m1	GO:000686	lipid transp	41/2606	319/23843	0.154383	0.576454	0.548145	Abca12/Ab
GO_BP_m1	GO:000669	prostanoid	7/2606	41/23843	0.154803	0.576454	0.548145	Akr1c12/Av
GO_BP_m1	GO:000669	prostaglan	7/2606	41/23843	0.154803	0.576454	0.548145	Akr1c12/Av
GO_BP_m1	GO:001047	regulation	7/2606	41/23843	0.154803	0.576454	0.548145	Col5a1/Fox
GO_BP_m1	GO:003237	regulation	7/2606	41/23843	0.154803	0.576454	0.548145	Abca12/Ar
GO_BP_m1	GO:003237	regulation	7/2606	41/23843	0.154803	0.576454	0.548145	Abca12/Ar
GO_BP_m1	GO:003292	activin rece	7/2606	41/23843	0.154803	0.576454	0.548145	Cfc1/Dand
GO_BP_m1	GO:004218	ketone bios	7/2606	41/23843	0.154803	0.576454	0.548145	Coq10b/Co
GO_BP_m1	GO:003237	positive reg	10/2606	64/23843	0.156653	0.576454	0.548145	Abca12/Ar
GO_BP_m1	GO:000008	G1/S transi	24/2606	177/23843	0.157291	0.576454	0.548145	Camk2a/Cc
GO_BP_m1	GO:000920	purine ribo	18/2606	128/23843	0.158871	0.576454	0.548145	Atp5a1/Atp
GO_BP_m1	GO:004559	regulation	18/2606	128/23843	0.158871	0.576454	0.548145	Adig/Arntl/

GO_BP_m1	GO:004427	sulfur com	11/2606	72/23843	0.158912	0.576454	0.548145	Apip/Chst1
GO_BP_m1	GO:00550	cardiac mu	11/2606	72/23843	0.158912	0.576454	0.548145	Ankrd1/Dll
GO_BP_m1	GO:004881	dendrite m	23/2606	169/23843	0.159041	0.576454	0.548145	Abi1/Abl2/
GO_BP_m1	GO:00171	regulation	12/2606	80/23843	0.1603	0.576454	0.548145	Catsper3/
GO_BP_m1	GO:00720	nephron e	12/2606	80/23843	0.1603	0.576454	0.548145	Fgf1/Gdnf/
GO_BP_m1	GO:19001	positive re	12/2606	80/23843	0.1603	0.576454	0.548145	Cct3/Cdk1
GO_BP_m1	GO:00461	alcohol bio	16/2606	112/23843	0.160564	0.576454	0.548145	Acer3/Adc
GO_BP_m1	GO:00109	regulation	50/2606	397/23843	0.160639	0.576454	0.548145	Adcyap1r1
GO_BP_m1	GO:00019	negative re	6/2606	34/23843	0.160984	0.576454	0.548145	Bcas3/Enp
GO_BP_m1	GO:00320	response t	6/2606	34/23843	0.160984	0.576454	0.548145	Bbs2/Cart
GO_BP_m1	GO:00336	regulation	6/2606	34/23843	0.160984	0.576454	0.548145	Cib1/Epha
GO_BP_m1	GO:00400	regulation	6/2606	34/23843	0.160984	0.576454	0.548145	Calr/Cdc2
GO_BP_m1	GO:00508	intestinal a	6/2606	34/23843	0.160984	0.576454	0.548145	Abcb1a/Cc
GO_BP_m1	GO:00973	response t	6/2606	34/23843	0.160984	0.576454	0.548145	Bcar1/Drd
GO_BP_m1	GO:00987	bone cell d	6/2606	34/23843	0.160984	0.576454	0.548145	Abi1/Anxa
GO_BP_m1	GO:20001	positive re	6/2606	34/23843	0.160984	0.576454	0.548145	Adam8/Hc
GO_BP_m1	GO:20007	regulation	6/2606	34/23843	0.160984	0.576454	0.548145	Arntl/Mb2
GO_BP_m1	GO:00469	nucleotide	13/2606	88/23843	0.161026	0.576454	0.548145	Bpgm/Eno
GO_BP_m1	GO:00609	regulation	13/2606	88/23843	0.161026	0.576454	0.548145	Arhgap44/
GO_BP_m1	GO:00717	response t	13/2606	88/23843	0.161026	0.576454	0.548145	Ctgf/Dll4/
GO_BP_m1	GO:00726	lymphocyt	13/2606	88/23843	0.161026	0.576454	0.548145	Adam8/Cc
GO_BP_m1	GO:00352	segmentati	15/2606	104/23843	0.16106	0.576454	0.548145	Abi1/Foxa
GO_BP_m1	GO:00019	positive re	8/2606	49/23843	0.161207	0.576454	0.548145	Ccl28/Cd3
GO_BP_m1	GO:003111	regulation	8/2606	49/23843	0.161207	0.576454	0.548145	Ankrd53/C
GO_BP_m1	GO:19020	regulation	8/2606	49/23843	0.161207	0.576454	0.548145	Atf3/Dapk
GO_BP_m1	GO:20006	regulation	8/2606	49/23843	0.161207	0.576454	0.548145	Cav3/Drd3
GO_BP_m1	GO:00105	regulation	14/2606	96/23843	0.161242	0.576454	0.548145	Adcyap1r1
GO_BP_m1	GO:00421	positive re	14/2606	96/23843	0.161242	0.576454	0.548145	Adk/Blm/B
GO_BP_m1	GO:00442	cellular pol	14/2606	96/23843	0.161242	0.576454	0.548145	Aoah/B3gr
GO_BP_m1	GO:00608	artery deve	14/2606	96/23843	0.161242	0.576454	0.548145	Adamts9/
GO_BP_m1	GO:00720	nephron tu	14/2606	96/23843	0.161242	0.576454	0.548145	Fgf1/Gdnf/
GO_BP_m1	GO:00506	nucleic aci	21/2606	153/23843	0.162408	0.576454	0.548145	Ahctf1/Dd
GO_BP_m1	GO:00506	RNA trans	21/2606	153/23843	0.162408	0.576454	0.548145	Ahctf1/Dd
GO_BP_m1	GO:00004	maturation	3/2606	13/23843	0.162749	0.576454	0.548145	Ftsj3/Rpf2/
GO_BP_m1	GO:00020	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Adora1/Gl
GO_BP_m1	GO:000641	translation	3/2606	13/23843	0.162749	0.576454	0.548145	Gspt2/Mtrf
GO_BP_m1	GO:00065	thyroid ho	3/2606	13/23843	0.162749	0.576454	0.548145	Dio2/Duox
GO_BP_m1	GO:00071	meiosis II	3/2606	13/23843	0.162749	0.576454	0.548145	Mastl/Ppp
GO_BP_m1	GO:00071	adenylate	3/2606	13/23843	0.162749	0.576454	0.548145	Adra1d/Dr
GO_BP_m1	GO:00090	methionin	3/2606	13/23843	0.162749	0.576454	0.548145	Apip/Enop
GO_BP_m1	GO:00103	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Abcb1a/Pr
GO_BP_m1	GO:001087	cholesterol	3/2606	13/23843	0.162749	0.576454	0.548145	Cd36/Nr1h
GO_BP_m1	GO:00108	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Fkbp1b/Hr
GO_BP_m1	GO:00109	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Cd36/Gprc
GO_BP_m1	GO:00109	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Eif2ak1/Eif
GO_BP_m1	GO:001481	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Cav3/Myh
GO_BP_m1	GO:00190	modulatio	3/2606	13/23843	0.162749	0.576454	0.548145	Park2/Vap
GO_BP_m1	GO:00216	cranial ner	3/2606	13/23843	0.162749	0.576454	0.548145	Hoxb1/Kcn

GO_BP_m1	GO:003165	positive reg	3/2606	13/23843	0.162749	0.576454	0.548145	Abat/Ptgs2
GO_BP_m1	GO:003209	negative re	3/2606	13/23843	0.162749	0.576454	0.548145	Bbs2/Cartp
GO_BP_m1	GO:003408	maintenan	3/2606	13/23843	0.162749	0.576454	0.548145	H2afy/Naa
GO_BP_m1	GO:003587	nucleotide-	3/2606	13/23843	0.162749	0.576454	0.548145	5730559C1
GO_BP_m1	GO:004249	gamma-de	3/2606	13/23843	0.162749	0.576454	0.548145	Gpr18/Nck
GO_BP_m1	GO:004269	muscle cell	3/2606	13/23843	0.162749	0.576454	0.548145	Tbx1/Wnt3
GO_BP_m1	GO:004311	positive reg	3/2606	13/23843	0.162749	0.576454	0.548145	Ccl4/Tacr2/
GO_BP_m1	GO:004454	NLRP3 infla	3/2606	13/23843	0.162749	0.576454	0.548145	Cd36/Eif2a
GO_BP_m1	GO:004565	positive reg	3/2606	13/23843	0.162749	0.576454	0.548145	Casp8/Prkc
GO_BP_m1	GO:004583	negative re	3/2606	13/23843	0.162749	0.576454	0.548145	Arl6ip5/Bni
GO_BP_m1	GO:004590	negative re	3/2606	13/23843	0.162749	0.576454	0.548145	Adm/Dock
GO_BP_m1	GO:004618	aldehyde c	3/2606	13/23843	0.162749	0.576454	0.548145	Adh5/Esd/
GO_BP_m1	GO:004647	phosphatic	3/2606	13/23843	0.162749	0.576454	0.548145	Agpat2/Dg
GO_BP_m1	GO:004650	S-adenosy	3/2606	13/23843	0.162749	0.576454	0.548145	Ahcyl2/Ma
GO_BP_m1	GO:004801	hepatocyte	3/2606	13/23843	0.162749	0.576454	0.548145	Bcar1/Pak1
GO_BP_m1	GO:005264	alditol pho	3/2606	13/23843	0.162749	0.576454	0.548145	Acp6/Gk2/
GO_BP_m1	GO:005508	fatty acid h	3/2606	13/23843	0.162749	0.576454	0.548145	Dgat1/Got
GO_BP_m1	GO:006019	negative re	3/2606	13/23843	0.162749	0.576454	0.548145	Angptl3/Pl
GO_BP_m1	GO:006027	embryonic	3/2606	13/23843	0.162749	0.576454	0.548145	Nog/Osr1/
GO_BP_m1	GO:006028	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Npr2/Ppp2
GO_BP_m1	GO:006073	positive reg	3/2606	13/23843	0.162749	0.576454	0.548145	Adcyap1r1
GO_BP_m1	GO:006085	establishm	3/2606	13/23843	0.162749	0.576454	0.548145	Abcb1a/Ac
GO_BP_m1	GO:006115	3'-UTR-me	3/2606	13/23843	0.162749	0.576454	0.548145	Cpeb3/Khs
GO_BP_m1	GO:006198	meiosis II c	3/2606	13/23843	0.162749	0.576454	0.548145	Mastl/Ppp2
GO_BP_m1	GO:009011	cargo load	3/2606	13/23843	0.162749	0.576454	0.548145	Mia3/Sec24
GO_BP_m1	GO:009033	negative re	3/2606	13/23843	0.162749	0.576454	0.548145	Abat/Alox1
GO_BP_m1	GO:009033	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Mecom/Ptg
GO_BP_m1	GO:009709	presynapti	3/2606	13/23843	0.162749	0.576454	0.548145	Lrp4/Lrrtm
GO_BP_m1	GO:009905	presynapse	3/2606	13/23843	0.162749	0.576454	0.548145	Lrp4/Nlgn3
GO_BP_m1	GO:190012	negative re	3/2606	13/23843	0.162749	0.576454	0.548145	Il10/Nog/P
GO_BP_m1	GO:190074	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Adgra2/Cd
GO_BP_m1	GO:190228	semaphori	3/2606	13/23843	0.162749	0.576454	0.548145	Plxna2/Plxn
GO_BP_m1	GO:190381	positive reg	3/2606	13/23843	0.162749	0.576454	0.548145	Akap6/Kcn
GO_BP_m1	GO:190587	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Npr2/Ppp2
GO_BP_m1	GO:200005	positive reg	3/2606	13/23843	0.162749	0.576454	0.548145	Abl2/Csnk1
GO_BP_m1	GO:200103	regulation	3/2606	13/23843	0.162749	0.576454	0.548145	Dek/Nudt1
GO_BP_m1	GO:005104	positive reg	61/2606	492/23843	0.162795	0.576454	0.548145	Abat/Abl2/
GO_BP_m1	GO:001908	viral gene e	9/2606	57/23843	0.165443	0.576454	0.548145	Ccl4/Eif3f/
GO_BP_m1	GO:005067	positive reg	19/2606	137/23843	0.165499	0.576454	0.548145	Adk/Blm/B
GO_BP_m1	GO:190355	regulation	19/2606	137/23843	0.165499	0.576454	0.548145	Adam8/Ca
GO_BP_m1	GO:001080	regulation	5/2606	27/23843	0.165974	0.576454	0.548145	Ccdc3/Park
GO_BP_m1	GO:003048	tRNA meth	5/2606	27/23843	0.165974	0.576454	0.548145	Gtpbp3/Me
GO_BP_m1	GO:004810	somatic ste	5/2606	27/23843	0.165974	0.576454	0.548145	Dct/Dock7/
GO_BP_m1	GO:005506	zinc ion ho	5/2606	27/23843	0.165974	0.576454	0.548145	Atp7b/Mt2
GO_BP_m1	GO:007023	negative re	5/2606	27/23843	0.165974	0.576454	0.548145	Blm/Dock8
GO_BP_m1	GO:190223	regulation	5/2606	27/23843	0.165974	0.576454	0.548145	Bok/Nck2/
GO_BP_m1	GO:001025	endomemb	44/2606	347/23843	0.166507	0.576454	0.548145	Ahnak2/Ar
GO_BP_m1	GO:000911	vitamin bio	4/2606	20/23843	0.168079	0.576454	0.548145	Ifng/Mmac

GO_BP_m1	GO:001003	response t	4/2606	20/23843	0.168079	0.576454	0.548145	Abat/Casp
GO_BP_m1	GO:001407	response t	4/2606	20/23843	0.168079	0.576454	0.548145	Drd3/Drd5
GO_BP_m1	GO:003164	negative re	4/2606	20/23843	0.168079	0.576454	0.548145	Avpr1a/Ifn
GO_BP_m1	GO:003251	negative re	4/2606	20/23843	0.168079	0.576454	0.548145	Fkbp1b/Ma
GO_BP_m1	GO:003268	negative re	4/2606	20/23843	0.168079	0.576454	0.548145	C1qtnf3/Ep
GO_BP_m1	GO:003359	regulation	4/2606	20/23843	0.168079	0.576454	0.548145	Gpx1/Pygc
GO_BP_m1	GO:004398	histone H4	4/2606	20/23843	0.168079	0.576454	0.548145	Kansl1/Kan
GO_BP_m1	GO:004413	negative re	4/2606	20/23843	0.168079	0.576454	0.548145	Cd36/Ifng/
GO_BP_m1	GO:006000	Sertoli cell	4/2606	20/23843	0.168079	0.576454	0.548145	Dmrt1/Hsd
GO_BP_m1	GO:007207	nephron tu	4/2606	20/23843	0.168079	0.576454	0.548145	Gdnf/Irx2/
GO_BP_m1	GO:007224	metanephr	4/2606	20/23843	0.168079	0.576454	0.548145	Lamb2/Lgr
GO_BP_m1	GO:008011	DNA deme	4/2606	20/23843	0.168079	0.576454	0.548145	Apobec1/T
GO_BP_m1	GO:009033	regulation	4/2606	20/23843	0.168079	0.576454	0.548145	Abat/Alox1
GO_BP_m1	GO:009963	protein tra	4/2606	20/23843	0.168079	0.576454	0.548145	Arhgap44/
GO_BP_m1	GO:009963	neurotrans	4/2606	20/23843	0.168079	0.576454	0.548145	Arhgap44/
GO_BP_m1	GO:190010	regulation	4/2606	20/23843	0.168079	0.576454	0.548145	Bok/Ficd/N
GO_BP_m1	GO:190520	negative re	4/2606	20/23843	0.168079	0.576454	0.548145	Cav3/Pak1
GO_BP_m1	GO:000222	pattern rec	17/2606	121/23843	0.168147	0.576454	0.548145	5730559C1
GO_BP_m1	GO:001810	peptidyl-th	17/2606	121/23843	0.168147	0.576454	0.548145	Camk2a/Cc
GO_BP_m1	GO:000740	neuroblast	10/2606	65/23843	0.168172	0.576454	0.548145	Dct/Dmrta
GO_BP_m1	GO:003508	axoneme a	10/2606	65/23843	0.168172	0.576454	0.548145	Bbs2/Cc2d
GO_BP_m1	GO:004477	mitotic DN	10/2606	65/23843	0.168172	0.576454	0.548145	Blm/Ccng1
GO_BP_m1	GO:190495	negative re	25/2606	187/23843	0.168704	0.576454	0.548145	C1qtnf3/Cc
GO_BP_m1	GO:000269	regulation	45/2606	356/23843	0.168761	0.576454	0.548145	Aplf/Arg1/
GO_BP_m1	GO:001090	regulation	16/2606	113/23843	0.169228	0.576454	0.548145	C1qtnf3/Cc
GO_BP_m1	GO:004654	developme	16/2606	113/23843	0.169228	0.576454	0.548145	Ccdc182/A
GO_BP_m1	GO:009877	skin epider	16/2606	113/23843	0.169228	0.576454	0.548145	Ctsl/Fgf7/F
GO_BP_m1	GO:004001	positive reg	7/2606	42/23843	0.169385	0.576454	0.548145	Bbs2/Ezr/G
GO_BP_m1	GO:004348	RNA stabili	7/2606	42/23843	0.169385	0.576454	0.548145	Apobec1/N
GO_BP_m1	GO:003081	regulation	11/2606	73/23843	0.169814	0.576454	0.548145	Adm/Adra
GO_BP_m1	GO:000072	double-str	15/2606	105/23843	0.170088	0.576454	0.548145	Blm/Cdc7/
GO_BP_m1	GO:000072	recombina	15/2606	105/23843	0.170088	0.576454	0.548145	Blm/Cdc7/
GO_BP_m1	GO:000182	mesoneph	15/2606	105/23843	0.170088	0.576454	0.548145	Fgf1/Foxc1
GO_BP_m1	GO:003496	histone lysi	15/2606	105/23843	0.170088	0.576454	0.548145	Ash2l/Dmr
GO_BP_m1	GO:000647	protein dea	12/2606	81/23843	0.170656	0.576454	0.548145	BC004004/
GO_BP_m1	GO:000721	glutamate	12/2606	81/23843	0.170656	0.576454	0.548145	Cacng5/Ca
GO_BP_m1	GO:001574	organopho	12/2606	81/23843	0.170656	0.576454	0.548145	Abca12/Ab
GO_BP_m1	GO:007202	nephron m	12/2606	81/23843	0.170656	0.576454	0.548145	Fgf1/Gdnf/
GO_BP_m1	GO:190406	negative re	12/2606	81/23843	0.170656	0.576454	0.548145	Adra1d/Ca
GO_BP_m1	GO:004852	negative re	14/2606	97/23843	0.17067	0.576454	0.548145	Ccl4/Eif2ak
GO_BP_m1	GO:005500	cardiac cell	13/2606	89/23843	0.170893	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:005502	regulation	13/2606	89/23843	0.170893	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:000910	glycoprote	34/2606	263/23843	0.171489	0.576454	0.548145	A4gnt/Alg
GO_BP_m1	GO:004632	regulation	23/2606	171/23843	0.173072	0.576454	0.548145	Ctgf/Dusp
GO_BP_m1	GO:000821	regulation	26/2606	196/23843	0.173136	0.576454	0.548145	Abat/Acta
GO_BP_m1	GO:000045	exonucleol	2/2606	7/23843	0.173184	0.576454	0.548145	Eri1/Exosc
GO_BP_m1	GO:000046	exonucleol	2/2606	7/23843	0.173184	0.576454	0.548145	Eri1/Exosc
GO_BP_m1	GO:000269	negative re	2/2606	7/23843	0.173184	0.576454	0.548145	Bcr/Ccl28

GO_BP_m1	GO:000301	voluntary s	2/2606	7/23843	0.173184	0.576454	0.548145	Myh7/Mylk
GO_BP_m1	GO:000332	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Adra1d/Dr
GO_BP_m1	GO:000614	purine nuc	2/2606	7/23843	0.173184	0.576454	0.548145	Dpyd/Gda
GO_BP_m1	GO:000637	7-methylg	2/2606	7/23843	0.173184	0.576454	0.548145	Cmtr2/Rnm
GO_BP_m1	GO:000655	leucine me	2/2606	7/23843	0.173184	0.576454	0.548145	Bcat2/Mcc
GO_BP_m1	GO:000721	tachykinin	2/2606	7/23843	0.173184	0.576454	0.548145	Tac1/Tacr2
GO_BP_m1	GO:000862	intrinsic ap	2/2606	7/23843	0.173184	0.576454	0.548145	Ptgs2/Ybx3
GO_BP_m1	GO:000963	response t	2/2606	7/23843	0.173184	0.576454	0.548145	Mapk13/Zc
GO_BP_m1	GO:001051	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Fpr2/Pdgfa
GO_BP_m1	GO:001082	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Plk4/Poc1a
GO_BP_m1	GO:001088	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Cd36/Scark
GO_BP_m1	GO:001089	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Fitm1/Plin5
GO_BP_m1	GO:001472	twitch skel	2/2606	7/23843	0.173184	0.576454	0.548145	Myh7/Mylk
GO_BP_m1	GO:001481	skeletal mu	2/2606	7/23843	0.173184	0.576454	0.548145	Ephb1/Myl
GO_BP_m1	GO:003224	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Adora1/Rb
GO_BP_m1	GO:003253	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Ezr/Pls1
GO_BP_m1	GO:003414	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Cav1/Ptpn
GO_BP_m1	GO:003415	toll-like rec	2/2606	7/23843	0.173184	0.576454	0.548145	Ptpn22/Tre
GO_BP_m1	GO:003416	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Ptpn22/Tre
GO_BP_m1	GO:003576	cell chemo	2/2606	7/23843	0.173184	0.576454	0.548145	Fgf1/Fgf16
GO_BP_m1	GO:003576	endothelial	2/2606	7/23843	0.173184	0.576454	0.548145	Fgf1/Fgf16
GO_BP_m1	GO:003606	protein O-	2/2606	7/23843	0.173184	0.576454	0.548145	Slc35c1/Slc
GO_BP_m1	GO:004227	susceptibili	2/2606	7/23843	0.173184	0.576454	0.548145	Cadm1/Ulb
GO_BP_m1	GO:004232	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Htr7/Uts2r
GO_BP_m1	GO:004232	negative re	2/2606	7/23843	0.173184	0.576454	0.548145	Adora1/Htr
GO_BP_m1	GO:004274	circadian sl	2/2606	7/23843	0.173184	0.576454	0.548145	Htr7/Uts2r
GO_BP_m1	GO:004278	tRNA 3'-en	2/2606	7/23843	0.173184	0.576454	0.548145	Elac1/Ptcd
GO_BP_m1	GO:004310	amino acid	2/2606	7/23843	0.173184	0.576454	0.548145	Apip/Enop
GO_BP_m1	GO:004354	molybdopt	2/2606	7/23843	0.173184	0.576454	0.548145	Gphn/Moc
GO_BP_m1	GO:004435	modulation	2/2606	7/23843	0.173184	0.576454	0.548145	Anxa2/Nuc
GO_BP_m1	GO:004554	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Fgf1/Por
GO_BP_m1	GO:004563	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Adamts9/K
GO_BP_m1	GO:004643	L-cysteine	2/2606	7/23843	0.173184	0.576454	0.548145	Ahcyl2/Mtr
GO_BP_m1	GO:004660	negative re	2/2606	7/23843	0.173184	0.576454	0.548145	Kat2a/Kat2
GO_BP_m1	GO:004665	tetrahydro	2/2606	7/23843	0.173184	0.576454	0.548145	Gch1/Mthf
GO_BP_m1	GO:004822	plasma me	2/2606	7/23843	0.173184	0.576454	0.548145	Sgsm3/Usp
GO_BP_m1	GO:004847	replication	2/2606	7/23843	0.173184	0.576454	0.548145	Fbxo18/Tip
GO_BP_m1	GO:004870	embryonic	2/2606	7/23843	0.173184	0.576454	0.548145	Mthfd1l/Tu
GO_BP_m1	GO:005065	dermatan s	2/2606	7/23843	0.173184	0.576454	0.548145	Dse/Dsel
GO_BP_m1	GO:005113	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Hsph1/Il12
GO_BP_m1	GO:005118	prosthetic	2/2606	7/23843	0.173184	0.576454	0.548145	Gphn/Moc
GO_BP_m1	GO:005220	modulation	2/2606	7/23843	0.173184	0.576454	0.548145	Anxa2/Nuc
GO_BP_m1	GO:005242	modulation	2/2606	7/23843	0.173184	0.576454	0.548145	Anxa2/Nuc
GO_BP_m1	GO:006001	parathyroi	2/2606	7/23843	0.173184	0.576454	0.548145	Hoxa3/Tbx
GO_BP_m1	GO:006005	positive re	2/2606	7/23843	0.173184	0.576454	0.548145	Mmp12/W
GO_BP_m1	GO:006037	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Cav3/Smac
GO_BP_m1	GO:006055	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Ifng/Nfkb1
GO_BP_m1	GO:006067	ureteric bu	2/2606	7/23843	0.173184	0.576454	0.548145	Gdnf/Nog

GO_BP_m1	GO:006068	epithelial-r	2/2606	7/23843	0.173184	0.576454	0.548145	Pdgfa/Smc
GO_BP_m1	GO:00607 8	hair follicle	2/2606	7/23843	0.173184	0.576454	0.548145	Hdac1/Hda
GO_BP_m1	GO:006119	fungiform	2/2606	7/23843	0.173184	0.576454	0.548145	Hdac1/Hda
GO_BP_m1	GO:006131	Notch sign	2/2606	7/23843	0.173184	0.576454	0.548145	Dll4/Jag1
GO_BP_m1	GO:006152	acetylcholi	2/2606	7/23843	0.173184	0.576454	0.548145	Htr6/Tacr2
GO_BP_m1	GO:007031	G1 to G0 tr	2/2606	7/23843	0.173184	0.576454	0.548145	1500015O
GO_BP_m1	GO:007034	negative re	2/2606	7/23843	0.173184	0.576454	0.548145	E2f1/E2f3
GO_BP_m1	GO:007045	prolactin se	2/2606	7/23843	0.173184	0.576454	0.548145	Abat/Tacr2
GO_BP_m1	GO:007126	L-methioni	2/2606	7/23843	0.173184	0.576454	0.548145	Apip/Enop
GO_BP_m1	GO:007135	cellular res	2/2606	7/23843	0.173184	0.576454	0.548145	Ifng/Ticam
GO_BP_m1	GO:007164	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Ticam2/Trp
GO_BP_m1	GO:008606	cell commu	2/2606	7/23843	0.173184	0.576454	0.548145	Cav1/Gjc1
GO_BP_m1	GO:009020	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Fgf1/Por
GO_BP_m1	GO:009030	spindle ass	2/2606	7/23843	0.173184	0.576454	0.548145	Washc5/Fb
GO_BP_m1	GO:009033	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Mecom/Ptg
GO_BP_m1	GO:009764	calcitonin f	2/2606	7/23843	0.173184	0.576454	0.548145	Adm/Calcr
GO_BP_m1	GO:009894	neurotrans	2/2606	7/23843	0.173184	0.576454	0.548145	Cacng5/Ca
GO_BP_m1	GO:190004	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Abl2/Btnl2
GO_BP_m1	GO:190010	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Dand5/Dm
GO_BP_m1	GO:190024	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Ddx60/Dhx
GO_BP_m1	GO:190102	negative re	2/2606	7/23843	0.173184	0.576454	0.548145	Bok/Tmem
GO_BP_m1	GO:190116	neural cres	2/2606	7/23843	0.173184	0.576454	0.548145	Gdnf/Sema
GO_BP_m1	GO:190134	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Asph/Stim2
GO_BP_m1	GO:190149	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Epha2/Fox
GO_BP_m1	GO:190189	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Akap6/Pde
GO_BP_m1	GO:190306	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Bcap31/Us
GO_BP_m1	GO:190325	multi-ciliat	2/2606	7/23843	0.173184	0.576454	0.548145	Deup1/Plk4
GO_BP_m1	GO:190330	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Pfkfb1/Tiga
GO_BP_m1	GO:190354	protein loc	2/2606	7/23843	0.173184	0.576454	0.548145	Tulp1/Tulp
GO_BP_m1	GO:190398	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Itgam/Ttbk
GO_BP_m1	GO:190477	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Epb41/Gna
GO_BP_m1	GO:190484	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Fgf1/Fgf16
GO_BP_m1	GO:200009	positive reg	2/2606	7/23843	0.173184	0.576454	0.548145	Abl2/Mllt3
GO_BP_m1	GO:200035	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Amh/Hyal3
GO_BP_m1	GO:200054	regulation	2/2606	7/23843	0.173184	0.576454	0.548145	Fgf1/Fgf16
GO_BP_m1	GO:000705	cell cycle a	19/2606	138/23843	0.173432	0.576454	0.548145	AY074887/
GO_BP_m1	GO:005068	negative re	19/2606	138/23843	0.173432	0.576454	0.548145	A4gnt/Atp5
GO_BP_m1	GO:001603	viral proces	35/2606	272/23843	0.174543	0.576454	0.548145	Cav1/Ccl4/
GO_BP_m1	GO:000916	nucleotide	39/2606	306/23843	0.174698	0.576454	0.548145	Adcy4/Adk
GO_BP_m1	GO:000999	oocyte diff	8/2606	50/23843	0.174749	0.576454	0.548145	Dmrt1/Was
GO_BP_m1	GO:004214	cellular res	8/2606	50/23843	0.174749	0.576454	0.548145	Cpeb4/Gm
GO_BP_m1	GO:003001	establishm	18/2606	130/23843	0.175122	0.576454	0.548145	Bcas3/Cen
GO_BP_m1	GO:005508	lipid home	18/2606	130/23843	0.175122	0.576454	0.548145	Abca12/Ar
GO_BP_m1	GO:000726	small GTPa	61/2606	495/23843	0.175143	0.576454	0.548145	Aatk/Abl2/
GO_BP_m1	GO:005178	regulation	25/2606	188/23843	0.175522	0.576454	0.548145	Bora/Calr/
GO_BP_m1	GO:006029	long-term	30/2606	230/23843	0.175981	0.576454	0.548145	Cpeb3/Grir
GO_BP_m1	GO:000916	nucleotide	17/2606	122/23843	0.176698	0.576454	0.548145	Bpgm/Dera
GO_BP_m1	GO:000269	positive reg	54/2606	435/23843	0.177007	0.576454	0.548145	Adam8/Ad

GO_BP_m1	GO:000714	female mei	6/2606	35/23843	0.177519	0.576454	0.548145	Washc5/Fb
GO_BP_m1	GO:000815	negative re	6/2606	35/23843	0.177519	0.576454	0.548145	Atr/Fbxo18
GO_BP_m1	GO:001403	Schwann c	6/2606	35/23843	0.177519	0.576454	0.548145	Ahnak2/Cc
GO_BP_m1	GO:003167	cellular res	6/2606	35/23843	0.177519	0.576454	0.548145	Foxa2/Hsp
GO_BP_m1	GO:003579	positive reg	6/2606	35/23843	0.177519	0.576454	0.548145	Bnip3/Bok/
GO_BP_m1	GO:004519	regulation	6/2606	35/23843	0.177519	0.576454	0.548145	Aplf/Ifng/Il
GO_BP_m1	GO:005502	negative re	6/2606	35/23843	0.177519	0.576454	0.548145	Cav3/Hdac
GO_BP_m1	GO:009730	programm	6/2606	35/23843	0.177519	0.576454	0.548145	Bok/Casp8
GO_BP_m1	GO:004685	regulation	9/2606	58/23843	0.178108	0.576454	0.548145	Adam8/Ca
GO_BP_m1	GO:002240	molting cyc	16/2606	114/23843	0.178127	0.576454	0.548145	Ctsl/Fgf7/F
GO_BP_m1	GO:002240	hair cycle p	16/2606	114/23843	0.178127	0.576454	0.548145	Ctsl/Fgf7/F
GO_BP_m1	GO:004354	protein acy	29/2606	222/23843	0.178623	0.576454	0.548145	Arntl/Brpf3
GO_BP_m1	GO:000688	exocytosis	41/2606	324/23843	0.17974	0.576454	0.548145	Abca12/Ar
GO_BP_m1	GO:000263	regulation	10/2606	66/23843	0.180082	0.576454	0.548145	Aplf/Ifng/Il
GO_BP_m1	GO:003043	ubiquitin-c	10/2606	66/23843	0.180082	0.576454	0.548145	Bcap31/Hs
GO_BP_m1	GO:005502	regulation	10/2606	66/23843	0.180082	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:006068	regulation	10/2606	66/23843	0.180082	0.576454	0.548145	Cav3/Cdh1
GO_BP_m1	GO:006109	regulation	10/2606	66/23843	0.180082	0.576454	0.548145	Adora1/Ca
GO_BP_m1	GO:190551	non-motile	10/2606	66/23843	0.180082	0.576454	0.548145	Bbs10/Bbs
GO_BP_m1	GO:003315	regulation	35/2606	273/23843	0.180275	0.576454	0.548145	Arih2/Asph
GO_BP_m1	GO:004506	regulation	13/2606	90/23843	0.181054	0.576454	0.548145	Eif2ak2/Fkb
GO_BP_m1	GO:007145	cellular res	13/2606	90/23843	0.181054	0.576454	0.548145	Adam8/Bn
GO_BP_m1	GO:190288	regulation	13/2606	90/23843	0.181054	0.576454	0.548145	Cd36/Endo
GO_BP_m1	GO:000862	extrinsic ap	11/2606	74/23843	0.181068	0.576454	0.548145	Atf3/Casp8
GO_BP_m1	GO:001401	positive reg	11/2606	74/23843	0.181068	0.576454	0.548145	Enpp2/Hda
GO_BP_m1	GO:003246	regulation	11/2606	74/23843	0.181068	0.576454	0.548145	Ahctf1/Ank
GO_BP_m1	GO:003020	glycosamin	12/2606	82/23843	0.181331	0.576454	0.548145	Chst13/Csg
GO_BP_m1	GO:003264	regulation	12/2606	82/23843	0.181331	0.576454	0.548145	C1qtnf3/Eif
GO_BP_m1	GO:005081	regulation	12/2606	82/23843	0.181331	0.576454	0.548145	Abat/Alox1
GO_BP_m1	GO:004477	mitotic cell	44/2606	350/23843	0.181495	0.576454	0.548145	Abcb1a/Blm
GO_BP_m1	GO:000181	negative re	30/2606	231/23843	0.182263	0.576454	0.548145	Arg1/C1qtn
GO_BP_m1	GO:000640	RNA localiz	25/2606	189/23843	0.182486	0.576454	0.548145	Ahctf1/Atr/
GO_BP_m1	GO:003505	cardiocyte	22/2606	164/23843	0.182734	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:004212	regulation	22/2606	164/23843	0.182734	0.576454	0.548145	Adk/Arg1/I
GO_BP_m1	GO:190198	regulation	36/2606	282/23843	0.183166	0.576454	0.548145	Atp2b4/Blm
GO_BP_m1	GO:001060	posttranscr	58/2606	471/23843	0.183549	0.576454	0.548145	Apobec1/B
GO_BP_m1	GO:000920	ribonucleo	18/2606	131/23843	0.183556	0.576454	0.548145	Atp5a1/Atp
GO_BP_m1	GO:004230	molting cyc	18/2606	131/23843	0.183556	0.576454	0.548145	Arntl/Clock
GO_BP_m1	GO:004263	hair cycle	18/2606	131/23843	0.183556	0.576454	0.548145	Arntl/Clock
GO_BP_m1	GO:004885	brain morp	7/2606	43/23843	0.184539	0.576454	0.548145	Bbs2/Cdh2
GO_BP_m1	GO:007052	platelet ag	7/2606	43/23843	0.184539	0.576454	0.548145	Abat/Alox1
GO_BP_m1	GO:190103	regulation	7/2606	43/23843	0.184539	0.576454	0.548145	Cd36/Endo
GO_BP_m1	GO:190274	regulation	7/2606	43/23843	0.184539	0.576454	0.548145	Cfl1/Enpp2
GO_BP_m1	GO:200005	negative re	7/2606	43/23843	0.184539	0.576454	0.548145	N4bp1/Og
GO_BP_m1	GO:200125	negative re	7/2606	43/23843	0.184539	0.576454	0.548145	Adra1d/Ca
GO_BP_m1	GO:000030	response to	5/2606	28/23843	0.185082	0.576454	0.548145	Cd36/Fbln5
GO_BP_m1	GO:001075	regulation	5/2606	28/23843	0.185082	0.576454	0.548145	Cxcl17/Ddt
GO_BP_m1	GO:003315	regulation	5/2606	28/23843	0.185082	0.576454	0.548145	Cdk1/Cdkn

GO_BP_m1	GO:003319	response t	5/2606	28/23843	0.185082	0.576454	0.548145	Asph/Dgkc
GO_BP_m1	GO:004400	modificatic	5/2606	28/23843	0.185082	0.576454	0.548145	Hyal2/Myc
GO_BP_m1	GO:004506	regulatory	5/2606	28/23843	0.185082	0.576454	0.548145	Ctla4/Ifng/
GO_BP_m1	GO:004591	negative re	5/2606	28/23843	0.185082	0.576454	0.548145	Blm/Fbxo1
GO_BP_m1	GO:007239	signal trans	5/2606	28/23843	0.185082	0.576454	0.548145	Babam2/C
GO_BP_m1	GO:007240	signal trans	5/2606	28/23843	0.185082	0.576454	0.548145	Babam2/C
GO_BP_m1	GO:007242	signal trans	5/2606	28/23843	0.185082	0.576454	0.548145	Babam2/C
GO_BP_m1	GO:200027	negative re	5/2606	28/23843	0.185082	0.576454	0.548145	Cnrip1/Crh
GO_BP_m1	GO:006040	cytosolic ca	21/2606	156/23843	0.185134	0.576454	0.548145	Adcyap1r1
GO_BP_m1	GO:000275	innate imm	17/2606	123/23843	0.185465	0.576454	0.548145	5730559C1
GO_BP_m1	GO:000276	regulation	17/2606	123/23843	0.185465	0.576454	0.548145	Adam8/Ca
GO_BP_m1	GO:190018	regulation	17/2606	123/23843	0.185465	0.576454	0.548145	Cct3/Cdk1/
GO_BP_m1	GO:190165	cellular res	33/2606	257/23843	0.186053	0.576454	0.548145	Appl1/Bcar
GO_BP_m1	GO:000752	neuromusc	8/2606	51/23843	0.188777	0.576454	0.548145	Cacnb2/Dc
GO_BP_m1	GO:003007	regulation	8/2606	51/23843	0.188777	0.576454	0.548145	Cdc23/Klhl
GO_BP_m1	GO:004582	negative re	8/2606	51/23843	0.188777	0.576454	0.548145	Arg1/Cacti
GO_BP_m1	GO:004690	regulation	8/2606	51/23843	0.188777	0.576454	0.548145	Bnip3/Bok/
GO_BP_m1	GO:004824	lymphocyte	8/2606	51/23843	0.188777	0.576454	0.548145	Adam8/Ccl
GO_BP_m1	GO:000834	adult locor	15/2606	107/23843	0.188894	0.576454	0.548145	Abl2/Cend
GO_BP_m1	GO:007265	protein loc	32/2606	249/23843	0.189032	0.576454	0.548145	Abca12/Ar
GO_BP_m1	GO:014001	mitotic nuc	34/2606	266/23843	0.189114	0.576454	0.548145	Ankrd53/B
GO_BP_m1	GO:007170	tumor necr	19/2606	140/23843	0.189876	0.576454	0.548145	Adam8/Ca
GO_BP_m1	GO:001975	polyol met	14/2606	99/23843	0.190329	0.576454	0.548145	Acer3/Adcy
GO_BP_m1	GO:006113	regulation	22/2606	165/23843	0.190391	0.576454	0.548145	Arih2/Bcap
GO_BP_m1	GO:000208	regulation	4/2606	21/23843	0.190823	0.576454	0.548145	Cdk1/Myc/
GO_BP_m1	GO:000328	atrial septu	4/2606	21/23843	0.190823	0.576454	0.548145	Cfc1/Dand
GO_BP_m1	GO:000762	grooming		4/2606	21/23843	0.190823	0.576454	0.548145	Aprt/Avpr1
GO_BP_m1	GO:001491	negative re	4/2606	21/23843	0.190823	0.576454	0.548145	Igfbp3/Ndr
GO_BP_m1	GO:001812	protein hyc	4/2606	21/23843	0.190823	0.576454	0.548145	Asph/Egln3
GO_BP_m1	GO:003157	mitotic G1	4/2606	21/23843	0.190823	0.576454	0.548145	Cdkn1a/Fb
GO_BP_m1	GO:004412	regulation	4/2606	21/23843	0.190823	0.576454	0.548145	Cd36/Ifng/
GO_BP_m1	GO:004668	response t	4/2606	21/23843	0.190823	0.576454	0.548145	As3mt/Ma
GO_BP_m1	GO:004848	parasympa	4/2606	21/23843	0.190823	0.576454	0.548145	Gdnf/Hoxb
GO_BP_m1	GO:006105	regulation	4/2606	21/23843	0.190823	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:009706	dendritic s	4/2606	21/23843	0.190823	0.576454	0.548145	Abl2/Cfl1/
GO_BP_m1	GO:000666	phosphatic	9/2606	59/23843	0.191194	0.576454	0.548145	Fpr2/Pdgfa
GO_BP_m1	GO:000680	superoxide	9/2606	59/23843	0.191194	0.576454	0.548145	Cd36/Fbln5
GO_BP_m1	GO:003272	positive re	9/2606	59/23843	0.191194	0.576454	0.548145	Eif2ak2/Hd
GO_BP_m1	GO:004684	filopodium	9/2606	59/23843	0.191194	0.576454	0.548145	Bcas3/Dnm
GO_BP_m1	GO:005130	mitotic sist	9/2606	59/23843	0.191194	0.576454	0.548145	Cdc23/Klhl
GO_BP_m1	GO:007020	protein trir	9/2606	59/23843	0.191194	0.576454	0.548145	Arg1/C1qt
GO_BP_m1	GO:190351	mucopolys	9/2606	59/23843	0.191194	0.576454	0.548145	Chst13/Cs
GO_BP_m1	GO:000177	immunolo	3/2606	14/23843	0.191261	0.576454	0.548145	Dock8/Eph
GO_BP_m1	GO:000209	tRNA wobl	3/2606	14/23843	0.191261	0.576454	0.548145	6430573F1
GO_BP_m1	GO:000282	negative re	3/2606	14/23843	0.191261	0.576454	0.548145	Arg1/Il27ra
GO_BP_m1	GO:000315	morphoge	3/2606	14/23843	0.191261	0.576454	0.548145	Cxcl10/Dll4
GO_BP_m1	GO:000653	cysteine m	3/2606	14/23843	0.191261	0.576454	0.548145	Ahcyl2/Gcl
GO_BP_m1	GO:000657	amino-acic	3/2606	14/23843	0.191261	0.576454	0.548145	Aldh9a1/C

GO_BP_m1	GO:001064	negative re	3/2606	14/23843	0.191261	0.576454	0.548145	Ndrg4/Ptp
GO_BP_m1	GO:001080	negative re	3/2606	14/23843	0.191261	0.576454	0.548145	Dgkq/Ogt/
GO_BP_m1	GO:001087	positive reg	3/2606	14/23843	0.191261	0.576454	0.548145	Abca12/Nr
GO_BP_m1	GO:001593	coenzyme	3/2606	14/23843	0.191261	0.576454	0.548145	Crot/Dcakd
GO_BP_m1	GO:001632	neuron ren	3/2606	14/23843	0.191261	0.576454	0.548145	Abl2/C1ql1
GO_BP_m1	GO:003209	negative re	3/2606	14/23843	0.191261	0.576454	0.548145	Bbs2/Cartp
GO_BP_m1	GO:003253	regulation	3/2606	14/23843	0.191261	0.576454	0.548145	Ezr/Pls1/W
GO_BP_m1	GO:003509	sperm chro	3/2606	14/23843	0.191261	0.576454	0.548145	Psme4/Syc
GO_BP_m1	GO:003556	positive reg	3/2606	14/23843	0.191261	0.576454	0.548145	Hmbox1/K
GO_BP_m1	GO:004312	surfactant l	3/2606	14/23843	0.191261	0.576454	0.548145	Abca12/Fg
GO_BP_m1	GO:004355	regulation	3/2606	14/23843	0.191261	0.576454	0.548145	Eif2ak1/Eif2
GO_BP_m1	GO:004365	dicarboxyli	3/2606	14/23843	0.191261	0.576454	0.548145	Gls/Got1/M
GO_BP_m1	GO:004589	positive reg	3/2606	14/23843	0.191261	0.576454	0.548145	Cand1/Psm
GO_BP_m1	GO:004831	Golgi inher	3/2606	14/23843	0.191261	0.576454	0.548145	Cdk1/Gbf1
GO_BP_m1	GO:005066	homocyste	3/2606	14/23843	0.191261	0.576454	0.548145	Blmh/Mtrr/
GO_BP_m1	GO:005138	kinetochor	3/2606	14/23843	0.191261	0.576454	0.548145	Cenpa/Cen
GO_BP_m1	GO:005178	negative re	3/2606	14/23843	0.191261	0.576454	0.548145	Blm/E2f7/N
GO_BP_m1	GO:005189	negative re	3/2606	14/23843	0.191261	0.576454	0.548145	Bcas3/Itgb
GO_BP_m1	GO:006083	smoothene	3/2606	14/23843	0.191261	0.576454	0.548145	Prkacb/Tra
GO_BP_m1	GO:006115	endothelial	3/2606	14/23843	0.191261	0.576454	0.548145	Cxcl10/Dll4
GO_BP_m1	GO:007137	cellular res	3/2606	14/23843	0.191261	0.576454	0.548145	Epha8/Ppa
GO_BP_m1	GO:007194	nitrogen cy	3/2606	14/23843	0.191261	0.576454	0.548145	Arg1/Otc/S
GO_BP_m1	GO:009906	postsynaps	3/2606	14/23843	0.191261	0.576454	0.548145	Cdh2/Lrp4/
GO_BP_m1	GO:190254	regulation	3/2606	14/23843	0.191261	0.576454	0.548145	Adgra2/Cd
GO_BP_m1	GO:190335	regulation	3/2606	14/23843	0.191261	0.576454	0.548145	Rbsn/Stx5a
GO_BP_m1	GO:200104	regulation	3/2606	14/23843	0.191261	0.576454	0.548145	Cd63/Itgb1
GO_BP_m1	GO:003650	ERAD path	13/2606	91/23843	0.191498	0.576454	0.548145	Bcap31/Hs
GO_BP_m1	GO:005140	neuron apo	35/2606	275/23843	0.192042	0.576454	0.548145	Aatk/Adam
GO_BP_m1	GO:000858	regulation	12/2606	83/23843	0.192314	0.576454	0.548145	Ankmy2/Fc
GO_BP_m1	GO:001403	mesenchym	12/2606	83/23843	0.192314	0.576454	0.548145	Cfl1/Ednrb
GO_BP_m1	GO:003276	positive reg	12/2606	83/23843	0.192314	0.576454	0.548145	Ccl4/Cd36/
GO_BP_m1	GO:004263	cholesterol	12/2606	83/23843	0.192314	0.576454	0.548145	Angptl3/Ca
GO_BP_m1	GO:005509	sterol hom	12/2606	83/23843	0.192314	0.576454	0.548145	Angptl3/Ca
GO_BP_m1	GO:190187	regulation	12/2606	83/23843	0.192314	0.576454	0.548145	Asph/Cfl1/
GO_BP_m1	GO:003238	negative re	10/2606	67/23843	0.192367	0.576454	0.548145	Cdk5/Ei24/
GO_BP_m1	GO:003265	regulation	10/2606	67/23843	0.192367	0.576454	0.548145	5730559C1
GO_BP_m1	GO:003410	homotypic	10/2606	67/23843	0.192367	0.576454	0.548145	Abat/Alox1
GO_BP_m1	GO:000648	protein N-	11/2606	75/23843	0.192659	0.576454	0.548145	Alg6/Ccdc1
GO_BP_m1	GO:009775	positive reg	11/2606	75/23843	0.192659	0.576454	0.548145	Adm/Adora
GO_BP_m1	GO:000611	regulation	6/2606	36/23843	0.194703	0.576454	0.548145	Esrrb/Myc/
GO_BP_m1	GO:000725	activation o	6/2606	36/23843	0.194703	0.576454	0.548145	Gab1/Map
GO_BP_m1	GO:004816	regulation	6/2606	36/23843	0.194703	0.576454	0.548145	Drd5/Grin2
GO_BP_m1	GO:005093	pigment ce	6/2606	36/23843	0.194703	0.576454	0.548145	Adamts9/B
GO_BP_m1	GO:005108	'de novo' p	6/2606	36/23843	0.194703	0.576454	0.548145	Ero1l/H2-D
GO_BP_m1	GO:008600	regulation	6/2606	36/23843	0.194703	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:001931	hexose me	28/2606	216/23843	0.194705	0.576454	0.548145	Atf3/Bpgm
GO_BP_m1	GO:003210	positive reg	36/2606	284/23843	0.194846	0.576454	0.548145	Adam8/Ao
GO_BP_m1	GO:003090	forebrain d	46/2606	370/23843	0.196047	0.576454	0.548145	Aldh1a3/A

GO_BP_m1	GO:000279	regulation	59/2606	483/23843	0.198584	0.576454	0.548145	Abat/Abl2/
GO_BP_m1	GO:000597	polysaccha	15/2606	108/23843	0.198657	0.576454	0.548145	Aoah/B3gr
GO_BP_m1	GO:003524	synaptic tra	15/2606	108/23843	0.198657	0.576454	0.548145	Adora1/Ad
GO_BP_m1	GO:005120	sequesterir	15/2606	108/23843	0.198657	0.576454	0.548145	Akap6/Asp
GO_BP_m1	GO:005122	negative re	24/2606	183/23843	0.199903	0.576454	0.548145	C1qtnf3/Cc
GO_BP_m1	GO:200102	regulation	24/2606	183/23843	0.199903	0.576454	0.548145	Ankrd1/Atr
GO_BP_m1	GO:000690	vesicle doc	7/2606	44/23843	0.200227	0.576454	0.548145	Ncam1/Scf
GO_BP_m1	GO:003289	positive reg	7/2606	44/23843	0.200227	0.576454	0.548145	Abat/Avpr1
GO_BP_m1	GO:000940	response to	14/2606	100/23843	0.200544	0.576454	0.548145	Ano1/Clpb
GO_BP_m1	GO:004346	regulation	14/2606	100/23843	0.200544	0.576454	0.548145	Bnip3/Cdk1
GO_BP_m1	GO:006007	regulation	14/2606	100/23843	0.200544	0.576454	0.548145	Abat/Adora
GO_BP_m1	GO:002195	central ner	28/2606	217/23843	0.201591	0.576454	0.548145	Arx/Btg2/C
GO_BP_m1	GO:001656	covalent ch	55/2606	449/23843	0.201974	0.576454	0.548145	Apobec1/A
GO_BP_m1	GO:005501	cardiac mu	13/2606	92/23843	0.202215	0.576454	0.548145	Akap6/Cav
GO_BP_m1	GO:004593	positive reg	8/2606	52/23843	0.20326	0.576454	0.548145	Abat/Adra1
GO_BP_m1	GO:007162	regulation	8/2606	52/23843	0.20326	0.576454	0.548145	Cxcl17/Kars
GO_BP_m1	GO:190209	regulation	8/2606	52/23843	0.20326	0.576454	0.548145	Cdc23/Klhl
GO_BP_m1	GO:190236	negative re	8/2606	52/23843	0.20326	0.576454	0.548145	Apobec1/N
GO_BP_m1	GO:004227	ribosomal l	12/2606	84/23843	0.203593	0.576454	0.548145	Dhx30/Ebn
GO_BP_m1	GO:006133	renal tubul	12/2606	84/23843	0.203593	0.576454	0.548145	Fgf1/Gdnf/
GO_BP_m1	GO:000649	protein O-	11/2606	76/23843	0.204574	0.576454	0.548145	A4gnt/B3g
GO_BP_m1	GO:004352	positive reg	11/2606	76/23843	0.204574	0.576454	0.548145	Aifm1/Casp
GO_BP_m1	GO:005127	regulation	11/2606	76/23843	0.204574	0.576454	0.548145	Akap6/Asp
GO_BP_m1	GO:006118	mammary	11/2606	76/23843	0.204574	0.576454	0.548145	Cav3/Epha
GO_BP_m1	GO:000276	positive reg	9/2606	60/23843	0.20468	0.576454	0.548145	Casp8/Ccr1
GO_BP_m1	GO:001061	regulation	9/2606	60/23843	0.20468	0.576454	0.548145	Adk/Akap6
GO_BP_m1	GO:002151	cell differen	9/2606	60/23843	0.20468	0.576454	0.548145	Dbx1/Dll4/
GO_BP_m1	GO:003439	protein loc	9/2606	60/23843	0.20468	0.576454	0.548145	Abca12/Cc
GO_BP_m1	GO:003590	aorta deve	9/2606	60/23843	0.20468	0.576454	0.548145	Adamts9/C
GO_BP_m1	GO:006099	positive reg	9/2606	60/23843	0.20468	0.576454	0.548145	Caprin2/Cc
GO_BP_m1	GO:000300	heart morp	33/2606	260/23843	0.204759	0.576454	0.548145	Adamts1/A
GO_BP_m1	GO:000191	regulation	5/2606	29/23843	0.204941	0.576454	0.548145	Ache/Anxa
GO_BP_m1	GO:000609	tricarboxyli	5/2606	29/23843	0.204941	0.576454	0.548145	Idh2/Idh3a
GO_BP_m1	GO:000653	glutamate	5/2606	29/23843	0.204941	0.576454	0.548145	Dglucy/Ald
GO_BP_m1	GO:000922	nucleotide-	5/2606	29/23843	0.204941	0.576454	0.548145	Csgalnact1
GO_BP_m1	GO:001092	positive reg	5/2606	29/23843	0.204941	0.576454	0.548145	Akap6/Ifng
GO_BP_m1	GO:001404	Schwann ce	5/2606	29/23843	0.204941	0.576454	0.548145	Ahnak2/Cc
GO_BP_m1	GO:003111	positive reg	5/2606	29/23843	0.204941	0.576454	0.548145	Ankrd53/C
GO_BP_m1	GO:003462	cellular pro	5/2606	29/23843	0.204941	0.576454	0.548145	Akap6/Exo
GO_BP_m1	GO:004445	motile ciliu	5/2606	29/23843	0.204941	0.576454	0.548145	Cc2d2a/Dr
GO_BP_m1	GO:004518	regulation	5/2606	29/23843	0.204941	0.576454	0.548145	Adora1/Dr
GO_BP_m1	GO:004838	retinoic aci	5/2606	29/23843	0.204941	0.576454	0.548145	Aldh1a3/As
GO_BP_m1	GO:005108	chaperone	5/2606	29/23843	0.204941	0.576454	0.548145	Ero1l/H2-D
GO_BP_m1	GO:006175	leukocyte a	5/2606	29/23843	0.204941	0.576454	0.548145	Ccl28/Gcnt
GO_BP_m1	GO:007154	response to	5/2606	29/23843	0.204941	0.576454	0.548145	Eif4e/Fibin/
GO_BP_m1	GO:190403	positive reg	5/2606	29/23843	0.204941	0.576454	0.548145	Cd248/Gsr
GO_BP_m1	GO:000007	regulation	10/2606	68/23843	0.205009	0.576454	0.548145	Blm/Ccnl1/
GO_BP_m1	GO:003088	regulation	10/2606	68/23843	0.205009	0.576454	0.548145	Cdkn1a/Ct

GO_BP_m1	GO:007037	negative re	10/2606	68/23843	0.205009	0.576454	0.548145	Atf3/Camk
GO_BP_m1	GO:014005	organelle l	10/2606	68/23843	0.205009	0.576454	0.548145	Ncam1/Nd
GO_BP_m1	GO:190198	regulation	10/2606	68/23843	0.205009	0.576454	0.548145	Arntl/Fam1
GO_BP_m1	GO:190442	positive reg	10/2606	68/23843	0.205009	0.576454	0.548145	Akap6/Asp
GO_BP_m1	GO:001972	calcium-m	22/2606	167/23843	0.206179	0.576454	0.548145	Akap6/Asp
GO_BP_m1	GO:003440	nucleobase	22/2606	167/23843	0.206179	0.576454	0.548145	Adk/Aprt/E
GO_BP_m1	GO:001715	calcium ior	16/2606	117/23843	0.206179	0.576454	0.548145	Catsper3/C
GO_BP_m1	GO:000011	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Esrrb
GO_BP_m1	GO:000029	nuclear-tra	1/2606	2/23843	0.206655	0.576454	0.548145	Zc3h12a
GO_BP_m1	GO:000034	generation	1/2606	2/23843	0.206655	0.576454	0.548145	Prpf19
GO_BP_m1	GO:000045	enzyme-di	1/2606	2/23843	0.206655	0.576454	0.548145	Mrm1
GO_BP_m1	GO:000045	enzyme-di	1/2606	2/23843	0.206655	0.576454	0.548145	Rpusd1
GO_BP_m1	GO:000096	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Pnpt1
GO_BP_m1	GO:000155	ovarian foll	1/2606	2/23843	0.206655	0.576454	0.548145	Hyal3
GO_BP_m1	GO:000169	histamine b	1/2606	2/23843	0.206655	0.576454	0.548145	Hdc
GO_BP_m1	GO:000192	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Ncam1
GO_BP_m1	GO:000198	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Manf
GO_BP_m1	GO:000203	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Arl6ip5
GO_BP_m1	GO:000204	intussuscep	1/2606	2/23843	0.206655	0.576454	0.548145	Lemd3
GO_BP_m1	GO:000218	cytoplasmi	1/2606	2/23843	0.206655	0.576454	0.548145	Gspt2
GO_BP_m1	GO:000227	basophil ac	1/2606	2/23843	0.206655	0.576454	0.548145	Kars
GO_BP_m1	GO:000230	CD8-positi	1/2606	2/23843	0.206655	0.576454	0.548145	Ifng
GO_BP_m1	GO:000230	gamma-de	1/2606	2/23843	0.206655	0.576454	0.548145	Gpr18
GO_BP_m1	GO:000230	CD8-positi	1/2606	2/23843	0.206655	0.576454	0.548145	Gpr18
GO_BP_m1	GO:000239	MHC prote	1/2606	2/23843	0.206655	0.576454	0.548145	Calr
GO_BP_m1	GO:000250	peptide an	1/2606	2/23843	0.206655	0.576454	0.548145	Calr
GO_BP_m1	GO:000258	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Pycard
GO_BP_m1	GO:000258	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Pycard
GO_BP_m1	GO:000294	tRNA N2-g	1/2606	2/23843	0.206655	0.576454	0.548145	Trmt1
GO_BP_m1	GO:000305	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Corin
GO_BP_m1	GO:000329	atrial septu	1/2606	2/23843	0.206655	0.576454	0.548145	Nsd2
GO_BP_m1	GO:000342	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Por
GO_BP_m1	GO:000601	UDP-gluco	1/2606	2/23843	0.206655	0.576454	0.548145	Ugp2
GO_BP_m1	GO:000609	glyoxylate	1/2606	2/23843	0.206655	0.576454	0.548145	Idh2
GO_BP_m1	GO:000616	adenine sa	1/2606	2/23843	0.206655	0.576454	0.548145	Aprt
GO_BP_m1	GO:000643	tryptophan	1/2606	2/23843	0.206655	0.576454	0.548145	Wars
GO_BP_m1	GO:000650	N-terminal	1/2606	2/23843	0.206655	0.576454	0.548145	Map6d1
GO_BP_m1	GO:000655	isoleucine	1/2606	2/23843	0.206655	0.576454	0.548145	Bcat2
GO_BP_m1	GO:000658	melanin bio	1/2606	2/23843	0.206655	0.576454	0.548145	Dct
GO_BP_m1	GO:000671	glucocortic	1/2606	2/23843	0.206655	0.576454	0.548145	Hsd11b1
GO_BP_m1	GO:000678	heme a bio	1/2606	2/23843	0.206655	0.576454	0.548145	Cox15
GO_BP_m1	GO:000685	mitochond	1/2606	2/23843	0.206655	0.576454	0.548145	Mpc2
GO_BP_m1	GO:000686	pyrimidine	1/2606	2/23843	0.206655	0.576454	0.548145	Slc25a33
GO_BP_m1	GO:000698	response to	1/2606	2/23843	0.206655	0.576454	0.548145	Mgst1
GO_BP_m1	GO:000705	spindle ass	1/2606	2/23843	0.206655	0.576454	0.548145	Fbxo5
GO_BP_m1	GO:000711	endomitoti	1/2606	2/23843	0.206655	0.576454	0.548145	Cib1
GO_BP_m1	GO:000714	female mei	1/2606	2/23843	0.206655	0.576454	0.548145	Mastl
GO_BP_m1	GO:000735	zygotic spe	1/2606	2/23843	0.206655	0.576454	0.548145	Smad6

GO_BP_m1	GO:000859	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Peli3
GO_BP_m1	GO:000908	branched-	1/2606	2/23843	0.206655	0.576454	0.548145	Bcat2
GO_BP_m1	GO:000909	leucine bio	1/2606	2/23843	0.206655	0.576454	0.548145	Bcat2
GO_BP_m1	GO:000909	valine bios	1/2606	2/23843	0.206655	0.576454	0.548145	Bcat2
GO_BP_m1	GO:000915	purine deo	1/2606	2/23843	0.206655	0.576454	0.548145	Adk
GO_BP_m1	GO:000915	deoxyribon	1/2606	2/23843	0.206655	0.576454	0.548145	Dnph1
GO_BP_m1	GO:000921	purine deo	1/2606	2/23843	0.206655	0.576454	0.548145	Adk
GO_BP_m1	GO:000924	lipid A bios	1/2606	2/23843	0.206655	0.576454	0.548145	Zfp593
GO_BP_m1	GO:000925	10-formylt	1/2606	2/23843	0.206655	0.576454	0.548145	Mthfd1l
GO_BP_m1	GO:000945	gamma-am	1/2606	2/23843	0.206655	0.576454	0.548145	Abat
GO_BP_m1	GO:000963	cold acclim	1/2606	2/23843	0.206655	0.576454	0.548145	Saxo1
GO_BP_m1	GO:001007	zygote asy	1/2606	2/23843	0.206655	0.576454	0.548145	Rgs14
GO_BP_m1	GO:001014	farnesyl dip	1/2606	2/23843	0.206655	0.576454	0.548145	Hmgcs2
GO_BP_m1	GO:001026	SCF compl	1/2606	2/23843	0.206655	0.576454	0.548145	Cand1
GO_BP_m1	GO:001026	response to	1/2606	2/23843	0.206655	0.576454	0.548145	Gpx1
GO_BP_m1	GO:001051	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Pdgfa
GO_BP_m1	GO:001072	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Snca
GO_BP_m1	GO:001084	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Map1s
GO_BP_m1	GO:001089	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Scarb1
GO_BP_m1	GO:001472	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Myh7
GO_BP_m1	GO:001485	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Ephb1
GO_BP_m1	GO:001486	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Myh7
GO_BP_m1	GO:001568	intracellula	1/2606	2/23843	0.206655	0.576454	0.548145	Atp7b
GO_BP_m1	GO:001578	GDP-fucos	1/2606	2/23843	0.206655	0.576454	0.548145	Slc35c1
GO_BP_m1	GO:001591	peroxisoma	1/2606	2/23843	0.206655	0.576454	0.548145	Abcd3
GO_BP_m1	GO:001592	lipopolysac	1/2606	2/23843	0.206655	0.576454	0.548145	Scarb1
GO_BP_m1	GO:001609	monoterpe	1/2606	2/23843	0.206655	0.576454	0.548145	Cyp2e1
GO_BP_m1	GO:001626	selenocyste	1/2606	2/23843	0.206655	0.576454	0.548145	Sephs1
GO_BP_m1	GO:001907	viral genom	1/2606	2/23843	0.206655	0.576454	0.548145	Pcx
GO_BP_m1	GO:001907	viral RNA g	1/2606	2/23843	0.206655	0.576454	0.548145	Pcx
GO_BP_m1	GO:001926	glycine bio	1/2606	2/23843	0.206655	0.576454	0.548145	Shmt1
GO_BP_m1	GO:001938	glucuronos	1/2606	2/23843	0.206655	0.576454	0.548145	Abhd10
GO_BP_m1	GO:001940	dolichol bi	1/2606	2/23843	0.206655	0.576454	0.548145	Nus1
GO_BP_m1	GO:001947	D-amino a	1/2606	2/23843	0.206655	0.576454	0.548145	Ddo
GO_BP_m1	GO:001954	arginine ca	1/2606	2/23843	0.206655	0.576454	0.548145	Arg1
GO_BP_m1	GO:001955	glutamate	1/2606	2/23843	0.206655	0.576454	0.548145	Got1
GO_BP_m1	GO:001955	glutamate	1/2606	2/23843	0.206655	0.576454	0.548145	Got1
GO_BP_m1	GO:001956	glycerol ca	1/2606	2/23843	0.206655	0.576454	0.548145	Tkfc
GO_BP_m1	GO:001985	cytosine m	1/2606	2/23843	0.206655	0.576454	0.548145	Tet2
GO_BP_m1	GO:002152	medial mo	1/2606	2/23843	0.206655	0.576454	0.548145	Lhx4
GO_BP_m1	GO:002159	fourth vent	1/2606	2/23843	0.206655	0.576454	0.548145	Kdm2b
GO_BP_m1	GO:002163	optic nerve	1/2606	2/23843	0.206655	0.576454	0.548145	Kcna2
GO_BP_m1	GO:002164	vagus nerv	1/2606	2/23843	0.206655	0.576454	0.548145	Tbx1
GO_BP_m1	GO:002175	facial nucle	1/2606	2/23843	0.206655	0.576454	0.548145	Hoxb1
GO_BP_m1	GO:002175	globus pall	1/2606	2/23843	0.206655	0.576454	0.548145	Arx
GO_BP_m1	GO:002178	postgangli	1/2606	2/23843	0.206655	0.576454	0.548145	Gdnf
GO_BP_m1	GO:002183	embryonic	1/2606	2/23843	0.206655	0.576454	0.548145	Arx
GO_BP_m1	GO:002184	directional	1/2606	2/23843	0.206655	0.576454	0.548145	Nrg1

GO_BP_m1	GO:002184	chemorepu	1/2606	2/23843	0.206655	0.576454	0.548145	Nrg1
GO_BP_m1	GO:002187	Wnt signali	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:002189	forebrain a	1/2606	2/23843	0.206655	0.576454	0.548145	Nf1
GO_BP_m1	GO:002189	forebrain a	1/2606	2/23843	0.206655	0.576454	0.548145	Nf1
GO_BP_m1	GO:002193	radial glia	1/2606	2/23843	0.206655	0.576454	0.548145	Cend1
GO_BP_m1	GO:002193	cerebellar	1/2606	2/23843	0.206655	0.576454	0.548145	Plxna2
GO_BP_m1	GO:002194	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Cend1
GO_BP_m1	GO:003010	vasopressi	1/2606	2/23843	0.206655	0.576454	0.548145	Trpv4
GO_BP_m1	GO:003045	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Susd4
GO_BP_m1	GO:003124	actin rod a	1/2606	2/23843	0.206655	0.576454	0.548145	Hsp90b1
GO_BP_m1	GO:003144	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Tpr
GO_BP_m1	GO:003144	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Myh7
GO_BP_m1	GO:003145	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Tpr
GO_BP_m1	GO:003159	wybutosine	1/2606	2/23843	0.206655	0.576454	0.548145	Tyw5
GO_BP_m1	GO:003159	wybutosine	1/2606	2/23843	0.206655	0.576454	0.548145	Tyw5
GO_BP_m1	GO:003199	mRNA exp	1/2606	2/23843	0.206655	0.576454	0.548145	Tpr
GO_BP_m1	GO:003207	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Dffa
GO_BP_m1	GO:003241	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Drd3
GO_BP_m1	GO:003280	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Anxa2
GO_BP_m1	GO:003280	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Pcsk9
GO_BP_m1	GO:003287	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	E2f7
GO_BP_m1	GO:003319	response t	1/2606	2/23843	0.206655	0.576454	0.548145	Eif2ak2
GO_BP_m1	GO:003330	phytol met	1/2606	2/23843	0.206655	0.576454	0.548145	Pecr
GO_BP_m1	GO:003348	nitric oxide	1/2606	2/23843	0.206655	0.576454	0.548145	Cav1
GO_BP_m1	GO:003408	establishm	1/2606	2/23843	0.206655	0.576454	0.548145	Naa50
GO_BP_m1	GO:003414	toll-like rec	1/2606	2/23843	0.206655	0.576454	0.548145	Tlr5
GO_BP_m1	GO:003417	toll-like rec	1/2606	2/23843	0.206655	0.576454	0.548145	Treml4
GO_BP_m1	GO:003441	tRNA 3'-tra	1/2606	2/23843	0.206655	0.576454	0.548145	Elac1
GO_BP_m1	GO:003497	histone H3	1/2606	2/23843	0.206655	0.576454	0.548145	Prmt6
GO_BP_m1	GO:003506	nuclear spe	1/2606	2/23843	0.206655	0.576454	0.548145	Srpk2
GO_BP_m1	GO:003512	post-embr	1/2606	2/23843	0.206655	0.576454	0.548145	Mir23a
GO_BP_m1	GO:003512	post-embr	1/2606	2/23843	0.206655	0.576454	0.548145	Mir23a
GO_BP_m1	GO:003540	histone H3	1/2606	2/23843	0.206655	0.576454	0.548145	Prkca
GO_BP_m1	GO:003550	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Wt1
GO_BP_m1	GO:003552	retrograde	1/2606	2/23843	0.206655	0.576454	0.548145	Usp6nl
GO_BP_m1	GO:003558	sequesterin	1/2606	2/23843	0.206655	0.576454	0.548145	Fbn1
GO_BP_m1	GO:003566	TRAM-dep	1/2606	2/23843	0.206655	0.576454	0.548145	Ticam2
GO_BP_m1	GO:003566	TRAM-dep	1/2606	2/23843	0.206655	0.576454	0.548145	Ticam2
GO_BP_m1	GO:003569	CD8-positi	1/2606	2/23843	0.206655	0.576454	0.548145	Ripk3
GO_BP_m1	GO:003570	astrocyte c	1/2606	2/23843	0.206655	0.576454	0.548145	Gpr183
GO_BP_m1	GO:003570	memory T	1/2606	2/23843	0.206655	0.576454	0.548145	Fam49b
GO_BP_m1	GO:003580	adrenal cor	1/2606	2/23843	0.206655	0.576454	0.548145	Wt1
GO_BP_m1	GO:003580	adrenal cor	1/2606	2/23843	0.206655	0.576454	0.548145	Wt1
GO_BP_m1	GO:003584	oviduct epi	1/2606	2/23843	0.206655	0.576454	0.548145	Cdh1
GO_BP_m1	GO:003584	uterine epi	1/2606	2/23843	0.206655	0.576454	0.548145	Cdh1
GO_BP_m1	GO:003598	tongue mu	1/2606	2/23843	0.206655	0.576454	0.548145	Tbx1
GO_BP_m1	GO:003622	protein loc	1/2606	2/23843	0.206655	0.576454	0.548145	Nup54
GO_BP_m1	GO:003632	vascular en	1/2606	2/23843	0.206655	0.576454	0.548145	Pdcd6

GO_BP_m1	GO:003633	hepatocyte	1/2606	2/23843	0.206655	0.576454	0.548145	Ezh1
GO_BP_m1	GO:003633	epidermal	1/2606	2/23843	0.206655	0.576454	0.548145	Ift88
GO_BP_m1	GO:003645	cap mRNA	1/2606	2/23843	0.206655	0.576454	0.548145	Cmtr2
GO_BP_m1	GO:003648	neuron intr	1/2606	2/23843	0.206655	0.576454	0.548145	Park2
GO_BP_m1	GO:003650	trimming c	1/2606	2/23843	0.206655	0.576454	0.548145	Man1b1
GO_BP_m1	GO:003800	netrin-acti	1/2606	2/23843	0.206655	0.576454	0.548145	Shtn1
GO_BP_m1	GO:003815	granulocyt	1/2606	2/23843	0.206655	0.576454	0.548145	Jagn1
GO_BP_m1	GO:003816	thrombopo	1/2606	2/23843	0.206655	0.576454	0.548145	Cib1
GO_BP_m1	GO:004212	nitrate assi	1/2606	2/23843	0.206655	0.576454	0.548145	Suox
GO_BP_m1	GO:004226	DNA prote	1/2606	2/23843	0.206655	0.576454	0.548145	Nudt1
GO_BP_m1	GO:004226	peptidyl-as	1/2606	2/23843	0.206655	0.576454	0.548145	Asph
GO_BP_m1	GO:004232	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Adora1
GO_BP_m1	GO:004240	thyroid hor	1/2606	2/23843	0.206655	0.576454	0.548145	Dio2
GO_BP_m1	GO:004245	arginine bi	1/2606	2/23843	0.206655	0.576454	0.548145	Otc
GO_BP_m1	GO:004253	hypotonic	1/2606	2/23843	0.206655	0.576454	0.548145	Trpv4
GO_BP_m1	GO:004259	behavioral	1/2606	2/23843	0.206655	0.576454	0.548145	Galp
GO_BP_m1	GO:004277	tRNA 3'-tra	1/2606	2/23843	0.206655	0.576454	0.548145	Elac1
GO_BP_m1	GO:004311	replication	1/2606	2/23843	0.206655	0.576454	0.548145	Tipin
GO_BP_m1	GO:004331	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Stx4a
GO_BP_m1	GO:004331	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Bcr
GO_BP_m1	GO:004337	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Nckap1l
GO_BP_m1	GO:004360	cellular am	1/2606	2/23843	0.206655	0.576454	0.548145	Pm20d1
GO_BP_m1	GO:004433	canonical W	1/2606	2/23843	0.206655	0.576454	0.548145	Myc
GO_BP_m1	GO:004434	canonical W	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:004469	tooth erup	1/2606	2/23843	0.206655	0.576454	0.548145	Tnfsf11
GO_BP_m1	GO:004472	DNA deme	1/2606	2/23843	0.206655	0.576454	0.548145	Tet3
GO_BP_m1	GO:004478	metaphase	1/2606	2/23843	0.206655	0.576454	0.548145	Ttk
GO_BP_m1	GO:004500	DNA replic	1/2606	2/23843	0.206655	0.576454	0.548145	Pole
GO_BP_m1	GO:004521	FasL biosyn	1/2606	2/23843	0.206655	0.576454	0.548145	Jak3
GO_BP_m1	GO:004521	neurotrans	1/2606	2/23843	0.206655	0.576454	0.548145	Ache
GO_BP_m1	GO:004564	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Trib1
GO_BP_m1	GO:004564	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Trib1
GO_BP_m1	GO:004565	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Trib1
GO_BP_m1	GO:004575	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Peli3
GO_BP_m1	GO:004576	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Atp2b4
GO_BP_m1	GO:004608	adenine m	1/2606	2/23843	0.206655	0.576454	0.548145	Aprt
GO_BP_m1	GO:004608	adenine bi	1/2606	2/23843	0.206655	0.576454	0.548145	Aprt
GO_BP_m1	GO:004608	adenosine	1/2606	2/23843	0.206655	0.576454	0.548145	Adk
GO_BP_m1	GO:004616	heme a me	1/2606	2/23843	0.206655	0.576454	0.548145	Cox15
GO_BP_m1	GO:004649	lipid A met	1/2606	2/23843	0.206655	0.576454	0.548145	Zfp593
GO_BP_m1	GO:004651	sphinganin	1/2606	2/23843	0.206655	0.576454	0.548145	Sptlc2
GO_BP_m1	GO:004672	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Vapb
GO_BP_m1	GO:004807	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Spns2
GO_BP_m1	GO:004820	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Preb
GO_BP_m1	GO:004834	paraxial me	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:004834	paraxial me	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:004838	intermedia	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:004869	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a

GO_BP_m1	GO:004874	compound	1/2606	2/23843	0.206655	0.576454	0.548145	Abcb5
GO_BP_m1	GO:004886	stem cell fa	1/2606	2/23843	0.206655	0.576454	0.548145	Ntf5
GO_BP_m1	GO:005097	detection c	1/2606	2/23843	0.206655	0.576454	0.548145	Sox2
GO_BP_m1	GO:005103	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Zfp386
GO_BP_m1	GO:005145	attachmen	1/2606	2/23843	0.206655	0.576454	0.548145	Cenpc1
GO_BP_m1	GO:005159	response t	1/2606	2/23843	0.206655	0.576454	0.548145	Arsb
GO_BP_m1	GO:005189	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:005195	methotrexa	1/2606	2/23843	0.206655	0.576454	0.548145	Slc46a1
GO_BP_m1	GO:005507	cadmium i	1/2606	2/23843	0.206655	0.576454	0.548145	Mt3
GO_BP_m1	GO:006000	copper ion	1/2606	2/23843	0.206655	0.576454	0.548145	Atp7b
GO_BP_m1	GO:006031	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Bcr
GO_BP_m1	GO:006032	cytoplasmi	1/2606	2/23843	0.206655	0.576454	0.548145	Shtn1
GO_BP_m1	GO:006037	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Itgam
GO_BP_m1	GO:006038	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Nucks1
GO_BP_m1	GO:006043	bronchus r	1/2606	2/23843	0.206655	0.576454	0.548145	Tulp3
GO_BP_m1	GO:006054	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Ripk3
GO_BP_m1	GO:006073	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Slc22a5
GO_BP_m1	GO:006099	cell-cell sig	1/2606	2/23843	0.206655	0.576454	0.548145	Lgr4
GO_BP_m1	GO:006103	secretion b	1/2606	2/23843	0.206655	0.576454	0.548145	Fgf7
GO_BP_m1	GO:006118	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Rflna
GO_BP_m1	GO:006119	taste bud c	1/2606	2/23843	0.206655	0.576454	0.548145	Ntf5
GO_BP_m1	GO:006122	pattern spe	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:006128	Wnt signali	1/2606	2/23843	0.206655	0.576454	0.548145	Lgr4
GO_BP_m1	GO:006129	canonical V	1/2606	2/23843	0.206655	0.576454	0.548145	Lgr4
GO_BP_m1	GO:006144	endocardia	1/2606	2/23843	0.206655	0.576454	0.548145	Jag1
GO_BP_m1	GO:006158	intestinal e	1/2606	2/23843	0.206655	0.576454	0.548145	Arsb
GO_BP_m1	GO:007025	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Adora1
GO_BP_m1	GO:007031	G1 to G0 tr	1/2606	2/23843	0.206655	0.576454	0.548145	Zfp503
GO_BP_m1	GO:007032	tRNA selen	1/2606	2/23843	0.206655	0.576454	0.548145	Sephs1
GO_BP_m1	GO:007034	brown fat c	1/2606	2/23843	0.206655	0.576454	0.548145	Fgf16
GO_BP_m1	GO:007034	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Fgf16
GO_BP_m1	GO:007042	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Peli3
GO_BP_m1	GO:007043	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Peli3
GO_BP_m1	GO:007056	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Kank2
GO_BP_m1	GO:007065	actin filame	1/2606	2/23843	0.206655	0.576454	0.548145	Shtn1
GO_BP_m1	GO:007083	divalent me	1/2606	2/23843	0.206655	0.576454	0.548145	Slc40a1
GO_BP_m1	GO:007095	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Arg1
GO_BP_m1	GO:007096	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Arg1
GO_BP_m1	GO:007110	response t	1/2606	2/23843	0.206655	0.576454	0.548145	Jak3
GO_BP_m1	GO:007138	cellular res	1/2606	2/23843	0.206655	0.576454	0.548145	Npas4
GO_BP_m1	GO:007147	cellular hyp	1/2606	2/23843	0.206655	0.576454	0.548145	Trpv4
GO_BP_m1	GO:007159	thymocyte	1/2606	2/23843	0.206655	0.576454	0.548145	Adam8
GO_BP_m1	GO:007164	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Mefv
GO_BP_m1	GO:007164	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Trpv4
GO_BP_m1	GO:007181	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Tnfsf11
GO_BP_m1	GO:007184	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Tnfsf11
GO_BP_m1	GO:007187	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Atp2b4
GO_BP_m1	GO:007191	urea transp	1/2606	2/23843	0.206655	0.576454	0.548145	Slc14a2

GO_BP_m1	GO:007192	alpha-tubu	1/2606	2/23843	0.206655	0.576454	0.548145	Kat2a
GO_BP_m1	GO:007193	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Esrrb
GO_BP_m1	GO:007202	ascending	1/2606	2/23843	0.206655	0.576454	0.548145	Pou3f3
GO_BP_m1	GO:007202	thick ascen	1/2606	2/23843	0.206655	0.576454	0.548145	Pou3f3
GO_BP_m1	GO:007207	kidney inte	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:007209	anterior/po	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:007214	renal inters	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:007220	cell-cell sig	1/2606	2/23843	0.206655	0.576454	0.548145	Lgr4
GO_BP_m1	GO:007221	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Pou3f3
GO_BP_m1	GO:007223	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Pou3f3
GO_BP_m1	GO:007224	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Lamb2
GO_BP_m1	GO:007224	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Lamb2
GO_BP_m1	GO:007227	proximal/d	1/2606	2/23843	0.206655	0.576454	0.548145	Irx2
GO_BP_m1	GO:007227	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Wt1
GO_BP_m1	GO:007230	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Wt1
GO_BP_m1	GO:007231	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Lamb2
GO_BP_m1	GO:007231	metanephr	1/2606	2/23843	0.206655	0.576454	0.548145	Lamb2
GO_BP_m1	GO:007255	blood vess	1/2606	2/23843	0.206655	0.576454	0.548145	Dll4
GO_BP_m1	GO:007256	blood micr	1/2606	2/23843	0.206655	0.576454	0.548145	Cd36
GO_BP_m1	GO:007273	response to	1/2606	2/23843	0.206655	0.576454	0.548145	Mapk13
GO_BP_m1	GO:007275	cellular resp	1/2606	2/23843	0.206655	0.576454	0.548145	Ranbp1
GO_BP_m1	GO:008609	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Slc9a1
GO_BP_m1	GO:008609	angiotensin	1/2606	2/23843	0.206655	0.576454	0.548145	Cav1
GO_BP_m1	GO:009010	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Nr1h2
GO_BP_m1	GO:009018	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Nr1h2
GO_BP_m1	GO:009036	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Ptgs2
GO_BP_m1	GO:009036	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Hnrnpc
GO_BP_m1	GO:009061	mitochond	1/2606	2/23843	0.206655	0.576454	0.548145	Pnpt1
GO_BP_m1	GO:009067	endothelial	1/2606	2/23843	0.206655	0.576454	0.548145	Adamts9
GO_BP_m1	GO:009701	renal prote	1/2606	2/23843	0.206655	0.576454	0.548145	Gsn
GO_BP_m1	GO:009708	methyl-bra	1/2606	2/23843	0.206655	0.576454	0.548145	Phyh
GO_BP_m1	GO:009711	endoplasm	1/2606	2/23843	0.206655	0.576454	0.548145	Gbf1
GO_BP_m1	GO:009721	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Mt3
GO_BP_m1	GO:009727	ammonia h	1/2606	2/23843	0.206655	0.576454	0.548145	Otc
GO_BP_m1	GO:009727	urea home	1/2606	2/23843	0.206655	0.576454	0.548145	Slc25a23
GO_BP_m1	GO:009730	cap1 mRNA	1/2606	2/23843	0.206655	0.576454	0.548145	Cmtr2
GO_BP_m1	GO:009768	double-stra	1/2606	2/23843	0.206655	0.576454	0.548145	Lig3
GO_BP_m1	GO:009870	copper ion	1/2606	2/23843	0.206655	0.576454	0.548145	Slc31a1
GO_BP_m1	GO:009874	cerebellar r	1/2606	2/23843	0.206655	0.576454	0.548145	Samd4b
GO_BP_m1	GO:009888	modificatio	1/2606	2/23843	0.206655	0.576454	0.548145	Arhgap44
GO_BP_m1	GO:009896	dendritic tr	1/2606	2/23843	0.206655	0.576454	0.548145	Stau2
GO_BP_m1	GO:009896	dendritic tr	1/2606	2/23843	0.206655	0.576454	0.548145	Stau2
GO_BP_m1	GO:009896	anterograd	1/2606	2/23843	0.206655	0.576454	0.548145	Stau2
GO_BP_m1	GO:009902	vesicle teth	1/2606	2/23843	0.206655	0.576454	0.548145	Stard3nl
GO_BP_m1	GO:009903	sphingolipi	1/2606	2/23843	0.206655	0.576454	0.548145	Abcb1a
GO_BP_m1	GO:009904	vesicle teth	1/2606	2/23843	0.206655	0.576454	0.548145	Stard3nl
GO_BP_m1	GO:009908	retrograde	1/2606	2/23843	0.206655	0.576454	0.548145	Ntf5
GO_BP_m1	GO:009916	synaptic sig	1/2606	2/23843	0.206655	0.576454	0.548145	Gucy1b1

GO_BP_m1	GO:009940	maintenan	1/2606	2/23843	0.206655	0.576454	0.548145	Tnks
GO_BP_m1	GO:009940	mitotic sist	1/2606	2/23843	0.206655	0.576454	0.548145	Tnks
GO_BP_m1	GO:009954	trans-syna	1/2606	2/23843	0.206655	0.576454	0.548145	Gucy1b1
GO_BP_m1	GO:009954	trans-syna	1/2606	2/23843	0.206655	0.576454	0.548145	Gucy1b1
GO_BP_m1	GO:009956	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Grin2b
GO_BP_m1	GO:014019	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Atp2b4
GO_BP_m1	GO:190003	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Kcnk2
GO_BP_m1	GO:190011	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Dmrtc2
GO_BP_m1	GO:190011	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Dmrtc2
GO_BP_m1	GO:190014	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Dand5
GO_BP_m1	GO:190017	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Dand5
GO_BP_m1	GO:190067	olefin meta	1/2606	2/23843	0.206655	0.576454	0.548145	Ephx2
GO_BP_m1	GO:190075	protein pro	1/2606	2/23843	0.206655	0.576454	0.548145	Gsn
GO_BP_m1	GO:190109	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Pex5
GO_BP_m1	GO:190109	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Pex5
GO_BP_m1	GO:190109	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Pex5
GO_BP_m1	GO:190109	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Pex5
GO_BP_m1	GO:190126	lipooligosa	1/2606	2/23843	0.206655	0.576454	0.548145	Zfp593
GO_BP_m1	GO:190127	lipooligosa	1/2606	2/23843	0.206655	0.576454	0.548145	Zfp593
GO_BP_m1	GO:190134	response t	1/2606	2/23843	0.206655	0.576454	0.548145	Ranbp1
GO_BP_m1	GO:190140	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Clybl
GO_BP_m1	GO:190173	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Dgat1
GO_BP_m1	GO:190186	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Ppargc1a
GO_BP_m1	GO:190189	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Pde4b
GO_BP_m1	GO:190210	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Ttk
GO_BP_m1	GO:190210	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Ttk
GO_BP_m1	GO:190225	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Foxc1
GO_BP_m1	GO:190251	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Dffa
GO_BP_m1	GO:190252	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Nmi
GO_BP_m1	GO:190252	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Park2
GO_BP_m1	GO:190253	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Park2
GO_BP_m1	GO:190256	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Stx4a
GO_BP_m1	GO:190268	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Tigar
GO_BP_m1	GO:190272	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Ephb1
GO_BP_m1	GO:190272	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Ephb1
GO_BP_m1	GO:190276	isoprenoid	1/2606	2/23843	0.206655	0.576454	0.548145	Hmgcs2
GO_BP_m1	GO:190281	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Tbx1
GO_BP_m1	GO:190295	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Dnajc13
GO_BP_m1	GO:190310	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Sirt3
GO_BP_m1	GO:190310	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Sirt3
GO_BP_m1	GO:190317	fatty alcoh	1/2606	2/23843	0.206655	0.576454	0.548145	Pecr
GO_BP_m1	GO:190328	positive re	1/2606	2/23843	0.206655	0.576454	0.548145	Slc9a1
GO_BP_m1	GO:190338	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Park2
GO_BP_m1	GO:190338	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Park2
GO_BP_m1	GO:190341	response t	1/2606	2/23843	0.206655	0.576454	0.548145	Kcnmb1
GO_BP_m1	GO:190341	cellular res	1/2606	2/23843	0.206655	0.576454	0.548145	Kcnmb1
GO_BP_m1	GO:190341	response t	1/2606	2/23843	0.206655	0.576454	0.548145	Nfkb1
GO_BP_m1	GO:190351	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Xrcc1

GO_BP_m1	GO:190351	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Xrcc1
GO_BP_m1	GO:190369	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Rreb1
GO_BP_m1	GO:190387	ferrous iron	1/2606	2/23843	0.206655	0.576454	0.548145	Slc40a1
GO_BP_m1	GO:190392	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Gsn
GO_BP_m1	GO:190392	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Gsn
GO_BP_m1	GO:190402	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Tigar
GO_BP_m1	GO:190404	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Park2
GO_BP_m1	GO:190444	folic acid ir	1/2606	2/23843	0.206655	0.576454	0.548145	Slc46a1
GO_BP_m1	GO:190446	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Idh2
GO_BP_m1	GO:190470	granulosa c	1/2606	2/23843	0.206655	0.576454	0.548145	Bok
GO_BP_m1	GO:190470	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Bok
GO_BP_m1	GO:190471	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Snca
GO_BP_m1	GO:190474	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Tnks
GO_BP_m1	GO:190477	response to	1/2606	2/23843	0.206655	0.576454	0.548145	Ezh1
GO_BP_m1	GO:190481	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	H2afy
GO_BP_m1	GO:190486	inhibitory s	1/2606	2/23843	0.206655	0.576454	0.548145	Npas4
GO_BP_m1	GO:190486	telomerase	1/2606	2/23843	0.206655	0.576454	0.548145	Atr
GO_BP_m1	GO:190487	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Cacnb2
GO_BP_m1	GO:190488	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Atr
GO_BP_m1	GO:190488	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Atr
GO_BP_m1	GO:190488	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt7a
GO_BP_m1	GO:190489	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt7a
GO_BP_m1	GO:190490	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Tnks
GO_BP_m1	GO:190490	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Tnks
GO_BP_m1	GO:190500	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Nog
GO_BP_m1	GO:190513	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Ttk
GO_BP_m1	GO:190513	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Ttk
GO_BP_m1	GO:190516	protein loc	1/2606	2/23843	0.206655	0.576454	0.548145	Rab34
GO_BP_m1	GO:190516	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Rab34
GO_BP_m1	GO:190517	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Rab34
GO_BP_m1	GO:190526	endonucle	1/2606	2/23843	0.206655	0.576454	0.548145	Elac1
GO_BP_m1	GO:190540	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:190540	negative re	1/2606	2/23843	0.206655	0.576454	0.548145	Osr1
GO_BP_m1	GO:190555	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Ddrgk1
GO_BP_m1	GO:190555	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Ddrgk1
GO_BP_m1	GO:190562	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Gch1
GO_BP_m1	GO:190566	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Calcr
GO_BP_m1	GO:190587	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Cfl1
GO_BP_m1	GO:190593	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Cib1
GO_BP_m1	GO:199011	ribosome-a	1/2606	2/23843	0.206655	0.576454	0.548145	Nemf
GO_BP_m1	GO:199026	peptidyl-ty	1/2606	2/23843	0.206655	0.576454	0.548145	Ptpn1
GO_BP_m1	GO:199040	embryonic	1/2606	2/23843	0.206655	0.576454	0.548145	Pdgfa
GO_BP_m1	GO:199051	pyrimidine	1/2606	2/23843	0.206655	0.576454	0.548145	Slc25a33
GO_BP_m1	GO:199077	matrix met	1/2606	2/23843	0.206655	0.576454	0.548145	Idh2
GO_BP_m1	GO:199085	cellular res	1/2606	2/23843	0.206655	0.576454	0.548145	Bcar1
GO_BP_m1	GO:200004	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:200007	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Wnt3a
GO_BP_m1	GO:200012	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Mgll

GO_BP_m1	GO:200025	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Cib1
GO_BP_m1	GO:200028	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Atp2b4
GO_BP_m1	GO:200029	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Snca
GO_BP_m1	GO:200033	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Nlgn3
GO_BP_m1	GO:200033	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Cd36
GO_BP_m1	GO:200033	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Cd36
GO_BP_m1	GO:200034	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Trpv4
GO_BP_m1	GO:200036	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Itgam
GO_BP_m1	GO:200036	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Itgam
GO_BP_m1	GO:200036	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Hyal3
GO_BP_m1	GO:200036	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Hyal3
GO_BP_m1	GO:200037	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Mt3
GO_BP_m1	GO:200045	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Ripk3
GO_BP_m1	GO:200045	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Gpr183
GO_BP_m1	GO:200047	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Ptprc
GO_BP_m1	GO:200047	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Ptprc
GO_BP_m1	GO:200056	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Fam49b
GO_BP_m1	GO:200056	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Fam49b
GO_BP_m1	GO:200070	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Prkca
GO_BP_m1	GO:200076	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Cfl1
GO_BP_m1	GO:200077	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Cfl1
GO_BP_m1	GO:200081	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Cfl1
GO_BP_m1	GO:200085	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Tac1
GO_BP_m1	GO:200086	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Spp1
GO_BP_m1	GO:200103	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Tbx1
GO_BP_m1	GO:200103	positive reg	1/2606	2/23843	0.206655	0.576454	0.548145	Tbx1
GO_BP_m1	GO:200122	regulation	1/2606	2/23843	0.206655	0.576454	0.548145	Prkdc
GO_BP_m1	GO:200130	lipoxin met	1/2606	2/23843	0.206655	0.576454	0.548145	Alox12
GO_BP_m1	GO:200130	lipoxin bios	1/2606	2/23843	0.206655	0.576454	0.548145	Alox12
GO_BP_m1	GO:200130	lipoxin A4	1/2606	2/23843	0.206655	0.576454	0.548145	Alox12
GO_BP_m1	GO:200130	lipoxin A4	1/2606	2/23843	0.206655	0.576454	0.548145	Alox12
GO_BP_m1	GO:000914	nucleoside	19/2606	142/23843	0.207063	0.577409	0.549053	Adk/Atp5a
GO_BP_m1	GO:001921	regulation	39/2606	312/23843	0.208426	0.578275	0.549877	Adora1/An
GO_BP_m1	GO:003166	cellular res	28/2606	218/23843	0.208596	0.578275	0.549877	Aoc1/Atf3/
GO_BP_m1	GO:000941	response to	18/2606	134/23843	0.210038	0.578275	0.549877	Atr/Cdc25a
GO_BP_m1	GO:001401	regulation	18/2606	134/23843	0.210038	0.578275	0.549877	Cdh2/Drd3
GO_BP_m1	GO:007132	cellular res	18/2606	134/23843	0.210038	0.578275	0.549877	Ano1/Fkbp
GO_BP_m1	GO:007066	leukocyte p	40/2606	321/23843	0.210757	0.578275	0.549877	Adk/Arg1/
GO_BP_m1	GO:000616	purine nuc	33/2606	261/23843	0.211199	0.578275	0.549877	Adcy4/Adk
GO_BP_m1	GO:002241	cellular cor	43/2606	347/23843	0.211564	0.578275	0.549877	Aifm1/Asp
GO_BP_m1	GO:000018	nuclear-tra	6/2606	37/23843	0.212479	0.578275	0.549877	Gspt2/Mag
GO_BP_m1	GO:000300	skeletal mu	6/2606	37/23843	0.212479	0.578275	0.549877	Cav3/Chrn
GO_BP_m1	GO:003085	granulocyt	6/2606	37/23843	0.212479	0.578275	0.549877	Cebpe/Csf
GO_BP_m1	GO:004598	positive reg	6/2606	37/23843	0.212479	0.578275	0.549877	Abat/Adra
GO_BP_m1	GO:006023	regulation	6/2606	37/23843	0.212479	0.578275	0.549877	Ankrd53/B
GO_BP_m1	GO:007117	mitotic spi	6/2606	37/23843	0.212479	0.578275	0.549877	Klhl22/Mad
GO_BP_m1	GO:007182	protein-lip	6/2606	37/23843	0.212479	0.578275	0.549877	Dgat1/Mtt
GO_BP_m1	GO:007260	interleukin-	6/2606	37/23843	0.212479	0.578275	0.549877	C1qtnf3/Hy

GO_BP_m1	GO:190210	regulation	6/2606	37/23843	0.212479	0.578275	0.549877	Bnip3/Bok/
GO_BP_m1	GO:004856	embryonic	59/2606	486/23843	0.212608	0.578275	0.549877	Adm/Aldh1
GO_BP_m1	GO:004864	muscle org	13/2606	93/23843	0.213194	0.578275	0.549877	Ankrd1/Dll
GO_BP_m1	GO:007148	cellular res	13/2606	93/23843	0.213194	0.578275	0.549877	Atr/Cdc25
GO_BP_m1	GO:190382	organic aci	13/2606	93/23843	0.213194	0.578275	0.549877	Arl6ip5/AU
GO_BP_m1	GO:190503	carboxylic	13/2606	93/23843	0.213194	0.578275	0.549877	Arl6ip5/AU
GO_BP_m1	GO:190129	nucleoside	39/2606	313/23843	0.214351	0.578275	0.549877	Adcy4/Adk
GO_BP_m1	GO:000713	synaptone	4/2606	22/23843	0.214458	0.578275	0.549877	Syce2/Syc
GO_BP_m1	GO:001058	miRNA me	4/2606	22/23843	0.214458	0.578275	0.549877	Khsrp/Nfk
GO_BP_m1	GO:001587	norepineph	4/2606	22/23843	0.214458	0.578275	0.549877	Hrh3/P2ry1
GO_BP_m1	GO:003551	DNA dealk	4/2606	22/23843	0.214458	0.578275	0.549877	Apobec1/T
GO_BP_m1	GO:004202	protein ref	4/2606	22/23843	0.214458	0.578275	0.549877	Dnaja4/Hs
GO_BP_m1	GO:004414	negative re	4/2606	22/23843	0.214458	0.578275	0.549877	Cd36/Ifng/
GO_BP_m1	GO:004478	G1 DNA da	4/2606	22/23843	0.214458	0.578275	0.549877	Cdkn1a/Fb
GO_BP_m1	GO:004481	mitotic G1/	4/2606	22/23843	0.214458	0.578275	0.549877	Cdkn1a/Fb
GO_BP_m1	GO:004581	positive re	4/2606	22/23843	0.214458	0.578275	0.549877	Apobec1/
GO_BP_m1	GO:005188	mitochond	4/2606	22/23843	0.214458	0.578275	0.549877	Alox12/Bo
GO_BP_m1	GO:007023	positive re	4/2606	22/23843	0.214458	0.578275	0.549877	Adam8/Il1
GO_BP_m1	GO:007145	protein loc	4/2606	22/23843	0.214458	0.578275	0.549877	Cdk1/Cen
GO_BP_m1	GO:007147	cellular hy	4/2606	22/23843	0.214458	0.578275	0.549877	Mir7b/Mir
GO_BP_m1	GO:007221	regulation	4/2606	22/23843	0.214458	0.578275	0.549877	Gdnf/Myc/
GO_BP_m1	GO:007227	metanephr	4/2606	22/23843	0.214458	0.578275	0.549877	Gdnf/Lgr4/
GO_BP_m1	GO:200076	regulation	4/2606	22/23843	0.214458	0.578275	0.549877	Cpeb3/Cp
GO_BP_m1	GO:000005	citrulline m	2/2606	8/23843	0.214944	0.578275	0.549877	Atp2b4/Ot
GO_BP_m1	GO:000009	sulfur amin	2/2606	8/23843	0.214944	0.578275	0.549877	Blmh/Mtrr
GO_BP_m1	GO:000151	selenocyst	2/2606	8/23843	0.214944	0.578275	0.549877	Pstk/Sepse
GO_BP_m1	GO:000177	plasma me	2/2606	8/23843	0.214944	0.578275	0.549877	Cav3/Myof
GO_BP_m1	GO:000199	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Adra1d/Dr
GO_BP_m1	GO:000645	translation	2/2606	8/23843	0.214944	0.578275	0.549877	Pstk/Sepse
GO_BP_m1	GO:000693	substrate-	2/2606	8/23843	0.214944	0.578275	0.549877	Abl2/Shtn1
GO_BP_m1	GO:000704	lysosomal l	2/2606	8/23843	0.214944	0.578275	0.549877	Atp6v0c/P
GO_BP_m1	GO:000912	deoxyribo	2/2606	8/23843	0.214944	0.578275	0.549877	Dera/Dpyd
GO_BP_m1	GO:000916	deoxyribo	2/2606	8/23843	0.214944	0.578275	0.549877	Dnph1/Shr
GO_BP_m1	GO:000945	7-methylg	2/2606	8/23843	0.214944	0.578275	0.549877	Cmtr2/Rnn
GO_BP_m1	GO:001088	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Fkbp1b/Hr
GO_BP_m1	GO:001094	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Dach1/Sm
GO_BP_m1	GO:001567	copper ion	2/2606	8/23843	0.214944	0.578275	0.549877	Atp7b/Slc3
GO_BP_m1	GO:001587	acetylcholi	2/2606	8/23843	0.214944	0.578275	0.549877	Htr6/Tacr2
GO_BP_m1	GO:001587	carnitine tr	2/2606	8/23843	0.214944	0.578275	0.549877	Slc22a5/Sl
GO_BP_m1	GO:001632	female mei	2/2606	8/23843	0.214944	0.578275	0.549877	Sycp3/Ttk
GO_BP_m1	GO:001809	protein pol	2/2606	8/23843	0.214944	0.578275	0.549877	Tpgs1/Ttll5
GO_BP_m1	GO:002154	corpus call	2/2606	8/23843	0.214944	0.578275	0.549877	Pafah1b1/
GO_BP_m1	GO:002178	branchiom	2/2606	8/23843	0.214944	0.578275	0.549877	Plxna2/Sen
GO_BP_m1	GO:002189	cerebral co	2/2606	8/23843	0.214944	0.578275	0.549877	Arx/Rac3
GO_BP_m1	GO:002191	smoothen	2/2606	8/23843	0.214944	0.578275	0.549877	Smo/Tulp3
GO_BP_m1	GO:002303	CD40 sign	2/2606	8/23843	0.214944	0.578275	0.549877	Sharpin/Tn
GO_BP_m1	GO:003021	hyalurona	2/2606	8/23843	0.214944	0.578275	0.549877	Hyal2/Hyal
GO_BP_m1	GO:003111	rRNA pseu	2/2606	8/23843	0.214944	0.578275	0.549877	Nop10/Rp

GO_BP_m1	GO:003139	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Avpr1a/Ptg
GO_BP_m1	GO:003166	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Cactin/Trib
GO_BP_m1	GO:003253	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Atp8b1/Fsc
GO_BP_m1	GO:003281	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Il12b/Ptpn2
GO_BP_m1	GO:003431	primary alc	2/2606	8/23843	0.214944	0.578275	0.549877	Adh1/Adh5
GO_BP_m1	GO:003581	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Adora1/Uts
GO_BP_m1	GO:003649	IRE1-media	2/2606	8/23843	0.214944	0.578275	0.549877	Ficd/Ptpn1
GO_BP_m1	GO:003804	dimeric G-	2/2606	8/23843	0.214944	0.578275	0.549877	Adm/Calcr
GO_BP_m1	GO:004279	snRNA trar	2/2606	8/23843	0.214944	0.578275	0.549877	Ell2/Ice1
GO_BP_m1	GO:004317	nucleoside	2/2606	8/23843	0.214944	0.578275	0.549877	Adk/Aprt
GO_BP_m1	GO:004331	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Bcr/Itgam
GO_BP_m1	GO:004361	astrocyte c	2/2606	8/23843	0.214944	0.578275	0.549877	Arhgef7/Gp
GO_BP_m1	GO:004363	polyadenyl	2/2606	8/23843	0.214944	0.578275	0.549877	Exosc9/Pnp
GO_BP_m1	GO:004482	positive reg	2/2606	8/23843	0.214944	0.578275	0.549877	Nucks1/Va
GO_BP_m1	GO:004502	G0 to G1 tr	2/2606	8/23843	0.214944	0.578275	0.549877	Ctgf/Orc1
GO_BP_m1	GO:004534	positive reg	2/2606	8/23843	0.214944	0.578275	0.549877	Ifng/Il10
GO_BP_m1	GO:004606	dATP meta	2/2606	8/23843	0.214944	0.578275	0.549877	Adk/Nudt1
GO_BP_m1	GO:004649	S-adenosy	2/2606	8/23843	0.214944	0.578275	0.549877	Ahcyl2/Mtr
GO_BP_m1	GO:004695	nonassocia	2/2606	8/23843	0.214944	0.578275	0.549877	Drd5/Grin2
GO_BP_m1	GO:004824	epinephrin	2/2606	8/23843	0.214944	0.578275	0.549877	Cartpt/Ly6
GO_BP_m1	GO:004853	bone marr	2/2606	8/23843	0.214944	0.578275	0.549877	Asxl1/Ptprc
GO_BP_m1	GO:004879	pronephros	2/2606	8/23843	0.214944	0.578275	0.549877	Osr1/Osr2
GO_BP_m1	GO:005113	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Hsph1/Il12
GO_BP_m1	GO:006033	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Cactin/Mm
GO_BP_m1	GO:006092	cardiac mu	2/2606	8/23843	0.214944	0.578275	0.549877	Wnt3a/Wt1
GO_BP_m1	GO:006100	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Dnm3/Nlgn
GO_BP_m1	GO:006168	detoxificati	2/2606	8/23843	0.214944	0.578275	0.549877	Mt2/Mt3
GO_BP_m1	GO:006173	mitochond	2/2606	8/23843	0.214944	0.578275	0.549877	Mpc2/Pdh
GO_BP_m1	GO:007031	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Ctgf/Orc1
GO_BP_m1	GO:007126	L-methioni	2/2606	8/23843	0.214944	0.578275	0.549877	Apip/Enop
GO_BP_m1	GO:007160	chemokine	2/2606	8/23843	0.214944	0.578275	0.549877	Ticam2/Trp
GO_BP_m1	GO:009004	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Fnta/Nek3
GO_BP_m1	GO:009016	Golgi to lys	2/2606	8/23843	0.214944	0.578275	0.549877	Ankfy1/Rbs
GO_BP_m1	GO:009711	AMPA glut	2/2606	8/23843	0.214944	0.578275	0.549877	Lrrtm4/Ssh
GO_BP_m1	GO:009715	positive reg	2/2606	8/23843	0.214944	0.578275	0.549877	Abat/Nlgn3
GO_BP_m1	GO:009738	cellular lipi	2/2606	8/23843	0.214944	0.578275	0.549877	Fasn/Fdft1
GO_BP_m1	GO:009870	neurotrans	2/2606	8/23843	0.214944	0.578275	0.549877	Slc18a2/Th
GO_BP_m1	GO:009955	trans-synap	2/2606	8/23843	0.214944	0.578275	0.549877	Gucy1b1/N
GO_BP_m1	GO:010607	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Atp2b4/Op
GO_BP_m1	GO:190012	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Has2/Nfkb
GO_BP_m1	GO:190137	acetate est	2/2606	8/23843	0.214944	0.578275	0.549877	Htr6/Tacr2
GO_BP_m1	GO:190164	nucleoside	2/2606	8/23843	0.214944	0.578275	0.549877	Slc29a3/Slc
GO_BP_m1	GO:190203	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Eif2ak2/Fox
GO_BP_m1	GO:190371	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Bnip3/Trpv
GO_BP_m1	GO:190474	negative re	2/2606	8/23843	0.214944	0.578275	0.549877	Foxc1/Wt1
GO_BP_m1	GO:199031	cellular res	2/2606	8/23843	0.214944	0.578275	0.549877	Cfl1/Slc25a
GO_BP_m1	GO:200077	positive reg	2/2606	8/23843	0.214944	0.578275	0.549877	Mb21d1/Yp
GO_BP_m1	GO:200080	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Cdh2/Nlgn

GO_BP_m1	GO:200084	positive reg	2/2606	8/23843	0.214944	0.578275	0.549877	Galr1/Tac1
GO_BP_m1	GO:200126	positive reg	2/2606	8/23843	0.214944	0.578275	0.549877	Gsn/Tfap4
GO_BP_m1	GO:200127	regulation	2/2606	8/23843	0.214944	0.578275	0.549877	Avpr1a/Ptg
GO_BP_m1	GO:000717	transmemb	42/2606	339/23843	0.215151	0.578486	0.550078	Bmp3/Cav1
GO_BP_m1	GO:006041	muscle tiss	12/2606	85/23843	0.215154	0.578486	0.550078	Ankrd1/Dll
GO_BP_m1	GO:200005	regulation	19/2606	143/23843	0.215921	0.580113	0.551624	Arih2/Bcap
GO_BP_m1	GO:000666	sphingolipi	16/2606	118/23843	0.215957	0.580113	0.551624	Acer3/Asah
GO_BP_m1	GO:005072	positive reg	16/2606	118/23843	0.215957	0.580113	0.551624	Adam8/Ao
GO_BP_m1	GO:003019	collagen fib	7/2606	45/23843	0.216409	0.580261	0.551766	Anxa2/Col1
GO_BP_m1	GO:003301	tetrapyrrol	7/2606	45/23843	0.216409	0.580261	0.551766	Clybl/Cox1
GO_BP_m1	GO:004590	positive reg	7/2606	45/23843	0.216409	0.580261	0.551766	Adra1d/Alc
GO_BP_m1	GO:006032	head morp	7/2606	45/23843	0.216409	0.580261	0.551766	Asph/Crisp
GO_BP_m1	GO:190044	regulation	7/2606	45/23843	0.216409	0.580261	0.551766	Cacng5/Ca
GO_BP_m1	GO:190179	negative re	7/2606	45/23843	0.216409	0.580261	0.551766	N4bp1/Og
GO_BP_m1	GO:007149	cellular res	35/2606	279/23843	0.216746	0.580412	0.551909	Ankrd1/Ao
GO_BP_m1	GO:003577	insulin secr	11/2606	77/23843	0.216795	0.580412	0.551909	Ano1/Fkbp
GO_BP_m1	GO:005178	positive reg	11/2606	77/23843	0.216795	0.580412	0.551909	Cxcr5/Drd3
GO_BP_m1	GO:009063	activation o	11/2606	77/23843	0.216795	0.580412	0.551909	Bcas3/Docl
GO_BP_m1	GO:190331	negative re	11/2606	77/23843	0.216795	0.580412	0.551909	Apobec1/N
GO_BP_m1	GO:012003	plasma me	59/2606	487/23843	0.217393	0.581626	0.553063	Abl2/Arhge
GO_BP_m1	GO:006019	regulation	10/2606	69/23843	0.217988	0.581626	0.553063	Abl2/Adcya
GO_BP_m1	GO:006067	ureteric bu	10/2606	69/23843	0.217988	0.581626	0.553063	Fgf1/Gdnf/
GO_BP_m1	GO:006117	regulation	10/2606	69/23843	0.217988	0.581626	0.553063	Ano1/Fkbp
GO_BP_m1	GO:005501	ventricular	8/2606	53/23843	0.21817	0.581626	0.553063	Dll4/Foxc1/
GO_BP_m1	GO:000322	ventricular	9/2606	61/23843	0.218542	0.581626	0.553063	Adamts9/D
GO_BP_m1	GO:001017	body morp	9/2606	61/23843	0.218542	0.581626	0.553063	Asph/Crisp
GO_BP_m1	GO:001067	positive reg	9/2606	61/23843	0.218542	0.581626	0.553063	Adcyap1r1
GO_BP_m1	GO:004338	positive reg	9/2606	61/23843	0.218542	0.581626	0.553063	Ddrgk1/Fo
GO_BP_m1	GO:009055	regulation	9/2606	61/23843	0.218542	0.581626	0.553063	Bnip3/Bok/
GO_BP_m1	GO:190280	negative re	9/2606	61/23843	0.218542	0.581626	0.553063	Cdkn1a/E2
GO_BP_m1	GO:190437	positive reg	9/2606	61/23843	0.218542	0.581626	0.553063	Cib1/Epb41
GO_BP_m1	GO:200125	positive reg	9/2606	61/23843	0.218542	0.581626	0.553063	Akap6/Asp
GO_BP_m1	GO:000858	female gon	15/2606	110/23843	0.218863	0.581626	0.553063	Ccdc182/A
GO_BP_m1	GO:005126	protein dep	15/2606	110/23843	0.218863	0.581626	0.553063	Asph/Cfl1/
GO_BP_m1	GO:009009	negative re	15/2606	110/23843	0.218863	0.581626	0.553063	Cav1/Cdh1
GO_BP_m1	GO:003268	regulation	18/2606	135/23843	0.21924	0.581626	0.553063	Cactin/Ccl4
GO_BP_m1	GO:005092	positive reg	18/2606	135/23843	0.21924	0.581626	0.553063	Calr/Ccl4/C
GO_BP_m1	GO:009730	response to	18/2606	135/23843	0.21924	0.581626	0.553063	Abat/Adh1
GO_BP_m1	GO:003134	negative re	25/2606	194/23843	0.219386	0.581626	0.553063	Aatk/Cdk5/
GO_BP_m1	GO:006082	regulation	27/2606	211/23843	0.219437	0.581626	0.553063	Arntl/Capri
GO_BP_m1	GO:005070	regulation	54/2606	444/23843	0.220218	0.581626	0.553063	Abat/Abl2/
GO_BP_m1	GO:000007	DNA replic	3/2606	15/23843	0.220891	0.581626	0.553063	Rad9b/Tipi
GO_BP_m1	GO:000668	sphingomy	3/2606	15/23843	0.220891	0.581626	0.553063	Smpd2/Sm
GO_BP_m1	GO:000689	Golgi to va	3/2606	15/23843	0.220891	0.581626	0.553063	Ankfy1/Rbs
GO_BP_m1	GO:000699	nuclear po	3/2606	15/23843	0.220891	0.581626	0.553063	Ahctf1/Nup
GO_BP_m1	GO:000827	sulfate tran	3/2606	15/23843	0.220891	0.581626	0.553063	Racgap1/S
GO_BP_m1	GO:001088	negative re	3/2606	15/23843	0.220891	0.581626	0.553063	Nr1h2/Osb
GO_BP_m1	GO:001093	macrophag	3/2606	15/23843	0.220891	0.581626	0.553063	Cd36/Gprc

GO_BP_m1	GO:001591	peroxisom	3/2606	15/23843	0.220891	0.581626	0.553063	Pex10/Pex
GO_BP_m1	GO:003027	maintenan	3/2606	15/23843	0.220891	0.581626	0.553063	5730559C1
GO_BP_m1	GO:00346	response t	3/2606	15/23843	0.220891	0.581626	0.553063	Epha8/Ppa
GO_BP_m1	GO:00355	G-protein	3/2606	15/23843	0.220891	0.581626	0.553063	Acpp/Ador
GO_BP_m1	GO:00423	vitamin D r	3/2606	15/23843	0.220891	0.581626	0.553063	Cyp24a1/If
GO_BP_m1	GO:004241	dopamine	3/2606	15/23843	0.220891	0.581626	0.553063	Gch1/Snca
GO_BP_m1	GO:004514	meiotic tel	3/2606	15/23843	0.220891	0.581626	0.553063	Terb1/Lem
GO_BP_m1	GO:004577	negative re	3/2606	15/23843	0.220891	0.581626	0.553063	Cartpt/Cld
GO_BP_m1	GO:004611	nucleobase	3/2606	15/23843	0.220891	0.581626	0.553063	Aprt/Mthf
GO_BP_m1	GO:004651	sphingoid	3/2606	15/23843	0.220891	0.581626	0.553063	Acer3/Asa
GO_BP_m1	GO:00483	regulation	3/2606	15/23843	0.220891	0.581626	0.553063	Aldh1a3/A
GO_BP_m1	GO:00601	phospholip	3/2606	15/23843	0.220891	0.581626	0.553063	Adra1d/Dr
GO_BP_m1	GO:006057	intestinal e	3/2606	15/23843	0.220891	0.581626	0.553063	Cdh1/Gsd
GO_BP_m1	GO:00610	negative re	3/2606	15/23843	0.220891	0.581626	0.553063	Dnm3/Hda
GO_BP_m1	GO:00610	eyelid deve	3/2606	15/23843	0.220891	0.581626	0.553063	Hdac1/Hd
GO_BP_m1	GO:007107	regulation	3/2606	15/23843	0.220891	0.581626	0.553063	Fpr2/Pcx/P
GO_BP_m1	GO:007207	kidney mes	3/2606	15/23843	0.220891	0.581626	0.553063	Myc/Osr1/
GO_BP_m1	GO:00724	embryonic	3/2606	15/23843	0.220891	0.581626	0.553063	Nog/Osr1/
GO_BP_m1	GO:00900	negative re	3/2606	15/23843	0.220891	0.581626	0.553063	Dll4/Itgb1b
GO_BP_m1	GO:00970	type B pan	3/2606	15/23843	0.220891	0.581626	0.553063	Hdac1/Psm
GO_BP_m1	GO:00972	hepatocyte	3/2606	15/23843	0.220891	0.581626	0.553063	Casp8/Gsn
GO_BP_m1	GO:19000	regulation	3/2606	15/23843	0.220891	0.581626	0.553063	Chchd2/Kc
GO_BP_m1	GO:19004	regulation	3/2606	15/23843	0.220891	0.581626	0.553063	Adora1/Fm
GO_BP_m1	GO:19033	negative re	3/2606	15/23843	0.220891	0.581626	0.553063	Bcas3/Itgb
GO_BP_m1	GO:19900	amyloid fib	3/2606	15/23843	0.220891	0.581626	0.553063	Cd36/Gsn/
GO_BP_m1	GO:200047	regulation	3/2606	15/23843	0.220891	0.581626	0.553063	Akap6/Atp
GO_BP_m1	GO:00091	purine ribo	32/2606	254/23843	0.221533	0.582529	0.553922	Adcy4/Adr
GO_BP_m1	GO:004854	response t	32/2606	254/23843	0.221533	0.582529	0.553922	Adh1/Alpl/
GO_BP_m1	GO:00016	ureteric bu	14/2606	102/23843	0.221698	0.582529	0.553922	Fgf1/Foxc1
GO_BP_m1	GO:00613	renal tubul	14/2606	102/23843	0.221698	0.582529	0.553922	Fgf1/Gdnf/
GO_BP_m1	GO:00721	mesoneph	14/2606	102/23843	0.221698	0.582529	0.553922	Fgf1/Foxc1
GO_BP_m1	GO:00721	mesoneph	14/2606	102/23843	0.221698	0.582529	0.553922	Fgf1/Foxc1
GO_BP_m1	GO:190401	epithelial c	14/2606	102/23843	0.221698	0.582529	0.553922	Abl2/Bok/
GO_BP_m1	GO:00903	nucleic aci	17/2606	127/23843	0.222582	0.584677	0.555964	Aifm1/Bms
GO_BP_m1	GO:003051	regulation	13/2606	94/23843	0.224423	0.58916	0.560227	Cav1/Danc
GO_BP_m1	GO:19021	negative re	13/2606	94/23843	0.224423	0.58916	0.560227	Cartpt/Cld
GO_BP_m1	GO:00199	second-me	41/2606	332/23843	0.224731	0.589792	0.560828	Adcyap1r1
GO_BP_m1	GO:003564	exploratio	5/2606	30/23843	0.225461	0.591003	0.561979	Abat/Abl2/
GO_BP_m1	GO:00459	negative re	5/2606	30/23843	0.225461	0.591003	0.561979	Bcr/Fmr1/
GO_BP_m1	GO:00508	circadian sl	5/2606	30/23843	0.225461	0.591003	0.561979	Adora1/Dr
GO_BP_m1	GO:19058	positive re	5/2606	30/23843	0.225461	0.591003	0.561979	Bcap31/Bo
GO_BP_m1	GO:00082	cholesterol	16/2606	119/23843	0.225937	0.59172	0.562661	Angptl3/C
GO_BP_m1	GO:00468	regulation	16/2606	119/23843	0.225937	0.59172	0.562661	Cdk1/Cdk5
GO_BP_m1	GO:00519	positive re	16/2606	119/23843	0.225937	0.59172	0.562661	Adcyap1r1
GO_BP_m1	GO:00485	embryonic	39/2606	315/23843	0.226448	0.592883	0.563767	Aldh1a3/A
GO_BP_m1	GO:00326	chemokine	12/2606	86/23843	0.226984	0.594034	0.564862	C1qtnf3/Ei
GO_BP_m1	GO:00507	regulation	23/2606	178/23843	0.227023	0.594034	0.564862	Ccl4/Cfl1/E
GO_BP_m1	GO:001657	histone m	53/2606	437/23843	0.229045	0.599145	0.569721	Ash2l/Asxl

GO_BP_m1	GO:00086	intrinsic ap	15/2606	111/23843	0.229288	0.599297	0.569867	Bok/Cdkn1
GO_BP_m1	GO:004254	response t	15/2606	111/23843	0.229288	0.599297	0.569867	Aptx/Bnip
GO_BP_m1	GO:00519	regulation	11/2606	78/23843	0.229308	0.599297	0.569867	Adora1/Ad
GO_BP_m1	GO:00082	steroid me	35/2606	281/23843	0.229655	0.599849	0.570392	Adm/Akr1
GO_BP_m1	GO:000941	response t	35/2606	281/23843	0.229655	0.599849	0.570392	Abl2/Adam
GO_BP_m1	GO:00183	peptidyl-ly	20/2606	153/23843	0.2302	0.600914	0.571404	Brpf3/Nat8
GO_BP_m1	GO:00468	regulation	20/2606	153/23843	0.2302	0.600914	0.571404	Avpr1a/Cc
GO_BP_m1	GO:001607	rRNA meta	28/2606	221/23843	0.230308	0.601019	0.571504	Bms1/Cd3
GO_BP_m1	GO:00032	cardiac atri	6/2606	38/23843	0.230787	0.601376	0.571843	Cfc1/Dand
GO_BP_m1	GO:003081	regulation	6/2606	38/23843	0.230787	0.601376	0.571843	Esrrb/Myc/
GO_BP_m1	GO:004584	negative re	6/2606	38/23843	0.230787	0.601376	0.571843	Klhl22/Ma
GO_BP_m1	GO:00487	calcium ior	6/2606	38/23843	0.230787	0.601376	0.571843	Rims3/Rph
GO_BP_m1	GO:20004	regulation	6/2606	38/23843	0.230787	0.601376	0.571843	Adam8/Cc
GO_BP_m1	GO:00098	negative re	33/2606	264/23843	0.231104	0.601778	0.572225	Adora1/An
GO_BP_m1	GO:00447	multi-mult	24/2606	187/23843	0.231176	0.601778	0.572225	Arhgdib/A
GO_BP_m1	GO:004211	macrophag	10/2606	70/23843	0.231284	0.601778	0.572225	Cd200/Fpr
GO_BP_m1	GO:00454	bone resor	10/2606	70/23843	0.231284	0.601778	0.572225	Adam8/Ca
GO_BP_m1	GO:004884	artery mor	10/2606	70/23843	0.231284	0.601778	0.572225	Adamts9/
GO_BP_m1	GO:00015	skeletal sys	59/2606	490/23843	0.232076	0.603181	0.57356	Abi1/Alpl/
GO_BP_m1	GO:00468	regulation	36/2606	290/23843	0.232116	0.603181	0.57356	Abat/Ador
GO_BP_m1	GO:00456	negative re	31/2606	247/23843	0.232411	0.603181	0.57356	Aatk/Calr/
GO_BP_m1	GO:000204	sprouting	14/2606	103/23843	0.232616	0.603181	0.57356	Adamts9/
GO_BP_m1	GO:003264	regulation	14/2606	103/23843	0.232616	0.603181	0.57356	Abl2/Fam4
GO_BP_m1	GO:00466	alpha-beta	14/2606	103/23843	0.232616	0.603181	0.57356	Abl2/Blm/
GO_BP_m1	GO:001474	regulation	9/2606	62/23843	0.232754	0.603181	0.57356	Adk/Akap
GO_BP_m1	GO:004244	pigment m	9/2606	62/23843	0.232754	0.603181	0.57356	Aprt/Cox1
GO_BP_m1	GO:190367	regulation	9/2606	62/23843	0.232754	0.603181	0.57356	Adamts9/
GO_BP_m1	GO:00015	retinoid m	7/2606	46/23843	0.233041	0.603181	0.57356	Adh1/Adh
GO_BP_m1	GO:00090	aspartate f	7/2606	46/23843	0.233041	0.603181	0.57356	Adss/Ahcy
GO_BP_m1	GO:003411	heterotypi	7/2606	46/23843	0.233041	0.603181	0.57356	Gcnt2/Il10
GO_BP_m1	GO:00430	T cell hom	7/2606	46/23843	0.233041	0.603181	0.57356	Gpam/Gpr
GO_BP_m1	GO:00514	regulation	7/2606	46/23843	0.233041	0.603181	0.57356	Arrdc4/Cd
GO_BP_m1	GO:00514	regulation	7/2606	46/23843	0.233041	0.603181	0.57356	Bcas3/Dn
GO_BP_m1	GO:00901	cochlea de	7/2606	46/23843	0.233041	0.603181	0.57356	Cdh1/Cthr
GO_BP_m1	GO:20012	regulation	7/2606	46/23843	0.233041	0.603181	0.57356	Cdh1/Fbxo
GO_BP_m1	GO:001604	cell growth	60/2606	499/23843	0.233308	0.603181	0.57356	Aatk/Adip
GO_BP_m1	GO:00027	negative re	8/2606	54/23843	0.233472	0.603181	0.57356	Arg1/Bcr/
GO_BP_m1	GO:00028	positive re	8/2606	54/23843	0.233472	0.603181	0.57356	Arg1/Ddx6
GO_BP_m1	GO:00105	positive re	8/2606	54/23843	0.233472	0.603181	0.57356	Adcyap1r1
GO_BP_m1	GO:004507	negative re	8/2606	54/23843	0.233472	0.603181	0.57356	Eif2ak2/Ifit
GO_BP_m1	GO:004617	polyol bios	8/2606	54/23843	0.233472	0.603181	0.57356	Acer3/Adc
GO_BP_m1	GO:00482	positive re	8/2606	54/23843	0.233472	0.603181	0.57356	Anxa2/Cd6
GO_BP_m1	GO:00356	protein de	13/2606	95/23843	0.23589	0.608891	0.578989	BC004004/
GO_BP_m1	GO:004684	bone remo	13/2606	95/23843	0.23589	0.608891	0.578989	Adam8/Ca
GO_BP_m1	GO:00610	somite dev	13/2606	95/23843	0.23589	0.608891	0.578989	Abi1/Foxa
GO_BP_m1	GO:00109	regulation	16/2606	120/23843	0.236109	0.609278	0.579357	2810408A1
GO_BP_m1	GO:003294	mononucle	38/2606	308/23843	0.236714	0.610659	0.58067	Adk/Arg1/
GO_BP_m1	GO:006007	canonical	33/2606	265/23843	0.237927	0.612358	0.582286	Arntl/Capri

GO_BP_m1	GO:000912	purine nuc	18/2606	137/23843	0.238165	0.612358	0.582286	Adss/Atp5a
GO_BP_m1	GO:000916	purine ribo	18/2606	137/23843	0.238165	0.612358	0.582286	Adss/Atp5a
GO_BP_m1	GO:003264	tumor necr	18/2606	137/23843	0.238165	0.612358	0.582286	Cactin/Ccl4
GO_BP_m1	GO:000271	negative re	4/2606	23/23843	0.238836	0.612358	0.582286	Arg1/Il10/J
GO_BP_m1	GO:000629	mismatch r	4/2606	23/23843	0.238836	0.612358	0.582286	Msh3/Msh4
GO_BP_m1	GO:002301	signal trans	4/2606	23/23843	0.238836	0.612358	0.582286	Dand5/Fox
GO_BP_m1	GO:003020	chondroitin	4/2606	23/23843	0.238836	0.612358	0.582286	Chst13/Csg
GO_BP_m1	GO:003209	regulation	4/2606	23/23843	0.238836	0.612358	0.582286	Bbs2/Cartp
GO_BP_m1	GO:003410	negative re	4/2606	23/23843	0.238836	0.612358	0.582286	Bcr/Cartpt/
GO_BP_m1	GO:003431	diol metab	4/2606	23/23843	0.238836	0.612358	0.582286	Acer3/Asah
GO_BP_m1	GO:003580	regulation	4/2606	23/23843	0.238836	0.612358	0.582286	Adm/Ednrb
GO_BP_m1	GO:004309	cellular me	4/2606	23/23843	0.238836	0.612358	0.582286	Adk/Apip/
GO_BP_m1	GO:004357	regulation	4/2606	23/23843	0.238836	0.612358	0.582286	Adora1/Gls
GO_BP_m1	GO:004414	modulation	4/2606	23/23843	0.238836	0.612358	0.582286	Cd36/Ifng/
GO_BP_m1	GO:004659	negative re	4/2606	23/23843	0.238836	0.612358	0.582286	Gsn/Ifitm2/
GO_BP_m1	GO:005196	regulation	4/2606	23/23843	0.238836	0.612358	0.582286	Avpr1a/Car
GO_BP_m1	GO:006097	left/right pa	4/2606	23/23843	0.238836	0.612358	0.582286	Dnaaf1/Ift1
GO_BP_m1	GO:007116	protein loc	4/2606	23/23843	0.238836	0.612358	0.582286	H2afy/Hda
GO_BP_m1	GO:007220	metanephr	4/2606	23/23843	0.238836	0.612358	0.582286	Lamb2/Lgr
GO_BP_m1	GO:190367	negative re	4/2606	23/23843	0.238836	0.612358	0.582286	Adamts9/D
GO_BP_m1	GO:004643	organopho	24/2606	188/23843	0.23932	0.61342	0.583296	Angptl3/Bp
GO_BP_m1	GO:001619	endosomal	22/2606	171/23843	0.239536	0.613614	0.583481	Ankfy1/Arh
GO_BP_m1	GO:003050	BMP signal	22/2606	171/23843	0.239536	0.613614	0.583481	Bmp3/Cav1
GO_BP_m1	GO:000315	endotheliu	15/2606	112/23843	0.239916	0.614409	0.584236	Alox12/Cld
GO_BP_m1	GO:004217	regulation	43/2606	352/23843	0.240595	0.615968	0.585718	Adam8/An
GO_BP_m1	GO:003009	myeloid ce	47/2606	387/23843	0.241651	0.61836	0.587994	Abi1/Adam
GO_BP_m1	GO:003261	interleukin-	11/2606	79/23843	0.242093	0.61836	0.587994	5730559C1
GO_BP_m1	GO:003410	regulation	11/2606	79/23843	0.242093	0.61836	0.587994	Adam8/Bcr
GO_BP_m1	GO:003450	protein loc	11/2606	79/23843	0.242093	0.61836	0.587994	Atr/Cdk1/C
GO_BP_m1	GO:003803	signal trans	11/2606	79/23843	0.242093	0.61836	0.587994	Bok/Erbb3/
GO_BP_m1	GO:004410	cellular am	11/2606	79/23843	0.242093	0.61836	0.587994	Abat/Agma
GO_BP_m1	GO:009719	extrinsic ap	11/2606	79/23843	0.242093	0.61836	0.587994	Bok/Erbb3/
GO_BP_m1	GO:190186	positive reg	11/2606	79/23843	0.242093	0.61836	0.587994	Akap6/Arn
GO_BP_m1	GO:007147	cellular res	19/2606	146/23843	0.243488	0.621744	0.591211	Atr/Blm/Cc
GO_BP_m1	GO:000913	nucleoside	14/2606	104/23843	0.243747	0.622224	0.591667	Bpgm/Eno3
GO_BP_m1	GO:003254	mitochond	10/2606	71/23843	0.244876	0.623365	0.592752	Gfm1/Mrpl
GO_BP_m1	GO:004336	CD4-positi	10/2606	71/23843	0.244876	0.623365	0.592752	Gpr183/Ifn
GO_BP_m1	GO:005076	negative re	39/2606	318/23843	0.245188	0.623365	0.592752	Aatk/Calr/C
GO_BP_m1	GO:000269	negative re	16/2606	121/23843	0.246465	0.623365	0.592752	Arg1/Bcr/C
GO_BP_m1	GO:000829	isoprenoid	5/2606	31/23843	0.246552	0.623365	0.592752	Aldh1a3/Fo
GO_BP_m1	GO:001827	protein N-	5/2606	31/23843	0.246552	0.623365	0.592752	Fut8/St3ga
GO_BP_m1	GO:003274	positive reg	5/2606	31/23843	0.246552	0.623365	0.592752	Abl2/Btnl2/
GO_BP_m1	GO:004274	regulation	5/2606	31/23843	0.246552	0.623365	0.592752	Adora1/Dr
GO_BP_m1	GO:004324	positive reg	5/2606	31/23843	0.246552	0.623365	0.592752	Bnip3/Cfl1/
GO_BP_m1	GO:005118	vitamin tran	5/2606	31/23843	0.246552	0.623365	0.592752	Folr2/Gif/S
GO_BP_m1	GO:005149	positive reg	5/2606	31/23843	0.246552	0.623365	0.592752	Bcas3/Dnm
GO_BP_m1	GO:200040	positive reg	5/2606	31/23843	0.246552	0.623365	0.592752	Adam8/Ccl
GO_BP_m1	GO:003164	regulation	31/2606	249/23843	0.246666	0.623365	0.592752	Aptx/Asph/

GO_BP_m1	GO:000998	cell-cell rec	9/2606	63/23843	0.24729	0.623365	0.592752	Cct3/Dock8
GO_BP_m1	GO:000628	regulation	13/2606	96/23843	0.247582	0.623365	0.592752	Blm/Baban
GO_BP_m1	GO:005077	positive reg	13/2606	96/23843	0.247582	0.623365	0.592752	Ache/Cdkl5
GO_BP_m1	GO:006099	kidney mor	13/2606	96/23843	0.247582	0.623365	0.592752	Fgf1/Gcnt1
GO_BP_m1	GO:009873	macromole	13/2606	96/23843	0.247582	0.623365	0.592752	BC004004/
GO_BP_m1	GO:000150	action pote	18/2606	138/23843	0.247874	0.623365	0.592752	Cacnb2/Ca
GO_BP_m1	GO:000167	cellular glu	18/2606	138/23843	0.247874	0.623365	0.592752	Ano1/Cartp
GO_BP_m1	GO:190199	negative re	18/2606	138/23843	0.247874	0.623365	0.592752	Blm/Ccng1
GO_BP_m1	GO:001993	cyclic-nucl	20/2606	155/23843	0.248374	0.623365	0.592752	Adcyap1r1
GO_BP_m1	GO:000709	metaphase	8/2606	55/23843	0.249133	0.623365	0.592752	Cdc23/Klhl
GO_BP_m1	GO:003081	regulation	8/2606	55/23843	0.249133	0.623365	0.592752	Adra1d/Ak
GO_BP_m1	GO:004574	negative re	8/2606	55/23843	0.249133	0.623365	0.592752	Adm/Atp2
GO_BP_m1	GO:000188	receptor re	6/2606	39/23843	0.249568	0.623365	0.592752	Ache/Anxa
GO_BP_m1	GO:004274	hydrogen p	6/2606	39/23843	0.249568	0.623365	0.592752	Duoxa2/Gp
GO_BP_m1	GO:004355	regulation	6/2606	39/23843	0.249568	0.623365	0.592752	Epha8/Fpr2
GO_BP_m1	GO:004474	protein tra	6/2606	39/23843	0.249568	0.623365	0.592752	Grpel1/Pex
GO_BP_m1	GO:004574	positive reg	6/2606	39/23843	0.249568	0.623365	0.592752	Dll4/Enho/
GO_BP_m1	GO:005085	regulation	6/2606	39/23843	0.249568	0.623365	0.592752	Btnl2/Dusp
GO_BP_m1	GO:009700	energy hor	6/2606	39/23843	0.249568	0.623365	0.592752	Cd36/Fcor/
GO_BP_m1	GO:190210	negative re	6/2606	39/23843	0.249568	0.623365	0.592752	Klhl22/Mac
GO_BP_m1	GO:190317	negative re	6/2606	39/23843	0.249568	0.623365	0.592752	Adra1d/Fkb
GO_BP_m1	GO:200081	negative re	6/2606	39/23843	0.249568	0.623365	0.592752	Klhl22/Mac
GO_BP_m1	GO:002153	neural tube	7/2606	47/23843	0.250079	0.623365	0.592752	Foxa2/Kdm
GO_BP_m1	GO:003089	positive reg	7/2606	47/23843	0.250079	0.623365	0.592752	Cdkn1a/Gp
GO_BP_m1	GO:004801	inositol pho	7/2606	47/23843	0.250079	0.623365	0.592752	Akap6/Atp
GO_BP_m1	GO:004848	autonomic	7/2606	47/23843	0.250079	0.623365	0.592752	Ednrb/Gdn
GO_BP_m1	GO:004871	regulation	7/2606	47/23843	0.250079	0.623365	0.592752	Drd3/Enpp
GO_BP_m1	GO:009960	regulation	7/2606	47/23843	0.250079	0.623365	0.592752	Cacng5/Ca
GO_BP_m1	GO:000863	apoptotic r	15/2606	113/23843	0.250736	0.623365	0.592752	Aifm1/Aifm
GO_BP_m1	GO:003298	protein-co	25/2606	198/23843	0.251211	0.623365	0.592752	Asph/Bnip3
GO_BP_m1	GO:004209	T cell prolif	25/2606	198/23843	0.251211	0.623365	0.592752	Adk/Arg1/I
GO_BP_m1	GO:003350	carbohydra	30/2606	241/23843	0.251228	0.623365	0.592752	Adipor2/Ar
GO_BP_m1	GO:004259	glucose ho	30/2606	241/23843	0.251228	0.623365	0.592752	Adipor2/Ar
GO_BP_m1	GO:000009	sulfur amin	3/2606	16/23843	0.251344	0.623365	0.592752	Apip/Enop
GO_BP_m1	GO:000203	G-protein c	3/2606	16/23843	0.251344	0.623365	0.592752	Adm/Drd3/
GO_BP_m1	GO:000228	neutrophil	3/2606	16/23843	0.251344	0.623365	0.592752	Anxa3/Bcr/
GO_BP_m1	GO:000635	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Foxa2/Ice1
GO_BP_m1	GO:000685	mitochond	3/2606	16/23843	0.251344	0.623365	0.592752	Micu2/Slc2
GO_BP_m1	GO:000907	serine fami	3/2606	16/23843	0.251344	0.623365	0.592752	Psph/Seph
GO_BP_m1	GO:001052	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Btbd18/Dd
GO_BP_m1	GO:001052	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Btbd18/Dd
GO_BP_m1	GO:001056	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Coq3/Dgkq
GO_BP_m1	GO:001091	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Adcyap1r1
GO_BP_m1	GO:001699	cell wall ma	3/2606	16/23843	0.251344	0.623365	0.592752	1700016D0
GO_BP_m1	GO:003270	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Ifng/Il12b/I
GO_BP_m1	GO:003363	positive reg	3/2606	16/23843	0.251344	0.623365	0.592752	Cib1/Nckap
GO_BP_m1	GO:003523	ionotropic	3/2606	16/23843	0.251344	0.623365	0.592752	Camk2a/Cp
GO_BP_m1	GO:003572	response to	3/2606	16/23843	0.251344	0.623365	0.592752	Bcar1/Gab1

GO_BP_m1	GO:004001	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Bbs2/H19/
GO_BP_m1	GO:004392	positive reg	3/2606	16/23843	0.251344	0.623365	0.592752	Nucks1/Ta
GO_BP_m1	GO:004406	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Adora1/Gls
GO_BP_m1	GO:004406	modulation	3/2606	16/23843	0.251344	0.623365	0.592752	Park2/Vapb
GO_BP_m1	GO:004589	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Cand1/Psm
GO_BP_m1	GO:004662	gamma-de	3/2606	16/23843	0.251344	0.623365	0.592752	Gpr18/Nck
GO_BP_m1	GO:004683	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Nup153/Rb
GO_BP_m1	GO:004830	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Ifng/Il27ra/
GO_BP_m1	GO:004887	chemical h	3/2606	16/23843	0.251344	0.623365	0.592752	Abca12/Fg
GO_BP_m1	GO:006004	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Hdac2/Kcn
GO_BP_m1	GO:006057	ventral spin	3/2606	16/23843	0.251344	0.623365	0.592752	Dbx1/Dll4/
GO_BP_m1	GO:006058	cell fate co	3/2606	16/23843	0.251344	0.623365	0.592752	Dbx1/Dll4/
GO_BP_m1	GO:007057	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Klk8/Map4
GO_BP_m1	GO:007136	cellular resp	3/2606	16/23843	0.251344	0.623365	0.592752	Cav1/Mb21
GO_BP_m1	GO:009019	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Ifng/Nog/V
GO_BP_m1	GO:009022	chromosom	3/2606	16/23843	0.251344	0.623365	0.592752	Terb1/Lem
GO_BP_m1	GO:009917	presynapse	3/2606	16/23843	0.251344	0.623365	0.592752	Lrp4/Nlgn3
GO_BP_m1	GO:190015	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Btg2/Cpeb
GO_BP_m1	GO:190015	positive reg	3/2606	16/23843	0.251344	0.623365	0.592752	Btg2/Cpeb
GO_BP_m1	GO:190271	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Abl2/Ptpn2
GO_BP_m1	GO:190466	regulation	3/2606	16/23843	0.251344	0.623365	0.592752	Cdc20/Fbx
GO_BP_m1	GO:200010	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Fbxo18/Lig
GO_BP_m1	GO:200072	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Cav3/Pak1/
GO_BP_m1	GO:200117	negative re	3/2606	16/23843	0.251344	0.623365	0.592752	Flcn/Pparg
GO_BP_m1	GO:004847	oogenesis	12/2606	88/23843	0.251391	0.623365	0.592752	Amh/Dmrt
GO_BP_m1	GO:190260	proton tran	12/2606	88/23843	0.251391	0.623365	0.592752	Atp5a1/Atp
GO_BP_m1	GO:000155	regulation	50/2606	415/23843	0.251879	0.623365	0.592752	Aatk/Adipo
GO_BP_m1	GO:004206	gliogenesis	36/2606	293/23843	0.251918	0.623365	0.592752	Abl2/Ahna
GO_BP_m1	GO:003030	negative re	23/2606	181/23843	0.252236	0.623365	0.592752	Aatk/Adipo
GO_BP_m1	GO:004877	tissue remo	23/2606	181/23843	0.252236	0.623365	0.592752	Adam8/Bcr
GO_BP_m1	GO:001612	sterol meta	17/2606	130/23843	0.252376	0.623365	0.592752	Angptl3/Cy
GO_BP_m1	GO:190186	regulation	21/2606	164/23843	0.252873	0.623365	0.592752	Akap6/Arn
GO_BP_m1	GO:000912	nucleoside	19/2606	147/23843	0.252987	0.623365	0.592752	Adss/Atp5a
GO_BP_m1	GO:190121	negative re	28/2606	224/23843	0.253002	0.623365	0.592752	Adam8/Bo
GO_BP_m1	GO:003505	embryonic	11/2606	80/23843	0.255132	0.623365	0.592752	Cfc1/Dnaaf
GO_BP_m1	GO:007030	cellular resp	11/2606	80/23843	0.255132	0.623365	0.592752	Bnip3/Cfl1/
GO_BP_m1	GO:001097	positive reg	41/2606	337/23843	0.255374	0.623365	0.592752	Abl2/Ache/
GO_BP_m1	GO:005110	regulation	16/2606	122/23843	0.256996	0.623365	0.592752	Ddrgk1/E2
GO_BP_m1	GO:000024	spliceosom	2/2606	9/23843	0.257455	0.623365	0.592752	Prpf19/Prp
GO_BP_m1	GO:000049	box C/D sn	2/2606	9/23843	0.257455	0.623365	0.592752	Gm3086/Ta
GO_BP_m1	GO:000157	ganglioside	2/2606	9/23843	0.257455	0.623365	0.592752	St6galnac1
GO_BP_m1	GO:000167	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Map1s/Tpr
GO_BP_m1	GO:000183	neural plat	2/2606	9/23843	0.257455	0.623365	0.592752	Nog/Zfp56
GO_BP_m1	GO:000272	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Arg1/Smac
GO_BP_m1	GO:000314	determinat	2/2606	9/23843	0.257455	0.623365	0.592752	Dand5/Sm
GO_BP_m1	GO:000656	proline me	2/2606	9/23843	0.257455	0.623365	0.592752	Aldh4a1/Py
GO_BP_m1	GO:000656	L-serine m	2/2606	9/23843	0.257455	0.623365	0.592752	Psph/Shmt
GO_BP_m1	GO:000719	adenylate c	2/2606	9/23843	0.257455	0.623365	0.592752	Drd3/Drd5

GO_BP_m1	GO:000821	spermidine	2/2606	9/23843	0.257455	0.623365	0.592752	Agmat/Sat
GO_BP_m1	GO:000835	germ cell n	2/2606	9/23843	0.257455	0.623365	0.592752	Dmrt1/Fox
GO_BP_m1	GO:001063	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Bnip3/Park
GO_BP_m1	GO:001087	positive re	2/2606	9/23843	0.257455	0.623365	0.592752	Hdac1/Hd
GO_BP_m1	GO:001579	polyol tran	2/2606	9/23843	0.257455	0.623365	0.592752	Pgap1/Slc
GO_BP_m1	GO:001924	lactate bios	2/2606	9/23843	0.257455	0.623365	0.592752	Ldha/Tigar
GO_BP_m1	GO:001937	lipoxygena	2/2606	9/23843	0.257455	0.623365	0.592752	Alox12/Alo
GO_BP_m1	GO:001951	peptidyl-p	2/2606	9/23843	0.257455	0.623365	0.592752	Egln3/Ogf
GO_BP_m1	GO:002183	interneuro	2/2606	9/23843	0.257455	0.623365	0.592752	Arx/Nrg1
GO_BP_m1	GO:002187	forebrain n	2/2606	9/23843	0.257455	0.623365	0.592752	Dct/Wnt3a
GO_BP_m1	GO:003020	chondroiti	2/2606	9/23843	0.257455	0.623365	0.592752	Chst13/Cs
GO_BP_m1	GO:003030	poly-N-ac	2/2606	9/23843	0.257455	0.623365	0.592752	B3gnt3/B3
GO_BP_m1	GO:003031	poly-N-ac	2/2606	9/23843	0.257455	0.623365	0.592752	B3gnt3/B3
GO_BP_m1	GO:003162	positive re	2/2606	9/23843	0.257455	0.623365	0.592752	Ptgs2/Tnfs
GO_BP_m1	GO:003164	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Ifng/Klk8
GO_BP_m1	GO:003207	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Dffa/Pcna
GO_BP_m1	GO:003247	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Bcap31/Ra
GO_BP_m1	GO:003283	glomerular	2/2606	9/23843	0.257455	0.623365	0.592752	Lamb2/Wt
GO_BP_m1	GO:003360	positive re	2/2606	9/23843	0.257455	0.623365	0.592752	Rreb1/Zfp
GO_BP_m1	GO:003413	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Cav1/Ptpn
GO_BP_m1	GO:003497	protein fol	2/2606	9/23843	0.257455	0.623365	0.592752	Emc3/Ero1
GO_BP_m1	GO:003523	ectopic ge	2/2606	9/23843	0.257455	0.623365	0.592752	Kitl/Prkdc
GO_BP_m1	GO:003552	monoubiq	2/2606	9/23843	0.257455	0.623365	0.592752	Asxl1/Usp
GO_BP_m1	GO:003554	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Trim9/Vps
GO_BP_m1	GO:003556	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Fbxo18/W
GO_BP_m1	GO:003626	RNA cappi	2/2606	9/23843	0.257455	0.623365	0.592752	Cmtr2/Rn
GO_BP_m1	GO:003648	neuron int	2/2606	9/23843	0.257455	0.623365	0.592752	Park2/Ralb
GO_BP_m1	GO:004236	vitamin D	2/2606	9/23843	0.257455	0.623365	0.592752	Ifng/Nfkb1
GO_BP_m1	GO:004310	purine-co	2/2606	9/23843	0.257455	0.623365	0.592752	Adk/Aprt
GO_BP_m1	GO:004558	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Nckap1l/Pt
GO_BP_m1	GO:004598	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Adora1/Zc
GO_BP_m1	GO:004664	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Nckap1l/Pt
GO_BP_m1	GO:004831	axial meso	2/2606	9/23843	0.257455	0.623365	0.592752	Epha2/No
GO_BP_m1	GO:004834	paraxial m	2/2606	9/23843	0.257455	0.623365	0.592752	Foxc1/Wnt
GO_BP_m1	GO:005095	equilibrioc	2/2606	9/23843	0.257455	0.623365	0.592752	Sox2/Ush1
GO_BP_m1	GO:005141	microtubul	2/2606	9/23843	0.257455	0.623365	0.592752	Tubgcp2/T
GO_BP_m1	GO:005154	positive re	2/2606	9/23843	0.257455	0.623365	0.592752	Fgf7/Has2
GO_BP_m1	GO:005179	medium-c	2/2606	9/23843	0.257455	0.623365	0.592752	Abhd1/Crc
GO_BP_m1	GO:005509	phospholi	2/2606	9/23843	0.257455	0.623365	0.592752	Angptl3/G
GO_BP_m1	GO:006035	cell adhesi	2/2606	9/23843	0.257455	0.623365	0.592752	Cav1/Gcnt
GO_BP_m1	GO:006055	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Ifng/Nfkb1
GO_BP_m1	GO:006100	pattern sp	2/2606	9/23843	0.257455	0.623365	0.592752	Irx2/Osr1
GO_BP_m1	GO:007023	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Gpam/Rip
GO_BP_m1	GO:007041	cellular res	2/2606	9/23843	0.257455	0.623365	0.592752	Fcor/Saxo1
GO_BP_m1	GO:007047	positive re	2/2606	9/23843	0.257455	0.623365	0.592752	Abat/Tacr2
GO_BP_m1	GO:007098	oxidative d	2/2606	9/23843	0.257455	0.623365	0.592752	Tet2/Tet3
GO_BP_m1	GO:007137	cellular res	2/2606	9/23843	0.257455	0.623365	0.592752	Epha8/Ppa
GO_BP_m1	GO:007204	renal syste	2/2606	9/23843	0.257455	0.623365	0.592752	Irx2/Osr1

GO_BP_m1	GO:007264	type I inter	2/2606	9/23843	0.257455	0.623365	0.592752	Mmp12/Pt
GO_BP_m1	GO:007264	interferon-	2/2606	9/23843	0.257455	0.623365	0.592752	Mmp12/Pt
GO_BP_m1	GO:007271	cellular res	2/2606	9/23843	0.257455	0.623365	0.592752	Blm/Fmr1
GO_BP_m1	GO:008610	G-protein	2/2606	9/23843	0.257455	0.623365	0.592752	Atp2b4/Ca
GO_BP_m1	GO:009004	positive reg	2/2606	9/23843	0.257455	0.623365	0.592752	BC004004/
GO_BP_m1	GO:009043	protein loc	2/2606	9/23843	0.257455	0.623365	0.592752	Nup54/Os
GO_BP_m1	GO:009706	cellular res	2/2606	9/23843	0.257455	0.623365	0.592752	Lmo2/Ppar
GO_BP_m1	GO:009768	glutamate	2/2606	9/23843	0.257455	0.623365	0.592752	Lrrtm4/Ssh
GO_BP_m1	GO:009853	histone H3	2/2606	9/23843	0.257455	0.623365	0.592752	Ezh1/Hist1
GO_BP_m1	GO:009859	observatio	2/2606	9/23843	0.257455	0.623365	0.592752	Nf1/Pak1
GO_BP_m1	GO:009881	spontaneo	2/2606	9/23843	0.257455	0.623365	0.592752	Park2/Stx1
GO_BP_m1	GO:009882	modulatio	2/2606	9/23843	0.257455	0.623365	0.592752	Abat/Nlgn
GO_BP_m1	GO:190010	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Nck2/Ptpn
GO_BP_m1	GO:190202	L-arginine	2/2606	9/23843	0.257455	0.623365	0.592752	Arg1/AU01
GO_BP_m1	GO:190203	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Eif2ak2/Kit
GO_BP_m1	GO:190209	positive reg	2/2606	9/23843	0.257455	0.623365	0.592752	Rnase10/T
GO_BP_m1	GO:190256	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Bcr/Itgam
GO_BP_m1	GO:190273	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Mmp12/Pt
GO_BP_m1	GO:190274	positive reg	2/2606	9/23843	0.257455	0.623365	0.592752	Mmp12/Pt
GO_BP_m1	GO:190337	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Park2/Ralb
GO_BP_m1	GO:190386	positive reg	2/2606	9/23843	0.257455	0.623365	0.592752	Cdk1/Myc
GO_BP_m1	GO:190397	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Itgam/Ttbk
GO_BP_m1	GO:190439	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Lrp4/Mesd
GO_BP_m1	GO:190466	negative re	2/2606	9/23843	0.257455	0.623365	0.592752	Fbxo5/Rpl
GO_BP_m1	GO:200039	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Enpp2/Rre
GO_BP_m1	GO:200048	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Acta2/Dga
GO_BP_m1	GO:200118	regulation	2/2606	9/23843	0.257455	0.623365	0.592752	Nckap1l/Pt
GO_BP_m1	GO:003300	muscle cell	27/2606	216/23843	0.257782	0.623365	0.592752	Alox12/Ca
GO_BP_m1	GO:003030	cholesterol	10/2606	72/23843	0.258742	0.623365	0.592752	Abca12/Ar
GO_BP_m1	GO:004567	regulation	10/2606	72/23843	0.258742	0.623365	0.592752	Adam8/Ca
GO_BP_m1	GO:200002	regulation	25/2606	199/23843	0.259457	0.623365	0.592752	Abl2/Casp
GO_BP_m1	GO:004312	positive reg	13/2606	97/23843	0.259485	0.623365	0.592752	5730559C1
GO_BP_m1	GO:005123	maintenan	37/2606	303/23843	0.260745	0.623365	0.592752	Akap6/Ang
GO_BP_m1	GO:001097	negative re	21/2606	165/23843	0.261985	0.623365	0.592752	Aatk/Cdk5/
GO_BP_m1	GO:004827	vesicle doc	9/2606	64/23843	0.262121	0.623365	0.592752	Ncam1/Nd
GO_BP_m1	GO:006137	determinat	9/2606	64/23843	0.262121	0.623365	0.592752	Cfc1/Dand
GO_BP_m1	GO:003434	response t	17/2606	131/23843	0.262639	0.623365	0.592752	Arg1/Ccl2
GO_BP_m1	GO:004327	positive reg	35/2606	286/23843	0.263428	0.623365	0.592752	Abat/Abcb
GO_BP_m1	GO:000681	potassium	29/2606	234/23843	0.263582	0.623365	0.592752	Adora1/Ad
GO_BP_m1	GO:000692	inflammato	4/2606	24/23843	0.263809	0.623365	0.592752	Hcar2/Ifng/
GO_BP_m1	GO:000709	mitotic G2	4/2606	24/23843	0.263809	0.623365	0.592752	Blm/Ccng1
GO_BP_m1	GO:000906	aspartate f	4/2606	24/23843	0.263809	0.623365	0.592752	Apip/Enop
GO_BP_m1	GO:001061	negative re	4/2606	24/23843	0.263809	0.623365	0.592752	Atp2b4/Ca
GO_BP_m1	GO:001819	peptidyl-a	4/2606	24/23843	0.263809	0.623365	0.592752	Ndufaf7/Pr
GO_BP_m1	GO:002189	cerebral co	4/2606	24/23843	0.263809	0.623365	0.592752	Arx/Pafah1
GO_BP_m1	GO:004533	phospholi	4/2606	24/23843	0.263809	0.623365	0.592752	Abcb1a/At
GO_BP_m1	GO:004682	negative re	4/2606	24/23843	0.263809	0.623365	0.592752	Cdk5/Ei24/
GO_BP_m1	GO:004867	regulation	4/2606	24/23843	0.263809	0.623365	0.592752	Epha7/Fgf1

GO_BP_m1	GO:005148	negative re	4/2606	24/23843	0.263809	0.623365	0.592752	Adra1d/Hr
GO_BP_m1	GO:006500	protein-lip	4/2606	24/23843	0.263809	0.623365	0.592752	Dgat1/Mttp
GO_BP_m1	GO:190101	positive reg	4/2606	24/23843	0.263809	0.623365	0.592752	Akap6/Atp
GO_BP_m1	GO:190179	positive reg	4/2606	24/23843	0.263809	0.623365	0.592752	Ankrd1/Atr
GO_BP_m1	GO:200117	positive reg	4/2606	24/23843	0.263809	0.623365	0.592752	Esrrb/Myc/
GO_BP_m1	GO:001096	regulation	8/2606	56/23843	0.265118	0.623365	0.592752	Cdc23/Klhl
GO_BP_m1	GO:001644	somatic rec	8/2606	56/23843	0.265118	0.623365	0.592752	Aplf/Ifng/Il
GO_BP_m1	GO:002151	ventral spir	8/2606	56/23843	0.265118	0.623365	0.592752	Dbx1/Dll4/
GO_BP_m1	GO:004478	metaphase	8/2606	56/23843	0.265118	0.623365	0.592752	Cdc23/Klhl
GO_BP_m1	GO:004512	cellular ext	8/2606	56/23843	0.265118	0.623365	0.592752	Adam8/Bcr
GO_BP_m1	GO:000694	striated mu	20/2606	157/23843	0.267107	0.623365	0.592752	Adora1/Ak
GO_BP_m1	GO:000701	microtubul	7/2606	48/23843	0.267477	0.623365	0.592752	Cib1/Fgf13
GO_BP_m1	GO:000713	reciprocal r	7/2606	48/23843	0.267477	0.623365	0.592752	Mnd1/Msh
GO_BP_m1	GO:001059	negative re	7/2606	48/23843	0.267477	0.623365	0.592752	Adamts9/S
GO_BP_m1	GO:003582	homologou	7/2606	48/23843	0.267477	0.623365	0.592752	Mnd1/Msh
GO_BP_m1	GO:004255	neuron ma	7/2606	48/23843	0.267477	0.623365	0.592752	Abl2/C1ql1
GO_BP_m1	GO:200123	regulation	7/2606	48/23843	0.267477	0.623365	0.592752	Gdnf/Il7/Ja
GO_BP_m1	GO:001821	peptidyl-th	18/2606	140/23843	0.267752	0.623365	0.592752	Camk2a/Cc
GO_BP_m1	GO:004663	alpha-beta	18/2606	140/23843	0.267752	0.623365	0.592752	Abl2/Blm/C
GO_BP_m1	GO:000003	very long-c	5/2606	32/23843	0.268122	0.623365	0.592752	Abcd3/Acc
GO_BP_m1	GO:000268	negative re	5/2606	32/23843	0.268122	0.623365	0.592752	Adora1/Bcr
GO_BP_m1	GO:000270	negative re	5/2606	32/23843	0.268122	0.623365	0.592752	Arg1/Il10/J
GO_BP_m1	GO:000329	physiologic	5/2606	32/23843	0.268122	0.623365	0.592752	Akap6/Cav
GO_BP_m1	GO:000330	physiologic	5/2606	32/23843	0.268122	0.623365	0.592752	Akap6/Cav
GO_BP_m1	GO:000608	acetyl-CoA	5/2606	32/23843	0.268122	0.623365	0.592752	Fasn/Hmgc
GO_BP_m1	GO:001819	peptidyl-as	5/2606	32/23843	0.268122	0.623365	0.592752	Fut8/St3ga
GO_BP_m1	GO:002241	circadian sl	5/2606	32/23843	0.268122	0.623365	0.592752	Adora1/Drd
GO_BP_m1	GO:003623	granulocyte	5/2606	32/23843	0.268122	0.623365	0.592752	Anxa3/Bcr/
GO_BP_m1	GO:004283	defense res	5/2606	32/23843	0.268122	0.623365	0.592752	Arg1/Ifng/I
GO_BP_m1	GO:004507	positive reg	5/2606	32/23843	0.268122	0.623365	0.592752	Fkbp6/Nuc
GO_BP_m1	GO:004632	negative re	5/2606	32/23843	0.268122	0.623365	0.592752	Dusp3/Mec
GO_BP_m1	GO:004664	regulation	5/2606	32/23843	0.268122	0.623365	0.592752	Blm/Cd80/
GO_BP_m1	GO:005164	nucleus loc	5/2606	32/23843	0.268122	0.623365	0.592752	Cav3/Dock
GO_BP_m1	GO:006104	cell growth	5/2606	32/23843	0.268122	0.623365	0.592752	Akap6/Cav
GO_BP_m1	GO:190268	mitochond	5/2606	32/23843	0.268122	0.623365	0.592752	Bnip3/Bok/
GO_BP_m1	GO:190342	regulation	5/2606	32/23843	0.268122	0.623365	0.592752	Ednrb/Npr
GO_BP_m1	GO:007050	calcium ior	11/2606	81/23843	0.268407	0.623365	0.592752	Cacnb2/Ca
GO_BP_m1	GO:009758	lamellipodi	11/2606	81/23843	0.268407	0.623365	0.592752	Abi1/Arhge
GO_BP_m1	GO:190040	regulation	11/2606	81/23843	0.268407	0.623365	0.592752	Cd36/Endo
GO_BP_m1	GO:000637	mRNA poly	6/2606	40/23843	0.268757	0.623365	0.592752	Cpeb3/Cps
GO_BP_m1	GO:004873	epidermis r	6/2606	40/23843	0.268757	0.623365	0.592752	Ctsl/Fgf7/F
GO_BP_m1	GO:004887	homeostas	6/2606	40/23843	0.268757	0.623365	0.592752	Gigyf2/Il7/I
GO_BP_m1	GO:007154	dopaminer	6/2606	40/23843	0.268757	0.623365	0.592752	Cdnf/Dmrt
GO_BP_m1	GO:009022	regulation	6/2606	40/23843	0.268757	0.623365	0.592752	Ankrd53/B
GO_BP_m1	GO:190581	negative re	6/2606	40/23843	0.268757	0.623365	0.592752	Klhl22/Mac
GO_BP_m1	GO:200072	regulation	6/2606	40/23843	0.268757	0.623365	0.592752	Akap6/Cav
GO_BP_m1	GO:003030	positive reg	23/2606	183/23843	0.269653	0.623365	0.592752	Adnp2/Aka
GO_BP_m1	GO:005086	negative re	23/2606	183/23843	0.269653	0.623365	0.592752	Abat/Alox1

GO_BP_m1	GO:00447	cilium orga	39/2606	322/23843	0.271209	0.623365	0.592752	B9d1/Bbs1
GO_BP_m1	GO:001631	dephosph	43/2606	357/23843	0.271347	0.623365	0.592752	2810408A1
GO_BP_m1	GO:00307	regulation	13/2606	98/23843	0.271585	0.623365	0.592752	Adm/Adra
GO_BP_m1	GO:00995	chemical s	13/2606	98/23843	0.271585	0.623365	0.592752	Abat/Ador
GO_BP_m1	GO:000647	internal pr	19/2606	149/23843	0.272409	0.623365	0.592752	Brpf3/Nat8
GO_BP_m1	GO:001591	sterol trans	10/2606	73/23843	0.272857	0.623365	0.592752	Abca12/Ar
GO_BP_m1	GO:00224	membrane	10/2606	73/23843	0.272857	0.623365	0.592752	Ncam1/Nd
GO_BP_m1	GO:00362	cellular res	15/2606	115/23843	0.272909	0.623365	0.592752	Adam8/Bn
GO_BP_m1	GO:000762	circadian r	24/2606	192/23843	0.273077	0.623365	0.592752	Adora1/Ar
GO_BP_m1	GO:00316	cellular res	24/2606	192/23843	0.273077	0.623365	0.592752	Aoc1/Atf3/
GO_BP_m1	GO:003214	activation	30/2606	244/23843	0.273868	0.623365	0.592752	5730559C1
GO_BP_m1	GO:00092	response t	20/2606	158/23843	0.276668	0.623365	0.592752	Adora1/An
GO_BP_m1	GO:00511	negative r	20/2606	158/23843	0.276668	0.623365	0.592752	Cav1/Csnk
GO_BP_m1	GO:000271	regulation	9/2606	65/23843	0.277221	0.623365	0.592752	Arg1/Cd36
GO_BP_m1	GO:00481	regulation	9/2606	65/23843	0.277221	0.623365	0.592752	Camk2a/D
GO_BP_m1	GO:00032	cardiac ch	18/2606	141/23843	0.277904	0.623365	0.592752	Adamts1/
GO_BP_m1	GO:00091	ribonucleo	18/2606	141/23843	0.277904	0.623365	0.592752	Adss/Atp5
GO_BP_m1	GO:001907	viral geno	14/2606	107/23843	0.278298	0.623365	0.592752	Eif2ak2/Fk
GO_BP_m1	GO:004324	regulation	14/2606	107/23843	0.278298	0.623365	0.592752	Asph/Bnip
GO_BP_m1	GO:00512	regulation	14/2606	107/23843	0.278298	0.623365	0.592752	Akap6/Asp
GO_BP_m1	GO:003007	peptide ho	32/2606	262/23843	0.278528	0.623365	0.592752	Abat/Ano1
GO_BP_m1	GO:00975	calcium io	16/2606	124/23843	0.278544	0.623365	0.592752	Akap6/Asp
GO_BP_m1	GO:19026	secondary	16/2606	124/23843	0.278544	0.623365	0.592752	Angptl3/C
GO_BP_m1	GO:00456	regulation	26/2606	210/23843	0.279241	0.623365	0.592752	Adam8/Ca
GO_BP_m1	GO:000691	nucleocyto	37/2606	306/23843	0.281232	0.623365	0.592752	1700123L1
GO_BP_m1	GO:00466	lymphocyt	37/2606	306/23843	0.281232	0.623365	0.592752	Adk/Arg1/
GO_BP_m1	GO:003412	regulation	8/2606	57/23843	0.281391	0.623365	0.592752	Cactin/Cav
GO_BP_m1	GO:004851	circadian b	8/2606	57/23843	0.281391	0.623365	0.592752	Adora1/Cs
GO_BP_m1	GO:20001	negative r	8/2606	57/23843	0.281391	0.623365	0.592752	Cdkn1a/E2
GO_BP_m1	GO:20007	regulation	8/2606	57/23843	0.281391	0.623365	0.592752	Eif2ak2/Esr
GO_BP_m1	GO:19030	regulation	24/2606	193/23843	0.281788	0.623365	0.592752	Arih2/Bcap
GO_BP_m1	GO:00353	regulation	11/2606	82/23843	0.281898	0.623365	0.592752	2810408A1
GO_BP_m1	GO:00432	regulation	51/2606	429/23843	0.281917	0.623365	0.592752	Ankra2/An
GO_BP_m1	GO:00434	positive re	27/2606	219/23843	0.282024	0.623365	0.592752	5730559C1
GO_BP_m1	GO:00000	ribosomal	3/2606	17/23843	0.282346	0.623365	0.592752	Nmd3/Ras
GO_BP_m1	GO:000204	blood vess	3/2606	17/23843	0.282346	0.623365	0.592752	Dll4/Epha2
GO_BP_m1	GO:00062	pyrimidine	3/2606	17/23843	0.282346	0.623365	0.592752	Dpyd/Dpy
GO_BP_m1	GO:000821	estrogen m	3/2606	17/23843	0.282346	0.623365	0.592752	Hsd17b4/
GO_BP_m1	GO:00090	glutamine	3/2606	17/23843	0.282346	0.623365	0.592752	Gls/Otc/Py
GO_BP_m1	GO:003162	synaptic ve	3/2606	17/23843	0.282346	0.623365	0.592752	Snap29/St
GO_BP_m1	GO:003222	regulation	3/2606	17/23843	0.282346	0.623365	0.592752	Gdnf/Ptgs
GO_BP_m1	GO:00329	protein-D	3/2606	17/23843	0.282346	0.623365	0.592752	Myc/Rpl23
GO_BP_m1	GO:00337	ribosome	3/2606	17/23843	0.282346	0.623365	0.592752	Nmd3/Ras
GO_BP_m1	GO:00343	telomere l	3/2606	17/23843	0.282346	0.623365	0.592752	Terb1/Lem
GO_BP_m1	GO:003502	regulation	3/2606	17/23843	0.282346	0.623365	0.592752	Arhgap44/
GO_BP_m1	GO:00360	fucosylatio	3/2606	17/23843	0.282346	0.623365	0.592752	Fut8/Slc35
GO_BP_m1	GO:00380	nodal sign	3/2606	17/23843	0.282346	0.623365	0.592752	Cfc1/Dand
GO_BP_m1	GO:00435	nose devel	3/2606	17/23843	0.282346	0.623365	0.592752	Aldh1a3/G

GO_BP_m1	GO:004403	cell wall ma	3/2606	17/23843	0.282346	0.623365	0.592752	1700016D0
GO_BP_m1	GO:004557	positive reg	3/2606	17/23843	0.282346	0.623365	0.592752	Il2rg/Mmp
GO_BP_m1	GO:004572	positive reg	3/2606	17/23843	0.282346	0.623365	0.592752	Kat2a/Kat2
GO_BP_m1	GO:004633	diacylglyce	3/2606	17/23843	0.282346	0.623365	0.592752	Dgat1/Dgk
GO_BP_m1	GO:004669	decidualiza	3/2606	17/23843	0.282346	0.623365	0.592752	Cdh1/Ctsl/
GO_BP_m1	GO:004685	negative re	3/2606	17/23843	0.282346	0.623365	0.592752	Cartpt/Cldn
GO_BP_m1	GO:004829	isotype swi	3/2606	17/23843	0.282346	0.623365	0.592752	Ifng/Il27ra/
GO_BP_m1	GO:005144	negative re	3/2606	17/23843	0.282346	0.623365	0.592752	Fbxo5/Rpl2
GO_BP_m1	GO:006041	atrial septu	3/2606	17/23843	0.282346	0.623365	0.592752	Cfc1/Smo/
GO_BP_m1	GO:007155	cell wall org	3/2606	17/23843	0.282346	0.623365	0.592752	1700016D0
GO_BP_m1	GO:007223	metanephr	3/2606	17/23843	0.282346	0.623365	0.592752	Lgr4/Osr1/
GO_BP_m1	GO:009750	mannosyla	3/2606	17/23843	0.282346	0.623365	0.592752	Nus1/Pigb/
GO_BP_m1	GO:009950	vesicle fusi	3/2606	17/23843	0.282346	0.623365	0.592752	Snap29/Stx
GO_BP_m1	GO:190217	negative re	3/2606	17/23843	0.282346	0.623365	0.592752	Gpx1/Hsph
GO_BP_m1	GO:200000	regulation	3/2606	17/23843	0.282346	0.623365	0.592752	Cul4a/Nek1
GO_BP_m1	GO:001635	dendrite de	34/2606	280/23843	0.282701	0.623365	0.592752	Abi1/Abl2/
GO_BP_m1	GO:003527	endocrine s	17/2606	133/23843	0.283609	0.623365	0.592752	Arntl/Cdkn
GO_BP_m1	GO:005071	positive reg	17/2606	133/23843	0.283609	0.623365	0.592752	Abl2/Btnl2/
GO_BP_m1	GO:000680	xenobiotic	13/2606	99/23843	0.283867	0.623365	0.592752	Acsl1/Akr1
GO_BP_m1	GO:000919	cyclic nucle	13/2606	99/23843	0.283867	0.623365	0.592752	Adcy4/Adr
GO_BP_m1	GO:000754	sex differen	35/2606	289/23843	0.284628	0.623365	0.592752	Ccdc182/A
GO_BP_m1	GO:000204	cell migrati	7/2606	49/23843	0.285189	0.623365	0.592752	Cib1/Dll4/E
GO_BP_m1	GO:003019	negative re	7/2606	49/23843	0.285189	0.623365	0.592752	Abat/Alox1
GO_BP_m1	GO:003294	secretion b	7/2606	49/23843	0.285189	0.623365	0.592752	Adora1/Ch
GO_BP_m1	GO:004568	positive reg	7/2606	49/23843	0.285189	0.623365	0.592752	Enpp2/Hda
GO_BP_m1	GO:005502	positive reg	7/2606	49/23843	0.285189	0.623365	0.592752	Akap6/Cdk
GO_BP_m1	GO:007097	protein loc	7/2606	49/23843	0.285189	0.623365	0.592752	Bcap29/Bca
GO_BP_m1	GO:190004	negative re	7/2606	49/23843	0.285189	0.623365	0.592752	Abat/Alox1
GO_BP_m1	GO:004441	interspecie	49/2606	412/23843	0.285564	0.623365	0.592752	Anxa2/Arg
GO_BP_m1	GO:000683	mitochond	32/2606	263/23843	0.28603	0.623365	0.592752	Arih2/Atp5
GO_BP_m1	GO:000926	ribonucleo	32/2606	263/23843	0.28603	0.623365	0.592752	Adcy4/Adr
GO_BP_m1	GO:005129	protein het	20/2606	159/23843	0.286349	0.623365	0.592752	Anxa2/Cbr
GO_BP_m1	GO:007190	positive reg	36/2606	298/23843	0.286457	0.623365	0.592752	5730559C1
GO_BP_m1	GO:003272	positive reg	10/2606	74/23843	0.287199	0.623365	0.592752	Abl2/Fam4
GO_BP_m1	GO:003432	cell junctio	23/2606	185/23843	0.287511	0.623365	0.592752	Bcas3/Cav1
GO_BP_m1	GO:000165	eye develo	46/2606	386/23843	0.288076	0.623365	0.592752	Abcb5/Ach
GO_BP_m1	GO:005116	nuclear tra	37/2606	307/23843	0.288197	0.623365	0.592752	1700123L1
GO_BP_m1	GO:000018	activation o	6/2606	41/23843	0.288291	0.623365	0.592752	Adora1/Ca
GO_BP_m1	GO:001067	negative re	6/2606	41/23843	0.288291	0.623365	0.592752	C1qtnf3/Cd
GO_BP_m1	GO:004592	positive reg	6/2606	41/23843	0.288291	0.623365	0.592752	Avpr1a/Dg
GO_BP_m1	GO:005159	positive reg	6/2606	41/23843	0.288291	0.623365	0.592752	Htr6/Park2
GO_BP_m1	GO:009034	regulation	6/2606	41/23843	0.288291	0.623365	0.592752	Arntl/Mb21
GO_BP_m1	GO:190266	regulation	6/2606	41/23843	0.288291	0.623365	0.592752	Plxna2/Sen
GO_BP_m1	GO:000046	cleavage in	4/2606	25/23843	0.289231	0.623365	0.592752	Bms1/Eri1/
GO_BP_m1	GO:000282	regulation	4/2606	25/23843	0.289231	0.623365	0.592752	Il12b/Il1rl1/
GO_BP_m1	GO:001086	positive reg	4/2606	25/23843	0.289231	0.623365	0.592752	Abl2/Adcy
GO_BP_m1	GO:001089	positive reg	4/2606	25/23843	0.289231	0.623365	0.592752	Fgf1/Ifng/P
GO_BP_m1	GO:003420	lipid transl	4/2606	25/23843	0.289231	0.623365	0.592752	Abcb1a/At

GO_BP_m1	GO:003634	post-anal t	4/2606	25/23843	0.289231	0.623365	0.592752	Epha2/Tcf1
GO_BP_m1	GO:004210	positive reg	4/2606	25/23843	0.289231	0.623365	0.592752	Gpam/Il12
GO_BP_m1	GO:004337	positive reg	4/2606	25/23843	0.289231	0.623365	0.592752	Ifng/Il2rg/
GO_BP_m1	GO:004411	growth of s	4/2606	25/23843	0.289231	0.623365	0.592752	Cd36/Ifng/
GO_BP_m1	GO:004558	regulation	4/2606	25/23843	0.289231	0.623365	0.592752	Ctla4/Ifng/
GO_BP_m1	GO:004636	monosacch	4/2606	25/23843	0.289231	0.623365	0.592752	Ldha/Rpe/
GO_BP_m1	GO:005090	leukocyte t	4/2606	25/23843	0.289231	0.623365	0.592752	Ccl28/Gcnt
GO_BP_m1	GO:005095	sensory pe	4/2606	25/23843	0.289231	0.623365	0.592752	Adora1/An
GO_BP_m1	GO:006000	Sertoli cell	4/2606	25/23843	0.289231	0.623365	0.592752	Dmrt1/Hsd
GO_BP_m1	GO:007019	synaptonem	4/2606	25/23843	0.289231	0.623365	0.592752	Syce2/Sycp
GO_BP_m1	GO:007201	glomerulus	4/2606	25/23843	0.289231	0.623365	0.592752	Ifng/Osr1/
GO_BP_m1	GO:009014	regulation	4/2606	25/23843	0.289231	0.623365	0.592752	Bnip3/Dcn/
GO_BP_m1	GO:000599	monosacch	30/2606	246/23843	0.289387	0.623365	0.592752	Atf3/Bpgm
GO_BP_m1	GO:000610	citrate met	5/2606	33/23843	0.290081	0.623365	0.592752	Idh2/Idh3a
GO_BP_m1	GO:001059	regulation	5/2606	33/23843	0.290081	0.623365	0.592752	Cfl1/Epha2
GO_BP_m1	GO:001482	response to	5/2606	33/23843	0.290081	0.623365	0.592752	Gpam/Myh
GO_BP_m1	GO:003430	primary alc	5/2606	33/23843	0.290081	0.623365	0.592752	Adh1/Adh5
GO_BP_m1	GO:004587	negative re	5/2606	33/23843	0.290081	0.623365	0.592752	Kif7/Prkacb
GO_BP_m1	GO:004591	positive reg	5/2606	33/23843	0.290081	0.623365	0.592752	Blm/Ifng/P
GO_BP_m1	GO:190358	positive reg	5/2606	33/23843	0.290081	0.623365	0.592752	Cdk1/Esrrb
GO_BP_m1	GO:000008	G2/M trans	14/2606	108/23843	0.290159	0.623365	0.592752	Abcb1a/Blm
GO_BP_m1	GO:003236	regulation	14/2606	108/23843	0.290159	0.623365	0.592752	Abca12/Ar
GO_BP_m1	GO:001648	protein pro	31/2606	255/23843	0.291558	0.623365	0.592752	Aph1a/Aph
GO_BP_m1	GO:000028	mitotic cyto	9/2606	66/23843	0.292558	0.623365	0.592752	Ankrd53/C
GO_BP_m1	GO:190179	regulation	9/2606	66/23843	0.292558	0.623365	0.592752	Ankrd1/Atr
GO_BP_m1	GO:190372	regulation	9/2606	66/23843	0.292558	0.623365	0.592752	Epha8/Fpr2
GO_BP_m1	GO:002261	ribonucleo	50/2606	422/23843	0.292686	0.623365	0.592752	Atr/Bms1/
GO_BP_m1	GO:000023	pachytene	1/2606	3/23843	0.293373	0.623365	0.592752	Topaz1
GO_BP_m1	GO:000043	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Foxa2
GO_BP_m1	GO:000043	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Foxa2
GO_BP_m1	GO:000045	rRNA 2'-O	1/2606	3/23843	0.293373	0.623365	0.592752	Mrm1
GO_BP_m1	GO:000095	mitochond	1/2606	3/23843	0.293373	0.623365	0.592752	Pnpt1
GO_BP_m1	GO:000154	preantral o	1/2606	3/23843	0.293373	0.623365	0.592752	Amh
GO_BP_m1	GO:000182	inner cell m	1/2606	3/23843	0.293373	0.623365	0.592752	Lats1
GO_BP_m1	GO:000182	inner cell m	1/2606	3/23843	0.293373	0.623365	0.592752	Lats1
GO_BP_m1	GO:000183	trophectod	1/2606	3/23843	0.293373	0.623365	0.592752	Esrrb
GO_BP_m1	GO:000198	barorecept	1/2606	3/23843	0.293373	0.623365	0.592752	Adra1d
GO_BP_m1	GO:000227	myeloid de	1/2606	3/23843	0.293373	0.623365	0.592752	Pycard
GO_BP_m1	GO:000233	B-1a B cell	1/2606	3/23843	0.293373	0.623365	0.592752	Cmtm7
GO_BP_m1	GO:000237	immunoglo	1/2606	3/23843	0.293373	0.623365	0.592752	Ptprc
GO_BP_m1	GO:000254	leukotriene	1/2606	3/23843	0.293373	0.623365	0.592752	Alox5
GO_BP_m1	GO:000255	serotonin s	1/2606	3/23843	0.293373	0.623365	0.592752	P2rx1
GO_BP_m1	GO:000258	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Pycard
GO_BP_m1	GO:000287	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Il10
GO_BP_m1	GO:000294	tRNA C5-c	1/2606	3/23843	0.293373	0.623365	0.592752	Mettl6
GO_BP_m1	GO:000294	tRNA threo	1/2606	3/23843	0.293373	0.623365	0.592752	Osgepl1
GO_BP_m1	GO:000322	right ventri	1/2606	3/23843	0.293373	0.623365	0.592752	Zfpm2
GO_BP_m1	GO:000327	apoptotic p	1/2606	3/23843	0.293373	0.623365	0.592752	Foxc1

GO_BP_m1	GO:00032	septum sec	1/2606	3/23843	0.293373	0.623365	0.592752	Nsd2
GO_BP_m1	GO:00033	brainstem	1/2606	3/23843	0.293373	0.623365	0.592752	Cntfr
GO_BP_m1	GO:00059	trehalose n	1/2606	3/23843	0.293373	0.623365	0.592752	Pgghg
GO_BP_m1	GO:00060	fructose ca	1/2606	3/23843	0.293373	0.623365	0.592752	Tkfc
GO_BP_m1	GO:00061	fumarate	1/2606	3/23843	0.293373	0.623365	0.592752	Got1
GO_BP_m1	GO:00062	dTMP bios	1/2606	3/23843	0.293373	0.623365	0.592752	Shmt1
GO_BP_m1	GO:00062	base-excisi	1/2606	3/23843	0.293373	0.623365	0.592752	Ung
GO_BP_m1	GO:00062	nucleotide-	1/2606	3/23843	0.293373	0.623365	0.592752	Ercc5
GO_BP_m1	GO:00063	transcripti	1/2606	3/23843	0.293373	0.623365	0.592752	Tfb2m
GO_BP_m1	GO:00063	terminatio	1/2606	3/23843	0.293373	0.623365	0.592752	Mterf2
GO_BP_m1	GO:00064	RNA impor	1/2606	3/23843	0.293373	0.623365	0.592752	Tpr
GO_BP_m1	GO:00064	valyl-tRNA	1/2606	3/23843	0.293373	0.623365	0.592752	Vars2
GO_BP_m1	GO:00065	aspartate	1/2606	3/23843	0.293373	0.623365	0.592752	Got1
GO_BP_m1	GO:000654	glutamine	1/2606	3/23843	0.293373	0.623365	0.592752	Gls
GO_BP_m1	GO:000654	glycine cat	1/2606	3/23843	0.293373	0.623365	0.592752	Gldc
GO_BP_m1	GO:00065	S-adenosy	1/2606	3/23843	0.293373	0.623365	0.592752	Mat2b
GO_BP_m1	GO:00065	L-serine ca	1/2606	3/23843	0.293373	0.623365	0.592752	Shmt1
GO_BP_m1	GO:00066	sphinganin	1/2606	3/23843	0.293373	0.623365	0.592752	Sptlc2
GO_BP_m1	GO:00066	ergosterol	1/2606	3/23843	0.293373	0.623365	0.592752	Fdft1
GO_BP_m1	GO:000671	androgen	1/2606	3/23843	0.293373	0.623365	0.592752	Spp1
GO_BP_m1	GO:000677	thiamine	1/2606	3/23843	0.293373	0.623365	0.592752	Acpp
GO_BP_m1	GO:00070	spindle ass	1/2606	3/23843	0.293373	0.623365	0.592752	Fbxo5
GO_BP_m1	GO:00070	female mei	1/2606	3/23843	0.293373	0.623365	0.592752	Sycp3
GO_BP_m1	GO:00070	traversing	1/2606	3/23843	0.293373	0.623365	0.592752	Mtbp
GO_BP_m1	GO:000722	positive re	1/2606	3/23843	0.293373	0.623365	0.592752	Smo
GO_BP_m1	GO:00073	thorax and	1/2606	3/23843	0.293373	0.623365	0.592752	Wt1
GO_BP_m1	GO:000752	establishm	1/2606	3/23843	0.293373	0.623365	0.592752	Gphn
GO_BP_m1	GO:00082	ergosterol	1/2606	3/23843	0.293373	0.623365	0.592752	Fdft1
GO_BP_m1	GO:000944	gamma-a	1/2606	3/23843	0.293373	0.623365	0.592752	Abat
GO_BP_m1	GO:00097	detection	1/2606	3/23843	0.293373	0.623365	0.592752	Foxa2
GO_BP_m1	GO:00097	detection	1/2606	3/23843	0.293373	0.623365	0.592752	Foxa2
GO_BP_m1	GO:00101	proline cat	1/2606	3/23843	0.293373	0.623365	0.592752	Aldh4a1
GO_BP_m1	GO:00101	specificati	1/2606	3/23843	0.293373	0.623365	0.592752	Hoxa3
GO_BP_m1	GO:001024	establishm	1/2606	3/23843	0.293373	0.623365	0.592752	Slc22a1
GO_BP_m1	GO:00103	COP9 sign	1/2606	3/23843	0.293373	0.623365	0.592752	Wnt3a
GO_BP_m1	GO:00107	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Atp2b4
GO_BP_m1	GO:00108	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Xrcc1
GO_BP_m1	GO:00109	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Nfkb1
GO_BP_m1	GO:00109	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Arg1
GO_BP_m1	GO:00109	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Eif2ak1
GO_BP_m1	GO:001401	neuroblast	1/2606	3/23843	0.293373	0.623365	0.592752	Bche
GO_BP_m1	GO:00140	positive re	1/2606	3/23843	0.293373	0.623365	0.592752	Tacr2
GO_BP_m1	GO:001491	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Gch1
GO_BP_m1	GO:001567	plasma me	1/2606	3/23843	0.293373	0.623365	0.592752	Slc31a1
GO_BP_m1	GO:00156	ferrous iro	1/2606	3/23843	0.293373	0.623365	0.592752	Slc40a1
GO_BP_m1	GO:001591	aminophos	1/2606	3/23843	0.293373	0.623365	0.592752	Atp8b1
GO_BP_m1	GO:00159	diadenosin	1/2606	3/23843	0.293373	0.623365	0.592752	Kars
GO_BP_m1	GO:00159	diadenosin	1/2606	3/23843	0.293373	0.623365	0.592752	Kars

GO_BP_m1	GO:00159	diadenosin	1/2606	3/23843	0.293373	0.623365	0.592752	Kars
GO_BP_m1	GO:00160	polyprenol	1/2606	3/23843	0.293373	0.623365	0.592752	Nus1
GO_BP_m1	GO:00164	negative r	1/2606	3/23843	0.293373	0.623365	0.592752	Maf1
GO_BP_m1	GO:00165	protein im	1/2606	3/23843	0.293373	0.623365	0.592752	Pex5
GO_BP_m1	GO:00171	peptidyl-g	1/2606	3/23843	0.293373	0.623365	0.592752	Vkorc1l1
GO_BP_m1	GO:00181	peptidyl-a	1/2606	3/23843	0.293373	0.623365	0.592752	Asph
GO_BP_m1	GO:001904	latent virus	1/2606	3/23843	0.293373	0.623365	0.592752	Nucks1
GO_BP_m1	GO:001904	release fro	1/2606	3/23843	0.293373	0.623365	0.592752	Nucks1
GO_BP_m1	GO:00190	fusion of vi	1/2606	3/23843	0.293373	0.623365	0.592752	Hyal2
GO_BP_m1	GO:00190	receptor-	1/2606	3/23843	0.293373	0.623365	0.592752	Cav1
GO_BP_m1	GO:00192	isopenteny	1/2606	3/23843	0.293373	0.623365	0.592752	Mvd
GO_BP_m1	GO:001932	pentose ca	1/2606	3/23843	0.293373	0.623365	0.592752	Rpe
GO_BP_m1	GO:001937	cyclooxyge	1/2606	3/23843	0.293373	0.623365	0.592752	Ptgs2
GO_BP_m1	GO:00194	alditol cata	1/2606	3/23843	0.293373	0.623365	0.592752	Tkfc
GO_BP_m1	GO:00194	glycine de	1/2606	3/23843	0.293373	0.623365	0.592752	Gldc
GO_BP_m1	GO:001974	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Dgat1
GO_BP_m1	GO:001991	peptidyl-a	1/2606	3/23843	0.293373	0.623365	0.592752	Ndufaf7
GO_BP_m1	GO:00215	vagus nerv	1/2606	3/23843	0.293373	0.623365	0.592752	Tbx1
GO_BP_m1	GO:002157	rhombome	1/2606	3/23843	0.293373	0.623365	0.592752	Hoxb1
GO_BP_m1	GO:00216	cerebellar	1/2606	3/23843	0.293373	0.623365	0.592752	Cend1
GO_BP_m1	GO:002184	ventricular	1/2606	3/23843	0.293373	0.623365	0.592752	Dct
GO_BP_m1	GO:00219	hindbrain t	1/2606	3/23843	0.293373	0.623365	0.592752	Plxna2
GO_BP_m1	GO:002301	signal tran	1/2606	3/23843	0.293373	0.623365	0.592752	Osr1
GO_BP_m1	GO:00302	dermatan	1/2606	3/23843	0.293373	0.623365	0.592752	Dse
GO_BP_m1	GO:003144	slow-twitc	1/2606	3/23843	0.293373	0.623365	0.592752	Myh7
GO_BP_m1	GO:003144	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Mylk2
GO_BP_m1	GO:003144	positive re	1/2606	3/23843	0.293373	0.623365	0.592752	Mylk2
GO_BP_m1	GO:003247	otolith mo	1/2606	3/23843	0.293373	0.623365	0.592752	Bloc1s5
GO_BP_m1	GO:00324	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Dennd4b
GO_BP_m1	GO:00327	saturated	1/2606	3/23843	0.293373	0.623365	0.592752	Acot3
GO_BP_m1	GO:00327	unsaturate	1/2606	3/23843	0.293373	0.623365	0.592752	Acot3
GO_BP_m1	GO:00328	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Adora1
GO_BP_m1	GO:003291	polyamine	1/2606	3/23843	0.293373	0.623365	0.592752	Sat1
GO_BP_m1	GO:003291	spermidine	1/2606	3/23843	0.293373	0.623365	0.592752	Sat1
GO_BP_m1	GO:003312	negative r	1/2606	3/23843	0.293373	0.623365	0.592752	H2afy
GO_BP_m1	GO:003361	mitochond	1/2606	3/23843	0.293373	0.623365	0.592752	Atpaf1
GO_BP_m1	GO:00338	negative r	1/2606	3/23843	0.293373	0.623365	0.592752	Drd5
GO_BP_m1	GO:00342	detection	1/2606	3/23843	0.293373	0.623365	0.592752	Foxa2
GO_BP_m1	GO:00343	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Slc40a1
GO_BP_m1	GO:003442	post-transl	1/2606	3/23843	0.293373	0.623365	0.592752	Esco1
GO_BP_m1	GO:00344	glycoprote	1/2606	3/23843	0.293373	0.623365	0.592752	Vldlr
GO_BP_m1	GO:003447	U1 snRNA	1/2606	3/23843	0.293373	0.623365	0.592752	Exosc9
GO_BP_m1	GO:003447	U5 snRNA	1/2606	3/23843	0.293373	0.623365	0.592752	Exosc9
GO_BP_m1	GO:003554	negative r	1/2606	3/23843	0.293373	0.623365	0.592752	Trim9
GO_BP_m1	GO:00357	platelet-de	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfra
GO_BP_m1	GO:00357	positive re	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfa
GO_BP_m1	GO:00359	testostero	1/2606	3/23843	0.293373	0.623365	0.592752	Igfbp3
GO_BP_m1	GO:00359	estradiol s	1/2606	3/23843	0.293373	0.623365	0.592752	Spp1

GO_BP_m1	GO:003611	medium-cl	1/2606	3/23843	0.293373	0.623365	0.592752	Hsd17b4
GO_BP_m1	GO:003614	dendritic c	1/2606	3/23843	0.293373	0.623365	0.592752	Gpr183
GO_BP_m1	GO:003649	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Nck2
GO_BP_m1	GO:003808	VEGF-activ	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfra
GO_BP_m1	GO:003809	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfra
GO_BP_m1	GO:003966	membrane	1/2606	3/23843	0.293373	0.623365	0.592752	Hyal2
GO_BP_m1	GO:004211	monocyte	1/2606	3/23843	0.293373	0.623365	0.592752	Hyal2
GO_BP_m1	GO:004232	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Htr7
GO_BP_m1	GO:004236	vitamin E n	1/2606	3/23843	0.293373	0.623365	0.592752	Pltp
GO_BP_m1	GO:004272	thiamine-c	1/2606	3/23843	0.293373	0.623365	0.592752	Acpp
GO_BP_m1	GO:004330	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Stx4a
GO_BP_m1	GO:004420	'de novo' A	1/2606	3/23843	0.293373	0.623365	0.592752	Adss
GO_BP_m1	GO:004433	canonical W	1/2606	3/23843	0.293373	0.623365	0.592752	Myc
GO_BP_m1	GO:004472	chromatin	1/2606	3/23843	0.293373	0.623365	0.592752	Tet3
GO_BP_m1	GO:004480	multi-orga	1/2606	3/23843	0.293373	0.623365	0.592752	Hyal2
GO_BP_m1	GO:004486	protein loc	1/2606	3/23843	0.293373	0.623365	0.592752	Flot2
GO_BP_m1	GO:004486	modulation	1/2606	3/23843	0.293373	0.623365	0.592752	Nucks1
GO_BP_m1	GO:004522	extracellula	1/2606	3/23843	0.293373	0.623365	0.592752	Has2
GO_BP_m1	GO:004533	farnesyl dip	1/2606	3/23843	0.293373	0.623365	0.592752	Hmgcs2
GO_BP_m1	GO:004535	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Nmi
GO_BP_m1	GO:004536	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ccl20
GO_BP_m1	GO:004536	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ccl20
GO_BP_m1	GO:004557	basophil ac	1/2606	3/23843	0.293373	0.623365	0.592752	Kars
GO_BP_m1	GO:004562	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Jak3
GO_BP_m1	GO:004565	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Trib1
GO_BP_m1	GO:004579	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Tpr
GO_BP_m1	GO:004600	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Uts2r
GO_BP_m1	GO:004606	dATP catab	1/2606	3/23843	0.293373	0.623365	0.592752	Nudt1
GO_BP_m1	GO:004607	dTMP meta	1/2606	3/23843	0.293373	0.623365	0.592752	Shmt1
GO_BP_m1	GO:004609	guanine m	1/2606	3/23843	0.293373	0.623365	0.592752	Gda
GO_BP_m1	GO:004610	thymidine	1/2606	3/23843	0.293373	0.623365	0.592752	Dpyd
GO_BP_m1	GO:004613	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ifng
GO_BP_m1	GO:004637	extracellula	1/2606	3/23843	0.293373	0.623365	0.592752	Has2
GO_BP_m1	GO:004641	D-amino a	1/2606	3/23843	0.293373	0.623365	0.592752	Ddo
GO_BP_m1	GO:004660	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Plk4
GO_BP_m1	GO:004698	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Prmt1
GO_BP_m1	GO:004816	multi-layer	1/2606	3/23843	0.293373	0.623365	0.592752	Amh
GO_BP_m1	GO:004832	axial meso	1/2606	3/23843	0.293373	0.623365	0.592752	Epha2
GO_BP_m1	GO:004869	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Wnt3a
GO_BP_m1	GO:004886	stem cell fa	1/2606	3/23843	0.293373	0.623365	0.592752	Sox18
GO_BP_m1	GO:005088	musculoske	1/2606	3/23843	0.293373	0.623365	0.592752	Drd3
GO_BP_m1	GO:005131	attachmen	1/2606	3/23843	0.293373	0.623365	0.592752	Cenpc1
GO_BP_m1	GO:005146	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Tnfsf11
GO_BP_m1	GO:005159	detection c	1/2606	3/23843	0.293373	0.623365	0.592752	Foxa2
GO_BP_m1	GO:005159	response to	1/2606	3/23843	0.293373	0.623365	0.592752	Atp2b4
GO_BP_m1	GO:005509	lipoprotein	1/2606	3/23843	0.293373	0.623365	0.592752	Cd36
GO_BP_m1	GO:005509	low-densit	1/2606	3/23843	0.293373	0.623365	0.592752	Cd36
GO_BP_m1	GO:006016	olfactory p	1/2606	3/23843	0.293373	0.623365	0.592752	Aldh1a3

GO_BP_m1	GO:006016	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Acpp
GO_BP_m1	GO:006039	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Pbld1
GO_BP_m1	GO:006045	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Oprl1
GO_BP_m1	GO:006046	left lung m	1/2606	3/23843	0.293373	0.623365	0.592752	Cfc1
GO_BP_m1	GO:006055	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ifng
GO_BP_m1	GO:006055	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ifng
GO_BP_m1	GO:006082	fibroblast g	1/2606	3/23843	0.293373	0.623365	0.592752	Nog
GO_BP_m1	GO:006091	cardiac cell	1/2606	3/23843	0.293373	0.623365	0.592752	Wnt3a
GO_BP_m1	GO:006098	lipid tube a	1/2606	3/23843	0.293373	0.623365	0.592752	Snx9
GO_BP_m1	GO:006118	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Rflna
GO_BP_m1	GO:006118	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Wnt3a
GO_BP_m1	GO:006131	canonical W	1/2606	3/23843	0.293373	0.623365	0.592752	Wnt3a
GO_BP_m1	GO:006150	early endos	1/2606	3/23843	0.293373	0.623365	0.592752	Dnajc13
GO_BP_m1	GO:006162	fructose ca	1/2606	3/23843	0.293373	0.623365	0.592752	Tkfc
GO_BP_m1	GO:006162	glycolytic p	1/2606	3/23843	0.293373	0.623365	0.592752	Tkfc
GO_BP_m1	GO:006189	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ttbk1
GO_BP_m1	GO:006194	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Nmi
GO_BP_m1	GO:007038	DNA cytosi	1/2606	3/23843	0.293373	0.623365	0.592752	Apobec1
GO_BP_m1	GO:007042	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Ptpn22
GO_BP_m1	GO:007042	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Peli3
GO_BP_m1	GO:007043	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Ptpn22
GO_BP_m1	GO:007046	thyroid-stim	1/2606	3/23843	0.293373	0.623365	0.592752	Dio2
GO_BP_m1	GO:007048	T cell aggre	1/2606	3/23843	0.293373	0.623365	0.592752	Adam8
GO_BP_m1	GO:007049	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Snca
GO_BP_m1	GO:007049	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Snca
GO_BP_m1	GO:007053	histone H2	1/2606	3/23843	0.293373	0.623365	0.592752	Uimc1
GO_BP_m1	GO:007059	dendrite se	1/2606	3/23843	0.293373	0.623365	0.592752	Dscaml1
GO_BP_m1	GO:007063	transepithe	1/2606	3/23843	0.293373	0.623365	0.592752	Slc12a2
GO_BP_m1	GO:007067	intralumen	1/2606	3/23843	0.293373	0.623365	0.592752	Park2
GO_BP_m1	GO:007068	proteasom	1/2606	3/23843	0.293373	0.623365	0.592752	Psmd9
GO_BP_m1	GO:007096	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Arg1
GO_BP_m1	GO:007096	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Arg1
GO_BP_m1	GO:007131	cellular resp	1/2606	3/23843	0.293373	0.623365	0.592752	Crhbp
GO_BP_m1	GO:007161	granzyme B	1/2606	3/23843	0.293373	0.623365	0.592752	Ptpn22
GO_BP_m1	GO:007165	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Ticam2
GO_BP_m1	GO:007166	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ptpn22
GO_BP_m1	GO:007166	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ptpn22
GO_BP_m1	GO:007187	response to	1/2606	3/23843	0.293373	0.623365	0.592752	Rnls
GO_BP_m1	GO:007196	establishme	1/2606	3/23843	0.293373	0.623365	0.592752	Cfl1
GO_BP_m1	GO:007206	DCT cell di	1/2606	3/23843	0.293373	0.623365	0.592752	Pou3f3
GO_BP_m1	GO:007219	ureter urot	1/2606	3/23843	0.293373	0.623365	0.592752	Osr1
GO_BP_m1	GO:007219	kidney smo	1/2606	3/23843	0.293373	0.623365	0.592752	Osr1
GO_BP_m1	GO:007224	metanephr	1/2606	3/23843	0.293373	0.623365	0.592752	Pou3f3
GO_BP_m1	GO:007224	metanephr	1/2606	3/23843	0.293373	0.623365	0.592752	Lamb2
GO_BP_m1	GO:007227	metanephr	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfra
GO_BP_m1	GO:007227	metanephr	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfra
GO_BP_m1	GO:007227	metanephr	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfra
GO_BP_m1	GO:007228	metanephr	1/2606	3/23843	0.293373	0.623365	0.592752	Wt1

GO_BP_m1	GO:007256	chemokine	1/2606	3/23843	0.293373	0.623365	0.592752	Trpv4
GO_BP_m1	GO:007270	response t	1/2606	3/23843	0.293373	0.623365	0.592752	Mapk13
GO_BP_m1	GO:007271	cellular res	1/2606	3/23843	0.293373	0.623365	0.592752	Rpl23
GO_BP_m1	GO:007273	response t	1/2606	3/23843	0.293373	0.623365	0.592752	Casp6
GO_BP_m1	GO:007273	cellular res	1/2606	3/23843	0.293373	0.623365	0.592752	Casp6
GO_BP_m1	GO:007550	endocytosi	1/2606	3/23843	0.293373	0.623365	0.592752	Cav1
GO_BP_m1	GO:007573	intracellula	1/2606	3/23843	0.293373	0.623365	0.592752	Fmr1
GO_BP_m1	GO:008605	AV node c	1/2606	3/23843	0.293373	0.623365	0.592752	Gjc1
GO_BP_m1	GO:009020	protein loc	1/2606	3/23843	0.293373	0.623365	0.592752	Osbpl8
GO_BP_m1	GO:009021	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Adgra2
GO_BP_m1	GO:009027	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ptgs2
GO_BP_m1	GO:009029	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Lig3
GO_BP_m1	GO:009031	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Apobec1
GO_BP_m1	GO:009036	platelet-de	1/2606	3/23843	0.293373	0.623365	0.592752	Ptgs2
GO_BP_m1	GO:009036	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ptgs2
GO_BP_m1	GO:009048	purine nuc	1/2606	3/23843	0.293373	0.623365	0.592752	Slc35c1
GO_BP_m1	GO:009711	gamma-ar	1/2606	3/23843	0.293373	0.623365	0.592752	Gphn
GO_BP_m1	GO:009711	neuroligin	1/2606	3/23843	0.293373	0.623365	0.592752	Cdh2
GO_BP_m1	GO:009717	epoxide m	1/2606	3/23843	0.293373	0.623365	0.592752	Ephx2
GO_BP_m1	GO:009719	pilomotor	1/2606	3/23843	0.293373	0.623365	0.592752	Npnt
GO_BP_m1	GO:009721	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Mt3
GO_BP_m1	GO:009769	establishm	1/2606	3/23843	0.293373	0.623365	0.592752	Atr
GO_BP_m1	GO:009876	mitotic cell	1/2606	3/23843	0.293373	0.623365	0.592752	Cdc20
GO_BP_m1	GO:009891	membrane	1/2606	3/23843	0.293373	0.623365	0.592752	Cacnb2
GO_BP_m1	GO:009907	mitochond	1/2606	3/23843	0.293373	0.623365	0.592752	Park2
GO_BP_m1	GO:009907	mitochond	1/2606	3/23843	0.293373	0.623365	0.592752	Park2
GO_BP_m1	GO:009908	retrograde	1/2606	3/23843	0.293373	0.623365	0.592752	Ntf5
GO_BP_m1	GO:009917	postsynapt	1/2606	3/23843	0.293373	0.623365	0.592752	Fmr1
GO_BP_m1	GO:009954	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Fmr1
GO_BP_m1	GO:009955	trans-syna	1/2606	3/23843	0.293373	0.623365	0.592752	Ntf5
GO_BP_m1	GO:009955	maintenan	1/2606	3/23843	0.293373	0.623365	0.592752	C1ql1
GO_BP_m1	GO:009957	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Fmr1
GO_BP_m1	GO:010602	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ncam1
GO_BP_m1	GO:190004	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Ezr
GO_BP_m1	GO:190015	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Arg1
GO_BP_m1	GO:190023	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfa
GO_BP_m1	GO:190036	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Cpeb3
GO_BP_m1	GO:190062	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Has2
GO_BP_m1	GO:190062	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Has2
GO_BP_m1	GO:190100	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Tigar
GO_BP_m1	GO:190125	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Fmr1
GO_BP_m1	GO:190153	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Foxc1
GO_BP_m1	GO:190174	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Cxcl10
GO_BP_m1	GO:190184	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Cav1
GO_BP_m1	GO:190185	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Flcn
GO_BP_m1	GO:190187	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Flcn
GO_BP_m1	GO:190187	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Flcn
GO_BP_m1	GO:190197	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Cav1

GO_BP_m1	GO:190199	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Ttk
GO_BP_m1	GO:190217	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Gsn
GO_BP_m1	GO:190225	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Foxc1
GO_BP_m1	GO:190226	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Oaz1
GO_BP_m1	GO:190252	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ptpn22
GO_BP_m1	GO:190252	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Pdcd6
GO_BP_m1	GO:190256	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Bcr
GO_BP_m1	GO:190268	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Nptn
GO_BP_m1	GO:190268	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Tigar
GO_BP_m1	GO:190272	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Abat
GO_BP_m1	GO:190277	mitochond	1/2606	3/23843	0.293373	0.623365	0.592752	Dhx30
GO_BP_m1	GO:190299	mitotic telo	1/2606	3/23843	0.293373	0.623365	0.592752	Pcna
GO_BP_m1	GO:190307	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Usp14
GO_BP_m1	GO:190323	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Ccl28
GO_BP_m1	GO:190327	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Slc9a1
GO_BP_m1	GO:190328	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Atp1b2
GO_BP_m1	GO:190334	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Cldn1
GO_BP_m1	GO:190337	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ralbp1
GO_BP_m1	GO:190342	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Stx1b
GO_BP_m1	GO:190354	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Park2
GO_BP_m1	GO:190359	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Cav1
GO_BP_m1	GO:190362	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Dffa
GO_BP_m1	GO:190367	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ythdf2
GO_BP_m1	GO:190367	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ythdf2
GO_BP_m1	GO:190371	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ddrgk1
GO_BP_m1	GO:190372	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ddrgk1
GO_BP_m1	GO:190392	primary pa	1/2606	3/23843	0.293373	0.623365	0.592752	Ift88
GO_BP_m1	GO:190398	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Atf3
GO_BP_m1	GO:190402	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Tigar
GO_BP_m1	GO:190405	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Il10
GO_BP_m1	GO:190405	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Oprl1
GO_BP_m1	GO:190415	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Bcap31
GO_BP_m1	GO:190433	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Wnt3a
GO_BP_m1	GO:190438	endoplasm	1/2606	3/23843	0.293373	0.623365	0.592752	Man1b1
GO_BP_m1	GO:190469	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Ythdf2
GO_BP_m1	GO:190469	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Dock4
GO_BP_m1	GO:190478	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Cfl1
GO_BP_m1	GO:190488	response to	1/2606	3/23843	0.293373	0.623365	0.592752	Park2
GO_BP_m1	GO:190488	cellular res	1/2606	3/23843	0.293373	0.623365	0.592752	Park2
GO_BP_m1	GO:190560	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Snca
GO_BP_m1	GO:200031	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Nog
GO_BP_m1	GO:200033	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Trpv4
GO_BP_m1	GO:200037	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Mt3
GO_BP_m1	GO:200041	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Adam8
GO_BP_m1	GO:200044	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Ripk3
GO_BP_m1	GO:200046	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Snca
GO_BP_m1	GO:200055	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Arg1
GO_BP_m1	GO:200059	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Pdgfa

GO_BP_m1	GO:200064	negative re	1/2606	3/23843	0.293373	0.623365	0.592752	Anxa2
GO_BP_m1	GO:200067	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Jak3
GO_BP_m1	GO:200070	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Prkca
GO_BP_m1	GO:200072	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Npnt
GO_BP_m1	GO:200081	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Cul4a
GO_BP_m1	GO:200084	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Igfbp3
GO_BP_m1	GO:200086	regulation	1/2606	3/23843	0.293373	0.623365	0.592752	Spp1
GO_BP_m1	GO:200128	positive reg	1/2606	3/23843	0.293373	0.623365	0.592752	Cav3
GO_BP_m1	GO:001569	inorganic a	17/2606	134/23843	0.294299	0.62518	0.594479	Abcb1a/Ar
GO_BP_m1	GO:005501	cardiac mu	11/2606	83/23843	0.295584	0.625459	0.594743	Akap6/Cav
GO_BP_m1	GO:005109	positive reg	15/2606	117/23843	0.29572	0.625459	0.594743	Adam8/Am
GO_BP_m1	GO:005149	positive reg	26/2606	212/23843	0.296139	0.625459	0.594743	Ankrd53/B
GO_BP_m1	GO:005070	regulation	23/2606	186/23843	0.296591	0.625459	0.594743	Abl2/Btnl2/
GO_BP_m1	GO:000194	heart loopi	8/2606	58/23843	0.297917	0.625459	0.594743	Cfc1/Dnaa
GO_BP_m1	GO:004663	regulation	8/2606	58/23843	0.297917	0.625459	0.594743	Ifng/Il2rg/J
GO_BP_m1	GO:006003	cardiac mu	8/2606	58/23843	0.297917	0.625459	0.594743	Cdk1/Fgf1/
GO_BP_m1	GO:190379	positive reg	8/2606	58/23843	0.297917	0.625459	0.594743	Abat/Abcb
GO_BP_m1	GO:000005	ribosomal l	2/2606	10/23843	0.300055	0.625459	0.594743	Nmd3/Zfp5
GO_BP_m1	GO:000217	male germ	2/2606	10/23843	0.300055	0.625459	0.594743	Cib1/Dmrt1
GO_BP_m1	GO:000293	desmosom	2/2606	10/23843	0.300055	0.625459	0.594743	Perp/Prkca
GO_BP_m1	GO:000314	membrano	2/2606	10/23843	0.300055	0.625459	0.594743	Nog/Nsd2
GO_BP_m1	GO:000600	fructose m	2/2606	10/23843	0.300055	0.625459	0.594743	Pfkfb1/Tkfc
GO_BP_m1	GO:000600	fructose 6-	2/2606	10/23843	0.300055	0.625459	0.594743	Gfpt2/Pfkl
GO_BP_m1	GO:000600	glucose cat	2/2606	10/23843	0.300055	0.625459	0.594743	Ldha/Tigar
GO_BP_m1	GO:000628	transcriptic	2/2606	10/23843	0.300055	0.625459	0.594743	Ercc5/Usp7
GO_BP_m1	GO:000652	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Atp2b4/Slc
GO_BP_m1	GO:000659	ornithine m	2/2606	10/23843	0.300055	0.625459	0.594743	Arg1/Otc
GO_BP_m1	GO:000722	Notch rece	2/2606	10/23843	0.300055	0.625459	0.594743	Aph1a/Aph
GO_BP_m1	GO:000930	snRNA tran	2/2606	10/23843	0.300055	0.625459	0.594743	Ell2/Ice1
GO_BP_m1	GO:000965	UV protect	2/2606	10/23843	0.300055	0.625459	0.594743	Ercc5/Gpx1
GO_BP_m1	GO:001004	response to	2/2606	10/23843	0.300055	0.625459	0.594743	Atp7b/Fibin
GO_BP_m1	GO:001083	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Fgf7/Has2
GO_BP_m1	GO:001091	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Arl6ip5/Bni
GO_BP_m1	GO:001098	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Anxa2/Pcsk
GO_BP_m1	GO:001482	artery smo	2/2606	10/23843	0.300055	0.625459	0.594743	Bbs2/Smpd
GO_BP_m1	GO:001947	4-hydroxyp	2/2606	10/23843	0.300055	0.625459	0.594743	Egln3/Ero1
GO_BP_m1	GO:002155	optic nerve	2/2606	10/23843	0.300055	0.625459	0.594743	Ephb1/Kcn
GO_BP_m1	GO:002161	facial nerve	2/2606	10/23843	0.300055	0.625459	0.594743	Hoxb1/Sem
GO_BP_m1	GO:002182	substrate-i	2/2606	10/23843	0.300055	0.625459	0.594743	Arx/Nrg1
GO_BP_m1	GO:002184	substrate-i	2/2606	10/23843	0.300055	0.625459	0.594743	Arx/Nrg1
GO_BP_m1	GO:002202	interkinetic	2/2606	10/23843	0.300055	0.625459	0.594743	Dock7/Tac
GO_BP_m1	GO:003004	muscle fila	2/2606	10/23843	0.300055	0.625459	0.594743	Myh7/Mylk
GO_BP_m1	GO:003085	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Cul4a/Trib1
GO_BP_m1	GO:003094	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Pdcd6/Ptpr
GO_BP_m1	GO:003184	protection	2/2606	10/23843	0.300055	0.625459	0.594743	Dclre1a/Xr
GO_BP_m1	GO:003207	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Pcna/Vapb
GO_BP_m1	GO:003235	response to	2/2606	10/23843	0.300055	0.625459	0.594743	Epha8/Ppa
GO_BP_m1	GO:003321	leptin-mec	2/2606	10/23843	0.300055	0.625459	0.594743	Bbs2/Mt3

GO_BP_m1	GO:003411	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Il10/Il1rn
GO_BP_m1	GO:003414	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Ptpn22/Tic
GO_BP_m1	GO:003509	spermatog	2/2606	10/23843	0.300055	0.625459	0.594743	Psme4/Syc
GO_BP_m1	GO:003543	phosphate	2/2606	10/23843	0.300055	0.625459	0.594743	Ank/Slc20a
GO_BP_m1	GO:003573	hepatic ste	2/2606	10/23843	0.300055	0.625459	0.594743	Acta2/Dga
GO_BP_m1	GO:003644	calcium im	2/2606	10/23843	0.300055	0.625459	0.594743	Micu2/Slc2
GO_BP_m1	GO:004209	interleukin-	2/2606	10/23843	0.300055	0.625459	0.594743	Ifng/Nfkb1
GO_BP_m1	GO:004415	histone H3	2/2606	10/23843	0.300055	0.625459	0.594743	Kat2a/Kat2
GO_BP_m1	GO:004507	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Ifng/Nfkb1
GO_BP_m1	GO:004648	ether lipid	2/2606	10/23843	0.300055	0.625459	0.594743	Fasn/Tmen
GO_BP_m1	GO:004809	chromatin-	2/2606	10/23843	0.300055	0.625459	0.594743	Ash2l/Pabp
GO_BP_m1	GO:004867	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Epha7/Fgf1
GO_BP_m1	GO:004870	embryonic	2/2606	10/23843	0.300055	0.625459	0.594743	Mthfd1l/Tb
GO_BP_m1	GO:005117	meiotic sist	2/2606	10/23843	0.300055	0.625459	0.594743	Ppp2r1a/Sy
GO_BP_m1	GO:005129	nuclear po	2/2606	10/23843	0.300055	0.625459	0.594743	Ahctf1/Nup
GO_BP_m1	GO:006029	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Cav3/Hdac
GO_BP_m1	GO:006063	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Dmrt1/Fbx
GO_BP_m1	GO:006108	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	H2afy/Ogt
GO_BP_m1	GO:007052	tRNA threo	2/2606	10/23843	0.300055	0.625459	0.594743	Osgepl1/Tr
GO_BP_m1	GO:007058	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Il10/Il1rn
GO_BP_m1	GO:007107	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Fpr2/Pcx
GO_BP_m1	GO:007201	distal tubul	2/2606	10/23843	0.300055	0.625459	0.594743	Jag1/Pou3f
GO_BP_m1	GO:007271	response to	2/2606	10/23843	0.300055	0.625459	0.594743	Blm/Fmr1
GO_BP_m1	GO:008000	mRNA met	2/2606	10/23843	0.300055	0.625459	0.594743	Virma/Cmt
GO_BP_m1	GO:009004	tubulin dea	2/2606	10/23843	0.300055	0.625459	0.594743	Fnta/Nek3
GO_BP_m1	GO:009020	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Apobec1/P
GO_BP_m1	GO:009028	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Hrc/Mrln
GO_BP_m1	GO:009034	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Mb21d1/Yp
GO_BP_m1	GO:009048	pyrimidine	2/2606	10/23843	0.300055	0.625459	0.594743	Slc35a5/Slc
GO_BP_m1	GO:009052	actin filame	2/2606	10/23843	0.300055	0.625459	0.594743	Bcar1/Gsn
GO_BP_m1	GO:009708	vascular sm	2/2606	10/23843	0.300055	0.625459	0.594743	Adm/Smad
GO_BP_m1	GO:009710	presynaptic	2/2606	10/23843	0.300055	0.625459	0.594743	Lrp4/Nlgn3
GO_BP_m1	GO:009749	protein loc	2/2606	10/23843	0.300055	0.625459	0.594743	Tulp1/Tulp
GO_BP_m1	GO:009890	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Fmr1/Ifng
GO_BP_m1	GO:190045	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Cfl1/Nlgn3
GO_BP_m1	GO:190133	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Asph/Stim2
GO_BP_m1	GO:190138	positive reg	2/2606	10/23843	0.300055	0.625459	0.594743	Cacnb2/S1
GO_BP_m1	GO:190378	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Arl6ip5/Os
GO_BP_m1	GO:200004	negative re	2/2606	10/23843	0.300055	0.625459	0.594743	Fbxo18/Par
GO_BP_m1	GO:200084	regulation	2/2606	10/23843	0.300055	0.625459	0.594743	Galr1/Tac1
GO_BP_m1	GO:005125	positive reg	46/2606	388/23843	0.300651	0.626553	0.595784	Adam8/Ad
GO_BP_m1	GO:000647	protein dep	28/2606	230/23843	0.30097	0.627068	0.596274	2810408A1
GO_BP_m1	GO:005160	protein ma	37/2606	309/23843	0.302316	0.629724	0.598799	Aph1a/Aph
GO_BP_m1	GO:000704	lysosomal t	12/2606	92/23843	0.302739	0.630301	0.599348	Ankfy1/Cac
GO_BP_m1	GO:005189	membrane	12/2606	92/23843	0.302739	0.630301	0.599348	Alox12/Bok
GO_BP_m1	GO:000191	positive reg	7/2606	50/23843	0.303167	0.630301	0.599348	Arg1/Cadm
GO_BP_m1	GO:000645	'de novo' p	7/2606	50/23843	0.303167	0.630301	0.599348	Cct3/Ero1l/
GO_BP_m1	GO:001051	regulation	7/2606	50/23843	0.303167	0.630301	0.599348	Abl2/Adcy

GO_BP_m1	GO:003513	hindlimb m	7/2606	50/23843	0.303167	0.630301	0.599348	Alx3/Hoxd1
GO_BP_m1	GO:005189	regulation	7/2606	50/23843	0.303167	0.630301	0.599348	Bcas3/Cfl1/
GO_BP_m1	GO:009010	regulation	7/2606	50/23843	0.303167	0.630301	0.599348	Bcas3/Cfl1/
GO_BP_m1	GO:190406	positive reg	17/2606	135/23843	0.305112	0.634195	0.603051	Akap6/Asp
GO_BP_m1	GO:000320	cardiac cha	23/2606	187/23843	0.305765	0.635401	0.604198	Adamts1/C
GO_BP_m1	GO:190336	regulation	27/2606	222/23843	0.307062	0.637858	0.606534	Anxa2/Arih
GO_BP_m1	GO:006004	cardiac mu	15/2606	118/23843	0.307336	0.637858	0.606534	Adora1/Ak
GO_BP_m1	GO:190303	negative re	15/2606	118/23843	0.307336	0.637858	0.606534	Adam8/Arg
GO_BP_m1	GO:000617	cAMP biosy	9/2606	67/23843	0.308105	0.637858	0.606534	Adcy4/Adr
GO_BP_m1	GO:001063	negative re	9/2606	67/23843	0.308105	0.637858	0.606534	Adamts9/S
GO_BP_m1	GO:190589	regulation	9/2606	67/23843	0.308105	0.637858	0.606534	Bcap31/Bo
GO_BP_m1	GO:000026	mitochond	6/2606	42/23843	0.308109	0.637858	0.606534	Bnip3/Dcn/
GO_BP_m1	GO:000695	acute-phas	6/2606	42/23843	0.308109	0.637858	0.606534	Ednrb/Il1rn
GO_BP_m1	GO:001820	peptidyl-pr	6/2606	42/23843	0.308109	0.637858	0.606534	Egln3/Fkbp
GO_BP_m1	GO:003157	spindle che	6/2606	42/23843	0.308109	0.637858	0.606534	Klhl22/Mac
GO_BP_m1	GO:003419	cellular res	6/2606	42/23843	0.308109	0.637858	0.606534	Atf3/Cdkn1
GO_BP_m1	GO:004250	serine phos	6/2606	42/23843	0.308109	0.637858	0.606534	Cdk5/Gm1
GO_BP_m1	GO:004361	keratinocyt	6/2606	42/23843	0.308109	0.637858	0.606534	Slurp2/Ctsl
GO_BP_m1	GO:004363	RNA polya	6/2606	42/23843	0.308109	0.637858	0.606534	Cpeb3/Cps
GO_BP_m1	GO:005091	positive ch	6/2606	42/23843	0.308109	0.637858	0.606534	Fgf7/Fpr2/
GO_BP_m1	GO:009031	regulation	6/2606	42/23843	0.308109	0.637858	0.606534	BC004004/
GO_BP_m1	GO:001988	antigen pro	13/2606	101/23843	0.308921	0.639184	0.607795	Calr/Gm11
GO_BP_m1	GO:200037	positive reg	13/2606	101/23843	0.308921	0.639184	0.607795	Cd36/Cdkn
GO_BP_m1	GO:004639	ribose pho	32/2606	266/23843	0.308968	0.639184	0.607795	Adcy4/Adr
GO_BP_m1	GO:003017	negative re	18/2606	144/23843	0.309115	0.639187	0.607797	Cav1/Cdh1
GO_BP_m1	GO:006040	calcium ion	18/2606	144/23843	0.309115	0.639187	0.607797	Adcyap1r1/
GO_BP_m1	GO:004825	regulation	11/2606	84/23843	0.309446	0.63957	0.608161	Anxa2/Cd6
GO_BP_m1	GO:190352	positive reg	11/2606	84/23843	0.309446	0.63957	0.608161	Adm/Adra1
GO_BP_m1	GO:003134	positive reg	51/2606	434/23843	0.31179	0.64013	0.608694	Abl2/Ache/
GO_BP_m1	GO:004633	positive reg	16/2606	127/23843	0.311929	0.64013	0.608694	Ctgf/Gab1/
GO_BP_m1	GO:003139	regulation	22/2606	179/23843	0.312278	0.64013	0.608694	5730559C1
GO_BP_m1	GO:000267	positive reg	5/2606	34/23843	0.312339	0.64013	0.608694	Adam8/Ao
GO_BP_m1	GO:000320	cardiac atri	5/2606	34/23843	0.312339	0.64013	0.608694	Cfc1/Dll4/
GO_BP_m1	GO:003026	chromosom	5/2606	34/23843	0.312339	0.64013	0.608694	Cdk1/Hils1
GO_BP_m1	GO:003273	positive reg	5/2606	34/23843	0.312339	0.64013	0.608694	5730559C1
GO_BP_m1	GO:003314	negative re	5/2606	34/23843	0.312339	0.64013	0.608694	Arntl/Calr/
GO_BP_m1	GO:003511	embryonic	5/2606	34/23843	0.312339	0.64013	0.608694	Alx3/Meco
GO_BP_m1	GO:004274	circadian sl	5/2606	34/23843	0.312339	0.64013	0.608694	Adora1/Dr
GO_BP_m1	GO:007028	axonemal c	5/2606	34/23843	0.312339	0.64013	0.608694	Ccdc63/Dn
GO_BP_m1	GO:007182	plasma lipo	5/2606	34/23843	0.312339	0.64013	0.608694	Dgat1/Mttp
GO_BP_m1	GO:000152	pseudouric	3/2606	18/23843	0.313643	0.64013	0.608694	Nop10/Rpu
GO_BP_m1	GO:000195	positive reg	3/2606	18/23843	0.313643	0.64013	0.608694	Snca/Stx1b
GO_BP_m1	GO:000209	tRNA wobb	3/2606	18/23843	0.313643	0.64013	0.608694	6430573F1
GO_BP_m1	GO:000309	glomerular	3/2606	18/23843	0.313643	0.64013	0.608694	Adora1/Uts
GO_BP_m1	GO:000598	glycogen c	3/2606	18/23843	0.313643	0.64013	0.608694	Ppp1r3d/P
GO_BP_m1	GO:000649	N-glycan p	3/2606	18/23843	0.313643	0.64013	0.608694	Fut8/Man1
GO_BP_m1	GO:000659	polyamine	3/2606	18/23843	0.313643	0.64013	0.608694	Agmat/Oaz
GO_BP_m1	GO:000668	glycosphin	3/2606	18/23843	0.313643	0.64013	0.608694	B4galt3/St6

GO_BP_m1	GO:00092	glucan cat	3/2606	18/23843	0.313643	0.64013	0.608694	Ppp1r3d/P
GO_BP_m1	GO:00093	amine bios	3/2606	18/23843	0.313643	0.64013	0.608694	Agmat/Hd
GO_BP_m1	GO:00108	regulation	3/2606	18/23843	0.313643	0.64013	0.608694	Hdac1/Hd
GO_BP_m1	GO:00108	regulation	3/2606	18/23843	0.313643	0.64013	0.608694	Dhrs7c/Fk
GO_BP_m1	GO:00200	hemoglobi	3/2606	18/23843	0.313643	0.64013	0.608694	Eif2ak1/Pr
GO_BP_m1	GO:002151	ventral spi	3/2606	18/23843	0.313643	0.64013	0.608694	Dbx1/Dll4/
GO_BP_m1	GO:00217	preganglio	3/2606	18/23843	0.313643	0.64013	0.608694	Hoxb1/Sen
GO_BP_m1	GO:00308	negative r	3/2606	18/23843	0.313643	0.64013	0.608694	Ctla4/Il10/
GO_BP_m1	GO:00316	regulation	3/2606	18/23843	0.313643	0.64013	0.608694	Cactin/Prk
GO_BP_m1	GO:00321	transpositi	3/2606	18/23843	0.313643	0.64013	0.608694	Btbd18/Dd
GO_BP_m1	GO:00341	toll-like re	3/2606	18/23843	0.313643	0.64013	0.608694	Cav1/Ptpn
GO_BP_m1	GO:00345	protein loc	3/2606	18/23843	0.313643	0.64013	0.608694	Cdk1/Mtb
GO_BP_m1	GO:00355	purinergic	3/2606	18/23843	0.313643	0.64013	0.608694	Acpp/Ado
GO_BP_m1	GO:00361	outer dyne	3/2606	18/23843	0.313643	0.64013	0.608694	Ccdc63/Dn
GO_BP_m1	GO:00361	inner dyne	3/2606	18/23843	0.313643	0.64013	0.608694	Dnaaf1/Dn
GO_BP_m1	GO:00424	cellular bio	3/2606	18/23843	0.313643	0.64013	0.608694	Agmat/Hd
GO_BP_m1	GO:00424	melanin bi	3/2606	18/23843	0.313643	0.64013	0.608694	Dct/Ddt/Ty
GO_BP_m1	GO:004257	retinol met	3/2606	18/23843	0.313643	0.64013	0.608694	Adh1/Rets
GO_BP_m1	GO:004337	negative r	3/2606	18/23843	0.313643	0.64013	0.608694	Jak3/Smad
GO_BP_m1	GO:00435	regulation	3/2606	18/23843	0.313643	0.64013	0.608694	Eif2ak1/Eif
GO_BP_m1	GO:00456	negative r	3/2606	18/23843	0.313643	0.64013	0.608694	Jak3/Smad
GO_BP_m1	GO:00463	positive re	3/2606	18/23843	0.313643	0.64013	0.608694	Dgat1/Plin
GO_BP_m1	GO:004647	glyceroph	3/2606	18/23843	0.313643	0.64013	0.608694	Enpp2/Prd
GO_BP_m1	GO:004871	negative r	3/2606	18/23843	0.313643	0.64013	0.608694	Mbd1/Nf1
GO_BP_m1	GO:005091	detection	3/2606	18/23843	0.313643	0.64013	0.608694	Myc/Slc12
GO_BP_m1	GO:00509	detection	3/2606	18/23843	0.313643	0.64013	0.608694	Adora1/An
GO_BP_m1	GO:00509	detection	3/2606	18/23843	0.313643	0.64013	0.608694	Adora1/An
GO_BP_m1	GO:00718	regulation	3/2606	18/23843	0.313643	0.64013	0.608694	Fscn1/Gsn
GO_BP_m1	GO:009881	neurotrans	3/2606	18/23843	0.313643	0.64013	0.608694	Gdnf/Park
GO_BP_m1	GO:19034	regulation	3/2606	18/23843	0.313643	0.64013	0.608694	Dnm3/Stx1
GO_BP_m1	GO:19043	cellular res	3/2606	18/23843	0.313643	0.64013	0.608694	Camk2a/C
GO_BP_m1	GO:199077	response t	3/2606	18/23843	0.313643	0.64013	0.608694	Camk2a/C
GO_BP_m1	GO:00076	rhythmic b	8/2606	59/23843	0.314657	0.64013	0.608694	Adora1/Cs
GO_BP_m1	GO:00603	face devel	8/2606	59/23843	0.314657	0.64013	0.608694	Aldh1a3/A
GO_BP_m1	GO:00020	positive re	4/2606	26/23843	0.314964	0.64013	0.608694	Dct/Dmrta
GO_BP_m1	GO:00020	lens morp	4/2606	26/23843	0.314964	0.64013	0.608694	Bcar3/Eph
GO_BP_m1	GO:001474	negative r	4/2606	26/23843	0.314964	0.64013	0.608694	Atp2b4/Ca
GO_BP_m1	GO:003021	hyalurona	4/2606	26/23843	0.314964	0.64013	0.608694	Has2/Hyal
GO_BP_m1	GO:003097	retrograde	4/2606	26/23843	0.314964	0.64013	0.608694	Bcap31/Hs
GO_BP_m1	GO:00458	positive re	4/2606	26/23843	0.314964	0.64013	0.608694	Ifng/Ptprc/
GO_BP_m1	GO:00515	mitochond	4/2606	26/23843	0.314964	0.64013	0.608694	Bcap31/Bn
GO_BP_m1	GO:00519	positive re	4/2606	26/23843	0.314964	0.64013	0.608694	Abat/Avpr
GO_BP_m1	GO:006091	heart form	4/2606	26/23843	0.314964	0.64013	0.608694	Ift88/Lemd
GO_BP_m1	GO:006131	cell surface	4/2606	26/23843	0.314964	0.64013	0.608694	Dll4/Jag1/
GO_BP_m1	GO:00614	renal syste	4/2606	26/23843	0.314964	0.64013	0.608694	Ifng/Osr1/
GO_BP_m1	GO:006144	kidney vas	4/2606	26/23843	0.314964	0.64013	0.608694	Ifng/Osr1/
GO_BP_m1	GO:007154	cellular res	4/2606	26/23843	0.314964	0.64013	0.608694	Eif4e/Gdnf
GO_BP_m1	GO:00901	regulation	4/2606	26/23843	0.314964	0.64013	0.608694	Dgkq/Eph

GO_BP_m1	GO:009050	RNA phosp	4/2606	26/23843	0.314964	0.64013	0.608694	Bms1/Elac1
GO_BP_m1	GO:190275	positive reg	4/2606	26/23843	0.314964	0.64013	0.608694	Cdc25a/Cd
GO_BP_m1	GO:190351	endoplasm	4/2606	26/23843	0.314964	0.64013	0.608694	Bcap31/Hs
GO_BP_m1	GO:200017	negative re	4/2606	26/23843	0.314964	0.64013	0.608694	Btg2/Cend
GO_BP_m1	GO:000279	positive reg	36/2606	302/23843	0.315295	0.640655	0.609193	Abat/Abl2/
GO_BP_m1	GO:000700	mitochond	12/2606	93/23843	0.316005	0.641427	0.609928	Bnip3/Bok/
GO_BP_m1	GO:001077	negative re	12/2606	93/23843	0.316005	0.641427	0.609928	Aatk/Bcar1
GO_BP_m1	GO:003027	negative re	12/2606	93/23843	0.316005	0.641427	0.609928	Calcr/Ccr1/
GO_BP_m1	GO:190274	regulation	12/2606	93/23843	0.316005	0.641427	0.609928	Blm/Baban
GO_BP_m1	GO:001657	histone me	17/2606	136/23843	0.31604	0.641427	0.609928	Ash2l/Dmr
GO_BP_m1	GO:000175	somitogen	10/2606	76/23843	0.316466	0.641995	0.610468	Abi1/Foxa2
GO_BP_m1	GO:003433	adherens ju	10/2606	76/23843	0.316466	0.641995	0.610468	Bcas3/Cfl1/
GO_BP_m1	GO:004505	regulated e	24/2606	197/23843	0.317567	0.64408	0.612451	Abca12/Ar
GO_BP_m1	GO:000647	protein me	21/2606	171/23843	0.319059	0.646544	0.614793	Ash2l/Btg2
GO_BP_m1	GO:000821	protein alky	21/2606	171/23843	0.319059	0.646544	0.614793	Ash2l/Btg2
GO_BP_m1	GO:004259	response to	21/2606	171/23843	0.319059	0.646544	0.614793	Aoc1/Atf3/
GO_BP_m1	GO:004648	phosphatic	15/2606	119/23843	0.319076	0.646544	0.614793	Bpnt1/Fpr2
GO_BP_m1	GO:000834	glial cell mi	7/2606	51/23843	0.321366	0.649983	0.618064	Arhgef7/Cc
GO_BP_m1	GO:003260	interferon-	7/2606	51/23843	0.321366	0.649983	0.618064	Cactin/Nm
GO_BP_m1	GO:003265	regulation	7/2606	51/23843	0.321366	0.649983	0.618064	Cd36/Ifng/
GO_BP_m1	GO:005081	negative re	7/2606	51/23843	0.321366	0.649983	0.618064	Abat/Alox1
GO_BP_m1	GO:005085	regulation	7/2606	51/23843	0.321366	0.649983	0.618064	Btnl2/Dusp
GO_BP_m1	GO:005129	protein het	7/2606	51/23843	0.321366	0.649983	0.618064	Anxa2/Cbr
GO_BP_m1	GO:006500	intracellula	7/2606	51/23843	0.321366	0.649983	0.618064	Bcr/Grpel1/
GO_BP_m1	GO:200051	regulation	7/2606	51/23843	0.321366	0.649983	0.618064	Ifng/Il2rg/J
GO_BP_m1	GO:000195	regulation	13/2606	102/23843	0.321662	0.650432	0.618491	Bcas3/Ccl2
GO_BP_m1	GO:007145	cellular res	16/2606	128/23843	0.323299	0.65287	0.620809	Adam8/Bn
GO_BP_m1	GO:200125	negative re	16/2606	128/23843	0.323299	0.65287	0.620809	Apobec1/H
GO_BP_m1	GO:000236	cytokine pr	11/2606	85/23843	0.323462	0.65287	0.620809	5730559C1
GO_BP_m1	GO:000270	positive reg	11/2606	85/23843	0.323462	0.65287	0.620809	Cd36/Gprc
GO_BP_m1	GO:000721	neuropepti	11/2606	85/23843	0.323462	0.65287	0.620809	Cartpt/Cysl
GO_BP_m1	GO:004277	signal trans	11/2606	85/23843	0.323462	0.65287	0.620809	Ankrd1/Atr
GO_BP_m1	GO:004350	regulation	11/2606	85/23843	0.323462	0.65287	0.620809	Adk/Akap6
GO_BP_m1	GO:004568	regulation	11/2606	85/23843	0.323462	0.65287	0.620809	Drd3/Enpp
GO_BP_m1	GO:007180	cellular pot	23/2606	189/23843	0.324371	0.654404	0.622268	Akap6/Atp
GO_BP_m1	GO:007180	potassium	23/2606	189/23843	0.324371	0.654404	0.622268	Akap6/Atp
GO_BP_m1	GO:005125	protein pol	32/2606	268/23843	0.324587	0.65469	0.622539	Ankrd53/C
GO_BP_m1	GO:190370	positive reg	24/2606	198/23843	0.32672	0.65884	0.626486	Adam8/Cas
GO_BP_m1	GO:000641	regulation	47/2606	401/23843	0.327215	0.659687	0.62729	Btg2/Calr/C
GO_BP_m1	GO:000325	regulation	6/2606	43/23843	0.328148	0.660658	0.628214	Alox12/Bok
GO_BP_m1	GO:000604	amino suga	6/2606	43/23843	0.328148	0.660658	0.628214	Chil5/Csga
GO_BP_m1	GO:001025	NADH deh	6/2606	43/23843	0.328148	0.660658	0.628214	Aifm1/Ndu
GO_BP_m1	GO:001802	peptidyl-ly	6/2606	43/23843	0.328148	0.660658	0.628214	Dmrtc2/Ee
GO_BP_m1	GO:003016	proteoglyc	6/2606	43/23843	0.328148	0.660658	0.628214	Chst13/Csg
GO_BP_m1	GO:003298	mitochond	6/2606	43/23843	0.328148	0.660658	0.628214	Aifm1/Ndu
GO_BP_m1	GO:003241	positive reg	12/2606	94/23843	0.329407	0.662889	0.630336	Abcb1a/Ak
GO_BP_m1	GO:004563	negative re	12/2606	94/23843	0.329407	0.662889	0.630336	Cartpt/Cib1
GO_BP_m1	GO:000911	ribonucleos	10/2606	77/23843	0.331343	0.663168	0.630601	Acpp/Adk/

GO_BP_m1	GO:00331	mitochond	10/2606	77/23843	0.331343	0.663168	0.630601	Aifm1/Ndu
GO_BP_m1	GO:006164	cytoskeletc	10/2606	77/23843	0.331343	0.663168	0.630601	Ankrd53/C
GO_BP_m1	GO:00027	regulation	8/2606	60/23843	0.331577	0.663168	0.630601	Arg1/Clec4
GO_BP_m1	GO:00336	cellular pol	8/2606	60/23843	0.331577	0.663168	0.630601	B3gnt3/B3
GO_BP_m1	GO:007147	cellular res	8/2606	60/23843	0.331577	0.663168	0.630601	Atr/Blm/Cc
GO_BP_m1	GO:190581	regulation	8/2606	60/23843	0.331577	0.663168	0.630601	Cdc23/Klhl
GO_BP_m1	GO:20007	regulation	8/2606	60/23843	0.331577	0.663168	0.630601	Flcn/Hdac1
GO_BP_m1	GO:004851	rhythmic p	32/2606	269/23843	0.332485	0.663168	0.630601	Adamts1/A
GO_BP_m1	GO:00508	protein sta	19/2606	155/23843	0.333528	0.663168	0.630601	Atp1b2/Ca
GO_BP_m1	GO:003241	positive re	13/2606	103/23843	0.334524	0.663168	0.630601	Abcb1a/Ak
GO_BP_m1	GO:004867	axon exten	16/2606	129/23843	0.334772	0.663168	0.630601	Aatk/Cdk5
GO_BP_m1	GO:000727	neuromusc	5/2606	35/23843	0.334809	0.663168	0.630601	Chrm1/Chr
GO_BP_m1	GO:00310	hair follicle	5/2606	35/23843	0.334809	0.663168	0.630601	Ctsl/Fgf7/F
GO_BP_m1	GO:003314	positive re	5/2606	35/23843	0.334809	0.663168	0.630601	Gm13271/
GO_BP_m1	GO:00359	aorta morp	5/2606	35/23843	0.334809	0.663168	0.630601	Adamts9/D
GO_BP_m1	GO:004647	phosphatic	5/2606	35/23843	0.334809	0.663168	0.630601	Abhd1/Enp
GO_BP_m1	GO:00466	alpha-beta	5/2606	35/23843	0.334809	0.663168	0.630601	Blm/Cd80/
GO_BP_m1	GO:004814	negative re	5/2606	35/23843	0.334809	0.663168	0.630601	Dach1/Ifng
GO_BP_m1	GO:19013	positive re	5/2606	35/23843	0.334809	0.663168	0.630601	Akap6/Atp
GO_BP_m1	GO:00512	protein ho	41/2606	349/23843	0.335384	0.663168	0.630601	Acpp/Aldh
GO_BP_m1	GO:000611	energy res	11/2606	86/23843	0.337612	0.663168	0.630601	Esrrb/Gys1
GO_BP_m1	GO:00512	protein ho	11/2606	86/23843	0.337612	0.663168	0.630601	Acpp/Aldh
GO_BP_m1	GO:00513	chromosor	11/2606	86/23843	0.337612	0.663168	0.630601	Cdc23/Klhl
GO_BP_m1	GO:000027	polysaccha	9/2606	69/23843	0.339708	0.663168	0.630601	B3gnt3/B3
GO_BP_m1	GO:00455	negative re	7/2606	52/23843	0.339738	0.663168	0.630601	Arntl/Asxl1
GO_BP_m1	GO:00718	protein tra	7/2606	52/23843	0.339738	0.663168	0.630601	Bcr/Grpel1
GO_BP_m1	GO:00725	pyrimidine	7/2606	52/23843	0.339738	0.663168	0.630601	Acpp/Dpy
GO_BP_m1	GO:007267	T cell migr	7/2606	52/23843	0.339738	0.663168	0.630601	Adam8/Ccl
GO_BP_m1	GO:000191	regulation	4/2606	27/23843	0.340875	0.663168	0.630601	Fam49b/Il1
GO_BP_m1	GO:00033	metanephr	4/2606	27/23843	0.340875	0.663168	0.630601	Gdnf/Lgr4/
GO_BP_m1	GO:00107	regulation	4/2606	27/23843	0.340875	0.663168	0.630601	Akap6/C33
GO_BP_m1	GO:00215	cell differer	4/2606	27/23843	0.340875	0.663168	0.630601	Cend1/Fox
GO_BP_m1	GO:00331	negative re	4/2606	27/23843	0.340875	0.663168	0.630601	Cav1/Nck2
GO_BP_m1	GO:004411	growth inv	4/2606	27/23843	0.340875	0.663168	0.630601	Cd36/Ifng/
GO_BP_m1	GO:004411	growth of	4/2606	27/23843	0.340875	0.663168	0.630601	Cd36/Ifng/
GO_BP_m1	GO:00701	protein loc	4/2606	27/23843	0.340875	0.663168	0.630601	Atr/H2afy/
GO_BP_m1	GO:009031	positive re	4/2606	27/23843	0.340875	0.663168	0.630601	BC004004/
GO_BP_m1	GO:00973	mitochond	4/2606	27/23843	0.340875	0.663168	0.630601	Bnip3/Bok
GO_BP_m1	GO:20003	regulation	4/2606	27/23843	0.340875	0.663168	0.630601	Fmr1/Rab5
GO_BP_m1	GO:007177	response t	22/2606	182/23843	0.341158	0.663168	0.630601	Bmp3/Cav
GO_BP_m1	GO:007177	cellular res	22/2606	182/23843	0.341158	0.663168	0.630601	Bmp3/Cav
GO_BP_m1	GO:00000	urea cycle	2/2606	11/23843	0.342216	0.663168	0.630601	Arg1/Otc
GO_BP_m1	GO:00004	small nucle	2/2606	11/23843	0.342216	0.663168	0.630601	Gm3086/T
GO_BP_m1	GO:00017	natural kill	2/2606	11/23843	0.342216	0.663168	0.630601	Il12b/Ptpn
GO_BP_m1	GO:000257	positive re	2/2606	11/23843	0.342216	0.663168	0.630601	Nod1/Pyca
GO_BP_m1	GO:00061	succinate n	2/2606	11/23843	0.342216	0.663168	0.630601	Sdhaf3/Sdh
GO_BP_m1	GO:000627	lagging str	2/2606	11/23843	0.342216	0.663168	0.630601	Fen1/Lig3
GO_BP_m1	GO:00065	arginine ca	2/2606	11/23843	0.342216	0.663168	0.630601	Arg1/Atp2

GO_BP_m1	GO:000665	phosphatic	2/2606	11/23843	0.342216	0.663168	0.630601	Agpat2/Dg
GO_BP_m1	GO:000695	complemer	2/2606	11/23843	0.342216	0.663168	0.630601	Cfd/Susd4
GO_BP_m1	GO:000912	nucleoside	2/2606	11/23843	0.342216	0.663168	0.630601	Dnph1/Nt5
GO_BP_m1	GO:000926	2'-deoxyrib	2/2606	11/23843	0.342216	0.663168	0.630601	Adk/Shmt1
GO_BP_m1	GO:000939	folic acid-c	2/2606	11/23843	0.342216	0.663168	0.630601	Gch1/Mthf
GO_BP_m1	GO:001073	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	C330021F2
GO_BP_m1	GO:001580	arginine tra	2/2606	11/23843	0.342216	0.663168	0.630601	Arg1/AU01
GO_BP_m1	GO:001708	response to	2/2606	11/23843	0.342216	0.663168	0.630601	Mapk13/Zc
GO_BP_m1	GO:002189	cerebral co	2/2606	11/23843	0.342216	0.663168	0.630601	Arx/Rac3
GO_BP_m1	GO:003095	astral micro	2/2606	11/23843	0.342216	0.663168	0.630601	Ezr/Tacc2
GO_BP_m1	GO:003107	post-embr	2/2606	11/23843	0.342216	0.663168	0.630601	Krtap21-1/
GO_BP_m1	GO:003150	heterochro	2/2606	11/23843	0.342216	0.663168	0.630601	Bahd1/Tpr
GO_BP_m1	GO:003332	Leydig cell	2/2606	11/23843	0.342216	0.663168	0.630601	Map7/Pdg
GO_BP_m1	GO:003437	high-densi	2/2606	11/23843	0.342216	0.663168	0.630601	Pltp/Scarb1
GO_BP_m1	GO:003477	response to	2/2606	11/23843	0.342216	0.663168	0.630601	Aoc1/Drd3
GO_BP_m1	GO:003533	fatty-acyl-	2/2606	11/23843	0.342216	0.663168	0.630601	Dgat1/Hsd
GO_BP_m1	GO:003537	sterol impo	2/2606	11/23843	0.342216	0.663168	0.630601	Cd36/Scarb
GO_BP_m1	GO:003593	glucocortic	2/2606	11/23843	0.342216	0.663168	0.630601	Galr1/Tac1
GO_BP_m1	GO:003609	germ cell p	2/2606	11/23843	0.342216	0.663168	0.630601	Cib1/Dmrt
GO_BP_m1	GO:003806	collagen-a	2/2606	11/23843	0.342216	0.663168	0.630601	Col4a2/Ub
GO_BP_m1	GO:003816	angiotensir	2/2606	11/23843	0.342216	0.663168	0.630601	Camk2a/Ca
GO_BP_m1	GO:004356	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Ift88/Igfbp
GO_BP_m1	GO:004365	mitochond	2/2606	11/23843	0.342216	0.663168	0.630601	Bnip3/Park
GO_BP_m1	GO:004514	meiotic sist	2/2606	11/23843	0.342216	0.663168	0.630601	Ppp2r1a/Sy
GO_BP_m1	GO:004587	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Fen1/H2afy
GO_BP_m1	GO:004592	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Avpr1a/Drd
GO_BP_m1	GO:004600	negative re	2/2606	11/23843	0.342216	0.663168	0.630601	Arg1/Lrrc3
GO_BP_m1	GO:004604	IMP metab	2/2606	11/23843	0.342216	0.663168	0.630601	Adss/Nt5c2
GO_BP_m1	GO:004638	deoxyribos	2/2606	11/23843	0.342216	0.663168	0.630601	Adk/Shmt1
GO_BP_m1	GO:004831	intracellula	2/2606	11/23843	0.342216	0.663168	0.630601	Kat2a/Ogt
GO_BP_m1	GO:005113	NK T cell a	2/2606	11/23843	0.342216	0.663168	0.630601	Hsph1/Il12
GO_BP_m1	GO:005115	negative re	2/2606	11/23843	0.342216	0.663168	0.630601	Med28/Rb
GO_BP_m1	GO:005154	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Fgf7/Has2
GO_BP_m1	GO:005163	actin filame	2/2606	11/23843	0.342216	0.663168	0.630601	Pls1/Pls3
GO_BP_m1	GO:005190	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Alox12/Dcr
GO_BP_m1	GO:006007	micturition	2/2606	11/23843	0.342216	0.663168	0.630601	Adra1d/Htr
GO_BP_m1	GO:006015	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Drd3/Rgs8
GO_BP_m1	GO:006021	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Btg2/Cpeb
GO_BP_m1	GO:006021	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Btg2/Cpeb
GO_BP_m1	GO:007047	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Abat/Tacr2
GO_BP_m1	GO:007049	thrombin-a	2/2606	11/23843	0.342216	0.663168	0.630601	Dgkq/Snca
GO_BP_m1	GO:007050	cholesterol	2/2606	11/23843	0.342216	0.663168	0.630601	Cd36/Scarb
GO_BP_m1	GO:007058	cell-cell ad	2/2606	11/23843	0.342216	0.663168	0.630601	Il10/Il1rn
GO_BP_m1	GO:007131	cellular res	2/2606	11/23843	0.342216	0.663168	0.630601	Hsp90b1/S
GO_BP_m1	GO:007160	otic vesicle	2/2606	11/23843	0.342216	0.663168	0.630601	Stox1/Tbx1
GO_BP_m1	GO:007173	cellular res	2/2606	11/23843	0.342216	0.663168	0.630601	Bcar1/Kcnc
GO_BP_m1	GO:007212	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Ifng/Wt1
GO_BP_m1	GO:007217	nephric du	2/2606	11/23843	0.342216	0.663168	0.630601	Epha7/Osr

GO_BP_m1	GO:007258	caveolin-m	2/2606	11/23843	0.342216	0.663168	0.630601	Cav1/Cav3
GO_BP_m1	GO:009039	negative re	2/2606	11/23843	0.342216	0.663168	0.630601	Nlgn3/Park
GO_BP_m1	GO:009709	synaptic ve	2/2606	11/23843	0.342216	0.663168	0.630601	Cdh2/Nlgn
GO_BP_m1	GO:009872	asymmetric	2/2606	11/23843	0.342216	0.663168	0.630601	Dock7/Fgf1
GO_BP_m1	GO:009879	xenophagy	2/2606	11/23843	0.342216	0.663168	0.630601	Nod1/Wipi
GO_BP_m1	GO:010607	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Atp2b4/Op
GO_BP_m1	GO:190036	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Cpeb3/Sup
GO_BP_m1	GO:190223	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Fbxo18/Ski
GO_BP_m1	GO:190245	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Esrrb/Kdm2
GO_BP_m1	GO:190342	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Dnm3/Synj
GO_BP_m1	GO:199044	positive reg	2/2606	11/23843	0.342216	0.663168	0.630601	Atf3/Creb3
GO_BP_m1	GO:200032	regulation	2/2606	11/23843	0.342216	0.663168	0.630601	Arntl/Clock
GO_BP_m1	GO:000327	cardiac sep	15/2606	121/23843	0.342881	0.663168	0.630601	Cfc1/Cntrl/
GO_BP_m1	GO:007124	cellular res	15/2606	121/23843	0.342881	0.663168	0.630601	Aoc1/Asph
GO_BP_m1	GO:004580	positive reg	19/2606	156/23843	0.344048	0.663168	0.630601	Ankfy1/Anx
GO_BP_m1	GO:000249	antigen pro	3/2606	19/23843	0.345006	0.663168	0.630601	H2-DMb2/
GO_BP_m1	GO:000608	lactate met	3/2606	19/23843	0.345006	0.663168	0.630601	Haghl/Ldha
GO_BP_m1	GO:000610	2-oxogluta	3/2606	19/23843	0.345006	0.663168	0.630601	Got1/Idh3a
GO_BP_m1	GO:000634	methylation	3/2606	19/23843	0.345006	0.663168	0.630601	Apobec1/H
GO_BP_m1	GO:001062	programme	3/2606	19/23843	0.345006	0.663168	0.630601	Casp6/Kitl/
GO_BP_m1	GO:001608	synaptic ve	3/2606	19/23843	0.345006	0.663168	0.630601	Snap29/Stx
GO_BP_m1	GO:003545	cargo load	3/2606	19/23843	0.345006	0.663168	0.630601	Mia3/Sec24
GO_BP_m1	GO:004304	DNA methy	3/2606	19/23843	0.345006	0.663168	0.630601	Ddx4/Fkbp
GO_BP_m1	GO:004424	cellular pol	3/2606	19/23843	0.345006	0.663168	0.630601	Ppp1r3d/Py
GO_BP_m1	GO:004564	regulation	3/2606	19/23843	0.345006	0.663168	0.630601	Casp8/Prkc
GO_BP_m1	GO:004683	carbohydra	3/2606	19/23843	0.345006	0.663168	0.630601	Adk/Pfkfb1
GO_BP_m1	GO:004688	positive reg	3/2606	19/23843	0.345006	0.663168	0.630601	Ifng/Por/Pp
GO_BP_m1	GO:005084	negative re	3/2606	19/23843	0.345006	0.663168	0.630601	Atp2b4/Fkb
GO_BP_m1	GO:005088	neuromusc	3/2606	19/23843	0.345006	0.663168	0.630601	Gch1/Tcf15
GO_BP_m1	GO:005138	kinetochore	3/2606	19/23843	0.345006	0.663168	0.630601	Cenpa/Cen
GO_BP_m1	GO:005177	positive reg	3/2606	19/23843	0.345006	0.663168	0.630601	Ccl20/Fnta/
GO_BP_m1	GO:006029	cilium mov	3/2606	19/23843	0.345006	0.663168	0.630601	Bbs2/Dnah
GO_BP_m1	GO:006078	ectoderma	3/2606	19/23843	0.345006	0.663168	0.630601	Hdac1/Hda
GO_BP_m1	GO:007020	protein het	3/2606	19/23843	0.345006	0.663168	0.630601	Nup54/Og
GO_BP_m1	GO:007142	rRNA-cont	3/2606	19/23843	0.345006	0.663168	0.630601	Nmd3/Rasl
GO_BP_m1	GO:007169	ectoderma	3/2606	19/23843	0.345006	0.663168	0.630601	Hdac1/Hda
GO_BP_m1	GO:009020	negative re	3/2606	19/23843	0.345006	0.663168	0.630601	Gpx1/Higd
GO_BP_m1	GO:190188	negative re	3/2606	19/23843	0.345006	0.663168	0.630601	Bcas3/Itgb
GO_BP_m1	GO:190230	positive reg	3/2606	19/23843	0.345006	0.663168	0.630601	Atp1b2/Fxy
GO_BP_m1	GO:200001	positive reg	3/2606	19/23843	0.345006	0.663168	0.630601	Abca12/Nr
GO_BP_m1	GO:200078	negative re	3/2606	19/23843	0.345006	0.663168	0.630601	Fbxo18/Nu
GO_BP_m1	GO:003267	regulation	16/2606	130/23843	0.346336	0.663168	0.630601	5730559C1
GO_BP_m1	GO:190330	regulation	16/2606	130/23843	0.346336	0.663168	0.630601	Bcr/Catspe
GO_BP_m1	GO:004584	positive reg	10/2606	78/23843	0.346348	0.663168	0.630601	Akap6/Arn
GO_BP_m1	GO:004863	positive reg	10/2606	78/23843	0.346348	0.663168	0.630601	Akap6/Arn
GO_BP_m1	GO:004870	astrocyte d	10/2606	78/23843	0.346348	0.663168	0.630601	Abl2/Fpr2/
GO_BP_m1	GO:006007	excitatory p	10/2606	78/23843	0.346348	0.663168	0.630601	Adora1/Cd
GO_BP_m1	GO:006041	cardiac sep	10/2606	78/23843	0.346348	0.663168	0.630601	Cfc1/Ift88/

GO_BP_m1	GO:004863	regulation	20/2606	165/23843	0.34656	0.663168	0.630601	Akap6/Arn
GO_BP_m1	GO:000270	negative re	6/2606	44/23843	0.348346	0.663168	0.630601	Arg1/Clec4
GO_BP_m1	GO:004326	positive reg	6/2606	44/23843	0.348346	0.663168	0.630601	Adora1/Ak
GO_BP_m1	GO:000188	endothelial	8/2606	61/23843	0.348639	0.663168	0.630601	Cldn1/Ezr/
GO_BP_m1	GO:001644	somatic div	8/2606	61/23843	0.348639	0.663168	0.630601	Aplf/Ifng/Il
GO_BP_m1	GO:005077	negative re	8/2606	61/23843	0.348639	0.663168	0.630601	Aatk/Cdk5/
GO_BP_m1	GO:190305	negative re	8/2606	61/23843	0.348639	0.663168	0.630601	N4bp1/Og
GO_BP_m1	GO:005079	regulation	21/2606	174/23843	0.348844	0.663168	0.630601	Abat/Ano1
GO_BP_m1	GO:007137	cellular res	27/2606	227/23843	0.350247	0.663168	0.630601	Appl1/Bcar
GO_BP_m1	GO:003252	response to	11/2606	87/23843	0.351875	0.663168	0.630601	Abl2/Adh1
GO_BP_m1	GO:005165	establishm	47/2606	405/23843	0.353322	0.663168	0.630601	Ankrd53/B
GO_BP_m1	GO:004863	negative re	9/2606	70/23843	0.355705	0.663168	0.630601	Cav3/Ephb
GO_BP_m1	GO:009030	mitotic spir	9/2606	70/23843	0.355705	0.663168	0.630601	Cdc20/Chr
GO_BP_m1	GO:004578	positive reg	40/2606	343/23843	0.355802	0.663168	0.630601	BC004004/
GO_BP_m1	GO:001567	monovaler	53/2606	459/23843	0.356159	0.663168	0.630601	Adora1/Ad
GO_BP_m1	GO:003007	insulin secr	25/2606	210/23843	0.3562	0.663168	0.630601	Abat/Ano1
GO_BP_m1	GO:000704	cell-cell jur	12/2606	96/23843	0.356549	0.663168	0.630601	Cav1/Cdh1
GO_BP_m1	GO:004577	positive reg	12/2606	96/23843	0.356549	0.663168	0.630601	Clic1/Cthrc
GO_BP_m1	GO:009026	positive reg	12/2606	96/23843	0.356549	0.663168	0.630601	Arntl/Capri
GO_BP_m1	GO:004352	negative re	20/2606	166/23843	0.356881	0.663168	0.630601	Adam8/Bo
GO_BP_m1	GO:000046	maturation	5/2606	36/23843	0.357407	0.663168	0.630601	Bms1/Kri1/
GO_BP_m1	GO:000156	response to	5/2606	36/23843	0.357407	0.663168	0.630601	Arg1/Ifng/I
GO_BP_m1	GO:001009	specificatio	5/2606	36/23843	0.357407	0.663168	0.630601	Fgf1/Gdnf/
GO_BP_m1	GO:001073	protein kin	5/2606	36/23843	0.357407	0.663168	0.630601	Akap6/C33
GO_BP_m1	GO:003410	positive reg	5/2606	36/23843	0.357407	0.663168	0.630601	Adam8/Os
GO_BP_m1	GO:003511	embryonic	5/2606	36/23843	0.357407	0.663168	0.630601	Alx3/Meco
GO_BP_m1	GO:004231	vasodilatio	5/2606	36/23843	0.357407	0.663168	0.630601	Adora1/Bb
GO_BP_m1	GO:004239	cellular mo	5/2606	36/23843	0.357407	0.663168	0.630601	Tmem269/
GO_BP_m1	GO:004826	response to	5/2606	36/23843	0.357407	0.663168	0.630601	Ednrb/Gch
GO_BP_m1	GO:004871	regulation	5/2606	36/23843	0.357407	0.663168	0.630601	Mbd1/Nf1/
GO_BP_m1	GO:006138	heart trabe	5/2606	36/23843	0.357407	0.663168	0.630601	Adamts1/C
GO_BP_m1	GO:006190	glial cell ac	5/2606	36/23843	0.357407	0.663168	0.630601	Fpr2/Itgam
GO_BP_m1	GO:190269	regulation	5/2606	36/23843	0.357407	0.663168	0.630601	Dct/Dmrta2
GO_BP_m1	GO:001000	glial cell dif	26/2606	219/23843	0.357686	0.663168	0.630601	Abl2/Ahna
GO_BP_m1	GO:006113	morphoger	26/2606	219/23843	0.357686	0.663168	0.630601	Adm/Cav3/
GO_BP_m1	GO:000252	acute inflar	16/2606	131/23843	0.357981	0.663168	0.630601	Adam8/Ad
GO_BP_m1	GO:003265	regulation	7/2606	53/23843	0.358237	0.663168	0.630601	5730559C1
GO_BP_m1	GO:005099	regulation	7/2606	53/23843	0.358237	0.663168	0.630601	Adora1/An
GO_BP_m1	GO:005193	synaptic tra	7/2606	53/23843	0.358237	0.663168	0.630601	Adora1/Ga
GO_BP_m1	GO:190101	regulation	7/2606	53/23843	0.358237	0.663168	0.630601	Akap6/Atp
GO_BP_m1	GO:190275	negative re	7/2606	53/23843	0.358237	0.663168	0.630601	Blm/Babam
GO_BP_m1	GO:190339	regulation	7/2606	53/23843	0.358237	0.663168	0.630601	Bcas3/Cfl1/
GO_BP_m1	GO:200064	positive reg	7/2606	53/23843	0.358237	0.663168	0.630601	Dct/Dmrta2
GO_BP_m1	GO:000206	epithelial c	28/2606	237/23843	0.360333	0.663168	0.630601	Arntl/Cdh1
GO_BP_m1	GO:003133	positive reg	28/2606	237/23843	0.360333	0.663168	0.630601	Ankrd53/A
GO_BP_m1	GO:190437	regulation	13/2606	105/23843	0.360551	0.663168	0.630601	Appl1/Cam
GO_BP_m1	GO:200017	regulation	13/2606	105/23843	0.360551	0.663168	0.630601	Btg2/Cdh2
GO_BP_m1	GO:000974	response to	22/2606	184/23843	0.360761	0.663168	0.630601	Ano1/Casp

GO_BP_m1	GO:00032	cardiac ver	10/2606	79/23843	0.361457	0.663168	0.630601	Dll4/Foxc1
GO_BP_m1	GO:00485	positive re	10/2606	79/23843	0.361457	0.663168	0.630601	Cfl1/Fkbp6
GO_BP_m1	GO:00702	actin-medi	10/2606	79/23843	0.361457	0.663168	0.630601	Acta2/Aka
GO_BP_m1	GO:19039	negative re	10/2606	79/23843	0.361457	0.663168	0.630601	Eif2ak2/Gs
GO_BP_m1	GO:19040	regulation	10/2606	79/23843	0.361457	0.663168	0.630601	Abl2/Bok/
GO_BP_m1	GO:00487	gland deve	53/2606	460/23843	0.362389	0.663168	0.630601	Aldh1a3/A
GO_BP_m1	GO:00016	response t	23/2606	193/23843	0.362449	0.663168	0.630601	Abat/Adam
GO_BP_m1	GO:00486	regulation	18/2606	149/23843	0.363123	0.663168	0.630601	Alox12/Ca
GO_BP_m1	GO:19016	response t	41/2606	353/23843	0.363611	0.663168	0.630601	5730559C1
GO_BP_m1	GO:001657	protein de	14/2606	114/23843	0.364014	0.663168	0.630601	Asxl1/Eif3f
GO_BP_m1	GO:004217	negative re	14/2606	114/23843	0.364014	0.663168	0.630601	Anxa2/Il10
GO_BP_m1	GO:005071	positive re	32/2606	273/23843	0.364579	0.663168	0.630601	Abat/Abl2/
GO_BP_m1	GO:004521	cell-cell ju	25/2606	211/23843	0.365414	0.663168	0.630601	5730559C1
GO_BP_m1	GO:000267	regulation	8/2606	62/23843	0.365807	0.663168	0.630601	Adam8/Ad
GO_BP_m1	GO:003134	positive re	8/2606	62/23843	0.365807	0.663168	0.630601	Arg1/Cadn
GO_BP_m1	GO:004277	ATP synth	8/2606	62/23843	0.365807	0.663168	0.630601	Cdk1/Coq
GO_BP_m1	GO:000194	lymph vess	4/2606	28/23843	0.36684	0.663168	0.630601	Epha2/Fox
GO_BP_m1	GO:000202	response t	4/2606	28/23843	0.36684	0.663168	0.630601	Ppargc1a/
GO_BP_m1	GO:00067	folic acid-	4/2606	28/23843	0.36684	0.663168	0.630601	Gch1/Mthf
GO_BP_m1	GO:00075	sex determ	4/2606	28/23843	0.36684	0.663168	0.630601	Dmrt1/Nr5
GO_BP_m1	GO:00219	central ner	4/2606	28/23843	0.36684	0.663168	0.630601	Ephb1/Eph
GO_BP_m1	GO:00335	regulation	4/2606	28/23843	0.36684	0.663168	0.630601	Abca12/Al
GO_BP_m1	GO:00357	endothelial	4/2606	28/23843	0.36684	0.663168	0.630601	Fgf1/Fgf16
GO_BP_m1	GO:00435	positive re	4/2606	28/23843	0.36684	0.663168	0.630601	Epha8/Fpr
GO_BP_m1	GO:00445	secondary	4/2606	28/23843	0.36684	0.663168	0.630601	Bdh2/Dct/
GO_BP_m1	GO:00459	negative re	4/2606	28/23843	0.36684	0.663168	0.630601	Col5a1/Prk
GO_BP_m1	GO:004882	hair follicle	4/2606	28/23843	0.36684	0.663168	0.630601	Ctsl/Krtap2
GO_BP_m1	GO:00506	chondroiti	4/2606	28/23843	0.36684	0.663168	0.630601	Chst13/Cs
GO_BP_m1	GO:005164	centrosom	4/2606	28/23843	0.36684	0.663168	0.630601	Ezr/Nubp1
GO_BP_m1	GO:006021	hematopoi	4/2606	28/23843	0.36684	0.663168	0.630601	Eif2ak2/Fo
GO_BP_m1	GO:006044	branching	4/2606	28/23843	0.36684	0.663168	0.630601	Cdh1/Fgf7
GO_BP_m1	GO:00612	retina vasc	4/2606	28/23843	0.36684	0.663168	0.630601	Mir23a/Mi
GO_BP_m1	GO:007074	response t	4/2606	28/23843	0.36684	0.663168	0.630601	Cfl1/Foxa2
GO_BP_m1	GO:190027	regulation	4/2606	28/23843	0.36684	0.663168	0.630601	Abl2/Adcy
GO_BP_m1	GO:190217	regulation	4/2606	28/23843	0.36684	0.663168	0.630601	Gpx1/Hsph
GO_BP_m1	GO:190274	positive re	4/2606	28/23843	0.36684	0.663168	0.630601	Cfl1/Enpp2
GO_BP_m1	GO:19028	regulation	4/2606	28/23843	0.36684	0.663168	0.630601	Fmr1/Rab5
GO_BP_m1	GO:006027	cilium asse	35/2606	300/23843	0.367064	0.663168	0.630601	B9d1/Bbs1
GO_BP_m1	GO:00026	positive re	6/2606	45/23843	0.368644	0.663168	0.630601	Ifng/Ptprc/
GO_BP_m1	GO:003164	protein de	6/2606	45/23843	0.368644	0.663168	0.630601	Gsn/Isoc2a
GO_BP_m1	GO:003271	negative re	6/2606	45/23843	0.368644	0.663168	0.630601	C1qtnf3/Il1
GO_BP_m1	GO:004591	negative re	6/2606	45/23843	0.368644	0.663168	0.630601	C1qtnf3/C
GO_BP_m1	GO:00607	positive re	6/2606	45/23843	0.368644	0.663168	0.630601	Il7/Mmp12
GO_BP_m1	GO:00901	regulation	6/2606	45/23843	0.368644	0.663168	0.630601	Bnip3/Cide
GO_BP_m1	GO:00019	endothelial	16/2606	132/23843	0.369695	0.663168	0.630601	Arg1/Atp5
GO_BP_m1	GO:000032	re-entry in	1/2606	4/23843	0.370616	0.663168	0.630601	Myc
GO_BP_m1	GO:000042	carbon cat	1/2606	4/23843	0.370616	0.663168	0.630601	Foxa2
GO_BP_m1	GO:00004	carbon cat	1/2606	4/23843	0.370616	0.663168	0.630601	Foxa2

GO_BP_m1	GO:000045	snoRNA gu	1/2606	4/23843	0.370616	0.663168	0.630601	Nop10
GO_BP_m1	GO:000071	meiotic mis	1/2606	4/23843	0.370616	0.663168	0.630601	Msh3
GO_BP_m1	GO:000096	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Pnpt1
GO_BP_m1	GO:000096	mitochond	1/2606	4/23843	0.370616	0.663168	0.630601	Pnpt1
GO_BP_m1	GO:000169	histamine r	1/2606	4/23843	0.370616	0.663168	0.630601	Hdc
GO_BP_m1	GO:000175	somite spe	1/2606	4/23843	0.370616	0.663168	0.630601	Meox2
GO_BP_m1	GO:000183	trophectod	1/2606	4/23843	0.370616	0.663168	0.630601	Esrrb
GO_BP_m1	GO:000188	Mullerian c	1/2606	4/23843	0.370616	0.663168	0.630601	Amh
GO_BP_m1	GO:000188	selenium c	1/2606	4/23843	0.370616	0.663168	0.630601	Sephs1
GO_BP_m1	GO:000191	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Ptprc
GO_BP_m1	GO:000192	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Pcsk9
GO_BP_m1	GO:000192	B-1 B cell c	1/2606	4/23843	0.370616	0.663168	0.630601	Cmtm7
GO_BP_m1	GO:000192	exocyst ass	1/2606	4/23843	0.370616	0.663168	0.630601	Ncam1
GO_BP_m1	GO:000202	reduction c	1/2606	4/23843	0.370616	0.663168	0.630601	Prlh
GO_BP_m1	GO:000215	desmosom	1/2606	4/23843	0.370616	0.663168	0.630601	Prkca
GO_BP_m1	GO:000235	serotonin p	1/2606	4/23843	0.370616	0.663168	0.630601	P2rx1
GO_BP_m1	GO:000243	chronic infl	1/2606	4/23843	0.370616	0.663168	0.630601	Il10
GO_BP_m1	GO:000244	serotonin s	1/2606	4/23843	0.370616	0.663168	0.630601	P2rx1
GO_BP_m1	GO:000252	acute inflar	1/2606	4/23843	0.370616	0.663168	0.630601	Casp6
GO_BP_m1	GO:000258	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Pycard
GO_BP_m1	GO:000292	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Susd4
GO_BP_m1	GO:000319	tricuspid va	1/2606	4/23843	0.370616	0.663168	0.630601	Zfpm2
GO_BP_m1	GO:000341	growth pla	1/2606	4/23843	0.370616	0.663168	0.630601	Por
GO_BP_m1	GO:000343	growth pla	1/2606	4/23843	0.370616	0.663168	0.630601	Poc1a
GO_BP_m1	GO:000604	glucosamir	1/2606	4/23843	0.370616	0.663168	0.630601	Ogt
GO_BP_m1	GO:000620	dGTP catab	1/2606	4/23843	0.370616	0.663168	0.630601	Nudt1
GO_BP_m1	GO:000634	maintenanc	1/2606	4/23843	0.370616	0.663168	0.630601	Hdac2
GO_BP_m1	GO:000642	arginyl-tRN	1/2606	4/23843	0.370616	0.663168	0.630601	Rars2
GO_BP_m1	GO:000653	glutamate	1/2606	4/23843	0.370616	0.663168	0.630601	Gls
GO_BP_m1	GO:000655	leucine cat	1/2606	4/23843	0.370616	0.663168	0.630601	Mccc2
GO_BP_m1	GO:000656	proline bio	1/2606	4/23843	0.370616	0.663168	0.630601	Pycr2
GO_BP_m1	GO:000656	proline cat	1/2606	4/23843	0.370616	0.663168	0.630601	Aldh4a1
GO_BP_m1	GO:000656	L-serine bi	1/2606	4/23843	0.370616	0.663168	0.630601	Psph
GO_BP_m1	GO:000668	galactosylc	1/2606	4/23843	0.370616	0.663168	0.630601	B4galt3
GO_BP_m1	GO:000674	NADP bios	1/2606	4/23843	0.370616	0.663168	0.630601	Idh2
GO_BP_m1	GO:000698	activation c	1/2606	4/23843	0.370616	0.663168	0.630601	Vapb
GO_BP_m1	GO:000702	post-chape	1/2606	4/23843	0.370616	0.663168	0.630601	Tbca
GO_BP_m1	GO:000722	signal trans	1/2606	4/23843	0.370616	0.663168	0.630601	Smo
GO_BP_m1	GO:000741	ventral mic	1/2606	4/23843	0.370616	0.663168	0.630601	Smo
GO_BP_m1	GO:000762	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Avpr1a
GO_BP_m1	GO:000806	establishm	1/2606	4/23843	0.370616	0.663168	0.630601	Cldn1
GO_BP_m1	GO:000959	detection c	1/2606	4/23843	0.370616	0.663168	0.630601	Serinc5
GO_BP_m1	GO:001004	response tc	1/2606	4/23843	0.370616	0.663168	0.630601	Snca
GO_BP_m1	GO:001028	response tc	1/2606	4/23843	0.370616	0.663168	0.630601	Ncam1
GO_BP_m1	GO:001053	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Il12b
GO_BP_m1	GO:001063	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Park2
GO_BP_m1	GO:001072	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Senp1
GO_BP_m1	GO:001073	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Mkl1

GO_BP_m1	GO:001084	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Uts2r
GO_BP_m1	GO:001084	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Tpr
GO_BP_m1	GO:00108	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Nr1h2
GO_BP_m1	GO:00108	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Plin5
GO_BP_m1	GO:00140	microglia c	1/2606	4/23843	0.370616	0.663168	0.630601	Itgam
GO_BP_m1	GO:00140	microglia c	1/2606	4/23843	0.370616	0.663168	0.630601	Itgam
GO_BP_m1	GO:001402	neural plat	1/2606	4/23843	0.370616	0.663168	0.630601	Zfp568
GO_BP_m1	GO:001482	vein smoot	1/2606	4/23843	0.370616	0.663168	0.630601	Ednrb
GO_BP_m1	GO:00148	striated mu	1/2606	4/23843	0.370616	0.663168	0.630601	Gsn
GO_BP_m1	GO:00161	diterpenoi	1/2606	4/23843	0.370616	0.663168	0.630601	Crabp1
GO_BP_m1	GO:001612	phytostero	1/2606	4/23843	0.370616	0.663168	0.630601	Fdft1
GO_BP_m1	GO:001612	phytostero	1/2606	4/23843	0.370616	0.663168	0.630601	Fdft1
GO_BP_m1	GO:001624	autophago	1/2606	4/23843	0.370616	0.663168	0.630601	Snap29
GO_BP_m1	GO:00162	selenocyst	1/2606	4/23843	0.370616	0.663168	0.630601	Sephs1
GO_BP_m1	GO:00165	protein im	1/2606	4/23843	0.370616	0.663168	0.630601	Pex5
GO_BP_m1	GO:001807	N-terminal	1/2606	4/23843	0.370616	0.663168	0.630601	Kat2b
GO_BP_m1	GO:001821	protein car	1/2606	4/23843	0.370616	0.663168	0.630601	Vkorc1l1
GO_BP_m1	GO:00183	protein suc	1/2606	4/23843	0.370616	0.663168	0.630601	Kat2a
GO_BP_m1	GO:001834	protein far	1/2606	4/23843	0.370616	0.663168	0.630601	Fnta
GO_BP_m1	GO:001904	viral latenc	1/2606	4/23843	0.370616	0.663168	0.630601	Nucks1
GO_BP_m1	GO:001924	methylglyc	1/2606	4/23843	0.370616	0.663168	0.630601	Haghl
GO_BP_m1	GO:001924	lactate bios	1/2606	4/23843	0.370616	0.663168	0.630601	Ldha
GO_BP_m1	GO:001927	UDP-N-ac	1/2606	4/23843	0.370616	0.663168	0.630601	Csgalnact1
GO_BP_m1	GO:001937	galactolipi	1/2606	4/23843	0.370616	0.663168	0.630601	B4galt3
GO_BP_m1	GO:00194	beta-alani	1/2606	4/23843	0.370616	0.663168	0.630601	Dpys
GO_BP_m1	GO:00215	midbrain-	1/2606	4/23843	0.370616	0.663168	0.630601	Kdm2b
GO_BP_m1	GO:002157	rhombome	1/2606	4/23843	0.370616	0.663168	0.630601	Hoxb1
GO_BP_m1	GO:00215	cerebellum	1/2606	4/23843	0.370616	0.663168	0.630601	Cend1
GO_BP_m1	GO:002161	glossophar	1/2606	4/23843	0.370616	0.663168	0.630601	Hoxa3
GO_BP_m1	GO:00216	vestibuloc	1/2606	4/23843	0.370616	0.663168	0.630601	Atp8b1
GO_BP_m1	GO:002167	third ventri	1/2606	4/23843	0.370616	0.663168	0.630601	Kdm2b
GO_BP_m1	GO:00219	smoothene	1/2606	4/23843	0.370616	0.663168	0.630601	Smo
GO_BP_m1	GO:00220	convergen	1/2606	4/23843	0.370616	0.663168	0.630601	Zfp568
GO_BP_m1	GO:00220	central ner	1/2606	4/23843	0.370616	0.663168	0.630601	Wnt7a
GO_BP_m1	GO:00300	microspike	1/2606	4/23843	0.370616	0.663168	0.630601	Fscn1
GO_BP_m1	GO:003004	actin filame	1/2606	4/23843	0.370616	0.663168	0.630601	Cfl1
GO_BP_m1	GO:00300	protein rep	1/2606	4/23843	0.370616	0.663168	0.630601	Msrb1
GO_BP_m1	GO:003112	snRNA pse	1/2606	4/23843	0.370616	0.663168	0.630601	Nop10
GO_BP_m1	GO:003144	fast-twitch	1/2606	4/23843	0.370616	0.663168	0.630601	Mylk2
GO_BP_m1	GO:00322	telomere m	1/2606	4/23843	0.370616	0.663168	0.630601	Pcna
GO_BP_m1	GO:00322	peripheral	1/2606	4/23843	0.370616	0.663168	0.630601	Ahnak2
GO_BP_m1	GO:00324	detection c	1/2606	4/23843	0.370616	0.663168	0.630601	Scarb1
GO_BP_m1	GO:003284	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Avpr1a
GO_BP_m1	GO:003297	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Mylk2
GO_BP_m1	GO:003302	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Kitl
GO_BP_m1	GO:00346	retinoic aci	1/2606	4/23843	0.370616	0.663168	0.630601	Crabp1
GO_BP_m1	GO:00351	operant co	1/2606	4/23843	0.370616	0.663168	0.630601	Tacr2
GO_BP_m1	GO:00352	trunk segm	1/2606	4/23843	0.370616	0.663168	0.630601	Sema3f

GO_BP_m1	GO:003552	monoubiqu	1/2606	4/23843	0.370616	0.663168	0.630601	Asxl1
GO_BP_m1	GO:003552	monoubiqu	1/2606	4/23843	0.370616	0.663168	0.630601	Asxl1
GO_BP_m1	GO:003558	G-protein	1/2606	4/23843	0.370616	0.663168	0.630601	P2ry1
GO_BP_m1	GO:003561	histone H2	1/2606	4/23843	0.370616	0.663168	0.630601	Usp7
GO_BP_m1	GO:003569	CD8-positi	1/2606	4/23843	0.370616	0.663168	0.630601	Ripk3
GO_BP_m1	GO:003572	intraciliary	1/2606	4/23843	0.370616	0.663168	0.630601	Ift52
GO_BP_m1	GO:003578	cell migrati	1/2606	4/23843	0.370616	0.663168	0.630601	Pdgfa
GO_BP_m1	GO:003578	metanephr	1/2606	4/23843	0.370616	0.663168	0.630601	Pdgfa
GO_BP_m1	GO:003597	protein de	1/2606	4/23843	0.370616	0.663168	0.630601	Man1b1
GO_BP_m1	GO:003598	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Hdac2
GO_BP_m1	GO:003598	cellular res	1/2606	4/23843	0.370616	0.663168	0.630601	Hdac2
GO_BP_m1	GO:003599	tendon cell	1/2606	4/23843	0.370616	0.663168	0.630601	Mkx
GO_BP_m1	GO:003599	tendon for	1/2606	4/23843	0.370616	0.663168	0.630601	Mkx
GO_BP_m1	GO:003599	detection c	1/2606	4/23843	0.370616	0.663168	0.630601	Cav3
GO_BP_m1	GO:003648	trunk neur	1/2606	4/23843	0.370616	0.663168	0.630601	Sema3f
GO_BP_m1	GO:003648	ventral tru	1/2606	4/23843	0.370616	0.663168	0.630601	Sema3f
GO_BP_m1	GO:003650	protein de	1/2606	4/23843	0.370616	0.663168	0.630601	Man1b1
GO_BP_m1	GO:003650	protein alp	1/2606	4/23843	0.370616	0.663168	0.630601	Man1b1
GO_BP_m1	GO:003802	reelin-mec	1/2606	4/23843	0.370616	0.663168	0.630601	Vldlr
GO_BP_m1	GO:003809	Fc-epsilon	1/2606	4/23843	0.370616	0.663168	0.630601	Ms4a2
GO_BP_m1	GO:003810	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Bbs2
GO_BP_m1	GO:004222	interleukin	1/2606	4/23843	0.370616	0.663168	0.630601	Ccl20
GO_BP_m1	GO:004266	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Wnt3a
GO_BP_m1	GO:004277	mitochond	1/2606	4/23843	0.370616	0.663168	0.630601	Atp5o
GO_BP_m1	GO:004309	purine nuc	1/2606	4/23843	0.370616	0.663168	0.630601	Aprt
GO_BP_m1	GO:004313	DNA replic	1/2606	4/23843	0.370616	0.663168	0.630601	Fen1
GO_BP_m1	GO:004315	induction c	1/2606	4/23843	0.370616	0.663168	0.630601	Spon2
GO_BP_m1	GO:004331	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Itgam
GO_BP_m1	GO:004339	corticotrop	1/2606	4/23843	0.370616	0.663168	0.630601	Tnfsf11
GO_BP_m1	GO:004339	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Tnfsf11
GO_BP_m1	GO:004343	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Nr4a1
GO_BP_m1	GO:004346	proton-tra	1/2606	4/23843	0.370616	0.663168	0.630601	Atpaf1
GO_BP_m1	GO:004346	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Tigar
GO_BP_m1	GO:004398	histone H4	1/2606	4/23843	0.370616	0.663168	0.630601	Prmt1
GO_BP_m1	GO:004410	cellular alc	1/2606	4/23843	0.370616	0.663168	0.630601	Fdft1
GO_BP_m1	GO:004410	cellular alc	1/2606	4/23843	0.370616	0.663168	0.630601	Fdft1
GO_BP_m1	GO:004452	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Fastkd1
GO_BP_m1	GO:004480	multi-orga	1/2606	4/23843	0.370616	0.663168	0.630601	Hyal2
GO_BP_m1	GO:004559	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Ctla4
GO_BP_m1	GO:004590	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Cpeb3
GO_BP_m1	GO:004601	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Foxa2
GO_BP_m1	GO:004612	pyrimidine	1/2606	4/23843	0.370616	0.663168	0.630601	Dpyd
GO_BP_m1	GO:004616	glycerol-3-	1/2606	4/23843	0.370616	0.663168	0.630601	Gk2
GO_BP_m1	GO:004620	spermine c	1/2606	4/23843	0.370616	0.663168	0.630601	Sat1
GO_BP_m1	GO:004636	GDP-L-fuc	1/2606	4/23843	0.370616	0.663168	0.630601	Fut8
GO_BP_m1	GO:004660	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Ranbp1
GO_BP_m1	GO:004820	Golgi trans	1/2606	4/23843	0.370616	0.663168	0.630601	Gbf1
GO_BP_m1	GO:004820	COPI coati	1/2606	4/23843	0.370616	0.663168	0.630601	Gbf1

GO_BP_m1	GO:004876	sarcomerog	1/2606	4/23843	0.370616	0.663168	0.630601	Mylk2
GO_BP_m1	GO:005114	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Il12b
GO_BP_m1	GO:005114	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Il12b
GO_BP_m1	GO:005130	female mei	1/2606	4/23843	0.370616	0.663168	0.630601	Sycp3
GO_BP_m1	GO:005146	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Galr1
GO_BP_m1	GO:005159	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Bche
GO_BP_m1	GO:005159	methylglyc	1/2606	4/23843	0.370616	0.663168	0.630601	Haghl
GO_BP_m1	GO:005161	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Snca
GO_BP_m1	GO:005172	protein de	1/2606	4/23843	0.370616	0.663168	0.630601	Macrod2
GO_BP_m1	GO:005179	medium-cl	1/2606	4/23843	0.370616	0.663168	0.630601	Abhd1
GO_BP_m1	GO:005190	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Bok
GO_BP_m1	GO:005191	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	F11
GO_BP_m1	GO:006016	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Drd3
GO_BP_m1	GO:006016	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Acpp
GO_BP_m1	GO:006021	endocardiu	1/2606	4/23843	0.370616	0.663168	0.630601	Sox18
GO_BP_m1	GO:006037	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Itgam
GO_BP_m1	GO:006045	left lung de	1/2606	4/23843	0.370616	0.663168	0.630601	Cfc1
GO_BP_m1	GO:006047	acrosomal	1/2606	4/23843	0.370616	0.663168	0.630601	Hyal3
GO_BP_m1	GO:006059	mammary	1/2606	4/23843	0.370616	0.663168	0.630601	Pax3
GO_BP_m1	GO:006080	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Stk3
GO_BP_m1	GO:006083	ciliary recep	1/2606	4/23843	0.370616	0.663168	0.630601	Ssna1
GO_BP_m1	GO:006105	dermatome	1/2606	4/23843	0.370616	0.663168	0.630601	Wnt3a
GO_BP_m1	GO:006108	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	H2afy
GO_BP_m1	GO:006111	dense core	1/2606	4/23843	0.370616	0.663168	0.630601	Prkca
GO_BP_m1	GO:006111	pancreas m	1/2606	4/23843	0.370616	0.663168	0.630601	Smo
GO_BP_m1	GO:006118	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Wnt3a
GO_BP_m1	GO:006147	T follicular	1/2606	4/23843	0.370616	0.663168	0.630601	Gpr183
GO_BP_m1	GO:006172	methylglyc	1/2606	4/23843	0.370616	0.663168	0.630601	Haghl
GO_BP_m1	GO:006173	protein lipi	1/2606	4/23843	0.370616	0.663168	0.630601	Wipi2
GO_BP_m1	GO:006181	telomeric D	1/2606	4/23843	0.370616	0.663168	0.630601	Xrcc1
GO_BP_m1	GO:006188	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ttbk1
GO_BP_m1	GO:007009	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Cartpt
GO_BP_m1	GO:007012	mitochond	1/2606	4/23843	0.370616	0.663168	0.630601	Mtrf1
GO_BP_m1	GO:007021	protein pol	1/2606	4/23843	0.370616	0.663168	0.630601	Tnks
GO_BP_m1	GO:007021	protein aut	1/2606	4/23843	0.370616	0.663168	0.630601	Tnks
GO_BP_m1	GO:007034	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Fgf16
GO_BP_m1	GO:007035	actin polym	1/2606	4/23843	0.370616	0.663168	0.630601	Nckap1l
GO_BP_m1	GO:007038	Harderian g	1/2606	4/23843	0.370616	0.663168	0.630601	Aldh1a3
GO_BP_m1	GO:007060	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Naa10
GO_BP_m1	GO:007066	mast cell p	1/2606	4/23843	0.370616	0.663168	0.630601	Kitl
GO_BP_m1	GO:007066	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Kitl
GO_BP_m1	GO:007066	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Kitl
GO_BP_m1	GO:007067	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Ticam2
GO_BP_m1	GO:007083	dehydroasc	1/2606	4/23843	0.370616	0.663168	0.630601	Slc2a1
GO_BP_m1	GO:007094	neutrophil	1/2606	4/23843	0.370616	0.663168	0.630601	Arg1
GO_BP_m1	GO:007094	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Arg1
GO_BP_m1	GO:007107	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Pdgfa
GO_BP_m1	GO:007137	cellular resp	1/2606	4/23843	0.370616	0.663168	0.630601	Nr4a1

GO_BP_m1	GO:007172	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Cd36
GO_BP_m1	GO:007172	cellular res	1/2606	4/23843	0.370616	0.663168	0.630601	Cd36
GO_BP_m1	GO:007181	tail-anchor	1/2606	4/23843	0.370616	0.663168	0.630601	Wrb
GO_BP_m1	GO:007192	endocanna	1/2606	4/23843	0.370616	0.663168	0.630601	Mgll
GO_BP_m1	GO:007205	juxtaglome	1/2606	4/23843	0.370616	0.663168	0.630601	Pou3f3
GO_BP_m1	GO:007208	specificatio	1/2606	4/23843	0.370616	0.663168	0.630601	Irx2
GO_BP_m1	GO:007209	metanephr	1/2606	4/23843	0.370616	0.663168	0.630601	Smo
GO_BP_m1	GO:007210	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Gdnf
GO_BP_m1	GO:007210	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Gdnf
GO_BP_m1	GO:007210	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Gdnf
GO_BP_m1	GO:007216	metanephr	1/2606	4/23843	0.370616	0.663168	0.630601	Osr1
GO_BP_m1	GO:007218	mesonephr	1/2606	4/23843	0.370616	0.663168	0.630601	Osr1
GO_BP_m1	GO:007222	metanephr	1/2606	4/23843	0.370616	0.663168	0.630601	Wt1
GO_BP_m1	GO:007223	metanephr	1/2606	4/23843	0.370616	0.663168	0.630601	Pou3f3
GO_BP_m1	GO:007226	metanephr	1/2606	4/23843	0.370616	0.663168	0.630601	Wt1
GO_BP_m1	GO:007238	plus-end-c	1/2606	4/23843	0.370616	0.663168	0.630601	Kif23
GO_BP_m1	GO:007238	plus-end-c	1/2606	4/23843	0.370616	0.663168	0.630601	Kif23
GO_BP_m1	GO:007242	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Fbxo18
GO_BP_m1	GO:007271	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Rpl23
GO_BP_m1	GO:007271	cellular res	1/2606	4/23843	0.370616	0.663168	0.630601	Slc31a1
GO_BP_m1	GO:008970	protein kin	1/2606	4/23843	0.370616	0.663168	0.630601	Prkd3
GO_BP_m1	GO:009015	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Smpd3
GO_BP_m1	GO:009018	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Nr1h2
GO_BP_m1	GO:009029	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Lig3
GO_BP_m1	GO:009040	oxidative st	1/2606	4/23843	0.370616	0.663168	0.630601	Arntl
GO_BP_m1	GO:009721	lysosomal r	1/2606	4/23843	0.370616	0.663168	0.630601	Mt3
GO_BP_m1	GO:009736	chorionic t	1/2606	4/23843	0.370616	0.663168	0.630601	Bok
GO_BP_m1	GO:009749	sympatheti	1/2606	4/23843	0.370616	0.663168	0.630601	Sema3f
GO_BP_m1	GO:009749	sympatheti	1/2606	4/23843	0.370616	0.663168	0.630601	Sema3f
GO_BP_m1	GO:009953	synaptic sig	1/2606	4/23843	0.370616	0.663168	0.630601	Ntf5
GO_BP_m1	GO:009954	trans-synap	1/2606	4/23843	0.370616	0.663168	0.630601	Ntf5
GO_BP_m1	GO:010001	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Wnt3a
GO_BP_m1	GO:010607	histone suc	1/2606	4/23843	0.370616	0.663168	0.630601	Kat2a
GO_BP_m1	GO:010610	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ssh1
GO_BP_m1	GO:190010	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Dand5
GO_BP_m1	GO:190010	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Dmrtc2
GO_BP_m1	GO:190014	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Dand5
GO_BP_m1	GO:190015	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Rflna
GO_BP_m1	GO:190017	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Dand5
GO_BP_m1	GO:190020	mesenchyr	1/2606	4/23843	0.370616	0.663168	0.630601	Wt1
GO_BP_m1	GO:190021	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Wt1
GO_BP_m1	GO:190021	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Wt1
GO_BP_m1	GO:190130	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Endog
GO_BP_m1	GO:190138	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Bok
GO_BP_m1	GO:190152	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Abcb1a
GO_BP_m1	GO:190153	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Usp7
GO_BP_m1	GO:190166	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Szt2
GO_BP_m1	GO:190183	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	H2afy

GO_BP_m1	GO:190184	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Rrad
GO_BP_m1	GO:190184	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Cacnb2
GO_BP_m1	GO:190206	response t	1/2606	4/23843	0.370616	0.663168	0.630601	Park2
GO_BP_m1	GO:190210	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Bnip3
GO_BP_m1	GO:190220	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ptpn1
GO_BP_m1	GO:190226	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Akap6
GO_BP_m1	GO:190241	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ankrd53
GO_BP_m1	GO:190246	protein loc	1/2606	4/23843	0.370616	0.663168	0.630601	Cfl1
GO_BP_m1	GO:190252	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Pdcd6
GO_BP_m1	GO:190256	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Itgam
GO_BP_m1	GO:190256	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Stx4a
GO_BP_m1	GO:190274	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Cdkn1c
GO_BP_m1	GO:190289	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Cdh2
GO_BP_m1	GO:190305	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Antxr1
GO_BP_m1	GO:190311	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Acta2
GO_BP_m1	GO:190312	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Atf3
GO_BP_m1	GO:190322	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Col5a1
GO_BP_m1	GO:190328	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Atp1b2
GO_BP_m1	GO:190358	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Dll4
GO_BP_m1	GO:190359	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Cav1
GO_BP_m1	GO:190375	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Hsph1
GO_BP_m1	GO:190375	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Hsph1
GO_BP_m1	GO:190379	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Fxyd1
GO_BP_m1	GO:190384	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ephb4
GO_BP_m1	GO:190384	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Ephb4
GO_BP_m1	GO:190389	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Bok
GO_BP_m1	GO:190396	monounsat	1/2606	4/23843	0.370616	0.663168	0.630601	Scd4
GO_BP_m1	GO:190396	monounsat	1/2606	4/23843	0.370616	0.663168	0.630601	Scd4
GO_BP_m1	GO:190397	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Idh2
GO_BP_m1	GO:190438	mannose t	1/2606	4/23843	0.370616	0.663168	0.630601	Man1b1
GO_BP_m1	GO:190468	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ythdf2
GO_BP_m1	GO:190471	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Snca
GO_BP_m1	GO:190471	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ssh1
GO_BP_m1	GO:190474	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Tnks
GO_BP_m1	GO:190484	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Fgf16
GO_BP_m1	GO:190499	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Ccl28
GO_BP_m1	GO:190516	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Blm
GO_BP_m1	GO:190527	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Gdnf
GO_BP_m1	GO:190544	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Cdk1
GO_BP_m1	GO:190546	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	E2f3
GO_BP_m1	GO:190566	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Calcr
GO_BP_m1	GO:190576	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Xrcc1
GO_BP_m1	GO:190576	negative re	1/2606	4/23843	0.370616	0.663168	0.630601	Xrcc1
GO_BP_m1	GO:199008	lens fiber c	1/2606	4/23843	0.370616	0.663168	0.630601	E2f1
GO_BP_m1	GO:199041	adrenome	1/2606	4/23843	0.370616	0.663168	0.630601	Adm
GO_BP_m1	GO:199041	cellular res	1/2606	4/23843	0.370616	0.663168	0.630601	Nfkb1
GO_BP_m1	GO:199048	mRNA pse	1/2606	4/23843	0.370616	0.663168	0.630601	Trub1
GO_BP_m1	GO:200004	positive reg	1/2606	4/23843	0.370616	0.663168	0.630601	Wnt3a

GO_BP_m1	GO:20003	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Smpd3
GO_BP_m1	GO:200041	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Adam8
GO_BP_m1	GO:200041	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Adam8
GO_BP_m1	GO:20005	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Ccl4
GO_BP_m1	GO:200052	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Ephb4
GO_BP_m1	GO:200052	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Ephb4
GO_BP_m1	GO:200054	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Fgf16
GO_BP_m1	GO:20005	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Ptpn22
GO_BP_m1	GO:20005	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Pdgfa
GO_BP_m1	GO:20006	negative r	1/2606	4/23843	0.370616	0.663168	0.630601	Il1rn
GO_BP_m1	GO:20006	negative r	1/2606	4/23843	0.370616	0.663168	0.630601	Osr1
GO_BP_m1	GO:20008	regulation	1/2606	4/23843	0.370616	0.663168	0.630601	Tac1
GO_BP_m1	GO:200101	epithelial c	1/2606	4/23843	0.370616	0.663168	0.630601	Lgr4
GO_BP_m1	GO:20010	negative r	1/2606	4/23843	0.370616	0.663168	0.630601	Nudt16l1
GO_BP_m1	GO:20012	positive re	1/2606	4/23843	0.370616	0.663168	0.630601	Tnfsf11
GO_BP_m1	GO:000691	autophagy	43/2606	372/23843	0.371699	0.664463	0.631832	3110002H
GO_BP_m1	GO:006191	process uti	43/2606	372/23843	0.371699	0.664463	0.631832	3110002H
GO_BP_m1	GO:00072	tyrosine p	9/2606	71/23843	0.371793	0.664463	0.631832	Cav1/Hdac
GO_BP_m1	GO:00346	cellular car	9/2606	71/23843	0.371793	0.664463	0.631832	B3gnt3/B3
GO_BP_m1	GO:19018	negative r	9/2606	71/23843	0.371793	0.664463	0.631832	Cav3/Ephb
GO_BP_m1	GO:19033	negative r	9/2606	71/23843	0.371793	0.664463	0.631832	Anxa2/N4
GO_BP_m1	GO:00512	release of	13/2606	106/23843	0.373684	0.666581	0.633846	Akap6/Asp
GO_BP_m1	GO:00512	negative r	13/2606	106/23843	0.373684	0.666581	0.633846	Akap6/Asp
GO_BP_m1	GO:00072	Ras protei	49/2606	426/23843	0.373888	0.666581	0.633846	Aatk/Abl2/
GO_BP_m1	GO:00027	regulation	18/2606	150/23843	0.374142	0.666581	0.633846	Aplf/Arg1/
GO_BP_m1	GO:000194	lymphangi	3/2606	20/23843	0.376228	0.666581	0.633846	Epha2/Fox
GO_BP_m1	GO:00025	antigen pr	3/2606	20/23843	0.376228	0.666581	0.633846	H2-DMb2/
GO_BP_m1	GO:00065	melanin m	3/2606	20/23843	0.376228	0.666581	0.633846	Dct/Ddt/Ty
GO_BP_m1	GO:00068	cellular soc	3/2606	20/23843	0.376228	0.666581	0.633846	Atp1b2/C7
GO_BP_m1	GO:00070	vacuolar a	3/2606	20/23843	0.376228	0.666581	0.633846	Atp6v0c/P
GO_BP_m1	GO:00083	asymmetri	3/2606	20/23843	0.376228	0.666581	0.633846	Dock7/Fgf
GO_BP_m1	GO:001064	regulation	3/2606	20/23843	0.376228	0.666581	0.633846	Ndrg4/Ptp
GO_BP_m1	GO:001087	regulation	3/2606	20/23843	0.376228	0.666581	0.633846	Abca12/N
GO_BP_m1	GO:00148	release of	3/2606	20/23843	0.376228	0.666581	0.633846	Dhrs7c/Fk
GO_BP_m1	GO:00161	glycoside r	3/2606	20/23843	0.376228	0.666581	0.633846	Abhd10/A
GO_BP_m1	GO:00312	positive re	3/2606	20/23843	0.376228	0.666581	0.633846	Calcr/Guca
GO_BP_m1	GO:003214	activation	3/2606	20/23843	0.376228	0.666581	0.633846	Fgf1/Itgb1
GO_BP_m1	GO:00338	nucleoside	3/2606	20/23843	0.376228	0.666581	0.633846	Crot/Dcak
GO_BP_m1	GO:003387	ribonucleo	3/2606	20/23843	0.376228	0.666581	0.633846	Crot/Dcak
GO_BP_m1	GO:00340	purine nuc	3/2606	20/23843	0.376228	0.666581	0.633846	Crot/Dcak
GO_BP_m1	GO:00353	thioester b	3/2606	20/23843	0.376228	0.666581	0.633846	Mpc2/Pdh
GO_BP_m1	GO:00363	dendritic c	3/2606	20/23843	0.376228	0.666581	0.633846	Calr/Dock
GO_BP_m1	GO:004244	progestero	3/2606	20/23843	0.376228	0.666581	0.633846	Akr1c12/D
GO_BP_m1	GO:00457	negative r	3/2606	20/23843	0.376228	0.666581	0.633846	Fbxo18/Nu
GO_BP_m1	GO:00459	negative r	3/2606	20/23843	0.376228	0.666581	0.633846	Adora1/Dc
GO_BP_m1	GO:00504	positive re	3/2606	20/23843	0.376228	0.666581	0.633846	Nucks1/Ta
GO_BP_m1	GO:00511	positive re	3/2606	20/23843	0.376228	0.666581	0.633846	Esrrb/Myc/
GO_BP_m1	GO:005134	positive re	3/2606	20/23843	0.376228	0.666581	0.633846	Calcr/Guca

GO_BP_m1	GO:00600	inhibitory	3/2606	20/23843	0.376228	0.666581	0.633846	Abat/Nlgn
GO_BP_m1	GO:00603	interferon-	3/2606	20/23843	0.376228	0.666581	0.633846	Arg1/Ifng/
GO_BP_m1	GO:00611	establishm	3/2606	20/23843	0.376228	0.666581	0.633846	Fscn1/Gbf1
GO_BP_m1	GO:00702	pyroptosis	3/2606	20/23843	0.376228	0.666581	0.633846	Apip/Gsdm
GO_BP_m1	GO:00704	interleukin	3/2606	20/23843	0.376228	0.666581	0.633846	Il1rn/Irak2/
GO_BP_m1	GO:00711	negative re	3/2606	20/23843	0.376228	0.666581	0.633846	Calr/Rpl23/
GO_BP_m1	GO:007161	acyl-CoA	3/2606	20/23843	0.376228	0.666581	0.633846	Mpc2/Pdh
GO_BP_m1	GO:00716	ectoderma	3/2606	20/23843	0.376228	0.666581	0.633846	Hdac1/Hd
GO_BP_m1	GO:00720	renal vesicl	3/2606	20/23843	0.376228	0.666581	0.633846	Gdnf/Osr1/
GO_BP_m1	GO:007217	metanephr	3/2606	20/23843	0.376228	0.666581	0.633846	Lgr4/Osr1/
GO_BP_m1	GO:00903	phagosom	3/2606	20/23843	0.376228	0.666581	0.633846	Rab32/Rab
GO_BP_m1	GO:190167	regulation	3/2606	20/23843	0.376228	0.666581	0.633846	Chmp1b/H
GO_BP_m1	GO:00326	interferon-	14/2606	115/23843	0.376642	0.666581	0.633846	Abl2/Fam4
GO_BP_m1	GO:002167	nerve deve	10/2606	80/23843	0.376646	0.666581	0.633846	Ahnak2/At
GO_BP_m1	GO:00229	respiratory	10/2606	80/23843	0.376646	0.666581	0.633846	Cdk1/Coq
GO_BP_m1	GO:004472	DNA meth	10/2606	80/23843	0.376646	0.666581	0.633846	Apobec1/
GO_BP_m1	GO:00986	inorganic a	10/2606	80/23843	0.376646	0.666581	0.633846	Ank/Ano1/
GO_BP_m1	GO:000674	glutathion	7/2606	54/23843	0.376819	0.666581	0.633846	Gclm/Gpx1
GO_BP_m1	GO:00217	cerebral co	7/2606	54/23843	0.376819	0.666581	0.633846	Arx/Cdk5/
GO_BP_m1	GO:00304	maturation	7/2606	54/23843	0.376819	0.666581	0.633846	Bms1/Kri1/
GO_BP_m1	GO:003261	interleukin	7/2606	54/23843	0.376819	0.666581	0.633846	Cd36/Ifng/
GO_BP_m1	GO:004671	viral entry i	7/2606	54/23843	0.376819	0.666581	0.633846	Cav1/Gsn/
GO_BP_m1	GO:19039	positive re	7/2606	54/23843	0.376819	0.666581	0.633846	Fkbp6/Fmr
GO_BP_m1	GO:00070	vacuolar tr	15/2606	124/23843	0.379214	0.666581	0.633846	Ankfy1/Ca
GO_BP_m1	GO:00713	cellular res	15/2606	124/23843	0.379214	0.666581	0.633846	Ano1/Fkbp
GO_BP_m1	GO:00107	regulation	5/2606	37/23843	0.380052	0.666581	0.633846	Acta2/D1E
GO_BP_m1	GO:00162	telomere c	5/2606	37/23843	0.380052	0.666581	0.633846	Dclre1a/N
GO_BP_m1	GO:00219	central ner	5/2606	37/23843	0.380052	0.666581	0.633846	Ephb1/Eph
GO_BP_m1	GO:003302	myeloid ce	5/2606	37/23843	0.380052	0.666581	0.633846	Hcar2/Ifng
GO_BP_m1	GO:00331	regulation	5/2606	37/23843	0.380052	0.666581	0.633846	Gm13271/
GO_BP_m1	GO:00507	interleukin	5/2606	37/23843	0.380052	0.666581	0.633846	Cd36/Gsd
GO_BP_m1	GO:009004	regulation	5/2606	37/23843	0.380052	0.666581	0.633846	Cib1/Dll4/
GO_BP_m1	GO:190367	positive re	5/2606	37/23843	0.380052	0.666581	0.633846	Cib1/Fgf1/
GO_BP_m1	GO:200082	regulation	5/2606	37/23843	0.380052	0.666581	0.633846	Foxc1/Nog
GO_BP_m1	GO:00033	cardiac mu	11/2606	89/23843	0.380656	0.666581	0.633846	Adk/Akap6
GO_BP_m1	GO:004001	regulation	11/2606	89/23843	0.380656	0.666581	0.633846	Bbs2/Drd3
GO_BP_m1	GO:003262	interleukin	8/2606	63/23843	0.383046	0.666581	0.633846	Abl2/Btnl2/
GO_BP_m1	GO:00480	antigen pr	8/2606	63/23843	0.383046	0.666581	0.633846	Calr/Gm11
GO_BP_m1	GO:004801	phosphatic	17/2606	142/23843	0.383453	0.666581	0.633846	Csf3/Dcn/
GO_BP_m1	GO:000027	M phase	2/2606	12/23843	0.383527	0.666581	0.633846	Cdc20/Top
GO_BP_m1	GO:000184	neural plat	2/2606	12/23843	0.383527	0.666581	0.633846	Nog/Zfp56
GO_BP_m1	GO:000232	pro-B cell	2/2606	12/23843	0.383527	0.666581	0.633846	Flcn/Prkdc
GO_BP_m1	GO:000292	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Ptprc/Susd
GO_BP_m1	GO:00030	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Adora1/Ut
GO_BP_m1	GO:00031	endocardi	2/2606	12/23843	0.383527	0.666581	0.633846	Sox18/Stk3
GO_BP_m1	GO:00031	mitral valv	2/2606	12/23843	0.383527	0.666581	0.633846	Smad6/Zfp
GO_BP_m1	GO:00033	mesenchy	2/2606	12/23843	0.383527	0.666581	0.633846	Gdnf/Smo
GO_BP_m1	GO:00033	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Bbs2/Dnaa

GO_BP_m1	GO:000604	UDP-N-ac	2/2606	12/23843	0.383527	0.666581	0.633846	Gfpt2/Pgm
GO_BP_m1	GO:000607	glycerol-3-	2/2606	12/23843	0.383527	0.666581	0.633846	Gk2/Gpam
GO_BP_m1	GO:000608	acetyl-CoA	2/2606	12/23843	0.383527	0.666581	0.633846	Mpc2/Pdh
GO_BP_m1	GO:000862	granzyme-	2/2606	12/23843	0.383527	0.666581	0.633846	Bnip3/Ube
GO_BP_m1	GO:000907	serine fami	2/2606	12/23843	0.383527	0.666581	0.633846	Gldc/Shmt
GO_BP_m1	GO:000926	deoxyribor	2/2606	12/23843	0.383527	0.666581	0.633846	Dera/Nudt
GO_BP_m1	GO:001482	tonic smoo	2/2606	12/23843	0.383527	0.666581	0.633846	Bbs2/Smp
GO_BP_m1	GO:001962	urea metal	2/2606	12/23843	0.383527	0.666581	0.633846	Arg1/Otc
GO_BP_m1	GO:002156	facial nerve	2/2606	12/23843	0.383527	0.666581	0.633846	Hoxb1/Sem
GO_BP_m1	GO:002161	facial nerve	2/2606	12/23843	0.383527	0.666581	0.633846	Hoxb1/Sem
GO_BP_m1	GO:003063	polyketide	2/2606	12/23843	0.383527	0.666581	0.633846	Akr1c12/C
GO_BP_m1	GO:003064	aminoglyco	2/2606	12/23843	0.383527	0.666581	0.633846	Akr1c12/C
GO_BP_m1	GO:003112	rRNA 3'-er	2/2606	12/23843	0.383527	0.666581	0.633846	Eri1/Exosc
GO_BP_m1	GO:003230	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	P2ry2/Tnfs
GO_BP_m1	GO:003327	actin-myos	2/2606	12/23843	0.383527	0.666581	0.633846	Myh7/Mylk
GO_BP_m1	GO:003535	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Asxl1/Plin5
GO_BP_m1	GO:003546	vitamin tra	2/2606	12/23843	0.383527	0.666581	0.633846	Scarb1/Slc
GO_BP_m1	GO:003575	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Atp6v0c/Pp
GO_BP_m1	GO:003579	platelet-de	2/2606	12/23843	0.383527	0.666581	0.633846	Pdgfa/Ptpr
GO_BP_m1	GO:003581	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	Ednrb/Opr
GO_BP_m1	GO:004254	hemoglobi	2/2606	12/23843	0.383527	0.666581	0.633846	Eif2ak1/Prr
GO_BP_m1	GO:004275	long-chain	2/2606	12/23843	0.383527	0.666581	0.633846	Alox12/Asa
GO_BP_m1	GO:004298	sequesterir	2/2606	12/23843	0.383527	0.666581	0.633846	Gsn/Tmsb1
GO_BP_m1	GO:004459	daunorubic	2/2606	12/23843	0.383527	0.666581	0.633846	Akr1c12/C
GO_BP_m1	GO:004459	doxorubici	2/2606	12/23843	0.383527	0.666581	0.633846	Akr1c12/C
GO_BP_m1	GO:004534	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Ifng/Il10
GO_BP_m1	GO:004576	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	Calcr/Nf1
GO_BP_m1	GO:004582	negative re	2/2606	12/23843	0.383527	0.666581	0.633846	Ppargc1a/
GO_BP_m1	GO:004594	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	Foxa2/Ice1
GO_BP_m1	GO:004595	negative re	2/2606	12/23843	0.383527	0.666581	0.633846	Fmr1/Trim
GO_BP_m1	GO:004857	notochord	2/2606	12/23843	0.383527	0.666581	0.633846	Epha2/Nog
GO_BP_m1	GO:006003	anatomical	2/2606	12/23843	0.383527	0.666581	0.633846	Amh/Cd24
GO_BP_m1	GO:006010	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	Cd36/Ncka
GO_BP_m1	GO:006012	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	Arhgef7/Se
GO_BP_m1	GO:007044	oligodendr	2/2606	12/23843	0.383527	0.666581	0.633846	Cdh2/Nog
GO_BP_m1	GO:007044	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Cdh2/Nog
GO_BP_m1	GO:007047	uterine sm	2/2606	12/23843	0.383527	0.666581	0.633846	Abat/Tacr2
GO_BP_m1	GO:007098	left/right a	2/2606	12/23843	0.383527	0.666581	0.633846	Ift172/Smo
GO_BP_m1	GO:007211	glomerular	2/2606	12/23843	0.383527	0.666581	0.633846	Ifng/Wt1
GO_BP_m1	GO:007217	nephric du	2/2606	12/23843	0.383527	0.666581	0.633846	Epha7/Osr
GO_BP_m1	GO:007243	signal trans	2/2606	12/23843	0.383527	0.666581	0.633846	Cdkn1a/Prl
GO_BP_m1	GO:009019	positive re	2/2606	12/23843	0.383527	0.666581	0.633846	Il1rl1/Pycar
GO_BP_m1	GO:009732	response t	2/2606	12/23843	0.383527	0.666581	0.633846	Blm/Fmr1
GO_BP_m1	GO:009876	meiotic cel	2/2606	12/23843	0.383527	0.666581	0.633846	Topaz1/Ttk
GO_BP_m1	GO:009876	meiosis I c	2/2606	12/23843	0.383527	0.666581	0.633846	Topaz1/Ttk
GO_BP_m1	GO:009896	neurotrans	2/2606	12/23843	0.383527	0.666581	0.633846	Arhgap44/
GO_BP_m1	GO:190120	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Antxr1/Has
GO_BP_m1	GO:190129	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Endog/Hsp

GO_BP_m1	GO:190240	intracellula	2/2606	12/23843	0.383527	0.666581	0.633846	Cdkn1a/Prl
GO_BP_m1	GO:190257	protein loc	2/2606	12/23843	0.383527	0.666581	0.633846	Nmd3/Rpf2
GO_BP_m1	GO:190271	positive reg	2/2606	12/23843	0.383527	0.666581	0.633846	Abl2/Ptpn2
GO_BP_m1	GO:190295	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Cfl1/Grin2b
GO_BP_m1	GO:190302	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Ddrgk1/Zfp
GO_BP_m1	GO:190354	establishme	2/2606	12/23843	0.383527	0.666581	0.633846	Arhgap44/
GO_BP_m1	GO:190396	positive reg	2/2606	12/23843	0.383527	0.666581	0.633846	Abcb1a/Fxy
GO_BP_m1	GO:190397	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Gpr183/Idh
GO_BP_m1	GO:190429	positive reg	2/2606	12/23843	0.383527	0.666581	0.633846	Bcap31/Tm
GO_BP_m1	GO:190447	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Abcb1a/Dg
GO_BP_m1	GO:190486	excitatory s	2/2606	12/23843	0.383527	0.666581	0.633846	Nptn/Wnt7
GO_BP_m1	GO:190515	positive reg	2/2606	12/23843	0.383527	0.666581	0.633846	Cd36/Ncka
GO_BP_m1	GO:190521	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Fmr1/Nuck
GO_BP_m1	GO:200067	regulation	2/2606	12/23843	0.383527	0.666581	0.633846	Hdac1/Spc
GO_BP_m1	GO:200083	positive reg	2/2606	12/23843	0.383527	0.666581	0.633846	Galr1/Tac1
GO_BP_m1	GO:200105	negative re	2/2606	12/23843	0.383527	0.666581	0.633846	Tbx1/Wt1
GO_BP_m1	GO:000910	glycoprote	37/2606	320/23843	0.383606	0.666586	0.633851	A4gnt/Alg6
GO_BP_m1	GO:004513	developme	25/2606	213/23843	0.383978	0.666909	0.634158	Ccdc182/A
GO_BP_m1	GO:004215	lipoprotein	12/2606	98/23843	0.384019	0.666909	0.634158	Apobec1/A
GO_BP_m1	GO:005265	cyclic purin	12/2606	98/23843	0.384019	0.666909	0.634158	Adcy4/Adr
GO_BP_m1	GO:003476	positive reg	18/2606	151/23843	0.385212	0.668717	0.635877	Abcb1a/Ak
GO_BP_m1	GO:004666	male sex di	18/2606	151/23843	0.385212	0.668717	0.635877	Amh/Asb1/
GO_BP_m1	GO:004275	regulation	13/2606	107/23843	0.386875	0.671338	0.638369	Adora1/Ar
GO_BP_m1	GO:004881	regulation	13/2606	107/23843	0.386875	0.671338	0.638369	Ache/Arhg
GO_BP_m1	GO:001485	striated mu	9/2606	72/23843	0.387944	0.672793	0.639753	Cdk1/Ephb
GO_BP_m1	GO:003080	regulation	9/2606	72/23843	0.387944	0.672793	0.639753	Adra1d/Ak
GO_BP_m1	GO:004244	hormone b	9/2606	72/23843	0.387944	0.672793	0.639753	Dgkq/Dio2
GO_BP_m1	GO:000703	endosome	6/2606	46/23843	0.388984	0.673932	0.640836	Dnajc13/Pa
GO_BP_m1	GO:003513	forelimb m	6/2606	46/23843	0.388984	0.673932	0.640836	Alx3/Hoxd1
GO_BP_m1	GO:004542	positive reg	6/2606	46/23843	0.388984	0.673932	0.640836	Cd36/Ifng/
GO_BP_m1	GO:006004	regulation	6/2606	46/23843	0.388984	0.673932	0.640836	Cdk1/Hdac
GO_BP_m1	GO:190440	positive reg	6/2606	46/23843	0.388984	0.673932	0.640836	Cd36/Ifng/
GO_BP_m1	GO:004210	B cell prolif	14/2606	116/23843	0.389325	0.674389	0.641271	Cdkn1a/Ct
GO_BP_m1	GO:003227	positive reg	15/2606	125/23843	0.391443	0.67764	0.644362	Ankrd53/C
GO_BP_m1	GO:001715	regulation	23/2606	196/23843	0.391572	0.67764	0.644362	Bcr/Catspe
GO_BP_m1	GO:000193	positive reg	10/2606	81/23843	0.391891	0.67764	0.644362	Arg1/Cav1/
GO_BP_m1	GO:003220	regulation	10/2606	81/23843	0.391891	0.67764	0.644362	Atr/Cct3/H
GO_BP_m1	GO:004866	neuron fate	10/2606	81/23843	0.391891	0.67764	0.644362	Dbx1/Dll4/
GO_BP_m1	GO:000110	response to	40/2606	348/23843	0.392119	0.67764	0.644362	Abl2/Adh1
GO_BP_m1	GO:000177	microglial c	4/2606	29/23843	0.392744	0.67764	0.644362	Fpr2/Itgam
GO_BP_m1	GO:000195	endochond	4/2606	29/23843	0.392744	0.67764	0.644362	Alpl/Csgaln
GO_BP_m1	GO:000209	positive reg	4/2606	29/23843	0.392744	0.67764	0.644362	Cd63/Fmr1
GO_BP_m1	GO:000269	regulation	4/2606	29/23843	0.392744	0.67764	0.644362	Adam8/Bcr
GO_BP_m1	GO:000330	type B pan	4/2606	29/23843	0.392744	0.67764	0.644362	Arntl/Clock
GO_BP_m1	GO:000682	zinc ion tra	4/2606	29/23843	0.392744	0.67764	0.644362	Mt3/Slc30a
GO_BP_m1	GO:003326	nuclear DN	4/2606	29/23843	0.392744	0.67764	0.644362	Cdc7/Dach
GO_BP_m1	GO:003530	negative re	4/2606	29/23843	0.392744	0.67764	0.644362	Fkbp1b/Ma
GO_BP_m1	GO:003607	replacemen	4/2606	29/23843	0.392744	0.67764	0.644362	Alpl/Csgaln

GO_BP_m1	GO:004567	positive re	4/2606	29/23843	0.392744	0.67764	0.644362	Ccr1/Ifng/I
GO_BP_m1	GO:004595	positive re	4/2606	29/23843	0.392744	0.67764	0.644362	Cadm1/Il1
GO_BP_m1	GO:004864	positive re	4/2606	29/23843	0.392744	0.67764	0.644362	Arntl/Rps6
GO_BP_m1	GO:200051	positive re	4/2606	29/23843	0.392744	0.67764	0.644362	Ifng/Il2rg/
GO_BP_m1	GO:200101	regulation	4/2606	29/23843	0.392744	0.67764	0.644362	Arntl/Ephb
GO_BP_m1	GO:004247	ear morph	16/2606	134/23843	0.393287	0.678444	0.645126	Aldh1a3/B
GO_BP_m1	GO:001003	response t	27/2606	232/23843	0.394747	0.680288	0.64688	Abat/Aoc1
GO_BP_m1	GO:003032	embryonic	17/2606	143/23843	0.394903	0.680288	0.64688	Alx3/B9d1/
GO_BP_m1	GO:003511	embryonic	17/2606	143/23843	0.394903	0.680288	0.64688	Alx3/B9d1/
GO_BP_m1	GO:005095	sensory pe	17/2606	143/23843	0.394903	0.680288	0.64688	Bbs2/Cacn
GO_BP_m1	GO:000202	regulation	11/2606	90/23843	0.395133	0.680288	0.64688	Adm/Avpr
GO_BP_m1	GO:004668	response t	11/2606	90/23843	0.395133	0.680288	0.64688	Akap6/Asp
GO_BP_m1	GO:001580	L-amino a	7/2606	55/23843	0.39544	0.680288	0.64688	Arg1/Arl6i
GO_BP_m1	GO:004362	regulation	7/2606	55/23843	0.39544	0.680288	0.64688	Atf3/Bclaf1
GO_BP_m1	GO:004853	thymus de	7/2606	55/23843	0.39544	0.680288	0.64688	Asxl1/Ephb
GO_BP_m1	GO:006035	endochon	7/2606	55/23843	0.39544	0.680288	0.64688	Alpl/Csgal
GO_BP_m1	GO:006197	replaceme	7/2606	55/23843	0.39544	0.680288	0.64688	Alpl/Csgal
GO_BP_m1	GO:009890	regulation	7/2606	55/23843	0.39544	0.680288	0.64688	Cav1/Cav3
GO_BP_m1	GO:190307	positive re	7/2606	55/23843	0.39544	0.680288	0.64688	Cib1/Epha
GO_BP_m1	GO:200077	regulation	7/2606	55/23843	0.39544	0.680288	0.64688	Blm/Dek/F
GO_BP_m1	GO:000926	cellular res	18/2606	152/23843	0.396324	0.681675	0.648199	Aoc1/Atf3/
GO_BP_m1	GO:001620	regulation	19/2606	161/23843	0.397581	0.683702	0.650126	Akap6/Arn
GO_BP_m1	GO:190180	positive re	12/2606	99/23843	0.397833	0.684002	0.650412	Arih2/Bcap
GO_BP_m1	GO:200027	regulation	13/2606	108/23843	0.40011	0.68774	0.653966	Ankrd1/At
GO_BP_m1	GO:000694	syncytium	8/2606	64/23843	0.400321	0.68774	0.653966	Adam8/Ca
GO_BP_m1	GO:003261	interleukin	8/2606	64/23843	0.400321	0.68774	0.653966	5730559C1
GO_BP_m1	GO:004333	response t	8/2606	64/23843	0.400321	0.68774	0.653966	Cav1/Ddx2
GO_BP_m1	GO:007124	cellular res	22/2606	188/23843	0.400567	0.688029	0.654241	Aoc1/Asph
GO_BP_m1	GO:003526	multicellul	24/2606	206/23843	0.402058	0.690288	0.656389	Abl2/Bbs2/
GO_BP_m1	GO:000057	embryonic	5/2606	38/23843	0.402668	0.690288	0.656389	Foxa2/Sma
GO_BP_m1	GO:000272	positive re	5/2606	38/23843	0.402668	0.690288	0.656389	Cd36/Gprc
GO_BP_m1	GO:004478	cell cycle D	5/2606	38/23843	0.402668	0.690288	0.656389	Cdc7/Dach
GO_BP_m1	GO:004688	regulation	5/2606	38/23843	0.402668	0.690288	0.656389	Dgkq/Ifng/
GO_BP_m1	GO:007235	tricarboxyli	5/2606	38/23843	0.402668	0.690288	0.656389	Idh2/Idh3a
GO_BP_m1	GO:190595	negative re	5/2606	38/23843	0.402668	0.690288	0.656389	Igfbp3/Nr1
GO_BP_m1	GO:200000	regulation	5/2606	38/23843	0.402668	0.690288	0.656389	Abca12/C
GO_BP_m1	GO:200027	negative re	5/2606	38/23843	0.402668	0.690288	0.656389	Ankrd1/Da
GO_BP_m1	GO:200102	positive re	5/2606	38/23843	0.402668	0.690288	0.656389	Abcb1a/En
GO_BP_m1	GO:003017	positive re	15/2606	126/23843	0.403709	0.691802	0.657829	Abl2/Arntl/
GO_BP_m1	GO:007133	cellular res	15/2606	126/23843	0.403709	0.691802	0.657829	Ano1/Fkbp
GO_BP_m1	GO:000191	regulation	9/2606	73/23843	0.404128	0.692115	0.658127	Arg1/Cad
GO_BP_m1	GO:004632	regulation	9/2606	73/23843	0.404128	0.692115	0.658127	Adipor2/A
GO_BP_m1	GO:190137	regulation	9/2606	73/23843	0.404128	0.692115	0.658127	Akap6/Atp
GO_BP_m1	GO:003021	keratinocyt	16/2606	135/23843	0.405143	0.693594	0.659533	Abca12/Ce
GO_BP_m1	GO:009059	sensory or	34/2606	296/23843	0.40603	0.693594	0.659533	Aldh1a3/B
GO_BP_m1	GO:000690	phagocyto	36/2606	314/23843	0.406386	0.693594	0.659533	Abl2/Anxa
GO_BP_m1	GO:000332	type B pan	3/2606	21/23843	0.407129	0.693594	0.659533	Arntl/Clock
GO_BP_m1	GO:001066	epithelial s	3/2606	21/23843	0.407129	0.693594	0.659533	5730559C1

GO_BP_m1	GO:001932	hexose cat	3/2606	21/23843	0.407129	0.693594	0.659533	Ldha/Tigar
GO_BP_m1	GO:003129	retinal gan	3/2606	21/23843	0.407129	0.693594	0.659533	Epha7/Eph
GO_BP_m1	GO:003411	regulation	3/2606	21/23843	0.407129	0.693594	0.659533	Gcnt2/Il10/
GO_BP_m1	GO:003437	plasma lipo	3/2606	21/23843	0.407129	0.693594	0.659533	Dgat1/Mttp
GO_BP_m1	GO:003630	lymph vess	3/2606	21/23843	0.407129	0.693594	0.659533	Epha2/Foxc
GO_BP_m1	GO:003969	viral RNA g	3/2606	21/23843	0.407129	0.693594	0.659533	Fmr1/Rab5
GO_BP_m1	GO:004245	purine nuc	3/2606	21/23843	0.407129	0.693594	0.659533	Adk/Aprt/N
GO_BP_m1	GO:004572	positive reg	3/2606	21/23843	0.407129	0.693594	0.659533	Avpr1a/Nr1
GO_BP_m1	GO:004583	positive reg	3/2606	21/23843	0.407129	0.693594	0.659533	Gria1/Myc/
GO_BP_m1	GO:004612	purine ribo	3/2606	21/23843	0.407129	0.693594	0.659533	Adk/Aprt/N
GO_BP_m1	GO:004663	negative re	3/2606	21/23843	0.407129	0.693594	0.659533	Jak3/Smad
GO_BP_m1	GO:004802	positive reg	3/2606	21/23843	0.407129	0.693594	0.659533	Hmx2/Prdx
GO_BP_m1	GO:006133	establishm	3/2606	21/23843	0.407129	0.693594	0.659533	Fscn1/Gbf1
GO_BP_m1	GO:007086	regulation	3/2606	21/23843	0.407129	0.693594	0.659533	Bcap31/Se
GO_BP_m1	GO:007264	interferon-	3/2606	21/23843	0.407129	0.693594	0.659533	Abl2/Ptpn2
GO_BP_m1	GO:190351	release of s	3/2606	21/23843	0.407129	0.693594	0.659533	Dhrs7c/Fkb
GO_BP_m1	GO:200048	regulation	3/2606	21/23843	0.407129	0.693594	0.659533	Hyal2/Ptpr
GO_BP_m1	GO:003294	negative re	10/2606	82/23843	0.407168	0.693594	0.659533	Arg1/Cd80
GO_BP_m1	GO:005067	negative re	10/2606	82/23843	0.407168	0.693594	0.659533	Arg1/Cd80
GO_BP_m1	GO:007233	intrinsic ap	10/2606	82/23843	0.407168	0.693594	0.659533	Bok/Cdkn1
GO_BP_m1	GO:005126	protein tetr	19/2606	162/23843	0.408414	0.693594	0.659533	Ache/Acpp
GO_BP_m1	GO:190211	regulation	20/2606	171/23843	0.409242	0.693594	0.659533	Cav3/Chmp
GO_BP_m1	GO:004355	regulation	6/2606	47/23843	0.409312	0.693594	0.659533	Epha8/Fpr2
GO_BP_m1	GO:005197	regulation	6/2606	47/23843	0.409312	0.693594	0.659533	Hmbox1/M
GO_BP_m1	GO:003286	cellular res	21/2606	180/23843	0.409968	0.693594	0.659533	Appl1/Bcar
GO_BP_m1	GO:190290	positive reg	22/2606	189/23843	0.410605	0.693594	0.659533	Ankrd53/C
GO_BP_m1	GO:003139	positive reg	12/2606	100/23843	0.411676	0.693594	0.659533	5730559C1
GO_BP_m1	GO:190000	positive reg	12/2606	100/23843	0.411676	0.693594	0.659533	Ache/Capr
GO_BP_m1	GO:001050	regulation	27/2606	234/23843	0.412783	0.693594	0.659533	3110002H1
GO_BP_m1	GO:000018	activation c	13/2606	109/23843	0.413373	0.693594	0.659533	5730559C1
GO_BP_m1	GO:003011	regulation	32/2606	279/23843	0.413837	0.693594	0.659533	Abl2/Arntl/
GO_BP_m1	GO:007132	cellular res	15/2606	127/23843	0.416001	0.693594	0.659533	Ano1/Fkbp
GO_BP_m1	GO:004870	embryonic	16/2606	136/23843	0.417023	0.693594	0.659533	Alx3/Dscar
GO_BP_m1	GO:000256	somatic div	8/2606	65/23843	0.417598	0.693594	0.659533	Aplf/Ifng/Il
GO_BP_m1	GO:000314	embryonic	8/2606	65/23843	0.417598	0.693594	0.659533	Cfc1/Dnaa
GO_BP_m1	GO:000651	protein mo	8/2606	65/23843	0.417598	0.693594	0.659533	Cul1/Kdm2
GO_BP_m1	GO:001644	somatic cel	8/2606	65/23843	0.417598	0.693594	0.659533	Aplf/Ifng/Il
GO_BP_m1	GO:004801	inositol lipi	17/2606	145/23843	0.417893	0.693594	0.659533	Csf3/Dcn/E
GO_BP_m1	GO:000196	startle resp	4/2606	30/23843	0.41848	0.693594	0.659533	Drd3/Grin2
GO_BP_m1	GO:000271	positive reg	4/2606	30/23843	0.41848	0.693594	0.659533	Cadm1/Il12
GO_BP_m1	GO:003259	protein tra	4/2606	30/23843	0.41848	0.693594	0.659533	Arhgap44/
GO_BP_m1	GO:004431	wound hea	4/2606	30/23843	0.41848	0.693594	0.659533	Col5a1/Mn
GO_BP_m1	GO:004593	negative re	4/2606	30/23843	0.41848	0.693594	0.659533	Adora1/Dc
GO_BP_m1	GO:005068	positive reg	4/2606	30/23843	0.41848	0.693594	0.659533	Cpeb3/Hm
GO_BP_m1	GO:006184	microtubul	4/2606	30/23843	0.41848	0.693594	0.659533	Ezr/Nubp1
GO_BP_m1	GO:009050	epiboly inv	4/2606	30/23843	0.41848	0.693594	0.659533	Col5a1/Mn
GO_BP_m1	GO:190211	positive reg	4/2606	30/23843	0.41848	0.693594	0.659533	Bnip3/Bok/
GO_BP_m1	GO:200014	positive reg	4/2606	30/23843	0.41848	0.693594	0.659533	Bclaf1/Can

GO_BP_m1	GO:004865	smooth mu	18/2606	154/23843	0.418636	0.693594	0.659533	Alox12/Cav
GO_BP_m1	GO:003052	intracellula	23/2606	199/23843	0.420993	0.693594	0.659533	5730559C1
GO_BP_m1	GO:004873	appendage	23/2606	199/23843	0.420993	0.693594	0.659533	Alx3/Asph/
GO_BP_m1	GO:006017	limb devel	23/2606	199/23843	0.420993	0.693594	0.659533	Alx3/Asph/
GO_BP_m1	GO:009027	regulation	25/2606	217/23843	0.421497	0.693594	0.659533	Abat/Ano1
GO_BP_m1	GO:190199	regulation	29/2606	253/23843	0.42203	0.693594	0.659533	Blm/Ccng1
GO_BP_m1	GO:003243	positive re	10/2606	83/23843	0.422454	0.693594	0.659533	Arih2/Bcap
GO_BP_m1	GO:003275	positive re	10/2606	83/23843	0.422454	0.693594	0.659533	5730559C1
GO_BP_m1	GO:004249	mechanore	10/2606	83/23843	0.422454	0.693594	0.659533	Atp8b1/Ctl
GO_BP_m1	GO:000047	endonucle	2/2606	13/23843	0.423668	0.693594	0.659533	Bms1/Kri1
GO_BP_m1	GO:000155	luteinizatio	2/2606	13/23843	0.423668	0.693594	0.659533	Nr5a1/Pdg
GO_BP_m1	GO:000184	phagolysos	2/2606	13/23843	0.423668	0.693594	0.659533	Rab34/Srp
GO_BP_m1	GO:000317	mitral valve	2/2606	13/23843	0.423668	0.693594	0.659533	Smad6/Zfp
GO_BP_m1	GO:000317	pulmonary	2/2606	13/23843	0.423668	0.693594	0.659533	Jag1/Smad
GO_BP_m1	GO:000318	pulmonary	2/2606	13/23843	0.423668	0.693594	0.659533	Jag1/Smad
GO_BP_m1	GO:000626	mitochond	2/2606	13/23843	0.423668	0.693594	0.659533	Lig3/Polg
GO_BP_m1	GO:000659	polyamine	2/2606	13/23843	0.423668	0.693594	0.659533	Agmat/Oa
GO_BP_m1	GO:000686	nucleotide	2/2606	13/23843	0.423668	0.693594	0.659533	Slc25a23/S
GO_BP_m1	GO:000761	short-term	2/2606	13/23843	0.423668	0.693594	0.659533	Npas4/Ser
GO_BP_m1	GO:000906	aspartate f	2/2606	13/23843	0.423668	0.693594	0.659533	Ddo/Got1
GO_BP_m1	GO:001080	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Ccdc3/Peli
GO_BP_m1	GO:001091	positive re	2/2606	13/23843	0.423668	0.693594	0.659533	Myc/Park2
GO_BP_m1	GO:001580	basic amin	2/2606	13/23843	0.423668	0.693594	0.659533	Arg1/AU01
GO_BP_m1	GO:001918	nonribosor	2/2606	13/23843	0.423668	0.693594	0.659533	Bdh2/Gclm
GO_BP_m1	GO:001937	leukotriene	2/2606	13/23843	0.423668	0.693594	0.659533	Alox5/Ltc4
GO_BP_m1	GO:002179	thalamus d	2/2606	13/23843	0.423668	0.693594	0.659533	Ncam1/Sm
GO_BP_m1	GO:002193	regulation	2/2606	13/23843	0.423668	0.693594	0.659533	Cend1/Sm
GO_BP_m1	GO:003021	hyaluronar	2/2606	13/23843	0.423668	0.693594	0.659533	Has2/Nfkb
GO_BP_m1	GO:003025	lipid glycos	2/2606	13/23843	0.423668	0.693594	0.659533	Abo/Slc35
GO_BP_m1	GO:003049	fatty acid e	2/2606	13/23843	0.423668	0.693594	0.659533	Pecr/Tecr
GO_BP_m1	GO:003111	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Snca/Stmn
GO_BP_m1	GO:003195	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Cav1/Ptprc
GO_BP_m1	GO:003230	regulation	2/2606	13/23843	0.423668	0.693594	0.659533	P2ry2/Tnfs
GO_BP_m1	GO:003806	collagen-a	2/2606	13/23843	0.423668	0.693594	0.659533	Col4a2/Ub
GO_BP_m1	GO:003809	Fc recepto	2/2606	13/23843	0.423668	0.693594	0.659533	Ms4a2/Osc
GO_BP_m1	GO:004253	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Cav1/Traf3
GO_BP_m1	GO:004311	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Adm/Ptprj
GO_BP_m1	GO:004324	telomere m	2/2606	13/23843	0.423668	0.693594	0.659533	Dclre1a/Xr
GO_BP_m1	GO:004351	positive re	2/2606	13/23843	0.423668	0.693594	0.659533	Ankrd1/Atr
GO_BP_m1	GO:004534	MHC class	2/2606	13/23843	0.423668	0.693594	0.659533	Ifng/Il10
GO_BP_m1	GO:004559	positive re	2/2606	13/23843	0.423668	0.693594	0.659533	Ifng/Il2rg
GO_BP_m1	GO:004830	positive re	2/2606	13/23843	0.423668	0.693594	0.659533	Ifng/Ptprc
GO_BP_m1	GO:004834	paraxial me	2/2606	13/23843	0.423668	0.693594	0.659533	Foxc1/Wnt
GO_BP_m1	GO:004848	enteric ner	2/2606	13/23843	0.423668	0.693594	0.659533	Ednrb/Gdn
GO_BP_m1	GO:005119	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Ppargc1a/
GO_BP_m1	GO:005176	actin crossl	2/2606	13/23843	0.423668	0.693594	0.659533	Pls1/Pls3
GO_BP_m1	GO:005511	relaxation	2/2606	13/23843	0.423668	0.693594	0.659533	Akap6/Pde
GO_BP_m1	GO:006067	branching	2/2606	13/23843	0.423668	0.693594	0.659533	Adm/Il10

GO_BP_m1	GO:006091	cardiac cell	2/2606	13/23843	0.423668	0.693594	0.659533	Wnt3a/Wt1
GO_BP_m1	GO:007025	regulation	2/2606	13/23843	0.423668	0.693594	0.659533	Adora1/P2
GO_BP_m1	GO:007171	ER-associa	2/2606	13/23843	0.423668	0.693594	0.659533	Ufd1/Uggt
GO_BP_m1	GO:007242	signal trans	2/2606	13/23843	0.423668	0.693594	0.659533	Babam2/Ui
GO_BP_m1	GO:007253	fibroblast a	2/2606	13/23843	0.423668	0.693594	0.659533	Acta2/Dga
GO_BP_m1	GO:008606	AV node ce	2/2606	13/23843	0.423668	0.693594	0.659533	Cacnb2/Gj
GO_BP_m1	GO:009019	regulation	2/2606	13/23843	0.423668	0.693594	0.659533	Il1rl1/Pycar
GO_BP_m1	GO:009050	RNA phosp	2/2606	13/23843	0.423668	0.693594	0.659533	Eri1/Exosc9
GO_BP_m1	GO:009706	response to	2/2606	13/23843	0.423668	0.693594	0.659533	Lmo2/Ppar
GO_BP_m1	GO:009870	calcium ior	2/2606	13/23843	0.423668	0.693594	0.659533	Calcr/Trpv6
GO_BP_m1	GO:009887	neurotrans	2/2606	13/23843	0.423668	0.693594	0.659533	Arhgap44/
GO_BP_m1	GO:190002	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	Bcar1/Itgb1
GO_BP_m1	GO:190217	cellular res	2/2606	13/23843	0.423668	0.693594	0.659533	Bcar1/Kcnc
GO_BP_m1	GO:190265	calcium ior	2/2606	13/23843	0.423668	0.693594	0.659533	Calcr/Trpv6
GO_BP_m1	GO:190299	negative re	2/2606	13/23843	0.423668	0.693594	0.659533	C330021F2
GO_BP_m1	GO:190418	positive reg	2/2606	13/23843	0.423668	0.693594	0.659533	Alox12/Dcr
GO_BP_m1	GO:200009	regulation	2/2606	13/23843	0.423668	0.693594	0.659533	Abl2/Mllt3
GO_BP_m1	GO:200048	positive reg	2/2606	13/23843	0.423668	0.693594	0.659533	Hyal2/Pyca
GO_BP_m1	GO:200126	regulation	2/2606	13/23843	0.423668	0.693594	0.659533	Gsn/Tfap4
GO_BP_m1	GO:000202	regulation	11/2606	92/23843	0.424157	0.693594	0.659533	Atp1b2/Atp
GO_BP_m1	GO:001489	striated mu	11/2606	92/23843	0.424157	0.693594	0.659533	Adk/Akap6
GO_BP_m1	GO:000002	ribosomal l	5/2606	39/23843	0.425183	0.693594	0.659533	Dhx30/Mrp
GO_BP_m1	GO:003043	sleep	5/2606	39/23843	0.425183	0.693594	0.659533	Adora1/Dr
GO_BP_m1	GO:003107	embryonic	5/2606	39/23843	0.425183	0.693594	0.659533	Aldh1a3/Ko
GO_BP_m1	GO:006012	inner ear re	5/2606	39/23843	0.425183	0.693594	0.659533	Cthrc1/Ift27
GO_BP_m1	GO:006096	regulation	5/2606	39/23843	0.425183	0.693594	0.659533	Fmr1/Mael
GO_BP_m1	GO:007152	semaphori	5/2606	39/23843	0.425183	0.693594	0.659533	Mir23a/Mir
GO_BP_m1	GO:190199	toxin trans	5/2606	39/23843	0.425183	0.693594	0.659533	Antxr1/Ant
GO_BP_m1	GO:004326	regulation	12/2606	101/23843	0.425531	0.693594	0.659533	Adora1/Ad
GO_BP_m1	GO:005086	negative re	13/2606	110/23843	0.426648	0.693594	0.659533	Arg1/Cd80
GO_BP_m1	GO:006138	regulation	14/2606	119/23843	0.42756	0.693594	0.659533	Aatk/Cdk5/
GO_BP_m1	GO:000150	ossification	41/2606	362/23843	0.428811	0.693594	0.659533	Alpl/Ank/B
GO_BP_m1	GO:003263	interleukin-	16/2606	137/23843	0.428917	0.693594	0.659533	5730559C1
GO_BP_m1	GO:004666	female sex	17/2606	146/23843	0.429415	0.693594	0.659533	Ccdc182/A
GO_BP_m1	GO:005149	negative re	17/2606	146/23843	0.429415	0.693594	0.659533	Cav3/Cfl1/
GO_BP_m1	GO:004301	camera-typ	38/2606	335/23843	0.429431	0.693594	0.659533	Ache/Aldh1
GO_BP_m1	GO:003164	regulation	6/2606	48/23843	0.429574	0.693594	0.659533	Cdh2/Ifng/
GO_BP_m1	GO:004395	cellular cor	6/2606	48/23843	0.429574	0.693594	0.659533	5730559C1
GO_BP_m1	GO:004650	glycerolipic	6/2606	48/23843	0.429574	0.693594	0.659533	Enpp2/Mgl
GO_BP_m1	GO:005195	positive reg	6/2606	48/23843	0.429574	0.693594	0.659533	Abat/Avpr1
GO_BP_m1	GO:003530	regulation	19/2606	164/23843	0.430142	0.693594	0.659533	2810408A1
GO_BP_m1	GO:004875	branching	21/2606	182/23843	0.430592	0.693594	0.659533	Cav3/Dll4/
GO_BP_m1	GO:001905	viral life cy	22/2606	191/23843	0.430737	0.693594	0.659533	Cav1/Chm
GO_BP_m1	GO:000270	regulation	23/2606	200/23843	0.430837	0.693594	0.659533	Aplf/Arg1/
GO_BP_m1	GO:000840	gonad dev	24/2606	209/23843	0.430899	0.693594	0.659533	Ccdc182/A
GO_BP_m1	GO:003476	positive reg	24/2606	209/23843	0.430899	0.693594	0.659533	Abcb1a/Ac
GO_BP_m1	GO:003026	entry into h	7/2606	57/23843	0.432631	0.693594	0.659533	Cav1/Gsn/
GO_BP_m1	GO:004440	entry into h	7/2606	57/23843	0.432631	0.693594	0.659533	Cav1/Gsn/

GO_BP_m1	GO:005180	entry into c	7/2606	57/23843	0.432631	0.693594	0.659533	Cav1/Gsn/
GO_BP_m1	GO:005182	entry into c	7/2606	57/23843	0.432631	0.693594	0.659533	Cav1/Gsn/
GO_BP_m1	GO:006011	inner ear re	7/2606	57/23843	0.432631	0.693594	0.659533	Atp8b1/Ct
GO_BP_m1	GO:190342	positive reg	7/2606	57/23843	0.432631	0.693594	0.659533	Cd36/Ifng/
GO_BP_m1	GO:001605	Wnt signali	47/2606	417/23843	0.434263	0.693594	0.659533	Abl2/Arntl/
GO_BP_m1	GO:000154	ovarian foll	8/2606	66/23843	0.434845	0.693594	0.659533	Amh/Fancf
GO_BP_m1	GO:000333	amino acid	8/2606	66/23843	0.434845	0.693594	0.659533	Arl6ip5/AU
GO_BP_m1	GO:000988	embryonic	8/2606	66/23843	0.434845	0.693594	0.659533	Foxa2/Mec
GO_BP_m1	GO:190188	regulation	9/2606	75/23843	0.436487	0.693594	0.659533	Bcas3/Cav1
GO_BP_m1	GO:000002	ribosomal s	3/2606	22/23843	0.437551	0.693594	0.659533	Eral1/Rps2
GO_BP_m1	GO:000027	polysaccha	3/2606	22/23843	0.437551	0.693594	0.659533	Ppp1r3d/P
GO_BP_m1	GO:000191	positive reg	3/2606	22/23843	0.437551	0.693594	0.659533	Fam49b/Il1
GO_BP_m1	GO:000714	male meios	3/2606	22/23843	0.437551	0.693594	0.659533	Btbd18/Dd
GO_BP_m1	GO:000741	axonal fasc	3/2606	22/23843	0.437551	0.693594	0.659533	Ephb3/Nca
GO_BP_m1	GO:001097	positive reg	3/2606	22/23843	0.437551	0.693594	0.659533	Cdc7/Cdk1
GO_BP_m1	GO:001485	response to	3/2606	22/23843	0.437551	0.693594	0.659533	Perm1/Ppa
GO_BP_m1	GO:001604	detection o	3/2606	22/23843	0.437551	0.693594	0.659533	Adora1/An
GO_BP_m1	GO:003250	cytokinetic	3/2606	22/23843	0.437551	0.693594	0.659533	Kif23/Racg
GO_BP_m1	GO:003440	response to	3/2606	22/23843	0.437551	0.693594	0.659533	Ift88/Ptgs2
GO_BP_m1	GO:003502	negative re	3/2606	22/23843	0.437551	0.693594	0.659533	Abl2/Flcn/
GO_BP_m1	GO:003563	response to	3/2606	22/23843	0.437551	0.693594	0.659533	Cd36/Mup
GO_BP_m1	GO:004257	retinoic aci	3/2606	22/23843	0.437551	0.693594	0.659533	Adh1/Aldh
GO_BP_m1	GO:004485	hair cycle p	3/2606	22/23843	0.437551	0.693594	0.659533	Ctsl/Krtap2
GO_BP_m1	GO:004665	tetrahydrof	3/2606	22/23843	0.437551	0.693594	0.659533	Gch1/Mthf
GO_BP_m1	GO:004833	paraxial me	3/2606	22/23843	0.437551	0.693594	0.659533	Foxc1/Tcf1
GO_BP_m1	GO:004853	anatomical	3/2606	22/23843	0.437551	0.693594	0.659533	Hoxb1/Kcn
GO_BP_m1	GO:004885	neural nucl	3/2606	22/23843	0.437551	0.693594	0.659533	Aldh1a3/A
GO_BP_m1	GO:005099	negative re	3/2606	22/23843	0.437551	0.693594	0.659533	Adora1/Hc
GO_BP_m1	GO:005144	positive reg	3/2606	22/23843	0.437551	0.693594	0.659533	Dmrt1/Fbx
GO_BP_m1	GO:006026	positive reg	3/2606	22/23843	0.437551	0.693594	0.659533	Cand1/Psm
GO_BP_m1	GO:006057	intestinal e	3/2606	22/23843	0.437551	0.693594	0.659533	Cdh1/Gsdm
GO_BP_m1	GO:006108	myeloid leu	3/2606	22/23843	0.437551	0.693594	0.659533	Cd36/Gprc
GO_BP_m1	GO:010603	neuron pro	3/2606	22/23843	0.437551	0.693594	0.659533	Ephb3/Nca
GO_BP_m1	GO:190074	positive reg	3/2606	22/23843	0.437551	0.693594	0.659533	Kars/Prmt1
GO_BP_m1	GO:190153	regulation	3/2606	22/23843	0.437551	0.693594	0.659533	Eif2ak2/Flc
GO_BP_m1	GO:190165	glycosyl co	3/2606	22/23843	0.437551	0.693594	0.659533	Abhd10/De
GO_BP_m1	GO:190288	positive reg	3/2606	22/23843	0.437551	0.693594	0.659533	Endog/H2a
GO_BP_m1	GO:190330	negative re	3/2606	22/23843	0.437551	0.693594	0.659533	Bcr/Fmr1/T
GO_BP_m1	GO:001066	regulation	10/2606	84/23843	0.437725	0.693594	0.659533	Alox12/Bni
GO_BP_m1	GO:003571	CD4-positi	10/2606	84/23843	0.437725	0.693594	0.659533	Gpr183/Ifn
GO_BP_m1	GO:007209	regulation	10/2606	84/23843	0.437725	0.693594	0.659533	Dct/Dmrta
GO_BP_m1	GO:014002	exocytic pr	10/2606	84/23843	0.437725	0.693594	0.659533	Ncam1/P2r
GO_BP_m1	GO:000649	protein lipi	11/2606	93/23843	0.438665	0.693594	0.659533	Atg10/Map
GO_BP_m1	GO:001082	regulation	11/2606	93/23843	0.438665	0.693594	0.659533	Adipor2/Ad
GO_BP_m1	GO:003004	actin filame	12/2606	102/23843	0.43938	0.693594	0.659533	Acta2/Akap
GO_BP_m1	GO:000039	spliceosom	1/2606	5/23843	0.439418	0.693594	0.659533	Prpf19
GO_BP_m1	GO:000039	mRNA 5'-s	1/2606	5/23843	0.439418	0.693594	0.659533	Psip1
GO_BP_m1	GO:000072	double-stra	1/2606	5/23843	0.439418	0.693594	0.659533	Cdc7

GO_BP_m1	GO:000095	mitochond	1/2606	5/23843	0.439418	0.693594	0.659533	Pnpt1
GO_BP_m1	GO:000096	mitochond	1/2606	5/23843	0.439418	0.693594	0.659533	Pnpt1
GO_BP_m1	GO:000156	fatty acid a	1/2606	5/23843	0.439418	0.693594	0.659533	Phyh
GO_BP_m1	GO:000166	conditione	1/2606	5/23843	0.439418	0.693594	0.659533	Tbr1
GO_BP_m1	GO:000197	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Adra1d
GO_BP_m1	GO:000227	eosinophil	1/2606	5/23843	0.439418	0.693594	0.659533	Stx4a
GO_BP_m1	GO:000232	B cell linea	1/2606	5/23843	0.439418	0.693594	0.659533	Prkdc
GO_BP_m1	GO:000244	eosinophil	1/2606	5/23843	0.439418	0.693594	0.659533	Stx4a
GO_BP_m1	GO:000256	somatic div	1/2606	5/23843	0.439418	0.693594	0.659533	Prkdc
GO_BP_m1	GO:000258	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Pycard
GO_BP_m1	GO:000268	somatic rec	1/2606	5/23843	0.439418	0.693594	0.659533	Prkdc
GO_BP_m1	GO:000274	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Il10
GO_BP_m1	GO:000319	mitral valve	1/2606	5/23843	0.439418	0.693594	0.659533	Zfpm2
GO_BP_m1	GO:000328	atrial septu	1/2606	5/23843	0.439418	0.693594	0.659533	Nsd2
GO_BP_m1	GO:000611	glycerol bi	1/2606	5/23843	0.439418	0.693594	0.659533	Got1
GO_BP_m1	GO:000616	AMP biosy	1/2606	5/23843	0.439418	0.693594	0.659533	Adss
GO_BP_m1	GO:000639	mRNA 3'-e	1/2606	5/23843	0.439418	0.693594	0.659533	Cpsf2
GO_BP_m1	GO:000643	phenylalan	1/2606	5/23843	0.439418	0.693594	0.659533	Lrrc47
GO_BP_m1	GO:000644	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Ogfod1
GO_BP_m1	GO:000654	histidine ca	1/2606	5/23843	0.439418	0.693594	0.659533	Hdc
GO_BP_m1	GO:000654	isoleucine	1/2606	5/23843	0.439418	0.693594	0.659533	Bcat2
GO_BP_m1	GO:000659	polyamine	1/2606	5/23843	0.439418	0.693594	0.659533	Sat1
GO_BP_m1	GO:000665	phosphatic	1/2606	5/23843	0.439418	0.693594	0.659533	Tmem269
GO_BP_m1	GO:000677	vitamin A r	1/2606	5/23843	0.439418	0.693594	0.659533	Dgat1
GO_BP_m1	GO:000717	activation c	1/2606	5/23843	0.439418	0.693594	0.659533	Nrg1
GO_BP_m1	GO:000735	zygotic det	1/2606	5/23843	0.439418	0.693594	0.659533	Wt1
GO_BP_m1	GO:000829	spermidine	1/2606	5/23843	0.439418	0.693594	0.659533	Agmat
GO_BP_m1	GO:000861	ether lipid	1/2606	5/23843	0.439418	0.693594	0.659533	Fasn
GO_BP_m1	GO:000905	pentose-pl	1/2606	5/23843	0.439418	0.693594	0.659533	Rpe
GO_BP_m1	GO:000915	deoxyribor	1/2606	5/23843	0.439418	0.693594	0.659533	Shmt1
GO_BP_m1	GO:000917	pyrimidine	1/2606	5/23843	0.439418	0.693594	0.659533	Shmt1
GO_BP_m1	GO:000920	deoxyribor	1/2606	5/23843	0.439418	0.693594	0.659533	Adk
GO_BP_m1	GO:000925	10-formylt	1/2606	5/23843	0.439418	0.693594	0.659533	Mthfd1l
GO_BP_m1	GO:000944	gamma-ar	1/2606	5/23843	0.439418	0.693594	0.659533	Abat
GO_BP_m1	GO:001051	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Fpr2
GO_BP_m1	GO:001051	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Angptl3
GO_BP_m1	GO:001057	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Cdc7
GO_BP_m1	GO:001060	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Cnot6l
GO_BP_m1	GO:001063	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Bnip3
GO_BP_m1	GO:001069	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Npnt
GO_BP_m1	GO:001091	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Itgam
GO_BP_m1	GO:001091	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Itgam
GO_BP_m1	GO:001095	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Nfkb1
GO_BP_m1	GO:001098	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Anxa2
GO_BP_m1	GO:001098	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Pcsk9
GO_BP_m1	GO:001099	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Smad6
GO_BP_m1	GO:001099	free ubiqui	1/2606	5/23843	0.439418	0.693594	0.659533	Park2
GO_BP_m1	GO:001402	notochord	1/2606	5/23843	0.439418	0.693594	0.659533	Epha2

GO_BP_m1	GO:001404	establishm	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt7a
GO_BP_m1	GO:00148	skeletal mu	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt7a
GO_BP_m1	GO:001487	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Prkag3
GO_BP_m1	GO:001501	heparan su	1/2606	5/23843	0.439418	0.693594	0.659533	Hs6st1
GO_BP_m1	GO:00157	iodide tran	1/2606	5/23843	0.439418	0.693594	0.659533	Ano1
GO_BP_m1	GO:001584	urea trans	1/2606	5/23843	0.439418	0.693594	0.659533	Slc14a2
GO_BP_m1	GO:00158	cobalamin	1/2606	5/23843	0.439418	0.693594	0.659533	Gif
GO_BP_m1	GO:00161	synaptic ve	1/2606	5/23843	0.439418	0.693594	0.659533	Dnm3
GO_BP_m1	GO:00192	propriocep	1/2606	5/23843	0.439418	0.693594	0.659533	Tmem150c
GO_BP_m1	GO:001934	dolichol m	1/2606	5/23843	0.439418	0.693594	0.659533	Nus1
GO_BP_m1	GO:00215	glossophar	1/2606	5/23843	0.439418	0.693594	0.659533	Hoxa3
GO_BP_m1	GO:00216	trigeminal	1/2606	5/23843	0.439418	0.693594	0.659533	Sema3f
GO_BP_m1	GO:00216	trigeminal	1/2606	5/23843	0.439418	0.693594	0.659533	Sema3f
GO_BP_m1	GO:002191	negative r	1/2606	5/23843	0.439418	0.693594	0.659533	Tulp3
GO_BP_m1	GO:002241	protein ma	1/2606	5/23843	0.439418	0.693594	0.659533	Ero1l
GO_BP_m1	GO:003022	eosinophil	1/2606	5/23843	0.439418	0.693594	0.659533	Trib1
GO_BP_m1	GO:003024	autophagy	1/2606	5/23843	0.439418	0.693594	0.659533	Pik3r4
GO_BP_m1	GO:00303	membrane	1/2606	5/23843	0.439418	0.693594	0.659533	Pafah1b1
GO_BP_m1	GO:00312	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Guca1a
GO_BP_m1	GO:00315	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Asph
GO_BP_m1	GO:003207	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Pcna
GO_BP_m1	GO:00326	negative r	1/2606	5/23843	0.439418	0.693594	0.659533	Nmi
GO_BP_m1	GO:003274	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Ifng
GO_BP_m1	GO:003284	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Avpr1a
GO_BP_m1	GO:00328	neurotrop	1/2606	5/23843	0.439418	0.693594	0.659533	Adora1
GO_BP_m1	GO:00329	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	P2ry1
GO_BP_m1	GO:003302	mast cell h	1/2606	5/23843	0.439418	0.693594	0.659533	Kitl
GO_BP_m1	GO:003302	mast cell a	1/2606	5/23843	0.439418	0.693594	0.659533	Kitl
GO_BP_m1	GO:003302	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Kitl
GO_BP_m1	GO:00330	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Hcar2
GO_BP_m1	GO:00331	T cell rece	1/2606	5/23843	0.439418	0.693594	0.659533	Prkdc
GO_BP_m1	GO:00335	anterior/p	1/2606	5/23843	0.439418	0.693594	0.659533	Unc5c
GO_BP_m1	GO:00335	DNA replic	1/2606	5/23843	0.439418	0.693594	0.659533	Fen1
GO_BP_m1	GO:003357	protein gly	1/2606	5/23843	0.439418	0.693594	0.659533	Fut8
GO_BP_m1	GO:00336	negative r	1/2606	5/23843	0.439418	0.693594	0.659533	Abat
GO_BP_m1	GO:00336	negative r	1/2606	5/23843	0.439418	0.693594	0.659533	Tacr2
GO_BP_m1	GO:00341	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	H2afy
GO_BP_m1	GO:003422	tRNA thio-	1/2606	5/23843	0.439418	0.693594	0.659533	Urm1
GO_BP_m1	GO:003444	very-low-	1/2606	5/23843	0.439418	0.693594	0.659533	Vldlr
GO_BP_m1	GO:00354	determinat	1/2606	5/23843	0.439418	0.693594	0.659533	Dnaaf1
GO_BP_m1	GO:00354	gastric em	1/2606	5/23843	0.439418	0.693594	0.659533	Drd3
GO_BP_m1	GO:003552	proline tra	1/2606	5/23843	0.439418	0.693594	0.659533	Slc6a20a
GO_BP_m1	GO:003554	interferon-	1/2606	5/23843	0.439418	0.693594	0.659533	Ptpn22
GO_BP_m1	GO:003554	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Ptpn22
GO_BP_m1	GO:003554	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Ptpn22
GO_BP_m1	GO:00356	entry of ba	1/2606	5/23843	0.439418	0.693594	0.659533	Cav1
GO_BP_m1	GO:00356	mitochond	1/2606	5/23843	0.439418	0.693594	0.659533	Bnip3
GO_BP_m1	GO:003574	CD8-positi	1/2606	5/23843	0.439418	0.693594	0.659533	Ptpn22

GO_BP_m1	GO:003574	natural kille	1/2606	5/23843	0.439418	0.693594	0.659533	Ccl4
GO_BP_m1	GO:003577	interleukin-	1/2606	5/23843	0.439418	0.693594	0.659533	Jak3
GO_BP_m1	GO:003578	cell migrati	1/2606	5/23843	0.439418	0.693594	0.659533	Pdgfa
GO_BP_m1	GO:003579	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Bnip3
GO_BP_m1	GO:003586	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Crhbp
GO_BP_m1	GO:003586	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Crhbp
GO_BP_m1	GO:003589	parathyroid	1/2606	5/23843	0.439418	0.693594	0.659533	Trpv6
GO_BP_m1	GO:003590	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Aoc3
GO_BP_m1	GO:003593	corticostero	1/2606	5/23843	0.439418	0.693594	0.659533	Tac1
GO_BP_m1	GO:003596	COPI-coate	1/2606	5/23843	0.439418	0.693594	0.659533	Gbf1
GO_BP_m1	GO:003626	RNA (guan	1/2606	5/23843	0.439418	0.693594	0.659533	Rnmt
GO_BP_m1	GO:003817	cannabinoi	1/2606	5/23843	0.439418	0.693594	0.659533	Mgll
GO_BP_m1	GO:004253	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Il10
GO_BP_m1	GO:004330	eosinophil	1/2606	5/23843	0.439418	0.693594	0.659533	Stx4a
GO_BP_m1	GO:004340	cortisol sec	1/2606	5/23843	0.439418	0.693594	0.659533	Galr1
GO_BP_m1	GO:004357	maintenanc	1/2606	5/23843	0.439418	0.693594	0.659533	Msh3
GO_BP_m1	GO:004365	recognition	1/2606	5/23843	0.439418	0.693594	0.659533	Scarb1
GO_BP_m1	GO:004504	protein ins	1/2606	5/23843	0.439418	0.693594	0.659533	Wrb
GO_BP_m1	GO:004534	MHC class	1/2606	5/23843	0.439418	0.693594	0.659533	Hsph1
GO_BP_m1	GO:004534	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Hsph1
GO_BP_m1	GO:004534	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Hsph1
GO_BP_m1	GO:004534	interferon-	1/2606	5/23843	0.439418	0.693594	0.659533	Nmi
GO_BP_m1	GO:004535	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Nmi
GO_BP_m1	GO:004595	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Blm
GO_BP_m1	GO:004599	carbon cat	1/2606	5/23843	0.439418	0.693594	0.659533	Foxa2
GO_BP_m1	GO:004599	carbon cat	1/2606	5/23843	0.439418	0.693594	0.659533	Foxa2
GO_BP_m1	GO:004601	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Foxa2
GO_BP_m1	GO:004647	glycosylcer	1/2606	5/23843	0.439418	0.693594	0.659533	B4galt3
GO_BP_m1	GO:004650	protoporph	1/2606	5/23843	0.439418	0.693594	0.659533	Eif2ak1
GO_BP_m1	GO:004650	glycerol eth	1/2606	5/23843	0.439418	0.693594	0.659533	Fasn
GO_BP_m1	GO:004661	drug expor	1/2606	5/23843	0.439418	0.693594	0.659533	Abcb1a
GO_BP_m1	GO:004687	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Tac1
GO_BP_m1	GO:004831	axial meso	1/2606	5/23843	0.439418	0.693594	0.659533	Epha2
GO_BP_m1	GO:004866	collateral sp	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt3a
GO_BP_m1	GO:004867	axon exten	1/2606	5/23843	0.439418	0.693594	0.659533	Lamb2
GO_BP_m1	GO:004885	formation o	1/2606	5/23843	0.439418	0.693594	0.659533	Ntf5
GO_BP_m1	GO:005065	dermatan s	1/2606	5/23843	0.439418	0.693594	0.659533	Dse
GO_BP_m1	GO:005071	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Zc3h12a
GO_BP_m1	GO:005081	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Snca
GO_BP_m1	GO:005095	thermocep	1/2606	5/23843	0.439418	0.693594	0.659533	Cpeb3
GO_BP_m1	GO:005100	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Angptl3
GO_BP_m1	GO:005103	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Rab5a
GO_BP_m1	GO:005108	nuclear env	1/2606	5/23843	0.439418	0.693594	0.659533	Pafah1b1
GO_BP_m1	GO:005109	positive reg	1/2606	5/23843	0.439418	0.693594	0.659533	Msh3
GO_BP_m1	GO:005112	hepoxilin m	1/2606	5/23843	0.439418	0.693594	0.659533	Alox12
GO_BP_m1	GO:005112	hepoxilin b	1/2606	5/23843	0.439418	0.693594	0.659533	Alox12
GO_BP_m1	GO:005146	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Galr1
GO_BP_m1	GO:005156	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Micu2

GO_BP_m1	GO:005161	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Snca
GO_BP_m1	GO:005166	maintenan	1/2606	5/23843	0.439418	0.693594	0.659533	Pafah1b1
GO_BP_m1	GO:005166	actin cortic	1/2606	5/23843	0.439418	0.693594	0.659533	Wipf1
GO_BP_m1	GO:005175	meiotic sist	1/2606	5/23843	0.439418	0.693594	0.659533	Ppp2r1a
GO_BP_m1	GO:005179	medium-cl	1/2606	5/23843	0.439418	0.693594	0.659533	Abhd1
GO_BP_m1	GO:005196	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Epha7
GO_BP_m1	GO:006013	maternal p	1/2606	5/23843	0.439418	0.693594	0.659533	Arntl
GO_BP_m1	GO:006016	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Drd3
GO_BP_m1	GO:006031	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Akap6
GO_BP_m1	GO:006033	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Arg1
GO_BP_m1	GO:006033	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Arg1
GO_BP_m1	GO:006035	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Cav1
GO_BP_m1	GO:006062	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Wapl
GO_BP_m1	GO:006066	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Fgf7
GO_BP_m1	GO:006068	branch elo	1/2606	5/23843	0.439418	0.693594	0.659533	Fgf1
GO_BP_m1	GO:006069	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Scarb1
GO_BP_m1	GO:006094	cardiac vas	1/2606	5/23843	0.439418	0.693594	0.659533	Smad6
GO_BP_m1	GO:006095	endocardia	1/2606	5/23843	0.439418	0.693594	0.659533	Sox18
GO_BP_m1	GO:006104	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Pdgfra
GO_BP_m1	GO:006107	ciliary body	1/2606	5/23843	0.439418	0.693594	0.659533	Jag1
GO_BP_m1	GO:006131	canonical	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt3a
GO_BP_m1	GO:006174	motor lear	1/2606	5/23843	0.439418	0.693594	0.659533	C1ql1
GO_BP_m1	GO:007012	ciliary neur	1/2606	5/23843	0.439418	0.693594	0.659533	Cntfr
GO_BP_m1	GO:007012	mitochond	1/2606	5/23843	0.439418	0.693594	0.659533	Gfm1
GO_BP_m1	GO:007042	nucleotide-	1/2606	5/23843	0.439418	0.693594	0.659533	Peli3
GO_BP_m1	GO:007048	monocyte	1/2606	5/23843	0.439418	0.693594	0.659533	Has2
GO_BP_m1	GO:007066	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Jak3
GO_BP_m1	GO:007067	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Jak3
GO_BP_m1	GO:007103	nuclear pol	1/2606	5/23843	0.439418	0.693594	0.659533	Exosc9
GO_BP_m1	GO:007128	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Atp7b
GO_BP_m1	GO:007131	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Nfkb1
GO_BP_m1	GO:007144	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Kat2b
GO_BP_m1	GO:007145	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Cav1
GO_BP_m1	GO:007155	histone H3	1/2606	5/23843	0.439418	0.693594	0.659533	Kdm6b
GO_BP_m1	GO:007159	lymphocyte	1/2606	5/23843	0.439418	0.693594	0.659533	Adam8
GO_BP_m1	GO:007168	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Cdh1
GO_BP_m1	GO:007168	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Cdh1
GO_BP_m1	GO:007200	mesangial	1/2606	5/23843	0.439418	0.693594	0.659533	Osr1
GO_BP_m1	GO:007202	distal conv	1/2606	5/23843	0.439418	0.693594	0.659533	Pou3f3
GO_BP_m1	GO:007214	mesangial	1/2606	5/23843	0.439418	0.693594	0.659533	Osr1
GO_BP_m1	GO:007222	metanephr	1/2606	5/23843	0.439418	0.693594	0.659533	Pou3f3
GO_BP_m1	GO:007223	metanephr	1/2606	5/23843	0.439418	0.693594	0.659533	Pou3f3
GO_BP_m1	GO:007251	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Tbx1
GO_BP_m1	GO:007275	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Blm
GO_BP_m1	GO:008602	adenylate c	1/2606	5/23843	0.439418	0.693594	0.659533	Atp2b4
GO_BP_m1	GO:008604	membrane	1/2606	5/23843	0.439418	0.693594	0.659533	Cacnb2
GO_BP_m1	GO:009024	axis elonga	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt3a
GO_BP_m1	GO:009038	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt3a

GO_BP_m1	GO:009721	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Crhbp
GO_BP_m1	GO:009721	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Crhbp
GO_BP_m1	GO:009746	ubiquitin-c	1/2606	5/23843	0.439418	0.693594	0.659533	Man1b1
GO_BP_m1	GO:009763	L-arginine	1/2606	5/23843	0.439418	0.693594	0.659533	AU018091
GO_BP_m1	GO:009873	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Slc9a1
GO_BP_m1	GO:009888	neurotrans	1/2606	5/23843	0.439418	0.693594	0.659533	Arhgap44
GO_BP_m1	GO:009901	modificatio	1/2606	5/23843	0.439418	0.693594	0.659533	Arhgap44
GO_BP_m1	GO:009964	axo-dendr	1/2606	5/23843	0.439418	0.693594	0.659533	Stau2
GO_BP_m1	GO:014005	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Cd36
GO_BP_m1	GO:190022	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Mefv
GO_BP_m1	GO:190082	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Cav3
GO_BP_m1	GO:190107	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Pde4b
GO_BP_m1	GO:190116	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Syde1
GO_BP_m1	GO:190150	ether biosy	1/2606	5/23843	0.439418	0.693594	0.659533	Fasn
GO_BP_m1	GO:190167	nucleotide	1/2606	5/23843	0.439418	0.693594	0.659533	Slc25a33
GO_BP_m1	GO:190226	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Oaz1
GO_BP_m1	GO:190247	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Nlgn3
GO_BP_m1	GO:190271	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Zc3h12a
GO_BP_m1	GO:190307	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Bcap31
GO_BP_m1	GO:190323	melanosom	1/2606	5/23843	0.439418	0.693594	0.659533	Rab32
GO_BP_m1	GO:190337	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Park2
GO_BP_m1	GO:190391	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Nck2
GO_BP_m1	GO:190450	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Sptlc2
GO_BP_m1	GO:190450	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Sptlc2
GO_BP_m1	GO:190450	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Xrcc1
GO_BP_m1	GO:190450	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Xrcc1
GO_BP_m1	GO:190463	response t	1/2606	5/23843	0.439418	0.693594	0.659533	Zc3h12a
GO_BP_m1	GO:190463	cellular res	1/2606	5/23843	0.439418	0.693594	0.659533	Zc3h12a
GO_BP_m1	GO:190475	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Nmd3
GO_BP_m1	GO:190497	brush bord	1/2606	5/23843	0.439418	0.693594	0.659533	Myo7b
GO_BP_m1	GO:190544	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Cdk1
GO_BP_m1	GO:190565	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Ephb4
GO_BP_m1	GO:190570	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Bnip3
GO_BP_m1	GO:199044	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Nck2
GO_BP_m1	GO:199056	protein pol	1/2606	5/23843	0.439418	0.693594	0.659533	Ddrgk1
GO_BP_m1	GO:199059	protein K6	1/2606	5/23843	0.439418	0.693594	0.659533	Ddrgk1
GO_BP_m1	GO:200027	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Pm20d1
GO_BP_m1	GO:200030	negative re	1/2606	5/23843	0.439418	0.693594	0.659533	Fmr1
GO_BP_m1	GO:200038	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Wnt3a
GO_BP_m1	GO:200040	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Ripk3
GO_BP_m1	GO:200050	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Ccl4
GO_BP_m1	GO:200053	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Cav1
GO_BP_m1	GO:200056	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Ptpn22
GO_BP_m1	GO:200060	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Duoxa2
GO_BP_m1	GO:200081	regulation	1/2606	5/23843	0.439418	0.693594	0.659533	Cfl1
GO_BP_m1	GO:200096	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Nlgn3
GO_BP_m1	GO:200118	positive re	1/2606	5/23843	0.439418	0.693594	0.659533	Pycard
GO_BP_m1	GO:000176	morphoge	27/2606	237/23843	0.439966	0.694209	0.660118	Adm/Cav3

GO_BP_m1	GO:004657	regulation	27/2606	237/23843	0.439966	0.694209	0.660118	Abl2/Abra/
GO_BP_m1	GO:003629	response t	25/2606	219/23843	0.440364	0.694713	0.660597	Abat/Adam
GO_BP_m1	GO:000282	regulation	17/2606	147/23843	0.440941	0.694871	0.660747	Aplf/Arg1/
GO_BP_m1	GO:000176	neuron mig	20/2606	174/23843	0.440987	0.694871	0.660747	Arx/Cdh1/
GO_BP_m1	GO:003510	appendage	20/2606	174/23843	0.440987	0.694871	0.660747	Alx3/Asph/
GO_BP_m1	GO:003510	limb morph	20/2606	174/23843	0.440987	0.694871	0.660747	Alx3/Asph/
GO_BP_m1	GO:004576	positive reg	20/2606	174/23843	0.440987	0.694871	0.660747	Adm/Angp
GO_BP_m1	GO:004688	positive reg	18/2606	156/23843	0.441006	0.694871	0.660747	Abat/Ano1
GO_BP_m1	GO:190303	regulation	19/2606	165/23843	0.441019	0.694871	0.660747	Abat/Acta2
GO_BP_m1	GO:000702	negative re	4/2606	31/23843	0.443951	0.697864	0.663593	Cib1/Fgf13
GO_BP_m1	GO:001056	regulation	4/2606	31/23843	0.443951	0.697864	0.663593	Blm/Fbxo1
GO_BP_m1	GO:003206	regulation	4/2606	31/23843	0.443951	0.697864	0.663593	Dffa/Oas1f
GO_BP_m1	GO:003246	positive reg	4/2606	31/23843	0.443951	0.697864	0.663593	Cxcr5/Drd3
GO_BP_m1	GO:004362	ncRNA 3'-	4/2606	31/23843	0.443951	0.697864	0.663593	Elac1/Eri1/
GO_BP_m1	GO:005070	regulation	4/2606	31/23843	0.443951	0.697864	0.663593	Gsdmd/Ifng
GO_BP_m1	GO:006097	coronary va	4/2606	31/23843	0.443951	0.697864	0.663593	Fgf1/Smad
GO_BP_m1	GO:007052	protein kin	4/2606	31/23843	0.443951	0.697864	0.663593	Dgkq/Fibin
GO_BP_m1	GO:009007	relaxation	4/2606	31/23843	0.443951	0.697864	0.663593	Adora1/Ak
GO_BP_m1	GO:009021	positive reg	4/2606	31/23843	0.443951	0.697864	0.663593	Epha8/Fpr2
GO_BP_m1	GO:009050	epiboly	4/2606	31/23843	0.443951	0.697864	0.663593	Col5a1/Mn
GO_BP_m1	GO:200035	negative re	4/2606	31/23843	0.443951	0.697864	0.663593	Abl2/Il10/S
GO_BP_m1	GO:200046	positive reg	4/2606	31/23843	0.443951	0.697864	0.663593	Nlgn3/Ssh1
GO_BP_m1	GO:000193	negative re	5/2606	40/23843	0.44753	0.702358	0.667867	Atp5a1/Ca
GO_BP_m1	GO:000315	regulation	5/2606	40/23843	0.44753	0.702358	0.667867	Fgf1/Gdnf/
GO_BP_m1	GO:001660	Rac protein	5/2606	40/23843	0.44753	0.702358	0.667867	Arhgap44/
GO_BP_m1	GO:003334	cholesterol	5/2606	40/23843	0.44753	0.702358	0.667867	Abca12/Ca
GO_BP_m1	GO:003541	protein loc	5/2606	40/23843	0.44753	0.702358	0.667867	Arhgap44/
GO_BP_m1	GO:004582	positive reg	5/2606	40/23843	0.44753	0.702358	0.667867	Adm/Avpr1
GO_BP_m1	GO:006042	positive reg	5/2606	40/23843	0.44753	0.702358	0.667867	Akap6/Cdk
GO_BP_m1	GO:009878	ncRNA tran	5/2606	40/23843	0.44753	0.702358	0.667867	Cd3eap/Ell
GO_BP_m1	GO:190027	regulation	5/2606	40/23843	0.44753	0.702358	0.667867	Cpeb3/Grin
GO_BP_m1	GO:019873	cell-cell sig	47/2606	419/23843	0.447965	0.702916	0.668397	Abl2/Arntl/
GO_BP_m1	GO:000762	locomotory	28/2606	247/23843	0.448655	0.703873	0.669306	Abat/Abl2/
GO_BP_m1	GO:004858	developme	27/2606	238/23843	0.449043	0.704036	0.669462	Aatk/Akap6
GO_BP_m1	GO:000220	somatic rec	6/2606	49/23843	0.44972	0.704036	0.669462	Aplf/Ifng/Il
GO_BP_m1	GO:000220	somatic div	6/2606	49/23843	0.44972	0.704036	0.669462	Aplf/Ifng/Il
GO_BP_m1	GO:003101	endocrine	6/2606	49/23843	0.44972	0.704036	0.669462	Arntl/Clock
GO_BP_m1	GO:003248	positive reg	6/2606	49/23843	0.44972	0.704036	0.669462	Dhx58/Mb
GO_BP_m1	GO:003264	regulation	6/2606	49/23843	0.44972	0.704036	0.669462	Cactin/Nm
GO_BP_m1	GO:004405	regulation	6/2606	49/23843	0.44972	0.704036	0.669462	Abcb1a/Dg
GO_BP_m1	GO:004519	isotype swi	6/2606	49/23843	0.44972	0.704036	0.669462	Aplf/Ifng/Il
GO_BP_m1	GO:005077	positive reg	6/2606	49/23843	0.44972	0.704036	0.669462	Ache/Capr
GO_BP_m1	GO:005114	negative re	6/2606	49/23843	0.44972	0.704036	0.669462	Cav3/Cxcl1
GO_BP_m1	GO:005149	positive reg	6/2606	49/23843	0.44972	0.704036	0.669462	Ctgf/Itgb1b
GO_BP_m1	GO:200067	regulation	6/2606	49/23843	0.44972	0.704036	0.669462	Ddrgk1/Fo
GO_BP_m1	GO:003027	regulation	25/2606	220/23843	0.449806	0.704044	0.66947	Ank/Bglap3
GO_BP_m1	GO:005066	cytokine se	24/2606	211/23843	0.450179	0.704377	0.669786	Abl2/Btnl2/
GO_BP_m1	GO:190332	regulation	24/2606	211/23843	0.450179	0.704377	0.669786	5730559C1

GO_BP_m1	GO:000201	morphoge	7/2606	58/23843	0.451122	0.705349	0.670711	Col5a1/Dll
GO_BP_m1	GO:000644	regulation	7/2606	58/23843	0.451122	0.705349	0.670711	Eif2ak1/Eif
GO_BP_m1	GO:004277	mitochond	7/2606	58/23843	0.451122	0.705349	0.670711	Cdk1/Coq
GO_BP_m1	GO:005071	negative re	7/2606	58/23843	0.451122	0.705349	0.670711	C1qtnf3/Ez
GO_BP_m1	GO:000602	proteoglyc	8/2606	67/23843	0.45203	0.705922	0.671256	Chst13/Cs
GO_BP_m1	GO:000704	cell-substr	8/2606	67/23843	0.45203	0.705922	0.671256	Bcas3/Cfl1
GO_BP_m1	GO:00456	positive re	8/2606	67/23843	0.45203	0.705922	0.671256	Clic1/Cthrc
GO_BP_m1	GO:004804	focal adhe	8/2606	67/23843	0.45203	0.705922	0.671256	Bcas3/Cfl1
GO_BP_m1	GO:00075	female pre	18/2606	157/23843	0.45219	0.705922	0.671256	Arhgdib/A
GO_BP_m1	GO:000597	glycogen n	9/2606	76/23843	0.452609	0.705922	0.671256	Esrrb/Gys1
GO_BP_m1	GO:000607	cellular glu	9/2606	76/23843	0.452609	0.705922	0.671256	Esrrb/Gys1
GO_BP_m1	GO:004404	glucan me	9/2606	76/23843	0.452609	0.705922	0.671256	Esrrb/Gys1
GO_BP_m1	GO:00519	positive re	9/2606	76/23843	0.452609	0.705922	0.671256	Ephb1/Eph
GO_BP_m1	GO:00076	visual perc	16/2606	139/23843	0.452704	0.705922	0.671256	Bbs2/Cacn
GO_BP_m1	GO:19039	regulation	16/2606	139/23843	0.452704	0.705922	0.671256	Eif2ak2/Fk
GO_BP_m1	GO:00219	central ner	10/2606	85/23843	0.45296	0.705922	0.671256	Arx/Btg2/C
GO_BP_m1	GO:00229	electron tra	10/2606	85/23843	0.45296	0.705922	0.671256	Cdk1/Coq
GO_BP_m1	GO:00435	regulation	10/2606	85/23843	0.45296	0.705922	0.671256	Atp5a1/Ci
GO_BP_m1	GO:00459	positive re	10/2606	85/23843	0.45296	0.705922	0.671256	Adm/Calcr
GO_BP_m1	GO:00706	negative re	10/2606	85/23843	0.45296	0.705922	0.671256	Arg1/Cd80
GO_BP_m1	GO:190054	positive re	10/2606	85/23843	0.45296	0.705922	0.671256	Adm/Calcr
GO_BP_m1	GO:00148	muscle hyp	11/2606	94/23843	0.453145	0.705922	0.671256	Adk/Akap6
GO_BP_m1	GO:00519	regulation	11/2606	94/23843	0.453145	0.705922	0.671256	Epha7/Eph
GO_BP_m1	GO:00343	adherens j	13/2606	112/23843	0.453176	0.705922	0.671256	5730559C1
GO_BP_m1	GO:005082	defense re	13/2606	112/23843	0.453176	0.705922	0.671256	1700016D
GO_BP_m1	GO:00343	cell junctio	26/2606	230/23843	0.45868	0.713839	0.678784	5730559C1
GO_BP_m1	GO:00900	positive re	26/2606	230/23843	0.45868	0.713839	0.678784	Cdc25a/Cd
GO_BP_m1	GO:00063	mRNA pro	49/2606	439/23843	0.460477	0.713839	0.678784	Virma/Apo
GO_BP_m1	GO:00421	cellular ket	21/2606	185/23843	0.461566	0.713839	0.678784	Akr1c12/A
GO_BP_m1	GO:000047	endonucle	2/2606	14/23843	0.462403	0.713839	0.678784	Bms1/Kri1
GO_BP_m1	GO:000167	acrosome	2/2606	14/23843	0.462403	0.713839	0.678784	Ccdc136/P
GO_BP_m1	GO:00033	keratinocyt	2/2606	14/23843	0.462403	0.713839	0.678784	Flnb/Fosl2
GO_BP_m1	GO:00061	oxaloaceta	2/2606	14/23843	0.462403	0.713839	0.678784	Got1/Pcx
GO_BP_m1	GO:00061	cAMP cata	2/2606	14/23843	0.462403	0.713839	0.678784	Pde11a/Pd
GO_BP_m1	GO:000654	glycine me	2/2606	14/23843	0.462403	0.713839	0.678784	Gldc/Shmt
GO_BP_m1	GO:00071	SMAD prot	2/2606	14/23843	0.462403	0.713839	0.678784	Smad6/Zfy
GO_BP_m1	GO:000921	purine deo	2/2606	14/23843	0.462403	0.713839	0.678784	Adk/Nudt1
GO_BP_m1	GO:00092	deoxyribor	2/2606	14/23843	0.462403	0.713839	0.678784	Adk/Shmt1
GO_BP_m1	GO:001042	hydrogen	2/2606	14/23843	0.462403	0.713839	0.678784	Endog/Hsp
GO_BP_m1	GO:00108	regulation	2/2606	14/23843	0.462403	0.713839	0.678784	Plin5/Pnpla
GO_BP_m1	GO:001404	positive re	2/2606	14/23843	0.462403	0.713839	0.678784	Avpr1a/Gri
GO_BP_m1	GO:001654	protein aut	2/2606	14/23843	0.462403	0.713839	0.678784	Ctsl/Pcsk9
GO_BP_m1	GO:001811	peptidyl-c	2/2606	14/23843	0.462403	0.713839	0.678784	Adh5/Atp2
GO_BP_m1	GO:00198	antigen pr	2/2606	14/23843	0.462403	0.713839	0.678784	H2-DMb2/
GO_BP_m1	GO:002152	spinal cord	2/2606	14/23843	0.462403	0.713839	0.678784	Pax3/Wnt3
GO_BP_m1	GO:003081	negative re	2/2606	14/23843	0.462403	0.713839	0.678784	Ppargc1a/
GO_BP_m1	GO:00327	negative re	2/2606	14/23843	0.462403	0.713839	0.678784	Nelfb/Supt
GO_BP_m1	GO:003312	regulation	2/2606	14/23843	0.462403	0.713839	0.678784	Fmr1/H2af

GO_BP_m1	GO:003572	cellular res	2/2606	14/23843	0.462403	0.713839	0.678784	Bcar1/Il10
GO_BP_m1	GO:003598	chondrocy	2/2606	14/23843	0.462403	0.713839	0.678784	Ctgf/Mmp
GO_BP_m1	GO:003637	sodium ior	2/2606	14/23843	0.462403	0.713839	0.678784	Atp1b2/Fx
GO_BP_m1	GO:004292	glucocortic	2/2606	14/23843	0.462403	0.713839	0.678784	Arntl/Clock
GO_BP_m1	GO:004324	proteasom	2/2606	14/23843	0.462403	0.713839	0.678784	Psmd8/Psn
GO_BP_m1	GO:004364	dicarboxyli	2/2606	14/23843	0.462403	0.713839	0.678784	Ddo/Got1
GO_BP_m1	GO:004424	lipid digest	2/2606	14/23843	0.462403	0.713839	0.678784	Arx/Cd36
GO_BP_m1	GO:004518	regulation	2/2606	14/23843	0.462403	0.713839	0.678784	Adora1/Kc
GO_BP_m1	GO:004561	positive re	2/2606	14/23843	0.462403	0.713839	0.678784	Foxc1/H2a
GO_BP_m1	GO:004579	negative re	2/2606	14/23843	0.462403	0.713839	0.678784	Cav3/Cfl1
GO_BP_m1	GO:004867	positive re	2/2606	14/23843	0.462403	0.713839	0.678784	Ntf5/Wnt3
GO_BP_m1	GO:004868	negative re	2/2606	14/23843	0.462403	0.713839	0.678784	Klk8/Xylt1
GO_BP_m1	GO:005171	positive re	2/2606	14/23843	0.462403	0.713839	0.678784	Arg1/Ifng
GO_BP_m1	GO:006018	female ma	2/2606	14/23843	0.462403	0.713839	0.678784	Avpr1a/Dr
GO_BP_m1	GO:006062	regulation	2/2606	14/23843	0.462403	0.713839	0.678784	Preb/Scfd1
GO_BP_m1	GO:006154	ganglion d	2/2606	14/23843	0.462403	0.713839	0.678784	Sema3f/Tu
GO_BP_m1	GO:007007	proton-tra	2/2606	14/23843	0.462403	0.713839	0.678784	Atpaf1/Tcir
GO_BP_m1	GO:007048	leukocyte a	2/2606	14/23843	0.462403	0.713839	0.678784	Adam8/Ha
GO_BP_m1	GO:007185	mitotic cell	2/2606	14/23843	0.462403	0.713839	0.678784	Cdkn1a/Pn
GO_BP_m1	GO:009014	positive re	2/2606	14/23843	0.462403	0.713839	0.678784	Bnip3/Dcn
GO_BP_m1	GO:009019	chemokine	2/2606	14/23843	0.462403	0.713839	0.678784	Il1rl1/Pycar
GO_BP_m1	GO:009715	GABAergic	2/2606	14/23843	0.462403	0.713839	0.678784	Arx/Rac3
GO_BP_m1	GO:009746	programm	2/2606	14/23843	0.462403	0.713839	0.678784	Endog/Hsp
GO_BP_m1	GO:009871	sodium ior	2/2606	14/23843	0.462403	0.713839	0.678784	Slc9a1/Slc9
GO_BP_m1	GO:009885	intestinal li	2/2606	14/23843	0.462403	0.713839	0.678784	Cd36/Dgat
GO_BP_m1	GO:190343	negative re	2/2606	14/23843	0.462403	0.713839	0.678784	Ednrb/Npr
GO_BP_m1	GO:190474	regulation	2/2606	14/23843	0.462403	0.713839	0.678784	Foxc1/Wt1
GO_BP_m1	GO:200036	regulation	2/2606	14/23843	0.462403	0.713839	0.678784	Dnajc6/Sm
GO_BP_m1	GO:000091	cytokinesis	19/2606	167/23843	0.462758	0.714137	0.679067	Ahctf1/Ank
GO_BP_m1	GO:000974	response t	19/2606	167/23843	0.462758	0.714137	0.679067	Ano1/Casp
GO_BP_m1	GO:005105	regulation	30/2606	267/23843	0.465072	0.717172	0.681952	Abl2/Abra/
GO_BP_m1	GO:003572	sodium ior	13/2606	113/23843	0.4664	0.717172	0.681952	Atp1b2/At
GO_BP_m1	GO:005085	T cell recep	13/2606	113/23843	0.4664	0.717172	0.681952	Btnl2/Dusp
GO_BP_m1	GO:000272	regulation	3/2606	23/23843	0.467358	0.717172	0.681952	Arg1/Sash
GO_BP_m1	GO:000702	microtubul	3/2606	23/23843	0.467358	0.717172	0.681952	Tubg1/Tub
GO_BP_m1	GO:001906	virion asse	3/2606	23/23843	0.467358	0.717172	0.681952	Chmp1b/P
GO_BP_m1	GO:003090	notochord	3/2606	23/23843	0.467358	0.717172	0.681952	Epha2/Nog
GO_BP_m1	GO:003235	positive re	3/2606	23/23843	0.467358	0.717172	0.681952	Ifng/Por/P
GO_BP_m1	GO:003439	smooth mu	3/2606	23/23843	0.467358	0.717172	0.681952	E2f3/Ifng/Il
GO_BP_m1	GO:003439	regulation	3/2606	23/23843	0.467358	0.717172	0.681952	E2f3/Ifng/Il
GO_BP_m1	GO:004240	thyroid hor	3/2606	23/23843	0.467358	0.717172	0.681952	Dio2/Duox
GO_BP_m1	GO:004253	hyperosmo	3/2606	23/23843	0.467358	0.717172	0.681952	Mir7b/Mir9
GO_BP_m1	GO:004848	sympatheti	3/2606	23/23843	0.467358	0.717172	0.681952	Gdnf/Nf1/
GO_BP_m1	GO:005130	meiotic chr	3/2606	23/23843	0.467358	0.717172	0.681952	Cenpx/Syc
GO_BP_m1	GO:005145	maintenan	3/2606	23/23843	0.467358	0.717172	0.681952	Cdk5/Ciz1/
GO_BP_m1	GO:007127	cellular res	3/2606	23/23843	0.467358	0.717172	0.681952	Gsn/Mt2/M
GO_BP_m1	GO:007131	cellular res	3/2606	23/23843	0.467358	0.717172	0.681952	Blm/Casp6
GO_BP_m1	GO:007147	cellular res	3/2606	23/23843	0.467358	0.717172	0.681952	Mir7b/Mir9

GO_BP_m1	GO:014011	extracellula	3/2606	23/23843	0.467358	0.717172	0.681952	Arrdc4/Par
GO_BP_m1	GO:014011	export acr	3/2606	23/23843	0.467358	0.717172	0.681952	Atp1b2/Fx
GO_BP_m1	GO:004592	positive re	11/2606	95/23843	0.467579	0.717172	0.681952	Catsper3/C
GO_BP_m1	GO:00487	oligodendr	11/2606	95/23843	0.467579	0.717172	0.681952	Cdk5/Drd3
GO_BP_m1	GO:004227	ribosomal	9/2606	77/23843	0.468659	0.717172	0.681952	Bms1/Eral1
GO_BP_m1	GO:006011	inner ear r	9/2606	77/23843	0.468659	0.717172	0.681952	Atp8b1/Ct
GO_BP_m1	GO:006097	coronary v	9/2606	77/23843	0.468659	0.717172	0.681952	Cfc1/Cntrl/
GO_BP_m1	GO:000041	protein pe	4/2606	32/23843	0.469069	0.717172	0.681952	Fkbp11/Fk
GO_BP_m1	GO:00069	ER-nucleus	4/2606	32/23843	0.469069	0.717172	0.681952	Atg10/Bok
GO_BP_m1	GO:00092	deoxyribor	4/2606	32/23843	0.469069	0.717172	0.681952	Adk/Dera/
GO_BP_m1	GO:001004	response t	4/2606	32/23843	0.469069	0.717172	0.681952	Hvcn1/Mt2
GO_BP_m1	GO:001937	epoxygena	4/2606	32/23843	0.469069	0.717172	0.681952	Cyp2b10/C
GO_BP_m1	GO:003221	positive re	4/2606	32/23843	0.469069	0.717172	0.681952	Atr/Cct3/H
GO_BP_m1	GO:00327	positive re	4/2606	32/23843	0.469069	0.717172	0.681952	5730559C1
GO_BP_m1	GO:00350	response t	4/2606	32/23843	0.469069	0.717172	0.681952	Abat/Chrn
GO_BP_m1	GO:00358	enteroend	4/2606	32/23843	0.469069	0.717172	0.681952	Arntl/Clock
GO_BP_m1	GO:004481	mitotic G2	4/2606	32/23843	0.469069	0.717172	0.681952	Blm/Ccng1
GO_BP_m1	GO:004557	regulation	4/2606	32/23843	0.469069	0.717172	0.681952	Il2rg/Mmp
GO_BP_m1	GO:00486	collateral s	4/2606	32/23843	0.469069	0.717172	0.681952	Epha7/Fgf
GO_BP_m1	GO:00511	cofactor tr	4/2606	32/23843	0.469069	0.717172	0.681952	Folr2/Gif/P
GO_BP_m1	GO:00602	regulation	4/2606	32/23843	0.469069	0.717172	0.681952	Idh2/Ifng/
GO_BP_m1	GO:00606	embryonic	4/2606	32/23843	0.469069	0.717172	0.681952	Adm/Cdkn
GO_BP_m1	GO:190211	negative re	4/2606	32/23843	0.469069	0.717172	0.681952	Cav3/Kat2
GO_BP_m1	GO:00425	regulation	8/2606	68/23843	0.469123	0.717172	0.681952	Cav1/Hdac
GO_BP_m1	GO:004584	negative re	8/2606	68/23843	0.469123	0.717172	0.681952	Cav3/Ephb
GO_BP_m1	GO:000271	regulation	7/2606	59/23843	0.469492	0.717172	0.681952	Aplf/Ifng/Il
GO_BP_m1	GO:00028	regulation	7/2606	59/23843	0.469492	0.717172	0.681952	Aplf/Ifng/Il
GO_BP_m1	GO:00609	endocrine	7/2606	59/23843	0.469492	0.717172	0.681952	C1qtnf3/Cr
GO_BP_m1	GO:00019	positive re	5/2606	41/23843	0.469646	0.717172	0.681952	Il7/Mmp12
GO_BP_m1	GO:00140	glial cell pr	5/2606	41/23843	0.469646	0.717172	0.681952	Idh2/Ifng/L
GO_BP_m1	GO:003281	regulation	5/2606	41/23843	0.469646	0.717172	0.681952	Il12b/Ptpn
GO_BP_m1	GO:00454	photorece	5/2606	41/23843	0.469646	0.717172	0.681952	Bbs10/Bbs
GO_BP_m1	GO:00466	positive re	5/2606	41/23843	0.469646	0.717172	0.681952	Ifng/Il2rg/
GO_BP_m1	GO:005097	detection c	5/2606	41/23843	0.469646	0.717172	0.681952	Grin2b/Htr
GO_BP_m1	GO:006102	establishm	5/2606	41/23843	0.469646	0.717172	0.681952	Cldn1/Ezr/
GO_BP_m1	GO:003112	mRNA 3'-e	6/2606	50/23843	0.469705	0.717172	0.681952	Cpeb3/Cps
GO_BP_m1	GO:00323	regulation	6/2606	50/23843	0.469705	0.717172	0.681952	Dgkq/Duo
GO_BP_m1	GO:003517	social beha	6/2606	50/23843	0.469705	0.717172	0.681952	Avpr1a/Gn
GO_BP_m1	GO:00353	positive re	6/2606	50/23843	0.469705	0.717172	0.681952	Adora1/Ak
GO_BP_m1	GO:00354	response t	6/2606	50/23843	0.469705	0.717172	0.681952	Gm12185/
GO_BP_m1	GO:00487	embryonic	6/2606	50/23843	0.469705	0.717172	0.681952	Alx3/Mmp
GO_BP_m1	GO:00517	intraspecie	6/2606	50/23843	0.469705	0.717172	0.681952	Avpr1a/Gn
GO_BP_m1	GO:00702	negative re	6/2606	50/23843	0.469705	0.717172	0.681952	Blm/Dock8
GO_BP_m1	GO:00457	positive re	23/2606	204/23843	0.470236	0.717858	0.682605	Adam8/Ari
GO_BP_m1	GO:00080	cell recogn	30/2606	268/23843	0.473666	0.721602	0.686165	Cadm1/Cc
GO_BP_m1	GO:000281	regulation	18/2606	159/23843	0.474512	0.721602	0.686165	Aplf/Arg1/
GO_BP_m1	GO:00075	blood coag	18/2606	159/23843	0.474512	0.721602	0.686165	Abat/Alox1
GO_BP_m1	GO:00083	regulation	18/2606	159/23843	0.474512	0.721602	0.686165	Arhgef18/

GO_BP_m1	GO:000864	carbohydra	18/2606	159/23843	0.474512	0.721602	0.686165	Abcb1a/Ac
GO_BP_m1	GO:190210	positive re	18/2606	159/23843	0.474512	0.721602	0.686165	Adam8/Ca
GO_BP_m1	GO:001097	transport a	16/2606	141/23843	0.47642	0.721602	0.686165	Bloc1s5/Cc
GO_BP_m1	GO:009911	microtubul	16/2606	141/23843	0.47642	0.721602	0.686165	Bloc1s5/Cc
GO_BP_m1	GO:000985	determinat	15/2606	132/23843	0.477428	0.721602	0.686165	Cc2d2a/Cf
GO_BP_m1	GO:003121	biomineral	15/2606	132/23843	0.477428	0.721602	0.686165	Ambn/Ank
GO_BP_m1	GO:006104	regulation	15/2606	132/23843	0.477428	0.721602	0.686165	Abat/Acta2
GO_BP_m1	GO:000736	determinat	14/2606	123/23843	0.478479	0.721602	0.686165	Cc2d2a/Cf
GO_BP_m1	GO:004856	digestive tr	14/2606	123/23843	0.478479	0.721602	0.686165	Cdh1/Cfc1/
GO_BP_m1	GO:001082	regulation	22/2606	196/23843	0.481092	0.721602	0.686165	Arih2/Bnip
GO_BP_m1	GO:000245	T cell medi	11/2606	96/23843	0.481947	0.721602	0.686165	Arg1/Clec4
GO_BP_m1	GO:000225	activation	54/2606	488/23843	0.483193	0.721602	0.686165	5730559C1
GO_BP_m1	GO:003112	RNA 3'-en	10/2606	87/23843	0.483237	0.721602	0.686165	Cpeb3/Cps
GO_BP_m1	GO:000226	myeloid ce	19/2606	169/23843	0.484426	0.721602	0.686165	Bpgm/Hca
GO_BP_m1	GO:000085	regulation	9/2606	78/23843	0.484613	0.721602	0.686165	Dll4/Enho/
GO_BP_m1	GO:002202	telencepha	8/2606	69/23843	0.486095	0.721602	0.686165	Arx/Cdk5/
GO_BP_m1	GO:004213	negative re	8/2606	69/23843	0.486095	0.721602	0.686165	Arg1/Cd80
GO_BP_m1	GO:004358	ear develo	26/2606	233/23843	0.486384	0.721602	0.686165	Aldh1a3/A
GO_BP_m1	GO:000704	lysosome c	7/2606	60/23843	0.487707	0.721602	0.686165	Atp6v0c/Cl
GO_BP_m1	GO:005508	anion hom	7/2606	60/23843	0.487707	0.721602	0.686165	Angptl3/D
GO_BP_m1	GO:007005	intrinsic ap	7/2606	60/23843	0.487707	0.721602	0.686165	Aifm1/Bok/
GO_BP_m1	GO:008017	lytic vacuol	7/2606	60/23843	0.487707	0.721602	0.686165	Atp6v0c/Cl
GO_BP_m1	GO:000197	blood vess	6/2606	51/23843	0.489483	0.721602	0.686165	Bcr/Dll4/Fc
GO_BP_m1	GO:003272	negative re	6/2606	51/23843	0.489483	0.721602	0.686165	Cactin/Gpr
GO_BP_m1	GO:004573	positive re	6/2606	51/23843	0.489483	0.721602	0.686165	Blm/Baban
GO_BP_m1	GO:000979	specificatic	15/2606	133/23843	0.489627	0.721602	0.686165	Cc2d2a/Cf
GO_BP_m1	GO:001607	snRNA met	5/2606	42/23843	0.491475	0.721602	0.686165	Ell2/Exosc9
GO_BP_m1	GO:003195	regulation	5/2606	42/23843	0.491475	0.721602	0.686165	Cav1/Epha
GO_BP_m1	GO:005164	mitochond	5/2606	42/23843	0.491475	0.721602	0.686165	Kat2a/Ogt/
GO_BP_m1	GO:006014	regulation	5/2606	42/23843	0.491475	0.721602	0.686165	Fmr1/Mael
GO_BP_m1	GO:006096	regulation	5/2606	42/23843	0.491475	0.721602	0.686165	Fmr1/Mael
GO_BP_m1	GO:190372	positive re	5/2606	42/23843	0.491475	0.721602	0.686165	Epha8/Fpr
GO_BP_m1	GO:000188	liver develo	13/2606	115/23843	0.492697	0.721602	0.686165	Cadm1/Cfc
GO_BP_m1	GO:004568	negative re	4/2606	33/23843	0.493757	0.721602	0.686165	Drd3/Mbd
GO_BP_m1	GO:004574	negative re	4/2606	33/23843	0.493757	0.721602	0.686165	Dll4/Kctd1
GO_BP_m1	GO:004594	positive re	4/2606	33/23843	0.493757	0.721602	0.686165	Fgf1/Ifng/
GO_BP_m1	GO:006033	type I inter	4/2606	33/23843	0.493757	0.721602	0.686165	Cactin/Ifitm
GO_BP_m1	GO:006146	protein loc	4/2606	33/23843	0.493757	0.721602	0.686165	Cacng5/Ca
GO_BP_m1	GO:007135	cellular res	4/2606	33/23843	0.493757	0.721602	0.686165	Cactin/Ifitm
GO_BP_m1	GO:200024	regulation	4/2606	33/23843	0.493757	0.721602	0.686165	Arhgdib/Bc
GO_BP_m1	GO:000974	response t	19/2606	170/23843	0.495214	0.721602	0.686165	Ano1/Casp
GO_BP_m1	GO:000635	DNA-temp	11/2606	97/23843	0.496234	0.721602	0.686165	Bclaf1/Can
GO_BP_m1	GO:190307	regulation	11/2606	97/23843	0.496234	0.721602	0.686165	Appl1/Cam
GO_BP_m1	GO:000233	mature B c	3/2606	24/23843	0.496436	0.721602	0.686165	Cmtm7/Dc
GO_BP_m1	GO:000630	postreplica	3/2606	24/23843	0.496436	0.721602	0.686165	Pcna/Polh/
GO_BP_m1	GO:000720	protein kin	3/2606	24/23843	0.496436	0.721602	0.686165	Dgkh/Dgk
GO_BP_m1	GO:002188	olfactory b	3/2606	24/23843	0.496436	0.721602	0.686165	Arx/Mir141
GO_BP_m1	GO:003072	ovulation	3/2606	24/23843	0.496436	0.721602	0.686165	Adamts1/L

GO_BP_m1	GO:005099	positive reg	3/2606	24/23843	0.496436	0.721602	0.686165	Angptl3/Pl
GO_BP_m1	GO:005176	nitric-oxide	3/2606	24/23843	0.496436	0.721602	0.686165	Ccl20/Fnta/
GO_BP_m1	GO:005176	regulation	3/2606	24/23843	0.496436	0.721602	0.686165	Ccl20/Fnta/
GO_BP_m1	GO:006000	reflex	3/2606	24/23843	0.496436	0.721602	0.686165	Aldh1a3/D
GO_BP_m1	GO:006100	positive reg	3/2606	24/23843	0.496436	0.721602	0.686165	Caprin2/Pa
GO_BP_m1	GO:006143	establishm	3/2606	24/23843	0.496436	0.721602	0.686165	Abca12/Al
GO_BP_m1	GO:007139	cellular res	3/2606	24/23843	0.496436	0.721602	0.686165	Crhbp/H2a
GO_BP_m1	GO:007157	zinc ion tra	3/2606	24/23843	0.496436	0.721602	0.686165	Slc30a3/Sl
GO_BP_m1	GO:007257	liver morph	3/2606	24/23843	0.496436	0.721602	0.686165	Ifng/Tet2/
GO_BP_m1	GO:009718	amelogene	3/2606	24/23843	0.496436	0.721602	0.686165	Itga6/Perp/
GO_BP_m1	GO:190357	negative re	3/2606	24/23843	0.496436	0.721602	0.686165	Flcn/Pparg
GO_BP_m1	GO:190429	regulation	3/2606	24/23843	0.496436	0.721602	0.686165	Bcap31/Tm
GO_BP_m1	GO:190464	cellular res	3/2606	24/23843	0.496436	0.721602	0.686165	Cd36/Cdk5
GO_BP_m1	GO:200072	positive reg	3/2606	24/23843	0.496436	0.721602	0.686165	Akap6/Nrg
GO_BP_m1	GO:200073	negative re	3/2606	24/23843	0.496436	0.721602	0.686165	Esrrb/Jag1/
GO_BP_m1	GO:000759	hemostasis	18/2606	161/23843	0.496716	0.721602	0.686165	Abat/Alox1
GO_BP_m1	GO:005109	positive reg	25/2606	225/23843	0.496884	0.721602	0.686165	Abra/Adam
GO_BP_m1	GO:003134	regulation	10/2606	88/23843	0.498238	0.721602	0.686165	Arg1/Cadm
GO_BP_m1	GO:001820	peptidyl-ly	37/2606	335/23843	0.499147	0.721602	0.686165	Ash2l/Brpf3
GO_BP_m1	GO:000197	renal syste	2/2606	15/23843	0.499558	0.721602	0.686165	Adora1/Uts
GO_BP_m1	GO:000268	negative re	2/2606	15/23843	0.499558	0.721602	0.686165	Ddt/Gpr18
GO_BP_m1	GO:000273	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Il10/Kars
GO_BP_m1	GO:000670	glucocortic	2/2606	15/23843	0.499558	0.721602	0.686165	Dgkq/Hsd1
GO_BP_m1	GO:000692	activation-	2/2606	15/23843	0.499558	0.721602	0.686165	Gpam/Ripk
GO_BP_m1	GO:000734	fusion of sp	2/2606	15/23843	0.499558	0.721602	0.686165	Folr2/Spesp
GO_BP_m1	GO:000915	purine deo	2/2606	15/23843	0.499558	0.721602	0.686165	Adk/Nudt1
GO_BP_m1	GO:000916	nucleoside	2/2606	15/23843	0.499558	0.721602	0.686165	Dera/Dpyd
GO_BP_m1	GO:000931	amine cata	2/2606	15/23843	0.499558	0.721602	0.686165	Atp2b4/Sat
GO_BP_m1	GO:001017	embryonic	2/2606	15/23843	0.499558	0.721602	0.686165	Grem2/Zfp
GO_BP_m1	GO:001064	cell commu	2/2606	15/23843	0.499558	0.721602	0.686165	Cav1/Gjc1
GO_BP_m1	GO:001611	terpenoid	2/2606	15/23843	0.499558	0.721602	0.686165	Aldh1a3/H
GO_BP_m1	GO:001701	protein nitr	2/2606	15/23843	0.499558	0.721602	0.686165	Adh5/Atp2
GO_BP_m1	GO:001998	translesion	2/2606	15/23843	0.499558	0.721602	0.686165	Pcna/Poli
GO_BP_m1	GO:002181	layer forma	2/2606	15/23843	0.499558	0.721602	0.686165	Cdk5/Pafah
GO_BP_m1	GO:003023	male sex d	2/2606	15/23843	0.499558	0.721602	0.686165	Dmrt1/Sry
GO_BP_m1	GO:003032	stabilizatio	2/2606	15/23843	0.499558	0.721602	0.686165	Kcnk2/Kcn
GO_BP_m1	GO:003157	intra-S DN	2/2606	15/23843	0.499558	0.721602	0.686165	Rad9b/Tipi
GO_BP_m1	GO:003271	negative re	2/2606	15/23843	0.499558	0.721602	0.686165	Cactin/Ptpr
GO_BP_m1	GO:003308	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Adam8/Il2r
GO_BP_m1	GO:004242	serotonin r	2/2606	15/23843	0.499558	0.721602	0.686165	Gch1/Htr1a
GO_BP_m1	GO:004274	circadian sl	2/2606	15/23843	0.499558	0.721602	0.686165	Adora1/Kcn
GO_BP_m1	GO:004432	cellular res	2/2606	15/23843	0.499558	0.721602	0.686165	Bbs2/Mt3
GO_BP_m1	GO:004576	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Slc9a1/Tac
GO_BP_m1	GO:004582	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Esrrb/Myc
GO_BP_m1	GO:004594	negative re	2/2606	15/23843	0.499558	0.721602	0.686165	Fmr1/Tpr
GO_BP_m1	GO:004598	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Ctgf/Mylk2
GO_BP_m1	GO:004662	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Nucks1/Os
GO_BP_m1	GO:004871	negative re	2/2606	15/23843	0.499558	0.721602	0.686165	Drd3/Nf1

GO_BP_m1	GO:005087	white fat ce	2/2606	15/23843	0.499558	0.721602	0.686165	Adig/Tbl1x
GO_BP_m1	GO:005093	induction c	2/2606	15/23843	0.499558	0.721602	0.686165	Prkca/Scg2
GO_BP_m1	GO:005100	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Angptl3/Nr
GO_BP_m1	GO:005154	keratinocyt	2/2606	15/23843	0.499558	0.721602	0.686165	Fgf7/Has2
GO_BP_m1	GO:005170	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Arg1/Ifng
GO_BP_m1	GO:006005	angiogenes	2/2606	15/23843	0.499558	0.721602	0.686165	Adipor2/Gp
GO_BP_m1	GO:006009	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Cd36/Ncka
GO_BP_m1	GO:006025	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Myc/Plag1
GO_BP_m1	GO:006034	heart trabe	2/2606	15/23843	0.499558	0.721602	0.686165	Adamts1/C
GO_BP_m1	GO:007023	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Adam8/Sig
GO_BP_m1	GO:007025	mucus secr	2/2606	15/23843	0.499558	0.721602	0.686165	Adora1/P2
GO_BP_m1	GO:007093	3'-UTR-me	2/2606	15/23843	0.499558	0.721602	0.686165	Hnrnpa0/H
GO_BP_m1	GO:007159	otic vesicle	2/2606	15/23843	0.499558	0.721602	0.686165	Stox1/Tbx1
GO_BP_m1	GO:007173	response to	2/2606	15/23843	0.499558	0.721602	0.686165	Bcar1/Kcnc
GO_BP_m1	GO:007210	glomerular	2/2606	15/23843	0.499558	0.721602	0.686165	Ifng/Wt1
GO_BP_m1	GO:007228	metanephr	2/2606	15/23843	0.499558	0.721602	0.686165	Gdnf/Smo
GO_BP_m1	GO:007233	modified a	2/2606	15/23843	0.499558	0.721602	0.686165	Folr2/Slc46
GO_BP_m1	GO:007241	signal trans	2/2606	15/23843	0.499558	0.721602	0.686165	Cdkn1a/Prl
GO_BP_m1	GO:009710	postsynapt	2/2606	15/23843	0.499558	0.721602	0.686165	Cdh2/Cfl1
GO_BP_m1	GO:009908	postsynapt	2/2606	15/23843	0.499558	0.721602	0.686165	Cdh2/Cfl1
GO_BP_m1	GO:009956	modificatio	2/2606	15/23843	0.499558	0.721602	0.686165	Arhgap44/
GO_BP_m1	GO:190107	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Akap6/Pde
GO_BP_m1	GO:190131	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Rnase10/Ta
GO_BP_m1	GO:190152	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Park2/Tiga
GO_BP_m1	GO:190240	signal trans	2/2606	15/23843	0.499558	0.721602	0.686165	Cdkn1a/Prl
GO_BP_m1	GO:190240	signal trans	2/2606	15/23843	0.499558	0.721602	0.686165	Cdkn1a/Prl
GO_BP_m1	GO:190487	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Cct3/Nop1
GO_BP_m1	GO:200081	negative re	2/2606	15/23843	0.499558	0.721602	0.686165	Cav1/Ptrh2
GO_BP_m1	GO:200105	regulation	2/2606	15/23843	0.499558	0.721602	0.686165	Tbx1/Wt1
GO_BP_m1	GO:200127	positive reg	2/2606	15/23843	0.499558	0.721602	0.686165	Osbpl8/Pal
GO_BP_m1	GO:000323	cardiac ver	16/2606	143/23843	0.499982	0.721602	0.686165	Cntrl/Dand
GO_BP_m1	GO:003085	regulation	16/2606	143/23843	0.499982	0.721602	0.686165	Alox12/Arr
GO_BP_m1	GO:000001	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Blm
GO_BP_m1	GO:000014	actin cortic	1/2606	6/23843	0.500702	0.721602	0.686165	Wipf1
GO_BP_m1	GO:000016	phosphore	1/2606	6/23843	0.500702	0.721602	0.686165	Mtrf1
GO_BP_m1	GO:000170	ectoderm f	1/2606	6/23843	0.500702	0.721602	0.686165	Foxa2
GO_BP_m1	GO:000186	NK T cell p	1/2606	6/23843	0.500702	0.721602	0.686165	Il12b
GO_BP_m1	GO:000203	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Arl6ip5
GO_BP_m1	GO:000205	osteoblast	1/2606	6/23843	0.500702	0.721602	0.686165	Men1
GO_BP_m1	GO:000245	T cell antig	1/2606	6/23843	0.500702	0.721602	0.686165	Treml4
GO_BP_m1	GO:000260	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Nod1
GO_BP_m1	GO:000267	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Il10
GO_BP_m1	GO:000273	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Jak3
GO_BP_m1	GO:000310	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Uts2r
GO_BP_m1	GO:000327	apoptotic p	1/2606	6/23843	0.500702	0.721602	0.686165	Foxc1
GO_BP_m1	GO:000328	septum pri	1/2606	6/23843	0.500702	0.721602	0.686165	Nsd2
GO_BP_m1	GO:000337	dynamin fa	1/2606	6/23843	0.500702	0.721602	0.686165	Dnm3
GO_BP_m1	GO:000337	dynamin fa	1/2606	6/23843	0.500702	0.721602	0.686165	Dnm3

GO_BP_m1	GO:000341	growth pla	1/2606	6/23843	0.500702	0.721602	0.686165	Poc1a
GO_BP_m1	GO:000343	chondrocyt	1/2606	6/23843	0.500702	0.721602	0.686165	Poc1a
GO_BP_m1	GO:000604	UDP-N-ac	1/2606	6/23843	0.500702	0.721602	0.686165	Pgm3
GO_BP_m1	GO:000649	N-terminal	1/2606	6/23843	0.500702	0.721602	0.686165	Map6d1
GO_BP_m1	GO:000653	glutamate	1/2606	6/23843	0.500702	0.721602	0.686165	Got1
GO_BP_m1	GO:000654	glycine bio	1/2606	6/23843	0.500702	0.721602	0.686165	Shmt1
GO_BP_m1	GO:000657	tyrosine ca	1/2606	6/23843	0.500702	0.721602	0.686165	Hpdl
GO_BP_m1	GO:000668	sphingomy	1/2606	6/23843	0.500702	0.721602	0.686165	Sptlc2
GO_BP_m1	GO:000670	androgen	1/2606	6/23843	0.500702	0.721602	0.686165	Scarb1
GO_BP_m1	GO:000679	polyphospl	1/2606	6/23843	0.500702	0.721602	0.686165	Prune1
GO_BP_m1	GO:000679	polyphospl	1/2606	6/23843	0.500702	0.721602	0.686165	Prune1
GO_BP_m1	GO:000682	cobalt ion	1/2606	6/23843	0.500702	0.721602	0.686165	Gif
GO_BP_m1	GO:000701	cytoskeleta	1/2606	6/23843	0.500702	0.721602	0.686165	Gypa
GO_BP_m1	GO:000716	receptor g	1/2606	6/23843	0.500702	0.721602	0.686165	Npr2
GO_BP_m1	GO:000722	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Maml3
GO_BP_m1	GO:000822	opsonizati	1/2606	6/23843	0.500702	0.721602	0.686165	Spon2
GO_BP_m1	GO:000863	activation	1/2606	6/23843	0.500702	0.721602	0.686165	Bok
GO_BP_m1	GO:000917	pyrimidine	1/2606	6/23843	0.500702	0.721602	0.686165	Shmt1
GO_BP_m1	GO:000921	purine deo	1/2606	6/23843	0.500702	0.721602	0.686165	Nudt1
GO_BP_m1	GO:000924	isopenteny	1/2606	6/23843	0.500702	0.721602	0.686165	Mvd
GO_BP_m1	GO:000943	methylglyc	1/2606	6/23843	0.500702	0.721602	0.686165	Haghl
GO_BP_m1	GO:000944	putrescine	1/2606	6/23843	0.500702	0.721602	0.686165	Agmat
GO_BP_m1	GO:001057	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Ptprj
GO_BP_m1	GO:001074	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Atp2b4
GO_BP_m1	GO:001084	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Uts2r
GO_BP_m1	GO:001099	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Smad6
GO_BP_m1	GO:001404	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Ednrb
GO_BP_m1	GO:001572	canalicular	1/2606	6/23843	0.500702	0.721602	0.686165	Abcc3
GO_BP_m1	GO:001584	polyamine	1/2606	6/23843	0.500702	0.721602	0.686165	Oaz1
GO_BP_m1	GO:001587	choline tra	1/2606	6/23843	0.500702	0.721602	0.686165	Scn4a
GO_BP_m1	GO:001607	tRNA catab	1/2606	6/23843	0.500702	0.721602	0.686165	Exosc9
GO_BP_m1	GO:001611	terpenoid	1/2606	6/23843	0.500702	0.721602	0.686165	Crabp1
GO_BP_m1	GO:001655	cytidine to	1/2606	6/23843	0.500702	0.721602	0.686165	Apobec1
GO_BP_m1	GO:001840	peptidyl-p	1/2606	6/23843	0.500702	0.721602	0.686165	Egln3
GO_BP_m1	GO:001940	alditol bios	1/2606	6/23843	0.500702	0.721602	0.686165	Got1
GO_BP_m1	GO:002152	somatic m	1/2606	6/23843	0.500702	0.721602	0.686165	Lhx4
GO_BP_m1	GO:002164	vestibuloc	1/2606	6/23843	0.500702	0.721602	0.686165	Atp8b1
GO_BP_m1	GO:002185	cerebral co	1/2606	6/23843	0.500702	0.721602	0.686165	Arx
GO_BP_m1	GO:002193	cerebellar	1/2606	6/23843	0.500702	0.721602	0.686165	Smo
GO_BP_m1	GO:002260	mammalia	1/2606	6/23843	0.500702	0.721602	0.686165	Amh
GO_BP_m1	GO:003007	insulin pro	1/2606	6/23843	0.500702	0.721602	0.686165	Cpz
GO_BP_m1	GO:003032	transepithe	1/2606	6/23843	0.500702	0.721602	0.686165	Slc12a2
GO_BP_m1	GO:003091	olfactory p	1/2606	6/23843	0.500702	0.721602	0.686165	Sox2
GO_BP_m1	GO:003113	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Wnt7a
GO_BP_m1	GO:003129	membrane	1/2606	6/23843	0.500702	0.721602	0.686165	Aph1a
GO_BP_m1	GO:003199	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Plin5
GO_BP_m1	GO:003205	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Nck2
GO_BP_m1	GO:003241	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Drd3

GO_BP_m1	GO:00324	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	E2f7
GO_BP_m1	GO:00327	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Ccl20
GO_BP_m1	GO:003281	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Il12b
GO_BP_m1	GO:00329	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	P2ry1
GO_BP_m1	GO:00331	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Pfkfb1
GO_BP_m1	GO:00340	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	H2afy
GO_BP_m1	GO:003411	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Tnfsf11
GO_BP_m1	GO:003424	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Cxcl10
GO_BP_m1	GO:00355	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Nckap1l
GO_BP_m1	GO:00356	interleukin	1/2606	6/23843	0.500702	0.721602	0.686165	Ticam2
GO_BP_m1	GO:00364	intrinsic ap	1/2606	6/23843	0.500702	0.721602	0.686165	Hsph1
GO_BP_m1	GO:00380	opioid rece	1/2606	6/23843	0.500702	0.721602	0.686165	Oprd1
GO_BP_m1	GO:00400	snRNA mo	1/2606	6/23843	0.500702	0.721602	0.686165	Nop10
GO_BP_m1	GO:00400	polar body	1/2606	6/23843	0.500702	0.721602	0.686165	Washc5
GO_BP_m1	GO:00423	vitamin K	1/2606	6/23843	0.500702	0.721602	0.686165	Vkorc1l1
GO_BP_m1	GO:00424	serotonin	1/2606	6/23843	0.500702	0.721602	0.686165	Gch1
GO_BP_m1	GO:004271	sperm ejac	1/2606	6/23843	0.500702	0.721602	0.686165	Avpr1a
GO_BP_m1	GO:004274	circadian sl	1/2606	6/23843	0.500702	0.721602	0.686165	Uts2r
GO_BP_m1	GO:00427	long-chain	1/2606	6/23843	0.500702	0.721602	0.686165	Aig1
GO_BP_m1	GO:00427	snRNA tra	1/2606	6/23843	0.500702	0.721602	0.686165	Ice1
GO_BP_m1	GO:00433	eosinophil	1/2606	6/23843	0.500702	0.721602	0.686165	Stx4a
GO_BP_m1	GO:00435	mitochond	1/2606	6/23843	0.500702	0.721602	0.686165	Lig3
GO_BP_m1	GO:00443	canonical	1/2606	6/23843	0.500702	0.721602	0.686165	Myc
GO_BP_m1	GO:004434	canonical	1/2606	6/23843	0.500702	0.721602	0.686165	Wnt3a
GO_BP_m1	GO:00443	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Anxa2
GO_BP_m1	GO:00443	actin cortic	1/2606	6/23843	0.500702	0.721602	0.686165	Wipf1
GO_BP_m1	GO:00448	G-quadrup	1/2606	6/23843	0.500702	0.721602	0.686165	Blm
GO_BP_m1	GO:004504	protein im	1/2606	6/23843	0.500702	0.721602	0.686165	Pex5
GO_BP_m1	GO:004511	integrin bi	1/2606	6/23843	0.500702	0.721602	0.686165	Col5a1
GO_BP_m1	GO:00456	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Zfp35
GO_BP_m1	GO:004607	dGTP meta	1/2606	6/23843	0.500702	0.721602	0.686165	Nudt1
GO_BP_m1	GO:00461	pyrimidine	1/2606	6/23843	0.500702	0.721602	0.686165	Dpyd
GO_BP_m1	GO:00461	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Nfkb1
GO_BP_m1	GO:00464	glyoxylate	1/2606	6/23843	0.500702	0.721602	0.686165	Idh2
GO_BP_m1	GO:00464	isopenteny	1/2606	6/23843	0.500702	0.721602	0.686165	Mvd
GO_BP_m1	GO:00466	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Casp6
GO_BP_m1	GO:004671	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Vapb
GO_BP_m1	GO:00468	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Rbm27
GO_BP_m1	GO:00482	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Nsd2
GO_BP_m1	GO:00485	post-embr	1/2606	6/23843	0.500702	0.721602	0.686165	Mir23a
GO_BP_m1	GO:00486	positive re	1/2606	6/23843	0.500702	0.721602	0.686165	Rps6kb1
GO_BP_m1	GO:00486	sprouting	1/2606	6/23843	0.500702	0.721602	0.686165	Lamb2
GO_BP_m1	GO:004884	otolith dev	1/2606	6/23843	0.500702	0.721602	0.686165	Bloc1s5
GO_BP_m1	GO:00488	diencephal	1/2606	6/23843	0.500702	0.721602	0.686165	Sox2
GO_BP_m1	GO:005101	microtubul	1/2606	6/23843	0.500702	0.721602	0.686165	Katna1
GO_BP_m1	GO:00510	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Msh3
GO_BP_m1	GO:005161	serotonin	1/2606	6/23843	0.500702	0.721602	0.686165	Snca
GO_BP_m1	GO:005177	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Fnta

GO_BP_m1	GO:005220	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Anxa2
GO_BP_m1	GO:005240	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Anxa2
GO_BP_m1	GO:005280	imidazole-	1/2606	6/23843	0.500702	0.721602	0.686165	Hdc
GO_BP_m1	GO:005509	response to	1/2606	6/23843	0.500702	0.721602	0.686165	Cav1
GO_BP_m1	GO:006002	hard palate	1/2606	6/23843	0.500702	0.721602	0.686165	Foxe1
GO_BP_m1	GO:006002	rhythmic sy	1/2606	6/23843	0.500702	0.721602	0.686165	Nlgn3
GO_BP_m1	GO:006026	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Bcr
GO_BP_m1	GO:006031	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Fkbp1b
GO_BP_m1	GO:006037	mast cell d	1/2606	6/23843	0.500702	0.721602	0.686165	Itgam
GO_BP_m1	GO:006060	tube lumen	1/2606	6/23843	0.500702	0.721602	0.686165	Cdh1
GO_BP_m1	GO:006066	salivary gla	1/2606	6/23843	0.500702	0.721602	0.686165	Cdh1
GO_BP_m1	GO:006071	chorionic tr	1/2606	6/23843	0.500702	0.721602	0.686165	E2f7
GO_BP_m1	GO:006076	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Cav3
GO_BP_m1	GO:006103	uterus mor	1/2606	6/23843	0.500702	0.721602	0.686165	Wnt7a
GO_BP_m1	GO:006108	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Ogt
GO_BP_m1	GO:006131	BMP signal	1/2606	6/23843	0.500702	0.721602	0.686165	Nog
GO_BP_m1	GO:006134	cell adhesio	1/2606	6/23843	0.500702	0.721602	0.686165	Flrt2
GO_BP_m1	GO:006166	mitochond	1/2606	6/23843	0.500702	0.721602	0.686165	Dhx30
GO_BP_m1	GO:006168	chaperone	1/2606	6/23843	0.500702	0.721602	0.686165	Snca
GO_BP_m1	GO:006172	lipophagy	1/2606	6/23843	0.500702	0.721602	0.686165	Sptlc2
GO_BP_m1	GO:006173	parkin-med	1/2606	6/23843	0.500702	0.721602	0.686165	Park2
GO_BP_m1	GO:007023	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Gpam
GO_BP_m1	GO:007024	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Adam8
GO_BP_m1	GO:007027	extracellula	1/2606	6/23843	0.500702	0.721602	0.686165	Ctgf
GO_BP_m1	GO:007030	lens fiber c	1/2606	6/23843	0.500702	0.721602	0.686165	Epha2
GO_BP_m1	GO:007032	thyroid hor	1/2606	6/23843	0.500702	0.721602	0.686165	Ttr
GO_BP_m1	GO:007033	response to	1/2606	6/23843	0.500702	0.721602	0.686165	Cd36
GO_BP_m1	GO:007044	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Nog
GO_BP_m1	GO:007056	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Kank2
GO_BP_m1	GO:007084	aggresome	1/2606	6/23843	0.500702	0.721602	0.686165	Park2
GO_BP_m1	GO:007094	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Arg1
GO_BP_m1	GO:007102	nuclear ncR	1/2606	6/23843	0.500702	0.721602	0.686165	Exosc9
GO_BP_m1	GO:007103	nuclear pol	1/2606	6/23843	0.500702	0.721602	0.686165	Exosc9
GO_BP_m1	GO:007104	nuclear pol	1/2606	6/23843	0.500702	0.721602	0.686165	Exosc9
GO_BP_m1	GO:007122	cellular resp	1/2606	6/23843	0.500702	0.721602	0.686165	Cd36
GO_BP_m1	GO:007122	cellular resp	1/2606	6/23843	0.500702	0.721602	0.686165	Cd36
GO_BP_m1	GO:007147	cellular hyp	1/2606	6/23843	0.500702	0.721602	0.686165	Trpv4
GO_BP_m1	GO:007150	cellular resp	1/2606	6/23843	0.500702	0.721602	0.686165	Stox1
GO_BP_m1	GO:007156	protein ufm	1/2606	6/23843	0.500702	0.721602	0.686165	Ddrgk1
GO_BP_m1	GO:007169	olfactory p	1/2606	6/23843	0.500702	0.721602	0.686165	Sox2
GO_BP_m1	GO:007169	olfactory p	1/2606	6/23843	0.500702	0.721602	0.686165	Sox2
GO_BP_m1	GO:007191	determinat	1/2606	6/23843	0.500702	0.721602	0.686165	Dnaaf1
GO_BP_m1	GO:007204	comma-sh	1/2606	6/23843	0.500702	0.721602	0.686165	Wt1
GO_BP_m1	GO:007210	glomerulus	1/2606	6/23843	0.500702	0.721602	0.686165	Pdgfra
GO_BP_m1	GO:007210	glomerular	1/2606	6/23843	0.500702	0.721602	0.686165	Pdgfra
GO_BP_m1	GO:007217	mesonephr	1/2606	6/23843	0.500702	0.721602	0.686165	Osr1
GO_BP_m1	GO:007229	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Wt1
GO_BP_m1	GO:007253	pyrimidine-	1/2606	6/23843	0.500702	0.721602	0.686165	Slc25a33

GO_BP_m1	GO:007255	terminal bu	1/2606	6/23843	0.500702	0.721602	0.686165	Nlgn3
GO_BP_m1	GO:009032	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Drd3
GO_BP_m1	GO:009050	endocardia	1/2606	6/23843	0.500702	0.721602	0.686165	Has2
GO_BP_m1	GO:009711	NMDA glu	1/2606	6/23843	0.500702	0.721602	0.686165	Htr1a
GO_BP_m1	GO:009888	exocytic ins	1/2606	6/23843	0.500702	0.721602	0.686165	Stx1b
GO_BP_m1	GO:009890	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Cav3
GO_BP_m1	GO:009893	dendritic tr	1/2606	6/23843	0.500702	0.721602	0.686165	Stau2
GO_BP_m1	GO:009893	anterograd	1/2606	6/23843	0.500702	0.721602	0.686165	Stau2
GO_BP_m1	GO:009896	exocytic ins	1/2606	6/23843	0.500702	0.721602	0.686165	Stx1b
GO_BP_m1	GO:009963	neurotrans	1/2606	6/23843	0.500702	0.721602	0.686165	Arhgap44
GO_BP_m1	GO:190015	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Rflna
GO_BP_m1	GO:190019	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Npr2
GO_BP_m1	GO:190022	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Cd36
GO_BP_m1	GO:190116	primary am	1/2606	6/23843	0.500702	0.721602	0.686165	Gch1
GO_BP_m1	GO:190152	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Tigar
GO_BP_m1	GO:190156	response to	1/2606	6/23843	0.500702	0.721602	0.686165	Blm
GO_BP_m1	GO:190172	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	BC004004
GO_BP_m1	GO:190203	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Kitl
GO_BP_m1	GO:190204	polyamine	1/2606	6/23843	0.500702	0.721602	0.686165	Oaz1
GO_BP_m1	GO:190208	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Atp2b4
GO_BP_m1	GO:190247	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Nlgn3
GO_BP_m1	GO:190280	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Fmr1
GO_BP_m1	GO:190322	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Ralbp1
GO_BP_m1	GO:190324	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Atp2b4
GO_BP_m1	GO:190340	L-arginine	1/2606	6/23843	0.500702	0.721602	0.686165	AU018091
GO_BP_m1	GO:190368	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Rreb1
GO_BP_m1	GO:190382	arginine tra	1/2606	6/23843	0.500702	0.721602	0.686165	AU018091
GO_BP_m1	GO:190389	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Ficd
GO_BP_m1	GO:190405	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Oprl1
GO_BP_m1	GO:190449	protein loc	1/2606	6/23843	0.500702	0.721602	0.686165	Cc2d2a
GO_BP_m1	GO:190458	response to	1/2606	6/23843	0.500702	0.721602	0.686165	Man1b1
GO_BP_m1	GO:190474	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Nmd3
GO_BP_m1	GO:190493	interneuron	1/2606	6/23843	0.500702	0.721602	0.686165	Arx
GO_BP_m1	GO:190500	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Nog
GO_BP_m1	GO:190504	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Timp1
GO_BP_m1	GO:190520	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Endog
GO_BP_m1	GO:190528	vascular as	1/2606	6/23843	0.500702	0.721602	0.686165	E2f3
GO_BP_m1	GO:190532	telomerase	1/2606	6/23843	0.500702	0.721602	0.686165	Atr
GO_BP_m1	GO:190545	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	E2f3
GO_BP_m1	GO:190565	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Ephb4
GO_BP_m1	GO:199082	basic amin	1/2606	6/23843	0.500702	0.721602	0.686165	AU018091
GO_BP_m1	GO:200006	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Dgkq
GO_BP_m1	GO:200011	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	St6gal1
GO_BP_m1	GO:200021	positive reg	1/2606	6/23843	0.500702	0.721602	0.686165	Ptrh2
GO_BP_m1	GO:200034	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Sharpin
GO_BP_m1	GO:200041	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Adam8
GO_BP_m1	GO:200048	negative re	1/2606	6/23843	0.500702	0.721602	0.686165	Ptpn22
GO_BP_m1	GO:200065	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Il1rn

GO_BP_m1	GO:20012	regulation	1/2606	6/23843	0.500702	0.721602	0.686165	Cav3
GO_BP_m1	GO:00712	cellular res	21/2606	189/23843	0.502648	0.724288	0.68872	Bnip3/Cfl1
GO_BP_m1	GO:19018	negative re	8/2606	70/23843	0.50292	0.724442	0.688865	Cfl1/Cib1/
GO_BP_m1	GO:20001	negative re	8/2606	70/23843	0.50292	0.724442	0.688865	Blm/Dock8
GO_BP_m1	GO:00466	regulation	7/2606	61/23843	0.505734	0.727914	0.692167	Gpr21/Nuc
GO_BP_m1	GO:00515	response t	7/2606	61/23843	0.505734	0.727914	0.692167	Akap6/Cdk
GO_BP_m1	GO:00712	cellular res	7/2606	61/23843	0.505734	0.727914	0.692167	Ankrd1/Ca
GO_BP_m1	GO:00105	regulation	13/2606	116/23843	0.505744	0.727914	0.692167	Atp2b4/Av
GO_BP_m1	GO:00517	interaction	13/2606	116/23843	0.505744	0.727914	0.692167	Cav1/Gsn/
GO_BP_m1	GO:00342	response t	19/2606	171/23843	0.50596	0.728105	0.692349	Ano1/Casp
GO_BP_m1	GO:00431	regulation	18/2606	162/23843	0.507754	0.730448	0.694576	5730559C1
GO_BP_m1	GO:00615	actin filame	18/2606	162/23843	0.507754	0.730448	0.694576	Abl2/Cfl1/
GO_BP_m1	GO:00161	sterol biosy	6/2606	52/23843	0.509015	0.731543	0.695618	Fdft1/Fgf1
GO_BP_m1	GO:00215	cerebellum	6/2606	52/23843	0.509015	0.731543	0.695618	Abl2/Cdk5
GO_BP_m1	GO:00433	negative re	6/2606	52/23843	0.509015	0.731543	0.695618	E2f1/Hdac
GO_BP_m1	GO:00488	genitalia d	6/2606	52/23843	0.509015	0.731543	0.695618	Asb1/Hsd1
GO_BP_m1	GO:19035	negative re	6/2606	52/23843	0.509015	0.731543	0.695618	Cactin/Gpr
GO_BP_m1	GO:19052	regulation	6/2606	52/23843	0.509015	0.731543	0.695618	Akap6/Cav
GO_BP_m1	GO:00508	regulation	29/2606	263/23843	0.509321	0.731862	0.695922	Aplf/Cdkn1
GO_BP_m1	GO:00459	positive re	17/2606	153/23843	0.509656	0.732225	0.696266	Cdc7/Cdk1
GO_BP_m1	GO:00301	natural kill	11/2606	98/23843	0.510422	0.733205	0.697198	Gm13271/
GO_BP_m1	GO:00605	developme	28/2606	254/23843	0.510791	0.733615	0.697588	Aatk/Cadm
GO_BP_m1	GO:00183	internal pe	16/2606	144/23843	0.511682	0.734774	0.69869	Brpf3/Nat8
GO_BP_m1	GO:000191	T cell medi	5/2606	43/23843	0.512966	0.735896	0.699757	Fam49b/Il1
GO_BP_m1	GO:000721	dopamine	5/2606	43/23843	0.512966	0.735896	0.699757	Adra1d/Dr
GO_BP_m1	GO:003111	negative re	5/2606	43/23843	0.512966	0.735896	0.699757	Cib1/Fgf13
GO_BP_m1	GO:00507	interleukin	5/2606	43/23843	0.512966	0.735896	0.699757	Cd36/Gsd
GO_BP_m1	GO:00705	protein K6	5/2606	43/23843	0.512966	0.735896	0.699757	Arih2/Park
GO_BP_m1	GO:00713	cellular res	5/2606	43/23843	0.512966	0.735896	0.699757	Eif4e/Gdnf
GO_BP_m1	GO:00106	muscle cell	10/2606	89/23843	0.513121	0.735999	0.699855	Alox12/Bni
GO_BP_m1	GO:00164	cytosolic tr	15/2606	135/23843	0.513849	0.736802	0.700619	Ankfy1/Dn
GO_BP_m1	GO:00706	protein mo	15/2606	135/23843	0.513849	0.736802	0.700619	Asxl1/Eif3f
GO_BP_m1	GO:004211	T cell activ	53/2606	484/23843	0.516164	0.74	0.70366	Abl2/Adam
GO_BP_m1	GO:00023	T cell cytok	4/2606	34/23843	0.517947	0.740984	0.704595	Arg1/Il12b
GO_BP_m1	GO:00028	regulation	4/2606	34/23843	0.517947	0.740984	0.704595	Gpx1/Gpx
GO_BP_m1	GO:00080	neuron rec	4/2606	34/23843	0.517947	0.740984	0.704595	Dscaml1/E
GO_BP_m1	GO:001061	positive re	4/2606	34/23843	0.517947	0.740984	0.704595	Adk/Akap6
GO_BP_m1	GO:001474	positive re	4/2606	34/23843	0.517947	0.740984	0.704595	Adk/Akap6
GO_BP_m1	GO:003164	positive re	4/2606	34/23843	0.517947	0.740984	0.704595	Cartpt/Mir
GO_BP_m1	GO:003314	regulation	4/2606	34/23843	0.517947	0.740984	0.704595	Ddrgk1/Ka
GO_BP_m1	GO:004632	regulation	4/2606	34/23843	0.517947	0.740984	0.704595	Dgat1/Lon
GO_BP_m1	GO:00465	regulation	4/2606	34/23843	0.517947	0.740984	0.704595	Gsn/Ifitm2
GO_BP_m1	GO:004884	axon exten	4/2606	34/23843	0.517947	0.740984	0.704595	Plxna2/Sen
GO_BP_m1	GO:007057	regulation	4/2606	34/23843	0.517947	0.740984	0.704595	Fkbp1b/Klk
GO_BP_m1	GO:190001	regulation	4/2606	34/23843	0.517947	0.740984	0.704595	D1Ertd622
GO_BP_m1	GO:19022	neuron pro	4/2606	34/23843	0.517947	0.740984	0.704595	Plxna2/Sen
GO_BP_m1	GO:005081	coagulatio	18/2606	163/23843	0.518738	0.741996	0.705558	Abat/Alox1
GO_BP_m1	GO:00328	response t	23/2606	209/23843	0.51909	0.742379	0.705922	Appl1/Bcar

GO_BP_m1	GO:00022	somatic di	8/2606	71/23843	0.51957	0.742823	0.706344	Aplf/Ifng/Il
GO_BP_m1	GO:004362	response t	8/2606	71/23843	0.51957	0.742823	0.706344	Arsb/Ash2l
GO_BP_m1	GO:190401	positive re	21/2606	191/23843	0.522977	0.746621	0.709956	Adm/Angp
GO_BP_m1	GO:00199	cAMP-med	16/2606	145/23843	0.523314	0.746621	0.709956	Adcyap1r1
GO_BP_m1	GO:00007	syncytium	7/2606	62/23843	0.523543	0.746621	0.709956	Adam8/Ca
GO_BP_m1	GO:00018	release of	7/2606	62/23843	0.523543	0.746621	0.709956	Bnip3/Bok
GO_BP_m1	GO:00063	transcriptic	7/2606	62/23843	0.523543	0.746621	0.709956	Cand1/Gtf
GO_BP_m1	GO:00510	positive re	7/2606	62/23843	0.523543	0.746621	0.709956	Abra/Adcy
GO_BP_m1	GO:200017	positive re	7/2606	62/23843	0.523543	0.746621	0.709956	Dct/Dll4/D
GO_BP_m1	GO:00020	chondrocy	11/2606	99/23843	0.524495	0.746621	0.709956	Col11a2/C
GO_BP_m1	GO:00017	organ indu	3/2606	25/23843	0.524692	0.746621	0.709956	Fgf1/Gdnf
GO_BP_m1	GO:00104	positive re	3/2606	25/23843	0.524692	0.746621	0.709956	Adm/Avpr
GO_BP_m1	GO:001482	phasic smc	3/2606	25/23843	0.524692	0.746621	0.709956	Ednrb/Gdn
GO_BP_m1	GO:001572	bile acid ar	3/2606	25/23843	0.524692	0.746621	0.709956	Abcc3/Slc1
GO_BP_m1	GO:00159	energy cou	3/2606	25/23843	0.524692	0.746621	0.709956	Atp5a1/At
GO_BP_m1	GO:00159	ATP synthe	3/2606	25/23843	0.524692	0.746621	0.709956	Atp5a1/At
GO_BP_m1	GO:003051	positive re	3/2606	25/23843	0.524692	0.746621	0.709956	Flcn/Men1
GO_BP_m1	GO:00344	microtubul	3/2606	25/23843	0.524692	0.746621	0.709956	Ccdc68/Ce
GO_BP_m1	GO:004564	positive re	3/2606	25/23843	0.524692	0.746621	0.709956	Nckap1l/Pr
GO_BP_m1	GO:00508	defense re	3/2606	25/23843	0.524692	0.746621	0.709956	Arg1/Jagn
GO_BP_m1	GO:005144	positive re	3/2606	25/23843	0.524692	0.746621	0.709956	Arrdc4/Cd
GO_BP_m1	GO:006004	positive re	3/2606	25/23843	0.524692	0.746621	0.709956	Cdk1/Ncar
GO_BP_m1	GO:00610	negative re	3/2606	25/23843	0.524692	0.746621	0.709956	Cav1/Gprc
GO_BP_m1	GO:00712	cellular res	3/2606	25/23843	0.524692	0.746621	0.709956	Mir23a/Mi
GO_BP_m1	GO:00726	interleukin	3/2606	25/23843	0.524692	0.746621	0.709956	Hyal2/Ptpr
GO_BP_m1	GO:007267	eosinophil	3/2606	25/23843	0.524692	0.746621	0.709956	Adam8/Ccl
GO_BP_m1	GO:00800	response t	3/2606	25/23843	0.524692	0.746621	0.709956	Mir23a/Mi
GO_BP_m1	GO:00989	regulation	3/2606	25/23843	0.524692	0.746621	0.709956	Cav1/Cav3
GO_BP_m1	GO:190384	positive re	3/2606	25/23843	0.524692	0.746621	0.709956	Flcn/Men1
GO_BP_m1	GO:20000	regulation	3/2606	25/23843	0.524692	0.746621	0.709956	Abl2/Csnk
GO_BP_m1	GO:200051	negative re	3/2606	25/23843	0.524692	0.746621	0.709956	Jak3/Smad
GO_BP_m1	GO:00097	post-embr	15/2606	136/23843	0.525852	0.748151	0.711411	Abl2/Cfc1/
GO_BP_m1	GO:00063	DNA modi	10/2606	90/23843	0.52787	0.750842	0.713969	Apobec1/
GO_BP_m1	GO:00159	long-chain	6/2606	53/23843	0.528264	0.750842	0.713969	Abcd3/Acs
GO_BP_m1	GO:00425	positive re	6/2606	53/23843	0.528264	0.750842	0.713969	Hdac1/Hda
GO_BP_m1	GO:00427	exogenous	6/2606	53/23843	0.528264	0.750842	0.713969	Cyp2b10/C
GO_BP_m1	GO:00465	negative re	6/2606	53/23843	0.528264	0.750842	0.713969	Abl2/Arhg
GO_BP_m1	GO:00613	trabecula	6/2606	53/23843	0.528264	0.750842	0.713969	Adamts1/C
GO_BP_m1	GO:00604	mesenchyr	28/2606	256/23843	0.528342	0.750842	0.713969	Cfl1/Dand
GO_BP_m1	GO:00027	positive re	14/2606	127/23843	0.528593	0.750956	0.714077	Arg1/Cadn
GO_BP_m1	GO:003502	regulation	14/2606	127/23843	0.528593	0.750956	0.714077	Abl2/Abra/
GO_BP_m1	GO:00026	negative re	18/2606	164/23843	0.529661	0.751217	0.714325	Arg1/Bcr/C
GO_BP_m1	GO:00301	regulation	27/2606	247/23843	0.530175	0.751217	0.714325	Ankfy1/An
GO_BP_m1	GO:003304	regulation	36/2606	330/23843	0.53131	0.751217	0.714325	Apobec1/
GO_BP_m1	GO:00019	regulation	13/2606	118/23843	0.531572	0.751217	0.714325	Arg1/Atp5
GO_BP_m1	GO:00506	regulation	13/2606	118/23843	0.531572	0.751217	0.714325	Cpeb3/Fm
GO_BP_m1	GO:00610	hepaticobil	13/2606	118/23843	0.531572	0.751217	0.714325	Cadm1/Cf
GO_BP_m1	GO:006201	negative re	13/2606	118/23843	0.531572	0.751217	0.714325	Adra1d/Ak

GO_BP_m1	GO:000328	ventricular	9/2606	81/23843	0.531672	0.751217	0.714325	Cntrl/Dand
GO_BP_m1	GO:001590	fatty acid t	9/2606	81/23843	0.531672	0.751217	0.714325	Abcd3/Acs
GO_BP_m1	GO:001921	regulation	9/2606	81/23843	0.531672	0.751217	0.714325	Avpr1a/Ca
GO_BP_m1	GO:000724	I-kappaB k	21/2606	192/23843	0.533067	0.751217	0.714325	5730559C1
GO_BP_m1	GO:000247	antigen pr	5/2606	44/23843	0.534071	0.751217	0.714325	Calr/Gm11
GO_BP_m1	GO:000338	epithelial c	5/2606	44/23843	0.534071	0.751217	0.714325	Cdh1/Cgn/
GO_BP_m1	GO:000669	cholesterol	5/2606	44/23843	0.534071	0.751217	0.714325	Fdft1/Fgf1/
GO_BP_m1	GO:004312	negative re	5/2606	44/23843	0.534071	0.751217	0.714325	Casp8/Hda
GO_BP_m1	GO:006191	selective a	5/2606	44/23843	0.534071	0.751217	0.714325	Nod1/Park
GO_BP_m1	GO:190314	regulation	5/2606	44/23843	0.534071	0.751217	0.714325	Bnip3/Kat2
GO_BP_m1	GO:190370	negative re	16/2606	146/23843	0.534871	0.751217	0.714325	Cartpt/Cib
GO_BP_m1	GO:000096	RNA 5'-en	2/2606	16/23843	0.535018	0.751217	0.714325	Pnpt1/Rpp
GO_BP_m1	GO:000240	dendritic c	2/2606	16/23843	0.535018	0.751217	0.714325	Calr/Gpr18
GO_BP_m1	GO:000322	ventricular	2/2606	16/23843	0.535018	0.751217	0.714325	Dll4/Ube4
GO_BP_m1	GO:000335	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Bbs2/Dnaa
GO_BP_m1	GO:000665	phosphatic	2/2606	16/23843	0.535018	0.751217	0.714325	Fabp5/Fgf
GO_BP_m1	GO:000687	cellular co	2/2606	16/23843	0.535018	0.751217	0.714325	Atp7b/Slc3
GO_BP_m1	GO:000689	Golgi to en	2/2606	16/23843	0.535018	0.751217	0.714325	Gbf1/Rbsn
GO_BP_m1	GO:000751	adult heart	2/2606	16/23843	0.535018	0.751217	0.714325	Myh7/Slc2
GO_BP_m1	GO:000763	mechanose	2/2606	16/23843	0.535018	0.751217	0.714325	Abl2/Strbp
GO_BP_m1	GO:001404	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Ednrb/Rac
GO_BP_m1	GO:002175	striatum de	2/2606	16/23843	0.535018	0.751217	0.714325	Aldh1a3/B
GO_BP_m1	GO:003195	corticoster	2/2606	16/23843	0.535018	0.751217	0.714325	Arntl/Clock
GO_BP_m1	GO:003230	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	P2ry2/Tnfs
GO_BP_m1	GO:003231	prostaglan	2/2606	16/23843	0.535018	0.751217	0.714325	P2ry2/Tnfs
GO_BP_m1	GO:003246	negative re	2/2606	16/23843	0.535018	0.751217	0.714325	Oprd1/Pex
GO_BP_m1	GO:003251	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	Akap6/Ptp
GO_BP_m1	GO:003269	negative re	2/2606	16/23843	0.535018	0.751217	0.714325	Mefv/Zc3h
GO_BP_m1	GO:003526	protein ma	2/2606	16/23843	0.535018	0.751217	0.714325	Nus1/Pom
GO_BP_m1	GO:004255	pteridine-c	2/2606	16/23843	0.535018	0.751217	0.714325	Gch1/Mthf
GO_BP_m1	GO:004264	anagen	2/2606	16/23843	0.535018	0.751217	0.714325	Krtap21-1/
GO_BP_m1	GO:004476	multi-orga	2/2606	16/23843	0.535018	0.751217	0.714325	Cav1/Fmr1
GO_BP_m1	GO:004554	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Fgf1/Por
GO_BP_m1	GO:004583	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	Dmrt1/Fbx
GO_BP_m1	GO:004826	negative re	2/2606	16/23843	0.535018	0.751217	0.714325	Fmr1/Pcsk
GO_BP_m1	GO:004871	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	Prpf19/Ttb
GO_BP_m1	GO:005112	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	Gsn/Wipf1
GO_BP_m1	GO:005119	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	Esrrb/Myc
GO_BP_m1	GO:006097	vasculoge	2/2606	16/23843	0.535018	0.751217	0.714325	Fgf1/Zfpm
GO_BP_m1	GO:007081	phosphory	2/2606	16/23843	0.535018	0.751217	0.714325	Ccnl1/Gtf2
GO_BP_m1	GO:007149	cellular res	2/2606	16/23843	0.535018	0.751217	0.714325	Ptgs2/Spp
GO_BP_m1	GO:007162	vocalizatio	2/2606	16/23843	0.535018	0.751217	0.714325	Myh14/Nlg
GO_BP_m1	GO:009715	mesenchyr	2/2606	16/23843	0.535018	0.751217	0.714325	Tbx1/Wt1
GO_BP_m1	GO:190116	primary am	2/2606	16/23843	0.535018	0.751217	0.714325	Gch1/Htr1
GO_BP_m1	GO:190218	positive re	2/2606	16/23843	0.535018	0.751217	0.714325	Pcx/Vapb
GO_BP_m1	GO:190257	multi-orga	2/2606	16/23843	0.535018	0.751217	0.714325	Cav1/Fmr1
GO_BP_m1	GO:190353	protein loc	2/2606	16/23843	0.535018	0.751217	0.714325	Arhgap44/
GO_BP_m1	GO:190354	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Park2/Smp

GO_BP_m1	GO:190515	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Cd36/Ncka
GO_BP_m1	GO:199084	adaptive th	2/2606	16/23843	0.535018	0.751217	0.714325	Pm20d1/Tr
GO_BP_m1	GO:200034	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Ifng/Wnt3a
GO_BP_m1	GO:200038	regulation	2/2606	16/23843	0.535018	0.751217	0.714325	Dand5/Wn
GO_BP_m1	GO:000206	columnar/c	8/2606	72/23843	0.536024	0.751217	0.714325	Arntl/Cdh1
GO_BP_m1	GO:000854	fibroblast g	8/2606	72/23843	0.536024	0.751217	0.714325	Ctgf/Fgf1/F
GO_BP_m1	GO:002188	forebrain c	8/2606	72/23843	0.536024	0.751217	0.714325	Arx/Cdk5/F
GO_BP_m1	GO:003050	regulation	8/2606	72/23843	0.536024	0.751217	0.714325	Ank/Bglap3
GO_BP_m1	GO:004225	ribosome a	8/2606	72/23843	0.536024	0.751217	0.714325	Dhx30/Eral
GO_BP_m1	GO:005087	positive reg	24/2606	220/23843	0.536173	0.751217	0.714325	Cdkn1a/Gp
GO_BP_m1	GO:200123	negative re	24/2606	220/23843	0.536173	0.751217	0.714325	Bok/Dapk1
GO_BP_m1	GO:004566	positive reg	47/2606	432/23843	0.53671	0.751217	0.714325	Abl2/Ache/
GO_BP_m1	GO:005512	digestive sy	15/2606	137/23843	0.537771	0.751217	0.714325	Cdh1/Cdkn
GO_BP_m1	GO:007169	anatomical	19/2606	174/23843	0.537881	0.751217	0.714325	Abl2/C1ql1
GO_BP_m1	GO:003227	regulation	23/2606	211/23843	0.538365	0.751217	0.714325	Ankrd53/C
GO_BP_m1	GO:000718	adenylate c	11/2606	100/23843	0.538439	0.751217	0.714325	Adgrd1/Ac
GO_BP_m1	GO:005088	endocrine	11/2606	100/23843	0.538439	0.751217	0.714325	Avpr1a/C1
GO_BP_m1	GO:004215	lipoprotein	14/2606	128/23843	0.540909	0.751217	0.714325	Apobec1/A
GO_BP_m1	GO:000931	oligosacchа	7/2606	63/23843	0.541105	0.751217	0.714325	Pgghg/Gal
GO_BP_m1	GO:003003	lamellipodi	7/2606	63/23843	0.541105	0.751217	0.714325	Arhgef7/Cf
GO_BP_m1	GO:190247	chloride tra	7/2606	63/23843	0.541105	0.751217	0.714325	Ano1/Clcn4
GO_BP_m1	GO:000150	neurotrans	4/2606	35/23843	0.541577	0.751217	0.714325	Arl6ip5/Gd
GO_BP_m1	GO:000673	one-carbo	4/2606	35/23843	0.541577	0.751217	0.714325	Ahcyl2/Ma
GO_BP_m1	GO:000709	mitotic spir	4/2606	35/23843	0.541577	0.751217	0.714325	Klhl22/Mac
GO_BP_m1	GO:000995	proximal/d	4/2606	35/23843	0.541577	0.751217	0.714325	Hoxd10/Irx
GO_BP_m1	GO:003222	regulation	4/2606	35/23843	0.541577	0.751217	0.714325	Adora1/Nf
GO_BP_m1	GO:003577	positive reg	4/2606	35/23843	0.541577	0.751217	0.714325	Ano1/Mpc
GO_BP_m1	GO:004255	pteridine-c	4/2606	35/23843	0.541577	0.751217	0.714325	Gch1/Mthf
GO_BP_m1	GO:005145	intracellula	4/2606	35/23843	0.541577	0.751217	0.714325	Atp6v0c/Av
GO_BP_m1	GO:005196	positive reg	4/2606	35/23843	0.541577	0.751217	0.714325	Cacng5/Ca
GO_BP_m1	GO:005197	positive reg	4/2606	35/23843	0.541577	0.751217	0.714325	Hmbox1/M
GO_BP_m1	GO:007117	spindle ass	4/2606	35/23843	0.541577	0.751217	0.714325	Klhl22/Mac
GO_BP_m1	GO:009002	regulation	4/2606	35/23843	0.541577	0.751217	0.714325	Mospd2/M
GO_BP_m1	GO:190197	regulation	4/2606	35/23843	0.541577	0.751217	0.714325	Cul4a/Nek
GO_BP_m1	GO:190435	positive reg	4/2606	35/23843	0.541577	0.751217	0.714325	Atr/Cct3/H
GO_BP_m1	GO:200017	negative re	4/2606	35/23843	0.541577	0.751217	0.714325	Cyth2/Dnm
GO_BP_m1	GO:001082	positive reg	6/2606	54/23843	0.547194	0.751217	0.714325	Adipor2/Ac
GO_BP_m1	GO:004406	regulation	6/2606	54/23843	0.547194	0.751217	0.714325	C1qtnf3/Cr
GO_BP_m1	GO:006019	positive reg	6/2606	54/23843	0.547194	0.751217	0.714325	Abl2/Adcya
GO_BP_m1	GO:004860	reproductiv	48/2606	443/23843	0.548654	0.751217	0.714325	Ccdc182/A
GO_BP_m1	GO:000202	desensitiza	3/2606	26/23843	0.552048	0.751217	0.714325	Adm/Drd3/
GO_BP_m1	GO:000206	chondrocyt	3/2606	26/23843	0.552048	0.751217	0.714325	Rflna/Mia3
GO_BP_m1	GO:000673	NADH met	3/2606	26/23843	0.552048	0.751217	0.714325	Idh3a/Ldha
GO_BP_m1	GO:000959	detection c	3/2606	26/23843	0.552048	0.751217	0.714325	Nod1/Scar
GO_BP_m1	GO:001016	response tc	3/2606	26/23843	0.552048	0.751217	0.714325	Blm/Kars/N
GO_BP_m1	GO:001082	negative re	3/2606	26/23843	0.552048	0.751217	0.714325	Fabp5/Myc
GO_BP_m1	GO:002201	myelinatior	3/2606	26/23843	0.552048	0.751217	0.714325	Ahnak2/Lg
GO_BP_m1	GO:002240	negative ac	3/2606	26/23843	0.552048	0.751217	0.714325	Adm/Drd3/

GO_BP_m1	GO:003031	melanocyte	3/2606	26/23843	0.552048	0.751217	0.714325	Adamts9/E
GO_BP_m1	GO:003129	T cell costir	3/2606	26/23843	0.552048	0.751217	0.714325	Cav1/Cd80
GO_BP_m1	GO:003229	peripheral	3/2606	26/23843	0.552048	0.751217	0.714325	Ahnak2/Lg
GO_BP_m1	GO:003301	tetrapyrrol	3/2606	26/23843	0.552048	0.751217	0.714325	Cox15/Iba5
GO_BP_m1	GO:003450	centromere	3/2606	26/23843	0.552048	0.751217	0.714325	Cenpa/Cen
GO_BP_m1	GO:004000	establishm	3/2606	26/23843	0.552048	0.751217	0.714325	Cenpa/Nus
GO_BP_m1	GO:004595	positive reg	3/2606	26/23843	0.552048	0.751217	0.714325	Catsper3/C
GO_BP_m1	GO:005071	positive reg	3/2606	26/23843	0.552048	0.751217	0.714325	Gsdmd/Ifng
GO_BP_m1	GO:006003	pharyngea	3/2606	26/23843	0.552048	0.751217	0.714325	Nog/Plxna2
GO_BP_m1	GO:006006	uterus deve	3/2606	26/23843	0.552048	0.751217	0.714325	Cdh1/Cdkn
GO_BP_m1	GO:007007	histone lysi	3/2606	26/23843	0.552048	0.751217	0.714325	Kdm2b/Kd
GO_BP_m1	GO:007135	cellular res	3/2606	26/23843	0.552048	0.751217	0.714325	Cfl1/Gab1/
GO_BP_m1	GO:007148	cellular res	3/2606	26/23843	0.552048	0.751217	0.714325	Atr/Cdkn1a
GO_BP_m1	GO:007188	adenylate c	3/2606	26/23843	0.552048	0.751217	0.714325	Adra1d/Atp
GO_BP_m1	GO:009016	regulation	3/2606	26/23843	0.552048	0.751217	0.714325	Chmp1b/H
GO_BP_m1	GO:190299	regulation	3/2606	26/23843	0.552048	0.751217	0.714325	C330021F2
GO_BP_m1	GO:190435	regulation	3/2606	26/23843	0.552048	0.751217	0.714325	Nabp2/Tnk
GO_BP_m1	GO:190464	response to	3/2606	26/23843	0.552048	0.751217	0.714325	Cd36/Cdk5
GO_BP_m1	GO:200031	regulation	3/2606	26/23843	0.552048	0.751217	0.714325	Cacng5/Ca
GO_BP_m1	GO:200077	positive reg	3/2606	26/23843	0.552048	0.751217	0.714325	Hyal2/Pyca
GO_BP_m1	GO:000715	homophilic	11/2606	101/23843	0.552239	0.751217	0.714325	Cadm1/Cd
GO_BP_m1	GO:004544	endothelial	11/2606	101/23843	0.552239	0.751217	0.714325	Alox12/Cld
GO_BP_m1	GO:004350	positive reg	8/2606	73/23843	0.552257	0.751217	0.714325	Gab1/Il1rn/
GO_BP_m1	GO:009050	RNA phosp	8/2606	73/23843	0.552257	0.751217	0.714325	Bms1/Cpsf
GO_BP_m1	GO:003103	actomyosin	21/2606	194/23843	0.553067	0.751217	0.714325	Acta1/Cav3
GO_BP_m1	GO:000752	myoblast fu	5/2606	45/23843	0.554749	0.751217	0.714325	Cav3/Cxcl1
GO_BP_m1	GO:000863	intrinsic ap	5/2606	45/23843	0.554749	0.751217	0.714325	Arl6ip5/Gp
GO_BP_m1	GO:003085	negative re	5/2606	45/23843	0.554749	0.751217	0.714325	Cav1/Ifng/
GO_BP_m1	GO:004208	T-helper 1	5/2606	45/23843	0.554749	0.751217	0.714325	Il12b/Il18b
GO_BP_m1	GO:004632	positive reg	5/2606	45/23843	0.554749	0.751217	0.714325	Adipor2/Cr
GO_BP_m1	GO:004801	vascular en	5/2606	45/23843	0.554749	0.751217	0.714325	Bcar1/Foxc
GO_BP_m1	GO:005089	multicellula	5/2606	45/23843	0.554749	0.751217	0.714325	Abca12/Alo
GO_BP_m1	GO:007138	cellular res	5/2606	45/23843	0.554749	0.751217	0.714325	Eif4e/Gdnf/
GO_BP_m1	GO:190262	regulation	5/2606	45/23843	0.554749	0.751217	0.714325	Adam8/Mc
GO_BP_m1	GO:000044	endonucle	1/2606	7/23843	0.555288	0.751217	0.714325	Kri1
GO_BP_m1	GO:000207	optic cup r	1/2606	7/23843	0.555288	0.751217	0.714325	Aldh1a3
GO_BP_m1	GO:000215	osteoclast	1/2606	7/23843	0.555288	0.751217	0.714325	Tnfsf11
GO_BP_m1	GO:000219	cap-indepe	1/2606	7/23843	0.555288	0.751217	0.714325	Ythdf2
GO_BP_m1	GO:000237	dendritic ce	1/2606	7/23843	0.555288	0.751217	0.714325	Jak3
GO_BP_m1	GO:000257	platelet deg	1/2606	7/23843	0.555288	0.751217	0.714325	P2rx1
GO_BP_m1	GO:000258	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Pycard
GO_BP_m1	GO:000260	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Nod1
GO_BP_m1	GO:000292	positive reg	1/2606	7/23843	0.555288	0.751217	0.714325	Ptprc
GO_BP_m1	GO:000302	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Adra1d
GO_BP_m1	GO:000305	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cav1
GO_BP_m1	GO:000312	heart induc	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:000316	endocardiu	1/2606	7/23843	0.555288	0.751217	0.714325	Sox18
GO_BP_m1	GO:000318	tricuspid va	1/2606	7/23843	0.555288	0.751217	0.714325	Zfpm2

GO_BP_m1	GO:000334	cardiac enc	1/2606	7/23843	0.555288	0.751217	0.714325	Sox18
GO_BP_m1	GO:000598	disaccharic	1/2606	7/23843	0.555288	0.751217	0.714325	Pgghg
GO_BP_m1	GO:000610	malate met	1/2606	7/23843	0.555288	0.751217	0.714325	Me3
GO_BP_m1	GO:000629	pyrimidine	1/2606	7/23843	0.555288	0.751217	0.714325	Polh
GO_BP_m1	GO:000652	arginine bi	1/2606	7/23843	0.555288	0.751217	0.714325	Otc
GO_BP_m1	GO:000654	histidine m	1/2606	7/23843	0.555288	0.751217	0.714325	Hdc
GO_BP_m1	GO:000657	valine meta	1/2606	7/23843	0.555288	0.751217	0.714325	Bcat2
GO_BP_m1	GO:000661	ribosomal	1/2606	7/23843	0.555288	0.751217	0.714325	Ipo11
GO_BP_m1	GO:000662	protein prc	1/2606	7/23843	0.555288	0.751217	0.714325	Uqcrc2
GO_BP_m1	GO:000668	galactosylc	1/2606	7/23843	0.555288	0.751217	0.714325	B4galt3
GO_BP_m1	GO:000672	tetrahydrol	1/2606	7/23843	0.555288	0.751217	0.714325	Gch1
GO_BP_m1	GO:000702	tubulin cor	1/2606	7/23843	0.555288	0.751217	0.714325	Tbca
GO_BP_m1	GO:000806	Toll signali	1/2606	7/23843	0.555288	0.751217	0.714325	Peli3
GO_BP_m1	GO:000829	acetylcholi	1/2606	7/23843	0.555288	0.751217	0.714325	Ache
GO_BP_m1	GO:000914	purine nuc	1/2606	7/23843	0.555288	0.751217	0.714325	Nudt1
GO_BP_m1	GO:000915	purine deo	1/2606	7/23843	0.555288	0.751217	0.714325	Nudt1
GO_BP_m1	GO:000941	response t	1/2606	7/23843	0.555288	0.751217	0.714325	Atp2b4
GO_BP_m1	GO:000944	putrescine	1/2606	7/23843	0.555288	0.751217	0.714325	Agmat
GO_BP_m1	GO:001053	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Il12b
GO_BP_m1	GO:001061	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Atp2b4
GO_BP_m1	GO:001064	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cav1
GO_BP_m1	GO:001076	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Ddt
GO_BP_m1	GO:001098	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Pcsk9
GO_BP_m1	GO:001099	ubiquitin re	1/2606	7/23843	0.555288	0.751217	0.714325	Park2
GO_BP_m1	GO:001405	positive reg	1/2606	7/23843	0.555288	0.751217	0.714325	Htr6
GO_BP_m1	GO:001406	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cartpt
GO_BP_m1	GO:001582	ornithine tr	1/2606	7/23843	0.555288	0.751217	0.714325	AU018091
GO_BP_m1	GO:001605	rhodopsin	1/2606	7/23843	0.555288	0.751217	0.714325	Opn4
GO_BP_m1	GO:001613	glycoside c	1/2606	7/23843	0.555288	0.751217	0.714325	Abhd10
GO_BP_m1	GO:001647	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	H2afy
GO_BP_m1	GO:002157	hindbrain r	1/2606	7/23843	0.555288	0.751217	0.714325	Cend1
GO_BP_m1	GO:002162	central ner	1/2606	7/23843	0.555288	0.751217	0.714325	Cend1
GO_BP_m1	GO:002190	commitme	1/2606	7/23843	0.555288	0.751217	0.714325	Tbr1
GO_BP_m1	GO:002199	neural plat	1/2606	7/23843	0.555288	0.751217	0.714325	Nog
GO_BP_m1	GO:003071	germ-line	1/2606	7/23843	0.555288	0.751217	0.714325	Nanos2
GO_BP_m1	GO:003111	tRNA pseu	1/2606	7/23843	0.555288	0.751217	0.714325	Rpusd1
GO_BP_m1	GO:003128	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Guca1a
GO_BP_m1	GO:003193	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Apobec1
GO_BP_m1	GO:003207	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Dffa
GO_BP_m1	GO:003280	lacrimal gla	1/2606	7/23843	0.555288	0.751217	0.714325	Foxc1
GO_BP_m1	GO:003327	cell prolifer	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:003331	meiotic cel	1/2606	7/23843	0.555288	0.751217	0.714325	Ttk
GO_BP_m1	GO:003348	gas homec	1/2606	7/23843	0.555288	0.751217	0.714325	Cav1
GO_BP_m1	GO:003350	floor plate	1/2606	7/23843	0.555288	0.751217	0.714325	Stil
GO_BP_m1	GO:003386	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Drd5
GO_BP_m1	GO:003414	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Ticam2
GO_BP_m1	GO:003498	peptidyl-ly	1/2606	7/23843	0.555288	0.751217	0.714325	Sirt3
GO_BP_m1	GO:003533	long-chain	1/2606	7/23843	0.555288	0.751217	0.714325	Dgat1

GO_BP_m1	GO:003535	cellular trig	1/2606	7/23843	0.555288	0.751217	0.714325	C1qtnf3
GO_BP_m1	GO:003559	purinergic	1/2606	7/23843	0.555288	0.751217	0.714325	P2ry1
GO_BP_m1	GO:003570	hematopoi	1/2606	7/23843	0.555288	0.751217	0.714325	Ptprc
GO_BP_m1	GO:003574	T-helper 1	1/2606	7/23843	0.555288	0.751217	0.714325	Il12b
GO_BP_m1	GO:003575	B cell chem	1/2606	7/23843	0.555288	0.751217	0.714325	Hsd3b7
GO_BP_m1	GO:003608	cleavage fu	1/2606	7/23843	0.555288	0.751217	0.714325	Snx9
GO_BP_m1	GO:003612	histone H3	1/2606	7/23843	0.555288	0.751217	0.714325	Dmrtc2
GO_BP_m1	GO:003628	peptidyl-se	1/2606	7/23843	0.555288	0.751217	0.714325	Prkca
GO_BP_m1	GO:003630	atrioventric	1/2606	7/23843	0.555288	0.751217	0.714325	Has2
GO_BP_m1	GO:003647	neuron dea	1/2606	7/23843	0.555288	0.751217	0.714325	Il10
GO_BP_m1	GO:003649	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Nck2
GO_BP_m1	GO:003649	eiF2alpha p	1/2606	7/23843	0.555288	0.751217	0.714325	Nck2
GO_BP_m1	GO:003810	nodal signa	1/2606	7/23843	0.555288	0.751217	0.714325	Dand5
GO_BP_m1	GO:004266	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:004276	DNA dama	1/2606	7/23843	0.555288	0.751217	0.714325	Nek1
GO_BP_m1	GO:004363	polyadenyl	1/2606	7/23843	0.555288	0.751217	0.714325	Exosc9
GO_BP_m1	GO:004435	macropino	1/2606	7/23843	0.555288	0.751217	0.714325	Pycard
GO_BP_m1	GO:004500	DNA deam	1/2606	7/23843	0.555288	0.751217	0.714325	Apobec1
GO_BP_m1	GO:004503	protein imp	1/2606	7/23843	0.555288	0.751217	0.714325	Timm22
GO_BP_m1	GO:004565	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Myc
GO_BP_m1	GO:004571	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Sec24a
GO_BP_m1	GO:004591	positive reg	1/2606	7/23843	0.555288	0.751217	0.714325	Abat
GO_BP_m1	GO:004591	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Susd4
GO_BP_m1	GO:004596	positive reg	1/2606	7/23843	0.555288	0.751217	0.714325	Abat
GO_BP_m1	GO:004682	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Cdk5
GO_BP_m1	GO:004805	post-embr	1/2606	7/23843	0.555288	0.751217	0.714325	Mir23a
GO_BP_m1	GO:004806	eye pigmen	1/2606	7/23843	0.555288	0.751217	0.714325	Spns2
GO_BP_m1	GO:004829	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Nsd2
GO_BP_m1	GO:004838	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Calr
GO_BP_m1	GO:005158	positive reg	1/2606	7/23843	0.555288	0.751217	0.714325	Park2
GO_BP_m1	GO:005169	pointed-en	1/2606	7/23843	0.555288	0.751217	0.714325	Tmod3
GO_BP_m1	GO:005179	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Smo
GO_BP_m1	GO:005189	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:005197	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Avpr1a
GO_BP_m1	GO:006002	convergent	1/2606	7/23843	0.555288	0.751217	0.714325	Zfp568
GO_BP_m1	GO:006023	lens induct	1/2606	7/23843	0.555288	0.751217	0.714325	Sox2
GO_BP_m1	GO:006028	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Npr2
GO_BP_m1	GO:006029	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Bbs2
GO_BP_m1	GO:006029	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Bbs2
GO_BP_m1	GO:006031	definitive e	1/2606	7/23843	0.555288	0.751217	0.714325	Senp1
GO_BP_m1	GO:006035	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cav1
GO_BP_m1	GO:006050	positive reg	1/2606	7/23843	0.555288	0.751217	0.714325	Fgf7
GO_BP_m1	GO:006061	fat pad dev	1/2606	7/23843	0.555288	0.751217	0.714325	Tbl1xr1
GO_BP_m1	GO:006076	mammary	1/2606	7/23843	0.555288	0.751217	0.714325	Slc12a2
GO_BP_m1	GO:006077	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Serpinf1
GO_BP_m1	GO:006104	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Pdgfra
GO_BP_m1	GO:006107	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Dll4
GO_BP_m1	GO:006115	pulmonary	1/2606	7/23843	0.555288	0.751217	0.714325	Jag1

GO_BP_m1	GO:006143	renal syste	1/2606	7/23843	0.555288	0.751217	0.714325	Pdgfra
GO_BP_m1	GO:006143	kidney vas	1/2606	7/23843	0.555288	0.751217	0.714325	Pdgfra
GO_BP_m1	GO:006148	hematopoi	1/2606	7/23843	0.555288	0.751217	0.714325	Tet2
GO_BP_m1	GO:007014	synaptic ve	1/2606	7/23843	0.555288	0.751217	0.714325	Dnm3
GO_BP_m1	GO:007099	NADPH ox	1/2606	7/23843	0.555288	0.751217	0.714325	Fmo2
GO_BP_m1	GO:007116	establishm	1/2606	7/23843	0.555288	0.751217	0.714325	H2afy
GO_BP_m1	GO:007136	cellular res	1/2606	7/23843	0.555288	0.751217	0.714325	Zc3h12a
GO_BP_m1	GO:007144	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Kat2b
GO_BP_m1	GO:007163	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	C1qtnf3
GO_BP_m1	GO:007190	determinat	1/2606	7/23843	0.555288	0.751217	0.714325	Dnaaf1
GO_BP_m1	GO:007205	S-shaped	1/2606	7/23843	0.555288	0.751217	0.714325	Wt1
GO_BP_m1	GO:007216	mesenchyr	1/2606	7/23843	0.555288	0.751217	0.714325	Osr1
GO_BP_m1	GO:007228	metanephr	1/2606	7/23843	0.555288	0.751217	0.714325	Lgr4
GO_BP_m1	GO:007234	rescue of s	1/2606	7/23843	0.555288	0.751217	0.714325	Nemf
GO_BP_m1	GO:009026	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Tpr
GO_BP_m1	GO:009040	stress-indu	1/2606	7/23843	0.555288	0.751217	0.714325	Arntl
GO_BP_m1	GO:009704	dendritic c	1/2606	7/23843	0.555288	0.751217	0.714325	Jak3
GO_BP_m1	GO:009728	keratinocyt	1/2606	7/23843	0.555288	0.751217	0.714325	Gsn
GO_BP_m1	GO:009747	motor neu	1/2606	7/23843	0.555288	0.751217	0.714325	Nhsl1
GO_BP_m1	GO:009890	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cav1
GO_BP_m1	GO:009891	retrograde	1/2606	7/23843	0.555288	0.751217	0.714325	Ntf5
GO_BP_m1	GO:009900	calmodulin	1/2606	7/23843	0.555288	0.751217	0.714325	Camk2a
GO_BP_m1	GO:190008	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cav1
GO_BP_m1	GO:190009	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Dand5
GO_BP_m1	GO:190012	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Anxa2
GO_BP_m1	GO:190016	nodal sign	1/2606	7/23843	0.555288	0.751217	0.714325	Dand5
GO_BP_m1	GO:190061	acetate est	1/2606	7/23843	0.555288	0.751217	0.714325	Ache
GO_BP_m1	GO:190153	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Usp7
GO_BP_m1	GO:190172	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	BC004004
GO_BP_m1	GO:190201	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Bbs2
GO_BP_m1	GO:190217	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Gsn
GO_BP_m1	GO:190217	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Ralbp1
GO_BP_m1	GO:190233	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Foxc1
GO_BP_m1	GO:190251	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cacnb2
GO_BP_m1	GO:190296	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Ezr
GO_BP_m1	GO:190296	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Ezr
GO_BP_m1	GO:190300	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Zc3h12a
GO_BP_m1	GO:190302	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Zfp593
GO_BP_m1	GO:190304	protein loc	1/2606	7/23843	0.555288	0.751217	0.714325	Flot2
GO_BP_m1	GO:190320	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Il10
GO_BP_m1	GO:190320	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Il10
GO_BP_m1	GO:190322	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Col5a1
GO_BP_m1	GO:190326	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Park2
GO_BP_m1	GO:190335	L-ornithine	1/2606	7/23843	0.555288	0.751217	0.714325	AU018091
GO_BP_m1	GO:190466	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Cdc20
GO_BP_m1	GO:190552	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Ddt
GO_BP_m1	GO:190577	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:190588	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Npr2

GO_BP_m1	GO:190590	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:190593	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cib1
GO_BP_m1	GO:199014	intrinsic ap	1/2606	7/23843	0.555288	0.751217	0.714325	Bnip3
GO_BP_m1	GO:200025	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Cib1
GO_BP_m1	GO:200025	negative re	1/2606	7/23843	0.555288	0.751217	0.714325	Susd4
GO_BP_m1	GO:200034	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Wnt3a
GO_BP_m1	GO:200051	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Calr
GO_BP_m1	GO:200065	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	H19
GO_BP_m1	GO:200066	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Jak3
GO_BP_m1	GO:200069	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Gdnf
GO_BP_m1	GO:200073	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Pdgfra
GO_BP_m1	GO:200076	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Ythdf2
GO_BP_m1	GO:200097	regulation	1/2606	7/23843	0.555288	0.751217	0.714325	Flcn
GO_BP_m1	GO:200101	mesenchyr	1/2606	7/23843	0.555288	0.751217	0.714325	Osr1
GO_BP_m1	GO:200104	positive re	1/2606	7/23843	0.555288	0.751217	0.714325	Endog
GO_BP_m1	GO:000222	toll-like rec	10/2606	92/23843	0.556894	0.753136	0.716151	Cactin/Cav
GO_BP_m1	GO:00640	RNA expor	10/2606	92/23843	0.556894	0.753136	0.716151	Ddx19b/Nr
GO_BP_m1	GO:190353	regulation	13/2606	120/23843	0.556964	0.753136	0.716151	Arih2/Cdk5
GO_BP_m1	GO:000681	sodium ior	23/2606	213/23843	0.557423	0.753641	0.716631	Atp1b2/At
GO_BP_m1	GO:003081	positive re	7/2606	64/23843	0.558395	0.75449	0.717438	Calcr/Esrrb
GO_BP_m1	GO:003263	interleukin-	7/2606	64/23843	0.558395	0.75449	0.717438	Cactin/Hya
GO_BP_m1	GO:005076	positive re	7/2606	64/23843	0.558395	0.75449	0.717438	Bcr/Calr/Cc
GO_BP_m1	GO:190037	positive re	7/2606	64/23843	0.558395	0.75449	0.717438	Calcr/Esrrb
GO_BP_m1	GO:004876	mesenchyr	22/2606	204/23843	0.56012	0.756704	0.719544	Cfl1/Ednrb/
GO_BP_m1	GO:001657	histone ace	15/2606	139/23843	0.561315	0.758203	0.720968	Brpf3/Nat8
GO_BP_m1	GO:190303	negative re	9/2606	83/23843	0.562172	0.759243	0.721958	Abat/Alox1
GO_BP_m1	GO:003400	axis elonga	4/2606	36/23843	0.564598	0.759891	0.722574	Nat8f3/Fgf
GO_BP_m1	GO:001083	positive re	4/2606	36/23843	0.564598	0.759891	0.722574	Cav3/Mmp
GO_BP_m1	GO:003081	positive re	4/2606	36/23843	0.564598	0.759891	0.722574	Adm/Calcr/
GO_BP_m1	GO:003288	regulation	4/2606	36/23843	0.564598	0.759891	0.722574	Esrrb/Has2
GO_BP_m1	GO:004298	amyloid pr	4/2606	36/23843	0.564598	0.759891	0.722574	Aph1a/C33
GO_BP_m1	GO:004683	lipid phosp	4/2606	36/23843	0.564598	0.759891	0.722574	Bpnt1/Dgk
GO_BP_m1	GO:004683	phospholip	4/2606	36/23843	0.564598	0.759891	0.722574	Ephx2/Plpp
GO_BP_m1	GO:004866	neuron fate	4/2606	36/23843	0.564598	0.759891	0.722574	Dbx1/Dmrt
GO_BP_m1	GO:004882	erythrocyte	4/2606	36/23843	0.564598	0.759891	0.722574	Bpgm/Lyar
GO_BP_m1	GO:005070	regulation	4/2606	36/23843	0.564598	0.759891	0.722574	Gsdmd/Ifn
GO_BP_m1	GO:005115	negative re	4/2606	36/23843	0.564598	0.759891	0.722574	Cav3/Cxcl1
GO_BP_m1	GO:007132	cellular res	4/2606	36/23843	0.564598	0.759891	0.722574	Akap6/Crh
GO_BP_m1	GO:190336	positive re	14/2606	130/23843	0.565213	0.759891	0.722574	Arih2/Bcap
GO_BP_m1	GO:003266	regulation	6/2606	55/23843	0.565776	0.759891	0.722574	Abl2/Btnl2/
GO_BP_m1	GO:003808	peptidyl-ty	6/2606	55/23843	0.565776	0.759891	0.722574	Aatk/Abl2/
GO_BP_m1	GO:004642	negative re	6/2606	55/23843	0.565776	0.759891	0.722574	Cav1/Dcn/
GO_BP_m1	GO:004657	positive re	6/2606	55/23843	0.565776	0.759891	0.722574	Abra/Gpr1
GO_BP_m1	GO:008600	cardiac mu	6/2606	55/23843	0.565776	0.759891	0.722574	Akap6/Cac
GO_BP_m1	GO:190489	negative re	6/2606	55/23843	0.565776	0.759891	0.722574	Cav1/Dcn/
GO_BP_m1	GO:000682	chloride tra	11/2606	102/23843	0.565882	0.759891	0.722574	Abcb1a/Ar
GO_BP_m1	GO:190300	organelle c	11/2606	102/23843	0.565882	0.759891	0.722574	Atg2a/Bnip
GO_BP_m1	GO:000956	fertilization	20/2606	186/23843	0.565981	0.759891	0.722574	1700016D0

GO_BP_m1	GO:000231	B cell activ	8/2606	74/23843	0.56825	0.759891	0.722574	Aplf/Dock1
GO_BP_m1	GO:000906	aerobic res	8/2606	74/23843	0.56825	0.759891	0.722574	Bnip3/Cox
GO_BP_m1	GO:009873	import acr	8/2606	74/23843	0.56825	0.759891	0.722574	Arl6ip5/AU
GO_BP_m1	GO:000192	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Anxa2/Snc
GO_BP_m1	GO:000257	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Nod1/Pyca
GO_BP_m1	GO:000283	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Il12b/Ulbp
GO_BP_m1	GO:000283	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Il12b/Ulbp
GO_BP_m1	GO:000341	growth pla	2/2606	17/23843	0.568707	0.759891	0.722574	Poc1a/Por
GO_BP_m1	GO:000608	acetyl-Co	2/2606	17/23843	0.568707	0.759891	0.722574	Mpc2/Pdh
GO_BP_m1	GO:000670	C21-stero	2/2606	17/23843	0.568707	0.759891	0.722574	Dgkq/Ppar
GO_BP_m1	GO:000697	DNA dama	2/2606	17/23843	0.568707	0.759891	0.722574	Cdkn1a/Tf
GO_BP_m1	GO:000709	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Cdkn1c/M
GO_BP_m1	GO:000720	activation	2/2606	17/23843	0.568707	0.759891	0.722574	Adcyap1r1
GO_BP_m1	GO:000735	blastoderm	2/2606	17/23843	0.568707	0.759891	0.722574	Sema3f/Wt
GO_BP_m1	GO:000921	cyclic nucl	2/2606	17/23843	0.568707	0.759891	0.722574	Pde11a/Pd
GO_BP_m1	GO:001098	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Anxa2/Pcs
GO_BP_m1	GO:002168	cerebellar	2/2606	17/23843	0.568707	0.759891	0.722574	Cend1/Wn
GO_BP_m1	GO:003001	maintenan	2/2606	17/23843	0.568707	0.759891	0.722574	Lrrd1/Ncka
GO_BP_m1	GO:003081	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Esrrb/Myc
GO_BP_m1	GO:003149	chromatin	2/2606	17/23843	0.568707	0.759891	0.722574	Map1s/Sm
GO_BP_m1	GO:003164	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Mir23a/Nr
GO_BP_m1	GO:003240	melanoson	2/2606	17/23843	0.568707	0.759891	0.722574	Bloc1s5/Ra
GO_BP_m1	GO:003293	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Fpr2/Itgam
GO_BP_m1	GO:003360	negative re	2/2606	17/23843	0.568707	0.759891	0.722574	Abat/P2ry1
GO_BP_m1	GO:003414	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Ptpn22/Tic
GO_BP_m1	GO:003465	nucleobase	2/2606	17/23843	0.568707	0.759891	0.722574	Dera/Dpyd
GO_BP_m1	GO:003551	histone H2	2/2606	17/23843	0.568707	0.759891	0.722574	Kdm2b/Rir
GO_BP_m1	GO:003558	calcium-m	2/2606	17/23843	0.568707	0.759891	0.722574	Bcap31/Cc
GO_BP_m1	GO:004248	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Ift88/Wnt1
GO_BP_m1	GO:004275	negative re	2/2606	17/23843	0.568707	0.759891	0.722574	Adora1/Ht
GO_BP_m1	GO:004432	response t	2/2606	17/23843	0.568707	0.759891	0.722574	Bbs2/Mt3
GO_BP_m1	GO:004560	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Alox12/Ve
GO_BP_m1	GO:004565	negative re	2/2606	17/23843	0.568707	0.759891	0.722574	Cib1/Prmt1
GO_BP_m1	GO:004836	lateral mes	2/2606	17/23843	0.568707	0.759891	0.722574	Dand5/Sm
GO_BP_m1	GO:005065	chondroiti	2/2606	17/23843	0.568707	0.759891	0.722574	Chst13/Cs
GO_BP_m1	GO:005507	copper ion	2/2606	17/23843	0.568707	0.759891	0.722574	Atp7b/Slc3
GO_BP_m1	GO:006008	membrane	2/2606	17/23843	0.568707	0.759891	0.722574	Kcnq2/Kcn
GO_BP_m1	GO:007082	heterochro	2/2606	17/23843	0.568707	0.759891	0.722574	Bahd1/Tpr
GO_BP_m1	GO:008601	membrane	2/2606	17/23843	0.568707	0.759891	0.722574	Cacnb2/Ca
GO_BP_m1	GO:009003	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Sez6l2/Ulk
GO_BP_m1	GO:190225	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Akap6/Kcn
GO_BP_m1	GO:190320	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Endog/Ral
GO_BP_m1	GO:190359	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Bnip3/Park
GO_BP_m1	GO:190435	positive re	2/2606	17/23843	0.568707	0.759891	0.722574	Nabp2/Tnk
GO_BP_m1	GO:190531	semi-lunar	2/2606	17/23843	0.568707	0.759891	0.722574	Jag1/Smad
GO_BP_m1	GO:200064	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Dnajc13/Ez
GO_BP_m1	GO:200069	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Gdnf/Osr1
GO_BP_m1	GO:200084	regulation	2/2606	17/23843	0.568707	0.759891	0.722574	Galr1/Tac1

GO_BP_m1	GO:000669	steroid bio	16/2606	149/23843	0.569002	0.76017	0.722839	Dgkq/Fdft1
GO_BP_m1	GO:199013	neuron pro	19/2606	177/23843	0.569183	0.760295	0.722958	Aatk/Cdk5/
GO_BP_m1	GO:000991	epidermal	22/2606	205/23843	0.569744	0.760929	0.723561	Abca12/Ce
GO_BP_m1	GO:002178	glial cell de	10/2606	93/23843	0.571138	0.762676	0.725222	Ahnak2/Cc
GO_BP_m1	GO:190305	positive reg	12/2606	112/23843	0.574154	0.766048	0.728428	Arih2/Bcap
GO_BP_m1	GO:000024	spliceosom	5/2606	46/23843	0.574964	0.766048	0.728428	Prpf19/Psip
GO_BP_m1	GO:000232	natural kille	5/2606	46/23843	0.574964	0.766048	0.728428	Gm13271/I
GO_BP_m1	GO:000641	tRNA amin	5/2606	46/23843	0.574964	0.766048	0.728428	Kars/Lrrc47
GO_BP_m1	GO:000699	nuclear env	5/2606	46/23843	0.574964	0.766048	0.728428	Lemd2/Len
GO_BP_m1	GO:003052	intracellula	5/2606	46/23843	0.574964	0.766048	0.728428	Ddrgk1/Ka
GO_BP_m1	GO:003166	lipopolysac	5/2606	46/23843	0.574964	0.766048	0.728428	Cactin/Irak
GO_BP_m1	GO:003230	icosanoid s	5/2606	46/23843	0.574964	0.766048	0.728428	Drd3/P2ry2
GO_BP_m1	GO:003503	sperm-egg	5/2606	46/23843	0.574964	0.766048	0.728428	Cct3/Fetub
GO_BP_m1	GO:004226	regulation	5/2606	46/23843	0.574964	0.766048	0.728428	Cadm1/Il12
GO_BP_m1	GO:005118	cofactor ca	5/2606	46/23843	0.574964	0.766048	0.728428	Gpx1/Prdx1
GO_BP_m1	GO:007252	purine-cor	5/2606	46/23843	0.574964	0.766048	0.728428	Dpyd/Gda/
GO_BP_m1	GO:009881	modulation	5/2606	46/23843	0.574964	0.766048	0.728428	Nlgn3/Park
GO_BP_m1	GO:190265	secondary	5/2606	46/23843	0.574964	0.766048	0.728428	Fdft1/Fgf1/
GO_BP_m1	GO:006145	reproductiv	48/2606	447/23843	0.574972	0.766048	0.728428	Ccdc182/A
GO_BP_m1	GO:000253	production	7/2606	65/23843	0.575387	0.766137	0.728513	Alox5/D1Er
GO_BP_m1	GO:000630	DNA alkyla	7/2606	65/23843	0.575387	0.766137	0.728513	Ddx4/Fkbp
GO_BP_m1	GO:000630	DNA methy	7/2606	65/23843	0.575387	0.766137	0.728513	Ddx4/Fkbp
GO_BP_m1	GO:001657	histone dea	7/2606	65/23843	0.575387	0.766137	0.728513	BC004004/
GO_BP_m1	GO:000020	protein pol	20/2606	187/23843	0.576019	0.766745	0.729092	Arih2/Cdc2
GO_BP_m1	GO:001623	macroauto	20/2606	187/23843	0.576019	0.766745	0.729092	Atg2a/Bnip
GO_BP_m1	GO:000276	immune re	47/2606	438/23843	0.576709	0.766951	0.729288	5730559C1
GO_BP_m1	GO:190290	regulation	36/2606	336/23843	0.576949	0.766951	0.729288	Ankrd53/C
GO_BP_m1	GO:005507	transition r	14/2606	131/23843	0.577182	0.766951	0.729288	Atp7b/Bdh
GO_BP_m1	GO:000206	glandular e	3/2606	27/23843	0.578444	0.766951	0.729288	Arntl/Clock
GO_BP_m1	GO:000314	outflow tra	3/2606	27/23843	0.578444	0.766951	0.729288	Smad6/Tbx
GO_BP_m1	GO:000651	protein qua	3/2606	27/23843	0.578444	0.766951	0.729288	Lonp2/Ufd
GO_BP_m1	GO:000709	nuclear mig	3/2606	27/23843	0.578444	0.766951	0.729288	Dock7/Pafa
GO_BP_m1	GO:000760	phototrans	3/2606	27/23843	0.578444	0.766951	0.729288	Guca1a/Op
GO_BP_m1	GO:000907	aromatic ar	3/2606	27/23843	0.578444	0.766951	0.729288	Dct/Hpdl/T
GO_BP_m1	GO:000939	2'-deoxyrib	3/2606	27/23843	0.578444	0.766951	0.729288	Adk/Nudt1
GO_BP_m1	GO:001657	histone der	3/2606	27/23843	0.578444	0.766951	0.729288	Kdm2b/Kd
GO_BP_m1	GO:001969	deoxyribos	3/2606	27/23843	0.578444	0.766951	0.729288	Adk/Nudt1
GO_BP_m1	GO:003087	thyroid gla	3/2606	27/23843	0.578444	0.766951	0.729288	Foxe1/Hox
GO_BP_m1	GO:003236	negative re	3/2606	27/23843	0.578444	0.766951	0.729288	Igfbp3/Nr1
GO_BP_m1	GO:003264	regulation	3/2606	27/23843	0.578444	0.766951	0.729288	Mmp12/Nr
GO_BP_m1	GO:003266	regulation	3/2606	27/23843	0.578444	0.766951	0.729288	Ifng/Il12b/I
GO_BP_m1	GO:003368	osteoblast	3/2606	27/23843	0.578444	0.766951	0.729288	Cthrc1/Eif2
GO_BP_m1	GO:003420	amyloid-be	3/2606	27/23843	0.578444	0.766951	0.729288	Aph1a/C33
GO_BP_m1	GO:003466	ncRNA cata	3/2606	27/23843	0.578444	0.766951	0.729288	Exosc9/Pnp
GO_BP_m1	GO:004211	neutrophil	3/2606	27/23843	0.578444	0.766951	0.729288	Anxa3/Bcr/
GO_BP_m1	GO:005071	positive reg	3/2606	27/23843	0.578444	0.766951	0.729288	Gsdmd/Ifng
GO_BP_m1	GO:006026	regulation	3/2606	27/23843	0.578444	0.766951	0.729288	Cand1/Psm
GO_BP_m1	GO:006034	trabecula f	3/2606	27/23843	0.578444	0.766951	0.729288	Adamts1/C

GO_BP_m1	GO:00713	cellular res	3/2606	27/23843	0.578444	0.766951	0.729288	Kcnmb1/M
GO_BP_m1	GO:00901	cochlea mo	3/2606	27/23843	0.578444	0.766951	0.729288	Cthrc1/My
GO_BP_m1	GO:00902	positive re	3/2606	27/23843	0.578444	0.766951	0.729288	Bnip3/Cide
GO_BP_m1	GO:001407	response t	11/2606	103/23843	0.579354	0.767809	0.730104	Akap6/Asp
GO_BP_m1	GO:003051	regulation	11/2606	103/23843	0.579354	0.767809	0.730104	Aatk/Cdk5/
GO_BP_m1	GO:00435	muscle ada	11/2606	103/23843	0.579354	0.767809	0.730104	Adk/Akap6
GO_BP_m1	GO:19033	positive re	13/2606	122/23843	0.581834	0.770981	0.733119	5730559C1
GO_BP_m1	GO:00458	negative re	37/2606	346/23843	0.582225	0.771383	0.733501	Camk2n1/
GO_BP_m1	GO:002157	hindbrain r	6/2606	56/23843	0.583983	0.771485	0.733599	Abl2/Cdk5/
GO_BP_m1	GO:00311	neuron pro	6/2606	56/23843	0.583983	0.771485	0.733599	Adm/Fkbp
GO_BP_m1	GO:00355	non-canon	6/2606	56/23843	0.583983	0.771485	0.733599	Abl2/Csnk1
GO_BP_m1	GO:003314	regulation	8/2606	75/23843	0.583983	0.771485	0.733599	Arntl/Calr/
GO_BP_m1	GO:00512	negative re	15/2606	141/23843	0.584412	0.771485	0.733599	Arg1/Cd80
GO_BP_m1	GO:00725	establishm	46/2606	430/23843	0.585115	0.771485	0.733599	1700123L1
GO_BP_m1	GO:00335	multicellula	10/2606	94/23843	0.585185	0.771485	0.733599	Ednrb/Eif4
GO_BP_m1	GO:00380	NIK/NF-ka	10/2606	94/23843	0.585185	0.771485	0.733599	C1qtnf3/Ca
GO_BP_m1	GO:004691	cellular tra	10/2606	94/23843	0.585185	0.771485	0.733599	Atp7b/Mt2
GO_BP_m1	GO:20000	positive re	10/2606	94/23843	0.585185	0.771485	0.733599	Arih2/Bcap
GO_BP_m1	GO:000164	osteoblast	20/2606	188/23843	0.585971	0.771485	0.733599	Bmp3/Noc
GO_BP_m1	GO:00017	endoderm	4/2606	37/23843	0.586968	0.771485	0.733599	Col5a1/Du
GO_BP_m1	GO:00017	B cell hom	4/2606	37/23843	0.586968	0.771485	0.733599	Dock10/Nc
GO_BP_m1	GO:00020	positive re	4/2606	37/23843	0.586968	0.771485	0.733599	Myc/Pdgfa
GO_BP_m1	GO:00025	cytokine pr	4/2606	37/23843	0.586968	0.771485	0.733599	D1Ertd622
GO_BP_m1	GO:00028	positive re	4/2606	37/23843	0.586968	0.771485	0.733599	Arg1/Itgam
GO_BP_m1	GO:00074	salivary gla	4/2606	37/23843	0.586968	0.771485	0.733599	Cdh1/Fgf7/
GO_BP_m1	GO:00420	type 2 imm	4/2606	37/23843	0.586968	0.771485	0.733599	Arg1/Bcl6b
GO_BP_m1	GO:00456	regulation	4/2606	37/23843	0.586968	0.771485	0.733599	Alox12/Jag
GO_BP_m1	GO:00550	positive re	4/2606	37/23843	0.586968	0.771485	0.733599	Akap6/Cdk
GO_BP_m1	GO:19026	positive re	4/2606	37/23843	0.586968	0.771485	0.733599	Adam8/Mc
GO_BP_m1	GO:200014	regulation	4/2606	37/23843	0.586968	0.771485	0.733599	Bclaf1/Can
GO_BP_m1	GO:005077	regulation	19/2606	179/23843	0.589621	0.771485	0.733599	Ache/Arhg
GO_BP_m1	GO:19028	regulation	13/2606	123/23843	0.594049	0.771485	0.733599	Atp2b4/Cd
GO_BP_m1	GO:19046	glucose tra	13/2606	123/23843	0.594049	0.771485	0.733599	Adipor2/Ac
GO_BP_m1	GO:000271	regulation	5/2606	47/23843	0.594685	0.771485	0.733599	Cadm1/Il1
GO_BP_m1	GO:004564	regulation	5/2606	47/23843	0.594685	0.771485	0.733599	Lmo2/Nck
GO_BP_m1	GO:00509	negative re	5/2606	47/23843	0.594685	0.771485	0.733599	Ddt/Gpr18
GO_BP_m1	GO:00721	mesenchyr	5/2606	47/23843	0.594685	0.771485	0.733599	Foxc1/Myc
GO_BP_m1	GO:00097	hormone-r	20/2606	189/23843	0.595832	0.771485	0.733599	Acsl1/Adip
GO_BP_m1	GO:00426	muscle cell	40/2606	376/23843	0.597226	0.771485	0.733599	Acta1/Adm
GO_BP_m1	GO:200124	negative re	10/2606	95/23843	0.599021	0.771485	0.733599	Gpx1/Hdac
GO_BP_m1	GO:19021	regulation	30/2606	283/23843	0.599281	0.771485	0.733599	Adam8/Ca
GO_BP_m1	GO:000704	cell-substra	8/2606	76/23843	0.599438	0.771485	0.733599	Bcas3/Cfl1/
GO_BP_m1	GO:000307	regulation	12/2606	114/23843	0.599589	0.771485	0.733599	Adm/Ador
GO_BP_m1	GO:00511	regulation	12/2606	114/23843	0.599589	0.771485	0.733599	Akap6/Cav
GO_BP_m1	GO:000157	ganglioside	2/2606	18/23843	0.60059	0.771485	0.733599	St6galnac1
GO_BP_m1	GO:00028	positive re	2/2606	18/23843	0.60059	0.771485	0.733599	Il12b/Il27ra
GO_BP_m1	GO:000602	glycosamin	2/2606	18/23843	0.60059	0.771485	0.733599	Hyal2/Hyal
GO_BP_m1	GO:000612	mitochond	2/2606	18/23843	0.60059	0.771485	0.733599	Coq9/Ndu

GO_BP_m1	GO:000669	leukotriene	2/2606	18/23843	0.60059	0.771485	0.733599	Alox5/Ltc4s
GO_BP_m1	GO:000682	copper ion	2/2606	18/23843	0.60059	0.771485	0.733599	Atp7b/Slc3
GO_BP_m1	GO:000995	dorsal/vent	2/2606	18/23843	0.60059	0.771485	0.733599	Lrp4/Smad
GO_BP_m1	GO:001081	T cell chem	2/2606	18/23843	0.60059	0.771485	0.733599	Cxcl10/Gpr
GO_BP_m1	GO:001406	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Hrh3/P2ry1
GO_BP_m1	GO:002154	dentate gy	2/2606	18/23843	0.60059	0.771485	0.733599	Btg2/Smo
GO_BP_m1	GO:003015	protein imp	2/2606	18/23843	0.60059	0.771485	0.733599	Grpel1/Tim
GO_BP_m1	GO:003050	negative re	2/2606	18/23843	0.60059	0.771485	0.733599	Ccr1/Rflna
GO_BP_m1	GO:003199	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Lonp2/Plin
GO_BP_m1	GO:003240	establishm	2/2606	18/23843	0.60059	0.771485	0.733599	Bloc1s5/Ra
GO_BP_m1	GO:003269	negative re	2/2606	18/23843	0.60059	0.771485	0.733599	Il12b/Jak3
GO_BP_m1	GO:003357	response t	2/2606	18/23843	0.60059	0.771485	0.733599	Adh1/Spp1
GO_BP_m1	GO:003506	negative re	2/2606	18/23843	0.60059	0.771485	0.733599	Msx3/Snca
GO_BP_m1	GO:003508	establishm	2/2606	18/23843	0.60059	0.771485	0.733599	Fscn1/Tcf1
GO_BP_m1	GO:003593	corticoster	2/2606	18/23843	0.60059	0.771485	0.733599	Galr1/Tac1
GO_BP_m1	GO:003629	interstrand	2/2606	18/23843	0.60059	0.771485	0.733599	Dclre1a/Nu
GO_BP_m1	GO:004224	establishm	2/2606	18/23843	0.60059	0.771485	0.733599	Cthrc1/Pafa
GO_BP_m1	GO:004277	DNA dama	2/2606	18/23843	0.60059	0.771485	0.733599	Cdkn1a/Tfa
GO_BP_m1	GO:004547	locomotor	2/2606	18/23843	0.60059	0.771485	0.733599	Kcnd2/Opr
GO_BP_m1	GO:004617	polyol cata	2/2606	18/23843	0.60059	0.771485	0.733599	Synj1/Tkfc
GO_BP_m1	GO:004824	norepineph	2/2606	18/23843	0.60059	0.771485	0.733599	Hrh3/P2ry1
GO_BP_m1	GO:005096	detection c	2/2606	18/23843	0.60059	0.771485	0.733599	Grin2b/Htr
GO_BP_m1	GO:005119	negative re	2/2606	18/23843	0.60059	0.771485	0.733599	Ppargc1a/T
GO_BP_m1	GO:005190	pigment gr	2/2606	18/23843	0.60059	0.771485	0.733599	Bloc1s5/Ra
GO_BP_m1	GO:006033	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Cactin/Mm
GO_BP_m1	GO:006070	trophoblas	2/2606	18/23843	0.60059	0.771485	0.733599	E2f7/Plk4
GO_BP_m1	GO:007147	cellular hyp	2/2606	18/23843	0.60059	0.771485	0.733599	Mir7b/Mir9
GO_BP_m1	GO:007160	monocyte	2/2606	18/23843	0.60059	0.771485	0.733599	C1qtnf3/Tr
GO_BP_m1	GO:007163	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	C1qtnf3/Tr
GO_BP_m1	GO:007207	renal vesicl	2/2606	18/23843	0.60059	0.771485	0.733599	Gdnf/Smo
GO_BP_m1	GO:009003	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Dgkq/Por
GO_BP_m1	GO:190101	negative re	2/2606	18/23843	0.60059	0.771485	0.733599	Cav1/Cav3
GO_BP_m1	GO:190102	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Bok/Tmem
GO_BP_m1	GO:190162	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Ccl4/Cxcl10
GO_BP_m1	GO:190223	negative re	2/2606	18/23843	0.60059	0.771485	0.733599	Park2/Ptpn
GO_BP_m1	GO:190487	regulation	2/2606	18/23843	0.60059	0.771485	0.733599	Cct3/Nop1
GO_BP_m1	GO:001046	mesenchyr	6/2606	57/23843	0.601789	0.771485	0.733599	Fgf7/Myc/C
GO_BP_m1	GO:190370	regulation	41/2606	386/23843	0.601973	0.771485	0.733599	Adam8/Ca
GO_BP_m1	GO:004516	cell fate co	29/2606	274/23843	0.6021	0.771485	0.733599	Arx/Dbx1/D
GO_BP_m1	GO:005506	monovalen	16/2606	152/23843	0.60216	0.771485	0.733599	Adora1/Atp
GO_BP_m1	GO:000189	maternal p	3/2606	28/23843	0.603837	0.771485	0.733599	Cdh1/Ctsl/
GO_BP_m1	GO:000602	aminoglyca	3/2606	28/23843	0.603837	0.771485	0.733599	Chil5/Hyal2
GO_BP_m1	GO:001071	negative re	3/2606	28/23843	0.603837	0.771485	0.733599	Foxa2/Nog
GO_BP_m1	GO:002169	cerebellar	3/2606	28/23843	0.603837	0.771485	0.733599	Cdk5/Cenc
GO_BP_m1	GO:002305	adaptation	3/2606	28/23843	0.603837	0.771485	0.733599	Adm/Drd3/
GO_BP_m1	GO:003129	lymphocyte	3/2606	28/23843	0.603837	0.771485	0.733599	Cav1/Cd80
GO_BP_m1	GO:003260	interferon-	3/2606	28/23843	0.603837	0.771485	0.733599	Mmp12/Nr
GO_BP_m1	GO:003516	embryonic	3/2606	28/23843	0.603837	0.771485	0.733599	Kitl/Lmo2/S

GO_BP_m1	GO:004203	negative re	3/2606	28/23843	0.603837	0.771485	0.733599	Il10/Nfkb1/
GO_BP_m1	GO:004368	post-transl	3/2606	28/23843	0.603837	0.771485	0.733599	Esco1/Flcn/
GO_BP_m1	GO:004565	regulation	3/2606	28/23843	0.603837	0.771485	0.733599	Cib1/Prmt1
GO_BP_m1	GO:004685	phosphatic	3/2606	28/23843	0.603837	0.771485	0.733599	Bpnt1/Pik3
GO_BP_m1	GO:004859	embryonic	3/2606	28/23843	0.603837	0.771485	0.733599	Aldh1a3/Kc
GO_BP_m1	GO:006003	pericardiur	3/2606	28/23843	0.603837	0.771485	0.733599	Dll4/Mecor
GO_BP_m1	GO:006044	branching	3/2606	28/23843	0.603837	0.771485	0.733599	Cav3/Epha
GO_BP_m1	GO:007187	adrenergic	3/2606	28/23843	0.603837	0.771485	0.733599	Adra1d/Atp
GO_BP_m1	GO:200027	positive reg	3/2606	28/23843	0.603837	0.771485	0.733599	Adora1/Cfl
GO_BP_m1	GO:000176	membrane	1/2606	8/23843	0.603908	0.771485	0.733599	Gsn
GO_BP_m1	GO:000182	inner cell m	1/2606	8/23843	0.603908	0.771485	0.733599	Lats1
GO_BP_m1	GO:000218	cytoplasmi	1/2606	8/23843	0.603908	0.771485	0.733599	Cpeb3
GO_BP_m1	GO:000246	dendritic ce	1/2606	8/23843	0.603908	0.771485	0.733599	Nod1
GO_BP_m1	GO:000271	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Susd4
GO_BP_m1	GO:000289	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Susd4
GO_BP_m1	GO:000317	tricuspid va	1/2606	8/23843	0.603908	0.771485	0.733599	Zfpm2
GO_BP_m1	GO:000319	atrioventric	1/2606	8/23843	0.603908	0.771485	0.733599	Zfpm2
GO_BP_m1	GO:000322	atrial cardia	1/2606	8/23843	0.603908	0.771485	0.733599	Nog
GO_BP_m1	GO:000333	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Gdnf
GO_BP_m1	GO:000551	detection c	1/2606	8/23843	0.603908	0.771485	0.733599	Kcnmb1
GO_BP_m1	GO:000598	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ppp1r3d
GO_BP_m1	GO:000634	chromatin	1/2606	8/23843	0.603908	0.771485	0.733599	Hat1
GO_BP_m1	GO:000664	phosphatic	1/2606	8/23843	0.603908	0.771485	0.733599	Pisd
GO_BP_m1	GO:000697	hypotonic	1/2606	8/23843	0.603908	0.771485	0.733599	Trpv4
GO_BP_m1	GO:000714	female mei	1/2606	8/23843	0.603908	0.771485	0.733599	Fbxo5
GO_BP_m1	GO:000740	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Nf1
GO_BP_m1	GO:000821	spermine n	1/2606	8/23843	0.603908	0.771485	0.733599	Sat1
GO_BP_m1	GO:000913	pyrimidine	1/2606	8/23843	0.603908	0.771485	0.733599	Shmt1
GO_BP_m1	GO:000920	deoxyribor	1/2606	8/23843	0.603908	0.771485	0.733599	Nudt1
GO_BP_m1	GO:000931	oligosacch	1/2606	8/23843	0.603908	0.771485	0.733599	Pgghg
GO_BP_m1	GO:000999	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Wnt3a
GO_BP_m1	GO:001021	maintenan	1/2606	8/23843	0.603908	0.771485	0.733599	Usp7
GO_BP_m1	GO:001045	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Wnt3a
GO_BP_m1	GO:001060	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Cnot6l
GO_BP_m1	GO:001070	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	P2ry1
GO_BP_m1	GO:001095	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Arl6ip5
GO_BP_m1	GO:001588	heme trans	1/2606	8/23843	0.603908	0.771485	0.733599	Slc46a1
GO_BP_m1	GO:001595	diadenosin	1/2606	8/23843	0.603908	0.771485	0.733599	Kars
GO_BP_m1	GO:001609	polyprenol	1/2606	8/23843	0.603908	0.771485	0.733599	Nus1
GO_BP_m1	GO:001658	nucleosom	1/2606	8/23843	0.603908	0.771485	0.733599	Hist1h1c
GO_BP_m1	GO:001718	peptidyl-ly	1/2606	8/23843	0.603908	0.771485	0.733599	P3h3
GO_BP_m1	GO:001834	protein ger	1/2606	8/23843	0.603908	0.771485	0.733599	Fnta
GO_BP_m1	GO:001922	neuronal a	1/2606	8/23843	0.603908	0.771485	0.733599	Fkbp1b
GO_BP_m1	GO:001937	galactolipic	1/2606	8/23843	0.603908	0.771485	0.733599	B4galt3
GO_BP_m1	GO:001980	peptide crc	1/2606	8/23843	0.603908	0.771485	0.733599	Dcn
GO_BP_m1	GO:002160	cranial ner	1/2606	8/23843	0.603908	0.771485	0.733599	Atp8b1
GO_BP_m1	GO:003024	skeletal mu	1/2606	8/23843	0.603908	0.771485	0.733599	Acta1
GO_BP_m1	GO:003144	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Supt5

GO_BP_m1	GO:003158	membrane	1/2606	8/23843	0.603908	0.771485	0.733599	Gsn
GO_BP_m1	GO:003166	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Prkca
GO_BP_m1	GO:003194	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Dgkq
GO_BP_m1	GO:003204	cardiolipin	1/2606	8/23843	0.603908	0.771485	0.733599	Ptpmt1
GO_BP_m1	GO:003222	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Adora1
GO_BP_m1	GO:003227	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Tacr2
GO_BP_m1	GO:003242	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ppt1
GO_BP_m1	GO:003262	interleukin-	1/2606	8/23843	0.603908	0.771485	0.733599	Ifng
GO_BP_m1	GO:003265	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ccl20
GO_BP_m1	GO:003266	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ifng
GO_BP_m1	GO:003287	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	E2f7
GO_BP_m1	GO:003315	immunoglo	1/2606	8/23843	0.603908	0.771485	0.733599	Prkdc
GO_BP_m1	GO:003320	meiotic cyt	1/2606	8/23843	0.603908	0.771485	0.733599	Washc5
GO_BP_m1	GO:003368	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Tacr2
GO_BP_m1	GO:003433	adherens ju	1/2606	8/23843	0.603908	0.771485	0.733599	5730559C1
GO_BP_m1	GO:003437	very-low-d	1/2606	8/23843	0.603908	0.771485	0.733599	Dgat1
GO_BP_m1	GO:003438	high-densi	1/2606	8/23843	0.603908	0.771485	0.733599	Scarb1
GO_BP_m1	GO:003447	U4 snRNA	1/2606	8/23843	0.603908	0.771485	0.733599	Exosc9
GO_BP_m1	GO:003465	cortisol bio	1/2606	8/23843	0.603908	0.771485	0.733599	Dgkq
GO_BP_m1	GO:003548	gastric mot	1/2606	8/23843	0.603908	0.771485	0.733599	Drd3
GO_BP_m1	GO:003550	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Nckap1l
GO_BP_m1	GO:003581	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Uts2r
GO_BP_m1	GO:003591	dorsal aort	1/2606	8/23843	0.603908	0.771485	0.733599	Dll4
GO_BP_m1	GO:003649	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Nck2
GO_BP_m1	GO:003808	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Gab1
GO_BP_m1	GO:003809	Fc-gamma	1/2606	8/23843	0.603908	0.771485	0.733599	Oscar
GO_BP_m1	GO:004204	epithelial fl	1/2606	8/23843	0.603908	0.771485	0.733599	Ednrb
GO_BP_m1	GO:004236	fat-soluble	1/2606	8/23843	0.603908	0.771485	0.733599	Crabp1
GO_BP_m1	GO:004236	water-solu	1/2606	8/23843	0.603908	0.771485	0.733599	Mmachc
GO_BP_m1	GO:004243	indole-con	1/2606	8/23843	0.603908	0.771485	0.733599	Gch1
GO_BP_m1	GO:004263	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Smo
GO_BP_m1	GO:004263	catagen	1/2606	8/23843	0.603908	0.771485	0.733599	Ctsl
GO_BP_m1	GO:004276	very long-c	1/2606	8/23843	0.603908	0.771485	0.733599	Abcd3
GO_BP_m1	GO:004303	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Cd200
GO_BP_m1	GO:004304	DNA methy	1/2606	8/23843	0.603908	0.771485	0.733599	Tet3
GO_BP_m1	GO:004369	dedifferent	1/2606	8/23843	0.603908	0.771485	0.733599	Esrrb
GO_BP_m1	GO:004369	cell dediffe	1/2606	8/23843	0.603908	0.771485	0.733599	Esrrb
GO_BP_m1	GO:004398	histone H4	1/2606	8/23843	0.603908	0.771485	0.733599	Kat2a
GO_BP_m1	GO:004433	Wnt signali	1/2606	8/23843	0.603908	0.771485	0.733599	Lrp4
GO_BP_m1	GO:004508	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Ifng
GO_BP_m1	GO:004565	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Rcor1
GO_BP_m1	GO:004571	low-densit	1/2606	8/23843	0.603908	0.771485	0.733599	Sec24a
GO_BP_m1	GO:004606	cGMP cata	1/2606	8/23843	0.603908	0.771485	0.733599	Pde11a
GO_BP_m1	GO:004634	amino suga	1/2606	8/23843	0.603908	0.771485	0.733599	Pgm3
GO_BP_m1	GO:004810	autophagic	1/2606	8/23843	0.603908	0.771485	0.733599	Bnip3
GO_BP_m1	GO:004829	isotype swi	1/2606	8/23843	0.603908	0.771485	0.733599	Nsd2
GO_BP_m1	GO:004863	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Rps6kb1
GO_BP_m1	GO:004875	semicircula	1/2606	8/23843	0.603908	0.771485	0.733599	Tbx1

GO_BP_m1	GO:005088	voluntary r	1/2606	8/23843	0.603908	0.771485	0.733599	Xrcc1
GO_BP_m1	GO:005110	DNA ligatio	1/2606	8/23843	0.603908	0.771485	0.733599	Lig3
GO_BP_m1	GO:005145	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Crhbp
GO_BP_m1	GO:005500	atrial cardi	1/2606	8/23843	0.603908	0.771485	0.733599	Nog
GO_BP_m1	GO:006002	convergent	1/2606	8/23843	0.603908	0.771485	0.733599	Zfp568
GO_BP_m1	GO:006008	relaxation (	1/2606	8/23843	0.603908	0.771485	0.733599	Adora1
GO_BP_m1	GO:006067	ureteric bu	1/2606	8/23843	0.603908	0.771485	0.733599	Fgf1
GO_BP_m1	GO:006083	lymphatic e	1/2606	8/23843	0.603908	0.771485	0.733599	Sox18
GO_BP_m1	GO:006089	neural plat	1/2606	8/23843	0.603908	0.771485	0.733599	Nog
GO_BP_m1	GO:006104	vascular wo	1/2606	8/23843	0.603908	0.771485	0.733599	Adipor2
GO_BP_m1	GO:006162	pharyngea	1/2606	8/23843	0.603908	0.771485	0.733599	Nog
GO_BP_m1	GO:006182	telomeric D	1/2606	8/23843	0.603908	0.771485	0.733599	Blm
GO_BP_m1	GO:007025	somatostat	1/2606	8/23843	0.603908	0.771485	0.733599	Cartpt
GO_BP_m1	GO:007047	rRNA base	1/2606	8/23843	0.603908	0.771485	0.733599	Nop2
GO_BP_m1	GO:007056	vitamin D r	1/2606	8/23843	0.603908	0.771485	0.733599	Kank2
GO_BP_m1	GO:007142	cellular res	1/2606	8/23843	0.603908	0.771485	0.733599	Aoc1
GO_BP_m1	GO:007203	renal vesicl	1/2606	8/23843	0.603908	0.771485	0.733599	Smo
GO_BP_m1	GO:008502	protein K6-	1/2606	8/23843	0.603908	0.771485	0.733599	Park2
GO_BP_m1	GO:009008	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Dnaja4
GO_BP_m1	GO:009023	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Tpr
GO_BP_m1	GO:009026	fibroblast g	1/2606	8/23843	0.603908	0.771485	0.733599	Ptgs2
GO_BP_m1	GO:009027	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ptgs2
GO_BP_m1	GO:009038	phagosom	1/2606	8/23843	0.603908	0.771485	0.733599	Rab34
GO_BP_m1	GO:009065	telomeric lo	1/2606	8/23843	0.603908	0.771485	0.733599	Blm
GO_BP_m1	GO:009706	anterior he	1/2606	8/23843	0.603908	0.771485	0.733599	Arsb
GO_BP_m1	GO:009737	interneuron	1/2606	8/23843	0.603908	0.771485	0.733599	Mir9-3
GO_BP_m1	GO:009742	protein ma	1/2606	8/23843	0.603908	0.771485	0.733599	Isca2
GO_BP_m1	GO:009884	protein tran	1/2606	8/23843	0.603908	0.771485	0.733599	Stau2
GO_BP_m1	GO:009887	action pote	1/2606	8/23843	0.603908	0.771485	0.733599	Fkbp1b
GO_BP_m1	GO:009911	microtubul	1/2606	8/23843	0.603908	0.771485	0.733599	Stau2
GO_BP_m1	GO:190004	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ptpn22
GO_BP_m1	GO:190024	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Cpeb3
GO_BP_m1	GO:190036	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Supt5
GO_BP_m1	GO:190045	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Stau2
GO_BP_m1	GO:190129	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Hsph1
GO_BP_m1	GO:190153	changes to	1/2606	8/23843	0.603908	0.771485	0.733599	Tet3
GO_BP_m1	GO:190241	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Fmr1
GO_BP_m1	GO:190286	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Dll4
GO_BP_m1	GO:190301	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Tnfsf11
GO_BP_m1	GO:190314	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Tigar
GO_BP_m1	GO:190323	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Ccl28
GO_BP_m1	GO:190340	protein loc	1/2606	8/23843	0.603908	0.771485	0.733599	Cct3
GO_BP_m1	GO:190372	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Pdgfa
GO_BP_m1	GO:190374	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Hsph1
GO_BP_m1	GO:190379	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Fxyd1
GO_BP_m1	GO:190399	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Dgat1
GO_BP_m1	GO:190441	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Nod1
GO_BP_m1	GO:190441	positive reg	1/2606	8/23843	0.603908	0.771485	0.733599	Nod1

GO_BP_m1	GO:19044	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Zc3h12a
GO_BP_m1	GO:19048	protein loc	1/2606	8/23843	0.603908	0.771485	0.733599	Cct3
GO_BP_m1	GO:19048	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Cct3
GO_BP_m1	GO:190487	positive re	1/2606	8/23843	0.603908	0.771485	0.733599	Cct3
GO_BP_m1	GO:190524	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Fmr1
GO_BP_m1	GO:200004	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Wnt3a
GO_BP_m1	GO:20001	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Atp2b4
GO_BP_m1	GO:20003	regulation	1/2606	8/23843	0.603908	0.771485	0.733599	Smpd3
GO_BP_m1	GO:200031	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Smad7
GO_BP_m1	GO:200032	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Smad7
GO_BP_m1	GO:20004	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Prkar2b
GO_BP_m1	GO:200054	negative re	1/2606	8/23843	0.603908	0.771485	0.733599	Col5a1
GO_BP_m1	GO:200061	positive re	1/2606	8/23843	0.603908	0.771485	0.733599	Kat2b
GO_BP_m1	GO:200064	positive re	1/2606	8/23843	0.603908	0.771485	0.733599	Ezr
GO_BP_m1	GO:00105	positive re	11/2606	105/23843	0.605739	0.773711	0.735716	Bnip3/Dap
GO_BP_m1	GO:00027	immune re	45/2606	424/23843	0.606837	0.775001	0.736942	5730559C1
GO_BP_m1	GO:00071	establishm	22/2606	209/23843	0.607458	0.775682	0.737589	Bcas3/Cen
GO_BP_m1	GO:003087	mammary	17/2606	162/23843	0.608224	0.775962	0.737856	Aprt/Atp7
GO_BP_m1	GO:005114	smooth m	7/2606	67/23843	0.608399	0.775962	0.737856	Adm/Ednr
GO_BP_m1	GO:19048	cranial skel	7/2606	67/23843	0.608399	0.775962	0.737856	Alx3/Foxe1
GO_BP_m1	GO:00094	response t	4/2606	38/23843	0.60865	0.775962	0.737856	Dio2/Fcor/
GO_BP_m1	GO:00163	calcium-d	4/2606	38/23843	0.60865	0.775962	0.737856	Cdh1/Cdh
GO_BP_m1	GO:00440	regulation	4/2606	38/23843	0.60865	0.775962	0.737856	Anxa2/Ift8
GO_BP_m1	GO:00455	negative re	4/2606	38/23843	0.60865	0.775962	0.737856	Ctla4/Jak3/
GO_BP_m1	GO:00504	amyloid-b	4/2606	38/23843	0.60865	0.775962	0.737856	Apeh/Aph
GO_BP_m1	GO:00860	membrane	4/2606	38/23843	0.60865	0.775962	0.737856	Akap6/Atp
GO_BP_m1	GO:19016	glycosyl co	4/2606	38/23843	0.60865	0.775962	0.737856	Adk/Aprt/
GO_BP_m1	GO:19019	positive re	4/2606	38/23843	0.60865	0.775962	0.737856	Arntl/Fam1
GO_BP_m1	GO:00095	detection	5/2606	48/23843	0.613884	0.781841	0.743446	Prcd/Guca
GO_BP_m1	GO:00105	RNA secon	5/2606	48/23843	0.613884	0.781841	0.743446	Ddx19b/D
GO_BP_m1	GO:00107	fibroblast	5/2606	48/23843	0.613884	0.781841	0.743446	Acta2/D1E
GO_BP_m1	GO:00326	regulation	5/2606	48/23843	0.613884	0.781841	0.743446	5730559C1
GO_BP_m1	GO:00986	inorganic	5/2606	48/23843	0.613884	0.781841	0.743446	Calcr/Slc31
GO_BP_m1	GO:00995	inorganic i	5/2606	48/23843	0.613884	0.781841	0.743446	Calcr/Slc31
GO_BP_m1	GO:20003	regulation	5/2606	48/23843	0.613884	0.781841	0.743446	Abl2/Cd24
GO_BP_m1	GO:01200	regulation	18/2606	172/23843	0.614001	0.781877	0.74348	Atp8b1/Bc
GO_BP_m1	GO:00103	regulation	8/2606	77/23843	0.614601	0.782414	0.743991	Blm/Ccng1
GO_BP_m1	GO:004324	negative re	8/2606	77/23843	0.614601	0.782414	0.743991	Cfl1/Cib1/
GO_BP_m1	GO:000864	hexose tra	13/2606	125/23843	0.617993	0.786617	0.747988	Adipor2/A
GO_BP_m1	GO:00023	immunogl	6/2606	58/23843	0.619173	0.787664	0.748983	Aplf/Ifng/Il
GO_BP_m1	GO:00320	negative re	6/2606	58/23843	0.619173	0.787664	0.748983	Arntl/Flcn/
GO_BP_m1	GO:00322	positive re	6/2606	58/23843	0.619173	0.787664	0.748983	Ctgf/Itgb1
GO_BP_m1	GO:19033	positive re	6/2606	58/23843	0.619173	0.787664	0.748983	Catsper3/
GO_BP_m1	GO:005114	striated m	31/2606	295/23843	0.620066	0.788685	0.749954	Acta1/Aka
GO_BP_m1	GO:00068	post-Golgi	9/2606	87/23843	0.620457	0.788839	0.750101	Ankfy1/Bb
GO_BP_m1	GO:003101	pancreas d	9/2606	87/23843	0.620457	0.788839	0.750101	Arntl/Clock
GO_BP_m1	GO:004632	glucose im	9/2606	87/23843	0.620457	0.788839	0.750101	Adipor2/A
GO_BP_m1	GO:00485	eye morph	18/2606	173/23843	0.62407	0.793318	0.75436	Aldh1a3/B

GO_BP_m1	GO:003023	myofibril a	7/2606	68/23843	0.624382	0.79337	0.754409	Acta1/Cav3
GO_BP_m1	GO:004864	regulation	7/2606	68/23843	0.624382	0.79337	0.754409	Arntl/Ephb
GO_BP_m1	GO:006104	negative re	7/2606	68/23843	0.624382	0.79337	0.754409	Abat/Alox1
GO_BP_m1	GO:006034	bone morp	10/2606	97/23843	0.626014	0.794223	0.75522	Alpl/Csgal
GO_BP_m1	GO:200123	negative re	10/2606	97/23843	0.626014	0.794223	0.75522	Dapk1/Gcl
GO_BP_m1	GO:000648	protein de	3/2606	29/23843	0.628193	0.794223	0.75522	Kdm2b/Kd
GO_BP_m1	GO:000689	intra-Golgi	3/2606	29/23843	0.628193	0.794223	0.75522	Cog4/Copg
GO_BP_m1	GO:000821	protein de	3/2606	29/23843	0.628193	0.794223	0.75522	Kdm2b/Kd
GO_BP_m1	GO:003094	regulation	3/2606	29/23843	0.628193	0.794223	0.75522	Myof/Pdcd
GO_BP_m1	GO:003278	positive re	3/2606	29/23843	0.628193	0.794223	0.75522	Btbd18/Ell2
GO_BP_m1	GO:003295	inositol ph	3/2606	29/23843	0.628193	0.794223	0.75522	Adcyap1r1
GO_BP_m1	GO:003647	neuron de	3/2606	29/23843	0.628193	0.794223	0.75522	Il10/Park2/
GO_BP_m1	GO:004330	positive re	3/2606	29/23843	0.628193	0.794223	0.75522	Itgam/Ms4
GO_BP_m1	GO:006030	regulation	3/2606	29/23843	0.628193	0.794223	0.75522	Akap6/Cav
GO_BP_m1	GO:007030	lens fiber c	3/2606	29/23843	0.628193	0.794223	0.75522	Cdkn1c/Ep
GO_BP_m1	GO:009002	positive re	3/2606	29/23843	0.628193	0.794223	0.75522	Mospd2/N
GO_BP_m1	GO:190018	negative re	3/2606	29/23843	0.628193	0.794223	0.75522	Cldn18/Ei2
GO_BP_m1	GO:190320	regulation	3/2606	29/23843	0.628193	0.794223	0.75522	Il10/Park2/
GO_BP_m1	GO:000633	chromatin	15/2606	145/23843	0.629016	0.794223	0.75522	Ash2l/Bah
GO_BP_m1	GO:001092	negative re	8/2606	78/23843	0.629457	0.794223	0.75522	Csrnp3/Fkb
GO_BP_m1	GO:007122	cellular res	28/2606	268/23843	0.629483	0.794223	0.75522	Abl2/Adnp
GO_BP_m1	GO:000271	positive re	4/2606	39/23843	0.629618	0.794223	0.75522	Fam49b/Il1
GO_BP_m1	GO:000317	heart valve	4/2606	39/23843	0.629618	0.794223	0.75522	Adamts9/J
GO_BP_m1	GO:000668	glycosphin	4/2606	39/23843	0.629618	0.794223	0.75522	B4galt3/M
GO_BP_m1	GO:000939	phospholip	4/2606	39/23843	0.629618	0.794223	0.75522	Angptl3/Er
GO_BP_m1	GO:003112	developme	4/2606	39/23843	0.629618	0.794223	0.75522	Fgf1/Gdnf/
GO_BP_m1	GO:003434	response t	4/2606	39/23843	0.629618	0.794223	0.75522	Cactin/Ifitm
GO_BP_m1	GO:003545	cellular res	4/2606	39/23843	0.629618	0.794223	0.75522	Gm12185/
GO_BP_m1	GO:004327	apoptotic c	4/2606	39/23843	0.629618	0.794223	0.75522	Cd36/Pdia
GO_BP_m1	GO:004585	pH reducti	4/2606	39/23843	0.629618	0.794223	0.75522	Atp6v0c/A
GO_BP_m1	GO:005128	positive re	4/2606	39/23843	0.629618	0.794223	0.75522	Akap6/Cd1
GO_BP_m1	GO:190357	negative re	4/2606	39/23843	0.629618	0.794223	0.75522	Nck2/Park2
GO_BP_m1	GO:000150	cartilage c	2/2606	19/23843	0.630659	0.794223	0.75522	Ctgf/Wnt7a
GO_BP_m1	GO:000169	gastric acic	2/2606	19/23843	0.630659	0.794223	0.75522	Oprl1/Slc2
GO_BP_m1	GO:000231	mature B c	2/2606	19/23843	0.630659	0.794223	0.75522	Dock10/Gp
GO_BP_m1	GO:000321	cardiac rig	2/2606	19/23843	0.630659	0.794223	0.75522	Jag1/Zfpm
GO_BP_m1	GO:001015	regulation	2/2606	19/23843	0.630659	0.794223	0.75522	Drd3/Pm2
GO_BP_m1	GO:001076	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	Acta2/Pak1
GO_BP_m1	GO:001501	heparan su	2/2606	19/23843	0.630659	0.794223	0.75522	Extl3/Hs6st
GO_BP_m1	GO:001581	L-glutamat	2/2606	19/23843	0.630659	0.794223	0.75522	Arl6ip5/Slc
GO_BP_m1	GO:002153	cell migrati	2/2606	19/23843	0.630659	0.794223	0.75522	Cend1/Plxn
GO_BP_m1	GO:003085	regulation	2/2606	19/23843	0.630659	0.794223	0.75522	Cul4a/Trib1
GO_BP_m1	GO:003360	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	Cartpt/Htr6
GO_BP_m1	GO:003396	cytoplasmi	2/2606	19/23843	0.630659	0.794223	0.75522	Noct/Cnot
GO_BP_m1	GO:003535	peroxisom	2/2606	19/23843	0.630659	0.794223	0.75522	Asxl1/Plin5
GO_BP_m1	GO:003574	CD4-positi	2/2606	19/23843	0.630659	0.794223	0.75522	Arg1/Il12b
GO_BP_m1	GO:004278	mRNA tran	2/2606	19/23843	0.630659	0.794223	0.75522	Lmo2/Sox1
GO_BP_m1	GO:004395	negative re	2/2606	19/23843	0.630659	0.794223	0.75522	Atp2b4/Op

GO_BP_m1	GO:004682	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	Tpr/Wipf1
GO_BP_m1	GO:004831	mitochond	2/2606	19/23843	0.630659	0.794223	0.75522	Kat2a/Ogt
GO_BP_m1	GO:005077	negative re	2/2606	19/23843	0.630659	0.794223	0.75522	Dnm3/Nlg
GO_BP_m1	GO:005101	barbed-en	2/2606	19/23843	0.630659	0.794223	0.75522	Cfl1/Gsn
GO_BP_m1	GO:00519	establishm	2/2606	19/23843	0.630659	0.794223	0.75522	Bloc1s5/Ra
GO_BP_m1	GO:00550	cardiac my	2/2606	19/23843	0.630659	0.794223	0.75522	Mylk2/Pdg
GO_BP_m1	GO:006012	regulation	2/2606	19/23843	0.630659	0.794223	0.75522	Arhgef7/Se
GO_BP_m1	GO:006074	parental be	2/2606	19/23843	0.630659	0.794223	0.75522	Avpr1a/Zfx
GO_BP_m1	GO:007252	seminifero	2/2606	19/23843	0.630659	0.794223	0.75522	Rnase10/W
GO_BP_m1	GO:009067	RNA locali	2/2606	19/23843	0.630659	0.794223	0.75522	Cct3/Nop1
GO_BP_m1	GO:009067	telomerase	2/2606	19/23843	0.630659	0.794223	0.75522	Cct3/Nop1
GO_BP_m1	GO:009067	telomerase	2/2606	19/23843	0.630659	0.794223	0.75522	Cct3/Nop1
GO_BP_m1	GO:00906	RNA locali	2/2606	19/23843	0.630659	0.794223	0.75522	Cct3/Nop1
GO_BP_m1	GO:19004	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	Endog/Rall
GO_BP_m1	GO:20001	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	P2ry2/Tnfs
GO_BP_m1	GO:20002	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	Bcas3/Csf3
GO_BP_m1	GO:200122	positive re	2/2606	19/23843	0.630659	0.794223	0.75522	Fbxo31/Sh
GO_BP_m1	GO:000641	translation	11/2606	107/23843	0.63131	0.79493	0.755892	Eif1b/Eif2a
GO_BP_m1	GO:00323	response t	5/2606	49/23843	0.632539	0.79602	0.756929	Crhbp/Fosl
GO_BP_m1	GO:00329	collagen bi	5/2606	49/23843	0.632539	0.79602	0.756929	Arg1/Col5a
GO_BP_m1	GO:00430	tRNA amin	5/2606	49/23843	0.632539	0.79602	0.756929	Kars/Lrrc47
GO_BP_m1	GO:19052	negative re	5/2606	49/23843	0.632539	0.79602	0.756929	Apobec1/H
GO_BP_m1	GO:00604	regulation	18/2606	174/23843	0.634015	0.797652	0.758481	Atp8b1/Bc
GO_BP_m1	GO:00072	Rho protei	20/2606	193/23843	0.634264	0.797652	0.758481	Abl2/Abra/
GO_BP_m1	GO:000004	transition r	9/2606	88/23843	0.63438	0.797652	0.758481	Atp7b/Gif/
GO_BP_m1	GO:00435	regulation	9/2606	88/23843	0.63438	0.797652	0.758481	Gab1/Il1rn/
GO_BP_m1	GO:00455	positive re	9/2606	88/23843	0.63438	0.797652	0.758481	Adam8/Ifn
GO_BP_m1	GO:190122	regulation	9/2606	88/23843	0.63438	0.797652	0.758481	C1qtnf3/Ca
GO_BP_m1	GO:00022	CD4-positi	6/2606	59/23843	0.636118	0.798026	0.758836	Gpr183/Ifn
GO_BP_m1	GO:003267	regulation	6/2606	59/23843	0.636118	0.798026	0.758836	Cactin/Hya
GO_BP_m1	GO:00456	negative re	6/2606	59/23843	0.636118	0.798026	0.758836	Noct/Gdf1
GO_BP_m1	GO:00460	cGMP met	6/2606	59/23843	0.636118	0.798026	0.758836	Adcy4/Guc
GO_BP_m1	GO:00510	negative re	6/2606	59/23843	0.636118	0.798026	0.758836	Abl2/Arhg
GO_BP_m1	GO:001624	regulation	10/2606	98/23843	0.639149	0.798026	0.758836	Bnip3/Dcn/
GO_BP_m1	GO:00320	negative re	10/2606	98/23843	0.639149	0.798026	0.758836	Cav1/Csnk
GO_BP_m1	GO:00511	positive re	7/2606	69/23843	0.639995	0.798026	0.758836	Akap6/Cav
GO_BP_m1	GO:001574	monosacch	13/2606	127/23843	0.641236	0.798026	0.758836	Adipor2/Ad
GO_BP_m1	GO:00434	response t	31/2606	298/23843	0.642965	0.798026	0.758836	Appl1/Bcar
GO_BP_m1	GO:007134	cellular res	11/2606	108/23843	0.643767	0.798026	0.758836	Arg1/Ccl2
GO_BP_m1	GO:006144	connective	26/2606	251/23843	0.644665	0.798026	0.758836	Ap1s2/Bbs
GO_BP_m1	GO:000171	endoderma	1/2606	9/23843	0.647215	0.798026	0.758836	Sox2
GO_BP_m1	GO:000184	neural fold	1/2606	9/23843	0.647215	0.798026	0.758836	Cfl1
GO_BP_m1	GO:000231	myeloid pr	1/2606	9/23843	0.647215	0.798026	0.758836	Tet2
GO_BP_m1	GO:000274	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Kars
GO_BP_m1	GO:00028	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Il12b
GO_BP_m1	GO:00028	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Il12b
GO_BP_m1	GO:00028	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Bcr
GO_BP_m1	GO:000322	ventricular	1/2606	9/23843	0.647215	0.798026	0.758836	Nog

GO_BP_m1	GO:000334	pericardiur	1/2606	9/23843	0.647215	0.798026	0.758836	Dll4
GO_BP_m1	GO:000622	UTP biosyr	1/2606	9/23843	0.647215	0.798026	0.758836	Nme6
GO_BP_m1	GO:000734	penetratior	1/2606	9/23843	0.647215	0.798026	0.758836	Hyal3
GO_BP_m1	GO:000756	parturition	1/2606	9/23843	0.647215	0.798026	0.758836	Arntl
GO_BP_m1	GO:000830	isoprenoid	1/2606	9/23843	0.647215	0.798026	0.758836	Crabp1
GO_BP_m1	GO:000834	adult feedi	1/2606	9/23843	0.647215	0.798026	0.758836	Cartpt
GO_BP_m1	GO:000912	purine nuc	1/2606	9/23843	0.647215	0.798026	0.758836	Nt5c1a
GO_BP_m1	GO:000912	pyrimidine	1/2606	9/23843	0.647215	0.798026	0.758836	Shmt1
GO_BP_m1	GO:000922	pyrimidine	1/2606	9/23843	0.647215	0.798026	0.758836	Shmt1
GO_BP_m1	GO:001069	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Npnt
GO_BP_m1	GO:001080	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Stx1b
GO_BP_m1	GO:001402	neural cres	1/2606	9/23843	0.647215	0.798026	0.758836	Pdcd6
GO_BP_m1	GO:001482	intestine sr	1/2606	9/23843	0.647215	0.798026	0.758836	Tacr2
GO_BP_m1	GO:001486	skeletal my	1/2606	9/23843	0.647215	0.798026	0.758836	Acta1
GO_BP_m1	GO:001582	proline trar	1/2606	9/23843	0.647215	0.798026	0.758836	Slc6a20a
GO_BP_m1	GO:001655	peroxisom	1/2606	9/23843	0.647215	0.798026	0.758836	Sec16b
GO_BP_m1	GO:001706	respiratory	1/2606	9/23843	0.647215	0.798026	0.758836	Slc25a33
GO_BP_m1	GO:001802	peptidyl-ly	1/2606	9/23843	0.647215	0.798026	0.758836	Kmt5a
GO_BP_m1	GO:001933	phenol-co	1/2606	9/23843	0.647215	0.798026	0.758836	Dio2
GO_BP_m1	GO:002154	rhombome	1/2606	9/23843	0.647215	0.798026	0.758836	Hoxb1
GO_BP_m1	GO:002156	vestibulocc	1/2606	9/23843	0.647215	0.798026	0.758836	Atp8b1
GO_BP_m1	GO:002179	cerebral cc	1/2606	9/23843	0.647215	0.798026	0.758836	Dmrta2
GO_BP_m1	GO:002189	olfactory b	1/2606	9/23843	0.647215	0.798026	0.758836	Arx
GO_BP_m1	GO:002202	tangential	1/2606	9/23843	0.647215	0.798026	0.758836	Arx
GO_BP_m1	GO:003091	midbrain-h	1/2606	9/23843	0.647215	0.798026	0.758836	Kdm2b
GO_BP_m1	GO:003144	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Cpeb3
GO_BP_m1	GO:003200	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Plin5
GO_BP_m1	GO:003228	peripheral	1/2606	9/23843	0.647215	0.798026	0.758836	Ahnak2
GO_BP_m1	GO:003249	response t	1/2606	9/23843	0.647215	0.798026	0.758836	Cd36
GO_BP_m1	GO:003302	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Hcar2
GO_BP_m1	GO:003303	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Hcar2
GO_BP_m1	GO:003312	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Fmr1
GO_BP_m1	GO:003329	secretion o	1/2606	9/23843	0.647215	0.798026	0.758836	Nr1h2
GO_BP_m1	GO:003331	mitotic DN	1/2606	9/23843	0.647215	0.798026	0.758836	Topbp1
GO_BP_m1	GO:003368	nucleotide-	1/2606	9/23843	0.647215	0.798026	0.758836	Ercc5
GO_BP_m1	GO:003368	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Eif2ak2
GO_BP_m1	GO:003435	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Prkca
GO_BP_m1	GO:003445	microtubul	1/2606	9/23843	0.647215	0.798026	0.758836	Ccdc68
GO_BP_m1	GO:003455	mitochond	1/2606	9/23843	0.647215	0.798026	0.758836	Slc25a33
GO_BP_m1	GO:003477	histone H4	1/2606	9/23843	0.647215	0.798026	0.758836	Nsd2
GO_BP_m1	GO:003587	nail develo	1/2606	9/23843	0.647215	0.798026	0.758836	Itga6
GO_BP_m1	GO:004202	DNA endo	1/2606	9/23843	0.647215	0.798026	0.758836	E2f7
GO_BP_m1	GO:004211	endothelial	1/2606	9/23843	0.647215	0.798026	0.758836	Cxcl10
GO_BP_m1	GO:004218	ketone cat	1/2606	9/23843	0.647215	0.798026	0.758836	Haghl
GO_BP_m1	GO:004247	outer ear n	1/2606	9/23843	0.647215	0.798026	0.758836	Tbx1
GO_BP_m1	GO:004508	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Ifng
GO_BP_m1	GO:004541	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Ifng
GO_BP_m1	GO:004547	response t	1/2606	9/23843	0.647215	0.798026	0.758836	Zc3h12a

GO_BP_m1	GO:004575	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Cav3
GO_BP_m1	GO:004614	tetrahydrol	1/2606	9/23843	0.647215	0.798026	0.758836	Gch1
GO_BP_m1	GO:004660	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Ranbp1
GO_BP_m1	GO:004666	retinal cell	1/2606	9/23843	0.647215	0.798026	0.758836	Casp6
GO_BP_m1	GO:004687	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Tac1
GO_BP_m1	GO:004825	elastic fiber	1/2606	9/23843	0.647215	0.798026	0.758836	Fbln5
GO_BP_m1	GO:005071	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Zc3h12a
GO_BP_m1	GO:005150	adenine nu	1/2606	9/23843	0.647215	0.798026	0.758836	Slc25a23
GO_BP_m1	GO:005157	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Dmrtc2
GO_BP_m1	GO:005166	membrane	1/2606	9/23843	0.647215	0.798026	0.758836	Gsn
GO_BP_m1	GO:005269	flavonoid g	1/2606	9/23843	0.647215	0.798026	0.758836	Ugt1a9
GO_BP_m1	GO:005269	xenobiotic	1/2606	9/23843	0.647215	0.798026	0.758836	Ugt1a9
GO_BP_m1	GO:006002	convergent	1/2606	9/23843	0.647215	0.798026	0.758836	Zfp568
GO_BP_m1	GO:006013	embryonic	1/2606	9/23843	0.647215	0.798026	0.758836	Tle6
GO_BP_m1	GO:006031	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Bcr
GO_BP_m1	GO:006042	lung vascul	1/2606	9/23843	0.647215	0.798026	0.758836	Ift88
GO_BP_m1	GO:006053	diaphragm	1/2606	9/23843	0.647215	0.798026	0.758836	Wt1
GO_BP_m1	GO:006059	mammary	1/2606	9/23843	0.647215	0.798026	0.758836	Pax3
GO_BP_m1	GO:006063	mesenchym	1/2606	9/23843	0.647215	0.798026	0.758836	Fgf7
GO_BP_m1	GO:006071	chorion de	1/2606	9/23843	0.647215	0.798026	0.758836	E2f7
GO_BP_m1	GO:006103	visceral ser	1/2606	9/23843	0.647215	0.798026	0.758836	Wt1
GO_BP_m1	GO:006130	cornea dev	1/2606	9/23843	0.647215	0.798026	0.758836	Limk2
GO_BP_m1	GO:006137	testosteron	1/2606	9/23843	0.647215	0.798026	0.758836	Hsd17b3
GO_BP_m1	GO:006152	hindgut de	1/2606	9/23843	0.647215	0.798026	0.758836	Ift172
GO_BP_m1	GO:006154	sympatheti	1/2606	9/23843	0.647215	0.798026	0.758836	Sema3f
GO_BP_m1	GO:006157	calcium ion	1/2606	9/23843	0.647215	0.798026	0.758836	Cacnb2
GO_BP_m1	GO:007054	histone H3	1/2606	9/23843	0.647215	0.798026	0.758836	Kdm2b
GO_BP_m1	GO:007130	cellular res	1/2606	9/23843	0.647215	0.798026	0.758836	Kank2
GO_BP_m1	GO:007139	cellular res	1/2606	9/23843	0.647215	0.798026	0.758836	Spp1
GO_BP_m1	GO:007139	cellular res	1/2606	9/23843	0.647215	0.798026	0.758836	Smo
GO_BP_m1	GO:007148	cellular res	1/2606	9/23843	0.647215	0.798026	0.758836	Nucks1
GO_BP_m1	GO:007221	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Wt1
GO_BP_m1	GO:007249	mesenchym	1/2606	9/23843	0.647215	0.798026	0.758836	Pdgfra
GO_BP_m1	GO:007268	T cell extra	1/2606	9/23843	0.647215	0.798026	0.758836	Ripk3
GO_BP_m1	GO:008603	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Fxyd1
GO_BP_m1	GO:009003	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Por
GO_BP_m1	GO:009009	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Fscn1
GO_BP_m1	GO:009015	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Smpd3
GO_BP_m1	GO:009030	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Apobec1
GO_BP_m1	GO:009039	replicative	1/2606	9/23843	0.647215	0.798026	0.758836	Atr
GO_BP_m1	GO:009711	postsynapt	1/2606	9/23843	0.647215	0.798026	0.758836	Cdh2
GO_BP_m1	GO:009877	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Park2
GO_BP_m1	GO:009963	endosome	1/2606	9/23843	0.647215	0.798026	0.758836	Arhgap44
GO_BP_m1	GO:190103	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Endog
GO_BP_m1	GO:190140	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Ccnl1
GO_BP_m1	GO:190152	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Park2
GO_BP_m1	GO:190172	positive reg	1/2606	9/23843	0.647215	0.798026	0.758836	Myc
GO_BP_m1	GO:190222	ketone bod	1/2606	9/23843	0.647215	0.798026	0.758836	Dgat1

GO_BP_m1	GO:19026	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Tubb2b
GO_BP_m1	GO:19029	protein loc	1/2606	9/23843	0.647215	0.798026	0.758836	Ezr
GO_BP_m1	GO:19032	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Atp2b4
GO_BP_m1	GO:19037	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Zc3h12a
GO_BP_m1	GO:19043	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Wnt3a
GO_BP_m1	GO:19043	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Xrcc1
GO_BP_m1	GO:19047	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Dgat1
GO_BP_m1	GO:19050	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Smpd3
GO_BP_m1	GO:190521	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Fmr1
GO_BP_m1	GO:19054	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Flcn
GO_BP_m1	GO:20003	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Hdac1
GO_BP_m1	GO:20003	negative re	1/2606	9/23843	0.647215	0.798026	0.758836	Dand5
GO_BP_m1	GO:20003	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Adam8
GO_BP_m1	GO:20003	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Adam8
GO_BP_m1	GO:20005	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Calr
GO_BP_m1	GO:20005	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Arg1
GO_BP_m1	GO:20007	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Fgf7
GO_BP_m1	GO:200104	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Cd63
GO_BP_m1	GO:20011	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Ndrg4
GO_BP_m1	GO:200117	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Pycard
GO_BP_m1	GO:200121	positive re	1/2606	9/23843	0.647215	0.798026	0.758836	Adm
GO_BP_m1	GO:20012	regulation	1/2606	9/23843	0.647215	0.798026	0.758836	Abcb1a
GO_BP_m1	GO:00017	cell fate sp	9/2606	89/23843	0.648022	0.798909	0.759676	Dbx1/Dmr
GO_BP_m1	GO:00085	male gona	12/2606	118/23843	0.648241	0.799066	0.759825	Dmrt1/Hsd
GO_BP_m1	GO:00017	B cell apop	4/2606	40/23843	0.64985	0.799376	0.76012	Il10/Mir18
GO_BP_m1	GO:00061	cGMP bios	4/2606	40/23843	0.64985	0.799376	0.76012	Adcy4/Guc
GO_BP_m1	GO:003051	negative re	4/2606	40/23843	0.64985	0.799376	0.76012	Aatk/Cdk5
GO_BP_m1	GO:00308	negative re	4/2606	40/23843	0.64985	0.799376	0.76012	Cfl1/Gsn/P
GO_BP_m1	GO:003201	ARF protei	4/2606	40/23843	0.64985	0.799376	0.76012	Appl1/Asa
GO_BP_m1	GO:003201	regulation	4/2606	40/23843	0.64985	0.799376	0.76012	Appl1/Asa
GO_BP_m1	GO:009027	regulation	4/2606	40/23843	0.64985	0.799376	0.76012	Calcr/Cav3
GO_BP_m1	GO:19040	positive re	4/2606	40/23843	0.64985	0.799376	0.76012	Ccnl1/Stil/
GO_BP_m1	GO:00016	behavioral	5/2606	50/23843	0.650632	0.799376	0.76012	Eif4e/Grin2
GO_BP_m1	GO:000714	male meio	5/2606	50/23843	0.650632	0.799376	0.76012	Btbd18/Dd
GO_BP_m1	GO:001401	negative re	5/2606	50/23843	0.650632	0.799376	0.76012	Drd3/Idh2/
GO_BP_m1	GO:00301	water hom	5/2606	50/23843	0.650632	0.799376	0.76012	Abca12/Al
GO_BP_m1	GO:003221	regulation	5/2606	50/23843	0.650632	0.799376	0.76012	Atr/Cct3/H
GO_BP_m1	GO:00429	amyloid pr	5/2606	50/23843	0.650632	0.799376	0.76012	Aph1a/C3
GO_BP_m1	GO:00430	amino acid	5/2606	50/23843	0.650632	0.799376	0.76012	Kars/Lrrc47
GO_BP_m1	GO:004361	regulation	5/2606	50/23843	0.650632	0.799376	0.76012	Atf3/Cd36/
GO_BP_m1	GO:004394	regulation	5/2606	50/23843	0.650632	0.799376	0.76012	Adcyap1r1
GO_BP_m1	GO:00015	cilium or fl	3/2606	30/23843	0.651495	0.799376	0.76012	Bbs2/Dnah
GO_BP_m1	GO:00028	regulation	3/2606	30/23843	0.651495	0.799376	0.76012	Arg1/Il27r
GO_BP_m1	GO:00029	regulation	3/2606	30/23843	0.651495	0.799376	0.76012	Il10/Mir18
GO_BP_m1	GO:00095	detection	3/2606	30/23843	0.651495	0.799376	0.76012	Prcd/Opn4
GO_BP_m1	GO:00322	negative re	3/2606	30/23843	0.651495	0.799376	0.76012	Cfl1/Kank2
GO_BP_m1	GO:00435	negative re	3/2606	30/23843	0.651495	0.799376	0.76012	Dll4/Itgb1
GO_BP_m1	GO:00456	negative re	3/2606	30/23843	0.651495	0.799376	0.76012	Cxcl10/Mk

GO_BP_m1	GO:004603	GTP metab	3/2606	30/23843	0.651495	0.799376	0.76012	Gphn/Moc
GO_BP_m1	GO:004867	regulation	3/2606	30/23843	0.651495	0.799376	0.76012	Fkbp1b/Klk
GO_BP_m1	GO:004884	regulation	3/2606	30/23843	0.651495	0.799376	0.76012	Plxna2/Sem
GO_BP_m1	GO:005048	arachidoni	3/2606	30/23843	0.651495	0.799376	0.76012	Drd3/Pla2g
GO_BP_m1	GO:005156	regulation	3/2606	30/23843	0.651495	0.799376	0.76012	H2afy/Prm
GO_BP_m1	GO:006028	cilium-dep	3/2606	30/23843	0.651495	0.799376	0.76012	Bbs2/Dnah
GO_BP_m1	GO:007234	sulfur comp	3/2606	30/23843	0.651495	0.799376	0.76012	Racgap1/S
GO_BP_m1	GO:190007	positive reg	3/2606	30/23843	0.651495	0.799376	0.76012	Nucks1/Os
GO_BP_m1	GO:190396	arachidona	3/2606	30/23843	0.651495	0.799376	0.76012	Drd3/Pla2g
GO_BP_m1	GO:005087	regulation	35/2606	337/23843	0.65229	0.800072	0.760781	Abat/Abca
GO_BP_m1	GO:000229	alpha-beta	6/2606	60/23843	0.652608	0.800072	0.760781	Gpr183/Ifn
GO_BP_m1	GO:000627	RNA-depe	6/2606	60/23843	0.652608	0.800072	0.760781	Atr/Cct3/H
GO_BP_m1	GO:000700	telomere m	6/2606	60/23843	0.652608	0.800072	0.760781	Atr/Cct3/H
GO_BP_m1	GO:000808	axo-dendr	6/2606	60/23843	0.652608	0.800072	0.760781	Bloc1s5/Fm
GO_BP_m1	GO:003033	DNA dama	6/2606	60/23843	0.652608	0.800072	0.760781	Ankrd1/Atr
GO_BP_m1	GO:000173	morphoge	7/2606	70/23843	0.655225	0.803055	0.763619	Abl2/Cthrc
GO_BP_m1	GO:000749	endoderm	7/2606	70/23843	0.655225	0.803055	0.763619	Cfc1/Col5a
GO_BP_m1	GO:000244	production	31/2606	300/23843	0.657869	0.804626	0.765112	5730559C1
GO_BP_m1	GO:000237	cytokine se	2/2606	20/23843	0.658929	0.804626	0.765112	Il10/Kars
GO_BP_m1	GO:000275	MyD88-de	2/2606	20/23843	0.658929	0.804626	0.765112	Irak2/Tlr5
GO_BP_m1	GO:000308	positive reg	2/2606	20/23843	0.658929	0.804626	0.765112	Avpr1a/Ma
GO_BP_m1	GO:000678	heme biosy	2/2606	20/23843	0.658929	0.804626	0.765112	Cox15/Iba5
GO_BP_m1	GO:000681	phosphate	2/2606	20/23843	0.658929	0.804626	0.765112	Ank/Slc20a
GO_BP_m1	GO:000920	deoxyribor	2/2606	20/23843	0.658929	0.804626	0.765112	Adk/Nudt1
GO_BP_m1	GO:001573	prostaglan	2/2606	20/23843	0.658929	0.804626	0.765112	P2ry2/Tnfs
GO_BP_m1	GO:001648	peptide ho	2/2606	20/23843	0.658929	0.804626	0.765112	Corin/Cpz
GO_BP_m1	GO:003144	regulation	2/2606	20/23843	0.658929	0.804626	0.765112	Cpeb3/Sup
GO_BP_m1	GO:003230	regulation	2/2606	20/23843	0.658929	0.804626	0.765112	P2ry2/Tnfs
GO_BP_m1	GO:003303	negative re	2/2606	20/23843	0.658929	0.804626	0.765112	Kitl/St6gal1
GO_BP_m1	GO:003436	protein-lip	2/2606	20/23843	0.658929	0.804626	0.765112	Pltp/Scarb1
GO_BP_m1	GO:003436	plasma lipo	2/2606	20/23843	0.658929	0.804626	0.765112	Pltp/Scarb1
GO_BP_m1	GO:004273	fibrinolysis	2/2606	20/23843	0.658929	0.804626	0.765112	Anxa2/F11
GO_BP_m1	GO:004594	positive reg	2/2606	20/23843	0.658929	0.804626	0.765112	Rps6kb1/Y
GO_BP_m1	GO:005090	detection c	2/2606	20/23843	0.658929	0.804626	0.765112	Prcd/Tulp1
GO_BP_m1	GO:005096	detection c	2/2606	20/23843	0.658929	0.804626	0.765112	Prcd/Tulp1
GO_BP_m1	GO:007016	negative re	2/2606	20/23843	0.658929	0.804626	0.765112	Ccr1/Rflna
GO_BP_m1	GO:007063	transepithe	2/2606	20/23843	0.658929	0.804626	0.765112	Ednrb/Slc1
GO_BP_m1	GO:009005	positive reg	2/2606	20/23843	0.658929	0.804626	0.765112	Cib1/Ptgs2
GO_BP_m1	GO:009874	cell aggreg	2/2606	20/23843	0.658929	0.804626	0.765112	Ctgf/Wnt7a
GO_BP_m1	GO:190122	negative re	2/2606	20/23843	0.658929	0.804626	0.765112	C1qtnf3/Zc
GO_BP_m1	GO:199012	retrograde	2/2606	20/23843	0.658929	0.804626	0.765112	Arhgap44/
GO_BP_m1	GO:199018	exosomal s	2/2606	20/23843	0.658929	0.804626	0.765112	Park2/Smp
GO_BP_m1	GO:200102	regulation	2/2606	20/23843	0.658929	0.804626	0.765112	Fgf1/Fgf16
GO_BP_m1	GO:007123	cellular res	17/2606	167/23843	0.65898	0.804626	0.765112	Cdh1/Cpeb
GO_BP_m1	GO:004654	developme	12/2606	119/23843	0.659895	0.805631	0.766067	Dmrt1/Hsd
GO_BP_m1	GO:000244	myeloid leu	9/2606	90/23843	0.661372	0.807211	0.76757	Anxa3/Arg
GO_BP_m1	GO:005079	regulation	9/2606	90/23843	0.661372	0.807211	0.76757	Adora1/Dg
GO_BP_m1	GO:000836	regulation	20/2606	196/23843	0.661905	0.807748	0.768081	Aatk/Cav3/

GO_BP_m1	GO:00307	cytoskelet	16/2606	158/23843	0.664842	0.811219	0.771382	Bloc1s5/C
GO_BP_m1	GO:00026	positive re	21/2606	206/23843	0.665909	0.812408	0.772512	Arg1/Cadn
GO_BP_m1	GO:200004	regulation	11/2606	110/23843	0.667985	0.813758	0.773796	Cdkn1a/Cu
GO_BP_m1	GO:00018	retina hom	5/2606	51/23843	0.668148	0.813758	0.773796	Bbs10/Bbs
GO_BP_m1	GO:00022	behavioral	5/2606	51/23843	0.668148	0.813758	0.773796	Eif4e/Grin2
GO_BP_m1	GO:00322	positive re	5/2606	51/23843	0.668148	0.813758	0.773796	Atr/Cct3/H
GO_BP_m1	GO:003261	interleukin	5/2606	51/23843	0.668148	0.813758	0.773796	5730559C1
GO_BP_m1	GO:004577	positive re	5/2606	51/23843	0.668148	0.813758	0.773796	Cdkl5/Nrg
GO_BP_m1	GO:007171	icosanoid t	5/2606	51/23843	0.668148	0.813758	0.773796	Drd3/P2ry
GO_BP_m1	GO:00860	cardiac mu	5/2606	51/23843	0.668148	0.813758	0.773796	Cacnb2/Ca
GO_BP_m1	GO:190157	fatty acid d	5/2606	51/23843	0.668148	0.813758	0.773796	Drd3/P2ry
GO_BP_m1	GO:000961	response t	48/2606	462/23843	0.668538	0.813758	0.773796	4833427F1
GO_BP_m1	GO:00022	alpha-beta	6/2606	61/23843	0.668631	0.813758	0.773796	Gpr183/Ifn
GO_BP_m1	GO:00108	regulation	6/2606	61/23843	0.668631	0.813758	0.773796	Cav3/Cxcl1
GO_BP_m1	GO:00162	positive re	6/2606	61/23843	0.668631	0.813758	0.773796	Bnip3/Dcn
GO_BP_m1	GO:00308	positive re	6/2606	61/23843	0.668631	0.813758	0.773796	Alox12/Fox
GO_BP_m1	GO:00603	regulation	6/2606	61/23843	0.668631	0.813758	0.773796	Bmp3/Gdf
GO_BP_m1	GO:199082	response t	32/2606	311/23843	0.668991	0.813758	0.773796	Bcat2/Bcla
GO_BP_m1	GO:19908	cellular res	32/2606	311/23843	0.668991	0.813758	0.773796	Bcat2/Bcla
GO_BP_m1	GO:00074	salivary gla	4/2606	41/23843	0.669331	0.813758	0.773796	Cdh1/Fgf7
GO_BP_m1	GO:00092	response t	4/2606	41/23843	0.669331	0.813758	0.773796	Arsb/Gja3/
GO_BP_m1	GO:001051	positive re	4/2606	41/23843	0.669331	0.813758	0.773796	Abl2/Adcy
GO_BP_m1	GO:00109	positive re	4/2606	41/23843	0.669331	0.813758	0.773796	Esrrb/Kat2
GO_BP_m1	GO:002152	spinal cord	4/2606	41/23843	0.669331	0.813758	0.773796	Gigyf2/Hox
GO_BP_m1	GO:00216	cerebellar	4/2606	41/23843	0.669331	0.813758	0.773796	Cdk5/Cenc
GO_BP_m1	GO:006151	protein loc	4/2606	41/23843	0.669331	0.813758	0.773796	Bbs2/Cc2d
GO_BP_m1	GO:00970	regulation	4/2606	41/23843	0.669331	0.813758	0.773796	Abcb1a/At
GO_BP_m1	GO:00974	neuron pro	22/2606	216/23843	0.669797	0.814212	0.774228	Arx/Cdk5/
GO_BP_m1	GO:003227	negative re	7/2606	71/23843	0.670062	0.814422	0.774427	Cfl1/Gsn/K
GO_BP_m1	GO:00701	regulation	8/2606	81/23843	0.672065	0.815813	0.77575	Ank/Bglap
GO_BP_m1	GO:19019	positive re	8/2606	81/23843	0.672065	0.815813	0.77575	Cdc25a/Cd
GO_BP_m1	GO:00108	regulation	3/2606	31/23843	0.673732	0.815813	0.77575	Ctsl/Fgf7/
GO_BP_m1	GO:00158	neutral am	3/2606	31/23843	0.673732	0.815813	0.77575	Slc43a2/Sl
GO_BP_m1	GO:00326	negative re	3/2606	31/23843	0.673732	0.815813	0.77575	Il10/Il1rl1/
GO_BP_m1	GO:003412	negative re	3/2606	31/23843	0.673732	0.815813	0.77575	Cactin/Lgr
GO_BP_m1	GO:00426	regulation	3/2606	31/23843	0.673732	0.815813	0.77575	Arntl/Clock
GO_BP_m1	GO:004327	anoikis	3/2606	31/23843	0.673732	0.815813	0.77575	Cav1/E2f1/
GO_BP_m1	GO:004351	regulation	3/2606	31/23843	0.673732	0.815813	0.77575	Ankrd1/Atr
GO_BP_m1	GO:00443	cell-cell ad	3/2606	31/23843	0.673732	0.815813	0.77575	Cdh1/Cdh
GO_BP_m1	GO:004561	regulation	3/2606	31/23843	0.673732	0.815813	0.77575	Foxc1/H2a
GO_BP_m1	GO:004824	sperm cap	3/2606	31/23843	0.673732	0.815813	0.77575	Acrbp/Bspl
GO_BP_m1	GO:007162	positive re	3/2606	31/23843	0.673732	0.815813	0.77575	Mospd2/N
GO_BP_m1	GO:00725	clathrin-de	3/2606	31/23843	0.673732	0.815813	0.77575	Canx/Dnaj
GO_BP_m1	GO:003421	carbohydr	13/2606	130/23843	0.674669	0.815813	0.77575	Adipor2/A
GO_BP_m1	GO:005101	actin filam	16/2606	159/23843	0.674754	0.815813	0.77575	Abl2/Cfl1/
GO_BP_m1	GO:000227	myeloid le	19/2606	188/23843	0.676136	0.815813	0.77575	Anxa3/Bcr/
GO_BP_m1	GO:00302	bone mine	10/2606	101/23843	0.677006	0.815813	0.77575	Ank/Bglap
GO_BP_m1	GO:004562	positive re	10/2606	101/23843	0.677006	0.815813	0.77575	Adam8/Ifn

GO_BP_m1	GO:00020	columnar/	14/2606	140/23843	0.677983	0.815813	0.77575	Abl2/Arntl
GO_BP_m1	GO:00455	regulation	14/2606	140/23843	0.677983	0.815813	0.77575	Adam8/Ctl
GO_BP_m1	GO:00074	mesoderm	11/2606	111/23843	0.679732	0.815813	0.77575	Dand5/Ep
GO_BP_m1	GO:00511	nuclear ex	15/2606	150/23843	0.681263	0.815813	0.77575	Calr/Cdk5
GO_BP_m1	GO:00432	response t	18/2606	179/23843	0.681731	0.815813	0.77575	Cdh1/Cfl1
GO_BP_m1	GO:00020	lens devel	7/2606	72/23843	0.684497	0.815813	0.77575	Bcar3/Cdk
GO_BP_m1	GO:00605	neuroepith	7/2606	72/23843	0.684497	0.815813	0.77575	Abl2/B9d1
GO_BP_m1	GO:00308	positive re	5/2606	52/23843	0.685077	0.815813	0.77575	Adm/Calcr
GO_BP_m1	GO:00435	positive re	5/2606	52/23843	0.685077	0.815813	0.77575	Atp5a1/Ci
GO_BP_m1	GO:00507	negative r	5/2606	52/23843	0.685077	0.815813	0.77575	Cav1/Gprc
GO_BP_m1	GO:007257	endothelia	5/2606	52/23843	0.685077	0.815813	0.77575	Abl2/Cd24
GO_BP_m1	GO:000042	mitophagy	2/2606	21/23843	0.685434	0.815813	0.77575	Park2/Tiga
GO_BP_m1	GO:000197	neurologic	2/2606	21/23843	0.685434	0.815813	0.77575	Adra1d/M
GO_BP_m1	GO:000232	lymphoid	2/2606	21/23843	0.685434	0.815813	0.77575	Flcn/Prkdc
GO_BP_m1	GO:000247	antigen pr	2/2606	21/23843	0.685434	0.815813	0.77575	H2-DMb2
GO_BP_m1	GO:00063	DNA-tem	2/2606	21/23843	0.685434	0.815813	0.77575	Mterf2/Xrn
GO_BP_m1	GO:00105	positive re	2/2606	21/23843	0.685434	0.815813	0.77575	Cfl1/Fscn1
GO_BP_m1	GO:002151	dorsal spin	2/2606	21/23843	0.685434	0.815813	0.77575	Pax3/Wnt3
GO_BP_m1	GO:00324	melanoso	2/2606	21/23843	0.685434	0.815813	0.77575	Bloc1s5/Ra
GO_BP_m1	GO:003292	regulation	2/2606	21/23843	0.685434	0.815813	0.77575	Fpr2/Itgam
GO_BP_m1	GO:00329	positive re	2/2606	21/23843	0.685434	0.815813	0.77575	Btbd18/Ell
GO_BP_m1	GO:003362	integrin ac	2/2606	21/23843	0.685434	0.815813	0.77575	Fermt2/Itg
GO_BP_m1	GO:00343	protein-co	2/2606	21/23843	0.685434	0.815813	0.77575	Pltp/Scarb
GO_BP_m1	GO:004427	sulfur com	2/2606	21/23843	0.685434	0.815813	0.77575	Blmh/Mtrr
GO_BP_m1	GO:00448	autophagy	2/2606	21/23843	0.685434	0.815813	0.77575	Atg2a/Wip
GO_BP_m1	GO:004632	negative r	2/2606	21/23843	0.685434	0.815813	0.77575	Myc/Prkca
GO_BP_m1	GO:004824	eosinophil	2/2606	21/23843	0.685434	0.815813	0.77575	Ccl4/Scg2
GO_BP_m1	GO:00485	post-embr	2/2606	21/23843	0.685434	0.815813	0.77575	Krtap21-1
GO_BP_m1	GO:007084	inclusion b	2/2606	21/23843	0.685434	0.815813	0.77575	Dnaja4/Pa
GO_BP_m1	GO:00977	extracellul	2/2606	21/23843	0.685434	0.815813	0.77575	Park2/Smp
GO_BP_m1	GO:19020	regulation	2/2606	21/23843	0.685434	0.815813	0.77575	C330021F
GO_BP_m1	GO:20002	regulation	2/2606	21/23843	0.685434	0.815813	0.77575	Cav1/Ptrh
GO_BP_m1	GO:200127	regulation	2/2606	21/23843	0.685434	0.815813	0.77575	Osbpl8/Pa
GO_BP_m1	GO:00002	deadenylat	1/2606	10/23843	0.685789	0.815813	0.77575	Noct
GO_BP_m1	GO:00020	negative r	1/2606	10/23843	0.685789	0.815813	0.77575	Fmr1
GO_BP_m1	GO:000231	marginal z	1/2606	10/23843	0.685789	0.815813	0.77575	Dock10
GO_BP_m1	GO:00026	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Pkn1
GO_BP_m1	GO:00026	negative r	1/2606	10/23843	0.685789	0.815813	0.77575	Prkdc
GO_BP_m1	GO:00027	MyD88-in	1/2606	10/23843	0.685789	0.815813	0.77575	Ticam2
GO_BP_m1	GO:00032	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Tbx1
GO_BP_m1	GO:00060	chitin meta	1/2606	10/23843	0.685789	0.815813	0.77575	Chil5
GO_BP_m1	GO:00060	chitin cata	1/2606	10/23843	0.685789	0.815813	0.77575	Chil5
GO_BP_m1	GO:000624	CTP biosyn	1/2606	10/23843	0.685789	0.815813	0.77575	Nme6
GO_BP_m1	GO:000662	posttransla	1/2606	10/23843	0.685789	0.815813	0.77575	Folr2
GO_BP_m1	GO:00066	phosphati	1/2606	10/23843	0.685789	0.815813	0.77575	Ptpmt1
GO_BP_m1	GO:00070	protein cat	1/2606	10/23843	0.685789	0.815813	0.77575	Tcirg1
GO_BP_m1	GO:00071	neuron cel	1/2606	10/23843	0.685789	0.815813	0.77575	Nlgn3
GO_BP_m1	GO:000727	neuron-ne	1/2606	10/23843	0.685789	0.815813	0.77575	Vdac1

GO_BP_m1	GO:00760	phototrans	1/2606	10/23843	0.685789	0.815813	0.77575	Opn4
GO_BP_m1	GO:00104	histone H3	1/2606	10/23843	0.685789	0.815813	0.77575	Nsd2
GO_BP_m1	GO:001061	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Atp2b4
GO_BP_m1	GO:00108	positive re	1/2606	10/23843	0.685789	0.815813	0.77575	Pnpla2
GO_BP_m1	GO:00148	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Pax3
GO_BP_m1	GO:00148	transition	1/2606	10/23843	0.685789	0.815813	0.77575	Myh7
GO_BP_m1	GO:00148	muscle atr	1/2606	10/23843	0.685789	0.815813	0.77575	Gsn
GO_BP_m1	GO:001581	glycine tra	1/2606	10/23843	0.685789	0.815813	0.77575	Slc6a20a
GO_BP_m1	GO:00158	purine nuc	1/2606	10/23843	0.685789	0.815813	0.77575	Slc25a23
GO_BP_m1	GO:00159	coenzyme	1/2606	10/23843	0.685789	0.815813	0.77575	Dcakd
GO_BP_m1	GO:00218	cerebral c	1/2606	10/23843	0.685789	0.815813	0.77575	Arx
GO_BP_m1	GO:002194	positive re	1/2606	10/23843	0.685789	0.815813	0.77575	Smo
GO_BP_m1	GO:00308	positive re	1/2606	10/23843	0.685789	0.815813	0.77575	Trib1
GO_BP_m1	GO:003127	positive re	1/2606	10/23843	0.685789	0.815813	0.77575	Cdc42ep5
GO_BP_m1	GO:003134	positive re	1/2606	10/23843	0.685789	0.815813	0.77575	Anxa2
GO_BP_m1	GO:003194	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Dgkq
GO_BP_m1	GO:003211	sequesteri	1/2606	10/23843	0.685789	0.815813	0.77575	Slc30a3
GO_BP_m1	GO:003237	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Pcsk9
GO_BP_m1	GO:003237	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Pcsk9
GO_BP_m1	GO:003261	interleukin	1/2606	10/23843	0.685789	0.815813	0.77575	Ccl20
GO_BP_m1	GO:00329	inositol tris	1/2606	10/23843	0.685789	0.815813	0.77575	P2ry1
GO_BP_m1	GO:003357	transferrin	1/2606	10/23843	0.685789	0.815813	0.77575	Rep15
GO_BP_m1	GO:00343	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Prkca
GO_BP_m1	GO:00343	high-densi	1/2606	10/23843	0.685789	0.815813	0.77575	Nr1h2
GO_BP_m1	GO:003442	nuclear-tra	1/2606	10/23843	0.685789	0.815813	0.77575	Exosc9
GO_BP_m1	GO:00346	cortisol me	1/2606	10/23843	0.685789	0.815813	0.77575	Dgkq
GO_BP_m1	GO:003572	common	1/2606	10/23843	0.685789	0.815813	0.77575	Samd9l
GO_BP_m1	GO:00359	dorsal aort	1/2606	10/23843	0.685789	0.815813	0.77575	Dll4
GO_BP_m1	GO:00359	tetrahydro	1/2606	10/23843	0.685789	0.815813	0.77575	Shmt1
GO_BP_m1	GO:004242	norepinep	1/2606	10/23843	0.685789	0.815813	0.77575	Th
GO_BP_m1	GO:004276	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Snca
GO_BP_m1	GO:00433	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Bcr
GO_BP_m1	GO:00434	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Cd36
GO_BP_m1	GO:00436	linoleic aci	1/2606	10/23843	0.685789	0.815813	0.77575	Ephx2
GO_BP_m1	GO:004392	exonucleol	1/2606	10/23843	0.685789	0.815813	0.77575	Exosc9
GO_BP_m1	GO:00453	interferon-	1/2606	10/23843	0.685789	0.815813	0.77575	Nmi
GO_BP_m1	GO:00453	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Nmi
GO_BP_m1	GO:00456	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Jag1
GO_BP_m1	GO:00460	CTP metab	1/2606	10/23843	0.685789	0.815813	0.77575	Nme6
GO_BP_m1	GO:00460	UTP metab	1/2606	10/23843	0.685789	0.815813	0.77575	Nme6
GO_BP_m1	GO:00482	vesicle fus	1/2606	10/23843	0.685789	0.815813	0.77575	Stx5a
GO_BP_m1	GO:00489	peripheral	1/2606	10/23843	0.685789	0.815813	0.77575	Hoxd10
GO_BP_m1	GO:00489	peripheral	1/2606	10/23843	0.685789	0.815813	0.77575	Hoxd10
GO_BP_m1	GO:00510	positive re	1/2606	10/23843	0.685789	0.815813	0.77575	Nr1h2
GO_BP_m1	GO:005101	actin filam	1/2606	10/23843	0.685789	0.815813	0.77575	Gsn
GO_BP_m1	GO:005112	synaptic gr	1/2606	10/23843	0.685789	0.815813	0.77575	Lrp4
GO_BP_m1	GO:00514	corticotrop	1/2606	10/23843	0.685789	0.815813	0.77575	Crhbp
GO_BP_m1	GO:00516	maintenan	1/2606	10/23843	0.685789	0.815813	0.77575	Pafah1b1

GO_BP_m1	GO:005182	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Ncan
GO_BP_m1	GO:005191	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	F11
GO_BP_m1	GO:005197	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Cartpt
GO_BP_m1	GO:005280	imidazole-	1/2606	10/23843	0.685789	0.815813	0.77575	Hdc
GO_BP_m1	GO:006002	Bergmann	1/2606	10/23843	0.685789	0.815813	0.77575	Abl2
GO_BP_m1	GO:006021	primitive h	1/2606	10/23843	0.685789	0.815813	0.77575	Stk3
GO_BP_m1	GO:006051	prostatic b	1/2606	10/23843	0.685789	0.815813	0.77575	Nog
GO_BP_m1	GO:006089	neural plat	1/2606	10/23843	0.685789	0.815813	0.77575	Nog
GO_BP_m1	GO:006098	coronary a	1/2606	10/23843	0.685789	0.815813	0.77575	Tbx1
GO_BP_m1	GO:006108	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Slc30a3
GO_BP_m1	GO:007007	proton-tra	1/2606	10/23843	0.685789	0.815813	0.77575	Tcirg1
GO_BP_m1	GO:007007	vacuolar pr	1/2606	10/23843	0.685789	0.815813	0.77575	Tcirg1
GO_BP_m1	GO:007009	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Cartpt
GO_BP_m1	GO:007025	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	P2ry2
GO_BP_m1	GO:007039	response t	1/2606	10/23843	0.685789	0.815813	0.77575	Cd36
GO_BP_m1	GO:007088	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Atp2b4
GO_BP_m1	GO:007122	cellular res	1/2606	10/23843	0.685789	0.815813	0.77575	Cd36
GO_BP_m1	GO:007188	macrophag	1/2606	10/23843	0.685789	0.815813	0.77575	St6gal1
GO_BP_m1	GO:007217	metanephr	1/2606	10/23843	0.685789	0.815813	0.77575	Lgr4
GO_BP_m1	GO:007260	interleukin-	1/2606	10/23843	0.685789	0.815813	0.77575	Pycard
GO_BP_m1	GO:007552	IRES-depen	1/2606	10/23843	0.685789	0.815813	0.77575	Eif3f
GO_BP_m1	GO:009000	primitive st	1/2606	10/23843	0.685789	0.815813	0.77575	Foxa2
GO_BP_m1	GO:009012	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Cdc20
GO_BP_m1	GO:009018	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Nr1h2
GO_BP_m1	GO:009742	liver regen	1/2606	10/23843	0.685789	0.815813	0.77575	Ezh1
GO_BP_m1	GO:010605	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Atp2b4
GO_BP_m1	GO:190003	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Ogt
GO_BP_m1	GO:190010	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Bok
GO_BP_m1	GO:190011	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Dmrtc2
GO_BP_m1	GO:190011	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Dffa
GO_BP_m1	GO:190103	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Bok
GO_BP_m1	GO:190140	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Ccnl1
GO_BP_m1	GO:190167	iron coordi	1/2606	10/23843	0.685789	0.815813	0.77575	Slc46a1
GO_BP_m1	GO:190197	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Tpr
GO_BP_m1	GO:190241	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Fmr1
GO_BP_m1	GO:190293	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Nfkb1
GO_BP_m1	GO:190381	negative re	1/2606	10/23843	0.685789	0.815813	0.77575	Cav1
GO_BP_m1	GO:190566	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	Ezr
GO_BP_m1	GO:190566	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Ezr
GO_BP_m1	GO:199017	protein loc	1/2606	10/23843	0.685789	0.815813	0.77575	Cct3
GO_BP_m1	GO:200010	regulation	1/2606	10/23843	0.685789	0.815813	0.77575	St6gal1
GO_BP_m1	GO:200034	positive reg	1/2606	10/23843	0.685789	0.815813	0.77575	Hyal3
GO_BP_m1	GO:003297	regulation	39/2606	380/23843	0.68683	0.816942	0.776823	Abra/Abra
GO_BP_m1	GO:009874	cell-cell ad	17/2606	170/23843	0.687698	0.817068	0.776943	Cadm1/Cd
GO_BP_m1	GO:000597	glycogen b	4/2606	42/23843	0.688053	0.817068	0.776943	Esrrb/Gys1
GO_BP_m1	GO:000708	mitotic me	4/2606	42/23843	0.688053	0.817068	0.776943	Ankrd53/C
GO_BP_m1	GO:000925	glucan bios	4/2606	42/23843	0.688053	0.817068	0.776943	Esrrb/Gys1
GO_BP_m1	GO:001079	regulation	4/2606	42/23843	0.688053	0.817068	0.776943	Dgkq/Ogt/

GO_BP_m1	GO:001097	negative re	4/2606	42/23843	0.688053	0.817068	0.776943	Blm/Ccng1
GO_BP_m1	GO:003105	negative re	4/2606	42/23843	0.688053	0.817068	0.776943	H2afy/Msx
GO_BP_m1	GO:003288	regulation	4/2606	42/23843	0.688053	0.817068	0.776943	Esrrb/Has2
GO_BP_m1	GO:003305	cellular pig	4/2606	42/23843	0.688053	0.817068	0.776943	Bloc1s5/Cc
GO_BP_m1	GO:004277	intrinsic ap	4/2606	42/23843	0.688053	0.817068	0.776943	Cdkn1a/Nu
GO_BP_m1	GO:006013	maternal p	4/2606	42/23843	0.688053	0.817068	0.776943	Cdh1/Ctsl/
GO_BP_m1	GO:007266	establishm	4/2606	42/23843	0.688053	0.817068	0.776943	Cacng5/Ca
GO_BP_m1	GO:006054	respiratory	25/2606	247/23843	0.688677	0.8177	0.777544	Abca12/Al
GO_BP_m1	GO:000270	positive reg	10/2606	102/23843	0.689085	0.817963	0.777794	Cadm1/Far
GO_BP_m1	GO:004518	maintenan	10/2606	102/23843	0.689085	0.817963	0.777794	Cav1/Cdk5
GO_BP_m1	GO:000758	body fluid	11/2606	112/23843	0.691231	0.820288	0.780005	Adora1/An
GO_BP_m1	GO:004247	inner ear m	11/2606	112/23843	0.691231	0.820288	0.780005	Aldh1a3/B
GO_BP_m1	GO:003090	hindbrain	16/2606	161/23843	0.694083	0.823423	0.782986	Abl2/Cdk5/
GO_BP_m1	GO:001700	cytochrom	3/2606	32/23843	0.694904	0.823423	0.782986	Cox15/Slc2
GO_BP_m1	GO:004574	positive reg	3/2606	32/23843	0.694904	0.823423	0.782986	Acpp/Drd3
GO_BP_m1	GO:005086	negative re	3/2606	32/23843	0.694904	0.823423	0.782986	Ctla4/Il10/
GO_BP_m1	GO:006035	cartilage d	3/2606	32/23843	0.694904	0.823423	0.782986	Poc1a/Por/
GO_BP_m1	GO:008015	regulation	3/2606	32/23843	0.694904	0.823423	0.782986	Hyal3/Pkdr
GO_BP_m1	GO:008502	extracellula	3/2606	32/23843	0.694904	0.823423	0.782986	Antxr1/Fblr
GO_BP_m1	GO:190218	regulation	3/2606	32/23843	0.694904	0.823423	0.782986	Pcx/Trim31
GO_BP_m1	GO:190247	L-alpha-ar	3/2606	32/23843	0.694904	0.823423	0.782986	Arl6ip5/AU
GO_BP_m1	GO:190520	positive reg	3/2606	32/23843	0.694904	0.823423	0.782986	Akap6/Nrg
GO_BP_m1	GO:200003	regulation	3/2606	32/23843	0.694904	0.823423	0.782986	Esrrb/Kdm
GO_BP_m1	GO:000736	gastrulatio	17/2606	171/23843	0.696958	0.825745	0.785194	Cfc1/Nat8f
GO_BP_m1	GO:000334	cilium mov	7/2606	73/23843	0.698523	0.827377	0.786745	Bbs2/Ccdc
GO_BP_m1	GO:006096	regulation	7/2606	73/23843	0.698523	0.827377	0.786745	Apobec1/C
GO_BP_m1	GO:190007	regulation	8/2606	83/23843	0.698747	0.82753	0.786892	Gpr21/Nuc
GO_BP_m1	GO:004396	histone H4	6/2606	63/23843	0.699236	0.827887	0.787231	Hat1/Kansl
GO_BP_m1	GO:009730	cellular res	6/2606	63/23843	0.699236	0.827887	0.787231	Blm/Cdh1/
GO_BP_m1	GO:000661	protein tar	10/2606	103/23843	0.700884	0.829726	0.78898	Adora1/Cd
GO_BP_m1	GO:000304	regulation	5/2606	53/23843	0.701411	0.830015	0.789254	Adra1d/Av
GO_BP_m1	GO:003506	regulation	5/2606	53/23843	0.701411	0.830015	0.789254	Flcn/Kat2a/
GO_BP_m1	GO:190288	negative re	5/2606	53/23843	0.701411	0.830015	0.789254	Gpx1/H2af
GO_BP_m1	GO:002203	metenceph	11/2606	113/23843	0.702476	0.831162	0.790345	Abl2/Cdk5/
GO_BP_m1	GO:000182	blastocyst	4/2606	43/23843	0.70601	0.834423	0.793446	Cdh1/Esrrb
GO_BP_m1	GO:003110	axon reger	4/2606	43/23843	0.70601	0.834423	0.793446	Fkbp1b/Klk
GO_BP_m1	GO:003275	positive reg	4/2606	43/23843	0.70601	0.834423	0.793446	Hyal2/Pyca
GO_BP_m1	GO:008601	membrane	4/2606	43/23843	0.70601	0.834423	0.793446	Cacnb2/Ca
GO_BP_m1	GO:009031	negative re	4/2606	43/23843	0.70601	0.834423	0.793446	Cdk5/Ei24/
GO_BP_m1	GO:004859	camera-typ	13/2606	133/23843	0.706256	0.834423	0.793446	Aldh1a3/B
GO_BP_m1	GO:000191	negative re	2/2606	22/23843	0.710222	0.834423	0.793446	Ptprc/Sh2d
GO_BP_m1	GO:000283	regulation	2/2606	22/23843	0.710222	0.834423	0.793446	Il12b/Ulbp
GO_BP_m1	GO:000283	regulation	2/2606	22/23843	0.710222	0.834423	0.793446	Il12b/Ulbp
GO_BP_m1	GO:000335	epithelial c	2/2606	22/23843	0.710222	0.834423	0.793446	Dnah1/Ulk
GO_BP_m1	GO:000654	glutamine	2/2606	22/23843	0.710222	0.834423	0.793446	Gfpt2/Gls
GO_BP_m1	GO:000853	respiratory	2/2606	22/23843	0.710222	0.834423	0.793446	Cox15/Smi
GO_BP_m1	GO:002154	subpallium	2/2606	22/23843	0.710222	0.834423	0.793446	Aldh1a3/Bl
GO_BP_m1	GO:003025	growth hor	2/2606	22/23843	0.710222	0.834423	0.793446	Arhgef7/Se

GO_BP_m1	GO:003272	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Mmp12/Pt
GO_BP_m1	GO:004348	histone exc	2/2606	22/23843	0.710222	0.834423	0.793446	Psme4/Syc
GO_BP_m1	GO:004560	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Foxc1/H2a
GO_BP_m1	GO:004884	negative re	2/2606	22/23843	0.710222	0.834423	0.793446	Sema3f/Wr
GO_BP_m1	GO:005085	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Kcnn4/Ptpr
GO_BP_m1	GO:005187	pigment gr	2/2606	22/23843	0.710222	0.834423	0.793446	Bloc1s5/Ra
GO_BP_m1	GO:006007	synapse ma	2/2606	22/23843	0.710222	0.834423	0.793446	Cdc20/Sez
GO_BP_m1	GO:006096	negative re	2/2606	22/23843	0.710222	0.834423	0.793446	Apobec1/Z
GO_BP_m1	GO:007121	cellular res	2/2606	22/23843	0.710222	0.834423	0.793446	Ufd1/Uggt
GO_BP_m1	GO:007257	hepatocyte	2/2606	22/23843	0.710222	0.834423	0.793446	Ifng/Wnt3a
GO_BP_m1	GO:007257	epithelial c	2/2606	22/23843	0.710222	0.834423	0.793446	Ifng/Wnt3a
GO_BP_m1	GO:190027	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Cpeb3/Grir
GO_BP_m1	GO:190138	negative re	2/2606	22/23843	0.710222	0.834423	0.793446	Cav1/Cav3
GO_BP_m1	GO:190320	negative re	2/2606	22/23843	0.710222	0.834423	0.793446	Il10/Park2
GO_BP_m1	GO:190364	regulation	2/2606	22/23843	0.710222	0.834423	0.793446	Dnajc13/Ez
GO_BP_m1	GO:190386	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Cpne6/Parl
GO_BP_m1	GO:200063	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Fmr1/Nfkb
GO_BP_m1	GO:200073	positive reg	2/2606	22/23843	0.710222	0.834423	0.793446	Foxc1/Mir3
GO_BP_m1	GO:200083	regulation	2/2606	22/23843	0.710222	0.834423	0.793446	Galr1/Tac1
GO_BP_m1	GO:011002	regulation	9/2606	94/23843	0.711713	0.834423	0.793446	Cav3/Ctgf/
GO_BP_m1	GO:003250	maintenanc	7/2606	74/23843	0.712133	0.834423	0.793446	Cav1/Cdk5
GO_BP_m1	GO:004883	inner ear d	20/2606	202/23843	0.713736	0.834423	0.793446	Aldh1a3/A
GO_BP_m1	GO:006038	pathway-re	6/2606	64/23843	0.713806	0.834423	0.793446	Bmp3/Gdf1
GO_BP_m1	GO:006042	lung morph	6/2606	64/23843	0.713806	0.834423	0.793446	Cfc1/Fgf7/
GO_BP_m1	GO:000701	microtubul	26/2606	260/23843	0.714293	0.834423	0.793446	Bbs2/Bloc1
GO_BP_m1	GO:003021	erythrocyte	12/2606	124/23843	0.714807	0.834423	0.793446	Bpgm/Jak3
GO_BP_m1	GO:000177	myeloid de	3/2606	33/23843	0.715018	0.834423	0.793446	Il10/Pycarc
GO_BP_m1	GO:000761	mating beh	3/2606	33/23843	0.715018	0.834423	0.793446	Avpr1a/Drc
GO_BP_m1	GO:003262	interleukin-	3/2606	33/23843	0.715018	0.834423	0.793446	Ifng/Il12b/
GO_BP_m1	GO:003303	regulation	3/2606	33/23843	0.715018	0.834423	0.793446	Hcar2/Kitl/
GO_BP_m1	GO:004562	regulation	3/2606	33/23843	0.715018	0.834423	0.793446	Jak3/Smad
GO_BP_m1	GO:004646	neutral lipi	3/2606	33/23843	0.715018	0.834423	0.793446	Mgll/Plin5/
GO_BP_m1	GO:004646	acylglycerc	3/2606	33/23843	0.715018	0.834423	0.793446	Mgll/Plin5/
GO_BP_m1	GO:004804	embryonic	3/2606	33/23843	0.715018	0.834423	0.793446	Aldh1a3/Kc
GO_BP_m1	GO:005068	negative re	3/2606	33/23843	0.715018	0.834423	0.793446	Rbm42/Srs
GO_BP_m1	GO:005509	acylglycerc	3/2606	33/23843	0.715018	0.834423	0.793446	Angptl3/C1
GO_BP_m1	GO:006070	cell differer	3/2606	33/23843	0.715018	0.834423	0.793446	E2f7/Plk4/S
GO_BP_m1	GO:007032	triglyceride	3/2606	33/23843	0.715018	0.834423	0.793446	Angptl3/C1
GO_BP_m1	GO:190109	negative re	3/2606	33/23843	0.715018	0.834423	0.793446	Gdnf/Il7/St
GO_BP_m1	GO:190320	regulation	3/2606	33/23843	0.715018	0.834423	0.793446	Endog/Hsp
GO_BP_m1	GO:200124	negative re	3/2606	33/23843	0.715018	0.834423	0.793446	Gdnf/Il7/St
GO_BP_m1	GO:004206	wound hea	34/2606	337/23843	0.716105	0.834423	0.793446	Abat/Acta2
GO_BP_m1	GO:004274	defense res	45/2606	442/23843	0.716821	0.834423	0.793446	1700016D0
GO_BP_m1	GO:004259	fear respor	5/2606	54/23843	0.717148	0.834423	0.793446	Eif4e/Grin2
GO_BP_m1	GO:007266	protein loc	5/2606	54/23843	0.717148	0.834423	0.793446	Cacng5/Ca
GO_BP_m1	GO:000701	actin filame	39/2606	385/23843	0.717618	0.834423	0.793446	Abi1/Abl2/
GO_BP_m1	GO:000168	tRNA 5'-lea	1/2606	11/23843	0.720146	0.834423	0.793446	Rpp40
GO_BP_m1	GO:000213	retinoic aci	1/2606	11/23843	0.720146	0.834423	0.793446	Aldh1a3

GO_BP_m1	GO:000267	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Il10
GO_BP_m1	GO:000292	negative re	1/2606	11/23843	0.720146	0.834423	0.793446	Susd4
GO_BP_m1	GO:000326	cardioblast	1/2606	11/23843	0.720146	0.834423	0.793446	Tbx1
GO_BP_m1	GO:000326	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Tbx1
GO_BP_m1	GO:000330	Wnt signali	1/2606	11/23843	0.720146	0.834423	0.793446	Wnt3a
GO_BP_m1	GO:000605	N-acetylne	1/2606	11/23843	0.720146	0.834423	0.793446	St6gal1
GO_BP_m1	GO:000618	GTP biosyr	1/2606	11/23843	0.720146	0.834423	0.793446	Nme6
GO_BP_m1	GO:000650	C-terminal	1/2606	11/23843	0.720146	0.834423	0.793446	Wipi2
GO_BP_m1	GO:000675	glutathione	1/2606	11/23843	0.720146	0.834423	0.793446	Gclm
GO_BP_m1	GO:000697	DNA dama	1/2606	11/23843	0.720146	0.834423	0.793446	Cdkn1a
GO_BP_m1	GO:000698	ER overloa	1/2606	11/23843	0.720146	0.834423	0.793446	Atg10
GO_BP_m1	GO:000712	meiotic prc	1/2606	11/23843	0.720146	0.834423	0.793446	Topaz1
GO_BP_m1	GO:000809	retrograde	1/2606	11/23843	0.720146	0.834423	0.793446	Pafah1b1
GO_BP_m1	GO:000920	pyrimidine	1/2606	11/23843	0.720146	0.834423	0.793446	Nme6
GO_BP_m1	GO:000981	flavonoid r	1/2606	11/23843	0.720146	0.834423	0.793446	Ugt1a9
GO_BP_m1	GO:001074	positive re	1/2606	11/23843	0.720146	0.834423	0.793446	Cd36
GO_BP_m1	GO:001483	urinary bla	1/2606	11/23843	0.720146	0.834423	0.793446	Htr7
GO_BP_m1	GO:001484	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Ephb1
GO_BP_m1	GO:001487	response t	1/2606	11/23843	0.720146	0.834423	0.793446	Prkag3
GO_BP_m1	GO:001574	C4-dicarbo	1/2606	11/23843	0.720146	0.834423	0.793446	Abat
GO_BP_m1	GO:001610	diterpenoi	1/2606	11/23843	0.720146	0.834423	0.793446	Aldh1a3
GO_BP_m1	GO:001655	base conve	1/2606	11/23843	0.720146	0.834423	0.793446	Apobec1
GO_BP_m1	GO:001829	protein-ch	1/2606	11/23843	0.720146	0.834423	0.793446	Opn4
GO_BP_m1	GO:001953	oxalate tra	1/2606	11/23843	0.720146	0.834423	0.793446	Slc26a7
GO_BP_m1	GO:002155	trigeminal	1/2606	11/23843	0.720146	0.834423	0.793446	Sema3f
GO_BP_m1	GO:002168	cerebellar	1/2606	11/23843	0.720146	0.834423	0.793446	Wnt7a
GO_BP_m1	GO:002170	cerebellar	1/2606	11/23843	0.720146	0.834423	0.793446	Wnt7a
GO_BP_m1	GO:003103	myosin fila	1/2606	11/23843	0.720146	0.834423	0.793446	Rap1gds1
GO_BP_m1	GO:003127	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Cdc42ep5
GO_BP_m1	GO:003202	response t	1/2606	11/23843	0.720146	0.834423	0.793446	Snca
GO_BP_m1	GO:003204	cardiolipin	1/2606	11/23843	0.720146	0.834423	0.793446	Ptpmt1
GO_BP_m1	GO:003246	negative re	1/2606	11/23843	0.720146	0.834423	0.793446	Pex5
GO_BP_m1	GO:003323	negative re	1/2606	11/23843	0.720146	0.834423	0.793446	Hmg20a
GO_BP_m1	GO:003360	positive re	1/2606	11/23843	0.720146	0.834423	0.793446	Htr6
GO_BP_m1	GO:003363	cell-cell ad	1/2606	11/23843	0.720146	0.834423	0.793446	Npnt
GO_BP_m1	GO:003370	phospholip	1/2606	11/23843	0.720146	0.834423	0.793446	Abca12
GO_BP_m1	GO:003411	positive re	1/2606	11/23843	0.720146	0.834423	0.793446	Gcnt2
GO_BP_m1	GO:003526	protein O-	1/2606	11/23843	0.720146	0.834423	0.793446	Pomgnt2
GO_BP_m1	GO:003563	bone mine	1/2606	11/23843	0.720146	0.834423	0.793446	Rflna
GO_BP_m1	GO:003584	photorecep	1/2606	11/23843	0.720146	0.834423	0.793446	Tmem67
GO_BP_m1	GO:003588	amacrine c	1/2606	11/23843	0.720146	0.834423	0.793446	Foxn4
GO_BP_m1	GO:003818	nerve grow	1/2606	11/23843	0.720146	0.834423	0.793446	Ntf5
GO_BP_m1	GO:004358	skin morph	1/2606	11/23843	0.720146	0.834423	0.793446	Wnt7a
GO_BP_m1	GO:004361	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Cd36
GO_BP_m1	GO:004455	relaxation	1/2606	11/23843	0.720146	0.834423	0.793446	Adora1
GO_BP_m1	GO:004508	positive re	1/2606	11/23843	0.720146	0.834423	0.793446	Glmn
GO_BP_m1	GO:004519	maintenan	1/2606	11/23843	0.720146	0.834423	0.793446	Lrrd1
GO_BP_m1	GO:004564	negative re	1/2606	11/23843	0.720146	0.834423	0.793446	Lmo2

GO_BP_m1	GO:004638	deoxyribos	1/2606	11/23843	0.720146	0.834423	0.793446	Nudt1
GO_BP_m1	GO:004668	response t	1/2606	11/23843	0.720146	0.834423	0.793446	Pgam2
GO_BP_m1	GO:004826	determinat	1/2606	11/23843	0.720146	0.834423	0.793446	Grem2
GO_BP_m1	GO:004826	determinat	1/2606	11/23843	0.720146	0.834423	0.793446	Grem2
GO_BP_m1	GO:004856	post-embr	1/2606	11/23843	0.720146	0.834423	0.793446	Mir23a
GO_BP_m1	GO:004863	skeletal mu	1/2606	11/23843	0.720146	0.834423	0.793446	Rps6kb1
GO_BP_m1	GO:004868	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Fkbp1b
GO_BP_m1	GO:004884	venous blo	1/2606	11/23843	0.720146	0.834423	0.793446	Ephb4
GO_BP_m1	GO:005132	prophase	1/2606	11/23843	0.720146	0.834423	0.793446	Topaz1
GO_BP_m1	GO:005160	exocyst loc	1/2606	11/23843	0.720146	0.834423	0.793446	Exoc3l2
GO_BP_m1	GO:006001	righting ref	1/2606	11/23843	0.720146	0.834423	0.793446	Aldh1a3
GO_BP_m1	GO:006005	mammary	1/2606	11/23843	0.720146	0.834423	0.793446	Cav1
GO_BP_m1	GO:006017	limb bud fo	1/2606	11/23843	0.720146	0.834423	0.793446	Plxna2
GO_BP_m1	GO:006034	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Mmp12
GO_BP_m1	GO:006045	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Ctgf
GO_BP_m1	GO:006076	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Serpinf1
GO_BP_m1	GO:006087	semicircula	1/2606	11/23843	0.720146	0.834423	0.793446	Tbx1
GO_BP_m1	GO:006090	embryonic	1/2606	11/23843	0.720146	0.834423	0.793446	Aldh1a3
GO_BP_m1	GO:006130	cardiac neu	1/2606	11/23843	0.720146	0.834423	0.793446	Jag1
GO_BP_m1	GO:006136	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Nr1h2
GO_BP_m1	GO:006161	glycolytic p	1/2606	11/23843	0.720146	0.834423	0.793446	Pfkl
GO_BP_m1	GO:007009	glucagon s	1/2606	11/23843	0.720146	0.834423	0.793446	Cartpt
GO_BP_m1	GO:007094	neutrophil	1/2606	11/23843	0.720146	0.834423	0.793446	Arg1
GO_BP_m1	GO:007163	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Trpv4
GO_BP_m1	GO:007167	commissur	1/2606	11/23843	0.720146	0.834423	0.793446	Smo
GO_BP_m1	GO:007210	glomerulus	1/2606	11/23843	0.720146	0.834423	0.793446	Pdgfra
GO_BP_m1	GO:007218	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Osr1
GO_BP_m1	GO:007239	microtubul	1/2606	11/23843	0.720146	0.834423	0.793446	Ccdc68
GO_BP_m1	GO:008601	AV node ce	1/2606	11/23843	0.720146	0.834423	0.793446	Cacnb2
GO_BP_m1	GO:008602	AV node ce	1/2606	11/23843	0.720146	0.834423	0.793446	Cacnb2
GO_BP_m1	GO:009007	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Trhr
GO_BP_m1	GO:009014	membrane	1/2606	11/23843	0.720146	0.834423	0.793446	Dnm3
GO_BP_m1	GO:009016	Golgi ribbo	1/2606	11/23843	0.720146	0.834423	0.793446	Tmed5
GO_BP_m1	GO:009055	establishme	1/2606	11/23843	0.720146	0.834423	0.793446	Cldn1
GO_BP_m1	GO:009878	pre-mRNA	1/2606	11/23843	0.720146	0.834423	0.793446	Cpsf4
GO_BP_m1	GO:190166	calcium ior	1/2606	11/23843	0.720146	0.834423	0.793446	Atp2b4
GO_BP_m1	GO:190200	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Csnk1e
GO_BP_m1	GO:190235	sulfate trar	1/2606	11/23843	0.720146	0.834423	0.793446	Slc26a7
GO_BP_m1	GO:190243	negative re	1/2606	11/23843	0.720146	0.834423	0.793446	C330021F2
GO_BP_m1	GO:190358	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Dll4
GO_BP_m1	GO:190365	positive reg	1/2606	11/23843	0.720146	0.834423	0.793446	Ezr
GO_BP_m1	GO:190372	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Gsn
GO_BP_m1	GO:190386	extraembry	1/2606	11/23843	0.720146	0.834423	0.793446	E2f7
GO_BP_m1	GO:190415	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Bcap31
GO_BP_m1	GO:200003	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Esrrb
GO_BP_m1	GO:200057	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Pafah1b1
GO_BP_m1	GO:200061	regulation	1/2606	11/23843	0.720146	0.834423	0.793446	Kat2b
GO_BP_m1	GO:000979	axis specifi	9/2606	95/23843	0.723506	0.838206	0.797043	Foxa2/Ift17

GO_BP_m1	GO:001071	regulation	8/2606	85/23843	0.723992	0.838658	0.797473	Foxa2/Fox
GO_BP_m1	GO:00341	erythrocyt	13/2606	135/23843	0.726235	0.841146	0.799838	Bpgm/Jak3
GO_BP_m1	GO:00022	T cell differ	6/2606	65/23843	0.727883	0.842721	0.801336	Gpr183/Ifn
GO_BP_m1	GO:00105	negative re	6/2606	65/23843	0.727883	0.842721	0.801336	Dapl1/Mt3
GO_BP_m1	GO:00422	natural kill	6/2606	65/23843	0.727883	0.842721	0.801336	Cadm1/Il1
GO_BP_m1	GO:003104	gene silen	15/2606	155/23843	0.729063	0.843976	0.80253	Cnot10/Cn
GO_BP_m1	GO:000741	axon guida	21/2606	214/23843	0.732009	0.846004	0.804458	Arx/Cdk5/
GO_BP_m1	GO:003527	exocrine sy	5/2606	55/23843	0.732285	0.846004	0.804458	Cdh1/Fgf7/
GO_BP_m1	GO:00001	establishm	2/2606	23/23843	0.733352	0.846004	0.804458	Cenpa/Paf
GO_BP_m1	GO:00031	atrioventri	2/2606	23/23843	0.733352	0.846004	0.804458	Smad6/Zfp
GO_BP_m1	GO:000341	endochon	2/2606	23/23843	0.733352	0.846004	0.804458	Poc1a/Por
GO_BP_m1	GO:000821	glucocortic	2/2606	23/23843	0.733352	0.846004	0.804458	Dgkq/Hsd1
GO_BP_m1	GO:00094	toxin meta	2/2606	23/23843	0.733352	0.846004	0.804458	As3mt/Fm
GO_BP_m1	GO:003014	sphingolipi	2/2606	23/23843	0.733352	0.846004	0.804458	Asah2/Sm
GO_BP_m1	GO:00319	positive re	2/2606	23/23843	0.733352	0.846004	0.804458	Gpnmb/Pd
GO_BP_m1	GO:00326	negative re	2/2606	23/23843	0.733352	0.846004	0.804458	Mefv/Zc3h
GO_BP_m1	GO:00354	histone-se	2/2606	23/23843	0.733352	0.846004	0.804458	Gm14147/
GO_BP_m1	GO:004204	fluid trans	2/2606	23/23843	0.733352	0.846004	0.804458	Ednrb/Myl
GO_BP_m1	GO:00443	glucose im	2/2606	23/23843	0.733352	0.846004	0.804458	Osbpl8/Pal
GO_BP_m1	GO:00482	behavioral	2/2606	23/23843	0.733352	0.846004	0.804458	Grin2b/Htr
GO_BP_m1	GO:00483	mesoderm	2/2606	23/23843	0.733352	0.846004	0.804458	Kdm6b/Wr
GO_BP_m1	GO:00512	protein ins	2/2606	23/23843	0.733352	0.846004	0.804458	Reep1/Wrb
GO_BP_m1	GO:006004	regulation	2/2606	23/23843	0.733352	0.846004	0.804458	Hyal3/Pkdr
GO_BP_m1	GO:006014	positive re	2/2606	23/23843	0.733352	0.846004	0.804458	Fmr1/Nfkb
GO_BP_m1	GO:00701	establishm	2/2606	23/23843	0.733352	0.846004	0.804458	H2afy/Nab
GO_BP_m1	GO:00714	cellular res	2/2606	23/23843	0.733352	0.846004	0.804458	Hvcn1/Slc
GO_BP_m1	GO:008971	amino acid	2/2606	23/23843	0.733352	0.846004	0.804458	Arl6ip5/AU
GO_BP_m1	GO:00971	neuronal s	2/2606	23/23843	0.733352	0.846004	0.804458	Cdh2/Sox2
GO_BP_m1	GO:19026	negative re	2/2606	23/23843	0.733352	0.846004	0.804458	Sema3f/Wr
GO_BP_m1	GO:00061	purine nuc	3/2606	34/23843	0.73409	0.846004	0.804458	Nudt1/Pde
GO_BP_m1	GO:00082	C21-steroi	3/2606	34/23843	0.73409	0.846004	0.804458	Akr1c12/D
GO_BP_m1	GO:001907	viral releas	3/2606	34/23843	0.73409	0.846004	0.804458	Pcx/Trim31
GO_BP_m1	GO:00327	positive re	3/2606	34/23843	0.73409	0.846004	0.804458	Cd36/Ifng/
GO_BP_m1	GO:003424	regulation	3/2606	34/23843	0.73409	0.846004	0.804458	Btbd18/Ell
GO_BP_m1	GO:00358	exit from h	3/2606	34/23843	0.73409	0.846004	0.804458	Pcx/Trim31
GO_BP_m1	GO:00358	exit from h	3/2606	34/23843	0.73409	0.846004	0.804458	Pcx/Trim31
GO_BP_m1	GO:00424	ribonucleo	3/2606	34/23843	0.73409	0.846004	0.804458	Adk/Aprt/
GO_BP_m1	GO:005091	negative c	3/2606	34/23843	0.73409	0.846004	0.804458	Nrg1/Pdgf
GO_BP_m1	GO:00521	movement	3/2606	34/23843	0.73409	0.846004	0.804458	Pcx/Trim31
GO_BP_m1	GO:00521	movement	3/2606	34/23843	0.73409	0.846004	0.804458	Pcx/Trim31
GO_BP_m1	GO:00149	myotube d	11/2606	116/23843	0.734655	0.846545	0.804973	Acta1/Cav
GO_BP_m1	GO:00486	positive re	9/2606	96/23843	0.734976	0.846803	0.805218	Alox12/My
GO_BP_m1	GO:002261	gland mor	14/2606	146/23843	0.736885	0.84878	0.807098	Cav1/Cav3
GO_BP_m1	GO:00301	B cell differ	14/2606	146/23843	0.736885	0.84878	0.807098	Cmtm7/Dc
GO_BP_m1	GO:00019	regulation	4/2606	45/23843	0.739639	0.850837	0.809053	Avpr1a/Co
GO_BP_m1	GO:000271	positive re	4/2606	45/23843	0.739639	0.850837	0.809053	Ifng/Ptprc/
GO_BP_m1	GO:00028	positive re	4/2606	45/23843	0.739639	0.850837	0.809053	Ifng/Ptprc/
GO_BP_m1	GO:000657	cellular bio	4/2606	45/23843	0.739639	0.850837	0.809053	Agmat/Hd

GO_BP_m1	GO:001046	regulation	4/2606	45/23843	0.739639	0.850837	0.809053	Myc/Pdgfa
GO_BP_m1	GO:001071	positive reg	4/2606	45/23843	0.739639	0.850837	0.809053	Foxc1/Gcnt
GO_BP_m1	GO:003278	regulation	4/2606	45/23843	0.739639	0.850837	0.809053	Btbd18/Ell2
GO_BP_m1	GO:006041	ventricular	4/2606	45/23843	0.739639	0.850837	0.809053	Nog/Smad
GO_BP_m1	GO:007130	cellular res	4/2606	45/23843	0.739639	0.850837	0.809053	Abl2/Adnp
GO_BP_m1	GO:009893	axonal tran	4/2606	45/23843	0.739639	0.850837	0.809053	Bloc1s5/Fm
GO_BP_m1	GO:005085	antigen rec	28/2606	283/23843	0.740093	0.851247	0.809444	Bcar1/Btnl2
GO_BP_m1	GO:000190	leukocyte r	10/2606	107/23843	0.745209	0.852417	0.810556	Arg1/Cadm
GO_BP_m1	GO:000828	insulin rece	10/2606	107/23843	0.745209	0.852417	0.810556	Appl1/Bcar
GO_BP_m1	GO:005102	mRNA tran	10/2606	107/23843	0.745209	0.852417	0.810556	Ahctf1/Ddx
GO_BP_m1	GO:003133	negative re	13/2606	137/23843	0.745326	0.852417	0.810556	Cfl1/Gsn/K
GO_BP_m1	GO:190290	negative re	13/2606	137/23843	0.745326	0.852417	0.810556	Cav3/Cfl1/
GO_BP_m1	GO:006133	cardiac cor	5/2606	56/23843	0.746825	0.852417	0.810556	Cacnb2/Ca
GO_BP_m1	GO:002187	forebrain g	8/2606	87/23843	0.747774	0.852417	0.810556	Arx/Dct/Mi
GO_BP_m1	GO:005145	regulation	7/2606	77/23843	0.750446	0.852417	0.810556	Atp6v0c/A
GO_BP_m1	GO:000096	mitochond	1/2606	12/23843	0.750747	0.852417	0.810556	Pnpt1
GO_BP_m1	GO:000201	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Drd3
GO_BP_m1	GO:000208	protein dep	1/2606	12/23843	0.750747	0.852417	0.810556	Ppt1
GO_BP_m1	GO:000242	natural kille	1/2606	12/23843	0.750747	0.852417	0.810556	Il12b
GO_BP_m1	GO:000242	natural kille	1/2606	12/23843	0.750747	0.852417	0.810556	Il12b
GO_BP_m1	GO:000243	complemen	1/2606	12/23843	0.750747	0.852417	0.810556	Fpr2
GO_BP_m1	GO:000285	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Il12b
GO_BP_m1	GO:000285	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Il12b
GO_BP_m1	GO:000312	heart field	1/2606	12/23843	0.750747	0.852417	0.810556	Wnt3a
GO_BP_m1	GO:000341	chondrocyt	1/2606	12/23843	0.750747	0.852417	0.810556	Poc1a
GO_BP_m1	GO:000602	inositol me	1/2606	12/23843	0.750747	0.852417	0.810556	Slc5a3
GO_BP_m1	GO:000911	vitamin cat	1/2606	12/23843	0.750747	0.852417	0.810556	Crabp1
GO_BP_m1	GO:000920	pyrimidine	1/2606	12/23843	0.750747	0.852417	0.810556	Nme6
GO_BP_m1	GO:000921	pyrimidine	1/2606	12/23843	0.750747	0.852417	0.810556	Shmt1
GO_BP_m1	GO:001031	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Snca
GO_BP_m1	GO:001045	centriole-c	1/2606	12/23843	0.750747	0.852417	0.810556	Odf2
GO_BP_m1	GO:001081	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Cxcl10
GO_BP_m1	GO:001474	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Atp2b4
GO_BP_m1	GO:001484	skeletal mu	1/2606	12/23843	0.750747	0.852417	0.810556	Ephb1
GO_BP_m1	GO:001484	urinary trac	1/2606	12/23843	0.750747	0.852417	0.810556	Htr7
GO_BP_m1	GO:001644	somatic hy	1/2606	12/23843	0.750747	0.852417	0.810556	Ung
GO_BP_m1	GO:001692	protein des	1/2606	12/23843	0.750747	0.852417	0.810556	Senp1
GO_BP_m1	GO:001815	protein oxi	1/2606	12/23843	0.750747	0.852417	0.810556	Gpx1
GO_BP_m1	GO:001834	protein pre	1/2606	12/23843	0.750747	0.852417	0.810556	Fnta
GO_BP_m1	GO:002152	ventral spir	1/2606	12/23843	0.750747	0.852417	0.810556	Dbx1
GO_BP_m1	GO:002167	lateral vent	1/2606	12/23843	0.750747	0.852417	0.810556	Kdm2b
GO_BP_m1	GO:003029	intestinal c	1/2606	12/23843	0.750747	0.852417	0.810556	Cd36
GO_BP_m1	GO:003043	peristalsis	1/2606	12/23843	0.750747	0.852417	0.810556	Gdnf
GO_BP_m1	GO:003083	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Cfl1
GO_BP_m1	GO:003227	luteinizing	1/2606	12/23843	0.750747	0.852417	0.810556	Tacr2
GO_BP_m1	GO:003235	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Nfkb1
GO_BP_m1	GO:003272	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Il12b
GO_BP_m1	GO:003275	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Il1rl1

GO_BP_m1	GO:003314	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Pak1
GO_BP_m1	GO:003324	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Abat
GO_BP_m1	GO:003386	nucleoside	1/2606	12/23843	0.750747	0.852417	0.810556	Dcakd
GO_BP_m1	GO:003403	ribonucleos	1/2606	12/23843	0.750747	0.852417	0.810556	Dcakd
GO_BP_m1	GO:003403	purine nuc	1/2606	12/23843	0.750747	0.852417	0.810556	Dcakd
GO_BP_m1	GO:003424	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Nelfb
GO_BP_m1	GO:003498	mitochond	1/2606	12/23843	0.750747	0.852417	0.810556	Uqcrc2
GO_BP_m1	GO:003509	maintenanc	1/2606	12/23843	0.750747	0.852417	0.810556	Lrrd1
GO_BP_m1	GO:003597	peptidyl-th	1/2606	12/23843	0.750747	0.852417	0.810556	Dusp5
GO_BP_m1	GO:003629	cellular res	1/2606	12/23843	0.750747	0.852417	0.810556	Cav1
GO_BP_m1	GO:003631	cellular res	1/2606	12/23843	0.750747	0.852417	0.810556	Smo
GO_BP_m1	GO:004203	chemokine	1/2606	12/23843	0.750747	0.852417	0.810556	Ifng
GO_BP_m1	GO:004365	engulfmen	1/2606	12/23843	0.750747	0.852417	0.810556	Rac3
GO_BP_m1	GO:004397	histone H3	1/2606	12/23843	0.750747	0.852417	0.810556	Kat2b
GO_BP_m1	GO:004409	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Anxa2
GO_BP_m1	GO:004507	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Ifng
GO_BP_m1	GO:004532	late endoso	1/2606	12/23843	0.750747	0.852417	0.810556	Pik3r4
GO_BP_m1	GO:004562	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Jak3
GO_BP_m1	GO:004574	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Adora1
GO_BP_m1	GO:004632	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Plin5
GO_BP_m1	GO:004685	inositol pho	1/2606	12/23843	0.750747	0.852417	0.810556	Synj1
GO_BP_m1	GO:004873	sebaceous	1/2606	12/23843	0.750747	0.852417	0.810556	Wnt10a
GO_BP_m1	GO:004873	cardiac mu	1/2606	12/23843	0.750747	0.852417	0.810556	Mypn
GO_BP_m1	GO:005102	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Stx4a
GO_BP_m1	GO:005128	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Fkbp1b
GO_BP_m1	GO:005197	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Men1
GO_BP_m1	GO:005198	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Racgap1
GO_BP_m1	GO:006043	lung saccul	1/2606	12/23843	0.750747	0.852417	0.810556	Asxl1
GO_BP_m1	GO:006043	bronchus c	1/2606	12/23843	0.750747	0.852417	0.810556	Tulp3
GO_BP_m1	GO:006045	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Oprl1
GO_BP_m1	GO:006050	epithelial c	1/2606	12/23843	0.750747	0.852417	0.810556	Fgf7
GO_BP_m1	GO:006057	cell fate sp	1/2606	12/23843	0.750747	0.852417	0.810556	Dbx1
GO_BP_m1	GO:006076	epithelial c	1/2606	12/23843	0.750747	0.852417	0.810556	Serpinf1
GO_BP_m1	GO:006105	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Akap6
GO_BP_m1	GO:007026	peptidyl-se	1/2606	12/23843	0.750747	0.852417	0.810556	Ppp2r1a
GO_BP_m1	GO:007036	hepatocyte	1/2606	12/23843	0.750747	0.852417	0.810556	E2f7
GO_BP_m1	GO:007057	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Fkbp1b
GO_BP_m1	GO:007128	cellular res	1/2606	12/23843	0.750747	0.852417	0.810556	Slc40a1
GO_BP_m1	GO:007128	cellular res	1/2606	12/23843	0.750747	0.852417	0.810556	Cdh1
GO_BP_m1	GO:007129	cellular res	1/2606	12/23843	0.750747	0.852417	0.810556	Kank2
GO_BP_m1	GO:007146	cellular res	1/2606	12/23843	0.750747	0.852417	0.810556	Slc9a1
GO_BP_m1	GO:009019	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Nog
GO_BP_m1	GO:009720	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Nck2
GO_BP_m1	GO:009735	prenylation	1/2606	12/23843	0.750747	0.852417	0.810556	Fnta
GO_BP_m1	GO:190042	positive reg	1/2606	12/23843	0.750747	0.852417	0.810556	Rab34
GO_BP_m1	GO:190155	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Tnfrsf1a
GO_BP_m1	GO:190241	protein loc	1/2606	12/23843	0.750747	0.852417	0.810556	Nectin3
GO_BP_m1	GO:190290	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Scfd1

GO_BP_m1	GO:190314	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Tnfrsf1a
GO_BP_m1	GO:190429	negative re	1/2606	12/23843	0.750747	0.852417	0.810556	Usp14
GO_BP_m1	GO:190499	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Ccl28
GO_BP_m1	GO:190551	positive re	1/2606	12/23843	0.750747	0.852417	0.810556	Hyal3
GO_BP_m1	GO:200031	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Smad7
GO_BP_m1	GO:200034	regulation	1/2606	12/23843	0.750747	0.852417	0.810556	Hdac1
GO_BP_m1	GO:000292	regulation	3/2606	35/23843	0.752138	0.852417	0.810556	Ptprc/Spns
GO_BP_m1	GO:000965	response t	3/2606	35/23843	0.752138	0.852417	0.810556	Mir7b/Mir
GO_BP_m1	GO:003142	keratinizati	3/2606	35/23843	0.752138	0.852417	0.810556	Abca12/Sh
GO_BP_m1	GO:003200	positive re	3/2606	35/23843	0.752138	0.852417	0.810556	Flcn/Htr6/
GO_BP_m1	GO:003220	negative re	3/2606	35/23843	0.752138	0.852417	0.810556	Hnrnpc/Tn
GO_BP_m1	GO:003647	cell death i	3/2606	35/23843	0.752138	0.852417	0.810556	Endog/Hsp
GO_BP_m1	GO:004230	regulation	3/2606	35/23843	0.752138	0.852417	0.810556	Avpr1a/Nr
GO_BP_m1	GO:004304	ATP-deper	3/2606	35/23843	0.752138	0.852417	0.810556	Psme4/Sm
GO_BP_m1	GO:004663	negative re	3/2606	35/23843	0.752138	0.852417	0.810556	Jak3/Smad
GO_BP_m1	GO:004668	response t	3/2606	35/23843	0.752138	0.852417	0.810556	Gsn/Mt2/
GO_BP_m1	GO:004800	insulin-like	3/2606	35/23843	0.752138	0.852417	0.810556	Gigyf2/Ift8
GO_BP_m1	GO:005169	actin filam	3/2606	35/23843	0.752138	0.852417	0.810556	Cfl1/Gsn/T
GO_BP_m1	GO:006007	Wnt signali	3/2606	35/23843	0.752138	0.852417	0.810556	Abl2/Cthrc
GO_BP_m1	GO:006044	epithelial t	3/2606	35/23843	0.752138	0.852417	0.810556	Foxa2/Pdg
GO_BP_m1	GO:200078	regulation	3/2606	35/23843	0.752138	0.852417	0.810556	Ift88/Scfd1
GO_BP_m1	GO:200103	regulation	3/2606	35/23843	0.752138	0.852417	0.810556	Endog/Hsp
GO_BP_m1	GO:004211	B cell activ	40/2606	401/23843	0.754342	0.852417	0.810556	Aplf/Cdkn1
GO_BP_m1	GO:001082	positive re	13/2606	138/23843	0.754535	0.852417	0.810556	Arih2/Bnip
GO_BP_m1	GO:000222	natural kill	6/2606	67/23843	0.754553	0.852417	0.810556	Cadm1/Il1
GO_BP_m1	GO:003032	respiratory	21/2606	217/23843	0.754583	0.852417	0.810556	Abca12/As
GO_BP_m1	GO:005114	regulation	14/2606	148/23843	0.75488	0.852417	0.810556	Akap6/Cav
GO_BP_m1	GO:000182	trophectod	2/2606	24/23843	0.75489	0.852417	0.810556	Cdh1/Esrrb
GO_BP_m1	GO:000241	immune re	2/2606	24/23843	0.75489	0.852417	0.810556	Il12b/Ulbp
GO_BP_m1	GO:000308	negative re	2/2606	24/23843	0.75489	0.852417	0.810556	Adra1d/Cd
GO_BP_m1	GO:000622	pyrimidine	2/2606	24/23843	0.75489	0.852417	0.810556	Nme6/Shm
GO_BP_m1	GO:001057	positive re	2/2606	24/23843	0.75489	0.852417	0.810556	Cxcl17/Ptg
GO_BP_m1	GO:001943	triglyceride	2/2606	24/23843	0.75489	0.852417	0.810556	Plin5/Pnpla
GO_BP_m1	GO:002180	cerebral co	2/2606	24/23843	0.75489	0.852417	0.810556	Cdk5/Pafa
GO_BP_m1	GO:002203	telencepha	2/2606	24/23843	0.75489	0.852417	0.810556	Cdk5/Pafa
GO_BP_m1	GO:003020	heparan su	2/2606	24/23843	0.75489	0.852417	0.810556	Extl3/Hs6st
GO_BP_m1	GO:003106	negative re	2/2606	24/23843	0.75489	0.852417	0.810556	H2afy/Prm
GO_BP_m1	GO:003110	animal org	2/2606	24/23843	0.75489	0.852417	0.810556	Cdk1/Ezh1
GO_BP_m1	GO:003246	endoplasm	2/2606	24/23843	0.75489	0.852417	0.810556	Bcap31/Ra
GO_BP_m1	GO:003352	histone H2	2/2606	24/23843	0.75489	0.852417	0.810556	Kdm2b/Rir
GO_BP_m1	GO:003368	regulation	2/2606	24/23843	0.75489	0.852417	0.810556	Cthrc1/Eif2
GO_BP_m1	GO:003406	protein loc	2/2606	24/23843	0.75489	0.852417	0.810556	Cog7/Gbf1
GO_BP_m1	GO:004205	negative re	2/2606	24/23843	0.75489	0.852417	0.810556	Gprc5a/Ptp
GO_BP_m1	GO:004356	regulation	2/2606	24/23843	0.75489	0.852417	0.810556	Ift88/Igfbp
GO_BP_m1	GO:004572	positive re	2/2606	24/23843	0.75489	0.852417	0.810556	Saxo1/Tme
GO_BP_m1	GO:004685	phosphatic	2/2606	24/23843	0.75489	0.852417	0.810556	Synj1/Tme
GO_BP_m1	GO:004802	negative re	2/2606	24/23843	0.75489	0.852417	0.810556	Rbm42/Srs
GO_BP_m1	GO:005178	response t	2/2606	24/23843	0.75489	0.852417	0.810556	Ufd1/Uggt

GO_BP_m1	GO:006021	definitive h	2/2606	24/23843	0.75489	0.852417	0.810556	Bcr/Senp1
GO_BP_m1	GO:007058	mitochond	2/2606	24/23843	0.75489	0.852417	0.810556	Myh14/Pnp
GO_BP_m1	GO:009858	detection c	2/2606	24/23843	0.75489	0.852417	0.810556	Nod1/Scar
GO_BP_m1	GO:012003	negative re	2/2606	24/23843	0.75489	0.852417	0.810556	Cfl1/Plxnb3
GO_BP_m1	GO:190173	regulation	2/2606	24/23843	0.75489	0.852417	0.810556	Cxcl10/Scg
GO_BP_m1	GO:000209	regulation	4/2606	46/23843	0.755322	0.852576	0.810708	Cd63/Fmr1
GO_BP_m1	GO:000317	heart valve	4/2606	46/23843	0.755322	0.852576	0.810708	Adamts9/Ja
GO_BP_m1	GO:002260	ovulation c	4/2606	46/23843	0.755322	0.852576	0.810708	Adamts1/A
GO_BP_m1	GO:001092	cellular cor	10/2606	108/23843	0.75556	0.852735	0.810858	Acta1/Ahna
GO_BP_m1	GO:000170	formation c	9/2606	98/23843	0.756937	0.85407	0.812128	Col5a1/Du
GO_BP_m1	GO:003223	regulation	9/2606	98/23843	0.756937	0.85407	0.812128	Cfl1/Ctgf/It
GO_BP_m1	GO:005076	regulation	8/2606	88/23843	0.759114	0.856416	0.814359	Bcr/Calr/Cc
GO_BP_m1	GO:005130	establishm	7/2606	78/23843	0.762375	0.859874	0.817647	Ankrd53/Tc
GO_BP_m1	GO:007061	regulation	7/2606	78/23843	0.762375	0.859874	0.817647	Cdh1/Fmr1
GO_BP_m1	GO:004255	myelinatior	13/2606	139/23843	0.763517	0.861052	0.818767	Ahnak2/Cc
GO_BP_m1	GO:005083	defense res	12/2606	129/23843	0.763787	0.861109	0.818822	1700016D0
GO_BP_m1	GO:000703	vacuole org	15/2606	159/23843	0.763862	0.861109	0.818822	Anxa2/Atg
GO_BP_m1	GO:190165	response tc	15/2606	159/23843	0.763862	0.861109	0.818822	Adh1/Cav1
GO_BP_m1	GO:000189	placenta de	16/2606	169/23843	0.764369	0.86157	0.819259	Adm/Cdh1
GO_BP_m1	GO:012003	positive reg	9/2606	99/23843	0.767427	0.862006	0.819675	Bcas3/Cdc4
GO_BP_m1	GO:000838	RNA splicir	36/2606	365/23843	0.768289	0.862006	0.819675	Virma/Rtra
GO_BP_m1	GO:000170	gastrulatior	3/2606	36/23843	0.769187	0.862006	0.819675	Nat8f3/Fox
GO_BP_m1	GO:000916	nucleoside	3/2606	36/23843	0.769187	0.862006	0.819675	Adk/Aprt/N
GO_BP_m1	GO:000931	oligosacch	3/2606	36/23843	0.769187	0.862006	0.819675	Galnt9/St6g
GO_BP_m1	GO:001025	multicellula	3/2606	36/23843	0.769187	0.862006	0.819675	Ercc5/Hyal
GO_BP_m1	GO:002179	cerebral cc	3/2606	36/23843	0.769187	0.862006	0.819675	Cdk5/Pafah
GO_BP_m1	GO:003106	positive reg	3/2606	36/23843	0.769187	0.862006	0.819675	Dmrtc2/Me
GO_BP_m1	GO:003245	endocytic r	3/2606	36/23843	0.769187	0.862006	0.819675	Epg5/Ndrg
GO_BP_m1	GO:003530	positive reg	3/2606	36/23843	0.769187	0.862006	0.819675	Adora1/Ak
GO_BP_m1	GO:005129	establishm	3/2606	36/23843	0.769187	0.862006	0.819675	Cenpa/Nus
GO_BP_m1	GO:006025	regulation	3/2606	36/23843	0.769187	0.862006	0.819675	Dgat1/Htr1
GO_BP_m1	GO:007139	cellular res	3/2606	36/23843	0.769187	0.862006	0.819675	Bcas3/Crhb
GO_BP_m1	GO:007151	genetic imp	3/2606	36/23843	0.769187	0.862006	0.819675	Cdkn1c/H1
GO_BP_m1	GO:190222	regulation	3/2606	36/23843	0.769187	0.862006	0.819675	Fbxo18/Pg
GO_BP_m1	GO:005507	iron ion ho	8/2606	89/23843	0.770086	0.862006	0.819675	Bdh2/Eif2a
GO_BP_m1	GO:000636	transcriptic	4/2606	47/23843	0.770265	0.862006	0.819675	Btbd18/Ell2
GO_BP_m1	GO:003233	regulation	4/2606	47/23843	0.770265	0.862006	0.819675	Ctgf/Rflna/
GO_BP_m1	GO:004562	negative re	4/2606	47/23843	0.770265	0.862006	0.819675	Ctla4/Jak3/
GO_BP_m1	GO:190403	negative re	4/2606	47/23843	0.770265	0.862006	0.819675	Abl2/Il10/S
GO_BP_m1	GO:003253	regulation	38/2606	385/23843	0.771938	0.862006	0.819675	Aatk/Cav3/
GO_BP_m1	GO:005000	chromosor	7/2606	79/23843	0.773884	0.862006	0.819675	Ankrd53/Tc
GO_BP_m1	GO:003021	T cell differ	25/2606	259/23843	0.773941	0.862006	0.819675	Abl2/Adam
GO_BP_m1	GO:000288	regulation	5/2606	58/23843	0.774129	0.862006	0.819675	Arg1/Bcr/It
GO_BP_m1	GO:000715	heterophili	5/2606	58/23843	0.774129	0.862006	0.819675	Cadm1/Cd
GO_BP_m1	GO:003083	negative re	5/2606	58/23843	0.774129	0.862006	0.819675	Cfl1/Gsn/K
GO_BP_m1	GO:004209	T-helper ce	5/2606	58/23843	0.774129	0.862006	0.819675	Gpr183/Il1
GO_BP_m1	GO:004828	lung alveol	5/2606	58/23843	0.774129	0.862006	0.819675	Abca12/As
GO_BP_m1	GO:006044	mammary	5/2606	58/23843	0.774129	0.862006	0.819675	Cav1/Cav3

GO_BP_m1	GO:190435	regulation	5/2606	58/23843	0.774129	0.862006	0.819675	Atr/Cct3/H
GO_BP_m1	GO:000307	renal syste	2/2606	25/23843	0.774907	0.862006	0.819675	Adora1/Uts
GO_BP_m1	GO:000677	porphyrin-	2/2606	25/23843	0.774907	0.862006	0.819675	Cox15/Iba5
GO_BP_m1	GO:003019	positive reg	2/2606	25/23843	0.774907	0.862006	0.819675	Cd36/Ptprj
GO_BP_m1	GO:003114	SCF-deper	2/2606	25/23843	0.774907	0.862006	0.819675	Cul1/Fbxo3
GO_BP_m1	GO:003134	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Ptprc/Sh2d
GO_BP_m1	GO:003592	steroid hor	2/2606	25/23843	0.774907	0.862006	0.819675	Galr1/Tac1
GO_BP_m1	GO:004243	indole-con	2/2606	25/23843	0.774907	0.862006	0.819675	Gch1/Htr1a
GO_BP_m1	GO:004573	respiratory	2/2606	25/23843	0.774907	0.862006	0.819675	Bcr/Pgam1
GO_BP_m1	GO:004864	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Ephb1/Ybx
GO_BP_m1	GO:007110	protein K48	2/2606	25/23843	0.774907	0.862006	0.819675	Mindy2/Us
GO_BP_m1	GO:008600	ventricular	2/2606	25/23843	0.774907	0.862006	0.819675	Cav1/Cav3
GO_BP_m1	GO:009886	bone grow	2/2606	25/23843	0.774907	0.862006	0.819675	Poc1a/Por
GO_BP_m1	GO:190004	positive reg	2/2606	25/23843	0.774907	0.862006	0.819675	Cd36/Ptprj
GO_BP_m1	GO:190103	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Hsph1/Il10
GO_BP_m1	GO:190118	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Gprc5a/Ptp
GO_BP_m1	GO:190320	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Hsph1/Il10
GO_BP_m1	GO:190385	regulation	2/2606	25/23843	0.774907	0.862006	0.819675	Cpne6/Parl
GO_BP_m1	GO:190435	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Hnrnpc/Tn
GO_BP_m1	GO:200103	negative re	2/2606	25/23843	0.774907	0.862006	0.819675	Hsph1/Il10
GO_BP_m1	GO:003051	intracellula	10/2606	110/23843	0.77538	0.862006	0.819675	Arntl/Calr/
GO_BP_m1	GO:000717	epidermal	9/2606	100/23843	0.777592	0.862006	0.819675	Abl2/Adora
GO_BP_m1	GO:000154	ovulation fi	1/2606	13/23843	0.778004	0.862006	0.819675	Adamts1
GO_BP_m1	GO:000202	diet induce	1/2606	13/23843	0.778004	0.862006	0.819675	Trpv4
GO_BP_m1	GO:000256	somatic div	1/2606	13/23843	0.778004	0.862006	0.819675	Ung
GO_BP_m1	GO:000267	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Adora1
GO_BP_m1	GO:000649	oligosacch	1/2606	13/23843	0.778004	0.862006	0.819675	Alg6
GO_BP_m1	GO:000651	protein deg	1/2606	13/23843	0.778004	0.862006	0.819675	Man1b1
GO_BP_m1	GO:007100	mitotic cen	1/2606	13/23843	0.778004	0.862006	0.819675	Ranbp1
GO_BP_m1	GO:000735	tripartite re	1/2606	13/23843	0.778004	0.862006	0.819675	Wt1
GO_BP_m1	GO:000750	mesoderm	1/2606	13/23843	0.778004	0.862006	0.819675	Wnt3a
GO_BP_m1	GO:000859	anterior/pc	1/2606	13/23843	0.778004	0.862006	0.819675	Wt1
GO_BP_m1	GO:000922	nucleotide-	1/2606	13/23843	0.778004	0.862006	0.819675	Pgm3
GO_BP_m1	GO:001022	response to	1/2606	13/23843	0.778004	0.862006	0.819675	Cdh1
GO_BP_m1	GO:001056	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Jak3
GO_BP_m1	GO:001932	pentose m	1/2606	13/23843	0.778004	0.862006	0.819675	Rpe
GO_BP_m1	GO:001975	one-carbo	1/2606	13/23843	0.778004	0.862006	0.819675	Slc14a2
GO_BP_m1	GO:002152	spinal cord	1/2606	13/23843	0.778004	0.862006	0.819675	Hoxd10
GO_BP_m1	GO:002154	pons devel	1/2606	13/23843	0.778004	0.862006	0.819675	Hoxb1
GO_BP_m1	GO:002168	cerebellar	1/2606	13/23843	0.778004	0.862006	0.819675	Wnt7a
GO_BP_m1	GO:002192	cell prolifer	1/2606	13/23843	0.778004	0.862006	0.819675	Cend1
GO_BP_m1	GO:002193	cerebellar	1/2606	13/23843	0.778004	0.862006	0.819675	Cend1
GO_BP_m1	GO:003044	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Susd4
GO_BP_m1	GO:003057	nuclear bo	1/2606	13/23843	0.778004	0.862006	0.819675	Srpk2
GO_BP_m1	GO:003103	myosin fila	1/2606	13/23843	0.778004	0.862006	0.819675	Rap1gds1
GO_BP_m1	GO:003122	auditory be	1/2606	13/23843	0.778004	0.862006	0.819675	Abl2
GO_BP_m1	GO:003126	pseudopoc	1/2606	13/23843	0.778004	0.862006	0.819675	Cdc42ep5
GO_BP_m1	GO:003206	bleb assem	1/2606	13/23843	0.778004	0.862006	0.819675	Prdx6

GO_BP_m1	GO:003227	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Tacr2
GO_BP_m1	GO:003235	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Nfkb1
GO_BP_m1	GO:003249	detection c	1/2606	13/23843	0.778004	0.862006	0.819675	Scarb1
GO_BP_m1	GO:003249	response t	1/2606	13/23843	0.778004	0.862006	0.819675	5730559C1
GO_BP_m1	GO:003252	somite rost	1/2606	13/23843	0.778004	0.862006	0.819675	Foxa2
GO_BP_m1	GO:003274	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Il12b
GO_BP_m1	GO:003314	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Kank2
GO_BP_m1	GO:003316	histone H3	1/2606	13/23843	0.778004	0.862006	0.819675	Kdm3b
GO_BP_m1	GO:003369	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Cthrc1
GO_BP_m1	GO:003406	stress gran	1/2606	13/23843	0.778004	0.862006	0.819675	Ogfod1
GO_BP_m1	GO:003449	protein loc	1/2606	13/23843	0.778004	0.862006	0.819675	Wipi2
GO_BP_m1	GO:003574	T-helper 2	1/2606	13/23843	0.778004	0.862006	0.819675	Arg1
GO_BP_m1	GO:003629	response t	1/2606	13/23843	0.778004	0.862006	0.819675	Cav1
GO_BP_m1	GO:003970	viral buddi	1/2606	13/23843	0.778004	0.862006	0.819675	Chmp1b
GO_BP_m1	GO:004222	interleukin	1/2606	13/23843	0.778004	0.862006	0.819675	Nod1
GO_BP_m1	GO:004257	retinal met	1/2606	13/23843	0.778004	0.862006	0.819675	Aldh1a3
GO_BP_m1	GO:004276	very long-	1/2606	13/23843	0.778004	0.862006	0.819675	Tecr
GO_BP_m1	GO:004297	activation	1/2606	13/23843	0.778004	0.862006	0.819675	Il12b
GO_BP_m1	GO:004350	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Ptpn22
GO_BP_m1	GO:004369	reverse ch	1/2606	13/23843	0.778004	0.862006	0.819675	Scarb1
GO_BP_m1	GO:004562	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Zfp35
GO_BP_m1	GO:004593	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Uts2r
GO_BP_m1	GO:004603	AMP metal	1/2606	13/23843	0.778004	0.862006	0.819675	Adss
GO_BP_m1	GO:004875	branching	1/2606	13/23843	0.778004	0.862006	0.819675	Epha7
GO_BP_m1	GO:005128	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Fkbp1b
GO_BP_m1	GO:005131	attachmen	1/2606	13/23843	0.778004	0.862006	0.819675	Cenpc1
GO_BP_m1	GO:005269	cellular glu	1/2606	13/23843	0.778004	0.862006	0.819675	Ugt1a9
GO_BP_m1	GO:006013	prepulse in	1/2606	13/23843	0.778004	0.862006	0.819675	Drd3
GO_BP_m1	GO:006026	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Bcr
GO_BP_m1	GO:006060	lateral spro	1/2606	13/23843	0.778004	0.862006	0.819675	Nog
GO_BP_m1	GO:006076	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Hdac1
GO_BP_m1	GO:006096	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Zc3h12a
GO_BP_m1	GO:006141	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Stox1
GO_BP_m1	GO:007010	interleukin	1/2606	13/23843	0.778004	0.862006	0.819675	Gab1
GO_BP_m1	GO:007094	neutrophil	1/2606	13/23843	0.778004	0.862006	0.819675	Arg1
GO_BP_m1	GO:007102	nuclear RN	1/2606	13/23843	0.778004	0.862006	0.819675	Exosc9
GO_BP_m1	GO:007102	nuclear mR	1/2606	13/23843	0.778004	0.862006	0.819675	Exosc9
GO_BP_m1	GO:007143	potassium	1/2606	13/23843	0.778004	0.862006	0.819675	Kcnn4
GO_BP_m1	GO:007216	nephron tu	1/2606	13/23843	0.778004	0.862006	0.819675	Osr1
GO_BP_m1	GO:007256	chemokine	1/2606	13/23843	0.778004	0.862006	0.819675	Hdac1
GO_BP_m1	GO:009008	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Zc3h12a
GO_BP_m1	GO:009012	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Cdc20
GO_BP_m1	GO:009871	L-glutamat	1/2606	13/23843	0.778004	0.862006	0.819675	Arl6ip5
GO_BP_m1	GO:009873	macromole	1/2606	13/23843	0.778004	0.862006	0.819675	Ppt1
GO_BP_m1	GO:009878	mRNA clea	1/2606	13/23843	0.778004	0.862006	0.819675	Cpsf4
GO_BP_m1	GO:009891	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Cav1
GO_BP_m1	GO:009911	tRNA 5'-er	1/2606	13/23843	0.778004	0.862006	0.819675	Rpp40
GO_BP_m1	GO:190107	glucosamir	1/2606	13/23843	0.778004	0.862006	0.819675	Chil5

GO_BP_m1	GO:190114	insulin met	1/2606	13/23843	0.778004	0.862006	0.819675	Cpz
GO_BP_m1	GO:190183	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	H2afy
GO_BP_m1	GO:190233	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Foxc1
GO_BP_m1	GO:190285	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Tmem67
GO_BP_m1	GO:190289	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Hdac2
GO_BP_m1	GO:190299	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Csnk1e
GO_BP_m1	GO:190470	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Il10
GO_BP_m1	GO:190492	positive re	1/2606	13/23843	0.778004	0.862006	0.819675	Park2
GO_BP_m1	GO:200121	regulation	1/2606	13/23843	0.778004	0.862006	0.819675	Adm
GO_BP_m1	GO:200122	negative re	1/2606	13/23843	0.778004	0.862006	0.819675	Nrg1
GO_BP_m1	GO:005081	regulation	6/2606	69/23843	0.779261	0.863072	0.820688	Dgkq/Fgf1/
GO_BP_m1	GO:190199	positive re	6/2606	69/23843	0.779261	0.863072	0.820688	Cdc7/Cdk1
GO_BP_m1	GO:200057	positive re	6/2606	69/23843	0.779261	0.863072	0.820688	Atr/Cct3/H
GO_BP_m1	GO:003530	negative re	8/2606	90/23843	0.780692	0.864549	0.822092	Csrnp3/Fkb
GO_BP_m1	GO:007138	cellular res	19/2606	201/23843	0.781291	0.865103	0.822619	Arntl/Calr/
GO_BP_m1	GO:006156	axon devel	49/2606	493/23843	0.781832	0.865593	0.823085	Aatk/Ache/
GO_BP_m1	GO:001909	reproducti	4/2606	48/23843	0.784482	0.867753	0.825139	Avpr1a/Dr
GO_BP_m1	GO:004249	inner ear a	4/2606	48/23843	0.784482	0.867753	0.825139	Jag1/Mcol
GO_BP_m1	GO:004330	regulation	4/2606	48/23843	0.784482	0.867753	0.825139	Bcr/Itgam/
GO_BP_m1	GO:000227	myeloid ce	7/2606	80/23843	0.784977	0.867753	0.825139	Anxa3/Bcr/
GO_BP_m1	GO:000700	plasma me	7/2606	80/23843	0.784977	0.867753	0.825139	Ahnak2/Ca
GO_BP_m1	GO:190331	regulation	7/2606	80/23843	0.784977	0.867753	0.825139	Cdh1/Fmr1
GO_BP_m1	GO:000677	porphyrin-	3/2606	37/23843	0.785265	0.867753	0.825139	Cox15/Eif2
GO_BP_m1	GO:000808	anterograd	3/2606	37/23843	0.785265	0.867753	0.825139	Bloc1s5/Fn
GO_BP_m1	GO:003050	positive re	3/2606	37/23843	0.785265	0.867753	0.825139	Mia3/Osr1/
GO_BP_m1	GO:003312	positive re	3/2606	37/23843	0.785265	0.867753	0.825139	Hmx2/Prdx
GO_BP_m1	GO:004662	negative re	3/2606	37/23843	0.785265	0.867753	0.825139	Gpr21/Prk
GO_BP_m1	GO:008606	cell commu	3/2606	37/23843	0.785265	0.867753	0.825139	Cacnb2/Ca
GO_BP_m1	GO:009017	regulation	3/2606	37/23843	0.785265	0.867753	0.825139	Abl2/Cthrc
GO_BP_m1	GO:190106	guanosine-	3/2606	37/23843	0.785265	0.867753	0.825139	Gphn/Moc
GO_BP_m1	GO:190289	regulation	3/2606	37/23843	0.785265	0.867753	0.825139	Hdac2/Nfk
GO_BP_m1	GO:000243	inflammato	5/2606	59/23843	0.786907	0.86924	0.826553	Gpx1/Gpx2
GO_BP_m1	GO:004584	positive re	5/2606	59/23843	0.786907	0.86924	0.826553	Dmrt1/Drd
GO_BP_m1	GO:007115	regulation	5/2606	59/23843	0.786907	0.86924	0.826553	Calr/Cdkn1
GO_BP_m1	GO:002154	cerebellum	9/2606	101/23843	0.787432	0.86971	0.827	Abl2/Cdk5/
GO_BP_m1	GO:002261	ribonucleo	20/2606	212/23843	0.788795	0.871105	0.828327	Atr/Noct/C
GO_BP_m1	GO:000727	ensheathm	13/2606	142/23843	0.789103	0.871118	0.828339	Ahnak2/Cc
GO_BP_m1	GO:000733	single fertil	13/2606	142/23843	0.789103	0.871118	0.828339	1700016D0
GO_BP_m1	GO:000836	axon enshe	13/2606	142/23843	0.789103	0.871118	0.828339	Ahnak2/Cc
GO_BP_m1	GO:002170	developme	28/2606	291/23843	0.789876	0.871862	0.829046	Abl2/Acrbp
GO_BP_m1	GO:000317	atrioventric	2/2606	26/23843	0.793479	0.873862	0.830948	Smad6/Zfp
GO_BP_m1	GO:000329	muscle hyp	2/2606	26/23843	0.793479	0.873862	0.830948	Atp2b4/My
GO_BP_m1	GO:000631	mitotic rec	2/2606	26/23843	0.793479	0.873862	0.830948	Blm/Xrcc1
GO_BP_m1	GO:000688	cell volume	2/2606	26/23843	0.793479	0.873862	0.830948	Kcnn4/Slc1
GO_BP_m1	GO:000700	inner mito	2/2606	26/23843	0.793479	0.873862	0.830948	Myc/Timm
GO_BP_m1	GO:000805	mitochond	2/2606	26/23843	0.793479	0.873862	0.830948	Bnip3/Park
GO_BP_m1	GO:000929	mRNA tran	2/2606	26/23843	0.793479	0.873862	0.830948	Lmo2/Sox1
GO_BP_m1	GO:001489	cardiac mu	2/2606	26/23843	0.793479	0.873862	0.830948	Atp2b4/My

GO_BP_m1	GO:001618	snRNA pro	2/2606	26/23843	0.793479	0.873862	0.830948	Exosc9/Ints
GO_BP_m1	GO:003081	positive reg	2/2606	26/23843	0.793479	0.873862	0.830948	Calcr/Nf1
GO_BP_m1	GO:004275	positive reg	2/2606	26/23843	0.793479	0.873862	0.830948	Arntl/Uts2r
GO_BP_m1	GO:004309	amino acid	2/2606	26/23843	0.793479	0.873862	0.830948	Arl6ip5/AU
GO_BP_m1	GO:004646	membrane	2/2606	26/23843	0.793479	0.873862	0.830948	Asah2/Smp
GO_BP_m1	GO:004852	negative re	2/2606	26/23843	0.793479	0.873862	0.830948	Adora1/Htr
GO_BP_m1	GO:005092	positive reg	2/2606	26/23843	0.793479	0.873862	0.830948	Prkca/Scg2
GO_BP_m1	GO:005198	positive reg	2/2606	26/23843	0.793479	0.873862	0.830948	Fen1/H2afy
GO_BP_m1	GO:006103	negative re	2/2606	26/23843	0.793479	0.873862	0.830948	Rflna/Nog
GO_BP_m1	GO:190107	glucosamir	2/2606	26/23843	0.793479	0.873862	0.830948	Chil5/Ogt
GO_BP_m1	GO:000228	T cell activa	10/2606	112/23843	0.794028	0.874247	0.831314	Gm13271/
GO_BP_m1	GO:004333	response t	10/2606	112/23843	0.794028	0.874247	0.831314	Cav1/Ddx2
GO_BP_m1	GO:005500	muscle cell	18/2606	193/23843	0.794976	0.874455	0.831512	Acta1/Adm
GO_BP_m1	GO:003202	positive reg	7/2606	81/23843	0.795658	0.874455	0.831512	Abat/Ano1
GO_BP_m1	GO:004802	regulation	7/2606	81/23843	0.795658	0.874455	0.831512	Fmr1/Hmx
GO_BP_m1	GO:001066	regulation	4/2606	49/23843	0.797988	0.874455	0.831512	Bnip3/Cam
GO_BP_m1	GO:003021	megakaryc	4/2606	49/23843	0.797988	0.874455	0.831512	Abi1/Cib1/
GO_BP_m1	GO:003083	regulation	4/2606	49/23843	0.797988	0.874455	0.831512	Cfl1/Gsn/P
GO_BP_m1	GO:004329	apical junc	4/2606	49/23843	0.797988	0.874455	0.831512	Cdh1/Cgn/
GO_BP_m1	GO:004580	negative re	4/2606	49/23843	0.797988	0.874455	0.831512	Cav1/Fmr1
GO_BP_m1	GO:190320	negative re	4/2606	49/23843	0.797988	0.874455	0.831512	Gpx1/Hsph
GO_BP_m1	GO:000962	response t	3/2606	38/23843	0.800404	0.874455	0.831512	Arg1/Jagn
GO_BP_m1	GO:005148	positive reg	3/2606	38/23843	0.800404	0.874455	0.831512	Adra1d/Gp
GO_BP_m1	GO:007084	response t	3/2606	38/23843	0.800404	0.874455	0.831512	Cfl1/Foxc1/
GO_BP_m1	GO:007259	maintenan	3/2606	38/23843	0.800404	0.874455	0.831512	Cdk5/Ciz1/
GO_BP_m1	GO:004846	cell matura	17/2606	184/23843	0.801995	0.874455	0.831512	Abl2/Acrbp
GO_BP_m1	GO:005121	cartilage de	17/2606	184/23843	0.801995	0.874455	0.831512	Bbs2/Bmp
GO_BP_m1	GO:003032	lung develo	20/2606	214/23843	0.802032	0.874455	0.831512	Abca12/As
GO_BP_m1	GO:003106	regulation	6/2606	71/23843	0.802042	0.874455	0.831512	Dmrtc2/H2
GO_BP_m1	GO:000188	endothelial	1/2606	14/23843	0.802281	0.874455	0.831512	Ift88
GO_BP_m1	GO:000272	positive reg	1/2606	14/23843	0.802281	0.874455	0.831512	Sash3
GO_BP_m1	GO:000606	uronic acid	1/2606	14/23843	0.802281	0.874455	0.831512	Ugt1a9
GO_BP_m1	GO:000707	mitotic chr	1/2606	14/23843	0.802281	0.874455	0.831512	Nusap1
GO_BP_m1	GO:000717	negative re	1/2606	14/23843	0.802281	0.874455	0.831512	Gprc5a
GO_BP_m1	GO:000907	aromatic ar	1/2606	14/23843	0.802281	0.874455	0.831512	Hpdl
GO_BP_m1	GO:000914	pyrimidine	1/2606	14/23843	0.802281	0.874455	0.831512	Nme6
GO_BP_m1	GO:001071	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Fscn1
GO_BP_m1	GO:001083	negative re	1/2606	14/23843	0.802281	0.874455	0.831512	Ctsl
GO_BP_m1	GO:001483	gastro-inte	1/2606	14/23843	0.802281	0.874455	0.831512	Tacr2
GO_BP_m1	GO:001485	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Ephb1
GO_BP_m1	GO:001607	snoRNA m	1/2606	14/23843	0.802281	0.874455	0.831512	Nop10
GO_BP_m1	GO:001908	viral transla	1/2606	14/23843	0.802281	0.874455	0.831512	Eif3f
GO_BP_m1	GO:001958	glucuronat	1/2606	14/23843	0.802281	0.874455	0.831512	Ugt1a9
GO_BP_m1	GO:002153	cell prolifer	1/2606	14/23843	0.802281	0.874455	0.831512	Cend1
GO_BP_m1	GO:002170	cerebellar I	1/2606	14/23843	0.802281	0.874455	0.831512	Cend1
GO_BP_m1	GO:002178	glial cell fat	1/2606	14/23843	0.802281	0.874455	0.831512	Nrg1
GO_BP_m1	GO:002187	forebrain n	1/2606	14/23843	0.802281	0.874455	0.831512	Tbr1
GO_BP_m1	GO:002190	rostrocaud	1/2606	14/23843	0.802281	0.874455	0.831512	Kdm2b

GO_BP_m1	GO:00219	hindbrain r	1/2606	14/23843	0.802281	0.874455	0.831512	Cend1
GO_BP_m1	GO:00219	adenohyp	1/2606	14/23843	0.802281	0.874455	0.831512	Sox2
GO_BP_m1	GO:003082	positive re	1/2606	14/23843	0.802281	0.874455	0.831512	Guca1a
GO_BP_m1	GO:00319	locomotion	1/2606	14/23843	0.802281	0.874455	0.831512	Drd3
GO_BP_m1	GO:00326	granulocyt	1/2606	14/23843	0.802281	0.874455	0.831512	Il12b
GO_BP_m1	GO:003264	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Il12b
GO_BP_m1	GO:00341	toll-like re	1/2606	14/23843	0.802281	0.874455	0.831512	Tnip2
GO_BP_m1	GO:003434	glial cell ap	1/2606	14/23843	0.802281	0.874455	0.831512	Prkca
GO_BP_m1	GO:003447	ncRNA 5'-	1/2606	14/23843	0.802281	0.874455	0.831512	Rpp40
GO_BP_m1	GO:00347	iron ion tra	1/2606	14/23843	0.802281	0.874455	0.831512	Slc40a1
GO_BP_m1	GO:004217	xenobiotic	1/2606	14/23843	0.802281	0.874455	0.831512	Acsl1
GO_BP_m1	GO:00424	cellular bio	1/2606	14/23843	0.802281	0.874455	0.831512	Sat1
GO_BP_m1	GO:004321	myelin mai	1/2606	14/23843	0.802281	0.874455	0.831512	Ahnak2
GO_BP_m1	GO:00450	positive th	1/2606	14/23843	0.802281	0.874455	0.831512	Ptprc
GO_BP_m1	GO:00450	negative th	1/2606	14/23843	0.802281	0.874455	0.831512	Ptprc
GO_BP_m1	GO:00451	establishm	1/2606	14/23843	0.802281	0.874455	0.831512	Tcf15
GO_BP_m1	GO:00453	type I inter	1/2606	14/23843	0.802281	0.874455	0.831512	Nmi
GO_BP_m1	GO:004572	negative re	1/2606	14/23843	0.802281	0.874455	0.831512	C1qtnf3
GO_BP_m1	GO:00463	phosphatic	1/2606	14/23843	0.802281	0.874455	0.831512	Pisd
GO_BP_m1	GO:004647	phosphatic	1/2606	14/23843	0.802281	0.874455	0.831512	Ptpmt1
GO_BP_m1	GO:00468	phosphory	1/2606	14/23843	0.802281	0.874455	0.831512	Synj1
GO_BP_m1	GO:00507	chemokine	1/2606	14/23843	0.802281	0.874455	0.831512	Ifng
GO_BP_m1	GO:00508	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Ptprc
GO_BP_m1	GO:00508	positive re	1/2606	14/23843	0.802281	0.874455	0.831512	Kcnn4
GO_BP_m1	GO:00512	centrosom	1/2606	14/23843	0.802281	0.874455	0.831512	Ranbp1
GO_BP_m1	GO:006001	radial glial	1/2606	14/23843	0.802281	0.874455	0.831512	Cdh2
GO_BP_m1	GO:006004	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Mt3
GO_BP_m1	GO:00603	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Arg1
GO_BP_m1	GO:00603	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Arg1
GO_BP_m1	GO:00607	prostate gl	1/2606	14/23843	0.802281	0.874455	0.831512	Plag1
GO_BP_m1	GO:00613	cardiac ne	1/2606	14/23843	0.802281	0.874455	0.831512	Jag1
GO_BP_m1	GO:00702	renal abso	1/2606	14/23843	0.802281	0.874455	0.831512	Gsn
GO_BP_m1	GO:00703	lens fiber c	1/2606	14/23843	0.802281	0.874455	0.831512	Epha2
GO_BP_m1	GO:007154	inositol ph	1/2606	14/23843	0.802281	0.874455	0.831512	Synj1
GO_BP_m1	GO:00718	positive re	1/2606	14/23843	0.802281	0.874455	0.831512	Fscn1
GO_BP_m1	GO:00901	establishm	1/2606	14/23843	0.802281	0.874455	0.831512	Timm22
GO_BP_m1	GO:00902	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Tpr
GO_BP_m1	GO:01401	positive re	1/2606	14/23843	0.802281	0.874455	0.831512	Ccl4
GO_BP_m1	GO:190107	guanosine	1/2606	14/23843	0.802281	0.874455	0.831512	Nme6
GO_BP_m1	GO:190121	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Nog
GO_BP_m1	GO:19035	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Tpr
GO_BP_m1	GO:190481	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	H2afy
GO_BP_m1	GO:190492	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Park2
GO_BP_m1	GO:20002	regulation	1/2606	14/23843	0.802281	0.874455	0.831512	Susd4
GO_BP_m1	GO:20006	positive re	1/2606	14/23843	0.802281	0.874455	0.831512	Slc9a1
GO_BP_m1	GO:00018	embryonic	10/2606	113/23843	0.802917	0.874931	0.831965	Adm/Cdkn
GO_BP_m1	GO:009027	positive re	10/2606	113/23843	0.802917	0.874931	0.831965	Abat/Ano1
GO_BP_m1	GO:000691	phagocyto	14/2606	154/23843	0.803817	0.875803	0.832794	Cd36/Ighv

GO_BP_m1	GO:000276	immune re	31/2606	323/23843	0.804245	0.876161	0.833134	Bcar1/Btnl
GO_BP_m1	GO:000042	autophagy	7/2606	82/23843	0.805932	0.877672	0.834571	Atg2a/Bnip
GO_BP_m1	GO:003064	regulation	7/2606	82/23843	0.805932	0.877672	0.834571	Atp6v0c/A
GO_BP_m1	GO:006172	mitochond	7/2606	82/23843	0.805932	0.877672	0.834571	Atg2a/Bnip
GO_BP_m1	GO:005159	response t	9/2606	103/23843	0.806147	0.877798	0.834691	Apobec1/A
GO_BP_m1	GO:004642	regulation	18/2606	195/23843	0.808546	0.880301	0.83707	Cav1/Cdk5
GO_BP_m1	GO:003083	positive re	8/2606	93/23843	0.810344	0.880682	0.837433	Cdc42ep5/
GO_BP_m1	GO:000234	response t	2/2606	27/23843	0.810682	0.880682	0.837433	Il12b/Ulbp
GO_BP_m1	GO:001488	cardiac mu	2/2606	27/23843	0.810682	0.880682	0.837433	Atp2b4/My
GO_BP_m1	GO:001988	antigen pr	2/2606	27/23843	0.810682	0.880682	0.837433	H2-DMb2/
GO_BP_m1	GO:003082	regulation	2/2606	27/23843	0.810682	0.880682	0.837433	Guca1a/Lh
GO_BP_m1	GO:003163	plasminog	2/2606	27/23843	0.810682	0.880682	0.837433	F11/Tmprs
GO_BP_m1	GO:003281	positive re	2/2606	27/23843	0.810682	0.880682	0.837433	Il12b/Ulbp
GO_BP_m1	GO:003598	endoderma	2/2606	27/23843	0.810682	0.880682	0.837433	Col5a1/So
GO_BP_m1	GO:003600	positive re	2/2606	27/23843	0.810682	0.880682	0.837433	Atf3/Creb3
GO_BP_m1	GO:004874	smooth mu	2/2606	27/23843	0.810682	0.880682	0.837433	Nf1/Osr1
GO_BP_m1	GO:005092	regulation	2/2606	27/23843	0.810682	0.880682	0.837433	Prkca/Scg2
GO_BP_m1	GO:005115	regulation	2/2606	27/23843	0.810682	0.880682	0.837433	Med28/Rb
GO_BP_m1	GO:006071	labyrinthin	2/2606	27/23843	0.810682	0.880682	0.837433	Adm/Il10
GO_BP_m1	GO:007097	protein K1	2/2606	27/23843	0.810682	0.880682	0.837433	Cdc23/Par
GO_BP_m1	GO:190289	positive re	2/2606	27/23843	0.810682	0.880682	0.837433	Nfkb1/Sm
GO_BP_m1	GO:004396	histone H3	5/2606	61/23843	0.810767	0.880682	0.837433	Brpf3/Kat2
GO_BP_m1	GO:004566	regulation	5/2606	61/23843	0.810767	0.880682	0.837433	Cxcl10/Flot
GO_BP_m1	GO:200102	negative re	5/2606	61/23843	0.810767	0.880682	0.837433	Fbxo18/Nu
GO_BP_m1	GO:190040	negative re	4/2606	50/23843	0.810801	0.880682	0.837433	Gpx1/Hsp
GO_BP_m1	GO:000740	axonogene	45/2606	461/23843	0.811526	0.881361	0.838079	Aatk/Ache/
GO_BP_m1	GO:190320	regulation	6/2606	72/23843	0.812728	0.882557	0.839216	Endog/Gp
GO_BP_m1	GO:000734	acrosome	3/2606	39/23843	0.814636	0.884191	0.84077	Hyal3/Pkd
GO_BP_m1	GO:003817	neurotroph	3/2606	39/23843	0.814636	0.884191	0.84077	Bcar1/Ndn
GO_BP_m1	GO:004502	early endo	3/2606	39/23843	0.814636	0.884191	0.84077	Dnajc13/E
GO_BP_m1	GO:004874	skeletal mu	3/2606	39/23843	0.814636	0.884191	0.84077	Acta1/Gpx
GO_BP_m1	GO:003000	cellular mo	9/2606	104/23843	0.815028	0.88446	0.841026	Atp1b2/At
GO_BP_m1	GO:009902	plasma me	18/2606	196/23843	0.815085	0.88446	0.841026	Cd36/Gsn/
GO_BP_m1	GO:005114	positive re	7/2606	83/23843	0.815804	0.885022	0.84156	Akap6/Cav
GO_BP_m1	GO:005149	regulation	7/2606	83/23843	0.815804	0.885022	0.84156	Ctgf/Itgb1
GO_BP_m1	GO:190227	regulation	16/2606	176/23843	0.816252	0.885399	0.841918	Apobec1/
GO_BP_m1	GO:009872	maintenan	15/2606	166/23843	0.817202	0.885823	0.842322	Cdh2/Cul4
GO_BP_m1	GO:190489	regulation	18/2606	197/23843	0.821462	0.885823	0.842322	Cav1/Cdk5
GO_BP_m1	GO:002169	cerebellar	5/2606	62/23843	0.821871	0.885823	0.842322	Cdk5/Cenc
GO_BP_m1	GO:006103	regulation	5/2606	62/23843	0.821871	0.885823	0.842322	Ctgf/Rflna/
GO_BP_m1	GO:190122	positive re	5/2606	62/23843	0.821871	0.885823	0.842322	Calr/Eif2ak
GO_BP_m1	GO:000691	phagocyto	17/2606	187/23843	0.822083	0.885823	0.842322	Cd36/Gsn/
GO_BP_m1	GO:004566	regulation	12/2606	136/23843	0.822109	0.885823	0.842322	Noct/Clic1/
GO_BP_m1	GO:000173	establishm	4/2606	51/23843	0.822942	0.885823	0.842322	Abl2/Cthrc
GO_BP_m1	GO:001066	regulation	4/2606	51/23843	0.822942	0.885823	0.842322	Bnip3/Cam
GO_BP_m1	GO:003508	establishm	4/2606	51/23843	0.822942	0.885823	0.842322	Ezr/Fscn1/
GO_BP_m1	GO:004364	inositol ph	4/2606	51/23843	0.822942	0.885823	0.842322	Adcyap1r1
GO_BP_m1	GO:006124	establishm	4/2606	51/23843	0.822942	0.885823	0.842322	Ezr/Fscn1/

GO_BP_m1	GO:190201	regulation	4/2606	51/23843	0.822942	0.885823	0.842322	Ift88/Odf2/
GO_BP_m1	GO:001083	telomere m	6/2606	73/23843	0.822955	0.885823	0.842322	Atr/Cct3/H
GO_BP_m1	GO:000029	nuclear-tra	1/2606	15/23843	0.823904	0.885823	0.842322	Exosc9
GO_BP_m1	GO:000071	resolution (	1/2606	15/23843	0.823904	0.885823	0.842322	Cenpx
GO_BP_m1	GO:000072	DNA doub	1/2606	15/23843	0.823904	0.885823	0.842322	Blm
GO_BP_m1	GO:000318	heart valve	1/2606	15/23843	0.823904	0.885823	0.842322	Zfpm2
GO_BP_m1	GO:000612	mitochond	1/2606	15/23843	0.823904	0.885823	0.842322	Cox4i2
GO_BP_m1	GO:000633	nucleosom	1/2606	15/23843	0.823904	0.885823	0.842322	Smarce1
GO_BP_m1	GO:000667	glycosylcer	1/2606	15/23843	0.823904	0.885823	0.842322	B4galt3
GO_BP_m1	GO:000725	I-kappaB p	1/2606	15/23843	0.823904	0.885823	0.842322	Ddrgk1
GO_BP_m1	GO:000914	nucleoside	1/2606	15/23843	0.823904	0.885823	0.842322	Nudt1
GO_BP_m1	GO:001045	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Wnt3a
GO_BP_m1	GO:001052	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Fkbp1b
GO_BP_m1	GO:001096	magnesium	1/2606	15/23843	0.823904	0.885823	0.842322	Trmt10a
GO_BP_m1	GO:001473	regulation	1/2606	15/23843	0.823904	0.885823	0.842322	Myh7
GO_BP_m1	GO:001485	skeletal mu	1/2606	15/23843	0.823904	0.885823	0.842322	Ephb1
GO_BP_m1	GO:001568	ferric iron t	1/2606	15/23843	0.823904	0.885823	0.842322	Rep15
GO_BP_m1	GO:001802	peptidyl-ly	1/2606	15/23843	0.823904	0.885823	0.842322	Dmrtc2
GO_BP_m1	GO:001964	aerobic ele	1/2606	15/23843	0.823904	0.885823	0.842322	Cox4i2
GO_BP_m1	GO:002169	cerebellar I	1/2606	15/23843	0.823904	0.885823	0.842322	Cend1
GO_BP_m1	GO:003000	cellular pot	1/2606	15/23843	0.823904	0.885823	0.842322	Atp1b2
GO_BP_m1	GO:003015	pancreatic	1/2606	15/23843	0.823904	0.885823	0.842322	Nr1h2
GO_BP_m1	GO:003126	pseudopoc	1/2606	15/23843	0.823904	0.885823	0.842322	Cdc42ep5
GO_BP_m1	GO:003248	Cdc42 prot	1/2606	15/23843	0.823904	0.885823	0.842322	Shtn1
GO_BP_m1	GO:003278	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Cnn3
GO_BP_m1	GO:003295	inositol tris	1/2606	15/23843	0.823904	0.885823	0.842322	P2ry1
GO_BP_m1	GO:004230	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Ei24
GO_BP_m1	GO:004279	nucleolar la	1/2606	15/23843	0.823904	0.885823	0.842322	H2afy
GO_BP_m1	GO:004338	negative T	1/2606	15/23843	0.823904	0.885823	0.842322	Ptprc
GO_BP_m1	GO:004529	mRNA cis s	1/2606	15/23843	0.823904	0.885823	0.842322	Psip1
GO_BP_m1	GO:004565	regulation	1/2606	15/23843	0.823904	0.885823	0.842322	Myc
GO_BP_m1	GO:004613	pyrimidine	1/2606	15/23843	0.823904	0.885823	0.842322	Nme6
GO_BP_m1	GO:005113	chaperone	1/2606	15/23843	0.823904	0.885823	0.842322	Bbs10
GO_BP_m1	GO:005192	sulfation	1/2606	15/23843	0.823904	0.885823	0.842322	Sult1a1
GO_BP_m1	GO:005193	L-glutamat	1/2606	15/23843	0.823904	0.885823	0.842322	Arl6ip5
GO_BP_m1	GO:005506	phosphate	1/2606	15/23843	0.823904	0.885823	0.842322	Rnls
GO_BP_m1	GO:006014	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Zc3h12a
GO_BP_m1	GO:006070	regulation	1/2606	15/23843	0.823904	0.885823	0.842322	Oas1f
GO_BP_m1	GO:006096	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Zc3h12a
GO_BP_m1	GO:006130	cardiac neu	1/2606	15/23843	0.823904	0.885823	0.842322	Jag1
GO_BP_m1	GO:007016	enamel mir	1/2606	15/23843	0.823904	0.885823	0.842322	Tbx1
GO_BP_m1	GO:007020	establishm	1/2606	15/23843	0.823904	0.885823	0.842322	Nabp2
GO_BP_m1	GO:007072	response to	1/2606	15/23843	0.823904	0.885823	0.842322	Smo
GO_BP_m1	GO:007102	RNA survei	1/2606	15/23843	0.823904	0.885823	0.842322	Exosc9
GO_BP_m1	GO:007140	cellular res	1/2606	15/23843	0.823904	0.885823	0.842322	Cd36
GO_BP_m1	GO:007163	positive reg	1/2606	15/23843	0.823904	0.885823	0.842322	Ptgs2
GO_BP_m1	GO:007218	ureter deve	1/2606	15/23843	0.823904	0.885823	0.842322	Osr1
GO_BP_m1	GO:007250	divalent ino	1/2606	15/23843	0.823904	0.885823	0.842322	Rnls

GO_BP_m1	GO:00725	trivalent in	1/2606	15/23843	0.823904	0.885823	0.842322	Rnls
GO_BP_m1	GO:007251	trivalent in	1/2606	15/23843	0.823904	0.885823	0.842322	Rep15
GO_BP_m1	GO:007267	neutrophil	1/2606	15/23843	0.823904	0.885823	0.842322	Adam8
GO_BP_m1	GO:008601	atrial cardi	1/2606	15/23843	0.823904	0.885823	0.842322	Cacnb2
GO_BP_m1	GO:00860	atrial cardi	1/2606	15/23843	0.823904	0.885823	0.842322	Cacnb2
GO_BP_m1	GO:00860	atrial cardi	1/2606	15/23843	0.823904	0.885823	0.842322	Cacnb2
GO_BP_m1	GO:00900	regulation	1/2606	15/23843	0.823904	0.885823	0.842322	Dnaja4
GO_BP_m1	GO:190354	positive re	1/2606	15/23843	0.823904	0.885823	0.842322	Smpd3
GO_BP_m1	GO:19045	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Ei24
GO_BP_m1	GO:200064	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Nf1
GO_BP_m1	GO:200101	negative re	1/2606	15/23843	0.823904	0.885823	0.842322	Ephb1
GO_BP_m1	GO:20010	positive re	1/2606	15/23843	0.823904	0.885823	0.842322	Fgf16
GO_BP_m1	GO:19016	cellular res	11/2606	126/23843	0.824672	0.886111	0.842595	Eif4e/Gdnf
GO_BP_m1	GO:00434	steroid hor	14/2606	157/23843	0.825464	0.886111	0.842595	Arntl/Calr/
GO_BP_m1	GO:00018	blastocyst	2/2606	28/23843	0.826593	0.886111	0.842595	Esrrb/Prpf1
GO_BP_m1	GO:000597	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	Esrrb/Ppp1
GO_BP_m1	GO:000621	pyrimidine	2/2606	28/23843	0.826593	0.886111	0.842595	Dpyd/Nme
GO_BP_m1	GO:000637	mRNA clea	2/2606	28/23843	0.826593	0.886111	0.842595	Cpsf2/Cpsf
GO_BP_m1	GO:000717	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	Adora1/Gp
GO_BP_m1	GO:00093	rRNA trans	2/2606	28/23843	0.826593	0.886111	0.842595	Cd3eap/H2
GO_BP_m1	GO:00104	exit from m	2/2606	28/23843	0.826593	0.886111	0.842595	Cdkn1c/Ma
GO_BP_m1	GO:00109	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	Esrrb/Ppp1
GO_BP_m1	GO:001624	negative re	2/2606	28/23843	0.826593	0.886111	0.842595	Scfd1/Tiga
GO_BP_m1	GO:002187	forebrain r	2/2606	28/23843	0.826593	0.886111	0.842595	Dmrta2/Pg
GO_BP_m1	GO:003022	monocyte	2/2606	28/23843	0.826593	0.886111	0.842595	Fasn/Myc
GO_BP_m1	GO:003502	positive re	2/2606	28/23843	0.826593	0.886111	0.842595	Abra/Gpr1
GO_BP_m1	GO:00440	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	H19/Mpho
GO_BP_m1	GO:005082	positive re	2/2606	28/23843	0.826593	0.886111	0.842595	Cd36/Ptprj
GO_BP_m1	GO:005112	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	Gsn/Wipf1
GO_BP_m1	GO:006011	auditory re	2/2606	28/23843	0.826593	0.886111	0.842595	Myo3a/Paf
GO_BP_m1	GO:00606	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	Bbs2/Dnaa
GO_BP_m1	GO:00705	protein K6	2/2606	28/23843	0.826593	0.886111	0.842595	Uimc1/Usp
GO_BP_m1	GO:00713	cellular res	2/2606	28/23843	0.826593	0.886111	0.842595	Fasn/Jak3
GO_BP_m1	GO:190204	negative re	2/2606	28/23843	0.826593	0.886111	0.842595	Dapk1/Gpx
GO_BP_m1	GO:19031	mononucle	2/2606	28/23843	0.826593	0.886111	0.842595	Fasn/Myc
GO_BP_m1	GO:20001	regulation	2/2606	28/23843	0.826593	0.886111	0.842595	P2ry2/Tnfs
GO_BP_m1	GO:00901	establishm	18/2606	198/23843	0.827677	0.886858	0.843306	Adora1/Arl
GO_BP_m1	GO:00308	positive re	3/2606	40/23843	0.827997	0.886858	0.843306	Calcr/Guca
GO_BP_m1	GO:00324	regulation	3/2606	40/23843	0.827997	0.886858	0.843306	Oprd1/Pex
GO_BP_m1	GO:00432	sodium-in	3/2606	40/23843	0.827997	0.886858	0.843306	Slc22a1/Sl
GO_BP_m1	GO:00606	mammary	3/2606	40/23843	0.827997	0.886858	0.843306	Cav3/Epha
GO_BP_m1	GO:00708	bicellular ti	3/2606	40/23843	0.827997	0.886858	0.843306	Cdh1/Cgn/
GO_BP_m1	GO:00860	cardiac mu	3/2606	40/23843	0.827997	0.886858	0.843306	Cacnb2/Ca
GO_BP_m1	GO:20012	positive re	15/2606	168/23843	0.830692	0.889637	0.845948	Atr/BC004
GO_BP_m1	GO:00320	regulation	9/2606	106/23843	0.831858	0.890777	0.847032	Arntl/Dgkq
GO_BP_m1	GO:00517	positive re	6/2606	74/23843	0.832734	0.891497	0.847717	Dmrt1/Drd
GO_BP_m1	GO:007142	ribonucleo	6/2606	74/23843	0.832734	0.891497	0.847717	Ddx19b/Nr
GO_BP_m1	GO:00071	establishm	4/2606	52/23843	0.834431	0.893096	0.849237	Abl2/Cthrc

GO_BP_m1	GO:007093	protein K48	4/2606	52/23843	0.834431	0.893096	0.849237	Arih2/Nmi/
GO_BP_m1	GO:001921	regulation	8/2606	96/23843	0.836836	0.894594	0.850662	Dgkq/Ephx
GO_BP_m1	GO:000226	cell activati	24/2606	260/23843	0.837149	0.894594	0.850662	Anxa3/Aplf
GO_BP_m1	GO:006004	retina deve	14/2606	159/23843	0.838876	0.894594	0.850662	Ache/Dll4/
GO_BP_m1	GO:007333	binding of	3/2606	41/23843	0.840523	0.894594	0.850662	Cct3/Fetub
GO_BP_m1	GO:001076	positive reg	3/2606	41/23843	0.840523	0.894594	0.850662	Atp1b2/Fxy
GO_BP_m1	GO:001095	negative re	3/2606	41/23843	0.840523	0.894594	0.850662	Cdh1/Fmr1
GO_BP_m1	GO:001967	NAD metal	3/2606	41/23843	0.840523	0.894594	0.850662	Idh3a/Ldha
GO_BP_m1	GO:004749	vesicle tran	3/2606	41/23843	0.840523	0.894594	0.850662	Bloc1s5/Kif
GO_BP_m1	GO:005165	spindle loc	3/2606	41/23843	0.840523	0.894594	0.850662	Cenpa/Nus
GO_BP_m1	GO:009892	vesicle-me	3/2606	41/23843	0.840523	0.894594	0.850662	Dnajc13/Ez
GO_BP_m1	GO:190007	negative re	3/2606	41/23843	0.840523	0.894594	0.850662	Gpr21/Prkc
GO_BP_m1	GO:190331	negative re	3/2606	41/23843	0.840523	0.894594	0.850662	Cdh1/Fmr1
GO_BP_m1	GO:003105	regulation	13/2606	149/23843	0.840977	0.894594	0.850662	BC004004/
GO_BP_m1	GO:009915	purine ribo	2/2606	29/23843	0.841289	0.894594	0.850662	Pde11a/Pd
GO_BP_m1	GO:009926	ribonucleo	2/2606	29/23843	0.841289	0.894594	0.850662	Pde11a/Pd
GO_BP_m1	GO:001039	histone mc	2/2606	29/23843	0.841289	0.894594	0.850662	Kdm2b/Rir
GO_BP_m1	GO:003300	positive reg	2/2606	29/23843	0.841289	0.894594	0.850662	Cd300lb/M
GO_BP_m1	GO:003311	negative re	2/2606	29/23843	0.841289	0.894594	0.850662	Rbm42/Srs
GO_BP_m1	GO:003426	negative re	2/2606	29/23843	0.841289	0.894594	0.850662	Bcas3/Plxn
GO_BP_m1	GO:003506	positive reg	2/2606	29/23843	0.841289	0.894594	0.850662	Kat2a/Kat2
GO_BP_m1	GO:003588	vascular sm	2/2606	29/23843	0.841289	0.894594	0.850662	Adm/Smac
GO_BP_m1	GO:004216	heme meta	2/2606	29/23843	0.841289	0.894594	0.850662	Cox15/Iba5
GO_BP_m1	GO:005129	establishm	2/2606	29/23843	0.841289	0.894594	0.850662	Cenpa/Pafa
GO_BP_m1	GO:006031	cardiac epi	2/2606	29/23843	0.841289	0.894594	0.850662	Has2/Nog
GO_BP_m1	GO:006057	morphogei	2/2606	29/23843	0.841289	0.894594	0.850662	Cfl1/Nog
GO_BP_m1	GO:007252	pyrimidine	2/2606	29/23843	0.841289	0.894594	0.850662	Nme6/Shm
GO_BP_m1	GO:009735	autophago	2/2606	29/23843	0.841289	0.894594	0.850662	Epg5/Snap
GO_BP_m1	GO:005085	B cell recep	16/2606	180/23843	0.841893	0.894594	0.850662	Bcar1/Cd19
GO_BP_m1	GO:007116	ribonucleo	6/2606	75/23843	0.842074	0.894594	0.850662	Ddx19b/Nr
GO_BP_m1	GO:000170	mesoderm	5/2606	64/23843	0.842497	0.894594	0.850662	Epha2/Fox
GO_BP_m1	GO:007135	cellular res	5/2606	64/23843	0.842497	0.894594	0.850662	Cav1/Mb21
GO_BP_m1	GO:000242	immune re	29/2606	311/23843	0.842714	0.894594	0.850662	Bcar1/Btnl2
GO_BP_m1	GO:004315	negative re	7/2606	86/23843	0.843082	0.894594	0.850662	Gpx1/Mkl1
GO_BP_m1	GO:190113	carbohydra	10/2606	118/23843	0.843115	0.894594	0.850662	Abhd10/Ch
GO_BP_m1	GO:000072	telomere m	1/2606	16/23843	0.843163	0.894594	0.850662	Xrcc1
GO_BP_m1	GO:000092	cell separat	1/2606	16/23843	0.843163	0.894594	0.850662	Chmp1b
GO_BP_m1	GO:000171	endoderma	1/2606	16/23843	0.843163	0.894594	0.850662	Sox2
GO_BP_m1	GO:000183	inner cell m	1/2606	16/23843	0.843163	0.894594	0.850662	Prpf19
GO_BP_m1	GO:000246	germinal ce	1/2606	16/23843	0.843163	0.894594	0.850662	Pkn1
GO_BP_m1	GO:000254	chronic infl	1/2606	16/23843	0.843163	0.894594	0.850662	Il10
GO_BP_m1	GO:000316	cardiac cor	1/2606	16/23843	0.843163	0.894594	0.850662	Nrg1
GO_BP_m1	GO:000651	glycoprote	1/2606	16/23843	0.843163	0.894594	0.850662	Man1b1
GO_BP_m1	GO:000660	NLS-bearir	1/2606	16/23843	0.843163	0.894594	0.850662	Nup54
GO_BP_m1	GO:000683	water trans	1/2606	16/23843	0.843163	0.894594	0.850662	Mylk2
GO_BP_m1	GO:000721	G-protein	1/2606	16/23843	0.843163	0.894594	0.850662	Grm2
GO_BP_m1	GO:000833	histone mR	1/2606	16/23843	0.843163	0.894594	0.850662	Cpsf2
GO_BP_m1	GO:000922	pyrimidine	1/2606	16/23843	0.843163	0.894594	0.850662	Nme6

GO_BP_m1	GO:002197	telencepha	1/2606	16/23843	0.843163	0.894594	0.850662	Dmrta2
GO_BP_m1	GO:003082	positive reg	1/2606	16/23843	0.843163	0.894594	0.850662	Guca1a
GO_BP_m1	GO:003223	positive reg	1/2606	16/23843	0.843163	0.894594	0.850662	Tac1
GO_BP_m1	GO:003257	response to	1/2606	16/23843	0.843163	0.894594	0.850662	Cav1
GO_BP_m1	GO:003612	histone H3	1/2606	16/23843	0.843163	0.894594	0.850662	Dmrtc2
GO_BP_m1	GO:004275	drinking be	1/2606	16/23843	0.843163	0.894594	0.850662	Hrh3
GO_BP_m1	GO:004440	adhesion o	1/2606	16/23843	0.843163	0.894594	0.850662	Scarb1
GO_BP_m1	GO:004572	positive reg	1/2606	16/23843	0.843163	0.894594	0.850662	Esrrb
GO_BP_m1	GO:004651	ceramide c	1/2606	16/23843	0.843163	0.894594	0.850662	Asah2
GO_BP_m1	GO:004675	viral buddi	1/2606	16/23843	0.843163	0.894594	0.850662	Chmp1b
GO_BP_m1	GO:005185	disruption	1/2606	16/23843	0.843163	0.894594	0.850662	Arg1
GO_BP_m1	GO:005187	killing by h	1/2606	16/23843	0.843163	0.894594	0.850662	Arg1
GO_BP_m1	GO:006002	convergent	1/2606	16/23843	0.843163	0.894594	0.850662	Zfp568
GO_BP_m1	GO:006025	negative re	1/2606	16/23843	0.843163	0.894594	0.850662	Idh2
GO_BP_m1	GO:006030	regulation	1/2606	16/23843	0.843163	0.894594	0.850662	Cav3
GO_BP_m1	GO:008601	membrane	1/2606	16/23843	0.843163	0.894594	0.850662	Cav1
GO_BP_m1	GO:009017	establishm	1/2606	16/23843	0.843163	0.894594	0.850662	Cthrc1
GO_BP_m1	GO:009709	craniofacia	1/2606	16/23843	0.843163	0.894594	0.850662	Mmp14
GO_BP_m1	GO:009732	plasma me	1/2606	16/23843	0.843163	0.894594	0.850662	Snx9
GO_BP_m1	GO:190218	negative re	1/2606	16/23843	0.843163	0.894594	0.850662	Vapb
GO_BP_m1	GO:190301	negative re	1/2606	16/23843	0.843163	0.894594	0.850662	Jak3
GO_BP_m1	GO:190377	regulation	1/2606	16/23843	0.843163	0.894594	0.850662	Cav1
GO_BP_m1	GO:190379	regulation	1/2606	16/23843	0.843163	0.894594	0.850662	Zc3h12a
GO_BP_m1	GO:190426	negative re	1/2606	16/23843	0.843163	0.894594	0.850662	Szt2
GO_BP_m1	GO:200031	regulation	1/2606	16/23843	0.843163	0.894594	0.850662	Smad7
GO_BP_m1	GO:007182	protein-DN	19/2606	211/23843	0.844452	0.895853	0.851859	Cand1/Cer
GO_BP_m1	GO:000688	regulation	8/2606	97/23843	0.84499	0.895984	0.851984	Atp6v0c/Av
GO_BP_m1	GO:000687	cellular iron	4/2606	53/23843	0.845289	0.895984	0.851984	Myc/Nubp
GO_BP_m1	GO:001065	cardiac mu	4/2606	53/23843	0.845289	0.895984	0.851984	Bnip3/Cam
GO_BP_m1	GO:003004	actin filame	4/2606	53/23843	0.845289	0.895984	0.851984	Cfl1/Gsn/P
GO_BP_m1	GO:003531	hair cell dif	4/2606	53/23843	0.845289	0.895984	0.851984	Jag1/Mcoln
GO_BP_m1	GO:007127	cellular resp	4/2606	53/23843	0.845289	0.895984	0.851984	Asph/Cpne
GO_BP_m1	GO:009030	positive reg	4/2606	53/23843	0.845289	0.895984	0.851984	Cd36/Myc/
GO_BP_m1	GO:000282	positive reg	9/2606	108/23843	0.847475	0.898193	0.854084	Fam49b/Ifn
GO_BP_m1	GO:000237	immunoglo	20/2606	222/23843	0.849104	0.899811	0.855623	Aplf/Ifng/Ig
GO_BP_m1	GO:000632	DNA packa	15/2606	171/23843	0.849512	0.900026	0.855827	Bahd1/Cdk
GO_BP_m1	GO:004561	regulation	15/2606	171/23843	0.849512	0.900026	0.855827	Adam8/Ctl
GO_BP_m1	GO:002187	forebrain n	6/2606	76/23843	0.850986	0.90137	0.857105	Arx/Mir141
GO_BP_m1	GO:190395	positive reg	6/2606	76/23843	0.850986	0.90137	0.857105	Arih2/Kat2
GO_BP_m1	GO:190432	response to	5/2606	65/23843	0.852048	0.902058	0.857759	Gnai1/Mir1
GO_BP_m1	GO:190432	cellular resp	5/2606	65/23843	0.852048	0.902058	0.857759	Gnai1/Mir1
GO_BP_m1	GO:000319	endocardia	3/2606	42/23843	0.852252	0.902058	0.857759	Erbb3/Jag1
GO_BP_m1	GO:004246	eye photor	3/2606	42/23843	0.852252	0.902058	0.857759	Fscn2/Th/T
GO_BP_m1	GO:005167	membrane	3/2606	42/23843	0.852252	0.902058	0.857759	Defa29/De
GO_BP_m1	GO:007016	positive reg	3/2606	42/23843	0.852252	0.902058	0.857759	Mia3/Osr1/
GO_BP_m1	GO:005165	maintenan	8/2606	98/23843	0.852817	0.902548	0.858225	Cav1/Cdk5
GO_BP_m1	GO:001644	posttranscr	11/2606	130/23843	0.853424	0.902954	0.858612	Fmr1/Gigyf
GO_BP_m1	GO:007182	ribonucleo	20/2606	223/23843	0.854343	0.902954	0.858612	Atr/Noct/C

GO_BP_m1	GO:003812	ERBB signa	9/2606	109/23843	0.854843	0.902954	0.858612	Abl2/Adora
GO_BP_m1	GO:000236	T cell lineag	2/2606	30/23843	0.854846	0.902954	0.858612	Il7/Prkdc
GO_BP_m1	GO:000622	pyrimidine	2/2606	30/23843	0.854846	0.902954	0.858612	Nme6/Shm
GO_BP_m1	GO:003296	positive reg	2/2606	30/23843	0.854846	0.902954	0.858612	Ctgf/Mkx
GO_BP_m1	GO:003414	toll-like rec	2/2606	30/23843	0.854846	0.902954	0.858612	Ptpn22/Tic
GO_BP_m1	GO:003532	hippo signa	2/2606	30/23843	0.854846	0.902954	0.858612	Lats1/Stk3
GO_BP_m1	GO:004248	regulation	2/2606	30/23843	0.854846	0.902954	0.858612	Ift88/Wnt1
GO_BP_m1	GO:004255	superoxide	2/2606	30/23843	0.854846	0.902954	0.858612	Fpr2/Itgam
GO_BP_m1	GO:004395	positive reg	2/2606	30/23843	0.854846	0.902954	0.858612	Adcyap1r1
GO_BP_m1	GO:004801	neurotroph	2/2606	30/23843	0.854846	0.902954	0.858612	Bcar1/Ndn
GO_BP_m1	GO:005507	potassium	2/2606	30/23843	0.854846	0.902954	0.858612	Atp1b2/Slc
GO_BP_m1	GO:007067	response to	2/2606	30/23843	0.854846	0.902954	0.858612	Fasn/Jak3
GO_BP_m1	GO:190008	positive reg	2/2606	30/23843	0.854846	0.902954	0.858612	Cul4a/Mtb
GO_BP_m1	GO:190343	regulation	2/2606	30/23843	0.854846	0.902954	0.858612	Dgkq/Szt2
GO_BP_m1	GO:000833	endosome	4/2606	54/23843	0.855541	0.903471	0.859103	Cacng5/Ca
GO_BP_m1	GO:003501	somatic ste	4/2606	54/23843	0.855541	0.903471	0.859103	Cul4a/Nog
GO_BP_m1	GO:001032	membrane	18/2606	203/23843	0.856374	0.904242	0.859836	Cd36/Gsn/
GO_BP_m1	GO:001982	stem cell p	14/2606	162/23843	0.857506	0.904383	0.85997	Cdh2/Cul4
GO_BP_m1	GO:000641	translationa	6/2606	77/23843	0.859482	0.904383	0.85997	Abtb1/Cpe
GO_BP_m1	GO:000319	epithelial to	1/2606	17/23843	0.860317	0.904383	0.85997	Nog
GO_BP_m1	GO:000644	regulation	1/2606	17/23843	0.860317	0.904383	0.85997	Cpeb3
GO_BP_m1	GO:000696	cellular def	1/2606	17/23843	0.860317	0.904383	0.85997	Cd19
GO_BP_m1	GO:000914	pyrimidine	1/2606	17/23843	0.860317	0.904383	0.85997	Nme6
GO_BP_m1	GO:000921	pyrimidine	1/2606	17/23843	0.860317	0.904383	0.85997	Nme6
GO_BP_m1	GO:000988	post-embr	1/2606	17/23843	0.860317	0.904383	0.85997	Mir23a
GO_BP_m1	GO:001000	cardioblast	1/2606	17/23843	0.860317	0.904383	0.85997	Wnt3a
GO_BP_m1	GO:001083	negative re	1/2606	17/23843	0.860317	0.904383	0.85997	Cxcl10
GO_BP_m1	GO:003082	regulation	1/2606	17/23843	0.860317	0.904383	0.85997	Guca1a
GO_BP_m1	GO:003315	V(D)J recor	1/2606	17/23843	0.860317	0.904383	0.85997	Prkdc
GO_BP_m1	GO:003353	fatty acid b	1/2606	17/23843	0.860317	0.904383	0.85997	Acad11
GO_BP_m1	GO:003433	cell junctio	1/2606	17/23843	0.860317	0.904383	0.85997	5730559C1
GO_BP_m1	GO:003447	snRNA 3'-e	1/2606	17/23843	0.860317	0.904383	0.85997	Exosc9
GO_BP_m1	GO:003464	establishme	1/2606	17/23843	0.860317	0.904383	0.85997	Rhot2
GO_BP_m1	GO:003612	cellular res	1/2606	17/23843	0.860317	0.904383	0.85997	Has2
GO_BP_m1	GO:004215	lipoprotein	1/2606	17/23843	0.860317	0.904383	0.85997	Ppt1
GO_BP_m1	GO:004265	regulation	1/2606	17/23843	0.860317	0.904383	0.85997	Wnt3a
GO_BP_m1	GO:004327	response to	1/2606	17/23843	0.860317	0.904383	0.85997	Drd3
GO_BP_m1	GO:004506	T-helper 2	1/2606	17/23843	0.860317	0.904383	0.85997	Zfp35
GO_BP_m1	GO:004579	positive reg	1/2606	17/23843	0.860317	0.904383	0.85997	Ogt
GO_BP_m1	GO:004613	pyrimidine	1/2606	17/23843	0.860317	0.904383	0.85997	Nme6
GO_BP_m1	GO:004618	aldehyde b	1/2606	17/23843	0.860317	0.904383	0.85997	Adh1
GO_BP_m1	GO:004634	amino suga	1/2606	17/23843	0.860317	0.904383	0.85997	Chil5
GO_BP_m1	GO:004749	mitochond	1/2606	17/23843	0.860317	0.904383	0.85997	Rhot2
GO_BP_m1	GO:004849	anterograd	1/2606	17/23843	0.860317	0.904383	0.85997	Bloc1s5
GO_BP_m1	GO:006097	cell migrati	1/2606	17/23843	0.860317	0.904383	0.85997	Ndrg4
GO_BP_m1	GO:007092	regulation	1/2606	17/23843	0.860317	0.904383	0.85997	Zc3h12a
GO_BP_m1	GO:007178	endoplasm	1/2606	17/23843	0.860317	0.904383	0.85997	Reep1
GO_BP_m1	GO:009023	regulation	1/2606	17/23843	0.860317	0.904383	0.85997	Tpr

GO_BP_m1	GO:009951	synaptic ve	1/2606	17/23843	0.860317	0.904383	0.85997	Bloc1s5
GO_BP_m1	GO:009951	synaptic ve	1/2606	17/23843	0.860317	0.904383	0.85997	Bloc1s5
GO_BP_m1	GO:200035	positive reg	1/2606	17/23843	0.860317	0.904383	0.85997	Cd248
GO_BP_m1	GO:200077	negative re	1/2606	17/23843	0.860317	0.904383	0.85997	Prkdc
GO_BP_m1	GO:200078	positive reg	1/2606	17/23843	0.860317	0.904383	0.85997	Blm
GO_BP_m1	GO:200081	regulation	1/2606	17/23843	0.860317	0.904383	0.85997	Cldn1
GO_BP_m1	GO:006147	response to	5/2606	66/23843	0.861112	0.905003	0.860559	Gnai1/Mir1
GO_BP_m1	GO:190303	positive reg	5/2606	66/23843	0.861112	0.905003	0.860559	Cd36/Fkbp
GO_BP_m1	GO:001490	myotube c	3/2606	43/23843	0.86322	0.906892	0.862356	Acta1/Gpx
GO_BP_m1	GO:004682	regulation	3/2606	43/23843	0.86322	0.906892	0.862356	Cdk5/Tpr/
GO_BP_m1	GO:005091	detection c	3/2606	43/23843	0.86322	0.906892	0.862356	Olfr371/Ol
GO_BP_m1	GO:001065	striated mu	4/2606	55/23843	0.865208	0.908654	0.864032	Bnip3/Cam
GO_BP_m1	GO:004269	ovulation c	4/2606	55/23843	0.865208	0.908654	0.864032	Adamts1/A
GO_BP_m1	GO:004867	response to	4/2606	55/23843	0.865208	0.908654	0.864032	Fkbp1b/Klk
GO_BP_m1	GO:000236	leukocyte a	23/2606	256/23843	0.866709	0.909476	0.864814	Anxa3/Aplf
GO_BP_m1	GO:003208	negative re	7/2606	89/23843	0.867023	0.909476	0.864814	Cactin/Irak
GO_BP_m1	GO:003647	cell death i	7/2606	89/23843	0.867023	0.909476	0.864814	Arl6ip5/En
GO_BP_m1	GO:000662	protein targ	2/2606	31/23843	0.867337	0.909476	0.864814	Pik3r4/Zfyv
GO_BP_m1	GO:000860	attachment	2/2606	31/23843	0.867337	0.909476	0.864814	Cenpc1/Ra
GO_BP_m1	GO:001057	regulation	2/2606	31/23843	0.867337	0.909476	0.864814	Cxcl17/Ptg
GO_BP_m1	GO:001071	positive reg	2/2606	31/23843	0.867337	0.909476	0.864814	Ctgf/Mkx
GO_BP_m1	GO:003272	positive reg	2/2606	31/23843	0.867337	0.909476	0.864814	Polr3g/Ptp
GO_BP_m1	GO:003308	regulation	2/2606	31/23843	0.867337	0.909476	0.864814	Adam8/Il2r
GO_BP_m1	GO:003336	secretory g	2/2606	31/23843	0.867337	0.909476	0.864814	Ccdc136/P
GO_BP_m1	GO:009016	establishme	2/2606	31/23843	0.867337	0.909476	0.864814	Fbf1/Tcf15
GO_BP_m1	GO:190547	negative re	2/2606	31/23843	0.867337	0.909476	0.864814	Itgb1bp1/
GO_BP_m1	GO:200075	positive reg	2/2606	31/23843	0.867337	0.909476	0.864814	Kat2a/Kat2
GO_BP_m1	GO:190526	positive reg	8/2606	100/23843	0.867518	0.909509	0.864844	BC004004/
GO_BP_m1	GO:190374	positive reg	6/2606	78/23843	0.867574	0.909509	0.864844	Arih2/Kat2
GO_BP_m1	GO:000228	lymphocyte	16/2606	185/23843	0.870025	0.911866	0.867086	Aplf/Dock1
GO_BP_m1	GO:001645	gene silenc	25/2606	277/23843	0.870031	0.911866	0.867086	Apobec1/B
GO_BP_m1	GO:003192	TOR signal	10/2606	122/23843	0.870419	0.912165	0.86737	Arntl/Dgkq
GO_BP_m1	GO:006161	pri-miRNA	3/2606	44/23843	0.873465	0.913122	0.86828	Hdac2/Nfk
GO_BP_m1	GO:000206	glandular e	4/2606	56/23843	0.874314	0.913122	0.86828	Arntl/Clock
GO_BP_m1	GO:000244	leukocyte r	43/2606	458/23843	0.874898	0.913122	0.86828	Anxa3/Aplf
GO_BP_m1	GO:000171	mesoderm	1/2606	18/23843	0.875595	0.913122	0.86828	Wnt3a
GO_BP_m1	GO:000207	osteoblast	1/2606	18/23843	0.875595	0.913122	0.86828	Men1
GO_BP_m1	GO:000292	positive reg	1/2606	18/23843	0.875595	0.913122	0.86828	Ptprc
GO_BP_m1	GO:000662	protein targ	1/2606	18/23843	0.875595	0.913122	0.86828	Zfyve16
GO_BP_m1	GO:000719	activation c	1/2606	18/23843	0.875595	0.913122	0.86828	Adcy4
GO_BP_m1	GO:000739	ectoderm c	1/2606	18/23843	0.875595	0.913122	0.86828	Foxa2
GO_BP_m1	GO:001099	response to	1/2606	18/23843	0.875595	0.913122	0.86828	Abl2
GO_BP_m1	GO:001407	response to	1/2606	18/23843	0.875595	0.913122	0.86828	Drd3
GO_BP_m1	GO:001604	detection c	1/2606	18/23843	0.875595	0.913122	0.86828	Nod1
GO_BP_m1	GO:001607	rRNA catab	1/2606	18/23843	0.875595	0.913122	0.86828	Exosc9
GO_BP_m1	GO:001841	C-terminal	1/2606	18/23843	0.875595	0.913122	0.86828	Wipi2
GO_BP_m1	GO:003227	gonadotro	1/2606	18/23843	0.875595	0.913122	0.86828	Tacr2
GO_BP_m1	GO:003243	melanosom	1/2606	18/23843	0.875595	0.913122	0.86828	Rab32

GO_BP_m1	GO:003267	regulation	1/2606	18/23843	0.875595	0.913122	0.86828	Il1rl1
GO_BP_m1	GO:003585	megakaryc	1/2606	18/23843	0.875595	0.913122	0.86828	Abi1
GO_BP_m1	GO:003611	response tc	1/2606	18/23843	0.875595	0.913122	0.86828	Has2
GO_BP_m1	GO:003631	response tc	1/2606	18/23843	0.875595	0.913122	0.86828	Smo
GO_BP_m1	GO:004003	negative re	1/2606	18/23843	0.875595	0.913122	0.86828	Shisa2
GO_BP_m1	GO:004221	cellular mo	1/2606	18/23843	0.875595	0.913122	0.86828	Dio2
GO_BP_m1	GO:004271	maternal b	1/2606	18/23843	0.875595	0.913122	0.86828	Avpr1a
GO_BP_m1	GO:004393	ossification	1/2606	18/23843	0.875595	0.913122	0.86828	Rflna
GO_BP_m1	GO:004507	regulation	1/2606	18/23843	0.875595	0.913122	0.86828	Glmn
GO_BP_m1	GO:004595	negative re	1/2606	18/23843	0.875595	0.913122	0.86828	Sh2d1b2
GO_BP_m1	GO:004671	muscle cell	1/2606	18/23843	0.875595	0.913122	0.86828	Cav3
GO_BP_m1	GO:005506	chloride ioı	1/2606	18/23843	0.875595	0.913122	0.86828	Slc12a2
GO_BP_m1	GO:006008	auditory re	1/2606	18/23843	0.875595	0.913122	0.86828	Myo3a
GO_BP_m1	GO:006039	regulation	1/2606	18/23843	0.875595	0.913122	0.86828	Pbld1
GO_BP_m1	GO:006057	morphogeı	1/2606	18/23843	0.875595	0.913122	0.86828	Nog
GO_BP_m1	GO:006071	spongiotro	1/2606	18/23843	0.875595	0.913122	0.86828	Adm
GO_BP_m1	GO:006084	venous blo	1/2606	18/23843	0.875595	0.913122	0.86828	Ephb4
GO_BP_m1	GO:006094	cardiac vas	1/2606	18/23843	0.875595	0.913122	0.86828	Smad6
GO_BP_m1	GO:007087	positive reg	1/2606	18/23843	0.875595	0.913122	0.86828	Esrrb
GO_BP_m1	GO:009854	detection c	1/2606	18/23843	0.875595	0.913122	0.86828	Nod1
GO_BP_m1	GO:009962	ventricular	1/2606	18/23843	0.875595	0.913122	0.86828	Cav3
GO_BP_m1	GO:190225	negative re	1/2606	18/23843	0.875595	0.913122	0.86828	Park2
GO_BP_m1	GO:190285	regulation	1/2606	18/23843	0.875595	0.913122	0.86828	Tmem67
GO_BP_m1	GO:190442	regulation	1/2606	18/23843	0.875595	0.913122	0.86828	Arhgef7
GO_BP_m1	GO:199040	embryonic	1/2606	18/23843	0.875595	0.913122	0.86828	Cc2d2a
GO_BP_m1	GO:000725	JAK-STAT (	18/2606	207/23843	0.876581	0.914041	0.869154	Cav1/Dcn/
GO_BP_m1	GO:005500	striated mu	15/2606	176/23843	0.877258	0.91464	0.869723	Acta1/Akap
GO_BP_m1	GO:004329	leukocyte c	5/2606	68/23843	0.877845	0.915034	0.870098	Anxa3/Bcr/
GO_BP_m1	GO:004833	mesoderm	5/2606	68/23843	0.877845	0.915034	0.870098	Epha2/Foxc
GO_BP_m1	GO:000038	spliceosom	2/2606	32/23843	0.878832	0.915302	0.870353	Prpf19/Prp
GO_BP_m1	GO:002159	ventricular	2/2606	32/23843	0.878832	0.915302	0.870353	Kdm2b/Ulk
GO_BP_m1	GO:002261	extracellula	2/2606	32/23843	0.878832	0.915302	0.870353	Fscn1/Kif9
GO_BP_m1	GO:004003	regulation	2/2606	32/23843	0.878832	0.915302	0.870353	Nog/Shisa2
GO_BP_m1	GO:006014	regulation	2/2606	32/23843	0.878832	0.915302	0.870353	Cxcl10/Scg
GO_BP_m1	GO:006079	cell fate co	2/2606	32/23843	0.878832	0.915302	0.870353	Sox2/Wnt3
GO_BP_m1	GO:008609	regulation	2/2606	32/23843	0.878832	0.915302	0.870353	Cacnb2/Ca
GO_BP_m1	GO:000282	positive reg	8/2606	102/23843	0.881	0.917278	0.872232	Fam49b/Ifr
GO_BP_m1	GO:000170	in utero en	42/2606	450/23843	0.881084	0.917278	0.872232	Adm/B9d1
GO_BP_m1	GO:003105	positive reg	7/2606	91/23843	0.881251	0.917278	0.872232	BC004004/
GO_BP_m1	GO:004544	myoblast d	7/2606	91/23843	0.881251	0.917278	0.872232	Ankrd1/Cxc
GO_BP_m1	GO:190374	regulation	7/2606	91/23843	0.881251	0.917278	0.872232	Arih2/Hsph
GO_BP_m1	GO:003519	gene silenc	10/2606	124/23843	0.882562	0.918461	0.873357	Fmr1/Mael
GO_BP_m1	GO:000315	outflow tra	6/2606	80/23843	0.882596	0.918461	0.873357	Foxc1/Jag1
GO_BP_m1	GO:005131	metaphase	4/2606	57/23843	0.882883	0.918579	0.873469	Ankrd53/C
GO_BP_m1	GO:006061	adipose tis	3/2606	45/23843	0.883024	0.918579	0.873469	Ap1s2/Ppa
GO_BP_m1	GO:006195	establishm	3/2606	45/23843	0.883024	0.918579	0.873469	Arhgap44/
GO_BP_m1	GO:011005	regulation	22/2606	250/23843	0.884906	0.920428	0.875227	Cdc42ep5/
GO_BP_m1	GO:009769	STAT casca	18/2606	209/23843	0.885811	0.921068	0.875835	Cav1/Dcn/

GO_BP_m1	GO:00080	regulation	15/2606	178/23843	0.887153	0.921068	0.875835	Cdc42ep5/
GO_BP_m1	GO:200011	negative re	8/2606	103/23843	0.887303	0.921068	0.875835	Cst6/Gpx1/
GO_BP_m1	GO:00081	actin polyn	17/2606	199/23843	0.887572	0.921068	0.875835	Abi1/Cdc4
GO_BP_m1	GO:00310	regeneratio	10/2606	125/23843	0.888276	0.921068	0.875835	Adm/Cdk1
GO_BP_m1	GO:00104	negative re	22/2606	251/23843	0.888984	0.921068	0.875835	Col28a1/C
GO_BP_m1	GO:000211	store-oper	1/2606	19/23843	0.889202	0.921068	0.875835	Stim2
GO_BP_m1	GO:00021	cytoplasmi	1/2606	19/23843	0.889202	0.921068	0.875835	Ythdf2
GO_BP_m1	GO:000271	negative re	1/2606	19/23843	0.889202	0.921068	0.875835	Sh2d1b2
GO_BP_m1	GO:000321	cardiac left	1/2606	19/23843	0.889202	0.921068	0.875835	Rnls
GO_BP_m1	GO:00075	dosage cor	1/2606	19/23843	0.889202	0.921068	0.875835	H2afy
GO_BP_m1	GO:00104	response t	1/2606	19/23843	0.889202	0.921068	0.875835	Slc9a1
GO_BP_m1	GO:00108	retina layer	1/2606	19/23843	0.889202	0.921068	0.875835	Foxn4
GO_BP_m1	GO:00182	protein O-	1/2606	19/23843	0.889202	0.921068	0.875835	Galnt9
GO_BP_m1	GO:00216	cerebellar	1/2606	19/23843	0.889202	0.921068	0.875835	Cend1
GO_BP_m1	GO:00302	platelet for	1/2606	19/23843	0.889202	0.921068	0.875835	Cib1
GO_BP_m1	GO:00308	polarized e	1/2606	19/23843	0.889202	0.921068	0.875835	Tcf15
GO_BP_m1	GO:003221	negative re	1/2606	19/23843	0.889202	0.921068	0.875835	Hnrnpc
GO_BP_m1	GO:00326	interleukin	1/2606	19/23843	0.889202	0.921068	0.875835	Il1rl1
GO_BP_m1	GO:003361	mitochond	1/2606	19/23843	0.889202	0.921068	0.875835	Smim20
GO_BP_m1	GO:003601	protein loc	1/2606	19/23843	0.889202	0.921068	0.875835	Ezr
GO_BP_m1	GO:00454	regulation	1/2606	19/23843	0.889202	0.921068	0.875835	Ifng
GO_BP_m1	GO:00487	pigment gr	1/2606	19/23843	0.889202	0.921068	0.875835	Rab32
GO_BP_m1	GO:00510	regulation	1/2606	19/23843	0.889202	0.921068	0.875835	Stx4a
GO_BP_m1	GO:00516	establishm	1/2606	19/23843	0.889202	0.921068	0.875835	Rhot2
GO_BP_m1	GO:007097	bone matu	1/2606	19/23843	0.889202	0.921068	0.875835	Rflna
GO_BP_m1	GO:00721	epithelial c	1/2606	19/23843	0.889202	0.921068	0.875835	Arx
GO_BP_m1	GO:00972	amyloid-b	1/2606	19/23843	0.889202	0.921068	0.875835	Itgam
GO_BP_m1	GO:190001	positive re	1/2606	19/23843	0.889202	0.921068	0.875835	Kars
GO_BP_m1	GO:19004	regulation	1/2606	19/23843	0.889202	0.921068	0.875835	Rab34
GO_BP_m1	GO:19030	positive re	1/2606	19/23843	0.889202	0.921068	0.875835	Fscn1
GO_BP_m1	GO:190527	regulation	1/2606	19/23843	0.889202	0.921068	0.875835	Gdnf
GO_BP_m1	GO:20001	regulation	1/2606	19/23843	0.889202	0.921068	0.875835	Tbx1
GO_BP_m1	GO:001057	vascular en	2/2606	33/23843	0.889401	0.921068	0.875835	Cxcl17/Ptg
GO_BP_m1	GO:00216	cerebellar	2/2606	33/23843	0.889401	0.921068	0.875835	Cend1/Sez
GO_BP_m1	GO:00430	Golgi to pl	2/2606	33/23843	0.889401	0.921068	0.875835	Bbs2/Rab3
GO_BP_m1	GO:00434	skeletal mu	2/2606	33/23843	0.889401	0.921068	0.875835	Gpx1/Wnt
GO_BP_m1	GO:00434	negative re	14/2606	168/23843	0.889698	0.921267	0.876025	Cactin/Fox
GO_BP_m1	GO:00063	DNA-temp	4/2606	58/23843	0.890939	0.922335	0.877041	Btbd18/Ell
GO_BP_m1	GO:00424	photorece	4/2606	58/23843	0.890939	0.922335	0.877041	Fscn2/Th/T
GO_BP_m1	GO:00308	regulation	15/2606	179/23843	0.891855	0.92282	0.877502	Cdc42ep5/
GO_BP_m1	GO:00148	striated mu	3/2606	46/23843	0.891933	0.92282	0.877502	Atp2b4/Gs
GO_BP_m1	GO:00181	peptidyl-c	3/2606	46/23843	0.891933	0.92282	0.877502	Adh5/Atp2
GO_BP_m1	GO:002177	olfactory b	3/2606	46/23843	0.891933	0.92282	0.877502	Arx/Mir141
GO_BP_m1	GO:007054	response t	3/2606	46/23843	0.891933	0.92282	0.877502	Cd36/Ran
GO_BP_m1	GO:00215	diencephal	5/2606	70/23843	0.892829	0.923529	0.878176	Arx/Ncam1
GO_BP_m1	GO:004874	muscle fibe	5/2606	70/23843	0.892829	0.923529	0.878176	Acta1/Gpx
GO_BP_m1	GO:00329	regulation	30/2606	334/23843	0.894573	0.925224	0.879787	Arhgap44/
GO_BP_m1	GO:00109	negative re	17/2606	201/23843	0.896337	0.92694	0.881419	Cst6/Fetub

GO_BP_m1	GO:003083	regulation	13/2606	159/23843	0.897386	0.927915	0.882347	Cdc42ep5/
GO_BP_m1	GO:001814	peptide cro	4/2606	59/23843	0.898505	0.928596	0.882994	Dcn/Lce3c/
GO_BP_m1	GO:006071	labyrinthin	4/2606	59/23843	0.898505	0.928596	0.882994	Adm/Gab1
GO_BP_m1	GO:003519	posttranscr	10/2606	127/23843	0.899018	0.928596	0.882994	Fmr1/Mael
GO_BP_m1	GO:000695	complemen	14/2606	170/23843	0.899022	0.928596	0.882994	C1rl/Ighv1-
GO_BP_m1	GO:003004	actin filame	14/2606	170/23843	0.899022	0.928596	0.882994	Cdc42ep5/
GO_BP_m1	GO:004326	negative re	2/2606	34/23843	0.899108	0.928596	0.882994	Cav1/Cav3
GO_BP_m1	GO:005508	monovalen	2/2606	34/23843	0.899108	0.928596	0.882994	Rnls/Slc12a
GO_BP_m1	GO:007087	regulation	2/2606	34/23843	0.899108	0.928596	0.882994	Esrrb/Ppp1
GO_BP_m1	GO:007139	cellular res	2/2606	34/23843	0.899108	0.928596	0.882994	Ranbp1/Zc
GO_BP_m1	GO:007238	organelle t	5/2606	71/23843	0.899706	0.928596	0.882994	Bloc1s5/Cc
GO_BP_m1	GO:004521	sarcomere	3/2606	47/23843	0.900229	0.928596	0.882994	Cav3/Hdac
GO_BP_m1	GO:000834	determinat	1/2606	20/23843	0.901322	0.928596	0.882994	Ercc5
GO_BP_m1	GO:001824	protein O-	1/2606	20/23843	0.901322	0.928596	0.882994	Galnt9
GO_BP_m1	GO:003106	positive reg	1/2606	20/23843	0.901322	0.928596	0.882994	BC004004
GO_BP_m1	GO:003228	myelin asse	1/2606	20/23843	0.901322	0.928596	0.882994	Ahnak2
GO_BP_m1	GO:003233	positive reg	1/2606	20/23843	0.901322	0.928596	0.882994	Por
GO_BP_m1	GO:003634	platelet mo	1/2606	20/23843	0.901322	0.928596	0.882994	Cib1
GO_BP_m1	GO:004209	interleukin-	1/2606	20/23843	0.901322	0.928596	0.882994	Glmn
GO_BP_m1	GO:004222	interleukin-	1/2606	20/23843	0.901322	0.928596	0.882994	Ifng
GO_BP_m1	GO:004253	tumor necr	1/2606	20/23843	0.901322	0.928596	0.882994	Il10
GO_BP_m1	GO:004253	regulation	1/2606	20/23843	0.901322	0.928596	0.882994	Il10
GO_BP_m1	GO:004350	skeletal mu	1/2606	20/23843	0.901322	0.928596	0.882994	Myh7
GO_BP_m1	GO:004855	embryonic	1/2606	20/23843	0.901322	0.928596	0.882994	Pdgfra
GO_BP_m1	GO:005122	cytoplasmi	1/2606	20/23843	0.901322	0.928596	0.882994	Lats1
GO_BP_m1	GO:005181	disruption	1/2606	20/23843	0.901322	0.928596	0.882994	Arg1
GO_BP_m1	GO:005188	killing of ce	1/2606	20/23843	0.901322	0.928596	0.882994	Arg1
GO_BP_m1	GO:005509	response to	1/2606	20/23843	0.901322	0.928596	0.882994	Cd36
GO_BP_m1	GO:006132	cell prolifer	1/2606	20/23843	0.901322	0.928596	0.882994	Tbx1
GO_BP_m1	GO:007171	basement m	1/2606	20/23843	0.901322	0.928596	0.882994	Flrt2
GO_BP_m1	GO:009878	response to	1/2606	20/23843	0.901322	0.928596	0.882994	Park2
GO_BP_m1	GO:009962	regulation	1/2606	20/23843	0.901322	0.928596	0.882994	Cav3
GO_BP_m1	GO:005134	negative re	36/2606	397/23843	0.902357	0.929554	0.883905	Angptl3/Bc
GO_BP_m1	GO:000661	protein exp	10/2606	128/23843	0.904058	0.931197	0.885467	Calr/Cdk5/
GO_BP_m1	GO:000190	cell killing	11/2606	139/23843	0.904542	0.931586	0.885837	Arg1/Cadm
GO_BP_m1	GO:190211	positive reg	5/2606	72/23843	0.906197	0.933181	0.887354	Cnot6l/Fscn
GO_BP_m1	GO:002198	olfactory lo	3/2606	48/23843	0.907945	0.934396	0.888509	Arx/Mir141
GO_BP_m1	GO:009951	vesicle cyto	3/2606	48/23843	0.907945	0.934396	0.888509	Bloc1s5/Kif
GO_BP_m1	GO:000682	iron ion tra	2/2606	35/23843	0.908015	0.934396	0.888509	Rep15/Slc4
GO_BP_m1	GO:004568	positive reg	2/2606	35/23843	0.908015	0.934396	0.888509	Foxc1/H2a
GO_BP_m1	GO:007136	cellular res	2/2606	35/23843	0.908015	0.934396	0.888509	Cfl1/Foxc1
GO_BP_m1	GO:190274	apoptotic p	2/2606	35/23843	0.908015	0.934396	0.888509	Foxc1/Wt1
GO_BP_m1	GO:004583	negative re	6/2606	84/23843	0.908347	0.934628	0.88873	Adora1/Ap
GO_BP_m1	GO:000183	epithelial to	10/2606	129/23843	0.908886	0.935073	0.889153	Foxa2/Foxc
GO_BP_m1	GO:190382	negative re	8/2606	107/23843	0.909796	0.9359	0.889939	Cdk5/Cldn
GO_BP_m1	GO:003003	contractile	7/2606	96/23843	0.911341	0.936204	0.890228	Ctgf/Itgb1b
GO_BP_m1	GO:004314	stress fiber	7/2606	96/23843	0.911341	0.936204	0.890228	Ctgf/Itgb1b
GO_BP_m1	GO:000269	positive reg	1/2606	21/23843	0.912116	0.936204	0.890228	Adam8

GO_BP_m1	GO:001074	regulation	1/2606	21/23843	0.912116	0.936204	0.890228	Cd36
GO_BP_m1	GO:003193	regulation	1/2606	21/23843	0.912116	0.936204	0.890228	Apobec1
GO_BP_m1	GO:003233	negative re	1/2606	21/23843	0.912116	0.936204	0.890228	Rflna
GO_BP_m1	GO:003246	regulation	1/2606	21/23843	0.912116	0.936204	0.890228	Pex5
GO_BP_m1	GO:003300	positive reg	1/2606	21/23843	0.912116	0.936204	0.890228	Ms4a2
GO_BP_m1	GO:003314	positive reg	1/2606	21/23843	0.912116	0.936204	0.890228	Pak1
GO_BP_m1	GO:004330	positive reg	1/2606	21/23843	0.912116	0.936204	0.890228	Ms4a2
GO_BP_m1	GO:004505	transcytosis	1/2606	21/23843	0.912116	0.936204	0.890228	Rab5a
GO_BP_m1	GO:004506	T-helper 1	1/2606	21/23843	0.912116	0.936204	0.890228	Jak3
GO_BP_m1	GO:004568	negative re	1/2606	21/23843	0.912116	0.936204	0.890228	Smo
GO_BP_m1	GO:004613	pyrimidine	1/2606	21/23843	0.912116	0.936204	0.890228	Nme6
GO_BP_m1	GO:005123	sequesteri	1/2606	21/23843	0.912116	0.936204	0.890228	Slc30a3
GO_BP_m1	GO:005145	myoblast p	1/2606	21/23843	0.912116	0.936204	0.890228	Gpx1
GO_BP_m1	GO:009028	positive reg	1/2606	21/23843	0.912116	0.936204	0.890228	Calcr
GO_BP_m1	GO:190174	positive reg	1/2606	21/23843	0.912116	0.936204	0.890228	Scgb3a1
GO_BP_m1	GO:200067	negative re	1/2606	21/23843	0.912116	0.936204	0.890228	Zfp593
GO_BP_m1	GO:000245	humoral i	15/2606	184/23843	0.913037	0.937039	0.891022	C1rl/Ighv1-
GO_BP_m1	GO:001406	phosphati	9/2606	119/23843	0.913848	0.937652	0.891606	Csf3/Dcn/
GO_BP_m1	GO:004348	regulation	9/2606	119/23843	0.913848	0.937652	0.891606	Ahnak2/Fm
GO_BP_m1	GO:000244	lymphocyte	34/2606	381/23843	0.914253	0.937958	0.891897	Aplf/Arg1/
GO_BP_m1	GO:000634	chromatin	8/2606	108/23843	0.914782	0.938391	0.892308	Apobec1/
GO_BP_m1	GO:009748	dendrite ex	2/2606	36/23843	0.916181	0.939498	0.89336	Cpne6/Par
GO_BP_m1	GO:190470	regulation	2/2606	36/23843	0.916181	0.939498	0.89336	Il10/Pak1
GO_BP_m1	GO:199087	vascular s	2/2606	36/23843	0.916181	0.939498	0.89336	Il10/Pak1
GO_BP_m1	GO:004205	regulation	4/2606	62/23843	0.918494	0.941759	0.895511	Adora1/G
GO_BP_m1	GO:190321	regulation	6/2606	86/23843	0.919282	0.942457	0.896175	Arih2/Kat2
GO_BP_m1	GO:005160	detection	43/2606	474/23843	0.919727	0.942804	0.896504	Adora1/An
GO_BP_m1	GO:000218	cytoplasmi	7/2606	98/23843	0.921401	0.942986	0.896678	Cpeb3/Cp
GO_BP_m1	GO:000209	auditory re	1/2606	22/23843	0.92173	0.942986	0.896678	Myo3a
GO_BP_m1	GO:000327	endocardia	1/2606	22/23843	0.92173	0.942986	0.896678	Nog
GO_BP_m1	GO:003270	negative re	1/2606	22/23843	0.92173	0.942986	0.896678	Ezr
GO_BP_m1	GO:003275	positive reg	1/2606	22/23843	0.92173	0.942986	0.896678	Sash3
GO_BP_m1	GO:003450	tooth mine	1/2606	22/23843	0.92173	0.942986	0.896678	Tbx1
GO_BP_m1	GO:004349	regulation	1/2606	22/23843	0.92173	0.942986	0.896678	Trhr
GO_BP_m1	GO:004592	negative re	1/2606	22/23843	0.92173	0.942986	0.896678	Plin5
GO_BP_m1	GO:005160	response t	1/2606	22/23843	0.92173	0.942986	0.896678	Cdk2
GO_BP_m1	GO:005179	regulation	1/2606	22/23843	0.92173	0.942986	0.896678	Smo
GO_BP_m1	GO:006043	trachea de	1/2606	22/23843	0.92173	0.942986	0.896678	Ano1
GO_BP_m1	GO:006060	branch elo	1/2606	22/23843	0.92173	0.942986	0.896678	Fgf1
GO_BP_m1	GO:006074	mammary	1/2606	22/23843	0.92173	0.942986	0.896678	Tnfsf11
GO_BP_m1	GO:006137	mammary	1/2606	22/23843	0.92173	0.942986	0.896678	Tnfsf11
GO_BP_m1	GO:007140	cellular res	1/2606	22/23843	0.92173	0.942986	0.896678	Cd36
GO_BP_m1	GO:007198	multivesicu	1/2606	22/23843	0.92173	0.942986	0.896678	Rab27b
GO_BP_m1	GO:007253	T-helper 1	1/2606	22/23843	0.92173	0.942986	0.896678	Smad7
GO_BP_m1	GO:009887	vesicle-me	5/2606	75/23843	0.923514	0.944193	0.897825	Arhgap44/
GO_BP_m1	GO:000037	RNA splici	20/2606	240/23843	0.923655	0.944193	0.897825	Fmr1/Hmx
GO_BP_m1	GO:000039	mRNA splic	20/2606	240/23843	0.923655	0.944193	0.897825	Fmr1/Hmx
GO_BP_m1	GO:002188	forebrain n	2/2606	37/23843	0.923662	0.944193	0.897825	Arx/Rac3

GO_BP_m1	GO:003820	TORC1 sign	2/2606	37/23843	0.923662	0.944193	0.897825	Dgkq/Szt2
GO_BP_m1	GO:004573	positive reg	2/2606	37/23843	0.923662	0.944193	0.897825	Ccnl1/Stil
GO_BP_m1	GO:007115	positive reg	2/2606	37/23843	0.923662	0.944193	0.897825	Cdkn1a/Rp
GO_BP_m1	GO:000695	complemen	15/2606	187/23843	0.924009	0.944437	0.898057	C1rl/Cfd/Ig
GO_BP_m1	GO:003307	T cell differ	6/2606	87/23843	0.924309	0.944634	0.898244	Adam8/Il2r
GO_BP_m1	GO:005109	regulation	34/2606	385/23843	0.924589	0.94481	0.898412	Abra/Adam
GO_BP_m1	GO:000037	RNA splicin	20/2606	241/23843	0.926691	0.946848	0.90035	Fmr1/Hmx
GO_BP_m1	GO:000640	mRNA exp	3/2606	51/23843	0.927952	0.947695	0.901155	Ddx19b/Sa
GO_BP_m1	GO:003090	midbrain d	3/2606	51/23843	0.927952	0.947695	0.901155	Kat2a/Kdm
GO_BP_m1	GO:004560	regulation	3/2606	51/23843	0.927952	0.947695	0.901155	Foxc1/H2a
GO_BP_m1	GO:007142	mRNA-con	3/2606	51/23843	0.927952	0.947695	0.901155	Ddx19b/Sa
GO_BP_m1	GO:003296	collagen m	6/2606	88/23843	0.929058	0.948715	0.902125	Arg1/Col5a
GO_BP_m1	GO:006500	protein-DN	14/2606	178/23843	0.930078	0.949204	0.90259	Cand1/Cen
GO_BP_m1	GO:000290	negative re	1/2606	23/23843	0.930293	0.949204	0.90259	Mir18b
GO_BP_m1	GO:001095	positive reg	1/2606	23/23843	0.930293	0.949204	0.90259	Gsn
GO_BP_m1	GO:003246	positive reg	1/2606	23/23843	0.930293	0.949204	0.90259	Snx9
GO_BP_m1	GO:004879	animal org	1/2606	23/23843	0.930293	0.949204	0.90259	Rflna
GO_BP_m1	GO:009034	negative re	1/2606	23/23843	0.930293	0.949204	0.90259	Prkdc
GO_BP_m1	GO:190470	positive reg	1/2606	23/23843	0.930293	0.949204	0.90259	Pak1
GO_BP_m1	GO:009717	ruffle assem	2/2606	38/23843	0.93051	0.949204	0.90259	Cav1/Dbnl
GO_BP_m1	GO:190280	positive reg	2/2606	38/23843	0.93051	0.949204	0.90259	Cul4a/Mtb
GO_BP_m1	GO:004208	cytokine bi	8/2606	112/23843	0.932429	0.950941	0.904241	Ccl20/Cebp
GO_BP_m1	GO:004581	negative re	8/2606	112/23843	0.932429	0.950941	0.904241	Apobec1/B
GO_BP_m1	GO:001065	negative re	3/2606	52/23843	0.933677	0.951993	0.905242	Alox12/Cav
GO_BP_m1	GO:003085	prostate gl	3/2606	52/23843	0.933677	0.951993	0.905242	Nog/Plag1
GO_BP_m1	GO:000660	protein targ	27/2606	317/23843	0.934234	0.95245	0.905677	Adora1/Ari
GO_BP_m1	GO:002198	pituitary gl	2/2606	39/23843	0.936773	0.954707	0.907823	Nog/Sox2
GO_BP_m1	GO:003164	killing of ce	2/2606	39/23843	0.936773	0.954707	0.907823	Arg1/Ifng
GO_BP_m1	GO:004436	disruption	2/2606	39/23843	0.936773	0.954707	0.907823	Arg1/Ifng
GO_BP_m1	GO:000637	mRNA splic	1/2606	24/23843	0.937919	0.954877	0.907985	Psip1
GO_BP_m1	GO:001570	bicarbonat	1/2606	24/23843	0.937919	0.954877	0.907985	Slc26a7
GO_BP_m1	GO:001626	O-glycan p	1/2606	24/23843	0.937919	0.954877	0.907985	Galnt9
GO_BP_m1	GO:003057	collagen ca	1/2606	24/23843	0.937919	0.954877	0.907985	Mmp14
GO_BP_m1	GO:004504	protein targ	1/2606	24/23843	0.937919	0.954877	0.907985	Folr2
GO_BP_m1	GO:005157	regulation	1/2606	24/23843	0.937919	0.954877	0.907985	Dmrtc2
GO_BP_m1	GO:190223	negative re	1/2606	24/23843	0.937919	0.954877	0.907985	Pgap2
GO_BP_m1	GO:190446	regulation	1/2606	24/23843	0.937919	0.954877	0.907985	Zc3h12a
GO_BP_m1	GO:199077	tumor necr	1/2606	24/23843	0.937919	0.954877	0.907985	Zc3h12a
GO_BP_m1	GO:000994	anterior/po	3/2606	53/23843	0.938981	0.955626	0.908697	Foxa2/Pgap
GO_BP_m1	GO:004438	protein loc	3/2606	53/23843	0.938981	0.955626	0.908697	Klhl21/Stil/
GO_BP_m1	GO:004854	digestive tr	3/2606	53/23843	0.938981	0.955626	0.908697	Cfc1/Ephb3
GO_BP_m1	GO:007058	protein loc	12/2606	159/23843	0.939457	0.955964	0.909018	Arih2/Grpe
GO_BP_m1	GO:001406	positive reg	4/2606	66/23843	0.939639	0.955964	0.909018	Csf3/Dcn/N
GO_BP_m1	GO:190118	regulation	4/2606	66/23843	0.939639	0.955964	0.909018	Adora1/Gp
GO_BP_m1	GO:000246	adaptive im	34/2606	393/23843	0.942213	0.958472	0.911403	Aplf/Arg1/
GO_BP_m1	GO:001055	regulation	2/2606	40/23843	0.942498	0.958651	0.911573	Jak3/Mt3
GO_BP_m1	GO:007110	DNA confo	16/2606	204/23843	0.94283	0.958877	0.911788	Bahd1/Blm
GO_BP_m1	GO:000721	gamma-am	1/2606	25/23843	0.944711	0.959568	0.912445	Gabra6

GO_BP_m1	GO:001074	macrophag	1/2606	25/23843	0.944711	0.959568	0.912445	Cd36
GO_BP_m1	GO:00108	negative re	1/2606	25/23843	0.944711	0.959568	0.912445	Nfkb1
GO_BP_m1	GO:00459	negative re	1/2606	25/23843	0.944711	0.959568	0.912445	Nfkb1
GO_BP_m1	GO:00483	immunogl	1/2606	25/23843	0.944711	0.959568	0.912445	Stx4a
GO_BP_m1	GO:00514	negative re	1/2606	25/23843	0.944711	0.959568	0.912445	Kank2
GO_BP_m1	GO:00607	regulation	1/2606	25/23843	0.944711	0.959568	0.912445	Hdac1
GO_BP_m1	GO:00725	T-helper 1	1/2606	25/23843	0.944711	0.959568	0.912445	Smad7
GO_BP_m1	GO:008601	cell-cell sig	1/2606	25/23843	0.944711	0.959568	0.912445	Cacnb2
GO_BP_m1	GO:009962	cardiac mu	1/2606	25/23843	0.944711	0.959568	0.912445	Cav3
GO_BP_m1	GO:190331	positive re	1/2606	25/23843	0.944711	0.959568	0.912445	Gsn
GO_BP_m1	GO:000004	autophago	6/2606	92/23843	0.945524	0.960282	0.913124	Atg2a/Ift88
GO_BP_m1	GO:00421	cytokine m	8/2606	116/23843	0.946798	0.961466	0.91425	Ccl20/Cebp
GO_BP_m1	GO:00101	potassium	2/2606	41/23843	0.947728	0.962187	0.914936	Atp1b2/Slc
GO_BP_m1	GO:00329	regulation	2/2606	41/23843	0.947728	0.962187	0.914936	Ctgf/Mkx
GO_BP_m1	GO:00300	lymphocyt	33/2606	386/23843	0.948476	0.962836	0.915552	Abl2/Adam
GO_BP_m1	GO:00066	protein tar	10/2606	140/23843	0.949748	0.964015	0.916674	Arih2/Grpe
GO_BP_m1	GO:00310	regulation	1/2606	26/23843	0.950761	0.964152	0.916804	BC004004
GO_BP_m1	GO:00325	DNA duple	1/2606	26/23843	0.950761	0.964152	0.916804	Blm
GO_BP_m1	GO:00332	regulation	1/2606	26/23843	0.950761	0.964152	0.916804	Hmg20a
GO_BP_m1	GO:00450	thymic T c	1/2606	26/23843	0.950761	0.964152	0.916804	Ptprc
GO_BP_m1	GO:00451	intermedia	1/2606	26/23843	0.950761	0.964152	0.916804	Des
GO_BP_m1	GO:00603	innervatior	1/2606	26/23843	0.950761	0.964152	0.916804	Ntf5
GO_BP_m1	GO:006071	labyrinthin	1/2606	26/23843	0.950761	0.964152	0.916804	Hs6st1
GO_BP_m1	GO:009007	foam cell d	1/2606	26/23843	0.950761	0.964152	0.916804	Cd36
GO_BP_m1	GO:00003	regulation	2/2606	42/23843	0.952502	0.965706	0.918282	Fmr1/Rbm
GO_BP_m1	GO:00017	eye photor	3/2606	56/23843	0.952623	0.965706	0.918282	Fscn2/Th/T
GO_BP_m1	GO:000222	innate imm	3/2606	56/23843	0.952623	0.965706	0.918282	Defa29/De
GO_BP_m1	GO:00160	immunogl	20/2606	253/23843	0.95589	0.968832	0.921254	Aplf/C1rl/I
GO_BP_m1	GO:00456	positive re	1/2606	27/23843	0.956148	0.968832	0.921254	Igfbp3
GO_BP_m1	GO:006014	positive re	1/2606	27/23843	0.956148	0.968832	0.921254	Scgb3a1
GO_BP_m1	GO:00716	regulation	1/2606	27/23843	0.956148	0.968832	0.921254	Ptgs2
GO_BP_m1	GO:00015	branching	2/2606	43/23843	0.956857	0.968991	0.921406	Dll4/Tbx1
GO_BP_m1	GO:00017	cell fate de	2/2606	43/23843	0.956857	0.968991	0.921406	Ntf5/Wnt7
GO_BP_m1	GO:000762	adult walki	2/2606	43/23843	0.956857	0.968991	0.921406	Abl2/Cend
GO_BP_m1	GO:00451	establishm	2/2606	43/23843	0.956857	0.968991	0.921406	Lrrd1/Tcf1
GO_BP_m1	GO:006164	histone H3	2/2606	43/23843	0.956857	0.968991	0.921406	Dmrtc2/Ka
GO_BP_m1	GO:19050	autophago	6/2606	96/23843	0.958476	0.970519	0.922858	Atg2a/Ift88
GO_BP_m1	GO:00726	establishm	11/2606	155/23843	0.958894	0.97083	0.923154	Arih2/Grpe
GO_BP_m1	GO:007237	protein act	15/2606	200/23843	0.959036	0.970863	0.923185	C1rl/Cfd/Ig
GO_BP_m1	GO:001972	B cell medi	20/2606	255/23843	0.95962	0.971118	0.923428	Aplf/C1rl/I
GO_BP_m1	GO:00198	cytolysis	2/2606	44/23843	0.960828	0.971118	0.923428	Gsdmd/Lyz
GO_BP_m1	GO:00451	intermedia	2/2606	44/23843	0.960828	0.971118	0.923428	Des/Sync
GO_BP_m1	GO:00906	walking be	2/2606	44/23843	0.960828	0.971118	0.923428	Abl2/Cend
GO_BP_m1	GO:00063	DNA replic	1/2606	28/23843	0.960947	0.971118	0.923428	Hat1
GO_BP_m1	GO:00159	ATP hydrol	1/2606	28/23843	0.960947	0.971118	0.923428	Atp6v0c
GO_BP_m1	GO:003267	regulation	1/2606	28/23843	0.960947	0.971118	0.923428	Sash3
GO_BP_m1	GO:004574	positive re	1/2606	28/23843	0.960947	0.971118	0.923428	Adora1
GO_BP_m1	GO:00716	transformi	1/2606	28/23843	0.960947	0.971118	0.923428	Ptgs2

GO_BP_m1	GO:007259	establishm	1/2606	28/23843	0.960947	0.971118	0.923428	Folr2
GO_BP_m1	GO:009066	ATP hydrol	1/2606	28/23843	0.960947	0.971118	0.923428	Atp6v0c
GO_BP_m1	GO:009913	ATP hydrol	1/2606	28/23843	0.960947	0.971118	0.923428	Atp6v0c
GO_BP_m1	GO:009913	ATP hydrol	1/2606	28/23843	0.960947	0.971118	0.923428	Atp6v0c
GO_BP_m1	GO:190002	regulation	1/2606	28/23843	0.960947	0.971118	0.923428	Cav1
GO_BP_m1	GO:190225	regulation	1/2606	28/23843	0.960947	0.971118	0.923428	Park2
GO_BP_m1	GO:006039	SMAD prot	5/2606	85/23843	0.962526	0.972601	0.924839	Bmp3/Gdf1
GO_BP_m1	GO:000182	blastocyst	6/2606	98/23843	0.963842	0.973708	0.92589	Cdh1/Esrrb
GO_BP_m1	GO:004642	positive re	6/2606	98/23843	0.963842	0.973708	0.92589	Hdac1/Hda
GO_BP_m1	GO:190301	regulation	2/2606	45/23843	0.964447	0.974207	0.926365	Jak3/Mt3
GO_BP_m1	GO:008200	bile acid m	1/2606	29/23843	0.96522	0.974316	0.926468	Atp8b1
GO_BP_m1	GO:001080	positive re	1/2606	29/23843	0.96522	0.974316	0.926468	Stox1
GO_BP_m1	GO:003472	DNA replic	1/2606	29/23843	0.96522	0.974316	0.926468	Hat1
GO_BP_m1	GO:004317	peptide ca	1/2606	29/23843	0.96522	0.974316	0.926468	Lvrn
GO_BP_m1	GO:006103	positive re	1/2606	29/23843	0.96522	0.974316	0.926468	Por
GO_BP_m1	GO:190179	negative re	1/2606	29/23843	0.96522	0.974316	0.926468	Park2
GO_BP_m1	GO:004203	regulation	6/2606	99/23843	0.96628	0.975274	0.927379	Ccl20/Glm
GO_BP_m1	GO:007595	lactation	3/2606	60/23843	0.966412	0.975295	0.9274	Aprt/Atp7b
GO_BP_m1	GO:004002	regulation	23/2606	292/23843	0.96699	0.975765	0.927847	Apobec1/A
GO_BP_m1	GO:001973	antibacteri	4/2606	74/23843	0.967682	0.976189	0.92825	Defa29/De
GO_BP_m1	GO:001071	regulation	2/2606	46/23843	0.967743	0.976189	0.92825	Ctgf/Mkx
GO_BP_m1	GO:007269	protein loc	2/2606	46/23843	0.967743	0.976189	0.92825	Stil/Ttk
GO_BP_m1	GO:003425	positive re	9/2606	136/23843	0.967861	0.976196	0.928256	Cpeb3/Csn
GO_BP_m1	GO:000633	chromatin	10/2606	148/23843	0.968333	0.97656	0.928603	Bahd1/Cen
GO_BP_m1	GO:190489	positive re	6/2606	100/23843	0.968567	0.976684	0.92872	Hdac1/Hda
GO_BP_m1	GO:003200	endocardia	1/2606	30/23843	0.969026	0.976698	0.928734	Nog
GO_BP_m1	GO:006056	apoptotic	1/2606	30/23843	0.969026	0.976698	0.928734	Foxc1
GO_BP_m1	GO:007153	protein loc	1/2606	30/23843	0.969026	0.976698	0.928734	Stil
GO_BP_m1	GO:190118	positive re	1/2606	30/23843	0.969026	0.976698	0.928734	Adora1
GO_BP_m1	GO:003149	chromatin	8/2606	125/23843	0.969669	0.977231	0.92924	Bahd1/Cen
GO_BP_m1	GO:003472	nucleosom	9/2606	137/23843	0.969777	0.977231	0.92924	Cenpa/H2a
GO_BP_m1	GO:004568	regulation	4/2606	75/23843	0.97017	0.977515	0.929511	Foxc1/H2a
GO_BP_m1	GO:001657	histone ubi	2/2606	47/23843	0.970744	0.977756	0.92974	Kdm2b/Rin
GO_BP_m1	GO:004224	tissue rege	2/2606	47/23843	0.970744	0.977756	0.92974	Gpx1/Wnt7
GO_BP_m1	GO:005105	negative re	2/2606	47/23843	0.970744	0.977756	0.92974	Nfkb1/Pdg
GO_BP_m1	GO:003400	neural retir	3/2606	62/23843	0.971792	0.978319	0.930275	Dll4/Foxn4
GO_BP_m1	GO:005186	protein aut	3/2606	62/23843	0.971792	0.978319	0.930275	Park2/Rnf1
GO_BP_m1	GO:006004	retina mor	3/2606	62/23843	0.971792	0.978319	0.930275	Foxn4/Nec
GO_BP_m1	GO:001406	regulation	5/2606	89/23843	0.972186	0.978319	0.930275	Csf3/Dcn/N
GO_BP_m1	GO:000308	regulation	1/2606	31/23843	0.972416	0.978319	0.930275	Drd3
GO_BP_m1	GO:000633	DNA replic	1/2606	31/23843	0.972416	0.978319	0.930275	Hat1
GO_BP_m1	GO:001598	energy cou	1/2606	31/23843	0.972416	0.978319	0.930275	Atp6v0c
GO_BP_m1	GO:003239	DNA geom	1/2606	31/23843	0.972416	0.978319	0.930275	Blm
GO_BP_m1	GO:003472	DNA replic	1/2606	31/23843	0.972416	0.978319	0.930275	Hat1
GO_BP_m1	GO:190550	protein loc	1/2606	31/23843	0.972416	0.978319	0.930275	Stil
GO_BP_m1	GO:001086	positive re	2/2606	48/23843	0.973474	0.979271	0.931181	Bmp3/Gdf1
GO_BP_m1	GO:004210	positive re	3/2606	63/23843	0.974166	0.979855	0.931736	Ccl20/Glm
GO_BP_m1	GO:000695	humoral in	28/2606	352/23843	0.974659	0.980238	0.9321	C1rl/Cfd/D

GO_BP_m1	GO:000635	regulation	1/2606	32/23843	0.975435	0.980646	0.932488	H2afy
GO_BP_m1	GO:001045	regulation	1/2606	32/23843	0.975435	0.980646	0.932488	Wnt3a
GO_BP_m1	GO:006048	lung epithe	1/2606	32/23843	0.975435	0.980646	0.932488	Foxa2
GO_BP_m1	GO:000244	mast cell m	2/2606	49/23843	0.975957	0.980646	0.932488	Ms4a2/Spc
GO_BP_m1	GO:003152	ruffle orga	2/2606	49/23843	0.975957	0.980646	0.932488	Cav1/Dbnl
GO_BP_m1	GO:003300	regulation	2/2606	49/23843	0.975957	0.980646	0.932488	Cd300lb/M
GO_BP_m1	GO:004501	actin nucle	2/2606	49/23843	0.975957	0.980646	0.932488	Gsn/Wipf1
GO_BP_m1	GO:006042	lung epithe	2/2606	49/23843	0.975957	0.980646	0.932488	Fgf7/Foxa2
GO_BP_m1	GO:004653	photorecep	4/2606	78/23843	0.976601	0.981181	0.932997	Fscn2/Th/T
GO_BP_m1	GO:004572	positive re	7/2606	117/23843	0.977089	0.981559	0.933356	Cpeb3/Fmr
GO_BP_m1	GO:001834	protein pal	1/2606	33/23843	0.978123	0.982016	0.933791	Map6d1
GO_BP_m1	GO:004852	positive re	1/2606	33/23843	0.978123	0.982016	0.933791	Uts2r
GO_BP_m1	GO:004856	embryonic	1/2606	33/23843	0.978123	0.982016	0.933791	Pdgfra
GO_BP_m1	GO:006047	lung cell di	1/2606	33/23843	0.978123	0.982016	0.933791	Foxa2
GO_BP_m1	GO:006074	prostate gl	1/2606	33/23843	0.978123	0.982016	0.933791	Nog
GO_BP_m1	GO:000689	Golgi to pl	2/2606	50/23843	0.978215	0.982016	0.933791	Bbs2/Rab3
GO_BP_m1	GO:005156	histone H3	1/2606	34/23843	0.980518	0.984103	0.935775	Dmrtc2
GO_BP_m1	GO:006051	prostate gl	1/2606	34/23843	0.980518	0.984103	0.935775	Nog
GO_BP_m1	GO:000633	nucleosom	6/2606	107/23843	0.980984	0.984346	0.936006	Cenpa/H2a
GO_BP_m1	GO:009010	positive re	6/2606	107/23843	0.980984	0.984346	0.936006	Bmp3/Flcn/
GO_BP_m1	GO:003263	interleukin-	1/2606	35/23843	0.98265	0.98568	0.937275	Sash3
GO_BP_m1	GO:003300	regulation	1/2606	35/23843	0.98265	0.98568	0.937275	Ms4a2
GO_BP_m1	GO:004330	regulation	1/2606	35/23843	0.98265	0.98568	0.937275	Ms4a2
GO_BP_m1	GO:000238	mucosal im	3/2606	68/23843	0.983446	0.986253	0.937819	Defa29/De
GO_BP_m1	GO:004557	mast cell a	3/2606	68/23843	0.983446	0.986253	0.937819	Cd300lb/M
GO_BP_m1	GO:004336	positive T c	1/2606	36/23843	0.984549	0.987247	0.938764	Ptprc
GO_BP_m1	GO:000225	organ or ti	3/2606	69/23843	0.984872	0.987457	0.938965	Defa29/De
GO_BP_m1	GO:003241	lysosome l	3/2606	70/23843	0.986179	0.988491	0.939948	Map6d1/M
GO_BP_m1	GO:003051	positive re	1/2606	37/23843	0.98624	0.988491	0.939948	Kcp
GO_BP_m1	GO:006067	placenta bl	1/2606	37/23843	0.98624	0.988491	0.939948	Hs6st1
GO_BP_m1	GO:000038	alternative	2/2606	55/23843	0.986752	0.988891	0.940328	Fmr1/Rbm
GO_BP_m1	GO:006184	antimicrob	4/2606	85/23843	0.986898	0.988925	0.94036	Defa29/De
GO_BP_m1	GO:003278	positive re	1/2606	38/23843	0.987747	0.989662	0.941061	Atp1b2
GO_BP_m1	GO:004346	regulation	2/2606	57/23843	0.989162	0.990967	0.942302	Atp1b2/Cn
GO_BP_m1	GO:003519	production	1/2606	41/23843	0.991347	0.992958	0.944195	Zc3h12a
GO_BP_m1	GO:001973	antimicrob	5/2606	104/23843	0.991386	0.992958	0.944195	Defa29/De
GO_BP_m1	GO:005090	detection c	28/2606	377/23843	0.991488	0.992958	0.944195	Adora1/An
GO_BP_m1	GO:001692	protein sur	1/2606	42/23843	0.992294	0.993425	0.944639	Hmg20a
GO_BP_m1	GO:003105	dsRNA frag	1/2606	42/23843	0.992294	0.993425	0.944639	Zc3h12a
GO_BP_m1	GO:007091	production	1/2606	42/23843	0.992294	0.993425	0.944639	Zc3h12a
GO_BP_m1	GO:004510	intermedia	1/2606	43/23843	0.993138	0.994156	0.945335	Des
GO_BP_m1	GO:003052	androgen r	1/2606	45/23843	0.994558	0.995465	0.946579	Hdac1
GO_BP_m1	GO:000227	mast cell a	1/2606	48/23843	0.996157	0.996725	0.947777	Ms4a2
GO_BP_m1	GO:000636	transcripti	1/2606	48/23843	0.996157	0.996725	0.947777	H2afy
GO_BP_m1	GO:004330	mast cell d	1/2606	48/23843	0.996157	0.996725	0.947777	Ms4a2
GO_BP_m1	GO:005090	sensory pe	2/2606	70/23843	0.997123	0.997577	0.948588	Cd36/Trpm
GO_BP_m1	GO:001923	response t	4/2606	105/23843	0.997704	0.998045	0.949033	Gng8/Vmn
GO_BP_m1	GO:004505	T cell selec	1/2606	54/23843	0.998084	0.998312	0.949286	Ptprc

GO_BP_m1	GO:000959	detection c	21/2606	337/23843	0.998959	0.999073	0.95001	Foxa2/Kcn
GO_BP_m1	GO:005090	detection c	18/2606	308/23843	0.999337	0.999337	0.950261	Olfr1180/C
GO_BP_m2	GO:000641	regulation	21/470	401/23843	5.38E-05	0.14701	0.137635	2810006K2
GO_BP_m2	GO:001060	posttranscr	23/470	471/23843	7.01E-05	0.14701	0.137635	2810006K2
GO_BP_m2	GO:003424	regulation	21/470	441/23843	0.000202	0.175617	0.164418	2810006K2
GO_BP_m2	GO:003647	neuron de	3/470	7/23843	0.000251	0.175617	0.164418	Rack1/Nr4
GO_BP_m2	GO:190320	regulation	3/470	7/23843	0.000251	0.175617	0.164418	Rack1/Nr4
GO_BP_m2	GO:190320	negative re	3/470	7/23843	0.000251	0.175617	0.164418	Rack1/Nr4
GO_BP_m2	GO:190331	negative re	7/470	77/23843	0.00081	0.365555	0.342244	Dhx34/Dyr
GO_BP_m2	GO:190320	negative re	4/470	22/23843	0.000823	0.365555	0.342244	Atf4/Rack1
GO_BP_m2	GO:000243	Fc recepto	3/470	11/23843	0.001116	0.365555	0.342244	Csk/Myo1
GO_BP_m2	GO:000685	extracellul	2/470	3/23843	0.001148	0.365555	0.342244	Arrdc1/Tsg
GO_BP_m2	GO:005103	snRNA tra	2/470	3/23843	0.001148	0.365555	0.342244	Phax/Ran
GO_BP_m2	GO:007036	positive re	2/470	3/23843	0.001148	0.365555	0.342244	Bmp4/Fox
GO_BP_m2	GO:010602	regulation	2/470	3/23843	0.001148	0.365555	0.342244	Ralb/Stxbp
GO_BP_m2	GO:000655	leucine cat	2/470	4/23843	0.002266	0.365555	0.342244	Hmgcl/Ivd
GO_BP_m2	GO:003609	positive re	2/470	4/23843	0.002266	0.365555	0.342244	Atf4/Chd6
GO_BP_m2	GO:007036	regulation	2/470	4/23843	0.002266	0.365555	0.342244	Bmp4/Fox
GO_BP_m2	GO:009023	regulation	2/470	4/23843	0.002266	0.365555	0.342244	H3f3b/Tra
GO_BP_m2	GO:000619	cAMP catal	3/470	14/23843	0.002356	0.365555	0.342244	Rack1/Pde
GO_BP_m2	GO:000648	protein de	4/470	29/23843	0.002395	0.365555	0.342244	Alkbh4/Hr/
GO_BP_m2	GO:000821	protein de	4/470	29/23843	0.002395	0.365555	0.342244	Alkbh4/Hr/
GO_BP_m2	GO:003647	neuron de	4/470	29/23843	0.002395	0.365555	0.342244	Atf4/Rack1
GO_BP_m2	GO:190320	regulation	4/470	29/23843	0.002395	0.365555	0.342244	Atf4/Rack1
GO_BP_m2	GO:004580	negative re	5/470	49/23843	0.002722	0.365555	0.342244	Csk/Rack1/
GO_BP_m2	GO:003246	positive re	4/470	31/23843	0.003077	0.365555	0.342244	Aurkb/Chm
GO_BP_m2	GO:190331	regulation	11/470	213/23843	0.003499	0.365555	0.342244	Dhx34/Dyr
GO_BP_m2	GO:003209	positive re	7/470	100/23843	0.003669	0.365555	0.342244	Agrn/Bam
GO_BP_m2	GO:005103	regulation	2/470	5/23843	0.003728	0.365555	0.342244	Chmp3/Ra
GO_BP_m2	GO:005068	negative re	4/470	33/23843	0.003879	0.365555	0.342244	Dyrk1a/Hn
GO_BP_m2	GO:003466	ncRNA me	18/470	453/23843	0.004121	0.365555	0.342244	Chd7/Ell/E
GO_BP_m2	GO:006164	cytoskelet	6/470	77/23843	0.004142	0.365555	0.342244	Alkbh4/Au
GO_BP_m2	GO:000921	cyclic nucl	3/470	17/23843	0.004213	0.365555	0.342244	Rack1/Pde
GO_BP_m2	GO:004326	negative re	4/470	34/23843	0.004329	0.365555	0.342244	Agrn/Atf4/
GO_BP_m2	GO:005129	protein het	9/470	159/23843	0.004396	0.365555	0.342244	Agrn/Chm
GO_BP_m2	GO:003647	cell death i	4/470	35/23843	0.004813	0.365555	0.342244	Rack1/Nr4
GO_BP_m2	GO:005076	negative re	3/470	18/23843	0.004982	0.365555	0.342244	Csk/Rack1/
GO_BP_m2	GO:000640	mRNA cat	10/470	193/23843	0.00513	0.365555	0.342244	Dhx34/Ela
GO_BP_m2	GO:001714	negative re	11/470	225/23843	0.005268	0.365555	0.342244	Bmp4/Dnd
GO_BP_m2	GO:000016	phosphore	2/470	6/23843	0.005519	0.365555	0.342244	Kcnh2/Kcn
GO_BP_m2	GO:003648	intrinsic ap	2/470	6/23843	0.005519	0.365555	0.342244	Pdcd10/Pi
GO_BP_m2	GO:007210	glomerulu	2/470	6/23843	0.005519	0.365555	0.342244	Bmp4/Not
GO_BP_m2	GO:007210	glomerular	2/470	6/23843	0.005519	0.365555	0.342244	Bmp4/Not
GO_BP_m2	GO:003225	methylatio	14/470	327/23843	0.005741	0.365555	0.342244	Auts2/Ftsj1
GO_BP_m2	GO:000231	mature B c	3/470	19/23843	0.005831	0.365555	0.342244	Itfg2/Lfng/
GO_BP_m2	GO:000091	cytokinesis	9/470	167/23843	0.006033	0.365555	0.342244	Alkbh4/Au
GO_BP_m2	GO:190211	regulation	9/470	171/23843	0.00701	0.365555	0.342244	Cep120/Cr
GO_BP_m2	GO:012003	regulation	9/470	172/23843	0.007272	0.365555	0.342244	Agrn/Auts

GO_BP_m2	GO:000655	leucine me	2/470	7/23843	0.007626	0.365555	0.342244	Hmgcl/Ivd
GO_BP_m2	GO:003608	cleavage fu	2/470	7/23843	0.007626	0.365555	0.342244	Aurkb/Spin
GO_BP_m2	GO:004695	cellular ket	2/470	7/23843	0.007626	0.365555	0.342244	Hmgcl/Oxc
GO_BP_m2	GO:006023	lens induct	2/470	7/23843	0.007626	0.365555	0.342244	Bmp4/Six3
GO_BP_m2	GO:006143	renal system	2/470	7/23843	0.007626	0.365555	0.342244	Bmp4/Notc
GO_BP_m2	GO:006143	kidney vasc	2/470	7/23843	0.007626	0.365555	0.342244	Bmp4/Notc
GO_BP_m2	GO:007234	rescue of s	2/470	7/23843	0.007626	0.365555	0.342244	2810006K2
GO_BP_m2	GO:001660	Rac protein	4/470	40/23843	0.007777	0.365555	0.342244	Arap3/Auts
GO_BP_m2	GO:006049	regulation	9/470	174/23843	0.007819	0.365555	0.342244	Agrn/Auts2
GO_BP_m2	GO:001888	liver develo	7/470	115/23843	0.007823	0.365555	0.342244	Bmp4/Ceb
GO_BP_m2	GO:004341	macromole	12/470	273/23843	0.008322	0.365555	0.342244	Auts2/Ftsj1
GO_BP_m2	GO:000037	RNA splicin	11/470	240/23843	0.008397	0.365555	0.342244	Cdc5l/Dyrk
GO_BP_m2	GO:000039	mRNA splic	11/470	240/23843	0.008397	0.365555	0.342244	Cdc5l/Dyrk
GO_BP_m2	GO:004572	positive reg	7/470	117/23843	0.008565	0.365555	0.342244	Dnd1/Eif4g
GO_BP_m2	GO:000037	RNA splicin	11/470	241/23843	0.008648	0.365555	0.342244	Cdc5l/Dyrk
GO_BP_m2	GO:003424	negative re	11/470	241/23843	0.008648	0.365555	0.342244	Bmp4/Dnd
GO_BP_m2	GO:003250	cytokinetic	3/470	22/23843	0.008871	0.365555	0.342244	Alkbh4/Aur
GO_BP_m2	GO:007187	cellular res	3/470	22/23843	0.008871	0.365555	0.342244	Atf4/Nr4a3
GO_BP_m2	GO:005068	regulation	7/470	118/23843	0.008956	0.365555	0.342244	Dyrk1a/Hn
GO_BP_m2	GO:006100	hepaticobil	7/470	118/23843	0.008956	0.365555	0.342244	Bmp4/Ceb
GO_BP_m2	GO:001810	peptidyl-ty	13/470	310/23843	0.008973	0.365555	0.342244	Agrn/Angp
GO_BP_m2	GO:000026	mitochond	4/470	42/23843	0.009236	0.365555	0.342244	Cox10/Mtfp
GO_BP_m2	GO:007182	protein-DN	10/470	211/23843	0.009378	0.365555	0.342244	Asf1a/Chaf
GO_BP_m2	GO:001821	peptidyl-ty	13/470	313/23843	0.009675	0.365555	0.342244	Agrn/Angp
GO_BP_m2	GO:004875	semicircula	2/470	8/23843	0.010036	0.365555	0.342244	Chd7/Nr4a
GO_BP_m2	GO:007186	cellular res	3/470	23/23843	0.010054	0.365555	0.342244	Atf4/Nr4a3
GO_BP_m2	GO:007186	response to	3/470	23/23843	0.010054	0.365555	0.342244	Atf4/Nr4a3
GO_BP_m2	GO:014011	extracellula	3/470	23/23843	0.010054	0.365555	0.342244	Arrdc1/Rab
GO_BP_m2	GO:000233	mature B c	3/470	24/23843	0.011325	0.365555	0.342244	Itfg2/Lfng/
GO_BP_m2	GO:004572	positive reg	3/470	24/23843	0.011325	0.365555	0.342244	Cep120/Cr
GO_BP_m2	GO:004802	negative re	3/470	24/23843	0.011325	0.365555	0.342244	Dyrk1a/Hn
GO_BP_m2	GO:007186	response to	3/470	24/23843	0.011325	0.365555	0.342244	Atf4/Nr4a3
GO_BP_m2	GO:006195	establishme	4/470	45/23843	0.011742	0.365555	0.342244	Csk/Rack1/
GO_BP_m2	GO:007259	establishme	16/470	430/23843	0.011919	0.365555	0.342244	Bmp4/Ect2
GO_BP_m2	GO:004339	regulation	10/470	220/23843	0.012317	0.365555	0.342244	Agrn/Aplp2
GO_BP_m2	GO:000164	osteoblast	9/470	188/23843	0.01257	0.365555	0.342244	Asf1a/Bmp
GO_BP_m2	GO:003465	nucleobase	15/470	396/23843	0.012612	0.365555	0.342244	Dhx34/Elav
GO_BP_m2	GO:190103	negative re	3/470	25/23843	0.012685	0.365555	0.342244	Rack1/Nr4a
GO_BP_m2	GO:190320	negative re	3/470	25/23843	0.012685	0.365555	0.342244	Rack1/Nr4a
GO_BP_m2	GO:200103	negative re	3/470	25/23843	0.012685	0.365555	0.342244	Rack1/Nr4a
GO_BP_m2	GO:003232	alanine tran	2/470	9/23843	0.012736	0.365555	0.342244	Slc36a4/Slc
GO_BP_m2	GO:004299	regulation	2/470	9/23843	0.012736	0.365555	0.342244	Csk/Rack1
GO_BP_m2	GO:004825	elastic fiber	2/470	9/23843	0.012736	0.365555	0.342244	Mfap4/Myh
GO_BP_m2	GO:009853	histone H3	2/470	9/23843	0.012736	0.365555	0.342244	Hist1h1e/S
GO_BP_m2	GO:190222	ketone bod	2/470	9/23843	0.012736	0.365555	0.342244	Hmgcl/Oxc
GO_BP_m2	GO:000218	cytoplasmi	6/470	98/23843	0.013053	0.365555	0.342244	Eif5/Ftsj1/N
GO_BP_m2	GO:005188	regulation	5/470	71/23843	0.013083	0.365555	0.342244	Rack1/Heb
GO_BP_m2	GO:004427	cellular nitr	16/470	435/23843	0.013174	0.365555	0.342244	Dhx34/Elav

GO_BP_m2	GO:01200	positive re	6/470	99/23843	0.013672	0.365555	0.342244	Agrn/Auts
GO_BP_m2	GO:00315	protein-co	9/470	191/23843	0.013819	0.365555	0.342244	Ap2b1/Hn
GO_BP_m2	GO:00064	RNA catab	10/470	224/23843	0.013827	0.365555	0.342244	Dhx34/Elav
GO_BP_m2	GO:190211	positive re	5/470	72/23843	0.013838	0.365555	0.342244	Cep120/Cr
GO_BP_m2	GO:00083	RNA splici	14/470	365/23843	0.014161	0.365555	0.342244	Cdc5l/Clk1
GO_BP_m2	GO:00108	positive re	4/470	48/23843	0.014646	0.365555	0.342244	Bmp4/Gdf
GO_BP_m2	GO:00467	heterocycl	16/470	441/23843	0.014815	0.365555	0.342244	Dhx34/Elav
GO_BP_m2	GO:00512	protein tet	8/470	162/23843	0.015276	0.365555	0.342244	Acaca/Ads
GO_BP_m2	GO:00324	regulation	5/470	74/23843	0.015436	0.365555	0.342244	Aurkb/Chn
GO_BP_m2	GO:001657	histone de	3/470	27/23843	0.015671	0.365555	0.342244	Hr/Jmjd6/
GO_BP_m2	GO:00331	negative re	3/470	27/23843	0.015671	0.365555	0.342244	Rack1/Gpd
GO_BP_m2	GO:00360	positive re	3/470	27/23843	0.015671	0.365555	0.342244	Atf4/Chd6/
GO_BP_m2	GO:19032	negative re	4/470	49/23843	0.015706	0.365555	0.342244	Atf4/Rack1
GO_BP_m2	GO:000231	marginal z	2/470	10/23843	0.015714	0.365555	0.342244	Lfng/Ptk2b
GO_BP_m2	GO:000314	membrano	2/470	10/23843	0.015714	0.365555	0.342244	Bmp4/Id2
GO_BP_m2	GO:00442	small mole	12/470	298/23843	0.015767	0.365555	0.342244	Acat2/Echc
GO_BP_m2	GO:00068	mitochond	11/470	263/23843	0.015783	0.365555	0.342244	Bloc1s2/Cr
GO_BP_m2	GO:00711	ribonucleo	5/470	75/23843	0.016279	0.365555	0.342244	Hnrnpa2b1
GO_BP_m2	GO:00900	positive re	10/470	230/23843	0.016345	0.365555	0.342244	Aurkb/Cep
GO_BP_m2	GO:00351	hindlimb m	4/470	50/23843	0.016813	0.365555	0.342244	Aff3/Bmp4
GO_BP_m2	GO:19004	negative re	4/470	50/23843	0.016813	0.365555	0.342244	Atf4/Rack1
GO_BP_m2	GO:00459	negative re	3/470	28/23843	0.0173	0.365555	0.342244	Bmp4/Lfng
GO_BP_m2	GO:006101	regulation	6/470	105/23843	0.017816	0.365555	0.342244	Dhx34/Elav
GO_BP_m2	GO:190201	regulation	4/470	51/23843	0.017967	0.365555	0.342244	Cep120/Cr
GO_BP_m2	GO:00063	tRNA meta	8/470	167/23843	0.018014	0.365555	0.342244	Eprs/Exosc
GO_BP_m2	GO:00342	positive re	7/470	136/23843	0.01841	0.365555	0.342244	Dnd1/Eif4
GO_BP_m2	GO:00000	urea cycle	2/470	11/23843	0.018957	0.365555	0.342244	Cad/Cebpa
GO_BP_m2	GO:00182	protein-ch	2/470	11/23843	0.018957	0.365555	0.342244	Ambp/Cry
GO_BP_m2	GO:00309	astral micr	2/470	11/23843	0.018957	0.365555	0.342244	Cep120/Ra
GO_BP_m2	GO:004204	olfactory b	2/470	11/23843	0.018957	0.365555	0.342244	Chd7/Lmx
GO_BP_m2	GO:004361	regulation	2/470	11/23843	0.018957	0.365555	0.342244	Atf4/Chd6
GO_BP_m2	GO:006087	semicircula	2/470	11/23843	0.018957	0.365555	0.342244	Chd7/Nr4a
GO_BP_m2	GO:00721	glomerulus	2/470	11/23843	0.018957	0.365555	0.342244	Bmp4/Not
GO_BP_m2	GO:190024	regulation	2/470	11/23843	0.018957	0.365555	0.342244	Sh3gl1/Syt
GO_BP_m2	GO:199044	positive re	2/470	11/23843	0.018957	0.365555	0.342244	Atf4/Mbtp
GO_BP_m2	GO:20002	positive re	2/470	11/23843	0.018957	0.365555	0.342244	Agrp/Nr4a
GO_BP_m2	GO:00082	bile acid m	3/470	29/23843	0.01902	0.365555	0.342244	Fabp6/Gba
GO_BP_m2	GO:00091	purine ribo	3/470	29/23843	0.01902	0.365555	0.342244	Rack1/Pde
GO_BP_m2	GO:00092	ribonucleo	3/470	29/23843	0.01902	0.365555	0.342244	Rack1/Pde
GO_BP_m2	GO:003311	negative re	3/470	29/23843	0.01902	0.365555	0.342244	Dyrk1a/Hn
GO_BP_m2	GO:00421	heme meta	3/470	29/23843	0.01902	0.365555	0.342244	Alad/Cox1
GO_BP_m2	GO:00347	nucleosom	7/470	137/23843	0.019085	0.365555	0.342244	Asf1a/Chaf
GO_BP_m2	GO:00194	aromatic c	16/470	455/23843	0.01926	0.365555	0.342244	Dhx34/Elav
GO_BP_m2	GO:00457	positive re	13/470	343/23843	0.019294	0.365555	0.342244	Aurkb/Cep
GO_BP_m2	GO:00009	nuclear-tra	6/470	107/23843	0.019369	0.365555	0.342244	Dhx34/Exo
GO_BP_m2	GO:00032	right ventri	1/470	1/23843	0.019712	0.365555	0.342244	Chd7
GO_BP_m2	GO:000604	UDP-N-ac	1/470	1/23843	0.019712	0.365555	0.342244	Mgat1
GO_BP_m2	GO:00064	snRNA exp	1/470	1/23843	0.019712	0.365555	0.342244	Phax

GO_BP_m2	GO:000707	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Sirt7
GO_BP_m2	GO:000750	mesoderm	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:000944	pyruvate o	1/470	1/23843	0.019712	0.365555	0.342244	Nr4a3
GO_BP_m2	GO:001012	arginine ca	1/470	1/23843	0.019712	0.365555	0.342244	Oat
GO_BP_m2	GO:001839	peptidyl-ly	1/470	1/23843	0.019712	0.365555	0.342244	Jmjd6
GO_BP_m2	GO:001949	arginine ca	1/470	1/23843	0.019712	0.365555	0.342244	Oat
GO_BP_m2	GO:001954	arginine ca	1/470	1/23843	0.019712	0.365555	0.342244	Oat
GO_BP_m2	GO:002157	rhombome	1/470	1/23843	0.019712	0.365555	0.342244	Mafb
GO_BP_m2	GO:003080	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Rack1
GO_BP_m2	GO:003082	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Rack1
GO_BP_m2	GO:003127	lateral pseu	1/470	1/23843	0.019712	0.365555	0.342244	Klhl41
GO_BP_m2	GO:003127	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Klhl41
GO_BP_m2	GO:003128	actin phos	1/470	1/23843	0.019712	0.365555	0.342244	Twf1
GO_BP_m2	GO:003230	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Acsl4
GO_BP_m2	GO:003312	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Rack1
GO_BP_m2	GO:003349	cholesterol	1/470	1/23843	0.019712	0.365555	0.342244	Sc5d
GO_BP_m2	GO:003423	islet amylo	1/470	1/23843	0.019712	0.365555	0.342244	Pcsk2
GO_BP_m2	GO:003809	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Nr4a3
GO_BP_m2	GO:004294	D-alanine	1/470	1/23843	0.019712	0.365555	0.342244	Slc7a10
GO_BP_m2	GO:004309	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Gchfr
GO_BP_m2	GO:004310	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Gchfr
GO_BP_m2	GO:004353	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Twf1
GO_BP_m2	GO:004579	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Acat2
GO_BP_m2	GO:004629	formaldehy	1/470	1/23843	0.019712	0.365555	0.342244	Kdm3a
GO_BP_m2	GO:004665	folic acid c	1/470	1/23843	0.019712	0.365555	0.342244	Pm20d2
GO_BP_m2	GO:004803	heme o me	1/470	1/23843	0.019712	0.365555	0.342244	Cox10
GO_BP_m2	GO:004803	heme O bi	1/470	1/23843	0.019712	0.365555	0.342244	Cox10
GO_BP_m2	GO:004839	intermedia	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:004839	intermedia	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:004839	intermedia	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:004869	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Spg20
GO_BP_m2	GO:005501	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:005502	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:006050	bud dilatio	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:006114	BMP signal	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:006115	renal syste	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:006115	BMP signal	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:006115	pulmonary	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:006116	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Dkk4
GO_BP_m2	GO:006117	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Dkk4
GO_BP_m2	GO:006118	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Sfrp2
GO_BP_m2	GO:006121	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007007	histone arg	1/470	1/23843	0.019712	0.365555	0.342244	Jmjd6
GO_BP_m2	GO:007007	histone H3	1/470	1/23843	0.019712	0.365555	0.342244	Jmjd6
GO_BP_m2	GO:007007	histone H4	1/470	1/23843	0.019712	0.365555	0.342244	Jmjd6
GO_BP_m2	GO:007018	mitochond	1/470	1/23843	0.019712	0.365555	0.342244	Wars2
GO_BP_m2	GO:007161	IP-10 prod	1/470	1/23843	0.019712	0.365555	0.342244	Mavs
GO_BP_m2	GO:007165	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Mavs

GO_BP_m2	GO:007166	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Mavs
GO_BP_m2	GO:007189	BMP signal	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007197	cell gliding	1/470	1/23843	0.019712	0.365555	0.342244	Myo1g
GO_BP_m2	GO:007209	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007209	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007209	anterior/po	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007210	specificatio	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007210	specificatio	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007219	ureter epith	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:007220	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:009858	innate voca	1/470	1/23843	0.019712	0.365555	0.342244	Auts2
GO_BP_m2	GO:010602	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Stxbp1
GO_BP_m2	GO:012011	T cell mean	1/470	1/23843	0.019712	0.365555	0.342244	Myo1g
GO_BP_m2	GO:190024	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Syt11
GO_BP_m2	GO:190196	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:190216	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Pcbp4
GO_BP_m2	GO:190327	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Agrn
GO_BP_m2	GO:190340	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Agrn
GO_BP_m2	GO:190385	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Pink1
GO_BP_m2	GO:190385	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Pink1
GO_BP_m2	GO:190424	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Pabpn1
GO_BP_m2	GO:190448	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Acat2
GO_BP_m2	GO:190456	response to	1/470	1/23843	0.019712	0.365555	0.342244	Cdc5l
GO_BP_m2	GO:190456	cellular resp	1/470	1/23843	0.019712	0.365555	0.342244	Cdc5l
GO_BP_m2	GO:190473	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Acat2
GO_BP_m2	GO:190498	glycine imp	1/470	1/23843	0.019712	0.365555	0.342244	Slc25a38
GO_BP_m2	GO:190516	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Syt11
GO_BP_m2	GO:190545	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Zbtb1
GO_BP_m2	GO:190546	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Syt11
GO_BP_m2	GO:190546	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Syt11
GO_BP_m2	GO:200000	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:200000	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:200000	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:200000	negative re	1/470	1/23843	0.019712	0.365555	0.342244	Bmp4
GO_BP_m2	GO:200017	regulation	1/470	1/23843	0.019712	0.365555	0.342244	Zbtb1
GO_BP_m2	GO:200017	positive reg	1/470	1/23843	0.019712	0.365555	0.342244	Zbtb1
GO_BP_m2	GO:005068	negative re	7/470	138/23843	0.019776	0.365555	0.342244	Bmp4/Ift12
GO_BP_m2	GO:007098	demethylat	4/470	53/23843	0.020421	0.369792	0.346211	Alkbh4/Hr/
GO_BP_m2	GO:190288	negative re	4/470	53/23843	0.020421	0.369792	0.346211	Atf4/Rack1
GO_BP_m2	GO:000647	protein me	8/470	171/23843	0.020446	0.369792	0.346211	Auts2/Hist1
GO_BP_m2	GO:000821	protein alk	8/470	171/23843	0.020446	0.369792	0.346211	Auts2/Hist1
GO_BP_m2	GO:004259	response to	8/470	171/23843	0.020446	0.369792	0.346211	Atf4/Cad/F
GO_BP_m2	GO:007030	cellular resp	5/470	80/23843	0.020952	0.377316	0.353255	Ect2/Rack1
GO_BP_m2	GO:004802	regulation	5/470	81/23843	0.021981	0.386164	0.361538	Dyrk1a/Hn
GO_BP_m2	GO:003510	appendage	8/470	174/23843	0.022417	0.386164	0.361538	Aff3/Bmp4
GO_BP_m2	GO:003510	limb morph	8/470	174/23843	0.022417	0.386164	0.361538	Aff3/Bmp4
GO_BP_m2	GO:001834	protein pre	2/470	12/23843	0.022456	0.386164	0.361538	Agrn/Cox1
GO_BP_m2	GO:001962	urea metab	2/470	12/23843	0.022456	0.386164	0.361538	Cad/Cebpa

GO_BP_m2	GO:004594	positive re	2/470	12/23843	0.022456	0.386164	0.361538	Cebpa/Ell
GO_BP_m2	GO:004685	inositol ph	2/470	12/23843	0.022456	0.386164	0.361538	Mtmr2/Mt
GO_BP_m2	GO:004873	cardiac mu	2/470	12/23843	0.022456	0.386164	0.361538	Bmp4/Myh
GO_BP_m2	GO:007036	hepatocyte	2/470	12/23843	0.022456	0.386164	0.361538	Bmp4/Foxa
GO_BP_m2	GO:007128	cellular res	2/470	12/23843	0.022456	0.386164	0.361538	Cebpa/Id2
GO_BP_m2	GO:009735	prenylation	2/470	12/23843	0.022456	0.386164	0.361538	Agrn/Cox1
GO_BP_m2	GO:001580	neutral am	3/470	31/23843	0.022733	0.388014	0.363271	Slc25a38/S
GO_BP_m2	GO:004254	response t	6/470	111/23843	0.022748	0.388014	0.363271	Ect2/Rack1
GO_BP_m2	GO:004348	regulation	5/470	82/23843	0.023042	0.390357	0.365464	Elavl1/Mett
GO_BP_m2	GO:003808	peptidyl-ty	4/470	55/23843	0.023072	0.390357	0.365464	Csk/Dyrk1a
GO_BP_m2	GO:004325	regulation	15/470	429/23843	0.023999	0.391862	0.366873	Cebpa/Csf
GO_BP_m2	GO:009027	positive re	6/470	113/23843	0.024578	0.391862	0.366873	Glul/Oxct1/
GO_BP_m2	GO:008502	extracellula	3/470	32/23843	0.024727	0.391862	0.366873	Fam234b/
GO_BP_m2	GO:006500	protein-DN	8/470	178/23843	0.025248	0.391862	0.366873	Asf1a/Chaf
GO_BP_m2	GO:000155	luteinizatio	2/470	13/23843	0.026197	0.391862	0.366873	Gdf9/Sgpl1
GO_BP_m2	GO:001022	response t	2/470	13/23843	0.026197	0.391862	0.366873	Cebpa/Id2
GO_BP_m2	GO:003316	histone H3	2/470	13/23843	0.026197	0.391862	0.366873	Hr/Kdm3a
GO_BP_m2	GO:003809	Fc receptor	2/470	13/23843	0.026197	0.391862	0.366873	Myo1g/Nr
GO_BP_m2	GO:003970	viral buddi	2/470	13/23843	0.026197	0.391862	0.366873	Chmp3/Ts
GO_BP_m2	GO:006027	embryonic	2/470	13/23843	0.026197	0.391862	0.366873	Bmp4/Col2
GO_BP_m2	GO:006096	negative re	2/470	13/23843	0.026197	0.391862	0.366873	Dnd1/Elavl
GO_BP_m2	GO:007102	nuclear RN	2/470	13/23843	0.026197	0.391862	0.366873	Exosc2/Xrn
GO_BP_m2	GO:007102	nuclear mR	2/470	13/23843	0.026197	0.391862	0.366873	Exosc2/Xrn
GO_BP_m2	GO:007171	ER-associa	2/470	13/23843	0.026197	0.391862	0.366873	Derl1/Sdf2
GO_BP_m2	GO:009050	RNA phosp	2/470	13/23843	0.026197	0.391862	0.366873	Exosc2/Xrn
GO_BP_m2	GO:001059	regulation	3/470	33/23843	0.026812	0.391862	0.366873	Auts2/Rac2
GO_BP_m2	GO:004300	Golgi to pl	3/470	33/23843	0.026812	0.391862	0.366873	Csk/Rack1/
GO_BP_m2	GO:004852	positive re	3/470	33/23843	0.026812	0.391862	0.366873	Agrp/Nr4a
GO_BP_m2	GO:190320	regulation	3/470	33/23843	0.026812	0.391862	0.366873	Rack1/Nr4a
GO_BP_m2	GO:001703	protein imp	9/470	215/23843	0.027331	0.391862	0.366873	Bmp4/Ect2
GO_BP_m2	GO:190134	negative re	6/470	116/23843	0.027502	0.391862	0.366873	Angpt4/Bm
GO_BP_m2	GO:000633	chromatin	7/470	148/23843	0.027674	0.391862	0.366873	Actl6b/Asf1
GO_BP_m2	GO:005130	regulation	7/470	148/23843	0.027674	0.391862	0.366873	Aurkb/Chm
GO_BP_m2	GO:007177	response t	8/470	182/23843	0.028319	0.391862	0.366873	Bmp4/Col2
GO_BP_m2	GO:007177	cellular res	8/470	182/23843	0.028319	0.391862	0.366873	Bmp4/Col2
GO_BP_m2	GO:001003	response t	15/470	439/23843	0.028637	0.391862	0.366873	Aco1/Alad/
GO_BP_m2	GO:000619	purine nuc	3/470	34/23843	0.028987	0.391862	0.366873	Rack1/Pde
GO_BP_m2	GO:003511	embryonic	3/470	34/23843	0.028987	0.391862	0.366873	Aff3/Bmp4
GO_BP_m2	GO:003166	cellular res	9/470	218/23843	0.029509	0.391862	0.366873	Atf4/Fads1
GO_BP_m2	GO:190113	carbohydra	6/470	118/23843	0.029574	0.391862	0.366873	Gba2/Rack
GO_BP_m2	GO:001042	hydrogen	2/470	14/23843	0.03017	0.391862	0.366873	Pdcd10/Pir
GO_BP_m2	GO:001697	poly(A)+ m	2/470	14/23843	0.03017	0.391862	0.366873	Pabpn1/Zc
GO_BP_m2	GO:004683	phosphory	2/470	14/23843	0.03017	0.391862	0.366873	Mtmr2/Mt
GO_BP_m2	GO:007048	leukocyte	2/470	14/23843	0.03017	0.391862	0.366873	Nr4a3/Rac
GO_BP_m2	GO:007154	inositol ph	2/470	14/23843	0.03017	0.391862	0.366873	Mtmr2/Mt
GO_BP_m2	GO:007194	nitrogen cy	2/470	14/23843	0.03017	0.391862	0.366873	Cad/Cebpa
GO_BP_m2	GO:009746	programm	2/470	14/23843	0.03017	0.391862	0.366873	Pdcd10/Pir
GO_BP_m2	GO:200036	regulation	2/470	14/23843	0.03017	0.391862	0.366873	Arap3/Syt1

GO_BP_m2	GO:000151	RNA methy	4/470	60/23843	0.030576	0.391862	0.366873	Ftsj1/Mettl
GO_BP_m2	GO:004348	regulation	6/470	119/23843	0.030647	0.391862	0.366873	Clk1/Dyrk1
GO_BP_m2	GO:190136	organic cyc	16/470	483/23843	0.031128	0.391862	0.366873	Dhx34/Elav
GO_BP_m2	GO:005196	positive reg	3/470	35/23843	0.031254	0.391862	0.366873	Glul/Ptk2b/
GO_BP_m2	GO:200103	regulation	3/470	35/23843	0.031254	0.391862	0.366873	Rack1/Nr4a
GO_BP_m2	GO:000926	cellular res	7/470	152/23843	0.031359	0.391862	0.366873	Atf4/Fads1
GO_BP_m2	GO:003313	regulation	7/470	152/23843	0.031359	0.391862	0.366873	Rack1/Gpd
GO_BP_m2	GO:003647	cell death i	5/470	89/23843	0.0314	0.391862	0.366873	Atf4/Rack1
GO_BP_m2	GO:001607	rRNA meta	9/470	221/23843	0.031805	0.391862	0.366873	Chd7/Exos
GO_BP_m2	GO:006039	regulation	4/470	61/23843	0.03223	0.391862	0.366873	Bmp4/Gdf
GO_BP_m2	GO:005065	nucleic aci	7/470	153/23843	0.032329	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:005065	RNA transp	7/470	153/23843	0.032329	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:001593	nucleobase	8/470	188/23843	0.033396	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:003022	macrophag	3/470	36/23843	0.03361	0.391862	0.366873	Bmp4/Ceb
GO_BP_m2	GO:003400	neural retir	4/470	62/23843	0.033935	0.391862	0.366873	Irx5/Ptprm/
GO_BP_m2	GO:006400	RNA localiz	8/470	189/23843	0.034299	0.391862	0.366873	Exosc2/Hnr
GO_BP_m2	GO:000975	hormone-r	8/470	189/23843	0.034299	0.391862	0.366873	Agrp/Bmp4
GO_BP_m2	GO:000908	branched-	2/470	15/23843	0.034365	0.391862	0.366873	Hmgcl/Ivd
GO_BP_m2	GO:001700	antibiotic b	2/470	15/23843	0.034365	0.391862	0.366873	Cybb/Kdm
GO_BP_m2	GO:004351	negative re	2/470	15/23843	0.034365	0.391862	0.366873	Dyrk1a/Pck
GO_BP_m2	GO:004529	mRNA cis s	2/470	15/23843	0.034365	0.391862	0.366873	Ncbp2/Wb
GO_BP_m2	GO:004871	negative re	2/470	15/23843	0.034365	0.391862	0.366873	Bmp4/Id2
GO_BP_m2	GO:006014	negative re	2/470	15/23843	0.034365	0.391862	0.366873	Dnd1/Elavl
GO_BP_m2	GO:006070	regulation	2/470	15/23843	0.034365	0.391862	0.366873	Oas1b/Oas
GO_BP_m2	GO:006096	negative re	2/470	15/23843	0.034365	0.391862	0.366873	Dnd1/Elavl
GO_BP_m2	GO:007102	RNA survei	2/470	15/23843	0.034365	0.391862	0.366873	Exosc2/Xrn
GO_BP_m2	GO:007249	embryonic	2/470	15/23843	0.034365	0.391862	0.366873	Bmp4/Col2
GO_BP_m2	GO:003447	ncRNA pro	12/470	335/23843	0.034812	0.391862	0.366873	Chd7/Exos
GO_BP_m2	GO:005123	establishm	7/470	156/23843	0.035359	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:006400	RNA expor	5/470	92/23843	0.035494	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:000677	porphyrin-	3/470	37/23843	0.036057	0.391862	0.366873	Alad/Cox1
GO_BP_m2	GO:007115	positive reg	3/470	37/23843	0.036057	0.391862	0.366873	Foxo4/Id2/
GO_BP_m2	GO:200102	negative re	3/470	37/23843	0.036057	0.391862	0.366873	Rack1/Nr4a
GO_BP_m2	GO:007000	mitochond	5/470	93/23843	0.036928	0.391862	0.366873	Bloc1s2/He
GO_BP_m2	GO:004348	regulation	5/470	93/23843	0.036928	0.391862	0.366873	Elavl1/Mett
GO_BP_m2	GO:004533	cellular res	7/470	158/23843	0.03748	0.391862	0.366873	Aco1/Adsl/
GO_BP_m2	GO:000170	mesoderm	4/470	64/23843	0.037501	0.391862	0.366873	Bmp4/Nr4a
GO_BP_m2	GO:006038	pathway-re	4/470	64/23843	0.037501	0.391862	0.366873	Bmp4/Gdf
GO_BP_m2	GO:007135	cellular res	4/470	64/23843	0.037501	0.391862	0.366873	Bmp4/Hnrn
GO_BP_m2	GO:199054	mitochond	4/470	64/23843	0.037501	0.391862	0.366873	Slc25a28/S
GO_BP_m2	GO:190382	positive reg	12/470	340/23843	0.038281	0.391862	0.366873	Crocc/Ect2
GO_BP_m2	GO:000635	regulation	2/470	16/23843	0.038772	0.391862	0.366873	Cebpa/Ell
GO_BP_m2	GO:000674	ubiquinone	2/470	16/23843	0.038772	0.391862	0.366873	Coq8b/Coq
GO_BP_m2	GO:002197	telencepha	2/470	16/23843	0.038772	0.391862	0.366873	Bmp4/Six3
GO_BP_m2	GO:004675	viral buddin	2/470	16/23843	0.038772	0.391862	0.366873	Chmp3/Tsg
GO_BP_m2	GO:004826	negative re	2/470	16/23843	0.038772	0.391862	0.366873	Mtmr2/Syt
GO_BP_m2	GO:007136	cellular res	2/470	16/23843	0.038772	0.391862	0.366873	Mavs/Ralb
GO_BP_m2	GO:190166	quinone bi	2/470	16/23843	0.038772	0.391862	0.366873	Coq8b/Coq

GO_BP_m2	GO:190218	positive reg	2/470	16/23843	0.038772	0.391862	0.366873	Chmp3/Tsg
GO_BP_m2	GO:190426	negative re	2/470	16/23843	0.038772	0.391862	0.366873	Gatsl2/Itfg2
GO_BP_m2	GO:200034	regulation	2/470	16/23843	0.038772	0.391862	0.366873	Plau/Sulf2
GO_BP_m2	GO:000155	oocyte gro	1/470	2/23843	0.039037	0.391862	0.366873	Gdf9
GO_BP_m2	GO:000192	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Ralb
GO_BP_m2	GO:000196	thigmotaxi	1/470	2/23843	0.039037	0.391862	0.366873	Id2
GO_BP_m2	GO:000305	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Rasl10b
GO_BP_m2	GO:000340	optic vesicl	1/470	2/23843	0.039037	0.391862	0.366873	Six3
GO_BP_m2	GO:000642	glutamyl-tl	1/470	2/23843	0.039037	0.391862	0.366873	Eprs
GO_BP_m2	GO:000643	tryptophan	1/470	2/23843	0.039037	0.391862	0.366873	Wars2
GO_BP_m2	GO:000654	glutamine	1/470	2/23843	0.039037	0.391862	0.366873	Glul
GO_BP_m2	GO:000678	heme a bic	1/470	2/23843	0.039037	0.391862	0.366873	Cox10
GO_BP_m2	GO:000717	signal com	1/470	2/23843	0.039037	0.391862	0.366873	Ptk2b
GO_BP_m2	GO:000922	nucleotide-	1/470	2/23843	0.039037	0.391862	0.366873	Mgat1
GO_BP_m2	GO:001075	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Ptk2b
GO_BP_m2	GO:001484	esophagus	1/470	2/23843	0.039037	0.391862	0.366873	Sulf2
GO_BP_m2	GO:001580	aromatic a	1/470	2/23843	0.039037	0.391862	0.366873	Slc36a4
GO_BP_m2	GO:001582	tryptophan	1/470	2/23843	0.039037	0.391862	0.366873	Slc36a4
GO_BP_m2	GO:001603	tRNA impo	1/470	2/23843	0.039037	0.391862	0.366873	Tomm20
GO_BP_m2	GO:001814	keratan sul	1/470	2/23843	0.039037	0.391862	0.366873	Chst5
GO_BP_m2	GO:002156	abducens r	1/470	2/23843	0.039037	0.391862	0.366873	Mafb
GO_BP_m2	GO:002159	abducens r	1/470	2/23843	0.039037	0.391862	0.366873	Mafb
GO_BP_m2	GO:002159	abducens r	1/470	2/23843	0.039037	0.391862	0.366873	Mafb
GO_BP_m2	GO:003004	actin modi	1/470	2/23843	0.039037	0.391862	0.366873	Twf1
GO_BP_m2	GO:003080	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Rack1
GO_BP_m2	GO:003082	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Rack1
GO_BP_m2	GO:003221	riboflavin t	1/470	2/23843	0.039037	0.391862	0.366873	Slc52a3
GO_BP_m2	GO:003276	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Nr4a3
GO_BP_m2	GO:003312	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Rack1
GO_BP_m2	GO:003423	enkephalin	1/470	2/23843	0.039037	0.391862	0.366873	Pcsk2
GO_BP_m2	GO:003609	cleavage fu	1/470	2/23843	0.039037	0.391862	0.366873	Alkbh4
GO_BP_m2	GO:003626	7-methylgı	1/470	2/23843	0.039037	0.391862	0.366873	Tgs1
GO_BP_m2	GO:003648	neuron intr	1/470	2/23843	0.039037	0.391862	0.366873	Pink1
GO_BP_m2	GO:004263	cellular res	1/470	2/23843	0.039037	0.391862	0.366873	Sipa1
GO_BP_m2	GO:004294	D-serine tr	1/470	2/23843	0.039037	0.391862	0.366873	Slc7a10
GO_BP_m2	GO:004588	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Agrn
GO_BP_m2	GO:004616	heme a me	1/470	2/23843	0.039037	0.391862	0.366873	Cox10
GO_BP_m2	GO:004616	glycerol-3-	1/470	2/23843	0.039037	0.391862	0.366873	Gpd1l
GO_BP_m2	GO:004825	iron import	1/470	2/23843	0.039037	0.391862	0.366873	Slc25a28
GO_BP_m2	GO:004838	intermedia	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:004863	negative re	1/470	2/23843	0.039037	0.391862	0.366873	Tll2
GO_BP_m2	GO:005134	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Rack1
GO_BP_m2	GO:006019	cloacal sep	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:006099	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:006101	snRNA imp	1/470	2/23843	0.039037	0.391862	0.366873	Ran
GO_BP_m2	GO:006122	pattern spe	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:006176	multivesicu	1/470	2/23843	0.039037	0.391862	0.366873	Chmp3
GO_BP_m2	GO:007009	mitochond	1/470	2/23843	0.039037	0.391862	0.366873	Tomm20

GO_BP_m2	GO:007103	nuclear mR	1/470	2/23843	0.039037	0.391862	0.366873	Exosc2
GO_BP_m2	GO:007104	nuclear ret	1/470	2/23843	0.039037	0.391862	0.366873	Exosc2
GO_BP_m2	GO:007209	anterior/pc	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:007227	metanephr	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:009708	methyl-bra	1/470	2/23843	0.039037	0.391862	0.366873	Slc27a2
GO_BP_m2	GO:009740	neuroblast	1/470	2/23843	0.039037	0.391862	0.366873	Six3
GO_BP_m2	GO:190006	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Mavs
GO_BP_m2	GO:190189	negative re	1/470	2/23843	0.039037	0.391862	0.366873	Pde4d
GO_BP_m2	GO:190230	negative re	1/470	2/23843	0.039037	0.391862	0.366873	Kcnh2
GO_BP_m2	GO:190234	negative re	1/470	2/23843	0.039037	0.391862	0.366873	H3f3b
GO_BP_m2	GO:190235	Notch sign	1/470	2/23843	0.039037	0.391862	0.366873	Lfng
GO_BP_m2	GO:190236	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Lfng
GO_BP_m2	GO:190236	negative re	1/470	2/23843	0.039037	0.391862	0.366873	Lfng
GO_BP_m2	GO:190246	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:190246	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:190295	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Pink1
GO_BP_m2	GO:190338	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Pink1
GO_BP_m2	GO:190338	negative re	1/470	2/23843	0.039037	0.391862	0.366873	Pink1
GO_BP_m2	GO:190340	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Agrn
GO_BP_m2	GO:190424	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Pabpn1
GO_BP_m2	GO:190516	protein loc	1/470	2/23843	0.039037	0.391862	0.366873	Syt11
GO_BP_m2	GO:190516	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Syt11
GO_BP_m2	GO:190517	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Syt11
GO_BP_m2	GO:190522	clathrin-co	1/470	2/23843	0.039037	0.391862	0.366873	Syt11
GO_BP_m2	GO:190566	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:190566	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:199042	miRNA tran	1/470	2/23843	0.039037	0.391862	0.366873	Hnrnpa2b1
GO_BP_m2	GO:199092	calcium ion	1/470	2/23843	0.039037	0.391862	0.366873	Syt11
GO_BP_m2	GO:200013	negative re	1/470	2/23843	0.039037	0.391862	0.366873	Bmp4
GO_BP_m2	GO:200039	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Tsg101
GO_BP_m2	GO:200039	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Tsg101
GO_BP_m2	GO:200053	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Ptk2b
GO_BP_m2	GO:200053	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Ptk2b
GO_BP_m2	GO:200053	regulation	1/470	2/23843	0.039037	0.391862	0.366873	Agrn
GO_BP_m2	GO:200054	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Agrn
GO_BP_m2	GO:200062	positive reg	1/470	2/23843	0.039037	0.391862	0.366873	Auts2
GO_BP_m2	GO:005105	negative re	16/470	498/23843	0.039364	0.394199	0.369061	Acsl4/Agrn
GO_BP_m2	GO:000660	protein imp	7/470	160/23843	0.039683	0.396448	0.371166	Bmp4/Ect2
GO_BP_m2	GO:000002	ribosomal l	3/470	39/23843	0.041216	0.406536	0.380611	Fastkd2/Mr
GO_BP_m2	GO:004327	apoptotic c	3/470	39/23843	0.041216	0.406536	0.380611	Jmjd6/Rac2
GO_BP_m2	GO:006096	regulation	3/470	39/23843	0.041216	0.406536	0.380611	Bmp4/Dnd
GO_BP_m2	GO:000691	nucleocyto	11/470	306/23843	0.041241	0.406536	0.380611	Bmp4/Ect2
GO_BP_m2	GO:000333	amino acid	4/470	66/23843	0.041274	0.406536	0.380611	Slc6a21/Slc
GO_BP_m2	GO:003096	endoplasm	4/470	66/23843	0.041274	0.406536	0.380611	Atf4/Derl1/
GO_BP_m2	GO:004866	positive reg	5/470	96/23843	0.041441	0.407232	0.381263	Bmp4/Id2/
GO_BP_m2	GO:004851	rhythmic p	10/470	269/23843	0.041576	0.407599	0.381607	Atf4/Cry1/C
GO_BP_m2	GO:005116	nuclear tra	11/470	307/23843	0.042052	0.408503	0.382452	Bmp4/Ect2
GO_BP_m2	GO:000652	cellular am	10/470	270/23843	0.042452	0.408503	0.382452	Cad/Kyat3/

GO_BP_m2	GO:000728	germ cell c	10/470	270/23843	0.042452	0.408503	0.382452	Bmp4/Dnd
GO_BP_m2	GO:200123	negative re	5/470	97/23843	0.043017	0.408503	0.382452	Bmp4/Col2
GO_BP_m2	GO:001063	negative re	4/470	67/23843	0.043238	0.408503	0.382452	Angpt4/Mc
GO_BP_m2	GO:004566	positive reg	4/470	67/23843	0.043238	0.408503	0.382452	Bmp4/Ceb
GO_BP_m2	GO:000204	blood vess	2/470	17/23843	0.04338	0.408503	0.382452	Bmp4/Pdc
GO_BP_m2	GO:000674	ubiquinone	2/470	17/23843	0.04338	0.408503	0.382452	Coq8b/Coq
GO_BP_m2	GO:000908	glutamine	2/470	17/23843	0.04338	0.408503	0.382452	Cad/Glul
GO_BP_m2	GO:003502	regulation	2/470	17/23843	0.04338	0.408503	0.382452	Arap3/Auts
GO_BP_m2	GO:200064	regulation	2/470	17/23843	0.04338	0.408503	0.382452	Chmp3/Mt
GO_BP_m2	GO:000999	response t	13/470	386/23843	0.04372	0.408503	0.382452	Adsl/Alad/
GO_BP_m2	GO:004873	appendage	8/470	199/23843	0.044243	0.408503	0.382452	Aff3/Bmp4
GO_BP_m2	GO:006017	limb devel	8/470	199/23843	0.044243	0.408503	0.382452	Aff3/Bmp4
GO_BP_m2	GO:005117	import into	7/470	164/23843	0.044338	0.408503	0.382452	Bmp4/Ect2
GO_BP_m2	GO:000663	fatty acid b	4/470	68/23843	0.045253	0.408503	0.382452	Acat2/Echc
GO_BP_m2	GO:004833	mesoderm	4/470	68/23843	0.045253	0.408503	0.382452	Bmp4/Nr4a
GO_BP_m2	GO:000206	chondrocyt	5/470	99/23843	0.046274	0.408503	0.382452	Bmp4/Col2
GO_BP_m2	GO:001939	fatty acid c	5/470	99/23843	0.046274	0.408503	0.382452	Acat2/Echc
GO_BP_m2	GO:000717	epidermal	5/470	100/23843	0.047957	0.408503	0.382452	Aplp2/Cam
GO_BP_m2	GO:000171	mesoderm	2/470	18/23843	0.048179	0.408503	0.382452	Bmp4/Sfrp
GO_BP_m2	GO:001088	regulation	2/470	18/23843	0.048179	0.408503	0.382452	Chd7/Pde4
GO_BP_m2	GO:001607	rRNA catab	2/470	18/23843	0.048179	0.408503	0.382452	Exosc2/Xrn
GO_BP_m2	GO:003450	protein loc	2/470	18/23843	0.048179	0.408503	0.382452	Aurkb/Trap
GO_BP_m2	GO:004617	polyol cata	2/470	18/23843	0.048179	0.408503	0.382452	Mtmr2/Mtr
GO_BP_m2	GO:190285	regulation	2/470	18/23843	0.048179	0.408503	0.382452	Mir129-2/S
GO_BP_m2	GO:190342	regulation	2/470	18/23843	0.048179	0.408503	0.382452	Sh3gl1/Syt
GO_BP_m2	GO:004859	camera-typ	6/470	133/23843	0.048386	0.408503	0.382452	Bmp4/Ift12
GO_BP_m2	GO:001032	membrane	8/470	203/23843	0.048702	0.408503	0.382452	Alkbh4/Au
GO_BP_m2	GO:003025	lipid modif	8/470	203/23843	0.048702	0.408503	0.382452	Acat2/Echc
GO_BP_m2	GO:003241	lysosome l	4/470	70/23843	0.04944	0.408503	0.382452	Bloc1s2/Nr
GO_BP_m2	GO:006014	regulation	3/470	42/23843	0.049609	0.408503	0.382452	Bmp4/Dnd
GO_BP_m2	GO:006096	regulation	3/470	42/23843	0.049609	0.408503	0.382452	Bmp4/Dnd
GO_BP_m2	GO:003153	actin cytosl	5/470	101/23843	0.049675	0.408503	0.382452	Auts2/Farp
GO_BP_m2	GO:003444	lipid oxidat	5/470	101/23843	0.049675	0.408503	0.382452	Acat2/Echc
GO_BP_m2	GO:003596	cellular res	5/470	101/23843	0.049675	0.408503	0.382452	Atf4/Derl1/
GO_BP_m2	GO:004239	regulation	14/470	434/23843	0.050201	0.408503	0.382452	Agrn/Rack1
GO_BP_m2	GO:003350	carbohydra	9/470	241/23843	0.050328	0.408503	0.382452	Aspscr1/Ce
GO_BP_m2	GO:004259	glucose ho	9/470	241/23843	0.050328	0.408503	0.382452	Aspscr1/Ce
GO_BP_m2	GO:007149	cellular res	10/470	279/23843	0.050911	0.408503	0.382452	Atf4/Fads1
GO_BP_m2	GO:003106	regulation	4/470	71/23843	0.05161	0.408503	0.382452	Auts2/Kdm
GO_BP_m2	GO:003289	regulation	4/470	71/23843	0.05161	0.408503	0.382452	Acsl4/Erfe/
GO_BP_m2	GO:190331	positive reg	4/470	71/23843	0.05161	0.408503	0.382452	Mettl14/Nc
GO_BP_m2	GO:000991	hormone tr	12/470	357/23843	0.051883	0.408503	0.382452	Chd7/Cry1
GO_BP_m2	GO:190103	regulation	3/470	43/23843	0.052577	0.408503	0.382452	Rack1/Nr4a
GO_BP_m2	GO:190274	regulation	3/470	43/23843	0.052577	0.408503	0.382452	Auts2/Rac2
GO_BP_m2	GO:000686	amino acid	6/470	136/23843	0.052865	0.408503	0.382452	Slc6a21/Gr
GO_BP_m2	GO:001657	histone me	6/470	136/23843	0.052865	0.408503	0.382452	Auts2/Hist1
GO_BP_m2	GO:004566	regulation	6/470	136/23843	0.052865	0.408503	0.382452	Bmp4/Ceb
GO_BP_m2	GO:000652	arginine m	2/470	19/23843	0.053162	0.408503	0.382452	Cad/Oat

GO_BP_m2	GO:000763	chemosens	2/470	19/23843	0.053162	0.408503	0.382452	Chd7/Lmx1
GO_BP_m2	GO:000908	branched-	2/470	19/23843	0.053162	0.408503	0.382452	Hmgcl/Ivd
GO_BP_m2	GO:002169	cerebellar	2/470	19/23843	0.053162	0.408503	0.382452	Coq8b/Fair
GO_BP_m2	GO:004278	mRNA tran	2/470	19/23843	0.053162	0.408503	0.382452	Atf4/Zbtb1
GO_BP_m2	GO:006012	regulation	2/470	19/23843	0.053162	0.408503	0.382452	Chd7/Serp
GO_BP_m2	GO:003050	BMP signal	7/470	171/23843	0.053302	0.408503	0.382452	Bmp4/Gdf6
GO_BP_m2	GO:000910	glycoprote	11/470	320/23843	0.053611	0.408503	0.382452	Chst12/Col
GO_BP_m2	GO:004225	ribosome a	4/470	72/23843	0.053832	0.408503	0.382452	Fastkd2/Mr
GO_BP_m2	GO:190320	regulation	4/470	72/23843	0.053832	0.408503	0.382452	Atf4/Rack1
GO_BP_m2	GO:001820	peptidyl-se	12/470	360/23843	0.054585	0.408503	0.382452	Aurkb/Clk1
GO_BP_m2	GO:000599	monosacch	9/470	246/23843	0.055877	0.408503	0.382452	Atf4/Cry1/
GO_BP_m2	GO:009050	RNA phosp	4/470	73/23843	0.056105	0.408503	0.382452	Exosc2/Nck
GO_BP_m2	GO:003010	regulation	9/470	247/23843	0.057033	0.408503	0.382452	Arap3/Csk/
GO_BP_m2	GO:000688	exocytosis	11/470	324/23843	0.057558	0.408503	0.382452	Cplx4/Myo
GO_BP_m2	GO:190390	regulation	6/470	139/23843	0.057588	0.408503	0.382452	Chmp3/Ma
GO_BP_m2	GO:000182	inner cell m	1/470	3/23843	0.057981	0.408503	0.382452	Lats2
GO_BP_m2	GO:000182	inner cell m	1/470	3/23843	0.057981	0.408503	0.382452	Lats2
GO_BP_m2	GO:000231	germinal ce	1/470	3/23843	0.057981	0.408503	0.382452	Itfg2
GO_BP_m2	GO:000237	immunoglo	1/470	3/23843	0.057981	0.408503	0.382452	Galnt2
GO_BP_m2	GO:000257	pro-T cell	1/470	3/23843	0.057981	0.408503	0.382452	Zbtb1
GO_BP_m2	GO:000293	trabecular	1/470	3/23843	0.057981	0.408503	0.382452	Lmx1b
GO_BP_m2	GO:000313	BMP signal	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:000313	endoderma	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:000313	endoderma	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:000322	right ventri	1/470	3/23843	0.057981	0.408503	0.382452	Chd7
GO_BP_m2	GO:000599	xylulose me	1/470	3/23843	0.057981	0.408503	0.382452	Xylb
GO_BP_m2	GO:000626	pre-replica	1/470	3/23843	0.057981	0.408503	0.382452	Wdr18
GO_BP_m2	GO:000640	RNA impor	1/470	3/23843	0.057981	0.408503	0.382452	Ran
GO_BP_m2	GO:000643	prolyl-tRNA	1/470	3/23843	0.057981	0.408503	0.382452	Eprs
GO_BP_m2	GO:000668	glucosylcer	1/470	3/23843	0.057981	0.408503	0.382452	Gba2
GO_BP_m2	GO:000700	outer mito	1/470	3/23843	0.057981	0.408503	0.382452	Tomm20
GO_BP_m2	GO:000939	folic acid-c	1/470	3/23843	0.057981	0.408503	0.382452	Pm20d2
GO_BP_m2	GO:001015	specificatio	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:001079	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Rab11a
GO_BP_m2	GO:001401	neuroblast	1/470	3/23843	0.057981	0.408503	0.382452	Six3
GO_BP_m2	GO:001576	disaccharid	1/470	3/23843	0.057981	0.408503	0.382452	Slc45a4
GO_BP_m2	GO:001577	sucrose tra	1/470	3/23843	0.057981	0.408503	0.382452	Slc45a4
GO_BP_m2	GO:001577	oligosaccha	1/470	3/23843	0.057981	0.408503	0.382452	Slc45a4
GO_BP_m2	GO:001582	L-serine tra	1/470	3/23843	0.057981	0.408503	0.382452	Slc7a10
GO_BP_m2	GO:001967	ammonia a	1/470	3/23843	0.057981	0.408503	0.382452	Glul
GO_BP_m2	GO:002155	olfactory n	1/470	3/23843	0.057981	0.408503	0.382452	Chd7
GO_BP_m2	GO:003020	dermatan s	1/470	3/23843	0.057981	0.408503	0.382452	Chst12
GO_BP_m2	GO:003150	telomeric h	1/470	3/23843	0.057981	0.408503	0.382452	H3f3b
GO_BP_m2	GO:003205	ciliary basa	1/470	3/23843	0.057981	0.408503	0.382452	Crocc
GO_BP_m2	GO:003528	central ner	1/470	3/23843	0.057981	0.408503	0.382452	Mafb
GO_BP_m2	GO:003528	brain segm	1/470	3/23843	0.057981	0.408503	0.382452	Mafb
GO_BP_m2	GO:003584	cloaca dev	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:003586	glial cell-d	1/470	3/23843	0.057981	0.408503	0.382452	Sulf2

GO_BP_m2	GO:003599	deltoid tub	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:003625	multivesicu	1/470	3/23843	0.057981	0.408503	0.382452	Rab11a
GO_BP_m2	GO:003638	pre-replica	1/470	3/23843	0.057981	0.408503	0.382452	Wdr18
GO_BP_m2	GO:004233	keratan sul	1/470	3/23843	0.057981	0.408503	0.382452	Chst5
GO_BP_m2	GO:004236	water-solu	1/470	3/23843	0.057981	0.408503	0.382452	Pm20d2
GO_BP_m2	GO:004256	pteridine-c	1/470	3/23843	0.057981	0.408503	0.382452	Pm20d2
GO_BP_m2	GO:004273	D-xylose m	1/470	3/23843	0.057981	0.408503	0.382452	Xylb
GO_BP_m2	GO:004299	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Rack1
GO_BP_m2	GO:004398	histone H3	1/470	3/23843	0.057981	0.408503	0.382452	Aurkb
GO_BP_m2	GO:004420	'de novo' A	1/470	3/23843	0.057981	0.408503	0.382452	Adsl
GO_BP_m2	GO:004634	CDP-diacy	1/470	3/23843	0.057981	0.408503	0.382452	Cdipt
GO_BP_m2	GO:004695	ketone bo	1/470	3/23843	0.057981	0.408503	0.382452	Hmgcl
GO_BP_m2	GO:004869	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Spg20
GO_BP_m2	GO:006017	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Ralb
GO_BP_m2	GO:007064	formin-nu	1/470	3/23843	0.057981	0.408503	0.382452	Spire2
GO_BP_m2	GO:007146	cellular res	1/470	3/23843	0.057981	0.408503	0.382452	Sipa1
GO_BP_m2	GO:007213	mesenchy	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:007219	ureter urot	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:007228	metanephr	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:009003	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Gpd1l
GO_BP_m2	GO:009023	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Trappc12
GO_BP_m2	GO:009716	mesenchy	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:009907	mitochond	1/470	3/23843	0.057981	0.408503	0.382452	Pink1
GO_BP_m2	GO:009907	mitochond	1/470	3/23843	0.057981	0.408503	0.382452	Pink1
GO_BP_m2	GO:011000	formin-nu	1/470	3/23843	0.057981	0.408503	0.382452	Spire2
GO_BP_m2	GO:190018	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Syt11
GO_BP_m2	GO:190062	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Nr4a3
GO_BP_m2	GO:190062	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Nr4a3
GO_BP_m2	GO:190153	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Zbtb1
GO_BP_m2	GO:190184	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Pde4d
GO_BP_m2	GO:190196	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:190216	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Pcbp4
GO_BP_m2	GO:190229	pre-replica	1/470	3/23843	0.057981	0.408503	0.382452	Wdr18
GO_BP_m2	GO:190277	mitochond	1/470	3/23843	0.057981	0.408503	0.382452	Fastkd2
GO_BP_m2	GO:190295	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Pink1
GO_BP_m2	GO:190329	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Stxbp1
GO_BP_m2	GO:190329	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Stxbp1
GO_BP_m2	GO:190342	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Syt11
GO_BP_m2	GO:190356	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Crocc
GO_BP_m2	GO:190377	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Tsg101
GO_BP_m2	GO:190380	glycine im	1/470	3/23843	0.057981	0.408503	0.382452	Slc25a38
GO_BP_m2	GO:190478	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Pink1
GO_BP_m2	GO:190488	response t	1/470	3/23843	0.057981	0.408503	0.382452	Pink1
GO_BP_m2	GO:190488	cellular res	1/470	3/23843	0.057981	0.408503	0.382452	Pink1
GO_BP_m2	GO:190515	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Syt11
GO_BP_m2	GO:190529	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:190529	positive re	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:190531	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4

GO_BP_m2	GO:190531	positive reg	1/470	3/23843	0.057981	0.408503	0.382452	Bmp4
GO_BP_m2	GO:190555	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Fkbpl
GO_BP_m2	GO:200004	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Sfrp2
GO_BP_m2	GO:200004	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Sfrp2
GO_BP_m2	GO:200032	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Zcchc12
GO_BP_m2	GO:200032	positive reg	1/470	3/23843	0.057981	0.408503	0.382452	Zcchc12
GO_BP_m2	GO:200064	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Mtmr2
GO_BP_m2	GO:200083	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Cry1
GO_BP_m2	GO:200084	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Cry1
GO_BP_m2	GO:200085	negative re	1/470	3/23843	0.057981	0.408503	0.382452	Cry1
GO_BP_m2	GO:200087	regulation	1/470	3/23843	0.057981	0.408503	0.382452	Gdf9
GO_BP_m2	GO:000678	heme biosy	2/470	20/23843	0.058317	0.408503	0.382452	Alad/Cox10
GO_BP_m2	GO:001003	response to	2/470	20/23843	0.058317	0.408503	0.382452	Aco1/Cybr
GO_BP_m2	GO:001480	release of s	2/470	20/23843	0.058317	0.408503	0.382452	Chd7/Pde4
GO_BP_m2	GO:003144	regulation	2/470	20/23843	0.058317	0.408503	0.382452	Ncbp2/Rnf
GO_BP_m2	GO:004253	tumor necr	2/470	20/23843	0.058317	0.408503	0.382452	Cybb/Ube2
GO_BP_m2	GO:004253	regulation	2/470	20/23843	0.058317	0.408503	0.382452	Cybb/Ube2
GO_BP_m2	GO:199018	exosomal s	2/470	20/23843	0.058317	0.408503	0.382452	Rab11a/Tsg
GO_BP_m2	GO:200031	regulation	2/470	20/23843	0.058317	0.408503	0.382452	Pink1/Ptk2
GO_BP_m2	GO:000906	aerobic res	4/470	74/23843	0.058429	0.408503	0.382452	Aco1/Adsl/
GO_BP_m2	GO:007142	ribonucleo	4/470	74/23843	0.058429	0.408503	0.382452	Hnrnpa2b1
GO_BP_m2	GO:006082	regulation	8/470	211/23843	0.058471	0.408503	0.382452	Bambi/Dkk
GO_BP_m2	GO:001810	peptidyl-se	11/470	325/23843	0.058574	0.408503	0.382452	Aurkb/Clk1
GO_BP_m2	GO:001071	positive reg	3/470	45/23843	0.058764	0.408503	0.382452	Bambi/Bmp
GO_BP_m2	GO:003019	collagen fib	3/470	45/23843	0.058764	0.408503	0.382452	Col2a1/Lm
GO_BP_m2	GO:003052	androgen r	3/470	45/23843	0.058764	0.408503	0.382452	Kdm3a/Rnf
GO_BP_m2	GO:003301	tetrapyrrol	3/470	45/23843	0.058764	0.408503	0.382452	Alad/Cox10
GO_BP_m2	GO:006061	adipose tis	3/470	45/23843	0.058764	0.408503	0.382452	Fgl1/Id2/Sp
GO_BP_m2	GO:190237	negative re	3/470	45/23843	0.058764	0.408503	0.382452	Dhx34/Elav
GO_BP_m2	GO:001652	negative re	5/470	106/23843	0.058803	0.408503	0.382452	Angpt4/Fo
GO_BP_m2	GO:003476	regulation	14/470	445/23843	0.05926	0.411001	0.384791	Agrn/Bmp4
GO_BP_m2	GO:005165	establishm	13/470	405/23843	0.059483	0.411864	0.3856	Bloc1s2/Ce
GO_BP_m2	GO:000633	nucleosom	5/470	107/23843	0.060736	0.418795	0.392088	Asf1a/Chaf
GO_BP_m2	GO:009010	positive reg	5/470	107/23843	0.060736	0.418795	0.392088	Bmp4/Gdf6
GO_BP_m2	GO:009887	vesicle-me	4/470	75/23843	0.060804	0.418795	0.392088	Csk/Rack1/
GO_BP_m2	GO:004311	receptor m	7/470	177/23843	0.061828	0.418795	0.392088	Agrn/Ap2b
GO_BP_m2	GO:000641	tRNA amin	3/470	46/23843	0.06198	0.418795	0.392088	Eprs/Farsa/
GO_BP_m2	GO:002177	olfactory b	3/470	46/23843	0.06198	0.418795	0.392088	Chd7/Id2/S
GO_BP_m2	GO:007252	purine-cor	3/470	46/23843	0.06198	0.418795	0.392088	Rack1/Pde
GO_BP_m2	GO:009869	regulation	3/470	46/23843	0.06198	0.418795	0.392088	Sh3gl1/Stx
GO_BP_m2	GO:009881	modulation	3/470	46/23843	0.06198	0.418795	0.392088	Mtmr2/Ptk
GO_BP_m2	GO:000728	spermatog	15/470	489/23843	0.062095	0.418795	0.392088	Ankrd49/C
GO_BP_m2	GO:002241	cellular pro	12/470	368/23843	0.062251	0.418795	0.392088	Bmp4/Dnd
GO_BP_m2	GO:004688	regulation	10/470	290/23843	0.062688	0.418795	0.392088	Chd7/Cry1
GO_BP_m2	GO:001046	regulation	5/470	108/23843	0.062704	0.418795	0.392088	Aplp2/Pink
GO_BP_m2	GO:003236	regulation	5/470	108/23843	0.062704	0.418795	0.392088	Acat2/Acsl4
GO_BP_m2	GO:000232	lymphoid p	2/470	21/23843	0.063638	0.418795	0.392088	Bmp4/Zbtb
GO_BP_m2	GO:001059	positive reg	2/470	21/23843	0.063638	0.418795	0.392088	Auts2/Rac2

GO_BP_m2	GO:00431	entrainme	2/470	21/23843	0.063638	0.418795	0.392088	Cry1/Id2
GO_BP_m2	GO:00707	histone H3	2/470	21/23843	0.063638	0.418795	0.392088	Hist1h1e/S
GO_BP_m2	GO:00977	extracellula	2/470	21/23843	0.063638	0.418795	0.392088	Rab11a/Ts
GO_BP_m2	GO:190152	positive re	2/470	21/23843	0.063638	0.418795	0.392088	Atf4/Chd6
GO_BP_m2	GO:190351	release of	2/470	21/23843	0.063638	0.418795	0.392088	Chd7/Pde4
GO_BP_m2	GO:003032	embryonic	6/470	143/23843	0.064267	0.418795	0.392088	Aff3/Bmp4
GO_BP_m2	GO:003511	embryonic	6/470	143/23843	0.064267	0.418795	0.392088	Aff3/Bmp4
GO_BP_m2	GO:003812	ERBB signa	5/470	109/23843	0.064709	0.418795	0.392088	Aplp2/Cam
GO_BP_m2	GO:20001	negative re	5/470	109/23843	0.064709	0.418795	0.392088	Angpt4/Fo
GO_BP_m2	GO:001931	hexose me	8/470	216/23843	0.065163	0.418795	0.392088	Atf4/Cry1/
GO_BP_m2	GO:00517	positive re	4/470	77/23843	0.065704	0.418795	0.392088	Aurkb/Chm
GO_BP_m2	GO:003017	negative re	6/470	144/23843	0.066005	0.418795	0.392088	Dkk4/Lats2
GO_BP_m2	GO:00486	regulation	12/470	372/23843	0.066339	0.418795	0.392088	Agrn/Bmp
GO_BP_m2	GO:00900	regulation	8/470	217/23843	0.066556	0.418795	0.392088	Bambi/Bm
GO_BP_m2	GO:009027	regulation	8/470	217/23843	0.066556	0.418795	0.392088	Chd7/Glul/
GO_BP_m2	GO:004864	negative re	5/470	110/23843	0.066749	0.418795	0.392088	Bmp4/Rnf
GO_BP_m2	GO:00900	negative re	5/470	110/23843	0.066749	0.418795	0.392088	Dkk4/Lats2
GO_BP_m2	GO:00063	chromatin	6/470	145/23843	0.06777	0.418795	0.392088	Actl6b/Ch
GO_BP_m2	GO:00519	regulation	4/470	78/23843	0.06823	0.418795	0.392088	Glul/Grm7/
GO_BP_m2	GO:000227	mast cell a	3/470	48/23843	0.068652	0.418795	0.392088	Nr4a3/Rac
GO_BP_m2	GO:00063	transcriptic	3/470	48/23843	0.068652	0.418795	0.392088	Atf4/Cebp
GO_BP_m2	GO:00105	negative re	3/470	48/23843	0.068652	0.418795	0.392088	Angpt4/Pd
GO_BP_m2	GO:002154	cranial ner	3/470	48/23843	0.068652	0.418795	0.392088	Chd7/Maf
GO_BP_m2	GO:00219	olfactory l	3/470	48/23843	0.068652	0.418795	0.392088	Chd7/Id2/
GO_BP_m2	GO:00433	mast cell d	3/470	48/23843	0.068652	0.418795	0.392088	Nr4a3/Rac
GO_BP_m2	GO:000654	glutamine	2/470	22/23843	0.069114	0.418795	0.392088	Cad/Glul
GO_BP_m2	GO:000964	photoperic	2/470	22/23843	0.069114	0.418795	0.392088	Cry1/Id2
GO_BP_m2	GO:00302	growth ho	2/470	22/23843	0.069114	0.418795	0.392088	Chd7/Serp
GO_BP_m2	GO:005144	positive re	2/470	22/23843	0.069114	0.418795	0.392088	Eif4g3/Lfn
GO_BP_m2	GO:00609	negative re	2/470	22/23843	0.069114	0.418795	0.392088	Dnd1/Elavl
GO_BP_m2	GO:007121	cellular res	2/470	22/23843	0.069114	0.418795	0.392088	Derl1/Sdf2
GO_BP_m2	GO:00714	protein loc	2/470	22/23843	0.069114	0.418795	0.392088	Aurkb/Tra
GO_BP_m2	GO:007257	hepatocyte	2/470	22/23843	0.069114	0.418795	0.392088	Plau/Sulf2
GO_BP_m2	GO:007257	epithelial c	2/470	22/23843	0.069114	0.418795	0.392088	Plau/Sulf2
GO_BP_m2	GO:19013	negative re	2/470	22/23843	0.069114	0.418795	0.392088	Agrn/Kcnh
GO_BP_m2	GO:190364	regulation	2/470	22/23843	0.069114	0.418795	0.392088	Chmp3/Mt
GO_BP_m2	GO:20008	regulation	2/470	22/23843	0.069114	0.418795	0.392088	Cry1/Gdf9
GO_BP_m2	GO:003497	response t	8/470	219/23843	0.069397	0.418795	0.392088	Atf4/Derl1/
GO_BP_m2	GO:00301	B cell diffe	6/470	146/23843	0.069563	0.418795	0.392088	Id2/Ifna4/I
GO_BP_m2	GO:007147	cellular res	6/470	146/23843	0.069563	0.418795	0.392088	Aurkb/Ect2
GO_BP_m2	GO:00905	sensory or	10/470	296/23843	0.069796	0.418795	0.392088	Bmp4/Chd
GO_BP_m2	GO:00702	actin-medi	4/470	79/23843	0.070804	0.418795	0.392088	Frmd6/Gp
GO_BP_m2	GO:19039	negative re	4/470	79/23843	0.070804	0.418795	0.392088	Chmp3/M
GO_BP_m2	GO:00433	response t	5/470	112/23843	0.070935	0.418795	0.392088	Bmp4/Hnr
GO_BP_m2	GO:000244	mast cell r	3/470	49/23843	0.072105	0.418795	0.392088	Nr4a3/Rac
GO_BP_m2	GO:00330	regulation	3/470	49/23843	0.072105	0.418795	0.392088	Nr4a3/Rac
GO_BP_m2	GO:00430	tRNA amin	3/470	49/23843	0.072105	0.418795	0.392088	Eprs/Farsa/
GO_BP_m2	GO:00484	cell matura	7/470	184/23843	0.072771	0.418795	0.392088	Cebpa/Far

GO_BP_m2	GO:002167	nerve deve	4/470	80/23843	0.073428	0.418795	0.392088	Chd7/Mafb
GO_BP_m2	GO:003019	extracellula	8/470	222/23843	0.073796	0.418795	0.392088	Fam234b/A
GO_BP_m2	GO:004218	cellular ket	7/470	185/23843	0.074423	0.418795	0.392088	Acsl4/Coq8
GO_BP_m2	GO:001906	virion asser	2/470	23/23843	0.074739	0.418795	0.392088	Chmp3/Tsg
GO_BP_m2	GO:003014	sphingolipi	2/470	23/23843	0.074739	0.418795	0.392088	Gba2/Sgpl
GO_BP_m2	GO:004833	mesoderm	2/470	23/23843	0.074739	0.418795	0.392088	Bmp4/Sfrp
GO_BP_m2	GO:006115	mRNA des	2/470	23/23843	0.074739	0.418795	0.392088	Mettl14/Zc
GO_BP_m2	GO:014011	export acrc	2/470	23/23843	0.074739	0.418795	0.392088	Agrn/Kcnh
GO_BP_m2	GO:004866	regulation	6/470	149/23843	0.075103	0.418795	0.392088	Bmp4/Id2/
GO_BP_m2	GO:005067	regulation	11/470	340/23843	0.075246	0.418795	0.392088	Bmp4/Glul/
GO_BP_m2	GO:000689	Golgi to pl	3/470	50/23843	0.075634	0.418795	0.392088	Csk/Rack1/
GO_BP_m2	GO:003112	mRNA 3'-e	3/470	50/23843	0.075634	0.418795	0.392088	Ncbp2/Pab
GO_BP_m2	GO:004214	cellular res	3/470	50/23843	0.075634	0.418795	0.392088	Atf4/Itfg2/I
GO_BP_m2	GO:004303	amino acid	3/470	50/23843	0.075634	0.418795	0.392088	Eprs/Farsa/
GO_BP_m2	GO:004361	regulation	3/470	50/23843	0.075634	0.418795	0.392088	Atf4/Chd6/
GO_BP_m2	GO:003202	positive reg	4/470	81/23843	0.076101	0.418795	0.392088	Glul/Oxct1/
GO_BP_m2	GO:190040	regulation	4/470	81/23843	0.076101	0.418795	0.392088	Atf4/Rack1
GO_BP_m2	GO:007099	neuron dea	12/470	381/23843	0.076168	0.418795	0.392088	Agrn/Atf4/
GO_BP_m2	GO:003007	peptide ho	9/470	262/23843	0.076228	0.418795	0.392088	Chd7/Cyb5
GO_BP_m2	GO:000073	DNA stranc	1/470	4/23843	0.076553	0.418795	0.392088	Recql
GO_BP_m2	GO:000192	exocyst ass	1/470	4/23843	0.076553	0.418795	0.392088	Ralb
GO_BP_m2	GO:000243	immune re	1/470	4/23843	0.076553	0.418795	0.392088	Myo1g
GO_BP_m2	GO:000316	bundle of H	1/470	4/23843	0.076553	0.418795	0.392088	Id2
GO_BP_m2	GO:000338	apical cons	1/470	4/23843	0.076553	0.418795	0.392088	Frmd6
GO_BP_m2	GO:000722	signal trans	1/470	4/23843	0.076553	0.418795	0.392088	Ift122
GO_BP_m2	GO:000738	compartme	1/470	4/23843	0.076553	0.418795	0.392088	Lfng
GO_BP_m2	GO:000741	axon targe	1/470	4/23843	0.076553	0.418795	0.392088	Stxbp1
GO_BP_m2	GO:000941	response tc	1/470	4/23843	0.076553	0.418795	0.392088	Sipa1
GO_BP_m2	GO:000994	proximal/d	1/470	4/23843	0.076553	0.418795	0.392088	Six3
GO_BP_m2	GO:001004	response tc	1/470	4/23843	0.076553	0.418795	0.392088	Aco1
GO_BP_m2	GO:001656	protein imp	1/470	4/23843	0.076553	0.418795	0.392088	Pex5l
GO_BP_m2	GO:001834	protein far	1/470	4/23843	0.076553	0.418795	0.392088	Cox10
GO_BP_m2	GO:001924	citrulline bi	1/470	4/23843	0.076553	0.418795	0.392088	Cad
GO_BP_m2	GO:002157	rhombome	1/470	4/23843	0.076553	0.418795	0.392088	Mafb
GO_BP_m2	GO:003009	protein rep	1/470	4/23843	0.076553	0.418795	0.392088	Msrb3
GO_BP_m2	GO:003120	posttransla	1/470	4/23843	0.076553	0.418795	0.392088	Sec63
GO_BP_m2	GO:003150	pericentric	1/470	4/23843	0.076553	0.418795	0.392088	H3f3b
GO_BP_m2	GO:003230	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Acsl4
GO_BP_m2	GO:003232	serine trans	1/470	4/23843	0.076553	0.418795	0.392088	Slc7a10
GO_BP_m2	GO:003276	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Nr4a3
GO_BP_m2	GO:003455	respiratory	1/470	4/23843	0.076553	0.418795	0.392088	Sdhaf1
GO_BP_m2	GO:003455	mitochond	1/470	4/23843	0.076553	0.418795	0.392088	Sdhaf1
GO_BP_m2	GO:003502	positive reg	1/470	4/23843	0.076553	0.418795	0.392088	Auts2
GO_BP_m2	GO:003572	intraciliary	1/470	4/23843	0.076553	0.418795	0.392088	Ift122
GO_BP_m2	GO:003599	tendon cell	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:003599	tendon for	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:003625	multivesicu	1/470	4/23843	0.076553	0.418795	0.392088	Rab11a
GO_BP_m2	GO:003650	ATF6-med	1/470	4/23843	0.076553	0.418795	0.392088	Mbtps2

GO_BP_m2	GO:003809	Fc-epsilon	1/470	4/23843	0.076553	0.418795	0.392088	Nr4a3
GO_BP_m2	GO:003809	Fc-gamma	1/470	4/23843	0.076553	0.418795	0.392088	Myo1g
GO_BP_m2	GO:004266	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Sfrp2
GO_BP_m2	GO:004343	response t	1/470	4/23843	0.076553	0.418795	0.392088	Nr4a3
GO_BP_m2	GO:004431	protein K2	1/470	4/23843	0.076553	0.418795	0.392088	Rnf6
GO_BP_m2	GO:004557	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Id2
GO_BP_m2	GO:004629	formaldehy	1/470	4/23843	0.076553	0.418795	0.392088	Kdm3a
GO_BP_m2	GO:004695	ketone boc	1/470	4/23843	0.076553	0.418795	0.392088	Oxct1
GO_BP_m2	GO:004801	Tie signalir	1/470	4/23843	0.076553	0.418795	0.392088	Angpt4
GO_BP_m2	GO:006000	vestibular r	1/470	4/23843	0.076553	0.418795	0.392088	Nr4a3
GO_BP_m2	GO:006027	positive reg	1/470	4/23843	0.076553	0.418795	0.392088	Plau
GO_BP_m2	GO:006068	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:006083	ciliary rece	1/470	4/23843	0.076553	0.418795	0.392088	Ift122
GO_BP_m2	GO:006103	epithelial c	1/470	4/23843	0.076553	0.418795	0.392088	Id2
GO_BP_m2	GO:006103	endoderma	1/470	4/23843	0.076553	0.418795	0.392088	Id2
GO_BP_m2	GO:006105	dermatome	1/470	4/23843	0.076553	0.418795	0.392088	Sfrp2
GO_BP_m2	GO:006118	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Sfrp2
GO_BP_m2	GO:006120	cell prolifer	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:007008	ubiquitin-c	1/470	4/23843	0.076553	0.418795	0.392088	Tsg101
GO_BP_m2	GO:007012	mitochond	1/470	4/23843	0.076553	0.418795	0.392088	2810006K2
GO_BP_m2	GO:007031	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Foxo4
GO_BP_m2	GO:007103	CUT catabo	1/470	4/23843	0.076553	0.418795	0.392088	Exosc2
GO_BP_m2	GO:007104	CUT metab	1/470	4/23843	0.076553	0.418795	0.392088	Exosc2
GO_BP_m2	GO:007137	cellular res	1/470	4/23843	0.076553	0.418795	0.392088	Nr4a3
GO_BP_m2	GO:007209	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:007212	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:007219	ureter mor	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:007219	mesenchyr	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:007219	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:009013	actin filame	1/470	4/23843	0.076553	0.418795	0.392088	Mir129-2
GO_BP_m2	GO:009016	Golgi reass	1/470	4/23843	0.076553	0.418795	0.392088	Pdcd10
GO_BP_m2	GO:009019	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:009019	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Bmp4
GO_BP_m2	GO:009024	Wnt signali	1/470	4/23843	0.076553	0.418795	0.392088	Sfrp2
GO_BP_m2	GO:190356	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Crocc
GO_BP_m2	GO:190358	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Pdcd10
GO_BP_m2	GO:190375	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Pink1
GO_BP_m2	GO:190375	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Pink1
GO_BP_m2	GO:190534	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Trappc12
GO_BP_m2	GO:190534	positive reg	1/470	4/23843	0.076553	0.418795	0.392088	Trappc12
GO_BP_m2	GO:190544	positive reg	1/470	4/23843	0.076553	0.418795	0.392088	Pink1
GO_BP_m2	GO:190577	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Sfrp2
GO_BP_m2	GO:190590	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Sfrp2
GO_BP_m2	GO:199008	lens fiber c	1/470	4/23843	0.076553	0.418795	0.392088	Six3
GO_BP_m2	GO:199083	response t	1/470	4/23843	0.076553	0.418795	0.392088	Shc1
GO_BP_m2	GO:200009	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Plau
GO_BP_m2	GO:200062	regulation	1/470	4/23843	0.076553	0.418795	0.392088	Dhx34
GO_BP_m2	GO:200062	negative re	1/470	4/23843	0.076553	0.418795	0.392088	Dhx34

GO_BP_m2	GO:200116	positive reg	1/470	4/23843	0.076553	0.418795	0.392088	Rnf20
GO_BP_m2	GO:190121	negative re	8/470	224/23843	0.07682	0.419712	0.392947	Atf4/Faim2
GO_BP_m2	GO:000609	generation	11/470	342/23843	0.077674	0.423275	0.396283	Aco1/Adsl/
GO_BP_m2	GO:005196	negative re	11/470	342/23843	0.077674	0.423275	0.396283	Bmp4/Cit/I
GO_BP_m2	GO:005118	cofactor m	14/470	465/23843	0.078442	0.426903	0.39968	Acaca/Coq
GO_BP_m2	GO:000640	mRNA exp	3/470	51/23843	0.079239	0.42813	0.400828	Hnrnpa2b1
GO_BP_m2	GO:003090	midbrain d	3/470	51/23843	0.079239	0.42813	0.400828	Aplp2/Lmx
GO_BP_m2	GO:004364	inositol ph	3/470	51/23843	0.079239	0.42813	0.400828	Mtmr2/Mtr
GO_BP_m2	GO:006500	intracellula	3/470	51/23843	0.079239	0.42813	0.400828	Pex5l/Sec6
GO_BP_m2	GO:007142	mRNA-cor	3/470	51/23843	0.079239	0.42813	0.400828	Hnrnpa2b1
GO_BP_m2	GO:002306	signal relea	14/470	466/23843	0.079495	0.42813	0.400828	Chd7/Cplx
GO_BP_m2	GO:004643	organopho	7/470	188/23843	0.079507	0.42813	0.400828	Rack1/Gpd
GO_BP_m2	GO:001802	peptidyl-ly	5/470	116/23843	0.07973	0.42813	0.400828	Auts2/Hist
GO_BP_m2	GO:000293	response t	2/470	24/23843	0.080504	0.42813	0.400828	Faim2/Pan
GO_BP_m2	GO:000964	entrainmer	2/470	24/23843	0.080504	0.42813	0.400828	Cry1/Id2
GO_BP_m2	GO:001057	positive reg	2/470	24/23843	0.080504	0.42813	0.400828	Atf4/Sulf2
GO_BP_m2	GO:001404	regulation	2/470	24/23843	0.080504	0.42813	0.400828	Grm7/Stxb
GO_BP_m2	GO:004685	phosphatic	2/470	24/23843	0.080504	0.42813	0.400828	Mtmr2/Mtr
GO_BP_m2	GO:005178	response t	2/470	24/23843	0.080504	0.42813	0.400828	Derl1/Sdf2
GO_BP_m2	GO:006000	reflex	2/470	24/23843	0.080504	0.42813	0.400828	Auts2/Nr4a
GO_BP_m2	GO:007257	liver morph	2/470	24/23843	0.080504	0.42813	0.400828	Plau/Sulf2
GO_BP_m2	GO:190446	regulation	2/470	24/23843	0.080504	0.42813	0.400828	Mavs/Syt1
GO_BP_m2	GO:199077	tumor necr	2/470	24/23843	0.080504	0.42813	0.400828	Mavs/Syt1
GO_BP_m2	GO:003462	cellular res	4/470	83/23843	0.08159	0.432184	0.404624	Atf4/Derl1/
GO_BP_m2	GO:009723	cellular res	6/470	153/23843	0.08287	0.432184	0.404624	Ect2/Rack1
GO_BP_m2	GO:002158	cerebellum	3/470	52/23843	0.082916	0.432184	0.404624	Coq8b/Fair
GO_BP_m2	GO:005073	negative re	3/470	52/23843	0.082916	0.432184	0.404624	Sfrp2/Suz1
GO_BP_m2	GO:007093	protein K4	3/470	52/23843	0.082916	0.432184	0.404624	Rnf146/Rn
GO_BP_m2	GO:007180	protein tra	3/470	52/23843	0.082916	0.432184	0.404624	Pex5l/Sec6
GO_BP_m2	GO:190236	negative re	3/470	52/23843	0.082916	0.432184	0.404624	Dhx34/Elav
GO_BP_m2	GO:004306	extracellula	9/470	267/23843	0.083411	0.432184	0.404624	Fam234b/
GO_BP_m2	GO:004825	regulation	4/470	84/23843	0.084407	0.432184	0.404624	Arap3/Mtn
GO_BP_m2	GO:004865	smooth mu	6/470	154/23843	0.084878	0.432184	0.404624	Bmp4/Id2/
GO_BP_m2	GO:004687	hormone s	11/470	348/23843	0.085253	0.432184	0.404624	Chd7/Cry1
GO_BP_m2	GO:000677	porphyrin-	2/470	25/23843	0.086401	0.432184	0.404624	Alad/Cox1
GO_BP_m2	GO:003289	negative re	2/470	25/23843	0.086401	0.432184	0.404624	Acsl4/Grm
GO_BP_m2	GO:003592	steroid hor	2/470	25/23843	0.086401	0.432184	0.404624	Cry1/Gdf9
GO_BP_m2	GO:004573	respiratory	2/470	25/23843	0.086401	0.432184	0.404624	Cybb/Rac2
GO_BP_m2	GO:005077	RNA destal	2/470	25/23843	0.086401	0.432184	0.404624	Mettl14/Zc
GO_BP_m2	GO:007180	podosome	2/470	25/23843	0.086401	0.432184	0.404624	Csf2/Farp2
GO_BP_m2	GO:007201	glomerulus	2/470	25/23843	0.086401	0.432184	0.404624	Bmp4/Not
GO_BP_m2	GO:008600	ventricular	2/470	25/23843	0.086401	0.432184	0.404624	Gpd1l/Kcnl
GO_BP_m2	GO:005126	protein hor	11/470	349/23843	0.086559	0.432184	0.404624	Acaca/Alac
GO_BP_m2	GO:000636	rRNA proc	7/470	192/23843	0.086594	0.432184	0.404624	Chd7/Exos
GO_BP_m2	GO:000762	circadian r	7/470	192/23843	0.086594	0.432184	0.404624	Atf4/Cry1/
GO_BP_m2	GO:003166	cellular res	7/470	192/23843	0.086594	0.432184	0.404624	Atf4/Fads1
GO_BP_m2	GO:000687	cellular iro	3/470	53/23843	0.086666	0.432184	0.404624	Aco1/Erfe/
GO_BP_m2	GO:004854	digestive tr	3/470	53/23843	0.086666	0.432184	0.404624	Bmp4/Id2/

GO_BP_m2	GO:007127	cellular res	3/470	53/23843	0.086666	0.432184	0.404624	Ect2/Fosb/
GO_BP_m2	GO:004648	phosphatic	5/470	119/23843	0.086691	0.432184	0.404624	Cdipt/Fam
GO_BP_m2	GO:003104	gene silenc	6/470	155/23843	0.086914	0.432184	0.404624	Bmp4/Dnd
GO_BP_m2	GO:000721	neuropepti	4/470	85/23843	0.08727	0.432184	0.404624	Agrp/Gpr1
GO_BP_m2	GO:001071	regulation	4/470	85/23843	0.08727	0.432184	0.404624	Bambi/Bmp
GO_BP_m2	GO:006039	SMAD prot	4/470	85/23843	0.08727	0.432184	0.404624	Bmp4/Gdf6
GO_BP_m2	GO:000728	spermatid	6/470	156/23843	0.088976	0.432184	0.404624	H3f3b/Kdm
GO_BP_m2	GO:004688	positive reg	6/470	156/23843	0.088976	0.432184	0.404624	Glul/Oxct1/
GO_BP_m2	GO:001003	response to	8/470	232/23843	0.089652	0.432184	0.404624	Aco1/Alad/
GO_BP_m2	GO:000030	response to	7/470	194/23843	0.090267	0.432184	0.404624	Ect2/Rack1
GO_BP_m2	GO:005109	positive reg	7/470	194/23843	0.090267	0.432184	0.404624	Agrn/Bamb
GO_BP_m2	GO:004406	regulation	3/470	54/23843	0.090486	0.432184	0.404624	Cry1/Gdf9/
GO_BP_m2	GO:004507	negative re	3/470	54/23843	0.090486	0.432184	0.404624	Mavs/Oas1
GO_BP_m2	GO:190390	positive reg	3/470	54/23843	0.090486	0.432184	0.404624	Chmp3/Pp
GO_BP_m2	GO:004340	steroid hor	6/470	157/23843	0.091065	0.432184	0.404624	Bmp4/Cry1
GO_BP_m2	GO:007124	cellular res	5/470	121/23843	0.091503	0.432184	0.404624	Cebpa/Ect2
GO_BP_m2	GO:190160	alpha-amir	7/470	195/23843	0.092137	0.432184	0.404624	Cad/Kyat3/
GO_BP_m2	GO:000206	chondrocy	2/470	26/23843	0.092424	0.432184	0.404624	Sfrp2/Sulf2
GO_BP_m2	GO:000208	lens morph	2/470	26/23843	0.092424	0.432184	0.404624	Bmp4/Six3
GO_BP_m2	GO:000929	mRNA tran	2/470	26/23843	0.092424	0.432184	0.404624	Atf4/Zbtb1
GO_BP_m2	GO:003097	retrograde	2/470	26/23843	0.092424	0.432184	0.404624	Derl1/Ube2
GO_BP_m2	GO:003301	tetrapyrrol	2/470	26/23843	0.092424	0.432184	0.404624	Alad/Cox10
GO_BP_m2	GO:003450	centromere	2/470	26/23843	0.092424	0.432184	0.404624	H3f3b/Trap
GO_BP_m2	GO:004646	membrane	2/470	26/23843	0.092424	0.432184	0.404624	Gba2/Sgpl1
GO_BP_m2	GO:006038	innervation	2/470	26/23843	0.092424	0.432184	0.404624	Chd7/Sulf2
GO_BP_m2	GO:006143	renal syster	2/470	26/23843	0.092424	0.432184	0.404624	Bmp4/Notc
GO_BP_m2	GO:006144	kidney vasc	2/470	26/23843	0.092424	0.432184	0.404624	Bmp4/Notc
GO_BP_m2	GO:007007	histone lysi	2/470	26/23843	0.092424	0.432184	0.404624	Hr/Kdm3a
GO_BP_m2	GO:007029	sarcoplasm	2/470	26/23843	0.092424	0.432184	0.404624	Chd7/Pde4
GO_BP_m2	GO:190351	endoplasm	2/470	26/23843	0.092424	0.432184	0.404624	Derl1/Ube2
GO_BP_m2	GO:200017	negative re	2/470	26/23843	0.092424	0.432184	0.404624	Id2/Vax1
GO_BP_m2	GO:000681	potassium	8/470	234/23843	0.093042	0.432184	0.404624	Agrn/Atf4/
GO_BP_m2	GO:003112	RNA 3'-en	4/470	87/23843	0.093136	0.432184	0.404624	Exosc2/Ncb
GO_BP_m2	GO:003307	T cell differ	4/470	87/23843	0.093136	0.432184	0.404624	Bmp4/Jmjc
GO_BP_m2	GO:190161	organic hy	13/470	437/23843	0.093873	0.432184	0.404624	Aplp2/Ceb
GO_BP_m2	GO:009902	plasma me	7/470	196/23843	0.094028	0.432184	0.404624	Alkbh4/Au
GO_BP_m2	GO:000690	phagocyto	10/470	314/23843	0.094084	0.432184	0.404624	Csk/Rack1/
GO_BP_m2	GO:001580	L-amino a	3/470	55/23843	0.094375	0.432184	0.404624	Slc25a38/S
GO_BP_m2	GO:004362	regulation	3/470	55/23843	0.094375	0.432184	0.404624	Atf4/Chd6/
GO_BP_m2	GO:008600	cardiac mu	3/470	55/23843	0.094375	0.432184	0.404624	Gpd1l/Kcn
GO_BP_m2	GO:000156	fatty acid a	1/470	5/23843	0.094759	0.432184	0.404624	Slc27a2
GO_BP_m2	GO:000166	conditione	1/470	5/23843	0.094759	0.432184	0.404624	Grm7
GO_BP_m2	GO:000316	His-Purkinj	1/470	5/23843	0.094759	0.432184	0.404624	Id2
GO_BP_m2	GO:000600	fructose 2,	1/470	5/23843	0.094759	0.432184	0.404624	Pfkfb4
GO_BP_m2	GO:000616	AMP biosy	1/470	5/23843	0.094759	0.432184	0.404624	Adsl
GO_BP_m2	GO:000643	phenylalan	1/470	5/23843	0.094759	0.432184	0.404624	Farsa
GO_BP_m2	GO:000729	spermatid	1/470	5/23843	0.094759	0.432184	0.404624	Kdm3a
GO_BP_m2	GO:000858	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Agrn

GO_BP_m2	GO:001098	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Csk
GO_BP_m2	GO:001487	response t	1/470	5/23843	0.094759	0.432184	0.404624	Srl
GO_BP_m2	GO:001619	synaptic ve	1/470	5/23843	0.094759	0.432184	0.404624	Sh3gl1
GO_BP_m2	GO:002179	forebrain a	1/470	5/23843	0.094759	0.432184	0.404624	Six3
GO_BP_m2	GO:002191	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Ift122
GO_BP_m2	GO:003004	parallel act	1/470	5/23843	0.094759	0.432184	0.404624	Spire2
GO_BP_m2	GO:003020	dermatan s	1/470	5/23843	0.094759	0.432184	0.404624	Chst12
GO_BP_m2	GO:003274	positive re	1/470	5/23843	0.094759	0.432184	0.404624	Csf2
GO_BP_m2	GO:003308	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:003502	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Arap3
GO_BP_m2	GO:003554	interferon-	1/470	5/23843	0.094759	0.432184	0.404624	Mavs
GO_BP_m2	GO:003554	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Mavs
GO_BP_m2	GO:003554	positive re	1/470	5/23843	0.094759	0.432184	0.404624	Mavs
GO_BP_m2	GO:003592	RNA impor	1/470	5/23843	0.094759	0.432184	0.404624	Tomm20
GO_BP_m2	GO:004270	progestero	1/470	5/23843	0.094759	0.432184	0.404624	Gdf9
GO_BP_m2	GO:004299	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Csk
GO_BP_m2	GO:004365	recognitio	1/470	5/23843	0.094759	0.432184	0.404624	Jmjd6
GO_BP_m2	GO:004591	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Csf2
GO_BP_m2	GO:004601	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Rrp8
GO_BP_m2	GO:004866	collateral s	1/470	5/23843	0.094759	0.432184	0.404624	Spg20
GO_BP_m2	GO:005065	dermatan s	1/470	5/23843	0.094759	0.432184	0.404624	Chst12
GO_BP_m2	GO:005103	tRNA trans	1/470	5/23843	0.094759	0.432184	0.404624	Tomm20
GO_BP_m2	GO:005129	establishm	1/470	5/23843	0.094759	0.432184	0.404624	Spire2
GO_BP_m2	GO:005134	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Rack1
GO_BP_m2	GO:006027	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Plau
GO_BP_m2	GO:006062	regulation	1/470	5/23843	0.094759	0.432184	0.404624	H3f3b
GO_BP_m2	GO:006068	branch elo	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:006097	embryonic	1/470	5/23843	0.094759	0.432184	0.404624	Ift122
GO_BP_m2	GO:006104	positive re	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:006105	sclerotome	1/470	5/23843	0.094759	0.432184	0.404624	Sfrp2
GO_BP_m2	GO:006132	cell prolifer	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:006153	glutamate	1/470	5/23843	0.094759	0.432184	0.404624	Stxbp1
GO_BP_m2	GO:007048	monocyte	1/470	5/23843	0.094759	0.432184	0.404624	Nr4a3
GO_BP_m2	GO:007103	nuclear ret	1/470	5/23843	0.094759	0.432184	0.404624	Exosc2
GO_BP_m2	GO:007103	nuclear pol	1/470	5/23843	0.094759	0.432184	0.404624	Exosc2
GO_BP_m2	GO:007105	polyadenyl	1/470	5/23843	0.094759	0.432184	0.404624	Exosc2
GO_BP_m2	GO:007159	lymphocyt	1/470	5/23843	0.094759	0.432184	0.404624	Rac2
GO_BP_m2	GO:007165	positive re	1/470	5/23843	0.094759	0.432184	0.404624	Mavs
GO_BP_m2	GO:007217	nephric du	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:007219	ureter smo	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:007219	ureter smo	1/470	5/23843	0.094759	0.432184	0.404624	Bmp4
GO_BP_m2	GO:007265	maintenan	1/470	5/23843	0.094759	0.432184	0.404624	Pink1
GO_BP_m2	GO:009888	neurotrans	1/470	5/23843	0.094759	0.432184	0.404624	Rab11a
GO_BP_m2	GO:009901	neuronal d	1/470	5/23843	0.094759	0.432184	0.404624	Stxbp1
GO_BP_m2	GO:009952	presynapti	1/470	5/23843	0.094759	0.432184	0.404624	Stxbp1
GO_BP_m2	GO:190107	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Pde4d
GO_BP_m2	GO:190230	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Kcnh2
GO_BP_m2	GO:190327	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Agrn

GO_BP_m2	GO:190329	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Pink1
GO_BP_m2	GO:190329	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Pink1
GO_BP_m2	GO:190336	positive reg	1/470	5/23843	0.094759	0.432184	0.404624	Penk
GO_BP_m2	GO:190337	negative re	1/470	5/23843	0.094759	0.432184	0.404624	Pink1
GO_BP_m2	GO:190377	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Tsg101
GO_BP_m2	GO:190439	positive reg	1/470	5/23843	0.094759	0.432184	0.404624	Agrn
GO_BP_m2	GO:190495	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Sfrp2
GO_BP_m2	GO:190544	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Pink1
GO_BP_m2	GO:200098	positive reg	1/470	5/23843	0.094759	0.432184	0.404624	Penk
GO_BP_m2	GO:200116	regulation	1/470	5/23843	0.094759	0.432184	0.404624	Rnf20
GO_BP_m2	GO:000864	carbohydra	6/470	159/23843	0.095322	0.433806	0.406143	Aspscr1/M
GO_BP_m2	GO:006004	retina deve	6/470	159/23843	0.095322	0.433806	0.406143	Chd7/Irx5/
GO_BP_m2	GO:005140	neuron apo	9/470	275/23843	0.095721	0.435151	0.407401	Agrn/Atf4/
GO_BP_m2	GO:004505	regulated e	7/470	197/23843	0.09594	0.435676	0.407893	Cplx4/Nr4a
GO_BP_m2	GO:000639	mRNA proc	13/470	439/23843	0.09636	0.437112	0.409237	Cdc5l/Dyrk
GO_BP_m2	GO:002153	telencepha	8/470	236/23843	0.096505	0.437297	0.40941	Bmp4/Cep
GO_BP_m2	GO:190134	regulation	10/470	316/23843	0.097058	0.439328	0.411312	Angpt4/Bm
GO_BP_m2	GO:004327	negative re	6/470	160/23843	0.097489	0.440803	0.412693	Acsl4/Agrn
GO_BP_m2	GO:000006	protein imp	3/470	56/23843	0.098332	0.441852	0.413675	Mavs/Ran/
GO_BP_m2	GO:002157	hindbrain r	3/470	56/23843	0.098332	0.441852	0.413675	Coq8b/Fair
GO_BP_m2	GO:000651	protein qua	2/470	27/23843	0.098564	0.441852	0.413675	Derl1/Sdf2
GO_BP_m2	GO:003048	tRNA meth	2/470	27/23843	0.098564	0.441852	0.413675	Ftsj1/Nsun
GO_BP_m2	GO:003236	negative re	2/470	27/23843	0.098564	0.441852	0.413675	Acsl4/Cry1
GO_BP_m2	GO:003466	ncRNA cata	2/470	27/23843	0.098564	0.441852	0.413675	Exosc2/Xrn
GO_BP_m2	GO:005115	regulation	2/470	27/23843	0.098564	0.441852	0.413675	Bmp4/Foxc
GO_BP_m2	GO:009031	positive reg	2/470	27/23843	0.098564	0.441852	0.413675	Dyrk1a/Pin
GO_BP_m2	GO:003021	erythrocyte	5/470	124/23843	0.098973	0.442742	0.414509	Bmp4/Id2/
GO_BP_m2	GO:003519	gene silenc	5/470	124/23843	0.098973	0.442742	0.414509	Bmp4/Dnd
GO_BP_m2	GO:005507	iron ion ho	4/470	89/23843	0.099184	0.443212	0.414948	Aco1/Erfe/
GO_BP_m2	GO:003166	response to	11/470	359/23843	0.100292	0.447686	0.419138	Adsl/Alad/
GO_BP_m2	GO:003149	chromatin	5/470	125/23843	0.10153	0.452153	0.423319	Asf1a/Chaf
GO_BP_m2	GO:005090	neuromusc	5/470	125/23843	0.10153	0.452153	0.423319	Aplp2/Csm
GO_BP_m2	GO:003011	regulation	9/470	279/23843	0.102252	0.452153	0.423319	Bambi/Dkk
GO_BP_m2	GO:000202	regulation	4/470	90/23843	0.102275	0.452153	0.423319	Gpd1l/Irx5/
GO_BP_m2	GO:004506	regulation	4/470	90/23843	0.102275	0.452153	0.423319	Mavs/Oas1
GO_BP_m2	GO:005079	regulation	4/470	90/23843	0.102275	0.452153	0.423319	Agrp/Csf2/
GO_BP_m2	GO:190288	regulation	4/470	90/23843	0.102275	0.452153	0.423319	Atf4/Rack1
GO_BP_m2	GO:004560	positive reg	3/470	57/23843	0.102355	0.452153	0.423319	Cebpa/Id2/
GO_BP_m2	GO:004851	circadian b	3/470	57/23843	0.102355	0.452153	0.423319	Csf2/Id2/Si
GO_BP_m2	GO:012003	plasma me	14/470	487/23843	0.103728	0.452153	0.423319	2700049A0
GO_BP_m2	GO:005067	epithelial c	12/470	403/23843	0.103931	0.452153	0.423319	Bmp4/Glul/
GO_BP_m2	GO:001500	ossification	11/470	362/23843	0.10465	0.452153	0.423319	Asf1a/Bmp
GO_BP_m2	GO:000223	positive reg	2/470	28/23843	0.104815	0.452153	0.423319	Il12rb1/Ma
GO_BP_m2	GO:000717	regulation	2/470	28/23843	0.104815	0.452153	0.423319	Aplp2/Tsg1
GO_BP_m2	GO:002187	forebrain r	2/470	28/23843	0.104815	0.452153	0.423319	Bmp4/Six3
GO_BP_m2	GO:003022	monocyte	2/470	28/23843	0.104815	0.452153	0.423319	Bmp4/Csf2
GO_BP_m2	GO:190204	negative re	2/470	28/23843	0.104815	0.452153	0.423319	Faim2/Sfrp
GO_BP_m2	GO:190274	positive reg	2/470	28/23843	0.104815	0.452153	0.423319	Auts2/Rac2

GO_BP_m2	GO:190313	mononucle	2/470	28/23843	0.104815	0.452153	0.423319	Bmp4/Csf2
GO_BP_m2	GO:200019	regulation	2/470	28/23843	0.104815	0.452153	0.423319	Acsl4/Erfe
GO_BP_m2	GO:003650	ERAD path	4/470	91/23843	0.10541	0.452153	0.423319	Derl1/Psmc
GO_BP_m2	GO:000820	steroid me	9/470	281/23843	0.105611	0.452153	0.423319	Aplp2/Ceb
GO_BP_m2	GO:003200	negative re	3/470	58/23843	0.106442	0.452153	0.423319	Gatsl2/Itfg2
GO_BP_m2	GO:003283	glomerulus	3/470	58/23843	0.106442	0.452153	0.423319	Bmp4/Notc
GO_BP_m2	GO:004574	positive re	3/470	58/23843	0.106442	0.452153	0.423319	Bmp4/Csf2
GO_BP_m2	GO:003519	posttranscr	5/470	127/23843	0.10674	0.452153	0.423319	Bmp4/Dnd
GO_BP_m2	GO:005189	membrane	4/470	92/23843	0.108588	0.452153	0.423319	Rack1/Gpd
GO_BP_m2	GO:006002	roof of mo	4/470	92/23843	0.108588	0.452153	0.423319	Chd7/Col2
GO_BP_m2	GO:004851	spermatid	6/470	165/23843	0.108717	0.452153	0.423319	H3f3b/Kdm
GO_BP_m2	GO:004694	carboxylic	9/470	283/23843	0.109031	0.452153	0.423319	Slc6a21/Ac
GO_BP_m2	GO:003596	response t	5/470	128/23843	0.109394	0.452153	0.423319	Atf4/Derl1/
GO_BP_m2	GO:007110	DNA confo	7/470	204/23843	0.109924	0.452153	0.423319	Asf1a/Chaf
GO_BP_m2	GO:000680	superoxide	3/470	59/23843	0.110592	0.452153	0.423319	Cyb5r4/Cyb
GO_BP_m2	GO:000762	rhythmic b	3/470	59/23843	0.110592	0.452153	0.423319	Csf2/Id2/Si
GO_BP_m2	GO:004606	cGMP meta	3/470	59/23843	0.110592	0.452153	0.423319	Gucy2c/Pd
GO_BP_m2	GO:006098	endocrine	3/470	59/23843	0.110592	0.452153	0.423319	Cry1/Gdf9/
GO_BP_m2	GO:007115	regulation	3/470	59/23843	0.110592	0.452153	0.423319	Foxo4/Id2/
GO_BP_m2	GO:001584	organic aci	9/470	284/23843	0.110765	0.452153	0.423319	Slc6a21/Ac
GO_BP_m2	GO:004352	negative re	6/470	166/23843	0.111039	0.452153	0.423319	Faim2/Nr4a
GO_BP_m2	GO:000195	endochond	2/470	29/23843	0.11117	0.452153	0.423319	Bmp4/Col2
GO_BP_m2	GO:000653	glutamate	2/470	29/23843	0.11117	0.452153	0.423319	Glul/Oat
GO_BP_m2	GO:003300	positive re	2/470	29/23843	0.11117	0.452153	0.423319	Nr4a3/Stxb
GO_BP_m2	GO:003462	cellular pro	2/470	29/23843	0.11117	0.452153	0.423319	Ralb/Ran
GO_BP_m2	GO:003607	replacemen	2/470	29/23843	0.11117	0.452153	0.423319	Bmp4/Col2
GO_BP_m2	GO:004445	motile ciliu	2/470	29/23843	0.11117	0.452153	0.423319	Mir449b/M
GO_BP_m2	GO:006103	positive re	2/470	29/23843	0.11117	0.452153	0.423319	Bmp4/Gdf6
GO_BP_m2	GO:190179	negative re	2/470	29/23843	0.11117	0.452153	0.423319	Dyrk1a/Pcb
GO_BP_m2	GO:004364	dicarboxyli	4/470	93/23843	0.111808	0.452153	0.423319	Kyat3/Glul/
GO_BP_m2	GO:190382	organic aci	4/470	93/23843	0.111808	0.452153	0.423319	Slc6a21/Slc
GO_BP_m2	GO:190503	carboxylic	4/470	93/23843	0.111808	0.452153	0.423319	Slc6a21/Slc
GO_BP_m2	GO:003400	planar cell	1/470	6/23843	0.112607	0.452153	0.423319	Sfrp2
GO_BP_m2	GO:006200	'de novo' p	1/470	6/23843	0.112607	0.452153	0.423319	Cad
GO_BP_m2	GO:000647	protein sul	1/470	6/23843	0.112607	0.452153	0.423319	Hs3st3b1
GO_BP_m2	GO:000667	glucosylcer	1/470	6/23843	0.112607	0.452153	0.423319	Gba2
GO_BP_m2	GO:000697	DNA dama	1/470	6/23843	0.112607	0.452153	0.423319	Cry1
GO_BP_m2	GO:000718	common-p	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:000719	adenylate	1/470	6/23843	0.112607	0.452153	0.423319	Grm7
GO_BP_m2	GO:001066	ectoderma	1/470	6/23843	0.112607	0.452153	0.423319	Erf
GO_BP_m2	GO:001094	positive re	1/470	6/23843	0.112607	0.452153	0.423319	Hebp2
GO_BP_m2	GO:001580	L-alanine t	1/470	6/23843	0.112607	0.452153	0.423319	Slc36a4
GO_BP_m2	GO:001607	tRNA catab	1/470	6/23843	0.112607	0.452153	0.423319	Exosc2
GO_BP_m2	GO:001974	nitrogen ut	1/470	6/23843	0.112607	0.452153	0.423319	Glul
GO_BP_m2	GO:001985	pyrimidine	1/470	6/23843	0.112607	0.452153	0.423319	Cad
GO_BP_m2	GO:003007	insulin pro	1/470	6/23843	0.112607	0.452153	0.423319	Pcsk2
GO_BP_m2	GO:003017	regulation	1/470	6/23843	0.112607	0.452153	0.423319	Wdr18
GO_BP_m2	GO:003057	ubiquitin-c	1/470	6/23843	0.112607	0.452153	0.423319	Tgfb1i1

GO_BP_m2	GO:003129	membrane	1/470	6/23843	0.112607	0.452153	0.423319	Mbtps2
GO_BP_m2	GO:003205	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Slc35a4
GO_BP_m2	GO:003251	endosome	1/470	6/23843	0.112607	0.452153	0.423319	Chmp3
GO_BP_m2	GO:003276	mast cell cy	1/470	6/23843	0.112607	0.452153	0.423319	Nr4a3
GO_BP_m2	GO:003296	regulation	1/470	6/23843	0.112607	0.452153	0.423319	Ptk2b
GO_BP_m2	GO:003308	negative re	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:003313	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Pfkfb2
GO_BP_m2	GO:003318	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Rnf20
GO_BP_m2	GO:003376	response to	1/470	6/23843	0.112607	0.452153	0.423319	Cry1
GO_BP_m2	GO:003598	tendon dev	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:004003	polar body	1/470	6/23843	0.112607	0.452153	0.423319	Spire2
GO_BP_m2	GO:004279	snRNA trar	1/470	6/23843	0.112607	0.452153	0.423319	Ell
GO_BP_m2	GO:004294	D-amino a	1/470	6/23843	0.112607	0.452153	0.423319	Slc7a10
GO_BP_m2	GO:004453	long-chain	1/470	6/23843	0.112607	0.452153	0.423319	Slc27a2
GO_BP_m2	GO:004480	G-quadrup	1/470	6/23843	0.112607	0.452153	0.423319	Hnrnpa2b1
GO_BP_m2	GO:004521	neurotrans	1/470	6/23843	0.112607	0.452153	0.423319	Agrn
GO_BP_m2	GO:004647	glycosylcer	1/470	6/23843	0.112607	0.452153	0.423319	Gba2
GO_BP_m2	GO:004665	folic acid m	1/470	6/23843	0.112607	0.452153	0.423319	Pm20d2
GO_BP_m2	GO:006030	regulation	1/470	6/23843	0.112607	0.452153	0.423319	Mtmr2
GO_BP_m2	GO:006068	regulation	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:006090	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Eif4g3
GO_BP_m2	GO:006121	negative re	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:006130	smooth mu	1/470	6/23843	0.112607	0.452153	0.423319	Plau
GO_BP_m2	GO:006131	BMP signal	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:006166	mitochond	1/470	6/23843	0.112607	0.452153	0.423319	Fastkd2
GO_BP_m2	GO:007032	thyroid hor	1/470	6/23843	0.112607	0.452153	0.423319	Crym
GO_BP_m2	GO:007102	nuclear ncR	1/470	6/23843	0.112607	0.452153	0.423319	Exosc2
GO_BP_m2	GO:007103	nuclear pol	1/470	6/23843	0.112607	0.452153	0.423319	Exosc2
GO_BP_m2	GO:007104	nuclear pol	1/470	6/23843	0.112607	0.452153	0.423319	Exosc2
GO_BP_m2	GO:007204	comma-sh	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:009024	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Auts2
GO_BP_m2	GO:009025	negative re	1/470	6/23843	0.112607	0.452153	0.423319	Pink1
GO_BP_m2	GO:009026	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Psmc5
GO_BP_m2	GO:009963	neurotrans	1/470	6/23843	0.112607	0.452153	0.423319	Rab11a
GO_BP_m2	GO:190172	negative re	1/470	6/23843	0.112607	0.452153	0.423319	Bmp4
GO_BP_m2	GO:190172	positive reg	1/470	6/23843	0.112607	0.452153	0.423319	Pink1
GO_BP_m2	GO:190355	regulation	1/470	6/23843	0.112607	0.452153	0.423319	Tsg101
GO_BP_m2	GO:200032	negative re	1/470	6/23843	0.112607	0.452153	0.423319	Cry1
GO_BP_m2	GO:200061	regulation	1/470	6/23843	0.112607	0.452153	0.423319	Auts2
GO_BP_m2	GO:005073	regulation	8/470	245/23843	0.112981	0.453219	0.424317	Agrn/Angp
GO_BP_m2	GO:001644	posttranscr	5/470	130/23843	0.114797	0.459215	0.429931	Bmp4/Dnd
GO_BP_m2	GO:003292	circadian rh	3/470	60/23843	0.114804	0.459215	0.429931	Atf4/Cry1/I
GO_BP_m2	GO:007147	cellular res	3/470	60/23843	0.114804	0.459215	0.429931	Ect2/H2afx
GO_BP_m2	GO:000906	fatty acid c	4/470	94/23843	0.115071	0.459408	0.430112	Acat2/Echc
GO_BP_m2	GO:004691	cellular trar	4/470	94/23843	0.115071	0.459408	0.430112	Aco1/Aplp
GO_BP_m2	GO:003090	forebrain d	11/470	370/23843	0.116807	0.465453	0.435771	Aplp2/Bmp
GO_BP_m2	GO:005109	regulation	11/470	370/23843	0.116807	0.465453	0.435771	Agrn/Aplp2
GO_BP_m2	GO:005507	transition r	5/470	131/23843	0.117545	0.465608	0.435917	Aco1/Aplp

GO_BP_m2	GO:00196	startle resp	2/470	30/23843	0.117623	0.465608	0.435917	Csmd1/Per
GO_BP_m2	GO:00219	dorsal/vent	2/470	30/23843	0.117623	0.465608	0.435917	Bmp4/Ift12
GO_BP_m2	GO:00435	negative re	2/470	30/23843	0.117623	0.465608	0.435917	Angpt4/Pd
GO_BP_m2	GO:00506	positive re	2/470	30/23843	0.117623	0.465608	0.435917	Ncbp2/Thr
GO_BP_m2	GO:19034	regulation	2/470	30/23843	0.117623	0.465608	0.435917	Gatsl2/Itfg
GO_BP_m2	GO:200014	positive re	2/470	30/23843	0.117623	0.465608	0.435917	Cebpa/Psn
GO_BP_m2	GO:00705	spindle org	6/470	169/23843	0.118156	0.466838	0.437068	Aurkb/Cep
GO_BP_m2	GO:000721	Notch sign	6/470	169/23843	0.118156	0.466838	0.437068	Angpt4/Ar
GO_BP_m2	GO:003304	regulation	10/470	330/23843	0.119405	0.468277	0.438415	Aurkb/Auts
GO_BP_m2	GO:00422	ribosome b	9/470	289/23843	0.119661	0.468277	0.438415	Chd7/Exos
GO_BP_m2	GO:00106	regulation	7/470	209/23843	0.120539	0.468277	0.438415	Angpt4/Bn
GO_BP_m2	GO:00345	cellular res	8/470	249/23843	0.120763	0.468277	0.438415	Atf4/Bmp4
GO_BP_m2	GO:00015	regulation	12/470	415/23843	0.121316	0.468277	0.438415	Acsl4/Exos
GO_BP_m2	GO:00457	regulation	9/470	290/23843	0.121486	0.468277	0.438415	Angpt4/Cy
GO_BP_m2	GO:001052	regulation	4/470	96/23843	0.12172	0.468277	0.438415	Bmp4/Chd
GO_BP_m2	GO:004577	positive re	4/470	96/23843	0.12172	0.468277	0.438415	Bmp4/Ceb
GO_BP_m2	GO:006084	artery deve	4/470	96/23843	0.12172	0.468277	0.438415	Ap2b1/Bm
GO_BP_m2	GO:00902	positive re	4/470	96/23843	0.12172	0.468277	0.438415	Bambi/Rnf
GO_BP_m2	GO:00160	organic aci	7/470	210/23843	0.122724	0.468277	0.438415	Acat2/Echo
GO_BP_m2	GO:00463	carboxylic	7/470	210/23843	0.122724	0.468277	0.438415	Acat2/Echo
GO_BP_m2	GO:004352	regulation	8/470	250/23843	0.122752	0.468277	0.438415	Agrn/Atf4/
GO_BP_m2	GO:00902	negative re	5/470	133/23843	0.123135	0.468277	0.438415	Bambi/Sfrp
GO_BP_m2	GO:00217	developme	9/470	291/23843	0.123326	0.468277	0.438415	Cebpa/Far
GO_BP_m2	GO:004244	pigment m	3/470	62/23843	0.123404	0.468277	0.438415	Alad/Cox1
GO_BP_m2	GO:006004	retina mor	3/470	62/23843	0.123404	0.468277	0.438415	Irx5/Ptprm
GO_BP_m2	GO:000177	natural kill	2/470	31/23843	0.124167	0.468277	0.438415	Id2/Zbtb1
GO_BP_m2	GO:00063	DNA replic	2/470	31/23843	0.124167	0.468277	0.438415	Asf1a/Chaf
GO_BP_m2	GO:001057	regulation	2/470	31/23843	0.124167	0.468277	0.438415	Atf4/Sulf2
GO_BP_m2	GO:00320	regulation	2/470	31/23843	0.124167	0.468277	0.438415	Oas1b/Oas
GO_BP_m2	GO:00323	DNA geom	2/470	31/23843	0.124167	0.468277	0.438415	Hnrnpa2b1
GO_BP_m2	GO:00347	DNA replic	2/470	31/23843	0.124167	0.468277	0.438415	Asf1a/Chaf
GO_BP_m2	GO:004351	regulation	2/470	31/23843	0.124167	0.468277	0.438415	Dyrk1a/Pck
GO_BP_m2	GO:007162	positive re	2/470	31/23843	0.124167	0.468277	0.438415	Rac2/S100
GO_BP_m2	GO:00725	clathrin-de	2/470	31/23843	0.124167	0.468277	0.438415	Arap3/Syt1
GO_BP_m2	GO:006144	connective	8/470	251/23843	0.124759	0.468277	0.438415	Bmp4/Col2
GO_BP_m2	GO:004852	negative re	4/470	97/23843	0.125105	0.468277	0.438415	Chmp3/Ma
GO_BP_m2	GO:00719	regulation	12/470	418/23843	0.125906	0.468277	0.438415	Bmp4/Cks1
GO_BP_m2	GO:004592	positive re	9/470	293/23843	0.12705	0.468277	0.438415	Acsl4/Agrn
GO_BP_m2	GO:002261	ribonucleo	7/470	212/23843	0.127153	0.468277	0.438415	Eif5/Fastkd
GO_BP_m2	GO:00300	lamellipodi	3/470	63/23843	0.12779	0.468277	0.438415	Auts2/Rac2
GO_BP_m2	GO:00485	eye morph	6/470	173/23843	0.12799	0.468277	0.438415	Bmp4/Ift12
GO_BP_m2	GO:004301	camera-typ	10/470	335/23843	0.128025	0.468277	0.438415	Bmp4/Chd
GO_BP_m2	GO:00066	fatty acid n	11/470	377/23843	0.128074	0.468277	0.438415	Acaca/Aca
GO_BP_m2	GO:00017	formation	4/470	98/23843	0.12853	0.468277	0.438415	Bmp4/Nr4
GO_BP_m2	GO:00516	maintenan	4/470	98/23843	0.12853	0.468277	0.438415	Fthl17f/Pin
GO_BP_m2	GO:00341	erythrocyt	5/470	135/23843	0.128846	0.468277	0.438415	Bmp4/Id2/
GO_BP_m2	GO:00004	exonucleol	1/470	7/23843	0.130104	0.468277	0.438415	Exosc2
GO_BP_m2	GO:00004	exonucleol	1/470	7/23843	0.130104	0.468277	0.438415	Exosc2

GO_BP_m2	GO:000257	platelet de	1/470	7/23843	0.130104	0.468277	0.438415	Stxbp1
GO_BP_m2	GO:000312	heart induc	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:000317	aortic valve	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00031	aortic valve	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00032	cardiac neu	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:000652	arginine bi	1/470	7/23843	0.130104	0.468277	0.438415	Cad
GO_BP_m2	GO:000672	tetrahydrol	1/470	7/23843	0.130104	0.468277	0.438415	Pcbd1
GO_BP_m2	GO:00080	Toll signali	1/470	7/23843	0.130104	0.468277	0.438415	Palm3
GO_BP_m2	GO:000941	response t	1/470	7/23843	0.130104	0.468277	0.438415	Sipa1
GO_BP_m2	GO:001064	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Pde4d
GO_BP_m2	GO:001082	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Cep120
GO_BP_m2	GO:00109	negative re	1/470	7/23843	0.130104	0.468277	0.438415	Csk
GO_BP_m2	GO:00161	glycoside c	1/470	7/23843	0.130104	0.468277	0.438415	Gba2
GO_BP_m2	GO:00217	forebrain d	1/470	7/23843	0.130104	0.468277	0.438415	Six3
GO_BP_m2	GO:003222	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Pink1
GO_BP_m2	GO:003331	meiotic cel	1/470	7/23843	0.130104	0.468277	0.438415	Nsun2
GO_BP_m2	GO:00357	B cell chem	1/470	7/23843	0.130104	0.468277	0.438415	Ptk2b
GO_BP_m2	GO:00360	protein O-	1/470	7/23843	0.130104	0.468277	0.438415	Lfng
GO_BP_m2	GO:003612	histone H3	1/470	7/23843	0.130104	0.468277	0.438415	Kdm3a
GO_BP_m2	GO:00362	peptidyl-se	1/470	7/23843	0.130104	0.468277	0.438415	Pink1
GO_BP_m2	GO:00363	atrioventric	1/470	7/23843	0.130104	0.468277	0.438415	Chd7
GO_BP_m2	GO:00426	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Sfrp2
GO_BP_m2	GO:00436	polyadenyl	1/470	7/23843	0.130104	0.468277	0.438415	Exosc2
GO_BP_m2	GO:004574	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Fgfbp3
GO_BP_m2	GO:00506	dermatan	1/470	7/23843	0.130104	0.468277	0.438415	Chst12
GO_BP_m2	GO:00512	mitotic spi	1/470	7/23843	0.130104	0.468277	0.438415	Aurkb
GO_BP_m2	GO:00514	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Pex5l
GO_BP_m2	GO:00517	negative re	1/470	7/23843	0.130104	0.468277	0.438415	Dkk4
GO_BP_m2	GO:00603	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Csk
GO_BP_m2	GO:006037	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Gpd1l
GO_BP_m2	GO:006044	trachea for	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:006044	bud elong	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00606	epithelial-	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00606	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00607	hair follicle	1/470	7/23843	0.130104	0.468277	0.438415	Dkk4
GO_BP_m2	GO:006104	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:006107	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Six3
GO_BP_m2	GO:00611	pulmonary	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:007164	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Mavs
GO_BP_m2	GO:007197	extracellul	1/470	7/23843	0.130104	0.468277	0.438415	Tsg101
GO_BP_m2	GO:00720	S-shaped	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00721	mesenchy	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:00722	metanephr	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:007231	clathrin co	1/470	7/23843	0.130104	0.468277	0.438415	Sh3gl1
GO_BP_m2	GO:00860	cell comm	1/470	7/23843	0.130104	0.468277	0.438415	Pde4d
GO_BP_m2	GO:009741	hypoxia-in	1/470	7/23843	0.130104	0.468277	0.438415	Cybb
GO_BP_m2	GO:009762	potassium	1/470	7/23843	0.130104	0.468277	0.438415	Kcnh2
GO_BP_m2	GO:009891	membrane	1/470	7/23843	0.130104	0.468277	0.438415	Kcnh2

GO_BP_m2	GO:190134	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:190156	fatty acid d	1/470	7/23843	0.130104	0.468277	0.438415	Oxct1
GO_BP_m2	GO:190172	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Pink1
GO_BP_m2	GO:190189	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Pde4d
GO_BP_m2	GO:190330	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Pfkfb2
GO_BP_m2	GO:190335	response t	1/470	7/23843	0.130104	0.468277	0.438415	Atf4
GO_BP_m2	GO:190335	cellular res	1/470	7/23843	0.130104	0.468277	0.438415	Atf4
GO_BP_m2	GO:190577	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Sfrp2
GO_BP_m2	GO:190590	regulation	1/470	7/23843	0.130104	0.468277	0.438415	Sfrp2
GO_BP_m2	GO:199014	intrinsic ap	1/470	7/23843	0.130104	0.468277	0.438415	Pink1
GO_BP_m2	GO:200013	positive re	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:200076	negative re	1/470	7/23843	0.130104	0.468277	0.438415	Unk
GO_BP_m2	GO:200101	mesenchy	1/470	7/23843	0.130104	0.468277	0.438415	Bmp4
GO_BP_m2	GO:000038	spliceosom	2/470	32/23843	0.130796	0.468277	0.438415	Prpf31/Snr
GO_BP_m2	GO:000698	ER-nucleus	2/470	32/23843	0.130796	0.468277	0.438415	Atf4/Mbtps
GO_BP_m2	GO:000703	peroxisom	2/470	32/23843	0.130796	0.468277	0.438415	Mavs/Pex5
GO_BP_m2	GO:001045	regulation	2/470	32/23843	0.130796	0.468277	0.438415	Bmp4/Sfrp
GO_BP_m2	GO:004003	regulation	2/470	32/23843	0.130796	0.468277	0.438415	Fgfbp3/Sul
GO_BP_m2	GO:006029	long term	2/470	32/23843	0.130796	0.468277	0.438415	Ptk2b/Stxb
GO_BP_m2	GO:006079	cell fate co	2/470	32/23843	0.130796	0.468277	0.438415	Bmp4/Sfrp
GO_BP_m2	GO:190218	regulation	2/470	32/23843	0.130796	0.468277	0.438415	Chmp3/Ts
GO_BP_m2	GO:200003	regulation	2/470	32/23843	0.130796	0.468277	0.438415	Elavl1/Kdm
GO_BP_m2	GO:000963	response t	10/470	337/23843	0.131565	0.470628	0.440616	Alad/Ect2/
GO_BP_m2	GO:000979	post-embr	5/470	136/23843	0.131746	0.470873	0.440845	Aco1/Bmp
GO_BP_m2	GO:001975	polyol met	4/470	99/23843	0.131993	0.470999	0.440964	Mtmr2/Mt
GO_BP_m2	GO:002261	ribonucleo	12/470	422/23843	0.132176	0.470999	0.440964	Chd7/Eif5/
GO_BP_m2	GO:000906	glutamine	3/470	64/23843	0.13223	0.470999	0.440964	Cad/Glul/
GO_BP_m2	GO:004333	response t	3/470	64/23843	0.13223	0.470999	0.440964	Ifna4/Mavs
GO_BP_m2	GO:004828	organelle f	13/470	466/23843	0.133841	0.476335	0.445959	Aurkb/Bmp
GO_BP_m2	GO:190595	regulation	5/470	137/23843	0.134675	0.476399	0.446019	Acat2/Acsl
GO_BP_m2	GO:000717	transmemb	10/470	339/23843	0.135157	0.476399	0.446019	Bambi/Bm
GO_BP_m2	GO:003162	receptor in	4/470	100/23843	0.135495	0.476399	0.446019	Ap2b1/Cxc
GO_BP_m2	GO:005088	endocrine	4/470	100/23843	0.135495	0.476399	0.446019	Cry1/Gdf9/
GO_BP_m2	GO:003300	muscle cell	7/470	216/23843	0.136251	0.476399	0.446019	Bmp4/Id2/
GO_BP_m2	GO:005118	cofactor bi	7/470	216/23843	0.136251	0.476399	0.446019	Coq8b/Ala
GO_BP_m2	GO:005160	defense res	7/470	216/23843	0.136251	0.476399	0.446019	Ifna4/Ifnl3/
GO_BP_m2	GO:000638	transcripti	2/470	33/23843	0.137505	0.476399	0.446019	Cebpa/Ell
GO_BP_m2	GO:001057	vascular en	2/470	33/23843	0.137505	0.476399	0.446019	Atf4/Sulf2
GO_BP_m2	GO:001404	glutamate	2/470	33/23843	0.137505	0.476399	0.446019	Grm7/Stxb
GO_BP_m2	GO:002168	cerebellar	2/470	33/23843	0.137505	0.476399	0.446019	Coq8b/Fai
GO_BP_m2	GO:004568	negative re	2/470	33/23843	0.137505	0.476399	0.446019	Bmp4/Id2
GO_BP_m2	GO:004574	negative re	2/470	33/23843	0.137505	0.476399	0.446019	Arrdc1/Lfn
GO_BP_m2	GO:004587	negative re	2/470	33/23843	0.137505	0.476399	0.446019	Ift122/Sall3
GO_BP_m2	GO:190109	negative re	2/470	33/23843	0.137505	0.476399	0.446019	Col2a1/Csf
GO_BP_m2	GO:190166	quinone m	2/470	33/23843	0.137505	0.476399	0.446019	Coq8b/Co
GO_BP_m2	GO:200124	negative re	2/470	33/23843	0.137505	0.476399	0.446019	Col2a1/Csf
GO_BP_m2	GO:000729	female gan	5/470	138/23843	0.137633	0.476399	0.446019	Gdf9/H3f3
GO_BP_m2	GO:002154	cerebellum	4/470	101/23843	0.139034	0.476399	0.446019	Coq8b/Fai

GO_BP_m2	GO:00432	regulation	4/470	101/23843	0.139034	0.476399	0.446019	Agrn/Atf4/
GO_BP_m2	GO:004667	response t	9/470	300/23843	0.140551	0.476399	0.446019	Alad/Cyb5
GO_BP_m2	GO:006027	cilium asse	9/470	300/23843	0.140551	0.476399	0.446019	2700049A
GO_BP_m2	GO:00507	regulation	6/470	178/23843	0.140817	0.476399	0.446019	Chmp3/Ma
GO_BP_m2	GO:00002	mitotic cyt	3/470	66/23843	0.141269	0.476399	0.446019	Cit/Ect2/Se
GO_BP_m2	GO:00304	ubiquitin-c	3/470	66/23843	0.141269	0.476399	0.446019	Derl1/Psm
GO_BP_m2	GO:00610	regulation	3/470	66/23843	0.141269	0.476399	0.446019	Agrn/Aplp
GO_BP_m2	GO:190551	non-motil	3/470	66/23843	0.141269	0.476399	0.446019	Ift122/Mir1
GO_BP_m2	GO:000697	response t	11/470	385/23843	0.141655	0.476399	0.446019	Atf4/Bmp4
GO_BP_m2	GO:003004	actin filam	4/470	102/23843	0.142609	0.476399	0.446019	Frmd6/Gp
GO_BP_m2	GO:00451	maintenan	4/470	102/23843	0.142609	0.476399	0.446019	Pex5l/Pink
GO_BP_m2	GO:200102	regulation	4/470	102/23843	0.142609	0.476399	0.446019	Gdf9/Rack
GO_BP_m2	GO:001061	positive re	2/470	34/23843	0.144287	0.476399	0.446019	Nr4a3/Twf
GO_BP_m2	GO:001474	positive re	2/470	34/23843	0.144287	0.476399	0.446019	Nr4a3/Twf
GO_BP_m2	GO:001907	viral releas	2/470	34/23843	0.144287	0.476399	0.446019	Chmp3/Ts
GO_BP_m2	GO:002184	cell prolife	2/470	34/23843	0.144287	0.476399	0.446019	Cep120/Si
GO_BP_m2	GO:00358	exit from h	2/470	34/23843	0.144287	0.476399	0.446019	Chmp3/Ts
GO_BP_m2	GO:00358	exit from h	2/470	34/23843	0.144287	0.476399	0.446019	Chmp3/Ts
GO_BP_m2	GO:00508	intestinal a	2/470	34/23843	0.144287	0.476399	0.446019	Acat2/Aco
GO_BP_m2	GO:00521	movement	2/470	34/23843	0.144287	0.476399	0.446019	Chmp3/Ts
GO_BP_m2	GO:00521	movement	2/470	34/23843	0.144287	0.476399	0.446019	Chmp3/Ts
GO_BP_m2	GO:19037	negative re	2/470	34/23843	0.144287	0.476399	0.446019	Acsl4/Grm
GO_BP_m2	GO:190121	regulation	10/470	344/23843	0.144363	0.476399	0.446019	Agrn/Atf4/
GO_BP_m2	GO:003027	regulation	7/470	220/23843	0.145658	0.476399	0.446019	Bmp4/Ceb
GO_BP_m2	GO:004592	negative re	8/470	261/23843	0.14575	0.476399	0.446019	Bmp4/Gdf
GO_BP_m2	GO:000602	proteoglyc	3/470	67/23843	0.145864	0.476399	0.446019	Chst12/Col
GO_BP_m2	GO:000204	sprouting	4/470	103/23843	0.146221	0.476399	0.446019	Bmp4/Jmjc
GO_BP_m2	GO:00512	maintenan	9/470	303/23843	0.146553	0.476399	0.446019	Chd7/Cry1
GO_BP_m2	GO:00032	cardiac ch	5/470	141/23843	0.146678	0.476399	0.446019	Adgrg6/B
GO_BP_m2	GO:003461	cellular res	5/470	141/23843	0.146678	0.476399	0.446019	Ect2/Rack1
GO_BP_m2	GO:00990	vesicle-me	5/470	141/23843	0.146678	0.476399	0.446019	Bloc1s2/Cp
GO_BP_m2	GO:000002	mitotic spi	1/470	8/23843	0.147257	0.476399	0.446019	Aurkb
GO_BP_m2	GO:00005	citrulline m	1/470	8/23843	0.147257	0.476399	0.446019	Cad
GO_BP_m2	GO:00005	ribosomal	1/470	8/23843	0.147257	0.476399	0.446019	Ran
GO_BP_m2	GO:000151	selenocyst	1/470	8/23843	0.147257	0.476399	0.446019	Trnau1ap
GO_BP_m2	GO:000177	plasma me	1/470	8/23843	0.147257	0.476399	0.446019	Syt11
GO_BP_m2	GO:000182	inner cell	1/470	8/23843	0.147257	0.476399	0.446019	Lats2
GO_BP_m2	GO:00064	translation	1/470	8/23843	0.147257	0.476399	0.446019	Trnau1ap
GO_BP_m2	GO:00074	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Vax1
GO_BP_m2	GO:00094	7-methylg	1/470	8/23843	0.147257	0.476399	0.446019	Tgs1
GO_BP_m2	GO:00099	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Sfrp2
GO_BP_m2	GO:00165	nucleosom	1/470	8/23843	0.147257	0.476399	0.446019	Hist1h1e
GO_BP_m2	GO:00171	peptidyl-ly	1/470	8/23843	0.147257	0.476399	0.446019	Jmjd6
GO_BP_m2	GO:001834	protein ge	1/470	8/23843	0.147257	0.476399	0.446019	Agrn
GO_BP_m2	GO:00216	cranial ner	1/470	8/23843	0.147257	0.476399	0.446019	Mafb
GO_BP_m2	GO:00218	forebrain r	1/470	8/23843	0.147257	0.476399	0.446019	Mettl14
GO_BP_m2	GO:002191	smoothene	1/470	8/23843	0.147257	0.476399	0.446019	Ift122
GO_BP_m2	GO:00303	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Acat2

GO_BP_m2	GO:003105	primary mi	1/470	8/23843	0.147257	0.476399	0.446019	Hnrnpa2b1
GO_BP_m2	GO:003112	snoRNA 3'-	1/470	8/23843	0.147257	0.476399	0.446019	Exosc2
GO_BP_m2	GO:003144	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Rnf20
GO_BP_m2	GO:003222	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Stxbp1
GO_BP_m2	GO:003262	interleukin-	1/470	8/23843	0.147257	0.476399	0.446019	Csf2
GO_BP_m2	GO:003266	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Csf2
GO_BP_m2	GO:003320	meiotic cyt	1/470	8/23843	0.147257	0.476399	0.446019	Spire2
GO_BP_m2	GO:003421	protein he	1/470	8/23843	0.147257	0.476399	0.446019	Oat
GO_BP_m2	GO:003447	U4 snRNA	1/470	8/23843	0.147257	0.476399	0.446019	Exosc2
GO_BP_m2	GO:003809	Fc-gamma	1/470	8/23843	0.147257	0.476399	0.446019	Myo1g
GO_BP_m2	GO:004204	epithelial fl	1/470	8/23843	0.147257	0.476399	0.446019	Csf2
GO_BP_m2	GO:004263	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Dkk4
GO_BP_m2	GO:004276	very long-	1/470	8/23843	0.147257	0.476399	0.446019	Slc27a2
GO_BP_m2	GO:004279	snRNA trar	1/470	8/23843	0.147257	0.476399	0.446019	Ell
GO_BP_m2	GO:004363	polyadenyl	1/470	8/23843	0.147257	0.476399	0.446019	Exosc2
GO_BP_m2	GO:004482	positive re	1/470	8/23843	0.147257	0.476399	0.446019	Ppib
GO_BP_m2	GO:004502	G0 to G1 t	1/470	8/23843	0.147257	0.476399	0.446019	Foxo4
GO_BP_m2	GO:004606	cGMP cata	1/470	8/23843	0.147257	0.476399	0.446019	Pde1a
GO_BP_m2	GO:004863	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Tll2
GO_BP_m2	GO:005145	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Pex5l
GO_BP_m2	GO:005168	establishm	1/470	8/23843	0.147257	0.476399	0.446019	Pdcd10
GO_BP_m2	GO:006004	retinal bipo	1/470	8/23843	0.147257	0.476399	0.446019	Irx5
GO_BP_m2	GO:006036	cranial sutu	1/470	8/23843	0.147257	0.476399	0.446019	Bmp4
GO_BP_m2	GO:006067	ureteric bu	1/470	8/23843	0.147257	0.476399	0.446019	Bmp4
GO_BP_m2	GO:006075	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Rac2
GO_BP_m2	GO:006162	pharyngea	1/470	8/23843	0.147257	0.476399	0.446019	Bmp4
GO_BP_m2	GO:007012	tRNA amin	1/470	8/23843	0.147257	0.476399	0.446019	Wars2
GO_BP_m2	GO:007031	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Foxo4
GO_BP_m2	GO:007149	cellular res	1/470	8/23843	0.147257	0.476399	0.446019	Mfap4
GO_BP_m2	GO:007160	chemokine	1/470	8/23843	0.147257	0.476399	0.446019	Mavs
GO_BP_m2	GO:007220	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Bmp4
GO_BP_m2	GO:007231	vesicle unc	1/470	8/23843	0.147257	0.476399	0.446019	Sh3gl1
GO_BP_m2	GO:008502	protein K6-	1/470	8/23843	0.147257	0.476399	0.446019	Rnf6
GO_BP_m2	GO:009028	cytoskeleta	1/470	8/23843	0.147257	0.476399	0.446019	Syne3
GO_BP_m2	GO:009706	ncRNA exp	1/470	8/23843	0.147257	0.476399	0.446019	Phax
GO_BP_m2	GO:009706	anterior he	1/470	8/23843	0.147257	0.476399	0.446019	Col2a1
GO_BP_m2	GO:190036	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Rnf20
GO_BP_m2	GO:190129	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Pink1
GO_BP_m2	GO:190185	positive re	1/470	8/23843	0.147257	0.476399	0.446019	Pink1
GO_BP_m2	GO:190286	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Six3
GO_BP_m2	GO:190314	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Pink1
GO_BP_m2	GO:190336	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Penk
GO_BP_m2	GO:190380	positive re	1/470	8/23843	0.147257	0.476399	0.446019	Bmp4
GO_BP_m2	GO:190415	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Ube2j1
GO_BP_m2	GO:190446	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Syt11
GO_BP_m2	GO:199050	dense core	1/470	8/23843	0.147257	0.476399	0.446019	Stxbp1
GO_BP_m2	GO:200019	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Acsl4
GO_BP_m2	GO:200048	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Prkar1a

GO_BP_m2	GO:200054	negative re	1/470	8/23843	0.147257	0.476399	0.446019	Sfrp2
GO_BP_m2	GO:200064	positive reg	1/470	8/23843	0.147257	0.476399	0.446019	Mtmr2
GO_BP_m2	GO:200082	regulation	1/470	8/23843	0.147257	0.476399	0.446019	Penk
GO_BP_m2	GO:003133	negative re	7/470	221/23843	0.148057	0.47862	0.448098	Alad/Dhx34
GO_BP_m2	GO:003030	negative re	6/470	181/23843	0.14879	0.480617	0.449968	Gdf9/Rack1
GO_BP_m2	GO:003528	segmentati	4/470	104/23843	0.149868	0.483728	0.452881	Bmp4/Lfng
GO_BP_m2	GO:004230	regulation	3/470	68/23843	0.150508	0.483733	0.452885	Bmp4/Ect2
GO_BP_m2	GO:004329	leukocyte c	3/470	68/23843	0.150508	0.483733	0.452885	Nr4a3/Rac2
GO_BP_m2	GO:004557	mast cell a	3/470	68/23843	0.150508	0.483733	0.452885	Nr4a3/Rac2
GO_BP_m2	GO:003300	regulation	2/470	35/23843	0.151138	0.483733	0.452885	Rac2/Stxbp
GO_BP_m2	GO:003579	positive reg	2/470	35/23843	0.151138	0.483733	0.452885	Bloc1s2/He
GO_BP_m2	GO:004255	pteridine-c	2/470	35/23843	0.151138	0.483733	0.452885	Pcbd1/Pm2
GO_BP_m2	GO:004330	regulation	2/470	35/23843	0.151138	0.483733	0.452885	Rac2/Stxbp
GO_BP_m2	GO:005145	intracellula	2/470	35/23843	0.151138	0.483733	0.452885	Atp6v1h/G
GO_BP_m2	GO:005197	positive reg	2/470	35/23843	0.151138	0.483733	0.452885	Aurkb/Hnr
GO_BP_m2	GO:190435	positive reg	2/470	35/23843	0.151138	0.483733	0.452885	Aurkb/Hnr
GO_BP_m2	GO:200078	regulation	2/470	35/23843	0.151138	0.483733	0.452885	Pink1/Ralb
GO_BP_m2	GO:003053	adult beha	6/470	182/23843	0.151491	0.484495	0.453599	Agrp/Chd7
GO_BP_m2	GO:000673	coenzyme	9/470	306/23843	0.152683	0.487551	0.456459	Acaca/Coq
GO_BP_m2	GO:000323	cardiac ver	5/470	143/23843	0.152845	0.487551	0.456459	Ap2b1/Bm
GO_BP_m2	GO:000918	cyclic nucle	5/470	143/23843	0.152845	0.487551	0.456459	Rack1/Guc
GO_BP_m2	GO:007182	ribonucleo	7/470	223/23843	0.152911	0.487551	0.456459	Eif5/Fastkd
GO_BP_m2	GO:003496	histone lysi	4/470	105/23843	0.15355	0.487951	0.456834	Auts2/Hist1
GO_BP_m2	GO:007190	negative re	4/470	105/23843	0.15355	0.487951	0.456834	Bmp4/Lats
GO_BP_m2	GO:009010	negative re	4/470	105/23843	0.15355	0.487951	0.456834	Bambi/Sfrp
GO_BP_m2	GO:006007	canonical W	8/470	265/23843	0.154604	0.487951	0.456834	Bambi/Dkk
GO_BP_m2	GO:004213	negative re	3/470	69/23843	0.155198	0.487951	0.456834	Bmp4/Prka
GO_BP_m2	GO:200057	positive reg	3/470	69/23843	0.155198	0.487951	0.456834	Aurkb/Hnr
GO_BP_m2	GO:003400	axis elonga	2/470	36/23843	0.158051	0.487951	0.456834	Bmp4/Sfrp
GO_BP_m2	GO:001025	multicellula	2/470	36/23843	0.158051	0.487951	0.456834	Sec63/Serp
GO_BP_m2	GO:003106	positive reg	2/470	36/23843	0.158051	0.487951	0.456834	Auts2/Rnf2
GO_BP_m2	GO:004683	phospholip	2/470	36/23843	0.158051	0.487951	0.456834	Mtmr2/Mtr
GO_BP_m2	GO:006025	regulation	2/470	36/23843	0.158051	0.487951	0.456834	Agrp/Nr4a
GO_BP_m2	GO:006138	heart trabe	2/470	36/23843	0.158051	0.487951	0.456834	Adgrg6/Ch
GO_BP_m2	GO:190269	regulation	2/470	36/23843	0.158051	0.487951	0.456834	Six3/Vax1
GO_BP_m2	GO:001059	regulation	5/470	145/23843	0.159118	0.487951	0.456834	Angpt4/Bm
GO_BP_m2	GO:000606	alcohol me	8/470	267/23843	0.159126	0.487951	0.456834	Aplp2/Ceb
GO_BP_m2	GO:004545	bone resor	3/470	70/23843	0.159933	0.487951	0.456834	Csk/Ptk2b/
GO_BP_m2	GO:004874	muscle fibe	3/470	70/23843	0.159933	0.487951	0.456834	Bmp4/Klhl4
GO_BP_m2	GO:004884	artery mor	3/470	70/23843	0.159933	0.487951	0.456834	Bmp4/Chd
GO_BP_m2	GO:200024	positive reg	3/470	70/23843	0.159933	0.487951	0.456834	Eif4g3/Lfng
GO_BP_m2	GO:000641	translationa	4/470	107/23843	0.161014	0.487951	0.456834	Ddx3y/Eif4
GO_BP_m2	GO:001907	viral genon	4/470	107/23843	0.161014	0.487951	0.456834	Mavs/Oas1
GO_BP_m2	GO:004275	regulation	4/470	107/23843	0.161014	0.487951	0.456834	Cry1/Csf2/
GO_BP_m2	GO:005102	mRNA tran	4/470	107/23843	0.161014	0.487951	0.456834	Hnrnpa2b1
GO_BP_m2	GO:004666	female sex	5/470	146/23843	0.162294	0.487951	0.456834	Bmp4/Chd
GO_BP_m2	GO:004211	T cell activa	13/470	484/23843	0.162752	0.487951	0.456834	Bmp4/Chd
GO_BP_m2	GO:000018	chromatin	1/470	9/23843	0.164072	0.487951	0.456834	Rrp8

GO_BP_m2	GO:000024	spliceosom	1/470	9/23843	0.164072	0.487951	0.456834	Prpf31
GO_BP_m2	GO:00031	secondary	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:00032	ventricular	1/470	9/23843	0.164072	0.487951	0.456834	Chd7
GO_BP_m2	GO:000601	mannose	1/470	9/23843	0.164072	0.487951	0.456834	Man2c1
GO_BP_m2	GO:00062	UTP biosy	1/470	9/23843	0.164072	0.487951	0.456834	Cad
GO_BP_m2	GO:00065	L-phenylal	1/470	9/23843	0.164072	0.487951	0.456834	Pcbd1
GO_BP_m2	GO:00065	proline me	1/470	9/23843	0.164072	0.487951	0.456834	Oat
GO_BP_m2	GO:000834	adult feedi	1/470	9/23843	0.164072	0.487951	0.456834	Agrp
GO_BP_m2	GO:00108	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Stxbp1
GO_BP_m2	GO:00140	negative r	1/470	9/23843	0.164072	0.487951	0.456834	Grm7
GO_BP_m2	GO:00158	proline tra	1/470	9/23843	0.164072	0.487951	0.456834	Slc36a4
GO_BP_m2	GO:002154	rhombom	1/470	9/23843	0.164072	0.487951	0.456834	Mafb
GO_BP_m2	GO:00218	olfactory b	1/470	9/23843	0.164072	0.487951	0.456834	Sall3
GO_BP_m2	GO:00302	chondroiti	1/470	9/23843	0.164072	0.487951	0.456834	Chst12
GO_BP_m2	GO:00302	neutrophil	1/470	9/23843	0.164072	0.487951	0.456834	Csf2
GO_BP_m2	GO:003144	positive re	1/470	9/23843	0.164072	0.487951	0.456834	Ncbp2
GO_BP_m2	GO:003164	negative r	1/470	9/23843	0.164072	0.487951	0.456834	Mtmr2
GO_BP_m2	GO:00328	glomerular	1/470	9/23843	0.164072	0.487951	0.456834	Sulf2
GO_BP_m2	GO:003497	protein fol	1/470	9/23843	0.164072	0.487951	0.456834	Emc4
GO_BP_m2	GO:00362	RNA cappi	1/470	9/23843	0.164072	0.487951	0.456834	Tgs1
GO_BP_m2	GO:00364	neuron int	1/470	9/23843	0.164072	0.487951	0.456834	Pink1
GO_BP_m2	GO:00421	ketone cat	1/470	9/23843	0.164072	0.487951	0.456834	Oxct1
GO_BP_m2	GO:00433	enucleate	1/470	9/23843	0.164072	0.487951	0.456834	Id2
GO_BP_m2	GO:004614	tetrahydro	1/470	9/23843	0.164072	0.487951	0.456834	Pcbd1
GO_BP_m2	GO:00512	spindle elo	1/470	9/23843	0.164072	0.487951	0.456834	Aurkb
GO_BP_m2	GO:00512	spindle mi	1/470	9/23843	0.164072	0.487951	0.456834	Aurkb
GO_BP_m2	GO:00600	convergen	1/470	9/23843	0.164072	0.487951	0.456834	Sfrp2
GO_BP_m2	GO:00601	embryonic	1/470	9/23843	0.164072	0.487951	0.456834	Acsl4
GO_BP_m2	GO:00605	mammary	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:00610	pattern sp	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:00701	kynurenine	1/470	9/23843	0.164072	0.487951	0.456834	Kyat3
GO_BP_m2	GO:00708	negative r	1/470	9/23843	0.164072	0.487951	0.456834	Ube2j1
GO_BP_m2	GO:00714	cellular re	1/470	9/23843	0.164072	0.487951	0.456834	Sfrp2
GO_BP_m2	GO:007187	response t	1/470	9/23843	0.164072	0.487951	0.456834	Pde4d
GO_BP_m2	GO:007187	cellular re	1/470	9/23843	0.164072	0.487951	0.456834	Pde4d
GO_BP_m2	GO:007201	glomerular	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:007204	renal syste	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:007221	negative r	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:007231	glomerular	1/470	9/23843	0.164072	0.487951	0.456834	Bmp4
GO_BP_m2	GO:007264	type I inter	1/470	9/23843	0.164072	0.487951	0.456834	Mavs
GO_BP_m2	GO:007264	interferon-	1/470	9/23843	0.164072	0.487951	0.456834	Mavs
GO_BP_m2	GO:00860	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Agrn
GO_BP_m2	GO:009004	positive re	1/470	9/23843	0.164072	0.487951	0.456834	Pink1
GO_BP_m2	GO:009877	positive re	1/470	9/23843	0.164072	0.487951	0.456834	Pink1
GO_BP_m2	GO:00996	endosome	1/470	9/23843	0.164072	0.487951	0.456834	Rab11a
GO_BP_m2	GO:19001	negative r	1/470	9/23843	0.164072	0.487951	0.456834	Syt11
GO_BP_m2	GO:19015	positive re	1/470	9/23843	0.164072	0.487951	0.456834	Pink1
GO_BP_m2	GO:19022	erythrose	1/470	9/23843	0.164072	0.487951	0.456834	Pcbd1

GO_BP_m2	GO:190273	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Mavs
GO_BP_m2	GO:190274	positive reg	1/470	9/23843	0.164072	0.487951	0.456834	Mavs
GO_BP_m2	GO:190337	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Pink1
GO_BP_m2	GO:190386	positive reg	1/470	9/23843	0.164072	0.487951	0.456834	Pink1
GO_BP_m2	GO:190433	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Sfrp2
GO_BP_m2	GO:190439	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Agrn
GO_BP_m2	GO:190472	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Acat2
GO_BP_m2	GO:190545	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Zbtb1
GO_BP_m2	GO:200005	negative re	1/470	9/23843	0.164072	0.487951	0.456834	Sfrp2
GO_BP_m2	GO:200038	negative re	1/470	9/23843	0.164072	0.487951	0.456834	Sfrp2
GO_BP_m2	GO:200064	regulation	1/470	9/23843	0.164072	0.487951	0.456834	Mtmr2
GO_BP_m2	GO:004273	embryonic	3/470	71/23843	0.164712	0.487951	0.456834	Bmp4/Ift12
GO_BP_m2	GO:000008	G2/M trans	4/470	108/23843	0.164795	0.487951	0.456834	Cit/Foxo4/
GO_BP_m2	GO:000698	response t	4/470	108/23843	0.164795	0.487951	0.456834	Atf4/Derl1/
GO_BP_m2	GO:001092	cellular cor	4/470	108/23843	0.164795	0.487951	0.456834	Klhl41/Mtm
GO_BP_m2	GO:003524	synaptic tra	4/470	108/23843	0.164795	0.487951	0.456834	Glul/Grm7/
GO_BP_m2	GO:007134	cellular res	4/470	108/23843	0.164795	0.487951	0.456834	Eprs/Il12rb
GO_BP_m2	GO:000018	nuclear-tra	2/470	37/23843	0.165022	0.487951	0.456834	Dhx34/Ncb
GO_BP_m2	GO:001623	telomere ca	2/470	37/23843	0.165022	0.487951	0.456834	Aurkb/Hnrn
GO_BP_m2	GO:003085	granulocyt	2/470	37/23843	0.165022	0.487951	0.456834	Cebpa/Csf2
GO_BP_m2	GO:003312	positive reg	2/470	37/23843	0.165022	0.487951	0.456834	Dyrk1a/Thr
GO_BP_m2	GO:003820	TORC1 sign	2/470	37/23843	0.165022	0.487951	0.456834	Gatsl2/Itfg2
GO_BP_m2	GO:004600	regulation	2/470	37/23843	0.165022	0.487951	0.456834	Il12rb1/Prk
GO_BP_m2	GO:004616	alcohol cat	2/470	37/23843	0.165022	0.487951	0.456834	Mtmr2/Mtr
GO_BP_m2	GO:004825	mRNA stab	2/470	37/23843	0.165022	0.487951	0.456834	Elavl1/Thra
GO_BP_m2	GO:007260	interleukin-	2/470	37/23843	0.165022	0.487951	0.456834	Mavs/Syt11
GO_BP_m2	GO:190571	positive reg	2/470	37/23843	0.165022	0.487951	0.456834	Bloc1s2/He
GO_BP_m2	GO:200014	regulation	2/470	37/23843	0.165022	0.487951	0.456834	Cebpa/Psm
GO_BP_m2	GO:003320	cardiac cha	6/470	187/23843	0.165323	0.487951	0.456834	Adgrg6/Ap
GO_BP_m2	GO:000600	glucose me	6/470	187/23843	0.165323	0.487951	0.456834	Atf4/Cry1/
GO_BP_m2	GO:004424	cellular lipi	6/470	187/23843	0.165323	0.487951	0.456834	Acat2/Echo
GO_BP_m2	GO:000756	aging	7/470	228/23843	0.165364	0.487951	0.456834	Id2/Mirlet7
GO_BP_m2	GO:000007	mitotic sist	5/470	147/23843	0.165495	0.487996	0.456876	Aurkb/Cit/
GO_BP_m2	GO:004578	negative re	12/470	442/23843	0.166019	0.489195	0.457999	Aurkb/Bmp
GO_BP_m2	GO:000693	smooth mu	4/470	109/23843	0.168608	0.495781	0.464165	Myh11/Pde
GO_BP_m2	GO:000995	dorsal/vent	4/470	109/23843	0.168608	0.495781	0.464165	Bmp4/Ift12
GO_BP_m2	GO:004407	regulation	4/470	109/23843	0.168608	0.495781	0.464165	Acsl4/Erfe/
GO_BP_m2	GO:003050	regulation	3/470	72/23843	0.169533	0.498152	0.466385	Bmp4/Nbr1
GO_BP_m2	GO:007123	cellular res	6/470	189/23843	0.171002	0.501414	0.469439	Ect2/Rack1
GO_BP_m2	GO:007180	cellular pot	6/470	189/23843	0.171002	0.501414	0.469439	Agrn/Kcne4
GO_BP_m2	GO:007180	potassium	6/470	189/23843	0.171002	0.501414	0.469439	Agrn/Kcne4
GO_BP_m2	GO:003105	regulation	5/470	149/23843	0.171972	0.50237	0.470334	Auts2/Kdm
GO_BP_m2	GO:003252	protein exi	2/470	38/23843	0.172046	0.50237	0.470334	Derl1/Ube2
GO_BP_m2	GO:004408	regulation	2/470	38/23843	0.172046	0.50237	0.470334	Pink1/Ralb
GO_BP_m2	GO:004502	plasma me	2/470	38/23843	0.172046	0.50237	0.470334	Izumo1r/St
GO_BP_m2	GO:005043	amyloid-be	2/470	38/23843	0.172046	0.50237	0.470334	Bace1/Dyrk
GO_BP_m2	GO:190595	negative re	2/470	38/23843	0.172046	0.50237	0.470334	Acsl4/Cry1
GO_BP_m2	GO:000858	female gor	4/470	110/23843	0.172452	0.502855	0.470788	Bmp4/Gdf9

GO_BP_m2	GO:003051	intracellula	4/470	110/23843	0.172452	0.502855	0.470788	Cry1/Kdm
GO_BP_m2	GO:001571	organic ani	11/470	402/23843	0.17291	0.50304	0.470961	Slc6a21/Ac
GO_BP_m2	GO:00609	regulation	3/470	73/23843	0.174394	0.50304	0.470961	Bmp4/Dnd
GO_BP_m2	GO:19045	regulation	3/470	73/23843	0.174394	0.50304	0.470961	Bmp4/Ect2
GO_BP_m2	GO:00511	nuclear ex	5/470	150/23843	0.175247	0.50304	0.470961	Hnrnpa2b1
GO_BP_m2	GO:00074	mesoderm	4/470	111/23843	0.176326	0.50304	0.470961	Bmp4/Nr4
GO_BP_m2	GO:00723	monocarb	4/470	111/23843	0.176326	0.50304	0.470961	Acat2/Echo
GO_BP_m2	GO:00015	angiogene	13/470	492/23843	0.176554	0.50304	0.470961	Angpt4/Bm
GO_BP_m2	GO:00190	viral life cy	6/470	191/23843	0.17676	0.50304	0.470961	Chmp3/Ma
GO_BP_m2	GO:00712	cellular res	8/470	275/23843	0.177819	0.50304	0.470961	Aurkb/Ect2
GO_BP_m2	GO:01040	cellular res	8/470	275/23843	0.177819	0.50304	0.470961	Aurkb/Ect2
GO_BP_m2	GO:00507	negative re	9/470	318/23843	0.178422	0.50304	0.470961	Bmp4/Cit/
GO_BP_m2	GO:00018	receptor re	2/470	39/23843	0.179118	0.50304	0.470961	Caml/Vam
GO_BP_m2	GO:00219	pituitary gl	2/470	39/23843	0.179118	0.50304	0.470961	Bmp4/Six3
GO_BP_m2	GO:00311	developme	2/470	39/23843	0.179118	0.50304	0.470961	Bmp4/Six3
GO_BP_m2	GO:00427	hydrogen	2/470	39/23843	0.179118	0.50304	0.470961	Cybb/Pink
GO_BP_m2	GO:00447	protein tra	2/470	39/23843	0.179118	0.50304	0.470961	Pex5l/Tom
GO_BP_m2	GO:00450	early endo	2/470	39/23843	0.179118	0.50304	0.470961	Chmp3/Mt
GO_BP_m2	GO:00457	positive re	2/470	39/23843	0.179118	0.50304	0.470961	Lfng/Pdcd
GO_BP_m2	GO:00458	pH reducti	2/470	39/23843	0.179118	0.50304	0.470961	Atp6v1h/G
GO_BP_m2	GO:000231	B cell activ	3/470	74/23843	0.179294	0.50304	0.470961	Itfg2/Lfng/
GO_BP_m2	GO:00086	extrinsic a	3/470	74/23843	0.179294	0.50304	0.470961	Bloc1s2/Fa
GO_BP_m2	GO:00325	maintenan	3/470	74/23843	0.179294	0.50304	0.470961	Pink1/Syne
GO_BP_m2	GO:00080	tRNA proc	4/470	112/23843	0.180229	0.50304	0.470961	Ftsj1/Nsun
GO_BP_m2	GO:004247	inner ear m	4/470	112/23843	0.180229	0.50304	0.470961	Chd7/Col2
GO_BP_m2	GO:00000	ribosomal	1/470	10/23843	0.180556	0.50304	0.470961	Ran
GO_BP_m2	GO:00020	negative re	1/470	10/23843	0.180556	0.50304	0.470961	Mtmr2
GO_BP_m2	GO:00060	fructose m	1/470	10/23843	0.180556	0.50304	0.470961	Pfkfb4
GO_BP_m2	GO:00060	glucose ca	1/470	10/23843	0.180556	0.50304	0.470961	Pfkfb2
GO_BP_m2	GO:00063	tRNA splici	1/470	10/23843	0.180556	0.50304	0.470961	Rtcb
GO_BP_m2	GO:00066	posttransla	1/470	10/23843	0.180556	0.50304	0.470961	Sec63
GO_BP_m2	GO:00093	snRNA tra	1/470	10/23843	0.180556	0.50304	0.470961	Ell
GO_BP_m2	GO:00096	UV protect	1/470	10/23843	0.180556	0.50304	0.470961	Mfap4
GO_BP_m2	GO:001091	negative re	1/470	10/23843	0.180556	0.50304	0.470961	Hebp2
GO_BP_m2	GO:00109	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Csk
GO_BP_m2	GO:00148	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Lfng
GO_BP_m2	GO:001581	glycine tra	1/470	10/23843	0.180556	0.50304	0.470961	Slc25a38
GO_BP_m2	GO:00182	peptidyl-m	1/470	10/23843	0.180556	0.50304	0.470961	Metap2
GO_BP_m2	GO:00215	optic nerve	1/470	10/23843	0.180556	0.50304	0.470961	Tmem126
GO_BP_m2	GO:00220	interkinetic	1/470	10/23843	0.180556	0.50304	0.470961	Cep120
GO_BP_m2	GO:00310	chromatin	1/470	10/23843	0.180556	0.50304	0.470961	H3f3b
GO_BP_m2	GO:00324	positive re	1/470	10/23843	0.180556	0.50304	0.470961	Rack1
GO_BP_m2	GO:00329	inositol tris	1/470	10/23843	0.180556	0.50304	0.470961	Ptk2b
GO_BP_m2	GO:00330	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Bmp4
GO_BP_m2	GO:00330	negative re	1/470	10/23843	0.180556	0.50304	0.470961	Bmp4
GO_BP_m2	GO:00331	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Pfkfb2
GO_BP_m2	GO:00331	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Rnf20
GO_BP_m2	GO:00344	nuclear-tra	1/470	10/23843	0.180556	0.50304	0.470961	Exosc2

GO_BP_m2	GO:003572	common n	1/470	10/23843	0.180556	0.50304	0.470961	Nr4a3
GO_BP_m2	GO:003649	PERK-med	1/470	10/23843	0.180556	0.50304	0.470961	Atf4
GO_BP_m2	GO:004314	snoRNA pr	1/470	10/23843	0.180556	0.50304	0.470961	Exosc2
GO_BP_m2	GO:004392	exonucleol	1/470	10/23843	0.180556	0.50304	0.470961	Exosc2
GO_BP_m2	GO:004605	UTP metab	1/470	10/23843	0.180556	0.50304	0.470961	Cad
GO_BP_m2	GO:004809	chromatin-	1/470	10/23843	0.180556	0.50304	0.470961	Smarcd1
GO_BP_m2	GO:004867	negative re	1/470	10/23843	0.180556	0.50304	0.470961	Spg20
GO_BP_m2	GO:005112	synaptic gr	1/470	10/23843	0.180556	0.50304	0.470961	Agrn
GO_BP_m2	GO:005145	corticotrop	1/470	10/23843	0.180556	0.50304	0.470961	Pex5l
GO_BP_m2	GO:006051	prostatic b	1/470	10/23843	0.180556	0.50304	0.470961	Bmp4
GO_BP_m2	GO:006063	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Eif4g3
GO_BP_m2	GO:006071	chorio-alla	1/470	10/23843	0.180556	0.50304	0.470961	Erf
GO_BP_m2	GO:007024	negative re	1/470	10/23843	0.180556	0.50304	0.470961	Bmp4
GO_BP_m2	GO:008000	mRNA met	1/470	10/23843	0.180556	0.50304	0.470961	Mettl14
GO_BP_m2	GO:009048	pyrimidine	1/470	10/23843	0.180556	0.50304	0.470961	Slc35a4
GO_BP_m2	GO:009742	liver regen	1/470	10/23843	0.180556	0.50304	0.470961	Sulf2
GO_BP_m2	GO:190003	negative re	1/470	10/23843	0.180556	0.50304	0.470961	Pink1
GO_BP_m2	GO:190045	positive reg	1/470	10/23843	0.180556	0.50304	0.470961	Pink1
GO_BP_m2	GO:190133	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Bmp4
GO_BP_m2	GO:200084	regulation	1/470	10/23843	0.180556	0.50304	0.470961	Cry1
GO_BP_m2	GO:000170	in utero en	12/470	450/23843	0.180668	0.50304	0.470961	Cebpa/Chc
GO_BP_m2	GO:001645	gene silenc	8/470	277/23843	0.182639	0.508191	0.475784	Bmp4/Dnd
GO_BP_m2	GO:002203	metenceph	4/470	113/23843	0.184161	0.511267	0.478663	Coq8b/Fair
GO_BP_m2	GO:004654	developme	4/470	113/23843	0.184161	0.511267	0.478663	Bmp4/Gdf9
GO_BP_m2	GO:000648	protein N-	3/470	75/23843	0.184232	0.511267	0.478663	Mgat1/Ser
GO_BP_m2	GO:003464	cellular res	3/470	75/23843	0.184232	0.511267	0.478663	Aurkb/Mfa
GO_BP_m2	GO:000673	oxidoreduc	5/470	153/23843	0.185211	0.512753	0.480054	Coq8b/Coc
GO_BP_m2	GO:009017	organelle r	5/470	153/23843	0.185211	0.512753	0.480054	Chmp3/Sn
GO_BP_m2	GO:000193	negative re	2/470	40/23843	0.186233	0.512753	0.480054	Pdcd10/Pt
GO_BP_m2	GO:000602	glycosamir	2/470	40/23843	0.186233	0.512753	0.480054	Chst12/Chs
GO_BP_m2	GO:000618	cGMP bios	2/470	40/23843	0.186233	0.512753	0.480054	Gucy2c/Ptk
GO_BP_m2	GO:000637	mRNA poly	2/470	40/23843	0.186233	0.512753	0.480054	Pabpn1/Rr
GO_BP_m2	GO:001082	regulation	2/470	40/23843	0.186233	0.512753	0.480054	Cep120/Ch
GO_BP_m2	GO:003201	ARF protei	2/470	40/23843	0.186233	0.512753	0.480054	Arap3/Sma
GO_BP_m2	GO:003201	regulation	2/470	40/23843	0.186233	0.512753	0.480054	Arap3/Sma
GO_BP_m2	GO:007154	dopaminer	2/470	40/23843	0.186233	0.512753	0.480054	Lmx1b/Sfr
GO_BP_m2	GO:008600	cardiac mu	2/470	40/23843	0.186233	0.512753	0.480054	Gpd1l/Kcn
GO_BP_m2	GO:009878	ncRNA trar	2/470	40/23843	0.186233	0.512753	0.480054	Ell/Sirt7
GO_BP_m2	GO:004478	cilium orga	9/470	322/23843	0.187416	0.515669	0.482785	2700049A0
GO_BP_m2	GO:000648	protein gly	6/470	195/23843	0.188509	0.517658	0.484647	Galnt2/Lfn
GO_BP_m2	GO:000689	receptor-n	6/470	195/23843	0.188509	0.517658	0.484647	Ap2b1/Ara
GO_BP_m2	GO:004341	macromole	6/470	195/23843	0.188509	0.517658	0.484647	Galnt2/Lfn
GO_BP_m2	GO:003133	positive reg	7/470	237/23843	0.188858	0.518278	0.485228	Cebpa/Csf2
GO_BP_m2	GO:001604	cell growth	13/470	499/23843	0.189086	0.518551	0.485483	Acsl4/Auts2
GO_BP_m2	GO:005127	regulation	3/470	76/23843	0.189204	0.518551	0.485483	Chd7/Pde4
GO_BP_m2	GO:002169	cerebellar (	2/470	41/23843	0.193388	0.52077	0.487561	Coq8b/Fair
GO_BP_m2	GO:003519	production	2/470	41/23843	0.193388	0.52077	0.487561	Bmp4/Hnr
GO_BP_m2	GO:004218	ketone bio	2/470	41/23843	0.193388	0.52077	0.487561	Coq8b/Coc

GO_BP_m2	GO:005069	regulation	2/470	41/23843	0.193388	0.52077	0.487561	Il12rb1/Ma
GO_BP_m2	GO:006101	positive reg	2/470	41/23843	0.193388	0.52077	0.487561	Mettl14/Zc
GO_BP_m2	GO:006151	protein loc	2/470	41/23843	0.193388	0.52077	0.487561	Crocc/Ift12
GO_BP_m2	GO:009892	vesicle-me	2/470	41/23843	0.193388	0.52077	0.487561	Chmp3/Mt
GO_BP_m2	GO:000641	translationa	3/470	77/23843	0.194211	0.52077	0.487561	2810006K2
GO_BP_m2	GO:001038	regulation	3/470	77/23843	0.194211	0.52077	0.487561	Foxo4/Kcnl
GO_BP_m2	GO:009063	activation	3/470	77/23843	0.194211	0.52077	0.487561	Ect2/Eif5/P
GO_BP_m2	GO:190160	alpha-amin	3/470	77/23843	0.194211	0.52077	0.487561	Hmgcl/Ivd/
GO_BP_m2	GO:000173	formation	1/470	11/23843	0.196716	0.52077	0.487561	Eif5
GO_BP_m2	GO:000211	aggressive	1/470	11/23843	0.196716	0.52077	0.487561	Penk
GO_BP_m2	GO:000652	arginine ca	1/470	11/23843	0.196716	0.52077	0.487561	Oat
GO_BP_m2	GO:000688	intracellula	1/470	11/23843	0.196716	0.52077	0.487561	Fthl17f
GO_BP_m2	GO:000920	pyrimidine	1/470	11/23843	0.196716	0.52077	0.487561	Cad
GO_BP_m2	GO:001074	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Csf2
GO_BP_m2	GO:001487	response t	1/470	11/23843	0.196716	0.52077	0.487561	Srl
GO_BP_m2	GO:001618	synaptic ve	1/470	11/23843	0.196716	0.52077	0.487561	Stxbp1
GO_BP_m2	GO:003127	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Klhl41
GO_BP_m2	GO:003150	heterochro	1/470	11/23843	0.196716	0.52077	0.487561	H3f3b
GO_BP_m2	GO:003308	immature T	1/470	11/23843	0.196716	0.52077	0.487561	Bmp4
GO_BP_m2	GO:003332	Leydig cell	1/470	11/23843	0.196716	0.52077	0.487561	Sgpl1
GO_BP_m2	GO:003360	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Pink1
GO_BP_m2	GO:003593	glucocortic	1/470	11/23843	0.196716	0.52077	0.487561	Cry1
GO_BP_m2	GO:004564	negative re	1/470	11/23843	0.196716	0.52077	0.487561	Mafb
GO_BP_m2	GO:004600	negative re	1/470	11/23843	0.196716	0.52077	0.487561	Prkar1a
GO_BP_m2	GO:004660	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Cep120
GO_BP_m2	GO:004863	skeletal mu	1/470	11/23843	0.196716	0.52077	0.487561	Tll2
GO_BP_m2	GO:005066	hydrogen p	1/470	11/23843	0.196716	0.52077	0.487561	Cybb
GO_BP_m2	GO:005115	negative re	1/470	11/23843	0.196716	0.52077	0.487561	Foxo4
GO_BP_m2	GO:005160	exocyst loc	1/470	11/23843	0.196716	0.52077	0.487561	Ralb
GO_BP_m2	GO:005190	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Rack1
GO_BP_m2	GO:006001	righting ref	1/470	11/23843	0.196716	0.52077	0.487561	Auts2
GO_BP_m2	GO:006017	limb bud fo	1/470	11/23843	0.196716	0.52077	0.487561	Col2a1
GO_BP_m2	GO:006034	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Mavs
GO_BP_m2	GO:006108	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Nr4a3
GO_BP_m2	GO:006130	cardiac neu	1/470	11/23843	0.196716	0.52077	0.487561	Bmp4
GO_BP_m2	GO:007093	histone H4	1/470	11/23843	0.196716	0.52077	0.487561	Sirt7
GO_BP_m2	GO:007104	histone mR	1/470	11/23843	0.196716	0.52077	0.487561	Xrn1
GO_BP_m2	GO:007186	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Shc1
GO_BP_m2	GO:007212	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Bmp4
GO_BP_m2	GO:007217	nephric du	1/470	11/23843	0.196716	0.52077	0.487561	Bmp4
GO_BP_m2	GO:009039	negative re	1/470	11/23843	0.196716	0.52077	0.487561	Mtmr2
GO_BP_m2	GO:009757	sequesterin	1/470	11/23843	0.196716	0.52077	0.487561	Fthl17f
GO_BP_m2	GO:009878	pre-mRNA	1/470	11/23843	0.196716	0.52077	0.487561	Ncbp2
GO_BP_m2	GO:190036	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Rnf20
GO_BP_m2	GO:190329	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Pfkfb2
GO_BP_m2	GO:190358	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Pdcd10
GO_BP_m2	GO:190365	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Mtmr2
GO_BP_m2	GO:190415	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Ube2j1

GO_BP_m2	GO:200003	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Sfrp2
GO_BP_m2	GO:200032	regulation	1/470	11/23843	0.196716	0.52077	0.487561	Cry1
GO_BP_m2	GO:200078	positive reg	1/470	11/23843	0.196716	0.52077	0.487561	Ralb
GO_BP_m2	GO:009015	establishm	6/470	198/23843	0.197513	0.522551	0.489228	Csk/Rack1/
GO_BP_m2	GO:000859	regulation	3/470	78/23843	0.19925	0.525355	0.491853	Arrdc1/Lfn
GO_BP_m2	GO:006007	excitatory p	3/470	78/23843	0.19925	0.525355	0.491853	Mtmr2/Ptk
GO_BP_m2	GO:006041	cardiac sep	3/470	78/23843	0.19925	0.525355	0.491853	Bmp4/Chd
GO_BP_m2	GO:004873	gland deve	12/470	460/23843	0.199811	0.525355	0.491853	Bmp4/Ceb
GO_BP_m2	GO:001715	calcium ior	4/470	117/23843	0.200161	0.525355	0.491853	Cplx4/Stxb
GO_BP_m2	GO:000038	regulation	2/470	42/23843	0.200577	0.525355	0.491853	Dyrk1a/Thr
GO_BP_m2	GO:001607	snRNA met	2/470	42/23843	0.200577	0.525355	0.491853	Ell/Exosc2
GO_BP_m2	GO:003105	dsRNA frag	2/470	42/23843	0.200577	0.525355	0.491853	Bmp4/Hnrr
GO_BP_m2	GO:003419	cellular res	2/470	42/23843	0.200577	0.525355	0.491853	Atf4/Itfg2
GO_BP_m2	GO:004001	positive reg	2/470	42/23843	0.200577	0.525355	0.491853	Chd7/Ppib
GO_BP_m2	GO:004207	intraciliary	2/470	42/23843	0.200577	0.525355	0.491853	Ift122/Ttc3
GO_BP_m2	GO:004230	positive reg	2/470	42/23843	0.200577	0.525355	0.491853	Ect2/Mavs
GO_BP_m2	GO:004348	RNA stabili	2/470	42/23843	0.200577	0.525355	0.491853	Elavl1/Thra
GO_BP_m2	GO:004363	RNA polya	2/470	42/23843	0.200577	0.525355	0.491853	Pabpn1/Rr
GO_BP_m2	GO:007091	production	2/470	42/23843	0.200577	0.525355	0.491853	Bmp4/Hnrr
GO_BP_m2	GO:009031	regulation	2/470	42/23843	0.200577	0.525355	0.491853	Dyrk1a/Pin
GO_BP_m2	GO:003238	regulation	11/470	417/23843	0.203002	0.531377	0.497491	Bmp4/Chm
GO_BP_m2	GO:000627	regulation	4/470	118/23843	0.204225	0.533496	0.499475	Bmp4/Csf2
GO_BP_m2	GO:001699	antibiotic n	4/470	118/23843	0.204225	0.533496	0.499475	Aco1/Cybb
GO_BP_m2	GO:006004	cardiac mu	4/470	118/23843	0.204225	0.533496	0.499475	Agrn/Gpd1
GO_BP_m2	GO:004852	positive reg	3/470	79/23843	0.20432	0.533496	0.499475	Chmp3/Pp
GO_BP_m2	GO:004677	protein aut	7/470	243/23843	0.205234	0.535029	0.50091	Cad/Clk1/C
GO_BP_m2	GO:007138	cellular res	6/470	201/23843	0.206675	0.535029	0.50091	Bmp4/Cry1
GO_BP_m2	GO:001556	branching	2/470	43/23843	0.207796	0.535029	0.50091	Fkbpl/Sfrp2
GO_BP_m2	GO:003325	regulation	2/470	43/23843	0.207796	0.535029	0.50091	Rack1/Gpd
GO_BP_m2	GO:000604	amino suga	2/470	43/23843	0.207796	0.535029	0.50091	Chst5/Mga
GO_BP_m2	GO:008601	membrane	2/470	43/23843	0.207796	0.535029	0.50091	Kcnh2/Tpc
GO_BP_m2	GO:003033	negative re	7/470	244/23843	0.208015	0.535029	0.50091	Angpt4/Ara
GO_BP_m2	GO:007030	Golgi orga	4/470	119/23843	0.208313	0.535029	0.50091	Cit/Pdcd10
GO_BP_m2	GO:000820	cholesterol	4/470	119/23843	0.208313	0.535029	0.50091	Aplp2/Ceb
GO_BP_m2	GO:000227	myeloid ce	3/470	80/23843	0.20942	0.535029	0.50091	Nr4a3/Rac
GO_BP_m2	GO:004883	inner ear d	6/470	202/23843	0.209762	0.535029	0.50091	Bmp4/Ceb
GO_BP_m2	GO:006004	heart contr	6/470	202/23843	0.209762	0.535029	0.50091	Agrn/Gpd1
GO_BP_m2	GO:004269	muscle cell	10/470	376/23843	0.210355	0.535029	0.50091	Asf1a/Bmp
GO_BP_m2	GO:003313	positive reg	4/470	120/23843	0.212425	0.535029	0.50091	Ifna4/Pdcd
GO_BP_m2	GO:000039	RNA splicir	1/470	12/23843	0.212558	0.535029	0.50091	Rtcb
GO_BP_m2	GO:000312	heart field	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:000333	mesenchyr	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:000604	UDP-N-ac	1/470	12/23843	0.212558	0.535029	0.50091	Mgat1
GO_BP_m2	GO:000607	glycerol-3-	1/470	12/23843	0.212558	0.535029	0.50091	Gpd1l
GO_BP_m2	GO:000911	vitamin cat	1/470	12/23843	0.212558	0.535029	0.50091	Pm20d2
GO_BP_m2	GO:000920	pyrimidine	1/470	12/23843	0.212558	0.535029	0.50091	Cad
GO_BP_m2	GO:001031	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Pink1
GO_BP_m2	GO:001045	centriole-c	1/470	12/23843	0.212558	0.535029	0.50091	Crocc

GO_BP_m2	GO:00157	nucleotide	1/470	12/23843	0.212558	0.535029	0.50091	Slc35a4
GO_BP_m2	GO:00165	protein im	1/470	12/23843	0.212558	0.535029	0.50091	Pex5l
GO_BP_m2	GO:00199	cGMP-me	1/470	12/23843	0.212558	0.535029	0.50091	Ptk2b
GO_BP_m2	GO:00302	intestinal c	1/470	12/23843	0.212558	0.535029	0.50091	Acat2
GO_BP_m2	GO:00311	rRNA 3'-e	1/470	12/23843	0.212558	0.535029	0.50091	Exosc2
GO_BP_m2	GO:00328	positive re	1/470	12/23843	0.212558	0.535029	0.50091	Zbtb1
GO_BP_m2	GO:00330	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:00335	histone H2	1/470	12/23843	0.212558	0.535029	0.50091	Rnf20
GO_BP_m2	GO:00336	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Farp2
GO_BP_m2	GO:003597	peptidyl-t	1/470	12/23843	0.212558	0.535029	0.50091	Pdp1
GO_BP_m2	GO:00427	long-chain	1/470	12/23843	0.212558	0.535029	0.50091	Fads1
GO_BP_m2	GO:00429	sequesterin	1/470	12/23843	0.212558	0.535029	0.50091	Twf1
GO_BP_m2	GO:00436	engulfmen	1/470	12/23843	0.212558	0.535029	0.50091	Rac2
GO_BP_m2	GO:00440	positive re	1/470	12/23843	0.212558	0.535029	0.50091	Ralb
GO_BP_m2	GO:00519	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Ect2
GO_BP_m2	GO:00601	positive re	1/470	12/23843	0.212558	0.535029	0.50091	Serp1
GO_BP_m2	GO:00604	bronchus	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:00604	trachea m	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:00605	epithelial c	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:006117	negative re	1/470	12/23843	0.212558	0.535029	0.50091	Ucp2
GO_BP_m2	GO:00614	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Nr4a3
GO_BP_m2	GO:00709	histone H3	1/470	12/23843	0.212558	0.535029	0.50091	Sirt7
GO_BP_m2	GO:007134	skeletal mu	1/470	12/23843	0.212558	0.535029	0.50091	Agrn
GO_BP_m2	GO:00718	cell prolifer	1/470	12/23843	0.212558	0.535029	0.50091	Shc1
GO_BP_m2	GO:00718	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Shc1
GO_BP_m2	GO:007204	collecting	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:007211	glomerular	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:007217	nephric du	1/470	12/23843	0.212558	0.535029	0.50091	Bmp4
GO_BP_m2	GO:008601	membrane	1/470	12/23843	0.212558	0.535029	0.50091	Kcnh2
GO_BP_m2	GO:00902	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Auts2
GO_BP_m2	GO:00989	neurotrans	1/470	12/23843	0.212558	0.535029	0.50091	Rab11a
GO_BP_m2	GO:19012	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Pink1
GO_BP_m2	GO:190257	protein loc	1/470	12/23843	0.212558	0.535029	0.50091	Ran
GO_BP_m2	GO:19029	negative re	1/470	12/23843	0.212558	0.535029	0.50091	Pink1
GO_BP_m2	GO:190354	establishm	1/470	12/23843	0.212558	0.535029	0.50091	Rab11a
GO_BP_m2	GO:19042	negative re	1/470	12/23843	0.212558	0.535029	0.50091	Ube2j1
GO_BP_m2	GO:190447	regulation	1/470	12/23843	0.212558	0.535029	0.50091	Acat2
GO_BP_m2	GO:00309	hindbrain	5/470	161/23843	0.212735	0.535154	0.501027	Coq8b/Fai
GO_BP_m2	GO:000801	blood circu	12/470	467/23843	0.213731	0.536817	0.502585	Agrn/Chd7
GO_BP_m2	GO:00032	ventricular	3/470	81/23843	0.214548	0.536817	0.502585	Ap2b1/Bm
GO_BP_m2	GO:000647	protein de	3/470	81/23843	0.214548	0.536817	0.502585	Dyrk1a/Pin
GO_BP_m2	GO:000721	glutamate	3/470	81/23843	0.214548	0.536817	0.502585	Grm7/Pink
GO_BP_m2	GO:00159	fatty acid t	3/470	81/23843	0.214548	0.536817	0.502585	Acsl4/Erfe/
GO_BP_m2	GO:001921	regulation	3/470	81/23843	0.214548	0.536817	0.502585	Acsl4/Erfe/
GO_BP_m2	GO:00486	neuron fat	3/470	81/23843	0.214548	0.536817	0.502585	Bmp4/Id2/
GO_BP_m2	GO:00701	regulation	3/470	81/23843	0.214548	0.536817	0.502585	Bmp4/Nbr
GO_BP_m2	GO:00975	lamellipodi	3/470	81/23843	0.214548	0.536817	0.502585	Auts2/Rac
GO_BP_m2	GO:00069	vesicle doc	2/470	44/23843	0.215042	0.537093	0.502843	Ralb/Stxbp

GO_BP_m2	GO:003289	positive re	2/470	44/23843	0.215042	0.537093	0.502843	Erfe/Stxbp1
GO_BP_m2	GO:004848	synaptic ve	2/470	44/23843	0.215042	0.537093	0.502843	Sh3gl1/Syt
GO_BP_m2	GO:004340	regulation	8/470	290/23843	0.215281	0.53737	0.503102	Bmp4/Csk/
GO_BP_m2	GO:200123	regulation	5/470	162/23843	0.216265	0.538637	0.504288	Bmp4/Col2
GO_BP_m2	GO:001598	energy der	7/470	247/23843	0.216442	0.538637	0.504288	Aco1/Adsl/
GO_BP_m2	GO:004566	negative re	7/470	247/23843	0.216442	0.538637	0.504288	Cit/Id2/No
GO_BP_m2	GO:000327	cardiac sep	4/470	121/23843	0.216559	0.538637	0.504288	Ap2b1/Bm
GO_BP_m2	GO:004848	synaptic ve	4/470	121/23843	0.216559	0.538637	0.504288	Bloc1s2/Cp
GO_BP_m2	GO:009748	establishm	4/470	121/23843	0.216559	0.538637	0.504288	Bloc1s2/Cp
GO_BP_m2	GO:001470	striated mu	11/470	424/23843	0.217779	0.541282	0.506765	Bmp4/Chd
GO_BP_m2	GO:007200	renal syste	8/470	291/23843	0.21788	0.541282	0.506765	Bmp4/Id2/
GO_BP_m2	GO:000301	heart proce	6/470	205/23843	0.21912	0.54404	0.509347	Agrn/Gpd1
GO_BP_m2	GO:003294	negative re	3/470	82/23843	0.219702	0.54484	0.510096	Bmp4/Prka
GO_BP_m2	GO:005067	negative re	3/470	82/23843	0.219702	0.54484	0.510096	Bmp4/Prka
GO_BP_m2	GO:004002	regulation	8/470	292/23843	0.220491	0.545332	0.510556	Bmp4/Dnd
GO_BP_m2	GO:000916	nucleotide	4/470	122/23843	0.220715	0.545332	0.510556	Rack1/Pde
GO_BP_m2	GO:000301	circulatory	12/470	471/23843	0.221867	0.545332	0.510556	Agrn/Chd7
GO_BP_m2	GO:003526	multicellula	6/470	206/23843	0.22227	0.545332	0.510556	Chd7/H3f3
GO_BP_m2	GO:000863	intrinsic ap	2/470	45/23843	0.222311	0.545332	0.510556	Pdcd10/Pir
GO_BP_m2	GO:003271	negative re	2/470	45/23843	0.222311	0.545332	0.510556	Csk/Syt11
GO_BP_m2	GO:004801	vascular en	2/470	45/23843	0.222311	0.545332	0.510556	Bmp4/Ptk2
GO_BP_m2	GO:005079	activated T	2/470	45/23843	0.222311	0.545332	0.510556	Il12rb1/Prk
GO_BP_m2	GO:005195	regulation	2/470	45/23843	0.222311	0.545332	0.510556	Grm7/Stxb
GO_BP_m2	GO:006041	ventricular	2/470	45/23843	0.222311	0.545332	0.510556	Bmp4/Id2
GO_BP_m2	GO:009032	regulation	2/470	45/23843	0.222311	0.545332	0.510556	Bmp4/Wdr
GO_BP_m2	GO:190044	regulation	2/470	45/23843	0.222311	0.545332	0.510556	Pink1/Ptk2
GO_BP_m2	GO:190179	negative re	2/470	45/23843	0.222311	0.545332	0.510556	Alad/Ube2
GO_BP_m2	GO:005086	regulation	8/470	293/23843	0.223114	0.545332	0.510556	Bmp4/Csk/
GO_BP_m2	GO:003530	regulation	5/470	164/23843	0.223379	0.545332	0.510556	Elfn2/Ell/M
GO_BP_m2	GO:004212	regulation	5/470	164/23843	0.223379	0.545332	0.510556	Bmp4/Il12r
GO_BP_m2	GO:003220	telomere o	4/470	123/23843	0.224892	0.545332	0.510556	Aurkb/H3f3
GO_BP_m2	GO:007008	glycosylati	6/470	207/23843	0.225436	0.545332	0.510556	Galnt2/Lfng
GO_BP_m2	GO:000092	septin ring	1/470	13/23843	0.228088	0.545332	0.510556	9-Sep
GO_BP_m2	GO:000255	mast cell cl	1/470	13/23843	0.228088	0.545332	0.510556	Rac2
GO_BP_m2	GO:000317	pulmonary	1/470	13/23843	0.228088	0.545332	0.510556	Bmp4
GO_BP_m2	GO:000318	pulmonary	1/470	13/23843	0.228088	0.545332	0.510556	Bmp4
GO_BP_m2	GO:000641	translationa	1/470	13/23843	0.228088	0.545332	0.510556	2810006K2
GO_BP_m2	GO:000651	protein deg	1/470	13/23843	0.228088	0.545332	0.510556	Man2c1
GO_BP_m2	GO:000661	SRP-deper	1/470	13/23843	0.228088	0.545332	0.510556	Sec63
GO_BP_m2	GO:007500	mesoderm	1/470	13/23843	0.228088	0.545332	0.510556	Sfrp2
GO_BP_m2	GO:000761	short-term	1/470	13/23843	0.228088	0.545332	0.510556	Grm7
GO_BP_m2	GO:000829	intracellula	1/470	13/23843	0.228088	0.545332	0.510556	Exosc2
GO_BP_m2	GO:001932	pentose m	1/470	13/23843	0.228088	0.545332	0.510556	Xylb
GO_BP_m2	GO:003111	negative re	1/470	13/23843	0.228088	0.545332	0.510556	Dyrk1a
GO_BP_m2	GO:003126	pseudopoc	1/470	13/23843	0.228088	0.545332	0.510556	Klhl41
GO_BP_m2	GO:003230	regulation	1/470	13/23843	0.228088	0.545332	0.510556	Acsl4
GO_BP_m2	GO:003307	immature T	1/470	13/23843	0.228088	0.545332	0.510556	Bmp4
GO_BP_m2	GO:003572	intraciliary	1/470	13/23843	0.228088	0.545332	0.510556	Ift122

GO_BP_m2	GO:004226	regulation	1/470	13/23843	0.228088	0.545332	0.510556	Csf2
GO_BP_m2	GO:004253	negative re	1/470	13/23843	0.228088	0.545332	0.510556	Suz12
GO_BP_m2	GO:004253	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	Cybb
GO_BP_m2	GO:004297	activation (	1/470	13/23843	0.228088	0.545332	0.510556	Ptk2b
GO_BP_m2	GO:004311	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	Fgfbp3
GO_BP_m2	GO:004350	negative re	1/470	13/23843	0.228088	0.545332	0.510556	Sfrp2
GO_BP_m2	GO:004565	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	Id2
GO_BP_m2	GO:004583	negative re	1/470	13/23843	0.228088	0.545332	0.510556	Hebp2
GO_BP_m2	GO:004603	AMP metal	1/470	13/23843	0.228088	0.545332	0.510556	Adsl
GO_BP_m2	GO:004647	glycosphin	1/470	13/23843	0.228088	0.545332	0.510556	Gba2
GO_BP_m2	GO:004801	hepatocyte	1/470	13/23843	0.228088	0.545332	0.510556	Muc20
GO_BP_m2	GO:005157	negative re	1/470	13/23843	0.228088	0.545332	0.510556	Kdm3a
GO_BP_m2	GO:005264	alditol pho	1/470	13/23843	0.228088	0.545332	0.510556	Gpd1l
GO_BP_m2	GO:005511	relaxation (	1/470	13/23843	0.228088	0.545332	0.510556	Pde4d
GO_BP_m2	GO:006026	regulation	1/470	13/23843	0.228088	0.545332	0.510556	Rac2
GO_BP_m2	GO:006060	lateral spro	1/470	13/23843	0.228088	0.545332	0.510556	Bmp4
GO_BP_m2	GO:006115	3'-UTR-me	1/470	13/23843	0.228088	0.545332	0.510556	Zc3h12d
GO_BP_m2	GO:007143	potassium	1/470	13/23843	0.228088	0.545332	0.510556	Kcnh2
GO_BP_m2	GO:009701	cellular res	1/470	13/23843	0.228088	0.545332	0.510556	Csf2
GO_BP_m2	GO:009878	mRNA clea	1/470	13/23843	0.228088	0.545332	0.510556	Ncbp2
GO_BP_m2	GO:009887	neurotrans	1/470	13/23843	0.228088	0.545332	0.510556	Rab11a
GO_BP_m2	GO:009959	neurotrans	1/470	13/23843	0.228088	0.545332	0.510556	Ap2b1
GO_BP_m2	GO:190114	insulin met	1/470	13/23843	0.228088	0.545332	0.510556	Pcsk2
GO_BP_m2	GO:190285	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	9-Sep
GO_BP_m2	GO:190418	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	Rack1
GO_BP_m2	GO:190492	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	Pink1
GO_BP_m2	GO:200009	regulation	1/470	13/23843	0.228088	0.545332	0.510556	Sfrp2
GO_BP_m2	GO:200010	positive reg	1/470	13/23843	0.228088	0.545332	0.510556	Bmp4
GO_BP_m2	GO:200065	negative re	1/470	13/23843	0.228088	0.545332	0.510556	Agrn
GO_BP_m2	GO:004477	cell cycle p	10/470	384/23843	0.228559	0.54575	0.510948	Cit/Cks1b/I
GO_BP_m2	GO:004483	cell cycle G	4/470	124/23843	0.229089	0.54575	0.510948	Cit/Foxo4/I
GO_BP_m2	GO:190265	secondary	4/470	124/23843	0.229089	0.54575	0.510948	Aplp2/Ceb
GO_BP_m2	GO:000209	regulation	2/470	46/23843	0.229599	0.54575	0.510948	Mtmr2/Sel
GO_BP_m2	GO:000703	endosome	2/470	46/23843	0.229599	0.54575	0.510948	Rab11a/Tm
GO_BP_m2	GO:001071	regulation	2/470	46/23843	0.229599	0.54575	0.510948	Bmp4/Mfa
GO_BP_m2	GO:002260	ovulation c	2/470	46/23843	0.229599	0.54575	0.510948	Gdf9/Sgpl1
GO_BP_m2	GO:003503	sperm-egg	2/470	46/23843	0.229599	0.54575	0.510948	Izumo1r/Z
GO_BP_m2	GO:003513	forelimb m	2/470	46/23843	0.229599	0.54575	0.510948	Ift122/Sall3
GO_BP_m2	GO:004859	oocyte dev	2/470	46/23843	0.229599	0.54575	0.510948	Gdf9/Ptk2b
GO_BP_m2	GO:001066	regulation	3/470	84/23843	0.230084	0.54575	0.510948	Pde1a/Ptk2
GO_BP_m2	GO:004227	ribosomal l	3/470	84/23843	0.230084	0.54575	0.510948	Fastkd2/M
GO_BP_m2	GO:005080	negative re	3/470	84/23843	0.230084	0.54575	0.510948	Mtmr2/Ptk
GO_BP_m2	GO:007209	regulation	3/470	84/23843	0.230084	0.54575	0.510948	Bmp4/Six3
GO_BP_m2	GO:200024	regulation	5/470	166/23843	0.230562	0.546575	0.51172	Bmp4/Eif4g
GO_BP_m2	GO:009881	nuclear chr	7/470	252/23843	0.230754	0.546722	0.511857	Aurkb/Cit/I
GO_BP_m2	GO:000257	myeloid leu	6/470	209/23843	0.23181	0.548604	0.51362	Bmp4/Ceb
GO_BP_m2	GO:000840	gonad dev	6/470	209/23843	0.23181	0.548604	0.51362	Bmp4/Gdf9
GO_BP_m2	GO:000165	eye develo	10/470	386/23843	0.233203	0.551279	0.516124	Bmp4/Chd

GO_BP_m2	GO:003009	lymphocyte	10/470	386/23843	0.233203	0.551279	0.516124	Bmp4/Chd
GO_BP_m2	GO:003238	positive reg	7/470	253/23843	0.233655	0.551859	0.516667	Ect2/Mavs/
GO_BP_m2	GO:000801	regulation	5/470	167/23843	0.234179	0.551859	0.516667	Agrn/Gpd1
GO_BP_m2	GO:000974	response to	5/470	167/23843	0.234179	0.551859	0.516667	Glul/Rack1/
GO_BP_m2	GO:003440	nucleobase	5/470	167/23843	0.234179	0.551859	0.516667	Cad/Rack1/
GO_BP_m2	GO:003007	insulin secr	6/470	210/23843	0.235019	0.551859	0.516667	Cyb5r4/Glu
GO_BP_m2	GO:001607	synaptic ve	3/470	85/23843	0.235309	0.551859	0.516667	Cplx4/Stxb
GO_BP_m2	GO:002195	central ner	3/470	85/23843	0.235309	0.551859	0.516667	Gba2/Lmx1
GO_BP_m2	GO:004277	signal trans	3/470	85/23843	0.235309	0.551859	0.516667	Cdc5l/Dyrk
GO_BP_m2	GO:004350	regulation	3/470	85/23843	0.235309	0.551859	0.516667	Nr4a3/Srl/
GO_BP_m2	GO:007066	negative re	3/470	85/23843	0.235309	0.551859	0.516667	Bmp4/Prka
GO_BP_m2	GO:007190	positive reg	8/470	298/23843	0.236398	0.551859	0.516667	Bmp4/Cks1
GO_BP_m2	GO:000636	transcriptic	2/470	47/23843	0.236902	0.551859	0.516667	Ell/Eloa
GO_BP_m2	GO:001657	histone ubi	2/470	47/23843	0.236902	0.551859	0.516667	Rnf20/Suz1
GO_BP_m2	GO:002153	neural tube	2/470	47/23843	0.236902	0.551859	0.516667	Bmp4/Ift12
GO_BP_m2	GO:003233	regulation	2/470	47/23843	0.236902	0.551859	0.516667	Bmp4/Gdf6
GO_BP_m2	GO:004521	sarcomere	2/470	47/23843	0.236902	0.551859	0.516667	Klhl41/Prka
GO_BP_m2	GO:004562	negative re	2/470	47/23843	0.236902	0.551859	0.516667	Bmp4/Id2
GO_BP_m2	GO:004564	regulation	2/470	47/23843	0.236902	0.551859	0.516667	Id2/Mafb
GO_BP_m2	GO:004871	regulation	2/470	47/23843	0.236902	0.551859	0.516667	Bmp4/Id2
GO_BP_m2	GO:005197	regulation	2/470	47/23843	0.236902	0.551859	0.516667	Aurkb/Hnr
GO_BP_m2	GO:009960	regulation	2/470	47/23843	0.236902	0.551859	0.516667	Pink1/Ptk2
GO_BP_m2	GO:190459	positive reg	2/470	47/23843	0.236902	0.551859	0.516667	Ect2/Mavs
GO_BP_m2	GO:003017	positive reg	4/470	126/23843	0.237541	0.551859	0.516667	Bambi/Rnf1
GO_BP_m2	GO:200125	positive reg	5/470	168/23843	0.237811	0.551859	0.516667	Aurkb/Auts
GO_BP_m2	GO:000931	response to	10/470	388/23843	0.237882	0.551859	0.516667	Aurkb/Cry1
GO_BP_m2	GO:009028	regulation	7/470	255/23843	0.239492	0.551859	0.516667	Bambi/Bmp
GO_BP_m2	GO:003134	positive reg	11/470	434/23843	0.239623	0.551859	0.516667	Agrn/Auts2
GO_BP_m2	GO:003591	skeletal mu	3/470	86/23843	0.240554	0.551859	0.516667	Klhl41/Vax1
GO_BP_m2	GO:005128	protein hor	3/470	86/23843	0.240554	0.551859	0.516667	Acaca/Pcb
GO_BP_m2	GO:000226	myeloid ce	5/470	169/23843	0.241459	0.551859	0.516667	Bmp4/Id2/
GO_BP_m2	GO:009030	nucleic aci	4/470	127/23843	0.241795	0.551859	0.516667	Exosc2/Nc
GO_BP_m2	GO:000236	leukocyte a	7/470	256/23843	0.242428	0.551859	0.516667	Ifna4/Itfg2/
GO_BP_m2	GO:000167	acrosome a	1/470	14/23843	0.243313	0.551859	0.516667	Zpbp
GO_BP_m2	GO:000315	morphogen	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:000604	N-acetylglu	1/470	14/23843	0.243313	0.551859	0.516667	Chst5
GO_BP_m2	GO:000717	negative re	1/470	14/23843	0.243313	0.551859	0.516667	Tsg101
GO_BP_m2	GO:000914	pyrimidine	1/470	14/23843	0.243313	0.551859	0.516667	Cad
GO_BP_m2	GO:001404	positive reg	1/470	14/23843	0.243313	0.551859	0.516667	Stxbp1
GO_BP_m2	GO:001483	gastro-inte	1/470	14/23843	0.243313	0.551859	0.516667	Sulf2
GO_BP_m2	GO:001607	snoRNA m	1/470	14/23843	0.243313	0.551859	0.516667	Exosc2
GO_BP_m2	GO:001632	neuron ren	1/470	14/23843	0.243313	0.551859	0.516667	Farp2
GO_BP_m2	GO:001654	protein aut	1/470	14/23843	0.243313	0.551859	0.516667	Pcsk2
GO_BP_m2	GO:001937	glycolipid	1/470	14/23843	0.243313	0.551859	0.516667	Gba2
GO_BP_m2	GO:002170	cerebellar	1/470	14/23843	0.243313	0.551859	0.516667	Faim2
GO_BP_m2	GO:003094	positive reg	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:003475	iron ion tra	1/470	14/23843	0.243313	0.551859	0.516667	Slc25a28
GO_BP_m2	GO:003637	sodium io	1/470	14/23843	0.243313	0.551859	0.516667	Agrn

GO_BP_m2	GO:004292	glucocortic	1/470	14/23843	0.243313	0.551859	0.516667	Cry1
GO_BP_m2	GO:004364	dicarboxyli	1/470	14/23843	0.243313	0.551859	0.516667	Pm20d2
GO_BP_m2	GO:004424	lipid digest	1/470	14/23843	0.243313	0.551859	0.516667	Acat2
GO_BP_m2	GO:004589	positive re	1/470	14/23843	0.243313	0.551859	0.516667	Psmc5
GO_BP_m2	GO:004831	Golgi inher	1/470	14/23843	0.243313	0.551859	0.516667	Pdcd10
GO_BP_m2	GO:004853	mucosal-a	1/470	14/23843	0.243313	0.551859	0.516667	Id2
GO_BP_m2	GO:004854	Peyer's pat	1/470	14/23843	0.243313	0.551859	0.516667	Id2
GO_BP_m2	GO:005138	kinetochor	1/470	14/23843	0.243313	0.551859	0.516667	Trappc12
GO_BP_m2	GO:006001	radial glial	1/470	14/23843	0.243313	0.551859	0.516667	Mettl14
GO_BP_m2	GO:006039	positive re	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:006083	smoothene	1/470	14/23843	0.243313	0.551859	0.516667	Ift122
GO_BP_m2	GO:006115	endothelial	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:006130	cardiac neu	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:006131	renal filtrat	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:007138	cellular res	1/470	14/23843	0.243313	0.551859	0.516667	Acaca
GO_BP_m2	GO:007180	positive re	1/470	14/23843	0.243313	0.551859	0.516667	Csf2
GO_BP_m2	GO:007211	glomerular	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:007231	glomerular	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:009014	positive re	1/470	14/23843	0.243313	0.551859	0.516667	Pink1
GO_BP_m2	GO:009017	planar cell	1/470	14/23843	0.243313	0.551859	0.516667	Sfrp2
GO_BP_m2	GO:009701	response t	1/470	14/23843	0.243313	0.551859	0.516667	Csf2
GO_BP_m2	GO:009753	mast cell m	1/470	14/23843	0.243313	0.551859	0.516667	Rac2
GO_BP_m2	GO:009885	intestinal li	1/470	14/23843	0.243313	0.551859	0.516667	Acat2
GO_BP_m2	GO:014013	positive re	1/470	14/23843	0.243313	0.551859	0.516667	Ptk2b
GO_BP_m2	GO:190121	regulation	1/470	14/23843	0.243313	0.551859	0.516667	Bmp4
GO_BP_m2	GO:190230	negative re	1/470	14/23843	0.243313	0.551859	0.516667	Agrn
GO_BP_m2	GO:190492	regulation	1/470	14/23843	0.243313	0.551859	0.516667	Pink1
GO_BP_m2	GO:190494	midbrain d	1/470	14/23843	0.243313	0.551859	0.516667	Sfrp2
GO_BP_m2	GO:004255	neuron ma	2/470	48/23843	0.244217	0.552716	0.517469	Farp2/Irx5
GO_BP_m2	GO:004330	regulation	2/470	48/23843	0.244217	0.552716	0.517469	Rac2/Stxbp
GO_BP_m2	GO:005195	positive re	2/470	48/23843	0.244217	0.552716	0.517469	Pink1/Stxb
GO_BP_m2	GO:200123	regulation	2/470	48/23843	0.244217	0.552716	0.517469	Col2a1/Csf
GO_BP_m2	GO:000715	leukocyte	8/470	301/23843	0.244496	0.55305	0.517782	Bmp4/Il12r
GO_BP_m2	GO:004513	developme	6/470	213/23843	0.244725	0.553268	0.517986	Bmp4/Gdf
GO_BP_m2	GO:000974	response t	5/470	170/23843	0.245122	0.553868	0.518548	Glul/Rack1
GO_BP_m2	GO:000269	positive re	3/470	87/23843	0.245819	0.55421	0.518868	Ptk2b/Rac2
GO_BP_m2	GO:000689	post-Golgi	3/470	87/23843	0.245819	0.55421	0.518868	Csk/Rack1/
GO_BP_m2	GO:000661	protein exp	4/470	128/23843	0.246066	0.55421	0.518868	Hnrnpa2b1
GO_BP_m2	GO:000945	RNA modif	4/470	128/23843	0.246066	0.55421	0.518868	Ftsj1/Mettl
GO_BP_m2	GO:001021	response t	4/470	128/23843	0.246066	0.55421	0.518868	Ect2/H2afx
GO_BP_m2	GO:004559	regulation	4/470	128/23843	0.246066	0.55421	0.518868	Cebpa/Id2/
GO_BP_m2	GO:001657	histone mo	11/470	437/23843	0.246332	0.554511	0.51915	Aurkb/Auts
GO_BP_m2	GO:001025	endomemb	9/470	347/23843	0.247728	0.556691	0.521191	Agrn/Cit/P
GO_BP_m2	GO:003569	cellular res	9/470	347/23843	0.247728	0.556691	0.521191	Atf4/Bmp4
GO_BP_m2	GO:200014	negative re	7/470	258/23843	0.248335	0.556691	0.521191	Angpt4/Ar
GO_BP_m2	GO:000632	DNA packa	5/470	171/23843	0.2488	0.556691	0.521191	Asf1a/Chaf
GO_BP_m2	GO:000736	gastrulatio	5/470	171/23843	0.2488	0.556691	0.521191	Bmp4/Rack
GO_BP_m2	GO:003428	response t	5/470	171/23843	0.2488	0.556691	0.521191	Glul/Rack1

GO_BP_m2	GO:000183	epithelial t	4/470	129/23843	0.250354	0.556691	0.521191	Bambi/Bmp
GO_BP_m2	GO:000906	cellular am	3/470	88/23843	0.251102	0.556691	0.521191	Hmgcl/Ivd/
GO_BP_m2	GO:001059	positive reg	3/470	88/23843	0.251102	0.556691	0.521191	Angpt4/Bm
GO_BP_m2	GO:004847	oogenesis	3/470	88/23843	0.251102	0.556691	0.521191	Gdf9/H3f3
GO_BP_m2	GO:005076	regulation	3/470	88/23843	0.251102	0.556691	0.521191	Csk/Rack1/
GO_BP_m2	GO:004390	regulation	6/470	215/23843	0.25126	0.556691	0.521191	Chmp3/Ma
GO_BP_m2	GO:000602	aminoglyca	2/470	49/23843	0.251541	0.556691	0.521191	Chst12/Chs
GO_BP_m2	GO:004614	pigment bi	2/470	49/23843	0.251541	0.556691	0.521191	Alad/Cox10
GO_BP_m2	GO:190204	regulation	2/470	49/23843	0.251541	0.556691	0.521191	Faim2/Sfrp
GO_BP_m2	GO:200064	regulation	2/470	49/23843	0.251541	0.556691	0.521191	Agrn/Gpd1
GO_BP_m2	GO:004856	embryonic	12/470	486/23843	0.253456	0.556691	0.521191	Bmp4/Ceb
GO_BP_m2	GO:000226	cell activati	7/470	260/23843	0.254285	0.556691	0.521191	Ifna4/Itfg2/
GO_BP_m2	GO:001063	positive reg	4/470	130/23843	0.254657	0.556691	0.521191	Angpt4/Bm
GO_BP_m2	GO:001612	sterol meta	4/470	130/23843	0.254657	0.556691	0.521191	Aplp2/Ceb
GO_BP_m2	GO:005166	localization	4/470	130/23843	0.254657	0.556691	0.521191	Agrn/Ap2b
GO_BP_m2	GO:009747	synaptic ve	4/470	130/23843	0.254657	0.556691	0.521191	Bloc1s2/Cp
GO_BP_m2	GO:004477	mitotic cell	9/470	350/23843	0.255382	0.556691	0.521191	Cit/Cks1b/
GO_BP_m2	GO:004001	negative re	8/470	305/23843	0.255435	0.556691	0.521191	Angpt4/Ara
GO_BP_m2	GO:001065	muscle cell	3/470	89/23843	0.256402	0.556691	0.521191	Pde1a/Ptk2
GO_BP_m2	GO:004001	regulation	3/470	89/23843	0.256402	0.556691	0.521191	Chd7/Ppib/
GO_BP_m2	GO:000961	response t	7/470	261/23843	0.257276	0.556691	0.521191	Ifna4/Ifnl3/
GO_BP_m2	GO:001063	epithelial c	7/470	261/23843	0.257276	0.556691	0.521191	Angpt4/Bm
GO_BP_m2	GO:000021	meiotic spi	1/470	15/23843	0.258237	0.556691	0.521191	Espl1
GO_BP_m2	GO:000029	nuclear-tra	1/470	15/23843	0.258237	0.556691	0.521191	Exosc2
GO_BP_m2	GO:000633	nucleosom	1/470	15/23843	0.258237	0.556691	0.521191	Smarcd1
GO_BP_m2	GO:000667	glycosylcer	1/470	15/23843	0.258237	0.556691	0.521191	Gba2
GO_BP_m2	GO:000734	fusion of sp	1/470	15/23843	0.258237	0.556691	0.521191	Izumo1r
GO_BP_m2	GO:000737	segment sp	1/470	15/23843	0.258237	0.556691	0.521191	Mafb
GO_BP_m2	GO:001017	embryonic	1/470	15/23843	0.258237	0.556691	0.521191	Ift122
GO_BP_m2	GO:001045	negative re	1/470	15/23843	0.258237	0.556691	0.521191	Sfrp2
GO_BP_m2	GO:001064	cell commu	1/470	15/23843	0.258237	0.556691	0.521191	Pde4d
GO_BP_m2	GO:001591	peroxisoma	1/470	15/23843	0.258237	0.556691	0.521191	Pex5l
GO_BP_m2	GO:001802	peptidyl-ly	1/470	15/23843	0.258237	0.556691	0.521191	Kdm3a
GO_BP_m2	GO:001998	translesion	1/470	15/23843	0.258237	0.556691	0.521191	Zbtb1
GO_BP_m2	GO:002169	cerebellar	1/470	15/23843	0.258237	0.556691	0.521191	Faim2
GO_BP_m2	GO:003126	pseudopod	1/470	15/23843	0.258237	0.556691	0.521191	Klhl41
GO_BP_m2	GO:003278	negative re	1/470	15/23843	0.258237	0.556691	0.521191	Agrn
GO_BP_m2	GO:003295	inositol tris	1/470	15/23843	0.258237	0.556691	0.521191	Ptk2b
GO_BP_m2	GO:003323	positive reg	1/470	15/23843	0.258237	0.556691	0.521191	Tollip
GO_BP_m2	GO:003564	locomotory	1/470	15/23843	0.258237	0.556691	0.521191	Penk
GO_BP_m2	GO:004240	cristae form	1/470	15/23843	0.258237	0.556691	0.521191	Pink1
GO_BP_m2	GO:004316	ubiquitin-c	1/470	15/23843	0.258237	0.556691	0.521191	Tsg101
GO_BP_m2	GO:004432	cellular resp	1/470	15/23843	0.258237	0.556691	0.521191	Nr4a3
GO_BP_m2	GO:004479	positive reg	1/470	15/23843	0.258237	0.556691	0.521191	Ppib
GO_BP_m2	GO:004482	modulation	1/470	15/23843	0.258237	0.556691	0.521191	Ppib
GO_BP_m2	GO:004577	negative re	1/470	15/23843	0.258237	0.556691	0.521191	Csk
GO_BP_m2	GO:004611	nucleobase	1/470	15/23843	0.258237	0.556691	0.521191	Cad
GO_BP_m2	GO:004613	pyrimidine	1/470	15/23843	0.258237	0.556691	0.521191	Cad

GO_BP_m2	GO:00483	organelle i	1/470	15/23843	0.258237	0.556691	0.521191	Pdcd10
GO_BP_m2	GO:005087	white fat c	1/470	15/23843	0.258237	0.556691	0.521191	Cebpa
GO_BP_m2	GO:005157	positive re	1/470	15/23843	0.258237	0.556691	0.521191	Auts2
GO_BP_m2	GO:005164	Golgi locali	1/470	15/23843	0.258237	0.556691	0.521191	Pdcd10
GO_BP_m2	GO:005192	sulfation	1/470	15/23843	0.258237	0.556691	0.521191	Hs3st3b1
GO_BP_m2	GO:006034	heart trabe	1/470	15/23843	0.258237	0.556691	0.521191	Adgrg6
GO_BP_m2	GO:006044	branching	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:00613	cardiac ne	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:00709	3'-UTR-m	1/470	15/23843	0.258237	0.556691	0.521191	Elavl1
GO_BP_m2	GO:00715	otic vesicle	1/470	15/23843	0.258237	0.556691	0.521191	Col2a1
GO_BP_m2	GO:007207	kidney me	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:00721	glomerular	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:00721	ureter dev	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:00722	metanephr	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:00900	negative r	1/470	15/23843	0.258237	0.556691	0.521191	Pdcd10
GO_BP_m2	GO:00900	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Psmc5
GO_BP_m2	GO:009017	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Sfrp2
GO_BP_m2	GO:19000	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Pink1
GO_BP_m2	GO:190107	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Pde4d
GO_BP_m2	GO:19015	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Pink1
GO_BP_m2	GO:19017	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Bmp4
GO_BP_m2	GO:190354	positive re	1/470	15/23843	0.258237	0.556691	0.521191	Tsg101
GO_BP_m2	GO:19044	positive re	1/470	15/23843	0.258237	0.556691	0.521191	Mavs
GO_BP_m2	GO:20001	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Gdf9
GO_BP_m2	GO:200047	regulation	1/470	15/23843	0.258237	0.556691	0.521191	Prkar1a
GO_BP_m2	GO:200064	negative r	1/470	15/23843	0.258237	0.556691	0.521191	Vax1
GO_BP_m2	GO:00016	behavioral	2/470	50/23843	0.25887	0.556691	0.521191	Grm7/Pen
GO_BP_m2	GO:00099	oocyte diff	2/470	50/23843	0.25887	0.556691	0.521191	Gdf9/Ptk2
GO_BP_m2	GO:001401	negative r	2/470	50/23843	0.25887	0.556691	0.521191	Bmp4/Id2
GO_BP_m2	GO:00702	negative r	2/470	50/23843	0.25887	0.556691	0.521191	Aurkb/Bm
GO_BP_m2	GO:190161	organic hy	2/470	50/23843	0.25887	0.556691	0.521191	Mtmr2/Mt
GO_BP_m2	GO:00076	feeding be	4/470	131/23843	0.258975	0.556691	0.521191	Agrp/Aplp
GO_BP_m2	GO:003434	response t	4/470	131/23843	0.258975	0.556691	0.521191	Eprs/Il12rb
GO_BP_m2	GO:19015	fatty acid	4/470	131/23843	0.258975	0.556691	0.521191	Cyp2g1/Fa
GO_BP_m2	GO:00507	regulation	5/470	174/23843	0.259916	0.557932	0.522352	Glul/Oxct1
GO_BP_m2	GO:00716	anatomical	5/470	174/23843	0.259916	0.557932	0.522352	Farp2/Irx5
GO_BP_m2	GO:00486	reproducti	11/470	443/23843	0.259951	0.557932	0.522352	Bmp4/Ceb
GO_BP_m2	GO:00018	tissue hom	6/470	218/23843	0.261153	0.559938	0.524231	Acaca/Col
GO_BP_m2	GO:006102	membrane	6/470	218/23843	0.261153	0.559938	0.524231	Chmp3/Izu
GO_BP_m2	GO:000244	myeloid le	3/470	90/23843	0.261716	0.560859	0.525093	Nr4a3/Rac
GO_BP_m2	GO:00091	glycoprote	7/470	263/23843	0.263289	0.563653	0.527709	Chst12/Gal
GO_BP_m2	GO:00901	epithelium	7/470	263/23843	0.263289	0.563653	0.527709	Angpt4/Bm
GO_BP_m2	GO:00434	positive re	6/470	219/23843	0.264474	0.564296	0.528311	Bmp4/Csk
GO_BP_m2	GO:00605	muscle tiss	11/470	445/23843	0.264548	0.564296	0.528311	Bmp4/Chd
GO_BP_m2	GO:00022	behavioral	2/470	51/23843	0.266202	0.564296	0.528311	Grm7/Pen
GO_BP_m2	GO:00322	positive re	2/470	51/23843	0.266202	0.564296	0.528311	Aurkb/Hnr
GO_BP_m2	GO:003361	membrane	2/470	51/23843	0.266202	0.564296	0.528311	Bace1/Mbt
GO_BP_m2	GO:00469	regulation	2/470	51/23843	0.266202	0.564296	0.528311	Bloc1s2/He

GO_BP_m2	GO:00512	protein het	2/470	51/23843	0.266202	0.564296	0.528311	Agrn/Farsa
GO_BP_m2	GO:00514	regulation	2/470	51/23843	0.266202	0.564296	0.528311	Eif4g3/Lfn
GO_BP_m2	GO:00515	histone H3	2/470	51/23843	0.266202	0.564296	0.528311	Auts2/Hist
GO_BP_m2	GO:00860	cardiac mu	2/470	51/23843	0.266202	0.564296	0.528311	Gpd1l/Kcn
GO_BP_m2	GO:00098	negative re	7/470	264/23843	0.26631	0.564296	0.528311	Alad/Dhx3
GO_BP_m2	GO:00310	positive re	3/470	91/23843	0.267045	0.564296	0.528311	Auts2/Pink
GO_BP_m2	GO:000081	sister chro	5/470	176/23843	0.267391	0.564296	0.528311	Aurkb/Cit/
GO_BP_m2	GO:190227	regulation	5/470	176/23843	0.267391	0.564296	0.528311	Auts2/Kdm
GO_BP_m2	GO:20012	negative re	6/470	220/23843	0.267805	0.564296	0.528311	Bmp4/Col2
GO_BP_m2	GO:00614	reproducti	11/470	447/23843	0.269171	0.564296	0.528311	Bmp4/Ceb
GO_BP_m2	GO:00901	tissue migr	7/470	265/23843	0.269341	0.564296	0.528311	Angpt4/Bn
GO_BP_m2	GO:004247	ear morph	4/470	134/23843	0.272014	0.564296	0.528311	Chd7/Col2
GO_BP_m2	GO:19012	nucleoside	4/470	134/23843	0.272014	0.564296	0.528311	Rack1/Pde
GO_BP_m2	GO:014001	mitotic nuc	7/470	266/23843	0.272381	0.564296	0.528311	Aurkb/Bmp
GO_BP_m2	GO:000167	long-chain	3/470	92/23843	0.272386	0.564296	0.528311	Cyp2g1/Fa
GO_BP_m2	GO:000704	lysosomal	3/470	92/23843	0.272386	0.564296	0.528311	Chmp3/Pir
GO_BP_m2	GO:000092	cell separa	1/470	16/23843	0.272868	0.564296	0.528311	Chmp3
GO_BP_m2	GO:000182	histamine	1/470	16/23843	0.272868	0.564296	0.528311	Csf2
GO_BP_m2	GO:000207	epithelial c	1/470	16/23843	0.272868	0.564296	0.528311	Six3
GO_BP_m2	GO:00031	cardiac cor	1/470	16/23843	0.272868	0.564296	0.528311	Id2
GO_BP_m2	GO:000322	ventricular	1/470	16/23843	0.272868	0.564296	0.528311	Chd7
GO_BP_m2	GO:00064	signal pept	1/470	16/23843	0.272868	0.564296	0.528311	Sec11c
GO_BP_m2	GO:000661	cotranslati	1/470	16/23843	0.272868	0.564296	0.528311	Sec63
GO_BP_m2	GO:000687	cellular co	1/470	16/23843	0.272868	0.564296	0.528311	Aplp2
GO_BP_m2	GO:000721	G-protein	1/470	16/23843	0.272868	0.564296	0.528311	Grm7
GO_BP_m2	GO:000751	adult heart	1/470	16/23843	0.272868	0.564296	0.528311	Chd7
GO_BP_m2	GO:00083	histone mR	1/470	16/23843	0.272868	0.564296	0.528311	Xrn1
GO_BP_m2	GO:000922	pyrimidine	1/470	16/23843	0.272868	0.564296	0.528311	Cad
GO_BP_m2	GO:001022	response t	1/470	16/23843	0.272868	0.564296	0.528311	Mfap4
GO_BP_m2	GO:001091	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Ptk2b
GO_BP_m2	GO:00311	septin ring	1/470	16/23843	0.272868	0.564296	0.528311	9-Sep
GO_BP_m2	GO:00319	corticoster	1/470	16/23843	0.272868	0.564296	0.528311	Cry1
GO_BP_m2	GO:00321	septin cyto	1/470	16/23843	0.272868	0.564296	0.528311	9-Sep
GO_BP_m2	GO:003231	prostaglan	1/470	16/23843	0.272868	0.564296	0.528311	Acsl4
GO_BP_m2	GO:00343	lipid partic	1/470	16/23843	0.272868	0.564296	0.528311	Spg20
GO_BP_m2	GO:00352	ionotropic	1/470	16/23843	0.272868	0.564296	0.528311	Ptk2b
GO_BP_m2	GO:00425	pteridine-	1/470	16/23843	0.272868	0.564296	0.528311	Pcbd1
GO_BP_m2	GO:00458	positive re	1/470	16/23843	0.272868	0.564296	0.528311	Eif4g3
GO_BP_m2	GO:00458	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Psmc5
GO_BP_m2	GO:004651	ceramide c	1/470	16/23843	0.272868	0.564296	0.528311	Gba2
GO_BP_m2	GO:004871	positive re	1/470	16/23843	0.272868	0.564296	0.528311	Id2
GO_BP_m2	GO:006002	convergen	1/470	16/23843	0.272868	0.564296	0.528311	Sfrp2
GO_BP_m2	GO:00603	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Kcnh2
GO_BP_m2	GO:006064	mammary	1/470	16/23843	0.272868	0.564296	0.528311	Id2
GO_BP_m2	GO:007081	phosphory	1/470	16/23843	0.272868	0.564296	0.528311	Gtf2h1
GO_BP_m2	GO:007137	cellular res	1/470	16/23843	0.272868	0.564296	0.528311	Acaca
GO_BP_m2	GO:00714	cellular res	1/470	16/23843	0.272868	0.564296	0.528311	Ptk2b
GO_BP_m2	GO:007162	vocalizatio	1/470	16/23843	0.272868	0.564296	0.528311	Auts2

GO_BP_m2	GO:007201	glomerular	1/470	16/23843	0.272868	0.564296	0.528311	Bmp4
GO_BP_m2	GO:008601	membrane	1/470	16/23843	0.272868	0.564296	0.528311	Kcnh2
GO_BP_m2	GO:009017	establishm	1/470	16/23843	0.272868	0.564296	0.528311	Sfrp2
GO_BP_m2	GO:00901	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Bmp4
GO_BP_m2	GO:00970	craniofacia	1/470	16/23843	0.272868	0.564296	0.528311	Bmp4
GO_BP_m2	GO:00972	iron ion im	1/470	16/23843	0.272868	0.564296	0.528311	Slc25a28
GO_BP_m2	GO:19021	negative re	1/470	16/23843	0.272868	0.564296	0.528311	Chmp3
GO_BP_m2	GO:19035	protein loc	1/470	16/23843	0.272868	0.564296	0.528311	Rab11a
GO_BP_m2	GO:190354	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Tsg101
GO_BP_m2	GO:190377	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Pde4d
GO_BP_m2	GO:19037	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Bmp4
GO_BP_m2	GO:19051	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Syt11
GO_BP_m2	GO:199084	adaptive th	1/470	16/23843	0.272868	0.564296	0.528311	Ucp2
GO_BP_m2	GO:20002	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Klhl41
GO_BP_m2	GO:20003	regulation	1/470	16/23843	0.272868	0.564296	0.528311	Sfrp2
GO_BP_m2	GO:001631	dephospho	9/470	357/23843	0.273532	0.564559	0.528557	Elfn2/Ell/M
GO_BP_m2	GO:00106	negative re	2/470	52/23843	0.273534	0.564559	0.528557	Ptk2b/Sfrp
GO_BP_m2	GO:003051	negative re	2/470	52/23843	0.273534	0.564559	0.528557	Sfrp2/Spg2
GO_BP_m2	GO:007162	regulation	2/470	52/23843	0.273534	0.564559	0.528557	Rac2/S100
GO_BP_m2	GO:00165	covalent c	11/470	449/23843	0.27382	0.564871	0.52885	Aurkb/Auts
GO_BP_m2	GO:00902	regulation	6/470	222/23843	0.274499	0.565994	0.5299	Agrn/Nr4a
GO_BP_m2	GO:00080	regulation	5/470	178/23843	0.274913	0.566326	0.530212	Cit/Ptk2b/
GO_BP_m2	GO:00160	vesicle org	8/470	312/23843	0.27493	0.566326	0.530212	Rab11a/Sn
GO_BP_m2	GO:00164	cytosolic tr	4/470	135/23843	0.276386	0.567124	0.530959	Chmp3/De
GO_BP_m2	GO:00326	regulation	4/470	135/23843	0.276386	0.567124	0.530959	Cybb/Mavs
GO_BP_m2	GO:00720	stem cell p	4/470	135/23843	0.276386	0.567124	0.530959	Bmp4/Sfrp
GO_BP_m2	GO:00995	synaptic ve	4/470	135/23843	0.276386	0.567124	0.530959	Cplx4/Sh3
GO_BP_m2	GO:001077	negative re	3/470	93/23843	0.277739	0.567124	0.530959	Cit/Rnf6/S
GO_BP_m2	GO:001082	regulation	3/470	93/23843	0.277739	0.567124	0.530959	Aspscr1/N
GO_BP_m2	GO:003027	negative re	3/470	93/23843	0.277739	0.567124	0.530959	Id2/Nbr1/
GO_BP_m2	GO:00308	positive re	3/470	93/23843	0.277739	0.567124	0.530959	Ptk2b/Rac2
GO_BP_m2	GO:00714	cellular res	3/470	93/23843	0.277739	0.567124	0.530959	Aurkb/Mfa
GO_BP_m2	GO:190274	regulation	3/470	93/23843	0.277739	0.567124	0.530959	Foxo4/Kcn
GO_BP_m2	GO:000007	cell cycle c	5/470	179/23843	0.27869	0.567124	0.530959	Aurkb/Cdc
GO_BP_m2	GO:00308	regulation	5/470	179/23843	0.27869	0.567124	0.530959	Cit/Ptk2b/
GO_BP_m2	GO:000751	muscle org	10/470	405/23843	0.27895	0.567124	0.530959	Bmp4/Chd
GO_BP_m2	GO:00613	trabecula	2/470	53/23843	0.280862	0.567124	0.530959	Adgrg6/Ch
GO_BP_m2	GO:00482	organelle f	5/470	180/23843	0.282478	0.567124	0.530959	Chmp3/Sn
GO_BP_m2	GO:003051	regulation	3/470	94/23843	0.283102	0.567124	0.530959	Bmp4/Sfrp
GO_BP_m2	GO:19021	negative re	3/470	94/23843	0.283102	0.567124	0.530959	Bmp4/Id2/
GO_BP_m2	GO:20000	positive re	3/470	94/23843	0.283102	0.567124	0.530959	Rack1/Ptk2
GO_BP_m2	GO:19040	regulation	8/470	315/23843	0.28341	0.567124	0.530959	Agrn/Bmp
GO_BP_m2	GO:006024	anatomical	9/470	361/23843	0.28407	0.567124	0.530959	Acaca/Aur
GO_BP_m2	GO:003264	tumor necr	4/470	137/23843	0.285162	0.567124	0.530959	Cybb/Mavs
GO_BP_m2	GO:19035	regulation	4/470	137/23843	0.285162	0.567124	0.530959	Cybb/Mavs
GO_BP_m2	GO:001072	negative re	9/470	362/23843	0.286722	0.567124	0.530959	Bmp4/Cit/
GO_BP_m2	GO:00000	ribosomal	1/470	17/23843	0.287211	0.567124	0.530959	Ran
GO_BP_m2	GO:000192	positive re	1/470	17/23843	0.287211	0.567124	0.530959	Vamp3

GO_BP_m2	GO:00196	suckling be	1/470	17/23843	0.287211	0.567124	0.530959	Aplp2
GO_BP_m2	GO:00620	pyrimidine	1/470	17/23843	0.287211	0.567124	0.530959	Cad
GO_BP_m2	GO:00662	protein tar	1/470	17/23843	0.287211	0.567124	0.530959	Pex5l
GO_BP_m2	GO:00696	cellular def	1/470	17/23843	0.287211	0.567124	0.530959	Ptk2b
GO_BP_m2	GO:00697	DNA dama	1/470	17/23843	0.287211	0.567124	0.530959	Pcbp4
GO_BP_m2	GO:00720	activation	1/470	17/23843	0.287211	0.567124	0.530959	Sele
GO_BP_m2	GO:000821	estrogen m	1/470	17/23843	0.287211	0.567124	0.530959	Sgpl1
GO_BP_m2	GO:00910	coenzyme	1/470	17/23843	0.287211	0.567124	0.530959	Pm20d2
GO_BP_m2	GO:000914	pyrimidine	1/470	17/23843	0.287211	0.567124	0.530959	Cad
GO_BP_m2	GO:000921	pyrimidine	1/470	17/23843	0.287211	0.567124	0.530959	Cad
GO_BP_m2	GO:00107	negative re	1/470	17/23843	0.287211	0.567124	0.530959	Agrn
GO_BP_m2	GO:00109	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Csk
GO_BP_m2	GO:00216	cerebellar	1/470	17/23843	0.287211	0.567124	0.530959	Faim2
GO_BP_m2	GO:003081	positive re	1/470	17/23843	0.287211	0.567124	0.530959	Rack1
GO_BP_m2	GO:003082	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Ptk2b
GO_BP_m2	GO:00314	chromatin	1/470	17/23843	0.287211	0.567124	0.530959	Smarcd1
GO_BP_m2	GO:003162	synaptic ve	1/470	17/23843	0.287211	0.567124	0.530959	Stxbp1
GO_BP_m2	GO:003222	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Pink1
GO_BP_m2	GO:00324	melanoson	1/470	17/23843	0.287211	0.567124	0.530959	Rab11a
GO_BP_m2	GO:00325	endosome	1/470	17/23843	0.287211	0.567124	0.530959	Chmp3
GO_BP_m2	GO:00329	protein-DN	1/470	17/23843	0.287211	0.567124	0.530959	Smarcd1
GO_BP_m2	GO:00335	fatty acid b	1/470	17/23843	0.287211	0.567124	0.530959	Ivd
GO_BP_m2	GO:00337	ribosome l	1/470	17/23843	0.287211	0.567124	0.530959	Ran
GO_BP_m2	GO:003431	diol biosyn	1/470	17/23843	0.287211	0.567124	0.530959	Pcbd1
GO_BP_m2	GO:003447	snRNA 3'-	1/470	17/23843	0.287211	0.567124	0.530959	Exosc2
GO_BP_m2	GO:00346	nucleobase	1/470	17/23843	0.287211	0.567124	0.530959	Mgat1
GO_BP_m2	GO:00360	fucosylatio	1/470	17/23843	0.287211	0.567124	0.530959	Lfng
GO_BP_m2	GO:003952	RIG-I signa	1/470	17/23843	0.287211	0.567124	0.530959	Mavs
GO_BP_m2	GO:00424	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:00426	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Sfrp2
GO_BP_m2	GO:00427	negative re	1/470	17/23843	0.287211	0.567124	0.530959	Cry1
GO_BP_m2	GO:004357	peroxisom	1/470	17/23843	0.287211	0.567124	0.530959	Pex5l
GO_BP_m2	GO:00435	nose devel	1/470	17/23843	0.287211	0.567124	0.530959	Chd7
GO_BP_m2	GO:004432	response t	1/470	17/23843	0.287211	0.567124	0.530959	Nr4a3
GO_BP_m2	GO:00456	positive re	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:00461	pyrimidine	1/470	17/23843	0.287211	0.567124	0.530959	Cad
GO_BP_m2	GO:00461	aldehyde b	1/470	17/23843	0.287211	0.567124	0.530959	Kdm3a
GO_BP_m2	GO:004634	amino sug	1/470	17/23843	0.287211	0.567124	0.530959	Mgat1
GO_BP_m2	GO:00468	negative re	1/470	17/23843	0.287211	0.567124	0.530959	Csk
GO_BP_m2	GO:00484	anterograd	1/470	17/23843	0.287211	0.567124	0.530959	Bloc1s2
GO_BP_m2	GO:00506	chondroiti	1/470	17/23843	0.287211	0.567124	0.530959	Chst12
GO_BP_m2	GO:00510	positive re	1/470	17/23843	0.287211	0.567124	0.530959	Ptk2b
GO_BP_m2	GO:00519	negative re	1/470	17/23843	0.287211	0.567124	0.530959	Grm7
GO_BP_m2	GO:005507	copper ion	1/470	17/23843	0.287211	0.567124	0.530959	Aplp2
GO_BP_m2	GO:006031	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Pde4d
GO_BP_m2	GO:006097	cell migrati	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:007024	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:007082	heterochro	1/470	17/23843	0.287211	0.567124	0.530959	H3f3b

GO_BP_m2	GO:007092	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:007266	protein loc	1/470	17/23843	0.287211	0.567124	0.530959	Pex5l
GO_BP_m2	GO:007266	establishm	1/470	17/23843	0.287211	0.567124	0.530959	Pex5l
GO_BP_m2	GO:008018	histone H3	1/470	17/23843	0.287211	0.567124	0.530959	Hist1h1e
GO_BP_m2	GO:009003	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Gpd1l
GO_BP_m2	GO:009950	vesicle fusi	1/470	17/23843	0.287211	0.567124	0.530959	Stxbp1
GO_BP_m2	GO:009951	synaptic ve	1/470	17/23843	0.287211	0.567124	0.530959	Bloc1s2
GO_BP_m2	GO:009951	synaptic ve	1/470	17/23843	0.287211	0.567124	0.530959	Bloc1s2
GO_BP_m2	GO:190217	negative re	1/470	17/23843	0.287211	0.567124	0.530959	Pink1
GO_BP_m2	GO:190359	positive reg	1/470	17/23843	0.287211	0.567124	0.530959	Pink1
GO_BP_m2	GO:190435	positive reg	1/470	17/23843	0.287211	0.567124	0.530959	Aurkb
GO_BP_m2	GO:190531	semi-lunar	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:200000	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Cry1
GO_BP_m2	GO:200035	positive reg	1/470	17/23843	0.287211	0.567124	0.530959	Bmp4
GO_BP_m2	GO:200084	regulation	1/470	17/23843	0.287211	0.567124	0.530959	Cry1
GO_BP_m2	GO:000833	endosome	2/470	54/23843	0.288184	0.567709	0.531506	Chmp3/Tsg
GO_BP_m2	GO:003049	maturation	2/470	54/23843	0.288184	0.567709	0.531506	Pwp2/Utp1
GO_BP_m2	GO:003646	synaptic ve	2/470	54/23843	0.288184	0.567709	0.531506	Sh3gl1/Syt
GO_BP_m2	GO:004259	fear respon	2/470	54/23843	0.288184	0.567709	0.531506	Grm7/Penk
GO_BP_m2	GO:004617	polyol bios	2/470	54/23843	0.288184	0.567709	0.531506	Pcbd1/Ptk2
GO_BP_m2	GO:003560	protein dea	3/470	95/23843	0.288473	0.567746	0.53154	Dyrk1a/Pin
GO_BP_m2	GO:004684	bone remo	3/470	95/23843	0.288473	0.567746	0.53154	Csk/Ptk2b/
GO_BP_m2	GO:000705	chromoso	8/470	317/23843	0.289101	0.568714	0.532447	Aurkb/Cit/
GO_BP_m2	GO:000167	cellular glu	4/470	138/23843	0.289566	0.56883	0.532555	Foxa3/Rack
GO_BP_m2	GO:000268	positive reg	4/470	138/23843	0.289566	0.56883	0.532555	Ptk2b/Rac2
GO_BP_m2	GO:000705	cell cycle a	4/470	138/23843	0.289566	0.56883	0.532555	Foxo4/Id2/
GO_BP_m2	GO:190352	regulation	6/470	227/23843	0.2914	0.572165	0.535678	Agrn/Gpd1
GO_BP_m2	GO:009873	macromole	3/470	96/23843	0.293852	0.57487	0.53821	Dyrk1a/Pin
GO_BP_m2	GO:003030	positive reg	5/470	183/23843	0.2939	0.57487	0.53821	Acsl4/Exos
GO_BP_m2	GO:004354	endothelial	5/470	183/23843	0.2939	0.57487	0.53821	Angpt4/Bm
GO_BP_m2	GO:003315	regulation	7/470	273/23843	0.293902	0.57487	0.53821	Bmp4/Ect2
GO_BP_m2	GO:004255	myelinatio	4/470	139/23843	0.293979	0.57487	0.53821	Adgrg6/Fa
GO_BP_m2	GO:004544	fat cell diffe	6/470	228/23843	0.294807	0.57487	0.53821	Cebpa/Gdf
GO_BP_m2	GO:009719	extrinsic ap	6/470	228/23843	0.294807	0.57487	0.53821	Bloc1s2/Bm
GO_BP_m2	GO:000686	lipid transp	8/470	319/23843	0.29482	0.57487	0.53821	Acat2/Acsl4
GO_BP_m2	GO:000038	alternative	2/470	55/23843	0.295498	0.57487	0.53821	Dyrk1a/Thr
GO_BP_m2	GO:004269	ovulation c	2/470	55/23843	0.295498	0.57487	0.53821	Gdf9/Sgpl1
GO_BP_m2	GO:004660	regulation	2/470	55/23843	0.295498	0.57487	0.53821	Cep120/Ch
GO_BP_m2	GO:004853	thymus dev	2/470	55/23843	0.295498	0.57487	0.53821	Mafb/Zbtb
GO_BP_m2	GO:006035	endochonc	2/470	55/23843	0.295498	0.57487	0.53821	Bmp4/Col2
GO_BP_m2	GO:006197	replaceme	2/470	55/23843	0.295498	0.57487	0.53821	Bmp4/Col2
GO_BP_m2	GO:190307	positive reg	2/470	55/23843	0.295498	0.57487	0.53821	Rack1/Rab
GO_BP_m2	GO:001567	monovalen	11/470	459/23843	0.297428	0.57487	0.53821	Agrn/Atf4/
GO_BP_m2	GO:000974	response to	5/470	184/23843	0.297725	0.57487	0.53821	Glul/Rack1
GO_BP_m2	GO:005121	cartilage de	5/470	184/23843	0.297725	0.57487	0.53821	Bmp4/Col2
GO_BP_m2	GO:000662	protein targ	4/470	140/23843	0.298401	0.57487	0.53821	Pink1/Rac2
GO_BP_m2	GO:001821	peptidyl-th	4/470	140/23843	0.298401	0.57487	0.53821	Cad/Clk1/
GO_BP_m2	GO:007170	tumor necr	4/470	140/23843	0.298401	0.57487	0.53821	Cybb/Mavs

GO_BP_m2	GO:000193	negative re	10/470	413/23843	0.298968	0.57487	0.53821	Bmp4/Csk/
GO_BP_m2	GO:000635	DNA-temp	3/470	97/23843	0.299238	0.57487	0.53821	Cebpa/Psm
GO_BP_m2	GO:004605	cAMP meta	3/470	97/23843	0.299238	0.57487	0.53821	Rack1/Pde
GO_BP_m2	GO:006034	bone morp	3/470	97/23843	0.299238	0.57487	0.53821	Bmp4/Col2
GO_BP_m2	GO:190307	regulation	3/470	97/23843	0.299238	0.57487	0.53821	Csk/Rack1/
GO_BP_m2	GO:000195	positive reg	1/470	18/23843	0.301272	0.57487	0.53821	Stxbp1
GO_BP_m2	GO:000207	osteoblast	1/470	18/23843	0.301272	0.57487	0.53821	Jund
GO_BP_m2	GO:000282	positive reg	1/470	18/23843	0.301272	0.57487	0.53821	Il12rb1
GO_BP_m2	GO:000309	glomerular	1/470	18/23843	0.301272	0.57487	0.53821	Sulf2
GO_BP_m2	GO:000612	mitochond	1/470	18/23843	0.301272	0.57487	0.53821	Pink1
GO_BP_m2	GO:000649	N-glycan p	1/470	18/23843	0.301272	0.57487	0.53821	Prkcsh
GO_BP_m2	GO:000739	ectoderm	1/470	18/23843	0.301272	0.57487	0.53821	Erf
GO_BP_m2	GO:003015	protein imp	1/470	18/23843	0.301272	0.57487	0.53821	Tomm20
GO_BP_m2	GO:003050	negative re	1/470	18/23843	0.301272	0.57487	0.53821	Ptk2b
GO_BP_m2	GO:003240	establishm	1/470	18/23843	0.301272	0.57487	0.53821	Rab11a
GO_BP_m2	GO:003316	positive reg	1/470	18/23843	0.301272	0.57487	0.53821	Mavs
GO_BP_m2	GO:003593	corticoster	1/470	18/23843	0.301272	0.57487	0.53821	Cry1
GO_BP_m2	GO:003615	outer dyne	1/470	18/23843	0.301272	0.57487	0.53821	Mss51
GO_BP_m2	GO:003615	inner dyne	1/470	18/23843	0.301272	0.57487	0.53821	Mss51
GO_BP_m2	GO:004003	negative re	1/470	18/23843	0.301272	0.57487	0.53821	Sulf2
GO_BP_m2	GO:004221	cellular mo	1/470	18/23843	0.301272	0.57487	0.53821	Pm20d2
GO_BP_m2	GO:004224	establishm	1/470	18/23843	0.301272	0.57487	0.53821	Sfrp2
GO_BP_m2	GO:004277	DNA dama	1/470	18/23843	0.301272	0.57487	0.53821	Pcbp4
GO_BP_m2	GO:004355	regulation	1/470	18/23843	0.301272	0.57487	0.53821	Slc35a4
GO_BP_m2	GO:004547	locomotor	1/470	18/23843	0.301272	0.57487	0.53821	Id2
GO_BP_m2	GO:004632	positive reg	1/470	18/23843	0.301272	0.57487	0.53821	Nr4a3
GO_BP_m2	GO:005160	histamine t	1/470	18/23843	0.301272	0.57487	0.53821	Csf2
GO_BP_m2	GO:005190	pigment gr	1/470	18/23843	0.301272	0.57487	0.53821	Rab11a
GO_BP_m2	GO:006023	mesenchym	1/470	18/23843	0.301272	0.57487	0.53821	Bmp4
GO_BP_m2	GO:006033	regulation	1/470	18/23843	0.301272	0.57487	0.53821	Mavs
GO_BP_m2	GO:006039	regulation	1/470	18/23843	0.301272	0.57487	0.53821	Bmp4
GO_BP_m2	GO:006057	morphogen	1/470	18/23843	0.301272	0.57487	0.53821	Bmp4
GO_BP_m2	GO:006070	trophoblas	1/470	18/23843	0.301272	0.57487	0.53821	Erf
GO_BP_m2	GO:007180	regulation	1/470	18/23843	0.301272	0.57487	0.53821	Csf2
GO_BP_m2	GO:007207	renal vesicl	1/470	18/23843	0.301272	0.57487	0.53821	Bmp4
GO_BP_m2	GO:009002	positive reg	1/470	18/23843	0.301272	0.57487	0.53821	S100a14
GO_BP_m2	GO:009018	negative re	1/470	18/23843	0.301272	0.57487	0.53821	Bmp4
GO_BP_m2	GO:009962	ventricular	1/470	18/23843	0.301272	0.57487	0.53821	Kcnh2
GO_BP_m2	GO:190101	negative re	1/470	18/23843	0.301272	0.57487	0.53821	Agrn
GO_BP_m2	GO:190162	regulation	1/470	18/23843	0.301272	0.57487	0.53821	Ptk2b
GO_BP_m2	GO:199040	embryonic	1/470	18/23843	0.301272	0.57487	0.53821	Mir449b
GO_BP_m2	GO:001491	positive reg	2/470	56/23843	0.3028	0.577057	0.540258	Foxo4/Plau
GO_BP_m2	GO:006133	cardiac con	2/470	56/23843	0.3028	0.577057	0.540258	Kcnh2/Pde
GO_BP_m2	GO:005125	negative re	4/470	141/23843	0.302831	0.577057	0.540258	Bmp4/Id2/
GO_BP_m2	GO:003450	protein loc	7/470	276/23843	0.303242	0.577577	0.540745	Bmp4/Ect2
GO_BP_m2	GO:003010	natural kille	3/470	98/23843	0.304629	0.579167	0.542234	Id2/Ifna4/Z
GO_BP_m2	GO:003079	regulation	3/470	98/23843	0.304629	0.579167	0.542234	Rack1/Pde4
GO_BP_m2	GO:004642	positive reg	3/470	98/23843	0.304629	0.579167	0.542234	Csf2/Prl8a2

GO_BP_m2	GO:009956	chemical sy	3/470	98/23843	0.304629	0.579167	0.542234	Mtmr2/Ptk
GO_BP_m2	GO:000727	ensheathm	4/470	142/23843	0.307268	0.583657	0.546437	Adgrg6/Fa
GO_BP_m2	GO:000836	axon enshe	4/470	142/23843	0.307268	0.583657	0.546437	Adgrg6/Fa
GO_BP_m2	GO:001605	Wnt signali	10/470	417/23843	0.309115	0.585364	0.548035	Bambi/Dkk
GO_BP_m2	GO:003133	positive reg	8/470	324/23843	0.309233	0.585364	0.548035	Rack1/Met
GO_BP_m2	GO:000020	protein pol	5/470	187/23843	0.309248	0.585364	0.548035	Rnf146/Rnf
GO_BP_m2	GO:005122	positive reg	11/470	464/23843	0.309436	0.585364	0.548035	Ect2/Glul/R
GO_BP_m2	GO:001580	acidic amin	2/470	57/23843	0.310089	0.585364	0.548035	Grm7/Stxb
GO_BP_m2	GO:004311	receptor cl	2/470	57/23843	0.310089	0.585364	0.548035	Agrn/Ift122
GO_BP_m2	GO:005131	metaphase	2/470	57/23843	0.310089	0.585364	0.548035	Rab11a/Tra
GO_BP_m2	GO:200073	regulation	2/470	57/23843	0.310089	0.585364	0.548035	Bmp4/Kdm
GO_BP_m2	GO:004358	ear develop	6/470	233/23843	0.311952	0.585364	0.548035	Bmp4/Ceb
GO_BP_m2	GO:000227	myeloid leu	5/470	188/23843	0.313103	0.585364	0.548035	Csf2/Jmjd6
GO_BP_m2	GO:003461	response to	5/470	188/23843	0.313103	0.585364	0.548035	Aff3/Cebpa
GO_BP_m2	GO:007124	cellular resp	5/470	188/23843	0.313103	0.585364	0.548035	Cebpa/Ect2
GO_BP_m2	GO:019873	cell-cell sig	10/470	419/23843	0.31422	0.585364	0.548035	Bambi/Dkk
GO_BP_m2	GO:000150	cartilage co	1/470	19/23843	0.315056	0.585364	0.548035	Col2a1
GO_BP_m2	GO:000211	store-oper	1/470	19/23843	0.315056	0.585364	0.548035	Srl
GO_BP_m2	GO:000218	cytoplasmi	1/470	19/23843	0.315056	0.585364	0.548035	Eif5
GO_BP_m2	GO:000321	cardiac left	1/470	19/23843	0.315056	0.585364	0.548035	Sfrp2
GO_BP_m2	GO:000321	cardiac righ	1/470	19/23843	0.315056	0.585364	0.548035	Chd7
GO_BP_m2	GO:000608	lactate met	1/470	19/23843	0.315056	0.585364	0.548035	Pfkfb2
GO_BP_m2	GO:000610	2-oxogluta	1/470	19/23843	0.315056	0.585364	0.548035	Kyat3
GO_BP_m2	GO:000669	bile acid bi	1/470	19/23843	0.315056	0.585364	0.548035	Slc27a2
GO_BP_m2	GO:000820	androgen r	1/470	19/23843	0.315056	0.585364	0.548035	Sgpl1
GO_BP_m2	GO:001084	retina layer	1/470	19/23843	0.315056	0.585364	0.548035	Ptprm
GO_BP_m2	GO:001608	synaptic ve	1/470	19/23843	0.315056	0.585364	0.548035	Stxbp1
GO_BP_m2	GO:001824	protein O-	1/470	19/23843	0.315056	0.585364	0.548035	Galnt2
GO_BP_m2	GO:003282	regulation	1/470	19/23843	0.315056	0.585364	0.548035	Zbtb1
GO_BP_m2	GO:003360	positive reg	1/470	19/23843	0.315056	0.585364	0.548035	Pink1
GO_BP_m2	GO:003469	response to	1/470	19/23843	0.315056	0.585364	0.548035	Acaca
GO_BP_m2	GO:003549	SNARE com	1/470	19/23843	0.315056	0.585364	0.548035	Vamp3
GO_BP_m2	GO:003601	protein loc	1/470	19/23843	0.315056	0.585364	0.548035	Tollip
GO_BP_m2	GO:004564	regulation	1/470	19/23843	0.315056	0.585364	0.548035	Id2
GO_BP_m2	GO:005077	negative re	1/470	19/23843	0.315056	0.585364	0.548035	Cit
GO_BP_m2	GO:005101	barbed-en	1/470	19/23843	0.315056	0.585364	0.548035	Twf1
GO_BP_m2	GO:005138	kinetochor	1/470	19/23843	0.315056	0.585364	0.548035	Trappc12
GO_BP_m2	GO:005190	regulation	1/470	19/23843	0.315056	0.585364	0.548035	Rack1
GO_BP_m2	GO:005190	establishme	1/470	19/23843	0.315056	0.585364	0.548035	Rab11a
GO_BP_m2	GO:006029	cilium mov	1/470	19/23843	0.315056	0.585364	0.548035	Cfap46
GO_BP_m2	GO:006045	positive reg	1/470	19/23843	0.315056	0.585364	0.548035	Acat2
GO_BP_m2	GO:006078	ectoderma	1/470	19/23843	0.315056	0.585364	0.548035	Dkk4
GO_BP_m2	GO:007142	rRNA-cont	1/470	19/23843	0.315056	0.585364	0.548035	Ran
GO_BP_m2	GO:007169	ectoderma	1/470	19/23843	0.315056	0.585364	0.548035	Dkk4
GO_BP_m2	GO:009720	renal filtrat	1/470	19/23843	0.315056	0.585364	0.548035	Sulf2
GO_BP_m2	GO:190042	regulation	1/470	19/23843	0.315056	0.585364	0.548035	Syt11
GO_BP_m2	GO:190527	regulation	1/470	19/23843	0.315056	0.585364	0.548035	Sfrp2
GO_BP_m2	GO:190533	negative re	1/470	19/23843	0.315056	0.585364	0.548035	Bmp4

GO_BP_m2	GO:200001	positive re	1/470	19/23843	0.315056	0.585364	0.548035	Gpd1l
GO_BP_m2	GO:200013	regulation	1/470	19/23843	0.315056	0.585364	0.548035	Bmp4
GO_BP_m2	GO:200019	positive re	1/470	19/23843	0.315056	0.585364	0.548035	Erfe
GO_BP_m2	GO:000940	response t	3/470	100/23843	0.315421	0.585364	0.548035	Slc52a3/Tg
GO_BP_m2	GO:006007	regulation	3/470	100/23843	0.315421	0.585364	0.548035	Mtmr2/Ptk
GO_BP_m2	GO:190489	positive re	3/470	100/23843	0.315421	0.585364	0.548035	Csf2/Prl8a2
GO_BP_m2	GO:190526	positive re	3/470	100/23843	0.315421	0.585364	0.548035	Auts2/Pink
GO_BP_m2	GO:006040	calcium ion	4/470	144/23843	0.316162	0.586479	0.54908	Bmp4/Chd
GO_BP_m2	GO:000288	regulation	2/470	58/23843	0.317362	0.587148	0.549705	Rac2/Stxbp
GO_BP_m2	GO:000635	DNA-temp	2/470	58/23843	0.317362	0.587148	0.549705	Ell/Eloa
GO_BP_m2	GO:000644	regulation	2/470	58/23843	0.317362	0.587148	0.549705	Eif5/Ncbp2
GO_BP_m2	GO:190230	regulation	2/470	58/23843	0.317362	0.587148	0.549705	Agrn/Gpd1
GO_BP_m2	GO:190379	positive re	2/470	58/23843	0.317362	0.587148	0.549705	Erfe/Stxbp1
GO_BP_m2	GO:190435	regulation	2/470	58/23843	0.317362	0.587148	0.549705	Aurkb/Hnr
GO_BP_m2	GO:003028	bone mine	3/470	101/23843	0.320821	0.593024	0.555207	Bmp4/Nbr1
GO_BP_m2	GO:005195	regulation	3/470	101/23843	0.320821	0.593024	0.555207	Grm7/Pink
GO_BP_m2	GO:000301	muscle sys	9/470	375/23843	0.321751	0.594481	0.556571	Agrn/Gpd1
GO_BP_m2	GO:005105	positive re	6/470	236/23843	0.322317	0.595266	0.557305	Aurkb/Bmp
GO_BP_m2	GO:000666	phosphatic	2/470	59/23843	0.324617	0.59657	0.558527	Cdipt/Pigm
GO_BP_m2	GO:001936	arachidoni	2/470	59/23843	0.324617	0.59657	0.558527	Cyp2g1/Fa
GO_BP_m2	GO:003051	negative re	2/470	59/23843	0.324617	0.59657	0.558527	Bambi/Tgfb
GO_BP_m2	GO:004566	negative re	2/470	59/23843	0.324617	0.59657	0.558527	Id2/Nbr1
GO_BP_m2	GO:006032	face develo	2/470	59/23843	0.324617	0.59657	0.558527	Chd7/Sgpl1
GO_BP_m2	GO:190351	mucopolys	2/470	59/23843	0.324617	0.59657	0.558527	Chst12/Chs
GO_BP_m2	GO:000751	skeletal mu	5/470	191/23843	0.324705	0.59657	0.558527	Klhl41/Tll2/
GO_BP_m2	GO:190370	negative re	4/470	146/23843	0.325077	0.59657	0.558527	Bmp4/Id2/
GO_BP_m2	GO:000693	muscle con	7/470	283/23843	0.325256	0.59657	0.558527	Agrn/Gpd1
GO_BP_m2	GO:003241	regulation	6/470	237/23843	0.325784	0.59657	0.558527	Agrn/Bmp4
GO_BP_m2	GO:000703	vacuolar ac	1/470	20/23843	0.328569	0.59657	0.558527	Atp6v1h
GO_BP_m2	GO:001573	prostaglan	1/470	20/23843	0.328569	0.59657	0.558527	Acsl4
GO_BP_m2	GO:001613	glycoside r	1/470	20/23843	0.328569	0.59657	0.558527	Gba2
GO_BP_m2	GO:001648	peptide ho	1/470	20/23843	0.328569	0.59657	0.558527	Pcsk2
GO_BP_m2	GO:001824	protein O-	1/470	20/23843	0.328569	0.59657	0.558527	Galnt2
GO_BP_m2	GO:003054	female ger	1/470	20/23843	0.328569	0.59657	0.558527	Chd7
GO_BP_m2	GO:003106	positive re	1/470	20/23843	0.328569	0.59657	0.558527	Pink1
GO_BP_m2	GO:003164	negative re	1/470	20/23843	0.328569	0.59657	0.558527	Mtmr2
GO_BP_m2	GO:003228	myelin asse	1/470	20/23843	0.328569	0.59657	0.558527	Mtmr2
GO_BP_m2	GO:003230	regulation	1/470	20/23843	0.328569	0.59657	0.558527	Acsl4
GO_BP_m2	GO:003233	positive re	1/470	20/23843	0.328569	0.59657	0.558527	Gdf6
GO_BP_m2	GO:003268	negative re	1/470	20/23843	0.328569	0.59657	0.558527	Suz12
GO_BP_m2	GO:004273	fibrinolysis	1/470	20/23843	0.328569	0.59657	0.558527	Plau
GO_BP_m2	GO:004301	myeloid de	1/470	20/23843	0.328569	0.59657	0.558527	Csf2
GO_BP_m2	GO:004398	histone H4	1/470	20/23843	0.328569	0.59657	0.558527	Auts2
GO_BP_m2	GO:004855	embryonic	1/470	20/23843	0.328569	0.59657	0.558527	Id2
GO_BP_m2	GO:006132	cell prolifer	1/470	20/23843	0.328569	0.59657	0.558527	Bmp4
GO_BP_m2	GO:007016	negative re	1/470	20/23843	0.328569	0.59657	0.558527	Ptk2b
GO_BP_m2	GO:007063	transepithe	1/470	20/23843	0.328569	0.59657	0.558527	Csf2
GO_BP_m2	GO:007169	ectoderma	1/470	20/23843	0.328569	0.59657	0.558527	Dkk4

GO_BP_m2	GO:007208	renal vesicl	1/470	20/23843	0.328569	0.59657	0.558527	Bmp4
GO_BP_m2	GO:009038	phagosom	1/470	20/23843	0.328569	0.59657	0.558527	Syt11
GO_BP_m2	GO:009874	cell aggreg	1/470	20/23843	0.328569	0.59657	0.558527	Col2a1
GO_BP_m2	GO:009878	response t	1/470	20/23843	0.328569	0.59657	0.558527	Pink1
GO_BP_m2	GO:009962	regulation	1/470	20/23843	0.328569	0.59657	0.558527	Kcnh2
GO_BP_m2	GO:009963	protein tra	1/470	20/23843	0.328569	0.59657	0.558527	Rab11a
GO_BP_m2	GO:009963	neurotrans	1/470	20/23843	0.328569	0.59657	0.558527	Rab11a
GO_BP_m2	GO:199012	retrograde	1/470	20/23843	0.328569	0.59657	0.558527	Rab11a
GO_BP_m2	GO:200011	regulation	1/470	20/23843	0.328569	0.59657	0.558527	Ptk2b
GO_BP_m2	GO:005159	response t	3/470	103/23843	0.331621	0.601304	0.562959	Ect2/Fosb/
GO_BP_m2	GO:001061	regulation	2/470	60/23843	0.331852	0.601304	0.562959	Nr4a3/Twf1
GO_BP_m2	GO:003033	DNA dama	2/470	60/23843	0.331852	0.601304	0.562959	Dyrk1a/Pcb
GO_BP_m2	GO:003590	aorta deve	2/470	60/23843	0.331852	0.601304	0.562959	Ap2b1/Chd
GO_BP_m2	GO:000166	response t	5/470	193/23843	0.332465	0.601304	0.562959	Cybb/Pink1
GO_BP_m2	GO:001589	drug transp	5/470	193/23843	0.332465	0.601304	0.562959	Gdf9/Pink1
GO_BP_m2	GO:005165	establishm	5/470	193/23843	0.332465	0.601304	0.562959	Bloc1s2/Cp
GO_BP_m2	GO:005500	muscle cell	5/470	193/23843	0.332465	0.601304	0.562959	Bmp4/Klhl4
GO_BP_m2	GO:190305	regulation	5/470	193/23843	0.332465	0.601304	0.562959	Alad/Rack1
GO_BP_m2	GO:005104	negative re	6/470	239/23843	0.332732	0.601526	0.563167	Acsl4/Cry1/
GO_BP_m2	GO:000690	vesicle fusi	4/470	148/23843	0.334008	0.603574	0.565084	Snph/Stxbp
GO_BP_m2	GO:000165	urogenital	8/470	333/23843	0.335527	0.604152	0.565625	Bmp4/Id2/
GO_BP_m2	GO:003103	actomyosin	5/470	194/23843	0.336352	0.604152	0.565625	Alkbh4/Frm
GO_BP_m2	GO:009031	positive reg	5/470	194/23843	0.336352	0.604152	0.565625	Ect2/Mavs/
GO_BP_m2	GO:005127	negative re	7/470	287/23843	0.33795	0.604152	0.565625	Angpt4/Ara
GO_BP_m2	GO:190316	regulation	4/470	149/23843	0.338478	0.604152	0.565625	Bmp4/Chd
GO_BP_m2	GO:190495	positive reg	11/470	476/23843	0.338712	0.604152	0.565625	Ect2/Glul/R
GO_BP_m2	GO:000322	ventricular	2/470	61/23843	0.339065	0.604152	0.565625	Chd7/Id2
GO_BP_m2	GO:001017	body morp	2/470	61/23843	0.339065	0.604152	0.565625	Ift122/Sgpl
GO_BP_m2	GO:001623	positive reg	2/470	61/23843	0.339065	0.604152	0.565625	Pink1/Ralb
GO_BP_m2	GO:003085	positive reg	2/470	61/23843	0.339065	0.604152	0.565625	Bmp4/Foxa
GO_BP_m2	GO:004566	regulation	2/470	61/23843	0.339065	0.604152	0.565625	Bmp4/Klhl4
GO_BP_m2	GO:005077	negative re	2/470	61/23843	0.339065	0.604152	0.565625	Rnf6/Spg20
GO_BP_m2	GO:009055	regulation	2/470	61/23843	0.339065	0.604152	0.565625	Bloc1s2/He
GO_BP_m2	GO:190305	negative re	2/470	61/23843	0.339065	0.604152	0.565625	Alad/Ube2
GO_BP_m2	GO:190384	negative re	2/470	61/23843	0.339065	0.604152	0.565625	Bambi/Tgfb
GO_BP_m2	GO:190437	positive reg	2/470	61/23843	0.339065	0.604152	0.565625	Rack1/Rab
GO_BP_m2	GO:200102	negative re	2/470	61/23843	0.339065	0.604152	0.565625	Dyrk1a/Pcb
GO_BP_m2	GO:200125	positive reg	2/470	61/23843	0.339065	0.604152	0.565625	Bmp4/Pink
GO_BP_m2	GO:003367	negative re	6/470	241/23843	0.339698	0.604152	0.565625	Bmp4/Csk/
GO_BP_m2	GO:004642	regulation	5/470	195/23843	0.340243	0.604152	0.565625	Csf2/Ifna4/
GO_BP_m2	GO:000042	mitophagy	1/470	21/23843	0.341815	0.604152	0.565625	Pink1
GO_BP_m2	GO:000046	maturation	1/470	21/23843	0.341815	0.604152	0.565625	Exosc2
GO_BP_m2	GO:000208	regulation	1/470	21/23843	0.341815	0.604152	0.565625	Pink1
GO_BP_m2	GO:000332	type B pan	1/470	21/23843	0.341815	0.604152	0.565625	Bmp4
GO_BP_m2	GO:001066	epithelial s	1/470	21/23843	0.341815	0.604152	0.565625	Crocc
GO_BP_m2	GO:001074	regulation	1/470	21/23843	0.341815	0.604152	0.565625	Csf2
GO_BP_m2	GO:001655	mRNA mod	1/470	21/23843	0.341815	0.604152	0.565625	Mettl14
GO_BP_m2	GO:001812	protein hyd	1/470	21/23843	0.341815	0.604152	0.565625	Jmjd6

GO_BP_m2	GO:001932	hexose cat	1/470	21/23843	0.341815	0.604152	0.565625	Pfkfb2
GO_BP_m2	GO:003129	retinal gan	1/470	21/23843	0.341815	0.604152	0.565625	Ptprm
GO_BP_m2	GO:003233	negative re	1/470	21/23843	0.341815	0.604152	0.565625	Bmp4
GO_BP_m2	GO:003240	melanoson	1/470	21/23843	0.341815	0.604152	0.565625	Rab11a
GO_BP_m2	GO:003246	regulation	1/470	21/23843	0.341815	0.604152	0.565625	Rack1
GO_BP_m2	GO:003296	positive re	1/470	21/23843	0.341815	0.604152	0.565625	Ell
GO_BP_m2	GO:003300	positive re	1/470	21/23843	0.341815	0.604152	0.565625	Stxbp1
GO_BP_m2	GO:003362	integrin ac	1/470	21/23843	0.341815	0.604152	0.565625	Farp2
GO_BP_m2	GO:003438	low-densit	1/470	21/23843	0.341815	0.604152	0.565625	Csk
GO_BP_m2	GO:003469	response t	1/470	21/23843	0.341815	0.604152	0.565625	Acaca
GO_BP_m2	GO:003952	cytoplasmi	1/470	21/23843	0.341815	0.604152	0.565625	Mavs
GO_BP_m2	GO:004330	positive re	1/470	21/23843	0.341815	0.604152	0.565625	Stxbp1
GO_BP_m2	GO:004568	negative re	1/470	21/23843	0.341815	0.604152	0.565625	Dkk4
GO_BP_m2	GO:004613	pyrimidine	1/470	21/23843	0.341815	0.604152	0.565625	Cad
GO_BP_m2	GO:004632	negative re	1/470	21/23843	0.341815	0.604152	0.565625	Upk3b
GO_BP_m2	GO:004668	response t	1/470	21/23843	0.341815	0.604152	0.565625	Alad
GO_BP_m2	GO:004802	positive re	1/470	21/23843	0.341815	0.604152	0.565625	Thrap3
GO_BP_m2	GO:005123	sequesterir	1/470	21/23843	0.341815	0.604152	0.565625	Fthl17f
GO_BP_m2	GO:005145	myoblast p	1/470	21/23843	0.341815	0.604152	0.565625	Klhl41
GO_BP_m2	GO:007084	inclusion b	1/470	21/23843	0.341815	0.604152	0.565625	Psmc5
GO_BP_m2	GO:007086	regulation	1/470	21/23843	0.341815	0.604152	0.565625	Ube2j1
GO_BP_m2	GO:007211	cell prolifer	1/470	21/23843	0.341815	0.604152	0.565625	Bmp4
GO_BP_m2	GO:009706	dendritic s	1/470	21/23843	0.341815	0.604152	0.565625	Mtmr2
GO_BP_m2	GO:190174	positive re	1/470	21/23843	0.341815	0.604152	0.565625	Cd53
GO_BP_m2	GO:001050	positive re	3/470	105/23843	0.342416	0.604196	0.565666	Pink1/Ralb
GO_BP_m2	GO:001583	amine tran	3/470	105/23843	0.342416	0.604196	0.565666	Grm7/Pink
GO_BP_m2	GO:190437	regulation	3/470	105/23843	0.342416	0.604196	0.565666	Csk/Rack1/
GO_BP_m2	GO:200017	regulation	3/470	105/23843	0.342416	0.604196	0.565666	Id2/Six3/V
GO_BP_m2	GO:004873	cardiac mu	6/470	242/23843	0.343187	0.605301	0.566701	Bmp4/Chd
GO_BP_m2	GO:001715	regulation	5/470	196/23843	0.344137	0.606467	0.567793	Rac2/Ralb/
GO_BP_m2	GO:006034	bone devel	5/470	196/23843	0.344137	0.606467	0.567793	Bmp4/Col2
GO_BP_m2	GO:000754	sex differer	7/470	289/23843	0.344323	0.606541	0.567862	Bmp4/Chd
GO_BP_m2	GO:000636	transcriptic	2/470	62/23843	0.346253	0.608154	0.569372	Psmc5/Thr
GO_BP_m2	GO:001474	regulation	2/470	62/23843	0.346253	0.608154	0.569372	Nr4a3/Twf
GO_BP_m2	GO:002169	cerebellar	2/470	62/23843	0.346253	0.608154	0.569372	Coq8b/Fai
GO_BP_m2	GO:003112	cytoplasmi	2/470	62/23843	0.346253	0.608154	0.569372	Cep120/Ra
GO_BP_m2	GO:004205	regulation	2/470	62/23843	0.346253	0.608154	0.569372	Aplp2/Tsg
GO_BP_m2	GO:005186	protein aut	2/470	62/23843	0.346253	0.608154	0.569372	Rnf146/Rn
GO_BP_m2	GO:006103	regulation	2/470	62/23843	0.346253	0.608154	0.569372	Bmp4/Gdf
GO_BP_m2	GO:002289	regulation	6/470	243/23843	0.346679	0.608646	0.569833	Agrn/Bmp
GO_BP_m2	GO:003200	regulation	3/470	106/23843	0.347809	0.60961	0.570735	Gatsl2/Itfg
GO_BP_m2	GO:004353	blood vess	3/470	106/23843	0.347809	0.60961	0.570735	Angpt4/Pd
GO_BP_m2	GO:005120	release of	3/470	106/23843	0.347809	0.60961	0.570735	Chd7/Pde4
GO_BP_m2	GO:005128	negative re	3/470	106/23843	0.347809	0.60961	0.570735	Chd7/Pde4
GO_BP_m2	GO:190489	regulation	5/470	197/23843	0.348034	0.609749	0.570866	Csf2/Ifna4/
GO_BP_m2	GO:003253	regulation	9/470	385/23843	0.349255	0.610392	0.571467	Chmp3/Cit
GO_BP_m2	GO:003214	activation	6/470	244/23843	0.350175	0.610392	0.571467	Bmp4/Cks1
GO_BP_m2	GO:004209	T cell prolif	5/470	198/23843	0.351933	0.610392	0.571467	Bmp4/Il12

GO_BP_m2	GO:000007	DNA dama	3/470	107/23843	0.353197	0.610392	0.571467	Cdc5l/Cry1
GO_BP_m2	GO:005122	spindle ass	3/470	107/23843	0.353197	0.610392	0.571467	Aurkb/Rab
GO_BP_m2	GO:005128	regulation	3/470	107/23843	0.353197	0.610392	0.571467	Chd7/Pde4
GO_BP_m2	GO:000998	cell-cell rec	2/470	63/23843	0.353416	0.610392	0.571467	Izumo1r/Zf
GO_BP_m2	GO:003460	cellular res	2/470	63/23843	0.353416	0.610392	0.571467	Slc52a3/Zf
GO_BP_m2	GO:009730	cellular res	2/470	63/23843	0.353416	0.610392	0.571467	Acaca/Mir3
GO_BP_m2	GO:190160	alpha-amir	2/470	63/23843	0.353416	0.610392	0.571467	Cad/Glul
GO_BP_m2	GO:003009	myeloid ce	9/470	387/23843	0.354799	0.610392	0.571467	Bmp4/Ceb
GO_BP_m2	GO:000002	ribosomal	1/470	22/23843	0.354801	0.610392	0.571467	Pwp2
GO_BP_m2	GO:000853	respiratory	1/470	22/23843	0.354801	0.610392	0.571467	Cox10
GO_BP_m2	GO:001097	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Rab11a
GO_BP_m2	GO:001485	response to	1/470	22/23843	0.354801	0.610392	0.571467	Srl
GO_BP_m2	GO:003272	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Mavs
GO_BP_m2	GO:003440	response to	1/470	22/23843	0.354801	0.610392	0.571467	Ptk2b
GO_BP_m2	GO:003502	negative re	1/470	22/23843	0.354801	0.610392	0.571467	Arap3
GO_BP_m2	GO:003563	response to	1/470	22/23843	0.354801	0.610392	0.571467	Fgl1
GO_BP_m2	GO:004253	benzene-c	1/470	22/23843	0.354801	0.610392	0.571467	Kyat3
GO_BP_m2	GO:004348	histone exc	1/470	22/23843	0.354801	0.610392	0.571467	Vps72
GO_BP_m2	GO:004349	regulation	1/470	22/23843	0.354801	0.610392	0.571467	Pcbd1
GO_BP_m2	GO:004560	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:004581	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Smarcd1
GO_BP_m2	GO:004594	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Atf4
GO_BP_m2	GO:005179	regulation	1/470	22/23843	0.354801	0.610392	0.571467	Dkk4
GO_BP_m2	GO:005187	pigment gr	1/470	22/23843	0.354801	0.610392	0.571467	Rab11a
GO_BP_m2	GO:005188	mitochond	1/470	22/23843	0.354801	0.610392	0.571467	Rack1
GO_BP_m2	GO:006026	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Psmc5
GO_BP_m2	GO:006043	trachea dev	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:006060	branch elon	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:006074	mammary	1/470	22/23843	0.354801	0.610392	0.571467	Id2
GO_BP_m2	GO:006108	myeloid leu	1/470	22/23843	0.354801	0.610392	0.571467	Nr4a3
GO_BP_m2	GO:006137	mammary	1/470	22/23843	0.354801	0.610392	0.571467	Id2
GO_BP_m2	GO:007024	thymocyte	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:007198	multivesicu	1/470	22/23843	0.354801	0.610392	0.571467	Chmp3
GO_BP_m2	GO:007221	regulation	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:007227	metanephr	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:190074	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Gdf6
GO_BP_m2	GO:190153	regulation	1/470	22/23843	0.354801	0.610392	0.571467	Zbtb1
GO_BP_m2	GO:190165	glycosyl co	1/470	22/23843	0.354801	0.610392	0.571467	Gba2
GO_BP_m2	GO:200063	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:200073	positive reg	1/470	22/23843	0.354801	0.610392	0.571467	Bmp4
GO_BP_m2	GO:200076	regulation	1/470	22/23843	0.354801	0.610392	0.571467	Unk
GO_BP_m2	GO:000815	actin polyn	5/470	199/23843	0.355835	0.611669	0.572662	Cit/Ptk2b/
GO_BP_m2	GO:003052	intracellula	5/470	199/23843	0.355835	0.611669	0.572662	Cry1/Kdm3
GO_BP_m2	GO:007189	DNA biosy	4/470	153/23843	0.356373	0.612343	0.573294	Aurkb/Hnr
GO_BP_m2	GO:004586	positive reg	10/470	436/23843	0.358281	0.615127	0.575901	Agrn/Bmp4
GO_BP_m2	GO:000184	neural tube	3/470	108/23843	0.35858	0.615127	0.575901	Bmp4/Ift12
GO_BP_m2	GO:005120	sequesterir	3/470	108/23843	0.35858	0.615127	0.575901	Chd7/Pde4
GO_BP_m2	GO:200027	regulation	3/470	108/23843	0.35858	0.615127	0.575901	Aurkb/Hnr

GO_BP_m2	GO:00605	skeletal mu	5/470	200/23843	0.359738	0.616744	0.577414	Klhl41/Tll2/
GO_BP_m2	GO:00756	embryo im	2/470	64/23843	0.360551	0.616744	0.577414	H3f3b/Ooe
GO_BP_m2	GO:00217	hippocamp	2/470	64/23843	0.360551	0.616744	0.577414	Nr4a3/Zbt
GO_BP_m2	GO:003237	positive re	2/470	64/23843	0.360551	0.616744	0.577414	Acat2/Erfe
GO_BP_m2	GO:004682	positive re	2/470	64/23843	0.360551	0.616744	0.577414	Ect2/Mavs
GO_BP_m2	GO:004692	regulation	2/470	64/23843	0.360551	0.616744	0.577414	Cplx4/Stxb
GO_BP_m2	GO:004827	vesicle doc	2/470	64/23843	0.360551	0.616744	0.577414	Ralb/Stxbp
GO_BP_m2	GO:000691	phagocyto	4/470	154/23843	0.360848	0.617	0.577653	Ighv1-23/I
GO_BP_m2	GO:00486	positive re	5/470	201/23843	0.363643	0.619612	0.5801	Agrn/Chd7
GO_BP_m2	GO:00606	tube closu	3/470	109/23843	0.363957	0.619612	0.5801	Bmp4/Ift12
GO_BP_m2	GO:00716	granulocyt	3/470	109/23843	0.363957	0.619612	0.5801	Pde4d/Rac
GO_BP_m2	GO:19053	regulation	3/470	109/23843	0.363957	0.619612	0.5801	Bmp4/Fkb
GO_BP_m2	GO:20001	regulation	3/470	109/23843	0.363957	0.619612	0.5801	Aurkb/Bm
GO_BP_m2	GO:00508	protein sta	4/470	155/23843	0.365321	0.619612	0.5801	Pdcd10/Pi
GO_BP_m2	GO:00726	establishm	4/470	155/23843	0.365321	0.619612	0.5801	Pink1/Rac2
GO_BP_m2	GO:19035	positive re	10/470	439/23843	0.366154	0.619612	0.5801	Glul/Mavs/
GO_BP_m2	GO:00029	negative re	1/470	23/23843	0.367531	0.619612	0.5801	Aurkb
GO_BP_m2	GO:00302	chondroiti	1/470	23/23843	0.367531	0.619612	0.5801	Chst12
GO_BP_m2	GO:00309	notochord	1/470	23/23843	0.367531	0.619612	0.5801	Col2a1
GO_BP_m2	GO:003237	positive re	1/470	23/23843	0.367531	0.619612	0.5801	Acat2
GO_BP_m2	GO:003237	positive re	1/470	23/23843	0.367531	0.619612	0.5801	Acat2
GO_BP_m2	GO:00324	positive re	1/470	23/23843	0.367531	0.619612	0.5801	Rack1
GO_BP_m2	GO:00341	negative re	1/470	23/23843	0.367531	0.619612	0.5801	Csk
GO_BP_m2	GO:003431	diol metab	1/470	23/23843	0.367531	0.619612	0.5801	Pcbd1
GO_BP_m2	GO:00343	smooth mu	1/470	23/23843	0.367531	0.619612	0.5801	Pde1a
GO_BP_m2	GO:00343	regulation	1/470	23/23843	0.367531	0.619612	0.5801	Pde1a
GO_BP_m2	GO:00354	histone-se	1/470	23/23843	0.367531	0.619612	0.5801	Aurkb
GO_BP_m2	GO:004204	fluid transp	1/470	23/23843	0.367531	0.619612	0.5801	Csf2
GO_BP_m2	GO:00424	thyroid hor	1/470	23/23843	0.367531	0.619612	0.5801	Crym
GO_BP_m2	GO:00457	negative re	1/470	23/23843	0.367531	0.619612	0.5801	Lats2
GO_BP_m2	GO:00513	meiotic chr	1/470	23/23843	0.367531	0.619612	0.5801	Espl1
GO_BP_m2	GO:006014	positive re	1/470	23/23843	0.367531	0.619612	0.5801	Bmp4
GO_BP_m2	GO:006097	left/right p	1/470	23/23843	0.367531	0.619612	0.5801	Ift122
GO_BP_m2	GO:007167	positive re	1/470	23/23843	0.367531	0.619612	0.5801	S100a14
GO_BP_m2	GO:00722	cell differe	1/470	23/23843	0.367531	0.619612	0.5801	Bmp4
GO_BP_m2	GO:008971	amino acid	1/470	23/23843	0.367531	0.619612	0.5801	Slc25a38
GO_BP_m2	GO:00901	positive re	1/470	23/23843	0.367531	0.619612	0.5801	Bmp4
GO_BP_m2	GO:190307	negative re	1/470	23/23843	0.367531	0.619612	0.5801	Csk
GO_BP_m2	GO:190367	negative re	1/470	23/23843	0.367531	0.619612	0.5801	Pdcd10
GO_BP_m2	GO:000651	protein m	2/470	65/23843	0.367657	0.619612	0.5801	Rnf20/Tsg1
GO_BP_m2	GO:00740	neuroblast	2/470	65/23843	0.367657	0.619612	0.5801	Six3/Vax1
GO_BP_m2	GO:001657	histone de	2/470	65/23843	0.367657	0.619612	0.5801	Pink1/Sirt7
GO_BP_m2	GO:005511	regulation	2/470	65/23843	0.367657	0.619612	0.5801	Agrn/Pde4
GO_BP_m2	GO:00726	protein loc	6/470	249/23843	0.367692	0.619612	0.5801	Csk/Fam12
GO_BP_m2	GO:00092	ribonucleo	10/470	440/23843	0.368783	0.621202	0.581588	Adsl/Cad/
GO_BP_m2	GO:00026	regulation	3/470	110/23843	0.369326	0.621617	0.581976	Ptk2b/Rac2
GO_BP_m2	GO:00508	negative re	3/470	110/23843	0.369326	0.621617	0.581976	Bmp4/Prka
GO_BP_m2	GO:00604	cytosolic c	4/470	156/23843	0.369794	0.622155	0.58248	Bmp4/Chd

GO_BP_m2	GO:004343	response t	7/470	298/23843	0.373152	0.627553	0.587534	Cad/Cry1/
GO_BP_m2	GO:000694	striated mu	4/470	157/23843	0.374264	0.627694	0.587666	Agrn/Gpd1
GO_BP_m2	GO:000756	female pre	4/470	157/23843	0.374264	0.627694	0.587666	Acsl4/H3f3
GO_BP_m2	GO:000154	ovarian foll	2/470	66/23843	0.374731	0.627694	0.587666	Bmp4/Lfng
GO_BP_m2	GO:000865	cellular am	2/470	66/23843	0.374731	0.627694	0.587666	Cad/Glul
GO_BP_m2	GO:004340	negative re	2/470	66/23843	0.374731	0.627694	0.587666	Bmp4/Sfrp
GO_BP_m2	GO:005129	centrosom	2/470	66/23843	0.374731	0.627694	0.587666	Cep120/Ch
GO_BP_m2	GO:006068	regulation	2/470	66/23843	0.374731	0.627694	0.587666	Bmp4/Fkbp
GO_BP_m2	GO:190118	regulation	2/470	66/23843	0.374731	0.627694	0.587666	Aplp2/Tsg1
GO_BP_m2	GO:190179	regulation	2/470	66/23843	0.374731	0.627694	0.587666	Dyrk1a/Pcb
GO_BP_m2	GO:190372	regulation	2/470	66/23843	0.374731	0.627694	0.587666	Mtmr2/Ptk
GO_BP_m2	GO:001605	carbohydra	5/470	204/23843	0.375361	0.628497	0.588418	Atf4/Chst1
GO_BP_m2	GO:005104	positive reg	11/470	492/23843	0.378483	0.630045	0.589867	Glul/Mavs/
GO_BP_m2	GO:000926	response t	4/470	158/23843	0.378731	0.630045	0.589867	Slc52a3/Tg
GO_BP_m2	GO:000622	pyrimidine	1/470	24/23843	0.380011	0.630045	0.589867	Cad
GO_BP_m2	GO:000630	postreplica	1/470	24/23843	0.380011	0.630045	0.589867	Zbtb1
GO_BP_m2	GO:000709	mitotic G2	1/470	24/23843	0.380011	0.630045	0.589867	Foxo4
GO_BP_m2	GO:001093	regulation	1/470	24/23843	0.380011	0.630045	0.589867	Hebp2
GO_BP_m2	GO:001626	O-glycan p	1/470	24/23843	0.380011	0.630045	0.589867	Galnt2
GO_BP_m2	GO:002188	olfactory b	1/470	24/23843	0.380011	0.630045	0.589867	Sall3
GO_BP_m2	GO:003020	heparan su	1/470	24/23843	0.380011	0.630045	0.589867	Sulf2
GO_BP_m2	GO:003072	ovulation	1/470	24/23843	0.380011	0.630045	0.589867	Plau
GO_BP_m2	GO:003106	negative re	1/470	24/23843	0.380011	0.630045	0.589867	Kdm3a
GO_BP_m2	GO:003110	animal org	1/470	24/23843	0.380011	0.630045	0.589867	Sulf2
GO_BP_m2	GO:003277	positive reg	1/470	24/23843	0.380011	0.630045	0.589867	Ptk2b
GO_BP_m2	GO:004205	negative re	1/470	24/23843	0.380011	0.630045	0.589867	Tsg101
GO_BP_m2	GO:004434	type B pan	1/470	24/23843	0.380011	0.630045	0.589867	Nr4a3
GO_BP_m2	GO:004504	protein targ	1/470	24/23843	0.380011	0.630045	0.589867	Sec63
GO_BP_m2	GO:004867	regulation	1/470	24/23843	0.380011	0.630045	0.589867	Spg20
GO_BP_m2	GO:005157	regulation	1/470	24/23843	0.380011	0.630045	0.589867	Kdm3a
GO_BP_m2	GO:009002	regulation	1/470	24/23843	0.380011	0.630045	0.589867	S100a14
GO_BP_m2	GO:190173	regulation	1/470	24/23843	0.380011	0.630045	0.589867	Cd53
GO_BP_m2	GO:190429	regulation	1/470	24/23843	0.380011	0.630045	0.589867	Ube2j1
GO_BP_m2	GO:190593	regulation	1/470	24/23843	0.380011	0.630045	0.589867	Gdf9
GO_BP_m2	GO:200072	positive reg	1/470	24/23843	0.380011	0.630045	0.589867	Bmp4
GO_BP_m2	GO:004616	alcohol bio	3/470	112/23843	0.380039	0.630045	0.589867	Pcbd1/Ptk2
GO_BP_m2	GO:190305	positive reg	3/470	112/23843	0.380039	0.630045	0.589867	Rack1/Ptk2
GO_BP_m2	GO:000640	tRNA modi	2/470	67/23843	0.381774	0.632171	0.591858	Ftsj1/Nsun
GO_BP_m2	GO:005088	neuromusc	2/470	67/23843	0.381774	0.632171	0.591858	Aplp2/Nr4a
GO_BP_m2	GO:005114	smooth mu	2/470	67/23843	0.381774	0.632171	0.591858	Bmp4/Foxo
GO_BP_m2	GO:000665	glyceropho	5/470	206/23843	0.383172	0.633277	0.592893	Cdipt/Fam
GO_BP_m2	GO:000836	regulation	4/470	159/23843	0.383196	0.633277	0.592893	Arap3/Bam
GO_BP_m2	GO:003083	regulation	4/470	159/23843	0.383196	0.633277	0.592893	Ptk2b/Rac2
GO_BP_m2	GO:007058	protein loc	4/470	159/23843	0.383196	0.633277	0.592893	Pink1/Rac2
GO_BP_m2	GO:200125	regulation	4/470	159/23843	0.383196	0.633277	0.592893	Bmp4/Pde
GO_BP_m2	GO:003033	positive reg	11/470	494/23843	0.383494	0.63352	0.59312	Angpt4/Bm
GO_BP_m2	GO:004854	response t	6/470	254/23843	0.385246	0.635886	0.595336	Bmp4/Cry1
GO_BP_m2	GO:006056	developme	6/470	254/23843	0.385246	0.635886	0.595336	Auts2/Bmp

GO_BP_m2	GO:000189	embryonic	3/470	113/23843	0.385381	0.635886	0.595336	Cebpa/Csf
GO_BP_m2	GO:000279	positive reg	7/470	302/23843	0.386014	0.636491	0.595902	Glul/Mavs/
GO_BP_m2	GO:000725	JAK-STAT	5/470	207/23843	0.387077	0.636491	0.595902	Csf2/Ifna4/
GO_BP_m2	GO:004390	regulation	9/470	399/23843	0.388263	0.636491	0.595902	Chmp3/Il1
GO_BP_m2	GO:000007	regulation	2/470	68/23843	0.388782	0.636491	0.595902	Cks1b/Lats
GO_BP_m2	GO:003023	myofibril a	2/470	68/23843	0.388782	0.636491	0.595902	Klhl41/Prka
GO_BP_m2	GO:004250	regulation	2/470	68/23843	0.388782	0.636491	0.595902	Csf2/Suz12
GO_BP_m2	GO:004584	negative re	2/470	68/23843	0.388782	0.636491	0.595902	Bmp4/Tll2
GO_BP_m2	GO:004864	regulation	2/470	68/23843	0.388782	0.636491	0.595902	Klhl41/Tll2
GO_BP_m2	GO:014005	organelle l	2/470	68/23843	0.388782	0.636491	0.595902	Ralb/Stxbp
GO_BP_m2	GO:002240	molting cy	3/470	114/23843	0.390712	0.636491	0.595902	Dkk4/Farp
GO_BP_m2	GO:002240	hair cycle p	3/470	114/23843	0.390712	0.636491	0.595902	Dkk4/Farp
GO_BP_m2	GO:003157	DNA integ	3/470	114/23843	0.390712	0.636491	0.595902	Cdc5l/Cry1
GO_BP_m2	GO:005164	vesicle loca	5/470	208/23843	0.39098	0.636491	0.595902	Bloc1s2/Cp
GO_BP_m2	GO:000030	response t	1/470	25/23843	0.392244	0.636491	0.595902	Ucp2
GO_BP_m2	GO:000046	cleavage in	1/470	25/23843	0.392244	0.636491	0.595902	Exosc2
GO_BP_m2	GO:000175	organ indu	1/470	25/23843	0.392244	0.636491	0.595902	Bmp4
GO_BP_m2	GO:000282	regulation	1/470	25/23843	0.392244	0.636491	0.595902	Il12rb1
GO_BP_m2	GO:000721	gamma-ar	1/470	25/23843	0.392244	0.636491	0.595902	Atf4
GO_BP_m2	GO:000728	spermatid	1/470	25/23843	0.392244	0.636491	0.595902	Kdm3a
GO_BP_m2	GO:001074	macrophag	1/470	25/23843	0.392244	0.636491	0.595902	Csf2
GO_BP_m2	GO:001086	positive reg	1/470	25/23843	0.392244	0.636491	0.595902	Sele
GO_BP_m2	GO:003051	positive reg	1/470	25/23843	0.392244	0.636491	0.595902	Tgfb1i1
GO_BP_m2	GO:003280	receptor ca	1/470	25/23843	0.392244	0.636491	0.595902	Mtmr2
GO_BP_m2	GO:003287	regulation	1/470	25/23843	0.392244	0.636491	0.595902	Ptk2b
GO_BP_m2	GO:003634	post-anal t	1/470	25/23843	0.392244	0.636491	0.595902	Sfrp2
GO_BP_m2	GO:004210	positive reg	1/470	25/23843	0.392244	0.636491	0.595902	Il12rb1
GO_BP_m2	GO:004564	positive reg	1/470	25/23843	0.392244	0.636491	0.595902	Id2
GO_BP_m2	GO:004636	monosacch	1/470	25/23843	0.392244	0.636491	0.595902	Pfkfb2
GO_BP_m2	GO:004864	negative re	1/470	25/23843	0.392244	0.636491	0.595902	Tll2
GO_BP_m2	GO:005090	leukocyte t	1/470	25/23843	0.392244	0.636491	0.595902	Sele
GO_BP_m2	GO:006076	regulation	1/470	25/23843	0.392244	0.636491	0.595902	Rnf6
GO_BP_m2	GO:006109	negative re	1/470	25/23843	0.392244	0.636491	0.595902	Tsg101
GO_BP_m2	GO:006121	positive reg	1/470	25/23843	0.392244	0.636491	0.595902	Bmp4
GO_BP_m2	GO:007142	hematopoi	1/470	25/23843	0.392244	0.636491	0.595902	Sfrp2
GO_BP_m2	GO:009014	regulation	1/470	25/23843	0.392244	0.636491	0.595902	Pink1
GO_BP_m2	GO:009962	cardiac mu	1/470	25/23843	0.392244	0.636491	0.595902	Kcnh2
GO_BP_m2	GO:190118	negative re	1/470	25/23843	0.392244	0.636491	0.595902	Tsg101
GO_BP_m2	GO:190384	positive reg	1/470	25/23843	0.392244	0.636491	0.595902	Tgfb1i1
GO_BP_m2	GO:190403	negative re	1/470	25/23843	0.392244	0.636491	0.595902	Lats2
GO_BP_m2	GO:190437	negative re	1/470	25/23843	0.392244	0.636491	0.595902	Csk
GO_BP_m2	GO:200005	regulation	1/470	25/23843	0.392244	0.636491	0.595902	Sfrp2
GO_BP_m2	GO:003240	regulation	6/470	256/23843	0.39227	0.636491	0.595902	Agrn/Bmp
GO_BP_m2	GO:007259	reactive ox	6/470	256/23843	0.39227	0.636491	0.595902	Cyb5r4/Cy
GO_BP_m2	GO:004211	B cell activ	9/470	401/23843	0.393863	0.638829	0.598091	Id2/Ifna4/I
GO_BP_m2	GO:003287	regulation	5/470	209/23843	0.394881	0.639985	0.599173	Gdf6/Nbr1
GO_BP_m2	GO:009769	STAT casca	5/470	209/23843	0.394881	0.639985	0.599173	Csf2/Ifna4/
GO_BP_m2	GO:000609	gluconeog	2/470	69/23843	0.395754	0.640658	0.599803	Atf4/Cry1

GO_BP_m2	GO:005115	positive reg	2/470	69/23843	0.395754	0.640658	0.599803	Bmp4/Cd5
GO_BP_m2	GO:006117	regulation	2/470	69/23843	0.395754	0.640658	0.599803	Oxct1/Ucp
GO_BP_m2	GO:001402	primary ne	3/470	115/23843	0.396032	0.64086	0.599993	Bmp4/Ift12
GO_BP_m2	GO:001982	stem cell p	4/470	162/23843	0.396565	0.641475	0.600568	Elavl1/Kdm
GO_BP_m2	GO:007030	regulation	5/470	210/23843	0.39878	0.642006	0.601065	Gdf6/Nbr1
GO_BP_m2	GO:001969	ribose pho	10/470	452/23843	0.400462	0.642006	0.601065	Adsl/Cad/F
GO_BP_m2	GO:190054	regulation	4/470	163/23843	0.401012	0.642006	0.601065	Rack1/Pde4
GO_BP_m2	GO:001056	regulation	3/470	116/23843	0.40134	0.642006	0.601065	Acsl4/Erfe/
GO_BP_m2	GO:006201	regulation	9/470	404/23843	0.402268	0.642006	0.601065	Acsl4/Erfe/
GO_BP_m2	GO:003227	regulation	5/470	211/23843	0.402677	0.642006	0.601065	Dyrk1a/Ptk
GO_BP_m2	GO:190332	regulation	5/470	211/23843	0.402677	0.642006	0.601065	Cry1/Derl1
GO_BP_m2	GO:190353	negative re	5/470	211/23843	0.402677	0.642006	0.601065	Cry1/Grm7
GO_BP_m2	GO:000749	endoderm	2/470	70/23843	0.40269	0.642006	0.601065	Angpt4/Bm
GO_BP_m2	GO:002153	diencephal	2/470	70/23843	0.40269	0.642006	0.601065	Bmp4/Six3
GO_BP_m2	GO:004211	macrophag	2/470	70/23843	0.40269	0.642006	0.601065	Csf2/Jmjd6
GO_BP_m2	GO:004863	negative re	2/470	70/23843	0.40269	0.642006	0.601065	Bmp4/Tll2
GO_BP_m2	GO:009030	mitotic spir	2/470	70/23843	0.40269	0.642006	0.601065	Aurkb/Rab
GO_BP_m2	GO:200010	negative re	2/470	70/23843	0.40269	0.642006	0.601065	Aurkb/Bmp
GO_BP_m2	GO:003021	T cell differ	6/470	259/23843	0.402802	0.642006	0.601065	Bmp4/Chd
GO_BP_m2	GO:000673	NADH met	1/470	26/23843	0.404237	0.642006	0.601065	Gpd1l
GO_BP_m2	GO:000700	inner mitoc	1/470	26/23843	0.404237	0.642006	0.601065	Pink1
GO_BP_m2	GO:000906	glutamine	1/470	26/23843	0.404237	0.642006	0.601065	Oat
GO_BP_m2	GO:001016	response t	1/470	26/23843	0.404237	0.642006	0.601065	Sfrp2
GO_BP_m2	GO:001082	negative re	1/470	26/23843	0.404237	0.642006	0.601065	Upk3b
GO_BP_m2	GO:001618	snRNA pro	1/470	26/23843	0.404237	0.642006	0.601065	Exosc2
GO_BP_m2	GO:002151	spinal cord	1/470	26/23843	0.404237	0.642006	0.601065	Ift122
GO_BP_m2	GO:002201	myelinatior	1/470	26/23843	0.404237	0.642006	0.601065	Adgrg6
GO_BP_m2	GO:003106	regulation	1/470	26/23843	0.404237	0.642006	0.601065	Pink1
GO_BP_m2	GO:003136	N-terminal	1/470	26/23843	0.404237	0.642006	0.601065	Metap2
GO_BP_m2	GO:003229	peripheral	1/470	26/23843	0.404237	0.642006	0.601065	Adgrg6
GO_BP_m2	GO:003250	DNA duple	1/470	26/23843	0.404237	0.642006	0.601065	Recql
GO_BP_m2	GO:003323	regulation	1/470	26/23843	0.404237	0.642006	0.601065	Tollip
GO_BP_m2	GO:004275	positive reg	1/470	26/23843	0.404237	0.642006	0.601065	Thrap3
GO_BP_m2	GO:004309	amino acid	1/470	26/23843	0.404237	0.642006	0.601065	Slc25a38
GO_BP_m2	GO:004345	regulation	1/470	26/23843	0.404237	0.642006	0.601065	Pink1
GO_BP_m2	GO:004511	azole trans	1/470	26/23843	0.404237	0.642006	0.601065	Csf2
GO_BP_m2	GO:004582	negative re	1/470	26/23843	0.404237	0.642006	0.601065	Pde4d
GO_BP_m2	GO:004595	positive reg	1/470	26/23843	0.404237	0.642006	0.601065	Stxbp1
GO_BP_m2	GO:005195	positive reg	1/470	26/23843	0.404237	0.642006	0.601065	Stxbp1
GO_BP_m2	GO:006003	pharyngea	1/470	26/23843	0.404237	0.642006	0.601065	Bmp4
GO_BP_m2	GO:006021	camera-typ	1/470	26/23843	0.404237	0.642006	0.601065	Rom1
GO_BP_m2	GO:006091	heart form	1/470	26/23843	0.404237	0.642006	0.601065	Bmp4
GO_BP_m2	GO:006103	negative re	1/470	26/23843	0.404237	0.642006	0.601065	Bmp4
GO_BP_m2	GO:006131	cell surface	1/470	26/23843	0.404237	0.642006	0.601065	Bmp4
GO_BP_m2	GO:007148	cellular res	1/470	26/23843	0.404237	0.642006	0.601065	H2afx
GO_BP_m2	GO:007154	cellular res	1/470	26/23843	0.404237	0.642006	0.601065	Bmp4
GO_BP_m2	GO:009007	foam cell d	1/470	26/23843	0.404237	0.642006	0.601065	Csf2
GO_BP_m2	GO:009018	regulation	1/470	26/23843	0.404237	0.642006	0.601065	Bmp4

GO_BP_m2	GO:190107	glucosami	1/470	26/23843	0.404237	0.642006	0.601065	Chst5
GO_BP_m2	GO:190275	positive re	1/470	26/23843	0.404237	0.642006	0.601065	Rab11a
GO_BP_m2	GO:190435	regulation	1/470	26/23843	0.404237	0.642006	0.601065	Aurkb
GO_BP_m2	GO:200077	positive re	1/470	26/23843	0.404237	0.642006	0.601065	Mavs
GO_BP_m2	GO:000269	negative re	4/470	164/23843	0.405452	0.643692	0.602644	Bmp4/Id2/
GO_BP_m2	GO:000300	heart morp	6/470	260/23843	0.40631	0.644566	0.603462	Adgrg6/B
GO_BP_m2	GO:007600	sensory pe	6/470	260/23843	0.40631	0.644566	0.603462	Chd7/Col2
GO_BP_m2	GO:004671	acid secret	3/470	117/23843	0.406634	0.644836	0.603714	Acsl4/Grm
GO_BP_m2	GO:001087	lipid localiz	8/470	357/23843	0.40691	0.645029	0.603896	Acat2/Acsl
GO_BP_m2	GO:004232	negative re	10/470	455/23843	0.408405	0.647155	0.605886	Bmp4/Csk/
GO_BP_m2	GO:000726	tyrosine ph	2/470	71/23843	0.409588	0.647547	0.606253	Csf2/Suz12
GO_BP_m2	GO:003227	negative re	2/470	71/23843	0.409588	0.647547	0.606253	Dyrk1a/Tw
GO_BP_m2	GO:003254	mitochond	2/470	71/23843	0.409588	0.647547	0.606253	2810006K2
GO_BP_m2	GO:190186	negative re	2/470	71/23843	0.409588	0.647547	0.606253	Bmp4/Tll2
GO_BP_m2	GO:190336	negative re	2/470	71/23843	0.409588	0.647547	0.606253	Alad/Ube2
GO_BP_m2	GO:000679	sulfur com	6/470	261/23843	0.409817	0.647547	0.606253	Acaca/Chs
GO_BP_m2	GO:001097	negative re	4/470	165/23843	0.409887	0.647547	0.606253	Cit/Prkcsh/
GO_BP_m2	GO:006113	regulation	4/470	165/23843	0.409887	0.647547	0.606253	Alad/Rack1
GO_BP_m2	GO:004354	positive re	5/470	213/23843	0.410461	0.648149	0.606817	Agrn/Ect2/
GO_BP_m2	GO:000193	regulation	3/470	118/23843	0.411914	0.648149	0.606817	Bmp4/Pdc
GO_BP_m2	GO:000709	centrosom	3/470	118/23843	0.411914	0.648149	0.606817	Cep120/Ch
GO_BP_m2	GO:000858	male gona	3/470	118/23843	0.411914	0.648149	0.606817	H3f3b/Sfrp
GO_BP_m2	GO:190303	negative re	3/470	118/23843	0.411914	0.648149	0.606817	Bmp4/Prka
GO_BP_m2	GO:004390	positive re	4/470	166/23843	0.414315	0.648149	0.606817	Chmp3/Pla
GO_BP_m2	GO:009872	maintenan	4/470	166/23843	0.414315	0.648149	0.606817	Elavl1/Kdm
GO_BP_m2	GO:000206	glandular	1/470	27/23843	0.415994	0.648149	0.606817	Bmp4
GO_BP_m2	GO:000314	outflow tra	1/470	27/23843	0.415994	0.648149	0.606817	Bmp4
GO_BP_m2	GO:000333	metanephr	1/470	27/23843	0.415994	0.648149	0.606817	Bmp4
GO_BP_m2	GO:000709	nuclear mi	1/470	27/23843	0.415994	0.648149	0.606817	Cep120
GO_BP_m2	GO:000907	aromatic a	1/470	27/23843	0.415994	0.648149	0.606817	Pcbd1
GO_BP_m2	GO:002153	cell differe	1/470	27/23843	0.415994	0.648149	0.606817	Faim2
GO_BP_m2	GO:003082	regulation	1/470	27/23843	0.415994	0.648149	0.606817	Ptk2b
GO_BP_m2	GO:003163	plasminog	1/470	27/23843	0.415994	0.648149	0.606817	Plau
GO_BP_m2	GO:003264	regulation	1/470	27/23843	0.415994	0.648149	0.606817	Mavs
GO_BP_m2	GO:003281	positive re	1/470	27/23843	0.415994	0.648149	0.606817	Zbtb1
GO_BP_m2	GO:003420	amyloid-b	1/470	27/23843	0.415994	0.648149	0.606817	Dyrk1a
GO_BP_m2	GO:004478	modulatio	1/470	27/23843	0.415994	0.648149	0.606817	Ppib
GO_BP_m2	GO:004874	smooth mu	1/470	27/23843	0.415994	0.648149	0.606817	Bmp4
GO_BP_m2	GO:005112	RNA polym	1/470	27/23843	0.415994	0.648149	0.606817	Psmc5
GO_BP_m2	GO:006014	positive re	1/470	27/23843	0.415994	0.648149	0.606817	Cd53
GO_BP_m2	GO:006026	regulation	1/470	27/23843	0.415994	0.648149	0.606817	Psmc5
GO_BP_m2	GO:006034	trabecula f	1/470	27/23843	0.415994	0.648149	0.606817	Adgrg6
GO_BP_m2	GO:006071	labyrinthin	1/470	27/23843	0.415994	0.648149	0.606817	Erf
GO_BP_m2	GO:007023	negative re	1/470	27/23843	0.415994	0.648149	0.606817	Bmp4
GO_BP_m2	GO:007136	cellular res	1/470	27/23843	0.415994	0.648149	0.606817	Mir339
GO_BP_m2	GO:009020	positive re	1/470	27/23843	0.415994	0.648149	0.606817	Pink1
GO_BP_m2	GO:009734	mitochond	1/470	27/23843	0.415994	0.648149	0.606817	Bloc1s2
GO_BP_m2	GO:009907	regulation	1/470	27/23843	0.415994	0.648149	0.606817	Rab11a

GO_BP_m2	GO:190289	positive reg	1/470	27/23843	0.415994	0.648149	0.606817	Bmp4
GO_BP_m2	GO:190348	positive reg	1/470	27/23843	0.415994	0.648149	0.606817	Prl8a2
GO_BP_m2	GO:200030	regulation	1/470	27/23843	0.415994	0.648149	0.606817	Stxbp1
GO_BP_m2	GO:000208	lens develo	2/470	72/23843	0.416447	0.648149	0.606817	Bmp4/Six3
GO_BP_m2	GO:000854	fibroblast g	2/470	72/23843	0.416447	0.648149	0.606817	Fgfbp3/Sul
GO_BP_m2	GO:001931	hexose bio	2/470	72/23843	0.416447	0.648149	0.606817	Atf4/Cry1
GO_BP_m2	GO:004214	retrograde	2/470	72/23843	0.416447	0.648149	0.606817	Dennd2a/V
GO_BP_m2	GO:004427	sulfur comp	2/470	72/23843	0.416447	0.648149	0.606817	Chst12/Chs
GO_BP_m2	GO:005068	regulation	2/470	72/23843	0.416447	0.648149	0.606817	Il12rb1/Ma
GO_BP_m2	GO:005170	multi-orga	2/470	72/23843	0.416447	0.648149	0.606817	Aplp2/Pen
GO_BP_m2	GO:004654	developme	3/470	119/23843	0.417179	0.648568	0.607209	H3f3b/Sfrp
GO_BP_m2	GO:004682	regulation	3/470	119/23843	0.417179	0.648568	0.607209	Bmp4/Ect2
GO_BP_m2	GO:006138	regulation	3/470	119/23843	0.417179	0.648568	0.607209	Rab11a/Rn
GO_BP_m2	GO:000910	coenzyme	4/470	168/23843	0.423148	0.652537	0.610925	Coq8b/Coq
GO_BP_m2	GO:000334	cilium mov	2/470	73/23843	0.423265	0.652537	0.610925	Cfap46/Ro
GO_BP_m2	GO:001083	telomere m	2/470	73/23843	0.423265	0.652537	0.610925	Aurkb/Hnr
GO_BP_m2	GO:002240	membrane	2/470	73/23843	0.423265	0.652537	0.610925	Ralb/Stxbp
GO_BP_m2	GO:003081	regulation	2/470	73/23843	0.423265	0.652537	0.610925	Rack1/Pde4
GO_BP_m2	GO:004632	regulation	2/470	73/23843	0.423265	0.652537	0.610925	Aspscr1/Up
GO_BP_m2	GO:190137	regulation	2/470	73/23843	0.423265	0.652537	0.610925	Agrn/Kcnh
GO_BP_m2	GO:190402	regulation	2/470	73/23843	0.423265	0.652537	0.610925	Cks1b/Lats
GO_BP_m2	GO:000740	axonogene	10/470	461/23843	0.424296	0.652537	0.610925	Agrn/Auts2
GO_BP_m2	GO:002195	central ner	5/470	217/23843	0.425984	0.652537	0.610925	Faim2/Gba
GO_BP_m2	GO:000030	response to	1/470	28/23843	0.427519	0.652537	0.610925	Ucp2
GO_BP_m2	GO:000073	DNA synth	1/470	28/23843	0.427519	0.652537	0.610925	Zbtb1
GO_BP_m2	GO:000621	pyrimidine	1/470	28/23843	0.427519	0.652537	0.610925	Cad
GO_BP_m2	GO:000633	DNA replic	1/470	28/23843	0.427519	0.652537	0.610925	Asf1a
GO_BP_m2	GO:000637	mRNA clea	1/470	28/23843	0.427519	0.652537	0.610925	Ncbp2
GO_BP_m2	GO:000676	folic acid-c	1/470	28/23843	0.427519	0.652537	0.610925	Pm20d2
GO_BP_m2	GO:000930	rRNA trans	1/470	28/23843	0.427519	0.652537	0.610925	Sirt7
GO_BP_m2	GO:001045	exit from m	1/470	28/23843	0.427519	0.652537	0.610925	Sirt7
GO_BP_m2	GO:001071	negative re	1/470	28/23843	0.427519	0.652537	0.610925	Sfrp2
GO_BP_m2	GO:001075	regulation	1/470	28/23843	0.427519	0.652537	0.610925	Ptk2b
GO_BP_m2	GO:001599	ATP hydrol	1/470	28/23843	0.427519	0.652537	0.610925	Atp6v1h
GO_BP_m2	GO:001624	negative re	1/470	28/23843	0.427519	0.652537	0.610925	Pink1
GO_BP_m2	GO:002151	spinal cord	1/470	28/23843	0.427519	0.652537	0.610925	Ift122
GO_BP_m2	GO:002169	cerebellar	1/470	28/23843	0.427519	0.652537	0.610925	Faim2
GO_BP_m2	GO:003260	interferon-	1/470	28/23843	0.427519	0.652537	0.610925	Mavs
GO_BP_m2	GO:003315	regulation	1/470	28/23843	0.427519	0.652537	0.610925	Mavs
GO_BP_m2	GO:004355	positive reg	1/470	28/23843	0.427519	0.652537	0.610925	Ptk2b
GO_BP_m2	GO:004567	negative re	1/470	28/23843	0.427519	0.652537	0.610925	Mafb
GO_BP_m2	GO:004685	phosphatic	1/470	28/23843	0.427519	0.652537	0.610925	Fam126a
GO_BP_m2	GO:004859	embryonic	1/470	28/23843	0.427519	0.652537	0.610925	Six3
GO_BP_m2	GO:004882	hair follicle	1/470	28/23843	0.427519	0.652537	0.610925	Nsun2
GO_BP_m2	GO:005065	chondroitin	1/470	28/23843	0.427519	0.652537	0.610925	Chst12
GO_BP_m2	GO:006121	regulation	1/470	28/23843	0.427519	0.652537	0.610925	Bmp4
GO_BP_m2	GO:006129	retina vasc	1/470	28/23843	0.427519	0.652537	0.610925	Rom1
GO_BP_m2	GO:007135	cellular res	1/470	28/23843	0.427519	0.652537	0.610925	Alad

GO_BP_m2	GO:007239	signal trans	1/470	28/23843	0.427519	0.652537	0.610925	Cdc5l
GO_BP_m2	GO:007240	signal trans	1/470	28/23843	0.427519	0.652537	0.610925	Cdc5l
GO_BP_m2	GO:007242	signal trans	1/470	28/23843	0.427519	0.652537	0.610925	Cdc5l
GO_BP_m2	GO:007259	establishm	1/470	28/23843	0.427519	0.652537	0.610925	Sec63
GO_BP_m2	GO:009066	ATP hydrol	1/470	28/23843	0.427519	0.652537	0.610925	Atp6v1h
GO_BP_m2	GO:009913	ATP hydrol	1/470	28/23843	0.427519	0.652537	0.610925	Atp6v1h
GO_BP_m2	GO:009913	ATP hydrol	1/470	28/23843	0.427519	0.652537	0.610925	Atp6v1h
GO_BP_m2	GO:190027	regulation	1/470	28/23843	0.427519	0.652537	0.610925	Sele
GO_BP_m2	GO:190217	regulation	1/470	28/23843	0.427519	0.652537	0.610925	Pink1
GO_BP_m2	GO:190280	regulation	1/470	28/23843	0.427519	0.652537	0.610925	Stxbp1
GO_BP_m2	GO:200027	negative re	1/470	28/23843	0.427519	0.652537	0.610925	Tsg101
GO_BP_m2	GO:200027	positive reg	1/470	28/23843	0.427519	0.652537	0.610925	Pink1
GO_BP_m2	GO:000189	placenta de	4/470	169/23843	0.427553	0.652537	0.610925	Cebpa/Csf2
GO_BP_m2	GO:000072	telomere m	3/470	121/23843	0.427664	0.652537	0.610925	Aurkb/Hnr
GO_BP_m2	GO:001810	peptidyl-th	3/470	121/23843	0.427664	0.652537	0.610925	Cad/Clk1/D
GO_BP_m2	GO:190165	glycosyl co	3/470	121/23843	0.427664	0.652537	0.610925	Cad/Gba2/
GO_BP_m2	GO:004856	embryonic	7/470	315/23843	0.427819	0.652537	0.610925	Bmp4/Chd
GO_BP_m2	GO:003320	tumor necr	2/470	74/23843	0.430042	0.655689	0.613876	Ptk2b/Txnc
GO_BP_m2	GO:005105	regulation	6/470	267/23843	0.430809	0.65662	0.614747	Arap3/Auts
GO_BP_m2	GO:000614	regulation	4/470	170/23843	0.431949	0.657834	0.615884	Rack1/Pde
GO_BP_m2	GO:003004	actin filame	4/470	170/23843	0.431949	0.657834	0.615884	Ptk2b/Rac2
GO_BP_m2	GO:003192	TOR signal	3/470	122/23843	0.432881	0.657834	0.615884	Gatsl2/Itfg2
GO_BP_m2	GO:190332	positive reg	3/470	122/23843	0.432881	0.657834	0.615884	Derl1/Rnf2
GO_BP_m2	GO:003629	response to	5/470	219/23843	0.433717	0.657834	0.615884	Cybb/Pink1
GO_BP_m2	GO:000803	cell recogn	6/470	268/23843	0.434297	0.657834	0.615884	Ighv1-23/I
GO_BP_m2	GO:005125	protein pol	6/470	268/23843	0.434297	0.657834	0.615884	Chmp3/Dy
GO_BP_m2	GO:007122	cellular res	6/470	268/23843	0.434297	0.657834	0.615884	Acaca/Mir3
GO_BP_m2	GO:000028	nuclear div	9/470	416/23843	0.435886	0.657834	0.615884	Aurkb/Bmp
GO_BP_m2	GO:001619	endosomal	4/470	171/23843	0.436335	0.657834	0.615884	Chmp3/De
GO_BP_m2	GO:003314	regulation	2/470	75/23843	0.436777	0.657834	0.615884	Cry1/Rnf6
GO_BP_m2	GO:004568	regulation	2/470	75/23843	0.436777	0.657834	0.615884	Bmp4/Dkk
GO_BP_m2	GO:005067	regulation	5/470	220/23843	0.437575	0.657834	0.615884	Bmp4/Il12r
GO_BP_m2	GO:000182	kidney dev	6/470	269/23843	0.437782	0.657834	0.615884	Bmp4/Id2/
GO_BP_m2	GO:190303	regulation	6/470	269/23843	0.437782	0.657834	0.615884	Bmp4/Il12r
GO_BP_m2	GO:004599	regulation	3/470	123/23843	0.438081	0.657834	0.615884	Bmp4/Lfng
GO_BP_m2	GO:004856	digestive tr	3/470	123/23843	0.438081	0.657834	0.615884	Bmp4/Id2/
GO_BP_m2	GO:190018	regulation	3/470	123/23843	0.438081	0.657834	0.615884	Bmp4/Ect2
GO_BP_m2	GO:190465	glucose tra	3/470	123/23843	0.438081	0.657834	0.615884	Aspscr1/Nr
GO_BP_m2	GO:000155	oocyte mat	1/470	29/23843	0.438817	0.657834	0.615884	Ptk2b
GO_BP_m2	GO:000191	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Vamp3
GO_BP_m2	GO:000209	positive reg	1/470	29/23843	0.438817	0.657834	0.615884	Sele
GO_BP_m2	GO:000330	type B pan	1/470	29/23843	0.438817	0.657834	0.615884	Bmp4
GO_BP_m2	GO:000609	tricarboxyli	1/470	29/23843	0.438817	0.657834	0.615884	Aco1
GO_BP_m2	GO:000922	nucleotide-	1/470	29/23843	0.438817	0.657834	0.615884	Mgat1
GO_BP_m2	GO:001039	histone mo	1/470	29/23843	0.438817	0.657834	0.615884	Rnf20
GO_BP_m2	GO:001404	Schwann ce	1/470	29/23843	0.438817	0.657834	0.615884	Adgrg6
GO_BP_m2	GO:003094	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Bmp4
GO_BP_m2	GO:003278	positive reg	1/470	29/23843	0.438817	0.657834	0.615884	Ell

GO_BP_m2	GO:003295	inositol ph	1/470	29/23843	0.438817	0.657834	0.615884	Ptk2b
GO_BP_m2	GO:003326	nuclear D	1/470	29/23843	0.438817	0.657834	0.615884	Wdr18
GO_BP_m2	GO:003472	DNA replic	1/470	29/23843	0.438817	0.657834	0.615884	Asf1a
GO_BP_m2	GO:003506	positive re	1/470	29/23843	0.438817	0.657834	0.615884	Auts2
GO_BP_m2	GO:004311	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Fgfbp3
GO_BP_m2	GO:004330	positive re	1/470	29/23843	0.438817	0.657834	0.615884	Stxbp1
GO_BP_m2	GO:004518	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Csf2
GO_BP_m2	GO:006030	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Kcnh2
GO_BP_m2	GO:006057	morphoge	1/470	29/23843	0.438817	0.657834	0.615884	Bmp4
GO_BP_m2	GO:006175	leukocyte	1/470	29/23843	0.438817	0.657834	0.615884	Sele
GO_BP_m2	GO:007030	lens fiber c	1/470	29/23843	0.438817	0.657834	0.615884	Six3
GO_BP_m2	GO:007154	response t	1/470	29/23843	0.438817	0.657834	0.615884	Bmp4
GO_BP_m2	GO:007252	pyrimidine	1/470	29/23843	0.438817	0.657834	0.615884	Cad
GO_BP_m2	GO:009002	positive re	1/470	29/23843	0.438817	0.657834	0.615884	Rac2
GO_BP_m2	GO:190348	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Prl8a2
GO_BP_m2	GO:190403	positive re	1/470	29/23843	0.438817	0.657834	0.615884	Bmp4
GO_BP_m2	GO:200101	regulation	1/470	29/23843	0.438817	0.657834	0.615884	Klhl41
GO_BP_m2	GO:007135	cellular res	4/470	172/23843	0.440713	0.660439	0.618323	Cebpa/Mir
GO_BP_m2	GO:007048	response t	6/470	270/23843	0.441263	0.661027	0.618874	Cybb/Mir1
GO_BP_m2	GO:000646	negative re	5/470	221/23843	0.441428	0.661039	0.618885	Bmp4/Lats
GO_BP_m2	GO:000703	vacuolar tr	3/470	124/23843	0.443262	0.661968	0.619754	Chmp3/Pir
GO_BP_m2	GO:007133	cellular res	3/470	124/23843	0.443262	0.661968	0.619754	Rack1/Oxc
GO_BP_m2	GO:009755	calcium ior	3/470	124/23843	0.443262	0.661968	0.619754	Chd7/Pde4
GO_BP_m2	GO:000175	somitogen	2/470	76/23843	0.443468	0.661968	0.619754	Lfng/Sfrp2
GO_BP_m2	GO:000649	protein O-	2/470	76/23843	0.443468	0.661968	0.619754	Galnt2/Lfn
GO_BP_m2	GO:000667	ceramide n	2/470	76/23843	0.443468	0.661968	0.619754	Gba2/Sgpl
GO_BP_m2	GO:000683	dicarboxyli	2/470	76/23843	0.443468	0.661968	0.619754	Grm7/Stxb
GO_BP_m2	GO:004352	positive re	2/470	76/23843	0.443468	0.661968	0.619754	Agrn/Atf4
GO_BP_m2	GO:190395	positive re	2/470	76/23843	0.443468	0.661968	0.619754	Pink1/Rac2
GO_BP_m2	GO:006135	neural pre	4/470	173/23843	0.44508	0.662695	0.620435	Cep120/Id
GO_BP_m2	GO:003294	regulation	5/470	222/23843	0.445274	0.662695	0.620435	Bmp4/Il12r
GO_BP_m2	GO:190336	regulation	5/470	222/23843	0.445274	0.662695	0.620435	Alad/Rack1
GO_BP_m2	GO:001603	viral proce	6/470	272/23843	0.448211	0.662695	0.620435	Chmp3/Ma
GO_BP_m2	GO:000758	digestion	3/470	125/23843	0.448425	0.662695	0.620435	Acat2/Aco
GO_BP_m2	GO:000864	hexose tra	3/470	125/23843	0.448425	0.662695	0.620435	Aspscr1/N
GO_BP_m2	GO:003227	positive re	3/470	125/23843	0.448425	0.662695	0.620435	Ptk2b/Rac
GO_BP_m2	GO:003476	negative re	3/470	125/23843	0.448425	0.662695	0.620435	Agrn/Kcnh
GO_BP_m2	GO:000176	neuron mi	4/470	174/23843	0.449437	0.662695	0.620435	Auts2/Lmx
GO_BP_m2	GO:004576	positive re	4/470	174/23843	0.449437	0.662695	0.620435	Angpt4/Cy
GO_BP_m2	GO:000153	cilium or fl	1/470	30/23843	0.449893	0.662695	0.620435	Cfap46
GO_BP_m2	GO:000290	regulation	1/470	30/23843	0.449893	0.662695	0.620435	Aurkb
GO_BP_m2	GO:000622	pyrimidine	1/470	30/23843	0.449893	0.662695	0.620435	Cad
GO_BP_m2	GO:001066	negative re	1/470	30/23843	0.449893	0.662695	0.620435	Sfrp2
GO_BP_m2	GO:002160	cranial ner	1/470	30/23843	0.449893	0.662695	0.620435	Mafb
GO_BP_m2	GO:003259	protein tra	1/470	30/23843	0.449893	0.662695	0.620435	Rab11a
GO_BP_m2	GO:003296	positive re	1/470	30/23843	0.449893	0.662695	0.620435	Bmp4
GO_BP_m2	GO:003414	toll-like re	1/470	30/23843	0.449893	0.662695	0.620435	S100a14
GO_BP_m2	GO:003532	hippo sign	1/470	30/23843	0.449893	0.662695	0.620435	Lats2

GO_BP_m2	GO:003564	exploratior	1/470	30/23843	0.449893	0.662695	0.620435	Penk
GO_BP_m2	GO:004248	regulation	1/470	30/23843	0.449893	0.662695	0.620435	Bmp4
GO_BP_m2	GO:004255	superoxide	1/470	30/23843	0.449893	0.662695	0.620435	Cybb
GO_BP_m2	GO:004431	wound hea	1/470	30/23843	0.449893	0.662695	0.620435	Pdcd10
GO_BP_m2	GO:004566	negative re	1/470	30/23843	0.449893	0.662695	0.620435	Bmp4
GO_BP_m2	GO:004603	GTP metab	1/470	30/23843	0.449893	0.662695	0.620435	Ran
GO_BP_m2	GO:005080	circadian sl	1/470	30/23843	0.449893	0.662695	0.620435	Csf2
GO_BP_m2	GO:005156	regulation	1/470	30/23843	0.449893	0.662695	0.620435	Auts2
GO_BP_m2	GO:005507	potassium	1/470	30/23843	0.449893	0.662695	0.620435	Kcnh2
GO_BP_m2	GO:006028	cilium-dep	1/470	30/23843	0.449893	0.662695	0.620435	Cfap46
GO_BP_m2	GO:007067	response t	1/470	30/23843	0.449893	0.662695	0.620435	Alad
GO_BP_m2	GO:009050	epiboly inv	1/470	30/23843	0.449893	0.662695	0.620435	Pdcd10
GO_BP_m2	GO:190211	positive reg	1/470	30/23843	0.449893	0.662695	0.620435	Bloc1s2
GO_BP_m2	GO:190552	regulation	1/470	30/23843	0.449893	0.662695	0.620435	Ptk2b
GO_BP_m2	GO:000911	ribonucleo	2/470	77/23843	0.450115	0.662695	0.620435	Cad/Ran
GO_BP_m2	GO:003310	mitochond	2/470	77/23843	0.450115	0.662695	0.620435	Ndufaf8/Sc
GO_BP_m2	GO:003577	insulin secr	2/470	77/23843	0.450115	0.662695	0.620435	Oxct1/Ucp
GO_BP_m2	GO:004227	ribosomal	2/470	77/23843	0.450115	0.662695	0.620435	Pwp2/Utp1
GO_BP_m2	GO:005145	regulation	2/470	77/23843	0.450115	0.662695	0.620435	Atp6v1h/G
GO_BP_m2	GO:006097	coronary v	2/470	77/23843	0.450115	0.662695	0.620435	Ap2b1/Bm
GO_BP_m2	GO:001922	cytokine-m	8/470	372/23843	0.451626	0.664532	0.622155	Cebpa/Ifna
GO_BP_m2	GO:005134	negative re	6/470	273/23843	0.451679	0.664532	0.622155	Bmp4/Csk/
GO_BP_m2	GO:007265	protein loc	10/470	472/23843	0.453373	0.666377	0.623882	Agrn/Csk/F
GO_BP_m2	GO:003102	microtubul	3/470	126/23843	0.453569	0.666377	0.623882	Cep120/Ch
GO_BP_m2	GO:007133	cellular res	3/470	126/23843	0.453569	0.666377	0.623882	Rack1/Oxc
GO_BP_m2	GO:190165	cellular res	3/470	126/23843	0.453569	0.666377	0.623882	Acaca/Bmp
GO_BP_m2	GO:004516	cell fate co	6/470	274/23843	0.455142	0.668271	0.625655	Bmp4/Id2/
GO_BP_m2	GO:000663	acyl-CoA n	2/470	78/23843	0.456716	0.668271	0.625655	Acaca/Hmg
GO_BP_m2	GO:000694	regulation	2/470	78/23843	0.456716	0.668271	0.625655	Agrn/Pde4
GO_BP_m2	GO:001092	negative re	2/470	78/23843	0.456716	0.668271	0.625655	Elfn2/Ell
GO_BP_m2	GO:003538	thioester m	2/470	78/23843	0.456716	0.668271	0.625655	Acaca/Hmg
GO_BP_m2	GO:004636	monosacch	2/470	78/23843	0.456716	0.668271	0.625655	Atf4/Cry1
GO_BP_m2	GO:005130	establishm	2/470	78/23843	0.456716	0.668271	0.625655	Rab11a/Tra
GO_BP_m2	GO:007022	regulation	2/470	78/23843	0.456716	0.668271	0.625655	Aurkb/Bmp
GO_BP_m2	GO:190374	positive reg	2/470	78/23843	0.456716	0.668271	0.625655	Pink1/Rac2
GO_BP_m2	GO:005500	striated mu	4/470	176/23843	0.458117	0.668271	0.625655	Bmp4/Klhl4
GO_BP_m2	GO:001574	monosacch	3/470	127/23843	0.458692	0.668271	0.625655	Aspscr1/Nr
GO_BP_m2	GO:003502	regulation	3/470	127/23843	0.458692	0.668271	0.625655	Arap3/Ect2
GO_BP_m2	GO:007132	cellular res	3/470	127/23843	0.458692	0.668271	0.625655	Rack1/Oxc
GO_BP_m2	GO:000650	GPI anchor	1/470	31/23843	0.46075	0.668271	0.625655	Pigm
GO_BP_m2	GO:000860	attachment	1/470	31/23843	0.46075	0.668271	0.625655	Ect2
GO_BP_m2	GO:001071	positive reg	1/470	31/23843	0.46075	0.668271	0.625655	Bmp4
GO_BP_m2	GO:001598	energy cou	1/470	31/23843	0.46075	0.668271	0.625655	Atp6v1h
GO_BP_m2	GO:001827	protein N-	1/470	31/23843	0.46075	0.668271	0.625655	Ube2j1
GO_BP_m2	GO:003272	positive reg	1/470	31/23843	0.46075	0.668271	0.625655	Mavs
GO_BP_m2	GO:003308	regulation	1/470	31/23843	0.46075	0.668271	0.625655	Bmp4
GO_BP_m2	GO:003336	secretory g	1/470	31/23843	0.46075	0.668271	0.625655	Zpbp
GO_BP_m2	GO:004263	regulation	1/470	31/23843	0.46075	0.668271	0.625655	Dkk4

GO_BP_m2	GO:004274	regulation	1/470	31/23843	0.46075	0.668271	0.625655	Csf2
GO_BP_m2	GO:004362	ncRNA 3'-	1/470	31/23843	0.46075	0.668271	0.625655	Exosc2
GO_BP_m2	GO:004824	sperm cap	1/470	31/23843	0.46075	0.668271	0.625655	Ropn1l
GO_BP_m2	GO:00485	lymph nod	1/470	31/23843	0.46075	0.668271	0.625655	Id2
GO_BP_m2	GO:00509	regulation	1/470	31/23843	0.46075	0.668271	0.625655	Ptk2b
GO_BP_m2	GO:00511	vitamin tra	1/470	31/23843	0.46075	0.668271	0.625655	Slc52a3
GO_BP_m2	GO:00514	positive re	1/470	31/23843	0.46075	0.668271	0.625655	Agrn
GO_BP_m2	GO:007052	protein kin	1/470	31/23843	0.46075	0.668271	0.625655	Gpd1l
GO_BP_m2	GO:009007	relaxation	1/470	31/23843	0.46075	0.668271	0.625655	Pde4d
GO_BP_m2	GO:009021	positive re	1/470	31/23843	0.46075	0.668271	0.625655	Ptk2b
GO_BP_m2	GO:009032	regulation	1/470	31/23843	0.46075	0.668271	0.625655	Shc1
GO_BP_m2	GO:00905	epiboly	1/470	31/23843	0.46075	0.668271	0.625655	Pdcd10
GO_BP_m2	GO:190547	negative r	1/470	31/23843	0.46075	0.668271	0.625655	Csk
GO_BP_m2	GO:20004	positive re	1/470	31/23843	0.46075	0.668271	0.625655	Ptk2b
GO_BP_m2	GO:20007	positive re	1/470	31/23843	0.46075	0.668271	0.625655	Auts2
GO_BP_m2	GO:00508	positive re	7/470	326/23843	0.46294	0.670538	0.627778	Glul/Mir12
GO_BP_m2	GO:00032	cardiac ver	2/470	79/23843	0.463272	0.670538	0.627778	Chd7/Sfrp
GO_BP_m2	GO:00345	protein loc	2/470	79/23843	0.463272	0.670538	0.627778	Aurkb/Tra
GO_BP_m2	GO:00380	signal tran	2/470	79/23843	0.463272	0.670538	0.627778	Col2a1/Csf
GO_BP_m2	GO:00500	chromoso	2/470	79/23843	0.463272	0.670538	0.627778	Rab11a/Tr
GO_BP_m2	GO:00971	extrinsic a	2/470	79/23843	0.463272	0.670538	0.627778	Col2a1/Csf
GO_BP_m2	GO:004362	cellular pr	3/470	128/23843	0.463795	0.671064	0.62827	2810006K2
GO_BP_m2	GO:000184	neural tub	3/470	129/23843	0.468877	0.672093	0.629233	Bmp4/Ift12
GO_BP_m2	GO:004867	axon exten	3/470	129/23843	0.468877	0.672093	0.629233	Auts2/Rab
GO_BP_m2	GO:00975	granulocyt	3/470	129/23843	0.468877	0.672093	0.629233	Pde4d/Rac
GO_BP_m2	GO:00016	ameboidal	8/470	378/23843	0.469378	0.672093	0.629233	Angpt4/Bm
GO_BP_m2	GO:00031	outflow tra	2/470	80/23843	0.469781	0.672093	0.629233	Bmp4/Sfrp
GO_BP_m2	GO:00070	plasma me	2/470	80/23843	0.469781	0.672093	0.629233	Agrn/Syt11
GO_BP_m2	GO:001491	regulation	2/470	80/23843	0.469781	0.672093	0.629233	Foxo4/Pla
GO_BP_m2	GO:00171	regulation	2/470	80/23843	0.469781	0.672093	0.629233	Stxbp1/Syt
GO_BP_m2	GO:19001	positive re	2/470	80/23843	0.469781	0.672093	0.629233	Ect2/Mavs
GO_BP_m2	GO:00163	morphoge	4/470	179/23843	0.47105	0.672093	0.629233	Bmp4/Ift12
GO_BP_m2	GO:00313	regulation	4/470	179/23843	0.47105	0.672093	0.629233	Cry1/Derl1
GO_BP_m2	GO:009752	myeloid le	4/470	179/23843	0.47105	0.672093	0.629233	Pde4d/Ptk
GO_BP_m2	GO:00000	very long-	1/470	32/23843	0.471394	0.672093	0.629233	Slc27a2
GO_BP_m2	GO:000041	protein pe	1/470	32/23843	0.471394	0.672093	0.629233	Ppib
GO_BP_m2	GO:00060	acetyl-Co	1/470	32/23843	0.471394	0.672093	0.629233	Acaca
GO_BP_m2	GO:00063	regulation	1/470	32/23843	0.471394	0.672093	0.629233	Atf4
GO_BP_m2	GO:00065	GPI anchor	1/470	32/23843	0.471394	0.672093	0.629233	Pigm
GO_BP_m2	GO:00067	water-solu	1/470	32/23843	0.471394	0.672093	0.629233	Pm20d2
GO_BP_m2	GO:001004	response t	1/470	32/23843	0.471394	0.672093	0.629233	Alad
GO_BP_m2	GO:00170	cytochrom	1/470	32/23843	0.471394	0.672093	0.629233	Cox10
GO_BP_m2	GO:00181	peptidyl-a	1/470	32/23843	0.471394	0.672093	0.629233	Ube2j1
GO_BP_m2	GO:001937	epoxygena	1/470	32/23843	0.471394	0.672093	0.629233	Cyp2g1
GO_BP_m2	GO:00215	ventricular	1/470	32/23843	0.471394	0.672093	0.629233	Ak8
GO_BP_m2	GO:002241	circadian s	1/470	32/23843	0.471394	0.672093	0.629233	Csf2
GO_BP_m2	GO:003221	positive re	1/470	32/23843	0.471394	0.672093	0.629233	Aurkb
GO_BP_m2	GO:00335	mammary	1/470	32/23843	0.471394	0.672093	0.629233	Id2

GO_BP_m2	GO:003588	enteroendo	1/470	32/23843	0.471394	0.672093	0.629233	Bmp4
GO_BP_m2	GO:004481	mitotic G2/	1/470	32/23843	0.471394	0.672093	0.629233	Foxo4
GO_BP_m2	GO:004507	positive reg	1/470	32/23843	0.471394	0.672093	0.629233	Ppib
GO_BP_m2	GO:004557	regulation	1/470	32/23843	0.471394	0.672093	0.629233	Id2
GO_BP_m2	GO:004632	negative re	1/470	32/23843	0.471394	0.672093	0.629233	Sfrp2
GO_BP_m2	GO:004866	collateral s	1/470	32/23843	0.471394	0.672093	0.629233	Spg20
GO_BP_m2	GO:005086	negative re	1/470	32/23843	0.471394	0.672093	0.629233	Id2
GO_BP_m2	GO:005164	nucleus loc	1/470	32/23843	0.471394	0.672093	0.629233	Cep120
GO_BP_m2	GO:006014	regulation	1/470	32/23843	0.471394	0.672093	0.629233	Cd53
GO_BP_m2	GO:006035	cartilage de	1/470	32/23843	0.471394	0.672093	0.629233	Col2a1
GO_BP_m2	GO:006066	embryonic	1/470	32/23843	0.471394	0.672093	0.629233	Erf
GO_BP_m2	GO:007089	DNA-temp	1/470	32/23843	0.471394	0.672093	0.629233	Psmc5
GO_BP_m2	GO:008609	regulation	1/470	32/23843	0.471394	0.672093	0.629233	Kcnh2
GO_BP_m2	GO:190211	negative re	1/470	32/23843	0.471394	0.672093	0.629233	Pink1
GO_BP_m2	GO:190247	L-alpha-ar	1/470	32/23843	0.471394	0.672093	0.629233	Slc25a38
GO_BP_m2	GO:190268	mitochond	1/470	32/23843	0.471394	0.672093	0.629233	Bloc1s2
GO_BP_m2	GO:190520	positive reg	1/470	32/23843	0.471394	0.672093	0.629233	Bmp4
GO_BP_m2	GO:003267	regulation	3/470	130/23843	0.473937	0.674802	0.63177	Csk/Mavs/S
GO_BP_m2	GO:003421	carbohydra	3/470	130/23843	0.473937	0.674802	0.63177	Aspscr1/Nr
GO_BP_m2	GO:190330	regulation	3/470	130/23843	0.473937	0.674802	0.63177	Rac2/Stxbp
GO_BP_m2	GO:190336	positive reg	3/470	130/23843	0.473937	0.674802	0.63177	Rack1/Ptk2
GO_BP_m2	GO:000915	purine ribo	9/470	430/23843	0.47486	0.675886	0.632785	Adsl/Rack1
GO_BP_m2	GO:005073	positive reg	4/470	180/23843	0.475336	0.676334	0.633204	Agrn/Angp
GO_BP_m2	GO:000647	protein dep	5/470	230/23843	0.475784	0.676513	0.633372	Pdp1/Pink1
GO_BP_m2	GO:007066	regulation	5/470	230/23843	0.475784	0.676513	0.633372	Bmp4/Il12r
GO_BP_m2	GO:003220	regulation	2/470	81/23843	0.476243	0.676706	0.633553	Aurkb/Hnr
GO_BP_m2	GO:190406	negative re	2/470	81/23843	0.476243	0.676706	0.633553	Agrn/Kcnh
GO_BP_m2	GO:004230	molting cyc	3/470	131/23843	0.478976	0.678695	0.635414	Dkk4/Farp2
GO_BP_m2	GO:004263	hair cycle	3/470	131/23843	0.478976	0.678695	0.635414	Dkk4/Farp2
GO_BP_m2	GO:000645	protein fold	4/470	181/23843	0.479608	0.678695	0.635414	Emc4/Ppib
GO_BP_m2	GO:004877	tissue remo	4/470	181/23843	0.479608	0.678695	0.635414	Chd7/Csk/
GO_BP_m2	GO:000046	maturation	1/470	33/23843	0.481828	0.678695	0.635414	Exosc2
GO_BP_m2	GO:000177	myeloid de	1/470	33/23843	0.481828	0.678695	0.635414	Csf2
GO_BP_m2	GO:000275	cytoplasmi	1/470	33/23843	0.481828	0.678695	0.635414	Mavs
GO_BP_m2	GO:000610	citrate met	1/470	33/23843	0.481828	0.678695	0.635414	Aco1
GO_BP_m2	GO:000627	DNA replic	1/470	33/23843	0.481828	0.678695	0.635414	Wdr18
GO_BP_m2	GO:000761	mating beh	1/470	33/23843	0.481828	0.678695	0.635414	Aplp2
GO_BP_m2	GO:001066	negative re	1/470	33/23843	0.481828	0.678695	0.635414	Sfrp2
GO_BP_m2	GO:001482	response to	1/470	33/23843	0.481828	0.678695	0.635414	Srl
GO_BP_m2	GO:003438	plasma lipo	1/470	33/23843	0.481828	0.678695	0.635414	Csk
GO_BP_m2	GO:004340	skeletal mu	1/470	33/23843	0.481828	0.678695	0.635414	Plau
GO_BP_m2	GO:004804	embryonic	1/470	33/23843	0.481828	0.678695	0.635414	Six3
GO_BP_m2	GO:004856	embryonic	1/470	33/23843	0.481828	0.678695	0.635414	Id2
GO_BP_m2	GO:005195	negative re	1/470	33/23843	0.481828	0.678695	0.635414	Grm7
GO_BP_m2	GO:006033	type I inter	1/470	33/23843	0.481828	0.678695	0.635414	Mavs
GO_BP_m2	GO:006070	cell differen	1/470	33/23843	0.481828	0.678695	0.635414	Erf
GO_BP_m2	GO:006074	prostate gl	1/470	33/23843	0.481828	0.678695	0.635414	Bmp4
GO_BP_m2	GO:007135	cellular res	1/470	33/23843	0.481828	0.678695	0.635414	Mavs

GO_BP_m2	GO:190074	regulation	1/470	33/23843	0.481828	0.678695	0.635414	Gdf6
GO_BP_m2	GO:190102	positive re	1/470	33/23843	0.481828	0.678695	0.635414	Bmp4
GO_BP_m2	GO:19035	positive re	1/470	33/23843	0.481828	0.678695	0.635414	Pink1
GO_BP_m2	GO:200024	regulation	1/470	33/23843	0.481828	0.678695	0.635414	Ptk2b
GO_BP_m2	GO:00027	regulation	10/470	483/23843	0.482252	0.678695	0.635414	Chd7/Glul/
GO_BP_m2	GO:19019	regulation	6/470	282/23843	0.482642	0.678695	0.635414	Foxo4/Id2/
GO_BP_m2	GO:00302	glycosamir	2/470	82/23843	0.482656	0.678695	0.635414	Chst12/Ch
GO_BP_m2	GO:003064	regulation	2/470	82/23843	0.482656	0.678695	0.635414	Atp6v1h/G
GO_BP_m2	GO:003264	regulation	2/470	82/23843	0.482656	0.678695	0.635414	Mavs/Suz1
GO_BP_m2	GO:00353	regulation	2/470	82/23843	0.482656	0.678695	0.635414	Pink1/Ppp
GO_BP_m2	GO:00352	organ grov	4/470	182/23843	0.483867	0.678979	0.635681	Lats2/Lmx1
GO_BP_m2	GO:00439	negative re	4/470	182/23843	0.483867	0.678979	0.635681	Chmp3/Ma
GO_BP_m2	GO:200037	regulation	4/470	182/23843	0.483867	0.678979	0.635681	Pink1/Plau/
GO_BP_m2	GO:00019	endothelial	3/470	132/23843	0.483991	0.678979	0.635681	Bmp4/Pdc
GO_BP_m2	GO:000761	memory	3/470	132/23843	0.483991	0.678979	0.635681	Bace1/Grm
GO_BP_m2	GO:003121	biomineral	3/470	132/23843	0.483991	0.678979	0.635681	Bmp4/Nbr
GO_BP_m2	GO:00718	leukocyte	3/470	132/23843	0.483991	0.678979	0.635681	Aurkb/Bmp
GO_BP_m2	GO:19907	protein loc	6/470	283/23843	0.486051	0.681642	0.638173	Csk/Fam12
GO_BP_m2	GO:00508	negative re	4/470	183/23843	0.488112	0.683665	0.640068	Bmp4/Id2/
GO_BP_m2	GO:00512	negative re	4/470	183/23843	0.488112	0.683665	0.640068	Csk/Syt11/
GO_BP_m2	GO:00085	regulation	2/470	83/23843	0.489021	0.683665	0.640068	Ift122/Sall
GO_BP_m2	GO:00324	positive re	2/470	83/23843	0.489021	0.683665	0.640068	Rack1/Cop
GO_BP_m2	GO:00327	positive re	2/470	83/23843	0.489021	0.683665	0.640068	Cybb/Mav
GO_BP_m2	GO:005114	positive re	2/470	83/23843	0.489021	0.683665	0.640068	Bmp4/Cd5
GO_BP_m2	GO:005501	cardiac mu	2/470	83/23843	0.489021	0.683665	0.640068	Bmp4/Myh
GO_BP_m2	GO:00098	positive re	8/470	385/23843	0.489926	0.683665	0.640068	Rack1/Met
GO_BP_m2	GO:00182	peptidyl-ly	7/470	335/23843	0.491314	0.683665	0.640068	Auts2/Hist
GO_BP_m2	GO:00140	oligodendr	1/470	34/23843	0.492057	0.683665	0.640068	Id2
GO_BP_m2	GO:001404	dopamine	1/470	34/23843	0.492057	0.683665	0.640068	Pink1
GO_BP_m2	GO:00140	regulation	1/470	34/23843	0.492057	0.683665	0.640068	Pink1
GO_BP_m2	GO:00302	chromosor	1/470	34/23843	0.492057	0.683665	0.640068	H3f3b
GO_BP_m2	GO:003164	positive re	1/470	34/23843	0.492057	0.683665	0.640068	Fgfbp3
GO_BP_m2	GO:003314	negative re	1/470	34/23843	0.492057	0.683665	0.640068	Cry1
GO_BP_m2	GO:003362	regulation	1/470	34/23843	0.492057	0.683665	0.640068	Plau
GO_BP_m2	GO:003424	regulation	1/470	34/23843	0.492057	0.683665	0.640068	Ell
GO_BP_m2	GO:004002	regulation	1/470	34/23843	0.492057	0.683665	0.640068	Eif4g3
GO_BP_m2	GO:00424	ribonucleo	1/470	34/23843	0.492057	0.683665	0.640068	Cad
GO_BP_m2	GO:004274	circadian sl	1/470	34/23843	0.492057	0.683665	0.640068	Csf2
GO_BP_m2	GO:004632	regulation	1/470	34/23843	0.492057	0.683665	0.640068	Nr4a3
GO_BP_m2	GO:00515	histone H3	1/470	34/23843	0.492057	0.683665	0.640068	Kdm3a
GO_BP_m2	GO:006051	prostate gl	1/470	34/23843	0.492057	0.683665	0.640068	Bmp4
GO_BP_m2	GO:00702	axonemal	1/470	34/23843	0.492057	0.683665	0.640068	Mss51
GO_BP_m2	GO:00713	cellular res	1/470	34/23843	0.492057	0.683665	0.640068	Acaca
GO_BP_m2	GO:19900	response t	1/470	34/23843	0.492057	0.683665	0.640068	Cdc5l
GO_BP_m2	GO:19900	cellular res	1/470	34/23843	0.492057	0.683665	0.640068	Cdc5l
GO_BP_m2	GO:20001	positive re	1/470	34/23843	0.492057	0.683665	0.640068	Nr4a3
GO_BP_m2	GO:00026	regulation	4/470	184/23843	0.492343	0.683837	0.640229	Ptk2b/Rac
GO_BP_m2	GO:000941	response t	3/470	134/23843	0.493952	0.685618	0.641896	Aurkb/Mfa

GO_BP_m2	GO:007132	cellular res	3/470	134/23843	0.493952	0.685618	0.641896	Rack1/Oxc
GO_BP_m2	GO:001049	proteasom	9/470	437/23843	0.494144	0.685657	0.641933	Alad/Derl1
GO_BP_m2	GO:014002	exocytic pr	2/470	84/23843	0.495337	0.685789	0.642056	Ralb/Stxbp
GO_BP_m2	GO:190101	regulation	2/470	84/23843	0.495337	0.685789	0.642056	Bmp4/Pde
GO_BP_m2	GO:190355	positive re	2/470	84/23843	0.495337	0.685789	0.642056	Cybb/Mavs
GO_BP_m2	GO:190595	positive re	2/470	84/23843	0.495337	0.685789	0.642056	Acat2/Erfe
GO_BP_m2	GO:004327	positive re	6/470	286/23843	0.496236	0.685789	0.642056	Bmp4/Erfe
GO_BP_m2	GO:004358	skin develo	6/470	286/23843	0.496236	0.685789	0.642056	Dkk4/Gpr8
GO_BP_m2	GO:000228	lymphocyte	4/470	185/23843	0.496559	0.685789	0.642056	Ifna4/Itfg2
GO_BP_m2	GO:007050	regulation	4/470	185/23843	0.496559	0.685789	0.642056	Agrn/Cep1
GO_BP_m2	GO:004639	carboxylic	7/470	337/23843	0.497561	0.685789	0.642056	Acaca/Cad
GO_BP_m2	GO:007233	monocarbo	5/470	236/23843	0.498303	0.685789	0.642056	Acaca/Chst
GO_BP_m2	GO:003021	keratinocyt	3/470	135/23843	0.498897	0.685789	0.642056	Kazn/Lats2
GO_BP_m2	GO:004649	nicotinami	3/470	135/23843	0.498897	0.685789	0.642056	Cyb5r4/Gp
GO_BP_m2	GO:005092	positive re	3/470	135/23843	0.498897	0.685789	0.642056	Ptk2b/Rac2
GO_BP_m2	GO:009730	response t	3/470	135/23843	0.498897	0.685789	0.642056	Acaca/Alad
GO_BP_m2	GO:190406	positive re	3/470	135/23843	0.498897	0.685789	0.642056	Bmp4/Kcnh
GO_BP_m2	GO:005095	sensory pe	6/470	287/23843	0.499615	0.685789	0.642056	Chd7/Col2
GO_BP_m2	GO:001605	organic aci	7/470	338/23843	0.500676	0.685789	0.642056	Acaca/Cad
GO_BP_m2	GO:000956	fertilization	4/470	186/23843	0.500761	0.685789	0.642056	H3f3b/Izum
GO_BP_m2	GO:004353	regulation	2/470	85/23843	0.501602	0.685789	0.642056	Angpt4/Pd
GO_BP_m2	GO:004547	response t	2/470	85/23843	0.501602	0.685789	0.642056	Alad/Mir33
GO_BP_m2	GO:004568	regulation	2/470	85/23843	0.501602	0.685789	0.642056	Bmp4/Id2
GO_BP_m2	GO:004598	positive re	2/470	85/23843	0.501602	0.685789	0.642056	Rack1/Pink
GO_BP_m2	GO:190054	positive re	2/470	85/23843	0.501602	0.685789	0.642056	Rack1/Pink
GO_BP_m2	GO:004657	regulation	5/470	237/23843	0.502021	0.685789	0.642056	Arap3/Auts
GO_BP_m2	GO:005140	stress-activ	5/470	237/23843	0.502021	0.685789	0.642056	Gdf6/Nbr1
GO_BP_m2	GO:000150	neurotrans	1/470	35/23843	0.502084	0.685789	0.642056	Slc25a38
GO_BP_m2	GO:000682	iron ion tra	1/470	35/23843	0.502084	0.685789	0.642056	Slc25a28
GO_BP_m2	GO:000714	female mei	1/470	35/23843	0.502084	0.685789	0.642056	Spire2
GO_BP_m2	GO:000727	neuromusc	1/470	35/23843	0.502084	0.685789	0.642056	Stxbp1
GO_BP_m2	GO:000995	proximal/d	1/470	35/23843	0.502084	0.685789	0.642056	Six3
GO_BP_m2	GO:001403	Schwann c	1/470	35/23843	0.502084	0.685789	0.642056	Adgrg6
GO_BP_m2	GO:003142	keratinizati	1/470	35/23843	0.502084	0.685789	0.642056	Kazn
GO_BP_m2	GO:003222	regulation	1/470	35/23843	0.502084	0.685789	0.642056	Stxbp1
GO_BP_m2	GO:003314	positive re	1/470	35/23843	0.502084	0.685789	0.642056	Ifna4
GO_BP_m2	GO:003577	positive re	1/470	35/23843	0.502084	0.685789	0.642056	Oxct1
GO_BP_m2	GO:003590	aorta morp	1/470	35/23843	0.502084	0.685789	0.642056	Chd7
GO_BP_m2	GO:004304	ATP-depen	1/470	35/23843	0.502084	0.685789	0.642056	Vps72
GO_BP_m2	GO:004568	positive re	1/470	35/23843	0.502084	0.685789	0.642056	Bmp4
GO_BP_m2	GO:004668	response t	1/470	35/23843	0.502084	0.685789	0.642056	Alad
GO_BP_m2	GO:005169	actin filame	1/470	35/23843	0.502084	0.685789	0.642056	Twf1
GO_BP_m2	GO:006007	Wnt signali	1/470	35/23843	0.502084	0.685789	0.642056	Sfrp2
GO_BP_m2	GO:006044	epithelial t	1/470	35/23843	0.502084	0.685789	0.642056	Bmp4
GO_BP_m2	GO:009002	regulation	1/470	35/23843	0.502084	0.685789	0.642056	Rac2
GO_BP_m2	GO:190138	positive re	1/470	35/23843	0.502084	0.685789	0.642056	Kcnh2
GO_BP_m2	GO:190197	regulation	1/470	35/23843	0.502084	0.685789	0.642056	Cry1
GO_BP_m2	GO:190274	apoptotic	1/470	35/23843	0.502084	0.685789	0.642056	Six3

GO_BP_m2	GO:200017	negative re	1/470	35/23843	0.502084	0.685789	0.642056	Cit
GO_BP_m2	GO:200040	positive re	1/470	35/23843	0.502084	0.685789	0.642056	Ptk2b
GO_BP_m2	GO:003563	multicellula	3/470	136/23843	0.503817	0.687485	0.643644	Grm7/Kcnh
GO_BP_m2	GO:004870	embryonic	3/470	136/23843	0.503817	0.687485	0.643644	Bmp4/Col2
GO_BP_m2	GO:007233	signal trans	3/470	136/23843	0.503817	0.687485	0.643644	Dyrk1a/Pck
GO_BP_m2	GO:000691	phagocyto	4/470	187/23843	0.504947	0.688355	0.644458	Ighv1-23/I
GO_BP_m2	GO:004470	multi-mult	4/470	187/23843	0.504947	0.688355	0.644458	Acsl4/H3f3
GO_BP_m2	GO:190495	negative re	4/470	187/23843	0.504947	0.688355	0.644458	Csk/Syt11/
GO_BP_m2	GO:004858	developme	5/470	238/23843	0.505728	0.689196	0.645246	Auts2/Gdf9
GO_BP_m2	GO:004308	regulation	6/470	289/23843	0.506351	0.689821	0.645832	Agrn/Ect2/
GO_BP_m2	GO:000165	metanephr	2/470	86/23843	0.507818	0.690006	0.646004	Bmp4/Id2
GO_BP_m2	GO:000616	nucleoside	2/470	86/23843	0.507818	0.690006	0.646004	Ak8/Pfkfb2
GO_BP_m2	GO:003260	chemokine	2/470	86/23843	0.507818	0.690006	0.646004	Mavs/Suz1
GO_BP_m2	GO:004434	cellular res	2/470	86/23843	0.507818	0.690006	0.646004	Fgfbp3/Sul
GO_BP_m2	GO:005130	chromosor	2/470	86/23843	0.507818	0.690006	0.646004	Cit/Espl1
GO_BP_m2	GO:190321	regulation	2/470	86/23843	0.507818	0.690006	0.646004	Pink1/Rac2
GO_BP_m2	GO:006156	axon devel	10/470	493/23843	0.508213	0.690006	0.646004	Agrn/Auts2
GO_BP_m2	GO:000726	neurotrans	3/470	137/23843	0.508712	0.690006	0.646004	Cplx4/Stxb
GO_BP_m2	GO:001936	pyridine nu	3/470	137/23843	0.508712	0.690006	0.646004	Cyb5r4/Gp
GO_BP_m2	GO:003133	negative re	3/470	137/23843	0.508712	0.690006	0.646004	Dyrk1a/Stx
GO_BP_m2	GO:003263	interleukin	3/470	137/23843	0.508712	0.690006	0.646004	Csk/Mavs/
GO_BP_m2	GO:005512	digestive sy	3/470	137/23843	0.508712	0.690006	0.646004	Bmp4/Id2/
GO_BP_m2	GO:009964	signal relea	3/470	137/23843	0.508712	0.690006	0.646004	Cplx4/Stxb
GO_BP_m2	GO:000616	purine nuc	9/470	443/23843	0.510523	0.690006	0.646004	Adsl/Rack1
GO_BP_m2	GO:000046	maturation	1/470	36/23843	0.511913	0.690006	0.646004	Pwp2
GO_BP_m2	GO:000663	unsaturate	1/470	36/23843	0.511913	0.690006	0.646004	Fads1
GO_BP_m2	GO:000916	nucleoside	1/470	36/23843	0.511913	0.690006	0.646004	Cad
GO_BP_m2	GO:000931	oligosacch	1/470	36/23843	0.511913	0.690006	0.646004	Galnt2
GO_BP_m2	GO:001009	specificatic	1/470	36/23843	0.511913	0.690006	0.646004	Bmp4
GO_BP_m2	GO:001083	positive re	1/470	36/23843	0.511913	0.690006	0.646004	Cd53
GO_BP_m2	GO:003081	positive re	1/470	36/23843	0.511913	0.690006	0.646004	Rack1
GO_BP_m2	GO:003511	embryonic	1/470	36/23843	0.511913	0.690006	0.646004	Ift122
GO_BP_m2	GO:003530	positive re	1/470	36/23843	0.511913	0.690006	0.646004	Pink1
GO_BP_m2	GO:004298	amyloid pr	1/470	36/23843	0.511913	0.690006	0.646004	Dyrk1a
GO_BP_m2	GO:004476	multi-orga	1/470	36/23843	0.511913	0.690006	0.646004	Mavs
GO_BP_m2	GO:004683	lipid phosp	1/470	36/23843	0.511913	0.690006	0.646004	Fam126a
GO_BP_m2	GO:004816	regulation	1/470	36/23843	0.511913	0.690006	0.646004	Rab11a
GO_BP_m2	GO:004871	regulation	1/470	36/23843	0.511913	0.690006	0.646004	Id2
GO_BP_m2	GO:004882	erythrocyte	1/470	36/23843	0.511913	0.690006	0.646004	Jmjd6
GO_BP_m2	GO:005129	establishm	1/470	36/23843	0.511913	0.690006	0.646004	Spire2
GO_BP_m2	GO:008600	regulation	1/470	36/23843	0.511913	0.690006	0.646004	Pde4d
GO_BP_m2	GO:009702	dendritic c	1/470	36/23843	0.511913	0.690006	0.646004	Csf2
GO_BP_m2	GO:009748	dendrite e	1/470	36/23843	0.511913	0.690006	0.646004	Auts2
GO_BP_m2	GO:009719	intrinsic ap	6/470	291/23843	0.513054	0.6909	0.646841	Atf4/Casp1
GO_BP_m2	GO:004816	regulation	7/470	342/23843	0.513071	0.6909	0.646841	Bace1/Mir1
GO_BP_m2	GO:005132	meiotic cel	7/470	342/23843	0.513071	0.6909	0.646841	Eif4g3/Espl
GO_BP_m2	GO:000150	action pote	3/470	138/23843	0.513582	0.691019	0.646953	Gpd1l/Kcnl
GO_BP_m2	GO:000722	smoothene	3/470	138/23843	0.513582	0.691019	0.646953	2700049A

GO_BP_m2	GO:00149	smooth mu	2/470	87/23843	0.513982	0.691019	0.646953	Foxo4/Plau
GO_BP_m2	GO:002187	forebrain g	2/470	87/23843	0.513982	0.691019	0.646953	Mettl14/Sa
GO_BP_m2	GO:004632	glucose im	2/470	87/23843	0.513982	0.691019	0.646953	Aspscr1/U
GO_BP_m2	GO:005077	regulation	4/470	190/23843	0.51741	0.694295	0.65002	Agrn/Rab1
GO_BP_m2	GO:00760	visual perc	3/470	139/23843	0.518426	0.694295	0.65002	Col2a1/Irx
GO_BP_m2	GO:00217	limbic syst	2/470	88/23843	0.520096	0.694295	0.65002	Nr4a3/Zbt
GO_BP_m2	GO:00305	neutrophil	2/470	88/23843	0.520096	0.694295	0.65002	Pde4d/Rac
GO_BP_m2	GO:00329	collagen m	2/470	88/23843	0.520096	0.694295	0.65002	Bmp4/Mfa
GO_BP_m2	GO:00435	regulation	2/470	88/23843	0.520096	0.694295	0.65002	Ptk2b/Sfrp
GO_BP_m2	GO:00469	nucleotide	2/470	88/23843	0.520096	0.694295	0.65002	Ak8/Pfkfb2
GO_BP_m2	GO:007177	response t	2/470	88/23843	0.520096	0.694295	0.65002	Fgfbp3/Sul
GO_BP_m2	GO:007267	lymphocyt	2/470	88/23843	0.520096	0.694295	0.65002	Myo1g/Ptk
GO_BP_m2	GO:190401	positive re	4/470	191/23843	0.521532	0.694295	0.65002	Angpt4/Cy
GO_BP_m2	GO:000194	postsynapt	1/470	37/23843	0.521549	0.694295	0.65002	Agrn
GO_BP_m2	GO:00028	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Stxbp1
GO_BP_m2	GO:00067	NADP met	1/470	37/23843	0.521549	0.694295	0.65002	Cyb5r4
GO_BP_m2	GO:00080	anterograd	1/470	37/23843	0.521549	0.694295	0.65002	Bloc1s2
GO_BP_m2	GO:00218	forebrain n	1/470	37/23843	0.521549	0.694295	0.65002	Sall3
GO_BP_m2	GO:00305	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:003051	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:00331	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Ifna4
GO_BP_m2	GO:00358	epithelial c	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:00456	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:00457	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Cks1b
GO_BP_m2	GO:00610	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Agrn
GO_BP_m2	GO:00860	cell commu	1/470	37/23843	0.521549	0.694295	0.65002	Pde4d
GO_BP_m2	GO:009004	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Pdcd10
GO_BP_m2	GO:009017	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Sfrp2
GO_BP_m2	GO:19010	guanosine-	1/470	37/23843	0.521549	0.694295	0.65002	Ran
GO_BP_m2	GO:19021	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Bloc1s2
GO_BP_m2	GO:190262	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Rac2
GO_BP_m2	GO:19028	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:19053	positive re	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:200082	regulation	1/470	37/23843	0.521549	0.694295	0.65002	Bmp4
GO_BP_m2	GO:00720	nephron d	3/470	140/23843	0.523245	0.696332	0.651927	Bmp4/Not
GO_BP_m2	GO:00109	regulation	8/470	397/23843	0.524613	0.697932	0.653424	Agrn/Atf4/
GO_BP_m2	GO:00033	cardiac mu	2/470	89/23843	0.526158	0.6991	0.654518	Nr4a3/Twf
GO_BP_m2	GO:00066	glycolipid	2/470	89/23843	0.526158	0.6991	0.654518	Gba2/Pigm
GO_BP_m2	GO:00075	response t	2/470	89/23843	0.526158	0.6991	0.654518	Adsl/Alad
GO_BP_m2	GO:00550	cardiac cell	2/470	89/23843	0.526158	0.6991	0.654518	Bmp4/Myh
GO_BP_m2	GO:00028	regulation	3/470	141/23843	0.528036	0.700646	0.655966	Il12rb1/Ma
GO_BP_m2	GO:001097	transport a	3/470	141/23843	0.528036	0.700646	0.655966	Bloc1s2/Ift
GO_BP_m2	GO:00427	drug catab	3/470	141/23843	0.528036	0.700646	0.655966	Cyp2g1/Ox
GO_BP_m2	GO:009911	microtubul	3/470	141/23843	0.528036	0.700646	0.655966	Bloc1s2/Ift
GO_BP_m2	GO:00726	Rho protei	4/470	193/23843	0.529726	0.700646	0.655966	Arap3/Ect2
GO_BP_m2	GO:00305	leukocyte	4/470	193/23843	0.529726	0.700646	0.655966	Pde4d/Ptk
GO_BP_m2	GO:00019	synaptic tr	1/470	38/23843	0.530995	0.700646	0.655966	Pink1
GO_BP_m2	GO:000272	positive re	1/470	38/23843	0.530995	0.700646	0.655966	Nr4a3

GO_BP_m2	GO:00940	response t	1/470	38/23843	0.530995	0.700646	0.655966	Ucp2
GO_BP_m2	GO:003081	regulation	1/470	38/23843	0.530995	0.700646	0.655966	Rack1
GO_BP_m2	GO:004478	cell cycle D	1/470	38/23843	0.530995	0.700646	0.655966	Wdr18
GO_BP_m2	GO:004558	negative re	1/470	38/23843	0.530995	0.700646	0.655966	Bmp4
GO_BP_m2	GO:004879	calcium io	1/470	38/23843	0.530995	0.700646	0.655966	Syt11
GO_BP_m2	GO:007221	metanephr	1/470	38/23843	0.530995	0.700646	0.655966	Bmp4
GO_BP_m2	GO:007235	tricarboxyli	1/470	38/23843	0.530995	0.700646	0.655966	Aco1
GO_BP_m2	GO:007259	maintenan	1/470	38/23843	0.530995	0.700646	0.655966	Pink1
GO_BP_m2	GO:008600	membrane	1/470	38/23843	0.530995	0.700646	0.655966	Kcnh2
GO_BP_m2	GO:009712	receptor lo	1/470	38/23843	0.530995	0.700646	0.655966	Rab11a
GO_BP_m2	GO:190165	glycosyl co	1/470	38/23843	0.530995	0.700646	0.655966	Cad
GO_BP_m2	GO:190198	positive reg	1/470	38/23843	0.530995	0.700646	0.655966	Auts2
GO_BP_m2	GO:200000	regulation	1/470	38/23843	0.530995	0.700646	0.655966	Gpd1l
GO_BP_m2	GO:200102	positive reg	1/470	38/23843	0.530995	0.700646	0.655966	Pink1
GO_BP_m2	GO:003530	negative re	2/470	90/23843	0.532168	0.701312	0.656589	Elfn2/Ell
GO_BP_m2	GO:005084	regulation	2/470	90/23843	0.532168	0.701312	0.656589	Pde4d/Ptk2
GO_BP_m2	GO:007145	cellular res	2/470	90/23843	0.532168	0.701312	0.656589	Cybb/Pink1
GO_BP_m2	GO:190350	liposacchar	2/470	90/23843	0.532168	0.701312	0.656589	Gba2/Pigm
GO_BP_m2	GO:000733	single fertil	3/470	142/23843	0.532801	0.701463	0.656731	H3f3b/Izun
GO_BP_m2	GO:000914	nucleoside	3/470	142/23843	0.532801	0.701463	0.656731	Ak8/Cad/P
GO_BP_m2	GO:007252	pyridine-c	3/470	142/23843	0.532801	0.701463	0.656731	Cyb5r4/Gp
GO_BP_m2	GO:001604	lipid catab	6/470	297/23843	0.532952	0.701463	0.656731	Acat2/Echc
GO_BP_m2	GO:003134	negative re	4/470	194/23843	0.533797	0.702356	0.657566	Cit/Prkcsh/
GO_BP_m2	GO:001067	regulation	3/470	143/23843	0.537539	0.705543	0.66055	Fgl1/Pfkfb2
GO_BP_m2	GO:005095	sensory pe	3/470	143/23843	0.537539	0.705543	0.66055	Col2a1/Irx5
GO_BP_m2	GO:200005	regulation	3/470	143/23843	0.537539	0.705543	0.66055	Rack1/Ptk2
GO_BP_m2	GO:004544	myoblast d	2/470	91/23843	0.538126	0.705543	0.66055	Bmp4/Klhl4
GO_BP_m2	GO:190374	regulation	2/470	91/23843	0.538126	0.705543	0.66055	Pink1/Rac2
GO_BP_m2	GO:000762	locomotory	5/470	247/23843	0.538577	0.705543	0.66055	Aplp2/Chd
GO_BP_m2	GO:000271	positive reg	1/470	39/23843	0.540255	0.705543	0.66055	Zbtb1
GO_BP_m2	GO:000317	heart valve	1/470	39/23843	0.540255	0.705543	0.66055	Bmp4
GO_BP_m2	GO:000668	glycosphin	1/470	39/23843	0.540255	0.705543	0.66055	Gba2
GO_BP_m2	GO:003043	sleep	1/470	39/23843	0.540255	0.705543	0.66055	Csf2
GO_BP_m2	GO:003107	embryonic	1/470	39/23843	0.540255	0.705543	0.66055	Six3
GO_BP_m2	GO:003157	G2 DNA da	1/470	39/23843	0.540255	0.705543	0.66055	Foxo4
GO_BP_m2	GO:003287	negative re	1/470	39/23843	0.540255	0.705543	0.66055	Sfrp2
GO_BP_m2	GO:003434	response t	1/470	39/23843	0.540255	0.705543	0.66055	Mavs
GO_BP_m2	GO:004355	regulation	1/470	39/23843	0.540255	0.705543	0.66055	Ptk2b
GO_BP_m2	GO:004824	macrophag	1/470	39/23843	0.540255	0.705543	0.66055	Ptk2b
GO_BP_m2	GO:004874	skeletal mu	1/470	39/23843	0.540255	0.705543	0.66055	Klhl41
GO_BP_m2	GO:006032	face morph	1/470	39/23843	0.540255	0.705543	0.66055	Sgpl1
GO_BP_m2	GO:007030	negative re	1/470	39/23843	0.540255	0.705543	0.66055	Sfrp2
GO_BP_m2	GO:007152	semaphori	1/470	39/23843	0.540255	0.705543	0.66055	Farp2
GO_BP_m2	GO:009700	energy hor	1/470	39/23843	0.540255	0.705543	0.66055	Nr4a3
GO_BP_m2	GO:190293	regulation	1/470	39/23843	0.540255	0.705543	0.66055	Ptk2b
GO_BP_m2	GO:190352	negative re	1/470	39/23843	0.540255	0.705543	0.66055	Pde4d
GO_BP_m2	GO:190357	negative re	1/470	39/23843	0.540255	0.705543	0.66055	Ube2j1
GO_BP_m2	GO:004887	multicellula	7/470	351/23843	0.540549	0.705707	0.660704	Acaca/Col2

GO_BP_m2	GO:000004	autophago	2/470	92/23843	0.544031	0.70937	0.664134	Pink1/Ralb
GO_BP_m2	GO:000202	regulation	2/470	92/23843	0.544031	0.70937	0.664134	Agrn/Gpd1
GO_BP_m2	GO:001489	striated mu	2/470	92/23843	0.544031	0.70937	0.664134	Nr4a3/Twf1
GO_BP_m2	GO:004688	negative re	2/470	92/23843	0.544031	0.70937	0.664134	Cry1/Ucp2
GO_BP_m2	GO:003164	regulation	5/470	249/23843	0.54574	0.71137	0.666006	Derl1/Pdcc
GO_BP_m2	GO:190304	meiotic cel	4/470	197/23843	0.545904	0.71137	0.666006	Eif4g3/Espl
GO_BP_m2	GO:190165	response t	7/470	353/23843	0.54657	0.712017	0.666612	Cad/Cry1/C
GO_BP_m2	GO:000683	neurotrans	5/470	250/23843	0.549302	0.712159	0.666744	Cplx4/Csf2
GO_BP_m2	GO:004819	Golgi vesic	5/470	250/23843	0.549302	0.712159	0.666744	Csk/Rack1/
GO_BP_m2	GO:011005	regulation	5/470	250/23843	0.549302	0.712159	0.666744	Cit/Ptk2b/P
GO_BP_m2	GO:000178	B cell apop	1/470	40/23843	0.549332	0.712159	0.666744	Aurkb
GO_BP_m2	GO:000315	regulation	1/470	40/23843	0.549332	0.712159	0.666744	Bmp4
GO_BP_m2	GO:000911	nucleobase	1/470	40/23843	0.549332	0.712159	0.666744	Cad
GO_BP_m2	GO:003051	negative re	1/470	40/23843	0.549332	0.712159	0.666744	Rnf6
GO_BP_m2	GO:003083	negative re	1/470	40/23843	0.549332	0.712159	0.666744	Twf1
GO_BP_m2	GO:003245	regulation	1/470	40/23843	0.549332	0.712159	0.666744	Rack1
GO_BP_m2	GO:003541	protein loc	1/470	40/23843	0.549332	0.712159	0.666744	Rab11a
GO_BP_m2	GO:003806	p38MAPK (	1/470	40/23843	0.549332	0.712159	0.666744	Gdf6
GO_BP_m2	GO:007083	bicellular ti	1/470	40/23843	0.549332	0.712159	0.666744	Ect2
GO_BP_m2	GO:190403	positive re	1/470	40/23843	0.549332	0.712159	0.666744	Cks1b
GO_BP_m2	GO:200072	regulation	1/470	40/23843	0.549332	0.712159	0.666744	Bmp4
GO_BP_m2	GO:000157	vasculogen	2/470	93/23843	0.549884	0.712159	0.666744	Sgpl1/Wars
GO_BP_m2	GO:002178	glial cell de	2/470	93/23843	0.549884	0.712159	0.666744	Adgrg6/Id2
GO_BP_m2	GO:004864	muscle org	2/470	93/23843	0.549884	0.712159	0.666744	Chd7/Serp
GO_BP_m2	GO:190547	positive re	2/470	93/23843	0.549884	0.712159	0.666744	Rack1/Rab
GO_BP_m2	GO:003298	protein-co	4/470	198/23843	0.549903	0.712159	0.666744	2810006K2
GO_BP_m2	GO:001571	monocarbo	3/470	146/23843	0.551585	0.713676	0.668165	Acsl4/Erfe/
GO_BP_m2	GO:002261	gland morp	3/470	146/23843	0.551585	0.713676	0.668165	Bmp4/Plau
GO_BP_m2	GO:009953	presynapti	3/470	146/23843	0.551585	0.713676	0.668165	Cplx4/Stxb
GO_BP_m2	GO:200002	regulation	4/470	199/23843	0.553884	0.716092	0.670427	Bmp4/Plau
GO_BP_m2	GO:000195	regulation	2/470	94/23843	0.555683	0.716092	0.670427	Mavs/Palm
GO_BP_m2	GO:001489	muscle hyp	2/470	94/23843	0.555683	0.716092	0.670427	Nr4a3/Twf1
GO_BP_m2	GO:001701	regulation	2/470	94/23843	0.555683	0.716092	0.670427	Bambi/Tgfb
GO_BP_m2	GO:003241	positive re	2/470	94/23843	0.555683	0.716092	0.670427	Bmp4/Pink
GO_BP_m2	GO:003355	multicellula	2/470	94/23843	0.555683	0.716092	0.670427	Grm7/Penk
GO_BP_m2	GO:004563	negative re	2/470	94/23843	0.555683	0.716092	0.670427	Mafb/Ptk2b
GO_BP_m2	GO:000756	cell aging	3/470	147/23843	0.556211	0.716092	0.670427	Id2/Mirlet7
GO_BP_m2	GO:002154	pallium dev	3/470	147/23843	0.556211	0.716092	0.670427	Cep120/Nr
GO_BP_m2	GO:000018	activation (	1/470	41/23843	0.558231	0.716092	0.670427	Bmp4
GO_BP_m2	GO:000196	positive re	1/470	41/23843	0.558231	0.716092	0.670427	Mavs
GO_BP_m2	GO:000650	membrane	1/470	41/23843	0.558231	0.716092	0.670427	Bace1
GO_BP_m2	GO:000733	binding of	1/470	41/23843	0.558231	0.716092	0.670427	Zpbp
GO_BP_m2	GO:001047	regulation	1/470	41/23843	0.558231	0.716092	0.670427	Sfrp2
GO_BP_m2	GO:001051	positive re	1/470	41/23843	0.558231	0.716092	0.670427	Sele
GO_BP_m2	GO:001076	positive re	1/470	41/23843	0.558231	0.716092	0.670427	Gpd1l
GO_BP_m2	GO:001967	NAD metal	1/470	41/23843	0.558231	0.716092	0.670427	Gpd1l
GO_BP_m2	GO:003237	regulation	1/470	41/23843	0.558231	0.716092	0.670427	Acat2
GO_BP_m2	GO:003237	regulation	1/470	41/23843	0.558231	0.716092	0.670427	Acat2

GO_BP_m2	GO:003281	regulation	1/470	41/23843	0.558231	0.716092	0.670427	Zbtb1
GO_BP_m2	GO:003292	activin rece	1/470	41/23843	0.558231	0.716092	0.670427	Gdf6
GO_BP_m2	GO:003296	regulation	1/470	41/23843	0.558231	0.716092	0.670427	Bmp4
GO_BP_m2	GO:004549	photorecep	1/470	41/23843	0.558231	0.716092	0.670427	Crocc
GO_BP_m2	GO:004592	positive reg	1/470	41/23843	0.558231	0.716092	0.670427	Nr4a3
GO_BP_m2	GO:004749	vesicle tran	1/470	41/23843	0.558231	0.716092	0.670427	Bloc1s2
GO_BP_m2	GO:005159	positive reg	1/470	41/23843	0.558231	0.716092	0.670427	Stxbp1
GO_BP_m2	GO:005165	spindle loc	1/470	41/23843	0.558231	0.716092	0.670427	Spire2
GO_BP_m2	GO:190266	regulation	1/470	41/23843	0.558231	0.716092	0.670427	Agrn
GO_BP_m2	GO:190199	regulation	5/470	253/23843	0.559907	0.718023	0.672234	Foxo4/Id2/
GO_BP_m2	GO:005114	regulation	3/470	148/23843	0.560809	0.718438	0.672623	Bmp4/Cd5
GO_BP_m2	GO:000911	nucleoside	2/470	95/23843	0.56143	0.718438	0.672623	Cad/Ran
GO_BP_m2	GO:000979	axis specifi	2/470	95/23843	0.56143	0.718438	0.672623	Bmp4/Six3
GO_BP_m2	GO:003164	regulation	2/470	95/23843	0.56143	0.718438	0.672623	Fgfbp3/Mt
GO_BP_m2	GO:004592	positive reg	2/470	95/23843	0.56143	0.718438	0.672623	Stxbp1/Tsg
GO_BP_m2	GO:004870	oligodendr	2/470	95/23843	0.56143	0.718438	0.672623	Bmp4/Id2
GO_BP_m2	GO:006105	somite dev	2/470	95/23843	0.56143	0.718438	0.672623	Lfng/Sfrp2
GO_BP_m2	GO:003158	cell-substra	6/470	306/23843	0.562139	0.718469	0.672652	Myo1g/Pla
GO_BP_m2	GO:004648	glycerolipid	6/470	306/23843	0.562139	0.718469	0.672652	Acsl4/Cdip
GO_BP_m2	GO:004665	lymphocyte	6/470	306/23843	0.562139	0.718469	0.672652	Bmp4/Ifna4
GO_BP_m2	GO:004887	homeostas	6/470	306/23843	0.562139	0.718469	0.672652	Bmp4/Id2/
GO_BP_m2	GO:000669	steroid bio	3/470	149/23843	0.565377	0.719144	0.673284	Sc5d/Sdr42
GO_BP_m2	GO:000693	regulation	3/470	149/23843	0.565377	0.719144	0.673284	Agrn/Pde4
GO_BP_m2	GO:190547	regulation	3/470	149/23843	0.565377	0.719144	0.673284	Csk/Rack1/
GO_BP_m2	GO:005092	regulation	4/470	202/23843	0.565714	0.719144	0.673284	Agrn/Ptk2b
GO_BP_m2	GO:009865	anion trans	4/470	202/23843	0.565714	0.719144	0.673284	Slc6a21/Slc
GO_BP_m2	GO:001648	protein pro	5/470	255/23843	0.566908	0.719144	0.673284	Metap2/Pc
GO_BP_m2	GO:000095	mitochond	1/470	42/23843	0.566954	0.719144	0.673284	Wars2
GO_BP_m2	GO:000319	endocardia	1/470	42/23843	0.566954	0.719144	0.673284	Bmp4
GO_BP_m2	GO:000695	acute-phas	1/470	42/23843	0.566954	0.719144	0.673284	Serpina1b
GO_BP_m2	GO:000708	mitotic me	1/470	42/23843	0.566954	0.719144	0.673284	Rab11a
GO_BP_m2	GO:001097	negative re	1/470	42/23843	0.566954	0.719144	0.673284	Foxo4
GO_BP_m2	GO:001692	protein sur	1/470	42/23843	0.566954	0.719144	0.673284	Tollip
GO_BP_m2	GO:001820	peptidyl-pr	1/470	42/23843	0.566954	0.719144	0.673284	Ppib
GO_BP_m2	GO:003105	negative re	1/470	42/23843	0.566954	0.719144	0.673284	Kdm3a
GO_BP_m2	GO:003157	spindle che	1/470	42/23843	0.566954	0.719144	0.673284	Aurkb
GO_BP_m2	GO:003276	regulation	1/470	42/23843	0.566954	0.719144	0.673284	Ptk2b
GO_BP_m2	GO:003305	cellular pig	1/470	42/23843	0.566954	0.719144	0.673284	Rab11a
GO_BP_m2	GO:004250	serine phos	1/470	42/23843	0.566954	0.719144	0.673284	Ifna4
GO_BP_m2	GO:005189	negative re	1/470	42/23843	0.566954	0.719144	0.673284	Rack1
GO_BP_m2	GO:006013	maternal p	1/470	42/23843	0.566954	0.719144	0.673284	Prl8a2
GO_BP_m2	GO:007016	positive reg	1/470	42/23843	0.566954	0.719144	0.673284	Bmp4
GO_BP_m2	GO:190372	positive reg	1/470	42/23843	0.566954	0.719144	0.673284	Ptk2b
GO_BP_m2	GO:000245	T cell medi	2/470	96/23843	0.567123	0.719144	0.673284	Myo1g/Zbt
GO_BP_m2	GO:014005	mitochond	2/470	96/23843	0.567123	0.719144	0.673284	2810006K2
GO_BP_m2	GO:190384	regulation	2/470	96/23843	0.567123	0.719144	0.673284	Bambi/Tgfb
GO_BP_m2	GO:190503	autophago	2/470	96/23843	0.567123	0.719144	0.673284	Pink1/Ralb
GO_BP_m2	GO:003294	mononucle	6/470	308/23843	0.568508	0.720682	0.674724	Bmp4/Ifna4

GO_BP_m2	GO:003287	positive re	3/470	150/23843	0.569916	0.72225	0.676192	Gdf6/Pdcd
GO_BP_m2	GO:005160	protein ma	6/470	309/23843	0.571675	0.723434	0.6773	Ambp/Met
GO_BP_m2	GO:000688	regulation	2/470	97/23843	0.572762	0.723434	0.6773	Atp6v1h/G
GO_BP_m2	GO:003476	negative re	2/470	97/23843	0.572762	0.723434	0.6773	Agrn/Kcnh
GO_BP_m2	GO:004312	positive re	2/470	97/23843	0.572762	0.723434	0.6773	Pink1/Tme
GO_BP_m2	GO:004876	mesenchyr	4/470	204/23843	0.573503	0.723434	0.6773	Bambi/Bm
GO_BP_m2	GO:000183	embryonic	3/470	151/23843	0.574426	0.723434	0.6773	Bmp4/Ift12
GO_BP_m2	GO:003476	positive re	3/470	151/23843	0.574426	0.723434	0.6773	Bmp4/Kcn
GO_BP_m2	GO:004666	male sex d	3/470	151/23843	0.574426	0.723434	0.6773	H3f3b/Sfrp
GO_BP_m2	GO:007030	positive re	3/470	151/23843	0.574426	0.723434	0.6773	Gdf6/Pdcd
GO_BP_m2	GO:005090	leukocyte r	6/470	310/23843	0.574832	0.723434	0.6773	Myo1g/Pd
GO_BP_m2	GO:001700	cell fate de	1/470	43/23843	0.575506	0.723434	0.6773	Bmp4
GO_BP_m2	GO:000182	blastocyst	1/470	43/23843	0.575506	0.723434	0.6773	Lats2
GO_BP_m2	GO:000196	negative re	1/470	43/23843	0.575506	0.723434	0.6773	Palm3
GO_BP_m2	GO:000762	adult walki	1/470	43/23843	0.575506	0.723434	0.6773	Chd7
GO_BP_m2	GO:001025	NADH deh	1/470	43/23843	0.575506	0.723434	0.6773	Ndufaf8
GO_BP_m2	GO:001490	myotube c	1/470	43/23843	0.575506	0.723434	0.6773	Klhl41
GO_BP_m2	GO:001802	peptidyl-ly	1/470	43/23843	0.575506	0.723434	0.6773	Hist1h1e
GO_BP_m2	GO:003016	proteoglyc	1/470	43/23843	0.575506	0.723434	0.6773	Chst12
GO_BP_m2	GO:003111	negative re	1/470	43/23843	0.575506	0.723434	0.6773	Dyrk1a
GO_BP_m2	GO:003275	positive re	1/470	43/23843	0.575506	0.723434	0.6773	Mavs
GO_BP_m2	GO:003298	mitochond	1/470	43/23843	0.575506	0.723434	0.6773	Ndufaf8
GO_BP_m2	GO:006164	histone H3	1/470	43/23843	0.575506	0.723434	0.6773	Kdm3a
GO_BP_m2	GO:007052	platelet ag	1/470	43/23843	0.575506	0.723434	0.6773	Stxbp1
GO_BP_m2	GO:007138	cellular res	1/470	43/23843	0.575506	0.723434	0.6773	Bmp4
GO_BP_m2	GO:009031	negative re	1/470	43/23843	0.575506	0.723434	0.6773	Ube2j1
GO_BP_m2	GO:190311	regulation	1/470	43/23843	0.575506	0.723434	0.6773	Pde4d
GO_BP_m2	GO:190551	macrophag	1/470	43/23843	0.575506	0.723434	0.6773	Ptk2b
GO_BP_m2	GO:000991	epidermal	4/470	205/23843	0.577369	0.725269	0.679019	Bmp4/Kazr
GO_BP_m2	GO:000242	immune re	6/470	311/23843	0.577976	0.725269	0.679019	Csk/Ighv1-
GO_BP_m2	GO:000301	renal syste	2/470	98/23843	0.578349	0.725269	0.679019	Bmp4/Sulf
GO_BP_m2	GO:000609	pyruvate m	2/470	98/23843	0.578349	0.725269	0.679019	Nr4a3/Pfkf
GO_BP_m2	GO:001624	regulation	2/470	98/23843	0.578349	0.725269	0.679019	Pink1/Ralb
GO_BP_m2	GO:003209	negative re	2/470	98/23843	0.578349	0.725269	0.679019	Aurkb/Ralb
GO_BP_m2	GO:005265	cyclic puri	2/470	98/23843	0.578349	0.725269	0.679019	Gucy2c/Ptk
GO_BP_m2	GO:007022	lymphocyt	2/470	98/23843	0.578349	0.725269	0.679019	Aurkb/Bmp
GO_BP_m2	GO:005506	monovale	3/470	152/23843	0.578907	0.725737	0.679457	Atp6v1h/G
GO_BP_m2	GO:003000	regionaliza	7/470	364/23843	0.579067	0.725737	0.679457	Bmp4/Ift12
GO_BP_m2	GO:001921	regulation	6/470	312/23843	0.581109	0.727428	0.68104	Acsl4/Erfe/
GO_BP_m2	GO:000269	positive re	4/470	206/23843	0.581214	0.727428	0.68104	Nr4a3/Rac
GO_BP_m2	GO:000919	cyclic nucle	2/470	99/23843	0.583881	0.727428	0.68104	Gucy2c/Ptk
GO_BP_m2	GO:001481	muscle cell	2/470	99/23843	0.583881	0.727428	0.68104	Foxo4/Plau
GO_BP_m2	GO:004203	regulation	2/470	99/23843	0.583881	0.727428	0.68104	Cybb/Ube2
GO_BP_m2	GO:190180	positive re	2/470	99/23843	0.583881	0.727428	0.68104	Rack1/Cop
GO_BP_m2	GO:000338	epithelial c	1/470	44/23843	0.583888	0.727428	0.68104	Frmd6
GO_BP_m2	GO:000669	cholesterol	1/470	44/23843	0.583888	0.727428	0.68104	Sc5d
GO_BP_m2	GO:001983	cytolysis	1/470	44/23843	0.583888	0.727428	0.68104	Csf2
GO_BP_m2	GO:004275	eating beh	1/470	44/23843	0.583888	0.727428	0.68104	Agrp

GO_BP_m2	GO:004326	positive reg	1/470	44/23843	0.583888	0.727428	0.68104	Kcnh2
GO_BP_m2	GO:005135	positive reg	1/470	44/23843	0.583888	0.727428	0.68104	Ptk2b
GO_BP_m2	GO:006161	pri-miRNA	1/470	44/23843	0.583888	0.727428	0.68104	Bmp4
GO_BP_m2	GO:006191	selective au	1/470	44/23843	0.583888	0.727428	0.68104	Pink1
GO_BP_m2	GO:007023	regulation	1/470	44/23843	0.583888	0.727428	0.68104	Bmp4
GO_BP_m2	GO:007167	regulation	1/470	44/23843	0.583888	0.727428	0.68104	S100a14
GO_BP_m2	GO:009018	positive reg	1/470	44/23843	0.583888	0.727428	0.68104	Bmp4
GO_BP_m2	GO:009065	walking be	1/470	44/23843	0.583888	0.727428	0.68104	Chd7
GO_BP_m2	GO:190314	regulation	1/470	44/23843	0.583888	0.727428	0.68104	Pink1
GO_BP_m2	GO:000626	DNA replic	5/470	260/23843	0.584156	0.727428	0.68104	Bmp4/Cha
GO_BP_m2	GO:000701	microtubul	5/470	260/23843	0.584156	0.727428	0.68104	Bloc1s2/Cf
GO_BP_m2	GO:190129	nucleoside	6/470	313/23843	0.584231	0.727428	0.68104	Adsl/Ak8/C
GO_BP_m2	GO:004340	negative re	3/470	154/23843	0.587778	0.731628	0.684972	Bmp4/Csk/
GO_BP_m2	GO:002260	digestive sy	2/470	100/23843	0.58936	0.732745	0.686018	Acat2/Aco1
GO_BP_m2	GO:003139	positive reg	2/470	100/23843	0.58936	0.732745	0.686018	Derl1/Rnf2
GO_BP_m2	GO:005198	regulation	2/470	100/23843	0.58936	0.732745	0.686018	Cit/Ect2
GO_BP_m2	GO:000199	regulation	1/470	45/23843	0.592106	0.732745	0.686018	Rasl10b
GO_BP_m2	GO:000752	myoblast fu	1/470	45/23843	0.592106	0.732745	0.686018	Cd53
GO_BP_m2	GO:001046	regulation	1/470	45/23843	0.592106	0.732745	0.686018	Bmp4
GO_BP_m2	GO:003164	protein des	1/470	45/23843	0.592106	0.732745	0.686018	Derl1
GO_BP_m2	GO:003278	regulation	1/470	45/23843	0.592106	0.732745	0.686018	Ell
GO_BP_m2	GO:004208	T-helper 1	1/470	45/23843	0.592106	0.732745	0.686018	Il12rb1
GO_BP_m2	GO:004590	positive reg	1/470	45/23843	0.592106	0.732745	0.686018	Shc1
GO_BP_m2	GO:005087	brown fat c	1/470	45/23843	0.592106	0.732745	0.686018	Cebpa
GO_BP_m2	GO:006032	head morp	1/470	45/23843	0.592106	0.732745	0.686018	Sgpl1
GO_BP_m2	GO:006076	positive reg	1/470	45/23843	0.592106	0.732745	0.686018	Mavs
GO_BP_m2	GO:007124	cellular res	1/470	45/23843	0.592106	0.732745	0.686018	Atf4
GO_BP_m2	GO:007130	cellular res	1/470	45/23843	0.592106	0.732745	0.686018	Ptk2b
GO_BP_m2	GO:007138	cellular res	1/470	45/23843	0.592106	0.732745	0.686018	Bmp4
GO_BP_m2	GO:009019	regulation	1/470	45/23843	0.592106	0.732745	0.686018	Pink1
GO_BP_m2	GO:009893	axonal tran	1/470	45/23843	0.592106	0.732745	0.686018	Bloc1s2
GO_BP_m2	GO:190262	regulation	1/470	45/23843	0.592106	0.732745	0.686018	Rac2
GO_BP_m2	GO:001993	cyclic-nucl	3/470	155/23843	0.592169	0.732745	0.686018	Adgrg6/Pe
GO_BP_m2	GO:003286	response to	4/470	209/23843	0.592629	0.732883	0.686147	Cad/Cry1/F
GO_BP_m2	GO:003476	positive reg	4/470	209/23843	0.592629	0.732883	0.686147	Bmp4/Kcnh
GO_BP_m2	GO:000926	ribonucleo	5/470	263/23843	0.594325	0.734764	0.687908	Adsl/Cad/C
GO_BP_m2	GO:000602	aminoglyca	2/470	101/23843	0.594785	0.734899	0.688034	Chst12/Chs
GO_BP_m2	GO:200037	positive reg	2/470	101/23843	0.594785	0.734899	0.688034	Plau/Ptk2b
GO_BP_m2	GO:190161	organic hy	4/470	210/23843	0.596393	0.736487	0.689521	Pcbd1/Ptk2
GO_BP_m2	GO:000660	protein targ	6/470	317/23843	0.596596	0.736487	0.689521	Pex5l/Pink1
GO_BP_m2	GO:001076	regulation	6/470	317/23843	0.596596	0.736487	0.689521	Agrn/Cit/R
GO_BP_m2	GO:000275	immune re	8/470	424/23843	0.599204	0.737849	0.690797	Csk/Ighv1-
GO_BP_m2	GO:000195	regulation	2/470	102/23843	0.600156	0.737849	0.690797	Plau/Ptk2b
GO_BP_m2	GO:000282	positive reg	2/470	102/23843	0.600156	0.737849	0.690797	Il12rb1/Zbt
GO_BP_m2	GO:003355	unsaturate	2/470	102/23843	0.600156	0.737849	0.690797	Cyp2g1/Fa
GO_BP_m2	GO:190401	epithelial c	2/470	102/23843	0.600156	0.737849	0.690797	Bmp4/Six3
GO_BP_m2	GO:000232	natural kille	1/470	46/23843	0.600162	0.737849	0.690797	Ifna4
GO_BP_m2	GO:000317	heart valve	1/470	46/23843	0.600162	0.737849	0.690797	Bmp4

GO_BP_m2	GO:00323	icosanoid s	1/470	46/23843	0.600162	0.737849	0.690797	Acsl4
GO_BP_m2	GO:004542	positive re	1/470	46/23843	0.600162	0.737849	0.690797	Ptk2b
GO_BP_m2	GO:00511	cofactor ca	1/470	46/23843	0.600162	0.737849	0.690797	Pm20d2
GO_BP_m2	GO:00514	regulation	1/470	46/23843	0.600162	0.737849	0.690797	Agrn
GO_BP_m2	GO:007054	response t	1/470	46/23843	0.600162	0.737849	0.690797	Acaca
GO_BP_m2	GO:19026	secondary	1/470	46/23843	0.600162	0.737849	0.690797	Sc5d
GO_BP_m2	GO:19044	positive re	1/470	46/23843	0.600162	0.737849	0.690797	Ptk2b
GO_BP_m2	GO:000691	autophagy	7/470	372/23843	0.601984	0.739656	0.692488	Cym/Lmx1
GO_BP_m2	GO:006191	process uti	7/470	372/23843	0.601984	0.739656	0.692488	Cym/Lmx1
GO_BP_m2	GO:00488	stem cell d	4/470	212/23843	0.603859	0.741122	0.693861	Bmp4/Fox
GO_BP_m2	GO:00514	positive re	4/470	212/23843	0.603859	0.741122	0.693861	Cep120/Pt
GO_BP_m2	GO:00442	cellular car	5/470	266/23843	0.604355	0.741122	0.693861	Fgl1/Mtmr
GO_BP_m2	GO:00463	ribose pho	5/470	266/23843	0.604355	0.741122	0.693861	Adsl/Cad/
GO_BP_m2	GO:00072	Ras protei	8/470	426/23843	0.604499	0.741122	0.693861	Arap3/Aut
GO_BP_m2	GO:00307	cytoskelet	3/470	158/23843	0.605158	0.741122	0.693861	Bloc1s2/Ift
GO_BP_m2	GO:00511	negative re	3/470	158/23843	0.605158	0.741122	0.693861	Aurkb/Id2/
GO_BP_m2	GO:007217	epithelial t	3/470	158/23843	0.605158	0.741122	0.693861	Bmp4/Ift12
GO_BP_m2	GO:003051	regulation	2/470	103/23843	0.605474	0.741122	0.693861	Rab11a/Rn
GO_BP_m2	GO:003241	positive re	2/470	103/23843	0.605474	0.741122	0.693861	Bmp4/Pink
GO_BP_m2	GO:004347	pigmentati	2/470	103/23843	0.605474	0.741122	0.693861	Rack1/Rab
GO_BP_m2	GO:00435	muscle ada	2/470	103/23843	0.605474	0.741122	0.693861	Nr4a3/Twf
GO_BP_m2	GO:00607	regulation	2/470	103/23843	0.605474	0.741122	0.693861	Mavs/Palm
GO_BP_m2	GO:004224	tissue rege	1/470	47/23843	0.608059	0.743203	0.695809	Plau
GO_BP_m2	GO:00435	regulation	1/470	47/23843	0.608059	0.743203	0.695809	Ptk2b
GO_BP_m2	GO:00607	negative re	1/470	47/23843	0.608059	0.743203	0.695809	Palm3
GO_BP_m2	GO:00702	necrotic ce	1/470	47/23843	0.608059	0.743203	0.695809	Hebp2
GO_BP_m2	GO:00985	cellular res	1/470	47/23843	0.608059	0.743203	0.695809	Mavs
GO_BP_m2	GO:00706	leukocyte	6/470	321/23843	0.608765	0.743849	0.696413	Bmp4/Ifna
GO_BP_m2	GO:19016	response t	3/470	159/23843	0.609427	0.744441	0.696968	Acaca/Bmp
GO_BP_m2	GO:00431	proteasom	7/470	375/23843	0.610409	0.744958	0.697452	Derl1/Rack
GO_BP_m2	GO:00091	nucleoside	2/470	104/23843	0.610737	0.744958	0.697452	Ak8/Pfkfb2
GO_BP_m2	GO:00300	cellular mo	2/470	104/23843	0.610737	0.744958	0.697452	Atp6v1h/G
GO_BP_m2	GO:00487	embryonic	2/470	104/23843	0.610737	0.744958	0.697452	Bmp4/Col2
GO_BP_m2	GO:19034	reactive ox	2/470	104/23843	0.610737	0.744958	0.697452	Cybb/Ptk2
GO_BP_m2	GO:000741	axon guida	4/470	214/23843	0.611241	0.745355	0.697824	Agrn/Nr4a
GO_BP_m2	GO:00705	calcium io	5/470	269/23843	0.614243	0.74697	0.699336	Bmp4/Chd
GO_BP_m2	GO:00027	immune re	6/470	323/23843	0.614773	0.74697	0.699336	Csk/Ighv1-
GO_BP_m2	GO:000854	epidermis	6/470	323/23843	0.614773	0.74697	0.699336	Bmp4/Dkk
GO_BP_m2	GO:00027	negative re	1/470	48/23843	0.6158	0.74697	0.699336	Mafb
GO_BP_m2	GO:00105	RNA secon	1/470	48/23843	0.6158	0.74697	0.699336	Ddx3y
GO_BP_m2	GO:00107	fibroblast	1/470	48/23843	0.6158	0.74697	0.699336	Sgpl1
GO_BP_m2	GO:00190	reproducti	1/470	48/23843	0.6158	0.74697	0.699336	Aplp2
GO_BP_m2	GO:003164	regulation	1/470	48/23843	0.6158	0.74697	0.699336	Mtmr2
GO_BP_m2	GO:00439	cellular co	1/470	48/23843	0.6158	0.74697	0.699336	Mtmr2
GO_BP_m2	GO:004512	regulation	1/470	48/23843	0.6158	0.74697	0.699336	Csk
GO_BP_m2	GO:00610	cell differe	1/470	48/23843	0.6158	0.74697	0.699336	Bmp4
GO_BP_m2	GO:009951	vesicle cyt	1/470	48/23843	0.6158	0.74697	0.699336	Bloc1s2
GO_BP_m2	GO:190157	fatty acid d	1/470	48/23843	0.6158	0.74697	0.699336	Hmgcl

GO_BP_m2	GO:200035	regulation	1/470	48/23843	0.6158	0.74697	0.699336	Bmp4
GO_BP_m2	GO:200040	regulation	1/470	48/23843	0.6158	0.74697	0.699336	Ptk2b
GO_BP_m2	GO:000072	double-str	2/470	105/23843	0.615948	0.74697	0.699336	H2afx/Rec
GO_BP_m2	GO:000072	recombina	2/470	105/23843	0.615948	0.74697	0.699336	H2afx/Rec
GO_BP_m2	GO:002198	cerebral co	2/470	105/23843	0.615948	0.74697	0.699336	Cep120/Zb
GO_BP_m2	GO:003031	osteoclast	2/470	105/23843	0.615948	0.74697	0.699336	Farp2/Maf
GO_BP_m2	GO:003109	stress-activ	5/470	270/23843	0.617507	0.748645	0.700904	Gdf6/Nbr1
GO_BP_m2	GO:001620	regulation	3/470	161/23843	0.617871	0.748869	0.701114	Bmp4/Klhl
GO_BP_m2	GO:009748	neuron pro	4/470	216/23843	0.618537	0.749066	0.701298	Agrn/Nr4a
GO_BP_m2	GO:004647	glyceropho	2/470	106/23843	0.621104	0.749066	0.701298	Cdipt/Pigm
GO_BP_m2	GO:199026	neutrophil	2/470	106/23843	0.621104	0.749066	0.701298	Pde4d/Rac
GO_BP_m2	GO:007252	purine-con	9/470	486/23843	0.621877	0.749066	0.701298	Adsl/Rack1
GO_BP_m2	GO:003087	mammary	3/470	162/23843	0.622046	0.749066	0.701298	Bmp4/Id2/
GO_BP_m2	GO:000195	positive re	1/470	49/23843	0.623389	0.749066	0.701298	Ptk2b
GO_BP_m2	GO:000204	cell migrati	1/470	49/23843	0.623389	0.749066	0.701298	Pdcd10
GO_BP_m2	GO:001033	response t	1/470	49/23843	0.623389	0.749066	0.701298	H2afx
GO_BP_m2	GO:001066	regulation	1/470	49/23843	0.623389	0.749066	0.701298	Sfrp2
GO_BP_m2	GO:001587	dopamine	1/470	49/23843	0.623389	0.749066	0.701298	Pink1
GO_BP_m2	GO:001657	histone ph	1/470	49/23843	0.623389	0.749066	0.701298	Aurkb
GO_BP_m2	GO:001714	stem cell d	1/470	49/23843	0.623389	0.749066	0.701298	Sfrp2
GO_BP_m2	GO:003019	negative re	1/470	49/23843	0.623389	0.749066	0.701298	Plau
GO_BP_m2	GO:003083	regulation	1/470	49/23843	0.623389	0.749066	0.701298	Twf1
GO_BP_m2	GO:003101	endocrine	1/470	49/23843	0.623389	0.749066	0.701298	Bmp4
GO_BP_m2	GO:003111	regulation	1/470	49/23843	0.623389	0.749066	0.701298	Dyrk1a
GO_BP_m2	GO:003248	positive re	1/470	49/23843	0.623389	0.749066	0.701298	Mavs
GO_BP_m2	GO:003264	regulation	1/470	49/23843	0.623389	0.749066	0.701298	Mavs
GO_BP_m2	GO:003296	collagen bi	1/470	49/23843	0.623389	0.749066	0.701298	Bmp4
GO_BP_m2	GO:004329	apical junc	1/470	49/23843	0.623389	0.749066	0.701298	Ect2
GO_BP_m2	GO:004405	regulation	1/470	49/23843	0.623389	0.749066	0.701298	Acat2
GO_BP_m2	GO:004501	actin nucle	1/470	49/23843	0.623389	0.749066	0.701298	Spire2
GO_BP_m2	GO:004568	positive re	1/470	49/23843	0.623389	0.749066	0.701298	Id2
GO_BP_m2	GO:005077	positive re	1/470	49/23843	0.623389	0.749066	0.701298	Ss18l1
GO_BP_m2	GO:005114	negative re	1/470	49/23843	0.623389	0.749066	0.701298	Foxo4
GO_BP_m2	GO:005502	positive re	1/470	49/23843	0.623389	0.749066	0.701298	Bmp4
GO_BP_m2	GO:006042	lung epithe	1/470	49/23843	0.623389	0.749066	0.701298	Bmp4
GO_BP_m2	GO:007097	protein loc	1/470	49/23843	0.623389	0.749066	0.701298	Sec63
GO_BP_m2	GO:190004	negative re	1/470	49/23843	0.623389	0.749066	0.701298	Plau
GO_BP_m2	GO:190526	negative re	1/470	49/23843	0.623389	0.749066	0.701298	Kdm3a
GO_BP_m2	GO:003297	regulation	7/470	380/23843	0.624239	0.749873	0.702053	Cit/Frmd6/
GO_BP_m2	GO:003288	regulation	4/470	218/23843	0.625748	0.750733	0.702859	Agrn/Cep1
GO_BP_m2	GO:000828	insulin rece	2/470	107/23843	0.626207	0.750733	0.702859	Foxo4/Shc
GO_BP_m2	GO:000834	adult locom	2/470	107/23843	0.626207	0.750733	0.702859	Chd7/Id2
GO_BP_m2	GO:004662	regulation	2/470	107/23843	0.626207	0.750733	0.702859	Lats2/Serp
GO_BP_m2	GO:004881	regulation	2/470	107/23843	0.626207	0.750733	0.702859	Cit/Ss18l1
GO_BP_m2	GO:005158	regulation	2/470	107/23843	0.626207	0.750733	0.702859	Cplx4/Stxb
GO_BP_m2	GO:190382	negative re	2/470	107/23843	0.626207	0.750733	0.702859	Csk/Ube2j1
GO_BP_m2	GO:005071	positive re	5/470	273/23843	0.6272	0.751709	0.703773	Glul/Mavs/
GO_BP_m2	GO:001000	glial cell di	4/470	219/23843	0.62932	0.753689	0.705626	Adgrg6/Bm

GO_BP_m2	GO:190186	regulation	3/470	164/23843	0.630304	0.753689	0.705626	Bmp4/Klhl4
GO_BP_m2	GO:000914	nucleoside	5/470	274/23843	0.630399	0.753689	0.705626	Ak8/Cad/P
GO_BP_m2	GO:000028	nuclear-tra	1/470	50/23843	0.630828	0.753689	0.705626	Exosc2
GO_BP_m2	GO:001051	regulation	1/470	50/23843	0.630828	0.753689	0.705626	Sele
GO_BP_m2	GO:003221	regulation	1/470	50/23843	0.630828	0.753689	0.705626	Aurkb
GO_BP_m2	GO:003362	cell adhesi	1/470	50/23843	0.630828	0.753689	0.705626	Plau
GO_BP_m2	GO:003530	positive reg	1/470	50/23843	0.630828	0.753689	0.705626	Pink1
GO_BP_m2	GO:004298	amyloid pr	1/470	50/23843	0.630828	0.753689	0.705626	Dyrk1a
GO_BP_m2	GO:004394	regulation	1/470	50/23843	0.630828	0.753689	0.705626	Pex5l
GO_BP_m2	GO:004870	embryonic	1/470	50/23843	0.630828	0.753689	0.705626	Bmp4
GO_BP_m2	GO:000282	positive reg	2/470	108/23843	0.631257	0.753771	0.705703	Il12rb1/Zb
GO_BP_m2	GO:000634	chromatin	2/470	108/23843	0.631257	0.753771	0.705703	H2afx/Rrp8
GO_BP_m2	GO:001503	skeletal sys	9/470	490/23843	0.631559	0.753918	0.70584	Bmp4/Chd
GO_BP_m2	GO:004863	regulation	3/470	165/23843	0.634386	0.757077	0.708798	Bmp4/Klhl4
GO_BP_m2	GO:000276	immune re	8/470	438/23843	0.635501	0.757655	0.70934	Csk/Ighv1-
GO_BP_m2	GO:000018	activation c	2/470	109/23843	0.636253	0.757655	0.70934	Muc20/Shc
GO_BP_m2	GO:000173	establishm	1/470	51/23843	0.638121	0.757655	0.70934	Sfrp2
GO_BP_m2	GO:000189	retina hom	1/470	51/23843	0.638121	0.757655	0.70934	Crocc
GO_BP_m2	GO:000197	blood vess	1/470	51/23843	0.638121	0.757655	0.70934	Chd7
GO_BP_m2	GO:000752	neuromusc	1/470	51/23843	0.638121	0.757655	0.70934	Agrn
GO_BP_m2	GO:001066	regulation	1/470	51/23843	0.638121	0.757655	0.70934	Sfrp2
GO_BP_m2	GO:001082	negative re	1/470	51/23843	0.638121	0.757655	0.70934	Pink1
GO_BP_m2	GO:003260	interferon-	1/470	51/23843	0.638121	0.757655	0.70934	Mavs
GO_BP_m2	GO:003272	negative re	1/470	51/23843	0.638121	0.757655	0.70934	Syt11
GO_BP_m2	GO:003508	establishm	1/470	51/23843	0.638121	0.757655	0.70934	Ooep
GO_BP_m2	GO:004560	regulation	1/470	51/23843	0.638121	0.757655	0.70934	Bmp4
GO_BP_m2	GO:004577	positive reg	1/470	51/23843	0.638121	0.757655	0.70934	Rab11a
GO_BP_m2	GO:004824	lymphocyte	1/470	51/23843	0.638121	0.757655	0.70934	Ptk2b
GO_BP_m2	GO:005081	negative re	1/470	51/23843	0.638121	0.757655	0.70934	Plau
GO_BP_m2	GO:006124	establishm	1/470	51/23843	0.638121	0.757655	0.70934	Ooep
GO_BP_m2	GO:007171	icosanoid t	1/470	51/23843	0.638121	0.757655	0.70934	Acsl4
GO_BP_m2	GO:190157	fatty acid d	1/470	51/23843	0.638121	0.757655	0.70934	Acsl4
GO_BP_m2	GO:000664	phospholip	6/470	332/23843	0.641159	0.760661	0.712154	Cdipt/Fam1
GO_BP_m2	GO:005126	protein dep	2/470	110/23843	0.641196	0.760661	0.712154	Sh3gl1/Twf
GO_BP_m2	GO:200004	regulation	2/470	110/23843	0.641196	0.760661	0.712154	Id2/Zc3h12
GO_BP_m2	GO:000610	regulation	3/470	167/23843	0.642455	0.760975	0.712448	Fgl1/Pfkfb2
GO_BP_m2	GO:000995	anterior/pc	4/470	223/23843	0.643392	0.760975	0.712448	Bmp4/Lfng
GO_BP_m2	GO:000726	small GTPa	9/470	495/23843	0.643472	0.760975	0.712448	Arap3/Auts
GO_BP_m2	GO:000716	establishm	1/470	52/23843	0.645269	0.760975	0.712448	Sfrp2
GO_BP_m2	GO:000761	mating	1/470	52/23843	0.645269	0.760975	0.712448	Aplp2
GO_BP_m2	GO:001612	sterol biosy	1/470	52/23843	0.645269	0.760975	0.712448	Sc5d
GO_BP_m2	GO:003080	positive reg	1/470	52/23843	0.645269	0.760975	0.712448	Rack1
GO_BP_m2	GO:003085	prostate gl	1/470	52/23843	0.645269	0.760975	0.712448	Bmp4
GO_BP_m2	GO:004339	negative re	1/470	52/23843	0.645269	0.760975	0.712448	Id2
GO_BP_m2	GO:004353	positive reg	1/470	52/23843	0.645269	0.760975	0.712448	Angpt4
GO_BP_m2	GO:004559	negative re	1/470	52/23843	0.645269	0.760975	0.712448	Tgfb1i1
GO_BP_m2	GO:004577	positive reg	1/470	52/23843	0.645269	0.760975	0.712448	Id2
GO_BP_m2	GO:004583	negative re	1/470	52/23843	0.645269	0.760975	0.712448	Bmp4

GO_BP_m2	GO:004667	negative re	1/470	52/23843	0.645269	0.760975	0.712448	Ucp2
GO_BP_m2	GO:00488	genitalia d	1/470	52/23843	0.645269	0.760975	0.712448	Chd7
GO_BP_m2	GO:00700	chemokine	1/470	52/23843	0.645269	0.760975	0.712448	Ptk2b
GO_BP_m2	GO:007252	pyrimidine	1/470	52/23843	0.645269	0.760975	0.712448	Cad
GO_BP_m2	GO:007257	endothelial	1/470	52/23843	0.645269	0.760975	0.712448	Bmp4
GO_BP_m2	GO:007267	T cell migr	1/470	52/23843	0.645269	0.760975	0.712448	Myo1g
GO_BP_m2	GO:19035	negative re	1/470	52/23843	0.645269	0.760975	0.712448	Syt11
GO_BP_m2	GO:19052	regulation	1/470	52/23843	0.645269	0.760975	0.712448	Bmp4
GO_BP_m2	GO:004274	defense re	8/470	442/23843	0.645531	0.76107	0.712536	Defb37/Igh
GO_BP_m2	GO:000194	hair follicle	2/470	111/23843	0.646086	0.761297	0.712749	Dkk4/Nsun
GO_BP_m2	GO:190121	positive re	2/470	111/23843	0.646086	0.761297	0.712749	Agrn/Atf4
GO_BP_m2	GO:00066	icosanoid r	2/470	112/23843	0.650923	0.763916	0.715201	Cyp2g1/Fa
GO_BP_m2	GO:00343	adherens j	2/470	112/23843	0.650923	0.763916	0.715201	Csk/Ptk2b
GO_BP_m2	GO:00420	cytokine bi	2/470	112/23843	0.650923	0.763916	0.715201	Cybb/Ube
GO_BP_m2	GO:004581	negative re	2/470	112/23843	0.650923	0.763916	0.715201	H2afx/Rrp
GO_BP_m2	GO:00017	neural cres	1/470	53/23843	0.652277	0.763916	0.715201	Bmp4
GO_BP_m2	GO:000254	monocyte	1/470	53/23843	0.652277	0.763916	0.715201	S100a14
GO_BP_m2	GO:000304	regulation	1/470	53/23843	0.652277	0.763916	0.715201	Rasl10b
GO_BP_m2	GO:000994	anterior/pc	1/470	53/23843	0.652277	0.763916	0.715201	Bmp4
GO_BP_m2	GO:00106	cardiac mu	1/470	53/23843	0.652277	0.763916	0.715201	Sfrp2
GO_BP_m2	GO:00159	long-chain	1/470	53/23843	0.652277	0.763916	0.715201	Slc27a2
GO_BP_m2	GO:003004	actin filam	1/470	53/23843	0.652277	0.763916	0.715201	Twf1
GO_BP_m2	GO:00350	regulation	1/470	53/23843	0.652277	0.763916	0.715201	Auts2
GO_BP_m2	GO:00425	positive re	1/470	53/23843	0.652277	0.763916	0.715201	Csf2
GO_BP_m2	GO:00427	exogenous	1/470	53/23843	0.652277	0.763916	0.715201	Cyp2g1
GO_BP_m2	GO:00465	negative re	1/470	53/23843	0.652277	0.763916	0.715201	Arap3
GO_BP_m2	GO:004662	positive re	1/470	53/23843	0.652277	0.763916	0.715201	Serp1
GO_BP_m2	GO:00519	synaptic tr	1/470	53/23843	0.652277	0.763916	0.715201	Stxbp1
GO_BP_m2	GO:005501	ventricular	1/470	53/23843	0.652277	0.763916	0.715201	Chd7
GO_BP_m2	GO:190101	regulation	1/470	53/23843	0.652277	0.763916	0.715201	Agrn
GO_BP_m2	GO:19027	negative re	1/470	53/23843	0.652277	0.763916	0.715201	Foxo4
GO_BP_m2	GO:200064	positive re	1/470	53/23843	0.652277	0.763916	0.715201	Bmp4
GO_BP_m2	GO:000941	response t	5/470	281/23843	0.652315	0.763916	0.715201	Aurkb/Cry1
GO_BP_m2	GO:19029	regulation	6/470	336/23843	0.652534	0.76396	0.715242	Cit/Dyrk1a
GO_BP_m2	GO:000664	membrane	3/470	170/23843	0.654323	0.765413	0.716603	Gba2/Pigm
GO_BP_m2	GO:00069	compleme	3/470	170/23843	0.654323	0.765413	0.716603	Ighv1-23/I
GO_BP_m2	GO:00224	negative re	3/470	170/23843	0.654323	0.765413	0.716603	Bmp4/Prka
GO_BP_m2	GO:00086	apoptotic r	2/470	113/23843	0.655708	0.766179	0.71732	Bloc1s2/Pi
GO_BP_m2	GO:00109	regulation	2/470	113/23843	0.655708	0.766179	0.71732	Fgl1/Pfkfb
GO_BP_m2	GO:003572	sodium ior	2/470	113/23843	0.655708	0.766179	0.71732	Agrn/Gpd1
GO_BP_m2	GO:009877	skin epider	2/470	113/23843	0.655708	0.766179	0.71732	Dkk4/Nsun
GO_BP_m2	GO:007137	cellular res	4/470	227/23843	0.657109	0.767603	0.718653	Csk/Foxo4/
GO_BP_m2	GO:004561	regulation	3/470	171/23843	0.658215	0.768486	0.719479	Bmp4/Id2/
GO_BP_m2	GO:00075	respiratory	1/470	54/23843	0.659147	0.768486	0.719479	Mafb
GO_BP_m2	GO:001052	positive re	1/470	54/23843	0.659147	0.768486	0.719479	Bmp4
GO_BP_m2	GO:00108	positive re	1/470	54/23843	0.659147	0.768486	0.719479	Nr4a3
GO_BP_m2	GO:003501	somatic ste	1/470	54/23843	0.659147	0.768486	0.719479	Vps72
GO_BP_m2	GO:00482	positive re	1/470	54/23843	0.659147	0.768486	0.719479	Sele

GO_BP_m2	GO:006019	positive reg	1/470	54/23843	0.659147	0.768486	0.719479	Sele
GO_BP_m2	GO:004217	negative re	2/470	114/23843	0.66044	0.769352	0.72029	Alad/Ube2
GO_BP_m2	GO:005115	regulation	2/470	114/23843	0.66044	0.769352	0.72029	Bmp4/Cd5
GO_BP_m2	GO:009917	postsynaps	2/470	114/23843	0.66044	0.769352	0.72029	Agrn/Mtm
GO_BP_m2	GO:003514	tube forma	3/470	172/23843	0.662076	0.771044	0.721875	Bmp4/Ift12
GO_BP_m2	GO:006888	ER to Golg	2/470	115/23843	0.66512	0.773329	0.724014	Tmed4/Tra
GO_BP_m2	GO:007055	mitotic spir	2/470	115/23843	0.66512	0.773329	0.724014	Aurkb/Rab
GO_BP_m2	GO:003629	cellular res	2/470	115/23843	0.66512	0.773329	0.724014	Cybb/Pink1
GO_BP_m2	GO:006628	nucleotide-	1/470	55/23843	0.665881	0.773329	0.724014	Gtf2h1
GO_BP_m2	GO:007090	metaphase	1/470	55/23843	0.665881	0.773329	0.724014	Cit
GO_BP_m2	GO:001065	striated mu	1/470	55/23843	0.665881	0.773329	0.724014	Sfrp2
GO_BP_m2	GO:004574	negative re	1/470	55/23843	0.665881	0.773329	0.724014	Cry1
GO_BP_m2	GO:004642	negative re	1/470	55/23843	0.665881	0.773329	0.724014	Suz12
GO_BP_m2	GO:004657	positive reg	1/470	55/23843	0.665881	0.773329	0.724014	Auts2
GO_BP_m2	GO:190489	negative re	1/470	55/23843	0.665881	0.773329	0.724014	Suz12
GO_BP_m2	GO:200123	regulation	7/470	396/23843	0.666605	0.773955	0.7246	Bmp4/Col2
GO_BP_m2	GO:006029	long-term	4/470	230/23843	0.667161	0.774387	0.725004	Mir129-2/
GO_BP_m2	GO:005134	negative re	7/470	397/23843	0.669154	0.7761	0.726609	Agrn/Amb
GO_BP_m2	GO:007127	meiosis I	2/470	116/23843	0.669747	0.7761	0.726609	Eif4g3/Espl
GO_BP_m2	GO:001490	myotube d	2/470	116/23843	0.669747	0.7761	0.726609	Cd53/Klhl4
GO_BP_m2	GO:001569	ammonium	2/470	116/23843	0.669747	0.7761	0.726609	Csf2/Pink1
GO_BP_m2	GO:004210	cytokine m	2/470	116/23843	0.669747	0.7761	0.726609	Cybb/Ube2
GO_BP_m2	GO:005170	interaction	2/470	116/23843	0.669747	0.7761	0.726609	Chmp3/Ts
GO_BP_m2	GO:000175	eye photor	1/470	56/23843	0.672483	0.777766	0.728168	Rom1
GO_BP_m2	GO:000206	glandular e	1/470	56/23843	0.672483	0.777766	0.728168	Bmp4
GO_BP_m2	GO:001096	regulation	1/470	56/23843	0.672483	0.777766	0.728168	Cit
GO_BP_m2	GO:003556	non-canor	1/470	56/23843	0.672483	0.777766	0.728168	Sfrp2
GO_BP_m2	GO:004478	metaphase	1/470	56/23843	0.672483	0.777766	0.728168	Cit
GO_BP_m2	GO:004512	cellular ext	1/470	56/23843	0.672483	0.777766	0.728168	Sele
GO_BP_m2	GO:009039	cellular sen	1/470	56/23843	0.672483	0.777766	0.728168	Id2
GO_BP_m2	GO:000681	calcium ior	7/470	399/23843	0.674215	0.779555	0.729843	Bmp4/Chd
GO_BP_m2	GO:007388	pattern spe	8/470	454/23843	0.674658	0.779853	0.730122	Bmp4/Ift12
GO_BP_m2	GO:006666	sphingolipi	2/470	118/23843	0.678848	0.783308	0.733356	Gba2/Sgpl
GO_BP_m2	GO:006198	meiosis I ce	2/470	118/23843	0.678848	0.783308	0.733356	Eif4g3/Espl
GO_BP_m2	GO:001046	mesenchyr	1/470	57/23843	0.678954	0.783308	0.733356	Bmp4
GO_BP_m2	GO:004346	regulation	1/470	57/23843	0.678954	0.783308	0.733356	Agrn
GO_BP_m2	GO:004800	platelet-de	1/470	57/23843	0.678954	0.783308	0.733356	Sgpl1
GO_BP_m2	GO:190342	positive reg	1/470	57/23843	0.678954	0.783308	0.733356	Ptk2b
GO_BP_m2	GO:200013	negative re	1/470	57/23843	0.678954	0.783308	0.733356	Zc3h12d
GO_BP_m2	GO:001050	regulation	4/470	234/23843	0.680248	0.784586	0.734552	Lmx1b/Pin
GO_BP_m2	GO:000008	G1/S transi	3/470	177/23843	0.680907	0.784913	0.734859	Id2/Lats2/Z
GO_BP_m2	GO:199013	neuron prc	3/470	177/23843	0.680907	0.784913	0.734859	Auts2/Rab1
GO_BP_m2	GO:004440	symbiont p	6/470	347/23843	0.682658	0.786532	0.736375	Chmp3/Ma
GO_BP_m2	GO:003243	regulation	2/470	119/23843	0.68332	0.786532	0.736375	Rack1/Cop
GO_BP_m2	GO:000244	leukocyte r	8/470	458/23843	0.684037	0.786532	0.736375	Ighv1-23/I
GO_BP_m2	GO:000201	morphoger	1/470	58/23843	0.685298	0.786532	0.736375	Pdcd10
GO_BP_m2	GO:000715	heterophili	1/470	58/23843	0.685298	0.786532	0.736375	Sele
GO_BP_m2	GO:003083	negative re	1/470	58/23843	0.685298	0.786532	0.736375	Twf1

GO_BP_m2	GO:004277	mitochond	1/470	58/23843	0.685298	0.786532	0.736375	Pink1
GO_BP_m2	GO:004685	regulation	1/470	58/23843	0.685298	0.786532	0.736375	Csk
GO_BP_m2	GO:004828	lung alveol	1/470	58/23843	0.685298	0.786532	0.736375	Bmp4
GO_BP_m2	GO:005043	regulation	1/470	58/23843	0.685298	0.786532	0.736375	Pink1
GO_BP_m2	GO:005071	negative re	1/470	58/23843	0.685298	0.786532	0.736375	Syt11
GO_BP_m2	GO:006003	cardiac mu	1/470	58/23843	0.685298	0.786532	0.736375	Prkar1a
GO_BP_m2	GO:006044	mammary	1/470	58/23843	0.685298	0.786532	0.736375	Bmp4
GO_BP_m2	GO:009018	regulation	1/470	58/23843	0.685298	0.786532	0.736375	Bmp4
GO_BP_m2	GO:190330	positive re	1/470	58/23843	0.685298	0.786532	0.736375	Stxbp1
GO_BP_m2	GO:000110	response t	6/470	348/23843	0.68531	0.786532	0.736375	Acaca/Mir3
GO_BP_m2	GO:000181	positive re	7/470	404/23843	0.686655	0.787861	0.737619	Atf4/Csf2/C
GO_BP_m2	GO:001092	regulation	2/470	120/23843	0.687742	0.788676	0.738382	Elfn2/Ell
GO_BP_m2	GO:190353	regulation	2/470	120/23843	0.687742	0.788676	0.738382	Pink1/Rac2
GO_BP_m2	GO:003133	regulation	1/470	59/23843	0.691516	0.790843	0.740411	Stxbp1
GO_BP_m2	GO:003267	regulation	1/470	59/23843	0.691516	0.790843	0.740411	Mavs
GO_BP_m2	GO:003272	positive re	1/470	59/23843	0.691516	0.790843	0.740411	Mavs
GO_BP_m2	GO:004612	purine ribo	1/470	59/23843	0.691516	0.790843	0.740411	Ran
GO_BP_m2	GO:004684	filopodium	1/470	59/23843	0.691516	0.790843	0.740411	Agrn
GO_BP_m2	GO:005105	negative re	1/470	59/23843	0.691516	0.790843	0.740411	Arap3
GO_BP_m2	GO:005130	mitotic sist	1/470	59/23843	0.691516	0.790843	0.740411	Cit
GO_BP_m2	GO:006071	labyrinthin	1/470	59/23843	0.691516	0.790843	0.740411	Erf
GO_BP_m2	GO:007023	T cell apop	1/470	59/23843	0.691516	0.790843	0.740411	Bmp4
GO_BP_m2	GO:009700	regulation	1/470	59/23843	0.691516	0.790843	0.740411	Csk
GO_BP_m2	GO:005085	B cell recep	3/470	180/23843	0.691826	0.790981	0.74054	Ighv1-23/I
GO_BP_m2	GO:000222	pattern rec	2/470	121/23843	0.692113	0.791094	0.740646	Mavs/S100
GO_BP_m2	GO:005114	striated mu	5/470	295/23843	0.693604	0.792582	0.742039	Bmp4/Cd5
GO_BP_m2	GO:014001	meiotic nu	3/470	181/23843	0.695402	0.793919	0.743291	Eif4g3/Espl
GO_BP_m2	GO:000699	nucleus org	2/470	122/23843	0.696434	0.793919	0.743291	H3f3b/Kdm
GO_BP_m2	GO:000270	regulation	1/470	60/23843	0.697612	0.793919	0.743291	Zbtb1
GO_BP_m2	GO:000276	positive re	1/470	60/23843	0.697612	0.793919	0.743291	Id2
GO_BP_m2	GO:000627	RNA-depe	1/470	60/23843	0.697612	0.793919	0.743291	Aurkb
GO_BP_m2	GO:000685	drug transr	1/470	60/23843	0.697612	0.793919	0.743291	Slc25a38
GO_BP_m2	GO:000700	telomere m	1/470	60/23843	0.697612	0.793919	0.743291	Aurkb
GO_BP_m2	GO:000759	lactation	1/470	60/23843	0.697612	0.793919	0.743291	Prl8a2
GO_BP_m2	GO:000808	axo-dendr	1/470	60/23843	0.697612	0.793919	0.743291	Bloc1s2
GO_BP_m2	GO:003439	protein loc	1/470	60/23843	0.697612	0.793919	0.743291	Gpd1l
GO_BP_m2	GO:004477	mitotic DN	1/470	60/23843	0.697612	0.793919	0.743291	Foxo4
GO_BP_m2	GO:005119	regulation	1/470	60/23843	0.697612	0.793919	0.743291	Pink1
GO_BP_m2	GO:007005	intrinsic ap	1/470	60/23843	0.697612	0.793919	0.743291	Atf4
GO_BP_m2	GO:190581	regulation	1/470	60/23843	0.697612	0.793919	0.743291	Cit
GO_BP_m2	GO:200075	regulation	1/470	60/23843	0.697612	0.793919	0.743291	Auts2
GO_BP_m2	GO:004875	branching	3/470	182/23843	0.698948	0.795223	0.744512	Bmp4/Fkbp
GO_BP_m2	GO:004870	skeletal sys	4/470	240/23843	0.699198	0.795293	0.744577	Bmp4/Col2
GO_BP_m2	GO:000275	innate imm	2/470	123/23843	0.700704	0.796358	0.745575	Mavs/S100
GO_BP_m2	GO:000276	regulation	2/470	123/23843	0.700704	0.796358	0.745575	Id2/Mafb
GO_BP_m2	GO:190280	regulation	2/470	123/23843	0.700704	0.796358	0.745575	Id2/Zc3h12
GO_BP_m2	GO:006201	positive re	3/470	183/23843	0.702461	0.79726	0.746419	Rack1/Nr4a
GO_BP_m2	GO:200102	regulation	3/470	183/23843	0.702461	0.79726	0.746419	Cry1/Dyrk1

GO_BP_m2	GO:00510	regulation	7/470	411/23843	0.703557	0.79726	0.746419	Aurkb/Bmp
GO_BP_m2	GO:001067	positive re	1/470	61/23843	0.703588	0.79726	0.746419	Pfkfb2
GO_BP_m2	GO:00108	regulation	1/470	61/23843	0.703588	0.79726	0.746419	Cd53
GO_BP_m2	GO:00316	zymogen a	1/470	61/23843	0.703588	0.79726	0.746419	Plau
GO_BP_m2	GO:00504	catecholam	1/470	61/23843	0.703588	0.79726	0.746419	Pink1
GO_BP_m2	GO:00515	response t	1/470	61/23843	0.703588	0.79726	0.746419	Jund
GO_BP_m2	GO:00712	cellular res	1/470	61/23843	0.703588	0.79726	0.746419	Mir760
GO_BP_m2	GO:19028	negative re	1/470	61/23843	0.703588	0.79726	0.746419	Zc3h12d
GO_BP_m2	GO:200124	positive re	1/470	61/23843	0.703588	0.79726	0.746419	Rack1
GO_BP_m2	GO:007037	positive re	4/470	242/23843	0.705333	0.799022	0.748068	Bmp4/Fgfb
GO_BP_m2	GO:00024	humoral in	3/470	184/23843	0.705944	0.799354	0.74838	Ighv1-23/I
GO_BP_m2	GO:00026	regulation	6/470	356/23843	0.706008	0.799354	0.74838	Il12rb1/Ma
GO_BP_m2	GO:00310	regeneratio	2/470	125/23843	0.709095	0.800225	0.749194	Plau/Sulf2
GO_BP_m2	GO:00007	syncytium	1/470	62/23843	0.709446	0.800225	0.749194	Cd53
GO_BP_m2	GO:00018	release of	1/470	62/23843	0.709446	0.800225	0.749194	Pink1
GO_BP_m2	GO:000924	glycolipid	1/470	62/23843	0.709446	0.800225	0.749194	Pigm
GO_BP_m2	GO:001591	phospholip	1/470	62/23843	0.709446	0.800225	0.749194	Osbpl5
GO_BP_m2	GO:004277	ATP synthe	1/470	62/23843	0.709446	0.800225	0.749194	Pink1
GO_BP_m2	GO:004514	homologou	1/470	62/23843	0.709446	0.800225	0.749194	Espl1
GO_BP_m2	GO:004542	regulation	1/470	62/23843	0.709446	0.800225	0.749194	Ptk2b
GO_BP_m2	GO:00510	positive re	1/470	62/23843	0.709446	0.800225	0.749194	Auts2
GO_BP_m2	GO:009027	negative re	1/470	62/23843	0.709446	0.800225	0.749194	Ucp2
GO_BP_m2	GO:19012	carbohydra	1/470	62/23843	0.709446	0.800225	0.749194	Slc35a4
GO_BP_m2	GO:190367	regulation	1/470	62/23843	0.709446	0.800225	0.749194	Pdcd10
GO_BP_m2	GO:200024	negative re	1/470	62/23843	0.709446	0.800225	0.749194	Bmp4
GO_BP_m2	GO:200037	negative re	1/470	62/23843	0.709446	0.800225	0.749194	Pink1
GO_BP_m2	GO:00066	fatty acid b	2/470	126/23843	0.713217	0.804262	0.752974	Acaca/Fads
GO_BP_m2	GO:00016	branching	1/470	63/23843	0.715188	0.805187	0.75384	Bmp4
GO_BP_m2	GO:000931	oligosacch	1/470	63/23843	0.715188	0.805187	0.75384	Galnt2
GO_BP_m2	GO:00421	positive re	1/470	63/23843	0.715188	0.805187	0.75384	Cybb
GO_BP_m2	GO:004227	purine nuc	1/470	63/23843	0.715188	0.805187	0.75384	Ran
GO_BP_m2	GO:00439	histone H4	1/470	63/23843	0.715188	0.805187	0.75384	Auts2
GO_BP_m2	GO:00454	cell redox	1/470	63/23843	0.715188	0.805187	0.75384	Txndc5
GO_BP_m2	GO:00069	compleme	3/470	187/23843	0.716205	0.805899	0.754506	Ighv1-23/I
GO_BP_m2	GO:00162	macroauto	3/470	187/23843	0.716205	0.805899	0.754506	Nbr1/Pink1
GO_BP_m2	GO:00027	positive re	2/470	127/23843	0.717289	0.806902	0.755446	Stxbp1/Zbt
GO_BP_m2	GO:002191	neural tube	3/470	188/23843	0.719563	0.80881	0.757232	Bmp4/Ift12
GO_BP_m2	GO:005067	positive re	3/470	188/23843	0.719563	0.80881	0.757232	Bmp4/Glul
GO_BP_m2	GO:00517	regulation	3/470	188/23843	0.719563	0.80881	0.757232	Bmp4/Cit/
GO_BP_m2	GO:006054	respiratory	4/470	247/23843	0.720272	0.808826	0.757248	Bmp4/Ceb
GO_BP_m2	GO:000694	syncytium	1/470	64/23843	0.720818	0.808826	0.757248	Cd53
GO_BP_m2	GO:00313	negative re	1/470	64/23843	0.720818	0.808826	0.757248	Cry1
GO_BP_m2	GO:00326	interleukin	1/470	64/23843	0.720818	0.808826	0.757248	Mavs
GO_BP_m2	GO:00517	negative re	1/470	64/23843	0.720818	0.808826	0.757248	Bmp4
GO_BP_m2	GO:006042	lung morph	1/470	64/23843	0.720818	0.808826	0.757248	Bmp4
GO_BP_m2	GO:00550	cardiac mu	2/470	128/23843	0.721313	0.808826	0.757248	Bmp4/Myh
GO_BP_m2	GO:00714	cellular res	2/470	128/23843	0.721313	0.808826	0.757248	Cybb/Pink
GO_BP_m2	GO:20012	negative re	2/470	128/23843	0.721313	0.808826	0.757248	H3f3b/Kdm

GO_BP_m2	GO:00071	cell-matrix	3/470	189/23843	0.72289	0.80973	0.758093	Plau/Ptk2b
GO_BP_m2	GO:001081	regulation	3/470	189/23843	0.72289	0.80973	0.758093	Plau/Ptk2b
GO_BP_m2	GO:19029	positive re	3/470	189/23843	0.72289	0.80973	0.758093	Ptk2b/Rac
GO_BP_m2	GO:19030	positive re	3/470	189/23843	0.72289	0.80973	0.758093	Il12rb1/Nr
GO_BP_m2	GO:00224	regulation	6/470	363/23843	0.723347	0.809809	0.758168	Bmp4/Il12r
GO_BP_m2	GO:00324	response t	6/470	363/23843	0.723347	0.809809	0.758168	Jund/Mir1
GO_BP_m2	GO:00091	nucleotide	5/470	306/23843	0.723609	0.809886	0.75824	Adsl/Cad/
GO_BP_m2	GO:004484	cell cycle G	3/470	190/23843	0.726187	0.811639	0.759881	Id2/Lats2/
GO_BP_m2	GO:000271	regulation	1/470	65/23843	0.726336	0.811639	0.759881	Nr4a3
GO_BP_m2	GO:00105	negative re	1/470	65/23843	0.726336	0.811639	0.759881	Pink1
GO_BP_m2	GO:00350	axoneme a	1/470	65/23843	0.726336	0.811639	0.759881	Mss51
GO_BP_m2	GO:004477	mitotic DN	1/470	65/23843	0.726336	0.811639	0.759881	Foxo4
GO_BP_m2	GO:00481	regulation	1/470	65/23843	0.726336	0.811639	0.759881	Rab11a
GO_BP_m2	GO:00550	lipid home	2/470	130/23843	0.729216	0.81464	0.762691	Acaca/Ceb
GO_BP_m2	GO:00098	embryonic	1/470	66/23843	0.731745	0.816675	0.764596	Ooep
GO_BP_m2	GO:001991	lipid stora	1/470	66/23843	0.731745	0.816675	0.764596	Cry1
GO_BP_m2	GO:190357	regulation	1/470	66/23843	0.731745	0.816675	0.764596	Pink1
GO_BP_m2	GO:00091	ribonucleo	4/470	251/23843	0.731816	0.816675	0.764596	Cad/Pfkfb
GO_BP_m2	GO:00092	ribonucleo	2/470	131/23843	0.733095	0.817886	0.765729	Cad/Pfkfb
GO_BP_m2	GO:00015	regulation	5/470	310/23843	0.733984	0.81866	0.766454	Cplx4/Ptk2
GO_BP_m2	GO:000694	regulation	1/470	67/23843	0.737048	0.820332	0.768019	Shc1
GO_BP_m2	GO:000704	cell-substr	1/470	67/23843	0.737048	0.820332	0.768019	Ptk2b
GO_BP_m2	GO:00323	negative re	1/470	67/23843	0.737048	0.820332	0.768019	Ube2j1
GO_BP_m2	GO:003304	regulation	1/470	67/23843	0.737048	0.820332	0.768019	Cit
GO_BP_m2	GO:00341	homotypic	1/470	67/23843	0.737048	0.820332	0.768019	Stxbp1
GO_BP_m2	GO:004804	focal adhe	1/470	67/23843	0.737048	0.820332	0.768019	Ptk2b
GO_BP_m2	GO:19048	cranial skel	1/470	67/23843	0.737048	0.820332	0.768019	Bmp4
GO_BP_m2	GO:19058	regulation	1/470	67/23843	0.737048	0.820332	0.768019	Ube2j1
GO_BP_m2	GO:00106	negative re	6/470	369/23843	0.737634	0.820767	0.768427	Bmp4/Dyr
GO_BP_m2	GO:000301	vascular pr	3/470	194/23843	0.739067	0.822143	0.769715	Fgfbp3/Ptp
GO_BP_m2	GO:00091	purine ribo	4/470	254/23843	0.740237	0.822843	0.770371	Adsl/Gucy
GO_BP_m2	GO:005192	regulation	4/470	254/23843	0.740237	0.822843	0.770371	Bmp4/Chd
GO_BP_m2	GO:00062	DNA-depe	2/470	133/23843	0.740713	0.822843	0.770371	Bmp4/Wdr
GO_BP_m2	GO:003527	endocrine	2/470	133/23843	0.740713	0.822843	0.770371	Bmp4/Six3
GO_BP_m2	GO:00507	negative re	2/470	133/23843	0.740713	0.822843	0.770371	Syt11/Ucp
GO_BP_m2	GO:00067	vitamin me	1/470	68/23843	0.742246	0.822843	0.770371	Pm20d2
GO_BP_m2	GO:003241	negative re	1/470	68/23843	0.742246	0.822843	0.770371	Agrn
GO_BP_m2	GO:00324	Rab protei	1/470	68/23843	0.742246	0.822843	0.770371	Rab11a
GO_BP_m2	GO:006104	negative re	1/470	68/23843	0.742246	0.822843	0.770371	Plau
GO_BP_m2	GO:007037	negative re	1/470	68/23843	0.742246	0.822843	0.770371	Csk
GO_BP_m2	GO:009732	response t	1/470	68/23843	0.742246	0.822843	0.770371	Bmp4
GO_BP_m2	GO:19019	regulation	1/470	68/23843	0.742246	0.822843	0.770371	Auts2
GO_BP_m2	GO:190442	positive re	1/470	68/23843	0.742246	0.822843	0.770371	Bmp4
GO_BP_m2	GO:001401	regulation	2/470	134/23843	0.744452	0.825071	0.772457	Bmp4/Id2
GO_BP_m2	GO:00083	regulation	3/470	196/23843	0.745325	0.82582	0.773158	Rab11a/Rn
GO_BP_m2	GO:00604	mesenchy	4/470	256/23843	0.745739	0.826061	0.773383	Bambi/Bm
GO_BP_m2	GO:00060	cellular ald	1/470	69/23843	0.747341	0.826745	0.774023	Kdm3a
GO_BP_m2	GO:004864	animal org	1/470	69/23843	0.747341	0.826745	0.774023	Bmp4

GO_BP_m2	GO:006019	regulation	1/470	69/23843	0.747341	0.826745	0.774023	Sele
GO_BP_m2	GO:006067	ureteric bu	1/470	69/23843	0.747341	0.826745	0.774023	Bmp4
GO_BP_m2	GO:190199	positive reg	1/470	69/23843	0.747341	0.826745	0.774023	Rab11a
GO_BP_m2	GO:190285	microtubul	2/470	135/23843	0.748144	0.827415	0.774651	Aurkb/Rab
GO_BP_m2	GO:190165	cellular resp	4/470	257/23843	0.748457	0.827542	0.77477	Csk/Foxo4/
GO_BP_m2	GO:000225	activation o	8/470	488/23843	0.74888	0.827792	0.775004	Csk/Ighv1-
GO_BP_m2	GO:004566	positive reg	7/470	432/23843	0.750582	0.829456	0.776561	Bmp4/Ect2
GO_BP_m2	GO:000173	morphogen	1/470	70/23843	0.752336	0.830082	0.777148	Sfrp2
GO_BP_m2	GO:000609	glycolytic p	1/470	70/23843	0.752336	0.830082	0.777148	Pfkfb2
GO_BP_m2	GO:006800	nitric oxide	1/470	70/23843	0.752336	0.830082	0.777148	Ptk2b
GO_BP_m2	GO:000742	peripheral	1/470	70/23843	0.752336	0.830082	0.777148	Adgrg6
GO_BP_m2	GO:007217	mesonephr	1/470	70/23843	0.752336	0.830082	0.777148	Bmp4
GO_BP_m2	GO:190188	negative re	1/470	70/23843	0.752336	0.830082	0.777148	Twf1
GO_BP_m2	GO:007122	cellular resp	4/470	259/23843	0.753825	0.831348	0.778333	Mir146b/Pa
GO_BP_m2	GO:007037	regulation	5/470	318/23843	0.75388	0.831348	0.778333	Bmp4/Csk/
GO_BP_m2	GO:000912	purine nuc	2/470	137/23843	0.755392	0.83236	0.77928	Adsl/Pfkfb2
GO_BP_m2	GO:000916	purine ribo	2/470	137/23843	0.755392	0.83236	0.77928	Adsl/Pfkfb2
GO_BP_m2	GO:190290	negative re	2/470	137/23843	0.755392	0.83236	0.77928	Dyrk1a/Tw
GO_BP_m2	GO:000269	positive reg	7/470	435/23843	0.756846	0.833567	0.78041	Ighv1-23/Ig
GO_BP_m2	GO:006757	ATP genera	1/470	71/23843	0.757232	0.833567	0.78041	Pfkfb2
GO_BP_m2	GO:007238	organelle t	1/470	71/23843	0.757232	0.833567	0.78041	Bloc1s2
GO_BP_m2	GO:000270	regulation	3/470	200/23843	0.757481	0.833567	0.78041	Rac2/Stxbp
GO_BP_m2	GO:007237	protein act	3/470	200/23843	0.757481	0.833567	0.78041	Ighv1-23/Ig
GO_BP_m2	GO:001082	positive reg	2/470	138/23843	0.758948	0.834697	0.781469	Pink1/Rac2
GO_BP_m2	GO:190199	negative re	2/470	138/23843	0.758948	0.834697	0.781469	Foxo4/Zc3h
GO_BP_m2	GO:000616	purine nuc	4/470	261/23843	0.759105	0.834697	0.781469	Adsl/Gucy2
GO_BP_m2	GO:000206	columnar/c	1/470	72/23843	0.762032	0.836382	0.783046	Bmp4
GO_BP_m2	GO:001485	striated mu	1/470	72/23843	0.762032	0.836382	0.783046	Prkar1a
GO_BP_m2	GO:003030	cholesterol	1/470	72/23843	0.762032	0.836382	0.783046	Acat2
GO_BP_m2	GO:003080	regulation	1/470	72/23843	0.762032	0.836382	0.783046	Ptk2b
GO_BP_m2	GO:004567	regulation	1/470	72/23843	0.762032	0.836382	0.783046	Mafb
GO_BP_m2	GO:005185	modificatio	1/470	72/23843	0.762032	0.836382	0.783046	Ppib
GO_BP_m2	GO:005500	cardiac mu	1/470	72/23843	0.762032	0.836382	0.783046	Chd7
GO_BP_m2	GO:005134	positive reg	8/470	495/23843	0.762587	0.836772	0.783411	Agrn/Ect2/
GO_BP_m2	GO:000628	DNA repair	7/470	438/23843	0.762997	0.837003	0.783627	Asf1a/Cdc5
GO_BP_m2	GO:004244	hormone m	3/470	202/23843	0.763382	0.837206	0.783817	Crym/Pcsk1
GO_BP_m2	GO:005086	regulation	4/470	263/23843	0.764297	0.837991	0.784552	Id2/Ighv1-
GO_BP_m2	GO:000221	activation o	2/470	140/23843	0.765926	0.839119	0.785609	Mavs/S100
GO_BP_m2	GO:004501	glycerolipid	2/470	140/23843	0.765926	0.839119	0.785609	Cdipt/Pigm
GO_BP_m2	GO:004558	regulation	2/470	140/23843	0.765926	0.839119	0.785609	Bmp4/Zbtb
GO_BP_m2	GO:001591	sterol trans	1/470	73/23843	0.766737	0.839131	0.78562	Acat2
GO_BP_m2	GO:004350	positive reg	1/470	73/23843	0.766737	0.839131	0.78562	Ptk2b
GO_BP_m2	GO:004620	nitric oxide	1/470	73/23843	0.766737	0.839131	0.78562	Ptk2b
GO_BP_m2	GO:006151	myeloid ce	1/470	73/23843	0.766737	0.839131	0.78562	Jmjd6
GO_BP_m2	GO:004573	positive reg	3/470	204/23843	0.769166	0.841551	0.787885	Rack1/Ptk2
GO_BP_m2	GO:000915	ribonucleo	2/470	141/23843	0.769349	0.841551	0.787885	Adsl/Pfkfb2
GO_BP_m2	GO:000223	response to	6/470	384/23843	0.77103	0.841764	0.788085	Jund/Mir14
GO_BP_m2	GO:001401	positive reg	1/470	74/23843	0.77135	0.841764	0.788085	Id2

GO_BP_m2	GO:001973	antibacteria	1/470	74/23843	0.77135	0.841764	0.788085	Rnase6
GO_BP_m2	GO:003272	positive reg	1/470	74/23843	0.77135	0.841764	0.788085	Il12rb1
GO_BP_m2	GO:004286	pyruvate b	1/470	74/23843	0.77135	0.841764	0.788085	Pfkfb2
GO_BP_m2	GO:004678	microtubul	1/470	74/23843	0.77135	0.841764	0.788085	Dyrk1a
GO_BP_m2	GO:005178	positive reg	1/470	74/23843	0.77135	0.841764	0.788085	Eif4g3
GO_BP_m2	GO:007167	mononucle	1/470	74/23843	0.77135	0.841764	0.788085	S100a14
GO_BP_m2	GO:009873	import acro	1/470	74/23843	0.77135	0.841764	0.788085	Slc25a38
GO_BP_m2	GO:007252	purine-cor	4/470	266/23843	0.771922	0.84217	0.788464	Adsl/Gucy2
GO_BP_m2	GO:000279	negative re	2/470	142/23843	0.772729	0.842612	0.788878	Syt11/Ucp2
GO_BP_m2	GO:007146	cellular res	2/470	142/23843	0.772729	0.842612	0.788878	Bmp4/Cyp
GO_BP_m2	GO:000701	actin filame	6/470	385/23843	0.77314	0.842841	0.789093	Cit/Mir129
GO_BP_m2	GO:005070	regulation	7/470	444/23843	0.774959	0.844605	0.790744	Glul/Mavs/
GO_BP_m2	GO:001922	regulation	1/470	75/23843	0.775871	0.844932	0.79105	Shc1
GO_BP_m2	GO:003247	regulation	1/470	75/23843	0.775871	0.844932	0.79105	Mavs
GO_BP_m2	GO:009775	positive reg	1/470	75/23843	0.775871	0.844932	0.79105	Ptprm
GO_BP_m2	GO:003085	regulation	2/470	143/23843	0.776065	0.844932	0.79105	Bmp4/Foxa
GO_BP_m2	GO:007121	cellular res	4/470	268/23843	0.776897	0.845412	0.791501	Mir146b/Pa
GO_BP_m2	GO:007083	divalent m	7/470	445/23843	0.776909	0.845412	0.791501	Bmp4/Chd
GO_BP_m2	GO:001095	positive reg	2/470	144/23843	0.779358	0.846471	0.792492	Rack1/Sfrp
GO_BP_m2	GO:004583	positive reg	2/470	144/23843	0.779358	0.846471	0.792492	Nr4a3/Ptk2
GO_BP_m2	GO:000691	activation c	1/470	76/23843	0.780303	0.846471	0.792492	Rack1
GO_BP_m2	GO:000704	cell-substra	1/470	76/23843	0.780303	0.846471	0.792492	Ptk2b
GO_BP_m2	GO:002187	forebrain n	1/470	76/23843	0.780303	0.846471	0.792492	Sall3
GO_BP_m2	GO:003433	adherens ju	1/470	76/23843	0.780303	0.846471	0.792492	Ptk2b
GO_BP_m2	GO:004591	positive reg	1/470	76/23843	0.780303	0.846471	0.792492	Pfkfb2
GO_BP_m2	GO:005138	response to	1/470	76/23843	0.780303	0.846471	0.792492	Bmp4
GO_BP_m2	GO:005193	catecholam	1/470	76/23843	0.780303	0.846471	0.792492	Pink1
GO_BP_m2	GO:005196	positive reg	1/470	76/23843	0.780303	0.846471	0.792492	Agrn
GO_BP_m2	GO:006118	mammary	1/470	76/23843	0.780303	0.846471	0.792492	Id2
GO_BP_m2	GO:190332	negative re	1/470	76/23843	0.780303	0.846471	0.792492	Cry1
GO_BP_m2	GO:001993	cAMP-med	2/470	145/23843	0.782609	0.848616	0.794499	Adgrg6/Pe
GO_BP_m2	GO:007251	divalent ino	7/470	448/23843	0.782684	0.848616	0.794499	Bmp4/Chd
GO_BP_m2	GO:005086	positive reg	7/470	449/23843	0.784584	0.849427	0.795259	Ighv1-23/Ig
GO_BP_m2	GO:003241	negative re	1/470	77/23843	0.784647	0.849427	0.795259	Agrn
GO_BP_m2	GO:004324	negative re	1/470	77/23843	0.784647	0.849427	0.795259	Twf1
GO_BP_m2	GO:005134	regulation	1/470	77/23843	0.784647	0.849427	0.795259	Ptk2b
GO_BP_m2	GO:005170	interaction	1/470	77/23843	0.784647	0.849427	0.795259	Ppib
GO_BP_m2	GO:006011	inner ear re	1/470	77/23843	0.784647	0.849427	0.795259	Bmp4
GO_BP_m2	GO:005149	negative re	2/470	146/23843	0.785817	0.850267	0.796045	Dyrk1a/Tw
GO_BP_m2	GO:004563	regulation	3/470	210/23843	0.785828	0.850267	0.796045	Id2/Mafb/F
GO_BP_m2	GO:004521	cell-cell jur	3/470	211/23843	0.788506	0.850392	0.796163	Csk/Ect2/P
GO_BP_m2	GO:001403	neural cres	1/470	78/23843	0.788906	0.850392	0.796163	Bmp4
GO_BP_m2	GO:003016	platelet act	1/470	78/23843	0.788906	0.850392	0.796163	Stxbp1
GO_BP_m2	GO:003019	regulation	1/470	78/23843	0.788906	0.850392	0.796163	Plau
GO_BP_m2	GO:003260	type I inter	1/470	78/23843	0.788906	0.850392	0.796163	Mavs
GO_BP_m2	GO:004584	positive reg	1/470	78/23843	0.788906	0.850392	0.796163	Bmp4
GO_BP_m2	GO:004603	ADP metab	1/470	78/23843	0.788906	0.850392	0.796163	Pfkfb2
GO_BP_m2	GO:004653	photorecep	1/470	78/23843	0.788906	0.850392	0.796163	Rom1

GO_BP_m2	GO:004863	positive re	1/470	78/23843	0.788906	0.850392	0.796163	Bmp4
GO_BP_m2	GO:004870	astrocyte d	1/470	78/23843	0.788906	0.850392	0.796163	Id2
GO_BP_m2	GO:007207	nephron tu	1/470	78/23843	0.788906	0.850392	0.796163	Bmp4
GO_BP_m2	GO:190004	regulation	1/470	78/23843	0.788906	0.850392	0.796163	Plau
GO_BP_m2	GO:200105	reactive nit	1/470	78/23843	0.788906	0.850392	0.796163	Ptk2b
GO_BP_m2	GO:000282	regulation	2/470	147/23843	0.788984	0.850392	0.796163	Il12rb1/Zbt
GO_BP_m2	GO:000912	nucleoside	2/470	147/23843	0.788984	0.850392	0.796163	Adsl/Pfkfb2
GO_BP_m2	GO:000246	adaptive in	6/470	393/23843	0.789494	0.850723	0.796472	Ighv1-23/I
GO_BP_m2	GO:003295	regulation	5/470	334/23843	0.790302	0.851376	0.797083	Cit/Ptk2b/
GO_BP_m2	GO:006032	cell chemo	4/470	274/23843	0.791308	0.852241	0.797893	Pde4d/Ptk2
GO_BP_m2	GO:000719	adenylate	1/470	79/23843	0.793081	0.853055	0.798656	Grm7
GO_BP_m2	GO:003304	regulation	1/470	79/23843	0.793081	0.853055	0.798656	Cit
GO_BP_m2	GO:003410	regulation	1/470	79/23843	0.793081	0.853055	0.798656	Csk
GO_BP_m2	GO:190186	positive re	1/470	79/23843	0.793081	0.853055	0.798656	Bmp4
GO_BP_m2	GO:190403	regulation	1/470	79/23843	0.793081	0.853055	0.798656	Bmp4
GO_BP_m2	GO:000681	sodium io	3/470	213/23843	0.793779	0.853588	0.799154	Agrn/Mfsd
GO_BP_m2	GO:007037	ERK1 and	5/470	336/23843	0.794546	0.854193	0.799721	Bmp4/Csk/
GO_BP_m2	GO:000224	hematopoi	2/470	149/23843	0.795195	0.854452	0.799964	Bmp4/Zbtb
GO_BP_m2	GO:000717	transformin	2/470	149/23843	0.795195	0.854452	0.799964	Bambi/Tgfb
GO_BP_m2	GO:003032	lung develo	3/470	214/23843	0.796375	0.855265	0.800724	Bmp4/Ceb
GO_BP_m2	GO:001097	positive re	5/470	337/23843	0.796642	0.855265	0.800724	Bmp4/Ptk2
GO_BP_m2	GO:002290	respiratory	1/470	80/23843	0.797173	0.855265	0.800724	Pink1
GO_BP_m2	GO:003196	response to	1/470	80/23843	0.797173	0.855265	0.800724	Bmp4
GO_BP_m2	GO:003505	embryonic	1/470	80/23843	0.797173	0.855265	0.800724	Ift122
GO_BP_m2	GO:007208	nephron ep	1/470	80/23843	0.797173	0.855265	0.800724	Bmp4
GO_BP_m2	GO:000193	positive re	1/470	81/23843	0.801185	0.858533	0.803785	Bmp4
GO_BP_m2	GO:001574	organopho	1/470	81/23843	0.801185	0.858533	0.803785	Osbpl5
GO_BP_m2	GO:007202	nephron m	1/470	81/23843	0.801185	0.858533	0.803785	Bmp4
GO_BP_m2	GO:190198	positive re	1/470	81/23843	0.801185	0.858533	0.803785	Rab11a
GO_BP_m2	GO:001095	positive re	2/470	151/23843	0.801243	0.858533	0.803785	Rack1/Sfrp
GO_BP_m2	GO:003032	respiratory	3/470	217/23843	0.803998	0.861265	0.806342	Bmp4/Ceb
GO_BP_m2	GO:000042	autophagy	1/470	82/23843	0.805118	0.861365	0.806436	Pink1
GO_BP_m2	GO:003111	regulation	1/470	82/23843	0.805118	0.861365	0.806436	Dyrk1a
GO_BP_m2	GO:005081	regulation	1/470	82/23843	0.805118	0.861365	0.806436	Plau
GO_BP_m2	GO:006172	mitochond	1/470	82/23843	0.805118	0.861365	0.806436	Pink1
GO_BP_m2	GO:007233	intrinsic ap	1/470	82/23843	0.805118	0.861365	0.806436	Rrp8
GO_BP_m2	GO:000718	G-protein	3/470	218/23843	0.806485	0.862608	0.807599	Adgrg6/Gp
GO_BP_m2	GO:000961	response to	7/470	462/23843	0.808169	0.862849	0.807825	2210409D
GO_BP_m2	GO:001094	negative re	3/470	219/23843	0.808946	0.862849	0.807825	Bmp4/Foxc
GO_BP_m2	GO:006113	morphogen	3/470	219/23843	0.808946	0.862849	0.807825	Bmp4/Fkbp
GO_BP_m2	GO:000722	integrin-m	1/470	83/23843	0.808972	0.862849	0.807825	Ptk2b
GO_BP_m2	GO:000913	purine nuc	1/470	83/23843	0.808972	0.862849	0.807825	Pfkfb2
GO_BP_m2	GO:000917	purine ribo	1/470	83/23843	0.808972	0.862849	0.807825	Pfkfb2
GO_BP_m2	GO:001403	mesenchym	1/470	83/23843	0.808972	0.862849	0.807825	Bmp4
GO_BP_m2	GO:003275	positive re	1/470	83/23843	0.808972	0.862849	0.807825	Mavs
GO_BP_m2	GO:004249	mechanore	1/470	83/23843	0.808972	0.862849	0.807825	Bmp4
GO_BP_m2	GO:190187	regulation	1/470	83/23843	0.808972	0.862849	0.807825	Twf1
GO_BP_m2	GO:190303	negative re	1/470	83/23843	0.808972	0.862849	0.807825	Plau

GO_BP_m2	GO:190198	negative re	2/470	154/23843	0.810019	0.863746	0.808665	Foxo4/Zc3
GO_BP_m2	GO:005087	positive reg	3/470	220/23843	0.81138	0.864905	0.80975	Ighv1-23/Ig
GO_BP_m2	GO:190210	regulation	4/470	283/23843	0.811518	0.864905	0.80975	Bmp4/Id2/
GO_BP_m2	GO:001935	nicotinami	1/470	84/23843	0.812751	0.865024	0.809861	Pfkfb2
GO_BP_m2	GO:004886	stem cell d	1/470	84/23843	0.812751	0.865024	0.809861	Bmp4
GO_BP_m2	GO:006133	renal tubul	1/470	84/23843	0.812751	0.865024	0.809861	Bmp4
GO_BP_m2	GO:009706	dendritic s	1/470	84/23843	0.812751	0.865024	0.809861	Mtmr2
GO_BP_m2	GO:190352	positive reg	1/470	84/23843	0.812751	0.865024	0.809861	Shc1
GO_BP_m2	GO:000657	cellular mo	2/470	155/23843	0.812867	0.865024	0.809861	Crym/Pm2
GO_BP_m2	GO:004586	negative re	5/470	346/23843	0.814762	0.866425	0.811174	Alad/Ambp
GO_BP_m2	GO:000865	phospholip	2/470	156/23843	0.815676	0.866425	0.811174	Cdipt/Pigm
GO_BP_m2	GO:004580	positive reg	2/470	156/23843	0.815676	0.866425	0.811174	Sele/Tsg10
GO_BP_m2	GO:004593	negative re	3/470	222/23843	0.81617	0.866425	0.811174	Bmp4/Foxo
GO_BP_m2	GO:000236	cytokine pr	1/470	85/23843	0.816455	0.866425	0.811174	Nr4a3
GO_BP_m2	GO:000270	positive reg	1/470	85/23843	0.816455	0.866425	0.811174	Nr4a3
GO_BP_m2	GO:001403	neural cres	1/470	85/23843	0.816455	0.866425	0.811174	Bmp4
GO_BP_m2	GO:002290	electron tra	1/470	85/23843	0.816455	0.866425	0.811174	Pink1
GO_BP_m2	GO:004247	odontogen	1/470	85/23843	0.816455	0.866425	0.811174	Bmp4
GO_BP_m2	GO:006041	muscle tiss	1/470	85/23843	0.816455	0.866425	0.811174	Chd7
GO_BP_m2	GO:006184	antimicrob	1/470	85/23843	0.816455	0.866425	0.811174	Rnase6
GO_BP_m2	GO:002241	cellular cor	5/470	347/23843	0.816693	0.866459	0.811205	2810006K2
GO_BP_m2	GO:000611	oxidative p	1/470	86/23843	0.820086	0.86918	0.813752	Pink1
GO_BP_m2	GO:000930	amine met	1/470	86/23843	0.820086	0.86918	0.813752	Inmt
GO_BP_m2	GO:001922	transmissio	1/470	86/23843	0.820086	0.86918	0.813752	Grm7
GO_BP_m2	GO:004315	negative re	1/470	86/23843	0.820086	0.86918	0.813752	Sfrp2
GO_BP_m2	GO:002240	positive reg	3/470	224/23843	0.820856	0.869467	0.814021	Il12rb1/Nr4
GO_BP_m2	GO:007121	cellular res	4/470	288/23843	0.822039	0.869467	0.814021	Mir146b/Pa
GO_BP_m2	GO:005109	positive reg	3/470	225/23843	0.823161	0.869467	0.814021	Mavs/Mbtp
GO_BP_m2	GO:000918	ribonucleo	1/470	87/23843	0.823646	0.869467	0.814021	Pfkfb2
GO_BP_m2	GO:001936	pyridine nu	1/470	87/23843	0.823646	0.869467	0.814021	Pfkfb2
GO_BP_m2	GO:003101	pancreas d	1/470	87/23843	0.823646	0.869467	0.814021	Bmp4
GO_BP_m2	GO:003252	response t	1/470	87/23843	0.823646	0.869467	0.814021	Ptk2b
GO_BP_m2	GO:003444	substrate a	1/470	87/23843	0.823646	0.869467	0.814021	Vamp3
GO_BP_m2	GO:010602	neuron pro	1/470	87/23843	0.823646	0.869467	0.814021	Mtmr2
GO_BP_m2	GO:000281	regulation	2/470	159/23843	0.82388	0.869467	0.814021	Il12rb1/Zbt
GO_BP_m2	GO:000703	vacuole org	2/470	159/23843	0.82388	0.869467	0.814021	Pink1/Ralb
GO_BP_m2	GO:000708	regulation	2/470	159/23843	0.82388	0.869467	0.814021	Bmp4/Cit
GO_BP_m2	GO:000759	blood coag	2/470	159/23843	0.82388	0.869467	0.814021	Plau/Stxbp
GO_BP_m2	GO:003529	regulation	2/470	159/23843	0.82388	0.869467	0.814021	Ptprm/Shc
GO_BP_m2	GO:005101	actin filame	2/470	159/23843	0.82388	0.869467	0.814021	Ptk2b/Spire
GO_BP_m2	GO:009774	regulation	2/470	159/23843	0.82388	0.869467	0.814021	Ptprm/Shc
GO_BP_m2	GO:190210	positive reg	2/470	159/23843	0.82388	0.869467	0.814021	Id2/Zbtb1
GO_BP_m2	GO:004441	interspecie	6/470	412/23843	0.824714	0.870129	0.814641	Chmp3/Ma
GO_BP_m2	GO:000695	humoral im	5/470	352/23843	0.826109	0.871162	0.815608	Ifna4/Ighv1
GO_BP_m2	GO:004217	regulation	5/470	352/23843	0.826109	0.871162	0.815608	Alad/Rack1
GO_BP_m2	GO:000004	transition r	1/470	88/23843	0.827135	0.871368	0.815801	Slc25a28
GO_BP_m2	GO:004558	positive reg	1/470	88/23843	0.827135	0.871368	0.815801	Zbtb1
GO_BP_m2	GO:190260	proton tran	1/470	88/23843	0.827135	0.871368	0.815801	Atp6v1h

GO_BP_m2	GO:190342	regulation	1/470	88/23843	0.827135	0.871368	0.815801	Ptk2b
GO_BP_m2	GO:00759	hemostasis	2/470	161/23843	0.829166	0.873288	0.817599	Plau/Stxbp
GO_BP_m2	GO:00170	cell fate sp	1/470	89/23843	0.830555	0.874093	0.818352	Sfrp2
GO_BP_m2	GO:005502	regulation	1/470	89/23843	0.830555	0.874093	0.818352	Bmp4
GO_BP_m2	GO:007055	response t	1/470	89/23843	0.830555	0.874093	0.818352	Sele
GO_BP_m2	GO:004312	regulation	2/470	162/23843	0.831755	0.874698	0.818918	Pink1/Tme
GO_BP_m2	GO:006157	actin filame	2/470	162/23843	0.831755	0.874698	0.818918	Ptk2b/Spire
GO_BP_m2	GO:200124	regulation	2/470	162/23843	0.831755	0.874698	0.818918	Rack1/Pink
GO_BP_m2	GO:004206	gliogenesis	4/470	293/23843	0.832071	0.874811	0.819024	Adgrg6/Bn
GO_BP_m2	GO:004668	response t	1/470	90/23843	0.833908	0.876505	0.820611	Jund
GO_BP_m2	GO:005081	coagulatio	2/470	163/23843	0.834309	0.876505	0.820611	Plau/Stxbp
GO_BP_m2	GO:003433	cell junctio	3/470	230/23843	0.834309	0.876505	0.820611	Csk/Ect2/P
GO_BP_m2	GO:000181	negative re	3/470	231/23843	0.836465	0.87855	0.822525	Csk/Suz12/
GO_BP_m2	GO:003505	cardiocyte	2/470	164/23843	0.836827	0.87871	0.822675	Bmp4/Myh
GO_BP_m2	GO:007252	pyridine-cc	1/470	91/23843	0.837194	0.878876	0.82283	Pfkfb2
GO_BP_m2	GO:000222	toll-like rec	1/470	92/23843	0.840416	0.881376	0.82517	S100a14
GO_BP_m2	GO:005181	modificatic	1/470	92/23843	0.840416	0.881376	0.82517	Ppib
GO_BP_m2	GO:005501	cardiac mu	1/470	92/23843	0.840416	0.881376	0.82517	Prkar1a
GO_BP_m2	GO:006035	response t	1/470	92/23843	0.840416	0.881376	0.82517	Atf4
GO_BP_m2	GO:000649	protein lipi	1/470	93/23843	0.843574	0.884246	0.827857	Pigm
GO_BP_m2	GO:003475	cellular hor	1/470	93/23843	0.843574	0.884246	0.827857	Sgpl1
GO_BP_m2	GO:001972	calcium-m	2/470	167/23843	0.844177	0.884436	0.828035	Pde4d/Ptk2
GO_BP_m2	GO:007123	cellular res	2/470	167/23843	0.844177	0.884436	0.828035	Mir346/Mir
GO_BP_m2	GO:004343	negative re	2/470	168/23843	0.846559	0.886162	0.829652	Hr/Id2
GO_BP_m2	GO:000157	microtubul	1/470	94/23843	0.846669	0.886162	0.829652	Mss51
GO_BP_m2	GO:001584	monoamin	1/470	94/23843	0.846669	0.886162	0.829652	Pink1
GO_BP_m2	GO:005196	regulation	1/470	94/23843	0.846669	0.886162	0.829652	Agrn
GO_BP_m2	GO:000176	morphoge	3/470	237/23843	0.848899	0.887361	0.830774	Bmp4/Fkbp
GO_BP_m2	GO:000206	epithelial c	3/470	237/23843	0.848899	0.887361	0.830774	Bmp4/Frm
GO_BP_m2	GO:001077	positive re	2/470	169/23843	0.848908	0.887361	0.830774	Rab11a/Ss
GO_BP_m2	GO:004881	dendrite m	2/470	169/23843	0.848908	0.887361	0.830774	Cit/Ss18l1
GO_BP_m2	GO:000720	positive re	4/470	302/23843	0.848942	0.887361	0.830774	Bmp4/Chd
GO_BP_m2	GO:004325	regulation	1/470	95/23843	0.849704	0.887361	0.830774	Ptk2b
GO_BP_m2	GO:004513	meiotic chr	1/470	95/23843	0.849704	0.887361	0.830774	Espl1
GO_BP_m2	GO:200124	negative re	1/470	95/23843	0.849704	0.887361	0.830774	Pink1
GO_BP_m2	GO:005089	cognition	4/470	303/23843	0.850725	0.887361	0.830774	Bace1/Chd
GO_BP_m2	GO:000961	response t	2/470	170/23843	0.851225	0.887361	0.830774	Jund/Mir76
GO_BP_m2	GO:005088	regulation	2/470	170/23843	0.851225	0.887361	0.830774	Ptprm/Shc
GO_BP_m2	GO:009874	cell-cell ad	2/470	170/23843	0.851225	0.887361	0.830774	Ptprm/Sele
GO_BP_m2	GO:000664	triglyceride	1/470	96/23843	0.852678	0.887361	0.830774	Acsl4
GO_BP_m2	GO:000704	cell-cell jur	1/470	96/23843	0.852678	0.887361	0.830774	Ect2
GO_BP_m2	GO:000830	associative	1/470	96/23843	0.852678	0.887361	0.830774	Grm7
GO_BP_m2	GO:003003	contractile	1/470	96/23843	0.852678	0.887361	0.830774	Ptk2b
GO_BP_m2	GO:003031	flagellated	1/470	96/23843	0.852678	0.887361	0.830774	Ropn1l
GO_BP_m2	GO:004210	positive re	1/470	96/23843	0.852678	0.887361	0.830774	Il12rb1
GO_BP_m2	GO:004314	stress fiber	1/470	96/23843	0.852678	0.887361	0.830774	Ptk2b
GO_BP_m2	GO:004563	positive re	1/470	96/23843	0.852678	0.887361	0.830774	Id2
GO_BP_m2	GO:005077	positive re	1/470	96/23843	0.852678	0.887361	0.830774	Rab11a

GO_BP_m2	GO:00609	kidney mor	1/470	96/23843	0.852678	0.887361	0.830774	Bmp4
GO_BP_m2	GO:00720	nephron tu	1/470	96/23843	0.852678	0.887361	0.830774	Bmp4
GO_BP_m2	GO:00351	regulation	2/470	171/23843	0.853509	0.887785	0.83117	Ptprm/Shc
GO_BP_m2	GO:00463	regulation	2/470	171/23843	0.853509	0.887785	0.83117	Ptk2b/Sfrp
GO_BP_m2	GO:00018	blastocyst	1/470	98/23843	0.858452	0.892263	0.835363	Lats2
GO_BP_m2	GO:00421	lipoprotein	1/470	98/23843	0.858452	0.892263	0.835363	Pigm
GO_BP_m2	GO:004231	vasoconstr	1/470	98/23843	0.858452	0.892263	0.835363	Shc1
GO_BP_m2	GO:00068	xenobiotic	1/470	99/23843	0.861254	0.89451	0.837467	Cyp2g1
GO_BP_m2	GO:002151	spinal cord	1/470	99/23843	0.861254	0.89451	0.837467	Ift122
GO_BP_m2	GO:00421	neurotrans	1/470	99/23843	0.861254	0.89451	0.837467	Ptk2b
GO_BP_m2	GO:00071	adenylate	1/470	100/23843	0.864	0.896284	0.839128	Adgrg6
GO_BP_m2	GO:00434	regulation	1/470	100/23843	0.864	0.896284	0.839128	Pink1
GO_BP_m2	GO:00977	sperm mot	1/470	100/23843	0.864	0.896284	0.839128	Ropn1l
GO_BP_m2	GO:19000	positive re	1/470	100/23843	0.864	0.896284	0.839128	Ss18l1
GO_BP_m2	GO:19908	response t	4/470	311/23843	0.86436	0.896284	0.839128	Gtf2h1/Kdr
GO_BP_m2	GO:19908	cellular res	4/470	311/23843	0.86436	0.896284	0.839128	Gtf2h1/Kdr
GO_BP_m2	GO:20012	positive re	2/470	176/23843	0.864457	0.896284	0.839128	Rack1/Pink
GO_BP_m2	GO:00458	positive re	4/470	312/23843	0.865987	0.897493	0.84026	Rack1/Ptk2
GO_BP_m2	GO:00071	homophilic	1/470	101/23843	0.866692	0.897493	0.84026	Ptprm
GO_BP_m2	GO:004544	endothelial	1/470	101/23843	0.866692	0.897493	0.84026	Bmp4
GO_BP_m2	GO:00456	positive re	1/470	101/23843	0.866692	0.897493	0.84026	Zbtb1
GO_BP_m2	GO:006041	heart grow	1/470	101/23843	0.866692	0.897493	0.84026	Prkar1a
GO_BP_m2	GO:00091	purine ribo	3/470	247/23843	0.8678	0.898196	0.840918	Adsl/Pfkfb
GO_BP_m2	GO:00092	purine ribo	3/470	247/23843	0.8678	0.898196	0.840918	Pfkfb2/Pink
GO_BP_m2	GO:00016	ureteric bu	1/470	102/23843	0.869331	0.898452	0.841158	Bmp4
GO_BP_m2	GO:00027	positive re	1/470	102/23843	0.869331	0.898452	0.841158	Zbtb1
GO_BP_m2	GO:00613	renal tubul	1/470	102/23843	0.869331	0.898452	0.841158	Bmp4
GO_BP_m2	GO:00721	mesonephr	1/470	102/23843	0.869331	0.898452	0.841158	Bmp4
GO_BP_m2	GO:00721	mesonephr	1/470	102/23843	0.869331	0.898452	0.841158	Bmp4
GO_BP_m2	GO:19030	organelle c	1/470	102/23843	0.869331	0.898452	0.841158	Pink1
GO_BP_m2	GO:00091	purine nuc	3/470	248/23843	0.86957	0.898477	0.841181	Adsl/Pfkfb
GO_BP_m2	GO:00432	response t	2/470	179/23843	0.870661	0.89894	0.841615	Mir346/Mi
GO_BP_m2	GO:005077	regulation	2/470	179/23843	0.870661	0.89894	0.841615	Cit/Ss18l1
GO_BP_m2	GO:005087	positive re	2/470	179/23843	0.870661	0.89894	0.841615	Il12rb1/Zb
GO_BP_m2	GO:000661	protein tar	1/470	103/23843	0.871918	0.899132	0.841795	Sec63
GO_BP_m2	GO:001407	response t	1/470	103/23843	0.871918	0.899132	0.841795	Jund
GO_BP_m2	GO:00189	phenol-co	1/470	103/23843	0.871918	0.899132	0.841795	Crym
GO_BP_m2	GO:003264	regulation	1/470	103/23843	0.871918	0.899132	0.841795	Il12rb1
GO_BP_m2	GO:200011	negative re	1/470	103/23843	0.871918	0.899132	0.841795	Sfrp2
GO_BP_m2	GO:00328	cellular res	2/470	180/23843	0.872671	0.899687	0.842314	Foxo4/Shc
GO_BP_m2	GO:000244	lymphocyt	5/470	381/23843	0.873246	0.900059	0.842663	Ighv1-23/I
GO_BP_m2	GO:00197	antimicrob	1/470	104/23843	0.874454	0.900732	0.843292	Rnase6
GO_BP_m2	GO:00977	negative re	1/470	104/23843	0.874454	0.900732	0.843292	Shc1
GO_BP_m2	GO:00091	ribonucleo	3/470	251/23843	0.874757	0.900732	0.843292	Adsl/Pfkfb
GO_BP_m2	GO:00104	negative re	3/470	251/23843	0.874757	0.900732	0.843292	Ambp/Serp
GO_BP_m2	GO:00018	mesonephr	1/470	105/23843	0.87694	0.902536	0.844981	Bmp4
GO_BP_m2	GO:00192	response t	1/470	105/23843	0.87694	0.902536	0.844981	Vmn1r215
GO_BP_m2	GO:00160	immunogl	3/470	253/23843	0.878113	0.903522	0.845905	Ighv1-23/I

GO_BP_m2	GO:00268	negative re	6/470	448/23843	0.878493	0.903691	0.846062	Bmp4/Id2/
GO_BP_m2	GO:00510	regulation	5/470	385/23843	0.878815	0.903801	0.846166	Hr/Id2/Ma
GO_BP_m2	GO:19037	regulation	5/470	386/23843	0.880175	0.904978	0.847267	Bmp4/Id2/
GO_BP_m2	GO:001972	B cell medi	3/470	255/23843	0.88139	0.906005	0.848229	Ighv1-23/I
GO_BP_m2	GO:004324	regulation	1/470	107/23843	0.881765	0.906168	0.848382	Twf1
GO_BP_m2	GO:003432	cell junctio	2/470	185/23843	0.882293	0.906268	0.848475	Ect2/Ptk2b
GO_BP_m2	GO:007156	cellular res	2/470	185/23843	0.882293	0.906268	0.848475	Bambi/Tgf
GO_BP_m2	GO:005125	positive re	5/470	388/23843	0.882855	0.906548	0.848737	Ighv1-23/I
GO_BP_m2	GO:000914	purine nuc	3/470	256/23843	0.882998	0.906548	0.848737	Pfkfb2/Pin
GO_BP_m2	GO:007200	nephron e	1/470	108/23843	0.884106	0.907049	0.849207	Bmp4
GO_BP_m2	GO:000718	adenylate	2/470	186/23843	0.884135	0.907049	0.849207	Adgrg6/Gr
GO_BP_m2	GO:005070	regulation	2/470	186/23843	0.884135	0.907049	0.849207	Mavs/Syt1
GO_BP_m2	GO:007155	response t	2/470	187/23843	0.885951	0.90869	0.850743	Bambi/Tgf
GO_BP_m2	GO:000725	JNK cascad	2/470	188/23843	0.88774	0.910302	0.852252	Ptk2b/Sfrp
GO_BP_m2	GO:006300	double-str	2/470	189/23843	0.889503	0.911887	0.853736	H2afx/Rec
GO_BP_m2	GO:000912	nucleoside	3/470	261/23843	0.890753	0.912828	0.854617	Adsl/Pfkfb
GO_BP_m2	GO:000863	intrinsic ap	1/470	111/23843	0.890855	0.912828	0.854617	Casp16-ps
GO_BP_m2	GO:000228	T cell activ	1/470	112/23843	0.893017	0.913927	0.855646	Ifna4
GO_BP_m2	GO:000315	endotheliu	1/470	112/23843	0.893017	0.913927	0.855646	Bmp4
GO_BP_m2	GO:000758	body fluid	1/470	112/23843	0.893017	0.913927	0.855646	Prl8a2
GO_BP_m2	GO:004247	odontoger	1/470	112/23843	0.893017	0.913927	0.855646	Bmp4
GO_BP_m2	GO:005082	defense re	1/470	112/23843	0.893017	0.913927	0.855646	Rnase6
GO_BP_m2	GO:000716	negative re	3/470	263/23843	0.893724	0.914427	0.856114	Bmp4/Prka
GO_BP_m2	GO:000724	I-kappaB k	2/470	192/23843	0.89464	0.915141	0.856782	Pink1/Tme
GO_BP_m2	GO:003110	microtubul	1/470	113/23843	0.895136	0.915245	0.85688	Dyrk1a
GO_BP_m2	GO:001993	second-me	4/470	332/23843	0.895178	0.915245	0.85688	Adgrg6/Pd
GO_BP_m2	GO:000307	regulation	1/470	114/23843	0.897213	0.916656	0.858201	Rasl10b
GO_BP_m2	GO:001081	positive re	1/470	114/23843	0.897213	0.916656	0.858201	Ptk2b
GO_BP_m2	GO:001657	protein de	1/470	114/23843	0.897213	0.916656	0.858201	Usp17le
GO_BP_m2	GO:000663	acylglycer	1/470	115/23843	0.899249	0.918289	0.859729	Acsl4
GO_BP_m2	GO:003260	interferon-	1/470	115/23843	0.899249	0.918289	0.859729	Il12rb1
GO_BP_m2	GO:000821	regulation	2/470	196/23843	0.901143	0.919431	0.860799	Id2/Rasl10
GO_BP_m2	GO:001082	regulation	2/470	196/23843	0.901143	0.919431	0.860799	Pink1/Rac2
GO_BP_m2	GO:000827	regulation	1/470	116/23843	0.901244	0.919431	0.860799	Cry1
GO_BP_m2	GO:004210	B cell proli	1/470	116/23843	0.901244	0.919431	0.860799	Ifna4
GO_BP_m2	GO:004206	wound he	4/470	337/23843	0.901543	0.919513	0.860875	Pdcd10/Pl
GO_BP_m2	GO:005148	regulation	4/470	338/23843	0.902774	0.919638	0.860993	Bmp4/Chd
GO_BP_m2	GO:000663	neutral lip	1/470	117/23843	0.903201	0.919638	0.860993	Acsl4
GO_BP_m2	GO:000675	ATP biosyn	1/470	117/23843	0.903201	0.919638	0.860993	Pfkfb2
GO_BP_m2	GO:001605	carbohydr	1/470	117/23843	0.903201	0.919638	0.860993	Pfkfb2
GO_BP_m2	GO:004328	positive re	1/470	117/23843	0.903201	0.919638	0.860993	Rack1
GO_BP_m2	GO:006099	dendritic s	1/470	117/23843	0.903201	0.919638	0.860993	Acsl4
GO_BP_m2	GO:190037	regulation	1/470	117/23843	0.903201	0.919638	0.860993	Ptk2b
GO_BP_m2	GO:004508	positive re	2/470	198/23843	0.904253	0.920264	0.861578	Mavs/S100
GO_BP_m2	GO:190370	positive re	2/470	198/23843	0.904253	0.920264	0.861578	Id2/Zbtb1
GO_BP_m2	GO:003080	regulation	1/470	118/23843	0.905118	0.920697	0.861984	Ptk2b
GO_BP_m2	GO:004646	membrane	1/470	118/23843	0.905118	0.920697	0.861984	Pigm
GO_BP_m2	GO:000761	learning or	3/470	272/23843	0.906216	0.92159	0.86282	Bace1/Gr

GO_BP_m2	GO:005192	positive reg	1/470	119/23843	0.906998	0.922162	0.863356	Bmp4
GO_BP_m2	GO:001095	negative re	2/470	201/23843	0.908747	0.923717	0.864812	Serpina1b/
GO_BP_m2	GO:005110	regulation	1/470	122/23843	0.912417	0.927222	0.868093	Id2
GO_BP_m2	GO:004328	regulation	2/470	204/23843	0.913044	0.927635	0.868479	Rack1/Sfrp
GO_BP_m2	GO:001635	dendrite de	3/470	280/23843	0.916189	0.930605	0.87126	Acsl4/Cit/S
GO_BP_m2	GO:000270	regulation	1/470	126/23843	0.919155	0.933166	0.873658	Nr4a3
GO_BP_m2	GO:000709	mitotic cell	1/470	126/23843	0.919155	0.933166	0.873658	Foxo4
GO_BP_m2	GO:005085	antigen rec	3/470	283/23843	0.919673	0.933354	0.873834	Ighv1-23/Ig
GO_BP_m2	GO:000716	establishm	2/470	209/23843	0.919785	0.933354	0.873834	Ooep/Ptk2
GO_BP_m2	GO:004633	positive reg	1/470	127/23843	0.920757	0.933937	0.87438	Ptk2b
GO_BP_m2	GO:003210	positive reg	3/470	284/23843	0.920805	0.933937	0.87438	Ptk2b/Rac2
GO_BP_m2	GO:000920	purine ribo	1/470	128/23843	0.922327	0.934818	0.875205	Pfkfb2
GO_BP_m2	GO:004215	lipoprotein	1/470	128/23843	0.922327	0.934818	0.875205	Pigm
GO_BP_m2	GO:005066	cytokine se	2/470	211/23843	0.922342	0.934818	0.875205	Mavs/Syt11
GO_BP_m2	GO:000914	purine nuc	1/470	129/23843	0.923867	0.935685	0.876017	Pfkfb2
GO_BP_m2	GO:005083	defense res	1/470	129/23843	0.923867	0.935685	0.876017	Rnase6
GO_BP_m2	GO:200105	positive reg	1/470	129/23843	0.923867	0.935685	0.876017	Rack1
GO_BP_m2	GO:003001	establishm	1/470	130/23843	0.925376	0.936988	0.877236	Ptk2b
GO_BP_m2	GO:000252	acute inflar	1/470	131/23843	0.926855	0.938259	0.878426	Serpina1b
GO_BP_m2	GO:006104	regulation	1/470	132/23843	0.928305	0.9395	0.879588	Plau
GO_BP_m2	GO:000941	response to	2/470	217/23843	0.929559	0.940031	0.880085	Bmp4/Cyp
GO_BP_m2	GO:000979	specificatio	1/470	133/23843	0.929726	0.940031	0.880085	Bmp4
GO_BP_m2	GO:001923	sensory pe	1/470	133/23843	0.929726	0.940031	0.880085	Penk
GO_BP_m2	GO:005071	positive reg	1/470	133/23843	0.929726	0.940031	0.880085	Mavs
GO_BP_m2	GO:007064	protein mo	1/470	135/23843	0.932484	0.942593	0.882484	Usp17le
GO_BP_m2	GO:001585	organic hy	2/470	221/23843	0.934014	0.943685	0.883506	Acat2/Pink
GO_BP_m2	GO:004603	ATP metab	2/470	221/23843	0.934014	0.943685	0.883506	Pfkfb2/Pink
GO_BP_m2	GO:005067	positive reg	1/470	137/23843	0.935135	0.94459	0.884353	Il12rb1
GO_BP_m2	GO:006056	epithelial tu	4/470	371/23843	0.93646	0.945701	0.885394	Bmp4/Fkbp
GO_BP_m2	GO:001657	histone ace	1/470	139/23843	0.937681	0.946478	0.886122	Auts2
GO_BP_m2	GO:003294	positive reg	1/470	139/23843	0.937681	0.946478	0.886122	Il12rb1
GO_BP_m2	GO:000206	columnar/c	1/470	140/23843	0.938917	0.94727	0.886863	Bmp4
GO_BP_m2	GO:005189	regulation	1/470	140/23843	0.938917	0.94727	0.886863	Rack1
GO_BP_m2	GO:004213	neurotrans	1/470	141/23843	0.940128	0.948036	0.88758	Ptk2b
GO_BP_m2	GO:007207	kidney epit	1/470	141/23843	0.940128	0.948036	0.88758	Bmp4
GO_BP_m2	GO:004578	positive reg	4/470	379/23843	0.942844	0.950547	0.88993	Il12rb1/Nr4
GO_BP_m2	GO:001839	internal pe	1/470	144/23843	0.94362	0.9511	0.890448	Auts2
GO_BP_m2	GO:007066	positive reg	1/470	145/23843	0.944738	0.951998	0.891289	Il12rb1
GO_BP_m2	GO:200011	regulation	2/470	234/23843	0.94672	0.953767	0.892945	Rack1/Sfrp
GO_BP_m2	GO:003134	positive reg	3/470	312/23843	0.947135	0.953956	0.893122	Mavs/Penk
GO_BP_m2	GO:000647	internal pro	1/470	149/23843	0.948994	0.955598	0.89466	Auts2
GO_BP_m2	GO:000270	regulation	1/470	150/23843	0.950005	0.956387	0.895399	Zbtb1
GO_BP_m2	GO:000631	DNA recon	2/470	239/23843	0.950958	0.957116	0.896081	H2afx/Recq
GO_BP_m2	GO:004508	regulation	2/470	241/23843	0.952561	0.958404	0.897286	Mavs/S100
GO_BP_m2	GO:001839	peptidyl-ly	1/470	153/23843	0.952922	0.958404	0.897286	Auts2
GO_BP_m2	GO:004593	positive reg	1/470	153/23843	0.952922	0.958404	0.897286	Rab11a
GO_BP_m2	GO:000741	synapse as	1/470	158/23843	0.957411	0.962457	0.901081	Agrn
GO_BP_m2	GO:003582	modificatio	1/470	158/23843	0.957411	0.962457	0.901081	Ppib

GO_BP_m2	GO:000761	learning	1/470	161/23843	0.959896	0.964725	0.903204	Grm7
GO_BP_m2	GO:005254	regulation	4/470	407/23843	0.960849	0.965451	0.903884	Ambp/Rac
GO_BP_m2	GO:190303	regulation	1/470	165/23843	0.962987	0.967367	0.905678	Plau
GO_BP_m2	GO:005080	synapse or	3/470	337/23843	0.963524	0.967444	0.90575	Agrn/Lmx1
GO_BP_m2	GO:005087	regulation	3/470	337/23843	0.963524	0.967444	0.90575	Plau/Prl8a2
GO_BP_m2	GO:004349	protein kin	1/470	168/23843	0.965147	0.968842	0.907059	Rack1
GO_BP_m2	GO:005254	regulation	3/470	349/23843	0.969569	0.973048	0.910997	Rack1/Serp
GO_BP_m2	GO:000647	protein ace	1/470	179/23843	0.972047	0.975301	0.913106	Auts2
GO_BP_m2	GO:000687	cellular cal	4/470	433/23843	0.972721	0.975744	0.913521	Bmp4/Chd
GO_BP_m2	GO:005080	regulation	1/470	182/23843	0.97368	0.976473	0.914203	Agrn
GO_BP_m2	GO:005507	calcium ion	4/470	448/23843	0.977943	0.980513	0.917986	Bmp4/Chd
GO_BP_m2	GO:005080	regulation	1/470	194/23843	0.979313	0.981653	0.919053	Agrn
GO_BP_m2	GO:007250	cellular div	4/470	459/23843	0.981158	0.983267	0.920564	Bmp4/Chd
GO_BP_m2	GO:000244	production	2/470	300/23843	0.982565	0.984442	0.921664	Galnt2/Nr4
GO_BP_m2	GO:007250	divalent in	4/470	482/23843	0.986508	0.988157	0.925142	Bmp4/Chd
GO_BP_m2	GO:000237	immunoglo	1/470	222/23843	0.988212	0.989391	0.926297	Galnt2
GO_BP_m2	GO:004354	protein acy	1/470	222/23843	0.988212	0.989391	0.926297	Auts2
GO_BP_m2	GO:005090	detection o	1/470	308/23843	0.997913	0.99875	0.93506	Olfr282
GO_BP_m2	GO:003210	negative re	1/470	311/23843	0.998036	0.99875	0.93506	Plau
GO_BP_m2	GO:000959	detection o	1/470	337/23843	0.998838	0.999314	0.935588	Olfr282
GO_BP_m2	GO:005090	detection o	1/470	377/23843	0.999482	0.999721	0.935968	Olfr282
GO_BP_m2	GO:005160	detection o	1/470	474/23843	0.999928	0.999928	0.936162	Olfr282
GO_BP_m3	GO:004654	saliva secre	5/539	15/23843	1.44E-05	0.06196	0.058464	Aqp5/Neu
GO_BP_m3	GO:005080	positive reg	20/539	326/23843	5.96E-05	0.0971	0.09162	Bcl2l1/Calb
GO_BP_m3	GO:006045	negative re	5/539	20/23843	6.78E-05	0.0971	0.09162	Neurog1/C
GO_BP_m3	GO:009707	ductus arte	3/539	6/23843	0.000218	0.164862	0.155559	Foxf1/Hpg
GO_BP_m3	GO:006029	long-term	15/539	230/23843	0.000254	0.164862	0.155559	Calb2/Gip/
GO_BP_m3	GO:004816	regulation	19/539	342/23843	0.000322	0.164862	0.155559	Bcl2l1/Calb
GO_BP_m3	GO:190024	positive reg	3/539	7/23843	0.000376	0.164862	0.155559	Bcl2l1/Lrrk2
GO_BP_m3	GO:004001	negative re	4/539	16/23843	0.000379	0.164862	0.155559	Atxn2/Ptch
GO_BP_m3	GO:007162	masticatio	2/539	2/23843	0.00051	0.164862	0.155559	Neurog1/T
GO_BP_m3	GO:009858	learned vo	2/539	2/23843	0.00051	0.164862	0.155559	Neurog1/T
GO_BP_m3	GO:190574	negative re	2/539	2/23843	0.00051	0.164862	0.155559	Neurog1/T
GO_BP_m3	GO:190574	hard palate	2/539	2/23843	0.00051	0.164862	0.155559	Neurog1/T
GO_BP_m3	GO:003564	exploratio	5/539	30/23843	0.000517	0.164862	0.155559	Chrna4/Gip
GO_BP_m3	GO:000758	digestion	10/539	125/23843	0.000558	0.164862	0.155559	Adm2/Aqp
GO_BP_m3	GO:006045	negative re	3/539	8/23843	0.000591	0.164862	0.155559	Oxt/Tff2/U
GO_BP_m3	GO:001099	response t	4/539	18/23843	0.000614	0.164862	0.155559	Neurog1/T
GO_BP_m3	GO:003294	secretion b	6/539	49/23843	0.000796	0.189865	0.179151	Aqp5/Neu
GO_BP_m3	GO:004405	regulation	6/539	49/23843	0.000796	0.189865	0.179151	Neurog1/C
GO_BP_m3	GO:004687	regulation	3/539	9/23843	0.000872	0.197068	0.185948	Neurog1/T
GO_BP_m3	GO:200082	regulation	5/539	37/23843	0.00139	0.263359	0.248498	Bmp2/Foxc
GO_BP_m3	GO:007735	thorax and	2/539	3/23843	0.001507	0.263359	0.248498	Neurog1/T
GO_BP_m3	GO:001490	myotube d	2/539	3/23843	0.001507	0.263359	0.248498	Myod1/My
GO_BP_m3	GO:006179	secretory g	2/539	3/23843	0.001507	0.263359	0.248498	Ptprn/Syt4
GO_BP_m3	GO:005080	regulation	12/539	194/23843	0.001611	0.263359	0.248498	2610042L0
GO_BP_m3	GO:009709	synaptic ve	3/539	11/23843	0.001656	0.263359	0.248498	Bcl2l1/Nlgn
GO_BP_m3	GO:190024	regulation	3/539	11/23843	0.001656	0.263359	0.248498	Bcl2l1/Lrrk2

GO_BP_m3	GO:190342	positive re	3/539	11/23843	0.001656	0.263359	0.248498	Bcl2l1/Lrrk
GO_BP_m3	GO:006007	excitatory	7/539	78/23843	0.00192	0.289539	0.2732	Chrna4/Cu
GO_BP_m3	GO:002260	digestive s	8/539	100/23843	0.001955	0.289539	0.2732	Aqp5/Neur
GO_BP_m3	GO:000341	chondrocy	3/539	12/23843	0.002171	0.297797	0.280992	Axin2/Col2
GO_BP_m3	GO:006045	regulation	3/539	12/23843	0.002171	0.297797	0.280992	Oxt/Tff2/U
GO_BP_m3	GO:001400	glial cell pr	5/539	41/23843	0.002219	0.297797	0.280992	Areg/Hes1
GO_BP_m3	GO:007007	histone lysi	4/539	26/23843	0.002601	0.338486	0.319385	Hsf4/Kdm4
GO_BP_m3	GO:002170	developme	15/539	291/23843	0.002743	0.338978	0.319849	Bmp2/Cats
GO_BP_m3	GO:003316	histone H3	3/539	13/23843	0.002775	0.338978	0.319849	Hsf4/Kdm4
GO_BP_m3	GO:002165	vestibuloc	2/539	4/23843	0.00297	0.338978	0.319849	Neurog1/T
GO_BP_m3	GO:001657	histone de	4/539	27/23843	0.002999	0.338978	0.319849	Hsf4/Kdm4
GO_BP_m3	GO:200030	regulation	4/539	27/23843	0.002999	0.338978	0.319849	Bcl2l1/Lrrk
GO_BP_m3	GO:004846	cell matura	11/539	184/23843	0.003227	0.355362	0.335308	Catsper4/D
GO_BP_m3	GO:190280	regulation	4/539	28/23843	0.003437	0.363761	0.343233	Bcl2l1/Lrrk
GO_BP_m3	GO:002198	adenohypo	3/539	14/23843	0.003472	0.363761	0.343233	Bmp2/Ghr
GO_BP_m3	GO:009881	modulatio	5/539	46/23843	0.003701	0.378451	0.357095	Chrna4/Cu
GO_BP_m3	GO:000648	protein de	4/539	29/23843	0.003917	0.379624	0.358201	Hsf4/Kdm4
GO_BP_m3	GO:000821	protein de	4/539	29/23843	0.003917	0.379624	0.358201	Hsf4/Kdm4
GO_BP_m3	GO:004001	regulation	7/539	89/23843	0.004053	0.379624	0.358201	Atxn2/Gdf5
GO_BP_m3	GO:007213	mesenchy	5/539	47/23843	0.004066	0.379624	0.358201	Bmp2/Foxc
GO_BP_m3	GO:007335	zygotic det	2/539	5/23843	0.004875	0.390787	0.368735	Neurog1/T
GO_BP_m3	GO:001099	free ubiqui	2/539	5/23843	0.004875	0.390787	0.368735	Trim6/Ube
GO_BP_m3	GO:190107	negative re	2/539	5/23843	0.004875	0.390787	0.368735	Neurog1/T
GO_BP_m3	GO:190280	positive re	2/539	5/23843	0.004875	0.390787	0.368735	Bcl2l1/Nlg
GO_BP_m3	GO:200030	positive re	2/539	5/23843	0.004875	0.390787	0.368735	Bcl2l1/Nlg
GO_BP_m3	GO:005105	negative re	21/539	498/23843	0.004973	0.390787	0.368735	Abr/Atxn2/
GO_BP_m3	GO:000995	anterior/p	12/539	223/23843	0.005009	0.390787	0.368735	Axin2/Bmp
GO_BP_m3	GO:004884	artery mor	6/539	70/23843	0.005014	0.390787	0.368735	Foxc2/Foxf
GO_BP_m3	GO:004275	drinking be	3/539	16/23843	0.005166	0.390787	0.368735	Oxt/Tacr1/
GO_BP_m3	GO:009709	craniofacia	3/539	16/23843	0.005166	0.390787	0.368735	Neurog1/T
GO_BP_m3	GO:001082	regulation	11/539	196/23843	0.005186	0.390787	0.368735	2610042L0
GO_BP_m3	GO:005196	regulation	7/539	94/23843	0.005471	0.405149	0.382287	Amigo3/Cu
GO_BP_m3	GO:190353	positive re	19/539	439/23843	0.005612	0.405154	0.382291	Avp/Bcl2l1
GO_BP_m3	GO:004856	embryonic	15/539	315/23843	0.005685	0.405154	0.382291	Abr/Cryaa/
GO_BP_m3	GO:005170	multi-orga	6/539	72/23843	0.005754	0.405154	0.382291	Avp/Helt/
GO_BP_m3	GO:005507	sodium ior	5/539	52/23843	0.006284	0.435314	0.410749	Avp/Oxt/S
GO_BP_m3	GO:004854	digestive tr	5/539	53/23843	0.006812	0.445528	0.420386	Foxf1/Ihh/
GO_BP_m3	GO:009956	chemical s	7/539	98/23843	0.00685	0.445528	0.420386	Chrna4/Cu
GO_BP_m3	GO:002164	vestibuloc	2/539	6/23843	0.007204	0.445528	0.420386	Neurog1/T
GO_BP_m3	GO:003158	activation	2/539	6/23843	0.007204	0.445528	0.420386	Ccl5/Prkcz
GO_BP_m3	GO:004271	sperm ejac	2/539	6/23843	0.007204	0.445528	0.420386	Oxt/Tacr1
GO_BP_m3	GO:200080	positive re	2/539	6/23843	0.007204	0.445528	0.420386	Bcl2l1/Nlg
GO_BP_m3	GO:004817	regulation	3/539	18/23843	0.00728	0.445528	0.420386	Grik2/Syng
GO_BP_m3	GO:190342	regulation	3/539	18/23843	0.00728	0.445528	0.420386	Bcl2l1/Lrrk
GO_BP_m3	GO:003526	multicellula	11/539	206/23843	0.007452	0.445528	0.420386	Atf5/Atxn2
GO_BP_m3	GO:005196	positive re	6/539	76/23843	0.007469	0.445528	0.420386	Amigo3/Cu
GO_BP_m3	GO:006007	regulation	7/539	100/23843	0.007629	0.448833	0.423505	Chrna4/Cu
GO_BP_m3	GO:000169	gastric aci	3/539	19/23843	0.008501	0.45856	0.432683	Oxt/Tff2/U

GO_BP_m3	GO:004683	carbohydra	3/539	19/23843	0.008501	0.45856	0.432683	Fuk/Hk1/Ip
GO_BP_m3	GO:003081	positive re	4/539	36/23843	0.008581	0.45856	0.432683	Avp/Ghrhr/
GO_BP_m3	GO:00508C	regulation	10/539	182/23843	0.008662	0.45856	0.432683	Amigo3/Ca
GO_BP_m3	GO:004855	embryonic	3/539	20/23843	0.009836	0.45856	0.432683	Foxf1/Ihh/T
GO_BP_m3	GO:004577	negative re	5/539	58/23843	0.009926	0.45856	0.432683	Adm2/Ier3/
GO_BP_m3	GO:004516	cell fate co	13/539	274/23843	0.009928	0.45856	0.432683	Bmp2/Cdo
GO_BP_m3	GO:001099	ubiquitin re	2/539	7/23843	0.009935	0.45856	0.432683	Trim6/Ube
GO_BP_m3	GO:009891	retrograde	2/539	7/23843	0.009935	0.45856	0.432683	Nlgn1/Syt4
GO_BP_m3	GO:190011	negative re	2/539	7/23843	0.009935	0.45856	0.432683	Kdm4b/Kd
GO_BP_m3	GO:004866	neuron fate	6/539	81/23843	0.010095	0.45856	0.432683	Epop/Hes1
GO_BP_m3	GO:001063	negative re	16/539	369/23843	0.010334	0.45856	0.432683	Avp/Bcl2l1/
GO_BP_m3	GO:004566	negative re	5/539	59/23843	0.010649	0.45856	0.432683	Areg/Axin2
GO_BP_m3	GO:006133	establishm	3/539	21/23843	0.011285	0.45856	0.432683	Crb3/Foxf1
GO_BP_m3	GO:003027	regulation	11/539	220/23843	0.011839	0.45856	0.432683	Areg/Axin2
GO_BP_m3	GO:19033C	negative re	3/539	22/23843	0.012852	0.45856	0.432683	Abr/Foxf1/
GO_BP_m3	GO:004863	regulation	9/539	165/23843	0.012981	0.45856	0.432683	Bmp2/Cdo
GO_BP_m3	GO:00216C	cranial ner	2/539	8/23843	0.013049	0.45856	0.432683	Neurog1/T
GO_BP_m3	GO:006173	mitochond	2/539	8/23843	0.013049	0.45856	0.432683	Dlat/Dld
GO_BP_m3	GO:190033	regulation	2/539	8/23843	0.013049	0.45856	0.432683	Bag5/Pdia3
GO_BP_m3	GO:20008C	regulation	2/539	8/23843	0.013049	0.45856	0.432683	Bcl2l1/Nlgr
GO_BP_m3	GO:190321	regulation	6/539	86/23843	0.013319	0.45856	0.432683	Ablim3/He
GO_BP_m3	GO:000758	body fluid	7/539	112/23843	0.013736	0.45856	0.432683	Aqp5/Ghrh
GO_BP_m3	GO:004247	inner ear m	7/539	112/23843	0.013736	0.45856	0.432683	Abr/Foxi1/
GO_BP_m3	GO:003581	regulation	3/539	23/23843	0.014536	0.45856	0.432683	Avp/Oxt/Ta
GO_BP_m3	GO:000319	endocardia	4/539	42/23843	0.014669	0.45856	0.432683	Bmp2/Foxf
GO_BP_m3	GO:003581	renal sodiu	3/539	24/23843	0.016338	0.45856	0.432683	Avp/Oxt/Ta
GO_BP_m3	GO:000274	positive re	2/539	9/23843	0.016529	0.45856	0.432683	Hk1/Trim6
GO_BP_m3	GO:000288	negative re	2/539	9/23843	0.016529	0.45856	0.432683	Abr/Foxf1
GO_BP_m3	GO:001401	Schwann c	2/539	9/23843	0.016529	0.45856	0.432683	Nf2/Sox10
GO_BP_m3	GO:002156	vestibuloc	2/539	9/23843	0.016529	0.45856	0.432683	Neurog1/T
GO_BP_m3	GO:003153	positive re	2/539	9/23843	0.016529	0.45856	0.432683	Neurog1/U
GO_BP_m3	GO:003509	behavioral	2/539	9/23843	0.016529	0.45856	0.432683	Chrna4/Ch
GO_BP_m3	GO:006042	lung vascu	2/539	9/23843	0.016529	0.45856	0.432683	Foxf1/Tcf2
GO_BP_m3	GO:00611C	neuroendo	2/539	9/23843	0.016529	0.45856	0.432683	Bmp2/Hes
GO_BP_m3	GO:007047	positive re	2/539	9/23843	0.016529	0.45856	0.432683	Oxt/Tacr1
GO_BP_m3	GO:190545	regulation	2/539	9/23843	0.016529	0.45856	0.432683	Ankle1/Hes
GO_BP_m3	GO:00015C	skeletal sys	19/539	490/23843	0.016615	0.45856	0.432683	Axin2/Bmp
GO_BP_m3	GO:00181C	peptidyl-se	14/539	325/23843	0.016627	0.45856	0.432683	Avp/Fnip2/
GO_BP_m3	GO:190374	regulation	6/539	91/23843	0.017203	0.45856	0.432683	Ablim3/He
GO_BP_m3	GO:005104	positive re	19/539	492/23843	0.017259	0.45856	0.432683	Avp/Bcl2l1/
GO_BP_m3	GO:005088	neuromusc	5/539	67/23843	0.017756	0.45856	0.432683	Abr/Grin2c
GO_BP_m3	GO:190488	cranial skel	5/539	67/23843	0.017756	0.45856	0.432683	Foxc2/Neu
GO_BP_m3	GO:007201	glomerulus	3/539	25/23843	0.018261	0.45856	0.432683	Foxc2/Hes
GO_BP_m3	GO:000752	myoblast f	4/539	45/23843	0.018525	0.45856	0.432683	Cdon/Myo
GO_BP_m3	GO:001071	positive re	4/539	45/23843	0.018525	0.45856	0.432683	Axin2/Bmp
GO_BP_m3	GO:06100C	regulation	4/539	45/23843	0.018525	0.45856	0.432683	Caprin1/Cu
GO_BP_m3	GO:009869	regulation	4/539	46/23843	0.019937	0.45856	0.432683	Bcl2l1/Lrrk
GO_BP_m3	GO:000762	copulation	3/539	26/23843	0.020303	0.45856	0.432683	Avp/Oxt/Ta

GO_BP_m3	GO:00310	regulation	3/539	26/23843	0.020303	0.45856	0.432683	Jdp2/Lrrk2
GO_BP_m3	GO:00459	positive re	3/539	26/23843	0.020303	0.45856	0.432683	Bcl2l1/Nlg
GO_BP_m3	GO:00600	pharyngea	3/539	26/23843	0.020303	0.45856	0.432683	Hes1/Ptch
GO_BP_m3	GO:00614	renal syste	3/539	26/23843	0.020303	0.45856	0.432683	Foxc2/Hes
GO_BP_m3	GO:00614	kidney vas	3/539	26/23843	0.020303	0.45856	0.432683	Foxc2/Hes
GO_BP_m3	GO:00020	negative re	2/539	10/23843	0.020355	0.45856	0.432683	Atxn2/Lrrt
GO_BP_m3	GO:00433	negative re	2/539	10/23843	0.020355	0.45856	0.432683	Abr/Foxf1
GO_BP_m3	GO:00434	regulation	2/539	10/23843	0.020355	0.45856	0.432683	Cdon/Hes1
GO_BP_m3	GO:00985	learned vo	2/539	10/23843	0.020355	0.45856	0.432683	Neurog1/T
GO_BP_m3	GO:190011	regulation	2/539	10/23843	0.020355	0.45856	0.432683	Kdm4b/Kd
GO_BP_m3	GO:00608	artery deve	6/539	96/23843	0.021801	0.45856	0.432683	Foxc2/Foxf
GO_BP_m3	GO:004211	neutrophil	3/539	27/23843	0.022467	0.45856	0.432683	Abr/Ccl5/
GO_BP_m3	GO:00456	positive re	3/539	27/23843	0.022467	0.45856	0.432683	Cdon/Myo
GO_BP_m3	GO:000111	DNA-temp	1/539	1/23843	0.022606	0.45856	0.432683	Gtf2e1
GO_BP_m3	GO:000111	transcripti	1/539	1/23843	0.022606	0.45856	0.432683	Gtf2e1
GO_BP_m3	GO:000112	protein-D	1/539	1/23843	0.022606	0.45856	0.432683	Gtf2e1
GO_BP_m3	GO:00250	central tol	1/539	1/23843	0.022606	0.45856	0.432683	Aire
GO_BP_m3	GO:00071	transmem	1/539	1/23843	0.022606	0.45856	0.432683	Ptpre
GO_BP_m3	GO:000751	myoblast f	1/539	1/23843	0.022606	0.45856	0.432683	Myod1
GO_BP_m3	GO:00090	threonine	1/539	1/23843	0.022606	0.45856	0.432683	Thnsl2
GO_BP_m3	GO:000981	defense re	1/539	1/23843	0.022606	0.45856	0.432683	Tfeb
GO_BP_m3	GO:00101	response t	1/539	1/23843	0.022606	0.45856	0.432683	Ptch1
GO_BP_m3	GO:00101	response t	1/539	1/23843	0.022606	0.45856	0.432683	Tacr1
GO_BP_m3	GO:00148	detection	1/539	1/23843	0.022606	0.45856	0.432683	Foxf1
GO_BP_m3	GO:00149	myoblast f	1/539	1/23843	0.022606	0.45856	0.432683	Mymk
GO_BP_m3	GO:00157	glycerol-3-	1/539	1/23843	0.022606	0.45856	0.432683	Slc37a2
GO_BP_m3	GO:00218	GABAergic	1/539	1/23843	0.022606	0.45856	0.432683	Helt
GO_BP_m3	GO:00307	vitelline m	1/539	1/23843	0.022606	0.45856	0.432683	Ihh
GO_BP_m3	GO:00341	activation	1/539	1/23843	0.022606	0.45856	0.432683	Ucn
GO_BP_m3	GO:00356	helper T c	1/539	1/23843	0.022606	0.45856	0.432683	Ccl5
GO_BP_m3	GO:00356	T-helper 1	1/539	1/23843	0.022606	0.45856	0.432683	Ccl5
GO_BP_m3	GO:00356	T-helper 1	1/539	1/23843	0.022606	0.45856	0.432683	Ccl5
GO_BP_m3	GO:00423	GDP-L-fuc	1/539	1/23843	0.022606	0.45856	0.432683	Fuk
GO_BP_m3	GO:00435	skeletal m	1/539	1/23843	0.022606	0.45856	0.432683	Myod1
GO_BP_m3	GO:00450	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Trib2
GO_BP_m3	GO:00463	2-oxobuty	1/539	1/23843	0.022606	0.45856	0.432683	Thnsl2
GO_BP_m3	GO:00463	2-oxobuty	1/539	1/23843	0.022606	0.45856	0.432683	Thnsl2
GO_BP_m3	GO:00468	response t	1/539	1/23843	0.022606	0.45856	0.432683	Bcl2l1
GO_BP_m3	GO:004807	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Ihh
GO_BP_m3	GO:00480	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Ihh
GO_BP_m3	GO:004817	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:00485	ectoderma	1/539	1/23843	0.022606	0.45856	0.432683	Foxf1
GO_BP_m3	GO:004861	embryonic	1/539	1/23843	0.022606	0.45856	0.432683	Foxf1
GO_BP_m3	GO:004862	post-embr	1/539	1/23843	0.022606	0.45856	0.432683	Nkx2-3
GO_BP_m3	GO:00487	cytoskeleta	1/539	1/23843	0.022606	0.45856	0.432683	Nlgn1
GO_BP_m3	GO:005104	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Bmp2
GO_BP_m3	GO:00510	dihydrolip	1/539	1/23843	0.022606	0.45856	0.432683	Dld
GO_BP_m3	GO:00604	right lung	1/539	1/23843	0.022606	0.45856	0.432683	Foxf1

GO_BP_m3	GO:00608	positive re	1/539	1/23843	0.022606	0.45856	0.432683	Bmp2
GO_BP_m3	GO:00611	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Hes1
GO_BP_m3	GO:00611	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Hes1
GO_BP_m3	GO:00617	vesicle fusi	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:007267	mitochond	1/539	1/23843	0.022606	0.45856	0.432683	Ankzf1
GO_BP_m3	GO:00901	mesenchy	1/539	1/23843	0.022606	0.45856	0.432683	Foxf1
GO_BP_m3	GO:009017	microtubul	1/539	1/23843	0.022606	0.45856	0.432683	Ccdc155
GO_BP_m3	GO:009711	neurexin cl	1/539	1/23843	0.022606	0.45856	0.432683	Nlgn1
GO_BP_m3	GO:009727	creatinine	1/539	1/23843	0.022606	0.45856	0.432683	Tfap2b
GO_BP_m3	GO:009727	cellular am	1/539	1/23843	0.022606	0.45856	0.432683	Tfap2b
GO_BP_m3	GO:009727	cellular cre	1/539	1/23843	0.022606	0.45856	0.432683	Tfap2b
GO_BP_m3	GO:009727	cellular ure	1/539	1/23843	0.022606	0.45856	0.432683	Tfap2b
GO_BP_m3	GO:00988	reduced fo	1/539	1/23843	0.022606	0.45856	0.432683	Slc19a1
GO_BP_m3	GO:009894	retrograde	1/539	1/23843	0.022606	0.45856	0.432683	Nlgn1
GO_BP_m3	GO:00991	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:014004	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Twist1
GO_BP_m3	GO:01400	positive re	1/539	1/23843	0.022606	0.45856	0.432683	Twist1
GO_BP_m3	GO:19015	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Stoml1
GO_BP_m3	GO:19017	mesenchy	1/539	1/23843	0.022606	0.45856	0.432683	Ranbp3l
GO_BP_m3	GO:190247	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Tfeb
GO_BP_m3	GO:190304	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Chrna4
GO_BP_m3	GO:190312	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Lrrk2
GO_BP_m3	GO:190312	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Lrrk2
GO_BP_m3	GO:190312	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Lrrk2
GO_BP_m3	GO:19048	Wnt signal	1/539	1/23843	0.022606	0.45856	0.432683	Lrrk2
GO_BP_m3	GO:19051	manchette	1/539	1/23843	0.022606	0.45856	0.432683	Cep131
GO_BP_m3	GO:190522	epicardium	1/539	1/23843	0.022606	0.45856	0.432683	Tgfbr1
GO_BP_m3	GO:190541	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:190541	positive re	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:19054	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:19054	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Syt4
GO_BP_m3	GO:19054	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Ankle1
GO_BP_m3	GO:190551	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Nlgn1
GO_BP_m3	GO:190552	positive re	1/539	1/23843	0.022606	0.45856	0.432683	Nlgn1
GO_BP_m3	GO:19056	positive re	1/539	1/23843	0.022606	0.45856	0.432683	Nlgn1
GO_BP_m3	GO:199022	paranodal	1/539	1/23843	0.022606	0.45856	0.432683	Whrn
GO_BP_m3	GO:19909	intramanch	1/539	1/23843	0.022606	0.45856	0.432683	Cep131
GO_BP_m3	GO:20008	regulation	1/539	1/23843	0.022606	0.45856	0.432683	Twist1
GO_BP_m3	GO:20008	positive re	1/539	1/23843	0.022606	0.45856	0.432683	Twist1
GO_BP_m3	GO:200081	negative re	1/539	1/23843	0.022606	0.45856	0.432683	Myod1
GO_BP_m3	GO:000751	muscle org	16/539	405/23843	0.022771	0.45856	0.432683	Bmp2/Cdo
GO_BP_m3	GO:006034	bone morp	6/539	97/23843	0.022811	0.45856	0.432683	Axin2/Col2
GO_BP_m3	GO:00015	detection	4/539	48/23843	0.022955	0.45856	0.432683	Car6/Pigr/
GO_BP_m3	GO:00519	positive re	4/539	48/23843	0.022955	0.45856	0.432683	Avp/Chrna
GO_BP_m3	GO:00610	cell differe	4/539	48/23843	0.022955	0.45856	0.432683	Foxc2/Hes
GO_BP_m3	GO:00020	lens devel	5/539	72/23843	0.023494	0.46153	0.435486	Cdon/Crya
GO_BP_m3	GO:00305	regulation	5/539	72/23843	0.023494	0.46153	0.435486	Bmp2/Gp
GO_BP_m3	GO:00509	neuromusc	7/539	125/23843	0.023634	0.46153	0.435486	Abr/Atxn2/

GO_BP_m3	GO:200102	regulation	9/539	183/23843	0.023756	0.46153	0.435486	Ankle1/Arr
GO_BP_m3	GO:000211	aggressive	2/539	11/23843	0.02451	0.46153	0.435486	Avp/Tacr1
GO_BP_m3	GO:00215	trigeminal	2/539	11/23843	0.02451	0.46153	0.435486	Neurog1/T
GO_BP_m3	GO:004592	regulation	2/539	11/23843	0.02451	0.46153	0.435486	Avp/Oxt
GO_BP_m3	GO:006007	micturition	2/539	11/23843	0.02451	0.46153	0.435486	Chrnb4/Ta
GO_BP_m3	GO:00613	cardiac ne	2/539	11/23843	0.02451	0.46153	0.435486	Hes1/Twist
GO_BP_m3	GO:007047	regulation	2/539	11/23843	0.02451	0.46153	0.435486	Oxt/Tacr1
GO_BP_m3	GO:01400	neuron pro	2/539	11/23843	0.02451	0.46153	0.435486	Lrrk2/Nlgn
GO_BP_m3	GO:00458	negative re	4/539	49/23843	0.024562	0.46153	0.435486	Atxn2/Lrrtr
GO_BP_m3	GO:005077	positive re	4/539	49/23843	0.024562	0.46153	0.435486	Caprin1/Cu
GO_BP_m3	GO:00104	exit from n	3/539	28/23843	0.02475	0.46153	0.435486	Ctdp1/Neu
GO_BP_m3	GO:00485	embryonic	3/539	28/23843	0.02475	0.46153	0.435486	Cryaa/Ihh/
GO_BP_m3	GO:00020	chondrocy	6/539	99/23843	0.024924	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:00301	regulation	11/539	247/23843	0.025525	0.46153	0.435486	Abr/Atxn2/
GO_BP_m3	GO:001401	positive re	5/539	74/23843	0.026088	0.46153	0.435486	Bmp2/Hes
GO_BP_m3	GO:001401	negative re	4/539	50/23843	0.026236	0.46153	0.435486	Atf5/Hes1/
GO_BP_m3	GO:00301	water hom	4/539	50/23843	0.026236	0.46153	0.435486	Avp/Cela2a
GO_BP_m3	GO:00351	hindlimb m	4/539	50/23843	0.026236	0.46153	0.435486	Gdf5/Ptch1
GO_BP_m3	GO:003517	social beha	4/539	50/23843	0.026236	0.46153	0.435486	Avp/Mkks/
GO_BP_m3	GO:00517	intraspecie	4/539	50/23843	0.026236	0.46153	0.435486	Avp/Mkks/
GO_BP_m3	GO:00328	regulation	10/539	218/23843	0.027104	0.46153	0.435486	1110004E0
GO_BP_m3	GO:004311	regulation	3/539	29/23843	0.027154	0.46153	0.435486	Abr/Tacr1/
GO_BP_m3	GO:00440	regulation	3/539	29/23843	0.027154	0.46153	0.435486	Avp/Oxt/Ta
GO_BP_m3	GO:006031	cardiac epi	3/539	29/23843	0.027154	0.46153	0.435486	Bmp2/Tgfb
GO_BP_m3	GO:00302	bone mine	6/539	101/23843	0.027164	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:000741	synapse as	8/539	158/23843	0.027545	0.46153	0.435486	2610042L0
GO_BP_m3	GO:000164	osteoblast	9/539	188/23843	0.027634	0.46153	0.435486	Areg/Axin2
GO_BP_m3	GO:001082	negative re	4/539	51/23843	0.027976	0.46153	0.435486	Avp/Bcl2l1
GO_BP_m3	GO:005091	sensory pe	4/539	51/23843	0.027976	0.46153	0.435486	Car6/Pigr/
GO_BP_m3	GO:00016	ureteric bu	6/539	102/23843	0.028332	0.46153	0.435486	Bmp2/Crlf1
GO_BP_m3	GO:00721	mesoneph	6/539	102/23843	0.028332	0.46153	0.435486	Bmp2/Crlf1
GO_BP_m3	GO:00721	mesoneph	6/539	102/23843	0.028332	0.46153	0.435486	Bmp2/Crlf1
GO_BP_m3	GO:009747	synaptic ve	7/539	130/23843	0.02849	0.46153	0.435486	Ap3s1/Bcl2
GO_BP_m3	GO:19033	regulation	7/539	130/23843	0.02849	0.46153	0.435486	Abr/Bcl2l1/
GO_BP_m3	GO:19039	positive re	5/539	76/23843	0.028858	0.46153	0.435486	Ablim3/He
GO_BP_m3	GO:00485	embryonic	18/539	486/23843	0.028871	0.46153	0.435486	Abr/Cryaa/
GO_BP_m3	GO:00060	acetyl-Co	2/539	12/23843	0.028978	0.46153	0.435486	Dlat/Dld
GO_BP_m3	GO:000907	serine fam	2/539	12/23843	0.028978	0.46153	0.435486	Gcsh/Thnsl
GO_BP_m3	GO:00304	peristalsis	2/539	12/23843	0.028978	0.46153	0.435486	Neurog1/T
GO_BP_m3	GO:004521	cell-cell ju	2/539	12/23843	0.028978	0.46153	0.435486	Prtn3/Whr
GO_BP_m3	GO:007047	uterine sm	2/539	12/23843	0.028978	0.46153	0.435486	Oxt/Tacr1
GO_BP_m3	GO:00032	endocardia	3/539	30/23843	0.029678	0.46153	0.435486	Bmp2/Tgfb
GO_BP_m3	GO:004592	negative re	3/539	30/23843	0.029678	0.46153	0.435486	Abr/Foxf1/
GO_BP_m3	GO:00308	positive re	4/539	52/23843	0.029784	0.46153	0.435486	Avp/Ghrhr
GO_BP_m3	GO:00488	genitalia d	4/539	52/23843	0.029784	0.46153	0.435486	Dhcr24/Ne
GO_BP_m3	GO:005091	detection	4/539	52/23843	0.029784	0.46153	0.435486	Car6/Pigr/
GO_BP_m3	GO:003121	biomineral	7/539	132/23843	0.030609	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:00709	demethyla	4/539	53/23843	0.031659	0.46153	0.435486	Hsf4/Kdm4

GO_BP_m3	GO:190275	negative re	4/539	53/23843	0.031659	0.46153	0.435486	Atf5/Fanci/
GO_BP_m3	GO:005071	positive re	7/539	133/23843	0.031707	0.46153	0.435486	C1qtnf4/Hl
GO_BP_m3	GO:005196	regulation	5/539	78/23843	0.031807	0.46153	0.435486	Grik2/Grm
GO_BP_m3	GO:190374	positive re	5/539	78/23843	0.031807	0.46153	0.435486	Ablim3/He
GO_BP_m3	GO:000182	mesoneph	6/539	105/23843	0.032034	0.46153	0.435486	Bmp2/Crlf1
GO_BP_m3	GO:007052	protein kin	3/539	31/23843	0.032321	0.46153	0.435486	Avp/Prkch/
GO_BP_m3	GO:009016	establishm	3/539	31/23843	0.032321	0.46153	0.435486	Crb3/Foxf1
GO_BP_m3	GO:200046	positive re	3/539	31/23843	0.032321	0.46153	0.435486	Cux2/Nlgn
GO_BP_m3	GO:001401	regulation	7/539	134/23843	0.032831	0.46153	0.435486	Atf5/Bmp2
GO_BP_m3	GO:004247	ear morph	7/539	134/23843	0.032831	0.46153	0.435486	Abr/Foxi1/
GO_BP_m3	GO:000758	excretion	4/539	54/23843	0.033602	0.46153	0.435486	Avp/Chrnb
GO_BP_m3	GO:000732	inseminati	2/539	13/23843	0.033742	0.46153	0.435486	Oxt/Tacr1
GO_BP_m3	GO:000735	tripartite r	2/539	13/23843	0.033742	0.46153	0.435486	Neurog1/T
GO_BP_m3	GO:000859	anterior/p	2/539	13/23843	0.033742	0.46153	0.435486	Neurog1/T
GO_BP_m3	GO:000922	nucleotide	2/539	13/23843	0.033742	0.46153	0.435486	Fuk/Pmm1
GO_BP_m3	GO:001975	one-carbo	2/539	13/23843	0.033742	0.46153	0.435486	Aqp5/Slc1
GO_BP_m3	GO:003122	auditory b	2/539	13/23843	0.033742	0.46153	0.435486	Neurog1/T
GO_BP_m3	GO:003209	negative re	2/539	13/23843	0.033742	0.46153	0.435486	Mkks/Ucn
GO_BP_m3	GO:003369	positive re	2/539	13/23843	0.033742	0.46153	0.435486	Bmp2/Tme
GO_BP_m3	GO:003581	positive re	2/539	13/23843	0.033742	0.46153	0.435486	Oxt/Tacr1
GO_BP_m3	GO:004311	positive re	2/539	13/23843	0.033742	0.46153	0.435486	Tacr1/Ucn
GO_BP_m3	GO:004559	positive re	2/539	13/23843	0.033742	0.46153	0.435486	Cd46/Carm
GO_BP_m3	GO:005157	negative re	2/539	13/23843	0.033742	0.46153	0.435486	Kdm4b/Kd
GO_BP_m3	GO:007010	interleukin	2/539	13/23843	0.033742	0.46153	0.435486	C1qtnf4/Ct
GO_BP_m3	GO:007064	protein mc	7/539	135/23843	0.033981	0.46153	0.435486	Cops7a/Ep
GO_BP_m3	GO:009730	response t	7/539	135/23843	0.033981	0.46153	0.435486	Bcl2l1/Hpg
GO_BP_m3	GO:004881	regulation	6/539	107/23843	0.034669	0.46153	0.435486	Caprin1/Cu
GO_BP_m3	GO:006034	bone devel	9/539	196/23843	0.034733	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:001715	regulation	5/539	80/23843	0.034938	0.46153	0.435486	Bcl2l1/Lrrk
GO_BP_m3	GO:003509	response t	3/539	32/23843	0.035083	0.46153	0.435486	Chrna4/Ch
GO_BP_m3	GO:003623	granulocyt	3/539	32/23843	0.035083	0.46153	0.435486	Abr/Ccl5/D
GO_BP_m3	GO:004481	mitotic G2	3/539	32/23843	0.035083	0.46153	0.435486	Fanci/Ier3/
GO_BP_m3	GO:006025	regulation	3/539	32/23843	0.035083	0.46153	0.435486	Hes1/Prkch
GO_BP_m3	GO:006035	cartilage d	3/539	32/23843	0.035083	0.46153	0.435486	Axin2/Col2
GO_BP_m3	GO:004566	regulation	7/539	136/23843	0.035158	0.46153	0.435486	Areg/Axin2
GO_BP_m3	GO:000300	heart morp	11/539	260/23843	0.03516	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:001820	peptidyl-se	14/539	360/23843	0.035522	0.46153	0.435486	Avp/Fnip2/
GO_BP_m3	GO:004660	regulation	4/539	55/23843	0.035613	0.46153	0.435486	Atf5/Ccnf/
GO_BP_m3	GO:004853	thymus de	4/539	55/23843	0.035613	0.46153	0.435486	Aire/Hes1/
GO_BP_m3	GO:005122	positive re	17/539	464/23843	0.036018	0.46153	0.435486	Ablim3/C1
GO_BP_m3	GO:003524	synaptic tr	6/539	108/23843	0.036037	0.46153	0.435486	Grik2/Grik4
GO_BP_m3	GO:007200	nephron e	6/539	108/23843	0.036037	0.46153	0.435486	Bmp2/Foxc
GO_BP_m3	GO:007016	regulation	5/539	81/23843	0.036572	0.46153	0.435486	Bmp2/Gpn
GO_BP_m3	GO:000150	ossification	14/539	362/23843	0.036939	0.46153	0.435486	Areg/Axin2
GO_BP_m3	GO:000693	smooth mu	6/539	109/23843	0.037439	0.46153	0.435486	Chrnb4/Mk
GO_BP_m3	GO:000150	action pote	7/539	138/23843	0.037592	0.46153	0.435486	Catsper4/C
GO_BP_m3	GO:000683	mitochond	11/539	263/23843	0.037705	0.46153	0.435486	Ablim3/Bcl
GO_BP_m3	GO:009059	sensory or	12/539	296/23843	0.037804	0.46153	0.435486	Abr/Aqp5/

GO_BP_m3	GO:00456	positive re	16/539	432/23843	0.037827	0.46153	0.435486	Bend6/Bm
GO_BP_m3	GO:00456	negative re	3/539	33/23843	0.037962	0.46153	0.435486	Atf5/Hes1/
GO_BP_m3	GO:004804	embryonic	3/539	33/23843	0.037962	0.46153	0.435486	Cryaa/Ihh/
GO_BP_m3	GO:004852	positive re	3/539	33/23843	0.037962	0.46153	0.435486	Ghrhr/Nlg
GO_BP_m3	GO:00485	embryonic	3/539	33/23843	0.037962	0.46153	0.435486	Foxf1/Ihh/
GO_BP_m3	GO:00030	regionaliza	14/539	364/23843	0.038396	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:001404	positive re	2/539	14/23843	0.038787	0.46153	0.435486	Avp/Syt4
GO_BP_m3	GO:00320	negative re	2/539	14/23843	0.038787	0.46153	0.435486	Mkks/Ucn
GO_BP_m3	GO:00355	positive re	2/539	14/23843	0.038787	0.46153	0.435486	Kdm4d/Tu
GO_BP_m3	GO:004324	erythrocyt	2/539	14/23843	0.038787	0.46153	0.435486	Klf2/L3mbt
GO_BP_m3	GO:00451	establishm	2/539	14/23843	0.038787	0.46153	0.435486	Crb3/Foxf1
GO_BP_m3	GO:00517	negative re	2/539	14/23843	0.038787	0.46153	0.435486	Ptch1/Susc
GO_BP_m3	GO:00601	female ma	2/539	14/23843	0.038787	0.46153	0.435486	Avp/Oxt
GO_BP_m3	GO:00613	cardiac ne	2/539	14/23843	0.038787	0.46153	0.435486	Hes1/Twist
GO_BP_m3	GO:190002	positive re	2/539	14/23843	0.038787	0.46153	0.435486	Nlgn1/Car
GO_BP_m3	GO:00514	regulation	5/539	83/23843	0.03998	0.46153	0.435486	Mkks/Nf2/
GO_BP_m3	GO:00488	inner ear d	9/539	202/23843	0.040818	0.46153	0.435486	Abr/Bmp2/
GO_BP_m3	GO:004667	response t	12/539	300/23843	0.041169	0.46153	0.435486	Ankzf1/Bcl
GO_BP_m3	GO:007207	kidney epit	7/539	141/23843	0.041446	0.46153	0.435486	Bmp2/Crlf1
GO_BP_m3	GO:00215	telencepha	10/539	236/23843	0.042901	0.46153	0.435486	Atat1/Atf5/
GO_BP_m3	GO:00027	positive re	12/539	302/23843	0.042928	0.46153	0.435486	C1qtnf4/Ex
GO_BP_m3	GO:00487	mesenchyr	9/539	204/23843	0.042997	0.46153	0.435486	Axin2/Bmp
GO_BP_m3	GO:001607	synaptic ve	5/539	85/23843	0.043574	0.46153	0.435486	Bcl2l1/Lrrk
GO_BP_m3	GO:00459	positive re	5/539	85/23843	0.043574	0.46153	0.435486	Avp/Bcl2l1
GO_BP_m3	GO:190054	positive re	5/539	85/23843	0.043574	0.46153	0.435486	Avp/Bcl2l1
GO_BP_m3	GO:00508	cognition	12/539	303/23843	0.043826	0.46153	0.435486	Chrna4/Cu
GO_BP_m3	GO:19049	positive re	17/539	476/23843	0.043977	0.46153	0.435486	Ablim3/C1
GO_BP_m3	GO:000761	long-term	3/539	35/23843	0.044071	0.46153	0.435486	Prkcz/Sgk1
GO_BP_m3	GO:00027	regulation	2/539	15/23843	0.044098	0.46153	0.435486	Hk1/Trim6
GO_BP_m3	GO:00216	cerebellar	2/539	15/23843	0.044098	0.46153	0.435486	Atxn2/Whr
GO_BP_m3	GO:00613	cardiac ne	2/539	15/23843	0.044098	0.46153	0.435486	Hes1/Twist
GO_BP_m3	GO:007072	response t	2/539	15/23843	0.044098	0.46153	0.435486	Ptch1/Tgfb
GO_BP_m3	GO:190107	regulation	2/539	15/23843	0.044098	0.46153	0.435486	Neurog1/T
GO_BP_m3	GO:19044	positive re	2/539	15/23843	0.044098	0.46153	0.435486	C1qtnf4/Lr
GO_BP_m3	GO:001922	cytokine-m	14/539	372/23843	0.044633	0.46153	0.435486	C1qtnf4/C
GO_BP_m3	GO:000157	medium-cl	1/539	2/23843	0.044702	0.46153	0.435486	Slc27a4
GO_BP_m3	GO:000241	immunogl	1/539	2/23843	0.044702	0.46153	0.435486	Pigr
GO_BP_m3	GO:00024	peripheral	1/539	2/23843	0.044702	0.46153	0.435486	Aire
GO_BP_m3	GO:00024	peripheral	1/539	2/23843	0.044702	0.46153	0.435486	Aire
GO_BP_m3	GO:00025	central tol	1/539	2/23843	0.044702	0.46153	0.435486	Aire
GO_BP_m3	GO:000324	cardiac mu	1/539	2/23843	0.044702	0.46153	0.435486	S1pr1
GO_BP_m3	GO:000612	glyceroph	1/539	2/23843	0.044702	0.46153	0.435486	Slc37a2
GO_BP_m3	GO:000671	estrogen c	1/539	2/23843	0.044702	0.46153	0.435486	Ugt1a7c
GO_BP_m3	GO:00074	ectoderma	1/539	2/23843	0.044702	0.46153	0.435486	Foxf1
GO_BP_m3	GO:00091	lipoate me	1/539	2/23843	0.044702	0.46153	0.435486	Dld
GO_BP_m3	GO:000981	defense re	1/539	2/23843	0.044702	0.46153	0.435486	Tfeb
GO_BP_m3	GO:00190	suppressio	1/539	2/23843	0.044702	0.46153	0.435486	Bcl2l1
GO_BP_m3	GO:00219	neural plat	1/539	2/23843	0.044702	0.46153	0.435486	Ptch1

GO_BP_m3	GO:003242	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Axin2
GO_BP_m3	GO:00356	helper T ce	1/539	2/23843	0.044702	0.46153	0.435486	Ccl5
GO_BP_m3	GO:00358	egg coat f	1/539	2/23843	0.044702	0.46153	0.435486	Ihh
GO_BP_m3	GO:003952	modulatio	1/539	2/23843	0.044702	0.46153	0.435486	Bcl2l1
GO_BP_m3	GO:004331	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Abr
GO_BP_m3	GO:00451	cell-cell si	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:004597	positive re	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:004622	coumarin	1/539	2/23843	0.044702	0.46153	0.435486	Ugt1a7c
GO_BP_m3	GO:004627	phenylpro	1/539	2/23843	0.044702	0.46153	0.435486	Ugt1a7c
GO_BP_m3	GO:00463	lateral inhi	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:004807	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Ihh
GO_BP_m3	GO:004834	paraxial m	1/539	2/23843	0.044702	0.46153	0.435486	Foxc2
GO_BP_m3	GO:004834	paraxial m	1/539	2/23843	0.044702	0.46153	0.435486	Foxc2
GO_BP_m3	GO:004861	embryonic	1/539	2/23843	0.044702	0.46153	0.435486	Foxf1
GO_BP_m3	GO:005104	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Bmp2
GO_BP_m3	GO:00519	methotrex	1/539	2/23843	0.044702	0.46153	0.435486	Slc19a1
GO_BP_m3	GO:005274	inositol ph	1/539	2/23843	0.044702	0.46153	0.435486	Ippk
GO_BP_m3	GO:00601	somatotro	1/539	2/23843	0.044702	0.46153	0.435486	Ghrhr
GO_BP_m3	GO:006022	camera-ty	1/539	2/23843	0.044702	0.46153	0.435486	Ihh
GO_BP_m3	GO:006031	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Abr
GO_BP_m3	GO:00604	positive re	1/539	2/23843	0.044702	0.46153	0.435486	Oxt
GO_BP_m3	GO:00604	right lung	1/539	2/23843	0.044702	0.46153	0.435486	Foxf1
GO_BP_m3	GO:00605	dichotomo	1/539	2/23843	0.044702	0.46153	0.435486	Areg
GO_BP_m3	GO:00611	stomach n	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:00701	positive re	1/539	2/23843	0.044702	0.46153	0.435486	C1qtnf4
GO_BP_m3	GO:007191	urea trans	1/539	2/23843	0.044702	0.46153	0.435486	Slc14a1
GO_BP_m3	GO:007192	alpha-tub	1/539	2/23843	0.044702	0.46153	0.435486	Atat1
GO_BP_m3	GO:007201	glomerular	1/539	2/23843	0.044702	0.46153	0.435486	Foxc2
GO_BP_m3	GO:007207	kidney inte	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:007214	renal inters	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:008012	AMP trans	1/539	2/23843	0.044702	0.46153	0.435486	Slc25a17
GO_BP_m3	GO:009727	ammonia	1/539	2/23843	0.044702	0.46153	0.435486	Tfap2b
GO_BP_m3	GO:009727	urea home	1/539	2/23843	0.044702	0.46153	0.435486	Tfap2b
GO_BP_m3	GO:00975	stress resp	1/539	2/23843	0.044702	0.46153	0.435486	Klf2
GO_BP_m3	GO:00975	cellular stre	1/539	2/23843	0.044702	0.46153	0.435486	Klf2
GO_BP_m3	GO:00975	thymus epi	1/539	2/23843	0.044702	0.46153	0.435486	Aire
GO_BP_m3	GO:009874	cerebellar	1/539	2/23843	0.044702	0.46153	0.435486	Nanos1
GO_BP_m3	GO:00989	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Chrna4
GO_BP_m3	GO:009954	trans-syna	1/539	2/23843	0.044702	0.46153	0.435486	Nlgn1
GO_BP_m3	GO:19015	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Stoml1
GO_BP_m3	GO:19022	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Foxc2
GO_BP_m3	GO:190231	positive re	1/539	2/23843	0.044702	0.46153	0.435486	Dusp26
GO_BP_m3	GO:19024	positive re	1/539	2/23843	0.044702	0.46153	0.435486	Lrrk2
GO_BP_m3	GO:190407	presynapti	1/539	2/23843	0.044702	0.46153	0.435486	Nlgn1
GO_BP_m3	GO:19046	positive re	1/539	2/23843	0.044702	0.46153	0.435486	Ptprn
GO_BP_m3	GO:190527	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Lrrk2
GO_BP_m3	GO:19052	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Lrrk2
GO_BP_m3	GO:19905	dense core	1/539	2/23843	0.044702	0.46153	0.435486	Ptprn

GO_BP_m3	GO:200022	regulation	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:200022	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Hes1
GO_BP_m3	GO:200027	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Twist1
GO_BP_m3	GO:200046	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Lrrk2
GO_BP_m3	GO:200081	negative re	1/539	2/23843	0.044702	0.46153	0.435486	Carmil2
GO_BP_m3	GO:200116	positive reg	1/539	2/23843	0.044702	0.46153	0.435486	Ctr9
GO_BP_m3	GO:000165	metanephr	5/539	86/23843	0.045442	0.466919	0.440571	Foxc2/Hes1
GO_BP_m3	GO:001922	transmissio	5/539	86/23843	0.045442	0.466919	0.440571	Avp/Chrnb
GO_BP_m3	GO:005104	negative re	10/539	239/23843	0.046039	0.471471	0.444865	Abr/Btn1a1
GO_BP_m3	GO:000761	learning or	11/539	272/23843	0.046104	0.471471	0.444865	Cux2/Gip/C
GO_BP_m3	GO:004870	skeletal sys	10/539	240/23843	0.047118	0.478578	0.451572	Axin2/Col2
GO_BP_m3	GO:190227	regulation	8/539	176/23843	0.047215	0.478578	0.451572	Ctr9/Jdp2/
GO_BP_m3	GO:001025	multicellula	3/539	36/23843	0.047297	0.478578	0.451572	Ghrhr/Helt
GO_BP_m3	GO:004871	regulation	3/539	36/23843	0.047297	0.478578	0.451572	Atf5/Bmp2
GO_BP_m3	GO:003101	pancreas d	5/539	87/23843	0.047356	0.478578	0.451572	Foxf1/Gip/
GO_BP_m3	GO:005196	negative re	13/539	342/23843	0.048434	0.479167	0.452128	Atf5/Bag5/
GO_BP_m3	GO:000228	neutrophil	2/539	16/23843	0.049659	0.479167	0.452128	Abr/Dnase
GO_BP_m3	GO:000335	regulation	2/539	16/23843	0.049659	0.479167	0.452128	1110004E0
GO_BP_m3	GO:000683	water trans	2/539	16/23843	0.049659	0.479167	0.452128	Aqp5/Slc14
GO_BP_m3	GO:000763	mechanose	2/539	16/23843	0.049659	0.479167	0.452128	Neurog1/T
GO_BP_m3	GO:001404	regulation	2/539	16/23843	0.049659	0.479167	0.452128	Dleu2/Lrrk2
GO_BP_m3	GO:003210	negative re	2/539	16/23843	0.049659	0.479167	0.452128	Mkks/Ucn
GO_BP_m3	GO:003210	negative re	2/539	16/23843	0.049659	0.479167	0.452128	Mkks/Ucn
GO_BP_m3	GO:003223	positive reg	2/539	16/23843	0.049659	0.479167	0.452128	Nlgn1/Tacr
GO_BP_m3	GO:003363	positive reg	2/539	16/23843	0.049659	0.479167	0.452128	Ccl5/Foxc2
GO_BP_m3	GO:003511	genitalia m	2/539	16/23843	0.049659	0.479167	0.452128	Neurog1/T
GO_BP_m3	GO:003612	histone H3	2/539	16/23843	0.049659	0.479167	0.452128	Kdm4b/Kd
GO_BP_m3	GO:004308	penile erec	2/539	16/23843	0.049659	0.479167	0.452128	Avp/Oxt
GO_BP_m3	GO:004826	negative re	2/539	16/23843	0.049659	0.479167	0.452128	Atxn2/Lrrtm
GO_BP_m3	GO:004871	positive reg	2/539	16/23843	0.049659	0.479167	0.452128	Bmp2/Hes1
GO_BP_m3	GO:006025	negative re	2/539	16/23843	0.049659	0.479167	0.452128	Hes1/Sox1
GO_BP_m3	GO:006064	mammary	2/539	16/23843	0.049659	0.479167	0.452128	Foxf1/Ptch
GO_BP_m3	GO:007162	vocalizatio	2/539	16/23843	0.049659	0.479167	0.452128	Neurog1/T
GO_BP_m3	GO:009022	chromosor	2/539	16/23843	0.049659	0.479167	0.452128	Ankle1/Ccc
GO_BP_m3	GO:200072	negative re	2/539	16/23843	0.049659	0.479167	0.452128	Bmp2/Ctdp
GO_BP_m3	GO:003050	positive reg	3/539	37/23843	0.050636	0.479167	0.452128	Bmp2/Gpm
GO_BP_m3	GO:004662	negative re	3/539	37/23843	0.050636	0.479167	0.452128	Prkcz/Ptpre
GO_BP_m3	GO:003139	regulation	8/539	179/23843	0.051202	0.479167	0.452128	Bag5/Ctr9/
GO_BP_m3	GO:000076	syncytium	4/539	62/23843	0.051601	0.479167	0.452128	Cdon/Myo
GO_BP_m3	GO:006103	regulation	4/539	62/23843	0.051601	0.479167	0.452128	Axin2/Bmp
GO_BP_m3	GO:000709	centrosom	6/539	118/23843	0.051632	0.479167	0.452128	Atf5/Ccnf/C
GO_BP_m3	GO:003105	regulation	7/539	149/23843	0.052946	0.479167	0.452128	Ctr9/Jdp2/
GO_BP_m3	GO:000057	embryonic	3/539	38/23843	0.054087	0.479167	0.452128	Neurog1/P
GO_BP_m3	GO:000272	positive reg	3/539	38/23843	0.054087	0.479167	0.452128	Hk1/Prkcz/
GO_BP_m3	GO:000727	synaptic tra	3/539	38/23843	0.054087	0.479167	0.452128	Chrna4/Ch
GO_BP_m3	GO:007221	metanephr	3/539	38/23843	0.054087	0.479167	0.452128	Hes1/Tcf21
GO_BP_m3	GO:009880	regulation	3/539	38/23843	0.054087	0.479167	0.452128	Avp/Oxt/Ta
GO_BP_m3	GO:006099	dendritic sp	4/539	63/23843	0.054158	0.479167	0.452128	Caprin1/Cu

GO_BP_m3	GO:003313	positive reg	6/539	120/23843	0.055175	0.479167	0.452128	Avp/Fnip2/
GO_BP_m3	GO:190353	regulation	6/539	120/23843	0.055175	0.479167	0.452128	Ablim3/He
GO_BP_m3	GO:000608	acetyl-CoA	2/539	17/23843	0.055458	0.479167	0.452128	Dlat/Dld
GO_BP_m3	GO:000709	regulation	2/539	17/23843	0.055458	0.479167	0.452128	Neurog1/U
GO_BP_m3	GO:000735	blastoderm	2/539	17/23843	0.055458	0.479167	0.452128	Neurog1/T
GO_BP_m3	GO:003001	maintenan	2/539	17/23843	0.055458	0.479167	0.452128	Pdzd11/Ca
GO_BP_m3	GO:003433	cell junctio	2/539	17/23843	0.055458	0.479167	0.452128	Prtn3/Whr
GO_BP_m3	GO:003439	telomere lo	2/539	17/23843	0.055458	0.479167	0.452128	Ankle1/Ccd
GO_BP_m3	GO:003447	snRNA 3'-e	2/539	17/23843	0.055458	0.479167	0.452128	Exosc6/Ints
GO_BP_m3	GO:005144	negative re	2/539	17/23843	0.055458	0.479167	0.452128	Bag5/Mad2
GO_BP_m3	GO:000694	syncytium	4/539	64/23843	0.056781	0.479167	0.452128	Cdon/Myo
GO_BP_m3	GO:004692	regulation	4/539	64/23843	0.056781	0.479167	0.452128	Bcl2l1/Lrrk2
GO_BP_m3	GO:004848	synaptic ve	6/539	121/23843	0.057001	0.479167	0.452128	Ap3s1/Bcl2
GO_BP_m3	GO:009748	establishm	6/539	121/23843	0.057001	0.479167	0.452128	Ap3s1/Bcl2
GO_BP_m3	GO:002198	pituitary gl	3/539	39/23843	0.057647	0.479167	0.452128	Bmp2/Ghrh
GO_BP_m3	GO:003107	embryonic	3/539	39/23843	0.057647	0.479167	0.452128	Cryaa/Ihh/
GO_BP_m3	GO:005506	monovalen	7/539	152/23843	0.057727	0.479167	0.452128	Avp/Lrrk2/
GO_BP_m3	GO:000693	muscle con	11/539	283/23843	0.058	0.479167	0.452128	Chrnb4/Clc
GO_BP_m3	GO:005121	cartilage de	8/539	184/23843	0.058317	0.479167	0.452128	Axin2/Bmp
GO_BP_m3	GO:005076	negative re	12/539	318/23843	0.058901	0.479167	0.452128	Atf5/Bag5/
GO_BP_m3	GO:190432	response to	4/539	65/23843	0.059472	0.479167	0.452128	Fdx1/Mir10
GO_BP_m3	GO:190432	cellular res	4/539	65/23843	0.059472	0.479167	0.452128	Fdx1/Mir10
GO_BP_m3	GO:007050	regulation	8/539	185/23843	0.059811	0.479167	0.452128	Atat1/Atf5/
GO_BP_m3	GO:003027	negative re	5/539	93/23843	0.059836	0.479167	0.452128	Areg/Axin2
GO_BP_m3	GO:006144	connective	10/539	251/23843	0.060125	0.479167	0.452128	Axin2/Bmp
GO_BP_m3	GO:004856	digestive tr	6/539	123/23843	0.06076	0.479167	0.452128	Foxf1/Hes1
GO_BP_m3	GO:003541	protein loc	3/539	40/23843	0.061315	0.479167	0.452128	Grin2c/Lrrt
GO_BP_m3	GO:005070	regulation	8/539	186/23843	0.061329	0.479167	0.452128	Btn1a1/C1
GO_BP_m3	GO:000152	pseudourid	2/539	18/23843	0.06148	0.479167	0.452128	Pus7l/Rpus
GO_BP_m3	GO:000195	positive reg	2/539	18/23843	0.06148	0.479167	0.452128	Bcl2l1/Nlgn
GO_BP_m3	GO:001607	rRNA catab	2/539	18/23843	0.06148	0.479167	0.452128	Dis3/Exosc
GO_BP_m3	GO:003316	positive reg	2/539	18/23843	0.06148	0.479167	0.452128	Lrrk2/Ptpn
GO_BP_m3	GO:003458	piRNA met	2/539	18/23843	0.06148	0.479167	0.452128	Mov10l1/P
GO_BP_m3	GO:003508	establishm	2/539	18/23843	0.06148	0.479167	0.452128	Crb3/Foxf1
GO_BP_m3	GO:003631	response to	2/539	18/23843	0.06148	0.479167	0.452128	Ptch1/Tgfb
GO_BP_m3	GO:004271	maternal b	2/539	18/23843	0.06148	0.479167	0.452128	Avp/Oxt
GO_BP_m3	GO:011002	regulation	5/539	94/23843	0.062081	0.479167	0.452128	Mkks/Nf2/
GO_BP_m3	GO:000988	embryonic	4/539	66/23843	0.062229	0.479167	0.452128	Ihh/Neurog
GO_BP_m3	GO:006147	response to	4/539	66/23843	0.062229	0.479167	0.452128	Fdx1/Mir10
GO_BP_m3	GO:003238	positive reg	10/539	253/23843	0.062718	0.479167	0.452128	Ablim3/Bcl
GO_BP_m3	GO:007265	establishm	7/539	155/23843	0.062765	0.479167	0.452128	Ablim3/He
GO_BP_m3	GO:006105	somite dev	5/539	95/23843	0.064373	0.479167	0.452128	Axin2/Foxc
GO_BP_m3	GO:009917	regulation	4/539	67/23843	0.065053	0.479167	0.452128	Caprin1/Cu
GO_BP_m3	GO:000018	activation o	3/539	41/23843	0.06509	0.479167	0.452128	Lrrk2/Map3
GO_BP_m3	GO:002152	spinal cord	3/539	41/23843	0.06509	0.479167	0.452128	Mir19a/Nk
GO_BP_m3	GO:190007	negative re	3/539	41/23843	0.06509	0.479167	0.452128	Prkcz/Ptpre
GO_BP_m3	GO:007123	cellular res	8/539	189/23843	0.066027	0.479167	0.452128	Ankzf1/Fdx
GO_BP_m3	GO:009025	regulation	9/539	222/23843	0.066154	0.479167	0.452128	Chrnb4/Ctc

GO_BP_m3	GO:000212	maternal a	1/539	3/23843	0.0663	0.479167	0.452128	Avp
GO_BP_m3	GO:00023	immune re	1/539	3/23843	0.0663	0.479167	0.452128	Pigr
GO_BP_m3	GO:000241	immunogl	1/539	3/23843	0.0663	0.479167	0.452128	Pigr
GO_BP_m3	GO:00030	angiotensi	1/539	3/23843	0.0663	0.479167	0.452128	Tacr1
GO_BP_m3	GO:00031	BMP signal	1/539	3/23843	0.0663	0.479167	0.452128	Bmp2
GO_BP_m3	GO:00031	endoderm	1/539	3/23843	0.0663	0.479167	0.452128	Bmp2
GO_BP_m3	GO:00031	endoderm	1/539	3/23843	0.0663	0.479167	0.452128	Bmp2
GO_BP_m3	GO:000327	apoptotic	1/539	3/23843	0.0663	0.479167	0.452128	Foxc2
GO_BP_m3	GO:00064	valyl-tRNA	1/539	3/23843	0.0663	0.479167	0.452128	Vars
GO_BP_m3	GO:000654	glycine cat	1/539	3/23843	0.0663	0.479167	0.452128	Gcsh
GO_BP_m3	GO:00067	NADH reg	1/539	3/23843	0.0663	0.479167	0.452128	Hk1
GO_BP_m3	GO:00092	GDP-man	1/539	3/23843	0.0663	0.479167	0.452128	Pmm1
GO_BP_m3	GO:00147	branchiom	1/539	3/23843	0.0663	0.479167	0.452128	Tcf21
GO_BP_m3	GO:001591	aminophos	1/539	3/23843	0.0663	0.479167	0.452128	Tmem30b
GO_BP_m3	GO:00165	intein-mec	1/539	3/23843	0.0663	0.479167	0.452128	Ihh
GO_BP_m3	GO:00194	glycine dec	1/539	3/23843	0.0663	0.479167	0.452128	Gcsh
GO_BP_m3	GO:00215	trochlear n	1/539	3/23843	0.0663	0.479167	0.452128	Hes1
GO_BP_m3	GO:002191	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Nkx6-1
GO_BP_m3	GO:00309	protein spl	1/539	3/23843	0.0663	0.479167	0.452128	Ihh
GO_BP_m3	GO:00330	directional	1/539	3/23843	0.0663	0.479167	0.452128	Grin2c
GO_BP_m3	GO:003312	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Twist1
GO_BP_m3	GO:00336	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Bcl2l1
GO_BP_m3	GO:00347	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Hamp2
GO_BP_m3	GO:00347	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Hamp2
GO_BP_m3	GO:00347	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Hamp2
GO_BP_m3	GO:00350	embryonic	1/539	3/23843	0.0663	0.479167	0.452128	Bmp2
GO_BP_m3	GO:00364	synaptic ve	1/539	3/23843	0.0663	0.479167	0.452128	Bcl2l1
GO_BP_m3	GO:00420	interleukin-	1/539	3/23843	0.0663	0.479167	0.452128	Trib2
GO_BP_m3	GO:00423	GDP-L-fuc	1/539	3/23843	0.0663	0.479167	0.452128	Fuk
GO_BP_m3	GO:00426	auditory re	1/539	3/23843	0.0663	0.479167	0.452128	Hes1
GO_BP_m3	GO:00427	eye photor	1/539	3/23843	0.0663	0.479167	0.452128	Ihh
GO_BP_m3	GO:00431	hindgut co	1/539	3/23843	0.0663	0.479167	0.452128	Oxt
GO_BP_m3	GO:00431	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Oxt
GO_BP_m3	GO:00433	positive re	1/539	3/23843	0.0663	0.479167	0.452128	Cd46
GO_BP_m3	GO:004431	protein K6-	1/539	3/23843	0.0663	0.479167	0.452128	Otud3
GO_BP_m3	GO:004477	meiotic D	1/539	3/23843	0.0663	0.479167	0.452128	Oraov1
GO_BP_m3	GO:004507	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Trib2
GO_BP_m3	GO:00456	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Hes1
GO_BP_m3	GO:00465	photorece	1/539	3/23843	0.0663	0.479167	0.452128	Ihh
GO_BP_m3	GO:00483	lateral mes	1/539	3/23843	0.0663	0.479167	0.452128	Foxf1
GO_BP_m3	GO:004837	lateral mes	1/539	3/23843	0.0663	0.479167	0.452128	Foxf1
GO_BP_m3	GO:004837	lateral mes	1/539	3/23843	0.0663	0.479167	0.452128	Foxf1
GO_BP_m3	GO:00484	synaptic ve	1/539	3/23843	0.0663	0.479167	0.452128	Syngr1
GO_BP_m3	GO:005204	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Bcl2l1
GO_BP_m3	GO:00524	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Bcl2l1
GO_BP_m3	GO:006002	regulation	1/539	3/23843	0.0663	0.479167	0.452128	2610042L0
GO_BP_m3	GO:00600	synaptic tr	1/539	3/23843	0.0663	0.479167	0.452128	Chrnb4
GO_BP_m3	GO:006012	corticotrop	1/539	3/23843	0.0663	0.479167	0.452128	Bmp2

GO_BP_m3	GO:00601	cellular prc	1/539	3/23843	0.0663	0.479167	0.452128	Bcl2l1
GO_BP_m3	GO:00604	bronchiole	1/539	3/23843	0.0663	0.479167	0.452128	Tcf21
GO_BP_m3	GO:00609	response t	1/539	3/23843	0.0663	0.479167	0.452128	Bcl2l1
GO_BP_m3	GO:00610	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Bag5
GO_BP_m3	GO:00611	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Axin2
GO_BP_m3	GO:00616	canonical	1/539	3/23843	0.0663	0.479167	0.452128	Hk1
GO_BP_m3	GO:006171	glucose ca	1/539	3/23843	0.0663	0.479167	0.452128	Hk1
GO_BP_m3	GO:00716	nuclear prc	1/539	3/23843	0.0663	0.479167	0.452128	Ankzf1
GO_BP_m3	GO:00721	mesenchyr	1/539	3/23843	0.0663	0.479167	0.452128	Bmp2
GO_BP_m3	GO:007227	metanephr	1/539	3/23843	0.0663	0.479167	0.452128	Tcf21
GO_BP_m3	GO:007227	metanephr	1/539	3/23843	0.0663	0.479167	0.452128	Tcf21
GO_BP_m3	GO:007227	metanephr	1/539	3/23843	0.0663	0.479167	0.452128	Tcf21
GO_BP_m3	GO:00990	retrograde	1/539	3/23843	0.0663	0.479167	0.452128	Syt4
GO_BP_m3	GO:00995	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Calb2
GO_BP_m3	GO:00995	synaptic m	1/539	3/23843	0.0663	0.479167	0.452128	Nlgn1
GO_BP_m3	GO:19022	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Foxc2
GO_BP_m3	GO:19025	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Abr
GO_BP_m3	GO:19033	positive re	1/539	3/23843	0.0663	0.479167	0.452128	Pdia3
GO_BP_m3	GO:190507	occluding j	1/539	3/23843	0.0663	0.479167	0.452128	Tgfbr1
GO_BP_m3	GO:190507	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Tgfbr1
GO_BP_m3	GO:190507	positive re	1/539	3/23843	0.0663	0.479167	0.452128	Tgfbr1
GO_BP_m3	GO:19054	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Hes1
GO_BP_m3	GO:19056	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Nlgn1
GO_BP_m3	GO:19901	protein K2	1/539	3/23843	0.0663	0.479167	0.452128	Otud3
GO_BP_m3	GO:19907	presynapti	1/539	3/23843	0.0663	0.479167	0.452128	Nlgn1
GO_BP_m3	GO:20000	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Axin2
GO_BP_m3	GO:200011	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Stc2
GO_BP_m3	GO:20004	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Lrrk2
GO_BP_m3	GO:20007	cell prolifer	1/539	3/23843	0.0663	0.479167	0.452128	Twist1
GO_BP_m3	GO:200097	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Hes1
GO_BP_m3	GO:200097	negative re	1/539	3/23843	0.0663	0.479167	0.452128	Hes1
GO_BP_m3	GO:20011	regulation	1/539	3/23843	0.0663	0.479167	0.452128	Ctr9
GO_BP_m3	GO:00310	microtubul	6/539	126/23843	0.066668	0.479167	0.452128	Atf5/Ccnf/
GO_BP_m3	GO:00062	regulation	5/539	96/23843	0.066712	0.479167	0.452128	Axin2/D33
GO_BP_m3	GO:00300	contractile	5/539	96/23843	0.066712	0.479167	0.452128	Mkks/Nf2/
GO_BP_m3	GO:004314	stress fiber	5/539	96/23843	0.066712	0.479167	0.452128	Mkks/Nf2/
GO_BP_m3	GO:004577	positive re	5/539	96/23843	0.066712	0.479167	0.452128	Bmp2/Gpn
GO_BP_m3	GO:00609	kidney mo	5/539	96/23843	0.066712	0.479167	0.452128	Bmp2/Hes
GO_BP_m3	GO:00720	nephron tu	5/539	96/23843	0.066712	0.479167	0.452128	Bmp2/Hes
GO_BP_m3	GO:00023	leukocyte	10/539	256/23843	0.06674	0.479167	0.452128	Abr/Cd46/
GO_BP_m3	GO:00604	mesenchyr	10/539	256/23843	0.06674	0.479167	0.452128	Axin2/Bmp
GO_BP_m3	GO:00106	programm	2/539	19/23843	0.067713	0.479167	0.452128	Dnase1l3/
GO_BP_m3	GO:00216	cerebellar	2/539	19/23843	0.067713	0.479167	0.452128	Atxn2/Whr
GO_BP_m3	GO:00308	polarized	2/539	19/23843	0.067713	0.479167	0.452128	Crb3/Foxf1
GO_BP_m3	GO:00320	regulation	2/539	19/23843	0.067713	0.479167	0.452128	Mkks/Ucn
GO_BP_m3	GO:00336	positive re	2/539	19/23843	0.067713	0.479167	0.452128	Chrna4/Ox
GO_BP_m3	GO:004304	DNA meth	2/539	19/23843	0.067713	0.479167	0.452128	Mov10l1/P
GO_BP_m3	GO:00604	positive re	2/539	19/23843	0.067713	0.479167	0.452128	Oxt/Tacr1

GO_BP_m3	GO:006074	parental b	2/539	19/23843	0.067713	0.479167	0.452128	Avp/Oxt
GO_BP_m3	GO:00902	negative r	2/539	19/23843	0.067713	0.479167	0.452128	Avp/Bcl2l1
GO_BP_m3	GO:20007	negative r	2/539	19/23843	0.067713	0.479167	0.452128	D330045A
GO_BP_m3	GO:00720	renal syste	11/539	291/23843	0.067825	0.479167	0.452128	Bmp2/Crlf1
GO_BP_m3	GO:00425	regulation	4/539	68/23843	0.067942	0.479167	0.452128	Ccl5/Crlf1/
GO_BP_m3	GO:004584	negative r	4/539	68/23843	0.067942	0.479167	0.452128	Bmp2/Ctd
GO_BP_m3	GO:004864	regulation	4/539	68/23843	0.067942	0.479167	0.452128	Cdon/Myo
GO_BP_m3	GO:0003	regulation	3/539	42/23843	0.068968	0.481656	0.454476	Celf5/Mbn
GO_BP_m3	GO:001097	negative r	3/539	42/23843	0.068968	0.481656	0.454476	Fanci/Ier3/
GO_BP_m3	GO:001607	snRNA me	3/539	42/23843	0.068968	0.481656	0.454476	Exosc6/Int
GO_BP_m3	GO:00310	negative r	3/539	42/23843	0.068968	0.481656	0.454476	Kdm4b/Kd
GO_BP_m3	GO:00701	positive re	3/539	42/23843	0.068968	0.481656	0.454476	Bmp2/Gpn
GO_BP_m3	GO:009031	regulation	3/539	42/23843	0.068968	0.481656	0.454476	Jdp2/Lrrk2
GO_BP_m3	GO:001072	negative r	13/539	362/23843	0.069225	0.482666	0.455429	Atf5/Bag5/
GO_BP_m3	GO:00423	regulation	15/539	434/23843	0.069858	0.484926	0.457561	Bcl2l1/Cats
GO_BP_m3	GO:00705	protein loc	7/539	159/23843	0.069888	0.484926	0.457561	Ablim3/He
GO_BP_m3	GO:19016	response t	7/539	159/23843	0.069888	0.484926	0.457561	Bcl2l1/Fdx
GO_BP_m3	GO:006067	ureteric bu	4/539	69/23843	0.070897	0.491136	0.463421	Bmp2/Hes
GO_BP_m3	GO:000301	renal syste	5/539	98/23843	0.071531	0.493493	0.465645	Avp/Chrnb
GO_BP_m3	GO:00322	regulation	5/539	98/23843	0.071531	0.493493	0.465645	Mkks/Nf2/
GO_BP_m3	GO:00022	cell activati	10/539	260/23843	0.072354	0.493493	0.465645	Abr/Cd46/
GO_BP_m3	GO:00017	cell fate de	3/539	43/23843	0.072949	0.493493	0.465645	Hes1/Myo
GO_BP_m3	GO:001802	peptidyl-ly	3/539	43/23843	0.072949	0.493493	0.465645	Ctr9/Kdm4
GO_BP_m3	GO:00451	establishm	3/539	43/23843	0.072949	0.493493	0.465645	Crb3/Foxf1
GO_BP_m3	GO:003304	regulation	12/539	330/23843	0.0732	0.493493	0.465645	Axin2/Ctr9
GO_BP_m3	GO:00162	regulation	7/539	161/23843	0.073623	0.493493	0.465645	Bmp2/Cdo
GO_BP_m3	GO:00309	hindbrain	7/539	161/23843	0.073623	0.493493	0.465645	Atf5/Atxn2
GO_BP_m3	GO:00215	diencephal	4/539	70/23843	0.073917	0.493493	0.465645	Bmp2/Ghr
GO_BP_m3	GO:00486	negative r	4/539	70/23843	0.073917	0.493493	0.465645	Bmp2/Ctd
GO_BP_m3	GO:00509	sensory pe	4/539	70/23843	0.073917	0.493493	0.465645	Car6/Pigr/
GO_BP_m3	GO:007217	mesoneph	4/539	70/23843	0.073917	0.493493	0.465645	Bmp2/Hes
GO_BP_m3	GO:000237	cytokine se	2/539	20/23843	0.074144	0.493493	0.465645	Hk1/Trim6
GO_BP_m3	GO:000681	phosphate	2/539	20/23843	0.074144	0.493493	0.465645	Slc37a2/St
GO_BP_m3	GO:000834	determinat	2/539	20/23843	0.074144	0.493493	0.465645	Ghrhr/Lrrk
GO_BP_m3	GO:00310	positive re	2/539	20/23843	0.074144	0.493493	0.465645	Jdp2/Lrrk2
GO_BP_m3	GO:00353	thioester b	2/539	20/23843	0.074144	0.493493	0.465645	Dlat/Dld
GO_BP_m3	GO:00457	negative r	2/539	20/23843	0.074144	0.493493	0.465645	D330045A
GO_BP_m3	GO:00600	inhibitory	2/539	20/23843	0.074144	0.493493	0.465645	Chrna4/Gri
GO_BP_m3	GO:00611	establishm	2/539	20/23843	0.074144	0.493493	0.465645	Crb3/Foxf1
GO_BP_m3	GO:00706	transepithe	2/539	20/23843	0.074144	0.493493	0.465645	P2ry6/Prss
GO_BP_m3	GO:007161	acyl-CoA b	2/539	20/23843	0.074144	0.493493	0.465645	Dlat/Dld
GO_BP_m3	GO:19052	negative r	2/539	20/23843	0.074144	0.493493	0.465645	Bmp2/Ctd
GO_BP_m3	GO:00062	DNA repai	15/539	438/23843	0.074208	0.493493	0.465645	Axin2/Ccd
GO_BP_m3	GO:00510	positive re	8/539	194/23843	0.07434	0.493493	0.465645	Bmp2/Gnl
GO_BP_m3	GO:009031	positive re	8/539	194/23843	0.07434	0.493493	0.465645	Ablim3/Ce
GO_BP_m3	GO:004544	fat cell diff	9/539	228/23843	0.075337	0.496742	0.46871	Atat1/Atf5/
GO_BP_m3	GO:009772	sperm mot	5/539	100/23843	0.076535	0.496742	0.46871	Catsper4/
GO_BP_m3	GO:19000	positive re	5/539	100/23843	0.076535	0.496742	0.46871	Caprin1/Cu

GO_BP_m3	GO:000726	tyrosine ph	4/539	71/23843	0.077001	0.496742	0.46871	Ccl5/Crlf1/
GO_BP_m3	GO:190186	negative re	4/539	71/23843	0.077001	0.496742	0.46871	Bmp2/Ctdp
GO_BP_m3	GO:003289	positive re	3/539	44/23843	0.07703	0.496742	0.46871	Avp/Oxt/Sy
GO_BP_m3	GO:004848	synaptic ve	3/539	44/23843	0.07703	0.496742	0.46871	Bcl2l1/Lrrk
GO_BP_m3	GO:000821	regulation	8/539	196/23843	0.077834	0.496742	0.46871	Adm2/Avp
GO_BP_m3	GO:190186	regulation	7/539	164/23843	0.079443	0.496742	0.46871	Bmp2/Cdo
GO_BP_m3	GO:000761	memory	6/539	132/23843	0.079454	0.496742	0.46871	Cux2/Gip/
GO_BP_m3	GO:004505	regulated	8/539	197/23843	0.079618	0.496742	0.46871	Abr/Bcl2l1/
GO_BP_m3	GO:004244	hormone b	4/539	72/23843	0.080148	0.496742	0.46871	Bmp2/Fdx1
GO_BP_m3	GO:005500	cardiac mu	4/539	72/23843	0.080148	0.496742	0.46871	Bmp2/Foxc
GO_BP_m3	GO:000232	lymphoid p	2/539	21/23843	0.080761	0.496742	0.46871	Ankle1/Hes
GO_BP_m3	GO:000762	grooming	2/539	21/23843	0.080761	0.496742	0.46871	Avp/Oxt
GO_BP_m3	GO:003233	negative re	2/539	21/23843	0.080761	0.496742	0.46871	Gdf5/Tgfbr
GO_BP_m3	GO:007211	cell prolifer	2/539	21/23843	0.080761	0.496742	0.46871	Bmp2/Ptch
GO_BP_m3	GO:003019	collagen fi	3/539	45/23843	0.081209	0.496742	0.46871	Adamts14/
GO_BP_m3	GO:003052	androgen	3/539	45/23843	0.081209	0.496742	0.46871	Kdm5d/Me
GO_BP_m3	GO:005089	multicellula	3/539	45/23843	0.081209	0.496742	0.46871	Avp/Cela2a
GO_BP_m3	GO:006041	ventricular	3/539	45/23843	0.081209	0.496742	0.46871	Hes1/Mir1
GO_BP_m3	GO:004863	regulation	13/539	372/23843	0.081533	0.496742	0.46871	Atxn2/Ctdp
GO_BP_m3	GO:003527	endocrine	6/539	133/23843	0.081709	0.496742	0.46871	Bmp2/Ghr
GO_BP_m3	GO:005105	negative re	6/539	133/23843	0.081709	0.496742	0.46871	Ankle1/D3
GO_BP_m3	GO:006132	renal tubul	5/539	102/23843	0.081724	0.496742	0.46871	Bmp2/Hes
GO_BP_m3	GO:003081	regulation	4/539	73/23843	0.083359	0.496742	0.46871	Avp/Ghrhr/
GO_BP_m3	GO:004358	ear develo	9/539	233/23843	0.083559	0.496742	0.46871	Abr/Bmp2/
GO_BP_m3	GO:000279	regulation	16/539	483/23843	0.083774	0.496742	0.46871	Btn1a1/C1
GO_BP_m3	GO:005105	regulation	14/539	411/23843	0.085233	0.496742	0.46871	Ankle1/Are
GO_BP_m3	GO:000301	muscle sys	13/539	375/23843	0.08548	0.496742	0.46871	Chrnb4/Cl
GO_BP_m3	GO:000209	regulation	3/539	46/23843	0.085484	0.496742	0.46871	Atxn2/Lrrt
GO_BP_m3	GO:003513	forelimb m	3/539	46/23843	0.085484	0.496742	0.46871	Gdf5/Tfap
GO_BP_m3	GO:005143	regulation	3/539	46/23843	0.085484	0.496742	0.46871	Bag5/Mad
GO_BP_m3	GO:009010	cochlea de	3/539	46/23843	0.085484	0.496742	0.46871	Hes1/Neur
GO_BP_m3	GO:000182	kidney dev	10/539	269/23843	0.086044	0.496742	0.46871	Bmp2/Crlf
GO_BP_m3	GO:004649	nicotinami	6/539	135/23843	0.086327	0.496742	0.46871	Dlat/Dld/F
GO_BP_m3	GO:009950	synaptic ve	6/539	135/23843	0.086327	0.496742	0.46871	Bcl2l1/Lrrk
GO_BP_m3	GO:003528	segmentati	5/539	104/23843	0.087095	0.496742	0.46871	Axin2/Foxc
GO_BP_m3	GO:000032	re-entry in	1/539	4/23843	0.08741	0.496742	0.46871	Ccnf
GO_BP_m3	GO:000073	DNA catab	1/539	4/23843	0.08741	0.496742	0.46871	Isg20
GO_BP_m3	GO:000208	inhibition	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:000246	tolerance i	1/539	4/23843	0.08741	0.496742	0.46871	Aire
GO_BP_m3	GO:000343	growth pla	1/539	4/23843	0.08741	0.496742	0.46871	Col27a1
GO_BP_m3	GO:000762	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Avp
GO_BP_m3	GO:000995	epidermal	1/539	4/23843	0.08741	0.496742	0.46871	Ptch1
GO_BP_m3	GO:001084	positive re	1/539	4/23843	0.08741	0.496742	0.46871	Nlgn1
GO_BP_m3	GO:001608	synaptic ve	1/539	4/23843	0.08741	0.496742	0.46871	Nlgn1
GO_BP_m3	GO:001833	protein su	1/539	4/23843	0.08741	0.496742	0.46871	Dld
GO_BP_m3	GO:002155	midbrain-	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:002155	oculomoto	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:002191	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Nkx6-1

GO_BP_m3	GO:003234	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Bmp2
GO_BP_m3	GO:003234	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Bmp2
GO_BP_m3	GO:003284	positive re	1/539	4/23843	0.08741	0.496742	0.46871	Avp
GO_BP_m3	GO:003363	positive re	1/539	4/23843	0.08741	0.496742	0.46871	Ccl5
GO_BP_m3	GO:003472	histone H3	1/539	4/23843	0.08741	0.496742	0.46871	Ctr9
GO_BP_m3	GO:003510	operant co	1/539	4/23843	0.08741	0.496742	0.46871	Tacr1
GO_BP_m3	GO:003535	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Twist1
GO_BP_m3	GO:003547	positive re	1/539	4/23843	0.08741	0.496742	0.46871	Foxc2
GO_BP_m3	GO:003556	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Lrrk2
GO_BP_m3	GO:003561	histone H2	1/539	4/23843	0.08741	0.496742	0.46871	Epop
GO_BP_m3	GO:003569	CD8-positi	1/539	4/23843	0.08741	0.496742	0.46871	Ccl5
GO_BP_m3	GO:003572	intraciliary	1/539	4/23843	0.08741	0.496742	0.46871	Ttc30a1
GO_BP_m3	GO:003590	ascending	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:003591	ascending	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:003810	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Mkks
GO_BP_m3	GO:004338	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Cd46
GO_BP_m3	GO:004340	glucocortic	1/539	4/23843	0.08741	0.496742	0.46871	Sgk1
GO_BP_m3	GO:004563	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:004636	GDP-L-fuc	1/539	4/23843	0.08741	0.496742	0.46871	Fuk
GO_BP_m3	GO:004660	positive re	1/539	4/23843	0.08741	0.496742	0.46871	Ranbp3l
GO_BP_m3	GO:004688	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Ucn2
GO_BP_m3	GO:004862	myoblast fa	1/539	4/23843	0.08741	0.496742	0.46871	Myod1
GO_BP_m3	GO:005161	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Gpm6b
GO_BP_m3	GO:005179	short-chair	1/539	4/23843	0.08741	0.496742	0.46871	Thnsl2
GO_BP_m3	GO:006012	somatotrop	1/539	4/23843	0.08741	0.496742	0.46871	Ghrhr
GO_BP_m3	GO:006012	thyroid-sti	1/539	4/23843	0.08741	0.496742	0.46871	Bmp2
GO_BP_m3	GO:006046	prevention	1/539	4/23843	0.08741	0.496742	0.46871	Adam24
GO_BP_m3	GO:006047	acrosomal	1/539	4/23843	0.08741	0.496742	0.46871	Syt6
GO_BP_m3	GO:006103	epithelial c	1/539	4/23843	0.08741	0.496742	0.46871	Foxf1
GO_BP_m3	GO:006108	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Bag5
GO_BP_m3	GO:006120	cell prolifer	1/539	4/23843	0.08741	0.496742	0.46871	Bmp2
GO_BP_m3	GO:007009	positive re	1/539	4/23843	0.08741	0.496742	0.46871	Gip
GO_BP_m3	GO:007010	regulation	1/539	4/23843	0.08741	0.496742	0.46871	C1qtnf4
GO_BP_m3	GO:007060	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Axin2
GO_BP_m3	GO:007103	CUT catabo	1/539	4/23843	0.08741	0.496742	0.46871	Dis3
GO_BP_m3	GO:007104	CUT metab	1/539	4/23843	0.08741	0.496742	0.46871	Dis3
GO_BP_m3	GO:007200	glomerular	1/539	4/23843	0.08741	0.496742	0.46871	Foxc2
GO_BP_m3	GO:007205	juxtaglome	1/539	4/23843	0.08741	0.496742	0.46871	Mir330
GO_BP_m3	GO:007214	glomerular	1/539	4/23843	0.08741	0.496742	0.46871	Foxc2
GO_BP_m3	GO:007216	metanephr	1/539	4/23843	0.08741	0.496742	0.46871	Tcf21
GO_BP_m3	GO:009702	mature cor	1/539	4/23843	0.08741	0.496742	0.46871	Prtn3
GO_BP_m3	GO:009953	synaptic sig	1/539	4/23843	0.08741	0.496742	0.46871	Syt4
GO_BP_m3	GO:009954	trans-syna	1/539	4/23843	0.08741	0.496742	0.46871	Syt4
GO_BP_m3	GO:010607	histone suc	1/539	4/23843	0.08741	0.496742	0.46871	Dld
GO_BP_m3	GO:190249	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Lrrk2
GO_BP_m3	GO:190333	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Bag5
GO_BP_m3	GO:190336	protein loc	1/539	4/23843	0.08741	0.496742	0.46871	Pdzd11
GO_BP_m3	GO:200005	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Axin2

GO_BP_m3	GO:200006	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Bmp2
GO_BP_m3	GO:200041	regulation	1/539	4/23843	0.08741	0.496742	0.46871	Aire
GO_BP_m3	GO:200050	positive reg	1/539	4/23843	0.08741	0.496742	0.46871	Ccl5
GO_BP_m3	GO:200066	positive reg	1/539	4/23843	0.08741	0.496742	0.46871	Prkcz
GO_BP_m3	GO:200098	negative re	1/539	4/23843	0.08741	0.496742	0.46871	Hes1
GO_BP_m3	GO:200116	positive reg	1/539	4/23843	0.08741	0.496742	0.46871	Ctr9
GO_BP_m3	GO:004560	positive reg	2/539	22/23843	0.087551	0.496742	0.46871	Prkch/Ptch
GO_BP_m3	GO:005085	positive reg	2/539	22/23843	0.087551	0.496742	0.46871	Prkch/Usp1
GO_BP_m3	GO:006074	mammary	2/539	22/23843	0.087551	0.496742	0.46871	Areg/Foxf1
GO_BP_m3	GO:006137	mammary	2/539	22/23843	0.087551	0.496742	0.46871	Areg/Foxf1
GO_BP_m3	GO:190153	regulation	2/539	22/23843	0.087551	0.496742	0.46871	Ankle1/He
GO_BP_m3	GO:000170	in utero em	15/539	450/23843	0.088312	0.500397	0.472159	Bcl2l1/Bmp
GO_BP_m3	GO:004870	embryonic	6/539	136/23843	0.088689	0.501867	0.473547	Foxc2/Hox
GO_BP_m3	GO:004665	lymphocyte	11/539	306/23843	0.088995	0.502937	0.474556	Btn1a1/Ccl
GO_BP_m3	GO:000072	double-str	5/539	105/23843	0.089848	0.504463	0.475996	Ccdc155/D
GO_BP_m3	GO:000072	recombina	5/539	105/23843	0.089848	0.504463	0.475996	Ccdc155/D
GO_BP_m3	GO:200017	regulation	5/539	105/23843	0.089848	0.504463	0.475996	Cdon/Lrrk2
GO_BP_m3	GO:003233	regulation	3/539	47/23843	0.089852	0.504463	0.475996	Axin2/Gdf5
GO_BP_m3	GO:004848	autonomic	3/539	47/23843	0.089852	0.504463	0.475996	Hes1/Sox1
GO_BP_m3	GO:000176	morphogen	9/539	237/23843	0.09051	0.507496	0.478858	Areg/Bmp2
GO_BP_m3	GO:000726	neurotrans	6/539	137/23843	0.091085	0.508066	0.479396	Bcl2l1/Lrrk2
GO_BP_m3	GO:001936	pyridine nu	6/539	137/23843	0.091085	0.508066	0.479396	Dlat/Dld/F
GO_BP_m3	GO:005512	digestive sy	6/539	137/23843	0.091085	0.508066	0.479396	Foxf1/Hes1
GO_BP_m3	GO:009964	signal relea	6/539	137/23843	0.091085	0.508066	0.479396	Bcl2l1/Lrrk2
GO_BP_m3	GO:009874	cell-cell ad	7/539	170/23843	0.091859	0.511543	0.482677	Amigo3/Br
GO_BP_m3	GO:003294	mononucle	11/539	308/23843	0.092091	0.511543	0.482677	Btn1a1/Ccl
GO_BP_m3	GO:005071	positive reg	10/539	273/23843	0.0926	0.511543	0.482677	C1qtnf4/Ex
GO_BP_m3	GO:005138	response to	4/539	76/23843	0.09336	0.511543	0.482677	Areg/Ghrh
GO_BP_m3	GO:000738	pattern spe	15/539	454/23843	0.093368	0.511543	0.482677	Axin2/Bmp
GO_BP_m3	GO:000722	smoothene	6/539	138/23843	0.093517	0.511543	0.482677	Cdon/Foxf1
GO_BP_m3	GO:000631	DNA recon	9/539	239/23843	0.09411	0.511543	0.482677	Ankle1/Ccd
GO_BP_m3	GO:001086	positive reg	3/539	48/23843	0.094312	0.511543	0.482677	Bmp2/Gdf5
GO_BP_m3	GO:002154	cranial nerv	3/539	48/23843	0.094312	0.511543	0.482677	Hes1/Neur
GO_BP_m3	GO:003265	regulation	3/539	48/23843	0.094312	0.511543	0.482677	Cd46/Prkcz
GO_BP_m3	GO:004255	neuron ma	3/539	48/23843	0.094312	0.511543	0.482677	Dleu2/Lrrk2
GO_BP_m3	GO:000318	atrioventric	2/539	23/23843	0.094505	0.511543	0.482677	Bmp2/Twis
GO_BP_m3	GO:003209	regulation	2/539	23/23843	0.094505	0.511543	0.482677	Mkks/Ucn
GO_BP_m3	GO:003580	regulation	2/539	23/23843	0.094505	0.511543	0.482677	Oxt/Tfap2b
GO_BP_m3	GO:004204	fluid transp	2/539	23/23843	0.094505	0.511543	0.482677	Aqp5/Slc14
GO_BP_m3	GO:004833	mesoderm	2/539	23/23843	0.094505	0.511543	0.482677	Foxc2/Foxf
GO_BP_m3	GO:005196	regulation	2/539	23/23843	0.094505	0.511543	0.482677	Avp/Chrnb
GO_BP_m3	GO:200067	positive reg	2/539	23/23843	0.094505	0.511543	0.482677	Trim6/Twis
GO_BP_m3	GO:005158	regulation	5/539	107/23843	0.095488	0.511543	0.482677	Bcl2l1/Gpm
GO_BP_m3	GO:000001	regulation	4/539	77/23843	0.096815	0.511543	0.482677	Ankle1/D3
GO_BP_m3	GO:006135	neural prec	7/539	173/23843	0.098452	0.511543	0.482677	Atf5/Cdon/
GO_BP_m3	GO:000662	protein targ	6/539	140/23843	0.098484	0.511543	0.482677	Ablim3/He
GO_BP_m3	GO:007200	nephron de	6/539	140/23843	0.098484	0.511543	0.482677	Bmp2/Foxc
GO_BP_m3	GO:000725	JAK-STAT (	8/539	207/23843	0.098777	0.511543	0.482677	Ccl5/Crlf1/

GO_BP_m3	GO:003101	endocrine	3/539	49/23843	0.098861	0.511543	0.482677	Gip/Hes1/
GO_BP_m3	GO:004568	positive reg	3/539	49/23843	0.098861	0.511543	0.482677	Bmp2/Hes1
GO_BP_m3	GO:005114	negative re	3/539	49/23843	0.098861	0.511543	0.482677	Bmp2/Ctdp
GO_BP_m3	GO:005149	positive reg	3/539	49/23843	0.098861	0.511543	0.482677	Nf2/Tacr1/
GO_BP_m3	GO:190526	negative re	3/539	49/23843	0.098861	0.511543	0.482677	Kdm4b/Kd
GO_BP_m3	GO:200067	regulation	3/539	49/23843	0.098861	0.511543	0.482677	Hes1/Trim6
GO_BP_m3	GO:000701	actin filame	13/539	385/23843	0.099494	0.511543	0.482677	Arhgap25/
GO_BP_m3	GO:001403	neural cres	4/539	78/23843	0.100329	0.511543	0.482677	Foxc2/Hes1
GO_BP_m3	GO:007207	nephron tu	4/539	78/23843	0.100329	0.511543	0.482677	Bmp2/Hes1
GO_BP_m3	GO:007169	anatomical	7/539	174/23843	0.100706	0.511543	0.482677	Bmp2/Dleu
GO_BP_m3	GO:005164	vesicle loca	8/539	208/23843	0.100825	0.511543	0.482677	Ap3s1/Bcl2
GO_BP_m3	GO:009900	vesicle-me	6/539	141/23843	0.101019	0.511543	0.482677	Ap3s1/Bcl2
GO_BP_m3	GO:004407	regulation	5/539	109/23843	0.101303	0.511543	0.482677	Avp/Hk1/C
GO_BP_m3	GO:000293	response to	2/539	24/23843	0.101611	0.511543	0.482677	Bcl2l1/Hk1
GO_BP_m3	GO:000709	mitotic G2	2/539	24/23843	0.101611	0.511543	0.482677	Fanci/Ier3
GO_BP_m3	GO:001404	regulation	2/539	24/23843	0.101611	0.511543	0.482677	Avp/Syt4
GO_BP_m3	GO:003053	male genit	2/539	24/23843	0.101611	0.511543	0.482677	Dhcr24/Src
GO_BP_m3	GO:003106	negative re	2/539	24/23843	0.101611	0.511543	0.482677	Kdm4b/Kd
GO_BP_m3	GO:003368	regulation	2/539	24/23843	0.101611	0.511543	0.482677	Bmp2/Tme
GO_BP_m3	GO:003556	regulation	2/539	24/23843	0.101611	0.511543	0.482677	Kdm4d/Tu
GO_BP_m3	GO:004356	regulation	2/539	24/23843	0.101611	0.511543	0.482677	Bmp2/Ghr
GO_BP_m3	GO:004392	modulation	2/539	24/23843	0.101611	0.511543	0.482677	Ccl5/Ctdp1
GO_BP_m3	GO:004434	type B pan	2/539	24/23843	0.101611	0.511543	0.482677	Nkx6-1/Ptp
GO_BP_m3	GO:005157	regulation	2/539	24/23843	0.101611	0.511543	0.482677	Kdm4b/Kd
GO_BP_m3	GO:005231	modulation	2/539	24/23843	0.101611	0.511543	0.482677	Ccl5/Ctdp1
GO_BP_m3	GO:005247	modulation	2/539	24/23843	0.101611	0.511543	0.482677	Ccl5/Ctdp1
GO_BP_m3	GO:006100	positive reg	2/539	24/23843	0.101611	0.511543	0.482677	Caprin1/Cu
GO_BP_m3	GO:190446	regulation	2/539	24/23843	0.101611	0.511543	0.482677	C1qtnf4/Lr
GO_BP_m3	GO:190580	negative re	2/539	24/23843	0.101611	0.511543	0.482677	Mdga1/Nlg
GO_BP_m3	GO:199077	tumor necr	2/539	24/23843	0.101611	0.511543	0.482677	C1qtnf4/Lr
GO_BP_m3	GO:200073	negative re	2/539	24/23843	0.101611	0.511543	0.482677	Hes1/Trim6
GO_BP_m3	GO:000716	establishm	8/539	209/23843	0.102896	0.511543	0.482677	Crb3/Foxf1
GO_BP_m3	GO:009769	STAT casca	8/539	209/23843	0.102896	0.511543	0.482677	Ccl5/Crlf1/
GO_BP_m3	GO:004870	embryonic	3/539	50/23843	0.103496	0.511543	0.482677	Foxc2/Tgfb
GO_BP_m3	GO:007022	negative re	3/539	50/23843	0.103496	0.511543	0.482677	Ccl5/Mir10
GO_BP_m3	GO:007252	pyridine-co	6/539	142/23843	0.103588	0.511543	0.482677	Dlat/Dld/Fo
GO_BP_m3	GO:004864	negative re	5/539	110/23843	0.104276	0.511543	0.482677	Atxn2/Ctdp
GO_BP_m3	GO:004521	cell-cell ju	8/539	211/23843	0.10711	0.511543	0.482677	Cdh26/Crb
GO_BP_m3	GO:005066	cytokine se	8/539	211/23843	0.10711	0.511543	0.482677	Btn1a1/C1q
GO_BP_m3	GO:190332	regulation	8/539	211/23843	0.10711	0.511543	0.482677	Bag5/Ctr9/
GO_BP_m3	GO:003196	response to	4/539	80/23843	0.107531	0.511543	0.482677	Areg/Ghrh
GO_BP_m3	GO:007208	nephron ep	4/539	80/23843	0.107531	0.511543	0.482677	Bmp2/Hes1
GO_BP_m3	GO:000195	intramemb	1/539	5/23843	0.108044	0.511543	0.482677	Axin2
GO_BP_m3	GO:000231	plasma cell	1/539	5/23843	0.108044	0.511543	0.482677	Nkx2-3
GO_BP_m3	GO:000319	endocardia	1/539	5/23843	0.108044	0.511543	0.482677	Twist1
GO_BP_m3	GO:000324	growth inv	1/539	5/23843	0.108044	0.511543	0.482677	S1pr1
GO_BP_m3	GO:000330	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Bmp2
GO_BP_m3	GO:000611	NADH oxid	1/539	5/23843	0.108044	0.511543	0.482677	Slc37a2

GO_BP_m3	GO:00749	midgut dev	1/539	5/23843	0.108044	0.511543	0.482677	Foxf1
GO_BP_m3	GO:00979	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Hes1
GO_BP_m3	GO:001571	hexose pho	1/539	5/23843	0.108044	0.511543	0.482677	Slc37a2
GO_BP_m3	GO:001576	glucose-6-	1/539	5/23843	0.108044	0.511543	0.482677	Slc37a2
GO_BP_m3	GO:001584	urea transp	1/539	5/23843	0.108044	0.511543	0.482677	Slc14a1
GO_BP_m3	GO:001586	ATP transp	1/539	5/23843	0.108044	0.511543	0.482677	Slc25a17
GO_BP_m3	GO:001588	folic acid tr	1/539	5/23843	0.108044	0.511543	0.482677	Slc19a1
GO_BP_m3	GO:003194	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Bmp2
GO_BP_m3	GO:003194	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Bmp2
GO_BP_m3	GO:003284	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Avp
GO_BP_m3	GO:003308	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Ihh
GO_BP_m3	GO:003368	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Ucn2
GO_BP_m3	GO:003548	gastric emp	1/539	5/23843	0.108044	0.511543	0.482677	Ucn
GO_BP_m3	GO:003574	natural kille	1/539	5/23843	0.108044	0.511543	0.482677	Ccl5
GO_BP_m3	GO:003590	response to	1/539	5/23843	0.108044	0.511543	0.482677	Ptpn5
GO_BP_m3	GO:003607	direct ossif	1/539	5/23843	0.108044	0.511543	0.482677	Axin2
GO_BP_m3	GO:004337	memory T	1/539	5/23843	0.108044	0.511543	0.482677	Cd46
GO_BP_m3	GO:004357	maintenan	1/539	5/23843	0.108044	0.511543	0.482677	Axin2
GO_BP_m3	GO:004434	sodium-de	1/539	5/23843	0.108044	0.511543	0.482677	Stc2
GO_BP_m3	GO:004544	mitotic cell	1/539	5/23843	0.108044	0.511543	0.482677	Hes1
GO_BP_m3	GO:004595	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Ankle1
GO_BP_m3	GO:004687	positive reg	1/539	5/23843	0.108044	0.511543	0.482677	Tacr1
GO_BP_m3	GO:005090	diapedesis	1/539	5/23843	0.108044	0.511543	0.482677	Ccl5
GO_BP_m3	GO:005138	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Ptprf
GO_BP_m3	GO:005161	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Gpm6b
GO_BP_m3	GO:005196	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Mdga1
GO_BP_m3	GO:005215	modulation	1/539	5/23843	0.108044	0.511543	0.482677	Bcl2l1
GO_BP_m3	GO:006008	smooth mu	1/539	5/23843	0.108044	0.511543	0.482677	Tacr1
GO_BP_m3	GO:006016	positive reg	1/539	5/23843	0.108044	0.511543	0.482677	Lrrk2
GO_BP_m3	GO:006016	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Hes1
GO_BP_m3	GO:006059	chondrobla	1/539	5/23843	0.108044	0.511543	0.482677	Gdf5
GO_BP_m3	GO:006075	epithelial c	1/539	5/23843	0.108044	0.511543	0.482677	Areg
GO_BP_m3	GO:006104	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Foxc2
GO_BP_m3	GO:006176	CAMKK-AM	1/539	5/23843	0.108044	0.511543	0.482677	Lrrk2
GO_BP_m3	GO:007094	dephospho	1/539	5/23843	0.108044	0.511543	0.482677	Ctdp1
GO_BP_m3	GO:007105	polyadenyl	1/539	5/23843	0.108044	0.511543	0.482677	Exosc6
GO_BP_m3	GO:007128	cellular res	1/539	5/23843	0.108044	0.511543	0.482677	Lrrk2
GO_BP_m3	GO:007200	mesangial	1/539	5/23843	0.108044	0.511543	0.482677	Foxc2
GO_BP_m3	GO:007214	mesangial	1/539	5/23843	0.108044	0.511543	0.482677	Foxc2
GO_BP_m3	GO:007265	maintenan	1/539	5/23843	0.108044	0.511543	0.482677	Hk1
GO_BP_m3	GO:009071	immunolog	1/539	5/23843	0.108044	0.511543	0.482677	Cd46
GO_BP_m3	GO:009071	immunolog	1/539	5/23843	0.108044	0.511543	0.482677	Cd46
GO_BP_m3	GO:009917	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Nlgn1
GO_BP_m3	GO:190167	nucleotide	1/539	5/23843	0.108044	0.511543	0.482677	Slc25a17
GO_BP_m3	GO:190230	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Dusp26
GO_BP_m3	GO:190247	positive reg	1/539	5/23843	0.108044	0.511543	0.482677	Nlgn1
GO_BP_m3	GO:190321	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Lrrk2
GO_BP_m3	GO:190336	positive reg	1/539	5/23843	0.108044	0.511543	0.482677	Ucn

GO_BP_m3	GO:19050	positive re	1/539	5/23843	0.108044	0.511543	0.482677	Tgfbr1
GO_BP_m3	GO:200027	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Twist1
GO_BP_m3	GO:20003	negative re	1/539	5/23843	0.108044	0.511543	0.482677	Syt4
GO_BP_m3	GO:20005	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Ccl5
GO_BP_m3	GO:200081	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Carmil2
GO_BP_m3	GO:200097	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Hes1
GO_BP_m3	GO:20009	positive re	1/539	5/23843	0.108044	0.511543	0.482677	Ucn
GO_BP_m3	GO:20010	positive re	1/539	5/23843	0.108044	0.511543	0.482677	Kdm4d
GO_BP_m3	GO:20011	regulation	1/539	5/23843	0.108044	0.511543	0.482677	Ctr9
GO_BP_m3	GO:20011	positive re	1/539	5/23843	0.108044	0.511543	0.482677	Prkcz
GO_BP_m3	GO:00018	retina hom	3/539	51/23843	0.108216	0.511543	0.482677	Mkks/Nxnl
GO_BP_m3	GO:003261	interleukin	3/539	51/23843	0.108216	0.511543	0.482677	Cd46/Prkc
GO_BP_m3	GO:00350	establishm	3/539	51/23843	0.108216	0.511543	0.482677	Crb3/Foxf1
GO_BP_m3	GO:00456	regulation	3/539	51/23843	0.108216	0.511543	0.482677	Hes1/Prkc
GO_BP_m3	GO:00469	regulation	3/539	51/23843	0.108216	0.511543	0.482677	Bcl2l1/Ier3
GO_BP_m3	GO:006124	establishm	3/539	51/23843	0.108216	0.511543	0.482677	Crb3/Foxf1
GO_BP_m3	GO:00148	phasic smo	2/539	25/23843	0.108859	0.511543	0.482677	Neurog1/T
GO_BP_m3	GO:00321	regulation	2/539	25/23843	0.108859	0.511543	0.482677	Mkks/Ucn
GO_BP_m3	GO:00321	regulation	2/539	25/23843	0.108859	0.511543	0.482677	Mkks/Ucn
GO_BP_m3	GO:00455	regulation	2/539	25/23843	0.108859	0.511543	0.482677	Cd46/Carm
GO_BP_m3	GO:004864	negative re	2/539	25/23843	0.108859	0.511543	0.482677	Tsc22d3/T
GO_BP_m3	GO:00607	regulation	2/539	25/23843	0.108859	0.511543	0.482677	Kdm5d/Tcf
GO_BP_m3	GO:00712	cellular res	2/539	25/23843	0.108859	0.511543	0.482677	Mir539/Mi
GO_BP_m3	GO:00800	response t	2/539	25/23843	0.108859	0.511543	0.482677	Mir539/Mi
GO_BP_m3	GO:00230	signal relea	15/539	466/23843	0.109605	0.514487	0.485454	Bcl2l1/Ccl5
GO_BP_m3	GO:001574	organopho	4/539	81/23843	0.111217	0.520347	0.490984	Slc25a17/S
GO_BP_m3	GO:00480	regulation	4/539	81/23843	0.111217	0.520347	0.490984	Celf5/Khdr
GO_BP_m3	GO:00720	nephron m	4/539	81/23843	0.111217	0.520347	0.490984	Bmp2/Hes
GO_BP_m3	GO:190331	regulation	8/539	213/23843	0.111417	0.520715	0.491331	Axin2/Celf
GO_BP_m3	GO:000761	mating	3/539	52/23843	0.113018	0.520973	0.491574	Avp/Oxt/T
GO_BP_m3	GO:004577	positive re	3/539	52/23843	0.113018	0.520973	0.491574	Avp/Oxt/T
GO_BP_m3	GO:00459	positive re	3/539	52/23843	0.113018	0.520973	0.491574	Oxt/Tacr1/
GO_BP_m3	GO:007267	T cell migr	3/539	52/23843	0.113018	0.520973	0.491574	Aire/Ccl5/
GO_BP_m3	GO:00086	apoptotic	5/539	113/23843	0.113449	0.520973	0.491574	Avp/Bcl2l1
GO_BP_m3	GO:00220	metenceph	5/539	113/23843	0.113449	0.520973	0.491574	Atxn2/Dixd
GO_BP_m3	GO:00706	leukocyte	11/539	321/23843	0.113786	0.520973	0.491574	Btn1a1/Ccl
GO_BP_m3	GO:00514	negative re	6/539	146/23843	0.114201	0.520973	0.491574	Ccnf/Ckap
GO_BP_m3	GO:00995	presynapti	6/539	146/23843	0.114201	0.520973	0.491574	Bcl2l1/Lrrk
GO_BP_m3	GO:00020	chondrocy	2/539	26/23843	0.116239	0.520973	0.491574	Axin2/Col2
GO_BP_m3	GO:000317	atrioventri	2/539	26/23843	0.116239	0.520973	0.491574	Bmp2/Twis
GO_BP_m3	GO:00067	NADH met	2/539	26/23843	0.116239	0.520973	0.491574	Hk1/Slc37a
GO_BP_m3	GO:00161	snRNA pro	2/539	26/23843	0.116239	0.520973	0.491574	Exosc6/Ints
GO_BP_m3	GO:003081	positive re	2/539	26/23843	0.116239	0.520973	0.491574	Avp/Rln3
GO_BP_m3	GO:00427	positive re	2/539	26/23843	0.116239	0.520973	0.491574	Ghrhr/Nlgr
GO_BP_m3	GO:00515	negative re	2/539	26/23843	0.116239	0.520973	0.491574	Gpm6b/Sy
GO_BP_m3	GO:00519	positive re	2/539	26/23843	0.116239	0.520973	0.491574	Avp/Syt4
GO_BP_m3	GO:006071	labyrinthin	2/539	26/23843	0.116239	0.520973	0.491574	Esx1/Hes1
GO_BP_m3	GO:006091	heart form	2/539	26/23843	0.116239	0.520973	0.491574	Axin2/Hes1

GO_BP_m3	GO:006103	negative re	2/539	26/23843	0.116239	0.520973	0.491574	Gdf5/Tgfbr
GO_BP_m3	GO:007135	cellular res	2/539	26/23843	0.116239	0.520973	0.491574	C1qtnf4/Ct
GO_BP_m3	GO:200077	positive reg	2/539	26/23843	0.116239	0.520973	0.491574	C1qtnf4/Tv
GO_BP_m3	GO:001657	protein de	5/539	114/23843	0.11659	0.520973	0.491574	Epop/Otuc
GO_BP_m3	GO:002154	pallium dev	6/539	147/23843	0.116937	0.520973	0.491574	Atat1/Cdor
GO_BP_m3	GO:004253	positive reg	3/539	53/23843	0.1179	0.520973	0.491574	Ccl5/Crlf1/
GO_BP_m3	GO:001403	mesenchyr	4/539	83/23843	0.118756	0.520973	0.491574	Foxc2/Hes1
GO_BP_m3	GO:003275	positive reg	4/539	83/23843	0.118756	0.520973	0.491574	C1qtnf4/Il1
GO_BP_m3	GO:000688	exocytosis	11/539	324/23843	0.119175	0.520973	0.491574	Abr/Bcl2l1/
GO_BP_m3	GO:004875	branching	7/539	182/23843	0.119738	0.520973	0.491574	Areg/Bmp2
GO_BP_m3	GO:000693	regulation	6/539	149/23843	0.122506	0.520973	0.491574	Chrnb4/Ox
GO_BP_m3	GO:004886	stem cell d	4/539	84/23843	0.122606	0.520973	0.491574	Foxc2/Hes1
GO_BP_m3	GO:005080	negative re	4/539	84/23843	0.122606	0.520973	0.491574	Bcl2l1/Grik
GO_BP_m3	GO:006133	renal tubul	4/539	84/23843	0.122606	0.520973	0.491574	Bmp2/Hes1
GO_BP_m3	GO:009706	dendritic sp	4/539	84/23843	0.122606	0.520973	0.491574	Caprin1/Cu
GO_BP_m3	GO:003646	synaptic ve	3/539	54/23843	0.122859	0.520973	0.491574	Bcl2l1/Lrrk2
GO_BP_m3	GO:004507	negative re	3/539	54/23843	0.122859	0.520973	0.491574	Ccl5/Isg20/
GO_BP_m3	GO:004854	response to	9/539	254/23843	0.123714	0.520973	0.491574	Areg/Ghrh
GO_BP_m3	GO:003368	osteoblast	2/539	27/23843	0.123741	0.520973	0.491574	Bmp2/Tme
GO_BP_m3	GO:003466	ncRNA cata	2/539	27/23843	0.123741	0.520973	0.491574	Dis3/Exosc
GO_BP_m3	GO:003533	peptidyl-ty	2/539	27/23843	0.123741	0.520973	0.491574	Ptpn5/Ptpr
GO_BP_m3	GO:003600	positive reg	2/539	27/23843	0.123741	0.520973	0.491574	Hsf4/Klf2
GO_BP_m3	GO:007023	negative re	2/539	27/23843	0.123741	0.520973	0.491574	Ccl5/Tsc22
GO_BP_m3	GO:009010	cochlea mo	2/539	27/23843	0.123741	0.520973	0.491574	Neurog1/T
GO_BP_m3	GO:009031	positive reg	2/539	27/23843	0.123741	0.520973	0.491574	Jdp2/Lrrk2
GO_BP_m3	GO:190289	positive reg	2/539	27/23843	0.123741	0.520973	0.491574	Bmp2/Tgfb
GO_BP_m3	GO:006113	morphogen	8/539	219/23843	0.124894	0.520973	0.491574	Areg/Bmp2
GO_BP_m3	GO:001715	calcium ior	5/539	117/23843	0.126257	0.520973	0.491574	Bcl2l1/Lrrk2
GO_BP_m3	GO:004671	acid secret	5/539	117/23843	0.126257	0.520973	0.491574	Avp/Oxt/Sy
GO_BP_m3	GO:000270	positive reg	4/539	85/23843	0.126508	0.520973	0.491574	Exosc6/Hk1
GO_BP_m3	GO:001071	regulation	4/539	85/23843	0.126508	0.520973	0.491574	Axin2/Bmp
GO_BP_m3	GO:001403	neural cres	4/539	85/23843	0.126508	0.520973	0.491574	Foxc2/Hes1
GO_BP_m3	GO:004568	regulation	4/539	85/23843	0.126508	0.520973	0.491574	Atf5/Bmp2
GO_BP_m3	GO:006039	SMAD prot	4/539	85/23843	0.126508	0.520973	0.491574	Bmp2/Gdf5
GO_BP_m3	GO:006041	muscle tiss	4/539	85/23843	0.126508	0.520973	0.491574	Bmp2/Foxc
GO_BP_m3	GO:000228	lymphocyte	7/539	185/23843	0.127322	0.520973	0.491574	Cd46/Exos
GO_BP_m3	GO:000038	alternative	3/539	55/23843	0.127892	0.520973	0.491574	Celf5/Mbnl
GO_BP_m3	GO:006035	endochonc	3/539	55/23843	0.127892	0.520973	0.491574	Axin2/Col2
GO_BP_m3	GO:006197	replacemer	3/539	55/23843	0.127892	0.520973	0.491574	Axin2/Col2
GO_BP_m3	GO:200077	regulation	3/539	55/23843	0.127892	0.520973	0.491574	D330045A2
GO_BP_m3	GO:004666	male sex d	6/539	151/23843	0.128205	0.520973	0.491574	Bcl2l1/Dhc
GO_BP_m3	GO:000001	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Ankle1
GO_BP_m3	GO:000016	phosphore	1/539	6/23843	0.128212	0.520973	0.491574	Kcnh3
GO_BP_m3	GO:000245	T cell antig	1/539	6/23843	0.128212	0.520973	0.491574	Kdm5d
GO_BP_m3	GO:000251	tolerance ir	1/539	6/23843	0.128212	0.520973	0.491574	Aire
GO_BP_m3	GO:000327	apoptotic p	1/539	6/23843	0.128212	0.520973	0.491574	Foxc2
GO_BP_m3	GO:000340	retinal pigr	1/539	6/23843	0.128212	0.520973	0.491574	Ihh
GO_BP_m3	GO:000341	growth pla	1/539	6/23843	0.128212	0.520973	0.491574	Col27a1

GO_BP_m3	GO:000343	chondrocy	1/539	6/23843	0.128212	0.520973	0.491574	Col27a1
GO_BP_m3	GO:000636	terminatio	1/539	6/23843	0.128212	0.520973	0.491574	Dmtf1
GO_BP_m3	GO:000668	sphingomy	1/539	6/23843	0.128212	0.520973	0.491574	Enpp7
GO_BP_m3	GO:000670	androgen	1/539	6/23843	0.128212	0.520973	0.491574	Srd5a1
GO_BP_m3	GO:000719	adenylate	1/539	6/23843	0.128212	0.520973	0.491574	Grm4
GO_BP_m3	GO:001062	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Sox10
GO_BP_m3	GO:001070	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Oxt
GO_BP_m3	GO:001084	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Nlgn1
GO_BP_m3	GO:001404	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Dleu2
GO_BP_m3	GO:001719	N-terminal	1/539	6/23843	0.128212	0.520973	0.491574	Naa25
GO_BP_m3	GO:002186	forebrain v	1/539	6/23843	0.128212	0.520973	0.491574	Dixdc1
GO_BP_m3	GO:003032	transepithe	1/539	6/23843	0.128212	0.520973	0.491574	P2ry6
GO_BP_m3	GO:003133	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Syt4
GO_BP_m3	GO:003139	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Avp
GO_BP_m3	GO:003308	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Ihh
GO_BP_m3	GO:003318	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Ctr9
GO_BP_m3	GO:003411	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Ccl5
GO_BP_m3	GO:003461	response t	1/539	6/23843	0.128212	0.520973	0.491574	Klf2
GO_BP_m3	GO:003475	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Hamp2
GO_BP_m3	GO:003573	intraciliary	1/539	6/23843	0.128212	0.520973	0.491574	Cep131
GO_BP_m3	GO:003820	TORC2 sig	1/539	6/23843	0.128212	0.520973	0.491574	Prr5
GO_BP_m3	GO:004269	thelarche	1/539	6/23843	0.128212	0.520973	0.491574	Areg
GO_BP_m3	GO:004274	circadian sl	1/539	6/23843	0.128212	0.520973	0.491574	Nlgn1
GO_BP_m3	GO:004279	snRNA tra	1/539	6/23843	0.128212	0.520973	0.491574	Snapc1
GO_BP_m3	GO:004330	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Foxf1
GO_BP_m3	GO:004341	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Myod1
GO_BP_m3	GO:004350	mitochond	1/539	6/23843	0.128212	0.520973	0.491574	Mgme1
GO_BP_m3	GO:004453	modulatio	1/539	6/23843	0.128212	0.520973	0.491574	Bcl2l1
GO_BP_m3	GO:004453	modulatio	1/539	6/23843	0.128212	0.520973	0.491574	Bcl2l1
GO_BP_m3	GO:004453	long-chain	1/539	6/23843	0.128212	0.520973	0.491574	Slc27a4
GO_BP_m3	GO:004516	clustering	1/539	6/23843	0.128212	0.520973	0.491574	Sclt1
GO_BP_m3	GO:004592	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Oxt
GO_BP_m3	GO:004885	diencephal	1/539	6/23843	0.128212	0.520973	0.491574	Otx1
GO_BP_m3	GO:005158	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Gpm6b
GO_BP_m3	GO:005161	serotonin	1/539	6/23843	0.128212	0.520973	0.491574	Gpm6b
GO_BP_m3	GO:005204	modulatio	1/539	6/23843	0.128212	0.520973	0.491574	Bcl2l1
GO_BP_m3	GO:005224	modulatio	1/539	6/23843	0.128212	0.520973	0.491574	Bcl2l1
GO_BP_m3	GO:005243	modulatio	1/539	6/23843	0.128212	0.520973	0.491574	Bcl2l1
GO_BP_m3	GO:006074	mammary	1/539	6/23843	0.128212	0.520973	0.491574	Areg
GO_BP_m3	GO:006075	branch elo	1/539	6/23843	0.128212	0.520973	0.491574	Areg
GO_BP_m3	GO:006140	positive re	1/539	6/23843	0.128212	0.520973	0.491574	Hsf4
GO_BP_m3	GO:006162	glycolytic	1/539	6/23843	0.128212	0.520973	0.491574	Hk1
GO_BP_m3	GO:007023	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Tsc22d3
GO_BP_m3	GO:007030	lens fiber c	1/539	6/23843	0.128212	0.520973	0.491574	Cryaa
GO_BP_m3	GO:007094	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Dnase1l3
GO_BP_m3	GO:007149	cellular res	1/539	6/23843	0.128212	0.520973	0.491574	Klf2
GO_BP_m3	GO:007183	apoptotic	1/539	6/23843	0.128212	0.520973	0.491574	Bcl2l1
GO_BP_m3	GO:007204	comma-sh	1/539	6/23843	0.128212	0.520973	0.491574	Hes1

GO_BP_m3	GO:007210	glomerulus	1/539	6/23843	0.128212	0.520973	0.491574	Tcf21
GO_BP_m3	GO:007210	glomerular	1/539	6/23843	0.128212	0.520973	0.491574	Tcf21
GO_BP_m3	GO:007255	terminal bu	1/539	6/23843	0.128212	0.520973	0.491574	Nlgn1
GO_BP_m3	GO:007261	interleukin-	1/539	6/23843	0.128212	0.520973	0.491574	Prkcz
GO_BP_m3	GO:007267	thymocyte	1/539	6/23843	0.128212	0.520973	0.491574	Aire
GO_BP_m3	GO:009003	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Bmp2
GO_BP_m3	GO:009050	endocardia	1/539	6/23843	0.128212	0.520973	0.491574	Twist1
GO_BP_m3	GO:009711	NMDA glu	1/539	6/23843	0.128212	0.520973	0.491574	Nlgn1
GO_BP_m3	GO:190022	positive reg	1/539	6/23843	0.128212	0.520973	0.491574	Atat1
GO_BP_m3	GO:190172	positive reg	1/539	6/23843	0.128212	0.520973	0.491574	Lrrk2
GO_BP_m3	GO:190247	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Nlgn1
GO_BP_m3	GO:190280	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Syt4
GO_BP_m3	GO:190423	pericyte ce	1/539	6/23843	0.128212	0.520973	0.491574	Foxc2
GO_BP_m3	GO:190500	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Tgfbr1
GO_BP_m3	GO:200006	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Bmp2
GO_BP_m3	GO:200011	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Ccl5
GO_BP_m3	GO:200055	positive reg	1/539	6/23843	0.128212	0.520973	0.491574	Prkcz
GO_BP_m3	GO:200058	regulation	1/539	6/23843	0.128212	0.520973	0.491574	BC048507
GO_BP_m3	GO:200058	positive reg	1/539	6/23843	0.128212	0.520973	0.491574	BC048507
GO_BP_m3	GO:200066	positive reg	1/539	6/23843	0.128212	0.520973	0.491574	Prkcz
GO_BP_m3	GO:200066	regulation	1/539	6/23843	0.128212	0.520973	0.491574	Prkcz
GO_BP_m3	GO:200067	negative re	1/539	6/23843	0.128212	0.520973	0.491574	Crlf1
GO_BP_m3	GO:200128	positive reg	1/539	6/23843	0.128212	0.520973	0.491574	Avp
GO_BP_m3	GO:005068	regulation	5/539	118/23843	0.12956	0.525953	0.496273	Celf5/Ctr9/
GO_BP_m3	GO:003313	regulation	6/539	152/23843	0.131101	0.528745	0.498908	Avp/Fnip2/
GO_BP_m3	GO:000223	positive reg	2/539	28/23843	0.131355	0.528745	0.498908	Ccl5/Trim6
GO_BP_m3	GO:002169	cerebellar	2/539	28/23843	0.131355	0.528745	0.498908	Atxn2/Whr
GO_BP_m3	GO:003315	regulation	2/539	28/23843	0.131355	0.528745	0.498908	Lrrk2/Ptpn5
GO_BP_m3	GO:004506	regulatory	2/539	28/23843	0.131355	0.528745	0.498908	Cd46/Carm
GO_BP_m3	GO:004591	negative re	2/539	28/23843	0.131355	0.528745	0.498908	Ankle1/D33
GO_BP_m3	GO:006063	regulation	2/539	28/23843	0.131355	0.528745	0.498908	1110004E0
GO_BP_m3	GO:007074	response to	2/539	28/23843	0.131355	0.528745	0.498908	C1qtnf4/Ct
GO_BP_m3	GO:190002	regulation	2/539	28/23843	0.131355	0.528745	0.498908	Nlgn1/Carr
GO_BP_m3	GO:003019	extracellula	8/539	222/23843	0.131939	0.530598	0.500656	Adamts14/
GO_BP_m3	GO:000006	protein imp	3/539	56/23843	0.132998	0.532362	0.502321	Lrrk2/Ptpn5
GO_BP_m3	GO:002006	glandular e	3/539	56/23843	0.132998	0.532362	0.502321	Bmp2/Hes1
GO_BP_m3	GO:002151	ventral spir	3/539	56/23843	0.132998	0.532362	0.502321	Mir19a/Nk2
GO_BP_m3	GO:002157	hindbrain r	3/539	56/23843	0.132998	0.532362	0.502321	Atxn2/Hes1
GO_BP_m3	GO:004512	cellular ext	3/539	56/23843	0.132998	0.532362	0.502321	Abr/Ccl5/P
GO_BP_m3	GO:005070	regulation	14/539	444/23843	0.133687	0.532552	0.5025	Btn1a1/C1q
GO_BP_m3	GO:000673	oxidoreduc	6/539	153/23843	0.134028	0.532552	0.5025	Dlat/Dld/Fo
GO_BP_m3	GO:004593	positive reg	6/539	153/23843	0.134028	0.532552	0.5025	Hes1/Mad2
GO_BP_m3	GO:010602	neuron pro	4/539	87/23843	0.134468	0.532552	0.5025	Caprin1/Cu
GO_BP_m3	GO:000227	myeloid leu	7/539	188/23843	0.135142	0.532552	0.5025	Abr/Ccl5/D
GO_BP_m3	GO:003090	forebrain d	12/539	370/23843	0.135819	0.532552	0.5025	Atat1/Atf5/
GO_BP_m3	GO:000165	urogenital	11/539	333/23843	0.136188	0.532552	0.5025	Bmp2/Crlf1
GO_BP_m3	GO:190121	negative re	8/539	224/23843	0.136747	0.532552	0.5025	Bcl2l1/Ccl5
GO_BP_m3	GO:190198	negative re	6/539	154/23843	0.136987	0.532552	0.5025	Atf5/Fanci/

GO_BP_m3	GO:00063	double-str	7/539	189/23843	0.1378	0.532552	0.5025	Ccdc155/D
GO_BP_m3	GO:00104	mesenchy	3/539	57/23843	0.138173	0.532552	0.5025	Bmp2/Foxf
GO_BP_m3	GO:004311	receptor cl	3/539	57/23843	0.138173	0.532552	0.5025	Grik2/Nlgn
GO_BP_m3	GO:00455	positive re	4/539	88/23843	0.138523	0.532552	0.5025	Cd46/Ihh/
GO_BP_m3	GO:00609	regulation	4/539	88/23843	0.138523	0.532552	0.5025	Caprin1/Cu
GO_BP_m3	GO:000922	nucleotide-	2/539	29/23843	0.139074	0.532552	0.5025	Fuk/Pmm1
GO_BP_m3	GO:00103	histone mo	2/539	29/23843	0.139074	0.532552	0.5025	Ctr9/Uhrf1
GO_BP_m3	GO:00342	negative re	2/539	29/23843	0.139074	0.532552	0.5025	Lrrk2/Mkks
GO_BP_m3	GO:004864	positive re	2/539	29/23843	0.139074	0.532552	0.5025	Cdon/Myo
GO_BP_m3	GO:00610	positive re	2/539	29/23843	0.139074	0.532552	0.5025	Bmp2/Gdf
GO_BP_m3	GO:00703	lens fiber c	2/539	29/23843	0.139074	0.532552	0.5025	Cryaa/Nf2
GO_BP_m3	GO:00181	peptidyl-th	5/539	121/23843	0.139697	0.532552	0.5025	Hk1/Lrrk2/
GO_BP_m3	GO:00017	cell fate sp	4/539	89/23843	0.142626	0.532552	0.5025	Cdon/Ihh/
GO_BP_m3	GO:000751	skeletal mu	7/539	191/23843	0.143192	0.532552	0.5025	Cdon/Myo
GO_BP_m3	GO:00028	regulation	3/539	58/23843	0.143416	0.532552	0.5025	Abr/Dnase
GO_BP_m3	GO:00071	heterophili	3/539	58/23843	0.143416	0.532552	0.5025	Amigo3/Cr
GO_BP_m3	GO:00322	positive re	3/539	58/23843	0.143416	0.532552	0.5025	Nf2/Tacr1/
GO_BP_m3	GO:00328	glomerulus	3/539	58/23843	0.143416	0.532552	0.5025	Foxc2/Hes
GO_BP_m3	GO:00504	regulation	3/539	58/23843	0.143416	0.532552	0.5025	Chrna4/Ox
GO_BP_m3	GO:19033	positive re	3/539	58/23843	0.143416	0.532552	0.5025	Bcl2l1/Nlgr
GO_BP_m3	GO:19037	positive re	3/539	58/23843	0.143416	0.532552	0.5025	Avp/Oxt/S
GO_BP_m3	GO:00096	response t	11/539	337/23843	0.144147	0.532552	0.5025	Ankzf1/Bcl
GO_BP_m3	GO:00508	synapse or	11/539	337/23843	0.144147	0.532552	0.5025	2610042L0
GO_BP_m3	GO:005087	regulation	11/539	337/23843	0.144147	0.532552	0.5025	Aqp5/Avp/
GO_BP_m3	GO:000244	production	10/539	300/23843	0.144327	0.532552	0.5025	Exosc6/Hk
GO_BP_m3	GO:00072	spermatog	15/539	489/23843	0.145176	0.532552	0.5025	Adam24/A
GO_BP_m3	GO:00216	cranial ner	2/539	30/23843	0.146888	0.532552	0.5025	Neurog1/T
GO_BP_m3	GO:00329	positive re	2/539	30/23843	0.146888	0.532552	0.5025	Ihh/Ucn
GO_BP_m3	GO:00439	positive re	2/539	30/23843	0.146888	0.532552	0.5025	Gip/Ucn
GO_BP_m3	GO:004431	wound hea	2/539	30/23843	0.146888	0.532552	0.5025	Plet1/Carm
GO_BP_m3	GO:005507	potassium	2/539	30/23843	0.146888	0.532552	0.5025	Slc12a7/Tf
GO_BP_m3	GO:00605	apoptotic	2/539	30/23843	0.146888	0.532552	0.5025	Cryaa/Foxc
GO_BP_m3	GO:00905	epiboly inv	2/539	30/23843	0.146888	0.532552	0.5025	Plet1/Carm
GO_BP_m3	GO:00426	muscle cell	12/539	376/23843	0.147171	0.532552	0.5025	Bmp2/Cdo
GO_BP_m3	GO:00019	blood vess	1/539	7/23843	0.147924	0.532552	0.5025	S1pr1
GO_BP_m3	GO:00020	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Ndst2
GO_BP_m3	GO:00026	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Abr
GO_BP_m3	GO:000312	heart induc	1/539	7/23843	0.147924	0.532552	0.5025	Bmp2
GO_BP_m3	GO:000317	aortic valve	1/539	7/23843	0.147924	0.532552	0.5025	Twist1
GO_BP_m3	GO:00031	aortic valve	1/539	7/23843	0.147924	0.532552	0.5025	Twist1
GO_BP_m3	GO:00032	cardiac neu	1/539	7/23843	0.147924	0.532552	0.5025	Twist1
GO_BP_m3	GO:00033	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Bmp2
GO_BP_m3	GO:000337	sphingosin	1/539	7/23843	0.147924	0.532552	0.5025	S1pr1
GO_BP_m3	GO:00062	DNA topol	1/539	7/23843	0.147924	0.532552	0.5025	Top3b
GO_BP_m3	GO:00065	threonine	1/539	7/23843	0.147924	0.532552	0.5025	Thnsl2
GO_BP_m3	GO:000661	ribosomal	1/539	7/23843	0.147924	0.532552	0.5025	Tnpo2
GO_BP_m3	GO:000702	tubulin cor	1/539	7/23843	0.147924	0.532552	0.5025	Cryaa
GO_BP_m3	GO:000721	tachykinin	1/539	7/23843	0.147924	0.532552	0.5025	Tacr1

GO_BP_m3	GO:000924	protein lipo	1/539	7/23843	0.147924	0.532552	0.5025	Gcsh
GO_BP_m3	GO:000969	phenylprop	1/539	7/23843	0.147924	0.532552	0.5025	Ugt1a7c
GO_BP_m3	GO:000980	coumarin r	1/539	7/23843	0.147924	0.532552	0.5025	Ugt1a7c
GO_BP_m3	GO:000991	auditory re	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:001062	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Sox10
GO_BP_m3	GO:001096	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Stc2
GO_BP_m3	GO:001481	skeletal mu	1/539	7/23843	0.147924	0.532552	0.5025	Cdon
GO_BP_m3	GO:001936	fatty acid e	1/539	7/23843	0.147924	0.532552	0.5025	Elovl2
GO_BP_m3	GO:001936	fatty acid e	1/539	7/23843	0.147924	0.532552	0.5025	Elovl2
GO_BP_m3	GO:001967	GDP-manr	1/539	7/23843	0.147924	0.532552	0.5025	Pmm1
GO_BP_m3	GO:003111	tRNA pseu	1/539	7/23843	0.147924	0.532552	0.5025	Rpusd3
GO_BP_m3	GO:003234	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Bmp2
GO_BP_m3	GO:003280	lacrimal gla	1/539	7/23843	0.147924	0.532552	0.5025	Sox10
GO_BP_m3	GO:003300	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Foxf1
GO_BP_m3	GO:003331	meiotic cel	1/539	7/23843	0.147924	0.532552	0.5025	Oraov1
GO_BP_m3	GO:003362	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Foxc2
GO_BP_m3	GO:003462	fatty acid e	1/539	7/23843	0.147924	0.532552	0.5025	Elovl2
GO_BP_m3	GO:003462	fatty acid e	1/539	7/23843	0.147924	0.532552	0.5025	Elovl2
GO_BP_m3	GO:003472	histone H3	1/539	7/23843	0.147924	0.532552	0.5025	Kdm5d
GO_BP_m3	GO:003533	long-chain	1/539	7/23843	0.147924	0.532552	0.5025	Them4
GO_BP_m3	GO:003558	sequesterin	1/539	7/23843	0.147924	0.532552	0.5025	Cd46
GO_BP_m3	GO:004435	macropino	1/539	7/23843	0.147924	0.532552	0.5025	Mapkapk3
GO_BP_m3	GO:004500	DNA deam	1/539	7/23843	0.147924	0.532552	0.5025	Exosc6
GO_BP_m3	GO:004563	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Prkcz
GO_BP_m3	GO:004591	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Cd46
GO_BP_m3	GO:004806	eye pigmen	1/539	7/23843	0.147924	0.532552	0.5025	Ihh
GO_BP_m3	GO:005086	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Prkch
GO_BP_m3	GO:005146	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Ucn
GO_BP_m3	GO:005197	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Avp
GO_BP_m3	GO:006001	parathyroic	1/539	7/23843	0.147924	0.532552	0.5025	Tgfbr1
GO_BP_m3	GO:006012	inner ear re	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:006029	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Mkks
GO_BP_m3	GO:006029	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Mkks
GO_BP_m3	GO:006046	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Adam24
GO_BP_m3	GO:006050	Type I pneu	1/539	7/23843	0.147924	0.532552	0.5025	Klf2
GO_BP_m3	GO:006075	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Ccl5
GO_BP_m3	GO:006097	angiogene	1/539	7/23843	0.147924	0.532552	0.5025	Tgfbr1
GO_BP_m3	GO:006143	renal syster	1/539	7/23843	0.147924	0.532552	0.5025	Tcf21
GO_BP_m3	GO:006143	kidney vasc	1/539	7/23843	0.147924	0.532552	0.5025	Tcf21
GO_BP_m3	GO:007014	response to	1/539	7/23843	0.147924	0.532552	0.5025	Cryaa
GO_BP_m3	GO:007099	NADPH ox	1/539	7/23843	0.147924	0.532552	0.5025	Fdx1
GO_BP_m3	GO:007205	S-shaped b	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:007216	mesenchyr	1/539	7/23843	0.147924	0.532552	0.5025	Tcf21
GO_BP_m3	GO:007228	metanephr	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:007260	interleukin-	1/539	7/23843	0.147924	0.532552	0.5025	Prkcz
GO_BP_m3	GO:009026	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Mad2l1
GO_BP_m3	GO:009900	calmodulin	1/539	7/23843	0.147924	0.532552	0.5025	Lrrk2
GO_BP_m3	GO:190004	positive reg	1/539	7/23843	0.147924	0.532552	0.5025	Carmil2

GO_BP_m3	GO:190102	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Ier3
GO_BP_m3	GO:190153	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:190172	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Lrrk2
GO_BP_m3	GO:190201	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Mkks
GO_BP_m3	GO:190233	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Foxc2
GO_BP_m3	GO:190302	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:190335	response t	1/539	7/23843	0.147924	0.532552	0.5025	Lrrk2
GO_BP_m3	GO:190335	cellular res	1/539	7/23843	0.147924	0.532552	0.5025	Lrrk2
GO_BP_m3	GO:190398	positive re	1/539	7/23843	0.147924	0.532552	0.5025	Lrrk2
GO_BP_m3	GO:200025	negative re	1/539	7/23843	0.147924	0.532552	0.5025	Cd46
GO_BP_m3	GO:200057	positive re	1/539	7/23843	0.147924	0.532552	0.5025	BC048507
GO_BP_m3	GO:200065	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Ctr9
GO_BP_m3	GO:200066	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Prkcz
GO_BP_m3	GO:200097	regulation	1/539	7/23843	0.147924	0.532552	0.5025	Hes1
GO_BP_m3	GO:200101	mesenchyr	1/539	7/23843	0.147924	0.532552	0.5025	Tcf21
GO_BP_m3	GO:005165	establishm	7/539	193/23843	0.148685	0.534533	0.504369	Ap3s1/Bcl2
GO_BP_m3	GO:004584	positive re	3/539	59/23843	0.148723	0.534533	0.504369	Neurog1/
GO_BP_m3	GO:003466	ncRNA me	14/539	453/23843	0.149143	0.535594	0.505371	Trmo/Dis3/
GO_BP_m3	GO:003103	actomyosir	7/539	194/23843	0.151468	0.543486	0.512817	Mkks/Myb
GO_BP_m3	GO:003433	cell junctio	8/539	230/23843	0.151689	0.543825	0.513137	Cdh26/Crb
GO_BP_m3	GO:005101	actin filame	6/539	159/23843	0.152228	0.545305	0.514533	Mkks/Nf2/
GO_BP_m3	GO:003238	regulation	13/539	417/23843	0.153101	0.546492	0.515653	Ablim3/Bcl
GO_BP_m3	GO:002151	cell differer	3/539	60/23843	0.154093	0.546492	0.515653	Mir19a/Nk
GO_BP_m3	GO:004477	mitotic DN	3/539	60/23843	0.154093	0.546492	0.515653	Fanci/Ier3/
GO_BP_m3	GO:006099	positive re	3/539	60/23843	0.154093	0.546492	0.515653	Caprin1/C
GO_BP_m3	GO:007147	cellular res	3/539	60/23843	0.154093	0.546492	0.515653	Bcl2l1/Kdm
GO_BP_m3	GO:004642	regulation	7/539	195/23843	0.154275	0.546492	0.515653	Ccl5/Crlf1/
GO_BP_m3	GO:000308	regulation	2/539	31/23843	0.154789	0.546492	0.515653	Ndst2/Tac
GO_BP_m3	GO:001071	positive re	2/539	31/23843	0.154789	0.546492	0.515653	Ihh/Ucn
GO_BP_m3	GO:003336	secretory g	2/539	31/23843	0.154789	0.546492	0.515653	Ptprn/Syt4
GO_BP_m3	GO:004274	regulation	2/539	31/23843	0.154789	0.546492	0.515653	Ghrhr/Nlg
GO_BP_m3	GO:004362	ncRNA 3'-	2/539	31/23843	0.154789	0.546492	0.515653	Exosc6/Int
GO_BP_m3	GO:004824	sperm cap	2/539	31/23843	0.154789	0.546492	0.515653	Catsper4/
GO_BP_m3	GO:005149	positive re	2/539	31/23843	0.154789	0.546492	0.515653	Nlgn1/Tgf
GO_BP_m3	GO:009007	relaxation	2/539	31/23843	0.154789	0.546492	0.515653	Neurog1/T
GO_BP_m3	GO:009050	epiboly	2/539	31/23843	0.154789	0.546492	0.515653	Plet1/Car
GO_BP_m3	GO:000202	regulation	4/539	92/23843	0.155217	0.546492	0.515653	Nkain3/Prs
GO_BP_m3	GO:005189	membrane	4/539	92/23843	0.155217	0.546492	0.515653	Catsper4/
GO_BP_m3	GO:005501	cardiac mu	4/539	92/23843	0.155217	0.546492	0.515653	Ctdp1/Fox
GO_BP_m3	GO:004327	negative re	6/539	160/23843	0.155364	0.546492	0.515653	Gpm6b/Ha
GO_BP_m3	GO:001715	regulation	7/539	196/23843	0.157106	0.546492	0.515653	Abr/Bcl2l1/
GO_BP_m3	GO:000270	regulation	5/539	126/23843	0.15733	0.546492	0.515653	Exosc6/Hk
GO_BP_m3	GO:000709	mitotic cell	5/539	126/23843	0.15733	0.546492	0.515653	Bcl2l1/Fan
GO_BP_m3	GO:190165	cellular res	5/539	126/23843	0.15733	0.546492	0.515653	Fdx1/Mir1
GO_BP_m3	GO:003475	cellular hor	4/539	93/23843	0.159504	0.546492	0.515653	Bmp2/Lcn
GO_BP_m3	GO:004864	muscle org	4/539	93/23843	0.159504	0.546492	0.515653	Bmp2/Fox
GO_BP_m3	GO:190274	regulation	4/539	93/23843	0.159504	0.546492	0.515653	Atf5/Fanci/
GO_BP_m3	GO:004338	positive re	3/539	61/23843	0.159524	0.546492	0.515653	Hes1/Trim

GO_BP_m3	GO:004566	regulation	3/539	61/23843	0.159524	0.546492	0.515653	Cdon/Myo
GO_BP_m3	GO:004662	regulation	3/539	61/23843	0.159524	0.546492	0.515653	Prkcz/Ptpre
GO_BP_m3	GO:005043	catecholam	3/539	61/23843	0.159524	0.546492	0.515653	Chrna4/Ox
GO_BP_m3	GO:006039	regulation	3/539	61/23843	0.159524	0.546492	0.515653	Bmp2/Gdf5
GO_BP_m3	GO:009055	regulation	3/539	61/23843	0.159524	0.546492	0.515653	Bcl2l1/Ier3/
GO_BP_m3	GO:200102	negative re	3/539	61/23843	0.159524	0.546492	0.515653	Bcl2l1/D33
GO_BP_m3	GO:190489	regulation	7/539	197/23843	0.159961	0.546492	0.515653	Ccl5/Crlf1/
GO_BP_m3	GO:006157	actin filame	6/539	162/23843	0.161721	0.546492	0.515653	Mkks/Nf2/
GO_BP_m3	GO:000003	very long-	2/539	32/23843	0.16277	0.546492	0.515653	Elovl2/Slc2
GO_BP_m3	GO:000244	neutrophil	2/539	32/23843	0.16277	0.546492	0.515653	Abr/Dnase
GO_BP_m3	GO:006008	acetyl-CoA	2/539	32/23843	0.16277	0.546492	0.515653	Dlat/Dld
GO_BP_m3	GO:006300	DNA catab	2/539	32/23843	0.16277	0.546492	0.515653	Dnase1l3/I
GO_BP_m3	GO:002241	circadian sl	2/539	32/23843	0.16277	0.546492	0.515653	Ghrhr/Nlgr
GO_BP_m3	GO:003273	positive re	2/539	32/23843	0.16277	0.546492	0.515653	Cd46/Prkcz
GO_BP_m3	GO:003588	enteroend	2/539	32/23843	0.16277	0.546492	0.515653	Hes1/Nkx6
GO_BP_m3	GO:006079	cell fate co	2/539	32/23843	0.16277	0.546492	0.515653	Ctr9/Foxc2
GO_BP_m3	GO:008015	regulation	2/539	32/23843	0.16277	0.546492	0.515653	Adam24/Fa
GO_BP_m3	GO:008502	extracellula	2/539	32/23843	0.16277	0.546492	0.515653	Gpm6b/Ihh
GO_BP_m3	GO:190342	regulation	2/539	32/23843	0.16277	0.546492	0.515653	Dleu2/Lrrk2
GO_BP_m3	GO:004209	T cell prolif	7/539	198/23843	0.162839	0.546492	0.515653	Btn1a1/Ccl
GO_BP_m3	GO:001584	monoamin	4/539	94/23843	0.163833	0.546492	0.515653	Chrna4/Gp
GO_BP_m3	GO:004559	regulation	5/539	128/23843	0.164628	0.546492	0.515653	Atat1/Bmp
GO_BP_m3	GO:200125	negative re	5/539	128/23843	0.164628	0.546492	0.515653	Gnl3l/Kdm
GO_BP_m3	GO:190054	regulation	6/539	163/23843	0.16494	0.546492	0.515653	Avp/Bcl2l1/
GO_BP_m3	GO:000183	release of	3/539	62/23843	0.165011	0.546492	0.515653	Avp/Bcl2l1/
GO_BP_m3	GO:000267	regulation	3/539	62/23843	0.165011	0.546492	0.515653	Ccl5/Cd46/
GO_BP_m3	GO:002169	cerebellar	3/539	62/23843	0.165011	0.546492	0.515653	Atxn2/Dixd
GO_BP_m3	GO:200017	positive re	3/539	62/23843	0.165011	0.546492	0.515653	Cdon/Disp
GO_BP_m3	GO:000182	inner cell n	1/539	8/23843	0.167192	0.546492	0.515653	Ctr9
GO_BP_m3	GO:000203	brain renin	1/539	8/23843	0.167192	0.546492	0.515653	Tacr1
GO_BP_m3	GO:000551	detection c	1/539	8/23843	0.167192	0.546492	0.515653	Kcnmb4
GO_BP_m3	GO:000636	transcriptic	1/539	8/23843	0.167192	0.546492	0.515653	Dmtf1
GO_BP_m3	GO:001021	maintenanc	1/539	8/23843	0.167192	0.546492	0.515653	Uhrf1
GO_BP_m3	GO:001060	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Atxn2
GO_BP_m3	GO:001567	carbon dio	1/539	8/23843	0.167192	0.546492	0.515653	Aqp5
GO_BP_m3	GO:001809	protein pol	1/539	8/23843	0.167192	0.546492	0.515653	Ttll4
GO_BP_m3	GO:001922	neuronal a	1/539	8/23843	0.167192	0.546492	0.515653	Clcn1
GO_BP_m3	GO:002186	forebrain r	1/539	8/23843	0.167192	0.546492	0.515653	Hes1
GO_BP_m3	GO:003112	snoRNA 3'	1/539	8/23843	0.167192	0.546492	0.515653	Exosc6
GO_BP_m3	GO:003139	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Avp
GO_BP_m3	GO:003144	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Ctr9
GO_BP_m3	GO:003194	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Bmp2
GO_BP_m3	GO:003227	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Ucn2
GO_BP_m3	GO:003234	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Bmp2
GO_BP_m3	GO:003363	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ccl5
GO_BP_m3	GO:003368	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ucn2
GO_BP_m3	GO:003447	U4 snRNA	1/539	8/23843	0.167192	0.546492	0.515653	Exosc6
GO_BP_m3	GO:003465	cortisol bio	1/539	8/23843	0.167192	0.546492	0.515653	Bmp2

GO_BP_m3	GO:00354	gastric mo	1/539	8/23843	0.167192	0.546492	0.515653	Ucn
GO_BP_m3	GO:003581	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Oxt
GO_BP_m3	GO:00427	very long-	1/539	8/23843	0.167192	0.546492	0.515653	Slc27a4
GO_BP_m3	GO:00427	snRNA tra	1/539	8/23843	0.167192	0.546492	0.515653	Snapc1
GO_BP_m3	GO:00430	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Tff2
GO_BP_m3	GO:004331	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Abr
GO_BP_m3	GO:00443	Wnt signali	1/539	8/23843	0.167192	0.546492	0.515653	Axin2
GO_BP_m3	GO:00443	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Dusp26
GO_BP_m3	GO:00448	meiotic tel	1/539	8/23843	0.167192	0.546492	0.515653	Ankle1
GO_BP_m3	GO:00468	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ucn2
GO_BP_m3	GO:004874	positive re	1/539	8/23843	0.167192	0.546492	0.515653	Myod1
GO_BP_m3	GO:00514	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ucn
GO_BP_m3	GO:00600	embryonic	1/539	8/23843	0.167192	0.546492	0.515653	Cdon
GO_BP_m3	GO:00603	cranial sut	1/539	8/23843	0.167192	0.546492	0.515653	Twist1
GO_BP_m3	GO:00607	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ccl5
GO_BP_m3	GO:00610	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Nlgn1
GO_BP_m3	GO:006104	vascular w	1/539	8/23843	0.167192	0.546492	0.515653	Foxc2
GO_BP_m3	GO:00610	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Ctdp1
GO_BP_m3	GO:00616	pharyngea	1/539	8/23843	0.167192	0.546492	0.515653	Hes1
GO_BP_m3	GO:00701	meiotic att	1/539	8/23843	0.167192	0.546492	0.515653	Ankle1
GO_BP_m3	GO:00722	metanephr	1/539	8/23843	0.167192	0.546492	0.515653	Tcf21
GO_BP_m3	GO:00902	positive re	1/539	8/23843	0.167192	0.546492	0.515653	Mad2l1
GO_BP_m3	GO:009711	AMPA glut	1/539	8/23843	0.167192	0.546492	0.515653	Nlgn1
GO_BP_m3	GO:009724	chromoso	1/539	8/23843	0.167192	0.546492	0.515653	Ankle1
GO_BP_m3	GO:009884	protein tra	1/539	8/23843	0.167192	0.546492	0.515653	Cep131
GO_BP_m3	GO:009887	action pote	1/539	8/23843	0.167192	0.546492	0.515653	Clcn1
GO_BP_m3	GO:009911	microtubul	1/539	8/23843	0.167192	0.546492	0.515653	Cep131
GO_BP_m3	GO:190011	extracellula	1/539	8/23843	0.167192	0.546492	0.515653	Cd46
GO_BP_m3	GO:190011	extracellula	1/539	8/23843	0.167192	0.546492	0.515653	Cd46
GO_BP_m3	GO:19003	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Ctr9
GO_BP_m3	GO:190301	positive re	1/539	8/23843	0.167192	0.546492	0.515653	Tmem119
GO_BP_m3	GO:19033	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ucn
GO_BP_m3	GO:190374	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Lrrk2
GO_BP_m3	GO:190417	positive re	1/539	8/23843	0.167192	0.546492	0.515653	Mir103-2
GO_BP_m3	GO:190474	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Foxc2
GO_BP_m3	GO:19905	dense core	1/539	8/23843	0.167192	0.546492	0.515653	Syt4
GO_BP_m3	GO:200017	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Lrrk2
GO_BP_m3	GO:20004	negative re	1/539	8/23843	0.167192	0.546492	0.515653	Prkar1b
GO_BP_m3	GO:20008	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Ucn
GO_BP_m3	GO:200127	regulation	1/539	8/23843	0.167192	0.546492	0.515653	Avp
GO_BP_m3	GO:00421	regulation	6/539	164/23843	0.168187	0.548551	0.517596	Btn1a1/Ccl
GO_BP_m3	GO:00097	axis specifi	4/539	95/23843	0.168205	0.548551	0.517596	Axin2/Neu
GO_BP_m3	GO:003164	regulation	4/539	95/23843	0.168205	0.548551	0.517596	Avp/Chrnb
GO_BP_m3	GO:00605	skeletal mu	7/539	200/23843	0.168665	0.549632	0.518616	Cdon/Myo
GO_BP_m3	GO:00016	branching	3/539	63/23843	0.170554	0.55372	0.522474	Bmp2/Ptch
GO_BP_m3	GO:00300	lamellipodi	3/539	63/23843	0.170554	0.55372	0.522474	Ablim3/Ca
GO_BP_m3	GO:00973	cellular res	3/539	63/23843	0.170554	0.55372	0.522474	Mir362/P2
GO_BP_m3	GO:000761	mating beh	2/539	33/23843	0.170822	0.55372	0.522474	Avp/Oxt

GO_BP_m3	GO:001404	glutamate	2/539	33/23843	0.170822	0.55372	0.522474	Avp/Syt4
GO_BP_m3	GO:002168	cerebellar l	2/539	33/23843	0.170822	0.55372	0.522474	Atxn2/Whr
GO_BP_m3	GO:004340	skeletal mu	2/539	33/23843	0.170822	0.55372	0.522474	Myod1/My
GO_BP_m3	GO:003001	establishm	5/539	130/23843	0.172058	0.556887	0.525461	Crb3/Foxf1
GO_BP_m3	GO:003267	regulation	5/539	130/23843	0.172058	0.556887	0.525461	C1qtnf4/Il1
GO_BP_m3	GO:000245	T cell medi	4/539	96/23843	0.172618	0.557439	0.525983	Aire/Cd46/
GO_BP_m3	GO:003031	flagellated	4/539	96/23843	0.172618	0.557439	0.525983	Catsper4/C
GO_BP_m3	GO:004210	positive reg	4/539	96/23843	0.172618	0.557439	0.525983	Ccl5/Cd46/
GO_BP_m3	GO:004244	hormone m	7/539	202/23843	0.174581	0.561597	0.529906	Bmp2/Fdx1
GO_BP_m3	GO:000763	feeding be	5/539	131/23843	0.175821	0.561597	0.529906	Adm2/Helt
GO_BP_m3	GO:001700	mesoderm	3/539	64/23843	0.176149	0.561597	0.529906	Foxc2/Foxf
GO_BP_m3	GO:002176	hippocamp	3/539	64/23843	0.176149	0.561597	0.529906	Atat1/Mkks
GO_BP_m3	GO:003081	positive reg	3/539	64/23843	0.176149	0.561597	0.529906	Avp/Bcl2l1/
GO_BP_m3	GO:003139	negative re	3/539	64/23843	0.176149	0.561597	0.529906	Bag5/Gnl3l
GO_BP_m3	GO:006038	pathway-re	3/539	64/23843	0.176149	0.561597	0.529906	Bmp2/Gdf5
GO_BP_m3	GO:190037	positive reg	3/539	64/23843	0.176149	0.561597	0.529906	Avp/Bcl2l1/
GO_BP_m3	GO:000635	DNA-temp	4/539	97/23843	0.17707	0.561597	0.529906	Dmtf1/Gtf2
GO_BP_m3	GO:004605	cAMP meta	4/539	97/23843	0.17707	0.561597	0.529906	Avp/Ghrhr/
GO_BP_m3	GO:000820	C21-steroi	2/539	34/23843	0.178938	0.561597	0.529906	Bmp2/Srd5
GO_BP_m3	GO:001404	dopamine	2/539	34/23843	0.178938	0.561597	0.529906	Chrna4/Syt
GO_BP_m3	GO:001405	regulation	2/539	34/23843	0.178938	0.561597	0.529906	Chrna4/Syt
GO_BP_m3	GO:003164	positive reg	2/539	34/23843	0.178938	0.561597	0.529906	Chrnb4/So
GO_BP_m3	GO:003209	response to	2/539	34/23843	0.178938	0.561597	0.529906	Mkks/Ucn
GO_BP_m3	GO:003362	regulation	2/539	34/23843	0.178938	0.561597	0.529906	Ccl5/Foxc2
GO_BP_m3	GO:004274	circadian sl	2/539	34/23843	0.178938	0.561597	0.529906	Ghrhr/Nlgn
GO_BP_m3	GO:005156	histone H3	2/539	34/23843	0.178938	0.561597	0.529906	Kdm4b/Kd
GO_BP_m3	GO:005508	monovalen	2/539	34/23843	0.178938	0.561597	0.529906	Slc12a7/Tfa
GO_BP_m3	GO:001700	formation (	4/539	98/23843	0.181562	0.561597	0.529906	Ctr9/Foxc2
GO_BP_m3	GO:000609	pyruvate m	4/539	98/23843	0.181562	0.561597	0.529906	Dlat/Dld/H
GO_BP_m3	GO:003079	regulation	4/539	98/23843	0.181562	0.561597	0.529906	Avp/Ghrhr/
GO_BP_m3	GO:007022	lymphocyte	4/539	98/23843	0.181562	0.561597	0.529906	Ccl5/Mir10
GO_BP_m3	GO:000271	regulation	3/539	65/23843	0.181795	0.561597	0.529906	Hk1/Prkcz/
GO_BP_m3	GO:001657	histone dea	3/539	65/23843	0.181795	0.561597	0.529906	Jdp2/Lrrk2/
GO_BP_m3	GO:004477	mitotic DN	3/539	65/23843	0.181795	0.561597	0.529906	Fanci/Ier3/
GO_BP_m3	GO:004816	regulation	3/539	65/23843	0.181795	0.561597	0.529906	Grik2/Syng
GO_BP_m3	GO:004859	camera-typ	5/539	133/23843	0.183439	0.561597	0.529906	Aqp5/Cdon
GO_BP_m3	GO:004881	dendrite m	6/539	169/23843	0.184813	0.561597	0.529906	Caprin1/Cu
GO_BP_m3	GO:000231	myeloid pr	1/539	9/23843	0.186025	0.561597	0.529906	Ankle1
GO_BP_m3	GO:000313	secondary	1/539	9/23843	0.186025	0.561597	0.529906	Axin2
GO_BP_m3	GO:000322	ventricular	1/539	9/23843	0.186025	0.561597	0.529906	Tgfbr1
GO_BP_m3	GO:000331	pancreatic	1/539	9/23843	0.186025	0.561597	0.529906	Hes1
GO_BP_m3	GO:000601	mannose m	1/539	9/23843	0.186025	0.561597	0.529906	Pmm1
GO_BP_m3	GO:000734	egg activat	1/539	9/23843	0.186025	0.561597	0.529906	Adam24
GO_BP_m3	GO:000756	parturition	1/539	9/23843	0.186025	0.561597	0.529906	Hpgd
GO_BP_m3	GO:000835	germ cell m	1/539	9/23843	0.186025	0.561597	0.529906	Tgfbr1
GO_BP_m3	GO:001586	purine ribo	1/539	9/23843	0.186025	0.561597	0.529906	Slc25a17
GO_BP_m3	GO:001633	calcium-ind	1/539	9/23843	0.186025	0.561597	0.529906	Bmp2
GO_BP_m3	GO:001706	respiratory	1/539	9/23843	0.186025	0.561597	0.529906	Bcs1l

GO_BP_m3	GO:002189	olfactory b	1/539	9/23843	0.186025	0.561597	0.529906	Atf5
GO_BP_m3	GO:002202	tangential	1/539	9/23843	0.186025	0.561597	0.529906	Lrrk2
GO_BP_m3	GO:003030	poly-N-ac	1/539	9/23843	0.186025	0.561597	0.529906	B3gnt6
GO_BP_m3	GO:003031	poly-N-ac	1/539	9/23843	0.186025	0.561597	0.529906	B3gnt6
GO_BP_m3	GO:003091	midbrain-	1/539	9/23843	0.186025	0.561597	0.529906	Hes1
GO_BP_m3	GO:003162	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Ccl5
GO_BP_m3	GO:003200	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Twist1
GO_BP_m3	GO:003331	mitotic DN	1/539	9/23843	0.186025	0.561597	0.529906	Oraov1
GO_BP_m3	GO:003435	negative re	1/539	9/23843	0.186025	0.561597	0.529906	Prkch
GO_BP_m3	GO:003439	telomere te	1/539	9/23843	0.186025	0.561597	0.529906	Ankle1
GO_BP_m3	GO:003455	mitochond	1/539	9/23843	0.186025	0.561597	0.529906	Bcs1l
GO_BP_m3	GO:003523	ectopic ge	1/539	9/23843	0.186025	0.561597	0.529906	Rhox5
GO_BP_m3	GO:004317	nucleotide	1/539	9/23843	0.186025	0.561597	0.529906	Fuk
GO_BP_m3	GO:004341	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Myod1
GO_BP_m3	GO:004356	negative re	1/539	9/23843	0.186025	0.561597	0.529906	Bmp2
GO_BP_m3	GO:004560	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Hes1
GO_BP_m3	GO:004563	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Hes1
GO_BP_m3	GO:004601	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Ghrhr
GO_BP_m3	GO:004660	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Ranbp3l
GO_BP_m3	GO:004834	paraxial me	1/539	9/23843	0.186025	0.561597	0.529906	Foxc2
GO_BP_m3	GO:005150	adenine nu	1/539	9/23843	0.186025	0.561597	0.529906	Slc25a17
GO_BP_m3	GO:005269	flavonoid	1/539	9/23843	0.186025	0.561597	0.529906	Ugt1a7c
GO_BP_m3	GO:005269	xenobiotic	1/539	9/23843	0.186025	0.561597	0.529906	Ugt1a7c
GO_BP_m3	GO:006031	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Abr
GO_BP_m3	GO:006040	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Oxt
GO_BP_m3	GO:006046	lung lobe	1/539	9/23843	0.186025	0.561597	0.529906	Foxf1
GO_BP_m3	GO:006046	lung lobe	1/539	9/23843	0.186025	0.561597	0.529906	Foxf1
GO_BP_m3	GO:006053	diaphragm	1/539	9/23843	0.186025	0.561597	0.529906	Tcf21
GO_BP_m3	GO:006100	common b	1/539	9/23843	0.186025	0.561597	0.529906	Hes1
GO_BP_m3	GO:007023	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Tsc22d3
GO_BP_m3	GO:007054	histone H3	1/539	9/23843	0.186025	0.561597	0.529906	Kdm4b
GO_BP_m3	GO:007130	cellular res	1/539	9/23843	0.186025	0.561597	0.529906	Pdia3
GO_BP_m3	GO:007139	cellular res	1/539	9/23843	0.186025	0.561597	0.529906	Ptch1
GO_BP_m3	GO:007268	T cell extra	1/539	9/23843	0.186025	0.561597	0.529906	Ccl5
GO_BP_m3	GO:009004	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Lrrk2
GO_BP_m3	GO:009009	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Carmil2
GO_BP_m3	GO:009030	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Uhrf1
GO_BP_m3	GO:009052	sphingolipi	1/539	9/23843	0.186025	0.561597	0.529906	S1pr1
GO_BP_m3	GO:009710	postsynapt	1/539	9/23843	0.186025	0.561597	0.529906	Nlgn1
GO_BP_m3	GO:009711	postsynapt	1/539	9/23843	0.186025	0.561597	0.529906	Nlgn1
GO_BP_m3	GO:009768	glutamate	1/539	9/23843	0.186025	0.561597	0.529906	Nlgn1
GO_BP_m3	GO:190183	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Ippk
GO_BP_m3	GO:190209	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Tacr1
GO_BP_m3	GO:190256	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Abr
GO_BP_m3	GO:190397	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Lrrk2
GO_BP_m3	GO:190466	negative re	1/539	9/23843	0.186025	0.561597	0.529906	Mad2l1
GO_BP_m3	GO:200034	positive re	1/539	9/23843	0.186025	0.561597	0.529906	Ccl5
GO_BP_m3	GO:200055	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Prkcz

GO_BP_m3	GO:200067	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Crlf1
GO_BP_m3	GO:200098	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Hes1
GO_BP_m3	GO:200117	regulation	1/539	9/23843	0.186025	0.561597	0.529906	Prkcz
GO_BP_m3	GO:000727	neuromusc	2/539	35/23843	0.187112	0.561597	0.529906	Chrna4/Ch
GO_BP_m3	GO:000815	negative re	2/539	35/23843	0.187112	0.561597	0.529906	Enpp7/Nf2
GO_BP_m3	GO:003222	regulation	2/539	35/23843	0.187112	0.561597	0.529906	Nlgn1/Tacr
GO_BP_m3	GO:003314	positive reg	2/539	35/23843	0.187112	0.561597	0.529906	Gm13287/
GO_BP_m3	GO:003590	aorta morp	2/539	35/23843	0.187112	0.561597	0.529906	Hes1/Tfap2
GO_BP_m3	GO:004519	regulation	2/539	35/23843	0.187112	0.561597	0.529906	Exosc6/Mir
GO_BP_m3	GO:004568	positive reg	2/539	35/23843	0.187112	0.561597	0.529906	Prkch/Ptch
GO_BP_m3	GO:004800	insulin-like	2/539	35/23843	0.187112	0.561597	0.529906	Bmp2/Ghrl
GO_BP_m3	GO:005502	negative re	2/539	35/23843	0.187112	0.561597	0.529906	Bmp2/Ctdp
GO_BP_m3	GO:190274	apoptotic p	2/539	35/23843	0.187112	0.561597	0.529906	Cryaa/Foxc
GO_BP_m3	GO:001569	inorganic a	5/539	134/23843	0.187293	0.561749	0.53005	Clcn1/P2ry
GO_BP_m3	GO:001631	dephospho	11/539	357/23843	0.187426	0.561756	0.530056	Bmp2/Ctdp
GO_BP_m3	GO:000614	regulation	6/539	170/23843	0.188214	0.56333	0.531541	Avp/Bcl2l1/
GO_BP_m3	GO:000961	response t	6/539	170/23843	0.188214	0.56333	0.531541	Mir194-2/N
GO_BP_m3	GO:005134	negative re	12/539	397/23843	0.190623	0.569445	0.537311	9230104L0
GO_BP_m3	GO:003139	positive reg	4/539	100/23843	0.190655	0.569445	0.537311	Ctr9/Fanci/
GO_BP_m3	GO:005088	endocrine	4/539	100/23843	0.190655	0.569445	0.537311	Ndst2/Tacr
GO_BP_m3	GO:001657	histone mo	13/539	437/23843	0.193007	0.572728	0.540409	Ctr9/Epop/
GO_BP_m3	GO:000602	proteoglyc	3/539	67/23843	0.193228	0.572728	0.540409	Bmp2/Ihh/
GO_BP_m3	GO:000694	regulation	3/539	67/23843	0.193228	0.572728	0.540409	Chrnb4/Ox
GO_BP_m3	GO:003238	negative re	3/539	67/23843	0.193228	0.572728	0.540409	Foxf1/Lrrk2
GO_BP_m3	GO:003563	multicellula	5/539	136/23843	0.195089	0.572728	0.540409	Avp/Chrnb
GO_BP_m3	GO:002154	cerebellum	4/539	101/23843	0.195255	0.572728	0.540409	Atxn2/Dixd
GO_BP_m3	GO:003153	actin cytos	4/539	101/23843	0.195255	0.572728	0.540409	Cass4/Hck/
GO_BP_m3	GO:004562	positive reg	4/539	101/23843	0.195255	0.572728	0.540409	Cd46/Ihh/P
GO_BP_m3	GO:005195	regulation	4/539	101/23843	0.195255	0.572728	0.540409	Avp/Chrna
GO_BP_m3	GO:006041	heart grow	4/539	101/23843	0.195255	0.572728	0.540409	Ctdp1/Foxc
GO_BP_m3	GO:002179	cerebral co	2/539	36/23843	0.195336	0.572728	0.540409	Dixdc1/Md
GO_BP_m3	GO:003022	macrophag	2/539	36/23843	0.195336	0.572728	0.540409	L3mbtl3/N
GO_BP_m3	GO:004816	regulation	2/539	36/23843	0.195336	0.572728	0.540409	Grik2/Syng
GO_BP_m3	GO:004882	erythrocyte	2/539	36/23843	0.195336	0.572728	0.540409	Klf2/L3mbt
GO_BP_m3	GO:005115	negative re	2/539	36/23843	0.195336	0.572728	0.540409	Bmp2/Ctdp
GO_BP_m3	GO:006138	heart trabe	2/539	36/23843	0.195336	0.572728	0.540409	S1pr1/Tgfb
GO_BP_m3	GO:190269	regulation	2/539	36/23843	0.195336	0.572728	0.540409	Lrrk2/Sox1
GO_BP_m3	GO:004478	cilium orga	10/539	322/23843	0.195444	0.572728	0.540409	1110004E0
GO_BP_m3	GO:004833	mesoderm	3/539	68/23843	0.19901	0.572728	0.540409	Foxc2/Foxf
GO_BP_m3	GO:003263	interleukin-	5/539	137/23843	0.199028	0.572728	0.540409	C1qtnf4/Il1
GO_BP_m3	GO:005067	positive reg	5/539	137/23843	0.199028	0.572728	0.540409	Ccl5/Cd46/
GO_BP_m3	GO:190290	negative re	5/539	137/23843	0.199028	0.572728	0.540409	Ckap2/Mkl
GO_BP_m3	GO:200102	regulation	4/539	102/23843	0.199889	0.572728	0.540409	Chrna4/Lrr
GO_BP_m3	GO:004327	positive reg	9/539	286/23843	0.201131	0.572728	0.540409	Avp/Ccl5/C
GO_BP_m3	GO:003510	appendage	6/539	174/23843	0.202054	0.572728	0.540409	Gdf5/Ihh/P
GO_BP_m3	GO:003510	limb morph	6/539	174/23843	0.202054	0.572728	0.540409	Gdf5/Ihh/P
GO_BP_m3	GO:001082	positive reg	5/539	138/23843	0.202995	0.572728	0.540409	Ablim3/He
GO_BP_m3	GO:000205	positive reg	2/539	37/23843	0.203605	0.572728	0.540409	Foxf1/Ihh

GO_BP_m3	GO:00030	skeletal mu	2/539	37/23843	0.203605	0.572728	0.540409	Tnni2/Tnnt
GO_BP_m3	GO:003051	positive re	2/539	37/23843	0.203605	0.572728	0.540409	Gdf5/Hes1
GO_BP_m3	GO:00331	regulation	2/539	37/23843	0.203605	0.572728	0.540409	Gm13287/
GO_BP_m3	GO:00459	positive re	2/539	37/23843	0.203605	0.572728	0.540409	Oxt/Tacr1
GO_BP_m3	GO:006067	placenta bl	2/539	37/23843	0.203605	0.572728	0.540409	Esx1/Hes1
GO_BP_m3	GO:00726	interleukin	2/539	37/23843	0.203605	0.572728	0.540409	C1qtnf4/Tv
GO_BP_m3	GO:19021	regulation	2/539	37/23843	0.203605	0.572728	0.540409	Ier3/Them
GO_BP_m3	GO:19028	regulation	2/539	37/23843	0.203605	0.572728	0.540409	Bmp2/Tgfb
GO_BP_m3	GO:00457	negative re	13/539	442/23843	0.203681	0.572728	0.540409	Atf5/Bcl2l1
GO_BP_m3	GO:005067	epithelial c	12/539	403/23843	0.204029	0.572728	0.540409	Areg/Bmp
GO_BP_m3	GO:00003	protein der	1/539	10/23843	0.204433	0.572728	0.540409	Cops7a
GO_BP_m3	GO:00030	renal water	1/539	10/23843	0.204433	0.572728	0.540409	Tfap2b
GO_BP_m3	GO:00032	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Hes1
GO_BP_m3	GO:00060	glucose ca	1/539	10/23843	0.204433	0.572728	0.540409	Hk1
GO_BP_m3	GO:00071	neuron cell	1/539	10/23843	0.204433	0.572728	0.540409	Nlgn1
GO_BP_m3	GO:00093	snRNA tra	1/539	10/23843	0.204433	0.572728	0.540409	Snapc1
GO_BP_m3	GO:001004	response t	1/539	10/23843	0.204433	0.572728	0.540409	Lrrk2
GO_BP_m3	GO:001482	artery smo	1/539	10/23843	0.204433	0.572728	0.540409	Mkks
GO_BP_m3	GO:00158	nucleoside	1/539	10/23843	0.204433	0.572728	0.540409	Slc25a17
GO_BP_m3	GO:00158	purine nuc	1/539	10/23843	0.204433	0.572728	0.540409	Slc25a17
GO_BP_m3	GO:00180	protein-co	1/539	10/23843	0.204433	0.572728	0.540409	Gcsh
GO_BP_m3	GO:00182	peptidyl-m	1/539	10/23843	0.204433	0.572728	0.540409	Naa25
GO_BP_m3	GO:003162	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Ccl5
GO_BP_m3	GO:003194	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Bmp2
GO_BP_m3	GO:003222	positive re	1/539	10/23843	0.204433	0.572728	0.540409	Tacr1
GO_BP_m3	GO:003234	aldosteron	1/539	10/23843	0.204433	0.572728	0.540409	Bmp2
GO_BP_m3	GO:00330	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Ihh
GO_BP_m3	GO:00330	negative re	1/539	10/23843	0.204433	0.572728	0.540409	Ihh
GO_BP_m3	GO:00331	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Ctr9
GO_BP_m3	GO:003321	leptin-mec	1/539	10/23843	0.204433	0.572728	0.540409	Mkks
GO_BP_m3	GO:00343	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Prkch
GO_BP_m3	GO:003442	nuclear-tra	1/539	10/23843	0.204433	0.572728	0.540409	Exosc6
GO_BP_m3	GO:00346	cortisol me	1/539	10/23843	0.204433	0.572728	0.540409	Bmp2
GO_BP_m3	GO:00353	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Nf2
GO_BP_m3	GO:00354	phosphate	1/539	10/23843	0.204433	0.572728	0.540409	Slc37a2
GO_BP_m3	GO:003587	protein K1	1/539	10/23843	0.204433	0.572728	0.540409	Otud3
GO_BP_m3	GO:004314	snoRNA pr	1/539	10/23843	0.204433	0.572728	0.540409	Exosc6
GO_BP_m3	GO:004392	negative re	1/539	10/23843	0.204433	0.572728	0.540409	Ccl5
GO_BP_m3	GO:00451	neuronal ic	1/539	10/23843	0.204433	0.572728	0.540409	Sclt1
GO_BP_m3	GO:00456	negative re	1/539	10/23843	0.204433	0.572728	0.540409	Tgfbr1
GO_BP_m3	GO:004654	developme	1/539	10/23843	0.204433	0.572728	0.540409	Areg
GO_BP_m3	GO:00468	follicle-stin	1/539	10/23843	0.204433	0.572728	0.540409	Ucn2
GO_BP_m3	GO:00487	embryonic	1/539	10/23843	0.204433	0.572728	0.540409	Foxc2
GO_BP_m3	GO:005101	actin filam	1/539	10/23843	0.204433	0.572728	0.540409	Fmnl1
GO_BP_m3	GO:00514	corticotrop	1/539	10/23843	0.204433	0.572728	0.540409	Ucn
GO_BP_m3	GO:005197	positive re	1/539	10/23843	0.204433	0.572728	0.540409	Chrnb4
GO_BP_m3	GO:00608	neural plat	1/539	10/23843	0.204433	0.572728	0.540409	Ptch1
GO_BP_m3	GO:00609	coronary a	1/539	10/23843	0.204433	0.572728	0.540409	Tgfbr1

GO_BP_m3	GO:007009	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Gip
GO_BP_m3	GO:007168	striated mu	1/539	10/23843	0.204433	0.572728	0.540409	Mybph
GO_BP_m3	GO:007188	macrophag	1/539	10/23843	0.204433	0.572728	0.540409	Ccl5
GO_BP_m3	GO:007201	distal tubul	1/539	10/23843	0.204433	0.572728	0.540409	Tfap2b
GO_BP_m3	GO:007217	metanephr	1/539	10/23843	0.204433	0.572728	0.540409	Hes1
GO_BP_m3	GO:007220	cell prolifer	1/539	10/23843	0.204433	0.572728	0.540409	Ptch1
GO_BP_m3	GO:007260	interleukin-	1/539	10/23843	0.204433	0.572728	0.540409	Prkcz
GO_BP_m3	GO:009028	negative re	1/539	10/23843	0.204433	0.572728	0.540409	Hes1
GO_BP_m3	GO:009052	actin filame	1/539	10/23843	0.204433	0.572728	0.540409	Cass4
GO_BP_m3	GO:009708	vascular sm	1/539	10/23843	0.204433	0.572728	0.540409	Hes1
GO_BP_m3	GO:009710	presynapti	1/539	10/23843	0.204433	0.572728	0.540409	Nlgn1
GO_BP_m3	GO:190004	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Carmil2
GO_BP_m3	GO:190011	negative re	1/539	10/23843	0.204433	0.572728	0.540409	Bcl2l1
GO_BP_m3	GO:190197	positive reg	1/539	10/23843	0.204433	0.572728	0.540409	Mad2l1
GO_BP_m3	GO:190417	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Mir103-2
GO_BP_m3	GO:200004	negative re	1/539	10/23843	0.204433	0.572728	0.540409	D330045A2
GO_BP_m3	GO:200010	regulation	1/539	10/23843	0.204433	0.572728	0.540409	Ccl5
GO_BP_m3	GO:200034	positive reg	1/539	10/23843	0.204433	0.572728	0.540409	Fam170b
GO_BP_m3	GO:004663	alpha-beta	4/539	103/23843	0.204555	0.572728	0.540409	Ihh/Nkx2-3
GO_BP_m3	GO:200011	negative re	4/539	103/23843	0.204555	0.572728	0.540409	9230104L0
GO_BP_m3	GO:002202	telencepha	3/539	69/23843	0.204833	0.573133	0.540791	Dixdc1/Lrrk
GO_BP_m3	GO:004860	reproducti	13/539	443/23843	0.205847	0.575595	0.543114	Bcl2l1/Ccnt
GO_BP_m3	GO:003294	positive reg	5/539	139/23843	0.206988	0.578407	0.545767	Ccl5/Cd46/
GO_BP_m3	GO:000754	sex differer	9/539	289/23843	0.209267	0.584396	0.551418	Bcl2l1/Dhc
GO_BP_m3	GO:006053	muscle tiss	13/539	445/23843	0.21021	0.58665	0.553545	Bmp2/Cdo
GO_BP_m3	GO:200010	negative re	3/539	70/23843	0.210695	0.587621	0.554461	Ccl5/Mir10
GO_BP_m3	GO:001821	peptidyl-th	5/539	140/23843	0.211006	0.587958	0.55478	Hk1/Lrrk2/
GO_BP_m3	GO:009006	serine fami	2/539	38/23843	0.211911	0.587958	0.55478	Gcsh/Thnsl
GO_BP_m3	GO:001633	calcium-de	2/539	38/23843	0.211911	0.587958	0.55478	Cdh26/Nlg
GO_BP_m3	GO:004688	regulation	2/539	38/23843	0.211911	0.587958	0.55478	Bmp2/Stc2
GO_BP_m3	GO:004879	calcium ior	2/539	38/23843	0.211911	0.587958	0.55478	Syt4/Syt6
GO_BP_m3	GO:009717	ruffle asser	2/539	38/23843	0.211911	0.587958	0.55478	Nlgn1/Carr
GO_BP_m3	GO:200040	regulation	2/539	38/23843	0.211911	0.587958	0.55478	Aire/Ccl5
GO_BP_m3	GO:200102	positive reg	2/539	38/23843	0.211911	0.587958	0.55478	Chrna4/Ptp
GO_BP_m3	GO:002241	cellular prc	11/539	368/23843	0.213507	0.590333	0.55702	Bcl2l1/Cats
GO_BP_m3	GO:001583	amine tran	4/539	105/23843	0.213983	0.590333	0.55702	Avp/Chrna
GO_BP_m3	GO:002198	cerebral cc	4/539	105/23843	0.213983	0.590333	0.55702	Cdon/Dixd
GO_BP_m3	GO:006145	reproducti	13/539	447/23843	0.214614	0.590333	0.55702	Bcl2l1/Ccnt
GO_BP_m3	GO:00320	cardiac cha	5/539	141/23843	0.21505	0.590333	0.55702	Foxc2/Foxf
GO_BP_m3	GO:001097	transport a	5/539	141/23843	0.21505	0.590333	0.55702	Ap3s1/BC0
GO_BP_m3	GO:009911	microtubul	5/539	141/23843	0.21505	0.590333	0.55702	Ap3s1/BC0
GO_BP_m3	GO:012003	plasma me	14/539	487/23843	0.215492	0.590333	0.55702	1110004E0
GO_BP_m3	GO:003106	regulation	3/539	71/23843	0.216593	0.590333	0.55702	Ctr9/Kdm4
GO_BP_m3	GO:003227	negative re	3/539	71/23843	0.216593	0.590333	0.55702	Mkks/Carm
GO_BP_m3	GO:003289	regulation	3/539	71/23843	0.216593	0.590333	0.55702	Avp/Oxt/Sy
GO_BP_m3	GO:004336	CD4-positi	3/539	71/23843	0.216593	0.590333	0.55702	Nkx2-3/Prl
GO_BP_m3	GO:005507	calcium ior	13/539	448/23843	0.216831	0.590333	0.55702	Avp/Calb2/
GO_BP_m3	GO:005109	regulation	11/539	370/23843	0.218406	0.590333	0.55702	Bmp2/Cdo

GO_BP_m3	GO:001656	covalent ch	13/539	449/23843	0.219057	0.590333	0.55702	Ctr9/Epop/
GO_BP_m3	GO:005077	regulation	6/539	179/23843	0.219854	0.590333	0.55702	Caprin1/Cu
GO_BP_m3	GO:005087	positive reg	6/539	179/23843	0.219854	0.590333	0.55702	Ccl5/Cd46/
GO_BP_m3	GO:000317	heart valve	2/539	39/23843	0.22025	0.590333	0.55702	Bmp2/Twis
GO_BP_m3	GO:000734	acrosome r	2/539	39/23843	0.22025	0.590333	0.55702	Fam170b/S
GO_BP_m3	GO:003043	sleep	2/539	39/23843	0.22025	0.590333	0.55702	Ghrhr/Oxt
GO_BP_m3	GO:003157	G2 DNA da	2/539	39/23843	0.22025	0.590333	0.55702	Fanci/Ier3
GO_BP_m3	GO:006012	inner ear re	2/539	39/23843	0.22025	0.590333	0.55702	Hes1/Whrn
GO_BP_m3	GO:004592	positive reg	9/539	293/23843	0.220317	0.590333	0.55702	Avp/Cryaa/
GO_BP_m3	GO:002195	central nerv	7/539	217/23843	0.221592	0.590333	0.55702	Atf5/Atxn2
GO_BP_m3	GO:000292	negative re	1/539	11/23843	0.222425	0.590333	0.55702	Cd46
GO_BP_m3	GO:000326	cardioblast	1/539	11/23843	0.222425	0.590333	0.55702	Hes1
GO_BP_m3	GO:000326	regulation	1/539	11/23843	0.222425	0.590333	0.55702	Hes1
GO_BP_m3	GO:000330	Wnt signali	1/539	11/23843	0.222425	0.590333	0.55702	Bmp2
GO_BP_m3	GO:000670	mineralocc	1/539	11/23843	0.222425	0.590333	0.55702	Bmp2
GO_BP_m3	GO:000981	flavonoid m	1/539	11/23843	0.222425	0.590333	0.55702	Ugt1a7c
GO_BP_m3	GO:001074	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Prkch
GO_BP_m3	GO:001082	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Ccl5
GO_BP_m3	GO:001483	urinary bla	1/539	11/23843	0.222425	0.590333	0.55702	Tacr1
GO_BP_m3	GO:003103	myosin fila	1/539	11/23843	0.222425	0.590333	0.55702	Mybph
GO_BP_m3	GO:003234	aldosteron	1/539	11/23843	0.222425	0.590333	0.55702	Bmp2
GO_BP_m3	GO:003300	negative re	1/539	11/23843	0.222425	0.590333	0.55702	Foxf1
GO_BP_m3	GO:003308	immature T	1/539	11/23843	0.222425	0.590333	0.55702	Ihh
GO_BP_m3	GO:003323	negative re	1/539	11/23843	0.222425	0.590333	0.55702	Gnl3l
GO_BP_m3	GO:003360	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Chrna4
GO_BP_m3	GO:003363	cell-cell ad	1/539	11/23843	0.222425	0.590333	0.55702	Ccl5
GO_BP_m3	GO:003533	fatty-acyl-	1/539	11/23843	0.222425	0.590333	0.55702	Them4
GO_BP_m3	GO:003563	bone mine	1/539	11/23843	0.222425	0.590333	0.55702	Bmp2
GO_BP_m3	GO:004519	maintenan	1/539	11/23843	0.222425	0.590333	0.55702	Pdzd11
GO_BP_m3	GO:004600	negative re	1/539	11/23843	0.222425	0.590333	0.55702	Btn1a1
GO_BP_m3	GO:004660	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Ranbp3l
GO_BP_m3	GO:004831	intracellula	1/539	11/23843	0.222425	0.590333	0.55702	Lrrk2
GO_BP_m3	GO:004861	embryonic	1/539	11/23843	0.222425	0.590333	0.55702	Foxf1
GO_BP_m3	GO:004866	neuron fate	1/539	11/23843	0.222425	0.590333	0.55702	Hes1
GO_BP_m3	GO:005160	exocyst loc	1/539	11/23843	0.222425	0.590333	0.55702	Exoc1
GO_BP_m3	GO:005163	actin filame	1/539	11/23843	0.222425	0.590333	0.55702	Carmil2
GO_BP_m3	GO:006015	regulation	1/539	11/23843	0.222425	0.590333	0.55702	Lrrk2
GO_BP_m3	GO:006034	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Trim6
GO_BP_m3	GO:006040	regulation	1/539	11/23843	0.222425	0.590333	0.55702	Oxt
GO_BP_m3	GO:006045	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Ucn
GO_BP_m3	GO:006060	dichotomo	1/539	11/23843	0.222425	0.590333	0.55702	Areg
GO_BP_m3	GO:006090	embryonic	1/539	11/23843	0.222425	0.590333	0.55702	Twist1
GO_BP_m3	GO:006161	glycolytic p	1/539	11/23843	0.222425	0.590333	0.55702	Hk1
GO_BP_m3	GO:007009	glucagon s	1/539	11/23843	0.222425	0.590333	0.55702	Gip
GO_BP_m3	GO:007060	centromeri	1/539	11/23843	0.222425	0.590333	0.55702	Axin2
GO_BP_m3	GO:007086	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Tmem30b
GO_BP_m3	GO:007163	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Twist1
GO_BP_m3	GO:007167	commissur	1/539	11/23843	0.222425	0.590333	0.55702	Ptch1

GO_BP_m3	GO:007207	metanephr	1/539	11/23843	0.222425	0.590333	0.55702	Tcf21
GO_BP_m3	GO:007210	glomerulus	1/539	11/23843	0.222425	0.590333	0.55702	Tcf21
GO_BP_m3	GO:009007	positive reg	1/539	11/23843	0.222425	0.590333	0.55702	Gnl3l
GO_BP_m3	GO:009039	negative re	1/539	11/23843	0.222425	0.590333	0.55702	Lrrk2
GO_BP_m3	GO:190036	regulation	1/539	11/23843	0.222425	0.590333	0.55702	Ctr9
GO_BP_m3	GO:200057	regulation	1/539	11/23843	0.222425	0.590333	0.55702	BC048507
GO_BP_m3	GO:002188	forebrain c	3/539	72/23843	0.222526	0.590333	0.55702	Dixdc1/Lrrk
GO_BP_m3	GO:004567	regulation	3/539	72/23843	0.222526	0.590333	0.55702	Ccl5/Tmem
GO_BP_m3	GO:006056	neuroepith	3/539	72/23843	0.222526	0.590333	0.55702	Bmp2/Hes1
GO_BP_m3	GO:000323	cardiac ver	5/539	143/23843	0.223209	0.5908	0.557461	Foxc2/Foxf
GO_BP_m3	GO:003032	embryonic	5/539	143/23843	0.223209	0.5908	0.557461	Gdf5/Ihh/P
GO_BP_m3	GO:003511	embryonic	5/539	143/23843	0.223209	0.5908	0.557461	Gdf5/Ihh/P
GO_BP_m3	GO:003286	cellular res	6/539	180/23843	0.223476	0.5908	0.557461	Foxc2/Ghrl
GO_BP_m3	GO:000828	insulin rece	4/539	107/23843	0.223528	0.5908	0.557461	Foxc2/Prkc
GO_BP_m3	GO:009010	positive reg	4/539	107/23843	0.223528	0.5908	0.557461	Bmp2/Gdf5
GO_BP_m3	GO:005114	striated mu	9/539	295/23843	0.225925	0.595373	0.561776	Bmp2/Cdo
GO_BP_m3	GO:003295	regulation	10/539	334/23843	0.226255	0.595373	0.561776	Dixdc1/Gpr
GO_BP_m3	GO:001094	negative re	7/539	219/23843	0.228177	0.595373	0.561776	Atf5/Ccnf/I
GO_BP_m3	GO:000334	cilium mov	3/539	73/23843	0.22849	0.595373	0.561776	1110004E0
GO_BP_m3	GO:000178	B cell apop	2/539	40/23843	0.228615	0.595373	0.561776	Mir106b/M
GO_BP_m3	GO:000315	regulation	2/539	40/23843	0.228615	0.595373	0.561776	Bmp2/Hes1
GO_BP_m3	GO:001082	regulation	2/539	40/23843	0.228615	0.595373	0.561776	Ccnf/Cep13
GO_BP_m3	GO:003080	positive reg	2/539	40/23843	0.228615	0.595373	0.561776	Avp/Rln3
GO_BP_m3	GO:003334	cholesterol	2/539	40/23843	0.228615	0.595373	0.561776	Ptch1/Stx1
GO_BP_m3	GO:006060	mammary	2/539	40/23843	0.228615	0.595373	0.561776	Areg/Ptch1
GO_BP_m3	GO:009027	regulation	2/539	40/23843	0.228615	0.595373	0.561776	Hes1/Ucn
GO_BP_m3	GO:009878	ncRNA trar	2/539	40/23843	0.228615	0.595373	0.561776	Ippk/Snapc
GO_BP_m3	GO:190027	regulation	2/539	40/23843	0.228615	0.595373	0.561776	Calb2/Ptpr
GO_BP_m3	GO:200072	regulation	2/539	40/23843	0.228615	0.595373	0.561776	Bmp2/Ctdp
GO_BP_m3	GO:004301	camera-typ	10/539	335/23843	0.228905	0.595373	0.561776	Aqp5/Cdon
GO_BP_m3	GO:001993	cAMP-mec	5/539	145/23843	0.231461	0.595373	0.561776	Adm2/Ghrl
GO_BP_m3	GO:007066	positive reg	5/539	145/23843	0.231461	0.595373	0.561776	Ccl5/Cd46/
GO_BP_m3	GO:004339	regulation	7/539	220/23843	0.231495	0.595373	0.561776	Bmp2/Cdo
GO_BP_m3	GO:005067	regulation	7/539	220/23843	0.231495	0.595373	0.561776	Btn1a1/Ccl
GO_BP_m3	GO:003030	positive reg	6/539	183/23843	0.234458	0.595373	0.561776	Avp/Cryaa/
GO_BP_m3	GO:006201	positive reg	6/539	183/23843	0.234458	0.595373	0.561776	Avp/Bcl2l1/
GO_BP_m3	GO:000231	B cell activ	3/539	74/23843	0.234484	0.595373	0.561776	Exosc6/Mir
GO_BP_m3	GO:005178	positive reg	3/539	74/23843	0.234484	0.595373	0.561776	Neurog1/R
GO_BP_m3	GO:190370	negative re	5/539	146/23843	0.235619	0.595373	0.561776	Ctr9/Hes1/
GO_BP_m3	GO:000701	microtubul	8/539	260/23843	0.236751	0.595373	0.561776	1110004E0
GO_BP_m3	GO:000196	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	C1qtnf4/Tr
GO_BP_m3	GO:000650	membrane	2/539	41/23843	0.237001	0.595373	0.561776	Pacsin3/Prt
GO_BP_m3	GO:000669	prostanoid	2/539	41/23843	0.237001	0.595373	0.561776	Avp/Hpgd
GO_BP_m3	GO:000669	prostaglan	2/539	41/23843	0.237001	0.595373	0.561776	Avp/Hpgd
GO_BP_m3	GO:001010	potassium	2/539	41/23843	0.237001	0.595373	0.561776	Kcnj4/Slc12
GO_BP_m3	GO:001051	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	Ccl5/Prkcz
GO_BP_m3	GO:001076	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	Prss8/Sgk1
GO_BP_m3	GO:001095	negative re	2/539	41/23843	0.237001	0.595373	0.561776	Cd46/Lrrk2

GO_BP_m3	GO:001967	NAD metal	2/539	41/23843	0.237001	0.595373	0.561776	Hk1/Slc37a
GO_BP_m3	GO:002169	cerebellar (	2/539	41/23843	0.237001	0.595373	0.561776	Atxn2/Whr
GO_BP_m3	GO:003296	regulation	2/539	41/23843	0.237001	0.595373	0.561776	Ihh/Ucn
GO_BP_m3	GO:004549	photorecep	2/539	41/23843	0.237001	0.595373	0.561776	Mkks/Nxnl
GO_BP_m3	GO:004592	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	Avp/Twist1
GO_BP_m3	GO:004663	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	Ihh/Prkcz
GO_BP_m3	GO:004678	regulation	2/539	41/23843	0.237001	0.595373	0.561776	Ccl5/Ctdp1
GO_BP_m3	GO:004749	vesicle tran	2/539	41/23843	0.237001	0.595373	0.561776	Ap3s1/Prkc
GO_BP_m3	GO:005069	regulation	2/539	41/23843	0.237001	0.595373	0.561776	Ccl5/Trim6
GO_BP_m3	GO:005159	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	Bcl2l1/Nlgr
GO_BP_m3	GO:006101	positive reg	2/539	41/23843	0.237001	0.595373	0.561776	Hnrnpr/Na
GO_BP_m3	GO:190331	negative re	2/539	41/23843	0.237001	0.595373	0.561776	Cd46/Lrrk2
GO_BP_m3	GO:003051	intracellula	4/539	110/23843	0.238045	0.595373	0.561776	Ghrhr/Kdm
GO_BP_m3	GO:000237	immunoglo	7/539	222/23843	0.238179	0.595373	0.561776	Exosc6/Igk
GO_BP_m3	GO:003294	regulation	7/539	222/23843	0.238179	0.595373	0.561776	Btn1a1/Ccl
GO_BP_m3	GO:000184	neural plat	1/539	12/23843	0.240011	0.595373	0.561776	Ptch1
GO_BP_m3	GO:000201	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Tacr1
GO_BP_m3	GO:000232	pro-B cell (	1/539	12/23843	0.240011	0.595373	0.561776	Hes1
GO_BP_m3	GO:000232	pre-B cell (	1/539	12/23843	0.240011	0.595373	0.561776	Mir19a
GO_BP_m3	GO:000312	heart field	1/539	12/23843	0.240011	0.595373	0.561776	Axin2
GO_BP_m3	GO:000318	mitral valve	1/539	12/23843	0.240011	0.595373	0.561776	Twist1
GO_BP_m3	GO:000335	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Mkks
GO_BP_m3	GO:000602	inositol me	1/539	12/23843	0.240011	0.595373	0.561776	Ippk
GO_BP_m3	GO:000607	glycerol-3-	1/539	12/23843	0.240011	0.595373	0.561776	Slc37a2
GO_BP_m3	GO:000685	oligopeptic	1/539	12/23843	0.240011	0.595373	0.561776	Slc15a3
GO_BP_m3	GO:000744	foregut mc	1/539	12/23843	0.240011	0.595373	0.561776	Foxf1
GO_BP_m3	GO:000821	mineralocc	1/539	12/23843	0.240011	0.595373	0.561776	Bmp2
GO_BP_m3	GO:001081	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Ccl5
GO_BP_m3	GO:001082	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Ccnf
GO_BP_m3	GO:001482	tonic smoc	1/539	12/23843	0.240011	0.595373	0.561776	Mkks
GO_BP_m3	GO:001484	urinary trac	1/539	12/23843	0.240011	0.595373	0.561776	Tacr1
GO_BP_m3	GO:001692	protein des	1/539	12/23843	0.240011	0.595373	0.561776	Gm5415
GO_BP_m3	GO:002152	ventral spir	1/539	12/23843	0.240011	0.595373	0.561776	Nkx6-1
GO_BP_m3	GO:003083	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Carmil2
GO_BP_m3	GO:003112	rRNA 3'-er	1/539	12/23843	0.240011	0.595373	0.561776	Exosc6
GO_BP_m3	GO:003114	anaphase-	1/539	12/23843	0.240011	0.595373	0.561776	Ube2c
GO_BP_m3	GO:003227	luteinizing	1/539	12/23843	0.240011	0.595373	0.561776	Ucn2
GO_BP_m3	GO:003230	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Oxt
GO_BP_m3	GO:003235	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Bmp2
GO_BP_m3	GO:003272	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Il17d
GO_BP_m3	GO:003275	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Prkcz
GO_BP_m3	GO:003308	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Ihh
GO_BP_m3	GO:003328	response tc	1/539	12/23843	0.240011	0.595373	0.561776	Pdia3
GO_BP_m3	GO:003352	histone H2	1/539	12/23843	0.240011	0.595373	0.561776	Ctr9
GO_BP_m3	GO:003362	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Foxc2
GO_BP_m3	GO:003509	maintenan	1/539	12/23843	0.240011	0.595373	0.561776	Pdzd11
GO_BP_m3	GO:003535	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Twist1
GO_BP_m3	GO:003575	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Lrrk2

GO_BP_m3	GO:003581	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Tfap2b
GO_BP_m3	GO:003631	cellular res	1/539	12/23843	0.240011	0.595373	0.561776	Ptch1
GO_BP_m3	GO:004331	neutrophil	1/539	12/23843	0.240011	0.595373	0.561776	Abr
GO_BP_m3	GO:004337	CD8-positi	1/539	12/23843	0.240011	0.595373	0.561776	Satb1
GO_BP_m3	GO:004582	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Ier3
GO_BP_m3	GO:004595	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Syt4
GO_BP_m3	GO:004692	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Syt4
GO_BP_m3	GO:006012	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Ghrhr
GO_BP_m3	GO:006057	cell fate sp	1/539	12/23843	0.240011	0.595373	0.561776	Nkx6-1
GO_BP_m3	GO:006146	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Ptprn
GO_BP_m3	GO:007026	peptidyl-se	1/539	12/23843	0.240011	0.595373	0.561776	Dusp26
GO_BP_m3	GO:007097	interleukin-	1/539	12/23843	0.240011	0.595373	0.561776	Carmil2
GO_BP_m3	GO:007129	cellular res	1/539	12/23843	0.240011	0.595373	0.561776	Pdia3
GO_BP_m3	GO:007204	collecting	1/539	12/23843	0.240011	0.595373	0.561776	Tfap2b
GO_BP_m3	GO:009704	motor neu	1/539	12/23843	0.240011	0.595373	0.561776	Crlf1
GO_BP_m3	GO:190022	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Atat1
GO_BP_m3	GO:190271	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Carmil2
GO_BP_m3	GO:190290	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Lrrk2
GO_BP_m3	GO:190302	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Hes1
GO_BP_m3	GO:190481	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Gnl3l
GO_BP_m3	GO:190486	excitatory	1/539	12/23843	0.240011	0.595373	0.561776	Nlgn1
GO_BP_m3	GO:190551	positive reg	1/539	12/23843	0.240011	0.595373	0.561776	Fam170b
GO_BP_m3	GO:200000	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Gpm6b
GO_BP_m3	GO:200034	regulation	1/539	12/23843	0.240011	0.595373	0.561776	Ccl5
GO_BP_m3	GO:200105	negative re	1/539	12/23843	0.240011	0.595373	0.561776	Gdf5
GO_BP_m3	GO:006027	cilium asse	9/539	300/23843	0.240176	0.595373	0.561776	1110004E0
GO_BP_m3	GO:000648	protein N-	3/539	75/23843	0.240506	0.595373	0.561776	D730048I0
GO_BP_m3	GO:003314	regulation	3/539	75/23843	0.240506	0.595373	0.561776	Ghrhr/Kdm
GO_BP_m3	GO:004568	regulation	3/539	75/23843	0.240506	0.595373	0.561776	Hes1/Prkc
GO_BP_m3	GO:005067	regulation	10/539	340/23843	0.242328	0.599539	0.565707	Bmp2/Ccl5
GO_BP_m3	GO:004254	response t	4/539	111/23843	0.242933	0.600344	0.566466	Ankzf1/Cry
GO_BP_m3	GO:190121	positive reg	4/539	111/23843	0.242933	0.600344	0.566466	Grik2/Ptpn
GO_BP_m3	GO:005114	regulation	5/539	148/23843	0.243997	0.602626	0.568619	Bmp2/Ctd
GO_BP_m3	GO:004873	gland deve	13/539	460/23843	0.244167	0.602699	0.568688	Aire/Areg/
GO_BP_m3	GO:004001	positive reg	2/539	42/23843	0.245403	0.603648	0.569584	Ghrhr/Mkk
GO_BP_m3	GO:004207	intraciliary	2/539	42/23843	0.245403	0.603648	0.569584	Cep131/Tt
GO_BP_m3	GO:004230	positive reg	2/539	42/23843	0.245403	0.603648	0.569584	Lrrk2/Ptpn
GO_BP_m3	GO:004250	serine pho	2/539	42/23843	0.245403	0.603648	0.569584	Gm13287/
GO_BP_m3	GO:000718	adenylate	6/539	186/23843	0.245602	0.603648	0.569584	Adm2/Ghr
GO_BP_m3	GO:000956	fertilization	6/539	186/23843	0.245602	0.603648	0.569584	Adam24/B
GO_BP_m3	GO:007099	neuron dea	11/539	381/23843	0.246138	0.603648	0.569584	Bag5/Bcl2l
GO_BP_m3	GO:000175	somitogen	3/539	76/23843	0.246553	0.603648	0.569584	Axin2/Foxc
GO_BP_m3	GO:000683	dicarboxyli	3/539	76/23843	0.246553	0.603648	0.569584	Avp/Slc19a
GO_BP_m3	GO:004352	positive reg	3/539	76/23843	0.246553	0.603648	0.569584	Grik2/Ptprf
GO_BP_m3	GO:005193	catecholam	3/539	76/23843	0.246553	0.603648	0.569584	Chrna4/Ox
GO_BP_m3	GO:006118	mammary	3/539	76/23843	0.246553	0.603648	0.569584	Areg/Foxf1
GO_BP_m3	GO:190332	negative re	3/539	76/23843	0.246553	0.603648	0.569584	Bag5/Gnl3l
GO_BP_m3	GO:000228	T cell activa	4/539	112/23843	0.247843	0.603648	0.569584	Cd46/Gm1

GO_BP_m3	GO:004247	odontoger	4/539	112/23843	0.247843	0.603648	0.569584	Axin2/Bmp
GO_BP_m3	GO:00066	steroid bio	5/539	149/23843	0.248215	0.603648	0.569584	Bmp2/Dhc
GO_BP_m3	GO:00103	regulation	3/539	77/23843	0.252623	0.603648	0.569584	Fanci/Ier3/
GO_BP_m3	GO:009027	positive re	4/539	113/23843	0.252775	0.603648	0.569584	Ghrhr/Gip/
GO_BP_m3	GO:005067	positive re	6/539	188/23843	0.253117	0.603648	0.569584	Bmp2/Ccl5
GO_BP_m3	GO:190121	regulation	10/539	344/23843	0.253267	0.603648	0.569584	Bcl2l1/Ccl5
GO_BP_m3	GO:00015	branching	2/539	43/23843	0.253815	0.603648	0.569584	Foxc2/Ihh
GO_BP_m3	GO:003111	negative re	2/539	43/23843	0.253815	0.603648	0.569584	Ckap2/Sgk
GO_BP_m3	GO:00488	brain morp	2/539	43/23843	0.253815	0.603648	0.569584	Mkks/Otx1
GO_BP_m3	GO:006164	histone H3	2/539	43/23843	0.253815	0.603648	0.569584	Kdm4b/Kd
GO_BP_m3	GO:00713	cellular res	2/539	43/23843	0.253815	0.603648	0.569584	Myod1/Sgk
GO_BP_m3	GO:004477	cell cycle p	11/539	384/23843	0.253917	0.603648	0.569584	Atf5/Ctdp1
GO_BP_m3	GO:00147	striated mu	12/539	424/23843	0.253966	0.603648	0.569584	Bmp2/Cdo
GO_BP_m3	GO:00097	hormone-r	6/539	189/23843	0.256897	0.603648	0.569584	Ghrhr/Kdm
GO_BP_m3	GO:19030	positive re	6/539	189/23843	0.256897	0.603648	0.569584	Ccl5/Cd46/
GO_BP_m3	GO:00015	luteinizatio	1/539	13/23843	0.257201	0.603648	0.569584	Ptprn
GO_BP_m3	GO:00020	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Nlgn1
GO_BP_m3	GO:000251	T cell toler	1/539	13/23843	0.257201	0.603648	0.569584	Aire
GO_BP_m3	GO:00025	mast cell c	1/539	13/23843	0.257201	0.603648	0.569584	Ccl5
GO_BP_m3	GO:000317	mitral valv	1/539	13/23843	0.257201	0.603648	0.569584	Twist1
GO_BP_m3	GO:00062	mitochond	1/539	13/23843	0.257201	0.603648	0.569584	Mgme1
GO_BP_m3	GO:00068	nucleotide	1/539	13/23843	0.257201	0.603648	0.569584	Slc25a17
GO_BP_m3	GO:00071	mitotic cen	1/539	13/23843	0.257201	0.603648	0.569584	Ranbp3l
GO_BP_m3	GO:000761	short-term	1/539	13/23843	0.257201	0.603648	0.569584	Cux2
GO_BP_m3	GO:00094	NAD biosy	1/539	13/23843	0.257201	0.603648	0.569584	Hk1
GO_BP_m3	GO:00103	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Hk1
GO_BP_m3	GO:00190	modulatior	1/539	13/23843	0.257201	0.603648	0.569584	Bcl2l1
GO_BP_m3	GO:00215	spinal cord	1/539	13/23843	0.257201	0.603648	0.569584	Nkx6-1
GO_BP_m3	GO:00219	cell prolifer	1/539	13/23843	0.257201	0.603648	0.569584	Atf5
GO_BP_m3	GO:00219	cerebellar	1/539	13/23843	0.257201	0.603648	0.569584	Atf5
GO_BP_m3	GO:00304	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Cd46
GO_BP_m3	GO:00304	fatty acid e	1/539	13/23843	0.257201	0.603648	0.569584	Elovl2
GO_BP_m3	GO:00310	myosin fila	1/539	13/23843	0.257201	0.603648	0.569584	Mybph
GO_BP_m3	GO:003111	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Sgk1
GO_BP_m3	GO:00312	pseudopoc	1/539	13/23843	0.257201	0.603648	0.569584	Ccl5
GO_BP_m3	GO:00316	positive re	1/539	13/23843	0.257201	0.603648	0.569584	Ccl5
GO_BP_m3	GO:003227	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Ucn2
GO_BP_m3	GO:00323	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Oxt
GO_BP_m3	GO:00323	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Bmp2
GO_BP_m3	GO:003307	immature	1/539	13/23843	0.257201	0.603648	0.569584	Ihh
GO_BP_m3	GO:00340	stress gran	1/539	13/23843	0.257201	0.603648	0.569584	Atxn2
GO_BP_m3	GO:003574	T-helper 2	1/539	13/23843	0.257201	0.603648	0.569584	Prkcz
GO_BP_m3	GO:00380	Fc receptor	1/539	13/23843	0.257201	0.603648	0.569584	Pigr
GO_BP_m3	GO:00424	positive re	1/539	13/23843	0.257201	0.603648	0.569584	Bmp2
GO_BP_m3	GO:00425	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Nf2
GO_BP_m3	GO:00427	very long-	1/539	13/23843	0.257201	0.603648	0.569584	Elovl2
GO_BP_m3	GO:004454	NLRP3 infl	1/539	13/23843	0.257201	0.603648	0.569584	Atat1
GO_BP_m3	GO:00451	developme	1/539	13/23843	0.257201	0.603648	0.569584	Areg

GO_BP_m3	GO:004562	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Prkcz
GO_BP_m3	GO:004593	positive reg	1/539	13/23843	0.257201	0.603648	0.569584	Ghrhr
GO_BP_m3	GO:004645	short-chair	1/539	13/23843	0.257201	0.603648	0.569584	Thnsl2
GO_BP_m3	GO:004660	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Ccnf
GO_BP_m3	GO:004834	paraxial me	1/539	13/23843	0.257201	0.603648	0.569584	Foxc2
GO_BP_m3	GO:004848	enteric ner	1/539	13/23843	0.257201	0.603648	0.569584	Sox10
GO_BP_m3	GO:004850	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Hes1
GO_BP_m3	GO:004874	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Myod1
GO_BP_m3	GO:004875	branching	1/539	13/23843	0.257201	0.603648	0.569584	Lrrk2
GO_BP_m3	GO:005119	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Ier3
GO_BP_m3	GO:005264	alditol pho	1/539	13/23843	0.257201	0.603648	0.569584	Slc37a2
GO_BP_m3	GO:005269	cellular glu	1/539	13/23843	0.257201	0.603648	0.569584	Ugt1a7c
GO_BP_m3	GO:006076	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Tcf21
GO_BP_m3	GO:007005	neuron cell	1/539	13/23843	0.257201	0.603648	0.569584	Calb2
GO_BP_m3	GO:007094	neutrophil	1/539	13/23843	0.257201	0.603648	0.569584	Dnase1l3
GO_BP_m3	GO:007102	nuclear RN	1/539	13/23843	0.257201	0.603648	0.569584	Exosc6
GO_BP_m3	GO:007102	nuclear mR	1/539	13/23843	0.257201	0.603648	0.569584	Exosc6
GO_BP_m3	GO:007256	chemokine	1/539	13/23843	0.257201	0.603648	0.569584	Ccl5
GO_BP_m3	GO:009709	presynapti	1/539	13/23843	0.257201	0.603648	0.569584	Nlgn1
GO_BP_m3	GO:009905	presynapse	1/539	13/23843	0.257201	0.603648	0.569584	Nlgn1
GO_BP_m3	GO:190012	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Ptprf
GO_BP_m3	GO:190183	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Ippk
GO_BP_m3	GO:190233	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Foxc2
GO_BP_m3	GO:190289	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Tgfbr1
GO_BP_m3	GO:200065	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Stoml1
GO_BP_m3	GO:200103	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Kdm4d
GO_BP_m3	GO:200122	negative re	1/539	13/23843	0.257201	0.603648	0.569584	Gpr173
GO_BP_m3	GO:200125	regulation	1/539	13/23843	0.257201	0.603648	0.569584	Stc2
GO_BP_m3	GO:000307	regulation	4/539	114/23843	0.257728	0.604097	0.570008	Avp/Ier3/N
GO_BP_m3	GO:009917	postsynaps	4/539	114/23843	0.257728	0.604097	0.570008	Caprin1/Cu
GO_BP_m3	GO:004306	extracellula	8/539	267/23843	0.258651	0.604097	0.570008	Adamts14/
GO_BP_m3	GO:000663	acyl-CoA n	3/539	78/23843	0.258715	0.604097	0.570008	Dlat/Dld/Tl
GO_BP_m3	GO:000859	regulation	3/539	78/23843	0.258715	0.604097	0.570008	Bend6/Cd4
GO_BP_m3	GO:003538	thioester m	3/539	78/23843	0.258715	0.604097	0.570008	Dlat/Dld/Tl
GO_BP_m3	GO:004870	astrocyte d	3/539	78/23843	0.258715	0.604097	0.570008	Atf5/Bmp2
GO_BP_m3	GO:006041	cardiac sep	3/539	78/23843	0.258715	0.604097	0.570008	Hes1/Mir1
GO_BP_m3	GO:007022	regulation	3/539	78/23843	0.258715	0.604097	0.570008	Ccl5/Mir10
GO_BP_m3	GO:004586	negative re	10/539	346/23843	0.258798	0.604097	0.570008	9230104L0
GO_BP_m3	GO:190370	regulation	11/539	386/23843	0.259151	0.604592	0.570474	Ankle1/Ccl
GO_BP_m3	GO:007122	cellular res	8/539	268/23843	0.26183	0.607243	0.572976	Bcl2l1/Halr
GO_BP_m3	GO:000669	cholesterol	2/539	44/23843	0.262233	0.607243	0.572976	Dhcr24/Tm
GO_BP_m3	GO:001908	viral transc	2/539	44/23843	0.262233	0.607243	0.572976	Ccl5/Ctdp1
GO_BP_m3	GO:004275	eating beh	2/539	44/23843	0.262233	0.607243	0.572976	Oxt/Tacr1
GO_BP_m3	GO:004303	regulation	2/539	44/23843	0.262233	0.607243	0.572976	Lrrk2/Tff2
GO_BP_m3	GO:006161	pri-miRNA	2/539	44/23843	0.262233	0.607243	0.572976	Bmp2/Tgfb
GO_BP_m3	GO:007023	regulation	2/539	44/23843	0.262233	0.607243	0.572976	Ccl5/Tsc22
GO_BP_m3	GO:000110	response t	10/539	348/23843	0.26437	0.607243	0.572976	Bcl2l1/Halr
GO_BP_m3	GO:005125	positive reg	11/539	388/23843	0.264421	0.607243	0.572976	Ccl5/Cd46/

GO_BP_m3	GO:00032	cardiac ver	3/539	79/23843	0.264826	0.607243	0.572976	Foxc2/Foxf
GO_BP_m3	GO:003304	regulation	3/539	79/23843	0.264826	0.607243	0.572976	Axin2/Mad
GO_BP_m3	GO:19039	negative re	3/539	79/23843	0.264826	0.607243	0.572976	Ccl5/Isg20/
GO_BP_m3	GO:000647	protein de	7/539	230/23843	0.265507	0.607243	0.572976	Ctdp1/Dus
GO_BP_m3	GO:00706	regulation	7/539	230/23843	0.265507	0.607243	0.572976	Btn1a1/Ccl
GO_BP_m3	GO:00516	protein ma	9/539	309/23843	0.266581	0.607243	0.572976	Cd46/Dhcr
GO_BP_m3	GO:00149	myotube d	4/539	116/23843	0.267688	0.607243	0.572976	Cdon/Myo
GO_BP_m3	GO:00150	regulation	9/539	310/23843	0.26957	0.607243	0.572976	Bcl2l1/Gcsh
GO_BP_m3	GO:00199	regulation	2/539	45/23843	0.270653	0.607243	0.572976	Ndst2/Tacr
GO_BP_m3	GO:00104	regulation	2/539	45/23843	0.270653	0.607243	0.572976	Foxf1/Ihh
GO_BP_m3	GO:001922	neuronal a	2/539	45/23843	0.270653	0.607243	0.572976	Grik2/Kcnn
GO_BP_m3	GO:00308	negative re	2/539	45/23843	0.270653	0.607243	0.572976	Hes1/Tgfbr
GO_BP_m3	GO:00459	positive re	2/539	45/23843	0.270653	0.607243	0.572976	Avp/Tacr1
GO_BP_m3	GO:00507	activated T	2/539	45/23843	0.270653	0.607243	0.572976	Btn1a1/Sat
GO_BP_m3	GO:00519	regulation	2/539	45/23843	0.270653	0.607243	0.572976	Avp/Syt4
GO_BP_m3	GO:00607	positive re	2/539	45/23843	0.270653	0.607243	0.572976	C1qtnf4/Tr
GO_BP_m3	GO:007124	cellular res	2/539	45/23843	0.270653	0.607243	0.572976	Chrna4/Lrr
GO_BP_m3	GO:00713	cellular res	2/539	45/23843	0.270653	0.607243	0.572976	Myod1/Sgk
GO_BP_m3	GO:00901	regulation	2/539	45/23843	0.270653	0.607243	0.572976	Avp/Bcl2l1
GO_BP_m3	GO:000227	myeloid ce	3/539	80/23843	0.270954	0.607243	0.572976	Abr/Dnase
GO_BP_m3	GO:00031	outflow tra	3/539	80/23843	0.270954	0.607243	0.572976	Foxc2/Hes
GO_BP_m3	GO:001491	regulation	3/539	80/23843	0.270954	0.607243	0.572976	Ccl5/P2ry6
GO_BP_m3	GO:002167	nerve deve	3/539	80/23843	0.270954	0.607243	0.572976	Hes1/Neur
GO_BP_m3	GO:00350	embryonic	3/539	80/23843	0.270954	0.607243	0.572976	Foxc2/Hes
GO_BP_m3	GO:00703	cellular res	3/539	80/23843	0.270954	0.607243	0.572976	Ankzf1/Lrrk
GO_BP_m3	GO:00986	inorganic a	3/539	80/23843	0.270954	0.607243	0.572976	Clcn1/Slc1
GO_BP_m3	GO:00550	muscle cell	6/539	193/23843	0.272168	0.607243	0.572976	Ctdp1/Flnc
GO_BP_m3	GO:199082	response t	9/539	311/23843	0.272568	0.607243	0.572976	Adam23/M
GO_BP_m3	GO:19908	cellular res	9/539	311/23843	0.272568	0.607243	0.572976	Adam23/M
GO_BP_m3	GO:00510	positive re	4/539	117/23843	0.272695	0.607243	0.572976	Map3k13/
GO_BP_m3	GO:00609	dendritic s	4/539	117/23843	0.272695	0.607243	0.572976	Caprin1/Cu
GO_BP_m3	GO:190037	regulation	4/539	117/23843	0.272695	0.607243	0.572976	Avp/Bcl2l1/
GO_BP_m3	GO:004887	multicellula	10/539	351/23843	0.272799	0.607243	0.572976	Avp/Ccl5/C
GO_BP_m3	GO:00199	cyclic-nucl	5/539	155/23843	0.273893	0.607243	0.572976	Adm2/Ghrl
GO_BP_m3	GO:00016	fever gene	1/539	14/23843	0.274002	0.607243	0.572976	Ccl5
GO_BP_m3	GO:000272	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Prkcz
GO_BP_m3	GO:00031	morphoge	1/539	14/23843	0.274002	0.607243	0.572976	Rhob
GO_BP_m3	GO:00060	uronic acid	1/539	14/23843	0.274002	0.607243	0.572976	Ugt1a7c
GO_BP_m3	GO:000654	glycine me	1/539	14/23843	0.274002	0.607243	0.572976	Gcsh
GO_BP_m3	GO:00092	deoxyribor	1/539	14/23843	0.274002	0.607243	0.572976	Rrm2
GO_BP_m3	GO:001071	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Carmil2
GO_BP_m3	GO:001087	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Ptch1
GO_BP_m3	GO:001607	snoRNA m	1/539	14/23843	0.274002	0.607243	0.572976	Exosc6
GO_BP_m3	GO:00195	glucuronat	1/539	14/23843	0.274002	0.607243	0.572976	Ugt1a7c
GO_BP_m3	GO:00215	cell prolifer	1/539	14/23843	0.274002	0.607243	0.572976	Atf5
GO_BP_m3	GO:00217	cerebellar	1/539	14/23843	0.274002	0.607243	0.572976	Atxn2
GO_BP_m3	GO:00219	rostrocaud	1/539	14/23843	0.274002	0.607243	0.572976	Hes1
GO_BP_m3	GO:003081	negative re	1/539	14/23843	0.274002	0.607243	0.572976	Ier3

GO_BP_m3	GO:003260	granulocyt	1/539	14/23843	0.274002	0.607243	0.572976	Il17d
GO_BP_m3	GO:003264	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Il17d
GO_BP_m3	GO:003273	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Prkcz
GO_BP_m3	GO:003312	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Twist1
GO_BP_m3	GO:003434	glial cell ap	1/539	14/23843	0.274002	0.607243	0.572976	Prkch
GO_BP_m3	GO:003475	iron ion tra	1/539	14/23843	0.274002	0.607243	0.572976	Hamp2
GO_BP_m3	GO:003598	chondrocy	1/539	14/23843	0.274002	0.607243	0.572976	Ihh
GO_BP_m3	GO:004506	negative th	1/539	14/23843	0.274002	0.607243	0.572976	Aire
GO_BP_m3	GO:004518	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Ghrhr
GO_BP_m3	GO:004560	negative re	1/539	14/23843	0.274002	0.607243	0.572976	Hes1
GO_BP_m3	GO:004561	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Prkch
GO_BP_m3	GO:004579	negative re	1/539	14/23843	0.274002	0.607243	0.572976	Ucn
GO_BP_m3	GO:004853	mucosal-a	1/539	14/23843	0.274002	0.607243	0.572976	Nkx2-3
GO_BP_m3	GO:004854	Peyer's pat	1/539	14/23843	0.274002	0.607243	0.572976	Nkx2-3
GO_BP_m3	GO:005085	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Prkch
GO_BP_m3	GO:005086	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Usp12
GO_BP_m3	GO:005129	centrosom	1/539	14/23843	0.274002	0.607243	0.572976	Ranbp3l
GO_BP_m3	GO:006001	radial glial	1/539	14/23843	0.274002	0.607243	0.572976	Hes1
GO_BP_m3	GO:006039	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Tgfbr1
GO_BP_m3	GO:006083	smoothene	1/539	14/23843	0.274002	0.607243	0.572976	Ptch1
GO_BP_m3	GO:006115	endothelial	1/539	14/23843	0.274002	0.607243	0.572976	Rhob
GO_BP_m3	GO:006131	renal filtrat	1/539	14/23843	0.274002	0.607243	0.572976	Foxc2
GO_BP_m3	GO:007030	lens fiber c	1/539	14/23843	0.274002	0.607243	0.572976	Cryaa
GO_BP_m3	GO:007138	cellular res	1/539	14/23843	0.274002	0.607243	0.572976	P2ry6
GO_BP_m3	GO:007211	glomerular	1/539	14/23843	0.274002	0.607243	0.572976	Foxc2
GO_BP_m3	GO:007222	metanephr	1/539	14/23843	0.274002	0.607243	0.572976	Tcf21
GO_BP_m3	GO:007231	glomerular	1/539	14/23843	0.274002	0.607243	0.572976	Foxc2
GO_BP_m3	GO:007257	neurotrans	1/539	14/23843	0.274002	0.607243	0.572976	Nlgn1
GO_BP_m3	GO:009026	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Mad2l1
GO_BP_m3	GO:009715	GABAergic	1/539	14/23843	0.274002	0.607243	0.572976	Helt
GO_BP_m3	GO:009753	mast cell m	1/539	14/23843	0.274002	0.607243	0.572976	Ccl5
GO_BP_m3	GO:009906	postsynaps	1/539	14/23843	0.274002	0.607243	0.572976	Nlgn1
GO_BP_m3	GO:014013	positive re	1/539	14/23843	0.274002	0.607243	0.572976	Ccl5
GO_BP_m3	GO:190230	negative re	1/539	14/23843	0.274002	0.607243	0.572976	Stoml1
GO_BP_m3	GO:190343	negative re	1/539	14/23843	0.274002	0.607243	0.572976	Dleu2
GO_BP_m3	GO:190350	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Mad2l1
GO_BP_m3	GO:190474	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Foxc2
GO_BP_m3	GO:190481	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Gnl3l
GO_BP_m3	GO:200025	negative re	1/539	14/23843	0.274002	0.607243	0.572976	Ucn
GO_BP_m3	GO:200025	regulation	1/539	14/23843	0.274002	0.607243	0.572976	Cd46
GO_BP_m3	GO:000300	response t	6/539	194/23843	0.276021	0.609662	0.575258	Ankzf1/Cry
GO_BP_m3	GO:000301	vascular pr	6/539	194/23843	0.276021	0.609662	0.575258	Abr/Avp/F
GO_BP_m3	GO:003134	negative re	6/539	194/23843	0.276021	0.609662	0.575258	Bag5/Dleu
GO_BP_m3	GO:000687	cellular cal	12/539	433/23843	0.276613	0.609662	0.575258	Avp/Calb2/
GO_BP_m3	GO:000328	ventricular	3/539	81/23843	0.277098	0.609662	0.575258	Hes1/Mir1
GO_BP_m3	GO:000647	protein de	3/539	81/23843	0.277098	0.609662	0.575258	Jdp2/Lrrk2/
GO_BP_m3	GO:001590	fatty acid t	3/539	81/23843	0.277098	0.609662	0.575258	Oxt/Slc25a
GO_BP_m3	GO:009758	lamellipodi	3/539	81/23843	0.277098	0.609662	0.575258	Ablim3/Ca

GO_BP_m3	GO:190406	negative re	3/539	81/23843	0.277098	0.609662	0.575258	Hamp2/Stc
GO_BP_m3	GO:000627	regulation	4/539	118/23843	0.277717	0.609662	0.575258	Areg/Enpp
GO_BP_m3	GO:000858	male gona	4/539	118/23843	0.277717	0.609662	0.575258	Bcl2l1/Tcf2
GO_BP_m3	GO:003080	regulation	4/539	118/23843	0.277717	0.609662	0.575258	Avp/Bcl2l1/
GO_BP_m3	GO:003315	regulation	8/539	273/23843	0.277895	0.609662	0.575258	Ablim3/Ce
GO_BP_m3	GO:005134	negative re	8/539	273/23843	0.277895	0.609662	0.575258	Bag5/Dusp
GO_BP_m3	GO:004580	positive reg	5/539	156/23843	0.278228	0.609662	0.575258	Abr/Bcl2l1/
GO_BP_m3	GO:004688	positive reg	5/539	156/23843	0.278228	0.609662	0.575258	Ghrhr/Gip/
GO_BP_m3	GO:000232	natural kille	2/539	46/23843	0.27907	0.609662	0.575258	Gm13287/
GO_BP_m3	GO:000317	heart valve	2/539	46/23843	0.27907	0.609662	0.575258	Bmp2/Twis
GO_BP_m3	GO:001071	regulation	2/539	46/23843	0.27907	0.609662	0.575258	Ihh/Ucn
GO_BP_m3	GO:002177	olfactory b	2/539	46/23843	0.27907	0.609662	0.575258	Atf5/Lrrk2
GO_BP_m3	GO:004853	spleen dev	2/539	46/23843	0.27907	0.609662	0.575258	Nkx2-3/Tc
GO_BP_m3	GO:005148	regulation	2/539	46/23843	0.27907	0.609662	0.575258	Nlgn1/Tgfb
GO_BP_m3	GO:190265	secondary	2/539	46/23843	0.27907	0.609662	0.575258	Dhcr24/Tm
GO_BP_m3	GO:200116	regulation	2/539	46/23843	0.27907	0.609662	0.575258	Bcl2l1/Ier3
GO_BP_m3	GO:200122	regulation	2/539	46/23843	0.27907	0.609662	0.575258	Gpr173/Nk
GO_BP_m3	GO:000269	positive reg	12/539	435/23843	0.281732	0.609662	0.575258	Ccl5/Cd46/
GO_BP_m3	GO:004340	steroid hor	5/539	157/23843	0.282576	0.609662	0.575258	Ghrhr/Kdm
GO_BP_m3	GO:000820	cholesterol	4/539	119/23843	0.282754	0.609662	0.575258	Dhcr24/Fd
GO_BP_m3	GO:003243	regulation	4/539	119/23843	0.282754	0.609662	0.575258	Bag5/Lrrk2
GO_BP_m3	GO:004348	regulation	4/539	119/23843	0.282754	0.609662	0.575258	Celf5/Khdr
GO_BP_m3	GO:004654	developme	4/539	119/23843	0.282754	0.609662	0.575258	Bcl2l1/Tcf2
GO_BP_m3	GO:003070	cytoskeleto	5/539	158/23843	0.286937	0.609662	0.575258	Ap3s1/BC0
GO_BP_m3	GO:003582	modificatio	5/539	158/23843	0.286937	0.609662	0.575258	Bcl2l1/Ccl5
GO_BP_m3	GO:000269	regulation	10/539	356/23843	0.287025	0.609662	0.575258	Abr/Ccl5/C
GO_BP_m3	GO:000636	transcriptio	2/539	47/23843	0.287479	0.609662	0.575258	Ctr9/Sox10
GO_BP_m3	GO:001657	histone ubi	2/539	47/23843	0.287479	0.609662	0.575258	Ctr9/Uhrf1
GO_BP_m3	GO:002153	neural tube	2/539	47/23843	0.287479	0.609662	0.575258	Hes1/Ptch1
GO_BP_m3	GO:004224	tissue rege	2/539	47/23843	0.287479	0.609662	0.575258	Myod1/My
GO_BP_m3	GO:004521	sarcomere	2/539	47/23843	0.287479	0.609662	0.575258	Mybph/Tnı
GO_BP_m3	GO:009858	cellular res	2/539	47/23843	0.287479	0.609662	0.575258	Bcl2l1/Trim
GO_BP_m3	GO:009960	regulation	2/539	47/23843	0.287479	0.609662	0.575258	Chrna4/Nlg
GO_BP_m3	GO:190459	positive reg	2/539	47/23843	0.287479	0.609662	0.575258	Lrrk2/Ptpn5
GO_BP_m3	GO:001095	regulation	11/539	397/23843	0.288556	0.609662	0.575258	Ccl5/Hamp
GO_BP_m3	GO:003243	positive reg	3/539	83/23843	0.289424	0.609662	0.575258	Lrrk2/Rnf14
GO_BP_m3	GO:003276	positive reg	3/539	83/23843	0.289424	0.609662	0.575258	C1qtnf4/Lr
GO_BP_m3	GO:190007	regulation	3/539	83/23843	0.289424	0.609662	0.575258	Prkcz/Ptpre
GO_BP_m3	GO:000007	DNA replic	1/539	15/23843	0.290423	0.609662	0.575258	Oraov1
GO_BP_m3	GO:000029	nuclear-tra	1/539	15/23843	0.290423	0.609662	0.575258	Exosc6
GO_BP_m3	GO:000232	immature E	1/539	15/23843	0.290423	0.609662	0.575258	Mir19a
GO_BP_m3	GO:000283	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Prkcz
GO_BP_m3	GO:000318	heart valve	1/539	15/23843	0.290423	0.609662	0.575258	Twist1
GO_BP_m3	GO:000668	sphingomy	1/539	15/23843	0.290423	0.609662	0.575258	Enpp7
GO_BP_m3	GO:000670	glucocortic	1/539	15/23843	0.290423	0.609662	0.575258	Bmp2
GO_BP_m3	GO:000692	activation-	1/539	15/23843	0.290423	0.609662	0.575258	Tsc22d3
GO_BP_m3	GO:000728	sperm axor	1/539	15/23843	0.290423	0.609662	0.575258	Cep131
GO_BP_m3	GO:001017	embryonic	1/539	15/23843	0.290423	0.609662	0.575258	Cdon

GO_BP_m3	GO:001096	magnesiun	1/539	15/23843	0.290423	0.609662	0.575258	Tfap2b
GO_BP_m3	GO:001406	negative re	1/539	15/23843	0.290423	0.609662	0.575258	Twist1
GO_BP_m3	GO:003015	pancreatic	1/539	15/23843	0.290423	0.609662	0.575258	Ucn
GO_BP_m3	GO:003126	pseudopoc	1/539	15/23843	0.290423	0.609662	0.575258	Ccl5
GO_BP_m3	GO:003157	intra-S DN	1/539	15/23843	0.290423	0.609662	0.575258	Oraov1
GO_BP_m3	GO:003165	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Ccl5
GO_BP_m3	GO:003222	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Tacr1
GO_BP_m3	GO:003308	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Ihh
GO_BP_m3	GO:003564	locomotory	1/539	15/23843	0.290423	0.609662	0.575258	Lrrk2
GO_BP_m3	GO:004003	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Hes1
GO_BP_m3	GO:004274	circadian sl	1/539	15/23843	0.290423	0.609662	0.575258	Ghrhr
GO_BP_m3	GO:004279	nucleolar la	1/539	15/23843	0.290423	0.609662	0.575258	Ippk
GO_BP_m3	GO:004316	ubiquitin-c	1/539	15/23843	0.290423	0.609662	0.575258	Ubap1l
GO_BP_m3	GO:004338	negative T	1/539	15/23843	0.290423	0.609662	0.575258	Aire
GO_BP_m3	GO:004351	negative re	1/539	15/23843	0.290423	0.609662	0.575258	Twist1
GO_BP_m3	GO:004432	cellular res	1/539	15/23843	0.290423	0.609662	0.575258	Mkks
GO_BP_m3	GO:004514	meiotic telo	1/539	15/23843	0.290423	0.609662	0.575258	Ankle1
GO_BP_m3	GO:004576	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Tacr1
GO_BP_m3	GO:004598	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Ucn
GO_BP_m3	GO:004662	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Prkcz
GO_BP_m3	GO:004871	negative re	1/539	15/23843	0.290423	0.609662	0.575258	Hes1
GO_BP_m3	GO:005104	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Pacsin3
GO_BP_m3	GO:005113	chaperone	1/539	15/23843	0.290423	0.609662	0.575258	Mkks
GO_BP_m3	GO:005138	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Ptprf
GO_BP_m3	GO:005154	keratinocyt	1/539	15/23843	0.290423	0.609662	0.575258	Ltb4r2
GO_BP_m3	GO:005157	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Ctr9
GO_BP_m3	GO:005506	phosphate	1/539	15/23843	0.290423	0.609662	0.575258	Tfap2b
GO_BP_m3	GO:006005	angiogenes	1/539	15/23843	0.290423	0.609662	0.575258	Foxc2
GO_BP_m3	GO:006025	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Prkch
GO_BP_m3	GO:006100	negative re	1/539	15/23843	0.290423	0.609662	0.575258	Nlgn1
GO_BP_m3	GO:006102	eyelid deve	1/539	15/23843	0.290423	0.609662	0.575258	Twist1
GO_BP_m3	GO:007023	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Ccl5
GO_BP_m3	GO:007102	RNA survei	1/539	15/23843	0.290423	0.609662	0.575258	Exosc6
GO_BP_m3	GO:007163	positive reg	1/539	15/23843	0.290423	0.609662	0.575258	Cd46
GO_BP_m3	GO:007207	kidney mes	1/539	15/23843	0.290423	0.609662	0.575258	Tcf21
GO_BP_m3	GO:007210	glomerular	1/539	15/23843	0.290423	0.609662	0.575258	Foxc2
GO_BP_m3	GO:007218	ureter deve	1/539	15/23843	0.290423	0.609662	0.575258	Foxf1
GO_BP_m3	GO:007233	modified a	1/539	15/23843	0.290423	0.609662	0.575258	Slc19a1
GO_BP_m3	GO:007249	embryonic	1/539	15/23843	0.290423	0.609662	0.575258	Ihh
GO_BP_m3	GO:007250	divalent ino	1/539	15/23843	0.290423	0.609662	0.575258	Tfap2b
GO_BP_m3	GO:007250	trivalent ino	1/539	15/23843	0.290423	0.609662	0.575258	Tfap2b
GO_BP_m3	GO:007267	neutrophil	1/539	15/23843	0.290423	0.609662	0.575258	Prtn3
GO_BP_m3	GO:009008	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Bag5
GO_BP_m3	GO:009013	epithelial c	1/539	15/23843	0.290423	0.609662	0.575258	Ihh
GO_BP_m3	GO:009710	postsynapt	1/539	15/23843	0.290423	0.609662	0.575258	Nlgn1
GO_BP_m3	GO:009728	hepatocyte	1/539	15/23843	0.290423	0.609662	0.575258	Bcl2l1
GO_BP_m3	GO:009908	postsynapt	1/539	15/23843	0.290423	0.609662	0.575258	Nlgn1
GO_BP_m3	GO:190045	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Bcl2l1

GO_BP_m3	GO:190131	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Tacr1
GO_BP_m3	GO:200047	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Prkar1b
GO_BP_m3	GO:200081	negative re	1/539	15/23843	0.290423	0.609662	0.575258	Bcl2l1
GO_BP_m3	GO:20010	regulation	1/539	15/23843	0.290423	0.609662	0.575258	Gdf5
GO_BP_m3	GO:00066	protein tar	9/539	317/23843	0.290758	0.610067	0.57564	Ablim3/He
GO_BP_m3	GO:00512	protein het	5/539	159/23843	0.291311	0.610629	0.576171	Chrna4/Ch
GO_BP_m3	GO:19021	positive re	5/539	159/23843	0.291311	0.610629	0.576171	Ccl5/Cd46/
GO_BP_m3	GO:00487	appendage	6/539	199/23843	0.295463	0.614802	0.580109	Gdf5/Ihh/P
GO_BP_m3	GO:006017	limb devel	6/539	199/23843	0.295463	0.614802	0.580109	Gdf5/Ihh/P
GO_BP_m3	GO:003571	CD4-positi	3/539	84/23843	0.295603	0.614802	0.580109	Nkx2-3/Pr
GO_BP_m3	GO:004227	ribosomal	3/539	84/23843	0.295603	0.614802	0.580109	Rpl6l/Nip7/
GO_BP_m3	GO:00482	regulation	3/539	84/23843	0.295603	0.614802	0.580109	Atxn2/Lrrtr
GO_BP_m3	GO:00720	regulation	3/539	84/23843	0.295603	0.614802	0.580109	Lrrk2/Nf2/
GO_BP_m3	GO:190352	positive re	3/539	84/23843	0.295603	0.614802	0.580109	Avp/Tacr1/
GO_BP_m3	GO:19035	positive re	3/539	84/23843	0.295603	0.614802	0.580109	C1qtnf4/Lr
GO_BP_m3	GO:00066	protein im	5/539	160/23843	0.295696	0.614802	0.580109	Lrrk2/Nxt1/
GO_BP_m3	GO:00063	transcriptic	2/539	48/23843	0.295878	0.614802	0.580109	Dmtf1/Ipp
GO_BP_m3	GO:000701	microtubul	2/539	48/23843	0.295878	0.614802	0.580109	Ckap2/Sgk
GO_BP_m3	GO:00190	reproducti	2/539	48/23843	0.295878	0.614802	0.580109	Avp/Oxt
GO_BP_m3	GO:00219	olfactory l	2/539	48/23843	0.295878	0.614802	0.580109	Atf5/Lrrk2
GO_BP_m3	GO:00424	inner ear a	2/539	48/23843	0.295878	0.614802	0.580109	Hes1/Whrr
GO_BP_m3	GO:00433	regulation	2/539	48/23843	0.295878	0.614802	0.580109	Abr/Foxf1
GO_BP_m3	GO:00439	cellular cor	2/539	48/23843	0.295878	0.614802	0.580109	Prtn3/Whr
GO_BP_m3	GO:009951	vesicle cyto	2/539	48/23843	0.295878	0.614802	0.580109	Ap3s1/Prk
GO_BP_m3	GO:20004	regulation	2/539	48/23843	0.295878	0.614802	0.580109	Aire/Ccl5
GO_BP_m3	GO:00725	divalent in	13/539	482/23843	0.297353	0.617567	0.582718	Avp/Calb2/
GO_BP_m3	GO:190332	positive re	4/539	122/23843	0.297944	0.618496	0.583594	Ctr9/Fanci/
GO_BP_m3	GO:00027	regulation	6/539	200/23843	0.299385	0.619147	0.584208	Abr/Dnase
GO_BP_m3	GO:004211	B cell activ	11/539	401/23843	0.299483	0.619147	0.584208	Chrna4/Ex
GO_BP_m3	GO:00023	cytokine pr	3/539	85/23843	0.301789	0.619147	0.584208	Hk1/Prkcz/
GO_BP_m3	GO:004247	odontoger	3/539	85/23843	0.301789	0.619147	0.584208	Bmp2/Nf2/
GO_BP_m3	GO:004547	response t	3/539	85/23843	0.301789	0.619147	0.584208	Hpgd/Mir3
GO_BP_m3	GO:200102	positive re	3/539	85/23843	0.301789	0.619147	0.584208	Ankle1/Eid
GO_BP_m3	GO:00713	cellular res	6/539	201/23843	0.303317	0.619147	0.584208	Ghrhr/Kdm
GO_BP_m3	GO:00022	somatic re	2/539	49/23843	0.304262	0.619147	0.584208	Exosc6/Mir
GO_BP_m3	GO:00022	somatic di	2/539	49/23843	0.304262	0.619147	0.584208	Exosc6/Mir
GO_BP_m3	GO:000602	aminoglyc	2/539	49/23843	0.304262	0.619147	0.584208	B3gnt6/Nd
GO_BP_m3	GO:001587	dopamine	2/539	49/23843	0.304262	0.619147	0.584208	Chrna4/Syt
GO_BP_m3	GO:003152	ruffle orga	2/539	49/23843	0.304262	0.619147	0.584208	Nlgn1/Car
GO_BP_m3	GO:00323	response t	2/539	49/23843	0.304262	0.619147	0.584208	Areg/Myo
GO_BP_m3	GO:00329	collagen bi	2/539	49/23843	0.304262	0.619147	0.584208	Ihh/Ucn
GO_BP_m3	GO:00330	regulation	2/539	49/23843	0.304262	0.619147	0.584208	Foxf1/Ptpr
GO_BP_m3	GO:00451	isotype swi	2/539	49/23843	0.304262	0.619147	0.584208	Exosc6/Mir
GO_BP_m3	GO:19032	negative re	2/539	49/23843	0.304262	0.619147	0.584208	Bag5/Lrrk2
GO_BP_m3	GO:003087	mammary	5/539	162/23843	0.304499	0.619147	0.584208	Areg/Foxf1
GO_BP_m3	GO:000171	endoderm	1/539	16/23843	0.306474	0.619147	0.584208	Ctr9
GO_BP_m3	GO:000322	ventricular	1/539	16/23843	0.306474	0.619147	0.584208	Tgfbr1
GO_BP_m3	GO:00063	apoptotic	1/539	16/23843	0.306474	0.619147	0.584208	Dnase1l3

GO_BP_m3	GO:000647	N-terminal	1/539	16/23843	0.306474	0.619147	0.584208	Naa25
GO_BP_m3	GO:00066	NLS-bearir	1/539	16/23843	0.306474	0.619147	0.584208	Tnpo2
GO_BP_m3	GO:000682	manganes	1/539	16/23843	0.306474	0.619147	0.584208	Trpc1
GO_BP_m3	GO:000721	G-protein	1/539	16/23843	0.306474	0.619147	0.584208	Grm4
GO_BP_m3	GO:001052	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Piwil4
GO_BP_m3	GO:001052	negative re	1/539	16/23843	0.306474	0.619147	0.584208	Piwil4
GO_BP_m3	GO:001056	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Bmp2
GO_BP_m3	GO:001566	gas transp	1/539	16/23843	0.306474	0.619147	0.584208	Aqp5
GO_BP_m3	GO:002175	striatum de	1/539	16/23843	0.306474	0.619147	0.584208	Mkks
GO_BP_m3	GO:002197	telencepha	1/539	16/23843	0.306474	0.619147	0.584208	Bmp2
GO_BP_m3	GO:003095	establishm	1/539	16/23843	0.306474	0.619147	0.584208	Rhob
GO_BP_m3	GO:00323	positive re	1/539	16/23843	0.306474	0.619147	0.584208	Oxt
GO_BP_m3	GO:003231	prostaglan	1/539	16/23843	0.306474	0.619147	0.584208	Oxt
GO_BP_m3	GO:003257	response t	1/539	16/23843	0.306474	0.619147	0.584208	Oxt
GO_BP_m3	GO:004392	positive re	1/539	16/23843	0.306474	0.619147	0.584208	Ctdp1
GO_BP_m3	GO:004406	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Nlgn1
GO_BP_m3	GO:004406	modulatior	1/539	16/23843	0.306474	0.619147	0.584208	Bcl2l1
GO_BP_m3	GO:004807	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Ihh
GO_BP_m3	GO:006057	ventral spir	1/539	16/23843	0.306474	0.619147	0.584208	Nkx6-1
GO_BP_m3	GO:006058	cell fate co	1/539	16/23843	0.306474	0.619147	0.584208	Nkx6-1
GO_BP_m3	GO:007137	cellular res	1/539	16/23843	0.306474	0.619147	0.584208	P2ry6
GO_BP_m3	GO:007149	cellular res	1/539	16/23843	0.306474	0.619147	0.584208	Klf2
GO_BP_m3	GO:007201	glomerular	1/539	16/23843	0.306474	0.619147	0.584208	Foxc2
GO_BP_m3	GO:009715	mesenchyr	1/539	16/23843	0.306474	0.619147	0.584208	Gdf5
GO_BP_m3	GO:009732	plasma me	1/539	16/23843	0.306474	0.619147	0.584208	Pacsin3
GO_BP_m3	GO:00975	sialylation	1/539	16/23843	0.306474	0.619147	0.584208	St6galnac5
GO_BP_m3	GO:009917	presynaps	1/539	16/23843	0.306474	0.619147	0.584208	Nlgn1
GO_BP_m3	GO:190015	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Nanos1
GO_BP_m3	GO:190015	positive re	1/539	16/23843	0.306474	0.619147	0.584208	Nanos1
GO_BP_m3	GO:190188	positive re	1/539	16/23843	0.306474	0.619147	0.584208	Carmil2
GO_BP_m3	GO:190271	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Carmil2
GO_BP_m3	GO:190353	protein loc	1/539	16/23843	0.306474	0.619147	0.584208	Grin2c
GO_BP_m3	GO:190466	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Mad2l1
GO_BP_m3	GO:200029	regulation	1/539	16/23843	0.306474	0.619147	0.584208	Myod1
GO_BP_m3	GO:200117	negative re	1/539	16/23843	0.306474	0.619147	0.584208	Ier3
GO_BP_m3	GO:200124	positive re	1/539	16/23843	0.306474	0.619147	0.584208	Wwox
GO_BP_m3	GO:009865	anion trans	6/539	202/23843	0.307257	0.620148	0.585153	Clcn1/Hk1/
GO_BP_m3	GO:190198	regulation	8/539	282/23843	0.307439	0.620148	0.585153	Atf5/Fanci/
GO_BP_m3	GO:000181	positive re	11/539	404/23843	0.30775	0.620148	0.585153	C1qtnf4/C
GO_BP_m3	GO:000616	nucleoside	3/539	86/23843	0.307981	0.620148	0.585153	Ak7/Hk1/I
GO_BP_m3	GO:00326	chemokine	3/539	86/23843	0.307981	0.620148	0.585153	Aire/Ccl5/
GO_BP_m3	GO:004315	negative re	3/539	86/23843	0.307981	0.620148	0.585153	Avp/Cryaa/
GO_BP_m3	GO:004483	cell cycle G	4/539	124/23843	0.308125	0.620148	0.585153	Atf5/Fanci/
GO_BP_m3	GO:190265	secondary	4/539	124/23843	0.308125	0.620148	0.585153	Dhcr24/Fd
GO_BP_m3	GO:000166	behavioral	2/539	50/23843	0.312627	0.626859	0.591486	Grik2/Ucn
GO_BP_m3	GO:001051	regulation	2/539	50/23843	0.312627	0.626859	0.591486	Ccl5/Prkcz
GO_BP_m3	GO:003235	regulation	2/539	50/23843	0.312627	0.626859	0.591486	Bmp2/Stc2
GO_BP_m3	GO:003362	cell adhesi	2/539	50/23843	0.312627	0.626859	0.591486	Ccl5/Foxc2

GO_BP_m3	GO:00353	positive re	2/539	50/23843	0.312627	0.626859	0.591486	Bmp2/Dus
GO_BP_m3	GO:004361	regulation	2/539	50/23843	0.312627	0.626859	0.591486	Hsf4/Klf2
GO_BP_m3	GO:004394	regulation	2/539	50/23843	0.312627	0.626859	0.591486	Gip/Ucn
GO_BP_m3	GO:19004	negative re	2/539	50/23843	0.312627	0.626859	0.591486	Bag5/Lrrk2
GO_BP_m3	GO:00026	negative re	5/539	164/23843	0.313341	0.627412	0.592007	Abr/Btn1a1
GO_BP_m3	GO:00350	cardiocyte	5/539	164/23843	0.313341	0.627412	0.592007	Bmp2/Ctd
GO_BP_m3	GO:005117	import int	5/539	164/23843	0.313341	0.627412	0.592007	Lrrk2/Nxt1/
GO_BP_m3	GO:00149	smooth mu	3/539	87/23843	0.314178	0.628503	0.593036	Ccl5/P2ry6
GO_BP_m3	GO:00311	RNA 3'-en	3/539	87/23843	0.314178	0.628503	0.593036	Ctr9/Exosc
GO_BP_m3	GO:003214	activation	7/539	244/23843	0.315167	0.62934	0.593826	Bmp2/Grm
GO_BP_m3	GO:001097	negative re	5/539	165/23843	0.317775	0.62934	0.593826	Bag5/Dleu
GO_BP_m3	GO:004851	spermatid	5/539	165/23843	0.317775	0.62934	0.593826	Catsper4/C
GO_BP_m3	GO:00508	positive re	12/539	449/23843	0.318322	0.62934	0.593826	Ccl5/Cd46/
GO_BP_m3	GO:003017	positive re	4/539	126/23843	0.31834	0.62934	0.593826	Bmp2/Dixc
GO_BP_m3	GO:00217	limbic syst	3/539	88/23843	0.320378	0.62934	0.593826	Atat1/Mkk
GO_BP_m3	GO:00329	collagen m	3/539	88/23843	0.320378	0.62934	0.593826	Ihh/Prtn3/
GO_BP_m3	GO:00469	nucleotide	3/539	88/23843	0.320378	0.62934	0.593826	Ak7/Hk1/I
GO_BP_m3	GO:00507	regulation	3/539	88/23843	0.320378	0.62934	0.593826	Abr/Hck/P
GO_BP_m3	GO:007267	lymphocyt	3/539	88/23843	0.320378	0.62934	0.593826	Aire/Ccl5/
GO_BP_m3	GO:000197	blood vess	2/539	51/23843	0.32097	0.62934	0.593826	Abr/Foxc2
GO_BP_m3	GO:00022	behavioral	2/539	51/23843	0.32097	0.62934	0.593826	Grik2/Ucn
GO_BP_m3	GO:003007	regulation	2/539	51/23843	0.32097	0.62934	0.593826	Mad2l1/Ub
GO_BP_m3	GO:00309	midbrain d	2/539	51/23843	0.32097	0.62934	0.593826	Hes1/Otx1
GO_BP_m3	GO:003361	membrane	2/539	51/23843	0.32097	0.62934	0.593826	Pacsin3/Pr
GO_BP_m3	GO:00508	regulation	2/539	51/23843	0.32097	0.62934	0.593826	Prkch/Usp
GO_BP_m3	GO:00512	protein het	2/539	51/23843	0.32097	0.62934	0.593826	Nlgn1/Rrm
GO_BP_m3	GO:00019	suckling be	1/539	17/23843	0.322163	0.62934	0.593826	Helt
GO_BP_m3	GO:00019	regulation	1/539	17/23843	0.322163	0.62934	0.593826	Ndst2
GO_BP_m3	GO:00031	epithelial t	1/539	17/23843	0.322163	0.62934	0.593826	Tgfbr1
GO_BP_m3	GO:000341	growth pla	1/539	17/23843	0.322163	0.62934	0.593826	Col27a1
GO_BP_m3	GO:00067	C21-steroi	1/539	17/23843	0.322163	0.62934	0.593826	Bmp2
GO_BP_m3	GO:000821	estrogen m	1/539	17/23843	0.322163	0.62934	0.593826	Ugt1a7c
GO_BP_m3	GO:00098	post-embr	1/539	17/23843	0.322163	0.62934	0.593826	Nkx2-3
GO_BP_m3	GO:00107	negative re	1/539	17/23843	0.322163	0.62934	0.593826	Stoml1
GO_BP_m3	GO:003164	positive re	1/539	17/23843	0.322163	0.62934	0.593826	Sox10
GO_BP_m3	GO:00336	negative re	1/539	17/23843	0.322163	0.62934	0.593826	Syt4
GO_BP_m3	GO:003531	wound hea	1/539	17/23843	0.322163	0.62934	0.593826	Plet1
GO_BP_m3	GO:00421	neurotrans	1/539	17/23843	0.322163	0.62934	0.593826	Gcsh
GO_BP_m3	GO:004244	hormone c	1/539	17/23843	0.322163	0.62934	0.593826	Ugt1a7c
GO_BP_m3	GO:00424	regulation	1/539	17/23843	0.322163	0.62934	0.593826	Bmp2
GO_BP_m3	GO:004432	response t	1/539	17/23843	0.322163	0.62934	0.593826	Mkks
GO_BP_m3	GO:00450	T-helper 2	1/539	17/23843	0.322163	0.62934	0.593826	Prkcz
GO_BP_m3	GO:00461	aldehyde b	1/539	17/23843	0.322163	0.62934	0.593826	Bmp2
GO_BP_m3	GO:00483	lateral mes	1/539	17/23843	0.322163	0.62934	0.593826	Foxf1
GO_BP_m3	GO:00484	anterograd	1/539	17/23843	0.322163	0.62934	0.593826	Ap3s1
GO_BP_m3	GO:00488	forebrain n	1/539	17/23843	0.322163	0.62934	0.593826	Otx1
GO_BP_m3	GO:00600	membrane	1/539	17/23843	0.322163	0.62934	0.593826	Prkcz
GO_BP_m3	GO:006054	negative re	1/539	17/23843	0.322163	0.62934	0.593826	Ucn

GO_BP_m3	GO:006085	regulation	1/539	17/23843	0.322163	0.62934	0.593826	Nkx6-1
GO_BP_m3	GO:006097	cell migrati	1/539	17/23843	0.322163	0.62934	0.593826	Twist1
GO_BP_m3	GO:007223	metanephr	1/539	17/23843	0.322163	0.62934	0.593826	Hes1
GO_BP_m3	GO:008018	histone H3	1/539	17/23843	0.322163	0.62934	0.593826	Ctr9
GO_BP_m3	GO:009023	regulation	1/539	17/23843	0.322163	0.62934	0.593826	Mad2l1
GO_BP_m3	GO:009951	synaptic ve	1/539	17/23843	0.322163	0.62934	0.593826	Ap3s1
GO_BP_m3	GO:009951	synaptic ve	1/539	17/23843	0.322163	0.62934	0.593826	Ap3s1
GO_BP_m3	GO:190217	negative re	1/539	17/23843	0.322163	0.62934	0.593826	Bag5
GO_BP_m3	GO:190531	semi-lunar	1/539	17/23843	0.322163	0.62934	0.593826	Twist1
GO_BP_m3	GO:200077	negative re	1/539	17/23843	0.322163	0.62934	0.593826	Twist1
GO_BP_m3	GO:200078	positive re	1/539	17/23843	0.322163	0.62934	0.593826	Kdm4d
GO_BP_m3	GO:200081	regulation	1/539	17/23843	0.322163	0.62934	0.593826	Prkch
GO_BP_m3	GO:004352	negative re	5/539	166/23843	0.322216	0.62934	0.593826	Bcl2l1/Crlf1
GO_BP_m3	GO:000269	positive re	6/539	206/23843	0.323105	0.63079	0.595194	Cd46/Exos
GO_BP_m3	GO:004566	negative re	7/539	247/23843	0.326035	0.634806	0.598984	Bag5/Dixd
GO_BP_m3	GO:001406	regulation	3/539	89/23843	0.326579	0.634806	0.598984	Ccl5/Prr5/T
GO_BP_m3	GO:005502	regulation	3/539	89/23843	0.326579	0.634806	0.598984	Bmp2/Ctd
GO_BP_m3	GO:007123	cellular res	5/539	167/23843	0.326665	0.634806	0.598984	Bcl2l1/Mir1
GO_BP_m3	GO:003033	positive re	13/539	494/23843	0.327682	0.634806	0.598984	Bmp2/Ccl5
GO_BP_m3	GO:001612	sterol bios	2/539	52/23843	0.329288	0.634806	0.598984	Dhcr24/Tm
GO_BP_m3	GO:002158	cerebellum	2/539	52/23843	0.329288	0.634806	0.598984	Atxn2/Whr
GO_BP_m3	GO:004559	negative re	2/539	52/23843	0.329288	0.634806	0.598984	Jdp2/Trib2
GO_BP_m3	GO:005073	negative re	2/539	52/23843	0.329288	0.634806	0.598984	Nf2/Prkcz
GO_BP_m3	GO:005087	multicellula	2/539	52/23843	0.329288	0.634806	0.598984	Tnni2/Tnnt
GO_BP_m3	GO:005088	musculosk	2/539	52/23843	0.329288	0.634806	0.598984	Tnni2/Tnnt
GO_BP_m3	GO:007009	chemokine	2/539	52/23843	0.329288	0.634806	0.598984	Ccl5/Tff2
GO_BP_m3	GO:190209	regulation	2/539	52/23843	0.329288	0.634806	0.598984	Mad2l1/Ub
GO_BP_m3	GO:190520	regulation	2/539	52/23843	0.329288	0.634806	0.598984	Bmp2/Ctd
GO_BP_m3	GO:006056	epithelial t	10/539	371/23843	0.330823	0.634806	0.598984	Areg/Bmp2
GO_BP_m3	GO:004225	ribosome b	8/539	289/23843	0.330864	0.634806	0.598984	Dis3/Exosc
GO_BP_m3	GO:000244	myeloid le	3/539	90/23843	0.332779	0.634806	0.598984	Abr/Dnase
GO_BP_m3	GO:000630	DNA modi	3/539	90/23843	0.332779	0.634806	0.598984	Exosc6/Mo
GO_BP_m3	GO:004506	regulation	3/539	90/23843	0.332779	0.634806	0.598984	Ccl5/Isg20/
GO_BP_m3	GO:005079	regulation	3/539	90/23843	0.332779	0.634806	0.598984	Ghrhr/Nlgr
GO_BP_m3	GO:000183	epithelial t	4/539	129/23843	0.33371	0.634806	0.598984	Axin2/Bmp
GO_BP_m3	GO:004688	regulation	8/539	290/23843	0.334236	0.634806	0.598984	Ccl5/Ghrhr
GO_BP_m3	GO:000257	myeloid le	6/539	209/23843	0.335067	0.634806	0.598984	Ccl5/L3mb
GO_BP_m3	GO:003286	response t	6/539	209/23843	0.335067	0.634806	0.598984	Foxc2/Ghrh
GO_BP_m3	GO:000721	Notch sign	5/539	169/23843	0.33558	0.634806	0.598984	Bend6/Bmp
GO_BP_m3	GO:001077	positive re	5/539	169/23843	0.33558	0.634806	0.598984	Caprin1/Cu
GO_BP_m3	GO:000683	neurotrans	7/539	250/23843	0.336962	0.634806	0.598984	Bcl2l1/Gpm
GO_BP_m3	GO:000171	mesoderm	1/539	18/23843	0.337497	0.634806	0.598984	Foxc2
GO_BP_m3	GO:000612	mitochond	1/539	18/23843	0.337497	0.634806	0.598984	Dld
GO_BP_m3	GO:000668	glycosphin	1/539	18/23843	0.337497	0.634806	0.598984	St6galnac5
GO_BP_m3	GO:000719	activation	1/539	18/23843	0.337497	0.634806	0.598984	Ghrhr
GO_BP_m3	GO:000739	ectoderm	1/539	18/23843	0.337497	0.634806	0.598984	Nf2
GO_BP_m3	GO:000995	dorsal/vent	1/539	18/23843	0.337497	0.634806	0.598984	Axin2
GO_BP_m3	GO:001075	positive re	1/539	18/23843	0.337497	0.634806	0.598984	Ccl5

GO_BP_m3	GO:001081	T cell chem	1/539	18/23843	0.337497	0.634806	0.598984	Ccl5
GO_BP_m3	GO:001406	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Oxt
GO_BP_m3	GO:002151	ventral spi	1/539	18/23843	0.337497	0.634806	0.598984	Nkx6-1
GO_BP_m3	GO:002154	dentate gy	1/539	18/23843	0.337497	0.634806	0.598984	Atat1
GO_BP_m3	GO:002178	preganglio	1/539	18/23843	0.337497	0.634806	0.598984	Hes1
GO_BP_m3	GO:002201	central ner	1/539	18/23843	0.337497	0.634806	0.598984	Sox10
GO_BP_m3	GO:003199	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Twist1
GO_BP_m3	GO:003219	transpositi	1/539	18/23843	0.337497	0.634806	0.598984	Piwil4
GO_BP_m3	GO:003227	gonadotro	1/539	18/23843	0.337497	0.634806	0.598984	Ucn2
GO_BP_m3	GO:003229	axon enshe	1/539	18/23843	0.337497	0.634806	0.598984	Sox10
GO_BP_m3	GO:003265	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Prkcz
GO_BP_m3	GO:003267	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Prkcz
GO_BP_m3	GO:003269	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Trib2
GO_BP_m3	GO:003506	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Twist1
GO_BP_m3	GO:003603	CD8-positi	1/539	18/23843	0.337497	0.634806	0.598984	Satb1
GO_BP_m3	GO:004243	melanin bi	1/539	18/23843	0.337497	0.634806	0.598984	Trpc1
GO_BP_m3	GO:004393	ossification	1/539	18/23843	0.337497	0.634806	0.598984	Bmp2
GO_BP_m3	GO:004632	positive re	1/539	18/23843	0.337497	0.634806	0.598984	Twist1
GO_BP_m3	GO:004824	norepinep	1/539	18/23843	0.337497	0.634806	0.598984	Oxt
GO_BP_m3	GO:004871	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Atf5
GO_BP_m3	GO:005076	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Prtn3
GO_BP_m3	GO:005091	detection	1/539	18/23843	0.337497	0.634806	0.598984	Mkks
GO_BP_m3	GO:005119	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Ier3
GO_BP_m3	GO:005196	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Grik2
GO_BP_m3	GO:005506	chloride io	1/539	18/23843	0.337497	0.634806	0.598984	Slc12a7
GO_BP_m3	GO:006008	auditory re	1/539	18/23843	0.337497	0.634806	0.598984	Whrn
GO_BP_m3	GO:006033	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Trim6
GO_BP_m3	GO:006039	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Tgfbr1
GO_BP_m3	GO:006084	venous blo	1/539	18/23843	0.337497	0.634806	0.598984	Foxf1
GO_BP_m3	GO:007160	monocyte	1/539	18/23843	0.337497	0.634806	0.598984	Twist1
GO_BP_m3	GO:007163	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Twist1
GO_BP_m3	GO:007180	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Hck
GO_BP_m3	GO:009002	positive re	1/539	18/23843	0.337497	0.634806	0.598984	Ccl5
GO_BP_m3	GO:009003	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Bmp2
GO_BP_m3	GO:009881	neurotrans	1/539	18/23843	0.337497	0.634806	0.598984	Gpm6b
GO_BP_m3	GO:190102	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Ier3
GO_BP_m3	GO:190162	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Ccl5
GO_BP_m3	GO:190223	negative re	1/539	18/23843	0.337497	0.634806	0.598984	Lrrk2
GO_BP_m3	GO:200026	regulation	1/539	18/23843	0.337497	0.634806	0.598984	Ier3ip1
GO_BP_m3	GO:000175	neural cres	2/539	53/23843	0.337578	0.634806	0.598984	Sox10/Twis
GO_BP_m3	GO:000304	regulation	2/539	53/23843	0.337578	0.634806	0.598984	Ndst2/Tacr
GO_BP_m3	GO:000994	anterior/p	2/539	53/23843	0.337578	0.634806	0.598984	Neurog1/T
GO_BP_m3	GO:003531	hair cell dif	2/539	53/23843	0.337578	0.634806	0.598984	Hes1/Whr
GO_BP_m3	GO:004438	protein loc	2/539	53/23843	0.337578	0.634806	0.598984	Cep131/Fa
GO_BP_m3	GO:004806	developme	2/539	53/23843	0.337578	0.634806	0.598984	Ihh/Sox10
GO_BP_m3	GO:005193	synaptic tra	2/539	53/23843	0.337578	0.634806	0.598984	Nlgn1/Tacr
GO_BP_m3	GO:005501	ventricular	2/539	53/23843	0.337578	0.634806	0.598984	Foxc2/Tgfb
GO_BP_m3	GO:006138	trabecula	2/539	53/23843	0.337578	0.634806	0.598984	S1pr1/Tgfb

GO_BP_m3	GO:009030	positive reg	2/539	53/23843	0.337578	0.634806	0.598984	Foxc2/Myc
GO_BP_m3	GO:190288	negative re	2/539	53/23843	0.337578	0.634806	0.598984	Bag5/Lrrk2
GO_BP_m3	GO:001612	sterol meta	4/539	130/23843	0.338841	0.6366	0.600677	Dhcr24/Fdx
GO_BP_m3	GO:003105	positive reg	3/539	91/23843	0.338977	0.6366	0.600677	Ctr9/Jdp2/
GO_BP_m3	GO:004544	myoblast d	3/539	91/23843	0.338977	0.6366	0.600677	Cdon/Myo
GO_BP_m3	GO:005088	regulation	5/539	170/23843	0.340046	0.638329	0.602308	Avp/Foxc2/
GO_BP_m3	GO:001046	negative re	7/539	251/23843	0.340616	0.639119	0.603053	9230104L0
GO_BP_m3	GO:000244	leukocyte r	12/539	458/23843	0.342423	0.642231	0.60599	Abr/Aire/C
GO_BP_m3	GO:190353	negative re	6/539	211/23843	0.34307	0.643162	0.606868	Abr/Btn1a1
GO_BP_m3	GO:190156	fatty acid d	4/539	131/23843	0.343976	0.644132	0.607783	Avp/Cyp2c
GO_BP_m3	GO:001605	Wnt signali	11/539	417/23843	0.344173	0.644132	0.607783	Axin2/Bmp
GO_BP_m3	GO:004206	gliogenesis	8/539	293/23843	0.344383	0.644132	0.607783	Areg/Atf5/
GO_BP_m3	GO:000736	gastrulatio	5/539	171/23843	0.344516	0.644132	0.607783	Ctr9/Dld/F
GO_BP_m3	GO:003515	regulation	5/539	171/23843	0.344516	0.644132	0.607783	Avp/Foxc2/
GO_BP_m3	GO:007250	cellular diva	12/539	459/23843	0.345124	0.644132	0.607783	Avp/Calb2/
GO_BP_m3	GO:005181	modificatio	3/539	92/23843	0.345171	0.644132	0.607783	Bcl2l1/Ccl5
GO_BP_m3	GO:000270	negative re	2/539	54/23843	0.345837	0.644132	0.607783	Abr/Foxf1
GO_BP_m3	GO:000674	glutathione	2/539	54/23843	0.345837	0.644132	0.607783	Gdap1l1/G
GO_BP_m3	GO:000758	respiratory	2/539	54/23843	0.345837	0.644132	0.607783	Chrna4/Nlg
GO_BP_m3	GO:001082	positive reg	2/539	54/23843	0.345837	0.644132	0.607783	Gip/Prkcz
GO_BP_m3	GO:002179	cerebral co	2/539	54/23843	0.345837	0.644132	0.607783	Dixdc1/Md
GO_BP_m3	GO:004259	fear respor	2/539	54/23843	0.345837	0.644132	0.607783	Grik2/Ucn
GO_BP_m3	GO:004406	regulation	2/539	54/23843	0.345837	0.644132	0.607783	Ucn/Ucn2
GO_BP_m3	GO:006019	positive reg	2/539	54/23843	0.345837	0.644132	0.607783	Ccl5/Prkcz
GO_BP_m3	GO:001820	peptidyl-ly	9/539	335/23843	0.346962	0.644497	0.608128	Atat1/Ctr9/
GO_BP_m3	GO:003447	ncRNA pro	9/539	335/23843	0.346962	0.644497	0.608128	Trmo/Dis3/
GO_BP_m3	GO:004886	stem cell d	6/539	212/23843	0.347079	0.644497	0.608128	Epop/Foxc2
GO_BP_m3	GO:005149	positive reg	6/539	212/23843	0.347079	0.644497	0.608128	Hck/Nf2/Ra
GO_BP_m3	GO:000663	fatty acid n	10/539	377/23843	0.348708	0.644497	0.608128	Avp/Cyp2c
GO_BP_m3	GO:007188	leukocyte a	4/539	132/23843	0.349112	0.644497	0.608128	Ccl5/Mir10
GO_BP_m3	GO:019873	cell-cell sig	11/539	419/23843	0.349848	0.644497	0.608128	Axin2/Bmp
GO_BP_m3	GO:000700	mitochond	3/539	93/23843	0.35136	0.644497	0.608128	Bcl2l1/Ier3/
GO_BP_m3	GO:000211	store-oper	1/539	19/23843	0.352485	0.644497	0.608128	Stc2
GO_BP_m3	GO:000231	mature B c	1/539	19/23843	0.352485	0.644497	0.608128	Nkx2-3
GO_BP_m3	GO:000321	cardiac left	1/539	19/23843	0.352485	0.644497	0.608128	Foxf1
GO_BP_m3	GO:000610	2-oxogluta	1/539	19/23843	0.352485	0.644497	0.608128	Dld
GO_BP_m3	GO:000634	methylatio	1/539	19/23843	0.352485	0.644497	0.608128	Uhrf1
GO_BP_m3	GO:000690	pinocytosis	1/539	19/23843	0.352485	0.644497	0.608128	Mapkapk3
GO_BP_m3	GO:000820	androgen r	1/539	19/23843	0.352485	0.644497	0.608128	Srd5a1
GO_BP_m3	GO:001015	regulation	1/539	19/23843	0.352485	0.644497	0.608128	Twist1
GO_BP_m3	GO:001044	response to	1/539	19/23843	0.352485	0.644497	0.608128	Gip
GO_BP_m3	GO:001501	heparan su	1/539	19/23843	0.352485	0.644497	0.608128	Ndst2
GO_BP_m3	GO:003221	negative re	1/539	19/23843	0.352485	0.644497	0.608128	Gnl3l
GO_BP_m3	GO:003263	interleukin-	1/539	19/23843	0.352485	0.644497	0.608128	Prkcz
GO_BP_m3	GO:003361	mitochond	1/539	19/23843	0.352485	0.644497	0.608128	Bcs1l
GO_BP_m3	GO:003396	cytoplasmi	1/539	19/23843	0.352485	0.644497	0.608128	Atxn2
GO_BP_m3	GO:003469	response to	1/539	19/23843	0.352485	0.644497	0.608128	P2ry6
GO_BP_m3	GO:003535	peroxisome	1/539	19/23843	0.352485	0.644497	0.608128	Twist1

GO_BP_m3	GO:003574	CD4-positi	1/539	19/23843	0.352485	0.644497	0.608128	Prkcz
GO_BP_m3	GO:004562	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Prkcz
GO_BP_m3	GO:004831	mitochond	1/539	19/23843	0.352485	0.644497	0.608128	Lrrk2
GO_BP_m3	GO:005077	negative re	1/539	19/23843	0.352485	0.644497	0.608128	Nlgn1
GO_BP_m3	GO:005101	barbed-en	1/539	19/23843	0.352485	0.644497	0.608128	Carmil2
GO_BP_m3	GO:005158	regulation	1/539	19/23843	0.352485	0.644497	0.608128	Gpm6b
GO_BP_m3	GO:005177	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Lrrk2
GO_BP_m3	GO:005190	regulation	1/539	19/23843	0.352485	0.644497	0.608128	Lrrk2
GO_BP_m3	GO:006012	regulation	1/539	19/23843	0.352485	0.644497	0.608128	Ghrhr
GO_BP_m3	GO:006029	cilium mov	1/539	19/23843	0.352485	0.644497	0.608128	Mkks
GO_BP_m3	GO:007097	bone matu	1/539	19/23843	0.352485	0.644497	0.608128	Bmp2
GO_BP_m3	GO:007214	epithelial c	1/539	19/23843	0.352485	0.644497	0.608128	Hes1
GO_BP_m3	GO:190001	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Il17d
GO_BP_m3	GO:190042	regulation	1/539	19/23843	0.352485	0.644497	0.608128	Tfeb
GO_BP_m3	GO:190305	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Carmil2
GO_BP_m3	GO:190552	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Ccl5
GO_BP_m3	GO:200013	regulation	1/539	19/23843	0.352485	0.644497	0.608128	Hes1
GO_BP_m3	GO:200019	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Oxt
GO_BP_m3	GO:200025	positive reg	1/539	19/23843	0.352485	0.644497	0.608128	Hck
GO_BP_m3	GO:000961	response t	12/539	462/23843	0.353248	0.645181	0.608773	Foxc2/Foxf
GO_BP_m3	GO:001097	positive reg	9/539	337/23843	0.353318	0.645181	0.608773	Caprin1/Cu
GO_BP_m3	GO:004859	eye morph	5/539	173/23843	0.353467	0.645181	0.608773	Aqp5/Cdor
GO_BP_m3	GO:000709	metaphase	2/539	55/23843	0.354061	0.645181	0.608773	Mad2l1/Ub
GO_BP_m3	GO:003081	regulation	2/539	55/23843	0.354061	0.645181	0.608773	Avp/Rln3
GO_BP_m3	GO:004362	regulation	2/539	55/23843	0.354061	0.645181	0.608773	Hsf4/Klf2
GO_BP_m3	GO:004642	negative re	2/539	55/23843	0.354061	0.645181	0.608773	Lrrtm1/Nf2
GO_BP_m3	GO:190489	negative re	2/539	55/23843	0.354061	0.645181	0.608773	Lrrtm1/Nf2
GO_BP_m3	GO:001923	sensory pe	4/539	133/23843	0.354249	0.645251	0.608839	Chrna4/Gip
GO_BP_m3	GO:003032	lung devel	6/539	214/23843	0.355108	0.646541	0.610056	Foxf1/Hes1
GO_BP_m3	GO:001648	protein pro	7/539	255/23843	0.355277	0.646574	0.610088	Cd46/Dhcr
GO_BP_m3	GO:005148	regulation	9/539	338/23843	0.356502	0.648528	0.611932	Avp/Calb2/
GO_BP_m3	GO:000195	regulation	3/539	94/23843	0.357542	0.649046	0.61242	C1qtnf4/Pt
GO_BP_m3	GO:000906	fatty acid c	3/539	94/23843	0.357542	0.649046	0.61242	Slc25a17/S
GO_BP_m3	GO:003051	regulation	3/539	94/23843	0.357542	0.649046	0.61242	Gdf5/Hes1/
GO_BP_m3	GO:003355	multicellula	3/539	94/23843	0.357542	0.649046	0.61242	Grik2/Tacr1
GO_BP_m3	GO:200006	positive reg	3/539	94/23843	0.357542	0.649046	0.61242	Lrrk2/Rnf14
GO_BP_m3	GO:003297	regulation	10/539	380/23843	0.357708	0.649072	0.612445	Dixdc1/Gpr
GO_BP_m3	GO:000176	neuron mig	5/539	174/23843	0.357947	0.649232	0.612595	Gpr173/Mc
GO_BP_m3	GO:001096	regulation	2/539	56/23843	0.362248	0.654367	0.617441	Mad2l1/Ub
GO_BP_m3	GO:001491	positive reg	2/539	56/23843	0.362248	0.654367	0.617441	Ccl5/P2ry6
GO_BP_m3	GO:001644	somatic rec	2/539	56/23843	0.362248	0.654367	0.617441	Exosc6/Mir
GO_BP_m3	GO:004478	metaphase	2/539	56/23843	0.362248	0.654367	0.617441	Mad2l1/Ub
GO_BP_m3	GO:190382	positive reg	9/539	340/23843	0.362881	0.654367	0.617441	Ablim3/Cep
GO_BP_m3	GO:003300	muscle cell	6/539	216/23843	0.363151	0.654367	0.617441	Ccl5/Foxc2
GO_BP_m3	GO:003560	protein dea	3/539	95/23843	0.363716	0.654367	0.617441	Jdp2/Lrrk2/
GO_BP_m3	GO:004592	positive reg	3/539	95/23843	0.363716	0.654367	0.617441	Bcl2l1/Nlgn
GO_BP_m3	GO:004870	oligodendr	3/539	95/23843	0.363716	0.654367	0.617441	Hes1/Nkx6
GO_BP_m3	GO:200124	negative re	3/539	95/23843	0.363716	0.654367	0.617441	Bag5/Bcl2l1

GO_BP_m3	GO:000801	blood circu	12/539	467/23843	0.366856	0.654367	0.617441	Abr/Adm2/
GO_BP_m3	GO:005500	striated mu	5/539	176/23843	0.366911	0.654367	0.617441	Ctdp1/Flnc
GO_BP_m3	GO:000194	lymphangi	1/539	20/23843	0.367135	0.654367	0.617441	Foxc2
GO_BP_m3	GO:000308	positive reg	1/539	20/23843	0.367135	0.654367	0.617441	Avp
GO_BP_m3	GO:000658	melanin m	1/539	20/23843	0.367135	0.654367	0.617441	Trpc1
GO_BP_m3	GO:000688	cellular soc	1/539	20/23843	0.367135	0.654367	0.617441	Sgk1
GO_BP_m3	GO:001087	regulation	1/539	20/23843	0.367135	0.654367	0.617441	Ptch1
GO_BP_m3	GO:001573	prostaglan	1/539	20/23843	0.367135	0.654367	0.617441	Oxt
GO_BP_m3	GO:003054	female ger	1/539	20/23843	0.367135	0.654367	0.617441	Srd5a1
GO_BP_m3	GO:003095	establishm	1/539	20/23843	0.367135	0.654367	0.617441	Rhob
GO_BP_m3	GO:003144	regulation	1/539	20/23843	0.367135	0.654367	0.617441	Ctr9
GO_BP_m3	GO:003164	negative re	1/539	20/23843	0.367135	0.654367	0.617441	Avp
GO_BP_m3	GO:003214	activation	1/539	20/23843	0.367135	0.654367	0.617441	Prkcz
GO_BP_m3	GO:003230	regulation	1/539	20/23843	0.367135	0.654367	0.617441	Oxt
GO_BP_m3	GO:003233	positive reg	1/539	20/23843	0.367135	0.654367	0.617441	Gdf5
GO_BP_m3	GO:003261	interleukin	1/539	20/23843	0.367135	0.654367	0.617441	Prkcz
GO_BP_m3	GO:003303	negative re	1/539	20/23843	0.367135	0.654367	0.617441	Ccl5
GO_BP_m3	GO:004244	progestero	1/539	20/23843	0.367135	0.654367	0.617441	Srd5a1
GO_BP_m3	GO:004350	skeletal mu	1/539	20/23843	0.367135	0.654367	0.617441	Myod1
GO_BP_m3	GO:004434	fibroblast a	1/539	20/23843	0.367135	0.654367	0.617441	Ier3ip1
GO_BP_m3	GO:005043	positive reg	1/539	20/23843	0.367135	0.654367	0.617441	Ctdp1
GO_BP_m3	GO:006132	cell prolifer	1/539	20/23843	0.367135	0.654367	0.617441	Hes1
GO_BP_m3	GO:007217	metanephr	1/539	20/23843	0.367135	0.654367	0.617441	Hes1
GO_BP_m3	GO:007224	metanephr	1/539	20/23843	0.367135	0.654367	0.617441	Hes1
GO_BP_m3	GO:009005	positive reg	1/539	20/23843	0.367135	0.654367	0.617441	Foxc2
GO_BP_m3	GO:009550	acetylcholi	1/539	20/23843	0.367135	0.654367	0.617441	Chrna4
GO_BP_m3	GO:190383	signal trans	1/539	20/23843	0.367135	0.654367	0.617441	Chrna4
GO_BP_m3	GO:190514	response t	1/539	20/23843	0.367135	0.654367	0.617441	Chrna4
GO_BP_m3	GO:190514	cellular res	1/539	20/23843	0.367135	0.654367	0.617441	Chrna4
GO_BP_m3	GO:200031	regulation	1/539	20/23843	0.367135	0.654367	0.617441	Nlgn1
GO_BP_m3	GO:003032	respiratory	6/539	217/23843	0.367177	0.654367	0.617441	Foxf1/Hes1
GO_BP_m3	GO:009027	regulation	6/539	217/23843	0.367177	0.654367	0.617441	Ccl5/Ghrhr
GO_BP_m3	GO:000979	post-embr	4/539	136/23843	0.369657	0.656293	0.619258	Atf5/Helt/
GO_BP_m3	GO:001657	histone me	4/539	136/23843	0.369657	0.656293	0.619258	Ctr9/Kdm4
GO_BP_m3	GO:000830	associative	3/539	96/23843	0.36988	0.656293	0.619258	Sgk1/Tacr1
GO_BP_m3	GO:004426	cellular pol	3/539	96/23843	0.36988	0.656293	0.619258	B3gnt6/Ph
GO_BP_m3	GO:004866	positive reg	3/539	96/23843	0.36988	0.656293	0.619258	Ccl5/Hpgd
GO_BP_m3	GO:009026	positive reg	3/539	96/23843	0.36988	0.656293	0.619258	Dixdc1/Fa
GO_BP_m3	GO:009873	macromole	3/539	96/23843	0.36988	0.656293	0.619258	Jdp2/Lrrk2/
GO_BP_m3	GO:003021	T cell differ	7/539	259/23843	0.369997	0.656293	0.619258	Aire/Cd46/
GO_BP_m3	GO:001580	acidic ami	2/539	57/23843	0.370397	0.656293	0.619258	Avp/Syt4
GO_BP_m3	GO:001908	viral gene	2/539	57/23843	0.370397	0.656293	0.619258	Ccl5/Ctdp1
GO_BP_m3	GO:004346	regulation	2/539	57/23843	0.370397	0.656293	0.619258	BC048507/
GO_BP_m3	GO:004851	circadian b	2/539	57/23843	0.370397	0.656293	0.619258	Ghrhr/Nlg
GO_BP_m3	GO:006011	inner ear r	2/539	57/23843	0.370397	0.656293	0.619258	Hes1/Whr
GO_BP_m3	GO:200073	regulation	2/539	57/23843	0.370397	0.656293	0.619258	Hes1/Trim
GO_BP_m3	GO:000189	tissue hom	6/539	218/23843	0.371204	0.657181	0.620096	Ihh/Mkks/
GO_BP_m3	GO:000718	G-protein	6/539	218/23843	0.371204	0.657181	0.620096	Adm2/Ghr

GO_BP_m3	GO:000697	response t	10/539	385/23843	0.372775	0.659691	0.622464	Ankzf1/Ba
GO_BP_m3	GO:00626	DNA replic	7/539	260/23843	0.373684	0.660888	0.623594	Areg/Enpp
GO_BP_m3	GO:00313	negative re	4/539	137/23843	0.374789	0.660888	0.623594	Mkks/Prkcz
GO_BP_m3	GO:00016	eye develo	10/539	386/23843	0.375797	0.660888	0.623594	Aqp5/Cdo
GO_BP_m3	GO:00300	lymphocyt	10/539	386/23843	0.375797	0.660888	0.623594	Aire/Cd46/
GO_BP_m3	GO:00347	negative re	3/539	97/23843	0.376034	0.660888	0.623594	Hamp2/Stc
GO_BP_m3	GO:00485	negative re	3/539	97/23843	0.376034	0.660888	0.623594	Ccl5/Isg20/
GO_BP_m3	GO:000301	circulatory	12/539	471/23843	0.377795	0.660888	0.623594	Abr/Adm2/
GO_BP_m3	GO:000201	morphoge	2/539	58/23843	0.378503	0.660888	0.623594	Plet1/Carm
GO_BP_m3	GO:00023	immunogl	2/539	58/23843	0.378503	0.660888	0.623594	Exosc6/Mir
GO_BP_m3	GO:00063	DNA-temp	2/539	58/23843	0.378503	0.660888	0.623594	Ctr9/Sox1
GO_BP_m3	GO:00308	negative re	2/539	58/23843	0.378503	0.660888	0.623594	Mkks/Carm
GO_BP_m3	GO:00457	positive re	2/539	58/23843	0.378503	0.660888	0.623594	Areg/Ucn
GO_BP_m3	GO:00466	positive re	2/539	58/23843	0.378503	0.660888	0.623594	Ihh/Prkcz
GO_BP_m3	GO:00466	regulation	2/539	58/23843	0.378503	0.660888	0.623594	Ihh/Prkcz
GO_BP_m3	GO:00482	lung alveol	2/539	58/23843	0.378503	0.660888	0.623594	Foxf1/Tcf2
GO_BP_m3	GO:00600	cardiac mu	2/539	58/23843	0.378503	0.660888	0.623594	Foxc2/Tgfb
GO_BP_m3	GO:00604	mammary	2/539	58/23843	0.378503	0.660888	0.623594	Areg/Ptch1
GO_BP_m3	GO:20012	negative re	6/539	220/23843	0.379263	0.660888	0.623594	Avp/Bag5/
GO_BP_m3	GO:19019	negative re	4/539	138/23843	0.379917	0.660888	0.623594	Fanci/Ier3/
GO_BP_m3	GO:000007	cell cycle c	5/539	179/23843	0.380362	0.660888	0.623594	Bcl2l1/Fan
GO_BP_m3	GO:00432	response t	5/539	179/23843	0.380362	0.660888	0.623594	Bcl2l1/Mir1
GO_BP_m3	GO:003007	peptide ho	7/539	262/23843	0.381063	0.660888	0.623594	Ccl5/Ghrhr
GO_BP_m3	GO:00725	establishm	11/539	430/23843	0.381303	0.660888	0.623594	Ablim3/He
GO_BP_m3	GO:000197	neurologic	1/539	21/23843	0.381453	0.660888	0.623594	Tacr1
GO_BP_m3	GO:00063	DNA-temp	1/539	21/23843	0.381453	0.660888	0.623594	Dmtf1
GO_BP_m3	GO:00105	positive re	1/539	21/23843	0.381453	0.660888	0.623594	Carmil2
GO_BP_m3	GO:001074	regulation	1/539	21/23843	0.381453	0.660888	0.623594	Prkch
GO_BP_m3	GO:001932	hexose cat	1/539	21/23843	0.381453	0.660888	0.623594	Hk1
GO_BP_m3	GO:00319	regulation	1/539	21/23843	0.381453	0.660888	0.623594	Uhrf1
GO_BP_m3	GO:003204	mitochond	1/539	21/23843	0.381453	0.660888	0.623594	Mgme1
GO_BP_m3	GO:00329	positive re	1/539	21/23843	0.381453	0.660888	0.623594	Ctr9
GO_BP_m3	GO:003362	integrin ac	1/539	21/23843	0.381453	0.660888	0.623594	Foxc2
GO_BP_m3	GO:00343	protein-co	1/539	21/23843	0.381453	0.660888	0.623594	Gtf2e1
GO_BP_m3	GO:00346	response t	1/539	21/23843	0.381453	0.660888	0.623594	P2ry6
GO_BP_m3	GO:00363	lymph vess	1/539	21/23843	0.381453	0.660888	0.623594	Foxc2
GO_BP_m3	GO:00450	transcytosi	1/539	21/23843	0.381453	0.660888	0.623594	Pigr
GO_BP_m3	GO:00456	negative re	1/539	21/23843	0.381453	0.660888	0.623594	Hes1
GO_BP_m3	GO:004572	positive re	1/539	21/23843	0.381453	0.660888	0.623594	Avp
GO_BP_m3	GO:00466	negative re	1/539	21/23843	0.381453	0.660888	0.623594	Ihh
GO_BP_m3	GO:004824	eosinophil	1/539	21/23843	0.381453	0.660888	0.623594	Ccl5
GO_BP_m3	GO:00484	parasympa	1/539	21/23843	0.381453	0.660888	0.623594	Hes1
GO_BP_m3	GO:00514	myoblast p	1/539	21/23843	0.381453	0.660888	0.623594	Myod1
GO_BP_m3	GO:00610	regulation	1/539	21/23843	0.381453	0.660888	0.623594	Ctdp1
GO_BP_m3	GO:007084	inclusion b	1/539	21/23843	0.381453	0.660888	0.623594	Bag5
GO_BP_m3	GO:00708	regulation	1/539	21/23843	0.381453	0.660888	0.623594	Tmem30b
GO_BP_m3	GO:007264	interferon-	1/539	21/23843	0.381453	0.660888	0.623594	Carmil2
GO_BP_m3	GO:00902	positive re	1/539	21/23843	0.381453	0.660888	0.623594	Ucn

GO_BP_m3	GO:190012	regulation	1/539	21/23843	0.381453	0.660888	0.623594	Ptprf
GO_BP_m3	GO:190152	positive re	1/539	21/23843	0.381453	0.660888	0.623594	Bmp2
GO_BP_m3	GO:190174	positive re	1/539	21/23843	0.381453	0.660888	0.623594	Myod1
GO_BP_m3	GO:20002	regulation	1/539	21/23843	0.381453	0.660888	0.623594	Bcl2l1
GO_BP_m3	GO:200067	negative re	1/539	21/23843	0.381453	0.660888	0.623594	Hes1
GO_BP_m3	GO:00320	negative re	3/539	98/23843	0.382175	0.661338	0.624019	Gnl3l/Lrrk2
GO_BP_m3	GO:004231	vasoconstr	3/539	98/23843	0.382175	0.661338	0.624019	Avp/Mkks/
GO_BP_m3	GO:004642	positive re	3/539	98/23843	0.382175	0.661338	0.624019	Ccl5/Crlf1/
GO_BP_m3	GO:00064	negative re	6/539	221/23843	0.383294	0.662474	0.62509	Dusp26/Lr
GO_BP_m3	GO:00158	organic hy	6/539	221/23843	0.383294	0.662474	0.62509	Chrna4/Gp
GO_BP_m3	GO:001607	rRNA meta	6/539	221/23843	0.383294	0.662474	0.62509	Dis3/Exosc
GO_BP_m3	GO:00356	cellular res	9/539	347/23843	0.385295	0.663199	0.625774	Ankzf1/Ch
GO_BP_m3	GO:000271	regulation	2/539	59/23843	0.386566	0.663199	0.625774	Exosc6/Mir
GO_BP_m3	GO:00028	regulation	2/539	59/23843	0.386566	0.663199	0.625774	Exosc6/Mir
GO_BP_m3	GO:000762	rhythmic b	2/539	59/23843	0.386566	0.663199	0.625774	Ghrhr/Nlg
GO_BP_m3	GO:003272	positive re	2/539	59/23843	0.386566	0.663199	0.625774	Ccl5/Twist1
GO_BP_m3	GO:004684	filopodium	2/539	59/23843	0.386566	0.663199	0.625774	Nlgn1/Tgf
GO_BP_m3	GO:00510	negative re	2/539	59/23843	0.386566	0.663199	0.625774	Arhgap25/
GO_BP_m3	GO:00513	mitotic sist	2/539	59/23843	0.386566	0.663199	0.625774	Mad2l1/Ub
GO_BP_m3	GO:006071	labyrinthin	2/539	59/23843	0.386566	0.663199	0.625774	Esx1/Hes1
GO_BP_m3	GO:00609	endocrine	2/539	59/23843	0.386566	0.663199	0.625774	Ucn/Ucn2
GO_BP_m3	GO:00702	protein tri	2/539	59/23843	0.386566	0.663199	0.625774	Hsf4/Trim6
GO_BP_m3	GO:00702	T cell apop	2/539	59/23843	0.386566	0.663199	0.625774	Ccl5/Tsc22
GO_BP_m3	GO:001481	muscle cell	3/539	99/23843	0.388303	0.663199	0.625774	Ccl5/P2ry6
GO_BP_m3	GO:002151	spinal cord	3/539	99/23843	0.388303	0.663199	0.625774	Mir19a/Nk
GO_BP_m3	GO:01200	positive re	3/539	99/23843	0.388303	0.663199	0.625774	Nlgn1/Car
GO_BP_m3	GO:19018	positive re	3/539	99/23843	0.388303	0.663199	0.625774	Lrrk2/Rnf1
GO_BP_m3	GO:004687	hormone s	9/539	348/23843	0.388506	0.663199	0.625774	Ccl5/Ghrhr
GO_BP_m3	GO:00064	protein fol	5/539	181/23843	0.389326	0.663199	0.625774	Bag5/Crya
GO_BP_m3	GO:00020	columnar/	4/539	140/23843	0.390159	0.663199	0.625774	Bmp2/Hes
GO_BP_m3	GO:00455	regulation	4/539	140/23843	0.390159	0.663199	0.625774	Cd46/Ihh/
GO_BP_m3	GO:00466	alpha-beta	4/539	140/23843	0.390159	0.663199	0.625774	Ihh/Nkx2-
GO_BP_m3	GO:005072	negative re	4/539	140/23843	0.390159	0.663199	0.625774	Abr/Foxf1/
GO_BP_m3	GO:00901	tissue migr	7/539	265/23843	0.39214	0.663199	0.625774	Foxc2/Foxf
GO_BP_m3	GO:003134	positive re	11/539	434/23843	0.392814	0.663199	0.625774	Caprin1/Cu
GO_BP_m3	GO:00352	organ gro	5/539	182/23843	0.393804	0.663199	0.625774	Col27a1/C
GO_BP_m3	GO:000717	epidermal	3/539	100/23843	0.394416	0.663199	0.625774	Areg/Pigr/
GO_BP_m3	GO:00071	adenylate	3/539	100/23843	0.394416	0.663199	0.625774	Adm2/Ghrl
GO_BP_m3	GO:003162	receptor in	3/539	100/23843	0.394416	0.663199	0.625774	Atxn2/Lrrt
GO_BP_m3	GO:00320	positive re	3/539	100/23843	0.394416	0.663199	0.625774	Bmp2/Gnl
GO_BP_m3	GO:00519	regulation	3/539	100/23843	0.394416	0.663199	0.625774	Axin2/Mad
GO_BP_m3	GO:19048	positive re	3/539	100/23843	0.394416	0.663199	0.625774	Ccl5/Crlf1/
GO_BP_m3	GO:19052	positive re	3/539	100/23843	0.394416	0.663199	0.625774	Ctr9/Jdp2/
GO_BP_m3	GO:000704	lysosome	2/539	60/23843	0.394582	0.663199	0.625774	Lrrk2/Tfeb
GO_BP_m3	GO:00336	cellular pol	2/539	60/23843	0.394582	0.663199	0.625774	B3gnt6/Phl
GO_BP_m3	GO:00359	aorta deve	2/539	60/23843	0.394582	0.663199	0.625774	Hes1/Tfap
GO_BP_m3	GO:00550	anion hom	2/539	60/23843	0.394582	0.663199	0.625774	Slc12a7/Tf
GO_BP_m3	GO:008017	lytic vacuol	2/539	60/23843	0.394582	0.663199	0.625774	Lrrk2/Tfeb

GO_BP_m3	GO:190581	regulation	2/539	60/23843	0.394582	0.663199	0.625774	Mad2l1/Ub
GO_BP_m3	GO:004477	mitotic cell	9/539	350/23843	0.39493	0.663199	0.625774	Ctdp1/Fanc
GO_BP_m3	GO:000640	RNA catab	6/539	224/23843	0.395386	0.663199	0.625774	Axin2/Dis3
GO_BP_m3	GO:002240	positive reg	6/539	224/23843	0.395386	0.663199	0.625774	Ccl5/Cd46/
GO_BP_m3	GO:000209	auditory re	1/539	22/23843	0.395449	0.663199	0.625774	Whrn
GO_BP_m3	GO:000327	endocardia	1/539	22/23843	0.395449	0.663199	0.625774	Tgfbr1
GO_BP_m3	GO:000335	epithelial c	1/539	22/23843	0.395449	0.663199	0.625774	Ak7
GO_BP_m3	GO:000670	steroid cata	1/539	22/23843	0.395449	0.663199	0.625774	Ugt1a7c
GO_BP_m3	GO:000683	serotonin t	1/539	22/23843	0.395449	0.663199	0.625774	Gpm6b
GO_BP_m3	GO:000706	regulation	1/539	22/23843	0.395449	0.663199	0.625774	Axin2
GO_BP_m3	GO:000714	male meios	1/539	22/23843	0.395449	0.663199	0.625774	Mov10l1
GO_BP_m3	GO:000726	nitric oxide	1/539	22/23843	0.395449	0.663199	0.625774	Rasd1
GO_BP_m3	GO:000853	respiratory	1/539	22/23843	0.395449	0.663199	0.625774	Bcs1l
GO_BP_m3	GO:001587	norepineph	1/539	22/23843	0.395449	0.663199	0.625774	Oxt
GO_BP_m3	GO:001820	peptidyl-gl	1/539	22/23843	0.395449	0.663199	0.625774	Ttll4
GO_BP_m3	GO:002154	subpallium	1/539	22/23843	0.395449	0.663199	0.625774	Mkks
GO_BP_m3	GO:003025	growth hor	1/539	22/23843	0.395449	0.663199	0.625774	Ghrhr
GO_BP_m3	GO:003275	positive reg	1/539	22/23843	0.395449	0.663199	0.625774	Prkcz
GO_BP_m3	GO:003289	negative re	1/539	22/23843	0.395449	0.663199	0.625774	Ccl5
GO_BP_m3	GO:003440	response to	1/539	22/23843	0.395449	0.663199	0.625774	Klf2
GO_BP_m3	GO:003502	negative re	1/539	22/23843	0.395449	0.663199	0.625774	Scai
GO_BP_m3	GO:003563	response to	1/539	22/23843	0.395449	0.663199	0.625774	Gsta2
GO_BP_m3	GO:004202	protein refo	1/539	22/23843	0.395449	0.663199	0.625774	Bag5
GO_BP_m3	GO:004257	retinoic aci	1/539	22/23843	0.395449	0.663199	0.625774	Lcn5
GO_BP_m3	GO:004349	regulation	1/539	22/23843	0.395449	0.663199	0.625774	Gnl3l
GO_BP_m3	GO:004594	positive reg	1/539	22/23843	0.395449	0.663199	0.625774	Ippk
GO_BP_m3	GO:004833	paraxial me	1/539	22/23843	0.395449	0.663199	0.625774	Foxc2
GO_BP_m3	GO:005104	regulation	1/539	22/23843	0.395449	0.663199	0.625774	Pacsin3
GO_BP_m3	GO:005188	mitochond	1/539	22/23843	0.395449	0.663199	0.625774	Lrrk2
GO_BP_m3	GO:006043	trachea dev	1/539	22/23843	0.395449	0.663199	0.625774	Foxf1
GO_BP_m3	GO:006060	branch elon	1/539	22/23843	0.395449	0.663199	0.625774	Areg
GO_BP_m3	GO:007023	positive reg	1/539	22/23843	0.395449	0.663199	0.625774	Ccl5
GO_BP_m3	GO:007121	cellular res	1/539	22/23843	0.395449	0.663199	0.625774	Ankzf1
GO_BP_m3	GO:007187	cellular res	1/539	22/23843	0.395449	0.663199	0.625774	Lrrk2
GO_BP_m3	GO:007227	metanephr	1/539	22/23843	0.395449	0.663199	0.625774	Hes1
GO_BP_m3	GO:190027	positive reg	1/539	22/23843	0.395449	0.663199	0.625774	Ptpn5
GO_BP_m3	GO:190074	positive reg	1/539	22/23843	0.395449	0.663199	0.625774	Bmp2
GO_BP_m3	GO:190364	regulation	1/539	22/23843	0.395449	0.663199	0.625774	Lrrk2
GO_BP_m3	GO:190386	positive reg	1/539	22/23843	0.395449	0.663199	0.625774	Syt4
GO_BP_m3	GO:004426	cellular car	7/539	266/23843	0.395833	0.663585	0.626138	B3gnt6/Fu
GO_BP_m3	GO:005086	negative re	5/539	183/23843	0.39828	0.667427	0.629763	Abr/Btn1a1
GO_BP_m3	GO:000733	single fertil	4/539	142/23843	0.400378	0.66986	0.632059	Adam24/C
GO_BP_m3	GO:000914	nucleoside	4/539	142/23843	0.400378	0.66986	0.632059	Ak7/Bcl2l1/
GO_BP_m3	GO:004801	phosphatic	4/539	142/23843	0.400378	0.66986	0.632059	Ccl5/Exoc1
GO_BP_m3	GO:000602	aminoglyca	3/539	101/23843	0.400512	0.66986	0.632059	B3gnt6/Itih
GO_BP_m3	GO:000715	homophilic	3/539	101/23843	0.400512	0.66986	0.632059	Cdh26/Dsg
GO_BP_m3	GO:000695	humoral im	9/539	352/23843	0.401359	0.670803	0.632949	Aire/Cd46/
GO_BP_m3	GO:001810	peptidyl-ty	8/539	310/23843	0.402458	0.670803	0.632949	Areg/Ccl5/

GO_BP_m3	GO:000322	ventricular	2/539	61/23843	0.40255	0.670803	0.632949	Foxc2/Tgfb
GO_BP_m3	GO:001017	body morp	2/539	61/23843	0.40255	0.670803	0.632949	Cdon/Ihh
GO_BP_m3	GO:001644	somatic div	2/539	61/23843	0.40255	0.670803	0.632949	Exosc6/Mir
GO_BP_m3	GO:003085	positive reg	2/539	61/23843	0.40255	0.670803	0.632949	Prkch/Ptch
GO_BP_m3	GO:200123	positive reg	2/539	61/23843	0.40255	0.670803	0.632949	Pdia3/Wwc
GO_BP_m3	GO:005125	protein pol	7/539	268/23843	0.40322	0.670803	0.632949	Mkks/Map
GO_BP_m3	GO:00091	cyclic nucle	4/539	143/23843	0.405476	0.670803	0.632949	Avp/Ghrhr
GO_BP_m3	GO:003085	regulation	4/539	143/23843	0.405476	0.670803	0.632949	Hes1/Prkch
GO_BP_m3	GO:200005	regulation	4/539	143/23843	0.405476	0.670803	0.632949	Bag5/Lrrk2
GO_BP_m3	GO:000195	regulation	3/539	102/23843	0.406592	0.670803	0.632949	Gpm6b/Ple
GO_BP_m3	GO:000682	chloride tra	3/539	102/23843	0.406592	0.670803	0.632949	Clcn1/P2ry
GO_BP_m3	GO:003355	unsaturate	3/539	102/23843	0.406592	0.670803	0.632949	Avp/Cyp2c
GO_BP_m3	GO:004851	rhythmic p	7/539	269/23843	0.406912	0.670803	0.632949	Atf5/Ghrhr
GO_BP_m3	GO:190303	regulation	7/539	269/23843	0.406912	0.670803	0.632949	Btn1a1/Ccl
GO_BP_m3	GO:004218	cellular ket	5/539	185/23843	0.407222	0.670803	0.632949	Avp/Bmp2
GO_BP_m3	GO:001003	response to	11/539	439/23843	0.407234	0.670803	0.632949	Ankzf1/Cry
GO_BP_m3	GO:007137	cellular res	6/539	227/23843	0.407469	0.670803	0.632949	Foxc2/Ghrh
GO_BP_m3	GO:000073	DNA catab	1/539	23/23843	0.409128	0.670803	0.632949	Dnase1l3
GO_BP_m3	GO:000272	regulation	1/539	23/23843	0.409128	0.670803	0.632949	Prkcz
GO_BP_m3	GO:00029	negative re	1/539	23/23843	0.409128	0.670803	0.632949	Mir106b
GO_BP_m3	GO:000341	endochond	1/539	23/23843	0.409128	0.670803	0.632949	Col27a1
GO_BP_m3	GO:00062	mismatch r	1/539	23/23843	0.409128	0.670803	0.632949	Axin2
GO_BP_m3	GO:000821	glucocortic	1/539	23/23843	0.409128	0.670803	0.632949	Bmp2
GO_BP_m3	GO:001657	histone de	1/539	23/23843	0.409128	0.670803	0.632949	Epop
GO_BP_m3	GO:001904	modulatior	1/539	23/23843	0.409128	0.670803	0.632949	Bcl2l1
GO_BP_m3	GO:003014	sphingolipi	1/539	23/23843	0.409128	0.670803	0.632949	Enpp7
GO_BP_m3	GO:003164	heat gener	1/539	23/23843	0.409128	0.670803	0.632949	Ccl5
GO_BP_m3	GO:003237	positive reg	1/539	23/23843	0.409128	0.670803	0.632949	Ptch1
GO_BP_m3	GO:003237	positive reg	1/539	23/23843	0.409128	0.670803	0.632949	Ptch1
GO_BP_m3	GO:00341	negative re	1/539	23/23843	0.409128	0.670803	0.632949	Abr
GO_BP_m3	GO:00430	cellular me	1/539	23/23843	0.409128	0.670803	0.632949	Fuk
GO_BP_m3	GO:004357	regulation	1/539	23/23843	0.409128	0.670803	0.632949	Nlgn1
GO_BP_m3	GO:00482	behavioral	1/539	23/23843	0.409128	0.670803	0.632949	Tacr1
GO_BP_m3	GO:00484	sympatheti	1/539	23/23843	0.409128	0.670803	0.632949	Tfap2b
GO_BP_m3	GO:00487	animal org	1/539	23/23843	0.409128	0.670803	0.632949	Bmp2
GO_BP_m3	GO:006004	regulation	1/539	23/23843	0.409128	0.670803	0.632949	Fam170b
GO_BP_m3	GO:00611	mRNA des	1/539	23/23843	0.409128	0.670803	0.632949	Hnrnpr
GO_BP_m3	GO:007131	cellular res	1/539	23/23843	0.409128	0.670803	0.632949	Bcl2l1
GO_BP_m3	GO:007167	positive reg	1/539	23/23843	0.409128	0.670803	0.632949	Ccl5
GO_BP_m3	GO:00718	cellular res	1/539	23/23843	0.409128	0.670803	0.632949	Lrrk2
GO_BP_m3	GO:00718	response to	1/539	23/23843	0.409128	0.670803	0.632949	Lrrk2
GO_BP_m3	GO:00722	cell differen	1/539	23/23843	0.409128	0.670803	0.632949	Tcf21
GO_BP_m3	GO:00722	metanephr	1/539	23/23843	0.409128	0.670803	0.632949	Hes1
GO_BP_m3	GO:009034	negative re	1/539	23/23843	0.409128	0.670803	0.632949	Twist1
GO_BP_m3	GO:00971	neuronal st	1/539	23/23843	0.409128	0.670803	0.632949	Hes1
GO_BP_m3	GO:190307	negative re	1/539	23/23843	0.409128	0.670803	0.632949	Bcl2l1
GO_BP_m3	GO:190367	negative re	1/539	23/23843	0.409128	0.670803	0.632949	Klf2
GO_BP_m3	GO:19047	positive reg	1/539	23/23843	0.409128	0.670803	0.632949	Hpgd

GO_BP_m3	GO:200075	negative re	1/539	23/23843	0.409128	0.670803	0.632949	Twist1
GO_BP_m3	GO:000636	transcriptic	2/539	62/23843	0.410468	0.670803	0.632949	Gtf2e1/Me
GO_BP_m3	GO:001591	phospholip	2/539	62/23843	0.410468	0.670803	0.632949	Prelid3a/Tr
GO_BP_m3	GO:004514	homologou	2/539	62/23843	0.410468	0.670803	0.632949	Ankle1/Ccc
GO_BP_m3	GO:005186	protein aut	2/539	62/23843	0.410468	0.670803	0.632949	Lrrk2/Uhrf1
GO_BP_m3	GO:005192	negative re	2/539	62/23843	0.410468	0.670803	0.632949	Hes1/Pacsi
GO_BP_m3	GO:006004	retina mor	2/539	62/23843	0.410468	0.670803	0.632949	Cdon/Ihh
GO_BP_m3	GO:190126	carbohydra	2/539	62/23843	0.410468	0.670803	0.632949	Slc25a17/S
GO_BP_m3	GO:190367	regulation	2/539	62/23843	0.410468	0.670803	0.632949	Foxc2/Klf2
GO_BP_m3	GO:003017	negative re	4/539	144/23843	0.410566	0.670803	0.632949	Axin2/Bmp
GO_BP_m3	GO:000728	germ cell c	7/539	270/23843	0.410603	0.670803	0.632949	Bcl2l1/Cats
GO_BP_m3	GO:005159	response t	3/539	103/23843	0.412653	0.673278	0.635285	Kcnmb4/N
GO_BP_m3	GO:006075	regulation	3/539	103/23843	0.412653	0.673278	0.635285	C1qtnf4/Pt
GO_BP_m3	GO:001821	peptidyl-ty	8/539	313/23843	0.412745	0.673278	0.635285	Areg/Ccl5/
GO_BP_m3	GO:190129	nucleoside	8/539	313/23843	0.412745	0.673278	0.635285	Ak7/Avp/B
GO_BP_m3	GO:004211	T cell activa	12/539	484/23843	0.413548	0.674332	0.636279	Aire/Btn1a
GO_BP_m3	GO:004801	inositol lipi	4/539	145/23843	0.415647	0.677101	0.638892	Ccl5/Exoc1
GO_BP_m3	GO:000320	cardiac cha	5/539	187/23843	0.416147	0.677101	0.638892	Foxc2/Foxf
GO_BP_m3	GO:004470	multi-mult	5/539	187/23843	0.416147	0.677101	0.638892	Ggn/Hmx3
GO_BP_m3	GO:000690	phagocyto	8/539	314/23843	0.416173	0.677101	0.638892	Abr/Arhga
GO_BP_m3	GO:005072	regulation	8/539	314/23843	0.416173	0.677101	0.638892	Abr/Ccl5/C
GO_BP_m3	GO:000991	hormone t	9/539	357/23843	0.417437	0.677101	0.638892	Ccl5/Ghrhr
GO_BP_m3	GO:004545	cell redox	2/539	63/23843	0.418334	0.677101	0.638892	Dld/Pdia3
GO_BP_m3	GO:190247	chloride tra	2/539	63/23843	0.418334	0.677101	0.638892	Clcn1/Slc12
GO_BP_m3	GO:000913	nucleoside	3/539	104/23843	0.418694	0.677101	0.638892	Ak7/Hk1/Ie
GO_BP_m3	GO:003000	cellular mo	3/539	104/23843	0.418694	0.677101	0.638892	Avp/Lrrk2/
GO_BP_m3	GO:004870	embryonic	3/539	104/23843	0.418694	0.677101	0.638892	Foxc2/Tgfb
GO_BP_m3	GO:009775	negative re	3/539	104/23843	0.418694	0.677101	0.638892	Avp/Mkks/
GO_BP_m3	GO:005178	regulation	5/539	188/23843	0.420601	0.677101	0.638892	Gpr3/Mad2
GO_BP_m3	GO:003018	B cell differ	4/539	146/23843	0.420719	0.677101	0.638892	Gm13287/
GO_BP_m3	GO:004341	macromole	7/539	273/23843	0.421668	0.677101	0.638892	Trmo/Ctr9/
GO_BP_m3	GO:000182	trophectod	1/539	24/23843	0.422498	0.677101	0.638892	Ctr9
GO_BP_m3	GO:000233	mature B c	1/539	24/23843	0.422498	0.677101	0.638892	Nkx2-3
GO_BP_m3	GO:000308	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Ier3
GO_BP_m3	GO:000692	inflammato	1/539	24/23843	0.422498	0.677101	0.638892	Ccl5
GO_BP_m3	GO:000906	aspartate f	1/539	24/23843	0.422498	0.677101	0.638892	Thnsl2
GO_BP_m3	GO:001061	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Ctdp1
GO_BP_m3	GO:001093	regulation	1/539	24/23843	0.422498	0.677101	0.638892	Ucn
GO_BP_m3	GO:001482	vascular sn	1/539	24/23843	0.422498	0.677101	0.638892	Mkks
GO_BP_m3	GO:002188	olfactory b	1/539	24/23843	0.422498	0.677101	0.638892	Atf5
GO_BP_m3	GO:003020	heparan su	1/539	24/23843	0.422498	0.677101	0.638892	Ndst2
GO_BP_m3	GO:003057	collagen ca	1/539	24/23843	0.422498	0.677101	0.638892	Prtn3
GO_BP_m3	GO:004205	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Ptprf
GO_BP_m3	GO:004504	protein tar	1/539	24/23843	0.422498	0.677101	0.638892	Pmm1
GO_BP_m3	GO:005099	positive re	1/539	24/23843	0.422498	0.677101	0.638892	Twist1
GO_BP_m3	GO:005176	nitric-oxide	1/539	24/23843	0.422498	0.677101	0.638892	Lrrk2
GO_BP_m3	GO:005176	regulation	1/539	24/23843	0.422498	0.677101	0.638892	Lrrk2
GO_BP_m3	GO:005178	response t	1/539	24/23843	0.422498	0.677101	0.638892	Ankzf1

GO_BP_m3	GO:005502	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Ctdp1
GO_BP_m3	GO:00600	reflex	1/539	24/23843	0.422498	0.677101	0.638892	Satb1
GO_BP_m3	GO:006111	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Ctdp1
GO_BP_m3	GO:00614	establishm	1/539	24/23843	0.422498	0.677101	0.638892	Cela2a
GO_BP_m3	GO:00705	mitochond	1/539	24/23843	0.422498	0.677101	0.638892	Bcl2l1
GO_BP_m3	GO:00713	cellular res	1/539	24/23843	0.422498	0.677101	0.638892	Myod1
GO_BP_m3	GO:00718	response t	1/539	24/23843	0.422498	0.677101	0.638892	Lrrk2
GO_BP_m3	GO:009002	regulation	1/539	24/23843	0.422498	0.677101	0.638892	Ccl5
GO_BP_m3	GO:19017	regulation	1/539	24/23843	0.422498	0.677101	0.638892	Myod1
GO_BP_m3	GO:19019	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Twist1
GO_BP_m3	GO:19022	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Bcl2l1
GO_BP_m3	GO:190301	regulation	1/539	24/23843	0.422498	0.677101	0.638892	Tmem119
GO_BP_m3	GO:190357	negative re	1/539	24/23843	0.422498	0.677101	0.638892	Ier3
GO_BP_m3	GO:200117	positive re	1/539	24/23843	0.422498	0.677101	0.638892	Bcl2l1
GO_BP_m3	GO:00347	regulation	11/539	445/23843	0.424559	0.67964	0.641287	Catsper4/C
GO_BP_m3	GO:003031	osteoclast	3/539	105/23843	0.424715	0.67964	0.641287	Ccl5/Tmem
GO_BP_m3	GO:00349	histone lysi	3/539	105/23843	0.424715	0.67964	0.641287	Ctr9/Kdm4
GO_BP_m3	GO:006101	regulation	3/539	105/23843	0.424715	0.67964	0.641287	Axin2/Hnr
GO_BP_m3	GO:00756	embryo im	2/539	64/23843	0.426146	0.680661	0.642251	Ggn/Hmx3
GO_BP_m3	GO:003237	positive re	2/539	64/23843	0.426146	0.680661	0.642251	Oxt/Ptch1
GO_BP_m3	GO:00433	response t	2/539	64/23843	0.426146	0.680661	0.642251	Gm13287/
GO_BP_m3	GO:004682	positive re	2/539	64/23843	0.426146	0.680661	0.642251	Lrrk2/Ptpn
GO_BP_m3	GO:006042	lung morp	2/539	64/23843	0.426146	0.680661	0.642251	Foxf1/Tcf2
GO_BP_m3	GO:00107	regulation	8/539	317/23843	0.426451	0.680894	0.642471	Caprin1/C
GO_BP_m3	GO:00026	negative re	11/539	448/23843	0.433219	0.685259	0.64659	Abr/Btn1a
GO_BP_m3	GO:00068	lipid transp	8/539	319/23843	0.433294	0.685259	0.64659	Oxt/Ptch1/
GO_BP_m3	GO:00516	establishm	10/539	405/23843	0.433452	0.685259	0.64659	Ankle1/Ap
GO_BP_m3	GO:00022	T cell differ	2/539	65/23843	0.433903	0.685259	0.64659	Cd46/Prkc
GO_BP_m3	GO:00025	somatic div	2/539	65/23843	0.433903	0.685259	0.64659	Exosc6/Mi
GO_BP_m3	GO:000314	embryonic	2/539	65/23843	0.433903	0.685259	0.64659	Hes1/Ihh
GO_BP_m3	GO:00063	DNA alkyla	2/539	65/23843	0.433903	0.685259	0.64659	Mov10l1/P
GO_BP_m3	GO:00063	DNA meth	2/539	65/23843	0.433903	0.685259	0.64659	Mov10l1/P
GO_BP_m3	GO:000651	protein m	2/539	65/23843	0.433903	0.685259	0.64659	Ctr9/Uhrf1
GO_BP_m3	GO:00074	neuroblast	2/539	65/23843	0.433903	0.685259	0.64659	Lrrk2/Sox1
GO_BP_m3	GO:001644	somatic cel	2/539	65/23843	0.433903	0.685259	0.64659	Exosc6/Mi
GO_BP_m3	GO:00350	axoneme a	2/539	65/23843	0.433903	0.685259	0.64659	Ak7/Cep13
GO_BP_m3	GO:000151	prostaglan	1/539	25/23843	0.435566	0.685259	0.64659	Avp
GO_BP_m3	GO:00017	organ indu	1/539	25/23843	0.435566	0.685259	0.64659	Bmp2
GO_BP_m3	GO:001074	macrophag	1/539	25/23843	0.435566	0.685259	0.64659	Prkch
GO_BP_m3	GO:00108	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Bmp2
GO_BP_m3	GO:003114	SCF-depe	1/539	25/23843	0.435566	0.685259	0.64659	Ccnf
GO_BP_m3	GO:003327	response t	1/539	25/23843	0.435566	0.685259	0.64659	Pdia3
GO_BP_m3	GO:00344	microtubul	1/539	25/23843	0.435566	0.685259	0.64659	Ccdc187
GO_BP_m3	GO:004337	positive re	1/539	25/23843	0.435566	0.685259	0.64659	Prkcz
GO_BP_m3	GO:00459	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Bmp2
GO_BP_m3	GO:00463	monosacch	1/539	25/23843	0.435566	0.685259	0.64659	Hk1
GO_BP_m3	GO:00464	prostanoid	1/539	25/23843	0.435566	0.685259	0.64659	Avp
GO_BP_m3	GO:005077	RNA desta	1/539	25/23843	0.435566	0.685259	0.64659	Hnrnpr

GO_BP_m3	GO:00508	defense re	1/539	25/23843	0.435566	0.685259	0.64659	Hamp2
GO_BP_m3	GO:00514	positive re	1/539	25/23843	0.435566	0.685259	0.64659	Trib2
GO_BP_m3	GO:00514	negative re	1/539	25/23843	0.435566	0.685259	0.64659	S1pr1
GO_BP_m3	GO:00600	Sertoli cell	1/539	25/23843	0.435566	0.685259	0.64659	Tcf21
GO_BP_m3	GO:00711	protein K4	1/539	25/23843	0.435566	0.685259	0.64659	Otud3
GO_BP_m3	GO:00718	podosome	1/539	25/23843	0.435566	0.685259	0.64659	Hck
GO_BP_m3	GO:007267	eosinophil	1/539	25/23843	0.435566	0.685259	0.64659	Ccl5
GO_BP_m3	GO:009014	regulation	1/539	25/23843	0.435566	0.685259	0.64659	Mir539
GO_BP_m3	GO:00988	bone grow	1/539	25/23843	0.435566	0.685259	0.64659	Col27a1
GO_BP_m3	GO:19010	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Lrrk2
GO_BP_m3	GO:19011	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Ptprf
GO_BP_m3	GO:19032	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Lrrk2
GO_BP_m3	GO:19038	regulation	1/539	25/23843	0.435566	0.685259	0.64659	Syt4
GO_BP_m3	GO:19043	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Gnl3l
GO_BP_m3	GO:190437	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Bcl2l1
GO_BP_m3	GO:20010	negative re	1/539	25/23843	0.435566	0.685259	0.64659	Lrrk2
GO_BP_m3	GO:00486	regulation	4/539	149/23843	0.435867	0.68548	0.646798	Ccl5/Hpgd
GO_BP_m3	GO:00007	DNA dama	3/539	107/23843	0.436691	0.685553	0.646867	Fanci/Ier3/
GO_BP_m3	GO:001907	viral genon	3/539	107/23843	0.436691	0.685553	0.646867	Ccl5/Isg20
GO_BP_m3	GO:00466	regulation	3/539	107/23843	0.436691	0.685553	0.646867	Ctdp1/Fox
GO_BP_m3	GO:190382	negative re	3/539	107/23843	0.436691	0.685553	0.646867	Bcl2l1/Gpn
GO_BP_m3	GO:00224	regulation	9/539	363/23843	0.436711	0.685553	0.646867	Bmp2/Btn1
GO_BP_m3	GO:00063	rRNA proc	5/539	192/23843	0.438354	0.687881	0.649064	Dis3/Exosc
GO_BP_m3	GO:00002	mitotic cyt	2/539	66/23843	0.441604	0.690961	0.65197	Ckap2/Rhc
GO_BP_m3	GO:00026	regulation	2/539	66/23843	0.441604	0.690961	0.65197	Exosc6/Mir
GO_BP_m3	GO:00140	positive re	2/539	66/23843	0.441604	0.690961	0.65197	Ccl5/Prr5
GO_BP_m3	GO:00512	centrosom	2/539	66/23843	0.441604	0.690961	0.65197	Ccnf/Cep1
GO_BP_m3	GO:005502	regulation	2/539	66/23843	0.441604	0.690961	0.65197	Ctdp1/Tgf
GO_BP_m3	GO:19030	positive re	2/539	66/23843	0.441604	0.690961	0.65197	Foxc2/Myc
GO_BP_m3	GO:190357	regulation	2/539	66/23843	0.441604	0.690961	0.65197	Bcl2l1/Ier3
GO_BP_m3	GO:190551	non-motile	2/539	66/23843	0.441604	0.690961	0.65197	Cep131/Ml
GO_BP_m3	GO:00000	G2/M tran	3/539	108/23843	0.442644	0.691533	0.652509	Fanci/Ier3/
GO_BP_m3	GO:000597	polysaccha	3/539	108/23843	0.442644	0.691533	0.652509	B3gnt6/Ph
GO_BP_m3	GO:001092	cellular cor	3/539	108/23843	0.442644	0.691533	0.652509	Ihh/Mybph
GO_BP_m3	GO:00064	mRNA cat	5/539	193/23843	0.442774	0.691533	0.652509	Axin2/Dis3
GO_BP_m3	GO:00158	drug trans	5/539	193/23843	0.442774	0.691533	0.652509	Aqp5/Chrn
GO_BP_m3	GO:003011	regulation	7/539	279/23843	0.44373	0.692773	0.65368	Axin2/Bmp
GO_BP_m3	GO:00027	immune re	8/539	323/23843	0.446953	0.692823	0.653727	Btn1a1/Igh
GO_BP_m3	GO:00020	positive re	1/539	26/23843	0.44834	0.692823	0.653727	Sox10
GO_BP_m3	GO:00020	lens morph	1/539	26/23843	0.44834	0.692823	0.653727	Cryaa
GO_BP_m3	GO:00025	tolerance i	1/539	26/23843	0.44834	0.692823	0.653727	Aire
GO_BP_m3	GO:000631	mitotic rec	1/539	26/23843	0.44834	0.692823	0.653727	Ankle1
GO_BP_m3	GO:00068	cell volum	1/539	26/23843	0.44834	0.692823	0.653727	Slc12a7
GO_BP_m3	GO:001474	negative re	1/539	26/23843	0.44834	0.692823	0.653727	Ctdp1
GO_BP_m3	GO:002151	spinal cord	1/539	26/23843	0.44834	0.692823	0.653727	Nkx6-1
GO_BP_m3	GO:003021	hyaluronar	1/539	26/23843	0.44834	0.692823	0.653727	Itih1
GO_BP_m3	GO:00302	apoptotic	1/539	26/23843	0.44834	0.692823	0.653727	Dnase1l3
GO_BP_m3	GO:003031	melanocyt	1/539	26/23843	0.44834	0.692823	0.653727	Sox10

GO_BP_m3	GO:003136	N-terminal	1/539	26/23843	0.44834	0.692823	0.653727	Naa25
GO_BP_m3	GO:003323	regulation	1/539	26/23843	0.44834	0.692823	0.653727	Gnl3l
GO_BP_m3	GO:004506	thymic T ce	1/539	26/23843	0.44834	0.692823	0.653727	Aire
GO_BP_m3	GO:004583	positive reg	1/539	26/23843	0.44834	0.692823	0.653727	Exosc6
GO_BP_m3	GO:004646	membrane	1/539	26/23843	0.44834	0.692823	0.653727	Enpp7
GO_BP_m3	GO:004852	negative re	1/539	26/23843	0.44834	0.692823	0.653727	Ucn
GO_BP_m3	GO:005071	positive reg	1/539	26/23843	0.44834	0.692823	0.653727	Hk1
GO_BP_m3	GO:005092	positive reg	1/539	26/23843	0.44834	0.692823	0.653727	S1pr1
GO_BP_m3	GO:006021	camera-typ	1/539	26/23843	0.44834	0.692823	0.653727	Ihh
GO_BP_m3	GO:006131	cell surface	1/539	26/23843	0.44834	0.692823	0.653727	Bmp2
GO_BP_m3	GO:007148	cellular res	1/539	26/23843	0.44834	0.692823	0.653727	Bcl2l1
GO_BP_m3	GO:009007	foam cell d	1/539	26/23843	0.44834	0.692823	0.653727	Prkch
GO_BP_m3	GO:200031	regulation	1/539	26/23843	0.44834	0.692823	0.653727	Nlgn1
GO_BP_m3	GO:000018	activation c	3/539	109/23843	0.448572	0.692823	0.653727	Bmp2/Grm
GO_BP_m3	GO:000995	dorsal/vent	3/539	109/23843	0.448572	0.692823	0.653727	Axin2/Nkx6
GO_BP_m3	GO:003812	ERBB signa	3/539	109/23843	0.448572	0.692823	0.653727	Areg/Pigr/I
GO_BP_m3	GO:200010	regulation	3/539	109/23843	0.448572	0.692823	0.653727	Ccl5/Mir10
GO_BP_m3	GO:000617	cAMP bios	2/539	67/23843	0.449246	0.692823	0.653727	Avp/Rln3
GO_BP_m3	GO:000640	tRNA modi	2/539	67/23843	0.449246	0.692823	0.653727	Trmo/Rpus
GO_BP_m3	GO:003304	regulation	2/539	67/23843	0.449246	0.692823	0.653727	Mad2l1/Ub
GO_BP_m3	GO:004566	positive reg	2/539	67/23843	0.449246	0.692823	0.653727	Bmp2/Tme
GO_BP_m3	GO:005114	smooth mu	2/539	67/23843	0.449246	0.692823	0.653727	Foxf1/Hes1
GO_BP_m3	GO:009719	execution p	2/539	67/23843	0.449246	0.692823	0.653727	Bcl2l1/Dna
GO_BP_m3	GO:003133	positive reg	8/539	324/23843	0.45036	0.694292	0.655112	Hnrnpr/Lrr
GO_BP_m3	GO:000820	steroid me	7/539	281/23843	0.451055	0.695113	0.655887	Bmp2/Dhc
GO_BP_m3	GO:004232	negative re	11/539	455/23843	0.453394	0.698468	0.659053	2610042L0
GO_BP_m3	GO:005126	protein dep	3/539	110/23843	0.454475	0.699175	0.65972	Ckap2/Car
GO_BP_m3	GO:001604	cell growth	12/539	499/23843	0.454884	0.699175	0.65972	Avp/Cryaa/
GO_BP_m3	GO:009723	cellular res	4/539	153/23843	0.455885	0.699175	0.65972	Ankzf1/Lrrk
GO_BP_m3	GO:000238	mucosal im	2/539	68/23843	0.456829	0.699175	0.65972	Defa27/Pig
GO_BP_m3	GO:000663	fatty acid b	2/539	68/23843	0.456829	0.699175	0.65972	Slc25a17/T
GO_BP_m3	GO:003023	myofibril as	2/539	68/23843	0.456829	0.699175	0.65972	Mybph/Tn
GO_BP_m3	GO:004230	regulation	2/539	68/23843	0.456829	0.699175	0.65972	Lrrk2/Ptpn5
GO_BP_m3	GO:004329	leukocyte c	2/539	68/23843	0.456829	0.699175	0.65972	Abr/Foxf1
GO_BP_m3	GO:004557	mast cell ac	2/539	68/23843	0.456829	0.699175	0.65972	Foxf1/Ptpre
GO_BP_m3	GO:000193	negative re	10/539	413/23843	0.457682	0.699175	0.65972	2610042L0
GO_BP_m3	GO:005085	antigen rec	7/539	283/23843	0.458361	0.699175	0.65972	Btn1a1/Igh
GO_BP_m3	GO:190210	regulation	7/539	283/23843	0.458361	0.699175	0.65972	Ccl5/Cd46/
GO_BP_m3	GO:000037	RNA splicin	6/539	240/23843	0.459461	0.699175	0.65972	Celf5/Ddx4
GO_BP_m3	GO:000039	mRNA splic	6/539	240/23843	0.459461	0.699175	0.65972	Celf5/Ddx4
GO_BP_m3	GO:000749	mesoderm	3/539	111/23843	0.460351	0.699175	0.65972	Foxc2/Foxf
GO_BP_m3	GO:000863	intrinsic ap	3/539	111/23843	0.460351	0.699175	0.65972	Bcl2l1/Fnip
GO_BP_m3	GO:007232	monocarbo	3/539	111/23843	0.460351	0.699175	0.65972	Slc25a17/S
GO_BP_m3	GO:190304	meiotic cel	5/539	197/23843	0.460365	0.699175	0.65972	Ankle1/Ccc
GO_BP_m3	GO:003225	methylatio	8/539	327/23843	0.460561	0.699175	0.65972	Trmo/Armt
GO_BP_m3	GO:000333	metanephr	1/539	27/23843	0.460824	0.699175	0.65972	Hes1
GO_BP_m3	GO:000651	protein qua	1/539	27/23843	0.460824	0.699175	0.65972	Ankzf1
GO_BP_m3	GO:000692	cellular cor	1/539	27/23843	0.460824	0.699175	0.65972	Dnase1l3

GO_BP_m3	GO:00107	regulation	1/539	27/23843	0.460824	0.699175	0.65972	Lrrk2
GO_BP_m3	GO:00215	cell differer	1/539	27/23843	0.460824	0.699175	0.65972	Atxn2
GO_BP_m3	GO:00304	tRNA meth	1/539	27/23843	0.460824	0.699175	0.65972	Trmo
GO_BP_m3	GO:00316	plasminog	1/539	27/23843	0.460824	0.699175	0.65972	Dhcr24
GO_BP_m3	GO:00359	endoderm	1/539	27/23843	0.460824	0.699175	0.65972	Ctr9
GO_BP_m3	GO:00430	positive re	1/539	27/23843	0.460824	0.699175	0.65972	Lrrk2
GO_BP_m3	GO:00487	smooth mu	1/539	27/23843	0.460824	0.699175	0.65972	Ihh
GO_BP_m3	GO:005071	positive re	1/539	27/23843	0.460824	0.699175	0.65972	Hk1
GO_BP_m3	GO:00509	regulation	1/539	27/23843	0.460824	0.699175	0.65972	S1pr1
GO_BP_m3	GO:00511	regulation	1/539	27/23843	0.460824	0.699175	0.65972	Foxf1
GO_BP_m3	GO:00601	positive re	1/539	27/23843	0.460824	0.699175	0.65972	Myod1
GO_BP_m3	GO:006071	labyrinthin	1/539	27/23843	0.460824	0.699175	0.65972	Esx1
GO_BP_m3	GO:00701	protein loc	1/539	27/23843	0.460824	0.699175	0.65972	Gnl3l
GO_BP_m3	GO:00709	protein K1	1/539	27/23843	0.460824	0.699175	0.65972	Ube2c
GO_BP_m3	GO:00713	cellular res	1/539	27/23843	0.460824	0.699175	0.65972	Mir362
GO_BP_m3	GO:00716	regulation	1/539	27/23843	0.460824	0.699175	0.65972	Cd46
GO_BP_m3	GO:00717	membrane	1/539	27/23843	0.460824	0.699175	0.65972	Nlgn1
GO_BP_m3	GO:009734	mitochond	1/539	27/23843	0.460824	0.699175	0.65972	Ier3
GO_BP_m3	GO:190011	regulation	1/539	27/23843	0.460824	0.699175	0.65972	Bcl2l1
GO_BP_m3	GO:19022	regulation	1/539	27/23843	0.460824	0.699175	0.65972	Lrrk2
GO_BP_m3	GO:00486	smooth mu	4/539	154/23843	0.460853	0.699175	0.65972	Ccl5/Hpgd
GO_BP_m3	GO:000037	RNA splicir	6/539	241/23843	0.463421	0.70225	0.662622	Celf5/Ddx4
GO_BP_m3	GO:003367	negative re	6/539	241/23843	0.463421	0.70225	0.662622	Dusp26/Lr
GO_BP_m3	GO:00015	regulation	10/539	415/23843	0.463718	0.70225	0.662622	Avp/Cryaa
GO_BP_m3	GO:000027	polysaccha	2/539	69/23843	0.464351	0.70225	0.662622	B3gnt6/Ph
GO_BP_m3	GO:00022	organ or ti	2/539	69/23843	0.464351	0.70225	0.662622	Defa27/Pig
GO_BP_m3	GO:00421	negative re	2/539	69/23843	0.464351	0.70225	0.662622	Btn1a1/Ihh
GO_BP_m3	GO:004864	animal org	2/539	69/23843	0.464351	0.70225	0.662622	Axin2/Hes1
GO_BP_m3	GO:00601	regulation	2/539	69/23843	0.464351	0.70225	0.662622	Ccl5/Prkcz
GO_BP_m3	GO:19019	positive re	2/539	69/23843	0.464351	0.70225	0.662622	Neurog1/U
GO_BP_m3	GO:19037	positive re	5/539	198/23843	0.464739	0.702588	0.66294	Ccl5/Cd46/
GO_BP_m3	GO:00031	endotheliu	3/539	112/23843	0.4662	0.703559	0.663857	Foxc2/Rho
GO_BP_m3	GO:00066	icosanoid r	3/539	112/23843	0.4662	0.703559	0.663857	Avp/Cyp2c
GO_BP_m3	GO:00080	tRNA proc	3/539	112/23843	0.4662	0.703559	0.663857	Trmo/Pus7
GO_BP_m3	GO:00461	alcohol bio	3/539	112/23843	0.4662	0.703559	0.663857	Dhcr24/Ipp
GO_BP_m3	GO:19030	positive re	3/539	112/23843	0.4662	0.703559	0.663857	Lrrk2/Rnf1
GO_BP_m3	GO:00487	cardiac mu	6/539	242/23843	0.467373	0.703723	0.664012	Bmp2/Ctd
GO_BP_m3	GO:00305	intracellula	5/539	199/23843	0.469101	0.703723	0.664012	Ghrhr/Kdm
GO_BP_m3	GO:20000	regulation	5/539	199/23843	0.469101	0.703723	0.664012	Bmp2/Fox
GO_BP_m3	GO:00072	spermatid	4/539	156/23843	0.470742	0.703723	0.664012	Catsper4/C
GO_BP_m3	GO:004677	protein aut	6/539	243/23843	0.471318	0.703723	0.664012	Hck/Hk1/L
GO_BP_m3	GO:00017	morphoge	2/539	70/23843	0.471812	0.703723	0.664012	Crb3/Foxf1
GO_BP_m3	GO:00060	glycolytic	2/539	70/23843	0.471812	0.703723	0.664012	Hk1/Ier3
GO_BP_m3	GO:004211	macropha	2/539	70/23843	0.471812	0.703723	0.664012	Lrrk2/Tff2
GO_BP_m3	GO:00454	bone resor	2/539	70/23843	0.471812	0.703723	0.664012	Ihh/S1pr1
GO_BP_m3	GO:004874	muscle fibe	2/539	70/23843	0.471812	0.703723	0.664012	Flnc/Myod
GO_BP_m3	GO:19018	negative re	2/539	70/23843	0.471812	0.703723	0.664012	Ckap2/Car
GO_BP_m3	GO:200024	positive re	2/539	70/23843	0.471812	0.703723	0.664012	Fam170b/

GO_BP_m3	GO:000189	embryonic	3/539	113/23843	0.472021	0.703723	0.664012	Esx1/Hes1/
GO_BP_m3	GO:003110	microtubul	3/539	113/23843	0.472021	0.703723	0.664012	Ckap2/Ma
GO_BP_m3	GO:005085	T cell rece	3/539	113/23843	0.472021	0.703723	0.664012	Btn1a1/Ca
GO_BP_m3	GO:000183	blastocyst	1/539	28/23843	0.473027	0.703723	0.664012	Ctr9
GO_BP_m3	GO:000194	lymph vess	1/539	28/23843	0.473027	0.703723	0.664012	Foxc2
GO_BP_m3	GO:000692	substrate-	1/539	28/23843	0.473027	0.703723	0.664012	Fmnl1
GO_BP_m3	GO:000753	sex determ	1/539	28/23843	0.473027	0.703723	0.664012	Tcf21
GO_BP_m3	GO:000930	rRNA trans	1/539	28/23843	0.473027	0.703723	0.664012	Ippk
GO_BP_m3	GO:001075	regulation	1/539	28/23843	0.473027	0.703723	0.664012	Ccl5
GO_BP_m3	GO:001624	negative re	1/539	28/23843	0.473027	0.703723	0.664012	Lrrk2
GO_BP_m3	GO:002151	spinal cord	1/539	28/23843	0.473027	0.703723	0.664012	Nkx6-1
GO_BP_m3	GO:002187	forebrain r	1/539	28/23843	0.473027	0.703723	0.664012	Bmp2
GO_BP_m3	GO:003129	replication	1/539	28/23843	0.473027	0.703723	0.664012	Mms22l
GO_BP_m3	GO:003267	regulation	1/539	28/23843	0.473027	0.703723	0.664012	Prkcz
GO_BP_m3	GO:003356	regulation	1/539	28/23843	0.473027	0.703723	0.664012	Cela2a
GO_BP_m3	GO:004203	negative re	1/539	28/23843	0.473027	0.703723	0.664012	Trib2
GO_BP_m3	GO:004400	modificatic	1/539	28/23843	0.473027	0.703723	0.664012	Bcl2l1
GO_BP_m3	GO:004455	secondary	1/539	28/23843	0.473027	0.703723	0.664012	Trpc1
GO_BP_m3	GO:004567	negative re	1/539	28/23843	0.473027	0.703723	0.664012	Tmem178
GO_BP_m3	GO:005135	negative re	1/539	28/23843	0.473027	0.703723	0.664012	Lrrk2
GO_BP_m3	GO:006003	pericardiu	1/539	28/23843	0.473027	0.703723	0.664012	Bmp2
GO_BP_m3	GO:006011	auditory re	1/539	28/23843	0.473027	0.703723	0.664012	Whrn
GO_BP_m3	GO:006044	branching	1/539	28/23843	0.473027	0.703723	0.664012	Areg
GO_BP_m3	GO:007160	transformi	1/539	28/23843	0.473027	0.703723	0.664012	Cd46
GO_BP_m3	GO:007259	establishm	1/539	28/23843	0.473027	0.703723	0.664012	Pmm1
GO_BP_m3	GO:190204	negative re	1/539	28/23843	0.473027	0.703723	0.664012	Bcl2l1
GO_BP_m3	GO:190217	regulation	1/539	28/23843	0.473027	0.703723	0.664012	Bag5
GO_BP_m3	GO:190274	positive re	1/539	28/23843	0.473027	0.703723	0.664012	Carmil2
GO_BP_m3	GO:200019	regulation	1/539	28/23843	0.473027	0.703723	0.664012	Oxt
GO_BP_m3	GO:000694	striated m	4/539	157/23843	0.475661	0.707398	0.667479	Mybph/Tn
GO_BP_m3	GO:001993	second-m	8/539	332/23843	0.477478	0.708992	0.668984	Adm2/Ghr
GO_BP_m3	GO:001095	negative re	5/539	201/23843	0.477793	0.708992	0.668984	9230104L0
GO_BP_m3	GO:003157	DNA integ	3/539	114/23843	0.477812	0.708992	0.668984	Fanci/Ier3/
GO_BP_m3	GO:004217	negative re	3/539	114/23843	0.477812	0.708992	0.668984	Bag5/Grin
GO_BP_m3	GO:005115	regulation	3/539	114/23843	0.477812	0.708992	0.668984	Bmp2/Ctd
GO_BP_m3	GO:005073	regulation	6/539	245/23843	0.479183	0.708992	0.668984	Areg/Ccl5/
GO_BP_m3	GO:000220	somatic di	2/539	71/23843	0.47921	0.708992	0.668984	Exosc6/Mi
GO_BP_m3	GO:000675	ATP gener	2/539	71/23843	0.47921	0.708992	0.668984	Hk1/Ier3
GO_BP_m3	GO:001974	secondary	2/539	71/23843	0.47921	0.708992	0.668984	Trpc1/Ugt1
GO_BP_m3	GO:003463	cellular ca	2/539	71/23843	0.47921	0.708992	0.668984	B3gnt6/Ph
GO_BP_m3	GO:004273	embryonic	2/539	71/23843	0.47921	0.708992	0.668984	Ihh/Twist1
GO_BP_m3	GO:004362	response t	2/539	71/23843	0.47921	0.708992	0.668984	Ghrhr/Tgf
GO_BP_m3	GO:005188	regulation	2/539	71/23843	0.47921	0.708992	0.668984	Bcl2l1/Lrrk
GO_BP_m3	GO:007238	organelle t	2/539	71/23843	0.47921	0.708992	0.668984	Ap3s1/Prk
GO_BP_m3	GO:190331	positive re	2/539	71/23843	0.47921	0.708992	0.668984	Hnrnpr/Na
GO_BP_m3	GO:004533	cellular res	4/539	158/23843	0.480563	0.710506	0.670412	Dlat/Dld/S
GO_BP_m3	GO:005110	negative re	4/539	158/23843	0.480563	0.710506	0.670412	Gnl3l/Hes1
GO_BP_m3	GO:004340	regulation	7/539	290/23843	0.483757	0.710986	0.670864	Bmp2/Grm

GO_BP_m3	GO:002261	ribonucleo	10/539	422/23843	0.484751	0.710986	0.670864	Atxn2/Dis3
GO_BP_m3	GO:000047	maturation	1/539	29/23843	0.484954	0.710986	0.670864	Nsa2
GO_BP_m3	GO:000177	microglial (	1/539	29/23843	0.484954	0.710986	0.670864	Lrrk2
GO_BP_m3	GO:00020S	positive re(	1/539	29/23843	0.484954	0.710986	0.670864	Ptpn5
GO_BP_m3	GO:00026S	regulation	1/539	29/23843	0.484954	0.710986	0.670864	Abr
GO_BP_m3	GO:00033(	type B pan	1/539	29/23843	0.484954	0.710986	0.670864	Nkx6-1
GO_BP_m3	GO:00060S	tricarboxyli	1/539	29/23843	0.484954	0.710986	0.670864	Dlat
GO_BP_m3	GO:00069(	vesicle tar(	1/539	29/23843	0.484954	0.710986	0.670864	Nlgn1
GO_BP_m3	GO:00108(	positive re(	1/539	29/23843	0.484954	0.710986	0.670864	Trim6
GO_BP_m3	GO:001092	positive re(	1/539	29/23843	0.484954	0.710986	0.670864	Bmp2
GO_BP_m3	GO:00324:	negative re	1/539	29/23843	0.484954	0.710986	0.670864	Bag5
GO_BP_m3	GO:00327ɛ	positive re(	1/539	29/23843	0.484954	0.710986	0.670864	Ctr9
GO_BP_m3	GO:00329Ɛ	inositol ph(	1/539	29/23843	0.484954	0.710986	0.670864	Ippk
GO_BP_m3	GO:003411	regulation	1/539	29/23843	0.484954	0.710986	0.670864	Ccl5
GO_BP_m3	GO:003462	cellular pro	1/539	29/23843	0.484954	0.710986	0.670864	Exoc1
GO_BP_m3	GO:00358ɛ	vascular sn	1/539	29/23843	0.484954	0.710986	0.670864	Hes1
GO_BP_m3	GO:00451ɛ	regulation	1/539	29/23843	0.484954	0.710986	0.670864	Ghrhr
GO_BP_m3	GO:004567	positive re(	1/539	29/23843	0.484954	0.710986	0.670864	Ccl5
GO_BP_m3	GO:19017S	negative re	1/539	29/23843	0.484954	0.710986	0.670864	Twist1
GO_BP_m3	GO:200051	positive re(	1/539	29/23843	0.484954	0.710986	0.670864	Prkcz
GO_BP_m3	GO:00070ɛ	regulation	4/539	159/23843	0.485447	0.710986	0.670864	Mad2l1/Ne
GO_BP_m3	GO:000864	carbohydra	4/539	159/23843	0.485447	0.710986	0.670864	Gip/Prkcz/S
GO_BP_m3	GO:00352S	regulation	4/539	159/23843	0.485447	0.710986	0.670864	Avp/Mkks/
GO_BP_m3	GO:009774	regulation	4/539	159/23843	0.485447	0.710986	0.670864	Avp/Mkks/
GO_BP_m3	GO:00148Ɛ	striated mu	2/539	72/23843	0.486543	0.710986	0.670864	Foxc2/Tgfb
GO_BP_m3	GO:00303(	cholesterol	2/539	72/23843	0.486543	0.710986	0.670864	Ptch1/Stx1
GO_BP_m3	GO:00308(	regulation	2/539	72/23843	0.486543	0.710986	0.670864	Avp/Rln3
GO_BP_m3	GO:00422Ɛ	ribosome a	2/539	72/23843	0.486543	0.710986	0.670864	Rpl6l/Nip7
GO_BP_m3	GO:004427	sulfur com(	2/539	72/23843	0.486543	0.710986	0.670864	Dlat/Dld
GO_BP_m3	GO:00506ɛ	regulation	2/539	72/23843	0.486543	0.710986	0.670864	Ccl5/Trim6
GO_BP_m3	GO:00518Ɛ	modificatic	2/539	72/23843	0.486543	0.710986	0.670864	Ccl5/Ctdp1
GO_BP_m3	GO:00701S	chromosor	2/539	72/23843	0.486543	0.710986	0.670864	Ankle1/Ccc
GO_BP_m3	GO:19032(	regulation	2/539	72/23843	0.486543	0.710986	0.670864	Bag5/Lrrk2
GO_BP_m3	GO:000762	locomotory	6/539	247/23843	0.487013	0.710986	0.670864	Avp/Chrna
GO_BP_m3	GO:00159ɛ	energy der	6/539	247/23843	0.487013	0.710986	0.670864	Dlat/Dld/Pl
GO_BP_m3	GO:006054	respiratory	6/539	247/23843	0.487013	0.710986	0.670864	Foxf1/Hes1
GO_BP_m3	GO:00457ɛ	positive re(	9/539	379/23843	0.487685	0.711726	0.671563	Ccl5/Cd46/
GO_BP_m3	GO:000712	meiosis I	3/539	116/23843	0.489306	0.712879	0.672651	Ankle1/Ccc
GO_BP_m3	GO:00105€	regulation	3/539	116/23843	0.489306	0.712879	0.672651	Avp/Bmp2/
GO_BP_m3	GO:00156S	ammonium	3/539	116/23843	0.489306	0.712879	0.672651	Chrna4/Gp
GO_BP_m3	GO:001802	peptidyl-ly	3/539	116/23843	0.489306	0.712879	0.672651	Ctr9/Kdm4
GO_BP_m3	GO:00421(	B cell proli	3/539	116/23843	0.489306	0.712879	0.672651	Gm13287/
GO_BP_m3	GO:00457:	positive re(	5/539	204/23843	0.490741	0.714728	0.674395	Ier3/Lrrk2/
GO_BP_m3	GO:19029(	regulation	8/539	336/23843	0.49092	0.714746	0.674412	Ckap2/Mkk
GO_BP_m3	GO:001591	sterol trans	2/539	73/23843	0.493813	0.716234	0.675816	Ptch1/Stx1
GO_BP_m3	GO:006042	regulation	2/539	73/23843	0.493813	0.716234	0.675816	Ctdp1/Tgfb
GO_BP_m3	GO:006151	myeloid ce	2/539	73/23843	0.493813	0.716234	0.675816	Klf2/L3mbt
GO_BP_m3	GO:19045ɛ	regulation	2/539	73/23843	0.493813	0.716234	0.675816	Lrrk2/Ptpn5

GO_BP_m3	GO:000244	lymphocyt	9/539	381/23843	0.493987	0.716234	0.675816	Aire/Cd46/
GO_BP_m3	GO:005086	regulation	7/539	293/23843	0.494542	0.716234	0.675816	Btn1a1/Ccl
GO_BP_m3	GO:003164	regulation	6/539	249/23843	0.494805	0.716234	0.675816	Bmp2/Gnl3
GO_BP_m3	GO:000675	ATP biosyn	3/539	117/23843	0.495006	0.716234	0.675816	Bcl2l1/Hk1
GO_BP_m3	GO:000761	learning	4/539	161/23843	0.495159	0.716234	0.675816	Grm4/Sgk1
GO_BP_m3	GO:000153	cilium or fl	1/539	30/23843	0.496611	0.716234	0.675816	Mkks
GO_BP_m3	GO:000196	startle resp	1/539	30/23843	0.496611	0.716234	0.675816	Ucn
GO_BP_m3	GO:000282	regulation	1/539	30/23843	0.496611	0.716234	0.675816	Prkcz
GO_BP_m3	GO:000290	regulation	1/539	30/23843	0.496611	0.716234	0.675816	Mir106b
GO_BP_m3	GO:002190	dorsal/vent	1/539	30/23843	0.496611	0.716234	0.675816	Ptch1
GO_BP_m3	GO:003223	negative re	1/539	30/23843	0.496611	0.716234	0.675816	S1pr1
GO_BP_m3	GO:003532	hippo signa	1/539	30/23843	0.496611	0.716234	0.675816	Nf2
GO_BP_m3	GO:004248	regulation	1/539	30/23843	0.496611	0.716234	0.675816	Bmp2
GO_BP_m3	GO:004603	GTP metab	1/539	30/23843	0.496611	0.716234	0.675816	Lrrk2
GO_BP_m3	GO:004801	neurotroph	1/539	30/23843	0.496611	0.716234	0.675816	Ptprf
GO_BP_m3	GO:004867	regulation	1/539	30/23843	0.496611	0.716234	0.675816	Ptprf
GO_BP_m3	GO:005080	circadian sl	1/539	30/23843	0.496611	0.716234	0.675816	Ghrhr
GO_BP_m3	GO:005156	regulation	1/539	30/23843	0.496611	0.716234	0.675816	Ctr9
GO_BP_m3	GO:006028	cilium-dep	1/539	30/23843	0.496611	0.716234	0.675816	Mkks
GO_BP_m3	GO:007153	protein loc	1/539	30/23843	0.496611	0.716234	0.675816	Cep131
GO_BP_m3	GO:190007	positive reg	1/539	30/23843	0.496611	0.716234	0.675816	Prkcz
GO_BP_m3	GO:190211	positive reg	1/539	30/23843	0.496611	0.716234	0.675816	Ier3
GO_BP_m3	GO:190552	regulation	1/539	30/23843	0.496611	0.716234	0.675816	Ccl5
GO_BP_m3	GO:200014	positive reg	1/539	30/23843	0.496611	0.716234	0.675816	Twist1
GO_BP_m3	GO:004352	regulation	6/539	250/23843	0.498686	0.718744	0.678185	Bcl2l1/Crlf1
GO_BP_m3	GO:011005	regulation	6/539	250/23843	0.498686	0.718744	0.678185	Mkks/Nf2/
GO_BP_m3	GO:200123	regulation	4/539	162/23843	0.499986	0.720169	0.679529	Bcl2l1/Pdia
GO_BP_m3	GO:000666	sphingolipi	3/539	118/23843	0.500674	0.720169	0.679529	Elovl2/Enp
GO_BP_m3	GO:006004	cardiac mu	3/539	118/23843	0.500674	0.720169	0.679529	Tnni2/Tnnt
GO_BP_m3	GO:006198	meiosis I ce	3/539	118/23843	0.500674	0.720169	0.679529	Ankle1/Ccd
GO_BP_m3	GO:000906	aerobic res	2/539	74/23843	0.501016	0.720169	0.679529	Dlat/Ucn
GO_BP_m3	GO:003014	sphingolipi	2/539	74/23843	0.501016	0.720169	0.679529	Elovl2/St6g
GO_BP_m3	GO:004286	pyruvate b	2/539	74/23843	0.501016	0.720169	0.679529	Hk1/Ier3
GO_BP_m3	GO:004678	microtubul	2/539	74/23843	0.501016	0.720169	0.679529	Map7d3/Sg
GO_BP_m3	GO:004325	regulation	10/539	429/23843	0.505595	0.724127	0.683264	Atat1/Atxn
GO_BP_m3	GO:001406	phosphatic	3/539	119/23843	0.50631	0.724127	0.683264	Ccl5/Prr5/T
GO_BP_m3	GO:004682	regulation	3/539	119/23843	0.50631	0.724127	0.683264	Ier3/Lrrk2/
GO_BP_m3	GO:005192	positive reg	3/539	119/23843	0.50631	0.724127	0.683264	Ccl5/Trpc1
GO_BP_m3	GO:000989	positive reg	9/539	385/23843	0.506526	0.724127	0.683264	Hnrnpr/Ier3
GO_BP_m3	GO:005109	regulation	9/539	385/23843	0.506526	0.724127	0.683264	Hck/Map3k
GO_BP_m3	GO:000702	negative re	1/539	31/23843	0.508005	0.724127	0.683264	Ckap2
GO_BP_m3	GO:001056	regulation	1/539	31/23843	0.508005	0.724127	0.683264	D330045A
GO_BP_m3	GO:001827	protein N-	1/539	31/23843	0.508005	0.724127	0.683264	St6galnac5
GO_BP_m3	GO:003274	positive reg	1/539	31/23843	0.508005	0.724127	0.683264	Carmil2
GO_BP_m3	GO:003308	regulation	1/539	31/23843	0.508005	0.724127	0.683264	Ihh
GO_BP_m3	GO:004324	positive reg	1/539	31/23843	0.508005	0.724127	0.683264	Carmil2
GO_BP_m3	GO:004327	anoikis	1/539	31/23843	0.508005	0.724127	0.683264	Bcl2l1
GO_BP_m3	GO:004351	regulation	1/539	31/23843	0.508005	0.724127	0.683264	Twist1

GO_BP_m3	GO:004433	cell-cell ad	1/539	31/23843	0.508005	0.724127	0.683264	Cdh26
GO_BP_m3	GO:004561	regulation	1/539	31/23843	0.508005	0.724127	0.683264	Prkch
GO_BP_m3	GO:004853	lymph nod	1/539	31/23843	0.508005	0.724127	0.683264	Nkx2-3
GO_BP_m3	GO:005070	regulation	1/539	31/23843	0.508005	0.724127	0.683264	Hk1
GO_BP_m3	GO:005118	vitamin tra	1/539	31/23843	0.508005	0.724127	0.683264	Slc19a1
GO_BP_m3	GO:006097	coronary v	1/539	31/23843	0.508005	0.724127	0.683264	Tgfbr1
GO_BP_m3	GO:190547	negative re	1/539	31/23843	0.508005	0.724127	0.683264	Bcl2l1
GO_BP_m3	GO:190550	protein loc	1/539	31/23843	0.508005	0.724127	0.683264	Cep131
GO_BP_m3	GO:200040	positive re	1/539	31/23843	0.508005	0.724127	0.683264	Ccl5
GO_BP_m3	GO:001922	regulation	2/539	75/23843	0.508153	0.724127	0.683264	Avp/Tacr1
GO_BP_m3	GO:009775	positive re	2/539	75/23843	0.508153	0.724127	0.683264	Mkks/Ucn
GO_BP_m3	GO:190188	regulation	2/539	75/23843	0.508153	0.724127	0.683264	Gpm6b/Pr
GO_BP_m3	GO:001604	lipid catab	7/539	297/23843	0.508812	0.724825	0.683923	Ces1b/Enp
GO_BP_m3	GO:003530	regulation	4/539	164/23843	0.509579	0.725677	0.684727	Bmp2/Dus
GO_BP_m3	GO:190199	regulation	6/539	253/23843	0.510268	0.726417	0.685425	Fanci/Ier3/
GO_BP_m3	GO:000609	generation	8/539	342/23843	0.510898	0.727073	0.686044	Dlat/Dld/H
GO_BP_m3	GO:001092	regulation	3/539	120/23843	0.511913	0.728235	0.687141	Bmp2/Gpa
GO_BP_m3	GO:000840	gonad dev	5/539	209/23843	0.512054	0.728235	0.687141	Bcl2l1/Ptpr
GO_BP_m3	GO:005192	regulation	6/539	254/23843	0.514106	0.730096	0.688896	Ccl5/Hes1/
GO_BP_m3	GO:006056	developme	6/539	254/23843	0.514106	0.730096	0.688896	Areg/Nkx6
GO_BP_m3	GO:006113	regulation	4/539	165/23843	0.514344	0.730096	0.688896	Bag5/Lrrk2
GO_BP_m3	GO:000597	glycogen n	2/539	76/23843	0.515224	0.730096	0.688896	Phkg2/Ppp
GO_BP_m3	GO:000607	cellular glu	2/539	76/23843	0.515224	0.730096	0.688896	Phkg2/Ppp
GO_BP_m3	GO:002187	forebrain n	2/539	76/23843	0.515224	0.730096	0.688896	Atf5/Hes1
GO_BP_m3	GO:004404	glucan met	2/539	76/23843	0.515224	0.730096	0.688896	Phkg2/Ppp
GO_BP_m3	GO:001605	organic aci	5/539	210/23843	0.516273	0.730096	0.688896	Gcsh/Slc25
GO_BP_m3	GO:003007	insulin secr	5/539	210/23843	0.516273	0.730096	0.688896	Ccl5/Gip/N
GO_BP_m3	GO:004639	carboxylic	5/539	210/23843	0.516273	0.730096	0.688896	Gcsh/Slc25
GO_BP_m3	GO:190161	organic hy	5/539	210/23843	0.516273	0.730096	0.688896	Bmp2/Dhc
GO_BP_m3	GO:000269	negative re	3/539	121/23843	0.517482	0.730096	0.688896	Abr/Cd46/
GO_BP_m3	GO:000327	cardiac sep	3/539	121/23843	0.517482	0.730096	0.688896	Hes1/Mir19
GO_BP_m3	GO:200024	regulation	4/539	166/23843	0.519088	0.730096	0.688896	Adam24/Fa
GO_BP_m3	GO:000268	negative re	1/539	32/23843	0.519142	0.730096	0.688896	Abr
GO_BP_m3	GO:000301	respiratory	1/539	32/23843	0.519142	0.730096	0.688896	Nlgn1
GO_BP_m3	GO:000329	physiologic	1/539	32/23843	0.519142	0.730096	0.688896	Ctdp1
GO_BP_m3	GO:000330	physiologic	1/539	32/23843	0.519142	0.730096	0.688896	Ctdp1
GO_BP_m3	GO:000635	regulation	1/539	32/23843	0.519142	0.730096	0.688896	Ippk
GO_BP_m3	GO:000926	deoxyribor	1/539	32/23843	0.519142	0.730096	0.688896	Rrm2
GO_BP_m3	GO:001700	cytochrom	1/539	32/23843	0.519142	0.730096	0.688896	Bcs1l
GO_BP_m3	GO:001819	peptidyl-as	1/539	32/23843	0.519142	0.730096	0.688896	St6galnac5
GO_BP_m3	GO:001937	epoxygena	1/539	32/23843	0.519142	0.730096	0.688896	Cyp2c38
GO_BP_m3	GO:002261	extracellula	1/539	32/23843	0.519142	0.730096	0.688896	Carmil2
GO_BP_m3	GO:003359	mammary	1/539	32/23843	0.519142	0.730096	0.688896	Areg
GO_BP_m3	GO:004574	positive re	1/539	32/23843	0.519142	0.730096	0.688896	Lrrk2
GO_BP_m3	GO:005118	cofactor tra	1/539	32/23843	0.519142	0.730096	0.688896	Slc19a1
GO_BP_m3	GO:006014	regulation	1/539	32/23843	0.519142	0.730096	0.688896	Myod1
GO_BP_m3	GO:006029	long term	1/539	32/23843	0.519142	0.730096	0.688896	Bcl2l1
GO_BP_m3	GO:006048	lung epithe	1/539	32/23843	0.519142	0.730096	0.688896	Klf2

GO_BP_m3	GO:006066	embryonic	1/539	32/23843	0.519142	0.730096	0.688896	Esx1
GO_BP_m3	GO:006104	cell growth	1/539	32/23843	0.519142	0.730096	0.688896	Ctdp1
GO_BP_m3	GO:190211	negative re	1/539	32/23843	0.519142	0.730096	0.688896	Lrrk2
GO_BP_m3	GO:190268	mitochond	1/539	32/23843	0.519142	0.730096	0.688896	Ier3
GO_BP_m3	GO:006082	regulation	5/539	211/23843	0.520477	0.731734	0.690442	Axin2/Dixd
GO_BP_m3	GO:003241	negative re	2/539	77/23843	0.522226	0.732037	0.690728	Stoml1/Tw
GO_BP_m3	GO:004324	negative re	2/539	77/23843	0.522226	0.732037	0.690728	Ckap2/Car
GO_BP_m3	GO:005134	regulation	2/539	77/23843	0.522226	0.732037	0.690728	Fdx1/Lrrk2
GO_BP_m3	GO:005145	regulation	2/539	77/23843	0.522226	0.732037	0.690728	Avp/Lrrk2
GO_BP_m3	GO:005170	interaction	2/539	77/23843	0.522226	0.732037	0.690728	Ccl5/Ctdp1
GO_BP_m3	GO:006011	inner ear r	2/539	77/23843	0.522226	0.732037	0.690728	Hes1/Whr
GO_BP_m3	GO:006164	cytoskelet	2/539	77/23843	0.522226	0.732037	0.690728	Ckap2/Rhc
GO_BP_m3	GO:190160	alpha-ami	2/539	77/23843	0.522226	0.732037	0.690728	Gcsh/Thns
GO_BP_m3	GO:190331	negative re	2/539	77/23843	0.522226	0.732037	0.690728	Axin2/Ctr9
GO_BP_m3	GO:000715	leukocyte	7/539	301/23843	0.522943	0.732667	0.691322	Btn1a1/Ccl
GO_BP_m3	GO:005110	regulation	3/539	122/23843	0.523016	0.732667	0.691322	Hes1/Trim
GO_BP_m3	GO:000091	cytokinesis	4/539	167/23843	0.52381	0.732689	0.691343	Bcl2l1/Cka
GO_BP_m3	GO:000639	tRNA meta	4/539	167/23843	0.52381	0.732689	0.691343	Trmo/Pus7
GO_BP_m3	GO:190165	cellular res	6/539	257/23843	0.525553	0.732689	0.691343	Foxc2/Ghr
GO_BP_m3	GO:000720	positive re	7/539	302/23843	0.526452	0.732689	0.691343	Avp/Gpr3/
GO_BP_m3	GO:000910	coenzyme	4/539	168/23843	0.52851	0.732689	0.691343	Dlat/Dld/H
GO_BP_m3	GO:004349	protein kin	4/539	168/23843	0.52851	0.732689	0.691343	Ccl5/Otud
GO_BP_m3	GO:000276	regulation	3/539	123/23843	0.528516	0.732689	0.691343	Ccl5/Tme
GO_BP_m3	GO:190018	regulation	3/539	123/23843	0.528516	0.732689	0.691343	Lrrk2/Nf2/
GO_BP_m3	GO:190465	glucose tra	3/539	123/23843	0.528516	0.732689	0.691343	Gip/Prkcz/
GO_BP_m3	GO:000681	sodium io	5/539	213/23843	0.528838	0.732689	0.691343	Catsper4/
GO_BP_m3	GO:004513	developme	5/539	213/23843	0.528838	0.732689	0.691343	Bcl2l1/Ptpr
GO_BP_m3	GO:000694	regulation	2/539	78/23843	0.529161	0.732689	0.691343	Tnnt3/Ucn
GO_BP_m3	GO:001092	negative re	2/539	78/23843	0.529161	0.732689	0.691343	Gpatch2/S
GO_BP_m3	GO:004584	positive re	2/539	78/23843	0.529161	0.732689	0.691343	Cdon/Myo
GO_BP_m3	GO:004603	ADP meta	2/539	78/23843	0.529161	0.732689	0.691343	Hk1/Ier3
GO_BP_m3	GO:004863	positive re	2/539	78/23843	0.529161	0.732689	0.691343	Cdon/Myo
GO_BP_m3	GO:005130	establishm	2/539	78/23843	0.529161	0.732689	0.691343	Ankle1/Cc
GO_BP_m3	GO:007061	regulation	2/539	78/23843	0.529161	0.732689	0.691343	Cd46/Lrrk
GO_BP_m3	GO:000000	mitochond	1/539	33/23843	0.530027	0.732689	0.691343	Mgme1
GO_BP_m3	GO:000046	maturation	1/539	33/23843	0.530027	0.732689	0.691343	Nsa2
GO_BP_m3	GO:000610	citrate met	1/539	33/23843	0.530027	0.732689	0.691343	Dlat
GO_BP_m3	GO:000638	transcripti	1/539	33/23843	0.530027	0.732689	0.691343	Snapc1
GO_BP_m3	GO:001059	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Carmil2
GO_BP_m3	GO:003303	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Ccl5
GO_BP_m3	GO:004562	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Prkcz
GO_BP_m3	GO:004574	negative re	1/539	33/23843	0.530027	0.732689	0.691343	Bend6
GO_BP_m3	GO:004587	negative re	1/539	33/23843	0.530027	0.732689	0.691343	Ptch1
GO_BP_m3	GO:004591	positive re	1/539	33/23843	0.530027	0.732689	0.691343	Exosc6
GO_BP_m3	GO:005068	negative re	1/539	33/23843	0.530027	0.732689	0.691343	Ctr9
GO_BP_m3	GO:005195	negative re	1/539	33/23843	0.530027	0.732689	0.691343	Syt4
GO_BP_m3	GO:005509	acylglycer	1/539	33/23843	0.530027	0.732689	0.691343	Gip
GO_BP_m3	GO:006033	type I inter	1/539	33/23843	0.530027	0.732689	0.691343	Trim6

GO_BP_m3	GO:006047	lung cell di	1/539	33/23843	0.530027	0.732689	0.691343	Klf2
GO_BP_m3	GO:007032	triglycerid	1/539	33/23843	0.530027	0.732689	0.691343	Gip
GO_BP_m3	GO:007135	cellular res	1/539	33/23843	0.530027	0.732689	0.691343	Trim6
GO_BP_m3	GO:190074	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Bmp2
GO_BP_m3	GO:190305	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Carmil2
GO_BP_m3	GO:190320	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Lrrk2
GO_BP_m3	GO:190358	positive re	1/539	33/23843	0.530027	0.732689	0.691343	Bcl2l1
GO_BP_m3	GO:190395	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Hk1
GO_BP_m3	GO:200024	regulation	1/539	33/23843	0.530027	0.732689	0.691343	Hck
GO_BP_m3	GO:000246	adaptive in	9/539	393/23843	0.531317	0.734237	0.692804	Aire/Cd46/
GO_BP_m3	GO:000189	placenta d	4/539	169/23843	0.533187	0.736584	0.695018	Ccnf/Esx1/
GO_BP_m3	GO:000719	adenylate	2/539	79/23843	0.536027	0.737535	0.695916	Grm4/S1pr
GO_BP_m3	GO:003410	regulation	2/539	79/23843	0.536027	0.737535	0.695916	Abr/S1pr1
GO_BP_m3	GO:003803	signal tran	2/539	79/23843	0.536027	0.737535	0.695916	Bcl2l1/Ww
GO_BP_m3	GO:005000	chromoso	2/539	79/23843	0.536027	0.737535	0.695916	Ankle1/Cc
GO_BP_m3	GO:009719	extrinsic a	2/539	79/23843	0.536027	0.737535	0.695916	Bcl2l1/Ww
GO_BP_m3	GO:190186	positive re	2/539	79/23843	0.536027	0.737535	0.695916	Cdon/Myo
GO_BP_m3	GO:001703	protein im	5/539	215/23843	0.537133	0.737535	0.695916	Lrrk2/Nxt1/
GO_BP_m3	GO:002240	negative r	4/539	170/23843	0.537841	0.737535	0.695916	Bmp2/Btn1
GO_BP_m3	GO:000864	hexose tra	3/539	125/23843	0.539409	0.737535	0.695916	Gip/Prkcz/
GO_BP_m3	GO:003109	regenerati	3/539	125/23843	0.539409	0.737535	0.695916	Myod1/Pt
GO_BP_m3	GO:003476	negative r	3/539	125/23843	0.539409	0.737535	0.695916	Hamp2/St
GO_BP_m3	GO:000673	coenzyme	7/539	306/23843	0.54039	0.737535	0.695916	Dlat/Dld/F
GO_BP_m3	GO:000691	nucleocyto	7/539	306/23843	0.54039	0.737535	0.695916	Ankle1/Ier
GO_BP_m3	GO:000916	nucleotide	7/539	306/23843	0.54039	0.737535	0.695916	Avp/Bcl2l1/
GO_BP_m3	GO:004887	homeostas	7/539	306/23843	0.54039	0.737535	0.695916	Atxn2/Klf2/
GO_BP_m3	GO:003465	nucleobas	9/539	396/23843	0.540502	0.737535	0.695916	Axin2/Dis3
GO_BP_m3	GO:001063	epithelial	6/539	261/23843	0.540643	0.737535	0.695916	Foxc2/Ltb4
GO_BP_m3	GO:004592	negative r	6/539	261/23843	0.540643	0.737535	0.695916	Atxn2/Ctd
GO_BP_m3	GO:000195	negative r	1/539	34/23843	0.540666	0.737535	0.695916	Plet1
GO_BP_m3	GO:000236	T cell cyto	1/539	34/23843	0.540666	0.737535	0.695916	Prkcz
GO_BP_m3	GO:000267	positive re	1/539	34/23843	0.540666	0.737535	0.695916	Ccl5
GO_BP_m3	GO:001400	oligodend	1/539	34/23843	0.540666	0.737535	0.695916	Sox10
GO_BP_m3	GO:002184	cell prolife	1/539	34/23843	0.540666	0.737535	0.695916	Dixdc1
GO_BP_m3	GO:003111	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Ckap2
GO_BP_m3	GO:003273	positive re	1/539	34/23843	0.540666	0.737535	0.695916	Hk1
GO_BP_m3	GO:003314	negative r	1/539	34/23843	0.540666	0.737535	0.695916	Tcf21
GO_BP_m3	GO:003424	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Ctr9
GO_BP_m3	GO:003511	embryonic	1/539	34/23843	0.540666	0.737535	0.695916	Twist1
GO_BP_m3	GO:004002	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Gpr3
GO_BP_m3	GO:004409	membrane	1/539	34/23843	0.540666	0.737535	0.695916	Nlgn1
GO_BP_m3	GO:004500	DNA-depe	1/539	34/23843	0.540666	0.737535	0.695916	Mms22l
GO_BP_m3	GO:004632	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Twist1
GO_BP_m3	GO:007057	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Ptprf
GO_BP_m3	GO:007139	cellular res	1/539	34/23843	0.540666	0.737535	0.695916	P2ry6
GO_BP_m3	GO:190001	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Il17d
GO_BP_m3	GO:199008	response t	1/539	34/23843	0.540666	0.737535	0.695916	Hes1
GO_BP_m3	GO:199009	cellular res	1/539	34/23843	0.540666	0.737535	0.695916	Hes1

GO_BP_m3	GO:200010	positive reg	1/539	34/23843	0.540666	0.737535	0.695916	Ccl5
GO_BP_m3	GO:200077	regulation	1/539	34/23843	0.540666	0.737535	0.695916	Twist1
GO_BP_m3	GO:004670	heterocycle	10/539	441/23843	0.540745	0.737535	0.695916	Axin2/Dis3
GO_BP_m3	GO:000647	protein me	4/539	171/23843	0.542472	0.738494	0.696821	Ctr9/Kdm4
GO_BP_m3	GO:000821	protein alky	4/539	171/23843	0.542472	0.738494	0.696821	Ctr9/Kdm4
GO_BP_m3	GO:003050	BMP signal	4/539	171/23843	0.542472	0.738494	0.696821	Bmp2/Gdf5
GO_BP_m3	GO:004561	regulation	4/539	171/23843	0.542472	0.738494	0.696821	Cd46/Ihh/P
GO_BP_m3	GO:002290	respiratory	2/539	80/23843	0.542823	0.738494	0.696821	Dld/Slc37a
GO_BP_m3	GO:004472	DNA methy	2/539	80/23843	0.542823	0.738494	0.696821	Mov10l1/P
GO_BP_m3	GO:190018	positive reg	2/539	80/23843	0.542823	0.738494	0.696821	Lrrk2/Ptpn5
GO_BP_m3	GO:190331	regulation	2/539	80/23843	0.542823	0.738494	0.696821	Cd46/Lrrk2
GO_BP_m3	GO:004217	regulation	8/539	352/23843	0.543601	0.739318	0.697598	Bag5/Grin2
GO_BP_m3	GO:005116	nuclear tra	7/539	307/23843	0.543848	0.73942	0.697695	Ankle1/Ier3
GO_BP_m3	GO:000663	fatty acid b	3/539	126/23843	0.544801	0.740481	0.698695	Avp/Elovl2/
GO_BP_m3	GO:009009	regulation	5/539	217/23843	0.545362	0.740789	0.698986	Bmp2/Gdf5
GO_BP_m3	GO:009013	epithelium	6/539	263/23843	0.54811	0.740789	0.698986	Foxc2/Ltb4
GO_BP_m3	GO:000721	glutamate	2/539	81/23843	0.549551	0.740789	0.698986	Grm4/Nlgn
GO_BP_m3	GO:001921	regulation	2/539	81/23843	0.549551	0.740789	0.698986	Avp/Twist1
GO_BP_m3	GO:003202	positive reg	2/539	81/23843	0.549551	0.740789	0.698986	Gip/Nkx6-1
GO_BP_m3	GO:007050	calcium ion	2/539	81/23843	0.549551	0.740789	0.698986	Hes1/Ucn
GO_BP_m3	GO:190040	regulation	2/539	81/23843	0.549551	0.740789	0.698986	Bag5/Lrrk2
GO_BP_m3	GO:190198	positive reg	2/539	81/23843	0.549551	0.740789	0.698986	Neurog1/U
GO_BP_m3	GO:000681	calcium ion	9/539	399/23843	0.549619	0.740789	0.698986	Catsper4/C
GO_BP_m3	GO:001574	monosacch	3/539	127/23843	0.550156	0.740789	0.698986	Gip/Prkcz/S
GO_BP_m3	GO:000150	neurotrans	1/539	35/23843	0.551064	0.740789	0.698986	Gpm6b
GO_BP_m3	GO:000292	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Cd46
GO_BP_m3	GO:000673	one-carbo	1/539	35/23843	0.551064	0.740789	0.698986	Car6
GO_BP_m3	GO:000682	iron ion tra	1/539	35/23843	0.551064	0.740789	0.698986	Hamp2
GO_BP_m3	GO:000709	mitotic spin	1/539	35/23843	0.551064	0.740789	0.698986	Mad2l1
GO_BP_m3	GO:003167	cellular resp	1/539	35/23843	0.551064	0.740789	0.698986	Pdia3
GO_BP_m3	GO:003220	negative re	1/539	35/23843	0.551064	0.740789	0.698986	Gnl3l
GO_BP_m3	GO:003263	interleukin-	1/539	35/23843	0.551064	0.740789	0.698986	Prkcz
GO_BP_m3	GO:003300	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Foxf1
GO_BP_m3	GO:003579	positive reg	1/539	35/23843	0.551064	0.740789	0.698986	Ier3
GO_BP_m3	GO:003647	cell death i	1/539	35/23843	0.551064	0.740789	0.698986	Lrrk2
GO_BP_m3	GO:004230	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Avp
GO_BP_m3	GO:004330	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Foxf1
GO_BP_m3	GO:004662	negative re	1/539	35/23843	0.551064	0.740789	0.698986	Ctdp1
GO_BP_m3	GO:004663	negative re	1/539	35/23843	0.551064	0.740789	0.698986	Ihh
GO_BP_m3	GO:005145	intracellula	1/539	35/23843	0.551064	0.740789	0.698986	Avp
GO_BP_m3	GO:005169	actin filame	1/539	35/23843	0.551064	0.740789	0.698986	Carmil2
GO_BP_m3	GO:005196	positive reg	1/539	35/23843	0.551064	0.740789	0.698986	Nlgn1
GO_BP_m3	GO:006044	epithelial tu	1/539	35/23843	0.551064	0.740789	0.698986	Foxf1
GO_BP_m3	GO:007117	spindle ass	1/539	35/23843	0.551064	0.740789	0.698986	Mad2l1
GO_BP_m3	GO:190197	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Mad2l1
GO_BP_m3	GO:200017	negative re	1/539	35/23843	0.551064	0.740789	0.698986	Nlgn1
GO_BP_m3	GO:200040	positive reg	1/539	35/23843	0.551064	0.740789	0.698986	Ccl5
GO_BP_m3	GO:200078	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Lrrk2

GO_BP_m3	GO:200103	regulation	1/539	35/23843	0.551064	0.740789	0.698986	Lrrk2
GO_BP_m3	GO:000989	negative re	6/539	264/23843	0.551823	0.741577	0.699729	Axin2/Bag5
GO_BP_m3	GO:00100	glial cell di	5/539	219/23843	0.553521	0.74237	0.700477	Atf5/Bmp2
GO_BP_m3	GO:00434	positive re	5/539	219/23843	0.553521	0.74237	0.700477	Bmp2/Grm
GO_BP_m3	GO:00509	leukocyte r	7/539	310/23843	0.554158	0.74237	0.700477	Abr/Aire/C
GO_BP_m3	GO:00092	purine ribo	3/539	128/23843	0.555473	0.74237	0.700477	Bcl2l1/Hk1
GO_BP_m3	GO:000945	RNA modif	3/539	128/23843	0.555473	0.74237	0.700477	Trmo/Pus7
GO_BP_m3	GO:001021	response t	3/539	128/23843	0.555473	0.74237	0.700477	Bcl2l1/Kdm
GO_BP_m3	GO:004362	cellular prc	3/539	128/23843	0.555473	0.74237	0.700477	Ckap2/Car
GO_BP_m3	GO:00550	cardiac mu	3/539	128/23843	0.555473	0.74237	0.700477	Bmp2/Ctd
GO_BP_m3	GO:006007	canonical	6/539	265/23843	0.555522	0.74237	0.700477	Axin2/Dixd
GO_BP_m3	GO:00302	glycosamir	2/539	82/23843	0.556208	0.74237	0.700477	Itih1/Ndst2
GO_BP_m3	GO:003064	regulation	2/539	82/23843	0.556208	0.74237	0.700477	Avp/Lrrk2
GO_BP_m3	GO:003111	regulation	2/539	82/23843	0.556208	0.74237	0.700477	Ckap2/Sgk
GO_BP_m3	GO:003264	regulation	2/539	82/23843	0.556208	0.74237	0.700477	Ccl5/Twist1
GO_BP_m3	GO:003294	negative re	2/539	82/23843	0.556208	0.74237	0.700477	Btn1a1/Ihh
GO_BP_m3	GO:004348	regulation	2/539	82/23843	0.556208	0.74237	0.700477	Axin2/Hnr
GO_BP_m3	GO:005067	negative re	2/539	82/23843	0.556208	0.74237	0.700477	Btn1a1/Ihh
GO_BP_m3	GO:004576	positive re	4/539	174/23843	0.556219	0.74237	0.700477	Adm2/Ccl5
GO_BP_m3	GO:005079	regulation	4/539	174/23843	0.556219	0.74237	0.700477	Ccl5/Gip/N
GO_BP_m3	GO:000242	immune re	7/539	311/23843	0.557572	0.74237	0.700477	Btn1a1/Igh
GO_BP_m3	GO:001571	organic ani	9/539	402/23843	0.558665	0.74237	0.700477	Avp/Oxt/Sl
GO_BP_m3	GO:001087	lipid localiz	8/539	357/23843	0.559627	0.74237	0.700477	Oxt/Ptch1/
GO_BP_m3	GO:000914	purine nuc	3/539	129/23843	0.560754	0.74237	0.700477	Bcl2l1/Hk1
GO_BP_m3	GO:000046	maturation	1/539	36/23843	0.561228	0.74237	0.700477	Nol10
GO_BP_m3	GO:000156	response t	1/539	36/23843	0.561228	0.74237	0.700477	Ier3
GO_BP_m3	GO:00034	axis elonga	1/539	36/23843	0.561228	0.74237	0.700477	Areg
GO_BP_m3	GO:000611	regulation	1/539	36/23843	0.561228	0.74237	0.700477	Ier3
GO_BP_m3	GO:000663	unsaturate	1/539	36/23843	0.561228	0.74237	0.700477	Avp
GO_BP_m3	GO:000931	oligosacch	1/539	36/23843	0.561228	0.74237	0.700477	St6galnac5
GO_BP_m3	GO:001009	specificatio	1/539	36/23843	0.561228	0.74237	0.700477	Axin2
GO_BP_m3	GO:001073	protein kin	1/539	36/23843	0.561228	0.74237	0.700477	Lrrk2
GO_BP_m3	GO:001083	positive re	1/539	36/23843	0.561228	0.74237	0.700477	Myod1
GO_BP_m3	GO:003106	positive re	1/539	36/23843	0.561228	0.74237	0.700477	Ctr9
GO_BP_m3	GO:003511	embryonic	1/539	36/23843	0.561228	0.74237	0.700477	Twist1
GO_BP_m3	GO:00353	positive re	1/539	36/23843	0.561228	0.74237	0.700477	Dusp26
GO_BP_m3	GO:004001	positive re	1/539	36/23843	0.561228	0.74237	0.700477	Hes1
GO_BP_m3	GO:004231	vasodilatio	1/539	36/23843	0.561228	0.74237	0.700477	Mkks
GO_BP_m3	GO:004298	amyloid pr	1/539	36/23843	0.561228	0.74237	0.700477	Dhcr24
GO_BP_m3	GO:004826	response t	1/539	36/23843	0.561228	0.74237	0.700477	Tacr1
GO_BP_m3	GO:004866	neuron fat	1/539	36/23843	0.561228	0.74237	0.700477	Nkx6-1
GO_BP_m3	GO:00507	regulation	1/539	36/23843	0.561228	0.74237	0.700477	Hk1
GO_BP_m3	GO:005093	pigment ce	1/539	36/23843	0.561228	0.74237	0.700477	Sox10
GO_BP_m3	GO:006025	regulation	1/539	36/23843	0.561228	0.74237	0.700477	Ucn
GO_BP_m3	GO:00619	glial cell ac	1/539	36/23843	0.561228	0.74237	0.700477	Lrrk2
GO_BP_m3	GO:00702	protein ho	1/539	36/23843	0.561228	0.74237	0.700477	Hsf4
GO_BP_m3	GO:007132	cellular res	1/539	36/23843	0.561228	0.74237	0.700477	Fdx1
GO_BP_m3	GO:007151	genetic im	1/539	36/23843	0.561228	0.74237	0.700477	Ctr9

GO_BP_m3	GO:009702	dendritic c	1/539	36/23843	0.561228	0.74237	0.700477	Prtn3
GO_BP_m3	GO:009748	dendrite e	1/539	36/23843	0.561228	0.74237	0.700477	Syt4
GO_BP_m3	GO:190222	regulation	1/539	36/23843	0.561228	0.74237	0.700477	Bcl2l1
GO_BP_m3	GO:190470	regulation	1/539	36/23843	0.561228	0.74237	0.700477	Hpgd
GO_BP_m3	GO:199087	vascular sm	1/539	36/23843	0.561228	0.74237	0.700477	Hpgd
GO_BP_m3	GO:000858	regulation	2/539	83/23843	0.562795	0.743298	0.701354	Ihh/Ptch1
GO_BP_m3	GO:000913	purine nuc	2/539	83/23843	0.562795	0.743298	0.701354	Hk1/Ier3
GO_BP_m3	GO:000917	purine ribo	2/539	83/23843	0.562795	0.743298	0.701354	Hk1/Ier3
GO_BP_m3	GO:004249	mechanore	2/539	83/23843	0.562795	0.743298	0.701354	Hes1/Whr
GO_BP_m3	GO:190187	regulation	2/539	83/23843	0.562795	0.743298	0.701354	Ckap2/Car
GO_BP_m3	GO:004354	protein acy	5/539	222/23843	0.565623	0.746148	0.704043	Atat1/Dld/
GO_BP_m3	GO:004593	negative re	5/539	222/23843	0.565623	0.746148	0.704043	Bcl2l1/Fanc
GO_BP_m3	GO:001063	positive re	3/539	130/23843	0.565996	0.746148	0.704043	Foxc2/Rho
GO_BP_m3	GO:003421	carbohydra	3/539	130/23843	0.565996	0.746148	0.704043	Gip/Prkcz/
GO_BP_m3	GO:005166	localizatio	3/539	130/23843	0.565996	0.746148	0.704043	Grik2/Nlgn
GO_BP_m3	GO:190336	positive re	3/539	130/23843	0.565996	0.746148	0.704043	Lrrk2/Rnf1
GO_BP_m3	GO:001935	nicotinami	2/539	84/23843	0.569312	0.746819	0.704676	Hk1/Ier3
GO_BP_m3	GO:190595	positive re	2/539	84/23843	0.569312	0.746819	0.704676	Oxt/Ptch1
GO_BP_m3	GO:199013	neuron pro	4/539	177/23843	0.569742	0.746819	0.704676	Nkx6-1/Pr
GO_BP_m3	GO:000170	endoderm	1/539	37/23843	0.571162	0.746819	0.704676	Ctr9
GO_BP_m3	GO:000194	postsynapt	1/539	37/23843	0.571162	0.746819	0.704676	Nlgn1
GO_BP_m3	GO:000253	cytokine p	1/539	37/23843	0.571162	0.746819	0.704676	Il17d
GO_BP_m3	GO:000673	NADP met	1/539	37/23843	0.571162	0.746819	0.704676	Fdx1
GO_BP_m3	GO:000808	anterograd	1/539	37/23843	0.571162	0.746819	0.704676	Ap3s1
GO_BP_m3	GO:002188	forebrain n	1/539	37/23843	0.571162	0.746819	0.704676	Atf5
GO_BP_m3	GO:003085	granulocyt	1/539	37/23843	0.571162	0.746819	0.704676	L3mbtl3
GO_BP_m3	GO:003302	myeloid ce	1/539	37/23843	0.571162	0.746819	0.704676	Ccl5
GO_BP_m3	GO:003585	epithelial c	1/539	37/23843	0.571162	0.746819	0.704676	Foxc2
GO_BP_m3	GO:004209	type 2 imm	1/539	37/23843	0.571162	0.746819	0.704676	Prkcz
GO_BP_m3	GO:004560	regulation	1/539	37/23843	0.571162	0.746819	0.704676	Tgfbr1
GO_BP_m3	GO:004588	positive re	1/539	37/23843	0.571162	0.746819	0.704676	Ihh
GO_BP_m3	GO:004600	regulation	1/539	37/23843	0.571162	0.746819	0.704676	Btn1a1
GO_BP_m3	GO:004825	mRNA stab	1/539	37/23843	0.571162	0.746819	0.704676	Axin2
GO_BP_m3	GO:005070	interleukin-	1/539	37/23843	0.571162	0.746819	0.704676	Hk1
GO_BP_m3	GO:007117	mitotic spi	1/539	37/23843	0.571162	0.746819	0.704676	Mad2l1
GO_BP_m3	GO:009004	regulation	1/539	37/23843	0.571162	0.746819	0.704676	Foxc2
GO_BP_m3	GO:190106	guanosine-	1/539	37/23843	0.571162	0.746819	0.704676	Lrrk2
GO_BP_m3	GO:190367	positive re	1/539	37/23843	0.571162	0.746819	0.704676	Foxc2
GO_BP_m3	GO:190571	positive re	1/539	37/23843	0.571162	0.746819	0.704676	Ier3
GO_BP_m3	GO:200014	regulation	1/539	37/23843	0.571162	0.746819	0.704676	Twist1
GO_BP_m3	GO:200102	negative re	1/539	37/23843	0.571162	0.746819	0.704676	Lrrk2
GO_BP_m3	GO:000252	acute infla	3/539	131/23843	0.571199	0.746819	0.704676	Ccl5/Cd46/
GO_BP_m3	GO:000920	ribonucleo	3/539	131/23843	0.571199	0.746819	0.704676	Bcl2l1/Hk1
GO_BP_m3	GO:006024	anatomical	8/539	361/23843	0.572273	0.747996	0.705786	Calb2/Gnl3
GO_BP_m3	GO:005079	regulation	4/539	178/23843	0.574199	0.750284	0.707945	Ccl5/Ctdp1
GO_BP_m3	GO:000721	neuropepti	2/539	85/23843	0.575758	0.751408	0.709005	Ltb4r2/Ucr
GO_BP_m3	GO:002195	central ner	2/539	85/23843	0.575758	0.751408	0.709005	Atf5/Nano
GO_BP_m3	GO:002290	electron tr	2/539	85/23843	0.575758	0.751408	0.709005	Dld/Slc37a

GO_BP_m3	GO:00706	negative re	2/539	85/23843	0.575758	0.751408	0.709005	Btn1a1/Ihh
GO_BP_m3	GO:00510	positive re	5/539	225/23843	0.577557	0.753525	0.711004	Map3k13/
GO_BP_m3	GO:00324	response t	8/539	363/23843	0.578535	0.753909	0.711366	Abr/Ccl5/C
GO_BP_m3	GO:000647	protein ac	4/539	179/23843	0.57863	0.753909	0.711366	Atat1/Myo
GO_BP_m3	GO:00194	aromatic c	10/539	455/23843	0.580559	0.753909	0.711366	Axin2/Dis3
GO_BP_m3	GO:000962	response t	1/539	38/23843	0.580871	0.753909	0.711366	Hamp2
GO_BP_m3	GO:003081	regulation	1/539	38/23843	0.580871	0.753909	0.711366	Ier3
GO_BP_m3	GO:003252	protein exi	1/539	38/23843	0.580871	0.753909	0.711366	Tmem30b
GO_BP_m3	GO:00327	positive re	1/539	38/23843	0.580871	0.753909	0.711366	BC048507
GO_BP_m3	GO:00440	regulation	1/539	38/23843	0.580871	0.753909	0.711366	Lrrk2
GO_BP_m3	GO:004502	plasma me	1/539	38/23843	0.580871	0.753909	0.711366	Mymk
GO_BP_m3	GO:00455	negative re	1/539	38/23843	0.580871	0.753909	0.711366	Ihh
GO_BP_m3	GO:004584	negative re	1/539	38/23843	0.580871	0.753909	0.711366	Mad2l1
GO_BP_m3	GO:00514	positive re	1/539	38/23843	0.580871	0.753909	0.711366	S1pr1
GO_BP_m3	GO:00723	tricarboxyli	1/539	38/23843	0.580871	0.753909	0.711366	Dlat
GO_BP_m3	GO:00725	maintenan	1/539	38/23843	0.580871	0.753909	0.711366	Hk1
GO_BP_m3	GO:009712	receptor lo	1/539	38/23843	0.580871	0.753909	0.711366	Nlgn1
GO_BP_m3	GO:20000	regulation	1/539	38/23843	0.580871	0.753909	0.711366	Gpm6b
GO_BP_m3	GO:200027	negative re	1/539	38/23843	0.580871	0.753909	0.711366	Gnl3l
GO_BP_m3	GO:00160	viral proce	6/539	272/23843	0.58101	0.753909	0.711366	Bcl2l1/Ccl5
GO_BP_m3	GO:000611	energy res	2/539	86/23843	0.582134	0.754683	0.712096	Phkg2/Ppp
GO_BP_m3	GO:003591	skeletal mu	2/539	86/23843	0.582134	0.754683	0.712096	Cdon/Myo
GO_BP_m3	GO:00513	chromosor	2/539	86/23843	0.582134	0.754683	0.712096	Mad2l1/Ub
GO_BP_m3	GO:00507	positive re	4/539	180/23843	0.583034	0.755394	0.712766	Areg/Ccl5/
GO_BP_m3	GO:00508	B cell recep	4/539	180/23843	0.583034	0.755394	0.712766	Ighv1-53/I
GO_BP_m3	GO:004877	tissue rem	4/539	181/23843	0.587411	0.757787	0.715025	Abr/Foxc2/
GO_BP_m3	GO:014001	meiotic nu	4/539	181/23843	0.587411	0.757787	0.715025	Ankle1/Ccc
GO_BP_m3	GO:00091	glycoprote	7/539	320/23843	0.58776	0.757787	0.715025	B3gnt6/Bm
GO_BP_m3	GO:000914	nucleoside	6/539	274/23843	0.588156	0.757787	0.715025	Ak7/Bcl2l1/
GO_BP_m3	GO:00091	ribonucleo	2/539	87/23843	0.588439	0.757787	0.715025	Hk1/Ier3
GO_BP_m3	GO:00193	pyridine nu	2/539	87/23843	0.588439	0.757787	0.715025	Hk1/Ier3
GO_BP_m3	GO:002187	forebrain g	2/539	87/23843	0.588439	0.757787	0.715025	Atf5/Hes1
GO_BP_m3	GO:003307	T cell differ	2/539	87/23843	0.588439	0.757787	0.715025	Aire/Ihh
GO_BP_m3	GO:004632	glucose im	2/539	87/23843	0.588439	0.757787	0.715025	Prkcz/Slc2a
GO_BP_m3	GO:00075	aging	5/539	228/23843	0.589315	0.757787	0.715025	Krt83/Ghrh
GO_BP_m3	GO:000002	ribosomal	1/539	39/23843	0.590361	0.757787	0.715025	Rpl6l
GO_BP_m3	GO:000271	positive re	1/539	39/23843	0.590361	0.757787	0.715025	Prkcz
GO_BP_m3	GO:00063	double-str	1/539	39/23843	0.590361	0.757787	0.715025	Kdm4d
GO_BP_m3	GO:00066	glycosphin	1/539	39/23843	0.590361	0.757787	0.715025	St6galnac5
GO_BP_m3	GO:00093	phospholip	1/539	39/23843	0.590361	0.757787	0.715025	Enpp7
GO_BP_m3	GO:003112	developme	1/539	39/23843	0.590361	0.757787	0.715025	Bmp2
GO_BP_m3	GO:003164	killing of c	1/539	39/23843	0.590361	0.757787	0.715025	Hamp2
GO_BP_m3	GO:003434	response t	1/539	39/23843	0.590361	0.757787	0.715025	Trim6
GO_BP_m3	GO:00354	cellular res	1/539	39/23843	0.590361	0.757787	0.715025	Trim6
GO_BP_m3	GO:003817	neurotroph	1/539	39/23843	0.590361	0.757787	0.715025	Ptprf
GO_BP_m3	GO:00443	disruption	1/539	39/23843	0.590361	0.757787	0.715025	Hamp2
GO_BP_m3	GO:004574	positive re	1/539	39/23843	0.590361	0.757787	0.715025	Hes1
GO_BP_m3	GO:00458	pH reducti	1/539	39/23843	0.590361	0.757787	0.715025	Avp

GO_BP_m3	GO:004824	macrophag	1/539	39/23843	0.590361	0.757787	0.715025	Ccl5
GO_BP_m3	GO:004874	skeletal mu	1/539	39/23843	0.590361	0.757787	0.715025	Myod1
GO_BP_m3	GO:005085	regulation	1/539	39/23843	0.590361	0.757787	0.715025	Usp12
GO_BP_m3	GO:005128	positive reg	1/539	39/23843	0.590361	0.757787	0.715025	Trpc1
GO_BP_m3	GO:190199	toxin trans	1/539	39/23843	0.590361	0.757787	0.715025	Mtmr12
GO_BP_m3	GO:190210	negative re	1/539	39/23843	0.590361	0.757787	0.715025	Mad2l1
GO_BP_m3	GO:190357	negative re	1/539	39/23843	0.590361	0.757787	0.715025	Lrrk2
GO_BP_m3	GO:200081	negative re	1/539	39/23843	0.590361	0.757787	0.715025	Mad2l1
GO_BP_m3	GO:003268	regulation	3/539	135/23843	0.591623	0.757787	0.715025	C1qtnf4/Lr
GO_BP_m3	GO:007208	stem cell p	3/539	135/23843	0.591623	0.757787	0.715025	Lrrk2/Nf2/
GO_BP_m3	GO:001567	monovaler	10/539	459/23843	0.591657	0.757787	0.715025	Catsper4/K
GO_BP_m3	GO:005140	neuron apo	6/539	275/23843	0.591705	0.757787	0.715025	Bcl2l1/Crlf1
GO_BP_m3	GO:003053	adult beha	4/539	182/23843	0.591762	0.757787	0.715025	Chrna4/Ch
GO_BP_m3	GO:004390	negative re	4/539	182/23843	0.591762	0.757787	0.715025	Adam24/C
GO_BP_m3	GO:007177	response to	4/539	182/23843	0.591762	0.757787	0.715025	Bmp2/Gdf5
GO_BP_m3	GO:007177	cellular res	4/539	182/23843	0.591762	0.757787	0.715025	Bmp2/Gdf5
GO_BP_m3	GO:000004	transition r	2/539	88/23843	0.594673	0.760608	0.717686	Hamp2/Trp
GO_BP_m3	GO:000906	cellular am	2/539	88/23843	0.594673	0.760608	0.717686	Gcsh/Thnsl
GO_BP_m3	GO:001059	positive reg	2/539	88/23843	0.594673	0.760608	0.717686	Foxc2/Rhol
GO_BP_m3	GO:004847	oogenesis	2/539	88/23843	0.594673	0.760608	0.717686	Ccdc155/Ih
GO_BP_m3	GO:003450	protein loc	6/539	276/23843	0.595238	0.761104	0.718155	Lrrk2/Nf2/l
GO_BP_m3	GO:000193	negative re	1/539	40/23843	0.599637	0.763999	0.720886	Tgfbr1
GO_BP_m3	GO:000602	glycosamir	1/539	40/23843	0.599637	0.763999	0.720886	Ndst2
GO_BP_m3	GO:000637	mRNA poly	1/539	40/23843	0.599637	0.763999	0.720886	Ctr9
GO_BP_m3	GO:001569	organic cat	1/539	40/23843	0.599637	0.763999	0.720886	Slc25a17
GO_BP_m3	GO:003083	negative re	1/539	40/23843	0.599637	0.763999	0.720886	Carmil2
GO_BP_m3	GO:003273	positive reg	1/539	40/23843	0.599637	0.763999	0.720886	Hk1
GO_BP_m3	GO:003806	p38MAPK	1/539	40/23843	0.599637	0.763999	0.720886	Bmp2
GO_BP_m3	GO:004337	regulation	1/539	40/23843	0.599637	0.763999	0.720886	Prkcz
GO_BP_m3	GO:004582	positive reg	1/539	40/23843	0.599637	0.763999	0.720886	Ucn
GO_BP_m3	GO:004645	icosanoid	1/539	40/23843	0.599637	0.763999	0.720886	Avp
GO_BP_m3	GO:007083	bicellular ti	1/539	40/23843	0.599637	0.763999	0.720886	Prkch
GO_BP_m3	GO:190581	negative re	1/539	40/23843	0.599637	0.763999	0.720886	Mad2l1
GO_BP_m3	GO:000028	nuclear div	9/539	416/23843	0.599837	0.764027	0.720913	Ankle1/Ccc
GO_BP_m3	GO:002668	regulation	4/539	184/23843	0.600382	0.764495	0.721354	Abr/Aire/C
GO_BP_m3	GO:003647	cell death i	2/539	89/23843	0.600836	0.764619	0.721472	Bag5/Lrrk2
GO_BP_m3	GO:004663	regulation	2/539	89/23843	0.600836	0.764619	0.721472	Ihh/Prkcz
GO_BP_m3	GO:000912	purine nuc	3/539	137/23843	0.601596	0.76468	0.721529	Bcl2l1/Hk1
GO_BP_m3	GO:000916	purine ribo	3/539	137/23843	0.601596	0.76468	0.721529	Bcl2l1/Hk1
GO_BP_m3	GO:003264	tumor necr	3/539	137/23843	0.601596	0.76468	0.721529	C1qtnf4/Lr
GO_BP_m3	GO:190355	regulation	3/539	137/23843	0.601596	0.76468	0.721529	C1qtnf4/Lr
GO_BP_m3	GO:007156	cellular res	4/539	185/23843	0.604651	0.768336	0.724978	Bmp2/Hpg
GO_BP_m3	GO:005068	negative re	3/539	138/23843	0.606522	0.770486	0.727007	Gdf5/Ptch1
GO_BP_m3	GO:003530	negative re	2/539	90/23843	0.606928	0.770546	0.727064	Gpatch2/Sl
GO_BP_m3	GO:190288	regulation	2/539	90/23843	0.606928	0.770546	0.727064	Bag5/Lrrk2
GO_BP_m3	GO:000926	response to	1/539	41/23843	0.608703	0.770976	0.727469	Gip
GO_BP_m3	GO:001067	negative re	1/539	41/23843	0.608703	0.770976	0.727469	Ier3
GO_BP_m3	GO:003237	regulation	1/539	41/23843	0.608703	0.770976	0.727469	Ptch1

GO_BP_m3	GO:003237	regulation	1/539	41/23843	0.608703	0.770976	0.727469	Ptch1
GO_BP_m3	GO:00421	ketone bio	1/539	41/23843	0.608703	0.770976	0.727469	Bmp2
GO_BP_m3	GO:005097	detection	1/539	41/23843	0.608703	0.770976	0.727469	Mkks
GO_BP_m3	GO:00516	spindle loc	1/539	41/23843	0.608703	0.770976	0.727469	Ccdc155
GO_BP_m3	GO:009034	regulation	1/539	41/23843	0.608703	0.770976	0.727469	Twist1
GO_BP_m3	GO:00163	dendrite d	6/539	280/23843	0.609208	0.771387	0.727858	Caprin1/C
GO_BP_m3	GO:00482	organelle f	10/539	466/23843	0.610747	0.773109	0.729482	Ankle1/Cc
GO_BP_m3	GO:19039	regulation	3/539	139/23843	0.611408	0.773717	0.730056	Ccl5/Isg20
GO_BP_m3	GO:007252	pyridine-c	2/539	91/23843	0.61295	0.774723	0.731005	Hk1/Ier3
GO_BP_m3	GO:000691	phagocyto	4/539	187/23843	0.613105	0.774723	0.731005	Arhgap25/
GO_BP_m3	GO:00069	compleme	4/539	187/23843	0.613105	0.774723	0.731005	Cd46/Ighv
GO_BP_m3	GO:004424	cellular lip	4/539	187/23843	0.613105	0.774723	0.731005	Enpp7/Slc
GO_BP_m3	GO:00715	response t	4/539	187/23843	0.613105	0.774723	0.731005	Bmp2/Hpg
GO_BP_m3	GO:00431	proteasom	8/539	375/23843	0.615178	0.77534	0.731587	Ankzf1/Ba
GO_BP_m3	GO:00717	tumor necr	3/539	140/23843	0.616253	0.77534	0.731587	C1qtnf4/Lr
GO_BP_m3	GO:00159	nucleobas	4/539	188/23843	0.617289	0.77534	0.731587	Mcm3ap/N
GO_BP_m3	GO:007124	cellular res	4/539	188/23843	0.617289	0.77534	0.731587	Lrrk2/Mir1
GO_BP_m3	GO:00002	mitochond	1/539	42/23843	0.617564	0.77534	0.731587	Mir539
GO_BP_m3	GO:000597	glycogen b	1/539	42/23843	0.617564	0.77534	0.731587	Phkg2
GO_BP_m3	GO:00069	acute-pha	1/539	42/23843	0.617564	0.77534	0.731587	Ccl5
GO_BP_m3	GO:00092	glucan bio	1/539	42/23843	0.617564	0.77534	0.731587	Phkg2
GO_BP_m3	GO:00107	regulation	1/539	42/23843	0.617564	0.77534	0.731587	Trim6
GO_BP_m3	GO:001692	protein sur	1/539	42/23843	0.617564	0.77534	0.731587	Gnl3l
GO_BP_m3	GO:00308	negative re	1/539	42/23843	0.617564	0.77534	0.731587	Ier3
GO_BP_m3	GO:003157	spindle ch	1/539	42/23843	0.617564	0.77534	0.731587	Mad2l1
GO_BP_m3	GO:003304	negative re	1/539	42/23843	0.617564	0.77534	0.731587	Mad2l1
GO_BP_m3	GO:00434	RNA stabili	1/539	42/23843	0.617564	0.77534	0.731587	Axin2
GO_BP_m3	GO:004361	keratinocyt	1/539	42/23843	0.617564	0.77534	0.731587	Ptch1
GO_BP_m3	GO:00436	RNA polya	1/539	42/23843	0.617564	0.77534	0.731587	Ctr9
GO_BP_m3	GO:005091	positive ch	1/539	42/23843	0.617564	0.77534	0.731587	S1pr1
GO_BP_m3	GO:005164	mitochond	1/539	42/23843	0.617564	0.77534	0.731587	Lrrk2
GO_BP_m3	GO:005167	membrane	1/539	42/23843	0.617564	0.77534	0.731587	Defa27
GO_BP_m3	GO:00518	negative re	1/539	42/23843	0.617564	0.77534	0.731587	Otud3
GO_BP_m3	GO:00601	maternal p	1/539	42/23843	0.617564	0.77534	0.731587	Hmx3
GO_BP_m3	GO:190037	negative re	1/539	42/23843	0.617564	0.77534	0.731587	Ier3
GO_BP_m3	GO:000004	autophago	2/539	92/23843	0.6189	0.775657	0.731886	Lrrk2/Stx1
GO_BP_m3	GO:000167	long-chain	2/539	92/23843	0.6189	0.775657	0.731886	Cyp2c38/S
GO_BP_m3	GO:00064	RNA expor	2/539	92/23843	0.6189	0.775657	0.731886	Nxt1/Ranb
GO_BP_m3	GO:00468	negative re	2/539	92/23843	0.6189	0.775657	0.731886	Ucn/Ucn2
GO_BP_m3	GO:006002	roof of mo	2/539	92/23843	0.6189	0.775657	0.731886	Tcf21/Tgfb
GO_BP_m3	GO:00603	response t	2/539	92/23843	0.6189	0.775657	0.731886	Chrna4/Lrr
GO_BP_m3	GO:004694	carboxylic	6/539	283/23843	0.619508	0.776193	0.732392	Avp/Oxt/Sl
GO_BP_m3	GO:00723	monocarb	5/539	236/23843	0.619772	0.776296	0.732489	Avp/Elovl2
GO_BP_m3	GO:00028	regulation	3/539	141/23843	0.621057	0.777226	0.733366	Ccl5/Tfeb/
GO_BP_m3	GO:00091	ribonucleo	3/539	141/23843	0.621057	0.777226	0.733366	Bcl2l1/Hk1
GO_BP_m3	GO:003461	cellular res	3/539	141/23843	0.621057	0.777226	0.733366	Ankzf1/Lrr
GO_BP_m3	GO:001081	regulation	4/539	189/23843	0.621446	0.77726	0.733399	Foxf1/Gpm
GO_BP_m3	GO:19029	positive re	4/539	189/23843	0.621446	0.77726	0.733399	Nf2/Carmil

GO_BP_m3	GO:001584	organic aci	6/539	284/23843	0.622908	0.777801	0.733909	Avp/Oxt/Sl
GO_BP_m3	GO:003133	positive reg	5/539	237/23843	0.623484	0.777801	0.733909	Atat1/Fnip
GO_BP_m3	GO:00166	ameboidal	8/539	378/23843	0.624075	0.777801	0.733909	Foxc2/Ltb4
GO_BP_m3	GO:001082	regulation	2/539	93/23843	0.62478	0.777801	0.733909	Gip/Prkcz
GO_BP_m3	GO:004348	regulation	2/539	93/23843	0.62478	0.777801	0.733909	Axin2/Hnrr
GO_BP_m3	GO:000182	blastocyst	1/539	43/23843	0.626225	0.777801	0.733909	Ctr9
GO_BP_m3	GO:000196	negative re	1/539	43/23843	0.626225	0.777801	0.733909	Ptprf
GO_BP_m3	GO:000325	regulation	1/539	43/23843	0.626225	0.777801	0.733909	Lrrk2
GO_BP_m3	GO:000721	dopamine	1/539	43/23843	0.626225	0.777801	0.733909	Lrrk2
GO_BP_m3	GO:001025	NADH deh	1/539	43/23843	0.626225	0.777801	0.733909	Bcs1l
GO_BP_m3	GO:001490	myotube c	1/539	43/23843	0.626225	0.777801	0.733909	Myod1
GO_BP_m3	GO:003016	proteoglyc	1/539	43/23843	0.626225	0.777801	0.733909	Ndst2
GO_BP_m3	GO:003110	axon reger	1/539	43/23843	0.626225	0.777801	0.733909	Ptprf
GO_BP_m3	GO:003275	positive reg	1/539	43/23843	0.626225	0.777801	0.733909	Il17d
GO_BP_m3	GO:003298	mitochond	1/539	43/23843	0.626225	0.777801	0.733909	Bcs1l
GO_BP_m3	GO:004510	intermedia	1/539	43/23843	0.626225	0.777801	0.733909	Fam83h
GO_BP_m3	GO:005070	interleukin	1/539	43/23843	0.626225	0.777801	0.733909	Hk1
GO_BP_m3	GO:008601	membrane	1/539	43/23843	0.626225	0.777801	0.733909	Catsper4
GO_BP_m3	GO:009031	negative re	1/539	43/23843	0.626225	0.777801	0.733909	Lrrk2
GO_BP_m3	GO:190103	regulation	1/539	43/23843	0.626225	0.777801	0.733909	Lrrk2
GO_BP_m3	GO:190274	regulation	1/539	43/23843	0.626225	0.777801	0.733909	Carmil2
GO_BP_m3	GO:190551	macrophag	1/539	43/23843	0.626225	0.777801	0.733909	Ccl5
GO_BP_m3	GO:200005	negative re	1/539	43/23843	0.626225	0.777801	0.733909	Bag5
GO_BP_m3	GO:200125	negative re	1/539	43/23843	0.626225	0.777801	0.733909	Stoml1
GO_BP_m3	GO:004858	developme	5/539	238/23843	0.627174	0.778754	0.734809	Ctdp1/Nkx
GO_BP_m3	GO:004358	skin develo	6/539	286/23843	0.629654	0.781181	0.737098	Cela2a/Dh
GO_BP_m3	GO:003150	protein-co	4/539	191/23843	0.629673	0.781181	0.737098	Cep131/Ex
GO_BP_m3	GO:190401	positive reg	4/539	191/23843	0.629673	0.781181	0.737098	Adm2/Ccl5
GO_BP_m3	GO:005095	sensory pe	3/539	143/23843	0.630541	0.781415	0.737319	Hsf4/Nxnl2
GO_BP_m3	GO:000157	microtubul	2/539	94/23843	0.63059	0.781415	0.737319	Ak7/Cep13
GO_BP_m3	GO:004563	negative re	2/539	94/23843	0.63059	0.781415	0.737319	Ctr9/Tmem
GO_BP_m3	GO:190210	negative re	2/539	94/23843	0.63059	0.781415	0.737319	Ihh/Tmem
GO_BP_m3	GO:000762	circadian rl	4/539	192/23843	0.633744	0.784684	0.740404	Atf5/Ghrhr
GO_BP_m3	GO:003166	cellular res	4/539	192/23843	0.633744	0.784684	0.740404	Lrrk2/Myoc
GO_BP_m3	GO:000072	non-recom	1/539	44/23843	0.634689	0.784684	0.740404	Kdm4d
GO_BP_m3	GO:000338	epithelial c	1/539	44/23843	0.634689	0.784684	0.740404	Ihh
GO_BP_m3	GO:003304	negative re	1/539	44/23843	0.634689	0.784684	0.740404	Mad2l1
GO_BP_m3	GO:004510	intermedia	1/539	44/23843	0.634689	0.784684	0.740404	Fam83h
GO_BP_m3	GO:005135	positive reg	1/539	44/23843	0.634689	0.784684	0.740404	Fdx1
GO_BP_m3	GO:007167	regulation	1/539	44/23843	0.634689	0.784684	0.740404	Ccl5
GO_BP_m3	GO:001839	internal pe	3/539	144/23843	0.635221	0.78489	0.740598	Atat1/Myo
GO_BP_m3	GO:004583	positive reg	3/539	144/23843	0.635221	0.78489	0.740598	Avp/Disp3/
GO_BP_m3	GO:004513	meiotic chr	2/539	95/23843	0.636329	0.785806	0.741463	Ankle1/Ccc
GO_BP_m3	GO:004684	bone remo	2/539	95/23843	0.636329	0.785806	0.741463	Ihh/S1pr1
GO_BP_m3	GO:000166	response t	4/539	193/23843	0.637786	0.787152	0.742733	Bmp2/Chrr
GO_BP_m3	GO:190305	regulation	4/539	193/23843	0.637786	0.787152	0.742733	Bag5/Lrrk2
GO_BP_m3	GO:000915	purine ribo	9/539	430/23843	0.639062	0.788332	0.743846	Avp/Bcl2l1
GO_BP_m3	GO:000223	response t	8/539	384/23843	0.641532	0.788332	0.743846	Abr/Ccl5/C

GO_BP_m3	GO:000959	detection c	7/539	337/23843	0.641829	0.788332	0.743846	Car6/Kcnm
GO_BP_m3	GO:000704	cell-cell jur	2/539	96/23843	0.641998	0.788332	0.743846	Cdh26/Prk
GO_BP_m3	GO:190503	autophago	2/539	96/23843	0.641998	0.788332	0.743846	Lrrk2/Stx12
GO_BP_m3	GO:000165	temperatur	1/539	45/23843	0.642963	0.788332	0.743846	Ccl5
GO_BP_m3	GO:000263	positive re	1/539	45/23843	0.642963	0.788332	0.743846	Exosc6
GO_BP_m3	GO:000271	positive re	1/539	45/23843	0.642963	0.788332	0.743846	Exosc6
GO_BP_m3	GO:000289	positive re	1/539	45/23843	0.642963	0.788332	0.743846	Exosc6
GO_BP_m3	GO:000863	intrinsic ap	1/539	45/23843	0.642963	0.788332	0.743846	Bag5
GO_BP_m3	GO:003164	protein des	1/539	45/23843	0.642963	0.788332	0.743846	Bmp2
GO_BP_m3	GO:003271	negative re	1/539	45/23843	0.642963	0.788332	0.743846	Klf2
GO_BP_m3	GO:003278	regulation	1/539	45/23843	0.642963	0.788332	0.743846	Ctr9
GO_BP_m3	GO:004591	negative re	1/539	45/23843	0.642963	0.788332	0.743846	Ier3
GO_BP_m3	GO:004632	positive re	1/539	45/23843	0.642963	0.788332	0.743846	Prkcz
GO_BP_m3	GO:004801	vascular en	1/539	45/23843	0.642963	0.788332	0.743846	Foxc2
GO_BP_m3	GO:006032	head morp	1/539	45/23843	0.642963	0.788332	0.743846	Ihh
GO_BP_m3	GO:006061	adipose tis	1/539	45/23843	0.642963	0.788332	0.743846	Mir103-2
GO_BP_m3	GO:007130	cellular res	1/539	45/23843	0.642963	0.788332	0.743846	Halr1
GO_BP_m3	GO:009893	axonal tran	1/539	45/23843	0.642963	0.788332	0.743846	Ap3s1
GO_BP_m3	GO:190044	regulation	1/539	45/23843	0.642963	0.788332	0.743846	Nlgn1
GO_BP_m3	GO:190179	negative re	1/539	45/23843	0.642963	0.788332	0.743846	Bag5
GO_BP_m3	GO:190237	negative re	1/539	45/23843	0.642963	0.788332	0.743846	Axin2
GO_BP_m3	GO:001571	monocarbo	3/539	146/23843	0.644458	0.789263	0.744725	Oxt/Slc25a
GO_BP_m3	GO:002261	gland morp	3/539	146/23843	0.644458	0.789263	0.744725	Areg/Nkx2
GO_BP_m3	GO:004666	female sex	3/539	146/23843	0.644458	0.789263	0.744725	Bcl2l1/Ptpr
GO_BP_m3	GO:007147	cellular res	3/539	146/23843	0.644458	0.789263	0.744725	Bcl2l1/Kdm
GO_BP_m3	GO:002289	regulation	5/539	243/23843	0.645295	0.790063	0.745479	Chrna4/Hk
GO_BP_m3	GO:000648	protein gly	4/539	195/23843	0.645782	0.790209	0.745617	B3gnt6/D7
GO_BP_m3	GO:004341	macromole	4/539	195/23843	0.645782	0.790209	0.745617	B3gnt6/D7
GO_BP_m3	GO:009719	intrinsic ap	6/539	291/23843	0.64621	0.790507	0.745899	Bag5/Bcl2l
GO_BP_m3	GO:000688	regulation	2/539	97/23843	0.647597	0.790797	0.746172	Avp/Lrrk2
GO_BP_m3	GO:200123	negative re	2/539	97/23843	0.647597	0.790797	0.746172	Bcl2l1/Tgfb
GO_BP_m3	GO:000717	transmemb	7/539	339/23843	0.647914	0.790797	0.746172	Bmp2/Gdf5
GO_BP_m3	GO:000282	regulation	3/539	147/23843	0.649013	0.790797	0.746172	Exosc6/Mir
GO_BP_m3	GO:000912	nucleoside	3/539	147/23843	0.649013	0.790797	0.746172	Bcl2l1/Hk1
GO_BP_m3	GO:000836	regulation	4/539	196/23843	0.649736	0.790797	0.746172	Nkx6-1/Slc
GO_BP_m3	GO:009902	plasma me	4/539	196/23843	0.649736	0.790797	0.746172	Arhgap25/
GO_BP_m3	GO:003009	myeloid ce	8/539	387/23843	0.650087	0.790797	0.746172	Ccl5/Ctr9/
GO_BP_m3	GO:000024	spliceosom	1/539	46/23843	0.65105	0.790797	0.746172	Gcfc2
GO_BP_m3	GO:000152	retinoid me	1/539	46/23843	0.65105	0.790797	0.746172	Lcn5
GO_BP_m3	GO:000641	tRNA amin	1/539	46/23843	0.65105	0.790797	0.746172	Vars
GO_BP_m3	GO:000699	nuclear en	1/539	46/23843	0.65105	0.790797	0.746172	Ankle1
GO_BP_m3	GO:000906	aspartate f	1/539	46/23843	0.65105	0.790797	0.746172	Thnsl2
GO_BP_m3	GO:001488	striated mu	1/539	46/23843	0.65105	0.790797	0.746172	Myod1
GO_BP_m3	GO:002260	ovulation c	1/539	46/23843	0.65105	0.790797	0.746172	Ptprn
GO_BP_m3	GO:003166	lipopolysac	1/539	46/23843	0.65105	0.790797	0.746172	Ccl5
GO_BP_m3	GO:003230	icosanoid s	1/539	46/23843	0.65105	0.790797	0.746172	Oxt
GO_BP_m3	GO:004302	T cell home	1/539	46/23843	0.65105	0.790797	0.746172	Tsc22d3
GO_BP_m3	GO:004347	regulation	1/539	46/23843	0.65105	0.790797	0.746172	Ier3

GO_BP_m3	GO:004542	positive reg	1/539	46/23843	0.65105	0.790797	0.746172	Klf2
GO_BP_m3	GO:005198	negative re	1/539	46/23843	0.65105	0.790797	0.746172	Mad2l1
GO_BP_m3	GO:006004	regulation	1/539	46/23843	0.65105	0.790797	0.746172	Tgfbr1
GO_BP_m3	GO:007054	response to	1/539	46/23843	0.65105	0.790797	0.746172	P2ry6
GO_BP_m3	GO:007269	protein loc	1/539	46/23843	0.65105	0.790797	0.746172	Cep131
GO_BP_m3	GO:190440	positive reg	1/539	46/23843	0.65105	0.790797	0.746172	Klf2
GO_BP_m3	GO:004427	cellular nitr	9/539	435/23843	0.65255	0.7922	0.747496	Axin2/Dis3
GO_BP_m3	GO:000182	blastocyst	2/539	98/23843	0.653127	0.7922	0.747496	Ctr9/Tgfbr
GO_BP_m3	GO:000218	cytoplasmi	2/539	98/23843	0.653127	0.7922	0.747496	Rpl6l/Rps3
GO_BP_m3	GO:003010	natural kille	2/539	98/23843	0.653127	0.7922	0.747496	Gm13287/
GO_BP_m3	GO:005265	cyclic purin	2/539	98/23843	0.653127	0.7922	0.747496	Avp/Rln3
GO_BP_m3	GO:000690	vesicle fusi	3/539	148/23843	0.653528	0.792239	0.747532	Stx12/Syt4/
GO_BP_m3	GO:005130	regulation	3/539	148/23843	0.653528	0.792239	0.747532	Bcl2l1/Ptch
GO_BP_m3	GO:190136	organic cyc	10/539	483/23843	0.655193	0.794034	0.749226	Axin2/Dis3
GO_BP_m3	GO:000599	monosacch	5/539	246/23843	0.655899	0.794665	0.749821	Dlat/Hk1/P
GO_BP_m3	GO:005132	meiotic cel	7/539	342/23843	0.656926	0.794778	0.749928	Ankle1/Cc
GO_BP_m3	GO:000224	hematopoi	3/539	149/23843	0.658	0.794778	0.749928	Ankle1/He
GO_BP_m3	GO:000647	internal pro	3/539	149/23843	0.658	0.794778	0.749928	Atat1/Myo
GO_BP_m3	GO:000717	transformin	3/539	149/23843	0.658	0.794778	0.749928	Bmp2/Hpg
GO_BP_m3	GO:000680	xenobiotic	2/539	99/23843	0.658587	0.794778	0.749928	Cyp2c38/U
GO_BP_m3	GO:000919	cyclic nucle	2/539	99/23843	0.658587	0.794778	0.749928	Avp/Rln3
GO_BP_m3	GO:001939	fatty acid c	2/539	99/23843	0.658587	0.794778	0.749928	Slc25a17/T
GO_BP_m3	GO:004562	negative re	1/539	47/23843	0.658953	0.794778	0.749928	Ihh
GO_BP_m3	GO:004618	phenol-con	1/539	47/23843	0.658953	0.794778	0.749928	Trpc1
GO_BP_m3	GO:004871	regulation	1/539	47/23843	0.658953	0.794778	0.749928	Hes1
GO_BP_m3	GO:005105	negative re	1/539	47/23843	0.658953	0.794778	0.749928	Bmp2
GO_BP_m3	GO:005119	regulation	1/539	47/23843	0.658953	0.794778	0.749928	Ier3
GO_BP_m3	GO:005193	regulation	1/539	47/23843	0.658953	0.794778	0.749928	Oxt
GO_BP_m3	GO:005193	regulation	1/539	47/23843	0.658953	0.794778	0.749928	Oxt
GO_BP_m3	GO:006076	negative re	1/539	47/23843	0.658953	0.794778	0.749928	Ptprf
GO_BP_m3	GO:007026	necrotic ce	1/539	47/23843	0.658953	0.794778	0.749928	Ucn
GO_BP_m3	GO:000920	purine ribo	5/539	247/23843	0.659388	0.795079	0.750213	Bcl2l1/Dld/
GO_BP_m3	GO:000276	immune re	9/539	438/23843	0.660504	0.796202	0.751272	Btn1a1/Igh
GO_BP_m3	GO:000270	regulation	3/539	150/23843	0.662431	0.798076	0.75304	Exosc6/Mir
GO_BP_m3	GO:005116	nuclear exp	3/539	150/23843	0.662431	0.798076	0.75304	Ankle1/Nxt
GO_BP_m3	GO:000639	mRNA proc	9/539	439/23843	0.663132	0.798697	0.753626	Celf5/Ctr9/
GO_BP_m3	GO:000940	response to	2/539	100/23843	0.663979	0.799492	0.754376	Hsf4/Tacr1
GO_BP_m3	GO:003134	negative re	4/539	200/23843	0.665258	0.799828	0.754693	Abr/Foxf1/
GO_BP_m3	GO:007237	protein act	4/539	200/23843	0.665258	0.799828	0.754693	Cd46/Ighv
GO_BP_m3	GO:000925	ribonucleo	9/539	440/23843	0.665748	0.799828	0.754693	Avp/Bcl2l1/
GO_BP_m3	GO:000227	mast cell a	1/539	48/23843	0.666678	0.799828	0.754693	Foxf1
GO_BP_m3	GO:000276	negative re	1/539	48/23843	0.666678	0.799828	0.754693	Tmem178
GO_BP_m3	GO:000712	synapsis	1/539	48/23843	0.666678	0.799828	0.754693	Ccdc155
GO_BP_m3	GO:001050	RNA secon	1/539	48/23843	0.666678	0.799828	0.754693	Ddx46
GO_BP_m3	GO:001610	diterpenoi	1/539	48/23843	0.666678	0.799828	0.754693	Lcn5
GO_BP_m3	GO:003164	regulation	1/539	48/23843	0.666678	0.799828	0.754693	Sox10
GO_BP_m3	GO:004330	mast cell d	1/539	48/23843	0.666678	0.799828	0.754693	Foxf1
GO_BP_m3	GO:004512	regulation	1/539	48/23843	0.666678	0.799828	0.754693	S1pr1

GO_BP_m3	GO:190157	fatty acid d	1/539	48/23843	0.666678	0.799828	0.754693	Avp
GO_BP_m3	GO:20012	regulation	1/539	48/23843	0.666678	0.799828	0.754693	Wwox
GO_BP_m3	GO:00434	response t	6/539	298/23843	0.668623	0.801713	0.756472	Foxc2/Ghr
GO_BP_m3	GO:00442	small mole	6/539	298/23843	0.668623	0.801713	0.756472	Gcsh/Hk1/
GO_BP_m3	GO:00486	positive re	4/539	201/23843	0.669064	0.801854	0.756606	Ghrhr/Mkk
GO_BP_m3	GO:003444	lipid oxidat	2/539	101/23843	0.669301	0.801854	0.756606	Slc25a17/T
GO_BP_m3	GO:00359	cellular res	2/539	101/23843	0.669301	0.801854	0.756606	Ankzf1/Stc
GO_BP_m3	GO:00102	endomem	7/539	347/23843	0.671637	0.803644	0.758294	Ankle1/Ba
GO_BP_m3	GO:006004	heart contr	4/539	202/23843	0.672841	0.803644	0.758294	Oxt/Tnni2/
GO_BP_m3	GO:00091	ribonucleo	5/539	251/23843	0.673117	0.803644	0.758294	Bcl2l1/Dld/
GO_BP_m3	GO:00061	purine nuc	9/539	443/23843	0.673525	0.803644	0.758294	Avp/Bcl2l1
GO_BP_m3	GO:00019	positive re	1/539	49/23843	0.674229	0.803644	0.758294	Prkcz
GO_BP_m3	GO:000204	cell migrati	1/539	49/23843	0.674229	0.803644	0.758294	Foxc2
GO_BP_m3	GO:000244	mast cell n	1/539	49/23843	0.674229	0.803644	0.758294	Foxf1
GO_BP_m3	GO:00103	response t	1/539	49/23843	0.674229	0.803644	0.758294	Bcl2l1
GO_BP_m3	GO:001657	histone ph	1/539	49/23843	0.674229	0.803644	0.758294	Twist1
GO_BP_m3	GO:00308	regulation	1/539	49/23843	0.674229	0.803644	0.758294	Carmil2
GO_BP_m3	GO:003111	regulation	1/539	49/23843	0.674229	0.803644	0.758294	Sgk1
GO_BP_m3	GO:00430	tRNA amin	1/539	49/23843	0.674229	0.803644	0.758294	Vars
GO_BP_m3	GO:00432	apical junc	1/539	49/23843	0.674229	0.803644	0.758294	Prkch
GO_BP_m3	GO:004614	pigment bi	1/539	49/23843	0.674229	0.803644	0.758294	Trpc1
GO_BP_m3	GO:006042	lung epithe	1/539	49/23843	0.674229	0.803644	0.758294	Klf2
GO_BP_m3	GO:007097	protein loc	1/539	49/23843	0.674229	0.803644	0.758294	Pmm1
GO_BP_m3	GO:190204	regulation	1/539	49/23843	0.674229	0.803644	0.758294	Bcl2l1
GO_BP_m3	GO:200064	regulation	1/539	49/23843	0.674229	0.803644	0.758294	Stoml1
GO_BP_m3	GO:00027	positive re	2/539	102/23843	0.674555	0.803644	0.758294	Exosc6/Prk
GO_BP_m3	GO:000282	positive re	2/539	102/23843	0.674555	0.803644	0.758294	Exosc6/Prk
GO_BP_m3	GO:20012	regulation	8/539	396/23843	0.675036	0.803644	0.758294	Avp/Bag5/
GO_BP_m3	GO:00183	peptidyl-ly	3/539	153/23843	0.675473	0.803644	0.758294	Atat1/Myo
GO_BP_m3	GO:00506	nucleic aci	3/539	153/23843	0.675473	0.803644	0.758294	Mcm3ap/
GO_BP_m3	GO:00506	RNA trans	3/539	153/23843	0.675473	0.803644	0.758294	Mcm3ap/
GO_BP_m3	GO:009017	organelle r	3/539	153/23843	0.675473	0.803644	0.758294	Stx12/Syt4
GO_BP_m3	GO:009881	nuclear chr	5/539	252/23843	0.676491	0.804525	0.759125	Ankle1/Axi
GO_BP_m3	GO:001032	membrane	4/539	203/23843	0.676588	0.804525	0.759125	Arhgap25/
GO_BP_m3	GO:000152	angiogene	10/539	492/23843	0.677533	0.805426	0.759976	Adm2/Ccl5
GO_BP_m3	GO:00708	divalent m	9/539	445/23843	0.67865	0.806254	0.760757	Catsper4/
GO_BP_m3	GO:000691	phagocyto	3/539	154/23843	0.679737	0.806254	0.760757	Ighv1-53/I
GO_BP_m3	GO:00434	negative re	3/539	154/23843	0.679737	0.806254	0.760757	Dusp26/Nf
GO_BP_m3	GO:000204	sprouting	2/539	103/23843	0.679741	0.806254	0.760757	Foxc2/Klf2
GO_BP_m3	GO:004347	pigmentati	2/539	103/23843	0.679741	0.806254	0.760757	Ihh/Sox10
GO_BP_m3	GO:00435	muscle ad	2/539	103/23843	0.679741	0.806254	0.760757	Ctdp1/Myc
GO_BP_m3	GO:00160	immunogl	5/539	253/23843	0.679842	0.806254	0.760757	Exosc6/Igh
GO_BP_m3	GO:00002	nuclear-tr	1/539	50/23843	0.681608	0.806254	0.760757	Nanos1
GO_BP_m3	GO:00064	'de novo'	1/539	50/23843	0.681608	0.806254	0.760757	Mkks
GO_BP_m3	GO:00068	Golgi to pl	1/539	50/23843	0.681608	0.806254	0.760757	Exoc1
GO_BP_m3	GO:000714	male meio	1/539	50/23843	0.681608	0.806254	0.760757	Mov10l1
GO_BP_m3	GO:003112	mRNA 3'-	1/539	50/23843	0.681608	0.806254	0.760757	Ctr9
GO_BP_m3	GO:003221	regulation	1/539	50/23843	0.681608	0.806254	0.760757	Gnl3l

GO_BP_m3	GO:003545	response t	1/539	50/23843	0.681608	0.806254	0.760757	Trim6
GO_BP_m3	GO:004298	amyloid pr	1/539	50/23843	0.681608	0.806254	0.760757	Dhcr24
GO_BP_m3	GO:004303	amino acid	1/539	50/23843	0.681608	0.806254	0.760757	Vars
GO_BP_m3	GO:005189	regulation	1/539	50/23843	0.681608	0.806254	0.760757	Gpm6b
GO_BP_m3	GO:009010	regulation	1/539	50/23843	0.681608	0.806254	0.760757	Gpm6b
GO_BP_m3	GO:004390	regulation	8/539	399/23843	0.683106	0.807657	0.76208	Adam24/C
GO_BP_m3	GO:000915	purine ribo	5/539	254/23843	0.68317	0.807657	0.76208	Avp/Bcl2l1/
GO_BP_m3	GO:000301	heart proce	4/539	205/23843	0.683992	0.808183	0.762577	Oxt/Tnni2/
GO_BP_m3	GO:000991	epidermal	4/539	205/23843	0.683992	0.808183	0.762577	Hes1/Prkch
GO_BP_m3	GO:007251	divalent in	9/539	448/23843	0.686245	0.810622	0.764878	Catsper4/C
GO_BP_m3	GO:001972	B cell medi	5/539	255/23843	0.686475	0.810671	0.764925	Exosc6/Igh
GO_BP_m3	GO:005123	establishm	3/539	156/23843	0.68814	0.810766	0.765014	Mcm3ap/N
GO_BP_m3	GO:190165	response t	7/539	353/23843	0.688766	0.810766	0.765014	Foxc2/Ghrh
GO_BP_m3	GO:000752	neuromusc	1/539	51/23843	0.688821	0.810766	0.765014	Lrrk2
GO_BP_m3	GO:003272	negative re	1/539	51/23843	0.688821	0.810766	0.765014	Twist1
GO_BP_m3	GO:004364	inositol ph	1/539	51/23843	0.688821	0.810766	0.765014	Ippk
GO_BP_m3	GO:004573	positive re	1/539	51/23843	0.688821	0.810766	0.765014	Kdm4d
GO_BP_m3	GO:004824	lymphocyte	1/539	51/23843	0.688821	0.810766	0.765014	Ccl5
GO_BP_m3	GO:005144	regulation	1/539	51/23843	0.688821	0.810766	0.765014	Gpr3
GO_BP_m3	GO:005156	histone H3	1/539	51/23843	0.688821	0.810766	0.765014	Ctr9
GO_BP_m3	GO:007171	icosanoid t	1/539	51/23843	0.688821	0.810766	0.765014	Oxt
GO_BP_m3	GO:190157	fatty acid d	1/539	51/23843	0.688821	0.810766	0.765014	Oxt
GO_BP_m3	GO:200051	regulation	1/539	51/23843	0.688821	0.810766	0.765014	Prkcz
GO_BP_m3	GO:000914	purine nuc	5/539	256/23843	0.689757	0.811161	0.765386	Bcl2l1/Dld/
GO_BP_m3	GO:003240	regulation	5/539	256/23843	0.689757	0.811161	0.765386	Chrna4/Hk
GO_BP_m3	GO:001050	positive re	2/539	105/23843	0.689911	0.811161	0.765386	Lrrk2/Tfeb
GO_BP_m3	GO:007190	negative re	2/539	105/23843	0.689911	0.811161	0.765386	Prkar1b/Pt
GO_BP_m3	GO:007008	glycosylati	4/539	207/23843	0.691276	0.812543	0.766691	B3gnt6/D7
GO_BP_m3	GO:007756	female pre	3/539	157/23843	0.692279	0.813277	0.767383	Ggn/Hmx3
GO_BP_m3	GO:005077	negative re	3/539	157/23843	0.692279	0.813277	0.767383	Abr/Cd46/
GO_BP_m3	GO:199026	neutrophil	2/539	106/23843	0.694896	0.815488	0.76947	Ccl5/Prtn3
GO_BP_m3	GO:003086	cortical cyt	1/539	52/23843	0.695871	0.815488	0.76947	Nlgn1
GO_BP_m3	GO:004339	negative re	1/539	52/23843	0.695871	0.815488	0.76947	Hes1
GO_BP_m3	GO:004353	positive re	1/539	52/23843	0.695871	0.815488	0.76947	Foxc2
GO_BP_m3	GO:004583	negative re	1/539	52/23843	0.695871	0.815488	0.76947	Mad2l1
GO_BP_m3	GO:007093	protein K4	1/539	52/23843	0.695871	0.815488	0.76947	Ube2c
GO_BP_m3	GO:007162	regulation	1/539	52/23843	0.695871	0.815488	0.76947	Ccl5
GO_BP_m3	GO:190236	negative re	1/539	52/23843	0.695871	0.815488	0.76947	Axin2
GO_BP_m3	GO:190355	negative re	1/539	52/23843	0.695871	0.815488	0.76947	Twist1
GO_BP_m3	GO:001969	ribose pho	9/539	452/23843	0.696199	0.815522	0.769501	Avp/Bcl2l1/
GO_BP_m3	GO:006201	regulation	8/539	404/23843	0.696279	0.815522	0.769501	Avp/Bcl2l1/
GO_BP_m3	GO:005090	detection c	6/539	308/23843	0.699045	0.81754	0.771406	Car6/Olfr1
GO_BP_m3	GO:007122	cellular res	5/539	259/23843	0.69946	0.81754	0.771406	Ccl5/Ctr9/
GO_BP_m3	GO:000095	nuclear-tra	2/539	107/23843	0.699814	0.81754	0.771406	Exosc6/Na
GO_BP_m3	GO:004275	regulation	2/539	107/23843	0.699814	0.81754	0.771406	Ghrhr/Nlgn
GO_BP_m3	GO:004324	regulation	2/539	107/23843	0.699814	0.81754	0.771406	Ckap2/Car
GO_BP_m3	GO:005102	mRNA tran	2/539	107/23843	0.699814	0.81754	0.771406	Mcm3ap/N
GO_BP_m3	GO:000281	regulation	3/539	159/23843	0.700433	0.81754	0.771406	Exosc6/Mir

GO_BP_m3	GO:000703	vacuole or	3/539	159/23843	0.700433	0.81754	0.771406	Lrrk2/Stx1
GO_BP_m3	GO:000836	regulation	3/539	159/23843	0.700433	0.81754	0.771406	Fmnl1/Hck
GO_BP_m3	GO:200125	regulation	3/539	159/23843	0.700433	0.81754	0.771406	Chrna4/Nl
GO_BP_m3	GO:004563	regulation	4/539	210/23843	0.701978	0.81754	0.771406	Ccl5/Ctr9/
GO_BP_m3	GO:000760	sensory pe	5/539	260/23843	0.702648	0.81754	0.771406	Mir106b/M
GO_BP_m3	GO:000254	monocyte	1/539	53/23843	0.702761	0.81754	0.771406	Ccl5
GO_BP_m3	GO:000687	cellular iro	1/539	53/23843	0.702761	0.81754	0.771406	Hamp2
GO_BP_m3	GO:001590	long-chain	1/539	53/23843	0.702761	0.81754	0.771406	Slc27a4
GO_BP_m3	GO:003004	actin filam	1/539	53/23843	0.702761	0.81754	0.771406	Carmil2
GO_BP_m3	GO:003265	regulation	1/539	53/23843	0.702761	0.81754	0.771406	Hk1
GO_BP_m3	GO:003506	regulation	1/539	53/23843	0.702761	0.81754	0.771406	Twist1
GO_BP_m3	GO:004273	exogenous	1/539	53/23843	0.702761	0.81754	0.771406	Cyp2c38
GO_BP_m3	GO:004658	negative r	1/539	53/23843	0.702761	0.81754	0.771406	Scai
GO_BP_m3	GO:005099	regulation	1/539	53/23843	0.702761	0.81754	0.771406	Twist1
GO_BP_m3	GO:007127	cellular res	1/539	53/23843	0.702761	0.81754	0.771406	Nlgn1
GO_BP_m3	GO:190054	negative r	1/539	53/23843	0.702761	0.81754	0.771406	Ier3
GO_BP_m3	GO:190339	regulation	1/539	53/23843	0.702761	0.81754	0.771406	Gpm6b
GO_BP_m3	GO:200064	positive re	1/539	53/23843	0.702761	0.81754	0.771406	Sox10
GO_BP_m3	GO:000184	neural tub	2/539	108/23843	0.704666	0.818648	0.772452	Ptch1/Twis
GO_BP_m3	GO:000282	positive re	2/539	108/23843	0.704666	0.818648	0.772452	Exosc6/Prk
GO_BP_m3	GO:000634	chromatin	2/539	108/23843	0.704666	0.818648	0.772452	Hypm/Uhr
GO_BP_m3	GO:001046	regulation	2/539	108/23843	0.704666	0.818648	0.772452	Chrna4/Nl
GO_BP_m3	GO:003236	regulation	2/539	108/23843	0.704666	0.818648	0.772452	Oxt/Ptch1
GO_BP_m3	GO:000616	purine nuc	5/539	261/23843	0.705812	0.819314	0.77308	Avp/Bcl2l1
GO_BP_m3	GO:000679	sulfur com	5/539	261/23843	0.705812	0.819314	0.77308	Dlat/Dld/G
GO_BP_m3	GO:000961	response t	5/539	261/23843	0.705812	0.819314	0.77308	Bcl2l1/Ccl5
GO_BP_m3	GO:003210	negative r	6/539	311/23843	0.707797	0.820485	0.774185	Abr/Foxf1/
GO_BP_m3	GO:002261	ribonucleo	4/539	212/23843	0.708962	0.820485	0.774185	Atxn2/Gcf
GO_BP_m3	GO:000177	leukocyte	2/539	109/23843	0.709453	0.820485	0.774185	Nkx2-3/Ts
GO_BP_m3	GO:000720	phospholi	2/539	109/23843	0.709453	0.820485	0.774185	Ltb4r2/S1p
GO_BP_m3	GO:006060	tube closu	2/539	109/23843	0.709453	0.820485	0.774185	Ptch1/Twis
GO_BP_m3	GO:000706	sister chro	1/539	54/23843	0.709495	0.820485	0.774185	Axin2
GO_BP_m3	GO:000833	endosome	1/539	54/23843	0.709495	0.820485	0.774185	Rhob
GO_BP_m3	GO:001052	positive re	1/539	54/23843	0.709495	0.820485	0.774185	Trpc1
GO_BP_m3	GO:003049	maturation	1/539	54/23843	0.709495	0.820485	0.774185	Nol10
GO_BP_m3	GO:003501	somatic st	1/539	54/23843	0.709495	0.820485	0.774185	Hes1
GO_BP_m3	GO:004505	T cell selec	1/539	54/23843	0.709495	0.820485	0.774185	Aire
GO_BP_m3	GO:004598	negative r	1/539	54/23843	0.709495	0.820485	0.774185	Ier3
GO_BP_m3	GO:004617	polyol bios	1/539	54/23843	0.709495	0.820485	0.774185	Ippk
GO_BP_m3	GO:004826	positive re	1/539	54/23843	0.709495	0.820485	0.774185	Ptpn5
GO_BP_m3	GO:000716	negative r	5/539	263/23843	0.71207	0.822242	0.775843	Bmp2/Btn1
GO_BP_m3	GO:000910	glycoprote	5/539	263/23843	0.71207	0.822242	0.775843	B3gnt6/D7
GO_BP_m3	GO:000926	ribonucleo	5/539	263/23843	0.71207	0.822242	0.775843	Avp/Bcl2l1
GO_BP_m3	GO:005086	regulation	5/539	263/23843	0.71207	0.822242	0.775843	Exosc6/Igh
GO_BP_m3	GO:001982	stem cell p	3/539	162/23843	0.712355	0.822242	0.775843	Ctr9/Hes1/
GO_BP_m3	GO:005126	protein tet	3/539	162/23843	0.712355	0.822242	0.775843	Ccl5/Nlgn1
GO_BP_m3	GO:200124	regulation	3/539	162/23843	0.712355	0.822242	0.775843	Bag5/Bcl2l
GO_BP_m3	GO:000858	female go	2/539	110/23843	0.714175	0.823679	0.777199	Bcl2l1/Ptpr

GO_BP_m3	GO:00508	negative re	2/539	110/23843	0.714175	0.823679	0.777199	Btn1a1/Ihh
GO_BP_m3	GO:00900	negative re	2/539	110/23843	0.714175	0.823679	0.777199	Axin2/Sox1
GO_BP_m3	GO:00062	nucleotide	1/539	55/23843	0.716077	0.823882	0.77739	Oraov1
GO_BP_m3	GO:00067	terpenoid	1/539	55/23843	0.716077	0.823882	0.77739	Lcn5
GO_BP_m3	GO:00326	regulation	1/539	55/23843	0.716077	0.823882	0.77739	Carmil2
GO_BP_m3	GO:003527	exocrine sy	1/539	55/23843	0.716077	0.823882	0.77739	Sox10
GO_BP_m3	GO:00380	peptidyl-ty	1/539	55/23843	0.716077	0.823882	0.77739	Hck
GO_BP_m3	GO:00426	ovulation c	1/539	55/23843	0.716077	0.823882	0.77739	Ptprn
GO_BP_m3	GO:004574	negative re	1/539	55/23843	0.716077	0.823882	0.77739	Ccl5
GO_BP_m3	GO:004867	response t	1/539	55/23843	0.716077	0.823882	0.77739	Ptprf
GO_BP_m3	GO:00989	regulation	1/539	55/23843	0.716077	0.823882	0.77739	Tacr1
GO_BP_m3	GO:004441	interspecie	8/539	412/23843	0.716619	0.824284	0.777769	Bcl2l1/Ccl5
GO_BP_m3	GO:19040	regulation	6/539	315/23843	0.719196	0.826827	0.780169	Chrna4/Ha
GO_BP_m3	GO:00439	regulation	4/539	215/23843	0.719215	0.826827	0.780169	Ccl5/Ctdp1
GO_BP_m3	GO:00083	RNA splicir	7/539	365/23843	0.721269	0.828028	0.781302	Celf5/Ddx4
GO_BP_m3	GO:00463	ribose pho	5/539	266/23843	0.72128	0.828028	0.781302	Avp/Bcl2l1
GO_BP_m3	GO:00725	purine-cor	5/539	266/23843	0.72128	0.828028	0.781302	Avp/Bcl2l1
GO_BP_m3	GO:014001	mitotic nuc	5/539	266/23843	0.72128	0.828028	0.781302	Ctdp1/Mac
GO_BP_m3	GO:00017	eye photor	1/539	56/23843	0.722511	0.828028	0.781302	Ihh
GO_BP_m3	GO:00022	innate imm	1/539	56/23843	0.722511	0.828028	0.781302	Defa27
GO_BP_m3	GO:001081	negative re	1/539	56/23843	0.722511	0.828028	0.781302	Plet1
GO_BP_m3	GO:00311	neuron prc	1/539	56/23843	0.722511	0.828028	0.781302	Ptprf
GO_BP_m3	GO:00903	cellular sen	1/539	56/23843	0.722511	0.828028	0.781302	Twist1
GO_BP_m3	GO:001931	hexose me	4/539	216/23843	0.722572	0.828028	0.781302	Dlat/Hk1/P
GO_BP_m3	GO:00511	cofactor bi	4/539	216/23843	0.722572	0.828028	0.781302	Dlat/Dld/H
GO_BP_m3	GO:00516	defense res	4/539	216/23843	0.722572	0.828028	0.781302	Ccl5/Ifna13
GO_BP_m3	GO:00343	adherens ju	2/539	112/23843	0.723426	0.828122	0.781391	Cdh26/Gpr
GO_BP_m3	GO:00433	response t	2/539	112/23843	0.723426	0.828122	0.781391	Gm13287/
GO_BP_m3	GO:004581	negative re	2/539	112/23843	0.723426	0.828122	0.781391	Hypm/Uhr
GO_BP_m3	GO:00508	defense res	2/539	112/23843	0.723426	0.828122	0.781391	Defa27/Tfe
GO_BP_m3	GO:19030	regulation	3/539	165/23843	0.723908	0.828453	0.781703	Foxc2/Myc
GO_BP_m3	GO:00060	alcohol me	5/539	267/23843	0.724303	0.828684	0.781921	Dhcr24/Fd
GO_BP_m3	GO:00070	chromosor	6/539	317/23843	0.724779	0.829009	0.782227	Ankle1/Axi
GO_BP_m3	GO:00511	cofactor m	9/539	465/23843	0.727162	0.831438	0.78452	Dlat/Dld/F
GO_BP_m3	GO:007121	cellular res	5/539	268/23843	0.727302	0.831438	0.78452	Ccl5/Ctr9/
GO_BP_m3	GO:00439	positive re	3/539	166/23843	0.727678	0.831438	0.78452	Ctdp1/Fam
GO_BP_m3	GO:00987	maintenan	3/539	166/23843	0.727678	0.831438	0.78452	Ctr9/Hes1/
GO_BP_m3	GO:004654	developme	2/539	113/23843	0.727956	0.831534	0.784611	Bcl2l1/Ptpr
GO_BP_m3	GO:00456	positive re	1/539	57/23843	0.728798	0.832055	0.785101	Bmp2
GO_BP_m3	GO:19034	positive re	1/539	57/23843	0.728798	0.832055	0.785101	Klf2
GO_BP_m3	GO:00316	cellular res	4/539	218/23843	0.729198	0.832069	0.785115	Lrrk2/Myo
GO_BP_m3	GO:00610	membrane	4/539	218/23843	0.729198	0.832069	0.785115	Stx12/Syt4
GO_BP_m3	GO:00719	regulation	8/539	418/23843	0.73127	0.834211	0.787137	Bmp2/Grm
GO_BP_m3	GO:001081	positive re	2/539	114/23843	0.732422	0.834911	0.787797	Foxf1/Prkc
GO_BP_m3	GO:003497	response t	4/539	219/23843	0.732467	0.834911	0.787797	Ankzf1/Lrr
GO_BP_m3	GO:00362	response t	4/539	219/23843	0.732467	0.834911	0.787797	Bmp2/Chr
GO_BP_m3	GO:00704	response t	5/539	270/23843	0.733231	0.83556	0.788409	Bmp2/Chr
GO_BP_m3	GO:00019	heart loopi	1/539	58/23843	0.734944	0.83569	0.788532	Ihh

GO_BP_m3	GO:004209	T-helper c	1/539	58/23843	0.734944	0.83569	0.788532	Prkcz
GO_BP_m3	GO:004277	mitochond	1/539	58/23843	0.734944	0.83569	0.788532	Dld
GO_BP_m3	GO:004685	regulation	1/539	58/23843	0.734944	0.83569	0.788532	S1pr1
GO_BP_m3	GO:005071	negative r	1/539	58/23843	0.734944	0.83569	0.788532	Btn1a1
GO_BP_m3	GO:190230	regulation	1/539	58/23843	0.734944	0.83569	0.788532	Stoml1
GO_BP_m3	GO:190435	regulation	1/539	58/23843	0.734944	0.83569	0.788532	Gnl3l
GO_BP_m3	GO:004343	negative r	3/539	168/23843	0.735096	0.83569	0.788532	Ptch1/Trib
GO_BP_m3	GO:200125	positive re	3/539	168/23843	0.735096	0.83569	0.788532	Ctr9/Jdp2/
GO_BP_m3	GO:005087	positive re	4/539	220/23843	0.735706	0.836162	0.788977	Exosc6/Igh
GO_BP_m3	GO:001402	primary ne	2/539	115/23843	0.736827	0.837215	0.78997	Ptch1/Twis
GO_BP_m3	GO:000705	spindle or	3/539	169/23843	0.738745	0.838921	0.791581	Ccdc155/C
GO_BP_m3	GO:003133	negative r	4/539	221/23843	0.738915	0.838921	0.791581	Axin2/Bag
GO_BP_m3	GO:004603	ATP metab	4/539	221/23843	0.738915	0.838921	0.791581	Bcl2l1/Dld/
GO_BP_m3	GO:000229	CD4-positi	1/539	59/23843	0.74095	0.839041	0.791694	Prkcz
GO_BP_m3	GO:000243	inflammat	1/539	59/23843	0.74095	0.839041	0.791694	Ak7
GO_BP_m3	GO:001936	arachidoni	1/539	59/23843	0.74095	0.839041	0.791694	Cyp2c38
GO_BP_m3	GO:003133	regulation	1/539	59/23843	0.74095	0.839041	0.791694	Syt4
GO_BP_m3	GO:003267	regulation	1/539	59/23843	0.74095	0.839041	0.791694	Il17d
GO_BP_m3	GO:004612	purine ribo	1/539	59/23843	0.74095	0.839041	0.791694	Lrrk2
GO_BP_m3	GO:005098	detection	1/539	59/23843	0.74095	0.839041	0.791694	Mkks
GO_BP_m3	GO:006032	face devel	1/539	59/23843	0.74095	0.839041	0.791694	Mkks
GO_BP_m3	GO:190351	mucopolys	1/539	59/23843	0.74095	0.839041	0.791694	Itih1
GO_BP_m3	GO:000854	epidermis	6/539	323/23843	0.741062	0.839041	0.791694	Hes1/Prkc
GO_BP_m3	GO:000827	regulation	2/539	116/23843	0.741169	0.839041	0.791694	Ccl5/Lrrk2
GO_BP_m3	GO:190336	regulation	4/539	222/23843	0.742094	0.839497	0.792124	Bag5/Lrrk2
GO_BP_m3	GO:000664	membrane	3/539	170/23843	0.742354	0.839497	0.792124	Elovl2/Enp
GO_BP_m3	GO:000695	compleme	3/539	170/23843	0.742354	0.839497	0.792124	Ighv1-53/I
GO_BP_m3	GO:003004	actin filam	3/539	170/23843	0.742354	0.839497	0.792124	Mkks/Carm
GO_BP_m3	GO:007182	ribonucleo	4/539	223/23843	0.745245	0.839905	0.792509	Atxn2/Gcfc
GO_BP_m3	GO:000275	immune re	8/539	424/23843	0.745401	0.839905	0.792509	Btn1a1/Igh
GO_BP_m3	GO:001605	carbohydr	2/539	117/23843	0.74545	0.839905	0.792509	Hk1/Ier3
GO_BP_m3	GO:004572	positive re	2/539	117/23843	0.74545	0.839905	0.792509	Rps3a1/Uc
GO_BP_m3	GO:190211	regulation	3/539	171/23843	0.745923	0.839905	0.792509	Atxn2/Hck/
GO_BP_m3	GO:000151	RNA meth	1/539	60/23843	0.746821	0.839905	0.792509	Trmo
GO_BP_m3	GO:000229	alpha-beta	1/539	60/23843	0.746821	0.839905	0.792509	Prkcz
GO_BP_m3	GO:000270	regulation	1/539	60/23843	0.746821	0.839905	0.792509	Prkcz
GO_BP_m3	GO:000276	positive re	1/539	60/23843	0.746821	0.839905	0.792509	Ccl5
GO_BP_m3	GO:000627	RNA-depe	1/539	60/23843	0.746821	0.839905	0.792509	Gnl3l
GO_BP_m3	GO:000685	drug trans	1/539	60/23843	0.746821	0.839905	0.792509	Slc25a17
GO_BP_m3	GO:000700	telomere	1/539	60/23843	0.746821	0.839905	0.792509	Gnl3l
GO_BP_m3	GO:000759	lactation	1/539	60/23843	0.746821	0.839905	0.792509	Ghrhr
GO_BP_m3	GO:000808	axo-dendr	1/539	60/23843	0.746821	0.839905	0.792509	Ap3s1
GO_BP_m3	GO:001061	regulation	1/539	60/23843	0.746821	0.839905	0.792509	Ctdp1
GO_BP_m3	GO:003033	DNA dama	1/539	60/23843	0.746821	0.839905	0.792509	Twist1
GO_BP_m3	GO:003292	circadian r	1/539	60/23843	0.746821	0.839905	0.792509	Rai1
GO_BP_m3	GO:003439	protein loc	1/539	60/23843	0.746821	0.839905	0.792509	Gpm6b
GO_BP_m3	GO:005119	regulation	1/539	60/23843	0.746821	0.839905	0.792509	Ier3
GO_BP_m3	GO:007005	intrinsic ap	1/539	60/23843	0.746821	0.839905	0.792509	Lrrk2

GO_BP_m3	GO:200075	regulation	1/539	60/23843	0.746821	0.839905	0.792509	Twist1
GO_BP_m3	GO:005160	detection c	9/539	474/23843	0.747333	0.84026	0.792844	Car6/Foxf1
GO_BP_m3	GO:003514	tube forma	3/539	172/23843	0.749453	0.841127	0.793662	Ptch1/Sdcc
GO_BP_m3	GO:007135	cellular res	3/539	172/23843	0.749453	0.841127	0.793662	Ccl5/Mir10
GO_BP_m3	GO:012003	regulation	3/539	172/23843	0.749453	0.841127	0.793662	Nlgn1/Carr
GO_BP_m3	GO:000193	regulation	2/539	118/23843	0.749671	0.841127	0.793662	Bmp2/Tgfb
GO_BP_m3	GO:004646	membrane	2/539	118/23843	0.749671	0.841127	0.793662	Elovl2/St6g
GO_BP_m3	GO:005072	positive reg	2/539	118/23843	0.749671	0.841127	0.793662	Ccl5/Il17d
GO_BP_m3	GO:006201	negative re	2/539	118/23843	0.749671	0.841127	0.793662	Bmp2/Ier3
GO_BP_m3	GO:190303	negative re	2/539	118/23843	0.749671	0.841127	0.793662	Btn1a1/Ihh
GO_BP_m3	GO:005090	detection c	7/539	377/23843	0.751392	0.842388	0.794851	Car6/Mkks/
GO_BP_m3	GO:000228	alpha-beta	1/539	61/23843	0.752559	0.842388	0.794851	Prkcz
GO_BP_m3	GO:001083	regulation	1/539	61/23843	0.752559	0.842388	0.794851	Myod1
GO_BP_m3	GO:003163	zymogen a	1/539	61/23843	0.752559	0.842388	0.794851	Dhcr24
GO_BP_m3	GO:004396	histone H3	1/539	61/23843	0.752559	0.842388	0.794851	Myod1
GO_BP_m3	GO:005159	response t	1/539	61/23843	0.752559	0.842388	0.794851	Fdx1
GO_BP_m3	GO:007126	cellular res	1/539	61/23843	0.752559	0.842388	0.794851	Mir194-2
GO_BP_m3	GO:190280	negative re	1/539	61/23843	0.752559	0.842388	0.794851	Susd2
GO_BP_m3	GO:190305	negative re	1/539	61/23843	0.752559	0.842388	0.794851	Bag5
GO_BP_m3	GO:000703	Golgi orga	2/539	119/23843	0.753831	0.843591	0.795987	Bag5/Lrrk2
GO_BP_m3	GO:006049	regulation	3/539	174/23843	0.756395	0.845799	0.798071	Nlgn1/Carr
GO_BP_m3	GO:190352	regulation	4/539	227/23843	0.757553	0.845799	0.798071	Avp/Oxt/Ta
GO_BP_m3	GO:000340	neural retir	1/539	62/23843	0.758167	0.845799	0.798071	Ihh
GO_BP_m3	GO:000924	glycolipid b	1/539	62/23843	0.758167	0.845799	0.798071	St6galnac5
GO_BP_m3	GO:001474	regulation	1/539	62/23843	0.758167	0.845799	0.798071	Ctdp1
GO_BP_m3	GO:004205	regulation	1/539	62/23843	0.758167	0.845799	0.798071	Ptprf
GO_BP_m3	GO:004244	pigment m	1/539	62/23843	0.758167	0.845799	0.798071	Trpc1
GO_BP_m3	GO:004277	ATP synthe	1/539	62/23843	0.758167	0.845799	0.798071	Dld
GO_BP_m3	GO:004542	regulation	1/539	62/23843	0.758167	0.845799	0.798071	Klf2
GO_BP_m3	GO:005105	positive reg	1/539	62/23843	0.758167	0.845799	0.798071	Cdon
GO_BP_m3	GO:190122	positive reg	1/539	62/23843	0.758167	0.845799	0.798071	C1qtnf4
GO_BP_m3	GO:200024	negative re	1/539	62/23843	0.758167	0.845799	0.798071	Adam24
GO_BP_m3	GO:007149	cellular res	5/539	279/23843	0.758748	0.846228	0.798475	Lrrk2/Mir19
GO_BP_m3	GO:009719	extrinsic ap	4/539	228/23843	0.760557	0.848025	0.800171	Bcl2l1/Pdia
GO_BP_m3	GO:007124	cellular res	2/539	121/23843	0.761972	0.849382	0.801451	Lrrk2/Nlgn
GO_BP_m3	GO:000081	sister chror	3/539	176/23843	0.763181	0.849487	0.80155	Axin2/Mad
GO_BP_m3	GO:200123	positive reg	3/539	176/23843	0.763181	0.849487	0.80155	Pdia3/Tgfb
GO_BP_m3	GO:000931	oligosacch	1/539	63/23843	0.763648	0.849487	0.80155	St6galnac5
GO_BP_m3	GO:003262	interleukin-	1/539	63/23843	0.763648	0.849487	0.80155	Carmil2
GO_BP_m3	GO:003460	cellular res	1/539	63/23843	0.763648	0.849487	0.80155	Hsf4
GO_BP_m3	GO:004227	purine nuc	1/539	63/23843	0.763648	0.849487	0.80155	Lrrk2
GO_BP_m3	GO:004396	histone H4	1/539	63/23843	0.763648	0.849487	0.80155	Myod1
GO_BP_m3	GO:190160	alpha-amir	1/539	63/23843	0.763648	0.849487	0.80155	Thnsl2
GO_BP_m3	GO:000916	nucleotide	2/539	122/23843	0.765955	0.851832	0.803763	Hk1/Ier3
GO_BP_m3	GO:009006	positive reg	4/539	230/23843	0.766479	0.852015	0.803936	Mad2l1/Ne
GO_BP_m3	GO:004311	receptor m	3/539	177/23843	0.766516	0.852015	0.803936	Atxn2/Lrrtr
GO_BP_m3	GO:003261	interleukin-	1/539	64/23843	0.769005	0.853457	0.805296	Hk1
GO_BP_m3	GO:003263	interleukin-	1/539	64/23843	0.769005	0.853457	0.805296	Il17d

GO_BP_m3	GO:004827	vesicle doc	1/539	64/23843	0.769005	0.853457	0.805296	Stx12
GO_BP_m3	GO:005076	positive re	1/539	64/23843	0.769005	0.853457	0.805296	Abr
GO_BP_m3	GO:005178	negative re	1/539	64/23843	0.769005	0.853457	0.805296	Mad2l1
GO_BP_m3	GO:006137	determinat	1/539	64/23843	0.769005	0.853457	0.805296	Ihh
GO_BP_m3	GO:000181	negative re	4/539	231/23843	0.769397	0.853545	0.805379	Btn1a1/Klf2
GO_BP_m3	GO:199077	protein loc	5/539	283/23843	0.769486	0.853545	0.805379	Bcl2l1/Grin
GO_BP_m3	GO:000736	determinat	2/539	123/23843	0.769879	0.853545	0.805379	Foxf1/Ihh
GO_BP_m3	GO:000958	detection c	2/539	123/23843	0.769879	0.853545	0.805379	Foxf1/Mkks
GO_BP_m3	GO:004586	positive re	8/539	436/23843	0.772093	0.85573	0.807441	Axin2/Bmp
GO_BP_m3	GO:001003	response t	4/539	232/23843	0.772286	0.85573	0.807441	Kcnmb4/Lr
GO_BP_m3	GO:007252	purine-cor	9/539	486/23843	0.7726	0.85573	0.807441	Avp/Bcl2l1
GO_BP_m3	GO:000703	vacuolar tr	2/539	124/23843	0.773746	0.85573	0.807441	2610002M
GO_BP_m3	GO:003021	erythrocyte	2/539	124/23843	0.773746	0.85573	0.807441	Klf2/L3mbt
GO_BP_m3	GO:009755	calcium ior	2/539	124/23843	0.773746	0.85573	0.807441	Grin2c/Trp
GO_BP_m3	GO:007037	ERK1 and	6/539	336/23843	0.773945	0.85573	0.807441	Avp/Bmp2
GO_BP_m3	GO:001049	proteasom	8/539	437/23843	0.774223	0.85573	0.807441	Ankzf1/Bag
GO_BP_m3	GO:000253	production	1/539	65/23843	0.774241	0.85573	0.807441	Il17d
GO_BP_m3	GO:000854	visual learn	1/539	65/23843	0.774241	0.85573	0.807441	Sgk1
GO_BP_m3	GO:001050	negative re	1/539	65/23843	0.774241	0.85573	0.807441	Lrrk2
GO_BP_m3	GO:005511	regulation	1/539	65/23843	0.774241	0.85573	0.807441	Ucn
GO_BP_m3	GO:004828	organelle f	3/539	180/23843	0.776293	0.857608	0.809213	Stx12/Syt4
GO_BP_m3	GO:004206	wound hea	6/539	337/23843	0.77634	0.857608	0.809213	Foxc2/Myc
GO_BP_m3	GO:000225	activation	9/539	488/23843	0.77663	0.857708	0.809307	Btn1a1/Cd
GO_BP_m3	GO:000681	potassium	4/539	234/23843	0.777979	0.858514	0.810068	Kcnh3/Kcn
GO_BP_m3	GO:200011	regulation	4/539	234/23843	0.777979	0.858514	0.810068	9230104L0
GO_BP_m3	GO:000154	ovarian foll	1/539	66/23843	0.779359	0.858514	0.810068	Bcl2l1
GO_BP_m3	GO:000865	cellular am	1/539	66/23843	0.779359	0.858514	0.810068	Thnsl2
GO_BP_m3	GO:003043	ubiquitin-c	1/539	66/23843	0.779359	0.858514	0.810068	Ankzf1
GO_BP_m3	GO:003096	endoplasm	1/539	66/23843	0.779359	0.858514	0.810068	Stc2
GO_BP_m3	GO:004340	negative re	1/539	66/23843	0.779359	0.858514	0.810068	Ptpn5
GO_BP_m3	GO:006068	regulation	1/539	66/23843	0.779359	0.858514	0.810068	Lrrk2
GO_BP_m3	GO:190118	regulation	1/539	66/23843	0.779359	0.858514	0.810068	Ptprf
GO_BP_m3	GO:190179	regulation	1/539	66/23843	0.779359	0.858514	0.810068	Twist1
GO_BP_m3	GO:005095	sensory pe	5/539	287/23843	0.779856	0.858842	0.810377	Mir106b/M
GO_BP_m3	GO:007121	cellular res	5/539	288/23843	0.782392	0.861413	0.812803	Ccl5/Ctr9/
GO_BP_m3	GO:005105	positive re	4/539	236/23843	0.783559	0.861865	0.81323	Areg/Exosc
GO_BP_m3	GO:000704	cell-substra	1/539	67/23843	0.784361	0.861865	0.81323	Gpm6b
GO_BP_m3	GO:003265	regulation	1/539	67/23843	0.784361	0.861865	0.81323	Hk1
GO_BP_m3	GO:003410	homotypic	1/539	67/23843	0.784361	0.861865	0.81323	Ccl5
GO_BP_m3	GO:004804	focal adhes	1/539	67/23843	0.784361	0.861865	0.81323	Gpm6b
GO_BP_m3	GO:004814	positive re	1/539	67/23843	0.784361	0.861865	0.81323	Rps3a1
GO_BP_m3	GO:190589	regulation	1/539	67/23843	0.784361	0.861865	0.81323	Lrrk2
GO_BP_m3	GO:004308	regulation	5/539	289/23843	0.784905	0.861865	0.81323	Ccl5/Lrrk2/
GO_BP_m3	GO:000270	positive re	2/539	127/23843	0.785009	0.861865	0.81323	Exosc6/Prk
GO_BP_m3	GO:003502	regulation	2/539	127/23843	0.785009	0.861865	0.81323	Abr/Scai
GO_BP_m3	GO:009030	nucleic aci	2/539	127/23843	0.785009	0.861865	0.81323	Dnase1l3/I
GO_BP_m3	GO:004354	endothelial	3/539	183/23843	0.785731	0.862188	0.813534	Foxc2/Rho
GO_BP_m3	GO:005122	negative re	3/539	183/23843	0.785731	0.862188	0.813534	Btn1a1/Lrr

GO_BP_m3	GO:00206	epithelial c	4/539	237/23843	0.786307	0.862188	0.813534	Cryaa/Foxc
GO_BP_m3	GO:003241	regulation	4/539	237/23843	0.786307	0.862188	0.813534	Chrna4/Hk
GO_BP_m3	GO:005140	stress-activ	4/539	237/23843	0.786307	0.862188	0.813534	Bmp2/Dixc
GO_BP_m3	GO:004576	regulation	5/539	290/23843	0.787396	0.86299	0.814291	Adm2/Ccl5
GO_BP_m3	GO:000661	protein exp	2/539	128/23843	0.788653	0.86299	0.814291	Ankle1/Nxt
GO_BP_m3	GO:003596	response to	2/539	128/23843	0.788653	0.86299	0.814291	Ankzf1/Stc
GO_BP_m3	GO:007145	cellular res	2/539	128/23843	0.788653	0.86299	0.814291	Myod1/Tw
GO_BP_m3	GO:000245	humoral im	3/539	184/23843	0.788803	0.86299	0.814291	Ighv1-53/Ig
GO_BP_m3	GO:007663	visual beha	1/539	68/23843	0.789249	0.86299	0.814291	Sgk1
GO_BP_m3	GO:003241	negative re	1/539	68/23843	0.789249	0.86299	0.814291	Stoml1
GO_BP_m3	GO:007037	negative re	1/539	68/23843	0.789249	0.86299	0.814291	Dusp26
GO_BP_m3	GO:014005	organelle lo	1/539	68/23843	0.789249	0.86299	0.814291	Stx12
GO_BP_m3	GO:190198	regulation	1/539	68/23843	0.789249	0.86299	0.814291	Twist1
GO_BP_m3	GO:190442	positive reg	1/539	68/23843	0.789249	0.86299	0.814291	Trpc1
GO_BP_m3	GO:004578	positive reg	6/539	343/23843	0.79031	0.86393	0.815178	Hes1/Mad2
GO_BP_m3	GO:003432	cell junctio	3/539	185/23843	0.791839	0.864941	0.816132	Cdh26/Gpr
GO_BP_m3	GO:000184	neural tube	2/539	129/23843	0.792242	0.864941	0.816132	Ptch1/Twis
GO_BP_m3	GO:004867	axon exten	2/539	129/23843	0.792242	0.864941	0.816132	Nkx6-1/Ra
GO_BP_m3	GO:005083	defense res	2/539	129/23843	0.792242	0.864941	0.816132	Defa27/Hc
GO_BP_m3	GO:009753	granulocyt	2/539	129/23843	0.792242	0.864941	0.816132	Ccl5/Prtn3
GO_BP_m3	GO:000608	cellular ald	1/539	69/23843	0.794027	0.86623	0.817348	Bmp2
GO_BP_m3	GO:005081	regulation	1/539	69/23843	0.794027	0.86623	0.817348	Bmp2
GO_BP_m3	GO:005115	positive reg	1/539	69/23843	0.794027	0.86623	0.817348	Myod1
GO_BP_m3	GO:003350	carbohydra	4/539	241/23843	0.797022	0.869056	0.820015	Hk1/Ptch1/
GO_BP_m3	GO:004259	glucose ho	4/539	241/23843	0.797022	0.869056	0.820015	Hk1/Ptch1/
GO_BP_m3	GO:000020	protein pol	3/539	187/23843	0.797801	0.869243	0.820191	Rnf144b/Tr
GO_BP_m3	GO:000600	glucose me	3/539	187/23843	0.797801	0.869243	0.820191	Dlat/Hk1/T
GO_BP_m3	GO:190495	negative re	3/539	187/23843	0.797801	0.869243	0.820191	Btn1a1/Lrrl
GO_BP_m3	GO:000680	nitric oxide	1/539	70/23843	0.798697	0.869288	0.820233	Klf2
GO_BP_m3	GO:000742	peripheral	1/539	70/23843	0.798697	0.869288	0.820233	Sox10
GO_BP_m3	GO:000749	endoderm	1/539	70/23843	0.798697	0.869288	0.820233	Ctr9
GO_BP_m3	GO:003241	lysosome lo	1/539	70/23843	0.798697	0.869288	0.820233	Foxf1
GO_BP_m3	GO:004440	symbiont p	6/539	347/23843	0.799248	0.869288	0.820233	Bcl2l1/Ccl5
GO_BP_m3	GO:004230	molting cyc	2/539	131/23843	0.799259	0.869288	0.820233	Krt83/Prss8
GO_BP_m3	GO:004263	hair cycle	2/539	131/23843	0.799259	0.869288	0.820233	Krt83/Prss8
GO_BP_m3	GO:007037	positive reg	4/539	242/23843	0.799633	0.869474	0.820409	Bmp2/Ccl5
GO_BP_m3	GO:000725	JNK cascad	3/539	188/23843	0.800728	0.869784	0.820702	Dixdc1/Gril
GO_BP_m3	GO:002191	neural tube	3/539	188/23843	0.800728	0.869784	0.820702	Hes1/Ptch1
GO_BP_m3	GO:003461	response to	3/539	188/23843	0.800728	0.869784	0.820702	Ccl5/Mir10
GO_BP_m3	GO:004643	organopho	3/539	188/23843	0.800728	0.869784	0.820702	Enpp7/Hk1
GO_BP_m3	GO:000193	endothelial	2/539	132/23843	0.802688	0.871163	0.822003	Bmp2/Tgfb
GO_BP_m3	GO:000985	determinat	2/539	132/23843	0.802688	0.871163	0.822003	Foxf1/Ihh
GO_BP_m3	GO:006104	regulation	2/539	132/23843	0.802688	0.871163	0.822003	Foxc2/Myc
GO_BP_m3	GO:190336	negative re	1/539	71/23843	0.803261	0.871163	0.822003	Bag5
GO_BP_m3	GO:000640	RNA localiz	3/539	189/23843	0.80362	0.871163	0.822003	Mcm3ap/N
GO_BP_m3	GO:007160	cell-matrix	3/539	189/23843	0.80362	0.871163	0.822003	Gpm6b/Ple
GO_BP_m3	GO:007180	cellular pot	3/539	189/23843	0.80362	0.871163	0.822003	Kcnh3/Kcn
GO_BP_m3	GO:007180	potassium	3/539	189/23843	0.80362	0.871163	0.822003	Kcnh3/Kcn

GO_BP_m3	GO:00303	negative re	4/539	244/23843	0.804772	0.872192	0.822973	Abr/Gpr17
GO_BP_m3	GO:00062	DNA-depe	2/539	133/23843	0.806065	0.872932	0.823672	Mgme1/M
GO_BP_m3	GO:00097	specificatio	2/539	133/23843	0.806065	0.872932	0.823672	Foxf1/Ihh
GO_BP_m3	GO:00507	negative re	2/539	133/23843	0.806065	0.872932	0.823672	Btn1a1/Syt
GO_BP_m3	GO:00448	cell cycle G	3/539	190/23843	0.806476	0.872986	0.823723	Ranbp3l/S
GO_BP_m3	GO:00719	positive re	5/539	298/23843	0.806521	0.872986	0.823723	Bmp2/Grm
GO_BP_m3	GO:00020	columnar/	1/539	72/23843	0.807722	0.873625	0.824326	Whrn
GO_BP_m3	GO:00421	retrograde	1/539	72/23843	0.807722	0.873625	0.824326	Lrrk2
GO_BP_m3	GO:00610	chaperone	1/539	72/23843	0.807722	0.873625	0.824326	Mkks
GO_BP_m3	GO:00190	viral life cy	3/539	191/23843	0.809297	0.874989	0.825613	Ccl5/Isg20
GO_BP_m3	GO:19012	nucleoside	2/539	134/23843	0.809391	0.874989	0.825613	Hk1/Ier3
GO_BP_m3	GO:000191	regulation	1/539	73/23843	0.812082	0.876544	0.82708	Dnase1l3
GO_BP_m3	GO:00108	telomere m	1/539	73/23843	0.812082	0.876544	0.82708	Gnl3l
GO_BP_m3	GO:00224	membrane	1/539	73/23843	0.812082	0.876544	0.82708	Stx12
GO_BP_m3	GO:00462	nitric oxide	1/539	73/23843	0.812082	0.876544	0.82708	Klf2
GO_BP_m3	GO:00463	regulation	1/539	73/23843	0.812082	0.876544	0.82708	Prkcz
GO_BP_m3	GO:00609	regulation	1/539	73/23843	0.812082	0.876544	0.82708	Uhrf1
GO_BP_m3	GO:00091	purine ribo	4/539	247/23843	0.81228	0.876544	0.82708	Bcl2l1/Dld/
GO_BP_m3	GO:00341	erythrocyte	2/539	135/23843	0.812665	0.876544	0.82708	Klf2/L3mbt
GO_BP_m3	GO:00509	positive re	2/539	135/23843	0.812665	0.876544	0.82708	Ccl5/S1pr1
GO_BP_m3	GO:00091	purine nuc	4/539	248/23843	0.814729	0.877865	0.828327	Bcl2l1/Dld/
GO_BP_m3	GO:00072	Rho protei	3/539	193/23843	0.814836	0.877865	0.828327	Abr/Rhob/
GO_BP_m3	GO:00068	amino acid	2/539	136/23843	0.81589	0.877865	0.828327	Avp/Syt4
GO_BP_m3	GO:00342	positive re	2/539	136/23843	0.81589	0.877865	0.828327	Rps3a1/Uc
GO_BP_m3	GO:00723	signal tran	2/539	136/23843	0.81589	0.877865	0.828327	Twist1/Ww
GO_BP_m3	GO:00525	regulation	7/539	407/23843	0.816333	0.877865	0.828327	9230104L0
GO_BP_m3	GO:00086	extrinsic a	1/539	74/23843	0.816343	0.877865	0.828327	Bcl2l1
GO_BP_m3	GO:00197	antibacteri	1/539	74/23843	0.816343	0.877865	0.828327	Defa27
GO_BP_m3	GO:00324	regulation	1/539	74/23843	0.816343	0.877865	0.828327	Bcl2l1
GO_BP_m3	GO:00325	maintenan	1/539	74/23843	0.816343	0.877865	0.828327	Hk1
GO_BP_m3	GO:00327	positive re	1/539	74/23843	0.816343	0.877865	0.828327	Carmil2
GO_BP_m3	GO:00716	mononucle	1/539	74/23843	0.816343	0.877865	0.828327	Ccl5
GO_BP_m3	GO:00345	cellular res	4/539	249/23843	0.817152	0.878516	0.828941	Ankzf1/Ba
GO_BP_m3	GO:19059	regulation	2/539	137/23843	0.819064	0.880351	0.830672	Oxt/Ptch1
GO_BP_m3	GO:00068	receptor-m	3/539	195/23843	0.820238	0.88102	0.831304	Atxn2/Lrrt
GO_BP_m3	GO:00067	isoprenoid	1/539	75/23843	0.820507	0.88102	0.831304	Lcn5
GO_BP_m3	GO:00713	cellular res	1/539	75/23843	0.820507	0.88102	0.831304	Ccl5
GO_BP_m3	GO:00988	vesicle-me	1/539	75/23843	0.820507	0.88102	0.831304	Exoc1
GO_BP_m3	GO:00091	ribonucleo	4/539	251/23843	0.821921	0.881945	0.832176	Bcl2l1/Dld/
GO_BP_m3	GO:00016	cellular glu	2/539	138/23843	0.82219	0.881945	0.832176	Hk1/Ptprn
GO_BP_m3	GO:00026	positive re	2/539	138/23843	0.82219	0.881945	0.832176	Ccl5/Tacr1
GO_BP_m3	GO:00072	female gan	2/539	138/23843	0.82219	0.881945	0.832176	Ccdc155/I
GO_BP_m3	GO:00316	response t	6/539	359/23843	0.8243	0.883183	0.833344	Lrrk2/Mkks
GO_BP_m3	GO:00064	protein O-	1/539	76/23843	0.824578	0.883183	0.833344	B3gnt6
GO_BP_m3	GO:00069	response t	1/539	76/23843	0.824578	0.883183	0.833344	Tsc22d3
GO_BP_m3	GO:00070	cell-substr	1/539	76/23843	0.824578	0.883183	0.833344	Gpm6b
GO_BP_m3	GO:00343	adherens j	1/539	76/23843	0.824578	0.883183	0.833344	Gpm6b
GO_BP_m3	GO:00512	regulation	1/539	76/23843	0.824578	0.883183	0.833344	Trpc1

GO_BP_m3	GO:000190	cell killing	2/539	139/23843	0.825267	0.88326	0.833417	Dnase1l3/H
GO_BP_m3	GO:000760	visual perc	2/539	139/23843	0.825267	0.88326	0.833417	Hsf4/Nxnl2
GO_BP_m3	GO:001657	histone ac	2/539	139/23843	0.825267	0.88326	0.833417	Myod1/Tw
GO_BP_m3	GO:003298	protein-co	3/539	198/23843	0.828089	0.885236	0.835282	Ckap2/Car
GO_BP_m3	GO:005189	regulation	2/539	140/23843	0.828296	0.885236	0.835282	Otud3/Tgf
GO_BP_m3	GO:000911	ribonucleo	1/539	77/23843	0.828556	0.885236	0.835282	Lrrk2
GO_BP_m3	GO:003310	mitochond	1/539	77/23843	0.828556	0.885236	0.835282	Bcs1l
GO_BP_m3	GO:003577	insulin secr	1/539	77/23843	0.828556	0.885236	0.835282	Ptprn
GO_BP_m3	GO:004227	ribosomal	1/539	77/23843	0.828556	0.885236	0.835282	Nol10
GO_BP_m3	GO:006097	coronary v	1/539	77/23843	0.828556	0.885236	0.835282	Tgfbr1
GO_BP_m3	GO:000815	actin polyn	3/539	199/23843	0.83064	0.887041	0.836985	Mkks/Carm
GO_BP_m3	GO:009028	regulation	4/539	255/23843	0.831151	0.887041	0.836985	Gdf5/Hes1
GO_BP_m3	GO:004213	neurotrans	2/539	141/23843	0.831278	0.887041	0.836985	Gcsh/Klf2
GO_BP_m3	GO:004273	drug catab	2/539	141/23843	0.831278	0.887041	0.836985	Cyp2c38/G
GO_BP_m3	GO:005125	negative re	2/539	141/23843	0.831278	0.887041	0.836985	Btn1a1/Ihh
GO_BP_m3	GO:000226	lymphocyt	1/539	78/23843	0.832444	0.887624	0.837535	Tsc22d3
GO_BP_m3	GO:004653	photorece	1/539	78/23843	0.832444	0.887624	0.837535	Ihh
GO_BP_m3	GO:200105	reactive nit	1/539	78/23843	0.832444	0.887624	0.837535	Klf2
GO_BP_m3	GO:000279	negative re	2/539	142/23843	0.834213	0.889069	0.838898	Btn1a1/Syt
GO_BP_m3	GO:007146	cellular res	2/539	142/23843	0.834213	0.889069	0.838898	Cyp2c38/U
GO_BP_m3	GO:003261	interleukin	1/539	79/23843	0.836245	0.89035	0.840107	Hk1
GO_BP_m3	GO:003450	protein loc	1/539	79/23843	0.836245	0.89035	0.840107	Gnl3l
GO_BP_m3	GO:004327	response t	1/539	79/23843	0.836245	0.89035	0.840107	Bcl2l1
GO_BP_m3	GO:004852	positive re	1/539	79/23843	0.836245	0.89035	0.840107	Ctdp1
GO_BP_m3	GO:003134	positive re	5/539	312/23843	0.836681	0.890594	0.840337	Ccl5/Il17d/
GO_BP_m3	GO:200014	negative re	4/539	258/23843	0.837809	0.891574	0.841262	Abr/Gpr17
GO_BP_m3	GO:007265	protein loc	8/539	472/23843	0.83988	0.893197	0.842794	Bcl2l1/Grik
GO_BP_m3	GO:006040	calcium ior	2/539	144/23843	0.839946	0.893197	0.842794	Grin2c/Trp
GO_BP_m3	GO:000700	plasma me	1/539	80/23843	0.839959	0.893197	0.842794	Pacsin3
GO_BP_m3	GO:001059	regulation	2/539	145/23843	0.842744	0.895673	0.84513	Foxc2/Rho
GO_BP_m3	GO:001605	carbohydra	3/539	204/23843	0.842913	0.895673	0.84513	B3gnt6/Ph
GO_BP_m3	GO:004328	regulation	3/539	204/23843	0.842913	0.895673	0.84513	Avp/Cryaa/
GO_BP_m3	GO:000193	positive re	1/539	81/23843	0.843589	0.895948	0.84539	Bmp2
GO_BP_m3	GO:003220	regulation	1/539	81/23843	0.843589	0.895948	0.84539	Gnl3l
GO_BP_m3	GO:000912	nucleoside	4/539	261/23843	0.844247	0.896425	0.84584	Bcl2l1/Dld/
GO_BP_m3	GO:190134	regulation	5/539	316/23843	0.844557	0.896533	0.845942	Adm2/Ccl5
GO_BP_m3	GO:003530	regulation	1/539	82/23843	0.847137	0.898827	0.848106	Dusp26
GO_BP_m3	GO:007233	intrinsic ap	1/539	82/23843	0.847137	0.898827	0.848106	Wwox
GO_BP_m3	GO:000007	mitotic sist	2/539	147/23843	0.848208	0.899698	0.848928	Mad2l1/Ub
GO_BP_m3	GO:007037	regulation	5/539	318/23843	0.848377	0.899698	0.848928	Bmp2/Ccl5
GO_BP_m3	GO:003462	cellular res	1/539	83/23843	0.850604	0.901171	0.850317	Stc2
GO_BP_m3	GO:004688	positive re	1/539	83/23843	0.850604	0.901171	0.850317	Avp
GO_BP_m3	GO:005114	positive re	1/539	83/23843	0.850604	0.901171	0.850317	Myod1
GO_BP_m3	GO:005501	cardiac mu	1/539	83/23843	0.850604	0.901171	0.850317	Ctdp1
GO_BP_m3	GO:004583	negative re	1/539	84/23843	0.853994	0.904086	0.853068	Bmp2
GO_BP_m3	GO:014002	exocytic pr	1/539	84/23843	0.853994	0.904086	0.853068	Nlgn1
GO_BP_m3	GO:001063	regulation	3/539	209/23843	0.854409	0.904086	0.853068	Foxc2/Rho
GO_BP_m3	GO:003287	regulation	3/539	209/23843	0.854409	0.904086	0.853068	Bmp2/Dixc

GO_BP_m3	GO:003476	positive reg	3/539	209/23843	0.854409	0.904086	0.853068	Gip/Prkcz/
GO_BP_m3	GO:003287	positive reg	2/539	150/23843	0.856081	0.90559	0.854487	Bmp2/Dixc
GO_BP_m3	GO:005105	regulation	4/539	267/23843	0.856478	0.90559	0.854487	Abr/Arhga
GO_BP_m3	GO:007030	regulation	3/539	210/23843	0.856618	0.90559	0.854487	Bmp2/Dixc
GO_BP_m3	GO:004277	signal trans	1/539	85/23843	0.857306	0.90559	0.854487	Twist1
GO_BP_m3	GO:004350	regulation	1/539	85/23843	0.857306	0.90559	0.854487	Ctdp1
GO_BP_m3	GO:004353	regulation	1/539	85/23843	0.857306	0.90559	0.854487	Foxc2
GO_BP_m3	GO:006184	antimicrob	1/539	85/23843	0.857306	0.90559	0.854487	Defa27
GO_BP_m3	GO:000183	embryonic	2/539	151/23843	0.858622	0.906497	0.855343	Ptch1/Twis
GO_BP_m3	GO:007030	positive reg	2/539	151/23843	0.858622	0.906497	0.855343	Bmp2/Dixc
GO_BP_m3	GO:003227	regulation	3/539	211/23843	0.858798	0.906497	0.855343	Mkks/Carm
GO_BP_m3	GO:000611	oxidative p	1/539	86/23843	0.860543	0.908116	0.856871	Dld
GO_BP_m3	GO:000926	cellular resp	2/539	152/23843	0.861121	0.908503	0.857236	Lrrk2/Myo
GO_BP_m3	GO:003109	stress-activ	4/539	270/23843	0.862282	0.909504	0.858181	Bmp2/Dixc
GO_BP_m3	GO:004354	positive reg	3/539	213/23843	0.86307	0.90989	0.858545	Ccl5/Prtn3/
GO_BP_m3	GO:004689	regulation	2/539	153/23843	0.86358	0.90989	0.858545	Avp/Bmp2
GO_BP_m3	GO:000269	positive reg	1/539	87/23843	0.863707	0.90989	0.858545	Ccl5
GO_BP_m3	GO:000689	post-Golgi	1/539	87/23843	0.863707	0.90989	0.858545	Exoc1
GO_BP_m3	GO:003252	response to	1/539	87/23843	0.863707	0.90989	0.858545	Halr1
GO_BP_m3	GO:003059	neutrophil	1/539	88/23843	0.8668	0.911806	0.860352	Ccl5
GO_BP_m3	GO:003134	regulation	1/539	88/23843	0.8668	0.911806	0.860352	Dnase1l3
GO_BP_m3	GO:007177	response to	1/539	88/23843	0.8668	0.911806	0.860352	Ier2
GO_BP_m3	GO:190122	regulation	1/539	88/23843	0.8668	0.911806	0.860352	C1qtnf4
GO_BP_m3	GO:190260	proton tran	1/539	88/23843	0.8668	0.911806	0.860352	Twist1
GO_BP_m3	GO:190342	regulation	1/539	88/23843	0.8668	0.911806	0.860352	Klf2
GO_BP_m3	GO:190161	organic hyd	7/539	437/23843	0.867305	0.912114	0.860644	Bmp2/Dhc
GO_BP_m3	GO:000657	cellular mo	2/539	155/23843	0.868379	0.912573	0.861076	Gdap1l1/G
GO_BP_m3	GO:003104	gene silenc	2/539	155/23843	0.868379	0.912573	0.861076	Mov10l1/P
GO_BP_m3	GO:005082	protein sta	2/539	155/23843	0.868379	0.912573	0.861076	Otud3/Stx1
GO_BP_m3	GO:000330	cardiac mu	1/539	89/23843	0.869822	0.91275	0.861243	Ctdp1
GO_BP_m3	GO:000666	glycolipid r	1/539	89/23843	0.869822	0.91275	0.861243	St6galnac5
GO_BP_m3	GO:000758	response to	1/539	89/23843	0.869822	0.91275	0.861243	Pdia3
GO_BP_m3	GO:005500	cardiac cell	1/539	89/23843	0.869822	0.91275	0.861243	Ctdp1
GO_BP_m3	GO:005507	iron ion ho	1/539	89/23843	0.869822	0.91275	0.861243	Hamp2
GO_BP_m3	GO:007055	response to	1/539	89/23843	0.869822	0.91275	0.861243	Ccl5
GO_BP_m3	GO:003253	regulation	6/539	385/23843	0.870045	0.912761	0.861254	Mkks/Nkx6
GO_BP_m3	GO:006040	cytosolic ca	2/539	156/23843	0.870719	0.913245	0.861711	Grin2c/Trp
GO_BP_m3	GO:007121	cellular resp	4/539	275/23843	0.871509	0.913395	0.861851	Bcl2l1/Kdm
GO_BP_m3	GO:010400	cellular resp	4/539	275/23843	0.871509	0.913395	0.861851	Bcl2l1/Kdm
GO_BP_m3	GO:000999	response to	6/539	386/23843	0.871587	0.913395	0.861851	Lrrk2/Mkks
GO_BP_m3	GO:000202	regulation	1/539	90/23843	0.872776	0.913395	0.861851	Oxt
GO_BP_m3	GO:004668	response to	1/539	90/23843	0.872776	0.913395	0.861851	Fdx1
GO_BP_m3	GO:005084	regulation	1/539	90/23843	0.872776	0.913395	0.861851	Lrrk2
GO_BP_m3	GO:005189	positive reg	1/539	90/23843	0.872776	0.913395	0.861851	Tgfbr1
GO_BP_m3	GO:007145	cellular resp	1/539	90/23843	0.872776	0.913395	0.861851	Twist1
GO_BP_m3	GO:190350	liposacchar	1/539	90/23843	0.872776	0.913395	0.861851	St6galnac5
GO_BP_m3	GO:004274	defense res	7/539	442/23843	0.874558	0.915037	0.863401	Defa27/Ha
GO_BP_m3	GO:001645	gene silenc	4/539	277/23843	0.875048	0.91513	0.863489	Hypm/Mov

GO_BP_m3	GO:000926	response t	2/539	158/23843	0.875286	0.91513	0.863489	Hsf4/Tacr1
GO_BP_m3	GO:007217	epithelial t	2/539	158/23843	0.875286	0.91513	0.863489	Ptch1/Twis
GO_BP_m3	GO:003650	ERAD path	1/539	91/23843	0.875663	0.915301	0.86365	Ankzf1
GO_BP_m3	GO:003083	regulation	2/539	159/23843	0.877514	0.91679	0.865055	Mkks/Carm
GO_BP_m3	GO:006004	retina deve	2/539	159/23843	0.877514	0.91679	0.865055	Cdon/Ihh
GO_BP_m3	GO:000222	toll-like re	1/539	92/23843	0.878484	0.917134	0.86538	Mapkapk3
GO_BP_m3	GO:000704	lysosomal	1/539	92/23843	0.878484	0.917134	0.86538	Rhob
GO_BP_m3	GO:001489	striated m	1/539	92/23843	0.878484	0.917134	0.86538	Ctdp1
GO_BP_m3	GO:004639	carboxylic	5/539	337/23843	0.880919	0.918228	0.866412	Avp/Elovl2/
GO_BP_m3	GO:000157	vasculoger	1/539	93/23843	0.881242	0.918228	0.866412	Foxf1
GO_BP_m3	GO:001077	negative re	1/539	93/23843	0.881242	0.918228	0.866412	Nlgn1
GO_BP_m3	GO:002178	glial cell de	1/539	93/23843	0.881242	0.918228	0.866412	Sox10
GO_BP_m3	GO:003083	positive re	1/539	93/23843	0.881242	0.918228	0.866412	Carmil2
GO_BP_m3	GO:004364	dicarboxyli	1/539	93/23843	0.881242	0.918228	0.866412	Dld
GO_BP_m3	GO:190382	organic aci	1/539	93/23843	0.881242	0.918228	0.866412	Slc19a1
GO_BP_m3	GO:190503	carboxylic	1/539	93/23843	0.881242	0.918228	0.866412	Slc19a1
GO_BP_m3	GO:001605	organic aci	5/539	338/23843	0.882454	0.919267	0.867393	Avp/Elovl2/
GO_BP_m3	GO:001489	muscle hyp	1/539	94/23843	0.883937	0.920143	0.868219	Ctdp1
GO_BP_m3	GO:003806	NIK/NF-ka	1/539	94/23843	0.883937	0.920143	0.868219	C1qtnf4
GO_BP_m3	GO:004691	cellular tra	1/539	94/23843	0.883937	0.920143	0.868219	Hamp2
GO_BP_m3	GO:001714	negative re	3/539	225/23843	0.886395	0.922438	0.870384	Caprin1/Hr
GO_BP_m3	GO:000911	nucleoside	1/539	95/23843	0.886571	0.922438	0.870384	Lrrk2
GO_BP_m3	GO:000664	triglyceride	1/539	96/23843	0.889146	0.923997	0.871856	Nkx2-3
GO_BP_m3	GO:001052	regulation	1/539	96/23843	0.889146	0.923997	0.871856	Trpc1
GO_BP_m3	GO:001921	regulation	1/539	96/23843	0.889146	0.923997	0.871856	Bmp2
GO_BP_m3	GO:004563	positive re	1/539	96/23843	0.889146	0.923997	0.871856	Ccl5
GO_BP_m3	GO:005077	positive re	1/539	96/23843	0.889146	0.923997	0.871856	Dixdc1
GO_BP_m3	GO:005127	negative re	4/539	287/23843	0.891507	0.926164	0.8739	Abr/Gpr17
GO_BP_m3	GO:190307	regulation	1/539	97/23843	0.891662	0.926164	0.8739	Bcl2l1
GO_BP_m3	GO:000641	regulation	6/539	401/23843	0.892934	0.927261	0.874936	Caprin1/Hr
GO_BP_m3	GO:000801	regulation	2/539	167/23843	0.894054	0.927372	0.87504	Oxt/Ucn
GO_BP_m3	GO:001972	calcium-m	2/539	167/23843	0.894054	0.927372	0.87504	Lrrk2/Tff2
GO_BP_m3	GO:003440	nucleobase	2/539	167/23843	0.894054	0.927372	0.87504	Hk1/Ier3
GO_BP_m3	GO:001624	regulation	1/539	98/23843	0.894121	0.927372	0.87504	Lrrk2
GO_BP_m3	GO:005165	maintenan	1/539	98/23843	0.894121	0.927372	0.87504	Hk1
GO_BP_m3	GO:002241	cellular cor	5/539	347/23843	0.89552	0.9286	0.876199	Ckap2/Dna
GO_BP_m3	GO:001975	polyol met	1/539	99/23843	0.896524	0.928968	0.876546	Ippk
GO_BP_m3	GO:004203	regulation	1/539	99/23843	0.896524	0.928968	0.876546	Trib2
GO_BP_m3	GO:004213	neurotrans	1/539	99/23843	0.896524	0.928968	0.876546	Klf2
GO_BP_m3	GO:000226	myeloid ce	2/539	169/23843	0.897852	0.930119	0.877632	Klf2/L3mbt
GO_BP_m3	GO:005254	regulation	5/539	349/23843	0.898248	0.930305	0.877807	9230104L0
GO_BP_m3	GO:004346	regulation	1/539	100/23843	0.898873	0.930728	0.878207	Ier3
GO_BP_m3	GO:001988	antigen pr	1/539	101/23843	0.901169	0.932348	0.879736	Kdm5d
GO_BP_m3	GO:004544	endothelial	1/539	101/23843	0.901169	0.932348	0.879736	Tgfbr1
GO_BP_m3	GO:200037	positive re	1/539	101/23843	0.901169	0.932348	0.879736	Klf2
GO_BP_m3	GO:004259	response t	2/539	171/23843	0.901523	0.932348	0.879736	Lrrk2/Myo
GO_BP_m3	GO:004632	regulation	2/539	171/23843	0.901523	0.932348	0.879736	Dixdc1/Gril
GO_BP_m3	GO:004518	maintenan	1/539	102/23843	0.903413	0.933853	0.881155	Hk1

GO_BP_m3	GO:190401	epithelial c	1/539	102/23843	0.903413	0.933853	0.881155	Bcl2l1
GO_BP_m3	GO:001407	response t	1/539	103/23843	0.905606	0.934994	0.882232	Fdx1
GO_BP_m3	GO:001895	phenol-co	1/539	103/23843	0.905606	0.934994	0.882232	Trpc1
GO_BP_m3	GO:003051	regulation	1/539	103/23843	0.905606	0.934994	0.882232	Nkx6-1
GO_BP_m3	GO:003264	regulation	1/539	103/23843	0.905606	0.934994	0.882232	Carmil2
GO_BP_m3	GO:004814	regulation	1/539	103/23843	0.905606	0.934994	0.882232	Rps3a1
GO_BP_m3	GO:001973	antimicrob	1/539	104/23843	0.907749	0.936757	0.883895	Defa27
GO_BP_m3	GO:190340	reactive ox	1/539	104/23843	0.907749	0.936757	0.883895	Klf2
GO_BP_m3	GO:001923	response t	1/539	105/23843	0.909843	0.938242	0.885296	Vmn1r202
GO_BP_m3	GO:004814	fibroblast p	1/539	105/23843	0.909843	0.938242	0.885296	Rps3a1
GO_BP_m3	GO:190437	regulation	1/539	105/23843	0.909843	0.938242	0.885296	Bcl2l1
GO_BP_m3	GO:001060	posttranscr	7/539	471/23843	0.910419	0.93861	0.885644	Axin2/Capr
GO_BP_m3	GO:000008	G1/S transi	2/539	177/23843	0.911811	0.938621	0.885654	Ranbp3l/U
GO_BP_m3	GO:001652	negative re	1/539	106/23843	0.91189	0.938621	0.885654	Klf2
GO_BP_m3	GO:004353	blood vess	1/539	106/23843	0.91189	0.938621	0.885654	Foxc2
GO_BP_m3	GO:005120	release of s	1/539	106/23843	0.91189	0.938621	0.885654	Trpc1
GO_BP_m3	GO:005128	negative re	1/539	106/23843	0.91189	0.938621	0.885654	Trpc1
GO_BP_m3	GO:003424	negative re	3/539	241/23843	0.911959	0.938621	0.885654	Caprin1/Hr
GO_BP_m3	GO:004508	regulation	3/539	241/23843	0.911959	0.938621	0.885654	Mapkapk3/
GO_BP_m3	GO:000806	regulation	2/539	178/23843	0.913425	0.939259	0.886256	Mkks/Carm
GO_BP_m3	GO:000190	leukocyte r	1/539	107/23843	0.913891	0.939259	0.886256	Dnase1l3
GO_BP_m3	GO:000641	translation	1/539	107/23843	0.913891	0.939259	0.886256	Dhx29
GO_BP_m3	GO:000834	adult loco	1/539	107/23843	0.913891	0.939259	0.886256	Gip
GO_BP_m3	GO:005122	spindle ass	1/539	107/23843	0.913891	0.939259	0.886256	Ccdc155
GO_BP_m3	GO:005128	regulation	1/539	107/23843	0.913891	0.939259	0.886256	Trpc1
GO_BP_m3	GO:001633	morphoge	2/539	179/23843	0.915011	0.939694	0.886667	Ptch1/Twis
GO_BP_m3	GO:003083	regulation	2/539	179/23843	0.915011	0.939694	0.886667	Mkks/Carm
GO_BP_m3	GO:009752	myeloid le	2/539	179/23843	0.915011	0.939694	0.886667	Ccl5/Prtn3
GO_BP_m3	GO:000698	response t	1/539	108/23843	0.915846	0.939694	0.886667	Stc2
GO_BP_m3	GO:005120	sequesteri	1/539	108/23843	0.915846	0.939694	0.886667	Trpc1
GO_BP_m3	GO:007134	cellular res	1/539	108/23843	0.915846	0.939694	0.886667	Ccl5
GO_BP_m3	GO:200027	regulation	1/539	108/23843	0.915846	0.939694	0.886667	Gnl3l
GO_BP_m3	GO:004001	negative re	4/539	305/23843	0.916395	0.940032	0.886986	Abr/Gpr17
GO_BP_m3	GO:003158	cell-substr	4/539	306/23843	0.917615	0.940756	0.887669	Foxf1/Gpm
GO_BP_m3	GO:007162	granulocyt	1/539	109/23843	0.917758	0.940756	0.887669	Ccl5
GO_BP_m3	GO:200018	negative re	1/539	109/23843	0.917758	0.940756	0.887669	Klf2
GO_BP_m3	GO:003030	negative re	2/539	181/23843	0.918101	0.940884	0.887789	Ctdp1/Nf2
GO_BP_m3	GO:200037	regulation	2/539	182/23843	0.919606	0.941996	0.888839	Ier3/Klf2
GO_BP_m3	GO:000268	regulation	1/539	110/23843	0.919625	0.941996	0.888839	Ccl5
GO_BP_m3	GO:000194	hair follicle	1/539	111/23843	0.921451	0.943641	0.890391	Prss8
GO_BP_m3	GO:007265	protein loc	3/539	249/23843	0.922678	0.944673	0.891364	Bcl2l1/Prkc
GO_BP_m3	GO:004208	cytokine bi	1/539	112/23843	0.923235	0.945017	0.89169	Trib2
GO_BP_m3	GO:004819	Golgi vesic	3/539	250/23843	0.923931	0.94545	0.892098	Cux2/Exoc
GO_BP_m3	GO:001605	vesicle org	4/539	312/23843	0.924608	0.94545	0.892098	Ptprn/Stx1
GO_BP_m3	GO:001921	regulation	4/539	312/23843	0.924608	0.94545	0.892098	Avp/Bmp2/
GO_BP_m3	GO:004586	positive re	4/539	312/23843	0.924608	0.94545	0.892098	Lrrk2/Pacsi
GO_BP_m3	GO:003572	sodium io	1/539	113/23843	0.924978	0.94545	0.892098	Stoml1
GO_BP_m3	GO:009877	skin epider	1/539	113/23843	0.924978	0.94545	0.892098	Prss8

GO_BP_m3	GO:00224	molting cy	1/539	114/23843	0.926682	0.946586	0.89317	Prss8
GO_BP_m3	GO:00224	hair cycle	1/539	114/23843	0.926682	0.946586	0.89317	Prss8
GO_BP_m3	GO:00162	macroauto	2/539	187/23843	0.926751	0.946586	0.89317	Lrrk2/Stx1
GO_BP_m3	GO:0018	liver devel	1/539	115/23843	0.928348	0.947091	0.893646	Hes1
GO_BP_m3	GO:00066	acylglycer	1/539	115/23843	0.928348	0.947091	0.893646	Nkx2-3
GO_BP_m3	GO:00068	ER to Golg	1/539	115/23843	0.928348	0.947091	0.893646	Ier3ip1
GO_BP_m3	GO:00326	interferon-	1/539	115/23843	0.928348	0.947091	0.893646	Carmil2
GO_BP_m3	GO:00362	cellular res	1/539	115/23843	0.928348	0.947091	0.893646	Twist1
GO_BP_m3	GO:00421	cytokine m	1/539	116/23843	0.929975	0.948076	0.894576	Trib2
GO_BP_m3	GO:00517	interaction	1/539	116/23843	0.929975	0.948076	0.894576	Bcl2l1
GO_BP_m3	GO:19013	negative re	1/539	116/23843	0.929975	0.948076	0.894576	Klf2
GO_BP_m3	GO:005077	regulation	2/539	190/23843	0.930745	0.948636	0.895104	Dixdc1/Nk
GO_BP_m3	GO:00725	reactive ox	3/539	256/23843	0.931064	0.948735	0.895198	Ier3/Klf2/L
GO_BP_m3	GO:00066	neutral lipi	1/539	117/23843	0.931566	0.949022	0.895468	Nkx2-3
GO_BP_m3	GO:00513	positive re	7/539	495/23843	0.933082	0.94993	0.896325	BC048507/
GO_BP_m3	GO:00169	antibiotic	1/539	118/23843	0.933121	0.94993	0.896325	Dlat
GO_BP_m3	GO:00610	hepaticobil	1/539	118/23843	0.933121	0.94993	0.896325	Hes1
GO_BP_m3	GO:00305	leukocyte	2/539	193/23843	0.934533	0.951026	0.897359	Ccl5/S1pr1
GO_BP_m3	GO:00613	regulation	1/539	119/23843	0.93464	0.951026	0.897359	Nkx6-1
GO_BP_m3	GO:00342	regulation	6/539	441/23843	0.935646	0.951824	0.898112	Caprin1/Hr
GO_BP_m3	GO:19016	alpha-ami	2/539	195/23843	0.936949	0.952885	0.899113	Gcsh/Thnsl
GO_BP_m3	GO:000072	telomere m	1/539	121/23843	0.937576	0.952885	0.899113	Gnl3l
GO_BP_m3	GO:000222	pattern rec	1/539	121/23843	0.937576	0.952885	0.899113	Mapkapk3
GO_BP_m3	GO:19016	glycosyl co	1/539	121/23843	0.937576	0.952885	0.899113	Lrrk2
GO_BP_m3	GO:00069	nucleus or	1/539	122/23843	0.938995	0.953649	0.899834	Ankle1
GO_BP_m3	GO:00095	detection	1/539	122/23843	0.938995	0.953649	0.899834	Mkks
GO_BP_m3	GO:00319	TOR signal	1/539	122/23843	0.938995	0.953649	0.899834	Prr5
GO_BP_m3	GO:000931	response t	5/539	388/23843	0.940335	0.953738	0.899918	Bcl2l1/Crya
GO_BP_m3	GO:00027	innate imm	1/539	123/23843	0.940381	0.953738	0.899918	Mapkapk3
GO_BP_m3	GO:00322	telomere o	1/539	123/23843	0.940381	0.953738	0.899918	Gnl3l
GO_BP_m3	GO:00459	regulation	1/539	123/23843	0.940381	0.953738	0.899918	Hes1
GO_BP_m3	GO:19028	regulation	1/539	123/23843	0.940381	0.953738	0.899918	Susd2
GO_BP_m3	GO:00450	positive re	2/539	198/23843	0.940414	0.953738	0.899918	Mapkapk3/
GO_BP_m3	GO:00713	cellular res	1/539	124/23843	0.941736	0.954852	0.90097	Ptprn
GO_BP_m3	GO:003227	positive re	1/539	125/23843	0.94306	0.955969	0.902023	Carmil2
GO_BP_m3	GO:00080	cell recogn	3/539	268/23843	0.943519	0.956209	0.90225	Ighv1-53/I
GO_BP_m3	GO:00713	cellular res	1/539	126/23843	0.944354	0.956708	0.902721	Ptprn
GO_BP_m3	GO:00705	calcium io	3/539	269/23843	0.944457	0.956708	0.902721	Catsper4/
GO_BP_m3	GO:005092	regulation	2/539	202/23843	0.944755	0.956784	0.902792	Ccl5/S1pr1
GO_BP_m3	GO:000652	cellular am	3/539	270/23843	0.94538	0.956932	0.902932	Gcsh/Thnsl
GO_BP_m3	GO:00463	positive re	1/539	127/23843	0.945618	0.956932	0.902932	Dixdc1
GO_BP_m3	GO:007132	cellular res	1/539	127/23843	0.945618	0.956932	0.902932	Ptprn
GO_BP_m3	GO:00302	lipid modif	2/539	203/23843	0.945792	0.956932	0.902932	Slc25a17/T
GO_BP_m3	GO:006032	cell chemo	3/539	274/23843	0.948933	0.959884	0.905717	Ccl5/Hoxb
GO_BP_m3	GO:00550	lipid home	1/539	130/23843	0.949243	0.959971	0.9058	Gip
GO_BP_m3	GO:003434	response t	1/539	131/23843	0.950396	0.960685	0.906474	Ccl5
GO_BP_m3	GO:005507	transition	1/539	131/23843	0.950396	0.960685	0.906474	Hamp2
GO_BP_m3	GO:00902	negative re	1/539	133/23843	0.952626	0.962713	0.908386	Ptprf

GO_BP_m3	GO:000941	response t	1/539	134/23843	0.953703	0.963348	0.908985	Cryaa
GO_BP_m3	GO:007132	cellular res	1/539	134/23843	0.953703	0.963348	0.908985	Ptprn
GO_BP_m3	GO:001648	cytosolic tr	1/539	135/23843	0.954755	0.963731	0.909347	Lrrk2
GO_BP_m3	GO:003021	keratinocyt	1/539	135/23843	0.954755	0.963731	0.909347	Prkch
GO_BP_m3	GO:190406	positive re	1/539	135/23843	0.954755	0.963731	0.909347	Trpc1
GO_BP_m3	GO:003210	positive re	3/539	284/23843	0.956895	0.965664	0.911171	Ccl5/Il17d/
GO_BP_m3	GO:000941	response t	2/539	217/23843	0.958499	0.967055	0.912483	Cyp2c38/U
GO_BP_m3	GO:004255	myelinatio	1/539	139/23843	0.958732	0.967063	0.912491	Sox10
GO_BP_m3	GO:000221	activation	1/539	140/23843	0.95967	0.967782	0.91317	Mapkapk3
GO_BP_m3	GO:000727	ensheathm	1/539	142/23843	0.961484	0.969156	0.914466	Sox10
GO_BP_m3	GO:008036	axon enshe	1/539	142/23843	0.961484	0.969156	0.914466	Sox10
GO_BP_m3	GO:001067	regulation	1/539	143/23843	0.96236	0.969637	0.91492	Ier3
GO_BP_m3	GO:004002	regulation	3/539	292/23843	0.962412	0.969637	0.91492	Hypm/Klf2/
GO_BP_m3	GO:000633	chromatin	1/539	145/23843	0.964052	0.971061	0.916264	Satb1
GO_BP_m3	GO:007556	cell aging	1/539	147/23843	0.965669	0.972461	0.917585	Twist1
GO_BP_m3	GO:000633	chromatin	1/539	148/23843	0.96645	0.97302	0.918112	Chd3
GO_BP_m3	GO:190316	regulation	1/539	149/23843	0.967213	0.973332	0.918406	Trpc1
GO_BP_m3	GO:190547	regulation	1/539	149/23843	0.967213	0.973332	0.918406	Bcl2l1
GO_BP_m3	GO:006156	axon devel	6/539	493/23843	0.968313	0.97421	0.919235	Dixdc1/Nk
GO_BP_m3	GO:003476	positive re	1/539	151/23843	0.968688	0.974359	0.919376	Trpc1
GO_BP_m3	GO:000726	small GTPa	6/539	495/23843	0.969194	0.97464	0.919641	Abr/Arhga
GO_BP_m3	GO:007189	DNA biosy	1/539	153/23843	0.970096	0.975113	0.920087	Gnl3l
GO_BP_m3	GO:001050	regulation	2/539	234/23843	0.970118	0.975113	0.920087	Lrrk2/Tfeb
GO_BP_m3	GO:004657	regulation	2/539	237/23843	0.971813	0.976588	0.921479	Abr/Scai
GO_BP_m3	GO:000610	regulation	1/539	167/23843	0.978335	0.982453	0.927013	Ier3
GO_BP_m3	GO:000974	response t	1/539	167/23843	0.978335	0.982453	0.927013	Ptprn
GO_BP_m3	GO:009716	ammoniun	1/539	167/23843	0.978335	0.982453	0.927013	Enpp7
GO_BP_m3	GO:000740	axonogene	5/539	461/23843	0.979715	0.983445	0.927949	Dixdc1/Nk
GO_BP_m3	GO:000974	response t	1/539	170/23843	0.979782	0.983445	0.927949	Ptprn
GO_BP_m3	GO:001619	endosomal	1/539	171/23843	0.980242	0.983448	0.927951	Lrrk2
GO_BP_m3	GO:003428	response t	1/539	171/23843	0.980242	0.983448	0.927951	Ptprn
GO_BP_m3	GO:000974	response t	1/539	184/23843	0.985356	0.988347	0.932574	Ptprn
GO_BP_m3	GO:005126	protein ho	3/539	349/23843	0.986261	0.989025	0.933214	Cryaa/Hsf4
GO_BP_m3	GO:000726	Ras protei	4/539	426/23843	0.987752	0.990127	0.934254	Abr/Dhcr2
GO_BP_m3	GO:000724	I-kappaB k	1/539	192/23843	0.987822	0.990127	0.934254	Tifab
GO_BP_m3	GO:000941	response t	2/539	281/23843	0.988185	0.990261	0.93438	Cryaa/Sgk1
GO_BP_m3	GO:007110	DNA confo	1/539	204/23843	0.990765	0.992353	0.936354	Top3b
GO_BP_m3	GO:000691	autophagy	3/539	372/23843	0.990967	0.992353	0.936354	Lrrk2/Stx12
GO_BP_m3	GO:006191	process uti	3/539	372/23843	0.990967	0.992353	0.936354	Lrrk2/Stx12
GO_BP_m3	GO:007182	protein-D	1/539	211/23843	0.992142	0.993299	0.937247	Gtf2e1
GO_BP_m3	GO:005123	maintenan	2/539	303/23843	0.992412	0.993337	0.937283	Hk1/Trpc1
GO_BP_m3	GO:000741	axon guida	1/539	214/23843	0.992668	0.993362	0.937306	Ptch1
GO_BP_m3	GO:009748	neuron pro	1/539	216/23843	0.992999	0.993461	0.9374	Ptch1
GO_BP_m3	GO:004648	glyceroli	1/539	306/23843	0.999126	0.999359	0.942965	Nkx2-3
GO_BP_m3	GO:000664	phospholi	1/539	332/23843	0.999522	0.999522	0.943118	Enpp7
GO_BP_m4	GO:007129	cellular res	4/727	12/23843	0.000349	0.592594	0.583728	Folr1/Gas6
GO_BP_m4	GO:003327	response t	5/727	25/23843	0.000832	0.592594	0.583728	Folr1/Gas6
GO_BP_m4	GO:003057	bile acid c	2/727	2/23843	0.000928	0.592594	0.583728	Akr1d1/Cy

GO_BP_m4	GO:005085	regulation	6/727	39/23843	0.001088	0.592594	0.583728	Bcl10/Btn2
GO_BP_m4	GO:004350	regulation	9/727	88/23843	0.001448	0.592594	0.583728	Ager/Dusp
GO_BP_m4	GO:004361	keratinocyt	6/727	42/23843	0.00162	0.592594	0.583728	Cdh3/Fst/C
GO_BP_m4	GO:004350	positive reg	8/727	73/23843	0.001686	0.592594	0.583728	Ager/Ern2/
GO_BP_m4	GO:001083	regulation	5/727	31/23843	0.002287	0.592594	0.583728	Cdh3/Ovol
GO_BP_m4	GO:004564	regulation	4/727	19/23843	0.002305	0.592594	0.583728	Il34/Ripk1/
GO_BP_m4	GO:001582	L-serine tra	2/727	3/23843	0.002729	0.592594	0.583728	Slc1a4/Slc1
GO_BP_m4	GO:007149	cellular res	2/727	3/23843	0.002729	0.592594	0.583728	Mme/Ppid
GO_BP_m4	GO:200128	positive reg	2/727	3/23843	0.002729	0.592594	0.583728	Itsn1/Nedd
GO_BP_m4	GO:190370	positive reg	14/727	198/23843	0.003133	0.592594	0.583728	Ager/Btn2a
GO_BP_m4	GO:004412	regulation	4/727	21/23843	0.003392	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:007258	caveolin-m	3/727	11/23843	0.003878	0.592594	0.583728	Itsn1/Mlc1/
GO_BP_m4	GO:000965	response to	5/727	35/23843	0.003954	0.592594	0.583728	Mir29b-1/I
GO_BP_m4	GO:003167	cellular res	5/727	35/23843	0.003954	0.592594	0.583728	Folr1/Gas6
GO_BP_m4	GO:005085	regulation	6/727	51/23843	0.004414	0.592594	0.583728	Bcl10/Btn2
GO_BP_m4	GO:004414	modulation	4/727	23/23843	0.004782	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:007147	cellular res	4/727	23/23843	0.004782	0.592594	0.583728	Mir29b-1/I
GO_BP_m4	GO:001624	autophago	2/727	4/23843	0.005348	0.592594	0.583728	Stx17/Vam
GO_BP_m4	GO:003232	serine trans	2/727	4/23843	0.005348	0.592594	0.583728	Slc1a4/Slc1
GO_BP_m4	GO:006021	endocardiu	2/727	4/23843	0.005348	0.592594	0.583728	Ovol2/Sox1
GO_BP_m4	GO:000758	response to	8/727	89/23843	0.005802	0.592594	0.583728	Folr1/Gas6
GO_BP_m4	GO:004565	positive reg	3/727	13/23843	0.006424	0.592594	0.583728	Il34/Ripk1/
GO_BP_m4	GO:004411	growth of s	4/727	25/23843	0.006511	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:004558	regulation	4/727	25/23843	0.006511	0.592594	0.583728	Btn2a2/Du
GO_BP_m4	GO:007037	ERK1 and E	19/727	336/23843	0.007681	0.592594	0.583728	Ager/Btn2a
GO_BP_m4	GO:004411	growth inv	4/727	27/23843	0.00861	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:004411	growth of s	4/727	27/23843	0.00861	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:000686	glutamine	2/727	5/23843	0.008733	0.592594	0.583728	Slc1a5/Slc3
GO_BP_m4	GO:001980	quinolinate	2/727	5/23843	0.008733	0.592594	0.583728	Acmsd/Kyn
GO_BP_m4	GO:003278	bile acid se	2/727	5/23843	0.008733	0.592594	0.583728	Abcb4/Slc5
GO_BP_m4	GO:004484	estrous cyc	2/727	5/23843	0.008733	0.592594	0.583728	Erbb2/Esr2
GO_BP_m4	GO:004802	positive reg	2/727	5/23843	0.008733	0.592594	0.583728	Cdh3/Zeb2
GO_BP_m4	GO:007029	N-acyletha	2/727	5/23843	0.008733	0.592594	0.583728	Abhd4/Gdp
GO_BP_m4	GO:009901	modificatio	2/727	5/23843	0.008733	0.592594	0.583728	Synpo/Tiam
GO_BP_m4	GO:004563	positive reg	8/727	96/23843	0.009062	0.592594	0.583728	Car2/Gata1
GO_BP_m4	GO:007037	regulation	18/727	318/23843	0.009215	0.592594	0.583728	Ager/Btn2a
GO_BP_m4	GO:190210	positive reg	11/727	159/23843	0.0097	0.592594	0.583728	Ager/Btn2a
GO_BP_m4	GO:007233	modified a	3/727	15/23843	0.009767	0.592594	0.583728	Folr1/Slc16
GO_BP_m4	GO:200064	negative re	3/727	15/23843	0.009767	0.592594	0.583728	Ctnna1/Nfa
GO_BP_m4	GO:004506	regulatory	4/727	28/23843	0.009807	0.592594	0.583728	Btn2a2/Du
GO_BP_m4	GO:000218	cytoplasmi	8/727	98/23843	0.010205	0.592594	0.583728	Eif3a/Rpl22
GO_BP_m4	GO:200123	positive reg	6/727	61/23843	0.010548	0.592594	0.583728	Bcl10/Ctnn
GO_BP_m4	GO:007121	cellular res	16/727	275/23843	0.010665	0.592594	0.583728	Agap3/Gna
GO_BP_m4	GO:010400	cellular res	16/727	275/23843	0.010665	0.592594	0.583728	Agap3/Gna
GO_BP_m4	GO:005189	regulation	10/727	140/23843	0.010803	0.592594	0.583728	Btn2a2/Dd
GO_BP_m4	GO:200124	positive reg	3/727	16/23843	0.011752	0.592594	0.583728	Ctnna1/Inh
GO_BP_m4	GO:001572	canalicular	2/727	6/23843	0.012836	0.592594	0.583728	Aqp9/Mip
GO_BP_m4	GO:003154	brain-deriv	2/727	6/23843	0.012836	0.592594	0.583728	Fam72a/Tia

GO_BP_m4	GO:003279	negative re	2/727	6/23843	0.012836	0.592594	0.583728	Ddit3/Sik1
GO_BP_m4	GO:004687	quinolinate	2/727	6/23843	0.012836	0.592594	0.583728	Acmsd/Kyr
GO_BP_m4	GO:190037	positive reg	2/727	6/23843	0.012836	0.592594	0.583728	Cdh3/Zeb2
GO_BP_m4	GO:200128	regulation	2/727	6/23843	0.012836	0.592594	0.583728	Itsn1/Nedd
GO_BP_m4	GO:004263	regulation	4/727	31/23843	0.014028	0.592594	0.583728	Cdh3/Fst/In
GO_BP_m4	GO:007147	cellular res	10/727	146/23843	0.014197	0.592594	0.583728	Agap3/Gna
GO_BP_m4	GO:004349	protein kin	11/727	168/23843	0.014222	0.592594	0.583728	Btn2a2/Dd
GO_BP_m4	GO:007588	digestion	9/727	125/23843	0.014463	0.592594	0.583728	Akr1d1/Ap
GO_BP_m4	GO:003127	regulation	5/727	48/23843	0.0151	0.592594	0.583728	Cap2/Gng7
GO_BP_m4	GO:200123	regulation	5/727	48/23843	0.0151	0.592594	0.583728	Ctnna1/Ga
GO_BP_m4	GO:001589	drug transp	12/727	193/23843	0.015642	0.592594	0.583728	Abcb1b/Ab
GO_BP_m4	GO:000608	acetyl-CoA	4/727	32/23843	0.015655	0.592594	0.583728	Kynu/Nudt
GO_BP_m4	GO:004633	positive reg	9/727	127/23843	0.0159	0.592594	0.583728	Ager/Ern2/
GO_BP_m4	GO:004434	cellular res	7/727	86/23843	0.01602	0.592594	0.583728	Fgf17/Fgf4
GO_BP_m4	GO:003223	regulation	3/727	18/23843	0.016369	0.592594	0.583728	Rbm26/Rip
GO_BP_m4	GO:007147	cellular hyp	3/727	18/23843	0.016369	0.592594	0.583728	Mir29b-1/M
GO_BP_m4	GO:000316	endocardiu	2/727	7/23843	0.017609	0.592594	0.583728	Ovol2/Sox1
GO_BP_m4	GO:000317	aortic valve	2/727	7/23843	0.017609	0.592594	0.583728	Efna1/Nfat
GO_BP_m4	GO:000318	aortic valve	2/727	7/23843	0.017609	0.592594	0.583728	Efna1/Nfat
GO_BP_m4	GO:005179	negative re	2/727	7/23843	0.017609	0.592594	0.583728	Cdh3/Inhba
GO_BP_m4	GO:007014	response to	2/727	7/23843	0.017609	0.592594	0.583728	Mme/Ppid
GO_BP_m4	GO:190197	negative re	2/727	7/23843	0.017609	0.592594	0.583728	Aurka/Thoc
GO_BP_m4	GO:200057	positive reg	2/727	7/23843	0.017609	0.592594	0.583728	Dynll2/Mtc
GO_BP_m4	GO:007177	response to	7/727	88/23843	0.017978	0.592594	0.583728	Fgf17/Fgf4
GO_BP_m4	GO:005508	lipid home	9/727	130/23843	0.01825	0.592594	0.583728	Abcb4/Abh
GO_BP_m4	GO:007058	calcium ion	15/727	269/23843	0.018616	0.592594	0.583728	Cacna1b/C
GO_BP_m4	GO:000150	cartilage co	3/727	19/23843	0.019006	0.592594	0.583728	Fgf4/Mapk
GO_BP_m4	GO:001501	heparan su	3/727	19/23843	0.019006	0.592594	0.583728	Lipc/Pxylp1
GO_BP_m4	GO:003599	response to	3/727	19/23843	0.019006	0.592594	0.583728	Mapk14/Re
GO_BP_m4	GO:005089	intestinal a	4/727	34/23843	0.019251	0.592594	0.583728	Apoa4/Npc
GO_BP_m4	GO:007182	plasma lipo	4/727	34/23843	0.019251	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:200123	positive reg	11/727	176/23843	0.019439	0.592594	0.583728	Bcl10/Ctnn
GO_BP_m4	GO:000749	endoderm	6/727	70/23843	0.019833	0.592594	0.583728	Arc/Dusp2/
GO_BP_m4	GO:002261	ribonucleo	21/727	422/23843	0.019993	0.592594	0.583728	Cnot6/Eif3a
GO_BP_m4	GO:005189	positive reg	7/727	90/23843	0.020098	0.592594	0.583728	C1qtnf12/C
GO_BP_m4	GO:000815	negative re	4/727	35/23843	0.021225	0.592594	0.583728	Hcrt/Hus1/
GO_BP_m4	GO:004304	ATP-deper	4/727	35/23843	0.021225	0.592594	0.583728	Anp32b/S
GO_BP_m4	GO:003436	protein-lip	3/727	20/23843	0.021864	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:003436	plasma lipo	3/727	20/23843	0.021864	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:004413	negative re	3/727	20/23843	0.021864	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:004573	negative re	3/727	20/23843	0.021864	0.592594	0.583728	Recql5/Rps
GO_BP_m4	GO:009874	cell aggreg	3/727	20/23843	0.021864	0.592594	0.583728	Fgf4/Mapk
GO_BP_m4	GO:000854	fibroblast g	6/727	72/23843	0.022472	0.592594	0.583728	Fgf17/Fgf4
GO_BP_m4	GO:000912	deoxyribon	2/727	8/23843	0.023009	0.592594	0.583728	Dguok/Tk1
GO_BP_m4	GO:001567	carbon dio	2/727	8/23843	0.023009	0.592594	0.583728	Car2/Car4
GO_BP_m4	GO:003437	very-low-d	2/727	8/23843	0.023009	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:004263	negative re	2/727	8/23843	0.023009	0.592594	0.583728	Cdh3/Inhba
GO_BP_m4	GO:004565	positive reg	2/727	8/23843	0.023009	0.592594	0.583728	Il34/Zfp36l

GO_BP_m4	GO:004802	regulation	2/727	8/23843	0.023009	0.592594	0.583728	Cdh3/Zeb2
GO_BP_m4	GO:007056	vitamin D r	2/727	8/23843	0.023009	0.592594	0.583728	Pim1/Vdr
GO_BP_m4	GO:003022	macrophag	4/727	36/23843	0.023318	0.592594	0.583728	Il34/Ripk1/
GO_BP_m4	GO:001591	sterol trans	6/727	73/23843	0.023875	0.592594	0.583728	Abcb4/Abc
GO_BP_m4	GO:003436	protein-co	3/727	21/23843	0.024943	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:004568	negative re	3/727	21/23843	0.024943	0.592594	0.583728	Cdh3/Inhb
GO_BP_m4	GO:007182	protein-lip	4/727	37/23843	0.025532	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:004642	negative re	5/727	55/23843	0.025822	0.592594	0.583728	Flrt1/Lrrc19
GO_BP_m4	GO:190489	negative re	5/727	55/23843	0.025822	0.592594	0.583728	Flrt1/Lrrc19
GO_BP_m4	GO:004568	regulation	6/727	75/23843	0.026856	0.592594	0.583728	Cdh3/Fst/In
GO_BP_m4	GO:004671	acid secret	8/727	117/23843	0.026935	0.592594	0.583728	Abcb4/Abc
GO_BP_m4	GO:004694	carboxylic a	15/727	283/23843	0.027723	0.592594	0.583728	Abcb4/Abc
GO_BP_m4	GO:190210	regulation	15/727	283/23843	0.027723	0.592594	0.583728	Ager/Btn2a
GO_BP_m4	GO:001633	calcium-de	4/727	38/23843	0.027869	0.592594	0.583728	Cdh24/Cdh
GO_BP_m4	GO:005043	amyloid-be	4/727	38/23843	0.027869	0.592594	0.583728	Nat8f1/Efn
GO_BP_m4	GO:00670	steroid cat	3/727	22/23843	0.028242	0.592594	0.583728	Akr1d1/Cyp
GO_BP_m4	GO:004414	negative re	3/727	22/23843	0.028242	0.592594	0.583728	Mbl1/Mbl2
GO_BP_m4	GO:005179	regulation	3/727	22/23843	0.028242	0.592594	0.583728	Cdh3/Fst/In
GO_BP_m4	GO:007147	cellular hyp	3/727	22/23843	0.028242	0.592594	0.583728	Mir29b-1/M
GO_BP_m4	GO:000697	response to	6/727	76/23843	0.028434	0.592594	0.583728	Mir29b-1/M
GO_BP_m4	GO:001584	organic aci	15/727	284/23843	0.028481	0.592594	0.583728	Abcb4/Abc
GO_BP_m4	GO:190370	regulation	19/727	386/23843	0.028607	0.592594	0.583728	Ager/Btn2a
GO_BP_m4	GO:000267	respiratory	2/727	9/23843	0.028993	0.592594	0.583728	Dusp10/Mp
GO_BP_m4	GO:00670	cholesterol	2/727	9/23843	0.028993	0.592594	0.583728	Akr1d1/Cyp
GO_BP_m4	GO:001612	sterol catab	2/727	9/23843	0.028993	0.592594	0.583728	Akr1d1/Cyp
GO_BP_m4	GO:003437	triglyceride	2/727	9/23843	0.028993	0.592594	0.583728	Apoa4/Lipc
GO_BP_m4	GO:003437	low-densit	2/727	9/23843	0.028993	0.592594	0.583728	Lipc/Mpo
GO_BP_m4	GO:004243	ethanolam	2/727	9/23843	0.028993	0.592594	0.583728	Abhd4/Gdp
GO_BP_m4	GO:006100	common b	2/727	9/23843	0.028993	0.592594	0.583728	Gak/Sox17
GO_BP_m4	GO:007130	cellular res	2/727	9/23843	0.028993	0.592594	0.583728	Pim1/Vdr
GO_BP_m4	GO:007139	cellular res	2/727	9/23843	0.028993	0.592594	0.583728	Inhba/Mlc1
GO_BP_m4	GO:007163	negative re	2/727	9/23843	0.028993	0.592594	0.583728	Cdh3/Il13
GO_BP_m4	GO:190037	regulation	2/727	9/23843	0.028993	0.592594	0.583728	Cdh3/Zeb2
GO_BP_m4	GO:190343	positive reg	2/727	9/23843	0.028993	0.592594	0.583728	Aurka/Ret
GO_BP_m4	GO:002261	ribonucleo	12/727	212/23843	0.029861	0.592594	0.583728	Cnot6/Eif3a
GO_BP_m4	GO:000002	ribosomal l	4/727	39/23843	0.030328	0.592594	0.583728	Gm5093/M
GO_BP_m4	GO:004274	hydrogen p	4/727	39/23843	0.030328	0.592594	0.583728	Apoa4/Cyc
GO_BP_m4	GO:004576	regulation	4/727	39/23843	0.030328	0.592594	0.583728	Cap2/Gng7
GO_BP_m4	GO:000157	globoside l	1/727	1/23843	0.030491	0.592594	0.583728	A4galt
GO_BP_m4	GO:000214	hypochlorc	1/727	1/23843	0.030491	0.592594	0.583728	Mpo
GO_BP_m4	GO:000214	hypochlorc	1/727	1/23843	0.030491	0.592594	0.583728	Mpo
GO_BP_m4	GO:000241	T cell medi	1/727	1/23843	0.030491	0.592594	0.583728	Muc4
GO_BP_m4	GO:000246	tolerance in	1/727	1/23843	0.030491	0.592594	0.583728	C3ar1
GO_BP_m4	GO:000254	Factor XII a	1/727	1/23843	0.030491	0.592594	0.583728	F12
GO_BP_m4	GO:000284	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Muc4
GO_BP_m4	GO:000285	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Muc4
GO_BP_m4	GO:000285	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Muc4
GO_BP_m4	GO:000314	cardiogeni	1/727	1/23843	0.030491	0.592594	0.583728	Sox17

GO_BP_m4	GO:000314	neural cres	1/727	1/23843	0.030491	0.592594	0.583728	Folr1
GO_BP_m4	GO:000686	purine nuc	1/727	1/23843	0.030491	0.592594	0.583728	Aqp9
GO_BP_m4	GO:000982	alkaloid me	1/727	1/23843	0.030491	0.592594	0.583728	Cyp1a2
GO_BP_m4	GO:001041	mannan m	1/727	1/23843	0.030491	0.592594	0.583728	Manba
GO_BP_m4	GO:001049	intercellula	1/727	1/23843	0.030491	0.592594	0.583728	Mip
GO_BP_m4	GO:001058	glutamine	1/727	1/23843	0.030491	0.592594	0.583728	Slc1a5
GO_BP_m4	GO:001086	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Sik1
GO_BP_m4	GO:001582	threonine t	1/727	1/23843	0.030491	0.592594	0.583728	Slc1a4
GO_BP_m4	GO:001593	coenzyme	1/727	1/23843	0.030491	0.592594	0.583728	Nudt7
GO_BP_m4	GO:001930	D-ribose c	1/727	1/23843	0.030491	0.592594	0.583728	Nudt5
GO_BP_m4	GO:003022	basophil di	1/727	1/23843	0.030491	0.592594	0.583728	Gata1
GO_BP_m4	GO:003155	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Fam72a
GO_BP_m4	GO:003155	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Fam72a
GO_BP_m4	GO:003260	connective	1/727	1/23843	0.030491	0.592594	0.583728	Il13
GO_BP_m4	GO:003264	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Il13
GO_BP_m4	GO:003272	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Il13
GO_BP_m4	GO:003277	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Cdh3
GO_BP_m4	GO:003277	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Cdh3
GO_BP_m4	GO:003348	cholesterol	1/727	1/23843	0.030491	0.592594	0.583728	Cyp51
GO_BP_m4	GO:003386	nucleoside	1/727	1/23843	0.030491	0.592594	0.583728	Nudt7
GO_BP_m4	GO:003403	ribonucleo	1/727	1/23843	0.030491	0.592594	0.583728	Nudt7
GO_BP_m4	GO:003403	purine nuc	1/727	1/23843	0.030491	0.592594	0.583728	Nudt7
GO_BP_m4	GO:003434	response t	1/727	1/23843	0.030491	0.592594	0.583728	A230050P2
GO_BP_m4	GO:003451	response t	1/727	1/23843	0.030491	0.592594	0.583728	Kynu
GO_BP_m4	GO:003458	hydroxypro	1/727	1/23843	0.030491	0.592594	0.583728	Slc1a4
GO_BP_m4	GO:003819	thyroid-sti	1/727	1/23843	0.030491	0.592594	0.583728	Tshr
GO_BP_m4	GO:004342	anthranilat	1/727	1/23843	0.030491	0.592594	0.583728	Kynu
GO_BP_m4	GO:004412	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Osbp
GO_BP_m4	GO:004414	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Osbp
GO_BP_m4	GO:004432	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Ddit3
GO_BP_m4	GO:004635	mannan ca	1/727	1/23843	0.030491	0.592594	0.583728	Manba
GO_BP_m4	GO:004668	response t	1/727	1/23843	0.030491	0.592594	0.583728	Mt1
GO_BP_m4	GO:004867	collateral s	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:004868	formation (	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:004869	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:004869	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:004885	adenohypo	1/727	1/23843	0.030491	0.592594	0.583728	Duox2
GO_BP_m4	GO:005168	maintenan	1/727	1/23843	0.030491	0.592594	0.583728	Polr2m
GO_BP_m4	GO:005179	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Cdh3
GO_BP_m4	GO:006080	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Sox17
GO_BP_m4	GO:006090	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Cdh3
GO_BP_m4	GO:006148	response t	1/727	1/23843	0.030491	0.592594	0.583728	Rps3
GO_BP_m4	GO:006171	anterior ne	1/727	1/23843	0.030491	0.592594	0.583728	Folr1
GO_BP_m4	GO:007092	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Ripk1
GO_BP_m4	GO:007123	cellular res	1/727	1/23843	0.030491	0.592594	0.583728	Folr1
GO_BP_m4	GO:007124	cellular res	1/727	1/23843	0.030491	0.592594	0.583728	Mt1
GO_BP_m4	GO:007146	cellular res	1/727	1/23843	0.030491	0.592594	0.583728	Vasn
GO_BP_m4	GO:007161	oxidative d	1/727	1/23843	0.030491	0.592594	0.583728	Cyp1a2

GO_BP_m4	GO:009046	glutamate	1/727	1/23843	0.030491	0.592594	0.583728	Kctd7
GO_BP_m4	GO:009724	hematopoi	1/727	1/23843	0.030491	0.592594	0.583728	Gas6
GO_BP_m4	GO:009729	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Hp1bp3
GO_BP_m4	GO:009740	cellular res	1/727	1/23843	0.030491	0.592594	0.583728	Zfp36l1
GO_BP_m4	GO:009769	vascular en	1/727	1/23843	0.030491	0.592594	0.583728	Socs5
GO_BP_m4	GO:009915	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Tiam1
GO_BP_m4	GO:190154	response t	1/727	1/23843	0.030491	0.592594	0.583728	Zfp36l1
GO_BP_m4	GO:190155	response t	1/727	1/23843	0.030491	0.592594	0.583728	Abcb4
GO_BP_m4	GO:190227	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Vamp8
GO_BP_m4	GO:190254	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Rps3
GO_BP_m4	GO:190274	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Zeb2
GO_BP_m4	GO:190291	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Cdh3
GO_BP_m4	GO:190318	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Ube2i
GO_BP_m4	GO:190338	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Ptpn23
GO_BP_m4	GO:190338	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Ptpn23
GO_BP_m4	GO:190375	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Ube2i
GO_BP_m4	GO:190376	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Lgals3
GO_BP_m4	GO:190380	L-glutamin	1/727	1/23843	0.030491	0.592594	0.583728	Slc1a5
GO_BP_m4	GO:190426	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Tiam1
GO_BP_m4	GO:190426	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Tiam1
GO_BP_m4	GO:190458	cellular res	1/727	1/23843	0.030491	0.592594	0.583728	Tshr
GO_BP_m4	GO:190459	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Ager
GO_BP_m4	GO:190459	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Ager
GO_BP_m4	GO:190460	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Ager
GO_BP_m4	GO:190460	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Ager
GO_BP_m4	GO:190460	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Ager
GO_BP_m4	GO:190480	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Trabd2b
GO_BP_m4	GO:190480	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Trabd2b
GO_BP_m4	GO:190498	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Acmsd
GO_BP_m4	GO:190498	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Acmsd
GO_BP_m4	GO:190498	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Socs5
GO_BP_m4	GO:190498	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Socs5
GO_BP_m4	GO:190504	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Dusp10
GO_BP_m4	GO:190506	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Pim1
GO_BP_m4	GO:190522	response t	1/727	1/23843	0.030491	0.592594	0.583728	Tshr
GO_BP_m4	GO:190522	cellular res	1/727	1/23843	0.030491	0.592594	0.583728	Tshr
GO_BP_m4	GO:190523	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Tnn
GO_BP_m4	GO:190524	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Tnn
GO_BP_m4	GO:190527	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Tiam1
GO_BP_m4	GO:190535	spine appa	1/727	1/23843	0.030491	0.592594	0.583728	Synpo
GO_BP_m4	GO:190557	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:190558	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:190587	invadopod	1/727	1/23843	0.030491	0.592594	0.583728	Nav3
GO_BP_m4	GO:190592	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Nav3
GO_BP_m4	GO:190592	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Nav3
GO_BP_m4	GO:190594	regulation	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:190594	negative re	1/727	1/23843	0.030491	0.592594	0.583728	Rtn4
GO_BP_m4	GO:199034	gap juncti	1/727	1/23843	0.030491	0.592594	0.583728	Mip

GO_BP_m4	GO:19907	Schwann c	1/727	1/23843	0.030491	0.592594	0.583728	Tiam1
GO_BP_m4	GO:20002	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Il13
GO_BP_m4	GO:20012	positive re	1/727	1/23843	0.030491	0.592594	0.583728	Rps3
GO_BP_m4	GO:00425	hyperosmc	3/727	23/23843	0.031761	0.614773	0.605576	Mir29b-1/
GO_BP_m4	GO:00380	p38MAPK	4/727	40/23843	0.032912	0.618787	0.60953	Ager/Dusp
GO_BP_m4	GO:00708	divalent m	21/727	445/23843	0.033002	0.618787	0.60953	Cacna1b/C
GO_BP_m4	GO:00702	T cell apop	5/727	59/23843	0.033694	0.618787	0.60953	Bcl10/Efna
GO_BP_m4	GO:19046	glucose tra	8/727	123/23843	0.03482	0.618787	0.60953	C1qtnf12/
GO_BP_m4	GO:007251	divalent in	21/727	448/23843	0.035081	0.618787	0.60953	Cacna1b/C
GO_BP_m4	GO:00063	mRNA spli	3/727	24/23843	0.035498	0.618787	0.60953	Luc7l3/Snr
GO_BP_m4	GO:00302	heparan su	3/727	24/23843	0.035498	0.618787	0.60953	Lipc/Pxylp1
GO_BP_m4	GO:00460	UTP metab	2/727	10/23843	0.03552	0.618787	0.60953	Ak3/Nme5
GO_BP_m4	GO:006021	primitive h	2/727	10/23843	0.03552	0.618787	0.60953	Gata1/Tho
GO_BP_m4	GO:00703	response t	2/727	10/23843	0.03552	0.618787	0.60953	Mapk14/R
GO_BP_m4	GO:00712	cellular res	2/727	10/23843	0.03552	0.618787	0.60953	Mapk14/R
GO_BP_m4	GO:00712	cellular res	2/727	10/23843	0.03552	0.618787	0.60953	Gnat1/Grm
GO_BP_m4	GO:00901	positive re	2/727	10/23843	0.03552	0.618787	0.60953	Anapc2/N
GO_BP_m4	GO:00515	positive re	4/727	41/23843	0.03562	0.618787	0.60953	Cacna1b/
GO_BP_m4	GO:00714	cellular res	4/727	41/23843	0.03562	0.618787	0.60953	Mir29b-1/
GO_BP_m4	GO:00027	positive re	5/727	60/23843	0.03587	0.618787	0.60953	Car2/Il34/
GO_BP_m4	GO:00068	drug trans	5/727	60/23843	0.03587	0.618787	0.60953	Abcc4/Slc1
GO_BP_m4	GO:00068	lipid transp	16/727	319/23843	0.036428	0.618787	0.60953	Abcb4/Ab
GO_BP_m4	GO:00463	regulation	10/727	171/23843	0.037228	0.618787	0.60953	Ager/Dusp
GO_BP_m4	GO:00705	calcium ior	6/727	81/23843	0.037239	0.618787	0.60953	Cacna1b/C
GO_BP_m4	GO:00086	hexose tra	8/727	125/23843	0.037762	0.618787	0.60953	C1qtnf12/
GO_BP_m4	GO:00310	regenerati	8/727	125/23843	0.037762	0.618787	0.60953	Apoa4/Aur
GO_BP_m4	GO:000681	calcium ior	19/727	399/23843	0.038047	0.618787	0.60953	Cacna1b/C
GO_BP_m4	GO:00444	symbiont p	17/727	347/23843	0.038334	0.618787	0.60953	A230050P
GO_BP_m4	GO:00157	bile acid ar	3/727	25/23843	0.039451	0.618787	0.60953	Aqp9/Mip/
GO_BP_m4	GO:00313	negative re	3/727	25/23843	0.039451	0.618787	0.60953	Il13/Muc4/
GO_BP_m4	GO:00456	positive re	3/727	25/23843	0.039451	0.618787	0.60953	Gata1/Inh
GO_BP_m4	GO:001571	organic ani	19/727	402/23843	0.040517	0.618787	0.60953	Abcb4/Ab
GO_BP_m4	GO:00328	positive re	9/727	150/23843	0.040675	0.618787	0.60953	Ager/Ern2/
GO_BP_m4	GO:00157	monosacch	8/727	127/23843	0.040866	0.618787	0.60953	C1qtnf12/
GO_BP_m4	GO:008601	membrane	4/727	43/23843	0.041412	0.618787	0.60953	Cacna1b/C
GO_BP_m4	GO:190551	macropha	4/727	43/23843	0.041412	0.618787	0.60953	C3ar1/Lgal
GO_BP_m4	GO:00718	ribonucleo	12/727	223/23843	0.041455	0.618787	0.60953	Cnot6/Eif3
GO_BP_m4	GO:00109	positive re	9/727	151/23843	0.042138	0.618787	0.60953	Bcl10/Cycs
GO_BP_m4	GO:00703	positive re	9/727	151/23843	0.042138	0.618787	0.60953	Ager/Ern2/
GO_BP_m4	GO:00018	compleme	2/727	11/23843	0.042551	0.618787	0.60953	Mbl1/Mbl2
GO_BP_m4	GO:00069	ER overloa	2/727	11/23843	0.042551	0.618787	0.60953	Ddit3/Ppp
GO_BP_m4	GO:19904	positive re	2/727	11/23843	0.042551	0.618787	0.60953	Atf6b/Ddit
GO_BP_m4	GO:20000	regulation	2/727	11/23843	0.042551	0.618787	0.60953	Sox17/Tho
GO_BP_m4	GO:20005	regulation	2/727	11/23843	0.042551	0.618787	0.60953	Dynll2/Mtc
GO_BP_m4	GO:00422	ribosomal	6/727	84/23843	0.043274	0.618787	0.60953	Gm5093/
GO_BP_m4	GO:00720	regulation	6/727	84/23843	0.043274	0.618787	0.60953	Ctnna1/Nf
GO_BP_m4	GO:00713	cellular res	3/727	26/23843	0.043616	0.618787	0.60953	Mir155/Pid
GO_BP_m4	GO:00481	Golgi vesic	13/727	250/23843	0.043802	0.618787	0.60953	Arf3/Bet1l/

GO_BP_m4	GO:000669	cholesterol	4/727	44/23843	0.044496	0.618787	0.60953	Apoa4/Cyp
GO_BP_m4	GO:005076	positive reg	5/727	64/23843	0.045427	0.618787	0.60953	Ager/Gas6/
GO_BP_m4	GO:003421	carbohydra	8/727	130/23843	0.045833	0.618787	0.60953	C1qtnf12/F
GO_BP_m4	GO:007137	cellular res	12/727	227/23843	0.046358	0.618787	0.60953	Car2/C1qtn
GO_BP_m4	GO:001046	regulation	7/727	108/23843	0.047366	0.618787	0.60953	Ager/Arc/F
GO_BP_m4	GO:003238	positive reg	13/727	253/23843	0.047368	0.618787	0.60953	Cdh3/Erbb
GO_BP_m4	GO:000763	feeding be	8/727	131/23843	0.047573	0.618787	0.60953	Dmbx1/Esr
GO_BP_m4	GO:004230	molting cyc	8/727	131/23843	0.047573	0.618787	0.60953	Cdh3/Fst/In
GO_BP_m4	GO:004263	hair cycle	8/727	131/23843	0.047573	0.618787	0.60953	Cdh3/Fst/In
GO_BP_m4	GO:004632	positive reg	4/727	45/23843	0.047705	0.618787	0.60953	C1qtnf12/F
GO_BP_m4	GO:006100	regulation	4/727	45/23843	0.047705	0.618787	0.60953	Arc/Efna1/
GO_BP_m4	GO:001087	lipid localiz	17/727	357/23843	0.047791	0.618787	0.60953	Abcb4/Abc
GO_BP_m4	GO:007163	regulation	3/727	27/23843	0.047992	0.618787	0.60953	Cdh3/Il13/
GO_BP_m4	GO:004328	regulation	11/727	204/23843	0.048879	0.618787	0.60953	Anp32b/Bc
GO_BP_m4	GO:004441	interspecie	19/727	412/23843	0.049592	0.618787	0.60953	A230050P2
GO_BP_m4	GO:003286	cellular res	10/727	180/23843	0.049726	0.618787	0.60953	C1qtnf12/F
GO_BP_m4	GO:000315	endocardiu	2/727	12/23843	0.05005	0.618787	0.60953	Ovol2/Sox1
GO_BP_m4	GO:000920	pyrimidine	2/727	12/23843	0.05005	0.618787	0.60953	Ak3/Nme5
GO_BP_m4	GO:003029	intestinal c	2/727	12/23843	0.05005	0.618787	0.60953	Apoa4/Npc
GO_BP_m4	GO:003328	response to	2/727	12/23843	0.05005	0.618787	0.60953	Pim1/Vdr
GO_BP_m4	GO:003424	negative re	2/727	12/23843	0.05005	0.618787	0.60953	Nelfe/Recq
GO_BP_m4	GO:003631	cellular res	2/727	12/23843	0.05005	0.618787	0.60953	Inhba/Mlc1
GO_BP_m4	GO:004562	regulation	2/727	12/23843	0.05005	0.618787	0.60953	Il27/Socs5
GO_BP_m4	GO:009019	positive reg	2/727	12/23843	0.05005	0.618787	0.60953	C3ar1/Ret
GO_BP_m4	GO:200000	negative re	2/727	12/23843	0.05005	0.618787	0.60953	Astn2/Ned
GO_BP_m4	GO:000333	amino acid	5/727	66/23843	0.050722	0.618787	0.60953	Slc16a12/S
GO_BP_m4	GO:006109	regulation	5/727	66/23843	0.050722	0.618787	0.60953	Efna1/Fam
GO_BP_m4	GO:000641	tRNA amin	4/727	46/23843	0.051039	0.618787	0.60953	Dalrd3/Ears
GO_BP_m4	GO:190265	secondary	4/727	46/23843	0.051039	0.618787	0.60953	Apoa4/Cyp
GO_BP_m4	GO:200004	regulation	7/727	110/23843	0.051383	0.618787	0.60953	Anp32b/Bt
GO_BP_m4	GO:006099	regulation	6/727	88/23843	0.052223	0.618787	0.60953	Arc/Efna1/
GO_BP_m4	GO:190165	cellular res	13/727	257/23843	0.052427	0.618787	0.60953	Ager/Car2/
GO_BP_m4	GO:000621	pyrimidine	3/727	28/23843	0.052575	0.618787	0.60953	Ak3/Nme5
GO_BP_m4	GO:001071	negative re	3/727	28/23843	0.052575	0.618787	0.60953	Efna1/Ovol
GO_BP_m4	GO:003022	monocyte	3/727	28/23843	0.052575	0.618787	0.60953	Il34/Thoc5/
GO_BP_m4	GO:004455	secondary	3/727	28/23843	0.052575	0.618787	0.60953	Cdh3/Cyp1
GO_BP_m4	GO:005065	chondroitin	3/727	28/23843	0.052575	0.618787	0.60953	Pxylp1/Spo
GO_BP_m4	GO:007074	response to	3/727	28/23843	0.052575	0.618787	0.60953	Mir155/Pid
GO_BP_m4	GO:007160	transformin	3/727	28/23843	0.052575	0.618787	0.60953	Cdh3/Il13/
GO_BP_m4	GO:190313	mononucle	3/727	28/23843	0.052575	0.618787	0.60953	Il34/Thoc5/
GO_BP_m4	GO:200027	negative re	3/727	28/23843	0.052575	0.618787	0.60953	Ager/Fam7
GO_BP_m4	GO:200027	positive reg	3/727	28/23843	0.052575	0.618787	0.60953	Ager/Arc/N
GO_BP_m4	GO:000194	hair follicle	7/727	111/23843	0.053469	0.618787	0.60953	Cdh3/Fst/In
GO_BP_m4	GO:004564	regulation	4/727	47/23843	0.054497	0.618787	0.60953	Gata1/Inhb
GO_BP_m4	GO:199082	response to	15/727	311/23843	0.055181	0.618787	0.60953	Abcg4/Fgf4
GO_BP_m4	GO:199083	cellular res	15/727	311/23843	0.055181	0.618787	0.60953	Abcg4/Fgf4
GO_BP_m4	GO:003476	positive reg	11/727	209/23843	0.056258	0.618787	0.60953	Ager/Arc/C
GO_BP_m4	GO:007037	negative re	5/727	68/23843	0.056363	0.618787	0.60953	Btn2a2/Cnl

GO_BP_m4	GO:00435	skin develo	14/727	286/23843	0.056605	0.618787	0.60953	Cdh3/Dsp/
GO_BP_m4	GO:00686	amino acid	8/727	136/23843	0.056913	0.618787	0.60953	Htr2c/Slc1
GO_BP_m4	GO:009877	skin epider	7/727	113/23843	0.057799	0.618787	0.60953	Cdh3/Fst/I
GO_BP_m4	GO:00082	intracellula	2/727	13/23843	0.057982	0.618787	0.60953	Mthfsd/Zf
GO_BP_m4	GO:001932	pentose m	2/727	13/23843	0.057982	0.618787	0.60953	Nudt5/Oto
GO_BP_m4	GO:00197	one-carbo	2/727	13/23843	0.057982	0.618787	0.60953	Car2/Car4
GO_BP_m4	GO:00455	positive re	2/727	13/23843	0.057982	0.618787	0.60953	Btn2a2/Du
GO_BP_m4	GO:00460	AMP meta	2/727	13/23843	0.057982	0.618787	0.60953	Ak3/Prps2
GO_BP_m4	GO:009012	regulation	2/727	13/23843	0.057982	0.618787	0.60953	Anapc2/Ne
GO_BP_m4	GO:00903	regulation	2/727	13/23843	0.057982	0.618787	0.60953	Dusp10/M
GO_BP_m4	GO:00224	molting cy	7/727	114/23843	0.060043	0.618787	0.60953	Cdh3/Fst/I
GO_BP_m4	GO:00224	hair cycle	7/727	114/23843	0.060043	0.618787	0.60953	Cdh3/Fst/I
GO_BP_m4	GO:00011	RNA polym	1/727	2/23843	0.060054	0.618787	0.60953	Polr1e
GO_BP_m4	GO:000157	globoside	1/727	2/23843	0.060054	0.618787	0.60953	A4galt
GO_BP_m4	GO:00017	formation	1/727	2/23843	0.060054	0.618787	0.60953	Eif3a
GO_BP_m4	GO:00023	plasma kall	1/727	2/23843	0.060054	0.618787	0.60953	F12
GO_BP_m4	GO:000254	activation	1/727	2/23843	0.060054	0.618787	0.60953	F12
GO_BP_m4	GO:000287	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Ffar3
GO_BP_m4	GO:000334	proepicard	1/727	2/23843	0.060054	0.618787	0.60953	Zfp36l1
GO_BP_m4	GO:000334	septum tra	1/727	2/23843	0.060054	0.618787	0.60953	Zfp36l1
GO_BP_m4	GO:000642	glutamyl-t	1/727	2/23843	0.060054	0.618787	0.60953	Ears2
GO_BP_m4	GO:000642	isoleucyl-t	1/727	2/23843	0.060054	0.618787	0.60953	Iars
GO_BP_m4	GO:00067	AMP phos	1/727	2/23843	0.060054	0.618787	0.60953	Ak3
GO_BP_m4	GO:00069	response t	1/727	2/23843	0.060054	0.618787	0.60953	Apoa4
GO_BP_m4	GO:00070	spindle ass	1/727	2/23843	0.060054	0.618787	0.60953	Aurka
GO_BP_m4	GO:00074	endoderm	1/727	2/23843	0.060054	0.618787	0.60953	Sox17
GO_BP_m4	GO:00097	carbohydr	1/727	2/23843	0.060054	0.618787	0.60953	Slc2a2
GO_BP_m4	GO:001004	response t	1/727	2/23843	0.060054	0.618787	0.60953	Cacna1g
GO_BP_m4	GO:00107	meiotic DN	1/727	2/23843	0.060054	0.618787	0.60953	Brip1
GO_BP_m4	GO:00140	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Rela
GO_BP_m4	GO:001404	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Rela
GO_BP_m4	GO:00148	transition	1/727	2/23843	0.060054	0.618787	0.60953	Gtf2ird1
GO_BP_m4	GO:00158	nucleobase	1/727	2/23843	0.060054	0.618787	0.60953	Aqp9
GO_BP_m4	GO:00158	pyrimidine	1/727	2/23843	0.060054	0.618787	0.60953	Aqp9
GO_BP_m4	GO:00158	creatine tr	1/727	2/23843	0.060054	0.618787	0.60953	Slc16a12
GO_BP_m4	GO:00160	monoterp	1/727	2/23843	0.060054	0.618787	0.60953	Cyp1a2
GO_BP_m4	GO:00165	protein arg	1/727	2/23843	0.060054	0.618787	0.60953	1700016K1
GO_BP_m4	GO:00180	peptidyl-ly	1/727	2/23843	0.060054	0.618787	0.60953	Nat8f1
GO_BP_m4	GO:00188	dibenzo-p	1/727	2/23843	0.060054	0.618787	0.60953	Cyp1a2
GO_BP_m4	GO:001944	tryptophan	1/727	2/23843	0.060054	0.618787	0.60953	Kynu
GO_BP_m4	GO:00195	arabinose	1/727	2/23843	0.060054	0.618787	0.60953	Otog
GO_BP_m4	GO:00217	mammillar	1/727	2/23843	0.060054	0.618787	0.60953	Zeb2
GO_BP_m4	GO:00303	fructosami	1/727	2/23843	0.060054	0.618787	0.60953	Mdp1
GO_BP_m4	GO:003154	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Fam72a
GO_BP_m4	GO:003154	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Fam72a
GO_BP_m4	GO:00315	phospholip	1/727	2/23843	0.060054	0.618787	0.60953	Htr2c
GO_BP_m4	GO:003257	response t	1/727	2/23843	0.060054	0.618787	0.60953	Gas6
GO_BP_m4	GO:003291	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Cdh3

GO_BP_m4	GO:003318	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Trip12
GO_BP_m4	GO:003437	chylomicro	1/727	2/23843	0.060054	0.618787	0.60953	Lipc
GO_BP_m4	GO:003437	chylomicro	1/727	2/23843	0.060054	0.618787	0.60953	Plagl2
GO_BP_m4	GO:003444	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Apoa4
GO_BP_m4	GO:003444	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Apoa4
GO_BP_m4	GO:003544	dipeptide t	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:003552	retrograde	1/727	2/23843	0.060054	0.618787	0.60953	Rab43
GO_BP_m4	GO:003562	ER to Golg	1/727	2/23843	0.060054	0.618787	0.60953	Plekha8
GO_BP_m4	GO:003585	eosinophil	1/727	2/23843	0.060054	0.618787	0.60953	Gata1
GO_BP_m4	GO:003639	pancreatic	1/727	2/23843	0.060054	0.618787	0.60953	Vamp8
GO_BP_m4	GO:003812	ERBB3 sign	1/727	2/23843	0.060054	0.618787	0.60953	Rtn4
GO_BP_m4	GO:003818	bile acid si	1/727	2/23843	0.060054	0.618787	0.60953	Vdr
GO_BP_m4	GO:003819	urokinase p	1/727	2/23843	0.060054	0.618787	0.60953	Slurp1
GO_BP_m4	GO:004520	MAPK expo	1/727	2/23843	0.060054	0.618787	0.60953	Styx
GO_BP_m4	GO:004604	ITP metabo	1/727	2/23843	0.060054	0.618787	0.60953	Ak3
GO_BP_m4	GO:004635	acetyl-CoA	1/727	2/23843	0.060054	0.618787	0.60953	Nudt7
GO_BP_m4	GO:004637	L-arabinos	1/727	2/23843	0.060054	0.618787	0.60953	Otog
GO_BP_m4	GO:004825	iron import	1/727	2/23843	0.060054	0.618787	0.60953	Slc25a37
GO_BP_m4	GO:004868	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Rtn4
GO_BP_m4	GO:005134	positive reg	1/727	2/23843	0.060054	0.618787	0.60953	Gnat1
GO_BP_m4	GO:005164	endoplasm	1/727	2/23843	0.060054	0.618787	0.60953	Polr2m
GO_BP_m4	GO:006015	peroxisome	1/727	2/23843	0.060054	0.618787	0.60953	Pex1
GO_BP_m4	GO:006015	microtubul	1/727	2/23843	0.060054	0.618787	0.60953	Pex1
GO_BP_m4	GO:006054	positive reg	1/727	2/23843	0.060054	0.618787	0.60953	Ripk1
GO_BP_m4	GO:006079	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Sox17
GO_BP_m4	GO:006085	branching	1/727	2/23843	0.060054	0.618787	0.60953	Nfatc1
GO_BP_m4	GO:006097	cell migrati	1/727	2/23843	0.060054	0.618787	0.60953	Folr1
GO_BP_m4	GO:006137	mammillar	1/727	2/23843	0.060054	0.618787	0.60953	Zeb2
GO_BP_m4	GO:007062	zymogen g	1/727	2/23843	0.060054	0.618787	0.60953	Vamp8
GO_BP_m4	GO:007130	cellular res	1/727	2/23843	0.060054	0.618787	0.60953	Gas6
GO_BP_m4	GO:007234	pancreatic	1/727	2/23843	0.060054	0.618787	0.60953	Il13
GO_BP_m4	GO:009008	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:009008	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:009023	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Aurka
GO_BP_m4	GO:009711	endoplasm	1/727	2/23843	0.060054	0.618787	0.60953	Stx17
GO_BP_m4	GO:009732	melanocyte	1/727	2/23843	0.060054	0.618787	0.60953	Zeb2
GO_BP_m4	GO:009888	modificatio	1/727	2/23843	0.060054	0.618787	0.60953	Synpo
GO_BP_m4	GO:009956	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Grm1
GO_BP_m4	GO:190014	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Gas6
GO_BP_m4	GO:190014	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Gas6
GO_BP_m4	GO:190014	positive reg	1/727	2/23843	0.060054	0.618787	0.60953	Tiam1
GO_BP_m4	GO:190019	positive reg	1/727	2/23843	0.060054	0.618787	0.60953	Aurka
GO_BP_m4	GO:190125	nucleotide-	1/727	2/23843	0.060054	0.618787	0.60953	Xpa
GO_BP_m4	GO:190131	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Trip12
GO_BP_m4	GO:190131	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Trip12
GO_BP_m4	GO:190227	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Vamp8
GO_BP_m4	GO:190254	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Rps3
GO_BP_m4	GO:190290	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Cdh3

GO_BP_m4	GO:190305	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Zeb2
GO_BP_m4	GO:190329	protein loc	1/727	2/23843	0.060054	0.618787	0.60953	Arl5a
GO_BP_m4	GO:190341	response t	1/727	2/23843	0.060054	0.618787	0.60953	Abcb4
GO_BP_m4	GO:190341	cellular res	1/727	2/23843	0.060054	0.618787	0.60953	Abcb4
GO_BP_m4	GO:190389	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Atf6b
GO_BP_m4	GO:190458	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Zfp36l1
GO_BP_m4	GO:190488	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Vstm5
GO_BP_m4	GO:190489	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Vstm5
GO_BP_m4	GO:190504	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Dusp10
GO_BP_m4	GO:190505	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Rps3
GO_BP_m4	GO:190505	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Rps3
GO_BP_m4	GO:190520	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Ager
GO_BP_m4	GO:190522	clathrin-co	1/727	2/23843	0.060054	0.618787	0.60953	Gak
GO_BP_m4	GO:190555	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Rtn4
GO_BP_m4	GO:190555	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Rtn4
GO_BP_m4	GO:199026	peptidyl-ty	1/727	2/23843	0.060054	0.618787	0.60953	Dusp10
GO_BP_m4	GO:199039	epithelium	1/727	2/23843	0.060054	0.618787	0.60953	Dusp10
GO_BP_m4	GO:199096	multi-orga	1/727	2/23843	0.060054	0.618787	0.60953	Rab40b
GO_BP_m4	GO:200004	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Sox17
GO_BP_m4	GO:200015	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Bet1l
GO_BP_m4	GO:200022	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Il13
GO_BP_m4	GO:200052	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Lgals3
GO_BP_m4	GO:200087	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:200088	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:200104	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Ctnna1
GO_BP_m4	GO:200114	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:200115	positive re	1/727	2/23843	0.060054	0.618787	0.60953	Car2
GO_BP_m4	GO:200118	regulation	1/727	2/23843	0.060054	0.618787	0.60953	Lgals3
GO_BP_m4	GO:200118	negative re	1/727	2/23843	0.060054	0.618787	0.60953	Lgals3
GO_BP_m4	GO:005140	stress-activ	12/727	237/23843	0.060325	0.620247	0.610968	Ager/Dusp
GO_BP_m4	GO:200123	regulation	9/727	162/23843	0.060601	0.620718	0.611432	Bcl10/Ctnn
GO_BP_m4	GO:004225	ribosome b	14/727	289/23843	0.060631	0.620718	0.611432	Eri2/Mrm2/
GO_BP_m4	GO:000150	action pote	8/727	138/23843	0.060952	0.622679	0.613363	Cacna1b/C
GO_BP_m4	GO:004303	tRNA amin	4/727	49/23843	0.061783	0.628477	0.619075	Dalrd3/Ear
GO_BP_m4	GO:004568	positive re	4/727	49/23843	0.061783	0.628477	0.619075	Ager/Nkx6
GO_BP_m4	GO:190118	positive re	3/727	30/23843	0.062342	0.631366	0.621921	Esr2/Neurl
GO_BP_m4	GO:200010	negative re	5/727	70/23843	0.06235	0.631366	0.621921	Bcl10/Efna
GO_BP_m4	GO:000681	sodium ior	11/727	213/23843	0.062669	0.631366	0.621921	Atp1b4/Cn
GO_BP_m4	GO:000725	JNK cascac	10/727	188/23843	0.062959	0.631366	0.621921	Ager/Dusp
GO_BP_m4	GO:000190	cell killing	8/727	139/23843	0.063038	0.631366	0.621921	Ager/Dnas
GO_BP_m4	GO:000760	visual perc	8/727	139/23843	0.063038	0.631366	0.621921	Bfsp2/Cab
GO_BP_m4	GO:007148	cellular res	6/727	93/23843	0.064882	0.631366	0.621921	Agap3/Gna
GO_BP_m4	GO:190382	organic aci	6/727	93/23843	0.064882	0.631366	0.621921	Irs2/Slc16a
GO_BP_m4	GO:190503	carboxylic	6/727	93/23843	0.064882	0.631366	0.621921	Irs2/Slc16a
GO_BP_m4	GO:004303	amino acid	4/727	50/23843	0.065609	0.631366	0.621921	Dalrd3/Ear
GO_BP_m4	GO:005133	regulation	4/727	50/23843	0.065609	0.631366	0.621921	Cap2/Gng
GO_BP_m4	GO:007022	negative re	4/727	50/23843	0.065609	0.631366	0.621921	Bcl10/Efna
GO_BP_m4	GO:000907	aromatic a	2/727	14/23843	0.066314	0.631366	0.621921	Fah/Kynu

GO_BP_m4	GO:000921	purine deo	2/727	14/23843	0.066314	0.631366	0.621921	Ak3/Dguok
GO_BP_m4	GO:001083	negative re	2/727	14/23843	0.066314	0.631366	0.621921	Slurp1/Vdr
GO_BP_m4	GO:003278	negative re	2/727	14/23843	0.066314	0.631366	0.621921	Nelfe/Recq
GO_BP_m4	GO:003637	sodium ion	2/727	14/23843	0.066314	0.631366	0.621921	Atp1b4/Slc
GO_BP_m4	GO:004345	regulation	2/727	14/23843	0.066314	0.631366	0.621921	Cdh3/Zeb2
GO_BP_m4	GO:004365	dicarboxyli	2/727	14/23843	0.066314	0.631366	0.621921	Acmsd/Kyn
GO_BP_m4	GO:004424	lipid digest	2/727	14/23843	0.066314	0.631366	0.621921	Apoa4/Npc
GO_BP_m4	GO:004561	positive reg	2/727	14/23843	0.066314	0.631366	0.621921	Ovol2/Vdr
GO_BP_m4	GO:004572	negative re	2/727	14/23843	0.066314	0.631366	0.621921	C1qtnf12/S
GO_BP_m4	GO:004868	negative re	2/727	14/23843	0.066314	0.631366	0.621921	Rtn4/Rtn4r
GO_BP_m4	GO:005086	positive reg	2/727	14/23843	0.066314	0.631366	0.621921	Rela/Rps3
GO_BP_m4	GO:009871	sodium ion	2/727	14/23843	0.066314	0.631366	0.621921	Slc8a1/Slc9
GO_BP_m4	GO:009885	intestinal li	2/727	14/23843	0.066314	0.631366	0.621921	Apoa4/Npc
GO_BP_m4	GO:001715	calcium ion	7/727	117/23843	0.067092	0.631366	0.621921	Cacna1g/C
GO_BP_m4	GO:004328	positive reg	7/727	117/23843	0.067092	0.631366	0.621921	Bcl10/Cycs
GO_BP_m4	GO:000697	hyperosmo	3/727	31/23843	0.067519	0.631366	0.621921	Mir29b-1/
GO_BP_m4	GO:001580	neutral am	3/727	31/23843	0.067519	0.631366	0.621921	Slc1a4/Slc1
GO_BP_m4	GO:004561	regulation	3/727	31/23843	0.067519	0.631366	0.621921	Ovol2/Vdr/
GO_BP_m4	GO:003355	multicellula	6/727	94/23843	0.067612	0.631366	0.621921	Cacna1b/E
GO_BP_m4	GO:007037	positive reg	12/727	242/23843	0.068258	0.631366	0.621921	Ager/Erbb2
GO_BP_m4	GO:003030	cholesterol	5/727	72/23843	0.068682	0.631366	0.621921	Abcb4/Abc
GO_BP_m4	GO:004225	ribosome a	5/727	72/23843	0.068682	0.631366	0.621921	Gm5093/M
GO_BP_m4	GO:000636	rRNA proce	10/727	192/23843	0.070352	0.631366	0.621921	Eri2/Mrm2/
GO_BP_m4	GO:000911	nucleoside	6/727	95/23843	0.070407	0.631366	0.621921	Ak3/Dguok
GO_BP_m4	GO:001567	monovalen	20/727	459/23843	0.071217	0.631366	0.621921	Ager/Atp1b
GO_BP_m4	GO:005095	sensory pe	8/727	143/23843	0.071821	0.631366	0.621921	Bfsp2/Cabp
GO_BP_m4	GO:004632	regulation	5/727	73/23843	0.071977	0.631366	0.621921	C1qtnf12/F
GO_BP_m4	GO:000820	cholesterol	7/727	119/23843	0.072056	0.631366	0.621921	Akr1d1/Ap
GO_BP_m4	GO:000630	DNA catab	3/727	32/23843	0.072884	0.631366	0.621921	Dnase1/Dn
GO_BP_m4	GO:000698	ER-nucleus	3/727	32/23843	0.072884	0.631366	0.621921	Atf6b/Ddit3
GO_BP_m4	GO:000926	deoxyribon	3/727	32/23843	0.072884	0.631366	0.621921	Ak3/Dguok
GO_BP_m4	GO:003509	response to	3/727	32/23843	0.072884	0.631366	0.621921	Htr2c/Il13/
GO_BP_m4	GO:008609	regulation	3/727	32/23843	0.072884	0.631366	0.621921	Cacna1g/D
GO_BP_m4	GO:190247	L-alpha-am	3/727	32/23843	0.072884	0.631366	0.621921	Slc17a8/Slc
GO_BP_m4	GO:004340	positive reg	11/727	219/23843	0.07315	0.631366	0.621921	Ager/Cspg
GO_BP_m4	GO:001612	sterol biosy	4/727	52/23843	0.073621	0.631366	0.621921	Apoa4/Cyp
GO_BP_m4	GO:001095	positive reg	8/727	144/23843	0.074127	0.631366	0.621921	Bcl10/Cycs
GO_BP_m4	GO:000030	response to	10/727	194/23843	0.074247	0.631366	0.621921	Agap3/Apc
GO_BP_m4	GO:005080	regulation	10/727	194/23843	0.074247	0.631366	0.621921	Anapc2/Ar
GO_BP_m4	GO:000915	purine deo	2/727	15/23843	0.075014	0.631366	0.621921	Ak3/Dguok
GO_BP_m4	GO:001045	negative re	2/727	15/23843	0.075014	0.631366	0.621921	Nkx6-2/So
GO_BP_m4	GO:001406	negative re	2/727	15/23843	0.075014	0.631366	0.621921	Btn2a2/Pik
GO_BP_m4	GO:001473	regulation	2/727	15/23843	0.075014	0.631366	0.621921	Gtf2ird1/N
GO_BP_m4	GO:003000	cellular pot	2/727	15/23843	0.075014	0.631366	0.621921	Atp1b4/Kc
GO_BP_m4	GO:004479	positive reg	2/727	15/23843	0.075014	0.631366	0.621921	Ythdc2/Zfp
GO_BP_m4	GO:004565	regulation	2/727	15/23843	0.075014	0.631366	0.621921	Il34/Zfp36l
GO_BP_m4	GO:006034	heart trabe	2/727	15/23843	0.075014	0.631366	0.621921	Fhl2/Ovol2
GO_BP_m4	GO:007072	response to	2/727	15/23843	0.075014	0.631366	0.621921	Inhba/Mlc1

GO_BP_m4	GO:00995	modificatic	2/727	15/23843	0.075014	0.631366	0.621921	Synpo/Tiar
GO_BP_m4	GO:190011	positive reg	2/727	15/23843	0.075014	0.631366	0.621921	Bcl10/Rps3
GO_BP_m4	GO:001401	positive reg	5/727	74/23843	0.075357	0.631366	0.621921	Ager/Nkx6
GO_BP_m4	GO:00987	import acro	5/727	74/23843	0.075357	0.631366	0.621921	Slc1a5/Slc1
GO_BP_m4	GO:00508	positive reg	15/727	326/23843	0.075784	0.631366	0.621921	Ager/Arc/C
GO_BP_m4	GO:19016	response to	16/727	353/23843	0.075806	0.631366	0.621921	Ager/Car2/
GO_BP_m4	GO:00158	organic hyd	11/727	221/23843	0.076877	0.631366	0.621921	Abcb4/Abc
GO_BP_m4	GO:001607	rRNA meta	11/727	221/23843	0.076877	0.631366	0.621921	Eri2/Ern2/N
GO_BP_m4	GO:006027	cilium asse	14/727	300/23843	0.077024	0.631366	0.621921	Abcc4/Atxn
GO_BP_m4	GO:00017	neural cres	4/727	53/23843	0.077805	0.631366	0.621921	Folr1/Ovol
GO_BP_m4	GO:00068	retrograde	3/727	33/23843	0.078433	0.631366	0.621921	Arf3/Bet1l/
GO_BP_m4	GO:00550	acylglycero	3/727	33/23843	0.078433	0.631366	0.621921	Apoa4/Apo
GO_BP_m4	GO:007032	triglyceride	3/727	33/23843	0.078433	0.631366	0.621921	Apoa4/Apo
GO_BP_m4	GO:009031	regulation	3/727	33/23843	0.078433	0.631366	0.621921	Erbb2/Kcne
GO_BP_m4	GO:19010	negative re	3/727	33/23843	0.078433	0.631366	0.621921	Ctnna1/Ga
GO_BP_m4	GO:200124	negative re	3/727	33/23843	0.078433	0.631366	0.621921	Ctnna1/Ga
GO_BP_m4	GO:003464	cellular res	5/727	75/23843	0.078821	0.631366	0.621921	Agap3/Mm
GO_BP_m4	GO:001571	monocarbo	8/727	146/23843	0.078873	0.631366	0.621921	Abcb4/Abc
GO_BP_m4	GO:004561	regulation	9/727	171/23843	0.079047	0.631366	0.621921	Btn2a2/Du
GO_BP_m4	GO:007022	lymphocyte	6/727	98/23843	0.079187	0.631366	0.621921	Bcl10/Efna
GO_BP_m4	GO:00450	regulated e	10/727	197/23843	0.080336	0.631366	0.621921	Cacna1g/C
GO_BP_m4	GO:001082	positive reg	4/727	54/23843	0.082104	0.631366	0.621921	C1qtnf12/F
GO_BP_m4	GO:000691	activation o	5/727	76/23843	0.082369	0.631366	0.621921	Bcl10/Cycs
GO_BP_m4	GO:19028	regulation	7/727	123/23843	0.08262	0.631366	0.621921	Anp32b/Bt
GO_BP_m4	GO:003424	regulation	19/727	441/23843	0.08386	0.631366	0.621921	Cnot6/Efna
GO_BP_m4	GO:000207	epithelial c	2/727	16/23843	0.084051	0.631366	0.621921	Esr2/Kcne1
GO_BP_m4	GO:00024	dendritic ce	2/727	16/23843	0.084051	0.631366	0.621921	Gas6/Retnl
GO_BP_m4	GO:000651	glycoprote	2/727	16/23843	0.084051	0.631366	0.621921	Manba/Stt
GO_BP_m4	GO:00068	water trans	2/727	16/23843	0.084051	0.631366	0.621921	Aqp9/Mip
GO_BP_m4	GO:001022	response to	2/727	16/23843	0.084051	0.631366	0.621921	Mme/Rela
GO_BP_m4	GO:00156	gas transpo	2/727	16/23843	0.084051	0.631366	0.621921	Car2/Car4
GO_BP_m4	GO:00169	cell wall ma	2/727	16/23843	0.084051	0.631366	0.621921	Lyzl1/Manb
GO_BP_m4	GO:00324	response to	2/727	16/23843	0.084051	0.631366	0.621921	Mapk14/Re
GO_BP_m4	GO:00447	multi-orga	2/727	16/23843	0.084051	0.631366	0.621921	Rab40b/Th
GO_BP_m4	GO:00468	regulation	2/727	16/23843	0.084051	0.631366	0.621921	Rbm26/Tho
GO_BP_m4	GO:00518	disruption	2/727	16/23843	0.084051	0.631366	0.621921	Mbl1/Mbl2
GO_BP_m4	GO:005187	killing by h	2/727	16/23843	0.084051	0.631366	0.621921	Mbl1/Mbl2
GO_BP_m4	GO:007057	negative re	2/727	16/23843	0.084051	0.631366	0.621921	Rtn4/Rtn4r
GO_BP_m4	GO:00901	regulation	2/727	16/23843	0.084051	0.631366	0.621921	C3ar1/Ret
GO_BP_m4	GO:190257	multi-orga	2/727	16/23843	0.084051	0.631366	0.621921	Rab40b/Th
GO_BP_m4	GO:00327	positive reg	3/727	34/23843	0.08416	0.631366	0.621921	Ager/Mapk
GO_BP_m4	GO:00432	negative re	3/727	34/23843	0.08416	0.631366	0.621921	Hcrt/Kcne1
GO_BP_m4	GO:00226	digestive sy	6/727	100/23843	0.085366	0.631366	0.621921	Apoa4/Npc
GO_BP_m4	GO:19026	secondary	7/727	124/23843	0.085393	0.631366	0.621921	Akr1d1/Ap
GO_BP_m4	GO:00158	L-amino ac	4/727	55/23843	0.086519	0.631366	0.621921	Slc17a8/Slc
GO_BP_m4	GO:003081	regulation	4/727	55/23843	0.086519	0.631366	0.621921	Cap2/Gng
GO_BP_m4	GO:004867	response to	4/727	55/23843	0.086519	0.631366	0.621921	Erbb2/Folr
GO_BP_m4	GO:00071	homophilic	6/727	101/23843	0.088552	0.631366	0.621921	Cadm2/Cd

GO_BP_m4	GO:000043	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Usf2
GO_BP_m4	GO:000043	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Usf2
GO_BP_m4	GO:000071	nucleotide-	1/727	3/23843	0.088716	0.631366	0.621921	Xpa
GO_BP_m4	GO:000156	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Ppan
GO_BP_m4	GO:000182	inner cell m	1/727	3/23843	0.088716	0.631366	0.621921	Sox17
GO_BP_m4	GO:000225	kinin casca	1/727	3/23843	0.088716	0.631366	0.621921	F12
GO_BP_m4	GO:000233	B-1a B cell	1/727	3/23843	0.088716	0.631366	0.621921	Nfatc1
GO_BP_m4	GO:000287	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Ffar3
GO_BP_m4	GO:000306	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Ffar3
GO_BP_m4	GO:000601	D-ribose m	1/727	3/23843	0.088716	0.631366	0.621921	Nudt5
GO_BP_m4	GO:000601	5-phospho	1/727	3/23843	0.088716	0.631366	0.621921	Prps2
GO_BP_m4	GO:000617	ADP biosyn	1/727	3/23843	0.088716	0.631366	0.621921	Ak3
GO_BP_m4	GO:000705	spindle ass	1/727	3/23843	0.088716	0.631366	0.621921	Aurka
GO_BP_m4	GO:000720	phospholip	1/727	3/23843	0.088716	0.631366	0.621921	Htr2c
GO_BP_m4	GO:000728	spermatog	1/727	3/23843	0.088716	0.631366	0.621921	Brip1
GO_BP_m4	GO:000862	hormone-r	1/727	3/23843	0.088716	0.631366	0.621921	Esr2
GO_BP_m4	GO:001072	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Gata1
GO_BP_m4	GO:001079	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Rilp
GO_BP_m4	GO:001090	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Pxylp1
GO_BP_m4	GO:001090	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Pxylp1
GO_BP_m4	GO:001097	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Vdr
GO_BP_m4	GO:001098	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Vdr
GO_BP_m4	GO:001405	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Htr2c
GO_BP_m4	GO:001406	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Lgals3
GO_BP_m4	GO:001906	fusion of vi	1/727	3/23843	0.088716	0.631366	0.621921	Gas6
GO_BP_m4	GO:001928	isopenteny	1/727	3/23843	0.088716	0.631366	0.621921	Pmvk
GO_BP_m4	GO:001932	pentose ca	1/727	3/23843	0.088716	0.631366	0.621921	Nudt5
GO_BP_m4	GO:001991	peptidyl-ar	1/727	3/23843	0.088716	0.631366	0.621921	Prmt9
GO_BP_m4	GO:002177	striatal med	1/727	3/23843	0.088716	0.631366	0.621921	Inhba
GO_BP_m4	GO:002191	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Nkx6-2
GO_BP_m4	GO:003021	heparin bio	1/727	3/23843	0.088716	0.631366	0.621921	Xylt2
GO_BP_m4	GO:003248	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Ralgps1
GO_BP_m4	GO:003366	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Serpinb9
GO_BP_m4	GO:003386	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Il13
GO_BP_m4	GO:003444	plasma lipo	1/727	3/23843	0.088716	0.631366	0.621921	Apoa4
GO_BP_m4	GO:003567	oligopeptid	1/727	3/23843	0.088716	0.631366	0.621921	Car2
GO_BP_m4	GO:003639	amylase se	1/727	3/23843	0.088716	0.631366	0.621921	Vamp8
GO_BP_m4	GO:003966	membrane	1/727	3/23843	0.088716	0.631366	0.621921	Gas6
GO_BP_m4	GO:004293	dipeptide t	1/727	3/23843	0.088716	0.631366	0.621921	Car2
GO_BP_m4	GO:004368	co-translat	1/727	3/23843	0.088716	0.631366	0.621921	Stt3b
GO_BP_m4	GO:004477	meiotic DN	1/727	3/23843	0.088716	0.631366	0.621921	Hus1
GO_BP_m4	GO:004480	multi-orga	1/727	3/23843	0.088716	0.631366	0.621921	Gas6
GO_BP_m4	GO:004610	thymidine	1/727	3/23843	0.088716	0.631366	0.621921	Tk1
GO_BP_m4	GO:004612	purine deo	1/727	3/23843	0.088716	0.631366	0.621921	Dguok
GO_BP_m4	GO:004639	5-phospho	1/727	3/23843	0.088716	0.631366	0.621921	Prps2
GO_BP_m4	GO:004694	nucleoside	1/727	3/23843	0.088716	0.631366	0.621921	Ak3
GO_BP_m4	GO:004881	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Cdh3
GO_BP_m4	GO:004885	hypophysis	1/727	3/23843	0.088716	0.631366	0.621921	Duox2

GO_BP_m4	GO:00488	stem cell fa	1/727	3/23843	0.088716	0.631366	0.621921	Sox17
GO_BP_m4	GO:005101	microtubul	1/727	3/23843	0.088716	0.631366	0.621921	Casc1
GO_BP_m4	GO:005204	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Serpinb9
GO_BP_m4	GO:00524	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Serpinb9
GO_BP_m4	GO:005501	atrial cardia	1/727	3/23843	0.088716	0.631366	0.621921	Fhl2
GO_BP_m4	GO:005501	atrial cardia	1/727	3/23843	0.088716	0.631366	0.621921	Fhl2
GO_BP_m4	GO:006091	cardiac cell	1/727	3/23843	0.088716	0.631366	0.621921	Sox17
GO_BP_m4	GO:006101	gall bladde	1/727	3/23843	0.088716	0.631366	0.621921	Sox17
GO_BP_m4	GO:00610	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Abcb4
GO_BP_m4	GO:00610	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Abcb4
GO_BP_m4	GO:006114	Peyer's pat	1/727	3/23843	0.088716	0.631366	0.621921	Ret
GO_BP_m4	GO:00613	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Ptpn23
GO_BP_m4	GO:00618	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Ager
GO_BP_m4	GO:007037	cellular hea	1/727	3/23843	0.088716	0.631366	0.621921	Hsbp1l1
GO_BP_m4	GO:00705	dendrite se	1/727	3/23843	0.088716	0.631366	0.621921	Tnn
GO_BP_m4	GO:007067	intralumen	1/727	3/23843	0.088716	0.631366	0.621921	Rilp
GO_BP_m4	GO:00717	immunoglo	1/727	3/23843	0.088716	0.631366	0.621921	Polb
GO_BP_m4	GO:008014	amino acid	1/727	3/23843	0.088716	0.631366	0.621921	Kctd7
GO_BP_m4	GO:00902	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Pid1
GO_BP_m4	GO:00988	modificatio	1/727	3/23843	0.088716	0.631366	0.621921	Tiam1
GO_BP_m4	GO:010601	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Ager
GO_BP_m4	GO:010601	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Ager
GO_BP_m4	GO:19004	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Ager
GO_BP_m4	GO:190334	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Nphp1
GO_BP_m4	GO:19036	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Il13
GO_BP_m4	GO:19036	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Il13
GO_BP_m4	GO:19038	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Atf6b
GO_BP_m4	GO:19045	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Zfp36l1
GO_BP_m4	GO:19052	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Ager
GO_BP_m4	GO:19058	invadopod	1/727	3/23843	0.088716	0.631366	0.621921	Nav3
GO_BP_m4	GO:19901	protein K2	1/727	3/23843	0.088716	0.631366	0.621921	Otud6a
GO_BP_m4	GO:19901	protein K3	1/727	3/23843	0.088716	0.631366	0.621921	Otud6a
GO_BP_m4	GO:199044	intrinsic ap	1/727	3/23843	0.088716	0.631366	0.621921	Ddit3
GO_BP_m4	GO:199052	bone reger	1/727	3/23843	0.088716	0.631366	0.621921	Lgr6
GO_BP_m4	GO:199091	double-str	1/727	3/23843	0.088716	0.631366	0.621921	Brip1
GO_BP_m4	GO:200001	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Ddit3
GO_BP_m4	GO:200032	regulation	1/727	3/23843	0.088716	0.631366	0.621921	Cnot6
GO_BP_m4	GO:200032	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Cnot6
GO_BP_m4	GO:200036	negative re	1/727	3/23843	0.088716	0.631366	0.621921	Astl
GO_BP_m4	GO:20012	positive reg	1/727	3/23843	0.088716	0.631366	0.621921	Ager
GO_BP_m4	GO:007022	regulation	5/727	78/23843	0.089715	0.631366	0.621921	Bcl10/Efna
GO_BP_m4	GO:00067	one-carbo	3/727	35/23843	0.09006	0.631366	0.621921	Car2/Car4/
GO_BP_m4	GO:00456	positive reg	3/727	35/23843	0.09006	0.631366	0.621921	Fst/Ovol2/
GO_BP_m4	GO:004647	phosphatic	3/727	35/23843	0.09006	0.631366	0.621921	Apoa4/Gd
GO_BP_m4	GO:004301	camera-typ	15/727	335/23843	0.09029	0.631366	0.621921	Bfsp2/Cab
GO_BP_m4	GO:00311	neuron prc	4/727	56/23843	0.091046	0.631366	0.621921	Apoa4/Fol
GO_BP_m4	GO:00613	cardiac cor	4/727	56/23843	0.091046	0.631366	0.621921	Cacna1g/D
GO_BP_m4	GO:00000	G1/S transi	9/727	177/23843	0.093051	0.631366	0.621921	Anp32b/Bt

GO_BP_m4	GO:19901	neuron pro	9/727	177/23843	0.093051	0.631366	0.621921	Anapc2/Au
GO_BP_m4	GO:00091	pyrimidine	2/727	17/23843	0.093397	0.631366	0.621921	Ak3/Nme5
GO_BP_m4	GO:00092	pyrimidine	2/727	17/23843	0.093397	0.631366	0.621921	Ak3/Nme5
GO_BP_m4	GO:00324	melanoson	2/727	17/23843	0.093397	0.631366	0.621921	Cdh3/Mreg
GO_BP_m4	GO:00427	hydrogen p	2/727	17/23843	0.093397	0.631366	0.621921	Apoa4/Mp
GO_BP_m4	GO:00440	cell wall ma	2/727	17/23843	0.093397	0.631366	0.621921	Lyzl1/Manl
GO_BP_m4	GO:00488	forebrain n	2/727	17/23843	0.093397	0.631366	0.621921	Duox2/Gak
GO_BP_m4	GO:00506	chondroitir	2/727	17/23843	0.093397	0.631366	0.621921	Pxylp1/Xylt
GO_BP_m4	GO:00608	regulation	2/727	17/23843	0.093397	0.631366	0.621921	Nkx6-2/So
GO_BP_m4	GO:00715	cell wall or	2/727	17/23843	0.093397	0.631366	0.621921	Lyzl1/Manl
GO_BP_m4	GO:19032	positive reg	2/727	17/23843	0.093397	0.631366	0.621921	Ripk1/Sfpq
GO_BP_m4	GO:190531	semi-lunar	2/727	17/23843	0.093397	0.631366	0.621921	Efna1/Nfat
GO_BP_m4	GO:200081	regulation	2/727	17/23843	0.093397	0.631366	0.621921	Nedd4l/Np
GO_BP_m4	GO:00380	signal trans	5/727	79/23843	0.093511	0.631366	0.621921	Ctnna1/Ga
GO_BP_m4	GO:00971	extrinsic ap	5/727	79/23843	0.093511	0.631366	0.621921	Ctnna1/Ga
GO_BP_m4	GO:003241	positive reg	6/727	103/23843	0.095118	0.631366	0.621921	Ager/Arc/C
GO_BP_m4	GO:00456	positive reg	4/727	57/23843	0.095684	0.631366	0.621921	Htr2c/Map
GO_BP_m4	GO:00487	mesenchyr	10/727	204/23843	0.095708	0.631366	0.621921	Ager/Efna1
GO_BP_m4	GO:00072	activation	3/727	36/23843	0.096128	0.631366	0.621921	Ern2/Map3
GO_BP_m4	GO:00482	response t	3/727	36/23843	0.096128	0.631366	0.621921	Cacna1b/R
GO_BP_m4	GO:00613	heart trabe	3/727	36/23843	0.096128	0.631366	0.621921	Fhl2/Nfatc
GO_BP_m4	GO:00171	regulation	5/727	80/23843	0.097389	0.631366	0.621921	Cacna1g/C
GO_BP_m4	GO:00458	positive reg	14/727	312/23843	0.097911	0.631366	0.621921	Astl/Aurka/
GO_BP_m4	GO:00018	epithelial t	7/727	129/23843	0.100043	0.631366	0.621921	Ager/Efna1
GO_BP_m4	GO:20010	positive reg	7/727	129/23843	0.100043	0.631366	0.621921	Bcl10/Cycs
GO_BP_m4	GO:004327	positive reg	13/727	286/23843	0.100188	0.631366	0.621921	Abcb4/Age
GO_BP_m4	GO:19033	positive reg	4/727	58/23843	0.100431	0.631366	0.621921	Cacna1g/C
GO_BP_m4	GO:00346	ncRNA me	19/727	453/23843	0.101735	0.631366	0.621921	Dalrd3/Dus
GO_BP_m4	GO:00030	heart morp	12/727	260/23843	0.102245	0.631366	0.621921	Dsp/Efna1/
GO_BP_m4	GO:00017	endoderm	3/727	37/23843	0.102357	0.631366	0.621921	Dusp2/Inhl
GO_BP_m4	GO:00460	regulation	3/727	37/23843	0.102357	0.631366	0.621921	Ager/Btn2a
GO_BP_m4	GO:00610	positive reg	3/727	37/23843	0.102357	0.631366	0.621921	Efna1/Gas6
GO_BP_m4	GO:00860	cell commu	3/727	37/23843	0.102357	0.631366	0.621921	Cacna1g/D
GO_BP_m4	GO:00481	regulation	15/727	342/23843	0.102709	0.631366	0.621921	Ager/Anap
GO_BP_m4	GO:00072	JAK-STAT	10/727	207/23843	0.102793	0.631366	0.621921	Ager/Flrt1/
GO_BP_m4	GO:00019	positive reg	2/727	18/23843	0.103026	0.631366	0.621921	Cacna1b/H
GO_BP_m4	GO:00107	positive reg	2/727	18/23843	0.103026	0.631366	0.621921	C3ar1/Map
GO_BP_m4	GO:00220	corpus call	2/727	18/23843	0.103026	0.631366	0.621921	Rtn4r/Zeb
GO_BP_m4	GO:00324	establishm	2/727	18/23843	0.103026	0.631366	0.621921	Cdh3/Mreg
GO_BP_m4	GO:003357	response t	2/727	18/23843	0.103026	0.631366	0.621921	Cacna1b/E
GO_BP_m4	GO:00362	interstrand	2/727	18/23843	0.103026	0.631366	0.621921	Cenps/Xpa
GO_BP_m4	GO:003631	response t	2/727	18/23843	0.103026	0.631366	0.621921	Inhba/Mlc1
GO_BP_m4	GO:00424	melanin bi	2/727	18/23843	0.103026	0.631366	0.621921	Cdh3/Zeb2
GO_BP_m4	GO:004647	glycerophc	2/727	18/23843	0.103026	0.631366	0.621921	Gdpd3/Lip
GO_BP_m4	GO:00508	negative re	2/727	18/23843	0.103026	0.631366	0.621921	Btn2a2/Lga
GO_BP_m4	GO:00519	pigment gr	2/727	18/23843	0.103026	0.631366	0.621921	Cdh3/Mreg
GO_BP_m4	GO:00716	monocyte	2/727	18/23843	0.103026	0.631366	0.621921	Ager/Socs
GO_BP_m4	GO:00716	regulation	2/727	18/23843	0.103026	0.631366	0.621921	Ager/Socs

GO_BP_m4	GO:190101	negative re	2/727	18/23843	0.103026	0.631366	0.621921	Kcne1/Nec
GO_BP_m4	GO:190438	cellular res	2/727	18/23843	0.103026	0.631366	0.621921	Car2/Rela
GO_BP_m4	GO:199077	response t	2/727	18/23843	0.103026	0.631366	0.621921	Car2/Rela
GO_BP_m4	GO:001612	sterol meta	7/727	130/23843	0.103128	0.631366	0.621921	Akr1d1/Ap
GO_BP_m4	GO:190330	regulation	7/727	130/23843	0.103128	0.631366	0.621921	Cacna1g/C
GO_BP_m4	GO:000726	Ras protein	18/727	426/23843	0.103561	0.631366	0.621921	Agap3/Agf
GO_BP_m4	GO:200011	regulation	11/727	234/23843	0.103974	0.631366	0.621921	Anp32b/Bc
GO_BP_m4	GO:004232	negative re	19/727	455/23843	0.104931	0.631366	0.621921	Ager/Akt1s
GO_BP_m4	GO:001814	peptide cro	4/727	59/23843	0.105284	0.631366	0.621921	Dsp/Lce1g
GO_BP_m4	GO:009700	regulation	4/727	59/23843	0.105284	0.631366	0.621921	Apoa4/Lipc
GO_BP_m4	GO:005120	release of s	6/727	106/23843	0.105439	0.631366	0.621921	Ddit3/Htr2
GO_BP_m4	GO:005128	negative re	6/727	106/23843	0.105439	0.631366	0.621921	Ddit3/Htr2
GO_BP_m4	GO:005080	regulation	9/727	182/23843	0.10576	0.631366	0.621921	Anapc2/Ar
GO_BP_m4	GO:003286	response t	10/727	209/23843	0.107682	0.631366	0.621921	C1qtnf12/F
GO_BP_m4	GO:003287	regulation	10/727	209/23843	0.107682	0.631366	0.621921	Ager/Dusp
GO_BP_m4	GO:009769	STAT casca	10/727	209/23843	0.107682	0.631366	0.621921	Ager/Flrt1/
GO_BP_m4	GO:004340	regulation	13/727	290/23843	0.108353	0.631366	0.621921	Ager/Cspg
GO_BP_m4	GO:200102	positive reg	3/727	38/23843	0.108741	0.631366	0.621921	Htr2c/Ripk
GO_BP_m4	GO:000641	regulation	17/727	401/23843	0.108793	0.631366	0.621921	Cnot6/Eif3
GO_BP_m4	GO:000828	insulin rece	6/727	107/23843	0.109003	0.631366	0.621921	C1qtnf12/C
GO_BP_m4	GO:004881	regulation	6/727	107/23843	0.109003	0.631366	0.621921	Anapc2/Ar
GO_BP_m4	GO:005102	mRNA tran	6/727	107/23843	0.109003	0.631366	0.621921	Parp11/Sec
GO_BP_m4	GO:005128	regulation	6/727	107/23843	0.109003	0.631366	0.621921	Ddit3/Htr2
GO_BP_m4	GO:005158	regulation	6/727	107/23843	0.109003	0.631366	0.621921	Cacna1b/H
GO_BP_m4	GO:190382	negative re	6/727	107/23843	0.109003	0.631366	0.621921	Astn2/Dclk
GO_BP_m4	GO:007188	leukocyte a	7/727	132/23843	0.109451	0.631366	0.621921	Bcl10/Efna
GO_BP_m4	GO:004263	cholesterol	5/727	83/23843	0.109496	0.631366	0.621921	Apoa4/Cyp
GO_BP_m4	GO:005509	sterol hom	5/727	83/23843	0.109496	0.631366	0.621921	Apoa4/Cyp
GO_BP_m4	GO:190303	negative re	5/727	83/23843	0.109496	0.631366	0.621921	Ager/Dusp
GO_BP_m4	GO:007030	regulation	10/727	210/23843	0.110175	0.631366	0.621921	Ager/Dusp
GO_BP_m4	GO:000759	lactation	4/727	60/23843	0.110242	0.631366	0.621921	Neurl1a/Oa
GO_BP_m4	GO:007147	cellular res	4/727	60/23843	0.110242	0.631366	0.621921	Grb2/Hus1
GO_BP_m4	GO:005120	sequesterin	6/727	108/23843	0.112629	0.631366	0.621921	Ddit3/Htr2
GO_BP_m4	GO:005105	negative re	7/727	133/23843	0.112688	0.631366	0.621921	Hcrt/Hus1/
GO_BP_m4	GO:000218	cytoplasmi	2/727	19/23843	0.112911	0.631366	0.621921	Eif3a/Rps2
GO_BP_m4	GO:000669	bile acid bi	2/727	19/23843	0.112911	0.631366	0.621921	Akr1d1/Cy
GO_BP_m4	GO:001076	positive reg	2/727	19/23843	0.112911	0.631366	0.621921	Ager/Slc8a
GO_BP_m4	GO:001581	L-glutamat	2/727	19/23843	0.112911	0.631366	0.621921	Slc17a8/Slc
GO_BP_m4	GO:004278	mRNA tran	2/727	19/23843	0.112911	0.631366	0.621921	Ddit3/Sox1
GO_BP_m4	GO:005190	establishm	2/727	19/23843	0.112911	0.631366	0.621921	Cdh3/Mreg
GO_BP_m4	GO:190040	positive reg	2/727	19/23843	0.112911	0.631366	0.621921	Ripk1/Sfpq
GO_BP_m4	GO:190552	positive reg	2/727	19/23843	0.112911	0.631366	0.621921	C3ar1/Map
GO_BP_m4	GO:200078	negative re	2/727	19/23843	0.112911	0.631366	0.621921	Recql5/Trip
GO_BP_m4	GO:000864	carbohydra	8/727	159/23843	0.114003	0.631366	0.621921	C1qtnf12/F
GO_BP_m4	GO:003164	killing of ce	3/727	39/23843	0.115276	0.631366	0.621921	Mbl1/Mbl2
GO_BP_m4	GO:004436	disruption	3/727	39/23843	0.115276	0.631366	0.621921	Mbl1/Mbl2
GO_BP_m4	GO:004502	early endos	3/727	39/23843	0.115276	0.631366	0.621921	Kif16b/Ptpr
GO_BP_m4	GO:004824	macrophag	3/727	39/23843	0.115276	0.631366	0.621921	C3ar1/Lgal

GO_BP_m4	GO:200102	negative re	4/727	61/23843	0.115303	0.631366	0.621921	Recql5/Rps
GO_BP_m4	GO:200124	positive reg	4/727	61/23843	0.115303	0.631366	0.621921	Lck/Plagl2/
GO_BP_m4	GO:000941	response t	7/727	134/23843	0.115975	0.631366	0.621921	Agap3/Hus
GO_BP_m4	GO:200010	regulation	6/727	109/23843	0.116315	0.631366	0.621921	Bcl10/Efna
GO_BP_m4	GO:000042	carbon cata	1/727	4/23843	0.116506	0.631366	0.621921	Usf2
GO_BP_m4	GO:000043	carbon cata	1/727	4/23843	0.116506	0.631366	0.621921	Usf2
GO_BP_m4	GO:000070	meiotic DN	1/727	4/23843	0.116506	0.631366	0.621921	Brip1
GO_BP_m4	GO:000073	DNA catab	1/727	4/23843	0.116506	0.631366	0.621921	Eri2
GO_BP_m4	GO:000191	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Muc4
GO_BP_m4	GO:000192	B-1 B cell	1/727	4/23843	0.116506	0.631366	0.621921	Nfatc1
GO_BP_m4	GO:000195	intestinal D	1/727	4/23843	0.116506	0.631366	0.621921	Slc5a1
GO_BP_m4	GO:000218	translation	1/727	4/23843	0.116506	0.631366	0.621921	Eif3a
GO_BP_m4	GO:000240	myeloid de	1/727	4/23843	0.116506	0.631366	0.621921	Retnlg
GO_BP_m4	GO:000242	T cell medi	1/727	4/23843	0.116506	0.631366	0.621921	Muc4
GO_BP_m4	GO:000246	tolerance i	1/727	4/23843	0.116506	0.631366	0.621921	C3ar1
GO_BP_m4	GO:000252	acute infla	1/727	4/23843	0.116506	0.631366	0.621921	Ffar3
GO_BP_m4	GO:000283	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Muc4
GO_BP_m4	GO:000283	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Muc4
GO_BP_m4	GO:000284	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Muc4
GO_BP_m4	GO:000310	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Gas6
GO_BP_m4	GO:000642	arginyl-tRN	1/727	4/23843	0.116506	0.631366	0.621921	Dalrd3
GO_BP_m4	GO:000722	Wnt signali	1/727	4/23843	0.116506	0.631366	0.621921	Ror2
GO_BP_m4	GO:000913	purine nuc	1/727	4/23843	0.116506	0.631366	0.621921	Ak3
GO_BP_m4	GO:000918	purine ribo	1/727	4/23843	0.116506	0.631366	0.621921	Ak3
GO_BP_m4	GO:001028	heat acclim	1/727	4/23843	0.116506	0.631366	0.621921	Hsbp1l1
GO_BP_m4	GO:001072	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Gata1
GO_BP_m4	GO:001074	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Irs2
GO_BP_m4	GO:001483	myoblast d	1/727	4/23843	0.116506	0.631366	0.621921	Mapk14
GO_BP_m4	GO:001569	cadmium i	1/727	4/23843	0.116506	0.631366	0.621921	Slc39a8
GO_BP_m4	GO:002191	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Nkx6-2
GO_BP_m4	GO:003020	heparin me	1/727	4/23843	0.116506	0.631366	0.621921	Xylt2
GO_BP_m4	GO:003024	skeletal mu	1/727	4/23843	0.116506	0.631366	0.621921	Myom2
GO_BP_m4	GO:003053	embryonic	1/727	4/23843	0.116506	0.631366	0.621921	Ror2
GO_BP_m4	GO:003207	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Rps3
GO_BP_m4	GO:003284	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Car2
GO_BP_m4	GO:003315	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Gas6
GO_BP_m4	GO:003552	protein K2	1/727	4/23843	0.116506	0.631366	0.621921	Otud6a
GO_BP_m4	GO:003562	intrahepati	1/727	4/23843	0.116506	0.631366	0.621921	Gak
GO_BP_m4	GO:003579	ureter matu	1/727	4/23843	0.116506	0.631366	0.621921	Ret
GO_BP_m4	GO:003613	Schwann c	1/727	4/23843	0.116506	0.631366	0.621921	Tiam1
GO_BP_m4	GO:003650	ATF6-med	1/727	4/23843	0.116506	0.631366	0.621921	Atf6b
GO_BP_m4	GO:004266	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Sox17
GO_BP_m4	GO:004339	corticotrop	1/727	4/23843	0.116506	0.631366	0.621921	Htr2c
GO_BP_m4	GO:004339	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Htr2c
GO_BP_m4	GO:004355	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Pik3ip1
GO_BP_m4	GO:004433	canonical	1/727	4/23843	0.116506	0.631366	0.621921	Tnn
GO_BP_m4	GO:004480	multi-orga	1/727	4/23843	0.116506	0.631366	0.621921	Gas6
GO_BP_m4	GO:004591	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Htr2c

GO_BP_m4	GO:004596	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Htr2c
GO_BP_m4	GO:004601	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Usf2
GO_BP_m4	GO:004612	pyrimidine	1/727	4/23843	0.116506	0.631366	0.621921	Tk1
GO_BP_m4	GO:004644	creatinine	1/727	4/23843	0.116506	0.631366	0.621921	Mme
GO_BP_m4	GO:004681	receptor-m	1/727	4/23843	0.116506	0.631366	0.621921	Gas6
GO_BP_m4	GO:004810	establishm	1/727	4/23843	0.116506	0.631366	0.621921	Astn2
GO_BP_m4	GO:004810	establishm	1/727	4/23843	0.116506	0.631366	0.621921	Astn2
GO_BP_m4	GO:004838	mesendod	1/727	4/23843	0.116506	0.631366	0.621921	Zfp36l1
GO_BP_m4	GO:004868	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Rtn4
GO_BP_m4	GO:005159	response t	1/727	4/23843	0.116506	0.631366	0.621921	Folr1
GO_BP_m4	GO:005179	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Cdh3
GO_BP_m4	GO:005191	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	F12
GO_BP_m4	GO:006026	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Dusp10
GO_BP_m4	GO:006027	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Inhba
GO_BP_m4	GO:006028	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Aurka
GO_BP_m4	GO:006046	prevention	1/727	4/23843	0.116506	0.631366	0.621921	Astl
GO_BP_m4	GO:006074	epithelial c	1/727	4/23843	0.116506	0.631366	0.621921	Esr2
GO_BP_m4	GO:006091	cardiac cell	1/727	4/23843	0.116506	0.631366	0.621921	Sox17
GO_BP_m4	GO:006103	endoderma	1/727	4/23843	0.116506	0.631366	0.621921	Sox17
GO_BP_m4	GO:006135	Wnt protei	1/727	4/23843	0.116506	0.631366	0.621921	Ptpn23
GO_BP_m4	GO:006135	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Ptpn23
GO_BP_m4	GO:006188	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Ager
GO_BP_m4	GO:007034	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Pid1
GO_BP_m4	GO:007053	histone H2	1/727	4/23843	0.116506	0.631366	0.621921	Trip12
GO_BP_m4	GO:007057	cadmium i	1/727	4/23843	0.116506	0.631366	0.621921	Slc39a8
GO_BP_m4	GO:007083	dehydroas	1/727	4/23843	0.116506	0.631366	0.621921	Slc2a2
GO_BP_m4	GO:007096	nuclear-tra	1/727	4/23843	0.116506	0.631366	0.621921	Cnot6
GO_BP_m4	GO:007173	transcriptio	1/727	4/23843	0.116506	0.631366	0.621921	Gata1
GO_BP_m4	GO:007178	endoplasm	1/727	4/23843	0.116506	0.631366	0.621921	Rtn4
GO_BP_m4	GO:007189	protein loc	1/727	4/23843	0.116506	0.631366	0.621921	Dsp
GO_BP_m4	GO:008604	membrane	1/727	4/23843	0.116506	0.631366	0.621921	Cacna1g
GO_BP_m4	GO:009018	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Vamp8
GO_BP_m4	GO:009020	gene loopi	1/727	4/23843	0.116506	0.631366	0.621921	Gata1
GO_BP_m4	GO:009029	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Pid1
GO_BP_m4	GO:009057	dsDNA loo	1/727	4/23843	0.116506	0.631366	0.621921	Gata1
GO_BP_m4	GO:009725	oligodendr	1/727	4/23843	0.116506	0.631366	0.621921	Gas6
GO_BP_m4	GO:009727	compleme	1/727	4/23843	0.116506	0.631366	0.621921	Il13
GO_BP_m4	GO:009898	NMDA sele	1/727	4/23843	0.116506	0.631366	0.621921	Tiam1
GO_BP_m4	GO:010600	intestinal h	1/727	4/23843	0.116506	0.631366	0.621921	Slc5a1
GO_BP_m4	GO:190004	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Trip12
GO_BP_m4	GO:190014	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Tiam1
GO_BP_m4	GO:190184	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Rem2
GO_BP_m4	GO:190185	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Pid1
GO_BP_m4	GO:190262	assembly c	1/727	4/23843	0.116506	0.631366	0.621921	Rpl24
GO_BP_m4	GO:190273	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Pxylp1
GO_BP_m4	GO:190274	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Zeb2
GO_BP_m4	GO:190359	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Vamp8
GO_BP_m4	GO:190359	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Vamp8

GO_BP_m4	GO:190386	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Rtn4
GO_BP_m4	GO:190397	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Tiam1
GO_BP_m4	GO:190577	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Sox17
GO_BP_m4	GO:190588	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Aurka
GO_BP_m4	GO:190590	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Sox17
GO_BP_m4	GO:199080	endoplasm	1/727	4/23843	0.116506	0.631366	0.621921	Rtn4
GO_BP_m4	GO:199096	ATP genera	1/727	4/23843	0.116506	0.631366	0.621921	Nudt5
GO_BP_m4	GO:200035	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Astl
GO_BP_m4	GO:200052	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Lgals3
GO_BP_m4	GO:200062	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Nbas
GO_BP_m4	GO:200062	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Nbas
GO_BP_m4	GO:200066	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Gas6
GO_BP_m4	GO:200118	positive reg	1/727	4/23843	0.116506	0.631366	0.621921	Mapk14
GO_BP_m4	GO:200127	regulation	1/727	4/23843	0.116506	0.631366	0.621921	Rps3
GO_BP_m4	GO:200127	negative re	1/727	4/23843	0.116506	0.631366	0.621921	Pid1
GO_BP_m4	GO:000961	response t	19/727	462/23843	0.116607	0.631366	0.621921	2310075C1
GO_BP_m4	GO:004478	cilium orga	14/727	322/23843	0.117742	0.63507	0.625569	Abcc4/Atxn
GO_BP_m4	GO:005105	regulation	12/727	267/23843	0.117777	0.63507	0.625569	Agap3/Agf
GO_BP_m4	GO:000721	neuropepti	5/727	85/23843	0.117955	0.63507	0.625569	Gpr19/Hcrt
GO_BP_m4	GO:001071	regulation	5/727	85/23843	0.117955	0.63507	0.625569	Ager/Efna1
GO_BP_m4	GO:004568	regulation	5/727	85/23843	0.117955	0.63507	0.625569	Ager/Dusp
GO_BP_m4	GO:003021	keratinocyt	7/727	135/23843	0.119312	0.641656	0.632056	Cdh3/Dsp/
GO_BP_m4	GO:005254	regulation	17/727	407/23843	0.119713	0.643076	0.633455	Anp32b/Bc
GO_BP_m4	GO:000854	epidermis (	14/727	323/23843	0.119845	0.643076	0.633455	Cdh3/Dsp/
GO_BP_m4	GO:190122	positive reg	4/727	62/23843	0.120463	0.645666	0.636007	Ager/Rela/
GO_BP_m4	GO:003367	negative re	11/727	241/23843	0.120618	0.645774	0.636113	Akt1s1/Dus
GO_BP_m4	GO:003201	ARF protei	3/727	40/23843	0.121954	0.646365	0.636695	Agap3/Agf
GO_BP_m4	GO:003201	regulation	3/727	40/23843	0.121954	0.646365	0.636695	Agap3/Agf
GO_BP_m4	GO:008600	cardiac mu	3/727	40/23843	0.121954	0.646365	0.636695	Cacna1g/D
GO_BP_m4	GO:003461	response t	9/727	188/23843	0.122237	0.646365	0.636695	Gas6/Mapk
GO_BP_m4	GO:000658	melanin m	2/727	20/23843	0.123027	0.646365	0.636695	Cdh3/Zeb2
GO_BP_m4	GO:000688	cellular soc	2/727	20/23843	0.123027	0.646365	0.636695	Atp1b4/Slc
GO_BP_m4	GO:000920	deoxyribor	2/727	20/23843	0.123027	0.646365	0.636695	Ak3/Dguok
GO_BP_m4	GO:001943	removal of	2/727	20/23843	0.123027	0.646365	0.636695	Apoa4/Mp
GO_BP_m4	GO:003128	positive reg	2/727	20/23843	0.123027	0.646365	0.636695	Mapk14/Ts
GO_BP_m4	GO:003144	regulation	2/727	20/23843	0.123027	0.646365	0.636695	Nelfe/Zfp3
GO_BP_m4	GO:003633	dendritic ce	2/727	20/23843	0.123027	0.646365	0.636695	Gas6/Retnl
GO_BP_m4	GO:004350	skeletal mu	2/727	20/23843	0.123027	0.646365	0.636695	Gtf2ird1/N
GO_BP_m4	GO:005181	disruption	2/727	20/23843	0.123027	0.646365	0.636695	Mbl1/Mbl2
GO_BP_m4	GO:005188	killing of ce	2/727	20/23843	0.123027	0.646365	0.636695	Mbl1/Mbl2
GO_BP_m4	GO:007016	negative re	2/727	20/23843	0.123027	0.646365	0.636695	Gas6/Gata1
GO_BP_m4	GO:009038	phagosom	2/727	20/23843	0.123027	0.646365	0.636695	Rab31/Rab
GO_BP_m4	GO:190138	negative re	2/727	20/23843	0.123027	0.646365	0.636695	Cbarp/Rem
GO_BP_m4	GO:007026	small GTPa	20/727	495/23843	0.124222	0.649487	0.63977	Agap3/Agf
GO_BP_m4	GO:005134	positive reg	20/727	495/23843	0.124222	0.649487	0.63977	Apoa4/Arh
GO_BP_m4	GO:003109	stress-activ	12/727	270/23843	0.124825	0.649487	0.63977	Ager/Dusp
GO_BP_m4	GO:006099	dendritic sp	4/727	63/23843	0.125721	0.649487	0.63977	Arc/Efna1/
GO_BP_m4	GO:009730	cellular res	4/727	63/23843	0.125721	0.649487	0.63977	Ctnna1/Inh

GO_BP_m4	GO:007190	positive reg	13/727	298/23843	0.12583	0.649487	0.63977	Ager/Cspg
GO_BP_m4	GO:000726	neurotrans	7/727	137/23843	0.126133	0.649487	0.63977	Cacna1b/H
GO_BP_m4	GO:009964	signal relea	7/727	137/23843	0.126133	0.649487	0.63977	Cacna1b/H
GO_BP_m4	GO:004632	glucose im	5/727	87/23843	0.126712	0.649487	0.63977	C1qtnf12/
GO_BP_m4	GO:004484	cell cycle G	9/727	190/23843	0.128021	0.649487	0.63977	Anp32b/Bt
GO_BP_m4	GO:005077	regulation	9/727	190/23843	0.128021	0.649487	0.63977	Anapc2/Efn
GO_BP_m4	GO:000628	base-excisi	3/727	41/23843	0.12877	0.649487	0.63977	Polb/Rps3/
GO_BP_m4	GO:009875	detoxificati	3/727	41/23843	0.12877	0.649487	0.63977	Apoa4/Mp
GO_BP_m4	GO:009892	vesicle-me	3/727	41/23843	0.12877	0.649487	0.63977	Kif16b/Ptp
GO_BP_m4	GO:001603	viral proces	12/727	272/23843	0.129653	0.649487	0.63977	A230050P2
GO_BP_m4	GO:005073	regulation	11/727	245/23843	0.130763	0.649487	0.63977	Cspg4/Efna
GO_BP_m4	GO:004692	regulation	4/727	64/23843	0.131074	0.649487	0.63977	Cacna1b/H
GO_BP_m4	GO:003134	regulation	5/727	88/23843	0.131199	0.649487	0.63977	Ager/Dnas
GO_BP_m4	GO:005076	regulation	5/727	88/23843	0.131199	0.649487	0.63977	Ager/Gas6/
GO_BP_m4	GO:000193	negative re	17/727	413/23843	0.131261	0.649487	0.63977	Ager/Akt1s
GO_BP_m4	GO:003572	sodium ion	6/727	113/23843	0.131652	0.649487	0.63977	Atp1b4/Cn
GO_BP_m4	GO:005085	T cell recep	6/727	113/23843	0.131652	0.649487	0.63977	Bcl10/Btn2
GO_BP_m4	GO:003240	melanosom	2/727	21/23843	0.133352	0.649487	0.63977	Cdh3/Mreg
GO_BP_m4	GO:003300	positive reg	2/727	21/23843	0.133352	0.649487	0.63977	Il13/Vamp8
GO_BP_m4	GO:003437	plasma lipo	2/727	21/23843	0.133352	0.649487	0.63977	Apoa4/Plag
GO_BP_m4	GO:004330	positive reg	2/727	21/23843	0.133352	0.649487	0.63977	Il13/Vamp8
GO_BP_m4	GO:004506	T-helper 1	2/727	21/23843	0.133352	0.649487	0.63977	Il27/Socs5
GO_BP_m4	GO:004613	pyrimidine	2/727	21/23843	0.133352	0.649487	0.63977	Ak3/Nme5
GO_BP_m4	GO:009028	positive reg	2/727	21/23843	0.133352	0.649487	0.63977	Lgals3/Trpv
GO_BP_m4	GO:190200	regulation	2/727	21/23843	0.133352	0.649487	0.63977	Efna1/Tme
GO_BP_m4	GO:200067	negative re	2/727	21/23843	0.133352	0.649487	0.63977	Ddit3/Gata
GO_BP_m4	GO:200127	regulation	2/727	21/23843	0.133352	0.649487	0.63977	Ffar3/Pid1
GO_BP_m4	GO:003305	cellular pig	3/727	42/23843	0.135717	0.649487	0.63977	Cdh3/Mreg
GO_BP_m4	GO:005189	negative re	3/727	42/23843	0.135717	0.649487	0.63977	Btn2a2/Dd
GO_BP_m4	GO:190138	regulation	3/727	42/23843	0.135717	0.649487	0.63977	Cbarp/Kcn
GO_BP_m4	GO:001406	regulation	5/727	89/23843	0.135757	0.649487	0.63977	Btn2a2/Erb
GO_BP_m4	GO:000253	production	4/727	65/23843	0.136519	0.649487	0.63977	Dusp10/Ma
GO_BP_m4	GO:004816	regulation	4/727	65/23843	0.136519	0.649487	0.63977	Arc/Neurl1
GO_BP_m4	GO:004558	regulation	7/727	140/23843	0.136724	0.649487	0.63977	Btn2a2/Du
GO_BP_m4	GO:003238	regulation	17/727	417/23843	0.139307	0.649487	0.63977	Cdh3/Erbb
GO_BP_m4	GO:000688	ER to Golgi	6/727	115/23843	0.139664	0.649487	0.63977	Lman1l/Se
GO_BP_m4	GO:003461	cellular res	7/727	141/23843	0.140349	0.649487	0.63977	Agap3/Ap
GO_BP_m4	GO:004273	drug catab	7/727	141/23843	0.140349	0.649487	0.63977	Apoa4/Ctb
GO_BP_m4	GO:000202	regulation	5/727	90/23843	0.140385	0.649487	0.63977	Cacna1g/D
GO_BP_m4	GO:007145	cellular res	5/727	90/23843	0.140385	0.649487	0.63977	Fndc1/Hp1
GO_BP_m4	GO:190118	regulation	4/727	66/23843	0.142055	0.649487	0.63977	Esr2/Neurl
GO_BP_m4	GO:000191	T cell medi	3/727	43/23843	0.14279	0.649487	0.63977	Ager/Muc4
GO_BP_m4	GO:003016	proteoglyc	3/727	43/23843	0.14279	0.649487	0.63977	Lipc/Pxylp1
GO_BP_m4	GO:003110	axon regen	3/727	43/23843	0.14279	0.649487	0.63977	Folr1/Rtn4/
GO_BP_m4	GO:003275	positive reg	3/727	43/23843	0.14279	0.649487	0.63977	Bcl10/Ddit3
GO_BP_m4	GO:007138	cellular res	3/727	43/23843	0.14279	0.649487	0.63977	Mir155/Sst
GO_BP_m4	GO:200125	negative re	3/727	43/23843	0.14279	0.649487	0.63977	Cbarp/Kcn
GO_BP_m4	GO:004642	regulation	9/727	195/23843	0.143101	0.649487	0.63977	Flrt1/Ifna12

GO_BP_m4	GO:000039	mRNA 5'-s	1/727	5/23843	0.143449	0.649487	0.63977	Snrpc
GO_BP_m4	GO:000187	response t	1/727	5/23843	0.143449	0.649487	0.63977	Mpo
GO_BP_m4	GO:000224	connective	1/727	5/23843	0.143449	0.649487	0.63977	Ager
GO_BP_m4	GO:000229	T cell activ	1/727	5/23843	0.143449	0.649487	0.63977	Lgals3
GO_BP_m4	GO:000290	mature B c	1/727	5/23843	0.143449	0.649487	0.63977	Bcl10
GO_BP_m4	GO:000290	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Bcl10
GO_BP_m4	GO:000290	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Bcl10
GO_BP_m4	GO:000319	endocardi	1/727	5/23843	0.143449	0.649487	0.63977	Efna1
GO_BP_m4	GO:000330	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Sox17
GO_BP_m4	GO:000616	AMP biosy	1/727	5/23843	0.143449	0.649487	0.63977	Prps2
GO_BP_m4	GO:000628	base-excisi	1/727	5/23843	0.143449	0.649487	0.63977	Polb
GO_BP_m4	GO:000643	phenylalan	1/727	5/23843	0.143449	0.649487	0.63977	Fars2
GO_BP_m4	GO:000719	G-protein	1/727	5/23843	0.143449	0.649487	0.63977	Gnat1
GO_BP_m4	GO:000725	activation	1/727	5/23843	0.143449	0.649487	0.63977	Map3k11
GO_BP_m4	GO:000911	xanthine c	1/727	5/23843	0.143449	0.649487	0.63977	Aox3
GO_BP_m4	GO:000918	ribonucleo	1/727	5/23843	0.143449	0.649487	0.63977	Ak3
GO_BP_m4	GO:000940	toxin biosy	1/727	5/23843	0.143449	0.649487	0.63977	Cyp1a2
GO_BP_m4	GO:000975	carbohydr	1/727	5/23843	0.143449	0.649487	0.63977	Ager
GO_BP_m4	GO:000975	hexose me	1/727	5/23843	0.143449	0.649487	0.63977	Ager
GO_BP_m4	GO:001018	sugar med	1/727	5/23843	0.143449	0.649487	0.63977	Ager
GO_BP_m4	GO:001025	glucose m	1/727	5/23843	0.143449	0.649487	0.63977	Ager
GO_BP_m4	GO:001051	positive re	1/727	5/23843	0.143449	0.649487	0.63977	Htr2c
GO_BP_m4	GO:001060	positive re	1/727	5/23843	0.143449	0.649487	0.63977	Cnot6
GO_BP_m4	GO:001402	notochord	1/727	5/23843	0.143449	0.649487	0.63977	Efna1
GO_BP_m4	GO:001404	positive re	1/727	5/23843	0.143449	0.649487	0.63977	Ret
GO_BP_m4	GO:001404	establishm	1/727	5/23843	0.143449	0.649487	0.63977	Abcb1b
GO_BP_m4	GO:001588	folic acid tr	1/727	5/23843	0.143449	0.649487	0.63977	Folr1
GO_BP_m4	GO:002179	forebrain a	1/727	5/23843	0.143449	0.649487	0.63977	Fezf1
GO_BP_m4	GO:002304	neuronal si	1/727	5/23843	0.143449	0.649487	0.63977	Rtn4r
GO_BP_m4	GO:003022	eosinophil	1/727	5/23843	0.143449	0.649487	0.63977	Gata1
GO_BP_m4	GO:003026	apoptotic	1/727	5/23843	0.143449	0.649487	0.63977	Ern2
GO_BP_m4	GO:003057	PML body	1/727	5/23843	0.143449	0.649487	0.63977	Agap3
GO_BP_m4	GO:003207	positive re	1/727	5/23843	0.143449	0.649487	0.63977	Rps3
GO_BP_m4	GO:003248	Ral protein	1/727	5/23843	0.143449	0.649487	0.63977	Ralgps1
GO_BP_m4	GO:003284	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Car2
GO_BP_m4	GO:003291	positive re	1/727	5/23843	0.143449	0.649487	0.63977	Lum
GO_BP_m4	GO:003308	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Erbb2
GO_BP_m4	GO:003596	COPI-coat	1/727	5/23843	0.143449	0.649487	0.63977	Tmed10
GO_BP_m4	GO:003626	RNA (guan	1/727	5/23843	0.143449	0.649487	0.63977	Wdr4
GO_BP_m4	GO:004213	meiotic D	1/727	5/23843	0.143449	0.649487	0.63977	Gm960
GO_BP_m4	GO:004227	error-pron	1/727	5/23843	0.143449	0.649487	0.63977	Polk
GO_BP_m4	GO:004270	progestero	1/727	5/23843	0.143449	0.649487	0.63977	Inhba
GO_BP_m4	GO:004483	cell quiesc	1/727	5/23843	0.143449	0.649487	0.63977	Nfatc1
GO_BP_m4	GO:004563	positive re	1/727	5/23843	0.143449	0.649487	0.63977	Zeb2
GO_BP_m4	GO:004599	carbon cat	1/727	5/23843	0.143449	0.649487	0.63977	Usf2
GO_BP_m4	GO:004599	carbon cat	1/727	5/23843	0.143449	0.649487	0.63977	Usf2
GO_BP_m4	GO:004601	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Usf2
GO_BP_m4	GO:004868	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Rtn4

GO_BP_m4	GO:005103	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Rilp	
GO_BP_m4	GO:005134	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Gnat1	
GO_BP_m4	GO:005138	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Spry2	
GO_BP_m4	GO:005166	actin cortic	1/727	5/23843	0.143449	0.649487	0.63977	Wipf2	
GO_BP_m4	GO:005215	modulatior	1/727	5/23843	0.143449	0.649487	0.63977	Serpinb9	
GO_BP_m4	GO:006005	apoptotic p	1/727	5/23843	0.143449	0.649487	0.63977	Vdr	
GO_BP_m4	GO:006005	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Vdr	
GO_BP_m4	GO:006026	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Dusp10	
GO_BP_m4	GO:006027	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Inhba	
GO_BP_m4	GO:006059	chondrobla	1/727	5/23843	0.143449	0.649487	0.63977	Fgf4	
GO_BP_m4	GO:006095	endocardia	1/727	5/23843	0.143449	0.649487	0.63977	Sox17	
GO_BP_m4	GO:007131	cellular res	1/727	5/23843	0.143449	0.649487	0.63977	Rela	
GO_BP_m4	GO:007168	response to	1/727	5/23843	0.143449	0.649487	0.63977	Ctnna1	
GO_BP_m4	GO:007168	cellular res	1/727	5/23843	0.143449	0.649487	0.63977	Ctnna1	
GO_BP_m4	GO:007230	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Ret	
GO_BP_m4	GO:007233	cellular lact	1/727	5/23843	0.143449	0.649487	0.63977	Mme	
GO_BP_m4	GO:007275	cellular res	1/727	5/23843	0.143449	0.649487	0.63977	Recql5	
GO_BP_m4	GO:007552	viral transla	1/727	5/23843	0.143449	0.649487	0.63977	Eif3a	
GO_BP_m4	GO:008604	membrane	1/727	5/23843	0.143449	0.649487	0.63977	Cacna1g	
GO_BP_m4	GO:009021	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Pik3ip1	
GO_BP_m4	GO:009734	ripoptoson	1/727	5/23843	0.143449	0.649487	0.63977	Ripk1	
GO_BP_m4	GO:009774	de novo ce	1/727	5/23843	0.143449	0.649487	0.63977	Cep152	
GO_BP_m4	GO:009853	de novo ce	1/727	5/23843	0.143449	0.649487	0.63977	Cep152	
GO_BP_m4	GO:009873	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Slc8a1	
GO_BP_m4	GO:015000	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Ager	
GO_BP_m4	GO:190102	ripoptoson	1/727	5/23843	0.143449	0.649487	0.63977	Ripk1	
GO_BP_m4	GO:190233	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Vdr	
GO_BP_m4	GO:190291	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Trip12	
GO_BP_m4	GO:190351	regulation	1/727	5/23843	0.143449	0.649487	0.63977	Vdr	
GO_BP_m4	GO:190352	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Vdr	
GO_BP_m4	GO:190375	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Dusp10	
GO_BP_m4	GO:190391	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Ppp1r15b	
GO_BP_m4	GO:190474	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Vdr	
GO_BP_m4	GO:200000	negative re	1/727	5/23843	0.143449	0.649487	0.63977	Thoc5	
GO_BP_m4	GO:200096	positive reg	1/727	5/23843	0.143449	0.649487	0.63977	Arc	
GO_BP_m4	GO:000191	negative re	2/727	22/23843	0.143863	0.649487	0.63977	Muc4/Serp	
GO_BP_m4	GO:003563	response to	2/727	22/23843	0.143863	0.649487	0.63977	Apoa4/Usp	
GO_BP_m4	GO:004485	hair cycle p	2/727	22/23843	0.143863	0.649487	0.63977	Cdh3/Mreg	
GO_BP_m4	GO:004560	positive reg	2/727	22/23843	0.143863	0.649487	0.63977	Ovol2/Vdr	
GO_BP_m4	GO:005085	positive reg	2/727	22/23843	0.143863	0.649487	0.63977	Rela/Rps3	
GO_BP_m4	GO:005085	negative re	2/727	22/23843	0.143863	0.649487	0.63977	Btn2a2/Lga	
GO_BP_m4	GO:005160	response to	2/727	22/23843	0.143863	0.649487	0.63977	Gnat1/Grm	
GO_BP_m4	GO:005187	pigment gr	2/727	22/23843	0.143863	0.649487	0.63977	Cdh3/Mreg	
GO_BP_m4	GO:006007	synapse ma	2/727	22/23843	0.143863	0.649487	0.63977	Anapc2/Ne	
GO_BP_m4	GO:007145	cellular res	2/727	22/23843	0.143863	0.649487	0.63977	Apoa4/Mp	
GO_BP_m4	GO:007145	cellular res	2/727	22/23843	0.143863	0.649487	0.63977	Apoa4/Mp	
GO_BP_m4	GO:190138	negative re	2/727	22/23843	0.143863	0.649487	0.63977	Kcne1/Nec	
GO_BP_m4	GO:190288	positive reg	2/727	22/23843	0.143863	0.649487	0.63977	Ripk1/Sfpq	

GO_BP_m4	GO:000683	neurotrans	11/727	250/23843	0.144075	0.649835	0.640113	Cacna1b/H
GO_BP_m4	GO:003447	ncRNA pro	14/727	335/23843	0.146768	0.661357	0.651463	Dus2/Eri2/
GO_BP_m4	GO:000602	proteoglyc	4/727	67/23843	0.147677	0.662954	0.653035	Lipc/Pxylp1
GO_BP_m4	GO:000617	cAMP bios	4/727	67/23843	0.147677	0.662954	0.653035	Cap2/Gng
GO_BP_m4	GO:009719	execution	4/727	67/23843	0.147677	0.662954	0.653035	Bcl10/Dnas
GO_BP_m4	GO:009917	regulation	4/727	67/23843	0.147677	0.662954	0.653035	Arc/Efna1/
GO_BP_m4	GO:006099	dendritic s	6/727	117/23843	0.147898	0.663319	0.653396	Arc/Efna1/
GO_BP_m4	GO:190489	regulation	9/727	197/23843	0.149375	0.667261	0.657279	Flrt1/Ifna1
GO_BP_m4	GO:000202	regulation	5/727	92/23843	0.149842	0.667261	0.657279	Cnksr3/Fxy
GO_BP_m4	GO:005181	modificatic	5/727	92/23843	0.149842	0.667261	0.657279	Mbl1/Mbl2
GO_BP_m4	GO:005189	membrane	5/727	92/23843	0.149842	0.667261	0.657279	Cacna1b/C
GO_BP_m4	GO:000247	antigen pr	3/727	44/23843	0.149982	0.667261	0.657279	H2-M10.1/
GO_BP_m4	GO:007023	regulation	3/727	44/23843	0.149982	0.667261	0.657279	Efna1/Lgal
GO_BP_m4	GO:007167	regulation	3/727	44/23843	0.149982	0.667261	0.657279	C3ar1/Lgal
GO_BP_m4	GO:006040	calcium ior	7/727	144/23843	0.151497	0.667261	0.657279	Cacna1g/D
GO_BP_m4	GO:005080	synapse or	14/727	337/23843	0.151551	0.667261	0.657279	Anapc2/Ar
GO_BP_m4	GO:005068	regulation	6/727	118/23843	0.152095	0.667261	0.657279	Nelfe/Rbfo
GO_BP_m4	GO:009015	establishm	9/727	198/23843	0.152562	0.667261	0.657279	Blzf1/Erbb
GO_BP_m4	GO:003241	negative re	4/727	68/23843	0.153385	0.667261	0.657279	Cbarp/Kcn
GO_BP_m4	GO:000013	establishm	2/727	23/23843	0.154539	0.667261	0.657279	Spdl1/Spry
GO_BP_m4	GO:000073	DNA catab	2/727	23/23843	0.154539	0.667261	0.657279	Dnase1/Dr
GO_BP_m4	GO:000290	negative re	2/727	23/23843	0.154539	0.667261	0.657279	Bcl10/Irs2
GO_BP_m4	GO:001095	positive re	2/727	23/23843	0.154539	0.667261	0.657279	Astl/F12
GO_BP_m4	GO:004204	fluid transp	2/727	23/23843	0.154539	0.667261	0.657279	Aqp9/Mip
GO_BP_m4	GO:004438	glucose im	2/727	23/23843	0.154539	0.667261	0.657279	Ffar3/Pid1
GO_BP_m4	GO:004833	mesoderm	2/727	23/23843	0.154539	0.667261	0.657279	Inhba/Sox1
GO_BP_m4	GO:007127	cellular res	2/727	23/23843	0.154539	0.667261	0.657279	Cyp1a2/Mt
GO_BP_m4	GO:007131	cellular res	2/727	23/23843	0.154539	0.667261	0.657279	Recql5/Slc
GO_BP_m4	GO:008971	amino acid	2/727	23/23843	0.154539	0.667261	0.657279	Slc1a5/Slc1
GO_BP_m4	GO:009886	cellular oxi	2/727	23/23843	0.154539	0.667261	0.657279	Apoa4/Mp
GO_BP_m4	GO:014011	export acrc	2/727	23/23843	0.154539	0.667261	0.657279	Atp1b4/Slc
GO_BP_m4	GO:001082	regulation	5/727	93/23843	0.15467	0.667261	0.657279	C1qtnf12/
GO_BP_m4	GO:005192	regulation	11/727	254/23843	0.155218	0.667261	0.657279	Cacna1b/C
GO_BP_m4	GO:006056	developme	11/727	254/23843	0.155218	0.667261	0.657279	Anapc2/Au
GO_BP_m4	GO:004801	inositol lipi	7/727	145/23843	0.155302	0.667261	0.657279	Btn2a2/Erb
GO_BP_m4	GO:007135	cellular res	8/727	172/23843	0.156251	0.667261	0.657279	Gas6/Map
GO_BP_m4	GO:000703	Golgi orga	6/727	119/23843	0.156345	0.667261	0.657279	Blzf1/Gak/
GO_BP_m4	GO:001406	phosphatic	6/727	119/23843	0.156345	0.667261	0.657279	Btn2a2/Erb
GO_BP_m4	GO:000657	cellular bio	3/727	45/23843	0.157288	0.667261	0.657279	Abhd4/Gd
GO_BP_m4	GO:003278	regulation	3/727	45/23843	0.157288	0.667261	0.657279	Nelfe/Recq
GO_BP_m4	GO:004484	biological	3/727	45/23843	0.157288	0.667261	0.657279	Cdh3/Mre
GO_BP_m4	GO:005079	activated T	3/727	45/23843	0.157288	0.667261	0.657279	Ager/Btn2
GO_BP_m4	GO:005087	brown fat	3/727	45/23843	0.157288	0.667261	0.657279	Dusp10/M
GO_BP_m4	GO:007138	cellular res	3/727	45/23843	0.157288	0.667261	0.657279	Mir155/Sst
GO_BP_m4	GO:001095	regulation	16/727	397/23843	0.158106	0.667261	0.657279	Ager/Cacn
GO_BP_m4	GO:009953	presynaptic	7/727	146/23843	0.159151	0.667261	0.657279	Cacna1b/H
GO_BP_m4	GO:003241	positive re	5/727	94/23843	0.159561	0.667261	0.657279	Ager/Arc/
GO_BP_m4	GO:190353	regulation	6/727	120/23843	0.160646	0.667261	0.657279	Erbb2/Kcn

GO_BP_m4	GO:00604	mesenchyr	11/727	256/23843	0.16095	0.667261	0.657279	Ager/Efna1
GO_BP_m4	GO:00725	reactive ox	11/727	256/23843	0.16095	0.667261	0.657279	Ager/Apoa
GO_BP_m4	GO:00716	anatomical	8/727	174/23843	0.163336	0.667261	0.657279	Aurka/Cdh
GO_BP_m4	GO:000024	spliceosom	3/727	46/23843	0.164701	0.667261	0.657279	Luc7l3/Snr
GO_BP_m4	GO:00511	cofactor ca	3/727	46/23843	0.164701	0.667261	0.657279	Apoa4/Mp
GO_BP_m4	GO:006004	regulation	3/727	46/23843	0.164701	0.667261	0.657279	Mapk14/M
GO_BP_m4	GO:19016	glycosyl co	6/727	121/23843	0.164998	0.667261	0.657279	Ak3/Dguo
GO_BP_m4	GO:00507	regulation	13/727	314/23843	0.165237	0.667261	0.657279	Ager/Dnas
GO_BP_m4	GO:00030	negative re	2/727	24/23843	0.165361	0.667261	0.657279	Kcnk6/Ned
GO_BP_m4	GO:000964	entrainmer	2/727	24/23843	0.165361	0.667261	0.657279	Sik1/Sox14
GO_BP_m4	GO:001482	vascular sn	2/727	24/23843	0.165361	0.667261	0.657279	Cacna1g/S
GO_BP_m4	GO:00194	triglycerid	2/727	24/23843	0.165361	0.667261	0.657279	Apoa4/Lip
GO_BP_m4	GO:00336	regulation	2/727	24/23843	0.165361	0.667261	0.657279	Gata1/Tnn
GO_BP_m4	GO:00340	protein loc	2/727	24/23843	0.165361	0.667261	0.657279	Arl5a/Gak
GO_BP_m4	GO:00509	positive re	2/727	24/23843	0.165361	0.667261	0.657279	Apoa4/Irs2
GO_BP_m4	GO:00650	protein-lip	2/727	24/23843	0.165361	0.667261	0.657279	Apoa4/Pla
GO_BP_m4	GO:190101	positive re	2/727	24/23843	0.165361	0.667261	0.657279	Ager/Kcne
GO_BP_m4	GO:00602	long-term	10/727	230/23843	0.166667	0.667261	0.657279	Ager/Arc/
GO_BP_m4	GO:00690	vesicle fusi	7/727	148/23843	0.166977	0.667261	0.657279	Rundc1/Se
GO_BP_m4	GO:000704	cell-cell ju	5/727	96/23843	0.169527	0.667261	0.657279	Cdh24/Cd
GO_BP_m4	GO:005077	positive re	5/727	96/23843	0.169527	0.667261	0.657279	Anapc2/Rt
GO_BP_m4	GO:000014	actin cortic	1/727	6/23843	0.169572	0.667261	0.657279	Wipf2
GO_BP_m4	GO:00025	respiratory	1/727	6/23843	0.169572	0.667261	0.657279	Dusp10
GO_BP_m4	GO:00062	nucleotide	1/727	6/23843	0.169572	0.667261	0.657279	Polk
GO_BP_m4	GO:00065	L-phenylal	1/727	6/23843	0.169572	0.667261	0.657279	Fah
GO_BP_m4	GO:000657	tyrosine ca	1/727	6/23843	0.169572	0.667261	0.657279	Fah
GO_BP_m4	GO:00071	receptor g	1/727	6/23843	0.169572	0.667261	0.657279	Gng7
GO_BP_m4	GO:00071	adenylate	1/727	6/23843	0.169572	0.667261	0.657279	Grm1
GO_BP_m4	GO:00082	opsonizati	1/727	6/23843	0.169572	0.667261	0.657279	Sftpa1
GO_BP_m4	GO:00085	photorece	1/727	6/23843	0.169572	0.667261	0.657279	Cabp4
GO_BP_m4	GO:000861	queuosine	1/727	6/23843	0.169572	0.667261	0.657279	Pdcl3
GO_BP_m4	GO:00086	activation	1/727	6/23843	0.169572	0.667261	0.657279	Cycs
GO_BP_m4	GO:000924	isopenteny	1/727	6/23843	0.169572	0.667261	0.657279	Pmvk
GO_BP_m4	GO:000964	response t	1/727	6/23843	0.169572	0.667261	0.657279	Gnat1
GO_BP_m4	GO:001027	detoxificati	1/727	6/23843	0.169572	0.667261	0.657279	Mt1
GO_BP_m4	GO:001074	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Irs2
GO_BP_m4	GO:00107	positive re	1/727	6/23843	0.169572	0.667261	0.657279	F12
GO_BP_m4	GO:001094	positive re	1/727	6/23843	0.169572	0.667261	0.657279	Ripk1
GO_BP_m4	GO:00140	acetylcholi	1/727	6/23843	0.169572	0.667261	0.657279	Htr2c
GO_BP_m4	GO:00140	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Htr2c
GO_BP_m4	GO:001507	DNA integ	1/727	6/23843	0.169572	0.667261	0.657279	Nynrin
GO_BP_m4	GO:00158	L-alanine t	1/727	6/23843	0.169572	0.667261	0.657279	Slc1a4
GO_BP_m4	GO:00190	virion attac	1/727	6/23843	0.169572	0.667261	0.657279	Gas6
GO_BP_m4	GO:00330	negative re	1/727	6/23843	0.169572	0.667261	0.657279	Erbb2
GO_BP_m4	GO:00332	negative re	1/727	6/23843	0.169572	0.667261	0.657279	Htr2c
GO_BP_m4	GO:00343	chylomicro	1/727	6/23843	0.169572	0.667261	0.657279	Lipc
GO_BP_m4	GO:00346	phosphatic	1/727	6/23843	0.169572	0.667261	0.657279	Gdpd3
GO_BP_m4	GO:004227	protection	1/727	6/23843	0.169572	0.667261	0.657279	Serpinb9

GO_BP_m4	GO:004439	actin cortic	1/727	6/23843	0.169572	0.667261	0.657279	Wipf2
GO_BP_m4	GO:004453	modulatior	1/727	6/23843	0.169572	0.667261	0.657279	Serpinb9
GO_BP_m4	GO:004453	modulatior	1/727	6/23843	0.169572	0.667261	0.657279	Serpinb9
GO_BP_m4	GO:004478	modulatior	1/727	6/23843	0.169572	0.667261	0.657279	Zfp72
GO_BP_m4	GO:004479	positive reg	1/727	6/23843	0.169572	0.667261	0.657279	Zfp72
GO_BP_m4	GO:004504	protein imp	1/727	6/23843	0.169572	0.667261	0.657279	Tomm7
GO_BP_m4	GO:004558	positive reg	1/727	6/23843	0.169572	0.667261	0.657279	Lck
GO_BP_m4	GO:004562	negative re	1/727	6/23843	0.169572	0.667261	0.657279	Socs5
GO_BP_m4	GO:004565	negative re	1/727	6/23843	0.169572	0.667261	0.657279	Thoc5
GO_BP_m4	GO:004607	dGTP meta	1/727	6/23843	0.169572	0.667261	0.657279	Dguok
GO_BP_m4	GO:004611	xanthine m	1/727	6/23843	0.169572	0.667261	0.657279	Aox3
GO_BP_m4	GO:004611	queuosine	1/727	6/23843	0.169572	0.667261	0.657279	Pdcl3
GO_BP_m4	GO:004648	glyoxylate	1/727	6/23843	0.169572	0.667261	0.657279	Grhpr
GO_BP_m4	GO:004649	isopenteny	1/727	6/23843	0.169572	0.667261	0.657279	Pmvk
GO_BP_m4	GO:004664	positive reg	1/727	6/23843	0.169572	0.667261	0.657279	Lck
GO_BP_m4	GO:004665	folic acid m	1/727	6/23843	0.169572	0.667261	0.657279	Folr1
GO_BP_m4	GO:004683	positive reg	1/727	6/23843	0.169572	0.667261	0.657279	Rbm26
GO_BP_m4	GO:004868	sprouting o	1/727	6/23843	0.169572	0.667261	0.657279	Rtn4
GO_BP_m4	GO:004885	diencephal	1/727	6/23843	0.169572	0.667261	0.657279	Duox2
GO_BP_m4	GO:004886	stem cell fa	1/727	6/23843	0.169572	0.667261	0.657279	Sox17
GO_BP_m4	GO:005091	sensory pe	1/727	6/23843	0.169572	0.667261	0.657279	Gnat1
GO_BP_m4	GO:005204	modulatior	1/727	6/23843	0.169572	0.667261	0.657279	Serpinb9
GO_BP_m4	GO:005224	modulatior	1/727	6/23843	0.169572	0.667261	0.657279	Serpinb9
GO_BP_m4	GO:005243	modulatior	1/727	6/23843	0.169572	0.667261	0.657279	Serpinb9
GO_BP_m4	GO:006007	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Kcnk6
GO_BP_m4	GO:006026	negative re	1/727	6/23843	0.169572	0.667261	0.657279	Dusp10
GO_BP_m4	GO:006031	primitive er	1/727	6/23843	0.169572	0.667261	0.657279	Gata1
GO_BP_m4	GO:006043	lung growt	1/727	6/23843	0.169572	0.667261	0.657279	Spry2
GO_BP_m4	GO:006074	mammary	1/727	6/23843	0.169572	0.667261	0.657279	Vdr
GO_BP_m4	GO:007094	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Dnase1
GO_BP_m4	GO:007122	cellular res	1/727	6/23843	0.169572	0.667261	0.657279	Rela
GO_BP_m4	GO:007131	cellular res	1/727	6/23843	0.169572	0.667261	0.657279	Slc8a1
GO_BP_m4	GO:007150	cellular res	1/727	6/23843	0.169572	0.667261	0.657279	Ddit3
GO_BP_m4	GO:007183	triglyceride	1/727	6/23843	0.169572	0.667261	0.657279	Lipc
GO_BP_m4	GO:007229	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Ret
GO_BP_m4	GO:008607	bundle of H	1/727	6/23843	0.169572	0.667261	0.657279	Dsp
GO_BP_m4	GO:009015	endoplasm	1/727	6/23843	0.169572	0.667261	0.657279	Rtn4
GO_BP_m4	GO:009031	negative re	1/727	6/23843	0.169572	0.667261	0.657279	Kcne1
GO_BP_m4	GO:009050	endocardia	1/727	6/23843	0.169572	0.667261	0.657279	Efna1
GO_BP_m4	GO:009752	necroptotic	1/727	6/23843	0.169572	0.667261	0.657279	Ripk1
GO_BP_m4	GO:009888	exocytic ins	1/727	6/23843	0.169572	0.667261	0.657279	Snap47
GO_BP_m4	GO:009896	exocytic ins	1/727	6/23843	0.169572	0.667261	0.657279	Snap47
GO_BP_m4	GO:012000	intermemb	1/727	6/23843	0.169572	0.667261	0.657279	Plekha8
GO_BP_m4	GO:190156	response to	1/727	6/23843	0.169572	0.667261	0.657279	Recql5
GO_BP_m4	GO:190222	erythrose 4	1/727	6/23843	0.169572	0.667261	0.657279	Fah
GO_BP_m4	GO:190296	positive reg	1/727	6/23843	0.169572	0.667261	0.657279	Efna1
GO_BP_m4	GO:190458	response to	1/727	6/23843	0.169572	0.667261	0.657279	Tshr
GO_BP_m4	GO:190520	positive reg	1/727	6/23843	0.169572	0.667261	0.657279	Ripk1

GO_BP_m4	GO:190524	positive re	1/727	6/23843	0.169572	0.667261	0.657279	Efna1
GO_BP_m4	GO:19901	stress resp	1/727	6/23843	0.169572	0.667261	0.657279	Mt1
GO_BP_m4	GO:199041	replication	1/727	6/23843	0.169572	0.667261	0.657279	Recql5
GO_BP_m4	GO:200001	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Ddit3
GO_BP_m4	GO:200034	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Fanca
GO_BP_m4	GO:20004	positive re	1/727	6/23843	0.169572	0.667261	0.657279	Rps6ka1
GO_BP_m4	GO:20005	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Dynll2
GO_BP_m4	GO:20005	positive re	1/727	6/23843	0.169572	0.667261	0.657279	Dynll2
GO_BP_m4	GO:20006	positive re	1/727	6/23843	0.169572	0.667261	0.657279	Rela
GO_BP_m4	GO:200067	positive re	1/727	6/23843	0.169572	0.667261	0.657279	Ager
GO_BP_m4	GO:20011	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Mapk14
GO_BP_m4	GO:20011	regulation	1/727	6/23843	0.169572	0.667261	0.657279	Ager
GO_BP_m4	GO:00066	steroid bio	7/727	149/23843	0.170953	0.671721	0.661672	Akr1d1/Ap
GO_BP_m4	GO:001974	secondary	4/727	71/23843	0.170986	0.671721	0.661672	Cdh3/Cyp1
GO_BP_m4	GO:007121	cellular res	12/727	288/23843	0.171865	0.673228	0.663156	AY761184/
GO_BP_m4	GO:004224	tissue rege	3/727	47/23843	0.172214	0.673228	0.663156	Dusp10/Lg
GO_BP_m4	GO:00435	regulation	3/727	47/23843	0.172214	0.673228	0.663156	Pik3ip1/Rb
GO_BP_m4	GO:004801	inositol ph	3/727	47/23843	0.172214	0.673228	0.663156	Htr2c/Mir1
GO_BP_m4	GO:00519	regulation	3/727	47/23843	0.172214	0.673228	0.663156	Grm1/Htr2
GO_BP_m4	GO:00519	regulation	3/727	47/23843	0.172214	0.673228	0.663156	Grm1/Htr2
GO_BP_m4	GO:00062	DNA replic	11/727	260/23843	0.172724	0.674667	0.664574	Cenps/Gm
GO_BP_m4	GO:00027	regulation	6/727	123/23843	0.17385	0.678512	0.668361	Car2/Il34/
GO_BP_m4	GO:00347	negative re	5/727	97/23843	0.1746	0.680326	0.670148	Cbarp/Irs2
GO_BP_m4	GO:20012	negative re	5/727	97/23843	0.1746	0.680326	0.670148	Ctnna1/Ga
GO_BP_m4	GO:00003	response t	2/727	25/23843	0.17631	0.681987	0.671784	Apoa4/Mp
GO_BP_m4	GO:00028	regulation	2/727	25/23843	0.17631	0.681987	0.671784	Il27/Socs5
GO_BP_m4	GO:00421	positive re	2/727	25/23843	0.17631	0.681987	0.671784	Ager/Rps3
GO_BP_m4	GO:00457	respiratory	2/727	25/23843	0.17631	0.681987	0.671784	Dusp10/M
GO_BP_m4	GO:006004	positive re	2/727	25/23843	0.17631	0.681987	0.671784	Mapk14/Pi
GO_BP_m4	GO:00610	negative re	2/727	25/23843	0.17631	0.681987	0.671784	Fam72a/Sc
GO_BP_m4	GO:00860	ventricular	2/727	25/23843	0.17631	0.681987	0.671784	Dsp/Nedd
GO_BP_m4	GO:190331	positive re	2/727	25/23843	0.17631	0.681987	0.671784	Astl/F12
GO_BP_m4	GO:19038	regulation	2/727	25/23843	0.17631	0.681987	0.671784	Nedd4l/Rtr
GO_BP_m4	GO:00356	cellular res	14/727	347/23843	0.176681	0.682464	0.672254	Ctnna1/Dp
GO_BP_m4	GO:00020	lens develo	4/727	72/23843	0.177004	0.682464	0.672254	Bfsp2/Lim2
GO_BP_m4	GO:00308	regulation	4/727	72/23843	0.177004	0.682464	0.672254	Cap2/Gng
GO_BP_m4	GO:00518	modificatio	4/727	72/23843	0.177004	0.682464	0.672254	Mbl1/Mbl2
GO_BP_m4	GO:00975	calcium io	6/727	124/23843	0.178348	0.683305	0.673083	Ddit3/Htr2
GO_BP_m4	GO:00526	cyclic puri	5/727	98/23843	0.179729	0.683305	0.673083	Cap2/Gng
GO_BP_m4	GO:00071	reciprocal	3/727	48/23843	0.179824	0.683305	0.673083	Cenps/Brip
GO_BP_m4	GO:003582	homologou	3/727	48/23843	0.179824	0.683305	0.673083	Cenps/Brip
GO_BP_m4	GO:00465	glycerolipi	3/727	48/23843	0.179824	0.683305	0.673083	Apoa4/Gd
GO_BP_m4	GO:00986	inorganic c	3/727	48/23843	0.179824	0.683305	0.673083	Slc39a8/Sl
GO_BP_m4	GO:00995	inorganic i	3/727	48/23843	0.179824	0.683305	0.673083	Slc39a8/Sl
GO_BP_m4	GO:20003	regulation	3/727	48/23843	0.179824	0.683305	0.673083	Ager/Gas6
GO_BP_m4	GO:00217	developme	12/727	291/23843	0.180457	0.683305	0.673083	Anapc2/Au
GO_BP_m4	GO:00971	intrinsic ap	12/727	291/23843	0.180457	0.683305	0.673083	Ddit3/Ern2
GO_BP_m4	GO:000007	cell cycle c	8/727	179/23843	0.181681	0.683305	0.673083	Aurka/Hus

GO_BP_m4	GO:005077	regulation	8/727	179/23843	0.181681	0.683305	0.673083	Anapc2/Ar
GO_BP_m4	GO:005126	protein hor	14/727	349/23843	0.181943	0.683305	0.673083	Ak3/Atxn1
GO_BP_m4	GO:005254	regulation	14/727	349/23843	0.181943	0.683305	0.673083	Anp32b/Bc
GO_BP_m4	GO:003476	negative re	6/727	125/23843	0.182892	0.683305	0.673083	Cbarp/Irs2/
GO_BP_m4	GO:000191	regulation	4/727	73/23843	0.183092	0.683305	0.673083	Ager/Dnas
GO_BP_m4	GO:003081	regulation	4/727	73/23843	0.183092	0.683305	0.673083	Cap2/Gng
GO_BP_m4	GO:000919	cyclic nucle	5/727	99/23843	0.184915	0.683305	0.673083	Cap2/Gng
GO_BP_m4	GO:004828	organelle f	8/727	180/23843	0.185454	0.683305	0.673083	Chchd6/Ru
GO_BP_m4	GO:005073	positive reg	8/727	180/23843	0.185454	0.683305	0.673083	Cspg4/Efna
GO_BP_m4	GO:005065	nucleic acid	7/727	153/23843	0.187259	0.683305	0.673083	Parp11/Rb
GO_BP_m4	GO:005065	RNA transp	7/727	153/23843	0.187259	0.683305	0.673083	Parp11/Rb
GO_BP_m4	GO:009017	organelle r	7/727	153/23843	0.187259	0.683305	0.673083	Rundc1/Se
GO_BP_m4	GO:000688	cellular zin	2/727	26/23843	0.187367	0.683305	0.673083	Mt1/Slc39a
GO_BP_m4	GO:000929	mRNA tran	2/727	26/23843	0.187367	0.683305	0.673083	Ddit3/Sox1
GO_BP_m4	GO:003026	apoptotic r	2/727	26/23843	0.187367	0.683305	0.673083	Dnase2b/E
GO_BP_m4	GO:003031	melanocyte	2/727	26/23843	0.187367	0.683305	0.673083	Mreg/Zeb2
GO_BP_m4	GO:003323	regulation	2/727	26/23843	0.187367	0.683305	0.673083	Rela/Ube2i
GO_BP_m4	GO:004000	establishm	2/727	26/23843	0.187367	0.683305	0.673083	Spdl1/Spry
GO_BP_m4	GO:004309	amino acid	2/727	26/23843	0.187367	0.683305	0.673083	Slc1a5/Slc1
GO_BP_m4	GO:004595	positive reg	2/727	26/23843	0.187367	0.683305	0.673083	Cacna1g/C
GO_BP_m4	GO:006091	heart forma	2/727	26/23843	0.187367	0.683305	0.673083	Folr1/Pim1
GO_BP_m4	GO:190299	regulation	2/727	26/23843	0.187367	0.683305	0.673083	Efna1/Tme
GO_BP_m4	GO:000602	aminoglyca	3/727	49/23843	0.187522	0.683305	0.673083	B3gnt5/Pxy
GO_BP_m4	GO:000690	vesicle bud	3/727	49/23843	0.187522	0.683305	0.673083	Rilp/Sec13/
GO_BP_m4	GO:004329	apical junct	3/727	49/23843	0.187522	0.683305	0.673083	Ctnna1/Ne
GO_BP_m4	GO:200064	regulation	3/727	49/23843	0.187522	0.683305	0.673083	Cnksr3/Fxy
GO_BP_m4	GO:004657	regulation	10/727	237/23843	0.189223	0.683305	0.673083	Agap3/Agf
GO_BP_m4	GO:000257	myeloid leu	9/727	209/23843	0.189747	0.683305	0.673083	Car2/Gata1
GO_BP_m4	GO:009030	nucleic acid	6/727	127/23843	0.192116	0.683305	0.673083	Dnase1/Dr
GO_BP_m4	GO:004858	developme	10/727	238/23843	0.192553	0.683305	0.673083	Anapc2/Au
GO_BP_m4	GO:000688	exocytosis	13/727	324/23843	0.192698	0.683305	0.673083	Cacna1g/C
GO_BP_m4	GO:004563	regulation	9/727	210/23843	0.19331	0.683305	0.673083	Car2/Gata1
GO_BP_m4	GO:190161	organic hy	9/727	210/23843	0.19331	0.683305	0.673083	Akr1d1/Ap
GO_BP_m4	GO:004306	extracellula	11/727	267/23843	0.194285	0.683305	0.673083	Apoa4/Eln/
GO_BP_m4	GO:000045	exonucleol	1/727	7/23843	0.194899	0.683305	0.673083	Eri2
GO_BP_m4	GO:000046	exonucleol	1/727	7/23843	0.194899	0.683305	0.673083	Eri2
GO_BP_m4	GO:000195	blood vess	1/727	7/23843	0.194899	0.683305	0.673083	Ddit3
GO_BP_m4	GO:000325	cardiac neu	1/727	7/23843	0.194899	0.683305	0.673083	Folr1
GO_BP_m4	GO:000330	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Sox17
GO_BP_m4	GO:000334	cardiac end	1/727	7/23843	0.194899	0.683305	0.673083	Sox17
GO_BP_m4	GO:000614	purine nuc	1/727	7/23843	0.194899	0.683305	0.673083	Aox3
GO_BP_m4	GO:000629	pyrimidine	1/727	7/23843	0.194899	0.683305	0.673083	Polb
GO_BP_m4	GO:000656	tryptophan	1/727	7/23843	0.194899	0.683305	0.673083	Kynu
GO_BP_m4	GO:000969	phenylprop	1/727	7/23843	0.194899	0.683305	0.673083	Cyp2a22
GO_BP_m4	GO:000980	coumarin r	1/727	7/23843	0.194899	0.683305	0.673083	Cyp2a22
GO_BP_m4	GO:001051	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Htr2c
GO_BP_m4	GO:001089	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Apoc4
GO_BP_m4	GO:001405	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Htr2c

GO_BP_m4	GO:001605	rhodopsin	1/727	7/23843	0.194899	0.683305	0.673083	Gnat1
GO_BP_m4	GO:001944	tryptophan	1/727	7/23843	0.194899	0.683305	0.673083	Kynu
GO_BP_m4	GO:003207	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Rps3
GO_BP_m4	GO:003224	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Rbm26
GO_BP_m4	GO:003331	meiotic cel	1/727	7/23843	0.194899	0.683305	0.673083	Hus1
GO_BP_m4	GO:003386	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Il13
GO_BP_m4	GO:003562	ceramide t	1/727	7/23843	0.194899	0.683305	0.673083	Plekha8
GO_BP_m4	GO:003570	hematopoi	1/727	7/23843	0.194899	0.683305	0.673083	Gas6
GO_BP_m4	GO:003575	B cell chem	1/727	7/23843	0.194899	0.683305	0.673083	Gas6
GO_BP_m4	GO:003576	cell chemo	1/727	7/23843	0.194899	0.683305	0.673083	Fgf4
GO_BP_m4	GO:003576	endothelial	1/727	7/23843	0.194899	0.683305	0.673083	Fgf4
GO_BP_m4	GO:003628	peptidyl-se	1/727	7/23843	0.194899	0.683305	0.673083	Ripk1
GO_BP_m4	GO:003649	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Ppp1r15b
GO_BP_m4	GO:003649	eiF2alpha p	1/727	7/23843	0.194899	0.683305	0.673083	Ppp1r15b
GO_BP_m4	GO:004243	indole-con	1/727	7/23843	0.194899	0.683305	0.673083	Kynu
GO_BP_m4	GO:004266	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Sox17
GO_BP_m4	GO:004276	DNA dama	1/727	7/23843	0.194899	0.683305	0.673083	Rps3
GO_BP_m4	GO:004310	amino acid	1/727	7/23843	0.194899	0.683305	0.673083	Bhmt
GO_BP_m4	GO:004465	adhesion o	1/727	7/23843	0.194899	0.683305	0.673083	Gas6
GO_BP_m4	GO:004563	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Zeb2
GO_BP_m4	GO:004621	indolalkylai	1/727	7/23843	0.194899	0.683305	0.673083	Kynu
GO_BP_m4	GO:004678	viral mRNA	1/727	7/23843	0.194899	0.683305	0.673083	Thoc5
GO_BP_m4	GO:004817	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Neurl1a
GO_BP_m4	GO:005094	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Zeb2
GO_BP_m4	GO:005169	pointed-er	1/727	7/23843	0.194899	0.683305	0.673083	Tmod2
GO_BP_m4	GO:005197	negative re	1/727	7/23843	0.194899	0.683305	0.673083	Hcrt
GO_BP_m4	GO:006001	Sertoli cell	1/727	7/23843	0.194899	0.683305	0.673083	Esr2
GO_BP_m4	GO:006031	definitive e	1/727	7/23843	0.194899	0.683305	0.673083	Gata1
GO_BP_m4	GO:006044	bud elonga	1/727	7/23843	0.194899	0.683305	0.673083	Spry2
GO_BP_m4	GO:006046	negative re	1/727	7/23843	0.194899	0.683305	0.673083	Astl
GO_BP_m4	GO:006055	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Vdr
GO_BP_m4	GO:006152	acetylcholi	1/727	7/23843	0.194899	0.683305	0.673083	Htr2c
GO_BP_m4	GO:007126	L-methioni	1/727	7/23843	0.194899	0.683305	0.673083	Bhmt
GO_BP_m4	GO:007141	cellular res	1/727	7/23843	0.194899	0.683305	0.673083	Slc8a1
GO_BP_m4	GO:007163	negative re	1/727	7/23843	0.194899	0.683305	0.673083	Socs5
GO_BP_m4	GO:007212	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	C3ar1
GO_BP_m4	GO:007231	clathrin coa	1/727	7/23843	0.194899	0.683305	0.673083	Gak
GO_BP_m4	GO:008604	cardiac mu	1/727	7/23843	0.194899	0.683305	0.673083	Dsp
GO_BP_m4	GO:008606	cell commu	1/727	7/23843	0.194899	0.683305	0.673083	Slc8a1
GO_BP_m4	GO:009030	spindle ass	1/727	7/23843	0.194899	0.683305	0.673083	Aurka
GO_BP_m4	GO:009033	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Mapk14
GO_BP_m4	GO:009040	stress-indu	1/727	7/23843	0.194899	0.683305	0.673083	Mapk14
GO_BP_m4	GO:009064	modulation	1/727	7/23843	0.194899	0.683305	0.673083	Ager
GO_BP_m4	GO:009704	dendritic ce	1/727	7/23843	0.194899	0.683305	0.673083	Gas6
GO_BP_m4	GO:009728	keratinocyt	1/727	7/23843	0.194899	0.683305	0.673083	Zfp36l1
GO_BP_m4	GO:009770	connective	1/727	7/23843	0.194899	0.683305	0.673083	Ager
GO_BP_m4	GO:190001	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Ror2
GO_BP_m4	GO:190002	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Ror2

GO_BP_m4	GO:190185	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Pid1
GO_BP_m4	GO:190217	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Zfp36l1
GO_BP_m4	GO:190217	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Sfpq
GO_BP_m4	GO:190245	negative re	1/727	7/23843	0.194899	0.683305	0.673083	Zfp706
GO_BP_m4	GO:190302	negative re	1/727	7/23843	0.194899	0.683305	0.673083	Ddit3
GO_BP_m4	GO:190325	multi-ciliat	1/727	7/23843	0.194899	0.683305	0.673083	Cep152
GO_BP_m4	GO:190398	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Ager
GO_BP_m4	GO:190484	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Fgf4
GO_BP_m4	GO:190505	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Mapk14
GO_BP_m4	GO:190577	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Sox17
GO_BP_m4	GO:190590	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Sox17
GO_BP_m4	GO:200013	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Pim1
GO_BP_m4	GO:200051	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Gas6
GO_BP_m4	GO:200054	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Fgf4
GO_BP_m4	GO:200066	regulation	1/727	7/23843	0.194899	0.683305	0.673083	Gas6
GO_BP_m4	GO:200104	positive reg	1/727	7/23843	0.194899	0.683305	0.673083	Ripk1
GO_BP_m4	GO:000166	behavioral	3/727	50/23843	0.195304	0.683305	0.673083	Esr2/Gng7/
GO_BP_m4	GO:000602	aminoglyca	5/727	101/23843	0.195446	0.683305	0.673083	B3gnt5/Ctb
GO_BP_m4	GO:004562	positive reg	5/727	101/23843	0.195446	0.683305	0.673083	Btn2a2/Du
GO_BP_m4	GO:007265	protein loc	18/727	472/23843	0.196688	0.683305	0.673083	Ager/Arl5a
GO_BP_m4	GO:003596	response to	6/727	128/23843	0.196794	0.683305	0.673083	Atf6b/Ddit3
GO_BP_m4	GO:004215	lipoprotein	6/727	128/23843	0.196794	0.683305	0.673083	Abhd13/Ap
GO_BP_m4	GO:004559	regulation	6/727	128/23843	0.196794	0.683305	0.673083	Ddit3/Dusp
GO_BP_m4	GO:007122	cellular res	11/727	268/23843	0.19746	0.683305	0.673083	Abcb4/Ffar
GO_BP_m4	GO:000191	regulation	2/727	27/23843	0.198517	0.683305	0.673083	Ager/Muc4
GO_BP_m4	GO:000692	cellular cor	2/727	27/23843	0.198517	0.683305	0.673083	Dnase2b/E
GO_BP_m4	GO:000760	phototrans	2/727	27/23843	0.198517	0.683305	0.673083	Cabp4/Gna
GO_BP_m4	GO:000907	aromatic ar	2/727	27/23843	0.198517	0.683305	0.673083	Fah/Kynu
GO_BP_m4	GO:000939	2'-deoxyrib	2/727	27/23843	0.198517	0.683305	0.673083	Ak3/Dguok
GO_BP_m4	GO:001969	deoxyribos	2/727	27/23843	0.198517	0.683305	0.673083	Ak3/Dguok
GO_BP_m4	GO:003368	osteoblast	2/727	27/23843	0.198517	0.683305	0.673083	Gata1/Tnn
GO_BP_m4	GO:003420	amyloid-be	2/727	27/23843	0.198517	0.683305	0.673083	Efna1/Tme
GO_BP_m4	GO:003598	endoderma	2/727	27/23843	0.198517	0.683305	0.673083	Inhba/Sox1
GO_BP_m4	GO:003600	positive reg	2/727	27/23843	0.198517	0.683305	0.673083	Atf6b/Ddit3
GO_BP_m4	GO:004303	positive reg	2/727	27/23843	0.198517	0.683305	0.673083	Ager/Il13
GO_BP_m4	GO:004478	modulation	2/727	27/23843	0.198517	0.683305	0.673083	Ythdc2/Zfp
GO_BP_m4	GO:005506	zinc ion ho	2/727	27/23843	0.198517	0.683305	0.673083	Mt1/Slc39a
GO_BP_m4	GO:006034	trabecula fo	2/727	27/23843	0.198517	0.683305	0.673083	Fhl2/Ovol2
GO_BP_m4	GO:006071	labyrinthine	2/727	27/23843	0.198517	0.683305	0.673083	Grb2/Zfp36
GO_BP_m4	GO:007023	negative re	2/727	27/23843	0.198517	0.683305	0.673083	Efna1/Serp
GO_BP_m4	GO:009031	positive reg	2/727	27/23843	0.198517	0.683305	0.673083	Erbb2/Mtcl
GO_BP_m4	GO:190011	regulation	2/727	27/23843	0.198517	0.683305	0.673083	Bcl10/Rps3
GO_BP_m4	GO:004580	positive reg	7/727	156/23843	0.19989	0.686546	0.676275	Ager/Gas6/
GO_BP_m4	GO:005123	establishme	7/727	156/23843	0.19989	0.686546	0.676275	Parp11/Rbr
GO_BP_m4	GO:006040	cytosolic ca	7/727	156/23843	0.19989	0.686546	0.676275	Cacna1g/D
GO_BP_m4	GO:003253	regulation	15/727	385/23843	0.200226	0.687208	0.676927	Akt1s1/Ana
GO_BP_m4	GO:004343	response to	12/727	298/23843	0.201277	0.689785	0.679466	Car2/C1qtr
GO_BP_m4	GO:000165	eye develo	15/727	386/23843	0.202897	0.689785	0.679466	Bfsp2/Cabp

GO_BP_m4	GO:000999	response to	15/727	386/23843	0.202897	0.689785	0.679466	5330417C2
GO_BP_m4	GO:000220	behavioral	3/727	51/23843	0.203163	0.689785	0.679466	Esr2/Gng7/
GO_BP_m4	GO:000702	endoplasm	3/727	51/23843	0.203163	0.689785	0.679466	Gak/Lman1
GO_BP_m4	GO:000834	glial cell mi	3/727	51/23843	0.203163	0.689785	0.679466	Cspg4/Rtn4
GO_BP_m4	GO:003265	regulation	3/727	51/23843	0.203163	0.689785	0.679466	Ager/Mapk
GO_BP_m4	GO:004560	regulation	3/727	51/23843	0.203163	0.689785	0.679466	Ovol2/Vdr/
GO_BP_m4	GO:008600	cardiac mu	3/727	51/23843	0.203163	0.689785	0.679466	Cacna1g/D
GO_BP_m4	GO:200051	regulation	3/727	51/23843	0.203163	0.689785	0.679466	Ager/Il27/S
GO_BP_m4	GO:000661	protein tar	5/727	103/23843	0.20618	0.689785	0.679466	Erbb2/Folr1
GO_BP_m4	GO:003241	negative re	4/727	77/23843	0.208096	0.689785	0.679466	Cbarp/Kcn
GO_BP_m4	GO:005170	interaction	4/727	77/23843	0.208096	0.689785	0.679466	Mbl1/Mbl2
GO_BP_m4	GO:003582	modificatio	7/727	158/23843	0.208489	0.689785	0.679466	AY761184/
GO_BP_m4	GO:003166	response to	14/727	359/23843	0.209359	0.689785	0.679466	5330417C2
GO_BP_m4	GO:007190	regulation	16/727	418/23843	0.209598	0.689785	0.679466	Ager/Cspg
GO_BP_m4	GO:000030	response to	2/727	28/23843	0.209744	0.689785	0.679466	Apoa4/Mp
GO_BP_m4	GO:000717	regulation	2/727	28/23843	0.209744	0.689785	0.679466	Neurl1a/Sc
GO_BP_m4	GO:001075	regulation	2/727	28/23843	0.209744	0.689785	0.679466	C3ar1/Map
GO_BP_m4	GO:003319	response to	2/727	28/23843	0.209744	0.689785	0.679466	Sell/Slc8a1
GO_BP_m4	GO:003516	embryonic	2/727	28/23843	0.209744	0.689785	0.679466	Gata1/Tho
GO_BP_m4	GO:004574	positive reg	2/727	28/23843	0.209744	0.689785	0.679466	Esr2/Neurl1
GO_BP_m4	GO:004882	hair follicle	2/727	28/23843	0.209744	0.689785	0.679466	Cdh3/Mreg
GO_BP_m4	GO:006021	hematopoi	2/727	28/23843	0.209744	0.689785	0.679466	Mir155/Mir
GO_BP_m4	GO:190217	regulation	2/727	28/23843	0.209744	0.689785	0.679466	Nme5/Sfp
GO_BP_m4	GO:199074	cellular det	2/727	28/23843	0.209744	0.689785	0.679466	Apoa4/Mp
GO_BP_m4	GO:007162	regulation	3/727	52/23843	0.211094	0.689785	0.679466	C3ar1/Map
GO_BP_m4	GO:007252	pyrimidine-	3/727	52/23843	0.211094	0.689785	0.679466	Ak3/Nme5/
GO_BP_m4	GO:007257	endothelial	3/727	52/23843	0.211094	0.689785	0.679466	Ager/Gas6/
GO_BP_m4	GO:004390	regulation	9/727	215/23843	0.211544	0.689785	0.679466	A230050P2
GO_BP_m4	GO:003000	cellular mo	5/727	104/23843	0.211618	0.689785	0.679466	Atp1b4/Ca
GO_BP_m4	GO:005129	protein het	7/727	159/23843	0.212841	0.689785	0.679466	Bcl10/Ctnn
GO_BP_m4	GO:006004	retina deve	7/727	159/23843	0.212841	0.689785	0.679466	Cabp4/Gna
GO_BP_m4	GO:190165	response to	7/727	159/23843	0.212841	0.689785	0.679466	Abcb4/Cac
GO_BP_m4	GO:005134	negative re	11/727	273/23843	0.213674	0.689785	0.679466	Akt1s1/Dus
GO_BP_m4	GO:000663	acyl-CoA m	4/727	78/23843	0.214495	0.689785	0.679466	Kynu/Nudt
GO_BP_m4	GO:001403	neural cres	4/727	78/23843	0.214495	0.689785	0.679466	Folr1/Ovol2
GO_BP_m4	GO:003538	thioester m	4/727	78/23843	0.214495	0.689785	0.679466	Kynu/Nudt
GO_BP_m4	GO:001593	nucleobase	8/727	188/23843	0.21679	0.689785	0.679466	Parp11/Rb
GO_BP_m4	GO:004273	exogenous	3/727	53/23843	0.219091	0.689785	0.679466	Cyp1a2/Cy
GO_BP_m4	GO:006138	trabecula m	3/727	53/23843	0.219091	0.689785	0.679466	Fhl2/Nfatc1
GO_BP_m4	GO:190101	regulation	3/727	53/23843	0.219091	0.689785	0.679466	Ager/Kcne1
GO_BP_m4	GO:000182	inner cell m	1/727	8/23843	0.219454	0.689785	0.679466	Sox17
GO_BP_m4	GO:000224	wound hea	1/727	8/23843	0.219454	0.689785	0.679466	Ager
GO_BP_m4	GO:000634	chromatin	1/727	8/23843	0.219454	0.689785	0.679466	Dydc1
GO_BP_m4	GO:000636	transcriptio	1/727	8/23843	0.219454	0.689785	0.679466	Polr1e
GO_BP_m4	GO:000714	female mei	1/727	8/23843	0.219454	0.689785	0.679466	Aurka
GO_BP_m4	GO:000740	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Ctnna1
GO_BP_m4	GO:000913	nucleoside	1/727	8/23843	0.219454	0.689785	0.679466	Ak3
GO_BP_m4	GO:000919	ribonucleos	1/727	8/23843	0.219454	0.689785	0.679466	Nudt5

GO_BP_m4	GO:000931	oligosacch	1/727	8/23843	0.219454	0.689785	0.679466	Ctbs
GO_BP_m4	GO:000999	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Sox17
GO_BP_m4	GO:001045	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Nkx6-2
GO_BP_m4	GO:001060	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Cnot6
GO_BP_m4	GO:001079	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Thoc5
GO_BP_m4	GO:001088	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Slc8a1
GO_BP_m4	GO:001094	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Ovol2
GO_BP_m4	GO:001587	acetylcholi	1/727	8/23843	0.219454	0.689785	0.679466	Htr2c
GO_BP_m4	GO:001591	plasma me	1/727	8/23843	0.219454	0.689785	0.679466	Irs2
GO_BP_m4	GO:001658	nucleosom	1/727	8/23843	0.219454	0.689785	0.679466	Smarca5
GO_BP_m4	GO:001980	peptide cro	1/727	8/23843	0.219454	0.689785	0.679466	Spock3
GO_BP_m4	GO:001991	peptidyl-ar	1/727	8/23843	0.219454	0.689785	0.679466	Prmt9
GO_BP_m4	GO:002154	corpus call	1/727	8/23843	0.219454	0.689785	0.679466	Zeb2
GO_BP_m4	GO:002303	CD40 signa	1/727	8/23843	0.219454	0.689785	0.679466	Fanca
GO_BP_m4	GO:003024	skeletal mu	1/727	8/23843	0.219454	0.689785	0.679466	Myom2
GO_BP_m4	GO:003030	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Apoa4
GO_BP_m4	GO:003108	nuclear-tra	1/727	8/23843	0.219454	0.689785	0.679466	Zfp36l1
GO_BP_m4	GO:003144	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Nelfe
GO_BP_m4	GO:003165	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Pim1
GO_BP_m4	GO:003290	transformir	1/727	8/23843	0.219454	0.689785	0.679466	Cdh3
GO_BP_m4	GO:003290	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Cdh3
GO_BP_m4	GO:003315	immunoglo	1/727	8/23843	0.219454	0.689785	0.679466	Polb
GO_BP_m4	GO:003649	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Ppp1r15b
GO_BP_m4	GO:003804	dimeric G-	1/727	8/23843	0.219454	0.689785	0.679466	Grm1
GO_BP_m4	GO:004263	catagen	1/727	8/23843	0.219454	0.689785	0.679466	Cdh3
GO_BP_m4	GO:004369	dedifferent	1/727	8/23843	0.219454	0.689785	0.679466	Fezf1
GO_BP_m4	GO:004369	cell dediffe	1/727	8/23843	0.219454	0.689785	0.679466	Fezf1
GO_BP_m4	GO:004438	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Dusp10
GO_BP_m4	GO:004441	translocatio	1/727	8/23843	0.219454	0.689785	0.679466	Thoc5
GO_BP_m4	GO:004482	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Ythdc2
GO_BP_m4	GO:004508	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Rela
GO_BP_m4	GO:004541	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Bcl10
GO_BP_m4	GO:004562	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Socs5
GO_BP_m4	GO:004606	dATP meta	1/727	8/23843	0.219454	0.689785	0.679466	Ak3
GO_BP_m4	GO:004688	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Inhba
GO_BP_m4	GO:004808	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Zeb2
GO_BP_m4	GO:005177	response to	1/727	8/23843	0.219454	0.689785	0.679466	Vasn
GO_BP_m4	GO:005183	translocatio	1/727	8/23843	0.219454	0.689785	0.679466	Thoc5
GO_BP_m4	GO:006004	retinal bipo	1/727	8/23843	0.219454	0.689785	0.679466	Cabp4
GO_BP_m4	GO:006036	cranial sutu	1/727	8/23843	0.219454	0.689785	0.679466	Fgf4
GO_BP_m4	GO:006037	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Cacna1g
GO_BP_m4	GO:006100	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Efna1
GO_BP_m4	GO:006162	pharyngea	1/727	8/23843	0.219454	0.689785	0.679466	Folr1
GO_BP_m4	GO:006168	detoxificati	1/727	8/23843	0.219454	0.689785	0.679466	Mt1
GO_BP_m4	GO:006173	mitochond	1/727	8/23843	0.219454	0.689785	0.679466	Pdhx
GO_BP_m4	GO:007012	tRNA amin	1/727	8/23843	0.219454	0.689785	0.679466	Ears2
GO_BP_m4	GO:007126	L-methioni	1/727	8/23843	0.219454	0.689785	0.679466	Bhmt
GO_BP_m4	GO:007149	cellular res	1/727	8/23843	0.219454	0.689785	0.679466	Mme

GO_BP_m4	GO:007157	zinc ion im	1/727	8/23843	0.219454	0.689785	0.679466	Slc39a8
GO_BP_m4	GO:007231	vesicle unc	1/727	8/23843	0.219454	0.689785	0.679466	Gak
GO_BP_m4	GO:007261	interleukin-	1/727	8/23843	0.219454	0.689785	0.679466	Mapk14
GO_BP_m4	GO:009016	Golgi to lys	1/727	8/23843	0.219454	0.689785	0.679466	Gak
GO_BP_m4	GO:009737	interneuro	1/727	8/23843	0.219454	0.689785	0.679466	Mir200c
GO_BP_m4	GO:009750	stress resp	1/727	8/23843	0.219454	0.689785	0.679466	Mt1
GO_BP_m4	GO:009870	neurotrans	1/727	8/23843	0.219454	0.689785	0.679466	Slc17a8
GO_BP_m4	GO:190004	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Trip12
GO_BP_m4	GO:190027	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Ager
GO_BP_m4	GO:190036	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Nelfe
GO_BP_m4	GO:190137	acetate est	1/727	8/23843	0.219454	0.689785	0.679466	Htr2c
GO_BP_m4	GO:190200	fatty acid t	1/727	8/23843	0.219454	0.689785	0.679466	Irs2
GO_BP_m4	GO:190241	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Eif3e
GO_BP_m4	GO:190295	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Efna1
GO_BP_m4	GO:190372	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Pik3ip1
GO_BP_m4	GO:190524	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Tiam1
GO_BP_m4	GO:190524	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Efna1
GO_BP_m4	GO:200017	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Rtn4
GO_BP_m4	GO:200019	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Irs2
GO_BP_m4	GO:200054	negative re	1/727	8/23843	0.219454	0.689785	0.679466	Sox17
GO_BP_m4	GO:200064	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Ptpn23
GO_BP_m4	GO:200113	regulation	1/727	8/23843	0.219454	0.689785	0.679466	Abcb4
GO_BP_m4	GO:200114	positive reg	1/727	8/23843	0.219454	0.689785	0.679466	Abcb4
GO_BP_m4	GO:001923	sensory pe	6/727	133/23843	0.22079	0.689785	0.679466	Cacna1b/G
GO_BP_m4	GO:006400	RNA localiz	8/727	189/23843	0.220842	0.689785	0.679466	Mthfsd/Par
GO_BP_m4	GO:007180	cellular pot	8/727	189/23843	0.220842	0.689785	0.679466	Ager/Atp1l
GO_BP_m4	GO:007180	potassium	8/727	189/23843	0.220842	0.689785	0.679466	Ager/Atp1l
GO_BP_m4	GO:004410	cellular am	4/727	79/23843	0.220948	0.689785	0.679466	Abhd4/Gd
GO_BP_m4	GO:190403	regulation	4/727	79/23843	0.220948	0.689785	0.679466	Ager/Gas6/
GO_BP_m4	GO:000177	microglial	2/727	29/23843	0.221031	0.689785	0.679466	Ager/Il13
GO_BP_m4	GO:008200	bile acid m	2/727	29/23843	0.221031	0.689785	0.679466	Akr1d1/Cy
GO_BP_m4	GO:003111	positive reg	2/727	29/23843	0.221031	0.689785	0.679466	Nav3/Rps3
GO_BP_m4	GO:003300	positive reg	2/727	29/23843	0.221031	0.689785	0.679466	Il13/Vamp8
GO_BP_m4	GO:004330	positive reg	2/727	29/23843	0.221031	0.689785	0.679466	Il13/Vamp8
GO_BP_m4	GO:005129	establishm	2/727	29/23843	0.221031	0.689785	0.679466	Spdl1/Spry
GO_BP_m4	GO:006030	regulation	2/727	29/23843	0.221031	0.689785	0.679466	Kcne1/Nec
GO_BP_m4	GO:006031	cardiac epi	2/727	29/23843	0.221031	0.689785	0.679466	Efna1/Rtn4
GO_BP_m4	GO:007030	lens fiber c	2/727	29/23843	0.221031	0.689785	0.679466	Bfsp2/Zeb2
GO_BP_m4	GO:009002	positive reg	2/727	29/23843	0.221031	0.689785	0.679466	C3ar1/Sell
GO_BP_m4	GO:009735	autophago	2/727	29/23843	0.221031	0.689785	0.679466	Stx17/Vam
GO_BP_m4	GO:190018	negative re	2/727	29/23843	0.221031	0.689785	0.679466	Dclk3/Gas6
GO_BP_m4	GO:006102	membrane	9/727	218/23843	0.222803	0.694862	0.684466	Chchd6/Ga
GO_BP_m4	GO:190136	organic cyc	18/727	483/23843	0.223629	0.696538	0.686118	Akr1d1/Ao
GO_BP_m4	GO:003010	regulation	10/727	247/23843	0.223632	0.696538	0.686118	Ager/Ehd4/
GO_BP_m4	GO:001401	regulation	6/727	134/23843	0.225703	0.699878	0.689408	Ager/Dusp
GO_BP_m4	GO:000916	nucleotide	12/727	306/23843	0.226302	0.699878	0.689408	Ak3/Atp5c1
GO_BP_m4	GO:003261	interleukin-	3/727	54/23843	0.227149	0.699878	0.689408	Ager/Mapk
GO_BP_m4	GO:004259	fear respon	3/727	54/23843	0.227149	0.699878	0.689408	Esr2/Gng7/

GO_BP_m4	GO:19039	positive re	3/727	54/23843	0.227149	0.699878	0.689408	Ppid/Ythdc
GO_BP_m4	GO:00350	embryonic	4/727	80/23843	0.227451	0.699878	0.689408	Folr1/Ovol
GO_BP_m4	GO:00007	DNA dama	5/727	107/23843	0.2282	0.699878	0.689408	Hus1/Mapl
GO_BP_m4	GO:000641	translation	5/727	107/23843	0.2282	0.699878	0.689408	Eif3a/Eif3e/
GO_BP_m4	GO:001907	viral genon	5/727	107/23843	0.2282	0.699878	0.689408	A230050P
GO_BP_m4	GO:00190	viral life cy	8/727	191/23843	0.229029	0.699878	0.689408	A230050P
GO_BP_m4	GO:20012	regulation	15/727	396/23843	0.230483	0.699878	0.689408	Bcl10/Ctnn
GO_BP_m4	GO:00164	cytosolic tr	6/727	135/23843	0.230652	0.699878	0.689408	Bet1l/Gak/
GO_BP_m4	GO:00509	positive re	6/727	135/23843	0.230652	0.699878	0.689408	Ager/C3ar
GO_BP_m4	GO:00720	stem cell p	6/727	135/23843	0.230652	0.699878	0.689408	Ctnna1/Nf
GO_BP_m4	GO:19040	positive re	6/727	135/23843	0.230652	0.699878	0.689408	Ager/Arc/
GO_BP_m4	GO:00345	cellular res	10/727	249/23843	0.230794	0.699878	0.689408	Agap3/Apo
GO_BP_m4	GO:00290	regulation	2/727	30/23843	0.232366	0.699878	0.689408	Bcl10/Irs2
GO_BP_m4	GO:000622	pyrimidine	2/727	30/23843	0.232366	0.699878	0.689408	Ak3/Nme5
GO_BP_m4	GO:00140	astrocyte d	2/727	30/23843	0.232366	0.699878	0.689408	Ager/Ror2
GO_BP_m4	GO:00460	GTP metab	2/727	30/23843	0.232366	0.699878	0.689408	Ak3/Nme5
GO_BP_m4	GO:004801	neurotroph	2/727	30/23843	0.232366	0.699878	0.689408	Akt1s1/Spr
GO_BP_m4	GO:004867	regulation	2/727	30/23843	0.232366	0.699878	0.689408	Rtn4/Rtn4r
GO_BP_m4	GO:005507	potassium	2/727	30/23843	0.232366	0.699878	0.689408	Atp1b4/Kc
GO_BP_m4	GO:00605	apoptotic	2/727	30/23843	0.232366	0.699878	0.689408	Fgf4/Vdr
GO_BP_m4	GO:190007	positive re	2/727	30/23843	0.232366	0.699878	0.689408	C1qtnf12/
GO_BP_m4	GO:190552	regulation	2/727	30/23843	0.232366	0.699878	0.689408	C3ar1/Map
GO_BP_m4	GO:00069	response t	5/727	108/23843	0.23381	0.699878	0.689408	Atf6b/Ddit
GO_BP_m4	GO:003011	regulation	11/727	279/23843	0.23383	0.699878	0.689408	Ddit3/Folr1
GO_BP_m4	GO:19040	negative re	4/727	81/23843	0.234002	0.699878	0.689408	Cbarp/Kcn
GO_BP_m4	GO:00064	negative re	9/727	221/23843	0.234285	0.699878	0.689408	Akt1s1/Du
GO_BP_m4	GO:00350	cardiocyte	7/727	164/23843	0.235078	0.699878	0.689408	Fhl2/Folr1/
GO_BP_m4	GO:00062	nucleotide-	3/727	55/23843	0.235263	0.699878	0.689408	Hus1/Polk/
GO_BP_m4	GO:00426	ovulation c	3/727	55/23843	0.235263	0.699878	0.689408	Erbb2/Esr2
GO_BP_m4	GO:00436	regulation	3/727	55/23843	0.235263	0.699878	0.689408	Atf6b/Ddit
GO_BP_m4	GO:00860	cardiac mu	3/727	55/23843	0.235263	0.699878	0.689408	Cacna1g/D
GO_BP_m4	GO:00356	multicellul	6/727	136/23843	0.235634	0.699878	0.689408	Cacna1g/C
GO_BP_m4	GO:00181	peptidyl-ty	12/727	310/23843	0.239267	0.699878	0.689408	Cspg4/Efn
GO_BP_m4	GO:00001	activation	5/727	109/23843	0.239459	0.699878	0.689408	Cspg4/Ern
GO_BP_m4	GO:00069	smooth mu	5/727	109/23843	0.239459	0.699878	0.689408	Cacna1g/H
GO_BP_m4	GO:00099	dorsal/ven	5/727	109/23843	0.239459	0.699878	0.689408	Ddit3/Nkx
GO_BP_m4	GO:003812	ERBB signa	5/727	109/23843	0.239459	0.699878	0.689408	Esr2/Kif16
GO_BP_m4	GO:004407	regulation	5/727	109/23843	0.239459	0.699878	0.689408	Abcb4/Car
GO_BP_m4	GO:000941	response t	11/727	281/23843	0.240707	0.699878	0.689408	Agap3/Cab
GO_BP_m4	GO:00001	chromatin	1/727	9/23843	0.243262	0.699878	0.689408	Smarca5
GO_BP_m4	GO:000171	endoderm	1/727	9/23843	0.243262	0.699878	0.689408	Sox17
GO_BP_m4	GO:000184	neural fold	1/727	9/23843	0.243262	0.699878	0.689408	Ovol2
GO_BP_m4	GO:000274	positive re	1/727	9/23843	0.243262	0.699878	0.689408	Mapk14
GO_BP_m4	GO:000322	ventricular	1/727	9/23843	0.243262	0.699878	0.689408	Dsp
GO_BP_m4	GO:000622	UTP biosy	1/727	9/23843	0.243262	0.699878	0.689408	Nme5
GO_BP_m4	GO:00065	L-phenylal	1/727	9/23843	0.243262	0.699878	0.689408	Fah
GO_BP_m4	GO:00069	response t	1/727	9/23843	0.243262	0.699878	0.689408	Npc1l1
GO_BP_m4	GO:000721	serotonin r	1/727	9/23843	0.243262	0.699878	0.689408	Htr2c

GO_BP_m4	GO:000734	egg activat	1/727	9/23843	0.243262	0.699878	0.689408	Astl
GO_BP_m4	GO:000834	adult feedi	1/727	9/23843	0.243262	0.699878	0.689408	Dmbx1
GO_BP_m4	GO:000913	nucleoside	1/727	9/23843	0.243262	0.699878	0.689408	Nudt5
GO_BP_m4	GO:001087	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Apoa4
GO_BP_m4	GO:001486	skeletal my	1/727	9/23843	0.243262	0.699878	0.689408	Myom2
GO_BP_m4	GO:001579	polyol tran	1/727	9/23843	0.243262	0.699878	0.689408	Aqp9
GO_BP_m4	GO:001582	proline tran	1/727	9/23843	0.243262	0.699878	0.689408	Slc1a4
GO_BP_m4	GO:001802	peptidyl-ly	1/727	9/23843	0.243262	0.699878	0.689408	Smyd2
GO_BP_m4	GO:002195	corticospin	1/727	9/23843	0.243262	0.699878	0.689408	Zeb2
GO_BP_m4	GO:003030	poly-N-ac	1/727	9/23843	0.243262	0.699878	0.689408	B3gnt5
GO_BP_m4	GO:003031	poly-N-ac	1/727	9/23843	0.243262	0.699878	0.689408	B3gnt5
GO_BP_m4	GO:003165	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Pim1
GO_BP_m4	GO:003200	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Irs2
GO_BP_m4	GO:003207	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Rps3
GO_BP_m4	GO:003232	alanine tran	1/727	9/23843	0.243262	0.699878	0.689408	Slc1a4
GO_BP_m4	GO:003290	transformin	1/727	9/23843	0.243262	0.699878	0.689408	Lum
GO_BP_m4	GO:003290	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Lum
GO_BP_m4	GO:003331	mitotic DN	1/727	9/23843	0.243262	0.699878	0.689408	Hus1
GO_BP_m4	GO:003360	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Rtn4
GO_BP_m4	GO:003368	nucleotide-	1/727	9/23843	0.243262	0.699878	0.689408	Xpa
GO_BP_m4	GO:003368	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Tnn
GO_BP_m4	GO:003435	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Gas6
GO_BP_m4	GO:003509	behavioral	1/727	9/23843	0.243262	0.699878	0.689408	Htr2c
GO_BP_m4	GO:004211	endothelial	1/727	9/23843	0.243262	0.699878	0.689408	Socs5
GO_BP_m4	GO:004236	vitamin D b	1/727	9/23843	0.243262	0.699878	0.689408	Vdr
GO_BP_m4	GO:004547	response to	1/727	9/23843	0.243262	0.699878	0.689408	Abcb4
GO_BP_m4	GO:004558	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Lck
GO_BP_m4	GO:004561	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Ovol2
GO_BP_m4	GO:004611	nucleobase	1/727	9/23843	0.243262	0.699878	0.689408	Aox3
GO_BP_m4	GO:004664	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Lck
GO_BP_m4	GO:004881	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Cdh3
GO_BP_m4	GO:005071	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Gas6
GO_BP_m4	GO:005093	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Zeb2
GO_BP_m4	GO:005102	chiasma as	1/727	9/23843	0.243262	0.699878	0.689408	Brip1
GO_BP_m4	GO:005140	response to	1/727	9/23843	0.243262	0.699878	0.689408	Ddit3
GO_BP_m4	GO:006055	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Vdr
GO_BP_m4	GO:006083	blood vess	1/727	9/23843	0.243262	0.699878	0.689408	Ccm2
GO_BP_m4	GO:006130	cornea dev	1/727	9/23843	0.243262	0.699878	0.689408	Kera
GO_BP_m4	GO:007018	kynurenine	1/727	9/23843	0.243262	0.699878	0.689408	Kynu
GO_BP_m4	GO:007047	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Lck
GO_BP_m4	GO:007098	oxidative d	1/727	9/23843	0.243262	0.699878	0.689408	Cyp1a2
GO_BP_m4	GO:007137	cellular res	1/727	9/23843	0.243262	0.699878	0.689408	Inhba
GO_BP_m4	GO:007150	cellular res	1/727	9/23843	0.243262	0.699878	0.689408	Npc1l1
GO_BP_m4	GO:008601	SA node ce	1/727	9/23843	0.243262	0.699878	0.689408	Cacna1g
GO_BP_m4	GO:008601	SA node ce	1/727	9/23843	0.243262	0.699878	0.689408	Cacna1g
GO_BP_m4	GO:008603	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Slc8a1
GO_BP_m4	GO:008607	SA node ce	1/727	9/23843	0.243262	0.699878	0.689408	Cacna1g
GO_BP_m4	GO:009706	cellular res	1/727	9/23843	0.243262	0.699878	0.689408	Gata1

GO_BP_m4	GO:009866	G-protein	1/727	9/23843	0.243262	0.699878	0.689408	Htr2c
GO_BP_m4	GO:009877	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Tomm7
GO_BP_m4	GO:009881	spontaneou	1/727	9/23843	0.243262	0.699878	0.689408	Ager
GO_BP_m4	GO:190010	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Atf6b
GO_BP_m4	GO:190016	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Gas6
GO_BP_m4	GO:190103	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Ripk1
GO_BP_m4	GO:190152	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Tomm7
GO_BP_m4	GO:190172	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	C3ar1
GO_BP_m4	GO:190203	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Pim1
GO_BP_m4	GO:190222	erythrose 4	1/727	9/23843	0.243262	0.699878	0.689408	Fah
GO_BP_m4	GO:190226	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Kcne1
GO_BP_m4	GO:190397	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Ager
GO_BP_m4	GO:190426	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Sec13
GO_BP_m4	GO:190433	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Tiam1
GO_BP_m4	GO:190472	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Apoa4
GO_BP_m4	GO:190521	positive reg	1/727	9/23843	0.243262	0.699878	0.689408	Eif3e
GO_BP_m4	GO:200019	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Thoc5
GO_BP_m4	GO:200027	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Gas6
GO_BP_m4	GO:200038	negative re	1/727	9/23843	0.243262	0.699878	0.689408	Sox17
GO_BP_m4	GO:200048	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Rps6ka1
GO_BP_m4	GO:200050	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Gas6
GO_BP_m4	GO:200122	regulation	1/727	9/23843	0.243262	0.699878	0.689408	Car2
GO_BP_m4	GO:000650	GPI anchor	2/727	31/23843	0.243735	0.699878	0.689408	Pigp/Pigv
GO_BP_m4	GO:003206	regulation	2/727	31/23843	0.243735	0.699878	0.689408	Oas2/Rps3
GO_BP_m4	GO:004433	cell-cell ad	2/727	31/23843	0.243735	0.699878	0.689408	Cdh24/Cdh
GO_BP_m4	GO:005118	vitamin tran	2/727	31/23843	0.243735	0.699878	0.689408	Folr1/Slc2a
GO_BP_m4	GO:007162	positive reg	2/727	31/23843	0.243735	0.699878	0.689408	C3ar1/Sell
GO_BP_m4	GO:190102	negative re	2/727	31/23843	0.243735	0.699878	0.689408	Cbarp/Rem
GO_BP_m4	GO:190547	negative re	2/727	31/23843	0.243735	0.699878	0.689408	Kcne1/Pid1
GO_BP_m4	GO:200035	negative re	2/727	31/23843	0.243735	0.699878	0.689408	Gas6/Il13
GO_BP_m4	GO:000740	axonogene	17/727	461/23843	0.244629	0.702025	0.691522	Anapc2/Efn
GO_BP_m4	GO:000858	female gon	5/727	110/23843	0.245145	0.70266	0.692148	Esr2/Fanca
GO_BP_m4	GO:009009	negative re	5/727	110/23843	0.245145	0.70266	0.692148	Ddit3/Map
GO_BP_m4	GO:001605	vesicle orga	12/727	312/23843	0.245855	0.704273	0.693737	Rilp/Rundc
GO_BP_m4	GO:001403	mesenchym	4/727	83/23843	0.247235	0.706957	0.696381	Folr1/Ovol
GO_BP_m4	GO:005501	cardiac mu	4/727	83/23843	0.247235	0.706957	0.696381	Fhl2/Myom
GO_BP_m4	GO:190007	regulation	4/727	83/23843	0.247235	0.706957	0.696381	C1qtnf12/
GO_BP_m4	GO:000639	tRNA meta	7/727	167/23843	0.248774	0.710799	0.700165	Dalrd3/Dus
GO_BP_m4	GO:000915	purine ribo	10/727	254/23843	0.249067	0.710799	0.700165	Ak3/Atp5c
GO_BP_m4	GO:001821	peptidyl-ty	12/727	313/23843	0.249174	0.710799	0.700165	Cspg4/Efna
GO_BP_m4	GO:190129	nucleoside	12/727	313/23843	0.249174	0.710799	0.700165	Ak3/Atp5c
GO_BP_m4	GO:006156	axon devel	18/727	493/23843	0.249449	0.71108	0.700441	Anapc2/Efn
GO_BP_m4	GO:001715	regulation	8/727	196/23843	0.249953	0.71108	0.700441	Cacna1g/C
GO_BP_m4	GO:004254	response to	5/727	111/23843	0.250865	0.71108	0.700441	Lck/Ppp1r1
GO_BP_m4	GO:003210	positive reg	11/727	284/23843	0.25116	0.71108	0.700441	Ager/C3ar
GO_BP_m4	GO:200013	negative re	3/727	57/23843	0.251634	0.71108	0.700441	Btn2a2/Pid
GO_BP_m4	GO:004239	regulation	16/727	434/23843	0.253319	0.71108	0.700441	Cacna1b/C
GO_BP_m4	GO:004886	stem cell d	4/727	84/23843	0.253913	0.71108	0.700441	Folr1/Ovol

GO_BP_m4	GO:00970	dendritic s	4/727	84/23843	0.253913	0.71108	0.700441	Arc/Efna1/
GO_BP_m4	GO:00003	spliceosom	2/727	32/23843	0.255125	0.71108	0.700441	Gemin5/Sn
GO_BP_m4	GO:00065	GPI anchor	2/727	32/23843	0.255125	0.71108	0.700441	Pigp/Pigv
GO_BP_m4	GO:00067	water-solu	2/727	32/23843	0.255125	0.71108	0.700441	Folr1/Kynu
GO_BP_m4	GO:00104	regulation	2/727	32/23843	0.255125	0.71108	0.700441	Nkx6-2/So
GO_BP_m4	GO:00215	ventricular	2/727	32/23843	0.255125	0.71108	0.700441	Anp32b/N
GO_BP_m4	GO:004507	positive re	2/727	32/23843	0.255125	0.71108	0.700441	Ppid/Ythdc
GO_BP_m4	GO:00486	collateral s	2/727	32/23843	0.255125	0.71108	0.700441	Rtn4/Zeb2
GO_BP_m4	GO:00606	embryonic	2/727	32/23843	0.255125	0.71108	0.700441	Grb2/Zfp3
GO_BP_m4	GO:190342	regulation	2/727	32/23843	0.255125	0.71108	0.700441	Aurka/Ret
GO_BP_m4	GO:00324	regulation	10/727	256/23843	0.256514	0.71108	0.700441	Ager/Arc/
GO_BP_m4	GO:00075	body fluid	5/727	112/23843	0.256619	0.71108	0.700441	Neurl1a/O
GO_BP_m4	GO:00461	alcohol bio	5/727	112/23843	0.256619	0.71108	0.700441	Apoa4/Cy
GO_BP_m4	GO:00458	positive re	16/727	436/23843	0.25902	0.71108	0.700441	Ager/Cspg
GO_BP_m4	GO:000194	heart loopi	3/727	58/23843	0.259881	0.71108	0.700441	Folr1/Ovol
GO_BP_m4	GO:00028	regulation	3/727	58/23843	0.259881	0.71108	0.700441	Dnase1/Il1
GO_BP_m4	GO:00063	DNA-temp	3/727	58/23843	0.259881	0.71108	0.700441	Nelfe/Recq
GO_BP_m4	GO:00424	photorece	3/727	58/23843	0.259881	0.71108	0.700441	Cabp4/Gn
GO_BP_m4	GO:004577	negative re	3/727	58/23843	0.259881	0.71108	0.700441	Ffar3/Kcnk
GO_BP_m4	GO:00600	cardiac mu	3/727	58/23843	0.259881	0.71108	0.700441	Mapk14/M
GO_BP_m4	GO:19023	regulation	3/727	58/23843	0.259881	0.71108	0.700441	Cnksr3/Fxy
GO_BP_m4	GO:00140	neural cres	4/727	85/23843	0.260627	0.71108	0.700441	Folr1/Ovol
GO_BP_m4	GO:004277	signal tran	4/727	85/23843	0.260627	0.71108	0.700441	Grb2/Map
GO_BP_m4	GO:004544	fat cell diff	9/727	228/23843	0.261862	0.71108	0.700441	Ddit3/Dus
GO_BP_m4	GO:00971	extrinsic a	9/727	228/23843	0.261862	0.71108	0.700441	Bcl10/Ctnn
GO_BP_m4	GO:00109	regulation	5/727	113/23843	0.262405	0.71108	0.700441	C1qtnf12/
GO_BP_m4	GO:004654	developme	5/727	113/23843	0.262405	0.71108	0.700441	Esr2/Fanca
GO_BP_m4	GO:00107	regulation	12/727	317/23843	0.262609	0.71108	0.700441	Anapc2/Ar
GO_BP_m4	GO:009874	cell-cell ad	7/727	170/23843	0.262707	0.71108	0.700441	Cadm2/Cd
GO_BP_m4	GO:001604	cell growth	18/727	499/23843	0.26549	0.71108	0.700441	Anapc2/Au
GO_BP_m4	GO:004801	phosphatic	6/727	142/23843	0.266177	0.71108	0.700441	Btn2a2/Erb
GO_BP_m4	GO:00011	response t	13/727	348/23843	0.266185	0.71108	0.700441	Abcb4/Ffar
GO_BP_m4	GO:00003	protein de	1/727	10/23843	0.266345	0.71108	0.700441	Cops2
GO_BP_m4	GO:000234	histamine	1/727	10/23843	0.266345	0.71108	0.700441	Vamp8
GO_BP_m4	GO:000244	histamine	1/727	10/23843	0.266345	0.71108	0.700441	Vamp8
GO_BP_m4	GO:00025	histamine	1/727	10/23843	0.266345	0.71108	0.700441	Vamp8
GO_BP_m4	GO:00029	desmosom	1/727	10/23843	0.266345	0.71108	0.700441	Dsp
GO_BP_m4	GO:00060	chitin meta	1/727	10/23843	0.266345	0.71108	0.700441	Ctbs
GO_BP_m4	GO:00060	chitin cata	1/727	10/23843	0.266345	0.71108	0.700441	Ctbs
GO_BP_m4	GO:000624	CTP biosyn	1/727	10/23843	0.266345	0.71108	0.700441	Nme5
GO_BP_m4	GO:000662	posttransla	1/727	10/23843	0.266345	0.71108	0.700441	Folr1
GO_BP_m4	GO:00071	neuron cell	1/727	10/23843	0.266345	0.71108	0.700441	Ret
GO_BP_m4	GO:000727	neuron-ne	1/727	10/23843	0.266345	0.71108	0.700441	Tmod2
GO_BP_m4	GO:00076	phototrans	1/727	10/23843	0.266345	0.71108	0.700441	Gnat1
GO_BP_m4	GO:00096	UV protect	1/727	10/23843	0.266345	0.71108	0.700441	Xpa
GO_BP_m4	GO:00104	histone H3	1/727	10/23843	0.266345	0.71108	0.700441	Smyd2
GO_BP_m4	GO:00108	positive re	1/727	10/23843	0.266345	0.71108	0.700441	Cdh3
GO_BP_m4	GO:00108	positive re	1/727	10/23843	0.266345	0.71108	0.700441	Apoa4

GO_BP_m4	GO:001406	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Lgals3
GO_BP_m4	GO:001482	artery smo	1/727	10/23843	0.266345	0.71108	0.700441	Cacna1g
GO_BP_m4	GO:001488	transition b	1/727	10/23843	0.266345	0.71108	0.700441	Nfatc1
GO_BP_m4	GO:001626	gap junctio	1/727	10/23843	0.266345	0.71108	0.700441	Ctnna1
GO_BP_m4	GO:002155	optic nerve	1/727	10/23843	0.266345	0.71108	0.700441	Rpl24
GO_BP_m4	GO:003207	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Rps3
GO_BP_m4	GO:003222	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Htr2c
GO_BP_m4	GO:003235	response to	1/727	10/23843	0.266345	0.71108	0.700441	Inhba
GO_BP_m4	GO:003308	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Erbb2
GO_BP_m4	GO:003308	negative re	1/727	10/23843	0.266345	0.71108	0.700441	Erbb2
GO_BP_m4	GO:003318	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Trip12
GO_BP_m4	GO:003435	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Gas6
GO_BP_m4	GO:003438	high-densi	1/727	10/23843	0.266345	0.71108	0.700441	Apoa4
GO_BP_m4	GO:003524	peptidyl-ar	1/727	10/23843	0.266345	0.71108	0.700441	Prmt9
GO_BP_m4	GO:003524	peptidyl-ar	1/727	10/23843	0.266345	0.71108	0.700441	Prmt9
GO_BP_m4	GO:003573	hepatic ste	1/727	10/23843	0.266345	0.71108	0.700441	Rps6ka1
GO_BP_m4	GO:003587	protein K11	1/727	10/23843	0.266345	0.71108	0.700441	Otud6a
GO_BP_m4	GO:004209	interleukin-	1/727	10/23843	0.266345	0.71108	0.700441	Rela
GO_BP_m4	GO:004392	exonucleol	1/727	10/23843	0.266345	0.71108	0.700441	Cnot6
GO_BP_m4	GO:004507	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Rela
GO_BP_m4	GO:004603	CTP metab	1/727	10/23843	0.266345	0.71108	0.700441	Nme5
GO_BP_m4	GO:004654	developme	1/727	10/23843	0.266345	0.71108	0.700441	Irf2bpl
GO_BP_m4	GO:004688	follicle-stin	1/727	10/23843	0.266345	0.71108	0.700441	Inhba
GO_BP_m4	GO:004748	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Mlc1
GO_BP_m4	GO:004828	vesicle fusi	1/727	10/23843	0.266345	0.71108	0.700441	Sec22b
GO_BP_m4	GO:005100	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Apoa4
GO_BP_m4	GO:005129	nuclear po	1/727	10/23843	0.266345	0.71108	0.700441	Rtn4
GO_BP_m4	GO:005165	maintenan	1/727	10/23843	0.266345	0.71108	0.700441	Polr2m
GO_BP_m4	GO:005191	regulation	1/727	10/23843	0.266345	0.71108	0.700441	F12
GO_BP_m4	GO:005197	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Hcrt
GO_BP_m4	GO:006071	chorio-alla	1/727	10/23843	0.266345	0.71108	0.700441	Zfp36l1
GO_BP_m4	GO:007024	negative re	1/727	10/23843	0.266345	0.71108	0.700441	Efna1
GO_BP_m4	GO:007107	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Htr2c
GO_BP_m4	GO:007168	striated mu	1/727	10/23843	0.266345	0.71108	0.700441	Myom2
GO_BP_m4	GO:007552	IRES-depen	1/727	10/23843	0.266345	0.71108	0.700441	Eif3a
GO_BP_m4	GO:009018	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Vamp8
GO_BP_m4	GO:009020	negative re	1/727	10/23843	0.266345	0.71108	0.700441	Sik1
GO_BP_m4	GO:009059	inflammato	1/727	10/23843	0.266345	0.71108	0.700441	Ager
GO_BP_m4	GO:009708	vascular sm	1/727	10/23843	0.266345	0.71108	0.700441	Sgcb
GO_BP_m4	GO:009742	liver regen	1/727	10/23843	0.266345	0.71108	0.700441	Aurka
GO_BP_m4	GO:190019	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Aurka
GO_BP_m4	GO:190045	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Arc
GO_BP_m4	GO:190138	positive reg	1/727	10/23843	0.266345	0.71108	0.700441	Kcne1
GO_BP_m4	GO:190241	regulation	1/727	10/23843	0.266345	0.71108	0.700441	Eif3e
GO_BP_m4	GO:190381	negative re	1/727	10/23843	0.266345	0.71108	0.700441	Kcne1
GO_BP_m4	GO:200004	negative re	1/727	10/23843	0.266345	0.71108	0.700441	Recql5
GO_BP_m4	GO:000046	maturation	2/727	33/23843	0.266525	0.71108	0.700441	Eri2/Mphos
GO_BP_m4	GO:001482	response to	2/727	33/23843	0.266525	0.71108	0.700441	Mir709/Slc

GO_BP_m4	GO:003111	positive re	2/727	33/23843	0.266525	0.71108	0.700441	Nav3/Rps3
GO_BP_m4	GO:003430	primary alc	2/727	33/23843	0.266525	0.71108	0.700441	Abhd4/Gd
GO_BP_m4	GO:004300	Golgi to pl	2/727	33/23843	0.266525	0.71108	0.700441	Blzf1/Rab3
GO_BP_m4	GO:004562	regulation	2/727	33/23843	0.266525	0.71108	0.700441	Il27/Socs5
GO_BP_m4	GO:004568	negative re	2/727	33/23843	0.266525	0.71108	0.700441	Dusp10/N
GO_BP_m4	GO:004574	negative re	2/727	33/23843	0.266525	0.71108	0.700441	Neurl1a/O
GO_BP_m4	GO:004646	neutral lipi	2/727	33/23843	0.266525	0.71108	0.700441	Apoa4/Lip
GO_BP_m4	GO:004646	acylglycer	2/727	33/23843	0.266525	0.71108	0.700441	Apoa4/Lip
GO_BP_m4	GO:004801	ephrin rec	2/727	33/23843	0.266525	0.71108	0.700441	Efna1/Tia
GO_BP_m4	GO:004819	Golgi vesic	2/727	33/23843	0.266525	0.71108	0.700441	Sec13/Tm
GO_BP_m4	GO:005068	negative re	2/727	33/23843	0.266525	0.71108	0.700441	Nelfe/Srsf1
GO_BP_m4	GO:190074	regulation	2/727	33/23843	0.266525	0.71108	0.700441	Ager/Dusp
GO_BP_m4	GO:190395	regulation	2/727	33/23843	0.266525	0.71108	0.700441	Irs2/Ripk1
GO_BP_m4	GO:000930	amine met	4/727	86/23843	0.267375	0.712027	0.701375	Abhd4/Gd
GO_BP_m4	GO:005128	protein ho	4/727	86/23843	0.267375	0.712027	0.701375	Decr1/Mbl
GO_BP_m4	GO:003021	T cell diffe	10/727	259/23843	0.267821	0.712027	0.701375	Btn2a2/Du
GO_BP_m4	GO:007122	cellular res	10/727	259/23843	0.267821	0.712027	0.701375	AY761184/
GO_BP_m4	GO:000666	phosphati	3/727	59/23843	0.268163	0.712027	0.701375	Htr2c/Pigp
GO_BP_m4	GO:003267	regulation	3/727	59/23843	0.268163	0.712027	0.701375	Bcl10/Ddit
GO_BP_m4	GO:004684	filopodium	3/727	59/23843	0.268163	0.712027	0.701375	Neurl1a/Sp
GO_BP_m4	GO:006071	labyrinthin	3/727	59/23843	0.268163	0.712027	0.701375	Grb2/Ovol
GO_BP_m4	GO:003157	DNA integ	5/727	114/23843	0.26822	0.712027	0.701375	Hus1/Map
GO_BP_m4	GO:000760	sensory pe	10/727	260/23843	0.271625	0.720666	0.709884	Mir16-2/M
GO_BP_m4	GO:001060	posttransc	17/727	471/23843	0.272263	0.721957	0.711156	Cnot6/Eif3
GO_BP_m4	GO:003629	cellular res	5/727	115/23843	0.274064	0.723422	0.712599	Fndc1/Hp1
GO_BP_m4	GO:000269	positive re	4/727	87/23843	0.274154	0.723422	0.712599	C3ar1/Gas
GO_BP_m4	GO:000689	post-Golgi	4/727	87/23843	0.274154	0.723422	0.712599	Blzf1/Gak/
GO_BP_m4	GO:010602	neuron pr	4/727	87/23843	0.274154	0.723422	0.712599	Arc/Efna1/
GO_BP_m4	GO:000616	purine nuc	10/727	261/23843	0.275446	0.723422	0.712599	Ak3/Atp5c
GO_BP_m4	GO:004592	negative re	10/727	261/23843	0.275446	0.723422	0.712599	Dusp10/In
GO_BP_m4	GO:005092	regulation	8/727	202/23843	0.275822	0.723422	0.712599	Ager/C3ar
GO_BP_m4	GO:009865	anion tran	8/727	202/23843	0.275822	0.723422	0.712599	Irs2/Lrrc8c
GO_BP_m4	GO:006099	positive re	3/727	60/23843	0.276475	0.723422	0.712599	Itsn1/Neur
GO_BP_m4	GO:003017	negative re	6/727	144/23843	0.276576	0.723422	0.712599	Ddit3/Map
GO_BP_m4	GO:000267	positive re	2/727	34/23843	0.277923	0.723422	0.712599	F12/Ffar3
GO_BP_m4	GO:000803	neuron rec	2/727	34/23843	0.277923	0.723422	0.712599	Rtn4/Tnn
GO_BP_m4	GO:003026	chromoso	2/727	34/23843	0.277923	0.723422	0.712599	Ern2/Ncap
GO_BP_m4	GO:003209	response t	2/727	34/23843	0.277923	0.723422	0.712599	Bcl10/Slc2
GO_BP_m4	GO:003362	regulation	2/727	34/23843	0.277923	0.723422	0.712599	Efna1/Ret
GO_BP_m4	GO:003424	regulation	2/727	34/23843	0.277923	0.723422	0.712599	Nelfe/Recq
GO_BP_m4	GO:004245	ribonucleo	2/727	34/23843	0.277923	0.723422	0.712599	Nme5/Pdc
GO_BP_m4	GO:007057	regulation	2/727	34/23843	0.277923	0.723422	0.712599	Rtn4/Rtn4
GO_BP_m4	GO:007139	cellular res	2/727	34/23843	0.277923	0.723422	0.712599	Ffar3/Pid1
GO_BP_m4	GO:190001	regulation	2/727	34/23843	0.277923	0.723422	0.712599	Mapk14/M
GO_BP_m4	GO:000712	meiosis I	5/727	116/23843	0.279934	0.723422	0.712599	Cenps/Aur
GO_BP_m4	GO:005170	interaction	5/727	116/23843	0.279934	0.723422	0.712599	Gas6/Serpi
GO_BP_m4	GO:004558	positive re	4/727	88/23843	0.280961	0.723422	0.712599	Btn2a2/Du
GO_BP_m4	GO:190122	regulation	4/727	88/23843	0.280961	0.723422	0.712599	Ager/Rela/

GO_BP_m4	GO:000633	chromatin	6/727	145/23843	0.281811	0.723422	0.712599	Anp32b/N
GO_BP_m4	GO:000926	ribonucleo	10/727	263/23843	0.283135	0.723422	0.712599	Ak3/Atp5c
GO_BP_m4	GO:005086	regulation	11/727	293/23843	0.283425	0.723422	0.712599	Ager/Bcl10
GO_BP_m4	GO:003085	positive reg	3/727	61/23843	0.284811	0.723422	0.712599	Ovol2/Vdr/
GO_BP_m4	GO:004566	regulation	3/727	61/23843	0.284811	0.723422	0.712599	Ddit3/Map
GO_BP_m4	GO:004662	regulation	3/727	61/23843	0.284811	0.723422	0.712599	C1qtnf12/
GO_BP_m4	GO:005159	response t	3/727	61/23843	0.284811	0.723422	0.712599	Duox2/Slc8
GO_BP_m4	GO:190280	negative re	3/727	61/23843	0.284811	0.723422	0.712599	Btn2a2/Pid
GO_BP_m4	GO:200125	positive reg	3/727	61/23843	0.284811	0.723422	0.712599	Arc/Kcne1/
GO_BP_m4	GO:003476	regulation	16/727	445/23843	0.285243	0.723422	0.712599	Ager/Arc/C
GO_BP_m4	GO:005109	positive reg	5/727	117/23843	0.285828	0.723422	0.712599	Ager/Bcl10
GO_BP_m4	GO:190037	regulation	5/727	117/23843	0.285828	0.723422	0.712599	Cap2/Gng7
GO_BP_m4	GO:000681	potassium	9/727	234/23843	0.286264	0.723422	0.712599	Ager/Atp1
GO_BP_m4	GO:005500	cardiac cell	4/727	89/23843	0.287794	0.723422	0.712599	Fhl2/Myom
GO_BP_m4	GO:000173	formation (	1/727	11/23843	0.288724	0.723422	0.712599	Rps2
GO_BP_m4	GO:003326	cardioblast	1/727	11/23843	0.288724	0.723422	0.712599	Pim1
GO_BP_m4	GO:003326	regulation	1/727	11/23843	0.288724	0.723422	0.712599	Pim1
GO_BP_m4	GO:003300	Wnt signali	1/727	11/23843	0.288724	0.723422	0.712599	Sox17
GO_BP_m4	GO:000618	GTP biosyn	1/727	11/23843	0.288724	0.723422	0.712599	Nme5
GO_BP_m4	GO:000652	arginine ca	1/727	11/23843	0.288724	0.723422	0.712599	Fah
GO_BP_m4	GO:000656	tryptophan	1/727	11/23843	0.288724	0.723422	0.712599	Kynu
GO_BP_m4	GO:000658	indolalkyla	1/727	11/23843	0.288724	0.723422	0.712599	Kynu
GO_BP_m4	GO:000665	phosphatid	1/727	11/23843	0.288724	0.723422	0.712599	Lipc
GO_BP_m4	GO:000697	DNA dama	1/727	11/23843	0.288724	0.723422	0.712599	Pidd1
GO_BP_m4	GO:000920	pyrimidine	1/727	11/23843	0.288724	0.723422	0.712599	Nme5
GO_BP_m4	GO:001071	negative re	1/727	11/23843	0.288724	0.723422	0.712599	Ager
GO_BP_m4	GO:001087	regulation	1/727	11/23843	0.288724	0.723422	0.712599	Apoa4
GO_BP_m4	GO:001405	regulation	1/727	11/23843	0.288724	0.723422	0.712599	Htr2c
GO_BP_m4	GO:003103	myosin fila	1/727	11/23843	0.288724	0.723422	0.712599	Myom2
GO_BP_m4	GO:003296	negative re	1/727	11/23843	0.288724	0.723422	0.712599	Ager
GO_BP_m4	GO:003308	immature T	1/727	11/23843	0.288724	0.723422	0.712599	Erbb2
GO_BP_m4	GO:003323	negative re	1/727	11/23843	0.288724	0.723422	0.712599	Rela
GO_BP_m4	GO:003360	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Rtn4
GO_BP_m4	GO:003370	phospholip	1/727	11/23843	0.288724	0.723422	0.712599	Apoa4
GO_BP_m4	GO:003437	high-densi	1/727	11/23843	0.288724	0.723422	0.712599	Lipc
GO_BP_m4	GO:003545	cellular res	1/727	11/23843	0.288724	0.723422	0.712599	Gas6
GO_BP_m4	GO:003584	photorecep	1/727	11/23843	0.288724	0.723422	0.712599	Nphp1
GO_BP_m4	GO:003816	angiotensin	1/727	11/23843	0.288724	0.723422	0.712599	Car2
GO_BP_m4	GO:004356	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Cdh3
GO_BP_m4	GO:004455	relaxation (	1/727	11/23843	0.288724	0.723422	0.712599	Slc8a1
GO_BP_m4	GO:004564	negative re	1/727	11/23843	0.288724	0.723422	0.712599	Zfp36l1
GO_BP_m4	GO:004587	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Sfpq
GO_BP_m4	GO:004600	negative re	1/727	11/23843	0.288724	0.723422	0.712599	Btn2a2
GO_BP_m4	GO:004668	response t	1/727	11/23843	0.288724	0.723422	0.712599	Aqp9
GO_BP_m4	GO:004826	determinat	1/727	11/23843	0.288724	0.723422	0.712599	Ddit3
GO_BP_m4	GO:004826	determinat	1/727	11/23843	0.288724	0.723422	0.712599	Ddit3
GO_BP_m4	GO:004861	embryonic	1/727	11/23843	0.288724	0.723422	0.712599	Sox17
GO_BP_m4	GO:004868	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Rtn4

GO_BP_m4	GO:004884	venous blo	1/727	11/23843	0.288724	0.723422	0.712599	Ccm2
GO_BP_m4	GO:005066	hydrogen p	1/727	11/23843	0.288724	0.723422	0.712599	Cyp1a2
GO_BP_m4	GO:005501	ventricular	1/727	11/23843	0.288724	0.723422	0.712599	Fhl2
GO_BP_m4	GO:006005	mammary	1/727	11/23843	0.288724	0.723422	0.712599	Vdr
GO_BP_m4	GO:006130	cardiac neu	1/727	11/23843	0.288724	0.723422	0.712599	Folr1
GO_BP_m4	GO:006136	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Apoa4
GO_BP_m4	GO:007047	regulation	1/727	11/23843	0.288724	0.723422	0.712599	Lck
GO_BP_m4	GO:007091	UV-damag	1/727	11/23843	0.288724	0.723422	0.712599	Xpa
GO_BP_m4	GO:007129	cellular resp	1/727	11/23843	0.288724	0.723422	0.712599	Mt1
GO_BP_m4	GO:007163	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Ager
GO_BP_m4	GO:007212	regulation	1/727	11/23843	0.288724	0.723422	0.712599	C3ar1
GO_BP_m4	GO:008601	AV node ce	1/727	11/23843	0.288724	0.723422	0.712599	Cacna1g
GO_BP_m4	GO:008602	AV node ce	1/727	11/23843	0.288724	0.723422	0.712599	Cacna1g
GO_BP_m4	GO:009007	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Traf4
GO_BP_m4	GO:009709	synaptic ve	1/727	11/23843	0.288724	0.723422	0.712599	Syn1
GO_BP_m4	GO:190036	regulation	1/727	11/23843	0.288724	0.723422	0.712599	Nelfe
GO_BP_m4	GO:190166	calcium ion	1/727	11/23843	0.288724	0.723422	0.712599	Slc8a1
GO_BP_m4	GO:190200	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Efna1
GO_BP_m4	GO:190223	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Rps3
GO_BP_m4	GO:190365	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	Ptpn23
GO_BP_m4	GO:200078	positive reg	1/727	11/23843	0.288724	0.723422	0.712599	5330417C2
GO_BP_m4	GO:000991	epidermal	8/727	205/23843	0.289025	0.723422	0.712599	Cdh3/Dsp/
GO_BP_m4	GO:000009	sulfur amin	2/727	35/23843	0.289308	0.723422	0.712599	Bhmt/Dpep
GO_BP_m4	GO:000682	iron ion tra	2/727	35/23843	0.289308	0.723422	0.712599	Heph/Slc25
GO_BP_m4	GO:001700	antibiotic c	2/727	35/23843	0.289308	0.723422	0.712599	Apoa4/Mp
GO_BP_m4	GO:003200	positive reg	2/727	35/23843	0.289308	0.723422	0.712599	Gas6/Sec13
GO_BP_m4	GO:003300	regulation	2/727	35/23843	0.289308	0.723422	0.712599	Il13/Vamp8
GO_BP_m4	GO:003314	positive reg	2/727	35/23843	0.289308	0.723422	0.712599	Ifna12/Ret
GO_BP_m4	GO:004330	regulation	2/727	35/23843	0.289308	0.723422	0.712599	Il13/Vamp8
GO_BP_m4	GO:004668	response to	2/727	35/23843	0.289308	0.723422	0.712599	Cyp1a2/Mt
GO_BP_m4	GO:005169	actin filame	2/727	35/23843	0.289308	0.723422	0.712599	Sptan1/Tm
GO_BP_m4	GO:007136	cellular resp	2/727	35/23843	0.289308	0.723422	0.712599	Erbb2/Zfp3
GO_BP_m4	GO:009002	regulation	2/727	35/23843	0.289308	0.723422	0.712599	C3ar1/Sell
GO_BP_m4	GO:190138	positive reg	2/727	35/23843	0.289308	0.723422	0.712599	Ager/Kcne1
GO_BP_m4	GO:190197	regulation	2/727	35/23843	0.289308	0.723422	0.712599	Aurka/Thoc
GO_BP_m4	GO:190274	apoptotic p	2/727	35/23843	0.289308	0.723422	0.712599	Fgf4/Vdr
GO_BP_m4	GO:200078	regulation	2/727	35/23843	0.289308	0.723422	0.712599	5330417C2
GO_BP_m4	GO:003009	lymphocyte	14/727	386/23843	0.291317	0.726855	0.715981	Btn2a2/Dus
GO_BP_m4	GO:000858	male gona	5/727	118/23843	0.291745	0.726855	0.715981	Brip1/Esr2/
GO_BP_m4	GO:001699	antibiotic m	5/727	118/23843	0.291745	0.726855	0.715981	Apoa4/Cyc
GO_BP_m4	GO:003080	regulation	5/727	118/23843	0.291745	0.726855	0.715981	Cap2/Gng7
GO_BP_m4	GO:005072	positive reg	5/727	118/23843	0.291745	0.726855	0.715981	Ager/F12/F
GO_BP_m4	GO:006100	hepaticobil	5/727	118/23843	0.291745	0.726855	0.715981	Aurka/Gak/
GO_BP_m4	GO:006198	meiosis I ce	5/727	118/23843	0.291745	0.726855	0.715981	Cenps/Aur
GO_BP_m4	GO:000267	regulation	3/727	62/23843	0.293168	0.72888	0.717975	Dnase1/F1
GO_BP_m4	GO:000924	glycolipid b	3/727	62/23843	0.293168	0.72888	0.717975	A4galt/Pigp
GO_BP_m4	GO:001591	phospholip	3/727	62/23843	0.293168	0.72888	0.717975	Abcb4/Apo
GO_BP_m4	GO:004205	regulation	3/727	62/23843	0.293168	0.72888	0.717975	Esr2/Neurl1

GO_BP_m4	GO:00450	regulation	4/727	90/23843	0.29465	0.731368	0.720427	A230050P
GO_BP_m4	GO:00466	response t	4/727	90/23843	0.29465	0.731368	0.720427	Duox2/Sell
GO_BP_m4	GO:00463	ribose pho	10/727	266/23843	0.294781	0.731368	0.720427	Ak3/Atp5c
GO_BP_m4	GO:00725	purine-cor	10/727	266/23843	0.294781	0.731368	0.720427	Ak3/Atp5c
GO_BP_m4	GO:00465	developme	5/727	119/23843	0.297684	0.732658	0.721697	Brip1/Esr2/
GO_BP_m4	GO:00519	positive re	5/727	119/23843	0.297684	0.732658	0.721697	Hcrt/Il13/K
GO_BP_m4	GO:000931	response t	14/727	388/23843	0.297763	0.732658	0.721697	Agap3/Ca
GO_BP_m4	GO:003241	regulation	9/727	237/23843	0.298689	0.732658	0.721697	Ager/Arc/
GO_BP_m4	GO:00060	alcohol me	10/727	267/23843	0.298691	0.732658	0.721697	Abhd4/Akr
GO_BP_m4	GO:01987	cell-cell sig	15/727	419/23843	0.299136	0.732658	0.721697	Cdh3/Ddit
GO_BP_m4	GO:00091	nucleoside	2/727	36/23843	0.300672	0.732658	0.721697	Nme5/Pdc
GO_BP_m4	GO:00324	endocytic r	2/727	36/23843	0.300672	0.732658	0.721697	Ehd4/Ptpn
GO_BP_m4	GO:00341	positive re	2/727	36/23843	0.300672	0.732658	0.721697	Car2/Vdr
GO_BP_m4	GO:00429	amyloid pr	2/727	36/23843	0.300672	0.732658	0.721697	Efna1/Tme
GO_BP_m4	GO:00468	phospholip	2/727	36/23843	0.300672	0.732658	0.721697	Plppr3/Plp
GO_BP_m4	GO:00481	regulation	2/727	36/23843	0.300672	0.732658	0.721697	Neurl1a/Sy
GO_BP_m4	GO:00509	pigment ce	2/727	36/23843	0.300672	0.732658	0.721697	Mreg/Zeb
GO_BP_m4	GO:00512	establishm	2/727	36/23843	0.300672	0.732658	0.721697	Spdl1/Spry
GO_BP_m4	GO:00619	glial cell ac	2/727	36/23843	0.300672	0.732658	0.721697	Ager/Il13
GO_BP_m4	GO:00702	protein ho	2/727	36/23843	0.300672	0.732658	0.721697	Atxn10/Mb
GO_BP_m4	GO:00713	cellular res	2/727	36/23843	0.300672	0.732658	0.721697	Slc8a1/Zfp
GO_BP_m4	GO:00970	dendritic c	2/727	36/23843	0.300672	0.732658	0.721697	Ager/Gata
GO_BP_m4	GO:00974	dendrite e	2/727	36/23843	0.300672	0.732658	0.721697	Nedd4l/Rtr
GO_BP_m4	GO:00421	positive re	3/727	63/23843	0.30154	0.732658	0.721697	Bcl10/Il27/
GO_BP_m4	GO:004227	purine nuc	3/727	63/23843	0.30154	0.732658	0.721697	Ak3/Dguo
GO_BP_m4	GO:00480	antigen pr	3/727	63/23843	0.30154	0.732658	0.721697	H2-M10.1/
GO_BP_m4	GO:007121	cellular res	10/727	268/23843	0.302615	0.732658	0.721697	AY761184/
GO_BP_m4	GO:00308	regulation	7/727	179/23843	0.305684	0.732658	0.721697	Arhgap18/
GO_BP_m4	GO:005087	positive re	7/727	179/23843	0.305684	0.732658	0.721697	Ager/Bcl10
GO_BP_m4	GO:00026	negative re	5/727	121/23843	0.309618	0.732658	0.721697	Dusp10/Lg
GO_BP_m4	GO:00326	interleukin	3/727	64/23843	0.309924	0.732658	0.721697	Bcl10/Ddit
GO_BP_m4	GO:00468	positive re	3/727	64/23843	0.309924	0.732658	0.721697	Gas6/Map
GO_BP_m4	GO:006137	determinat	3/727	64/23843	0.309924	0.732658	0.721697	Folr1/Ovol
GO_BP_m4	GO:00020	protein de	1/727	12/23843	0.310422	0.732658	0.721697	Abhd13
GO_BP_m4	GO:00024	compleme	1/727	12/23843	0.310422	0.732658	0.721697	C3ar1
GO_BP_m4	GO:00030	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Gas6
GO_BP_m4	GO:00031	mitral valve	1/727	12/23843	0.310422	0.732658	0.721697	Efna1
GO_BP_m4	GO:00060	acetyl-CoA	1/727	12/23843	0.310422	0.732658	0.721697	Pdhx
GO_BP_m4	GO:00061	mitochond	1/727	12/23843	0.310422	0.732658	0.721697	Cycs
GO_BP_m4	GO:00065	tyrosine m	1/727	12/23843	0.310422	0.732658	0.721697	Fah
GO_BP_m4	GO:00068	oligopepti	1/727	12/23843	0.310422	0.732658	0.721697	Car2
GO_BP_m4	GO:00074	foregut m	1/727	12/23843	0.310422	0.732658	0.721697	Sox17
GO_BP_m4	GO:00107	regulation	1/727	12/23843	0.310422	0.732658	0.721697	F12
GO_BP_m4	GO:00108	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Apoc4
GO_BP_m4	GO:00148	tonic smo	1/727	12/23843	0.310422	0.732658	0.721697	Cacna1g
GO_BP_m4	GO:00164	somatic hy	1/727	12/23843	0.310422	0.732658	0.721697	Polb
GO_BP_m4	GO:00165	protein im	1/727	12/23843	0.310422	0.732658	0.721697	Pex1
GO_BP_m4	GO:00181	protein oxi	1/727	12/23843	0.310422	0.732658	0.721697	Trabd2b

GO_BP_m4	GO:002152	ventral spir	1/727	12/23843	0.310422	0.732658	0.721697	Nkx6-2
GO_BP_m4	GO:003112	rRNA 3'-er	1/727	12/23843	0.310422	0.732658	0.721697	Eri2
GO_BP_m4	GO:003191	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Anapc2
GO_BP_m4	GO:003282	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Gas6
GO_BP_m4	GO:003292	negative re	1/727	12/23843	0.310422	0.732658	0.721697	Fst
GO_BP_m4	GO:003308	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Erbb2
GO_BP_m4	GO:003496	histone arg	1/727	12/23843	0.310422	0.732658	0.721697	Prmt9
GO_BP_m4	GO:003597	peptidyl-th	1/727	12/23843	0.310422	0.732658	0.721697	Dusp10
GO_BP_m4	GO:004236	fat-soluble	1/727	12/23843	0.310422	0.732658	0.721697	Vdr
GO_BP_m4	GO:004254	hemoglobi	1/727	12/23843	0.310422	0.732658	0.721697	Inhba
GO_BP_m4	GO:004409	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	5330417C2
GO_BP_m4	GO:004507	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Il27
GO_BP_m4	GO:004541	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Bcl10
GO_BP_m4	GO:004574	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Neurl1a
GO_BP_m4	GO:004576	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Tshr
GO_BP_m4	GO:004594	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Erbb2
GO_BP_m4	GO:004595	negative re	1/727	12/23843	0.310422	0.732658	0.721697	Cbarp
GO_BP_m4	GO:004814	astrocyte a	1/727	12/23843	0.310422	0.732658	0.721697	Ager
GO_BP_m4	GO:004857	notochord	1/727	12/23843	0.310422	0.732658	0.721697	Efna1
GO_BP_m4	GO:004873	cardiac mu	1/727	12/23843	0.310422	0.732658	0.721697	Myom2
GO_BP_m4	GO:005179	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Fst
GO_BP_m4	GO:006006	vagina dev	1/727	12/23843	0.310422	0.732658	0.721697	Esr2
GO_BP_m4	GO:006010	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Ager
GO_BP_m4	GO:006012	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Itsn1
GO_BP_m4	GO:006057	cell fate sp	1/727	12/23843	0.310422	0.732658	0.721697	Nkx6-2
GO_BP_m4	GO:007026	peptidyl-se	1/727	12/23843	0.310422	0.732658	0.721697	Ppp1r15b
GO_BP_m4	GO:007034	fat cell prol	1/727	12/23843	0.310422	0.732658	0.721697	Pid1
GO_BP_m4	GO:007034	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Pid1
GO_BP_m4	GO:007042	nucleotide-	1/727	12/23843	0.310422	0.732658	0.721697	Rela
GO_BP_m4	GO:007043	nucleotide-	1/727	12/23843	0.310422	0.732658	0.721697	Rela
GO_BP_m4	GO:007047	uterine sm	1/727	12/23843	0.310422	0.732658	0.721697	Lck
GO_BP_m4	GO:007057	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Rtn4
GO_BP_m4	GO:007093	histone H3	1/727	12/23843	0.310422	0.732658	0.721697	Sfpq
GO_BP_m4	GO:007146	cellular res	1/727	12/23843	0.310422	0.732658	0.721697	Kcne1
GO_BP_m4	GO:007183	cell prolifer	1/727	12/23843	0.310422	0.732658	0.721697	Lgals3
GO_BP_m4	GO:007186	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Lgals3
GO_BP_m4	GO:007211	glomerular	1/727	12/23843	0.310422	0.732658	0.721697	C3ar1
GO_BP_m4	GO:007243	signal trans	1/727	12/23843	0.310422	0.732658	0.721697	Pidd1
GO_BP_m4	GO:009896	neurotrans	1/727	12/23843	0.310422	0.732658	0.721697	Snap47
GO_BP_m4	GO:190184	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Rem2
GO_BP_m4	GO:190240	intracellula	1/727	12/23843	0.310422	0.732658	0.721697	Pidd1
GO_BP_m4	GO:190241	protein loc	1/727	12/23843	0.310422	0.732658	0.721697	Dsp
GO_BP_m4	GO:190271	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Mir155
GO_BP_m4	GO:190290	negative re	1/727	12/23843	0.310422	0.732658	0.721697	Sec22b
GO_BP_m4	GO:190302	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Ddit3
GO_BP_m4	GO:190354	establishm	1/727	12/23843	0.310422	0.732658	0.721697	Snap47
GO_BP_m4	GO:190397	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Tiam1
GO_BP_m4	GO:190447	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Apoa4

GO_BP_m4	GO:190486	excitatory s	1/727	12/23843	0.310422	0.732658	0.721697	Vstm5
GO_BP_m4	GO:190515	positive reg	1/727	12/23843	0.310422	0.732658	0.721697	Ager
GO_BP_m4	GO:190521	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Eif3e
GO_BP_m4	GO:200062	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Rela
GO_BP_m4	GO:200067	regulation	1/727	12/23843	0.310422	0.732658	0.721697	Ager
GO_BP_m4	GO:007048	response to	10/727	270/23843	0.3105	0.732658	0.721697	Ager/Fndc
GO_BP_m4	GO:000018	nuclear-tra	2/727	37/23843	0.312004	0.732658	0.721697	Eif3e/Nbas
GO_BP_m4	GO:000253	cytokine pr	2/727	37/23843	0.312004	0.732658	0.721697	Mapk14/M
GO_BP_m4	GO:000288	positive reg	2/727	37/23843	0.312004	0.732658	0.721697	Il13/Vamp8
GO_BP_m4	GO:001076	regulation	2/727	37/23843	0.312004	0.732658	0.721697	Ager/Slc8a
GO_BP_m4	GO:003313	regulation	2/727	37/23843	0.312004	0.732658	0.721697	Ifna12/Ret
GO_BP_m4	GO:003820	TORC1 sign	2/727	37/23843	0.312004	0.732658	0.721697	Akt1s1/Sec
GO_BP_m4	GO:004616	alcohol cat	2/727	37/23843	0.312004	0.732658	0.721697	Akr1d1/Cy
GO_BP_m4	GO:004662	negative re	2/727	37/23843	0.312004	0.732658	0.721697	Pid1/Rela
GO_BP_m4	GO:005502	positive reg	2/727	37/23843	0.312004	0.732658	0.721697	Mapk14/Pi
GO_BP_m4	GO:190106	guanosine-	2/727	37/23843	0.312004	0.732658	0.721697	Ak3/Nme5
GO_BP_m4	GO:190262	positive reg	2/727	37/23843	0.312004	0.732658	0.721697	C3ar1/Sell
GO_BP_m4	GO:007115	leukocyte c	11/727	301/23843	0.31307	0.7348	0.723807	Ager/Apoa
GO_BP_m4	GO:003476	positive reg	6/727	151/23843	0.31364	0.735776	0.724768	Ager/Arc/C
GO_BP_m4	GO:000664	phospholip	12/727	332/23843	0.314973	0.738541	0.727492	Apoa4/Gd
GO_BP_m4	GO:004364	dicarboxyli	4/727	93/23843	0.315332	0.739021	0.727965	Acmsd/Fol
GO_BP_m4	GO:003227	regulation	8/727	211/23843	0.315872	0.739133	0.728076	Arhgap18/
GO_BP_m4	GO:004521	cell-cell jun	8/727	211/23843	0.315872	0.739133	0.728076	Ccm2/Cdh
GO_BP_m4	GO:000314	embryonic	3/727	65/23843	0.318314	0.739133	0.728076	Folr1/Ovol
GO_BP_m4	GO:190432	response to	3/727	65/23843	0.318314	0.739133	0.728076	Mir7-2/Mir
GO_BP_m4	GO:190432	cellular res	3/727	65/23843	0.318314	0.739133	0.728076	Mir7-2/Mir
GO_BP_m4	GO:005506	monovalen	6/727	152/23843	0.319003	0.739133	0.728076	Atp1b4/Ca
GO_BP_m4	GO:004873	cardiac mu	9/727	242/23843	0.319678	0.739133	0.728076	Dsp/Fhl2/M
GO_BP_m4	GO:200037	regulation	7/727	182/23843	0.320321	0.739133	0.728076	Ager/Esr2/
GO_BP_m4	GO:004886	stem cell d	8/727	212/23843	0.320395	0.739133	0.728076	Folr1/Mir1
GO_BP_m4	GO:003806	NIK/NF-ka	4/727	94/23843	0.322255	0.739133	0.728076	Ager/Rela/
GO_BP_m4	GO:000272	positive reg	2/727	38/23843	0.323296	0.739133	0.728076	Ffar3/Mapk
GO_BP_m4	GO:000962	response to	2/727	38/23843	0.323296	0.739133	0.728076	Bcl10/Mpo
GO_BP_m4	GO:004408	regulation	2/727	38/23843	0.323296	0.739133	0.728076	5330417C2
GO_BP_m4	GO:004558	negative re	2/727	38/23843	0.323296	0.739133	0.728076	Erbb2/Socs
GO_BP_m4	GO:004688	regulation	2/727	38/23843	0.323296	0.739133	0.728076	Ffar3/Vdr
GO_BP_m4	GO:004879	calcium ion	2/727	38/23843	0.323296	0.739133	0.728076	Rims4/Syt1
GO_BP_m4	GO:005148	positive reg	2/727	38/23843	0.323296	0.739133	0.728076	Grm1/Htr2
GO_BP_m4	GO:007084	response to	2/727	38/23843	0.323296	0.739133	0.728076	Erbb2/Zfp3
GO_BP_m4	GO:008600	membrane	2/727	38/23843	0.323296	0.739133	0.728076	Kcne1/Nec
GO_BP_m4	GO:190165	glycosyl co	2/727	38/23843	0.323296	0.739133	0.728076	Nme5/Pdc
GO_BP_m4	GO:200000	regulation	2/727	38/23843	0.323296	0.739133	0.728076	Astn2/Ned
GO_BP_m4	GO:002289	regulation	9/727	243/23843	0.323912	0.739133	0.728076	Ager/Arc/C
GO_BP_m4	GO:006032	cell chemo	10/727	274/23843	0.32641	0.739133	0.728076	C3ar1/Defb
GO_BP_m4	GO:000154	ovarian foll	3/727	66/23843	0.326708	0.739133	0.728076	Esr2/Inhba
GO_BP_m4	GO:001406	positive reg	3/727	66/23843	0.326708	0.739133	0.728076	Erbb2/Hcst
GO_BP_m4	GO:003096	endoplasm	3/727	66/23843	0.326708	0.739133	0.728076	Atf6b/Ddit3
GO_BP_m4	GO:005502	regulation	3/727	66/23843	0.326708	0.739133	0.728076	Mapk14/M

GO_BP_m4	GO:006147	response t	3/727	66/23843	0.326708	0.739133	0.728076	Mir7-2/Mi
GO_BP_m4	GO:190372	regulation	3/727	66/23843	0.326708	0.739133	0.728076	Htr2c/Pik3i
GO_BP_m4	GO:003021	erythrocyt	5/727	124/23843	0.327637	0.739133	0.728076	Gata1/Hep
GO_BP_m4	GO:00351	gene silen	5/727	124/23843	0.327637	0.739133	0.728076	Mir155/Mi
GO_BP_m4	GO:00097	axis specifi	4/727	95/23843	0.329189	0.739133	0.728076	Aurka/Ddit
GO_BP_m4	GO:003164	regulation	4/727	95/23843	0.329189	0.739133	0.728076	Grm1/Hcrt
GO_BP_m4	GO:004592	positive re	4/727	95/23843	0.329189	0.739133	0.728076	Cacna1g/C
GO_BP_m4	GO:00434	negative re	6/727	154/23843	0.32977	0.739133	0.728076	Btn2a2/Cnl
GO_BP_m4	GO:00484	cell matura	7/727	184/23843	0.330145	0.739133	0.728076	Aurka/Bfsp
GO_BP_m4	GO:00004	maturation	1/727	13/23843	0.331458	0.739133	0.728076	Rpl7l1
GO_BP_m4	GO:000092	septin ring	1/727	13/23843	0.331458	0.739133	0.728076	12-Sep
GO_BP_m4	GO:00015	luteinizatio	1/727	13/23843	0.331458	0.739133	0.728076	Inhba
GO_BP_m4	GO:00025	somatic div	1/727	13/23843	0.331458	0.739133	0.728076	Polb
GO_BP_m4	GO:000317	mitral valv	1/727	13/23843	0.331458	0.739133	0.728076	Efna1
GO_BP_m4	GO:000317	pulmonary	1/727	13/23843	0.331458	0.739133	0.728076	Nfatc1
GO_BP_m4	GO:00031	pulmonary	1/727	13/23843	0.331458	0.739133	0.728076	Nfatc1
GO_BP_m4	GO:00062	mitochond	1/727	13/23843	0.331458	0.739133	0.728076	Pid1
GO_BP_m4	GO:000651	protein de	1/727	13/23843	0.331458	0.739133	0.728076	Aga
GO_BP_m4	GO:00071	mitotic cen	1/727	13/23843	0.331458	0.739133	0.728076	Aurka
GO_BP_m4	GO:00075	mesoderm	1/727	13/23843	0.331458	0.739133	0.728076	Sox17
GO_BP_m4	GO:00090	methionin	1/727	13/23843	0.331458	0.739133	0.728076	Bhmt
GO_BP_m4	GO:00094	NAD biosy	1/727	13/23843	0.331458	0.739133	0.728076	Kynu
GO_BP_m4	GO:00108	negative re	1/727	13/23843	0.331458	0.739133	0.728076	Gas6
GO_BP_m4	GO:00108	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Slc8a1
GO_BP_m4	GO:00109	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Ppp1r15b
GO_BP_m4	GO:001821	peptidyl-a	1/727	13/23843	0.331458	0.739133	0.728076	Prmt9
GO_BP_m4	GO:002152	spinal cord	1/727	13/23843	0.331458	0.739133	0.728076	Nkx6-2
GO_BP_m4	GO:003057	nuclear bo	1/727	13/23843	0.331458	0.739133	0.728076	Agap3
GO_BP_m4	GO:00310	myosin fila	1/727	13/23843	0.331458	0.739133	0.728076	Myom2
GO_BP_m4	GO:003227	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Inhba
GO_BP_m4	GO:00324	response t	1/727	13/23843	0.331458	0.739133	0.728076	Rela
GO_BP_m4	GO:003307	immature	1/727	13/23843	0.331458	0.739133	0.728076	Erbb2
GO_BP_m4	GO:00336	positive re	1/727	13/23843	0.331458	0.739133	0.728076	Gata1
GO_BP_m4	GO:00340	stress gran	1/727	13/23843	0.331458	0.739133	0.728076	Grb7
GO_BP_m4	GO:00344	protein loc	1/727	13/23843	0.331458	0.739133	0.728076	Stx17
GO_BP_m4	GO:003572	intraciliary	1/727	13/23843	0.331458	0.739133	0.728076	Wdr35
GO_BP_m4	GO:003587	nucleotide	1/727	13/23843	0.331458	0.739133	0.728076	Rela
GO_BP_m4	GO:004222	interleukin	1/727	13/23843	0.331458	0.739133	0.728076	Bcl10
GO_BP_m4	GO:00424	gamma-de	1/727	13/23843	0.331458	0.739133	0.728076	Lck
GO_BP_m4	GO:00426	positive re	1/727	13/23843	0.331458	0.739133	0.728076	Fst
GO_BP_m4	GO:00435	negative re	1/727	13/23843	0.331458	0.739133	0.728076	Dusp10
GO_BP_m4	GO:00436	reverse ch	1/727	13/23843	0.331458	0.739133	0.728076	Apoa4
GO_BP_m4	GO:004507	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Il27
GO_BP_m4	GO:00451	developme	1/727	13/23843	0.331458	0.739133	0.728076	Irf2bpl
GO_BP_m4	GO:004562	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Socs5
GO_BP_m4	GO:004647	phosphatic	1/727	13/23843	0.331458	0.739133	0.728076	Lipc
GO_BP_m4	GO:00484	enteric ner	1/727	13/23843	0.331458	0.739133	0.728076	Ret
GO_BP_m4	GO:00487	branching	1/727	13/23843	0.331458	0.739133	0.728076	Rtn4

GO_BP_m4	GO:00602	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Dusp10
GO_BP_m4	GO:00602	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Aurka
GO_BP_m4	GO:00606	branching	1/727	13/23843	0.331458	0.739133	0.728076	Grb2
GO_BP_m4	GO:00607	negative re	1/727	13/23843	0.331458	0.739133	0.728076	Esr2
GO_BP_m4	GO:00608	establishm	1/727	13/23843	0.331458	0.739133	0.728076	Abcb1b
GO_BP_m4	GO:006091	cardiac cell	1/727	13/23843	0.331458	0.739133	0.728076	Sox17
GO_BP_m4	GO:00611	3'-UTR-me	1/727	13/23843	0.331458	0.739133	0.728076	Zfp36l1
GO_BP_m4	GO:007094	neutrophil	1/727	13/23843	0.331458	0.739133	0.728076	Dnase1
GO_BP_m4	GO:00712	cellular res	1/727	13/23843	0.331458	0.739133	0.728076	Mt1
GO_BP_m4	GO:007221	positive re	1/727	13/23843	0.331458	0.739133	0.728076	Ret
GO_BP_m4	GO:00725	fibroblast	1/727	13/23843	0.331458	0.739133	0.728076	Rps6ka1
GO_BP_m4	GO:00860	AV node c	1/727	13/23843	0.331458	0.739133	0.728076	Cacna1g
GO_BP_m4	GO:009011	cargo load	1/727	13/23843	0.331458	0.739133	0.728076	Sec13
GO_BP_m4	GO:00905	RNA phos	1/727	13/23843	0.331458	0.739133	0.728076	Eri2
GO_BP_m4	GO:009701	cellular res	1/727	13/23843	0.331458	0.739133	0.728076	Mir155
GO_BP_m4	GO:00970	response t	1/727	13/23843	0.331458	0.739133	0.728076	Gata1
GO_BP_m4	GO:009871	L-glutama	1/727	13/23843	0.331458	0.739133	0.728076	Slc1a6
GO_BP_m4	GO:00987	macromol	1/727	13/23843	0.331458	0.739133	0.728076	Abhd13
GO_BP_m4	GO:009887	neurotrans	1/727	13/23843	0.331458	0.739133	0.728076	Snap47
GO_BP_m4	GO:009891	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Dsp
GO_BP_m4	GO:190107	glucosami	1/727	13/23843	0.331458	0.739133	0.728076	Ctbs
GO_BP_m4	GO:19023	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Vdr
GO_BP_m4	GO:19029	positive re	1/727	13/23843	0.331458	0.739133	0.728076	Efna1
GO_BP_m4	GO:190381	positive re	1/727	13/23843	0.331458	0.739133	0.728076	Kcne1
GO_BP_m4	GO:190492	positive re	1/727	13/23843	0.331458	0.739133	0.728076	Tomm7
GO_BP_m4	GO:190504	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Mapk14
GO_BP_m4	GO:190587	regulation	1/727	13/23843	0.331458	0.739133	0.728076	Aurka
GO_BP_m4	GO:20006	negative re	1/727	13/23843	0.331458	0.739133	0.728076	Nedd4l
GO_BP_m4	GO:20012	negative re	1/727	13/23843	0.331458	0.739133	0.728076	Tnn
GO_BP_m4	GO:000317	heart valve	2/727	39/23843	0.334541	0.742544	0.731435	Efna1/Nfat
GO_BP_m4	GO:00093	phospholi	2/727	39/23843	0.334541	0.742544	0.731435	Gdpd3/Lip
GO_BP_m4	GO:003317	calcineurin	2/727	39/23843	0.334541	0.742544	0.731435	Mir1a-2/N
GO_BP_m4	GO:003434	response t	2/727	39/23843	0.334541	0.742544	0.731435	A230050P2
GO_BP_m4	GO:003817	neurotroph	2/727	39/23843	0.334541	0.742544	0.731435	Akt1s1/Spr
GO_BP_m4	GO:00435	regulation	2/727	39/23843	0.334541	0.742544	0.731435	Pik3ip1/Tn
GO_BP_m4	GO:004474	protein tra	2/727	39/23843	0.334541	0.742544	0.731435	Pex1/Tom
GO_BP_m4	GO:19019	toxin trans	2/727	39/23843	0.334541	0.742544	0.731435	Rab40b/Ra
GO_BP_m4	GO:190317	negative re	2/727	39/23843	0.334541	0.742544	0.731435	Cbarp/Rem
GO_BP_m4	GO:190357	negative re	2/727	39/23843	0.334541	0.742544	0.731435	Atf6b/Ppp
GO_BP_m4	GO:00106	negative re	3/727	67/23843	0.3351	0.742909	0.731795	Ager/Dusp
GO_BP_m4	GO:004814	positive re	3/727	67/23843	0.3351	0.742909	0.731795	Ager/Gas6
GO_BP_m4	GO:003104	gene silenc	6/727	155/23843	0.335172	0.742909	0.731795	Cnot6/Mir
GO_BP_m4	GO:00486	positive re	4/727	96/23843	0.336131	0.74469	0.733549	Abcc4/Age
GO_BP_m4	GO:00059	monosacch	9/727	246/23843	0.336679	0.74556	0.734406	Car5a/C1q
GO_BP_m4	GO:00330	muscle cell	8/727	216/23843	0.338604	0.746677	0.735507	Abcc4/Age
GO_BP_m4	GO:00076	locomotor	9/727	247/23843	0.340954	0.746677	0.735507	Cacna1b/D
GO_BP_m4	GO:00460	cAMP meta	4/727	97/23843	0.343078	0.746677	0.735507	Cap2/Gng
GO_BP_m4	GO:00023	mucosal in	3/727	68/23843	0.343487	0.746677	0.735507	Apoa4/AY

GO_BP_m4	GO:000676	vitamin me	3/727	68/23843	0.343487	0.746677	0.735507	Folr1/Kynu
GO_BP_m4	GO:003023	myofibril a	3/727	68/23843	0.343487	0.746677	0.735507	Myom2/Ne
GO_BP_m4	GO:003248	Rab protei	3/727	68/23843	0.343487	0.746677	0.735507	Rab31/Rab
GO_BP_m4	GO:004557	mast cell a	3/727	68/23843	0.343487	0.746677	0.735507	Bcl10/Il13/
GO_BP_m4	GO:006104	negative re	3/727	68/23843	0.343487	0.746677	0.735507	Ager/Dusp
GO_BP_m4	GO:009732	response t	3/727	68/23843	0.343487	0.746677	0.735507	Ctnna1/Mi
GO_BP_m4	GO:014005	organelle l	3/727	68/23843	0.343487	0.746677	0.735507	Rab40b/St
GO_BP_m4	GO:005067	regulation	12/727	340/23843	0.343898	0.746677	0.735507	Ager/Cdh3
GO_BP_m4	GO:000600	glucose me	7/727	187/23843	0.344962	0.746677	0.735507	Car5a/C1q
GO_BP_m4	GO:000178	B cell apop	2/727	40/23843	0.345729	0.746677	0.735507	Bcl10/Irs2
GO_BP_m4	GO:000602	glycosami	2/727	40/23843	0.345729	0.746677	0.735507	Pxylp1/Xylt
GO_BP_m4	GO:001055	regulation	2/727	40/23843	0.345729	0.746677	0.735507	Gata1/Pxyl
GO_BP_m4	GO:001088	regulation	2/727	40/23843	0.345729	0.746677	0.735507	Apoc4/Me
GO_BP_m4	GO:003051	negative re	2/727	40/23843	0.345729	0.746677	0.735507	Rtn4/Rtn4r
GO_BP_m4	GO:003083	negative re	2/727	40/23843	0.345729	0.746677	0.735507	Sptan1/Tm
GO_BP_m4	GO:004337	regulation	2/727	40/23843	0.345729	0.746677	0.735507	Il27/Socs5
GO_BP_m4	GO:006042	positive re	2/727	40/23843	0.345729	0.746677	0.735507	Mapk14/Pi
GO_BP_m4	GO:007083	bicellular ti	2/727	40/23843	0.345729	0.746677	0.735507	Nedd4l/Np
GO_BP_m4	GO:007154	dopaminer	2/727	40/23843	0.345729	0.746677	0.735507	Tiam1/Tsh
GO_BP_m4	GO:009027	regulation	2/727	40/23843	0.345729	0.746677	0.735507	Lgals3/Trp
GO_BP_m4	GO:190027	regulation	2/727	40/23843	0.345729	0.746677	0.735507	Ager/Arc
GO_BP_m4	GO:003502	regulation	5/727	127/23843	0.345758	0.746677	0.735507	Arap2/Itsn
GO_BP_m4	GO:003519	posttransc	5/727	127/23843	0.345758	0.746677	0.735507	Mir155/Mi
GO_BP_m4	GO:005067	epithelial c	14/727	403/23843	0.347287	0.746677	0.735507	Ager/Cdh3
GO_BP_m4	GO:003166	cellular res	8/727	218/23843	0.347767	0.746677	0.735507	5330417C2
GO_BP_m4	GO:002306	signal relea	16/727	466/23843	0.349368	0.746677	0.735507	Cacna1b/C
GO_BP_m4	GO:007265	protein loc	9/727	249/23843	0.349529	0.746677	0.735507	Blzf1/Gak/
GO_BP_m4	GO:000170	formation	4/727	98/23843	0.350029	0.746677	0.735507	Dusp2/Inh
GO_BP_m4	GO:000182	blastocyst	4/727	98/23843	0.350029	0.746677	0.735507	Ncapg2/Rp
GO_BP_m4	GO:003079	regulation	4/727	98/23843	0.350029	0.746677	0.735507	Cap2/Gng
GO_BP_m4	GO:000181	positive re	14/727	404/23843	0.35065	0.746677	0.735507	Ager/Bcl10
GO_BP_m4	GO:005500	cardiac mu	5/727	128/23843	0.351813	0.746677	0.735507	Fhl2/Myom
GO_BP_m4	GO:007145	cellular res	5/727	128/23843	0.351813	0.746677	0.735507	Fndc1/Hp1
GO_BP_m4	GO:000018	inactivatio	1/727	14/23843	0.351854	0.746677	0.735507	Dusp10
GO_BP_m4	GO:000177	immunolo	1/727	14/23843	0.351854	0.746677	0.735507	Lgals3
GO_BP_m4	GO:000282	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Socs5
GO_BP_m4	GO:000315	morphoge	1/727	14/23843	0.351854	0.746677	0.735507	Ccm2
GO_BP_m4	GO:000657	amino-aci	1/727	14/23843	0.351854	0.746677	0.735507	Bhmt
GO_BP_m4	GO:000717	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Socs5
GO_BP_m4	GO:000914	pyrimidine	1/727	14/23843	0.351854	0.746677	0.735507	Nme5
GO_BP_m4	GO:000926	deoxyribo	1/727	14/23843	0.351854	0.746677	0.735507	Rrm1
GO_BP_m4	GO:001080	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Spry2
GO_BP_m4	GO:001089	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Apoa4
GO_BP_m4	GO:001593	coenzyme	1/727	14/23843	0.351854	0.746677	0.735507	Nudt7
GO_BP_m4	GO:001632	neuron ren	1/727	14/23843	0.351854	0.746677	0.735507	Cspg4
GO_BP_m4	GO:001654	protein aut	1/727	14/23843	0.351854	0.746677	0.735507	F12
GO_BP_m4	GO:001908	viral transl	1/727	14/23843	0.351854	0.746677	0.735507	Eif3a
GO_BP_m4	GO:002190	rostrocaud	1/727	14/23843	0.351854	0.746677	0.735507	Sox17

GO_BP_m4	GO:002198	adenohypo	1/727	14/23843	0.351854	0.746677	0.735507	Duox2
GO_BP_m4	GO:003065	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Vdr
GO_BP_m4	GO:003100	response to	1/727	14/23843	0.351854	0.746677	0.735507	Slc8a1
GO_BP_m4	GO:003434	glial cell ap	1/727	14/23843	0.351854	0.746677	0.735507	Gas6
GO_BP_m4	GO:003443	steroid este	1/727	14/23843	0.351854	0.746677	0.735507	Apoa4
GO_BP_m4	GO:003443	sterol ester	1/727	14/23843	0.351854	0.746677	0.735507	Apoa4
GO_BP_m4	GO:003443	cholesterol	1/727	14/23843	0.351854	0.746677	0.735507	Apoa4
GO_BP_m4	GO:003475	iron ion tra	1/727	14/23843	0.351854	0.746677	0.735507	Slc25a37
GO_BP_m4	GO:003572	cellular res	1/727	14/23843	0.351854	0.746677	0.735507	Rela
GO_BP_m4	GO:003627	response to	1/727	14/23843	0.351854	0.746677	0.735507	Slc8a1
GO_BP_m4	GO:004240	cellular bio	1/727	14/23843	0.351854	0.746677	0.735507	Kynu
GO_BP_m4	GO:004312	surfactant l	1/727	14/23843	0.351854	0.746677	0.735507	Sftpa1
GO_BP_m4	GO:004355	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Ppp1r15b
GO_BP_m4	GO:004560	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Ovol2
GO_BP_m4	GO:004579	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Akt1s1
GO_BP_m4	GO:004633	phosphatic	1/727	14/23843	0.351854	0.746677	0.735507	Lipc
GO_BP_m4	GO:004853	mucosal-a	1/727	14/23843	0.351854	0.746677	0.735507	Ret
GO_BP_m4	GO:004854	Peyer's pat	1/727	14/23843	0.351854	0.746677	0.735507	Ret
GO_BP_m4	GO:004867	positive reg	1/727	14/23843	0.351854	0.746677	0.735507	Rtn4
GO_BP_m4	GO:005066	homocyste	1/727	14/23843	0.351854	0.746677	0.735507	Dpep1
GO_BP_m4	GO:005129	centrosom	1/727	14/23843	0.351854	0.746677	0.735507	Aurka
GO_BP_m4	GO:005138	kinetochor	1/727	14/23843	0.351854	0.746677	0.735507	Cenps
GO_BP_m4	GO:006054	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Ripk1
GO_BP_m4	GO:006062	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Yipf5
GO_BP_m4	GO:006115	endothelial	1/727	14/23843	0.351854	0.746677	0.735507	Ccm2
GO_BP_m4	GO:006130	cardiac neu	1/727	14/23843	0.351854	0.746677	0.735507	Folr1
GO_BP_m4	GO:007030	lens fiber c	1/727	14/23843	0.351854	0.746677	0.735507	Bfsp2
GO_BP_m4	GO:007137	cellular res	1/727	14/23843	0.351854	0.746677	0.735507	Inhba
GO_BP_m4	GO:007222	metanephr	1/727	14/23843	0.351854	0.746677	0.735507	Ret
GO_BP_m4	GO:008606	bundle of H	1/727	14/23843	0.351854	0.746677	0.735507	Dsp
GO_BP_m4	GO:009015	establishm	1/727	14/23843	0.351854	0.746677	0.735507	Tomm7
GO_BP_m4	GO:009701	response to	1/727	14/23843	0.351854	0.746677	0.735507	Mir155
GO_BP_m4	GO:009715	GABAergic	1/727	14/23843	0.351854	0.746677	0.735507	Inhba
GO_BP_m4	GO:190107	guanosine-	1/727	14/23843	0.351854	0.746677	0.735507	Nme5
GO_BP_m4	GO:190230	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Nedd4l
GO_BP_m4	GO:190474	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Vdr
GO_BP_m4	GO:190492	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Tomm7
GO_BP_m4	GO:200025	negative re	1/727	14/23843	0.351854	0.746677	0.735507	Esr2
GO_BP_m4	GO:200065	positive reg	1/727	14/23843	0.351854	0.746677	0.735507	Cnksr3
GO_BP_m4	GO:200104	regulation	1/727	14/23843	0.351854	0.746677	0.735507	Ctnna1
GO_BP_m4	GO:000225	organ or tis	3/727	69/23843	0.351864	0.746677	0.735507	Apoa4/AY7
GO_BP_m4	GO:000609	gluconeog	3/727	69/23843	0.351864	0.746677	0.735507	Car5a/C1q
GO_BP_m4	GO:000801	blood circu	16/727	467/23843	0.3525	0.747695	0.736509	C3ar1/Cacn
GO_BP_m4	GO:190303	positive reg	7/727	189/23843	0.354883	0.751271	0.740031	Ager/Bcl10
GO_BP_m4	GO:000018	activation o	2/727	41/23843	0.356856	0.751271	0.740031	Grm1/Map
GO_BP_m4	GO:001010	potassium	2/727	41/23843	0.356856	0.751271	0.740031	Atp1b4/Kcn
GO_BP_m4	GO:001067	negative re	2/727	41/23843	0.356856	0.751271	0.740031	C1qtnf12/S
GO_BP_m4	GO:001076	positive reg	2/727	41/23843	0.356856	0.751271	0.740031	Cnksr3/Ne

GO_BP_m4	GO:003237	regulation	2/727	41/23843	0.356856	0.751271	0.740031	Abcb4/Apc
GO_BP_m4	GO:003237	regulation	2/727	41/23843	0.356856	0.751271	0.740031	Abcb4/Apc
GO_BP_m4	GO:003292	activin rece	2/727	41/23843	0.356856	0.751271	0.740031	Fst/Inhba
GO_BP_m4	GO:004592	positive reg	2/727	41/23843	0.356856	0.751271	0.740031	Apoa4/Irs2
GO_BP_m4	GO:005165	spindle loc	2/727	41/23843	0.356856	0.751271	0.740031	Spdl1/Spry
GO_BP_m4	GO:190007	negative re	2/727	41/23843	0.356856	0.751271	0.740031	Pid1/Rela
GO_BP_m4	GO:003083	regulation	6/727	159/23843	0.356866	0.751271	0.740031	Arhgap18/
GO_BP_m4	GO:005067	regulation	8/727	220/23843	0.356962	0.751271	0.740031	Ager/Btn2a
GO_BP_m4	GO:004874	muscle fibe	3/727	70/23843	0.36023	0.751271	0.740031	Myom2/Sg
GO_BP_m4	GO:190188	negative re	3/727	70/23843	0.36023	0.751271	0.740031	Nav3/Spta
GO_BP_m4	GO:004327	negative re	6/727	160/23843	0.362307	0.751271	0.740031	Cbarp/Hcrt
GO_BP_m4	GO:199077	protein loc	10/727	283/23843	0.362748	0.751271	0.740031	Blzf1/Gak/
GO_BP_m4	GO:000639	mRNA proc	15/727	439/23843	0.36309	0.751271	0.740031	Aurkaip1/E
GO_BP_m4	GO:190353	positive reg	15/727	439/23843	0.36309	0.751271	0.740031	Cacna1b/C
GO_BP_m4	GO:000717	epidermal	4/727	100/23843	0.363933	0.751271	0.740031	Esr2/Kif16b
GO_BP_m4	GO:009772	sperm mot	4/727	100/23843	0.363933	0.751271	0.740031	Catsper2/N
GO_BP_m4	GO:190000	positive reg	4/727	100/23843	0.363933	0.751271	0.740031	Anapc2/Its
GO_BP_m4	GO:001644	posttranscr	5/727	130/23843	0.363938	0.751271	0.740031	Mir155/Mir
GO_BP_m4	GO:000301	circulatory	16/727	471/23843	0.365083	0.751271	0.740031	C3ar1/Cacr
GO_BP_m4	GO:003294	regulation	8/727	222/23843	0.366183	0.751271	0.740031	Ager/Btn2a
GO_BP_m4	GO:190199	regulation	9/727	253/23843	0.366765	0.751271	0.740031	Anp32b/Bt
GO_BP_m4	GO:001692	protein sur	2/727	42/23843	0.367912	0.751271	0.740031	Rela/Ube2i
GO_BP_m4	GO:003157	spindle che	2/727	42/23843	0.367912	0.751271	0.740031	Aurka/Spdl
GO_BP_m4	GO:003276	regulation	2/727	42/23843	0.367912	0.751271	0.740031	Cdh3/Vdr
GO_BP_m4	GO:004246	eye photor	2/727	42/23843	0.367912	0.751271	0.740031	Cabp4/Gna
GO_BP_m4	GO:004250	serine phos	2/727	42/23843	0.367912	0.751271	0.740031	Ifna12/Ret
GO_BP_m4	GO:005091	positive ch	2/727	42/23843	0.367912	0.751271	0.740031	Ager/Lgals
GO_BP_m4	GO:009772	calcineurin	2/727	42/23843	0.367912	0.751271	0.740031	Mir1a-2/N
GO_BP_m4	GO:190372	positive reg	2/727	42/23843	0.367912	0.751271	0.740031	Htr2c/Tnfa
GO_BP_m4	GO:003166	cellular res	7/727	192/23843	0.369813	0.751271	0.740031	5330417C2
GO_BP_m4	GO:000252	acute inflar	5/727	131/23843	0.370004	0.751271	0.740031	Dnase1/F1
GO_BP_m4	GO:003434	response t	5/727	131/23843	0.370004	0.751271	0.740031	A230050P2
GO_BP_m4	GO:000995	anterior/pc	8/727	223/23843	0.370801	0.751271	0.740031	Arc/Aurka/
GO_BP_m4	GO:004326	regulation	4/727	101/23843	0.370881	0.751271	0.740031	Ager/Hcrt/
GO_BP_m4	GO:200037	positive reg	4/727	101/23843	0.370881	0.751271	0.740031	Ager/Grb2/
GO_BP_m4	GO:000007	DNA replic	1/727	15/23843	0.371628	0.751271	0.740031	Hus1
GO_BP_m4	GO:000021	meiotic spi	1/727	15/23843	0.371628	0.751271	0.740031	Aurka
GO_BP_m4	GO:000029	nuclear-tra	1/727	15/23843	0.371628	0.751271	0.740031	Cnot6
GO_BP_m4	GO:000071	resolution	1/727	15/23843	0.371628	0.751271	0.740031	Cenps
GO_BP_m4	GO:000072	DNA doub	1/727	15/23843	0.371628	0.751271	0.740031	Brip1
GO_BP_m4	GO:000197	renal syster	1/727	15/23843	0.371628	0.751271	0.740031	Gas6
GO_BP_m4	GO:000273	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Mapk14
GO_BP_m4	GO:000318	heart valve	1/727	15/23843	0.371628	0.751271	0.740031	Efna1
GO_BP_m4	GO:000612	mitochond	1/727	15/23843	0.371628	0.751271	0.740031	Cycs
GO_BP_m4	GO:000633	nucleosom	1/727	15/23843	0.371628	0.751271	0.740031	Smarcd2
GO_BP_m4	GO:000689	Golgi to va	1/727	15/23843	0.371628	0.751271	0.740031	Gak
GO_BP_m4	GO:000699	nuclear por	1/727	15/23843	0.371628	0.751271	0.740031	Rtn4
GO_BP_m4	GO:000728	sperm axor	1/727	15/23843	0.371628	0.751271	0.740031	Neurl1a

GO_BP_m4	GO:000931	amine cata	1/727	15/23843	0.371628	0.751271	0.740031	Kynu
GO_BP_m4	GO:001064	cell commu	1/727	15/23843	0.371628	0.751271	0.740031	Slc8a1
GO_BP_m4	GO:001093	macrophag	1/727	15/23843	0.371628	0.751271	0.740031	Gas6
GO_BP_m4	GO:001569	magnesiun	1/727	15/23843	0.371628	0.751271	0.740031	Nipa2
GO_BP_m4	GO:001591	peroxisoma	1/727	15/23843	0.371628	0.751271	0.740031	Pex1
GO_BP_m4	GO:001700	antibiotic b	1/727	15/23843	0.371628	0.751271	0.740031	Cyp1a2
GO_BP_m4	GO:001802	peptidyl-ly	1/727	15/23843	0.371628	0.751271	0.740031	Smyd2
GO_BP_m4	GO:001964	aerobic ele	1/727	15/23843	0.371628	0.751271	0.740031	Cycs
GO_BP_m4	GO:001998	translesion	1/727	15/23843	0.371628	0.751271	0.740031	Polk
GO_BP_m4	GO:003015	pancreatic	1/727	15/23843	0.371628	0.751271	0.740031	Vamp8
GO_BP_m4	GO:003032	stabilizatio	1/727	15/23843	0.371628	0.751271	0.740031	Kcnk6
GO_BP_m4	GO:003073	sequesterir	1/727	15/23843	0.371628	0.751271	0.740031	Apoc4
GO_BP_m4	GO:003157	intra-S DN	1/727	15/23843	0.371628	0.751271	0.740031	Hus1
GO_BP_m4	GO:003222	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Htr2c
GO_BP_m4	GO:003323	positive reg	1/727	15/23843	0.371628	0.751271	0.740031	Ube2i
GO_BP_m4	GO:003469	response to	1/727	15/23843	0.371628	0.751271	0.740031	Inhba
GO_BP_m4	GO:004209	interferon-	1/727	15/23843	0.371628	0.751271	0.740031	Il27
GO_BP_m4	GO:004230	negative re	1/727	15/23843	0.371628	0.751271	0.740031	Gas6
GO_BP_m4	GO:004235	vitamin D r	1/727	15/23843	0.371628	0.751271	0.740031	Vdr
GO_BP_m4	GO:004240	cristae forn	1/727	15/23843	0.371628	0.751271	0.740031	Chchd6
GO_BP_m4	GO:004316	ubiquitin-c	1/727	15/23843	0.371628	0.751271	0.740031	Ptpn23
GO_BP_m4	GO:004432	cellular res	1/727	15/23843	0.371628	0.751271	0.740031	Pid1
GO_BP_m4	GO:004482	modulatior	1/727	15/23843	0.371628	0.751271	0.740031	Ythdc2
GO_BP_m4	GO:004529	mRNA cis s	1/727	15/23843	0.371628	0.751271	0.740031	Snrpc
GO_BP_m4	GO:004576	positive reg	1/727	15/23843	0.371628	0.751271	0.740031	Ffar3
GO_BP_m4	GO:004613	pyrimidine	1/727	15/23843	0.371628	0.751271	0.740031	Nme5
GO_BP_m4	GO:004662	positive reg	1/727	15/23843	0.371628	0.751271	0.740031	C1qtnf12
GO_BP_m4	GO:004871	negative re	1/727	15/23843	0.371628	0.751271	0.740031	Dusp10
GO_BP_m4	GO:005093	induction c	1/727	15/23843	0.371628	0.751271	0.740031	Ager
GO_BP_m4	GO:005100	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Apoa4
GO_BP_m4	GO:005138	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Spry2
GO_BP_m4	GO:005193	L-glutamat	1/727	15/23843	0.371628	0.751271	0.740031	Slc1a6
GO_BP_m4	GO:006009	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Ager
GO_BP_m4	GO:006057	intestinal e	1/727	15/23843	0.371628	0.751271	0.740031	Mir7-2
GO_BP_m4	GO:006070	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Oas2
GO_BP_m4	GO:006074	epithelial c	1/727	15/23843	0.371628	0.751271	0.740031	Esr2
GO_BP_m4	GO:006100	negative re	1/727	15/23843	0.371628	0.751271	0.740031	Efna1
GO_BP_m4	GO:006102	eyelid deve	1/727	15/23843	0.371628	0.751271	0.740031	Inhba
GO_BP_m4	GO:006130	cardiac neu	1/727	15/23843	0.371628	0.751271	0.740031	Folr1
GO_BP_m4	GO:007025	mucus secr	1/727	15/23843	0.371628	0.751271	0.740031	Vamp8
GO_BP_m4	GO:007107	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Htr2c
GO_BP_m4	GO:007140	cellular res	1/727	15/23843	0.371628	0.751271	0.740031	Socs5
GO_BP_m4	GO:007163	positive reg	1/727	15/23843	0.371628	0.751271	0.740031	Lum
GO_BP_m4	GO:007210	glomerular	1/727	15/23843	0.371628	0.751271	0.740031	C3ar1
GO_BP_m4	GO:007218	ureter deve	1/727	15/23843	0.371628	0.751271	0.740031	Ret
GO_BP_m4	GO:007241	signal trans	1/727	15/23843	0.371628	0.751271	0.740031	Pidd1
GO_BP_m4	GO:009013	epithelial c	1/727	15/23843	0.371628	0.751271	0.740031	Ctnna1
GO_BP_m4	GO:009705	type B pan	1/727	15/23843	0.371628	0.751271	0.740031	Ager

GO_BP_m4	GO:190045	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Ager
GO_BP_m4	GO:190152	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Tomm7
GO_BP_m4	GO:190172	regulation	1/727	15/23843	0.371628	0.751271	0.740031	C3ar1
GO_BP_m4	GO:19024C	signal trans	1/727	15/23843	0.371628	0.751271	0.740031	Pidd1
GO_BP_m4	GO:19024C	signal trans	1/727	15/23843	0.371628	0.751271	0.740031	Pidd1
GO_BP_m4	GO:190396	negative re	1/727	15/23843	0.371628	0.751271	0.740031	Irs2
GO_BP_m4	GO:190459	negative re	1/727	15/23843	0.371628	0.751271	0.740031	Gas6
GO_BP_m4	GO:19900C	amyloid fib	1/727	15/23843	0.371628	0.751271	0.740031	Ripk1
GO_BP_m4	GO:200047	regulation	1/727	15/23843	0.371628	0.751271	0.740031	Npffr2
GO_BP_m4	GO:200127	positive re	1/727	15/23843	0.371628	0.751271	0.740031	Ffar3
GO_BP_m4	GO:003087	mammary	6/727	162/23843	0.3732	0.75413	0.742848	Irs2/Neurl1
GO_BP_m4	GO:000166	response t	7/727	193/23843	0.374799	0.756443	0.745127	Ager/Fndc
GO_BP_m4	GO:007226	Rho protei	7/727	193/23843	0.374799	0.756443	0.745127	Arap2/Arh
GO_BP_m4	GO:00224C	positive re	8/727	224/23843	0.375424	0.756443	0.745127	Ager/Bcl10
GO_BP_m4	GO:000616	purine nuc	15/727	443/23843	0.37618	0.756443	0.745127	Ak3/Atp5c
GO_BP_m4	GO:001485	striated mu	3/727	72/23843	0.376908	0.756443	0.745127	Mapk14/M
GO_BP_m4	GO:001931	hexose bio	3/727	72/23843	0.376908	0.756443	0.745127	Car5a/C1q
GO_BP_m4	GO:004427	sulfur com	3/727	72/23843	0.376908	0.756443	0.745127	Bhmt/Pdh
GO_BP_m4	GO:19032C	regulation	3/727	72/23843	0.376908	0.756443	0.745127	Nme5/Rip
GO_BP_m4	GO:003004	actin filam	4/727	102/23843	0.377823	0.756443	0.745127	Cacna1g/D
GO_BP_m4	GO:190401	epithelial c	4/727	102/23843	0.377823	0.756443	0.745127	Ager/Gas6
GO_BP_m4	GO:005076	negative re	11/727	318/23843	0.378121	0.756443	0.745127	Cspg4/Ctn
GO_BP_m4	GO:000182	blastocyst	2/727	43/23843	0.378894	0.756443	0.745127	Rpl7l1/Sox
GO_BP_m4	GO:000325	regulation	2/727	43/23843	0.378894	0.756443	0.745127	Cacna1g/N
GO_BP_m4	GO:000604	amino sug	2/727	43/23843	0.378894	0.756443	0.745127	Ctbs/Mdp1
GO_BP_m4	GO:001025	NADH deh	2/727	43/23843	0.378894	0.756443	0.745127	Ndufb10/N
GO_BP_m4	GO:003298	mitochond	2/727	43/23843	0.378894	0.756443	0.745127	Ndufb10/N
GO_BP_m4	GO:00451C	intermedia	2/727	43/23843	0.378894	0.756443	0.745127	Bfsp2/Dsp
GO_BP_m4	GO:004682	regulation	2/727	43/23843	0.378894	0.756443	0.745127	Gas6/Thoc
GO_BP_m4	GO:004885	brain morp	2/727	43/23843	0.378894	0.756443	0.745127	Duox2/Gak
GO_BP_m4	GO:005091	detection c	2/727	43/23843	0.378894	0.756443	0.745127	Olfr850/Ol
GO_BP_m4	GO:009031	negative re	2/727	43/23843	0.378894	0.756443	0.745127	Gas6/Kcne
GO_BP_m4	GO:005095	sensory pe	10/727	287/23843	0.379068	0.756443	0.745127	Mir16-2/M
GO_BP_m4	GO:003134	negative re	7/727	194/23843	0.379789	0.756443	0.745127	Cspg4/Dg
GO_BP_m4	GO:009031	positive re	7/727	194/23843	0.379789	0.756443	0.745127	Erbb2/Gas
GO_BP_m4	GO:001714	negative re	8/727	225/23843	0.380052	0.756443	0.745127	Grb7/Mir1
GO_BP_m4	GO:005109	positive re	8/727	225/23843	0.380052	0.756443	0.745127	Ager/Bcl10
GO_BP_m4	GO:004477	mitotic cell	12/727	350/23843	0.380689	0.756443	0.745127	Anp32b/Bt
GO_BP_m4	GO:004212	regulation	6/727	164/23843	0.384103	0.756443	0.745127	Ager/Btn2
GO_BP_m4	GO:001407	response t	4/727	103/23843	0.384758	0.756443	0.745127	Duox2/Sell
GO_BP_m4	GO:001895	phenol-co	4/727	103/23843	0.384758	0.756443	0.745127	Cdh3/Duo
GO_BP_m4	GO:003051	regulation	4/727	103/23843	0.384758	0.756443	0.745127	Anapc2/Rt
GO_BP_m4	GO:000334	cilium mov	3/727	73/23843	0.385214	0.756443	0.745127	Ccdc114/N
GO_BP_m4	GO:00224C	membrane	3/727	73/23843	0.385214	0.756443	0.745127	Rab40b/St
GO_BP_m4	GO:006042	regulation	3/727	73/23843	0.385214	0.756443	0.745127	Mapk14/M
GO_BP_m4	GO:190137	regulation	3/727	73/23843	0.385214	0.756443	0.745127	Ager/Kcne
GO_BP_m4	GO:00091C	glycoprote	11/727	320/23843	0.38589	0.756443	0.745127	Aga/B3gnt
GO_BP_m4	GO:007132	cellular res	5/727	134/23843	0.388199	0.756443	0.745127	Ager/C1qt

GO_BP_m4	GO:200014	negative re	9/727	258/23843	0.388425	0.756443	0.745127	Ager/Ctnn
GO_BP_m4	GO:001097	negative re	6/727	165/23843	0.389556	0.756443	0.745127	Cspg4/Dg
GO_BP_m4	GO:004851	spermatid	6/727	165/23843	0.389556	0.756443	0.745127	Brip1/Cats
GO_BP_m4	GO:000821	regulation	7/727	196/23843	0.389774	0.756443	0.745127	C3ar1/Cac
GO_BP_m4	GO:00027	negative re	2/727	44/23843	0.389795	0.756443	0.745127	Muc4/Serp
GO_BP_m4	GO:00427	eating beh	2/727	44/23843	0.389795	0.756443	0.745127	Hcrt/Uchl3
GO_BP_m4	GO:00430	regulation	2/727	44/23843	0.389795	0.756443	0.745127	Ager/Il13
GO_BP_m4	GO:00432	positive re	2/727	44/23843	0.389795	0.756443	0.745127	Ager/Kcne
GO_BP_m4	GO:00451	intermedia	2/727	44/23843	0.389795	0.756443	0.745127	Bfsp2/Dsp
GO_BP_m4	GO:00513	positive re	2/727	44/23843	0.389795	0.756443	0.745127	Cdh3/Vdr
GO_BP_m4	GO:00901	positive re	2/727	44/23843	0.389795	0.756443	0.745127	C3ar1/Ret
GO_BP_m4	GO:00902	regulation	2/727	44/23843	0.389795	0.756443	0.745127	Apoa4/Sik
GO_BP_m4	GO:00000	sulfur amin	1/727	16/23843	0.3908	0.756443	0.745127	Bhmt
GO_BP_m4	GO:000171	endoderm	1/727	16/23843	0.3908	0.756443	0.745127	Sox17
GO_BP_m4	GO:000182	histamine	1/727	16/23843	0.3908	0.756443	0.745127	Vamp8
GO_BP_m4	GO:00018	inner cell	1/727	16/23843	0.3908	0.756443	0.745127	Ncapg2
GO_BP_m4	GO:00022	neutrophil	1/727	16/23843	0.3908	0.756443	0.745127	Dnase1
GO_BP_m4	GO:00031	cardiac cor	1/727	16/23843	0.3908	0.756443	0.745127	Mir1a-2
GO_BP_m4	GO:00063	apoptotic	1/727	16/23843	0.3908	0.756443	0.745127	Dnase2b
GO_BP_m4	GO:00063	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Erbb2
GO_BP_m4	GO:000674	ubiquinon	1/727	16/23843	0.3908	0.756443	0.745127	Coq6
GO_BP_m4	GO:00068	Golgi to en	1/727	16/23843	0.3908	0.756443	0.745127	Kif16b
GO_BP_m4	GO:000721	G-protein	1/727	16/23843	0.3908	0.756443	0.745127	Grm1
GO_BP_m4	GO:00072	activation	1/727	16/23843	0.3908	0.756443	0.745127	Traf4
GO_BP_m4	GO:000922	pyrimidine	1/727	16/23843	0.3908	0.756443	0.745127	Nme5
GO_BP_m4	GO:001404	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Ret
GO_BP_m4	GO:00217	striatum d	1/727	16/23843	0.3908	0.756443	0.745127	Inhba
GO_BP_m4	GO:00311	septin ring	1/727	16/23843	0.3908	0.756443	0.745127	12-Sep
GO_BP_m4	GO:00321	septin cyto	1/727	16/23843	0.3908	0.756443	0.745127	12-Sep
GO_BP_m4	GO:00322	positive re	1/727	16/23843	0.3908	0.756443	0.745127	Car2
GO_BP_m4	GO:003231	prostaglan	1/727	16/23843	0.3908	0.756443	0.745127	Abcc4
GO_BP_m4	GO:003251	positive re	1/727	16/23843	0.3908	0.756443	0.745127	Ppp1r15b
GO_BP_m4	GO:00336	positive re	1/727	16/23843	0.3908	0.756443	0.745127	Ret
GO_BP_m4	GO:00343	lipid particl	1/727	16/23843	0.3908	0.756443	0.745127	Ppid
GO_BP_m4	GO:003511	genitalia m	1/727	16/23843	0.3908	0.756443	0.745127	Ror2
GO_BP_m4	GO:00352	ionotropic	1/727	16/23843	0.3908	0.756443	0.745127	Tiam1
GO_BP_m4	GO:003572	response t	1/727	16/23843	0.3908	0.756443	0.745127	Rela
GO_BP_m4	GO:004264	anagen	1/727	16/23843	0.3908	0.756443	0.745127	Mreg
GO_BP_m4	GO:00440	modulatio	1/727	16/23843	0.3908	0.756443	0.745127	Serpinb9
GO_BP_m4	GO:00444	adhesion o	1/727	16/23843	0.3908	0.756443	0.745127	Gas6
GO_BP_m4	GO:004501	negative re	1/727	16/23843	0.3908	0.756443	0.745127	Wdr35
GO_BP_m4	GO:004572	positive re	1/727	16/23843	0.3908	0.756443	0.745127	Irs2
GO_BP_m4	GO:004654	retinal con	1/727	16/23843	0.3908	0.756443	0.745127	Cabp4
GO_BP_m4	GO:004662	gamma-de	1/727	16/23843	0.3908	0.756443	0.745127	Lck
GO_BP_m4	GO:00469	pore comp	1/727	16/23843	0.3908	0.756443	0.745127	Rtn4
GO_BP_m4	GO:004807	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Zeb2
GO_BP_m4	GO:004871	positive re	1/727	16/23843	0.3908	0.756443	0.745127	Ager
GO_BP_m4	GO:004887	chemical h	1/727	16/23843	0.3908	0.756443	0.745127	Sftpa1

GO_BP_m4	GO:005112	positive reg	1/727	16/23843	0.3908	0.756443	0.745127	Wipf2
GO_BP_m4	GO:006004	negative re	1/727	16/23843	0.3908	0.756443	0.745127	Mir1a-2
GO_BP_m4	GO:006057	ventral spir	1/727	16/23843	0.3908	0.756443	0.745127	Nkx6-2
GO_BP_m4	GO:006058	cell fate co	1/727	16/23843	0.3908	0.756443	0.745127	Nkx6-2
GO_BP_m4	GO:007149	cellular res	1/727	16/23843	0.3908	0.756443	0.745127	Socs5
GO_BP_m4	GO:008601	membrane	1/727	16/23843	0.3908	0.756443	0.745127	Kcne1
GO_BP_m4	GO:009709	craniofacia	1/727	16/23843	0.3908	0.756443	0.745127	Fgf4
GO_BP_m4	GO:009728	iron ion im	1/727	16/23843	0.3908	0.756443	0.745127	Slc25a37
GO_BP_m4	GO:190015	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Zfp36l1
GO_BP_m4	GO:190015	positive reg	1/727	16/23843	0.3908	0.756443	0.745127	Zfp36l1
GO_BP_m4	GO:190166	quinone bi	1/727	16/23843	0.3908	0.756443	0.745127	Coq6
GO_BP_m4	GO:190218	positive reg	1/727	16/23843	0.3908	0.756443	0.745127	Zfp72
GO_BP_m4	GO:190271	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Mir155
GO_BP_m4	GO:190353	protein loc	1/727	16/23843	0.3908	0.756443	0.745127	Snap47
GO_BP_m4	GO:190440	negative re	1/727	16/23843	0.3908	0.756443	0.745127	Wdr35
GO_BP_m4	GO:190515	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Ager
GO_BP_m4	GO:200010	negative re	1/727	16/23843	0.3908	0.756443	0.745127	Pid1
GO_BP_m4	GO:200038	regulation	1/727	16/23843	0.3908	0.756443	0.745127	Sox17
GO_BP_m4	GO:200117	negative re	1/727	16/23843	0.3908	0.756443	0.745127	Pid1
GO_BP_m4	GO:000913	nucleoside	4/727	104/23843	0.391684	0.75754	0.746207	Ak3/Nme5
GO_BP_m4	GO:009775	negative re	4/727	104/23843	0.391684	0.75754	0.746207	Cacna1g/H
GO_BP_m4	GO:000697	response t	13/727	385/23843	0.393471	0.76012	0.748748	Agap3/Ap
GO_BP_m4	GO:000989	positive reg	13/727	385/23843	0.393471	0.76012	0.748748	5330417C2
GO_BP_m4	GO:007167	mononucle	3/727	74/23843	0.393495	0.76012	0.748748	C3ar1/Lgal
GO_BP_m4	GO:003410	erythrocyte	5/727	135/23843	0.394259	0.760981	0.749597	Gata1/Hep
GO_BP_m4	GO:009950	synaptic ve	5/727	135/23843	0.394259	0.760981	0.749597	Rims4/Slc1
GO_BP_m4	GO:190304	meiotic cel	7/727	197/23843	0.394769	0.761456	0.750064	Cenps/Aur
GO_BP_m4	GO:001605	Wnt signali	14/727	417/23843	0.394823	0.761456	0.750064	Cdh3/Ddit3
GO_BP_m4	GO:004390	positive reg	6/727	166/23843	0.395007	0.761504	0.750111	Aurka/Inhb
GO_BP_m4	GO:003298	protein-co	7/727	198/23843	0.399763	0.767302	0.755823	Gak/Nav3/
GO_BP_m4	GO:007250	divalent in	16/727	482/23843	0.400026	0.767302	0.755823	Ager/C3ar1
GO_BP_m4	GO:007233	signal trans	5/727	136/23843	0.400313	0.767302	0.755823	Phlda3/Pid
GO_BP_m4	GO:000801	regulation	6/727	167/23843	0.400457	0.767302	0.755823	Cacna1b/C
GO_BP_m4	GO:007123	cellular res	6/727	167/23843	0.400457	0.767302	0.755823	Mir155/Mir
GO_BP_m4	GO:000611	regulation	2/727	45/23843	0.400609	0.767302	0.755823	C1qtnf12/S
GO_BP_m4	GO:000863	intrinsic ap	2/727	45/23843	0.400609	0.767302	0.755823	Nme5/Sfp
GO_BP_m4	GO:001922	neuronal a	2/727	45/23843	0.400609	0.767302	0.755823	Cacna1g/C
GO_BP_m4	GO:003271	negative re	2/727	45/23843	0.400609	0.767302	0.755823	Gas6/Socs5
GO_BP_m4	GO:004208	T-helper 1	2/727	45/23843	0.400609	0.767302	0.755823	Il27/Socs5
GO_BP_m4	GO:004591	negative re	2/727	45/23843	0.400609	0.767302	0.755823	C1qtnf12/S
GO_BP_m4	GO:006195	establishm	2/727	45/23843	0.400609	0.767302	0.755823	Blzf1/Rab3
GO_BP_m4	GO:190262	regulation	2/727	45/23843	0.400609	0.767302	0.755823	C3ar1/Sell
GO_BP_m4	GO:190301	regulation	2/727	45/23843	0.400609	0.767302	0.755823	Gata1/Pxyl
GO_BP_m4	GO:009887	vesicle-me	3/727	75/23843	0.401746	0.767302	0.755823	Blzf1/Rab3
GO_BP_m4	GO:000269	regulation	12/727	356/23843	0.402968	0.767302	0.755823	Ager/Dnas
GO_BP_m4	GO:003433	cell junctio	8/727	230/23843	0.403221	0.767302	0.755823	Ccm2/Cdh
GO_BP_m4	GO:007066	regulation	8/727	230/23843	0.403221	0.767302	0.755823	Ager/Btn2a
GO_BP_m4	GO:004592	positive reg	10/727	293/23843	0.403655	0.767302	0.755823	Anapc2/Er

GO_BP_m4	GO:000815	actin polyn	7/727	199/23843	0.404757	0.767302	0.755823	Arhgap18/
GO_BP_m4	GO:003472	nucleosom	5/727	137/23843	0.406361	0.767302	0.755823	Anp32b/Hp
GO_BP_m4	GO:190595	regulation	5/727	137/23843	0.406361	0.767302	0.755823	Abcb4/Apo
GO_BP_m4	GO:000182	serotonin s	1/727	17/23843	0.409388	0.767302	0.755823	Lgals3
GO_BP_m4	GO:000608	acetyl-CoA	1/727	17/23843	0.409388	0.767302	0.755823	Pdhx
GO_BP_m4	GO:000662	protein tar	1/727	17/23843	0.409388	0.767302	0.755823	Pex1
GO_BP_m4	GO:000674	ubiquinone	1/727	17/23843	0.409388	0.767302	0.755823	Coq6
GO_BP_m4	GO:000696	cellular def	1/727	17/23843	0.409388	0.767302	0.755823	Bcl10
GO_BP_m4	GO:000910	coenzyme	1/727	17/23843	0.409388	0.767302	0.755823	Nudt7
GO_BP_m4	GO:001076	negative re	1/727	17/23843	0.409388	0.767302	0.755823	Nedd4l
GO_BP_m4	GO:001405	gamma-ar	1/727	17/23843	0.409388	0.767302	0.755823	Htr2c
GO_BP_m4	GO:003149	chromatin	1/727	17/23843	0.409388	0.767302	0.755823	Smarcd2
GO_BP_m4	GO:003162	synaptic ve	1/727	17/23843	0.409388	0.767302	0.755823	Snap47
GO_BP_m4	GO:003250	endosome	1/727	17/23843	0.409388	0.767302	0.755823	Rilp
GO_BP_m4	GO:003298	protein-DN	1/727	17/23843	0.409388	0.767302	0.755823	Smarcd2
GO_BP_m4	GO:003315	V(D)J recor	1/727	17/23843	0.409388	0.767302	0.755823	Polb
GO_BP_m4	GO:003319	response to	1/727	17/23843	0.409388	0.767302	0.755823	Apoa4
GO_BP_m4	GO:003606	fucosylatio	1/727	17/23843	0.409388	0.767302	0.755823	Fut1
GO_BP_m4	GO:004207	cell migrati	1/727	17/23843	0.409388	0.767302	0.755823	Sox17
GO_BP_m4	GO:004215	lipoprotein	1/727	17/23843	0.409388	0.767302	0.755823	Abhd13
GO_BP_m4	GO:004265	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Sox17
GO_BP_m4	GO:004267	retinal con	1/727	17/23843	0.409388	0.767302	0.755823	Cabp4
GO_BP_m4	GO:004275	negative re	1/727	17/23843	0.409388	0.767302	0.755823	Sfpq
GO_BP_m4	GO:004357	peroxisoma	1/727	17/23843	0.409388	0.767302	0.755823	Pex1
GO_BP_m4	GO:004432	response to	1/727	17/23843	0.409388	0.767302	0.755823	Pid1
GO_BP_m4	GO:004506	T-helper 2	1/727	17/23843	0.409388	0.767302	0.755823	Socs5
GO_BP_m4	GO:004579	positive reg	1/727	17/23843	0.409388	0.767302	0.755823	Ret
GO_BP_m4	GO:004613	pyrimidine	1/727	17/23843	0.409388	0.767302	0.755823	Nme5
GO_BP_m4	GO:004634	amino suga	1/727	17/23843	0.409388	0.767302	0.755823	Ctbs
GO_BP_m4	GO:004819	vesicle targ	1/727	17/23843	0.409388	0.767302	0.755823	Tmed10
GO_BP_m4	GO:005501	ventricular	1/727	17/23843	0.409388	0.767302	0.755823	Fhl2
GO_BP_m4	GO:006008	membrane	1/727	17/23843	0.409388	0.767302	0.755823	Kctd7
GO_BP_m4	GO:006097	cell migrati	1/727	17/23843	0.409388	0.767302	0.755823	Folr1
GO_BP_m4	GO:007024	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Efna1
GO_BP_m4	GO:007082	heterochro	1/727	17/23843	0.409388	0.767302	0.755823	Hp1bp3
GO_BP_m4	GO:007178	endoplasm	1/727	17/23843	0.409388	0.767302	0.755823	Rtn4
GO_BP_m4	GO:007266	protein loc	1/727	17/23843	0.409388	0.767302	0.755823	Pex1
GO_BP_m4	GO:007266	establishm	1/727	17/23843	0.409388	0.767302	0.755823	Pex1
GO_BP_m4	GO:008601	membrane	1/727	17/23843	0.409388	0.767302	0.755823	Cacna1g
GO_BP_m4	GO:009023	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Aurka
GO_BP_m4	GO:009950	vesicle fusi	1/727	17/23843	0.409388	0.767302	0.755823	Snap47
GO_BP_m4	GO:190217	negative re	1/727	17/23843	0.409388	0.767302	0.755823	Nme5
GO_BP_m4	GO:190225	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Kcne1
GO_BP_m4	GO:190291	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Trip12
GO_BP_m4	GO:190359	positive reg	1/727	17/23843	0.409388	0.767302	0.755823	Tomm7
GO_BP_m4	GO:200000	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Thoc5
GO_BP_m4	GO:200035	positive reg	1/727	17/23843	0.409388	0.767302	0.755823	Ager
GO_BP_m4	GO:200064	regulation	1/727	17/23843	0.409388	0.767302	0.755823	Ptpn23

GO_BP_m4	GO:200077	negative re	1/727	17/23843	0.409388	0.767302	0.755823	Rbl1
GO_BP_m4	GO:000683	dicarboxyli	3/727	76/23843	0.409964	0.767302	0.755823	Folr1/Slc17
GO_BP_m4	GO:004352	positive reg	3/727	76/23843	0.409964	0.767302	0.755823	Ager/Ddit3
GO_BP_m4	GO:005138	response to	3/727	76/23843	0.409964	0.767302	0.755823	Mir155/Sst
GO_BP_m4	GO:005196	positive reg	3/727	76/23843	0.409964	0.767302	0.755823	Flrt1/Lrrc4
GO_BP_m4	GO:190332	negative re	3/727	76/23843	0.409964	0.767302	0.755823	Rela/Rps3/
GO_BP_m4	GO:190395	positive reg	3/727	76/23843	0.409964	0.767302	0.755823	Plagl2/Tom
GO_BP_m4	GO:000317	heart valve	2/727	46/23843	0.411332	0.767302	0.755823	Efna1/Nfat
GO_BP_m4	GO:001488	striated mu	2/727	46/23843	0.411332	0.767302	0.755823	Gtf2ird1/N
GO_BP_m4	GO:002177	olfactory b	2/727	46/23843	0.411332	0.767302	0.755823	Fezf1/Mir2
GO_BP_m4	GO:007054	response to	2/727	46/23843	0.411332	0.767302	0.755823	Ffar3/Pid1
GO_BP_m4	GO:007252	purine-cor	2/727	46/23843	0.411332	0.767302	0.755823	Aox3/Nudt
GO_BP_m4	GO:200122	regulation	2/727	46/23843	0.411332	0.767302	0.755823	Sox14/Tnn
GO_BP_m4	GO:004881	dendrite m	6/727	169/23843	0.411347	0.767302	0.755823	Anapc2/Ar
GO_BP_m4	GO:000095	nuclear-tra	4/727	107/23843	0.412384	0.767302	0.755823	Cnot6/Eif3
GO_BP_m4	GO:000190	leukocyte r	4/727	107/23843	0.412384	0.767302	0.755823	Ager/Dnas
GO_BP_m4	GO:000633	nucleosom	4/727	107/23843	0.412384	0.767302	0.755823	Anp32b/Hp
GO_BP_m4	GO:000834	adult locor	4/727	107/23843	0.412384	0.767302	0.755823	Dmbx1/Ot
GO_BP_m4	GO:004275	regulation	4/727	107/23843	0.412384	0.767302	0.755823	Hcrtr1/Sfp
GO_BP_m4	GO:000268	positive reg	5/727	138/23843	0.412401	0.767302	0.755823	C3ar1/Gas
GO_BP_m4	GO:005068	negative re	5/727	138/23843	0.412401	0.767302	0.755823	Ager/Dusp
GO_BP_m4	GO:190199	negative re	5/727	138/23843	0.412401	0.767302	0.755823	Btn2a2/Hu
GO_BP_m4	GO:000738	pattern spe	15/727	454/23843	0.412459	0.767302	0.755823	Arc/Aurka/
GO_BP_m4	GO:007252	purine-cor	16/727	486/23843	0.412815	0.767667	0.756182	Ak3/Aox3/
GO_BP_m4	GO:004863	positive reg	7/727	201/23843	0.414739	0.770944	0.759411	Anapc2/Ma
GO_BP_m4	GO:001943	aromatic co	15/727	455/23843	0.41577	0.77256	0.761002	Aox3/Cnot
GO_BP_m4	GO:012003	plasma me	16/727	487/23843	0.416017	0.772718	0.761158	Abcc4/Atxr
GO_BP_m4	GO:003004	actin filame	6/727	170/23843	0.416785	0.773844	0.762267	Arhgap18/
GO_BP_m4	GO:000911	ribonucleo	3/727	77/23843	0.418148	0.774325	0.76274	Ak3/Nme5
GO_BP_m4	GO:003310	mitochond	3/727	77/23843	0.418148	0.774325	0.76274	Coa5/Nduf
GO_BP_m4	GO:004324	negative re	3/727	77/23843	0.418148	0.774325	0.76274	Nav3/Sptar
GO_BP_m4	GO:005134	regulation	3/727	77/23843	0.418148	0.774325	0.76274	Cdh3/Il13/
GO_BP_m4	GO:009063	activation c	3/727	77/23843	0.418148	0.774325	0.76274	Rundc1/Tb
GO_BP_m4	GO:190331	negative re	3/727	77/23843	0.418148	0.774325	0.76274	Nbas/Nelfe
GO_BP_m4	GO:190390	regulation	5/727	139/23843	0.418432	0.774325	0.76274	A230050P2
GO_BP_m4	GO:006004	heart contr	7/727	202/23843	0.419726	0.774325	0.76274	Cacna1b/C
GO_BP_m4	GO:001604	lipid catabo	10/727	297/23843	0.420076	0.774325	0.76274	Abhd4/Akr
GO_BP_m4	GO:000636	transcriptio	2/727	47/23843	0.421959	0.774325	0.76274	Nelfe/Recq
GO_BP_m4	GO:003089	positive reg	2/727	47/23843	0.421959	0.774325	0.76274	Il13/Irs2
GO_BP_m4	GO:004521	sarcomere	2/727	47/23843	0.421959	0.774325	0.76274	Myom2/Ne
GO_BP_m4	GO:004562	negative re	2/727	47/23843	0.421959	0.774325	0.76274	Erbb2/Socs
GO_BP_m4	GO:004618	phenol-co	2/727	47/23843	0.421959	0.774325	0.76274	Cdh3/Zeb2
GO_BP_m4	GO:004848	autonomic	2/727	47/23843	0.421959	0.774325	0.76274	Erbb2/Ret
GO_BP_m4	GO:190403	negative re	2/727	47/23843	0.421959	0.774325	0.76274	Gas6/Il13
GO_BP_m4	GO:000632	DNA packa	6/727	171/23843	0.422217	0.774325	0.76274	Anp32b/Er
GO_BP_m4	GO:000720	phospholip	4/727	109/23843	0.426101	0.774325	0.76274	C3ar1/Grm
GO_BP_m4	GO:007162	granulocyt	4/727	109/23843	0.426101	0.774325	0.76274	C3ar1/Lgal
GO_BP_m4	GO:004584	positive reg	3/727	78/23843	0.426294	0.774325	0.76274	Mapk14/Pi

GO_BP_m4	GO:00463€	monosacch	3/727	78/23843	0.426294	0.774325	0.76274	Car5a/C1q
GO_BP_m4	GO:00465€	photorece¦	3/727	78/23843	0.426294	0.774325	0.76274	Cabp4/Gna
GO_BP_m4	GO:00486€	positive re(	3/727	78/23843	0.426294	0.774325	0.76274	Mapk14/Pi
GO_BP_m4	GO:190374	positive re(	3/727	78/23843	0.426294	0.774325	0.76274	Plagl2/Tom
GO_BP_m4	GO:000171	mesoderm	1/727	18/23843	0.427409	0.774325	0.76274	Sox17
GO_BP_m4	GO:00020₇	osteoblast	1/727	18/23843	0.427409	0.774325	0.76274	Tnn
GO_BP_m4	GO:000271	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Muc4
GO_BP_m4	GO:00028₂	positive re(	1/727	18/23843	0.427409	0.774325	0.76274	Socs5
GO_BP_m4	GO:00030€	glomerular	1/727	18/23843	0.427409	0.774325	0.76274	Gas6
GO_BP_m4	GO:00065€	methionine	1/727	18/23843	0.427409	0.774325	0.76274	Bhmt
GO_BP_m4	GO:00066€	glycosphin	1/727	18/23843	0.427409	0.774325	0.76274	A4galt
GO_BP_m4	GO:00068₂	copper ion	1/727	18/23843	0.427409	0.774325	0.76274	Heph
GO_BP_m4	GO:00071€	activation (	1/727	18/23843	0.427409	0.774325	0.76274	Tshr
GO_BP_m4	GO:00099€	dorsal/vent	1/727	18/23843	0.427409	0.774325	0.76274	Vax2
GO_BP_m4	GO:00108€	regulation	1/727	18/23843	0.427409	0.774325	0.76274	Slc8a1
GO_BP_m4	GO:001581	gamma-ar	1/727	18/23843	0.427409	0.774325	0.76274	Htr2c
GO_BP_m4	GO:00160₇	rRNA catal	1/727	18/23843	0.427409	0.774325	0.76274	Ern2
GO_BP_m4	GO:00200₂	hemoglobi	1/727	18/23843	0.427409	0.774325	0.76274	Inhba
GO_BP_m4	GO:002151	ventral spir	1/727	18/23843	0.427409	0.774325	0.76274	Nkx6-2
GO_BP_m4	GO:002201	central ner	1/727	18/23843	0.427409	0.774325	0.76274	Nkx6-2
GO_BP_m4	GO:00301€	protein im¦	1/727	18/23843	0.427409	0.774325	0.76274	Tomm7
GO_BP_m4	GO:00305(	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Gata1
GO_BP_m4	GO:00319€	regulation	1/727	18/23843	0.427409	0.774325	0.76274	Irs2
GO_BP_m4	GO:003227	gonadotro	1/727	18/23843	0.427409	0.774325	0.76274	Inhba
GO_BP_m4	GO:00322€	axon enshe	1/727	18/23843	0.427409	0.774325	0.76274	Nkx6-2
GO_BP_m4	GO:00324€	melanoson	1/727	18/23843	0.427409	0.774325	0.76274	Zeb2
GO_BP_m4	GO:00326€	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Ager
GO_BP_m4	GO:00345(	protein loc	1/727	18/23843	0.427409	0.774325	0.76274	Spdl1
GO_BP_m4	GO:00361€	outer dyne	1/727	18/23843	0.427409	0.774325	0.76274	Ccdc114
GO_BP_m4	GO:00400€	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Spry2
GO_BP_m4	GO:004337	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Socs5
GO_BP_m4	GO:00435€	regulation	1/727	18/23843	0.427409	0.774325	0.76274	Ppp1r15b
GO_BP_m4	GO:00456₂	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Socs5
GO_BP_m4	GO:00459€	negative re	1/727	18/23843	0.427409	0.774325	0.76274	Serpinb9
GO_BP_m4	GO:00463₂	positive re(	1/727	18/23843	0.427409	0.774325	0.76274	Irs2
GO_BP_m4	GO:004817	regulation	1/727	18/23843	0.427409	0.774325	0.76274	Syn1
GO_BP_m4	GO:00509€	detection (	1/727	18/23843	0.427409	0.774325	0.76274	Lxn
GO_BP_m4	GO:00509€	detection (	1/727	18/23843	0.427409	0.774325	0.76274	Lxn
GO_BP_m4	GO:00516(	histamine t	1/727	18/23843	0.427409	0.774325	0.76274	Vamp8
GO_BP_m4	GO:006071	spongiotro	1/727	18/23843	0.427409	0.774325	0.76274	Zfp36l1
GO_BP_m4	GO:006084	venous blo	1/727	18/23843	0.427409	0.774325	0.76274	Ccm2
GO_BP_m4	GO:007087	positive re(	1/727	18/23843	0.427409	0.774325	0.76274	Irs2
GO_BP_m4	GO:190204	positive re(	1/727	18/23843	0.427409	0.774325	0.76274	Pidd1
GO_BP_m4	GO:20002€	regulation	1/727	18/23843	0.427409	0.774325	0.76274	Gas6
GO_BP_m4	GO:00457€	positive re(	7/727	204/23843	0.429687	0.777863	0.766225	Aurka/Ned
GO_BP_m4	GO:00711(	DNA confc	7/727	204/23843	0.429687	0.777863	0.766225	Anp32b/Er
GO_BP_m4	GO:00015€	detection (	2/727	48/23843	0.432487	0.779307	0.767648	Gnat1/Tas2
GO_BP_m4	GO:000227	mast cell a	2/727	48/23843	0.432487	0.779307	0.767648	Il13/Vamp8

GO_BP_m4	GO:00636	transcriptic	2/727	48/23843	0.432487	0.779307	0.767648	Erbb2/Polr
GO_BP_m4	GO:00958	detection c	2/727	48/23843	0.432487	0.779307	0.767648	Cabp4/Gna
GO_BP_m4	GO:00107€	fibroblast r	2/727	48/23843	0.432487	0.779307	0.767648	Ager/Slc8a
GO_BP_m4	GO:00219€	olfactory lc	2/727	48/23843	0.432487	0.779307	0.767648	Fezf1/Mir2
GO_BP_m4	GO:00425€	neuron ma	2/727	48/23843	0.432487	0.779307	0.767648	Cspg4/Ret
GO_BP_m4	GO:00433(	regulation	2/727	48/23843	0.432487	0.779307	0.767648	Il13/Vamp8
GO_BP_m4	GO:00433(	mast cell d	2/727	48/23843	0.432487	0.779307	0.767648	Il13/Vamp8
GO_BP_m4	GO:00519€	positive re(	2/727	48/23843	0.432487	0.779307	0.767648	Htr2c/Rtn4
GO_BP_m4	GO:00300(	regionaliza	12/727	364/23843	0.432759	0.779307	0.767648	Arc/Aurka/
GO_BP_m4	GO:00268	regulation	4/727	110/23843	0.43293	0.779307	0.767648	C3ar1/Gas(
GO_BP_m4	GO:004864	negative re	4/727	110/23843	0.43293	0.779307	0.767648	Dusp10/Mi
GO_BP_m4	GO:00508€	negative re	4/727	110/23843	0.43293	0.779307	0.767648	Btn2a2/Erb
GO_BP_m4	GO:00512€	protein de|	4/727	110/23843	0.43293	0.779307	0.767648	Gak/Nav3/
GO_BP_m4	GO:00071€	adenylate (	3/727	79/23843	0.4344	0.780484	0.768807	Ffar3/Grm1
GO_BP_m4	GO:00341(	regulation	3/727	79/23843	0.4344	0.780484	0.768807	Ager/Car2/
GO_BP_m4	GO:00485ž	positive re(	3/727	79/23843	0.4344	0.780484	0.768807	Ppid/Ythdc
GO_BP_m4	GO:00702€	actin-medi	3/727	79/23843	0.4344	0.780484	0.768807	Cacna1g/D
GO_BP_m4	GO:19018€	positive re(	3/727	79/23843	0.4344	0.780484	0.768807	Mapk14/Pi
GO_BP_m4	GO:000301	heart proce	7/727	205/23843	0.43466	0.780658	0.768979	Cacna1b/C
GO_BP_m4	GO:19030€	regulation	9/727	269/23843	0.436206	0.781402	0.769712	Ager/Bcl10
GO_BP_m4	GO:00714€	cellular res	5/727	142/23843	0.436457	0.781402	0.769712	Cyp1a2/Cy
GO_BP_m4	GO:00303€	positive re(	16/727	494/23843	0.438448	0.781402	0.769712	Ager/C3ar1
GO_BP_m4	GO:00091€	purine ribo	14/727	430/23843	0.439439	0.781402	0.769712	Ak3/Atp5c1
GO_BP_m4	GO:00086€	intrinsic ap	4/727	111/23843	0.439736	0.781402	0.769712	Phlda3/Pol
GO_BP_m4	GO:00723ž	monocarb(	4/727	111/23843	0.439736	0.781402	0.769712	Akr1d1/Cy|
GO_BP_m4	GO:00072(	positive re(	10/727	302/23843	0.440585	0.781402	0.769712	C3ar1/Cacr
GO_BP_m4	GO:00091€	cyclic nucle	5/727	143/23843	0.442438	0.781402	0.769712	Cap2/Gng7
GO_BP_m4	GO:001067	regulation	5/727	143/23843	0.442438	0.781402	0.769712	C1qtnf12/I
GO_BP_m4	GO:000227	myeloid ce	3/727	80/23843	0.442463	0.781402	0.769712	Dnase1/Il1
GO_BP_m4	GO:00319€	response t(	3/727	80/23843	0.442463	0.781402	0.769712	Mir155/Sst
GO_BP_m4	GO:00703(	cellular res	3/727	80/23843	0.442463	0.781402	0.769712	Rela/Ripk1/
GO_BP_m4	GO:000244	mast cell m	2/727	49/23843	0.442911	0.781402	0.769712	Il13/Vamp8
GO_BP_m4	GO:001714	stem cell d	2/727	49/23843	0.442911	0.781402	0.769712	Sox17/Tho
GO_BP_m4	GO:00308€	regulation	2/727	49/23843	0.442911	0.781402	0.769712	Sptan1/Tm
GO_BP_m4	GO:003111	regulation	2/727	49/23843	0.442911	0.781402	0.769712	Nav3/Rps3
GO_BP_m4	GO:00330(	regulation	2/727	49/23843	0.442911	0.781402	0.769712	Il13/Vamp8
GO_BP_m4	GO:00440€	regulation	2/727	49/23843	0.442911	0.781402	0.769712	Apoa4/Var
GO_BP_m4	GO:004614	pigment bi	2/727	49/23843	0.442911	0.781402	0.769712	Cdh3/Zeb2
GO_BP_m4	GO:005077	positive re(	2/727	49/23843	0.442911	0.781402	0.769712	Anapc2/Tia
GO_BP_m4	GO:00550ž	positive re(	2/727	49/23843	0.442911	0.781402	0.769712	Mapk14/Pi
GO_BP_m4	GO:007097	protein loc	2/727	49/23843	0.442911	0.781402	0.769712	Folr1/Rtn4
GO_BP_m4	GO:190204	regulation	2/727	49/23843	0.442911	0.781402	0.769712	Lgals3/Pidc
GO_BP_m4	GO:200067	regulation	2/727	49/23843	0.442911	0.781402	0.769712	Ddit3/Gata
GO_BP_m4	GO:00439(	regulation	13/727	399/23843	0.443426	0.781402	0.769712	A230050P2
GO_BP_m4	GO:00016€	gastric acic	1/727	19/23843	0.444881	0.781402	0.769712	Slc9a4
GO_BP_m4	GO:000271	negative re	1/727	19/23843	0.444881	0.781402	0.769712	Serpinb9
GO_BP_m4	GO:00065ž	arginine m	1/727	19/23843	0.444881	0.781402	0.769712	Fah
GO_BP_m4	GO:00069(	pinocytosis	1/727	19/23843	0.444881	0.781402	0.769712	Ehd4

GO_BP_m4	GO:00082	androgen r	1/727	19/23843	0.444881	0.781402	0.769712	Akr1d1
GO_BP_m4	GO:00101	regulation	1/727	19/23843	0.444881	0.781402	0.769712	Il13
GO_BP_m4	GO:00104	response t	1/727	19/23843	0.444881	0.781402	0.769712	Kcne1
GO_BP_m4	GO:00106	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Fndc1
GO_BP_m4	GO:00106	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Fndc1
GO_BP_m4	GO:00160	synaptic ve	1/727	19/23843	0.444881	0.781402	0.769712	Snap47
GO_BP_m4	GO:00302	platelet for	1/727	19/23843	0.444881	0.781402	0.769712	Gata1
GO_BP_m4	GO:00323	intracellula	1/727	19/23843	0.444881	0.781402	0.769712	Plekha8
GO_BP_m4	GO:00328	regulation	1/727	19/23843	0.444881	0.781402	0.769712	Gas6
GO_BP_m4	GO:00336	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Rtn4
GO_BP_m4	GO:003361	mitochond	1/727	19/23843	0.444881	0.781402	0.769712	Coa5
GO_BP_m4	GO:00339	cytoplasmi	1/727	19/23843	0.444881	0.781402	0.769712	Cnot6
GO_BP_m4	GO:00354	cargo load	1/727	19/23843	0.444881	0.781402	0.769712	Sec13
GO_BP_m4	GO:00354	SNARE cor	1/727	19/23843	0.444881	0.781402	0.769712	Vamp8
GO_BP_m4	GO:00442	cellular pol	1/727	19/23843	0.444881	0.781402	0.769712	Manba
GO_BP_m4	GO:00456	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Socs5
GO_BP_m4	GO:00468	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Gas6
GO_BP_m4	GO:00487	pigment gr	1/727	19/23843	0.444881	0.781402	0.769712	Zeb2
GO_BP_m4	GO:00507	negative re	1/727	19/23843	0.444881	0.781402	0.769712	Efna1
GO_BP_m4	GO:00508	neuromusc	1/727	19/23843	0.444881	0.781402	0.769712	Slurp1
GO_BP_m4	GO:00513	kinetochor	1/727	19/23843	0.444881	0.781402	0.769712	Cenps
GO_BP_m4	GO:00550	cardiac my	1/727	19/23843	0.444881	0.781402	0.769712	Myom2
GO_BP_m4	GO:00601	regulation	1/727	19/23843	0.444881	0.781402	0.769712	Itsn1
GO_BP_m4	GO:00602	cilium mov	1/727	19/23843	0.444881	0.781402	0.769712	Tekt5
GO_BP_m4	GO:00604	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Vamp8
GO_BP_m4	GO:00725	seminiferou	1/727	19/23843	0.444881	0.781402	0.769712	Brip1
GO_BP_m4	GO:00972	renal filtrat	1/727	19/23843	0.444881	0.781402	0.769712	Gas6
GO_BP_m4	GO:009724	amyloid-b	1/727	19/23843	0.444881	0.781402	0.769712	Mme
GO_BP_m4	GO:190001	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Mir324
GO_BP_m4	GO:19023	positive re	1/727	19/23843	0.444881	0.781402	0.769712	Cnksr3
GO_BP_m4	GO:20001	regulation	1/727	19/23843	0.444881	0.781402	0.769712	Pim1
GO_BP_m4	GO:00022	T cell activ	4/727	112/23843	0.446518	0.783414	0.771694	Ifna12/Il27
GO_BP_m4	GO:00080	tRNA proc	4/727	112/23843	0.446518	0.783414	0.771694	Dus2/Fars2
GO_BP_m4	GO:00343	adherens ju	4/727	112/23843	0.446518	0.783414	0.771694	Cdh24/Cd
GO_BP_m4	GO:00550	striated mu	6/727	176/23843	0.449257	0.787715	0.775931	Fhl2/Myom
GO_BP_m4	GO:005164	vesicle loca	7/727	208/23843	0.449539	0.787715	0.775931	Cdh3/Mre
GO_BP_m4	GO:000721	glutamate	3/727	81/23843	0.450481	0.787715	0.775931	Arc/Grm1/
GO_BP_m4	GO:001574	organopho	3/727	81/23843	0.450481	0.787715	0.775931	Abcb4/Ap
GO_BP_m4	GO:00480	regulation	3/727	81/23843	0.450481	0.787715	0.775931	Rbfox3/Srs
GO_BP_m4	GO:00701	regulation	3/727	81/23843	0.450481	0.787715	0.775931	Gas6/Gata
GO_BP_m4	GO:19004	regulation	3/727	81/23843	0.450481	0.787715	0.775931	Nme5/Rip
GO_BP_m4	GO:00096	response t	11/727	337/23843	0.452132	0.787715	0.775931	Apoa4/Htr
GO_BP_m4	GO:00420	wound hea	11/727	337/23843	0.452132	0.787715	0.775931	Ager/Dusp
GO_BP_m4	GO:00508	regulation	11/727	337/23843	0.452132	0.787715	0.775931	F12/F5/Ga
GO_BP_m4	GO:004001	negative re	10/727	305/23843	0.45286	0.787715	0.775931	Ager/Ctnn
GO_BP_m4	GO:00028	nuclear-tra	2/727	50/23843	0.453228	0.787715	0.775931	Cnot6/Zfp
GO_BP_m4	GO:00068	Golgi to pl	2/727	50/23843	0.453228	0.787715	0.775931	Blzf1/Rab3
GO_BP_m4	GO:001401	negative re	2/727	50/23843	0.453228	0.787715	0.775931	Dusp10/N

GO_BP_m4	GO:003112	mRNA 3'-	2/727	50/23843	0.453228	0.787715	0.775931	Nelfe/Zfp3
GO_BP_m4	GO:003235	regulation	2/727	50/23843	0.453228	0.787715	0.775931	Ffar3/Vdr
GO_BP_m4	GO:003362	cell adhesi	2/727	50/23843	0.453228	0.787715	0.775931	Efna1/Ret
GO_BP_m4	GO:004298	amyloid pr	2/727	50/23843	0.453228	0.787715	0.775931	Efna1/Tme
GO_BP_m4	GO:004361	regulation	2/727	50/23843	0.453228	0.787715	0.775931	Atf6b/Ddit
GO_BP_m4	GO:190161	organic hy	2/727	50/23843	0.453228	0.787715	0.775931	Akr1d1/Cy
GO_BP_m4	GO:000189	embryonic	4/727	113/23843	0.453275	0.787715	0.775931	Grb2/Ovol
GO_BP_m4	GO:003315	regulation	9/727	273/23843	0.453521	0.787715	0.775931	Erbb2/Gas
GO_BP_m4	GO:003424	negative re	8/727	241/23843	0.454081	0.787715	0.775931	Grb7/Mir1
GO_BP_m4	GO:000716	establishm	7/727	209/23843	0.454484	0.787715	0.775931	Cap2/Ctnn
GO_BP_m4	GO:000840	gonad dev	7/727	209/23843	0.454484	0.787715	0.775931	Brip1/Esr2/
GO_BP_m4	GO:005148	regulation	11/727	338/23843	0.456018	0.787715	0.775931	C3ar1/Cac
GO_BP_m4	GO:004427	cellular nitr	14/727	435/23843	0.456594	0.787715	0.775931	Aox3/Cnot
GO_BP_m4	GO:003020	glycosami	3/727	82/23843	0.458451	0.787715	0.775931	Pxylp1/Sp
GO_BP_m4	GO:003264	regulation	3/727	82/23843	0.458451	0.787715	0.775931	Ager/Ffar3
GO_BP_m4	GO:007233	intrinsic ap	3/727	82/23843	0.458451	0.787715	0.775931	Phlda3/Zm
GO_BP_m4	GO:000806	regulation	6/727	178/23843	0.459999	0.787715	0.775931	Arhgap18/
GO_BP_m4	GO:005079	regulation	6/727	178/23843	0.459999	0.787715	0.775931	A230050P
GO_BP_m4	GO:006500	protein-D	6/727	178/23843	0.459999	0.787715	0.775931	Anp32b/C
GO_BP_m4	GO:000307	regulation	4/727	114/23843	0.460004	0.787715	0.775931	Gas6/Kcnk
GO_BP_m4	GO:004217	negative re	4/727	114/23843	0.460004	0.787715	0.775931	Efna1/Pdcl
GO_BP_m4	GO:009917	postsynap	4/727	114/23843	0.460004	0.787715	0.775931	Arc/Efna1/
GO_BP_m4	GO:002261	gland mor	5/727	146/23843	0.460287	0.787715	0.775931	Duox2/Esr
GO_BP_m4	GO:004666	female sex	5/727	146/23843	0.460287	0.787715	0.775931	Esr2/Fanca
GO_BP_m4	GO:006201	regulation	13/727	404/23843	0.461241	0.787715	0.775931	Acmsd/Ap
GO_BP_m4	GO:000028	nuclear-tr	1/727	20/23843	0.461821	0.787715	0.775931	Cnot6
GO_BP_m4	GO:000194	lymphangi	1/727	20/23843	0.461821	0.787715	0.775931	Nfatc1
GO_BP_m4	GO:000237	cytokine s	1/727	20/23843	0.461821	0.787715	0.775931	Mapk14
GO_BP_m4	GO:000911	vitamin bi	1/727	20/23843	0.461821	0.787715	0.775931	Vdr
GO_BP_m4	GO:001056	positive re	1/727	20/23843	0.461821	0.787715	0.775931	Pxylp1
GO_BP_m4	GO:001480	release of	1/727	20/23843	0.461821	0.787715	0.775931	Slc8a1
GO_BP_m4	GO:001573	prostaglan	1/727	20/23843	0.461821	0.787715	0.775931	Abcc4
GO_BP_m4	GO:001648	peptide ho	1/727	20/23843	0.461821	0.787715	0.775931	Ece2
GO_BP_m4	GO:002240	cell cycle p	1/727	20/23843	0.461821	0.787715	0.775931	Nfatc1
GO_BP_m4	GO:003054	female ger	1/727	20/23843	0.461821	0.787715	0.775931	Esr2
GO_BP_m4	GO:003164	negative re	1/727	20/23843	0.461821	0.787715	0.775931	Hcrt
GO_BP_m4	GO:003214	activation	1/727	20/23843	0.461821	0.787715	0.775931	Gas6
GO_BP_m4	GO:003233	positive re	1/727	20/23843	0.461821	0.787715	0.775931	Rela
GO_BP_m4	GO:003268	negative re	1/727	20/23843	0.461821	0.787715	0.775931	Socs5
GO_BP_m4	GO:003359	regulation	1/727	20/23843	0.461821	0.787715	0.775931	Rtn4
GO_BP_m4	GO:003386	nucleoside	1/727	20/23843	0.461821	0.787715	0.775931	Nudt7
GO_BP_m4	GO:003387	ribonucleo	1/727	20/23843	0.461821	0.787715	0.775931	Nudt7
GO_BP_m4	GO:003403	purine nuc	1/727	20/23843	0.461821	0.787715	0.775931	Nudt7
GO_BP_m4	GO:003538	thioester b	1/727	20/23843	0.461821	0.787715	0.775931	Pdhx
GO_BP_m4	GO:003634	platelet m	1/727	20/23843	0.461821	0.787715	0.775931	Gata1
GO_BP_m4	GO:004273	fibrinolysis	1/727	20/23843	0.461821	0.787715	0.775931	F12
GO_BP_m4	GO:004434	fibroblast	1/727	20/23843	0.461821	0.787715	0.775931	Gas6
GO_BP_m4	GO:004855	embryonic	1/727	20/23843	0.461821	0.787715	0.775931	Ovol2

GO_BP_m4	GO:00509	detection c	1/727	20/23843	0.461821	0.787715	0.775931	Gnat1
GO_BP_m4	GO:00509	detection c	1/727	20/23843	0.461821	0.787715	0.775931	Gnat1
GO_BP_m4	GO:005134	positive re	1/727	20/23843	0.461821	0.787715	0.775931	Tshr
GO_BP_m4	GO:00550	response t	1/727	20/23843	0.461821	0.787715	0.775931	Socs5
GO_BP_m4	GO:006132	cell prolifer	1/727	20/23843	0.461821	0.787715	0.775931	Pim1
GO_BP_m4	GO:007161	acyl-CoA	1/727	20/23843	0.461821	0.787715	0.775931	Pdhx
GO_BP_m4	GO:00955	acetylcholi	1/727	20/23843	0.461821	0.787715	0.775931	Ly6g6d
GO_BP_m4	GO:00987	response t	1/727	20/23843	0.461821	0.787715	0.775931	Tomm7
GO_BP_m4	GO:00996	protein tra	1/727	20/23843	0.461821	0.787715	0.775931	Snap47
GO_BP_m4	GO:00996	neurotrans	1/727	20/23843	0.461821	0.787715	0.775931	Snap47
GO_BP_m4	GO:19001	regulation	1/727	20/23843	0.461821	0.787715	0.775931	Atf6b
GO_BP_m4	GO:19012	negative re	1/727	20/23843	0.461821	0.787715	0.775931	Rela
GO_BP_m4	GO:19038	signal trans	1/727	20/23843	0.461821	0.787715	0.775931	Ly6g6d
GO_BP_m4	GO:190514	response t	1/727	20/23843	0.461821	0.787715	0.775931	Ly6g6d
GO_BP_m4	GO:190514	cellular res	1/727	20/23843	0.461821	0.787715	0.775931	Ly6g6d
GO_BP_m4	GO:20010	regulation	1/727	20/23843	0.461821	0.787715	0.775931	Fgf4
GO_BP_m4	GO:00017	establishm	2/727	51/23843	0.463435	0.787954	0.776166	Astn2/Ror
GO_BP_m4	GO:00640	mRNA exp	2/727	51/23843	0.463435	0.787954	0.776166	Srsf10/Tho
GO_BP_m4	GO:003361	membrane	2/727	51/23843	0.463435	0.787954	0.776166	Adam19/R
GO_BP_m4	GO:004577	positive re	2/727	51/23843	0.463435	0.787954	0.776166	Anapc2/Tr
GO_BP_m4	GO:00458	negative re	2/727	51/23843	0.463435	0.787954	0.776166	Dusp10/Se
GO_BP_m4	GO:005091	sensory pe	2/727	51/23843	0.463435	0.787954	0.776166	Gnat1/Tas
GO_BP_m4	GO:00650	intracellula	2/727	51/23843	0.463435	0.787954	0.776166	Pex1/Tom
GO_BP_m4	GO:00714	mRNA-cor	2/727	51/23843	0.463435	0.787954	0.776166	Srsf10/Tho
GO_BP_m4	GO:190161	organic hy	14/727	437/23843	0.463444	0.787954	0.776166	Abhd4/Ak
GO_BP_m4	GO:00608	regulation	7/727	211/23843	0.464345	0.788924	0.777121	Ddit3/Folr1
GO_BP_m4	GO:00718	protein-D	7/727	211/23843	0.464345	0.788924	0.777121	Anp32b/C
GO_BP_m4	GO:00432	response t	6/727	179/23843	0.465351	0.790073	0.778253	Mir155/Mi
GO_BP_m4	GO:00975	myeloid le	6/727	179/23843	0.465351	0.790073	0.778253	C3ar1/Lgal
GO_BP_m4	GO:00075	cell aging	5/727	147/23843	0.4662	0.790963	0.779129	Mapk14/M
GO_BP_m4	GO:00346	cellular res	3/727	83/23843	0.466372	0.790963	0.779129	Atf6b/Ddit
GO_BP_m4	GO:190187	regulation	3/727	83/23843	0.466372	0.790963	0.779129	Nav3/Spta
GO_BP_m4	GO:00018	liver devel	4/727	115/23843	0.466704	0.790966	0.779132	Aurka/Gak
GO_BP_m4	GO:001402	primary ne	4/727	115/23843	0.466704	0.790966	0.779132	Bcl10/Folr1
GO_BP_m4	GO:00303	negative re	8/727	244/23843	0.467843	0.792615	0.780757	Ager/Dpe
GO_BP_m4	GO:00100	response t	14/727	439/23843	0.470284	0.795853	0.783947	Apoa4/Aq
GO_BP_m4	GO:00519	negative re	11/727	342/23843	0.471523	0.795853	0.783947	Cspg4/Ctn
GO_BP_m4	GO:00063	chromatin	5/727	148/23843	0.472094	0.795853	0.783947	Anp32b/H
GO_BP_m4	GO:00513	regulation	5/727	148/23843	0.472094	0.795853	0.783947	Aurka/Fgf4
GO_BP_m4	GO:00156	ammonium	4/727	116/23843	0.473375	0.795853	0.783947	Htr2c/Lgal
GO_BP_m4	GO:00071	establishm	2/727	52/23843	0.473528	0.795853	0.783947	Astn2/Ror
GO_BP_m4	GO:00308	cortical cyt	2/727	52/23843	0.473528	0.795853	0.783947	Synpo/Wip
GO_BP_m4	GO:00433	negative re	2/727	52/23843	0.473528	0.795853	0.783947	Ddit3/Gata
GO_BP_m4	GO:00488	genitalia d	2/727	52/23843	0.473528	0.795853	0.783947	Esr2/Ror2
GO_BP_m4	GO:00507	negative re	2/727	52/23843	0.473528	0.795853	0.783947	Fam72a/Sc
GO_BP_m4	GO:005091	detection c	2/727	52/23843	0.473528	0.795853	0.783947	Gnat1/Tas
GO_BP_m4	GO:005507	sodium io	2/727	52/23843	0.473528	0.795853	0.783947	Atp1b4/Slc
GO_BP_m4	GO:00718	protein tra	2/727	52/23843	0.473528	0.795853	0.783947	Pex1/Tom

GO_BP_m4	GO:000301	muscle sys	12/727	375/23843	0.473596	0.795853	0.783947	Cacna1g/D
GO_BP_m4	GO:000925	ribonucleo	14/727	440/23843	0.473699	0.795853	0.783947	Ak3/Atp5c
GO_BP_m4	GO:004513	developme	7/727	213/23843	0.474164	0.795853	0.783947	Brip1/Esr2/
GO_BP_m4	GO:190331	regulation	7/727	213/23843	0.474164	0.795853	0.783947	Nbas/Nelf
GO_BP_m4	GO:003571	CD4-positi	3/727	84/23843	0.474241	0.795853	0.783947	Ager/Il27/
GO_BP_m4	GO:014002	exocytic pr	3/727	84/23843	0.474241	0.795853	0.783947	Rab40b/Sn
GO_BP_m4	GO:190101	regulation	3/727	84/23843	0.474241	0.795853	0.783947	Cbarp/Kcn
GO_BP_m4	GO:014001	meiotic nu	6/727	181/23843	0.476013	0.795853	0.783947	Cenps/Aur
GO_BP_m4	GO:004670	heterocycl	14/727	441/23843	0.477111	0.795853	0.783947	Aox3/Cnot
GO_BP_m4	GO:000224	hematopoi	5/727	149/23843	0.477966	0.795853	0.783947	Fst/Inhba/
GO_BP_m4	GO:004866	regulation	5/727	149/23843	0.477966	0.795853	0.783947	Abcc4/Age
GO_BP_m4	GO:190316	regulation	5/727	149/23843	0.477966	0.795853	0.783947	Cbarp/Il13/
GO_BP_m4	GO:190547	regulation	5/727	149/23843	0.477966	0.795853	0.783947	Erbb2/Kcn
GO_BP_m4	GO:000042	mitophagy	1/727	21/23843	0.478244	0.795853	0.783947	Tomm7
GO_BP_m4	GO:000046	maturation	1/727	21/23843	0.478244	0.795853	0.783947	Eri2
GO_BP_m4	GO:001066	epithelial s	1/727	21/23843	0.478244	0.795853	0.783947	Ldb2
GO_BP_m4	GO:001086	regulation	1/727	21/23843	0.478244	0.795853	0.783947	Sik1
GO_BP_m4	GO:003116	rRNA meth	1/727	21/23843	0.478244	0.795853	0.783947	Mrm2
GO_BP_m4	GO:003129	retinal gan	1/727	21/23843	0.478244	0.795853	0.783947	Rpl24
GO_BP_m4	GO:003157	mitotic G1	1/727	21/23843	0.478244	0.795853	0.783947	Pidd1
GO_BP_m4	GO:003204	mitochond	1/727	21/23843	0.478244	0.795853	0.783947	Pid1
GO_BP_m4	GO:003314	positive re	1/727	21/23843	0.478244	0.795853	0.783947	Ube2i
GO_BP_m4	GO:003438	low-densit	1/727	21/23843	0.478244	0.795853	0.783947	Lipc
GO_BP_m4	GO:003630	lymph vess	1/727	21/23843	0.478244	0.795853	0.783947	Nfatc1
GO_BP_m4	GO:004205	regulation	1/727	21/23843	0.478244	0.795853	0.783947	Htr2c
GO_BP_m4	GO:004245	purine nuc	1/727	21/23843	0.478244	0.795853	0.783947	Nme5
GO_BP_m4	GO:004315	entrainme	1/727	21/23843	0.478244	0.795853	0.783947	Sik1
GO_BP_m4	GO:004427	sulfur com	1/727	21/23843	0.478244	0.795853	0.783947	Nudt7
GO_BP_m4	GO:004572	positive re	1/727	21/23843	0.478244	0.795853	0.783947	Apoa4
GO_BP_m4	GO:004612	purine ribo	1/727	21/23843	0.478244	0.795853	0.783947	Nme5
GO_BP_m4	GO:004632	negative re	1/727	21/23843	0.478244	0.795853	0.783947	Pid1
GO_BP_m4	GO:004663	negative re	1/727	21/23843	0.478244	0.795853	0.783947	Socs5
GO_BP_m4	GO:004824	eosinophil	1/727	21/23843	0.478244	0.795853	0.783947	Lgals3
GO_BP_m4	GO:007211	cell prolife	1/727	21/23843	0.478244	0.795853	0.783947	C3ar1
GO_BP_m4	GO:007264	interferon-	1/727	21/23843	0.478244	0.795853	0.783947	Mir155
GO_BP_m4	GO:190152	positive re	1/727	21/23843	0.478244	0.795853	0.783947	Rela
GO_BP_m4	GO:190174	positive re	1/727	21/23843	0.478244	0.795853	0.783947	Mapk14
GO_BP_m4	GO:190351	release of	1/727	21/23843	0.478244	0.795853	0.783947	Slc8a1
GO_BP_m4	GO:004578	negative re	14/727	442/23843	0.48052	0.79818	0.786239	Aurka/Btn
GO_BP_m4	GO:003053	adult beha	6/727	182/23843	0.48132	0.79818	0.786239	Dmbx1/Ht
GO_BP_m4	GO:004390	negative re	6/727	182/23843	0.48132	0.79818	0.786239	A230050P
GO_BP_m4	GO:000236	cytokine p	3/727	85/23843	0.482056	0.79818	0.786239	Ffar3/Gas6
GO_BP_m4	GO:000270	positive re	3/727	85/23843	0.482056	0.79818	0.786239	Ffar3/Il13/
GO_BP_m4	GO:001607	synaptic ve	3/727	85/23843	0.482056	0.79818	0.786239	Rims4/Sna
GO_BP_m4	GO:006039	SMAD prot	3/727	85/23843	0.482056	0.79818	0.786239	Inhba/Mir7
GO_BP_m4	GO:000994	anterior/p	2/727	53/23843	0.483506	0.79818	0.786239	Aurka/Ddit
GO_BP_m4	GO:003004	actin filam	2/727	53/23843	0.483506	0.79818	0.786239	Sptan1/Tm
GO_BP_m4	GO:004253	positive re	2/727	53/23843	0.483506	0.79818	0.786239	Il13/Lck

GO_BP_m4	GO:004662	positive reg	2/727	53/23843	0.483506	0.79818	0.786239	Mapk14/Pi
GO_BP_m4	GO:004806	developme	2/727	53/23843	0.483506	0.79818	0.786239	Mreg/Zeb2
GO_BP_m4	GO:004854	digestive tr	2/727	53/23843	0.483506	0.79818	0.786239	Ovol2/Sox
GO_BP_m4	GO:005099	regulation	2/727	53/23843	0.483506	0.79818	0.786239	Apoa4/Irs2
GO_BP_m4	GO:001635	dendrite de	9/727	280/23843	0.483605	0.79818	0.786239	Anapc2/Ar
GO_BP_m4	GO:005116	nuclear exp	5/727	150/23843	0.483817	0.79818	0.786239	Gas6/Rbm
GO_BP_m4	GO:000166	ameboidal	12/727	378/23843	0.48466	0.79818	0.786239	Ager/Dusp
GO_BP_m4	GO:003030	positive reg	6/727	183/23843	0.486612	0.79818	0.786239	Anapc2/Er
GO_BP_m4	GO:000627	regulation	4/727	118/23843	0.48662	0.79818	0.786239	Hcrt/Hus1/
GO_BP_m4	GO:004646	membrane	4/727	118/23843	0.48662	0.79818	0.786239	A4galt/B3g
GO_BP_m4	GO:006004	cardiac mu	4/727	118/23843	0.48662	0.79818	0.786239	Cacna1g/D
GO_BP_m4	GO:006201	negative re	4/727	118/23843	0.48662	0.79818	0.786239	Acmsd/C1
GO_BP_m4	GO:190113	carbohydra	4/727	118/23843	0.48662	0.79818	0.786239	Ctbs/Manb
GO_BP_m4	GO:190303	negative re	4/727	118/23843	0.48662	0.79818	0.786239	Btn2a2/Erb
GO_BP_m4	GO:000820	steroid me	9/727	281/23843	0.487873	0.79818	0.786239	Akr1d1/Ap
GO_BP_m4	GO:004578	positive reg	12/727	379/23843	0.488338	0.79818	0.786239	Ager/Bcl10
GO_BP_m4	GO:001931	hexose me	7/727	216/23843	0.488805	0.79818	0.786239	Car5a/C1q
GO_BP_m4	GO:000183	embryonic	5/727	151/23843	0.489645	0.79818	0.786239	Bcl10/Folr1
GO_BP_m4	GO:004666	male sex d	5/727	151/23843	0.489645	0.79818	0.786239	Brip1/Esr2/
GO_BP_m4	GO:001922	transmissic	3/727	86/23843	0.489815	0.79818	0.786239	Cacna1g/C
GO_BP_m4	GO:003260	chemokine	3/727	86/23843	0.489815	0.79818	0.786239	Ager/Ffar3
GO_BP_m4	GO:004315	negative re	3/727	86/23843	0.489815	0.79818	0.786239	Dpep1/Gas
GO_BP_m4	GO:190321	regulation	3/727	86/23843	0.489815	0.79818	0.786239	Plagl2/Tom
GO_BP_m4	GO:002241	cellular cor	11/727	347/23843	0.490792	0.79818	0.786239	Dnase2b/E
GO_BP_m4	GO:000974	response to	6/727	184/23843	0.491886	0.79818	0.786239	Ager/C1qt
GO_BP_m4	GO:190198	regulation	9/727	282/23843	0.492132	0.79818	0.786239	Anp32b/Bt
GO_BP_m4	GO:004682	regulation	4/727	119/23843	0.493191	0.79818	0.786239	Gas6/Mapk
GO_BP_m4	GO:006138	regulation	4/727	119/23843	0.493191	0.79818	0.786239	Anapc2/Rt
GO_BP_m4	GO:000270	negative re	2/727	54/23843	0.493366	0.79818	0.786239	Muc4/Serp
GO_BP_m4	GO:004507	negative re	2/727	54/23843	0.493366	0.79818	0.786239	A230050P2
GO_BP_m4	GO:004671	viral entry i	2/727	54/23843	0.493366	0.79818	0.786239	Gas6/Vamp
GO_BP_m4	GO:190406	regulation	10/727	315/23843	0.493456	0.79818	0.786239	Ager/Arc/C
GO_BP_m4	GO:009027	regulation	7/727	217/23843	0.493659	0.79818	0.786239	C1qtnf12/F
GO_BP_m4	GO:000002	ribosomal	1/727	22/23843	0.494167	0.79818	0.786239	Rps2
GO_BP_m4	GO:000027	polysaccha	1/727	22/23843	0.494167	0.79818	0.786239	Manba
GO_BP_m4	GO:000283	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Muc4
GO_BP_m4	GO:000283	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Muc4
GO_BP_m4	GO:000335	epithelial c	1/727	22/23843	0.494167	0.79818	0.786239	Nme5
GO_BP_m4	GO:000683	serotonin t	1/727	22/23843	0.494167	0.79818	0.786239	Lgals3
GO_BP_m4	GO:000706	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Sfpq
GO_BP_m4	GO:000726	nitric oxide	1/727	22/23843	0.494167	0.79818	0.786239	Mt1
GO_BP_m4	GO:000741	axonal fasc	1/727	22/23843	0.494167	0.79818	0.786239	Rtn4
GO_BP_m4	GO:000853	respiratory	1/727	22/23843	0.494167	0.79818	0.786239	Coa5
GO_BP_m4	GO:000964	photoperic	1/727	22/23843	0.494167	0.79818	0.786239	Sik1
GO_BP_m4	GO:001058	miRNA me	1/727	22/23843	0.494167	0.79818	0.786239	Rela
GO_BP_m4	GO:001088	positive reg	1/727	22/23843	0.494167	0.79818	0.786239	Apoc4
GO_BP_m4	GO:001485	response to	1/727	22/23843	0.494167	0.79818	0.786239	Mir709
GO_BP_m4	GO:001604	detection c	1/727	22/23843	0.494167	0.79818	0.786239	Lxn

GO_BP_m4	GO:001823	peptidyl-L-	1/727	22/23843	0.494167	0.79818	0.786239	Zdhhc22
GO_BP_m4	GO:001823	peptidyl-S-	1/727	22/23843	0.494167	0.79818	0.786239	Zdhhc22
GO_BP_m4	GO:002154	subpallium	1/727	22/23843	0.494167	0.79818	0.786239	Inhba
GO_BP_m4	GO:003025	growth hor	1/727	22/23843	0.494167	0.79818	0.786239	Itsn1
GO_BP_m4	GO:003270	negative re	1/727	22/23843	0.494167	0.79818	0.786239	Nav3
GO_BP_m4	GO:003440	response t	1/727	22/23843	0.494167	0.79818	0.786239	Socs5
GO_BP_m4	GO:004206	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Htr2c
GO_BP_m4	GO:004253	benzene-c	1/727	22/23843	0.494167	0.79818	0.786239	Kynu
GO_BP_m4	GO:004348	histone exc	1/727	22/23843	0.494167	0.79818	0.786239	Anp32b
GO_BP_m4	GO:004349	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Traf4
GO_BP_m4	GO:004478	G1 DNA da	1/727	22/23843	0.494167	0.79818	0.786239	Pidd1
GO_BP_m4	GO:004481	mitotic G1/	1/727	22/23843	0.494167	0.79818	0.786239	Pidd1
GO_BP_m4	GO:004594	positive reg	1/727	22/23843	0.494167	0.79818	0.786239	Erbb2
GO_BP_m4	GO:006057	intestinal e	1/727	22/23843	0.494167	0.79818	0.786239	Mir7-2
GO_BP_m4	GO:006060	branch elo	1/727	22/23843	0.494167	0.79818	0.786239	Spry2
GO_BP_m4	GO:006108	myeloid leu	1/727	22/23843	0.494167	0.79818	0.786239	Gas6
GO_BP_m4	GO:007024	thymocyte	1/727	22/23843	0.494167	0.79818	0.786239	Efna1
GO_BP_m4	GO:007140	cellular res	1/727	22/23843	0.494167	0.79818	0.786239	Socs5
GO_BP_m4	GO:007145	protein loc	1/727	22/23843	0.494167	0.79818	0.786239	Spdl1
GO_BP_m4	GO:007198	multivesicu	1/727	22/23843	0.494167	0.79818	0.786239	Rilp
GO_BP_m4	GO:007221	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Ret
GO_BP_m4	GO:007257	hepatocyte	1/727	22/23843	0.494167	0.79818	0.786239	Rps6ka1
GO_BP_m4	GO:007257	epithelial c	1/727	22/23843	0.494167	0.79818	0.786239	Rps6ka1
GO_BP_m4	GO:010603	neuron pro	1/727	22/23843	0.494167	0.79818	0.786239	Rtn4
GO_BP_m4	GO:190074	positive reg	1/727	22/23843	0.494167	0.79818	0.786239	Ager
GO_BP_m4	GO:190302	positive reg	1/727	22/23843	0.494167	0.79818	0.786239	Pxylp1
GO_BP_m4	GO:190330	negative re	1/727	22/23843	0.494167	0.79818	0.786239	Cbarp
GO_BP_m4	GO:190364	regulation	1/727	22/23843	0.494167	0.79818	0.786239	Ptpn23
GO_BP_m4	GO:190386	positive reg	1/727	22/23843	0.494167	0.79818	0.786239	Nedd4l
GO_BP_m4	GO:003313	regulation	5/727	152/23843	0.495449	0.799981	0.788013	Cnksr3/Gas
GO_BP_m4	GO:000693	muscle con	9/727	283/23843	0.496382	0.801216	0.789229	Cacna1g/D
GO_BP_m4	GO:003112	RNA 3'-end	3/727	87/23843	0.497518	0.802507	0.790501	Eri2/Nelfe/
GO_BP_m4	GO:003252	response t	3/727	87/23843	0.497518	0.802507	0.790501	Mest/Ret/R
GO_BP_m4	GO:000718	G-protein c	7/727	218/23843	0.498499	0.80382	0.791794	Ffar3/Gnat
GO_BP_m4	GO:003313	positive reg	4/727	120/23843	0.499727	0.805528	0.793477	Gas6/Ifna1
GO_BP_m4	GO:005507	calcium ion	14/727	448/23843	0.500887	0.807125	0.79505	Ager/C3ar1
GO_BP_m4	GO:009723	cellular res	5/727	153/23843	0.501229	0.807404	0.795325	Apoa4/Mp
GO_BP_m4	GO:000660	protein targ	10/727	317/23843	0.501493	0.807557	0.795476	Ap1s3/Erbb
GO_BP_m4	GO:000038	alternative	2/727	55/23843	0.503106	0.808329	0.796236	Rbfox3/Sfp
GO_BP_m4	GO:003266	regulation	2/727	55/23843	0.503106	0.808329	0.796236	Nav3/Rps3
GO_BP_m4	GO:003808	peptidyl-ty	2/727	55/23843	0.503106	0.808329	0.796236	Grb2/Lck
GO_BP_m4	GO:004657	positive reg	2/727	55/23843	0.503106	0.808329	0.796236	Erbb2/Rtn4
GO_BP_m4	GO:009890	regulation	2/727	55/23843	0.503106	0.808329	0.796236	Dsp/Ffar3
GO_BP_m4	GO:200077	regulation	2/727	55/23843	0.503106	0.808329	0.796236	Recql5/Trip
GO_BP_m4	GO:001000	glial cell dif	7/727	219/23843	0.503325	0.808329	0.796236	Ager/Dusp
GO_BP_m4	GO:003629	response t	7/727	219/23843	0.503325	0.808329	0.796236	Ager/Fndc1
GO_BP_m4	GO:000004	transition r	3/727	88/23843	0.505161	0.809173	0.797068	Heph/Slc25
GO_BP_m4	GO:003059	neutrophil	3/727	88/23843	0.505161	0.809173	0.797068	C3ar1/Lgal

GO_BP_m4	GO:004847	oogenesis	3/727	88/23843	0.505161	0.809173	0.797068	Aurka/Figla
GO_BP_m4	GO:190260	proton tran	3/727	88/23843	0.505161	0.809173	0.797068	Atp5c1/Atp
GO_BP_m4	GO:004477	cell cycle p	12/727	384/23843	0.50664	0.809173	0.797068	Anp32b/Bt
GO_BP_m4	GO:004865	smooth mu	5/727	154/23843	0.506982	0.809173	0.797068	Abcc4/Age
GO_BP_m4	GO:190198	negative re	5/727	154/23843	0.506982	0.809173	0.797068	Btn2a2/Hu
GO_BP_m4	GO:000279	regulation	15/727	483/23843	0.508096	0.809173	0.797068	Btn2a2/C1
GO_BP_m4	GO:000318	atrioventric	1/727	23/23843	0.509605	0.809173	0.797068	Efna1
GO_BP_m4	GO:000940	toxin metal	1/727	23/23843	0.509605	0.809173	0.797068	Cyp1a2
GO_BP_m4	GO:001906	virion asse	1/727	23/23843	0.509605	0.809173	0.797068	Rab43
GO_BP_m4	GO:002301	signal trans	1/727	23/23843	0.509605	0.809173	0.797068	Sox17
GO_BP_m4	GO:003020	chondroitin	1/727	23/23843	0.509605	0.809173	0.797068	Spock3
GO_BP_m4	GO:003090	notochord	1/727	23/23843	0.509605	0.809173	0.797068	Efna1
GO_BP_m4	GO:003209	regulation	1/727	23/23843	0.509605	0.809173	0.797068	Htr2c
GO_BP_m4	GO:003237	positive reg	1/727	23/23843	0.509605	0.809173	0.797068	Abcb4
GO_BP_m4	GO:003237	positive reg	1/727	23/23843	0.509605	0.809173	0.797068	Abcb4
GO_BP_m4	GO:003246	positive reg	1/727	23/23843	0.509605	0.809173	0.797068	Trabd2b
GO_BP_m4	GO:003269	negative re	1/727	23/23843	0.509605	0.809173	0.797068	Gas6
GO_BP_m4	GO:003410	negative re	1/727	23/23843	0.509605	0.809173	0.797068	Ager
GO_BP_m4	GO:004240	thyroid hor	1/727	23/23843	0.509605	0.809173	0.797068	Duox2
GO_BP_m4	GO:004309	cellular me	1/727	23/23843	0.509605	0.809173	0.797068	Bhmt
GO_BP_m4	GO:004668	response to	1/727	23/23843	0.509605	0.809173	0.797068	Mt1
GO_BP_m4	GO:004826	behavioral	1/727	23/23843	0.509605	0.809173	0.797068	Vwa1
GO_BP_m4	GO:004848	sympatheti	1/727	23/23843	0.509605	0.809173	0.797068	Erbb2
GO_BP_m4	GO:004879	animal org	1/727	23/23843	0.509605	0.809173	0.797068	Ret
GO_BP_m4	GO:005130	meiotic chr	1/727	23/23843	0.509605	0.809173	0.797068	Cenps
GO_BP_m4	GO:005196	regulation	1/727	23/23843	0.509605	0.809173	0.797068	Hcrt
GO_BP_m4	GO:006115	mRNA des	1/727	23/23843	0.509605	0.809173	0.797068	Zfp36l1
GO_BP_m4	GO:007146	cellular res	1/727	23/23843	0.509605	0.809173	0.797068	Kcne1
GO_BP_m4	GO:007167	positive reg	1/727	23/23843	0.509605	0.809173	0.797068	Lgals3
GO_BP_m4	GO:009011	COPII-coat	1/727	23/23843	0.509605	0.809173	0.797068	Sec13
GO_BP_m4	GO:009034	negative re	1/727	23/23843	0.509605	0.809173	0.797068	Rbl1
GO_BP_m4	GO:190307	negative re	1/727	23/23843	0.509605	0.809173	0.797068	Pid1
GO_BP_m4	GO:005109	regulation	12/727	385/23843	0.51028	0.809977	0.797859	Ager/Bcl10
GO_BP_m4	GO:004211	T cell activa	15/727	484/23843	0.511348	0.810472	0.798347	Ager/Bcl10
GO_BP_m4	GO:005082	protein sta	5/727	155/23843	0.512709	0.810472	0.798347	Efna1/Pim1
GO_BP_m4	GO:000006	protein imp	2/727	56/23843	0.512724	0.810472	0.798347	Agap3/Gas
GO_BP_m4	GO:000175	eye photor	2/727	56/23843	0.512724	0.810472	0.798347	Cabp4/Gna
GO_BP_m4	GO:000222	innate imm	2/727	56/23843	0.512724	0.810472	0.798347	Apoa4/AY7
GO_BP_m4	GO:002151	ventral spin	2/727	56/23843	0.512724	0.810472	0.798347	Nkx6-2/Vs
GO_BP_m4	GO:003556	non-canon	2/727	56/23843	0.512724	0.810472	0.798347	Ror2/Tiam1
GO_BP_m4	GO:009039	cellular sen	2/727	56/23843	0.512724	0.810472	0.798347	Mapk14/Rb
GO_BP_m4	GO:000666	glycolipid r	3/727	89/23843	0.512743	0.810472	0.798347	A4galt/Pig
GO_BP_m4	GO:003647	cell death i	3/727	89/23843	0.512743	0.810472	0.798347	Nme5/Ripk
GO_BP_m4	GO:004663	regulation	3/727	89/23843	0.512743	0.810472	0.798347	Ager/Il27/S
GO_BP_m4	GO:005502	regulation	3/727	89/23843	0.512743	0.810472	0.798347	Mapk14/M
GO_BP_m4	GO:002191	neural tube	6/727	188/23843	0.512796	0.810472	0.798347	Bcl10/Folr1
GO_BP_m4	GO:005127	negative re	9/727	287/23843	0.51328	0.81097	0.798837	Ager/Ctnna
GO_BP_m4	GO:001969	ribose pho	14/727	452/23843	0.514366	0.812416	0.800262	Ak3/Atp5c1

GO_BP_m4	GO:003019	extracellula	7/727	222/23843	0.517707	0.812696	0.800537	Eln/Hpse2/
GO_BP_m4	GO:007123	cellular res	6/727	189/23843	0.517974	0.812696	0.800537	Mir7-2/Mi
GO_BP_m4	GO:007288	spermatid	5/727	156/23843	0.518409	0.812696	0.800537	Brip1/Cats
GO_BP_m4	GO:004688	positive re	5/727	156/23843	0.518409	0.812696	0.800537	C1qtnf12/H
GO_BP_m4	GO:004856	digestive tr	4/727	123/23843	0.519111	0.812696	0.800537	Gata1/Mir7
GO_BP_m4	GO:000244	myeloid leu	3/727	90/23843	0.520264	0.812696	0.800537	Dnase1/Il1
GO_BP_m4	GO:190288	regulation	3/727	90/23843	0.520264	0.812696	0.800537	Nme5/Ripk
GO_BP_m4	GO:190350	liposacchar	3/727	90/23843	0.520264	0.812696	0.800537	A4galt/Pig
GO_BP_m4	GO:000754	sex differer	9/727	289/23843	0.521664	0.812696	0.800537	Brip1/Dmrt
GO_BP_m4	GO:000914	purine nuc	8/727	256/23843	0.521998	0.812696	0.800537	Ak3/Atp5c
GO_BP_m4	GO:001046	mesenchyr	2/727	57/23843	0.522218	0.812696	0.800537	Fgf4/Irs2
GO_BP_m4	GO:001580	acidic amir	2/727	57/23843	0.522218	0.812696	0.800537	Slc17a8/Sl
GO_BP_m4	GO:003026	entry into	2/727	57/23843	0.522218	0.812696	0.800537	Gas6/Vam
GO_BP_m4	GO:004440	entry into	2/727	57/23843	0.522218	0.812696	0.800537	Gas6/Vam
GO_BP_m4	GO:005180	entry into	2/727	57/23843	0.522218	0.812696	0.800537	Gas6/Vam
GO_BP_m4	GO:005182	entry into	2/727	57/23843	0.522218	0.812696	0.800537	Gas6/Vam
GO_BP_m4	GO:000694	striated mu	5/727	157/23843	0.52408	0.812696	0.800537	Cacna1g/D
GO_BP_m4	GO:005077	negative re	5/727	157/23843	0.52408	0.812696	0.800537	Dusp10/Lg
GO_BP_m4	GO:000233	mature B c	1/727	24/23843	0.524572	0.812696	0.800537	Nfatc1
GO_BP_m4	GO:000241	immune re	1/727	24/23843	0.524572	0.812696	0.800537	Muc4
GO_BP_m4	GO:000614	purine nuc	1/727	24/23843	0.524572	0.812696	0.800537	Aox3
GO_BP_m4	GO:000622	pyrimidine	1/727	24/23843	0.524572	0.812696	0.800537	Nme5
GO_BP_m4	GO:000630	postreplica	1/727	24/23843	0.524572	0.812696	0.800537	Polk
GO_BP_m4	GO:000720	protein kin	1/727	24/23843	0.524572	0.812696	0.800537	Hcrt
GO_BP_m4	GO:000906	aspartate f	1/727	24/23843	0.524572	0.812696	0.800537	Bhmt
GO_BP_m4	GO:001057	positive re	1/727	24/23843	0.524572	0.812696	0.800537	C3ar1
GO_BP_m4	GO:001093	regulation	1/727	24/23843	0.524572	0.812696	0.800537	Ripk1
GO_BP_m4	GO:001570	bicarbonat	1/727	24/23843	0.524572	0.812696	0.800537	Car4
GO_BP_m4	GO:001819	peptidyl-ar	1/727	24/23843	0.524572	0.812696	0.800537	Prmt9
GO_BP_m4	GO:002180	cerebral cc	1/727	24/23843	0.524572	0.812696	0.800537	Rtn4
GO_BP_m4	GO:002188	olfactory b	1/727	24/23843	0.524572	0.812696	0.800537	Mir200c
GO_BP_m4	GO:002203	telencepha	1/727	24/23843	0.524572	0.812696	0.800537	Rtn4
GO_BP_m4	GO:003072	ovulation	1/727	24/23843	0.524572	0.812696	0.800537	Inhba
GO_BP_m4	GO:003110	animal org	1/727	24/23843	0.524572	0.812696	0.800537	Aurka
GO_BP_m4	GO:003277	positive re	1/727	24/23843	0.524572	0.812696	0.800537	Cdh3
GO_BP_m4	GO:003352	histone H2	1/727	24/23843	0.524572	0.812696	0.800537	Trip12
GO_BP_m4	GO:004205	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Socs5
GO_BP_m4	GO:004356	regulation	1/727	24/23843	0.524572	0.812696	0.800537	Cdh3
GO_BP_m4	GO:004504	protein tar	1/727	24/23843	0.524572	0.812696	0.800537	Folr1
GO_BP_m4	GO:004533	phospholip	1/727	24/23843	0.524572	0.812696	0.800537	Abcb4
GO_BP_m4	GO:004682	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Gas6
GO_BP_m4	GO:004802	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Srsf10
GO_BP_m4	GO:004867	regulation	1/727	24/23843	0.524572	0.812696	0.800537	Rtn4
GO_BP_m4	GO:005148	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Slc8a1
GO_BP_m4	GO:005178	response t	1/727	24/23843	0.524572	0.812696	0.800537	F12
GO_BP_m4	GO:005502	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Mir1a-2
GO_BP_m4	GO:006021	definitive h	1/727	24/23843	0.524572	0.812696	0.800537	Gata1
GO_BP_m4	GO:006100	positive re	1/727	24/23843	0.524572	0.812696	0.800537	Tiam1

GO_BP_m4	GO:006111	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Mir1a-2
GO_BP_m4	GO:006143	establishm	1/727	24/23843	0.524572	0.812696	0.800537	Gak
GO_BP_m4	GO:007058	mitochond	1/727	24/23843	0.524572	0.812696	0.800537	Pid1
GO_BP_m4	GO:007139	cellular res	1/727	24/23843	0.524572	0.812696	0.800537	Esr2
GO_BP_m4	GO:007157	zinc ion tra	1/727	24/23843	0.524572	0.812696	0.800537	Slc39a8
GO_BP_m4	GO:007257	liver morph	1/727	24/23843	0.524572	0.812696	0.800537	Rps6ka1
GO_BP_m4	GO:190173	regulation	1/727	24/23843	0.524572	0.812696	0.800537	Mapk14
GO_BP_m4	GO:190357	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Pid1
GO_BP_m4	GO:190464	cellular res	1/727	24/23843	0.524572	0.812696	0.800537	Ager
GO_BP_m4	GO:190580	negative re	1/727	24/23843	0.524572	0.812696	0.800537	Efna1
GO_BP_m4	GO:200117	positive reg	1/727	24/23843	0.524572	0.812696	0.800537	Pid1
GO_BP_m4	GO:007133	cellular res	4/727	124/23843	0.525493	0.81386	0.801684	Ager/C1qt
GO_BP_m4	GO:004688	regulation	9/727	290/23843	0.525838	0.814129	0.801949	C1qtnf12/
GO_BP_m4	GO:000640	RNA catab	7/727	224/23843	0.527211	0.815991	0.803783	Cnot6/Eif3
GO_BP_m4	GO:004544	myoblast d	3/727	91/23843	0.527721	0.816251	0.80404	Ddit3/Map
GO_BP_m4	GO:190374	regulation	3/727	91/23843	0.527721	0.816251	0.80404	Plagl2/Tom
GO_BP_m4	GO:001631	dephospho	11/727	357/23843	0.528799	0.817655	0.805422	4933415F2
GO_BP_m4	GO:000741	synapse as	5/727	158/23843	0.529722	0.818003	0.805766	Flrt1/Lrrc4
GO_BP_m4	GO:007217	epithelial tu	5/727	158/23843	0.529722	0.818003	0.805766	Bcl10/Folr1
GO_BP_m4	GO:000644	regulation	2/727	58/23843	0.531587	0.818003	0.805766	Mif4gd/Pp
GO_BP_m4	GO:003083	negative re	2/727	58/23843	0.531587	0.818003	0.805766	Sptan1/Tm
GO_BP_m4	GO:003283	glomerulus	2/727	58/23843	0.531587	0.818003	0.805766	C3ar1/Ret
GO_BP_m4	GO:004209	T-helper ce	2/727	58/23843	0.531587	0.818003	0.805766	Il27/Socs5
GO_BP_m4	GO:004663	regulation	2/727	58/23843	0.531587	0.818003	0.805766	Il27/Socs5
GO_BP_m4	GO:005071	negative re	2/727	58/23843	0.531587	0.818003	0.805766	Btn2a2/Ga
GO_BP_m4	GO:009018	regulation	2/727	58/23843	0.531587	0.818003	0.805766	C3ar1/Ret
GO_BP_m4	GO:190379	positive reg	2/727	58/23843	0.531587	0.818003	0.805766	Abcb4/Htr
GO_BP_m4	GO:003149	chromatin	4/727	125/23843	0.531835	0.818003	0.805766	Anp32b/H
GO_BP_m4	GO:003227	positive reg	4/727	125/23843	0.531835	0.818003	0.805766	Grb2/Nav3
GO_BP_m4	GO:000004	autophago	3/727	92/23843	0.535113	0.818003	0.805766	5330417C
GO_BP_m4	GO:000640	RNA expor	3/727	92/23843	0.535113	0.818003	0.805766	Rbm26/Srs
GO_BP_m4	GO:005501	cardiac mu	3/727	92/23843	0.535113	0.818003	0.805766	Mapk14/M
GO_BP_m4	GO:000281	regulation	5/727	159/23843	0.535335	0.818003	0.805766	Ager/Dusp
GO_BP_m4	GO:000759	blood coag	5/727	159/23843	0.535335	0.818003	0.805766	F12/F5/Ga
GO_BP_m4	GO:003529	regulation	5/727	159/23843	0.535335	0.818003	0.805766	Cacna1g/E
GO_BP_m4	GO:009774	regulation	5/727	159/23843	0.535335	0.818003	0.805766	Cacna1g/E
GO_BP_m4	GO:200125	regulation	5/727	159/23843	0.535335	0.818003	0.805766	Arc/Cbarp/
GO_BP_m4	GO:005104	positive reg	15/727	492/23843	0.537161	0.818003	0.805766	Cacna1b/C
GO_BP_m4	GO:007250	cellular div	14/727	459/23843	0.537717	0.818003	0.805766	C3ar1/Cac
GO_BP_m4	GO:003017	positive reg	4/727	126/23843	0.538134	0.818003	0.805766	Lgr6/Ror2/
GO_BP_m4	GO:007133	cellular res	4/727	126/23843	0.538134	0.818003	0.805766	Ager/C1qt
GO_BP_m4	GO:190165	cellular res	4/727	126/23843	0.538134	0.818003	0.805766	Mir155/Mi
GO_BP_m4	GO:004206	gliogenesis	9/727	293/23843	0.538283	0.818003	0.805766	Ager/Cspg
GO_BP_m4	GO:003059	leukocyte	6/727	193/23843	0.538463	0.818003	0.805766	C3ar1/Gas
GO_BP_m4	GO:005165	establishm	6/727	193/23843	0.538463	0.818003	0.805766	Cdh3/Mreg
GO_BP_m4	GO:005500	muscle cell	6/727	193/23843	0.538463	0.818003	0.805766	Fhl2/Myom
GO_BP_m4	GO:000046	cleavage in	1/727	25/23843	0.539083	0.818003	0.805766	Eri2
GO_BP_m4	GO:000307	renal syste	1/727	25/23843	0.539083	0.818003	0.805766	Gas6

GO_BP_m4	GO:001598	energy cou	1/727	25/23843	0.539083	0.818003	0.805766	Atp5c1
GO_BP_m4	GO:001598	ATP synthe	1/727	25/23843	0.539083	0.818003	0.805766	Atp5c1
GO_BP_m4	GO:003019	positive re	1/727	25/23843	0.539083	0.818003	0.805766	F12
GO_BP_m4	GO:003280	receptor ca	1/727	25/23843	0.539083	0.818003	0.805766	Kif16b
GO_BP_m4	GO:003289	negative re	1/727	25/23843	0.539083	0.818003	0.805766	Irs2
GO_BP_m4	GO:003420	lipid transl	1/727	25/23843	0.539083	0.818003	0.805766	Abcb4
GO_BP_m4	GO:003545	response t	1/727	25/23843	0.539083	0.818003	0.805766	Gas6
GO_BP_m4	GO:003592	steroid hor	1/727	25/23843	0.539083	0.818003	0.805766	Inhba
GO_BP_m4	GO:004243	indole-con	1/727	25/23843	0.539083	0.818003	0.805766	Kynu
GO_BP_m4	GO:004337	positive re	1/727	25/23843	0.539083	0.818003	0.805766	Socs5
GO_BP_m4	GO:004636	monosacch	1/727	25/23843	0.539083	0.818003	0.805766	Nudt5
GO_BP_m4	GO:005077	RNA destal	1/727	25/23843	0.539083	0.818003	0.805766	Zfp36l1
GO_BP_m4	GO:005083	defense res	1/727	25/23843	0.539083	0.818003	0.805766	Mpo
GO_BP_m4	GO:005090	leukocyte t	1/727	25/23843	0.539083	0.818003	0.805766	Sell
GO_BP_m4	GO:005095	sensory pe	1/727	25/23843	0.539083	0.818003	0.805766	Lxn
GO_BP_m4	GO:005144	positive re	1/727	25/23843	0.539083	0.818003	0.805766	Rps2
GO_BP_m4	GO:006076	regulation	1/727	25/23843	0.539083	0.818003	0.805766	Esr2
GO_BP_m4	GO:007142	hematopoi	1/727	25/23843	0.539083	0.818003	0.805766	Pim1
GO_BP_m4	GO:007201	glomerulus	1/727	25/23843	0.539083	0.818003	0.805766	C3ar1
GO_BP_m4	GO:007267	eosinophil	1/727	25/23843	0.539083	0.818003	0.805766	Lgals3
GO_BP_m4	GO:008601	cell-cell sig	1/727	25/23843	0.539083	0.818003	0.805766	Cacna1g
GO_BP_m4	GO:009890	regulation	1/727	25/23843	0.539083	0.818003	0.805766	Dsp
GO_BP_m4	GO:190004	positive re	1/727	25/23843	0.539083	0.818003	0.805766	F12
GO_BP_m4	GO:190118	negative re	1/727	25/23843	0.539083	0.818003	0.805766	Socs5
GO_BP_m4	GO:190437	negative re	1/727	25/23843	0.539083	0.818003	0.805766	Pid1
GO_BP_m4	GO:200005	regulation	1/727	25/23843	0.539083	0.818003	0.805766	Tiam1
GO_BP_m4	GO:200051	negative re	1/727	25/23843	0.539083	0.818003	0.805766	Socs5
GO_BP_m4	GO:000701	microtubul	8/727	260/23843	0.539631	0.818003	0.805766	Casc1/Ccd
GO_BP_m4	GO:000229	CD4-positi	2/727	59/23843	0.54083	0.818003	0.805766	Il27/Socs5
GO_BP_m4	GO:000243	inflammato	2/727	59/23843	0.54083	0.818003	0.805766	Mir155/Ser
GO_BP_m4	GO:000680	superoxide	2/727	59/23843	0.54083	0.818003	0.805766	Apoa4/Mp
GO_BP_m4	GO:003133	regulation	2/727	59/23843	0.54083	0.818003	0.805766	Rundc1/Tb
GO_BP_m4	GO:003272	positive re	2/727	59/23843	0.54083	0.818003	0.805766	Ager/Ffar3
GO_BP_m4	GO:004566	negative re	2/727	59/23843	0.54083	0.818003	0.805766	Nfatc1/Tnr
GO_BP_m4	GO:004612	purine ribo	2/727	59/23843	0.54083	0.818003	0.805766	Ak3/Nme5
GO_BP_m4	GO:005105	negative re	2/727	59/23843	0.54083	0.818003	0.805766	Cgnl1/Spry
GO_BP_m4	GO:007020	protein trin	2/727	59/23843	0.54083	0.818003	0.805766	Atxn10/Mb
GO_BP_m4	GO:190351	mucopolys	2/727	59/23843	0.54083	0.818003	0.805766	Spock3/Xyl
GO_BP_m4	GO:003225	methylatio	10/727	327/23843	0.541104	0.818159	0.805919	Bhmt/Cam
GO_BP_m4	GO:190352	regulation	7/727	227/23843	0.541331	0.818243	0.806002	Cacna1b/C
GO_BP_m4	GO:000157	vasculoger	3/727	93/23843	0.542439	0.818365	0.806122	Ccm2/Sox1
GO_BP_m4	GO:000649	protein lipi	3/727	93/23843	0.542439	0.818365	0.806122	Pigp/Pigv/
GO_BP_m4	GO:007000	mitochond	3/727	93/23843	0.542439	0.818365	0.806122	Chchd6/Cs
GO_BP_m4	GO:001077	negative re	3/727	93/23843	0.542439	0.818365	0.806122	Efna1/Rtn4
GO_BP_m4	GO:002178	glial cell de	3/727	93/23843	0.542439	0.818365	0.806122	Ager/Nkx6
GO_BP_m4	GO:003027	negative re	3/727	93/23843	0.542439	0.818365	0.806122	Gata1/Nfat
GO_BP_m4	GO:000679	sulfur com	8/727	261/23843	0.544001	0.818514	0.806268	Bhmt/Dpe
GO_BP_m4	GO:007132	cellular res	4/727	127/23843	0.54439	0.818514	0.806268	Ager/C1qt

GO_BP_m4	GO:000756	aging	7/727	228/23843	0.545999	0.818514	0.806268	Ager/Grb2/
GO_BP_m4	GO:000759	hemostasis	5/727	161/23843	0.546466	0.818514	0.806268	F12/F5/Gas
GO_BP_m4	GO:001072	negative re	11/727	362/23843	0.547462	0.818514	0.806268	Cspg4/Ctn
GO_BP_m4	GO:000157	microtubul	3/727	94/23843	0.549698	0.818514	0.806268	Ccdc114/M
GO_BP_m4	GO:004691	cellular tra	3/727	94/23843	0.549698	0.818514	0.806268	Heph/Mt1/
GO_BP_m4	GO:005196	regulation	3/727	94/23843	0.549698	0.818514	0.806268	Flrt1/Lrrc4b
GO_BP_m4	GO:190210	negative re	3/727	94/23843	0.549698	0.818514	0.806268	Erbb2/Socs
GO_BP_m4	GO:003465	nucleobase	12/727	396/23843	0.5498	0.818514	0.806268	Cnot6/Dna
GO_BP_m4	GO:000151	RNA methy	2/727	60/23843	0.549946	0.818514	0.806268	Mrm2/Wdr
GO_BP_m4	GO:000229	alpha-beta	2/727	60/23843	0.549946	0.818514	0.806268	Il27/Socs5
GO_BP_m4	GO:000270	regulation	2/727	60/23843	0.549946	0.818514	0.806268	Ager/Muc4
GO_BP_m4	GO:003033	DNA dama	2/727	60/23843	0.549946	0.818514	0.806268	Pidd1/Smy
GO_BP_m4	GO:003369	cellular pol	2/727	60/23843	0.549946	0.818514	0.806268	B3gnt5/Irs2
GO_BP_m4	GO:003439	protein loc	2/727	60/23843	0.549946	0.818514	0.806268	Astn2/Ned
GO_BP_m4	GO:004477	mitotic DN	2/727	60/23843	0.549946	0.818514	0.806268	Hus1/Pidd1
GO_BP_m4	GO:007005	intrinsic ap	2/727	60/23843	0.549946	0.818514	0.806268	Ddit3/Ern2
GO_BP_m4	GO:000661	protein exp	4/727	128/23843	0.550602	0.818514	0.806268	Gas6/Srsf1
GO_BP_m4	GO:000920	purine ribo	4/727	128/23843	0.550602	0.818514	0.806268	Ak3/Atp5c1
GO_BP_m4	GO:001021	response to	4/727	128/23843	0.550602	0.818514	0.806268	Grb2/Hus1
GO_BP_m4	GO:004362	cellular pro	4/727	128/23843	0.550602	0.818514	0.806268	Gak/Nav3/
GO_BP_m4	GO:002240	regulation	11/727	363/23843	0.551163	0.818514	0.806268	Ager/Bcl10
GO_BP_m4	GO:003249	response to	11/727	363/23843	0.551163	0.818514	0.806268	AY761184/
GO_BP_m4	GO:005126	protein tetr	5/727	162/23843	0.551984	0.818514	0.806268	Decr1/Mbl
GO_BP_m4	GO:200124	regulation	5/727	162/23843	0.551984	0.818514	0.806268	Lck/Nme5/
GO_BP_m4	GO:000910	glycoprote	8/727	263/23843	0.552689	0.818514	0.806268	B3gnt5/Fut
GO_BP_m4	GO:000250	tolerance in	1/727	26/23843	0.553152	0.818514	0.806268	C3ar1
GO_BP_m4	GO:000317	atrioventric	1/727	26/23843	0.553152	0.818514	0.806268	Efna1
GO_BP_m4	GO:000631	mitotic rec	1/727	26/23843	0.553152	0.818514	0.806268	Cenps
GO_BP_m4	GO:000700	inner mitoc	1/727	26/23843	0.553152	0.818514	0.806268	Chchd6
GO_BP_m4	GO:000805	mitochond	1/727	26/23843	0.553152	0.818514	0.806268	Chchd6
GO_BP_m4	GO:000906	glutamine	1/727	26/23843	0.553152	0.818514	0.806268	Fah
GO_BP_m4	GO:001082	negative re	1/727	26/23843	0.553152	0.818514	0.806268	Pid1
GO_BP_m4	GO:002151	spinal cord	1/727	26/23843	0.553152	0.818514	0.806268	Nkx6-2
GO_BP_m4	GO:003081	positive reg	1/727	26/23843	0.553152	0.818514	0.806268	Tshr
GO_BP_m4	GO:003250	DNA duple	1/727	26/23843	0.553152	0.818514	0.806268	Recql5
GO_BP_m4	GO:003292	regulation	1/727	26/23843	0.553152	0.818514	0.806268	Fst
GO_BP_m4	GO:003450	centromere	1/727	26/23843	0.553152	0.818514	0.806268	Cenps
GO_BP_m4	GO:004510	intermedia	1/727	26/23843	0.553152	0.818514	0.806268	Dsp
GO_BP_m4	GO:004511	azole trans	1/727	26/23843	0.553152	0.818514	0.806268	Vamp8
GO_BP_m4	GO:004578	positive reg	1/727	26/23843	0.553152	0.818514	0.806268	Car2
GO_BP_m4	GO:004685	positive reg	1/727	26/23843	0.553152	0.818514	0.806268	Car2
GO_BP_m4	GO:004852	negative re	1/727	26/23843	0.553152	0.818514	0.806268	Esr2
GO_BP_m4	GO:005092	positive reg	1/727	26/23843	0.553152	0.818514	0.806268	Ager
GO_BP_m4	GO:005195	positive reg	1/727	26/23843	0.553152	0.818514	0.806268	Htr2c
GO_BP_m4	GO:005198	positive reg	1/727	26/23843	0.553152	0.818514	0.806268	Sfpq
GO_BP_m4	GO:006003	pharyngea	1/727	26/23843	0.553152	0.818514	0.806268	Folr1
GO_BP_m4	GO:006006	uterus dev	1/727	26/23843	0.553152	0.818514	0.806268	Esr2
GO_BP_m4	GO:006021	camera-typ	1/727	26/23843	0.553152	0.818514	0.806268	Cabp4

GO_BP_m4	GO:00603	innervatio	1/727	26/23843	0.553152	0.818514	0.806268	Ret
GO_BP_m4	GO:006071	labyrinthin	1/727	26/23843	0.553152	0.818514	0.806268	Ovol2
GO_BP_m4	GO:006131	cell surface	1/727	26/23843	0.553152	0.818514	0.806268	Sox17
GO_BP_m4	GO:00614	renal syste	1/727	26/23843	0.553152	0.818514	0.806268	C3ar1
GO_BP_m4	GO:006144	kidney vas	1/727	26/23843	0.553152	0.818514	0.806268	C3ar1
GO_BP_m4	GO:00702	sarcoplasm	1/727	26/23843	0.553152	0.818514	0.806268	Slc8a1
GO_BP_m4	GO:007154	cellular res	1/727	26/23843	0.553152	0.818514	0.806268	Mir155
GO_BP_m4	GO:190107	glucosami	1/727	26/23843	0.553152	0.818514	0.806268	Ctbs
GO_BP_m4	GO:19033	positive re	1/727	26/23843	0.553152	0.818514	0.806268	Ptpn23
GO_BP_m4	GO:190464	response t	1/727	26/23843	0.553152	0.818514	0.806268	Ager
GO_BP_m4	GO:200017	negative re	1/727	26/23843	0.553152	0.818514	0.806268	Ctnna1
GO_BP_m4	GO:200031	regulation	1/727	26/23843	0.553152	0.818514	0.806268	Arc
GO_BP_m4	GO:00083	regulation	6/727	196/23843	0.553581	0.818896	0.806645	Akt1s1/An
GO_BP_m4	GO:005122	positive re	14/727	464/23843	0.554178	0.819526	0.807265	Erbb2/C1q
GO_BP_m4	GO:000184	neural tub	4/727	129/23843	0.55677	0.821754	0.80946	Bcl10/Folr1
GO_BP_m4	GO:000914	purine nuc	4/727	129/23843	0.55677	0.821754	0.80946	Ak3/Atp5c
GO_BP_m4	GO:004867	axon exten	4/727	129/23843	0.55677	0.821754	0.80946	Anapc2/Rt
GO_BP_m4	GO:00508	defense re	4/727	129/23843	0.55677	0.821754	0.80946	AY761184/
GO_BP_m4	GO:00975	granulocyt	4/727	129/23843	0.55677	0.821754	0.80946	C3ar1/Lgal
GO_BP_m4	GO:00432	regulation	3/727	95/23843	0.556888	0.821754	0.80946	C1qtnf12/I
GO_BP_m4	GO:00487	oligodendr	3/727	95/23843	0.556888	0.821754	0.80946	Dusp10/Er
GO_BP_m4	GO:005081	coagulatio	5/727	163/23843	0.55747	0.822104	0.809805	F12/F5/Ga
GO_BP_m4	GO:190054	regulation	5/727	163/23843	0.55747	0.822104	0.809805	Cap2/Gng
GO_BP_m4	GO:00018	endothelial	2/727	61/23843	0.558933	0.822487	0.810182	Abcb1b/C
GO_BP_m4	GO:00022	alpha-beta	2/727	61/23843	0.558933	0.822487	0.810182	Il27/Socs5
GO_BP_m4	GO:00108	regulation	2/727	61/23843	0.558933	0.822487	0.810182	Mapk14/Si
GO_BP_m4	GO:00162	positive re	2/727	61/23843	0.558933	0.822487	0.810182	5330417C2
GO_BP_m4	GO:00316	zymogen a	2/727	61/23843	0.558933	0.822487	0.810182	F12/Klk1b1
GO_BP_m4	GO:005077	negative re	2/727	61/23843	0.558933	0.822487	0.810182	Rtn4/Rtn4r
GO_BP_m4	GO:19030	negative re	2/727	61/23843	0.558933	0.822487	0.810182	Efna1/Pdcl
GO_BP_m4	GO:000181	negative re	7/727	231/23843	0.559882	0.823629	0.811307	Ager/Btn2a
GO_BP_m4	GO:006007	canonical	8/727	265/23843	0.561309	0.825474	0.813125	Cdh3/Ddit
GO_BP_m4	GO:009747	synaptic ve	4/727	130/23843	0.562891	0.826168	0.813808	Rims4/Sna
GO_BP_m4	GO:00420	T cell prolif	6/727	198/23843	0.563533	0.826168	0.813808	Ager/Btn2a
GO_BP_m4	GO:00024	T cell medi	3/727	96/23843	0.564009	0.826168	0.813808	Ager/Muc
GO_BP_m4	GO:00062	regulation	3/727	96/23843	0.564009	0.826168	0.813808	Recql5/Rps
GO_BP_m4	GO:000664	triglyceride	3/727	96/23843	0.564009	0.826168	0.813808	Apoa4/Lip
GO_BP_m4	GO:003031	flagellated	3/727	96/23843	0.564009	0.826168	0.813808	Catsper2/
GO_BP_m4	GO:00442	cellular pol	3/727	96/23843	0.564009	0.826168	0.813808	B3gnt5/Irs
GO_BP_m4	GO:19050	autophago	3/727	96/23843	0.564009	0.826168	0.813808	5330417C2
GO_BP_m4	GO:000234	response t	1/727	27/23843	0.566791	0.826168	0.813808	Muc4
GO_BP_m4	GO:00108	regulation	1/727	27/23843	0.566791	0.826168	0.813808	Gas6
GO_BP_m4	GO:003087	thyroid gla	1/727	27/23843	0.566791	0.826168	0.813808	Duox2
GO_BP_m4	GO:00316	plasminog	1/727	27/23843	0.566791	0.826168	0.813808	F12
GO_BP_m4	GO:00323	negative re	1/727	27/23843	0.566791	0.826168	0.813808	Irs2
GO_BP_m4	GO:003281	positive re	1/727	27/23843	0.566791	0.826168	0.813808	Gas6
GO_BP_m4	GO:00331	negative re	1/727	27/23843	0.566791	0.826168	0.813808	Cnksr3
GO_BP_m4	GO:00346	ncRNA cat	1/727	27/23843	0.566791	0.826168	0.813808	Ern2

GO_BP_m4	GO:003533	peptidyl-ty	1/727	27/23843	0.566791	0.826168	0.813808	Dusp10
GO_BP_m4	GO:004211	neutrophil	1/727	27/23843	0.566791	0.826168	0.813808	Dnase1
GO_BP_m4	GO:004566	positive reg	1/727	27/23843	0.566791	0.826168	0.813808	Mapk14
GO_BP_m4	GO:005092	regulation	1/727	27/23843	0.566791	0.826168	0.813808	Ager
GO_BP_m4	GO:006014	positive reg	1/727	27/23843	0.566791	0.826168	0.813808	Mapk14
GO_BP_m4	GO:007026	necroptotic	1/727	27/23843	0.566791	0.826168	0.813808	Ripk1
GO_BP_m4	GO:007097	protein K11	1/727	27/23843	0.566791	0.826168	0.813808	Anapc2
GO_BP_m4	GO:009010	cochlea mo	1/727	27/23843	0.566791	0.826168	0.813808	Tshr
GO_BP_m4	GO:009020	positive reg	1/727	27/23843	0.566791	0.826168	0.813808	Wdr35
GO_BP_m4	GO:009020	positive reg	1/727	27/23843	0.566791	0.826168	0.813808	Apoa4
GO_BP_m4	GO:009907	regulation	1/727	27/23843	0.566791	0.826168	0.813808	Snap47
GO_BP_m4	GO:190289	positive reg	1/727	27/23843	0.566791	0.826168	0.813808	Rela
GO_BP_m4	GO:200030	regulation	1/727	27/23843	0.566791	0.826168	0.813808	Rims4
GO_BP_m4	GO:004244	pigment m	2/727	62/23843	0.567792	0.826618	0.814252	Cdh3/Zeb2
GO_BP_m4	GO:005105	positive reg	2/727	62/23843	0.567792	0.826618	0.814252	Erbb2/Rtn4
GO_BP_m4	GO:005192	negative re	2/727	62/23843	0.567792	0.826618	0.814252	Cbarp/Rem
GO_BP_m4	GO:200037	negative re	2/727	62/23843	0.567792	0.826618	0.814252	Esr2/Wdr35
GO_BP_m4	GO:190303	regulation	5/727	165/23843	0.568339	0.827162	0.814788	Ager/Dusp
GO_BP_m4	GO:000920	ribonucleos	4/727	131/23843	0.568967	0.82753	0.81515	Ak3/Atp5c1
GO_BP_m4	GO:005507	transition r	4/727	131/23843	0.568967	0.82753	0.81515	Heph/Mt1/
GO_BP_m4	GO:002241	cellular pro	11/727	368/23843	0.569494	0.82753	0.81515	Aurka/Brip
GO_BP_m4	GO:000688	regulation	3/727	97/23843	0.57106	0.82753	0.81515	Car2/Car4/
GO_BP_m4	GO:004312	positive reg	3/727	97/23843	0.57106	0.82753	0.81515	Rela/Ripk1/
GO_BP_m4	GO:004852	negative re	3/727	97/23843	0.57106	0.82753	0.81515	A230050P2
GO_BP_m4	GO:000270	regulation	6/727	200/23843	0.573377	0.82753	0.81515	Ager/Dnas
GO_BP_m4	GO:005125	protein pol	8/727	268/23843	0.574102	0.82753	0.81515	Arhgap18/
GO_BP_m4	GO:000279	positive reg	9/727	302/23843	0.57485	0.82753	0.81515	C1qtnf12/I
GO_BP_m4	GO:000985	determinat	4/727	132/23843	0.574995	0.82753	0.81515	Ddit3/Folr1
GO_BP_m4	GO:003121	biomineral	4/727	132/23843	0.574995	0.82753	0.81515	Duox2/Gas
GO_BP_m4	GO:000931	oligosaccha	2/727	63/23843	0.576522	0.82753	0.81515	Ctbs/Mogs
GO_BP_m4	GO:000998	cell-cell rec	2/727	63/23843	0.576522	0.82753	0.81515	Astl/Lgals3
GO_BP_m4	GO:003262	interleukin-	2/727	63/23843	0.576522	0.82753	0.81515	Nav3/Rps3
GO_BP_m4	GO:004545	cell redox h	2/727	63/23843	0.576522	0.82753	0.81515	Ddit3/Tmx2
GO_BP_m4	GO:001624	regulation	3/727	98/23843	0.57804	0.82753	0.81515	5330417C2
GO_BP_m4	GO:004215	lipoprotein	3/727	98/23843	0.57804	0.82753	0.81515	Pigp/Pigv/
GO_BP_m4	GO:004231	vasoconstr	3/727	98/23843	0.57804	0.82753	0.81515	Cacna1g/H
GO_BP_m4	GO:007138	cellular resp	6/727	201/23843	0.578259	0.82753	0.81515	Esr2/Mir15
GO_BP_m4	GO:004851	rhythmic p	8/727	269/23843	0.578329	0.82753	0.81515	Erbb2/Esr2
GO_BP_m4	GO:005123	maintenanc	9/727	303/23843	0.578835	0.82753	0.81515	Apoc4/Ddi
GO_BP_m4	GO:000610	regulation	5/727	167/23843	0.57907	0.82753	0.81515	C1qtnf12/I
GO_BP_m4	GO:000974	response to	5/727	167/23843	0.57907	0.82753	0.81515	Ager/C1qtn
GO_BP_m4	GO:001972	calcium-m	5/727	167/23843	0.57907	0.82753	0.81515	Grm1/Mir1
GO_BP_m4	GO:000073	DNA synth	1/727	28/23843	0.580015	0.82753	0.81515	Polk
GO_BP_m4	GO:000183	blastocyst g	1/727	28/23843	0.580015	0.82753	0.81515	Ncapg2
GO_BP_m4	GO:000194	lymph vess	1/727	28/23843	0.580015	0.82753	0.81515	Nfatc1
GO_BP_m4	GO:000202	response to	1/727	28/23843	0.580015	0.82753	0.81515	Slc25a25
GO_BP_m4	GO:000223	positive reg	1/727	28/23843	0.580015	0.82753	0.81515	Il27
GO_BP_m4	GO:000597	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Irs2

GO_BP_m4	GO:000602	aminoglyca	1/727	28/23843	0.580015	0.82753	0.81515	Ctbs
GO_BP_m4	GO:000676	folic acid-c	1/727	28/23843	0.580015	0.82753	0.81515	Folr1
GO_BP_m4	GO:000930	rRNA trans	1/727	28/23843	0.580015	0.82753	0.81515	Npm3
GO_BP_m4	GO:001045	exit from m	1/727	28/23843	0.580015	0.82753	0.81515	Rpl24
GO_BP_m4	GO:001096	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Irs2
GO_BP_m4	GO:001599	ATP hydrol	1/727	28/23843	0.580015	0.82753	0.81515	Atp6v1e2
GO_BP_m4	GO:001624	negative re	1/727	28/23843	0.580015	0.82753	0.81515	Sec22b
GO_BP_m4	GO:002151	spinal cord	1/727	28/23843	0.580015	0.82753	0.81515	Nkx6-2
GO_BP_m4	GO:002187	forebrain r	1/727	28/23843	0.580015	0.82753	0.81515	Fezf1
GO_BP_m4	GO:002195	central ner	1/727	28/23843	0.580015	0.82753	0.81515	Zeb2
GO_BP_m4	GO:003129	replication	1/727	28/23843	0.580015	0.82753	0.81515	Cenps
GO_BP_m4	GO:003315	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Gas6
GO_BP_m4	GO:003356	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Gak
GO_BP_m4	GO:003502	positive reg	1/727	28/23843	0.580015	0.82753	0.81515	Rtn4r
GO_BP_m4	GO:003576	endothelial	1/727	28/23843	0.580015	0.82753	0.81515	Fgf4
GO_BP_m4	GO:004355	positive reg	1/727	28/23843	0.580015	0.82753	0.81515	Tnfaip8l3
GO_BP_m4	GO:004368	post-transl	1/727	28/23843	0.580015	0.82753	0.81515	Stt3b
GO_BP_m4	GO:004400	modificatic	1/727	28/23843	0.580015	0.82753	0.81515	Serpinb9
GO_BP_m4	GO:004591	negative re	1/727	28/23843	0.580015	0.82753	0.81515	Recql5
GO_BP_m4	GO:004599	negative re	1/727	28/23843	0.580015	0.82753	0.81515	Sox17
GO_BP_m4	GO:005082	positive reg	1/727	28/23843	0.580015	0.82753	0.81515	F12
GO_BP_m4	GO:005112	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Wipf2
GO_BP_m4	GO:005135	negative re	1/727	28/23843	0.580015	0.82753	0.81515	Il13
GO_BP_m4	GO:005164	centrosom	1/727	28/23843	0.580015	0.82753	0.81515	Aurka
GO_BP_m4	GO:006003	pericardiur	1/727	28/23843	0.580015	0.82753	0.81515	Ccm2
GO_BP_m4	GO:006044	branching	1/727	28/23843	0.580015	0.82753	0.81515	Vdr
GO_BP_m4	GO:007135	cellular res	1/727	28/23843	0.580015	0.82753	0.81515	Rps2
GO_BP_m4	GO:007239	signal trans	1/727	28/23843	0.580015	0.82753	0.81515	Pidd1
GO_BP_m4	GO:007240	signal trans	1/727	28/23843	0.580015	0.82753	0.81515	Pidd1
GO_BP_m4	GO:007242	signal trans	1/727	28/23843	0.580015	0.82753	0.81515	Pidd1
GO_BP_m4	GO:007259	establishm	1/727	28/23843	0.580015	0.82753	0.81515	Folr1
GO_BP_m4	GO:009066	ATP hydrol	1/727	28/23843	0.580015	0.82753	0.81515	Atp6v1e2
GO_BP_m4	GO:009913	ATP hydrol	1/727	28/23843	0.580015	0.82753	0.81515	Atp6v1e2
GO_BP_m4	GO:009913	ATP hydrol	1/727	28/23843	0.580015	0.82753	0.81515	Atp6v1e2
GO_BP_m4	GO:190280	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Rims4
GO_BP_m4	GO:200019	regulation	1/727	28/23843	0.580015	0.82753	0.81515	Irs2
GO_BP_m4	GO:000979	specificatic	4/727	133/23843	0.580975	0.828651	0.816254	Ddit3/Folr1
GO_BP_m4	GO:000652	cellular am	8/727	270/23843	0.582536	0.830383	0.81796	Bhmt/Dalrc
GO_BP_m4	GO:000728	germ cell c	8/727	270/23843	0.582536	0.830383	0.81796	Aurka/Brip
GO_BP_m4	GO:004883	inner ear d	6/727	202/23843	0.583112	0.830956	0.818524	Anp32b/Cc
GO_BP_m4	GO:001922	cytokine-m	11/727	372/23843	0.583937	0.831095	0.818662	Duox2/Flrt
GO_BP_m4	GO:000680	xenobiotic	3/727	99/23843	0.584948	0.831095	0.818662	Cyp1a2/Cy
GO_BP_m4	GO:001939	fatty acid c	3/727	99/23843	0.584948	0.831095	0.818662	Decr1/Irs2/
GO_BP_m4	GO:004203	regulation	3/727	99/23843	0.584948	0.831095	0.818662	Bcl10/Il27/
GO_BP_m4	GO:000170	mesoderm	2/727	64/23843	0.585122	0.831095	0.818662	Inhba/Sox1
GO_BP_m4	GO:000756	embryo im	2/727	64/23843	0.585122	0.831095	0.818662	Mirlet7c-2/
GO_BP_m4	GO:003081	positive reg	2/727	64/23843	0.585122	0.831095	0.818662	Pid1/Tshr
GO_BP_m4	GO:003139	negative re	2/727	64/23843	0.585122	0.831095	0.818662	Rps3/Trip1

GO_BP_m4	GO:004827	vesicle doc	2/727	64/23843	0.585122	0.831095	0.818662	Rab40b/Stx
GO_BP_m4	GO:190037	positive reg	2/727	64/23843	0.585122	0.831095	0.818662	Pid1/Tshr
GO_BP_m4	GO:199054	mitochond	2/727	64/23843	0.585122	0.831095	0.818662	Slc25a37/T
GO_BP_m4	GO:000206	epithelial c	7/727	237/23843	0.587059	0.832736	0.820277	Abcb1b/Bfs
GO_BP_m4	GO:003025	lipid modif	6/727	203/23843	0.587936	0.832736	0.820277	Apoa4/Dec
GO_BP_m4	GO:000189	placenta de	5/727	169/23843	0.589657	0.832736	0.820277	Grb2/Mapk
GO_BP_m4	GO:000226	myeloid ce	5/727	169/23843	0.589657	0.832736	0.820277	Gata1/Hep
GO_BP_m4	GO:001077	positive reg	5/727	169/23843	0.589657	0.832736	0.820277	Anapc2/Rtn
GO_BP_m4	GO:000691	nucleocyto	9/727	306/23843	0.590688	0.832736	0.820277	Agap3/Anp
GO_BP_m4	GO:004665	lymphocyte	9/727	306/23843	0.590688	0.832736	0.820277	Ager/Btn2a
GO_BP_m4	GO:004274	defense res	13/727	442/23843	0.592119	0.832736	0.820277	AY761184/
GO_BP_m4	GO:007064	protein mo	4/727	135/23843	0.592789	0.832736	0.820277	Cops2/Otu
GO_BP_m4	GO:009730	response to	4/727	135/23843	0.592789	0.832736	0.820277	Ctnna1/Inh
GO_BP_m4	GO:190495	positive reg	14/727	476/23843	0.592791	0.832736	0.820277	Erbb2/C1q
GO_BP_m4	GO:000047	maturation	1/727	29/23843	0.592836	0.832736	0.820277	Rpl7l1
GO_BP_m4	GO:000155	oocyte mat	1/727	29/23843	0.592836	0.832736	0.820277	Aurka
GO_BP_m4	GO:000191	regulation	1/727	29/23843	0.592836	0.832736	0.820277	Kif16b
GO_BP_m4	GO:000243	acute inflam	1/727	29/23843	0.592836	0.832736	0.820277	Serpinb9
GO_BP_m4	GO:000682	zinc ion tra	1/727	29/23843	0.592836	0.832736	0.820277	Slc39a8
GO_BP_m4	GO:000690	vesicle targ	1/727	29/23843	0.592836	0.832736	0.820277	Tmed10
GO_BP_m4	GO:000915	purine ribo	1/727	29/23843	0.592836	0.832736	0.820277	Nudt7
GO_BP_m4	GO:000926	ribonucleo	1/727	29/23843	0.592836	0.832736	0.820277	Nudt7
GO_BP_m4	GO:001092	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Ppp1r15b
GO_BP_m4	GO:003278	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Thoc5
GO_BP_m4	GO:003311	negative re	1/727	29/23843	0.592836	0.832736	0.820277	Srsf10
GO_BP_m4	GO:003426	negative re	1/727	29/23843	0.592836	0.832736	0.820277	Spry2
GO_BP_m4	GO:003588	vascular sm	1/727	29/23843	0.592836	0.832736	0.820277	Sgcb
GO_BP_m4	GO:004518	regulation	1/727	29/23843	0.592836	0.832736	0.820277	Hcrtr1
GO_BP_m4	GO:004567	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Car2
GO_BP_m4	GO:004864	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Sox17
GO_BP_m4	GO:005108	chaperone	1/727	29/23843	0.592836	0.832736	0.820277	Dnajb14
GO_BP_m4	GO:006057	morphogen	1/727	29/23843	0.592836	0.832736	0.820277	Ovol2
GO_BP_m4	GO:006103	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Rela
GO_BP_m4	GO:006175	leukocyte a	1/727	29/23843	0.592836	0.832736	0.820277	Sell
GO_BP_m4	GO:007154	response to	1/727	29/23843	0.592836	0.832736	0.820277	Mir155
GO_BP_m4	GO:007252	pyrimidine	1/727	29/23843	0.592836	0.832736	0.820277	Nme5
GO_BP_m4	GO:190348	regulation	1/727	29/23843	0.592836	0.832736	0.820277	Oas2
GO_BP_m4	GO:190403	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Ager
GO_BP_m4	GO:200051	positive reg	1/727	29/23843	0.592836	0.832736	0.820277	Socs5
GO_BP_m4	GO:000229	T cell differ	2/727	65/23843	0.593592	0.832736	0.820277	Il27/Socs5
GO_BP_m4	GO:000271	regulation	2/727	65/23843	0.593592	0.832736	0.820277	Ffar3/Mapk
GO_BP_m4	GO:000651	protein mo	2/727	65/23843	0.593592	0.832736	0.820277	Nedd4l/Ne
GO_BP_m4	GO:003508	axoneme a	2/727	65/23843	0.593592	0.832736	0.820277	Ccdc114/N
GO_BP_m4	GO:004477	mitotic DN	2/727	65/23843	0.593592	0.832736	0.820277	Hus1/Pidd1
GO_BP_m4	GO:005511	regulation	2/727	65/23843	0.593592	0.832736	0.820277	Dsp/Slc8a1
GO_BP_m4	GO:005116	nuclear tra	9/727	307/23843	0.594604	0.833297	0.82083	Agap3/Anp
GO_BP_m4	GO:000614	regulation	5/727	170/23843	0.594895	0.833297	0.82083	Cap2/Gng7
GO_BP_m4	GO:000974	response to	5/727	170/23843	0.594895	0.833297	0.82083	Ager/C1qtn

GO_BP_m4	GO:00224	negative r	5/727	170/23843	0.594895	0.833297	0.82083	Btn2a2/Erb
GO_BP_m4	GO:00508	regulation	5/727	170/23843	0.594895	0.833297	0.82083	Cacna1g/E
GO_BP_m4	GO:005071	positive re	8/727	273/23843	0.595038	0.833297	0.82083	C1qtnf12/I
GO_BP_m4	GO:00486	reproducti	13/727	443/23843	0.59539	0.833546	0.821075	Brip1/Esr2/
GO_BP_m4	GO:000631	DNA recon	7/727	239/23843	0.595932	0.83406	0.821582	Cenps/Brip
GO_BP_m4	GO:003294	mononucle	9/727	308/23843	0.598502	0.836006	0.823499	Ager/Btn2a
GO_BP_m4	GO:00198	antigen pr	3/727	101/23843	0.598546	0.836006	0.823499	H2-M10.1/
GO_BP_m4	GO:00302	bone mine	3/727	101/23843	0.598546	0.836006	0.823499	Duox2/Gat
GO_BP_m4	GO:003444	lipid oxidat	3/727	101/23843	0.598546	0.836006	0.823499	Decr1/Irs2/
GO_BP_m4	GO:00359	cellular res	3/727	101/23843	0.598546	0.836006	0.823499	Atf6b/Ddit
GO_BP_m4	GO:004544	endothelial	3/727	101/23843	0.598546	0.836006	0.823499	Abcb1b/Cc
GO_BP_m4	GO:006041	heart grow	3/727	101/23843	0.598546	0.836006	0.823499	Mapk14/M
GO_BP_m4	GO:000914	nucleoside	8/727	274/23843	0.599164	0.83611	0.823602	Ak3/Atp5c
GO_BP_m4	GO:000647	protein me	5/727	171/23843	0.600097	0.83611	0.823602	Bhmt/Cam
GO_BP_m4	GO:00073	gastrulatio	5/727	171/23843	0.600097	0.83611	0.823602	Nat8f1/Dus
GO_BP_m4	GO:000821	protein alk	5/727	171/23843	0.600097	0.83611	0.823602	Bhmt/Cam
GO_BP_m4	GO:00342	response t	5/727	171/23843	0.600097	0.83611	0.823602	Ager/C1qt
GO_BP_m4	GO:00351	regulation	5/727	171/23843	0.600097	0.83611	0.823602	Cacna1g/E
GO_BP_m4	GO:000037	RNA splici	7/727	240/23843	0.600332	0.83611	0.823602	Gemin5/Lu
GO_BP_m4	GO:00003	mRNA spli	7/727	240/23843	0.600332	0.83611	0.823602	Gemin5/Lu
GO_BP_m4	GO:001991	lipid stora	2/727	66/23843	0.601932	0.83611	0.823602	Apoc4/Me
GO_BP_m4	GO:00434	negative r	2/727	66/23843	0.601932	0.83611	0.823602	Dusp10/Sp
GO_BP_m4	GO:19030	positive re	2/727	66/23843	0.601932	0.83611	0.823602	F12/Rtn4
GO_BP_m4	GO:00066	glyceropho	6/727	206/23843	0.602234	0.83611	0.823602	Apoa4/Gd
GO_BP_m4	GO:00352	multicellul	6/727	206/23843	0.602234	0.83611	0.823602	Ccm2/Duo
GO_BP_m4	GO:00514	neuron ap	8/727	275/23843	0.603269	0.83611	0.823602	Ager/Akt1s
GO_BP_m4	GO:000912	purine nuc	4/727	137/23843	0.604403	0.83611	0.823602	Ak3/Atp5c
GO_BP_m4	GO:00091	purine ribo	4/727	137/23843	0.604403	0.83611	0.823602	Ak3/Atp5c
GO_BP_m4	GO:005067	positive re	4/727	137/23843	0.604403	0.83611	0.823602	Ager/Il13/I
GO_BP_m4	GO:005512	digestive s	4/727	137/23843	0.604403	0.83611	0.823602	Gata1/Mir
GO_BP_m4	GO:000037	RNA splici	7/727	241/23843	0.604707	0.83611	0.823602	Gemin5/Lu
GO_BP_m4	GO:200102	regulation	3/727	102/23843	0.605235	0.83611	0.823602	Htr2c/Ripk
GO_BP_m4	GO:003514	tube forma	5/727	172/23843	0.60526	0.83611	0.823602	Bcl10/Folr1
GO_BP_m4	GO:00015	cilium or fl	1/727	30/23843	0.605266	0.83611	0.823602	Tekt5
GO_BP_m4	GO:00028	regulation	1/727	30/23843	0.605266	0.83611	0.823602	Socs5
GO_BP_m4	GO:00070	centriole r	1/727	30/23843	0.605266	0.83611	0.823602	Cep152
GO_BP_m4	GO:000804	motor neu	1/727	30/23843	0.605266	0.83611	0.823602	Erbb2
GO_BP_m4	GO:00095	detection	1/727	30/23843	0.605266	0.83611	0.823602	Gnat1
GO_BP_m4	GO:00325	protein tra	1/727	30/23843	0.605266	0.83611	0.823602	Snap47
GO_BP_m4	GO:00439	positive re	1/727	30/23843	0.605266	0.83611	0.823602	Gpr61
GO_BP_m4	GO:00456	negative r	1/727	30/23843	0.605266	0.83611	0.823602	Ddit3
GO_BP_m4	GO:004592	negative r	1/727	30/23843	0.605266	0.83611	0.823602	Cbarp
GO_BP_m4	GO:00508	circadian s	1/727	30/23843	0.605266	0.83611	0.823602	Hcrtr1
GO_BP_m4	GO:00602	cilium-dep	1/727	30/23843	0.605266	0.83611	0.823602	Tekt5
GO_BP_m4	GO:006184	microtubul	1/727	30/23843	0.605266	0.83611	0.823602	Aurka
GO_BP_m4	GO:007067	response t	1/727	30/23843	0.605266	0.83611	0.823602	Rps2
GO_BP_m4	GO:00715	protein loc	1/727	30/23843	0.605266	0.83611	0.823602	Aurka
GO_BP_m4	GO:19000	positive re	1/727	30/23843	0.605266	0.83611	0.823602	Anp32b

GO_BP_m4	GO:190342	negative re	1/727	30/23843	0.605266	0.83611	0.823602	Wdr35
GO_BP_m4	GO:190343	regulation	1/727	30/23843	0.605266	0.83611	0.823602	Sec13
GO_BP_m4	GO:000150	regulation	9/727	310/23843	0.606243	0.837218	0.824693	Cacna1b/H
GO_BP_m4	GO:006145	reproductiv	13/727	447/23843	0.608357	0.838728	0.82618	Brip1/Esr2/
GO_BP_m4	GO:000167	cellular glu	4/727	138/23843	0.610135	0.838728	0.82618	Ager/C1qt
GO_BP_m4	GO:000705	cell cycle a	4/727	138/23843	0.610135	0.838728	0.82618	Ddit3/Ern2
GO_BP_m4	GO:000722	smoothene	4/727	138/23843	0.610135	0.838728	0.82618	Ctnna1/Kct
GO_BP_m4	GO:000729	female gan	4/727	138/23843	0.610135	0.838728	0.82618	Aurka/Figla
GO_BP_m4	GO:001082	positive reg	4/727	138/23843	0.610135	0.838728	0.82618	Plagl2/Tom
GO_BP_m4	GO:003238	negative re	2/727	67/23843	0.610142	0.838728	0.82618	Gas6/Kcne
GO_BP_m4	GO:003410	homotypic	2/727	67/23843	0.610142	0.838728	0.82618	Dsp/Gata1
GO_BP_m4	GO:190589	regulation	2/727	67/23843	0.610142	0.838728	0.82618	Atf6b/Ppp1
GO_BP_m4	GO:001645	gene silenc	8/727	277/23843	0.611416	0.838728	0.82618	Cnot6/Dyd
GO_BP_m4	GO:003264	regulation	3/727	103/23843	0.611849	0.838728	0.82618	Gas6/Il27/
GO_BP_m4	GO:004347	pigmentati	3/727	103/23843	0.611849	0.838728	0.82618	Cdh3/Mreg
GO_BP_m4	GO:004663	alpha-beta	3/727	103/23843	0.611849	0.838728	0.82618	Il27/Rpl22/
GO_BP_m4	GO:004814	regulation	3/727	103/23843	0.611849	0.838728	0.82618	Ager/Gas6/
GO_BP_m4	GO:200011	negative re	3/727	103/23843	0.611849	0.838728	0.82618	Dpep1/Gas
GO_BP_m4	GO:004677	protein aut	7/727	243/23843	0.613381	0.838728	0.82618	Erbb2/Grb2
GO_BP_m4	GO:005086	positive reg	13/727	449/23843	0.614768	0.838728	0.82618	Ager/Bcl10
GO_BP_m4	GO:000155	regulation	12/727	415/23843	0.615081	0.838728	0.82618	Anapc2/Erb
GO_BP_m4	GO:000176	neuron mig	5/727	174/23843	0.615471	0.838728	0.82618	Esr2/Fezf1/
GO_BP_m4	GO:003294	positive reg	4/727	139/23843	0.615815	0.838728	0.82618	Ager/Il13/I
GO_BP_m4	GO:001063	regulation	6/727	209/23843	0.616259	0.838728	0.82618	Ager/Dusp
GO_BP_m4	GO:001025	endomemb	10/727	347/23843	0.616477	0.838728	0.82618	A4galt/Blzf
GO_BP_m4	GO:000177	natural kille	1/727	31/23843	0.617317	0.838728	0.82618	Gas6
GO_BP_m4	GO:000202	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Slc8a1
GO_BP_m4	GO:000647	protein AD	1/727	31/23843	0.617317	0.838728	0.82618	Art4
GO_BP_m4	GO:000702	negative re	1/727	31/23843	0.617317	0.838728	0.82618	Nav3
GO_BP_m4	GO:000829	isoprenoid	1/727	31/23843	0.617317	0.838728	0.82618	Pmvk
GO_BP_m4	GO:001056	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Recql5
GO_BP_m4	GO:001057	regulation	1/727	31/23843	0.617317	0.838728	0.82618	C3ar1
GO_BP_m4	GO:001066	positive reg	1/727	31/23843	0.617317	0.838728	0.82618	Fndc1
GO_BP_m4	GO:001598	energy cou	1/727	31/23843	0.617317	0.838728	0.82618	Atp6v1e2
GO_BP_m4	GO:001827	protein N-	1/727	31/23843	0.617317	0.838728	0.82618	Stt3b
GO_BP_m4	GO:003239	DNA geom	1/727	31/23843	0.617317	0.838728	0.82618	Recql5
GO_BP_m4	GO:003246	positive reg	1/727	31/23843	0.617317	0.838728	0.82618	Sstr5
GO_BP_m4	GO:003268	negative re	1/727	31/23843	0.617317	0.838728	0.82618	Gas6
GO_BP_m4	GO:003274	positive reg	1/727	31/23843	0.617317	0.838728	0.82618	Rps3
GO_BP_m4	GO:003308	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Erbb2
GO_BP_m4	GO:004274	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Hcrtr1
GO_BP_m4	GO:004327	anoikis	1/727	31/23843	0.617317	0.838728	0.82618	Sik1
GO_BP_m4	GO:004351	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Smyd2
GO_BP_m4	GO:004362	ncRNA 3'-e	1/727	31/23843	0.617317	0.838728	0.82618	Eri2
GO_BP_m4	GO:004824	sperm capa	1/727	31/23843	0.617317	0.838728	0.82618	Catsper2
GO_BP_m4	GO:004853	lymph nod	1/727	31/23843	0.617317	0.838728	0.82618	Polb
GO_BP_m4	GO:005149	positive reg	1/727	31/23843	0.617317	0.838728	0.82618	Neurl1a
GO_BP_m4	GO:007088	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Mir1a-2

GO_BP_m4	GO:00725	clathrin-de	1/727	31/23843	0.617317	0.838728	0.82618	Gak
GO_BP_m4	GO:009007	relaxation	1/727	31/23843	0.617317	0.838728	0.82618	Slc8a1
GO_BP_m4	GO:009016	establishm	1/727	31/23843	0.617317	0.838728	0.82618	Frmd4b
GO_BP_m4	GO:009021	positive re	1/727	31/23843	0.617317	0.838728	0.82618	Tnfaip8l3
GO_BP_m4	GO:00985	centriole a	1/727	31/23843	0.617317	0.838728	0.82618	Cep152
GO_BP_m4	GO:01060	regulation	1/727	31/23843	0.617317	0.838728	0.82618	Mir1a-2
GO_BP_m4	GO:19018	positive re	1/727	31/23843	0.617317	0.838728	0.82618	Nphp1
GO_BP_m4	GO:19055	protein loc	1/727	31/23843	0.617317	0.838728	0.82618	Aurka
GO_BP_m4	GO:003214	activation	7/727	244/23843	0.617679	0.838728	0.82618	Cspg4/Ern
GO_BP_m4	GO:00017	in utero en	13/727	450/23843	0.617955	0.838728	0.82618	Btf3/Ccm2
GO_BP_m4	GO:00066	fatty acid b	2/727	68/23843	0.618223	0.838728	0.82618	Decr1/Irs2
GO_BP_m4	GO:00308	regulation	2/727	68/23843	0.618223	0.838728	0.82618	Il13/Irs2
GO_BP_m4	GO:00423	regulation	2/727	68/23843	0.618223	0.838728	0.82618	Gas6/Map
GO_BP_m4	GO:00425	regulation	2/727	68/23843	0.618223	0.838728	0.82618	Il13/Lck
GO_BP_m4	GO:00432	leukocyte	2/727	68/23843	0.618223	0.838728	0.82618	Il13/Vamp
GO_BP_m4	GO:00483	mesoderm	2/727	68/23843	0.618223	0.838728	0.82618	Inhba/Sox1
GO_BP_m4	GO:190442	positive re	2/727	68/23843	0.618223	0.838728	0.82618	Il13/Kcne1
GO_BP_m4	GO:19034	reactive ox	3/727	104/23843	0.618389	0.838728	0.82618	Cyp1a2/M
GO_BP_m4	GO:00714	cellular res	8/727	279/23843	0.619475	0.839963	0.827397	5330417C2
GO_BP_m4	GO:00160	organic aci	6/727	210/23843	0.620872	0.840485	0.82791	Akr1d1/Cy
GO_BP_m4	GO:00463	carboxylic	6/727	210/23843	0.620872	0.840485	0.82791	Akr1d1/Cy
GO_BP_m4	GO:004501	glycerolipi	4/727	140/23843	0.621443	0.840485	0.82791	Htr2c/Pigp
GO_BP_m4	GO:00466	alpha-beta	4/727	140/23843	0.621443	0.840485	0.82791	Ager/Il27/
GO_BP_m4	GO:005072	negative re	4/727	140/23843	0.621443	0.840485	0.82791	Ager/Dusp
GO_BP_m4	GO:00485	embryonic	14/727	486/23843	0.623837	0.840485	0.82791	Efna1/Folr1
GO_BP_m4	GO:000072	double-str	3/727	105/23843	0.624853	0.840485	0.82791	Hus1/Recq
GO_BP_m4	GO:000072	recombina	3/727	105/23843	0.624853	0.840485	0.82791	Hus1/Recq
GO_BP_m4	GO:00105	positive re	3/727	105/23843	0.624853	0.840485	0.82791	5330417C2
GO_BP_m4	GO:00158	amine tran	3/727	105/23843	0.624853	0.840485	0.82791	Aqp9/Htr2
GO_BP_m4	GO:00192	response t	3/727	105/23843	0.624853	0.840485	0.82791	Tmem145/
GO_BP_m4	GO:003031	osteoclast	3/727	105/23843	0.624853	0.840485	0.82791	Car2/Mapk
GO_BP_m4	GO:004814	fibroblast	3/727	105/23843	0.624853	0.840485	0.82791	Ager/Gas6
GO_BP_m4	GO:200017	regulation	3/727	105/23843	0.624853	0.840485	0.82791	Ctnna1/Ga
GO_BP_m4	GO:00485	embryonic	9/727	315/23843	0.625267	0.840485	0.82791	Efna1/Folr1
GO_BP_m4	GO:190332	regulation	6/727	211/23843	0.625453	0.840485	0.82791	Bcl10/Rela
GO_BP_m4	GO:00022	response t	11/727	384/23843	0.625927	0.840485	0.82791	AY761184/
GO_BP_m4	GO:000027	polysaccha	2/727	69/23843	0.626174	0.840485	0.82791	B3gnt5/Irs
GO_BP_m4	GO:00421	negative re	2/727	69/23843	0.626174	0.840485	0.82791	Btn2a2/Erb
GO_BP_m4	GO:004864	animal org	2/727	69/23843	0.626174	0.840485	0.82791	Folr1/Pim1
GO_BP_m4	GO:006117	regulation	2/727	69/23843	0.626174	0.840485	0.82791	C1qtnf12/T
GO_BP_m4	GO:00032	cardiac cha	4/727	141/23843	0.627019	0.840485	0.82791	Dsp/Fhl2/N
GO_BP_m4	GO:00091	ribonucleo	4/727	141/23843	0.627019	0.840485	0.82791	Ak3/Atp5c
GO_BP_m4	GO:00512	negative re	4/727	141/23843	0.627019	0.840485	0.82791	Btn2a2/Erb
GO_BP_m4	GO:00001	rRNA modi	1/727	32/23843	0.629001	0.840485	0.82791	Mrm2
GO_BP_m4	GO:000041	protein pe	1/727	32/23843	0.629001	0.840485	0.82791	Ppid
GO_BP_m4	GO:000244	neutrophil	1/727	32/23843	0.629001	0.840485	0.82791	Dnase1
GO_BP_m4	GO:00063	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Erbb2
GO_BP_m4	GO:000677	fat-soluble	1/727	32/23843	0.629001	0.840485	0.82791	Vdr

GO_BP_m4	GO:000703	peroxisome	1/727	32/23843	0.629001	0.840485	0.82791	Pex1
GO_BP_m4	GO:001004	response t	1/727	32/23843	0.629001	0.840485	0.82791	Mt1
GO_BP_m4	GO:001700	cytochrom	1/727	32/23843	0.629001	0.840485	0.82791	Coa5
GO_BP_m4	GO:001819	peptidyl-as	1/727	32/23843	0.629001	0.840485	0.82791	Stt3b
GO_BP_m4	GO:001937	epoxygena	1/727	32/23843	0.629001	0.840485	0.82791	Cyp2a22
GO_BP_m4	GO:002241	circadian sl	1/727	32/23843	0.629001	0.840485	0.82791	Hcrtr1
GO_BP_m4	GO:003359	mammary	1/727	32/23843	0.629001	0.840485	0.82791	Rtn4
GO_BP_m4	GO:003623	granulocyt	1/727	32/23843	0.629001	0.840485	0.82791	Dnase1
GO_BP_m4	GO:004003	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Spry2
GO_BP_m4	GO:004427	cellular car	1/727	32/23843	0.629001	0.840485	0.82791	Manba
GO_BP_m4	GO:004481	mitotic G2/	1/727	32/23843	0.629001	0.840485	0.82791	Hus1
GO_BP_m4	GO:004557	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Zfp36l1
GO_BP_m4	GO:004574	positive reg	1/727	32/23843	0.629001	0.840485	0.82791	Tmod2
GO_BP_m4	GO:004632	negative re	1/727	32/23843	0.629001	0.840485	0.82791	Dusp10
GO_BP_m4	GO:005118	cofactor tra	1/727	32/23843	0.629001	0.840485	0.82791	Folr1
GO_BP_m4	GO:006014	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Mapk14
GO_BP_m4	GO:006029	long term s	1/727	32/23843	0.629001	0.840485	0.82791	Ager
GO_BP_m4	GO:006079	cell fate co	1/727	32/23843	0.629001	0.840485	0.82791	Sox17
GO_BP_m4	GO:007089	DNA-temp	1/727	32/23843	0.629001	0.840485	0.82791	Polr1e
GO_BP_m4	GO:008015	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Astl
GO_BP_m4	GO:190211	negative re	1/727	32/23843	0.629001	0.840485	0.82791	Sec22b
GO_BP_m4	GO:190218	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Zfp72
GO_BP_m4	GO:200003	regulation	1/727	32/23843	0.629001	0.840485	0.82791	Zfp706
GO_BP_m4	GO:000701	actin filame	11/727	385/23843	0.629328	0.840687	0.82811	Arhgap18/
GO_BP_m4	GO:000916	purine ribo	7/727	247/23843	0.630417	0.841437	0.828848	Ak3/Atp5c
GO_BP_m4	GO:000920	purine ribo	7/727	247/23843	0.630417	0.841437	0.828848	Ak3/Atp5c
GO_BP_m4	GO:004566	negative re	7/727	247/23843	0.630417	0.841437	0.828848	Cspg4/Dgu
GO_BP_m4	GO:003200	regulation	3/727	106/23843	0.631242	0.841832	0.829238	Akt1s1/Gas
GO_BP_m4	GO:004647	glyceropho	3/727	106/23843	0.631242	0.841832	0.829238	Htr2c/Pigp
GO_BP_m4	GO:199026	neutrophil	3/727	106/23843	0.631242	0.841832	0.829238	C3ar1/Lgal
GO_BP_m4	GO:000914	nucleoside	4/727	142/23843	0.632543	0.843332	0.830715	Ak3/Atp5c
GO_BP_m4	GO:000173	morphogen	2/727	70/23843	0.633996	0.843622	0.831001	Astn2/Ror2
GO_BP_m4	GO:000742	peripheral	2/727	70/23843	0.633996	0.843622	0.831001	Erbb2/Rela
GO_BP_m4	GO:002153	diencephal	2/727	70/23843	0.633996	0.843622	0.831001	Duox2/Zeb
GO_BP_m4	GO:003241	lysosome l	2/727	70/23843	0.633996	0.843622	0.831001	Il13/Vamp8
GO_BP_m4	GO:004211	macrophag	2/727	70/23843	0.633996	0.843622	0.831001	Ager/Il13
GO_BP_m4	GO:005090	sensory pe	2/727	70/23843	0.633996	0.843622	0.831001	Gnat1/Tas2
GO_BP_m4	GO:200024	positive reg	2/727	70/23843	0.633996	0.843622	0.831001	Aurka/Inhb
GO_BP_m4	GO:004217	regulation	10/727	352/23843	0.634328	0.843735	0.831112	Aurka/Efna
GO_BP_m4	GO:004354	positive reg	6/727	213/23843	0.63452	0.843735	0.831112	Arhgap23/
GO_BP_m4	GO:000912	purine nuc	7/727	248/23843	0.63461	0.843735	0.831112	Ak3/Atp5c
GO_BP_m4	GO:003009	myeloid ce	11/727	387/23843	0.636083	0.844225	0.831595	Car2/Gata1
GO_BP_m4	GO:004324	regulation	3/727	107/23843	0.637555	0.844225	0.831595	Nav3/Sptan
GO_BP_m4	GO:004662	regulation	3/727	107/23843	0.637555	0.844225	0.831595	Mapk14/M
GO_BP_m4	GO:003032	embryonic	4/727	143/23843	0.638014	0.844225	0.831595	Fgf4/Ror2/
GO_BP_m4	GO:003085	regulation	4/727	143/23843	0.638014	0.844225	0.831595	Ovol2/Vdr/
GO_BP_m4	GO:003511	embryonic	4/727	143/23843	0.638014	0.844225	0.831595	Fgf4/Ror2/
GO_BP_m4	GO:003164	regulation	7/727	249/23843	0.638775	0.844225	0.831595	Aurka/Efna

GO_BP_m4	GO:000741	axon guida	6/727	214/23843	0.639004	0.844225	0.831595	Efna1/Erbb
GO_BP_m4	GO:005125	positive re	11/727	388/23843	0.639436	0.844225	0.831595	Ager/Bcl10
GO_BP_m4	GO:001633	morphoge	5/727	179/23843	0.640308	0.844225	0.831595	Bcl10/Folr1
GO_BP_m4	GO:00000	mitochond	1/727	33/23843	0.640328	0.844225	0.831595	Pid1
GO_BP_m4	GO:000275	cytoplasmi	1/727	33/23843	0.640328	0.844225	0.831595	Rela
GO_BP_m4	GO:000627	DNA replic	1/727	33/23843	0.640328	0.844225	0.831595	Gmnc
GO_BP_m4	GO:000638	transcriptic	1/727	33/23843	0.640328	0.844225	0.831595	Erbb2
GO_BP_m4	GO:001057	vascular en	1/727	33/23843	0.640328	0.844225	0.831595	C3ar1
GO_BP_m4	GO:001834	protein pal	1/727	33/23843	0.640328	0.844225	0.831595	Zdhhc22
GO_BP_m4	GO:001943	triglyceride	1/727	33/23843	0.640328	0.844225	0.831595	Sik1
GO_BP_m4	GO:003438	plasma lipc	1/727	33/23843	0.640328	0.844225	0.831595	Lipc
GO_BP_m4	GO:00434	skeletal mu	1/727	33/23843	0.640328	0.844225	0.831595	Mapk14
GO_BP_m4	GO:004587	negative re	1/727	33/23843	0.640328	0.844225	0.831595	Kctd6
GO_BP_m4	GO:004594	positive re	1/727	33/23843	0.640328	0.844225	0.831595	Apoa4
GO_BP_m4	GO:004804	embryonic	1/727	33/23843	0.640328	0.844225	0.831595	Vax2
GO_BP_m4	GO:004856	embryonic	1/727	33/23843	0.640328	0.844225	0.831595	Ovol2
GO_BP_m4	GO:006033	type I inter	1/727	33/23843	0.640328	0.844225	0.831595	Oas2
GO_BP_m4	GO:006074	prostate gl	1/727	33/23843	0.640328	0.844225	0.831595	Esr2
GO_BP_m4	GO:007135	cellular res	1/727	33/23843	0.640328	0.844225	0.831595	Oas2
GO_BP_m4	GO:190102	positive re	1/727	33/23843	0.640328	0.844225	0.831595	Kcne1
GO_BP_m4	GO:190166	quinone m	1/727	33/23843	0.640328	0.844225	0.831595	Coq6
GO_BP_m4	GO:19032	regulation	1/727	33/23843	0.640328	0.844225	0.831595	Ripk1
GO_BP_m4	GO:190358	positive re	1/727	33/23843	0.640328	0.844225	0.831595	Pid1
GO_BP_m4	GO:000726	tyrosine ph	2/727	71/23843	0.641689	0.844225	0.831595	Il13/Lck
GO_BP_m4	GO:003227	negative re	2/727	71/23843	0.641689	0.844225	0.831595	Sptan1/Tm
GO_BP_m4	GO:003254	mitochond	2/727	71/23843	0.641689	0.844225	0.831595	Ears2/Mrps
GO_BP_m4	GO:003289	regulation	2/727	71/23843	0.641689	0.844225	0.831595	Htr2c/Irs2
GO_BP_m4	GO:003463	cellular car	2/727	71/23843	0.641689	0.844225	0.831595	B3gnt5/Irs2
GO_BP_m4	GO:004273	embryonic	2/727	71/23843	0.641689	0.844225	0.831595	Ror2/Tmem
GO_BP_m4	GO:004336	CD4-positi	2/727	71/23843	0.641689	0.844225	0.831595	Il27/Socs5
GO_BP_m4	GO:190336	negative re	2/727	71/23843	0.641689	0.844225	0.831595	Efna1/Pdcl3
GO_BP_m4	GO:004352	regulation	7/727	250/23843	0.642913	0.844795	0.832157	Ager/Akt1s
GO_BP_m4	GO:011005	regulation	7/727	250/23843	0.642913	0.844795	0.832157	Arhgap18/
GO_BP_m4	GO:004583	positive re	4/727	144/23843	0.643431	0.844795	0.832157	Apoa4/Htr
GO_BP_m4	GO:000184	neural tube	3/727	108/23843	0.643792	0.844795	0.832157	Bcl10/Folr1
GO_BP_m4	GO:000597	polysaccha	3/727	108/23843	0.643792	0.844795	0.832157	B3gnt5/Irs2
GO_BP_m4	GO:001092	cellular cor	3/727	108/23843	0.643792	0.844795	0.832157	Myom2/Ne
GO_BP_m4	GO:003236	regulation	3/727	108/23843	0.643792	0.844795	0.832157	Abcb4/Apo
GO_BP_m4	GO:003524	synaptic tra	3/727	108/23843	0.643792	0.844795	0.832157	Grm1/Ror2
GO_BP_m4	GO:007134	cellular res	3/727	108/23843	0.643792	0.844795	0.832157	Kif16b/Rab
GO_BP_m4	GO:00147	striated mu	12/727	424/23843	0.644357	0.844795	0.832157	Cops2/Dsp
GO_BP_m4	GO:000916	ribonucleo	7/727	251/23843	0.647024	0.844795	0.832157	Ak3/Atp5c1
GO_BP_m4	GO:000919	ribonucleo	7/727	251/23843	0.647024	0.844795	0.832157	Ak3/Atp5c1
GO_BP_m4	GO:001046	negative re	7/727	251/23843	0.647024	0.844795	0.832157	Dpep1/Gas
GO_BP_m4	GO:007066	leukocyte	9/727	321/23843	0.64744	0.844795	0.832157	Ager/Btn2a
GO_BP_m4	GO:009748	neuron prc	6/727	216/23843	0.647874	0.844795	0.832157	Efna1/Erbb
GO_BP_m4	GO:007066	positive re	4/727	145/23843	0.648795	0.844795	0.832157	Ager/Il13/I
GO_BP_m4	GO:004873	gland deve	13/727	460/23843	0.649107	0.844795	0.832157	Aurka/Duo

GO_BP_m4	GO:00305	regulation	2/727	72/23843	0.649254	0.844795	0.832157	Gata1/Slc8
GO_BP_m4	GO:004244	hormone b	2/727	72/23843	0.649254	0.844795	0.832157	Ffar3/Vdr
GO_BP_m4	GO:00550	cardiac mu	2/727	72/23843	0.649254	0.844795	0.832157	Dsp/Myom
GO_BP_m4	GO:006107	chaperone	2/727	72/23843	0.649254	0.844795	0.832157	Dnajb14/P
GO_BP_m4	GO:190211	positive re	2/727	72/23843	0.649254	0.844795	0.832157	5330417C
GO_BP_m4	GO:00606	tube closu	3/727	109/23843	0.649954	0.844795	0.832157	Bcl10/Folr1
GO_BP_m4	GO:00303	negative re	5/727	181/23843	0.64996	0.844795	0.832157	Inhba/Rtn4
GO_BP_m4	GO:004877	tissue rem	5/727	181/23843	0.64996	0.844795	0.832157	Ager/Car2/
GO_BP_m4	GO:000195	negative re	1/727	34/23843	0.65131	0.844795	0.832157	Muc4
GO_BP_m4	GO:000619	purine nuc	1/727	34/23843	0.65131	0.844795	0.832157	Nudt7
GO_BP_m4	GO:00082	C21-steroi	1/727	34/23843	0.65131	0.844795	0.832157	Akr1d1
GO_BP_m4	GO:00140	oligodendr	1/727	34/23843	0.65131	0.844795	0.832157	Nkx6-2
GO_BP_m4	GO:001404	dopamine	1/727	34/23843	0.65131	0.844795	0.832157	Rtn4
GO_BP_m4	GO:001405	regulation	1/727	34/23843	0.65131	0.844795	0.832157	Rtn4
GO_BP_m4	GO:001907	viral releas	1/727	34/23843	0.65131	0.844795	0.832157	Zfp72
GO_BP_m4	GO:002184	cell prolifer	1/727	34/23843	0.65131	0.844795	0.832157	Zeb2
GO_BP_m4	GO:003111	regulation	1/727	34/23843	0.65131	0.844795	0.832157	Nav3
GO_BP_m4	GO:003164	positive re	1/727	34/23843	0.65131	0.844795	0.832157	Hcrt
GO_BP_m4	GO:003314	negative re	1/727	34/23843	0.65131	0.844795	0.832157	Esr2
GO_BP_m4	GO:003323	regulation	1/727	34/23843	0.65131	0.844795	0.832157	Htr2c
GO_BP_m4	GO:003511	embryonic	1/727	34/23843	0.65131	0.844795	0.832157	Fgf4
GO_BP_m4	GO:003589	exit from h	1/727	34/23843	0.65131	0.844795	0.832157	Zfp72
GO_BP_m4	GO:003589	exit from h	1/727	34/23843	0.65131	0.844795	0.832157	Zfp72
GO_BP_m4	GO:004274	circadian sl	1/727	34/23843	0.65131	0.844795	0.832157	Hcrtr1
GO_BP_m4	GO:00450	DNA-depe	1/727	34/23843	0.65131	0.844795	0.832157	Cenps
GO_BP_m4	GO:004632	regulation	1/727	34/23843	0.65131	0.844795	0.832157	Irs2
GO_BP_m4	GO:005212	movement	1/727	34/23843	0.65131	0.844795	0.832157	Zfp72
GO_BP_m4	GO:005219	movement	1/727	34/23843	0.65131	0.844795	0.832157	Zfp72
GO_BP_m4	GO:006051	prostate gl	1/727	34/23843	0.65131	0.844795	0.832157	Esr2
GO_BP_m4	GO:007028	axonemal	1/727	34/23843	0.65131	0.844795	0.832157	Ccdc114
GO_BP_m4	GO:007087	regulation	1/727	34/23843	0.65131	0.844795	0.832157	Irs2
GO_BP_m4	GO:190379	negative re	1/727	34/23843	0.65131	0.844795	0.832157	Irs2
GO_BP_m4	GO:199008	response t	1/727	34/23843	0.65131	0.844795	0.832157	Rps3
GO_BP_m4	GO:199009	cellular res	1/727	34/23843	0.65131	0.844795	0.832157	Rps3
GO_BP_m4	GO:200077	regulation	1/727	34/23843	0.65131	0.844795	0.832157	Rbl1
GO_BP_m4	GO:000941	response t	6/727	217/23843	0.65226	0.845797	0.833143	Abcb4/Cyp
GO_BP_m4	GO:003018	B cell differ	4/727	146/23843	0.654105	0.84773	0.835047	Ifna12/Nfa
GO_BP_m4	GO:19037	negative re	4/727	146/23843	0.654105	0.84773	0.835047	Erbb2/Socs
GO_BP_m4	GO:00905	RNA phosp	2/727	73/23843	0.656692	0.850621	0.837896	Eri2/Rnase
GO_BP_m4	GO:190458	regulation	2/727	73/23843	0.656692	0.850621	0.837896	Gas6/Mapk
GO_BP_m4	GO:000282	regulation	4/727	147/23843	0.659361	0.850644	0.837918	Ager/Il27/
GO_BP_m4	GO:000912	nucleoside	4/727	147/23843	0.659361	0.850644	0.837918	Ak3/Atp5c
GO_BP_m4	GO:200102	regulation	5/727	183/23843	0.659446	0.850644	0.837918	Recql5/Rps
GO_BP_m4	GO:003497	response t	6/727	219/23843	0.660929	0.850644	0.837918	Atf6b/Ddit
GO_BP_m4	GO:00181	peptidyl-s	9/727	325/23843	0.661807	0.850644	0.837918	Camk1g/C
GO_BP_m4	GO:00182	peptidyl-s	10/727	360/23843	0.661947	0.850644	0.837918	Camk1g/C
GO_BP_m4	GO:00015	neurotrans	1/727	35/23843	0.661957	0.850644	0.837918	Slc1a6
GO_BP_m4	GO:000714	female mei	1/727	35/23843	0.661957	0.850644	0.837918	Aurka

GO_BP_m4	GO:000995	proximal/d	1/727	35/23843	0.661957	0.850644	0.837918	Sp8
GO_BP_m4	GO:001403	Schwann c	1/727	35/23843	0.661957	0.850644	0.837918	Rela
GO_BP_m4	GO:003106	hair follicle	1/727	35/23843	0.661957	0.850644	0.837918	Fst
GO_BP_m4	GO:003142	keratinizati	1/727	35/23843	0.661957	0.850644	0.837918	Cdh3
GO_BP_m4	GO:003222	regulation	1/727	35/23843	0.661957	0.850644	0.837918	Car2
GO_BP_m4	GO:003577	positive re	1/727	35/23843	0.661957	0.850644	0.837918	C1qtnf12
GO_BP_m4	GO:003647	cell death i	1/727	35/23843	0.661957	0.850644	0.837918	Ripk1
GO_BP_m4	GO:004230	regulation	1/727	35/23843	0.661957	0.850644	0.837918	Apoa4
GO_BP_m4	GO:004255	pteridine-c	1/727	35/23843	0.661957	0.850644	0.837918	Folr1
GO_BP_m4	GO:004662	negative re	1/727	35/23843	0.661957	0.850644	0.837918	Mir1a-2
GO_BP_m4	GO:004663	negative re	1/727	35/23843	0.661957	0.850644	0.837918	Socs5
GO_BP_m4	GO:004800	insulin-like	1/727	35/23843	0.661957	0.850644	0.837918	Cdh3
GO_BP_m4	GO:005145	intracellula	1/727	35/23843	0.661957	0.850644	0.837918	Car2
GO_BP_m4	GO:005196	positive re	1/727	35/23843	0.661957	0.850644	0.837918	Ror2
GO_BP_m4	GO:005502	negative re	1/727	35/23843	0.661957	0.850644	0.837918	Mir1a-2
GO_BP_m4	GO:006007	Wnt signali	1/727	35/23843	0.661957	0.850644	0.837918	Ror2
GO_BP_m4	GO:006044	epithelial tu	1/727	35/23843	0.661957	0.850644	0.837918	Spry2
GO_BP_m4	GO:009730	programm	1/727	35/23843	0.661957	0.850644	0.837918	Ripk1
GO_BP_m4	GO:200017	negative re	1/727	35/23843	0.661957	0.850644	0.837918	Efna1
GO_BP_m4	GO:200103	regulation	1/727	35/23843	0.661957	0.850644	0.837918	Ripk1
GO_BP_m4	GO:000749	mesoderm	3/727	111/23843	0.662047	0.850644	0.837918	Inhba/Sox1
GO_BP_m4	GO:190121	positive re	3/727	111/23843	0.662047	0.850644	0.837918	Ager/Ddit3
GO_BP_m4	GO:000862	extrinsic ap	2/727	74/23843	0.664003	0.851257	0.838522	Lgals3/Pidc
GO_BP_m4	GO:000906	aerobic res	2/727	74/23843	0.664003	0.851257	0.838522	Cycs/Mtfr1
GO_BP_m4	GO:003014	sphingolipi	2/727	74/23843	0.664003	0.851257	0.838522	A4galt/B3g
GO_BP_m4	GO:003246	regulation	2/727	74/23843	0.664003	0.851257	0.838522	Aurka/Sstr5
GO_BP_m4	GO:003272	positive re	2/727	74/23843	0.664003	0.851257	0.838522	Il27/Mir155
GO_BP_m4	GO:003320	tumor necr	2/727	74/23843	0.664003	0.851257	0.838522	Gas6/Rela
GO_BP_m4	GO:004678	microtubul	2/727	74/23843	0.664003	0.851257	0.838522	Nav3/Rps3
GO_BP_m4	GO:007142	ribonucleo	2/727	74/23843	0.664003	0.851257	0.838522	Srsf10/Tho
GO_BP_m4	GO:000268	regulation	5/727	184/23843	0.664126	0.851257	0.838522	C3ar1/Gas6
GO_BP_m4	GO:200123	negative re	6/727	220/23843	0.665213	0.852421	0.839669	Ctnna1/Ga
GO_BP_m4	GO:000236	leukocyte a	7/727	256/23843	0.667154	0.853644	0.840873	Dnase1/Ifn
GO_BP_m4	GO:000315	endotheliu	3/727	112/23843	0.667979	0.853644	0.840873	Abcb1b/Cc
GO_BP_m4	GO:004208	cytokine bi	3/727	112/23843	0.667979	0.853644	0.840873	Bcl10/Il27/
GO_BP_m4	GO:004247	inner ear m	3/727	112/23843	0.667979	0.853644	0.840873	Ror2/Spry2
GO_BP_m4	GO:004247	odontogen	3/727	112/23843	0.667979	0.853644	0.840873	Fgf4/Fst/In
GO_BP_m4	GO:005082	defense res	3/727	112/23843	0.667979	0.853644	0.840873	AY761184/
GO_BP_m4	GO:003432	cell junctio	5/727	185/23843	0.668765	0.853644	0.840873	Cdh24/Cdh
GO_BP_m4	GO:004603	ATP metab	6/727	221/23843	0.669463	0.853644	0.840873	Ak3/Atp5c1
GO_BP_m4	GO:000648	protein N-	2/727	75/23843	0.671188	0.853644	0.840873	Mogs/Stt3b
GO_BP_m4	GO:000672	isoprenoid	2/727	75/23843	0.671188	0.853644	0.840873	Cyp1a2/Pm
GO_BP_m4	GO:003314	regulation	2/727	75/23843	0.671188	0.853644	0.840873	Esr2/Ube2i
GO_BP_m4	GO:007116	ribonucleo	2/727	75/23843	0.671188	0.853644	0.840873	Srsf10/Tho
GO_BP_m4	GO:190188	regulation	2/727	75/23843	0.671188	0.853644	0.840873	Nedd4l/Np
GO_BP_m4	GO:000046	maturation	1/727	36/23843	0.67228	0.853644	0.840873	Krr1
GO_BP_m4	GO:000170	gastrulatio	1/727	36/23843	0.67228	0.853644	0.840873	Nat8f1
GO_BP_m4	GO:000340	axis elonga	1/727	36/23843	0.67228	0.853644	0.840873	Spry2

GO_BP_m4	GO:001083	positive reg	1/727	36/23843	0.67228	0.853644	0.840873	Mapk14
GO_BP_m4	GO:002179	cerebral co	1/727	36/23843	0.67228	0.853644	0.840873	Rtn4
GO_BP_m4	GO:003081	positive reg	1/727	36/23843	0.67228	0.853644	0.840873	Tshr
GO_BP_m4	GO:003288	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Irs2
GO_BP_m4	GO:003530	positive reg	1/727	36/23843	0.67228	0.853644	0.840873	Ppp1r15b
GO_BP_m4	GO:004476	multi-orga	1/727	36/23843	0.67228	0.853644	0.840873	Gas6
GO_BP_m4	GO:004646	neutral lipi	1/727	36/23843	0.67228	0.853644	0.840873	Sik1
GO_BP_m4	GO:004646	acylglycero	1/727	36/23843	0.67228	0.853644	0.840873	Sik1
GO_BP_m4	GO:004866	neuron fate	1/727	36/23843	0.67228	0.853644	0.840873	Nkx6-2
GO_BP_m4	GO:004871	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Ager
GO_BP_m4	GO:004882	erythrocyte	1/727	36/23843	0.67228	0.853644	0.840873	Gata1
GO_BP_m4	GO:005070	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Gas6
GO_BP_m4	GO:005108	'de novo' p	1/727	36/23843	0.67228	0.853644	0.840873	Dnajb14
GO_BP_m4	GO:006025	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Esr2
GO_BP_m4	GO:007139	cellular res	1/727	36/23843	0.67228	0.853644	0.840873	Mir451a
GO_BP_m4	GO:008600	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Dsp
GO_BP_m4	GO:190222	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Rps3
GO_BP_m4	GO:190269	regulation	1/727	36/23843	0.67228	0.853644	0.840873	Ctnna1
GO_BP_m4	GO:000687	cellular calc	12/727	433/23843	0.672417	0.853644	0.840873	C3ar1/Cacn
GO_BP_m4	GO:007188	adenylate c	5/727	186/23843	0.673361	0.854616	0.841831	Ffar3/Gnat
GO_BP_m4	GO:004593	negative re	6/727	222/23843	0.673678	0.854763	0.841975	Btn2a2/Hu
GO_BP_m4	GO:009027	positive reg	3/727	113/23843	0.673834	0.854763	0.841975	C1qtnf12/I
GO_BP_m4	GO:001623	macroauto	5/727	187/23843	0.677915	0.858994	0.846143	5330417C2
GO_BP_m4	GO:004424	cellular lipi	5/727	187/23843	0.677915	0.858994	0.846143	Apoa4/Dec
GO_BP_m4	GO:000175	somitogen	2/727	76/23843	0.678248	0.858994	0.846143	Ror2/Zeb2
GO_BP_m4	GO:002187	forebrain n	2/727	76/23843	0.678248	0.858994	0.846143	Inhba/Mir2
GO_BP_m4	GO:005127	regulation	2/727	76/23843	0.678248	0.858994	0.846143	Il13/Slc8a1
GO_BP_m4	GO:006118	mammary	2/727	76/23843	0.678248	0.858994	0.846143	Rtn4/Vdr
GO_BP_m4	GO:000269	positive reg	12/727	435/23843	0.678478	0.859053	0.846201	Ager/Bcl10
GO_BP_m4	GO:001657	protein deu	3/727	114/23843	0.679613	0.859053	0.846201	Otud6a/Uc
GO_BP_m4	GO:005114	striated mu	8/727	295/23843	0.680583	0.859053	0.846201	Fhl2/Mapk
GO_BP_m4	GO:000178	B cell home	1/727	37/23843	0.682288	0.859053	0.846201	Bcl10
GO_BP_m4	GO:000205	positive reg	1/727	37/23843	0.682288	0.859053	0.846201	Irs2
GO_BP_m4	GO:000282	negative re	1/727	37/23843	0.682288	0.859053	0.846201	Muc4
GO_BP_m4	GO:000677	porphyrin-	1/727	37/23843	0.682288	0.859053	0.846201	Cyp1a2
GO_BP_m4	GO:000743	salivary gla	1/727	37/23843	0.682288	0.859053	0.846201	Polb
GO_BP_m4	GO:002195	central ner	1/727	37/23843	0.682288	0.859053	0.846201	Zeb2
GO_BP_m4	GO:003050	positive reg	1/727	37/23843	0.682288	0.859053	0.846201	Slc8a1
GO_BP_m4	GO:003085	granulocyte	1/727	37/23843	0.682288	0.859053	0.846201	Gata1
GO_BP_m4	GO:004209	type 2 imm	1/727	37/23843	0.682288	0.859053	0.846201	Socs5
GO_BP_m4	GO:004573	positive reg	1/727	37/23843	0.682288	0.859053	0.846201	Pim1
GO_BP_m4	GO:004588	positive reg	1/727	37/23843	0.682288	0.859053	0.846201	Ctnna1
GO_BP_m4	GO:004598	positive reg	1/727	37/23843	0.682288	0.859053	0.846201	Lck
GO_BP_m4	GO:006067	placenta bl	1/727	37/23843	0.682288	0.859053	0.846201	Ovol2
GO_BP_m4	GO:007115	positive reg	1/727	37/23843	0.682288	0.859053	0.846201	Pidd1
GO_BP_m4	GO:007260	interleukin-	1/727	37/23843	0.682288	0.859053	0.846201	Gas6
GO_BP_m4	GO:009017	regulation	1/727	37/23843	0.682288	0.859053	0.846201	Ror2
GO_BP_m4	GO:190289	regulation	1/727	37/23843	0.682288	0.859053	0.846201	Rela

GO_BP_m4	GO:200082	regulation	1/727	37/23843	0.682288	0.859053	0.846201	Pim1
GO_BP_m4	GO:000227	myeloid le	5/727	188/23843	0.682427	0.859053	0.846201	Ager/Bcl10
GO_BP_m4	GO:005067	positive re	5/727	188/23843	0.682427	0.859053	0.846201	Cdh3/Erbb
GO_BP_m4	GO:000226	cell activati	7/727	260/23843	0.682741	0.859222	0.846367	Dnase1/Ifn
GO_BP_m4	GO:003577	insulin secr	2/727	77/23843	0.685184	0.860877	0.847998	C1qtnf12/T
GO_BP_m4	GO:004227	ribosomal	2/727	77/23843	0.685184	0.860877	0.847998	Krr1/Rps2
GO_BP_m4	GO:005145	regulation	2/727	77/23843	0.685184	0.860877	0.847998	Car2/Slc9a
GO_BP_m4	GO:005178	positive re	2/727	77/23843	0.685184	0.860877	0.847998	Fgf4/Sstr5
GO_BP_m4	GO:190160	alpha-ami	2/727	77/23843	0.685184	0.860877	0.847998	Fah/Kynu
GO_BP_m4	GO:000663	acylglycero	3/727	115/23843	0.685316	0.860877	0.847998	Apoa4/Lip
GO_BP_m4	GO:003260	interferon-	3/727	115/23843	0.685316	0.860877	0.847998	Gas6/Il27/
GO_BP_m4	GO:001993	second-me	9/727	332/23843	0.686111	0.861502	0.848614	Gpr61/Grm
GO_BP_m4	GO:000912	nucleoside	7/727	261/23843	0.686564	0.861502	0.848614	Ak3/Atp5c
GO_BP_m4	GO:000961	response t	7/727	261/23843	0.686564	0.861502	0.848614	A230050P
GO_BP_m4	GO:001063	epithelial c	7/727	261/23843	0.686564	0.861502	0.848614	Ager/Dusp
GO_BP_m4	GO:000630	double-str	5/727	189/23843	0.686895	0.861502	0.848614	Brip1/Hus1
GO_BP_m4	GO:190290	positive re	5/727	189/23843	0.686895	0.861502	0.848614	Grb2/Nav3
GO_BP_m4	GO:000628	DNA repai	12/727	438/23843	0.687447	0.861968	0.849072	Faap100/C
GO_BP_m4	GO:004689	regulation	4/727	153/23843	0.689754	0.86292	0.850011	Apoa4/Htr
GO_BP_m4	GO:007189	DNA biosy	4/727	153/23843	0.689754	0.86292	0.850011	C3ar1/Polb
GO_BP_m4	GO:003007	peptide ho	7/727	262/23843	0.690358	0.86292	0.850011	C1qtnf12/F
GO_BP_m4	GO:001802	peptidyl-ly	3/727	116/23843	0.690943	0.86292	0.850011	Camkmt/D
GO_BP_m4	GO:004210	B cell proli	3/727	116/23843	0.690943	0.86292	0.850011	Ifna12/Il13/
GO_BP_m4	GO:004210	cytokine m	3/727	116/23843	0.690943	0.86292	0.850011	Bcl10/Il27/
GO_BP_m4	GO:000057	embryonic	1/727	38/23843	0.69199	0.86292	0.850011	Peg12
GO_BP_m4	GO:000727	synaptic tr	1/727	38/23843	0.69199	0.86292	0.850011	Htr2c
GO_BP_m4	GO:003278	positive re	1/727	38/23843	0.69199	0.86292	0.850011	Dynll2
GO_BP_m4	GO:004502	plasma me	1/727	38/23843	0.69199	0.86292	0.850011	Snap47
GO_BP_m4	GO:007221	metanephr	1/727	38/23843	0.69199	0.86292	0.850011	Ret
GO_BP_m4	GO:009712	receptor lo	1/727	38/23843	0.69199	0.86292	0.850011	Snap47
GO_BP_m4	GO:009880	regulation	1/727	38/23843	0.69199	0.86292	0.850011	Gas6
GO_BP_m4	GO:190280	positive re	1/727	38/23843	0.69199	0.86292	0.850011	Anp32b
GO_BP_m4	GO:190595	negative re	1/727	38/23843	0.69199	0.86292	0.850011	Irs2
GO_BP_m4	GO:000694	regulation	2/727	78/23843	0.691997	0.86292	0.850011	Dsp/Slc8a1
GO_BP_m4	GO:000859	regulation	2/727	78/23843	0.691997	0.86292	0.850011	Neurl1a/O
GO_BP_m4	GO:001092	negative re	2/727	78/23843	0.691997	0.86292	0.850011	Rbm26/Tsk
GO_BP_m4	GO:004870	astrocyte d	2/727	78/23843	0.691997	0.86292	0.850011	Ager/Ror2
GO_BP_m4	GO:005196	regulation	2/727	78/23843	0.691997	0.86292	0.850011	Grm1/Ror2
GO_BP_m4	GO:007061	regulation	2/727	78/23843	0.691997	0.86292	0.850011	Astl/F12
GO_BP_m4	GO:000716	negative re	7/727	263/23843	0.694122	0.86512	0.852177	Ager/Btn2a
GO_BP_m4	GO:009013	epithelium	7/727	263/23843	0.694122	0.86512	0.852177	Ager/Dusp
GO_BP_m4	GO:000663	neutral lipi	3/727	117/23843	0.696494	0.867397	0.85442	Apoa4/Lip
GO_BP_m4	GO:000675	ATP biosyn	3/727	117/23843	0.696494	0.867397	0.85442	Ak3/Atp5c
GO_BP_m4	GO:001605	carbohydra	3/727	117/23843	0.696494	0.867397	0.85442	Ctbs/Manb
GO_BP_m4	GO:006056	epithelial t	10/727	371/23843	0.697904	0.868056	0.855069	Bcl10/Ccm
GO_BP_m4	GO:000244	production	8/727	300/23843	0.69838	0.868056	0.855069	Ffar3/Gas6
GO_BP_m4	GO:004667	response t	8/727	300/23843	0.69838	0.868056	0.855069	Lck/Mir7-2
GO_BP_m4	GO:003304	regulation	2/727	79/23843	0.698688	0.868056	0.855069	Rmi2/Sfpq

GO_BP_m4	GO:004327	response t	2/727	79/23843	0.698688	0.868056	0.855069	Recql5/Slc8
GO_BP_m4	GO:190390	negative re	2/727	79/23843	0.698688	0.868056	0.855069	A230050P2
GO_BP_m4	GO:007265	establishm	4/727	155/23843	0.699447	0.868056	0.855069	Ddit3/Plag
GO_BP_m4	GO:190290	regulation	9/727	336/23843	0.699508	0.868056	0.855069	Arhgap18/
GO_BP_m4	GO:000762	circadian r	5/727	192/23843	0.700045	0.868056	0.855069	Hcrtr1/Prol
GO_BP_m4	GO:004863	regulation	10/727	372/23843	0.701053	0.868056	0.855069	Anapc2/Du
GO_BP_m4	GO:000188	receptor re	1/727	39/23843	0.701397	0.868056	0.855069	Kif16b
GO_BP_m4	GO:000283	negative re	1/727	39/23843	0.701397	0.868056	0.855069	Muc4
GO_BP_m4	GO:000668	glycosphin	1/727	39/23843	0.701397	0.868056	0.855069	A4galt
GO_BP_m4	GO:002198	pituitary gl	1/727	39/23843	0.701397	0.868056	0.855069	Duox2
GO_BP_m4	GO:003043	sleep	1/727	39/23843	0.701397	0.868056	0.855069	Hcrtr1
GO_BP_m4	GO:003086	cortical act	1/727	39/23843	0.701397	0.868056	0.855069	Wipf2
GO_BP_m4	GO:003287	negative re	1/727	39/23843	0.701397	0.868056	0.855069	Dusp10
GO_BP_m4	GO:003545	cellular res	1/727	39/23843	0.701397	0.868056	0.855069	F830016B0
GO_BP_m4	GO:004327	apoptotic	1/727	39/23843	0.701397	0.868056	0.855069	Gas6
GO_BP_m4	GO:004585	pH reducti	1/727	39/23843	0.701397	0.868056	0.855069	Car2
GO_BP_m4	GO:005128	positive reg	1/727	39/23843	0.701397	0.868056	0.855069	Il13
GO_BP_m4	GO:006012	inner ear r	1/727	39/23843	0.701397	0.868056	0.855069	Tshr
GO_BP_m4	GO:007030	negative re	1/727	39/23843	0.701397	0.868056	0.855069	Dusp10
GO_BP_m4	GO:190293	regulation	1/727	39/23843	0.701397	0.868056	0.855069	Vdr
GO_BP_m4	GO:009013	tissue migr	7/727	265/23843	0.701562	0.868056	0.855069	Ager/Dusp
GO_BP_m4	GO:000193	regulation	3/727	118/23843	0.701969	0.868335	0.855344	Ager/Mydg
GO_BP_m4	GO:001097	positive reg	9/727	337/23843	0.7028	0.869138	0.856135	Anapc2/Its
GO_BP_m4	GO:000865	phospholip	4/727	156/23843	0.704211	0.870595	0.857571	Htr2c/Pigp
GO_BP_m4	GO:000640	mRNA cata	5/727	193/23843	0.704343	0.870595	0.857571	Cnot6/Eif3
GO_BP_m4	GO:005070	regulation	12/727	444/23843	0.704935	0.870601	0.857576	Btn2a2/C1
GO_BP_m4	GO:004426	cellular car	7/727	266/23843	0.705237	0.870601	0.857576	B3gnt5/C1
GO_BP_m4	GO:000315	outflow tra	2/727	80/23843	0.705258	0.870601	0.857576	Folr1/Sox1
GO_BP_m4	GO:002167	nerve deve	2/727	80/23843	0.705258	0.870601	0.857576	Ret/Rpl24
GO_BP_m4	GO:190331	regulation	2/727	80/23843	0.705258	0.870601	0.857576	Astl/F12
GO_BP_m4	GO:000647	protein dep	6/727	230/23843	0.706149	0.871476	0.858438	4933415F2
GO_BP_m4	GO:004348	regulation	3/727	119/23843	0.707368	0.871914	0.85887	Rbfox3/Srs
GO_BP_m4	GO:004648	phosphatic	3/727	119/23843	0.707368	0.871914	0.85887	Htr2c/Pigp
GO_BP_m4	GO:006053	muscle tiss	12/727	445/23843	0.707791	0.871914	0.85887	Cops2/Dsp
GO_BP_m4	GO:000301	vascular pr	5/727	194/23843	0.708597	0.871914	0.85887	Cacna1g/E
GO_BP_m4	GO:003103	actomyosin	5/727	194/23843	0.708597	0.871914	0.85887	Eln/Myom2
GO_BP_m4	GO:000193	negative re	1/727	40/23843	0.710516	0.871914	0.85887	Ager
GO_BP_m4	GO:000282	negative re	1/727	40/23843	0.710516	0.871914	0.85887	Muc4
GO_BP_m4	GO:000315	regulation	1/727	40/23843	0.710516	0.871914	0.85887	Pim1
GO_BP_m4	GO:000618	cGMP bios	1/727	40/23843	0.710516	0.871914	0.85887	Htr2c
GO_BP_m4	GO:000637	mRNA poly	1/727	40/23843	0.710516	0.871914	0.85887	Nelfe
GO_BP_m4	GO:000911	nucleobase	1/727	40/23843	0.710516	0.871914	0.85887	Aox3
GO_BP_m4	GO:001569	organic cat	1/727	40/23843	0.710516	0.871914	0.85887	Htr2c
GO_BP_m4	GO:001660	Rac protein	1/727	40/23843	0.710516	0.871914	0.85887	Tiam1
GO_BP_m4	GO:003080	positive reg	1/727	40/23843	0.710516	0.871914	0.85887	Tshr
GO_BP_m4	GO:003245	regulation	1/727	40/23843	0.710516	0.871914	0.85887	Trabd2b
GO_BP_m4	GO:003334	cholesterol	1/727	40/23843	0.710516	0.871914	0.85887	Apoa4
GO_BP_m4	GO:003541	protein loc	1/727	40/23843	0.710516	0.871914	0.85887	Snap47

GO_BP_m4	GO:004873	epidermis r	1/727	40/23843	0.710516	0.871914	0.85887	Fst
GO_BP_m4	GO:004887	homeostas	1/727	40/23843	0.710516	0.871914	0.85887	Gata1
GO_BP_m4	GO:006060	mammary	1/727	40/23843	0.710516	0.871914	0.85887	Vdr
GO_BP_m4	GO:009878	ncRNA trar	1/727	40/23843	0.710516	0.871914	0.85887	Npm3
GO_BP_m4	GO:190403	positive reg	1/727	40/23843	0.710516	0.871914	0.85887	Pim1
GO_BP_m4	GO:000193	positive reg	2/727	81/23843	0.711708	0.872481	0.859428	Mydgf/Pdc
GO_BP_m4	GO:001590	fatty acid tr	2/727	81/23843	0.711708	0.872481	0.859428	Abcc4/Irs2
GO_BP_m4	GO:001921	regulation	2/727	81/23843	0.711708	0.872481	0.859428	Apoa4/Irs2
GO_BP_m4	GO:003202	positive reg	2/727	81/23843	0.711708	0.872481	0.859428	C1qtnf12/I
GO_BP_m4	GO:001092	regulation	3/727	120/23843	0.712692	0.873128	0.860065	Ppp1r15b/
GO_BP_m4	GO:004533	cellular res	4/727	158/23843	0.713575	0.873128	0.860065	Cycs/Cyp1a
GO_BP_m4	GO:001003	response to	6/727	232/23843	0.713914	0.873128	0.860065	Aqp9/Cacn
GO_BP_m4	GO:001082	regulation	5/727	196/23843	0.716977	0.873128	0.860065	Pid1/Plagl2
GO_BP_m4	GO:004358	ear develop	6/727	233/23843	0.717744	0.873128	0.860065	Anp32b/Cc
GO_BP_m4	GO:001810	peptidyl-th	3/727	121/23843	0.717942	0.873128	0.860065	Camk1g/D
GO_BP_m4	GO:004848	synaptic ve	3/727	121/23843	0.717942	0.873128	0.860065	Rims4/Snap
GO_BP_m4	GO:009748	establishm	3/727	121/23843	0.717942	0.873128	0.860065	Rims4/Snap
GO_BP_m4	GO:000042	autophagy	2/727	82/23843	0.718039	0.873128	0.860065	Fundc2/To
GO_BP_m4	GO:003064	regulation	2/727	82/23843	0.718039	0.873128	0.860065	Car2/Slc9a
GO_BP_m4	GO:003111	regulation	2/727	82/23843	0.718039	0.873128	0.860065	Nav3/Rps3
GO_BP_m4	GO:003294	negative re	2/727	82/23843	0.718039	0.873128	0.860065	Btn2a2/Erb
GO_BP_m4	GO:003530	regulation	2/727	82/23843	0.718039	0.873128	0.860065	4933415F2
GO_BP_m4	GO:005067	negative re	2/727	82/23843	0.718039	0.873128	0.860065	Btn2a2/Erb
GO_BP_m4	GO:006172	mitochond	2/727	82/23843	0.718039	0.873128	0.860065	Fundc2/To
GO_BP_m4	GO:000703	vacuole org	4/727	159/23843	0.718175	0.873128	0.860065	5330417C2
GO_BP_m4	GO:007058	protein loc	4/727	159/23843	0.718175	0.873128	0.860065	Ddit3/Plag
GO_BP_m4	GO:000196	positive reg	1/727	41/23843	0.719358	0.873128	0.860065	Gas6
GO_BP_m4	GO:000650	membrane	1/727	41/23843	0.719358	0.873128	0.860065	Adam19
GO_BP_m4	GO:000669	prostanoid	1/727	41/23843	0.719358	0.873128	0.860065	Ces2h
GO_BP_m4	GO:000669	prostaglan	1/727	41/23843	0.719358	0.873128	0.860065	Ces2h
GO_BP_m4	GO:000733	binding of	1/727	41/23843	0.719358	0.873128	0.860065	Astl
GO_BP_m4	GO:000743	salivary gla	1/727	41/23843	0.719358	0.873128	0.860065	Polb
GO_BP_m4	GO:000926	response to	1/727	41/23843	0.719358	0.873128	0.860065	Kcne1
GO_BP_m4	GO:001047	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Sox17
GO_BP_m4	GO:001090	positive reg	1/727	41/23843	0.719358	0.873128	0.860065	Irs2
GO_BP_m4	GO:001967	NAD metal	1/727	41/23843	0.719358	0.873128	0.860065	Kynu
GO_BP_m4	GO:002152	spinal cord	1/727	41/23843	0.719358	0.873128	0.860065	Nkx6-2
GO_BP_m4	GO:003281	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Gas6
GO_BP_m4	GO:003296	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Ager
GO_BP_m4	GO:004218	ketone bio	1/727	41/23843	0.719358	0.873128	0.860065	Coq6
GO_BP_m4	GO:004663	positive reg	1/727	41/23843	0.719358	0.873128	0.860065	Socs5
GO_BP_m4	GO:005069	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Il27
GO_BP_m4	GO:006101	positive reg	1/727	41/23843	0.719358	0.873128	0.860065	Zfp36l1
GO_BP_m4	GO:006102	establishm	1/727	41/23843	0.719358	0.873128	0.860065	Abcb1b
GO_BP_m4	GO:006151	protein loc	1/727	41/23843	0.719358	0.873128	0.860065	Wdr35
GO_BP_m4	GO:009034	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Rbl1
GO_BP_m4	GO:009703	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Abcb4
GO_BP_m4	GO:190266	regulation	1/727	41/23843	0.719358	0.873128	0.860065	Zswim4

GO_BP_m4	GO:00105	regulation	6/727	234/23843	0.721538	0.875551	0.862452	5330417C2
GO_BP_m4	GO:00069	nucleus or	3/727	122/23843	0.723116	0.875654	0.862554	Agap3/Par
GO_BP_m4	GO:00095	detection	3/727	122/23843	0.723116	0.875654	0.862554	Cabp4/Gn
GO_BP_m4	GO:003192	TOR signal	3/727	122/23843	0.723116	0.875654	0.862554	Akt1s1/Ga
GO_BP_m4	GO:00511	regulation	3/727	122/23843	0.723116	0.875654	0.862554	Ager/Ddit
GO_BP_m4	GO:190332	positive re	3/727	122/23843	0.723116	0.875654	0.862554	Bcl10/Rps2
GO_BP_m4	GO:00085	regulation	2/727	83/23843	0.724253	0.875654	0.862554	Ctnna1/Kct
GO_BP_m4	GO:00324	positive re	2/727	83/23843	0.724253	0.875654	0.862554	Aurka/Soc
GO_BP_m4	GO:00468	positive re	2/727	83/23843	0.724253	0.875654	0.862554	Apoa4/Htr
GO_BP_m4	GO:00162	regulation	4/727	161/23843	0.72721	0.875654	0.862554	Mapk14/M
GO_BP_m4	GO:00002	mitochond	1/727	42/23843	0.72793	0.875654	0.862554	Mtfr1
GO_BP_m4	GO:00003	regulation	1/727	42/23843	0.72793	0.875654	0.862554	Rbfox3
GO_BP_m4	GO:00009	mitochond	1/727	42/23843	0.72793	0.875654	0.862554	Ears2
GO_BP_m4	GO:000597	glycogen	1/727	42/23843	0.72793	0.875654	0.862554	Irs2
GO_BP_m4	GO:00070	mitotic me	1/727	42/23843	0.72793	0.875654	0.862554	Spdl1
GO_BP_m4	GO:00092	glucan bio	1/727	42/23843	0.72793	0.875654	0.862554	Irs2
GO_BP_m4	GO:00107	regulation	1/727	42/23843	0.72793	0.875654	0.862554	Spry2
GO_BP_m4	GO:001097	negative re	1/727	42/23843	0.72793	0.875654	0.862554	Hus1
GO_BP_m4	GO:00182	peptidyl-p	1/727	42/23843	0.72793	0.875654	0.862554	Ppid
GO_BP_m4	GO:00308	negative re	1/727	42/23843	0.72793	0.875654	0.862554	Pid1
GO_BP_m4	GO:00310	negative re	1/727	42/23843	0.72793	0.875654	0.862554	Trip12
GO_BP_m4	GO:00328	regulation	1/727	42/23843	0.72793	0.875654	0.862554	Irs2
GO_BP_m4	GO:003592	cellular res	1/727	42/23843	0.72793	0.875654	0.862554	Mapk14
GO_BP_m4	GO:004001	positive re	1/727	42/23843	0.72793	0.875654	0.862554	Tshr
GO_BP_m4	GO:004207	intraciliary	1/727	42/23843	0.72793	0.875654	0.862554	Wdr35
GO_BP_m4	GO:00423	positive re	1/727	42/23843	0.72793	0.875654	0.862554	Mapk14
GO_BP_m4	GO:004241	dopamine	1/727	42/23843	0.72793	0.875654	0.862554	Htr2c
GO_BP_m4	GO:004277	intrinsic ap	1/727	42/23843	0.72793	0.875654	0.862554	Phlda3
GO_BP_m4	GO:00436	RNA polya	1/727	42/23843	0.72793	0.875654	0.862554	Nelfe
GO_BP_m4	GO:005167	membrane	1/727	42/23843	0.72793	0.875654	0.862554	AY761184
GO_BP_m4	GO:00601	maternal p	1/727	42/23843	0.72793	0.875654	0.862554	Vdr
GO_BP_m4	GO:00701	positive re	1/727	42/23843	0.72793	0.875654	0.862554	Slc8a1
GO_BP_m4	GO:190037	negative re	1/727	42/23843	0.72793	0.875654	0.862554	Pid1
GO_BP_m4	GO:00073	determinat	3/727	123/23843	0.728216	0.875654	0.862554	Folr1/Ovol
GO_BP_m4	GO:00095	detection	3/727	123/23843	0.728216	0.875654	0.862554	Cabp4/Gn
GO_BP_m4	GO:00459	regulation	3/727	123/23843	0.728216	0.875654	0.862554	Gata1/Sox
GO_BP_m4	GO:19001	regulation	3/727	123/23843	0.728216	0.875654	0.862554	Dclk3/Gas
GO_BP_m4	GO:00215	telencepha	6/727	236/23843	0.729019	0.876399	0.863288	Fezf1/Inhb
GO_BP_m4	GO:00305	intracellula	5/727	199/23843	0.729223	0.876424	0.863312	Esr2/Pim1/
GO_BP_m4	GO:004341	macromole	7/727	273/23843	0.730117	0.877118	0.863996	Bhmt/Cam
GO_BP_m4	GO:00458	negative re	2/727	84/23843	0.730351	0.877118	0.863996	Pik3ip1/Sik
GO_BP_m4	GO:19059	positive re	2/727	84/23843	0.730351	0.877118	0.863996	Abcb4/Ap
GO_BP_m4	GO:00072	spermatog	13/727	489/23843	0.731227	0.877924	0.864789	Brip1/Cats
GO_BP_m4	GO:00458	negative re	9/727	346/23843	0.731389	0.877924	0.864789	Dpep1/Efn
GO_BP_m4	GO:00313	positive re	6/727	237/23843	0.732706	0.879224	0.86607	Cnot6/Grb
GO_BP_m4	GO:003134	negative re	5/727	200/23843	0.733219	0.879224	0.86607	Ager/Dusp
GO_BP_m4	GO:000242	immune re	8/727	311/23843	0.735243	0.879224	0.86607	Bcl10/Btn2
GO_BP_m4	GO:00017	cell fate de	1/727	43/23843	0.73624	0.879224	0.86607	Sox17

GO_BP_m4	GO:00196	negative re	1/727	43/23843	0.73624	0.879224	0.86607	Gas6
GO_BP_m4	GO:00762	adult walki	1/727	43/23843	0.73624	0.879224	0.86607	Uchl3
GO_BP_m4	GO:003111	negative re	1/727	43/23843	0.73624	0.879224	0.86607	Nav3
GO_BP_m4	GO:00451	establishm	1/727	43/23843	0.73624	0.879224	0.86607	Mtcl1
GO_BP_m4	GO:00507	interleukin	1/727	43/23843	0.73624	0.879224	0.86607	Gas6
GO_BP_m4	GO:007052	platelet ag	1/727	43/23843	0.73624	0.879224	0.86607	Gata1
GO_BP_m4	GO:00705	protein K6	1/727	43/23843	0.73624	0.879224	0.86607	Trip12
GO_BP_m4	GO:19010	regulation	1/727	43/23843	0.73624	0.879224	0.86607	Ripk1
GO_BP_m4	GO:190311	regulation	1/727	43/23843	0.73624	0.879224	0.86607	Dsp
GO_BP_m4	GO:20000	negative re	1/727	43/23843	0.73624	0.879224	0.86607	Pdcl3
GO_BP_m4	GO:004247	odontoger	2/727	85/23843	0.736334	0.879224	0.86607	Fgf4/Fst
GO_BP_m4	GO:00435	regulation	2/727	85/23843	0.736334	0.879224	0.86607	Gtf2ird1/N
GO_BP_m4	GO:00459	positive re	2/727	85/23843	0.736334	0.879224	0.86607	Pid1/Tshr
GO_BP_m4	GO:006041	muscle tiss	2/727	85/23843	0.736334	0.879224	0.86607	Dsp/Myom
GO_BP_m4	GO:006184	antimicrob	2/727	85/23843	0.736334	0.879224	0.86607	AY761184/
GO_BP_m4	GO:00706	negative re	2/727	85/23843	0.736334	0.879224	0.86607	Btn2a2/Erb
GO_BP_m4	GO:190054	positive re	2/727	85/23843	0.736334	0.879224	0.86607	Pid1/Tshr
GO_BP_m4	GO:00109	negative re	5/727	201/23843	0.737172	0.880005	0.866839	Dpep1/Gas
GO_BP_m4	GO:004687	hormone s	9/727	348/23843	0.737485	0.880159	0.866991	C1qtnf12/
GO_BP_m4	GO:001921	regulation	8/727	312/23843	0.738436	0.881074	0.867892	Apoa4/Htr
GO_BP_m4	GO:00026	negative re	4/727	164/23843	0.740356	0.882483	0.869281	Btn2a2/Erb
GO_BP_m4	GO:00353	regulation	4/727	164/23843	0.740356	0.882483	0.869281	4933415F2
GO_BP_m4	GO:005117	import into	4/727	164/23843	0.740356	0.882483	0.869281	Agap3/Gas
GO_BP_m4	GO:19018	regulation	4/727	164/23843	0.740356	0.882483	0.869281	Mapk14/M
GO_BP_m4	GO:004244	hormone n	5/727	202/23843	0.741082	0.883129	0.869917	Akr1d1/Du
GO_BP_m4	GO:00016	metanephr	2/727	86/23843	0.742203	0.884024	0.870799	Ret/Slc5a1
GO_BP_m4	GO:00513	chromosor	2/727	86/23843	0.742203	0.884024	0.870799	Cenps/Rec
GO_BP_m4	GO:00027	regulation	3/727	126/23843	0.743074	0.884315	0.871085	Ffar3/Il13/
GO_BP_m4	GO:00066	fatty acid b	3/727	126/23843	0.743074	0.884315	0.871085	Apoa4/Lip
GO_BP_m4	GO:00070	mitotic cell	3/727	126/23843	0.743074	0.884315	0.871085	Hus1/Pidd
GO_BP_m4	GO:00069	vesicle doc	1/727	44/23843	0.744297	0.884315	0.871085	Rab40b
GO_BP_m4	GO:00328	positive re	1/727	44/23843	0.744297	0.884315	0.871085	Htr2c
GO_BP_m4	GO:004312	negative re	1/727	44/23843	0.744297	0.884315	0.871085	Ripk1
GO_BP_m4	GO:006161	pri-miRNA	1/727	44/23843	0.744297	0.884315	0.871085	Rela
GO_BP_m4	GO:006191	selective a	1/727	44/23843	0.744297	0.884315	0.871085	Tomm7
GO_BP_m4	GO:00906	walking be	1/727	44/23843	0.744297	0.884315	0.871085	Uchl3
GO_BP_m4	GO:190314	regulation	1/727	44/23843	0.744297	0.884315	0.871085	Tomm7
GO_BP_m4	GO:00486	regulation	4/727	165/23843	0.744629	0.88449	0.871258	Mapk14/M
GO_BP_m4	GO:00335	carbohydra	6/727	241/23843	0.747099	0.886764	0.873498	Ager/C1qt
GO_BP_m4	GO:00425	glucose ho	6/727	241/23843	0.747099	0.886764	0.873498	Ager/C1qt
GO_BP_m4	GO:00091	ribonucleo	2/727	87/23843	0.747961	0.886764	0.873498	Ak3/Nudt5
GO_BP_m4	GO:002187	forebrain g	2/727	87/23843	0.747961	0.886764	0.873498	Inhba/Mir2
GO_BP_m4	GO:003307	T cell differ	2/727	87/23843	0.747961	0.886764	0.873498	Erbb2/Zfp
GO_BP_m4	GO:003444	substrate a	2/727	87/23843	0.747961	0.886764	0.873498	Efna1/Parv
GO_BP_m4	GO:00160	carbohydra	5/727	204/23843	0.748774	0.886764	0.873498	B3gnt5/Ca
GO_BP_m4	GO:00016	temperatu	1/727	45/23843	0.752108	0.886764	0.873498	Hcrt
GO_BP_m4	GO:00026	positive re	1/727	45/23843	0.752108	0.886764	0.873498	Il13
GO_BP_m4	GO:00075	myoblast f	1/727	45/23843	0.752108	0.886764	0.873498	Mapk14

GO_BP_m4	GO:00104	regulation	1/727	45/23843	0.752108	0.886764	0.873498	Irs2
GO_BP_m4	GO:001071	positive re	1/727	45/23843	0.752108	0.886764	0.873498	Ager
GO_BP_m4	GO:00301	collagen fi	1/727	45/23843	0.752108	0.886764	0.873498	Lum
GO_BP_m4	GO:00305	androgen	1/727	45/23843	0.752108	0.886764	0.873498	Esr2
GO_BP_m4	GO:00308	negative re	1/727	45/23843	0.752108	0.886764	0.873498	Ovol2
GO_BP_m4	GO:003164	protein de	1/727	45/23843	0.752108	0.886764	0.873498	Sox17
GO_BP_m4	GO:003301	tetrapyrrol	1/727	45/23843	0.752108	0.886764	0.873498	Cyp1a2
GO_BP_m4	GO:00459	positive re	1/727	45/23843	0.752108	0.886764	0.873498	Htr2c
GO_BP_m4	GO:004801	vascular e	1/727	45/23843	0.752108	0.886764	0.873498	Mapk14
GO_BP_m4	GO:00508	multicellul	1/727	45/23843	0.752108	0.886764	0.873498	Gak
GO_BP_m4	GO:00519	regulation	1/727	45/23843	0.752108	0.886764	0.873498	Htr2c
GO_BP_m4	GO:006041	ventricular	1/727	45/23843	0.752108	0.886764	0.873498	Nfatc1
GO_BP_m4	GO:006061	adipose ti	1/727	45/23843	0.752108	0.886764	0.873498	Slc25a25
GO_BP_m4	GO:00607	positive re	1/727	45/23843	0.752108	0.886764	0.873498	Gas6
GO_BP_m4	GO:00712	cellular re	1/727	45/23843	0.752108	0.886764	0.873498	Ly6g6d
GO_BP_m4	GO:00713	cellular re	1/727	45/23843	0.752108	0.886764	0.873498	Ret
GO_BP_m4	GO:00901	regulation	1/727	45/23843	0.752108	0.886764	0.873498	Wdr35
GO_BP_m4	GO:00903	regulation	1/727	45/23843	0.752108	0.886764	0.873498	Pid1
GO_BP_m4	GO:19004	regulation	1/727	45/23843	0.752108	0.886764	0.873498	Arc
GO_BP_m4	GO:19023	negative re	1/727	45/23843	0.752108	0.886764	0.873498	Nbas
GO_BP_m4	GO:00344	nucleobas	4/727	167/23843	0.753016	0.887397	0.874121	Nme5/Nuc
GO_BP_m4	GO:00971	ammoniu	4/727	167/23843	0.753016	0.887397	0.874121	Apoa4/Gd
GO_BP_m4	GO:00090	cellular am	2/727	88/23843	0.753607	0.887875	0.874592	Fah/Kynu
GO_BP_m4	GO:00070	chromoso	8/727	317/23843	0.754003	0.888122	0.874835	Cenps/Brip
GO_BP_m4	GO:00026	positive re	5/727	206/23843	0.756295	0.889115	0.875813	Ffar3/Il13/
GO_BP_m4	GO:00434	negative re	4/727	168/23843	0.757129	0.889115	0.875813	Ddit3/Gas
GO_BP_m4	GO:00017	cell fate sp	2/727	89/23843	0.759144	0.889115	0.875813	Nkx6-2/So
GO_BP_m4	GO:005507	iron ion ho	2/727	89/23843	0.759144	0.889115	0.875813	Heph/Slc2
GO_BP_m4	GO:00705	response t	2/727	89/23843	0.759144	0.889115	0.875813	Rela/Ythdc
GO_BP_m4	GO:00023	natural kill	1/727	46/23843	0.759681	0.889115	0.875813	Ifna12
GO_BP_m4	GO:00069	nuclear en	1/727	46/23843	0.759681	0.889115	0.875813	Parp11
GO_BP_m4	GO:00070	endosome	1/727	46/23843	0.759681	0.889115	0.875813	Rilp
GO_BP_m4	GO:00090	aspartate f	1/727	46/23843	0.759681	0.889115	0.875813	Bhmt
GO_BP_m4	GO:001071	regulation	1/727	46/23843	0.759681	0.889115	0.875813	Ager
GO_BP_m4	GO:00181	peptidyl-c	1/727	46/23843	0.759681	0.889115	0.875813	Zdhhc22
GO_BP_m4	GO:00226	ovulation c	1/727	46/23843	0.759681	0.889115	0.875813	Inhba
GO_BP_m4	GO:00305	intracellula	1/727	46/23843	0.759681	0.889115	0.875813	Esr2
GO_BP_m4	GO:00316	lipopolysa	1/727	46/23843	0.759681	0.889115	0.875813	Mapk14
GO_BP_m4	GO:00323	icosanoid	1/727	46/23843	0.759681	0.889115	0.875813	Abcc4
GO_BP_m4	GO:003411	heterotypi	1/727	46/23843	0.759681	0.889115	0.875813	Dsp
GO_BP_m4	GO:00350	sperm-eg	1/727	46/23843	0.759681	0.889115	0.875813	Astl
GO_BP_m4	GO:00422	regulation	1/727	46/23843	0.759681	0.889115	0.875813	Serpinb9
GO_BP_m4	GO:00485	spleen dev	1/727	46/23843	0.759681	0.889115	0.875813	Polb
GO_BP_m4	GO:00485	oocyte dev	1/727	46/23843	0.759681	0.889115	0.875813	Aurka
GO_BP_m4	GO:00514	regulation	1/727	46/23843	0.759681	0.889115	0.875813	Rps2
GO_BP_m4	GO:00514	regulation	1/727	46/23843	0.759681	0.889115	0.875813	Neurl1a
GO_BP_m4	GO:00726	protein loc	1/727	46/23843	0.759681	0.889115	0.875813	Aurka
GO_BP_m4	GO:00901	cochlea de	1/727	46/23843	0.759681	0.889115	0.875813	Tshr

GO_BP_m4	GO:009869	regulation	1/727	46/23843	0.759681	0.889115	0.875813	Rims4
GO_BP_m4	GO:200116	regulation	1/727	46/23843	0.759681	0.889115	0.875813	Pid1
GO_BP_m4	GO:003001	establishm	3/727	130/23843	0.761871	0.89146	0.878123	Frmd4b/Sp
GO_BP_m4	GO:000246	adaptive in	10/727	393/23843	0.762342	0.891793	0.878451	Ager/Bcl10
GO_BP_m4	GO:005085	antigen rec	7/727	283/23843	0.763083	0.892442	0.87909	Bcl10/Btn2
GO_BP_m4	GO:000991	hormone t	9/727	357/23843	0.763751	0.893004	0.879644	C1qtnf12/F
GO_BP_m4	GO:003530	negative re	2/727	90/23843	0.764573	0.893529	0.880161	Rbm26/Tsk
GO_BP_m4	GO:005079	regulation	2/727	90/23843	0.764573	0.893529	0.880161	Esr2/Hcrtr1
GO_BP_m4	GO:000664	membrane	4/727	170/23843	0.765196	0.893551	0.880183	A4galt/B3g
GO_BP_m4	GO:000961	response t	4/727	170/23843	0.765196	0.893551	0.880183	Lck/Mapk1
GO_BP_m4	GO:000271	regulation	1/727	47/23843	0.767023	0.893551	0.880183	Serpinb9
GO_BP_m4	GO:001657	histone ubi	1/727	47/23843	0.767023	0.893551	0.880183	Trip12
GO_BP_m4	GO:002153	neural tube	1/727	47/23843	0.767023	0.893551	0.880183	Sox17
GO_BP_m4	GO:003233	regulation	1/727	47/23843	0.767023	0.893551	0.880183	Rela
GO_BP_m4	GO:004871	regulation	1/727	47/23843	0.767023	0.893551	0.880183	Dusp10
GO_BP_m4	GO:005105	negative re	1/727	47/23843	0.767023	0.893551	0.880183	Sik1
GO_BP_m4	GO:006076	negative re	1/727	47/23843	0.767023	0.893551	0.880183	Gas6
GO_BP_m4	GO:007026	necrotic ce	1/727	47/23843	0.767023	0.893551	0.880183	Ripk1
GO_BP_m4	GO:009858	cellular res	1/727	47/23843	0.767023	0.893551	0.880183	Mapk14
GO_BP_m4	GO:009960	regulation	1/727	47/23843	0.767023	0.893551	0.880183	Arc
GO_BP_m4	GO:190459	positive reg	1/727	47/23843	0.767023	0.893551	0.880183	Mapk14
GO_BP_m4	GO:001619	endosomal	4/727	171/23843	0.76915	0.895594	0.882195	Bet1l/Ehd4
GO_BP_m4	GO:004259	response t	4/727	171/23843	0.76915	0.895594	0.882195	5330417C2
GO_BP_m4	GO:007252	pyridine-co	2/727	91/23843	0.769896	0.896244	0.882835	Acmsd/Kyn
GO_BP_m4	GO:000193	endothelial	3/727	132/23843	0.770843	0.896909	0.883491	Ager/Myd
GO_BP_m4	GO:006104	regulation	3/727	132/23843	0.770843	0.896909	0.883491	Ager/Dusp
GO_BP_m4	GO:000276	immune re	8/727	323/23843	0.771808	0.897813	0.884381	Bcl10/Btn2
GO_BP_m4	GO:005134	negative re	10/727	397/23843	0.772958	0.897905	0.884472	Dpep1/Gas
GO_BP_m4	GO:000276	negative re	1/727	48/23843	0.77414	0.897905	0.884472	Thoc5
GO_BP_m4	GO:000701	microtubul	1/727	48/23843	0.77414	0.897905	0.884472	Nav3
GO_BP_m4	GO:000712	synapsis	1/727	48/23843	0.77414	0.897905	0.884472	Brip1
GO_BP_m4	GO:001059	negative re	1/727	48/23843	0.77414	0.897905	0.884472	Ager
GO_BP_m4	GO:001086	positive reg	1/727	48/23843	0.77414	0.897905	0.884472	Inhba
GO_BP_m4	GO:002154	cranial ner	1/727	48/23843	0.77414	0.897905	0.884472	Rpl24
GO_BP_m4	GO:003164	regulation	1/727	48/23843	0.77414	0.897905	0.884472	Nkx6-2
GO_BP_m4	GO:003265	regulation	1/727	48/23843	0.77414	0.897905	0.884472	Ager
GO_BP_m4	GO:004366	regulation	1/727	48/23843	0.77414	0.897905	0.884472	Ppp1r15b
GO_BP_m4	GO:004512	regulation	1/727	48/23843	0.77414	0.897905	0.884472	Car2
GO_BP_m4	GO:004866	negative re	1/727	48/23843	0.77414	0.897905	0.884472	Esr2
GO_BP_m4	GO:003133	positive reg	8/727	324/23843	0.774683	0.898074	0.884638	5330417C2
GO_BP_m4	GO:000704	lysosomal t	2/727	92/23843	0.775113	0.898074	0.884638	Gak/Rilp
GO_BP_m4	GO:006002	roof of mo	2/727	92/23843	0.775113	0.898074	0.884638	Anp32b/In
GO_BP_m4	GO:000626	DNA-depe	3/727	133/23843	0.775225	0.898074	0.884638	Cenps/Gm
GO_BP_m4	GO:009028	negative re	3/727	133/23843	0.775225	0.898074	0.884638	Fam72a/Sp
GO_BP_m4	GO:006135	neural prec	4/727	173/23843	0.776903	0.89958	0.886122	Ctnna1/Ga
GO_BP_m4	GO:005149	positive reg	5/727	212/23843	0.777845	0.89958	0.886122	Grb2/Nav3
GO_BP_m4	GO:004247	ear morph	3/727	134/23843	0.779537	0.89958	0.886122	Ror2/Spry2
GO_BP_m4	GO:003083	positive reg	2/727	93/23843	0.780227	0.89958	0.886122	Grb2/Wipf

GO_BP_m4	GO:004864	muscle org	2/727	93/23843	0.780227	0.89958	0.886122	Dsp/Myom
GO_BP_m4	GO:190547	positive reg	2/727	93/23843	0.780227	0.89958	0.886122	Erbb2/Mtcl
GO_BP_m4	GO:006144	connective	6/727	251/23843	0.780609	0.89958	0.886122	C3ar1/Fgf4
GO_BP_m4	GO:003510	appendage	4/727	174/23843	0.780701	0.89958	0.886122	Fgf4/Ror2/
GO_BP_m4	GO:003510	limb morph	4/727	174/23843	0.780701	0.89958	0.886122	Fgf4/Ror2/
GO_BP_m4	GO:004576	positive reg	4/727	174/23843	0.780701	0.89958	0.886122	C3ar1/Lgal
GO_BP_m4	GO:005079	regulation	4/727	174/23843	0.780701	0.89958	0.886122	C1qtnf12/I
GO_BP_m4	GO:001066	regulation	1/727	49/23843	0.781041	0.89958	0.886122	Fndc1
GO_BP_m4	GO:001587	dopamine	1/727	49/23843	0.781041	0.89958	0.886122	Rtn4
GO_BP_m4	GO:003019	negative re	1/727	49/23843	0.781041	0.89958	0.886122	F12
GO_BP_m4	GO:003021	megakaryc	1/727	49/23843	0.781041	0.89958	0.886122	Gata1
GO_BP_m4	GO:003101	endocrine	1/727	49/23843	0.781041	0.89958	0.886122	Nkx6-2
GO_BP_m4	GO:003235	response to	1/727	49/23843	0.781041	0.89958	0.886122	Esr2
GO_BP_m4	GO:003294	secretion b	1/727	49/23843	0.781041	0.89958	0.886122	Vamp8
GO_BP_m4	GO:003296	collagen bi	1/727	49/23843	0.781041	0.89958	0.886122	Ager
GO_BP_m4	GO:004501	actin nucle	1/727	49/23843	0.781041	0.89958	0.886122	Wipf2
GO_BP_m4	GO:004580	negative re	1/727	49/23843	0.781041	0.89958	0.886122	Lgals3
GO_BP_m4	GO:190004	negative re	1/727	49/23843	0.781041	0.89958	0.886122	F12
GO_BP_m4	GO:190320	negative re	1/727	49/23843	0.781041	0.89958	0.886122	Nme5
GO_BP_m4	GO:190526	negative re	1/727	49/23843	0.781041	0.89958	0.886122	Trip12
GO_BP_m4	GO:004308	regulation	7/727	289/23843	0.781411	0.89979	0.886329	Arhgap23/
GO_BP_m4	GO:190285	microtubul	3/727	135/23843	0.783782	0.902302	0.888803	Aurka/Spdl
GO_BP_m4	GO:000906	fatty acid c	2/727	94/23843	0.785239	0.902876	0.889369	Decr1/Irs2
GO_BP_m4	GO:001584	monoamin	2/727	94/23843	0.785239	0.902876	0.889369	Lgals3/Rtn
GO_BP_m4	GO:001701	regulation	2/727	94/23843	0.785239	0.902876	0.889369	Folr1/Vasn
GO_BP_m4	GO:004563	negative re	2/727	94/23843	0.785239	0.902876	0.889369	Thoc5/Zfp
GO_BP_m4	GO:200006	positive reg	2/727	94/23843	0.785239	0.902876	0.889369	Aurka/Socs
GO_BP_m4	GO:000838	RNA splicir	9/727	365/23843	0.785496	0.902876	0.889369	Gemin5/Lg
GO_BP_m4	GO:000645	'de novo' p	1/727	50/23843	0.787731	0.902876	0.889369	Dnajb14
GO_BP_m4	GO:000714	male meio	1/727	50/23843	0.787731	0.902876	0.889369	Fanca
GO_BP_m4	GO:000999	oocyte diff	1/727	50/23843	0.787731	0.902876	0.889369	Aurka
GO_BP_m4	GO:003010	water hom	1/727	50/23843	0.787731	0.902876	0.889369	Gak
GO_BP_m4	GO:003513	hindlimb m	1/727	50/23843	0.787731	0.902876	0.889369	Fgf4
GO_BP_m4	GO:003530	positive reg	1/727	50/23843	0.787731	0.902876	0.889369	Ppp1r15b
GO_BP_m4	GO:003545	response to	1/727	50/23843	0.787731	0.902876	0.889369	F830016B0
GO_BP_m4	GO:004214	cellular res	1/727	50/23843	0.787731	0.902876	0.889369	Tbl2
GO_BP_m4	GO:004394	regulation	1/727	50/23843	0.787731	0.902876	0.889369	Gpr61
GO_BP_m4	GO:190040	negative re	1/727	50/23843	0.787731	0.902876	0.889369	Nme5
GO_BP_m4	GO:000979	post-embr	3/727	136/23843	0.787958	0.902876	0.889369	Cyp1a2/Pla
GO_BP_m4	GO:001657	histone me	3/727	136/23843	0.787958	0.902876	0.889369	Dydc1/Prm
GO_BP_m4	GO:003425	positive reg	3/727	136/23843	0.787958	0.902876	0.889369	Efna1/Eif3e
GO_BP_m4	GO:001703	protein imp	5/727	215/23843	0.788057	0.902876	0.889369	Agap3/Gas
GO_BP_m4	GO:004854	response to	6/727	254/23843	0.789981	0.903854	0.890332	Esr2/Mir15
GO_BP_m4	GO:003560	protein dea	2/727	95/23843	0.790149	0.903854	0.890332	Abhd13/Sf
GO_BP_m4	GO:004513	meiotic chr	2/727	95/23843	0.790149	0.903854	0.890332	Cenps/Brip
GO_BP_m4	GO:006105	somite dev	2/727	95/23843	0.790149	0.903854	0.890332	Ror2/Zeb2
GO_BP_m4	GO:004002	regulation	7/727	292/23843	0.790172	0.903854	0.890332	Dydc1/Mir
GO_BP_m4	GO:005160	defense res	5/727	216/23843	0.791379	0.903854	0.890332	A230050P2

GO_BP_m4	GO:19029	negative re	3/727	137/23843	0.792068	0.903854	0.890332	Nav3/Spta
GO_BP_m4	GO:00516	establishm	10/727	405/23843	0.793172	0.903854	0.890332	Cdh3/Il13/
GO_BP_m4	GO:00018	retina hom	1/727	51/23843	0.794217	0.903854	0.890332	Cdh3
GO_BP_m4	GO:00075	neuromusc	1/727	51/23843	0.794217	0.903854	0.890332	Erbb2
GO_BP_m4	GO:00106	regulation	1/727	51/23843	0.794217	0.903854	0.890332	Fndc1
GO_BP_m4	GO:00108	negative re	1/727	51/23843	0.794217	0.903854	0.890332	Pid1
GO_BP_m4	GO:003261	interleukin	1/727	51/23843	0.794217	0.903854	0.890332	Ager
GO_BP_m4	GO:00327	negative re	1/727	51/23843	0.794217	0.903854	0.890332	Gas6
GO_BP_m4	GO:00350	establishm	1/727	51/23843	0.794217	0.903854	0.890332	Mtcl1
GO_BP_m4	GO:00457	positive re	1/727	51/23843	0.794217	0.903854	0.890332	Rps3
GO_BP_m4	GO:00482	lymphocyt	1/727	51/23843	0.794217	0.903854	0.890332	Gas6
GO_BP_m4	GO:005081	negative re	1/727	51/23843	0.794217	0.903854	0.890332	F12
GO_BP_m4	GO:00512	protein het	1/727	51/23843	0.794217	0.903854	0.890332	Rrm1
GO_BP_m4	GO:00515	histone H3	1/727	51/23843	0.794217	0.903854	0.890332	Dydc1
GO_BP_m4	GO:00612	establishm	1/727	51/23843	0.794217	0.903854	0.890332	Mtcl1
GO_BP_m4	GO:007171	icosanoid t	1/727	51/23843	0.794217	0.903854	0.890332	Abcc4
GO_BP_m4	GO:190157	fatty acid d	1/727	51/23843	0.794217	0.903854	0.890332	Abcc4
GO_BP_m4	GO:00105	regulation	2/727	96/23843	0.794961	0.903854	0.890332	Il13/Slc8a1
GO_BP_m4	GO:001921	regulation	2/727	96/23843	0.794961	0.903854	0.890332	Apoa4/Vdr
GO_BP_m4	GO:00300	contractile	2/727	96/23843	0.794961	0.903854	0.890332	Eln/Synpo
GO_BP_m4	GO:00421	positive re	2/727	96/23843	0.794961	0.903854	0.890332	Ager/Rps3
GO_BP_m4	GO:00431	stress fiber	2/727	96/23843	0.794961	0.903854	0.890332	Eln/Synpo
GO_BP_m4	GO:00902	positive re	2/727	96/23843	0.794961	0.903854	0.890332	Ror2/Zbed
GO_BP_m4	GO:00987	macromole	2/727	96/23843	0.794961	0.903854	0.890332	Abhd13/Sf
GO_BP_m4	GO:01400	mitochond	2/727	96/23843	0.794961	0.903854	0.890332	Ears2/Mrp
GO_BP_m4	GO:19038	regulation	2/727	96/23843	0.794961	0.903854	0.890332	Folr1/Vasn
GO_BP_m4	GO:00018	tissue hom	5/727	218/23843	0.797901	0.906981	0.893412	Car2/Cdh3
GO_BP_m4	GO:00309	forebrain d	9/727	370/23843	0.798327	0.90725	0.893677	Duox2/Fez
GO_BP_m4	GO:00313	regulation	4/727	179/23843	0.798928	0.907353	0.893778	Bcl10/Rps2
GO_BP_m4	GO:00063	DNA-temp	2/727	97/23843	0.799675	0.907353	0.893778	Polr1e/Sm
GO_BP_m4	GO:190307	regulation	2/727	97/23843	0.799675	0.907353	0.893778	Pid1/Vamp
GO_BP_m4	GO:00308	positive re	1/727	52/23843	0.800505	0.907353	0.893778	Tshr
GO_BP_m4	GO:00308	prostate gl	1/727	52/23843	0.800505	0.907353	0.893778	Esr2
GO_BP_m4	GO:00455	negative re	1/727	52/23843	0.800505	0.907353	0.893778	Ddit3
GO_BP_m4	GO:00459	positive re	1/727	52/23843	0.800505	0.907353	0.893778	Lck
GO_BP_m4	GO:00709	protein K4	1/727	52/23843	0.800505	0.907353	0.893778	Nedd4l
GO_BP_m4	GO:19023	negative re	1/727	52/23843	0.800505	0.907353	0.893778	Nbas
GO_BP_m4	GO:19035	negative re	1/727	52/23843	0.800505	0.907353	0.893778	Gas6
GO_BP_m4	GO:19052	regulation	1/727	52/23843	0.800505	0.907353	0.893778	Sox17
GO_BP_m4	GO:00109	negative re	5/727	219/23843	0.801101	0.907813	0.894232	Btn2a2/Hu
GO_BP_m4	GO:00329	regulation	8/727	334/23843	0.801992	0.908608	0.895014	Arhgap18/
GO_BP_m4	GO:000691	autophagy	9/727	372/23843	0.803298	0.90909	0.895489	5330417C
GO_BP_m4	GO:006191	process uti	9/727	372/23843	0.803298	0.90909	0.895489	5330417C
GO_BP_m4	GO:00066	protein tar	3/727	140/23843	0.804	0.90909	0.895489	Plagl2/Tom
GO_BP_m4	GO:001821	peptidyl-th	3/727	140/23843	0.804	0.90909	0.895489	Camk1g/D
GO_BP_m4	GO:003027	regulation	5/727	220/23843	0.804261	0.90909	0.895489	Gata1/Map
GO_BP_m4	GO:00301	natural kill	2/727	98/23843	0.804292	0.90909	0.895489	Gas6/Ifna1
GO_BP_m4	GO:00464	positive re	2/727	98/23843	0.804292	0.90909	0.895489	Il13/Lck

GO_BP_m4	GO:009956	chemical sy	2/727	98/23843	0.804292	0.90909	0.895489	Grm1/Hcrt
GO_BP_m4	GO:000254	monocyte	1/727	53/23843	0.806601	0.90909	0.895489	Lgals3
GO_BP_m4	GO:000687	cellular iron	1/727	53/23843	0.806601	0.90909	0.895489	Heph
GO_BP_m4	GO:001065	cardiac mu	1/727	53/23843	0.806601	0.90909	0.895489	Fndc1
GO_BP_m4	GO:001590	long-chain	1/727	53/23843	0.806601	0.90909	0.895489	Irs2
GO_BP_m4	GO:004438	protein loc	1/727	53/23843	0.806601	0.90909	0.895489	Aurka
GO_BP_m4	GO:004658	negative re	1/727	53/23843	0.806601	0.90909	0.895489	Spry2
GO_BP_m4	GO:005193	synaptic tra	1/727	53/23843	0.806601	0.90909	0.895489	Car2
GO_BP_m4	GO:005501	ventricular	1/727	53/23843	0.806601	0.90909	0.895489	Dsp
GO_BP_m4	GO:007098	demethylat	1/727	53/23843	0.806601	0.90909	0.895489	Cyp1a2
GO_BP_m4	GO:009030	positive reg	1/727	53/23843	0.806601	0.90909	0.895489	F12
GO_BP_m4	GO:190054	negative re	1/727	53/23843	0.806601	0.90909	0.895489	Pid1
GO_BP_m4	GO:190275	negative re	1/727	53/23843	0.806601	0.90909	0.895489	Hus1
GO_BP_m4	GO:190288	negative re	1/727	53/23843	0.806601	0.90909	0.895489	Nme5
GO_BP_m4	GO:190339	regulation	1/727	53/23843	0.806601	0.90909	0.895489	Ptpn23
GO_BP_m4	GO:004428	small mole	7/727	298/23843	0.806897	0.909209	0.895607	Akr1d1/Cy
GO_BP_m4	GO:009900	vesicle-me	3/727	141/23843	0.807847	0.909714	0.896104	Rims4/Sna
GO_BP_m4	GO:000206	chondrocy	2/727	99/23843	0.808814	0.909714	0.896104	Mapk14/Re
GO_BP_m4	GO:002151	spinal cord	2/727	99/23843	0.808814	0.909714	0.896104	Nkx6-2/Vs
GO_BP_m4	GO:190180	positive reg	2/727	99/23843	0.808814	0.909714	0.896104	Aurka/Socs
GO_BP_m4	GO:003526	organ grow	4/727	182/23843	0.809265	0.909714	0.896104	Mapk14/M
GO_BP_m4	GO:004639	carboxylic	8/727	337/23843	0.80968	0.909714	0.896104	Acmsd/Akr
GO_BP_m4	GO:000237	immunoglo	5/727	222/23843	0.810462	0.909714	0.896104	Igkv16-104
GO_BP_m4	GO:009025	regulation	5/727	222/23843	0.810462	0.909714	0.896104	Dsp/Gtf2irc
GO_BP_m4	GO:004316	proteasom	9/727	375/23843	0.810581	0.909714	0.896104	Agap3/Aur
GO_BP_m4	GO:007252	pyridine-c	3/727	142/23843	0.811631	0.909714	0.896104	Acmsd/Kyr
GO_BP_m4	GO:001605	organic aci	8/727	338/23843	0.812192	0.909714	0.896104	Acmsd/Akr
GO_BP_m4	GO:000706	sister chror	1/727	54/23843	0.812511	0.909714	0.896104	Sfpq
GO_BP_m4	GO:007558	respiratory	1/727	54/23843	0.812511	0.909714	0.896104	Traf4
GO_BP_m4	GO:007558	excretion	1/727	54/23843	0.812511	0.909714	0.896104	Grhpr
GO_BP_m4	GO:000833	endosome	1/727	54/23843	0.812511	0.909714	0.896104	Rilp
GO_BP_m4	GO:001052	positive reg	1/727	54/23843	0.812511	0.909714	0.896104	Il13
GO_BP_m4	GO:002179	cerebral co	1/727	54/23843	0.812511	0.909714	0.896104	Rtn4
GO_BP_m4	GO:003049	maturation	1/727	54/23843	0.812511	0.909714	0.896104	Krr1
GO_BP_m4	GO:003501	somatic ste	1/727	54/23843	0.812511	0.909714	0.896104	Ldb2
GO_BP_m4	GO:004406	regulation	1/727	54/23843	0.812511	0.909714	0.896104	Inhba
GO_BP_m4	GO:004598	negative re	1/727	54/23843	0.812511	0.909714	0.896104	Pid1
GO_BP_m4	GO:006019	positive reg	1/727	54/23843	0.812511	0.909714	0.896104	Apoa4
GO_BP_m4	GO:005086	negative re	4/727	183/23843	0.812613	0.909714	0.896104	Btn2a2/Erb
GO_BP_m4	GO:006201	positive reg	4/727	183/23843	0.812613	0.909714	0.896104	Apoa4/Irs2
GO_BP_m4	GO:009940	response t	2/727	100/23843	0.813244	0.909714	0.896104	Hsbp1l1/Tr
GO_BP_m4	GO:003139	positive reg	2/727	100/23843	0.813244	0.909714	0.896104	Bcl10/Rps2
GO_BP_m4	GO:003162	receptor in	2/727	100/23843	0.813244	0.909714	0.896104	Grb2/Rab3
GO_BP_m4	GO:003209	positive reg	2/727	100/23843	0.813244	0.909714	0.896104	Tiam1/Traf
GO_BP_m4	GO:004346	regulation	2/727	100/23843	0.813244	0.909714	0.896104	Irs2/Nkx1-
GO_BP_m4	GO:005198	regulation	2/727	100/23843	0.813244	0.909714	0.896104	Rmi2/Sfpq
GO_BP_m4	GO:190489	positive reg	2/727	100/23843	0.813244	0.909714	0.896104	Il13/Lck
GO_BP_m4	GO:200005	regulation	3/727	143/23843	0.815351	0.911858	0.898216	Aurka/Pdcl

GO_BP_m4	GO:005121	cartilage d	4/727	184/23843	0.815912	0.912273	0.898624	Fgf4/Mapk
GO_BP_m4	GO:00068	mitochond	6/727	263/23843	0.816262	0.91245	0.8988	Plagl2/Slc2
GO_BP_m4	GO:19038	positive re	8/727	340/23843	0.81714	0.913218	0.899556	Erbb2/Gas
GO_BP_m4	GO:00315	actin cytos	2/727	101/23843	0.817581	0.913284	0.899621	Parvg/Spta
GO_BP_m4	GO:00519	regulation	2/727	101/23843	0.817581	0.913284	0.899621	Htr2c/Rtn4
GO_BP_m4	GO:00067	terpenoid	1/727	55/23843	0.818241	0.913381	0.899716	Cyp1a2
GO_BP_m4	GO:00106	striated mu	1/727	55/23843	0.818241	0.913381	0.899716	Fndc1
GO_BP_m4	GO:003527	exocrine sy	1/727	55/23843	0.818241	0.913381	0.899716	Polb
GO_BP_m4	GO:00098	negative re	6/727	264/23843	0.819016	0.913558	0.899891	Efna1/Nba
GO_BP_m4	GO:00022	lymphocyt	4/727	185/23843	0.819164	0.913558	0.899891	Ifna12/Il27
GO_BP_m4	GO:00421	cellular ket	4/727	185/23843	0.819164	0.913558	0.899891	Apoa4/Coc
GO_BP_m4	GO:00715	cellular res	4/727	185/23843	0.819164	0.913558	0.899891	Folr1/Mir1
GO_BP_m4	GO:00335	unsaturate	2/727	102/23843	0.821828	0.916064	0.902359	Ces2h/Cyp
GO_BP_m4	GO:19030	organelle	2/727	102/23843	0.821828	0.916064	0.902359	Fundc2/To
GO_BP_m4	GO:00015	angiogene	12/727	492/23843	0.8222	0.916064	0.902359	Angptl6/C
GO_BP_m4	GO:003297	regulation	9/727	380/23843	0.822266	0.916064	0.902359	Arhgap18/
GO_BP_m4	GO:00507	regulation	4/727	186/23843	0.822369	0.916064	0.902359	Btn2a2/Ga
GO_BP_m4	GO:00105	regulation	3/727	145/23843	0.822605	0.916113	0.902408	Ager/Efna1
GO_BP_m4	GO:001081	negative re	1/727	56/23843	0.823796	0.916585	0.902873	Muc4
GO_BP_m4	GO:001491	positive re	1/727	56/23843	0.823796	0.916585	0.902873	Ager
GO_BP_m4	GO:001644	somatic re	1/727	56/23843	0.823796	0.916585	0.902873	Polb
GO_BP_m4	GO:004512	cellular ext	1/727	56/23843	0.823796	0.916585	0.902873	Sell
GO_BP_m4	GO:00709	neuron de	9/727	381/23843	0.824536	0.917195	0.903473	Ager/Akt1s
GO_BP_m4	GO:00002	protein pol	4/727	187/23843	0.825526	0.917657	0.903928	Anapc2/Ne
GO_BP_m4	GO:00032	cardiac ch	4/727	187/23843	0.825526	0.917657	0.903928	Dsp/Fhl2/N
GO_BP_m4	GO:00715	response t	4/727	187/23843	0.825526	0.917657	0.903928	Folr1/Mir1
GO_BP_m4	GO:00435	muscle ad	2/727	103/23843	0.825986	0.917912	0.904179	Gtf2ird1/N
GO_BP_m4	GO:00514	negative re	3/727	146/23843	0.82614	0.917912	0.904179	Nav3/Spta
GO_BP_m4	GO:190121	regulation	8/727	344/23843	0.826734	0.918303	0.904565	Ager/Akt1s
GO_BP_m4	GO:00315	cell-substr	7/727	306/23843	0.827581	0.918303	0.904565	Efna1/Gas6
GO_BP_m4	GO:00464	glycerolipi	7/727	306/23843	0.827581	0.918303	0.904565	Apoa4/Gd
GO_BP_m4	GO:004887	homeostas	7/727	306/23843	0.827581	0.918303	0.904565	Bcl10/Gata
GO_BP_m4	GO:00164	osteoblast	4/727	188/23843	0.828637	0.918303	0.904565	Fhl2/Nfatc
GO_BP_m4	GO:00464	organopho	4/727	188/23843	0.828637	0.918303	0.904565	Gdpd3/Lip
GO_BP_m4	GO:007124	cellular res	4/727	188/23843	0.828637	0.918303	0.904565	Cyp1a2/Mi
GO_BP_m4	GO:00065	catecholan	1/727	57/23843	0.829181	0.918303	0.904565	Htr2c
GO_BP_m4	GO:000971	catechol-c	1/727	57/23843	0.829181	0.918303	0.904565	Htr2c
GO_BP_m4	GO:00190	viral gene	1/727	57/23843	0.829181	0.918303	0.904565	Eif3a
GO_BP_m4	GO:00434	regulation	1/727	57/23843	0.829181	0.918303	0.904565	Dynll2
GO_BP_m4	GO:004851	circadian b	1/727	57/23843	0.829181	0.918303	0.904565	Hcrtr1
GO_BP_m4	GO:005131	metaphase	1/727	57/23843	0.829181	0.918303	0.904565	Spdl1
GO_BP_m4	GO:006011	inner ear r	1/727	57/23843	0.829181	0.918303	0.904565	Tshr
GO_BP_m4	GO:00080	cell recogn	6/727	268/23843	0.829706	0.918634	0.904891	Astl/Cadm
GO_BP_m4	GO:00197	antimicrob	2/727	104/23843	0.830056	0.918634	0.904891	AY761184/
GO_BP_m4	GO:00352	segmentati	2/727	104/23843	0.830056	0.918634	0.904891	Ror2/Zeb2
GO_BP_m4	GO:00097	hormone-r	4/727	189/23843	0.831702	0.920242	0.906475	Esr2/Tshr/
GO_BP_m4	GO:00509	detection	7/727	308/23843	0.832471	0.920248	0.906481	Gnat1/Olfr
GO_BP_m4	GO:00349	histone lysi	2/727	105/23843	0.834041	0.920248	0.906481	Dydc1/Smy

GO_BP_m4	GO:006101	regulation	2/727	105/23843	0.834041	0.920248	0.906481	Nbas/Zfp3
GO_BP_m4	GO:007190	negative re	2/727	105/23843	0.834041	0.920248	0.906481	Dusp10/Sp
GO_BP_m4	GO:009010	negative re	2/727	105/23843	0.834041	0.920248	0.906481	Fst/Vasn
GO_BP_m4	GO:190437	regulation	2/727	105/23843	0.834041	0.920248	0.906481	Pid1/Vamp
GO_BP_m4	GO:007155	heterophili	1/727	58/23843	0.834402	0.920248	0.906481	Cadm2
GO_BP_m4	GO:003200	negative re	1/727	58/23843	0.834402	0.920248	0.906481	Akt1s1
GO_BP_m4	GO:003223	positive re	1/727	58/23843	0.834402	0.920248	0.906481	Synpo
GO_BP_m4	GO:004277	mitochond	1/727	58/23843	0.834402	0.920248	0.906481	Cycs
GO_BP_m4	GO:004663	positive re	1/727	58/23843	0.834402	0.920248	0.906481	Socs5
GO_BP_m4	GO:004685	regulation	1/727	58/23843	0.834402	0.920248	0.906481	Car2
GO_BP_m4	GO:005043	regulation	1/727	58/23843	0.834402	0.920248	0.906481	Rtn4
GO_BP_m4	GO:006044	mammary	1/727	58/23843	0.834402	0.920248	0.906481	Vdr
GO_BP_m4	GO:000693	regulation	3/727	149/23843	0.836385	0.922223	0.908426	Dsp/Lck/Sl
GO_BP_m4	GO:005090	leukocyte r	7/727	310/23843	0.837251	0.922815	0.909009	C3ar1/Gas
GO_BP_m4	GO:000751	skeletal mu	4/727	191/23843	0.837694	0.922815	0.909009	Cops2/Eln/
GO_BP_m4	GO:003150	protein-co	4/727	191/23843	0.837694	0.922815	0.909009	Snap47/Srs
GO_BP_m4	GO:190401	positive re	4/727	191/23843	0.837694	0.922815	0.909009	C3ar1/Lgal
GO_BP_m4	GO:000762	rhythmic b	1/727	59/23843	0.839464	0.923303	0.90949	Hcrtr1
GO_BP_m4	GO:001936	arachidoni	1/727	59/23843	0.839464	0.923303	0.90949	Cyp2a22
GO_BP_m4	GO:003051	negative re	1/727	59/23843	0.839464	0.923303	0.90949	Vasn
GO_BP_m4	GO:004606	cGMP meta	1/727	59/23843	0.839464	0.923303	0.90949	Htr2c
GO_BP_m4	GO:006098	endocrine	1/727	59/23843	0.839464	0.923303	0.90949	Inhba
GO_BP_m4	GO:007115	regulation	1/727	59/23843	0.839464	0.923303	0.90949	Pidd1
GO_BP_m4	GO:003210	negative re	7/727	311/23843	0.8396	0.923303	0.90949	Ager/Dusp
GO_BP_m4	GO:000270	regulation	3/727	150/23843	0.839683	0.923303	0.90949	Ager/Muc
GO_BP_m4	GO:000724	I-kappaB k	4/727	192/23843	0.840623	0.924125	0.910299	Bcl10/Rela/
GO_BP_m4	GO:005122	spindle ass	2/727	107/23843	0.841758	0.925127	0.911286	Aurka/Rps
GO_BP_m4	GO:003134	positive re	7/727	312/23843	0.841921	0.925127	0.911286	Ager/F12/
GO_BP_m4	GO:190305	regulation	4/727	193/23843	0.843507	0.926656	0.912793	Aurka/Efna
GO_BP_m4	GO:000704	lysosome c	1/727	60/23843	0.844371	0.926753	0.912888	Tpcn2
GO_BP_m4	GO:002151	cell differe	1/727	60/23843	0.844371	0.926753	0.912888	Nkx6-2
GO_BP_m4	GO:005508	anion hom	1/727	60/23843	0.844371	0.926753	0.912888	Kctd7
GO_BP_m4	GO:008017	lytic vacuol	1/727	60/23843	0.844371	0.926753	0.912888	Tpcn2
GO_BP_m4	GO:000634	chromatin	2/727	108/23843	0.845493	0.927772	0.913892	Dydc1/Sma
GO_BP_m4	GO:004325	regulation	10/727	429/23843	0.845871	0.927974	0.914091	Arhgap18/
GO_BP_m4	GO:000926	cellular res	3/727	152/23843	0.846106	0.928018	0.914135	5330417C2
GO_BP_m4	GO:000322	ventricular	1/727	61/23843	0.849128	0.928891	0.914994	Dsp
GO_BP_m4	GO:001067	positive re	1/727	61/23843	0.849128	0.928891	0.914994	Irs2
GO_BP_m4	GO:001644	somatic div	1/727	61/23843	0.849128	0.928891	0.914994	Polb
GO_BP_m4	GO:004396	histone H3	1/727	61/23843	0.849128	0.928891	0.914994	Dr1
GO_BP_m4	GO:005043	catecholam	1/727	61/23843	0.849128	0.928891	0.914994	Rtn4
GO_BP_m4	GO:006039	regulation	1/727	61/23843	0.849128	0.928891	0.914994	Inhba
GO_BP_m4	GO:190384	negative re	1/727	61/23843	0.849128	0.928891	0.914994	Vasn
GO_BP_m4	GO:000648	protein gly	4/727	195/23843	0.849144	0.928891	0.914994	B3gnt5/Fut
GO_BP_m4	GO:000689	receptor-m	4/727	195/23843	0.849144	0.928891	0.914994	Gak/Grb2/
GO_BP_m4	GO:004341	macromole	4/727	195/23843	0.849144	0.928891	0.914994	B3gnt5/Fut
GO_BP_m4	GO:190160	alpha-ami	4/727	195/23843	0.849144	0.928891	0.914994	Bhmt/Dpe
GO_BP_m4	GO:000673	oxidoreduc	3/727	153/23843	0.849233	0.928891	0.914994	Coq6/Kynu

GO_BP_m4	GO:007233	monocarbc	5/727	236/23843	0.84958	0.929058	0.915159	Akr1d1/Ap
GO_BP_m4	GO:004566	positive reg	10/727	432/23843	0.851652	0.930627	0.916705	Anapc2/Fe
GO_BP_m4	GO:000176	morphogei	5/727	237/23843	0.852099	0.930627	0.916705	Grb2/Nfatc
GO_BP_m4	GO:003051	intracellula	2/727	110/23843	0.852724	0.930627	0.916705	Esr2/Ube2i
GO_BP_m4	GO:000076	syncytium	1/727	62/23843	0.85374	0.930627	0.916705	Mapk14
GO_BP_m4	GO:000183	release of (	1/727	62/23843	0.85374	0.930627	0.916705	Wdr35
GO_BP_m4	GO:003400	neural retir	1/727	62/23843	0.85374	0.930627	0.916705	Cabp4
GO_BP_m4	GO:004277	ATP synthe	1/727	62/23843	0.85374	0.930627	0.916705	Cycs
GO_BP_m4	GO:004514	homologou	1/727	62/23843	0.85374	0.930627	0.916705	Brip1
GO_BP_m4	GO:004542	regulation	1/727	62/23843	0.85374	0.930627	0.916705	Wdr35
GO_BP_m4	GO:006004	retina morp	1/727	62/23843	0.85374	0.930627	0.916705	Cabp4
GO_BP_m4	GO:006103	regulation	1/727	62/23843	0.85374	0.930627	0.916705	Rela
GO_BP_m4	GO:190126	carbohydra	1/727	62/23843	0.85374	0.930627	0.916705	Vamp8
GO_BP_m4	GO:200017	positive reg	1/727	62/23843	0.85374	0.930627	0.916705	Gak
GO_BP_m4	GO:200024	negative re	1/727	62/23843	0.85374	0.930627	0.916705	Astl
GO_BP_m4	GO:000657	cellular mo	3/727	155/23843	0.855322	0.932022	0.918079	Duox2/Folr
GO_BP_m4	GO:003134	positive reg	10/727	434/23843	0.85541	0.932022	0.918079	Anapc2/Its
GO_BP_m4	GO:003003	lamellipodi	1/727	63/23843	0.858211	0.934436	0.920456	Spata13
GO_BP_m4	GO:003460	cellular res	1/727	63/23843	0.858211	0.934436	0.920456	Hsbp1l1
GO_BP_m4	GO:190160	alpha-amir	1/727	63/23843	0.858211	0.934436	0.920456	Bhmt
GO_BP_m4	GO:000669	icosanoid r	2/727	112/23843	0.859645	0.935001	0.921013	Ces2h/Cyp
GO_BP_m4	GO:004581	negative re	2/727	112/23843	0.859645	0.935001	0.921013	Dydc1/Sma
GO_BP_m4	GO:190305	positive reg	2/727	112/23843	0.859645	0.935001	0.921013	Aurka/Socs
GO_BP_m4	GO:004873	appendage	4/727	199/23843	0.859904	0.935001	0.921013	Fgf4/Ror2/
GO_BP_m4	GO:006017	limb develo	4/727	199/23843	0.859904	0.935001	0.921013	Fgf4/Ror2/
GO_BP_m4	GO:200002	regulation	4/727	199/23843	0.859904	0.935001	0.921013	Pim1/Ror2/
GO_BP_m4	GO:000756	female pre	3/727	157/23843	0.861194	0.935534	0.921538	Mirlet7c-2/
GO_BP_m4	GO:004340	steroid hor	3/727	157/23843	0.861194	0.935534	0.921538	Esr2/Ube2i
GO_BP_m4	GO:006053	skeletal mu	4/727	200/23843	0.862489	0.935534	0.921538	Cops2/Eln/
GO_BP_m4	GO:007237	protein act	4/727	200/23843	0.862489	0.935534	0.921538	F12/Ighv9-
GO_BP_m4	GO:000694	syncytium	1/727	64/23843	0.862546	0.935534	0.921538	Mapk14
GO_BP_m4	GO:000906	glutamine	1/727	64/23843	0.862546	0.935534	0.921538	Fah
GO_BP_m4	GO:002176	hippocamp	1/727	64/23843	0.862546	0.935534	0.921538	Zeb2
GO_BP_m4	GO:003237	positive reg	1/727	64/23843	0.862546	0.935534	0.921538	Abcb4
GO_BP_m4	GO:004333	response to	1/727	64/23843	0.862546	0.935534	0.921538	Ifna12
GO_BP_m4	GO:006038	pathway-re	1/727	64/23843	0.862546	0.935534	0.921538	Inhba
GO_BP_m4	GO:006042	lung morpl	1/727	64/23843	0.862546	0.935534	0.921538	Spry2
GO_BP_m4	GO:003110	microtubul	2/727	113/23843	0.862993	0.935807	0.921806	Nav3/Rps3
GO_BP_m4	GO:000926	response to	3/727	158/23843	0.864051	0.936529	0.922518	Hsbp1l1/Lx
GO_BP_m4	GO:005110	negative re	3/727	158/23843	0.864051	0.936529	0.922518	Aurka/Ddit
GO_BP_m4	GO:000150	ossification	8/727	362/23843	0.865135	0.937444	0.92342	Duox2/Fhl2
GO_BP_m4	GO:005115	regulation	2/727	114/23843	0.866268	0.937444	0.92342	Mapk14/Si
GO_BP_m4	GO:000256	somatic div	1/727	65/23843	0.866748	0.937444	0.92342	Polb
GO_BP_m4	GO:007400	neuroblast	1/727	65/23843	0.866748	0.937444	0.92342	Ctnna1
GO_BP_m4	GO:000854	visual learn	1/727	65/23843	0.866748	0.937444	0.92342	Synpo
GO_BP_m4	GO:001050	negative re	1/727	65/23843	0.866748	0.937444	0.92342	Sec22b
GO_BP_m4	GO:001644	somatic cel	1/727	65/23843	0.866748	0.937444	0.92342	Polb
GO_BP_m4	GO:001657	histone dea	1/727	65/23843	0.866748	0.937444	0.92342	Sfpq

GO_BP_m4	GO:00422	natural kill	1/727	65/23843	0.866748	0.937444	0.92342	Serpinb9
GO_BP_m4	GO:00836	regulation	3/727	159/23843	0.866857	0.937444	0.92342	Arhgap18/
GO_BP_m4	GO:00066	protein im	3/727	160/23843	0.869611	0.939608	0.925551	Agap3/Gas
GO_BP_m4	GO:00002	mitotic cyt	1/727	66/23843	0.870822	0.939608	0.925551	12-Sep
GO_BP_m4	GO:00026	regulation	1/727	66/23843	0.870822	0.939608	0.925551	Il13
GO_BP_m4	GO:00086	cellular am	1/727	66/23843	0.870822	0.939608	0.925551	Bhmt
GO_BP_m4	GO:00098	embryonic	1/727	66/23843	0.870822	0.939608	0.925551	Peg12
GO_BP_m4	GO:00304	ubiquitin-c	1/727	66/23843	0.870822	0.939608	0.925551	Stt3b
GO_BP_m4	GO:00512	centrosom	1/727	66/23843	0.870822	0.939608	0.925551	Cep152
GO_BP_m4	GO:00606	regulation	1/727	66/23843	0.870822	0.939608	0.925551	Rtn4
GO_BP_m4	GO:19017	regulation	1/727	66/23843	0.870822	0.939608	0.925551	Smyd2
GO_BP_m4	GO:190357	regulation	1/727	66/23843	0.870822	0.939608	0.925551	Pid1
GO_BP_m4	GO:000751	muscle org	9/727	405/23843	0.87256	0.940892	0.926815	Cops2/Dsp
GO_BP_m4	GO:00105	regulation	2/727	116/23843	0.872603	0.940892	0.926815	Apoa4/Irs2
GO_BP_m4	GO:00149	myotube d	2/727	116/23843	0.872603	0.940892	0.926815	Mapk14/Si
GO_BP_m4	GO:000222	natural kill	1/727	67/23843	0.874772	0.941532	0.927446	Serpinb9
GO_BP_m4	GO:00064	tRNA modi	1/727	67/23843	0.874772	0.941532	0.927446	Wdr4
GO_BP_m4	GO:000694	regulation	1/727	67/23843	0.874772	0.941532	0.927446	Lck
GO_BP_m4	GO:00326	regulation	1/727	67/23843	0.874772	0.941532	0.927446	Gas6
GO_BP_m4	GO:00508	neuromusc	1/727	67/23843	0.874772	0.941532	0.927446	Nkx6-2
GO_BP_m4	GO:005114	smooth mu	1/727	67/23843	0.874772	0.941532	0.927446	Sgcb
GO_BP_m4	GO:19048	cranial skel	1/727	67/23843	0.874772	0.941532	0.927446	Fgf4
GO_BP_m4	GO:001982	stem cell p	3/727	162/23843	0.874969	0.941532	0.927446	Fgf4/Ldb2/
GO_BP_m4	GO:004312	regulation	3/727	162/23843	0.874969	0.941532	0.927446	Rela/Ripk1
GO_BP_m4	GO:00159	energy der	5/727	247/23843	0.875408	0.941792	0.927702	Cycs/Cyp1
GO_BP_m4	GO:004572	positive re	2/727	117/23843	0.875665	0.941857	0.927767	Eif3e/Erbb
GO_BP_m4	GO:000007	regulation	1/727	68/23843	0.878601	0.943805	0.929685	Pim1
GO_BP_m4	GO:00076	visual beha	1/727	68/23843	0.878601	0.943805	0.929685	Synpo
GO_BP_m4	GO:004584	negative re	1/727	68/23843	0.878601	0.943805	0.929685	Mir1a-2
GO_BP_m4	GO:004864	regulation	1/727	68/23843	0.878601	0.943805	0.929685	Sox17
GO_BP_m4	GO:00066	sphingolipi	2/727	118/23843	0.87866	0.943805	0.929685	A4galt/B3
GO_BP_m4	GO:00070	centrosom	2/727	118/23843	0.87866	0.943805	0.929685	Aurka/Cep
GO_BP_m4	GO:00700	glycosylati	4/727	207/23843	0.879467	0.944341	0.930213	B3gnt5/Fu
GO_BP_m4	GO:00026	negative re	10/727	448/23843	0.879647	0.944341	0.930213	Bcl10/Btn2
GO_BP_m4	GO:00457	regulation	6/727	290/23843	0.879752	0.944341	0.930213	C3ar1/Efna
GO_BP_m4	GO:00324	regulation	2/727	119/23843	0.881588	0.945181	0.93104	Aurka/Soc
GO_BP_m4	GO:00022	activation	11/727	488/23843	0.88188	0.945181	0.93104	Bcl10/Btn2
GO_BP_m4	GO:00060	cellular ald	1/727	69/23843	0.882313	0.945181	0.93104	Grhpr
GO_BP_m4	GO:002202	telencepha	1/727	69/23843	0.882313	0.945181	0.93104	Rtn4
GO_BP_m4	GO:005081	regulation	1/727	69/23843	0.882313	0.945181	0.93104	Vdr
GO_BP_m4	GO:00511	positive re	1/727	69/23843	0.882313	0.945181	0.93104	Mapk14
GO_BP_m4	GO:00601	regulation	1/727	69/23843	0.882313	0.945181	0.93104	Apoa4
GO_BP_m4	GO:19019	positive re	1/727	69/23843	0.882313	0.945181	0.93104	Anp32b
GO_BP_m4	GO:200057	positive re	1/727	69/23843	0.882313	0.945181	0.93104	C3ar1
GO_BP_m4	GO:009872	maintenan	3/727	166/23843	0.885102	0.94755	0.933374	Fgf4/Ldb2/
GO_BP_m4	GO:200024	regulation	3/727	166/23843	0.885102	0.94755	0.933374	Astl/Aurka/
GO_BP_m4	GO:009881	nuclear ch	5/727	252/23843	0.885844	0.94755	0.933374	Cenps/Brip
GO_BP_m4	GO:00068	nitric oxide	1/727	70/23843	0.885912	0.94755	0.933374	Wdr35

GO_BP_m4	GO:004545	bone resor	1/727	70/23843	0.885912	0.94755	0.933374	Car2
GO_BP_m4	GO:004863	negative re	1/727	70/23843	0.885912	0.94755	0.933374	Mir1a-2
GO_BP_m4	GO:004884	artery mor	1/727	70/23843	0.885912	0.94755	0.933374	Folr1
GO_BP_m4	GO:003007	insulin secr	4/727	210/23843	0.886169	0.947612	0.933435	C1qtnf12/
GO_BP_m4	GO:007124	cellular res	2/727	121/23843	0.887249	0.948555	0.934364	Cyp1a2/Mt
GO_BP_m4	GO:000091	cytokinesis	3/727	167/23843	0.887519	0.948631	0.934439	Aurka/Sept
GO_BP_m4	GO:001820	peptidyl-ly	7/727	335/23843	0.888254	0.948862	0.934666	Camkmt/N
GO_BP_m4	GO:005066	cytokine se	4/727	211/23843	0.88833	0.948862	0.934666	Btn2a2/Ga
GO_BP_m4	GO:190353	negative re	4/727	211/23843	0.88833	0.948862	0.934666	Btn2a2/Cb
GO_BP_m4	GO:000220	somatic div	1/727	71/23843	0.889401	0.948946	0.934749	Polb
GO_BP_m4	GO:004362	response t	1/727	71/23843	0.889401	0.948946	0.934749	Mir451a
GO_BP_m4	GO:005188	regulation	1/727	71/23843	0.889401	0.948946	0.934749	Pid1
GO_BP_m4	GO:190186	negative re	1/727	71/23843	0.889401	0.948946	0.934749	Mir1a-2
GO_BP_m4	GO:190331	positive re	1/727	71/23843	0.889401	0.948946	0.934749	Zfp36l1
GO_BP_m4	GO:000910	coenzyme	3/727	168/23843	0.889889	0.949134	0.934934	Coq6/Kyn
GO_BP_m4	GO:004269	muscle cell	8/727	376/23843	0.889974	0.949134	0.934934	Fhl2/Mapk
GO_BP_m4	GO:009059	sensory or	6/727	296/23843	0.891039	0.949377	0.935174	Cabp4/Gn
GO_BP_m4	GO:000663	fatty acid n	8/727	377/23843	0.891593	0.949377	0.935174	Apoa4/Ces
GO_BP_m4	GO:005090	detection	8/727	377/23843	0.891593	0.949377	0.935174	Gnat1/Lxn/
GO_BP_m4	GO:000959	detection	7/727	337/23843	0.891683	0.949377	0.935174	Gnat1/Olfr
GO_BP_m4	GO:009028	regulation	5/727	255/23843	0.891739	0.949377	0.935174	Fam72a/F
GO_BP_m4	GO:000721	Notch sign	3/727	169/23843	0.892215	0.949377	0.935174	Akt1s1/Ne
GO_BP_m4	GO:000206	columnar/	1/727	72/23843	0.892784	0.949377	0.935174	Mir7-2
GO_BP_m4	GO:002188	forebrain c	1/727	72/23843	0.892784	0.949377	0.935174	Rtn4
GO_BP_m4	GO:004214	retrograde	1/727	72/23843	0.892784	0.949377	0.935174	Bet1l
GO_BP_m4	GO:004567	regulation	1/727	72/23843	0.892784	0.949377	0.935174	Car2
GO_BP_m4	GO:005068	regulation	1/727	72/23843	0.892784	0.949377	0.935174	Il27
GO_BP_m4	GO:006056	neuroepith	1/727	72/23843	0.892784	0.949377	0.935174	Tmem231
GO_BP_m4	GO:007019	chromoso	1/727	72/23843	0.892784	0.949377	0.935174	Brip1
GO_BP_m4	GO:000695	compleme	3/727	170/23843	0.894497	0.950987	0.93676	Ighv9-4/M
GO_BP_m4	GO:000244	leukocyte	10/727	458/23843	0.894855	0.951124	0.936895	Ager/Bcl10
GO_BP_m4	GO:000717	transmemb	7/727	339/23843	0.895023	0.951124	0.936895	Folr1/Fst/I
GO_BP_m4	GO:000703	vacuolar tr	2/727	124/23843	0.895272	0.951177	0.936947	Gak/Rilp
GO_BP_m4	GO:004620	nitric oxide	1/727	73/23843	0.896063	0.951382	0.937149	Wdr35
GO_BP_m4	GO:006151	myeloid ce	1/727	73/23843	0.896063	0.951382	0.937149	Gata1
GO_BP_m4	GO:190402	regulation	1/727	73/23843	0.896063	0.951382	0.937149	Pim1
GO_BP_m4	GO:005105	negative re	11/727	498/23843	0.896329	0.951454	0.93722	Btn2a2/Cb
GO_BP_m4	GO:190211	regulation	3/727	171/23843	0.896735	0.951674	0.937437	5330417C2
GO_BP_m4	GO:005090	neuromusc	2/727	125/23843	0.897826	0.95262	0.938369	Nkx6-2/Sl
GO_BP_m4	GO:005118	cofactor bi	4/727	216/23843	0.898603	0.953233	0.938972	Coq6/Cyp1
GO_BP_m4	GO:001973	antibacteri	1/727	74/23843	0.899241	0.953699	0.939431	AY761184
GO_BP_m4	GO:005132	meiotic cel	7/727	342/23843	0.89987	0.954034	0.939761	Cenps/Aur
GO_BP_m4	GO:003102	microtubul	2/727	126/23843	0.900322	0.954034	0.939761	Aurka/Cep
GO_BP_m4	GO:002195	central ner	4/727	217/23843	0.900555	0.954034	0.939761	Inhba/Mir2
GO_BP_m4	GO:003032	respiratory	4/727	217/23843	0.900555	0.954034	0.939761	Cyp1a2/Sp
GO_BP_m4	GO:009009	regulation	4/727	217/23843	0.900555	0.954034	0.939761	Folr1/Fst/I
GO_BP_m4	GO:004859	eye morph	3/727	173/23843	0.901084	0.954383	0.940105	Cabp4/Gn
GO_BP_m4	GO:004578	positive re	7/727	343/23843	0.901443	0.954551	0.940271	Anp32b/A

GO_BP_m4	GO:001922	regulation	1/727	75/23843	0.902323	0.954797	0.940513	Htr2c
GO_BP_m4	GO:007134	cellular res	1/727	75/23843	0.902323	0.954797	0.940513	Rela
GO_BP_m4	GO:00977	positive re	1/727	75/23843	0.902323	0.954797	0.940513	Esr2
GO_BP_m4	GO:00328	regulation	4/727	218/23843	0.902474	0.954797	0.940513	Erbb2/Mer
GO_BP_m4	GO:00027	positive re	2/727	127/23843	0.902761	0.95489	0.940604	Il13/Vamp
GO_BP_m4	GO:00508	cognition	6/727	303/23843	0.903056	0.95499	0.940703	Ager/Esr2/
GO_BP_m4	GO:00611	morphoge	4/727	219/23843	0.90436	0.955473	0.941178	Grb2/Nfat
GO_BP_m4	GO:00511	cofactor m	10/727	465/23843	0.904528	0.955473	0.941178	Apoa4/Co
GO_BP_m4	GO:00094	RNA modif	2/727	128/23843	0.905145	0.955473	0.941178	Mrm2/Wd
GO_BP_m4	GO:000597	glycogen n	1/727	76/23843	0.905311	0.955473	0.941178	Irs2
GO_BP_m4	GO:000607	cellular glu	1/727	76/23843	0.905311	0.955473	0.941178	Irs2
GO_BP_m4	GO:00064	protein O-	1/727	76/23843	0.905311	0.955473	0.941178	B3gnt5
GO_BP_m4	GO:004404	glucan me	1/727	76/23843	0.905311	0.955473	0.941178	Irs2
GO_BP_m4	GO:004591	positive re	1/727	76/23843	0.905311	0.955473	0.941178	Irs2
GO_BP_m4	GO:00519	catecholar	1/727	76/23843	0.905311	0.955473	0.941178	Rtn4
GO_BP_m4	GO:000081	sister chro	3/727	176/23843	0.907299	0.956636	0.942324	Rmi2/Sfpq
GO_BP_m4	GO:00067	coenzyme	6/727	306/23843	0.907847	0.956636	0.942324	Coq6/Folr1
GO_BP_m4	GO:00313	negative re	4/727	221/23843	0.908036	0.956636	0.942324	Efna1/Nba
GO_BP_m4	GO:000001	regulation	1/727	77/23843	0.908207	0.956636	0.942324	Recql5
GO_BP_m4	GO:00103	regulation	1/727	77/23843	0.908207	0.956636	0.942324	Hus1
GO_BP_m4	GO:006011	inner ear r	1/727	77/23843	0.908207	0.956636	0.942324	Tshr
GO_BP_m4	GO:006097	coronary v	1/727	77/23843	0.908207	0.956636	0.942324	Prokr1
GO_BP_m4	GO:006164	cytoskelet	1/727	77/23843	0.908207	0.956636	0.942324	12-Sep
GO_BP_m4	GO:004311	receptor m	3/727	177/23843	0.90929	0.956636	0.942324	Grb2/Kif16
GO_BP_m4	GO:003267	regulation	2/727	130/23843	0.909748	0.956636	0.942324	Gas6/Socs
GO_BP_m4	GO:00516	localizatior	2/727	130/23843	0.909748	0.956636	0.942324	Sec13/Sna
GO_BP_m4	GO:19033	positive re	2/727	130/23843	0.909748	0.956636	0.942324	Aurka/Socs
GO_BP_m4	GO:19033	regulation	4/727	222/23843	0.909826	0.956636	0.942324	Aurka/Efna
GO_BP_m4	GO:00725	establishm	9/727	430/23843	0.910647	0.956636	0.942324	Agap3/Ddi
GO_BP_m4	GO:00022	lymphocyt	1/727	78/23843	0.911015	0.956636	0.942324	Bcl10
GO_BP_m4	GO:00301	platelet act	1/727	78/23843	0.911015	0.956636	0.942324	Gata1
GO_BP_m4	GO:00301	regulation	1/727	78/23843	0.911015	0.956636	0.942324	F12
GO_BP_m4	GO:00460	ADP meta	1/727	78/23843	0.911015	0.956636	0.942324	Ak3
GO_BP_m4	GO:00513	establishm	1/727	78/23843	0.911015	0.956636	0.942324	Spdl1
GO_BP_m4	GO:006007	excitatory	1/727	78/23843	0.911015	0.956636	0.942324	Hcrt
GO_BP_m4	GO:006041	cardiac sep	1/727	78/23843	0.911015	0.956636	0.942324	Nfatc1
GO_BP_m4	GO:190004	regulation	1/727	78/23843	0.911015	0.956636	0.942324	F12
GO_BP_m4	GO:20010	reactive nit	1/727	78/23843	0.911015	0.956636	0.942324	Wdr35
GO_BP_m4	GO:19015	fatty acid d	2/727	131/23843	0.911971	0.957429	0.943106	Ces2h/Cyp
GO_BP_m4	GO:004887	multicellul	7/727	351/23843	0.913285	0.958022	0.943689	Car2/Cdh3
GO_BP_m4	GO:190121	negative re	4/727	224/23843	0.913314	0.958022	0.943689	Esr2/Il13/It
GO_BP_m4	GO:00032	cardiac ver	1/727	79/23843	0.913737	0.958022	0.943689	Dsp
GO_BP_m4	GO:003261	interleukin	1/727	79/23843	0.913737	0.958022	0.943689	Gas6
GO_BP_m4	GO:00345	protein loc	1/727	79/23843	0.913737	0.958022	0.943689	Spdl1
GO_BP_m4	GO:00500	chromosor	1/727	79/23843	0.913737	0.958022	0.943689	Spdl1
GO_BP_m4	GO:00516	detection	10/727	474/23843	0.915861	0.959106	0.944757	Cabp4/Gna
GO_BP_m4	GO:003527	endocrine	2/727	133/23843	0.916263	0.959106	0.944757	Duox2/Nk
GO_BP_m4	GO:00507	negative re	2/727	133/23843	0.916263	0.959106	0.944757	Btn2a2/Ga

GO_BP_m4	GO:005071	positive reg	2/727	133/23843	0.916263	0.959106	0.944757	Mapk14/M
GO_BP_m4	GO:00700	plasma me	1/727	80/23843	0.916376	0.959106	0.944757	A4galt
GO_BP_m4	GO:001491	regulation	1/727	80/23843	0.916376	0.959106	0.944757	Ager
GO_BP_m4	GO:00229	respiratory	1/727	80/23843	0.916376	0.959106	0.944757	Cycs
GO_BP_m4	GO:19001	positive reg	1/727	80/23843	0.916376	0.959106	0.944757	Mapk14
GO_BP_m4	GO:190129	nucleoside	2/727	134/23843	0.918334	0.960312	0.945945	Nudt5/Nuc
GO_BP_m4	GO:004875	branching	3/727	182/23843	0.918678	0.960312	0.945945	Nfatc1/Spr
GO_BP_m4	GO:00032	ventricular	1/727	81/23843	0.918935	0.960312	0.945945	Nfatc1
GO_BP_m4	GO:000647	protein de	1/727	81/23843	0.918935	0.960312	0.945945	Sfpq
GO_BP_m4	GO:00486	neuron fat	1/727	81/23843	0.918935	0.960312	0.945945	Nkx6-2
GO_BP_m4	GO:00975	lamellipodi	1/727	81/23843	0.918935	0.960312	0.945945	Spata13
GO_BP_m4	GO:19019	positive reg	1/727	81/23843	0.918935	0.960312	0.945945	Anp32b
GO_BP_m4	GO:001049	proteasom	9/727	437/23843	0.919408	0.960596	0.946225	Agap3/Aur
GO_BP_m4	GO:00690	phagocyto	6/727	314/23843	0.919635	0.960624	0.946253	Ager/Gas6/
GO_BP_m4	GO:00326	regulation	2/727	135/23843	0.920358	0.960631	0.946259	Gas6/Ripk1
GO_BP_m4	GO:004649	nicotinami	2/727	135/23843	0.920358	0.960631	0.946259	Kynu/Pdhx
GO_BP_m4	GO:004354	endothelial	3/727	183/23843	0.920445	0.960631	0.946259	Ager/Efna1
GO_BP_m4	GO:005122	negative re	3/727	183/23843	0.920445	0.960631	0.946259	Btn2a2/Ga
GO_BP_m4	GO:00434	regulation	1/727	82/23843	0.921415	0.960632	0.94626	Zfp36l1
GO_BP_m4	GO:005081	regulation	1/727	82/23843	0.921415	0.960632	0.94626	F12
GO_BP_m4	GO:000245	humoral im	3/727	184/23843	0.922178	0.960632	0.94626	Ighv9-4/M
GO_BP_m4	GO:00456	regulation	2/727	136/23843	0.922334	0.960632	0.94626	Nfatc1/Tnr
GO_BP_m4	GO:190134	regulation	6/727	316/23843	0.922368	0.960632	0.94626	C3ar1/Efna
GO_BP_m4	GO:00900	positive reg	4/727	230/23843	0.923067	0.960632	0.94626	Anp32b/Pi
GO_BP_m4	GO:00451	cell fate co	5/727	274/23843	0.923304	0.960632	0.94626	Gata1/Nkx
GO_BP_m4	GO:000722	integrin-m	1/727	83/23843	0.923819	0.960632	0.94626	Ctnna1
GO_BP_m4	GO:00091	purine nuc	1/727	83/23843	0.923819	0.960632	0.94626	Ak3
GO_BP_m4	GO:000917	purine ribo	1/727	83/23843	0.923819	0.960632	0.94626	Ak3
GO_BP_m4	GO:00327	positive reg	1/727	83/23843	0.923819	0.960632	0.94626	Ripk1
GO_BP_m4	GO:004249	mechanore	1/727	83/23843	0.923819	0.960632	0.94626	Tshr
GO_BP_m4	GO:005114	positive reg	1/727	83/23843	0.923819	0.960632	0.94626	Mapk14
GO_BP_m4	GO:005149	regulation	1/727	83/23843	0.923819	0.960632	0.94626	Synpo
GO_BP_m4	GO:00193	pyridine nu	2/727	137/23843	0.924264	0.960632	0.94626	Kynu/Pdhx
GO_BP_m4	GO:00313	negative re	2/727	137/23843	0.924264	0.960632	0.94626	Sptan1/Tm
GO_BP_m4	GO:00326	interleukin	2/727	137/23843	0.924264	0.960632	0.94626	Gas6/Socs
GO_BP_m4	GO:003264	tumor necr	2/727	137/23843	0.924264	0.960632	0.94626	Gas6/Ripk1
GO_BP_m4	GO:190355	regulation	2/727	137/23843	0.924264	0.960632	0.94626	Gas6/Ripk1
GO_BP_m4	GO:00095	fertilization	3/727	186/23843	0.92554	0.96113	0.946751	Astl/Catspe
GO_BP_m4	GO:00345	protein loc	5/727	276/23843	0.9261	0.96113	0.946751	Agap3/Dcl
GO_BP_m4	GO:00106	regulation	1/727	84/23843	0.92615	0.96113	0.946751	Fndc1
GO_BP_m4	GO:00193	nicotinami	1/727	84/23843	0.92615	0.96113	0.946751	Kynu
GO_BP_m4	GO:00508	negative re	1/727	84/23843	0.92615	0.96113	0.946751	Ager
GO_BP_m4	GO:190352	positive reg	1/727	84/23843	0.92615	0.96113	0.946751	Htr2c
GO_BP_m4	GO:190355	positive reg	1/727	84/23843	0.92615	0.96113	0.946751	Ripk1
GO_BP_m4	GO:000695	compleme	3/727	187/23843	0.927171	0.961563	0.947177	Ighv9-4/M
GO_BP_m4	GO:00447	multi-mult	3/727	187/23843	0.927171	0.961563	0.947177	Mirlet7c-2/
GO_BP_m4	GO:190495	negative re	3/727	187/23843	0.927171	0.961563	0.947177	Btn2a2/Ga
GO_BP_m4	GO:004255	myelinatio	2/727	139/23843	0.927989	0.961805	0.947416	Erbb2/Nkx

GO_BP_m4	GO:002195	central ner	1/727	85/23843	0.92841	0.961805	0.947416	Zeb2
GO_BP_m4	GO:002290	electron tra	1/727	85/23843	0.92841	0.961805	0.947416	Cycs
GO_BP_m4	GO:004353	regulation	1/727	85/23843	0.92841	0.961805	0.947416	Efna1
GO_BP_m4	GO:200102	positive re	1/727	85/23843	0.92841	0.961805	0.947416	Rps3
GO_BP_m4	GO:000206	columnar/	2/727	140/23843	0.929786	0.962198	0.947803	Mir7-2/Tm
GO_BP_m4	GO:000221	activation	2/727	140/23843	0.929786	0.962198	0.947803	Rela/Sfpq
GO_BP_m4	GO:007170	tumor necr	2/727	140/23843	0.929786	0.962198	0.947803	Gas6/Ripk1
GO_BP_m4	GO:007200	nephron de	2/727	140/23843	0.929786	0.962198	0.947803	C3ar1/Ret
GO_BP_m4	GO:000716	cell-matrix	3/727	189/23843	0.930334	0.962198	0.947803	Muc4/Tiam
GO_BP_m4	GO:000611	energy rese	1/727	86/23843	0.930601	0.962198	0.947803	Irs2
GO_BP_m4	GO:000611	oxidative p	1/727	86/23843	0.930601	0.962198	0.947803	Cycs
GO_BP_m4	GO:000616	nucleoside	1/727	86/23843	0.930601	0.962198	0.947803	Nme5
GO_BP_m4	GO:003591	skeletal mu	1/727	86/23843	0.930601	0.962198	0.947803	Cops2
GO_BP_m4	GO:000283	regulation	2/727	141/23843	0.93154	0.962545	0.948144	Il27/Muc4
GO_BP_m4	GO:001097	transport a	2/727	141/23843	0.93154	0.962545	0.948144	Dynll2/Wd
GO_BP_m4	GO:009911	microtubul	2/727	141/23843	0.93154	0.962545	0.948144	Dynll2/Wd
GO_BP_m4	GO:001490	smooth mu	1/727	87/23843	0.932724	0.963066	0.948658	Ager
GO_BP_m4	GO:001936	pyridine nu	1/727	87/23843	0.932724	0.963066	0.948658	Kynu
GO_BP_m4	GO:003101	pancreas d	1/727	87/23843	0.932724	0.963066	0.948658	Nkx6-2
GO_BP_m4	GO:000279	negative re	2/727	142/23843	0.933253	0.963066	0.948658	Btn2a2/Ga
GO_BP_m4	GO:000727	ensheathm	2/727	142/23843	0.933253	0.963066	0.948658	Erbb2/Nkx
GO_BP_m4	GO:000836	axon enshe	2/727	142/23843	0.933253	0.963066	0.948658	Erbb2/Nkx
GO_BP_m4	GO:002176	limbic syste	1/727	88/23843	0.934783	0.963544	0.949129	Zeb2
GO_BP_m4	GO:003296	collagen m	1/727	88/23843	0.934783	0.963544	0.949129	Ager
GO_BP_m4	GO:004693	nucleotide	1/727	88/23843	0.934783	0.963544	0.949129	Nme5
GO_BP_m4	GO:007267	lymphocyte	1/727	88/23843	0.934783	0.963544	0.949129	Gas6
GO_BP_m4	GO:190342	regulation	1/727	88/23843	0.934783	0.963544	0.949129	Wdr35
GO_BP_m4	GO:000323	cardiac ver	2/727	143/23843	0.934926	0.963544	0.949129	Dsp/Nfatc1
GO_BP_m4	GO:005105	regulation	8/727	411/23843	0.935854	0.963999	0.949577	C3ar1/Hcrt
GO_BP_m4	GO:005104	negative re	4/727	239/23843	0.935856	0.963999	0.949577	Btn2a2/Cb
GO_BP_m4	GO:001839	internal pe	2/727	144/23843	0.936558	0.963999	0.949577	Nat8f1/Dr1
GO_BP_m4	GO:005109	regulation	7/727	370/23843	0.936606	0.963999	0.949577	Ager/Aurk
GO_BP_m4	GO:000330	cardiac mu	1/727	89/23843	0.936779	0.963999	0.949577	Tiam1
GO_BP_m4	GO:001065	muscle cell	1/727	89/23843	0.936779	0.963999	0.949577	Fndc1
GO_BP_m4	GO:004001	regulation	1/727	89/23843	0.936779	0.963999	0.949577	Tshr
GO_BP_m4	GO:004870	skeletal sys	4/727	240/23843	0.937151	0.964174	0.94975	Fgf4/Hoxa
GO_BP_m4	GO:005109	positive re	3/727	194/23843	0.937698	0.96453	0.9501	Eif3e/Tiam
GO_BP_m4	GO:001993	cAMP-med	2/727	145/23843	0.938152	0.964789	0.950355	Gpr61/Tsh
GO_BP_m4	GO:004508	regulation	4/727	241/23843	0.938422	0.96486	0.950425	Dusp10/Re
GO_BP_m4	GO:005084	regulation	1/727	90/23843	0.938714	0.964952	0.950516	Mir1a-2
GO_BP_m4	GO:003650	ERAD path	1/727	91/23843	0.94059	0.966672	0.95221	Stt3b
GO_BP_m4	GO:000028	nuclear div	8/727	416/23843	0.940811	0.966692	0.95223	Cenps/Aur
GO_BP_m4	GO:002154	pallium de	2/727	147/23843	0.941226	0.966911	0.952445	Rtn4/Zeb2
GO_BP_m4	GO:000167	long-chain	1/727	92/23843	0.942408	0.967501	0.953027	Cyp2a22
GO_BP_m4	GO:001489	striated mu	1/727	92/23843	0.942408	0.967501	0.953027	Tiam1
GO_BP_m4	GO:006035	response t	1/727	92/23843	0.942408	0.967501	0.953027	Ly6g6d
GO_BP_m4	GO:005114	regulation	2/727	148/23843	0.942708	0.967602	0.953126	Mapk14/Si
GO_BP_m4	GO:000647	internal pr	2/727	149/23843	0.944155	0.968064	0.953581	Nat8f1/Dr1

GO_BP_m4	GO:000717	transformir	2/727	149/23843	0.944155	0.968064	0.953581	Folr1/Vasn
GO_BP_m4	GO:003475	cellular hor	1/727	93/23843	0.944171	0.968064	0.953581	Akr1d1
GO_BP_m4	GO:004348	regulation	1/727	93/23843	0.944171	0.968064	0.953581	Zfp36l1
GO_BP_m4	GO:190274	regulation	1/727	93/23843	0.944171	0.968064	0.953581	Hus1
GO_BP_m4	GO:000195	regulation	1/727	94/23843	0.94588	0.969193	0.954693	Gas6
GO_BP_m4	GO:001489	muscle hyp	1/727	94/23843	0.94588	0.969193	0.954693	Tiam1
GO_BP_m4	GO:011002	regulation	1/727	94/23843	0.94588	0.969193	0.954693	Synpo
GO_BP_m4	GO:000244	lymphocyte	7/727	381/23843	0.947418	0.970266	0.955751	Ager/Bcl10
GO_BP_m4	GO:004684	bone remo	1/727	95/23843	0.947537	0.970266	0.955751	Car2
GO_BP_m4	GO:200124	negative re	1/727	95/23843	0.947537	0.970266	0.955751	Nme5
GO_BP_m4	GO:000275	immune re	8/727	424/23843	0.948044	0.970577	0.956057	Bcl10/Btn2
GO_BP_m4	GO:004828	organelle f	9/727	466/23843	0.948302	0.970634	0.956113	Cenps/Aur
GO_BP_m4	GO:000830	associative	1/727	96/23843	0.949143	0.970871	0.956346	Synpo
GO_BP_m4	GO:004577	positive re	1/727	96/23843	0.949143	0.970871	0.956346	Slc8a1
GO_BP_m4	GO:006084	artery deve	1/727	96/23843	0.949143	0.970871	0.956346	Folr1
GO_BP_m4	GO:001839	peptidyl-ly	2/727	153/23843	0.949601	0.971132	0.956603	Nat8f1/Dr1
GO_BP_m4	GO:006034	bone morp	1/727	97/23843	0.9507	0.971928	0.957388	Fgf4
GO_BP_m4	GO:000609	generation	6/727	342/23843	0.951137	0.971928	0.957388	Cycs/Cyp1a
GO_BP_m4	GO:001606	immunoglo	4/727	253/23843	0.951954	0.971928	0.957388	Bcl10/Ighv
GO_BP_m4	GO:001993	cyclic-nucl	2/727	155/23843	0.95213	0.971928	0.957388	Gpr61/Tshr
GO_BP_m4	GO:000301	renal syster	1/727	98/23843	0.952209	0.971928	0.957388	Gas6
GO_BP_m4	GO:000609	pyruvate m	1/727	98/23843	0.952209	0.971928	0.957388	Pdhx
GO_BP_m4	GO:003209	negative re	1/727	98/23843	0.952209	0.971928	0.957388	Aurka
GO_BP_m4	GO:003223	regulation	1/727	98/23843	0.952209	0.971928	0.957388	Synpo
GO_BP_m4	GO:005165	maintenan	1/727	98/23843	0.952209	0.971928	0.957388	Polr2m
GO_BP_m4	GO:001481	muscle cell	1/727	99/23843	0.953672	0.97264	0.958089	Ager
GO_BP_m4	GO:004213	neurotrans	1/727	99/23843	0.953672	0.97264	0.958089	Wdr35
GO_BP_m4	GO:012003	positive re	1/727	99/23843	0.953672	0.97264	0.958089	Neurl1a
GO_BP_m4	GO:001648	protein pro	4/727	255/23843	0.953924	0.97264	0.958089	Astl/Ece2/F
GO_BP_m4	GO:001972	B cell medi	4/727	255/23843	0.953924	0.97264	0.958089	Bcl10/Ighv
GO_BP_m4	GO:000718	adenylate	1/727	100/23843	0.955091	0.973207	0.958648	Tshr
GO_BP_m4	GO:005088	endocrine	1/727	100/23843	0.955091	0.973207	0.958648	Inhba
GO_BP_m4	GO:006007	regulation	1/727	100/23843	0.955091	0.973207	0.958648	Hcrt
GO_BP_m4	GO:003070	cytoskeleto	2/727	158/23843	0.955698	0.973619	0.959053	Dynll2/Wdr
GO_BP_m4	GO:005101	actin filame	2/727	159/23843	0.95683	0.974306	0.95973	Eln/Synpo
GO_BP_m4	GO:000165	ureteric bu	1/727	102/23843	0.957799	0.974306	0.95973	Ret
GO_BP_m4	GO:000195	regulation	1/727	102/23843	0.957799	0.974306	0.95973	Muc4
GO_BP_m4	GO:000282	positive re	1/727	102/23843	0.957799	0.974306	0.95973	Socs5
GO_BP_m4	GO:000682	chloride tra	1/727	102/23843	0.957799	0.974306	0.95973	Car2
GO_BP_m4	GO:007216	mesonephr	1/727	102/23843	0.957799	0.974306	0.95973	Ret
GO_BP_m4	GO:007216	mesonephr	1/727	102/23843	0.957799	0.974306	0.95973	Ret
GO_BP_m4	GO:000276	immune re	8/727	438/23843	0.958834	0.975151	0.960563	Bcl10/Btn2
GO_BP_m4	GO:006075	regulation	1/727	103/23843	0.959091	0.975205	0.960616	Gas6
GO_BP_m4	GO:000695	humoral in	6/727	352/23843	0.959358	0.975269	0.960678	AY761184/
GO_BP_m4	GO:006157	actin filame	2/727	162/23843	0.960062	0.975777	0.961179	Eln/Synpo
GO_BP_m4	GO:004870	embryonic	1/727	104/23843	0.960344	0.975823	0.961224	Hoxa6
GO_BP_m4	GO:003032	lung develo	3/727	214/23843	0.960515	0.975823	0.961224	Cyp1a2/Sp
GO_BP_m4	GO:005160	protein ma	5/727	309/23843	0.960799	0.975904	0.961304	Aga/Astl/E

GO_BP_m4	GO:00508	regulation	4/727	263/23843	0.961082	0.975984	0.961382	Ighv9-4/Il1
GO_BP_m4	GO:00182	mesonephr	1/727	105/23843	0.961558	0.976053	0.961451	Ret
GO_BP_m4	GO:00219	cerebral c	1/727	105/23843	0.961558	0.976053	0.961451	Rtn4
GO_BP_m4	GO:00165	negative re	1/727	106/23843	0.962736	0.976748	0.962136	Spry2
GO_BP_m4	GO:00435	blood vess	1/727	106/23843	0.962736	0.976748	0.962136	Efna1
GO_BP_m4	GO:004211	B cell activ	7/727	401/23843	0.962944	0.976748	0.962136	Ifna12/Ighv
GO_BP_m4	GO:00611	regulation	2/727	165/23843	0.963061	0.976748	0.962136	Aurka/Socs
GO_BP_m4	GO:00901	positive re	1/727	107/23843	0.963877	0.977298	0.962677	Inhba
GO_BP_m4	GO:00435	negative re	2/727	166/23843	0.964011	0.977298	0.962677	Itsn1/Mt1
GO_BP_m4	GO:00000	G2/M trans	1/727	108/23843	0.964983	0.977662	0.963035	Hus1
GO_BP_m4	GO:00028	positive re	1/727	108/23843	0.964983	0.977662	0.963035	Socs5
GO_BP_m4	GO:20002	regulation	1/727	108/23843	0.964983	0.977662	0.963035	C3ar1
GO_BP_m4	GO:00433	regulation	3/727	220/23843	0.965656	0.977713	0.963085	Aurka/Tia
GO_BP_m4	GO:00508	positive re	3/727	220/23843	0.965656	0.977713	0.963085	Ighv9-4/Il1
GO_BP_m4	GO:00017	leukocyte	1/727	109/23843	0.966056	0.977713	0.963085	Bcl10
GO_BP_m4	GO:19053	regulation	1/727	109/23843	0.966056	0.977713	0.963085	Ror2
GO_BP_m4	GO:20001	negative re	1/727	109/23843	0.966056	0.977713	0.963085	Spry2
GO_BP_m4	GO:00070	spindle or	2/727	169/23843	0.966724	0.978182	0.963548	Aurka/Rps
GO_BP_m4	GO:00435	protein acy	3/727	222/23843	0.967225	0.978481	0.963842	Nat8f1/Dr1
GO_BP_m4	GO:00076	learning or	4/727	272/23843	0.967896	0.978953	0.964307	Ager/Esr2/
GO_BP_m4	GO:00305	BMP signal	2/727	171/23843	0.968423	0.979279	0.964628	Fst/Ror2
GO_BP_m4	GO:00433	response t	1/727	112/23843	0.969081	0.979737	0.965079	Ifna12
GO_BP_m4	GO:00086	apoptotic	1/727	113/23843	0.970028	0.980487	0.965818	Wdr35
GO_BP_m4	GO:00106	negative re	6/727	369/23843	0.970499	0.980756	0.966083	Nav3/Pid1/
GO_BP_m4	GO:001081	positive re	1/727	114/23843	0.970946	0.981	0.966324	Vit
GO_BP_m4	GO:00070	mitotic spi	1/727	115/23843	0.971836	0.981692	0.967006	Aurka
GO_BP_m4	GO:000827	regulation	1/727	116/23843	0.972699	0.982149	0.967455	Tmod2
GO_BP_m4	GO:19013	negative re	1/727	116/23843	0.972699	0.982149	0.967455	Spry2
GO_BP_m4	GO:00064	protein ac	2/727	179/23843	0.974418	0.983677	0.96896	Nat8f1/Dr1
GO_BP_m4	GO:00508	B cell rece	2/727	180/23843	0.975085	0.984142	0.969419	Ighv9-4/Lc
GO_BP_m4	GO:00064	protein fol	2/727	181/23843	0.975736	0.984458	0.96973	Dnajb14/P
GO_BP_m4	GO:00016	urogenital	5/727	333/23843	0.975838	0.984458	0.96973	C3ar1/Esr2
GO_BP_m4	GO:00717	response t	2/727	182/23843	0.97637	0.984458	0.96973	Fst/Ror2
GO_BP_m4	GO:00717	cellular res	2/727	182/23843	0.97637	0.984458	0.96973	Fst/Ror2
GO_BP_m4	GO:00022	pattern rec	1/727	121/23843	0.976634	0.984458	0.96973	Rela
GO_BP_m4	GO:00032	cardiac sep	1/727	121/23843	0.976634	0.984458	0.96973	Nfatc1
GO_BP_m4	GO:00091	nucleotide	1/727	122/23843	0.97735	0.984972	0.970237	Nudt7
GO_BP_m4	GO:00027	innate imm	1/727	123/23843	0.978044	0.985391	0.970649	Rela
GO_BP_m4	GO:00705	regulation	2/727	185/23843	0.978177	0.985391	0.970649	Nav3/Rps3
GO_BP_m4	GO:00448	cell cycle G	1/727	124/23843	0.978717	0.985595	0.97085	Hus1
GO_BP_m4	GO:00720	renal syste	4/727	291/23843	0.978792	0.985595	0.97085	C3ar1/Ret/
GO_BP_m4	GO:000691	phagocyto	2/727	187/23843	0.979307	0.985905	0.971156	Ager/Ighv
GO_BP_m4	GO:001081	regulation	2/727	189/23843	0.98038	0.986778	0.972015	Muc4/Vit
GO_BP_m4	GO:20012	negative re	1/727	128/23843	0.981209	0.987405	0.972632	Trip12
GO_BP_m4	GO:006054	respiratory	3/727	247/23843	0.981909	0.987902	0.973122	Cyp1a2/Sp
GO_BP_m4	GO:00106	positive re	1/727	130/23843	0.982343	0.98813	0.973347	Rtn4
GO_BP_m4	GO:00015	skeletal sys	8/727	490/23843	0.983481	0.989067	0.97427	Fgf4/Fst/H
GO_BP_m4	GO:00990	plasma me	2/727	196/23843	0.983727	0.98909	0.974293	Ager/Ighv

GO_BP_m4	GO:004859	camera-typ	1/727	133/23843	0.983918	0.98909	0.974293	Cabp4
GO_BP_m4	GO:001569	inorganic a	1/727	134/23843	0.984411	0.989336	0.974535	Car2
GO_BP_m4	GO:004508	positive reg	2/727	198/23843	0.984576	0.989336	0.974535	Rela/Sfpq
GO_BP_m4	GO:004870	embryonic	1/727	136/23843	0.985352	0.989908	0.975098	Hoxa6
GO_BP_m4	GO:001032	membrane	2/727	203/23843	0.986516	0.990596	0.975776	Ager/Ighv9
GO_BP_m4	GO:006024	anatomical	5/727	361/23843	0.986548	0.990596	0.975776	Car2/Cdh3
GO_BP_m4	GO:001657	histone ace	1/727	139/23843	0.986659	0.990596	0.975776	Dr1
GO_BP_m4	GO:004213	neurotrans	1/727	141/23843	0.987465	0.990989	0.976163	Wdr35
GO_BP_m4	GO:007207	kidney epit	1/727	141/23843	0.987465	0.990989	0.976163	Ret
GO_BP_m4	GO:000733	single fertil	1/727	142/23843	0.987849	0.991166	0.976338	Astl
GO_BP_m4	GO:014001	mitotic nuc	3/727	266/23843	0.988611	0.991723	0.976886	Aurka/Rpl2
GO_BP_m4	GO:000182	kidney dev	3/727	269/23843	0.989422	0.9923	0.977455	C3ar1/Ret/
GO_BP_m4	GO:000007	mitotic sist	1/727	147/23843	0.989602	0.9923	0.977455	Spdl1
GO_BP_m4	GO:003105	regulation	1/727	149/23843	0.99023	0.992722	0.97787	Trip12
GO_BP_m4	GO:004593	positive reg	1/727	153/23843	0.991376	0.993662	0.978796	Anp32b
GO_BP_m4	GO:000691	phagocytos	1/727	154/23843	0.99164	0.993719	0.978852	Ighv9-4
GO_BP_m4	GO:001657	histone mo	6/727	437/23843	0.992441	0.994313	0.979438	Dr1/Dydc1
GO_BP_m4	GO:000761	learning	1/727	161/23843	0.993279	0.994944	0.980059	Synpo
GO_BP_m4	GO:001656	covalent ch	6/727	449/23843	0.994125	0.995583	0.980688	Dr1/Dydc1
GO_BP_m4	GO:005105	positive reg	2/727	236/23843	0.99451	0.995638	0.980743	C3ar1/Rps3
GO_BP_m4	GO:200125	positive reg	1/727	168/23843	0.994597	0.995638	0.980743	Sfpq
GO_BP_m4	GO:012003	regulation	1/727	172/23843	0.995231	0.996064	0.981163	Neurl1a
GO_BP_m4	GO:006049	regulation	1/727	174/23843	0.995519	0.996144	0.981242	Neurl1a
GO_BP_m4	GO:190227	regulation	1/727	176/23843	0.99579	0.996207	0.981303	Trip12
GO_BP_m4	GO:003304	regulation	3/727	330/23843	0.997736	0.997745	0.982818	Rmi2/Sfpq/
GO_BP_m4	GO:006034	bone devel	1/727	196/23843	0.997745	0.997745	0.982818	Fgf4
GO_CC_m1	GO:000577	peroxisome	32/2589	142/23583	5.61E-05	0.030225	0.028481	Abcd3/Aca
GO_CC_m1	GO:004257	microbody	32/2589	142/23583	5.61E-05	0.030225	0.028481	Abcd3/Aca
GO_CC_m1	GO:003099	intraciliary	9/2589	22/23583	0.000298	0.107249	0.10106	Ift172/Ift22
GO_CC_m1	GO:003099	intraciliary	11/2589	34/23583	0.000706	0.149275	0.14066	Ift172/Ift22
GO_CC_m1	GO:004308	synaptic cle	6/2589	12/23583	0.000894	0.149275	0.14066	Ache/C1ql
GO_CC_m1	GO:004443	microbody	15/2589	57/23583	0.000969	0.149275	0.14066	Abcd3/Acs
GO_CC_m1	GO:004443	peroxisoma	15/2589	57/23583	0.000969	0.149275	0.14066	Abcd3/Acs
GO_CC_m1	GO:003339	chromatoid	6/2589	14/23583	0.002392	0.293357	0.276428	Arntl/Clock
GO_CC_m1	GO:000575	mitochond	43/2589	253/23583	0.002449	0.293357	0.276428	Dglucy/Aba
GO_CC_m1	GO:009885	actin-base	35/2589	199/23583	0.003339	0.294083	0.277112	Abi1/Acpp/
GO_CC_m1	GO:003243	actin filame	18/2589	83/23583	0.003457	0.294083	0.277112	Acta1/Acta
GO_CC_m1	GO:004521	postsynapt	43/2589	258/23583	0.003551	0.294083	0.277112	Abi1/Ache/
GO_CC_m1	GO:009957	postsynapt	43/2589	258/23583	0.003551	0.294083	0.277112	Adora1/Arl
GO_CC_m1	GO:003002	lamellipodi	29/2589	160/23583	0.004603	0.294083	0.277112	Abi1/Abi3/
GO_CC_m1	GO:000578	endoplasm	71/2589	476/23583	0.004637	0.294083	0.277112	Acer3/Akap
GO_CC_m1	GO:000577	peroxisoma	11/2589	42/23583	0.004638	0.294083	0.277112	Abcd3/Acs
GO_CC_m1	GO:003190	microbody	11/2589	42/23583	0.004638	0.294083	0.277112	Abcd3/Acs
GO_CC_m1	GO:000579	rough endo	20/2589	100/23583	0.005647	0.295177	0.278143	Ache/Adcy
GO_CC_m1	GO:009882	endoplasm	72/2589	489/23583	0.005985	0.295177	0.278143	Acer3/Akap
GO_CC_m1	GO:009706	synaptic m	52/2589	334/23583	0.00612	0.295177	0.278143	Abi1/Ache/
GO_CC_m1	GO:004217	nuclear out	73/2589	498/23583	0.006315	0.295177	0.278143	Acer3/Akap
GO_CC_m1	GO:003227	asymmetric	42/2589	260/23583	0.006843	0.295177	0.278143	Adora1/Arl

GO_CC_m1	GO:007065	HAUS com	4/2589	8/23583	0.007045	0.295177	0.278143	Haus1/Hau
GO_CC_m1	GO:003146	Cul3-RING	15/2589	70/23583	0.008107	0.295177	0.278143	Btbd18/Glr
GO_CC_m1	GO:009898	neuron to	42/2589	263/23583	0.00833	0.295177	0.278143	Adora1/Arl
GO_CC_m1	GO:001406	postsynapt	41/2589	256/23583	0.008628	0.295177	0.278143	Adora1/Arl
GO_CC_m1	GO:001562	actin cytosl	69/2589	474/23583	0.009055	0.295177	0.278143	Abl2/Abra/
GO_CC_m1	GO:000565	nuclear lan	5/2589	13/23583	0.009585	0.295177	0.278143	Hlcs/Lbr/N
GO_CC_m1	GO:003194	filamentou	11/2589	46/23583	0.009604	0.295177	0.278143	Fermt2/Fsc
GO_CC_m1	GO:001986	organelle ii	68/2589	468/23583	0.009906	0.295177	0.278143	2010107E0
GO_CC_m1	GO:000578	peroxisoma	6/2589	18/23583	0.010056	0.295177	0.278143	Abcd3/Eci2
GO_CC_m1	GO:003104	dense core	6/2589	18/23583	0.010056	0.295177	0.278143	1500015O1
GO_CC_m1	GO:003190	microbody	6/2589	18/23583	0.010056	0.295177	0.278143	Abcd3/Eci2
GO_CC_m1	GO:003586	ciliary trans	15/2589	72/23583	0.010541	0.295177	0.278143	B9d1/Cc2d
GO_CC_m1	GO:000582	polar micro	3/2589	5/23583	0.011139	0.295177	0.278143	Klhl21/Klhl
GO_CC_m1	GO:003141	NatA comp	3/2589	5/23583	0.011139	0.295177	0.278143	Naa10/Naa
GO_CC_m1	GO:007179	LUBAC cor	3/2589	5/23583	0.011139	0.295177	0.278143	Park2/Rbck
GO_CC_m1	GO:003190	endosome	2/2589	2/23583	0.012048	0.295177	0.278143	Cd63/Pdlin
GO_CC_m1	GO:003650	UFD1-NPL	2/2589	2/23583	0.012048	0.295177	0.278143	Nploc4/Ufd
GO_CC_m1	GO:007055	PCNA-p21	2/2589	2/23583	0.012048	0.295177	0.278143	Cdkn1a/Pc
GO_CC_m1	GO:009712	cyclin A1-C	2/2589	2/23583	0.012048	0.295177	0.278143	Ccna1/Cdk
GO_CC_m1	GO:009713	cyclin E1-C	2/2589	2/23583	0.012048	0.295177	0.278143	Ccne1/Cdk
GO_CC_m1	GO:009713	cyclin E2-C	2/2589	2/23583	0.012048	0.295177	0.278143	Ccne2/Cdk
GO_CC_m1	GO:199066	PCSK9-Anx	2/2589	2/23583	0.012048	0.295177	0.278143	Anxa2/Pcsk
GO_CC_m1	GO:003017	filopodium	17/2589	87/23583	0.012817	0.298561	0.281331	Abi1/Acpp
GO_CC_m1	GO:000574	mitochond	62/2589	426/23583	0.012848	0.298561	0.281331	2010107E0
GO_CC_m1	GO:000581	centrosom	71/2589	498/23583	0.013017	0.298561	0.281331	Rtraf/B9d1
GO_CC_m1	GO:000587	microtubul	60/2589	412/23583	0.014016	0.314781	0.296615	Bcas3/Cct3
GO_CC_m1	GO:003146	cullin-RING	32/2589	199/23583	0.01759	0.367131	0.345944	Abtb1/Arih
GO_CC_m1	GO:003141	N-terminal	4/2589	10/23583	0.017653	0.367131	0.345944	Naa10/Naa
GO_CC_m1	GO:004466	MLL3/4 co	4/2589	10/23583	0.017653	0.367131	0.345944	Ash2l/Kdm
GO_CC_m1	GO:003013	transport v	44/2589	291/23583	0.017709	0.367131	0.345944	Adra1d/Ap
GO_CC_m1	GO:001632	basolateral	35/2589	223/23583	0.019101	0.36772	0.346499	Abcc3/Adc
GO_CC_m1	GO:004654	U4/U6 x U5	7/2589	26/23583	0.019135	0.36772	0.346499	Lsm5/Naa3
GO_CC_m1	GO:007097	endoplasm	7/2589	26/23583	0.019135	0.36772	0.346499	H2-Q2/Mia
GO_CC_m1	GO:000015	ubiquitin li	50/2589	340/23583	0.019688	0.36772	0.346499	Abtb1/Arih
GO_CC_m1	GO:003125	cell leading	53/2589	364/23583	0.019969	0.36772	0.346499	Abi1/Abi3/
GO_CC_m1	GO:000567	transcriptio	3/2589	6/23583	0.020467	0.36772	0.346499	Gtf2a1/Gtf
GO_CC_m1	GO:004435	pinosome	3/2589	6/23583	0.020467	0.36772	0.346499	Ankfy1/Anx
GO_CC_m1	GO:004435	macropino	3/2589	6/23583	0.020467	0.36772	0.346499	Ankfy1/Anx
GO_CC_m1	GO:003159	neuromusc	14/2589	71/23583	0.020949	0.370212	0.348848	Ache/Ascc
GO_CC_m1	GO:004264	actomyosir	16/2589	85/23583	0.021599	0.375538	0.353866	Acta1/Acta
GO_CC_m1	GO:004485	plasma me	20/2589	114/23583	0.023054	0.388763	0.366328	Adcyap1r1
GO_CC_m1	GO:009879	presynapse	56/2589	391/23583	0.023081	0.388763	0.366328	Ache/Ador
GO_CC_m1	GO:004319	varicosity	5/2589	16/23583	0.024612	0.408166	0.384611	Cadm1/Crh
GO_CC_m1	GO:000557	proteinace	52/2589	361/23583	0.025184	0.408166	0.384611	2300002M
GO_CC_m1	GO:001711	Golgi trans	4/2589	11/23583	0.025368	0.408166	0.384611	Cog4/Cog
GO_CC_m1	GO:000587	spindle mic	11/2589	53/23583	0.026982	0.411609	0.387856	Cdk1/Fam1
GO_CC_m1	GO:000210	podosome	7/2589	28/23583	0.028387	0.411609	0.387856	Adam8/Db
GO_CC_m1	GO:000571	nuclear eu	7/2589	28/23583	0.028387	0.411609	0.387856	Ash2l/H2af

GO_CC_m1	GO:000929	nucleoid	10/2589	47/23583	0.029084	0.411609	0.387856	Clpx/Dhx30
GO_CC_m1	GO:004264	mitochond	10/2589	47/23583	0.029084	0.411609	0.387856	Clpx/Dhx30
GO_CC_m1	GO:000172	stress fiber	14/2589	74/23583	0.029149	0.411609	0.387856	Acta1/Acta
GO_CC_m1	GO:009751	contractile	14/2589	74/23583	0.029149	0.411609	0.387856	Acta1/Acta
GO_CC_m1	GO:003196	nuclear me	36/2589	238/23583	0.029387	0.411609	0.387856	Ahctf1/Aka
GO_CC_m1	GO:004329	contractile	34/2589	223/23583	0.030256	0.411609	0.387856	Abra/Acta1
GO_CC_m1	GO:000560	basement r	18/2589	103/23583	0.031023	0.411609	0.387856	Ache/Adam
GO_CC_m1	GO:003243	filopodium	5/2589	17/23583	0.031793	0.411609	0.387856	Abi1/Cib1/
GO_CC_m1	GO:003197	organelle e	15/2589	82/23583	0.032274	0.411609	0.387856	Aifm1/Alox
GO_CC_m1	GO:000581	lipid drople	14/2589	75/23583	0.032344	0.411609	0.387856	Adig/Aifm2
GO_CC_m1	GO:004461	nuclear po	3/2589	7/23583	0.032924	0.411609	0.387856	Nup153/Pc
GO_CC_m1	GO:000080	transverse	2/2589	3/23583	0.033501	0.411609	0.387856	Sycp1/Sycp
GO_CC_m1	GO:003109	platelet alp	2/2589	3/23583	0.033501	0.411609	0.387856	Snca/Sparc
GO_CC_m1	GO:004439	microspike	2/2589	3/23583	0.033501	0.411609	0.387856	Ezr/Fscn1
GO_CC_m1	GO:009714	centralspin	2/2589	3/23583	0.033501	0.411609	0.387856	Kif23/Racg
GO_CC_m1	GO:009718	serine prot	2/2589	3/23583	0.033501	0.411609	0.387856	Klk8/Serpir
GO_CC_m1	GO:199045	Parkin-FBX	2/2589	3/23583	0.033501	0.411609	0.387856	Cul1/Park2
GO_CC_m1	GO:000031	organellar	7/2589	29/23583	0.033983	0.411609	0.387856	Mrpl42/Mr
GO_CC_m1	GO:000576	mitochond	7/2589	29/23583	0.033983	0.411609	0.387856	Mrpl42/Mr
GO_CC_m1	GO:003577	ribonucleo	29/2589	188/23583	0.03741	0.44809	0.422231	Arntl/Noct
GO_CC_m1	GO:006169	transferase	40/2589	275/23583	0.039335	0.465969	0.439078	Ccna1/Ccn
GO_CC_m1	GO:004429	dendrite te	5/2589	18/23583	0.040153	0.469541	0.442444	Cdkl5/Fmr1
GO_CC_m1	GO:003326	axon part	60/2589	437/23583	0.040671	0.469541	0.442444	Aatk/Adora
GO_CC_m1	GO:000208	acrosomal	6/2589	24/23583	0.041239	0.469541	0.442444	Cav1/Ccdc
GO_CC_m1	GO:003013	COPII-coat	10/2589	50/23583	0.042781	0.469541	0.442444	Pcsk9/Pdcc
GO_CC_m1	GO:004444	contractile	30/2589	199/23583	0.045229	0.469541	0.442444	Abra/Acta1
GO_CC_m1	GO:000590	caveola	16/2589	93/23583	0.04568	0.469541	0.442444	Adcyap1r1
GO_CC_m1	GO:000564	nuclear env	4/2589	13/23583	0.046026	0.469541	0.442444	Alox5/Bche
GO_CC_m1	GO:004258	specific gra	4/2589	13/23583	0.046026	0.469541	0.442444	Adam8/An
GO_CC_m1	GO:009893	intrinsic co	4/2589	13/23583	0.046026	0.469541	0.442444	Adora1/Cd
GO_CC_m1	GO:009905	integral co	4/2589	13/23583	0.046026	0.469541	0.442444	Adora1/Cd
GO_CC_m1	GO:009924	intrinsic co	4/2589	13/23583	0.046026	0.469541	0.442444	Adora1/Cd
GO_CC_m1	GO:009969	integral co	4/2589	13/23583	0.046026	0.469541	0.442444	Adora1/Cd
GO_CC_m1	GO:199012	messenger	4/2589	13/23583	0.046026	0.469541	0.442444	Cpeb3/Cpe
GO_CC_m1	GO:000030	cyclin-dep	9/2589	44/23583	0.046805	0.469541	0.442444	Ccna1/Ccn
GO_CC_m1	GO:000579	Golgi-asso	20/2589	123/23583	0.047058	0.469541	0.442444	Copg2/Igf2
GO_CC_m1	GO:009752	spliceosom	7/2589	31/23583	0.047257	0.469541	0.442444	Lsm5/Naa3
GO_CC_m1	GO:003122	anchored c	26/2589	169/23583	0.048005	0.469541	0.442444	Ache/Alpl/
GO_CC_m1	GO:000595	cAMP-dep	3/2589	8/23583	0.048452	0.469541	0.442444	Akap14/Prl
GO_CC_m1	GO:003409	VCP-NPL4	3/2589	8/23583	0.048452	0.469541	0.442444	Cav1/Nplo
GO_CC_m1	GO:003001	sarcomere	28/2589	185/23583	0.049457	0.469541	0.442444	Abra/Acta1
GO_CC_m1	GO:003109	platelet alp	5/2589	19/23583	0.049723	0.469541	0.442444	Igfbp3/Snc
GO_CC_m1	GO:004423	organelle r	5/2589	19/23583	0.049723	0.469541	0.442444	Canx/Pik3r
GO_CC_m1	GO:000079	euchromat	8/2589	38/23583	0.050941	0.469541	0.442444	Ash2l/H2af
GO_CC_m1	GO:000080	sex chromo	8/2589	38/23583	0.050941	0.469541	0.442444	Atr/Cdk2/D
GO_CC_m1	GO:009754	ciliary base	8/2589	38/23583	0.050941	0.469541	0.442444	Cfap36/Ift5
GO_CC_m1	GO:003001	myofibril	31/2589	209/23583	0.050961	0.469541	0.442444	Abra/Acta1
GO_CC_m1	GO:003646	cytoplasmi	27/2589	178/23583	0.05172	0.472491	0.445224	Arntl/Noct

GO_CC_m1	GO:015003	distal axon	50/2589	364/23583	0.056831	0.507866	0.478557	Aatk/Adora
GO_CC_m1	GO:001652	sarcoplasm	13/2589	74/23583	0.058306	0.507866	0.478557	Akap6/Art1
GO_CC_m1	GO:003603	MKS comp	4/2589	14/23583	0.059004	0.507866	0.478557	B9d1/Cc2d
GO_CC_m1	GO:007143	invadopod	4/2589	14/23583	0.059004	0.507866	0.478557	Ezr/Fscn1/I
GO_CC_m1	GO:003014	secretory g	54/2589	398/23583	0.059542	0.507866	0.478557	1500015O1
GO_CC_m1	GO:001250	ER to Golg	5/2589	20/23583	0.060516	0.507866	0.478557	Pdcd6/Sec
GO_CC_m1	GO:000563	nuclear env	54/2589	399/23583	0.061769	0.507866	0.478557	1700123L1
GO_CC_m1	GO:000021	tRNA-intro	2/2589	4/23583	0.062149	0.507866	0.478557	Tsen2/Tser
GO_CC_m1	GO:000032	storage vac	2/2589	4/23583	0.062149	0.507866	0.478557	Arhgef7/St
GO_CC_m1	GO:000575	mitochond	2/2589	4/23583	0.062149	0.507866	0.478557	Spg7/Vdac
GO_CC_m1	GO:007087	SOSS comp	2/2589	4/23583	0.062149	0.507866	0.478557	Nabp1/Nal
GO_CC_m1	GO:009717	protease ir	2/2589	4/23583	0.062149	0.507866	0.478557	Klk8/Serpir
GO_CC_m1	GO:190409	peptidase i	2/2589	4/23583	0.062149	0.507866	0.478557	Klk8/Serpir
GO_CC_m1	GO:009856	cytoplasmi	29/2589	197/23583	0.062188	0.507866	0.478557	Abl2/Cdh1
GO_CC_m1	GO:003167	I band	21/2589	135/23583	0.063507	0.514737	0.485032	Ahnak2/Ar
GO_CC_m1	GO:000193	female pro	3/2589	9/23583	0.066884	0.526288	0.495916	Slc2a1/Tbp
GO_CC_m1	GO:001977	proteasom	3/2589	9/23583	0.066884	0.526288	0.495916	Psma3/Psm
GO_CC_m1	GO:004432	endoplasm	3/2589	9/23583	0.066884	0.526288	0.495916	Calr/Canx/
GO_CC_m1	GO:012010	centriolar s	3/2589	9/23583	0.066884	0.526288	0.495916	Ccdc68/Cn
GO_CC_m1	GO:000588	actin filame	19/2589	121/23583	0.06927	0.537934	0.50689	Acta1/Aif1l
GO_CC_m1	GO:004442	extracellula	20/2589	129/23583	0.070756	0.537934	0.50689	Ache/Adan
GO_CC_m1	GO:009858	membrane	49/2589	362/23583	0.071945	0.537934	0.50689	Adcyap1r1
GO_CC_m1	GO:000174	XY body	5/2589	21/23583	0.072528	0.537934	0.50689	Atr/Dmrtc2
GO_CC_m1	GO:000566	DNA replic	4/2589	15/23583	0.073709	0.537934	0.50689	Ercc5/Prpf1
GO_CC_m1	GO:003146	Cul2-RING	4/2589	15/23583	0.073709	0.537934	0.50689	Cul2/Glmn
GO_CC_m1	GO:003001	Z disc	19/2589	122/23583	0.073979	0.537934	0.50689	Ahnak2/At
GO_CC_m1	GO:003101	extracellula	59/2589	447/23583	0.077542	0.537934	0.50689	2300002M
GO_CC_m1	GO:003066	secretory g	14/2589	85/23583	0.07912	0.537934	0.50689	Abca3/Ada
GO_CC_m1	GO:000583	heterotrim	7/2589	35/23583	0.082593	0.537934	0.50689	Gnai1/Gnb
GO_CC_m1	GO:190536	GTPase cor	7/2589	35/23583	0.082593	0.537934	0.50689	Gnai1/Gnb
GO_CC_m1	GO:000572	nuclear het	8/2589	42/23583	0.083568	0.537934	0.50689	Cenpa/Cer
GO_CC_m1	GO:004512	membrane	47/2589	350/23583	0.0848	0.537934	0.50689	Adcyap1r1
GO_CC_m1	GO:009888	membrane	47/2589	350/23583	0.0848	0.537934	0.50689	Adcyap1r1
GO_CC_m1	GO:000016	protein pho	3/2589	10/23583	0.087984	0.537934	0.50689	2810408A1
GO_CC_m1	GO:001660	flotillin con	3/2589	10/23583	0.087984	0.537934	0.50689	Cdh1/Flot2
GO_CC_m1	GO:004429	dendritic g	3/2589	10/23583	0.087984	0.537934	0.50689	Cdkl5/Fmr1
GO_CC_m1	GO:004524	dihydrolipo	3/2589	10/23583	0.087984	0.537934	0.50689	Bckdhb/Ka
GO_CC_m1	GO:009754	ciliary tip	3/2589	10/23583	0.087984	0.537934	0.50689	Ift52/Ift88/
GO_CC_m1	GO:003439	nuclear pe	18/2589	117/23583	0.088051	0.537934	0.50689	Ahctf1/Alo
GO_CC_m1	GO:000563	integral co	4/2589	16/23583	0.090075	0.537934	0.50689	Lbr/Lemd2
GO_CC_m1	GO:003122	intrinsic co	4/2589	16/23583	0.090075	0.537934	0.50689	Lbr/Lemd2
GO_CC_m1	GO:004259	lamellar bo	4/2589	16/23583	0.090075	0.537934	0.50689	Abca12/Ab
GO_CC_m1	GO:009879	mitochond	36/2589	262/23583	0.093116	0.537934	0.50689	2010107E0
GO_CC_m1	GO:000580	cis-Golgi n	8/2589	43/23583	0.093279	0.537934	0.50689	Bok/Ctgf/G
GO_CC_m1	GO:009863	protein cor	7/2589	36/23583	0.093287	0.537934	0.50689	Cd80/Ctla4
GO_CC_m1	GO:001652	sarcoplasm	11/2589	65/23583	0.095551	0.537934	0.50689	Akap6/Art1
GO_CC_m1	GO:000166	acrosomal	20/2589	134/23583	0.095846	0.537934	0.50689	1700016D0
GO_CC_m1	GO:190255	serine/thre	13/2589	80/23583	0.095941	0.537934	0.50689	Ccna1/Ccn

GO_CC_m1	GO:001000	cytoplasmi	2/2589	5/23583	0.096156	0.537934	0.50689	Rab5a/Rbs
GO_CC_m1	GO:003048	smooth mu	2/2589	5/23583	0.096156	0.537934	0.50689	Acta2/Npn
GO_CC_m1	GO:004276	GPI-ancho	2/2589	5/23583	0.096156	0.537934	0.50689	Pigs/Pigu
GO_CC_m1	GO:004454	NSL compl	2/2589	5/23583	0.096156	0.537934	0.50689	Kansl1/Kan
GO_CC_m1	GO:007154	piP-body	2/2589	5/23583	0.096156	0.537934	0.50689	Ddx4/Mael
GO_CC_m1	GO:009853	deuterosor	2/2589	5/23583	0.096156	0.537934	0.50689	Deup1/Plk4
GO_CC_m1	GO:009888	intrinsic co	2/2589	5/23583	0.096156	0.537934	0.50689	Adora1/Cd
GO_CC_m1	GO:009905	integral co	2/2589	5/23583	0.096156	0.537934	0.50689	Adora1/Cd
GO_CC_m1	GO:001989	extrinsic cc	40/2589	296/23583	0.097489	0.537934	0.50689	Abl2/Anxa2
GO_CC_m1	GO:000989	cytoplasmi	26/2589	182/23583	0.097541	0.537934	0.50689	Abl2/Cdh1
GO_CC_m1	GO:000568	U5 snRNP	5/2589	23/23583	0.100114	0.537934	0.50689	Naa38/Prp
GO_CC_m1	GO:000583	proteasom	5/2589	23/23583	0.100114	0.537934	0.50689	Psma3/Psm
GO_CC_m1	GO:003090	retromer c	5/2589	23/23583	0.100114	0.537934	0.50689	Ankfy1/Den
GO_CC_m1	GO:004512	pronucleus	5/2589	23/23583	0.100114	0.537934	0.50689	Blm/Hnrnp
GO_CC_m1	GO:004430	main axon	13/2589	81/23583	0.103389	0.537934	0.50689	Adora1/Ca
GO_CC_m1	GO:003014	trans-Golg	6/2589	30/23583	0.104019	0.537934	0.50689	Igf2r/Ldlra
GO_CC_m1	GO:000566	transcriptic	7/2589	37/23583	0.104714	0.537934	0.50689	Gtf2a1/Gtf2
GO_CC_m1	GO:009963	postsynapt	7/2589	37/23583	0.104714	0.537934	0.50689	Cacng5/Ca
GO_CC_m1	GO:000031	organellar	14/2589	89/23583	0.106145	0.537934	0.50689	Mrpl10/Mr
GO_CC_m1	GO:000576	mitochond	14/2589	89/23583	0.106145	0.537934	0.50689	Mrpl10/Mr
GO_CC_m1	GO:003198	Golgi ciste	10/2589	59/23583	0.107747	0.537934	0.50689	Acpp/Bcap
GO_CC_m1	GO:004445	nuclear me	4/2589	17/23583	0.108008	0.537934	0.50689	Lbr/Lemd2
GO_CC_m1	GO:004443	cytoplasmi	61/2589	475/23583	0.109363	0.537934	0.50689	3110002H1
GO_CC_m1	GO:000558	collagen ty	1/2589	1/23583	0.109782	0.537934	0.50689	Dcn
GO_CC_m1	GO:000561	cell wall	1/2589	1/23583	0.109782	0.537934	0.50689	Pgghg
GO_CC_m1	GO:000583	steroid hor	1/2589	1/23583	0.109782	0.537934	0.50689	Sra1
GO_CC_m1	GO:000862	CHRAC	1/2589	1/23583	0.109782	0.537934	0.50689	Baz1a
GO_CC_m1	GO:000984	mitochond	1/2589	1/23583	0.109782	0.537934	0.50689	Clpx
GO_CC_m1	GO:001711	single-stra	1/2589	1/23583	0.109782	0.537934	0.50689	Helq
GO_CC_m1	GO:003100	actin rod	1/2589	1/23583	0.109782	0.537934	0.50689	Cfl1
GO_CC_m1	GO:003190	early endo	1/2589	1/23583	0.109782	0.537934	0.50689	Pdlim4
GO_CC_m1	GO:003214	4-aminobu	1/2589	1/23583	0.109782	0.537934	0.50689	Abat
GO_CC_m1	GO:003467	integrin alp	1/2589	1/23583	0.109782	0.537934	0.50689	Itga6
GO_CC_m1	GO:003467	integrin alp	1/2589	1/23583	0.109782	0.537934	0.50689	Npnt
GO_CC_m1	GO:003477	recycling e	1/2589	1/23583	0.109782	0.537934	0.50689	Pdlim4
GO_CC_m1	GO:003557	specific gra	1/2589	1/23583	0.109782	0.537934	0.50689	Vamp1
GO_CC_m1	GO:004354	6-phosphc	1/2589	1/23583	0.109782	0.537934	0.50689	Pfkfb1
GO_CC_m1	GO:004419	nucleoplas	1/2589	1/23583	0.109782	0.537934	0.50689	Myc
GO_CC_m1	GO:006182	basal tubul	1/2589	1/23583	0.109782	0.537934	0.50689	Dnm3
GO_CC_m1	GO:007042	DNA ligase	1/2589	1/23583	0.109782	0.537934	0.50689	Lig3
GO_CC_m1	GO:007044	integrin alp	1/2589	1/23583	0.109782	0.537934	0.50689	Tspan32
GO_CC_m1	GO:007156	nucleus-va	1/2589	1/23583	0.109782	0.537934	0.50689	Pik3r4
GO_CC_m1	GO:007258	box H/ACA	1/2589	1/23583	0.109782	0.537934	0.50689	Nop10
GO_CC_m1	GO:009065	apical cyto	1/2589	1/23583	0.109782	0.537934	0.50689	Myo7b
GO_CC_m1	GO:009073	cofilin-acti	1/2589	1/23583	0.109782	0.537934	0.50689	Cfl1
GO_CC_m1	GO:009864	collagen be	1/2589	1/23583	0.109782	0.537934	0.50689	Dcn
GO_CC_m1	GO:009894	intrinsic co	1/2589	1/23583	0.109782	0.537934	0.50689	Cdh2
GO_CC_m1	GO:009899	neuronal d	1/2589	1/23583	0.109782	0.537934	0.50689	Scg2

GO_CC_m1	GO:009905	integral co	1/2589	1/23583	0.109782	0.537934	0.50689	Cdh2
GO_CC_m1	GO:009957	glutamater	1/2589	1/23583	0.109782	0.537934	0.50689	Camk2a
GO_CC_m1	GO:199082	nucleoplas	1/2589	1/23583	0.109782	0.537934	0.50689	Hnrnpc
GO_CC_m1	GO:199084	subsarcole	1/2589	1/23583	0.109782	0.537934	0.50689	Ppargc1a
GO_CC_m1	GO:199084	interfibrilla	1/2589	1/23583	0.109782	0.537934	0.50689	Ppargc1a
GO_CC_m1	GO:199087	nucleoplas	1/2589	1/23583	0.109782	0.537934	0.50689	Nup153
GO_CC_m1	GO:004461	nuclear po	3/2589	11/23583	0.111464	0.543704	0.512327	Nup153/N
GO_CC_m1	GO:003301	sarcoplasm	5/2589	24/23583	0.115608	0.561374	0.528977	Akap6/Dhr
GO_CC_m1	GO:004367	axon termi	27/2589	194/23583	0.117139	0.566258	0.53358	Adora1/Cd
GO_CC_m1	GO:004238	sarcolemm	22/2589	154/23583	0.119493	0.575061	0.541875	Ahnak2/Ak
GO_CC_m1	GO:000802	synaptic ve	27/2589	195/23583	0.122442	0.58483	0.551079	Adra1d/Ca
GO_CC_m1	GO:000566	DNA-direc	4/2589	18/23583	0.127395	0.58483	0.551079	Polr2f/Polr
GO_CC_m1	GO:001658	NuRD com	4/2589	18/23583	0.127395	0.58483	0.551079	Appl1/Hda
GO_CC_m1	GO:009054	CHD-type	4/2589	18/23583	0.127395	0.58483	0.551079	Appl1/Hda
GO_CC_m1	GO:000590	microvillus	14/2589	92/23583	0.129647	0.58483	0.551079	Aoc3/Bbs2
GO_CC_m1	GO:001250	vesicle me	40/2589	304/23583	0.13007	0.58483	0.551079	Abca3/Acp
GO_CC_m1	GO:007038	exocytic ve	29/2589	213/23583	0.131177	0.58483	0.551079	Adra1d/Ca
GO_CC_m1	GO:000575	mitochond	11/2589	69/23583	0.131316	0.58483	0.551079	Aifm1/Chcl
GO_CC_m1	GO:000578	endoplasm	9/2589	54/23583	0.132776	0.58483	0.551079	Ache/Bche
GO_CC_m1	GO:003049	midbody	19/2589	132/23583	0.13282	0.58483	0.551079	Anxa2/BC0
GO_CC_m1	GO:000040	EKC/KEOPS	2/2589	6/23583	0.134001	0.58483	0.551079	Osgepl1/T
GO_CC_m1	GO:000092	equatorial	2/2589	6/23583	0.134001	0.58483	0.551079	Tubgcp2/T
GO_CC_m1	GO:003089	VCB compl	2/2589	6/23583	0.134001	0.58483	0.551079	Cul2/Elob
GO_CC_m1	GO:003258	multivesicu	2/2589	6/23583	0.134001	0.58483	0.551079	Cd63/Rab2
GO_CC_m1	GO:003316	melanoson	2/2589	6/23583	0.134001	0.58483	0.551079	Rab32/Th
GO_CC_m1	GO:003574	myelin she	2/2589	6/23583	0.134001	0.58483	0.551079	Anxa2/Stx4
GO_CC_m1	GO:004500	chitosome	2/2589	6/23583	0.134001	0.58483	0.551079	Rab32/Th
GO_CC_m1	GO:007076	pre-snoRN	2/2589	6/23583	0.134001	0.58483	0.551079	Nop56/Taf
GO_CC_m1	GO:009074	pigment g	2/2589	6/23583	0.134001	0.58483	0.551079	Rab32/Th
GO_CC_m1	GO:009734	ripoptoson	2/2589	6/23583	0.134001	0.58483	0.551079	Casp8/Rip
GO_CC_m1	GO:009755	transcriptic	2/2589	6/23583	0.134001	0.58483	0.551079	Gtf2h3/Tb
GO_CC_m1	GO:009894	intrinsic co	2/2589	6/23583	0.134001	0.58483	0.551079	Cdh2/Gria
GO_CC_m1	GO:009906	integral co	2/2589	6/23583	0.134001	0.58483	0.551079	Cdh2/Gria
GO_CC_m1	GO:004443	Golgi appa	60/2589	474/23583	0.134731	0.585645	0.551848	Acer3/Acp
GO_CC_m1	GO:000567	holo TFIIH	3/2589	12/23583	0.137014	0.586118	0.552293	Cdk7/Ercc5
GO_CC_m1	GO:000584	mRNA cap	3/2589	12/23583	0.137014	0.586118	0.552293	Eif4e/Fmr1
GO_CC_m1	GO:003451	RNA cap b	3/2589	12/23583	0.137014	0.586118	0.552293	Eif4e/Fmr1
GO_CC_m1	GO:004818	Set1C/CON	3/2589	12/23583	0.137014	0.586118	0.552293	Ash2l/Rbb
GO_CC_m1	GO:000576	early endo	32/2589	239/23583	0.13772	0.586806	0.552942	Angptl3/Ar
GO_CC_m1	GO:190291	protein kin	16/2589	109/23583	0.139768	0.590647	0.556562	Ccna1/Ccn
GO_CC_m1	GO:000566	transcriptic	51/2589	399/23583	0.140287	0.590647	0.556562	Ankrd1/Arı
GO_CC_m1	GO:000093	P-body	11/2589	70/23583	0.141259	0.590647	0.556562	Noct/Eif4e
GO_CC_m1	GO:009057	RNA polym	22/2589	158/23583	0.14487	0.590647	0.556562	Ascl3/Cdk7
GO_CC_m1	GO:003065	cytoplasmi	36/2589	274/23583	0.146428	0.590647	0.556562	Abca3/Ada
GO_CC_m1	GO:004479	nuclear tra	26/2589	191/23583	0.146512	0.590647	0.556562	Ascl3/Cdk7
GO_CC_m1	GO:003470	methyltran	14/2589	94/23583	0.14682	0.590647	0.556562	Virma/Ash
GO_CC_m1	GO:000592	gap junctic	6/2589	33/23583	0.147364	0.590647	0.556562	Des/Gja3/
GO_CC_m1	GO:003068	90S preribo	6/2589	33/23583	0.147364	0.590647	0.556562	Bms1/Casp

GO_CC_m1	GO:00328	neuronal c	6/2589	33/23583	0.147364	0.590647	0.556562	Gabra6/Kc
GO_CC_m1	GO:00165	DNA-direc	16/2589	110/23583	0.147853	0.590647	0.556562	Cdk7/Ercc5
GO_CC_m1	GO:00009	gamma-tu	4/2589	19/23583	0.148108	0.590647	0.556562	Pde4b/Tub
GO_CC_m1	GO:003031	T-tubule	10/2589	63/23583	0.148539	0.590647	0.556562	Ahnak2/Ak
GO_CC_m1	GO:00324	stereociliu	8/2589	48/23583	0.150843	0.590647	0.556562	Atp8b1/Bb
GO_CC_m1	GO:00442	cell-cell co	12/2589	79/23583	0.153682	0.590647	0.556562	Akap6/Cav
GO_CC_m1	GO:00972	sperm part	32/2589	242/23583	0.153958	0.590647	0.556562	1700016D
GO_CC_m1	GO:00059	focal adhe	19/2589	135/23583	0.154646	0.590647	0.556562	Aif1l/Arhg
GO_CC_m1	GO:00550	nuclear DN	19/2589	135/23583	0.154646	0.590647	0.556562	Cd3eap/Cc
GO_CC_m1	GO:00726	mitotic spi	14/2589	95/23583	0.155846	0.590647	0.556562	Rtraf/Cdc7
GO_CC_m1	GO:00306	transport v	17/2589	119/23583	0.155893	0.590647	0.556562	Adra1d/Ld
GO_CC_m1	GO:004517	apical part	51/2589	403/23583	0.157175	0.590647	0.556562	Abcb1a/Ac
GO_CC_m1	GO:00005	proteasom	11/2589	72/23583	0.16229	0.590647	0.556562	Psma3/Ps
GO_CC_m1	GO:00004	DNA-direc	19/2589	136/23583	0.162335	0.590647	0.556562	Cd3eap/Cc
GO_CC_m1	GO:00016	fibrillar cen	18/2589	128/23583	0.163329	0.590647	0.556562	Ankrd1/Cc
GO_CC_m1	GO:00360	ciliary basa	18/2589	128/23583	0.163329	0.590647	0.556562	B9d1/Bbs2
GO_CC_m1	GO:00057	smooth en	6/2589	34/23583	0.163376	0.590647	0.556562	Calr/Canx/
GO_CC_m1	GO:00442	cell body n	6/2589	34/23583	0.163376	0.590647	0.556562	Gabra6/Kc
GO_CC_m1	GO:00301	coated ves	23/2589	169/23583	0.164151	0.590647	0.556562	Bcap31/Cl
GO_CC_m1	GO:000854	proteasom	3/2589	13/23583	0.164311	0.590647	0.556562	Psmc2/Ps
GO_CC_m1	GO:003012	COPII vesic	3/2589	13/23583	0.164311	0.590647	0.556562	Pdcd6/Sec
GO_CC_m1	GO:00442	ER-mitoch	3/2589	13/23583	0.164311	0.590647	0.556562	Canx/Plekh
GO_CC_m1	GO:00452	tricarboxyli	3/2589	13/23583	0.164311	0.590647	0.556562	Bckdhb/Ka
GO_CC_m1	GO:009744	astrocyte p	3/2589	13/23583	0.164311	0.590647	0.556562	Ezr/Gjb2/K
GO_CC_m1	GO:00306	preriboson	5/2589	27/23583	0.168165	0.590647	0.556562	Casp8/Ebn
GO_CC_m1	GO:00973	glial cell pr	4/2589	20/23583	0.170006	0.590647	0.556562	Ezr/Fmr1/
GO_CC_m1	GO:00164	myosin cor	10/2589	65/23583	0.171503	0.590647	0.556562	Cgn/Myh1
GO_CC_m1	GO:19053	endopeptic	11/2589	73/23583	0.173356	0.590647	0.556562	Psma3/Ps
GO_CC_m1	GO:00312	extrinsic cc	16/2589	113/23583	0.173591	0.590647	0.556562	Abl2/Ferm
GO_CC_m1	GO:000581	centriole	15/2589	105/23583	0.174312	0.590647	0.556562	Deup1/Ccc
GO_CC_m1	GO:00306	preriboson	12/2589	81/23583	0.17439	0.590647	0.556562	Bms1/Casp
GO_CC_m1	GO:00308	cortical act	12/2589	81/23583	0.17439	0.590647	0.556562	Cdh1/Cdh
GO_CC_m1	GO:000194	male pron	2/2589	7/23583	0.174431	0.590647	0.556562	Tbp/Tet3
GO_CC_m1	GO:000581	spindle pol	2/2589	7/23583	0.174431	0.590647	0.556562	Tubgcp2/T
GO_CC_m1	GO:003254	cortical en	2/2589	7/23583	0.174431	0.590647	0.556562	Asph/Osbp
GO_CC_m1	GO:00332	CORVET cc	2/2589	7/23583	0.174431	0.590647	0.556562	Tgfbrap1/
GO_CC_m1	GO:004321	lateral loop	2/2589	7/23583	0.174431	0.590647	0.556562	Cdh1/Stx4
GO_CC_m1	GO:00452	oxoglutara	2/2589	7/23583	0.174431	0.590647	0.556562	Kat2a/Ogd
GO_CC_m1	GO:00707	gamma-se	2/2589	7/23583	0.174431	0.590647	0.556562	Aph1a/Ap
GO_CC_m1	GO:00708	tertiary gra	2/2589	7/23583	0.174431	0.590647	0.556562	Adam8/Va
GO_CC_m1	GO:00725	NLRP3 infla	2/2589	7/23583	0.174431	0.590647	0.556562	Gsdmd/Py
GO_CC_m1	GO:19906	proximal d	2/2589	7/23583	0.174431	0.590647	0.556562	Fmr1/Gigy
GO_CC_m1	GO:003124	protein ac	13/2589	89/23583	0.174804	0.590647	0.556562	Brpf3/Gm3
GO_CC_m1	GO:19024	acetyltrans	13/2589	89/23583	0.174804	0.590647	0.556562	Brpf3/Gm3
GO_CC_m1	GO:00308	RNA polym	19/2589	138/23583	0.178314	0.590647	0.556562	Cd3eap/Cc
GO_CC_m1	GO:000581	spindle	33/2589	255/23583	0.180734	0.590647	0.556562	Rtraf/Ankr
GO_CC_m1	GO:00324	stereociliu	9/2589	58/23583	0.181374	0.590647	0.556562	Atp8b1/Bb
GO_CC_m1	GO:00007	heterochro	13/2589	90/23583	0.185125	0.590647	0.556562	Cenpa/Cer

GO_CC_m1	GO:000579	Golgi stack	12/2589	82/23583	0.185227	0.590647	0.556562	Acpp/Bcap
GO_CC_m1	GO:004466	MLL1/2 co	5/2589	28/23583	0.187458	0.590647	0.556562	Ash2l/Kans
GO_CC_m1	GO:007133	MLL1 comp	5/2589	28/23583	0.187458	0.590647	0.556562	Ash2l/Kans
GO_CC_m1	GO:000167	male germ	4/2589	21/23583	0.192942	0.590647	0.556562	Blm/Sycp1/
GO_CC_m1	GO:003067	axolemma	4/2589	21/23583	0.192942	0.590647	0.556562	Adora1/Kc
GO_CC_m1	GO:000567	Ada2/Gcn5	3/2589	14/23583	0.193031	0.590647	0.556562	Kat2a/Kat2
GO_CC_m1	GO:000573	DNA-direc	3/2589	14/23583	0.193031	0.590647	0.556562	Cd3eap/Pc
GO_CC_m1	GO:004258	zymogen g	3/2589	14/23583	0.193031	0.590647	0.556562	Cuzd1/Rab
GO_CC_m1	GO:003509	histone me	11/2589	75/23583	0.196527	0.590647	0.556562	Ash2l/Ezh1
GO_CC_m1	GO:001503	Cajal body	6/2589	36/23583	0.19745	0.590647	0.556562	Cdk2/Fmr1
GO_CC_m1	GO:001659	mediator c	6/2589	36/23583	0.19745	0.590647	0.556562	Med10/Me
GO_CC_m1	GO:199039	DNA repair	6/2589	36/23583	0.19745	0.590647	0.556562	Msh3/Msh
GO_CC_m1	GO:009886	cluster of a	24/2589	182/23583	0.198381	0.590647	0.556562	Abcb1a/At
GO_CC_m1	GO:003005	cell-substr	20/2589	149/23583	0.201166	0.590647	0.556562	Aif1l/Arhge
GO_CC_m1	GO:003239	photorecep	7/2589	44/23583	0.203294	0.590647	0.556562	Fam161a/I
GO_CC_m1	GO:000592	cell-substr	19/2589	141/23583	0.203722	0.590647	0.556562	Aif1l/Arhge
GO_CC_m1	GO:001989	extrinsic cc	24/2589	183/23583	0.206003	0.590647	0.556562	Abl2/Anxa
GO_CC_m1	GO:003215	cell divisior	8/2589	52/23583	0.206607	0.590647	0.556562	Cenpc1/Ma
GO_CC_m1	GO:009743	mitotic spir	5/2589	29/23583	0.207497	0.590647	0.556562	Cntrl/Fam1
GO_CC_m1	GO:000080	Y chromos	1/2589	2/23583	0.207517	0.590647	0.556562	Cdk2
GO_CC_m1	GO:000571	recombina	1/2589	2/23583	0.207517	0.590647	0.556562	Msh4
GO_CC_m1	GO:000576	gamma DN	1/2589	2/23583	0.207517	0.590647	0.556562	Polg
GO_CC_m1	GO:000585	nascent po	1/2589	2/23583	0.207517	0.590647	0.556562	Nacad
GO_CC_m1	GO:000595	CAAX-prot	1/2589	2/23583	0.207517	0.590647	0.556562	Fnta
GO_CC_m1	GO:000596	glycine cle	1/2589	2/23583	0.207517	0.590647	0.556562	Gldc
GO_CC_m1	GO:000596	protein far	1/2589	2/23583	0.207517	0.590647	0.556562	Fnta
GO_CC_m1	GO:000936	endopeptic	1/2589	2/23583	0.207517	0.590647	0.556562	Clpx
GO_CC_m1	GO:001480	longitudina	1/2589	2/23583	0.207517	0.590647	0.556562	Dhrs7c
GO_CC_m1	GO:001710	glutamate-	1/2589	2/23583	0.207517	0.590647	0.556562	Gclm
GO_CC_m1	GO:001900	molybdopt	1/2589	2/23583	0.207517	0.590647	0.556562	Mocs2
GO_CC_m1	GO:001903	viral replica	1/2589	2/23583	0.207517	0.590647	0.556562	Fmr1
GO_CC_m1	GO:003069	Noc1p-No	1/2589	2/23583	0.207517	0.590647	0.556562	Casp8
GO_CC_m1	GO:003084	autosome	1/2589	2/23583	0.207517	0.590647	0.556562	Mael
GO_CC_m1	GO:003090	retromer, t	1/2589	2/23583	0.207517	0.590647	0.556562	Snx2
GO_CC_m1	GO:003153	mRNA cap	1/2589	2/23583	0.207517	0.590647	0.556562	Rnmt
GO_CC_m1	GO:003230	MutSbeta c	1/2589	2/23583	0.207517	0.590647	0.556562	Msh3
GO_CC_m1	GO:003299	Fc receptor	1/2589	2/23583	0.207517	0.590647	0.556562	Ms4a2
GO_CC_m1	GO:003299	Fc-epsilon	1/2589	2/23583	0.207517	0.590647	0.556562	Ms4a2
GO_CC_m1	GO:003466	integrin alp	1/2589	2/23583	0.207517	0.590647	0.556562	Itga3
GO_CC_m1	GO:003586	alphav-bet	1/2589	2/23583	0.207517	0.590647	0.556562	Prkca
GO_CC_m1	GO:004256	insulin-like	1/2589	2/23583	0.207517	0.590647	0.556562	Igfbp3
GO_CC_m1	GO:004351	interleukin	1/2589	2/23583	0.207517	0.590647	0.556562	Il12b
GO_CC_m1	GO:004362	PCNA com	1/2589	2/23583	0.207517	0.590647	0.556562	Pcna
GO_CC_m1	GO:004430	climbing fi	1/2589	2/23583	0.207517	0.590647	0.556562	C1ql1
GO_CC_m1	GO:004479	DNA polyn	1/2589	2/23583	0.207517	0.590647	0.556562	Pcna
GO_CC_m1	GO:004502	mitochond	1/2589	2/23583	0.207517	0.590647	0.556562	Pnpt1
GO_CC_m1	GO:004532	interleukin	1/2589	2/23583	0.207517	0.590647	0.556562	Ticam2
GO_CC_m1	GO:004826	methionine	1/2589	2/23583	0.207517	0.590647	0.556562	Mat2b

GO_CC_m1	GO:006182	apical tubu	1/2589	2/23583	0.207517	0.590647	0.556562	Dnm3
GO_CC_m1	GO:007074	interleukin	1/2589	2/23583	0.207517	0.590647	0.556562	Il12b
GO_CC_m1	GO:007098	TFIIK comp	1/2589	2/23583	0.207517	0.590647	0.556562	Cdk7
GO_CC_m1	GO:007106	alpha9-bet	1/2589	2/23583	0.207517	0.590647	0.556562	Adam8
GO_CC_m1	GO:007113	alpha9-bet	1/2589	2/23583	0.207517	0.590647	0.556562	Adam8
GO_CC_m1	GO:009705	CNTFR-CL	1/2589	2/23583	0.207517	0.590647	0.556562	Cntfr
GO_CC_m1	GO:009712	cyclin A2-C	1/2589	2/23583	0.207517	0.590647	0.556562	Cdk2
GO_CC_m1	GO:009712	cyclin B1-C	1/2589	2/23583	0.207517	0.590647	0.556562	Cdk1
GO_CC_m1	GO:009719	Shu compl	1/2589	2/23583	0.207517	0.590647	0.556562	Zswim7
GO_CC_m1	GO:009723	lamellar bc	1/2589	2/23583	0.207517	0.590647	0.556562	Abca3
GO_CC_m1	GO:009723	alveolar lar	1/2589	2/23583	0.207517	0.590647	0.556562	Abca3
GO_CC_m1	GO:009736	MCM8-MC	1/2589	2/23583	0.207517	0.590647	0.556562	Mcm8
GO_CC_m1	GO:009744	spine appa	1/2589	2/23583	0.207517	0.590647	0.556562	Fmr1
GO_CC_m1	GO:009754	axonemal	1/2589	2/23583	0.207517	0.590647	0.556562	Ift88
GO_CC_m1	GO:009884	postsynapt	1/2589	2/23583	0.207517	0.590647	0.556562	Rab5a
GO_CC_m1	GO:190273	dendritic fi	1/2589	2/23583	0.207517	0.590647	0.556562	Fmr1
GO_CC_m1	GO:190520	methylcrot	1/2589	2/23583	0.207517	0.590647	0.556562	Mccc2
GO_CC_m1	GO:199011	RQC comp	1/2589	2/23583	0.207517	0.590647	0.556562	Nemf
GO_CC_m1	GO:199062	CHOP-ATF	1/2589	2/23583	0.207517	0.590647	0.556562	Atf3
GO_CC_m1	GO:199066	PCSK9-LDL	1/2589	2/23583	0.207517	0.590647	0.556562	Pcsk9
GO_CC_m1	GO:003066	Golgi-asso	9/2589	60/23583	0.208277	0.590647	0.556562	Copg2/Ldl
GO_CC_m1	GO:001623	inclusion b	11/2589	76/23583	0.208601	0.590647	0.556562	Gpx1/Gys1
GO_CC_m1	GO:003042	growth cor	25/2589	192/23583	0.210545	0.590647	0.556562	Aatk/Arhge
GO_CC_m1	GO:003086	cortical cyt	16/2589	117/23583	0.211164	0.590647	0.556562	Cdh1/Cdh2
GO_CC_m1	GO:199035	transporter	38/2589	303/23583	0.213971	0.590647	0.556562	Akap6/Anc
GO_CC_m1	GO:000023	astral micr	2/2589	8/23583	0.216425	0.590647	0.556562	Fam161a/F
GO_CC_m1	GO:000080	central eler	2/2589	8/23583	0.216425	0.590647	0.556562	Syce2/Sycp
GO_CC_m1	GO:001705	serine C-pa	2/2589	8/23583	0.216425	0.590647	0.556562	Sptlc2/Spts
GO_CC_m1	GO:003121	endoplasm	2/2589	8/23583	0.216425	0.590647	0.556562	Sptlc2/Spts
GO_CC_m1	GO:003159	nuclear prc	2/2589	8/23583	0.216425	0.590647	0.556562	Psmc2/Psm
GO_CC_m1	GO:004258	glycogen g	2/2589	8/23583	0.216425	0.590647	0.556562	Fasn/Ppp1r
GO_CC_m1	GO:004320	axon hilloc	2/2589	8/23583	0.216425	0.590647	0.556562	Htr1a/Serp
GO_CC_m1	GO:004325	laminin cor	2/2589	8/23583	0.216425	0.590647	0.556562	Lama5/Lan
GO_CC_m1	GO:007053	BRCA1-A c	2/2589	8/23583	0.216425	0.590647	0.556562	Babam2/Ui
GO_CC_m1	GO:007084	core media	2/2589	8/23583	0.216425	0.590647	0.556562	Med10/Me
GO_CC_m1	GO:007266	tRNA-splic	2/2589	8/23583	0.216425	0.590647	0.556562	Rtraf/Zbtb8
GO_CC_m1	GO:190596	protein-cys	2/2589	8/23583	0.216425	0.590647	0.556562	Sptlc2/Spts
GO_CC_m1	GO:001049	cytoplasmi	7/2589	45/23583	0.219643	0.59564	0.561266	Eif4e/Fmr1
GO_CC_m1	GO:000576	lysosomal	16/2589	118/23583	0.221094	0.59564	0.561266	Anxa2/Cd6
GO_CC_m1	GO:009885	lytic vacuol	16/2589	118/23583	0.221094	0.59564	0.561266	Anxa2/Cd6
GO_CC_m1	GO:001470	intercalate	9/2589	61/23583	0.2223	0.59564	0.561266	Akap6/Cav
GO_CC_m1	GO:003258	Golgi cister	3/2589	15/23583	0.222861	0.59564	0.561266	Bcap31/Cs
GO_CC_m1	GO:004322	Schmidt-La	3/2589	15/23583	0.222861	0.59564	0.561266	Anxa2/Cdh
GO_CC_m1	GO:004324	Fanconi an	3/2589	15/23583	0.222861	0.59564	0.561266	Fance/Fanc
GO_CC_m1	GO:009054	Flemming	3/2589	15/23583	0.222861	0.59564	0.561266	Cenpc1/Ol
GO_CC_m1	GO:190249	transmemb	37/2589	296/23583	0.223692	0.59564	0.561266	Akap6/Anc
GO_CC_m1	GO:003013	endocytic	21/2589	160/23583	0.223779	0.59564	0.561266	Adam8/An
GO_CC_m1	GO:004430	neuron prc	27/2589	211/23583	0.226334	0.600955	0.566274	Adora1/Cd

GO_CC_m1	GO:003190	late endoso	7/2589	46/23583	0.236438	0.623509	0.587527	3110002H1
GO_CC_m1	GO:000031	organellar	8/2589	54/23583	0.237142	0.623509	0.587527	Mrpl10/Mr
GO_CC_m1	GO:000576	mitochond	8/2589	54/23583	0.237142	0.623509	0.587527	Mrpl10/Mr
GO_CC_m1	GO:000802	transcriptio	8/2589	54/23583	0.237142	0.623509	0.587527	Ccnl1/Ell2/
GO_CC_m1	GO:004360	nuclear rep	4/2589	23/23583	0.241323	0.63296	0.596432	Ercc5/Prpf1
GO_CC_m1	GO:003470	ion channe	35/2589	282/23583	0.244532	0.633728	0.597157	Akap6/Anc
GO_CC_m1	GO:000040	phagophor	5/2589	31/23583	0.249453	0.633728	0.597157	Atg2a/Plek
GO_CC_m1	GO:004247	melanosom	5/2589	31/23583	0.249453	0.633728	0.597157	Dct/Rab27b
GO_CC_m1	GO:004877	pigment gr	5/2589	31/23583	0.249453	0.633728	0.597157	Dct/Rab27b
GO_CC_m1	GO:003042	site of pola	25/2589	197/23583	0.250115	0.633728	0.597157	Aatk/Arhge
GO_CC_m1	GO:003470	calcium cha	8/2589	55/23583	0.252958	0.633728	0.597157	Akap6/Cac
GO_CC_m1	GO:003001	CCR4-NOT	3/2589	16/23583	0.253504	0.633728	0.597157	Cnot10/Cn
GO_CC_m1	GO:003320	DNA helica	3/2589	16/23583	0.253504	0.633728	0.597157	Gm3086/H
GO_CC_m1	GO:009703	perinuclear	3/2589	16/23583	0.253504	0.633728	0.597157	Bcap31/Kcn
GO_CC_m1	GO:000080	X chromos	2/2589	9/23583	0.25915	0.633728	0.597157	Cdk2/H2afy
GO_CC_m1	GO:000211	semaphorin	2/2589	9/23583	0.25915	0.633728	0.597157	Plxna2/Plxn
GO_CC_m1	GO:000581	aster	2/2589	9/23583	0.25915	0.633728	0.597157	Fam161a/F
GO_CC_m1	GO:003120	SCAR comp	2/2589	9/23583	0.25915	0.633728	0.597157	Abi1/Nckap
GO_CC_m1	GO:003161	nuclear per	2/2589	9/23583	0.25915	0.633728	0.597157	Cenpa/Cen
GO_CC_m1	GO:004261	MHC class	2/2589	9/23583	0.25915	0.633728	0.597157	H2-DMb2/
GO_CC_m1	GO:009720	alveolar lar	2/2589	9/23583	0.25915	0.633728	0.597157	Abca3/Nap
GO_CC_m1	GO:009899	anchored c	2/2589	9/23583	0.25915	0.633728	0.597157	Rab27b/Ra
GO_CC_m1	GO:190536	peptidase c	13/2589	97/23583	0.264616	0.633728	0.597157	Psma3/Psm
GO_CC_m1	GO:000583	proteasom	4/2589	24/23583	0.266466	0.633728	0.597157	Psmc2/Psm
GO_CC_m1	GO:003089	replisome	4/2589	24/23583	0.266466	0.633728	0.597157	Ercc5/Prpf1
GO_CC_m1	GO:004258	zymogen g	4/2589	24/23583	0.266466	0.633728	0.597157	Cuzd1/Ogt
GO_CC_m1	GO:009744	apical dend	4/2589	24/23583	0.266466	0.633728	0.597157	Cpeb3/Grin
GO_CC_m1	GO:009879	Golgi subc	50/2589	416/23583	0.26808	0.633728	0.597157	Acer3/Acp
GO_CC_m1	GO:000587	microtubul	19/2589	148/23583	0.268978	0.633728	0.597157	Dctn5/Dna
GO_CC_m1	GO:009056	nuclear tra	5/2589	32/23583	0.271184	0.633728	0.597157	Appl1/Bah
GO_CC_m1	GO:199020	oxidoreduc	14/2589	106/23583	0.272028	0.633728	0.597157	Bckdhb/Cb
GO_CC_m1	GO:001623	aggresome	6/2589	40/23583	0.272162	0.633728	0.597157	Hspa1a/Pa
GO_CC_m1	GO:003215	cleavage fu	6/2589	40/23583	0.272162	0.633728	0.597157	Cenpc1/Ma
GO_CC_m1	GO:004359	nuclear rep	6/2589	40/23583	0.272162	0.633728	0.597157	Ercc5/Pcna
GO_CC_m1	GO:004878	presynaptic	6/2589	40/23583	0.272162	0.633728	0.597157	Adora1/Arl
GO_CC_m1	GO:003470	cation chan	26/2589	209/23583	0.278572	0.633728	0.597157	Akap6/Cac
GO_CC_m1	GO:004444	endosomal	26/2589	209/23583	0.278572	0.633728	0.597157	3110002H1
GO_CC_m1	GO:004445	microtubul	19/2589	149/23583	0.278889	0.633728	0.597157	Deup1/Ccc
GO_CC_m1	GO:009902	tethering c	9/2589	65/23583	0.281578	0.633728	0.597157	Cog4/Cog
GO_CC_m1	GO:000564	nuclear out	3/2589	17/23583	0.284682	0.633728	0.597157	Akap6/Rets
GO_CC_m1	GO:000577	integral con	3/2589	17/23583	0.284682	0.633728	0.597157	Pex10/Pex1
GO_CC_m1	GO:003298	myosin fila	3/2589	17/23583	0.284682	0.633728	0.597157	Myh14/My
GO_CC_m1	GO:003326	node of Ra	3/2589	17/23583	0.284682	0.633728	0.597157	Cdh1/Kcnq
GO_CC_m1	GO:004444	ciliary part	52/2589	437/23583	0.288423	0.633728	0.597157	Akap14/At
GO_CC_m1	GO:000191	photorecep	7/2589	49/23583	0.28904	0.633728	0.597157	Dnm3/Fam
GO_CC_m1	GO:003151	PcG protein	7/2589	49/23583	0.28904	0.633728	0.597157	Asxl1/Ezh1
GO_CC_m1	GO:000078	nuclear chr	10/2589	74/23583	0.291911	0.633728	0.597157	Terb1/Dclr
GO_CC_m1	GO:003532	transcriptio	4/2589	25/23583	0.292048	0.633728	0.597157	Bcas3/Hist1

GO_CC_m1	GO:00083	integrin co	5/2589	33/23583	0.293295	0.633728	0.597157	Itga3/Itga6
GO_CC_m1	GO:00004	core TFIIH	1/2589	3/23583	0.294525	0.633728	0.597157	Gtf2h3
GO_CC_m1	GO:00009	condensed	1/2589	3/23583	0.294525	0.633728	0.597157	Cenpa
GO_CC_m1	GO:00055	collagen ty	1/2589	3/23583	0.294525	0.633728	0.597157	Col5a1
GO_CC_m1	GO:00056	laminin-3	1/2589	3/23583	0.294525	0.633728	0.597157	Lamb2
GO_CC_m1	GO:000574	m-AAA co	1/2589	3/23583	0.294525	0.633728	0.597157	Spg7
GO_CC_m1	GO:000594	phosphatic	1/2589	3/23583	0.294525	0.633728	0.597157	Pik3r6
GO_CC_m1	GO:000594	6-phosphc	1/2589	3/23583	0.294525	0.633728	0.597157	Pfkl
GO_CC_m1	GO:00059	DNA-depe	1/2589	3/23583	0.294525	0.633728	0.597157	Prkdc
GO_CC_m1	GO:000827	gamma-tu	1/2589	3/23583	0.294525	0.633728	0.597157	Tubgcp2
GO_CC_m1	GO:00147	junctional	1/2589	3/23583	0.294525	0.633728	0.597157	Akap6
GO_CC_m1	GO:00165	cyclin-dep	1/2589	3/23583	0.294525	0.633728	0.597157	Cdk5
GO_CC_m1	GO:00169	kinesin II c	1/2589	3/23583	0.294525	0.633728	0.597157	Kifap3
GO_CC_m1	GO:001844	translation	1/2589	3/23583	0.294525	0.633728	0.597157	Gspt2
GO_CC_m1	GO:002001	ciliary pock	1/2589	3/23583	0.294525	0.633728	0.597157	Snap29
GO_CC_m1	GO:002001	ciliary pock	1/2589	3/23583	0.294525	0.633728	0.597157	Snap29
GO_CC_m1	GO:003031	external en	1/2589	3/23583	0.294525	0.633728	0.597157	Pgghg
GO_CC_m1	GO:00309	retromer, c	1/2589	3/23583	0.294525	0.633728	0.597157	Vps29
GO_CC_m1	GO:003141	NatC comp	1/2589	3/23583	0.294525	0.633728	0.597157	Naa38
GO_CC_m1	GO:003201	phagolyso	1/2589	3/23583	0.294525	0.633728	0.597157	Adam8
GO_CC_m1	GO:003204	DSIF comp	1/2589	3/23583	0.294525	0.633728	0.597157	Supt5
GO_CC_m1	GO:00321	dense core	1/2589	3/23583	0.294525	0.633728	0.597157	Adam8
GO_CC_m1	GO:00322	ribonuclea	1/2589	3/23583	0.294525	0.633728	0.597157	Rnaseh2b
GO_CC_m1	GO:00331	cis-Golgi n	1/2589	3/23583	0.294525	0.633728	0.597157	Bok
GO_CC_m1	GO:00351	FACT comp	1/2589	3/23583	0.294525	0.633728	0.597157	Tonsl
GO_CC_m1	GO:00362	tubulobulb	1/2589	3/23583	0.294525	0.633728	0.597157	Dnm3
GO_CC_m1	GO:00420	host cell nu	1/2589	3/23583	0.294525	0.633728	0.597157	Fmr1
GO_CC_m1	GO:00432	laminin-10	1/2589	3/23583	0.294525	0.633728	0.597157	Lama5
GO_CC_m1	GO:00440	host cell nu	1/2589	3/23583	0.294525	0.633728	0.597157	Fmr1
GO_CC_m1	GO:004527	plasma me	1/2589	3/23583	0.294525	0.633728	0.597157	Ndufs1
GO_CC_m1	GO:007011	ciliary neur	1/2589	3/23583	0.294525	0.633728	0.597157	Cntfr
GO_CC_m1	GO:00708	tertiary gra	1/2589	3/23583	0.294525	0.633728	0.597157	Vamp1
GO_CC_m1	GO:00710	U4/U6 snR	1/2589	3/23583	0.294525	0.633728	0.597157	Prpf4
GO_CC_m1	GO:00906	box H/AC	1/2589	3/23583	0.294525	0.633728	0.597157	Nop10
GO_CC_m1	GO:00974	Schwann c	1/2589	3/23583	0.294525	0.633728	0.597157	Ezr
GO_CC_m1	GO:009751	myosin II fi	1/2589	3/23583	0.294525	0.633728	0.597157	Myh14
GO_CC_m1	GO:00975	sperm cytc	1/2589	3/23583	0.294525	0.633728	0.597157	Ift172
GO_CC_m1	GO:00985	cytoplasmi	1/2589	3/23583	0.294525	0.633728	0.597157	Rab5a
GO_CC_m1	GO:00985	cytoplasmi	1/2589	3/23583	0.294525	0.633728	0.597157	Ezr
GO_CC_m1	GO:009884	postsynapt	1/2589	3/23583	0.294525	0.633728	0.597157	Dnm3
GO_CC_m1	GO:009907	mitochond	1/2589	3/23583	0.294525	0.633728	0.597157	Park2
GO_CC_m1	GO:00995	region of c	1/2589	3/23583	0.294525	0.633728	0.597157	Camk2a
GO_CC_m1	GO:00995	postsynapt	1/2589	3/23583	0.294525	0.633728	0.597157	Camk2a
GO_CC_m1	GO:199041	Pex17p-Pe	1/2589	3/23583	0.294525	0.633728	0.597157	Pex12
GO_CC_m1	GO:19904	RZZ compl	1/2589	3/23583	0.294525	0.633728	0.597157	Zwilch
GO_CC_m1	GO:19904	peroxisom	1/2589	3/23583	0.294525	0.633728	0.597157	Pex12
GO_CC_m1	GO:199081	growth cor	1/2589	3/23583	0.294525	0.633728	0.597157	Fmr1
GO_CC_m1	GO:000574	mitochond	2/2589	10/23583	0.301942	0.640735	0.603759	Grpel1/Tim

GO_CC_m1	GO:003230	mismatch r	2/2589	10/23583	0.301942	0.640735	0.603759	Msh3/Msh4
GO_CC_m1	GO:004878	presynaptic	2/2589	10/23583	0.301942	0.640735	0.603759	Cdh2/Stx1b
GO_CC_m1	GO:007120	WASH com	2/2589	10/23583	0.301942	0.640735	0.603759	Dnajc13/W
GO_CC_m1	GO:009053	cation-tran	2/2589	10/23583	0.301942	0.640735	0.603759	Atp1b2/Slc
GO_CC_m1	GO:009753	ciliary trans	2/2589	10/23583	0.301942	0.640735	0.603759	Fbf1/Odf2
GO_CC_m1	GO:015000	enzyme ac	2/2589	10/23583	0.301942	0.640735	0.603759	Cdk5/Cdk7
GO_CC_m1	GO:005503	recycling e	16/2589	126/23583	0.306904	0.649986	0.612476	Aatk/Bok/D
GO_CC_m1	GO:009880	inner mitoc	17/2589	135/23583	0.311598	0.656486	0.618601	2010107E0
GO_CC_m1	GO:000563	nuclear inn	6/2589	42/23583	0.3118	0.656486	0.618601	Terb1/Lbr/
GO_CC_m1	GO:190256	H4 histone	6/2589	42/23583	0.3118	0.656486	0.618601	Gm3086/Ka
GO_CC_m1	GO:000807	voltage-ga	11/2589	84/23583	0.314614	0.659185	0.621144	Kcna2/Kcna
GO_CC_m1	GO:003123	intrinsic co	3/2589	18/23583	0.31614	0.659185	0.621144	Pex10/Pex1
GO_CC_m1	GO:003152	microvillus	3/2589	18/23583	0.31614	0.659185	0.621144	Ezr/Mttp/S
GO_CC_m1	GO:003509	ESC/E(Z) co	3/2589	18/23583	0.31614	0.659185	0.621144	Ezh1/H2afy
GO_CC_m1	GO:004693	pore comp	3/2589	18/23583	0.31614	0.659185	0.621144	C7/Spg7/V
GO_CC_m1	GO:002262	proteasom	4/2589	26/23583	0.317929	0.660361	0.622252	Psmc2/Psm
GO_CC_m1	GO:009722	sperm mid	4/2589	26/23583	0.317929	0.660361	0.622252	Hyal3/Ift17
GO_CC_m1	GO:004319	dendritic sp	22/2589	179/23583	0.319805	0.66298	0.62472	Abl2/Adora
GO_CC_m1	GO:000013	Golgi mem	28/2589	232/23583	0.326234	0.670566	0.631868	Acer3/Atp7
GO_CC_m1	GO:000564	nuclear po	9/2589	68/23583	0.328576	0.670566	0.631868	1700123L1
GO_CC_m1	GO:000579	endoplasm	9/2589	68/23583	0.328576	0.670566	0.631868	Copg2/Gbf
GO_CC_m1	GO:000992	basal plasm	6/2589	43/23583	0.331968	0.670566	0.631868	Cav1/Erbb3
GO_CC_m1	GO:003190	early endos	6/2589	43/23583	0.331968	0.670566	0.631868	Bok/Dnajc1
GO_CC_m1	GO:004509	keratin fila	6/2589	43/23583	0.331968	0.670566	0.631868	Fbf1/Krt77/
GO_CC_m1	GO:000092	spindle pol	15/2589	120/23583	0.337243	0.670566	0.631868	Ankrd53/C
GO_CC_m1	GO:000577	multivesicu	5/2589	35/23583	0.338295	0.670566	0.631868	Acpp/Cd63
GO_CC_m1	GO:004430	neuron spi	22/2589	181/23583	0.339197	0.670566	0.631868	Abl2/Adora
GO_CC_m1	GO:004445	nucleolar p	22/2589	181/23583	0.339197	0.670566	0.631868	Ankrd1/Cc
GO_CC_m1	GO:007101	catalytic ste	13/2589	103/23583	0.340403	0.670566	0.631868	Cactin/Ddx
GO_CC_m1	GO:190494	ATPase co	11/2589	86/23583	0.343011	0.670566	0.631868	Appl1/Atp1
GO_CC_m1	GO:000013	Golgi cis ci	2/2589	11/23583	0.34427	0.670566	0.631868	Lyz1/Smpd
GO_CC_m1	GO:000152	microfibril	2/2589	11/23583	0.34427	0.670566	0.631868	Fbn1/Mfap
GO_CC_m1	GO:000193	uropod	2/2589	11/23583	0.34427	0.670566	0.631868	Ezr/Flot2
GO_CC_m1	GO:000217	palmitoyltr	2/2589	11/23583	0.34427	0.670566	0.631868	Sptlc2/Spts
GO_CC_m1	GO:000568	U4 snRNP	2/2589	11/23583	0.34427	0.670566	0.631868	Naa38/Snr
GO_CC_m1	GO:003125	cell trailing	2/2589	11/23583	0.34427	0.670566	0.631868	Ezr/Flot2
GO_CC_m1	GO:003146	Cul4A-RIN	2/2589	11/23583	0.34427	0.670566	0.631868	Cul4a/Glm
GO_CC_m1	GO:003510	PRC1 comp	2/2589	11/23583	0.34427	0.670566	0.631868	Phc2/Ring1
GO_CC_m1	GO:004255	MCM comp	2/2589	11/23583	0.34427	0.670566	0.631868	Mcm8/Ton
GO_CC_m1	GO:006170	GATOR2 co	2/2589	11/23583	0.34427	0.670566	0.631868	Szt2/Wdr2
GO_CC_m1	GO:007254	ER membra	2/2589	11/23583	0.34427	0.670566	0.631868	Emc3/Emc8
GO_CC_m1	GO:000565	replication	9/2589	69/23583	0.344567	0.670566	0.631868	Blm/Ercc5/
GO_CC_m1	GO:000594	phosphatic	3/2589	19/23583	0.347646	0.670566	0.631868	Pik3r3/Pik3
GO_CC_m1	GO:004321	compact m	3/2589	19/23583	0.347646	0.670566	0.631868	Anxa2/Cdh
GO_CC_m1	GO:003013	clathrin-co	12/2589	95/23583	0.348626	0.670566	0.631868	Bcap31/Clv
GO_CC_m1	GO:004273	presynaptic	10/2589	78/23583	0.351539	0.670566	0.631868	Ache/Ador
GO_CC_m1	GO:001900	SCF ubiqui	9/2589	70/23583	0.360671	0.670566	0.631868	Abtb1/Cul1
GO_CC_m1	GO:000590	brush bord	16/2589	131/23583	0.36475	0.670566	0.631868	Abcb1a/At

GO_CC_m1	GO:004307	germ cell r	4/2589	28/23583	0.370061	0.670566	0.631868	Blm/Sycp1/
GO_CC_m1	GO:000012	PCAF comp	1/2589	4/23583	0.371984	0.670566	0.631868	Taf9
GO_CC_m1	GO:000093	GARP com	1/2589	4/23583	0.371984	0.670566	0.631868	Vps53
GO_CC_m1	GO:000174	Barr body	1/2589	4/23583	0.371984	0.670566	0.631868	H2afy
GO_CC_m1	GO:000218	ribose pho	1/2589	4/23583	0.371984	0.670566	0.631868	Prpsap2
GO_CC_m1	GO:000561	laminin-5 c	1/2589	4/23583	0.371984	0.670566	0.631868	Lama5
GO_CC_m1	GO:000574	mitochond	1/2589	4/23583	0.371984	0.670566	0.631868	Sdhb
GO_CC_m1	GO:000578	Sec61 trans	1/2589	4/23583	0.371984	0.670566	0.631868	Bcap31
GO_CC_m1	GO:000586	muscle thir	1/2589	4/23583	0.371984	0.670566	0.631868	Tpm4
GO_CC_m1	GO:000594	mitochond	1/2589	4/23583	0.371984	0.670566	0.631868	Bckdhb
GO_CC_m1	GO:000862	epsilon DN	1/2589	4/23583	0.371984	0.670566	0.631868	Pole
GO_CC_m1	GO:000932	phenylalan	1/2589	4/23583	0.371984	0.670566	0.631868	Lrrc47
GO_CC_m1	GO:001707	intracellula	1/2589	4/23583	0.371984	0.670566	0.631868	Cnga2
GO_CC_m1	GO:003047	actin cap	1/2589	4/23583	0.371984	0.670566	0.631868	Gsn
GO_CC_m1	GO:003068	Noc compl	1/2589	4/23583	0.371984	0.670566	0.631868	Casp8
GO_CC_m1	GO:003126	CD95 deatl	1/2589	4/23583	0.371984	0.670566	0.631868	Casp8
GO_CC_m1	GO:003202	NELF comp	1/2589	4/23583	0.371984	0.670566	0.631868	Nelfb
GO_CC_m1	GO:003280	DNA ligase	1/2589	4/23583	0.371984	0.670566	0.631868	Lig3
GO_CC_m1	GO:003427	phosphatic	1/2589	4/23583	0.371984	0.670566	0.631868	Pik3r4
GO_CC_m1	GO:003427	phosphatic	1/2589	4/23583	0.371984	0.670566	0.631868	Pik3r4
GO_CC_m1	GO:003518	Rb-E2F cor	1/2589	4/23583	0.371984	0.670566	0.631868	E2f1
GO_CC_m1	GO:003536	histone loc	1/2589	4/23583	0.371984	0.670566	0.631868	Ice1
GO_CC_m1	GO:003551	PR-DUB cc	1/2589	4/23583	0.371984	0.670566	0.631868	Asxl1
GO_CC_m1	GO:003565	Mon1-Ccz	1/2589	4/23583	0.371984	0.670566	0.631868	3110002H1
GO_CC_m1	GO:003639	RNA N6-m	1/2589	4/23583	0.371984	0.670566	0.631868	Virma
GO_CC_m1	GO:004256	insulin-like	1/2589	4/23583	0.371984	0.670566	0.631868	Igfbp3
GO_CC_m1	GO:004430	calyx of He	1/2589	4/23583	0.371984	0.670566	0.631868	Kcnk2
GO_CC_m1	GO:004430	axonal spir	1/2589	4/23583	0.371984	0.670566	0.631868	Gria1
GO_CC_m1	GO:004525	succinate c	1/2589	4/23583	0.371984	0.670566	0.631868	Sdhb
GO_CC_m1	GO:004527	respiratory	1/2589	4/23583	0.371984	0.670566	0.631868	Sdhb
GO_CC_m1	GO:004528	succinate c	1/2589	4/23583	0.371984	0.670566	0.631868	Sdhb
GO_CC_m1	GO:004528	fumarate re	1/2589	4/23583	0.371984	0.670566	0.631868	Sdhb
GO_CC_m1	GO:007044	elongin cor	1/2589	4/23583	0.371984	0.670566	0.631868	Elob
GO_CC_m1	GO:007047	plasma me	1/2589	4/23583	0.371984	0.670566	0.631868	Ndufs1
GO_CC_m1	GO:007125	translocon	1/2589	4/23583	0.371984	0.670566	0.631868	Bcap31
GO_CC_m1	GO:007182	FANCM-M	1/2589	4/23583	0.371984	0.670566	0.631868	Cenpx
GO_CC_m1	GO:007195	elastic fibe	1/2589	4/23583	0.371984	0.670566	0.631868	Fbln5
GO_CC_m1	GO:007255	NLRP1 infla	1/2589	4/23583	0.371984	0.670566	0.631868	Pycard
GO_CC_m1	GO:009720	epidermal	1/2589	4/23583	0.371984	0.670566	0.631868	Abca12
GO_CC_m1	GO:009736	CIA comple	1/2589	4/23583	0.371984	0.670566	0.631868	Ciao1
GO_CC_m1	GO:009748	multivesicu	1/2589	4/23583	0.371984	0.670566	0.631868	Cd63
GO_CC_m1	GO:009762	extrinsic cc	1/2589	4/23583	0.371984	0.670566	0.631868	Plekhf2
GO_CC_m1	GO:009765	phosphatic	1/2589	4/23583	0.371984	0.670566	0.631868	Pik3r6
GO_CC_m1	GO:190344	amylin rece	1/2589	4/23583	0.371984	0.670566	0.631868	Calcr
GO_CC_m1	GO:199035	terminal we	1/2589	4/23583	0.371984	0.670566	0.631868	Pls1
GO_CC_m1	GO:199039	3M comple	1/2589	4/23583	0.371984	0.670566	0.631868	Ankra2
GO_CC_m1	GO:199074	EARP comp	1/2589	4/23583	0.371984	0.670566	0.631868	Vps53
GO_CC_m1	GO:199085	Wnt-Frizzle	1/2589	4/23583	0.371984	0.670566	0.631868	Wnt3a

GO_CC_m1	GO:00347	chloride ch	6/2589	45/23583	0.372691	0.67072	0.632013	Ano1/Ano
GO_CC_m1	GO:00432	perikaryon	16/2589	132/23583	0.376555	0.676544	0.637501	Bglap3/Cn
GO_CC_m1	GO:000592	connexin c	3/2589	20/23583	0.378994	0.678663	0.639498	Gja3/Gjb2/
GO_CC_m1	GO:000807	guanylate	3/2589	20/23583	0.378994	0.678663	0.639498	Adcy4/Guc
GO_CC_m1	GO:000593	axoneme	14/2589	115/23583	0.383083	0.680528	0.641255	Akap14/Cc
GO_CC_m1	GO:00313	integral co	5/2589	37/23583	0.383764	0.680528	0.641255	Cox11/Mp
GO_CC_m1	GO:000015	cytoplasmi	2/2589	12/23583	0.385722	0.680528	0.641255	Cul2/Elob
GO_CC_m1	GO:000017	nuclear ex	2/2589	12/23583	0.385722	0.680528	0.641255	Exosc1/Ex
GO_CC_m1	GO:003091	STAGA cor	2/2589	12/23583	0.385722	0.680528	0.641255	Kat2a/Taf9
GO_CC_m1	GO:003123	intrinsic co	2/2589	12/23583	0.385722	0.680528	0.641255	Nf1/Synga
GO_CC_m1	GO:003466	endoplasm	2/2589	12/23583	0.385722	0.680528	0.641255	Hsp90b1/P
GO_CC_m1	GO:00424	nuclear inc	2/2589	12/23583	0.385722	0.680528	0.641255	Nup153/T
GO_CC_m1	GO:009853	ATPase de	2/2589	12/23583	0.385722	0.680528	0.641255	Atp1b2/Slc
GO_CC_m1	GO:007046	respiratory	11/2589	89/23583	0.386348	0.680528	0.641255	Cox4i2/Co
GO_CC_m1	GO:000577	vacuolar m	21/2589	177/23583	0.387203	0.680921	0.641626	Anxa2/Atp
GO_CC_m1	GO:00100	endosome	22/2589	186/23583	0.38878	0.682582	0.64319	3110002H
GO_CC_m1	GO:00432	myelin she	25/2589	213/23583	0.392771	0.688468	0.648737	Anxa2/Atp
GO_CC_m1	GO:009701	ciliary plas	14/2589	116/23583	0.395847	0.690882	0.651011	Akap14/Cc
GO_CC_m1	GO:190255	endoribonu	4/2589	29/23583	0.396071	0.690882	0.651011	Mir27a/Rp
GO_CC_m1	GO:190534	endonucle	4/2589	29/23583	0.396071	0.690882	0.651011	Mir27a/Rp
GO_CC_m1	GO:000587	kinesin con	7/2589	55/23583	0.399978	0.696569	0.656371	Kif23/Kif4/
GO_CC_m1	GO:00313	intrinsic co	5/2589	38/23583	0.406475	0.696971	0.656749	Cox11/Mp
GO_CC_m1	GO:000569	telomerase	3/2589	21/23583	0.410002	0.696971	0.656749	Hmbox1/H
GO_CC_m1	GO:000558	collagen tri	10/2589	82/23583	0.412719	0.696971	0.656749	C1ql1/C1q
GO_CC_m1	GO:000574	mitochond	10/2589	82/23583	0.412719	0.696971	0.656749	Cox4i2/Co
GO_CC_m1	GO:003283	plasma me	19/2589	162/23583	0.416195	0.696971	0.656749	Akap14/Ca
GO_CC_m1	GO:000577	late endos	21/2589	180/23583	0.418175	0.696971	0.656749	3110002H
GO_CC_m1	GO:004517	intercellula	7/2589	56/23583	0.418676	0.696971	0.656749	Cdc7/Cenp
GO_CC_m1	GO:003228	AMPA glut	4/2589	30/23583	0.421899	0.696971	0.656749	Cacng5/Ca
GO_CC_m1	GO:003122	intrinsic co	16/2589	136/23583	0.424184	0.696971	0.656749	Acer3/Asp
GO_CC_m1	GO:000077	condensed	2/2589	13/23583	0.425978	0.696971	0.656749	Cenpa/Cen
GO_CC_m1	GO:000591	fascia adhe	2/2589	13/23583	0.425978	0.696971	0.656749	Cdh2/Des
GO_CC_m1	GO:001251	trans-Golg	2/2589	13/23583	0.425978	0.696971	0.656749	Ldlrap1/Ra
GO_CC_m1	GO:001658	Sin3 compl	2/2589	13/23583	0.425978	0.696971	0.656749	Hdac1/Hd
GO_CC_m1	GO:003159	cytosolic p	2/2589	13/23583	0.425978	0.696971	0.656749	Psmc2/Psm
GO_CC_m1	GO:004432	dendritic s	2/2589	13/23583	0.425978	0.696971	0.656749	Dnm3/Fmr
GO_CC_m1	GO:000574	mitochond	6/2589	48/23583	0.43388	0.696971	0.656749	Ndufa12/N
GO_CC_m1	GO:003096	NADH deh	6/2589	48/23583	0.43388	0.696971	0.656749	Ndufa12/N
GO_CC_m1	GO:004527	respiratory	6/2589	48/23583	0.43388	0.696971	0.656749	Ndufa12/N
GO_CC_m1	GO:00560	basal lami	3/2589	22/23583	0.440513	0.696971	0.656749	Ache/Lam
GO_CC_m1	GO:000572	pericentric	3/2589	22/23583	0.440513	0.696971	0.656749	Cenpa/Cen
GO_CC_m1	GO:000575	mitochond	3/2589	22/23583	0.440513	0.696971	0.656749	2010107E0
GO_CC_m1	GO:006007	inhibitory s	3/2589	22/23583	0.440513	0.696971	0.656749	Gphn/Maf
GO_CC_m1	GO:007178	endoplasm	3/2589	22/23583	0.440513	0.696971	0.656749	Asph/Osbp
GO_CC_m1	GO:000001	phosphopy	1/2589	5/23583	0.440941	0.696971	0.656749	Eno3
GO_CC_m1	GO:000012	RNA polym	1/2589	5/23583	0.440941	0.696971	0.656749	Tbp
GO_CC_m1	GO:000022	vacuolar p	1/2589	5/23583	0.440941	0.696971	0.656749	Atp6v0c
GO_CC_m1	GO:000027	mitochond	1/2589	5/23583	0.440941	0.696971	0.656749	Atp5a1

GO_CC_m1	GO:00140	presequen	1/2589	5/23583	0.440941	0.696971	0.656749	Grpel1
GO_CC_m1	GO:00020	outer acros	1/2589	5/23583	0.440941	0.696971	0.656749	Ift88
GO_CC_m1	GO:00056	annulate la	1/2589	5/23583	0.440941	0.696971	0.656749	Nup153
GO_CC_m1	GO:00056	DNA replic	1/2589	5/23583	0.440941	0.696971	0.656749	Rfc1
GO_CC_m1	GO:00058	axonemal	1/2589	5/23583	0.440941	0.696971	0.656749	Saxo1
GO_CC_m1	GO:00059	phosphory	1/2589	5/23583	0.440941	0.696971	0.656749	Phkb
GO_CC_m1	GO:00162	eukaryotic	1/2589	5/23583	0.440941	0.696971	0.656749	Eif4e
GO_CC_m1	GO:00169	insulin-like	1/2589	5/23583	0.440941	0.696971	0.656749	Igfbp3
GO_CC_m1	GO:00301	AP-4 adap	1/2589	5/23583	0.440941	0.696971	0.656749	Ap4e1
GO_CC_m1	GO:00314	box H/AC	1/2589	5/23583	0.440941	0.696971	0.656749	Nop10
GO_CC_m1	GO:00318	haptoglobi	1/2589	5/23583	0.440941	0.696971	0.656749	Hbb-bs
GO_CC_m1	GO:00336	host intrac	1/2589	5/23583	0.440941	0.696971	0.656749	Fmr1
GO_CC_m1	GO:00336	host intrac	1/2589	5/23583	0.440941	0.696971	0.656749	Fmr1
GO_CC_m1	GO:00364	growth fac	1/2589	5/23583	0.440941	0.696971	0.656749	Igfbp3
GO_CC_m1	GO:00428	MHC class	1/2589	5/23583	0.440941	0.696971	0.656749	Calr
GO_CC_m1	GO:00450	type III inte	1/2589	5/23583	0.440941	0.696971	0.656749	Des
GO_CC_m1	GO:00452	proton-tra	1/2589	5/23583	0.440941	0.696971	0.656749	Atp5a1
GO_CC_m1	GO:00452	mRNA edit	1/2589	5/23583	0.440941	0.696971	0.656749	Virma
GO_CC_m1	GO:00452	tubulin cor	1/2589	5/23583	0.440941	0.696971	0.656749	Ttbk1
GO_CC_m1	GO:00705	ERCC4-ER	1/2589	5/23583	0.440941	0.696971	0.656749	Xrcc1
GO_CC_m1	GO:00714	invadopod	1/2589	5/23583	0.440941	0.696971	0.656749	Itga3
GO_CC_m1	GO:007181	MMXD cor	1/2589	5/23583	0.440941	0.696971	0.656749	Ciao1
GO_CC_m1	GO:00725	box H/AC	1/2589	5/23583	0.440941	0.696971	0.656749	Nop10
GO_CC_m1	GO:00971	AIM2 infla	1/2589	5/23583	0.440941	0.696971	0.656749	Pycard
GO_CC_m1	GO:00974	tubular en	1/2589	5/23583	0.440941	0.696971	0.656749	Snx6
GO_CC_m1	GO:00974	basal dend	1/2589	5/23583	0.440941	0.696971	0.656749	Ykt6
GO_CC_m1	GO:00974	sorting en	1/2589	5/23583	0.440941	0.696971	0.656749	Ptpn1
GO_CC_m1	GO:00988	postsynapt	1/2589	5/23583	0.440941	0.696971	0.656749	Dnm3
GO_CC_m1	GO:00990	integral co	1/2589	5/23583	0.440941	0.696971	0.656749	Gria1
GO_CC_m1	GO:00991	intrinsic co	1/2589	5/23583	0.440941	0.696971	0.656749	Gria1
GO_CC_m1	GO:01400	KICSTOR c	1/2589	5/23583	0.440941	0.696971	0.656749	Szt2
GO_CC_m1	GO:19033	omegasom	1/2589	5/23583	0.440941	0.696971	0.656749	Plekhf2
GO_CC_m1	GO:19034	calcitonin f	1/2589	5/23583	0.440941	0.696971	0.656749	Calcr
GO_CC_m1	GO:199011	spermatop	1/2589	5/23583	0.440941	0.696971	0.656749	Psme4
GO_CC_m1	GO:19902	uniplex cor	1/2589	5/23583	0.440941	0.696971	0.656749	Micu2
GO_CC_m1	GO:19907	Lsm1-7-Pa	1/2589	5/23583	0.440941	0.696971	0.656749	Lsm5
GO_CC_m1	GO:00170	transcriptio	10/2589	84/23583	0.443406	0.699842	0.659455	Appl1/Bah
GO_CC_m1	GO:00347	potassium	11/2589	93/23583	0.444641	0.700765	0.660324	Kcna2/Kcn
GO_CC_m1	GO:00995	cytoplasmi	50/2589	444/23583	0.446359	0.702446	0.661908	Akap14/Ar
GO_CC_m1	GO:00001	nuclear ubi	5/2589	40/23583	0.451487	0.709479	0.668536	Babam2/C
GO_CC_m1	GO:00163	lateral plas	7/2589	58/23583	0.455869	0.715324	0.674043	Cdh1/Cldn
GO_CC_m1	GO:00159	small ribos	10/2589	85/23583	0.458694	0.717663	0.676248	Fau/Mrpl42
GO_CC_m1	GO:00361	sperm flag	13/2589	112/23583	0.45975	0.717663	0.676248	Akap14/At
GO_CC_m1	GO:00301	integral co	15/2589	130/23583	0.45999	0.717663	0.676248	Acer3/Asp
GO_CC_m1	GO:00017	ruffle	16/2589	139/23583	0.460024	0.717663	0.676248	Anxa2/Bca
GO_CC_m1	GO:00432	receptor co	42/2589	374/23583	0.462359	0.720265	0.678699	Adcyap1r1
GO_CC_m1	GO:00057	secondary	2/2589	14/23583	0.464803	0.720946	0.67934	Adam8/Cr
GO_CC_m1	GO:00332	transcriptio	2/2589	14/23583	0.464803	0.720946	0.67934	Kat2a/Taf9

GO_CC_m1	GO:003568	sperm fibr	2/2589	14/23583	0.464803	0.720946	0.67934	Akap14/Ld
GO_CC_m1	GO:000584	ribosome	31/2589	275/23583	0.46624	0.722013	0.680347	Canx/Fau/
GO_CC_m1	GO:000017	exosome (	3/2589	23/23583	0.470392	0.722013	0.680347	Exosc1/Exo
GO_CC_m1	GO:004261	MHC prote	3/2589	23/23583	0.470392	0.722013	0.680347	H2-DMb2/
GO_CC_m1	GO:004525	proton-tra	3/2589	23/23583	0.470392	0.722013	0.680347	2010107E0
GO_CC_m1	GO:190535	exoribonuc	3/2589	23/23583	0.470392	0.722013	0.680347	Exosc1/Exo
GO_CC_m1	GO:009772	9+2 motile	13/2589	114/23583	0.486227	0.722013	0.680347	Akap14/At
GO_CC_m1	GO:001636	nuclear ma	10/2589	87/23583	0.48905	0.722013	0.680347	Ahctf1/Alo
GO_CC_m1	GO:003067	synaptic ve	10/2589	87/23583	0.48905	0.722013	0.680347	Adra1d/Ol
GO_CC_m1	GO:009950	exocytic ve	10/2589	87/23583	0.48905	0.722013	0.680347	Adra1d/Ol
GO_CC_m1	GO:004443	vacuolar pa	21/2589	187/23583	0.490675	0.722013	0.680347	Anxa2/Atp
GO_CC_m1	GO:000591	adherens ju	32/2589	287/23583	0.490916	0.722013	0.680347	Aif1l/Anxa
GO_CC_m1	GO:003066	coated ves	8/2589	69/23583	0.491277	0.722013	0.680347	Copg2/Ldl
GO_CC_m1	GO:003152	brush bord	8/2589	69/23583	0.491277	0.722013	0.680347	Abcb1a/At
GO_CC_m1	GO:003215	cell divisio	8/2589	69/23583	0.491277	0.722013	0.680347	Cenpc1/M
GO_CC_m1	GO:003120	SNARE cor	6/2589	51/23583	0.493947	0.722013	0.680347	Snap29/St
GO_CC_m1	GO:001632	apical plas	34/2589	306/23583	0.497518	0.722013	0.680347	Abcb1a/Ac
GO_CC_m1	GO:003506	micro-ribo	13/2589	115/23583	0.499373	0.722013	0.680347	Mir16-1/M
GO_CC_m1	GO:001646	myosin II c	3/2589	24/23583	0.499524	0.722013	0.680347	Myh14/My
GO_CC_m1	GO:000078	chromoso	12/2589	106/23583	0.500806	0.722013	0.680347	Blm/Terb1/
GO_CC_m1	GO:000017	cytoplasmi	2/2589	15/23583	0.502024	0.722013	0.680347	Exosc9/Pn
GO_CC_m1	GO:003101	Ino80 com	2/2589	15/23583	0.502024	0.722013	0.680347	Gm3086/N
GO_CC_m1	GO:004257	DNA poly	2/2589	15/23583	0.502024	0.722013	0.680347	Pole/Polg
GO_CC_m1	GO:004318	P granule	2/2589	15/23583	0.502024	0.722013	0.680347	Ddx4/Mael
GO_CC_m1	GO:004549	pole plasm	2/2589	15/23583	0.502024	0.722013	0.680347	Ddx4/Mael
GO_CC_m1	GO:006029	germ plas	2/2589	15/23583	0.502024	0.722013	0.680347	Ddx4/Mael
GO_CC_m1	GO:000012	transcripti	1/2589	6/23583	0.502328	0.722013	0.680347	Gtf3c3
GO_CC_m1	GO:000173	sex chroma	1/2589	6/23583	0.502328	0.722013	0.680347	Ring1
GO_CC_m1	GO:000558	collagen ty	1/2589	6/23583	0.502328	0.722013	0.680347	Col4a2
GO_CC_m1	GO:000572	perichroma	1/2589	6/23583	0.502328	0.722013	0.680347	Clock
GO_CC_m1	GO:001601	sarcoglyca	1/2589	6/23583	0.502328	0.722013	0.680347	Sgcz
GO_CC_m1	GO:003006	mitochond	1/2589	6/23583	0.502328	0.722013	0.680347	Bckdhb
GO_CC_m1	GO:003012	AP-1 adap	1/2589	6/23583	0.502328	0.722013	0.680347	Ldlrap1
GO_CC_m1	GO:003089	checkpoint	1/2589	6/23583	0.502328	0.722013	0.680347	Rad9b
GO_CC_m1	GO:003126	death-indu	1/2589	6/23583	0.502328	0.722013	0.680347	Casp8
GO_CC_m1	GO:003142	box C/D s	1/2589	6/23583	0.502328	0.722013	0.680347	Nop56
GO_CC_m1	GO:003146	Cul5-RING	1/2589	6/23583	0.502328	0.722013	0.680347	Arih2
GO_CC_m1	GO:004240	extrinsic c	1/2589	6/23583	0.502328	0.722013	0.680347	Zc3h12a
GO_CC_m1	GO:004272	mitochond	1/2589	6/23583	0.502328	0.722013	0.680347	Timm22
GO_CC_m1	GO:004432	dendritic s	1/2589	6/23583	0.502328	0.722013	0.680347	Fmr1
GO_CC_m1	GO:004823	rough end	1/2589	6/23583	0.502328	0.722013	0.680347	Lyz1
GO_CC_m1	GO:004878	cytoskelet	1/2589	6/23583	0.502328	0.722013	0.680347	Rims3
GO_CC_m1	GO:007055	BRISC com	1/2589	6/23583	0.502328	0.722013	0.680347	Babam2
GO_CC_m1	GO:007077	H3 histone	1/2589	6/23583	0.502328	0.722013	0.680347	Brpf3
GO_CC_m1	GO:007077	MOZ/MOR	1/2589	6/23583	0.502328	0.722013	0.680347	Brpf3
GO_CC_m1	GO:007120	histone pre	1/2589	6/23583	0.502328	0.722013	0.680347	Eri1
GO_CC_m1	GO:008970	U2AF	1/2589	6/23583	0.502328	0.722013	0.680347	Zrsr2
GO_CC_m1	GO:009072	central reg	1/2589	6/23583	0.502328	0.722013	0.680347	Pafah1b1

GO_CC_m1	GO:009741	Lewy body	1/2589	6/23583	0.502328	0.722013	0.680347	Gpx1
GO_CC_m1	GO:009742	microtubul	1/2589	6/23583	0.502328	0.722013	0.680347	Tppp3
GO_CC_m1	GO:009864	network-fc	1/2589	6/23583	0.502328	0.722013	0.680347	Col4a2
GO_CC_m1	GO:009864	collagen ne	1/2589	6/23583	0.502328	0.722013	0.680347	Col4a2
GO_CC_m1	GO:009865	basement	1/2589	6/23583	0.502328	0.722013	0.680347	Col4a2
GO_CC_m1	GO:199007	periciliary r	1/2589	6/23583	0.502328	0.722013	0.680347	Kifap3
GO_CC_m1	GO:199013	GATOR1 c	1/2589	6/23583	0.502328	0.722013	0.680347	Szt2
GO_CC_m1	GO:199045	L-type volt	1/2589	6/23583	0.502328	0.722013	0.680347	Cacnb2
GO_CC_m1	GO:000012	histone ace	9/2589	79/23583	0.505982	0.726296	0.684382	Brpf3/Gm3
GO_CC_m1	GO:000577	autophago	8/2589	70/23583	0.50813	0.72841	0.686374	Plekhf2/Ra
GO_CC_m1	GO:000011	histone de	7/2589	61/23583	0.510599	0.730977	0.688793	Appl1/Hda
GO_CC_m1	GO:009773	photorecep	12/2589	107/23583	0.514407	0.735452	0.69301	Fam161a/F
GO_CC_m1	GO:004444	axoneme p	4/2589	34/23583	0.521585	0.743741	0.70082	Dnah1/Dna
GO_CC_m1	GO:009883	postsynapt	4/2589	34/23583	0.521585	0.743741	0.70082	Cacng5/Ca
GO_CC_m1	GO:004444	cell cortex	20/2589	181/23583	0.523047	0.744841	0.701857	Asph/Cdh1
GO_CC_m1	GO:003280	carboxy-te	3/2589	25/23583	0.527816	0.749652	0.70639	Cdk7/Ercc5
GO_CC_m1	GO:004533	clathrin-co	3/2589	25/23583	0.527816	0.749652	0.70639	Cpne6/Ctla
GO_CC_m1	GO:003011	membrane	11/2589	99/23583	0.530657	0.751706	0.708326	Ap1s2/Ap4
GO_CC_m1	GO:004847	coated me	11/2589	99/23583	0.530657	0.751706	0.708326	Ap1s2/Ap4
GO_CC_m1	GO:009880	respiratory	9/2589	81/23583	0.537235	0.754498	0.710956	Cox4i2/Nd
GO_CC_m1	GO:000566	DNA-direc	2/2589	16/23583	0.537527	0.754498	0.710956	Polr2f/Polr
GO_CC_m1	GO:003152	filopodium	2/2589	16/23583	0.537527	0.754498	0.710956	Antxr1/Itga
GO_CC_m1	GO:003585	Seh1-asso	2/2589	16/23583	0.537527	0.754498	0.710956	Szt2/Wdr2
GO_CC_m1	GO:004319	axon initial	2/2589	16/23583	0.537527	0.754498	0.710956	Kcnq2/Kcn
GO_CC_m1	GO:006170	inflammaso	2/2589	16/23583	0.537527	0.754498	0.710956	Gsdmd/Py
GO_CC_m1	GO:007082	Sin3-type	2/2589	16/23583	0.537527	0.754498	0.710956	Hdac1/Hda
GO_CC_m1	GO:001660	nuclear spe	33/2589	302/23583	0.538989	0.755565	0.711962	Virma/Basp
GO_CC_m1	GO:007060	SWI/SNF s	8/2589	72/23583	0.541262	0.756853	0.713176	Appl1/Baz1
GO_CC_m1	GO:000818	COP9 signa	4/2589	35/23583	0.545235	0.756853	0.713176	Atp5a1/Bas
GO_CC_m1	GO:008000	Cul4-RING	4/2589	35/23583	0.545235	0.756853	0.713176	Cul4a/Dcaf
GO_CC_m1	GO:000078	condensed	3/2589	26/23583	0.555193	0.756853	0.713176	Cenpa/Cen
GO_CC_m1	GO:003158	nucleotide	3/2589	26/23583	0.555193	0.756853	0.713176	Gm14147/
GO_CC_m1	GO:000043	core TFIIH	1/2589	7/23583	0.556978	0.756853	0.713176	Gtf2h3
GO_CC_m1	GO:000557	membrane	1/2589	7/23583	0.556978	0.756853	0.713176	C7
GO_CC_m1	GO:000565	nucleolar ri	1/2589	7/23583	0.556978	0.756853	0.713176	Rpp40
GO_CC_m1	GO:001601	dystroglyca	1/2589	7/23583	0.556978	0.756853	0.713176	Sgcz
GO_CC_m1	GO:001627	prefoldin c	1/2589	7/23583	0.556978	0.756853	0.713176	Pdrg1
GO_CC_m1	GO:001990	cyclin-dep	1/2589	7/23583	0.556978	0.756853	0.713176	Cdk7
GO_CC_m1	GO:003047	actin cortic	1/2589	7/23583	0.556978	0.756853	0.713176	Wipf1
GO_CC_m1	GO:003067	phagocytic	1/2589	7/23583	0.556978	0.756853	0.713176	Anxa3
GO_CC_m1	GO:003325	I-kappaB/N	1/2589	7/23583	0.556978	0.756853	0.713176	Nfkb1
GO_CC_m1	GO:003503	phosphatic	1/2589	7/23583	0.556978	0.756853	0.713176	Pik3r4
GO_CC_m1	GO:004430	cerebellar	1/2589	7/23583	0.556978	0.756853	0.713176	Syde1
GO_CC_m1	GO:006164	endocytic	1/2589	7/23583	0.556978	0.756853	0.713176	Wipf1
GO_CC_m1	GO:007018	shelterin c	1/2589	7/23583	0.556978	0.756853	0.713176	Terb1
GO_CC_m1	GO:007154	pi-body	1/2589	7/23583	0.556978	0.756853	0.713176	Ddx4
GO_CC_m1	GO:009057	RNA polym	1/2589	7/23583	0.556978	0.756853	0.713176	Hdac2
GO_CC_m1	GO:009725	R2TP comp	1/2589	7/23583	0.556978	0.756853	0.713176	Gm3086

GO_CC_m1	GO:00995	presynapti	1/2589	7/23583	0.556978	0.756853	0.713176	Rims3
GO_CC_m1	GO:19904	omegasom	1/2589	7/23583	0.556978	0.756853	0.713176	Plekhf2
GO_CC_m1	GO:199091	sperm hea	1/2589	7/23583	0.556978	0.756853	0.713176	Adam4
GO_CC_m1	GO:00082	protein ser	5/2589	45/23583	0.558864	0.756853	0.713176	2810408A1
GO_CC_m1	GO:012011	neuron prc	5/2589	45/23583	0.558864	0.756853	0.713176	Camk2a/C
GO_CC_m1	GO:19032	phosphata	5/2589	45/23583	0.558864	0.756853	0.713176	2810408A1
GO_CC_m1	GO:00975	spliceosom	7/2589	64/23583	0.563286	0.761443	0.7175	Lsm5/Naa
GO_CC_m1	GO:00431	terminal bc	13/2589	120/23583	0.563665	0.761443	0.7175	Adora1/Fm
GO_CC_m1	GO:00453	phagocytic	9/2589	83/23583	0.56773	0.762124	0.718143	Adam8/An
GO_CC_m1	GO:00058	voltage-ga	4/2589	36/23583	0.568263	0.762124	0.718143	Cacnb2/Ca
GO_CC_m1	GO:000561	interstitial	2/2589	17/23583	0.57124	0.762124	0.718143	2300002M
GO_CC_m1	GO:000584	mRNA clea	2/2589	17/23583	0.57124	0.762124	0.718143	Cpsf2/Cpsf
GO_CC_m1	GO:00058	acetylcholi	2/2589	17/23583	0.57124	0.762124	0.718143	Chrne/Chr
GO_CC_m1	GO:001601	dystrophin	2/2589	17/23583	0.57124	0.762124	0.718143	Cav3/Sgcz
GO_CC_m1	GO:006182	sperm hea	2/2589	17/23583	0.57124	0.762124	0.718143	Adam4/Ta
GO_CC_m1	GO:00710	U2-type pr	2/2589	17/23583	0.57124	0.762124	0.718143	Naa38/Snr
GO_CC_m1	GO:00906	glycoprote	2/2589	17/23583	0.57124	0.762124	0.718143	Cav3/Sgcz
GO_CC_m1	GO:009864	complex o	2/2589	17/23583	0.57124	0.762124	0.718143	Col4a2/Co
GO_CC_m1	GO:00444	mitochond	23/2589	214/23583	0.575777	0.767229	0.722952	2010107E0
GO_CC_m1	GO:00079	nuclear chr	42/2589	390/23583	0.577312	0.768323	0.723984	Appl1/Apt
GO_CC_m1	GO:00325	dendrite m	5/2589	46/23583	0.579075	0.768772	0.724407	Gabra6/Gri
GO_CC_m1	GO:006017	ciliary mer	5/2589	46/23583	0.579075	0.768772	0.724407	Drd5/Prcd
GO_CC_m1	GO:00977	9+0 non-n	12/2589	112/23583	0.580568	0.769806	0.725381	Fam161a/
GO_CC_m1	GO:00059	cell cortex	31/2589	290/23583	0.590928	0.77815	0.733243	Anxa2/Asp
GO_CC_m1	GO:004517	basal part	7/2589	66/23583	0.596925	0.77815	0.733243	Cav1/Erbb
GO_CC_m1	GO:003151	motile ciliu	19/2589	179/23583	0.597661	0.77815	0.733243	Akap14/At
GO_CC_m1	GO:00057	mitochond	2/2589	18/23583	0.603127	0.77815	0.733243	Cox4i2/Uq
GO_CC_m1	GO:001647	vacuolar pr	2/2589	18/23583	0.603127	0.77815	0.733243	Atp6v0c/T
GO_CC_m1	GO:00301	clathrin co	2/2589	18/23583	0.603127	0.77815	0.733243	Ldlrap1/Sy
GO_CC_m1	GO:00080	origin reco	1/2589	8/23583	0.605628	0.77815	0.733243	Orc1
GO_CC_m1	GO:00566	nuclear ori	1/2589	8/23583	0.605628	0.77815	0.733243	Orc1
GO_CC_m1	GO:000567	chromatin	1/2589	8/23583	0.605628	0.77815	0.733243	Bahd1
GO_CC_m1	GO:00568	U6 snRNP	1/2589	8/23583	0.605628	0.77815	0.733243	Lsm5
GO_CC_m1	GO:00058	sodium:po	1/2589	8/23583	0.605628	0.77815	0.733243	Atp1b2
GO_CC_m1	GO:003031	junctional	1/2589	8/23583	0.605628	0.77815	0.733243	Jph3
GO_CC_m1	GO:00309	intraciliary	1/2589	8/23583	0.605628	0.77815	0.733243	Tulp3
GO_CC_m1	GO:00312	lamellipodi	1/2589	8/23583	0.605628	0.77815	0.733243	Antxr1
GO_CC_m1	GO:003131	extrinsic cc	1/2589	8/23583	0.605628	0.77815	0.733243	Usp8
GO_CC_m1	GO:00325	insulin-res	1/2589	8/23583	0.605628	0.77815	0.733243	Dennd4c
GO_CC_m1	GO:00344	BBSome	1/2589	8/23583	0.605628	0.77815	0.733243	Bbs2
GO_CC_m1	GO:00380	G-protein	1/2589	8/23583	0.605628	0.77815	0.733243	Calcr
GO_CC_m1	GO:00452	pyruvate d	1/2589	8/23583	0.605628	0.77815	0.733243	Pdhb
GO_CC_m1	GO:007041	nonhomol	1/2589	8/23583	0.605628	0.77815	0.733243	Prkdc
GO_CC_m1	GO:007154	eukaryotic	1/2589	8/23583	0.605628	0.77815	0.733243	Eif3f
GO_CC_m1	GO:00715	neuronal ri	1/2589	8/23583	0.605628	0.77815	0.733243	Fmr1
GO_CC_m1	GO:009057	RNA polym	1/2589	8/23583	0.605628	0.77815	0.733243	Gtf3c3
GO_CC_m1	GO:009764	G-protein	1/2589	8/23583	0.605628	0.77815	0.733243	Calcr
GO_CC_m1	GO:009884	postsynapt	1/2589	8/23583	0.605628	0.77815	0.733243	Rab5a

GO_CC_m1	GO:190411	axon cytop	1/2589	8/23583	0.605628	0.77815	0.733243	Ranbp1
GO_CC_m1	GO:003258	neuron prc	7/2589	67/23583	0.613234	0.786984	0.741568	Adora1/Ga
GO_CC_m1	GO:009773	non-motile	15/2589	143/23583	0.614085	0.787138	0.741713	Ano2/Drd5
GO_CC_m1	GO:000584	polysome	8/2589	77/23583	0.619758	0.792609	0.746869	Calr/Fmr1/
GO_CC_m1	GO:007016	anchoring	32/2589	303/23583	0.619824	0.792609	0.746869	Aif1l/Anxa2
GO_CC_m1	GO:004665	anchored c	6/2589	58/23583	0.623627	0.796529	0.750562	Car15/Folr
GO_CC_m1	GO:003259	integral co	7/2589	68/23583	0.629181	0.800261	0.754078	Bnip3/Cox1
GO_CC_m1	GO:000989	external sic	52/2589	491/23583	0.630982	0.800261	0.754078	Adam4/An
GO_CC_m1	GO:001634	catenin cor	3/2589	29/23583	0.631315	0.800261	0.754078	Cdh1/Cdh2
GO_CC_m1	GO:000015	protein phc	2/2589	19/23583	0.633184	0.800261	0.754078	Ppp2r1a/Pt
GO_CC_m1	GO:000584	mRNA clea	2/2589	19/23583	0.633184	0.800261	0.754078	Cpsf2/Cpsf
GO_CC_m1	GO:003203	integrator	2/2589	19/23583	0.633184	0.800261	0.754078	Esrrb/Ints8
GO_CC_m1	GO:009072	growth cor	2/2589	19/23583	0.633184	0.800261	0.754078	Fmr1/Pafal
GO_CC_m1	GO:190271	GABA-A re	2/2589	19/23583	0.633184	0.800261	0.754078	Gabra6/Ga
GO_CC_m1	GO:004429	axonal gro	4/2589	39/23583	0.63323	0.800261	0.754078	Aatk/Fmr1/
GO_CC_m1	GO:001646	proton-tra	5/2589	49/23583	0.636577	0.803548	0.757176	2010107E0
GO_CC_m1	GO:004329	apical junc	14/2589	136/23583	0.641593	0.805012	0.758555	Adcyap1r1
GO_CC_m1	GO:000013	Golgi trans	1/2589	9/23583	0.648938	0.805012	0.758555	St6gal1
GO_CC_m1	GO:000050	glycosylph	1/2589	9/23583	0.648938	0.805012	0.758555	Pigyl
GO_CC_m1	GO:000081	Swr1 comp	1/2589	9/23583	0.648938	0.805012	0.758555	Gm3086
GO_CC_m1	GO:000081	ESCRT III c	1/2589	9/23583	0.648938	0.805012	0.758555	Chmp1b
GO_CC_m1	GO:000583	hemoglobi	1/2589	9/23583	0.648938	0.805012	0.758555	Hbb-bs
GO_CC_m1	GO:000586	dynactin c	1/2589	9/23583	0.648938	0.805012	0.758555	Dctn5
GO_CC_m1	GO:000838	IkappaB kir	1/2589	9/23583	0.648938	0.805012	0.758555	Pycard
GO_CC_m1	GO:000854	proteasom	1/2589	9/23583	0.648938	0.805012	0.758555	Psmd8
GO_CC_m1	GO:003129	replication	1/2589	9/23583	0.648938	0.805012	0.758555	Tipin
GO_CC_m1	GO:003317	proton-tra	1/2589	9/23583	0.648938	0.805012	0.758555	Atp6v0c
GO_CC_m1	GO:009751	cardiac my	1/2589	9/23583	0.648938	0.805012	0.758555	Des
GO_CC_m1	GO:009855	cytoplasmi	1/2589	9/23583	0.648938	0.805012	0.758555	Ptpn1
GO_CC_m1	GO:009883	presynaptic	1/2589	9/23583	0.648938	0.805012	0.758555	Rims3
GO_CC_m1	GO:199090	Wnt signal	1/2589	9/23583	0.648938	0.805012	0.758555	Wnt3a
GO_CC_m1	GO:006007	excitatory	4/2589	40/23583	0.653424	0.809645	0.762921	Gria1/Itga3
GO_CC_m1	GO:009722	sperm prin	3/2589	30/23583	0.654583	0.81015	0.763397	Atp2b4/Ift1
GO_CC_m1	GO:000588	cytoplasmi	7/2589	70/23583	0.659931	0.81302	0.766101	Bcas3/Fam
GO_CC_m1	GO:003053	small nucle	7/2589	70/23583	0.659931	0.81302	0.766101	Lsm5/Naa3
GO_CC_m1	GO:009857	intrinsic co	7/2589	70/23583	0.659931	0.81302	0.766101	Bnip3/Cox1
GO_CC_m1	GO:000024	pericentrio	2/2589	20/23583	0.661427	0.81302	0.766101	Nek1/Tubg
GO_CC_m1	GO:003136	anchored c	2/2589	20/23583	0.661427	0.81302	0.766101	Folr2/Hyal2
GO_CC_m1	GO:004527	respiratory	2/2589	20/23583	0.661427	0.81302	0.766101	Cox4i2/Uq
GO_CC_m1	GO:003012	vesicle coa	5/2589	51/23583	0.672092	0.823029	0.775532	Copg2/Ldl
GO_CC_m1	GO:001986	outer mem	19/2589	187/23583	0.674642	0.823029	0.775532	Acsl1/Aifm
GO_CC_m1	GO:003196	organelle c	19/2589	187/23583	0.674642	0.823029	0.775532	Acsl1/Aifm
GO_CC_m1	GO:000032	lytic vacuol	45/2589	433/23583	0.675689	0.823029	0.775532	3110002H1
GO_CC_m1	GO:000576	lysosome	45/2589	433/23583	0.675689	0.823029	0.775532	3110002H1
GO_CC_m1	GO:003283	dendrite cy	3/2589	31/23583	0.676777	0.823029	0.775532	Camk2a/Ca
GO_CC_m1	GO:000588	neurofilam	1/2589	10/23583	0.687493	0.823029	0.775532	Ldlrap1
GO_CC_m1	GO:003005	hemidesmo	1/2589	10/23583	0.687493	0.823029	0.775532	Itga6
GO_CC_m1	GO:003013	clathrin co	1/2589	10/23583	0.687493	0.823029	0.775532	Ldlrap1

GO_CC_m1	GO:00306	multimeric	1/2589	10/23583	0.687493	0.823029	0.775532	Rpp40
GO_CC_m1	GO:003101	ISWI-type	1/2589	10/23583	0.687493	0.823029	0.775532	Baz1a
GO_CC_m1	GO:00310	nuclear po	1/2589	10/23583	0.687493	0.823029	0.775532	Ahctf1
GO_CC_m1	GO:00347	methyloso	1/2589	10/23583	0.687493	0.823029	0.775532	Prmt1
GO_CC_m1	GO:00442	juxtaparan	1/2589	10/23583	0.687493	0.823029	0.775532	Kcna2
GO_CC_m1	GO:00465	intercellula	1/2589	10/23583	0.687493	0.823029	0.775532	Abcb1a
GO_CC_m1	GO:00512	cell tip	1/2589	10/23583	0.687493	0.823029	0.775532	Ezr
GO_CC_m1	GO:00600	kinocilium	1/2589	10/23583	0.687493	0.823029	0.775532	Ift88
GO_CC_m1	GO:00977	9+2 non-m	1/2589	10/23583	0.687493	0.823029	0.775532	Ift88
GO_CC_m1	GO:00042	autophago	2/2589	21/23583	0.687893	0.823029	0.775532	Rpn2/Vmp
GO_CC_m1	GO:00056	anaphase-	2/2589	21/23583	0.687893	0.823029	0.775532	Cdc20/Cdc
GO_CC_m1	GO:00056	U2 snRNP	2/2589	21/23583	0.687893	0.823029	0.775532	Naa38/Snr
GO_CC_m1	GO:00351	exon-exon	2/2589	21/23583	0.687893	0.823029	0.775532	Magohb/R
GO_CC_m1	GO:009734	INO80-typ	2/2589	21/23583	0.687893	0.823029	0.775532	Gm3086/N
GO_CC_m1	GO:190271	GABA rece	2/2589	21/23583	0.687893	0.823029	0.775532	Gabra6/Ga
GO_CC_m1	GO:00056	spliceosom	20/2589	199/23583	0.696053	0.831305	0.783331	Cactin/Dd
GO_CC_m1	GO:00007	condensed	3/2589	32/23583	0.697896	0.831305	0.783331	Ahctf1/Cer
GO_CC_m1	GO:00058	striated mu	3/2589	32/23583	0.697896	0.831305	0.783331	Acta1/Tmo
GO_CC_m1	GO:00700	cytochrom	3/2589	32/23583	0.697896	0.831305	0.783331	Cox15/Cox
GO_CC_m1	GO:000591	cell-cell ad	12/2589	122/23583	0.69944	0.832225	0.784198	Anxa2/Cad
GO_CC_m1	GO:00083	ionotropic	5/2589	53/23583	0.705232	0.833102	0.785024	Cacng5/Ca
GO_CC_m1	GO:00058	intermedia	12/2589	123/23583	0.710116	0.833102	0.785024	Des/Fbf1/
GO_CC_m1	GO:00056	U1 snRNP	2/2589	22/23583	0.712631	0.833102	0.785024	Naa38/Snr
GO_CC_m1	GO:00057	Golgi medi	2/2589	22/23583	0.712631	0.833102	0.785024	H2-Q2/St6
GO_CC_m1	GO:00306	endocytic	2/2589	22/23583	0.712631	0.833102	0.785024	Anxa3/Ldlr
GO_CC_m1	GO:007101	prespliceos	2/2589	22/23583	0.712631	0.833102	0.785024	Naa38/Snr
GO_CC_m1	GO:00001	nucleotide	1/2589	11/23583	0.721816	0.833102	0.785024	Xrcc1
GO_CC_m1	GO:00007	telomere c	1/2589	11/23583	0.721816	0.833102	0.785024	Terb1
GO_CC_m1	GO:00007	nuclear tel	1/2589	11/23583	0.721816	0.833102	0.785024	Terb1
GO_CC_m1	GO:000217	manchette	1/2589	11/23583	0.721816	0.833102	0.785024	1110017D
GO_CC_m1	GO:00055	fibrillar coll	1/2589	11/23583	0.721816	0.833102	0.785024	Col5a1
GO_CC_m1	GO:00057	mitochond	1/2589	11/23583	0.721816	0.833102	0.785024	Uqcrc2
GO_CC_m1	GO:00057	signal reco	1/2589	11/23583	0.721816	0.833102	0.785024	Rp9
GO_CC_m1	GO:00082	oligosacch	1/2589	11/23583	0.721816	0.833102	0.785024	Rpn2
GO_CC_m1	GO:001644	RISC comp	1/2589	11/23583	0.721816	0.833102	0.785024	Eif4e
GO_CC_m1	GO:00308	HOPS com	1/2589	11/23583	0.721816	0.833102	0.785024	Vps18
GO_CC_m1	GO:00313	RNAi effec	1/2589	11/23583	0.721816	0.833102	0.785024	Eif4e
GO_CC_m1	GO:00325	dendritic s	1/2589	11/23583	0.721816	0.833102	0.785024	Gria1
GO_CC_m1	GO:00327	SMN comp	1/2589	11/23583	0.721816	0.833102	0.785024	Fmr1
GO_CC_m1	GO:00361	inner dyne	1/2589	11/23583	0.721816	0.833102	0.785024	Dnah1
GO_CC_m1	GO:00361	outer dyne	1/2589	11/23583	0.721816	0.833102	0.785024	Dnaic2
GO_CC_m1	GO:004262	photorece	1/2589	11/23583	0.721816	0.833102	0.785024	Prcd
GO_CC_m1	GO:007057	RISC-loadi	1/2589	11/23583	0.721816	0.833102	0.785024	Mir27a
GO_CC_m1	GO:00708	cell body fi	1/2589	11/23583	0.721816	0.833102	0.785024	Cadm1
GO_CC_m1	GO:00710	U2-type ca	1/2589	11/23583	0.721816	0.833102	0.785024	Prpf19
GO_CC_m1	GO:00726	meiotic spi	1/2589	11/23583	0.721816	0.833102	0.785024	Bora
GO_CC_m1	GO:009864	banded co	1/2589	11/23583	0.721816	0.833102	0.785024	Col5a1
GO_CC_m1	GO:19909	beta-caten	1/2589	11/23583	0.721816	0.833102	0.785024	Pygo2

GO_CC_m1	GO:00312	leading ed	14/2589	145/23583	0.73365	0.845802	0.796991	Adora1/An
GO_CC_m1	GO:00058	axonemal	2/2589	23/23583	0.735701	0.845802	0.796991	Dnah1/Dn
GO_CC_m1	GO:00312	intrinsic co	2/2589	23/23583	0.735701	0.845802	0.796991	Folr2/Hyal
GO_CC_m1	GO:00988	neurotrans	5/2589	55/23583	0.735957	0.845802	0.796991	Cacng5/Ca
GO_CC_m1	GO:00363	myofilame	3/2589	34/23583	0.736952	0.846043	0.797218	Acta1/Tmo
GO_CC_m1	GO:00007	nucleosom	8/2589	86/23583	0.740643	0.846713	0.79785	Cenpa/Gly
GO_CC_m1	GO:00312	cell project	28/2589	282/23583	0.741819	0.846713	0.79785	Abcb1a/Ac
GO_CC_m1	GO:00058	trans-Golg	18/2589	186/23583	0.748989	0.846713	0.79785	Ap4e1/Atp
GO_CC_m1	GO:00313	intrinsic co	18/2589	186/23583	0.748989	0.846713	0.79785	Acer3/Bnip
GO_CC_m1	GO:00986	chromoso	29/2589	293/23583	0.750726	0.846713	0.79785	Ahctf1/Blm
GO_CC_m1	GO:00003	transcripti	1/2589	12/23583	0.75237	0.846713	0.79785	Sarnp
GO_CC_m1	GO:00058	chaperoni	1/2589	12/23583	0.75237	0.846713	0.79785	Cct3
GO_CC_m1	GO:00082	cohesin co	1/2589	12/23583	0.75237	0.846713	0.79785	Wapl
GO_CC_m1	GO:00171	NMDA sel	1/2589	12/23583	0.75237	0.846713	0.79785	Grin2b
GO_CC_m1	GO:00301	AP-2 adap	1/2589	12/23583	0.75237	0.846713	0.79785	Ldlrap1
GO_CC_m1	GO:00301	AP-3 adap	1/2589	12/23583	0.75237	0.846713	0.79785	Vps18
GO_CC_m1	GO:00306	ribonuclea	1/2589	12/23583	0.75237	0.846713	0.79785	Rpp40
GO_CC_m1	GO:00340	phagopho	1/2589	12/23583	0.75237	0.846713	0.79785	Wipi2
GO_CC_m1	GO:00361	CatSper co	1/2589	12/23583	0.75237	0.846713	0.79785	Catsper3
GO_CC_m1	GO:00426	MHC class	1/2589	12/23583	0.75237	0.846713	0.79785	H2-Q2
GO_CC_m1	GO:00452	respiratory	1/2589	12/23583	0.75237	0.846713	0.79785	Uqcrc2
GO_CC_m1	GO:00715	npBAF con	1/2589	12/23583	0.75237	0.846713	0.79785	Smarce1
GO_CC_m1	GO:00975	sperm plas	1/2589	12/23583	0.75237	0.846713	0.79785	Adam4
GO_CC_m1	GO:00017	immunolo	3/2589	35/23583	0.754925	0.846713	0.79785	Dusp3/Ezr/
GO_CC_m1	GO:00444	cytosolic p	29/2589	294/23583	0.757077	0.846713	0.79785	Adcy4/Blo
GO_CC_m1	GO:00308	rough end	2/2589	24/23583	0.757172	0.846713	0.79785	Bcap31/Rp
GO_CC_m1	GO:00325	trans-Golg	2/2589	24/23583	0.757172	0.846713	0.79785	Atp7b/Bok
GO_CC_m1	GO:00331	proton-tra	2/2589	24/23583	0.757172	0.846713	0.79785	Atp6v0c/T
GO_CC_m1	GO:00331	proton-tra	2/2589	24/23583	0.757172	0.846713	0.79785	Atp5o/Atp
GO_CC_m1	GO:00343	high-densi	2/2589	24/23583	0.757172	0.846713	0.79785	Pltp/Saa2
GO_CC_m1	GO:00431	dendritic s	6/2589	67/23583	0.758418	0.847228	0.798335	Fmr1/Gria1
GO_CC_m1	GO:00059	bicellular t	11/2589	119/23583	0.769513	0.85404	0.804754	Adcyap1r1
GO_CC_m1	GO:00057	mitochond	16/2589	169/23583	0.770424	0.85404	0.804754	Acsl1/Aifm
GO_CC_m1	GO:00329	protein-D	17/2589	179/23583	0.77127	0.85404	0.804754	Terb1/Cen
GO_CC_m1	GO:00320	small-subu	3/2589	36/23583	0.771895	0.85404	0.804754	Nop56/Pd
GO_CC_m1	GO:00343	plasma lip	3/2589	36/23583	0.771895	0.85404	0.804754	Pltp/Saa2/
GO_CC_m1	GO:19907	lipoprotein	3/2589	36/23583	0.771895	0.85404	0.804754	Pltp/Saa2/
GO_CC_m1	GO:00007	chromoso	18/2589	189/23583	0.772249	0.85404	0.804754	Ahctf1/Cer
GO_CC_m1	GO:00313	integral co	2/2589	25/23583	0.777116	0.85404	0.804754	Bnip3/Rho
GO_CC_m1	GO:00704	SAGA-typ	2/2589	25/23583	0.777116	0.85404	0.804754	Kat2a/Taf9
GO_CC_m1	GO:00007	kinetocho	12/2589	130/23583	0.778032	0.85404	0.804754	Ahctf1/Cer
GO_CC_m1	GO:00001	SAGA com	1/2589	13/23583	0.779569	0.85404	0.804754	Taf9
GO_CC_m1	GO:00002	mitochond	1/2589	13/23583	0.779569	0.85404	0.804754	Atp5o
GO_CC_m1	GO:00015	voltage-ga	1/2589	13/23583	0.779569	0.85404	0.804754	Scn4a
GO_CC_m1	GO:00021	zona pellu	1/2589	13/23583	0.779569	0.85404	0.804754	Cct3
GO_CC_m1	GO:00165	SWI/SNF c	1/2589	13/23583	0.779569	0.85404	0.804754	Smarce1
GO_CC_m1	GO:00171	aminoacyl-	1/2589	13/23583	0.779569	0.85404	0.804754	Kars
GO_CC_m1	GO:00301	clathrin co	1/2589	13/23583	0.779569	0.85404	0.804754	Ldlrap1

GO_CC_m1	GO:006501	extracellula	1/2589	13/23583	0.779569	0.85404	0.804754	Alpl
GO_CC_m1	GO:010103	chaperone	1/2589	13/23583	0.779569	0.85404	0.804754	Cct3
GO_CC_m1	GO:000077	condensed	4/2589	48/23583	0.78749	0.861842	0.812106	Ahctf1/Cen
GO_CC_m1	GO:012011	Sm-like pr	7/2589	80/23583	0.788885	0.862493	0.812719	Lsm5/Naa3
GO_CC_m1	GO:003130	integral co	16/2589	172/23583	0.79345	0.865611	0.815657	Acer3/Bnip
GO_CC_m1	GO:003130	intrinsic co	2/2589	26/23583	0.79561	0.865611	0.815657	Bnip3/Rho
GO_CC_m1	GO:007016	occluding j	11/2589	122/23583	0.796599	0.865611	0.815657	Adcyap1r1
GO_CC_m1	GO:004511	intermedia	15/2589	163/23583	0.800974	0.865611	0.815657	Bcas3/Ddx
GO_CC_m1	GO:003299	protein-lip	3/2589	38/23583	0.80294	0.865611	0.815657	Pltp/Saa2/
GO_CC_m1	GO:000097	Prp19 com	1/2589	14/23583	0.803782	0.865611	0.815657	Prpf19
GO_CC_m1	GO:003000	TRAPP con	1/2589	14/23583	0.803782	0.865611	0.815657	Trappc9
GO_CC_m1	GO:003012	COPI vesicl	1/2589	14/23583	0.803782	0.865611	0.815657	Copg2
GO_CC_m1	GO:003066	clathrin-co	1/2589	14/23583	0.803782	0.865611	0.815657	Ldlrap1
GO_CC_m1	GO:003317	proton-tra	1/2589	14/23583	0.803782	0.865611	0.815657	Atp5a1
GO_CC_m1	GO:003525	ciliary rootl	1/2589	14/23583	0.803782	0.865611	0.815657	Klc3
GO_CC_m1	GO:007093	contractile	1/2589	14/23583	0.803782	0.865611	0.815657	Prc1
GO_CC_m1	GO:007101	catalytic st	1/2589	14/23583	0.803782	0.865611	0.815657	Prpf19
GO_CC_m1	GO:007156	nBAF comp	1/2589	14/23583	0.803782	0.865611	0.815657	Smarce1
GO_CC_m1	GO:199002	mitotic spi	1/2589	14/23583	0.803782	0.865611	0.815657	Olfr13
GO_CC_m1	GO:007100	U2-type ca	2/2589	27/23583	0.812731	0.874375	0.823916	Ppie/Prpf1
GO_CC_m1	GO:003131	extrinsic co	3/2589	39/23583	0.817083	0.878181	0.827501	Plekhf2/Us
GO_CC_m1	GO:004481	DNA packa	8/2589	94/23583	0.823312	0.883995	0.83298	Cenpa/Gly
GO_CC_m1	GO:003108	BLOC-1 co	1/2589	15/23583	0.825336	0.884406	0.833367	Bloc1s5
GO_CC_m1	GO:004526	proton-tra	1/2589	15/23583	0.825336	0.884406	0.833367	Atp5o
GO_CC_m1	GO:001660	PML body	6/2589	73/23583	0.826241	0.884497	0.833453	Atr/Blm/N
GO_CC_m1	GO:000573	small nucle	2/2589	28/23583	0.828558	0.886097	0.834961	Nop10/No
GO_CC_m1	GO:000591	cell-cell ju	46/2589	473/23583	0.829877	0.886257	0.835112	Abcb1a/Ac
GO_CC_m1	GO:009973	cell cortex	3/2589	40/23583	0.830352	0.886257	0.835112	Epb41/Gna
GO_CC_m1	GO:190356	extracellula	8/2589	95/23583	0.832036	0.887176	0.835977	Acy1/Anxa
GO_CC_m1	GO:009856	intrinsic co	2/2589	29/23583	0.843168	0.895178	0.843518	Rab27b/Ra
GO_CC_m1	GO:004323	extracellula	9/2589	107/23583	0.843557	0.895178	0.843518	Acy1/Alpl/
GO_CC_m1	GO:000585	eukaryotic	1/2589	16/23583	0.844523	0.895178	0.843518	Eif3f
GO_CC_m1	GO:000585	muscle my	1/2589	16/23583	0.844523	0.895178	0.843518	Myh7
GO_CC_m1	GO:001036	chromocen	1/2589	16/23583	0.844523	0.895178	0.843518	Fmr1
GO_CC_m1	GO:003066	COPI-coat	1/2589	16/23583	0.844523	0.895178	0.843518	Copg2
GO_CC_m1	GO:004439	ribosomal	21/2589	231/23583	0.848643	0.898661	0.8468	Fau/Mrpl1
GO_CC_m1	GO:004278	polysomal	2/2589	30/23583	0.856639	0.906238	0.85394	Pnpt1/Rps
GO_CC_m1	GO:000153	cornified e	4/2589	54/23583	0.857978	0.906764	0.854436	Cst6/Lce3c
GO_CC_m1	GO:001990	nuclear cyc	1/2589	17/23583	0.861603	0.907926	0.85553	Cdk7
GO_CC_m1	GO:003364	host intrac	1/2589	17/23583	0.861603	0.907926	0.85553	Fmr1
GO_CC_m1	GO:004365	intracellula	1/2589	17/23583	0.861603	0.907926	0.85553	Fmr1
GO_CC_m1	GO:003167	A band	3/2589	43/23583	0.865297	0.910928	0.858359	Kat2b/Rpl7
GO_CC_m1	GO:003066	clathrin-co	2/2589	31/23583	0.869043	0.913088	0.860395	Ldlrap1/Ra
GO_CC_m1	GO:005123	spindle mic	2/2589	31/23583	0.869043	0.913088	0.860395	Olfr13/Rac
GO_CC_m1	GO:007006	extracellula	7/2589	89/23583	0.870005	0.913208	0.860508	Acy1/Anxa
GO_CC_m1	GO:009880	plasma me	15/2589	175/23583	0.876176	0.91589	0.863035	Cacng5/Ca
GO_CC_m1	GO:002262	cytosolic s	4/2589	56/23583	0.876558	0.91589	0.863035	Fau/Mrps9
GO_CC_m1	GO:000189	phagocytic	1/2589	18/23583	0.876808	0.91589	0.863035	Abl2

GO_CC_m1	GO:00343	very-low-	1/2589	18/23583	0.876808	0.91589	0.863035	Vldlr
GO_CC_m1	GO:00343	triglycerid	1/2589	18/23583	0.876808	0.91589	0.863035	Vldlr
GO_CC_m1	GO:00001	exocyst	1/2589	19/23583	0.890343	0.925544	0.872132	Exoc3l2
GO_CC_m1	GO:00189	host	1/2589	19/23583	0.890343	0.925544	0.872132	Fmr1
GO_CC_m1	GO:00324	stereociliu	1/2589	19/23583	0.890343	0.925544	0.872132	Myo3a
GO_CC_m1	GO:00336	host cell p	1/2589	19/23583	0.890343	0.925544	0.872132	Fmr1
GO_CC_m1	GO:00436	host cell	1/2589	19/23583	0.890343	0.925544	0.872132	Fmr1
GO_CC_m1	GO:00310	BLOC com	1/2589	20/23583	0.902391	0.934464	0.880537	Bloc1s5
GO_CC_m1	GO:00352	NuA4 hist	1/2589	20/23583	0.902391	0.934464	0.880537	Gm3086
GO_CC_m1	GO:00430	costamere	1/2589	20/23583	0.902391	0.934464	0.880537	Ahnak2
GO_CC_m1	GO:00431	H4/H2A hi	1/2589	20/23583	0.902391	0.934464	0.880537	Gm3086
GO_CC_m1	GO:00159	large ribos	12/2589	149/23583	0.903872	0.9351	0.881136	Mrpl10/Mr
GO_CC_m1	GO:00358	site of dou	2/2589	35/23583	0.909388	0.939196	0.884996	Aplf/Prpf1
GO_CC_m1	GO:003011	AP-type m	3/2589	48/23583	0.909574	0.939196	0.884996	Ap4e1/Ldl
GO_CC_m1	GO:00163	apicolatera	1/2589	21/23583	0.913116	0.941951	0.887592	Mpdz
GO_CC_m1	GO:00059	clathrin-co	4/2589	61/23583	0.914044	0.942007	0.887645	Ap1s2/Ldl
GO_CC_m1	GO:004257	immunogl	11/2589	141/23583	0.916362	0.942902	0.888488	Ighv1-15/I
GO_CC_m1	GO:003011	clathrin co	3/2589	49/23583	0.916661	0.942902	0.888488	Igf2r/Ldlra
GO_CC_m1	GO:00007	condensed	15/2589	185/23583	0.919899	0.94533	0.890776	Blm/Cenpa
GO_CC_m1	GO:00017	photorece	5/2589	76/23583	0.930326	0.95049	0.895638	Prcd/Guca
GO_CC_m1	GO:00301	clathrin ve	1/2589	23/23583	0.931161	0.95049	0.895638	Ldlrap1
GO_CC_m1	GO:00301	COPI-coat	1/2589	23/23583	0.931161	0.95049	0.895638	Copg2
GO_CC_m1	GO:00347	sodium ch	1/2589	23/23583	0.931161	0.95049	0.895638	Scn4a
GO_CC_m1	GO:003017	integral co	2/2589	38/23583	0.931655	0.95049	0.895638	Acer3/Yif1
GO_CC_m1	GO:00907	site of DN	2/2589	38/23583	0.931655	0.95049	0.895638	Aplf/Prpf1
GO_CC_m1	GO:00725	blood micr	12/2589	156/23583	0.931966	0.95049	0.895638	Hspa1a/Ig
GO_CC_m1	GO:001981	immunogl	11/2589	145/23583	0.931974	0.95049	0.895638	Ighv1-15/I
GO_CC_m1	GO:00056	U2-type s	4/2589	65/23583	0.936335	0.953766	0.898725	Naa38/Ppi
GO_CC_m1	GO:00007	nuclear nu	2/2589	39/23583	0.937848	0.953766	0.898725	Cenpa/Mp
GO_CC_m1	GO:00314	M band	1/2589	24/23583	0.938725	0.953766	0.898725	S100a1
GO_CC_m1	GO:00364	ESCRT con	1/2589	24/23583	0.938725	0.953766	0.898725	Chmp1b
GO_CC_m1	GO:003122	intrinsic co	2/2589	40/23583	0.943505	0.956618	0.901412	Acer3/Yif1
GO_CC_m1	GO:004421	other orga	1/2589	25/23583	0.945459	0.956618	0.901412	Fmr1
GO_CC_m1	GO:004421	other orga	1/2589	25/23583	0.945459	0.956618	0.901412	Fmr1
GO_CC_m1	GO:004421	other orga	1/2589	25/23583	0.945459	0.956618	0.901412	Fmr1
GO_CC_m1	GO:00007	synaptone	9/2589	127/23583	0.946856	0.956618	0.901412	Blm/Fkbp6
GO_CC_m1	GO:00990	synaptone	9/2589	127/23583	0.946856	0.956618	0.901412	Blm/Fkbp6
GO_CC_m1	GO:00007	condensed	19/2589	238/23583	0.94933	0.958219	0.902921	Ahctf1/Blm
GO_CC_m1	GO:00056	U12-type	1/2589	26/23583	0.951453	0.959464	0.904094	Zrsr2
GO_CC_m1	GO:00058	cytoplasm	1/2589	27/23583	0.956789	0.963725	0.908109	Tpr
GO_CC_m1	GO:00302	dynein con	3/2589	57/23583	0.957467	0.963725	0.908109	Dnah1/Dn
GO_CC_m1	GO:00226	cytosolic ri	11/2589	157/23583	0.964697	0.970097	0.914113	Fau/Mrps9
GO_CC_m1	GO:00301	clathrin ad	1/2589	29/23583	0.965765	0.970266	0.914272	Ldlrap1
GO_CC_m1	GO:00325	ruffle mem	3/2589	66/23583	0.980731	0.984384	0.927576	Cdkl5/Ptpr
GO_CC_m1	GO:007101	precatalyti	1/2589	35/23583	0.982978	0.985721	0.928836	Prpf38a
GO_CC_m1	GO:00550	recycling e	1/2589	36/23583	0.984849	0.98668	0.929739	Bok
GO_CC_m1	GO:00226	cytosolic la	4/2589	94/23583	0.994158	0.995081	0.937655	Rpl23/Rpl3
GO_CC_m1	GO:00008	lateral elen	4/2589	104/23583	0.997595	0.997595	0.940025	Blm/Sycp1

GO_CC_m2	GO:004878	presynapti	3/470	10/23583	0.00085	0.459187	0.446655	Grm7/Stxb
GO_CC_m2	GO:00715€	nBAF comp	3/470	14/23583	0.002431	0.506977	0.493141	Actl6b/Sma
GO_CC_m2	GO:00304S	midbody	8/470	132/23583	0.005033	0.506977	0.493141	Alkbh4/Au
GO_CC_m2	GO:00018S	phagocytic	3/470	18/23583	0.005136	0.506977	0.493141	Rack1/Myc
GO_CC_m2	GO:00057S	Golgi lume	2/470	6/23583	0.005638	0.506977	0.493141	Agrp/Galnt
GO_CC_m2	GO:00321£	cleavage fu	4/470	40/23583	0.008076	0.506977	0.493141	Cit/Ect2/Ra
GO_CC_m2	GO:00321£	cell divisior	5/470	69/23583	0.012176	0.506977	0.493141	Cit/Ect2/Ra
GO_CC_m2	GO:000574	mitochond	2/470	10/23583	0.016043	0.506977	0.493141	Pink1/Tom
GO_CC_m2	GO:00166C	nuclear spe	12/470	302/23583	0.018683	0.506977	0.493141	Cdc5l/Dyrk
GO_CC_m2	GO:00056E	U4 snRNP	2/470	11/23583	0.019353	0.506977	0.493141	Prpf31/Snr
GO_CC_m2	GO:00321£	cell divisior	4/470	52/23583	0.019867	0.506977	0.493141	Cit/Ect2/Ra
GO_CC_m2	GO:00055E	collagen ty	1/470	1/23583	0.01993	0.506977	0.493141	Col2a1
GO_CC_m2	GO:00057З	nucleolus c	1/470	1/23583	0.01993	0.506977	0.493141	Sirt7
GO_CC_m2	GO:003087	nucleolar c	1/470	1/23583	0.01993	0.506977	0.493141	Sirt7
GO_CC_m2	GO:004202	interleukin	1/470	1/23583	0.01993	0.506977	0.493141	Il12rb1
GO_CC_m2	GO:00704З	Shc-EGFR (	1/470	1/23583	0.01993	0.506977	0.493141	Shc1
GO_CC_m2	GO:000567	holo TFIIH	2/470	12/23583	0.022921	0.506977	0.493141	Gtf2h1/Psn
GO_CC_m2	GO:00453З	phagocytic	5/470	83/23583	0.025151	0.506977	0.493141	Cybb/Rab1
GO_CC_m2	GO:001651	SWI/SNF co	2/470	13/23583	0.026735	0.506977	0.493141	Actl6b/Sma
GO_CC_m2	GO:00442З	ER-mitoch	2/470	13/23583	0.026735	0.506977	0.493141	Acsl4/Tom
GO_CC_m2	GO:00987S	outer mito	2/470	14/23583	0.030786	0.506977	0.493141	Pink1/Tom
GO_CC_m2	GO:00150З	Cajal body	3/470	36/23583	0.034553	0.506977	0.493141	Ell/Hnrnpa
GO_CC_m2	GO:00056S	U4atac snR	1/470	2/23583	0.039463	0.506977	0.493141	Prpf31
GO_CC_m2	GO:000584	nuclear cap	1/470	2/23583	0.039463	0.506977	0.493141	Ncbp2
GO_CC_m2	GO:00165E	RSC-type (	1/470	2/23583	0.039463	0.506977	0.493141	Suz12
GO_CC_m2	GO:001717	glucosidas	1/470	2/23583	0.039463	0.506977	0.493141	Prkcsh
GO_CC_m2	GO:00365C	Derlin-1-V	1/470	2/23583	0.039463	0.506977	0.493141	Derl1
GO_CC_m2	GO:00425€	RNA nucle	1/470	2/23583	0.039463	0.506977	0.493141	Ran
GO_CC_m2	GO:00710C	U2-type pr	1/470	2/23583	0.039463	0.506977	0.493141	Prpf31
GO_CC_m2	GO:00725З	interleukin	1/470	2/23583	0.039463	0.506977	0.493141	Il12rb1
GO_CC_m2	GO:009734	Rix1 compl	1/470	2/23583	0.039463	0.506977	0.493141	Wdr18
GO_CC_m2	GO:19015E	dendritic n	1/470	2/23583	0.039463	0.506977	0.493141	Clip2
GO_CC_m2	GO:19905E	ATF4-CREE	1/470	2/23583	0.039463	0.506977	0.493141	Atf4
GO_CC_m2	GO:19905S	ATF1-ATF4	1/470	2/23583	0.039463	0.506977	0.493141	Atf4
GO_CC_m2	GO:199061	CHOP-ATF	1/470	2/23583	0.039463	0.506977	0.493141	Atf4
GO_CC_m2	GO:19906З	IRE1-RACK	1/470	2/23583	0.039463	0.506977	0.493141	Rack1
GO_CC_m2	GO:00347C	methyltran	5/470	94/23583	0.039938	0.506977	0.493141	Mettl14/Pr
GO_CC_m2	GO:004367	axon termi	8/470	194/23583	0.041206	0.506977	0.493141	Cad/Cplx4/
GO_CC_m2	GO:001601	dystrophin	2/470	17/23583	0.044247	0.506977	0.493141	Magee1/Sg
GO_CC_m2	GO:00906€	glycoprote	2/470	17/23583	0.044247	0.506977	0.493141	Magee1/Sg
GO_CC_m2	GO:00487E	presynapti	3/470	40/23583	0.045131	0.506977	0.493141	Grm7/Stxb
GO_CC_m2	GO:000577	peroxisom	3/470	42/23583	0.050953	0.506977	0.493141	Mavs/Pex5
GO_CC_m2	GO:00319C	microbody	3/470	42/23583	0.050953	0.506977	0.493141	Mavs/Pex5
GO_CC_m2	GO:00442З	organelle r	2/470	19/23583	0.054209	0.506977	0.493141	Acsl4/Tom
GO_CC_m2	GO:00706C	SWI/SNF su	4/470	72/23583	0.055612	0.506977	0.493141	Actl6b/Sma
GO_CC_m2	GO:00002Z	vacuolar pr	1/470	3/23583	0.058608	0.506977	0.493141	Atp6v1h
GO_CC_m2	GO:00056£	nuclear pre	1/470	3/23583	0.058608	0.506977	0.493141	Wdr18
GO_CC_m2	GO:00093З	glycerol-3-	1/470	3/23583	0.058608	0.506977	0.493141	Gpd1l

GO_CC_m2	GO:003107	nucleocyto	1/470	3/23583	0.058608	0.506977	0.493141	Ran
GO_CC_m2	GO:003228	symmetric	1/470	3/23583	0.058608	0.506977	0.493141	Penk
GO_CC_m2	GO:003318	CAF-1 com	1/470	3/23583	0.058608	0.506977	0.493141	Chaf1a
GO_CC_m2	GO:003638	pre-replica	1/470	3/23583	0.058608	0.506977	0.493141	Wdr18
GO_CC_m2	GO:003648	CHOP-C/E	1/470	3/23583	0.058608	0.506977	0.493141	Cebpa
GO_CC_m2	GO:009714	centralspin	1/470	3/23583	0.058608	0.506977	0.493141	Ect2
GO_CC_m2	GO:190293	inward rect	1/470	3/23583	0.058608	0.506977	0.493141	Kcnh2
GO_CC_m2	GO:199003	Lewy body	1/470	3/23583	0.058608	0.506977	0.493141	Atf4
GO_CC_m2	GO:009738	glial cell pr	2/470	20/23583	0.059458	0.506977	0.493141	Glul/Pink1
GO_CC_m2	GO:004430	neuron pro	8/470	211/23583	0.061507	0.506977	0.493141	Cad/Cplx4/
GO_CC_m2	GO:015003	distal axon	12/470	364/23583	0.062243	0.506977	0.493141	Agrn/Auts2
GO_CC_m2	GO:000577	vacuolar m	7/470	177/23583	0.064749	0.506977	0.493141	Atp6v1h/C
GO_CC_m2	GO:000167	male germ	2/470	21/23583	0.064874	0.506977	0.493141	H2afx/Ran
GO_CC_m2	GO:001623	inclusion b	4/470	76/23583	0.065279	0.506977	0.493141	Atf4/Pabp
GO_CC_m2	GO:003299	protein-DN	7/470	179/23583	0.067886	0.506977	0.493141	Cdc5l/H2a
GO_CC_m2	GO:000577	late endoso	7/470	180/23583	0.069488	0.506977	0.493141	Bace1/Chm
GO_CC_m2	GO:004273	presynaptic	4/470	78/23583	0.070419	0.506977	0.493141	Grm7/Snp
GO_CC_m2	GO:000568	U5 snRNP	2/470	23/23583	0.07617	0.506977	0.493141	Dcaf4/Snrp
GO_CC_m2	GO:000932	phenylalan	1/470	4/23583	0.077372	0.506977	0.493141	Farsa
GO_CC_m2	GO:001707	intracellula	1/470	4/23583	0.077372	0.506977	0.493141	Pex5l
GO_CC_m2	GO:003518	Rb-E2F cor	1/470	4/23583	0.077372	0.506977	0.493141	Cebpa
GO_CC_m2	GO:003536	histone loc	1/470	4/23583	0.077372	0.506977	0.493141	Ell
GO_CC_m2	GO:003639	RNA N6-m	1/470	4/23583	0.077372	0.506977	0.493141	Mettl14
GO_CC_m2	GO:007044	elongin cor	1/470	4/23583	0.077372	0.506977	0.493141	Eloa
GO_CC_m2	GO:007195	elastic fiber	1/470	4/23583	0.077372	0.506977	0.493141	Mfap4
GO_CC_m2	GO:009745	GAIT comp	1/470	4/23583	0.077372	0.506977	0.493141	Eprs
GO_CC_m2	GO:009883	postsynapt	1/470	4/23583	0.077372	0.506977	0.493141	Rab11a
GO_CC_m2	GO:004445	microtubul	6/470	149/23583	0.078218	0.506977	0.493141	2700049A0
GO_CC_m2	GO:001986	outer mem	7/470	187/23583	0.081332	0.506977	0.493141	Acsl4/Mavs
GO_CC_m2	GO:003196	organelle o	7/470	187/23583	0.081332	0.506977	0.493141	Acsl4/Mavs
GO_CC_m2	GO:004443	vacuolar pa	7/470	187/23583	0.081332	0.506977	0.493141	Atp6v1h/C
GO_CC_m2	GO:003645	ESCRT com	2/470	24/23583	0.082034	0.506977	0.493141	Chmp3/Tsg
GO_CC_m2	GO:009744	apical den	2/470	24/23583	0.082034	0.506977	0.493141	Ptk2b/Slc7a
GO_CC_m2	GO:000807	voltage-ga	4/470	84/23583	0.087035	0.506977	0.493141	Kcne4/Kcn
GO_CC_m2	GO:000576	lysosomal	5/470	118/23583	0.087384	0.506977	0.493141	Atp6v1h/C
GO_CC_m2	GO:009885	lytic vacuol	5/470	118/23583	0.087384	0.506977	0.493141	Atp6v1h/C
GO_CC_m2	GO:003130	integral co	2/470	25/23583	0.088031	0.506977	0.493141	Pink1/Tom
GO_CC_m2	GO:003280	carboxy-te	2/470	25/23583	0.088031	0.506977	0.493141	Gtf2h1/Psm
GO_CC_m2	GO:004319	terminal bo	5/470	120/23583	0.092271	0.506977	0.493141	Cad/Cplx4/
GO_CC_m2	GO:000802	transcriptio	3/470	54/23583	0.092773	0.506977	0.493141	Aff3/Ell/Elo
GO_CC_m2	GO:190494	ATPase cor	4/470	86/23583	0.09296	0.506977	0.493141	Actl6b/Sma
GO_CC_m2	GO:000078	condensed	2/470	26/23583	0.094155	0.506977	0.493141	Aurkb/Ss18
GO_CC_m2	GO:003130	intrinsic co	2/470	26/23583	0.094155	0.506977	0.493141	Pink1/Tom
GO_CC_m2	GO:004654	U4/U6 x U5	2/470	26/23583	0.094155	0.506977	0.493141	Prpf31/Snr
GO_CC_m2	GO:001562	actin cytosk	14/470	474/23583	0.094262	0.506977	0.493141	Acaca/Auts
GO_CC_m2	GO:000568	U7 snRNP	1/470	5/23583	0.095762	0.506977	0.493141	Snrpb
GO_CC_m2	GO:000592	muscle ten	1/470	5/23583	0.095762	0.506977	0.493141	Nrap
GO_CC_m2	GO:003048	smooth mu	1/470	5/23583	0.095762	0.506977	0.493141	Myh11

GO_CC_m2	GO:003213	chromosor	1/470	5/23583	0.095762	0.506977	0.493141	Aurkb
GO_CC_m2	GO:003350	HULC com	1/470	5/23583	0.095762	0.506977	0.493141	Rnf20
GO_CC_m2	GO:003355	rDNA hete	1/470	5/23583	0.095762	0.506977	0.493141	Rrp8
GO_CC_m2	GO:003597	transcriptic	1/470	5/23583	0.095762	0.506977	0.493141	Jund
GO_CC_m2	GO:004529	mRNA edit	1/470	5/23583	0.095762	0.506977	0.493141	Mettl14
GO_CC_m2	GO:014000	KICSTOR c	1/470	5/23583	0.095762	0.506977	0.493141	Itfg2
GO_CC_m2	GO:009057	RNA polym	6/470	158/23583	0.096905	0.508043	0.494179	Atf4/Cebpa
GO_CC_m2	GO:007100	U2-type ca	2/470	27/23583	0.100397	0.518338	0.504192	Cdc5l/Snrp
GO_CC_m2	GO:002262	cytosolic sr	3/470	56/23583	0.100788	0.518338	0.504192	Rack1/Mrp
GO_CC_m2	GO:004443	microbody	3/470	57/23583	0.104896	0.525172	0.51084	Mavs/Pex5
GO_CC_m2	GO:004443	peroxisoma	3/470	57/23583	0.104896	0.525172	0.51084	Mavs/Pex5
GO_CC_m2	GO:004307	germ cell r	2/470	28/23583	0.10675	0.525172	0.51084	H2afx/Ran
GO_CC_m2	GO:005503	recycling e	5/470	126/23583	0.107747	0.525172	0.51084	Bloc1s2/Ra
GO_CC_m2	GO:000173	sex chroma	1/470	6/23583	0.113787	0.525172	0.51084	Suz12
GO_CC_m2	GO:000578	signal pept	1/470	6/23583	0.113787	0.525172	0.51084	Sec11c
GO_CC_m2	GO:000582	kinetochor	1/470	6/23583	0.113787	0.525172	0.51084	Rab11a
GO_CC_m2	GO:001601	sarcoglycar	1/470	6/23583	0.113787	0.525172	0.51084	Sgcd
GO_CC_m2	GO:003278	ELL-EAF cc	1/470	6/23583	0.113787	0.525172	0.51084	Aff3
GO_CC_m2	GO:003438	Pwp2p-cor	1/470	6/23583	0.113787	0.525172	0.51084	Pwp2
GO_CC_m2	GO:007120	histone pre	1/470	6/23583	0.113787	0.525172	0.51084	Snrpb
GO_CC_m2	GO:009741	Lewy body	1/470	6/23583	0.113787	0.525172	0.51084	Atf4
GO_CC_m2	GO:003470	potassium	4/470	93/23583	0.115133	0.526878	0.5125	Kcne4/Kcn
GO_CC_m2	GO:190356	extracellula	4/470	95/23583	0.121858	0.551296	0.536251	Arrdc1/Hnr
GO_CC_m2	GO:000574	mitochond	6/470	169/23583	0.122665	0.551296	0.536251	Acsl4/Mavs
GO_CC_m2	GO:000581	centrosom	14/470	498/23583	0.125563	0.551296	0.536251	2700049A0
GO_CC_m2	GO:003470	cation char	7/470	209/23583	0.12558	0.551296	0.536251	Kcne4/Kcn
GO_CC_m2	GO:009752	spliceosom	2/470	31/23583	0.126409	0.551296	0.536251	Prpf31/Snr
GO_CC_m2	GO:000043	core TFIIH	1/470	7/23583	0.131454	0.551296	0.536251	Gtf2h1
GO_CC_m2	GO:000565	nucleolar ri	1/470	7/23583	0.131454	0.551296	0.536251	Rpp38
GO_CC_m2	GO:001601	dystroglyca	1/470	7/23583	0.131454	0.551296	0.536251	Sgcd
GO_CC_m2	GO:003318	proton-tra	1/470	7/23583	0.131454	0.551296	0.536251	Atp6v1h
GO_CC_m2	GO:009752	spliceosom	3/470	64/23583	0.135377	0.551296	0.536251	Dcaf4/Prpf
GO_CC_m2	GO:000579	rough endo	4/470	100/23583	0.139378	0.551296	0.536251	Cybb/Derl1
GO_CC_m2	GO:000592	gap junctic	2/470	33/23583	0.139951	0.551296	0.536251	Gja4/Panx2
GO_CC_m2	GO:000568	U2-type sp	3/470	65/23583	0.139957	0.551296	0.536251	Cdc5l/Prpf3
GO_CC_m2	GO:001645	myosin cor	3/470	65/23583	0.139957	0.551296	0.536251	Myh11/My
GO_CC_m2	GO:003099	intraciliary	2/470	34/23583	0.146835	0.551296	0.536251	Ift122/Ttc3
GO_CC_m2	GO:000567	chromatin	1/470	8/23583	0.148769	0.551296	0.536251	Rrp8
GO_CC_m2	GO:000595	cAMP-dep	1/470	8/23583	0.148769	0.551296	0.536251	Prkar1a
GO_CC_m2	GO:003099	intraciliary	1/470	8/23583	0.148769	0.551296	0.536251	Ift122
GO_CC_m2	GO:003131	extrinsic cc	1/470	8/23583	0.148769	0.551296	0.536251	Coq8b
GO_CC_m2	GO:003159	nuclear prc	1/470	8/23583	0.148769	0.551296	0.536251	Psmc5
GO_CC_m2	GO:003200	early phag	1/470	8/23583	0.148769	0.551296	0.536251	Syt11
GO_CC_m2	GO:007159	neuronal ri	1/470	8/23583	0.148769	0.551296	0.536251	Hnrnpa2b1
GO_CC_m2	GO:007266	tRNA-splic	1/470	8/23583	0.148769	0.551296	0.536251	Rtcb
GO_CC_m2	GO:009884	postsynapt	1/470	8/23583	0.148769	0.551296	0.536251	Rab11a
GO_CC_m2	GO:009907	BORC com	1/470	8/23583	0.148769	0.551296	0.536251	Bloc1s2
GO_CC_m2	GO:007101	catalytic st	4/470	103/23583	0.150345	0.551296	0.536251	Cdc5l/Dcaf

GO_CC_m2	GO:000177	immunolog	2/470	35/23583	0.153786	0.551296	0.536251	Cd53/Prkar
GO_CC_m2	GO:000577	multivesicu	2/470	35/23583	0.153786	0.551296	0.536251	Bace1/Rab
GO_CC_m2	GO:007101	precatalytic	2/470	35/23583	0.153786	0.551296	0.536251	Dcaf4/Prpf
GO_CC_m2	GO:00800	Cul4-RING	2/470	35/23583	0.153786	0.551296	0.536251	Dcaf4/Cop
GO_CC_m2	GO:000577	peroxisome	5/470	142/23583	0.154587	0.551296	0.536251	Acsl4/Hmg
GO_CC_m2	GO:004257	microbody	5/470	142/23583	0.154587	0.551296	0.536251	Acsl4/Hmg
GO_CC_m2	GO:000581	centriole	4/470	105/23583	0.157835	0.551296	0.536251	2700049A0
GO_CC_m2	GO:00079	nuclear chr	11/470	390/23583	0.158337	0.551296	0.536251	Actl6b/Asf1
GO_CC_m2	GO:00987	presynapse	11/470	391/23583	0.160211	0.551296	0.536251	Cad/Cplx4/
GO_CC_m2	GO:003204	small-subu	2/470	36/23583	0.1608	0.551296	0.536251	Pwp2/Utp1
GO_CC_m2	GO:00058	cytoplasmi	3/470	70/23583	0.163601	0.551296	0.536251	Clip2/Serp1
GO_CC_m2	GO:00305	small nucle	3/470	70/23583	0.163601	0.551296	0.536251	Dcaf4/Prpf
GO_CC_m2	GO:00432	extracellula	4/470	107/23583	0.165459	0.551296	0.536251	Arrdc1/Hn
GO_CC_m2	GO:00332	axon part	12/470	437/23583	0.165669	0.551296	0.536251	Agrn/Auts2
GO_CC_m2	GO:000081	ESCRT III c	1/470	9/23583	0.165739	0.551296	0.536251	Chmp3
GO_CC_m2	GO:003137	ubiquitin c	1/470	9/23583	0.165739	0.551296	0.536251	Rnf20
GO_CC_m2	GO:190291	protein kin	4/470	109/23583	0.173213	0.551296	0.536251	Cks1b/Gtf2
GO_CC_m2	GO:003577	ribonucleo	6/470	188/23583	0.17406	0.551296	0.536251	Ddx3y/Fast
GO_CC_m2	GO:00080	sex chromo	2/470	38/23583	0.174993	0.551296	0.536251	H2afx/Suz1
GO_CC_m2	GO:00056	nuclear env	11/470	399/23583	0.175598	0.551296	0.536251	Cybb/Gchf
GO_CC_m2	GO:00165	DNA-direc	4/470	110/23583	0.177136	0.551296	0.536251	Chd6/Gtf2
GO_CC_m2	GO:00007	nuclear nu	2/470	39/23583	0.182163	0.551296	0.536251	H3f3b/Hist
GO_CC_m2	GO:000081	ESCRT I co	1/470	10/23583	0.182372	0.551296	0.536251	Tsg101
GO_CC_m2	GO:00058	neurofilam	1/470	10/23583	0.182372	0.551296	0.536251	Dyrk1a
GO_CC_m2	GO:00306	multimeric	1/470	10/23583	0.182372	0.551296	0.536251	Rpp38
GO_CC_m2	GO:00347	methyloso	1/470	10/23583	0.182372	0.551296	0.536251	Snrpb
GO_CC_m2	GO:00349	microtubul	1/470	10/23583	0.182372	0.551296	0.536251	Syne3
GO_CC_m2	GO:00349	meiotic nu	1/470	10/23583	0.182372	0.551296	0.536251	Syne3
GO_CC_m2	GO:004302	NADPH ox	1/470	10/23583	0.182372	0.551296	0.536251	Cybb
GO_CC_m2	GO:00485	signal reco	1/470	10/23583	0.182372	0.551296	0.536251	Derl1
GO_CC_m2	GO:00512	cell tip	1/470	10/23583	0.182372	0.551296	0.536251	Pex5l
GO_CC_m2	GO:01060	nuclear me	1/470	10/23583	0.182372	0.551296	0.536251	Syne3
GO_CC_m2	GO:01060	nuclear me	1/470	10/23583	0.182372	0.551296	0.536251	Syne3
GO_CC_m2	GO:00447	nuclear tra	6/470	191/23583	0.182887	0.551296	0.536251	Atf4/Cebp
GO_CC_m2	GO:000581	lipid drople	3/470	75/23583	0.188326	0.551296	0.536251	Acsl4/Mett
GO_CC_m2	GO:00350	histone me	3/470	75/23583	0.188326	0.551296	0.536251	Prdm10/Pr
GO_CC_m2	GO:00059	axoneme	4/470	115/23583	0.197185	0.551296	0.536251	Ak8/Cfap4
GO_CC_m2	GO:000152	microfibril	1/470	11/23583	0.198674	0.551296	0.536251	Mfap4
GO_CC_m2	GO:000217	manchette	1/470	11/23583	0.198674	0.551296	0.536251	Ran
GO_CC_m2	GO:00055	fibrillar coll	1/470	11/23583	0.198674	0.551296	0.536251	Col2a1
GO_CC_m2	GO:00057	signal reco	1/470	11/23583	0.198674	0.551296	0.536251	Derl1
GO_CC_m2	GO:00314	Cul4A-RIN	1/470	11/23583	0.198674	0.551296	0.536251	Cop1
GO_CC_m2	GO:004262	photorece	1/470	11/23583	0.198674	0.551296	0.536251	Rom1
GO_CC_m2	GO:00617	GATOR2 c	1/470	11/23583	0.198674	0.551296	0.536251	Gatsl2
GO_CC_m2	GO:00708	cell body fi	1/470	11/23583	0.198674	0.551296	0.536251	Penk
GO_CC_m2	GO:007254	ER membra	1/470	11/23583	0.198674	0.551296	0.536251	Emc4
GO_CC_m2	GO:009864	banded co	1/470	11/23583	0.198674	0.551296	0.536251	Col2a1
GO_CC_m2	GO:009701	ciliary plas	4/470	116/23583	0.201276	0.551296	0.536251	Ak8/Cfap4

GO_CC_m2	GO:002262	cytosolic ri	5/470	157/23583	0.204779	0.551296	0.536251	Rack1/Mrp
GO_CC_m2	GO:003439	nuclear pe	4/470	117/23583	0.205392	0.551296	0.536251	Atf4/Cad/C
GO_CC_m2	GO:000568	spliceosom	6/470	199/23583	0.207254	0.551296	0.536251	Cdc5l/Dcaf
GO_CC_m2	GO:012011	Sm-like pro	3/470	80/23583	0.213929	0.551296	0.536251	Dcaf4/Prpf
GO_CC_m2	GO:190255	serine/thre	3/470	80/23583	0.213929	0.551296	0.536251	Cks1b/Gtf2
GO_CC_m2	GO:000017	nuclear exo	1/470	12/23583	0.214651	0.551296	0.536251	Exosc2
GO_CC_m2	GO:000034	transcriptic	1/470	12/23583	0.214651	0.551296	0.536251	Zc3h11a
GO_CC_m2	GO:000584	mRNA cap	1/470	12/23583	0.214651	0.551296	0.536251	Ncbp2
GO_CC_m2	GO:001714	NMDA sele	1/470	12/23583	0.214651	0.551296	0.536251	Ptk2b
GO_CC_m2	GO:003067	ribonucleas	1/470	12/23583	0.214651	0.551296	0.536251	Rpp38
GO_CC_m2	GO:003114	pseudopoc	1/470	12/23583	0.214651	0.551296	0.536251	Klhl41
GO_CC_m2	GO:003451	RNA cap b	1/470	12/23583	0.214651	0.551296	0.536251	Ncbp2
GO_CC_m2	GO:003466	endoplasm	1/470	12/23583	0.214651	0.551296	0.536251	Ppib
GO_CC_m2	GO:003651	Derlin-1 re	1/470	12/23583	0.214651	0.551296	0.536251	Derl1
GO_CC_m2	GO:004240	nuclear inc	1/470	12/23583	0.214651	0.551296	0.536251	Pabpn1
GO_CC_m2	GO:004308	synaptic cle	1/470	12/23583	0.214651	0.551296	0.536251	Agrn
GO_CC_m2	GO:007156	npBAF con	1/470	12/23583	0.214651	0.551296	0.536251	Smarcd1
GO_CC_m2	GO:003002	lamellipodi	5/470	160/23583	0.215414	0.551296	0.536251	Arap3/Myc
GO_CC_m2	GO:003013	endocytic \	5/470	160/23583	0.215414	0.551296	0.536251	Cybb/Rab1
GO_CC_m2	GO:003283	plasma me	5/470	162/23583	0.222599	0.557704	0.542484	Ak8/Cfap4
GO_CC_m2	GO:000579	Golgi stack	3/470	82/23583	0.224372	0.557704	0.542484	Cit/Galnt2/
GO_CC_m2	GO:000219	zona pelluc	1/470	13/23583	0.230311	0.557704	0.542484	Zpbp
GO_CC_m2	GO:000591	fascia adhe	1/470	13/23583	0.230311	0.557704	0.542484	Nrap
GO_CC_m2	GO:000594	septin ring	1/470	13/23583	0.230311	0.557704	0.542484	9-Sep
GO_CC_m2	GO:000854	proteasom	1/470	13/23583	0.230311	0.557704	0.542484	Psmc5
GO_CC_m2	GO:001710	aminoacyl-	1/470	13/23583	0.230311	0.557704	0.542484	Eprs
GO_CC_m2	GO:003110	septin com	1/470	13/23583	0.230311	0.557704	0.542484	9-Sep
GO_CC_m2	GO:003159	cytosolic pr	1/470	13/23583	0.230311	0.557704	0.542484	Psmc5
GO_CC_m2	GO:003193	TORC2 cor	1/470	13/23583	0.230311	0.557704	0.542484	Pink1
GO_CC_m2	GO:003216	septin filan	1/470	13/23583	0.230311	0.557704	0.542484	9-Sep
GO_CC_m2	GO:009744	astrocyte p	1/470	13/23583	0.230311	0.557704	0.542484	Pink1
GO_CC_m2	GO:004444	cytosolic pa	8/470	294/23583	0.234347	0.564944	0.549526	Bloc1s2/Ra
GO_CC_m2	GO:001593	small ribos	3/470	85/23583	0.240215	0.569339	0.553801	Rack1/Mrp
GO_CC_m2	GO:000078	nucleosom	3/470	86/23583	0.245537	0.569339	0.553801	H2afx/H3f3
GO_CC_m2	GO:000097	Prp19 com	1/470	14/23583	0.245659	0.569339	0.553801	Cdc5l
GO_CC_m2	GO:003000	TRAPP con	1/470	14/23583	0.245659	0.569339	0.553801	Trappc12
GO_CC_m2	GO:003317	proton-tra	1/470	14/23583	0.245659	0.569339	0.553801	Atp6v1h
GO_CC_m2	GO:003339	chromatoic	1/470	14/23583	0.245659	0.569339	0.553801	Nsun2
GO_CC_m2	GO:003525	ciliary rootl	1/470	14/23583	0.245659	0.569339	0.553801	Crocc
GO_CC_m2	GO:007093	contractile	1/470	14/23583	0.245659	0.569339	0.553801	Alkbh4
GO_CC_m2	GO:199002	mitotic spir	1/470	14/23583	0.245659	0.569339	0.553801	Aurkb
GO_CC_m2	GO:000077	condensed	2/470	48/23583	0.24809	0.572515	0.556891	Aurkb/Ss18
GO_CC_m2	GO:001636	nuclear ma	3/470	87/23583	0.250878	0.576486	0.560753	Cad/Cebpa
GO_CC_m2	GO:003011	clathrin coa	2/470	49/23583	0.255499	0.576608	0.560873	Ap2b1/Kcn
GO_CC_m2	GO:003130	integral coi	5/470	172/23583	0.259517	0.576608	0.560873	Lfng/Pink1
GO_CC_m2	GO:000017	cytoplasmi	1/470	15/23583	0.260702	0.576608	0.560873	Exosc2
GO_CC_m2	GO:000566	DNA replic	1/470	15/23583	0.260702	0.576608	0.560873	Cdc5l
GO_CC_m2	GO:003108	BLOC-1 co	1/470	15/23583	0.260702	0.576608	0.560873	Bloc1s2

GO_CC_m2	GO:003215	septin cyto	1/470	15/23583	0.260702	0.576608	0.560873	9-Sep
GO_CC_m2	GO:003258	Golgi cister	1/470	15/23583	0.260702	0.576608	0.560873	Gpr89
GO_CC_m2	GO:003471	SMN-Sm p	1/470	15/23583	0.260702	0.576608	0.560873	Snrpb
GO_CC_m2	GO:003017	integral co	4/470	130/23583	0.26084	0.576608	0.560873	Derl1/Emc4
GO_CC_m2	GO:007006	extracellula	3/470	89/23583	0.261609	0.576608	0.560873	Hnrnpa2b1
GO_CC_m2	GO:000079	heterochro	3/470	90/23583	0.266997	0.583295	0.567377	Rnf20/Rrp8
GO_CC_m2	GO:004320	perikaryon	4/470	132/23583	0.269628	0.583295	0.567377	Glul/Hnrnp
GO_CC_m2	GO:003120	SNARE co	2/470	51/23583	0.270325	0.583295	0.567377	Cplx4/Vam
GO_CC_m2	GO:009956	cytoplasmi	11/470	444/23583	0.27356	0.583295	0.567377	Ak8/Cfap4
GO_CC_m2	GO:000566	DNA-direc	1/470	16/23583	0.275445	0.583295	0.567377	Chd6
GO_CC_m2	GO:000585	muscle my	1/470	16/23583	0.275445	0.583295	0.567377	Myh11
GO_CC_m2	GO:001036	chromocen	1/470	16/23583	0.275445	0.583295	0.567377	Aurkb
GO_CC_m2	GO:003585	Seh1-asso	1/470	16/23583	0.275445	0.583295	0.567377	Gatsl2
GO_CC_m2	GO:003820	TOR comp	1/470	16/23583	0.275445	0.583295	0.567377	Pink1
GO_CC_m2	GO:004259	lamellar bo	1/470	16/23583	0.275445	0.583295	0.567377	Clip2
GO_CC_m2	GO:003646	cytoplasmi	5/470	178/23583	0.282326	0.586304	0.570304	Ddx3y/Hnr
GO_CC_m2	GO:005502	nuclear DN	4/470	135/23583	0.282905	0.586304	0.570304	Chd6/Gtf2
GO_CC_m2	GO:000587	spindle mic	2/470	53/23583	0.285143	0.586304	0.570304	Aurkb/Rab
GO_CC_m2	GO:000042	DNA-direc	4/470	136/23583	0.287353	0.586304	0.570304	Chd6/Gtf2
GO_CC_m2	GO:003122	intrinsic co	4/470	136/23583	0.287353	0.586304	0.570304	Derl1/Emc4
GO_CC_m2	GO:004481	DNA packa	3/470	94/23583	0.288664	0.586304	0.570304	H2afx/H3f3
GO_CC_m2	GO:000564	nuclear out	1/470	17/23583	0.289895	0.586304	0.570304	Syne3
GO_CC_m2	GO:000577	integral co	1/470	17/23583	0.289895	0.586304	0.570304	Slc27a2
GO_CC_m2	GO:003161	spindle pol	1/470	17/23583	0.289895	0.586304	0.570304	Aurkb
GO_CC_m2	GO:003298	myosin fila	1/470	17/23583	0.289895	0.586304	0.570304	Myh11
GO_CC_m2	GO:007100	U2-type pr	1/470	17/23583	0.289895	0.586304	0.570304	Snrpb
GO_CC_m2	GO:009864	complex of	1/470	17/23583	0.289895	0.586304	0.570304	Col2a1
GO_CC_m2	GO:000578	endoplasm	2/470	54/23583	0.292542	0.588207	0.572155	Slc27a2/Tx
GO_CC_m2	GO:004445	nucleolar p	5/470	181/23583	0.293874	0.588207	0.572155	Acaca/Jmjc
GO_CC_m2	GO:007268	mitotic spin	3/470	95/23583	0.294104	0.588207	0.572155	Aurkb/Ect2
GO_CC_m2	GO:003088	RNA polym	4/470	138/23583	0.296278	0.590369	0.574257	Chd6/Gtf2
GO_CC_m2	GO:001647	vacuolar pr	1/470	18/23583	0.304057	0.59891	0.582566	Atp6v1h
GO_CC_m2	GO:003123	intrinsic co	1/470	18/23583	0.304057	0.59891	0.582566	Slc27a2
GO_CC_m2	GO:003509	ESC/E(Z) co	1/470	18/23583	0.304057	0.59891	0.582566	Suz12
GO_CC_m2	GO:190536	peptidase	3/470	97/23583	0.305001	0.59891	0.582566	Alad/Psmc
GO_CC_m2	GO:000584	ribosome	7/470	275/23583	0.309592	0.6038	0.587322	2810006K2
GO_CC_m2	GO:000592	cell-substra	4/470	141/23583	0.309727	0.6038	0.587322	Nrap/Ptk2
GO_CC_m2	GO:003130	intrinsic co	5/470	186/23583	0.313292	0.60741	0.590834	Lfng/Pink1
GO_CC_m2	GO:004439	ribosomal	6/470	231/23583	0.313829	0.60741	0.590834	2810006K2
GO_CC_m2	GO:000014	exocyst	1/470	19/23583	0.317938	0.608817	0.592202	Ralb
GO_CC_m2	GO:000093	gamma-tu	1/470	19/23583	0.317938	0.608817	0.592202	Bloc1s2
GO_CC_m2	GO:003109	platelet alp	1/470	19/23583	0.317938	0.608817	0.592202	Stxbp1
GO_CC_m2	GO:003198	Golgi cister	2/470	59/23583	0.329332	0.622374	0.605389	Cit/Gpr89
GO_CC_m2	GO:000592	connexin c	1/470	20/23583	0.331542	0.622374	0.605389	Gja4
GO_CC_m2	GO:000807	guanylate	1/470	20/23583	0.331542	0.622374	0.605389	Gucy2c
GO_CC_m2	GO:003108	BLOC comp	1/470	20/23583	0.331542	0.622374	0.605389	Bloc1s2
GO_CC_m2	GO:003136	anchored c	1/470	20/23583	0.331542	0.622374	0.605389	Izumo1r
GO_CC_m2	GO:003470	ion channe	7/470	282/23583	0.331933	0.622374	0.605389	Kcne4/Kcn

GO_CC_m	GO:00059	clathrin-co	2/470	61/23583	0.34391	0.630895	0.613678	Ap2b1/Sel
GO_CC_m	GO:000574	mitochond	10/470	426/23583	0.344416	0.630895	0.613678	Coq8b/Co
GO_CC_m	GO:000174	XY body	1/470	21/23583	0.344875	0.630895	0.613678	H2afx
GO_CC_m	GO:00056	U2 snRNP	1/470	21/23583	0.344875	0.630895	0.613678	Snrpb
GO_CC_m	GO:00056	telomerase	1/470	21/23583	0.344875	0.630895	0.613678	Snrpb
GO_CC_m	GO:003514	exon-exon	1/470	21/23583	0.344875	0.630895	0.613678	Thrap3
GO_CC_m	GO:003537	microtubul	1/470	21/23583	0.344875	0.630895	0.613678	Clip2
GO_CC_m	GO:00300	cell-substr	4/470	149/23583	0.345824	0.630895	0.613678	Nrap/Ptk2
GO_CC_m	GO:00007	chromosor	3/470	106/23583	0.354108	0.637919	0.62051	H2afx/H3f
GO_CC_m	GO:00059	cell cortex	7/470	290/23583	0.357737	0.637919	0.62051	Grm7/Ooe
GO_CC_m	GO:00056	basal lamir	1/470	22/23583	0.357943	0.637919	0.62051	Agrn
GO_CC_m	GO:00056	U1 snRNP	1/470	22/23583	0.357943	0.637919	0.62051	Snrpb
GO_CC_m	GO:00309	intraciliary	1/470	22/23583	0.357943	0.637919	0.62051	Ttc30b
GO_CC_m	GO:006007	inhibitory s	1/470	22/23583	0.357943	0.637919	0.62051	Syt11
GO_CC_m	GO:007101	prespliceos	1/470	22/23583	0.357943	0.637919	0.62051	Snrpb
GO_CC_m	GO:000017	exosome (	1/470	23/23583	0.370751	0.648853	0.631146	Exosc2
GO_CC_m	GO:00058	proteasom	1/470	23/23583	0.370751	0.648853	0.631146	Alad
GO_CC_m	GO:00312	intrinsic co	1/470	23/23583	0.370751	0.648853	0.631146	Izumo1r
GO_CC_m	GO:00436	nuclear rep	1/470	23/23583	0.370751	0.648853	0.631146	Cdc5l
GO_CC_m	GO:19053	exoribonuc	1/470	23/23583	0.370751	0.648853	0.631146	Exosc2
GO_CC_m	GO:001652	sarcoplasm	2/470	65/23583	0.372741	0.648853	0.631146	Klhl41/Srl
GO_CC_m	GO:009902	tethering c	2/470	65/23583	0.372741	0.648853	0.631146	Ralb/Trapp
GO_CC_m	GO:19024	transmemb	7/470	296/23583	0.37721	0.648853	0.631146	Kcne4/Kcn
GO_CC_m	GO:00058	proteasom	1/470	24/23583	0.383304	0.648853	0.631146	Psmc5
GO_CC_m	GO:00164	myosin II c	1/470	24/23583	0.383304	0.648853	0.631146	Myh11
GO_CC_m	GO:00300	desmosom	1/470	24/23583	0.383304	0.648853	0.631146	Kazn
GO_CC_m	GO:00308	rough endo	1/470	24/23583	0.383304	0.648853	0.631146	Derl1
GO_CC_m	GO:00308	replisome	1/470	24/23583	0.383304	0.648853	0.631146	Cdc5l
GO_CC_m	GO:00314	M band	1/470	24/23583	0.383304	0.648853	0.631146	Klhl41
GO_CC_m	GO:003301	sarcoplasm	1/470	24/23583	0.383304	0.648853	0.631146	Klhl41
GO_CC_m	GO:003317	proton-tra	1/470	24/23583	0.383304	0.648853	0.631146	Atp6v1h
GO_CC_m	GO:00312	extrinsic co	3/470	113/23583	0.392028	0.660789	0.642756	Csk/Frk/Pt
GO_CC_m	GO:00057	endoplasm	2/470	68/23583	0.394026	0.660789	0.642756	Tmed4/Tra
GO_CC_m	GO:00325	integral co	2/470	68/23583	0.394026	0.660789	0.642756	Pink1/Tom
GO_CC_m	GO:00353	transcriptic	1/470	25/23583	0.395607	0.661387	0.643337	Ell
GO_CC_m	GO:19903	transporte	7/470	303/23583	0.399984	0.663666	0.645555	Kcne4/Kcn
GO_CC_m	GO:00056	replication	2/470	69/23583	0.401048	0.663666	0.645555	Cdc5l/H2a
GO_CC_m	GO:00056	U12-type s	1/470	26/23583	0.407665	0.663666	0.645555	Snrpb
GO_CC_m	GO:00226	proteasom	1/470	26/23583	0.407665	0.663666	0.645555	Psmc5
GO_CC_m	GO:00315	nucleotide	1/470	26/23583	0.407665	0.663666	0.645555	Prkar1a
GO_CC_m	GO:00344	centriolar s	1/470	26/23583	0.407665	0.663666	0.645555	Mss51
GO_CC_m	GO:00009	P-body	2/470	70/23583	0.408032	0.663666	0.645555	Xrn1/Zc3h
GO_CC_m	GO:000577	autophago	2/470	70/23583	0.408032	0.663666	0.645555	Nbr1/Ralb
GO_CC_m	GO:009857	intrinsic co	2/470	70/23583	0.408032	0.663666	0.645555	Pink1/Tom
GO_CC_m	GO:00005	proteasom	2/470	72/23583	0.421879	0.682588	0.66396	Alad/Psmc
GO_CC_m	GO:19053	endopeptic	2/470	73/23583	0.42874	0.682588	0.66396	Alad/Psmc
GO_CC_m	GO:000092	spindle pol	3/470	120/23583	0.429362	0.682588	0.66396	Aurkb/Lats
GO_CC_m	GO:00446	MLL1/2 co	1/470	28/23583	0.431066	0.682588	0.66396	Prpf31

GO_CC_m2	GO:007133	MLL1 comp	1/470	28/23583	0.431066	0.682588	0.66396	Prpf31
GO_CC_m2	GO:199075	microtubul	1/470	28/23583	0.431066	0.682588	0.66396	Clip2
GO_CC_m2	GO:000588	actin filame	3/470	121/23583	0.434631	0.682588	0.66396	Dyrk1a/Rac
GO_CC_m2	GO:000172	stress fiber	2/470	74/23583	0.435557	0.682588	0.66396	Myh11/Sep
GO_CC_m2	GO:001652	sarcoplasm	2/470	74/23583	0.435557	0.682588	0.66396	Klhl41/Srl
GO_CC_m2	GO:009751	contractile	2/470	74/23583	0.435557	0.682588	0.66396	Myh11/Sep
GO_CC_m2	GO:000587	microtubul	9/470	412/23583	0.437405	0.682588	0.66396	Aurkb/Clip
GO_CC_m2	GO:003125	cell leading	8/470	364/23583	0.43978	0.682588	0.66396	Arap3/Atf4
GO_CC_m2	GO:000031	organellar	1/470	29/23583	0.442418	0.682588	0.66396	Mrps5
GO_CC_m2	GO:000576	mitochond	1/470	29/23583	0.442418	0.682588	0.66396	Mrps5
GO_CC_m2	GO:003013	clathrin ada	1/470	29/23583	0.442418	0.682588	0.66396	Ap2b1
GO_CC_m2	GO:009743	mitotic spir	1/470	29/23583	0.442418	0.682588	0.66396	Aurkb
GO_CC_m2	GO:190255	endoribonu	1/470	29/23583	0.442418	0.682588	0.66396	Rpp38
GO_CC_m2	GO:190534	endonuclea	1/470	29/23583	0.442418	0.682588	0.66396	Rpp38
GO_CC_m2	GO:009879	Golgi subc	9/470	416/23583	0.448703	0.690312	0.671473	Bace1/Chst
GO_CC_m2	GO:004278	polysomal	1/470	30/23583	0.453544	0.695778	0.67679	Zc3h15
GO_CC_m2	GO:000584	polysome	2/470	77/23583	0.455741	0.696255	0.677254	Unk/Zc3h1
GO_CC_m2	GO:001986	organelle ir	10/470	468/23583	0.456434	0.696255	0.677254	Coq8b/Coc
GO_CC_m2	GO:004329	contractile	5/470	223/23583	0.458534	0.696673	0.677661	Itgb1bp2/K
GO_CC_m2	GO:000040	phagophor	1/470	31/23583	0.464449	0.696673	0.677661	Nbr1
GO_CC_m2	GO:003066	clathrin-co	1/470	31/23583	0.464449	0.696673	0.677661	Vamp3
GO_CC_m2	GO:004247	melanoson	1/470	31/23583	0.464449	0.696673	0.677661	Gchfr
GO_CC_m2	GO:004877	pigment gr	1/470	31/23583	0.464449	0.696673	0.677661	Gchfr
GO_CC_m2	GO:005123	spindle mic	1/470	31/23583	0.464449	0.696673	0.677661	Aurkb
GO_CC_m2	GO:006169	transferase	6/470	275/23583	0.469058	0.700504	0.681387	Chd6/Cks1
GO_CC_m2	GO:000591	cell-cell jur	10/470	473/23583	0.469729	0.700504	0.681387	Cd53/Csk/I
GO_CC_m2	GO:003606	ciliary basa	3/470	128/23583	0.470976	0.700504	0.681387	2700049A0
GO_CC_m2	GO:004443	Golgi appa	10/470	474/23583	0.472381	0.700504	0.681387	Agrp/Bace1
GO_CC_m2	GO:007006	cytochrom	1/470	32/23583	0.475136	0.700504	0.681387	Cox10
GO_CC_m2	GO:009056	nuclear tra	1/470	32/23583	0.475136	0.700504	0.681387	Rrp8
GO_CC_m2	GO:004442	extracellula	3/470	129/23583	0.476083	0.700504	0.681387	Agrn/Col2a
GO_CC_m2	GO:000077	kinetochor	3/470	130/23583	0.481168	0.705357	0.686108	Aurkb/Ss18
GO_CC_m2	GO:003068	preribosom	2/470	81/23583	0.481994	0.705357	0.686108	Pwp2/Utp1
GO_CC_m2	GO:003068	90S preribo	1/470	33/23583	0.485611	0.708729	0.689388	Pwp2
GO_CC_m2	GO:000989	cytoplasmi	4/470	182/23583	0.492385	0.71555	0.696023	Aspscr1/Cs
GO_CC_m2	GO:000013	Golgi mem	5/470	232/23583	0.492935	0.71555	0.696023	Chst5/Gpr8
GO_CC_m2	GO:003243	actin filame	2/470	83/23583	0.494825	0.715972	0.696432	Myh11/Sep
GO_CC_m2	GO:000579	smooth en	1/470	34/23583	0.495877	0.715972	0.696432	Ppib
GO_CC_m2	GO:009706	synaptic m	7/470	334/23583	0.499698	0.719565	0.699928	Faim2/Grm
GO_CC_m2	GO:003586	site of dou	1/470	35/23583	0.505938	0.723019	0.703287	H2afx
GO_CC_m2	GO:000592	focal adhes	3/470	135/23583	0.50623	0.723019	0.703287	Ptk2b/Tgfb
GO_CC_m2	GO:004444	ciliary part	9/470	437/23583	0.507318	0.723019	0.703287	2700049A0
GO_CC_m2	GO:004264	actomyosir	2/470	85/23583	0.507452	0.723019	0.703287	Myh11/Sep
GO_CC_m2	GO:001000	endosome	4/470	186/23583	0.509344	0.723805	0.704052	Chmp3/Sh
GO_CC_m2	GO:000589	voltage-ga	1/470	36/23583	0.515799	0.72914	0.709242	Pde4d
GO_CC_m2	GO:001659	mediator c	1/470	36/23583	0.515799	0.72914	0.709242	Thrap3
GO_CC_m2	GO:000576	early endo	5/470	239/23583	0.519126	0.73107	0.711119	Bace1/Chm
GO_CC_m2	GO:003017	filopodium	2/470	87/23583	0.519872	0.73107	0.711119	Myo1g/Tw

GO_CC_m2	GO:00566	transcriptic	1/470	37/23583	0.525464	0.732011	0.712034	Taf13
GO_CC_m2	GO:000172	ruffle	3/470	139/23583	0.52582	0.732011	0.712034	Arap3/Cit/
GO_CC_m2	GO:00986	chromosor	6/470	293/23583	0.530433	0.732011	0.712034	Aurkb/H2a
GO_CC_m2	GO:000031	organellar	2/470	89/23583	0.532081	0.732011	0.712034	2810006K2
GO_CC_m2	GO:00057	mitochond	2/470	89/23583	0.532081	0.732011	0.712034	2810006K2
GO_CC_m2	GO:003042	growth cor	4/470	192/23583	0.53429	0.732011	0.712034	Agrn/Auts2
GO_CC_m2	GO:003017	integral co	1/470	38/23583	0.534936	0.732011	0.712034	Lfng
GO_CC_m2	GO:00907	site of DN	1/470	38/23583	0.534936	0.732011	0.712034	H2afx
GO_CC_m2	GO:009754	ciliary base	1/470	38/23583	0.534936	0.732011	0.712034	Ift122
GO_CC_m2	GO:004217	nuclear ou	10/470	498/23583	0.535051	0.732011	0.712034	Derl1/Emc
GO_CC_m2	GO:004257	immunoglc	3/470	141/23583	0.535453	0.732011	0.712034	Ighv1-23/I
GO_CC_m2	GO:00566	transcriptic	8/470	399/23583	0.542783	0.735816	0.715735	Atf4/Cebpa
GO_CC_m2	GO:003131	extrinsic cc	1/470	39/23583	0.54422	0.735816	0.715735	Coq8b
GO_CC_m2	GO:00442	axonal grov	1/470	39/23583	0.54422	0.735816	0.715735	Agrn
GO_CC_m2	GO:00977	non-motile	3/470	143/23583	0.544974	0.735816	0.715735	Ift122/Rom
GO_CC_m2	GO:00162	aggresome	1/470	40/23583	0.553318	0.735816	0.715735	Rnf32
GO_CC_m2	GO:003122	intrinsic co	1/470	40/23583	0.553318	0.735816	0.715735	Lfng
GO_CC_m2	GO:00435	nuclear rep	1/470	40/23583	0.553318	0.735816	0.715735	Cdc5l
GO_CC_m2	GO:006007	excitatory	1/470	40/23583	0.553318	0.735816	0.715735	Syt11
GO_CC_m2	GO:001981	immunoglc	3/470	145/23583	0.554381	0.735816	0.715735	Ighv1-23/I
GO_CC_m2	GO:00312	leading ed	3/470	145/23583	0.554381	0.735816	0.715735	Atf4/Myo1
GO_CC_m2	GO:003042	site of pola	4/470	197/23583	0.554587	0.735816	0.715735	Agrn/Auts2
GO_CC_m2	GO:00985	cytoplasmi	4/470	197/23583	0.554587	0.735816	0.715735	Aspscr1/Cs
GO_CC_m2	GO:002262	cytosolic la	2/470	94/23583	0.561665	0.741834	0.721589	Mrto4/Rpl2
GO_CC_m2	GO:00314	cullin-RIN	4/470	199/23583	0.562573	0.741834	0.721589	Cks1b/Dca
GO_CC_m2	GO:00701	anchoring	6/470	303/23583	0.563245	0.741834	0.721589	Kazn/Nrap
GO_CC_m2	GO:00057	mitochond	5/470	253/23583	0.569675	0.748365	0.727942	2810006K2
GO_CC_m2	GO:000572	nuclear het	1/470	42/23583	0.570975	0.748365	0.727942	Suz12
GO_CC_m2	GO:00159	large ribos	3/470	149/23583	0.572843	0.748995	0.728555	2810006K2
GO_CC_m2	GO:000581	spindle	5/470	255/23583	0.576671	0.75218	0.731653	Aurkb/Ect2
GO_CC_m2	GO:00099	basal plasn	1/470	43/23583	0.579541	0.752288	0.731758	Muc20
GO_CC_m2	GO:003167	A band	1/470	43/23583	0.579541	0.752288	0.731758	Klhl41
GO_CC_m2	GO:00030	cyclin-dep	1/470	44/23583	0.587936	0.758427	0.737729	Cks1b
GO_CC_m2	GO:00323	photorecep	1/470	44/23583	0.587936	0.758427	0.737729	Ift122
GO_CC_m2	GO:003011	membrane	2/470	99/23583	0.589888	0.758427	0.737729	Ap2b1/Kcn
GO_CC_m2	GO:004847	coated me	2/470	99/23583	0.589888	0.758427	0.737729	Ap2b1/Kcn
GO_CC_m2	GO:012011	neuron prc	1/470	45/23583	0.596163	0.764128	0.743274	Hnrnpa2b1
GO_CC_m2	GO:003001	myofibril	4/470	209/23583	0.601295	0.764128	0.743274	Itgb1bp2/K
GO_CC_m2	GO:004444	endosomal	4/470	209/23583	0.601295	0.764128	0.743274	Chmp3/Sh
GO_CC_m2	GO:00725	blood micr	3/470	156/23583	0.603983	0.764128	0.743274	Ighv1-23/I
GO_CC_m2	GO:00989	neuron to	5/470	263/23583	0.604045	0.764128	0.743274	Grm7/Mtm
GO_CC_m2	GO:00325	dendrite m	1/470	46/23583	0.604227	0.764128	0.743274	Atf4
GO_CC_m2	GO:006017	ciliary mem	1/470	46/23583	0.604227	0.764128	0.743274	Rom1
GO_CC_m2	GO:00057	endoplasm	9/470	476/23583	0.610227	0.766938	0.746008	Derl1/Emc
GO_CC_m2	GO:00056	basement	2/470	103/23583	0.611478	0.766938	0.746008	Agrn/Col2a
GO_CC_m2	GO:00092	nucleoid	1/470	47/23583	0.61213	0.766938	0.746008	Fastkd2
GO_CC_m2	GO:004264	mitochond	1/470	47/23583	0.61213	0.766938	0.746008	Fastkd2
GO_CC_m2	GO:003011	AP-type m	1/470	48/23583	0.619875	0.774844	0.753698	Ap2b1

GO_CC_m2	GO:199020	oxidoreduc	2/470	106/23583	0.627094	0.777138	0.755929	Cybb/Gpd1
GO_CC_m2	GO:000191	photorecep	1/470	49/23583	0.627467	0.777138	0.755929	Crocc
GO_CC_m2	GO:001646	proton-tra	1/470	49/23583	0.627467	0.777138	0.755929	Atp6v1h
GO_CC_m2	GO:003151	PcG protein	1/470	49/23583	0.627467	0.777138	0.755929	Suz12
GO_CC_m2	GO:009773	photorecep	2/470	107/23583	0.63219	0.779259	0.757992	Ift122/Rom
GO_CC_m2	GO:003013	COPII-coat	1/470	50/23583	0.634907	0.779259	0.757992	Tmed4
GO_CC_m2	GO:000032	lytic vacuol	8/470	433/23583	0.634952	0.779259	0.757992	Atp6v1h/Bl
GO_CC_m2	GO:000576	lysosome	8/470	433/23583	0.634952	0.779259	0.757992	Atp6v1h/Bl
GO_CC_m2	GO:009882	endoplasm	9/470	489/23583	0.642056	0.78619	0.764735	Derl1/Emc4
GO_CC_m2	GO:000832	ionotropic	1/470	53/23583	0.656348	0.798879	0.777077	Ptk2b
GO_CC_m2	GO:003612	sperm flag	2/470	112/23583	0.656856	0.798879	0.777077	Ak8/Ran
GO_CC_m2	GO:009773	9+0 non-m	2/470	112/23583	0.656856	0.798879	0.777077	Ift122/Rom
GO_CC_m2	GO:000031	organellar	1/470	54/23583	0.663213	0.800371	0.778528	2810006K2
GO_CC_m2	GO:000153	cornified en	1/470	54/23583	0.663213	0.800371	0.778528	Kazn
GO_CC_m2	GO:000576	mitochond	1/470	54/23583	0.663213	0.800371	0.778528	2810006K2
GO_CC_m2	GO:004485	plasma me	2/470	114/23583	0.666346	0.800371	0.778528	Prkar1a/Se
GO_CC_m2	GO:009772	9+2 motile	2/470	114/23583	0.666346	0.800371	0.778528	Ak8/Ran
GO_CC_m2	GO:003101	extracellula	8/470	447/23583	0.66976	0.800371	0.778528	Agrn/Ambp
GO_CC_m2	GO:003470	calcium cha	1/470	55/23583	0.66994	0.800371	0.778528	Pde4d
GO_CC_m2	GO:009887	neurotrans	1/470	55/23583	0.66994	0.800371	0.778528	Ptk2b
GO_CC_m2	GO:004517	intercellula	1/470	56/23583	0.676533	0.806464	0.784455	Fastkd2
GO_CC_m2	GO:000591	adherens ju	5/470	287/23583	0.679759	0.808524	0.786459	Nrap/Ptk2b
GO_CC_m2	GO:003014	secretory g	7/470	398/23583	0.682704	0.810242	0.78813	Clip2/Klk10
GO_CC_m2	GO:004665	anchored c	1/470	58/23583	0.689328	0.81631	0.794033	Izumo1r
GO_CC_m2	GO:003013	transport v	5/470	291/23583	0.69139	0.816439	0.794158	Mtmr2/Rab
GO_CC_m2	GO:003151	motile ciliu	3/470	179/23583	0.695339	0.816439	0.794158	Ak8/Ran/R
GO_CC_m2	GO:004319	dendritic sp	3/470	179/23583	0.695339	0.816439	0.794158	Mtmr2/Ptk
GO_CC_m2	GO:003196	nuclear me	4/470	238/23583	0.701152	0.816439	0.794158	Gchfr/Rnf6
GO_CC_m2	GO:003066	Golgi-asso	1/470	60/23583	0.701618	0.816439	0.794158	Gpr89
GO_CC_m2	GO:000591	cell-cell ad	2/470	122/23583	0.7022	0.816439	0.794158	Nrap/Ptprn
GO_CC_m2	GO:004430	neuron spi	3/470	181/23583	0.702477	0.816439	0.794158	Mtmr2/Ptk
GO_CC_m2	GO:004444	cell cortex	3/470	181/23583	0.702477	0.816439	0.794158	Ralb/Sele/S
GO_CC_m2	GO:001989	extrinsic cc	5/470	296/23583	0.705519	0.816439	0.794158	Coq8b/Asp
GO_CC_m2	GO:000579	Golgi-asso	2/470	123/23583	0.706449	0.816439	0.794158	Gpr89/Tme
GO_CC_m2	GO:000011	histone dea	1/470	61/23583	0.70758	0.816439	0.794158	Hr
GO_CC_m2	GO:001470	intercalated	1/470	61/23583	0.70758	0.816439	0.794158	Nrap
GO_CC_m2	GO:001989	extrinsic cc	3/470	183/23583	0.709487	0.816894	0.7946	Csk/Frk/Ptk
GO_CC_m2	GO:000079	condensed	3/470	185/23583	0.71637	0.823064	0.800602	Aurkb/H2a
GO_CC_m2	GO:000165	fibrillar cen	2/470	128/23583	0.726943	0.833438	0.810693	Acaca/Rpp
GO_CC_m2	GO:000077	chromosom	3/470	189/23583	0.729757	0.834891	0.812106	Aurkb/Ss18
GO_CC_m2	GO:004443	cytoplasmi	8/470	475/23583	0.733074	0.836321	0.813497	Chmp3/Gp
GO_CC_m2	GO:003258	ruffle mem	1/470	66/23583	0.735653	0.836321	0.813497	Twf1
GO_CC_m2	GO:004517	basal part o	1/470	66/23583	0.735653	0.836321	0.813497	Muc20
GO_CC_m2	GO:000590	brush bord	2/470	131/23583	0.738649	0.83704	0.814197	Cybrd1/My
GO_CC_m2	GO:003258	neuron pro	1/470	67/23583	0.740936	0.83704	0.814197	Atf4
GO_CC_m2	GO:004319	dendritic sh	1/470	67/23583	0.740936	0.83704	0.814197	Grm7
GO_CC_m2	GO:000564	nuclear po	1/470	68/23583	0.746114	0.839838	0.816918	Ran
GO_CC_m2	GO:000802	synaptic ve	3/470	195/23583	0.7489	0.839838	0.816918	Mtmr2/Syt

GO_CC_m2	GO:00575	mitochond	1/470	69/23583	0.751188	0.839838	0.816918	Pink1
GO_CC_m2	GO:00306	coated ves	1/470	69/23583	0.751188	0.839838	0.816918	Vamp3
GO_CC_m2	GO:00315	brush bord	1/470	69/23583	0.751188	0.839838	0.816918	Cybrd1
GO_CC_m2	GO:00190	SCF ubiqui	1/470	70/23583	0.756161	0.841342	0.818381	Cks1b
GO_CC_m2	GO:00314	Cul3-RING	1/470	70/23583	0.756161	0.841342	0.818381	Klhl41
GO_CC_m2	GO:00432	apical junc	2/470	136/23583	0.757208	0.841342	0.818381	Ect2/Frmd
GO_CC_m2	GO:00315	neuromusc	1/470	71/23583	0.761035	0.842146	0.819163	Prkar1a
GO_CC_m2	GO:00444	contractile	3/470	199/23583	0.76105	0.842146	0.819163	Itgb1bp2/
GO_CC_m2	GO:00322	asymmetri	4/470	260/23583	0.763985	0.843664	0.82064	Grm7/Mtm
GO_CC_m2	GO:00358	ciliary trans	1/470	72/23583	0.765812	0.843956	0.820924	Ift122
GO_CC_m2	GO:00987	mitochond	4/470	262/23583	0.769151	0.845664	0.822585	2810006K2
GO_CC_m2	GO:00166	PML body	1/470	73/23583	0.770494	0.845664	0.822585	Rnf6
GO_CC_m2	GO:00007	nuclear chr	1/470	74/23583	0.775082	0.848974	0.825805	H3f3b
GO_CC_m2	GO:00017	photorece	1/470	76/23583	0.783986	0.856988	0.833601	Rom1
GO_CC_m2	GO:00442	cell-cell co	1/470	79/23583	0.796686	0.869112	0.845393	Nrap
GO_CC_m2	GO:00703	exocytic ve	3/470	213/23583	0.799863	0.870818	0.847053	Mtmr2/Syt
GO_CC_m2	GO:00444	mitochond	3/470	214/23583	0.802422	0.871847	0.848054	Coq8b/Pin
GO_CC_m2	GO:00055	collagen tri	1/470	82/23583	0.808641	0.875082	0.851201	Col2a1
GO_CC_m2	GO:00319	organelle e	1/470	82/23583	0.808641	0.875082	0.851201	Pink1
GO_CC_m2	GO:00001	ubiquitin li	5/470	340/23583	0.810384	0.875215	0.85133	Cks1b/Dca
GO_CC_m2	GO:00423	sarcolemm	2/470	154/23583	0.814864	0.876258	0.852345	Agrn/Sgcd
GO_CC_m2	GO:00312	cell project	4/470	282/23583	0.816047	0.876258	0.852345	Atf4/Cybrd
GO_CC_m2	GO:00170	transcriptic	1/470	84/23583	0.816218	0.876258	0.852345	Rrp8
GO_CC_m2	GO:00451	membrane	5/470	350/23583	0.829538	0.887031	0.862824	Csk/Faim2/
GO_CC_m2	GO:00988	membrane	5/470	350/23583	0.829538	0.887031	0.862824	Csk/Faim2/
GO_CC_m2	GO:00059	microvillus	1/470	92/23583	0.84365	0.899889	0.875331	Myo1g
GO_CC_m2	GO:00059	caveola	1/470	93/23583	0.846779	0.899889	0.875331	Sele
GO_CC_m2	GO:00055	proteinace	5/470	361/23583	0.848764	0.899889	0.875331	Agrn/Bmp
GO_CC_m2	GO:00985	membrane	5/470	362/23583	0.850419	0.899889	0.875331	Csk/Faim2/
GO_CC_m2	GO:00301	clathrin-co	1/470	95/23583	0.852849	0.899889	0.875331	Vamp3
GO_CC_m2	GO:00301	coated ves	2/470	169/23583	0.853228	0.899889	0.875331	Tmed4/Va
GO_CC_m2	GO:00312	anchored	2/470	169/23583	0.853228	0.899889	0.875331	Izumo1r/Ly
GO_CC_m2	GO:00007	condensed	3/470	238/23583	0.856034	0.901088	0.876497	Aurkb/H2a
GO_CC_m2	GO:00125	vesicle me	4/470	304/23583	0.858308	0.901725	0.877116	Aspscr1/Sp
GO_CC_m2	GO:00972	sperm part	3/470	242/23583	0.863617	0.90554	0.880827	Ak8/Ran/Z
GO_CC_m2	GO:00988	plasma me	2/470	175/23583	0.866436	0.906736	0.881991	Il12rb1/Ptk
GO_CC_m2	GO:00432	receptor c	5/470	374/23583	0.869137	0.907803	0.883028	Grm7/Il12r
GO_CC_m2	GO:00988	cluster of a	2/470	182/23583	0.880464	0.917858	0.89281	Cybrd1/My
GO_CC_m2	GO:003001	sarcomere	2/470	185/23583	0.886049	0.919492	0.894399	Itgb1bp2/
GO_CC_m2	GO:00140	postsynapt	3/470	256/23583	0.88746	0.919492	0.894399	Mtmr2/Ptk
GO_CC_m2	GO:00058	trans-Golg	2/470	186/23583	0.887857	0.919492	0.894399	Bace1/Rab
GO_CC_m2	GO:004521	postsynapt	3/470	258/23583	0.890545	0.919492	0.894399	Faim2/Grm
GO_CC_m2	GO:009957	postsynapt	3/470	258/23583	0.890545	0.919492	0.894399	Mtmr2/Ptk
GO_CC_m2	GO:00350	micro-ribo	1/470	115/23583	0.901797	0.929333	0.903971	Mirlet7f-1
GO_CC_m2	GO:00308	cortical cyt	1/470	117/23583	0.905692	0.931568	0.906146	Sele
GO_CC_m2	GO:00988	actin-base	2/470	199/23583	0.909055	0.931865	0.906434	Myo1g/Tw
GO_CC_m2	GO:000592	bicellular ti	1/470	119/23583	0.909432	0.931865	0.906434	Ect2
GO_CC_m2	GO:00306	cytoplasmi	3/470	274/23583	0.912617	0.932007	0.906572	Spire2/Van

GO_CC_m2	GO:003001	Z disc	1/470	122/23583	0.914766	0.932007	0.906572	Itgb1bp2
GO_CC_m2	GO:007016	occluding j	1/470	122/23583	0.914766	0.932007	0.906572	Ect2
GO_CC_m2	GO:000588	intermedia	1/470	123/23583	0.916473	0.932007	0.906572	Dyrk1a
GO_CC_m2	GO:004320	myelin she	2/470	213/23583	0.92766	0.941609	0.915912	Glul/Stxbp1
GO_CC_m2	GO:000166	acrosomal	1/470	134/23583	0.933146	0.944986	0.919197	Zpbp
GO_CC_m2	GO:003167	I band	1/470	135/23583	0.934486	0.944986	0.919197	Itgb1bp2
GO_CC_m2	GO:001632	apical plasr	3/470	306/23583	0.945081	0.953914	0.927881	Kcne4/Muc
GO_CC_m2	GO:000587	microtubul	1/470	148/23583	0.949652	0.956739	0.930629	Aurkb
GO_CC_m2	GO:004517	apical part	4/470	403/23583	0.961102	0.966429	0.940054	Kcne4/Muc
GO_CC_m2	GO:004511	intermedia	1/470	163/23583	0.962849	0.966429	0.940054	Dyrk1a
GO_CC_m2	GO:000989	external sic	5/470	491/23583	0.968914	0.970711	0.94422	Ighv1-23/Ig
GO_CC_m2	GO:001632	basolateral	1/470	223/23583	0.989009	0.989009	0.962018	Muc20
GO_CC_m3	GO:004430	neuron prc	13/540	211/23583	0.001217	0.430625	0.403725	Calb2/Dixd
GO_CC_m3	GO:004367	axon termi	12/540	194/23583	0.001791	0.430625	0.403725	Calb2/Dixd
GO_CC_m3	GO:004319	terminal bc	8/540	120/23583	0.006443	0.430625	0.403725	Calb2/Grik2
GO_CC_m3	GO:003012	AP-1 adap	2/540	6/23583	0.007385	0.430625	0.403725	Ap1g2/Slc1
GO_CC_m3	GO:003298	kainate sel	2/540	6/23583	0.007385	0.430625	0.403725	Grik2/Grik4
GO_CC_m3	GO:199046	omegasom	2/540	7/23583	0.010183	0.430625	0.403725	Trim12c/Tr
GO_CC_m3	GO:009722	sperm part	12/540	242/23583	0.01028	0.430625	0.403725	Adam24/C
GO_CC_m3	GO:006007	excitatory s	4/540	40/23583	0.012952	0.430625	0.403725	Lrrtm1/Nlg
GO_CC_m3	GO:000586	troponin cc	2/540	8/23583	0.013373	0.430625	0.403725	Tnni2/Tnnt
GO_CC_m3	GO:004525	pyruvate d	2/540	8/23583	0.013373	0.430625	0.403725	Dlat/Dld
GO_CC_m3	GO:009858	membrane	15/540	362/23583	0.020468	0.430625	0.403725	Cd46/Fam1
GO_CC_m3	GO:000081	ESCRT I co	2/540	10/23583	0.020851	0.430625	0.403725	Ubap1l/Vp
GO_CC_m3	GO:003013	clathrin coa	2/540	10/23583	0.020851	0.430625	0.403725	Ap1g2/Slc1
GO_CC_m3	GO:009753	ciliary trans	2/540	10/23583	0.020851	0.430625	0.403725	Cep164/Sc
GO_CC_m3	GO:015003	distal axon	15/540	364/23583	0.021378	0.430625	0.403725	Calb2/Dixd
GO_CC_m3	GO:001601	dystrobrev	1/540	1/23583	0.022898	0.430625	0.403725	Dtna
GO_CC_m3	GO:001628	eukaryotic	1/540	1/23583	0.022898	0.430625	0.403725	Dhx29
GO_CC_m3	GO:003247	cytoplasmi	1/540	1/23583	0.022898	0.430625	0.403725	Lrrk2
GO_CC_m3	GO:003626	Cdc48p-Np	1/540	1/23583	0.022898	0.430625	0.403725	Ankzf1
GO_CC_m3	GO:009061	meiotic spi	1/540	1/23583	0.022898	0.430625	0.403725	Ccdc155
GO_CC_m3	GO:009940	caveola ne	1/540	1/23583	0.022898	0.430625	0.403725	Lrrk2
GO_CC_m3	GO:004443	cytoplasmi	18/540	475/23583	0.026482	0.430625	0.403725	Ap1g2/App
GO_CC_m3	GO:000017	nuclear exc	2/540	12/23583	0.029673	0.430625	0.403725	Dis3/Exosc
GO_CC_m3	GO:001714	NMDA sele	2/540	12/23583	0.029673	0.430625	0.403725	Grin2c/Nlg
GO_CC_m3	GO:003612	CatSper co	2/540	12/23583	0.029673	0.430625	0.403725	Catsper4/C
GO_CC_m3	GO:009722	sperm prin	3/540	30/23583	0.030663	0.430625	0.403725	Catsper4/C
GO_CC_m3	GO:000832	ionotropic	4/540	53/23583	0.032957	0.430625	0.403725	Grik2/Grik4
GO_CC_m3	GO:001632	basolateral	10/540	223/23583	0.033377	0.430625	0.403725	Aqp5/Cd46
GO_CC_m3	GO:000581	centriole	6/540	105/23583	0.033781	0.430625	0.403725	Ccdc92/Cc
GO_CC_m3	GO:001251	trans-Golg	2/540	13/23583	0.034545	0.430625	0.403725	Ap1g2/Slc1
GO_CC_m3	GO:000166	acrosomal	7/540	134/23583	0.034814	0.430625	0.403725	Catsper4/C
GO_CC_m3	GO:000586	striated mu	3/540	32/23583	0.036233	0.430625	0.403725	Mybph/Tn
GO_CC_m3	GO:009879	presynapse	15/540	391/23583	0.036847	0.430625	0.403725	Bcl2l1/Calb
GO_CC_m3	GO:009887	neurotrans	4/540	55/23583	0.037057	0.430625	0.403725	Grik2/Grik4
GO_CC_m3	GO:000581	centrosom	18/540	498/23583	0.039276	0.430625	0.403725	Ccdc187/A
GO_CC_m3	GO:003014	secretory g	15/540	398/23583	0.041923	0.430625	0.403725	Avp/Catspe

GO_CC_m3	GO:003637	myofilamer	3/540	34/23583	0.042284	0.430625	0.403725	Mybph/Tn
GO_CC_m3	GO:009883	postsynapt	3/540	34/23583	0.042284	0.430625	0.403725	Grik2/Grik4
GO_CC_m3	GO:000017	cytoplasmi	2/540	15/23583	0.04513	0.430625	0.403725	Dis3/Exosc
GO_CC_m3	GO:004318	P granule	2/540	15/23583	0.04513	0.430625	0.403725	Mov10l1/P
GO_CC_m3	GO:004549	pole plasm	2/540	15/23583	0.04513	0.430625	0.403725	Mov10l1/P
GO_CC_m3	GO:006029	germ plasn	2/540	15/23583	0.04513	0.430625	0.403725	Mov10l1/P
GO_CC_m3	GO:000567	transcriptic	1/540	2/23583	0.045272	0.430625	0.403725	Gtf2e1
GO_CC_m3	GO:000596	glycine cle	1/540	2/23583	0.045272	0.430625	0.403725	Gcsh
GO_CC_m3	GO:001918	snRNA-act	1/540	2/23583	0.045272	0.430625	0.403725	Snapc1
GO_CC_m3	GO:003141	NatB comp	1/540	2/23583	0.045272	0.430625	0.403725	Naa25
GO_CC_m3	GO:003557	azurophil g	1/540	2/23583	0.045272	0.430625	0.403725	Prtn3
GO_CC_m3	GO:004475	amphisom	1/540	2/23583	0.045272	0.430625	0.403725	Lrrk2
GO_CC_m3	GO:007072	BMP recep	1/540	2/23583	0.045272	0.430625	0.403725	Bmp2
GO_CC_m3	GO:007099	translation	1/540	2/23583	0.045272	0.430625	0.403725	Dhx29
GO_CC_m3	GO:190263	kinociliary	1/540	2/23583	0.045272	0.430625	0.403725	Mkks
GO_CC_m3	GO:199074	microvesicl	1/540	2/23583	0.045272	0.430625	0.403725	Syt4
GO_CC_m3	GO:003326	axon part	16/540	437/23583	0.045374	0.430625	0.403725	Calb2/Dixd
GO_CC_m3	GO:004485	plasma me	6/540	114/23583	0.047329	0.44086	0.413321	Hck/Hk1/L
GO_CC_m3	GO:001636	nuclear ma	5/540	87/23583	0.049535	0.45298	0.424684	Ghrhr/Hes
GO_CC_m3	GO:009963	postsynapt	3/540	37/23583	0.052243	0.45298	0.424684	Grik2/Grik4
GO_CC_m3	GO:003439	nuclear pe	6/540	117/23583	0.052494	0.45298	0.424684	Ghrhr/Hes
GO_CC_m3	GO:003151	motile ciliu	8/540	179/23583	0.054388	0.45298	0.424684	Catsper4/C
GO_CC_m3	GO:003017	integral co	3/540	38/23583	0.055792	0.45298	0.424684	Ier3ip1/Pcs
GO_CC_m3	GO:004445	microtubul	7/540	149/23583	0.055953	0.45298	0.424684	Ccdc92/Cc
GO_CC_m3	GO:000564	nuclear ou	2/540	17/23583	0.056735	0.45298	0.424684	Ccdc155/G
GO_CC_m3	GO:000589	acetylcholi	2/540	17/23583	0.056735	0.45298	0.424684	Chrna4/Ch
GO_CC_m3	GO:006182	sperm hea	2/540	17/23583	0.056735	0.45298	0.424684	Adam24/Ta
GO_CC_m3	GO:000590	microvillus	5/540	92/23583	0.060224	0.458943	0.430274	Aqp5/Enpp
GO_CC_m3	GO:004512	membrane	13/540	350/23583	0.060832	0.458943	0.430274	Gpm6b/Hc
GO_CC_m3	GO:009885	membrane	13/540	350/23583	0.060832	0.458943	0.430274	Gpm6b/Hc
GO_CC_m3	GO:000590	caveola	5/540	93/23583	0.062507	0.458943	0.430274	Hck/Hk1/L
GO_CC_m3	GO:003122	intrinsic co	3/540	40/23583	0.063223	0.458943	0.430274	Ier3ip1/Pcs
GO_CC_m3	GO:000596	mitochond	1/540	3/23583	0.067135	0.458943	0.430274	Dlat
GO_CC_m3	GO:000597	ribonucleo	1/540	3/23583	0.067135	0.458943	0.430274	Rrm2
GO_CC_m3	GO:003510	FACT comp	1/540	3/23583	0.067135	0.458943	0.430274	Mms22l
GO_CC_m3	GO:009705	CRLF-CLCF	1/540	3/23583	0.067135	0.458943	0.430274	Crlf1
GO_CC_m3	GO:009859	cytoplasmi	1/540	3/23583	0.067135	0.458943	0.430274	Exoc1
GO_CC_m3	GO:004319	dendritic s	4/540	67/23583	0.067518	0.458943	0.430274	Grm4/Nlgr
GO_CC_m3	GO:000563	nuclear inn	3/540	42/23583	0.071085	0.47047	0.441081	Ankle1/Gh
GO_CC_m3	GO:000572	nuclear het	3/540	42/23583	0.071085	0.47047	0.441081	Kdm4b/Sat
GO_CC_m3	GO:004521	postsynapt	10/540	258/23583	0.074254	0.482685	0.452533	Chrna4/Ch
GO_CC_m3	GO:004509	keratin fila	3/540	43/23583	0.075173	0.482685	0.452533	Fam83h/Kr
GO_CC_m3	GO:004303	costamere	2/540	20/23583	0.075809	0.482685	0.452533	Svil/Trpc1
GO_CC_m3	GO:004320	perikaryon	6/540	132/23583	0.083287	0.489174	0.458617	Grik2/Grik4
GO_CC_m3	GO:009706	synaptic m	12/540	334/23583	0.084277	0.489174	0.458617	Chrna4/Ch
GO_CC_m3	GO:009885	actin-base	8/540	199/23583	0.088041	0.489174	0.458617	Aqp5/Enpp
GO_CC_m3	GO:000207	inner acros	1/540	4/23583	0.088499	0.489174	0.458617	Cd46
GO_CC_m3	GO:003477	secretory g	1/540	4/23583	0.088499	0.489174	0.458617	Prtn3

GO_CC_m3	GO:004282	TAP compl	1/540	4/23583	0.088499	0.489174	0.458617	Pdia3
GO_CC_m3	GO:006020	cytoplasmi	1/540	4/23583	0.088499	0.489174	0.458617	Prtn3
GO_CC_m3	GO:007044	elongin co	1/540	4/23583	0.088499	0.489174	0.458617	Epop
GO_CC_m3	GO:007100	U2-type pc	1/540	4/23583	0.088499	0.489174	0.458617	Gcfc2
GO_CC_m3	GO:009748	multivesicu	1/540	4/23583	0.088499	0.489174	0.458617	Lrrk2
GO_CC_m3	GO:009883	postsynapt	1/540	4/23583	0.088499	0.489174	0.458617	Stx12
GO_CC_m3	GO:199069	USH2 com	1/540	4/23583	0.088499	0.489174	0.458617	Whrn
GO_CC_m3	GO:000572	pericentric	2/540	22/23583	0.089486	0.489253	0.45869	Kdm4b/Kd
GO_CC_m3	GO:001632	apical plasr	11/540	306/23583	0.095139	0.498334	0.467205	Aqp5/Crb3
GO_CC_m3	GO:000017	exosome (R	2/540	23/23583	0.096576	0.498334	0.467205	Dis3/Exosc
GO_CC_m3	GO:003012	clathrin ves	2/540	23/23583	0.096576	0.498334	0.467205	Ap1g2/Slc1
GO_CC_m3	GO:003470	sodium cha	2/540	23/23583	0.096576	0.498334	0.467205	Grik2/Grik4
GO_CC_m3	GO:190535	exoribonuc	2/540	23/23583	0.096576	0.498334	0.467205	Dis3/Exosc
GO_CC_m3	GO:003011	AP-type m	3/540	48/23583	0.097091	0.498334	0.467205	Ap1g2/Ap3
GO_CC_m3	GO:003011	clathrin coa	3/540	49/23583	0.101754	0.504724	0.473196	Ap1g2/Sclt
GO_CC_m3	GO:000208	acrosomal	2/540	24/23583	0.103819	0.504724	0.473196	Cd46/Fam1
GO_CC_m3	GO:003645	ESCRT com	2/540	24/23583	0.103819	0.504724	0.473196	Ubap1l/Vp
GO_CC_m3	GO:009880	plasma me	7/540	175/23583	0.108214	0.504724	0.473196	Bmp2/Chrn
GO_CC_m3	GO:000208	outer acros	1/540	5/23583	0.109374	0.504724	0.473196	Fam170b
GO_CC_m3	GO:005596	phosphory	1/540	5/23583	0.109374	0.504724	0.473196	Phkg2
GO_CC_m3	GO:003131	extrinsic cc	1/540	5/23583	0.109374	0.504724	0.473196	Sox10
GO_CC_m3	GO:003645	keratohyali	1/540	5/23583	0.109374	0.504724	0.473196	Cela2a
GO_CC_m3	GO:004282	MHC class	1/540	5/23583	0.109374	0.504724	0.473196	Pdia3
GO_CC_m3	GO:004315	acrosomal	1/540	5/23583	0.109374	0.504724	0.473196	Dld
GO_CC_m3	GO:007154	piP-body	1/540	5/23583	0.109374	0.504724	0.473196	Piwil4
GO_CC_m3	GO:003612	sperm flag	5/540	112/23583	0.114812	0.518056	0.485694	Catsper4/C
GO_CC_m3	GO:003470	ion channe	10/540	282/23583	0.115183	0.518056	0.485694	Catsper4/C
GO_CC_m3	GO:003646	cytoplasmi	7/540	178/23583	0.115508	0.518056	0.485694	Atxn2/Capr
GO_CC_m3	GO:003445	centriolar s	2/540	26/23583	0.118721	0.518056	0.485694	Cep131/Sd
GO_CC_m3	GO:009772	9+2 motile	5/540	114/23583	0.121255	0.518056	0.485694	Catsper4/C
GO_CC_m3	GO:003506	micro-ribo	5/540	115/23583	0.124539	0.518056	0.485694	Mir106b/M
GO_CC_m3	GO:000802	transcriptic	3/540	54/23583	0.126332	0.518056	0.485694	Ctr9/Epop/
GO_CC_m3	GO:003068	preribosom	2/540	27/23583	0.126361	0.518056	0.485694	Nip7/Nsa2
GO_CC_m3	GO:000214	stereocilia	1/540	6/23583	0.129771	0.518056	0.485694	Whrn
GO_CC_m3	GO:000214	stereocilia	1/540	6/23583	0.129771	0.518056	0.485694	Whrn
GO_CC_m3	GO:003089	checkpoint	1/540	6/23583	0.129771	0.518056	0.485694	Oraov1
GO_CC_m3	GO:004435	pinosome	1/540	6/23583	0.129771	0.518056	0.485694	Carmil2
GO_CC_m3	GO:004435	macropino	1/540	6/23583	0.129771	0.518056	0.485694	Carmil2
GO_CC_m3	GO:009713	Bcl-2 famil	1/540	6/23583	0.129771	0.518056	0.485694	Bcl2l1
GO_CC_m3	GO:009742	microtubul	1/540	6/23583	0.129771	0.518056	0.485694	Atat1
GO_CC_m3	GO:009755	transcriptic	1/540	6/23583	0.129771	0.518056	0.485694	Gtf2e1
GO_CC_m3	GO:199007	periciliary r	1/540	6/23583	0.129771	0.518056	0.485694	Whrn
GO_CC_m3	GO:004517	intercellula	3/540	56/23583	0.136705	0.527338	0.494397	Cep131/Fa
GO_CC_m3	GO:003065	transport v	5/540	119/23583	0.138076	0.527338	0.494397	Ap1g2/Bcl2
GO_CC_m3	GO:001986	outer mem	7/540	187/23583	0.138874	0.527338	0.494397	Ankzf1/Bcl2
GO_CC_m3	GO:003196	organelle c	7/540	187/23583	0.138874	0.527338	0.494397	Ankzf1/Bcl2
GO_CC_m3	GO:003577	ribonucleo	7/540	188/23583	0.141603	0.527338	0.494397	Atxn2/Capr
GO_CC_m3	GO:003013	clathrin ada	2/540	29/23583	0.141969	0.527338	0.494397	Ap1g2/Slc1

GO_CC_m3	GO:190249	transmemb	10/540	296/23583	0.143908	0.527338	0.494397	Catsper4/C
GO_CC_m3	GO:046655	anchored c	3/540	58/23583	0.147357	0.527338	0.494397	Mdga1/Prr
GO_CC_m3	GO:000213	stereocilia	1/540	7/23583	0.149703	0.527338	0.494397	Whrn
GO_CC_m3	GO:001627	prefoldin c	1/540	7/23583	0.149703	0.527338	0.494397	Pfdn4
GO_CC_m3	GO:003091	Smc5-Smc	1/540	7/23583	0.149703	0.527338	0.494397	Eid3
GO_CC_m3	GO:004525	oxoglutara	1/540	7/23583	0.149703	0.527338	0.494397	Dld
GO_CC_m3	GO:007154	pi-body	1/540	7/23583	0.149703	0.527338	0.494397	Mov10l1
GO_CC_m3	GO:010606	SUMO liga	1/540	7/23583	0.149703	0.527338	0.494397	Eid3
GO_CC_m3	GO:199063	proximal d	1/540	7/23583	0.149703	0.527338	0.494397	Ptpn5
GO_CC_m3	GO:199091	sperm hea	1/540	7/23583	0.149703	0.527338	0.494397	Adam24
GO_CC_m3	GO:003014	trans-Golg	2/540	30/23583	0.149919	0.527338	0.494397	Ap1g2/Slc1
GO_CC_m3	GO:000079	heterochro	4/540	90/23583	0.151628	0.529646	0.496561	Kdm4b/Kd
GO_CC_m3	GO:003066	clathrin-co	2/540	31/23583	0.157956	0.541785	0.507941	Ap1g2/Slc1
GO_CC_m3	GO:003283	dendrite cy	2/540	31/23583	0.157956	0.541785	0.507941	Grik2/Lrrk2
GO_CC_m3	GO:199035	transporter	10/540	303/23583	0.15954	0.541785	0.507941	Catsper4/C
GO_CC_m3	GO:000590	clathrin-co	3/540	61/23583	0.163815	0.541785	0.507941	Atat1/Bcl2l
GO_CC_m3	GO:009856	cytoplasmi	7/540	197/23583	0.167293	0.541785	0.507941	Dsg1a/Dtn
GO_CC_m3	GO:000595	cAMP-dep	1/540	8/23583	0.169179	0.541785	0.507941	Prkar1b
GO_CC_m3	GO:000829	F-actin cap	1/540	8/23583	0.169179	0.541785	0.507941	Carmil2
GO_CC_m3	GO:001659	Cdc73/Paf1	1/540	8/23583	0.169179	0.541785	0.507941	Ctr9
GO_CC_m3	GO:004320	axon hilloc	1/540	8/23583	0.169179	0.541785	0.507941	Prkcz
GO_CC_m3	GO:009884	postsynapt	1/540	8/23583	0.169179	0.541785	0.507941	Stx12
GO_CC_m3	GO:003017	integral co	5/540	130/23583	0.178361	0.541785	0.507941	Elovl2/Pdia
GO_CC_m3	GO:003065	cytoplasmi	9/540	274/23583	0.178895	0.541785	0.507941	Ap1g2/App
GO_CC_m3	GO:000838	IkappaB kin	1/540	9/23583	0.188209	0.541785	0.507941	Map3k13
GO_CC_m3	GO:003161	nuclear pe	1/540	9/23583	0.188209	0.541785	0.507941	Kdm4b
GO_CC_m3	GO:003574	myelin she	1/540	9/23583	0.188209	0.541785	0.507941	Prkcz
GO_CC_m3	GO:004517	apical corte	1/540	9/23583	0.188209	0.541785	0.507941	Prkcz
GO_CC_m3	GO:007101	post-mRN	1/540	9/23583	0.188209	0.541785	0.507941	Gcfc2
GO_CC_m3	GO:007143	clathrin co	1/540	9/23583	0.188209	0.541785	0.507941	Sclt1
GO_CC_m3	GO:199090	Wnt signal	1/540	9/23583	0.188209	0.541785	0.507941	Lrrk2
GO_CC_m3	GO:000583	heterotrim	2/540	35/23583	0.190808	0.541785	0.507941	Gng10/Gng
GO_CC_m3	GO:000818	COP9 signa	2/540	35/23583	0.190808	0.541785	0.507941	Cops7a/Nc
GO_CC_m3	GO:003586	site of dou	2/540	35/23583	0.190808	0.541785	0.507941	Kdm4d/Ora
GO_CC_m3	GO:190536	GTPase co	2/540	35/23583	0.190808	0.541785	0.507941	Gng10/Gng
GO_CC_m3	GO:003011	membrane	4/540	99/23583	0.191904	0.541785	0.507941	Ap1g2/Ap3
GO_CC_m3	GO:004847	coated me	4/540	99/23583	0.191904	0.541785	0.507941	Ap1g2/Ap3
GO_CC_m3	GO:005502	nuclear DN	5/540	135/23583	0.197984	0.541785	0.507941	Ctdp1/Ctr9
GO_CC_m3	GO:000589	voltage-ga	2/540	36/23583	0.199161	0.541785	0.507941	Catsper4/C
GO_CC_m3	GO:001503	Cajal body	2/540	36/23583	0.199161	0.541785	0.507941	Ak6/Isg20
GO_CC_m3	GO:000042	DNA-direc	5/540	136/23583	0.201995	0.541785	0.507941	Ctdp1/Ctr9
GO_CC_m3	GO:003122	intrinsic co	5/540	136/23583	0.201995	0.541785	0.507941	Elovl2/Pdia
GO_CC_m3	GO:003130	integral co	6/540	172/23583	0.202798	0.541785	0.507941	Ankle1/Ier3
GO_CC_m3	GO:000564	nuclear po	3/540	68/23583	0.204099	0.541785	0.507941	Mad2l1/Mc
GO_CC_m3	GO:003001	myofibril	7/540	209/23583	0.204444	0.541785	0.507941	Rpl6l/Mybp
GO_CC_m3	GO:003470	cation cha	7/540	209/23583	0.204444	0.541785	0.507941	Catsper4/C
GO_CC_m3	GO:004444	endosomal	7/540	209/23583	0.204444	0.541785	0.507941	Cyb561a3/
GO_CC_m3	GO:000563	nuclear env	12/540	399/23583	0.206614	0.541785	0.507941	Ankle1/Ccc

GO_CC_m3	GO:000577	vacuolar lu	1/540	10/23583	0.206804	0.541785	0.507941	Prtn3
GO_CC_m3	GO:003141	N-terminal	1/540	10/23583	0.206804	0.541785	0.507941	Naa25
GO_CC_m3	GO:003198	vesicle lum	1/540	10/23583	0.206804	0.541785	0.507941	Prtn3
GO_CC_m3	GO:003499	microtubul	1/540	10/23583	0.206804	0.541785	0.507941	Ccdc155
GO_CC_m3	GO:003499	meiotic nu	1/540	10/23583	0.206804	0.541785	0.507941	Ccdc155
GO_CC_m3	GO:004429	dendritic g	1/540	10/23583	0.206804	0.541785	0.507941	Ptch1
GO_CC_m3	GO:004524	dihydrolipo	1/540	10/23583	0.206804	0.541785	0.507941	Dld
GO_CC_m3	GO:004878	presynapti	1/540	10/23583	0.206804	0.541785	0.507941	Grm4
GO_CC_m3	GO:006009	kinocilium	1/540	10/23583	0.206804	0.541785	0.507941	Mkks
GO_CC_m3	GO:009773	9+2 non-n	1/540	10/23583	0.206804	0.541785	0.507941	Mkks
GO_CC_m3	GO:010608	nuclear me	1/540	10/23583	0.206804	0.541785	0.507941	Ccdc155
GO_CC_m3	GO:010609	nuclear me	1/540	10/23583	0.206804	0.541785	0.507941	Ccdc155
GO_CC_m3	GO:000565	replication	3/540	69/23583	0.210033	0.542169	0.508302	D330045A
GO_CC_m3	GO:003088	RNA polym	5/540	138/23583	0.210099	0.542169	0.508302	Ctdp1/Ctr9
GO_CC_m3	GO:004517	apical part	12/540	403/23583	0.215947	0.542169	0.508302	Aqp5/Crb3
GO_CC_m3	GO:009073	site of DN	2/540	38/23583	0.215988	0.542169	0.508302	Kdm4d/Or
GO_CC_m3	GO:000093	P-body	3/540	70/23583	0.216004	0.542169	0.508302	Caprin1/Tr
GO_CC_m3	GO:000217	manchette	1/540	11/23583	0.224975	0.542169	0.508302	Cep131
GO_CC_m3	GO:000558	fibrillar coll	1/540	11/23583	0.224975	0.542169	0.508302	Col27a1
GO_CC_m3	GO:003006	mitochond	1/540	11/23583	0.224975	0.542169	0.508302	Fdx1
GO_CC_m3	GO:004255	MCM comp	1/540	11/23583	0.224975	0.542169	0.508302	Mms22l
GO_CC_m3	GO:004461	nuclear po	1/540	11/23583	0.224975	0.542169	0.508302	Nxt1
GO_CC_m3	GO:004475	autolysoso	1/540	11/23583	0.224975	0.542169	0.508302	Lrrk2
GO_CC_m3	GO:007057	RISC-loadi	1/540	11/23583	0.224975	0.542169	0.508302	Mir28a
GO_CC_m3	GO:007085	cell body fi	1/540	11/23583	0.224975	0.542169	0.508302	Srd5a1
GO_CC_m3	GO:007268	meiotic spi	1/540	11/23583	0.224975	0.542169	0.508302	Ccdc155
GO_CC_m3	GO:009864	banded co	1/540	11/23583	0.224975	0.542169	0.508302	Col27a1
GO_CC_m3	GO:199090	beta-caten	1/540	11/23583	0.224975	0.542169	0.508302	Tle4
GO_CC_m3	GO:199020	oxidoreduc	4/540	106/23583	0.225275	0.542169	0.508302	Dlat/Dld/G
GO_CC_m3	GO:003215	cleavage fu	2/540	40/23583	0.232935	0.557935	0.523082	Nf2/Rhob
GO_CC_m3	GO:000989	cytoplasmi	6/540	182/23583	0.239426	0.56633	0.530953	Dsg1a/Dtn
GO_CC_m3	GO:004323	receptor cc	11/540	374/23583	0.240531	0.56633	0.530953	Bmp2/Chr
GO_CC_m3	GO:003012	AP-2 adap	1/540	12/23583	0.242729	0.56633	0.530953	Slc18a3
GO_CC_m3	GO:003012	AP-3 adap	1/540	12/23583	0.242729	0.56633	0.530953	Ap3s1
GO_CC_m3	GO:009752	sperm plas	1/540	12/23583	0.242729	0.56633	0.530953	Adam24
GO_CC_m3	GO:001989	extrinsic cc	6/540	183/23583	0.243196	0.56633	0.530953	Cdh26/Dtn
GO_CC_m3	GO:001659	DNA-direc	4/540	110/23583	0.244973	0.56784	0.532368	Ctdp1/Ctr9
GO_CC_m3	GO:004329	contractile	7/540	223/23583	0.25129	0.571263	0.535578	Rpl6l/Myb
GO_CC_m3	GO:000580	trans-Golg	6/540	186/23583	0.254607	0.571263	0.535578	Ap1g2/Ap
GO_CC_m3	GO:001000	endosome	6/540	186/23583	0.254607	0.571263	0.535578	Cyb561a3/
GO_CC_m3	GO:003130	intrinsic co	6/540	186/23583	0.254607	0.571263	0.535578	Ankle1/Ier
GO_CC_m3	GO:003167	A band	2/540	43/23583	0.258483	0.571263	0.535578	Rpl6l/Myb
GO_CC_m3	GO:003123	extrinsic cc	4/540	113/23583	0.259987	0.571263	0.535578	Dtna/Gng1
GO_CC_m3	GO:000576	primary lys	1/540	13/23583	0.260078	0.571263	0.535578	Prtn3
GO_CC_m3	GO:003012	clathrin co	1/540	13/23583	0.260078	0.571263	0.535578	Slc18a3
GO_CC_m3	GO:003193	TORC2 cor	1/540	13/23583	0.260078	0.571263	0.535578	Prr5
GO_CC_m3	GO:004258	azurophil g	1/540	13/23583	0.260078	0.571263	0.535578	Prtn3
GO_CC_m3	GO:004523	tricarboxyli	1/540	13/23583	0.260078	0.571263	0.535578	Dld

GO_CC_m	GO:009744	astrocyte p	1/540	13/23583	0.260078	0.571263	0.535578	Syt4
GO_CC_m	GO:00125	vesicle mer	9/540	304/23583	0.263352	0.575939	0.539961	Ap1g2/App
GO_CC_m	GO:00427	presynapti	3/540	78/23583	0.264855	0.57672	0.540694	Grik2/Grik
GO_CC_m	GO:00104	cytoplasmi	2/540	45/23583	0.275541	0.587958	0.55123	Atxn2/Cap
GO_CC_m	GO:012011	neuron prc	2/540	45/23583	0.275541	0.587958	0.55123	Grik2/Lrrk2
GO_CC_m	GO:00057	DNA-direc	1/540	14/23583	0.27703	0.587958	0.55123	Ippk
GO_CC_m	GO:00057	secondary	1/540	14/23583	0.27703	0.587958	0.55123	Lrrk2
GO_CC_m	GO:00306	clathrin-co	1/540	14/23583	0.27703	0.587958	0.55123	Slc18a3
GO_CC_m	GO:00987	outer mito	1/540	14/23583	0.27703	0.587958	0.55123	Ankzf1
GO_CC_m	GO:00306	preriboson	3/540	81/23583	0.283526	0.599217	0.561786	Nip7/Nol1
GO_CC_m	GO:00310	BLOC-1 co	1/540	15/23583	0.293594	0.615325	0.576887	Stx12
GO_CC_m	GO:004324	Fanconi an	1/540	15/23583	0.293594	0.615325	0.576887	Fanci
GO_CC_m	GO:00453	phagocytic	3/540	83/23583	0.296036	0.617867	0.57927	Fmnl1/Pld
GO_CC_m	GO:00319	nuclear me	7/540	238/23583	0.304606	0.618535	0.579897	Ankle1/Cc
GO_CC_m	GO:004444	contractile	6/540	199/23583	0.305539	0.618535	0.579897	Rpl6l/Myb
GO_CC_m	GO:00306	secretory g	3/540	85/23583	0.308577	0.618535	0.579897	Cd46/Fam
GO_CC_m	GO:000191	photorece	2/540	49/23583	0.309558	0.618535	0.579897	Sag/Whrn
GO_CC_m	GO:00056	integral co	1/540	16/23583	0.30978	0.618535	0.579897	Ankle1
GO_CC_m	GO:00058	muscle my	1/540	16/23583	0.30978	0.618535	0.579897	Mybph
GO_CC_m	GO:00312	intrinsic co	1/540	16/23583	0.30978	0.618535	0.579897	Ankle1
GO_CC_m	GO:00382	TOR comp	1/540	16/23583	0.30978	0.618535	0.579897	Prr5
GO_CC_m	GO:00431	varicosity	1/540	16/23583	0.30978	0.618535	0.579897	Ucn
GO_CC_m	GO:00970	perinuclea	1/540	16/23583	0.30978	0.618535	0.579897	Syt6
GO_CC_m	GO:00057	Golgi-asso	4/540	123/23583	0.311112	0.618535	0.579897	Ap1g2/Ier
GO_CC_m	GO:00058	intermedia	4/540	123/23583	0.311112	0.618535	0.579897	Fam83h/Kr
GO_CC_m	GO:004511	intermedia	5/540	163/23583	0.318223	0.621995	0.583141	Fam83h/Kr
GO_CC_m	GO:003067	synaptic ve	3/540	87/23583	0.321136	0.621995	0.583141	Bcl2l1/Stx1
GO_CC_m	GO:00995	exocytic ve	3/540	87/23583	0.321136	0.621995	0.583141	Bcl2l1/Stx1
GO_CC_m	GO:000577	integral co	1/540	17/23583	0.325595	0.621995	0.583141	Slc25a17
GO_CC_m	GO:001601	dystrophin	1/540	17/23583	0.325595	0.621995	0.583141	Dtna
GO_CC_m	GO:00324	filopodium	1/540	17/23583	0.325595	0.621995	0.583141	Nlgn1
GO_CC_m	GO:00329	myosin fila	1/540	17/23583	0.325595	0.621995	0.583141	Mybph
GO_CC_m	GO:00444	nuclear me	1/540	17/23583	0.325595	0.621995	0.583141	Ankle1
GO_CC_m	GO:00906	glycoprote	1/540	17/23583	0.325595	0.621995	0.583141	Dtna
GO_CC_m	GO:009864	complex o	1/540	17/23583	0.325595	0.621995	0.583141	Col27a1
GO_CC_m	GO:003012	vesicle coa	2/540	51/23583	0.326455	0.621995	0.583141	Ap1g2/Slc
GO_CC_m	GO:00321	cell divisio	2/540	52/23583	0.334863	0.628379	0.589126	Nf2/Rhob
GO_CC_m	GO:00018	phagocytic	1/540	18/23583	0.341049	0.628379	0.589126	Arhgap25
GO_CC_m	GO:00165	NuRD com	1/540	18/23583	0.341049	0.628379	0.589126	Chd3
GO_CC_m	GO:00301	clathrin co	1/540	18/23583	0.341049	0.628379	0.589126	Slc18a3
GO_CC_m	GO:003104	dense core	1/540	18/23583	0.341049	0.628379	0.589126	Syt4
GO_CC_m	GO:00312	intrinsic co	1/540	18/23583	0.341049	0.628379	0.589126	Slc25a17
GO_CC_m	GO:00350	ESC/E(Z) c	1/540	18/23583	0.341049	0.628379	0.589126	Epop
GO_CC_m	GO:00442	dendrite te	1/540	18/23583	0.341049	0.628379	0.589126	Ptch1
GO_CC_m	GO:009054	CHD-type	1/540	18/23583	0.341049	0.628379	0.589126	Chd3
GO_CC_m	GO:000574	mitochond	5/540	169/23583	0.345318	0.633923	0.594323	Ankzf1/Bcl
GO_CC_m	GO:00301	transport v	8/540	291/23583	0.350329	0.640783	0.600755	Ap1g2/Bcl
GO_CC_m	GO:000014	exocyst	1/540	19/23583	0.356149	0.642858	0.6027	Exoc1

GO_CC_m3	GO:00320	integrator	1/540	19/23583	0.356149	0.642858	0.6027	Ints2
GO_CC_m3	GO:00324	stereociliur	1/540	19/23583	0.356149	0.642858	0.6027	Whrn
GO_CC_m3	GO:00987	Golgi subc	11/540	416/23583	0.356575	0.642858	0.6027	Ap1g2/Ap3
GO_CC_m3	GO:00347	potassium	3/540	93/23583	0.358781	0.644211	0.603969	Grik2/Grik4
GO_CC_m3	GO:00347	calcium ch	2/540	55/23583	0.359888	0.644211	0.603969	Catsper4/C
GO_CC_m3	GO:00703	exocytic ve	6/540	213/23583	0.362133	0.645933	0.605583	Bcl2l1/Lrrk
GO_CC_m3	GO:00198	extrinsic co	8/540	296/23583	0.367586	0.65005	0.609443	Cdh26/Dtn
GO_CC_m3	GO:00302	integral co	1/540	20/23583	0.370903	0.65005	0.609443	Stx12
GO_CC_m3	GO:00310	BLOC com	1/540	20/23583	0.370903	0.65005	0.609443	Stx12
GO_CC_m3	GO:00313	anchored c	1/540	20/23583	0.370903	0.65005	0.609443	Prn
GO_CC_m3	GO:00973	glial cell pr	1/540	20/23583	0.370903	0.65005	0.609443	Syt4
GO_CC_m3	GO:00324	stereociliur	2/540	58/23583	0.384557	0.668332	0.626583	Mkks/Whrr
GO_CC_m3	GO:00056	anaphase-	1/540	21/23583	0.385321	0.668332	0.626583	Ube2c
GO_CC_m3	GO:00056	telomerase	1/540	21/23583	0.385321	0.668332	0.626583	Gnl3l
GO_CC_m3	GO:00306	endocytic	1/540	22/23583	0.399408	0.686874	0.643967	Slc18a3
GO_CC_m3	GO:00309	intraciliary	1/540	22/23583	0.399408	0.686874	0.643967	Ttc30a1
GO_CC_m3	GO:00306	Golgi-asso	2/540	60/23583	0.400773	0.686874	0.643967	Ap1g2/Slc
GO_CC_m3	GO:00156	actin cytos	12/540	474/23583	0.402838	0.686874	0.643967	Ablim3/Fln
GO_CC_m3	GO:00444	Golgi appa	12/540	474/23583	0.402838	0.686874	0.643967	Ap1g2/Ap3
GO_CC_m3	GO:000011	histone de	2/540	61/23583	0.408805	0.694692	0.651297	Chd3/Dntti
GO_CC_m3	GO:00312	intrinsic co	1/540	23/23583	0.413173	0.699751	0.656039	Prn
GO_CC_m3	GO:004444	ciliary part	11/540	437/23583	0.417737	0.702981	0.659068	Catsper4/C
GO_CC_m3	GO:003001	sarcomere	5/540	185/23583	0.417876	0.702981	0.659068	Rpl6l/Myb
GO_CC_m3	GO:00164	myosin II c	1/540	24/23583	0.426623	0.708223	0.663982	Mybph
GO_CC_m3	GO:00300	desmosom	1/540	24/23583	0.426623	0.708223	0.663982	Dsg1a
GO_CC_m3	GO:00314	M band	1/540	24/23583	0.426623	0.708223	0.663982	Mybph
GO_CC_m3	GO:00325	trans-Golg	1/540	24/23583	0.426623	0.708223	0.663982	Pld4
GO_CC_m3	GO:00001	Golgi mem	6/540	232/23583	0.439542	0.722883	0.677726	Cux2/Ier3i
GO_CC_m3	GO:00353	transcriptic	1/540	25/23583	0.439766	0.722883	0.677726	Ctr9
GO_CC_m3	GO:00453	clathrin-co	1/540	25/23583	0.439766	0.722883	0.677726	Slc18a3
GO_CC_m3	GO:00616	transferase	7/540	275/23583	0.442077	0.724315	0.679069	Ctdp1/Ctr9
GO_CC_m3	GO:00447	nuclear tra	5/540	191/23583	0.444832	0.726463	0.681083	Gtf2e1/Ho
GO_CC_m3	GO:00304	growth cor	5/540	192/23583	0.449297	0.73138	0.685692	Hnrnpr/Lrr
GO_CC_m3	GO:00972	sperm mid	1/540	26/23583	0.452608	0.734392	0.688517	Tacr1
GO_CC_m3	GO:00080	synaptic ve	5/540	195/23583	0.462634	0.745756	0.699171	Bcl2l1/Lrrk
GO_CC_m3	GO:00058	cytoplasmi	1/540	27/23583	0.465155	0.745756	0.699171	BC048507
GO_CC_m3	GO:00423	sarcolemm	4/540	154/23583	0.470692	0.745756	0.699171	Clcn1/Dtna
GO_CC_m3	GO:00057	mitochond	2/540	69/23583	0.471023	0.745756	0.699171	Pdia3/Preli
GO_CC_m3	GO:00306	coated ves	2/540	69/23583	0.471023	0.745756	0.699171	Ap1g2/Slc
GO_CC_m3	GO:00315	brush bord	2/540	69/23583	0.471023	0.745756	0.699171	Slc19a1/Sl
GO_CC_m3	GO:00321	cell divisior	2/540	69/23583	0.471023	0.745756	0.699171	Nf2/Rhob
GO_CC_m3	GO:00304	site of pola	5/540	197/23583	0.471472	0.745756	0.699171	Hnrnpr/Lrr
GO_CC_m3	GO:00058	cytoplasmi	2/540	70/23583	0.478524	0.752179	0.705193	Ckap2/Mtu
GO_CC_m3	GO:00190	SCF ubiqui	2/540	70/23583	0.478524	0.752179	0.705193	Ccnf/Tdpo
GO_CC_m3	GO:001634	catenin cor	1/540	29/23583	0.489397	0.75917	0.711746	Cdh26
GO_CC_m3	GO:00985	intrinsic co	1/540	29/23583	0.489397	0.75917	0.711746	Stx12
GO_CC_m3	GO:19025	endoribonu	1/540	29/23583	0.489397	0.75917	0.711746	Mir28a
GO_CC_m3	GO:190534	endonucle	1/540	29/23583	0.489397	0.75917	0.711746	Mir28a

GO_CC_m3	GO:009057	RNA polym	4/540	158/23583	0.490517	0.75917	0.711746	Gtf2e1/Hox
GO_CC_m3	GO:003586	ciliary trans	2/540	72/23583	0.493327	0.761177	0.713628	Cep131/W
GO_CC_m3	GO:003013	endocytic v	4/540	160/23583	0.500314	0.766124	0.718266	Fmnl1/Pld4
GO_CC_m3	GO:001660	PML body	2/540	73/23583	0.500629	0.766124	0.718266	Isg20/Satb
GO_CC_m3	GO:004278	polysomal	1/540	30/23583	0.501103	0.766124	0.718266	Rpl6l
GO_CC_m3	GO:001986	organelle i	11/540	468/23583	0.507701	0.771767	0.723557	Ankle1/Bcl
GO_CC_m3	GO:001652	sarcoplasm	2/540	74/23583	0.507863	0.771767	0.723557	Flnc/Rasd1
GO_CC_m3	GO:000040	phagophor	1/540	31/23583	0.512541	0.774198	0.725836	Stx12
GO_CC_m3	GO:005123	spindle mic	1/540	31/23583	0.512541	0.774198	0.725836	Ctdp1
GO_CC_m3	GO:000592	bicellular ti	3/540	119/23583	0.514923	0.775468	0.727026	Crb3/Prkcz
GO_CC_m3	GO:000092	spindle pol	3/540	120/23583	0.520546	0.781595	0.732771	Ccdc155/C
GO_CC_m3	GO:001623	inclusion b	2/540	76/23583	0.522123	0.781631	0.732804	Bag5/Lrrk2
GO_CC_m3	GO:009056	nuclear tra	1/540	32/23583	0.523717	0.781691	0.732861	Chd3
GO_CC_m3	GO:000588	actin filame	3/540	121/23583	0.526133	0.782973	0.734062	Hck/Prkcz/
GO_CC_m3	GO:000584	polysome	2/540	77/23583	0.529149	0.784032	0.735055	Atxn2/Rpl6
GO_CC_m3	GO:007016	occluding j	3/540	122/23583	0.531684	0.784032	0.735055	Crb3/Prkcz
GO_CC_m3	GO:001406	postsynapt	6/540	256/23583	0.534284	0.784032	0.735055	Grik2/Grik4
GO_CC_m3	GO:000592	gap junctic	1/540	33/23583	0.534638	0.784032	0.735055	Calb2
GO_CC_m3	GO:003068	90S preribo	1/540	33/23583	0.534638	0.784032	0.735055	Nol10
GO_CC_m3	GO:004320	myelin shea	5/540	213/23583	0.54024	0.788191	0.738954	Dlat/Dld/P
GO_CC_m3	GO:009957	postsynapt	6/540	258/23583	0.541893	0.788191	0.738954	Grik2/Grik4
GO_CC_m3	GO:003122	anchored c	4/540	169/23583	0.543328	0.788191	0.738954	Mdga1/Ple
GO_CC_m3	GO:000579	smooth en	1/540	34/23583	0.545309	0.788191	0.738954	Pdia3
GO_CC_m3	GO:003099	intraciliary	1/540	34/23583	0.545309	0.788191	0.738954	Ttc30a1
GO_CC_m3	GO:003227	asymmetric	6/540	260/23583	0.549448	0.78853	0.739273	Grik2/Grik4
GO_CC_m3	GO:190255	serine/thre	2/540	80/23583	0.549801	0.78853	0.739273	Map3k13/
GO_CC_m3	GO:000177	immunolog	1/540	35/23583	0.555735	0.78853	0.739273	Carmil2
GO_CC_m3	GO:000577	multivesicu	1/540	35/23583	0.555735	0.78853	0.739273	Lrrk2
GO_CC_m3	GO:007101	precatalytic	1/540	35/23583	0.555735	0.78853	0.739273	Smu1
GO_CC_m3	GO:008000	Cul4-RING	1/540	35/23583	0.555735	0.78853	0.739273	Dcaf12l2
GO_CC_m3	GO:009898	neuron to	6/540	263/23583	0.560674	0.78853	0.739273	Grik2/Grik4
GO_CC_m3	GO:003197	organelle e	2/540	82/23583	0.563211	0.78853	0.739273	Pdia3/Preli
GO_CC_m3	GO:003606	ciliary basa	3/540	128/23583	0.564203	0.78853	0.739273	Cetn4/Mkk
GO_CC_m3	GO:000566	transcriptic	9/540	399/23583	0.565114	0.78853	0.739273	Atf5/Gtf2e
GO_CC_m3	GO:001659	mediator c	1/540	36/23583	0.565923	0.78853	0.739273	Med30
GO_CC_m3	GO:003204	small-subu	1/540	36/23583	0.565923	0.78853	0.739273	Nol10
GO_CC_m3	GO:005503	recycling e	1/540	36/23583	0.565923	0.78853	0.739273	Pigr
GO_CC_m3	GO:000566	transcriptic	1/540	37/23583	0.575878	0.800184	0.750198	Gtf2e1
GO_CC_m3	GO:003049	midbody	3/540	132/23583	0.585102	0.809228	0.758678	Ctdp1/Lap
GO_CC_m3	GO:000079	euchromat	1/540	38/23583	0.585604	0.809228	0.758678	Uhrf1
GO_CC_m3	GO:003131	extrinsic co	1/540	39/23583	0.595109	0.816135	0.765153	Sox10
GO_CC_m3	GO:004429	axonal grow	1/540	39/23583	0.595109	0.816135	0.765153	Ptch1
GO_CC_m3	GO:003017	filopodium	2/540	87/23583	0.59547	0.816135	0.765153	Nf2/Nlgn1
GO_CC_m3	GO:009886	cluster of a	4/540	182/23583	0.601901	0.816331	0.765337	Mkks/Slc19
GO_CC_m3	GO:000015	nuclear ubi	1/540	40/23583	0.604395	0.816331	0.765337	Ube2c
GO_CC_m3	GO:004359	nuclear rep	1/540	40/23583	0.604395	0.816331	0.765337	Mms22l
GO_CC_m3	GO:004878	presynaptic	1/540	40/23583	0.604395	0.816331	0.765337	Grm4
GO_CC_m3	GO:009973	cell cortex	1/540	40/23583	0.604395	0.816331	0.765337	Prkcz

GO_CC_m3	GO:004329	apical junc	3/540	136/23583	0.605351	0.816331	0.765337	Crb3/Prkcz
GO_CC_m3	GO:000577	peroxisoma	1/540	42/23583	0.622335	0.833675	0.781598	Slc25a17
GO_CC_m3	GO:003190	microbody	1/540	42/23583	0.622335	0.833675	0.781598	Slc25a17
GO_CC_m3	GO:004443	vacuolar pa	4/540	187/23583	0.623185	0.833675	0.781598	Cyb561a3/
GO_CC_m3	GO:004257	immunoglo	3/540	141/23583	0.629726	0.835899	0.783683	Ighv1-53/I
GO_CC_m3	GO:000992	basal plasn	1/540	43/23583	0.630998	0.835899	0.783683	Aqp5
GO_CC_m3	GO:003190	early endos	1/540	43/23583	0.630998	0.835899	0.783683	Syndig1
GO_CC_m3	GO:000077	chromosor	4/540	189/23583	0.631494	0.835899	0.783683	Fbxo28/Kd
GO_CC_m3	GO:002262	cytosolic la	2/540	94/23583	0.637582	0.836136	0.783905	Rpl6l/Rpl39
GO_CC_m3	GO:000079	condensed	5/540	238/23583	0.638399	0.836136	0.783905	Ccdc155/E
GO_CC_m3	GO:009773	non-motile	3/540	143/23583	0.63918	0.836136	0.783905	Mkks/Sag/
GO_CC_m3	GO:003239	photorecep	1/540	44/23583	0.639463	0.836136	0.783905	Whrn
GO_CC_m3	GO:003013	clathrin-co	2/540	95/23583	0.643309	0.836136	0.783905	Ap1g2/Slc1
GO_CC_m3	GO:007268	mitotic spir	2/540	95/23583	0.643309	0.836136	0.783905	Atat1/Mad
GO_CC_m3	GO:190356	extracellula	2/540	95/23583	0.643309	0.836136	0.783905	Mir106b/Sy
GO_CC_m3	GO:000591	cell-cell jur	10/540	473/23583	0.645282	0.836352	0.784108	Calb2/Cdh
GO_CC_m3	GO:003470	chloride ch	1/540	45/23583	0.647734	0.836352	0.784108	Clcn1
GO_CC_m3	GO:001981	immunoglo	3/540	145/23583	0.648464	0.836352	0.784108	Ighv1-53/I
GO_CC_m3	GO:003190	late endoso	1/540	46/23583	0.655815	0.841518	0.788951	Cyb561a3
GO_CC_m3	GO:003194	filamentou	1/540	46/23583	0.655815	0.841518	0.788951	Prkcz
GO_CC_m3	GO:009868	chromosor	6/540	293/23583	0.664814	0.85065	0.797512	Ccdc155/E
GO_CC_m3	GO:001593	large ribos	3/540	149/23583	0.666519	0.85065	0.797512	Rpl6l/Mrpl4
GO_CC_m3	GO:004444	cytosolic pa	6/540	294/23583	0.668006	0.85065	0.797512	Rpl6l/Map3
GO_CC_m3	GO:003146	cullin-RINC	4/540	199/23583	0.671247	0.8507	0.79756	Ccnf/Dcaf1
GO_CC_m3	GO:003242	stereociliur	1/540	48/23583	0.671428	0.8507	0.79756	Whrn
GO_CC_m3	GO:003151	PcG protei	1/540	49/23583	0.678967	0.858091	0.804488	Epop
GO_CC_m3	GO:003013	COPII-coat	1/540	50/23583	0.686333	0.865227	0.811178	Ier3ip1
GO_CC_m3	GO:000989	external sic	10/540	491/23583	0.690392	0.865622	0.811549	Adam24/B
GO_CC_m3	GO:000080	lateral elen	2/540	104/23583	0.691666	0.865622	0.811549	Ccdc155/X
GO_CC_m3	GO:001660	nuclear spe	6/540	302/23583	0.692837	0.865622	0.811549	Ddx46/Gpa
GO_CC_m3	GO:003120	SNARE cor	1/540	51/23583	0.69353	0.865622	0.811549	Stx12
GO_CC_m3	GO:007256	blood micr	3/540	156/23583	0.696468	0.867137	0.81297	Ighv1-53/I
GO_CC_m3	GO:002262	cytosolic ril	3/540	157/23583	0.700576	0.869284	0.814983	Rpl6l/Rpl39
GO_CC_m3	GO:000078	chromosor	2/540	106/23583	0.701649	0.869284	0.814983	Ccdc155/E
GO_CC_m3	GO:004323	extracellula	2/540	107/23583	0.706539	0.869436	0.815124	Mir106b/Sy
GO_CC_m3	GO:009773	photorecep	2/540	107/23583	0.706539	0.869436	0.815124	Sag/Whrn
GO_CC_m3	GO:004217	nuclear out	10/540	498/23583	0.706957	0.869436	0.815124	Ccdc155/E
GO_CC_m3	GO:003002	lamellipodi	3/540	160/23583	0.712646	0.871886	0.817421	Ablim3/Nf2
GO_CC_m3	GO:000031	organellar	1/540	54/23583	0.714149	0.871886	0.817421	Mrpl41
GO_CC_m3	GO:000576	mitochond	1/540	54/23583	0.714149	0.871886	0.817421	Mrpl41
GO_CC_m3	GO:190291	protein kin	2/540	109/23583	0.716119	0.872174	0.817691	Map3k13/F
GO_CC_m3	GO:004445	mitochond	4/540	214/23583	0.725146	0.880409	0.825412	Ankzf1/Fdx
GO_CC_m3	GO:002262	cytosolic sr	1/540	56/23583	0.727119	0.880409	0.825412	Rps3a1
GO_CC_m3	GO:009773	9+0 non-n	2/540	112/23583	0.729995	0.880409	0.825412	Sag/Whrn
GO_CC_m3	GO:003028	dynein con	1/540	57/23583	0.733383	0.880409	0.825412	BC048507
GO_CC_m3	GO:004443	microbody	1/540	57/23583	0.733383	0.880409	0.825412	Slc25a17
GO_CC_m3	GO:004443	peroxisoma	1/540	57/23583	0.733383	0.880409	0.825412	Slc25a17
GO_CC_m3	GO:001632	lateral plas	1/540	58/23583	0.739502	0.885642	0.830319	Dsg1a

GO_CC_m3	GO:003013	coated ves	3/540	169/23583	0.746604	0.892023	0.836301	Ap1g2/Ier3
GO_CC_m3	GO:000576	lysosomal r	2/540	118/23583	0.756024	0.898696	0.842557	Cyb561a3/
GO_CC_m3	GO:009885	lytic vacuol	2/540	118/23583	0.756024	0.898696	0.842557	Cyb561a3/
GO_CC_m3	GO:000584	ribosome	5/540	275/23583	0.757549	0.898696	0.842557	Rpl6l/Mrpl4
GO_CC_m3	GO:000574	mitochond	8/540	426/23583	0.762354	0.902268	0.845906	Bcl2l1/Bcs1
GO_CC_m3	GO:004439	ribosomal s	4/540	231/23583	0.777962	0.908365	0.851622	Rpl6l/Mrpl4
GO_CC_m3	GO:000568	U2-type sp	1/540	65/23583	0.778589	0.908365	0.851622	Gcfc2
GO_CC_m3	GO:001645	myosin con	1/540	65/23583	0.778589	0.908365	0.851622	Mybph
GO_CC_m3	GO:001652	sarcoplasm	1/540	65/23583	0.778589	0.908365	0.851622	Rasd1
GO_CC_m3	GO:009902	tethering c	1/540	65/23583	0.778589	0.908365	0.851622	Exoc1
GO_CC_m3	GO:000577	late endoso	3/540	180/23583	0.783669	0.908365	0.851622	Cyb561a3/
GO_CC_m3	GO:004517	basal part o	1/540	66/23583	0.783673	0.908365	0.851622	Aqp5
GO_CC_m3	GO:004444	cell cortex	3/540	181/23583	0.786805	0.908365	0.851622	Exoc1/Nf2/
GO_CC_m3	GO:004445	nucleolar p	3/540	181/23583	0.786805	0.908365	0.851622	Ddx46/Ippl
GO_CC_m3	GO:005503	recycling e	2/540	126/23583	0.787338	0.908365	0.851622	Pigr/Stx12
GO_CC_m3	GO:000079	synaptonem	2/540	127/23583	0.790994	0.908365	0.851622	Ccdc155/X
GO_CC_m3	GO:009908	synaptonem	2/540	127/23583	0.790994	0.908365	0.851622	Ccdc155/X
GO_CC_m3	GO:000079	nuclear chr	7/540	390/23583	0.79221	0.908365	0.851622	Chd3/Hypm
GO_CC_m3	GO:000015	ubiquitin lig	6/540	340/23583	0.793479	0.908365	0.851622	Ccnf/Dcaf1
GO_CC_m3	GO:000165	fibrillar cen	2/540	128/23583	0.794593	0.908365	0.851622	Ddx46/Kdm
GO_CC_m3	GO:000079	condensed	3/540	185/23583	0.798978	0.911305	0.854379	Ccdc155/C
GO_CC_m3	GO:000077	kinetochore	2/540	130/23583	0.801629	0.91161	0.854665	Fbxo28/Ma
GO_CC_m3	GO:000577	autophago	1/540	70/23583	0.80287	0.91161	0.854665	Lrrk2
GO_CC_m3	GO:000590	brush bord	2/540	131/23583	0.805066	0.912046	0.855073	Slc19a1/Slc
GO_CC_m3	GO:003159	neuromusc	1/540	71/23583	0.807397	0.912631	0.855621	Syngr1
GO_CC_m3	GO:007060	SWI/SNF su	1/540	72/23583	0.81182	0.915573	0.85838	Chd3
GO_CC_m3	GO:000172	stress fiber	1/540	74/23583	0.820366	0.92108	0.863543	Ablim3
GO_CC_m3	GO:009751	contractile	1/540	74/23583	0.820366	0.92108	0.863543	Ablim3
GO_CC_m3	GO:003509	histone me	1/540	75/23583	0.824492	0.923651	0.865953	Epop
GO_CC_m3	GO:000175	photorecep	1/540	76/23583	0.828523	0.926105	0.868254	Sag
GO_CC_m3	GO:000172	ruffle	2/540	139/23583	0.830706	0.926486	0.868611	Nf2/Carmil
GO_CC_m3	GO:000568	spliceosom	3/540	199/23583	0.837079	0.928075	0.870101	Gcfc2/Hnrn
GO_CC_m3	GO:000581	spindle	4/540	255/23583	0.838478	0.928075	0.870101	Atat1/Ccdc
GO_CC_m3	GO:000577	peroxisome	2/540	142/23583	0.839511	0.928075	0.870101	Ccdc33/Slc
GO_CC_m3	GO:004257	microbody	2/540	142/23583	0.839511	0.928075	0.870101	Ccdc33/Slc
GO_CC_m3	GO:003086	cortical act	1/540	81/23583	0.847336	0.932039	0.873817	Nf2
GO_CC_m3	GO:004430	main axon	1/540	81/23583	0.847336	0.932039	0.873817	Ucn
GO_CC_m3	GO:000558	collagen tri	1/540	82/23583	0.850844	0.932039	0.873817	Col27a1
GO_CC_m3	GO:003243	actin filame	1/540	83/23583	0.854271	0.932039	0.873817	Ablim3
GO_CC_m3	GO:000578	endoplasm	8/540	476/23583	0.85584	0.932039	0.873817	Elovl2/Ier3i
GO_CC_m3	GO:000807	voltage-ga	1/540	84/23583	0.85762	0.932039	0.873817	Kcnmb4
GO_CC_m3	GO:001705	transcriptio	1/540	84/23583	0.85762	0.932039	0.873817	Chd3
GO_CC_m3	GO:001593	small ribos	1/540	85/23583	0.860892	0.932039	0.873817	Rps3a1
GO_CC_m3	GO:004264	actomyosin	1/540	85/23583	0.860892	0.932039	0.873817	Ablim3
GO_CC_m3	GO:000078	nucleosom	1/540	86/23583	0.864089	0.932039	0.873817	Hypm
GO_CC_m3	GO:190494	ATPase com	1/540	86/23583	0.864089	0.932039	0.873817	Chd3
GO_CC_m3	GO:000031	organellar	1/540	89/23583	0.873246	0.932039	0.873817	Mrpl41
GO_CC_m3	GO:000576	mitochond	1/540	89/23583	0.873246	0.932039	0.873817	Mrpl41

GO_CC_m3	GO:003124	protein ace	1/540	89/23583	0.873246	0.932039	0.873817	Naa25
GO_CC_m3	GO:007006	extracellula	1/540	89/23583	0.873246	0.932039	0.873817	Mir106b
GO_CC_m3	GO:190249	acetyltrans	1/540	89/23583	0.873246	0.932039	0.873817	Naa25
GO_CC_m3	GO:009882	endoplasm	8/540	489/23583	0.874597	0.932039	0.873817	Elovl2/Ier3
GO_CC_m3	GO:003470	methyltran	1/540	94/23583	0.887159	0.940692	0.88193	Epop
GO_CC_m3	GO:004481	DNA packa	1/540	94/23583	0.887159	0.940692	0.88193	Hypm
GO_CC_m3	GO:003283	plasma me	2/540	162/23583	0.888327	0.940692	0.88193	Grik2/Lrrk2
GO_CC_m3	GO:000593	cell cortex	4/540	290/23583	0.901534	0.952672	0.893161	Exoc1/Nf2/
GO_CC_m3	GO:007101	catalytic st	1/540	103/23583	0.908474	0.957993	0.89815	Hnrnpr
GO_CC_m3	GO:000576	early endo	3/540	239/23583	0.913516	0.95819	0.898334	Nf2/Rhob/
GO_CC_m3	GO:000577	vacuolar m	2/540	177/23583	0.915485	0.95819	0.898334	Cyb561a3/
GO_CC_m3	GO:003299	protein-DN	2/540	179/23583	0.918599	0.95819	0.898334	Gtf2e1/Hyp
GO_CC_m3	GO:004319	dendritic s	2/540	179/23583	0.918599	0.95819	0.898334	Nlgn1/Syn
GO_CC_m3	GO:007016	anchoring	4/540	303/23583	0.918739	0.95819	0.898334	Cdh26/Ds
GO_CC_m3	GO:004430	neuron spi	2/540	181/23583	0.921604	0.95819	0.898334	Nlgn1/Syn
GO_CC_m3	GO:003125	cell leading	5/540	364/23583	0.921996	0.95819	0.898334	Ablim3/Nf2
GO_CC_m3	GO:000575	mitochond	3/540	253/23583	0.931389	0.965956	0.905616	Dlat/Lrrk2/
GO_CC_m3	GO:003086	cortical cyt	1/540	117/23583	0.933925	0.966593	0.906213	Nf2
GO_CC_m3	GO:009879	mitochond	3/540	262/23583	0.941016	0.967694	0.907245	Ankzf1/Dla
GO_CC_m3	GO:000591	cell-cell ad	1/540	122/23583	0.941186	0.967694	0.907245	Cdh26
GO_CC_m3	GO:003001	Z disc	1/540	122/23583	0.941186	0.967694	0.907245	Mybph
GO_CC_m3	GO:009956	cytoplasmi	6/540	444/23583	0.942684	0.967694	0.907245	Exoc1/Grik
GO_CC_m3	GO:004442	extracellula	1/540	129/23583	0.950033	0.973252	0.912456	Col27a1
GO_CC_m3	GO:000592	focal adhe	1/540	135/23583	0.956551	0.9758	0.914844	Hck
GO_CC_m3	GO:003167	I band	1/540	135/23583	0.956551	0.9758	0.914844	Mybph
GO_CC_m3	GO:000587	microtubul	5/540	412/23583	0.960887	0.9758	0.914844	Appbp2/At
GO_CC_m3	GO:000591	adherens j	3/540	287/23583	0.961583	0.9758	0.914844	Cdh26/Hck
GO_CC_m3	GO:000592	cell-substr	1/540	141/23583	0.96222	0.9758	0.914844	Hck
GO_CC_m3	GO:000587	microtubul	1/540	148/23583	0.967908	0.977313	0.916262	BC048507
GO_CC_m3	GO:003005	cell-substr	1/540	149/23583	0.968647	0.977313	0.916262	Hck
GO_CC_m3	GO:000032	lytic vacuol	5/540	433/23583	0.971484	0.977313	0.916262	Cyb561a3/
GO_CC_m3	GO:000576	lysosome	5/540	433/23583	0.971484	0.977313	0.916262	Cyb561a3/
GO_CC_m3	GO:003125	cell project	2/540	282/23583	0.989241	0.991831	0.929874	Slc19a1/Sl
GO_CC_m3	GO:000557	proteinace	3/540	361/23583	0.98986	0.991831	0.929874	Col27a1/F
GO_CC_m3	GO:003101	extracellula	4/540	447/23583	0.992245	0.992245	0.930263	Col27a1/F
GO_CC_m4	GO:000591	cell-cell ju	28/714	473/23583	0.000631	0.261803	0.257274	Abcb1b/A
GO_CC_m4	GO:007115	NF-kappa	2/714	2/23583	0.000915	0.261803	0.257274	Rela/Rps3
GO_CC_m4	GO:003013	COPII-coat	6/714	50/23583	0.00386	0.542006	0.53263	Lman1l/Se
GO_CC_m4	GO:001632	basolateral	14/714	223/23583	0.008282	0.542006	0.53263	Abcc4/Age
GO_CC_m4	GO:004324	Fanconi an	3/714	15/23583	0.00958	0.542006	0.53263	Faap100/C
GO_CC_m4	GO:000579	endoplasm	6/714	68/23583	0.016875	0.542006	0.53263	Car4/Nat8
GO_CC_m4	GO:001658	NURF com	2/714	7/23583	0.017374	0.542006	0.53263	Smarca1/S
GO_CC_m4	GO:000177	immunolog	4/714	35/23583	0.020739	0.542006	0.53263	Bcl10/Lck/
GO_CC_m4	GO:002262	cytosolic ri	10/714	157/23583	0.021455	0.542006	0.53263	Gemin5/Gr
GO_CC_m4	GO:003136	anchored	3/714	20/23583	0.021462	0.542006	0.53263	Car4/Folr1/
GO_CC_m4	GO:003167	I band	9/714	135/23583	0.021813	0.542006	0.53263	Fhl2/Kcne1
GO_CC_m4	GO:009719	tetraspanin	2/714	8/23583	0.022705	0.542006	0.53263	Scimp/Tsp
GO_CC_m4	GO:004329	apical junc	9/714	136/23583	0.022757	0.542006	0.53263	Cgnl1/Cld

GO_CC_m4	GO:002262	cytosolic la	7/714	94/23583	0.024023	0.542006	0.53263	Gemin5/Gr
GO_CC_m4	GO:001632	apical plasr	16/714	306/23583	0.024828	0.542006	0.53263	Abcb1b/Ab
GO_CC_m4	GO:000592	bicellular ti	8/714	119/23583	0.028362	0.542006	0.53263	Cgnl1/Cldr
GO_CC_m4	GO:000595	calcium- ai	1/714	1/23583	0.030276	0.542006	0.53263	Camk1g
GO_CC_m4	GO:003125	cell trailing	1/714	1/23583	0.030276	0.542006	0.53263	Scimp
GO_CC_m4	GO:003125	uropod me	1/714	1/23583	0.030276	0.542006	0.53263	Scimp
GO_CC_m4	GO:003147	myosin V c	1/714	1/23583	0.030276	0.542006	0.53263	Dynll2
GO_CC_m4	GO:003471	SMN-Gem	1/714	1/23583	0.030276	0.542006	0.53263	Gemin5
GO_CC_m4	GO:003552	NF-kappaE	1/714	1/23583	0.030276	0.542006	0.53263	Rela
GO_CC_m4	GO:003803	G-protein (	1/714	1/23583	0.030276	0.542006	0.53263	Grm1
GO_CC_m4	GO:004350	activin A cc	1/714	1/23583	0.030276	0.542006	0.53263	Inhba
GO_CC_m4	GO:004818	activin com	1/714	1/23583	0.030276	0.542006	0.53263	Inhba
GO_CC_m4	GO:006047	cortical gra	1/714	1/23583	0.030276	0.542006	0.53263	Astl
GO_CC_m4	GO:007154	eukaryotic	1/714	1/23583	0.030276	0.542006	0.53263	Eif3a
GO_CC_m4	GO:009855	mucin grar	1/714	1/23583	0.030276	0.542006	0.53263	Vamp8
GO_CC_m4	GO:199035	sumoylatec	1/714	1/23583	0.030276	0.542006	0.53263	Ube2i
GO_CC_m4	GO:003123	intrinsic co	3/714	23/23583	0.031191	0.542006	0.53263	Car4/Folr1/
GO_CC_m4	GO:003001	Z disc	8/714	122/23583	0.032235	0.542006	0.53263	Fhl2/Kcne1
GO_CC_m4	GO:007016	occluding j	8/714	122/23583	0.032235	0.542006	0.53263	Cgnl1/Cldr
GO_CC_m4	GO:003122	anchored c	10/714	169/23583	0.03338	0.542006	0.53263	Alppl2/Art4
GO_CC_m4	GO:003436	high-densi	3/714	24/23583	0.034867	0.542006	0.53263	Apoa4/Apc
GO_CC_m4	GO:009744	apical denc	3/714	24/23583	0.034867	0.542006	0.53263	Itsn1/Neur
GO_CC_m4	GO:003101	ISWI-type (	2/714	10/23583	0.03506	0.542006	0.53263	Smarca1/S
GO_CC_m4	GO:004658	intercellula	2/714	10/23583	0.03506	0.542006	0.53263	Abcb1b/Ab
GO_CC_m4	GO:000825	oligosacch	2/714	11/23583	0.042006	0.588141	0.577967	Ostc/Stt3b
GO_CC_m4	GO:003001	myofibril	11/714	209/23583	0.054016	0.588141	0.577967	Alppl2/Fhl2
GO_CC_m4	GO:001562	actin cytosl	21/714	474/23583	0.054018	0.588141	0.577967	Abcb4/Ack
GO_CC_m4	GO:003001	sarcomere	10/714	185/23583	0.055591	0.588141	0.577967	Fhl2/Kcne1
GO_CC_m4	GO:001634	catenin cor	3/714	29/23583	0.056383	0.588141	0.577967	Cdh24/Cdh
GO_CC_m4	GO:000576	primary lys	2/714	13/23583	0.057256	0.588141	0.577967	Mpo/Vamp
GO_CC_m4	GO:000591	fascia adhe	2/714	13/23583	0.057256	0.588141	0.577967	Dsp/Sptan
GO_CC_m4	GO:004258	azurophil g	2/714	13/23583	0.057256	0.588141	0.577967	Mpo/Vamp
GO_CC_m4	GO:003152	brush bord	5/714	69/23583	0.057882	0.588141	0.577967	Car4/Folr1/
GO_CC_m4	GO:003121	RSF compl	1/714	2/23583	0.059637	0.588141	0.577967	Smarca5
GO_CC_m4	GO:003557	azurophil g	1/714	2/23583	0.059637	0.588141	0.577967	Vamp8
GO_CC_m4	GO:004351	inhibin A c	1/714	2/23583	0.059637	0.588141	0.577967	Inhba
GO_CC_m4	GO:004361	multi-eIF c	1/714	2/23583	0.059637	0.588141	0.577967	Eif3a
GO_CC_m4	GO:006018	cell pole	1/714	2/23583	0.059637	0.588141	0.577967	Astn2
GO_CC_m4	GO:007043	Grb2-EGFF	1/714	2/23583	0.059637	0.588141	0.577967	Grb2
GO_CC_m4	GO:009053	CERF comp	1/714	2/23583	0.059637	0.588141	0.577967	Smarca1
GO_CC_m4	GO:009744	spine appa	1/714	2/23583	0.059637	0.588141	0.577967	Synpo
GO_CC_m4	GO:199002	hippocamp	1/714	2/23583	0.059637	0.588141	0.577967	Tnn
GO_CC_m4	GO:199003	pericellular	1/714	2/23583	0.059637	0.588141	0.577967	Slc17a8
GO_CC_m4	GO:199061	CHOP-ATF	1/714	2/23583	0.059637	0.588141	0.577967	Ddit3
GO_CC_m4	GO:199062	CHOP-ATF	1/714	2/23583	0.059637	0.588141	0.577967	Ddit3
GO_CC_m4	GO:004278	polysomal	3/714	30/23583	0.06129	0.5942	0.583921	Rpl24/Rpl3
GO_CC_m4	GO:004444	cytosolic p	14/714	294/23583	0.064739	0.611315	0.60074	Borcs7/Ger
GO_CC_m4	GO:003317	proton-tra	2/714	14/23583	0.065492	0.611315	0.60074	Atp5c1/Atp

GO_CC_m4	GO:004517	apical part	18/714	403/23583	0.066261	0.611315	0.60074	Abcb1b/Ab
GO_CC_m4	GO:003120	SNARE cor	4/714	51/23583	0.06814	0.612896	0.602293	Sec22b/Sn
GO_CC_m4	GO:001660	PML body	5/714	73/23583	0.070286	0.612896	0.602293	Agap3/Cb
GO_CC_m4	GO:000586	striated mu	3/714	32/23583	0.071675	0.612896	0.602293	Myom2/Ne
GO_CC_m4	GO:000566	DNA replic	2/714	15/23583	0.074094	0.612896	0.602293	Purb/Xpa
GO_CC_m4	GO:004329	contractile	11/714	223/23583	0.077693	0.612896	0.602293	Alppl2/Fhl2
GO_CC_m4	GO:004444	contractile	10/714	199/23583	0.08159	0.612896	0.602293	Fhl2/Kcne1
GO_CC_m4	GO:003637	myofilame	3/714	34/23583	0.082789	0.612896	0.602293	Myom2/Ne
GO_CC_m4	GO:000585	eukaryotic	2/714	16/23583	0.083032	0.612896	0.602293	Eif3a/Eif3e
GO_CC_m4	GO:000011	nucleotide-	1/714	3/23583	0.08811	0.612896	0.602293	Xpa
GO_CC_m4	GO:000597	ribonucleo	1/714	3/23583	0.08811	0.612896	0.602293	Rrm1
GO_CC_m4	GO:003108	platelet de	1/714	3/23583	0.08811	0.612896	0.602293	Abcc4
GO_CC_m4	GO:003648	CHOP-C/E	1/714	3/23583	0.08811	0.612896	0.602293	Ddit3
GO_CC_m4	GO:004351	inhibin con	1/714	3/23583	0.08811	0.612896	0.602293	Inhba
GO_CC_m4	GO:004669	intracellula	1/714	3/23583	0.08811	0.612896	0.602293	Mip
GO_CC_m4	GO:007093	Dsl1/NZR	1/714	3/23583	0.08811	0.612896	0.602293	Nbas
GO_CC_m4	GO:009744	CA3 pyram	1/714	3/23583	0.08811	0.612896	0.602293	Tnn
GO_CC_m4	GO:009745	glial limitin	1/714	3/23583	0.08811	0.612896	0.602293	Slc17a8
GO_CC_m4	GO:009745	hippocamp	1/714	3/23583	0.08811	0.612896	0.602293	Tnn
GO_CC_m4	GO:004429	cell-cell co	5/714	79/23583	0.091402	0.612896	0.602293	Ctnna1/Ds
GO_CC_m4	GO:000561	interstitial	2/714	17/23583	0.092278	0.612896	0.602293	Vit/Vwa1
GO_CC_m4	GO:004439	ribosomal	11/714	231/23583	0.093758	0.612896	0.602293	Gemin5/Gr
GO_CC_m4	GO:000589	voltage-ga	3/714	36/23583	0.09459	0.612896	0.602293	Cacna1b/C
GO_CC_m4	GO:003435	plasma lip	3/714	36/23583	0.09459	0.612896	0.602293	Apoa4/Ap
GO_CC_m4	GO:199077	lipoprotein	3/714	36/23583	0.09459	0.612896	0.602293	Apoa4/Ap
GO_CC_m4	GO:004665	anchored	4/714	58/23583	0.098493	0.612896	0.602293	Car4/Efna1
GO_CC_m4	GO:003436	very-low-	2/714	18/23583	0.101805	0.612896	0.602293	Apoa4/Ap
GO_CC_m4	GO:003438	triglyceride	2/714	18/23583	0.101805	0.612896	0.602293	Apoa4/Ap
GO_CC_m4	GO:003299	protein-lip	3/714	38/23583	0.107033	0.612896	0.602293	Apoa4/Ap
GO_CC_m4	GO:001470	intercalate	4/714	61/23583	0.11313	0.612896	0.602293	Ctnna1/Ds
GO_CC_m4	GO:004429	axonal gro	3/714	39/23583	0.113481	0.612896	0.602293	Rtn4r/Tiam
GO_CC_m4	GO:003066	secretory g	5/714	85/23583	0.115403	0.612896	0.602293	Abcc4/Car
GO_CC_m4	GO:000218	ribose pho	1/714	4/23583	0.115722	0.612896	0.602293	Prps2
GO_CC_m4	GO:003086	smooth en	1/714	4/23583	0.115722	0.612896	0.602293	Stx17
GO_CC_m4	GO:003150	mannosyltr	1/714	4/23583	0.115722	0.612896	0.602293	Pigv
GO_CC_m4	GO:003202	NELF comp	1/714	4/23583	0.115722	0.612896	0.602293	Nelfe
GO_CC_m4	GO:003244	CBM comp	1/714	4/23583	0.115722	0.612896	0.602293	Bcl10
GO_CC_m4	GO:004258	germinal v	1/714	4/23583	0.115722	0.612896	0.602293	Aurka
GO_CC_m4	GO:004282	platelet de	1/714	4/23583	0.115722	0.612896	0.602293	Abcc4
GO_CC_m4	GO:004352	tRNA meth	1/714	4/23583	0.115722	0.612896	0.602293	Wdr4
GO_CC_m4	GO:004430	dentate gy	1/714	4/23583	0.115722	0.612896	0.602293	Tnn
GO_CC_m4	GO:007182	FANCM-M	1/714	4/23583	0.115722	0.612896	0.602293	Cenps
GO_CC_m4	GO:007195	elastic fibe	1/714	4/23583	0.115722	0.612896	0.602293	Eln
GO_CC_m4	GO:009742	smooth en	1/714	4/23583	0.115722	0.612896	0.602293	Stx17
GO_CC_m4	GO:009745	astrocyte e	1/714	4/23583	0.115722	0.612896	0.602293	Slc17a8
GO_CC_m4	GO:012000	apical plas	1/714	4/23583	0.115722	0.612896	0.602293	Upk2
GO_CC_m4	GO:199060	IRE1-TRAF	1/714	4/23583	0.115722	0.612896	0.602293	Ern2
GO_CC_m4	GO:004359	nuclear rep	3/714	40/23583	0.120073	0.621033	0.61029	Purb/Smar

GO_CC_m4	GO:000024	pericentrio	2/714	20/23583	0.121601	0.621033	0.61029	Cep152/Lc
GO_CC_m4	GO:001250	ER to Golg	2/714	20/23583	0.121601	0.621033	0.61029	Sec13/Sec2
GO_CC_m4	GO:009738	glial cell pr	2/714	20/23583	0.121601	0.621033	0.61029	Lgals3/Slc1
GO_CC_m4	GO:003612	sperm flag	6/714	112/23583	0.124687	0.626994	0.616148	Catsper2/C
GO_CC_m4	GO:001660	nuclear spe	13/714	302/23583	0.130132	0.626994	0.616148	Arhgap18/
GO_CC_m4	GO:000584	ribosome	12/714	275/23583	0.132255	0.626994	0.616148	Aurkaip1/G
GO_CC_m4	GO:009772	9+2 motile	6/714	114/23583	0.13244	0.626994	0.616148	Catsper2/C
GO_CC_m4	GO:007006	extracellula	5/714	89/23583	0.132903	0.626994	0.616148	Bhmt/Car4
GO_CC_m4	GO:000563	nuclear inn	3/714	42/23583	0.133662	0.626994	0.616148	Atp1b4/Tm
GO_CC_m4	GO:001645	myosin cor	4/714	65/23583	0.134028	0.626994	0.616148	Cgnl1/Dyn
GO_CC_m4	GO:003101	extracellula	18/714	447/23583	0.135695	0.626994	0.616148	Apoa4/Csp
GO_CC_m4	GO:000557	proteinace	15/714	361/23583	0.135802	0.626994	0.616148	Eln/Emilin3
GO_CC_m4	GO:000568	U1 snRNP	2/714	22/23583	0.142232	0.626994	0.616148	Luc7l3/Snr
GO_CC_m4	GO:007101	prespliceos	2/714	22/23583	0.142232	0.626994	0.616148	Luc7l3/Snr
GO_CC_m4	GO:000027	mitochond	1/714	5/23583	0.142499	0.626994	0.616148	Atp5c1
GO_CC_m4	GO:003213	chromosor	1/714	5/23583	0.142499	0.626994	0.616148	Aurka
GO_CC_m4	GO:003597	transcriptic	1/714	5/23583	0.142499	0.626994	0.616148	Ddit3
GO_CC_m4	GO:004526	proton-tra	1/714	5/23583	0.142499	0.626994	0.616148	Atp5c1
GO_CC_m4	GO:009744	basal dend	1/714	5/23583	0.142499	0.626994	0.616148	Slc17a8
GO_CC_m4	GO:009853	deuterosor	1/714	5/23583	0.142499	0.626994	0.616148	Cep152
GO_CC_m4	GO:009882	endoplasm	1/714	5/23583	0.142499	0.626994	0.616148	Rtn4
GO_CC_m4	GO:003065	transport v	6/714	119/23583	0.152787	0.629355	0.618468	Car4/Sec13
GO_CC_m4	GO:000585	axonemal	2/714	23/23583	0.152808	0.629355	0.618468	Casc1/Ccd
GO_CC_m4	GO:004360	nuclear rep	2/714	23/23583	0.152808	0.629355	0.618468	Purb/Xpa
GO_CC_m4	GO:003014	secretory g	16/714	398/23583	0.154013	0.629355	0.618468	Abcc4/Ang
GO_CC_m4	GO:000566	transcriptic	16/714	399/23583	0.156249	0.629355	0.618468	Atf6b/Ddit3
GO_CC_m4	GO:190356	extracellula	5/714	95/23583	0.161202	0.629355	0.618468	Bhmt/Car4
GO_CC_m4	GO:001646	myosin II c	2/714	24/23583	0.16353	0.629355	0.618468	Myl12a/My
GO_CC_m4	GO:003089	replisome	2/714	24/23583	0.16353	0.629355	0.618468	Purb/Xpa
GO_CC_m4	GO:003143	M band	2/714	24/23583	0.16353	0.629355	0.618468	Fhl2/Myom
GO_CC_m4	GO:004258	zymogen g	2/714	24/23583	0.16353	0.629355	0.618468	Tmed10/Va
GO_CC_m4	GO:000591	cell-cell ad	6/714	122/23583	0.165621	0.629355	0.618468	Cadm2/Cd
GO_CC_m4	GO:001593	large ribos	7/714	149/23583	0.166786	0.629355	0.618468	Gemin5/Gr
GO_CC_m4	GO:000165	dense fibril	1/714	6/23583	0.168466	0.629355	0.618468	Vdr
GO_CC_m4	GO:000591	zonula adh	1/714	6/23583	0.168466	0.629355	0.618468	Ctnna1
GO_CC_m4	GO:001601	sarcoglycar	1/714	6/23583	0.168466	0.629355	0.618468	Sgcb
GO_CC_m4	GO:003089	checkpoint	1/714	6/23583	0.168466	0.629355	0.618468	Hus1
GO_CC_m4	GO:003126	death-indu	1/714	6/23583	0.168466	0.629355	0.618468	Ripk1
GO_CC_m4	GO:004669	lipopolysac	1/714	6/23583	0.168466	0.629355	0.618468	Bcl10
GO_CC_m4	GO:004878	cytoskeleto	1/714	6/23583	0.168466	0.629355	0.618468	Rims4
GO_CC_m4	GO:009722	sperm ann	1/714	6/23583	0.168466	0.629355	0.618468	12-Sep
GO_CC_m4	GO:009734	ripoptoson	1/714	6/23583	0.168466	0.629355	0.618468	Ripk1
GO_CC_m4	GO:009742	microtubul	1/714	6/23583	0.168466	0.629355	0.618468	Mtcl1
GO_CC_m4	GO:000579	Golgi-asso	6/714	123/23583	0.169998	0.629355	0.618468	Lman1l/Se
GO_CC_m4	GO:003130	integral co	2/714	25/23583	0.17438	0.629355	0.618468	Fundc2/To
GO_CC_m4	GO:003299	protein-DN	8/714	179/23583	0.176974	0.629355	0.618468	Atf6b/Ddit3
GO_CC_m4	GO:000577	late endos	8/714	180/23583	0.180677	0.629355	0.618468	5330417C2
GO_CC_m4	GO:003130	intrinsic co	2/714	26/23583	0.18534	0.629355	0.618468	Fundc2/To

GO_CC_m	GO:007097	endoplasm	2/714	26/23583	0.18534	0.629355	0.618468	H2-Q10/Yi
GO_CC_m	GO:000587	microtubul	16/714	412/23583	0.18687	0.629355	0.618468	Aurka/Bcl1
GO_CC_m	GO:00198	extrinsic cc	8/714	183/23583	0.191987	0.629355	0.618468	Cdh24/Cdh
GO_CC_m	GO:00016	fibrillar cen	6/714	128/23583	0.192579	0.629355	0.618468	Ager/Arhg
GO_CC_m	GO:000034	THO comp	1/714	7/23583	0.193648	0.629355	0.618468	Thoc5
GO_CC_m	GO:000044	THO comp	1/714	7/23583	0.193648	0.629355	0.618468	Thoc5
GO_CC_m	GO:001601	dystroglyc	1/714	7/23583	0.193648	0.629355	0.618468	Sgcb
GO_CC_m	GO:00164	unconventi	1/714	7/23583	0.193648	0.629355	0.618468	Dynll2
GO_CC_m	GO:003047	actin cortic	1/714	7/23583	0.193648	0.629355	0.618468	Wipf2
GO_CC_m	GO:00319	TORC1 cor	1/714	7/23583	0.193648	0.629355	0.618468	Akt1s1
GO_CC_m	GO:00324	cuticular pl	1/714	7/23583	0.193648	0.629355	0.618468	Sptan1
GO_CC_m	GO:00325	growth cor	1/714	7/23583	0.193648	0.629355	0.618468	Trpv2
GO_CC_m	GO:00332	I-kappaB/	1/714	7/23583	0.193648	0.629355	0.618468	Rela
GO_CC_m	GO:00423	paraspeckl	1/714	7/23583	0.193648	0.629355	0.618468	Sfpq
GO_CC_m	GO:004321	lateral loop	1/714	7/23583	0.193648	0.629355	0.618468	Erbb2
GO_CC_m	GO:00443	cerebellar	1/714	7/23583	0.193648	0.629355	0.618468	Lrrc4b
GO_CC_m	GO:006164	endocytic	1/714	7/23583	0.193648	0.629355	0.618468	Wipf2
GO_CC_m	GO:00707	gamma-se	1/714	7/23583	0.193648	0.629355	0.618468	Tmed10
GO_CC_m	GO:00995	presynapti	1/714	7/23583	0.193648	0.629355	0.618468	Rims4
GO_CC_m	GO:00306	preriboson	2/714	27/23583	0.196394	0.634676	0.623697	Mdn1/Ppa
GO_CC_m	GO:000584	polysome	4/714	77/23583	0.204655	0.641587	0.630489	Rpl24/Rpl3
GO_CC_m	GO:00059	brush bord	6/714	131/23583	0.206647	0.641587	0.630489	Car4/Folr1/
GO_CC_m	GO:004307	germ cell n	2/714	28/23583	0.207527	0.641587	0.630489	Aurka/Kif6
GO_CC_m	GO:00007	condensin	1/714	8/23583	0.218068	0.641587	0.630489	Ncapg2
GO_CC_m	GO:000167	female ger	1/714	8/23583	0.218068	0.641587	0.630489	Aurka
GO_CC_m	GO:000567	chromatin	1/714	8/23583	0.218068	0.641587	0.630489	Smarca5
GO_CC_m	GO:00058	sodium:po	1/714	8/23583	0.218068	0.641587	0.630489	Atp1b4
GO_CC_m	GO:00309	intraciliary	1/714	8/23583	0.218068	0.641587	0.630489	Wdr35
GO_CC_m	GO:003311	endoplasm	1/714	8/23583	0.218068	0.641587	0.630489	Nat8f1
GO_CC_m	GO:00380	G-protein	1/714	8/23583	0.218068	0.641587	0.630489	Grm1
GO_CC_m	GO:00432	axon hilloc	1/714	8/23583	0.218068	0.641587	0.630489	Aurka
GO_CC_m	GO:00452	pyruvate d	1/714	8/23583	0.218068	0.641587	0.630489	Pdhx
GO_CC_m	GO:006161	MICOS cor	1/714	8/23583	0.218068	0.641587	0.630489	Chchd6
GO_CC_m	GO:007154	eukaryotic	1/714	8/23583	0.218068	0.641587	0.630489	Eif3a
GO_CC_m	GO:00726	tRNA-splic	1/714	8/23583	0.218068	0.641587	0.630489	Fam98c
GO_CC_m	GO:009764	G-protein	1/714	8/23583	0.218068	0.641587	0.630489	Grm1
GO_CC_m	GO:009907	BORC com	1/714	8/23583	0.218068	0.641587	0.630489	Borcs7
GO_CC_m	GO:00985	intrinsic co	2/714	29/23583	0.218723	0.641587	0.630489	Slc17a8/Sy
GO_CC_m	GO:00447	nuclear tra	8/714	191/23583	0.223508	0.647348	0.63615	Atf6b/Ddit
GO_CC_m	GO:00432	extracellula	5/714	107/23583	0.224002	0.647348	0.63615	Bhmt/Car4
GO_CC_m	GO:00015	cornified e	3/714	54/23583	0.224082	0.647348	0.63615	Dsp/Lce1g
GO_CC_m	GO:004511	intermedia	7/714	163/23583	0.22543	0.647969	0.63676	Faap100/B
GO_CC_m	GO:00308	cortical act	4/714	81/23583	0.230262	0.652269	0.640986	Cap2/Polr2
GO_CC_m	GO:00056	nuclear env	15/714	399/23583	0.231001	0.652269	0.640986	Ackr2/Atp1
GO_CC_m	GO:00347	calcium ch	3/714	55/23583	0.232117	0.652269	0.640986	Cacna1b/C
GO_CC_m	GO:00312	cell project	11/714	282/23583	0.237296	0.652269	0.640986	Car4/Folr1/
GO_CC_m	GO:002262	cytosolic sr	3/714	56/23583	0.240203	0.652269	0.640986	Rps11/Rps
GO_CC_m	GO:004517	intercellula	3/714	56/23583	0.240203	0.652269	0.640986	Krr1/Rfxan

GO_CC_m4	GO:000024	commitme	1/714	9/23583	0.24175	0.652269	0.640986	Snrpc
GO_CC_m4	GO:000050	glycosylph	1/714	9/23583	0.24175	0.652269	0.640986	Pigp
GO_CC_m4	GO:000152	outer dens	1/714	9/23583	0.24175	0.652269	0.640986	Odf3
GO_CC_m4	GO:004421	spanning c	1/714	9/23583	0.24175	0.652269	0.640986	Npc1l1
GO_CC_m4	GO:008971	spanning c	1/714	9/23583	0.24175	0.652269	0.640986	Npc1l1
GO_CC_m4	GO:009883	presynapti	1/714	9/23583	0.24175	0.652269	0.640986	Rims4
GO_CC_m4	GO:009899	anchored c	1/714	9/23583	0.24175	0.652269	0.640986	Syn1
GO_CC_m4	GO:004533	phagocytic	4/714	83/23583	0.243353	0.65351	0.642206	Kif16b/Rab
GO_CC_m4	GO:003028	dynein con	3/714	57/23583	0.248335	0.659262	0.647858	Casc1/Ccd
GO_CC_m4	GO:004217	nuclear ou	18/714	498/23583	0.253375	0.659262	0.647858	Atf6b/Nat8
GO_CC_m4	GO:000591	adherens ju	11/714	287/23583	0.254594	0.659262	0.647858	Abcb4/Cac
GO_CC_m4	GO:001593	small ribos	4/714	85/23583	0.256604	0.659262	0.647858	Mrps16/Rp
GO_CC_m4	GO:003123	extrinsic cc	5/714	113/23583	0.257798	0.659262	0.647858	Gnat1/Gng
GO_CC_m4	GO:190494	ATPase co	4/714	86/23583	0.263284	0.659262	0.647858	Atp1b4/Sm
GO_CC_m4	GO:003280	neuronal c	2/714	33/23583	0.263871	0.659262	0.647858	Cadm2/Flrt
GO_CC_m4	GO:000016	protein ph	1/714	10/23583	0.264716	0.659262	0.647858	Ppp1r15b
GO_CC_m4	GO:000574	mitochond	1/714	10/23583	0.264716	0.659262	0.647858	Tomm7
GO_CC_m4	GO:001660	flotillin con	1/714	10/23583	0.264716	0.659262	0.647858	Ctnna1
GO_CC_m4	GO:003108	nuclear po	1/714	10/23583	0.264716	0.659262	0.647858	Sec13
GO_CC_m4	GO:004429	dendritic g	1/714	10/23583	0.264716	0.659262	0.647858	Rtn4
GO_CC_m4	GO:006009	kinocilium	1/714	10/23583	0.264716	0.659262	0.647858	Tiam1
GO_CC_m4	GO:009053	cation-tra	1/714	10/23583	0.264716	0.659262	0.647858	Atp1b4
GO_CC_m4	GO:009773	9+2 non-n	1/714	10/23583	0.264716	0.659262	0.647858	Tiam1
GO_CC_m4	GO:003506	micro-ribo	5/714	115/23583	0.269328	0.659262	0.647858	Mir16-2/M
GO_CC_m4	GO:004429	cell body n	2/714	34/23583	0.275189	0.659262	0.647858	Cadm2/Flrt
GO_CC_m4	GO:004444	axoneme p	2/714	34/23583	0.275189	0.659262	0.647858	Casc1/Ccd
GO_CC_m4	GO:000578	endoplasm	17/714	476/23583	0.276894	0.659262	0.647858	Atf6b/Nat8
GO_CC_m4	GO:003086	cortical cyt	5/714	117/23583	0.280968	0.659262	0.647858	Cap2/Polr2
GO_CC_m4	GO:000590	clathrin-co	3/714	61/23583	0.281225	0.659262	0.647858	Ap1s3/Itsn
GO_CC_m4	GO:000577	multivesicu	2/714	35/23583	0.286497	0.659262	0.647858	Sftpa1/Slc1
GO_CC_m4	GO:000583	heterotrim	2/714	35/23583	0.286497	0.659262	0.647858	Gnat1/Gng
GO_CC_m4	GO:000818	COP9 sign	2/714	35/23583	0.286497	0.659262	0.647858	Cops2/Grb
GO_CC_m4	GO:190536	GTPase co	2/714	35/23583	0.286497	0.659262	0.647858	Gnat1/Gng
GO_CC_m4	GO:000010	nucleotide-	1/714	11/23583	0.286987	0.659262	0.647858	Xpa
GO_CC_m4	GO:000193	uropod	1/714	11/23583	0.286987	0.659262	0.647858	Scimp
GO_CC_m4	GO:000558	fibrillar coll	1/714	11/23583	0.286987	0.659262	0.647858	Lum
GO_CC_m4	GO:003089	HOPS com	1/714	11/23583	0.286987	0.659262	0.647858	Stx17
GO_CC_m4	GO:003125	cell trailing	1/714	11/23583	0.286987	0.659262	0.647858	Scimp
GO_CC_m4	GO:003279	SMN comp	1/714	11/23583	0.286987	0.659262	0.647858	Gemin5
GO_CC_m4	GO:003615	inner dyne	1/714	11/23583	0.286987	0.659262	0.647858	Casc1
GO_CC_m4	GO:003615	outer dyne	1/714	11/23583	0.286987	0.659262	0.647858	Ccdc114
GO_CC_m4	GO:006170	GATOR2 c	1/714	11/23583	0.286987	0.659262	0.647858	Sec13
GO_CC_m4	GO:007268	meiotic spi	1/714	11/23583	0.286987	0.659262	0.647858	Aurka
GO_CC_m4	GO:009864	banded co	1/714	11/23583	0.286987	0.659262	0.647858	Lum
GO_CC_m4	GO:000587	microtubul	6/714	148/23583	0.292117	0.668365	0.656803	Aurka/Casc
GO_CC_m4	GO:003151	motile ciliu	7/714	179/23583	0.299567	0.669884	0.658296	Catsper2/C
GO_CC_m4	GO:004319	dendritic s	7/714	179/23583	0.299567	0.669884	0.658296	Grm1/Itsn1
GO_CC_m4	GO:000590	microvillus	4/714	92/23583	0.303949	0.669884	0.658296	Car2/Erbb2

GO_CC_m4	GO:000017	nuclear exc	1/714	12/23583	0.308584	0.669884	0.658296	Mphosph6
GO_CC_m4	GO:000034	transcriptic	1/714	12/23583	0.308584	0.669884	0.658296	Thoc5
GO_CC_m4	GO:003612	CatSper co	1/714	12/23583	0.308584	0.669884	0.658296	Catsper2
GO_CC_m4	GO:004261	MHC class	1/714	12/23583	0.308584	0.669884	0.658296	H2-Q10
GO_CC_m4	GO:004262	chylomicro	1/714	12/23583	0.308584	0.669884	0.658296	Apoa4
GO_CC_m4	GO:004818	Set1C/COM	1/714	12/23583	0.308584	0.669884	0.658296	Dydc1
GO_CC_m4	GO:009853	ATPase de	1/714	12/23583	0.308584	0.669884	0.658296	Atp1b4
GO_CC_m4	GO:004430	neuron spi	7/714	181/23583	0.309204	0.669884	0.658296	Grm1/Itsn1
GO_CC_m4	GO:004444	cell cortex	7/714	181/23583	0.309204	0.669884	0.658296	Cap2/Myl1
GO_CC_m4	GO:004445	nucleolar p	7/714	181/23583	0.309204	0.669884	0.658296	Ager/Arhga
GO_CC_m4	GO:009722	sperm part	9/714	242/23583	0.312478	0.669884	0.658296	Atp6v1e2/
GO_CC_m4	GO:007016	anchoring	11/714	303/23583	0.312554	0.669884	0.658296	Abcb4/Cac
GO_CC_m4	GO:009886	cluster of a	7/714	182/23583	0.314045	0.669884	0.658296	Car4/Folr1/
GO_CC_m4	GO:009882	endoplasm	17/714	489/23583	0.314279	0.669884	0.658296	Atf6b/Nat8
GO_CC_m4	GO:001250	vesicle mer	11/714	304/23583	0.316285	0.669884	0.658296	Abcc4/Car4
GO_CC_m4	GO:003470	methyltran	4/714	94/23583	0.317666	0.669884	0.658296	Cbx5/Dydc
GO_CC_m4	GO:004320	myelin she	8/714	213/23583	0.318123	0.669884	0.658296	Atp5c1/Car
GO_CC_m4	GO:003065	cytoplasmi	10/714	274/23583	0.318701	0.669884	0.658296	Abcc4/Car4
GO_CC_m4	GO:009073	site of DNA	2/714	38/23583	0.320269	0.669884	0.658296	Hus1/Polk
GO_CC_m4	GO:003258	ruffle mem	3/714	66/23583	0.3228	0.669884	0.658296	Rps3/Spata
GO_CC_m4	GO:000594	septin ring	1/714	13/23583	0.329528	0.669884	0.658296	12-Sep
GO_CC_m4	GO:001651	SWI/SNF c	1/714	13/23583	0.329528	0.669884	0.658296	Smarcd2
GO_CC_m4	GO:001710	aminoacyl-	1/714	13/23583	0.329528	0.669884	0.658296	Iars
GO_CC_m4	GO:003012	COPII vesic	1/714	13/23583	0.329528	0.669884	0.658296	Sec13
GO_CC_m4	GO:003110	septin com	1/714	13/23583	0.329528	0.669884	0.658296	12-Sep
GO_CC_m4	GO:003216	septin filam	1/714	13/23583	0.329528	0.669884	0.658296	12-Sep
GO_CC_m4	GO:004423	ER-mitoch	1/714	13/23583	0.329528	0.669884	0.658296	Stx17
GO_CC_m4	GO:009744	astrocyte p	1/714	13/23583	0.329528	0.669884	0.658296	Slc17a8
GO_CC_m4	GO:004319	dendritic sh	3/714	67/23583	0.331133	0.669884	0.658296	Cacna1b/R
GO_CC_m4	GO:003130	intrinsic co	7/714	186/23583	0.333537	0.669884	0.658296	Bet1l/Chch
GO_CC_m4	GO:000032	lytic vacuol	15/714	433/23583	0.333771	0.669884	0.658296	Borcs7/533
GO_CC_m4	GO:000576	lysosome	15/714	433/23583	0.333771	0.669884	0.658296	Borcs7/533
GO_CC_m4	GO:003259	integral co	3/714	68/23583	0.339463	0.678331	0.666596	Chchd6/Fu
GO_CC_m4	GO:004878	presynapti	2/714	40/23583	0.342571	0.678331	0.666596	Rims4/Syn
GO_CC_m4	GO:009973	cell cortex	2/714	40/23583	0.342571	0.678331	0.666596	Myl12a/Rir
GO_CC_m4	GO:000565	replication	3/714	69/23583	0.347786	0.678331	0.666596	Purb/Smar
GO_CC_m4	GO:000094	condensed	1/714	14/23583	0.349838	0.678331	0.666596	Spdl1
GO_CC_m4	GO:000567	Ada2/Gcn5	1/714	14/23583	0.349838	0.678331	0.666596	Dr1
GO_CC_m4	GO:000573	DNA-direc	1/714	14/23583	0.349838	0.678331	0.666596	Polr1e
GO_CC_m4	GO:003603	MKS comp	1/714	14/23583	0.349838	0.678331	0.666596	Tmem231
GO_CC_m4	GO:004258	zymogen g	1/714	14/23583	0.349838	0.678331	0.666596	Tmed10
GO_CC_m4	GO:009879	outer mito	1/714	14/23583	0.349838	0.678331	0.666596	Tomm7
GO_CC_m4	GO:000588	cytoplasmi	3/714	70/23583	0.356098	0.683652	0.671825	Bcl10/Casc
GO_CC_m4	GO:009857	intrinsic co	3/714	70/23583	0.356098	0.683652	0.671825	Chchd6/Fu
GO_CC_m4	GO:003013	endocytic	6/714	160/23583	0.356168	0.683652	0.671825	Itsn1/Kif16
GO_CC_m4	GO:000572	nuclear het	2/714	42/23583	0.364635	0.697563	0.685496	Cbx5/Vdr
GO_CC_m4	GO:003108	BLOC-1 co	1/714	15/23583	0.369534	0.697603	0.685535	Snap47
GO_CC_m4	GO:003146	Cul2-RING	1/714	15/23583	0.369534	0.697603	0.685535	Zswim4

GO_CC_m4	GO:003215	septin cyto	1/714	15/23583	0.369534	0.697603	0.685535	12-Sep	
GO_CC_m4	GO:003471	SMN-Sm p	1/714	15/23583	0.369534	0.697603	0.685535	Gemin5	
GO_CC_m4	GO:003586	ciliary trans	3/714	72/23583	0.372676	0.698921	0.686831	Gnat1/Nph	
GO_CC_m4	GO:007060	SWI/SNF su	3/714	72/23583	0.372676	0.698921	0.686831	Smarca1/S	
GO_CC_m4	GO:000992	basal plasn	2/714	43/23583	0.375561	0.699743	0.687638	Ager/Erbb2	
GO_CC_m4	GO:003167	A band	2/714	43/23583	0.375561	0.699743	0.687638	Fhl2/Myom	
GO_CC_m4	GO:000802	synaptic ve	7/714	195/23583	0.377915	0.701843	0.689702	Cttnbp2/M	
GO_CC_m4	GO:000593	cell cortex	10/714	290/23583	0.382972	0.703478	0.691308	Arhgap32/	
GO_CC_m4	GO:003239	photorecep	2/714	44/23583	0.386409	0.703478	0.691308	Gnat1/Nph	
GO_CC_m4	GO:003013	transport v	10/714	291/23583	0.387037	0.703478	0.691308	Car4/Cttnb	
GO_CC_m4	GO:000585	muscle my	1/714	16/23583	0.388634	0.703478	0.691308	Myom2	
GO_CC_m4	GO:001036	chromocer	1/714	16/23583	0.388634	0.703478	0.691308	Cbx5	
GO_CC_m4	GO:003001	CCR4-NOT	1/714	16/23583	0.388634	0.703478	0.691308	Cnot6	
GO_CC_m4	GO:003585	Seh1-asso	1/714	16/23583	0.388634	0.703478	0.691308	Sec13	
GO_CC_m4	GO:003820	TOR comp	1/714	16/23583	0.388634	0.703478	0.691308	Akt1s1	
GO_CC_m4	GO:003509	histone me	3/714	75/23583	0.397378	0.712213	0.699893	Cbx5/Dydc	
GO_CC_m4	GO:199020	oxidoreduc	4/714	106/23583	0.400337	0.712213	0.699893	Ndufb10/N	
GO_CC_m4	GO:003013	coated ves	6/714	169/23583	0.404857	0.712213	0.699893	Lman1l/Sec	
GO_CC_m4	GO:000013	Golgi mem	8/714	232/23583	0.404907	0.712213	0.699893	Abcb1b/Ab	
GO_CC_m4	GO:001601	dystrophin	1/714	17/23583	0.407157	0.712213	0.699893	Sgcb	
GO_CC_m4	GO:003161	spindle pol	1/714	17/23583	0.407157	0.712213	0.699893	Aurka	
GO_CC_m4	GO:003327	paranode r	1/714	17/23583	0.407157	0.712213	0.699893	Sptan1	
GO_CC_m4	GO:004210	T cell recep	1/714	17/23583	0.407157	0.712213	0.699893	Bcl10	
GO_CC_m4	GO:007100	U2-type pr	1/714	17/23583	0.407157	0.712213	0.699893	Luc7l3	
GO_CC_m4	GO:009066	glycoprote	1/714	17/23583	0.407157	0.712213	0.699893	Sgcb	
GO_CC_m4	GO:009864	complex of	1/714	17/23583	0.407157	0.712213	0.699893	Lum	
GO_CC_m4	GO:000172	ruffle	5/714	139/23583	0.412516	0.719388	0.706944	Frmd4b/M	
GO_CC_m4	GO:003130	integral co	6/714	172/23583	0.421057	0.732051	0.719387	Bet1l/Chch	
GO_CC_m4	GO:003152	microvillus	1/714	18/23583	0.425119	0.732364	0.719695	Muc4	
GO_CC_m4	GO:004429	dendrite te	1/714	18/23583	0.425119	0.732364	0.719695	Rtn4	
GO_CC_m4	GO:000077	condensed	2/714	48/23583	0.42892	0.732364	0.719695	Aurka/Spdl	
GO_CC_m4	GO:000574	mitochond	2/714	48/23583	0.42892	0.732364	0.719695	Ndufb10/N	
GO_CC_m4	GO:003096	NADH deh	2/714	48/23583	0.42892	0.732364	0.719695	Ndufb10/N	
GO_CC_m4	GO:004527	respiratory	2/714	48/23583	0.42892	0.732364	0.719695	Ndufb10/N	
GO_CC_m4	GO:000576	early endos	8/714	239/23583	0.43709	0.74232	0.729479	Kif16b/Lipo	
GO_CC_m4	GO:012011	Sm-like pro	3/714	80/23583	0.43791	0.74232	0.729479	Gemin5/Lu	
GO_CC_m4	GO:001646	proton-tra	2/714	49/23583	0.439305	0.74232	0.729479	Atp5c1/Atp	
GO_CC_m4	GO:003109	platelet alp	1/714	19/23583	0.442537	0.74232	0.729479	F5	
GO_CC_m4	GO:004423	organelle r	1/714	19/23583	0.442537	0.74232	0.729479	Stx17	
GO_CC_m4	GO:009072	growth cor	1/714	19/23583	0.442537	0.74232	0.729479	Trpv2	
GO_CC_m4	GO:003068	preribosom	3/714	81/23583	0.445896	0.745768	0.732867	Krr1/Mdn1	
GO_CC_m4	GO:001986	organelle i	15/714	468/23583	0.447906	0.746945	0.734024	Atp1b4/Atp	
GO_CC_m4	GO:000558	collagen tri	3/714	82/23583	0.453837	0.754636	0.741582	Lum/Mbl1/	
GO_CC_m4	GO:004430	neuron pro	7/714	211/23583	0.457008	0.757329	0.744228	Cacna1b/F	
GO_CC_m4	GO:003028	integral co	1/714	20/23583	0.459428	0.757329	0.744228	Slc17a8	
GO_CC_m4	GO:003108	BLOC comp	1/714	20/23583	0.459428	0.757329	0.744228	Snap47	
GO_CC_m4	GO:007038	exocytic ve	7/714	213/23583	0.466789	0.767251	0.753979	Cttnbp2/M	
GO_CC_m4	GO:001705	transcriptic	3/714	84/23583	0.469573	0.768033	0.754748	Cbx5/Gata	

GO_CC_m4	GO:004443	cytoplasmi	15/714	475/23583	0.470885	0.768033	0.754748	Abcc4/Car4
GO_CC_m4	GO:000042	autophago	1/714	21/23583	0.475809	0.768033	0.754748	Stx17
GO_CC_m4	GO:000167	male germ	1/714	21/23583	0.475809	0.768033	0.754748	Kif6
GO_CC_m4	GO:000568	anaphase-	1/714	21/23583	0.475809	0.768033	0.754748	Anapc2
GO_CC_m4	GO:001632	apicolatera	1/714	21/23583	0.475809	0.768033	0.754748	Mtcl1
GO_CC_m4	GO:009956	cytoplasmi	14/714	444/23583	0.476664	0.768033	0.754748	Abhd13/Ar
GO_CC_m4	GO:000587	spindle mic	2/714	53/23583	0.479772	0.77087	0.757535	Aurka/Polb
GO_CC_m4	GO:000572	pericentric	1/714	22/23583	0.491693	0.772277	0.758918	Cbx5
GO_CC_m4	GO:000575	mitochond	1/714	22/23583	0.491693	0.772277	0.758918	Atp5c1
GO_CC_m4	GO:000579	Golgi medi	1/714	22/23583	0.491693	0.772277	0.758918	H2-Q10
GO_CC_m4	GO:007178	endoplasm	1/714	22/23583	0.491693	0.772277	0.758918	Rtn4
GO_CC_m4	GO:003067	synaptic ve	3/714	87/23583	0.492785	0.772277	0.758918	Slc17a8/Sn
GO_CC_m4	GO:009950	exocytic ve	3/714	87/23583	0.492785	0.772277	0.758918	Slc17a8/Sn
GO_CC_m4	GO:004512	membrane	11/714	350/23583	0.492831	0.772277	0.758918	Bcl10/Ctnn
GO_CC_m4	GO:009885	membrane	11/714	350/23583	0.492831	0.772277	0.758918	Bcl10/Ctnn
GO_CC_m4	GO:009879	Golgi subc	13/714	416/23583	0.493345	0.772277	0.758918	5330417C2
GO_CC_m4	GO:000092	spindle pol	4/714	120/23583	0.494188	0.772277	0.758918	Aurka/Map
GO_CC_m4	GO:001000	endosome	6/714	186/23583	0.495499	0.772277	0.758918	Ehd4/Erbb
GO_CC_m4	GO:000587	kinesin con	2/714	55/23583	0.499323	0.77556	0.762144	Kif16b/Kif6
GO_CC_m4	GO:000017	exosome (	1/714	23/23583	0.507097	0.77556	0.762144	Mphosph6
GO_CC_m4	GO:003013	COPI-coat	1/714	23/23583	0.507097	0.77556	0.762144	Tmed10
GO_CC_m4	GO:004261	MHC prote	1/714	23/23583	0.507097	0.77556	0.762144	H2-Q10
GO_CC_m4	GO:004512	pronucleus	1/714	23/23583	0.507097	0.77556	0.762144	Aurka
GO_CC_m4	GO:004525	proton-tra	1/714	23/23583	0.507097	0.77556	0.762144	Atp5c1
GO_CC_m4	GO:190535	exoribonuc	1/714	23/23583	0.507097	0.77556	0.762144	Mphosph6
GO_CC_m4	GO:000581	spindle	8/714	255/23583	0.509521	0.777189	0.763745	Aurka/Map
GO_CC_m4	GO:000588	intermedia	4/714	123/23583	0.513531	0.7798	0.766311	Bfsp2/Dsp/
GO_CC_m4	GO:001406	postsynapt	8/714	256/23583	0.513959	0.7798	0.766311	Cap2/Grm1
GO_CC_m4	GO:003005	desmosom	1/714	24/23583	0.522035	0.781721	0.768198	Dsp
GO_CC_m4	GO:003258	trans-Golg	1/714	24/23583	0.522035	0.781721	0.768198	Rab31
GO_CC_m4	GO:009879	presynapse	12/714	391/23583	0.522037	0.781721	0.768198	Cacna1b/C
GO_CC_m4	GO:004521	postsynapt	8/714	258/23583	0.522796	0.781721	0.768198	Arc/Arhgap
GO_CC_m4	GO:009957	postsynapt	8/714	258/23583	0.522796	0.781721	0.768198	Cap2/Grm1
GO_CC_m4	GO:009057	RNA polym	5/714	158/23583	0.523425	0.781721	0.768198	Atf6b/Ddit3
GO_CC_m4	GO:003042	growth cor	6/714	192/23583	0.526442	0.784084	0.77052	Cbarp/Rtn4
GO_CC_m4	GO:001632	lateral plas	2/714	58/23583	0.527749	0.784084	0.77052	Mtcl1/Spta
GO_CC_m4	GO:003227	asymmetric	8/714	260/23583	0.531575	0.787094	0.773478	Cap2/Grm1
GO_CC_m4	GO:005503	recycling e	4/714	126/23583	0.532527	0.787094	0.773478	Ehd4/Mlc1
GO_CC_m4	GO:000590	caveola	3/714	93/23583	0.537626	0.791045	0.777361	Ctnna1/Ml
GO_CC_m4	GO:009858	membrane	11/714	362/23583	0.537966	0.791045	0.777361	Bcl10/Ctnn
GO_CC_m4	GO:001989	extrinsic cc	9/714	296/23583	0.542043	0.792787	0.779073	Cdh24/Cdh
GO_CC_m4	GO:009898	neuron to	8/714	263/23583	0.54463	0.792787	0.779073	Cap2/Grm1
GO_CC_m4	GO:003606	ciliary basa	4/714	128/23583	0.544984	0.792787	0.779073	Cep41/Ptp
GO_CC_m4	GO:015003	distal axon	11/714	364/23583	0.54536	0.792787	0.779073	Cacna1b/C
GO_CC_m4	GO:003066	Golgi-asso	2/714	60/23583	0.546082	0.792787	0.779073	Sec13/Sec2
GO_CC_m4	GO:000078	condensed	1/714	26/23583	0.550568	0.792787	0.779073	Aurka
GO_CC_m4	GO:003158	nucleotide-	1/714	26/23583	0.550568	0.792787	0.779073	Prkag1
GO_CC_m4	GO:004442	extracellula	4/714	129/23583	0.551148	0.792787	0.779073	Eln/Hmcn2

GO_CC_m4	GO:003042	site of pola	6/714	197/23583	0.551625	0.792787	0.779073	Cbarp/Rtn4
GO_CC_m4	GO:000077	kinetochor	4/714	130/23583	0.557268	0.79889	0.785071	Cenps/Cbx
GO_CC_m4	GO:000586	cytoplasmi	1/714	27/23583	0.56419	0.80434	0.790426	Dynll2
GO_CC_m4	GO:003326	axon part	13/714	437/23583	0.565288	0.80434	0.790426	Aurka/Cacr
GO_CC_m4	GO:004444	ciliary part	13/714	437/23583	0.565288	0.80434	0.790426	Casc1/Ccd
GO_CC_m4	GO:004320	perikaryon	4/714	132/23583	0.569371	0.805727	0.79179	Esr2/Neurl
GO_CC_m4	GO:003031	T-tubule	2/714	63/23583	0.572636	0.805727	0.79179	Slc8a1/Vdr
GO_CC_m4	GO:004443	Golgi appa	14/714	474/23583	0.575775	0.805727	0.79179	5330417C2
GO_CC_m4	GO:004466	MLL1/2 co	1/714	28/23583	0.5774	0.805727	0.79179	Max
GO_CC_m4	GO:007133	MLL1 comp	1/714	28/23583	0.5774	0.805727	0.79179	Max
GO_CC_m4	GO:199075	microtubul	1/714	28/23583	0.5774	0.805727	0.79179	Nav3
GO_CC_m4	GO:009752	spliceosom	2/714	64/23583	0.581233	0.805727	0.79179	Luc7l3/Snr
GO_CC_m4	GO:000079	condensed	7/714	238/23583	0.584022	0.805727	0.79179	Aurka/Hus
GO_CC_m4	GO:003196	nuclear me	7/714	238/23583	0.584022	0.805727	0.79179	Ackr2/Atp1
GO_CC_m4	GO:000579	rough end	3/714	100/23583	0.586953	0.805727	0.79179	Car4/F12/S
GO_CC_m4	GO:000592	focal adhe	4/714	135/23583	0.587175	0.805727	0.79179	Abcb4/Flrt
GO_CC_m4	GO:009880	inner mito	4/714	135/23583	0.587175	0.805727	0.79179	Atp5c1/Ch
GO_CC_m4	GO:000568	U2-type sp	2/714	65/23583	0.589701	0.805727	0.79179	Luc7l3/Snr
GO_CC_m4	GO:009902	tethering c	2/714	65/23583	0.589701	0.805727	0.79179	Nbas/Stx17
GO_CC_m4	GO:000031	organellar	1/714	29/23583	0.590209	0.805727	0.79179	Mrps16
GO_CC_m4	GO:000576	mitochond	1/714	29/23583	0.590209	0.805727	0.79179	Mrps16
GO_CC_m4	GO:009743	mitotic spi	1/714	29/23583	0.590209	0.805727	0.79179	Aurka
GO_CC_m4	GO:004517	basal part	2/714	66/23583	0.598042	0.814476	0.800387	Ager/Erbb2
GO_CC_m4	GO:009722	sperm prin	1/714	30/23583	0.602632	0.818777	0.804614	Catspere2
GO_CC_m4	GO:004444	endosomal	6/714	209/23583	0.609395	0.823409	0.809165	Ehd4/Erbb
GO_CC_m4	GO:000564	nuclear po	2/714	68/23583	0.614339	0.823409	0.809165	Parp11/Sec
GO_CC_m4	GO:003283	dendrite cy	1/714	31/23583	0.614678	0.823409	0.809165	Abhd13
GO_CC_m4	GO:004247	melanoson	1/714	31/23583	0.614678	0.823409	0.809165	Mreg
GO_CC_m4	GO:004877	pigment gr	1/714	31/23583	0.614678	0.823409	0.809165	Mreg
GO_CC_m4	GO:005123	spindle mic	1/714	31/23583	0.614678	0.823409	0.809165	Aurka
GO_CC_m4	GO:000581	centriole	3/714	105/23583	0.620055	0.824465	0.810203	Cep152/Ce
GO_CC_m4	GO:000592	cell-substr	4/714	141/23583	0.62146	0.824465	0.810203	Abcb4/Flrt
GO_CC_m4	GO:000575	mitochond	2/714	69/23583	0.622296	0.824465	0.810203	Ak3/Cycs
GO_CC_m4	GO:003066	coated ves	2/714	69/23583	0.622296	0.824465	0.810203	Sec13/Sec2
GO_CC_m4	GO:000077	condensed	1/714	32/23583	0.626359	0.824465	0.810203	Spdl1
GO_CC_m4	GO:009056	nuclear tra	1/714	32/23583	0.626359	0.824465	0.810203	Smarca5
GO_CC_m4	GO:000577	peroxisom	4/714	142/23583	0.626997	0.824465	0.810203	Nudt7/Pex
GO_CC_m4	GO:004257	microbody	4/714	142/23583	0.626997	0.824465	0.810203	Nudt7/Pex
GO_CC_m4	GO:003053	small nucle	2/714	70/23583	0.630125	0.824487	0.810224	Luc7l3/Snr
GO_CC_m4	GO:004445	mitochond	6/714	214/23583	0.632216	0.824487	0.810224	Atp5c1/Ch
GO_CC_m4	GO:009773	non-motile	4/714	143/23583	0.632481	0.824487	0.810224	Gnat1/Nph
GO_CC_m4	GO:009773	photorecep	3/714	107/23583	0.632779	0.824487	0.810224	Gnat1/Nph
GO_CC_m4	GO:000592	gap junctio	1/714	33/23583	0.637687	0.828993	0.814652	Mip
GO_CC_m4	GO:000574	mitochond	12/714	426/23583	0.641157	0.831614	0.817229	Atp5c1/Ch
GO_CC_m4	GO:003125	leading ed	4/714	145/23583	0.643294	0.831929	0.817537	Rps3/Scim
GO_CC_m4	GO:000989	cytoplasmi	5/714	182/23583	0.64859	0.831929	0.817537	Gnat1/Gng
GO_CC_m4	GO:000579	smooth en	1/714	34/23583	0.648672	0.831929	0.817537	Stx17
GO_CC_m4	GO:003099	intraciliary	1/714	34/23583	0.648672	0.831929	0.817537	Wdr35

GO_CC_m4	GO:009883	postsynapt	1/714	34/23583	0.648672	0.831929	0.817537	Grm1
GO_CC_m4	GO:003586	site of dou	1/714	35/23583	0.659324	0.833673	0.819252	Hus1
GO_CC_m4	GO:008000	Cul4-RING	1/714	35/23583	0.659324	0.833673	0.819252	Dcaf17
GO_CC_m4	GO:000078	nuclear chr	2/714	74/23583	0.660178	0.833673	0.819252	Cbx5/Thoc
GO_CC_m4	GO:000172	stress fiber	2/714	74/23583	0.660178	0.833673	0.819252	Myl12a/Syr
GO_CC_m4	GO:009751	contractile	2/714	74/23583	0.660178	0.833673	0.819252	Myl12a/Syr
GO_CC_m4	GO:009773	9+0 non-n	3/714	112/23583	0.66328	0.833673	0.819252	Gnat1/Nph
GO_CC_m4	GO:003005	cell-substr	4/714	149/23583	0.664285	0.833673	0.819252	Abcb4/Flrt
GO_CC_m4	GO:004445	microtubul	4/714	149/23583	0.664285	0.833673	0.819252	Cep152/Ce
GO_CC_m4	GO:003125	cell leading	10/714	364/23583	0.66677	0.833673	0.819252	Ctnna1/Frr
GO_CC_m4	GO:005580	trans-Golg	5/714	186/23583	0.667312	0.833673	0.819252	5330417C2
GO_CC_m4	GO:003204	small-subu	1/714	36/23583	0.669653	0.833673	0.819252	Krr1
GO_CC_m4	GO:005503	recycling e	1/714	36/23583	0.669653	0.833673	0.819252	Ehd4
GO_CC_m4	GO:199039	DNA repair	1/714	36/23583	0.669653	0.833673	0.819252	Xpa
GO_CC_m4	GO:000175	photorecep	2/714	76/23583	0.674454	0.833673	0.819252	Gnat1/Prpl
GO_CC_m4	GO:004485	plasma me	3/714	114/23583	0.674954	0.833673	0.819252	Ctnna1/Ml
GO_CC_m4	GO:003130	integral co	1/714	37/23583	0.67967	0.833673	0.819252	Chchd6
GO_CC_m4	GO:009963	postsynapt	1/714	37/23583	0.67967	0.833673	0.819252	Grm1
GO_CC_m4	GO:000593	axoneme	3/714	115/23583	0.680677	0.833673	0.819252	Casc1/Ccd
GO_CC_m4	GO:000077	chromosor	5/714	189/23583	0.680918	0.833673	0.819252	Cenps/Aur
GO_CC_m4	GO:009706	synaptic m	9/714	334/23583	0.684905	0.833673	0.819252	Arc/Arhgap
GO_CC_m4	GO:009701	ciliary plas	3/714	116/23583	0.686326	0.833673	0.819252	Casc1/Ccd
GO_CC_m4	GO:004273	presynapti	2/714	78/23583	0.688239	0.833673	0.819252	Grm1/Rims
GO_CC_m4	GO:004238	sarcolemm	4/714	154/23583	0.689317	0.833673	0.819252	Car4/Sgcb/
GO_CC_m4	GO:000079	euchromat	1/714	38/23583	0.689384	0.833673	0.819252	Vdr
GO_CC_m4	GO:003017	integral co	1/714	38/23583	0.689384	0.833673	0.819252	Bet1l
GO_CC_m4	GO:003130	intrinsic co	1/714	38/23583	0.689384	0.833673	0.819252	Chchd6
GO_CC_m4	GO:009754	ciliary base	1/714	38/23583	0.689384	0.833673	0.819252	Nphp1
GO_CC_m4	GO:000576	lysosomal	3/714	118/23583	0.697398	0.839814	0.825287	Sec13/Tpcr
GO_CC_m4	GO:009885	lytic vacuol	3/714	118/23583	0.697398	0.839814	0.825287	Sec13/Tpcr
GO_CC_m4	GO:004367	axon termi	5/714	194/23583	0.702754	0.840403	0.825866	Cacna1b/It
GO_CC_m4	GO:000015	nuclear ubi	1/714	40/23583	0.707937	0.840403	0.825866	Anapc2
GO_CC_m4	GO:003122	intrinsic co	1/714	40/23583	0.707937	0.840403	0.825866	Bet1l
GO_CC_m4	GO:006007	excitatory	1/714	40/23583	0.707937	0.840403	0.825866	Slc17a8
GO_CC_m4	GO:004430	main axon	2/714	81/23583	0.708012	0.840403	0.825866	Sptan1/Tia
GO_CC_m4	GO:009880	respiratory	2/714	81/23583	0.708012	0.840403	0.825866	Ndufb10/N
GO_CC_m4	GO:004319	terminal bo	3/714	120/23583	0.708172	0.840403	0.825866	Itsn1/Syn1/
GO_CC_m4	GO:000574	mitochond	2/714	82/23583	0.714367	0.841932	0.827368	Ndufb10/N
GO_CC_m4	GO:000579	Golgi stack	2/714	82/23583	0.714367	0.841932	0.827368	Bet1l/H2-Q
GO_CC_m4	GO:003197	organelle e	2/714	82/23583	0.714367	0.841932	0.827368	Ak3/Cycs
GO_CC_m4	GO:009856	cytoplasmi	5/714	197/23583	0.715348	0.841932	0.827368	Gnat1/Gng
GO_CC_m4	GO:003002	lamellipodi	4/714	160/23583	0.717572	0.842816	0.828236	Ctnna1/Itsr
GO_CC_m4	GO:003243	actin filame	2/714	83/23583	0.720605	0.842985	0.828403	Myl12a/Syr
GO_CC_m4	GO:009885	actin-base	5/714	199/23583	0.723531	0.842985	0.828403	Car2/Erbb2
GO_CC_m4	GO:000577	peroxisom	1/714	42/23583	0.725384	0.842985	0.828403	Pex1
GO_CC_m4	GO:003190	microbody	1/714	42/23583	0.725384	0.842985	0.828403	Pex1
GO_CC_m4	GO:190256	H4 histone	1/714	42/23583	0.725384	0.842985	0.828403	Dr1
GO_CC_m4	GO:003283	plasma me	4/714	162/23583	0.726559	0.842985	0.828403	Abhd13/Ca

GO_CC_m	GO:004264	actomyosir	2/714	85/23583	0.732736	0.847846	0.83318	Myl12a/Sy
GO_CC_m	GO:00580	cis-Golgi n	1/714	43/23583	0.733713	0.847846	0.83318	Tmed10
GO_CC_m	GO:001636	nuclear ma	2/714	87/23583	0.744417	0.857568	0.842733	Sfpq/Vdr
GO_CC_m	GO:00828	protein ser	1/714	45/23583	0.749622	0.857568	0.842733	Ppp1r15b
GO_CC_m	GO:00104	cytoplasmi	1/714	45/23583	0.749622	0.857568	0.842733	Grb7
GO_CC_m	GO:012011	neuron prc	1/714	45/23583	0.749622	0.857568	0.842733	Abhd13
GO_CC_m	GO:19032	phosphata	1/714	45/23583	0.749622	0.857568	0.842733	Ppp1r15b
GO_CC_m	GO:00704	respiratory	2/714	89/23583	0.755657	0.859381	0.844515	Ndufb10/N
GO_CC_m	GO:000574	mitochond	4/714	169/23583	0.75633	0.859381	0.844515	Cstad/Cyb
GO_CC_m	GO:00319	late endos	1/714	46/23583	0.757217	0.859381	0.844515	Vamp8
GO_CC_m	GO:006017	ciliary mem	1/714	46/23583	0.757217	0.859381	0.844515	Tmem231
GO_CC_m	GO:00079	heterochro	2/714	90/23583	0.761116	0.862095	0.847182	Cbx5/Vdr
GO_CC_m	GO:00166	acrosomal	3/714	134/23583	0.775445	0.87659	0.861427	Atp6v1e2/
GO_CC_m	GO:000191	photorece	1/714	49/23583	0.778649	0.877957	0.86277	Gnat1
GO_CC_m	GO:00550	nuclear DN	3/714	135/23583	0.779724	0.877957	0.86277	Polr1e/Pol
GO_CC_m	GO:004481	DNA packa	2/714	94/23583	0.781904	0.878682	0.863482	Hp1bp3/N
GO_CC_m	GO:00042	DNA-direc	3/714	136/23583	0.783936	0.879238	0.864028	Polr1e/Pol
GO_CC_m	GO:00726	mitotic spir	2/714	95/23583	0.786847	0.87947	0.864256	Aurka/Rps
GO_CC_m	GO:000577	vacuolar m	4/714	177/23583	0.787218	0.87947	0.864256	Sec13/Stx1
GO_CC_m	GO:00301	vesicle coa	1/714	51/23583	0.791877	0.881547	0.866297	Sec13
GO_CC_m	GO:00308	RNA polym	3/714	138/23583	0.792159	0.881547	0.866297	Polr1e/Pol
GO_CC_m	GO:00432	receptor cc	9/714	374/23583	0.80173	0.890466	0.875062	Bcl10/Erbb
GO_CC_m	GO:003011	membrane	2/714	99/23583	0.805644	0.891351	0.875932	Ap1s3/Sec
GO_CC_m	GO:004847	coated me	2/714	99/23583	0.805644	0.891351	0.875932	Ap1s3/Sec
GO_CC_m	GO:00987	mitochond	6/714	262/23583	0.808236	0.892493	0.877054	Atp5c1/Ch
GO_CC_m	GO:00080	transcriptic	1/714	54/23583	0.810253	0.892996	0.877548	Nelfe
GO_CC_m	GO:00079	condensed	4/714	185/23583	0.8149	0.89639	0.880884	Aurka/Hus
GO_CC_m	GO:00198	outer mem	4/714	187/23583	0.821341	0.898292	0.882753	Cstad/Cyb
GO_CC_m	GO:00319	organelle c	4/714	187/23583	0.821341	0.898292	0.882753	Cstad/Cyb
GO_CC_m	GO:00444	vacuolar pa	4/714	187/23583	0.821341	0.898292	0.882753	Sec13/Stx1
GO_CC_m	GO:00560	basement	2/714	103/23583	0.822953	0.898338	0.882798	Hmcn2/Vw
GO_CC_m	GO:00444	microbody	1/714	57/23583	0.827009	0.899333	0.883776	Pex1
GO_CC_m	GO:00444	peroxisoma	1/714	57/23583	0.827009	0.899333	0.883776	Pex1
GO_CC_m	GO:003242	stereociliur	1/714	58/23583	0.832259	0.903325	0.887699	Tiam1
GO_CC_m	GO:00078	chromosor	2/714	106/23583	0.835013	0.904597	0.888949	Cbx5/Thoc
GO_CC_m	GO:00319	Golgi ciste	1/714	59/23583	0.83735	0.904654	0.889004	H2-Q10
GO_CC_m	GO:00079	nuclear chr	9/714	390/23583	0.838228	0.904654	0.889004	Cbx5/Max/
GO_CC_m	GO:000011	histone de	1/714	61/23583	0.847074	0.912479	0.896694	Cbx5
GO_CC_m	GO:00165	DNA-direc	2/714	110/23583	0.849937	0.913842	0.898034	Polr2m/Re
GO_CC_m	GO:001652	sarcoplasm	1/714	65/23583	0.864815	0.928094	0.912039	Car4
GO_CC_m	GO:00343	nuclear pe	2/714	117/23583	0.873126	0.935258	0.91908	Sfpq/Vdr
GO_CC_m	GO:00321	cell divisior	1/714	69/23583	0.8805	0.935552	0.919368	12-Sep
GO_CC_m	GO:00347	cation char	4/714	209/23583	0.880658	0.935552	0.919368	Cacna1b/C
GO_CC_m	GO:00098	external sic	11/714	491/23583	0.881192	0.935552	0.919368	Ager/Btn2a
GO_CC_m	GO:00986	chromosor	6/714	293/23583	0.88157	0.935552	0.919368	Cenps/Aur
GO_CC_m	GO:00093	P-body	1/714	70/23583	0.884128	0.935552	0.919368	Zfp36l1
GO_CC_m	GO:000577	autophago	1/714	70/23583	0.884128	0.935552	0.919368	Stx17
GO_CC_m	GO:00058	actin filame	2/714	121/23583	0.884849	0.935552	0.919368	Ackr2/Wip

GO_CC_m4	GO:190249	transmemb	6/714	296/23583	0.887218	0.936326	0.920129	Atp1b4/Ca
GO_CC_m4	GO:001652	sarcoplasm	1/714	74/23583	0.897575	0.943449	0.927129	Car4
GO_CC_m4	GO:199035	transporter	6/714	303/23583	0.899515	0.943449	0.927129	Atp1b4/Ca
GO_CC_m4	GO:000079	synaptoner	2/714	127/23583	0.900565	0.943449	0.927129	Polb/Syn1
GO_CC_m4	GO:009908	synaptoner	2/714	127/23583	0.900565	0.943449	0.927129	Polb/Syn1
GO_CC_m4	GO:003017	integral co	2/714	130/23583	0.907651	0.948576	0.932167	Atf6b/Rtn4
GO_CC_m4	GO:003646	cytoplasmi	3/714	178/23583	0.908776	0.948576	0.932167	Grb7/Tuba
GO_CC_m4	GO:003049	midbody	2/714	132/23583	0.912109	0.948702	0.932291	Mtcl1/Sept
GO_CC_m4	GO:000012	histone ace	1/714	79/23583	0.912214	0.948702	0.932291	Dr1
GO_CC_m4	GO:003122	intrinsic co	2/714	136/23583	0.920427	0.953863	0.937363	Atf6b/Rtn4
GO_CC_m4	GO:006169	transferase	5/714	275/23583	0.921957	0.953863	0.937363	Polr1e/Polr
GO_CC_m4	GO:000807	voltage-ga	1/714	84/23583	0.924763	0.953863	0.937363	Kcne1
GO_CC_m4	GO:003577	ribonucleo	3/714	188/23583	0.926635	0.953863	0.937363	Grb7/Tuba
GO_CC_m4	GO:000078	nucleosom	1/714	86/23583	0.929265	0.953863	0.937363	Hp1bp3
GO_CC_m4	GO:003017	filopodium	1/714	87/23583	0.931415	0.953863	0.937363	Spata13
GO_CC_m4	GO:003470	ion channe	5/714	282/23583	0.931435	0.953863	0.937363	Cacna1b/C
GO_CC_m4	GO:000031	organellar	1/714	89/23583	0.93552	0.953863	0.937363	Mrps16
GO_CC_m4	GO:000576	mitochond	1/714	89/23583	0.93552	0.953863	0.937363	Mrps16
GO_CC_m4	GO:003124	protein ace	1/714	89/23583	0.93552	0.953863	0.937363	Dr1
GO_CC_m4	GO:190249	acetyltrans	1/714	89/23583	0.93552	0.953863	0.937363	Dr1
GO_CC_m4	GO:000568	spliceosom	3/714	199/23583	0.942536	0.956385	0.939841	Lgals3/Luc
GO_CC_m4	GO:003146	cullin-RING	3/714	199/23583	0.942536	0.956385	0.939841	Anapc2/Dc
GO_CC_m4	GO:003470	potassium	1/714	93/23583	0.943009	0.956385	0.939841	Kcne1
GO_CC_m4	GO:000575	mitochond	4/714	253/23583	0.950129	0.9619	0.945261	Ak3/Mrps1
GO_CC_m4	GO:007256	blood micr	2/714	156/23583	0.951999	0.962091	0.945448	Apoa4/Igh
GO_CC_m4	GO:190291	protein kin	1/714	109/23583	0.965226	0.973738	0.956894	Prkag1
GO_CC_m4	GO:009880	plasma me	2/714	175/23583	0.970629	0.977465	0.960556	Bcl10/Grm
GO_CC_m4	GO:000581	centrosom	8/714	498/23583	0.984789	0.989981	0.972856	Aurka/Cep
GO_CC_m4	GO:004257	immunoglo	1/714	141/23583	0.987067	0.990304	0.973173	Ighv9-4
GO_CC_m4	GO:001981	immunoglo	1/714	145/23583	0.988573	0.990304	0.973173	Ighv9-4
GO_CC_m4	GO:000015	ubiquitin lig	3/714	340/23583	0.998141	0.998141	0.980874	Anapc2/Dc
GO_MF_m1	GO:000500	transmemb	7/2529	14/23049	0.000324	0.247529	0.238551	Epha10/Ep
GO_MF_m1	GO:001984	vitamin bin	28/2529	133/23049	0.000515	0.247529	0.238551	Abat/Akr1b
GO_MF_m1	GO:001685	isomerase	30/2529	147/23049	0.000576	0.247529	0.238551	Bpgm/Dct/
GO_MF_m1	GO:001674	transferase	39/2529	211/23049	0.000775	0.247529	0.238551	6430573F1
GO_MF_m1	GO:001048	H4 histone	8/2529	20/23049	0.000775	0.247529	0.238551	Nat8f3/Hat
GO_MF_m1	GO:000500	ephrin rece	7/2529	16/23049	0.000884	0.247529	0.238551	Epha10/Ep
GO_MF_m1	GO:000816	methyltran	37/2529	199/23049	0.00093	0.247529	0.238551	6430573F1
GO_MF_m1	GO:000452	exonucleas	17/2529	70/23049	0.001218	0.247529	0.238551	Aplf/Aptx/
GO_MF_m1	GO:000408	bisphospho	3/2529	3/23049	0.00132	0.247529	0.238551	Bpgm/Pga
GO_MF_m1	GO:000461	phosphogly	3/2529	3/23049	0.00132	0.247529	0.238551	Bpgm/Pga
GO_MF_m1	GO:004653	2,3-bispho	3/2529	3/23049	0.00132	0.247529	0.238551	Bpgm/Pga
GO_MF_m1	GO:000875	S-adenosy	29/2529	148/23049	0.001378	0.247529	0.238551	As3mt/Ash
GO_MF_m1	GO:009952	G-protein	12/2529	43/23049	0.001756	0.291044	0.280488	Chrm1/Chr
GO_MF_m1	GO:005066	coenzyme	47/2529	281/23049	0.002194	0.337643	0.325397	Abat/Acad
GO_MF_m1	GO:000460	glutathione	7/2529	20/23049	0.004038	0.4122	0.397251	Gpx1/Gpx2
GO_MF_m1	GO:005121	dioxygenas	19/2529	91/23049	0.004204	0.4122	0.397251	6430573F1
GO_MF_m1	GO:000817	RNA methy	14/2529	60/23049	0.004696	0.4122	0.397251	6430573F1

GO_MF_m	GO:00704	ammonium	17/2529	79/23049	0.004772	0.4122	0.397251	Ache/Acp
GO_MF_m	GO:00017	rRNA (ader	3/2529	4/23049	0.004844	0.4122	0.397251	Gm1818/T
GO_MF_m	GO:00502	prostaglan	3/2529	4/23049	0.004844	0.4122	0.397251	Mgst1/Ptg
GO_MF_m	GO:00341	apolipopro	6/2529	16/23049	0.005242	0.4122	0.397251	Canx/Lrp4/
GO_MF_m	GO:00046	peroxidase	11/2529	43/23049	0.005601	0.4122	0.397251	Gpx1/Gpx
GO_MF_m	GO:00305	neurotrans	22/2529	114/23049	0.005916	0.4122	0.397251	Adra1d/Ch
GO_MF_m	GO:004301	alpha-tubu	9/2529	32/23049	0.006087	0.4122	0.397251	1110017D
GO_MF_m	GO:00048	cyclin-dep	5/2529	12/23049	0.006462	0.4122	0.397251	Cdkn1a/Cc
GO_MF_m	GO:00434	protein me	5/2529	12/23049	0.006462	0.4122	0.397251	Akap6/Cib
GO_MF_m	GO:00081	N-methyltı	18/2529	88/23049	0.006556	0.4122	0.397251	Ash2l/Eef2
GO_MF_m	GO:00167	oxidoreduc	11/2529	45/23049	0.008058	0.4122	0.397251	6430573F
GO_MF_m	GO:00302	protein ser	8/2529	28/23049	0.008606	0.4122	0.397251	Cdkn1a/Cc
GO_MF_m	GO:00082	G-protein	15/2529	71/23049	0.009214	0.4122	0.397251	Adra1d/Ch
GO_MF_m	GO:00167	phosphata	42/2529	265/23049	0.009372	0.4122	0.397251	Acp6/Acp
GO_MF_m	GO:00551	ubiquitin-	6/2529	18/23049	0.010029	0.4122	0.397251	Cdc20/Fbx
GO_MF_m	GO:000411	creatine kir	3/2529	5/23049	0.011121	0.4122	0.397251	Ckm/Ckmt
GO_MF_m	GO:00103	double-str	3/2529	5/23049	0.011121	0.4122	0.397251	H2afy/Mbc
GO_MF_m	GO:003524	protein-ar	3/2529	5/23049	0.011121	0.4122	0.397251	Prmt1/Prm
GO_MF_m	GO:00166	oxidoreduc	11/2529	47/23049	0.011279	0.4122	0.397251	Gpx1/Gpx
GO_MF_m	GO:003141	cobalamin	4/2529	9/23049	0.011564	0.4122	0.397251	Gif/Mmab/
GO_MF_m	GO:00466	sphingolipi	4/2529	9/23049	0.011564	0.4122	0.397251	Abcb1a/Plt
GO_MF_m	GO:00002	magnesiun	31/2529	186/23049	0.011807	0.4122	0.397251	Abl2/Atp8
GO_MF_m	GO:00020	uracil bindi	2/2529	2/23049	0.012035	0.4122	0.397251	Dpyd/Dpy
GO_MF_m	GO:00020	pyrimidine	2/2529	2/23049	0.012035	0.4122	0.397251	Dpyd/Dpy
GO_MF_m	GO:00038	3-hydroxyl	2/2529	2/23049	0.012035	0.4122	0.397251	Bdh1/Bdh
GO_MF_m	GO:00039	acetylcholi	2/2529	2/23049	0.012035	0.4122	0.397251	Ache/Bche
GO_MF_m	GO:00046	phosphatic	2/2529	2/23049	0.012035	0.4122	0.397251	Got1/Pisd
GO_MF_m	GO:00081	protein tyr	2/2529	2/23049	0.012035	0.4122	0.397251	Igfbp3/Ptp
GO_MF_m	GO:003061	transformir	2/2529	2/23049	0.012035	0.4122	0.397251	Smad6/Sm
GO_MF_m	GO:00339	hyaluronoc	2/2529	2/23049	0.012035	0.4122	0.397251	Hyal2/Hyal
GO_MF_m	GO:00341	very-low-c	2/2529	2/23049	0.012035	0.4122	0.397251	Pcsk9/Vldl
GO_MF_m	GO:00477	chondroitir	2/2529	2/23049	0.012035	0.4122	0.397251	Dse/Dsel
GO_MF_m	GO:005264	lysophosph	2/2529	2/23049	0.012035	0.4122	0.397251	Acp6/Acp
GO_MF_m	GO:00973	protein O-	2/2529	2/23049	0.012035	0.4122	0.397251	Ogt/Pomg
GO_MF_m	GO:19901	peptide-gl	2/2529	2/23049	0.012035	0.4122	0.397251	Naa10/Naa
GO_MF_m	GO:00470	MAP kinas	16/2529	80/23049	0.012393	0.4122	0.397251	Epha10/Ep
GO_MF_m	GO:003421	peptide N-	14/2529	67/23049	0.012812	0.4122	0.397251	Clock/Nat
GO_MF_m	GO:00049	G-protein	8/2529	30/23049	0.013299	0.4122	0.397251	Olfr1564/H
GO_MF_m	GO:00995	serotonin r	8/2529	30/23049	0.013299	0.4122	0.397251	Olfr1564/H
GO_MF_m	GO:00049	dopamine	5/2529	14/23049	0.013551	0.4122	0.397251	Adra1d/Dr
GO_MF_m	GO:00050	GDP-disso	5/2529	14/23049	0.013551	0.4122	0.397251	Arhgdib/G
GO_MF_m	GO:00082	nucleotidas	5/2529	14/23049	0.013551	0.4122	0.397251	Acpp/Bpnt
GO_MF_m	GO:00162	antioxidant	16/2529	81/23049	0.013914	0.4122	0.397251	Gpx1/Gpx
GO_MF_m	GO:00080	N-acetyltra	17/2529	88/23049	0.014231	0.4122	0.397251	Clock/Nat
GO_MF_m	GO:00164	acetyltrans	20/2529	109/23049	0.014516	0.4122	0.397251	Clock/Nat
GO_MF_m	GO:00156	tubulin bin	47/2529	311/23049	0.014637	0.4122	0.397251	1110017D
GO_MF_m	GO:004257	phosphoric	52/2529	351/23049	0.015369	0.4122	0.397251	Acp6/Acp
GO_MF_m	GO:001921	kinase inhil	17/2529	89/23049	0.015845	0.4122	0.397251	Camk2n1/

GO_MF_m	GO:000837	acetylgluc	12/2529	56/23049	0.016784	0.4122	0.397251	A4gnt/B3g
GO_MF_m	GO:000864	rRNA meth	6/2529	20/23049	0.0173	0.4122	0.397251	Ftsj3/Gm18
GO_MF_m	GO:014010	catalytic ac	6/2529	20/23049	0.0173	0.4122	0.397251	Ftsj3/Gm18
GO_MF_m	GO:000804	enzyme ac	63/2529	441/23049	0.017496	0.4122	0.397251	1700006A1
GO_MF_m	GO:001686	intramolec	4/2529	10/23049	0.017619	0.4122	0.397251	Bpgm/Pga
GO_MF_m	GO:004399	histone ac	4/2529	10/23049	0.017619	0.4122	0.397251	Kansl1/Kan
GO_MF_m	GO:004399	histone ac	4/2529	10/23049	0.017619	0.4122	0.397251	Kansl1/Kan
GO_MF_m	GO:004697	histone ac	4/2529	10/23049	0.017619	0.4122	0.397251	Kansl1/Kan
GO_MF_m	GO:190161	phosphatic	4/2529	10/23049	0.017619	0.4122	0.397251	Atp8b1/Ck
GO_MF_m	GO:004803	quinone bi	5/2529	15/23049	0.018522	0.4122	0.397251	Aoc1/Aoc3
GO_MF_m	GO:000840	3'-5' exon	10/2529	44/23049	0.018758	0.4122	0.397251	Aplf/Noct/
GO_MF_m	GO:001686	intramolec	7/2529	26/23049	0.019081	0.4122	0.397251	Bpgm/Mut
GO_MF_m	GO:001662	oxidoredu	12/2529	57/23049	0.019199	0.4122	0.397251	Acad11/Bd
GO_MF_m	GO:001682	lyase activi	29/2529	178/23049	0.019366	0.4122	0.397251	Dglucy/Ad
GO_MF_m	GO:001641	N-acyltran	19/2529	105/23049	0.019395	0.4122	0.397251	Cers3/Cers
GO_MF_m	GO:001653	cyclin-dep	8/2529	32/23049	0.019627	0.4122	0.397251	Ccne1/Ccn
GO_MF_m	GO:000451	nuclease a	32/2529	201/23049	0.019931	0.4122	0.397251	Aplf/Aptx/
GO_MF_m	GO:000040	Y-form DN	3/2529	6/23049	0.020436	0.4122	0.397251	Blm/Men1/
GO_MF_m	GO:000205	nucleobas	3/2529	6/23049	0.020436	0.4122	0.397251	Aprt/Dpyd/
GO_MF_m	GO:000476	stearoyl-C	3/2529	6/23049	0.020436	0.4122	0.397251	Cyb5a/Fad
GO_MF_m	GO:000485	phospholip	3/2529	6/23049	0.020436	0.4122	0.397251	Angptl3/Ar
GO_MF_m	GO:001643	rRNA (ade	3/2529	6/23049	0.020436	0.4122	0.397251	Gm1818/T
GO_MF_m	GO:001690	G-protein	3/2529	6/23049	0.020436	0.4122	0.397251	Chrm1/Chr
GO_MF_m	GO:003326	choline bin	3/2529	6/23049	0.020436	0.4122	0.397251	Ache/Acpp
GO_MF_m	GO:003419	apolipopro	3/2529	6/23049	0.020436	0.4122	0.397251	Abca12/Nr
GO_MF_m	GO:001686	intramolec	11/2529	51/23049	0.020556	0.4122	0.397251	Dct/Ddt/Ec
GO_MF_m	GO:001670	oxidoredu	32/2529	202/23049	0.021269	0.4122	0.397251	6430573F1
GO_MF_m	GO:004801	receptor li	68/2529	486/23049	0.021402	0.4122	0.397251	Adm/Amb
GO_MF_m	GO:003107	heat shock	23/2529	135/23049	0.021497	0.4122	0.397251	Adora1/Ar
GO_MF_m	GO:001709	AU-rich el	7/2529	27/23049	0.023384	0.4122	0.397251	Apobec1/C
GO_MF_m	GO:000110	RNA polym	8/2529	33/23049	0.023485	0.4122	0.397251	Bbs10/Bbs
GO_MF_m	GO:000486	protein kin	16/2529	86/23049	0.023805	0.4122	0.397251	Camk2n1/
GO_MF_m	GO:006173	peptide-ly	12/2529	59/23049	0.024792	0.4122	0.397251	Clock/Nat8
GO_MF_m	GO:001627	arginine N	4/2529	11/23049	0.025322	0.4122	0.397251	Ndufaf7/Pr
GO_MF_m	GO:001627	protein-ar	4/2529	11/23049	0.025322	0.4122	0.397251	Ndufaf7/Pr
GO_MF_m	GO:003098	mismatche	4/2529	11/23049	0.025322	0.4122	0.397251	Aptx/Msh3
GO_MF_m	GO:000550	iron ion bi	28/2529	175/23049	0.026401	0.4122	0.397251	6430573F1
GO_MF_m	GO:001674	transferase	34/2529	221/23049	0.026729	0.4122	0.397251	Acsm5/Ag
GO_MF_m	GO:014010	catalytic ac	6/2529	22/23049	0.027544	0.4122	0.397251	Abo/B3gnt
GO_MF_m	GO:190133	catecholan	6/2529	22/23049	0.027544	0.4122	0.397251	Adra1d/Dr
GO_MF_m	GO:003140	carboxylic	33/2529	214/23049	0.027867	0.4122	0.397251	2300002M
GO_MF_m	GO:000368	damaged	12/2529	60/23049	0.027997	0.4122	0.397251	Aptx/Blm/
GO_MF_m	GO:004216	neurotrans	12/2529	60/23049	0.027997	0.4122	0.397251	Ache/Acpp
GO_MF_m	GO:000453	exoribonu	7/2529	28/23049	0.02831	0.4122	0.397251	Noct/Cnot
GO_MF_m	GO:000808	growth fac	24/2529	146/23049	0.028347	0.4122	0.397251	Ambn/Ang
GO_MF_m	GO:000509	GTPase act	37/2529	246/23049	0.029512	0.4122	0.397251	1700006A1
GO_MF_m	GO:004848	beta-tubul	9/2529	41/23049	0.030995	0.4122	0.397251	Bcas3/Fgf1
GO_MF_m	GO:000471	transmem	12/2529	61/23049	0.031492	0.4122	0.397251	Epha10/Ep

GO_MF_m	GO:00306	GTPase re	39/2529	263/23049	0.031716	0.4122	0.397251	1700006A1
GO_MF_m	GO:00084	5'-3' exon	5/2529	17/23049	0.031725	0.4122	0.397251	Aptx/Dclre
GO_MF_m	GO:003524	dopamine	5/2529	17/23049	0.031725	0.4122	0.397251	Adra1d/Dr
GO_MF_m	GO:00016	G-protein	3/2529	7/23049	0.032876	0.4122	0.397251	Adora1/Ox
GO_MF_m	GO:001621	acyl-CoA c	3/2529	7/23049	0.032876	0.4122	0.397251	Cyb5a/Fad
GO_MF_m	GO:001987	potassium	3/2529	7/23049	0.032876	0.4122	0.397251	Cav1/Cav3
GO_MF_m	GO:00364	K48-linked	3/2529	7/23049	0.032876	0.4122	0.397251	Mindy2/Np
GO_MF_m	GO:00551	ubiquitin-	3/2529	7/23049	0.032876	0.4122	0.397251	Fbxo5/Glm
GO_MF_m	GO:00039	NAD(P)H d	2/2529	3/23049	0.033465	0.4122	0.397251	Cbr4/Nqo1
GO_MF_m	GO:00041	cholinester	2/2529	3/23049	0.033465	0.4122	0.397251	Ache/Bche
GO_MF_m	GO:000417	electron-tr	2/2529	3/23049	0.033465	0.4122	0.397251	Aifm1/Aif
GO_MF_m	GO:00081	C-methyltr	2/2529	3/23049	0.033465	0.4122	0.397251	Coq3/Nop
GO_MF_m	GO:00081	glycogen	2/2529	3/23049	0.033465	0.4122	0.397251	Pygb/Pyg
GO_MF_m	GO:000842	calcium-d	2/2529	3/23049	0.033465	0.4122	0.397251	Camk2n1/
GO_MF_m	GO:00162	protein N-	2/2529	3/23049	0.033465	0.4122	0.397251	B3gnt8/Og
GO_MF_m	GO:001664	oxidoreduc	2/2529	3/23049	0.033465	0.4122	0.397251	Aifm1/Aif
GO_MF_m	GO:00191	trans-2-en	2/2529	3/23049	0.033465	0.4122	0.397251	Decr2/Pec
GO_MF_m	GO:001997	interleukin	2/2529	3/23049	0.033465	0.4122	0.397251	Il2rb/Il2rg
GO_MF_m	GO:00303	DNA polyn	2/2529	3/23049	0.033465	0.4122	0.397251	Pcna/Tefm
GO_MF_m	GO:003117	phosphop	2/2529	3/23049	0.033465	0.4122	0.397251	Fasn/Zfp5
GO_MF_m	GO:00316	A1 adenos	2/2529	3/23049	0.033465	0.4122	0.397251	P2ry1/P2ry
GO_MF_m	GO:00321	dinucleotid	2/2529	3/23049	0.033465	0.4122	0.397251	Msh3/Pcna
GO_MF_m	GO:00341	apolipopro	2/2529	3/23049	0.033465	0.4122	0.397251	Abca12/Nr
GO_MF_m	GO:00358	Krueppel-	2/2529	3/23049	0.033465	0.4122	0.397251	Hdac1/Hd
GO_MF_m	GO:004312	ErbB-3 cla	2/2529	3/23049	0.033465	0.4122	0.397251	Cdk5/Nrg2
GO_MF_m	GO:19901	peptide-se	2/2529	3/23049	0.033465	0.4122	0.397251	Naa10/Na
GO_MF_m	GO:001662	oxidoreduc	6/2529	23/23049	0.033905	0.4122	0.397251	Bdh2/Decr
GO_MF_m	GO:003037	translation	6/2529	23/23049	0.033905	0.4122	0.397251	Cpeb3/Cp
GO_MF_m	GO:007084	dynein con	6/2529	23/23049	0.033905	0.4122	0.397251	Dnaaf1/Fm
GO_MF_m	GO:000472	protein tyr	17/2529	97/23049	0.034343	0.4122	0.397251	Cdc25a/Dr
GO_MF_m	GO:00082	5'-nucleoti	4/2529	12/23049	0.034751	0.4122	0.397251	Acpp/Nt5c
GO_MF_m	GO:00167	sulfurtrans	4/2529	12/23049	0.034751	0.4122	0.397251	Mocs2/Tst
GO_MF_m	GO:003107	histone de	4/2529	12/23049	0.034751	0.4122	0.397251	Hdac1/Hd
GO_MF_m	GO:003204	NAD-depe	4/2529	12/23049	0.034751	0.4122	0.397251	Hdac1/Hd
GO_MF_m	GO:004454	S100 prote	4/2529	12/23049	0.034751	0.4122	0.397251	Anxa2/Ezr/
GO_MF_m	GO:00704	repressing	12/2529	62/23049	0.03529	0.4122	0.397251	Arntl/Bbs1
GO_MF_m	GO:000372	double-str	14/2529	76/23049	0.035637	0.4122	0.397251	Aptx/Ddx2
GO_MF_m	GO:004317	organic aci	33/2529	219/23049	0.037182	0.4122	0.397251	2300002M
GO_MF_m	GO:000402	aldehyde d	5/2529	18/23049	0.04007	0.4122	0.397251	Adh5/Aldh
GO_MF_m	GO:00050	signal tran	24/2529	151/23049	0.040206	0.4122	0.397251	Cd19/Epha
GO_MF_m	GO:00351	miRNA bin	6/2529	24/23049	0.041142	0.4122	0.397251	Ddx21/Fm
GO_MF_m	GO:004292	neuropepti	6/2529	24/23049	0.041142	0.4122	0.397251	Adcyap1r1
GO_MF_m	GO:00605	nucleoside	43/2529	301/23049	0.043081	0.4122	0.397251	1700006A1
GO_MF_m	GO:00044	histone ac	11/2529	57/23049	0.04353	0.4122	0.397251	Clock/Nat
GO_MF_m	GO:00512	NAD bindi	12/2529	64/23049	0.043835	0.4122	0.397251	Adh1/Aldh
GO_MF_m	GO:000392	GTPase act	40/2529	278/23049	0.045092	0.4122	0.397251	Arhgdib/A
GO_MF_m	GO:00080	5S rRNA bi	4/2529	13/23049	0.045946	0.4122	0.397251	Mrpl18/Rp
GO_MF_m	GO:003154	peptidyl-p	4/2529	13/23049	0.045946	0.4122	0.397251	Egln3/Ogf

GO_MF_m	GO:007000	serine-type	4/2529	13/23049	0.045946	0.4122	0.397251	Cpm/Cpvl/
GO_MF_m	GO:000801	microtubul	33/2529	223/23049	0.046194	0.4122	0.397251	Cep350/Cg
GO_MF_m	GO:001679	exonucleas	9/2529	44/23049	0.046664	0.4122	0.397251	Aptx/Noct/
GO_MF_m	GO:000470	signal trans	20/2529	123/23049	0.046826	0.4122	0.397251	Epha10/Ep
GO_MF_m	GO:014009	catalytic ac	50/2529	360/23049	0.048043	0.4122	0.397251	6430573F1
GO_MF_m	GO:000107	transcriptic	3/2529	8/23049	0.048384	0.4122	0.397251	Dach1/Taf4
GO_MF_m	GO:000804	axon guida	3/2529	8/23049	0.048384	0.4122	0.397251	Epha7/Eph
GO_MF_m	GO:001519	L-serine tra	3/2529	8/23049	0.048384	0.4122	0.397251	Serinc2/Ser
GO_MF_m	GO:001671	oxidoreduc	3/2529	8/23049	0.048384	0.4122	0.397251	Cyb5a/Fad
GO_MF_m	GO:001688	ligase activ	3/2529	8/23049	0.048384	0.4122	0.397251	Mccc2/Pcc
GO_MF_m	GO:001689	endoribonu	3/2529	8/23049	0.048384	0.4122	0.397251	Rida/Tsen2
GO_MF_m	GO:002288	serine trans	3/2529	8/23049	0.048384	0.4122	0.397251	Serinc2/Ser
GO_MF_m	GO:003524	protein-arg	3/2529	8/23049	0.048384	0.4122	0.397251	Prmt1/Prm
GO_MF_m	GO:004291	xenobiotic	3/2529	8/23049	0.048384	0.4122	0.397251	Abcb1a/Ab
GO_MF_m	GO:190161	cardiolipin	3/2529	8/23049	0.048384	0.4122	0.397251	Atp8b1/Ck
GO_MF_m	GO:005084	extracellula	11/2529	58/23049	0.048601	0.4122	0.397251	2300002M
GO_MF_m	GO:000017	3'-5'-exori	6/2529	25/23049	0.049283	0.4122	0.397251	Noct/Cnot
GO_MF_m	GO:003558	purinergic	6/2529	25/23049	0.049283	0.4122	0.397251	Adora1/Hc
GO_MF_m	GO:000395	NAD+ ADP	5/2529	19/23049	0.049623	0.4122	0.397251	Art1/Art5/
GO_MF_m	GO:003016	low-density	5/2529	19/23049	0.049623	0.4122	0.397251	Cd36/Mptx
GO_MF_m	GO:003141	L-ascorbic	5/2529	19/23049	0.049623	0.4122	0.397251	Egln3/Ogf
GO_MF_m	GO:003126	small GTPa	59/2529	435/23049	0.050771	0.4122	0.397251	1700123L1
GO_MF_m	GO:001677	nucleotidyl	21/2529	132/23049	0.05184	0.4122	0.397251	Aptx/Ficd/
GO_MF_m	GO:004748	protein N-	20/2529	126/23049	0.05779	0.4122	0.397251	Akap6/Apt
GO_MF_m	GO:004339	proteoglyc	8/2529	39/23049	0.058012	0.4122	0.397251	Col5a1/Gp
GO_MF_m	GO:005075	low-density	6/2529	26/23049	0.058343	0.4122	0.397251	Ankra2/Hsp
GO_MF_m	GO:000554	1-phospha	4/2529	14/23049	0.058904	0.4122	0.397251	Epb41/Snx
GO_MF_m	GO:001674	transferase	36/2529	252/23049	0.059729	0.4122	0.397251	Acsm5/Agp
GO_MF_m	GO:001683	carbon-car	10/2529	53/23049	0.060125	0.4122	0.397251	Clybl/Ddt/
GO_MF_m	GO:000021	tRNA-intro	2/2529	4/23049	0.062086	0.4122	0.397251	Tsen2/Tsen
GO_MF_m	GO:000158	dopamine	2/2529	4/23049	0.062086	0.4122	0.397251	Drd5/Gpr2
GO_MF_m	GO:000404	aminoacyla	2/2529	4/23049	0.062086	0.4122	0.397251	Acy1/Acy3
GO_MF_m	GO:000416	dodecenoy	2/2529	4/23049	0.062086	0.4122	0.397251	Eci2/Ehhad
GO_MF_m	GO:000417	ATP-depen	2/2529	4/23049	0.062086	0.4122	0.397251	Clpx/Lonp2
GO_MF_m	GO:000452	RNA-DNA	2/2529	4/23049	0.062086	0.4122	0.397251	Fen1/Rnase
GO_MF_m	GO:000469	eukaryotic	2/2529	4/23049	0.062086	0.4122	0.397251	Eif2ak1/Eif2
GO_MF_m	GO:000479	thiosulfate	2/2529	4/23049	0.062086	0.4122	0.397251	Tst/Tstd3
GO_MF_m	GO:000517	ErbB-2 clas	2/2529	4/23049	0.062086	0.4122	0.397251	Cdk5/Nrg1
GO_MF_m	GO:000531	inorganic p	2/2529	4/23049	0.062086	0.4122	0.397251	Ank/Slc20a
GO_MF_m	GO:000894	oxaloaceta	2/2529	4/23049	0.062086	0.4122	0.397251	Fahd1/Me3
GO_MF_m	GO:000937	biotin bind	2/2529	4/23049	0.062086	0.4122	0.397251	Hlcs/Pcx
GO_MF_m	GO:001085	calcium-de	2/2529	4/23049	0.062086	0.4122	0.397251	Camk2n1/
GO_MF_m	GO:001628	small cond	2/2529	4/23049	0.062086	0.4122	0.397251	Kcnn1/Kcn
GO_MF_m	GO:001680	cysteine-ty	2/2529	4/23049	0.062086	0.4122	0.397251	Ctsl/Mindy
GO_MF_m	GO:001923	centromeri	2/2529	4/23049	0.062086	0.4122	0.397251	Cenpc1/Ms
GO_MF_m	GO:001983	phospholip	2/2529	4/23049	0.062086	0.4122	0.397251	Anxa2/Anx
GO_MF_m	GO:003154	peptidyl-pr	2/2529	4/23049	0.062086	0.4122	0.397251	Ogfod1/P3
GO_MF_m	GO:003374	peptide-m	2/2529	4/23049	0.062086	0.4122	0.397251	Msrb1/Txn

GO_MF_m	GO:003562	ceramide t	2/2529	4/23049	0.062086	0.4122	0.397251	Abcb1a/Plt
GO_MF_m	GO:004402	histone me	2/2529	4/23049	0.062086	0.4122	0.397251	Prmt1/Prm
GO_MF_m	GO:005083	pyruvate tr	2/2529	4/23049	0.062086	0.4122	0.397251	Mpc2/Slc1
GO_MF_m	GO:00700	cysteine-ty	2/2529	4/23049	0.062086	0.4122	0.397251	Ctsl/Mindy
GO_MF_m	GO:007057	methylcyto	2/2529	4/23049	0.062086	0.4122	0.397251	Tet2/Tet3
GO_MF_m	GO:007254	protein ph	2/2529	4/23049	0.062086	0.4122	0.397251	Igfbp3/Ptp
GO_MF_m	GO:009958	neurotrans	2/2529	4/23049	0.062086	0.4122	0.397251	Gria1/Grin2
GO_MF_m	GO:190412	phosphatic	2/2529	4/23049	0.062086	0.4122	0.397251	Abcb1a/Plt
GO_MF_m	GO:000517	integrin bir	18/2529	112/23049	0.062666	0.4122	0.397251	Adam8/An
GO_MF_m	GO:001661	oxidoreduc	21/2529	135/23049	0.063202	0.4122	0.397251	Adh1/Adh5
GO_MF_m	GO:001650	peptidase a	7/2529	33/23049	0.06328	0.4122	0.397251	Acrbp/Cav
GO_MF_m	GO:003329	monocarbo	13/2529	75/23049	0.063521	0.4122	0.397251	Adh5/Akr1
GO_MF_m	GO:000418	serine-type	3/2529	9/23049	0.066793	0.4122	0.397251	Cpm/Cpvl/
GO_MF_m	GO:000846	histone-arg	3/2529	9/23049	0.066793	0.4122	0.397251	Prmt1/Prm
GO_MF_m	GO:000993	calcium-de	3/2529	9/23049	0.066793	0.4122	0.397251	Camk2a/M
GO_MF_m	GO:001662	oxidoreduc	3/2529	9/23049	0.066793	0.4122	0.397251	Bckdhb/Og
GO_MF_m	GO:004518	translation	9/2529	47/23049	0.066857	0.4122	0.397251	Cpeb3/Cpe
GO_MF_m	GO:001681	hydrolase a	21/2529	136/23049	0.067345	0.4122	0.397251	Acer3/Acy1
GO_MF_m	GO:000388	DNA-direc	6/2529	27/23049	0.068332	0.4122	0.397251	Pole/Polg/
GO_MF_m	GO:000525	delayed re	6/2529	27/23049	0.068332	0.4122	0.397251	Kcna2/Kcn
GO_MF_m	GO:001689	exoribonuc	6/2529	27/23049	0.068332	0.4122	0.397251	Noct/Cnot
GO_MF_m	GO:000508	guanyl-nuc	28/2529	192/23049	0.071971	0.4122	0.397251	Arhgef18/
GO_MF_m	GO:000429	threonine-	5/2529	21/23049	0.072389	0.4122	0.397251	Psma3/Psn
GO_MF_m	GO:001503	protein dis	5/2529	21/23049	0.072389	0.4122	0.397251	Ero1l/Gstk1
GO_MF_m	GO:001546	acetylcholi	5/2529	21/23049	0.072389	0.4122	0.397251	Chrm1/Chr
GO_MF_m	GO:007000	threonine-	5/2529	21/23049	0.072389	0.4122	0.397251	Psma3/Psn
GO_MF_m	GO:007033	aromatase	7/2529	34/23049	0.072467	0.4122	0.397251	Cyp2b10/C
GO_MF_m	GO:000820	heparin bir	22/2529	145/23049	0.072704	0.4122	0.397251	2300002M
GO_MF_m	GO:007085	growth fac	22/2529	145/23049	0.072704	0.4122	0.397251	Csf3/Fgf1/
GO_MF_m	GO:000551	collagen bi	11/2529	62/23049	0.072817	0.4122	0.397251	2300002M
GO_MF_m	GO:000521	ion channe	54/2529	404/23049	0.073228	0.4122	0.397251	Ano1/Ano2
GO_MF_m	GO:000817	adenylate c	4/2529	15/23049	0.073588	0.4122	0.397251	Adcyap1r1
GO_MF_m	GO:001691	retinal binc	4/2529	15/23049	0.073588	0.4122	0.397251	Akr1b10/C
GO_MF_m	GO:004317	amine binc	4/2529	15/23049	0.073588	0.4122	0.397251	Aldh9a1/H
GO_MF_m	GO:004652	glucosyltra	4/2529	15/23049	0.073588	0.4122	0.397251	Alg6/Gys1/
GO_MF_m	GO:007040	NADPH bir	4/2529	15/23049	0.073588	0.4122	0.397251	Akr1b10/C
GO_MF_m	GO:000454	ribonuclea	17/2529	107/23049	0.075153	0.4122	0.397251	Noct/Cnot
GO_MF_m	GO:005101	actin filame	26/2529	177/23049	0.075221	0.4122	0.397251	Aif1l/Antxr
GO_MF_m	GO:000526	calcium cha	18/2529	115/23049	0.077008	0.4122	0.397251	Cacnb2/Ca
GO_MF_m	GO:001984	rRNA bindi	12/2529	70/23049	0.07773	0.4122	0.397251	Ddx21/Eral
GO_MF_m	GO:001526	channel ac	58/2529	439/23049	0.077737	0.4122	0.397251	Ano1/Ano2
GO_MF_m	GO:002280	passive tra	58/2529	439/23049	0.077737	0.4122	0.397251	Ano1/Ano2
GO_MF_m	GO:004690	tetrapyrrol	23/2529	154/23049	0.077887	0.4122	0.397251	Cyb5a/Cyb
GO_MF_m	GO:000526	cation char	42/2529	307/23049	0.0785	0.4122	0.397251	Ano1/Cacn
GO_MF_m	GO:007181	lipoprotein	6/2529	28/23049	0.079247	0.4122	0.397251	Cd36/Mptx
GO_MF_m	GO:007181	protein-lip	6/2529	28/23049	0.079247	0.4122	0.397251	Cd36/Mptx
GO_MF_m	GO:001676	transferase	11/2529	63/23049	0.079886	0.4122	0.397251	Fdft1/Fnta/
GO_MF_m	GO:000004	tRNA bindi	10/2529	56/23049	0.081694	0.4122	0.397251	6430573F1

GO_MF_m1	GO:001666	oxidoreduc	10/2529	56/23049	0.081694	0.4122	0.397251	Ero1l/Gstk1
GO_MF_m1	GO:000469	cyclin-dep	7/2529	35/23049	0.0824	0.4122	0.397251	Cdk1/Cdk2
GO_MF_m1	GO:001989	kinesin bin	9/2529	49/23049	0.082954	0.4122	0.397251	Ift88/Kcna2
GO_MF_m1	GO:001503	disulfide ox	8/2529	42/23049	0.083356	0.4122	0.397251	Ero1l/Gstk1
GO_MF_m1	GO:000524	voltage-ga	27/2529	187/23049	0.08365	0.4122	0.397251	Ano1/Cacn
GO_MF_m1	GO:002283	voltage-ga	27/2529	187/23049	0.08365	0.4122	0.397251	Ano1/Cacn
GO_MF_m1	GO:001920	kinase regu	29/2529	203/23049	0.083651	0.4122	0.397251	Abi1/Camk
GO_MF_m1	GO:000503	tumor necr	5/2529	22/23049	0.085578	0.4122	0.397251	Tnfrsf10b/T
GO_MF_m1	GO:000503	death recep	5/2529	22/23049	0.085578	0.4122	0.397251	Tnfrsf10b/T
GO_MF_m1	GO:000848	transamina	5/2529	22/23049	0.085578	0.4122	0.397251	Abat/Bcat2
GO_MF_m1	GO:001663	oxidoreduc	5/2529	22/23049	0.085578	0.4122	0.397251	Aoc1/Aoc3
GO_MF_m1	GO:005099	nitric-oxide	5/2529	22/23049	0.085578	0.4122	0.397251	Atp2b4/Ca
GO_MF_m1	GO:001675	transferase	38/2529	277/23049	0.087582	0.4122	0.397251	A4gnt/Abc
GO_MF_m1	GO:000159	dopamine	3/2529	10/23049	0.087868	0.4122	0.397251	Adra1d/Dr
GO_MF_m1	GO:000850	monoamin	3/2529	10/23049	0.087868	0.4122	0.397251	Slc18a2/Slc
GO_MF_m1	GO:001085	calcium-de	3/2529	10/23049	0.087868	0.4122	0.397251	Camk2a/M
GO_MF_m1	GO:003471	type I trans	3/2529	10/23049	0.087868	0.4122	0.397251	Smad6/Sm
GO_MF_m1	GO:005030	sugar-phos	3/2529	10/23049	0.087868	0.4122	0.397251	G6pc2/Pfkf
GO_MF_m1	GO:005101	microtubul	3/2529	10/23049	0.087868	0.4122	0.397251	Tmod3/Tub
GO_MF_m1	GO:002283	gated char	42/2529	310/23049	0.088174	0.4122	0.397251	Ano1/Ano2
GO_MF_m1	GO:004205	histone me	10/2529	57/23049	0.089814	0.4122	0.397251	Ash2l/Ezh1
GO_MF_m1	GO:001667	oxidoreduc	4/2529	16/23049	0.089931	0.4122	0.397251	Ero1l/Msrb
GO_MF_m1	GO:001685	racemase a	4/2529	16/23049	0.089931	0.4122	0.397251	Dse/Dsel/N
GO_MF_m1	GO:001686	intramolecu	4/2529	16/23049	0.089931	0.4122	0.397251	Dct/Eci2/Eh
GO_MF_m1	GO:001713	NAD-depe	4/2529	16/23049	0.089931	0.4122	0.397251	Hdac1/Hda
GO_MF_m1	GO:003029	protein tyro	4/2529	16/23049	0.089931	0.4122	0.397251	Abi1/Dgkq
GO_MF_m1	GO:190168	sulfur comp	33/2529	237/23049	0.090433	0.4122	0.397251	2300002M
GO_MF_m1	GO:000522	calcium act	6/2529	29/23049	0.091079	0.4122	0.397251	Ano1/Kcnn
GO_MF_m1	GO:000817	tRNA meth	6/2529	29/23049	0.091079	0.4122	0.397251	6430573F1
GO_MF_m1	GO:003051	snoRNA bin	6/2529	29/23049	0.091079	0.4122	0.397251	Bms1/Ddx2
GO_MF_m1	GO:001988	protein kin	26/2529	181/23049	0.092392	0.4122	0.397251	Abi1/Camk
GO_MF_m1	GO:000550	fatty acid b	8/2529	43/23049	0.093047	0.4122	0.397251	Adh5/Cd36
GO_MF_m1	GO:000800	chemokine	8/2529	43/23049	0.093047	0.4122	0.397251	Ccl20/Ccl2
GO_MF_m1	GO:003054	Hsp70 prot	8/2529	43/23049	0.093047	0.4122	0.397251	Cdk1/Fgf1/
GO_MF_m1	GO:005066	NADP binc	8/2529	43/23049	0.093047	0.4122	0.397251	Akr1b10/C
GO_MF_m1	GO:001683	carboxy-lya	7/2529	36/23049	0.093074	0.4122	0.397251	Ddt/Fahd1/
GO_MF_m1	GO:003406	DNA polym	7/2529	36/23049	0.093074	0.4122	0.397251	Hmbox1/P
GO_MF_m1	GO:003517	histone kin	7/2529	36/23049	0.093074	0.4122	0.397251	Cdk1/Cdk2
GO_MF_m1	GO:009747	cyclin-dep	7/2529	36/23049	0.093074	0.4122	0.397251	Cdk1/Cdk2
GO_MF_m1	GO:000188	purine nuc	47/2529	353/23049	0.093674	0.4122	0.397251	Adora1/Ad
GO_MF_m1	GO:000010	succinate c	2/2529	5/23049	0.096063	0.4122	0.397251	Sdhaf4/Sdh
GO_MF_m1	GO:000040	bubble DN	2/2529	5/23049	0.096063	0.4122	0.397251	Blm/Ercc5
GO_MF_m1	GO:000163	cysteinyl le	2/2529	5/23049	0.096063	0.4122	0.397251	Cysltr2/Ltb
GO_MF_m1	GO:000392	GPI-ancho	2/2529	5/23049	0.096063	0.4122	0.397251	Pigs/Pigu
GO_MF_m1	GO:000433	fructose-2,	2/2529	5/23049	0.096063	0.4122	0.397251	Pfkfb1/Tiga
GO_MF_m1	GO:000464	phosphory	2/2529	5/23049	0.096063	0.4122	0.397251	Pygb/Pygm
GO_MF_m1	GO:000475	serine C-pa	2/2529	5/23049	0.096063	0.4122	0.397251	Sptlc2/Spts
GO_MF_m1	GO:000497	leukotriene	2/2529	5/23049	0.096063	0.4122	0.397251	Cysltr2/Ltb

GO_MF_m	GO:00049	opioid rece	2/2529	5/23049	0.096063	0.4122	0.397251	Oprd1/Op
GO_MF_m	GO:000817	succinate c	2/2529	5/23049	0.096063	0.4122	0.397251	Sdhaf4/Sdh
GO_MF_m	GO:000851	folic acid tr	2/2529	5/23049	0.096063	0.4122	0.397251	Folr2/Slc46
GO_MF_m	GO:00108	cyclase act	2/2529	5/23049	0.096063	0.4122	0.397251	Guca1a/Gu
GO_MF_m	GO:00164	C-palmitoy	2/2529	5/23049	0.096063	0.4122	0.397251	Sptlc2/Spts
GO_MF_m	GO:001704	N-acylsphi	2/2529	5/23049	0.096063	0.4122	0.397251	Acer3/Asa
GO_MF_m	GO:00302	guanylate	2/2529	5/23049	0.096063	0.4122	0.397251	Guca1a/Gu
GO_MF_m	GO:00321	DNA insert	2/2529	5/23049	0.096063	0.4122	0.397251	Msh3/Pcna
GO_MF_m	GO:00324	MutLalpha	2/2529	5/23049	0.096063	0.4122	0.397251	Atr/Pcna
GO_MF_m	GO:004312	tumor necr	2/2529	5/23049	0.096063	0.4122	0.397251	Tnfrsf1a/Tr
GO_MF_m	GO:004691	transferase	2/2529	5/23049	0.096063	0.4122	0.397251	Clybl/Hmg
GO_MF_m	GO:00469	1-phospha	2/2529	5/23049	0.096063	0.4122	0.397251	Pik3r3/Pik
GO_MF_m	GO:00700	fructose-6	2/2529	5/23049	0.096063	0.4122	0.397251	Pfkfb1/Pfk
GO_MF_m	GO:00508	cell adhesi	62/2529	480/23049	0.098137	0.4122	0.397251	Abcf3/Abi1
GO_MF_m	GO:000817	O-methylt	5/2529	23/23049	0.099932	0.4122	0.397251	Cmtr2/Coc
GO_MF_m	GO:00081	ferrous iro	5/2529	23/23049	0.099932	0.4122	0.397251	6430573F1
GO_MF_m	GO:00167	hydrolase	5/2529	23/23049	0.099932	0.4122	0.397251	Art5/Dnph
GO_MF_m	GO:00433	heparan su	5/2529	23/23049	0.099932	0.4122	0.397251	Gpc4/Itga
GO_MF_m	GO:00048	enzyme in	53/2529	405/23049	0.100028	0.4122	0.397251	2810408A1
GO_MF_m	GO:00051	transformi	9/2529	51/23049	0.101184	0.4122	0.397251	Amh/Bmp
GO_MF_m	GO:003017	pyridoxal p	9/2529	51/23049	0.101184	0.4122	0.397251	Abat/Gldc/
GO_MF_m	GO:001701	Ras GTPas	52/2529	397/23049	0.101233	0.4122	0.397251	1700123L1
GO_MF_m	GO:001661	oxidoredu	22/2529	151/23049	0.10192	0.4122	0.397251	Adh1/Adh
GO_MF_m	GO:007032	lipoprotein	6/2529	30/23049	0.103808	0.4122	0.397251	Ankra2/Hs
GO_MF_m	GO:00228	substrate-	54/2529	415/23049	0.105259	0.4122	0.397251	Ano1/Ano
GO_MF_m	GO:007234	modified a	14/2529	89/23049	0.105786	0.4122	0.397251	Cpne6/Fas
GO_MF_m	GO:00228	ion gated	41/2529	307/23049	0.107188	0.4122	0.397251	Ano1/Ano
GO_MF_m	GO:000471	protein tyr	22/2529	152/23049	0.107424	0.4122	0.397251	Aatk/Abl2/
GO_MF_m	GO:00314	mitogen-a	12/2529	74/23049	0.107636	0.4122	0.397251	Epha10/Ep
GO_MF_m	GO:003022	lipoprotein	4/2529	17/23049	0.107841	0.4122	0.397251	Cd36/Scar
GO_MF_m	GO:003497	NAD-depe	4/2529	17/23049	0.107841	0.4122	0.397251	Hdac1/Hda
GO_MF_m	GO:003604	long-chain	4/2529	17/23049	0.107841	0.4122	0.397251	Cd36/Cyp4
GO_MF_m	GO:00421	acetylcholi	4/2529	17/23049	0.107841	0.4122	0.397251	Ache/Chrm
GO_MF_m	GO:00432	glutathion	4/2529	17/23049	0.107841	0.4122	0.397251	Ltc4s/Mgst
GO_MF_m	GO:19007	oligopepti	4/2529	17/23049	0.107841	0.4122	0.397251	Ltc4s/Mgst
GO_MF_m	GO:00009	RNA polym	1/2529	1/23049	0.109723	0.4122	0.397251	Maf1
GO_MF_m	GO:00016	nociceptin	1/2529	1/23049	0.109723	0.4122	0.397251	Oprl1
GO_MF_m	GO:00016	sialate O-a	1/2529	1/23049	0.109723	0.4122	0.397251	Siae
GO_MF_m	GO:00020	adenine bi	1/2529	1/23049	0.109723	0.4122	0.397251	Aprt
GO_MF_m	GO:00020	thymine bi	1/2529	1/23049	0.109723	0.4122	0.397251	Dpys
GO_MF_m	GO:000211	interleukin	1/2529	1/23049	0.109723	0.4122	0.397251	Il1rl1
GO_MF_m	GO:00038	1-pyrroline	1/2529	1/23049	0.109723	0.4122	0.397251	Aldh4a1
GO_MF_m	GO:00038	3-hydroxy	1/2529	1/23049	0.109723	0.4122	0.397251	Hibch
GO_MF_m	GO:00038	4-aminob	1/2529	1/23049	0.109723	0.4122	0.397251	Abat
GO_MF_m	GO:000387	ATP adeny	1/2529	1/23049	0.109723	0.4122	0.397251	Kars
GO_MF_m	GO:00039	alkylbase	1/2529	1/23049	0.109723	0.4122	0.397251	Mpg
GO_MF_m	GO:00039	GTP cycloh	1/2529	1/23049	0.109723	0.4122	0.397251	Gch1
GO_MF_m	GO:000394	N-acetylga	1/2529	1/23049	0.109723	0.4122	0.397251	Arsb

GO_MF_m	GO:000397	UDP-gluc	1/2529	1/23049	0.109723	0.4122	0.397251	Ugdh
GO_MF_m	GO:000398	UTP:glucos	1/2529	1/23049	0.109723	0.4122	0.397251	Ugp2
GO_MF_m	GO:000399	adenine ph	1/2529	1/23049	0.109723	0.4122	0.397251	Aprt
GO_MF_m	GO:000400	adenosine	1/2529	1/23049	0.109723	0.4122	0.397251	Adk
GO_MF_m	GO:000407	biotin-[ace	1/2529	1/23049	0.109723	0.4122	0.397251	Hlcs
GO_MF_m	GO:000407	biotin-[me	1/2529	1/23049	0.109723	0.4122	0.397251	Hlcs
GO_MF_m	GO:000407	biotin-[me	1/2529	1/23049	0.109723	0.4122	0.397251	Hlcs
GO_MF_m	GO:000408	biotin-[pro	1/2529	1/23049	0.109723	0.4122	0.397251	Hlcs
GO_MF_m	GO:000408	bisphosph	1/2529	1/23049	0.109723	0.4122	0.397251	Tigar
GO_MF_m	GO:000413	cytosine de	1/2529	1/23049	0.109723	0.4122	0.397251	Apobec1
GO_MF_m	GO:000413	deoxyribos	1/2529	1/23049	0.109723	0.4122	0.397251	Dera
GO_MF_m	GO:000415	dihydropyr	1/2529	1/23049	0.109723	0.4122	0.397251	Dpys
GO_MF_m	GO:000415	dihydroura	1/2529	1/23049	0.109723	0.4122	0.397251	Dpyd
GO_MF_m	GO:000416	diphospho	1/2529	1/23049	0.109723	0.4122	0.397251	Mvd
GO_MF_m	GO:000430	ethanolam	1/2529	1/23049	0.109723	0.4122	0.397251	Pcyt2
GO_MF_m	GO:000431	farnesyl-di	1/2529	1/23049	0.109723	0.4122	0.397251	Fdft1
GO_MF_m	GO:000431	[acyl-carrie	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:000431	3-oxoacyl-	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:000431	3-hydroxy	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:000431	enoyl-[acyl	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:000437	glycerone	1/2529	1/23049	0.109723	0.4122	0.397251	Tkfc
GO_MF_m	GO:000437	glycine del	1/2529	1/23049	0.109723	0.4122	0.397251	Gldc
GO_MF_m	GO:000438	glycoprote	1/2529	1/23049	0.109723	0.4122	0.397251	Abo
GO_MF_m	GO:000438	fucosylgala	1/2529	1/23049	0.109723	0.4122	0.397251	Abo
GO_MF_m	GO:000439	hexaprenyl	1/2529	1/23049	0.109723	0.4122	0.397251	Coq3
GO_MF_m	GO:000439	histidine de	1/2529	1/23049	0.109723	0.4122	0.397251	Hdc
GO_MF_m	GO:000447	malate syn	1/2529	1/23049	0.109723	0.4122	0.397251	Clybl
GO_MF_m	GO:000449	methylmal	1/2529	1/23049	0.109723	0.4122	0.397251	Mcee
GO_MF_m	GO:000449	methylmal	1/2529	1/23049	0.109723	0.4122	0.397251	Mut
GO_MF_m	GO:000450	monophen	1/2529	1/23049	0.109723	0.4122	0.397251	Tyr
GO_MF_m	GO:000451	tyrosine 3-	1/2529	1/23049	0.109723	0.4122	0.397251	Th
GO_MF_m	GO:000458	ornithine c	1/2529	1/23049	0.109723	0.4122	0.397251	Otc
GO_MF_m	GO:000459	peptide-as	1/2529	1/23049	0.109723	0.4122	0.397251	Asph
GO_MF_m	GO:000460	phenyletha	1/2529	1/23049	0.109723	0.4122	0.397251	Pnmt
GO_MF_m	GO:000461	phosphoac	1/2529	1/23049	0.109723	0.4122	0.397251	Pgm3
GO_MF_m	GO:000465	polyribonu	1/2529	1/23049	0.109723	0.4122	0.397251	Pnpt1
GO_MF_m	GO:000472	prenylated	1/2529	1/23049	0.109723	0.4122	0.397251	Ptp4a1
GO_MF_m	GO:000473	pyruvate ca	1/2529	1/23049	0.109723	0.4122	0.397251	Pcx
GO_MF_m	GO:000475	ribulose-pl	1/2529	1/23049	0.109723	0.4122	0.397251	Rpe
GO_MF_m	GO:000482	lysine-tRN	1/2529	1/23049	0.109723	0.4122	0.397251	Kars
GO_MF_m	GO:000501	platelet-de	1/2529	1/23049	0.109723	0.4122	0.397251	Pdgfra
GO_MF_m	GO:000509	Sar guanyl	1/2529	1/23049	0.109723	0.4122	0.397251	Preb
GO_MF_m	GO:000514	interleukin	1/2529	1/23049	0.109723	0.4122	0.397251	Il10
GO_MF_m	GO:000515	interleukin	1/2529	1/23049	0.109723	0.4122	0.397251	Il1rn
GO_MF_m	GO:000531	high-affinit	1/2529	1/23049	0.109723	0.4122	0.397251	Slc20a1
GO_MF_m	GO:000840	25-hydrox	1/2529	1/23049	0.109723	0.4122	0.397251	Cyp24a1
GO_MF_m	GO:000842	glycoprote	1/2529	1/23049	0.109723	0.4122	0.397251	Fut8
GO_MF_m	GO:000842	2-polypre	1/2529	1/23049	0.109723	0.4122	0.397251	Coq3

GO_MF_m	GO:000844	D-aspartat	1/2529	1/23049	0.109723	0.4122	0.397251	Ddo
GO_MF_m	GO:000845	carnitine O	1/2529	1/23049	0.109723	0.4122	0.397251	Crot
GO_MF_m	GO:000848	sulfite oxid	1/2529	1/23049	0.109723	0.4122	0.397251	Suox
GO_MF_m	GO:000868	3-demethy	1/2529	1/23049	0.109723	0.4122	0.397251	Coq3
GO_MF_m	GO:000872	DNA-3-me	1/2529	1/23049	0.109723	0.4122	0.397251	Mpg
GO_MF_m	GO:000875	NADPH de	1/2529	1/23049	0.109723	0.4122	0.397251	Cbr4
GO_MF_m	GO:000878	agmatinase	1/2529	1/23049	0.109723	0.4122	0.397251	Agmat
GO_MF_m	GO:000881	cob(I)yrinic	1/2529	1/23049	0.109723	0.4122	0.397251	Mmab
GO_MF_m	GO:000888	glycerate k	1/2529	1/23049	0.109723	0.4122	0.397251	Glyctk
GO_MF_m	GO:000889	guanine de	1/2529	1/23049	0.109723	0.4122	0.397251	Gda
GO_MF_m	GO:000894	nitric oxide	1/2529	1/23049	0.109723	0.4122	0.397251	Por
GO_MF_m	GO:000895	peptidogly	1/2529	1/23049	0.109723	0.4122	0.397251	Csgalnact1
GO_MF_m	GO:000900	site-specifi	1/2529	1/23049	0.109723	0.4122	0.397251	Mettl4
GO_MF_m	GO:001042	polyprenyl	1/2529	1/23049	0.109723	0.4122	0.397251	Coq3
GO_MF_m	GO:001509	molybdate	1/2529	1/23049	0.109723	0.4122	0.397251	Mfsd5
GO_MF_m	GO:001519	L-leucine t	1/2529	1/23049	0.109723	0.4122	0.397251	Slc38a7
GO_MF_m	GO:001519	L-methioni	1/2529	1/23049	0.109723	0.4122	0.397251	Slc38a7
GO_MF_m	GO:001543	bile acid-e	1/2529	1/23049	0.109723	0.4122	0.397251	Abcc3
GO_MF_m	GO:001565	branched-	1/2529	1/23049	0.109723	0.4122	0.397251	Slc38a7
GO_MF_m	GO:001592	aspartate c	1/2529	1/23049	0.109723	0.4122	0.397251	Ddo
GO_MF_m	GO:001627	[cytochrom	1/2529	1/23049	0.109723	0.4122	0.397251	Prmt1
GO_MF_m	GO:001641	O-octanoy	1/2529	1/23049	0.109723	0.4122	0.397251	Crot
GO_MF_m	GO:001641	octanoyltra	1/2529	1/23049	0.109723	0.4122	0.397251	Crot
GO_MF_m	GO:001649	substance	1/2529	1/23049	0.109723	0.4122	0.397251	Tacr2
GO_MF_m	GO:001664	oxidoreduc	1/2529	1/23049	0.109723	0.4122	0.397251	Gldc
GO_MF_m	GO:001670	oxidoreduc	1/2529	1/23049	0.109723	0.4122	0.397251	Por
GO_MF_m	GO:001678	transferase	1/2529	1/23049	0.109723	0.4122	0.397251	Sepsecs
GO_MF_m	GO:001702	myosin I bi	1/2529	1/23049	0.109723	0.4122	0.397251	Pycard
GO_MF_m	GO:001706	tyrosine-es	1/2529	1/23049	0.109723	0.4122	0.397251	Sult1a1
GO_MF_m	GO:001711	dihydropyr	1/2529	1/23049	0.109723	0.4122	0.397251	Dpyd
GO_MF_m	GO:001827	biotin-prot	1/2529	1/23049	0.109723	0.4122	0.397251	Hlcs
GO_MF_m	GO:001846	formaldehy	1/2529	1/23049	0.109723	0.4122	0.397251	Adh5
GO_MF_m	GO:001873	S-formylgl	1/2529	1/23049	0.109723	0.4122	0.397251	Esd
GO_MF_m	GO:001877	acetylpyruv	1/2529	1/23049	0.109723	0.4122	0.397251	Fahd1
GO_MF_m	GO:001914	aminobuty	1/2529	1/23049	0.109723	0.4122	0.397251	Aldh9a1
GO_MF_m	GO:001917	3-hydroxya	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:002289	Intermedia	1/2529	1/23049	0.109723	0.4122	0.397251	Kcnn4
GO_MF_m	GO:003017	voltage-ga	1/2529	1/23049	0.109723	0.4122	0.397251	Hvcn1
GO_MF_m	GO:003034	1-alpha,25	1/2529	1/23049	0.109723	0.4122	0.397251	Cyp24a1
GO_MF_m	GO:003050	inorganic c	1/2529	1/23049	0.109723	0.4122	0.397251	Ank
GO_MF_m	GO:003051	snoRNP bi	1/2529	1/23049	0.109723	0.4122	0.397251	Prmt1
GO_MF_m	GO:003058	quinone cc	1/2529	1/23049	0.109723	0.4122	0.397251	Coq3
GO_MF_m	GO:003058	[methionin	1/2529	1/23049	0.109723	0.4122	0.397251	Mtrr
GO_MF_m	GO:003079	arsenite me	1/2529	1/23049	0.109723	0.4122	0.397251	As3mt
GO_MF_m	GO:003079	methylarso	1/2529	1/23049	0.109723	0.4122	0.397251	As3mt
GO_MF_m	GO:003124	denatured	1/2529	1/23049	0.109723	0.4122	0.397251	Hspa1a
GO_MF_m	GO:003137	eukaryotic	1/2529	1/23049	0.109723	0.4122	0.397251	Eif4e
GO_MF_m	GO:003170	adrenome	1/2529	1/23049	0.109723	0.4122	0.397251	Adm

GO_MF_m	GO:003171	cannabinoi	1/2529	1/23049	0.109723	0.4122	0.397251	Cnrip1
GO_MF_m	GO:003171	type 1 cann	1/2529	1/23049	0.109723	0.4122	0.397251	Cnrip1
GO_MF_m	GO:003186	prolactin-r	1/2529	1/23049	0.109723	0.4122	0.397251	Prlh
GO_MF_m	GO:003186	EP4 subtyp	1/2529	1/23049	0.109723	0.4122	0.397251	Fem1a
GO_MF_m	GO:003284	calcitonin b	1/2529	1/23049	0.109723	0.4122	0.397251	Calcr
GO_MF_m	GO:003328	organic aci	1/2529	1/23049	0.109723	0.4122	0.397251	Abcc3
GO_MF_m	GO:003328	carboxylic a	1/2529	1/23049	0.109723	0.4122	0.397251	Abcc3
GO_MF_m	GO:003328	monocarbo	1/2529	1/23049	0.109723	0.4122	0.397251	Abcc3
GO_MF_m	GO:003369	DNA 5'-ad	1/2529	1/23049	0.109723	0.4122	0.397251	Aptx
GO_MF_m	GO:003378	cholesterol	1/2529	1/23049	0.109723	0.4122	0.397251	Cyp46a1
GO_MF_m	GO:003378	cyanocoba	1/2529	1/23049	0.109723	0.4122	0.397251	Mmachc
GO_MF_m	GO:003388	10-hydroxy	1/2529	1/23049	0.109723	0.4122	0.397251	Ephx2
GO_MF_m	GO:003397	hydroxyiso	1/2529	1/23049	0.109723	0.4122	0.397251	Urah
GO_MF_m	GO:003398	D-dopachr	1/2529	1/23049	0.109723	0.4122	0.397251	Ddt
GO_MF_m	GO:003398	3alpha,7alp	1/2529	1/23049	0.109723	0.4122	0.397251	Hsd17b4
GO_MF_m	GO:003401	FAD-AMP	1/2529	1/23049	0.109723	0.4122	0.397251	Tkfc
GO_MF_m	GO:003454	fumarylpyr	1/2529	1/23049	0.109723	0.4122	0.397251	Fahd1
GO_MF_m	GO:003522	glutamate-	1/2529	1/23049	0.109723	0.4122	0.397251	Gclm
GO_MF_m	GO:003543	cyclic-di-G	1/2529	1/23049	0.109723	0.4122	0.397251	Tmem173
GO_MF_m	GO:003621	GTP dipho	1/2529	1/23049	0.109723	0.4122	0.397251	Nudt1
GO_MF_m	GO:003631	tyrosyl-RN	1/2529	1/23049	0.109723	0.4122	0.397251	Tdp2
GO_MF_m	GO:003648	nitric-oxide	1/2529	1/23049	0.109723	0.4122	0.397251	Atp2b4
GO_MF_m	GO:003804	enkephalin	1/2529	1/23049	0.109723	0.4122	0.397251	Oprd1
GO_MF_m	GO:004200	interleukin-	1/2529	1/23049	0.109723	0.4122	0.397251	Il18bp
GO_MF_m	GO:004213	thiamine p	1/2529	1/23049	0.109723	0.4122	0.397251	Acpp
GO_MF_m	GO:004216	interleukin-	1/2529	1/23049	0.109723	0.4122	0.397251	Il12b
GO_MF_m	GO:004325	sodium-de	1/2529	1/23049	0.109723	0.4122	0.397251	Slc10a6
GO_MF_m	GO:004373	DNA-3-me	1/2529	1/23049	0.109723	0.4122	0.397251	Mpg
GO_MF_m	GO:004375	acetate-Co	1/2529	1/23049	0.109723	0.4122	0.397251	Acsl1
GO_MF_m	GO:004386	methionine	1/2529	1/23049	0.109723	0.4122	0.397251	Slc38a7
GO_MF_m	GO:004387	acireductor	1/2529	1/23049	0.109723	0.4122	0.397251	Enoph1
GO_MF_m	GO:004389	N-acetylga	1/2529	1/23049	0.109723	0.4122	0.397251	Galns
GO_MF_m	GO:004391	DNA-7-me	1/2529	1/23049	0.109723	0.4122	0.397251	Mpg
GO_MF_m	GO:004399	histone ace	1/2529	1/23049	0.109723	0.4122	0.397251	Kat2a
GO_MF_m	GO:004459	17-beta-hy	1/2529	1/23049	0.109723	0.4122	0.397251	Hsd17b4
GO_MF_m	GO:004471	2-hydroxy-	1/2529	1/23049	0.109723	0.4122	0.397251	Nudt1
GO_MF_m	GO:004471	2-hydroxy-	1/2529	1/23049	0.109723	0.4122	0.397251	Nudt1
GO_MF_m	GO:004473	bone sialop	1/2529	1/23049	0.109723	0.4122	0.397251	Anxa2
GO_MF_m	GO:004503	ATP-activa	1/2529	1/23049	0.109723	0.4122	0.397251	P2ry1
GO_MF_m	GO:004503	ADP-activa	1/2529	1/23049	0.109723	0.4122	0.397251	P2ry1
GO_MF_m	GO:004535	interleukin-	1/2529	1/23049	0.109723	0.4122	0.397251	Il1rn
GO_MF_m	GO:004535	interleukin-	1/2529	1/23049	0.109723	0.4122	0.397251	Il1rn
GO_MF_m	GO:004543	uridine nuc	1/2529	1/23049	0.109723	0.4122	0.397251	Ung
GO_MF_m	GO:004550	interleukin-	1/2529	1/23049	0.109723	0.4122	0.397251	Il27ra
GO_MF_m	GO:004657	methylthio	1/2529	1/23049	0.109723	0.4122	0.397251	Apip
GO_MF_m	GO:004692	alpha-(1->	1/2529	1/23049	0.109723	0.4122	0.397251	Fut8
GO_MF_m	GO:004701	cholest-5-	1/2529	1/23049	0.109723	0.4122	0.397251	Hsd3b7
GO_MF_m	GO:004710	4-trimethy	1/2529	1/23049	0.109723	0.4122	0.397251	Aldh9a1

GO_MF_m	GO:004711	enoyl-[acyl	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:00471	aquacobal	1/2529	1/23049	0.109723	0.4122	0.397251	Mtrr
GO_MF_m	GO:00471	1-alkenylg	1/2529	1/23049	0.109723	0.4122	0.397251	Lpcat4
GO_MF_m	GO:00472	(S)-3-amin	1/2529	1/23049	0.109723	0.4122	0.397251	Abat
GO_MF_m	GO:00474	protein-gl	1/2529	1/23049	0.109723	0.4122	0.397251	Pgghg
GO_MF_m	GO:00474	3-hydroxy	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:004762	acylpyruva	1/2529	1/23049	0.109723	0.4122	0.397251	Fahd1
GO_MF_m	GO:00476	ATP dipho	1/2529	1/23049	0.109723	0.4122	0.397251	Nudt1
GO_MF_m	GO:004772	iron-cytoc	1/2529	1/23049	0.109723	0.4122	0.397251	Por
GO_MF_m	GO:004777	(3S)-citra	1/2529	1/23049	0.109723	0.4122	0.397251	Clybl
GO_MF_m	GO:00478	L-cysteine:	1/2529	1/23049	0.109723	0.4122	0.397251	Got1
GO_MF_m	GO:004782	D-glutama	1/2529	1/23049	0.109723	0.4122	0.397251	Dglucy
GO_MF_m	GO:004824	phytanoyl-	1/2529	1/23049	0.109723	0.4122	0.397251	Phyh
GO_MF_m	GO:004827	methionin	1/2529	1/23049	0.109723	0.4122	0.397251	Mat2b
GO_MF_m	GO:005014	nucleoside	1/2529	1/23049	0.109723	0.4122	0.397251	Dnph1
GO_MF_m	GO:00501	phosphati	1/2529	1/23049	0.109723	0.4122	0.397251	Pgap1
GO_MF_m	GO:00502	ribosylpyri	1/2529	1/23049	0.109723	0.4122	0.397251	Ung
GO_MF_m	GO:00503	triokinase	1/2529	1/23049	0.109723	0.4122	0.397251	Tkfc
GO_MF_m	GO:005042	calcium-d	1/2529	1/23049	0.109723	0.4122	0.397251	Plch1
GO_MF_m	GO:005044	aquacobal	1/2529	1/23049	0.109723	0.4122	0.397251	Mtrr
GO_MF_m	GO:005052	acyloxyacy	1/2529	1/23049	0.109723	0.4122	0.397251	Aoah
GO_MF_m	GO:005174	UTP-mon	1/2529	1/23049	0.109723	0.4122	0.397251	Ugp2
GO_MF_m	GO:00517	all-trans-r	1/2529	1/23049	0.109723	0.4122	0.397251	Retsat
GO_MF_m	GO:00519	S-(hydroxy	1/2529	1/23049	0.109723	0.4122	0.397251	Adh5
GO_MF_m	GO:00519	squalene s	1/2529	1/23049	0.109723	0.4122	0.397251	Fdft1
GO_MF_m	GO:00523	tRNA dime	1/2529	1/23049	0.109723	0.4122	0.397251	Trit1
GO_MF_m	GO:00525	diamine ox	1/2529	1/23049	0.109723	0.4122	0.397251	Aoc1
GO_MF_m	GO:00525	histamine	1/2529	1/23049	0.109723	0.4122	0.397251	Aoc1
GO_MF_m	GO:00525	methylputr	1/2529	1/23049	0.109723	0.4122	0.397251	Aoc1
GO_MF_m	GO:00526	propane-1	1/2529	1/23049	0.109723	0.4122	0.397251	Aoc1
GO_MF_m	GO:005282	DNA-7-m	1/2529	1/23049	0.109723	0.4122	0.397251	Mpg
GO_MF_m	GO:005282	DNA-3-m	1/2529	1/23049	0.109723	0.4122	0.397251	Mpg
GO_MF_m	GO:00528	peptidyl-ly	1/2529	1/23049	0.109723	0.4122	0.397251	Naa50
GO_MF_m	GO:00607	deoxyribo	1/2529	1/23049	0.109723	0.4122	0.397251	Dffa
GO_MF_m	GO:00615	cyclic-GM	1/2529	1/23049	0.109723	0.4122	0.397251	Mb21d1
GO_MF_m	GO:00615	cyclic-GM	1/2529	1/23049	0.109723	0.4122	0.397251	Tmem173
GO_MF_m	GO:006154	3-demethy	1/2529	1/23049	0.109723	0.4122	0.397251	Coq3
GO_MF_m	GO:006154	glycogen s	1/2529	1/23049	0.109723	0.4122	0.397251	Gys1
GO_MF_m	GO:00615	molybdopt	1/2529	1/23049	0.109723	0.4122	0.397251	Gphn
GO_MF_m	GO:00615	molybdopt	1/2529	1/23049	0.109723	0.4122	0.397251	Gphn
GO_MF_m	GO:00700	serine-typ	1/2529	1/23049	0.109723	0.4122	0.397251	F11
GO_MF_m	GO:00702	5'-tyrosyl-	1/2529	1/23049	0.109723	0.4122	0.397251	Tdp2
GO_MF_m	GO:007032	inward rect	1/2529	1/23049	0.109723	0.4122	0.397251	Cav1
GO_MF_m	GO:007052	11-beta-h	1/2529	1/23049	0.109723	0.4122	0.397251	Hsd11b1
GO_MF_m	GO:00705	nicotinic a	1/2529	1/23049	0.109723	0.4122	0.397251	Hcar2
GO_MF_m	GO:007061	histone me	1/2529	1/23049	0.109723	0.4122	0.397251	Prmt6
GO_MF_m	GO:007061	histone me	1/2529	1/23049	0.109723	0.4122	0.397251	Prmt6
GO_MF_m	GO:00706	deoxyribo	1/2529	1/23049	0.109723	0.4122	0.397251	Dnph1

GO_MF_m	GO:00707	protein ad	1/2529	1/23049	0.109723	0.4122	0.397251	Ficd
GO_MF_m	GO:007077	phytoceran	1/2529	1/23049	0.109723	0.4122	0.397251	Acer3
GO_MF_m	GO:00708	lipoteichoi	1/2529	1/23049	0.109723	0.4122	0.397251	Cd36
GO_MF_m	GO:00717	K11-linked	1/2529	1/23049	0.109723	0.4122	0.397251	Mindy2
GO_MF_m	GO:00725	citrate-L-g	1/2529	1/23049	0.109723	0.4122	0.397251	Rimklb
GO_MF_m	GO:009762	monoamin	1/2529	1/23049	0.109723	0.4122	0.397251	Rnls
GO_MF_m	GO:00976	iron chann	1/2529	1/23049	0.109723	0.4122	0.397251	Slc40a1
GO_MF_m	GO:00990	ceramide-t	1/2529	1/23049	0.109723	0.4122	0.397251	Abcb1a
GO_MF_m	GO:01021	3-oxo-glut	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:01021	3-oxo-pim	1/2529	1/23049	0.109723	0.4122	0.397251	Fasn
GO_MF_m	GO:01023	mycophen	1/2529	1/23049	0.109723	0.4122	0.397251	Abhd10
GO_MF_m	GO:010607	peptide N-	1/2529	1/23049	0.109723	0.4122	0.397251	Kat2a
GO_MF_m	GO:010607	histone suc	1/2529	1/23049	0.109723	0.4122	0.397251	Kat2a
GO_MF_m	GO:015002	oxidised lo	1/2529	1/23049	0.109723	0.4122	0.397251	Cd36
GO_MF_m	GO:190401	platinum b	1/2529	1/23049	0.109723	0.4122	0.397251	Rida
GO_MF_m	GO:190401	xenon ator	1/2529	1/23049	0.109723	0.4122	0.397251	Rida
GO_MF_m	GO:19901	single-stra	1/2529	1/23049	0.109723	0.4122	0.397251	Aptx
GO_MF_m	GO:199044	F-box dom	1/2529	1/23049	0.109723	0.4122	0.397251	Park2
GO_MF_m	GO:19905	mast cell s	1/2529	1/23049	0.109723	0.4122	0.397251	Mrgprx2
GO_MF_m	GO:199082	deaminase	1/2529	1/23049	0.109723	0.4122	0.397251	Hnrnpc
GO_MF_m	GO:20010	mannan bi	1/2529	1/23049	0.109723	0.4122	0.397251	Reg4
GO_MF_m	GO:00325	guanyl ribo	48/2529	366/23049	0.109723	0.4122	0.397251	Adss/Arf5/
GO_MF_m	GO:003321	amide binc	45/2529	341/23049	0.109958	0.4122	0.397251	Adcyap1r1
GO_MF_m	GO:007027	vitamin B6	9/2529	52/23049	0.111091	0.4122	0.397251	Abat/Gldc/
GO_MF_m	GO:00040	3-chloroall	3/2529	11/23049	0.111323	0.4122	0.397251	Aldh1a3/Al
GO_MF_m	GO:00045	peptide alp	3/2529	11/23049	0.111323	0.4122	0.397251	Naa10/Naa
GO_MF_m	GO:00048	protein ser	3/2529	11/23049	0.111323	0.4122	0.397251	Ppp1r14a/
GO_MF_m	GO:00049	galanin rec	3/2529	11/23049	0.111323	0.4122	0.397251	Cysltr2/Gal
GO_MF_m	GO:001517	basic amin	3/2529	11/23049	0.111323	0.4122	0.397251	AU018091/
GO_MF_m	GO:001677	phosphotr	3/2529	11/23049	0.111323	0.4122	0.397251	Ckm/Ckmt
GO_MF_m	GO:00168	racemase	3/2529	11/23049	0.111323	0.4122	0.397251	Dse/Dsel/R
GO_MF_m	GO:00192	carbohydr	3/2529	11/23049	0.111323	0.4122	0.397251	G6pc2/Pfk
GO_MF_m	GO:00308	actin-depe	3/2529	11/23049	0.111323	0.4122	0.397251	Myh14/My
GO_MF_m	GO:00344	ubiquitin-	3/2529	11/23049	0.111323	0.4122	0.397251	Prpf19/Ub
GO_MF_m	GO:00423	phosphate	3/2529	11/23049	0.111323	0.4122	0.397251	Gng12/Otc
GO_MF_m	GO:00551	lipase inhil	3/2529	11/23049	0.111323	0.4122	0.397251	Angptl3/Ar
GO_MF_m	GO:010601	phosphatic	3/2529	11/23049	0.111323	0.4122	0.397251	Ptpmt1/Sy
GO_MF_m	GO:00171	Rab GTPas	23/2529	161/23049	0.113	0.417607	0.402461	Ankfy1/An
GO_MF_m	GO:00510	unfolded p	14/2529	90/23049	0.113295	0.417607	0.402461	Calr/Canx/
GO_MF_m	GO:00190	guanyl nuc	48/2529	367/23049	0.113364	0.417607	0.402461	Adss/Arf5/
GO_MF_m	GO:00167	transferase	5/2529	24/23049	0.115403	0.423668	0.408303	Abat/Bcat2
GO_MF_m	GO:00305	cAMP bind	5/2529	24/23049	0.115403	0.423668	0.408303	Cnbd2/Cn
GO_MF_m	GO:00305	cyclic nucl	7/2529	38/23049	0.116601	0.426613	0.41114	Cnbd2/Cn
GO_MF_m	GO:00515	4 iron, 4 su	7/2529	38/23049	0.116601	0.426613	0.41114	Dpyd/Isca2
GO_MF_m	GO:001517	L-amino ac	10/2529	60/23049	0.116958	0.427196	0.411702	AU018091/
GO_MF_m	GO:000851	ammoniur	6/2529	31/23049	0.11741	0.427395	0.411894	Rhd/Slc12a
GO_MF_m	GO:00619	regulatory	6/2529	31/23049	0.11741	0.427395	0.411894	Ddx21/Fm
GO_MF_m	GO:00426	ATPase act	49/2529	377/23049	0.119347	0.433715	0.417985	Abca12/Ab

GO_MF_m	GO:000452	endoribonu	9/2529	53/23049	0.121516	0.440252	0.424285	Cpsf4/Elac
GO_MF_m	GO:000552	GTP bindin	45/2529	344/23049	0.121554	0.440252	0.424285	Adss/Arf5/
GO_MF_m	GO:000372	mRNA binc	31/2529	228/23049	0.123053	0.444932	0.428795	Apobec1/C
GO_MF_m	GO:001526	calcium-ac	4/2529	18/23049	0.127204	0.457637	0.441039	Kcnmb1/Kc
GO_MF_m	GO:001664	oxidoreduc	4/2529	18/23049	0.127204	0.457637	0.441039	Aoc1/Aoc3
GO_MF_m	GO:003279	GTPase act	4/2529	18/23049	0.127204	0.457637	0.441039	Camk2a/Cc
GO_MF_m	GO:000554	phospholip	51/2529	396/23049	0.12752	0.458011	0.4414	Ankfy1/Anx
GO_MF_m	GO:000551	calmodulin	26/2529	188/23049	0.128233	0.459805	0.443129	Atp2b4/Ca
GO_MF_m	GO:001593	nucleobase	7/2529	39/23049	0.129417	0.46087	0.444155	Slc25a23/S
GO_MF_m	GO:000373	mRNA 3'-U	11/2529	69/23049	0.13095	0.46087	0.444155	Cpeb3/Cpe
GO_MF_m	GO:004302	ribonucleo	20/2529	140/23049	0.132128	0.46087	0.444155	Apobec1/C
GO_MF_m	GO:000395	NAD(P)+-p	2/2529	6/23049	0.133877	0.46087	0.444155	Art1/Art5
GO_MF_m	GO:000402	alcohol deh	2/2529	6/23049	0.133877	0.46087	0.444155	Adh1/Adh5
GO_MF_m	GO:000444	isocitrate d	2/2529	6/23049	0.133877	0.46087	0.444155	Idh2/Idh3a
GO_MF_m	GO:000507	transformin	2/2529	6/23049	0.133877	0.46087	0.444155	Smad6/Sm
GO_MF_m	GO:000537	copper ion	2/2529	6/23049	0.133877	0.46087	0.444155	Atp7b/Slc3
GO_MF_m	GO:000813	primary am	2/2529	6/23049	0.133877	0.46087	0.444155	Aoc1/Aoc3
GO_MF_m	GO:000855	xenobiotic	2/2529	6/23049	0.133877	0.46087	0.444155	Abcb1a/Ab
GO_MF_m	GO:000897	phosphatic	2/2529	6/23049	0.133877	0.46087	0.444155	Abhd1/Pla
GO_MF_m	GO:001512	lactate trar	2/2529	6/23049	0.133877	0.46087	0.444155	Slc16a1/Slc
GO_MF_m	GO:001640	carnitine O	2/2529	6/23049	0.133877	0.46087	0.444155	Cpt2/Crot
GO_MF_m	GO:001642	CoA carbo:	2/2529	6/23049	0.133877	0.46087	0.444155	Mccc2/Pcc
GO_MF_m	GO:001643	rRNA (guar	2/2529	6/23049	0.133877	0.46087	0.444155	Ftsj3/Mrm1
GO_MF_m	GO:001663	oxidoreduc	2/2529	6/23049	0.133877	0.46087	0.444155	Sdhaf4/Sdh
GO_MF_m	GO:001681	hydrolase a	2/2529	6/23049	0.133877	0.46087	0.444155	Dpys/Urah
GO_MF_m	GO:001921	phosphata:	2/2529	6/23049	0.133877	0.46087	0.444155	Igfbp3/Ptp
GO_MF_m	GO:003024	guanylate c	2/2529	6/23049	0.133877	0.46087	0.444155	Guca1a/Gu
GO_MF_m	GO:003531	5'-3' exode	2/2529	6/23049	0.133877	0.46087	0.444155	Aptx/Dclre
GO_MF_m	GO:003640	proteasom	2/2529	6/23049	0.133877	0.46087	0.444155	Psmc2/Psm
GO_MF_m	GO:003813	neuregulin	2/2529	6/23049	0.133877	0.46087	0.444155	Erbb3/Itga
GO_MF_m	GO:004354	molybdopt	2/2529	6/23049	0.133877	0.46087	0.444155	Gphn/Suox
GO_MF_m	GO:004718	1-acylglyce	2/2529	6/23049	0.133877	0.46087	0.444155	Lpcat3/Lpc
GO_MF_m	GO:199094	ubiquitin li	2/2529	6/23049	0.133877	0.46087	0.444155	Fbxo5/Rpl2
GO_MF_m	GO:000188	nucleoside	47/2529	364/23049	0.13453	0.462381	0.445612	Adora1/Ad
GO_MF_m	GO:000827	protein me	13/2529	85/23049	0.136112	0.464417	0.447573	Ash2l/Eef2
GO_MF_m	GO:000090	translation	3/2529	12/23049	0.136847	0.464417	0.447573	Cpeb3/Cpe
GO_MF_m	GO:000819	metalloenc	3/2529	12/23049	0.136847	0.464417	0.447573	Fetub/Timp
GO_MF_m	GO:001565	quaternary	3/2529	12/23049	0.136847	0.464417	0.447573	Slc22a1/Slc
GO_MF_m	GO:001680	hydrolase a	3/2529	12/23049	0.136847	0.464417	0.447573	Ahcyl2/Eph
GO_MF_m	GO:004302	ribosomal l	3/2529	12/23049	0.136847	0.464417	0.447573	Nemf/Nmc
GO_MF_m	GO:004302	ribosomal s	3/2529	12/23049	0.136847	0.464417	0.447573	Eral1/Ptcd3
GO_MF_m	GO:004840	platelet-de	3/2529	12/23049	0.136847	0.464417	0.447573	Col5a1/Pdg
GO_MF_m	GO:001679	thiolester h	8/2529	47/23049	0.137863	0.46713	0.450188	Acot1/Aco
GO_MF_m	GO:003255	purine ribo	45/2529	349/23049	0.142556	0.482275	0.464784	Adss/Arf5/
GO_MF_m	GO:000417	aminopept	7/2529	40/23049	0.142903	0.482691	0.465185	Blmh/Ctsl/
GO_MF_m	GO:001919	transmemb	12/2529	78/23049	0.143419	0.483676	0.466134	Epha10/Ep
GO_MF_m	GO:000802	monocarbo	9/2529	55/23049	0.143876	0.484457	0.466886	Abcc3/Mpc
GO_MF_m	GO:001675	transferase	27/2529	199/23049	0.144444	0.485613	0.468	A4gnt/Abc

GO_MF_m	GO:000534	organic aci	21/2529	150/23049	0.145188	0.485859	0.468237	Abcc3/AU
GO_MF_m	GO:004694	carboxylic	21/2529	150/23049	0.145188	0.485859	0.468237	Abcc3/AU
GO_MF_m	GO:001665	oxidoreduc	13/2529	86/23049	0.145194	0.485859	0.468237	Aifm1/Cbr
GO_MF_m	GO:00085	anion trans	41/2529	316/23049	0.145824	0.486895	0.469237	Abcc3/Ank
GO_MF_m	GO:00152	drug transp	15/2529	102/23049	0.147053	0.486895	0.469237	Abcb1a/Ab
GO_MF_m	GO:00019	G-protein	6/2529	33/23049	0.147087	0.486895	0.469237	Drd5/Gria1
GO_MF_m	GO:00043	glutathione	6/2529	33/23049	0.147087	0.486895	0.469237	Gstk1/Gstm
GO_MF_m	GO:005101	mitogen-a	6/2529	33/23049	0.147087	0.486895	0.469237	Gch1/Mica
GO_MF_m	GO:000514	interleukin	4/2529	19/23049	0.147892	0.486895	0.469237	Grin2b/Il1r
GO_MF_m	GO:00051	fibroblast g	5/2529	26/23049	0.149454	0.486895	0.469237	Fgf1/Fgf16
GO_MF_m	GO:000997	cyclase act	5/2529	26/23049	0.149454	0.486895	0.469237	Dglucy/Ad
GO_MF_m	GO:001702	TBP-class p	5/2529	26/23049	0.149454	0.486895	0.469237	Cand1/Gtf
GO_MF_m	GO:007194	FAD bindin	5/2529	26/23049	0.149454	0.486895	0.469237	Aifm1/Ddo
GO_MF_m	GO:00526	carboxylic	22/2529	159/23049	0.151058	0.486895	0.469237	Abhd1/Abh
GO_MF_m	GO:00169	oxidoreduc	9/2529	56/23049	0.155783	0.486895	0.469237	Adh5/Aldh
GO_MF_m	GO:00483	Rac GTPas	10/2529	64/23049	0.159419	0.486895	0.469237	Arhgap44/
GO_MF_m	GO:00081	UDP-glyco	20/2529	144/23049	0.160607	0.486895	0.469237	A4gnt/Abc
GO_MF_m	GO:00052	structural c	11/2529	72/23049	0.161863	0.486895	0.469237	Des/Epb41
GO_MF_m	GO:00090	electron tra	11/2529	72/23049	0.161863	0.486895	0.469237	Aifm1/Aifm
GO_MF_m	GO:001517	neutral am	6/2529	34/23049	0.163076	0.486895	0.469237	Serinc2/Se
GO_MF_m	GO:00303	cyclin bind	6/2529	34/23049	0.163076	0.486895	0.469237	Cdk1/Cdk2
GO_MF_m	GO:00337	steroid deh	6/2529	34/23049	0.163076	0.486895	0.469237	Akr1c12/Hs
GO_MF_m	GO:00705	adenylyltra	6/2529	34/23049	0.163076	0.486895	0.469237	Aptx/Ficd/
GO_MF_m	GO:004802	monosacch	12/2529	80/23049	0.16342	0.486895	0.469237	Cd209d/Eg
GO_MF_m	GO:00045	poly(A)-sp	3/2529	13/23049	0.164117	0.486895	0.469237	Noct/Cnot
GO_MF_m	GO:000524	gap junctic	3/2529	13/23049	0.164117	0.486895	0.469237	Gja3/Gjb2/
GO_MF_m	GO:00166	oxidoreduc	3/2529	13/23049	0.164117	0.486895	0.469237	Cox15/Mtr
GO_MF_m	GO:003354	MAP kinas	3/2529	13/23049	0.164117	0.486895	0.469237	Dusp3/Dus
GO_MF_m	GO:003592	mRNA 3'-U	3/2529	13/23049	0.164117	0.486895	0.469237	Cpeb3/Khs
GO_MF_m	GO:005137	serotonin b	3/2529	13/23049	0.164117	0.486895	0.469237	Htr1a/Htr5
GO_MF_m	GO:00971	cysteine-ty	3/2529	13/23049	0.164117	0.486895	0.469237	Casp6/Cas
GO_MF_m	GO:003254	ribonucleo	45/2529	354/23049	0.165635	0.486895	0.469237	Adss/Arf5/
GO_MF_m	GO:001664	oxidoreduc	5/2529	27/23049	0.167891	0.486895	0.469237	Aifm1/Aifm
GO_MF_m	GO:003074	GTP-deper	5/2529	27/23049	0.167891	0.486895	0.469237	Gch1/Mras
GO_MF_m	GO:00150	calcium ior	19/2529	137/23049	0.169623	0.486895	0.469237	Atp2b4/Ca
GO_MF_m	GO:000161	purinergic	4/2529	20/23049	0.169766	0.486895	0.469237	Hcar2/P2rx
GO_MF_m	GO:00082	poly(U) RN	4/2529	20/23049	0.169766	0.486895	0.469237	Fmr1/Hnrn
GO_MF_m	GO:00165	nucleotide	4/2529	20/23049	0.169766	0.486895	0.469237	Hcar2/P2rx
GO_MF_m	GO:00081	protein tyr	7/2529	42/23049	0.171766	0.486895	0.469237	Dusp16/Du
GO_MF_m	GO:00083	O-acyltran	7/2529	42/23049	0.171766	0.486895	0.469237	Agpat2/Cp
GO_MF_m	GO:00000	L-ornithine	2/2529	7/23049	0.174277	0.486895	0.469237	AU018091/
GO_MF_m	GO:000374	translation	2/2529	7/23049	0.174277	0.486895	0.469237	Gspt2/Mtrf
GO_MF_m	GO:00044	phosphatic	2/2529	7/23049	0.174277	0.486895	0.469237	Ptpmt1/Sy
GO_MF_m	GO:00050	GPI-linked	2/2529	7/23049	0.174277	0.486895	0.469237	Epha7/Eph
GO_MF_m	GO:000807	translation	2/2529	7/23049	0.174277	0.486895	0.469237	Gspt2/Mtrf
GO_MF_m	GO:000844	phosphofru	2/2529	7/23049	0.174277	0.486895	0.469237	Pfkfb1/Pfkl
GO_MF_m	GO:00085	bile acid:sc	2/2529	7/23049	0.174277	0.486895	0.469237	Slc10a4/Sl
GO_MF_m	GO:00108	cyclase reg	2/2529	7/23049	0.174277	0.486895	0.469237	Guca1a/Gu

GO_MF_m	GO:001522	carnitine tr	2/2529	7/23049	0.174277	0.486895	0.469237	Slc22a5/Sl
GO_MF_m	GO:001642	tRNA (cyto	2/2529	7/23049	0.174277	0.486895	0.469237	Mettl6/Ns
GO_MF_m	GO:001923	cyclohydro	2/2529	7/23049	0.174277	0.486895	0.469237	Gch1/Mthf
GO_MF_m	GO:001979	procollage	2/2529	7/23049	0.174277	0.486895	0.469237	P3h3/P4ha
GO_MF_m	GO:003168	adenosine	2/2529	7/23049	0.174277	0.486895	0.469237	P2ry1/P2ry
GO_MF_m	GO:003433	short-chai	2/2529	7/23049	0.174277	0.486895	0.469237	Abhd1/Sia
GO_MF_m	GO:003518	histone thr	2/2529	7/23049	0.174277	0.486895	0.469237	Pkn1/Prkc
GO_MF_m	GO:005029	sphingosin	2/2529	7/23049	0.174277	0.486895	0.469237	Cers3/Cers
GO_MF_m	GO:005065	3'-phosph	2/2529	7/23049	0.174277	0.486895	0.469237	Sult1a1/Su
GO_MF_m	GO:007032	thyroid ho	2/2529	7/23049	0.174277	0.486895	0.469237	Aldh1a3/Tt
GO_MF_m	GO:007069	activin rec	2/2529	7/23049	0.174277	0.486895	0.469237	Cfc1/Smad
GO_MF_m	GO:009732	7SK snRNA	2/2529	7/23049	0.174277	0.486895	0.469237	Ddx21/He
GO_MF_m	GO:199024	N6-methyl	2/2529	7/23049	0.174277	0.486895	0.469237	Hnrnpc/Yt
GO_MF_m	GO:005101	protein kin	8/2529	50/23049	0.177381	0.486895	0.469237	Akap14/Ak
GO_MF_m	GO:000553	glycosami	26/2529	196/23049	0.178187	0.486895	0.469237	2300002M
GO_MF_m	GO:001711	Rab guany	6/2529	35/23049	0.179768	0.486895	0.469237	Dennd4b/
GO_MF_m	GO:004302	ribosome	9/2529	58/23049	0.180964	0.486895	0.469237	Cpeb3/Cp
GO_MF_m	GO:003097	receptor ty	10/2529	66/23049	0.183138	0.486895	0.469237	Dock4/Elm
GO_MF_m	GO:004237	chemokine	10/2529	66/23049	0.183138	0.486895	0.469237	Ccl20/Ccl2
GO_MF_m	GO:000512	cytokine ac	29/2529	222/23049	0.184097	0.486895	0.469237	Bmp3/Ccl2
GO_MF_m	GO:000851	organic an	29/2529	222/23049	0.184097	0.486895	0.469237	Abcc3/Atp
GO_MF_m	GO:005111	ATPase bin	13/2529	90/23049	0.184611	0.486895	0.469237	Atp1b2/Ca
GO_MF_m	GO:000520	extracellula	7/2529	43/23049	0.187072	0.486895	0.469237	Ambn/Col
GO_MF_m	GO:001670	oxidoreduc	5/2529	28/23049	0.187162	0.486895	0.469237	Alox12/Alo
GO_MF_m	GO:001540	P-P-bond-	17/2529	123/23049	0.189661	0.486895	0.469237	Abca12/Ab
GO_MF_m	GO:000512	cytokine re	41/2529	325/23049	0.191827	0.486895	0.469237	Amh/Bmp
GO_MF_m	GO:000187	pattern bin	4/2529	21/23049	0.192678	0.486895	0.469237	Clec4g/En
GO_MF_m	GO:000837	sialyltransf	4/2529	21/23049	0.192678	0.486895	0.469237	St3gal3/St
GO_MF_m	GO:002282	wide pore	4/2529	21/23049	0.192678	0.486895	0.469237	Gja3/Gjb2/
GO_MF_m	GO:003024	polysaccha	4/2529	21/23049	0.192678	0.486895	0.469237	Clec4g/En
GO_MF_m	GO:007069	transmemb	4/2529	21/23049	0.192678	0.486895	0.469237	Bmp3/Cfc1
GO_MF_m	GO:000465	prenyltrans	3/2529	14/23049	0.192811	0.486895	0.469237	Fdft1/Fnta/
GO_MF_m	GO:000552	macrolide	3/2529	14/23049	0.192811	0.486895	0.469237	Fkbp11/Fk
GO_MF_m	GO:000552	FK506 bin	3/2529	14/23049	0.192811	0.486895	0.469237	Fkbp11/Fk
GO_MF_m	GO:001649	C-C chem	3/2529	14/23049	0.192811	0.486895	0.469237	Ccr1/Ccrl2/
GO_MF_m	GO:001910	DNA N-gly	3/2529	14/23049	0.192811	0.486895	0.469237	Mpg/Pcna/
GO_MF_m	GO:004529	gamma-ca	3/2529	14/23049	0.192811	0.486895	0.469237	Cdh1/Cdh
GO_MF_m	GO:001995	cytokine bi	15/2529	107/23049	0.192859	0.486895	0.469237	Ccr1/Cd36
GO_MF_m	GO:004256	hormone	15/2529	107/23049	0.192859	0.486895	0.469237	Ache/Adip
GO_MF_m	GO:004349	ATPase act	18/2529	132/23049	0.196625	0.486895	0.469237	Abca12/Ab
GO_MF_m	GO:001662	oxidoreduc	7/2529	44/23049	0.20291	0.486895	0.469237	Adh5/Aldh
GO_MF_m	GO:001802	histone-lys	7/2529	44/23049	0.20291	0.486895	0.469237	Ash2l/Ezh1
GO_MF_m	GO:005121	phosphopr	14/2529	100/23049	0.204517	0.486895	0.469237	Abl2/Aptx/
GO_MF_m	GO:003509	phosphati	31/2529	242/23049	0.204613	0.486895	0.469237	Ankfy1/An
GO_MF_m	GO:014009	catalytic ac	24/2529	183/23049	0.205226	0.486895	0.469237	Aplf/Aptx/
GO_MF_m	GO:000165	peptide re	18/2529	133/23049	0.205589	0.486895	0.469237	Avpr1a/Ca
GO_MF_m	GO:003149	chromatin	13/2529	92/23049	0.206049	0.486895	0.469237	Cenpa/Clo
GO_MF_m	GO:001683	hydro-lyas	8/2529	52/23049	0.206188	0.486895	0.469237	Dglucy/Api

GO_MF_m1	GO:000524	calcium cha	5/2529	29/23049	0.207179	0.486895	0.469237	Cacnb2/Ca
GO_MF_m1	GO:000552	insulin-like	5/2529	29/23049	0.207179	0.486895	0.469237	Ctgf/Igf2r/I
GO_MF_m1	GO:001670	oxidoreduc	5/2529	29/23049	0.207179	0.486895	0.469237	Alox12/Alo
GO_MF_m1	GO:004301	gamma-tu	5/2529	29/23049	0.207179	0.486895	0.469237	Ndn/Pde4b
GO_MF_m1	GO:000003	acyl bindin	1/2529	2/23049	0.207411	0.486895	0.469237	Zfp593
GO_MF_m1	GO:000003	acyl carrier	1/2529	2/23049	0.207411	0.486895	0.469237	Zfp593
GO_MF_m1	GO:000040	heterodupl	1/2529	2/23049	0.207411	0.486895	0.469237	Msh3
GO_MF_m1	GO:000040	double-stra	1/2529	2/23049	0.207411	0.486895	0.469237	Msh3
GO_MF_m1	GO:000070	purine-spe	1/2529	2/23049	0.207411	0.486895	0.469237	Pcna
GO_MF_m1	GO:000103	RNA polym	1/2529	2/23049	0.207411	0.486895	0.469237	Tbp
GO_MF_m1	GO:000114	transcriptio	1/2529	2/23049	0.207411	0.486895	0.469237	Xrn2
GO_MF_m1	GO:000116	transcriptio	1/2529	2/23049	0.207411	0.486895	0.469237	Xrn2
GO_MF_m1	GO:000160	urotensin II	1/2529	2/23049	0.207411	0.486895	0.469237	Uts2r
GO_MF_m1	GO:000163	leukotriene	1/2529	2/23049	0.207411	0.486895	0.469237	Ltb4r1
GO_MF_m1	GO:000164	group II me	1/2529	2/23049	0.207411	0.486895	0.469237	Grm2
GO_MF_m1	GO:000188	glucuronyl-	1/2529	2/23049	0.207411	0.486895	0.469237	Extl3
GO_MF_m1	GO:000196	alpha-1,3-	1/2529	2/23049	0.207411	0.486895	0.469237	Abo
GO_MF_m1	GO:000211	interleukin-	1/2529	2/23049	0.207411	0.486895	0.469237	Il1rl1
GO_MF_m1	GO:000382	alpha-keto	1/2529	2/23049	0.207411	0.486895	0.469237	Bckdhb
GO_MF_m1	GO:000383	beta-galac	1/2529	2/23049	0.207411	0.486895	0.469237	St6gal1
GO_MF_m1	GO:000384	11-beta-hy	1/2529	2/23049	0.207411	0.486895	0.469237	Hsd11b1
GO_MF_m1	GO:000386	3-methyl-2	1/2529	2/23049	0.207411	0.486895	0.469237	Bckdhb
GO_MF_m1	GO:000386	4-hydroxyp	1/2529	2/23049	0.207411	0.486895	0.469237	Hpdl
GO_MF_m1	GO:000388	CDP-diacy	1/2529	2/23049	0.207411	0.486895	0.469237	Tmem269
GO_MF_m1	GO:000388	D-amino-a	1/2529	2/23049	0.207411	0.486895	0.469237	Ddo
GO_MF_m1	GO:000393	GTP cycloh	1/2529	2/23049	0.207411	0.486895	0.469237	Gch1
GO_MF_m1	GO:000398	UDP-gluco	1/2529	2/23049	0.207411	0.486895	0.469237	Uggt1
GO_MF_m1	GO:000399	acylphosph	1/2529	2/23049	0.207411	0.486895	0.469237	Acyp1
GO_MF_m1	GO:000400	copper-exp	1/2529	2/23049	0.207411	0.486895	0.469237	Atp7b
GO_MF_m1	GO:000401	adenylosuc	1/2529	2/23049	0.207411	0.486895	0.469237	Adss
GO_MF_m1	GO:000402	L-alanine:2	1/2529	2/23049	0.207411	0.486895	0.469237	Gpt
GO_MF_m1	GO:000405	arachidona	1/2529	2/23049	0.207411	0.486895	0.469237	Alox5
GO_MF_m1	GO:000405	arginase ac	1/2529	2/23049	0.207411	0.486895	0.469237	Arg1
GO_MF_m1	GO:000408	branched-c	1/2529	2/23049	0.207411	0.486895	0.469237	Bcat2
GO_MF_m1	GO:000414	dephospho	1/2529	2/23049	0.207411	0.486895	0.469237	Dcakd
GO_MF_m1	GO:000416	dopachrom	1/2529	2/23049	0.207411	0.486895	0.469237	Dct
GO_MF_m1	GO:000431	[acyl-carrie	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m1	GO:000431	3-oxoacyl-	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m1	GO:000432	oleoyl-[acy	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m1	GO:000432	formate-te	1/2529	2/23049	0.207411	0.486895	0.469237	Mthfd1l
GO_MF_m1	GO:000435	glutamate-	1/2529	2/23049	0.207411	0.486895	0.469237	Gclm
GO_MF_m1	GO:000436	glutamine-	1/2529	2/23049	0.207411	0.486895	0.469237	Gfpt2
GO_MF_m1	GO:000437	glycine hyd	1/2529	2/23049	0.207411	0.486895	0.469237	Shmt1
GO_MF_m1	GO:000437	glycogen (s	1/2529	2/23049	0.207411	0.486895	0.469237	Gys1
GO_MF_m1	GO:000442	hydroxyme	1/2529	2/23049	0.207411	0.486895	0.469237	Hmgcs2
GO_MF_m1	GO:000444	inositol-1,4	1/2529	2/23049	0.207411	0.486895	0.469237	Bpnt1
GO_MF_m1	GO:000445	isocitrate d	1/2529	2/23049	0.207411	0.486895	0.469237	Idh2
GO_MF_m1	GO:000448	mRNA (gua	1/2529	2/23049	0.207411	0.486895	0.469237	Rnmt

GO_MF_m	GO:00044	mRNA (nu	1/2529	2/23049	0.207411	0.486895	0.469237	Cmtr2
GO_MF_m	GO:00044	methylcrot	1/2529	2/23049	0.207411	0.486895	0.469237	Mccc2
GO_MF_m	GO:00045	alpha,alph	1/2529	2/23049	0.207411	0.486895	0.469237	Pgghg
GO_MF_m	GO:000464	phosphose	1/2529	2/23049	0.207411	0.486895	0.469237	Psph
GO_MF_m	GO:00046	propionyl-	1/2529	2/23049	0.207411	0.486895	0.469237	Pcca
GO_MF_m	GO:00046	protein far	1/2529	2/23049	0.207411	0.486895	0.469237	Fnta
GO_MF_m	GO:00046	CAAX-prot	1/2529	2/23049	0.207411	0.486895	0.469237	Fnta
GO_MF_m	GO:00046	prostaglan	1/2529	2/23049	0.207411	0.486895	0.469237	Ptgs2
GO_MF_m	GO:000467	DNA-depe	1/2529	2/23049	0.207411	0.486895	0.469237	Prkdc
GO_MF_m	GO:00046	calcium-de	1/2529	2/23049	0.207411	0.486895	0.469237	Prkca
GO_MF_m	GO:00047	selenide, w	1/2529	2/23049	0.207411	0.486895	0.469237	Sephs1
GO_MF_m	GO:00048	tryptophan	1/2529	2/23049	0.207411	0.486895	0.469237	Wars
GO_MF_m	GO:000491	interleukin	1/2529	2/23049	0.207411	0.486895	0.469237	Il2rb
GO_MF_m	GO:000494	calcitonin r	1/2529	2/23049	0.207411	0.486895	0.469237	Calcr
GO_MF_m	GO:00049	thyrotropir	1/2529	2/23049	0.207411	0.486895	0.469237	Trhr
GO_MF_m	GO:000501	platelet-de	1/2529	2/23049	0.207411	0.486895	0.469237	Pdgfra
GO_MF_m	GO:00050	osmosensc	1/2529	2/23049	0.207411	0.486895	0.469237	Trpv4
GO_MF_m	GO:00050	peroxisom	1/2529	2/23049	0.207411	0.486895	0.469237	Pex5
GO_MF_m	GO:00050	Rab GDP-c	1/2529	2/23049	0.207411	0.486895	0.469237	Gdi2
GO_MF_m	GO:00051	granulocyt	1/2529	2/23049	0.207411	0.486895	0.469237	Csf3
GO_MF_m	GO:00051	interferon-	1/2529	2/23049	0.207411	0.486895	0.469237	Ifng
GO_MF_m	GO:00051	interleukin	1/2529	2/23049	0.207411	0.486895	0.469237	Il7
GO_MF_m	GO:00051	interleukin	1/2529	2/23049	0.207411	0.486895	0.469237	Il1rn
GO_MF_m	GO:00051	interleukin	1/2529	2/23049	0.207411	0.486895	0.469237	Il1rn
GO_MF_m	GO:000517	hepatocyte	1/2529	2/23049	0.207411	0.486895	0.469237	Glmn
GO_MF_m	GO:00054	GDP-fucos	1/2529	2/23049	0.207411	0.486895	0.469237	Slc35c1
GO_MF_m	GO:000804	calcium ser	1/2529	2/23049	0.207411	0.486895	0.469237	Guca1a
GO_MF_m	GO:00081	N-acetylla	1/2529	2/23049	0.207411	0.486895	0.469237	Gcnt2
GO_MF_m	GO:000811	peptide-m	1/2529	2/23049	0.207411	0.486895	0.469237	Txn2
GO_MF_m	GO:000811	N-acetylla	1/2529	2/23049	0.207411	0.486895	0.469237	St3gal3
GO_MF_m	GO:00082	tRNA-spec	1/2529	2/23049	0.207411	0.486895	0.469237	Adat1
GO_MF_m	GO:000841	8-oxo-7,8-	1/2529	2/23049	0.207411	0.486895	0.469237	Nudt1
GO_MF_m	GO:000844	3'(2'),5'-bis	1/2529	2/23049	0.207411	0.486895	0.469237	Bpnt1
GO_MF_m	GO:000851	secondary	1/2529	2/23049	0.207411	0.486895	0.469237	Slc22a1
GO_MF_m	GO:00086	rRNA (uridi	1/2529	2/23049	0.207411	0.486895	0.469237	Ftsj3
GO_MF_m	GO:000867	2,4-dienoy	1/2529	2/23049	0.207411	0.486895	0.469237	Decr2
GO_MF_m	GO:00089	phosphatic	1/2529	2/23049	0.207411	0.486895	0.469237	Ptpmt1
GO_MF_m	GO:00089	phosphogl	1/2529	2/23049	0.207411	0.486895	0.469237	Aptx
GO_MF_m	GO:00093	rRNA (cyto	1/2529	2/23049	0.207411	0.486895	0.469237	Nop2
GO_MF_m	GO:00106	acetyltrans	1/2529	2/23049	0.207411	0.486895	0.469237	Bcas3
GO_MF_m	GO:00151	L-asparagi	1/2529	2/23049	0.207411	0.486895	0.469237	Slc38a7
GO_MF_m	GO:001521	pyrimidine	1/2529	2/23049	0.207411	0.486895	0.469237	Slc25a33
GO_MF_m	GO:001522	acyl carniti	1/2529	2/23049	0.207411	0.486895	0.469237	Slc25a20
GO_MF_m	GO:00153	methotrexa	1/2529	2/23049	0.207411	0.486895	0.469237	Slc46a1
GO_MF_m	GO:001592	trehalase a	1/2529	2/23049	0.207411	0.486895	0.469237	Pgghg
GO_MF_m	GO:00161	linoleate 1	1/2529	2/23049	0.207411	0.486895	0.469237	Alox12
GO_MF_m	GO:00162	sphingomy	1/2529	2/23049	0.207411	0.486895	0.469237	Stx4a
GO_MF_m	GO:00162	myristoyl-[	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn

GO_MF_m	GO:001629	palmitoyl-[	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m	GO:001629	acyl-[acyl-	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m	GO:001641	S-acetyltra	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m	GO:001641	S-malonylt	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m	GO:001642	malonyltra	1/2529	2/23049	0.207411	0.486895	0.469237	Fasn
GO_MF_m	GO:001649	G-protein	1/2529	2/23049	0.207411	0.486895	0.469237	Ntsr2
GO_MF_m	GO:001671	oxidoreduc	1/2529	2/23049	0.207411	0.486895	0.469237	Tyr
GO_MF_m	GO:001678	phosphotra	1/2529	2/23049	0.207411	0.486895	0.469237	Sephs1
GO_MF_m	GO:001686	intramolec	1/2529	2/23049	0.207411	0.486895	0.469237	Ddt
GO_MF_m	GO:001690	oxidoreduc	1/2529	2/23049	0.207411	0.486895	0.469237	Vkorc1l1
GO_MF_m	GO:001977	Atg12 tran	1/2529	2/23049	0.207411	0.486895	0.469237	Atg10
GO_MF_m	GO:001991	cyclin-dep	1/2529	2/23049	0.207411	0.486895	0.469237	Cdkn1a
GO_MF_m	GO:001997	interleukin	1/2529	2/23049	0.207411	0.486895	0.469237	Il12b
GO_MF_m	GO:002302	MHC class	1/2529	2/23049	0.207411	0.486895	0.469237	Fam49b
GO_MF_m	GO:002303	MHC class	1/2529	2/23049	0.207411	0.486895	0.469237	Fam49b
GO_MF_m	GO:003011	glial cell-d	1/2529	2/23049	0.207411	0.486895	0.469237	Gdnf
GO_MF_m	GO:003029	receptor si	1/2529	2/23049	0.207411	0.486895	0.469237	Hyal2
GO_MF_m	GO:003036	molybdopt	1/2529	2/23049	0.207411	0.486895	0.469237	Mocs2
GO_MF_m	GO:003172	hemoglobi	1/2529	2/23049	0.207411	0.486895	0.469237	Hbb-bs
GO_MF_m	GO:003179	type 1 met	1/2529	2/23049	0.207411	0.486895	0.469237	Dnm3
GO_MF_m	GO:003183	neurokinin	1/2529	2/23049	0.207411	0.486895	0.469237	Tac1
GO_MF_m	GO:003183	substance	1/2529	2/23049	0.207411	0.486895	0.469237	Tac1
GO_MF_m	GO:003186	prostanoid	1/2529	2/23049	0.207411	0.486895	0.469237	Fem1a
GO_MF_m	GO:003189	V1A vasop	1/2529	2/23049	0.207411	0.486895	0.469237	Avpr1a
GO_MF_m	GO:003209	Pyrin doma	1/2529	2/23049	0.207411	0.486895	0.469237	Pycard
GO_MF_m	GO:003218	dinucleotid	1/2529	2/23049	0.207411	0.486895	0.469237	Msh3
GO_MF_m	GO:003314	FFAT motif	1/2529	2/23049	0.207411	0.486895	0.469237	Vapb
GO_MF_m	GO:003441	bisphosph	1/2529	2/23049	0.207411	0.486895	0.469237	Tigar
GO_MF_m	GO:003443	glycoprote	1/2529	2/23049	0.207411	0.486895	0.469237	Vldlr
GO_MF_m	GO:003503	histone ac	1/2529	2/23049	0.207411	0.486895	0.469237	Pygo2
GO_MF_m	GO:003540	histone kin	1/2529	2/23049	0.207411	0.486895	0.469237	Pkn1
GO_MF_m	GO:003540	histone kin	1/2529	2/23049	0.207411	0.486895	0.469237	Prkca
GO_MF_m	GO:003571	chemokine	1/2529	2/23049	0.207411	0.486895	0.469237	Ccr1
GO_MF_m	GO:003608	purine nuc	1/2529	2/23049	0.207411	0.486895	0.469237	Slc35c1
GO_MF_m	GO:003646	BLOC-2 co	1/2529	2/23049	0.207411	0.486895	0.469237	Rab32
GO_MF_m	GO:003802	reelin rece	1/2529	2/23049	0.207411	0.486895	0.469237	Vldlr
GO_MF_m	GO:003813	neuregulin	1/2529	2/23049	0.207411	0.486895	0.469237	Erbb3
GO_MF_m	GO:004228	dolichyl py	1/2529	2/23049	0.207411	0.486895	0.469237	Alg6
GO_MF_m	GO:004278	3'-tRNA pr	1/2529	2/23049	0.207411	0.486895	0.469237	Elac1
GO_MF_m	GO:004368	copper-tra	1/2529	2/23049	0.207411	0.486895	0.469237	Atp7b
GO_MF_m	GO:004462	ACP phosp	1/2529	2/23049	0.207411	0.486895	0.469237	Zfp593
GO_MF_m	GO:004503	UTP-activa	1/2529	2/23049	0.207411	0.486895	0.469237	P2ry2
GO_MF_m	GO:004551	interleukin	1/2529	2/23049	0.207411	0.486895	0.469237	Il12b
GO_MF_m	GO:004556	TRAIL bind	1/2529	2/23049	0.207411	0.486895	0.469237	Tnfrsf10b
GO_MF_m	GO:004640	polynucleo	1/2529	2/23049	0.207411	0.486895	0.469237	Aptx
GO_MF_m	GO:004702	3-oxoacyl-	1/2529	2/23049	0.207411	0.486895	0.469237	Cbr4
GO_MF_m	GO:004705	vitamin-K-	1/2529	2/23049	0.207411	0.486895	0.469237	Vkorc1l1
GO_MF_m	GO:004722	beta-1,3-g	1/2529	2/23049	0.207411	0.486895	0.469237	B3gnt3

GO_MF_m	GO:004740	alkenylglyc	1/2529	2/23049	0.207411	0.486895	0.469237	Tmem86b
GO_MF_m	GO:004740	alkenylglyc	1/2529	2/23049	0.207411	0.486895	0.469237	Tmem86b
GO_MF_m	GO:004763	alanine-ox	1/2529	2/23049	0.207411	0.486895	0.469237	Gpt
GO_MF_m	GO:004780	cytidylate	1/2529	2/23049	0.207411	0.486895	0.469237	Gucy1b1
GO_MF_m	GO:005017	phenylpyru	1/2529	2/23049	0.207411	0.486895	0.469237	Ddt
GO_MF_m	GO:005025	rhodopsin	1/2529	2/23049	0.207411	0.486895	0.469237	Grk4
GO_MF_m	GO:005026	ribosylnico	1/2529	2/23049	0.207411	0.486895	0.469237	Nmrk2
GO_MF_m	GO:005119	prosthetic	1/2529	2/23049	0.207411	0.486895	0.469237	Zfp593
GO_MF_m	GO:005142	corticotrop	1/2529	2/23049	0.207411	0.486895	0.469237	Crhbp
GO_MF_m	GO:005259	tryptamine	1/2529	2/23049	0.207411	0.486895	0.469237	Aoc3
GO_MF_m	GO:005259	aminoacet	1/2529	2/23049	0.207411	0.486895	0.469237	Aoc3
GO_MF_m	GO:005259	aliphatic-a	1/2529	2/23049	0.207411	0.486895	0.469237	Aoc3
GO_MF_m	GO:005259	phenethyla	1/2529	2/23049	0.207411	0.486895	0.469237	Aoc3
GO_MF_m	GO:005265	L-leucine t	1/2529	2/23049	0.207411	0.486895	0.469237	Bcat2
GO_MF_m	GO:005265	L-valine tr	1/2529	2/23049	0.207411	0.486895	0.469237	Bcat2
GO_MF_m	GO:005265	L-isoleucin	1/2529	2/23049	0.207411	0.486895	0.469237	Bcat2
GO_MF_m	GO:005287	tocopherol	1/2529	2/23049	0.207411	0.486895	0.469237	Cyp4f14
GO_MF_m	GO:005287	alpha-tocc	1/2529	2/23049	0.207411	0.486895	0.469237	Cyp4f14
GO_MF_m	GO:006000	plus-end d	1/2529	2/23049	0.207411	0.486895	0.469237	Myo3a
GO_MF_m	GO:006171	N(6)-L-thr	1/2529	2/23049	0.207411	0.486895	0.469237	Osgepl1
GO_MF_m	GO:006171	folic acid r	1/2529	2/23049	0.207411	0.486895	0.469237	Folr2
GO_MF_m	GO:006174	forked DN	1/2529	2/23049	0.207411	0.486895	0.469237	Blm
GO_MF_m	GO:006176	ribosylnico	1/2529	2/23049	0.207411	0.486895	0.469237	Nmrk2
GO_MF_m	GO:007019	methionin	1/2529	2/23049	0.207411	0.486895	0.469237	Msrb1
GO_MF_m	GO:007025	tyrosyl-DN	1/2529	2/23049	0.207411	0.486895	0.469237	Tdp2
GO_MF_m	GO:007050	high-densi	1/2529	2/23049	0.207411	0.486895	0.469237	Scarb1
GO_MF_m	GO:007057	vitamin D	1/2529	2/23049	0.207411	0.486895	0.469237	Cyp24a1
GO_MF_m	GO:007120	histone pr	1/2529	2/23049	0.207411	0.486895	0.469237	Eri1
GO_MF_m	GO:007156	UFM1 hydr	1/2529	2/23049	0.207411	0.486895	0.469237	Ufsp1
GO_MF_m	GO:007179	chemokine	1/2529	2/23049	0.207411	0.486895	0.469237	Ccr1
GO_MF_m	GO:007179	K6-linked	1/2529	2/23049	0.207411	0.486895	0.469237	Mindy2
GO_MF_m	GO:007259	N-acetyl-L	1/2529	2/23049	0.207411	0.486895	0.469237	Rimklb
GO_MF_m	GO:009055	phosphatic	1/2529	2/23049	0.207411	0.486895	0.469237	Abcb1a
GO_MF_m	GO:009700	adipokineti	1/2529	2/23049	0.207411	0.486895	0.469237	Adipor2
GO_MF_m	GO:009864	integrin bi	1/2529	2/23049	0.207411	0.486895	0.469237	Madcam1
GO_MF_m	GO:190503	voltage-ga	1/2529	2/23049	0.207411	0.486895	0.469237	Kcnd2
GO_MF_m	GO:199018	euchromat	1/2529	2/23049	0.207411	0.486895	0.469237	Ash2l
GO_MF_m	GO:001539	primary ac	17/2529	125/23049	0.208092	0.487964	0.470266	Abca12/Ab
GO_MF_m	GO:004262	ATPase act	16/2529	117/23049	0.210534	0.4921	0.474253	Abca12/Ab
GO_MF_m	GO:000377	actin bindi	50/2529	406/23049	0.211552	0.4921	0.474253	Abra/Abra
GO_MF_m	GO:000166	G-protein	36/2529	286/23049	0.213674	0.4921	0.474253	Adm/Ador
GO_MF_m	GO:001708	sodium ch	6/2529	37/23049	0.215035	0.4921	0.474253	Atp2b4/Ca
GO_MF_m	GO:001984	isoprenoid	6/2529	37/23049	0.215035	0.4921	0.474253	Akr1b10/C
GO_MF_m	GO:000395	NADPH-h	2/2529	8/23049	0.216242	0.4921	0.474253	Mtrr/Por
GO_MF_m	GO:000403	aldehyde d	2/2529	8/23049	0.216242	0.4921	0.474253	Aldh1a3/Al
GO_MF_m	GO:000430	enoyl-CoA	2/2529	8/23049	0.216242	0.4921	0.474253	Echs1/Ehha
GO_MF_m	GO:000476	sphingomy	2/2529	8/23049	0.216242	0.4921	0.474253	Smpd2/Sm
GO_MF_m	GO:000533	nucleoside	2/2529	8/23049	0.216242	0.4921	0.474253	Slc29a3/Sl

GO_MF_m	GO:000803	high-densi	2/2529	8/23049	0.216242	0.4921	0.474253	Cd36/Scarb
GO_MF_m	GO:000842	phosphatic	2/2529	8/23049	0.216242	0.4921	0.474253	Nf1/Pltp
GO_MF_m	GO:001999	diacylglyce	2/2529	8/23049	0.216242	0.4921	0.474253	Dgat1/Pltp
GO_MF_m	GO:003034	protein ph	2/2529	8/23049	0.216242	0.4921	0.474253	Atp2b4/Slc
GO_MF_m	GO:003199	insulin-like	2/2529	8/23049	0.216242	0.4921	0.474253	Igf2r/Igfbp
GO_MF_m	GO:003240	mismatch r	2/2529	8/23049	0.216242	0.4921	0.474253	Atr/Pcna
GO_MF_m	GO:003404	poly(G) bin	2/2529	8/23049	0.216242	0.4921	0.474253	Fmr1/Pnpt
GO_MF_m	GO:003459	phosphatic	2/2529	8/23049	0.216242	0.4921	0.474253	Ptpmt1/Syn
GO_MF_m	GO:003459	phosphatic	2/2529	8/23049	0.216242	0.4921	0.474253	Synj1/Tmer
GO_MF_m	GO:004554	syndecan b	2/2529	8/23049	0.216242	0.4921	0.474253	Gpnmb/Nf
GO_MF_m	GO:005102	GDP-disso	2/2529	8/23049	0.216242	0.4921	0.474253	Plxnb3/Rab
GO_MF_m	GO:009702	ubiquitin-p	2/2529	8/23049	0.216242	0.4921	0.474253	Cdc20/Ring
GO_MF_m	GO:199022	histone me	2/2529	8/23049	0.216242	0.4921	0.474253	Nop56/Prd
GO_MF_m	GO:000554	hyaluronic	4/2529	22/23049	0.216478	0.4921	0.474253	2300002M
GO_MF_m	GO:001560	organophc	4/2529	22/23049	0.216478	0.4921	0.474253	Atp8b1/Slc
GO_MF_m	GO:001705	structural c	4/2529	22/23049	0.216478	0.4921	0.474253	Nup153/Nu
GO_MF_m	GO:004549	chemorepe	4/2529	22/23049	0.216478	0.4921	0.474253	Epha7/Flrt2
GO_MF_m	GO:004802	mRNA 5'-U	4/2529	22/23049	0.216478	0.4921	0.474253	Fmr1/Igf2b
GO_MF_m	GO:007053	K63-linked	4/2529	22/23049	0.216478	0.4921	0.474253	Mindy2/Np
GO_MF_m	GO:000462	phospholip	12/2529	85/23049	0.218975	0.497252	0.479217	Abhd1/Adc
GO_MF_m	GO:002284	voltage-ga	19/2529	143/23049	0.220849	0.499729	0.481605	Cacnb2/Ca
GO_MF_m	GO:001676	transferase	8/2529	53/23049	0.221241	0.499729	0.481605	Aprt/Art1/A
GO_MF_m	GO:001683	carbon-oxy	9/2529	61/23049	0.221829	0.499729	0.481605	Dglucy/Api
GO_MF_m	GO:000379	lysozyme a	3/2529	15/23049	0.222617	0.499729	0.481605	1700016D0
GO_MF_m	GO:000469	protein kin	3/2529	15/23049	0.222617	0.499729	0.481605	Pkn1/Prkca
GO_MF_m	GO:000516	platelet-de	3/2529	15/23049	0.222617	0.499729	0.481605	Pdgfa/Pdg
GO_MF_m	GO:001521	nucleotide	3/2529	15/23049	0.222617	0.499729	0.481605	Slc25a23/S
GO_MF_m	GO:001620	AMP bindir	3/2529	15/23049	0.222617	0.499729	0.481605	Aprt/Oxgr1
GO_MF_m	GO:001629	palmitoyl-(	3/2529	15/23049	0.222617	0.499729	0.481605	Acot1/Acot
GO_MF_m	GO:003054	acetylcholir	3/2529	15/23049	0.222617	0.499729	0.481605	Cdk5/Fnta/
GO_MF_m	GO:009960	neurotrans	3/2529	15/23049	0.222617	0.499729	0.481605	Cdk5/Fnta/
GO_MF_m	GO:003162	ubiquitin p	40/2529	322/23049	0.224001	0.502313	0.484095	Abtb1/Ank
GO_MF_m	GO:001681	hydrolase a	5/2529	30/23049	0.227853	0.509889	0.491396	Adat1/Apo
GO_MF_m	GO:001923	deaminase	5/2529	30/23049	0.227853	0.509889	0.491396	Adat1/Apo
GO_MF_m	GO:014010	catalytic ac	16/2529	119/23049	0.230555	0.515401	0.496708	6430573F1
GO_MF_m	GO:004227	peptide bir	38/2529	306/23049	0.231499	0.516975	0.498226	Adcyap1r1
GO_MF_m	GO:000548	SNAP rece	6/2529	38/23049	0.233491	0.520344	0.501473	Snap29/Stx
GO_MF_m	GO:190150	carbohydra	6/2529	38/23049	0.233491	0.520344	0.501473	Slc25a23/S
GO_MF_m	GO:001712	SH3 domai	17/2529	128/23049	0.237197	0.528057	0.508905	Abi1/Bcar1
GO_MF_m	GO:002003	heme bind	19/2529	145/23049	0.239324	0.532242	0.512938	Cyb5a/Cyb
GO_MF_m	GO:000813	nuclear loc	4/2529	23/23049	0.241014	0.534898	0.515499	Brap/Lbr/N
GO_MF_m	GO:003361	receptor se	4/2529	23/23049	0.241014	0.534898	0.515499	Bmp3/Cfc1
GO_MF_m	GO:000852	G-protein c	17/2529	129/23049	0.247257	0.542683	0.523001	Avpr1a/Cal
GO_MF_m	GO:000550	retinoid bir	5/2529	31/23049	0.249092	0.542683	0.523001	Akr1b10/C
GO_MF_m	GO:000820	ion channe	5/2529	31/23049	0.249092	0.542683	0.523001	Cav1/Cav3
GO_MF_m	GO:004323	laminin bin	5/2529	31/23049	0.249092	0.542683	0.523001	2300002M
GO_MF_m	GO:000554	phosphatic	6/2529	39/23049	0.252414	0.542683	0.523001	Arhgap9/Fe
GO_MF_m	GO:001622	steroid deh	6/2529	39/23049	0.252414	0.542683	0.523001	Akr1c12/Hs

GO_MF_m	GO:00428	amide tran	6/2529	39/23049	0.252414	0.542683	0.523001	Folr2/Slc14
GO_MF_m	GO:004691	transition r	6/2529	39/23049	0.252414	0.542683	0.523001	Atp7b/Slc3
GO_MF_m	GO:190161	organic hy	7/2529	47/23049	0.253191	0.542683	0.523001	Abcc3/Slc1
GO_MF_m	GO:00014	microfilam	3/2529	16/23049	0.253237	0.542683	0.523001	Myh14/My
GO_MF_m	GO:00010	RNA polym	3/2529	16/23049	0.253237	0.542683	0.523001	Polr2f/Polr
GO_MF_m	GO:000184	opsonin bi	3/2529	16/23049	0.253237	0.542683	0.523001	Cd93/Itgar
GO_MF_m	GO:000454	tRNA-spec	3/2529	16/23049	0.253237	0.542683	0.523001	Rpp40/Tse
GO_MF_m	GO:000512	death rece	3/2529	16/23049	0.253237	0.542683	0.523001	Casp8/Bex
GO_MF_m	GO:00083	voltage-ga	3/2529	16/23049	0.253237	0.542683	0.523001	Ano1/Clcn
GO_MF_m	GO:00310	filamin bin	3/2529	16/23049	0.253237	0.542683	0.523001	Dpysl4/Rfln
GO_MF_m	GO:00422	MHC class	3/2529	16/23049	0.253237	0.542683	0.523001	Atp5a1/Bc
GO_MF_m	GO:00428	histone me	3/2529	16/23049	0.253237	0.542683	0.523001	Ash2l/Rbb
GO_MF_m	GO:19019	phosphatic	20/2529	155/23049	0.253896	0.542683	0.523001	Ankfy1/Anx
GO_MF_m	GO:00168	ATPase act	54/2529	449/23049	0.255653	0.542683	0.523001	Abca12/Ab
GO_MF_m	GO:000451	endonucle	17/2529	130/23049	0.257483	0.542683	0.523001	Aplf/Cpsf4/
GO_MF_m	GO:000371	transcriptic	56/2529	467/23049	0.258428	0.542683	0.523001	Ankra2/An
GO_MF_m	GO:00001	rDNA bind	2/2529	9/23049	0.258941	0.542683	0.523001	H2afy/Maf
GO_MF_m	GO:00077	adenyl-nuc	2/2529	9/23049	0.258941	0.542683	0.523001	Grpel1/Hsp
GO_MF_m	GO:00010	RNA polym	2/2529	9/23049	0.258941	0.542683	0.523001	Polr2f/Polr
GO_MF_m	GO:00038	3-beta-hy	2/2529	9/23049	0.258941	0.542683	0.523001	Hsd3b3/Hs
GO_MF_m	GO:00038	3-hydroxy	2/2529	9/23049	0.258941	0.542683	0.523001	Ehhadh/Hs
GO_MF_m	GO:00039	acid phosp	2/2529	9/23049	0.258941	0.542683	0.523001	Acp6/Acp
GO_MF_m	GO:000441	hyaluronor	2/2529	9/23049	0.258941	0.542683	0.523001	Hyal2/Hyal
GO_MF_m	GO:000534	ATP transm	2/2529	9/23049	0.258941	0.542683	0.523001	Slc25a23/S
GO_MF_m	GO:00083	mechanose	2/2529	9/23049	0.258941	0.542683	0.523001	Tmem150
GO_MF_m	GO:00084	selenium b	2/2529	9/23049	0.258941	0.542683	0.523001	Rph3a/Sele
GO_MF_m	GO:000852	phosphatic	2/2529	9/23049	0.258941	0.542683	0.523001	Abcb1a/Plt
GO_MF_m	GO:00085	N-acetylla	2/2529	9/23049	0.258941	0.542683	0.523001	B3gnt3/B3
GO_MF_m	GO:001642	tRNA (cyto	2/2529	9/23049	0.258941	0.542683	0.523001	Mettl6/Nsu
GO_MF_m	GO:001672	oxidoreduc	2/2529	9/23049	0.258941	0.542683	0.523001	Mmachc/M
GO_MF_m	GO:00168	ether hydr	2/2529	9/23049	0.258941	0.542683	0.523001	Ephx2/Tme
GO_MF_m	GO:00171	aryl hydro	2/2529	9/23049	0.258941	0.542683	0.523001	Arntl/Tbp
GO_MF_m	GO:002302	MHC prote	2/2529	9/23049	0.258941	0.542683	0.523001	Fam49b/H
GO_MF_m	GO:00302	structural c	2/2529	9/23049	0.258941	0.542683	0.523001	Krt36/Sprr
GO_MF_m	GO:003154	peptidyl-p	2/2529	9/23049	0.258941	0.542683	0.523001	Egln3/P4ha
GO_MF_m	GO:00352	UDP-gluc	2/2529	9/23049	0.258941	0.542683	0.523001	Gys1/Uggt
GO_MF_m	GO:005054	arachidoni	2/2529	9/23049	0.258941	0.542683	0.523001	Cyp4f14/Sr
GO_MF_m	GO:003802	cargo rece	11/2529	80/23049	0.259187	0.542683	0.523001	Cd36/Corir
GO_MF_m	GO:00443	ubiquitin-li	41/2529	337/23049	0.263601	0.542683	0.523001	Abtb1/Ank
GO_MF_m	GO:000021	DNA secor	4/2529	24/23049	0.266137	0.542683	0.523001	Blm/Ercc5/
GO_MF_m	GO:00016	G-protein	4/2529	24/23049	0.266137	0.542683	0.523001	Ccr1/Ccrl2/
GO_MF_m	GO:00049	chemokine	4/2529	24/23049	0.266137	0.542683	0.523001	Ccr1/Ccrl2/
GO_MF_m	GO:003054	receptor in	4/2529	24/23049	0.266137	0.542683	0.523001	Il18bp/Il1r
GO_MF_m	GO:00517	misfolded	4/2529	24/23049	0.266137	0.542683	0.523001	Hspa1a/Hs
GO_MF_m	GO:007041	R-SMAD b	4/2529	24/23049	0.266137	0.542683	0.523001	Ankrd1/Me
GO_MF_m	GO:00423	histone bin	23/2529	182/23049	0.267011	0.542683	0.523001	Bcas3/Ctsl/
GO_MF_m	GO:001627	lysine N-m	8/2529	56/23049	0.268597	0.542683	0.523001	Ash2l/Eef2
GO_MF_m	GO:001627	protein-lys	8/2529	56/23049	0.268597	0.542683	0.523001	Ash2l/Eef2

GO_MF_m	GO:00315	polyubiqui	7/2529	48/23049	0.270722	0.542683	0.523001	Babam2/M
GO_MF_m	GO:00510	NF-kappa	5/2529	32/23049	0.270804	0.542683	0.523001	Hdac1/Hd
GO_MF_m	GO:19907	protein tyr	11/2529	81/23049	0.272586	0.542683	0.523001	Dock4/Elm
GO_MF_m	GO:004432	ion channe	17/2529	132/23049	0.278397	0.542683	0.523001	Akap6/Cav
GO_MF_m	GO:00037	transcriptic	14/2529	107/23049	0.283163	0.542683	0.523001	Arx/Esrrb/
GO_MF_m	GO:00050	Ras guanyl	16/2529	124/23049	0.283775	0.542683	0.523001	Arhgef18/
GO_MF_m	GO:000832	methyl-Cp	3/2529	17/23049	0.284393	0.542683	0.523001	Mbd1/Prm
GO_MF_m	GO:00083	RNA polym	3/2529	17/23049	0.284393	0.542683	0.523001	Cdk1/Cdk7
GO_MF_m	GO:001527	outward re	3/2529	17/23049	0.284393	0.542683	0.523001	Kcna2/Kcn
GO_MF_m	GO:001664	oxidoredu	3/2529	17/23049	0.284393	0.542683	0.523001	Aldh4a1/M
GO_MF_m	GO:003561	RNA stem-	3/2529	17/23049	0.284393	0.542683	0.523001	Cpeb3/Fm
GO_MF_m	GO:00703	phosphatic	3/2529	17/23049	0.284393	0.542683	0.523001	Gsdmd/Plt
GO_MF_m	GO:000014	SNARE bin	17/2529	133/23049	0.289067	0.542683	0.523001	Cav1/Dapk
GO_MF_m	GO:000504	signal sequ	6/2529	41/23049	0.291403	0.542683	0.523001	Brap/Lbr/
GO_MF_m	GO:00081	poly-pyrim	4/2529	25/23049	0.291699	0.542683	0.523001	Fmr1/Hnrn
GO_MF_m	GO:00162	CoA hydro	4/2529	25/23049	0.291699	0.542683	0.523001	Acot1/Aco
GO_MF_m	GO:001667	oxidoredu	4/2529	25/23049	0.291699	0.542683	0.523001	Cox15/Cox
GO_MF_m	GO:001684	phosphoru	4/2529	25/23049	0.291699	0.542683	0.523001	Adcy4/Guc
GO_MF_m	GO:00168	endoribon	4/2529	25/23049	0.291699	0.542683	0.523001	Elac1/Fen1
GO_MF_m	GO:00048	protein ph	5/2529	33/23049	0.292896	0.542683	0.523001	2810408A
GO_MF_m	GO:001624	channel in	5/2529	33/23049	0.292896	0.542683	0.523001	Cav1/Cav3
GO_MF_m	GO:00011	RNA polym	1/2529	3/23049	0.294383	0.542683	0.523001	Tbp
GO_MF_m	GO:00011	RNA polym	1/2529	3/23049	0.294383	0.542683	0.523001	Tbp
GO_MF_m	GO:00012	RNA polym	1/2529	3/23049	0.294383	0.542683	0.523001	Hdac2
GO_MF_m	GO:00038	beta-1,3-g	1/2529	3/23049	0.294383	0.542683	0.523001	Gcnt1
GO_MF_m	GO:000387	6-phosph	1/2529	3/23049	0.294383	0.542683	0.523001	Pfkl
GO_MF_m	GO:00039	acetate-C	1/2529	3/23049	0.294383	0.542683	0.523001	Acss3
GO_MF_m	GO:000401	adenosylh	1/2529	3/23049	0.294383	0.542683	0.523001	Ahcyl2
GO_MF_m	GO:00040	alcohol de	1/2529	3/23049	0.294383	0.542683	0.523001	Adh1
GO_MF_m	GO:00040	L-aspartat	1/2529	3/23049	0.294383	0.542683	0.523001	Got1
GO_MF_m	GO:000411	cGMP-stir	1/2529	3/23049	0.294383	0.542683	0.523001	Pde11a
GO_MF_m	GO:000414	diamine N	1/2529	3/23049	0.294383	0.542683	0.523001	Sat1
GO_MF_m	GO:000434	glucose-6-	1/2529	3/23049	0.294383	0.542683	0.523001	G6pc2
GO_MF_m	GO:00043	glutaminas	1/2529	3/23049	0.294383	0.542683	0.523001	Gls
GO_MF_m	GO:000441	hydroxyac	1/2529	3/23049	0.294383	0.542683	0.523001	Haghl
GO_MF_m	GO:000447	malic enzy	1/2529	3/23049	0.294383	0.542683	0.523001	Me3
GO_MF_m	GO:000447	malate de	1/2529	3/23049	0.294383	0.542683	0.523001	Me3
GO_MF_m	GO:000447	malate de	1/2529	3/23049	0.294383	0.542683	0.523001	Me3
GO_MF_m	GO:00045	5'-3' exori	1/2529	3/23049	0.294383	0.542683	0.523001	Xrn2
GO_MF_m	GO:000461	phosphogl	1/2529	3/23049	0.294383	0.542683	0.523001	Glyr1
GO_MF_m	GO:00046	Rab gerany	1/2529	3/23049	0.294383	0.542683	0.523001	Fnta
GO_MF_m	GO:00046	prostaglan	1/2529	3/23049	0.294383	0.542683	0.523001	Ptges
GO_MF_m	GO:000471	protein-L-	1/2529	3/23049	0.294383	0.542683	0.523001	Pcmtd1
GO_MF_m	GO:00047	pyrroline-	1/2529	3/23049	0.294383	0.542683	0.523001	Pycr2
GO_MF_m	GO:00047	pyruvate d	1/2529	3/23049	0.294383	0.542683	0.523001	Pdhb
GO_MF_m	GO:00047	threonine	1/2529	3/23049	0.294383	0.542683	0.523001	Shmt1
GO_MF_m	GO:00048	thyroxine	1/2529	3/23049	0.294383	0.542683	0.523001	Dio2
GO_MF_m	GO:00048	tRNA (gua	1/2529	3/23049	0.294383	0.542683	0.523001	Trmt1

GO_MF_m	GO:000483	valine-tRN	1/2529	3/23049	0.294383	0.542683	0.523001	Vars2
GO_MF_m	GO:000493	alpha1-adr	1/2529	3/23049	0.294383	0.542683	0.523001	Adra1d
GO_MF_m	GO:000496	endothelin	1/2529	3/23049	0.294383	0.542683	0.523001	Ednrb
GO_MF_m	GO:000499	tachykinin	1/2529	3/23049	0.294383	0.542683	0.523001	Tacr2
GO_MF_m	GO:000499	vasoactive	1/2529	3/23049	0.294383	0.542683	0.523001	Adcyap1r1
GO_MF_m	GO:000500	epidermal	1/2529	3/23049	0.294383	0.542683	0.523001	Nrg2
GO_MF_m	GO:000509	Rho GDP-c	1/2529	3/23049	0.294383	0.542683	0.523001	Arhgdib
GO_MF_m	GO:000516	neurotroph	1/2529	3/23049	0.294383	0.542683	0.523001	Ntf5
GO_MF_m	GO:000517	stem cell fa	1/2529	3/23049	0.294383	0.542683	0.523001	Kitl
GO_MF_m	GO:000527	acetylcholi	1/2529	3/23049	0.294383	0.542683	0.523001	Slc22a1
GO_MF_m	GO:000529	L-histidine	1/2529	3/23049	0.294383	0.542683	0.523001	Slc38a7
GO_MF_m	GO:000533	norepineph	1/2529	3/23049	0.294383	0.542683	0.523001	Slc22a1
GO_MF_m	GO:000547	carnitine:ac	1/2529	3/23049	0.294383	0.542683	0.523001	Slc25a20
GO_MF_m	GO:000550	11-cis retir	1/2529	3/23049	0.294383	0.542683	0.523001	Opn4
GO_MF_m	GO:000807	ornithine d	1/2529	3/23049	0.294383	0.542683	0.523001	Oaz1
GO_MF_m	GO:000814	oxysterol b	1/2529	3/23049	0.294383	0.542683	0.523001	Gpr183
GO_MF_m	GO:000814	structural c	1/2529	3/23049	0.294383	0.542683	0.523001	Bglap3
GO_MF_m	GO:000815	hedgehog	1/2529	3/23049	0.294383	0.542683	0.523001	B9d1
GO_MF_m	GO:000824	tripeptidyl-	1/2529	3/23049	0.294383	0.542683	0.523001	Tpp2
GO_MF_m	GO:000845	alpha-1,3-	1/2529	3/23049	0.294383	0.542683	0.523001	Mgat4a
GO_MF_m	GO:000851	sodium:po	1/2529	3/23049	0.294383	0.542683	0.523001	Slc12a2
GO_MF_m	GO:000873	L-allo-thre	1/2529	3/23049	0.294383	0.542683	0.523001	Shmt1
GO_MF_m	GO:000879	aromatic-a	1/2529	3/23049	0.294383	0.542683	0.523001	Got1
GO_MF_m	GO:000894	nitrate redu	1/2529	3/23049	0.294383	0.542683	0.523001	Gphn
GO_MF_m	GO:000967	potassium:	1/2529	3/23049	0.294383	0.542683	0.523001	Slc12a2
GO_MF_m	GO:001506	uridine nuc	1/2529	3/23049	0.294383	0.542683	0.523001	P2ry2
GO_MF_m	GO:001511	iodide tran	1/2529	3/23049	0.294383	0.542683	0.523001	Ano1
GO_MF_m	GO:001522	serotonin t	1/2529	3/23049	0.294383	0.542683	0.523001	Slc18a2
GO_MF_m	GO:001524	aminophos	1/2529	3/23049	0.294383	0.542683	0.523001	Atp8b1
GO_MF_m	GO:001525	proton cha	1/2529	3/23049	0.294383	0.542683	0.523001	Hvcn1
GO_MF_m	GO:001527	stretch-act	1/2529	3/23049	0.294383	0.542683	0.523001	Trpv4
GO_MF_m	GO:001531	sodium:ino	1/2529	3/23049	0.294383	0.542683	0.523001	Slc20a1
GO_MF_m	GO:001537	sodium:chl	1/2529	3/23049	0.294383	0.542683	0.523001	Slc12a2
GO_MF_m	GO:001601	morphoge	1/2529	3/23049	0.294383	0.542683	0.523001	Dand5
GO_MF_m	GO:001643	rRNA (cyto	1/2529	3/23049	0.294383	0.542683	0.523001	Nop2
GO_MF_m	GO:001643	rRNA (uridi	1/2529	3/23049	0.294383	0.542683	0.523001	Ftsj3
GO_MF_m	GO:001650	long-chain	1/2529	3/23049	0.294383	0.542683	0.523001	Hsd17b4
GO_MF_m	GO:001674	carboxyl- c	1/2529	3/23049	0.294383	0.542683	0.523001	Otc
GO_MF_m	GO:001680	trialkylsulfo	1/2529	3/23049	0.294383	0.542683	0.523001	Ahcyl2
GO_MF_m	GO:001682	hydrolase a	1/2529	3/23049	0.294383	0.542683	0.523001	Fahd1
GO_MF_m	GO:001682	hydrolase a	1/2529	3/23049	0.294383	0.542683	0.523001	Fahd1
GO_MF_m	GO:001694	natriuretic	1/2529	3/23049	0.294383	0.542683	0.523001	Npr2
GO_MF_m	GO:001709	heparan su	1/2529	3/23049	0.294383	0.542683	0.523001	Hs6st1
GO_MF_m	GO:001709	very-long-	1/2529	3/23049	0.294383	0.542683	0.523001	Acad11
GO_MF_m	GO:001979	procollage	1/2529	3/23049	0.294383	0.542683	0.523001	P3h3
GO_MF_m	GO:001980	spermidine	1/2529	3/23049	0.294383	0.542683	0.523001	Sat1
GO_MF_m	GO:003002	extracellula	1/2529	3/23049	0.294383	0.542683	0.523001	Ambn
GO_MF_m	GO:003014	alpha-1,6-	1/2529	3/23049	0.294383	0.542683	0.523001	Ccdc126

GO_MF_m	GO:003015	protein xyl	1/2529	3/23049	0.294383	0.542683	0.523001	Xylt1
GO_MF_m	GO:003034	structural c	1/2529	3/23049	0.294383	0.542683	0.523001	Ambn
GO_MF_m	GO:003054	acetylcholi	1/2529	3/23049	0.294383	0.542683	0.523001	Cdk5
GO_MF_m	GO:003172	CCR1 chen	1/2529	3/23049	0.294383	0.542683	0.523001	Ccl4
GO_MF_m	GO:003189	vasopressi	1/2529	3/23049	0.294383	0.542683	0.523001	Avpr1a
GO_MF_m	GO:003214	single guar	1/2529	3/23049	0.294383	0.542683	0.523001	Msh3
GO_MF_m	GO:003374	L-methioni	1/2529	3/23049	0.294383	0.542683	0.523001	Msrb1
GO_MF_m	GO:003461	tetrahydrol	1/2529	3/23049	0.294383	0.542683	0.523001	Th
GO_MF_m	GO:003473	histone de	1/2529	3/23049	0.294383	0.542683	0.523001	Hdac2
GO_MF_m	GO:003553	8-oxo-7,8-	1/2529	3/23049	0.294383	0.542683	0.523001	Nudt1
GO_MF_m	GO:003565	AP-3 adap	1/2529	3/23049	0.294383	0.542683	0.523001	Rab32
GO_MF_m	GO:003587	death effec	1/2529	3/23049	0.294383	0.542683	0.523001	Casp8
GO_MF_m	GO:004201	interleukin-	1/2529	3/23049	0.294383	0.542683	0.523001	Il22ra1
GO_MF_m	GO:004381	phosphatic	1/2529	3/23049	0.294383	0.542683	0.523001	Synj1
GO_MF_m	GO:004472	hemi-meth	1/2529	3/23049	0.294383	0.542683	0.523001	Wt1
GO_MF_m	GO:004515	myosin II b	1/2529	3/23049	0.294383	0.542683	0.523001	Gsn
GO_MF_m	GO:004640	ATP-deper	1/2529	3/23049	0.294383	0.542683	0.523001	N4bp2
GO_MF_m	GO:004704	testosteror	1/2529	3/23049	0.294383	0.542683	0.523001	Hsd17b3
GO_MF_m	GO:004719	1-alkylglyc	1/2529	3/23049	0.294383	0.542683	0.523001	Lpcat4
GO_MF_m	GO:004723	glucuronyl	1/2529	3/23049	0.294383	0.542683	0.523001	Csgalnact1
GO_MF_m	GO:004775	chondroitir	1/2529	3/23049	0.294383	0.542683	0.523001	Chst13
GO_MF_m	GO:005025	retinol O-f	1/2529	3/23049	0.294383	0.542683	0.523001	Dgat1
GO_MF_m	GO:005030	sugar-term	1/2529	3/23049	0.294383	0.542683	0.523001	G6pc2
GO_MF_m	GO:005153	3 iron, 4 su	1/2529	3/23049	0.294383	0.542683	0.523001	Sdhb
GO_MF_m	GO:005173	polydeoxyr	1/2529	3/23049	0.294383	0.542683	0.523001	N4bp2
GO_MF_m	GO:005173	ATP-deper	1/2529	3/23049	0.294383	0.542683	0.523001	N4bp2
GO_MF_m	GO:005187	methotrex	1/2529	3/23049	0.294383	0.542683	0.523001	Folr2
GO_MF_m	GO:005290	tRNA (guar	1/2529	3/23049	0.294383	0.542683	0.523001	Trmt10a
GO_MF_m	GO:005510	adiponecti	1/2529	3/23049	0.294383	0.542683	0.523001	Adipor2
GO_MF_m	GO:007003	rRNA (guar	1/2529	3/23049	0.294383	0.542683	0.523001	Mrm1
GO_MF_m	GO:007013	ubiquitin-li	1/2529	3/23049	0.294383	0.542683	0.523001	Senp1
GO_MF_m	GO:007014	SUMO-spe	1/2529	3/23049	0.294383	0.542683	0.523001	Senp1
GO_MF_m	GO:007040	NADP+ bir	1/2529	3/23049	0.294383	0.542683	0.523001	Akr1b10
GO_MF_m	GO:007053	oleic acid b	1/2529	3/23049	0.294383	0.542683	0.523001	Cd36
GO_MF_m	GO:007054	L-glutamin	1/2529	3/23049	0.294383	0.542683	0.523001	Gfpt2
GO_MF_m	GO:007069	type I activ	1/2529	3/23049	0.294383	0.542683	0.523001	Smad6
GO_MF_m	GO:007074	tubulin-glu	1/2529	3/23049	0.294383	0.542683	0.523001	Tpgs1
GO_MF_m	GO:007090	serine bind	1/2529	3/23049	0.294383	0.542683	0.523001	Shmt1
GO_MF_m	GO:007099	medium-cl	1/2529	3/23049	0.294383	0.542683	0.523001	Acad11
GO_MF_m	GO:007155	G-protein	1/2529	3/23049	0.294383	0.542683	0.523001	P2ry2
GO_MF_m	GO:008013	L-phenylal	1/2529	3/23049	0.294383	0.542683	0.523001	Got1
GO_MF_m	GO:008605	voltage-ga	1/2529	3/23049	0.294383	0.542683	0.523001	Cacnb2
GO_MF_m	GO:008607	gap junctic	1/2529	3/23049	0.294383	0.542683	0.523001	Gjc1
GO_MF_m	GO:009710	supercoile	1/2529	3/23049	0.294383	0.542683	0.523001	Psip1
GO_MF_m	GO:190137	acetate est	1/2529	3/23049	0.294383	0.542683	0.523001	Slc22a1
GO_MF_m	GO:190577	8-hydroxy-	1/2529	3/23049	0.294383	0.542683	0.523001	Blm
GO_MF_m	GO:199046	leptin rece	1/2529	3/23049	0.294383	0.542683	0.523001	Snx2
GO_MF_m	GO:199075	protein bin	1/2529	3/23049	0.294383	0.542683	0.523001	Arrdc4

GO_MF_m	GO:001679	hydrolase a	17/2529	134/23049	0.299867	0.549606	0.529672	1700016D0
GO_MF_m	GO:001681	hydrolase a	11/2529	83/23049	0.299999	0.549606	0.529672	Acer3/Acy1
GO_MF_m	GO:000034	RNA 7-me	2/2529	10/23049	0.301709	0.549606	0.529672	Eif4e/Fmr1
GO_MF_m	GO:000184	compleme	2/2529	10/23049	0.301709	0.549606	0.529672	Cd93/Mptx
GO_MF_m	GO:000817	mRNA met	2/2529	10/23049	0.301709	0.549606	0.529672	Cmtr2/Rnm
GO_MF_m	GO:000834	MAP kinas	2/2529	10/23049	0.301709	0.549606	0.529672	Map4k2/M
GO_MF_m	GO:001521	ADP transr	2/2529	10/23049	0.301709	0.549606	0.529672	Slc25a23/S
GO_MF_m	GO:001538	potassium:	2/2529	10/23049	0.301709	0.549606	0.529672	Slc9a1/Slc9
GO_MF_m	GO:003235	oxidized D	2/2529	10/23049	0.301709	0.549606	0.529672	Blm/Xrcc1
GO_MF_m	GO:003501	phosphatic	2/2529	10/23049	0.301709	0.549606	0.529672	Pik3r3/Pik3
GO_MF_m	GO:005054	icosanoid b	2/2529	10/23049	0.301709	0.549606	0.529672	Cyp4f14/Sr
GO_MF_m	GO:005054	icosatetrae	2/2529	10/23049	0.301709	0.549606	0.529672	Cyp4f14/Sr
GO_MF_m	GO:005192	peroxiredo	2/2529	10/23049	0.301709	0.549606	0.529672	Prdx1/Prdx
GO_MF_m	GO:010299	myristoyl-(	2/2529	10/23049	0.301709	0.549606	0.529672	Acot1/Aco
GO_MF_m	GO:000203	p53 bindin	10/2529	75/23049	0.305982	0.556919	0.536721	Ankrd1/Blm
GO_MF_m	GO:004687	metal ion t	52/2529	441/23049	0.310823	0.565251	0.54475	Atp1b2/Atp
GO_MF_m	GO:001704	Rho GTPas	20/2529	161/23049	0.31224	0.56735	0.546773	Arhgap44/
GO_MF_m	GO:000452	exodeoxyri	3/2529	18/23049	0.315831	0.572428	0.551667	Aptx/Dclre
GO_MF_m	GO:000462	phospholip	3/2529	18/23049	0.315831	0.572428	0.551667	Adora1/Cc
GO_MF_m	GO:001689	exodeoxyri	3/2529	18/23049	0.315831	0.572428	0.551667	Aptx/Dclre
GO_MF_m	GO:000526	potassium	16/2529	127/23049	0.317486	0.573635	0.55283	Cnga2/Kcn
GO_MF_m	GO:001624	channel re	16/2529	127/23049	0.317486	0.573635	0.55283	Atp2b4/Ca
GO_MF_m	GO:000467	AMP-activa	4/2529	26/23049	0.317562	0.573635	0.55283	Gm14147/
GO_MF_m	GO:009863	cell-cell ad	4/2529	26/23049	0.317562	0.573635	0.55283	Anxa2/Cnn
GO_MF_m	GO:000489	cytokine re	12/2529	93/23049	0.320799	0.578997	0.557998	Ccr1/Ccrl2/
GO_MF_m	GO:001704	peptide ho	7/2529	51/23049	0.324971	0.586036	0.564782	Avpr1a/Cal
GO_MF_m	GO:000472	phosphopr	21/2529	171/23049	0.325551	0.586591	0.565316	Cdc25a/Dr
GO_MF_m	GO:001988	protein ph	9/2529	68/23049	0.327987	0.590486	0.56907	2810408A1
GO_MF_m	GO:001507	potassium	20/2529	163/23049	0.332527	0.59816	0.576466	Atp1b2/Cn
GO_MF_m	GO:004529	cadherin bi	38/2529	321/23049	0.334093	0.600476	0.578698	Abcf3/Abi1
GO_MF_m	GO:000531	dicarboxyli	5/2529	35/23049	0.337864	0.601549	0.579731	Folr2/Slc1a
GO_MF_m	GO:000853	Ran GTPas	5/2529	35/23049	0.337864	0.601549	0.579731	1700123L1
GO_MF_m	GO:009863	cell adhesi	5/2529	35/23049	0.337864	0.601549	0.579731	Anxa2/Cnn
GO_MF_m	GO:000468	calmodulin	4/2529	27/23049	0.343592	0.601549	0.579731	Camk2a/Da
GO_MF_m	GO:000119	transcriptic	9/2529	69/23049	0.343964	0.601549	0.579731	Ankrd1/Arr
GO_MF_m	GO:000414	diacylglyce	2/2529	11/23049	0.344017	0.601549	0.579731	Dgkh/Dgkq
GO_MF_m	GO:000479	thioredoxin	2/2529	11/23049	0.344017	0.601549	0.579731	Selenot/Txn
GO_MF_m	GO:000504	low-densit	2/2529	11/23049	0.344017	0.601549	0.579731	Cd36/Tnfai
GO_MF_m	GO:000524	voltage-ga	2/2529	11/23049	0.344017	0.601549	0.579731	Ano1/Clcn4
GO_MF_m	GO:000856	microtubul	2/2529	11/23049	0.344017	0.601549	0.579731	Fign/Katna
GO_MF_m	GO:001538	sodium:prc	2/2529	11/23049	0.344017	0.601549	0.579731	Slc9a1/Slc9
GO_MF_m	GO:001681	hydrolase a	2/2529	11/23049	0.344017	0.601549	0.579731	Agmat/Arg
GO_MF_m	GO:001683	aldehyde-l	2/2529	11/23049	0.344017	0.601549	0.579731	Dera/Shmt
GO_MF_m	GO:001715	semaphorin	2/2529	11/23049	0.344017	0.601549	0.579731	Plxna2/Plxn
GO_MF_m	GO:004737	acylglycerc	2/2529	11/23049	0.344017	0.601549	0.579731	Abhd1/Mg
GO_MF_m	GO:007041	co-SMAD I	2/2529	11/23049	0.344017	0.601549	0.579731	Smad6/Trir
GO_MF_m	GO:007041	I-SMAD bir	2/2529	11/23049	0.344017	0.601549	0.579731	Smad6/Sm
GO_MF_m	GO:009720	cysteine-ty	2/2529	11/23049	0.344017	0.601549	0.579731	Casp6/Cas

GO_MF_m	GO:199082	sequence-	2/2529	11/23049	0.344017	0.601549	0.579731	Fmr1/Srsf4
GO_MF_m	GO:000122	transcripti	3/2529	19/23049	0.34732	0.601549	0.579731	Hdac2/Ne
GO_MF_m	GO:000375	protein dis	3/2529	19/23049	0.34732	0.601549	0.579731	Ero1l/Pdia
GO_MF_m	GO:001686	intramolec	3/2529	19/23049	0.34732	0.601549	0.579731	Ero1l/Pdia
GO_MF_m	GO:001689	endonucle	3/2529	19/23049	0.34732	0.601549	0.579731	Rida/Tsen2
GO_MF_m	GO:001704	GTP-Rho b	3/2529	19/23049	0.34732	0.601549	0.579731	Cdc42ep5/
GO_MF_m	GO:003459	phosphati	3/2529	19/23049	0.34732	0.601549	0.579731	Ptpmt1/Sy
GO_MF_m	GO:004327	phospholi	3/2529	19/23049	0.34732	0.601549	0.579731	Dgkq/Park
GO_MF_m	GO:006178	peptidogly	3/2529	19/23049	0.34732	0.601549	0.579731	1700016D
GO_MF_m	GO:009864	cadherin bi	3/2529	19/23049	0.34732	0.601549	0.579731	Anxa2/Cnn
GO_MF_m	GO:000823	cysteine-ty	22/2529	182/23049	0.348022	0.601549	0.579731	Blmh/Capr
GO_MF_m	GO:000524	voltage-ga	6/2529	44/23049	0.351798	0.601549	0.579731	Cacnb2/Ca
GO_MF_m	GO:001671	oxidoreduc	8/2529	61/23049	0.352682	0.601549	0.579731	Cyp2b10/
GO_MF_m	GO:000371	transcripti	31/2529	262/23049	0.355509	0.601549	0.579731	Ankrd1/As
GO_MF_m	GO:009711	scaffold pr	9/2529	70/23049	0.360055	0.601549	0.579731	Atp2b4/Ca
GO_MF_m	GO:000375	peptidyl-p	5/2529	36/23049	0.360567	0.601549	0.579731	Fkbp11/Fk
GO_MF_m	GO:001921	phosphata	5/2529	36/23049	0.360567	0.601549	0.579731	2810408A
GO_MF_m	GO:007088	E-box bin	5/2529	36/23049	0.360567	0.601549	0.579731	Arntl/Cloc
GO_MF_m	GO:000453	deoxyribo	8/2529	62/23049	0.369941	0.601549	0.579731	Aplf/Aptx/
GO_MF_m	GO:000070	mismatch	1/2529	4/23049	0.371816	0.601549	0.579731	Pcna
GO_MF_m	GO:000099	transcripti	1/2529	4/23049	0.371816	0.601549	0.579731	Gtf3c3
GO_MF_m	GO:000103	RNA polym	1/2529	4/23049	0.371816	0.601549	0.579731	Maf1
GO_MF_m	GO:000109	TFIIB-class	1/2529	4/23049	0.371816	0.601549	0.579731	Tbp
GO_MF_m	GO:000185	compleme	1/2529	4/23049	0.371816	0.601549	0.579731	Itgam
GO_MF_m	GO:000187	lipopolysa	1/2529	4/23049	0.371816	0.601549	0.579731	Scarb1
GO_MF_m	GO:000206	purine nuc	1/2529	4/23049	0.371816	0.601549	0.579731	Aprt
GO_MF_m	GO:000384	2-acylglyc	1/2529	4/23049	0.371816	0.601549	0.579731	Dgat1
GO_MF_m	GO:000387	6-phosph	1/2529	4/23049	0.371816	0.601549	0.579731	Pfkfb1
GO_MF_m	GO:000394	N-acetylla	1/2529	4/23049	0.371816	0.601549	0.579731	B4galt3
GO_MF_m	GO:000395	NAD+ nuc	1/2529	4/23049	0.371816	0.601549	0.579731	Art5
GO_MF_m	GO:000405	arachidona	1/2529	4/23049	0.371816	0.601549	0.579731	Alox12
GO_MF_m	GO:000406	arylamine	1/2529	4/23049	0.371816	0.601549	0.579731	Nat2
GO_MF_m	GO:000406	aryl sulfotr	1/2529	4/23049	0.371816	0.601549	0.579731	Sult1a1
GO_MF_m	GO:000406	arylsulfatas	1/2529	4/23049	0.371816	0.601549	0.579731	Arsb
GO_MF_m	GO:000409	carnitine O	1/2529	4/23049	0.371816	0.601549	0.579731	Cpt2
GO_MF_m	GO:000414	diacylglyce	1/2529	4/23049	0.371816	0.601549	0.579731	Dgat1
GO_MF_m	GO:000437	glycerol ki	1/2529	4/23049	0.371816	0.601549	0.579731	Gk2
GO_MF_m	GO:000442	inorganic c	1/2529	4/23049	0.371816	0.601549	0.579731	Prune1
GO_MF_m	GO:000444	isocitrate d	1/2529	4/23049	0.371816	0.601549	0.579731	Idh3a
GO_MF_m	GO:000445	L-lactate d	1/2529	4/23049	0.371816	0.601549	0.579731	Ldha
GO_MF_m	GO:000446	leukotrien	1/2529	4/23049	0.371816	0.601549	0.579731	Ltc4s
GO_MF_m	GO:000446	long-chain	1/2529	4/23049	0.371816	0.601549	0.579731	Acad11
GO_MF_m	GO:000447	methenylt	1/2529	4/23049	0.371816	0.601549	0.579731	Mthfd1l
GO_MF_m	GO:000448	methylene	1/2529	4/23049	0.371816	0.601549	0.579731	Mthfd1l
GO_MF_m	GO:000459	oxoglutara	1/2529	4/23049	0.371816	0.601549	0.579731	Ogdhl
GO_MF_m	GO:000465	procollage	1/2529	4/23049	0.371816	0.601549	0.579731	P4ha3
GO_MF_m	GO:000466	protein ge	1/2529	4/23049	0.371816	0.601549	0.579731	Fnta
GO_MF_m	GO:000468	myosin lig	1/2529	4/23049	0.371816	0.601549	0.579731	Mylk2

GO_MF_m	GO:000469	cAMP-dep	1/2529	4/23049	0.371816	0.601549	0.579731	Prkacb
GO_MF_m	GO:000470	NF-kappaB	1/2529	4/23049	0.371816	0.601549	0.579731	Ripk3
GO_MF_m	GO:000474	ribose pho	1/2529	4/23049	0.371816	0.601549	0.579731	Prpsap2
GO_MF_m	GO:000481	arginine-tR	1/2529	4/23049	0.371816	0.601549	0.579731	Rars2
GO_MF_m	GO:000484	uracil DNA	1/2529	4/23049	0.371816	0.601549	0.579731	Ung
GO_MF_m	GO:000489	ciliary neur	1/2529	4/23049	0.371816	0.601549	0.579731	Cntfr
GO_MF_m	GO:000496	histamine r	1/2529	4/23049	0.371816	0.601549	0.579731	Hrh3
GO_MF_m	GO:000497	AMPA glut	1/2529	4/23049	0.371816	0.601549	0.579731	Gria1
GO_MF_m	GO:000504	netrin rece	1/2529	4/23049	0.371816	0.601549	0.579731	Unc5c
GO_MF_m	GO:000508	Ran guanyl	1/2529	4/23049	0.371816	0.601549	0.579731	Sergef
GO_MF_m	GO:000512	scavenger	1/2529	4/23049	0.371816	0.601549	0.579731	Fpr2
GO_MF_m	GO:000525	A-type (tra	1/2529	4/23049	0.371816	0.601549	0.579731	Kcnd2
GO_MF_m	GO:000527	amine tran	1/2529	4/23049	0.371816	0.601549	0.579731	Slc18a2
GO_MF_m	GO:000812	acetylester	1/2529	4/23049	0.371816	0.601549	0.579731	Siae
GO_MF_m	GO:000831	single-stra	1/2529	4/23049	0.371816	0.601549	0.579731	Pole
GO_MF_m	GO:000900	DNA-meth	1/2529	4/23049	0.371816	0.601549	0.579731	Mettl4
GO_MF_m	GO:000901	tRNA (guar	1/2529	4/23049	0.371816	0.601549	0.579731	Trmt10a
GO_MF_m	GO:001048	H3 histone	1/2529	4/23049	0.371816	0.601549	0.579731	Kat2a
GO_MF_m	GO:001518	L-aspartate	1/2529	4/23049	0.371816	0.601549	0.579731	Slc38a7
GO_MF_m	GO:001518	L-glutamin	1/2529	4/23049	0.371816	0.601549	0.579731	Slc38a7
GO_MF_m	GO:001630	tRNA (urac	1/2529	4/23049	0.371816	0.601549	0.579731	6430573F1
GO_MF_m	GO:001641	O-palmitoy	1/2529	4/23049	0.371816	0.601549	0.579731	Cpt2
GO_MF_m	GO:001711	single-stra	1/2529	4/23049	0.371816	0.601549	0.579731	Helq
GO_MF_m	GO:001976	IgE recepto	1/2529	4/23049	0.371816	0.601549	0.579731	Ms4a2
GO_MF_m	GO:002302	MHC class	1/2529	4/23049	0.371816	0.601549	0.579731	Fam49b
GO_MF_m	GO:003022	very-low-c	1/2529	4/23049	0.371816	0.601549	0.579731	Vldlr
GO_MF_m	GO:003029	transmemb	1/2529	4/23049	0.371816	0.601549	0.579731	Dgkq
GO_MF_m	GO:003094	mitochond	1/2529	4/23049	0.371816	0.601549	0.579731	Timm22
GO_MF_m	GO:003098	kininogen l	1/2529	4/23049	0.371816	0.601549	0.579731	Ctsl
GO_MF_m	GO:003172	haptoglobi	1/2529	4/23049	0.371816	0.601549	0.579731	Hbb-bs
GO_MF_m	GO:003172	hemoglobi	1/2529	4/23049	0.371816	0.601549	0.579731	Hbb-bs
GO_MF_m	GO:003213	single base	1/2529	4/23049	0.371816	0.601549	0.579731	Msh3
GO_MF_m	GO:003242	purine-rich	1/2529	4/23049	0.371816	0.601549	0.579731	Purg
GO_MF_m	GO:003289	palmitoyl-(	1/2529	4/23049	0.371816	0.601549	0.579731	Scd4
GO_MF_m	GO:003330	dehydroas	1/2529	4/23049	0.371816	0.601549	0.579731	Slc2a1
GO_MF_m	GO:003418	apolipopro	1/2529	4/23049	0.371816	0.601549	0.579731	Scarb1
GO_MF_m	GO:003423	GPI anchor	1/2529	4/23049	0.371816	0.601549	0.579731	Pigu
GO_MF_m	GO:003459	phosphatic	1/2529	4/23049	0.371816	0.601549	0.579731	Tmem55a
GO_MF_m	GO:003524	protein-arg	1/2529	4/23049	0.371816	0.601549	0.579731	Ndufaf7
GO_MF_m	GO:003527	ethanol bir	1/2529	4/23049	0.371816	0.601549	0.579731	Adh1
GO_MF_m	GO:003565	AP-1 adap	1/2529	4/23049	0.371816	0.601549	0.579731	Rab32
GO_MF_m	GO:003810	nodal bind	1/2529	4/23049	0.371816	0.601549	0.579731	Cfc1
GO_MF_m	GO:004353	angiostatin	1/2529	4/23049	0.371816	0.601549	0.579731	Atp5a1
GO_MF_m	GO:004723	glucuronos	1/2529	4/23049	0.371816	0.601549	0.579731	Csgalnact1
GO_MF_m	GO:005050	hyaluronar	1/2529	4/23049	0.371816	0.601549	0.579731	Has2
GO_MF_m	GO:005173	polynucleo	1/2529	4/23049	0.371816	0.601549	0.579731	N4bp2
GO_MF_m	GO:005265	NADP-retir	1/2529	4/23049	0.371816	0.601549	0.579731	Akr1b10
GO_MF_m	GO:005505	D-glucose	1/2529	4/23049	0.371816	0.601549	0.579731	Slc2a1

GO_MF_m	GO:006182	telomeric D	1/2529	4/23049	0.371816	0.601549	0.579731	Blm
GO_MF_m	GO:007001	oligopeptic	1/2529	4/23049	0.371816	0.601549	0.579731	Nln
GO_MF_m	GO:007005	collagen V	1/2529	4/23049	0.371816	0.601549	0.579731	2300002M
GO_MF_m	GO:007005	thrombosp	1/2529	4/23049	0.371816	0.601549	0.579731	Cd36
GO_MF_m	GO:007013	ubiquitin-li	1/2529	4/23049	0.371816	0.601549	0.579731	Senp1
GO_MF_m	GO:007013	SUMO-spe	1/2529	4/23049	0.371816	0.601549	0.579731	Senp1
GO_MF_m	GO:007032	very-low-c	1/2529	4/23049	0.371816	0.601549	0.579731	Pcsk9
GO_MF_m	GO:007040	NADH binc	1/2529	4/23049	0.371816	0.601549	0.579731	Rnls
GO_MF_m	GO:007054	L-phenylal	1/2529	4/23049	0.371816	0.601549	0.579731	Got1
GO_MF_m	GO:008607	gap junctic	1/2529	4/23049	0.371816	0.601549	0.579731	Gjc1
GO_MF_m	GO:009055	phosphatic	1/2529	4/23049	0.371816	0.601549	0.579731	Abcb1a
GO_MF_m	GO:009750	deaminate	1/2529	4/23049	0.371816	0.601549	0.579731	Ung
GO_MF_m	GO:009764	amylin rece	1/2529	4/23049	0.371816	0.601549	0.579731	Calcr
GO_MF_m	GO:009764	calcitonin f	1/2529	4/23049	0.371816	0.601549	0.579731	Calcr
GO_MF_m	GO:009851	polynucleo	1/2529	4/23049	0.371816	0.601549	0.579731	Aptx
GO_MF_m	GO:009910	channel ac	1/2529	4/23049	0.371816	0.601549	0.579731	Lrrc26
GO_MF_m	GO:009910	potassium	1/2529	4/23049	0.371816	0.601549	0.579731	Lrrc26
GO_MF_m	GO:014013	mechanose	1/2529	4/23049	0.371816	0.601549	0.579731	Trpv4
GO_MF_m	GO:199059	3' overhan	1/2529	4/23049	0.371816	0.601549	0.579731	Xrcc1
GO_MF_m	GO:00438	guanylate	3/2529	20/23049	0.378653	0.611692	0.589507	Adcy4/Guc
GO_MF_m	GO:003423	protein kin	3/2529	20/23049	0.378653	0.611692	0.589507	Akap14/Ak
GO_MF_m	GO:000484	ubiquitin-p	51/2529	443/23049	0.379028	0.611839	0.589648	Arih2/Asb1
GO_MF_m	GO:000550	copper ion	7/2529	54/23049	0.380717	0.613024	0.590791	Aoc1/Aoc3
GO_MF_m	GO:000484	thiol-depe	10/2529	80/23049	0.381366	0.613024	0.590791	Eif3f/Mindy
GO_MF_m	GO:001517	amino acid	10/2529	80/23049	0.381366	0.613024	0.590791	AU018091/
GO_MF_m	GO:001640	palmitoyltr	5/2529	37/23049	0.383306	0.613024	0.590791	Cpt2/Sptlc2
GO_MF_m	GO:003136	translation	5/2529	37/23049	0.383306	0.613024	0.590791	Eif3f/Eif4e/
GO_MF_m	GO:000029	adenine nu	2/2529	12/23049	0.385452	0.613024	0.590791	Slc25a23/S
GO_MF_m	GO:001055	RNA polym	2/2529	12/23049	0.385452	0.613024	0.590791	Polr2f/Polr
GO_MF_m	GO:001600	G-protein	2/2529	12/23049	0.385452	0.613024	0.590791	P2ry1/P2ry
GO_MF_m	GO:00534	purine ribo	2/2529	12/23049	0.385452	0.613024	0.590791	Slc25a23/S
GO_MF_m	GO:00545	monovalen	2/2529	12/23049	0.385452	0.613024	0.590791	Slc9a1/Slc9
GO_MF_m	GO:00553	glucose bir	2/2529	12/23049	0.385452	0.613024	0.590791	Gys1/Ugp2
GO_MF_m	GO:001521	purine nuc	2/2529	12/23049	0.385452	0.613024	0.590791	Slc25a23/S
GO_MF_m	GO:001650	peptidase	2/2529	12/23049	0.385452	0.613024	0.590791	Pycard/Tnf
GO_MF_m	GO:001701	MAP kinase	2/2529	12/23049	0.385452	0.613024	0.590791	Dusp5/Dus
GO_MF_m	GO:003054	receptor ac	2/2529	12/23049	0.385452	0.613024	0.590791	Cdk5/Dgkc
GO_MF_m	GO:003173	CCR6 chem	2/2529	12/23049	0.385452	0.613024	0.590791	Ccl20/Defb
GO_MF_m	GO:004502	G-protein	2/2529	12/23049	0.385452	0.613024	0.590791	P2ry1/P2ry
GO_MF_m	GO:007234	modified a	2/2529	12/23049	0.385452	0.613024	0.590791	Folr2/Slc46
GO_MF_m	GO:014016	monocarbo	2/2529	12/23049	0.385452	0.613024	0.590791	Slc10a4/Slc
GO_MF_m	GO:199038	Lys48-spec	2/2529	12/23049	0.385452	0.613024	0.590791	Mindy2/Us
GO_MF_m	GO:199084	promoter-	6/2529	46/23049	0.392618	0.623961	0.601331	Foxc1/Hda
GO_MF_m	GO:000440	histone dea	4/2529	29/23049	0.395661	0.626949	0.60421	Hdac1/Hda
GO_MF_m	GO:000462	phospholip	4/2529	29/23049	0.395661	0.626949	0.60421	Abhd1/Pla2
GO_MF_m	GO:007071	poly-purin	4/2529	29/23049	0.395661	0.626949	0.60421	Fmr1/Pabp
GO_MF_m	GO:007250	divalent inc	4/2529	29/23049	0.395661	0.626949	0.60421	Slc30a3/Slc
GO_MF_m	GO:00082	exopeptida	12/2529	99/23049	0.403145	0.638338	0.615187	Apeh/Blmh

GO_MF_m	GO:00051	frizzled bin	5/2529	38/23049	0.406005	0.640983	0.617736	Cthrc1/Wn
GO_MF_m	GO:00083	arachidoni	5/2529	38/23049	0.406005	0.640983	0.617736	Cyp2b10/C
GO_MF_m	GO:00166	oxidoreduc	5/2529	38/23049	0.406005	0.640983	0.617736	Cbr4/Nduf
GO_MF_m	GO:00168	cis-trans is	5/2529	38/23049	0.406005	0.640983	0.617736	Fkbp11/Fk
GO_MF_m	GO:000401	phospholip	3/2529	21/23049	0.409649	0.645261	0.621859	Abcb1a/At
GO_MF_m	GO:000401	adenylate	3/2529	21/23049	0.409649	0.645261	0.621859	Adcy4/Guc
GO_MF_m	GO:00164	C-acyltran	3/2529	21/23049	0.409649	0.645261	0.621859	Acsm5/Spt
GO_MF_m	GO:00081	translation	10/2529	82/23049	0.412034	0.645261	0.621859	Abtb1/Cpe
GO_MF_m	GO:000524	voltage-ga	11/2529	91/23049	0.414767	0.645261	0.621859	Cnga2/Kcn
GO_MF_m	GO:000554	phospholip	7/2529	56/23049	0.418107	0.645261	0.621859	Abcb1a/At
GO_MF_m	GO:00197	ubiquitin-li	13/2529	109/23049	0.418987	0.645261	0.621859	Eif3f/Mind
GO_MF_m	GO:00019	fibronectin	4/2529	30/23049	0.421478	0.645261	0.621859	2300002M
GO_MF_m	GO:00039	NADH deh	4/2529	30/23049	0.421478	0.645261	0.621859	Ndufa12/N
GO_MF_m	GO:00335	protein de	4/2529	30/23049	0.421478	0.645261	0.621859	Hdac1/Hd
GO_MF_m	GO:00515	iron-sulfur	8/2529	65/23049	0.421959	0.645261	0.621859	Abat/Dpyd
GO_MF_m	GO:005154	metal clust	8/2529	65/23049	0.421959	0.645261	0.621859	Abat/Dpyd
GO_MF_m	GO:01400	modificatio	15/2529	127/23049	0.422064	0.645261	0.621859	Babam2/M
GO_MF_m	GO:00430	estradiol 1	2/2529	13/23049	0.425694	0.645261	0.621859	Hsd17b3/H
GO_MF_m	GO:00053	nucleotide-	2/2529	13/23049	0.425694	0.645261	0.621859	Slc35a5/Sl
GO_MF_m	GO:000552	tropomyos	2/2529	13/23049	0.425694	0.645261	0.621859	Pycard/Tm
GO_MF_m	GO:000554	folic acid b	2/2529	13/23049	0.425694	0.645261	0.621859	Folr2/Slc46
GO_MF_m	GO:00081	phosphatic	2/2529	13/23049	0.425694	0.645261	0.621859	Lpin3/Plpp
GO_MF_m	GO:00083	DNA bindi	2/2529	13/23049	0.425694	0.645261	0.621859	Foxc1/Sry
GO_MF_m	GO:00084	sulfuric est	2/2529	13/23049	0.425694	0.645261	0.621859	Arsb/Galns
GO_MF_m	GO:00099	pseudouric	2/2529	13/23049	0.425694	0.645261	0.621859	Rpusd1/Tr
GO_MF_m	GO:00101	FMN bindi	2/2529	13/23049	0.425694	0.645261	0.621859	Mtrr/Por
GO_MF_m	GO:001642	tRNA (gua	2/2529	13/23049	0.425694	0.645261	0.621859	Trmt1/Trm
GO_MF_m	GO:001984	retinol binc	2/2529	13/23049	0.425694	0.645261	0.621859	Crabp1/Rb
GO_MF_m	GO:00319	insulin-like	2/2529	13/23049	0.425694	0.645261	0.621859	Igfbp3/Itga
GO_MF_m	GO:00452	alpha-cate	2/2529	13/23049	0.425694	0.645261	0.621859	Cdh1/Cdh
GO_MF_m	GO:007074	C2H2 zinc	2/2529	13/23049	0.425694	0.645261	0.621859	Taf9/Wt1
GO_MF_m	GO:007161	lysophosph	2/2529	13/23049	0.425694	0.645261	0.621859	Agpat2/Lp
GO_MF_m	GO:009761	annealing	2/2529	13/23049	0.425694	0.645261	0.621859	Blm/Fmr1
GO_MF_m	GO:00012	transcriptic	5/2529	39/23049	0.428592	0.645261	0.621859	Esrrb/Foxa
GO_MF_m	GO:00041	carboxype	5/2529	39/23049	0.428592	0.645261	0.621859	Cpm/Cpvl/
GO_MF_m	GO:00441	protein bin	5/2529	39/23049	0.428592	0.645261	0.621859	Cct3/Dffa/
GO_MF_m	GO:005187	Hsp90 prot	5/2529	39/23049	0.428592	0.645261	0.621859	Arntl/Fkbp
GO_MF_m	GO:009952	neurotrans	5/2529	39/23049	0.428592	0.645261	0.621859	Chrne/Chr
GO_MF_m	GO:00044	monooxyg	17/2529	146/23049	0.435949	0.645261	0.621859	Akr1c12/C
GO_MF_m	GO:00009	transcriptic	3/2529	22/23049	0.440149	0.645261	0.621859	Dach1/Taf
GO_MF_m	GO:00053	zinc ion tra	3/2529	22/23049	0.440149	0.645261	0.621859	Slc30a3/Sl
GO_MF_m	GO:001512	bile acid tr	3/2529	22/23049	0.440149	0.645261	0.621859	Abcc3/Slc1
GO_MF_m	GO:00192	carbohydr	3/2529	22/23049	0.440149	0.645261	0.621859	Adk/Pfkfb1
GO_MF_m	GO:009007	translation	3/2529	22/23049	0.440149	0.645261	0.621859	Cpeb3/Cp
GO_MF_m	GO:00904	vitamin tra	3/2529	22/23049	0.440149	0.645261	0.621859	Folr2/Slc2a
GO_MF_m	GO:00000	sulfur amin	1/2529	5/23049	0.440754	0.645261	0.621859	Slc38a7
GO_MF_m	GO:00002	peroxisom	1/2529	5/23049	0.440754	0.645261	0.621859	Pex5
GO_MF_m	GO:00010	RNA polym	1/2529	5/23049	0.440754	0.645261	0.621859	Maf1

GO_MF_m	GO:000103	RNA polym	1/2529	5/23049	0.440754	0.645261	0.621859	Maf1
GO_MF_m	GO:000108	transcripti	1/2529	5/23049	0.440754	0.645261	0.621859	Tbp
GO_MF_m	GO:000122	RNA polym	1/2529	5/23049	0.440754	0.645261	0.621859	Hdac2
GO_MF_m	GO:000153	N-acetylga	1/2529	5/23049	0.440754	0.645261	0.621859	Chst13
GO_MF_m	GO:000382	alpha-N-a	1/2529	5/23049	0.440754	0.645261	0.621859	St8sia3
GO_MF_m	GO:000383	beta-N-ac	1/2529	5/23049	0.440754	0.645261	0.621859	B4galt3
GO_MF_m	GO:000399	acyl-CoA li	1/2529	5/23049	0.440754	0.645261	0.621859	Acsm5
GO_MF_m	GO:000404	aminoacyl-	1/2529	5/23049	0.440754	0.645261	0.621859	Ptrh2
GO_MF_m	GO:000430	exopolyph	1/2529	5/23049	0.440754	0.645261	0.621859	Prune1
GO_MF_m	GO:000431	farnesyltra	1/2529	5/23049	0.440754	0.645261	0.621859	Fdft1
GO_MF_m	GO:000436	glycerol-3-	1/2529	5/23049	0.440754	0.645261	0.621859	Gpam
GO_MF_m	GO:000461	phosphogl	1/2529	5/23049	0.440754	0.645261	0.621859	Pgm3
GO_MF_m	GO:000463	phosphopy	1/2529	5/23049	0.440754	0.645261	0.621859	Eno3
GO_MF_m	GO:000468	phosphory	1/2529	5/23049	0.440754	0.645261	0.621859	Phkb
GO_MF_m	GO:000470	JUN kinase	1/2529	5/23049	0.440754	0.645261	0.621859	Map3k10
GO_MF_m	GO:000472	non-memb	1/2529	5/23049	0.440754	0.645261	0.621859	Ptpn4
GO_MF_m	GO:000476	steroid del	1/2529	5/23049	0.440754	0.645261	0.621859	Hsd3b3
GO_MF_m	GO:000478	superoxide	1/2529	5/23049	0.440754	0.645261	0.621859	Nqo1
GO_MF_m	GO:000482	phenylalan	1/2529	5/23049	0.440754	0.645261	0.621859	Lrrc47
GO_MF_m	GO:000511	type 2 fibr	1/2529	5/23049	0.440754	0.645261	0.621859	Fgf7
GO_MF_m	GO:000514	interleukin-	1/2529	5/23049	0.440754	0.645261	0.621859	Il12b
GO_MF_m	GO:000833	low voltag	1/2529	5/23049	0.440754	0.645261	0.621859	Catsper3
GO_MF_m	GO:000837	thioredoxi	1/2529	5/23049	0.440754	0.645261	0.621859	Prdx1
GO_MF_m	GO:000937	four-way ju	1/2529	5/23049	0.440754	0.645261	0.621859	Blm
GO_MF_m	GO:001099	anaphase-	1/2529	5/23049	0.440754	0.645261	0.621859	Cdc20
GO_MF_m	GO:001520	urea transp	1/2529	5/23049	0.440754	0.645261	0.621859	Slc14a2
GO_MF_m	GO:001537	anion:sodi	1/2529	5/23049	0.440754	0.645261	0.621859	Slc12a2
GO_MF_m	GO:001561	DNA transl	1/2529	5/23049	0.440754	0.645261	0.621859	Fbxo18
GO_MF_m	GO:001617	NAD(P)H o	1/2529	5/23049	0.440754	0.645261	0.621859	Aifm1
GO_MF_m	GO:001631	inositol bis	1/2529	5/23049	0.440754	0.645261	0.621859	Bpnt1
GO_MF_m	GO:001672	oxidoreduc	1/2529	5/23049	0.440754	0.645261	0.621859	Nqo1
GO_MF_m	GO:001677	diphospho	1/2529	5/23049	0.440754	0.645261	0.621859	Prpsap2
GO_MF_m	GO:001683	oxo-acid-l	1/2529	5/23049	0.440754	0.645261	0.621859	Clybl
GO_MF_m	GO:001710	5'-flap end	1/2529	5/23049	0.440754	0.645261	0.621859	Fen1
GO_MF_m	GO:001881	3-hydroxya	1/2529	5/23049	0.440754	0.645261	0.621859	Hsd17b4
GO_MF_m	GO:002284	glutamate-	1/2529	5/23049	0.440754	0.645261	0.621859	Grin2b
GO_MF_m	GO:003029	protein tyr	1/2529	5/23049	0.440754	0.645261	0.621859	Hyal2
GO_MF_m	GO:003062	U4 snRNA	1/2529	5/23049	0.440754	0.645261	0.621859	Prpf4
GO_MF_m	GO:003184	olfactory re	1/2529	5/23049	0.440754	0.645261	0.621859	Reep1
GO_MF_m	GO:003240	MutSalpha	1/2529	5/23049	0.440754	0.645261	0.621859	Atr
GO_MF_m	GO:003255	pyrimidine	1/2529	5/23049	0.440754	0.645261	0.621859	Ugp2
GO_MF_m	GO:003359	RNA strand	1/2529	5/23049	0.440754	0.645261	0.621859	Fmr1
GO_MF_m	GO:003404	lipid-transp	1/2529	5/23049	0.440754	0.645261	0.621859	Abcc3
GO_MF_m	GO:003448	chondroiti	1/2529	5/23049	0.440754	0.645261	0.621859	Chst13
GO_MF_m	GO:003451	box H/ACA	1/2529	5/23049	0.440754	0.645261	0.621859	Nop10
GO_MF_m	GO:004693	phosphati	1/2529	5/23049	0.440754	0.645261	0.621859	Pik3r6
GO_MF_m	GO:004824	CXCR3 che	1/2529	5/23049	0.440754	0.645261	0.621859	Cxcl10
GO_MF_m	GO:005005	leukotrien	1/2529	5/23049	0.440754	0.645261	0.621859	Cyp4f14

GO_MF_m	GO:005102	Rho GDP-	1/2529	5/23049	0.440754	0.645261	0.621859	Plxnb3
GO_MF_m	GO:005281	phosphatic	1/2529	5/23049	0.440754	0.645261	0.621859	Pik3r6
GO_MF_m	GO:005513	C3HC4-typ	1/2529	5/23049	0.440754	0.645261	0.621859	Hspa1a
GO_MF_m	GO:007006	fructose bi	1/2529	5/23049	0.440754	0.645261	0.621859	Pfkl
GO_MF_m	GO:007008	chromo sh	1/2529	5/23049	0.440754	0.645261	0.621859	Lbr
GO_MF_m	GO:007012	isopeptidas	1/2529	5/23049	0.440754	0.645261	0.621859	Senp1
GO_MF_m	GO:007073	protein-glu	1/2529	5/23049	0.440754	0.645261	0.621859	Tpgs1
GO_MF_m	GO:007107	eukaryotic	1/2529	5/23049	0.440754	0.645261	0.621859	Myc
GO_MF_m	GO:007155	histone de	1/2529	5/23049	0.440754	0.645261	0.621859	Kdm6b
GO_MF_m	GO:008008	5S rDNA bi	1/2529	5/23049	0.440754	0.645261	0.621859	Maf1
GO_MF_m	GO:008600	voltage-ga	1/2529	5/23049	0.440754	0.645261	0.621859	Cacnb2
GO_MF_m	GO:009072	receptor-r	1/2529	5/23049	0.440754	0.645261	0.621859	Htr1a
GO_MF_m	GO:009719	cysteine-ty	1/2529	5/23049	0.440754	0.645261	0.621859	Casp8
GO_MF_m	GO:009851	nucleotide	1/2529	5/23049	0.440754	0.645261	0.621859	Ntpcr
GO_MF_m	GO:190376	gap junctic	1/2529	5/23049	0.440754	0.645261	0.621859	Gjc1
GO_MF_m	GO:001678	transferase	9/2529	75/23049	0.441196	0.645471	0.622061	Chst13/Dse
GO_MF_m	GO:004419	cysteine-ty	10/2529	84/23049	0.442707	0.646802	0.623343	Blmh/Capn
GO_MF_m	GO:009910	ion channe	10/2529	84/23049	0.442707	0.646802	0.623343	Cacnb2/Ca
GO_MF_m	GO:003369	single-stra	12/2529	102/23049	0.444866	0.649516	0.62596	Aptx/Blm/E
GO_MF_m	GO:004000	ATP-deper	4/2529	31/23049	0.447017	0.650014	0.626439	Blm/Fbxo1
GO_MF_m	GO:000513	type I inter	4/2529	31/23049	0.447017	0.650014	0.626439	Gm13271/
GO_MF_m	GO:001714	Wnt-prote	4/2529	31/23049	0.447017	0.650014	0.626439	Cthrc1/Lrp
GO_MF_m	GO:003050	spectrin bi	4/2529	31/23049	0.447017	0.650014	0.626439	Epb41/Gnb
GO_MF_m	GO:004342	bHLH trans	4/2529	31/23049	0.447017	0.650014	0.626439	Arntl/Lmo2
GO_MF_m	GO:004687	ephrin rece	4/2529	31/23049	0.447017	0.650014	0.626439	Cdk5/Chn1
GO_MF_m	GO:001978	ubiquitin-li	52/2529	463/23049	0.450878	0.654482	0.630745	Arih2/Asb1
GO_MF_m	GO:001921	deacetylase	5/2529	40/23049	0.451	0.654482	0.630745	Hdac1/Hda
GO_MF_m	GO:003245	demethylas	5/2529	40/23049	0.451	0.654482	0.630745	Cyp3a11/K
GO_MF_m	GO:001670	oxidoreduc	6/2529	49/23049	0.453553	0.657744	0.633889	Akr1c12/Cy
GO_MF_m	GO:003700	steroid hor	7/2529	58/23049	0.455286	0.659812	0.635882	Esrrb/Nr1h
GO_MF_m	GO:000801	beta-caten	10/2529	85/23049	0.457989	0.663283	0.639227	Ash2l/Cdh1
GO_MF_m	GO:000104	core prom	18/2529	157/23049	0.459008	0.663582	0.639515	Ifi207/Arnt
GO_MF_m	GO:000202	protease b	17/2529	148/23049	0.459083	0.663582	0.639515	Anxa2/Cst6
GO_MF_m	GO:000377	motor acti	15/2529	130/23049	0.459118	0.663582	0.639515	Cgn/Dnah1
GO_MF_m	GO:000033	RNA cap b	2/2529	14/23049	0.464508	0.664684	0.640577	Eif4e/Fmr1
GO_MF_m	GO:000197	retinoic aci	2/2529	14/23049	0.464508	0.664684	0.640577	Crabp1/Igf
GO_MF_m	GO:000531	L-glutamat	2/2529	14/23049	0.464508	0.664684	0.640577	Slc1a7/Slc3
GO_MF_m	GO:000832	protein tra	2/2529	14/23049	0.464508	0.664684	0.640577	Timm17b/
GO_MF_m	GO:000832	signaling p	2/2529	14/23049	0.464508	0.664684	0.640577	Cd36/Scarb
GO_MF_m	GO:001535	secondary	2/2529	14/23049	0.464508	0.664684	0.640577	Slc10a4/Slc
GO_MF_m	GO:003313	acetylcholi	2/2529	14/23049	0.464508	0.664684	0.640577	Ly6e/Rapsn
GO_MF_m	GO:003818	pattern rec	2/2529	14/23049	0.464508	0.664684	0.640577	Cd36/Scarb
GO_MF_m	GO:004204	neurexin fa	2/2529	14/23049	0.464508	0.664684	0.640577	Nlgn3/Sytl3
GO_MF_m	GO:004313	3'-5' DNA	2/2529	14/23049	0.464508	0.664684	0.640577	Blm/Fbxo1
GO_MF_m	GO:004512	bioactive li	2/2529	14/23049	0.464508	0.664684	0.640577	Gpr174/S1
GO_MF_m	GO:004523	CXCR chen	2/2529	14/23049	0.464508	0.664684	0.640577	Cxcl10/Ppb
GO_MF_m	GO:004801	receptor ar	2/2529	14/23049	0.464508	0.664684	0.640577	Il18bp/Il1rn
GO_MF_m	GO:007040	NAD+ binc	2/2529	14/23049	0.464508	0.664684	0.640577	Aldh1a3/Si

GO_MF_m	GO:00707	BMP recep	2/2529	14/23049	0.464508	0.664684	0.640577	Bmp3/Pyca
GO_MF_m	GO:000417	endopeptic	49/2529	438/23049	0.465186	0.665213	0.641087	Adam2/Ad
GO_MF_m	GO:001687	ligase activ	20/2529	176/23049	0.469392	0.669017	0.644753	Acsl1/Acsm
GO_MF_m	GO:00151	organic cat	3/2529	23/23049	0.470019	0.669017	0.644753	Slc22a1/Slc
GO_MF_m	GO:00164	CoA-ligase	3/2529	23/23049	0.470019	0.669017	0.644753	Acsl1/Acsm
GO_MF_m	GO:001692	ligand-dep	3/2529	23/23049	0.470019	0.669017	0.644753	Ppargc1a/
GO_MF_m	GO:00314	nucleosom	3/2529	23/23049	0.470019	0.669017	0.644753	Cenpa/H2a
GO_MF_m	GO:004761	acyl-CoA h	3/2529	23/23049	0.470019	0.669017	0.644753	Acot1/Aco
GO_MF_m	GO:00718	HMG box	3/2529	23/23049	0.470019	0.669017	0.644753	Hoxa3/Pax
GO_MF_m	GO:00168	endonucle	4/2529	32/23049	0.47219	0.67062	0.646298	Elac1/Fen1
GO_MF_m	GO:00447	ATPase act	4/2529	32/23049	0.47219	0.67062	0.646298	Atp5a1/At
GO_MF_m	GO:00364	thiol-depe	11/2529	95/23049	0.472902	0.67062	0.646298	Eif3f/Mindy
GO_MF_m	GO:01010	ubiquitinyl	11/2529	95/23049	0.472902	0.67062	0.646298	Eif3f/Mindy
GO_MF_m	GO:00989	postsynapt	5/2529	41/23049	0.473166	0.67062	0.646298	Chrne/Chr
GO_MF_m	GO:00052	anion chan	10/2529	86/23049	0.473205	0.67062	0.646298	Ano1/Ano
GO_MF_m	GO:001687	ligase activ	6/2529	50/23049	0.473584	0.67062	0.646298	Adss/Gclm
GO_MF_m	GO:00302	protein kin	8/2529	68/23049	0.473635	0.67062	0.646298	Abi1/Cdkn
GO_MF_m	GO:00228	active trans	42/2529	376/23049	0.475451	0.672749	0.648349	Abca12/Ab
GO_MF_m	GO:000531	lipid transp	14/2529	123/23049	0.484537	0.674619	0.650151	Abca12/Ab
GO_MF_m	GO:00085	protein tra	9/2529	78/23049	0.489444	0.674619	0.650151	Calcr/Ipo1
GO_MF_m	GO:000554	calcium-de	6/2529	51/23049	0.493399	0.674619	0.650151	Anxa2/Anx
GO_MF_m	GO:003014	manganes	6/2529	51/23049	0.493399	0.674619	0.650151	Abl2/Abo/
GO_MF_m	GO:00422	MHC prote	4/2529	33/23049	0.49692	0.674619	0.650151	Atp5a1/Bc
GO_MF_m	GO:00513	alpha-acti	4/2529	33/23049	0.49692	0.674619	0.650151	Lrrc10/Myp
GO_MF_m	GO:00162	lipase activ	14/2529	124/23049	0.497195	0.674619	0.650151	Abhd1/Ad
GO_MF_m	GO:000184	compleme	3/2529	24/23049	0.499146	0.674619	0.650151	Cd93/Itgam
GO_MF_m	GO:000412	cytochrom	3/2529	24/23049	0.499146	0.674619	0.650151	Cox15/Cox
GO_MF_m	GO:000511	Notch binc	3/2529	24/23049	0.499146	0.674619	0.650151	Dll4/Jag1/
GO_MF_m	GO:00150	heme-cop	3/2529	24/23049	0.499146	0.674619	0.650151	Cox15/Cox
GO_MF_m	GO:001667	oxidoreduc	3/2529	24/23049	0.499146	0.674619	0.650151	Cox15/Cox
GO_MF_m	GO:00316	G-protein	3/2529	24/23049	0.499146	0.674619	0.650151	Adcy4/Adc
GO_MF_m	GO:00528	phosphatic	3/2529	24/23049	0.499146	0.674619	0.650151	Ptpmt1/Sy
GO_MF_m	GO:000522	intracellula	2/2529	15/23049	0.501722	0.674619	0.650151	Ano1/Ano
GO_MF_m	GO:001517	acidic amir	2/2529	15/23049	0.501722	0.674619	0.650151	Slc1a7/Slc
GO_MF_m	GO:001641	acylglycerc	2/2529	15/23049	0.501722	0.674619	0.650151	Agpat2/Dg
GO_MF_m	GO:00165	glycine bin	2/2529	15/23049	0.501722	0.674619	0.650151	Gldc/Grin2
GO_MF_m	GO:00166	oxidoreduc	2/2529	15/23049	0.501722	0.674619	0.650151	Selenot/Tx
GO_MF_m	GO:002282	potassium	2/2529	15/23049	0.501722	0.674619	0.650151	Slc9a1/Slc
GO_MF_m	GO:00301	receptor si	2/2529	15/23049	0.501722	0.674619	0.650151	Ldlrap1/Rg
GO_MF_m	GO:00342	protein kin	2/2529	15/23049	0.501722	0.674619	0.650151	Ezr/Prkar2
GO_MF_m	GO:00469	proton-tra	2/2529	15/23049	0.501722	0.674619	0.650151	Atp5a1/At
GO_MF_m	GO:00617	intracellula	2/2529	15/23049	0.501722	0.674619	0.650151	Ano1/Ano
GO_MF_m	GO:00016	alpha-N-a	1/2529	6/23049	0.502129	0.674619	0.650151	St6galnac1
GO_MF_m	GO:00039	DNA ligase	1/2529	6/23049	0.502129	0.674619	0.650151	Lig3
GO_MF_m	GO:000391	DNA ligase	1/2529	6/23049	0.502129	0.674619	0.650151	Lig3
GO_MF_m	GO:00040	alkaline ph	1/2529	6/23049	0.502129	0.674619	0.650151	Alpl
GO_MF_m	GO:000412	cytochrom	1/2529	6/23049	0.502129	0.674619	0.650151	Por
GO_MF_m	GO:00043	epoxide hy	1/2529	6/23049	0.502129	0.674619	0.650151	Ephx2

GO_MF_m	GO:000432	fatty-acyl-	1/2529	6/23049	0.502129	0.674619	0.650151	Acsm5
GO_MF_m	GO:000445	lactate deh	1/2529	6/23049	0.502129	0.674619	0.650151	Ldha
GO_MF_m	GO:000446	lysine N-ac	1/2529	6/23049	0.502129	0.674619	0.650151	Kat2b
GO_MF_m	GO:000452	phosphodi	1/2529	6/23049	0.502129	0.674619	0.650151	Enpp2
GO_MF_m	GO:000456	beta-galac	1/2529	6/23049	0.502129	0.674619	0.650151	Glb1l
GO_MF_m	GO:000469	cyclic nucle	1/2529	6/23049	0.502129	0.674619	0.650151	Prkacb
GO_MF_m	GO:000470	G-protein	1/2529	6/23049	0.502129	0.674619	0.650151	Grk4
GO_MF_m	GO:000471	ribosomal	1/2529	6/23049	0.502129	0.674619	0.650151	Rps6kb1
GO_MF_m	GO:000473	pyruvate d	1/2529	6/23049	0.502129	0.674619	0.650151	Pdhb
GO_MF_m	GO:000493	alpha-adre	1/2529	6/23049	0.502129	0.674619	0.650151	Adra1d
GO_MF_m	GO:000516	neurotroph	1/2529	6/23049	0.502129	0.674619	0.650151	Ntf5
GO_MF_m	GO:000532	long-chain	1/2529	6/23049	0.502129	0.674619	0.650151	Abcd3
GO_MF_m	GO:000532	dopamine	1/2529	6/23049	0.502129	0.674619	0.650151	Slc22a1
GO_MF_m	GO:000831	protein pre	1/2529	6/23049	0.502129	0.674619	0.650151	Fnta
GO_MF_m	GO:000860	cAMP-dep	1/2529	6/23049	0.502129	0.674619	0.650151	Prkar2b
GO_MF_m	GO:001509	ferrous iro	1/2529	6/23049	0.502129	0.674619	0.650151	Slc40a1
GO_MF_m	GO:001523	heme trans	1/2529	6/23049	0.502129	0.674619	0.650151	Slc46a1
GO_MF_m	GO:001528	porin activi	1/2529	6/23049	0.502129	0.674619	0.650151	Vdac1
GO_MF_m	GO:001545	P-P-bond-	1/2529	6/23049	0.502129	0.674619	0.650151	Timm17b
GO_MF_m	GO:001556	efflux trans	1/2529	6/23049	0.502129	0.674619	0.650151	Abcb5
GO_MF_m	GO:001661	malate deh	1/2529	6/23049	0.502129	0.674619	0.650151	Me3
GO_MF_m	GO:001980	polyamine	1/2529	6/23049	0.502129	0.674619	0.650151	Sat1
GO_MF_m	GO:001986	IgE bindin	1/2529	6/23049	0.502129	0.674619	0.650151	Ms4a2
GO_MF_m	GO:002302	MHC class	1/2529	6/23049	0.502129	0.674619	0.650151	H2-DMb2
GO_MF_m	GO:003036	interleukin-	1/2529	6/23049	0.502129	0.674619	0.650151	Il27ra
GO_MF_m	GO:003037	thyroid hor	1/2529	6/23049	0.502129	0.674619	0.650151	Sra1
GO_MF_m	GO:003174	D2 dopami	1/2529	6/23049	0.502129	0.674619	0.650151	Grin2b
GO_MF_m	GO:003180	type 5 met	1/2529	6/23049	0.502129	0.674619	0.650151	Dnm3
GO_MF_m	GO:003202	myosin ligh	1/2529	6/23049	0.502129	0.674619	0.650151	Mylk2
GO_MF_m	GO:003451	U3 snoRN	1/2529	6/23049	0.502129	0.674619	0.650151	Bms1
GO_MF_m	GO:003458	piRNA bin	1/2529	6/23049	0.502129	0.674619	0.650151	Tex19.2
GO_MF_m	GO:003460	pyruvate d	1/2529	6/23049	0.502129	0.674619	0.650151	Pdhb
GO_MF_m	GO:003460	pyruvate d	1/2529	6/23049	0.502129	0.674619	0.650151	Pdhb
GO_MF_m	GO:003547	lipase bind	1/2529	6/23049	0.502129	0.674619	0.650151	Plin5
GO_MF_m	GO:003806	collagen re	1/2529	6/23049	0.502129	0.674619	0.650151	Oscar
GO_MF_m	GO:003808	vascular en	1/2529	6/23049	0.502129	0.674619	0.650151	Pdgfra
GO_MF_m	GO:004295	lipoprotein	1/2529	6/23049	0.502129	0.674619	0.650151	Mia3
GO_MF_m	GO:004297	ornithine d	1/2529	6/23049	0.502129	0.674619	0.650151	Oaz1
GO_MF_m	GO:004351	kinetochor	1/2529	6/23049	0.502129	0.674619	0.650151	Ttk
GO_MF_m	GO:004703	testostero	1/2529	6/23049	0.502129	0.674619	0.650151	Hsd17b3
GO_MF_m	GO:004739	alkylglycer	1/2529	6/23049	0.502129	0.674619	0.650151	Enpp2
GO_MF_m	GO:004749	calcium-in	1/2529	6/23049	0.502129	0.674619	0.650151	Prdx6
GO_MF_m	GO:004770	bile-salt su	1/2529	6/23049	0.502129	0.674619	0.650151	Sult2a5
GO_MF_m	GO:004776	butyrate-C	1/2529	6/23049	0.502129	0.674619	0.650151	Acsm5
GO_MF_m	GO:004803	ubiquinone	1/2529	6/23049	0.502129	0.674619	0.650151	Coq10b
GO_MF_m	GO:005073	RS domain	1/2529	6/23049	0.502129	0.674619	0.650151	Sarnp
GO_MF_m	GO:005157	5'-deoxyrib	1/2529	6/23049	0.502129	0.674619	0.650151	Poll
GO_MF_m	GO:006162	RNA polym	1/2529	6/23049	0.502129	0.674619	0.650151	Ankrd1

GO_MF_m	GO:007018	large ribos	1/2529	6/23049	0.502129	0.674619	0.650151	Rpl23
GO_MF_m	GO:190313	cuprous io	1/2529	6/23049	0.502129	0.674619	0.650151	Snca
GO_MF_m	GO:199005	phosphatic	1/2529	6/23049	0.502129	0.674619	0.650151	Pltp
GO_MF_m	GO:000809	DNA-depe	9/2529	79/23049	0.505304	0.677616	0.65304	Blm/Cdk7/
GO_MF_m	GO:001920	phosphata	9/2529	79/23049	0.505304	0.677616	0.65304	2810408A1
GO_MF_m	GO:004633	SMAD binc	9/2529	79/23049	0.505304	0.677616	0.65304	Ankrd1/Fo
GO_MF_m	GO:000508	Rho guany	8/2529	70/23049	0.507491	0.680127	0.65546	Arhgef18/
GO_MF_m	GO:000802	protein C-	26/2529	235/23049	0.513129	0.687255	0.66233	Arl6ip5/Ca
GO_MF_m	GO:001545	potassium	5/2529	43/23049	0.516553	0.690982	0.665921	Cav1/Cav3
GO_MF_m	GO:004280	actinin binc	5/2529	43/23049	0.516553	0.690982	0.665921	Lrrc10/Myp
GO_MF_m	GO:000372	single-stra	10/2529	89/23049	0.518263	0.692839	0.667711	Ddx60/Dh
GO_MF_m	GO:000837	galactosylt	4/2529	34/23049	0.521139	0.695821	0.670584	Abo/B3gnt
GO_MF_m	GO:003503	histone ac	4/2529	34/23049	0.521139	0.695821	0.670584	Bcas3/Kans
GO_MF_m	GO:001659	amino acid	8/2529	71/23049	0.524159	0.698987	0.673636	Dpys/Gldc/
GO_MF_m	GO:004830	calcium-de	8/2529	71/23049	0.524159	0.698987	0.673636	Anxa2/Anx
GO_MF_m	GO:000167	ATPase act	3/2529	25/23049	0.527434	0.701617	0.676171	Ahsa2/Atp
GO_MF_m	GO:003517	histone ser	3/2529	25/23049	0.527434	0.701617	0.676171	Gm14147/
GO_MF_m	GO:007062	proteasom	3/2529	25/23049	0.527434	0.701617	0.676171	Psme4/Psn
GO_MF_m	GO:008002	phosphatic	3/2529	25/23049	0.527434	0.701617	0.676171	Clvs1/Gbf1
GO_MF_m	GO:000040	four-way ju	2/2529	16/23049	0.53722	0.70938	0.683652	Blm/Men1
GO_MF_m	GO:001529	solute:prot	2/2529	16/23049	0.53722	0.70938	0.683652	Slc9a1/Slc
GO_MF_m	GO:001650	protein-ho	2/2529	16/23049	0.53722	0.70938	0.683652	Adipor2/Lg
GO_MF_m	GO:001672	oxidoreduc	2/2529	16/23049	0.53722	0.70938	0.683652	Mmachc/M
GO_MF_m	GO:001716	Ral GTPase	2/2529	16/23049	0.53722	0.70938	0.683652	Rab34/Ralb
GO_MF_m	GO:002284	acetylcholi	2/2529	16/23049	0.53722	0.70938	0.683652	Chrne/Chr
GO_MF_m	GO:003055	cGMP bind	2/2529	16/23049	0.53722	0.70938	0.683652	Cnga2/Pde
GO_MF_m	GO:007000	metalloami	2/2529	16/23049	0.53722	0.70938	0.683652	Lvrn/Mmp
GO_MF_m	GO:007003	telomerase	2/2529	16/23049	0.53722	0.70938	0.683652	Hnrnpc/Nc
GO_MF_m	GO:007057	lysine-acet	2/2529	16/23049	0.53722	0.70938	0.683652	Mllt3/Psme
GO_MF_m	GO:007067	inositol 1,4	2/2529	16/23049	0.53722	0.70938	0.683652	Cyth2/Rph
GO_MF_m	GO:014003	acetylation	2/2529	16/23049	0.53722	0.70938	0.683652	Mllt3/Psme
GO_MF_m	GO:000839	arachidoni	4/2529	35/23049	0.544787	0.710807	0.685027	Cyp2b10/C
GO_MF_m	GO:003525	ionotropic	4/2529	35/23049	0.544787	0.710807	0.685027	Canx/Flot2
GO_MF_m	GO:005172	protein ph	4/2529	35/23049	0.544787	0.710807	0.685027	Akap6/Ptp
GO_MF_m	GO:001687	acid-thiol l	3/2529	26/23049	0.554808	0.710807	0.685027	Acsl1/Acsn
GO_MF_m	GO:003245	histone de	3/2529	26/23049	0.554808	0.710807	0.685027	Kdm2b/Kd
GO_MF_m	GO:005153	2 iron, 2 su	3/2529	26/23049	0.554808	0.710807	0.685027	Isca2/Nduf
GO_MF_m	GO:000101	RNA polym	1/2529	7/23049	0.556771	0.710807	0.685027	Maf1
GO_MF_m	GO:000164	adenylate	1/2529	7/23049	0.556771	0.710807	0.685027	Grm2
GO_MF_m	GO:000383	beta-galac	1/2529	7/23049	0.556771	0.710807	0.685027	St3gal3
GO_MF_m	GO:000402	alcohol sul	1/2529	7/23049	0.556771	0.710807	0.685027	Sult2a5
GO_MF_m	GO:000412	cytidine de	1/2529	7/23049	0.556771	0.710807	0.685027	Apobec1
GO_MF_m	GO:000471	signal trans	1/2529	7/23049	0.556771	0.710807	0.685027	Erbb3
GO_MF_m	GO:000490	interleukin	1/2529	7/23049	0.556771	0.710807	0.685027	Il1rl1
GO_MF_m	GO:000493	extracellula	1/2529	7/23049	0.556771	0.710807	0.685027	P2rx1
GO_MF_m	GO:000497	NMDA glu	1/2529	7/23049	0.556771	0.710807	0.685027	Grin2b
GO_MF_m	GO:000498	N-formyl p	1/2529	7/23049	0.556771	0.710807	0.685027	Fpr2
GO_MF_m	GO:000500	vasopressi	1/2529	7/23049	0.556771	0.710807	0.685027	Avpr1a

GO_MF_m	GO:000502	vascular en	1/2529	7/23049	0.556771	0.710807	0.685027	Pdgfra
GO_MF_m	GO:000511	patched bi	1/2529	7/23049	0.556771	0.710807	0.685027	Smo
GO_MF_m	GO:000513	interleukin-	1/2529	7/23049	0.556771	0.710807	0.685027	Pycard
GO_MF_m	GO:000522	intracellula	1/2529	7/23049	0.556771	0.710807	0.685027	Cnga2
GO_MF_m	GO:000819	ferric iron	1/2529	7/23049	0.556771	0.710807	0.685027	Th
GO_MF_m	GO:000829	single-stra	1/2529	7/23049	0.556771	0.710807	0.685027	Pole
GO_MF_m	GO:001034	carboxyl-C	1/2529	7/23049	0.556771	0.710807	0.685027	Pcmtd1
GO_MF_m	GO:001518	L-alanine t	1/2529	7/23049	0.556771	0.710807	0.685027	Slc38a7
GO_MF_m	GO:001518	arginine tra	1/2529	7/23049	0.556771	0.710807	0.685027	AU018091
GO_MF_m	GO:001518	L-lysine tra	1/2529	7/23049	0.556771	0.710807	0.685027	AU018091
GO_MF_m	GO:001555	C4-dicarbo	1/2529	7/23049	0.556771	0.710807	0.685027	Slc38a7
GO_MF_m	GO:001667	oxidoreduc	1/2529	7/23049	0.556771	0.710807	0.685027	Suox
GO_MF_m	GO:001671	oxidoreduc	1/2529	7/23049	0.556771	0.710807	0.685027	Th
GO_MF_m	GO:001716	CDP-alcoh	1/2529	7/23049	0.556771	0.710807	0.685027	Tmem269
GO_MF_m	GO:001717	phosphati	1/2529	7/23049	0.556771	0.710807	0.685027	Pigyl
GO_MF_m	GO:001987	sodium cha	1/2529	7/23049	0.556771	0.710807	0.685027	Pcsk9
GO_MF_m	GO:001996	interleukin-	1/2529	7/23049	0.556771	0.710807	0.685027	Il1rn
GO_MF_m	GO:002285	alanine tra	1/2529	7/23049	0.556771	0.710807	0.685027	Slc38a7
GO_MF_m	GO:003015	molybdenu	1/2529	7/23049	0.556771	0.710807	0.685027	Suox
GO_MF_m	GO:003055	acetylcholi	1/2529	7/23049	0.556771	0.710807	0.685027	Ly6e
GO_MF_m	GO:003173	CCR5 chem	1/2529	7/23049	0.556771	0.710807	0.685027	Ccl4
GO_MF_m	GO:003182	G-protein	1/2529	7/23049	0.556771	0.710807	0.685027	Gnai1
GO_MF_m	GO:003279	heterotrim	1/2529	7/23049	0.556771	0.710807	0.685027	Adora1
GO_MF_m	GO:003525	UDP-xylos	1/2529	7/23049	0.556771	0.710807	0.685027	Xylt1
GO_MF_m	GO:004260	CD4 recept	1/2529	7/23049	0.556771	0.710807	0.685027	Spg21
GO_MF_m	GO:004697	histone me	1/2529	7/23049	0.556771	0.710807	0.685027	Ezh1
GO_MF_m	GO:004713	protein-dis	1/2529	7/23049	0.556771	0.710807	0.685027	Txndc8
GO_MF_m	GO:004825	flap endon	1/2529	7/23049	0.556771	0.710807	0.685027	Fen1
GO_MF_m	GO:004827	mitogen-a	1/2529	7/23049	0.556771	0.710807	0.685027	Prmt1
GO_MF_m	GO:005029	steroid sulf	1/2529	7/23049	0.556771	0.710807	0.685027	Sult2a5
GO_MF_m	GO:005188	G-quadrup	1/2529	7/23049	0.556771	0.710807	0.685027	Blm
GO_MF_m	GO:005199	protein car	1/2529	7/23049	0.556771	0.710807	0.685027	Pcmtd1
GO_MF_m	GO:006167	importin-a	1/2529	7/23049	0.556771	0.710807	0.685027	Ei24
GO_MF_m	GO:007056	uridylyltran	1/2529	7/23049	0.556771	0.710807	0.685027	Ugp2
GO_MF_m	GO:007125	connexin b	1/2529	7/23049	0.556771	0.710807	0.685027	Cav3
GO_MF_m	GO:007234	NAADP-se	1/2529	7/23049	0.556771	0.710807	0.685027	Mcoln3
GO_MF_m	GO:009764	calcitonin	1/2529	7/23049	0.556771	0.710807	0.685027	Calcr
GO_MF_m	GO:009863	cell-matrix	1/2529	7/23049	0.556771	0.710807	0.685027	Madcam1
GO_MF_m	GO:190147	azole trans	1/2529	7/23049	0.556771	0.710807	0.685027	Slc38a7
GO_MF_m	GO:000481	aminoacyl-	5/2529	45/23049	0.558361	0.711572	0.685764	Kars/Lrrc47
GO_MF_m	GO:001687	ligase activ	5/2529	45/23049	0.558361	0.711572	0.685764	Kars/Lrrc47
GO_MF_m	GO:003281	tumor necr	5/2529	45/23049	0.558361	0.711572	0.685764	Babam2/C
GO_MF_m	GO:003024	carbohydra	29/2529	268/23049	0.561032	0.714554	0.688638	Calr/Canx/
GO_MF_m	GO:001982	cation-tra	7/2529	64/23049	0.562689	0.715395	0.689449	Atp1b2/At
GO_MF_m	GO:002285	active ion t	7/2529	64/23049	0.562689	0.715395	0.689449	Atp1b2/At
GO_MF_m	GO:004262	ATPase co	7/2529	64/23049	0.562689	0.715395	0.689449	Atp1b2/At
GO_MF_m	GO:000808	phosphoric	9/2529	83/23049	0.567052	0.720092	0.693976	Adora1/Cc
GO_MF_m	GO:005066	flavin aden	9/2529	83/23049	0.567052	0.720092	0.693976	Acad11/Ai

GO_MF_m	GO:000389	DNA-direc	4/2529	36/23049	0.567815	0.720637	0.694501	Polr2f/Polr
GO_MF_m	GO:000443	phosphatic	2/2529	17/23049	0.57093	0.721214	0.695057	Ccr1/Plch1
GO_MF_m	GO:000462	lysophosph	2/2529	17/23049	0.57093	0.721214	0.695057	Enpp2/Pnp
GO_MF_m	GO:000493	adrenergic	2/2529	17/23049	0.57093	0.721214	0.695057	Adra1d/Ol
GO_MF_m	GO:000495	icosanoid r	2/2529	17/23049	0.57093	0.721214	0.695057	Cysltr2/Ltb
GO_MF_m	GO:001688	acid-aminc	2/2529	17/23049	0.57093	0.721214	0.695057	Gclm/Tpgs
GO_MF_m	GO:002288	macromole	2/2529	17/23049	0.57093	0.721214	0.695057	Timm17b/
GO_MF_m	GO:003027	LRR domai	2/2529	17/23049	0.57093	0.721214	0.695057	Mkl1/Ncam
GO_MF_m	GO:000110	RNA polym	11/2529	102/23049	0.571282	0.721214	0.695057	Ankrd1/Hd
GO_MF_m	GO:190293	phosphatic	11/2529	102/23049	0.571282	0.721214	0.695057	Anxa2/Cfl1
GO_MF_m	GO:000525	chloride ch	8/2529	74/23049	0.572842	0.722761	0.696548	Ano1/Ano2
GO_MF_m	GO:006113	peptidase r	26/2529	242/23049	0.576234	0.726615	0.700262	Acrbp/Cav
GO_MF_m	GO:000837	acetylgalac	5/2529	46/23049	0.578573	0.728454	0.702034	Abo/B3gnt
GO_MF_m	GO:004802	CCR chemc	5/2529	46/23049	0.578573	0.728454	0.702034	Ccl20/Ccl2
GO_MF_m	GO:006163	ubiquitin p	25/2529	233/23049	0.578707	0.728454	0.702034	Arih2/Asb1
GO_MF_m	GO:000806	glutamate	3/2529	27/23049	0.58121	0.729593	0.703132	Gria1/Grin2
GO_MF_m	GO:000813	NADH deh	3/2529	27/23049	0.58121	0.729593	0.703132	Ndufa12/N
GO_MF_m	GO:005013	NADH deh	3/2529	27/23049	0.58121	0.729593	0.703132	Ndufa12/N
GO_MF_m	GO:007188	14-3-3 prc	3/2529	27/23049	0.58121	0.729593	0.703132	Nek1/Srpk
GO_MF_m	GO:001717	serine hydr	24/2529	224/23049	0.581304	0.729593	0.703132	Ache/Apeh
GO_MF_m	GO:000122	transcriptic	46/2529	428/23049	0.582938	0.731218	0.704698	Arid3c/Arn
GO_MF_m	GO:003506	methylatec	6/2529	56/23049	0.587939	0.736604	0.709889	Fmr1/Glyr1
GO_MF_m	GO:014003	methylatio	6/2529	56/23049	0.587939	0.736604	0.709889	Fmr1/Glyr1
GO_MF_m	GO:001920	kinase acti	8/2529	75/23049	0.588561	0.736604	0.709889	Abi1/Cdkn
GO_MF_m	GO:003162	ubiquitin c	4/2529	37/23049	0.59018	0.736604	0.709889	Arih2/Lonr
GO_MF_m	GO:003406	5'-3' RNA	4/2529	37/23049	0.59018	0.736604	0.709889	Polr2f/Polr
GO_MF_m	GO:004216	SH2 domai	4/2529	37/23049	0.59018	0.736604	0.709889	Ms4a2/Sit1
GO_MF_m	GO:009774	RNA polym	4/2529	37/23049	0.59018	0.736604	0.709889	Polr2f/Polr
GO_MF_m	GO:000802	ATP-deper	10/2529	94/23049	0.590309	0.736604	0.709889	Blm/Ddx19
GO_MF_m	GO:007003	purine NTF	10/2529	94/23049	0.590309	0.736604	0.709889	Blm/Ddx19
GO_MF_m	GO:000471	non-meml	7/2529	66/23049	0.596332	0.736689	0.709971	Abl2/Eif2ak
GO_MF_m	GO:001990	protein ph	16/2529	151/23049	0.597704	0.736689	0.709971	Akap6/Atp
GO_MF_m	GO:000122	transcriptic	5/2529	47/23049	0.598282	0.736689	0.709971	Foxc1/Hda
GO_MF_m	GO:000818	neuropepti	5/2529	47/23049	0.598282	0.736689	0.709971	Cysltr2/Gal
GO_MF_m	GO:001510	inorganic a	15/2529	142/23049	0.602032	0.736689	0.709971	Ank/Ano1/
GO_MF_m	GO:000474	retinol deh	2/2529	18/23049	0.602817	0.736689	0.709971	Adh1/Dhrs
GO_MF_m	GO:000523	extracellula	2/2529	18/23049	0.602817	0.736689	0.709971	Gria1/Grin2
GO_MF_m	GO:001592	hexosamin	2/2529	18/23049	0.602817	0.736689	0.709971	Hyal2/Hyal
GO_MF_m	GO:007018	DNA polyn	2/2529	18/23049	0.602817	0.736689	0.709971	Nabp2/Pcn
GO_MF_m	GO:001529	antiporter	8/2529	76/23049	0.603996	0.736689	0.709971	Clcn4/Slc2
GO_MF_m	GO:001507	proton trar	12/2529	114/23049	0.605176	0.736689	0.709971	Atp5a1/Atp
GO_MF_m	GO:000099	transcriptic	1/2529	8/23049	0.605418	0.736689	0.709971	Gtf3c3
GO_MF_m	GO:000449	N,N-dimet	1/2529	8/23049	0.605418	0.736689	0.709971	Fmo2
GO_MF_m	GO:000457	mannosyl-	1/2529	8/23049	0.605418	0.736689	0.709971	Man1b1
GO_MF_m	GO:000486	cAMP-dep	1/2529	8/23049	0.605418	0.736689	0.709971	Prkar2b
GO_MF_m	GO:000541	glucose:so	1/2529	8/23049	0.605418	0.736689	0.709971	Slc5a4a
GO_MF_m	GO:000802	G-protein	1/2529	8/23049	0.605418	0.736689	0.709971	Opn4
GO_MF_m	GO:000852	phosphatic	1/2529	8/23049	0.605418	0.736689	0.709971	Pitpnm2

GO_MF_m	GO:001519	L-proline t	1/2529	8/23049	0.605418	0.736689	0.709971	Slc6a20a
GO_MF_m	GO:001592	galactosida	1/2529	8/23049	0.605418	0.736689	0.709971	Glb1l
GO_MF_m	GO:001617	superoxide	1/2529	8/23049	0.605418	0.736689	0.709971	Sh3pxd2a
GO_MF_m	GO:001641	O-acetyltra	1/2529	8/23049	0.605418	0.736689	0.709971	Lpcat4
GO_MF_m	GO:001649	C-X-C che	1/2529	8/23049	0.605418	0.736689	0.709971	Cxcr5
GO_MF_m	GO:001666	oxidoreduc	1/2529	8/23049	0.605418	0.736689	0.709971	Gphn
GO_MF_m	GO:001674	hydroxyme	1/2529	8/23049	0.605418	0.736689	0.709971	Shmt1
GO_MF_m	GO:001985	calcium cha	1/2529	8/23049	0.605418	0.736689	0.709971	Fkbp1b
GO_MF_m	GO:003023	nitric-oxide	1/2529	8/23049	0.605418	0.736689	0.709971	Atp2b4
GO_MF_m	GO:003030	ADP-ribosy	1/2529	8/23049	0.605418	0.736689	0.709971	Adcyap1r1
GO_MF_m	GO:003049	hemoglobi	1/2529	8/23049	0.605418	0.736689	0.709971	Hbb-bs
GO_MF_m	GO:003062	pre-mRNA	1/2529	8/23049	0.605418	0.736689	0.709971	Zrsr2
GO_MF_m	GO:003169	beta-2 adr	1/2529	8/23049	0.605418	0.736689	0.709971	Gria1
GO_MF_m	GO:003195	medium-cl	1/2529	8/23049	0.605418	0.736689	0.709971	Acsl1
GO_MF_m	GO:003538	ATP-gated	1/2529	8/23049	0.605418	0.736689	0.709971	P2rx1
GO_MF_m	GO:003631	annealing	1/2529	8/23049	0.605418	0.736689	0.709971	Blm
GO_MF_m	GO:003803	sphingosin	1/2529	8/23049	0.605418	0.736689	0.709971	S1pr5
GO_MF_m	GO:004280	vitamin D r	1/2529	8/23049	0.605418	0.736689	0.709971	Taf11
GO_MF_m	GO:004314	ATP-deper	1/2529	8/23049	0.605418	0.736689	0.709971	Blm
GO_MF_m	GO:005064	testosteror	1/2529	8/23049	0.605418	0.736689	0.709971	Cyp3a11
GO_MF_m	GO:005078	RAGE recep	1/2529	8/23049	0.605418	0.736689	0.709971	Fpr2
GO_MF_m	GO:005137	epinephrin	1/2529	8/23049	0.605418	0.736689	0.709971	Rnls
GO_MF_m	GO:007009	delta-cater	1/2529	8/23049	0.605418	0.736689	0.709971	Ptprj
GO_MF_m	GO:007056	cytidylyltra	1/2529	8/23049	0.605418	0.736689	0.709971	Pcyt2
GO_MF_m	GO:010239	decanoate	1/2529	8/23049	0.605418	0.736689	0.709971	Acsl1
GO_MF_m	GO:199045	transferrin	1/2529	8/23049	0.605418	0.736689	0.709971	Snx2
GO_MF_m	GO:001549	cation:catic	3/2529	28/23049	0.606596	0.737289	0.710549	Slc22a5/Slc
GO_MF_m	GO:009960	ligand-gat	3/2529	28/23049	0.606596	0.737289	0.710549	Grin2b/Jph
GO_MF_m	GO:004205	chemoattra	4/2529	38/23049	0.611847	0.742416	0.71549	Defb4/Fgf7
GO_MF_m	GO:006059	ATPase reg	4/2529	38/23049	0.611847	0.742416	0.71549	Ahsa2/Atp
GO_MF_m	GO:190431	transmitter	4/2529	38/23049	0.611847	0.742416	0.71549	Chrne/Chrn
GO_MF_m	GO:000098	RNA polym	7/2529	67/23049	0.612646	0.742549	0.715618	Arx/Esrrb/H
GO_MF_m	GO:003027	clathrin bin	7/2529	67/23049	0.612646	0.742549	0.715618	Dnajc6/Ldl
GO_MF_m	GO:006165	ubiquitin-li	25/2529	237/23049	0.614034	0.743814	0.716837	Arih2/Asb1
GO_MF_m	GO:000110	RNA polym	5/2529	48/23049	0.61746	0.746581	0.719504	Ankrd1/Hy
GO_MF_m	GO:000178	phosphatic	5/2529	48/23049	0.61746	0.746581	0.719504	Cpne6/Gsc
GO_MF_m	GO:000523	excitatory	5/2529	48/23049	0.61746	0.746581	0.719504	Chrne/Chrn
GO_MF_m	GO:001990	syntaxin bi	10/2529	96/23049	0.617705	0.746581	0.719504	Cav1/Dapk
GO_MF_m	GO:003361	activating t	8/2529	77/23049	0.619131	0.747885	0.720761	Dgkq/Exos
GO_MF_m	GO:000823	serine-type	23/2529	219/23049	0.62061	0.749252	0.722078	Apeh/C1rl/
GO_MF_m	GO:001510	chloride tra	9/2529	87/23049	0.625248	0.754429	0.727067	Ano1/Ano2
GO_MF_m	GO:000372	RNA helica	7/2529	68/23049	0.628598	0.756013	0.728594	Ddx19b/Dc
GO_MF_m	GO:000400	ATP-deper	7/2529	68/23049	0.628598	0.756013	0.728594	Ddx19b/Dc
GO_MF_m	GO:001702	myosin bin	7/2529	68/23049	0.628598	0.756013	0.728594	Fxyd1/Gria
GO_MF_m	GO:005068	androgen r	3/2529	29/23049	0.630934	0.756013	0.728594	Calr/Pkn1/
GO_MF_m	GO:000178	phosphoty	4/2529	39/23049	0.632791	0.756013	0.728594	Abl2/Ldlrap
GO_MF_m	GO:000161	virus recep	2/2529	19/23049	0.632876	0.756013	0.728594	Cldn1/Hyal
GO_MF_m	GO:000374	translation	2/2529	19/23049	0.632876	0.756013	0.728594	Abtb1/Gfm

GO_MF_m	GO:000419	calcium-de	2/2529	19/23049	0.632876	0.756013	0.728594	Capn13/Pc
GO_MF_m	GO:000489	GABA-A re	2/2529	19/23049	0.632876	0.756013	0.728594	Gabra6/Ga
GO_MF_m	GO:000497	ionotropic	2/2529	19/23049	0.632876	0.756013	0.728594	Gria1/Grin2
GO_MF_m	GO:000508	ARF guany	2/2529	19/23049	0.632876	0.756013	0.728594	Cyth2/Gbf1
GO_MF_m	GO:001564	fatty acid li	2/2529	19/23049	0.632876	0.756013	0.728594	Acsl1/Acsm
GO_MF_m	GO:001678	phosphotra	2/2529	19/23049	0.632876	0.756013	0.728594	Tmem269/
GO_MF_m	GO:001982	oxygen bin	2/2529	19/23049	0.632876	0.756013	0.728594	Hbb-bs/Th
GO_MF_m	GO:004696	proton-tra	2/2529	19/23049	0.632876	0.756013	0.728594	Atp6v0c/Tc
GO_MF_m	GO:005043	transformin	2/2529	19/23049	0.632876	0.756013	0.728594	Cd36/Hyal2
GO_MF_m	GO:005274	inositol ph	2/2529	19/23049	0.632876	0.756013	0.728594	Bpnt1/Sec1
GO_MF_m	GO:010400	hijacked m	2/2529	19/23049	0.632876	0.756013	0.728594	Cldn1/Hyal
GO_MF_m	GO:000455	hydrolase a	11/2529	107/23049	0.636573	0.760008	0.732444	1700016D0
GO_MF_m	GO:000818	RNA-depe	7/2529	69/23049	0.644174	0.7602	0.732629	Ddx19b/Dc
GO_MF_m	GO:003525	nuclear hor	15/2529	146/23049	0.645901	0.7602	0.732629	Asxl1/Bcas3
GO_MF_m	GO:000001	single-stra	1/2529	9/23049	0.648728	0.7602	0.732629	Xrcc1
GO_MF_m	GO:000175	retinal deh	1/2529	9/23049	0.648728	0.7602	0.732629	Aldh1a3
GO_MF_m	GO:000215	G-quadrup	1/2529	9/23049	0.648728	0.7602	0.732629	Fmr1
GO_MF_m	GO:000368	DNA clamp	1/2529	9/23049	0.648728	0.7602	0.732629	Rfc1
GO_MF_m	GO:000369	double-str	1/2529	9/23049	0.648728	0.7602	0.732629	Hmbox1
GO_MF_m	GO:000372	telomerase	1/2529	9/23049	0.648728	0.7602	0.732629	Hmbox1
GO_MF_m	GO:000384	1-acylglyce	1/2529	9/23049	0.648728	0.7602	0.732629	Agpat2
GO_MF_m	GO:000396	RNA-direc	1/2529	9/23049	0.648728	0.7602	0.732629	Hmbox1
GO_MF_m	GO:000444	inositol-po	1/2529	9/23049	0.648728	0.7602	0.732629	Sec16a
GO_MF_m	GO:000457	oligosacch	1/2529	9/23049	0.648728	0.7602	0.732629	Rpn2
GO_MF_m	GO:000457	dolichyl-di	1/2529	9/23049	0.648728	0.7602	0.732629	Rpn2
GO_MF_m	GO:000465	polynucleo	1/2529	9/23049	0.648728	0.7602	0.732629	Papd7
GO_MF_m	GO:000516	neurotroph	1/2529	9/23049	0.648728	0.7602	0.732629	Ntf5
GO_MF_m	GO:000522	intracellula	1/2529	9/23049	0.648728	0.7602	0.732629	Cnga2
GO_MF_m	GO:000522	volume-se	1/2529	9/23049	0.648728	0.7602	0.732629	Lrrc8b
GO_MF_m	GO:000538	iron ion tra	1/2529	9/23049	0.648728	0.7602	0.732629	Slc40a1
GO_MF_m	GO:000824	omega pep	1/2529	9/23049	0.648728	0.7602	0.732629	Apeh
GO_MF_m	GO:000829	3'-5'-exod	1/2529	9/23049	0.648728	0.7602	0.732629	Pole
GO_MF_m	GO:001537	cation:chlo	1/2529	9/23049	0.648728	0.7602	0.732629	Slc12a2
GO_MF_m	GO:001537	potassium:	1/2529	9/23049	0.648728	0.7602	0.732629	Slc12a2
GO_MF_m	GO:001600	phospholip	1/2529	9/23049	0.648728	0.7602	0.732629	Stx4a
GO_MF_m	GO:001688	ligase activ	1/2529	9/23049	0.648728	0.7602	0.732629	Lig3
GO_MF_m	GO:001976	immunoglo	1/2529	9/23049	0.648728	0.7602	0.732629	Ms4a2
GO_MF_m	GO:003143	titin bindin	1/2529	9/23049	0.648728	0.7602	0.732629	Ankrd1
GO_MF_m	GO:003235	oxidized pu	1/2529	9/23049	0.648728	0.7602	0.732629	Blm
GO_MF_m	GO:003317	protein-DN	1/2529	9/23049	0.648728	0.7602	0.732629	Rfc1
GO_MF_m	GO:003445	dynactin bi	1/2529	9/23049	0.648728	0.7602	0.732629	Snx6
GO_MF_m	GO:004228	xylosyltrans	1/2529	9/23049	0.648728	0.7602	0.732629	Xylt1
GO_MF_m	GO:004289	antibiotic t	1/2529	9/23049	0.648728	0.7602	0.732629	Slc22a5
GO_MF_m	GO:004603	inositol tris	1/2529	9/23049	0.648728	0.7602	0.732629	Sec16a
GO_MF_m	GO:004702	androstero	1/2529	9/23049	0.648728	0.7602	0.732629	Akr1c12
GO_MF_m	GO:009898	G-protein c	1/2529	9/23049	0.648728	0.7602	0.732629	Grm2
GO_MF_m	GO:000857	ATP-depen	3/2529	30/23049	0.654207	0.765789	0.738015	Dnaic2/Kif4
GO_MF_m	GO:001529	solute:catio	3/2529	30/23049	0.654207	0.765789	0.738015	Slc22a5/Slc

GO_MF_m	GO:003525	glutamate	6/2529	60/23049	0.656447	0.767993	0.740139	Camk2a/Ca
GO_MF_m	GO:000422	metalloenc	10/2529	99/23049	0.656979	0.768198	0.740337	Adam2/Ad
GO_MF_m	GO:000122	transcriptic	2/2529	20/23049	0.661123	0.770952	0.742991	Foxc1/Rpl2
GO_MF_m	GO:003121	phosphatic	2/2529	20/23049	0.661123	0.770952	0.742991	Nf1/Pltp
GO_MF_m	GO:003148	myosin V b	2/2529	20/23049	0.661123	0.770952	0.742991	Gria1/Rab2
GO_MF_m	GO:004297	peroxisome	2/2529	20/23049	0.661123	0.770952	0.742991	Asxl1/Ppar
GO_MF_m	GO:005099	quaternary	2/2529	20/23049	0.661123	0.770952	0.742991	Nf1/Pltp
GO_MF_m	GO:000532	neurotrans	5/2529	51/23049	0.671613	0.782762	0.754373	Slc18a2/Slc
GO_MF_m	GO:000523	extracellula	7/2529	71/23049	0.674149	0.785292	0.756811	Chrne/Chr
GO_MF_m	GO:001641	S-acyltrans	3/2529	31/23049	0.676406	0.787332	0.758777	Fasn/Ykt6/
GO_MF_m	GO:000122	transcriptic	24/2529	235/23049	0.676631	0.787332	0.758777	Ifi207/Arx/
GO_MF_m	GO:004000	adenosine	1/2529	10/23049	0.687285	0.788592	0.759991	Adat1
GO_MF_m	GO:000443	phosphatic	1/2529	10/23049	0.687285	0.788592	0.759991	Synj1
GO_MF_m	GO:000456	chitinase a	1/2529	10/23049	0.687285	0.788592	0.759991	Chil5
GO_MF_m	GO:000543	sodium:ph	1/2529	10/23049	0.687285	0.788592	0.759991	Slc20a1
GO_MF_m	GO:000865	cysteine-ty	1/2529	10/23049	0.687285	0.788592	0.759991	Tnfrsf10b
GO_MF_m	GO:000988	photorecep	1/2529	10/23049	0.687285	0.788592	0.759991	Opn4
GO_MF_m	GO:001516	pyrimidine	1/2529	10/23049	0.687285	0.788592	0.759991	Slc35a5
GO_MF_m	GO:001592	mannosyl-	1/2529	10/23049	0.687285	0.788592	0.759991	Man1b1
GO_MF_m	GO:001688	endodeoxy	1/2529	10/23049	0.687285	0.788592	0.759991	Fen1
GO_MF_m	GO:001707	U6 snRNA	1/2529	10/23049	0.687285	0.788592	0.759991	Prpf4
GO_MF_m	GO:001995	C-C chemo	1/2529	10/23049	0.687285	0.788592	0.759991	Ccr1
GO_MF_m	GO:003170	type 1 ang	1/2529	10/23049	0.687285	0.788592	0.759991	Ednrb
GO_MF_m	GO:003199	thioesteras	1/2529	10/23049	0.687285	0.788592	0.759991	Haus7
GO_MF_m	GO:003519	siRNA bind	1/2529	10/23049	0.687285	0.788592	0.759991	Fmr1
GO_MF_m	GO:003561	clathrin ad	1/2529	10/23049	0.687285	0.788592	0.759991	Ldlrap1
GO_MF_m	GO:004257	lipid phosp	1/2529	10/23049	0.687285	0.788592	0.759991	Ephx2
GO_MF_m	GO:004708	ketosteroi	1/2529	10/23049	0.687285	0.788592	0.759991	Akr1c12
GO_MF_m	GO:004742	nucleoside	1/2529	10/23049	0.687285	0.788592	0.759991	Nudt1
GO_MF_m	GO:005070	CARD dom	1/2529	10/23049	0.687285	0.788592	0.759991	Nod1
GO_MF_m	GO:007051	death dom	1/2529	10/23049	0.687285	0.788592	0.759991	Dapl1
GO_MF_m	GO:007193	Arp2/3 co	1/2529	10/23049	0.687285	0.788592	0.759991	Snx9
GO_MF_m	GO:009700	ceramide b	1/2529	10/23049	0.687285	0.788592	0.759991	Pltp
GO_MF_m	GO:009850	G-rich stra	1/2529	10/23049	0.687285	0.788592	0.759991	Nabp2
GO_MF_m	GO:009874	endocytic a	1/2529	10/23049	0.687285	0.788592	0.759991	Ldlrap1
GO_MF_m	GO:010102	estrogen 1	1/2529	10/23049	0.687285	0.788592	0.759991	Cyp3a11
GO_MF_m	GO:199040	protein ant	1/2529	10/23049	0.687285	0.788592	0.759991	Ppp2r1a
GO_MF_m	GO:000403	alditol:NAD	2/2529	21/23049	0.687594	0.788592	0.759991	Akr1b10/A
GO_MF_m	GO:000367	DNA helica	4/2529	42/23049	0.691103	0.791774	0.763058	Blm/Fbxo1
GO_MF_m	GO:000452	endodeoxy	4/2529	42/23049	0.691103	0.791774	0.763058	Aplf/Ercc5/
GO_MF_m	GO:000108	RNA polym	15/2529	151/23049	0.697007	0.797444	0.768522	Ankrd1/Bb
GO_MF_m	GO:000507	SH3/SH2 a	3/2529	32/23049	0.697532	0.797444	0.768522	Bcar3/Nck2
GO_MF_m	GO:004297	retinoic aci	3/2529	32/23049	0.697532	0.797444	0.768522	Asxl1/Nr1h
GO_MF_m	GO:007027	phosphatic	3/2529	32/23049	0.697532	0.797444	0.768522	Gsdmc2/G
GO_MF_m	GO:000554	phosphatic	7/2529	73/23049	0.702494	0.802265	0.773168	Anxa2/Gsd
GO_MF_m	GO:000839	steroid hyd	7/2529	73/23049	0.702494	0.802265	0.773168	Cyp2b10/C
GO_MF_m	GO:001900	GDP bindi	6/2529	63/23049	0.702916	0.802322	0.773224	Gnai1/Rab
GO_MF_m	GO:002282	transmitter	5/2529	53/23049	0.70477	0.803586	0.774442	Chrne/Chr

GO_MF_m	GO:002283	transmitter	5/2529	53/23049	0.70477	0.803586	0.774442	Chrne/Chrn
GO_MF_m	GO:001566	ATPase act	4/2529	43/23049	0.709006	0.807212	0.777936	Atp1b2/Atp
GO_MF_m	GO:004439	ubiquitin-li	4/2529	43/23049	0.709006	0.807212	0.777936	Arih2/Lonr
GO_MF_m	GO:004425	serine-type	19/2529	191/23049	0.709073	0.807212	0.777936	Apeh/C1rl/
GO_MF_m	GO:000814	poly(A) bin	2/2529	22/23049	0.712338	0.807411	0.778128	Pabpc1l/Pp
GO_MF_m	GO:001527	calcium-re	2/2529	22/23049	0.712338	0.807411	0.778128	Jph3/Mcoln
GO_MF_m	GO:001691	GABA rece	2/2529	22/23049	0.712338	0.807411	0.778128	Gabra6/Ga
GO_MF_m	GO:003050	ankyrin bin	2/2529	22/23049	0.712338	0.807411	0.778128	Cdh1/Kcnq
GO_MF_m	GO:004281	Wnt-activa	2/2529	22/23049	0.712338	0.807411	0.778128	Lrp4/Smo
GO_MF_m	GO:004696	retinoid X r	2/2529	22/23049	0.712338	0.807411	0.778128	Nr1h2/Uim
GO_MF_m	GO:000516	tumor necr	3/2529	33/23049	0.717593	0.807411	0.778128	Babam2/Ca
GO_MF_m	GO:190156	fatty acid d	3/2529	33/23049	0.717593	0.807411	0.778128	Cyp4f14/Ec
GO_MF_m	GO:000116	RNA polym	1/2529	11/23049	0.721612	0.807411	0.778128	Tbx1
GO_MF_m	GO:000120	transcriptic	1/2529	11/23049	0.721612	0.807411	0.778128	Arx
GO_MF_m	GO:000431	fatty acid s	1/2529	11/23049	0.721612	0.807411	0.778128	Fasn
GO_MF_m	GO:000452	ribonucleas	1/2529	11/23049	0.721612	0.807411	0.778128	Rpp40
GO_MF_m	GO:000522	intracellula	1/2529	11/23049	0.721612	0.807411	0.778128	Cnga2
GO_MF_m	GO:000806	chitin bindi	1/2529	11/23049	0.721612	0.807411	0.778128	Chil5
GO_MF_m	GO:000841	fucosyltran	1/2529	11/23049	0.721612	0.807411	0.778128	Fut8
GO_MF_m	GO:000850	benzodiaze	1/2529	11/23049	0.721612	0.807411	0.778128	Gabra6
GO_MF_m	GO:001529	anion:catio	1/2529	11/23049	0.721612	0.807411	0.778128	Slc12a2
GO_MF_m	GO:001684	carbon-sul	1/2529	11/23049	0.721612	0.807411	0.778128	Ltc4s
GO_MF_m	GO:001910	pyrimidine	1/2529	11/23049	0.721612	0.807411	0.778128	Ugp2
GO_MF_m	GO:001953	oxalate tra	1/2529	11/23049	0.721612	0.807411	0.778128	Slc26a7
GO_MF_m	GO:003203	myosin hea	1/2529	11/23049	0.721612	0.807411	0.778128	Myl9
GO_MF_m	GO:003500	phosphatic	1/2529	11/23049	0.721612	0.807411	0.778128	Pik3r6
GO_MF_m	GO:003561	AP-2 adap	1/2529	11/23049	0.721612	0.807411	0.778128	Ldlrap1
GO_MF_m	GO:003612	BMP bindir	1/2529	11/23049	0.721612	0.807411	0.778128	Grem2
GO_MF_m	GO:004217	lysophosph	1/2529	11/23049	0.721612	0.807411	0.778128	Agpat2
GO_MF_m	GO:004352	leucine zip	1/2529	11/23049	0.721612	0.807411	0.778128	Mkl1
GO_MF_m	GO:004385	cyclic nucle	1/2529	11/23049	0.721612	0.807411	0.778128	Cnga2
GO_MF_m	GO:004697	TAP bindin	1/2529	11/23049	0.721612	0.807411	0.778128	H2-Q2
GO_MF_m	GO:004818	activin binc	1/2529	11/23049	0.721612	0.807411	0.778128	Smad7
GO_MF_m	GO:005032	tau-protei	1/2529	11/23049	0.721612	0.807411	0.778128	Cdk5
GO_MF_m	GO:005186	histone de	1/2529	11/23049	0.721612	0.807411	0.778128	Kdm2b
GO_MF_m	GO:005274	phosphatic	1/2529	11/23049	0.721612	0.807411	0.778128	Synj1
GO_MF_m	GO:006022	lipase activ	1/2529	11/23049	0.721612	0.807411	0.778128	Stx4a
GO_MF_m	GO:000504	scavenger	4/2529	44/23049	0.726139	0.811633	0.782197	Corin/Enpp
GO_MF_m	GO:004260	peptide an	4/2529	44/23049	0.726139	0.811633	0.782197	Gm11127/
GO_MF_m	GO:000418	metallocarl	2/2529	23/23049	0.735416	0.819986	0.790246	Cpm/Cpz
GO_MF_m	GO:000553	mannose b	2/2529	23/23049	0.735416	0.819986	0.790246	Cd209d/Ig
GO_MF_m	GO:003525	UDP-galac	2/2529	23/23049	0.735416	0.819986	0.790246	Abo/B4gal
GO_MF_m	GO:005078	dopamine	2/2529	23/23049	0.735416	0.819986	0.790246	Drd3/Grin2
GO_MF_m	GO:000814	sulfotransf	5/2529	55/23049	0.735514	0.819986	0.790246	Chst13/Dse
GO_MF_m	GO:000521	intracellula	3/2529	34/23049	0.736605	0.820778	0.79101	Cnga2/Jph
GO_MF_m	GO:003067	protein bin	12/2529	127/23049	0.749748	0.82785	0.797826	Arrdc4/Bca
GO_MF_m	GO:001983	growth fac	14/2529	147/23049	0.751172	0.82785	0.797826	Cd36/Col5
GO_MF_m	GO:000173	2'-5'-oligo	1/2529	12/23049	0.752172	0.82785	0.797826	Oas1f

GO_MF_m	GO:000216	aminoacyl-	1/2529	12/23049	0.752172	0.82785	0.797826	Vars2
GO_MF_m	GO:000395	NAD+ kina	1/2529	12/23049	0.752172	0.82785	0.797826	Dgkq
GO_MF_m	GO:000487	complemer	1/2529	12/23049	0.752172	0.82785	0.797826	Fpr2
GO_MF_m	GO:000539	sodium:pot	1/2529	12/23049	0.752172	0.82785	0.797826	Atp1b2
GO_MF_m	GO:000827	secondary	1/2529	12/23049	0.752172	0.82785	0.797826	Slc26a7
GO_MF_m	GO:000833	high voltag	1/2529	12/23049	0.752172	0.82785	0.797826	Cacnb2
GO_MF_m	GO:000855	potassium-	1/2529	12/23049	0.752172	0.82785	0.797826	Atp1b2
GO_MF_m	GO:001503	peptide dis	1/2529	12/23049	0.752172	0.82785	0.797826	Pdia6
GO_MF_m	GO:001511	phosphate	1/2529	12/23049	0.752172	0.82785	0.797826	Ank
GO_MF_m	GO:001692	SUMO-spe	1/2529	12/23049	0.752172	0.82785	0.797826	Senp1
GO_MF_m	GO:002285	GABA-gate	1/2529	12/23049	0.752172	0.82785	0.797826	Gabra6
GO_MF_m	GO:003088	beta-2-mic	1/2529	12/23049	0.752172	0.82785	0.797826	H2-Q2
GO_MF_m	GO:003168	G-protein	1/2529	12/23049	0.752172	0.82785	0.797826	Gria1
GO_MF_m	GO:003170	angiotensir	1/2529	12/23049	0.752172	0.82785	0.797826	Ednrb
GO_MF_m	GO:003174	D1 dopami	1/2529	12/23049	0.752172	0.82785	0.797826	Drd3
GO_MF_m	GO:003245	histone der	1/2529	12/23049	0.752172	0.82785	0.797826	Kdm3b
GO_MF_m	GO:003525	G-protein	1/2529	12/23049	0.752172	0.82785	0.797826	Dnm3
GO_MF_m	GO:003549	cAMP resp	1/2529	12/23049	0.752172	0.82785	0.797826	Creb3l3
GO_MF_m	GO:003970	co-recepto	1/2529	12/23049	0.752172	0.82785	0.797826	Wnt3a
GO_MF_m	GO:004304	single-strar	1/2529	12/23049	0.752172	0.82785	0.797826	Nabp2
GO_MF_m	GO:005066	oxidoreduc	1/2529	12/23049	0.752172	0.82785	0.797826	Aifm1
GO_MF_m	GO:004317	alcohol bin	7/2529	77/23049	0.754133	0.829239	0.799164	Adh1/Crab
GO_MF_m	GO:000515	epidermal	3/2529	35/23049	0.754588	0.829239	0.799164	Ms4a1/Nrg
GO_MF_m	GO:004216	telomeric D	3/2529	35/23049	0.754588	0.829239	0.799164	Hmbox1/N
GO_MF_m	GO:000373	structural c	18/2529	187/23049	0.756125	0.830505	0.800384	Mrpl10/Mr
GO_MF_m	GO:000411	3',5'-cyclic-	2/2529	24/23049	0.756895	0.830927	0.800791	Pde11a/Pd
GO_MF_m	GO:003016	PDZ doma	11/2529	118/23049	0.759329	0.83275	0.802548	Atp2b4/Ca
GO_MF_m	GO:004282	histone dea	11/2529	118/23049	0.759329	0.83275	0.802548	Ankra2/An
GO_MF_m	GO:000549	steroid bin	10/2529	109/23049	0.769865	0.843876	0.81327	Akr1c12/At
GO_MF_m	GO:004317	RNA polym	3/2529	36/23049	0.771567	0.845311	0.814654	Rtraf/Esrrb/
GO_MF_m	GO:000153	lipopolysac	2/2529	25/23049	0.776848	0.846553	0.81585	Scarb1/Spc
GO_MF_m	GO:000411	cyclic-nucl	2/2529	25/23049	0.776848	0.846553	0.81585	Pde11a/Pd
GO_MF_m	GO:000107	transcriptic	15/2529	160/23049	0.777161	0.846553	0.81585	Ifi207/Atf3/
GO_MF_m	GO:000371	transcriptic	17/2529	180/23049	0.778179	0.846553	0.81585	Ankrd1/Bas
GO_MF_m	GO:000390	DNA-(apur	1/2529	13/23049	0.779379	0.846553	0.81585	Aplf
GO_MF_m	GO:000411	3',5'-cyclic-	1/2529	13/23049	0.779379	0.846553	0.81585	Pde4b
GO_MF_m	GO:000446	long-chain	1/2529	13/23049	0.779379	0.846553	0.81585	Acsl1
GO_MF_m	GO:000847	palmitoyl-(	1/2529	13/23049	0.779379	0.846553	0.81585	Ppt1
GO_MF_m	GO:001511	sulfate trar	1/2529	13/23049	0.779379	0.846553	0.81585	Slc26a7
GO_MF_m	GO:001527	store-oper	1/2529	13/23049	0.779379	0.846553	0.81585	Stim2
GO_MF_m	GO:001564	toxic subst	1/2529	13/23049	0.779379	0.846553	0.81585	Ephx2
GO_MF_m	GO:001592	glucosidas	1/2529	13/23049	0.779379	0.846553	0.81585	Pgghg
GO_MF_m	GO:001920	nucleoside	1/2529	13/23049	0.779379	0.846553	0.81585	Adk
GO_MF_m	GO:003532	Toll-like re	1/2529	13/23049	0.779379	0.846553	0.81585	Cd36
GO_MF_m	GO:003631	phosphatic	1/2529	13/23049	0.779379	0.846553	0.81585	Ptpn13
GO_MF_m	GO:004755	3',5'-cyclic-	1/2529	13/23049	0.779379	0.846553	0.81585	Pde11a
GO_MF_m	GO:009859	palmitoyl h	1/2529	13/23049	0.779379	0.846553	0.81585	Ppt1
GO_MF_m	GO:000487	nuclear rec	4/2529	48/23049	0.787128	0.853302	0.822354	Nr1h2/Nr4

GO_MF_m	GO:009853	transcriptic	4/2529	48/23049	0.787128	0.853302	0.822354	Nr1h2/Nr4
GO_MF_m	GO:000097	RNA polym	3/2529	37/23049	0.787572	0.853302	0.822354	H2afy/H2a
GO_MF_m	GO:001687	ligase activ	3/2529	37/23049	0.787572	0.853302	0.822354	Acsl1/Acsm
GO_MF_m	GO:004353	ADP bindir	3/2529	37/23049	0.787572	0.853302	0.822354	Atp5a1/My
GO_MF_m	GO:000378	actin monc	2/2529	26/23049	0.795352	0.860002	0.828811	Mkl1/Tmsb
GO_MF_m	GO:000419	aspartic-ty	2/2529	26/23049	0.795352	0.860002	0.828811	Napsa/Nrip
GO_MF_m	GO:000515	insulin rece	2/2529	26/23049	0.795352	0.860002	0.828811	Ptpn1/Snx2
GO_MF_m	GO:000535	glucose tra	2/2529	26/23049	0.795352	0.860002	0.828811	Slc2a1/Slc5
GO_MF_m	GO:000107	transcriptic	18/2529	193/23049	0.800232	0.863719	0.832394	Ankrd1/Arr
GO_MF_m	GO:001529	symporter	13/2529	143/23049	0.801654	0.863719	0.832394	Slc10a4/Slc
GO_MF_m	GO:000116	intronic tra	1/2529	14/23049	0.8036	0.863719	0.832394	Tbx1
GO_MF_m	GO:000408	carbonate	1/2529	14/23049	0.8036	0.863719	0.832394	Car15
GO_MF_m	GO:000455	alpha-man	1/2529	14/23049	0.8036	0.863719	0.832394	Man1b1
GO_MF_m	GO:001031	phosphatic	1/2529	14/23049	0.8036	0.863719	0.832394	Wipi2
GO_MF_m	GO:001659	glutamate	1/2529	14/23049	0.8036	0.863719	0.832394	Grin2b
GO_MF_m	GO:003448	heparan su	1/2529	14/23049	0.8036	0.863719	0.832394	Hs6st1
GO_MF_m	GO:004815	tau protein	1/2529	14/23049	0.8036	0.863719	0.832394	Snca
GO_MF_m	GO:005081	GABA rece	1/2529	14/23049	0.8036	0.863719	0.832394	Maf1
GO_MF_m	GO:005140	BH domair	1/2529	14/23049	0.8036	0.863719	0.832394	Bok
GO_MF_m	GO:009884	sequence-	1/2529	14/23049	0.8036	0.863719	0.832394	Nabp2
GO_MF_m	GO:000377	microtubul	7/2529	82/23049	0.809197	0.869024	0.837506	Dnah1/Dna
GO_MF_m	GO:000518	neuropepti	2/2529	27/23049	0.812483	0.869024	0.837506	Cartpt/Prlh
GO_MF_m	GO:000534	organic aci	2/2529	27/23049	0.812483	0.869024	0.837506	Slc10a4/Slc
GO_MF_m	GO:000810	alcohol del	2/2529	27/23049	0.812483	0.869024	0.837506	Akr1b10/A
GO_MF_m	GO:001514	hexose trai	2/2529	27/23049	0.812483	0.869024	0.837506	Slc2a1/Slc5
GO_MF_m	GO:001970	protein-cys	2/2529	27/23049	0.812483	0.869024	0.837506	Ykt6/Zdhhc
GO_MF_m	GO:001970	protein-cys	2/2529	27/23049	0.812483	0.869024	0.837506	Ykt6/Zdhhc
GO_MF_m	GO:007000	aspartic-ty	2/2529	27/23049	0.812483	0.869024	0.837506	Napsa/Nrip
GO_MF_m	GO:190468	peptide tra	2/2529	27/23049	0.812483	0.869024	0.837506	Timm17b/T
GO_MF_m	GO:000823	metalloexo	4/2529	50/23049	0.813285	0.869024	0.837506	Cpm/Cpz/L
GO_MF_m	GO:004530	protein phc	4/2529	50/23049	0.813285	0.869024	0.837506	Abl2/Ldlrap
GO_MF_m	GO:000508	protein kin	5/2529	61/23049	0.813522	0.869024	0.837506	Adcy4/Pkn
GO_MF_m	GO:000115	enhancer s	8/2529	93/23049	0.813777	0.869024	0.837506	Arx/Esrrb/F
GO_MF_m	GO:001534	sodium-inc	3/2529	39/23049	0.816788	0.871807	0.840188	Slc22a1/Slc
GO_MF_m	GO:000159	trace-amin	1/2529	15/23049	0.825162	0.876164	0.844387	Taar9
GO_MF_m	GO:000470	MAP kinase	1/2529	15/23049	0.825162	0.876164	0.844387	Mapk13
GO_MF_m	GO:000516	neurotroph	1/2529	15/23049	0.825162	0.876164	0.844387	Ntf5
GO_MF_m	GO:000538	calcium-tra	1/2529	15/23049	0.825162	0.876164	0.844387	Atp2b4
GO_MF_m	GO:001592	mannosida	1/2529	15/23049	0.825162	0.876164	0.844387	Man1b1
GO_MF_m	GO:002284	potassium	1/2529	15/23049	0.825162	0.876164	0.844387	Kcnk2
GO_MF_m	GO:003205	bile acid bi	1/2529	15/23049	0.825162	0.876164	0.844387	Akr1c12
GO_MF_m	GO:004314	single-stra	1/2529	15/23049	0.825162	0.876164	0.844387	Helq
GO_MF_m	GO:004421	intronic tra	1/2529	15/23049	0.825162	0.876164	0.844387	Tbx1
GO_MF_m	GO:004550	dynein hea	1/2529	15/23049	0.825162	0.876164	0.844387	Dnaic2
GO_MF_m	GO:199093	ATP-deper	4/2529	51/23049	0.825342	0.876164	0.844387	Dnah1/Dna
GO_MF_m	GO:001529	secondary	23/2529	247/23049	0.826287	0.876735	0.844937	Ank/Clcn4/
GO_MF_m	GO:190168	sulfur comp	2/2529	28/23049	0.828321	0.878077	0.84623	Slc26a7/Slc
GO_MF_m	GO:003525	steroid hor	7/2529	84/23049	0.828366	0.878077	0.84623	Calr/Lats1/

GO_MF_m	GO:001706	snRNA bin	3/2529	40/23049	0.830069	0.879449	0.847553	Ddx21/Hex
GO_MF_m	GO:001507	monovaler	35/2529	369/23049	0.842868	0.889341	0.857087	Atp1b2/Atp
GO_MF_m	GO:000110	RNA polym	2/2529	29/23049	0.842942	0.889341	0.857087	Hdac1/Hsp
GO_MF_m	GO:001514	monosacch	2/2529	29/23049	0.842942	0.889341	0.857087	Slc2a1/Slc5
GO_MF_m	GO:003644	proton-exp	2/2529	29/23049	0.842942	0.889341	0.857087	Atp6v0c/Tc
GO_MF_m	GO:004550	dynein ligh	2/2529	29/23049	0.842942	0.889341	0.857087	Dnah1/Dna
GO_MF_m	GO:003041	peptidase i	19/2529	210/23049	0.84352	0.889341	0.857087	Col28a1/Cs
GO_MF_m	GO:000486	endopeptic	18/2529	200/23049	0.84419	0.889341	0.857087	Col28a1/Cs
GO_MF_m	GO:000399	acyl-CoA c	1/2529	16/23049	0.844358	0.889341	0.857087	Acad11
GO_MF_m	GO:001509	magnesiun	1/2529	16/23049	0.844358	0.889341	0.857087	Zdhhc13
GO_MF_m	GO:004260	T cell recep	1/2529	16/23049	0.844358	0.889341	0.857087	H2-Q2
GO_MF_m	GO:005137	muscle alp	1/2529	16/23049	0.844358	0.889341	0.857087	Mypn
GO_MF_m	GO:199038	ubiquitin-s	1/2529	16/23049	0.844358	0.889341	0.857087	Park2
GO_MF_m	GO:001537	solute:sodi	6/2529	75/23049	0.844788	0.889359	0.857104	Slc10a4/Slc
GO_MF_m	GO:000486	serine-type	10/2529	119/23049	0.853658	0.898258	0.86568	Col28a1/Pl
GO_MF_m	GO:000403	aldo-keto	2/2529	30/23049	0.856423	0.89985	0.867214	Akr1b10/A
GO_MF_m	GO:005111	sugar trans	2/2529	30/23049	0.856423	0.89985	0.867214	Slc2a1/Slc5
GO_MF_m	GO:007185	neuropepti	2/2529	30/23049	0.856423	0.89985	0.867214	Prlh/Tac1
GO_MF_m	GO:000517	hormone a	11/2529	130/23049	0.856856	0.899866	0.867229	Adm/Amh/
GO_MF_m	GO:009951	ion antipor	4/2529	54/23049	0.857686	0.900299	0.867647	Slc22a5/Slc
GO_MF_m	GO:005142	hormone r	15/2529	172/23049	0.859348	0.901175	0.868491	Asxl1/Bcas
GO_MF_m	GO:000109	RNA polym	1/2529	17/23049	0.861448	0.901175	0.868491	Tbp
GO_MF_m	GO:000455	nucleoside	1/2529	17/23049	0.861448	0.901175	0.868491	Nme6
GO_MF_m	GO:000455	nucleotide	1/2529	17/23049	0.861448	0.901175	0.868491	Enpp2
GO_MF_m	GO:000523	inhibitory e	1/2529	17/23049	0.861448	0.901175	0.868491	Gabra6
GO_MF_m	GO:004342	protein kin	1/2529	17/23049	0.861448	0.901175	0.868491	Appl1
GO_MF_m	GO:004670	natural kille	1/2529	17/23049	0.861448	0.901175	0.868491	Ulbp1
GO_MF_m	GO:000823	metallopep	15/2529	173/23049	0.864974	0.903625	0.870852	Acy1/Adan
GO_MF_m	GO:001920	nucleobase	3/2529	43/23049	0.865048	0.903625	0.870852	Adk/N4bp2
GO_MF_m	GO:003293	sterol bind	3/2529	43/23049	0.865048	0.903625	0.870852	Gpr183/Os
GO_MF_m	GO:000099	RNA polym	2/2529	31/23049	0.868838	0.906705	0.87382	Rtraf/Esrrb
GO_MF_m	GO:000545	inorganic a	2/2529	31/23049	0.868838	0.906705	0.87382	Slc22a1/Slc
GO_MF_m	GO:004313	ubiquitin b	5/2529	67/23049	0.871937	0.909498	0.876513	Nploc4/Par
GO_MF_m	GO:001986	immunoglc	1/2529	18/23049	0.876661	0.912659	0.879559	Ms4a2
GO_MF_m	GO:002284	leak chann	1/2529	18/23049	0.876661	0.912659	0.879559	Kcnk2
GO_MF_m	GO:002284	narrow por	1/2529	18/23049	0.876661	0.912659	0.879559	Kcnk2
GO_MF_m	GO:005118	cofactor tra	1/2529	18/23049	0.876661	0.912659	0.879559	Slc46a1
GO_MF_m	GO:009909	ligand-gat	8/2529	101/23049	0.877102	0.912677	0.879576	Chrne/Chr
GO_MF_m	GO:000438	helicase ac	12/2529	144/23049	0.877961	0.913131	0.880013	Blm/Ddx19
GO_MF_m	GO:004550	dynein inte	2/2529	32/23049	0.880258	0.914393	0.88123	Dnah1/Pafa
GO_MF_m	GO:006163	ubiquitin c	2/2529	32/23049	0.880258	0.914393	0.88123	Ube2d1/Ub
GO_MF_m	GO:006113	endopeptic	18/2529	207/23049	0.880448	0.914393	0.88123	Col28a1/Cs
GO_MF_m	GO:003559	signaling a	4/2529	57/23049	0.884776	0.918445	0.885135	Bcar3/Ldlra
GO_MF_m	GO:000465	polypeptid	1/2529	19/23049	0.890205	0.921449	0.88803	Galnt9
GO_MF_m	GO:000540	carbohydra	1/2529	19/23049	0.890205	0.921449	0.88803	Slc5a4a
GO_MF_m	GO:000855	proton-exp	1/2529	19/23049	0.890205	0.921449	0.88803	Atp6v0c
GO_MF_m	GO:005186	glycolipid	1/2529	19/23049	0.890205	0.921449	0.88803	Pigu
GO_MF_m	GO:009760	cullin famil	1/2529	19/23049	0.890205	0.921449	0.88803	Park2

GO_MF_m	GO:005108	chaperone	7/2529	92/23049	0.890235	0.921449	0.88803	Ahsa2/Cdc
GO_MF_m	GO:006165	ubiquitin-li	2/2529	33/23049	0.890753	0.921542	0.888119	Ube2d1/Ub
GO_MF_m	GO:003033	estrogen re	3/2529	46/23049	0.893521	0.923963	0.890452	Lats1/Pcna
GO_MF_m	GO:003532	enhancer b	8/2529	104/23049	0.895751	0.925824	0.892246	Arx/Esrrb/F
GO_MF_m	GO:001502	glucuronos	2/2529	34/23049	0.900387	0.926775	0.893163	Csgalnact1
GO_MF_m	GO:003600	pre-mRNA	2/2529	34/23049	0.900387	0.926775	0.893163	Eri1/Zrsr2
GO_MF_m	GO:009771	disordered	2/2529	34/23049	0.900387	0.926775	0.893163	Ezr/Hspa1a
GO_MF_m	GO:000107	transcriptio	26/2529	294/23049	0.900858	0.926775	0.893163	Arid3c/Arn
GO_MF_m	GO:000109	basal trans	3/2529	47/23049	0.901739	0.926775	0.893163	Rtraf/Esrrb
GO_MF_m	GO:000109	basal RNA	3/2529	47/23049	0.901739	0.926775	0.893163	Rtraf/Esrrb
GO_MF_m	GO:003149	nucleosom	3/2529	47/23049	0.901739	0.926775	0.893163	Cenpa/H2a
GO_MF_m	GO:000113	RNA polym	1/2529	20/23049	0.902262	0.926775	0.893163	Nr1h2
GO_MF_m	GO:000815	protein pho	1/2529	20/23049	0.902262	0.926775	0.893163	Shoc2
GO_MF_m	GO:003525	glucocortic	1/2529	20/23049	0.902262	0.926775	0.893163	Nr4a1
GO_MF_m	GO:003819	neuropilin	1/2529	20/23049	0.902262	0.926775	0.893163	Sema3f
GO_MF_m	GO:007006	proline-ric	1/2529	20/23049	0.902262	0.926775	0.893163	Gigyf2
GO_MF_m	GO:009909	ligand-gat	1/2529	20/23049	0.902262	0.926775	0.893163	Gabra6
GO_MF_m	GO:000098	transcriptio	41/2529	446/23049	0.904092	0.928114	0.894453	Ifi207/Arid3
GO_MF_m	GO:003294	protein-co	6/2529	83/23049	0.904426	0.928114	0.894453	Akap6/Cav
GO_MF_m	GO:000382	antigen bin	18/2529	213/23049	0.905916	0.9292	0.8955	Abo/Gm11
GO_MF_m	GO:001990	phosphata	17/2529	203/23049	0.907708	0.930595	0.896844	Akap6/Atp
GO_MF_m	GO:000856	ATP-depen	1/2529	21/23049	0.912995	0.934238	0.900355	Dnah1
GO_MF_m	GO:003021	semaphori	1/2529	21/23049	0.912995	0.934238	0.900355	Sema3f
GO_MF_m	GO:003169	adrenergic	1/2529	21/23049	0.912995	0.934238	0.900355	Gria1
GO_MF_m	GO:004662	sphingolipi	1/2529	21/23049	0.912995	0.934238	0.900355	Pltp
GO_MF_m	GO:000486	cysteine-ty	5/2529	73/23049	0.914048	0.934872	0.900965	Cst6/Ctla2b
GO_MF_m	GO:000374	translation	3/2529	49/23049	0.916478	0.936911	0.902931	Eif1b/Eif3f/
GO_MF_m	GO:000003	mannosyltr	1/2529	22/23049	0.92255	0.942226	0.908053	Pigb
GO_MF_m	GO:001510	bicarbonat	1/2529	22/23049	0.92255	0.942226	0.908053	Slc26a7
GO_MF_m	GO:000097	RNA polym	42/2529	466/23049	0.928532	0.947885	0.913507	Ifi207/Arid3
GO_MF_m	GO:000154	amyloid-be	3/2529	51/23049	0.929172	0.947894	0.913516	Gria1/Ldlra
GO_MF_m	GO:000098	proximal p	43/2529	477/23049	0.93053	0.947894	0.913516	Ifi207/Arid3
GO_MF_m	GO:000101	transcriptio	1/2529	23/23049	0.931057	0.947894	0.913516	Nr1h2
GO_MF_m	GO:003143	mitogen-a	1/2529	23/23049	0.931057	0.947894	0.913516	Map4k2
GO_MF_m	GO:003037	ligand-dep	4/2529	64/23049	0.931135	0.947894	0.913516	Nr1h2/Pkn
GO_MF_m	GO:000471	protein ser	2/2529	38/23049	0.931518	0.947894	0.913516	Rps6kb1/T
GO_MF_m	GO:001527	ligand-gat	10/2529	134/23049	0.932059	0.947894	0.913516	Chrne/Chrn
GO_MF_m	GO:002283	ligand-gat	10/2529	134/23049	0.932059	0.947894	0.913516	Chrne/Chrn
GO_MF_m	GO:003498	immunoglo	11/2529	146/23049	0.935198	0.950538	0.916064	Ighv1-15/Ig
GO_MF_m	GO:001514	carbohydra	2/2529	39/23049	0.93772	0.950538	0.916064	Slc2a1/Slc5
GO_MF_m	GO:001548	cholesterol	2/2529	39/23049	0.93772	0.950538	0.916064	Osbpl8/Sta
GO_MF_m	GO:003226	phosphatid	2/2529	39/23049	0.93772	0.950538	0.916064	Plekhf2/Wi
GO_MF_m	GO:000006	fatty-acyl-	1/2529	24/23049	0.938629	0.950538	0.916064	Eci2
GO_MF_m	GO:000521	structural c	1/2529	24/23049	0.938629	0.950538	0.916064	Crybb3
GO_MF_m	GO:000524	voltage-ga	1/2529	24/23049	0.938629	0.950538	0.916064	Scn4a
GO_MF_m	GO:001707	syntaxin-1	1/2529	24/23049	0.938629	0.950538	0.916064	Dapk1
GO_MF_m	GO:001995	chemokine	1/2529	24/23049	0.938629	0.950538	0.916064	Ccr1
GO_MF_m	GO:000119	transcriptio	3/2529	53/23049	0.940069	0.95155	0.917039	Esrrb/Hdac

GO_MF_m1	GO:004362	protein sel	4/2529	66/23049	0.940856	0.951899	0.917375	Abcd3/Ach
GO_MF_m1	GO:000104	core prom	6/2529	91/23049	0.943169	0.953791	0.919199	Arntl/Clock
GO_MF_m1	GO:007006	RNA polym	3/2529	54/23049	0.944915	0.955109	0.920469	Rtraf/Esrrb/
GO_MF_m1	GO:004696	thyroid hor	1/2529	25/23049	0.94537	0.95512	0.92048	Taf11
GO_MF_m1	GO:004302	cysteine-ty	2/2529	41/23049	0.948559	0.957444	0.92272	Snca/Tnfrsf
GO_MF_m1	GO:004354	phosphatic	2/2529	41/23049	0.948559	0.957444	0.92272	Pdgfra/Ptp
GO_MF_m1	GO:000532	neurotrans	1/2529	26/23049	0.95137	0.959384	0.924589	Slc6a20a
GO_MF_m1	GO:001530	anion:anior	1/2529	26/23049	0.95137	0.959384	0.924589	Slc26a7
GO_MF_m1	GO:001508	sodium ior	11/2529	153/23049	0.955618	0.963216	0.928282	Atp1b2/Scn
GO_MF_m1	GO:000527	sodium cha	2/2529	43/23049	0.957582	0.964745	0.929756	Scn4a/Trpr
GO_MF_m1	GO:006009	molecular a	13/2529	178/23049	0.961164	0.967754	0.932656	Arrdc4/Bca
GO_MF_m1	GO:008300	structural c	1/2529	28/23049	0.961467	0.967754	0.932656	Tpm4
GO_MF_m1	GO:003218	ubiquitin-li	5/2529	86/23049	0.966083	0.971946	0.936696	Nploc4/Par
GO_MF_m1	GO:004302	cysteine-ty	1/2529	30/23049	0.969469	0.974897	0.93954	Snca
GO_MF_m1	GO:005069	WW doma	1/2529	31/23049	0.972823	0.977814	0.942351	Tceal9
GO_MF_m1	GO:001529	solute:catic	6/2529	102/23049	0.973511	0.978049	0.942577	Slc10a4/Slc
GO_MF_m1	GO:000110	RNA polym	2/2529	49/23049	0.976428	0.980523	0.944962	Exosc9/Lm
GO_MF_m1	GO:005195	dynein ligh	1/2529	33/23049	0.978467	0.981656	0.946053	Dnah1
GO_MF_m1	GO:014010	molecular	1/2529	33/23049	0.978467	0.981656	0.946053	Zfp593
GO_MF_m1	GO:000113	transcriptic	1/2529	35/23049	0.982939	0.985225	0.949493	Nr1h2
GO_MF_m1	GO:000480	triglyceride	1/2529	35/23049	0.982939	0.985225	0.949493	Pnpla2
GO_MF_m1	GO:001677	phosphotra	1/2529	36/23049	0.984814	0.986645	0.950861	Nme6
GO_MF_m1	GO:000555	pheromone	3/2529	90/23049	0.997939	0.99933	0.963086	Mup3/Vmr
GO_MF_m1	GO:001650	pheromone	3/2529	99/23049	0.99914	0.999638	0.963383	Vmn1r232/
GO_MF_m1	GO:000472	protein ser	1/2529	61/23049	0.999174	0.999638	0.963383	Ppp2r1a
GO_MF_m1	GO:000554	odorant bi	27/2529	463/23049	0.999961	0.999961	0.963694	Mup3/Obp
GO_MF_m2	GO:000104	core prom	7/451	91/23049	0.002067	0.181458	0.153718	Atf4/Cry1/
GO_MF_m2	GO:000371	transcriptic	13/451	262/23049	0.002084	0.181458	0.153718	Cebpa/Gm
GO_MF_m2	GO:000387	6-phospho	2/451	4/23049	0.002233	0.181458	0.153718	Pfkfb2/Pfkf
GO_MF_m2	GO:199071	mRNA CDS	2/451	4/23049	0.002233	0.181458	0.153718	Hnrnpa2b1
GO_MF_m2	GO:001682	lyase activi	10/451	178/23049	0.002745	0.181458	0.153718	Aco1/Adsl/
GO_MF_m2	GO:001674	transferase	11/451	211/23049	0.003075	0.181458	0.153718	Cad/Ftsj1/
GO_MF_m2	GO:003014	manganese	5/451	51/23049	0.003145	0.181458	0.153718	Cdipt/Galn
GO_MF_m2	GO:000015	phosphore	2/451	5/23049	0.003674	0.181458	0.153718	Kcnh2/Kcn
GO_MF_m2	GO:000151	opioid pep	2/451	5/23049	0.003674	0.181458	0.153718	Penk/Pnoc
GO_MF_m2	GO:000433	fructose-2,	2/451	5/23049	0.003674	0.181458	0.153718	Pfkfb2/Pfkf
GO_MF_m2	GO:005513	C3HC4-typ	2/451	5/23049	0.003674	0.181458	0.153718	Kcnh2/Pink
GO_MF_m2	GO:000524	voltage-ga	10/451	187/23049	0.003903	0.181458	0.153718	Cybb/Gpr8
GO_MF_m2	GO:002283	voltage-ga	10/451	187/23049	0.003903	0.181458	0.153718	Cybb/Gpr8
GO_MF_m2	GO:004432	ion channe	8/451	132/23049	0.004512	0.181458	0.153718	Agrn/Gpd1
GO_MF_m2	GO:001921	phosphata	4/451	36/23049	0.005193	0.181458	0.153718	Elfn2/Phac
GO_MF_m2	GO:000371	transcriptic	18/451	467/23049	0.005195	0.181458	0.153718	Cebpa/Cry
GO_MF_m2	GO:000412	cytochrom	2/451	6/23049	0.005439	0.181458	0.153718	Cyb5r4/Cy
GO_MF_m2	GO:000467	protein his	2/451	6/23049	0.005439	0.181458	0.153718	Kcnh2/Kcn
GO_MF_m2	GO:000816	methyltran	10/451	199/23049	0.006013	0.181458	0.153718	Ftsj1/Inmt/
GO_MF_m2	GO:005142	hormone r	9/451	172/23049	0.006936	0.181458	0.153718	Cry1/Hr/Ju
GO_MF_m2	GO:002284	voltage-ga	8/451	143/23049	0.007243	0.181458	0.153718	Grm7/Kcne
GO_MF_m2	GO:000844	phosphofru	2/451	7/23049	0.007517	0.181458	0.153718	Pfkfb2/Pfkf

GO_MF_m	GO:001687	ligase activ	9/451	176/23049	0.008013	0.181458	0.153718	Acaca/Acsl
GO_MF_m	GO:003525	nuclear ho	8/451	146/23049	0.008168	0.181458	0.153718	Cry1/Hr/Ju
GO_MF_m	GO:000003	mannosyltr	3/451	22/23049	0.008692	0.181458	0.153718	Alg9/Pigm
GO_MF_m	GO:001920	carbohydra	3/451	22/23049	0.008692	0.181458	0.153718	Pfkfb2/Pfkf
GO_MF_m	GO:014010	catalytic ac	7/451	119/23049	0.009003	0.181458	0.153718	2810006K2
GO_MF_m	GO:000471	non-memb	5/451	66/23049	0.009432	0.181458	0.153718	Csk/Dyrk1a
GO_MF_m	GO:005066	coenzyme	12/451	281/23049	0.009755	0.181458	0.153718	Acaca/Kyat
GO_MF_m	GO:004239	histone bin	9/451	182/23049	0.009861	0.181458	0.153718	Asf1a/Cks1
GO_MF_m	GO:001671	oxidoreduc	2/451	8/23049	0.009893	0.181458	0.153718	Fads1/Sc5
GO_MF_m	GO:003195	medium-c	2/451	8/23049	0.009893	0.181458	0.153718	Acsl4/Slc27
GO_MF_m	GO:010239	decanoate	2/451	8/23049	0.009893	0.181458	0.153718	Acsl4/Slc27
GO_MF_m	GO:001707	syntaxin-1	3/451	24/23049	0.0111	0.181458	0.153718	Snph/Stxb
GO_MF_m	GO:001990	syntaxin bi	6/451	96/23049	0.011477	0.181458	0.153718	Cplx4/Hect
GO_MF_m	GO:014009	catalytic ac	14/451	360/23049	0.011948	0.181458	0.153718	2810006K2
GO_MF_m	GO:001642	tRNA (cyto	2/451	9/23049	0.012556	0.181458	0.153718	Ftsj1/Nsun
GO_MF_m	GO:003162	opioid rece	2/451	9/23049	0.012556	0.181458	0.153718	Penk/Pnoc
GO_MF_m	GO:003195	very long-	2/451	9/23049	0.012556	0.181458	0.153718	Acsl4/Slc27
GO_MF_m	GO:000122	transcripti	4/451	47/23049	0.013296	0.181458	0.153718	Cdc5l/Chd
GO_MF_m	GO:003245	histone de	3/451	26/23049	0.013855	0.181458	0.153718	Hr/Jmjd6/
GO_MF_m	GO:000518	neuropepti	3/451	27/23049	0.015364	0.181458	0.153718	Agrp/Penk
GO_MF_m	GO:005030	sugar-pho	2/451	10/23049	0.015494	0.181458	0.153718	Pfkfb2/Pfkf
GO_MF_m	GO:007099	snRNP bin	2/451	10/23049	0.015494	0.181458	0.153718	Prpf31/Snr
GO_MF_m	GO:000516	transformi	4/451	51/23049	0.017531	0.181458	0.153718	Bmp4/Gdf
GO_MF_m	GO:005068	androgen	3/451	29/23049	0.018651	0.181458	0.153718	Kdm3a/Rn
GO_MF_m	GO:000116	RNA polym	2/451	11/23049	0.018694	0.181458	0.153718	Vax1/Zc3h
GO_MF_m	GO:001677	phosphotra	2/451	11/23049	0.018694	0.181458	0.153718	Kcnh2/Kcn
GO_MF_m	GO:001920	carbohydra	2/451	11/23049	0.018694	0.181458	0.153718	Pfkfb2/Pfkf
GO_MF_m	GO:004352	leucine zip	2/451	11/23049	0.018694	0.181458	0.153718	Atf4/Cdc5l
GO_MF_m	GO:001683	hydro-lyas	4/451	52/23049	0.018707	0.181458	0.153718	Aco1/Alad
GO_MF_m	GO:000024	C-5 sterol	1/451	1/23049	0.019567	0.181458	0.153718	Sc5d
GO_MF_m	GO:000169	pseudopho	1/451	1/23049	0.019567	0.181458	0.153718	Sbf1
GO_MF_m	GO:000388	CDP-diacy	1/451	1/23049	0.019567	0.181458	0.153718	Cdipt
GO_MF_m	GO:000397	RNA ligase	1/451	1/23049	0.019567	0.181458	0.153718	Rtcb
GO_MF_m	GO:000401	N6-(1,2-di	1/451	1/23049	0.019567	0.181458	0.153718	Adsl
GO_MF_m	GO:000458	ornithine-	1/451	1/23049	0.019567	0.181458	0.153718	Oat
GO_MF_m	GO:000465	porphobili	1/451	1/23049	0.019567	0.181458	0.153718	Alad
GO_MF_m	GO:000479	thioether S	1/451	1/23049	0.019567	0.181458	0.153718	Inmt
GO_MF_m	GO:000485	xylulokinas	1/451	1/23049	0.019567	0.181458	0.153718	Xylb
GO_MF_m	GO:000512	granulocyt	1/451	1/23049	0.019567	0.181458	0.153718	Csf2
GO_MF_m	GO:000811	sphinganin	1/451	1/23049	0.019567	0.181458	0.153718	Sgpl1
GO_MF_m	GO:000845	RNA ligase	1/451	1/23049	0.019567	0.181458	0.153718	Rtcb
GO_MF_m	GO:000847	isovaleryl-	1/451	1/23049	0.019567	0.181458	0.153718	Ivd
GO_MF_m	GO:000849	protoheme	1/451	1/23049	0.019567	0.181458	0.153718	Cox10
GO_MF_m	GO:000902	tRNA (gua	1/451	1/23049	0.019567	0.181458	0.153718	Ftsj1
GO_MF_m	GO:001085	adenylate	1/451	1/23049	0.019567	0.181458	0.153718	Grm7
GO_MF_m	GO:001085	adenylate	1/451	1/23049	0.019567	0.181458	0.153718	Grm7
GO_MF_m	GO:001519	L-tryptoph	1/451	1/23049	0.019567	0.181458	0.153718	Slc36a4
GO_MF_m	GO:001621	linoleoyl-C	1/451	1/23049	0.019567	0.181458	0.153718	Fads1

GO_MF_m	GO:001651	interleukin	1/451	1/23049	0.019567	0.181458	0.153718	Il12rb1
GO_MF_m	GO:003074	amine N-	1/451	1/23049	0.019567	0.181458	0.153718	Inmt
GO_MF_m	GO:003374	histone de	1/451	1/23049	0.019567	0.181458	0.153718	Jmjd6
GO_MF_m	GO:003374	histone de	1/451	1/23049	0.019567	0.181458	0.153718	Jmjd6
GO_MF_m	GO:003387	[heparan s	1/451	1/23049	0.019567	0.181458	0.153718	Hs3st3b1
GO_MF_m	GO:004454	GTP cycloh	1/451	1/23049	0.019567	0.181458	0.153718	Gchfr
GO_MF_m	GO:004699	oxidoreduc	1/451	1/23049	0.019567	0.181458	0.153718	Sc5d
GO_MF_m	GO:004712	thiomorph	1/451	1/23049	0.019567	0.181458	0.153718	Crym
GO_MF_m	GO:004731	kynurenine	1/451	1/23049	0.019567	0.181458	0.153718	Kyat3
GO_MF_m	GO:004767	arachidona	1/451	1/23049	0.019567	0.181458	0.153718	Acsl4
GO_MF_m	GO:004780	cysteamine	1/451	1/23049	0.019567	0.181458	0.153718	Ado
GO_MF_m	GO:005004	lathosterol	1/451	1/23049	0.019567	0.181458	0.153718	Sc5d
GO_MF_m	GO:005019	phytanate-	1/451	1/23049	0.019567	0.181458	0.153718	Slc27a2
GO_MF_m	GO:005266	tRNA (cyto	1/451	1/23049	0.019567	0.181458	0.153718	Ftsj1
GO_MF_m	GO:005291	dol-P-Mar	1/451	1/23049	0.019567	0.181458	0.153718	Alg9
GO_MF_m	GO:005292	dol-P-Mar	1/451	1/23049	0.019567	0.181458	0.153718	Alg9
GO_MF_m	GO:007025	pristanate-	1/451	1/23049	0.019567	0.181458	0.153718	Slc27a2
GO_MF_m	GO:007062	(S)-2-(5-ar	1/451	1/23049	0.019567	0.181458	0.153718	Adsl
GO_MF_m	GO:007070	sterol desa	1/451	1/23049	0.019567	0.181458	0.153718	Sc5d
GO_MF_m	GO:007171	para-amin	1/451	1/23049	0.019567	0.181458	0.153718	Pm20d2
GO_MF_m	GO:007257	poly-ADP-	1/451	1/23049	0.019567	0.181458	0.153718	Rnf146
GO_MF_m	GO:008004	GDP-D-gl	1/451	1/23049	0.019567	0.181458	0.153718	Gdpgp1
GO_MF_m	GO:009737	NAD-depe	1/451	1/23049	0.019567	0.181458	0.153718	Sirt7
GO_MF_m	GO:010605	tRNA 2'-O	1/451	1/23049	0.019567	0.181458	0.153718	Ftsj1
GO_MF_m	GO:199044	U2 snRNP	1/451	1/23049	0.019567	0.181458	0.153718	Snrpb
GO_MF_m	GO:000173	2'-5'-oligo	2/451	12/23049	0.022146	0.197075	0.166947	Oas1b/Oas
GO_MF_m	GO:001716	vinculin bir	2/451	12/23049	0.022146	0.197075	0.166947	Nrap/Rtcb
GO_MF_m	GO:003245	histone de	2/451	12/23049	0.022146	0.197075	0.166947	Hr/Kdm3a
GO_MF_m	GO:003970	co-recepto	2/451	12/23049	0.022146	0.197075	0.166947	Bmp4/Dkk
GO_MF_m	GO:003254	ribonucleo	13/451	354/23049	0.022938	0.202082	0.171188	Arl15/Cad/
GO_MF_m	GO:003162	ubiquitin p	12/451	322/23049	0.025527	0.216079	0.183046	Arrdc1/Der
GO_MF_m	GO:000411	3',5'-cyclic	2/451	13/23049	0.025838	0.216079	0.183046	Pde1a/Pde
GO_MF_m	GO:000446	long-chain	2/451	13/23049	0.025838	0.216079	0.183046	Acsl4/Slc27
GO_MF_m	GO:001564	toxic subst	2/451	13/23049	0.025838	0.216079	0.183046	Gucy2c/Ph
GO_MF_m	GO:001665	oxidoreduc	2/451	13/23049	0.025838	0.216079	0.183046	Cyb5r4/Cy
GO_MF_m	GO:000486	protein ph	3/451	33/23049	0.026303	0.216079	0.183046	Elfn2/Phac
GO_MF_m	GO:000875	S-adenosy	7/451	148/23049	0.026715	0.216079	0.183046	Ftsj1/Inmt/
GO_MF_m	GO:003218	ubiquitin-li	5/451	86/23049	0.026856	0.216079	0.183046	Cks1b/Nbr
GO_MF_m	GO:000512	cytokine re	12/451	325/23049	0.02716	0.216079	0.183046	Angpt4/Bm
GO_MF_m	GO:000188	nucleoside	13/451	364/23049	0.027921	0.216079	0.183046	Arl15/Cad/
GO_MF_m	GO:001517	neutral am	3/451	34/23049	0.028441	0.216079	0.183046	Slc25a38/S
GO_MF_m	GO:003256	guanyl ribo	13/451	366/23049	0.029006	0.216079	0.183046	Arl15/Eif5/
GO_MF_m	GO:001900	guanyl nuc	13/451	367/23049	0.02956	0.216079	0.183046	Arl15/Eif5/
GO_MF_m	GO:000033	RNA cap b	2/451	14/23049	0.02976	0.216079	0.183046	Eif4g3/Ncb
GO_MF_m	GO:000116	intronic tra	2/451	14/23049	0.02976	0.216079	0.183046	Vax1/Zc3h
GO_MF_m	GO:001659	glutamate	2/451	14/23049	0.02976	0.216079	0.183046	Glul/Grm7
GO_MF_m	GO:000817	RNA meth	4/451	60/23049	0.029865	0.216079	0.183046	Ftsj1/Mettl
GO_MF_m	GO:000471	protein tyr	7/451	152/23049	0.030287	0.216079	0.183046	Clk1/Csk/D

GO_MF_m	GO:00168	carbon-ox	4/451	61/23049	0.031484	0.216079	0.183046	Aco1/Alad/
GO_MF_m	GO:00052	voltage-ga	5/451	91/23049	0.033175	0.216079	0.183046	Kcne4/Kcn
GO_MF_m	GO:00305	acetylcholi	2/451	15/23049	0.033901	0.216079	0.183046	Agrn/Lypd
GO_MF_m	GO:00321	SUMO bin	2/451	15/23049	0.033901	0.216079	0.183046	Tollip/Zcch
GO_MF_m	GO:00342	protein kin	2/451	15/23049	0.033901	0.216079	0.183046	Csk/Prkar1
GO_MF_m	GO:004421	intronic tra	2/451	15/23049	0.033901	0.216079	0.183046	Vax1/Zc3h
GO_MF_m	GO:00996	neurotrans	2/451	15/23049	0.033901	0.216079	0.183046	Agrn/Lypd
GO_MF_m	GO:00443	ubiquitin-li	12/451	337/23049	0.034455	0.216079	0.183046	Arrdc1/Der
GO_MF_m	GO:00314	chromatin	5/451	92/23049	0.03454	0.216079	0.183046	H3f3b/Hr/
GO_MF_m	GO:000104	core prom	7/451	157/23049	0.035186	0.216079	0.183046	Atf4/Cry1/
GO_MF_m	GO:000097	RNA polym	3/451	37/23049	0.035388	0.216079	0.183046	H3f3b/Kdm
GO_MF_m	GO:000372	mRNA bin	9/451	228/23049	0.036157	0.216079	0.183046	Aco1/Elavl
GO_MF_m	GO:000471	protein ser	3/451	38/23049	0.03788	0.216079	0.183046	Aurkb/Clk1
GO_MF_m	GO:19903	ubiquitin-s	2/451	16/23049	0.038251	0.216079	0.183046	Chmp3/De
GO_MF_m	GO:000382	alpha-1,3-	1/451	2/23049	0.038752	0.216079	0.183046	Mgat1
GO_MF_m	GO:00039	acetyl-Co	1/451	2/23049	0.038752	0.216079	0.183046	Acaca
GO_MF_m	GO:00039	aconitate h	1/451	2/23049	0.038752	0.216079	0.183046	Aco1
GO_MF_m	GO:000407	aspartate c	1/451	2/23049	0.038752	0.216079	0.183046	Cad
GO_MF_m	GO:000407	biotin carb	1/451	2/23049	0.038752	0.216079	0.183046	Acaca
GO_MF_m	GO:00040	carbamoyl-	1/451	2/23049	0.038752	0.216079	0.183046	Cad
GO_MF_m	GO:00040	carbamoyl-	1/451	2/23049	0.038752	0.216079	0.183046	Cad
GO_MF_m	GO:00041	dihydroorc	1/451	2/23049	0.038752	0.216079	0.183046	Cad
GO_MF_m	GO:000434	glucosylce	1/451	2/23049	0.038752	0.216079	0.183046	Gba2
GO_MF_m	GO:00043	glutamate-	1/451	2/23049	0.038752	0.216079	0.183046	Glul
GO_MF_m	GO:000441	hydroxyme	1/451	2/23049	0.038752	0.216079	0.183046	Hmgcl
GO_MF_m	GO:000481	glutamate-	1/451	2/23049	0.038752	0.216079	0.183046	Eprs
GO_MF_m	GO:00048	tryptophan	1/451	2/23049	0.038752	0.216079	0.183046	Wars2
GO_MF_m	GO:000491	interleukin	1/451	2/23049	0.038752	0.216079	0.183046	Cxcr1
GO_MF_m	GO:00050	peroxisom	1/451	2/23049	0.038752	0.216079	0.183046	Pex5l
GO_MF_m	GO:00051	interleukin	1/451	2/23049	0.038752	0.216079	0.183046	Tollip
GO_MF_m	GO:00081	4-alpha-hy	1/451	2/23049	0.038752	0.216079	0.183046	Pcbd1
GO_MF_m	GO:001517	aromatic a	1/451	2/23049	0.038752	0.216079	0.183046	Slc36a4
GO_MF_m	GO:00161	translation	1/451	2/23049	0.038752	0.216079	0.183046	2810006K2
GO_MF_m	GO:001621	ammonia li	1/451	2/23049	0.038752	0.216079	0.183046	Glul
GO_MF_m	GO:00166	oxidoreduc	1/451	2/23049	0.038752	0.216079	0.183046	Crym
GO_MF_m	GO:004201	interleukin	1/451	2/23049	0.038752	0.216079	0.183046	Il12rb1
GO_MF_m	GO:004202	interleukin	1/451	2/23049	0.038752	0.216079	0.183046	Il12rb1
GO_MF_m	GO:00478	cysteine-S	1/451	2/23049	0.038752	0.216079	0.183046	Kyat3
GO_MF_m	GO:00711	RNA trime	1/451	2/23049	0.038752	0.216079	0.183046	Tgs1
GO_MF_m	GO:19048	proteasom	1/451	2/23049	0.038752	0.216079	0.183046	Alad
GO_MF_m	GO:000552	GTP bindin	12/451	344/23049	0.039304	0.217781	0.184488	Arl15/Eif5/
GO_MF_m	GO:00228	ion gated	11/451	307/23049	0.0402	0.220742	0.186996	Cybb/Gpr8
GO_MF_m	GO:003097	receptor ty	4/451	66/23049	0.04034	0.220742	0.186996	Angpt4/Fiz
GO_MF_m	GO:00431	ubiquitin b	4/451	67/23049	0.042264	0.226151	0.191578	Cks1b/Nbr
GO_MF_m	GO:00228	gated char	11/451	310/23049	0.042605	0.226151	0.191578	Cybb/Gpr8
GO_MF_m	GO:003027	LRR domai	2/451	17/23049	0.042801	0.226151	0.191578	Atf4/Cdc5l
GO_MF_m	GO:000517	hormone a	6/451	130/23049	0.042841	0.226151	0.191578	Agrp/Erfe/
GO_MF_m	GO:00325	purine ribo	12/451	349/23049	0.043049	0.226151	0.191578	Arl15/Eif5/

GO_MF_m	GO:00170	snRNA bin	3/451	40/23049	0.043125	0.226151	0.191578	Ncbp2/Prp
GO_MF_m	GO:00324	demethyla	3/451	40/23049	0.043125	0.226151	0.191578	Hr/Jmjd6/K
GO_MF_m	GO:00018	purine nuc	12/451	353/23049	0.046219	0.236525	0.200366	Arl15/Eif5/
GO_MF_m	GO:00037	mRNA 3'-U	4/451	69/23049	0.046266	0.236525	0.200366	Elavl1/Hnrr
GO_MF_m	GO:000014	SNARE bin	6/451	133/23049	0.046968	0.236525	0.200366	Cplx4/Hect
GO_MF_m	GO:00199	phosphata	8/451	203/23049	0.046984	0.236525	0.200366	Cdc5l/Cry1
GO_MF_m	GO:00165	amino acid	4/451	71/23049	0.050471	0.236525	0.200366	Cad/Gchfr/
GO_MF_m	GO:000122	transcriptic	2/451	19/23049	0.052463	0.236525	0.200366	Cdc5l/Six3
GO_MF_m	GO:001564	fatty acid li	2/451	19/23049	0.052463	0.236525	0.200366	Acsl4/Slc27
GO_MF_m	GO:004327	phospholip	2/451	19/23049	0.052463	0.236525	0.200366	Sele/Stxbp
GO_MF_m	GO:00081	protein ph	2/451	20/23049	0.057556	0.236525	0.200366	Cdc5l/Phac
GO_MF_m	GO:00700	proline-ricl	2/451	20/23049	0.057556	0.236525	0.200366	Csk/Wbp4
GO_MF_m	GO:000002	alpha-1,2-	1/451	3/23049	0.057562	0.236525	0.200366	Alg9
GO_MF_m	GO:000411	calmodulin	1/451	3/23049	0.057562	0.236525	0.200366	Pde1a
GO_MF_m	GO:00043	glutamate	1/451	3/23049	0.057562	0.236525	0.200366	Glul
GO_MF_m	GO:00045	phenylalan	1/451	3/23049	0.057562	0.236525	0.200366	Pcbd1
GO_MF_m	GO:00045	5'-3' exorib	1/451	3/23049	0.057562	0.236525	0.200366	Xrn1
GO_MF_m	GO:000472	magnesium	1/451	3/23049	0.057562	0.236525	0.200366	Pdp1
GO_MF_m	GO:000474	[pyruvate c	1/451	3/23049	0.057562	0.236525	0.200366	Pdp1
GO_MF_m	GO:000482	proline-tRI	1/451	3/23049	0.057562	0.236525	0.200366	Eprs
GO_MF_m	GO:00082	3-oxoacid	1/451	3/23049	0.057562	0.236525	0.200366	Oxct1
GO_MF_m	GO:000844	N-acetylgl	1/451	3/23049	0.057562	0.236525	0.200366	Sulf2
GO_MF_m	GO:00085	sucrose:pro	1/451	3/23049	0.057562	0.236525	0.200366	Slc45a4
GO_MF_m	GO:000851	sucrose tra	1/451	3/23049	0.057562	0.236525	0.200366	Slc45a4
GO_MF_m	GO:00096	sucrose:cat	1/451	3/23049	0.057562	0.236525	0.200366	Slc45a4
GO_MF_m	GO:00151	disaccharic	1/451	3/23049	0.057562	0.236525	0.200366	Slc45a4
GO_MF_m	GO:00151	oligosacch	1/451	3/23049	0.057562	0.236525	0.200366	Slc45a4
GO_MF_m	GO:001642	mRNA (2'-	1/451	3/23049	0.057562	0.236525	0.200366	Mettl14
GO_MF_m	GO:001674	carboxyl- c	1/451	3/23049	0.057562	0.236525	0.200366	Cad
GO_MF_m	GO:001707	oxidative p	1/451	3/23049	0.057562	0.236525	0.200366	Ucp2
GO_MF_m	GO:00198	IgA binding	1/451	3/23049	0.057562	0.236525	0.200366	Ambp
GO_MF_m	GO:00199	interleukin-	1/451	3/23049	0.057562	0.236525	0.200366	Cxcr1
GO_MF_m	GO:00303	iron-respo	1/451	3/23049	0.057562	0.236525	0.200366	Aco1
GO_MF_m	GO:003062	U4atac snR	1/451	3/23049	0.057562	0.236525	0.200366	Prpf31
GO_MF_m	GO:00315	thyrotropir	1/451	3/23049	0.057562	0.236525	0.200366	Psmc5
GO_MF_m	GO:003221	riboflavin t	1/451	3/23049	0.057562	0.236525	0.200366	Slc52a3
GO_MF_m	GO:003374	L-methioni	1/451	3/23049	0.057562	0.236525	0.200366	Msrb3
GO_MF_m	GO:003382	O-fucosylp	1/451	3/23049	0.057562	0.236525	0.200366	Lfng
GO_MF_m	GO:00347	histone de	1/451	3/23049	0.057562	0.236525	0.200366	Sirt7
GO_MF_m	GO:004342	3-phospho	1/451	3/23049	0.057562	0.236525	0.200366	Ptk2b
GO_MF_m	GO:00477	chondroitir	1/451	3/23049	0.057562	0.236525	0.200366	Chst12
GO_MF_m	GO:00481	calcium- a	1/451	3/23049	0.057562	0.236525	0.200366	Pde1a
GO_MF_m	GO:00484	epidermal	1/451	3/23049	0.057562	0.236525	0.200366	Shc1
GO_MF_m	GO:00515	3 iron, 4 su	1/451	3/23049	0.057562	0.236525	0.200366	Aco1
GO_MF_m	GO:00709	serine bind	1/451	3/23049	0.057562	0.236525	0.200366	Grm7
GO_MF_m	GO:00712	histone pre	1/451	3/23049	0.057562	0.236525	0.200366	Snrpb
GO_MF_m	GO:19907	protein bin	1/451	3/23049	0.057562	0.236525	0.200366	Arrdc1
GO_MF_m	GO:000481	aminoacyl-	3/451	45/23049	0.057722	0.236525	0.200366	Eprs/Farsa/

GO_MF_m	GO:001687	ligase activ	3/451	45/23049	0.057722	0.236525	0.200366	Eprs/Farsa/
GO_MF_m	GO:001678	transferase	4/451	75/23049	0.059487	0.242629	0.205537	Chst12/Chs
GO_MF_m	GO:003140	carboxylic	8/451	214/23049	0.060308	0.244843	0.207412	Acaca/Cad
GO_MF_m	GO:199084	promoter-	3/451	46/23049	0.060887	0.246062	0.208445	Chd7/Foxo
GO_MF_m	GO:004317	organic aci	8/451	219/23049	0.067076	0.269833	0.228582	Acaca/Cad
GO_MF_m	GO:000808	growth fac	6/451	146/23049	0.067625	0.270003	0.228726	Bmp4/Csf2
GO_MF_m	GO:000848	transamina	2/451	22/23049	0.068225	0.270003	0.228726	Kyat3/Oat
GO_MF_m	GO:001920	phosphata	4/451	79/23049	0.0693	0.270003	0.228726	Elfn2/Phac
GO_MF_m	GO:001517	amino acid	4/451	80/23049	0.071876	0.270003	0.228726	Slc6a21/Slc
GO_MF_m	GO:001640	CoA-ligase	2/451	23/23049	0.073784	0.270003	0.228726	Acsl4/Slc27
GO_MF_m	GO:001687	ligase activ	3/451	50/23049	0.074331	0.270003	0.228726	Acaca/Cad
GO_MF_m	GO:199078	protein tyr	4/451	81/23049	0.0745	0.270003	0.228726	Angpt4/Fiz
GO_MF_m	GO:000029	ferric-chela	1/451	4/23049	0.076005	0.270003	0.228726	Cybrd1
GO_MF_m	GO:000164	group III m	1/451	4/23049	0.076005	0.270003	0.228726	Grm7
GO_MF_m	GO:000213	UTP bindin	1/451	4/23049	0.076005	0.270003	0.228726	Cad
GO_MF_m	GO:000398	acetyl-CoA	1/451	4/23049	0.076005	0.270003	0.228726	Acat2
GO_MF_m	GO:000406	arylsulfatas	1/451	4/23049	0.076005	0.270003	0.228726	Sulf2
GO_MF_m	GO:000412	cytidylate k	1/451	4/23049	0.076005	0.270003	0.228726	Ak8
GO_MF_m	GO:000436	glycerol-3-	1/451	4/23049	0.076005	0.270003	0.228726	Gpd1l
GO_MF_m	GO:000500	transmemb	1/451	4/23049	0.076005	0.270003	0.228726	Ptprm
GO_MF_m	GO:000850	melatonin	1/451	4/23049	0.076005	0.270003	0.228726	Gpr50
GO_MF_m	GO:000937	biotin bind	1/451	4/23049	0.076005	0.270003	0.228726	Acaca
GO_MF_m	GO:001621	kynurenine	1/451	4/23049	0.076005	0.270003	0.228726	Kyat3
GO_MF_m	GO:001688	acid-ammo	1/451	4/23049	0.076005	0.270003	0.228726	Glul
GO_MF_m	GO:001919	transmemb	1/451	4/23049	0.076005	0.270003	0.228726	Ptprm
GO_MF_m	GO:003029	transmemb	1/451	4/23049	0.076005	0.270003	0.228726	Angpt4
GO_MF_m	GO:003094	mitochond	1/451	4/23049	0.076005	0.270003	0.228726	Tomm20
GO_MF_m	GO:003169	beta-1 adr	1/451	4/23049	0.076005	0.270003	0.228726	Sh3gl1
GO_MF_m	GO:003255	pyrimidine	1/451	4/23049	0.076005	0.270003	0.228726	Cad
GO_MF_m	GO:003256	dATP bindi	1/451	4/23049	0.076005	0.270003	0.228726	Hist1h1e
GO_MF_m	GO:003374	peptide-m	1/451	4/23049	0.076005	0.270003	0.228726	Msrb3
GO_MF_m	GO:003613	kynurenine	1/451	4/23049	0.076005	0.270003	0.228726	Kyat3
GO_MF_m	GO:005262	phosphatic	1/451	4/23049	0.076005	0.270003	0.228726	Mtmr2
GO_MF_m	GO:007081	peptidyl-ly	1/451	4/23049	0.076005	0.270003	0.228726	Jmjd6
GO_MF_m	GO:003017	pyridoxal p	3/451	51/23049	0.077881	0.275554	0.233428	Kyat3/Oat/
GO_MF_m	GO:000411	3',5'-cyclic-	2/451	24/23049	0.079483	0.276777	0.234464	Pde1a/Pde
GO_MF_m	GO:001676	transferase	2/451	24/23049	0.079483	0.276777	0.234464	Kyat3/Oat
GO_MF_m	GO:004332	phosphatic	2/451	24/23049	0.079483	0.276777	0.234464	Arap3/Myo
GO_MF_m	GO:005286	phosphatic	2/451	24/23049	0.079483	0.276777	0.234464	Mtmr2/Mtr
GO_MF_m	GO:005066	flavin aden	4/451	83/23049	0.079891	0.277104	0.234741	Cyb5r4/Cyb
GO_MF_m	GO:007027	vitamin B6	3/451	52/23049	0.081504	0.280989	0.238033	Kyat3/Oat/
GO_MF_m	GO:003525	steroid hor	4/451	84/23049	0.082658	0.280989	0.238033	Kdm3a/Nr4
GO_MF_m	GO:001683	carbon-car	3/451	53/23049	0.085198	0.280989	0.238033	Glul/Hmgc
GO_MF_m	GO:000411	cyclic-nucl	2/451	25/23049	0.085313	0.280989	0.238033	Pde1a/Pde
GO_MF_m	GO:003517	histone ser	2/451	25/23049	0.085313	0.280989	0.238033	Aurkb/Stk-
GO_MF_m	GO:004696	thyroid hor	2/451	25/23049	0.085313	0.280989	0.238033	Hr/Thrap3
GO_MF_m	GO:001665	oxidoreduc	4/451	86/23049	0.08833	0.280989	0.238033	Cyb5r4/Cyb
GO_MF_m	GO:000419	aspartic-ty	2/451	26/23049	0.091268	0.280989	0.238033	Bace1/Cym

GO_MF_m	GO:001687	acid-thiol l	2/451	26/23049	0.091268	0.280989	0.238033	Acsl4/Slc27
GO_MF_m	GO:007194	FAD bindin	2/451	26/23049	0.091268	0.280989	0.238033	Cyb5r4/Cy
GO_MF_m	GO:000814	sulfotransf	3/451	55/23049	0.092796	0.280989	0.238033	Chst12/Ch
GO_MF_m	GO:000026	peroxisom	1/451	5/23049	0.094088	0.280989	0.238033	Pex5l
GO_MF_m	GO:000106	regulatory	1/451	5/23049	0.094088	0.280989	0.238033	Hnrnpa2b1
GO_MF_m	GO:000188	pyrimidine	1/451	5/23049	0.094088	0.280989	0.238033	Cad
GO_MF_m	GO:000404	aminoacyl-	1/451	5/23049	0.094088	0.280989	0.238033	2810006K2
GO_MF_m	GO:000416	dolichyl-p	1/451	5/23049	0.094088	0.280989	0.238033	Sdf2
GO_MF_m	GO:000431	farnesyltra	1/451	5/23049	0.094088	0.280989	0.238033	Cox10
GO_MF_m	GO:000464	phosphory	1/451	5/23049	0.094088	0.280989	0.238033	Gdpgp1
GO_MF_m	GO:000482	phenylalan	1/451	5/23049	0.094088	0.280989	0.238033	Farsa
GO_MF_m	GO:000492	interleukin	1/451	5/23049	0.094088	0.280989	0.238033	Il10rb
GO_MF_m	GO:000514	interleukin	1/451	5/23049	0.094088	0.280989	0.238033	Il12rb1
GO_MF_m	GO:000841	CoA-trans	1/451	5/23049	0.094088	0.280989	0.238033	Oxct1
GO_MF_m	GO:000842	beta-gluc	1/451	5/23049	0.094088	0.280989	0.238033	Gba2
GO_MF_m	GO:000846	[heparan s	1/451	5/23049	0.094088	0.280989	0.238033	Hs3st3b1
GO_MF_m	GO:000937	four-way j	1/451	5/23049	0.094088	0.280989	0.238033	Recql
GO_MF_m	GO:001631	inositol bis	1/451	5/23049	0.094088	0.280989	0.238033	Mtmr7
GO_MF_m	GO:001645	C-acetyltra	1/451	5/23049	0.094088	0.280989	0.238033	Acat2
GO_MF_m	GO:001683	oxo-acid-l	1/451	5/23049	0.094088	0.280989	0.238033	Hmgcl
GO_MF_m	GO:003029	protein tyr	1/451	5/23049	0.094088	0.280989	0.238033	Rack1
GO_MF_m	GO:003062	U4 snRNA	1/451	5/23049	0.094088	0.280989	0.238033	Prpf31
GO_MF_m	GO:003255	pyrimidine	1/451	5/23049	0.094088	0.280989	0.238033	Cad
GO_MF_m	GO:003255	adenyl dec	1/451	5/23049	0.094088	0.280989	0.238033	Hist1h1e
GO_MF_m	GO:003448	chondroiti	1/451	5/23049	0.094088	0.280989	0.238033	Chst12
GO_MF_m	GO:004203	ATPase inh	1/451	5/23049	0.094088	0.280989	0.238033	Agrn
GO_MF_m	GO:004849	Roundabo	1/451	5/23049	0.094088	0.280989	0.238033	Tgfb1i1
GO_MF_m	GO:006157	cyclin-dep	1/451	5/23049	0.094088	0.280989	0.238033	Cks1b
GO_MF_m	GO:007008	chromo sh	1/451	5/23049	0.094088	0.280989	0.238033	Chaf1a
GO_MF_m	GO:007107	eukaryotic	1/451	5/23049	0.094088	0.280989	0.238033	Eif5
GO_MF_m	GO:007198	WD40-rep	1/451	5/23049	0.094088	0.280989	0.238033	Cdc5l
GO_MF_m	GO:010601	phosphatic	1/451	5/23049	0.094088	0.280989	0.238033	Mtmr2
GO_MF_m	GO:190228	voltage-ga	1/451	5/23049	0.094088	0.280989	0.238033	Kcnh2
GO_MF_m	GO:000004	tRNA bindi	3/451	56/23049	0.096696	0.284907	0.241352	Farsa/Nsur
GO_MF_m	GO:001675	transferase	7/451	199/23049	0.096948	0.284907	0.241352	Alg9/Galnt
GO_MF_m	GO:000525	delayed re	2/451	27/23049	0.097341	0.284907	0.241352	Kcnh2/Kcn
GO_MF_m	GO:000806	glutamate	2/451	27/23049	0.097341	0.284907	0.241352	Grm7/Ptk2
GO_MF_m	GO:001709	AU-rich el	2/451	27/23049	0.097341	0.284907	0.241352	Dnd1/Elavl
GO_MF_m	GO:007000	aspartic-ty	2/451	27/23049	0.097341	0.284907	0.241352	Bace1/Cym
GO_MF_m	GO:004801	receptor lig	14/451	486/23049	0.098018	0.285939	0.242226	Agrp/Bmp
GO_MF_m	GO:005121	dioxygenas	4/451	91/23049	0.103301	0.300358	0.25444	Ado/Alkbh
GO_MF_m	GO:000526	potassium	5/451	127/23049	0.104278	0.302201	0.256001	Kcne4/Kcn
GO_MF_m	GO:000817	tRNA meth	2/451	29/23049	0.10981	0.306891	0.259974	Ftsj1/Nsun
GO_MF_m	GO:000151	N-acetylgl	1/451	6/23049	0.111818	0.306891	0.259974	Chst5
GO_MF_m	GO:000516	neurotrop	1/451	6/23049	0.111818	0.306891	0.259974	Shc1
GO_MF_m	GO:000817	S-methyltr	1/451	6/23049	0.111818	0.306891	0.259974	Inmt
GO_MF_m	GO:000860	cAMP-dep	1/451	6/23049	0.111818	0.306891	0.259974	Prkar1a
GO_MF_m	GO:001509	ferrous iro	1/451	6/23049	0.111818	0.306891	0.259974	Slc25a28

GO_MF_m	GO:001545	P-P-bond-	1/451	6/23049	0.111818	0.306891	0.259974	Tomm20
GO_MF_m	GO:001642	CoA carbo	1/451	6/23049	0.111818	0.306891	0.259974	Acaca
GO_MF_m	GO:001681	hydrolase a	1/451	6/23049	0.111818	0.306891	0.259974	Cad
GO_MF_m	GO:001995	C-X-C che	1/451	6/23049	0.111818	0.306891	0.259974	Cxcr1
GO_MF_m	GO:003062	U2 snRNA	1/451	6/23049	0.111818	0.306891	0.259974	Snrpb
GO_MF_m	GO:003255	purine deo	1/451	6/23049	0.111818	0.306891	0.259974	Hist1h1e
GO_MF_m	GO:003537	chondroiti	1/451	6/23049	0.111818	0.306891	0.259974	Agrn
GO_MF_m	GO:003640	proteasom	1/451	6/23049	0.111818	0.306891	0.259974	Psmc5
GO_MF_m	GO:004679	virion bind	1/451	6/23049	0.111818	0.306891	0.259974	Tsg101
GO_MF_m	GO:007088	pre-miRNA	1/451	6/23049	0.111818	0.306891	0.259974	Ran
GO_MF_m	GO:199076	arrestin fa	1/451	6/23049	0.111818	0.306891	0.259974	Arrdc1
GO_MF_m	GO:001517	L-amino ac	3/451	60/23049	0.112938	0.309001	0.261762	Slc25a38/S
GO_MF_m	GO:000164	adenylate c	1/451	7/23049	0.129202	0.329054	0.27875	Grm7
GO_MF_m	GO:000374	translation	1/451	7/23049	0.129202	0.329054	0.27875	2810006K2
GO_MF_m	GO:000497	NMDA glu	1/451	7/23049	0.129202	0.329054	0.27875	Ptk2b
GO_MF_m	GO:000807	translation	1/451	7/23049	0.129202	0.329054	0.27875	2810006K2
GO_MF_m	GO:001085	cyclase reg	1/451	7/23049	0.129202	0.329054	0.27875	Grm7
GO_MF_m	GO:001518	L-alanine t	1/451	7/23049	0.129202	0.329054	0.27875	Slc36a4
GO_MF_m	GO:001524	fatty acid t	1/451	7/23049	0.129202	0.329054	0.27875	Slc27a2
GO_MF_m	GO:001621	acyl-CoA c	1/451	7/23049	0.129202	0.329054	0.27875	Fads1
GO_MF_m	GO:001642	tRNA (cyto	1/451	7/23049	0.129202	0.329054	0.27875	Nsun2
GO_MF_m	GO:001671	oxidoreduc	1/451	7/23049	0.129202	0.329054	0.27875	Pcbd1
GO_MF_m	GO:001684	amidine-ly	1/451	7/23049	0.129202	0.329054	0.27875	Adsl
GO_MF_m	GO:001716	CDP-alcoh	1/451	7/23049	0.129202	0.329054	0.27875	Cdipt
GO_MF_m	GO:002285	alanine tra	1/451	7/23049	0.129202	0.329054	0.27875	Slc36a4
GO_MF_m	GO:003369	sialic acid b	1/451	7/23049	0.129202	0.329054	0.27875	Sele
GO_MF_m	GO:004228	MHC class	1/451	7/23049	0.129202	0.329054	0.27875	Col2a1
GO_MF_m	GO:004697	histone me	1/451	7/23049	0.129202	0.329054	0.27875	Suz12
GO_MF_m	GO:004713	protein-dis	1/451	7/23049	0.129202	0.329054	0.27875	Txndc17
GO_MF_m	GO:005188	G-quadrup	1/451	7/23049	0.129202	0.329054	0.27875	Xrn1
GO_MF_m	GO:006113	endopeptic	1/451	7/23049	0.129202	0.329054	0.27875	Sfrp2
GO_MF_m	GO:006167	importin-a	1/451	7/23049	0.129202	0.329054	0.27875	Ran
GO_MF_m	GO:007032	thyroid hor	1/451	7/23049	0.129202	0.329054	0.27875	Crym
GO_MF_m	GO:007234	NAADP-se	1/451	7/23049	0.129202	0.329054	0.27875	Tpcn1
GO_MF_m	GO:199024	N6-methyl	1/451	7/23049	0.129202	0.329054	0.27875	Hnrnpa2b1
GO_MF_m	GO:006163	ubiquitin c	2/451	32/23049	0.129231	0.329054	0.27875	Ube2j1/Ub
GO_MF_m	GO:001650	peptidase a	2/451	33/23049	0.135872	0.342989	0.290554	Rack1/Sfrp
GO_MF_m	GO:004228	MHC prote	2/451	33/23049	0.135872	0.342989	0.290554	Col2a1/De
GO_MF_m	GO:006165	ubiquitin-li	2/451	33/23049	0.135872	0.342989	0.290554	Ube2j1/Ub
GO_MF_m	GO:009909	ligand-gat	4/451	101/23049	0.136393	0.343321	0.290835	Kcnh2/Pex
GO_MF_m	GO:190293	phosphatic	4/451	102/23049	0.139915	0.346963	0.29392	Arap3/Chm
GO_MF_m	GO:000521	intracellula	2/451	34/23049	0.142586	0.346963	0.29392	Pex5l/Tpcn
GO_MF_m	GO:003033	cyclin bind	2/451	34/23049	0.142586	0.346963	0.29392	Rack1/Klhc
GO_MF_m	GO:007056	adenylyltra	2/451	34/23049	0.142586	0.346963	0.29392	Oas1b/Oas
GO_MF_m	GO:000395	NADPH-he	1/451	8/23049	0.146246	0.346963	0.29392	Cyb5r4
GO_MF_m	GO:000430	enoyl-CoA	1/451	8/23049	0.146246	0.346963	0.29392	Echdc2
GO_MF_m	GO:000486	cAMP-dep	1/451	8/23049	0.146246	0.346963	0.29392	Prkar1a
GO_MF_m	GO:001518	glycine tra	1/451	8/23049	0.146246	0.346963	0.29392	Slc25a38

GO_MF_m	GO:001519	L-proline t	1/451	8/23049	0.146246	0.346963	0.29392	Slc36a4
GO_MF_m	GO:001519	L-serine tra	1/451	8/23049	0.146246	0.346963	0.29392	Slc7a10
GO_MF_m	GO:001617	superoxide	1/451	8/23049	0.146246	0.346963	0.29392	Cybb
GO_MF_m	GO:001649	C-X-C che	1/451	8/23049	0.146246	0.346963	0.29392	Cxcr1
GO_MF_m	GO:001688	ligase activ	1/451	8/23049	0.146246	0.346963	0.29392	Acaca
GO_MF_m	GO:001999	diacylglyce	1/451	8/23049	0.146246	0.346963	0.29392	Cdipt
GO_MF_m	GO:002288	serine tran	1/451	8/23049	0.146246	0.346963	0.29392	Slc7a10
GO_MF_m	GO:003255	deoxyribon	1/451	8/23049	0.146246	0.346963	0.29392	Hist1h1e
GO_MF_m	GO:003631	annealing	1/451	8/23049	0.146246	0.346963	0.29392	Recql
GO_MF_m	GO:004280	vitamin D r	1/451	8/23049	0.146246	0.346963	0.29392	Hr
GO_MF_m	GO:004314	ATP-depen	1/451	8/23049	0.146246	0.346963	0.29392	Recql
GO_MF_m	GO:009715	pre-mRNA	1/451	8/23049	0.146246	0.346963	0.29392	Hnrnpa2b1
GO_MF_m	GO:199044	U1 snRNP	1/451	8/23049	0.146246	0.346963	0.29392	Snrpb
GO_MF_m	GO:000512	cytokine ac	7/451	222/23049	0.146504	0.346963	0.29392	Bmp4/Csf2
GO_MF_m	GO:001988	protein pho	3/451	68/23049	0.148177	0.349984	0.296479	Elfn2/Phac
GO_MF_m	GO:000853	Ran GTPas	2/451	35/23049	0.149369	0.350918	0.297271	Ipo7/Ipo8
GO_MF_m	GO:001711	Rab guany	2/451	35/23049	0.149369	0.350918	0.297271	Dennd2a/S
GO_MF_m	GO:000526	cation chan	9/451	307/23049	0.150046	0.351571	0.297824	Grm7/Kcne
GO_MF_m	GO:000438	helicase ac	5/451	144/23049	0.152644	0.35671	0.302177	Chd6/Chd7
GO_MF_m	GO:000417	endopeptid	12/451	438/23049	0.153251	0.357179	0.302575	Bace1/Cap
GO_MF_m	GO:001526	channel ac	12/451	439/23049	0.154964	0.359271	0.304347	Cybb/Gpr8
GO_MF_m	GO:002280	passive tra	12/451	439/23049	0.154964	0.359271	0.304347	Cybb/Gpr8
GO_MF_m	GO:007085	growth fac	5/451	145/23049	0.155743	0.359337	0.304402	Angpt4/Cs
GO_MF_m	GO:001683	carboxy-ly	2/451	36/23049	0.156216	0.359337	0.304402	Glul/Sgpl1
GO_MF_m	GO:003517	histone kin	2/451	36/23049	0.156216	0.359337	0.304402	Aurkb/Stk-
GO_MF_m	GO:000028	magnesium	6/451	186/23049	0.158681	0.361077	0.305877	Cib3/Glul/
GO_MF_m	GO:000101	RNA polym	1/451	9/23049	0.162957	0.361077	0.305877	Cebpa
GO_MF_m	GO:000215	G-quadrup	1/451	9/23049	0.162957	0.361077	0.305877	Xrn1
GO_MF_m	GO:000385	3-beta-hyd	1/451	9/23049	0.162957	0.361077	0.305877	Sdr42e1
GO_MF_m	GO:000398	acetyl-CoA	1/451	9/23049	0.162957	0.361077	0.305877	Acat2
GO_MF_m	GO:000401	adenylate	1/451	9/23049	0.162957	0.361077	0.305877	Ak8
GO_MF_m	GO:000516	neurotroph	1/451	9/23049	0.162957	0.361077	0.305877	Shc1
GO_MF_m	GO:000535	carbohydra	1/451	9/23049	0.162957	0.361077	0.305877	Slc45a4
GO_MF_m	GO:000538	iron ion tra	1/451	9/23049	0.162957	0.361077	0.305877	Slc25a28
GO_MF_m	GO:001672	oxidoreduc	1/451	9/23049	0.162957	0.361077	0.305877	Cybrd1
GO_MF_m	GO:001688	ligase activ	1/451	9/23049	0.162957	0.361077	0.305877	Rtcb
GO_MF_m	GO:008600	voltage-ga	1/451	9/23049	0.162957	0.361077	0.305877	Kcnh2
GO_MF_m	GO:009898	G-protein	1/451	9/23049	0.162957	0.361077	0.305877	Grm7
GO_MF_m	GO:001687	ligase activ	2/451	37/23049	0.16312	0.361077	0.305877	Acsl4/Slc27
GO_MF_m	GO:003136	translation	2/451	37/23049	0.16312	0.361077	0.305877	Eif5/Syt11
GO_MF_m	GO:000551	calmodulin	6/451	188/23049	0.16422	0.362602	0.307169	Grm7/Kcnh
GO_MF_m	GO:003055	cyclic nucle	2/451	38/23049	0.170078	0.374408	0.31717	Pde1a/Prka
GO_MF_m	GO:000534	organic aci	5/451	150/23049	0.171617	0.374408	0.31717	Slc6a21/Slc
GO_MF_m	GO:004694	carboxylic	5/451	150/23049	0.171617	0.374408	0.31717	Slc6a21/Slc
GO_MF_m	GO:000554	phosphatic	3/451	73/23049	0.171776	0.374408	0.31717	Chmp3/My
GO_MF_m	GO:006163	ubiquitin p	7/451	233/23049	0.173752	0.374408	0.31717	Fbxo40/He
GO_MF_m	GO:000377	actin bindi	11/451	406/23049	0.174802	0.374408	0.31717	Alkbh4/Crc
GO_MF_m	GO:001990	protein pho	5/451	151/23049	0.174865	0.374408	0.31717	Cdc5l/Csk/

GO_MF_m	GO:000554	phosphatic	2/451	39/23049	0.177084	0.374408	0.31717	Arap3/Myc
GO_MF_m	GO:001514	carbohydra	2/451	39/23049	0.177084	0.374408	0.31717	Mfsd4b3/S
GO_MF_m	GO:00167	transferase	8/451	277/23049	0.177687	0.374408	0.31717	Alg9/B4gal
GO_MF_m	GO:000802	protein C-t	7/451	235/23049	0.178928	0.374408	0.31717	Atf4/Bloc1
GO_MF_m	GO:000034	RNA 7-me	1/451	10/23049	0.179342	0.374408	0.31717	Ncbp2
GO_MF_m	GO:00011	transcriptic	1/451	10/23049	0.179342	0.374408	0.31717	Cdc5l
GO_MF_m	GO:00021	dystroglyca	1/451	10/23049	0.179342	0.374408	0.31717	Agrn
GO_MF_m	GO:00044	phosphatic	1/451	10/23049	0.179342	0.374408	0.31717	Mtmr2
GO_MF_m	GO:000817	mRNA met	1/451	10/23049	0.179342	0.374408	0.31717	Mettl14
GO_MF_m	GO:00086	cysteine-ty	1/451	10/23049	0.179342	0.374408	0.31717	Rack1
GO_MF_m	GO:00098	photorecep	1/451	10/23049	0.179342	0.374408	0.31717	Cry1
GO_MF_m	GO:00108	calcium-de	1/451	10/23049	0.179342	0.374408	0.31717	Pink1
GO_MF_m	GO:00151	pyrimidine	1/451	10/23049	0.179342	0.374408	0.31717	Slc35a4
GO_MF_m	GO:00168	carbon-nit	1/451	10/23049	0.179342	0.374408	0.31717	Cad
GO_MF_m	GO:00507	CARD dom	1/451	10/23049	0.179342	0.374408	0.31717	Mavs
GO_MF_m	GO:00985	G-rich stra	1/451	10/23049	0.179342	0.374408	0.31717	Hnrnpa2b1
GO_MF_m	GO:000417	aminopept	2/451	40/23049	0.184135	0.382672	0.324171	Metap2/N
GO_MF_m	GO:00616	ubiquitin-li	7/451	237/23049	0.184169	0.382672	0.324171	Fbxo40/He
GO_MF_m	GO:000372	double-str	3/451	76/23049	0.186416	0.386428	0.327353	Elavl1/Oas
GO_MF_m	GO:19019	phosphatic	5/451	155/23049	0.188087	0.388978	0.329513	Arap3/Chm
GO_MF_m	GO:000504	signal sequ	2/451	41/23049	0.191225	0.393944	0.333719	Pex5l/Tom
GO_MF_m	GO:000452	ribonuclea	1/451	11/23049	0.195407	0.393944	0.333719	Rpp38
GO_MF_m	GO:00048	protein ser	1/451	11/23049	0.195407	0.393944	0.333719	Ppp1r14c
GO_MF_m	GO:000522	intracellula	1/451	11/23049	0.195407	0.393944	0.333719	Pex5l
GO_MF_m	GO:00168	aldehyde-l	1/451	11/23049	0.195407	0.393944	0.333719	Sgpl1
GO_MF_m	GO:001684	carbon-sul	1/451	11/23049	0.195407	0.393944	0.333719	Kyat3
GO_MF_m	GO:00191	pyrimidine	1/451	11/23049	0.195407	0.393944	0.333719	Cad
GO_MF_m	GO:003612	BMP bindir	1/451	11/23049	0.195407	0.393944	0.333719	Agrn
GO_MF_m	GO:00438	cyclic nucle	1/451	11/23049	0.195407	0.393944	0.333719	Pex5l
GO_MF_m	GO:005274	phosphatic	1/451	11/23049	0.195407	0.393944	0.333719	Mtmr2
GO_MF_m	GO:007041	I-SMAD bi	1/451	11/23049	0.195407	0.393944	0.333719	Tgfb1i1
GO_MF_m	GO:00085	protein tra	3/451	78/23049	0.19635	0.394942	0.334564	Ipo7/Ipo8/
GO_MF_m	GO:004282	histone de	4/451	118/23049	0.200685	0.402741	0.341172	Cebpa/Cry
GO_MF_m	GO:00080	DNA-depe	3/451	79/23049	0.201365	0.403188	0.34155	Chd6/Gtf2
GO_MF_m	GO:00165	peptidase	1/451	12/23049	0.211158	0.417108	0.353342	Rack1
GO_MF_m	GO:003054	receptor a	1/451	12/23049	0.211158	0.417108	0.353342	Angpt4
GO_MF_m	GO:004304	single-stra	1/451	12/23049	0.211158	0.417108	0.353342	Hnrnpa2b1
GO_MF_m	GO:00484	platelet-de	1/451	12/23049	0.211158	0.417108	0.353342	Col2a1
GO_MF_m	GO:00506	oxidoreduc	1/451	12/23049	0.211158	0.417108	0.353342	Cybb
GO_MF_m	GO:005101	microtubul	1/451	12/23049	0.211158	0.417108	0.353342	Clip2
GO_MF_m	GO:000524	voltage-ga	2/451	44/23049	0.212692	0.419197	0.355112	Grm7/Tpcr
GO_MF_m	GO:001507	potassium	5/451	163/23049	0.215543	0.423868	0.359069	Kcne4/Kcn
GO_MF_m	GO:00081	translation	3/451	82/23049	0.216584	0.424968	0.36	2810006K2
GO_MF_m	GO:00050	Ras guanyl	4/451	124/23049	0.225248	0.430741	0.364891	Dennd2a/
GO_MF_m	GO:000517	vascular er	1/451	13/23049	0.226601	0.430741	0.364891	Angpt4
GO_MF_m	GO:000524	gap junctic	1/451	13/23049	0.226601	0.430741	0.364891	Panx2
GO_MF_m	GO:00053	nucleotide-	1/451	13/23049	0.226601	0.430741	0.364891	Slc35a4
GO_MF_m	GO:00084	sulfuric est	1/451	13/23049	0.226601	0.430741	0.364891	Sulf2

GO_MF_m	GO:001592	glucosidas	1/451	13/23049	0.226601	0.430741	0.364891	Gba2
GO_MF_m	GO:001642	tRNA (gua	1/451	13/23049	0.226601	0.430741	0.364891	Ftsj1
GO_MF_m	GO:001684	carbon-nit	1/451	13/23049	0.226601	0.430741	0.364891	Adsl
GO_MF_m	GO:00192	nucleoside	1/451	13/23049	0.226601	0.430741	0.364891	Ak8
GO_MF_m	GO:003532	Toll-like re	1/451	13/23049	0.226601	0.430741	0.364891	Tollip
GO_MF_m	GO:003592	mRNA 3'-	1/451	13/23049	0.226601	0.430741	0.364891	Elavl1
GO_MF_m	GO:00475	3',5'-cyclic	1/451	13/23049	0.226601	0.430741	0.364891	Pde1a
GO_MF_m	GO:00971	cysteine-ty	1/451	13/23049	0.226601	0.430741	0.364891	Casp16-ps
GO_MF_m	GO:009761	annealing	1/451	13/23049	0.226601	0.430741	0.364891	Recql
GO_MF_m	GO:00041	cysteine-ty	3/451	84/23049	0.22686	0.430741	0.364891	Capn15/Ca
GO_MF_m	GO:00312	small GTPa	11/451	435/23049	0.23468	0.444631	0.376657	Arap3/Cit/
GO_MF_m	GO:00045	alpha-man	1/451	14/23049	0.241743	0.448369	0.379824	Man2c1
GO_MF_m	GO:00046	prenyltrans	1/451	14/23049	0.241743	0.448369	0.379824	Cox10
GO_MF_m	GO:000832	protein tra	1/451	14/23049	0.241743	0.448369	0.379824	Tomm20
GO_MF_m	GO:00344	heparan su	1/451	14/23049	0.241743	0.448369	0.379824	Hs3st3b1
GO_MF_m	GO:00431	3'-5' DNA	1/451	14/23049	0.241743	0.448369	0.379824	Recql
GO_MF_m	GO:004801	receptor ar	1/451	14/23049	0.241743	0.448369	0.379824	Dkk4
GO_MF_m	GO:00481	tau protein	1/451	14/23049	0.241743	0.448369	0.379824	Dyrk1a
GO_MF_m	GO:00704	NAD+ bin	1/451	14/23049	0.241743	0.448369	0.379824	Sirt7
GO_MF_m	GO:00707	BMP recep	1/451	14/23049	0.241743	0.448369	0.379824	Bmp4
GO_MF_m	GO:009884	sequence-	1/451	14/23049	0.241743	0.448369	0.379824	Hnrnpa2b1
GO_MF_m	GO:000472	phosphopr	5/451	171/23049	0.244158	0.451897	0.382813	Mtmr2/Mtr
GO_MF_m	GO:000374	translation	2/451	49/23049	0.248896	0.4597	0.389423	Eif4g3/Eif5
GO_MF_m	GO:004257	phosphoric	9/451	351/23049	0.251288	0.463149	0.392344	Mtmr2/Mtr
GO_MF_m	GO:000484	ubiquitin-	11/451	443/23049	0.252458	0.464178	0.393216	Fbxo40/He
GO_MF_m	GO:00082	metalloexo	2/451	50/23049	0.256169	0.464178	0.393216	Metap2/N
GO_MF_m	GO:005101	protein kin	2/451	50/23049	0.256169	0.464178	0.393216	Csk/Prkar1
GO_MF_m	GO:00051	insulin-like	1/451	15/23049	0.256589	0.464178	0.393216	Shc1
GO_MF_m	GO:00051	neurotrop	1/451	15/23049	0.256589	0.464178	0.393216	Shc1
GO_MF_m	GO:001592	mannosida	1/451	15/23049	0.256589	0.464178	0.393216	Man2c1
GO_MF_m	GO:00162	AMP bindi	1/451	15/23049	0.256589	0.464178	0.393216	Hist1h1e
GO_MF_m	GO:00166	oxidoredu	1/451	15/23049	0.256589	0.464178	0.393216	Txndc17
GO_MF_m	GO:00320	bile acid bi	1/451	15/23049	0.256589	0.464178	0.393216	Fabp6
GO_MF_m	GO:005111	ATPase bin	3/451	90/23049	0.258189	0.466116	0.394858	Derl1/Pde
GO_MF_m	GO:001984	vitamin bin	4/451	133/23049	0.26339	0.471857	0.399721	Acaca/Kyat
GO_MF_m	GO:00167	phosphata	7/451	265/23049	0.26341	0.471857	0.399721	Mtmr2/Mtr
GO_MF_m	GO:001527	ligand-gat	4/451	134/23049	0.267705	0.471857	0.399721	Kcnh2/Pex
GO_MF_m	GO:00228	ligand-gat	4/451	134/23049	0.267705	0.471857	0.399721	Kcnh2/Pex
GO_MF_m	GO:000851	organic ani	6/451	222/23049	0.269006	0.471857	0.399721	Slc6a21/Sl
GO_MF_m	GO:000521	ion channe	10/451	404/23049	0.269109	0.471857	0.399721	Gpr89/Grm
GO_MF_m	GO:00039	acyl-CoA c	1/451	16/23049	0.271144	0.471857	0.399721	Ivd
GO_MF_m	GO:000454	tRNA-spec	1/451	16/23049	0.271144	0.471857	0.399721	Rpp38
GO_MF_m	GO:00083	voltage-ga	1/451	16/23049	0.271144	0.471857	0.399721	Gpr89
GO_MF_m	GO:001667	oxidoredu	1/451	16/23049	0.271144	0.471857	0.399721	Msrb3
GO_MF_m	GO:001672	oxidoredu	1/451	16/23049	0.271144	0.471857	0.399721	Cybrd1
GO_MF_m	GO:00168	dipeptidas	1/451	16/23049	0.271144	0.471857	0.399721	Pm20d2
GO_MF_m	GO:00171	NAD-depe	1/451	16/23049	0.271144	0.471857	0.399721	Sirt7
GO_MF_m	GO:00302	protein tyr	1/451	16/23049	0.271144	0.471857	0.399721	Angpt4

GO_MF_m2	GO:003055	cGMP bind	1/451	16/23049	0.271144	0.471857	0.399721	Pde1a
GO_MF_m2	GO:004228	MHC class	1/451	16/23049	0.271144	0.471857	0.399721	Derl1
GO_MF_m2	GO:005137	muscle alph	1/451	16/23049	0.271144	0.471857	0.399721	Nrap
GO_MF_m2	GO:007003	telomerase	1/451	16/23049	0.271144	0.471857	0.399721	Snrpb
GO_MF_m2	GO:000485	enzyme inh	10/451	405/23049	0.271545	0.471857	0.399721	Agrn/Ambp
GO_MF_m2	GO:000115	enhancer s	3/451	93/23049	0.274069	0.47437	0.40185	H3f3b/Six3
GO_MF_m2	GO:000489	cytokine re	3/451	93/23049	0.274069	0.47437	0.40185	Cxcr1/Il10r
GO_MF_m2	GO:000371	transcriptio	5/451	180/23049	0.277447	0.479277	0.406006	Crym/Erf/H
GO_MF_m2	GO:000802	ATP-depen	3/451	94/23049	0.279385	0.479869	0.406508	Ddx3y/Dhx
GO_MF_m2	GO:007003	purine NTP	3/451	94/23049	0.279385	0.479869	0.406508	Ddx3y/Dhx
GO_MF_m2	GO:001988	protein kin	5/451	181/23049	0.281204	0.479869	0.406508	Angpt4/Ck
GO_MF_m2	GO:007006	RNA polym	2/451	54/23049	0.28527	0.479869	0.406508	Pabpn1/Pp
GO_MF_m2	GO:000455	nucleoside	1/451	17/23049	0.285416	0.479869	0.406508	Ak8
GO_MF_m2	GO:000835	RNA polym	1/451	17/23049	0.285416	0.479869	0.406508	Gtf2h1
GO_MF_m2	GO:000840	5'-3' exonu	1/451	17/23049	0.285416	0.479869	0.406508	Xrn1
GO_MF_m2	GO:001664	oxidoreduc	1/451	17/23049	0.285416	0.479869	0.406508	Crym
GO_MF_m2	GO:002288	macromole	1/451	17/23049	0.285416	0.479869	0.406508	Tomm20
GO_MF_m2	GO:003067	Rac guanyl	1/451	17/23049	0.285416	0.479869	0.406508	Farp2
GO_MF_m2	GO:003497	NAD-depe	1/451	17/23049	0.285416	0.479869	0.406508	Sirt7
GO_MF_m2	GO:003561	RNA stem-	1/451	17/23049	0.285416	0.479869	0.406508	Eprs
GO_MF_m2	GO:004342	protein kin	1/451	17/23049	0.285416	0.479869	0.406508	Pink1
GO_MF_m2	GO:007049	oligosaccha	1/451	17/23049	0.285416	0.479869	0.406508	Sele
GO_MF_m2	GO:004529	cadherin bi	8/451	321/23049	0.293749	0.492746	0.417417	Eif5/Rack1/
GO_MF_m2	GO:000472	protein tyro	3/451	97/23049	0.295387	0.492746	0.417417	Mtmr2/Mtm
GO_MF_m2	GO:002283	substrate-s	10/451	415/23049	0.296264	0.492746	0.417417	Gpr89/Grm
GO_MF_m2	GO:001978	ubiquitin-li	11/451	463/23049	0.298793	0.492746	0.417417	Fbxo40/He
GO_MF_m2	GO:001986	immunoglo	1/451	18/23049	0.299408	0.492746	0.417417	Ambp
GO_MF_m2	GO:007018	DNA polym	1/451	18/23049	0.299408	0.492746	0.417417	Hnrnpa2b1
GO_MF_m2	GO:000837	acetylgluco	2/451	56/23049	0.299787	0.492746	0.417417	Lfng/Mgat1
GO_MF_m2	GO:001627	lysine N-m	2/451	56/23049	0.299787	0.492746	0.417417	Eef1akmt2/
GO_MF_m2	GO:001627	protein-lys	2/451	56/23049	0.299787	0.492746	0.417417	Eef1akmt2/
GO_MF_m2	GO:001666	oxidoreduc	2/451	56/23049	0.299787	0.492746	0.417417	Msrb3/Txn
GO_MF_m2	GO:003506	methylated	2/451	56/23049	0.299787	0.492746	0.417417	Rrp8/Suz12
GO_MF_m2	GO:014003	methylation	2/451	56/23049	0.299787	0.492746	0.417417	Rrp8/Suz12
GO_MF_m2	GO:000392	GTPase act	7/451	278/23049	0.303073	0.497221	0.421207	Rab11a/Ra
GO_MF_m2	GO:000097	RNA polym	11/451	466/23049	0.305941	0.499756	0.423355	Atf4/Cebpa
GO_MF_m2	GO:000823	exopeptida	3/451	99/23049	0.306086	0.499756	0.423355	Metap2/Np
GO_MF_m2	GO:005121	phosphopr	3/451	100/23049	0.311443	0.499756	0.423355	Prkcsh/Shc
GO_MF_m2	GO:000375	protein dis	1/451	19/23049	0.313128	0.499756	0.423355	Txndc5
GO_MF_m2	GO:000419	calcium-de	1/451	19/23049	0.313128	0.499756	0.423355	Capn15
GO_MF_m2	GO:000465	polypeptid	1/451	19/23049	0.313128	0.499756	0.423355	Galnt2
GO_MF_m2	GO:000497	ionotropic	1/451	19/23049	0.313128	0.499756	0.423355	Ptk2b
GO_MF_m2	GO:000514	interleukin-	1/451	19/23049	0.313128	0.499756	0.423355	Tollip
GO_MF_m2	GO:000540	carbohydra	1/451	19/23049	0.313128	0.499756	0.423355	Slc45a4
GO_MF_m2	GO:001678	phosphotra	1/451	19/23049	0.313128	0.499756	0.423355	Cdipt
GO_MF_m2	GO:001686	intramolecu	1/451	19/23049	0.313128	0.499756	0.423355	Txndc5
GO_MF_m2	GO:003459	phosphatic	1/451	19/23049	0.313128	0.499756	0.423355	Mtmr2
GO_MF_m2	GO:004696	proton-tra	1/451	19/23049	0.313128	0.499756	0.423355	Atp6v1h

GO_MF_m	GO:005043	transformir	1/451	19/23049	0.313128	0.499756	0.423355	Agrn
GO_MF_m	GO:005274	inositol ph	1/451	19/23049	0.313128	0.499756	0.423355	Mtmr7
GO_MF_m	GO:002003	heme bind	4/451	145/23049	0.315854	0.503196	0.426269	Ambp/Cyb
GO_MF_m	GO:190168	sulfur com	6/451	237/23049	0.319723	0.508441	0.430712	Acaca/Agr
GO_MF_m	GO:001523	drug trans	3/451	102/23049	0.322161	0.510134	0.432147	Slc25a38/S
GO_MF_m	GO:000508	guanyl-nu	5/451	192/23049	0.323092	0.510134	0.432147	Dennd2a/
GO_MF_m	GO:001983	growth fac	4/451	147/23049	0.324703	0.510134	0.432147	Agrn/Col2
GO_MF_m	GO:000122	transcriptic	1/451	20/23049	0.326579	0.510134	0.432147	Nr4a3
GO_MF_m	GO:004383	guanylate	1/451	20/23049	0.326579	0.510134	0.432147	Gucy2c
GO_MF_m	GO:000524	inward rec	1/451	20/23049	0.326579	0.510134	0.432147	Kcnh2
GO_MF_m	GO:003121	phosphatic	1/451	20/23049	0.326579	0.510134	0.432147	Chmp3
GO_MF_m	GO:003148	myosin V b	1/451	20/23049	0.326579	0.510134	0.432147	Rab11a
GO_MF_m	GO:003525	glucocortic	1/451	20/23049	0.326579	0.510134	0.432147	Nr4a3
GO_MF_m	GO:005099	quaternary	1/451	20/23049	0.326579	0.510134	0.432147	Chmp3
GO_MF_m	GO:000202	protease b	4/451	148/23049	0.329134	0.513216	0.434757	Chmp3/De
GO_MF_m	GO:000098	proximal p	11/451	477/23049	0.332497	0.517229	0.438157	Atf4/Cebp
GO_MF_m	GO:003532	enhancer b	3/451	104/23049	0.332882	0.517229	0.438157	H3f3b/Six3
GO_MF_m	GO:000472	protein ser	2/451	61/23049	0.335823	0.518778	0.439469	Pdp1/Ppm
GO_MF_m	GO:000508	protein kin	2/451	61/23049	0.335823	0.518778	0.439469	Rack1/Prkc
GO_MF_m	GO:000401	adenylate	1/451	21/23049	0.339767	0.518778	0.439469	Gucy2c
GO_MF_m	GO:001529	solute:prot	1/451	21/23049	0.339767	0.518778	0.439469	Slc45a4
GO_MF_m	GO:001640	C-acyltrans	1/451	21/23049	0.339767	0.518778	0.439469	Acat2
GO_MF_m	GO:001920	nucleotide	1/451	21/23049	0.339767	0.518778	0.439469	Ak8
GO_MF_m	GO:002282	wide pore	1/451	21/23049	0.339767	0.518778	0.439469	Panx2
GO_MF_m	GO:003169	adrenergic	1/451	21/23049	0.339767	0.518778	0.439469	Sh3gl1
GO_MF_m	GO:005142	peptide ho	1/451	21/23049	0.339767	0.518778	0.439469	Psmc5
GO_MF_m	GO:007069	transmemb	1/451	21/23049	0.339767	0.518778	0.439469	Bmp4
GO_MF_m	GO:000454	ribonuclea	3/451	107/23049	0.348949	0.527549	0.446899	Rnase6/Rp
GO_MF_m	GO:001995	cytokine bi	3/451	107/23049	0.348949	0.527549	0.446899	Agrn/Cxcr
GO_MF_m	GO:001900	GDP bindir	2/451	63/23049	0.350092	0.527549	0.446899	Ralb/Ran
GO_MF_m	GO:000098	transcriptic	1/451	22/23049	0.352698	0.527549	0.446899	Lmx1b
GO_MF_m	GO:000814	poly(A) bin	1/451	22/23049	0.352698	0.527549	0.446899	Pabpn1
GO_MF_m	GO:001527	calcium-re	1/451	22/23049	0.352698	0.527549	0.446899	Tpcn1
GO_MF_m	GO:001663	oxidoreduc	1/451	22/23049	0.352698	0.527549	0.446899	Crym
GO_MF_m	GO:004281	Wnt-activa	1/451	22/23049	0.352698	0.527549	0.446899	Sfrp2
GO_MF_m	GO:004802	mRNA 5'-	1/451	22/23049	0.352698	0.527549	0.446899	Aco1
GO_MF_m	GO:007053	K63-linked	1/451	22/23049	0.352698	0.527549	0.446899	Zbtb1
GO_MF_m	GO:009048	vitamin tra	1/451	22/23049	0.352698	0.527549	0.446899	Slc52a3
GO_MF_m	GO:014010	catalytic ac	1/451	22/23049	0.352698	0.527549	0.446899	Mgat1
GO_MF_m	GO:000107	transcriptic	7/451	294/23049	0.353367	0.527655	0.446989	Atf4/Cebp
GO_MF_m	GO:004690	tetrapyrrol	4/451	154/23049	0.355769	0.530343	0.449266	Ambp/Cyb
GO_MF_m	GO:003037	ligand-dep	2/451	64/23049	0.357188	0.530662	0.449536	Tsg101/Zc
GO_MF_m	GO:005128	NAD bindir	2/451	64/23049	0.357188	0.530662	0.449536	Gpd1l/Sirt
GO_MF_m	GO:001670	oxidoreduc	5/451	202/23049	0.361733	0.535944	0.454011	Cyp2g1/Fa
GO_MF_m	GO:000817	O-methylt	1/451	23/23049	0.365375	0.535944	0.454011	Ftsj1
GO_MF_m	GO:001692	ligand-dep	1/451	23/23049	0.365375	0.535944	0.454011	Jund
GO_MF_m	GO:003149	nucleosom	1/451	23/23049	0.365375	0.535944	0.454011	H3f3b
GO_MF_m	GO:003361	receptor se	1/451	23/23049	0.365375	0.535944	0.454011	Bmp4

GO_MF_m	GO:00433	heparan su	1/451	23/23049	0.365375	0.535944	0.454011	Agrn
GO_MF_m	GO:00718	HMG box	1/451	23/23049	0.365375	0.535944	0.454011	Cebpa
GO_MF_m	GO:00192	kinase regu	5/451	203/23049	0.36561	0.535944	0.454011	Angpt4/Ck
GO_MF_m	GO:004362	protein sel	2/451	66/23049	0.371292	0.541041	0.458328	Dyrk1a/Pa
GO_MF_m	GO:001701	Ras GTPas	9/451	397/23049	0.374483	0.541041	0.458328	Cit/Dennd
GO_MF_m	GO:00006	fatty-acyl-	1/451	24/23049	0.377806	0.541041	0.458328	Hmgcl
GO_MF_m	GO:00016	G-protein	1/451	24/23049	0.377806	0.541041	0.458328	Cxcr1
GO_MF_m	GO:000412	cytochrom	1/451	24/23049	0.377806	0.541041	0.458328	Cox10
GO_MF_m	GO:00049	chemokine	1/451	24/23049	0.377806	0.541041	0.458328	Cxcr1
GO_MF_m	GO:00150	heme-cop	1/451	24/23049	0.377806	0.541041	0.458328	Cox10
GO_MF_m	GO:001667	oxidoreduc	1/451	24/23049	0.377806	0.541041	0.458328	Cox10
GO_MF_m	GO:00199	chemokine	1/451	24/23049	0.377806	0.541041	0.458328	Cxcr1
GO_MF_m	GO:003054	receptor in	1/451	24/23049	0.377806	0.541041	0.458328	Dkk4
GO_MF_m	GO:00305	cAMP bind	1/451	24/23049	0.377806	0.541041	0.458328	Prkar1a
GO_MF_m	GO:00351	miRNA bin	1/451	24/23049	0.377806	0.541041	0.458328	Hnrnpa2b1
GO_MF_m	GO:004292	neuropepti	1/451	24/23049	0.377806	0.541041	0.458328	Gpr1
GO_MF_m	GO:00009	RNA polym	2/451	67/23049	0.378299	0.541041	0.458328	H3f3b/Six3
GO_MF_m	GO:003027	clathrin bir	2/451	67/23049	0.378299	0.541041	0.458328	Ap2b1/Syt
GO_MF_m	GO:000372	RNA helica	2/451	68/23049	0.385272	0.548344	0.464515	Ddx3y/Dhx
GO_MF_m	GO:00040	ATP-deper	2/451	68/23049	0.385272	0.548344	0.464515	Ddx3y/Dhx
GO_MF_m	GO:00302	protein kin	2/451	68/23049	0.385272	0.548344	0.464515	Angpt4/Ck
GO_MF_m	GO:001507	proton trar	3/451	114/23049	0.386235	0.548783	0.464887	Atp6v1h/C
GO_MF_m	GO:00171	Rab GTPas	4/451	161/23049	0.386827	0.548783	0.464887	Dennd2a/F
GO_MF_m	GO:001667	oxidoreduc	1/451	25/23049	0.389993	0.550615	0.466439	Cox10
GO_MF_m	GO:001684	phosphoru	1/451	25/23049	0.389993	0.550615	0.466439	Gucy2c
GO_MF_m	GO:00168	endoribonu	1/451	25/23049	0.389993	0.550615	0.466439	Rpp38
GO_MF_m	GO:00081	RNA-depe	2/451	69/23049	0.392211	0.552861	0.468341	Ddx3y/Dhx
GO_MF_m	GO:00050	Rho guany	2/451	70/23049	0.399115	0.558534	0.473147	Ect2/Farp2
GO_MF_m	GO:009711	scaffold pr	2/451	70/23049	0.399115	0.558534	0.473147	Cit/Kcnh2
GO_MF_m	GO:00037	actin monc	1/451	26/23049	0.401942	0.558534	0.473147	Twf1
GO_MF_m	GO:000467	AMP-activ	1/451	26/23049	0.401942	0.558534	0.473147	Stk-ps2
GO_MF_m	GO:00051	insulin rece	1/451	26/23049	0.401942	0.558534	0.473147	Shc1
GO_MF_m	GO:00053	glucose tra	1/451	26/23049	0.401942	0.558534	0.473147	Mfsd4b3
GO_MF_m	GO:000997	cyclase act	1/451	26/23049	0.401942	0.558534	0.473147	Gucy2c
GO_MF_m	GO:001702	TBP-class	1/451	26/23049	0.401942	0.558534	0.473147	Psmc5
GO_MF_m	GO:00171	fibroblast	1/451	26/23049	0.401942	0.558534	0.473147	Fgfbp3
GO_MF_m	GO:00483	calcium-de	2/451	71/23049	0.405982	0.56326	0.47715	Grm7/Tsg1
GO_MF_m	GO:00301	PDZ doma	3/451	118/23049	0.407325	0.564235	0.477977	Cit/Grm7/L
GO_MF_m	GO:00052	structural	2/451	72/23049	0.412811	0.565011	0.478634	Frmd6/Tub
GO_MF_m	GO:00090	electron tra	2/451	72/23049	0.412811	0.565011	0.478634	Cox10/Cyb
GO_MF_m	GO:00046	calmodulin	1/451	27/23049	0.413657	0.565011	0.478634	Ptk2b
GO_MF_m	GO:000514	prolactin re	1/451	27/23049	0.413657	0.565011	0.478634	Prl8a2
GO_MF_m	GO:001514	hexose trar	1/451	27/23049	0.413657	0.565011	0.478634	Mfsd4b3
GO_MF_m	GO:001664	oxidoreduc	1/451	27/23049	0.413657	0.565011	0.478634	Crym
GO_MF_m	GO:00168	exoribonuc	1/451	27/23049	0.413657	0.565011	0.478634	Xrn1
GO_MF_m	GO:003074	GTP-deper	1/451	27/23049	0.413657	0.565011	0.478634	Gchfr
GO_MF_m	GO:19046	peptide tra	1/451	27/23049	0.413657	0.565011	0.478634	Tomm20
GO_MF_m	GO:00085	anion trans	7/451	316/23049	0.42356	0.574465	0.486643	Slc6a21/Gp

GO_MF_m	GO:000453	exoribonuc	1/451	28/23049	0.425144	0.574465	0.486643	Xrn1
GO_MF_m	GO:000830	structural c	1/451	28/23049	0.425144	0.574465	0.486643	Myh11
GO_MF_m	GO:001670	oxidoreduc	1/451	28/23049	0.425144	0.574465	0.486643	Ado
GO_MF_m	GO:003029	protein ser	1/451	28/23049	0.425144	0.574465	0.486643	Prkar1a
GO_MF_m	GO:004353	protein ser	1/451	28/23049	0.425144	0.574465	0.486643	Cks1b
GO_MF_m	GO:009960	ligand-gat	1/451	28/23049	0.425144	0.574465	0.486643	Tpcn1
GO_MF_m	GO:000823	serine-type	5/451	219/23049	0.427484	0.576422	0.4883	Pcsk2/Plau
GO_MF_m	GO:001920	kinase activ	2/451	75/23049	0.433058	0.576422	0.4883	Angpt4/Ck
GO_MF_m	GO:003329	monocarbo	2/451	75/23049	0.433058	0.576422	0.4883	Acaca/Fab
GO_MF_m	GO:001540	P-P-bond-	3/451	123/23049	0.433371	0.576422	0.4883	Atp6v1h/Ip
GO_MF_m	GO:001507	monovaler	8/451	369/23049	0.434624	0.576422	0.4883	Atp6v1h/C
GO_MF_m	GO:000440	histone de	1/451	29/23049	0.436405	0.576422	0.4883	Sirt7
GO_MF_m	GO:000524	calcium ch	1/451	29/23049	0.436405	0.576422	0.4883	Grm7
GO_MF_m	GO:001514	monosacch	1/451	29/23049	0.436405	0.576422	0.4883	Mfsd4b3
GO_MF_m	GO:001670	oxidoreduc	1/451	29/23049	0.436405	0.576422	0.4883	Ado
GO_MF_m	GO:003051	snoRNA bi	1/451	29/23049	0.436405	0.576422	0.4883	Pwp2
GO_MF_m	GO:003644	proton-exp	1/451	29/23049	0.436405	0.576422	0.4883	Atp6v1h
GO_MF_m	GO:004301	gamma-tu	1/451	29/23049	0.436405	0.576422	0.4883	Bloc1s2
GO_MF_m	GO:004550	dynein ligh	1/451	29/23049	0.436405	0.576422	0.4883	Glul
GO_MF_m	GO:007071	poly-purin	1/451	29/23049	0.436405	0.576422	0.4883	Pabpn1
GO_MF_m	GO:007250	divalent in	1/451	29/23049	0.436405	0.576422	0.4883	Slc25a28
GO_MF_m	GO:000823	metallopep	4/451	173/23049	0.439516	0.579661	0.491045	Mbtps2/M
GO_MF_m	GO:001539	primary act	3/451	125/23049	0.443673	0.584269	0.494948	Atp6v1h/Ip
GO_MF_m	GO:004317	alcohol bin	2/451	77/23049	0.446347	0.585737	0.496192	Cdipt/Osb
GO_MF_m	GO:001717	serine hydr	5/451	224/23049	0.446624	0.585737	0.496192	Pcsk2/Plau
GO_MF_m	GO:003355	protein de	1/451	30/23049	0.447447	0.585737	0.496192	Sirt7
GO_MF_m	GO:005111	sugar trans	1/451	30/23049	0.447447	0.585737	0.496192	Mfsd4b3
GO_MF_m	GO:000550	iron ion bin	4/451	175/23049	0.448183	0.585829	0.49627	Fthl17f/Jmj
GO_MF_m	GO:001624	channel reg	3/451	127/23049	0.453902	0.590064	0.499857	Rack1/Gpd
GO_MF_m	GO:014003	modificatio	3/451	127/23049	0.453902	0.590064	0.499857	Rrp8/Suz1
GO_MF_m	GO:004262	ATPase act	8/451	377/23049	0.458226	0.590064	0.499857	Atp6v1h/C
GO_MF_m	GO:000400	ATP-depen	1/451	31/23049	0.458273	0.590064	0.499857	Recql
GO_MF_m	GO:000513	type I inter	1/451	31/23049	0.458273	0.590064	0.499857	Ifna4
GO_MF_m	GO:000820	ion channe	1/451	31/23049	0.458273	0.590064	0.499857	Rack1
GO_MF_m	GO:001714	Wnt-prote	1/451	31/23049	0.458273	0.590064	0.499857	Sfrp2
GO_MF_m	GO:004323	laminin bin	1/451	31/23049	0.458273	0.590064	0.499857	Adgrg6
GO_MF_m	GO:004687	ephrin rece	1/451	31/23049	0.458273	0.590064	0.499857	Shc1
GO_MF_m	GO:006198	regulatory	1/451	31/23049	0.458273	0.590064	0.499857	Hnrnpa2b1
GO_MF_m	GO:001712	SH3 domai	3/451	128/23049	0.458987	0.590064	0.499857	Cit/Itgb1bp
GO_MF_m	GO:004633	SMAD bind	2/451	79/23049	0.45946	0.590064	0.499857	Ipo7/Tgfb1
GO_MF_m	GO:000122	transcriptio	9/451	428/23049	0.460578	0.590639	0.500345	Atf4/Cdc5l
GO_MF_m	GO:005083	cell adhesi	10/451	480/23049	0.465138	0.594637	0.503731	Caml/Eif5/I
GO_MF_m	GO:001653	cyclin-dep	1/451	32/23049	0.468887	0.594637	0.503731	Cks1b
GO_MF_m	GO:001689	endonucle	1/451	32/23049	0.468887	0.594637	0.503731	Rpp38
GO_MF_m	GO:004476	ATPase act	1/451	32/23049	0.468887	0.594637	0.503731	Atp6v1h
GO_MF_m	GO:004550	dynein inte	1/451	32/23049	0.468887	0.594637	0.503731	Ran
GO_MF_m	GO:007027	phosphatid	1/451	32/23049	0.468887	0.594637	0.503731	Osbpl5
GO_MF_m	GO:000377	motor activ	3/451	130/23049	0.469095	0.594637	0.503731	Myh11/My

GO_MF_m	GO:000451	endonucle	3/451	130/23049	0.469095	0.594637	0.503731	Rnase6/Rp
GO_MF_m	GO:000823	cysteine-ty	4/451	182/23049	0.478161	0.602365	0.510278	Capn15/Ca
GO_MF_m	GO:001677	nucleotidyl	3/451	132/23049	0.479118	0.602365	0.510278	Gdpgp1/O
GO_MF_m	GO:001624	channel inl	1/451	33/23049	0.479294	0.602365	0.510278	Rack1
GO_MF_m	GO:005101	mitogen-a	1/451	33/23049	0.479294	0.602365	0.510278	Nbr1
GO_MF_m	GO:005139	alpha-actir	1/451	33/23049	0.479294	0.602365	0.510278	Nrap
GO_MF_m	GO:190156	fatty acid d	1/451	33/23049	0.479294	0.602365	0.510278	Hmgcl
GO_MF_m	GO:000808	phosphoric	2/451	83/23049	0.485133	0.607105	0.514293	Pde1a/Pde
GO_MF_m	GO:001681	hydrolase a	2/451	83/23049	0.485133	0.607105	0.514293	Pm20d2/Si
GO_MF_m	GO:003294	protein-co	2/451	83/23049	0.485133	0.607105	0.514293	Sept9/Sma
GO_MF_m	GO:000166	G-protein	6/451	286/23049	0.489105	0.609106	0.515988	Bambi/Pen
GO_MF_m	GO:003376	steroid deh	1/451	34/23049	0.489497	0.609106	0.515988	Sdr42e1
GO_MF_m	GO:003503	histone ace	1/451	34/23049	0.489497	0.609106	0.515988	Nr4a3
GO_MF_m	GO:003600	pre-mRNA	1/451	34/23049	0.489497	0.609106	0.515988	Hnrnpa2b1
GO_MF_m	GO:009910	ion channe	2/451	84/23049	0.491432	0.610652	0.517297	Rack1/Grm
GO_MF_m	GO:000804	enzyme ac	9/451	441/23049	0.496226	0.612898	0.5192	Angpt4/Ar
GO_MF_m	GO:000827	protein me	2/451	85/23049	0.497683	0.612898	0.5192	Eef1akmt2/
GO_MF_m	GO:001681	hydrolase a	3/451	136/23049	0.498893	0.612898	0.5192	Cad/Pm20
GO_MF_m	GO:000373	structural c	4/451	187/23049	0.499186	0.612898	0.5192	Mrps5/Mrt
GO_MF_m	GO:000113	transcriptic	1/451	35/23049	0.499501	0.612898	0.5192	Cdc5l
GO_MF_m	GO:000515	epidermal	1/451	35/23049	0.499501	0.612898	0.5192	Shc1
GO_MF_m	GO:000839	arachidoni	1/451	35/23049	0.499501	0.612898	0.5192	Cyp2g1
GO_MF_m	GO:004216	telomeric D	1/451	35/23049	0.499501	0.612898	0.5192	Hnrnpa2b1
GO_MF_m	GO:005172	protein pho	1/451	35/23049	0.499501	0.612898	0.5192	Shc1
GO_MF_m	GO:000486	protein kin	2/451	86/23049	0.503884	0.617416	0.523028	Rack1/Prka
GO_MF_m	GO:000375	peptidyl-p	1/451	36/23049	0.509309	0.622332	0.527192	Ppib
GO_MF_m	GO:001677	phosphotra	1/451	36/23049	0.509309	0.622332	0.527192	Ak8
GO_MF_m	GO:003509	phosphatic	5/451	242/23049	0.513925	0.627102	0.531233	Arap3/Chn
GO_MF_m	GO:000425	serine-type	4/451	191/23049	0.515739	0.627124	0.531252	Pcsk2/Plau
GO_MF_m	GO:000817	N-methyltr	2/451	88/23049	0.516137	0.627124	0.531252	Eef1akmt2/
GO_MF_m	GO:004302	ribonucleo	3/451	140/23049	0.518282	0.627124	0.531252	Rack1/Prpf
GO_MF_m	GO:001708	sodium cha	1/451	37/23049	0.518926	0.627124	0.531252	Gpd1l
GO_MF_m	GO:003162	ubiquitin c	1/451	37/23049	0.518926	0.627124	0.531252	Tollip
GO_MF_m	GO:004216	SH2 domai	1/451	37/23049	0.518926	0.627124	0.531252	Rack1
GO_MF_m	GO:004353	ADP bindir	1/451	37/23049	0.518926	0.627124	0.531252	Hist1h1e
GO_MF_m	GO:000372	single-stra	2/451	89/23049	0.522188	0.629124	0.532946	Jmjd6/Pab
GO_MF_m	GO:001921	kinase inhil	2/451	89/23049	0.522188	0.629124	0.532946	Rack1/Prka
GO_MF_m	GO:000510	frizzled bin	1/451	38/23049	0.528354	0.629124	0.532946	Bambi
GO_MF_m	GO:000548	SNAP rece	1/451	38/23049	0.528354	0.629124	0.532946	Vamp3
GO_MF_m	GO:000839	arachidoni	1/451	38/23049	0.528354	0.629124	0.532946	Cyp2g1
GO_MF_m	GO:001685	cis-trans is	1/451	38/23049	0.528354	0.629124	0.532946	Ppib
GO_MF_m	GO:004205	chemoattra	1/451	38/23049	0.528354	0.629124	0.532946	Bmp4
GO_MF_m	GO:005153	4 iron, 4 su	1/451	38/23049	0.528354	0.629124	0.532946	Aco1
GO_MF_m	GO:006059	ATPase reg	1/451	38/23049	0.528354	0.629124	0.532946	Agrn
GO_MF_m	GO:190150	carbohydra	1/451	38/23049	0.528354	0.629124	0.532946	Slc35a4
GO_MF_m	GO:000509	GTPase act	5/451	246/23049	0.528436	0.629124	0.532946	Arap3/Ect2
GO_MF_m	GO:001529	symporter	3/451	143/23049	0.532555	0.630657	0.534245	Mfsd4b3/S
GO_MF_m	GO:000553	glycosamir	4/451	196/23049	0.536067	0.630657	0.534245	Agrn/Aplp

GO_MF_m	GO:00819	UDP-glyco	3/451	144/23049	0.537259	0.630657	0.534245	Galnt2/Lfng
GO_MF_m	GO:00120	transcriptio	1/451	39/23049	0.537598	0.630657	0.534245	Six3
GO_MF_m	GO:00178	phosphoty	1/451	39/23049	0.537598	0.630657	0.534245	Shc1
GO_MF_m	GO:00154	cholesterol	1/451	39/23049	0.537598	0.630657	0.534245	Osbpl5
GO_MF_m	GO:00159	nucleobase	1/451	39/23049	0.537598	0.630657	0.534245	Slc35a4
GO_MF_m	GO:00162	steroid deh	1/451	39/23049	0.537598	0.630657	0.534245	Sdr42e1
GO_MF_m	GO:00428	amide tran	1/451	39/23049	0.537598	0.630657	0.534245	Tomm20
GO_MF_m	GO:00433	proteoglyc	1/451	39/23049	0.537598	0.630657	0.534245	Agrn
GO_MF_m	GO:004691	transition r	1/451	39/23049	0.537598	0.630657	0.534245	Slc25a28
GO_MF_m	GO:00605	nucleoside	6/451	301/23049	0.538823	0.631254	0.53475	Agrn/Arap
GO_MF_m	GO:00082	heparin bir	3/451	145/23049	0.541937	0.634059	0.537126	Aplp2/Bmp
GO_MF_m	GO:00349	immunoglo	3/451	146/23049	0.546587	0.637892	0.540373	Ighv1-23/I
GO_MF_m	GO:001921	deacetylase	1/451	40/23049	0.546661	0.637892	0.540373	Sirt7
GO_MF_m	GO:00430	cysteine-ty	1/451	41/23049	0.555547	0.646176	0.547391	Rack1
GO_MF_m	GO:00484	beta-tubul	1/451	41/23049	0.555547	0.646176	0.547391	Syt11
GO_MF_m	GO:000451	nuclease a	4/451	201/23049	0.55596	0.646176	0.547391	Rnase6/Rp
GO_MF_m	GO:000367	DNA helica	1/451	42/23049	0.564259	0.654095	0.554099	Recql
GO_MF_m	GO:00150	disulfide o	1/451	42/23049	0.564259	0.654095	0.554099	Txndc17
GO_MF_m	GO:00156	tubulin bin	6/451	311/23049	0.570786	0.656226	0.555904	Bloc1s2/Cli
GO_MF_m	GO:00046	peroxidase	1/451	43/23049	0.572801	0.656226	0.555904	Txndc17
GO_MF_m	GO:00052	extracellula	1/451	43/23049	0.572801	0.656226	0.555904	Col2a1
GO_MF_m	GO:00055	fatty acid b	1/451	43/23049	0.572801	0.656226	0.555904	Fabp6
GO_MF_m	GO:00192	nucleobase	1/451	43/23049	0.572801	0.656226	0.555904	Ak8
GO_MF_m	GO:00329	sterol bind	1/451	43/23049	0.572801	0.656226	0.555904	Osbpl5
GO_MF_m	GO:00428	actinin bin	1/451	43/23049	0.572801	0.656226	0.555904	Nrap
GO_MF_m	GO:00443	ubiquitin-li	1/451	43/23049	0.572801	0.656226	0.555904	Tollip
GO_MF_m	GO:00506	NADP bin	1/451	43/23049	0.572801	0.656226	0.555904	Crym
GO_MF_m	GO:00042	metalloenc	2/451	99/23049	0.579853	0.663233	0.56184	Mbtps2/Tll
GO_MF_m	GO:00167	exonucleas	1/451	44/23049	0.581175	0.663233	0.56184	Xrn1
GO_MF_m	GO:00180	histone-lys	1/451	44/23049	0.581175	0.663233	0.56184	Suz12
GO_MF_m	GO:00306	GTPase reg	5/451	263/23049	0.587801	0.669926	0.56751	Arap3/Ect2
GO_MF_m	GO:00167	oxidoreduc	1/451	45/23049	0.589386	0.670865	0.568305	Jmjd6
GO_MF_m	GO:000837	acetylgalac	1/451	46/23049	0.597436	0.67915	0.575324	Galnt2
GO_MF_m	GO:00166	oxidoreduc	1/451	47/23049	0.605329	0.685658	0.580837	Txndc17
GO_MF_m	GO:00314	nucleosom	1/451	47/23049	0.605329	0.685658	0.580837	H3f3b
GO_MF_m	GO:00228	active trans	7/451	376/23049	0.605496	0.685658	0.580837	Atp6v1h/M
GO_MF_m	GO:001704	Rho GTPas	3/451	161/23049	0.612892	0.689799	0.584345	Cit/Ect2/Fa
GO_MF_m	GO:00017	phosphatic	1/451	48/23049	0.613067	0.689799	0.584345	Osbpl5
GO_MF_m	GO:000487	nuclear rec	1/451	48/23049	0.613067	0.689799	0.584345	Nr4a3
GO_MF_m	GO:00315	polyubiqui	1/451	48/23049	0.613067	0.689799	0.584345	Zbtb1
GO_MF_m	GO:00985	transcriptio	1/451	48/23049	0.613067	0.689799	0.584345	Nr4a3
GO_MF_m	GO:00198	kinesin bin	1/451	49/23049	0.620654	0.696508	0.590028	Crocc
GO_MF_m	GO:00037	transcriptio	2/451	107/23049	0.622193	0.696508	0.590028	Cebpa/Six
GO_MF_m	GO:00045	hydrolase a	2/451	107/23049	0.622193	0.696508	0.590028	Gba2/Man
GO_MF_m	GO:00425	hormone b	2/451	107/23049	0.622193	0.696508	0.590028	Crym/Shc1
GO_MF_m	GO:00453	protein ph	1/451	50/23049	0.628093	0.702221	0.594868	Shc1
GO_MF_m	GO:00054	steroid bin	2/451	109/23049	0.63225	0.705006	0.597227	Osbpl5/Sc
GO_MF_m	GO:004687	metal ion t	8/451	441/23049	0.634934	0.705006	0.597227	Grm7/Kcn

GO_MF_m	GO:000154	amyloid-b	1/451	51/23049	0.635386	0.705006	0.597227	Bace1
GO_MF_m	GO:000532	neurotrans	1/451	51/23049	0.635386	0.705006	0.597227	Slc25a38
GO_MF_m	GO:000554	calcium-d	1/451	51/23049	0.635386	0.705006	0.597227	Syt11
GO_MF_m	GO:00168	intramole	1/451	51/23049	0.635386	0.705006	0.597227	Txndc5
GO_MF_m	GO:00011	transcripti	1/451	53/23049	0.649546	0.717106	0.607477	Id2
GO_MF_m	GO:000452	endoribon	1/451	53/23049	0.649546	0.717106	0.607477	Rpp38
GO_MF_m	GO:002282	transmitter	1/451	53/23049	0.649546	0.717106	0.607477	Ptk2b
GO_MF_m	GO:00228	transmitter	1/451	53/23049	0.649546	0.717106	0.607477	Ptk2b
GO_MF_m	GO:00168	ATPase act	8/451	449/23049	0.654717	0.72191	0.611547	Atp6v1h/C
GO_MF_m	GO:00052	calcium ch	2/451	115/23049	0.661165	0.728108	0.616797	Grm7/Tpcn
GO_MF_m	GO:000802	monocarb	1/451	55/23049	0.663158	0.729391	0.617884	Slc27a2
GO_MF_m	GO:000554	phospholi	1/451	56/23049	0.669765	0.735508	0.623066	Osbpl5
GO_MF_m	GO:004262	ATPase act	2/451	117/23049	0.670389	0.735508	0.623066	Atp6v1h/I
GO_MF_m	GO:005101	actin filam	3/451	177/23049	0.676093	0.738252	0.625391	Myh11/Sy
GO_MF_m	GO:001662	oxidoredu	1/451	57/23049	0.676242	0.738252	0.625391	Ivd
GO_MF_m	GO:00355	signaling a	1/451	57/23049	0.676242	0.738252	0.625391	Rack1
GO_MF_m	GO:00420	histone me	1/451	57/23049	0.676242	0.738252	0.625391	Suz12
GO_MF_m	GO:00048	serine-typ	2/451	119/23049	0.67941	0.740792	0.627542	Ambp/Ser
GO_MF_m	GO:00037	steroid hor	1/451	58/23049	0.682593	0.74151	0.62815	Nr4a3
GO_MF_m	GO:004302	ribosome	1/451	58/23049	0.682593	0.74151	0.62815	Rack1
GO_MF_m	GO:005084	extracellul	1/451	58/23049	0.682593	0.74151	0.62815	Adgrg6
GO_MF_m	GO:00036	damaged	1/451	60/23049	0.694924	0.753975	0.63871	H2afx
GO_MF_m	GO:000531	lipid trans	2/451	123/23049	0.696846	0.755131	0.639689	Osbpl5/Slc
GO_MF_m	GO:00611	peptidase	4/451	242/23049	0.699904	0.757513	0.641707	Ambp/Rac
GO_MF_m	GO:001671	oxidoredu	1/451	61/23049	0.700909	0.75767	0.64184	Cyp2g1
GO_MF_m	GO:00474	protein N-	2/451	126/23049	0.709402	0.765911	0.648821	Pdcd10/St
GO_MF_m	GO:00167	transferase	1/451	63/23049	0.71253	0.768346	0.650884	Cox10
GO_MF_m	GO:00152	secondary	4/451	247/23049	0.714939	0.769718	0.652046	Mfsd4b3/S
GO_MF_m	GO:001982	cation-tra	1/451	64/23049	0.71817	0.769718	0.652046	Atp6v1h
GO_MF_m	GO:00228	active ion	1/451	64/23049	0.71817	0.769718	0.652046	Atp6v1h
GO_MF_m	GO:004262	ATPase co	1/451	64/23049	0.71817	0.769718	0.652046	Atp6v1h
GO_MF_m	GO:00483	Rac GTPas	1/451	64/23049	0.71817	0.769718	0.652046	Farp2
GO_MF_m	GO:00515	iron-sulfur	1/451	65/23049	0.7237	0.773762	0.655472	Aco1
GO_MF_m	GO:005154	metal clust	1/451	65/23049	0.7237	0.773762	0.655472	Aco1
GO_MF_m	GO:004237	chemokine	1/451	66/23049	0.729122	0.778614	0.659582	S100a14
GO_MF_m	GO:000107	transcripti	3/451	193/23049	0.731353	0.780051	0.660799	Cdc5l/Id2/
GO_MF_m	GO:00434	ATPase act	2/451	132/23049	0.733213	0.781089	0.661679	Atp6v1h/I
GO_MF_m	GO:001702	myosin bin	1/451	68/23049	0.739649	0.786993	0.66668	Rab11a
GO_MF_m	GO:00167	hydrolase	2/451	134/23049	0.740773	0.787239	0.666889	Gba2/Man
GO_MF_m	GO:001661	oxidoredu	2/451	135/23049	0.744484	0.79023	0.669422	Gpd1l/Sdr
GO_MF_m	GO:000452	exonucleas	1/451	70/23049	0.749767	0.793924	0.672552	Xrn1
GO_MF_m	GO:001984	rRNA bindi	1/451	70/23049	0.749767	0.793924	0.672552	Fastkd2
GO_MF_m	GO:00150	calcium io	2/451	137/23049	0.75177	0.79509	0.673539	Grm7/Tpcn
GO_MF_m	GO:00052	extracellul	1/451	71/23049	0.754678	0.797208	0.675334	Ptk2b
GO_MF_m	GO:00083	steroid hy	1/451	73/23049	0.764214	0.806315	0.683048	Cyp2g1
GO_MF_m	GO:00009	transcripti	7/451	446/23049	0.772519	0.813072	0.688772	Atf4/Cebp
GO_MF_m	GO:00020	p53 bindin	1/451	75/23049	0.77338	0.813072	0.688772	Rnf20
GO_MF_m	GO:00611	endopepti	3/451	207/23049	0.773387	0.813072	0.688772	Ambp/Ser

GO_MF_m2	GO:001529	antiporter a	1/451	76/23049	0.777829	0.816767	0.691902	Slc7a10
GO_MF_m2	GO:000449	monooxyg	2/451	146/23049	0.78238	0.820567	0.695122	Cyp2g1/Pc
GO_MF_m2	GO:001685	isomerase	2/451	147/23049	0.785568	0.822932	0.697125	Ppib/Txndc
GO_MF_m2	GO:000382	antigen bir	3/451	213/23049	0.789683	0.825321	0.699149	Ighv1-23/I
GO_MF_m2	GO:000554	phospholip	6/451	396/23049	0.789732	0.825321	0.699149	Arap3/Chm
GO_MF_m2	GO:007040	ammonium	1/451	79/23049	0.790659	0.825321	0.699149	Chmp3
GO_MF_m2	GO:000484	thiol-depe	1/451	80/23049	0.794769	0.828629	0.701951	Usp17le
GO_MF_m2	GO:000108	RNA polym	2/451	151/23049	0.797915	0.829884	0.703015	Atf4/Id2
GO_MF_m2	GO:001661	oxidoreduc	2/451	151/23049	0.797915	0.829884	0.703015	Gpd1l/Sdr4
GO_MF_m2	GO:001620	antioxidant	1/451	81/23049	0.798799	0.829884	0.703015	Txndc17
GO_MF_m2	GO:003321	amide binc	5/451	341/23049	0.799792	0.829937	0.703059	Acaca/Bace
GO_MF_m2	GO:000801	beta-caten	1/451	85/23049	0.814144	0.843394	0.714459	Foxo4
GO_MF_m2	GO:000801	microtubul	3/451	223/23049	0.814675	0.843394	0.714459	Clip2/Eml3
GO_MF_m2	GO:000525	anion chan	1/451	86/23049	0.817794	0.84563	0.716353	Gpr89
GO_MF_m2	GO:007234	modified a	1/451	89/23049	0.828321	0.855511	0.724723	Osbpl5
GO_MF_m2	GO:000555	pheromon	1/451	90/23049	0.831693	0.856984	0.725971	Vmn1r215
GO_MF_m2	GO:005108	unfolded p	1/451	90/23049	0.831693	0.856984	0.725971	Tomm20
GO_MF_m2	GO:003645	thiol-depe	1/451	95/23049	0.847588	0.871325	0.73812	Usp17le
GO_MF_m2	GO:010100	ubiquitinyl	1/451	95/23049	0.847588	0.871325	0.73812	Usp17le
GO_MF_m2	GO:004227	peptide bir	4/451	306/23049	0.852094	0.874936	0.741179	Bace1/Gpr1
GO_MF_m2	GO:001650	pheromon	1/451	99/23049	0.859219	0.881225	0.746506	Vmn1r215
GO_MF_m2	GO:006009	molecular a	2/451	178/23049	0.865926	0.885448	0.750084	Arrdc1/Rac
GO_MF_m2	GO:000110	RNA polym	1/451	102/23049	0.867357	0.885448	0.750084	Thrap3
GO_MF_m2	GO:000369	single-stra	1/451	102/23049	0.867357	0.885448	0.750084	Hnrnpa2b1
GO_MF_m2	GO:001529	solute:catic	1/451	102/23049	0.867357	0.885448	0.750084	Slc45a4
GO_MF_m2	GO:001640	acetyltrans	1/451	109/23049	0.884566	0.900928	0.763197	Acat2
GO_MF_m2	GO:001978	ubiquitin-li	1/451	109/23049	0.884566	0.900928	0.763197	Usp17le
GO_MF_m2	GO:000517	integrin bir	1/451	112/23049	0.891242	0.906679	0.768069	Itgb1bp2
GO_MF_m2	GO:003059	neurotrans	1/451	114/23049	0.895477	0.909937	0.770829	Ptk2b
GO_MF_m2	GO:003024	carbohydra	3/451	268/23049	0.898118	0.911569	0.772211	Cdipt/Man
GO_MF_m2	GO:000486	endopeptic	2/451	200/23049	0.905079	0.917577	0.777301	Ambp/Serp
GO_MF_m2	GO:003041	peptidase i	2/451	210/23049	0.919095	0.92982	0.787673	Ambp/Serp
GO_MF_m2	GO:003067	protein bin	1/451	127/23049	0.919266	0.92982	0.787673	Arrdc1
GO_MF_m2	GO:000852	G-protein	1/451	129/23049	0.922412	0.931932	0.789462	Cxcr1
GO_MF_m2	GO:000165	peptide rec	1/451	133/23049	0.928341	0.936848	0.793626	Cxcr1
GO_MF_m2	GO:003107	heat shock	1/451	135/23049	0.931134	0.938592	0.795103	Tomm34
GO_MF_m2	GO:001510	inorganic a	1/451	142/23049	0.940081	0.946527	0.801826	Gpr89
GO_MF_m2	GO:000554	odorant bi	5/451	463/23049	0.950257	0.955681	0.80958	Olfr1062/C
GO_MF_m2	GO:005268	carboxylic	1/451	159/23049	0.957273	0.961639	0.814627	2810006K2
GO_MF_m2	GO:014009	catalytic ac	1/451	183/23049	0.973504	0.97683	0.827496	Recql
GO_MF_m2	GO:001674	transferase	1/451	221/23049	0.987579	0.989826	0.838505	Acat2
GO_MF_m2	GO:000122	transcriptic	1/451	235/23049	0.990607	0.991733	0.84012	Vax1
GO_MF_m2	GO:001674	transferase	1/451	252/23049	0.993311	0.993311	0.841457	Acat2
GO_MF_m3	GO:000518	neurohypo	2/520	2/23049	0.000508	0.272587	0.248033	Avp/Oxt
GO_MF_m3	GO:000517	hormone a	10/520	130/23049	0.000745	0.272587	0.248033	Adm2/Avp
GO_MF_m3	GO:007088	E-box binc	5/520	36/23049	0.001213	0.272587	0.248033	Hes1/Myoc
GO_MF_m3	GO:001560	organopho	4/520	22/23049	0.001356	0.272587	0.248033	Slc25a17/S
GO_MF_m3	GO:005143	corticotrop	2/520	4/23049	0.002958	0.27483	0.250074	Ucn/Ucn2

GO_MF_m	GO:000806	glutamate	4/520	27/23049	0.002977	0.27483	0.250074	Grik2/Grik4
GO_MF_m	GO:000523	excitatory	5/520	48/23049	0.004416	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:004216	acetylcholi	3/520	17/23049	0.006133	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:000098	proximal p	20/520	477/23049	0.00626	0.27483	0.250074	Cux2/Dmtf
GO_MF_m	GO:002282	transmitter	5/520	53/23049	0.006753	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:002283	transmitter	5/520	53/23049	0.006753	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:000473	pyruvate d	2/520	6/23049	0.007175	0.27483	0.250074	Dlat/Dld
GO_MF_m	GO:001527	kainate sel	2/520	6/23049	0.007175	0.27483	0.250074	Grik2/Grik4
GO_MF_m	GO:003458	piRNA bin	2/520	6/23049	0.007175	0.27483	0.250074	Mov10l1/P
GO_MF_m	GO:003460	pyruvate d	2/520	6/23049	0.007175	0.27483	0.250074	Dlat/Dld
GO_MF_m	GO:003460	pyruvate d	2/520	6/23049	0.007175	0.27483	0.250074	Dlat/Dld
GO_MF_m	GO:005142	corticotrop	2/520	6/23049	0.007175	0.27483	0.250074	Ucn/Ucn2
GO_MF_m	GO:000523	extracellula	3/520	18/23049	0.007238	0.27483	0.250074	Grik2/Grik4
GO_MF_m	GO:004801	receptor li	20/520	486/23049	0.007622	0.27483	0.250074	Adm2/Are
GO_MF_m	GO:009909	ligand-gat	7/520	101/23049	0.007953	0.27483	0.250074	Catsper4/C
GO_MF_m	GO:000497	ionotropic	3/520	19/23049	0.008453	0.27483	0.250074	Grik2/Grik4
GO_MF_m	GO:000511	patched bi	2/520	7/23049	0.009896	0.27483	0.250074	Ihh/Ptch1
GO_MF_m	GO:000829	single-stra	2/520	7/23049	0.009896	0.27483	0.250074	Isg20/Mgm
GO_MF_m	GO:000097	RNA polym	19/520	466/23049	0.010037	0.27483	0.250074	Cux2/Dmtf
GO_MF_m	GO:190431	transmitter	4/520	38/23049	0.010306	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:000107	transcriptio	9/520	160/23049	0.010632	0.27483	0.250074	Cux2/Gcfc2
GO_MF_m	GO:009952	neurotrans	4/520	39/23049	0.011284	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:009896	postsynapt	4/520	41/23049	0.013413	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:001662	oxidoreduc	3/520	23/23049	0.014456	0.27483	0.250074	Dhcr24/Sr
GO_MF_m	GO:000401	adenylate k	2/520	9/23049	0.016465	0.27483	0.250074	Ak6/Ak7
GO_MF_m	GO:003027	clathrin bin	5/520	67/23049	0.017612	0.27483	0.250074	Bcl2l1/Lrrk2
GO_MF_m	GO:000122	transcriptio	11/520	235/23049	0.018218	0.27483	0.250074	Cux2/Gcfc2
GO_MF_m	GO:001686	intramolec	3/520	26/23049	0.020194	0.27483	0.250074	Pmm1/Pus
GO_MF_m	GO:003245	histone de	3/520	26/23049	0.020194	0.27483	0.250074	Kdm4b/Kd
GO_MF_m	GO:000523	extracellula	5/520	71/23049	0.022085	0.27483	0.250074	Chrna4/Ch
GO_MF_m	GO:004885	enzyme inh	16/520	405/23049	0.022366	0.27483	0.250074	9230104L0
GO_MF_m	GO:000024	delta24(24	1/520	1/23049	0.022561	0.27483	0.250074	Dhcr24
GO_MF_m	GO:001099	TFIIF-class	1/520	1/23049	0.022561	0.27483	0.250074	Ctdp1
GO_MF_m	GO:000179	polymeric i	1/520	1/23049	0.022561	0.27483	0.250074	Pigr
GO_MF_m	GO:000414	dihydrolipo	1/520	1/23049	0.022561	0.27483	0.250074	Dld
GO_MF_m	GO:000474	dihydrolipo	1/520	1/23049	0.022561	0.27483	0.250074	Dlat
GO_MF_m	GO:000479	threonine s	1/520	1/23049	0.022561	0.27483	0.250074	Thnsl2
GO_MF_m	GO:000851	reduced fo	1/520	1/23049	0.022561	0.27483	0.250074	Slc19a1
GO_MF_m	GO:000885	exoribonuc	1/520	1/23049	0.022561	0.27483	0.250074	Isg20
GO_MF_m	GO:001516	glycerol-3-	1/520	1/23049	0.022561	0.27483	0.250074	Slc37a2
GO_MF_m	GO:001640	15-hydrox	1/520	1/23049	0.022561	0.27483	0.250074	Hpgd
GO_MF_m	GO:001643	tRNA (ader	1/520	1/23049	0.022561	0.27483	0.250074	Trmo
GO_MF_m	GO:001649	substance	1/520	1/23049	0.022561	0.27483	0.250074	Tacr1
GO_MF_m	GO:001979	tubulin N-a	1/520	1/23049	0.022561	0.27483	0.250074	Atat1
GO_MF_m	GO:001996	interleukin-	1/520	1/23049	0.022561	0.27483	0.250074	Il10ra
GO_MF_m	GO:003052	dihydrolipo	1/520	1/23049	0.022561	0.27483	0.250074	Dlat
GO_MF_m	GO:003172	CXCR4 che	1/520	1/23049	0.022561	0.27483	0.250074	Tff2
GO_MF_m	GO:003185	oxytocin re	1/520	1/23049	0.022561	0.27483	0.250074	Oxt

GO_MF_m3	GO:003189	V1B vasopr	1/520	1/23049	0.022561	0.27483	0.250074	Avp
GO_MF_m3	GO:003529	inositol per	1/520	1/23049	0.022561	0.27483	0.250074	Ippk
GO_MF_m3	GO:003647	peroxidase	1/520	1/23049	0.022561	0.27483	0.250074	Lrrk2
GO_MF_m3	GO:004354	lipoamide l	1/520	1/23049	0.022561	0.27483	0.250074	Dld
GO_MF_m3	GO:004461	FMN transr	1/520	1/23049	0.022561	0.27483	0.250074	Slc25a17
GO_MF_m3	GO:004502	UDP-activa	1/520	1/23049	0.022561	0.27483	0.250074	P2ry6
GO_MF_m3	GO:004681	chemokine	1/520	1/23049	0.022561	0.27483	0.250074	Ccl5
GO_MF_m3	GO:004722	acetylgalac	1/520	1/23049	0.022561	0.27483	0.250074	B3gnt6
GO_MF_m3	GO:005020	fucokinase	1/520	1/23049	0.022561	0.27483	0.250074	Fuk
GO_MF_m3	GO:005061	delta14-ste	1/520	1/23049	0.022561	0.27483	0.250074	Tm7sf2
GO_MF_m3	GO:005061	delta24-ste	1/520	1/23049	0.022561	0.27483	0.250074	Dhcr24
GO_MF_m3	GO:005172	NAD transr	1/520	1/23049	0.022561	0.27483	0.250074	Slc25a17
GO_MF_m3	GO:007182	N-box binc	1/520	1/23049	0.022561	0.27483	0.250074	Hes1
GO_MF_m3	GO:007041	I-SMAD bi	2/520	11/23049	0.024417	0.293	0.266607	Axin2/Tgfb
GO_MF_m3	GO:001624	channel re	7/520	127/23049	0.025248	0.298516	0.271626	Kcnmb4/Pa
GO_MF_m3	GO:000098	transcriptio	17/520	446/23049	0.025656	0.298945	0.272017	Cux2/Dmtf
GO_MF_m3	GO:000029	adenine nu	2/520	12/23049	0.028868	0.317948	0.289309	Slc25a17/S
GO_MF_m3	GO:000534	purine ribo	2/520	12/23049	0.028868	0.317948	0.289309	Slc25a17/S
GO_MF_m3	GO:001521	purine nuc	2/520	12/23049	0.028868	0.317948	0.289309	Slc25a17/S
GO_MF_m3	GO:003245	histone de	2/520	12/23049	0.028868	0.317948	0.289309	Kdm4b/Kd
GO_MF_m3	GO:004302	cysteine-ty	3/520	30/23049	0.029522	0.319527	0.290746	Avp/Bcl2l1/
GO_MF_m3	GO:000512	cytokine ac	10/520	222/23049	0.029807	0.319527	0.290746	Areg/Bmp2
GO_MF_m3	GO:004342	bHLH trans	3/520	31/23049	0.032152	0.332121	0.302205	Tcf21/Tsc2
GO_MF_m3	GO:001527	ligand-gat	7/520	134/23049	0.032513	0.332121	0.302205	Catsper4/C
GO_MF_m3	GO:002283	ligand-gat	7/520	134/23049	0.032513	0.332121	0.302205	Catsper4/C
GO_MF_m3	GO:000537	water trans	2/520	13/23049	0.033616	0.332121	0.302205	Aqp5/Slc14
GO_MF_m3	GO:000998	pseudouric	2/520	13/23049	0.033616	0.332121	0.302205	Pus7l/Rpus
GO_MF_m3	GO:000370	transcriptio	6/520	107/23049	0.034369	0.332121	0.302205	Foxc2/Foxf
GO_MF_m3	GO:001978	ubiquitin-li	6/520	109/23049	0.037119	0.332121	0.302205	Ankzf1/Gm
GO_MF_m3	GO:000436	glutathione	3/520	33/23049	0.037767	0.332121	0.302205	Gdap1l1/G
GO_MF_m3	GO:000832	signaling p	2/520	14/23049	0.038643	0.332121	0.302205	Trim12c/Tr
GO_MF_m3	GO:003818	pattern rec	2/520	14/23049	0.038643	0.332121	0.302205	Trim12c/Tr
GO_MF_m3	GO:009910	ion channe	5/520	84/23049	0.041443	0.332121	0.302205	Kcnmb4/Pa
GO_MF_m3	GO:000515	epidermal	3/520	35/23049	0.043847	0.332121	0.302205	Areg/Atxn2
GO_MF_m3	GO:000853	Ran GTPas	3/520	35/23049	0.043847	0.332121	0.302205	Nxt1/Ranb
GO_MF_m3	GO:000469	protein kin	2/520	15/23049	0.043935	0.332121	0.302205	Prkch/Prkc
GO_MF_m3	GO:001521	nucleotide	2/520	15/23049	0.043935	0.332121	0.302205	Slc25a17/S
GO_MF_m3	GO:001666	oxidoreduc	2/520	15/23049	0.043935	0.332121	0.302205	Dld/Nxnl2
GO_MF_m3	GO:001672	oxidoreduc	2/520	15/23049	0.043935	0.332121	0.302205	Cyp2c38/R
GO_MF_m3	GO:000163	leukotriene	1/520	2/23049	0.044613	0.332121	0.302205	Ltb4r2
GO_MF_m3	GO:000404	aminometh	1/520	2/23049	0.044613	0.332121	0.302205	Gcsh
GO_MF_m3	GO:000461	phosphom	1/520	2/23049	0.044613	0.332121	0.302205	Pmm1
GO_MF_m3	GO:000464	phosphoe	1/520	2/23049	0.044613	0.332121	0.302205	Dusp26
GO_MF_m3	GO:000496	gonadotro	1/520	2/23049	0.044613	0.332121	0.302205	Gpr173
GO_MF_m3	GO:000838	cholesterol	1/520	2/23049	0.044613	0.332121	0.302205	Fdx1
GO_MF_m3	GO:001503	NADPH-ac	1/520	2/23049	0.044613	0.332121	0.302205	Fdx1
GO_MF_m3	GO:001523	FAD transn	1/520	2/23049	0.044613	0.332121	0.302205	Slc25a17
GO_MF_m3	GO:001535	methotrexa	1/520	2/23049	0.044613	0.332121	0.302205	Slc19a1

GO_MF_m	GO:001641	S-acetyltra	1/520	2/23049	0.044613	0.332121	0.302205	Dlat
GO_MF_m	GO:003172	CCR4 chem	1/520	2/23049	0.044613	0.332121	0.302205	Ccl5
GO_MF_m	GO:003189	V1A vasop	1/520	2/23049	0.044613	0.332121	0.302205	Avp
GO_MF_m	GO:003421	GTP-deper	1/520	2/23049	0.044613	0.332121	0.302205	Lrrk2
GO_MF_m	GO:004681	histone de	1/520	2/23049	0.044613	0.332121	0.302205	Ucn
GO_MF_m	GO:004696	3'-phosph	1/520	2/23049	0.044613	0.332121	0.302205	Slc35b3
GO_MF_m	GO:190471	beta-caten	1/520	2/23049	0.044613	0.332121	0.302205	Lrrk2
GO_MF_m	GO:002284	acetylcholi	2/520	16/23049	0.049478	0.338854	0.308331	Chrna4/Ch
GO_MF_m	GO:190150	carbohydra	3/520	38/23049	0.053818	0.338854	0.308331	Slc25a17/S
GO_MF_m	GO:000109	RNA polym	2/520	17/23049	0.055257	0.338854	0.308331	Ctdp1/Gtf2
GO_MF_m	GO:000495	icosanoid r	2/520	17/23049	0.055257	0.338854	0.308331	Hpgd/Ltb4
GO_MF_m	GO:005108	chaperone	5/520	92/23049	0.057227	0.338854	0.308331	Bag5/Fnip2
GO_MF_m	GO:004288	amide tran	3/520	39/23049	0.057362	0.338854	0.308331	Slc14a1/Slc
GO_MF_m	GO:003245	demethylas	3/520	40/23049	0.061014	0.338854	0.308331	Kdm4b/Kd
GO_MF_m	GO:000452	exodeoxyri	2/520	18/23049	0.06126	0.338854	0.308331	Isg20/Mgm
GO_MF_m	GO:001689	exodeoxyri	2/520	18/23049	0.06126	0.338854	0.308331	Isg20/Mgm
GO_MF_m	GO:003645	thiol-depe	5/520	95/23049	0.063921	0.338854	0.308331	Ankzf1/Otu
GO_MF_m	GO:010100	ubiquitinyl	5/520	95/23049	0.063921	0.338854	0.308331	Ankzf1/Otu
GO_MF_m	GO:004302	cysteine-ty	3/520	41/23049	0.064772	0.338854	0.308331	Avp/Bcl2l1
GO_MF_m	GO:000109	TFIIH-class	1/520	3/23049	0.066169	0.338854	0.308331	Gtf2e1
GO_MF_m	GO:000386	3-oxo-5-a	1/520	3/23049	0.066169	0.338854	0.308331	Srd5a1
GO_MF_m	GO:000469	calcium-in	1/520	3/23049	0.066169	0.338854	0.308331	Prkch
GO_MF_m	GO:000474	ribonucleo	1/520	3/23049	0.066169	0.338854	0.308331	Rrm2
GO_MF_m	GO:000483	valine-tRN	1/520	3/23049	0.066169	0.338854	0.308331	Vars
GO_MF_m	GO:000499	tachykinin	1/520	3/23049	0.066169	0.338854	0.308331	Tacr1
GO_MF_m	GO:000511	smoothene	1/520	3/23049	0.066169	0.338854	0.308331	Ptch1
GO_MF_m	GO:000527	acetylcholi	1/520	3/23049	0.066169	0.338854	0.308331	Slc18a3
GO_MF_m	GO:000815	hedgehog	1/520	3/23049	0.066169	0.338854	0.308331	Ptch1
GO_MF_m	GO:001506	uridine nuc	1/520	3/23049	0.066169	0.338854	0.308331	P2ry6
GO_MF_m	GO:001511	hexose pho	1/520	3/23049	0.066169	0.338854	0.308331	Slc37a2
GO_MF_m	GO:001522	coenzyme	1/520	3/23049	0.066169	0.338854	0.308331	Slc25a17
GO_MF_m	GO:001524	aminophos	1/520	3/23049	0.066169	0.338854	0.308331	Tmem30b
GO_MF_m	GO:001526	urea chanr	1/520	3/23049	0.066169	0.338854	0.308331	Slc14a1
GO_MF_m	GO:001531	organopho	1/520	3/23049	0.066169	0.338854	0.308331	Slc37a2
GO_MF_m	GO:001552	hexose-ph	1/520	3/23049	0.066169	0.338854	0.308331	Slc37a2
GO_MF_m	GO:001642	tRNA (ader	1/520	3/23049	0.066169	0.338854	0.308331	Trmo
GO_MF_m	GO:001652	growth hor	1/520	3/23049	0.066169	0.338854	0.308331	Ghrhr
GO_MF_m	GO:001672	oxidoreduc	1/520	3/23049	0.066169	0.338854	0.308331	Rrm2
GO_MF_m	GO:001683	carbon-ox	1/520	3/23049	0.066169	0.338854	0.308331	Thnsl2
GO_MF_m	GO:001915	protein-dis	1/520	3/23049	0.066169	0.338854	0.308331	Pdia3
GO_MF_m	GO:003017	troponin C	1/520	3/23049	0.066169	0.338854	0.308331	Tnnt3
GO_MF_m	GO:003029	receptor si	1/520	3/23049	0.066169	0.338854	0.308331	Ccl5
GO_MF_m	GO:003034	syntaxin-3	1/520	3/23049	0.066169	0.338854	0.308331	Syt4
GO_MF_m	GO:003172	CCR1 chen	1/520	3/23049	0.066169	0.338854	0.308331	Ccl5
GO_MF_m	GO:003189	vasopressir	1/520	3/23049	0.066169	0.338854	0.308331	Avp
GO_MF_m	GO:003537	chondroitir	1/520	3/23049	0.066169	0.338854	0.308331	Ptprf
GO_MF_m	GO:004342	3-phospho	1/520	3/23049	0.066169	0.338854	0.308331	Sgk1
GO_MF_m	GO:004472	hemi-meth	1/520	3/23049	0.066169	0.338854	0.308331	Uhrf1

GO_MF_m	GO:004775	cholesteno	1/520	3/23049	0.066169	0.338854	0.308331	Srd5a1
GO_MF_m	GO:006151	glucose 6-	1/520	3/23049	0.066169	0.338854	0.308331	Slc37a2
GO_MF_m	GO:006173	ribonucleo	1/520	3/23049	0.066169	0.338854	0.308331	Rrm2
GO_MF_m	GO:007090	serine bind	1/520	3/23049	0.066169	0.338854	0.308331	Thnsl2
GO_MF_m	GO:007107	adenosine	1/520	3/23049	0.066169	0.338854	0.308331	Slc25a17
GO_MF_m	GO:007155	G-protein	1/520	3/23049	0.066169	0.338854	0.308331	P2ry6
GO_MF_m	GO:008012	AMP transı	1/520	3/23049	0.066169	0.338854	0.308331	Slc25a17
GO_MF_m	GO:190137	acetate est	1/520	3/23049	0.066169	0.338854	0.308331	Slc18a3
GO_MF_m	GO:000472	protein tyr	5/520	97/23049	0.068618	0.347056	0.315795	Dusp26/Pa
GO_MF_m	GO:000813	protein tyr	3/520	42/23049	0.068634	0.347056	0.315795	Ccdc155/D
GO_MF_m	GO:001545	potassium	3/520	43/23049	0.072598	0.364805	0.331945	Kcnmb4/Pı
GO_MF_m	GO:004830	calcium-de	4/520	71/23049	0.076549	0.38047	0.346199	Grm4/S10C
GO_MF_m	GO:001679	exonucleas	3/520	44/23049	0.076662	0.38047	0.346199	Dis3/Isg20/
GO_MF_m	GO:001529	solute:prot	2/520	21/23049	0.080478	0.383283	0.348758	Slc15a3/Slc
GO_MF_m	GO:001546	acetylcholi	2/520	21/23049	0.080478	0.383283	0.348758	Chrna4/Ch
GO_MF_m	GO:001920	nucleotide	2/520	21/23049	0.080478	0.383283	0.348758	Ak6/Ak7
GO_MF_m	GO:005142	peptide ho	2/520	21/23049	0.080478	0.383283	0.348758	Ucn/Ucn2
GO_MF_m	GO:000486	cysteine-ty	4/520	73/23049	0.082876	0.383283	0.348758	9230104L0
GO_MF_m	GO:000164	group III m	1/520	4/23049	0.08724	0.383283	0.348758	Grm4
GO_MF_m	GO:000204	opsin bindi	1/520	4/23049	0.08724	0.383283	0.348758	Sag
GO_MF_m	GO:000383	gamma-gl	1/520	4/23049	0.08724	0.383283	0.348758	Ggct
GO_MF_m	GO:000391	DNA topoi	1/520	4/23049	0.08724	0.383283	0.348758	Top3b
GO_MF_m	GO:000412	cytidylate k	1/520	4/23049	0.08724	0.383283	0.348758	Ak7
GO_MF_m	GO:000500	transmemb	1/520	4/23049	0.08724	0.383283	0.348758	Ptprf
GO_MF_m	GO:000502	transformir	1/520	4/23049	0.08724	0.383283	0.348758	Tgfbr1
GO_MF_m	GO:000831	single-stra	1/520	4/23049	0.08724	0.383283	0.348758	Isg20
GO_MF_m	GO:001501	[heparan sı	1/520	4/23049	0.08724	0.383283	0.348758	Ndst2
GO_MF_m	GO:001919	transmemb	1/520	4/23049	0.08724	0.383283	0.348758	Ptprf
GO_MF_m	GO:003101	troponin T	1/520	4/23049	0.08724	0.383283	0.348758	Tnni2
GO_MF_m	GO:003149	nucleosom	1/520	4/23049	0.08724	0.383283	0.348758	Uhrf1
GO_MF_m	GO:003376	steroid deh	1/520	4/23049	0.08724	0.383283	0.348758	Srd5a1
GO_MF_m	GO:005143	corticotrop	1/520	4/23049	0.08724	0.383283	0.348758	Ucn
GO_MF_m	GO:009710	hedgehog	1/520	4/23049	0.08724	0.383283	0.348758	Ptch1
GO_MF_m	GO:199093	5.8S rRNA	1/520	4/23049	0.08724	0.383283	0.348758	Rpl6l
GO_MF_m	GO:000109	basal trans	3/520	47/23049	0.089432	0.388665	0.353656	Ctdp1/Ctr9
GO_MF_m	GO:000109	basal RNA	3/520	47/23049	0.089432	0.388665	0.353656	Ctdp1/Ctr9
GO_MF_m	GO:000472	phosphopr	7/520	171/23049	0.093255	0.4031	0.366791	Ccdc155/C
GO_MF_m	GO:001510	organic cat	2/520	23/23049	0.09418	0.403256	0.366932	Slc18a3/Slc
GO_MF_m	GO:001995	cytokine bi	5/520	107/23049	0.094859	0.403256	0.366932	Crlf1/Cxcr6
GO_MF_m	GO:004256	hormone b	5/520	107/23049	0.094859	0.403256	0.366932	Chrna4/Ch
GO_MF_m	GO:000521	structural c	2/520	24/23049	0.101265	0.403256	0.366932	Cryaa/Cryg
GO_MF_m	GO:001707	syntaxin-1	2/520	24/23049	0.101265	0.403256	0.366932	Lrrk2/Syt4
GO_MF_m	GO:001920	phosphata	4/520	79/23049	0.103321	0.403256	0.366932	Bmp2/Mtm
GO_MF_m	GO:004633	SMAD binc	4/520	79/23049	0.103321	0.403256	0.366932	Axin2/Bmp
GO_MF_m	GO:000484	thiol-depe	4/520	80/23049	0.106934	0.403256	0.366932	Ankzf1/Otu
GO_MF_m	GO:000516	transformir	3/520	51/23049	0.107724	0.403256	0.366932	Bmp2/Gdf5
GO_MF_m	GO:000015	phosphore	1/520	5/23049	0.107836	0.403256	0.366932	Kcnh3
GO_MF_m	GO:000163	cysteinyl le	1/520	5/23049	0.107836	0.403256	0.366932	Ltb4r2

GO_MF_m	GO:000434	glucokinas	1/520	5/23049	0.107836	0.403256	0.366932	Hk1
GO_MF_m	GO:000439	hexokinase	1/520	5/23049	0.107836	0.403256	0.366932	Hk1
GO_MF_m	GO:000468	phosphory	1/520	5/23049	0.107836	0.403256	0.366932	Phkg2
GO_MF_m	GO:000492	interleukin-	1/520	5/23049	0.107836	0.403256	0.366932	Il10ra
GO_MF_m	GO:000497	leukotriene	1/520	5/23049	0.107836	0.403256	0.366932	Ltb4r2
GO_MF_m	GO:000851	folic acid tr	1/520	5/23049	0.107836	0.403256	0.366932	Slc19a1
GO_MF_m	GO:000886	fructokinas	1/520	5/23049	0.107836	0.403256	0.366932	Hk1
GO_MF_m	GO:001520	urea transp	1/520	5/23049	0.107836	0.403256	0.366932	Slc14a1
GO_MF_m	GO:001533	peptide:pr	1/520	5/23049	0.107836	0.403256	0.366932	Slc15a3
GO_MF_m	GO:001915	mannokina	1/520	5/23049	0.107836	0.403256	0.366932	Hk1
GO_MF_m	GO:002284	glutamate-	1/520	5/23049	0.107836	0.403256	0.366932	Grin2c
GO_MF_m	GO:003089	calcium-de	1/520	5/23049	0.107836	0.403256	0.366932	Tnnt3
GO_MF_m	GO:003101	troponin I	1/520	5/23049	0.107836	0.403256	0.366932	Tnnt3
GO_MF_m	GO:003503	histone dea	1/520	5/23049	0.107836	0.403256	0.366932	Ucn
GO_MF_m	GO:003567	enone redu	1/520	5/23049	0.107836	0.403256	0.366932	Srd5a1
GO_MF_m	GO:004203	ATPase inh	1/520	5/23049	0.107836	0.403256	0.366932	Fnip2
GO_MF_m	GO:005143	BH3 domai	1/520	5/23049	0.107836	0.403256	0.366932	Bcl2l1
GO_MF_m	GO:007073	protein-glu	1/520	5/23049	0.107836	0.403256	0.366932	Ttll4
GO_MF_m	GO:000017	3'-5'-exori	2/520	25/23049	0.108491	0.403829	0.367453	Dis3/Isg20
GO_MF_m	GO:003059	neurotrans	5/520	114/23049	0.115852	0.429238	0.390574	Chrna4/Ch
GO_MF_m	GO:000468	calmodulin	2/520	27/23049	0.12333	0.432295	0.393356	Mapkapk3/
GO_MF_m	GO:000518	neuropepti	2/520	27/23049	0.12333	0.432295	0.393356	Avp/Oxt
GO_MF_m	GO:001689	exoribonuc	2/520	27/23049	0.12333	0.432295	0.393356	Dis3/Isg20
GO_MF_m	GO:000166	alpha-N-a	1/520	6/23049	0.127968	0.432295	0.393356	St6galnac5
GO_MF_m	GO:000446	lysine N-ac	1/520	6/23049	0.127968	0.432295	0.393356	Atat1
GO_MF_m	GO:000467	protein his	1/520	6/23049	0.127968	0.432295	0.393356	Kcnh3
GO_MF_m	GO:000495	prostaglan	1/520	6/23049	0.127968	0.432295	0.393356	Hpgd
GO_MF_m	GO:000512	ciliary neur	1/520	6/23049	0.127968	0.432295	0.393356	Crlf1
GO_MF_m	GO:000549	vitamin D b	1/520	6/23049	0.127968	0.432295	0.393356	S100g
GO_MF_m	GO:000860	cAMP-dep	1/520	6/23049	0.127968	0.432295	0.393356	Prkar1b
GO_MF_m	GO:001921	phosphata	1/520	6/23049	0.127968	0.432295	0.393356	Bmp2
GO_MF_m	GO:001995	C-X-C che	1/520	6/23049	0.127968	0.432295	0.393356	Cxcr6
GO_MF_m	GO:003036	interleukin-	1/520	6/23049	0.127968	0.432295	0.393356	Il17rd
GO_MF_m	GO:003062	U2 snRNA	1/520	6/23049	0.127968	0.432295	0.393356	Isg20
GO_MF_m	GO:003369	oxidoreduc	1/520	6/23049	0.127968	0.432295	0.393356	Cyp2c38
GO_MF_m	GO:003451	U3 snoRNA	1/520	6/23049	0.127968	0.432295	0.393356	Isg20
GO_MF_m	GO:003487	caffeine ox	1/520	6/23049	0.127968	0.432295	0.393356	Cyp2c38
GO_MF_m	GO:004342	MRF bindin	1/520	6/23049	0.127968	0.432295	0.393356	Tsc22d3
GO_MF_m	GO:007029	N-acylpho	1/520	6/23049	0.127968	0.432295	0.393356	Pld4
GO_MF_m	GO:199005	phosphatid	1/520	6/23049	0.127968	0.432295	0.393356	Prelid3a
GO_MF_m	GO:199025	keratin fila	1/520	6/23049	0.127968	0.432295	0.393356	Fam83h
GO_MF_m	GO:003016	PDZ doma	5/520	118/23049	0.128757	0.43314	0.394125	Dtna/Grik2
GO_MF_m	GO:000453	exoribonuc	2/520	28/23049	0.130923	0.436771	0.397429	Dis3/Isg20
GO_MF_m	GO:009960	ligand-gat	2/520	28/23049	0.130923	0.436771	0.397429	Catsper4/C
GO_MF_m	GO:001666	oxidoreduc	3/520	56/23049	0.132414	0.439922	0.400295	Dld/Nxnl2/
GO_MF_m	GO:001662	oxidoreduc	3/520	57/23049	0.137571	0.448293	0.407913	Dhcr24/Src
GO_MF_m	GO:000110	RNA polym	2/520	29/23049	0.13862	0.448293	0.407913	Bend6/Tfap
GO_MF_m	GO:000522	calcium act	2/520	29/23049	0.13862	0.448293	0.407913	Catsper4/K

GO_MF_m	GO:005068	androgen r	2/520	29/23049	0.13862	0.448293	0.407913	Kdm5d/Tcf
GO_MF_m	GO:007234	modified a	4/520	89/23049	0.141878	0.448293	0.407913	Gsta2/Slc1
GO_MF_m	GO:007185	neuropepti	2/520	30/23049	0.146413	0.448293	0.407913	Ucn/Ucn2
GO_MF_m	GO:000107	transcripti	7/520	193/23049	0.147583	0.448293	0.407913	Bend6/Dm
GO_MF_m	GO:000164	adenylate c	1/520	7/23049	0.147647	0.448293	0.407913	Grm4
GO_MF_m	GO:000497	NMDA glu	1/520	7/23049	0.147647	0.448293	0.407913	Grin2c
GO_MF_m	GO:000511	type II tran	1/520	7/23049	0.147647	0.448293	0.407913	Tgfbr1
GO_MF_m	GO:000819	ferric iron b	1/520	7/23049	0.147647	0.448293	0.407913	Rrm2
GO_MF_m	GO:000992	fatty acid e	1/520	7/23049	0.147647	0.448293	0.407913	Elovl2
GO_MF_m	GO:001034	carboxyl-C	1/520	7/23049	0.147647	0.448293	0.407913	Armt1
GO_MF_m	GO:001684	amidine-ly	1/520	7/23049	0.147647	0.448293	0.407913	Ggct
GO_MF_m	GO:003173	CCR5 chem	1/520	7/23049	0.147647	0.448293	0.407913	Ccl5
GO_MF_m	GO:003279	heterotrim	1/520	7/23049	0.147647	0.448293	0.407913	Cetn4
GO_MF_m	GO:005118	coenzyme	1/520	7/23049	0.147647	0.448293	0.407913	Slc25a17
GO_MF_m	GO:005199	protein car	1/520	7/23049	0.147647	0.448293	0.407913	Armt1
GO_MF_m	GO:007234	NAADP-se	1/520	7/23049	0.147647	0.448293	0.407913	Catsper4
GO_MF_m	GO:010233	3-oxo-arac	1/520	7/23049	0.147647	0.448293	0.407913	Elovl2
GO_MF_m	GO:010233	3-oxo-cer	1/520	7/23049	0.147647	0.448293	0.407913	Elovl2
GO_MF_m	GO:010233	3-oxo-lign	1/520	7/23049	0.147647	0.448293	0.407913	Elovl2
GO_MF_m	GO:002283	substrate-s	13/520	415/23049	0.147758	0.448293	0.407913	Aqp5/Cats
GO_MF_m	GO:004216	neurotrans	3/520	60/23049	0.153437	0.458125	0.416859	Chrna4/Ch
GO_MF_m	GO:000099	RNA polym	2/520	31/23049	0.154293	0.458125	0.416859	Ctr9/Gtf2e
GO_MF_m	GO:000513	type I inter	2/520	31/23049	0.154293	0.458125	0.416859	Gm13287/
GO_MF_m	GO:000820	ion channe	2/520	31/23049	0.154293	0.458125	0.416859	Pacsin3/St
GO_MF_m	GO:003050	spectrin bi	2/520	31/23049	0.154293	0.458125	0.416859	Ptprn/Sag
GO_MF_m	GO:003149	chromatin	4/520	92/23049	0.154418	0.458125	0.416859	Ankle1/Fox
GO_MF_m	GO:000526	cation char	10/520	307/23049	0.158332	0.466295	0.424293	Catsper4/C
GO_MF_m	GO:002283	ion gated c	10/520	307/23049	0.158332	0.466295	0.424293	Catsper4/C
GO_MF_m	GO:000526	potassium	5/520	127/23049	0.160015	0.467503	0.425392	Grik2/Grik4
GO_MF_m	GO:001507	potassium	6/520	163/23049	0.163859	0.467503	0.425392	Grik2/Grik4
GO_MF_m	GO:000453	deoxyribon	3/520	62/23049	0.164318	0.467503	0.425392	Dnase1l3/I
GO_MF_m	GO:002283	gated char	10/520	310/23049	0.165149	0.467503	0.425392	Catsper4/C
GO_MF_m	GO:000391	DNA topoi	1/520	8/23049	0.166882	0.467503	0.425392	Top3b
GO_MF_m	GO:000476	sphingomy	1/520	8/23049	0.166882	0.467503	0.425392	Enpp7
GO_MF_m	GO:000486	cAMP-dep	1/520	8/23049	0.166882	0.467503	0.425392	Prkar1b
GO_MF_m	GO:000502	transformin	1/520	8/23049	0.166882	0.467503	0.425392	Tgfbr1
GO_MF_m	GO:000842	CTD phosp	1/520	8/23049	0.166882	0.467503	0.425392	Ctdp1
GO_MF_m	GO:001649	C-X-C che	1/520	8/23049	0.166882	0.467503	0.425392	Cxcr6
GO_MF_m	GO:001985	calcium ch	1/520	8/23049	0.166882	0.467503	0.425392	Pacsin3
GO_MF_m	GO:003061	U1 snRNA	1/520	8/23049	0.166882	0.467503	0.425392	Isg20
GO_MF_m	GO:003245	histone de	1/520	8/23049	0.166882	0.467503	0.425392	Kdm5d
GO_MF_m	GO:003803	sphingosin	1/520	8/23049	0.166882	0.467503	0.425392	S1pr1
GO_MF_m	GO:001676	transferase	3/520	63/23049	0.169843	0.470474	0.428096	Gdap1l1/G
GO_MF_m	GO:000486	protein ph	2/520	33/23049	0.170284	0.470474	0.428096	Ppp1r1a/Sl
GO_MF_m	GO:001624	channel inh	2/520	33/23049	0.170284	0.470474	0.428096	Pacsin3/St
GO_MF_m	GO:005101	mitogen-a	2/520	33/23049	0.170284	0.470474	0.428096	Mapkapk3/
GO_MF_m	GO:004257	phosphoric	11/520	351/23049	0.172236	0.473853	0.43117	Ccdc155/C
GO_MF_m	GO:000122	transcripti	13/520	428/23049	0.172685	0.473853	0.43117	Dmtf1/Fox

GO_MF_m	GO:000534	ATP transm	1/520	9/23049	0.185684	0.487877	0.443931	Slc25a17
GO_MF_m	GO:000535	carbohydra	1/520	9/23049	0.185684	0.487877	0.443931	Slc2a10
GO_MF_m	GO:000829	3'-5'-exod	1/520	9/23049	0.185684	0.487877	0.443931	Isg20
GO_MF_m	GO:000853	N-acetyllac	1/520	9/23049	0.185684	0.487877	0.443931	B3gnt6
GO_MF_m	GO:000993	calcium-de	1/520	9/23049	0.185684	0.487877	0.443931	Mapkapk3
GO_MF_m	GO:001537	cation:chlo	1/520	9/23049	0.185684	0.487877	0.443931	Slc12a7
GO_MF_m	GO:001537	potassium:	1/520	9/23049	0.185684	0.487877	0.443931	Slc12a7
GO_MF_m	GO:001600	phospholip	1/520	9/23049	0.185684	0.487877	0.443931	Ccl5
GO_MF_m	GO:001976	immunoglo	1/520	9/23049	0.185684	0.487877	0.443931	Pigr
GO_MF_m	GO:003095	Tat protein	1/520	9/23049	0.185684	0.487877	0.443931	Ctdp1
GO_MF_m	GO:003195	very long-(	1/520	9/23049	0.185684	0.487877	0.443931	Slc27a4
GO_MF_m	GO:009737	MDM2/MD	1/520	9/23049	0.185684	0.487877	0.443931	Bcl2l1
GO_MF_m	GO:009898	G-protein	1/520	9/23049	0.185684	0.487877	0.443931	Grm4
GO_MF_m	GO:003303	bitter taste	2/520	35/23049	0.186533	0.48851	0.444507	Tas2r107/T
GO_MF_m	GO:005142	hormone r	6/520	172/23049	0.19387	0.494177	0.449663	Kdm5d/Me
GO_MF_m	GO:001677	phosphotra	2/520	36/23049	0.194737	0.494177	0.449663	Ak6/Ak7
GO_MF_m	GO:001921	phosphata	2/520	36/23049	0.194737	0.494177	0.449663	Ppp1r1a/Sl
GO_MF_m	GO:004317	RNA polym	2/520	36/23049	0.194737	0.494177	0.449663	Ctr9/Gtf2e
GO_MF_m	GO:001526	channel ac	13/520	439/23049	0.1953	0.494177	0.449663	Aqp5/Cats
GO_MF_m	GO:002280	passive tra	13/520	439/23049	0.1953	0.494177	0.449663	Aqp5/Cats
GO_MF_m	GO:003041	peptidase i	7/520	210/23049	0.197747	0.494177	0.449663	9230104L0
GO_MF_m	GO:000372	RNA helica	3/520	68/23049	0.198211	0.494177	0.449663	Ddx46/Dh
GO_MF_m	GO:000400	ATP-deper	3/520	68/23049	0.198211	0.494177	0.449663	Ddx46/Dh
GO_MF_m	GO:000110	RNA polym	4/520	102/23049	0.198925	0.494177	0.449663	Bend6/Me
GO_MF_m	GO:000166	G-protein	9/520	286/23049	0.199545	0.494177	0.449663	Avp/Ccl5/C
GO_MF_m	GO:001708	sodium ch	2/520	37/23049	0.202986	0.494177	0.449663	Prss8/Sclt1
GO_MF_m	GO:003162	ubiquitin c	2/520	37/23049	0.202986	0.494177	0.449663	Grik2/Rnf1
GO_MF_m	GO:004216	SH2 domai	2/520	37/23049	0.202986	0.494177	0.449663	Ctr9/Khdrb
GO_MF_m	GO:000119	transcriptic	3/520	69/23049	0.204017	0.494177	0.449663	Sox10/Tfap
GO_MF_m	GO:000818	RNA-depe	3/520	69/23049	0.204017	0.494177	0.449663	Ddx46/Dh
GO_MF_m	GO:000113	transcriptic	1/520	10/23049	0.204063	0.494177	0.449663	Dmtf1
GO_MF_m	GO:000850	monoamin	1/520	10/23049	0.204063	0.494177	0.449663	Slc18a3
GO_MF_m	GO:001085	calcium-de	1/520	10/23049	0.204063	0.494177	0.449663	Mapkapk3
GO_MF_m	GO:001521	ADP transr	1/520	10/23049	0.204063	0.494177	0.449663	Slc25a17
GO_MF_m	GO:001671	oxidoreduc	1/520	10/23049	0.204063	0.494177	0.449663	Fdx1
GO_MF_m	GO:001686	intramolec	1/520	10/23049	0.204063	0.494177	0.449663	Pmm1
GO_MF_m	GO:007051	death dom	1/520	10/23049	0.204063	0.494177	0.449663	Bcl2l1
GO_MF_m	GO:010102	estrogen 1	1/520	10/23049	0.204063	0.494177	0.449663	Cyp2c38
GO_MF_m	GO:010299	myristoyl-(	1/520	10/23049	0.204063	0.494177	0.449663	Them4
GO_MF_m	GO:000452	exonucleas	3/520	70/23049	0.209862	0.505695	0.460144	Dis3/Isg20/
GO_MF_m	GO:000471	protein ser	2/520	38/23049	0.211273	0.505695	0.460144	Lrrk2/Sgk1
GO_MF_m	GO:000178	phosphoty	2/520	39/23049	0.219593	0.505695	0.460144	Hck/Ptpn5
GO_MF_m	GO:001593	nucleobase	2/520	39/23049	0.219593	0.505695	0.460144	Slc25a17/S
GO_MF_m	GO:000107	transcriptic	9/520	294/23049	0.221419	0.505695	0.460144	Dmtf1/Fox
GO_MF_m	GO:000431	fatty acid s	1/520	11/23049	0.222028	0.505695	0.460144	Elovl2
GO_MF_m	GO:000459	peptide alp	1/520	11/23049	0.222028	0.505695	0.460144	Naa25
GO_MF_m	GO:000470	MAP kinase	1/520	11/23049	0.222028	0.505695	0.460144	Lrrk2
GO_MF_m	GO:000479	thioredoxir	1/520	11/23049	0.222028	0.505695	0.460144	Nxnl2

GO_MF_m	GO:00486	protein ser	1/520	11/23049	0.222028	0.505695	0.460144	Ppp1r1a
GO_MF_m	GO:00495	prostaglan	1/520	11/23049	0.222028	0.505695	0.460144	Hpgd
GO_MF_m	GO:00496	galanin rec	1/520	11/23049	0.222028	0.505695	0.460144	Ltb4r2
GO_MF_m	GO:000524	voltage-ga	1/520	11/23049	0.222028	0.505695	0.460144	Clcn1
GO_MF_m	GO:00806	chitin bindi	1/520	11/23049	0.222028	0.505695	0.460144	Fibcd1
GO_MF_m	GO:00152	anion:catio	1/520	11/23049	0.222028	0.505695	0.460144	Slc12a7
GO_MF_m	GO:001677	phosphotra	1/520	11/23049	0.222028	0.505695	0.460144	Kcnh3
GO_MF_m	GO:00191	pyrimidine	1/520	11/23049	0.222028	0.505695	0.460144	P2ry6
GO_MF_m	GO:003612	BMP bindi	1/520	11/23049	0.222028	0.505695	0.460144	Gdf5
GO_MF_m	GO:00423	phosphate	1/520	11/23049	0.222028	0.505695	0.460144	Ptprf
GO_MF_m	GO:00518	histone de	1/520	11/23049	0.222028	0.505695	0.460144	Kdm4b
GO_MF_m	GO:006022	lipase activ	1/520	11/23049	0.222028	0.505695	0.460144	Ccl5
GO_MF_m	GO:00082	cysteine-ty	6/520	182/23049	0.229415	0.517818	0.471175	Ankzf1/Gm
GO_MF_m	GO:00443	ubiquitin-li	10/520	337/23049	0.232382	0.517818	0.471175	Axin2/Bag
GO_MF_m	GO:00085	taste recep	2/520	41/23049	0.236307	0.517818	0.471175	Tas2r107/T
GO_MF_m	GO:00168	isomerase	5/520	147/23049	0.238545	0.517818	0.471175	Pdia3/Pmn
GO_MF_m	GO:00016	G-protein	1/520	12/23049	0.239588	0.517818	0.471175	P2ry6
GO_MF_m	GO:00021	aminoacyl-	1/520	12/23049	0.239588	0.517818	0.471175	Vars
GO_MF_m	GO:00495	prostanoid	1/520	12/23049	0.239588	0.517818	0.471175	Hpgd
GO_MF_m	GO:00055	profilin bin	1/520	12/23049	0.239588	0.517818	0.471175	Fmnl1
GO_MF_m	GO:00055	glucose bir	1/520	12/23049	0.239588	0.517818	0.471175	Hk1
GO_MF_m	GO:00150	peptide dis	1/520	12/23049	0.239588	0.517818	0.471175	Pdia3
GO_MF_m	GO:001511	phosphate	1/520	12/23049	0.239588	0.517818	0.471175	Slc37a2
GO_MF_m	GO:00152	water chan	1/520	12/23049	0.239588	0.517818	0.471175	Aqp5
GO_MF_m	GO:00169	SUMO-spe	1/520	12/23049	0.239588	0.517818	0.471175	Gm5415
GO_MF_m	GO:00316	G-protein	1/520	12/23049	0.239588	0.517818	0.471175	Gng2
GO_MF_m	GO:00397	co-recepto	1/520	12/23049	0.239588	0.517818	0.471175	Bmp2
GO_MF_m	GO:00430	ribosomal	1/520	12/23049	0.239588	0.517818	0.471175	Dhx29
GO_MF_m	GO:00450	G-protein	1/520	12/23049	0.239588	0.517818	0.471175	P2ry6
GO_MF_m	GO:007234	modified a	1/520	12/23049	0.239588	0.517818	0.471175	Slc19a1
GO_MF_m	GO:00974	structural r	1/520	12/23049	0.239588	0.517818	0.471175	Mybph
GO_MF_m	GO:00150	disulfide o	2/520	42/23049	0.24469	0.527429	0.47992	Nxnl2/Pdia
GO_MF_m	GO:00167	phosphata	8/520	265/23049	0.250623	0.538772	0.490242	Ccdc155/C
GO_MF_m	GO:000527	sodium ch	2/520	43/23049	0.253085	0.538978	0.490429	Grik2/Grik
GO_MF_m	GO:00192	nucleobase	2/520	43/23049	0.253085	0.538978	0.490429	Ak6/Ak7
GO_MF_m	GO:00443	ubiquitin-li	2/520	43/23049	0.253085	0.538978	0.490429	Grik2/Rnf1
GO_MF_m	GO:00044	long-chain	1/520	13/23049	0.256752	0.538978	0.490429	Slc27a4
GO_MF_m	GO:00055	tropomyos	1/520	13/23049	0.256752	0.538978	0.490429	Tnnt3
GO_MF_m	GO:000554	folic acid b	1/520	13/23049	0.256752	0.538978	0.490429	Slc19a1
GO_MF_m	GO:001527	store-oper	1/520	13/23049	0.256752	0.538978	0.490429	Trpc1
GO_MF_m	GO:001684	carbon-nit	1/520	13/23049	0.256752	0.538978	0.490429	Ggct
GO_MF_m	GO:00192	nucleoside	1/520	13/23049	0.256752	0.538978	0.490429	Ak7
GO_MF_m	GO:00085	protein tra	3/520	78/23049	0.257753	0.53967	0.491059	Dscr3/Nxt1
GO_MF_m	GO:000504	scavenger	2/520	44/23049	0.261486	0.543242	0.494309	Crb3/Susd
GO_MF_m	GO:00084	3'-5' exon	2/520	44/23049	0.261486	0.543242	0.494309	Dis3/Isg20
GO_MF_m	GO:00166	oxidoreduc	2/520	44/23049	0.261486	0.543242	0.494309	Dlat/Dld
GO_MF_m	GO:00704	ammonium	3/520	79/23049	0.263849	0.546738	0.49749	Chrna4/Ch
GO_MF_m	GO:00040	carbonate	1/520	14/23049	0.273529	0.549794	0.500271	Car6

GO_MF_m	GO:000843	JUN kinase	1/520	14/23049	0.273529	0.549794	0.500271	Hes1
GO_MF_m	GO:003448	heparan su	1/520	14/23049	0.273529	0.549794	0.500271	Ndst2
GO_MF_m	GO:004204	neurexin fa	1/520	14/23049	0.273529	0.549794	0.500271	Nlgn1
GO_MF_m	GO:004512	bioactive li	1/520	14/23049	0.273529	0.549794	0.500271	S1pr1
GO_MF_m	GO:004523	CXCR chen	1/520	14/23049	0.273529	0.549794	0.500271	Tff2
GO_MF_m	GO:004529	gamma-ca	1/520	14/23049	0.273529	0.549794	0.500271	Dsg1a
GO_MF_m	GO:004801	receptor ar	1/520	14/23049	0.273529	0.549794	0.500271	Ccl5
GO_MF_m	GO:004815	tau protein	1/520	14/23049	0.273529	0.549794	0.500271	Sgk1
GO_MF_m	GO:005140	BH domair	1/520	14/23049	0.273529	0.549794	0.500271	Bcl2l1
GO_MF_m	GO:007040	NAD+ binc	1/520	14/23049	0.273529	0.549794	0.500271	Hpgd
GO_MF_m	GO:007070	BMP recep	1/520	14/23049	0.273529	0.549794	0.500271	Bmp2
GO_MF_m	GO:199084	promoter-	2/520	46/23049	0.278289	0.557967	0.507707	Foxc2/Sox1
GO_MF_m	GO:000818	neuropepti	2/520	47/23049	0.286683	0.568544	0.517332	Ltb4r2/Tac
GO_MF_m	GO:003149	nucleosom	2/520	47/23049	0.286683	0.568544	0.517332	Dnttip1/Uh
GO_MF_m	GO:000808	phosphoric	3/520	83/23049	0.288389	0.568544	0.517332	Ccl5/Enpp
GO_MF_m	GO:001629	palmitoyl-	1/520	15/23049	0.289929	0.568544	0.517332	Them4
GO_MF_m	GO:001921	intermedia	1/520	15/23049	0.289929	0.568544	0.517332	Fam83h
GO_MF_m	GO:003015	receptor si	1/520	15/23049	0.289929	0.568544	0.517332	Lrrk2
GO_MF_m	GO:003423	protein kin	1/520	15/23049	0.289929	0.568544	0.517332	Prkar1b
GO_MF_m	GO:004283	peptidogly	1/520	15/23049	0.289929	0.568544	0.517332	Hk1
GO_MF_m	GO:007040	NADPH bir	1/520	15/23049	0.289929	0.568544	0.517332	Srd5a1
GO_MF_m	GO:000110	RNA polyn	2/520	48/23049	0.295066	0.575808	0.523942	Tfap2b/W
GO_MF_m	GO:000178	phosphatic	2/520	48/23049	0.295066	0.575808	0.523942	Syt4/Syt6
GO_MF_m	GO:000486	endopeptic	6/520	200/23049	0.297791	0.576525	0.524594	9230104L0
GO_MF_m	GO:000462	phospholip	3/520	85/23049	0.300727	0.576525	0.524594	Ccl5/Enpp
GO_MF_m	GO:003162	ubiquitin p	9/520	322/23049	0.304118	0.576525	0.524594	Axin2/Bag
GO_MF_m	GO:000521	ion channe	11/520	404/23049	0.305467	0.576525	0.524594	Catsper4/C
GO_MF_m	GO:000518	pheromon	1/520	16/23049	0.305959	0.576525	0.524594	Esp38
GO_MF_m	GO:000830	voltage-ga	1/520	16/23049	0.305959	0.576525	0.524594	Clcn1
GO_MF_m	GO:001650	protein-ho	1/520	16/23049	0.305959	0.576525	0.524594	Gpr173
GO_MF_m	GO:001667	oxidoreduc	1/520	16/23049	0.305959	0.576525	0.524594	Pdia3
GO_MF_m	GO:001716	Ral GTPase	1/520	16/23049	0.305959	0.576525	0.524594	Prkch
GO_MF_m	GO:003029	protein tyr	1/520	16/23049	0.305959	0.576525	0.524594	Ccl5
GO_MF_m	GO:004228	MHC class	1/520	16/23049	0.305959	0.576525	0.524594	Pdia3
GO_MF_m	GO:005137	muscle alp	1/520	16/23049	0.305959	0.576525	0.524594	Mybph
GO_MF_m	GO:007067	inositol 1,4	1/520	16/23049	0.305959	0.576525	0.524594	Trpc1
GO_MF_m	GO:006113	peptidase	7/520	242/23049	0.30619	0.576525	0.524594	9230104L0
GO_MF_m	GO:001629	lipase activ	4/520	124/23049	0.306846	0.576525	0.524594	Ccl5/Ces1
GO_MF_m	GO:000486	protein kin	3/520	86/23049	0.306906	0.576525	0.524594	Lrrtm1/Prk
GO_MF_m	GO:004530	protein ph	2/520	50/23049	0.311785	0.582965	0.530454	Hck/Ptpn5
GO_MF_m	GO:005101	protein kin	2/520	50/23049	0.311785	0.582965	0.530454	Lrrk2/Prkar
GO_MF_m	GO:000512	cytokine re	9/520	325/23049	0.313414	0.584651	0.531988	Bmp2/Ccl5
GO_MF_m	GO:000554	calcium-de	2/520	51/23049	0.320114	0.58731	0.534408	Syt4/Syt6
GO_MF_m	GO:003017	pyridoxal p	2/520	51/23049	0.320114	0.58731	0.534408	Accs/Thnsl
GO_MF_m	GO:000443	phosphatic	1/520	17/23049	0.321628	0.58731	0.534408	Ccl5
GO_MF_m	GO:000455	nucleoside	1/520	17/23049	0.321628	0.58731	0.534408	Ak7
GO_MF_m	GO:000467	transmem	1/520	17/23049	0.321628	0.58731	0.534408	Tgfbr1
GO_MF_m	GO:000832	methyl-Cp	1/520	17/23049	0.321628	0.58731	0.534408	Uhrf1

GO_MF_m	GO:001688	acid-aminc	1/520	17/23049	0.321628	0.58731	0.534408	Ttll4
GO_MF_m	GO:004329	glutathione	1/520	17/23049	0.321628	0.58731	0.534408	Gsta2
GO_MF_m	GO:190075	oligopeptic	1/520	17/23049	0.321628	0.58731	0.534408	Gsta2
GO_MF_m	GO:003067	protein bin	4/520	127/23049	0.322144	0.58731	0.534408	Khdrbs2/Tr
GO_MF_m	GO:006113	endopeptic	6/520	207/23049	0.325415	0.590687	0.53748	9230104L0
GO_MF_m	GO:001921	kinase inhil	3/520	89/23049	0.325466	0.590687	0.53748	Lrrtm1/Prk
GO_MF_m	GO:007027	vitamin B6	2/520	52/23049	0.328418	0.594703	0.541135	Accs/Thnsl
GO_MF_m	GO:000119	transcriptic	2/520	53/23049	0.336695	0.599343	0.545356	Bend6/Tfap
GO_MF_m	GO:000462	phospholip	1/520	18/23049	0.336944	0.599343	0.545356	Ccl5
GO_MF_m	GO:000474	retinol deh	1/520	18/23049	0.336944	0.599343	0.545356	Bmp2
GO_MF_m	GO:001526	calcium-ac	1/520	18/23049	0.336944	0.599343	0.545356	Kcnmb4
GO_MF_m	GO:003279	GTPase act	1/520	18/23049	0.336944	0.599343	0.545356	Fmnl1
GO_MF_m	GO:005118	cofactor tra	1/520	18/23049	0.336944	0.599343	0.545356	Slc25a17
GO_MF_m	GO:005510	ubiquitin-p	1/520	18/23049	0.336944	0.599343	0.545356	Trib2
GO_MF_m	GO:007018	DNA polym	1/520	18/23049	0.336944	0.599343	0.545356	Fanci
GO_MF_m	GO:005121	dioxygenas	3/520	91/23049	0.33784	0.59961	0.545599	Kdm4b/Kd
GO_MF_m	GO:007006	RNA polym	2/520	54/23049	0.34494	0.610126	0.555168	Ctr9/Gtf2e
GO_MF_m	GO:000489	cytokine re	3/520	93/23049	0.3502	0.610126	0.555168	Cxcr6/Il10r
GO_MF_m	GO:000375	protein dis	1/520	19/23049	0.351914	0.610126	0.555168	Pdia3
GO_MF_m	GO:000514	interleukin-	1/520	19/23049	0.351914	0.610126	0.555168	Il1f10
GO_MF_m	GO:000540	carbohydra	1/520	19/23049	0.351914	0.610126	0.555168	Slc2a10
GO_MF_m	GO:001564	fatty acid li	1/520	19/23049	0.351914	0.610126	0.555168	Slc27a4
GO_MF_m	GO:001686	intramolecu	1/520	19/23049	0.351914	0.610126	0.555168	Pdia3
GO_MF_m	GO:001704	GTP-Rho b	1/520	19/23049	0.351914	0.610126	0.555168	Exoc1
GO_MF_m	GO:004327	phospholip	1/520	19/23049	0.351914	0.610126	0.555168	Prkcz
GO_MF_m	GO:005043	transformir	1/520	19/23049	0.351914	0.610126	0.555168	Tgfbr1
GO_MF_m	GO:000014	SNARE bin	4/520	133/23049	0.352871	0.610126	0.555168	Lrrk2/Stx1
GO_MF_m	GO:001984	vitamin bin	4/520	133/23049	0.352871	0.610126	0.555168	Accs/S100
GO_MF_m	GO:000802	ATP-deper	3/520	94/23049	0.356372	0.613539	0.558274	Ddx46/Dh
GO_MF_m	GO:007003	purine NTF	3/520	94/23049	0.356372	0.613539	0.558274	Ddx46/Dh
GO_MF_m	GO:000554	phospholip	2/520	56/23049	0.361327	0.616788	0.56123	Prelid3a/Tr
GO_MF_m	GO:001690	oxidoreduc	2/520	56/23049	0.361327	0.616788	0.56123	Dlat/Dld
GO_MF_m	GO:003506	methylatec	2/520	56/23049	0.361327	0.616788	0.56123	Spin2d/Uh
GO_MF_m	GO:014003	methylatio	2/520	56/23049	0.361327	0.616788	0.56123	Spin2d/Uh
GO_MF_m	GO:000161	purinergic	1/520	20/23049	0.366548	0.619127	0.563358	P2ry6
GO_MF_m	GO:000524	inward rect	1/520	20/23049	0.366548	0.619127	0.563358	Kcnj4
GO_MF_m	GO:000815	protein ph	1/520	20/23049	0.366548	0.619127	0.563358	Sh3rf2
GO_MF_m	GO:000826	poly(U) RN	1/520	20/23049	0.366548	0.619127	0.563358	Khdrbs2
GO_MF_m	GO:001650	nucleotide	1/520	20/23049	0.366548	0.619127	0.563358	P2ry6
GO_MF_m	GO:001990	syntaxin bi	3/520	96/23049	0.36869	0.621439	0.565462	Lrrk2/Syt4/
GO_MF_m	GO:005101	actin filame	5/520	177/23049	0.369794	0.621996	0.565969	Ablim3/Fln
GO_MF_m	GO:000823	serine-type	6/520	219/23049	0.373451	0.626837	0.570374	Cela2a/Klk
GO_MF_m	GO:000187	pattern bin	1/520	21/23049	0.380851	0.632654	0.575667	Susd2
GO_MF_m	GO:000837	sialyltransf	1/520	21/23049	0.380851	0.632654	0.575667	St6galnac5
GO_MF_m	GO:003024	polysaccha	1/520	21/23049	0.380851	0.632654	0.575667	Susd2
GO_MF_m	GO:004662	sphingolipi	1/520	21/23049	0.380851	0.632654	0.575667	S1pr1
GO_MF_m	GO:007069	transmemb	1/520	21/23049	0.380851	0.632654	0.575667	Bmp2
GO_MF_m	GO:000422	metalloenc	3/520	99/23049	0.387083	0.638723	0.581189	Adam23/A

GO_MF_m	GO:005121	phosphopr	3/520	100/23049	0.393187	0.638723	0.581189	Hck/Ptpn5
GO_MF_m	GO:001717	serine hydr	6/520	224/23049	0.393566	0.638723	0.581189	Cela2a/Klk
GO_MF_m	GO:00352	glutamate	2/520	60/23049	0.393617	0.638723	0.581189	Ptpn5/Syn
GO_MF_m	GO:00009	transcripti	1/520	22/23049	0.394832	0.638723	0.581189	Tfap2b
GO_MF_m	GO:000477	sterol ester	1/520	22/23049	0.394832	0.638723	0.581189	Ces1b
GO_MF_m	GO:000814	poly(A) bin	1/520	22/23049	0.394832	0.638723	0.581189	Khdrbs2
GO_MF_m	GO:001502	coreceptor	1/520	22/23049	0.394832	0.638723	0.581189	Cxcr6
GO_MF_m	GO:001527	calcium-re	1/520	22/23049	0.394832	0.638723	0.581189	Catsper4
GO_MF_m	GO:00192	carbohydr	1/520	22/23049	0.394832	0.638723	0.581189	Hk1
GO_MF_m	GO:00305	ankyrin bin	1/520	22/23049	0.394832	0.638723	0.581189	Flnc
GO_MF_m	GO:00904	vitamin tra	1/520	22/23049	0.394832	0.638723	0.581189	Slc19a1
GO_MF_m	GO:01401	catalytic ac	1/520	22/23049	0.394832	0.638723	0.581189	B3gnt6
GO_MF_m	GO:000472	protein ser	2/520	61/23049	0.401575	0.641764	0.583957	Ctdp1/Pal
GO_MF_m	GO:00168	carbon-ox	2/520	61/23049	0.401575	0.641764	0.583957	Car6/Thns
GO_MF_m	GO:000417	endopeptid	11/520	438/23049	0.401794	0.641764	0.583957	Adam23/A
GO_MF_m	GO:00156	tubulin bin	8/520	311/23049	0.403736	0.641764	0.583957	Ccdc187/A
GO_MF_m	GO:002284	voltage-ga	4/520	143/23049	0.404011	0.641764	0.583957	Catsper4/
GO_MF_m	GO:00152	drug trans	3/520	102/23049	0.405347	0.641764	0.583957	Slc18a3/Sl
GO_MF_m	GO:00152	solute:catic	3/520	102/23049	0.405347	0.641764	0.583957	Slc12a7/Sl
GO_MF_m	GO:00081	nuclear loc	1/520	23/23049	0.408498	0.641764	0.583957	Tnpo2
GO_MF_m	GO:000817	O-methylt	1/520	23/23049	0.408498	0.641764	0.583957	Armt1
GO_MF_m	GO:00164	CoA-ligase	1/520	23/23049	0.408498	0.641764	0.583957	Slc27a4
GO_MF_m	GO:00314	mitogen-a	1/520	23/23049	0.408498	0.641764	0.583957	Dixdc1
GO_MF_m	GO:003361	receptor se	1/520	23/23049	0.408498	0.641764	0.583957	Bmp2
GO_MF_m	GO:004761	acyl-CoA	1/520	23/23049	0.408498	0.641764	0.583957	Them4
GO_MF_m	GO:007084	dynein con	1/520	23/23049	0.408498	0.641764	0.583957	Ccdc155
GO_MF_m	GO:00043	helicase ac	4/520	144/23049	0.409094	0.641764	0.583957	Ddx46/Dh
GO_MF_m	GO:00704	repressing	2/520	62/23049	0.409484	0.641764	0.583957	Mkks/Tle4
GO_MF_m	GO:00082	heparin bir	4/520	145/23049	0.414168	0.643309	0.585362	Ccl5/Fbln7
GO_MF_m	GO:00708	growth fac	4/520	145/23049	0.414168	0.643309	0.585362	Areg/Atxn
GO_MF_m	GO:00037	structural	5/520	187/23049	0.41447	0.643309	0.585362	Rpl6l/Mrpl
GO_MF_m	GO:000524	voltage-ga	5/520	187/23049	0.41447	0.643309	0.585362	Catsper4/
GO_MF_m	GO:00228	voltage-ga	5/520	187/23049	0.41447	0.643309	0.585362	Catsper4/
GO_MF_m	GO:003532	enhancer	3/520	104/23049	0.417434	0.643591	0.585619	Rai1/Sox1
GO_MF_m	GO:00352	nuclear ho	4/520	146/23049	0.419232	0.643591	0.585619	Kdm5d/Me
GO_MF_m	GO:00016	G-protein	1/520	24/23049	0.421856	0.643591	0.585619	Cxcr6
GO_MF_m	GO:000184	compleme	1/520	24/23049	0.421856	0.643591	0.585619	Cd46
GO_MF_m	GO:00049	chemokine	1/520	24/23049	0.421856	0.643591	0.585619	Cxcr6
GO_MF_m	GO:00199	chemokine	1/520	24/23049	0.421856	0.643591	0.585619	Cxcr6
GO_MF_m	GO:003054	receptor in	1/520	24/23049	0.421856	0.643591	0.585619	Ccl5
GO_MF_m	GO:00305	cAMP bind	1/520	24/23049	0.421856	0.643591	0.585619	Prkar1b
GO_MF_m	GO:00316	G-protein	1/520	24/23049	0.421856	0.643591	0.585619	Cetn4
GO_MF_m	GO:00512	NAD bindi	2/520	64/23049	0.425145	0.64738	0.589066	Dld/Hpgd
GO_MF_m	GO:00042	serine-typ	5/520	191/23049	0.432226	0.654813	0.59583	Cela2a/Klk
GO_MF_m	GO:000377	actin bindi	10/520	406/23049	0.434007	0.654813	0.59583	Ablim3/Dix
GO_MF_m	GO:00081	poly-pyrim	1/520	25/23049	0.434913	0.654813	0.59583	Khdrbs2
GO_MF_m	GO:00162	CoA hydro	1/520	25/23049	0.434913	0.654813	0.59583	Them4
GO_MF_m	GO:00355	purinergic	1/520	25/23049	0.434913	0.654813	0.59583	P2ry6

GO_MF_m	GO:00469	thyroid hor	1/520	25/23049	0.434913	0.654813	0.59583	Med30
GO_MF_m	GO:004237	chemokine	2/520	66/23049	0.440587	0.661152	0.601598	Ccl5/Tff2
GO_MF_m	GO:00010	RNA polym	4/520	151/23049	0.444387	0.661152	0.601598	Ctdp1/Dus
GO_MF_m	GO:19016	sulfur com	6/520	237/23049	0.445645	0.661152	0.601598	Ccl5/Dld/F
GO_MF_m	GO:00054	steroid bin	3/520	109/23049	0.447278	0.661152	0.601598	Paqr6/Ptch
GO_MF_m	GO:00164	acetyltrans	3/520	109/23049	0.447278	0.661152	0.601598	Atat1/Dlat/
GO_MF_m	GO:00051	insulin rece	1/520	26/23049	0.447676	0.661152	0.601598	Ptprf
GO_MF_m	GO:00053	glucose tra	1/520	26/23049	0.447676	0.661152	0.601598	Slc2a10
GO_MF_m	GO:00153	anion:anio	1/520	26/23049	0.447676	0.661152	0.601598	Slc37a2
GO_MF_m	GO:001687	acid-thiol l	1/520	26/23049	0.447676	0.661152	0.601598	Slc27a4
GO_MF_m	GO:00515	2 iron, 2 su	1/520	26/23049	0.447676	0.661152	0.601598	Fdx1
GO_MF_m	GO:003421	peptide N-	2/520	67/23049	0.448222	0.661152	0.601598	Atat1/Naa
GO_MF_m	GO:00506	coenzyme	7/520	281/23049	0.448991	0.661152	0.601598	Accs/Atat1
GO_MF_m	GO:00055	glycosami	5/520	196/23049	0.454256	0.667682	0.60754	Ccl5/Fbln7
GO_MF_m	GO:00198	protein ph	2/520	68/23049	0.455798	0.668725	0.608489	Ppp1r1a/Sl
GO_MF_m	GO:001514	hexose tra	1/520	27/23049	0.460151	0.671436	0.610956	Slc2a10
GO_MF_m	GO:00718	14-3-3 pr	1/520	27/23049	0.460151	0.671436	0.610956	Prkcz
GO_MF_m	GO:19046	peptide tra	1/520	27/23049	0.460151	0.671436	0.610956	Slc15a3
GO_MF_m	GO:00083	structural c	1/520	28/23049	0.472344	0.685496	0.623749	Mybph
GO_MF_m	GO:00302	protein ser	1/520	28/23049	0.472344	0.685496	0.623749	Prkar1b
GO_MF_m	GO:19016	sulfur com	1/520	28/23049	0.472344	0.685496	0.623749	Slc35b3
GO_MF_m	GO:000554	odorant bi	11/520	463/23049	0.473691	0.686212	0.624401	Olfr1009/C
GO_MF_m	GO:000451	nuclease a	5/520	201/23049	0.476048	0.688386	0.626379	Ankle1/Dis
GO_MF_m	GO:00050	GTPase act	6/520	246/23049	0.481174	0.690332	0.62815	Abr/Arhga
GO_MF_m	GO:00052	calcium ch	3/520	115/23049	0.48225	0.690332	0.62815	Catsper4/C
GO_MF_m	GO:000524	calcium ch	1/520	29/23049	0.484263	0.690332	0.62815	Pacsin3
GO_MF_m	GO:000817	tRNA meth	1/520	29/23049	0.484263	0.690332	0.62815	Trmo
GO_MF_m	GO:001514	monosacch	1/520	29/23049	0.484263	0.690332	0.62815	Slc2a10
GO_MF_m	GO:003051	snoRNA bi	1/520	29/23049	0.484263	0.690332	0.62815	Isg20
GO_MF_m	GO:004301	gamma-tu	1/520	29/23049	0.484263	0.690332	0.62815	Dixdc1
GO_MF_m	GO:007071	poly-purin	1/520	29/23049	0.484263	0.690332	0.62815	Khdrbs2
GO_MF_m	GO:00090	electron tr	2/520	72/23049	0.485489	0.690855	0.628625	Dld/Fdx1
GO_MF_m	GO:00083	steroid hy	2/520	73/23049	0.492753	0.699498	0.63649	Cyp2c38/F
GO_MF_m	GO:001704	Rho GTPas	4/520	161/23049	0.493601	0.699498	0.63649	Abr/Exoc1/
GO_MF_m	GO:000857	ATP-depe	1/520	30/23049	0.495913	0.699498	0.63649	BC048507
GO_MF_m	GO:00192	deaminase	1/520	30/23049	0.495913	0.699498	0.63649	Rpusd3
GO_MF_m	GO:005111	sugar trans	1/520	30/23049	0.495913	0.699498	0.63649	Slc2a10
GO_MF_m	GO:003321	amide bin	8/520	341/23049	0.505327	0.710574	0.646568	Dhcr24/Dl
GO_MF_m	GO:00055	retinoid bi	1/520	31/23049	0.5073	0.710574	0.646568	Lcn5
GO_MF_m	GO:000851	ammonium	1/520	31/23049	0.5073	0.710574	0.646568	Slc18a3
GO_MF_m	GO:001641	S-acyltrans	1/520	31/23049	0.5073	0.710574	0.646568	Dlat
GO_MF_m	GO:000507	SH3/SH2 a	1/520	32/23049	0.518431	0.722389	0.657319	Khdrbs2
GO_MF_m	GO:00455	dynein inte	1/520	32/23049	0.518431	0.722389	0.657319	BC048507
GO_MF_m	GO:00616	ubiquitin c	1/520	32/23049	0.518431	0.722389	0.657319	Ube2c
GO_MF_m	GO:00605	nucleoside	7/520	301/23049	0.520833	0.723671	0.658486	Abr/Arhga
GO_MF_m	GO:004317	alcohol bin	2/520	77/23049	0.521151	0.723671	0.658486	Ptch1/Trpc
GO_MF_m	GO:00011	RNA polym	1/520	33/23049	0.529311	0.728708	0.663069	Mkks
GO_MF_m	GO:00422	MHC prote	1/520	33/23049	0.529311	0.728708	0.663069	Pdia3

GO_MF_m	GO:005139	alpha-actir	1/520	33/23049	0.529311	0.728708	0.663069	Mybph
GO_MF_m	GO:005195	dynein ligh	1/520	33/23049	0.529311	0.728708	0.663069	BC048507
GO_MF_m	GO:006165	ubiquitin-li	1/520	33/23049	0.529311	0.728708	0.663069	Ube2c
GO_MF_m	GO:000521	intracellula	1/520	34/23049	0.539945	0.735789	0.669512	Catsper4
GO_MF_m	GO:000837	galactosylt	1/520	34/23049	0.539945	0.735789	0.669512	B3gnt6
GO_MF_m	GO:001502	glucuronos	1/520	34/23049	0.539945	0.735789	0.669512	Ugt1a7c
GO_MF_m	GO:003033	cyclin bind	1/520	34/23049	0.539945	0.735789	0.669512	Ptch1
GO_MF_m	GO:003503	histone ace	1/520	34/23049	0.539945	0.735789	0.669512	Zbtb7a
GO_MF_m	GO:007033	aromatase	1/520	34/23049	0.539945	0.735789	0.669512	Cyp2c38
GO_MF_m	GO:003802	cargo rece	2/520	80/23049	0.541741	0.736987	0.670602	Crb3/Susd
GO_MF_m	GO:003069	GTPase reg	6/520	263/23049	0.546162	0.739921	0.673272	Abr/Arhga
GO_MF_m	GO:199078	protein tyr	2/520	81/23049	0.548466	0.739921	0.673272	Ptprf/Trim
GO_MF_m	GO:000823	metallopep	4/520	173/23049	0.550085	0.739921	0.673272	Adam23/A
GO_MF_m	GO:000113	transcriptic	1/520	35/23049	0.550339	0.739921	0.673272	Dmtf1
GO_MF_m	GO:00480	triglyceride	1/520	35/23049	0.550339	0.739921	0.673272	Ces1b
GO_MF_m	GO:000531	dicarboxyli	1/520	35/23049	0.550339	0.739921	0.673272	Slc19a1
GO_MF_m	GO:000839	arachidoni	1/520	35/23049	0.550339	0.739921	0.673272	Cyp2c38
GO_MF_m	GO:000852	G-protein	3/520	129/23049	0.559399	0.750847	0.683213	Cxcr6/Ltb4
GO_MF_m	GO:003294	protein-co	2/520	83/23049	0.561708	0.751436	0.683749	Ippk/Lrrk2
GO_MF_m	GO:005066	flavin aden	2/520	83/23049	0.561708	0.751436	0.683749	Dhcr24/Dl
GO_MF_m	GO:000851	organic ani	5/520	222/23049	0.563854	0.752855	0.685041	Slc19a1/Sl
GO_MF_m	GO:000451	endonucle	3/520	130/23049	0.564641	0.752855	0.685041	Ankle1/Dis
GO_MF_m	GO:003525	steroid hor	2/520	84/23049	0.568224	0.754319	0.686373	Kdm5d/Tcf
GO_MF_m	GO:000097	RNA polym	1/520	37/23049	0.57043	0.754319	0.686373	Tfap2b
GO_MF_m	GO:001687	ligase activ	1/520	37/23049	0.57043	0.754319	0.686373	Slc27a4
GO_MF_m	GO:001984	isoprenoid	1/520	37/23049	0.57043	0.754319	0.686373	Lcn5
GO_MF_m	GO:003136	translation	1/520	37/23049	0.57043	0.754319	0.686373	Rps3a1
GO_MF_m	GO:00850	anion trans	7/520	316/23049	0.572367	0.754738	0.686754	Clcn1/Slc1
GO_MF_m	GO:006009	molecular	4/520	178/23049	0.572625	0.754738	0.686754	Khdrbs2/Tr
GO_MF_m	GO:000801	beta-caten	2/520	85/23049	0.574669	0.755242	0.687213	Axin2/Nf2
GO_MF_m	GO:000165	peptide rec	3/520	133/23049	0.580136	0.755242	0.687213	Cxcr6/Ltb4
GO_MF_m	GO:000548	SNAP rece	1/520	38/23049	0.580137	0.755242	0.687213	Stx12
GO_MF_m	GO:000839	arachidoni	1/520	38/23049	0.580137	0.755242	0.687213	Cyp2c38
GO_MF_m	GO:003055	cyclic nucle	1/520	38/23049	0.580137	0.755242	0.687213	Prkar1b
GO_MF_m	GO:004205	chemoattra	1/520	38/23049	0.580137	0.755242	0.687213	Ccl5
GO_MF_m	GO:006059	ATPase reg	1/520	38/23049	0.580137	0.755242	0.687213	Fnip2
GO_MF_m	GO:001665	oxidoreduc	2/520	86/23049	0.581045	0.755242	0.687213	Dld/Nxnl2
GO_MF_m	GO:000371	transcriptic	4/520	180/23049	0.581462	0.755242	0.687213	Bend6/Sca
GO_MF_m	GO:001988	protein kin	4/520	181/23049	0.58584	0.757282	0.689069	Ccl5/Lrrtm
GO_MF_m	GO:00151	chloride tra	2/520	87/23049	0.587349	0.757282	0.689069	Clcn1/Slc1
GO_MF_m	GO:001514	carbohydra	1/520	39/23049	0.589625	0.757282	0.689069	Slc2a10
GO_MF_m	GO:001548	cholesterol	1/520	39/23049	0.589625	0.757282	0.689069	Ptch1
GO_MF_m	GO:001622	steroid deh	1/520	39/23049	0.589625	0.757282	0.689069	Srd5a1
GO_MF_m	GO:004339	proteoglyc	1/520	39/23049	0.589625	0.757282	0.689069	Ptprf
GO_MF_m	GO:004418	protein bin	1/520	39/23049	0.589625	0.757282	0.689069	Mkks
GO_MF_m	GO:000808	N-acetyltra	2/520	88/23049	0.593584	0.760326	0.691839	Atat1/Naa
GO_MF_m	GO:014009	catalytic ac	4/520	183/23049	0.594518	0.760326	0.691839	Dnase1l3/I
GO_MF_m	GO:001507	monovaler	8/520	369/23049	0.594832	0.760326	0.691839	Grik2/Grik

GO_MF_m	GO:000417	aminopept	1/520	40/23049	0.598899	0.761305	0.69273	Lap3
GO_MF_m	GO:001706	snRNA bin	1/520	40/23049	0.598899	0.761305	0.69273	Isg20
GO_MF_m	GO:001921	deacetylas	1/520	40/23049	0.598899	0.761305	0.69273	Ndst2
GO_MF_m	GO:001508	calcium ior	3/520	137/23049	0.600247	0.761305	0.69273	Catsper4/G
GO_MF_m	GO:000392	GTPase act	6/520	278/23049	0.600333	0.761305	0.69273	Diras1/Gng
GO_MF_m	GO:005108	unfolded p	2/520	90/23049	0.60584	0.767034	0.697943	Cryaa/Mkk
GO_MF_m	GO:006163	ubiquitin p	5/520	233/23049	0.606758	0.767034	0.697943	Med30/Rnf
GO_MF_m	GO:000504	signal sequ	1/520	41/23049	0.607964	0.767352	0.698232	Tnpo2
GO_MF_m	GO:000371	transcriptic	10/520	467/23049	0.610965	0.769855	0.70051	Aire/Bend6
GO_MF_m	GO:000524	voltage-ga	2/520	91/23049	0.611863	0.769855	0.70051	Kcnh3/Kcn
GO_MF_m	GO:000551	calmodulin	4/520	188/23049	0.615734	0.773516	0.70384	Grm4/Map
GO_MF_m	GO:000452	endodeoxy	1/520	42/23049	0.616824	0.773677	0.703987	Dnase1l3
GO_MF_m	GO:006165	ubiquitin-li	5/520	237/23049	0.621747	0.774869	0.705072	Med30/Rnf
GO_MF_m	GO:000115	enhancer s	2/520	93/23049	0.623696	0.774869	0.705072	Sox10/Tfap
GO_MF_m	GO:001510	inorganic a	3/520	142/23049	0.624481	0.774869	0.705072	Clcn1/Slc12
GO_MF_m	GO:000520	extracellula	1/520	43/23049	0.625485	0.774869	0.705072	Col27a1
GO_MF_m	GO:000800	chemokine	1/520	43/23049	0.625485	0.774869	0.705072	Ccl5
GO_MF_m	GO:003293	sterol bind	1/520	43/23049	0.625485	0.774869	0.705072	Ptch1
GO_MF_m	GO:004280	actinin bin	1/520	43/23049	0.625485	0.774869	0.705072	Mybph
GO_MF_m	GO:005066	NADP binc	1/520	43/23049	0.625485	0.774869	0.705072	Srd5a1
GO_MF_m	GO:001529	symporter	3/520	143/23049	0.629206	0.778279	0.708175	Slc12a7/Slc
GO_MF_m	GO:000524	voltage-ga	1/520	44/23049	0.63395	0.781742	0.711326	Catsper4
GO_MF_m	GO:004260	peptide an	1/520	44/23049	0.63395	0.781742	0.711326	Dhcr24
GO_MF_m	GO:000481	aminoacyl-	1/520	45/23049	0.642224	0.787029	0.716136	Vars
GO_MF_m	GO:001670	oxidoreduc	1/520	45/23049	0.642224	0.787029	0.716136	Kdm4b
GO_MF_m	GO:001687	ligase activ	1/520	45/23049	0.642224	0.787029	0.716136	Vars
GO_MF_m	GO:000808	growth fac	3/520	146/23049	0.643132	0.787029	0.716136	Areg/Bmp2
GO_MF_m	GO:003498	immunoglo	3/520	146/23049	0.643132	0.787029	0.716136	Ighv1-53/Ig
GO_MF_m	GO:001983	growth fac	3/520	147/23049	0.647691	0.791403	0.720117	Ghrhr/Il10r
GO_MF_m	GO:000837	acetylgalac	1/520	46/23049	0.650312	0.792198	0.72084	B3gnt6
GO_MF_m	GO:004802	CCR chem	1/520	46/23049	0.650312	0.792198	0.72084	Ccl5
GO_MF_m	GO:001529	secondary	5/520	247/23049	0.657693	0.798199	0.726301	Slc12a7/Slc
GO_MF_m	GO:001679	thiolester h	1/520	47/23049	0.658216	0.798199	0.726301	Them4
GO_MF_m	GO:004518	translation	1/520	47/23049	0.658216	0.798199	0.726301	Aire
GO_MF_m	GO:001661	oxidoreduc	3/520	151/23049	0.665513	0.804131	0.731698	Bmp2/Dhc
GO_MF_m	GO:000804	enzyme ac	9/520	441/23049	0.666109	0.804131	0.731698	Abr/Arhgap
GO_MF_m	GO:004687	metal ion t	9/520	441/23049	0.666109	0.804131	0.731698	Catsper4/G
GO_MF_m	GO:000484	ubiquitin-p	9/520	443/23049	0.671293	0.809175	0.736288	Ccnf/Fbxo4
GO_MF_m	GO:000110	RNA polym	1/520	49/23049	0.673495	0.809402	0.736495	Dusp26
GO_MF_m	GO:000374	translation	1/520	49/23049	0.673495	0.809402	0.736495	Dhx29
GO_MF_m	GO:001920	kinase regu	4/520	203/23049	0.675092	0.809562	0.73664	Ccl5/Lrrtm
GO_MF_m	GO:001701	Ras GTPas	8/520	397/23049	0.675642	0.809562	0.73664	Abr/Exoc1/
GO_MF_m	GO:000823	metalloexo	1/520	50/23049	0.680877	0.813411	0.740142	Lap3
GO_MF_m	GO:001687	ligase activ	1/520	50/23049	0.680877	0.813411	0.740142	Ttll4
GO_MF_m	GO:000532	neurotrans	1/520	51/23049	0.688092	0.815681	0.742208	Slc18a3
GO_MF_m	GO:001686	intramolec	1/520	51/23049	0.688092	0.815681	0.742208	Pdia3
GO_MF_m	GO:001704	peptide ho	1/520	51/23049	0.688092	0.815681	0.742208	Ghrhr
GO_MF_m	GO:003014	manganes	1/520	51/23049	0.688092	0.815681	0.742208	Lap3

GO_MF_m	GO:19909	ATP-depe	1/520	51/23049	0.688092	0.815681	0.742208	BC048507
GO_MF_m	GO:001641	N-acyltran	2/520	105/23049	0.688865	0.815681	0.742208	Atat1/Naa
GO_MF_m	GO:00168	hydro-lyas	1/520	52/23049	0.695145	0.821907	0.747873	Car6
GO_MF_m	GO:000454	ribonuclea	2/520	107/23049	0.698776	0.824236	0.749992	Dis3/Isg20
GO_MF_m	GO:00526	carboxylic	3/520	159/23049	0.699165	0.824236	0.749992	Ces1b/Nlg
GO_MF_m	GO:01400	catalytic ac	7/520	360/23049	0.706119	0.830694	0.755868	Trmo/Ddx
GO_MF_m	GO:000371	transcripti	5/520	262/23049	0.707344	0.830694	0.755868	Helz2/Myo
GO_MF_m	GO:00055	copper ion	1/520	54/23049	0.708776	0.830694	0.755868	Prn
GO_MF_m	GO:009951	ion antipo	1/520	54/23049	0.708776	0.830694	0.755868	Slc37a2
GO_MF_m	GO:000382	antigen bi	4/520	213/23049	0.710971	0.832053	0.757105	Dhcr24/Ig
GO_MF_m	GO:000814	sulfotransf	1/520	55/23049	0.715362	0.835975	0.760674	Ndst2
GO_MF_m	GO:00197	ubiquitin-li	9/520	463/23049	0.720447	0.839335	0.763731	Ccnf/Fbxo
GO_MF_m	GO:000004	tRNA bindi	1/520	56/23049	0.721798	0.839335	0.763731	Rpl6l
GO_MF_m	GO:000837	acetylgluc	1/520	56/23049	0.721798	0.839335	0.763731	B3gnt6
GO_MF_m	GO:000517	integrin bi	2/520	112/23049	0.722413	0.839335	0.763731	Adam24/N
GO_MF_m	GO:00355	signaling a	1/520	57/23049	0.72809	0.844711	0.768623	Khdrbs2
GO_MF_m	GO:001507	proton tra	2/520	114/23049	0.731421	0.847352	0.771026	Slc15a3/Sl
GO_MF_m	GO:00037	steroid ho	1/520	58/23049	0.73424	0.849394	0.772884	Paqr6
GO_MF_m	GO:001674	transferase	4/520	221/23049	0.737529	0.851974	0.775231	Atat1/Dlat
GO_MF_m	GO:00617	peptide-ly	1/520	59/23049	0.740251	0.85389	0.776975	Atat1
GO_MF_m	GO:000801	microtubul	4/520	223/23049	0.743873	0.85684	0.779659	Ccdc187/A
GO_MF_m	GO:00036	damaged	1/520	60/23049	0.746126	0.856979	0.779786	Kdm4d
GO_MF_m	GO:000817	RNA meth	1/520	60/23049	0.746126	0.856979	0.779786	Trmo
GO_MF_m	GO:004282	histone de	2/520	118/23049	0.748693	0.8587	0.781352	Hes1/Tcf21
GO_MF_m	GO:001671	oxidoredu	1/520	61/23049	0.751868	0.859799	0.782352	Cyp2c38
GO_MF_m	GO:00048	serine-typ	2/520	119/23049	0.752859	0.859799	0.782352	Itih1/Serpi
GO_MF_m	GO:01401	catalytic ac	2/520	119/23049	0.752859	0.859799	0.782352	Trmo/Vars
GO_MF_m	GO:00055	iron ion bi	3/520	175/23049	0.75864	0.865172	0.787241	Cyp2c38/F
GO_MF_m	GO:001687	ligase activ	3/520	176/23049	0.762021	0.867072	0.788969	Slc27a4/Tt
GO_MF_m	GO:00190	GDP bindi	1/520	63/23049	0.762967	0.867072	0.788969	Rhob
GO_MF_m	GO:00312	small GTPa	8/520	435/23049	0.768139	0.867072	0.788969	Abr/Exoc1
GO_MF_m	GO:003037	ligand-de	1/520	64/23049	0.76833	0.867072	0.788969	Helz2
GO_MF_m	GO:00483	Rac GTPas	1/520	64/23049	0.76833	0.867072	0.788969	Fmnl1
GO_MF_m	GO:001682	lyase activ	3/520	178/23049	0.768667	0.867072	0.788969	Car6/Ggct
GO_MF_m	GO:00047	signal tran	2/520	123/23049	0.768933	0.867072	0.788969	Map3k13/
GO_MF_m	GO:000531	lipid trans	2/520	123/23049	0.768933	0.867072	0.788969	Prelid3a/T
GO_MF_m	GO:00515	iron-sulfur	1/520	65/23049	0.773571	0.869861	0.791508	Fdx1
GO_MF_m	GO:005154	metal clust	1/520	65/23049	0.773571	0.869861	0.791508	Fdx1
GO_MF_m	GO:000471	non-mem	1/520	66/23049	0.778694	0.871655	0.79314	Hck
GO_MF_m	GO:003097	receptor ty	1/520	66/23049	0.778694	0.871655	0.79314	Ptprf
GO_MF_m	GO:004362	protein sel	1/520	66/23049	0.778694	0.871655	0.79314	Ccl5
GO_MF_m	GO:000802	protein C-	4/520	235/23049	0.779503	0.871655	0.79314	Atxn2/Pdz
GO_MF_m	GO:00423	histone bin	3/520	182/23049	0.781506	0.871934	0.793394	Aire/Spin2
GO_MF_m	GO:00009	RNA poly	1/520	67/23049	0.783701	0.871934	0.793394	Sox10
GO_MF_m	GO:00431	ubiquitin b	1/520	67/23049	0.783701	0.871934	0.793394	Ubap1l
GO_MF_m	GO:01400	modificati	2/520	127/23049	0.78409	0.871934	0.793394	Spin2d/Uh
GO_MF_m	GO:001712	SH3 domai	2/520	128/23049	0.78774	0.874524	0.795751	Khdrbs2/N
GO_MF_m	GO:00302	protein kin	1/520	68/23049	0.788595	0.874524	0.795751	Ccl5

GO_MF_m	GO:000373	mRNA 3'-U	1/520	69/23049	0.793378	0.878617	0.799475	Hnrnpr
GO_MF_m	GO:000508	Rho guany	1/520	70/23049	0.798054	0.880158	0.800877	Abr
GO_MF_m	GO:001984	rRNA bindi	1/520	70/23049	0.798054	0.880158	0.800877	Rpl6l
GO_MF_m	GO:009711	scaffold pr	1/520	70/23049	0.798054	0.880158	0.800877	Nlgn1
GO_MF_m	GO:004432	ion channe	2/520	132/23049	0.801804	0.882776	0.803259	Lrrk2/Trpc
GO_MF_m	GO:001659	amino acid	1/520	71/23049	0.802624	0.882776	0.803259	Thnsl2
GO_MF_m	GO:000554	phosphatic	1/520	73/23049	0.811456	0.890435	0.810229	Exoc1
GO_MF_m	GO:001661	oxidoreduc	2/520	135/23049	0.811802	0.890435	0.810229	Bmp2/Hpg
GO_MF_m	GO:000525	chloride ch	1/520	74/23049	0.815723	0.892302	0.811927	Clcn1
GO_MF_m	GO:003143	mitogen-a	1/520	74/23049	0.815723	0.892302	0.811927	Trib2
GO_MF_m	GO:000203	p53 bindin	1/520	75/23049	0.819894	0.893218	0.812761	Dusp26
GO_MF_m	GO:001678	transferase	1/520	75/23049	0.819894	0.893218	0.812761	Ndst2
GO_MF_m	GO:001920	kinase acti	1/520	75/23049	0.819894	0.893218	0.812761	Ccl5
GO_MF_m	GO:004227	peptide bir	5/520	306/23049	0.822997	0.894025	0.813495	Dhcr24/Gh
GO_MF_m	GO:001674	transferase	4/520	252/23049	0.823126	0.894025	0.813495	Atat1/Dlat/
GO_MF_m	GO:001529	antiporter a	1/520	76/23049	0.823971	0.894025	0.813495	Slc37a2
GO_MF_m	GO:003361	activating t	1/520	77/23049	0.827955	0.897138	0.816327	Dusp26
GO_MF_m	GO:000816	methyltran	3/520	199/23049	0.829656	0.897771	0.816903	Trmo/Armt
GO_MF_m	GO:001919	transmemb	1/520	78/23049	0.83185	0.898934	0.817962	Tgfbr1
GO_MF_m	GO:001670	oxidoreduc	3/520	202/23049	0.837139	0.902218	0.82095	Cyp2c38/F
GO_MF_m	GO:000819	UDP-glyco	2/520	144/23049	0.839149	0.902218	0.82095	B3gnt6/Ug
GO_MF_m	GO:000470	MAP kinase	1/520	80/23049	0.839377	0.902218	0.82095	Map3k13
GO_MF_m	GO:004802	monosacch	1/520	80/23049	0.839377	0.902218	0.82095	Hk1
GO_MF_m	GO:002003	heme bind	2/520	145/23049	0.841955	0.90371	0.822307	Cyp2c38/S
GO_MF_m	GO:001620	antioxidant	1/520	81/23049	0.843013	0.90371	0.822307	Nxnl2
GO_MF_m	GO:000449	monooxyg	2/520	146/23049	0.844717	0.903904	0.822484	Cyp2c38/F
GO_MF_m	GO:000377	microtubul	1/520	82/23049	0.846567	0.903904	0.822484	BC048507
GO_MF_m	GO:000813	translation	1/520	82/23049	0.846567	0.903904	0.822484	Dhx29
GO_MF_m	GO:000875	S-adenosy	2/520	148/23049	0.850108	0.906211	0.824583	Trmo/Armt
GO_MF_m	GO:000419	cysteine-ty	1/520	84/23049	0.853437	0.906211	0.824583	Usp12
GO_MF_m	GO:002280	active trans	6/520	376/23049	0.854252	0.906211	0.824583	Slc12a7/Slc
GO_MF_m	GO:000827	protein me	1/520	85/23049	0.856755	0.906211	0.824583	Armt1
GO_MF_m	GO:003024	carbohydra	4/520	268/23049	0.857429	0.906211	0.824583	Grifin/Hk1/
GO_MF_m	GO:000505	signal trans	2/520	151/23049	0.857877	0.906211	0.824583	Map3k13/T
GO_MF_m	GO:001990	protein pho	2/520	151/23049	0.857877	0.906211	0.824583	Hsf4/Sh3rf
GO_MF_m	GO:001674	transferase	3/520	211/23049	0.857911	0.906211	0.824583	Trmo/Armt
GO_MF_m	GO:000525	anion chan	1/520	86/23049	0.859999	0.906211	0.824583	Clcn1
GO_MF_m	GO:003218	ubiquitin-li	1/520	86/23049	0.859999	0.906211	0.824583	Ubap1l
GO_MF_m	GO:001508	sodium ion	2/520	153/23049	0.862851	0.908026	0.826235	Grik2/Grik
GO_MF_m	GO:004690	tetrapyrrol	2/520	154/23049	0.865277	0.909242	0.827341	Cyp2c38/S
GO_MF_m	GO:000817	N-methyltr	1/520	88/23049	0.866268	0.909242	0.827341	Trmo
GO_MF_m	GO:000372	single-stra	1/520	89/23049	0.869297	0.911231	0.829151	Khdrbs2
GO_MF_m	GO:000555	pheromone	1/520	90/23049	0.872257	0.912025	0.829873	Vmn1r202
GO_MF_m	GO:000104	core prom	2/520	157/23049	0.872322	0.912025	0.829873	Myod1/Tfa
GO_MF_m	GO:000104	core prom	1/520	91/23049	0.87515	0.913793	0.831482	Tfap2b
GO_MF_m	GO:000552	GTP bindin	5/520	344/23049	0.890375	0.927818	0.844244	Diras1/Gnl
GO_MF_m	GO:000372	mRNA binc	3/520	228/23049	0.89089	0.927818	0.844244	Rpl6l/Hnrn
GO_MF_m	GO:000823	exopeptida	1/520	99/23049	0.896061	0.930792	0.84695	Lap3

GO_MF_m3	GO:00165	pheromon	1/520	99/23049	0.896061	0.930792	0.84695	Vmn1r202
GO_MF_m3	GO:00325	purine ribo	5/520	349/23049	0.897353	0.930931	0.847076	Diras1/Gnl
GO_MF_m3	GO:0018	purine nuc	5/520	353/23049	0.902655	0.932952	0.848916	Diras1/Gnl
GO_MF_m3	GO:00036	single-stra	1/520	102/23049	0.902968	0.932952	0.848916	D330045A
GO_MF_m3	GO:19029	phosphatic	1/520	102/23049	0.902968	0.932952	0.848916	Exoc1
GO_MF_m3	GO:003254	ribonucleo	5/520	354/23049	0.903943	0.932952	0.848916	Diras1/Gnl
GO_MF_m3	GO:0018	nucleoside	5/520	364/23049	0.916026	0.944038	0.859003	Diras1/Gnl
GO_MF_m3	GO:00325	guanyl ribo	5/520	366/23049	0.918276	0.944038	0.859003	Diras1/Gnl
GO_MF_m3	GO:00508	cell adhesi	7/520	480/23049	0.91872	0.944038	0.859003	Adam24/C
GO_MF_m3	GO:00190	guanyl nuc	5/520	367/23049	0.91938	0.944038	0.859003	Diras1/Gnl
GO_MF_m3	GO:004262	ATPase act	5/520	377/23049	0.929724	0.953442	0.867559	BC048507/
GO_MF_m3	GO:0050	guanyl-nu	2/520	192/23049	0.93283	0.954876	0.868865	Abr/Dis3
GO_MF_m3	GO:00452	cadherin b	4/520	321/23049	0.933498	0.954876	0.868865	Cd46/Cdh
GO_MF_m3	GO:00167	transferase	2/520	199/23049	0.941106	0.960527	0.874006	B3gnt6/Ug
GO_MF_m3	GO:0050	Ras guanyl	1/520	124/23049	0.941412	0.960527	0.874006	Abr
GO_MF_m3	GO:0047	protein N-	1/520	126/23049	0.94404	0.961723	0.875095	Grin2c
GO_MF_m3	GO:00199	phosphata	2/520	203/23049	0.945391	0.961723	0.875095	Hsf4/Sh3rf
GO_MF_m3	GO:000554	phospholip	5/520	396/23049	0.946173	0.961723	0.875095	Exoc1/Pacs
GO_MF_m3	GO:000377	motor acti	1/520	130/23049	0.948948	0.963325	0.876553	BC048507
GO_MF_m3	GO:00167	transferase	3/520	277/23049	0.951024	0.964216	0.877363	B3gnt6/St
GO_MF_m3	GO:003107	heat shock	1/520	135/23049	0.954483	0.966504	0.879445	Atf5
GO_MF_m3	GO:00314	carboxylic	2/520	214/23049	0.955698	0.966517	0.879457	Slc19a1/Th
GO_MF_m3	GO:004302	ribonucleo	1/520	140/23049	0.959419	0.968171	0.880962	Dhx29
GO_MF_m3	GO:004317	organic aci	2/520	219/23049	0.959742	0.968171	0.880962	Slc19a1/Th
GO_MF_m3	GO:000202	protease b	1/520	148/23049	0.966229	0.972584	0.884978	9230104L0
GO_MF_m3	GO:000534	organic aci	1/520	150/23049	0.967745	0.972584	0.884978	Slc19a1
GO_MF_m3	GO:004694	carboxylic	1/520	150/23049	0.967745	0.972584	0.884978	Slc19a1
GO_MF_m3	GO:000471	protein tyr	1/520	152/23049	0.969194	0.972824	0.885196	Hck
GO_MF_m3	GO:19019	phosphatic	1/520	155/23049	0.971245	0.973667	0.885963	Exoc1
GO_MF_m3	GO:00168	ATPase act	5/520	449/23049	0.975322	0.976536	0.888574	BC048507/
GO_MF_m3	GO:00350	phosphatic	1/520	242/23049	0.996119	0.996119	0.906392	Exoc1
GO_MF_m4	GO:004827	mitogen-a	3/690	7/23049	0.000854	0.323587	0.304853	Dusp10/M
GO_MF_m4	GO:00507	advanced	2/690	2/23049	0.000895	0.323587	0.304853	Ager/Lgals
GO_MF_m4	GO:00152	drug trans	10/690	102/23049	0.000971	0.323587	0.304853	Abcb1b/A
GO_MF_m4	GO:00046	lysophosp	4/690	17/23049	0.001388	0.347043	0.326951	Abhd4/Gd
GO_MF_m4	GO:001682	hydrolase	2/690	3/23049	0.002631	0.378061	0.356173	Fah/Kynu
GO_MF_m4	GO:001682	hydrolase	2/690	3/23049	0.002631	0.378061	0.356173	Fah/Kynu
GO_MF_m4	GO:000531	lipid trans	10/690	123/23049	0.003918	0.378061	0.356173	Abcb4/Ab
GO_MF_m4	GO:00055	mannose	4/690	23/23049	0.00448	0.378061	0.356173	Lman1l/Ma
GO_MF_m4	GO:00152	water chan	3/690	12/23049	0.004801	0.378061	0.356173	Aqp12/Aq
GO_MF_m4	GO:007234	modified a	3/690	12/23049	0.004801	0.378061	0.356173	Folr1/Slc16
GO_MF_m4	GO:00191	deoxynucl	2/690	4/23049	0.005158	0.378061	0.356173	Dguok/Tk1
GO_MF_m4	GO:00054	SNAP rece	5/690	38/23049	0.005251	0.378061	0.356173	Bet1l/Sec2
GO_MF_m4	GO:000537	water trans	3/690	13/23049	0.006104	0.378061	0.356173	Aqp12/Aq
GO_MF_m4	GO:004302	cysteine-ty	5/690	41/23049	0.007286	0.378061	0.356173	Bcl10/Dpe
GO_MF_m4	GO:00040	carbonate	3/690	14/23049	0.007597	0.378061	0.356173	Car2/Car4/
GO_MF_m4	GO:00083	low voltag	2/690	5/23049	0.008427	0.378061	0.356173	Cacna1g/C
GO_MF_m4	GO:001672	oxidoreduc	3/690	15/23049	0.009288	0.378061	0.356173	Aox3/Cyp1

GO_MF_m	GO:014010	catalytic ac	9/690	119/23049	0.009582	0.378061	0.356173	Dalrd3/Dus
GO_MF_m	GO:000524	voltage-ga	5/690	44/23049	0.009815	0.378061	0.356173	Cacna1b/C
GO_MF_m	GO:004302	cysteine-ty	4/690	30/23049	0.011758	0.378061	0.356173	Dpep1/Gas
GO_MF_m	GO:000855	xenobiotic	2/690	6/23049	0.01239	0.378061	0.356173	Abcb1b/Ab
GO_MF_m	GO:007027	phosphatid	4/690	32/23049	0.014722	0.378061	0.356173	Mbl1/Mbl2
GO_MF_m	GO:005101	mitogen-a	4/690	33/23049	0.016365	0.378061	0.356173	Dusp10/Du
GO_MF_m	GO:000817	N-methyltr	7/690	88/23049	0.016418	0.378061	0.356173	Camkmt/D
GO_MF_m	GO:005186	glycolipid	3/690	19/23049	0.018104	0.378061	0.356173	Plekha8/Rt
GO_MF_m	GO:000541	glucose:so	2/690	8/23049	0.022228	0.378061	0.356173	Gm5134/Sl
GO_MF_m	GO:001519	L-serine tra	2/690	8/23049	0.022228	0.378061	0.356173	Slc1a4/Slc1
GO_MF_m	GO:002288	serine tran	2/690	8/23049	0.022228	0.378061	0.356173	Slc1a4/Slc1
GO_MF_m	GO:004291	xenobiotic	2/690	8/23049	0.022228	0.378061	0.356173	Abcb1b/Ab
GO_MF_m	GO:001524	sterol trans	3/690	21/23049	0.023778	0.378061	0.356173	Abcg4/Apo
GO_MF_m	GO:014009	catalytic ac	18/690	360/23049	0.024296	0.378061	0.356173	Ang6/Cnot
GO_MF_m	GO:000122	transcriptio	13/690	235/23049	0.025274	0.378061	0.356173	Dmbx1/Fez
GO_MF_m	GO:000814	cAMP resp	2/690	9/23049	0.028018	0.378061	0.356173	Ddit3/Sik1
GO_MF_m	GO:001514	carbohydra	4/690	39/23049	0.028606	0.378061	0.356173	Aqp9/Gm5
GO_MF_m	GO:000117	RNA polym	1/690	1/23049	0.029936	0.378061	0.356173	Polr1e
GO_MF_m	GO:000158	Gq/11-cou	1/690	1/23049	0.029936	0.378061	0.356173	Htr2c
GO_MF_m	GO:000176	aminocarb	1/690	1/23049	0.029936	0.378061	0.356173	Acmsd
GO_MF_m	GO:000394	N4-(beta-	1/690	1/23049	0.029936	0.378061	0.356173	Aga
GO_MF_m	GO:000413	deoxyguan	1/690	1/23049	0.029936	0.378061	0.356173	Dguok
GO_MF_m	GO:000433	fumarylace	1/690	1/23049	0.029936	0.378061	0.356173	Fah
GO_MF_m	GO:000456	beta-mann	1/690	1/23049	0.029936	0.378061	0.356173	Manba
GO_MF_m	GO:000457	mannosyl-	1/690	1/23049	0.029936	0.378061	0.356173	Mogs
GO_MF_m	GO:000458	dolichyl-ph	1/690	1/23049	0.029936	0.378061	0.356173	Pigv
GO_MF_m	GO:000463	phosphom	1/690	1/23049	0.029936	0.378061	0.356173	Pmvk
GO_MF_m	GO:000487	complemen	1/690	1/23049	0.029936	0.378061	0.356173	C3ar1
GO_MF_m	GO:000499	thyroid-stir	1/690	1/23049	0.029936	0.378061	0.356173	Tshr
GO_MF_m	GO:000514	interleukin	1/690	1/23049	0.029936	0.378061	0.356173	Il13
GO_MF_m	GO:000811	nicotinami	1/690	1/23049	0.029936	0.378061	0.356173	Nnmt
GO_MF_m	GO:000838	steroid 7-a	1/690	1/23049	0.029936	0.378061	0.356173	Cyp39a1
GO_MF_m	GO:000839	sterol 14-d	1/690	1/23049	0.029936	0.378061	0.356173	Cyp51
GO_MF_m	GO:000843	calcitriol re	1/690	1/23049	0.029936	0.378061	0.356173	Vdr
GO_MF_m	GO:000845	beta-galac	1/690	1/23049	0.029936	0.378061	0.356173	B3gnt5
GO_MF_m	GO:000846	glycerate d	1/690	1/23049	0.029936	0.378061	0.356173	Grhpr
GO_MF_m	GO:001519	L-threonin	1/690	1/23049	0.029936	0.378061	0.356173	Slc1a4
GO_MF_m	GO:001708	glycolipid t	1/690	1/23049	0.029936	0.378061	0.356173	Plekha8
GO_MF_m	GO:001802	calmodulin	1/690	1/23049	0.029936	0.378061	0.356173	Camkmt
GO_MF_m	GO:001914	ADP-sugar	1/690	1/23049	0.029936	0.378061	0.356173	Nudt5
GO_MF_m	GO:001978	ISG15-spe	1/690	1/23049	0.029936	0.378061	0.356173	Usp18
GO_MF_m	GO:003042	kynurenina	1/690	1/23049	0.029936	0.378061	0.356173	Kynu
GO_MF_m	GO:003177	type 1 hyp	1/690	1/23049	0.029936	0.378061	0.356173	Hcrt
GO_MF_m	GO:003177	type 2 hyp	1/690	1/23049	0.029936	0.378061	0.356173	Hcrt
GO_MF_m	GO:003235	oxidized p	1/690	1/23049	0.029936	0.378061	0.356173	Rps3
GO_MF_m	GO:003254	sulfiredoxi	1/690	1/23049	0.029936	0.378061	0.356173	Srxn1
GO_MF_m	GO:003459	L-hydroxyp	1/690	1/23049	0.029936	0.378061	0.356173	Slc1a4
GO_MF_m	GO:003818	lithocholic	1/690	1/23049	0.029936	0.378061	0.356173	Vdr

GO_MF_m	GO:004232	hypocretin	1/690	1/23049	0.029936	0.378061	0.356173	Hcrt
GO_MF_m	GO:004725	lactosylcera	1/690	1/23049	0.029936	0.378061	0.356173	B3gnt5
GO_MF_m	GO:004756	3-oxo-5-b	1/690	1/23049	0.029936	0.378061	0.356173	Akr1d1
GO_MF_m	GO:005051	lactosylcera	1/690	1/23049	0.029936	0.378061	0.356173	A4galt
GO_MF_m	GO:005056	glutamate-	1/690	1/23049	0.029936	0.378061	0.356173	Ears2
GO_MF_m	GO:005057	1,5-anhydr	1/690	1/23049	0.029936	0.378061	0.356173	Akr1e1
GO_MF_m	GO:006165	SUMO con	1/690	1/23049	0.029936	0.378061	0.356173	Ube2i
GO_MF_m	GO:006198	3-hydroxy	1/690	1/23049	0.029936	0.378061	0.356173	Kynu
GO_MF_m	GO:007000	glutamic-t	1/690	1/23049	0.029936	0.378061	0.356173	Astl
GO_MF_m	GO:007037	high mobil	1/690	1/23049	0.029936	0.378061	0.356173	Ager
GO_MF_m	GO:007061	nucleosom	1/690	1/23049	0.029936	0.378061	0.356173	Smarca1
GO_MF_m	GO:190209	calcitriol bi	1/690	1/23049	0.029936	0.378061	0.356173	Vdr
GO_MF_m	GO:190459	advanced	1/690	1/23049	0.029936	0.378061	0.356173	Ager
GO_MF_m	GO:004339	heparan su	3/690	23/23049	0.030302	0.378061	0.356173	Fst/Hpse2/
GO_MF_m	GO:002003	heme bind	9/690	145/23049	0.030639	0.378061	0.356173	Cyb5b/Cyc
GO_MF_m	GO:003509	phosphatic	13/690	242/23049	0.031052	0.378061	0.356173	Arap2/Arh
GO_MF_m	GO:001517	amino acid	6/690	80/23049	0.032752	0.378061	0.356173	Slc16a12/S
GO_MF_m	GO:004802	monosacch	6/690	80/23049	0.032752	0.378061	0.356173	Lgals3/Lm
GO_MF_m	GO:001517	L-amino a	5/690	60/23049	0.033533	0.378061	0.356173	Slc17a8/Sl
GO_MF_m	GO:004354	phosphatic	4/690	41/23049	0.033626	0.378061	0.356173	Hcst/Irs2/L
GO_MF_m	GO:000521	structural c	3/690	24/23049	0.033881	0.378061	0.356173	Bfsp2/Lim
GO_MF_m	GO:000875	S-adenosy	9/690	148/23049	0.034285	0.378061	0.356173	Camkmt/D
GO_MF_m	GO:009700	ceramide b	2/690	10/23049	0.034338	0.378061	0.356173	Plekha8/Rt
GO_MF_m	GO:000813	protein tyr	4/690	42/23049	0.036316	0.378061	0.356173	Dupd1/Du
GO_MF_m	GO:000534	organic aci	9/690	150/23049	0.036876	0.378061	0.356173	Abcc4/Folr
GO_MF_m	GO:004694	carboxylic	9/690	150/23049	0.036876	0.378061	0.356173	Abcc4/Folr
GO_MF_m	GO:001920	nucleobase	4/690	43/23049	0.039127	0.378061	0.356173	Ak3/Dguo
GO_MF_m	GO:000510	fibroblast	3/690	26/23049	0.041663	0.378061	0.356173	Fgf17/Fgf4
GO_MF_m	GO:000535	glucose tra	3/690	26/23049	0.041663	0.378061	0.356173	Gm5134/Sl
GO_MF_m	GO:004690	tetrapyrrol	9/690	154/23049	0.042451	0.378061	0.356173	Cyb5b/Cyc
GO_MF_m	GO:000372	mRNA bin	12/690	228/23049	0.042471	0.378061	0.356173	Eif3a/Gemi
GO_MF_m	GO:001920	kinase reg	11/690	203/23049	0.042585	0.378061	0.356173	Bcl10/Cnks
GO_MF_m	GO:000486	protein kin	6/690	86/23049	0.04423	0.378061	0.356173	Dus2/Flrt1/
GO_MF_m	GO:000481	aminoacyl-	4/690	45/23049	0.04511	0.378061	0.356173	Dalrd3/Ear
GO_MF_m	GO:001687	ligase activ	4/690	45/23049	0.04511	0.378061	0.356173	Dalrd3/Ear
GO_MF_m	GO:001514	hexose tra	3/690	27/23049	0.045861	0.378061	0.356173	Gm5134/Sl
GO_MF_m	GO:000014	SNARE bin	8/690	133/23049	0.04686	0.378061	0.356173	Nbas/Sec2
GO_MF_m	GO:000819	metalloen	2/690	12/23049	0.048421	0.378061	0.356173	Lxn/Spock
GO_MF_m	GO:001701	MAP kinas	2/690	12/23049	0.048421	0.378061	0.356173	Dusp10/Du
GO_MF_m	GO:003173	CCR6 che	2/690	12/23049	0.048421	0.378061	0.356173	Defb33/De
GO_MF_m	GO:005268	carboxylic	9/690	159/23049	0.050182	0.378061	0.356173	Abhd4/Car
GO_MF_m	GO:001921	kinase inhi	6/690	89/23049	0.050802	0.378061	0.356173	Dus2/Flrt1/
GO_MF_m	GO:001514	monosacc	3/690	29/23049	0.054856	0.378061	0.356173	Gm5134/Sl
GO_MF_m	GO:000373	structural c	10/690	187/23049	0.055437	0.378061	0.356173	Gm5093/
GO_MF_m	GO:000819	phosphatic	2/690	13/23049	0.056115	0.378061	0.356173	Plppr3/Plp
GO_MF_m	GO:001642	tRNA (gua	2/690	13/23049	0.056115	0.378061	0.356173	Trmt11/W
GO_MF_m	GO:001920	nucleoside	2/690	13/23049	0.056115	0.378061	0.356173	Dguok/Tk1
GO_MF_m	GO:003354	MAP kinas	2/690	13/23049	0.056115	0.378061	0.356173	Dusp10/Du

GO_MF_m	GO:001679	phosphata	13/690	265/23049	0.056699	0.378061	0.356173	Alppl2/Dup
GO_MF_m	GO:001670	oxidoreduc	4/690	49/23049	0.058517	0.378061	0.356173	Akr1d1/Co
GO_MF_m	GO:000122	RNA polym	1/690	2/23049	0.058978	0.378061	0.356173	Nfatc1
GO_MF_m	GO:000163	PLC activat	1/690	2/23049	0.058978	0.378061	0.356173	Grm1
GO_MF_m	GO:000185	compleme	1/690	2/23049	0.058978	0.378061	0.356173	C3ar1
GO_MF_m	GO:000453	deoxyribor	1/690	2/23049	0.058978	0.378061	0.356173	Dnase1
GO_MF_m	GO:000453	deoxyribor	1/690	2/23049	0.058978	0.378061	0.356173	Dnase2b
GO_MF_m	GO:000479	thymidine	1/690	2/23049	0.058978	0.378061	0.356173	Tk1
GO_MF_m	GO:000481	glutamate-	1/690	2/23049	0.058978	0.378061	0.356173	Ears2
GO_MF_m	GO:000482	isoleucine-	1/690	2/23049	0.058978	0.378061	0.356173	Iars
GO_MF_m	GO:000530	creatine tra	1/690	2/23049	0.058978	0.378061	0.356173	Slc16a12
GO_MF_m	GO:000817	tRNA (guai	1/690	2/23049	0.058978	0.378061	0.356173	Wdr4
GO_MF_m	GO:000839	oxysterol 7	1/690	2/23049	0.058978	0.378061	0.356173	Cyp39a1
GO_MF_m	GO:000865	rRNA (uridi	1/690	2/23049	0.058978	0.378061	0.356173	Mrm2
GO_MF_m	GO:000867	2,4-dienoy	1/690	2/23049	0.058978	0.378061	0.356173	Decr1
GO_MF_m	GO:001513	prostaglan	1/690	2/23049	0.058978	0.378061	0.356173	Abcc4
GO_MF_m	GO:001649	orexin rece	1/690	2/23049	0.058978	0.378061	0.356173	Hcrtr1
GO_MF_m	GO:003062	pre-mRNA	1/690	2/23049	0.058978	0.378061	0.356173	Snrpc
GO_MF_m	GO:003547	chylomicro	1/690	2/23049	0.058978	0.378061	0.356173	Lipc
GO_MF_m	GO:003631	phosphatic	1/690	2/23049	0.058978	0.378061	0.356173	Pik3ip1
GO_MF_m	GO:003805	RNA polym	1/690	2/23049	0.058978	0.378061	0.356173	Esr2
GO_MF_m	GO:003813	neuregulin	1/690	2/23049	0.058978	0.378061	0.356173	Rtn4r
GO_MF_m	GO:004261	CD8 recept	1/690	2/23049	0.058978	0.378061	0.356173	Lck
GO_MF_m	GO:004471	8-oxo-dGI	1/690	2/23049	0.058978	0.378061	0.356173	Nudt5
GO_MF_m	GO:004515	electron tra	1/690	2/23049	0.058978	0.378061	0.356173	Cycs
GO_MF_m	GO:004518	translation	1/690	2/23049	0.058978	0.378061	0.356173	Neurl1a
GO_MF_m	GO:004552	interleukin	1/690	2/23049	0.058978	0.378061	0.356173	Il27
GO_MF_m	GO:004655	alpha-L-ar	1/690	2/23049	0.058978	0.378061	0.356173	Otog
GO_MF_m	GO:004689	nucleoside	1/690	2/23049	0.058978	0.378061	0.356173	Ak3
GO_MF_m	GO:004715	betaine-hc	1/690	2/23049	0.058978	0.378061	0.356173	Bhmt
GO_MF_m	GO:004778	delta4-3-c	1/690	2/23049	0.058978	0.378061	0.356173	Akr1d1
GO_MF_m	GO:006171	folic acid re	1/690	2/23049	0.058978	0.378061	0.356173	Folr1
GO_MF_m	GO:007171	icosanoid t	1/690	2/23049	0.058978	0.378061	0.356173	Abcc4
GO_MF_m	GO:007188	1-(4-iodo-	1/690	2/23049	0.058978	0.378061	0.356173	Htr2c
GO_MF_m	GO:008603	calcium:soc	1/690	2/23049	0.058978	0.378061	0.356173	Slc8a1
GO_MF_m	GO:008605	voltage-ga	1/690	2/23049	0.058978	0.378061	0.356173	Cacna1g
GO_MF_m	GO:009913	estrogen b	1/690	2/23049	0.058978	0.378061	0.356173	Esr2
GO_MF_m	GO:009953	G-protein	1/690	2/23049	0.058978	0.378061	0.356173	Grm1
GO_MF_m	GO:009958	ion antipor	1/690	2/23049	0.058978	0.378061	0.356173	Slc8a1
GO_MF_m	GO:190212	lithocholic	1/690	2/23049	0.058978	0.378061	0.356173	Vdr
GO_MF_m	GO:190227	D3 vitamin	1/690	2/23049	0.058978	0.378061	0.356173	Vdr
GO_MF_m	GO:190392	estradiol bi	1/690	2/23049	0.058978	0.378061	0.356173	Esr2
GO_MF_m	GO:190557	ganglioside	1/690	2/23049	0.058978	0.378061	0.356173	Rtn4r
GO_MF_m	GO:005111	sugar trans	3/690	30/23049	0.059644	0.379899	0.357905	Gm5134/Sl
GO_MF_m	GO:002280	active trans	17/690	376/23049	0.061356	0.38224	0.36011	Abcb1b/Ab
GO_MF_m	GO:004262	ATPase act	7/690	117/23049	0.06207	0.38224	0.36011	Abcb1b/Ab
GO_MF_m	GO:000531	L-glutamat	2/690	14/23049	0.064201	0.38224	0.36011	Slc17a8/Slc
GO_MF_m	GO:004342	bHLH trans	3/690	31/23049	0.064622	0.38224	0.36011	Ncapg2/Ub

GO_MF_m	GO:004687	ephrin rece	3/690	31/23049	0.064622	0.38224	0.36011	Efna1/Grb2
GO_MF_m	GO:005069	WW doma	3/690	31/23049	0.064622	0.38224	0.36011	Tceal3/Tce
GO_MF_m	GO:001529	symporter	8/690	143/23049	0.066051	0.38224	0.36011	Gm5134/Sl
GO_MF_m	GO:002284	voltage-ga	8/690	143/23049	0.066051	0.38224	0.36011	Cacna1b/C
GO_MF_m	GO:001990	syntaxin bi	6/690	96/23049	0.068348	0.38224	0.36011	Sec22b/Sn
GO_MF_m	GO:000472	protein tyr	6/690	97/23049	0.071108	0.38224	0.36011	Dupd1/Du
GO_MF_m	GO:000851	organic ani	11/690	222/23049	0.071266	0.38224	0.36011	Abcc4/Folr
GO_MF_m	GO:000472	phosphopr	9/690	171/23049	0.072342	0.38224	0.36011	Dupd1/Du
GO_MF_m	GO:000449	monooxyg	8/690	146/23049	0.072632	0.38224	0.36011	Akr1d1/Co
GO_MF_m	GO:001517	acidic amir	2/690	15/23049	0.072649	0.38224	0.36011	Slc17a8/Sl
GO_MF_m	GO:001620	AMP bindi	2/690	15/23049	0.072649	0.38224	0.36011	Prkag1/Prp
GO_MF_m	GO:003054	acetylcholi	2/690	15/23049	0.072649	0.38224	0.36011	Ly6g6d/Slu
GO_MF_m	GO:007040	NADPH bir	2/690	15/23049	0.072649	0.38224	0.36011	Decr1/Grh
GO_MF_m	GO:009960	neurotrans	2/690	15/23049	0.072649	0.38224	0.36011	Ly6g6d/Slu
GO_MF_m	GO:004687	metal ion t	19/690	441/23049	0.073093	0.38224	0.36011	Atp1b4/Ca
GO_MF_m	GO:001676	transferase	4/690	53/23049	0.073812	0.38224	0.36011	Art4/Parp1
GO_MF_m	GO:001540	P-P-bond-	7/690	123/23049	0.076634	0.38224	0.36011	Abcb1b/Ab
GO_MF_m	GO:008816	methyltran	10/690	199/23049	0.077021	0.38224	0.36011	Bhmt/Cam
GO_MF_m	GO:000550	copper ion	4/690	54/23049	0.077922	0.38224	0.36011	Apoa4/F5/
GO_MF_m	GO:007006	RNA polym	4/690	54/23049	0.077922	0.38224	0.36011	Erbb2/Rec
GO_MF_m	GO:001517	neutral am	3/690	34/23049	0.080642	0.38224	0.36011	Slc1a4/Slc1
GO_MF_m	GO:001650	protein-ho	2/690	16/23049	0.08143	0.38224	0.36011	Lgr6/Tshr
GO_MF_m	GO:004260	T cell recep	2/690	16/23049	0.08143	0.38224	0.36011	H2-Q10/Lc
GO_MF_m	GO:001539	primary ac	7/690	125/23049	0.081897	0.38224	0.36011	Abcb1b/Ab
GO_MF_m	GO:004800	triglyceride	3/690	35/23049	0.086329	0.38224	0.36011	Ces2h/Lipc
GO_MF_m	GO:000531	dicarboxyli	3/690	35/23049	0.086329	0.38224	0.36011	Folr1/Slc17
GO_MF_m	GO:000004	tRNA bindi	4/690	56/23049	0.086478	0.38224	0.36011	Ears2/Fars2
GO_MF_m	GO:001627	lysine N-m	4/690	56/23049	0.086478	0.38224	0.36011	Camkmt/D
GO_MF_m	GO:001627	protein-lys	4/690	56/23049	0.086478	0.38224	0.36011	Camkmt/D
GO_MF_m	GO:000104	RNA polym	1/690	3/23049	0.087151	0.38224	0.36011	Erbb2
GO_MF_m	GO:003998	acetyl-CoA	1/690	3/23049	0.087151	0.38224	0.36011	Nudt7
GO_MF_m	GO:000452	ribonucleas	1/690	3/23049	0.087151	0.38224	0.36011	Rnase1
GO_MF_m	GO:000474	[pyruvate c	1/690	3/23049	0.087151	0.38224	0.36011	Pdpr
GO_MF_m	GO:000474	ribonucleo	1/690	3/23049	0.087151	0.38224	0.36011	Rrm1
GO_MF_m	GO:004800	tRNA (guar	1/690	3/23049	0.087151	0.38224	0.36011	Trmt11
GO_MF_m	GO:000515	macrophag	1/690	3/23049	0.087151	0.38224	0.36011	Il34
GO_MF_m	GO:000534	purine nuc	1/690	3/23049	0.087151	0.38224	0.36011	Aqp9
GO_MF_m	GO:000535	pyrimidine	1/690	3/23049	0.087151	0.38224	0.36011	Aqp9
GO_MF_m	GO:000551	cytoskeleta	1/690	3/23049	0.087151	0.38224	0.36011	Cttnbp2
GO_MF_m	GO:008010	galactoside	1/690	3/23049	0.087151	0.38224	0.36011	Fut1
GO_MF_m	GO:000832	Ral guanyl-	1/690	3/23049	0.087151	0.38224	0.36011	Ralgps1
GO_MF_m	GO:000853	oxidized pu	1/690	3/23049	0.087151	0.38224	0.36011	Rps3
GO_MF_m	GO:001520	nucleobase	1/690	3/23049	0.087151	0.38224	0.36011	Aqp9
GO_MF_m	GO:001525	glycerol ch	1/690	3/23049	0.087151	0.38224	0.36011	Aqp9
GO_MF_m	GO:001526	urea chanr	1/690	3/23049	0.087151	0.38224	0.36011	Aqp9
GO_MF_m	GO:001643	rRNA (uridi	1/690	3/23049	0.087151	0.38224	0.36011	Mrm2
GO_MF_m	GO:001661	hydroxypyr	1/690	3/23049	0.087151	0.38224	0.36011	Grhpr
GO_MF_m	GO:001672	oxidoreduc	1/690	3/23049	0.087151	0.38224	0.36011	Rrm1

GO_MF_m4	GO:003015	protein xyl	1/690	3/23049	0.087151	0.38224	0.36011	Xylt2
GO_MF_m4	GO:003026	glyoxylate	1/690	3/23049	0.087151	0.38224	0.36011	Grhpr
GO_MF_m4	GO:003054	acetylcholi	1/690	3/23049	0.087151	0.38224	0.36011	Slurp1
GO_MF_m4	GO:003062	U4atac snR	1/690	3/23049	0.087151	0.38224	0.36011	Gemin5
GO_MF_m4	GO:003112	alpha-(1,2)	1/690	3/23049	0.087151	0.38224	0.36011	Fut1
GO_MF_m4	GO:003404	sterol-tran	1/690	3/23049	0.087151	0.38224	0.36011	Abcg4
GO_MF_m4	GO:003498	Fc-gamma	1/690	3/23049	0.087151	0.38224	0.36011	Lgals3
GO_MF_m4	GO:003818	bile acid re	1/690	3/23049	0.087151	0.38224	0.36011	Vdr
GO_MF_m4	GO:004339	HLH doma	1/690	3/23049	0.087151	0.38224	0.36011	Ube2i
GO_MF_m4	GO:004803	disaccharid	1/690	3/23049	0.087151	0.38224	0.36011	Lgals3
GO_MF_m4	GO:005187	methotrex	1/690	3/23049	0.087151	0.38224	0.36011	Folr1
GO_MF_m4	GO:006173	ribonucleo	1/690	3/23049	0.087151	0.38224	0.36011	Rrm1
GO_MF_m4	GO:007057	metallodip	1/690	3/23049	0.087151	0.38224	0.36011	Dpep1
GO_MF_m4	GO:007064	vitamin D r	1/690	3/23049	0.087151	0.38224	0.36011	Vdr
GO_MF_m4	GO:007069	type II acti	1/690	3/23049	0.087151	0.38224	0.36011	Inhba
GO_MF_m4	GO:007153	RING-like z	1/690	3/23049	0.087151	0.38224	0.36011	Ube2i
GO_MF_m4	GO:008605	voltage-ga	1/690	3/23049	0.087151	0.38224	0.36011	Cacna1g
GO_MF_m4	GO:009710	supercoile	1/690	3/23049	0.087151	0.38224	0.36011	Rps3
GO_MF_m4	GO:190557	ganglioside	1/690	3/23049	0.087151	0.38224	0.36011	Rtn4r
GO_MF_m4	GO:000554	phospholip	17/690	396/23049	0.0885	0.386464	0.36409	Apoa4/Ara
GO_MF_m4	GO:001508	sodium ion	8/690	153/23049	0.089479	0.389039	0.366516	Atp1b4/Ca
GO_MF_m4	GO:003067	Rac guanyl	2/690	17/23049	0.090517	0.390159	0.367571	Spata13/Ti
GO_MF_m4	GO:007049	oligosacch	2/690	17/23049	0.090517	0.390159	0.367571	Lgals3/Sell
GO_MF_m4	GO:004205	histone me	4/690	57/23049	0.090919	0.390211	0.367619	Dydc1/Prm
GO_MF_m4	GO:001677	phosphotra	3/690	36/23049	0.09218	0.392256	0.369547	Ak3/Nme5
GO_MF_m4	GO:004317	RNA polym	3/690	36/23049	0.09218	0.392256	0.369547	Erbb2/Rec
GO_MF_m4	GO:001988	protein kin	9/690	181/23049	0.094807	0.401723	0.378465	Cnksr3/Du
GO_MF_m4	GO:014009	catalytic ac	9/690	183/23049	0.099737	0.419677	0.39538	Brip1/Dnas
GO_MF_m4	GO:005118	cofactor tra	2/690	18/23049	0.099883	0.419677	0.39538	Flvcr2/Slc1
GO_MF_m4	GO:004349	ATPase act	7/690	132/23049	0.10191	0.422441	0.397984	Abcb1b/Ab
GO_MF_m4	GO:001674	transferase	10/690	211/23049	0.103191	0.422441	0.397984	Bhmt/Cam
GO_MF_m4	GO:004205	chemoattra	3/690	38/23049	0.104355	0.422441	0.397984	Defb33/De
GO_MF_m4	GO:000368	damaged D	4/690	60/23049	0.104877	0.422441	0.397984	Polb/Polk/
GO_MF_m4	GO:004257	phosphoric	15/690	351/23049	0.107575	0.422441	0.397984	Alppl2/Dup
GO_MF_m4	GO:001679	hydrolase a	7/690	134/23049	0.108076	0.422441	0.397984	Ctbs/Hpse2
GO_MF_m4	GO:000540	carbohydra	2/690	19/23049	0.109504	0.422441	0.397984	Gm5134/Sl
GO_MF_m4	GO:001689	endonucle	2/690	19/23049	0.109504	0.422441	0.397984	Dnase2b/R
GO_MF_m4	GO:001712	cholesterol	2/690	19/23049	0.109504	0.422441	0.397984	Abcg4/Apo
GO_MF_m4	GO:001200	transcriptio	3/690	39/23049	0.110667	0.422441	0.397984	Nfatc1/Rel
GO_MF_m4	GO:000554	phosphatid	3/690	39/23049	0.110667	0.422441	0.397984	Arap2/Kif1
GO_MF_m4	GO:004288	amide tran	3/690	39/23049	0.110667	0.422441	0.397984	Aqp9/Folr1
GO_MF_m4	GO:004339	proteoglyc	3/690	39/23049	0.110667	0.422441	0.397984	Fst/Hpse2/
GO_MF_m4	GO:005187	Hsp90 prot	3/690	39/23049	0.110667	0.422441	0.397984	Erbb2/Ppic
GO_MF_m4	GO:000827	protein me	5/690	85/23049	0.111425	0.422441	0.397984	Camkmt/D
GO_MF_m4	GO:000391	DNA topoi	1/690	4/23049	0.114481	0.422441	0.397984	Gm960
GO_MF_m4	GO:000474	ribose pho	1/690	4/23049	0.114481	0.422441	0.397984	Prps2
GO_MF_m4	GO:000481	arginine-tR	1/690	4/23049	0.114481	0.422441	0.397984	Dalrd3
GO_MF_m4	GO:000517	ErbB-2 clas	1/690	4/23049	0.114481	0.422441	0.397984	Muc4

GO_MF_m	GO:000833	protein tyr	1/690	4/23049	0.114481	0.422441	0.397984	Dusp10
GO_MF_m	GO:001518	L-glutamin	1/690	4/23049	0.114481	0.422441	0.397984	Slc38a1
GO_MF_m	GO:001715	tRNA dihyd	1/690	4/23049	0.114481	0.422441	0.397984	Dus2
GO_MF_m	GO:003242	purine-rich	1/690	4/23049	0.114481	0.422441	0.397984	Purb
GO_MF_m	GO:003330	dehydroas	1/690	4/23049	0.114481	0.422441	0.397984	Slc2a2
GO_MF_m	GO:003376	steroid deh	1/690	4/23049	0.114481	0.422441	0.397984	Akr1d1
GO_MF_m	GO:003405	estrogen re	1/690	4/23049	0.114481	0.422441	0.397984	Esr2
GO_MF_m	GO:003524	protein-arg	1/690	4/23049	0.114481	0.422441	0.397984	Prmt9
GO_MF_m	GO:003559	ganglioside	1/690	4/23049	0.114481	0.422441	0.397984	Rtn4r
GO_MF_m	GO:004353	inositol 1,3	1/690	4/23049	0.114481	0.422441	0.397984	Astn2
GO_MF_m	GO:005505	D-glucose	1/690	4/23049	0.114481	0.422441	0.397984	Slc2a2
GO_MF_m	GO:006150	DNA topoi	1/690	4/23049	0.114481	0.422441	0.397984	Gm960
GO_MF_m	GO:009055	phosphatid	1/690	4/23049	0.114481	0.422441	0.397984	Abcb4
GO_MF_m	GO:009958	neurotrans	1/690	4/23049	0.114481	0.422441	0.397984	Grm1
GO_MF_m	GO:001508	calcium ion	7/690	137/23049	0.117688	0.432678	0.407628	Cacna1b/C
GO_MF_m	GO:004836	Rac GTPase	4/690	64/23049	0.12489	0.446187	0.420355	Map3k11/S
GO_MF_m	GO:000403	alditol:NAD	2/690	21/23049	0.129417	0.446187	0.420355	Akr1d1/Ak
GO_MF_m	GO:004662	sphingolipi	2/690	21/23049	0.129417	0.446187	0.420355	Plekha8/Rt
GO_MF_m	GO:000452	endodeoxy	3/690	42/23049	0.130437	0.446187	0.420355	Dnase1/Dn
GO_MF_m	GO:000526	calcium cha	6/690	115/23049	0.131317	0.446187	0.420355	Cacna1b/C
GO_MF_m	GO:003097	receptor ty	4/690	66/23049	0.135457	0.446187	0.420355	Eif3a/Gas6/
GO_MF_m	GO:004362	protein self	4/690	66/23049	0.135457	0.446187	0.420355	Aga/Bcl10/
GO_MF_m	GO:005066	NADP binc	3/690	43/23049	0.137285	0.446187	0.420355	Decr1/Fmc
GO_MF_m	GO:000098	transcriptic	2/690	22/23049	0.139666	0.446187	0.420355	Max/Rela
GO_MF_m	GO:003050	ankyrin bin	2/690	22/23049	0.139666	0.446187	0.420355	Kctd6/Slc8a
GO_MF_m	GO:009007	translation	2/690	22/23049	0.139666	0.446187	0.420355	Mif4gd/Pu
GO_MF_m	GO:009048	vitamin tra	2/690	22/23049	0.139666	0.446187	0.420355	Folr1/Slc2a
GO_MF_m	GO:000098	RNA polym	4/690	67/23049	0.140872	0.446187	0.420355	Atf6b/Nfat
GO_MF_m	GO:000070	oxidized ba	1/690	5/23049	0.140995	0.446187	0.420355	Rps3
GO_MF_m	GO:000122	RNA polym	1/690	5/23049	0.140995	0.446187	0.420355	Nfatc1
GO_MF_m	GO:000403	aldehyde c	1/690	5/23049	0.140995	0.446187	0.420355	Aox3
GO_MF_m	GO:000404	aminoacyl-	1/690	5/23049	0.140995	0.446187	0.420355	Ptrhd1
GO_MF_m	GO:000470	JUN kinase	1/690	5/23049	0.140995	0.446187	0.420355	Map3k11
GO_MF_m	GO:000482	phenylalan	1/690	5/23049	0.140995	0.446187	0.420355	Fars2
GO_MF_m	GO:000485	xanthine de	1/690	5/23049	0.140995	0.446187	0.420355	Aox3
GO_MF_m	GO:000492	interleukin-	1/690	5/23049	0.140995	0.446187	0.420355	Ifngr2
GO_MF_m	GO:000499	somatostat	1/690	5/23049	0.140995	0.446187	0.420355	Sstr5
GO_MF_m	GO:000510	type 1 fibro	1/690	5/23049	0.140995	0.446187	0.420355	Fgf17
GO_MF_m	GO:000511	type 2 fibro	1/690	5/23049	0.140995	0.446187	0.420355	Fgf17
GO_MF_m	GO:000851	folic acid tr	1/690	5/23049	0.140995	0.446187	0.420355	Folr1
GO_MF_m	GO:000937	four-way ju	1/690	5/23049	0.140995	0.446187	0.420355	Recql5
GO_MF_m	GO:001516	polyol tran	1/690	5/23049	0.140995	0.446187	0.420355	Aqp9
GO_MF_m	GO:001516	glycerol tra	1/690	5/23049	0.140995	0.446187	0.420355	Aqp9
GO_MF_m	GO:001520	urea transp	1/690	5/23049	0.140995	0.446187	0.420355	Aqp9
GO_MF_m	GO:001617	NAD(P)H o	1/690	5/23049	0.140995	0.446187	0.420355	Duox2
GO_MF_m	GO:001662	oxidoreduc	1/690	5/23049	0.140995	0.446187	0.420355	Aox3
GO_MF_m	GO:001672	oxidoreduc	1/690	5/23049	0.140995	0.446187	0.420355	Aox3
GO_MF_m	GO:001677	diphospho	1/690	5/23049	0.140995	0.446187	0.420355	Prps2

GO_MF_m	GO:003028	estrogen re	1/690	5/23049	0.140995	0.446187	0.420355	Esr2
GO_MF_m	GO:003062	U4 snRNA	1/690	5/23049	0.140995	0.446187	0.420355	Gemin5
GO_MF_m	GO:003404	lipid-transp	1/690	5/23049	0.140995	0.446187	0.420355	Abcg4
GO_MF_m	GO:003524	protein-arg	1/690	5/23049	0.140995	0.446187	0.420355	Prmt9
GO_MF_m	GO:003567	enone redu	1/690	5/23049	0.140995	0.446187	0.420355	Akr1d1
GO_MF_m	GO:004438	small prote	1/690	5/23049	0.140995	0.446187	0.420355	Ube2i
GO_MF_m	GO:004697	histone me	1/690	5/23049	0.140995	0.446187	0.420355	Smyd2
GO_MF_m	GO:004840	brain-deriv	1/690	5/23049	0.140995	0.446187	0.420355	Pzp
GO_MF_m	GO:005152	NFAT prote	1/690	5/23049	0.140995	0.446187	0.420355	Mapk14
GO_MF_m	GO:006022	phosphatic	1/690	5/23049	0.140995	0.446187	0.420355	Apoa4
GO_MF_m	GO:008600	voltage-ga	1/690	5/23049	0.140995	0.446187	0.420355	Cacna1g
GO_MF_m	GO:008408	3'-5' exonu	3/690	44/23049	0.144253	0.452203	0.426023	Cnot6/Eri2/
GO_MF_m	GO:001802	histone-lys	3/690	44/23049	0.144253	0.452203	0.426023	Dydc1/Setd
GO_MF_m	GO:004260	peptide an	3/690	44/23049	0.144253	0.452203	0.426023	H2-M10.1/
GO_MF_m	GO:000115	enhancer s	5/690	93/23049	0.146573	0.45804	0.431522	Atf6b/Gata
GO_MF_m	GO:001662	oxidoreduc	2/690	23/23049	0.150081	0.459273	0.432683	Akr1d1/De
GO_MF_m	GO:000451	nuclease ac	9/690	201/23049	0.150474	0.459273	0.432683	Ang6/Cnot
GO_MF_m	GO:001990	phosphatas	9/690	203/23049	0.156787	0.459273	0.432683	Cacna1b/E
GO_MF_m	GO:000524	voltage-ga	2/690	24/23049	0.160645	0.459273	0.432683	Cacna1g/C
GO_MF_m	GO:004332	phosphatic	2/690	24/23049	0.160645	0.459273	0.432683	Kif16b/Phlo
GO_MF_m	GO:004262	ATPase act	15/690	377/23049	0.162533	0.459273	0.432683	Abcb1b/Ab
GO_MF_m	GO:000818	neuropepti	3/690	47/23049	0.165816	0.459273	0.432683	Npffr2/Pro
GO_MF_m	GO:003149	nucleosom	3/690	47/23049	0.165816	0.459273	0.432683	Hp1bp3/Sr
GO_MF_m	GO:004518	translation	3/690	47/23049	0.165816	0.459273	0.432683	Mif4gd/Ne
GO_MF_m	GO:190161	organic hy	3/690	47/23049	0.165816	0.459273	0.432683	Abcg4/Aqp
GO_MF_m	GO:000160	pancreatic	1/690	6/23049	0.166716	0.459273	0.432683	Prokr1
GO_MF_m	GO:000395	NAD(P)+-p	1/690	6/23049	0.166716	0.459273	0.432683	Art4
GO_MF_m	GO:000403	alkaline ph	1/690	6/23049	0.166716	0.459273	0.432683	Alppl2
GO_MF_m	GO:000432	ferroxidase	1/690	6/23049	0.166716	0.459273	0.432683	Heph
GO_MF_m	GO:000446	lysine N-ac	1/690	6/23049	0.166716	0.459273	0.432683	Nat8f1
GO_MF_m	GO:000471	ribosomal p	1/690	6/23049	0.166716	0.459273	0.432683	Rps6ka1
GO_MF_m	GO:000473	pyruvate d	1/690	6/23049	0.166716	0.459273	0.432683	Pdhx
GO_MF_m	GO:000516	neurotroph	1/690	6/23049	0.166716	0.459273	0.432683	Grb2
GO_MF_m	GO:000531	high-affinit	1/690	6/23049	0.166716	0.459273	0.432683	Slc1a6
GO_MF_m	GO:000543	calcium:so	1/690	6/23049	0.166716	0.459273	0.432683	Slc8a1
GO_MF_m	GO:000549	vitamin D b	1/690	6/23049	0.166716	0.459273	0.432683	Vdr
GO_MF_m	GO:000553	galactose b	1/690	6/23049	0.166716	0.459273	0.432683	Mbl2
GO_MF_m	GO:000817	S-methyltr	1/690	6/23049	0.166716	0.459273	0.432683	Bhmt
GO_MF_m	GO:000897	phosphatic	1/690	6/23049	0.166716	0.459273	0.432683	Lipc
GO_MF_m	GO:001509	ferrous iron	1/690	6/23049	0.166716	0.459273	0.432683	Slc25a37
GO_MF_m	GO:001523	heme trans	1/690	6/23049	0.166716	0.459273	0.432683	Flvcr2
GO_MF_m	GO:001550	glutamate:	1/690	6/23049	0.166716	0.459273	0.432683	Slc1a6
GO_MF_m	GO:001601	cyclosporin	1/690	6/23049	0.166716	0.459273	0.432683	Ppid
GO_MF_m	GO:001672	oxidoreduc	1/690	6/23049	0.166716	0.459273	0.432683	Heph
GO_MF_m	GO:001986	IgE binding	1/690	6/23049	0.166716	0.459273	0.432683	Lgals3
GO_MF_m	GO:003369	oxidoreduc	1/690	6/23049	0.166716	0.459273	0.432683	Cyp1a2
GO_MF_m	GO:003460	pyruvate d	1/690	6/23049	0.166716	0.459273	0.432683	Pdhx
GO_MF_m	GO:003460	pyruvate d	1/690	6/23049	0.166716	0.459273	0.432683	Pdhx

GO_MF_m	GO:003487	caffeine ox	1/690	6/23049	0.166716	0.459273	0.432683	Cyp1a2
GO_MF_m	GO:00353	selenocyst	1/690	6/23049	0.166716	0.459273	0.432683	Rpl30
GO_MF_m	GO:003537	chondroiti	1/690	6/23049	0.166716	0.459273	0.432683	Rtn4r
GO_MF_m	GO:00431	vascular en	1/690	6/23049	0.166716	0.459273	0.432683	Pdcl3
GO_MF_m	GO:004351	kinetochor	1/690	6/23049	0.166716	0.459273	0.432683	Spdl1
GO_MF_m	GO:00473	alkylglycer	1/690	6/23049	0.166716	0.459273	0.432683	Gdpd1
GO_MF_m	GO:00476	ADP-ribos	1/690	6/23049	0.166716	0.459273	0.432683	Nudt5
GO_MF_m	GO:00715	ankyrin rep	1/690	6/23049	0.166716	0.459273	0.432683	Rela
GO_MF_m	GO:012001	intermemb	1/690	6/23049	0.166716	0.459273	0.432683	Plekha8
GO_MF_m	GO:19902	steroid hor	1/690	6/23049	0.166716	0.459273	0.432683	Esr2
GO_MF_m	GO:00199	protein ph	7/690	151/23049	0.167998	0.461078	0.434384	Cacna1b/E
GO_MF_m	GO:00162	lipase activ	6/690	124/23049	0.168293	0.461078	0.434384	Abhd4/Ces
GO_MF_m	GO:000017	3'-5'-exori	2/690	25/23049	0.171338	0.466862	0.439833	Cnot6/Eri2
GO_MF_m	GO:00800	phosphatic	2/690	25/23049	0.171338	0.466862	0.439833	Kif16b/Phl
GO_MF_m	GO:000804	enzyme ac	17/690	441/23049	0.174072	0.473021	0.445635	Agap3/Agf
GO_MF_m	GO:00486	cysteine-ty	4/690	73/23049	0.175053	0.474398	0.446932	Dpep1/Ga
GO_MF_m	GO:000422	metalloenc	5/690	99/23049	0.175643	0.474712	0.447228	Adam19/A
GO_MF_m	GO:00314	mitogen-a	4/690	74/23049	0.181006	0.483827	0.455816	Erbb2/Map
GO_MF_m	GO:00051	insulin rec	2/690	26/23049	0.182144	0.483827	0.455816	Irs2/Slc2a2
GO_MF_m	GO:00228	substrate-	16/690	415/23049	0.182781	0.483827	0.455816	Aqp12/Aq
GO_MF_m	GO:19019	phosphatic	7/690	155/23049	0.183883	0.483827	0.455816	Arap2/Kif1
GO_MF_m	GO:00020	p53 bindin	4/690	75/23049	0.187026	0.483827	0.455816	Gata1/Smy
GO_MF_m	GO:00192	kinase acti	4/690	75/23049	0.187026	0.483827	0.455816	Bcl10/Gas
GO_MF_m	GO:00085	G-protein	6/690	129/23049	0.190525	0.483827	0.455816	Ackr2/Hcrt
GO_MF_m	GO:000471	signal trans	1/690	7/23049	0.191668	0.483827	0.455816	Erbb2
GO_MF_m	GO:000847	queuine tR	1/690	7/23049	0.191668	0.483827	0.455816	Pdcl3
GO_MF_m	GO:00151	L-alanine t	1/690	7/23049	0.191668	0.483827	0.455816	Slc1a4
GO_MF_m	GO:001524	fatty acid t	1/690	7/23049	0.191668	0.483827	0.455816	Abcc4
GO_MF_m	GO:001717	phosphatic	1/690	7/23049	0.191668	0.483827	0.455816	Pigp
GO_MF_m	GO:001987	potassium	1/690	7/23049	0.191668	0.483827	0.455816	Nedd4l
GO_MF_m	GO:001987	sodium ch	1/690	7/23049	0.191668	0.483827	0.455816	Nedd4l
GO_MF_m	GO:00228	alanine tra	1/690	7/23049	0.191668	0.483827	0.455816	Slc1a4
GO_MF_m	GO:00301	molybden	1/690	7/23049	0.191668	0.483827	0.455816	Aox3
GO_MF_m	GO:003027	LIM domai	1/690	7/23049	0.191668	0.483827	0.455816	Ldb2
GO_MF_m	GO:00305	acetylcholi	1/690	7/23049	0.191668	0.483827	0.455816	Ly6g6d
GO_MF_m	GO:003471	inhibin bin	1/690	7/23049	0.191668	0.483827	0.455816	Inhba
GO_MF_m	GO:00352	UDP-xylos	1/690	7/23049	0.191668	0.483827	0.455816	Xylt2
GO_MF_m	GO:00426	CD4 recep	1/690	7/23049	0.191668	0.483827	0.455816	Lck
GO_MF_m	GO:00706	activin rec	1/690	7/23049	0.191668	0.483827	0.455816	Inhba
GO_MF_m	GO:007234	NAADP-se	1/690	7/23049	0.191668	0.483827	0.455816	Tpcn2
GO_MF_m	GO:199024	N6-methyl	1/690	7/23049	0.191668	0.483827	0.455816	Ythdc2
GO_MF_m	GO:00168	ATPase act	17/690	449/23049	0.19269	0.483827	0.455816	Abcb1b/Ab
GO_MF_m	GO:00038	DNA-direc	2/690	27/23049	0.193047	0.483827	0.455816	Polb/Polk
GO_MF_m	GO:00081	alcohol de	2/690	27/23049	0.193047	0.483827	0.455816	Akr1d1/Ak
GO_MF_m	GO:00168	exoribonu	2/690	27/23049	0.193047	0.483827	0.455816	Cnot6/Eri2
GO_MF_m	GO:00718	14-3-3 pr	2/690	27/23049	0.193047	0.483827	0.455816	Irs2/Zfp36l
GO_MF_m	GO:000451	endonucle	6/690	130/23049	0.195102	0.487754	0.459516	Ang6/Dna
GO_MF_m	GO:000524	voltage-ga	8/690	187/23049	0.19931	0.495796	0.467092	Cacna1b/C

GO_MF_m	GO:00228	voltage-ga	8/690	187/23049	0.19931	0.495796	0.467092	Cacna1b/C
GO_MF_m	GO:00353	enhancer b	5/690	104/23049	0.201391	0.499731	0.470799	Atf6b/Gata
GO_MF_m	GO:00168	hydro-lyas	3/690	52/23049	0.203614	0.49997	0.471024	Car2/Car4/
GO_MF_m	GO:00045	exoribonuc	2/690	28/23049	0.204031	0.49997	0.471024	Cnot6/Eri2
GO_MF_m	GO:00154	cation:catic	2/690	28/23049	0.204031	0.49997	0.471024	Slc8a1/Slc
GO_MF_m	GO:001677	nucleotidyl	6/690	132/23049	0.204377	0.49997	0.471024	Nudt5/Oas
GO_MF_m	GO:004432	ion channe	6/690	132/23049	0.204377	0.49997	0.471024	Cabp4/Cba
GO_MF_m	GO:00050	GTPase act	10/690	246/23049	0.204488	0.49997	0.471024	Agap3/Agf
GO_MF_m	GO:00152	secondary	10/690	247/23049	0.207868	0.502032	0.472967	Gm5134/Sl
GO_MF_m	GO:00016	peptide re	6/690	133/23049	0.209073	0.502032	0.472967	Ackr2/Hcrt
GO_MF_m	GO:00080	DNA-depe	4/690	79/23049	0.211714	0.502032	0.472967	Brip1/Gm9
GO_MF_m	GO:000817	tRNA meth	2/690	29/23049	0.215081	0.502032	0.472967	Trmt11/W
GO_MF_m	GO:003051	snoRNA bi	2/690	29/23049	0.215081	0.502032	0.472967	Nudt5/Nuc
GO_MF_m	GO:00725	divalent in	2/690	29/23049	0.215081	0.502032	0.472967	Slc25a37/S
GO_MF_m	GO:000122	transcriptic	16/690	428/23049	0.215388	0.502032	0.472967	Atf6b/Ddit
GO_MF_m	GO:000391	DNA topoi	1/690	8/23049	0.215874	0.502032	0.472967	Gm960
GO_MF_m	GO:00040	arylesteras	1/690	8/23049	0.215874	0.502032	0.472967	Car2
GO_MF_m	GO:00044	N,N-dimet	1/690	8/23049	0.215874	0.502032	0.472967	Fmo5
GO_MF_m	GO:000852	phosphatic	1/690	8/23049	0.215874	0.502032	0.472967	Tnfaip8l3
GO_MF_m	GO:00151	L-proline t	1/690	8/23049	0.215874	0.502032	0.472967	Slc1a4
GO_MF_m	GO:00168	endoribonu	1/690	8/23049	0.215874	0.502032	0.472967	Rnase1
GO_MF_m	GO:00171	sodium:dic	1/690	8/23049	0.215874	0.502032	0.472967	Slc1a6
GO_MF_m	GO:003061	U1 snRNA	1/690	8/23049	0.215874	0.502032	0.472967	Gemin5
GO_MF_m	GO:003524	protein-ar	1/690	8/23049	0.215874	0.502032	0.472967	Prmt9
GO_MF_m	GO:003631	annealing	1/690	8/23049	0.215874	0.502032	0.472967	Smarca1
GO_MF_m	GO:004314	ATP-deper	1/690	8/23049	0.215874	0.502032	0.472967	Recql5
GO_MF_m	GO:00700	delta-cater	1/690	8/23049	0.215874	0.502032	0.472967	Cdh24
GO_MF_m	GO:00701	small ribos	1/690	8/23049	0.215874	0.502032	0.472967	Rps3
GO_MF_m	GO:19904	U1 snRNP	1/690	8/23049	0.215874	0.502032	0.472967	Snrpc
GO_MF_m	GO:00037	transcriptic	5/690	107/23049	0.217417	0.502118	0.473048	Nfatc1/Rel
GO_MF_m	GO:000454	ribonuclea	5/690	107/23049	0.217417	0.502118	0.473048	Ang6/Cnot
GO_MF_m	GO:00045	hydrolase	5/690	107/23049	0.217417	0.502118	0.473048	Ctbs/Lyzl1/
GO_MF_m	GO:00047	MAP kinas	4/690	80/23049	0.218025	0.502362	0.473278	Erbb2/Map
GO_MF_m	GO:001507	monovaler	14/690	369/23049	0.218723	0.50281	0.4737	Atp1b4/At
GO_MF_m	GO:19907	protein tyr	4/690	81/23049	0.224386	0.511444	0.481834	Eif3a/Gas6
GO_MF_m	GO:003321	amide binc	13/690	341/23049	0.224519	0.511444	0.481834	Folr1/H2-N
GO_MF_m	GO:00040	aldo-keto	2/690	30/23049	0.226183	0.511444	0.481834	Akr1d1/Ak
GO_MF_m	GO:00049	G-protein	2/690	30/23049	0.226183	0.511444	0.481834	Htr2c/Olfr
GO_MF_m	GO:000857	ATP-deper	2/690	30/23049	0.226183	0.511444	0.481834	Dynll2/Kif1
GO_MF_m	GO:00152	solute:catic	2/690	30/23049	0.226183	0.511444	0.481834	Slc8a1/Slc
GO_MF_m	GO:00995	serotonin r	2/690	30/23049	0.226183	0.511444	0.481834	Htr2c/Olfr
GO_MF_m	GO:000802	monocarbo	3/690	55/23049	0.227163	0.511444	0.481834	Abcc4/Slc1
GO_MF_m	GO:00055	glycosamir	8/690	196/23049	0.234972	0.511444	0.481834	Ager/Lipc/
GO_MF_m	GO:000837	acetylgluco	3/690	56/23049	0.235127	0.511444	0.481834	B3gnt5/Pig
GO_MF_m	GO:00350	methylatec	3/690	56/23049	0.235127	0.511444	0.481834	Cbx5/Cdyl
GO_MF_m	GO:01400	methylatio	3/690	56/23049	0.235127	0.511444	0.481834	Cbx5/Cdyl
GO_MF_m	GO:00506	flavin aden	4/690	83/23049	0.237247	0.511444	0.481834	Aox3/Coq
GO_MF_m	GO:00009	RNA polyn	2/690	31/23049	0.237325	0.511444	0.481834	Recql5/Sm

GO_MF_m	GO:000400	ATP-deper	2/690	31/23049	0.237325	0.511444	0.481834	Brip1/Recq
GO_MF_m	GO:000820	ion channe	2/690	31/23049	0.237325	0.511444	0.481834	Nedd4l/Va
GO_MF_m	GO:001714	Wnt-prote	2/690	31/23049	0.237325	0.511444	0.481834	Ror2/Trab
GO_MF_m	GO:000401	adenylate	1/690	9/23049	0.239356	0.511444	0.481834	Ak3
GO_MF_m	GO:000457	oligosacch	1/690	9/23049	0.239356	0.511444	0.481834	Stt3b
GO_MF_m	GO:000457	dolichyl-di	1/690	9/23049	0.239356	0.511444	0.481834	Stt3b
GO_MF_m	GO:000516	neurotrop	1/690	9/23049	0.239356	0.511444	0.481834	Grb2
GO_MF_m	GO:000522	volume-se	1/690	9/23049	0.239356	0.511444	0.481834	Lrrc8c
GO_MF_m	GO:000534	ATP transm	1/690	9/23049	0.239356	0.511444	0.481834	Slc25a25
GO_MF_m	GO:000538	iron ion tra	1/690	9/23049	0.239356	0.511444	0.481834	Slc25a37
GO_MF_m	GO:000823	dipeptidyl-	1/690	9/23049	0.239356	0.511444	0.481834	Dpep1
GO_MF_m	GO:000846	histone-ar	1/690	9/23049	0.239356	0.511444	0.481834	Prmt9
GO_MF_m	GO:000852	phosphatic	1/690	9/23049	0.239356	0.511444	0.481834	Abcb4
GO_MF_m	GO:000853	N-acetylla	1/690	9/23049	0.239356	0.511444	0.481834	B3gnt5
GO_MF_m	GO:001986	chloride ch	1/690	9/23049	0.239356	0.511444	0.481834	Vamp8
GO_MF_m	GO:003162	opioid rec	1/690	9/23049	0.239356	0.511444	0.481834	Npffr2
GO_MF_m	GO:003235	oxidized p	1/690	9/23049	0.239356	0.511444	0.481834	Rps3
GO_MF_m	GO:004228	xylosyltran	1/690	9/23049	0.239356	0.511444	0.481834	Xylt2
GO_MF_m	GO:009898	G-protein	1/690	9/23049	0.239356	0.511444	0.481834	Grm1
GO_MF_m	GO:000850	anion trans	12/690	316/23049	0.240073	0.511882	0.482247	Abcc4/Folr
GO_MF_m	GO:001662	oxidoreduc	3/690	57/23049	0.243138	0.517316	0.487366	Akr1d1/De
GO_MF_m	GO:009910	ion channe	4/690	84/23049	0.243742	0.517498	0.487538	Cabp4/Kcn
GO_MF_m	GO:001526	channel ac	16/690	439/23049	0.244853	0.51766	0.48769	Aqp12/Aq
GO_MF_m	GO:002280	passive tra	16/690	439/23049	0.244853	0.51766	0.48769	Aqp12/Aq
GO_MF_m	GO:000507	SH3/SH2 a	2/690	32/23049	0.248495	0.521144	0.490972	Grb2/Grb7
GO_MF_m	GO:004476	ATPase act	2/690	32/23049	0.248495	0.521144	0.490972	Atp5c1/At
GO_MF_m	GO:005105	NF-kappa	2/690	32/23049	0.248495	0.521144	0.490972	Bcl10/Rela
GO_MF_m	GO:003255	purine ribo	13/690	349/23049	0.248966	0.521144	0.490972	Agap3/Ak
GO_MF_m	GO:000462	phospholi	4/690	85/23049	0.250276	0.521144	0.490972	Abhd4/Gd
GO_MF_m	GO:005084	extracellula	3/690	58/23049	0.251193	0.521144	0.490972	Eln/Lgals3/
GO_MF_m	GO:004529	cadherin bi	12/690	321/23049	0.25638	0.521144	0.490972	Arhgap18/
GO_MF_m	GO:001624	channel in	2/690	33/23049	0.25968	0.521144	0.490972	Nedd4l/Va
GO_MF_m	GO:005195	dynein ligh	2/690	33/23049	0.25968	0.521144	0.490972	Dynll2/Rilp
GO_MF_m	GO:001670	oxidoreduc	8/690	202/23049	0.259889	0.521144	0.490972	Akr1d1/Co
GO_MF_m	GO:000188	purine nuc	13/690	353/23049	0.26155	0.521144	0.490972	Agap3/Ak
GO_MF_m	GO:000823	metallope	7/690	173/23049	0.262024	0.521144	0.490972	Adam19/A
GO_MF_m	GO:000034	RNA 7-me	1/690	10/23049	0.262135	0.521144	0.490972	Gemin5
GO_MF_m	GO:000443	phosphatic	1/690	10/23049	0.262135	0.521144	0.490972	Mtmr14
GO_MF_m	GO:000456	chitinase a	1/690	10/23049	0.262135	0.521144	0.490972	Ctbs
GO_MF_m	GO:000498	neuropepti	1/690	10/23049	0.262135	0.521144	0.490972	Prokr1
GO_MF_m	GO:000849	translation	1/690	10/23049	0.262135	0.521144	0.490972	Mif4gd
GO_MF_m	GO:000865	cysteine-ty	1/690	10/23049	0.262135	0.521144	0.490972	Bcl10
GO_MF_m	GO:001521	ADP transr	1/690	10/23049	0.262135	0.521144	0.490972	Slc25a25
GO_MF_m	GO:001538	potassium	1/690	10/23049	0.262135	0.521144	0.490972	Slc9a4
GO_MF_m	GO:001688	endodeoxy	1/690	10/23049	0.262135	0.521144	0.490972	Dnase1
GO_MF_m	GO:001995	C-C chem	1/690	10/23049	0.262135	0.521144	0.490972	Ackr2
GO_MF_m	GO:003199	thioesteras	1/690	10/23049	0.262135	0.521144	0.490972	Traf4
GO_MF_m	GO:003235	oxidized D	1/690	10/23049	0.262135	0.521144	0.490972	Rps3

GO_MF_m	GO:004257	lipid phosp	1/690	10/23049	0.262135	0.521144	0.490972	Plppr3
GO_MF_m	GO:00432	glycosphin	1/690	10/23049	0.262135	0.521144	0.490972	Rtn4r
GO_MF_m	GO:00470	ketosteroi	1/690	10/23049	0.262135	0.521144	0.490972	Akr1d1
GO_MF_m	GO:007051	death dom	1/690	10/23049	0.262135	0.521144	0.490972	Ripk1
GO_MF_m	GO:00709	snRNP bin	1/690	10/23049	0.262135	0.521144	0.490972	Snrpc
GO_MF_m	GO:19904	protein ant	1/690	10/23049	0.262135	0.521144	0.490972	Lck
GO_MF_m	GO:003254	ribonucleo	13/690	354/23049	0.264731	0.524437	0.494075	Agap3/Ak
GO_MF_m	GO:00306	GTPase re	10/690	263/23049	0.264841	0.524437	0.494075	Agap3/Agf
GO_MF_m	GO:000817	RNA methy	3/690	60/23049	0.267413	0.526643	0.496153	Mrm2/Trm
GO_MF_m	GO:000107	transcripti	11/690	294/23049	0.267663	0.526643	0.496153	Ddit3/Esr2/
GO_MF_m	GO:00082	heparin bi	6/690	145/23049	0.268061	0.526643	0.496153	Ager/Lipc/
GO_MF_m	GO:00708	growth fac	6/690	145/23049	0.268061	0.526643	0.496153	Fgf17/Fgf4
GO_MF_m	GO:000837	galactosylt	2/690	34/23049	0.27087	0.531117	0.500368	A4galt/B3g
GO_MF_m	GO:000471	transmem	3/690	61/23049	0.275569	0.533272	0.502398	Erbb2/Ret/
GO_MF_m	GO:001671	oxidoreduc	3/690	61/23049	0.275569	0.533272	0.502398	Cyp1a2/Cy
GO_MF_m	GO:00168	carbon-ox	3/690	61/23049	0.275569	0.533272	0.502398	Car2/Car4/
GO_MF_m	GO:00428	histone de	5/690	118/23049	0.27908	0.533272	0.502398	Cbx5/Rela/
GO_MF_m	GO:00051	epidermal	2/690	35/23049	0.282054	0.533272	0.502398	Grb2/Socs
GO_MF_m	GO:00045	deoxyribo	3/690	62/23049	0.283749	0.533272	0.502398	Dnase1/Dr
GO_MF_m	GO:00011	RNA poly	1/690	11/23049	0.284234	0.533272	0.502398	Vax2
GO_MF_m	GO:00048	protein ser	1/690	11/23049	0.284234	0.533272	0.502398	4933415F2
GO_MF_m	GO:00080	chitin bindi	1/690	11/23049	0.284234	0.533272	0.502398	Ctbs
GO_MF_m	GO:000841	fucosyltran	1/690	11/23049	0.284234	0.533272	0.502398	Fut1
GO_MF_m	GO:00153	calcium:cat	1/690	11/23049	0.284234	0.533272	0.502398	Slc8a1
GO_MF_m	GO:00153	sodium:pr	1/690	11/23049	0.284234	0.533272	0.502398	Slc9a4
GO_MF_m	GO:001627	arginine N	1/690	11/23049	0.284234	0.533272	0.502398	Prmt9
GO_MF_m	GO:001627	protein-ar	1/690	11/23049	0.284234	0.533272	0.502398	Prmt9
GO_MF_m	GO:00168	endodeoxy	1/690	11/23049	0.284234	0.533272	0.502398	Dnase2b
GO_MF_m	GO:00423	phosphate	1/690	11/23049	0.284234	0.533272	0.502398	Rela
GO_MF_m	GO:00435	leucine zip	1/690	11/23049	0.284234	0.533272	0.502398	Ddit3
GO_MF_m	GO:00435	insulin rece	1/690	11/23049	0.284234	0.533272	0.502398	Grb2
GO_MF_m	GO:004697	TAP bindin	1/690	11/23049	0.284234	0.533272	0.502398	H2-Q10
GO_MF_m	GO:004737	acylglycer	1/690	11/23049	0.284234	0.533272	0.502398	Lipc
GO_MF_m	GO:00481	activin bin	1/690	11/23049	0.284234	0.533272	0.502398	Fst
GO_MF_m	GO:005274	phosphati	1/690	11/23049	0.284234	0.533272	0.502398	Mtmr14
GO_MF_m	GO:199082	sequence-	1/690	11/23049	0.284234	0.533272	0.502398	Srsf3
GO_MF_m	GO:00605	nucleoside	11/690	301/23049	0.292677	0.538154	0.506998	Agap3/Agf
GO_MF_m	GO:00038	DNA-direc	2/690	36/23049	0.293223	0.538154	0.506998	Polr1e/Pol
GO_MF_m	GO:00340	DNA poly	2/690	36/23049	0.293223	0.538154	0.506998	Polb/Polk
GO_MF_m	GO:00018	nucleoside	13/690	364/23049	0.29723	0.538154	0.506998	Agap3/Ak
GO_MF_m	GO:00050	signal trans	6/690	151/23049	0.29899	0.538154	0.506998	Erbb2/Map
GO_MF_m	GO:00198	cation-tra	3/690	64/23049	0.300166	0.538154	0.506998	Atp1b4/At
GO_MF_m	GO:00228	active ion t	3/690	64/23049	0.300166	0.538154	0.506998	Atp1b4/At
GO_MF_m	GO:00426	ATPase co	3/690	64/23049	0.300166	0.538154	0.506998	Atp1b4/At
GO_MF_m	GO:00325	guanyl ribo	13/690	366/23049	0.303867	0.538154	0.506998	Agap3/Ak
GO_MF_m	GO:00170	sodium cha	2/690	37/23049	0.304368	0.538154	0.506998	Fxyd6/Ned
GO_MF_m	GO:00340	5'-3' RNA	2/690	37/23049	0.304368	0.538154	0.506998	Polr1e/Pol
GO_MF_m	GO:00435	ADP bindi	2/690	37/23049	0.304368	0.538154	0.506998	Prkag1/Pr

GO_MF_m	GO:009774	RNA polym	2/690	37/23049	0.304368	0.538154	0.506998	Polr1e/Pol
GO_MF_m	GO:000029	adenine nu	1/690	12/23049	0.305671	0.538154	0.506998	Slc25a25
GO_MF_m	GO:000090	translation	1/690	12/23049	0.305671	0.538154	0.506998	Purb
GO_MF_m	GO:000105	RNA polym	1/690	12/23049	0.305671	0.538154	0.506998	Polr1e
GO_MF_m	GO:000173	2'-5'-oligo	1/690	12/23049	0.305671	0.538154	0.506998	Oas2
GO_MF_m	GO:000216	aminoacyl-	1/690	12/23049	0.305671	0.538154	0.506998	Iars
GO_MF_m	GO:000487	compleme	1/690	12/23049	0.305671	0.538154	0.506998	C3ar1
GO_MF_m	GO:000534	purine ribo	1/690	12/23049	0.305671	0.538154	0.506998	Slc25a25
GO_MF_m	GO:000539	sodium:po	1/690	12/23049	0.305671	0.538154	0.506998	Atp1b4
GO_MF_m	GO:000545	monovale	1/690	12/23049	0.305671	0.538154	0.506998	Slc9a4
GO_MF_m	GO:000833	high volta	1/690	12/23049	0.305671	0.538154	0.506998	Cacna1b
GO_MF_m	GO:000855	potassium-	1/690	12/23049	0.305671	0.538154	0.506998	Atp1b4
GO_MF_m	GO:001521	purine nuc	1/690	12/23049	0.305671	0.538154	0.506998	Slc25a25
GO_MF_m	GO:001650	peptidase	1/690	12/23049	0.305671	0.538154	0.506998	Bcl10
GO_MF_m	GO:001716	vinculin bi	1/690	12/23049	0.305671	0.538154	0.506998	Ctnna1
GO_MF_m	GO:003054	receptor a	1/690	12/23049	0.305671	0.538154	0.506998	Slurp1
GO_MF_m	GO:003088	beta-2-mi	1/690	12/23049	0.305671	0.538154	0.506998	H2-Q10
GO_MF_m	GO:003549	cAMP resp	1/690	12/23049	0.305671	0.538154	0.506998	Atf6b
GO_MF_m	GO:004302	ribosomal	1/690	12/23049	0.305671	0.538154	0.506998	Pim1
GO_MF_m	GO:004454	S100 prote	1/690	12/23049	0.305671	0.538154	0.506998	Ager
GO_MF_m	GO:004840	nerve grow	1/690	12/23049	0.305671	0.538154	0.506998	Pzp
GO_MF_m	GO:005066	oxidoredu	1/690	12/23049	0.305671	0.538154	0.506998	Duox2
GO_MF_m	GO:009749	structural	1/690	12/23049	0.305671	0.538154	0.506998	Myom2
GO_MF_m	GO:001900	guanyl nuc	13/690	367/23049	0.3072	0.539895	0.508638	Agap3/Ak
GO_MF_m	GO:000470	signal tran	5/690	123/23049	0.308201	0.540704	0.5094	Erbb2/Ma
GO_MF_m	GO:000471	protein ser	2/690	38/23049	0.31548	0.550676	0.518795	Aurka/Rps
GO_MF_m	GO:001675	transferase	10/690	277/23049	0.318267	0.550676	0.518795	A4galt/Art
GO_MF_m	GO:000097	RNA polym	16/690	466/23049	0.323029	0.550676	0.518795	Atf6b/Ddit
GO_MF_m	GO:003126	small GTPa	15/690	435/23049	0.324602	0.550676	0.518795	Agap3/Agf
GO_MF_m	GO:000390	DNA-(apu	1/690	13/23049	0.326468	0.550676	0.518795	Rps3
GO_MF_m	GO:000453	poly(A)-sp	1/690	13/23049	0.326468	0.550676	0.518795	Cnot6
GO_MF_m	GO:000517	vascular en	1/690	13/23049	0.326468	0.550676	0.518795	Pdcl3
GO_MF_m	GO:000552	tropomyos	1/690	13/23049	0.326468	0.550676	0.518795	Tmod2
GO_MF_m	GO:000554	folic acid b	1/690	13/23049	0.326468	0.550676	0.518795	Folr1
GO_MF_m	GO:000830	DNA bindi	1/690	13/23049	0.326468	0.550676	0.518795	Gata1
GO_MF_m	GO:000847	palmitoyl-(	1/690	13/23049	0.326468	0.550676	0.518795	Abhd13
GO_MF_m	GO:001564	toxic subst	1/690	13/23049	0.326468	0.550676	0.518795	A4galt
GO_MF_m	GO:001592	glucosidas	1/690	13/23049	0.326468	0.550676	0.518795	Mogs
GO_MF_m	GO:003592	mRNA 3'-	1/690	13/23049	0.326468	0.550676	0.518795	Zfp36l1
GO_MF_m	GO:004529	alpha-cate	1/690	13/23049	0.326468	0.550676	0.518795	Cdh24
GO_MF_m	GO:005137	serotonin	1/690	13/23049	0.326468	0.550676	0.518795	Htr2c
GO_MF_m	GO:007074	C2H2 zinc	1/690	13/23049	0.326468	0.550676	0.518795	Gata1
GO_MF_m	GO:009761	annealing	1/690	13/23049	0.326468	0.550676	0.518795	Smarca1
GO_MF_m	GO:009859	palmitoyl h	1/690	13/23049	0.326468	0.550676	0.518795	Abhd13
GO_MF_m	GO:000178	phosphoty	2/690	39/23049	0.326551	0.550676	0.518795	Grb2/Lck
GO_MF_m	GO:001548	cholesterol	2/690	39/23049	0.326551	0.550676	0.518795	Apoa4/Sta
GO_MF_m	GO:003226	phosphatic	2/690	39/23049	0.326551	0.550676	0.518795	Kif16b/Phl
GO_MF_m	GO:004691	transition	2/690	39/23049	0.326551	0.550676	0.518795	Slc25a37/S

GO_MF_m	GO:000485	enzyme inh	14/690	405/23049	0.329327	0.554422	0.522324	4933415F2
GO_MF_m	GO:001624	channel reg	5/690	127/23049	0.331795	0.556704	0.524474	Cabp4/Fxy
GO_MF_m	GO:003067	protein bin	5/690	127/23049	0.331795	0.556704	0.524474	Cbx5/Dsp/
GO_MF_m	GO:000552	GTP bindin	12/690	344/23049	0.335661	0.562246	0.529695	Agap3/Ak3
GO_MF_m	GO:003245	demethylas	2/690	40/23049	0.337573	0.563811	0.531169	Cyp1a2/Cy
GO_MF_m	GO:001712	SH3 domai	5/690	128/23049	0.337722	0.563811	0.531169	Adam19/C
GO_MF_m	GO:000107	transcriptic	6/690	160/23049	0.346485	0.566409	0.533617	Fezf1/Gata
GO_MF_m	GO:000033	RNA cap b	1/690	14/23049	0.346642	0.566409	0.533617	Gemin5
GO_MF_m	GO:000116	intronic tra	1/690	14/23049	0.346642	0.566409	0.533617	Vax2
GO_MF_m	GO:000528	amino acid	1/690	14/23049	0.346642	0.566409	0.533617	Slc1a6
GO_MF_m	GO:000552	macrolide l	1/690	14/23049	0.346642	0.566409	0.533617	Ppid
GO_MF_m	GO:000552	FK506 binc	1/690	14/23049	0.346642	0.566409	0.533617	Ppid
GO_MF_m	GO:000832	protein trai	1/690	14/23049	0.346642	0.566409	0.533617	Tomm7
GO_MF_m	GO:000843	JUN kinase	1/690	14/23049	0.346642	0.566409	0.533617	Dusp10
GO_MF_m	GO:001031	phosphatic	1/690	14/23049	0.346642	0.566409	0.533617	Phlda3
GO_MF_m	GO:001649	C-C chemc	1/690	14/23049	0.346642	0.566409	0.533617	Ackr2
GO_MF_m	GO:001910	DNA N-gly	1/690	14/23049	0.346642	0.566409	0.533617	Rps3
GO_MF_m	GO:004313	3'-5' DNA	1/690	14/23049	0.346642	0.566409	0.533617	Recql5
GO_MF_m	GO:004529	gamma-ca	1/690	14/23049	0.346642	0.566409	0.533617	Ctnna1
GO_MF_m	GO:000452	exonucleas	3/690	70/23049	0.349565	0.566613	0.533809	Cnot6/Eri2
GO_MF_m	GO:000508	Rho guany	3/690	70/23049	0.349565	0.566613	0.533809	Itsn1/Spata
GO_MF_m	GO:001984	rRNA bindi	3/690	70/23049	0.349565	0.566613	0.533809	Ppan/Rps1
GO_MF_m	GO:009711	scaffold pr	3/690	70/23049	0.349565	0.566613	0.533809	Cacna1g/D
GO_MF_m	GO:000517	hormone a	5/690	130/23049	0.3496	0.566613	0.533809	C1qtnf12/
GO_MF_m	GO:001713	Rab GTPas	6/690	161/23049	0.351815	0.56881	0.535879	Kif16b/Npc
GO_MF_m	GO:000801	microtubul	8/690	223/23049	0.352094	0.56881	0.535879	Casc1/Kif1
GO_MF_m	GO:000098	proximal p	16/690	477/23049	0.356621	0.573193	0.540008	Atf6b/Ddit
GO_MF_m	GO:004830	calcium-de	3/690	71/23049	0.357781	0.573193	0.540008	Mbl1/Mbl2
GO_MF_m	GO:000098	transcriptic	15/690	446/23049	0.359433	0.573193	0.540008	Ddit3/Esr2
GO_MF_m	GO:000367	DNA helica	2/690	42/23049	0.359446	0.573193	0.540008	Brip1/Recq
GO_MF_m	GO:001507	potassium	6/690	163/23049	0.362492	0.573193	0.540008	Atp1b4/Kc
GO_MF_m	GO:005083	cell adhesi	16/690	480/23049	0.3659	0.573193	0.540008	Arhgap18/
GO_MF_m	GO:000379	lysozyme a	1/690	15/23049	0.366213	0.573193	0.540008	Lyzl1
GO_MF_m	GO:000470	MAP kinase	1/690	15/23049	0.366213	0.573193	0.540008	Mapk14
GO_MF_m	GO:000516	neurotroph	1/690	15/23049	0.366213	0.573193	0.540008	Grb2
GO_MF_m	GO:000817	adenylate	1/690	15/23049	0.366213	0.573193	0.540008	Cap2
GO_MF_m	GO:001521	nucleotide	1/690	15/23049	0.366213	0.573193	0.540008	Slc25a25
GO_MF_m	GO:001592	mannosida	1/690	15/23049	0.366213	0.573193	0.540008	Manba
GO_MF_m	GO:001708	chloride ch	1/690	15/23049	0.366213	0.573193	0.540008	Vamp8
GO_MF_m	GO:002282	potassium	1/690	15/23049	0.366213	0.573193	0.540008	Slc9a4
GO_MF_m	GO:002284	potassium	1/690	15/23049	0.366213	0.573193	0.540008	Kcnk6
GO_MF_m	GO:003205	bile acid bi	1/690	15/23049	0.366213	0.573193	0.540008	Vdr
GO_MF_m	GO:004317	amine binc	1/690	15/23049	0.366213	0.573193	0.540008	Htr2c
GO_MF_m	GO:004421	intronic tra	1/690	15/23049	0.366213	0.573193	0.540008	Vax2
GO_MF_m	GO:004693	proton-tra	1/690	15/23049	0.366213	0.573193	0.540008	Atp5c1
GO_MF_m	GO:000520	extracellula	2/690	43/23049	0.370283	0.573193	0.540008	Eln/Tectb
GO_MF_m	GO:000527	sodium cha	2/690	43/23049	0.370283	0.573193	0.540008	Cacna1g/C
GO_MF_m	GO:001545	potassium	2/690	43/23049	0.370283	0.573193	0.540008	Kcne1/Nec

GO_MF_m	GO:00156	ATPase act	2/690	43/23049	0.370283	0.573193	0.540008	Atp1b4/At
GO_MF_m	GO:003054	Hsp70 prot	2/690	43/23049	0.370283	0.573193	0.540008	Dnajb14/R
GO_MF_m	GO:00329	sterol bind	2/690	43/23049	0.370283	0.573193	0.540008	Apoa4/Sta
GO_MF_m	GO:00428	actinin bin	2/690	43/23049	0.370283	0.573193	0.540008	Myom2/Re
GO_MF_m	GO:00995	G-protein	2/690	43/23049	0.370283	0.573193	0.540008	Htr2c/Olfr
GO_MF_m	GO:00083	steroid hy	3/690	73/23049	0.374164	0.578306	0.544825	Cyp2a22/C
GO_MF_m	GO:003107	heat shock	5/690	135/23049	0.379364	0.580118	0.546533	Camkmt/D
GO_MF_m	GO:00167	exonucleas	2/690	44/23049	0.381046	0.580118	0.546533	Cnot6/Eri2
GO_MF_m	GO:00051	cytokine re	11/690	325/23049	0.382332	0.580118	0.546533	Defb33/De
GO_MF_m	GO:004801	receptor li	16/690	486/23049	0.384572	0.580118	0.546533	Defb33/De
GO_MF_m	GO:00051	death rece	1/690	16/23049	0.385199	0.580118	0.546533	Ripk1
GO_MF_m	GO:00051	pheromon	1/690	16/23049	0.385199	0.580118	0.546533	Esp16
GO_MF_m	GO:00150	magnesiu	1/690	16/23049	0.385199	0.580118	0.546533	Nipa2
GO_MF_m	GO:00152	solute:prot	1/690	16/23049	0.385199	0.580118	0.546533	Slc9a4
GO_MF_m	GO:00167	oxidoreduc	1/690	16/23049	0.385199	0.580118	0.546533	Heph
GO_MF_m	GO:00168	dipeptidas	1/690	16/23049	0.385199	0.580118	0.546533	Dpep1
GO_MF_m	GO:001711	nucleoside	1/690	16/23049	0.385199	0.580118	0.546533	Nudt5
GO_MF_m	GO:00171	Ral GTPase	1/690	16/23049	0.385199	0.580118	0.546533	Ralgps1
GO_MF_m	GO:00302	protein tyr	1/690	16/23049	0.385199	0.580118	0.546533	Gas6
GO_MF_m	GO:00341	apolipopro	1/690	16/23049	0.385199	0.580118	0.546533	Lipc
GO_MF_m	GO:00428	histone me	1/690	16/23049	0.385199	0.580118	0.546533	Dydc1
GO_MF_m	GO:00431	neurotroph	1/690	16/23049	0.385199	0.580118	0.546533	Pzp
GO_MF_m	GO:005137	muscle alp	1/690	16/23049	0.385199	0.580118	0.546533	Myom2
GO_MF_m	GO:00167	transferase	7/690	199/23049	0.38667	0.581459	0.547796	A4galt/B3g
GO_MF_m	GO:001537	solute:sodi	3/690	75/23049	0.390463	0.586281	0.552338	Gm5134/Sl
GO_MF_m	GO:00048	endopepti	7/690	200/23049	0.391573	0.586423	0.552472	Dpep1/Gas
GO_MF_m	GO:003281	tumor necr	2/690	45/23049	0.39173	0.586423	0.552472	Ripk1/Traf
GO_MF_m	GO:00425	hormone b	4/690	107/23049	0.398954	0.596344	0.561819	Esr2/Hcrtr1
GO_MF_m	GO:00480	CCR chemo	2/690	46/23049	0.402331	0.597066	0.562499	Defb33/De
GO_MF_m	GO:199084	promoter-	2/690	46/23049	0.402331	0.597066	0.562499	Esr2/Rbl1
GO_MF_m	GO:00045	nucleoside	1/690	17/23049	0.403616	0.597066	0.562499	Nme5
GO_MF_m	GO:00197	SUMO tran	1/690	17/23049	0.403616	0.597066	0.562499	Ube2i
GO_MF_m	GO:00228	macromole	1/690	17/23049	0.403616	0.597066	0.562499	Tomm7
GO_MF_m	GO:003027	LRR domai	1/690	17/23049	0.403616	0.597066	0.562499	Ddit3
GO_MF_m	GO:00434	protein kin	1/690	17/23049	0.403616	0.597066	0.562499	Bcl10
GO_MF_m	GO:00080	protein C-	8/690	235/23049	0.406574	0.598901	0.564228	Bcl10/Cacn
GO_MF_m	GO:003361	activating t	3/690	77/23049	0.406654	0.598901	0.564228	Ldb2/Rbl1/
GO_MF_m	GO:004317	alcohol bin	3/690	77/23049	0.406654	0.598901	0.564228	Apoa4/Ast
GO_MF_m	GO:00302	carbohydra	9/690	268/23049	0.410681	0.603571	0.568627	Clec4a2/Lg
GO_MF_m	GO:00054	steroid bin	4/690	109/23049	0.412486	0.603571	0.568627	Apoa4/Esr
GO_MF_m	GO:00010	basal trans	2/690	47/23049	0.412842	0.603571	0.568627	Recql5/Sm
GO_MF_m	GO:00010	basal RNA	2/690	47/23049	0.412842	0.603571	0.568627	Recql5/Sm
GO_MF_m	GO:00167	thiolester h	2/690	47/23049	0.412842	0.603571	0.568627	Abhd13/N
GO_MF_m	GO:00191	transmemb	3/690	78/23049	0.414702	0.605404	0.570354	Erbb2/Ret/
GO_MF_m	GO:19016	sulfur com	8/690	237/23049	0.415676	0.605942	0.570861	Ager/Fst/H
GO_MF_m	GO:000541	amino acid	1/690	18/23049	0.421483	0.610845	0.57548	Slc1a6
GO_MF_m	GO:00198	immunoglo	1/690	18/23049	0.421483	0.610845	0.57548	Lgals3
GO_MF_m	GO:00228	leak chann	1/690	18/23049	0.421483	0.610845	0.57548	Kcnk6

GO_MF_m	GO:002284	narrow por	1/690	18/23049	0.421483	0.610845	0.57548	Kcnk6
GO_MF_m	GO:000487	nuclear rec	2/690	48/23049	0.423261	0.611649	0.576238	Esr2/Vdr
GO_MF_m	GO:009853	transcriptic	2/690	48/23049	0.423261	0.611649	0.576238	Esr2/Vdr
GO_MF_m	GO:006113	endopeptic	7/690	207/23049	0.425866	0.614526	0.578948	Dpep1/Gas
GO_MF_m	GO:000438	helicase ac	5/690	144/23049	0.432729	0.618921	0.583089	Brip1/Recq
GO_MF_m	GO:000110	RNA polym	2/690	49/23049	0.433584	0.618921	0.583089	Ldb2/Rbl1
GO_MF_m	GO:000374	translation	2/690	49/23049	0.433584	0.618921	0.583089	Eif3a/Eif3e
GO_MF_m	GO:004227	peptide bir	10/690	306/23049	0.434155	0.618921	0.583089	H2-M10.1/
GO_MF_m	GO:000521	ion channe	13/690	404/23049	0.43503	0.618921	0.583089	Cacna1b/C
GO_MF_m	GO:000526	cation char	10/690	307/23049	0.43818	0.618921	0.583089	Cacna1b/C
GO_MF_m	GO:006113	peptidase r	8/690	242/23049	0.438391	0.618921	0.583089	Bcl10/Dpep
GO_MF_m	GO:001620	antioxidant	3/690	81/23049	0.438624	0.618921	0.583089	Apoa4/Mp
GO_MF_m	GO:000395	NAD+ ADF	1/690	19/23049	0.438815	0.618921	0.583089	Parp11
GO_MF_m	GO:000855	proton-exp	1/690	19/23049	0.438815	0.618921	0.583089	Atp6v1e2
GO_MF_m	GO:003016	low-densit	1/690	19/23049	0.438815	0.618921	0.583089	Lipc
GO_MF_m	GO:004327	phospholip	1/690	19/23049	0.438815	0.618921	0.583089	Srsf3
GO_MF_m	GO:004696	proton-tra	1/690	19/23049	0.438815	0.618921	0.583089	Atp6v1e2
GO_MF_m	GO:005043	transformir	1/690	19/23049	0.438815	0.618921	0.583089	Vasn
GO_MF_m	GO:006178	peptidogly	1/690	19/23049	0.438815	0.618921	0.583089	Lyzl1
GO_MF_m	GO:009760	cullin famil	1/690	19/23049	0.438815	0.618921	0.583089	Kctd6
GO_MF_m	GO:003041	peptidase i	7/690	210/23049	0.440509	0.620435	0.584515	Dpep1/Gas
GO_MF_m	GO:001682	lyase activi	6/690	178/23049	0.442571	0.621577	0.585591	Acmsd/Car
GO_MF_m	GO:006009	molecular a	6/690	178/23049	0.442571	0.621577	0.585591	Cbx5/Dsp/
GO_MF_m	GO:000823	metalloexo	2/690	50/23049	0.443806	0.621577	0.585591	Cpa2/Dpep
GO_MF_m	GO:004530	protein pho	2/690	50/23049	0.443806	0.621577	0.585591	Grb2/Lck
GO_MF_m	GO:000377	microtubul	3/690	82/23049	0.446516	0.623176	0.587097	Dynll2/Kif1
GO_MF_m	GO:001983	growth fac	5/690	147/23049	0.450329	0.623176	0.587097	Erbb2/Igfb
GO_MF_m	GO:000392	GTPase act	9/690	278/23049	0.453265	0.623176	0.587097	Agap3/F83
GO_MF_m	GO:000532	neurotrans	2/690	51/23049	0.453925	0.623176	0.587097	Slc17a8/Slc
GO_MF_m	GO:001704	peptide ho	2/690	51/23049	0.453925	0.623176	0.587097	Hcrtr1/Inhb
GO_MF_m	GO:003014	manganese	2/690	51/23049	0.453925	0.623176	0.587097	Nudt7/Pim
GO_MF_m	GO:199093	ATP-deper	2/690	51/23049	0.453925	0.623176	0.587097	Dynll2/Kif1
GO_MF_m	GO:000113	RNA polym	1/690	20/23049	0.455629	0.623176	0.587097	Vdr
GO_MF_m	GO:000122	transcriptic	1/690	20/23049	0.455629	0.623176	0.587097	Nfatc1
GO_MF_m	GO:000524	inward rect	1/690	20/23049	0.455629	0.623176	0.587097	Kcnj14
GO_MF_m	GO:000864	rRNA meth	1/690	20/23049	0.455629	0.623176	0.587097	Mrm2
GO_MF_m	GO:003121	phosphatic	1/690	20/23049	0.455629	0.623176	0.587097	Apoa4
GO_MF_m	GO:003148	myosin V b	1/690	20/23049	0.455629	0.623176	0.587097	Npc1l1
GO_MF_m	GO:004297	peroxisom	1/690	20/23049	0.455629	0.623176	0.587097	Esr2
GO_MF_m	GO:005099	quaternary	1/690	20/23049	0.455629	0.623176	0.587097	Apoa4
GO_MF_m	GO:007006	proline-ricl	1/690	20/23049	0.455629	0.623176	0.587097	Itsn1
GO_MF_m	GO:014010	catalytic ac	1/690	20/23049	0.455629	0.623176	0.587097	Mrm2
GO_MF_m	GO:000202	protease b	5/690	148/23049	0.456165	0.623176	0.587097	Bcl10/Mbl1
GO_MF_m	GO:004239	histone bin	6/690	182/23049	0.463675	0.632572	0.595949	Anp32b/Cb
GO_MF_m	GO:000801	beta-caten	3/690	85/23049	0.469917	0.638619	0.601646	Cdh24/Ctn
GO_MF_m	GO:000187	pattern bin	1/690	21/23049	0.471939	0.638619	0.601646	Mbl1
GO_MF_m	GO:000401	phospholip	1/690	21/23049	0.471939	0.638619	0.601646	Abcb4
GO_MF_m	GO:001920	nucleotide	1/690	21/23049	0.471939	0.638619	0.601646	Ak3

GO_MF_m	GO:003024	polysaccha	1/690	21/23049	0.471939	0.638619	0.601646	Mbl1
GO_MF_m	GO:00706	transmem	1/690	21/23049	0.471939	0.638619	0.601646	Inhba
GO_MF_m	GO:000471	protein tyr	5/690	152/23049	0.479324	0.647735	0.610234	Erbb2/Grb
GO_MF_m	GO:009951	ion antipor	2/690	54/23049	0.483633	0.651217	0.613515	Slc8a1/Slc
GO_MF_m	GO:00002	magnesiu	6/690	186/23049	0.484568	0.651217	0.613515	Ern2/Nudt
GO_MF_m	GO:00000	mannosyltr	1/690	22/23049	0.487762	0.651217	0.613515	Pigv
GO_MF_m	GO:000477	sterol ester	1/690	22/23049	0.487762	0.651217	0.613515	Ces2h
GO_MF_m	GO:00053	zinc ion tra	1/690	22/23049	0.487762	0.651217	0.613515	Slc39a8
GO_MF_m	GO:001512	bile acid tr	1/690	22/23049	0.487762	0.651217	0.613515	Slc51a
GO_MF_m	GO:001527	calcium-re	1/690	22/23049	0.487762	0.651217	0.613515	Tpcn2
GO_MF_m	GO:00156	organoph	1/690	22/23049	0.487762	0.651217	0.613515	Slc25a25
GO_MF_m	GO:00469	retinoid X	1/690	22/23049	0.487762	0.651217	0.613515	Vdr
GO_MF_m	GO:003162	ubiquitin p	10/690	322/23049	0.498046	0.660251	0.622026	Anapc2/Au
GO_MF_m	GO:007234	modified a	3/690	89/23049	0.5004	0.660251	0.622026	Dpep1/Fol
GO_MF_m	GO:000554	phospholi	2/690	56/23049	0.502873	0.660251	0.622026	Abcb4/Tnf
GO_MF_m	GO:00169	oxidoredu	2/690	56/23049	0.502873	0.660251	0.622026	Aox3/Pdhx
GO_MF_m	GO:000101	transcripti	1/690	23/23049	0.503111	0.660251	0.622026	Vdr
GO_MF_m	GO:00041	metallocar	1/690	23/23049	0.503111	0.660251	0.622026	Cpa2
GO_MF_m	GO:000817	O-methylt	1/690	23/23049	0.503111	0.660251	0.622026	Mrm2
GO_MF_m	GO:00081	ferrous iro	1/690	23/23049	0.503111	0.660251	0.622026	Heph
GO_MF_m	GO:00167	hydrolase	1/690	23/23049	0.503111	0.660251	0.622026	Rps3
GO_MF_m	GO:003037	translation	1/690	23/23049	0.503111	0.660251	0.622026	Purb
GO_MF_m	GO:00314	mitogen-a	1/690	23/23049	0.503111	0.660251	0.622026	Map3k11
GO_MF_m	GO:003361	receptor se	1/690	23/23049	0.503111	0.660251	0.622026	Inhba
GO_MF_m	GO:00352	UDP-galac	1/690	23/23049	0.503111	0.660251	0.622026	A4galt
GO_MF_m	GO:00050	Ras guanyl	4/690	124/23049	0.511011	0.668388	0.629692	Itsn1/Ralgp
GO_MF_m	GO:00355	signaling a	2/690	57/23049	0.512318	0.668388	0.629692	Grb2/Grb7
GO_MF_m	GO:000104	core prom	3/690	91/23049	0.515304	0.668388	0.629692	Esr2/Gata1
GO_MF_m	GO:000524	voltage-ga	3/690	91/23049	0.515304	0.668388	0.629692	Kcne1/Kcn
GO_MF_m	GO:00016	G-protein	1/690	24/23049	0.518001	0.668388	0.629692	Ackr2
GO_MF_m	GO:000184	compleme	1/690	24/23049	0.518001	0.668388	0.629692	C3ar1
GO_MF_m	GO:00049	chemokine	1/690	24/23049	0.518001	0.668388	0.629692	Ackr2
GO_MF_m	GO:00199	chemokine	1/690	24/23049	0.518001	0.668388	0.629692	Ackr2
GO_MF_m	GO:003054	receptor in	1/690	24/23049	0.518001	0.668388	0.629692	Ly6g6d
GO_MF_m	GO:00316	G-protein	1/690	24/23049	0.518001	0.668388	0.629692	Gnat1
GO_MF_m	GO:004292	neuropepti	1/690	24/23049	0.518001	0.668388	0.629692	Sstr5
GO_MF_m	GO:00528	phosphati	1/690	24/23049	0.518001	0.668388	0.629692	Mtmr14
GO_MF_m	GO:007041	R-SMAD b	1/690	24/23049	0.518001	0.668388	0.629692	Zeb2
GO_MF_m	GO:00037	steroid hor	2/690	58/23049	0.521644	0.672221	0.633303	Esr2/Vdr
GO_MF_m	GO:00314	chromatin	3/690	92/23049	0.522666	0.672671	0.633727	Gata1/Rela
GO_MF_m	GO:001701	Ras GTPas	12/690	397/23049	0.527578	0.677411	0.638193	Itsn1/Kif16
GO_MF_m	GO:00052	potassium	4/690	127/23049	0.529841	0.677411	0.638193	Kcne1/Kcn
GO_MF_m	GO:01400	modificati	4/690	127/23049	0.529841	0.677411	0.638193	Agap3/Cb
GO_MF_m	GO:001704	Rho GTPas	5/690	161/23049	0.5301	0.677411	0.638193	Itsn1/Map
GO_MF_m	GO:00015	lipopolysa	1/690	25/23049	0.532445	0.677411	0.638193	Sftpa1
GO_MF_m	GO:000167	ATPase act	1/690	25/23049	0.532445	0.677411	0.638193	Atp1b4
GO_MF_m	GO:00162	CoA hydro	1/690	25/23049	0.532445	0.677411	0.638193	Nudt7
GO_MF_m	GO:003517	histone ser	1/690	25/23049	0.532445	0.677411	0.638193	Aurka

GO_MF_m	GO:004696	thyroid hor	1/690	25/23049	0.532445	0.677411	0.638193	Trip12
GO_MF_m	GO:000802	ATP-depen	3/690	94/23049	0.537203	0.68173	0.642262	Brip1/Recq
GO_MF_m	GO:007003	purine NT	3/690	94/23049	0.537203	0.68173	0.642262	Brip1/Recq
GO_MF_m	GO:003645	thiol-depe	3/690	95/23049	0.544377	0.686504	0.646759	Otud6a/Uc
GO_MF_m	GO:010100	ubiquitinyl	3/690	95/23049	0.544377	0.686504	0.646759	Otud6a/Uc
GO_MF_m	GO:000467	AMP-activ	1/690	26/23049	0.546457	0.686504	0.646759	Prkag1
GO_MF_m	GO:000532	neurotrans	1/690	26/23049	0.546457	0.686504	0.646759	Slc1a6
GO_MF_m	GO:001702	TBP-class	1/690	26/23049	0.546457	0.686504	0.646759	Dr1
GO_MF_m	GO:001713	fibroblast	1/690	26/23049	0.546457	0.686504	0.646759	Rps2
GO_MF_m	GO:005153	2 iron, 2 su	1/690	26/23049	0.546457	0.686504	0.646759	Aox3
GO_MF_m	GO:007194	FAD bindin	1/690	26/23049	0.546457	0.686504	0.646759	Coq6
GO_MF_m	GO:000377	motor acti	4/690	130/23049	0.548309	0.687966	0.648136	Cgnl1/Dyn
GO_MF_m	GO:004438	ubiquitin-li	10/690	337/23049	0.556131	0.690567	0.650587	Anapc2/Au
GO_MF_m	GO:000551	collagen bi	2/690	62/23049	0.557733	0.690567	0.650587	Cspg4/Lum
GO_MF_m	GO:007049	repressing	2/690	62/23049	0.557733	0.690567	0.650587	Cbx5/Rela
GO_MF_m	GO:000377	actin bindi	12/690	406/23049	0.559039	0.690567	0.650587	Arc/Cap2/
GO_MF_m	GO:000468	calmodulin	1/690	27/23049	0.56005	0.690567	0.650587	Camk1g
GO_MF_m	GO:000518	neuropepti	1/690	27/23049	0.56005	0.690567	0.650587	Hcrt
GO_MF_m	GO:000525	delayed re	1/690	27/23049	0.56005	0.690567	0.650587	Kcne1
GO_MF_m	GO:000534	organic aci	1/690	27/23049	0.56005	0.690567	0.650587	Slc1a6
GO_MF_m	GO:000806	glutamate	1/690	27/23049	0.56005	0.690567	0.650587	Grm1
GO_MF_m	GO:001709	AU-rich ele	1/690	27/23049	0.56005	0.690567	0.650587	Zfp36l1
GO_MF_m	GO:001970	protein-cy	1/690	27/23049	0.56005	0.690567	0.650587	Zdhhc22
GO_MF_m	GO:001970	protein-cy	1/690	27/23049	0.56005	0.690567	0.650587	Zdhhc22
GO_MF_m	GO:007000	aspartic-ty	1/690	27/23049	0.56005	0.690567	0.650587	Astl
GO_MF_m	GO:190468	peptide tra	1/690	27/23049	0.56005	0.690567	0.650587	Tomm7
GO_MF_m	GO:001900	GDP bindi	2/690	63/23049	0.566447	0.697595	0.657208	Prps2/Rab
GO_MF_m	GO:000823	exopeptida	3/690	99/23049	0.572411	0.700777	0.660206	Cpa2/Dpe
GO_MF_m	GO:000830	structural c	1/690	28/23049	0.573236	0.700777	0.660206	Myom2
GO_MF_m	GO:004353	protein ser	1/690	28/23049	0.573236	0.700777	0.660206	Spry2
GO_MF_m	GO:007181	lipoprotein	1/690	28/23049	0.573236	0.700777	0.660206	Lipc
GO_MF_m	GO:007181	protein-lip	1/690	28/23049	0.573236	0.700777	0.660206	Lipc
GO_MF_m	GO:009960	ligand-gat	1/690	28/23049	0.573236	0.700777	0.660206	Tpcn2
GO_MF_m	GO:005128	NAD bindi	2/690	64/23049	0.575037	0.702121	0.661472	Aox3/Grhp
GO_MF_m	GO:005121	phosphopr	3/690	100/23049	0.57925	0.706403	0.665506	Grb2/Lck/T
GO_MF_m	GO:005153	iron-sulfur	2/690	65/23049	0.583502	0.709476	0.668401	Aox3/Brip1
GO_MF_m	GO:005154	metal clust	2/690	65/23049	0.583502	0.709476	0.668401	Aox3/Brip1
GO_MF_m	GO:000522	calcium act	1/690	29/23049	0.586027	0.709476	0.668401	Catsper2
GO_MF_m	GO:000524	calcium ch	1/690	29/23049	0.586027	0.709476	0.668401	Cabp4
GO_MF_m	GO:000552	insulin-like	1/690	29/23049	0.586027	0.709476	0.668401	Igfbpl1
GO_MF_m	GO:003644	proton-ex	1/690	29/23049	0.586027	0.709476	0.668401	Atp6v1e2
GO_MF_m	GO:000471	non-mem	2/690	66/23049	0.591842	0.714784	0.673402	Grb2/Lck
GO_MF_m	GO:004237	chemokine	2/690	66/23049	0.591842	0.714784	0.673402	Defb33/De
GO_MF_m	GO:001529	solute:cati	3/690	102/23049	0.59272	0.714982	0.673588	Gm5134/Sl
GO_MF_m	GO:007185	neuropepti	1/690	30/23049	0.598435	0.721006	0.679264	Hcrt
GO_MF_m	GO:003027	clathrin bi	2/690	67/23049	0.600056	0.722089	0.680284	Gak/Syt16
GO_MF_m	GO:000550	iron ion bi	5/690	175/23049	0.604289	0.726309	0.68426	Aox3/Cyp1
GO_MF_m	GO:004302	ribonucleo	4/690	140/23049	0.606972	0.727619	0.685494	Cbx5/Gem

GO_MF_m	GO:00198	protein ph	2/690	68/23049	0.608146	0.727619	0.685494	4933415F2
GO_MF_m	GO:00302	protein kin	2/690	68/23049	0.608146	0.727619	0.685494	Gas6/Spry
GO_MF_m	GO:00051	type I inter	1/690	31/23049	0.610472	0.727619	0.685494	Ifna12
GO_MF_m	GO:001641	S-acyltrans	1/690	31/23049	0.610472	0.727619	0.685494	Zdhhc22
GO_MF_m	GO:00305	spectrin bi	1/690	31/23049	0.610472	0.727619	0.685494	Sptan1
GO_MF_m	GO:00432	laminin bin	1/690	31/23049	0.610472	0.727619	0.685494	Lgals3
GO_MF_m	GO:00037	mRNA 3'-	2/690	69/23049	0.61611	0.733437	0.690975	Gemin5/Zf
GO_MF_m	GO:00038	antigen bi	6/690	213/23049	0.61682	0.733437	0.690975	H2-M10.1
GO_MF_m	GO:00168	endonucle	1/690	32/23049	0.622149	0.736271	0.693645	Dnase1
GO_MF_m	GO:004297	retinoic aci	1/690	32/23049	0.622149	0.736271	0.693645	Vdr
GO_MF_m	GO:004301	alpha-tub	1/690	32/23049	0.622149	0.736271	0.693645	Casc1
GO_MF_m	GO:00455	dynein inte	1/690	32/23049	0.622149	0.736271	0.693645	Dynll2
GO_MF_m	GO:00199	cytokine bi	3/690	107/23049	0.625149	0.738947	0.696166	Ackr2/Age
GO_MF_m	GO:00081	UDP-glyco	4/690	144/23049	0.629091	0.740908	0.698013	A4galt/B3
GO_MF_m	GO:000371	transcripti	5/690	180/23049	0.629108	0.740908	0.698013	Cdyl2/Cop
GO_MF_m	GO:00082	G-protein	2/690	71/23049	0.631665	0.740908	0.698013	Htr2c/Olfr
GO_MF_m	GO:00043	glutathion	1/690	33/23049	0.633476	0.740908	0.698013	Gstm6
GO_MF_m	GO:00048	protein ph	1/690	33/23049	0.633476	0.740908	0.698013	4933415F2
GO_MF_m	GO:00051	tumor necr	1/690	33/23049	0.633476	0.740908	0.698013	Traf4
GO_MF_m	GO:00165	peptidase	1/690	33/23049	0.633476	0.740908	0.698013	Bcl10
GO_MF_m	GO:00513	alpha-acti	1/690	33/23049	0.633476	0.740908	0.698013	Myom2
GO_MF_m	GO:00616	ubiquitin-li	1/690	33/23049	0.633476	0.740908	0.698013	Ube2i
GO_MF_m	GO:00197	ubiquitin-li	3/690	109/23049	0.637615	0.744875	0.70175	Otud6a/U
GO_MF_m	GO:00052	structural	2/690	72/23049	0.639256	0.744875	0.70175	Myom2/Tu
GO_MF_m	GO:00090	electron tr	2/690	72/23049	0.639256	0.744875	0.70175	Aox3/Cycs
GO_MF_m	GO:00080	growth fac	4/690	146/23049	0.639847	0.744875	0.70175	Fgf17/Fgf4
GO_MF_m	GO:000521	intracellula	1/690	34/23049	0.644464	0.745045	0.701911	Tpcn2
GO_MF_m	GO:00303	cyclin bind	1/690	34/23049	0.644464	0.745045	0.701911	Gak
GO_MF_m	GO:00360	pre-mRNA	1/690	34/23049	0.644464	0.745045	0.701911	Snrpc
GO_MF_m	GO:00703	aromatase	1/690	34/23049	0.644464	0.745045	0.701911	Cyp1a2
GO_MF_m	GO:00705	adenylyltra	1/690	34/23049	0.644464	0.745045	0.701911	Oas2
GO_MF_m	GO:009771	disordered	1/690	34/23049	0.644464	0.745045	0.701911	Rrm1
GO_MF_m	GO:00011	transcripti	1/690	35/23049	0.655123	0.753882	0.710236	Vdr
GO_MF_m	GO:00083	arachidoni	1/690	35/23049	0.655123	0.753882	0.710236	Cyp2a22
GO_MF_m	GO:00330	bitter taste	1/690	35/23049	0.655123	0.753882	0.710236	Tas2r143
GO_MF_m	GO:00517	protein ph	1/690	35/23049	0.655123	0.753882	0.710236	Cacna1b
GO_MF_m	GO:00051	cytokine a	6/690	222/23049	0.656428	0.754515	0.710832	Ifna12/Il13
GO_MF_m	GO:00037	peptidyl-p	1/690	36/23049	0.665463	0.758672	0.714749	Ppid
GO_MF_m	GO:00168	carboxy-ly	1/690	36/23049	0.665463	0.758672	0.714749	Acmsd
GO_MF_m	GO:001921	phosphata	1/690	36/23049	0.665463	0.758672	0.714749	4933415F2
GO_MF_m	GO:003517	histone kin	1/690	36/23049	0.665463	0.758672	0.714749	Aurka
GO_MF_m	GO:00708	E-box bin	1/690	36/23049	0.665463	0.758672	0.714749	Max
GO_MF_m	GO:00010	RNA poly	4/690	151/23049	0.665834	0.758672	0.714749	Gata1/Ldb
GO_MF_m	GO:001661	oxidoredu	4/690	151/23049	0.665834	0.758672	0.714749	Akr1d1/Ak
GO_MF_m	GO:001507	proton tra	3/690	114/23049	0.667495	0.758672	0.714749	Atp5c1/At
GO_MF_m	GO:00305	neurotrans	3/690	114/23049	0.667495	0.758672	0.714749	Grm1/Htr2
GO_MF_m	GO:00037	double-str	2/690	76/23049	0.66839	0.758672	0.714749	Dus2/Oas2
GO_MF_m	GO:00152	antiporter	2/690	76/23049	0.66839	0.758672	0.714749	Slc8a1/Slc

GO_MF_m	GO:000097	RNA polym	1/690	37/23049	0.675494	0.76327	0.719081	Gata1
GO_MF_m	GO:001640	palmitoyltr	1/690	37/23049	0.675494	0.76327	0.719081	Zdhhc22
GO_MF_m	GO:003136	translation	1/690	37/23049	0.675494	0.76327	0.719081	Tbl2
GO_MF_m	GO:004216	SH2 domai	1/690	37/23049	0.675494	0.76327	0.719081	Lck
GO_MF_m	GO:000856	protein tra	2/690	78/23049	0.682229	0.768188	0.723714	Mlc1/Tomr
GO_MF_m	GO:000510	frizzled bin	1/690	38/23049	0.685224	0.768188	0.723714	Ror2
GO_MF_m	GO:000839	arachidoni	1/690	38/23049	0.685224	0.768188	0.723714	Cyp2a22
GO_MF_m	GO:001685	cis-trans is	1/690	38/23049	0.685224	0.768188	0.723714	Ppid
GO_MF_m	GO:005153	4 iron, 4 su	1/690	38/23049	0.685224	0.768188	0.723714	Brip1
GO_MF_m	GO:006059	ATPase reg	1/690	38/23049	0.685224	0.768188	0.723714	Atp1b4
GO_MF_m	GO:190150	carbohydra	1/690	38/23049	0.685224	0.768188	0.723714	Slc25a25
GO_MF_m	GO:001920	phosphata	2/690	79/23049	0.68897	0.769799	0.725231	4933415F2
GO_MF_m	GO:004633	SMAD binc	2/690	79/23049	0.68897	0.769799	0.725231	Purb/Zeb2
GO_MF_m	GO:007040	ammonium	2/690	79/23049	0.68897	0.769799	0.725231	Apoa4/Htr
GO_MF_m	GO:000418	carboxype	1/690	39/23049	0.694663	0.771167	0.72652	Cpa2
GO_MF_m	GO:001593	nucleobase	1/690	39/23049	0.694663	0.771167	0.72652	Slc25a25
GO_MF_m	GO:001622	steroid deh	1/690	39/23049	0.694663	0.771167	0.72652	Akr1d1
GO_MF_m	GO:004418	protein bin	1/690	39/23049	0.694663	0.771167	0.72652	Pdcl3
GO_MF_m	GO:000104	core prom	4/690	157/23049	0.695289	0.771167	0.72652	Esr2/Gata1
GO_MF_m	GO:000484	thiol-depe	2/690	80/23049	0.695592	0.771167	0.72652	Otud6a/Uc
GO_MF_m	GO:003802	cargo rece	2/690	80/23049	0.695592	0.771167	0.72652	Ackr2/Folr
GO_MF_m	GO:006163	ubiquitin p	6/690	233/23049	0.701254	0.776583	0.731623	Anapc2/Ne
GO_MF_m	GO:002283	ion gated	8/690	307/23049	0.703306	0.776842	0.731867	Cacna1b/C
GO_MF_m	GO:000417	aminopept	1/690	40/23049	0.703819	0.776842	0.731867	Dpep1
GO_MF_m	GO:001706	snRNA bin	1/690	40/23049	0.703819	0.776842	0.731867	Gemin5
GO_MF_m	GO:000813	translation	2/690	82/23049	0.708487	0.781133	0.735909	Eif3a/Eif3e
GO_MF_m	GO:000852	taste recep	1/690	41/23049	0.712701	0.782015	0.736741	Tas2r143
GO_MF_m	GO:004848	beta-tubul	1/690	41/23049	0.712701	0.782015	0.736741	Casc1
GO_MF_m	GO:009896	postsynapt	1/690	41/23049	0.712701	0.782015	0.736741	Grm1
GO_MF_m	GO:002283	gated char	8/690	310/23049	0.71338	0.782015	0.736741	Cacna1b/C
GO_MF_m	GO:000808	phosphoric	2/690	83/23049	0.714762	0.782015	0.736741	Gdpd1/Gd
GO_MF_m	GO:001681	hydrolase	2/690	83/23049	0.714762	0.782015	0.736741	Aga/Klk1b
GO_MF_m	GO:003294	protein-co	2/690	83/23049	0.714762	0.782015	0.736741	Itsn1/Sept1
GO_MF_m	GO:006165	ubiquitin-li	6/690	237/23049	0.716542	0.78241	0.737113	Anapc2/Ne
GO_MF_m	GO:001563	tubulin bin	8/690	311/23049	0.716688	0.78241	0.737113	Casc1/Kif1
GO_MF_m	GO:000460	peroxidase	1/690	43/23049	0.729675	0.794853	0.748835	Mpo
GO_MF_m	GO:004439	ubiquitin-li	1/690	43/23049	0.729675	0.794853	0.748835	Rps3
GO_MF_m	GO:004748	protein N-	3/690	126/23049	0.731735	0.796229	0.750132	Eif3e/Rela/
GO_MF_m	GO:000525	anion chan	2/690	86/23049	0.732908	0.796639	0.750518	Lrrc8c/Slc1
GO_MF_m	GO:000504	scavenger	1/690	44/23049	0.737782	0.800198	0.753871	Ackr2
GO_MF_m	GO:001662	oxidoreduc	1/690	44/23049	0.737782	0.800198	0.753871	Pdhx
GO_MF_m	GO:005066	coenzyme	7/690	281/23049	0.73995	0.80168	0.755267	Aox3/Coq
GO_MF_m	GO:000808	N-acetyltra	2/690	88/23049	0.744453	0.805685	0.75904	Nat8f1/Na
GO_MF_m	GO:000837	acetylgalac	1/690	46/23049	0.753276	0.813473	0.766378	B3gnt5
GO_MF_m	GO:003033	estrogen re	1/690	46/23049	0.753276	0.813473	0.766378	Grm1
GO_MF_m	GO:000122	transcriptic	1/690	47/23049	0.760677	0.819695	0.772239	Nfatc1
GO_MF_m	GO:001668	oxidoreduc	1/690	47/23049	0.760677	0.819695	0.772239	Mpo
GO_MF_m	GO:001984	vitamin bin	3/690	133/23049	0.764459	0.822884	0.775243	Folr1/Kynu

GO_MF_m	GO:00178	phosphatic	1/690	48/23049	0.767856	0.824765	0.777015	Gas6
GO_MF_m	GO:00315	polyubiqui	1/690	48/23049	0.767856	0.824765	0.777015	Agap3
GO_MF_m	GO:00489	cytokine re	2/690	93/23049	0.771456	0.827742	0.77982	Ackr2/Ifngr
GO_MF_m	GO:001661	oxidoreduc	3/690	135/23049	0.773192	0.828716	0.780738	Akr1d1/Ak
GO_MF_m	GO:001687	ligase activ	4/690	176/23049	0.776099	0.830942	0.782834	Dalrd3/Ear
GO_MF_m	GO:005101	actin filame	4/690	177/23049	0.77984	0.834053	0.785766	Ctnna1/My
GO_MF_m	GO:005101	protein kin	1/690	50/23049	0.781576	0.835017	0.786674	Rps3
GO_MF_m	GO:00051	transformir	1/690	51/23049	0.788129	0.839328	0.790735	Inhba
GO_MF_m	GO:000554	calcium-de	1/690	51/23049	0.788129	0.839328	0.790735	Syt16
GO_MF_m	GO:003017	pyridoxal p	1/690	51/23049	0.788129	0.839328	0.790735	Kynu
GO_MF_m	GO:007027	vitamin B6	1/690	52/23049	0.794485	0.845197	0.796265	Kynu
GO_MF_m	GO:00165	pheromon	2/690	99/23049	0.800545	0.849047	0.799892	Vmn1r43/V
GO_MF_m	GO:000452	endoribon	1/690	53/23049	0.800652	0.849047	0.799892	Rnase1
GO_MF_m	GO:00168	carbon-car	1/690	53/23049	0.800652	0.849047	0.799892	Acmsd
GO_MF_m	GO:00990	ligand-gat	2/690	101/23049	0.809487	0.857507	0.807862	Kcnj14/Tpc
GO_MF_m	GO:19029	phosphatic	2/690	102/23049	0.813822	0.861187	0.811329	Kif16b/Phl
GO_MF_m	GO:00352	nuclear ho	3/690	146/23049	0.816577	0.862936	0.812977	Grm1/Trip
GO_MF_m	GO:000551	calmodulin	4/690	188/23049	0.817778	0.862936	0.812977	Camk1g/Sl
GO_MF_m	GO:00166	oxidoreduc	1/690	56/23049	0.818064	0.862936	0.812977	Srxn1
GO_MF_m	GO:001641	N-acyltran	2/690	105/23049	0.826304	0.87071	0.8203	Nat8f1/Na
GO_MF_m	GO:004302	ribosome b	1/690	58/23049	0.82882	0.872442	0.821932	Gemin5
GO_MF_m	GO:00050	guanyl-nu	4/690	192/23049	0.830173	0.872948	0.822409	Itsn1/Ralg
GO_MF_m	GO:00352	glutamate	1/690	60/23049	0.838941	0.880315	0.82935	Myl12a
GO_MF_m	GO:00421	neurotrans	1/690	60/23049	0.838941	0.880315	0.82935	Htr2c
GO_MF_m	GO:00164	acetyltrans	2/690	109/23049	0.841773	0.882362	0.831278	Nat8f1/Na
GO_MF_m	GO:000472	protein ser	1/690	61/23049	0.843775	0.882609	0.831511	Lck
GO_MF_m	GO:00050	protein kin	1/690	61/23049	0.843775	0.882609	0.831511	Dsp
GO_MF_m	GO:00167	transferase	1/690	63/23049	0.853012	0.89134	0.839736	Gstm6
GO_MF_m	GO:00303	ligand-dep	1/690	64/23049	0.857425	0.895015	0.843199	Vdr
GO_MF_m	GO:00016	G-protein	6/690	286/23049	0.860549	0.89734	0.845388	Defb33/De
GO_MF_m	GO:00431	ubiquitin b	1/690	67/23049	0.869884	0.906129	0.853669	Uchl3
GO_MF_m	GO:000372	RNA helica	1/690	68/23049	0.87379	0.907363	0.854831	Ythdc2
GO_MF_m	GO:00040	ATP-deper	1/690	68/23049	0.87379	0.907363	0.854831	Ythdc2
GO_MF_m	GO:001702	myosin bin	1/690	68/23049	0.87379	0.907363	0.854831	Npc1l1
GO_MF_m	GO:00048	serine-typ	2/690	119/23049	0.875124	0.907805	0.855248	Pzp/Serpin
GO_MF_m	GO:001674	transferase	5/690	252/23049	0.8763	0.908083	0.85551	Nat8f1/Lip
GO_MF_m	GO:00081	RNA-depe	1/690	69/23049	0.87758	0.908468	0.855872	Ythdc2
GO_MF_m	GO:00314	carboxylic	4/690	214/23049	0.886387	0.916636	0.863568	Folr1/Grhp
GO_MF_m	GO:000554	phosphatic	1/690	73/23049	0.891635	0.920426	0.867138	Phlda3
GO_MF_m	GO:005142	hormone r	3/690	172/23049	0.891893	0.920426	0.867138	Grm1/Trip
GO_MF_m	GO:00052	chloride ch	1/690	74/23049	0.894889	0.922378	0.868978	Slc1a4
GO_MF_m	GO:000371	transcriptic	10/690	467/23049	0.895629	0.922378	0.868978	Bcl10/Cdyl
GO_MF_m	GO:004317	organic aci	4/690	219/23049	0.896637	0.922466	0.86906	Folr1/Grhp
GO_MF_m	GO:00332	monocarbo	1/690	75/23049	0.898046	0.922966	0.869531	Vdr
GO_MF_m	GO:00082	cysteine-ty	3/690	182/23049	0.912546	0.935622	0.881454	Otud6a/Uc
GO_MF_m	GO:001527	ligand-gat	2/690	134/23049	0.913167	0.935622	0.881454	Kcnj14/Tpc
GO_MF_m	GO:00228	ligand-gat	2/690	134/23049	0.913167	0.935622	0.881454	Kcnj14/Tpc
GO_MF_m	GO:001681	hydrolase	2/690	136/23049	0.917329	0.938924	0.884565	Aga/Klk1b

GO_MF_m	GO:003525	steroid hor	1/690	84/23049	0.92252	0.943272	0.888661	Grm1
GO_MF_m	GO:001665	oxidoreduc	1/690	86/23049	0.927106	0.946026	0.891256	Duox2
GO_MF_m	GO:003218	ubiquitin-li	1/690	86/23049	0.927106	0.946026	0.891256	Uchl3
GO_MF_m	GO:001510	inorganic a	2/690	142/23049	0.928717	0.94633	0.891542	Lrrc8c/Slc1
GO_MF_m	GO:001510	chloride tra	1/690	87/23049	0.929296	0.94633	0.891542	Slc1a4
GO_MF_m	GO:003498	immunogl	2/690	146/23049	0.935468	0.948763	0.893835	Ighv9-4/L
GO_MF_m	GO:000555	pheromon	1/690	90/23049	0.935481	0.948763	0.893835	Vmn1r9
GO_MF_m	GO:005108	unfolded p	1/690	90/23049	0.935481	0.948763	0.893835	Srsf10
GO_MF_m	GO:005111	ATPase bin	1/690	90/23049	0.935481	0.948763	0.893835	Lck
GO_MF_m	GO:001685	isomerase	2/690	147/23049	0.937058	0.949401	0.894435	Gm960/Pp
GO_MF_m	GO:000369	single-stra	1/690	102/23049	0.955267	0.96687	0.910893	Purb
GO_MF_m	GO:001674	transferase	3/690	221/23049	0.963146	0.973859	0.917477	Nat8f1/Na
GO_MF_m	GO:000517	integrin bi	1/690	112/23049	0.967039	0.976807	0.920255	Tnn
GO_MF_m	GO:003016	PDZ doma	1/690	118/23049	0.972559	0.981391	0.924574	Lzts3
GO_MF_m	GO:000417	endopepti	7/690	438/23049	0.978187	0.986017	0.928932	Adam19/A
GO_MF_m	GO:000425	serine-typ	2/690	191/23049	0.979587	0.986017	0.928932	F12/Klk1b1
GO_MF_m	GO:000484	ubiquitin-p	7/690	443/23049	0.980101	0.986017	0.928932	Anapc2/N
GO_MF_m	GO:000371	transcripti	3/690	262/23049	0.985885	0.990266	0.932934	Bcl10/Sox1
GO_MF_m	GO:001978	ubiquitin-li	7/690	463/23049	0.986305	0.990266	0.932934	Anapc2/N
GO_MF_m	GO:000823	serine-typ	2/690	219/23049	0.990255	0.993235	0.935732	F12/Klk1b1
GO_MF_m	GO:001717	serine hydr	2/690	224/23049	0.991473	0.99346	0.935944	F12/Klk1b1
GO_MF_m	GO:000107	transcripti	1/690	193/23049	0.997235	0.998234	0.940441	Vdr
GO_MF_m	GO:000554	odorant bi	4/690	463/23049	0.999576	0.999576	0.941706	Olfr301/Ol
KEGG_Path	mmu01200	Carbon m	28/1025	120/8294	0.00057	0.178866	0.175089	11532/937
KEGG_Path	mmu01230	Biosynthes	19/1025	78/8294	0.002484	0.310803	0.304239	109652/11
KEGG_Path	mmu00640	Propanoat	10/1025	31/8294	0.003054	0.310803	0.304239	268860/38
KEGG_Path	mmu00410	beta-Alani	10/1025	32/8294	0.003959	0.310803	0.304239	268860/56
KEGG_Path	mmu04146	Peroxisom	19/1025	84/8294	0.005962	0.358229	0.350663	19299/140
KEGG_Path	mmu00350	Tyrosine m	11/1025	40/8294	0.007525	0.358229	0.350663	11522/115
KEGG_Path	mmu03410	Base excisi	10/1025	35/8294	0.007986	0.358229	0.350663	14156/168
KEGG_Path	mmu04110	Cell cycle	24/1025	123/8294	0.014715	0.520085	0.509101	245000/12
KEGG_Path	mmu00561	Glycerolipi	14/1025	61/8294	0.014907	0.520085	0.509101	67512/678
KEGG_Path	mmu00220	Arginine bi	6/1025	19/8294	0.022968	0.655629	0.641782	109652/11
KEGG_Path	mmu01210	2-Oxocarb	6/1025	19/8294	0.022968	0.655629	0.641782	109652/12
KEGG_Path	mmu05206	MicroRNA	46/1025	281/8294	0.026691	0.668004	0.653896	18671/124
KEGG_Path	mmu00250	Alanine, as	9/1025	37/8294	0.03273	0.668004	0.653896	268860/11
KEGG_Path	mmu04330	Notch sign	11/1025	49/8294	0.033821	0.668004	0.653896	226548/20
KEGG_Path	mmu05204	Chemical c	18/1025	94/8294	0.037543	0.668004	0.653896	11522/115
KEGG_Path	mmu00280	Valine, leu	12/1025	56/8294	0.038124	0.668004	0.653896	268860/56
KEGG_Path	mmu00330	Arginine ar	11/1025	50/8294	0.038702	0.668004	0.653896	75986/212
KEGG_Path	mmu00650	Butanoate	7/1025	27/8294	0.041411	0.668004	0.653896	268860/27
KEGG_Path	mmu00590	Arachidoni	17/1025	89/8294	0.04332	0.668004	0.653896	11684/116
KEGG_Path	mmu04931	Insulin resi	20/1025	109/8294	0.044059	0.668004	0.653896	12491/208
KEGG_Path	mmu04623	Cytosolic D	13/1025	64/8294	0.046803	0.668004	0.653896	20303/159
KEGG_Path	mmu05230	Central car	13/1025	64/8294	0.046803	0.668004	0.653896	14660/168
KEGG_Path	mmu03050	Proteasom	10/1025	46/8294	0.050971	0.695862	0.681165	15978/191
KEGG_Path	mmu04726	Serotoner	23/1025	132/8294	0.054392	0.707723	0.692776	11684/116
KEGG_Path	mmu05166	Human T-	39/1025	246/8294	0.059158	0.707723	0.692776	104110/24

KEGG_Path	mmu04725	Cholinergic	20/1025	113/8294	0.060653	0.707723	0.692776	11423/104
KEGG_Path	mmu04514	Cell adhesi	28/1025	169/8294	0.063301	0.707723	0.692776	54725/125
KEGG_Path	mmu00010	Glycolysis /	13/1025	67/8294	0.06412	0.707723	0.692776	11522/115
KEGG_Path	mmu04122	Sulfur relay	3/1025	8/8294	0.065363	0.707723	0.692776	17434/221
KEGG_Path	mmu04922	Glucagon s	18/1025	102/8294	0.074045	0.753844	0.737924	12322/208
KEGG_Path	mmu03420	Nucleotide	9/1025	43/8294	0.076209	0.753844	0.737924	12572/993
KEGG_Path	mmu00471	D-Glutamin	2/1025	4/8294	0.077194	0.753844	0.737924	217830/14
KEGG_Path	mmu00563	Glycosylph	6/1025	25/8294	0.079226	0.753844	0.737924	241062/55
KEGG_Path	mmu04371	Apelin sign	23/1025	139/8294	0.086967	0.76628	0.750097	11475/104
KEGG_Path	mmu00920	Sulfur meta	3/1025	9/8294	0.089297	0.76628	0.750097	23827/211
KEGG_Path	mmu05330	Allograft re	12/1025	64/8294	0.09038	0.76628	0.750097	12519/697
KEGG_Path	mmu04066	HIF-1 signa	18/1025	105/8294	0.092375	0.76628	0.750097	12322/125
KEGG_Path	mmu00790	Folate bios	6/1025	26/8294	0.092735	0.76628	0.750097	67861/116
KEGG_Path	mmu05032	Morphine a	16/1025	92/8294	0.097885	0.788101	0.771457	104110/11
KEGG_Path	mmu04141	Protein pro	26/1025	163/8294	0.10172	0.789155	0.772489	27061/123
KEGG_Path	mmu05320	Autoimmun	14/1025	79/8294	0.103269	0.789155	0.772489	12519/124
KEGG_Path	mmu00260	Glycine, ser	8/1025	40/8294	0.112835	0.789155	0.772489	11754/121
KEGG_Path	mmu04934	Cushing sy	25/1025	158/8294	0.114514	0.789155	0.772489	104110/23
KEGG_Path	mmu05203	Viral carcin	35/1025	231/8294	0.115489	0.789155	0.772489	12370/124
KEGG_Path	mmu05170	Human imm	36/1025	239/8294	0.118733	0.789155	0.772489	108012/24
KEGG_Path	mmu04971	Gastric acid	13/1025	74/8294	0.119465	0.789155	0.772489	104110/11
KEGG_Path	mmu04014	Ras signalin	35/1025	233/8294	0.125958	0.789155	0.772489	11352/723
KEGG_Path	mmu03430	Mismatch r	5/1025	22/8294	0.126398	0.789155	0.772489	17686/185
KEGG_Path	mmu05163	Human cyt	38/1025	256/8294	0.130094	0.789155	0.772489	104110/12
KEGG_Path	mmu05030	Cocaine ad	9/1025	48/8294	0.131064	0.789155	0.772489	12568/208
KEGG_Path	mmu03030	DNA replic	7/1025	35/8294	0.13307	0.789155	0.772489	14156/185
KEGG_Path	mmu04727	GABAergic	15/1025	90/8294	0.139247	0.789155	0.772489	268860/10
KEGG_Path	mmu00072	Synthesis a	3/1025	11/8294	0.145834	0.789155	0.772489	71911/697
KEGG_Path	mmu00130	Ubiquinone	3/1025	11/8294	0.145834	0.789155	0.772489	230027/18
KEGG_Path	mmu04080	Neuroactiv	42/1025	289/8294	0.146638	0.789155	0.772489	11517/115
KEGG_Path	mmu05169	Epstein-Ba	34/1025	230/8294	0.15131	0.789155	0.772489	12317/123
KEGG_Path	mmu04728	Dopaminer	21/1025	135/8294	0.156874	0.789155	0.772489	11865/123
KEGG_Path	mmu00071	Fatty acid c	9/1025	50/8294	0.1576	0.789155	0.772489	14081/115
KEGG_Path	mmu00270	Cysteine ar	9/1025	50/8294	0.1576	0.789155	0.772489	74340/563
KEGG_Path	mmu01523	Antifolate r	6/1025	30/8294	0.157857	0.789155	0.772489	76408/116
KEGG_Path	mmu05222	Small cell lu	15/1025	92/8294	0.158745	0.789155	0.772489	12447/124
KEGG_Path	mmu01212	Fatty acid r	10/1025	57/8294	0.159611	0.789155	0.772489	14081/128
KEGG_Path	mmu04970	Salivary sec	13/1025	78/8294	0.160534	0.789155	0.772489	104110/11
KEGG_Path	mmu04115	p53 signali	12/1025	71/8294	0.160847	0.789155	0.772489	71361/245
KEGG_Path	mmu00340	Histidine m	5/1025	24/8294	0.166837	0.792292	0.775559	56847/621
KEGG_Path	mmu03022	Basal trans	8/1025	44/8294	0.169345	0.792292	0.775559	12572/836
KEGG_Path	mmu03460	Fanconi an	9/1025	51/8294	0.171771	0.792292	0.775559	245000/12
KEGG_Path	mmu04010	MAPK sign	42/1025	294/8294	0.174777	0.792292	0.775559	12296/122
KEGG_Path	mmu05205	Proteoglyc	30/1025	204/8294	0.176624	0.792292	0.775559	12322/123
KEGG_Path	mmu00630	Glyoxylate	6/1025	31/8294	0.176626	0.792292	0.775559	104174/23
KEGG_Path	mmu04918	Thyroid ho	12/1025	73/8294	0.18501	0.807964	0.7909	104110/11
KEGG_Path	mmu00980	Metabolism	11/1025	66/8294	0.186141	0.807964	0.7909	11522/115
KEGG_Path	mmu05416	Viral myoca	14/1025	88/8294	0.193089	0.807964	0.7909	11352/123

KEGG_Path	mmu0002	Citrate cycl	6/1025	32/8294	0.196244	0.807964	0.7909	269951/67
KEGG_Path	mmu0104	Biosynthes	6/1025	32/8294	0.196244	0.807964	0.7909	26897/171
KEGG_Path	mmu0345	Non-homo	3/1025	13/8294	0.210822	0.807964	0.7909	14156/566
KEGG_Path	mmu0421	Cellular ser	27/1025	186/8294	0.211253	0.807964	0.7909	245000/12
KEGG_Path	mmu0098	Drug meta	11/1025	68/8294	0.21341	0.807964	0.7909	11522/115
KEGG_Path	mmu0462	RIG-I-like	11/1025	68/8294	0.21341	0.807964	0.7909	12370/159
KEGG_Path	mmu0501	Huntingto	28/1025	194/8294	0.215126	0.807964	0.7909	11946/280
KEGG_Path	mmu0413	SNARE inte	6/1025	33/8294	0.216627	0.807964	0.7909	67474/562
KEGG_Path	mmu0497	Fat digesti	7/1025	40/8294	0.21854	0.807964	0.7909	67512/124
KEGG_Path	mmu0201	ABC transp	8/1025	47/8294	0.218616	0.807964	0.7909	74591/679
KEGG_Path	mmu0301	RNA degra	13/1025	83/8294	0.220602	0.807964	0.7909	12227/788
KEGG_Path	mmu0472	Retrograd	22/1025	150/8294	0.224959	0.807964	0.7909	104110/14
KEGG_Path	mmu0471	Circadian	15/1025	98/8294	0.225066	0.807964	0.7909	104110/11
KEGG_Path	mmu0053	Glycosami	4/1025	20/8294	0.228188	0.807964	0.7909	71797/234
KEGG_Path	mmu0421	Longevity	10/1025	62/8294	0.230874	0.807964	0.7909	104110/20
KEGG_Path	mmu0401	ErbB signal	13/1025	84/8294	0.233635	0.807964	0.7909	11352/123
KEGG_Path	mmu0492	Regulation	9/1025	55/8294	0.23377	0.807964	0.7909	104110/11
KEGG_Path	mmu00601	Glycosphin	5/1025	27/8294	0.23528	0.807964	0.7909	80908/722
KEGG_Path	mmu0344	Homologo	7/1025	41/8294	0.237619	0.807964	0.7909	12144/107
KEGG_Path	mmu04151	PI3K-Akt si	49/1025	358/8294	0.239301	0.807964	0.7909	12447/124
KEGG_Path	mmu0494	Type I diab	11/1025	70/8294	0.242222	0.809123	0.792035	12519/697
KEGG_Path	mmu0053	Glycosami	3/1025	14/8294	0.245336	0.810901	0.793775	57370/536
KEGG_Path	mmu0426	Cardiac m	12/1025	78/8294	0.252018	0.813378	0.7962	11932/122
KEGG_Path	mmu0497	Cholestero	8/1025	49/8294	0.254098	0.813378	0.7962	30924/124
KEGG_Path	mmu0514	Toxoplasm	16/1025	108/8294	0.256186	0.813378	0.7962	11689/123
KEGG_Path	mmu00531	Glycosami	4/1025	21/8294	0.256447	0.813378	0.7962	11881/509
KEGG_Path	mmu0481	Regulation	30/1025	215/8294	0.264161	0.829465	0.811947	54126/129
KEGG_Path	mmu0467	Intestinal i	7/1025	43/8294	0.27725	0.839257	0.821532	56838/125
KEGG_Path	mmu0533	Graft-vers	10/1025	65/8294	0.27851	0.839257	0.821532	12519/697
KEGG_Path	mmu0051	Other type	4/1025	22/8294	0.285347	0.839257	0.821532	57370/108
KEGG_Path	mmu0497	Pancreatic	15/1025	103/8294	0.287841	0.839257	0.821532	104110/54
KEGG_Path	mmu0436	Axon guid	25/1025	180/8294	0.295863	0.839257	0.821532	12322/125
KEGG_Path	mmu0434	Hedgehog	7/1025	44/8294	0.297664	0.839257	0.821532	27373/269
KEGG_Path	mmu0056	Glyceroph	14/1025	97/8294	0.308976	0.839257	0.821532	11423/675
KEGG_Path	mmu0471	Circadian	5/1025	30/8294	0.309918	0.839257	0.821532	11865/127
KEGG_Path	mmu0036	Phenylalan	4/1025	23/8294	0.31468	0.839257	0.821532	56847/621
KEGG_Path	mmu0090	Terpenoid	4/1025	23/8294	0.31468	0.839257	0.821532	14272/153
KEGG_Path	mmu0012	Primary bil	3/1025	16/8294	0.316332	0.839257	0.821532	13116/154
KEGG_Path	mmu0491	Progestero	13/1025	90/8294	0.31736	0.839257	0.821532	104110/12
KEGG_Path	mmu0497	Mineral ab	7/1025	45/8294	0.318385	0.839257	0.821532	11932/177
KEGG_Path	mmu0402	cAMP sign	27/1025	198/8294	0.321114	0.839257	0.821532	104110/11
KEGG_Path	mmu0501	Parkinson	20/1025	144/8294	0.322713	0.839257	0.821532	11946/280
KEGG_Path	mmu0520	Transcripti	25/1025	183/8294	0.32634	0.839257	0.821532	12427/125
KEGG_Path	mmu0062	Pyruvate m	6/1025	38/8294	0.326844	0.839257	0.821532	66204/567
KEGG_Path	mmu0078	Biotin met	1/1025	3/8294	0.326853	0.839257	0.821532	110948
KEGG_Path	mmu0461	Antigen pr	13/1025	91/8294	0.332031	0.839257	0.821532	12317/123
KEGG_Path	mmu0516	Herpes sim	29/1025	215/8294	0.335106	0.839257	0.821532	11865/123
KEGG_Path	mmu04071	Sphingolip	17/1025	122/8294	0.336296	0.839257	0.821532	11539/544

KEGG_Path	mmu04620	Toll-like re	14/1025	99/8294	0.337096	0.839257	0.821532	12370/203
KEGG_Path	mmu04144	Endocytosi	36/1025	270/8294	0.337504	0.839257	0.821532	11844/211
KEGG_Path	mmu04977	Vitamin dig	4/1025	24/8294	0.344248	0.839257	0.821532	14603/670
KEGG_Path	mmu04916	Melanoger	14/1025	100/8294	0.351361	0.839257	0.821532	104110/12
KEGG_Path	mmu00450	Selenocom	3/1025	17/8294	0.352094	0.839257	0.821532	214580/10
KEGG_Path	mmu03320	PPAR signa	12/1025	85/8294	0.357249	0.839257	0.821532	14081/124
KEGG_Path	mmu04350	TGF-beta s	12/1025	85/8294	0.357249	0.839257	0.821532	11705/269
KEGG_Path	mmu04911	Insulin secr	12/1025	85/8294	0.357249	0.839257	0.821532	104110/11
KEGG_Path	mmu04261	Adrenergic	20/1025	147/8294	0.357904	0.839257	0.821532	104110/11
KEGG_Path	mmu00030	Pentose ph	5/1025	32/8294	0.361348	0.839257	0.821532	232449/23
KEGG_Path	mmu00062	Fatty acid e	5/1025	32/8294	0.361348	0.839257	0.821532	26897/171
KEGG_Path	mmu05310	Asthma	4/1025	25/8294	0.373869	0.839257	0.821532	15000/149
KEGG_Path	mmu04920	Adipocytok	10/1025	71/8294	0.38047	0.839257	0.821532	14081/684
KEGG_Path	mmu00600	Sphingolip	7/1025	48/8294	0.3817	0.839257	0.821532	66190/544
KEGG_Path	mmu00500	Starch and	5/1025	33/8294	0.387191	0.839257	0.821532	14378/149
KEGG_Path	mmu00770	Pantothena	3/1025	18/8294	0.38762	0.839257	0.821532	12036/995
KEGG_Path	mmu04658	Th1 and Th	12/1025	87/8294	0.388683	0.839257	0.821532	54485/150
KEGG_Path	mmu04640	Hematopo	13/1025	95/8294	0.391917	0.839257	0.821532	12478/124
KEGG_Path	mmu05226	Gastric can	20/1025	150/8294	0.393816	0.839257	0.821532	18671/124
KEGG_Path	mmu05219	Bladder car	6/1025	41/8294	0.396302	0.839257	0.821532	12550/125
KEGG_Path	mmu05218	Melanoma	10/1025	72/8294	0.397907	0.839257	0.821532	12550/125
KEGG_Path	mmu01521	EGFR tyros	11/1025	80/8294	0.40148	0.839257	0.821532	13684/138
KEGG_Path	mmu00510	N-Glycan b	7/1025	49/8294	0.402967	0.839257	0.821532	320438/57
KEGG_Path	mmu05144	Malaria	7/1025	49/8294	0.402967	0.839257	0.821532	12491/129
KEGG_Path	mmu04392	Hippo sign	4/1025	26/8294	0.403372	0.839257	0.821532	27373/167
KEGG_Path	mmu04714	Thermoger	30/1025	230/8294	0.404603	0.839257	0.821532	14081/104
KEGG_Path	mmu00290	Valine, leuc	1/1025	4/8294	0.410073	0.839257	0.821532	12036
KEGG_Path	mmu00040	Pentose an	5/1025	34/8294	0.412968	0.839257	0.821532	67861/666
KEGG_Path	mmu05020	Prion disea	5/1025	34/8294	0.412968	0.839257	0.821532	109828/19
KEGG_Path	mmu05162	Measles	18/1025	136/8294	0.415757	0.839257	0.821532	12447/124
KEGG_Path	mmu05160	Hepatitis C	21/1025	160/8294	0.418952	0.839257	0.821532	12370/125
KEGG_Path	mmu05164	Influenza A	22/1025	168/8294	0.419807	0.839257	0.821532	54188/159
KEGG_Path	mmu05414	Dilated car	12/1025	89/8294	0.420335	0.839257	0.821532	104110/12
KEGG_Path	mmu04062	Chemokine	26/1025	200/8294	0.422482	0.839257	0.821532	104110/12
KEGG_Path	mmu05134	Legionellos	8/1025	58/8294	0.427792	0.839257	0.821532	12176/123
KEGG_Path	mmu05167	Kaposi sarc	28/1025	217/8294	0.433697	0.839257	0.821532	12370/127
KEGG_Path	mmu05146	Amoebiasis	14/1025	106/8294	0.4385	0.839257	0.821532	11846/128
KEGG_Path	mmu00051	Fructose ar	5/1025	35/8294	0.438574	0.839257	0.821532	67861/186
KEGG_Path	mmu04724	Glutamater	15/1025	114/8294	0.4394	0.839257	0.821532	104110/14
KEGG_Path	mmu04962	Vasopressi	6/1025	43/8294	0.442548	0.839257	0.821532	11857/208
KEGG_Path	mmu05321	Inflammatc	8/1025	59/8294	0.447452	0.839257	0.821532	15000/149
KEGG_Path	mmu05140	Leishmania	9/1025	67/8294	0.449036	0.839257	0.821532	15000/149
KEGG_Path	mmu04919	Thyroid ho	15/1025	115/8294	0.453477	0.839257	0.821532	11932/133
KEGG_Path	mmu04926	Relaxin sigr	17/1025	131/8294	0.454016	0.839257	0.821532	11475/104
KEGG_Path	mmu04020	Calcium sig	24/1025	187/8294	0.454459	0.839257	0.821532	104110/11
KEGG_Path	mmu05143	African tryp	5/1025	36/8294	0.463914	0.839257	0.821532	100503605
KEGG_Path	mmu05340	Primary im	5/1025	36/8294	0.463914	0.839257	0.821532	12478/161
KEGG_Path	mmu05014	Amyotroph	7/1025	52/8294	0.466385	0.839257	0.821532	14775/147

KEGG_Path	mmu05031	Amphetam	9/1025	68/8294	0.467392	0.839257	0.821532	12322/208
KEGG_Path	mmu05211	Renal cell	9/1025	68/8294	0.467392	0.839257	0.821532	12575/717
KEGG_Path	mmu04114	Oocyte me	15/1025	116/8294	0.467526	0.839257	0.821532	104110/12
KEGG_Path	mmu05133	Pertussis	10/1025	76/8294	0.467623	0.839257	0.821532	12631/146
KEGG_Path	mmu05220	Chronic m	10/1025	76/8294	0.467623	0.839257	0.821532	110279/12
KEGG_Path	mmu05410	Hypertrop	11/1025	84/8294	0.467739	0.839257	0.821532	12296/122
KEGG_Path	mmu01524	Platinum d	10/1025	77/8294	0.484881	0.865071	0.846801	11979/123
KEGG_Path	mmu04152	AMPK sign	16/1025	126/8294	0.494419	0.873056	0.854617	68465/124
KEGG_Path	mmu04668	TNF signali	14/1025	110/8294	0.496594	0.873056	0.854617	12370/202
KEGG_Path	mmu05165	Human pa	45/1025	361/8294	0.499912	0.873056	0.854617	11984/245
KEGG_Path	mmu04540	Gap juncti	11/1025	86/8294	0.500478	0.873056	0.854617	104110/12
KEGG_Path	mmu03020	RNA poly	4/1025	30/8294	0.517392	0.897576	0.878619	69833/664
KEGG_Path	mmu04976	Bile secret	9/1025	71/8294	0.521593	0.89801	0.879045	18671/764
KEGG_Path	mmu04217	Necroptosi	22/1025	177/8294	0.523363	0.89801	0.879045	26926/123
KEGG_Path	mmu00061	Fatty acid	2/1025	14/8294	0.531021	0.903447	0.884367	14081/141
KEGG_Path	mmu00565	Ether lipid	6/1025	47/8294	0.532286	0.903447	0.884367	18606/990
KEGG_Path	mmu05412	Arrhythmo	9/1025	72/8294	0.539263	0.903895	0.884805	12296/122
KEGG_Path	mmu00480	Glutathion	8/1025	64/8294	0.543299	0.903895	0.884805	14630/147
KEGG_Path	mmu05215	Prostate ca	12/1025	97/8294	0.545132	0.903895	0.884805	12447/124
KEGG_Path	mmu00232	Caffeine m	1/1025	6/8294	0.546943	0.903895	0.884805	17961
KEGG_Path	mmu00440	Phosphon	1/1025	6/8294	0.546943	0.903895	0.884805	68671
KEGG_Path	mmu00515	Mannose t	3/1025	23/8294	0.553976	0.904526	0.885423	57370/215
KEGG_Path	mmu04072	Phospholi	18/1025	147/8294	0.55503	0.904526	0.885423	104110/67
KEGG_Path	mmu04211	Longevity	11/1025	90/8294	0.564169	0.904526	0.885423	104110/68
KEGG_Path	mmu04145	Phagosom	22/1025	181/8294	0.568131	0.904526	0.885423	11984/123
KEGG_Path	mmu00730	Thiamine n	2/1025	15/8294	0.569542	0.904526	0.885423	11647/665
KEGG_Path	mmu04910	Insulin sig	17/1025	140/8294	0.570251	0.904526	0.885423	13684/141
KEGG_Path	mmu00052	Galactose	4/1025	32/8294	0.570472	0.904526	0.885423	67861/143
KEGG_Path	mmu04136	Autophagy	4/1025	32/8294	0.570472	0.904526	0.885423	66795/329
KEGG_Path	mmu04630	JAK-STAT	20/1025	165/8294	0.573386	0.904526	0.885423	12575/128
KEGG_Path	mmu04216	Ferroptosis	5/1025	41/8294	0.583869	0.904526	0.885423	14081/146
KEGG_Path	mmu00534	Glycosami	3/1025	24/8294	0.583937	0.904526	0.885423	54616/507
KEGG_Path	mmu04512	ECM-rece	10/1025	83/8294	0.584773	0.904526	0.885423	12491/128
KEGG_Path	mmu05323	Rheumatoi	10/1025	83/8294	0.584773	0.904526	0.885423	11984/202
KEGG_Path	mmu00591	Linoleic aci	6/1025	50/8294	0.595385	0.91639	0.897036	13096/226
KEGG_Path	mmu00190	Oxidative	16/1025	134/8294	0.598808	0.91639	0.897036	11946/280
KEGG_Path	mmu00310	Lysine deg	7/1025	59/8294	0.60561	0.91639	0.897036	56752/937
KEGG_Path	mmu05161	Hepatitis B	17/1025	143/8294	0.607036	0.91639	0.897036	12370/124
KEGG_Path	mmu05418	Fluid shear	17/1025	143/8294	0.607036	0.91639	0.897036	12389/123
KEGG_Path	mmu00592	alpha-Lino	3/1025	25/8294	0.612583	0.92034	0.900903	56473/663
KEGG_Path	mmu00230	Purine met	16/1025	136/8294	0.623467	0.932116	0.91243	104110/11
KEGG_Path	mmu04921	Oxytocin si	18/1025	153/8294	0.626358	0.932116	0.91243	104110/12
KEGG_Path	mmu04060	Cytokine-c	35/1025	296/8294	0.639038	0.932904	0.913201	11705/110
KEGG_Path	mmu05132	Salmonella	9/1025	78/8294	0.639238	0.932904	0.913201	20303/286
KEGG_Path	mmu04625	C-type lect	13/1025	112/8294	0.639377	0.932904	0.913201	12370/202
KEGG_Path	mmu04270	Vascular s	15/1025	129/8294	0.640669	0.932904	0.913201	11475/104
KEGG_Path	mmu04730	Long-term	7/1025	61/8294	0.641743	0.932904	0.913201	666513/14
KEGG_Path	mmu04666	Fc gamma	10/1025	87/8294	0.646219	0.935082	0.915333	211914/12

KEGG_Path	mmu0040	Phenylalan	1/1025	8/8294	0.652081	0.935993	0.916225	14718
KEGG_Path	mmu0414	Autophagy	15/1025	130/8294	0.65281	0.935993	0.916225	66795/329
KEGG_Path	mmu0005	Ascorbate	3/1025	27/8294	0.66578	0.938422	0.918603	56752/222
KEGG_Path	mmu0014	Steroid ho	10/1025	89/8294	0.674984	0.938422	0.918603	13088/130
KEGG_Path	mmu0413	Mitophagy	7/1025	63/8294	0.675879	0.938422	0.918603	12176/135
KEGG_Path	mmu0521	Basal cell c	7/1025	63/8294	0.675879	0.938422	0.918603	12575/165
KEGG_Path	mmu0467	Leukocyte	13/1025	115/8294	0.677631	0.938422	0.918603	12927/127
KEGG_Path	mmu0401	Rap1 signa	24/1025	209/8294	0.683036	0.938422	0.918603	104110/12
KEGG_Path	mmu0453	Tight juncti	19/1025	167/8294	0.686569	0.938422	0.918603	102098/70
KEGG_Path	mmu0521	Thyroid ca	4/1025	37/8294	0.687471	0.938422	0.918603	12550/125
KEGG_Path	mmu0038	Tryptopha	5/1025	46/8294	0.687715	0.938422	0.918603	56752/765
KEGG_Path	mmu0304	Spliceoso	15/1025	133/8294	0.6879	0.938422	0.918603	15381/193
KEGG_Path	mmu0497	Protein dig	10/1025	90/8294	0.688836	0.938422	0.918603	11932/128
KEGG_Path	mmu0493	Non-alcoh	17/1025	151/8294	0.697523	0.938422	0.918603	68465/123
KEGG_Path	mmu0010	Steroid bio	2/1025	19/8294	0.70024	0.938422	0.918603	13081/141
KEGG_Path	mmu0067	One carbo	2/1025	19/8294	0.70024	0.938422	0.918603	270685/20
KEGG_Path	mmu0083	Retinol me	10/1025	91/8294	0.702322	0.938422	0.918603	11522/115
KEGG_Path	mmu0465	IL-17 signa	10/1025	91/8294	0.702322	0.938422	0.918603	12370/202
KEGG_Path	mmu0515	Staphyloco	6/1025	56/8294	0.706486	0.939761	0.919914	11537/142
KEGG_Path	mmu0510	Bacterial in	8/1025	74/8294	0.710025	0.939761	0.919914	12927/123
KEGG_Path	mmu0514	Chagas dis	11/1025	101/8294	0.718469	0.939761	0.919914	12317/123
KEGG_Path	mmu0421	Apoptosis	15/1025	136/8294	0.72086	0.939761	0.919914	26926/123
KEGG_Path	mmu0491	Ovarian ste	6/1025	57/8294	0.72282	0.939761	0.919914	104110/11
KEGG_Path	mmu0521	Pancreatic	8/1025	75/8294	0.724274	0.939761	0.919914	12575/135
KEGG_Path	mmu0521	Glioma	8/1025	75/8294	0.724274	0.939761	0.919914	12322/125
KEGG_Path	mmu0152	Endocrine	10/1025	93/8294	0.728175	0.940935	0.921062	104110/12
KEGG_Path	mmu0522	Breast can	16/1025	147/8294	0.744488	0.955798	0.935612	12575/544
KEGG_Path	mmu0503	Nicotine ac	4/1025	40/8294	0.745914	0.955798	0.935612	14399/144
KEGG_Path	mmu0466	Fc epsilon	7/1025	68/8294	0.751854	0.955798	0.935612	11689/666
KEGG_Path	mmu0492	Cortisol sy	7/1025	68/8294	0.751854	0.955798	0.935612	104110/20
KEGG_Path	mmu0501	Alzheimer	19/1025	175/8294	0.761948	0.961349	0.941045	226548/20
KEGG_Path	mmu0098	Drug meta	9/1025	87/8294	0.763799	0.961349	0.941045	13106/995
KEGG_Path	mmu0522	Acute mye	7/1025	69/8294	0.765405	0.961349	0.941045	12427/110
KEGG_Path	mmu0421	Apoptosis	3/1025	32/8294	0.774841	0.963943	0.943585	51800/123
KEGG_Path	mmu0496	Proximal t	2/1025	22/8294	0.775149	0.963943	0.943585	11932/146
KEGG_Path	mmu0462	NOD-like	18/1025	168/8294	0.77668	0.963943	0.943585	226691/69
KEGG_Path	mmu0492	Parathyroi	11/1025	107/8294	0.785979	0.971643	0.951123	104110/12
KEGG_Path	mmu0523	Choline m	10/1025	99/8294	0.796566	0.980869	0.960154	380921/11
KEGG_Path	mmu0492	Aldosteron	10/1025	100/8294	0.806628	0.98229	0.961545	104110/11
KEGG_Path	mmu0439	Hippo sign	16/1025	154/8294	0.806818	0.98229	0.961545	11705/125
KEGG_Path	mmu0466	T cell rece	10/1025	101/8294	0.816316	0.98229	0.961545	12477/159
KEGG_Path	mmu0076	Nicotinate	3/1025	36/8294	0.839464	0.98229	0.961545	69564/230
KEGG_Path	mmu0097	Aminoacyl	6/1025	66/8294	0.841399	0.98229	0.961545	85305/214
KEGG_Path	mmu0522	Non-small	6/1025	66/8294	0.841399	0.98229	0.961545	12575/135
KEGG_Path	mmu0402	cGMP-PK	17/1025	168/8294	0.844038	0.98229	0.961545	104110/11
KEGG_Path	mmu0515	Tuberculos	18/1025	178/8294	0.850577	0.98229	0.961545	11984/123
KEGG_Path	mmu0431	Wnt signal	16/1025	160/8294	0.850898	0.98229	0.961545	12322/273
KEGG_Path	mmu0301	mRNA sur	9/1025	96/8294	0.854514	0.98229	0.961545	51786/541

KEGG_Path	mmu04142	Lysosome	12/1025	124/8294	0.854775	0.98229	0.961545	108012/10
KEGG_Path	mmu04611	Platelet act	12/1025	124/8294	0.854775	0.98229	0.961545	104110/66
KEGG_Path	mmu00240	Pyrimidine	5/1025	58/8294	0.859991	0.98229	0.961545	99586/647
KEGG_Path	mmu04370	VEGF signa	5/1025	58/8294	0.859991	0.98229	0.961545	26415/187
KEGG_Path	mmu04750	Inflammato	12/1025	125/8294	0.861982	0.98229	0.961545	104110/11
KEGG_Path	mmu05225	Hepatocell	17/1025	171/8294	0.863196	0.98229	0.961545	12575/135
KEGG_Path	mmu04744	Phototrans	2/1025	27/8294	0.863943	0.98229	0.961545	14913/196
KEGG_Path	mmu04950	Maturity or	2/1025	27/8294	0.863943	0.98229	0.961545	15376/153
KEGG_Path	mmu04966	Collecting	2/1025	27/8294	0.863943	0.98229	0.961545	11984/270
KEGG_Path	mmu04960	Aldosteron	3/1025	38/8294	0.865298	0.98229	0.961545	11932/187
KEGG_Path	mmu04742	Taste trans	8/1025	88/8294	0.866811	0.98229	0.961545	104110/12
KEGG_Path	mmu04510	Focal adhe	20/1025	199/8294	0.868273	0.98229	0.961545	12927/123
KEGG_Path	mmu00520	Amino sug	4/1025	49/8294	0.871437	0.98229	0.961545	14584/109
KEGG_Path	mmu00512	Mucin type	2/1025	28/8294	0.8773	0.98229	0.961545	14537/204
KEGG_Path	mmu04550	Signaling p	13/1025	137/8294	0.879827	0.98229	0.961545	26380/154
KEGG_Path	mmu04120	Ubiquitin n	13/1025	139/8294	0.891582	0.98229	0.961545	107995/52
KEGG_Path	mmu00910	Nitrogen m	1/1025	17/8294	0.894056	0.98229	0.961545	80733
KEGG_Path	mmu04520	Adherens j	6/1025	72/8294	0.894797	0.98229	0.961545	12550/192
KEGG_Path	mmu04917	Prolactin si	6/1025	72/8294	0.894797	0.98229	0.961545	16866/264
KEGG_Path	mmu04722	Neurotrop	11/1025	121/8294	0.896625	0.98229	0.961545	11857/123
KEGG_Path	mmu00860	Porphyrin a	3/1025	41/8294	0.897185	0.98229	0.961545	226139/77
KEGG_Path	mmu04659	Th17 cell d	9/1025	102/8294	0.897826	0.98229	0.961545	15000/149
KEGG_Path	mmu04068	FoxO signa	12/1025	132/8294	0.904817	0.986501	0.965667	12176/125
KEGG_Path	mmu05034	Alcoholism	19/1025	199/8294	0.911868	0.987061	0.966215	208677/66
KEGG_Path	mmu04973	Carbohydra	3/1025	43/8294	0.914493	0.987061	0.966215	11932/143
KEGG_Path	mmu04961	Endocrine	4/1025	54/8294	0.91476	0.987061	0.966215	11932/103
KEGG_Path	mmu04721	Synaptic ve	6/1025	77/8294	0.926777	0.989576	0.968676	11984/103
KEGG_Path	mmu03010	Ribosome	16/1025	175/8294	0.927448	0.989576	0.968676	14109/107
KEGG_Path	mmu04720	Long-term	5/1025	67/8294	0.929446	0.989576	0.968676	12322/147
KEGG_Path	mmu05210	Colorectal	7/1025	88/8294	0.930473	0.989576	0.968676	72993/125
KEGG_Path	mmu03013	RNA transp	15/1025	167/8294	0.932848	0.989576	0.968676	68969/660
KEGG_Path	mmu05213	Endometria	4/1025	58/8294	0.93949	0.990159	0.969247	12550/125
KEGG_Path	mmu04912	GnRH signa	7/1025	90/8294	0.939705	0.990159	0.969247	104110/12
KEGG_Path	mmu04662	B cell recep	5/1025	72/8294	0.952974	0.996849	0.975796	12478/666
KEGG_Path	mmu04924	Renin secre	5/1025	72/8294	0.952974	0.996849	0.975796	11517/115
KEGG_Path	mmu04150	mTOR sign	13/1025	155/8294	0.955634	0.996849	0.975796	13684/216
KEGG_Path	mmu03008	Ribosome	9/1025	116/8294	0.958753	0.996849	0.975796	434234/21
KEGG_Path	mmu04650	Natural kill	9/1025	118/8294	0.964073	0.999073	0.977972	242517/15
KEGG_Path	mmu05322	Systemic lu	11/1025	143/8294	0.973372	0.999284	0.978179	109828/12
KEGG_Path	mmu03060	Protein exp	1/1025	28/8294	0.975277	0.999284	0.978179	1E+08
KEGG_Path	mmu04064	NF-kappa	7/1025	104/8294	0.979111	0.999284	0.978179	20303/666
KEGG_Path	mmu04380	Osteoclast	9/1025	128/8294	0.982494	0.999284	0.978179	12311/142
KEGG_Path	mmu04070	Phosphatic	6/1025	98/8294	0.986435	0.999284	0.978179	380921/11
KEGG_Path	mmu04915	Estrogen si	9/1025	133/8294	0.987981	0.999284	0.978179	104110/20
KEGG_Path	mmu04610	Compleme	5/1025	88/8294	0.988335	0.999284	0.978179	109828/11
KEGG_Path	mmu04614	Renin-angi	1/1025	36/8294	0.991431	0.999284	0.978179	75805
KEGG_Path	mmu04933	AGE-RAGE	5/1025	100/8294	0.996204	0.999284	0.978179	12827/264
KEGG_Path	mmu04930	Type II diab	1/1025	48/8294	0.998255	0.999284	0.978179	18710

KEGG_Path	mmu00562	Inositol pho	2/1025	73/8294	0.999284	0.999284	0.978179	269437/10
KEGG_Path	mmu00072	Synthesis a	3/178	11/8294	0.001413	0.312176	0.312176	110460/15
KEGG_Path	mmu00650	Butanoate	3/178	27/8294	0.019477	0.991141	0.991141	110460/15
KEGG_Path	mmu00630	Glyoxylate	3/178	31/8294	0.028128	0.991141	0.991141	110460/11
KEGG_Path	mmu00280	Valine, leuc	4/178	56/8294	0.031717	0.991141	0.991141	110460/15
KEGG_Path	mmu01212	Fatty acid r	4/178	57/8294	0.033559	0.991141	0.991141	107476/11
KEGG_Path	mmu00061	Fatty acid b	2/178	14/8294	0.035188	0.991141	0.991141	107476/50
KEGG_Path	mmu04350	TGF-beta s	5/178	85/8294	0.035616	0.991141	0.991141	68010/121
KEGG_Path	mmu00250	Alanine, as	3/178	37/8294	0.044318	0.991141	0.991141	11564/697
KEGG_Path	mmu00450	Selenocom	2/178	17/8294	0.050437	0.991141	0.991141	229905/21
KEGG_Path	mmu00511	Other glyca	2/178	18/8294	0.05596	0.991141	0.991141	230101/73
KEGG_Path	mmu00860	Porphyrin a	3/178	41/8294	0.057179	0.991141	0.991141	17025/703
KEGG_Path	mmu04141	Protein pro	7/178	163/8294	0.061166	0.991141	0.991141	11911/678
KEGG_Path	mmu04144	Endocytosi	10/178	270/8294	0.065121	0.991141	0.991141	71770/106
KEGG_Path	mmu03013	RNA transp	7/178	167/8294	0.067823	0.991141	0.991141	230861/21
KEGG_Path	mmu00380	Tryptophan	3/178	46/8294	0.075436	0.991141	0.991141	110460/22
KEGG_Path	mmu04721	Synaptic ve	4/178	77/8294	0.083187	0.991141	0.991141	71770/108
KEGG_Path	mmu05202	Transcriptio	7/178	183/8294	0.098651	0.991141	0.991141	68938/126
KEGG_Path	mmu03008	Ribosome b	5/178	116/8294	0.10381	0.991141	0.991141	110816/19
KEGG_Path	mmu04060	Cytokine-c	10/178	296/8294	0.104086	0.991141	0.991141	12159/129
KEGG_Path	mmu04146	Peroxisome	4/178	84/8294	0.106048	0.991141	0.991141	50790/153
KEGG_Path	mmu04392	Hippo sign	2/178	26/8294	0.106479	0.991141	0.991141	319710/50
KEGG_Path	mmu04650	Natural kille	5/178	118/8294	0.109566	0.991141	0.991141	12981/159
KEGG_Path	mmu00512	Mucin type	2/178	28/8294	0.120513	0.991141	0.991141	56336/108
KEGG_Path	mmu03060	Protein exp	2/178	28/8294	0.120513	0.991141	0.991141	66286/140
KEGG_Path	mmu04657	IL-17 signa	4/178	91/8294	0.131435	0.991141	0.991141	12981/155
KEGG_Path	mmu00640	Propanoate	2/178	31/8294	0.142339	0.991141	0.991141	107476/11
KEGG_Path	mmu05164	Influenza A	6/178	168/8294	0.152526	0.991141	0.991141	15967/228
KEGG_Path	mmu04137	Mitophagy	3/178	63/8294	0.152749	0.991141	0.991141	11911/179
KEGG_Path	mmu00230	Purine met	5/178	136/8294	0.167839	0.991141	0.991141	11564/688
KEGG_Path	mmu05162	Measles	5/178	136/8294	0.167839	0.991141	0.991141	14694/159
KEGG_Path	mmu00970	Aminoacyl-	3/178	66/8294	0.168336	0.991141	0.991141	107508/66
KEGG_Path	mmu00051	Fructose an	2/178	35/8294	0.172579	0.991141	0.991141	18640/270
KEGG_Path	mmu00620	Pyruvate m	2/178	38/8294	0.195884	0.991141	0.991141	107476/11
KEGG_Path	mmu04928	Parathyroid	4/178	107/8294	0.197378	0.991141	0.991141	11911/164
KEGG_Path	mmu04520	Adherens j	3/178	72/8294	0.200775	0.991141	0.991141	227377/19
KEGG_Path	mmu00562	Inositol pho	3/178	73/8294	0.206322	0.991141	0.991141	52858/771
KEGG_Path	mmu04072	Phospholip	5/178	147/8294	0.208374	0.991141	0.991141	227288/10
KEGG_Path	mmu00430	Taurine and	1/178	11/8294	0.21242	0.991141	0.991141	211488
KEGG_Path	mmu04216	Ferroptosis	2/178	41/8294	0.219552	0.991141	0.991141	50790/130
KEGG_Path	mmu04670	Leukocyte t	4/178	115/8294	0.233541	0.991141	0.991141	13058/192
KEGG_Path	mmu04390	Hippo sign	5/178	154/8294	0.235693	0.991141	0.991141	12159/319
KEGG_Path	mmu03022	Basal trans	2/178	44/8294	0.243445	0.991141	0.991141	14884/997
KEGG_Path	mmu00533	Glycosamin	1/178	14/8294	0.262117	0.991141	0.991141	56773
KEGG_Path	mmu03320	PPAR signa	3/178	85/8294	0.275065	0.991141	0.991141	50790/162
KEGG_Path	mmu00600	Sphingolip	2/178	48/8294	0.275443	0.991141	0.991141	230101/20
KEGG_Path	mmu05030	Cocaine ad	2/178	48/8294	0.275443	0.991141	0.991141	11911/142
KEGG_Path	mmu00730	Thiamine n	1/178	15/8294	0.27798	0.991141	0.991141	68870

KEGG_Path	mmu0463	JAK-STAT	5/178	165/8294	0.280445	0.991141	0.991141	12981/159
KEGG_Path	mmu0051	N-Glycan	2/178	49/8294	0.283442	0.991141	0.991141	102580/17
KEGG_Path	mmu0052	Amino sug	2/178	49/8294	0.283442	0.991141	0.991141	266690/23
KEGG_Path	mmu0433	Notch sign	2/178	49/8294	0.283442	0.991141	0.991141	16848/181
KEGG_Path	mmu0415	AMPK sign	4/178	126/8294	0.285548	0.991141	0.991141	107476/15
KEGG_Path	mmu0007	Fatty acid	2/178	50/8294	0.291433	0.991141	0.991141	110460/50
KEGG_Path	mmu0401	Rap1 signa	6/178	209/8294	0.292421	0.991141	0.991141	11602/106
KEGG_Path	mmu0541	Viral myoc	3/178	88/8294	0.292666	0.991141	0.991141	230861/19
KEGG_Path	mmu0462	NOD-like	5/178	168/8294	0.292949	0.991141	0.991141	13058/159
KEGG_Path	mmu0091	Nitrogen	1/178	17/8294	0.308695	0.991141	0.991141	14645
KEGG_Path	mmu0304	Spliceoso	4/178	133/8294	0.319502	0.991141	0.991141	71702/680
KEGG_Path	mmu0496	Endocrine	2/178	54/8294	0.323256	0.991141	0.991141	71770/538
KEGG_Path	mmu0421	Necroptosi	5/178	177/8294	0.330977	0.991141	0.991141	66700/130
KEGG_Path	mmu0010	Steroid bio	1/178	19/8294	0.338111	0.991141	0.991141	235293
KEGG_Path	mmu0022	Arginine bi	1/178	19/8294	0.338111	0.991141	0.991141	14645
KEGG_Path	mmu0121	2-Oxocarb	1/178	19/8294	0.338111	0.991141	0.991141	11428
KEGG_Path	mmu0407	Phosphatic	3/178	98/8294	0.351658	0.991141	0.991141	52858/771
KEGG_Path	mmu0053	Glycosamir	1/178	20/8294	0.352348	0.991141	0.991141	59031
KEGG_Path	mmu0516	Hepatitis B	4/178	143/8294	0.368464	0.991141	0.991141	11911/159
KEGG_Path	mmu0051	Other type	1/178	22/8294	0.379916	0.991141	0.991141	16848
KEGG_Path	mmu0090	Terpenoid	1/178	23/8294	0.393259	0.991141	0.991141	110460
KEGG_Path	mmu0462	Cytosolic D	2/178	64/8294	0.400878	0.991141	0.991141	15967/228
KEGG_Path	mmu0053	Glycosamir	1/178	24/8294	0.406317	0.991141	0.991141	54710
KEGG_Path	mmu0497	Vitamin di	1/178	24/8294	0.406317	0.991141	0.991141	69698
KEGG_Path	mmu0056	Glycosylph	1/178	25/8294	0.419095	0.991141	0.991141	67556
KEGG_Path	mmu0466	TNF signali	3/178	110/8294	0.421628	0.991141	0.991141	11911/129
KEGG_Path	mmu0503	Alcoholism	5/178	199/8294	0.425065	0.991141	0.991141	11911/142
KEGG_Path	mmu0462	RIG-I-like	2/178	68/8294	0.430791	0.991141	0.991141	15967/228
KEGG_Path	mmu0466	Fc epsilon	2/178	68/8294	0.430791	0.991141	0.991141	12981/193
KEGG_Path	mmu0503	Amphetam	2/178	68/8294	0.430791	0.991141	0.991141	11911/142
KEGG_Path	mmu0079	Folate bios	1/178	26/8294	0.4316	0.991141	0.991141	13180
KEGG_Path	mmu0522	Acute mye	2/178	69/8294	0.438147	0.991141	0.991141	12606/129
KEGG_Path	mmu0495	Maturity o	1/178	27/8294	0.443837	0.991141	0.991141	15377
KEGG_Path	mmu0491	Thyroid ho	3/178	115/8294	0.450087	0.991141	0.991141	12159/181
KEGG_Path	mmu0431	Wnt signali	4/178	160/8294	0.450924	0.991141	0.991141	68010/234
KEGG_Path	mmu0516	Hepatitis C	4/178	160/8294	0.450924	0.991141	0.991141	15967/228
KEGG_Path	mmu0492	Adipocyto	2/178	71/8294	0.452703	0.991141	0.991141	50790/116
KEGG_Path	mmu0510	Bacterial in	2/178	74/8294	0.474132	0.991141	0.991141	53860/204
KEGG_Path	mmu0152	Antifolate	1/178	30/8294	0.478998	0.991141	0.991141	64931
KEGG_Path	mmu0471	Circadian	1/178	30/8294	0.478998	0.991141	0.991141	12952
KEGG_Path	mmu0521	Pancreatic	2/178	75/8294	0.481162	0.991141	0.991141	19354/641
KEGG_Path	mmu0516	Herpes sim	5/178	215/8294	0.492142	0.991141	0.991141	15967/228
KEGG_Path	mmu0002	Citrate cycl	1/178	32/8294	0.501201	0.991141	0.991141	11428
KEGG_Path	mmu0104	Biosynthes	1/178	32/8294	0.501201	0.991141	0.991141	76267
KEGG_Path	mmu0123	Biosynthes	2/178	78/8294	0.501905	0.991141	0.991141	11428/146
KEGG_Path	mmu0413	SNARE inte	1/178	33/8294	0.511948	0.991141	0.991141	22319
KEGG_Path	mmu0004	Pentose an	1/178	34/8294	0.522464	0.991141	0.991141	102448
KEGG_Path	mmu0301	RNA degra	2/178	83/8294	0.535276	0.991141	0.991141	227715/24

KEGG_Path	mmu04512	ECM-recep	2/178	83/8294	0.535276	0.991141	0.991141	11603/128
KEGG_Path	mmu05323	Rheumatoi	2/178	83/8294	0.535276	0.991141	0.991141	108664/12
KEGG_Path	mmu05143	African tryp	1/178	36/8294	0.542825	0.991141	0.991141	20339
KEGG_Path	mmu04145	Phagosom	4/178	181/8294	0.547508	0.991141	0.991141	108664/13
KEGG_Path	mmu04714	Thermogen	5/178	230/8294	0.552343	0.991141	0.991141	50790/837
KEGG_Path	mmu05169	Epstein-Ba	5/178	230/8294	0.552343	0.991141	0.991141	15967/228
KEGG_Path	mmu04658	Th1 and Th	2/178	87/8294	0.560855	0.991141	0.991141	16161/181
KEGG_Path	mmu05206	MicroRNAs	6/178	281/8294	0.563831	0.991141	0.991141	723953/75
KEGG_Path	mmu04014	Ras signalin	5/178	233/8294	0.563975	0.991141	0.991141	11602/546
KEGG_Path	mmu04610	Compleme	2/178	88/8294	0.567092	0.991141	0.991141	18792/207
KEGG_Path	mmu05210	Colorectal	2/178	88/8294	0.567092	0.991141	0.991141	19354/641
KEGG_Path	mmu04550	Signaling p	3/178	137/8294	0.567379	0.991141	0.991141	12159/159
KEGG_Path	mmu04120	Ubiquitin m	3/178	139/8294	0.577274	0.991141	0.991141	26374/562
KEGG_Path	mmu04912	GnRH signa	2/178	90/8294	0.579375	0.991141	0.991141	11911/192
KEGG_Path	mmu04974	Protein dig	2/178	90/8294	0.579375	0.991141	0.991141	12824/436
KEGG_Path	mmu04975	Fat digestio	1/178	40/8294	0.580993	0.991141	0.991141	110460
KEGG_Path	mmu04910	Insulin sign	3/178	140/8294	0.582168	0.991141	0.991141	107476/19
KEGG_Path	mmu05032	Morphine a	2/178	92/8294	0.591402	0.991141	0.991141	18573/238
KEGG_Path	mmu05322	Systemic lu	3/178	143/8294	0.596637	0.991141	0.991141	15270/150
KEGG_Path	mmu05418	Fluid shear	3/178	143/8294	0.596637	0.991141	0.991141	12159/193
KEGG_Path	mmu01522	Endocrine	2/178	93/8294	0.59732	0.991141	0.991141	18131/204
KEGG_Path	mmu03420	Nucleotide	1/178	43/8294	0.607523	0.991141	0.991141	14884
KEGG_Path	mmu04962	Vasopressin	1/178	43/8294	0.607523	0.991141	0.991141	53869
KEGG_Path	mmu03015	mRNA surv	2/178	96/8294	0.614689	0.991141	0.991141	68092/541
KEGG_Path	mmu00564	Glycerophо	2/178	97/8294	0.62035	0.991141	0.991141	52858/333
KEGG_Path	mmu05215	Prostate ca	2/178	97/8294	0.62035	0.991141	0.991141	11911/187
KEGG_Path	mmu04978	Mineral abs	1/178	45/8294	0.624276	0.991141	0.991141	73649
KEGG_Path	mmu04062	Chemokine	4/178	200/8294	0.626807	0.991141	0.991141	227288/19
KEGG_Path	mmu04620	Toll-like re	2/178	99/8294	0.631482	0.991141	0.991141	15967/544
KEGG_Path	mmu03050	Proteasom	1/178	46/8294	0.632383	0.991141	0.991141	19184
KEGG_Path	mmu04933	AGE-RAGE	2/178	100/8294	0.636952	0.991141	0.991141	13058/203
KEGG_Path	mmu04922	Glucagon s	2/178	102/8294	0.647703	0.991141	0.991141	107476/11
KEGG_Path	mmu05163	Human cyt	5/178	256/8294	0.647735	0.991141	0.991141	11911/159
KEGG_Path	mmu04972	Pancreatic	2/178	103/8294	0.652984	0.991141	0.991141	53869/436
KEGG_Path	mmu04979	Cholestero	1/178	49/8294	0.655677	0.991141	0.991141	79196
KEGG_Path	mmu05144	Malaria	1/178	49/8294	0.655677	0.991141	0.991141	20339
KEGG_Path	mmu00270	Cysteine an	1/178	50/8294	0.66311	0.991141	0.991141	229905
KEGG_Path	mmu00330	Arginine an	1/178	50/8294	0.66311	0.991141	0.991141	18242
KEGG_Path	mmu04066	HIF-1 signa	2/178	105/8294	0.663357	0.991141	0.991141	11602/130
KEGG_Path	mmu05014	Amyotroph	1/178	52/8294	0.677502	0.991141	0.991141	67819
KEGG_Path	mmu04725	Cholinergic	2/178	113/8294	0.702383	0.991141	0.991141	11911/226
KEGG_Path	mmu04724	Glutamater	2/178	114/8294	0.706989	0.991141	0.991141	14645/108
KEGG_Path	mmu05225	Hepatocell	3/178	171/8294	0.715507	0.991141	0.991141	83766/204
KEGG_Path	mmu00240	Pyrimidine	1/178	58/8294	0.71711	0.991141	0.991141	69719
KEGG_Path	mmu04370	VEGF signa	1/178	58/8294	0.71711	0.991141	0.991141	19354
KEGG_Path	mmu05134	Legionellos	1/178	58/8294	0.71711	0.991141	0.991141	12747
KEGG_Path	mmu00310	Lysine deg	1/178	59/8294	0.723224	0.991141	0.991141	110460
KEGG_Path	mmu05321	Inflammato	1/178	59/8294	0.723224	0.991141	0.991141	16161

KEGG_Path	mmu0301(	Ribosome	3/178	175/8294	0.730083	0.991141	0.991141	77721/199
KEGG_Path	mmu0120(	Carbon me	2/178	120/8294	0.733397	0.991141	0.991141	110460/11
KEGG_Path	mmu04722	Neurotropl	2/178	121/8294	0.737597	0.991141	0.991141	11911/204
KEGG_Path	mmu05152	Tuberculos	3/178	178/8294	0.740629	0.991141	0.991141	108664/15
KEGG_Path	mmu04071	Sphingolip	2/178	122/8294	0.741741	0.991141	0.991141	19354/203
KEGG_Path	mmu05217	Basal cell c	1/178	63/8294	0.746394	0.991141	0.991141	12159
KEGG_Path	mmu0438(	Osteoclast	2/178	128/8294	0.765453	0.991141	0.991141	14282/164
KEGG_Path	mmu0472(	Long-term	1/178	67/8294	0.767633	0.991141	0.991141	11911
KEGG_Path	mmu0514(	Leishmania	1/178	67/8294	0.767633	0.991141	0.991141	13058
KEGG_Path	mmu04927	Cortisol syr	1/178	68/8294	0.772661	0.991141	0.991141	11911
KEGG_Path	mmu04926	Relaxin sigi	2/178	131/8294	0.776588	0.991141	0.991141	11911/204
KEGG_Path	mmu05166	Human T-(	4/178	246/8294	0.779381	0.991141	0.991141	11911/129
KEGG_Path	mmu04915	Estrogen si	2/178	133/8294	0.783754	0.991141	0.991141	11911/204
KEGG_Path	mmu04115	p53 signali	1/178	71/8294	0.787104	0.991141	0.991141	26374
KEGG_Path	mmu0019(	Oxidative p	2/178	134/8294	0.787262	0.991141	0.991141	108664/70
KEGG_Path	mmu04662	B cell recep	1/178	72/8294	0.791712	0.991141	0.991141	19354
KEGG_Path	mmu04917	Prolactin si	1/178	72/8294	0.791712	0.991141	0.991141	20416
KEGG_Path	mmu04924	Renin secre	1/178	72/8294	0.791712	0.991141	0.991141	18573
KEGG_Path	mmu05412	Arrhythmo	1/178	72/8294	0.791712	0.991141	0.991141	24052
KEGG_Path	mmu04918	Thyroid ho	1/178	73/8294	0.796221	0.991141	0.991141	11911
KEGG_Path	mmu04024	cAMP signa	3/178	198/8294	0.802809	0.991141	0.991141	106952/23
KEGG_Path	mmu05214	Glioma	1/178	75/8294	0.804951	0.991141	0.991141	20416
KEGG_Path	mmu0451(	Focal adhe	3/178	199/8294	0.805564	0.991141	0.991141	12824/193
KEGG_Path	mmu0522(	Chronic my	1/178	76/8294	0.809175	0.991141	0.991141	20416
KEGG_Path	mmu05132	Salmonella	1/178	78/8294	0.817352	0.991141	0.991141	12981
KEGG_Path	mmu05012	Parkinson (	2/178	144/8294	0.819677	0.991141	0.991141	68943/562
KEGG_Path	mmu0532(	Autoimmu	1/178	79/8294	0.821309	0.991141	0.991141	15967
KEGG_Path	mmu01521	EGFR tyros	1/178	80/8294	0.825181	0.991141	0.991141	20416
KEGG_Path	mmu05224	Breast canc	2/178	147/8294	0.828506	0.991141	0.991141	18131/204
KEGG_Path	mmu04932	Non-alcoh	2/178	151/8294	0.839676	0.991141	0.991141	11911/126
KEGG_Path	mmu04012	ErbB signal	1/178	84/8294	0.839852	0.991141	0.991141	20416
KEGG_Path	mmu0541(	Hypertroph	1/178	84/8294	0.839852	0.991141	0.991141	24052
KEGG_Path	mmu04911	Insulin secr	1/178	85/8294	0.843324	0.991141	0.991141	11911
KEGG_Path	mmu0454(	Gap junctic	1/178	86/8294	0.846721	0.991141	0.991141	545486
KEGG_Path	mmu04666	Fc gamma	1/178	87/8294	0.850045	0.991141	0.991141	19354
KEGG_Path	mmu0415(	mTOR sign	2/178	155/8294	0.850186	0.991141	0.991141	108664/80
KEGG_Path	mmu04742	Taste trans	1/178	88/8294	0.853298	0.991141	0.991141	18573
KEGG_Path	mmu05414	Dilated car	1/178	89/8294	0.85648	0.991141	0.991141	24052
KEGG_Path	mmu04211	Longevity r	1/178	90/8294	0.859593	0.991141	0.991141	11911
KEGG_Path	mmu04727	GABAergic	1/178	90/8294	0.859593	0.991141	0.991141	14645
KEGG_Path	mmu05222	Small cell lu	1/178	92/8294	0.86562	0.991141	0.991141	54124
KEGG_Path	mmu05204	Chemical c	1/178	94/8294	0.87139	0.991141	0.991141	229905
KEGG_Path	mmu0464(	Hematopo	1/178	95/8294	0.874182	0.991141	0.991141	12981
KEGG_Path	mmu0401(	MAPK sign	4/178	294/8294	0.881545	0.991141	0.991141	11602/119
KEGG_Path	mmu04514	Cell adhesi	2/178	169/8294	0.882233	0.991141	0.991141	19274/203
KEGG_Path	mmu05231	Choline me	1/178	99/8294	0.884759	0.991141	0.991141	19354
KEGG_Path	mmu04925	Aldosteron	1/178	100/8294	0.887262	0.991141	0.991141	11911
KEGG_Path	mmu0466(	T cell recep	1/178	101/8294	0.889711	0.991141	0.991141	12981

KEGG_Path	mmu0517	Human im	3/178	239/8294	0.891943	0.991141	0.991141	15967/192
KEGG_Path	mmu0465	Th17 cell d	1/178	102/8294	0.892107	0.991141	0.991141	16161
KEGG_Path	mmu0516	Human pa	5/178	361/8294	0.892881	0.991141	0.991141	108664/12
KEGG_Path	mmu0406	NF-kappa	1/178	104/8294	0.896745	0.991141	0.991141	18792
KEGG_Path	mmu0514	Amoebiasi	1/178	106/8294	0.901185	0.991141	0.991141	12981
KEGG_Path	mmu0514	Toxoplasm	1/178	108/8294	0.905435	0.991141	0.991141	16155
KEGG_Path	mmu0493	Insulin resi	1/178	109/8294	0.907491	0.991141	0.991141	26458
KEGG_Path	mmu0402	Calcium si	2/178	187/8294	0.914178	0.991141	0.991141	18573/192
KEGG_Path	mmu0411	Oocyte me	1/178	116/8294	0.920692	0.991141	0.991141	105988
KEGG_Path	mmu0411	Cell cycle	1/178	123/8294	0.932018	0.991141	0.991141	105988
KEGG_Path	mmu0414	Lysosome	1/178	124/8294	0.933499	0.991141	0.991141	108664
KEGG_Path	mmu0427	Vascular s	1/178	129/8294	0.940436	0.991141	0.991141	17880
KEGG_Path	mmu0406	FoxO signa	1/178	132/8294	0.944248	0.991141	0.991141	54601
KEGG_Path	mmu0472	Dopamine	1/178	135/8294	0.947817	0.991141	0.991141	11911
KEGG_Path	mmu0421	Apoptosis	1/178	136/8294	0.948955	0.991141	0.991141	11911
KEGG_Path	mmu0516	Kaposi sar	2/178	217/8294	0.9501	0.991141	0.991141	12981/159
KEGG_Path	mmu0408	Neuroactiv	3/178	289/8294	0.951024	0.991141	0.991141	14765/108
KEGG_Path	mmu0437	Apelin sign	1/178	139/8294	0.952225	0.991141	0.991141	18131
KEGG_Path	mmu0415	PI3K-Akt si	4/178	358/8294	0.952794	0.991141	0.991141	11602/119
KEGG_Path	mmu0426	Adrenergic	1/178	147/8294	0.95996	0.991141	0.991141	11911
KEGG_Path	mmu0520	Viral carcin	2/178	231/8294	0.96147	0.991141	0.991141	11911/148
KEGG_Path	mmu0522	Gastric can	1/178	150/8294	0.962528	0.991141	0.991141	20416
KEGG_Path	mmu0493	Cushing sy	1/178	158/8294	0.968602	0.991141	0.991141	11911
KEGG_Path	mmu0453	Tight junct	1/178	167/8294	0.974273	0.991141	0.991141	17880
KEGG_Path	mmu0402	cGMP-PK	1/178	168/8294	0.974836	0.991141	0.991141	11911
KEGG_Path	mmu0501	Alzheimer	1/178	175/8294	0.978452	0.991141	0.991141	23821
KEGG_Path	mmu0436	Axon guid	1/178	180/8294	0.980713	0.991141	0.991141	19354
KEGG_Path	mmu0501	Huntingto	1/178	194/8294	0.985865	0.991141	0.991141	71770
KEGG_Path	mmu0520	Proteoglyc	1/178	204/8294	0.988683	0.991141	0.991141	18792
KEGG_Path	mmu0481	Regulation	1/178	215/8294	0.991141	0.991141	0.991141	19354
KEGG_Path	mmu0472	Glutamate	7/164	114/8294	0.007294	0.793293	0.793293	14700/147
KEGG_Path	mmu0048	Glutathion	5/164	64/8294	0.008478	0.793293	0.793293	110175/14
KEGG_Path	mmu0408	Neuroactiv	12/164	289/8294	0.011959	0.793293	0.793293	11438/108
KEGG_Path	mmu0472	Cholinergi	6/164	113/8294	0.024311	0.984834	0.984834	11438/108
KEGG_Path	mmu0005	Fructose a	3/164	35/8294	0.031288	0.984834	0.984834	234730/15
KEGG_Path	mmu0439	Hippo sign	7/164	154/8294	0.032868	0.984834	0.984834	11839/120
KEGG_Path	mmu0010	Steroid bio	2/164	19/8294	0.053333	0.984834	0.984834	74754/731
KEGG_Path	mmu0434	Hedgehog	3/164	44/8294	0.055735	0.984834	0.984834	57810/161
KEGG_Path	mmu0052	Amino sug	3/164	49/8294	0.072272	0.984834	0.984834	234730/15
KEGG_Path	mmu0346	Fanconi an	3/164	51/8294	0.079434	0.984834	0.984834	208836/15
KEGG_Path	mmu0098	Drug meta	4/164	87/8294	0.093258	0.984834	0.984834	14858/103
KEGG_Path	mmu0052	Neomycin,	1/164	5/8294	0.095055	0.984834	0.984834	15275
KEGG_Path	mmu0495	Maturity o	2/164	27/8294	0.098916	0.984834	0.984834	15205/180
KEGG_Path	mmu0520	Chemical c	4/164	94/8294	0.115301	0.984834	0.984834	13097/148
KEGG_Path	mmu0492	Relaxin sig	5/164	131/8294	0.117615	0.984834	0.984834	14700/147
KEGG_Path	mmu0063	Glyoxylate	2/164	31/8294	0.12463	0.984834	0.984834	13382/681
KEGG_Path	mmu0521	Basal cell c	3/164	63/8294	0.128215	0.984834	0.984834	12006/121
KEGG_Path	mmu0471	Circadian	4/164	98/8294	0.128835	0.984834	0.984834	14700/147

KEGG_Path	mmu0002(	Citrate cycl	2/164	32/8294	0.131289	0.984834	0.984834	235339/13
KEGG_Path	mmu00062	Fatty acid e	2/164	32/8294	0.131289	0.984834	0.984834	54326/757
KEGG_Path	mmu0406(	Cytokine-c	9/164	296/8294	0.131962	0.984834	0.984834	12156/203
KEGG_Path	mmu0098(	Metabolisn	3/164	66/8294	0.141766	0.984834	0.984834	14858/103
KEGG_Path	mmu0491(	Insulin sigr	5/164	140/8294	0.143868	0.984834	0.984834	15275/689
KEGG_Path	mmu0001(	Glycolysis /	3/164	67/8294	0.146387	0.984834	0.984834	235339/13
KEGG_Path	mmu00982	Drug meta	3/164	68/8294	0.151056	0.984834	0.984834	14858/103
KEGG_Path	mmu04115	p53 signali	3/164	71/8294	0.165342	0.984834	0.984834	12048/125
KEGG_Path	mmu0062(	Pyruvate m	2/164	38/8294	0.172729	0.984834	0.984834	235339/13
KEGG_Path	mmu0026(	Glycine, sei	2/164	40/8294	0.186984	0.984834	0.984834	13382/681
KEGG_Path	mmu05033	Nicotine ac	2/164	40/8294	0.186984	0.984834	0.984834	11438/148
KEGG_Path	mmu0517(	Human imi	7/164	239/8294	0.194537	0.984834	0.984834	11766/120
KEGG_Path	mmu01524	Platinum d	3/164	77/8294	0.195018	0.984834	0.984834	12048/148
KEGG_Path	mmu04062	Chemokine	6/164	200/8294	0.204163	0.984834	0.984834	20304/809
KEGG_Path	mmu0120(	Carbon me	4/164	120/8294	0.213305	0.984834	0.984834	235339/13
KEGG_Path	mmu0435(	TGF-beta s	3/164	85/8294	0.23638	0.984834	0.984834	12156/145
KEGG_Path	mmu0493(	Type II diak	2/164	48/8294	0.245254	0.984834	0.984834	15275/187
KEGG_Path	mmu05225	Hepatocell	5/164	171/8294	0.249927	0.984834	0.984834	12006/120
KEGG_Path	mmu04742	Taste trans	3/164	88/8294	0.252279	0.984834	0.984834	268934/38
KEGG_Path	mmu0521(	Colorectal	3/164	88/8294	0.252279	0.984834	0.984834	11839/120
KEGG_Path	mmu0014(	Steroid hor	3/164	89/8294	0.257614	0.984834	0.984834	13097/789
KEGG_Path	mmu00604	Glycosphin	1/164	15/8294	0.259054	0.984834	0.984834	26938
KEGG_Path	mmu0073(	Thiamine n	1/164	15/8294	0.259054	0.984834	0.984834	78801
KEGG_Path	mmu04068	FoxO signa	4/164	132/8294	0.264602	0.984834	0.984834	16598/136
KEGG_Path	mmu04726	Serotonerg	4/164	132/8294	0.264602	0.984834	0.984834	13097/147
KEGG_Path	mmu05014	Amyotroph	2/164	52/8294	0.27472	0.984834	0.984834	12048/148
KEGG_Path	mmu0436(	Axon guida	5/164	180/8294	0.283946	0.984834	0.984834	319713/18
KEGG_Path	mmu0455(	Signaling p	4/164	137/8294	0.286644	0.984834	0.984834	12006/139
KEGG_Path	mmu0091(	Nitrogen m	1/164	17/8294	0.28812	0.984834	0.984834	12353
KEGG_Path	mmu04371	Apelin sign	4/164	139/8294	0.295539	0.984834	0.984834	14700/147
KEGG_Path	mmu05418	Fluid shear	4/164	143/8294	0.313429	0.984834	0.984834	14858/103
KEGG_Path	mmu05206	MicroRNAs	7/164	281/8294	0.320824	0.984834	0.984834	723825/72
KEGG_Path	mmu04137	Mitophagy	2/164	63/8294	0.355016	0.984834	0.984834	12048/214
KEGG_Path	mmu04623	Cytosolic D	2/164	64/8294	0.362188	0.984834	0.984834	20304/230
KEGG_Path	mmu04931	Insulin resi	3/164	109/8294	0.365928	0.984834	0.984834	18762/192
KEGG_Path	mmu00534	Glycosamir	1/164	24/8294	0.381209	0.984834	0.984834	17423
KEGG_Path	mmu04977	Vitamin dig	1/164	24/8294	0.381209	0.984834	0.984834	20509
KEGG_Path	mmu0472(	Long-term	2/164	67/8294	0.383521	0.984834	0.984834	14813/582
KEGG_Path	mmu05163	Human cyt	6/164	256/8294	0.39512	0.984834	0.984834	20304/147
KEGG_Path	mmu03008	Ribosome l	3/164	116/8294	0.403581	0.984834	0.984834	102216272
KEGG_Path	mmu04392	Hippo sign	1/164	26/8294	0.405509	0.984834	0.984834	18016
KEGG_Path	mmu0463(	JAK-STAT s	4/164	165/8294	0.412506	0.984834	0.984834	12048/230
KEGG_Path	mmu00053	Ascorbate	1/164	27/8294	0.417301	0.984834	0.984834	394432
KEGG_Path	mmu04744	Phototrans	1/164	27/8294	0.417301	0.984834	0.984834	20215
KEGG_Path	mmu04966	Collecting	1/164	27/8294	0.417301	0.984834	0.984834	20499
KEGG_Path	mmu0452(	Adherens j	2/164	72/8294	0.418373	0.984834	0.984834	19268/218
KEGG_Path	mmu00512	Mucin type	1/164	28/8294	0.42886	0.984834	0.984834	272411
KEGG_Path	mmu05212	Pancreatic	2/164	75/8294	0.438807	0.984834	0.984834	12048/218

KEGG_Path	mmu0522	Chronic my	2/164	76/8294	0.445532	0.984834	0.984834	12048/218
KEGG_Path	mmu0152	Antifolate r	1/164	30/8294	0.4513	0.984834	0.984834	20509
KEGG_Path	mmu0064	Propanoat	1/164	31/8294	0.462189	0.984834	0.984834	13382
KEGG_Path	mmu0005	Galactose r	1/164	32/8294	0.472863	0.984834	0.984834	15275
KEGG_Path	mmu0104	Biosynthes	1/164	32/8294	0.472863	0.984834	0.984834	54326
KEGG_Path	mmu0421	Apoptosis	1/164	32/8294	0.472863	0.984834	0.984834	12048
KEGG_Path	mmu0050	Starch and	1/164	33/8294	0.483327	0.984834	0.984834	15275
KEGG_Path	mmu0301	RNA degra	2/164	83/8294	0.491311	0.984834	0.984834	72662/725
KEGG_Path	mmu0004	Pentose an	1/164	34/8294	0.493584	0.984834	0.984834	394432
KEGG_Path	mmu0502	Prion disea	1/164	34/8294	0.493584	0.984834	0.984834	20304
KEGG_Path	mmu0491	Insulin secr	2/164	85/8294	0.503953	0.984834	0.984834	14607/588
KEGG_Path	mmu0023	Purine met	3/164	136/8294	0.506784	0.984834	0.984834	102216272
KEGG_Path	mmu0516	Measles	3/164	136/8294	0.506784	0.984834	0.984834	17221/230
KEGG_Path	mmu0402	Calcium sig	4/164	187/8294	0.508435	0.984834	0.984834	14813/572
KEGG_Path	mmu0534	Primary im	1/164	36/8294	0.513495	0.984834	0.984834	11634
KEGG_Path	mmu0401	MAPK sign	6/164	294/8294	0.527634	0.984834	0.984834	11839/687
KEGG_Path	mmu0496	Aldosteron	1/164	38/8294	0.532628	0.984834	0.984834	20393
KEGG_Path	mmu0472	GABAergic	2/164	90/8294	0.534662	0.984834	0.984834	14700/147
KEGG_Path	mmu0497	Protein dig	2/164	90/8294	0.534662	0.984834	0.984834	13706/373
KEGG_Path	mmu0083	Retinol me	2/164	91/8294	0.540647	0.984834	0.984834	13097/394
KEGG_Path	mmu0503	Morphine	2/164	92/8294	0.546579	0.984834	0.984834	14700/147
KEGG_Path	mmu0497	Fat digesti	1/164	40/8294	0.551013	0.984834	0.984834	26569
KEGG_Path	mmu0086	Porphyrin	1/164	41/8294	0.559934	0.984834	0.984834	394432
KEGG_Path	mmu0344	Homologo	1/164	41/8294	0.559934	0.984834	0.984834	21976
KEGG_Path	mmu0415	PI3K-Akt si	7/164	358/8294	0.567045	0.984834	0.984834	11839/120
KEGG_Path	mmu0467	Intestinal i	1/164	43/8294	0.577251	0.984834	0.984834	18703
KEGG_Path	mmu0496	Vasopressi	1/164	43/8294	0.577251	0.984834	0.984834	11998
KEGG_Path	mmu0497	Carbohydr	1/164	43/8294	0.577251	0.984834	0.984834	15275
KEGG_Path	mmu0520	Proteoglyc	4/164	204/8294	0.577571	0.984834	0.984834	68794/161
KEGG_Path	mmu0302	Basal trans	1/164	44/8294	0.585653	0.984834	0.984834	74197
KEGG_Path	mmu0462	Toll-like re	2/164	99/8294	0.586601	0.984834	0.984834	20304/230
KEGG_Path	mmu0493	AGE-RAGE	2/164	100/8294	0.592102	0.984834	0.984834	18762/218
KEGG_Path	mmu0497	Mineral ab	1/164	45/8294	0.59389	0.984834	0.984834	12309
KEGG_Path	mmu0415	mTOR sign	3/164	155/8294	0.595699	0.984834	0.984834	329679/10
KEGG_Path	mmu0514	Chagas dis	2/164	101/8294	0.597549	0.984834	0.984834	20304/218
KEGG_Path	mmu0465	Th17 cell d	2/164	102/8294	0.602941	0.984834	0.984834	239114/21
KEGG_Path	mmu0497	Pancreatic	2/164	103/8294	0.608279	0.984834	0.984834	13706/220
KEGG_Path	mmu0056	Ether lipid	1/164	47/8294	0.609878	0.984834	0.984834	104759
KEGG_Path	mmu0060	Sphingolip	1/164	48/8294	0.617636	0.984834	0.984834	238011
KEGG_Path	mmu0503	Cocaine ac	1/164	48/8294	0.617636	0.984834	0.984834	14813
KEGG_Path	mmu0433	Notch sign	1/164	49/8294	0.625241	0.984834	0.984834	15205
KEGG_Path	mmu0516	Kaposi sar	4/164	217/8294	0.626586	0.984834	0.984834	14700/147
KEGG_Path	mmu0033	Arginine ar	1/164	50/8294	0.632695	0.984834	0.984834	66988
KEGG_Path	mmu0059	Linoleic aci	1/164	50/8294	0.632695	0.984834	0.984834	13097
KEGG_Path	mmu0514	Toxoplasm	2/164	108/8294	0.634158	0.984834	0.984834	12048/161
KEGG_Path	mmu0453	Tight juncti	3/164	167/8294	0.646255	0.984834	0.984834	224912/18
KEGG_Path	mmu0462	NOD-like r	3/164	168/8294	0.650261	0.984834	0.984834	12048/203
KEGG_Path	mmu0516	Influenza A	3/164	168/8294	0.650261	0.984834	0.984834	20304/230

KEGG_Path	mmu00280	Valine, leuc	1/164	56/8294	0.674425	0.984834	0.984834	13382
KEGG_Path	mmu05150	Staphyloco	1/164	56/8294	0.674425	0.984834	0.984834	13510
KEGG_Path	mmu01212	Fatty acid r	1/164	57/8294	0.680907	0.984834	0.984834	54326
KEGG_Path	mmu00240	Pyrimidine	1/164	58/8294	0.68726	0.984834	0.984834	20135
KEGG_Path	mmu04370	VEGF signa	1/164	58/8294	0.68726	0.984834	0.984834	102626
KEGG_Path	mmu05213	Endometria	1/164	58/8294	0.68726	0.984834	0.984834	12006
KEGG_Path	mmu04071	Sphingolip	2/164	122/8294	0.699528	0.984834	0.984834	18762/136
KEGG_Path	mmu04142	Lysosome	2/164	124/8294	0.708038	0.984834	0.984834	11766/117
KEGG_Path	mmu04750	Inflammato	2/164	125/8294	0.712217	0.984834	0.984834	13097/187
KEGG_Path	mmu05230	Central car	1/164	64/8294	0.722823	0.984834	0.984834	15275
KEGG_Path	mmu04270	Vascular sn	2/164	129/8294	0.728439	0.984834	0.984834	58802/187
KEGG_Path	mmu00970	Aminoacyl-	1/164	66/8294	0.733761	0.984834	0.984834	22321
KEGG_Path	mmu04622	RIG-I-like r	1/164	68/8294	0.744269	0.984834	0.984834	230396
KEGG_Path	mmu05031	Amphetam	1/164	68/8294	0.744269	0.984834	0.984834	14813
KEGG_Path	mmu04728	Dopaminer	2/164	135/8294	0.751325	0.984834	0.984834	14700/147
KEGG_Path	mmu04940	Type I diab	1/164	70/8294	0.754365	0.984834	0.984834	19275
KEGG_Path	mmu05034	Alcoholism	3/164	199/8294	0.758652	0.984834	0.984834	14700/147
KEGG_Path	mmu04120	Ubiquitin n	2/164	139/8294	0.76565	0.984834	0.984834	11634/686
KEGG_Path	mmu00562	Inositol ph	1/164	73/8294	0.76877	0.984834	0.984834	75678
KEGG_Path	mmu04971	Gastric aci	1/164	74/8294	0.773383	0.984834	0.984834	20604
KEGG_Path	mmu05161	Hepatitis B	2/164	143/8294	0.779257	0.984834	0.984834	230396/21
KEGG_Path	mmu04721	Synaptic ve	1/164	77/8294	0.78668	0.984834	0.984834	20508
KEGG_Path	mmu04144	Endocytosi	4/164	270/8294	0.786874	0.984834	0.984834	67028/187
KEGG_Path	mmu04970	Salivary sec	1/164	78/8294	0.790938	0.984834	0.984834	11830
KEGG_Path	mmu05132	Salmonella	1/164	78/8294	0.790938	0.984834	0.984834	68794
KEGG_Path	mmu04072	Phospholip	2/164	147/8294	0.792173	0.984834	0.984834	11998/268
KEGG_Path	mmu05224	Breast canc	2/164	147/8294	0.792173	0.984834	0.984834	12006/152
KEGG_Path	mmu05320	Autoimmu	1/164	79/8294	0.795111	0.984834	0.984834	230396
KEGG_Path	mmu01521	EGFR tyros	1/164	80/8294	0.799201	0.984834	0.984834	12048
KEGG_Path	mmu04723	Retrograde	2/164	150/8294	0.80142	0.984834	0.984834	14700/147
KEGG_Path	mmu05226	Gastric can	2/164	150/8294	0.80142	0.984834	0.984834	12006/218
KEGG_Path	mmu04921	Oxytocin si	2/164	153/8294	0.810303	0.984834	0.984834	16520/184
KEGG_Path	mmu05323	Rheumatoi	1/164	83/8294	0.810991	0.984834	0.984834	20304
KEGG_Path	mmu04012	ErbB signal	1/164	84/8294	0.814766	0.984834	0.984834	11839
KEGG_Path	mmu04146	Peroxisome	1/164	84/8294	0.814766	0.984834	0.984834	20524
KEGG_Path	mmu03320	PPAR signa	1/164	85/8294	0.818466	0.984834	0.984834	26569
KEGG_Path	mmu04934	Cushing sy	2/164	158/8294	0.824327	0.984834	0.984834	12006/194
KEGG_Path	mmu04666	Fc gamma	1/164	87/8294	0.825648	0.984834	0.984834	15162
KEGG_Path	mmu04610	Compleme	1/164	88/8294	0.829132	0.984834	0.984834	17221
KEGG_Path	mmu04310	Wnt signali	2/164	160/8294	0.829673	0.984834	0.984834	12006/408
KEGG_Path	mmu00590	Arachidoni	1/164	89/8294	0.832547	0.984834	0.984834	13097
KEGG_Path	mmu04914	Progestero	1/164	90/8294	0.835894	0.984834	0.984834	56150
KEGG_Path	mmu04141	Protein pro	2/164	163/8294	0.837419	0.984834	0.984834	12954/148
KEGG_Path	mmu05169	Epstein-Ba	3/164	230/8294	0.838388	0.984834	0.984834	15205/230
KEGG_Path	mmu04612	Antigen pr	1/164	91/8294	0.839174	0.984834	0.984834	14827
KEGG_Path	mmu04657	IL-17 signa	1/164	91/8294	0.839174	0.984834	0.984834	239114
KEGG_Path	mmu05222	Small cell lu	1/164	92/8294	0.84239	0.984834	0.984834	12048
KEGG_Path	mmu04014	Ras signalin	3/164	233/8294	0.844757	0.984834	0.984834	12048/147

KEGG_Path	mmu0301	RNA transp	2/164	167/8294	0.847254	0.984834	0.984834	408191/56
KEGG_Path	mmu0516	Human pa	5/164	361/8294	0.847848	0.984834	0.984834	12006/224
KEGG_Path	mmu0451	Cell adhesi	2/164	169/8294	0.851968	0.984834	0.984834	192167/19
KEGG_Path	mmu0301	mRNA surv	1/164	96/8294	0.854625	0.984834	0.984834	56488
KEGG_Path	mmu0056	Glycerophc	1/164	97/8294	0.857533	0.984834	0.984834	104759
KEGG_Path	mmu0407	Phosphatic	1/164	98/8294	0.860383	0.984834	0.984834	75678
KEGG_Path	mmu0301	Ribosome	2/164	175/8294	0.865328	0.984834	0.984834	68172/200
KEGG_Path	mmu0421	Necroptosi	2/164	177/8294	0.869531	0.984834	0.984834	67028/230
KEGG_Path	mmu0516	Human T-c	3/164	246/8294	0.869913	0.984834	0.984834	12048/561
KEGG_Path	mmu0492	Glucagon s	1/164	102/8294	0.871229	0.984834	0.984834	68961
KEGG_Path	mmu0515	Tuberculos	2/164	178/8294	0.871588	0.984834	0.984834	230396/16
KEGG_Path	mmu0406	NF-kappa	1/164	104/8294	0.876333	0.984834	0.984834	12048
KEGG_Path	mmu0406	HIF-1 signa	1/164	105/8294	0.87881	0.984834	0.984834	15275
KEGG_Path	mmu0520	Transcriptic	2/164	183/8294	0.881433	0.984834	0.984834	12048/154
KEGG_Path	mmu0466	TNF signali	1/164	110/8294	0.890471	0.984834	0.984834	20304
KEGG_Path	mmu0462	C-type lect	1/164	112/8294	0.894817	0.984834	0.984834	239114
KEGG_Path	mmu0491	Thyroid ho	1/164	115/8294	0.901017	0.984834	0.984834	69790
KEGG_Path	mmu0411	Oocyte me	1/164	116/8294	0.903002	0.984834	0.984834	56150
KEGG_Path	mmu0465	Natural kill	1/164	118/8294	0.906853	0.984834	0.984834	230396
KEGG_Path	mmu0402	cAMP signa	2/164	198/8294	0.906951	0.984834	0.984834	14813/192
KEGG_Path	mmu0411	Cell cycle	1/164	123/8294	0.91583	0.984834	0.984834	56150
KEGG_Path	mmu0461	Platelet act	1/164	124/8294	0.91752	0.984834	0.984834	18762
KEGG_Path	mmu0438	Osteoclast	1/164	128/8294	0.923947	0.984834	0.984834	21812
KEGG_Path	mmu0414	Autophagy	1/164	130/8294	0.926971	0.984834	0.984834	12048
KEGG_Path	mmu0516	Herpes sim	2/164	215/8294	0.929659	0.984834	0.984834	20304/230
KEGG_Path	mmu0304	Spliceosom	1/164	133/8294	0.931285	0.984834	0.984834	212880
KEGG_Path	mmu0421	Apoptosis	1/164	136/8294	0.935345	0.984834	0.984834	12048
KEGG_Path	mmu0501	Parkinson (	1/164	144/8294	0.945044	0.988015	0.988015	66725
KEGG_Path	mmu0426	Adrenergic	1/164	147/8294	0.948296	0.988015	0.988015	58200
KEGG_Path	mmu0516	Hepatitis C	1/164	160/8294	0.960315	0.990393	0.990393	230396
KEGG_Path	mmu0402	cGMP-PKG	1/164	168/8294	0.966284	0.990393	0.990393	58802
KEGG_Path	mmu0501	Alzheimer	1/164	175/8294	0.97077	0.990393	0.990393	14813
KEGG_Path	mmu0414	Phagosom	1/164	181/8294	0.97414	0.990393	0.990393	100226
KEGG_Path	mmu0421	Cellular ser	1/164	186/8294	0.97665	0.990393	0.990393	21812
KEGG_Path	mmu0451	Focal adhe	1/164	199/8294	0.982101	0.990393	0.990393	68794
KEGG_Path	mmu0401	Rap1 signa	1/164	209/8294	0.985416	0.990393	0.990393	18762
KEGG_Path	mmu0520	Viral carcin	1/164	231/8294	0.990714	0.990714	0.990714	74197
KEGG_Path	mmu0497	Bile secreti	8/275	71/8294	0.002295	0.29818	0.29818	18669/186
KEGG_Path	mmu0520	MicroRNAs	19/275	281/8294	0.002475	0.29818	0.29818	18669/138
KEGG_Path	mmu0497	Mineral ab	6/275	45/8294	0.003454	0.29818	0.29818	67821/152
KEGG_Path	mmu0346	Fanconi an	6/275	51/8294	0.006473	0.419159	0.419159	71885/699
KEGG_Path	mmu0091	Nitrogen m	3/275	17/8294	0.017369	0.899701	0.899701	12349/123
KEGG_Path	mmu0413	SNARE inte	4/275	33/8294	0.022718	0.930659	0.930659	54399/203
KEGG_Path	mmu0491	Prolactin si	6/275	72/8294	0.03167	0.930659	0.930659	13983/147
KEGG_Path	mmu0496	Proximal tu	3/275	22/8294	0.034845	0.930659	0.930659	67821/123
KEGG_Path	mmu0401	MAPK sign	16/275	294/8294	0.035124	0.930659	0.930659	12287/122
KEGG_Path	mmu0414	Phagosom	11/275	181/8294	0.038165	0.930659	0.930659	74915/149
KEGG_Path	mmu0453	Tight juncti	10/275	167/8294	0.050822	0.930659	0.930659	68178/581

KEGG_Path	mmu00601	Glycosphin	3/275	27/8294	0.058693	0.930659	0.930659	239559/10
KEGG_Path	mmu04380	Osteoclast	8/275	128/8294	0.062242	0.930659	0.930659	14200/147
KEGG_Path	mmu00380	Tryptophan	4/275	46/8294	0.065099	0.930659	0.930659	266645/71
KEGG_Path	mmu03010	Ribosome	10/275	175/8294	0.065571	0.930659	0.930659	66242/199
KEGG_Path	mmu04658	Th1 and Th	6/275	87/8294	0.068382	0.930659	0.930659	15980/161
KEGG_Path	mmu02010	ABC transp	4/275	47/8294	0.069385	0.930659	0.930659	18669/186
KEGG_Path	mmu04930	Type II diab	4/275	48/8294	0.073813	0.930659	0.930659	12287/122
KEGG_Path	mmu01523	Antifolate r	3/275	30/8294	0.075846	0.930659	0.930659	239273/14
KEGG_Path	mmu04974	Protein dig	6/275	90/8294	0.077825	0.930659	0.930659	67821/232
KEGG_Path	mmu04218	Cellular ser	10/275	186/8294	0.089948	0.930659	0.930659	14985/150
KEGG_Path	mmu00120	Primary bile	2/275	16/8294	0.096896	0.930659	0.930659	208665/56
KEGG_Path	mmu00603	Glycosphin	2/275	16/8294	0.096896	0.930659	0.930659	239559/14
KEGG_Path	mmu04961	Endocrine	4/275	54/8294	0.103244	0.930659	0.930659	67821/166
KEGG_Path	mmu04144	Endocytosi	13/275	270/8294	0.113457	0.930659	0.930659	213990/21
KEGG_Path	mmu04660	T cell recep	6/275	101/8294	0.11834	0.930659	0.930659	12042/147
KEGG_Path	mmu00511	Other glyca	2/275	18/8294	0.118394	0.930659	0.930659	11593/110
KEGG_Path	mmu05320	Autoimmun	5/275	79/8294	0.121006	0.930659	0.930659	14985/150
KEGG_Path	mmu05226	Gastric can	8/275	150/8294	0.125123	0.930659	0.930659	18669/123
KEGG_Path	mmu05213	Endometria	4/275	58/8294	0.125409	0.930659	0.930659	12385/138
KEGG_Path	mmu04932	Non-alcoh	8/275	151/8294	0.128574	0.930659	0.930659	13063/131
KEGG_Path	mmu04064	NF-kappa	6/275	104/8294	0.130924	0.930659	0.930659	12042/168
KEGG_Path	mmu05321	Inflammato	4/275	59/8294	0.131242	0.930659	0.930659	15980/161
KEGG_Path	mmu04714	Thermogen	11/275	230/8294	0.142166	0.930659	0.930659	67605/119
KEGG_Path	mmu05163	Human cyt	12/275	256/8294	0.143297	0.930659	0.930659	12915/130
KEGG_Path	mmu04975	Fat digestio	3/275	40/8294	0.145872	0.930659	0.930659	11808/237
KEGG_Path	mmu00983	Drug meta	5/275	87/8294	0.161683	0.930659	0.930659	436059/14
KEGG_Path	mmu05160	Hepatitis C	8/275	160/8294	0.161775	0.930659	0.930659	58187/130
KEGG_Path	mmu05230	Central car	4/275	64/8294	0.161992	0.930659	0.930659	13866/197
KEGG_Path	mmu04210	Apoptosis	7/275	136/8294	0.165247	0.930659	0.930659	13063/131
KEGG_Path	mmu04610	Compleme	5/275	88/8294	0.167118	0.930659	0.930659	12267/589
KEGG_Path	mmu05416	Viral myoca	5/275	88/8294	0.167118	0.930659	0.930659	13063/149
KEGG_Path	mmu04973	Carbohydra	3/275	43/8294	0.169949	0.930659	0.930659	67821/205
KEGG_Path	mmu05170	Human imm	11/275	239/8294	0.170218	0.930659	0.930659	252903/13
KEGG_Path	mmu05168	Herpes sim	10/275	215/8294	0.176788	0.930659	0.930659	13063/570
KEGG_Path	mmu04211	Longevity r	5/275	90/8294	0.178202	0.930659	0.930659	67605/129
KEGG_Path	mmu00232	Caffeine m	1/275	6/8294	0.18321	0.930659	0.930659	13077
KEGG_Path	mmu00982	Drug meta	4/275	68/8294	0.188285	0.930659	0.930659	71724/130
KEGG_Path	mmu04622	RIG-I-like r	4/275	68/8294	0.188285	0.930659	0.930659	242519/26
KEGG_Path	mmu05222	Small cell lu	5/275	92/8294	0.189555	0.930659	0.930659	13063/171
KEGG_Path	mmu05221	Acute mye	4/275	69/8294	0.195064	0.930659	0.930659	14784/175
KEGG_Path	mmu04650	Natural kill	6/275	118/8294	0.197264	0.930659	0.930659	14784/239
KEGG_Path	mmu00563	Glycosylph	2/275	25/8294	0.200429	0.930659	0.930659	56176/230
KEGG_Path	mmu05224	Breast canc	7/275	147/8294	0.215401	0.930659	0.930659	13866/139
KEGG_Path	mmu04662	B cell recep	4/275	72/8294	0.215831	0.930659	0.930659	12042/147
KEGG_Path	mmu05412	Arrhythmo	4/275	72/8294	0.215831	0.930659	0.930659	12385/109
KEGG_Path	mmu04918	Thyroid ho	4/275	73/8294	0.222886	0.930659	0.930659	12915/678
KEGG_Path	mmu04966	Collecting	2/275	27/8294	0.224997	0.930659	0.930659	74915/123
KEGG_Path	mmu04723	Retrograde	7/275	150/8294	0.229967	0.930659	0.930659	12287/147

KEGG_Path	mmu0516	Epstein-Ba	10/275	230/8294	0.233078	0.930659	0.930659	13063/149
KEGG_Path	mmu0493	AGE-RAGE	5/275	100/8294	0.23731	0.930659	0.930659	11596/264
KEGG_Path	mmu0515	Tuberculos	8/275	178/8294	0.238393	0.930659	0.930659	12042/130
KEGG_Path	mmu0465	Th17 cell d	5/275	102/8294	0.249746	0.930659	0.930659	15980/168
KEGG_Path	mmu0152	Platinum d	4/275	77/8294	0.251665	0.930659	0.930659	13063/138
KEGG_Path	mmu0472	Synaptic ve	4/275	77/8294	0.251665	0.930659	0.930659	74915/122
KEGG_Path	mmu0497	Pancreatic	5/275	103/8294	0.256026	0.930659	0.930659	67821/123
KEGG_Path	mmu0513	Salmonella	4/275	78/8294	0.258982	0.930659	0.930659	15980/264
KEGG_Path	mmu0075	Vitamin B6	1/275	9/8294	0.261856	0.930659	0.930659	71724
KEGG_Path	mmu0515	Staphyloco	3/275	56/8294	0.283775	0.930659	0.930659	12267/171
KEGG_Path	mmu0516	Kaposi sarc	9/275	217/8294	0.293293	0.930659	0.930659	13063/147
KEGG_Path	mmu0493	Insulin resis	5/275	109/8294	0.294432	0.930659	0.930659	384783/19
KEGG_Path	mmu0513	Legionellos	3/275	58/8294	0.302026	0.930659	0.930659	13063/196
KEGG_Path	mmu0463	JAK-STAT	7/275	165/8294	0.307052	0.930659	0.930659	71724/147
KEGG_Path	mmu0013	Ubiquinon	1/275	11/8294	0.310048	0.930659	0.930659	217707
KEGG_Path	mmu0301	RNA transp	7/275	167/8294	0.317735	0.930659	0.930659	13669/163
KEGG_Path	mmu0454	Gap junctio	4/275	86/8294	0.318727	0.930659	0.930659	14784/148
KEGG_Path	mmu0472	Glutamater	5/275	114/8294	0.327144	0.930659	0.930659	14708/148
KEGG_Path	mmu0451	Cell adhesi	7/275	169/8294	0.328483	0.930659	0.930659	12560/581
KEGG_Path	mmu0056	Glycerolipi	3/275	61/8294	0.329492	0.930659	0.930659	15450/189
KEGG_Path	mmu0076	Nicotinate	2/275	36/8294	0.336361	0.930659	0.930659	71724/181
KEGG_Path	mmu0461	Renin-angi	2/275	36/8294	0.336361	0.930659	0.930659	16613/173
KEGG_Path	mmu0534	Primary im	2/275	36/8294	0.336361	0.930659	0.930659	16818/197
KEGG_Path	mmu0516	Hepatitis B	6/275	143/8294	0.337524	0.930659	0.930659	12915/130
KEGG_Path	mmu0421	Longevity	3/275	62/8294	0.33865	0.930659	0.930659	67605/384
KEGG_Path	mmu0521	Thyroid ca	2/275	37/8294	0.34855	0.930659	0.930659	27015/197
KEGG_Path	mmu0491	Progestero	4/275	90/8294	0.349057	0.930659	0.930659	99152/208
KEGG_Path	mmu0461	Antigen pr	4/275	91/8294	0.356653	0.930659	0.930659	14985/150
KEGG_Path	mmu0465	IL-17 signa	4/275	91/8294	0.356653	0.930659	0.930659	16163/264
KEGG_Path	mmu0048	Glutathion	3/275	64/8294	0.356939	0.930659	0.930659	66116/148
KEGG_Path	mmu0462	Cytosolic	3/275	64/8294	0.356939	0.930659	0.930659	242519/19
KEGG_Path	mmu0533	Allograft re	3/275	64/8294	0.356939	0.930659	0.930659	14985/150
KEGG_Path	mmu0520	Viral carcin	9/275	231/8294	0.358418	0.930659	0.930659	12915/991
KEGG_Path	mmu0496	Aldosteron	2/275	38/8294	0.360664	0.930659	0.930659	67821/838
KEGG_Path	mmu0533	Graft-vers	3/275	65/8294	0.36606	0.930659	0.930659	14985/150
KEGG_Path	mmu0152	Endocrine	4/275	93/8294	0.371841	0.930659	0.930659	13866/139
KEGG_Path	mmu0097	Aminoacyl-	3/275	66/8294	0.37516	0.930659	0.930659	67417/699
KEGG_Path	mmu0522	Non-small	3/275	66/8294	0.37516	0.930659	0.930659	13866/147
KEGG_Path	mmu0514	Leishmania	3/275	67/8294	0.384233	0.930659	0.930659	15980/264
KEGG_Path	mmu0026	Glycine, se	2/275	40/8294	0.384631	0.930659	0.930659	12116/762
KEGG_Path	mmu0035	Tyrosine m	2/275	40/8294	0.384631	0.930659	0.930659	71724/140
KEGG_Path	mmu0503	Nicotine a	2/275	40/8294	0.384631	0.930659	0.930659	12287/216
KEGG_Path	mmu0466	Fc epsilon	3/275	68/8294	0.393277	0.930659	0.930659	14784/161
KEGG_Path	mmu0086	Porphyrin	2/275	41/8294	0.39647	0.930659	0.930659	67417/152
KEGG_Path	mmu0073	Thiamine n	1/275	15/8294	0.397227	0.930659	0.930659	11650
KEGG_Path	mmu0494	Type I diab	3/275	70/8294	0.411259	0.930659	0.930659	14985/150
KEGG_Path	mmu0462	Toll-like re	4/275	99/8294	0.41717	0.930659	0.930659	242519/26
KEGG_Path	mmu0492	Adipocyto	3/275	71/8294	0.420189	0.930659	0.930659	384783/19

KEGG_Path	mmu04925	Aldosteron	4/275	100/8294	0.424664	0.930659	0.930659	12915/678
KEGG_Path	mmu04020	Calcium sig	7/275	187/8294	0.426665	0.930659	0.930659	12287/122
KEGG_Path	mmu05218	Melanoma	3/275	72/8294	0.429074	0.930659	0.930659	14171/141
KEGG_Path	mmu05166	Human T-c	9/275	246/8294	0.4299	0.930659	0.930659	99152/129
KEGG_Path	mmu03022	Basal trans	2/275	44/8294	0.431331	0.930659	0.930659	99169/570
KEGG_Path	mmu04140	Autophagy	5/275	130/8294	0.432991	0.930659	0.930659	67605/384
KEGG_Path	mmu04926	Relaxin sigi	5/275	131/8294	0.439547	0.930659	0.930659	12915/147
KEGG_Path	mmu04068	FoxO signa	5/275	132/8294	0.446086	0.930659	0.930659	14784/148
KEGG_Path	mmu04971	Gastric acic	3/275	74/8294	0.446696	0.930659	0.930659	67821/123
KEGG_Path	mmu05212	Pancreatic	3/275	75/8294	0.455426	0.930659	0.930659	13866/270
KEGG_Path	mmu05214	Glioma	3/275	75/8294	0.455426	0.930659	0.930659	215303/14
KEGG_Path	mmu04141	Protein prc	6/275	163/8294	0.456466	0.930659	0.930659	12915/131
KEGG_Path	mmu05133	Pertussis	3/275	76/8294	0.464098	0.930659	0.930659	26416/196
KEGG_Path	mmu05220	Chronic my	3/275	76/8294	0.464098	0.930659	0.930659	14784/270
KEGG_Path	mmu00565	Ether lipid	2/275	47/8294	0.465097	0.930659	0.930659	66569/686
KEGG_Path	mmu00230	Purine met	5/275	136/8294	0.472041	0.930659	0.930659	56248/273
KEGG_Path	mmu05162	Measles	5/275	136/8294	0.472041	0.930659	0.930659	242519/15
KEGG_Path	mmu00100	Steroid bio	1/275	19/8294	0.473425	0.930659	0.930659	13121
KEGG_Path	mmu05030	Cocaine ac	2/275	48/8294	0.476089	0.930659	0.930659	12915/196
KEGG_Path	mmu05145	Toxoplasm	4/275	108/8294	0.483584	0.930659	0.930659	13063/159
KEGG_Path	mmu04022	cGMP-PKG	6/275	168/8294	0.485676	0.930659	0.930659	12915/678
KEGG_Path	mmu04621	NOD-like r	6/275	168/8294	0.485676	0.930659	0.930659	242519/26
KEGG_Path	mmu05164	Influenza A	6/275	168/8294	0.485676	0.930659	0.930659	13063/242
KEGG_Path	mmu04024	cAMP signa	7/275	198/8294	0.486198	0.930659	0.930659	239273/67
KEGG_Path	mmu00510	N-Glycan b	2/275	49/8294	0.486942	0.930659	0.930659	57377/682
KEGG_Path	mmu04979	Cholestero	2/275	49/8294	0.486942	0.930659	0.930659	11808/154
KEGG_Path	mmu00532	Glycosamir	1/275	20/8294	0.490925	0.930659	0.930659	217119
KEGG_Path	mmu04120	Ubiquitin m	5/275	139/8294	0.491255	0.930659	0.930659	99152/838
KEGG_Path	mmu00591	Linoleic aci	2/275	50/8294	0.497655	0.930659	0.930659	13077/745
KEGG_Path	mmu04668	TNF signali	4/275	110/8294	0.497954	0.930659	0.930659	12915/264
KEGG_Path	mmu01521	EGFR tyros	3/275	80/8294	0.498159	0.930659	0.930659	13866/144
KEGG_Path	mmu00531	Glycosamir	1/275	21/8294	0.507845	0.930659	0.930659	545291
KEGG_Path	mmu04625	C-type lect	4/275	112/8294	0.512152	0.930659	0.930659	12042/264
KEGG_Path	mmu05014	Amyotroph	2/275	52/8294	0.518649	0.930659	0.930659	13063/264
KEGG_Path	mmu03018	RNA degra	3/275	83/8294	0.522978	0.930659	0.930659	104625/68
KEGG_Path	mmu05010	Alzheimer	6/275	175/8294	0.525705	0.930659	0.930659	11949/130
KEGG_Path	mmu04146	Peroxisome	3/275	84/8294	0.531102	0.930659	0.930659	67528/713
KEGG_Path	mmu05410	Hypertroph	3/275	84/8294	0.531102	0.930659	0.930659	19082/240
KEGG_Path	mmu04670	Leukocyte	4/275	115/8294	0.533101	0.930659	0.930659	58187/123
KEGG_Path	mmu04350	TGF-beta s	3/275	85/8294	0.539148	0.930659	0.930659	14313/163
KEGG_Path	mmu04911	Insulin secr	3/275	85/8294	0.539148	0.930659	0.930659	12915/678
KEGG_Path	mmu00900	Terpenoid	1/275	23/8294	0.540022	0.930659	0.930659	68603
KEGG_Path	mmu04261	Adrenergic	5/275	147/8294	0.541155	0.930659	0.930659	12915/678
KEGG_Path	mmu04923	Regulation	2/275	55/8294	0.549028	0.930659	0.930659	384783/22
KEGG_Path	mmu00534	Glycosamir	1/275	24/8294	0.555316	0.930659	0.930659	217119
KEGG_Path	mmu04977	Vitamin dic	1/275	24/8294	0.555316	0.930659	0.930659	11808
KEGG_Path	mmu05210	Colorectal	3/275	88/8294	0.562806	0.930659	0.930659	13063/147
KEGG_Path	mmu05310	Asthma	1/275	25/8294	0.570103	0.930659	0.930659	16163

KEGG_Path	mmu0472	Neurotropl	4/275	121/8294	0.573612	0.930659	0.930659	14784/264
KEGG_Path	mmu0024	Pyrimidine	2/275	58/8294	0.578041	0.930659	0.930659	20133/218
KEGG_Path	mmu0472	GABAergic	3/275	90/8294	0.578164	0.930659	0.930659	12287/147
KEGG_Path	mmu0079	Folate bios	1/275	26/8294	0.5844	0.930659	0.930659	11650
KEGG_Path	mmu0031	Lysine deg	2/275	59/8294	0.587405	0.930659	0.930659	73582/208
KEGG_Path	mmu0415	mTOR sign	5/275	155/8294	0.58868	0.930659	0.930659	67605/749
KEGG_Path	mmu0414	Lysosome	4/275	124/8294	0.593115	0.930659	0.930659	11593/252
KEGG_Path	mmu04611	Platelet act	4/275	124/8294	0.593115	0.930659	0.930659	14724/264
KEGG_Path	mmu0474	Phototrans	1/275	27/8294	0.598223	0.930659	0.930659	14685
KEGG_Path	mmu0495	Maturity or	1/275	27/8294	0.598223	0.930659	0.930659	20526
KEGG_Path	mmu0475	Inflammato	4/275	125/8294	0.599499	0.930659	0.930659	74519/155
KEGG_Path	mmu0431	Wnt signali	5/275	160/8294	0.616986	0.930659	0.930659	329252/18
KEGG_Path	mmu0413	Mitophagy	2/275	63/8294	0.623317	0.930659	0.930659	19697/661
KEGG_Path	mmu0521	Prostate ca	3/275	97/8294	0.629185	0.930659	0.930659	13866/147
KEGG_Path	mmu0302	RNA polym	1/275	30/8294	0.637003	0.930659	0.930659	64424
KEGG_Path	mmu0471	Circadian r	1/275	30/8294	0.637003	0.930659	0.930659	19082
KEGG_Path	mmu0472	Serotonerg	4/275	132/8294	0.64247	0.930659	0.930659	12287/745
KEGG_Path	mmu0491	Estrogen si	4/275	133/8294	0.648357	0.930659	0.930659	12915/139
KEGG_Path	mmu0098	Metabolism	2/275	66/8294	0.648636	0.930659	0.930659	13077/148
KEGG_Path	mmu0063	Glyoxylate	1/275	31/8294	0.649083	0.930659	0.930659	76238
KEGG_Path	mmu0019	Oxidative p	4/275	134/8294	0.654181	0.930659	0.930659	11949/749
KEGG_Path	mmu0514	Chagas dis	3/275	101/8294	0.656372	0.930659	0.930659	15980/264
KEGG_Path	mmu0472	Long-term	2/275	67/8294	0.656772	0.930659	0.930659	14816/201
KEGG_Path	mmu0401	Ras signali	7/275	233/8294	0.658952	0.930659	0.930659	13636/141
KEGG_Path	mmu0472	Dopaminer	4/275	135/8294	0.659939	0.930659	0.930659	12915/122
KEGG_Path	mmu0003	Pentose ph	1/275	32/8294	0.660762	0.930659	0.930659	110639
KEGG_Path	mmu0421	Apoptosis	1/275	32/8294	0.660762	0.930659	0.930659	13063
KEGG_Path	mmu0492	Glucagon s	3/275	102/8294	0.662941	0.930659	0.930659	19082/176
KEGG_Path	mmu0492	Cortisol syr	2/275	68/8294	0.664756	0.930659	0.930659	12915/122
KEGG_Path	mmu05031	Amphetam	2/275	68/8294	0.664756	0.930659	0.930659	11838/129
KEGG_Path	mmu0522	Hepatocell	5/275	171/8294	0.675067	0.935126	0.935126	14784/148
KEGG_Path	mmu0520	Proteoglyc	6/275	204/8294	0.675168	0.935126	0.935126	13866/147
KEGG_Path	mmu0406	HIF-1 signa	3/275	105/8294	0.682103	0.937808	0.937808	13866/159
KEGG_Path	mmu0411	p53 signali	2/275	71/8294	0.687816	0.937808	0.937808	13063/579
KEGG_Path	mmu0341	Base excisi	1/275	35/8294	0.693525	0.937808	0.937808	18970
KEGG_Path	mmu0492	Parathyroic	3/275	107/8294	0.694423	0.937808	0.937808	12915/173
KEGG_Path	mmu0452	Adherens j	2/275	72/8294	0.695209	0.937808	0.937808	12385/138
KEGG_Path	mmu0501	Parkinson	4/275	144/8294	0.708833	0.947301	0.947301	11949/130
KEGG_Path	mmu0510	Bacterial in	2/275	74/8294	0.709561	0.947301	0.947301	12385/710
KEGG_Path	mmu0062	Pyruvate m	1/275	38/8294	0.723135	0.951327	0.951327	76238
KEGG_Path	mmu0472	Cholinergic	3/275	113/8294	0.729219	0.951327	0.951327	12287/147
KEGG_Path	mmu0520	Transcriptic	5/275	183/8294	0.731455	0.951327	0.951327	13198/171
KEGG_Path	mmu0426	Cardiac mu	2/275	78/8294	0.736576	0.951327	0.951327	67821/205
KEGG_Path	mmu0411	Oocyte me	3/275	116/8294	0.74542	0.951327	0.951327	99152/208
KEGG_Path	mmu0344	Homologo	1/275	41/8294	0.749893	0.951327	0.951327	237911
KEGG_Path	mmu0421	Ferroptosis	1/275	41/8294	0.749893	0.951327	0.951327	67547
KEGG_Path	mmu0521	Bladder car	1/275	41/8294	0.749893	0.951327	0.951327	13866
KEGG_Path	mmu04921	Oxytocin si	4/275	153/8294	0.752431	0.951327	0.951327	215303/21

KEGG_Path	mmu04151	PI3K-Akt si	10/275	358/8294	0.756134	0.951327	0.951327	12915/136
KEGG_Path	mmu03420	Nucleotide	1/275	43/8294	0.766284	0.951327	0.951327	22590
KEGG_Path	mmu04962	Vasopressi	1/275	43/8294	0.766284	0.951327	0.951327	68097
KEGG_Path	mmu04512	ECM-recep	2/275	83/8294	0.767315	0.951327	0.951327	14724/329
KEGG_Path	mmu04012	ErbB signal	2/275	84/8294	0.773076	0.951327	0.951327	13866/147
KEGG_Path	mmu04152	AMPK sign	3/275	126/8294	0.793898	0.951327	0.951327	67605/384
KEGG_Path	mmu04742	Taste trans	2/275	88/8294	0.794895	0.951327	0.951327	14816/387
KEGG_Path	mmu04510	Focal adhe	5/275	199/8294	0.795165	0.951327	0.951327	13866/147
KEGG_Path	mmu00140	Steroid hor	2/275	89/8294	0.800053	0.951327	0.951327	208665/13
KEGG_Path	mmu05414	Dilated car	2/275	89/8294	0.800053	0.951327	0.951327	24051/205
KEGG_Path	mmu04912	GnRH sign	2/275	90/8294	0.805096	0.951327	0.951327	14784/264
KEGG_Path	mmu00830	Retinol me	2/275	91/8294	0.810026	0.951327	0.951327	71724/130
KEGG_Path	mmu05032	Morphine	2/275	92/8294	0.814845	0.951327	0.951327	12287/147
KEGG_Path	mmu00270	Cysteine ar	1/275	50/8294	0.815668	0.951327	0.951327	12116
KEGG_Path	mmu03040	Spliceosom	3/275	133/8294	0.823071	0.951327	0.951327	20630/141
KEGG_Path	mmu05204	Chemical c	2/275	94/8294	0.824157	0.951327	0.951327	13077/148
KEGG_Path	mmu04015	Rap1 signa	5/275	209/8294	0.828594	0.951327	0.951327	13636/141
KEGG_Path	mmu04640	Hematopo	2/275	95/8294	0.828654	0.951327	0.951327	14724/173
KEGG_Path	mmu04550	Signaling p	3/275	137/8294	0.838112	0.951327	0.951327	14784/163
KEGG_Path	mmu04713	Circadian e	2/275	98/8294	0.841531	0.951327	0.951327	12291/147
KEGG_Path	mmu04217	Necroptosi	4/275	177/8294	0.844173	0.951327	0.951327	242519/15
KEGG_Path	mmu04371	Apelin sign	3/275	139/8294	0.845212	0.951327	0.951327	14708/190
KEGG_Path	mmu04810	Regulation	5/275	215/8294	0.846445	0.951327	0.951327	14171/141
KEGG_Path	mmu04910	Insulin sign	3/275	140/8294	0.84866	0.951327	0.951327	14784/384
KEGG_Path	mmu00280	Valine, leu	1/275	56/8294	0.849628	0.951327	0.951327	71724
KEGG_Path	mmu04080	Neuroactiv	7/275	289/8294	0.850336	0.951327	0.951327	12267/148
KEGG_Path	mmu05165	Human pa	9/275	361/8294	0.853133	0.951327	0.951327	74915/147
KEGG_Path	mmu04360	Axon guida	4/275	180/8294	0.853348	0.951327	0.951327	13636/672
KEGG_Path	mmu04913	Ovarian ste	1/275	57/8294	0.854647	0.951327	0.951327	74519
KEGG_Path	mmu05418	Fluid shear	3/275	143/8294	0.858607	0.951327	0.951327	14867/264
KEGG_Path	mmu04370	VEGF signa	1/275	58/8294	0.8595	0.951327	0.951327	26416
KEGG_Path	mmu05146	Amoebiasis	2/275	106/8294	0.871699	0.958202	0.958202	19697/207
KEGG_Path	mmu04730	Long-term	1/275	61/8294	0.873111	0.958202	0.958202	14816
KEGG_Path	mmu05217	Basal cell c	1/275	63/8294	0.881446	0.963269	0.963269	27015
KEGG_Path	mmu05016	Huntington	4/275	194/8294	0.890337	0.968896	0.968896	11949/130
KEGG_Path	mmu05211	Renal cell c	1/275	68/8294	0.899975	0.975052	0.975052	14784
KEGG_Path	mmu04062	Chemokine	4/275	200/8294	0.903524	0.975052	0.975052	14708/147
KEGG_Path	mmu00562	Inositol ph	1/275	73/8294	0.915617	0.979586	0.979586	97287
KEGG_Path	mmu04071	Sphingolip	2/275	122/8294	0.916813	0.979586	0.979586	26416/196
KEGG_Path	mmu04110	Cell cycle	2/275	123/8294	0.919071	0.979586	0.979586	99152/196
KEGG_Path	mmu01230	Biosynthes	1/275	78/8294	0.92882	0.981645	0.981645	110639
KEGG_Path	mmu04970	Salivary se	1/275	78/8294	0.92882	0.981645	0.981645	67821
KEGG_Path	mmu04060	Cytokine-c	6/275	296/8294	0.932373	0.981645	0.981645	242519/15
KEGG_Path	mmu05323	Rheumatoi	1/275	83/8294	0.939964	0.984208	0.984208	74915
KEGG_Path	mmu00590	Arachidoni	1/275	89/8294	0.951065	0.984208	0.984208	74519
KEGG_Path	mmu04072	Phospholip	2/275	147/8294	0.958729	0.984208	0.984208	14784/148
KEGG_Path	mmu03015	mRNA surv	1/275	96/8294	0.961457	0.984208	0.984208	241989
KEGG_Path	mmu00564	Glyceroph	1/275	97/8294	0.96275	0.984208	0.984208	381925

KEGG_Path	mmu0503	Alcoholism	3/275	199/8294	0.963807	0.984208	0.984208	12915/147
KEGG_Path	mmu0407	Phosphatic	1/275	98/8294	0.964	0.984208	0.984208	97287
KEGG_Path	mmu0523	Choline me	1/275	99/8294	0.965208	0.984208	0.984208	14784
KEGG_Path	mmu0493	Cushing sy	2/275	158/8294	0.969912	0.985126	0.985126	12915/122
KEGG_Path	mmu0491	Thyroid ho	1/275	115/8294	0.979859	0.986836	0.986836	67821
KEGG_Path	mmu0300	Ribosome	1/275	116/8294	0.980536	0.986836	0.986836	100019
KEGG_Path	mmu0120	Carbon me	1/275	120/8294	0.983026	0.986836	0.986836	110639
KEGG_Path	mmu0439	Hippo sign	1/275	154/8294	0.99471	0.99471	0.99471	12385

Count
5
5
5
62
75
39
6
10
28
5
16
24
48
34
13
11
34
63
52
41
19
32
74
9
4
5
25
48
54
76
27
22
23
24
31
31
21
21
12
73
23
24
3
3
3
52

7
5
45
76
73
33
34
21
76
6
26
55
42
68
45
15
26
42
24
29
46
13
45
60
11
61
51
15
7
22
10
37
8
8
9
59
29
31
15
64
26
6
6
6
37
37
22
54

19
62
69
18
32
8
8
8
11
23
19
73
38
57
50
20
45
49
67
17
6
6
52
61
4
4
4
30
8
27
7
63
5
5
5
5
49
16
73
53
21
53
36
9
68
3
3
3

3
3
3
3
52
8
8
19
10
20
12
21
22
25
9
20
18
66
5
5
5
5
5
10
31
11
48
8
8
8
65
20
15
28
4
4
4
4
4
4
4
4
22
26
25
25
67
18

7
6
6
6
63
33
16
16
16
9
9
13
12
10
11
11
55
41
50
31
36
26
8
33
22
37
9
25
7
7
7
7
10
29
48
5
31
26
45
18
13
40
15
54
19
20
47
31

8
27
32
11
17
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
23
4
4
4
4
4
4
4
4
4
4
4
4
4
38
48
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
7
7
7
42
56
12
12
14
14
48
41
19
59
11
40
35
15
6
10

13
5
5
5
5
5
30
39
63
64
21
20
20
38
14
14
50
28
28
42
39
30
47
15
38
26
7
7
7
7
13
21
21
56
40
8
8
38
14
29
69
40
37
37
21
21
25
16

66
6
58
60
43
4
4
4
4
4
4
4
4
4
40
23
32
32
58
5
5
5
5
5
5
33
50
10
10
10
31
31
15
15
24
57
12
12
12
7
7
34
16
16
41
41
35
62

33
58
25
25
13
50
3
3
3
3
3
3
3
3
3
3
3
3
3
3
14
14
32
35
15
33
46
17
17
17
31
37
34
51
43
6
6
6
24
36
13
9
9
14
7
7
7
7

15
11
11
11
39
8
8
8
8
8
16
37
61
5
5
5
5
35
35
27
53
19
10
64
13
13
42
4
4
4
46
15
40
23
27
25
19
19
6
6
6
6
39
12
12
8
8
8

8
40
40
18
17
7
10
10
20
26
24
44
47
49
29
18
21
27
34
9
9
23
17
17
42
53
12
12
5
5
5
5
5
5
5
5
14
22
33
68
8
8
30
66
60
10
21
25

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
23
23
64
28
28
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
7
6
6
6
6
6
6
29
11
24
4
4
4
4
4
4
4
4
4
4
4
4
4
4

4
15
12
12
12
13
61
28
9
9
9
9
18
48
29
29
62
20
17
17
10
42
19
8
8
54
15
15
34
11
35
51
12
12
12
13
22
22
32
7
5
5
5
5
5
5
5
5

53
17
17
28
28
28
59
25
6
6
6
6
6
6
6
6
6
6
21
30
15
10
61
14
14
14
25
60
29
29
13
13
13
12
17
26
8
8
8
57
19
16
16
36
51
15
4
4

4
4
4
4
4
4
4
4
4
4
4
4
4
9
9
9
9
26
23
14
7
7
7
7
7
7
7
32
13
10
10
10
24
37
50
12
11
11
11
11
29
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
16
6
6
6
6
6
26
5
5
5
5
43
41
35
15
15
15
59
8
29
19
30
43
22
32
13
9
9
9
48
16
20

27
12
12
18
10
10
11
11
11
11
51
15
7
7
7
7
40
32
25
38
19
17
47
26
63
20
20
28
29
16
18
30
30
13
60
60
8
46
55
6
6
6
6
6
25
12
54
4

4
4
4
4
4
4
4
4
9
9
22
42
10
28
38
5
5
5
5
5
5
5
5
5
5
37
32
14
18
52
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
13
13
7
7
7
7
7
28
30
32
23
15
15
17
12
12
12
12
12
47
20
8
8
8
8
8
10
9
9
35
52
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
22
23
6
6
6
6
6
6
13
24
59
20
35
21
21
18
14
23
11
11
11
7
7
7
7
7
5
5
5
5
5
5
5
5

5
5
5
10
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
20
8
8
8
8
30
17
40
9
9
9
9
9
9
58
15
12
12
40
25
16
16
31

48
27
29
29
28
14
20
20
37
6
6
6
6
6
6
11
17
17
35
22
13
13
13
13
10
24
29
26
27
7
7
7
9
9
9
9
55
8
8
8
8
8
8
8
16
20
20
40

40
12
17
17
17
22
42
30
5
5
5
5
5
5
5
5
5
5
5
25
36
11
11
11
11
11
11
15
15
35
34
13
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
20
20
10
30
22
29
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
27
27
26
14
35
6
6
6
6
6
6
12
12

12
9
9
9
18
59
32
8
8
8
48
7
7
7
7
7
19
15
31
31
53
21
13
22
16
16
23
23
34
42
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
17
60
31
14
14
40
10
10
10
18
30
30
29
12
12
12
12
20
20
15
26
5
5
5
5
5
5
5
5
5
5
5
5
5
5
22
33
9
16
16
58

11
11
17
8
8
8
8
6
6
6
6
6
6
7
7
7
7
7
7
7
7
37
14
14
19
19
20
46
43
36
15
15
12
12
12
10
10
38
4
4
4
4
4
4
4
4
4
4

4
4
4
4
4
4
4
4
4
4
4
4
4
16
16
40
18
18
18
18
9
9
9
9
9
42
24
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
19
47
21
11
11
11
11
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
14
34
29
8
8
8
8
8
8
15
27
12
16
16
16
5
5
5
5
5
5
5
35
24
10
10
7
7
7
7
7
23
18
18
22
48
6
6
6
20
20
13
13
13

32
32
27
27
14
38
26
9
9
9
9
9
15
30
30
16
22
36
17
17
18
18
18
20
12
12
12
12
38
48
8
8
8
56
26
26
10
13
13
30
25
4
4
4
4
4
4
4

4
4
4
4
4
7
7
7
7
7
7
7
7
22
15
16
45
20
20
17
17
18
34
26
6
6
6
6
6
6
30
9
9
5
5
5
5
5
5
5
5
5
12
41
56
24
38
32

45
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
13
13
13
42
22
60
21
14
14
46
10
10
20
20
20
15
15

15
26
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
8
8
8
16
16
16
18
17
17
11
11
23
48

22
12
12
12
12
12
12
7
7
7
9
20
13
13
13
13
19
44
44
17
16
6
6
6
6
6
6
6
6
36
36
10
10
49
33
33
4
4
4
4
4
4
4
4
4
4
4
4

4
4
4
4
22
26
5
5
5
5
5
5
5
5
5
5
5
5
8
8
8
8
8
29
20
19
36
13
13
17
27
14
16
9
9
9
41
7
7
7
7
7
7
7
10
24
18
18

11
11
23
12
12
12
16
50
6
6
6
6
6
6
6
6
6
13
13
13
13
15
8
8
8
8
14
14
14
14
14
21
21
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
61
9
19
19
5
5
5
5
5
5
44
4

4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
17
17
10
10
10
25
45
16
16
16
7
7
11
15
15
15
15
12
12
12
12
12
14
13
13
34
23
26
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
19
19
35
39
8
8
18
18
61
25
30
17
54

6
6
6
6
6
6
6
6
9
16
16
29
41
10
10
10
10
10
10
35
13
13
13
11
11
11
12
12
12
44
30
25
22
22
36
58
18
18
18
7
7
7
7
7
7
5
5
5

5
5
5
5
5
5
5
5
21
17
17
17
33
8
8
8
8
8
15
32
34
19
14
22
4
4
4
4
4
4
4
4
4
4
4
9
9
9
9
9
9
9
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
13
35
12
12
12
12
12
12
10
10
10
11
11
6
6
6
6
6
6
28
36
46

59
15
15
15
24
24
7
7
14
14
14
28
55
13
8
8
8
8
12
12
11
11
11
11
9
9
9
9
9
9
33
5
5
5
5
5
5
5
5
5
5
5
5
5
5
5
10
10

10
10
10
10
22
22
16
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
19
39
28
18
18
18
40
33
43
6
6
6
6
6
6
6
6

6
59
13
13
13
13
39
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
42
12
19
16
16
7
7
7
7
7
7
35
11
11
11
11
59
10
10
10
8
9
9
9
9
9
9
9
9
15
15
15
18
18
18
25
27
54
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
32
32
14
14
14
14
14
17
13
13
41
5
5
5
5
16
16
16
39
12
23
53

15
15
11
35
35
20
20
28
6
6
6
6
6
33
24
10
10
10
59
36
31
14
14
14
9
9
9
7
7
7
7
7
7
7
7
60
8
8
8
8
8
8
13
13
13
16
38
33

18
18
18
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
24
22
22
15
43
47
11
11
11
11
11
11
11
19
14
10
10
39
16
5
5
5
5
5
5
5
5
31

9
13
13
13
13
18
18
18
20
8
8
8
6
6
6
6
6
6
6
6
6
6
7
7
7
7
7
7
15
25
25
30
30
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
12
12
50
36
23
23
17
21
19
28
11
11
41
16
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
27
10
10
25
13
37
21
9
9
17
35
29
4
4
4
4
4
4
4
4
4

4
4
4
4
4
8
8
8
8
8
20
7
7
7
7
7
7
18
18
5
5
5
5
5
5
5
5
5
5
5
5
5
5
5
5
5
11
11
11
6
6
6
6
6
6
6
23
23

39
43
13
13
19
10
10
15
24
24
30
20
20
9
9
18
18
14
14
14
32
16
16
26
37
37
8
8
8
8
24
11
51
27
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
34
17
17
13
13
35
7
7
7
7
7
7
7
49
32
32
20
36
10
23
46
37
6
6
6
6
6
6
4
4
4
4
4

4
4
4
4
4
4
4
4
4
4
4
4
30
5
5
5
5
5
5
5
14
14
31
9
9
9
50
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
17
11
15
26
23
8
8
8
8
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
46
28
37
12
12
7
7
7

7
7
7
17
23
27
15
15
9
9
9
6
6
6
6
6
6
6
6
6
6
13
13
32
18
18
11
11
51
16
22
5
5
5
5
5
5
5
5
5
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
8
8
4
4
4
4
4
4
4
4
4
4
4
4
4
4

4
4
4
4
36
12
12
12
12
17
10
10
24
21
21
21
15
7
7
7
7
7
7
7
7
13
16
16
11
11
11
11
11
11
23
23
32
24
47
6
6
6
6
6
6
12
12
10

10
10
8
8
8
8
8
32
19
13
16
5
5
5
5
5
5
5
5
41
11
11
11
9
7
7
7
7
4
4
4
4
4
4
4
4
4
4
4
22
22
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
15
15
19
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
16
16
10
10
10
10
10

20
6
6
8
8
8
8
21
27
11
47
9
9
40
53
25
12
12
12
20
5
5
5
5
5
5
5
5
5
5
5
5
5
26
26
16
7
7
7
7
7
7
7
28
28
13
13
22

10
10
10
10
10
53
23
18
41
14
14
32
25
8
8
8
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
35
6
6
6
6
6
6
16
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
43
43
9
9
9
9
13
13
49
18
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
14
10
10
10
10
7
7
7
7
7
7
15
15
5
5
5
5
5
5
5
5
5
11
11
8
8
17
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
37
25
12
12
18
18
13
13
9
9
9
6
6
6
6
6
14
15
23
10
10
10
40
4
4
4
4
4
4
4
4
4

4
4
4
4
4
16
27
17
17
17
11
11
7
7
7
7
7
7
7
7
18
19
12
13
8
8
8
22
24
5
5
5
5
5
5
5
5
5
15
15
9
9
9
16
34
36
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
10
10
10
19
20
6
6
21
22
12
12
27
13
32
15
16
8
8
8
8
17
4
4
4
4
4
4
4
4
4
4

18
23
23
23
25
29
10
10
10
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
11
11
5
5
5
5
5
5
5
12
13
14
41
16
17
17
38
6
6
6
6
19
21
22
23
24
24
7
7

7
7
7
7
47
8
8
8
9
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
10
10
10
10
11
11
12
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
27

27
25
17
20
20
20
20
18
19
4
4
4
4
4
4
4
4
4
4
4
4
4
5
5
5
5
5
5
5
5
5
47
28
27
6
6
6
6
6
6
6
6
6
6
6
25
24
24

7
7
7
7
8
8
8
8
18
9
9
9
9
16
16
10
10
10
10
10
10
11
11
13
13
26
26
49
21
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
19
19
30
13
13
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
11
11
9
9
9
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
8
8
7
7
7
5
5
5
5
5
5
5
6
6
6
6
6
6
6
6
23
30
18
18
18

18
18
16
16
15
15
15
14
14
22
11
54
10
19
9
8
8
26
7
7
7
7
6
6
6
15
5
5
5
5
5
5
13
4
4
4
4
4
4
4
19
11
11
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
18
25
10
37
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
16
16
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
21
8
8
7
7
7
13
13
19
18
18
6
6
6
6
6
6
29
17
11
28
16
5
5
5
5
5
5
10
15
15
53
4
4
4
4
4
4
4
4
4
4
4
4
4
18
23

8
8
21
16
7
7
7
7
7
11
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
15
10
6
6
6
6
6
28
14
14
18
27
36
13
13
13
13

9
9
9
21
5
5
5
5
5
5
16
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
8
8
8
8
8
24
24
47
15
19
23
11
11
14
7
7
7
4
4
4
4
4
4
4
4
4
4
4
4
4
4
4
6
6
6
48
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
11
11
8
8
21
5
5
5
5
5
5
5
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
10
10
13
23
7
7
7
7
22
15
9
4
4
4
4
4
4
4
4
4
4
4
4
14
6
6
6
6
6
6
11
11
20

8
8
8
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

16
19
22
10
12
5
5
5
5
5
5
5
5
5
5
5
5
5
48
7
7
7
7
20
20
47
36
14
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3

3
3
3
11
11
11
13
37
6
6
6
8
15
46
10
10
10
10
20
4
4
4
4
4
4
4
4
4
4
4
19
13
13
5
5
5
5
20
40
10
30
8
12
12
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
6
41
29
16
3
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
11
45
22
17
7
7
4
4
4
4
4
4
4
4
5
5
5
5
5
5
5
18
8
8
13
6
6
6
6
31
9
9
9
18

7
7
7
10
10
3
3
3
3
3
3
3
3
3
3
3
3
3
15
8
28
4
4
4
4
4
4
4
4
4
4
4
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
11
5
5
5
5
18
20
9
9
9
9
6
6
6
6
6
10
10
7
13
31
11
26
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
9
12
4
4
4
4
4
4
4
4
5
5
5
5
5
5
5
5
5
3
3
3
3
3
3
3

3
3
3
3
3
3
3
3
3
35
6
6
6
6
6
7
7
31
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
17
12
9
9
20

16
21
11
5
5
5
5
5
5
5
5
48
6
6
6
6
6
32
32
4
4
4
4
4
4
4
4
22
7
8
8
3
3
3
3
3
3
3
3
3
3
3
3
13
16
19
10
10

14
14
11
15
18
7
7
5
5
5
5
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
39
17
4
4
4
4

4
4
4
4
4
4
4
25
10
10
11
11
16
3
3
3
3
3
3
3
3
3
3
17
7
7
8
6
6
10
5
5
5
11
4
4
4
4
4
13
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
9
7
20
6
6
26
12
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
34
45
5
5
39
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
9

8
13
6
6
6
15
21
5
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
3
3
3
3
3
3
3
3
3
3
3
11
9
14
14
4
4
4
4

4
4
4
4
4
4
28
10
10
10
13
13
5
8
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
3
40
13
6
21
14
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
4
4
4
10
9
9
8
7
7
13
12
15
15
16
9
36
3
3
3
3
3
3
3
3
3
3
3
3
3
8
4
4
4
4
38
7
25
5
5
5
5
5
5

5
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
10
9
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
6
6
6
8
19
49
4
4
4
7
7
7
3
3
3
3
3
3
3
3
3
5
5
5
9
20
13
13
13
28
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
10
10
18
7
7
4
4
4
4
4
4
3
3
3
3
17
17
20
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
10
10
14

31
7
7
7
9
18
8
2
2
2
2
2
2
2
2
2
2
2
2
2
2
5
5
5
4
45
6
3
3
3
3
9
18
7
7
16
15
18
5
5
5
17
12
4
4
4
4
4

4
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
11
14
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
18
3
3
3
3
3
3
15
9
6
6
4

4
8
24
14
3
3
3
3
3
3
3
3
3
13
2
2
2
2
2
2
2
2
2
2
2
2
2
2
16
6
5
5
29
7
10
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
19
8
4
4
4
4
4
4
9
20
15
15
6
6
5
5
3
3
3
3
8
11
20

9
2
2
2
2
2
2
2
2
2
2
2
2
2
4
4
18
14
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
5
5
3
3
3
4
4
4
23
7
7
2
2
2
2
2
2
2
2
2
2
8
6
16
25
10
3
4
43
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
18
15
5
5
2
2
2
2
2
2
2
8
42
7
7
7
10
6
4
3
3
22
18

15
8
17
10
22
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
14
4
4
15
3
3
3
3
5
5
30
17

13
4
4
10
14
14
2
2
2
2
5
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
36
10
11
5
3
3
2
2
2
2
6
10
8
7
7
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
15
9
9
34
8
2
2
2
4
6
43
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
20
20
2

2
2
2
15
6
34
20
3
3
3
3
6
14
1
1
1
1
1
1
2
2
8
8
3
3
27
2
2
2
1
1
1
1
1
1
1
1
1
3
3
3
12
4
4
34
2
16
1

1
1
1
1
1
1
1
1
1
1
6
8
2
2
33
10
1
1
1
1
1
1
1
1
2
3
3
20
1
1
1
2
2
2
2
2
6
11
15
20
2
2
2
1
1
1
1
1

1
1
1
1
1
1
5
6
6
2
1
1
1
1
1
1
6
3
23
4
2
2
9
10
6
1
1
1
1
8
9
4
2
2
2
3
3
3
5
1
1
1
1
1
1
2
3
28

1
1
1
2
2
2
2
2
4
7
1
1
1
1
1
2
1
1
6
6
1
1
1
3
3
1
3
3
1
1
2
4
1
2
1
5
28
1
1
1
1
1
1
1
1
2
4
1

21
18
21
23
21
3
3
3
7
4
3
2
2
2
2
2
2
2
2
3
4
4
4
4
5
4
11
7
2
4
18
6
3
4
9
4
3
10
11
2
2
2
2
14
3
9
9
9

2
2
2
2
2
2
2
4
9
7
12
11
11
7
11
11
3
3
7
7
13
4
10
13
2
3
3
3
3
3
3
3
4
16
10
9
15
3
3
3
2
2
2
2
2
6
5
16

6
9
10
5
14
4
16
8
5
3
3
3
4
2
2
12
11
5
10
4
4
3
6
4
8
7
2
2
2
2
2
2
2
2
2
2
3
3
3
3
3
7
16
13
6
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
4
4
8
8
8
5
5
8
8
2
2

2
2
2
2
2
2
3
6
5
4
15
6
3
8
2
2
2
2
2
2
2
2
2
2
2
3
3
3
3
9
6
7
7
8
8
15
3
3
9
6
2
2
2
2
2
2
2
2

4
6
16
3
3
7
7
5
9
4
7
7
8
3
4
8
8
2
2
2
2
2
2
2
2
2
2
12
7
5
3
3
3
5
5
7
4
4
4
4
12
2
2
2
2
2
2
2

2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
16
7
3
3
3
11
4
4
5
10
11
10

10
5
4
4
2
2
2
2
2
13
8
8
7
4
4
5
5
5
2
2
2
2
2
2
2
6
8
8
4
3
3
5
5
5
14
9
9
10
4
4
4
12
3
3
6
6
6
2

2
2
2
2
2
7
11
4
4
12
9
4
9
11
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
4
4
8
11
3
3
3
3
3
3
5
14
13
5
5
4
7
3
3
3
3
3
15
12
10
5
5
2
2

2
2
2
2
2
6
6
5
5
8
4
6
12
8
8
5
5
6
4
3
3
3
3
3
3
2
2
2
2
2
2
2
2
2
2
2
2
8
6
6
10
4
4
5
3
3
3
7

4
8
7
2
2
2
2
2
6
11
3
3
3
3
3
4
4
12
9
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
8
11
11
14
3
3
3
3
3
14
7
5
2
2
2
2
2
2
2
2
2
2
4
6
3
3
3
3
3
9
4
6
11
2
2
2
2
2
2
2
2
11
7
7
7
3
3

3
5
6
4
4
4
6
6
8
7
7
3
3
3
6
5
7
2
2
2
2
2
2
2
2
2
2
2
2
2
2
8
4
4
13
7
10
3
3
3
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
6
6
9
7
13
8
10
6
3
3
2
2
2
2
2
2
5
5
4
11
5
5
9
4
4
4
4
3
3
14
12
11
2
2
2
2
2
2

2
2
4
9
3
3
3
5
4
4
6
9
5
7
3
3
3
3
3
9
6
2
2
2
2
2
2
2
2
4
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
8
5
3
3
4
4
11
11
5

2
2
2
2
2
2
6
6
10
9
7
8
12
9
4
4
4
4
7
7
8
5
9
3
3
2
2
2
2
2
2
2
2
2
8
4
12
9
7
3
6
10
11
4
4
5
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
2
10
5
4
12
3
3
13
5
10
4
4
7
7
7
2
2
2
2
2
2
2
2
2
2
5
4

4
9
9
6
3
3
3
3
11
4
4
4
2
2
2
2
2
2
2
2
2
2
10
7
8
3
4
9
5
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
7
6
4
3
3
3
2
2
2
2
2
2
2
2
6
9
5
5
7
4
4
4
8
3
3
2
2
2
2
2
2
2
5
8
3
3
3
3
4
4
4
4
5
13
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
3
4
4
4
4
4
2
2
2
2
2
2
2
2
2
2
2
6
6
6
7
5
12
4
4
4
3
6
6
6
5
2
2
2
2
2
4

4
11
3
3
5
4
4
13
6
8
8
9
2
2
2
2
2
2
2
2
3
3
3
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
8
4
4
3
3
5
5
2
2
2
2
2
2
2
2
2
2
9
6
6
6
7
13
3
2
2
2

2
2
2
2
3
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
6
3
3
3
12
4
2
2
2
2
2
2
2
2
2
2
2
11
4
4
4
3
7
6
2
2
2
2
7
4
4
3
6
6
10
4
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
12
3
3
3
3
3
3
3
3
2

2
2
8
5
7
7
4
4
4
11
8
6
3
3
8
4
12
6
2
2
2
2
2
2
2
2
2
8
5
5
4
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
10
4
4
2
2
2
2
2
2
2
3
3
3
3
5
7
6
6
10

10
7
5
5
5
6
3
3
3
3
3
8
2
2
2
2
2
2
2
2
2
2
2
4
5
10
7
11
3
3
5
4
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
8
6
5
3
3
4
4
4
4
11
9
9
7
5
5
5

4
3
3
3
3
6
2
2
2
2
12
7
4
4
4
4
9
8
3
3
7
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
4
4
4
5
5
11
6
6
3
7
7
6
11
2
2
2
2

2
2
2
2
7
3
5
5
6
11
7
4
4
7
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
9
2
2
2
11
6
5
8
4
4
4
4
3
3
3
3
3
3
5
5
10
2
5
3
3
3
8
9
4
4
9
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
3
3
8
4
4
4
6
3
5
5
7
4
6
6
8
2
2
2
2
2
2
2
11
5
5
4
4
4

10
3
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
4
7
3
3
3

3
4
4
10
8
5
11
2
2
2
2
6
5
5
5
10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
3
3
3
3
4
2
2
2
2
2
2
3
3
9
6
2
2
2
2
2
2
5
4
7
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
3
2
2
2
5
5
5
5
5
6
4
8
5
5
7
4
11
2
2
2
2
2
2
2
2
2
2
2
2
6
5
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
3
3
6
5
5
7
2
2
2
2
2
2
2
6
3
3
3
3
5
9
6
5

3
3
3
2
2
2
2
9
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
5
4
10
3
3
3

5
2
2
2
2
2
2
4
5
3
3
3
3
4
4
10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
6
10
3
3
4

7
4
4
2
2
2
2
2
2
2
2
5
11
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
2
2
2
5
4
4
4
4
11
6
6

3
7
5
9
2
2
2
2
2
2
3
3
3
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
6
9
5
5
2

2
2
3
4
5
10
4
3
9
5
5
5
2
2
2
2
2
2
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
4
6
6
3
8
10
2
2
2
2
2
6
4
4
5
3
3
3
3
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
2
2
2
2
2
2
2
3
3
3
4
2
2
2
2
2
2
2
10
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
4
3
3
3
7
2
6
4
4
3
3
5
6
6
6
9
4
2
2
5
6
6
3
3
3
3
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
6
5
3
3
3
2
2
2
2
2
2
4
5
5
6
3
3
3
3
4
4
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
8
6
10
3
3
3
6
2
2
2
2
2
2
2
2
4
3
3
3
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
2
2
2
2
2
3
3
3
3
8
2
2
2
2
2
4
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
3
3
9
4
5
5
2
2
3
3
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
10
6
2
2
2
2
4
4
4
3
3
3
3
6
4
4
2
2
2
2
2
8
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
3

3
9
2
2
2
2
6
6
4
4
7
5
3
3
3
3
3
6
7
4
2
2
2
2
2
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
3
3
3
4
4
4
5
6
2
2
2
2
2
2
10
3
3
3
3
3
3
9
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
7
7
3
3

2
2
2
4
3
2
2
2
2
2
2
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
8
2
2
2
2
3
3
3
3
4
4
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
3
3
3
6
4
3
3
3
2
2
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7

2
2
2
2
5
4
7
5
5
5
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
4
3
3
3
4
2
2
2
2
2
2
3
3
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
5
3
2
2
2
2
2
2
6
6
6
6
3
3
3
4
4
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
6

3
6
2
2
2
4
3
3
3
3
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
6
2
2
2
2
2
2
3
7
6
4
2
2
2
2
1
1
1
1

1
1
1
1
1
1
1
1
1
5
5
6
3
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
4
4
5
2
2
4
6
6
8
2
2
2
2
1
1

1
1
1
1
1
1
1
7
7
4
4
5
5
8
3
3
3
2
2
2
2
2
1
1
1
1
1
6
3
7
2
2
2
2
4
5
6
6
1
1
1
1
1
1
1
1
1
1

1
1
2
2
2
2
5
3
4
2
2
9
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
4
2
2
2
2
2
2
5
4

3
5
1
1
1
1
1
1
1
1
2
2
9
3
8
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
2
2
3
4
9
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
8
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
6
3
3
3
2
2
2
2
4
3
1
1
1
1
1

1
2
2
2
3
2
2
2
1
1
1
1
1
1
1
7
4
7
2
2
2
2
2
1
1
1
1
1
1
1
7
8
2
2
1
1
1
1
1
4
3
3
6
2
8
1
1
1

1
1
1
1
1
1
1
1
1
6
7
2
2
1
1
1
1
1
1
1
1
1
1
3
2
5
3
2
1
1
1
1
1
1
1
1
1
1
1
1
1
3
4
2
2
2
3
3

7
1
1
1
1
1
1
1
1
4
3
6
2
1
1
1
1
1
1
1
1
1
1
1
1
1
2
1
1
1
1
1
1
3
3
2
3
3
3
4
1
1
1
1
1
2
2
2

3
3
3
3
6
6
5
3
1
1
1
1
1
2
1
1
1
4
2
5
1
1
1
1
1
1
1
1
6
3
4
4
2
2
2
1
1
1
1
1
1
1
1
2
3
4
1
1

1
1
1
2
4
8
7
1
1
1
1
1
1
4
5
2
2
2
7
1
1
3
3
2
2
4
1
1
1
1
1
1
1
8
7
3
4
2
2
2
1
1
1
1
3
2
6
1

1
1
1
1
1
1
1
4
2
2
6
7
1
1
1
2
4
7
2
2
1
1
1
1
1
1
1
1
1
1
2
7
7
1
1
1
1
1
2
3
3
1
1
1
1
1
1
1

1
1
1
1
1
2
2
6
5
4
1
1
1
1
1
3
5
2
2
3
5
1
1
1
1
1
1
1
1
2
3
1
1
1
1
1
3
7
3
3
1
1
1
1
1
1
1
1

2
3
4
1
1
1
1
1
2
5
2
2
3
1
1
1
1
1
1
1
5
1
1
1
1
3
4
3
1
1
1
1
1
1
2
2
2
2
2
2
2
2
6
5
5
1
1
1

1
2
1
1
1
2
2
2
4
1
2
3
3
2
1
1
1
1
1
1
1
2
2
2
1
1
1
3
3
2
2
4
1
1
1
4
2
2
2
1
1
1
1
1
1
1
1
1

1
1
2
2
1
1
1
1
1
1
1
1
1
1
4
4
2
4
1
1
1
1
3
3
1
1
1
1
1
1
3
2
2
2
1
1
1
1
1
2
5
1
1
3
3
1
1
3

6
5
5
3
1
2
2
5
3
1
2
2
2
2
2
3
1
1
1
1
1
1
3
2
1
4
1
1
1
1
1
2
2
1
1
4
4
1
1
1
1
1
1
2
2
1
1
3

1
2
1
2
3
1
1
3
2
1
3
1
1
2
1
1
1
1
1
1
2
1
1
1
1
2
2
1
4
1
1
1
1
1
1
4
1
1
2
3
1
1
2
2
1
1
1
1

1
4
1
3
3
1
3
1
4
1
4
1
4
2
4
1
1
1
1
1
1
1
5
20
5
3
15
19
3
4
2
2
2
2
5
10
3
4
6
6
3
5
2
2
2
12
3
3

3
7
8
3
3
5
4
15
3
2
4
4
11
4
3
5
4
4
7
5
2
2
2
2
2
21
12
6
3
3
11
7
19
15
6
5
5
7
2
2
2
2
3
3
11
6
7
3

3
4
10
3
5
13
2
2
2
6
16
5
3
11
3
9
2
2
2
2
6
7
7
3
4
3
2
2
2
2
2
2
2
2
2
2
19
14
6
19
5
5
3
4
4
4
4
3

3
3
3
3
3
2
2
2
2
2
6
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
16
6
4
4
4
5
5
7

9
2
2
2
2
2
2
2
4
4
3
3
6
11
5
4
4
4
4
4
10
3
3
3
6
8
9
4
4
6
6
6
7
7
5
18
2
2
2
2
2
3
3
4
4
4
7
4

4
7
5
5
6
3
3
3
7
7
4
2
2
2
2
2
2
2
2
2
2
2
2
2
7
7
6
9
5
3
3
3
3
3
7
11
14
4
4
17
6
6
5
14
6
7
11
12

16
3
3
3
3
14
2
2
2
2
2
2
2
2
2
5
9
12
7
10
12
9
5
5
5
12
17
3
2
2
2
2
2
2
14
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
5
5
10
11
10
8
3
3
5
13
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
3
3
8
4
4
6
7
3
3
3
3
3
4

6
6
2
2
2
2
2
2
2
2
4
4
6
6
3
3
7
11
8
12
4
4
8
5
10
6
3
8
2
2
2
2
2
2
2
2
5
4
4
10
7
5
4
3
3
3
8
9

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
5
5
5
5
5
5
10
10
2
2
2
2
2
2
2

2
2
2
11
4
4
4
3
3
3
3
3
3
13
15
7
7
4
5
5
10
3
3
3
12
7
7
4
4
4
4
2
2
2
2
2
2
2
2
2
2
2
15
8
8
9
5
5

4
4
3
3
8
7
6
8
4
4
2
2
2
2
3
3
3
3
13
6
6
5
4
9
16
14
13
3
3
3
3
10
6
6
5
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
2
2
2
2
2
15
6
11
5
5
5
3
3
9
6
6
6
6
7
11
10
4
15
6
9
3
3
3
3
2
2
2
2
2
2
2
5
4
7
6
6
8

3
3
3
3
3
3
13
4
4
7
8
6
5
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
8
8
3
3
6
5
8
8
8
4
4
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
3
3
3
3
3
3
2
2
2
2
2
2
2
2
15
4
4
4
8
3
3
3
3
5
5
11
6
6
2
2
2
2
2
2
2
2
2
2

2
2
2
5
6
3
4
4
11
7
6
4
4
4
4
3
3
9
2
2
2
2
2
2
2
2
8
5
5
4
4
4
4
4
4
7
3
3
3
3
6
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
6
2
2
2
2
2
2
2
2
8
3
3
3
3
3
14
6
6
4
7
12
11
8
6

7
3
3
4
4
2
2
2
2
2
2
5
4
7
3
3
3
3
3
3
3
11
11
11
10
15
2
2
2
2
2
2
2
12
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
14
7
8
6
13
3
3
3
3
7
2
2
2
2
2
2
2
2
2
4
4
4
6
7
5
5
5
4
4
4
3

3
3
3
3
3
3
7
6
2
2
2
2
2
2
2
2
2
2
2
7
4
5
5
6
3
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
4
4
7
3
3
3
2

2
2
2
5
5
4
4
4
7
5
3
3
3
3
3
3
4
4
2
2
2
2
2
2
2
2
2
4
4
4
4
3
3
3
3
5
6
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
2
2
2
2
2
2
2
2
2
2
5
11
6
6
12
4
4
13
3
3
3
5
4
4
4
4
4
2
2
2
2
2
2
2
10
3
5
5
5
4
9
6
6
5
2

2
2
2
2
2
2
2
2
13
12
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
3
13
5
9
13
3
5
2
2
2
2
2
2
2
11
4
4
13
5
5
5
14
3
3
3
3
13
11

13
6
6
2
2
2
2
2
9
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
3
3
3
5
5
5
6
4
4
9
10
7
3
2
2
2
2
2
2
2
2
2
2
10
5
5
7
7
6
6
3
3
5
8
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
4
7
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
9
3
3
3
10
4
4
5
13
2
2
2
2
6
6
11
3
3
3
3
3
3
4

4
5
3
4
6
10
2
2
2
2
2
11
12
6
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
8
3
3
3
3
3
3
10
11
8
2
2
2
2
2
2
10
11

3
3
3
7
7
9
4
9
2
2
2
2
2
2
2
2
2
2
2
3
3
3
3
3
3
3
6
9
9
4
4
4
10
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
6
6
12
3
3
3
3

3
4
4
4
8
8
5
5
2
2
2
2
2
2
2
2
2
12
5
4
4
4
4
5
5
10
2
2
2
2
2
2
2
2
11
3
3
3
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
9
5
5
6
6
3
3
3
3
3
3
5
2
2
2
2
2
2
2
2
2
13
4
6
11
3
3
3
3
6
2
2
2
2
2
2
2
2
2
2
5
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
8
11
3
3
3
4
4
2
2
2
2

2
2
2
2
5
5
5
3
3
7
5
5
12
4
3
3
3
3
3
2
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
5
6
7
3
3
5
13
2
2
2
2
2
2
2
2
2
10
8
3
3
3
3
4
8
6
6
5
5
7
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
2

2
2
4
3
3
5
7
12
6
4
11
8
5
5
12
3
2
2
2
2
2
2
2
2
9
9
6
6
10
4
11
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
9
5
2
2
2
2
2
4
6
7
9
3
3
3
3
3
10
5
2
2
2
2
9
6
3
3
3
3

12
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
6
4
4
3
3
3
3
3
7
2
2
2
2
2
2
6
6

10
7
4
10
10
3
3
12
2
2
2
2
2
2
2
2
2
2
6
4
5
5
7
11
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
3
3
3
6
6
6
9
2
2
2
2
2
2
2
2
2
2
2
3
3
3
3
9
5
4
4
4
4
7
11
5
3
3
3
3
3
3
3
2
2
2
2
2

2
9
6
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
5
4
4
4
3
3
9
8

2
2
2
2
2
7
4
4
4
3
3
3
7
7
5
11
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
2
2
2
2
2
2
2
2
4
7
3
3
8
8
12
4
5
5
8
8
9
2
2
3
3
3
3
5
4
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
11
3
3
3
2
2
2
2
2
8
11
8
10
2
2
2
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
3
3
3
3
9
5
2
2
2
2
2
2
2
2
3
3
3
5
5
7
8
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
3
3
2
2
2
2
2
2
8
7
11
3
12
4
2
2
2
2
2
2
10
7
7
6
6
3
3
3
5
8
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
6
6
10
2
2
2
2
2
2
5
3
3
3
3
3
6
5
5
4
6
2
2
2
2
2
2
2

3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
8
5
3
3
3
6
2
2
2
2
2
2
2
2
2
4
4
7

10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
4
4
2
2
2
2
2
2
2
2
2
6
6
6
9
3
3
3
3
3
5
8
2
2
2
2

9
7
6
3
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
6
4
3
3
3
2
2
2
2
10
3
3
3
9
9
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
2
2
2
7
4
6
8
3
5
6
6
4
2
2
2
2
5
5
5
5
3
3
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
5
2
2
2
2
2
2
2
2
2
7
3
4
4
6
7
4
4
3
3
3
5
5
2
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
9
4
2
2
2
2
2
2
5
4
3
3
3
7
7
7
7
9
6
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
10
4
4
4
4
2
2
2
2
8
7
3
5
6
2
2
2
2
2
2
9
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
6
5
5
7
3
3
3
3
3
6
2
2
2
2
2
2
2
4
4
7
9
8
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
2
2
2
2
2
5
5
3
3
3
3
2
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
8
4
2
2
2

2
5
8
4
10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
2
2
2
4
4
4
4
7
6
2
2
2
2
2
5
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
3
3
10
6
4
4
4
4
2
2
2
2
6
1
1
1
1
1
1
1
1
1
1
1
1
9
4
2
2
3
3
3
3
4
3
2
2
1
1
1

1
1
1
1
1
6
10
3
2
4
4
4
4
8
3
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
6
5
3
3
3
4
4

6
5
8
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
6
4
4
3
2
2
2
4
4
1
1
1
1
1
1
3
3
2
2
4
4
9
8

7
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
3
3
5
4
4
6
2
2
7
3
3
4
4
8
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
9
2
2
2
2
3
3
10
5
7
3
3
3
2
2
2
1
1
1
1
1
1
1
1
1
5
9
3
3
9
2
4
4
9
1
1
1
1
1
1
1
1

1
1
6
6
4
2
2
7
4
5
9
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
8
3
3
3
3
5
4
10
9
3
3
2
2
2
5
1
1
1
1
1
1

1
1
1
1
1
8
5
4
4
9
5
3
7
1
1
1
1
1
1
1
1
1
1
5
5
2
2
4
3
3
2
1
1
1
1
1
1
1
1
9
8
6
5
2
2
2
2
3

3
3
3
4
5
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
5
5
5
6
4
2
2
2
1
1
1
1
1
1
1
1
1
5
5
5
5
3
3
3
2

2
2
1
1
1
1
1
1
1
1
1
8
6
4
7
5
5
5
1
1
1
1
1
4
4
4
2
2
2
2
3
5
6
9
5
3
3
2
1
1
4
4
8
2
4
4
5
1

1
1
1
1
1
1
3
3
4
2
3
4
4
1
1
1
1
1
1
1
1
1
6
2
4
3
3
3
4
8
2
2
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
9
3
3
3
2
2
2
2
2
7
1
1
1
1
1
1
1
1
2
3
4
1
1
1
1
1
1
1
1
1
1
5
4
2
3
3
1
1
1
1
1
1
2
4
3
1
1

1
1
1
1
4
5
2
2
8
4
9
2
2
2
6
8
1
1
1
1
3
6
9
4
4
1
1
1
1
1
1
1
1
5
5
4
1
1
1
1
1
1
5
2
2
2
3
3

4
4
4
5
2
2
2
3
1
1
1
1
1
1
6
3
2
2
2
2
1
1
1
4
4
3
3
3
1
1
1
1
6
2
2
4
3
3
3
3
2
2
2
1
3
3
3
3

4
2
2
2
3
5
1
1
1
3
2
1
1
1
1
1
1
4
2
2
4
3
2
2
2
7
1
1
1
1
1
1
4
2
3
1
1
1
4
2
2
2
6
1
1
1
1
1

2
2
2
3
2
1
1
1
1
1
3
4
2
2
2
1
1
1
2
2
1
1
1
1
5
4
8
2
1
2
3
3
1
1
4
5
1
1
2
5
1
1
1
1
1
1
3
3

3
2
4
3
1
1
1
1
2
2
3
1
2
4
3
2
1
1
1
1
1
1
1
1
1
7
2
2
2
1
1
1
1
1
1
6
2
4
4
6
1
1
1
1
1
1
7
4

2
2
1
2
2
1
1
1
5
1
1
1
1
1
1
1
5
1
1
1
3
1
1
1
1
1
1
4
1
6
2
2
2
1
1
5
1
1
1
2
5
1
1
1
1
2
2
1

1
1
1
1
1
1
1
1
1
1
1
7
2
1
1
1
1
3
3
2
1
1
1
1
1
2
2
2
1
1
1
1
4
4
1
1
2
2
1
1
3
1
3
4
4
4
1
1

1
1
2
1
1
1
1
1
1
1
1
2
3
1
7
1
1
2
1
6
2
1
1
1
1
1
1
5
1
1
1
1
2
1
1
3
1
3
2
3
1
1
2
3
1
1
1
1

1
1
1
1
1
3
2
1
1
1
1
1
3
1
1
1
1
1
6
1
6
1
2
2
1
1
1
5
1
1
1
1
3
4
1
2
1
3
3
1
2
1
1
1
1
4
5
2

6
9
6
8
5
4
2
2
2
14
4
3
5
5
6
4
4
2
2
2
8
3
4
4
19
4
4
2
2
2
2
2
2
2
8
18
11
3
3
4
8
6
16
16
10
3
2
2

2
2
2
2
4
10
11
9
5
5
12
4
9
7
3
3
2
2
2
2
2
2
2
7
9
15
3
3
3
4
4
11
6
21
7
4
4
3
3
3
3
3
6
2
2
2
2
2

2
2
4
6
3
3
4
5
5
6
8
15
15
4
4
3
3
3
3
6
15
19
2
2
2
2
2
2
2
2
2
2
2
2
12
4
4
4
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
3
4
21
5
8
21
3
3
2
2
2
2
2
2
4
4
5
5
16
10
6
8
8
19
17
3
3
3
19
9
8
4
4
12
9
9
2
2
2
2
2
6
6
3
13

4
5
8
12
7
13
8
8
8
4
4
17
3
11
19
10
2
2
2
2
2
2
2
2
2
5
5
4
4
7
6
13
3
3
3
3
3
3
3
3
3
3
7
4
15
15
11
5

14
8
7
2
2
2
2
2
2
2
7
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
9
14
8
4
4
3
5
11
10
8
8
6
6
6
4
4
4
2

2
2
2
2
2
2
2
2
2
2
2
2
2
7
7
3
3
3
6
12
5
5
10
6
20
8
5
7
3
3
3
3
3
3
11
4
8
10
10
2
2
2
2
2
2
2
2
2

2
2
5
5
15
16
11
11
14
4
3
3
3
3
3
3
5
8
9
6
10
4
5
7
19
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
3
3
6
7
4
4
4
6

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
3
3
3
15
4
4
9

9
2
2
2
2
2
2
2
2
2
2
2
2
5
5
6
4
10
3
3
3
5
14
7
7
13
4
19
12
3
3
3
3
15
10
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
7
7
18
11
19
4
4
6
6
9
10
10
10
13
3
17
6
6
6
6
6
6
7
5
5
5
10
4
4
6
7
2
2
2
2
2
2
2
2
2
8
3
3
3
3

4
4
7
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
19
14
12
5
5
5
7
17
14
4
11
3
3
3
9
2
2
2
2
2
2
2
2
2
2
2
2
2
20
20
12
4
4

13
7
7
5
9
9
3
3
3
12
11
4
5
5
17
6
6
2
2
2
2
2
2
2
2
2
2
3
3
3
5
4
4
7
17
6
7
7
5
5
4
3
3
3
3
3
3
9

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
2
2
2
2
2

11
14
4
4
4
4
6
9
5
5
5
3
3
3
7
14
6
9
4
2
2
2
2
2
2
2
2
2
2
2
2
5
11
11
7
8
6
6
3
3
3
3
3
3
16
7
5
6

11
11
8
3
3
3
6
13
2
2
2
2
2
2
2
2
2
10
7
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
7
4
12
3
3
3
3
3
11
6
5
5
2
2
2
2
2
2
2
2
2
14
4
4
4
6
5
3
3
3
3
3
3
12
12
8

8
14
14
6
4
4
5
8
8
7
7
7
2
2
2
2
2
2
2
2
2
2
3
3
3
3
10
9
6
10
13
9
9
11
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
5
5
18
6
6
6
11
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
7
7
7
15
12
15

15
3
3
3
3
3
3
3
5
4
4
7
14
16
2
2
2
2
2
2
2
2
2
2
3
3
3
9
5
7
7
7
11
4
4
4
8
3
3
3
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
8
8
8
4
4
2
2
2
2
2
2
2
2
2
2
2
2
9
18
10
6
12
3
3

3
4
5
5
5
8
15
6
6
6
6
10
2
2
2
2
2
2
2
2
2
2
5
11
4
9
7
3
3
3
3
6
12
5
5
5
5
5
11
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
17
5
5
12
4
4
4
7
10
12
12
18
8
5
11
3
16
4

4
2
2
2
2
2
2
2
2
2
10
5
5
16
3
3
3
3
3
3
3
4
4
9
9
5
5
12
7
18
6
13
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
4
4
10
10
3
3
3
3
5
10
17
5
4
4
4
10
10
8
8
3
6
2
2
2
2
2
2
2
2
2
2
5
5
4
4

6
10
11
3
3
3
3
3
3
16
5
5
9
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
8
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
14
5
5
5
5
5
5
3
3
3
3

4
4
10
10
5
5
14
9
10
15
2
2
2
2
2
2
2
2
2
2
2
2
2
3
3
3
10
7
7
5
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
10
2
2
2
2
2
2
2
2
2
2
2
11
6
12
4
8
8
3
3
3
6
9
7
8
4
2
2
2
2
2
2
2
2
2
2
2
9
10
3
3
3
3

3
3
5
5
4
4
4
6
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
2
2
3
3
6
4
9
8
9
4
3

3
3
3
3
3
3
3
12
7
2
2
2
2
2
2
2
2
2
2
2
2
5
5
14
8
16
9
4
4
4
14
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
16
7
2
2
2
2

2
2
2
2
2
2
6
8
3
3
6
10
15
15
4
4
4
5
16
8
9
2
2
2
2
2
2
2
2
7
5
5
8
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
6
7
7
8
15
3
3
3
3
4
4
11
2
2
2
2
2
2
2
2
2
2
10
7
7
8
8
12
6
4
4
4
3
3
3
3
11
5

9
6
6
7
2
2
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
13
13
3
5
5
7
14
6
7
16
5
6
6
2
2
2
2
2
2
2
2
2
3
12
8
8
10

7
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
3
3
3
3
3
3
2
2
2
2
2
2
6
4
4
4
4
4
5
5
5
15
16
7
15
16
6
3
3
3
3
3
3
5
7
10
2
2
2
2
2
2
2
6
4
4
3

3
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
7
2
2

2
2
2
2
2
2
2
2
12
4
4
4
4
3
3
3
3
3
7
9
5
16
14
4
4
10
5
5
3
3
3
2
2
2
2
2
2
2
2
2
2
2
2
13
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
4
6
7
3
3
3
3
3
11
11
11
10
2
2
2

2
2
2
2
2
2
4
9
8
7
7
11
14
3
3
3
6
6
6
4
4
4
5
5
13
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
14
7
7
6
6
5
3
3
4
4
8
14
11
5
5
4
2
2
2
2
2
2
2
2

12
14
7
7
3
3
3
6
14
5
5
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
14
6
6
3
3
3
3
2
2
2

2
2
2
2
9
5
12
6
4
4
4
4
4
4
9
12
7
5
5
3
3
3
3
11
6
9
4
4
2
2
2
10
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
9
3
3
7
4
14
5
10
2
2
2
2
2
2
7
7
3
3

3
3
12
5
5
15
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
15
5
2
2
2
2
2
2
3
3
3
3
6
9
14

7
6
5
5
4
3
3
3
9
8
2
2
2
2
2
2
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
4
9
7
3
3
11
5
5
2
2
2
2
2
2
2
2
4
4
3
3
3
5
5
5
5
5
15
14
4
4
4
9
6
6
6
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
8
2
2
2
2
2
2
2
2
2
2
10
7
3
3
3
3
3
3
8
4

7
5
11
3
3
3
3
12
2
2
2
2
2
2
2
2
4
4
4
4
11
11
5
5
8
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
6
14
4
4
4
4
4
3
3
5
5
2
2
2
2
2
2
2
7
8
4
6
3
3
3
3
3
3
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
5
4
4
11
3
3
3
6
8
9
4
4
2
2
2
2
3
3
3
6
8
9
5
5
5
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
8
8
6
11
3
3
3
2
2
2
2

2
2
2
7
6
5
5
5
9
9
13
4
4
14
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
9
5
5

5
5
8
13
7
9
3
3
3
3
3
3
8
5
5
5
5
5
7
7
2
2
2
6
6
8
4
4
4
4
7
3
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
9
13
4
4
4
4
4
2
2
2
8
3
3
3
3
3
7
13
12
5
4
6
10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
7
13
2
2
2
2
2
2
2
3
8
6
6
4
4
4
14
3
3
3
3
3
3
3
3
9
6
11
2
2
2
2
4
4
4
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
11
7
7
7
3
3
3
4
2
2
2
2
2
2
2
10
6
7
11
3
3
4
4
4
7

6
11
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
7
7
4
3
3
3
3
3
3
12
7
7
7
9
6
4
13

2
2
2
2
2
3
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
6
4
4
2
2
4
4
5
6
9
10
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
2
2
2
2
2
2
2
2
5
6
7
3
3
3
3
3
5
6
2
2
2
2
2
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
5
6
3
5
5
2
2
2
2
12
3
8
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
5
5
7
2
2
2
2
2
3
3
9
7
7
7
5
5
12
4
4
7
3
3
3
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
7
7
3
3
3
10
8
8
2

2
2
4
9
5
10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
9
4
5
12
7
2
2
2
6
3
3
12
5
5
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
2
2
2
2
3
4
6
5
6
3
3
3
2
2
2
2
2
2
2
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

6
3
3
3
3
3
2
2
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
3
3
6
5
7
2
2
13
9
6
5
8
1

1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
5
9
8
4
4
4
4
5
2
2
3
3
3
1
1
1
1
1
1
1
4
6
6
2
2
2
2
5
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
2
8
5
4
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
3
10
7
9
2
2
4
4
1
1
1
1
1
1
1
1
1
1
1
4
4
2
3
3
8
10
1
1
1
1
1
1
1
1
1
1
1
8
2
2
3
3
4
5
3
2

2
2
6
4
4
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
2
2
2
2
2
9
1
1
1
1
1
1
1
1
1
1
3
3
3
5
6
2
2
2
7
5

3
10
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
2
2
2
5
9
4
2
2
1
1
1
1
1
1
1
1
5
8
9
9
3
3
5
2
2

2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
2
2
2
4
8
5
5
9
3
8
1
1
1
1
1
1
1
1
1
1
1
4
4
2
2
2
2
2
2
2
3

4
6
8
2
2
1
1
1
6
4
4
4
2
2
12
9
4
3
1
1
1
1
9
4
4
4
2
3
8
7
7
7
4
4
4
1
1
1
1
1
1
1
6
2
2
4
7
2

2
2
2
2
1
1
1
1
1
1
1
1
3
7
4
4
4
1
1
1
1
1
1
7
3
4
2
7
4
1
1
1
1
2
10
3
1
1
1
1
1
1
1
4
4
4
4
3

5
10
5
2
1
1
1
1
1
1
1
1
1
1
1
3
10
1
1
1
2
2
2
4
4
4
3
3
4
4
1
1
1
1
1
1
1
2
3
3
8
2
1
1
1
1
1
1

1
3
3
1
1
1
1
1
1
1
1
1
9
2
2
1
1
1
1
1
1
1
3
3
5
2
1
1
1
1
2
2
4
10
6
2
11
1
1
1
1
1
1
1
3
3
5
1

1
1
1
4
2
3
7
4
4
1
1
1
1
1
3
8
6
8
8
7
5
3
1
1
1
1
1
1
1
3
10
7
2
1
1
1
11
3
2
4
1
7
2
4
4
4
3
7

1
1
1
4
2
6
4
10
2
1
1
1
1
1
1
3
6
4
1
1
1
1
1
3
2
2
2
4
9
1
1
1
1
1
1
1
1
1
2
7
4
1
1
1
1
10
2
2

2
1
1
1
1
2
3
1
1
1
1
1
9
6
2
2
3
3
1
1
3
2
6
4
5
1
1
1
1
1
1
1
2
2
2
2
2
3
5
1
1
1
1
1
3
3
3
2

1
1
1
1
2
2
2
2
3
1
1
1
1
2
2
2
1
1
1
2
2
2
1
1
1
1
1
2
8
4
2
7
1
1
1
4
3
2
4
1
1
8
2
1
1
1
2
2

2
1
1
1
1
1
1
7
1
1
8
9
1
1
1
2
1
6
4
2
1
1
1
1
1
1
1
1
4
4
1
1
1
2
2
1
1
1
1
1
1
8
1
6
2
1
3
5

4
1
1
1
1
7
2
1
2
1
1
1
3
3
1
1
1
2
3
4
2
1
1
6
1
1
1
1
2
2
2
5
2
2
1
1
1
1
2
1
4
2
2
1
3
1
8
2

1
1
2
1
2
5
1
1
1
1
3
3
1
1
1
1
6
1
6
2
1
1
1
1
3
1
32
32
9
11
6
15
15
6
43
35
18
43
43
29
71
11
11
20
72
52
73
42

4
15
42
41
69
5
11
68
6
6
6
15
3
3
3
2
2
2
2
2
2
2
17
62
71
60
32
4
4
44
35
7
7
50
53
3
3
3
14
16
20
56
5
52
4
11
7
7

10
10
14
14
36
34
18
5
15
14
3
2
2
2
2
2
2
7
7
29
40
5
60
6
10
30
16
4
4
4
4
4
4
4
9
20
7
26
3
3
28
5
5
8
8
8
31
27

50
13
4
4
54
5
54
2
2
2
2
2
2
29
21
3
3
3
3
19
20
49
5
4
4
19
59
14
7
7
8
47
47
3
3
3
3
3
18
4
4
4
36
8
7
11
20
13

2
2
2
2
2
2
2
2
40
26
5
5
5
5
13
6
7
7
14
14
10
4
61
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
3
5
27
22
27
4
4
4
14
40
29
11
9
19
2
2
2
2
2
2
2
2
2
2
2
2
2
60
3
3
3
3
32
16
51
11
22
36
26
14
6
6

6
16
4
10
8
12
32
19
19
14
17
51
11
19
18
18
6
6
23
3
3
3
3
3
5
4
10
11
16
15
12
12
2
2
2
2
2
2
2
2
2
2
13
13
19
33
9
13

12
5
5
4
4
3
3
3
11
6
6
6
24
20
7
19
24
8
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
9
11
25
16
38
2
2
2
2
2
2
2
2
2
2
2
2
7
16
16
9
3
3
3
3
37
21
27

7
8
8
8
4
35
5
5
5
25
8
3
3
3
2
2
2
2
2
2
2
2
13
4
4
4
4
50
19
5
14
6
6
6
6
26
26
19
9
3
3
3
3
52
7
7
10
4

5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2

2
2
2
2
2
2
16
17
6
6
11
3
3
3
3
4
4
22
28
9
9
6
6
6
15
5
22
22
13
11
2
2
2
2
2
2
2
2
2
2
2
9
3
3
12
10
9
16

4

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

1

6
16
3
3
14
5
2
2
2
2
2
2
2
11
21
22
25
14
4
4
7
5
3
10
10
19
21
7
4
16
2
2
2
2
2
2
6
6
6
3
3
3
3
3
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
10
11
50
5
7
10
13
15
16
42
2
2

2
31
3
3
3
3
13
10
10
10
21
32
8
8
8
6
34
13
3
12
2
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
9
8
7
12
4
4
20
3
3
11
11
9
2
2
2
2
2
2
33
8
4
4
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
5
5
5
7
13
9
4
2
2
2
2
2
2
2
2
23
42
5
5
12
31
7
19
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
7
15
8
32
6
7
52
3
2
2
2
2
2
4
5
14
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
3
7
7
7
2
2
2
5
19
19
45
45
3
1
1
1

1
1
1
1
1
1
1
1
1
2
2
2
2
2
2
20
3
3
3
12
5
12
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

14
2
2
5
3
8
28
18
18
29
1
1
1
1
1
1
1
1
1
1
1
1
1
3
29
2
2
2
2
2
6
11
16
17
3
3
3
18
2
2
12
1
1
1
1
1
1
1

1
1
4
7
16
2
11
15
3
1
1
1
1
1
1
1
1
1
1
2
3
8
1
1
6
2
46
3
8
2
9
1
1
1
1
21
2
4
1
1
1
3
2
2
7
15
4
1

1
1
1
1
1
1
1
1
1
1
1
12
2
3
1
4
11
3
15
5
1
1
1
2
2
12
11
4
2
1
1
2
1
1
1
9
9
19
1
1
3
11
1
3
1
1
4
4

3
3
8
3
2
4
5
2
12
2
4
1
1
1
1
1
2
5
2
2
2
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
8
2
2
3
3
3
2
4
1
1
1

1
1
1
1
1
1
1
1
2
8
12
7
2
4
7
7
4
2
1
1
1
1
1
1
1
1
1
6
7
7
7
2
2
4
5
5
2
2
5
3
4
2
2
2
14
1
1
1

1
1
1
1
1
1
6
2
3
3
3
2
5
1
1
1
1
1
1
1
1
4
4
6
14
7
2
1
1
1
1
3
4
2
3
3
2
1
1
1
1
1
1
1
1
1
1
4

2
2
2
2
5
5
4
11
11
2
3
3
4
12
1
1
4
6
2
11
4
2
1
1
1
1
1
1
1
1
1
1
1
6
3
3
4
1
1
1
1
1
1
1
1
1
1
4

5
4
6
3
3
1
1
1
1
1
1
1
1
1
1
1
1
5
5
5
3
1
1
1
1
1
1
1
1
1
1
8
3
3
1
1
1
1
1
1
1
2
3
2
5
1
1
1

1
1
1
4
3
3
4
2
11
1
1
1
1
1
1
5
4
2
4
4
3
1
1
1
1
1
1
2
5
3
4
1
1
1
3
7
4
5
6
1
1
1
2
1
1
1
1
7

2
10
1
1
1
1
1
4
3
7
1
1
1
1
1
1
1
1
1
1
2
2
7
1
1
1
1
1
1
1
1
3
2
2
1
7
2
1
1
1
1
2
2
2
2
2
3
1

1
1
3
2
2
2
9
8
1
1
1
1
1
1
9
1
2
10
5
1
1
1
1
1
6
10
3
10
1
1
3
3
2
1
4
5
2
1
7
1
3
9
2
4
1
1
5
2

1
3
6
2
2
4
1
1
1
10
3
8
1
1
3
1
1
1
1
3
3
4
4
2
4
6
5
1
3
5
1
1
1
1
2
2
1
4
4
3
5
1
1
9
2
1
1
1

2
1
1
1
2
1
8
8
9
1
2
2
1
1
1
2
2
8
1
1
1
5
7
1
5
3
3
4
1
2
3
3
5
2
1
1
3
3
2
3
8
1
1
2
1
1
1
3

1
1
1
1
1
2
1
3
4
1
4
1
1
1
1
3
3
1
1
5
2
4
1
5
5
1
1
5
5
1
2
2
3
4
3
2
5
2
2
3
2
3
3
1
1
2
1
3

1
1
1
2
1
1
3
1
4
1
5
1
13
12
8
2
2
2
12
4
2
2
15
2
2
2
15
1
1
1
1
1
1
18
2
2
2
3
4
10
6
2
7
3
15
4
18
15

3
3
2
2
2
2
1
1
1
1
1
1
1
1
1
1
16
6
5
3
6
8
3
7
2
2
2
5
13
13
5
3
1
1
1
1
1
4
3
3
10
3
2
6
12
8
1
1

1
1
1
1
1
1
1
2
11
2
2
2
2
3
3
2
2
7
1
1
1
1
1
1
1
5
10
7
2
5
5
3
2
1
1
1
1
1
1
1
1
1
3
5
7
7
7
2

10
3
1
1
1
1
1
1
1
1
2
4
2
2
10
3
7
1
1
1
1
1
5
9
1
1
1
1
1
1
1
2
2
2
2
4
4
5
2
2
5
5
6
3
7
7
7
12

1
1
1
1
1
1
1
1
1
1
1
1
3
5
12
2
3
1
1
1
1
1
1
1
1
1
1
1
4
2
6
11
1
1
1
6
4
7
6
6
6
2
4
1
1
1
1
1

1
9
3
2
2
1
1
1
1
3
1
1
3
7
6
3
2
1
1
1
1
1
1
4
4
5
3
3
1
1
1
1
1
1
1
2
2
1
1
1
1
1
1
1
1
5
8
1

1
1
11
3
2
6
8
1
1
1
1
2
1
1
1
1
2
12
12
2
1
11
5
1
1
1
1
6
1
1
7
5
5
1
5
1
4
2
2
2
2
5
2
2
1
1
1
1

4
2
4
2
1
11
2
1
1
3
3
2
1
3
2
3
6
1
1
5
6
4
1
1
6
2
1
1
1
1
6
2
3
9
1
1
1
1
3
1
1
1
2
4
1
1
1
1

3
1
1
4
3
1
1
4
2
5
3
1
2
2
2
10
1
3
1
1
6
3
6
4
1
1
1
10
2
6
1
3
3
2
2
2
10
3
1
1
2
4
1
2
1
1
1
1

3
2
2
5
8
4
1
1
1
1
3
1
3
3
2
2
2
7
6
2
3
2
1
2
1
1
1
1
1
1
2
3
4
2
2
1
1
1
1
8
1
1
1
1
1
1
1
1

1
1
1
8
1
1
2
4
1
3
2
2
2
4
2
5
3
1
3
1
1
6
1
1
1
5
3
1
1
1
5
5
2
3
4
28
2
6
14
3
6
2
4
10
3
9
2
9

7
16
8
1
1
1
1
1
1
1
1
1
1
1
1
1
3
8
8
10
3
3
2
2
2
11
21
10
3
2
2
2
5
1
1
1
1
1
1
1
1
1
1
1
1
3
14
2

18
4
5
3
2
11
10
3
2
1
1
1
1
1
1
1
1
1
1
5
2
11
3
3
3
4
2
2
3
4
3
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3

2
2
2
6
13
12
6
5
3
4
18
15
2
2
1
1
1
1
1
1
1
6
2
2
16
16
5
2
2
2
2
6
7
1
1
1
1
1
1
1
1
1
1
6
2
8
8
2

2
16
8
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
4
6
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
8
5
3
7
4
15
3
11
3
3

1
1
1
1
1
1
1
4
3
18
11
4
5
4
2
1
1
1
1
1
1
1
1
5
2
2
17
5
3
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
6
7
7
4

1
1
1
1
1
1
1
7
7
7
9
11
7
17
11
4
8
10
2
3
1
1
1
1
1
1
1
1
3
7
15
15
3
2
2
3
1
1
1
1
1
1
3
3
6
2
1
1

1
1
3
3
2
2
7
10
2
10
1
1
1
1
1
3
4
6
8
1
1
1
1
1
1
1
5
6
1
1
2
2
2
2
8
3
2
1
1
1
3
15
3
7
1
1
7
3

15
1
1
1
1
14
2
1
1
1
1
3
3
11
11
13
4
6
2
1
1
1
1
1
1
8
4
8
1
1
12
8
8
5
6
2
8
4
3
11
9
8
4
11
2
1
1
4

6
4
1
13
13
4
2
14
1
1
1
2
7
7
3
4
4
2
2
1
1
1
2
1
6
2
1
1
1
1
3
4
2
2
1
1
4
4
2
6
4
3
1
12
4
5
1
1

1
1
1
2
2
2
3
4
4
10
5
1
1
1
2
3
1
1
3
5
9
3
2
4
1
1
1
1
3
3
5
1
1
1
2
2
3
2
2
2
5
4
2
5
1
1
1
4

2
1
2
1
1
1
1
2
4
1
1
2
3
1
3
2
3
2
4
1
3
9
2
2
6
1
4
4
4
4
2
1
1
1
2
1
9
1
2
1
2
1
4
11
6
1
1
2

6
1
6
2
2
2
3
2
1
2
5
1
3
1
1
5
1
1
1
1
3
3
1
4
2
1
2
8
1
1
3
7
28
30
39
8
7
37
17
3
3
3
29
12
47
7
19
14

17
3
3
6
11
22
9
5
5
18
11
8
15
42
6
3
3
3
11
4
4
31
2
2
2
2
2
2
2
2
2
2
2
2
2
16
14
8
8
5
5
5
16
17
20
47
52
17

12
6
6
63
4
4
4
4
4
5
10
7
12
29
19
8
32
3
3
3
3
3
3
3
3
11
32
68
23
7
8
16
12
4
4
4
28
34
6
6
33
12
12
7
24
37
9
12

39
5
5
3
3
3
3
3
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
6
6
6
17
4
4
4
4
4
12
14
33
5
24
6
6
43
11
12
40
4
4

4
33
9
20
50
3
3
3
3
3
3
3
3
3
3
11
6
6
5
5
5
59
21
20
8
6
4
36
10
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
18
21
7
13
3
3
3
3
9
21
6
6
6
28
5
5
5
5
7
22
22
11
54
4
4
4
4
4
17
26
18
12
58
58
23
42
6
6
11
10

10
7
9
8
27
27
29
5
5
5
5
5
38
3
3
3
3
3
3
42
10
4
4
4
4
4
33
6
6
6
26
8
8
8
8
7
7
7
7
47
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
62
5
5
5
5
53
9
9
52
22
6
54
14
41
22
12
4
4
4
4
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
48
45
9
3
3
3
3
3
3
3
3
3
3
3
3
3
23
14
48
5
5
7
7
10
6
6
49

9
45
31
4
4
4
51
26
7
11
20
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
47
13
3
3
3
3
3
3
3
8
45
7
12
9
27

21
21
13
41
15
6
6
6
4
5
5
5
5
22
9
10
20
11
11
6
6
6
6
12
3
3
3
3
3
3
3
45
5
5
19
4
4
4
7
7
2
2
2
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
8
26
6
9
10
10
29
29
13
7
5
17
41
4
4
4
4
4
3
3
3
3
3
3
15
15
18
7
7
14
31
24
18
13
8

5
5
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
17
16
50
36
6
6
2
2
2
2
2

2
2
2
2
2
2
2
2
2
2
2
2
2
4
4
4
4
4
4
12
19
8
9
3
3
3
3
3
3
3
3
40
5
5
16
38
6
6
17
19
4
4
17
5
5
5
6
6

6
6
7
3
3
3
3
3
3
3
3
3
20
54
17
56
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
11
41
4
4
4
4
4
4
23
8
8

7
5
11
17
14
16
3
3
3
3
3
3
17
6
4
4
4
4
4
5
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

17
11
2
2
2
2
2
2
2
2
2
2
2
2
10
52
20
3
3
3
16
16
4
4
12
7
21
9
20
38
5
5
5
4
9
2
2
2
2
2
2
2
2
2
2
2
2
2

2
3
3
3
3
3
3
3
3
3
22
6
8
31
9
5
5
5
8
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
51
7
10
10
5
5
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
6
4
4
4
4
12

5
5
5
5
3
3
3
10
11
7
13
4
4
4
8
8
15
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
2
5
5
5
5
5
17
3
3
3
3
3
3
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
9
10
10
12
4
4
4
4
4
4
52
5
5
6
7
10
18
17
15
2
2
2
2
2
2
2
2
2
2
2
2
2
2

2
49
20
3
3
3
3
3
3
4
4
11
11
5
10
6
8
42
14
9
6
6
4
4
14
3
3
3
3
3
3
3
2
2
2
2
2
2
2
2
2
2
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
9
9
9
8
26
5
5
10
4
4
8
8
3
3
3
3
2
2
2
2
2
2
2
2
2
2
2
2
4
4
4
3
3
3
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
5
5
29
7
7
7
9
9

4
2
2
2
2
2
2
2
11
11
8
26
5
5
25
3
3
3
3
24
46
6
6
8
4
4
4
4
10
10
7
16
5
5
15
2
2
2
2
8
12
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
4
4
4
7
7
25
5
5
5
10
8
23
9
7
7
7
3
4
2
2

2
2
2
2
2
2
2
2
2
2
2
11
7
15
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3

6
10
2
2
2
2
2
5
7
3
24
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
4
4
15
3
3
3
7
7
6
5

5
4
4
19
2
2
2
2
2
2
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
4
4
2
2
2
2
5
3
12
14
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
3
18
2
11
11
10
3
2
2
15
17
1
1
1
1
1
1
1
1
1
1
1
1
1
4

4
3
3
3
2
2
2
2
18
13
1
1
1
1
1
1
1
1
1
1
7
2
2
2
2
2
2
2
2
4
4
5
8
3
1
1
1
1
1
1
1
1
1
1
4
23
2
7

3
35
2
2
2
2
19
18
1
1
1
1
1
6
10
2
2
2
11
4
15
1
1
1
1
1
1
15
3
3
2
2
5
1
1
1
1
8
12
2
2
18
4
1
1
1
1
1

7
2
3
8
2
2
2
26
3
3
3
1
1
1
1
1
1
41
6
18
17
1
1
1
1
5
3
1
1
42
3
43
1
1
4
2
10
10
11
2
2
2
1
1
1
1
1
3

4
6
3
1
2
2
1
1
11
2
13
1
5
1
1
6
2
1
1
1
1
1
3
3
1
27
7
13
2
2
10
11
5
2
2
2
2
10
10
8
4
18
2
2
10
9
8
2

9
8
3
3
7
5
12
9
2
2
2
3
6
14
2
2
2
4
3
3
2
2
4
3
2
2
2
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
13
12
2
2
2
2
3
7
5
12
13
3
13
13
2
2
2
4
7

4
5
2
2
2
2
2
12
5
7
3
9
3
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
11
4
4
11
2
6
12

3
3
12
4
6
8
4
2
2
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3

3
4
8
3
8
6
2
4
4
2
3
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
2
2
2
2
4
3
4
3
2
2
2
4
2

2
2
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
7
2
2
2
2
14
4
5
2
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
4
4
2
2
2
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
2
2
9
5
12
12
12
5
2
2
6
1
1
1
1
1
1
1
1
1
1
1
1
2
2
6
2
5
5
3
7
11
5

2
2
8
7
1
1
1
1
1
1
1
1
1
1
1
1
2
7
3
5
2
1
1
1
1
1
1
1
1
1
1
3
4
3
1
1
1
1
1
1
2
5
3
4
1
1
1
1

1
1
1
1
1
1
1
1
1
3
11
1
1
1
1
1
1
1
1
1
1
5
2
9
11
2
2
1
1
1
1
1
1
3
4
7
4
4
6
10
1
1
1
1
1
1
1
1

1
1
1
1
10
3
3
5
3
3
5
2
1
1
1
1
1
1
1
1
1
1
8
3
10
11
1
1
2
2
2
2
2
2
7
11
3
3
1
1
1
1
1
1
1
1
1
1

1
1
4
6
3
5
4
1
1
1
1
1
1
1
4
11
3
2
2
1
1
1
1
1
1
1
1
3
3
2
1
1
1
1
1
1
1
1
1
7
4
2
2
5
1
1
1
1

1
1
5
2
9
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2
2
3
4
1
1
1
2
2
2
1
1
1
1
1
1
1
2
3
2
2
1
1
1
1
1
1
1
7

1
1
1
1
1
1
5
2
2
3
8
1
1
1
1
1
1
1
1
1
1
4
3
2
5
1
1
4
3
3
8
1
1
1
1
1
1
1
3
2
9
10
1
1
1
1
1
3

3
4
3
1
1
1
1
2
2
2
6
1
1
1
2
9
2
3
4
1
1
1
1
1
2
1
1
5
4
2
3
1
1
1
1
2
2
1
1
1
1
1
1
1
1
5
3
4

3
1
1
1
1
1
1
1
1
6
3
3
1
1
1
4
1
1
6
1
1
1
1
1
1
1
1
2
1
1
5
1
1
1
1
7
3
1
1
1
1
1
2
2
2
1
2
8

1
1
1
1
1
1
1
1
8
2
1
1
2
3
1
1
1
2
1
1
1
1
2
4
1
2
1
4
1
1
1
1
1
1
1
3
2
1
2
2
1
1
2
1
1
7
1
3

1
2
2
3
6
1
1
2
2
1
5
1
3
1
1
1
1
1
1
4
1
2
1
1
1
1
1
1
1
3
2
2
1
1
1
1
1
5
1
1
1
1
1
2
10
5
4
2

4
5
3
20
5
5
2
2
2
2
2
2
3
20
7
3
2
2
19
4
9
4
4
3
2
5
11
3
3
5
16
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
2
7
17
2
2
2
2
3
10
3
7
7
2
2
6
6
3
2
2
5
3
3
2
2
2
2
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
2
3
2
2
5
3
3
2
2
5
5
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
5
3
3
4
3
2
2
2
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
3
7
2
5
5
2
2
4
4
4
3
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
5
2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
2
2
3
3
2
2

2
4
2
7
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
13
3
2
2
2
2
4
10
10
5
6
3
10
1
1
1
1
1
1
1
1
1
1
3
2
2
2
11
13

1
1
1
1
1
1
1
1
1
1
1
1
1
2
6
2
2
2
13
13
7
3
3
4
9
2
2
2
3
3
1
1
1
1
1
1
1
1
1
3
2
2
2
9
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
6
10
2
5
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
8
2
2
2
1
1
1
1
1
1
3
2
2
2
3
1

1
1
1
1
1
1
1
1
1
1
1
2
2
2
3
1
1
1
1
1
1
2
2
6
3
9
11
1
1
1
1
1
1
1
1
1
7
4
3
2
2
9
2
2
1
1
1
1

1
1
1
4
6
3
2
2
1
1
1
1
1
1
1
3
2
3
1
1
1
1
1
1
1
1
4
4
3
3
2
2
2
2
1
1
1
1
1
3
5
6
1
1
1
1
1
3

3
6
2
1
1
1
1
1
1
1
1
1
2
2
11
8
4
3
3
1
1
1
1
1
1
1
4
2
4
4
5
5
5
3
4
1
1
1
1
1
1
1
2
5
10
1
1
1

1
2
4
6
3
3
1
1
1
1
1
2
7
5
2
1
1
1
1
1
1
11
5
6
3
1
1
1
1
1
1
2
2
4
1
1
1
8
1
1
1
1
1
1
7
2
1
1

1
1
1
1
1
1
1
1
1
2
6
2
4
1
1
1
1
3
2
2
5
3
2
1
1
1
1
7
4
2
3
1
1
1
1
1
2
4
4
2
1
1
1
1
1
2
4
8

1
1
1
3
6
2
5
1
10
2
4
1
5
2
3
1
1
1
1
1
3
1
1
1
1
1
3
3
3
1
1
5
1
1
3
9
9
9
1
1
4
8
1
1
1
1
1
1

1
2
1
2
3
7
5
1
1
4
1
9
1
1
2
1
2
1
4
1
4
1
1
2
1
2
2
3
3
1
8
1
1
3
2
2
1
1
1
1
1
4
3
1
1
2
2
1

1
1
1
1
2
1
1
2
1
1
1
1
1
5
4
1
1
3
1
3
2
1
1
2
1
2
1
1
2
1
6
1
4
2
2
3
1
1
2
2
1
1
1
2
1
5
3
1

1
5
5
1
1
5
5
5
7
5
5
2
4
2
1
1
2
5
1
3
1
2
1
2
1
1
1
1
1
5
1
3
2
10
4
2
2
10
4
3
3
2
5
3
5
3
2
3

9
5
4
2
4
4
7
3
2
2
2
2
3
18
13
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
3
9
13
6
6
5
4
3
9
2
4
9
9
4
3
3
9
12
11
6
4
4
3
8
2
2
2
9
6
3
10
2
2
2
2

13
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
3
17
7
2
3

3
3
8
8
6
6
11
9
8
2
2
2
2
2
19
4
7
10
4
4
3
2
2
7
3
3
4
4
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
17
8
2
2
4
3
3
9
9
2
7
10
3
4
15
7
2
2
2
3
3
3
3
3
5
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
1
1
1
7
4
2
2
3
6
4
4
3
2
2
2
2
4
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
1
3
3
3
5
2
9
9
2
2
15
3
3
3
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
1
1
1
1
7
6
2
2
17
4
5
4
2
16
7
4
4
6
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
17
2
2
2
2
6
8

8
5
3
2
2
6
6
10
10
6
4
2
2
2
16
1
1
1
1
1
1
1
1
1
1
1
1
1
1
5
5
5
4
14
4
13
2
2
2
2
2
3
8
3
3
3
4
2

2
2
2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
12
3
4
16
16
2
2
2
13
4
3
12
2
2
8
13
7
1
1
1
1
1
1
1
1
1
1
1
1

1
1
1
1
1
1
13
10
3
11
6
6
2
3
3
3
5
2
3
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
11
2
2
13
6
3
3
3
13
2
2
2

2
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
13
5
2
10
16
15
1
1
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2
2

14
5
5
12
2
5
6
1
1
1
1
1
1
1
1
1
1
1
1
3
3
3
3
5
6
8
16
3
15
2
6
16
1
1
1
1
1
1
1
1
1
1
1
1
1
2
2
2

2
2
2
2
2
3
5
2
11
16
1
1
1
1
1
1
1
1
1
1
1
1
1
7
3
7
2
4
2
2
1
1
1
1
1
8
3
3
9
4
2
2
2
3
8
1
1
1

1
2
2
7
5
2
2
10
13
10
8
3
1
1
1
1
1
1
1
1
7
6
6
2
2
3
5
9
2
2
2
2
1
1
1
1
1
1
1
1
1
1
5
6
3
1
1
1

1
1
5
2
6
1
1
1
1
1
1
1
10
3
2
2
1
1
1
1
1
1
1
1
1
4
2
3
3
1
1
1
1
1
1
1
1
1
2
3
12
4
4
5
1
1
1
1

1
3
3
3
3
1
1
1
1
1
1
4
10
2
2
12
1
1
1
1
1
1
1
1
1
1
2
3
1
1
1
1
1
2
3
2
2
1
1
1
1
2
2
3
1
2
5
4

2
2
1
1
1
1
2
6
1
1
1
1
3
4
5
2
1
1
1
1
1
1
3
2
2
4
1
1
1
1
1
1
1
1
1
1
6
1
1
1
1
1
4
4
3
3
2
2

1
1
1
1
2
1
1
1
1
1
1
2
2
2
1
1
1
1
4
2
2
6
8
1
1
2
1
1
1
8
2
2
2
6
8
1
1
3
2
1
1
7
2
1
1
1
1
3

1
1
2
3
4
4
1
1
1
1
1
2
1
1
2
2
3
4
1
2
1
4
1
1
2
1
1
1
1
6
1
1
1
1
2
5
1
4
1
3
1
10
4
1
3
2
2
2

1
1
1
2
1
2
1
1
1
2
1
3
1
1
7
2
7
3
7
2
2
1
4
28
19
10
10
19
11
10
24
14
6
6
46
9
11
18
12
11
7
17
20
13
13
10
23
39

20
28
13
3
18
9
2
6
23
3
12
18
6
16
26
14
8
25
35
36
13
35
5
38
9
7
15
3
3
42
34
21
9
9
6
15
10
13
12
5
8
9
42
30
6
12
11
14

6
6
3
27
11
11
28
6
7
8
13
22
15
4
10
13
9
5
7
49
11
3
12
8
16
4
30
7
10
4
15
25
7
14
5
4
4
3
13
7
27
20
25
6
1
13
29
17

14
36
4
14
3
12
12
12
20
5
5
4
10
7
5
3
12
13
20
6
10
11
7
7
4
30
1
5
5
18
21
22
12
26
8
28
14
5
15
6
8
9
15
17
24
5
5
7

9
9
15
10
10
11
10
16
14
45
11
4
9
22
2
6
9
8
12
1
1
3
18
11
22
2
17
4
4
20
5
3
10
10
6
16
7
17
17
3
16
18
35
9
13
15
7
10

1
15
3
10
7
7
13
24
19
4
5
15
10
17
2
2
10
10
6
8
11
15
6
8
8
10
16
4
7
7
19
9
7
3
2
18
11
10
10
16
10
3
6
6
17
18
16
9

12
12
5
5
12
17
2
2
2
3
8
20
4
2
13
13
1
6
6
11
3
9
12
19
3
4
6
16
5
7
15
4
7
5
5
13
9
9
11
1
7
9
6
9
5
1
5
1

2
3
3
3
4
4
2
5
3
2
2
3
7
10
7
3
4
7
5
10
4
2
5
2
2
4
2
6
3
5
5
3
2
2
4
3
3
5
1
2
4
5
2
1
3
2
2
1

5
2
2
2
4
2
6
3
5
1
4
2
5
1
1
1
3
1
4
1
1
2
1
1
1
3
5
2
2
2
1
2
1
3
4
4
2
2
1
1
2
5
1
1
2
1
1
2

2
2
1
4
5
5
2
6
5
2
2
3
3
2
2
1
3
2
3
3
2
1
1
2
2
2
1
4
2
1
2
2
5
2
1
1
1
1
2
1
2
2
3
1
1
1
1
1

3
2
2
3
2
1
2
1
1
1
2
4
2
1
2
1
1
1
1
1
3
1
3
1
1
2
1
1
2
2
1
1
1
1
1
2
1
1
1
1
1
1
1
4
2
1
1
1

3
1
5
1
1
1
1
2
1
1
1
1
1
1
1
2
3
1
4
1
2
1
1
1
1
1
1
1
1
1
7
5
12
6
3
7
2
3
3
3
4
1
2
4
5
2
3
4

2
2
9
3
5
3
3
3
2
2
2
7
3
6
4
3
2
5
3
3
3
1
1
4
4
2
5
4
1
4
4
7
2
2
3
1
1
2
6
3
1
4
1
1
1
2
1
2

2
1
1
1
1
1
1
2
1
1
2
3
3
4
1
6
1
2
2
2
2
1
1
1
7
1
1
1
4
1
2
2
1
3
2
2
2
1
1
1
1
4
1
1
2
3
3
3

1
1
1
1
1
1
2
2
2
1
2
1
1
1
2
1
3
2
1
1
2
1
4
1
1
2
2
1
1
2
2
2
1
1
1
1
2
1
1
2
1
1
2
3
1
1
1
3

2
5
2
1
1
1
2
2
3
1
2
1
1
2
1
1
1
1
1
2
1
1
1
1
2
1
1
1
1
1
1
1
1
1
1
1
1
8
19
6
6
3
4
6
3
16
11
10

3
8
4
10
6
4
4
3
6
10
2
2
4
13
6
2
5
8
4
8
6
4
11
12
3
5
8
4
7
5
5
3
11
10
5
1
4
4
5
4
6
2
7
4
4
4
2
7

10
5
8
5
4
4
5
4
1
3
9
5
3
7
1
7
4
5
7
3
2
2
2
6
3
2
4
4
4
3
3
3
9
2
3
4
3
3
3
2
2
2
3
2
1
3
4
3

4
7
3
9
2
5
5
5
3
3
3
6
3
3
2
5
5
1
2
4
6
6
6
7
2
2
1
5
2
4
3
1
4
2
3
6
3
3
4
3
3
1
5
2
1
1
3
1

4
2
3
1
2
5
4
4
1
1
4
5
2
3
1
1
4
4
2
1
4
3
2
7
4
1
1
3
2
2
5
6
3
2
1
3
2
4
2
1
3
5
2
3
1
1
1
4

10
1
1
2
2
3
2
5
2
2
2
2
2
1
3
2
5
2
3
2
4
3
5
3
1
7
9
4
1
3
1
2
1
1
4
1
4
1
2
2
1
1
6
1
1
2
1
1

3
1
1
2
1
1
1
1