Supplementary Table S1-S13

Supplementary Table S1

Species	Symbol	Ensembl	Family	Protein	Entrez ID
Homo_sapiens	ZBTB8B	ENSG00000273274	ZBTB	ENSP00000476499;	728116
Homo_sapiens	GSX2	ENSG00000180613	Homeobox	ENSP00000319118;	170825
Homo_sapiens	TBX2	ENSG00000121068	T-box	ENSP00000404781;	6909
Homo_sapiens	PAX8	ENSG00000125618	PAX	ENSP00000395498;	7849
Homo_sapiens	CREB3L1	ENSG00000157613	TF_bZIP	ENSP00000481956;	90993
Homo_sapiens	NKX6-1	ENSG00000163623	Homeobox	ENSP00000295886;	4825
Homo_sapiens	ZNF621	ENSG00000172888	zf-C2H2	ENSP00000386051;	285268
Homo_sapiens	ZNF138	ENSG00000197008	zf-C2H2	ENSP00000303533;	7697
Homo_sapiens	ZNF654	ENSG00000175105	zf-C2H2	ENSP00000312141;	55279
Homo_sapiens	POU3F3	ENSG00000198914	Pou	ENSP00000355001;	5455
Homo_sapiens	ALX1	ENSG00000180318	Homeobox	ENSP00000315417;	8092
Homo_sapiens	EMX1	ENSG00000135638	Homeobox	ENSP00000258106;	2016
Homo_sapiens	ZNF718	ENSG00000250312	zf-C2H2	ENSP00000476435;	255403
Homo_sapiens	VSX2	ENSG00000119614	Homeobox	ENSP00000261980;	338917
Homo_sapiens	POU1F1	ENSG00000064835	Pou	ENSP00000454072;	5449
Homo_sapiens	RARA	ENSG00000131759	THR-like	ENSP00000377649;	5914
Homo_sapiens	TLX3	ENSG00000164438	Homeobox	ENSP00000296921;	30012
Homo_sapiens	ZIC2	ENSG00000043355	zf-C2H2	ENSP00000365514;	7546
Homo_sapiens	ZNF226	ENSG00000167380	zf-C2H2	ENSP00000465121;	7769
Homo_sapiens	ZNF808	ENSG00000198482	zf-C2H2	ENSP00000420522;	388558
Homo_sapiens	AC067968.1	ENSG00000267022	zf-C2H2	ENSP00000467018;	-
Homo_sapiens	NR3C1	ENSG00000113580	ESR-like	ENSP00000427672;	2908
Homo_sapiens	HIC2	ENSG00000169635	ZBTB	ENSP00000385319;	23119
Homo_sapiens	ZNF442	ENSG00000198342	zf-C2H2	ENSP00000440162;	79973
Homo_sapiens	FOSL1	ENSG00000175592	TF_bZIP	ENSP00000310170;	8061
Homo_sapiens	MTF1	ENSG00000188786	zf-C2H2	ENSP00000362127;	4520
Homo_sapiens	YBX3	ENSG00000060138	CSD	ENSP00000279550;	8531
Homo_sapiens	ZNF705A	ENSG00000196946	zf-C2H2	ENSP00000379816;	440077
Homo_sapiens	NFE2	ENSG00000123405	TF_bZIP	ENSP00000397185;	4778
Homo_sapiens	RAX2	ENSG00000173976	Homeobox	ENSP00000450687;	84839
Homo_sapiens	SP1	ENSG00000185591	zf-C2H2	ENSP00000329357;	6667
Homo_sapiens	ARID3A	ENSG00000116017	ARID	ENSP00000263620;	1820
Homo_sapiens	FEZF1	ENSG00000128610	zf-C2H2	ENSP00000392727;	389549
Homo_sapiens	THAP4	ENSG00000176946	THAP	ENSP00000385006;	51078
Homo_sapiens	ZNF286A	ENSG00000187607	zf-C2H2	ENSP00000466154;	57335
Homo_sapiens	FOXQ1	ENSG00000164379	Fork_head	ENSP00000296839;	94234
Homo_sapiens	AIRE	ENSG00000160224	SAND	ENSP00000291582;	326
Homo_sapiens	SNAI3	ENSG00000185669	zf-C2H2	ENSP00000327968;	333929
Homo_sapiens	ZNF224	ENSG00000267680	zf-C2H2	ENSP00000337368;	7767
Homo_sapiens	ATOH8	ENSG00000168874	bHLH	ENSP00000304676;	84913
Homo_sapiens	MECOM	ENSG00000085276	zf-C2H2	ENSP00000420072;	2122
Homo_sapiens	ZNF45	ENSG00000124459	zf-C2H2	ENSP00000269973;	7596
Homo_sapiens	ZNF674	ENSG00000251192	zf-C2H2	ENSP00000428248;	641339
Homo_sapiens	ZXDA	ENSG00000198205	zf-C2H2	ENSP00000351530;	7789
Homo_sapiens	ST18	ENSG00000147488	zf-C2HC	ENSP00000428521;	9705
Homo_sapiens	NKX6-2	ENSG00000148826	Homeobox	ENSP00000357581;	84504
Homo_sapiens	ZNF689	ENSG00000156853	zf-C2H2	ENSP00000287461;	115509
Homo_sapiens	ZNF449	ENSG00000173275	zf-C2H2	ENSP00000339585;	203523
Homo_sapiens	ZNF2	ENSG00000275111	zf-C2H2	ENSP00000480057;	7549
Homo_sapiens	TFDP2	ENSG00000114126	E2F	ENSP00000418122;	7029
Homo_sapiens	ZBTB25	ENSG00000089775	ZBTB	ENSP00000378204;	7597
Homo_sapiens	PIAS4	ENSG00000105229	zf-MIZ	ENSP00000262971;	51588
Homo_sapiens	HES4	ENSG00000188290	bHLH	ENSP00000393198;	57801
Homo_sapiens	ZNF592	ENSG00000166716	zf-C2H2	ENSP00000452877;	9640
Homo_sapiens	WT1	ENSG00000184937	zf-C2H2	ENSP00000491511;	7490
Homo_sapiens	ZBTB49	ENSG00000168826	ZBTB	ENSP00000338807;	166793
Homo_sapiens	PAX5	ENSG00000196092	PAX	ENSP00000429197;	5079

Homo_sapiens	MAFG	ENSG00000197063	TF_bZIP	ENSP00000376173;	4097
Homo_sapiens	ZNF837	ENSG00000152475	zf-C2H2	ENSP00000405699;	116412
Homo_sapiens	FOXD4	ENSG00000170122	Fork_head	ENSP00000371940;	2298
Homo_sapiens	GATA3	ENSG00000107485	zf-GATA	ENSP00000341619;	2625
Homo_sapiens	HOMEZ	ENSG00000215271	Homeobox	ENSP00000453979;	57594
Homo_sapiens	ZNF26	ENSG00000198393	zf-C2H2	ENSP00000333725;	7574
Homo_sapiens	ZSCAN20	ENSG00000121903	zf-C2H2	ENSP00000355053;	7579
Homo_sapiens	MEOX2	ENSG00000106511	Homeobox	ENSP00000262041;	4223
Homo_sapiens	DMRTA1	ENSG00000176399	DM	ENSP00000319651;	63951
Homo_sapiens	ZNF567	ENSG00000189042	zf-C2H2	ENSP00000467712;	163081
Homo_sapiens	OVOL1	ENSG00000172818	zf-C2H2	ENSP00000434220;	5017
Homo_sapiens	PRRX2	ENSG00000167157	Homeobox	ENSP00000361547;	51450
Homo_sapiens	MAFB	ENSG00000204103	TF_bZIP	ENSP00000362410;	9935
Homo_sapiens	ZNF195	ENSG00000005801	zf-C2H2	ENSP00000387998;	7748
Homo_sapiens	ZNF75D	ENSG00000186376	zf-C2H2	ENSP00000359800;	7626
Homo_sapiens	PIAS2	ENSG00000078043	zf-MIZ	ENSP00000317163;	9063
Homo_sapiens	FOXJ1	ENSG00000129654	Fork_head	ENSP00000323880;	2302
Homo_sapiens	GRHL1	ENSG00000134317	CP2	ENSP00000418275;	29841
Homo_sapiens	KLF11	ENSG00000172059	zf-C2H2	ENSP00000444690;	8462
Homo_sapiens	ATF2	ENSG00000115966	TF_bZIP	ENSP00000407911;	1386
Homo_sapiens	NFAT5	ENSG00000102908	RHD	ENSP00000455628;	10725
Homo_sapiens	MXD1	ENSG00000059728	bHLH	ENSP00000410672;	4084
Homo_sapiens	SMAD3	ENSG00000166949	MH1	ENSP00000332973;	4088
Homo_sapiens	DMRT2	ENSG00000173253	DM	ENSP00000397494;	10655
Homo_sapiens	BARHL1	ENSG00000125492	Homeobox	ENSP00000263610;	56751
Homo_sapiens	IKZF4	ENSG00000123411	zf-C2H2	ENSP00000450020;	64375
Homo_sapiens	ZNF607	ENSG00000198182	zf-C2H2	ENSP00000347338;	84775
Homo_sapiens	E2F7	ENSG00000165891	E2F	ENSP00000449284;	144455
Homo_sapiens	ZNF595	ENSG00000272602	zf-C2H2	ENSP00000477392;	152687
Homo_sapiens	ETV5	ENSG00000244405	ETS	ENSP00000413755;	2119
Homo_sapiens	CSRNP3	ENSG00000178662	CSRNP_N	ENSP00000344042;	80034
Homo_sapiens	CEBPD	ENSG00000221869	TF_bZIP	ENSP00000386165;	1052
Homo_sapiens	ZNF669	ENSG00000188295	zf-C2H2	ENSP00000342818;	79862
Homo_sapiens	TBX22	ENSG00000122145	T-box	ENSP00000487527;	50945
Homo_sapiens	ZNF304	ENSG00000131845	zf-C2H2	ENSP00000401642;	57343
Homo_sapiens	FOXN4	ENSG00000139445	Fork_head	ENSP00000347354;	121643
Homo_sapiens	TBX6	ENSG00000149922	T-box	ENSP00000279386;	6911
Homo_sapiens	ZBED2	ENSG00000177494	zf-BED	ENSP00000321370;	79413
Homo_sapiens	HES5	ENSG00000197921	bHLH	ENSP00000367714;	388585
Homo_sapiens	ZNF283	ENSG00000167637	zf-C2H2	ENSP00000468708;	284349
Homo_sapiens	PLAG1	ENSG00000181690	zf-C2H2	ENSP00000404067;	5324
Homo_sapiens	ZNF512B	ENSG00000196700	zf-C2H2	ENSP00000358904;	57473
Homo_sapiens	ZNF486	ENSG00000256229	zf-C2H2	ENSP00000335042;	90649
Homo_sapiens	ZMIZ2	ENSG00000122515	zf-MIZ	ENSP00000409648;	83637
Homo_sapiens	TERF2	ENSG00000132604	MYB	ENSP00000254942;	7014
Homo_sapiens	TFAM	ENSG00000108064	HMG	ENSP00000363002;	7019
Homo_sapiens	LCORL	ENSG00000178177	HTH	ENSP00000371661;	254251
Homo_sapiens	THAP5	ENSG00000177683	THAP	ENSP00000400500;	168451
Homo_sapiens	TCF15	ENSG00000125878	bHLH	ENSP00000246080;	6939
Homo_sapiens	ZNF75A	ENSG00000162086	zf-C2H2	ENSP00000482769;	7627
Homo_sapiens	HMGB2	ENSG00000164104	HMG	ENSP00000296503;	3148
Homo_sapiens	EGR3	ENSG00000179388	zf-C2H2	ENSP00000318057;	1960
Homo_sapiens	ZFP69B	ENSG00000187801	zf-C2H2	ENSP00000354547;	65243
Homo_sapiens	USF1	ENSG00000158773	bHLH	ENSP00000356998;	7391
Homo_sapiens	TBR1	ENSG00000136535	T-box	ENSP00000387023;	10716
Homo_sapiens	SMAD2	ENSG00000175387	MH1	ENSP00000467075;	4087
Homo_sapiens	ZNF165	ENSG00000197279	zf-C2H2	ENSP00000366542;	7718
Homo_sapiens	HOXA11	ENSG00000005073	Homeobox	ENSP00000448962;	3207

Homo_sapiens	LMX1A	ENSG00000162761	Homeobox	ENSP00000356868;	4009
Homo_sapiens	LHX6	ENSG00000106852	Homeobox	ENSP00000362860;	26468
Homo_sapiens	ZNF155	ENSG00000204920	zf-C2H2	ENSP00000385163;	7711
Homo_sapiens	ZNF16	ENSG00000170631	zf-C2H2	ENSP00000378369;	7564
Homo_sapiens	ZNF225	ENSG00000256294	zf-C2H2	ENSP00000468686;	7768
Homo_sapiens	ZSCAN10	ENSG00000130182	zf-C2H2	ENSP00000459520;	84891
Homo_sapiens	HNF1B	ENSG00000275410	Homeobox	ENSP00000482529;	6928
Homo_sapiens	AC008758.1	ENSG00000196826	zf-C2H2	ENSP00000404127;	-
Homo_sapiens	HOXA13	ENSG00000106031	Homeobox	ENSP00000222753;	3209
Homo_sapiens	MKX	ENSG00000150051	Homeobox	ENSP00000452751;	283078
Homo_sapiens	TBX1	ENSG00000184058	T-box	ENSP00000331791;	6899
Homo_sapiens	ZNF70	ENSG00000187792	zf-C2H2	ENSP00000339314;	7621
Homo_sapiens	ZNF282	ENSG00000170265	zf-C2H2	ENSP00000477841;	8427
Homo_sapiens	PRDM13	ENSG00000112238	zf-C2H2	ENSP00000358217;	59336
Homo_sapiens	ZNF786	ENSG00000197362	zf-C2H2	ENSP00000313516;	136051
Homo_sapiens	ZNF547	ENSG00000152433	zf-C2H2	ENSP00000282282;	284306
Homo_sapiens	EOMES	ENSG00000163508	T-box	ENSP00000295743;	8320
Homo_sapiens	HOXB1	ENSG00000120094	Homeobox	ENSP00000355140;	3211
Homo_sapiens	ZKSCAN3	ENSG00000189298	zf-C2H2	ENSP00000341883;	80317
Homo_sapiens	ZNF648	ENSG00000179930	zf-C2H2	ENSP00000344129;	127665
Homo_sapiens	MECP2	ENSG00000169057	MBD	ENSP00000301948;	4204
Homo_sapiens	WIZ	ENSG00000011451	zf-C2H2	ENSP00000445824;	58525
Homo_sapiens	ZNF317	ENSG00000130803	zf-C2H2	ENSP00000353554;	57693
Homo_sapiens	ZGLP1	ENSG00000220201	zf-GATA	ENSP00000385403;	100125288
Homo_sapiens	BACH2	ENSG00000112182	TF_bZIP	ENSP00000437473;	60468
Homo_sapiens	IRX4	ENSG00000113430	Homeobox	ENSP00000424235;	50805
Homo_sapiens	IRF4	ENSG00000137265	IRF	ENSP00000436094;	3662
Homo_sapiens	HOXA9	ENSG00000078399	Homeobox	ENSP00000343619;	3205
Homo_sapiens	SMAD7	ENSG00000101665	MH1	ENSP00000467621;	4092
Homo_sapiens	ZNF613	ENSG00000176024	zf-C2H2	ENSP00000490115;	79898
Homo_sapiens	SOX30	ENSG00000039600	HMG	ENSP00000427984;	11063
Homo_sapiens	TSC22D4	ENSG00000166925	TSC22	ENSP00000377560;	81628
Homo_sapiens	MEOX1	ENSG00000005102	Homeobox	ENSP00000321684;	4222
Homo_sapiens	ZNF438	ENSG00000183621	zf-C2H2	ENSP00000406934;	220929
Homo_sapiens	TCF4	ENSG00000196628	bHLH	ENSP00000457649;	6925
Homo_sapiens	ZBTB18	ENSG00000179456	ZBTB	ENSP00000481278;	10472
Homo_sapiens	RBPJL	ENSG00000124232	CSL	ENSP00000361826;	11317
Homo_sapiens	LYL1	ENSG00000104903	bHLH	ENSP00000264824;	4066
Homo_sapiens	BHLHE22	ENSG00000180828	bHLH	ENSP00000318799;	27319
Homo_sapiens	AC010422.6	ENSG00000269693	zf-C2H2	ENSP00000473043;	-
Homo_sapiens	IRF3	ENSG00000126456	IRF	ENSP00000469113;	3661
Homo_sapiens	ZNF260	ENSG00000254004	zf-C2H2	ENSP00000467219;	339324
Homo_sapiens	PROX2	ENSG00000119608	HPD	ENSP00000451223;	283571
Homo_sapiens	TP63	ENSG00000073282	P53	ENSP00000389485;	8626
Homo_sapiens	HOXA6	ENSG00000106006	Homeobox	ENSP00000222728;	3203
Homo_sapiens	DMRTB1	ENSG00000143006	DM	ENSP00000360500;	63948
Homo_sapiens	CCDC169-SOHLH2	ENSG00000250709	bHLH	ENSP00000421868;	100526761
Homo_sapiens	YY2	ENSG00000230797	zf-C2H2	ENSP00000389381;	404281
Homo_sapiens	ZNF143	ENSG00000166478	zf-C2H2	ENSP00000379849;	7702
Homo_sapiens	PBRM1	ENSG00000163939	HMG	ENSP00000386643;	55193
Homo_sapiens	ZNF841	ENSG00000197608	zf-C2H2	ENSP00000415453;	284371
Homo_sapiens	ADNP	ENSG00000101126	Homeobox	ENSP00000495540;	23394
Homo_sapiens	SPIB	ENSG00000269404	ETS	ENSP00000391877;	6689
Homo_sapiens	BCL11B	ENSG00000127152	zf-C2H2	ENSP00000387419;	64919
Homo_sapiens	ZNF513	ENSG00000163795	zf-C2H2	ENSP00000318373;	130557
Homo_sapiens	NEUROD6	ENSG00000164600	bHLH	ENSP00000297142;	63974
Homo_sapiens	SRF	ENSG00000112658	SRF	ENSP00000265354;	6722
Homo_sapiens	TBXT	ENSG00000164458	T-box	ENSP00000355836;	6862

Homo_sapiens	HOXD9	ENSG00000128709	Homeobox	ENSP00000249499;	3235
Homo_sapiens	ZBTB47	ENSG00000114853	ZBTB	ENSP00000420968;	92999
Homo_sapiens	ZNF22	ENSG00000165512	zf-C2H2	ENSP00000298299;	7570
Homo_sapiens	NFXL1	ENSG00000170448	zf-NF-X1	ENSP00000370949;	152518
Homo_sapiens	ZNF543	ENSG00000178229	zf-C2H2	ENSP00000322545;	125919
Homo_sapiens	ZNF540	ENSG00000171817	zf-C2H2	ENSP00000465503;	163255
Homo_sapiens	SOX14	ENSG00000168875	HMG	ENSP00000305343;	8403
Homo_sapiens	TFAP4	ENSG00000090447	bHLH	ENSP00000459390;	7023
Homo_sapiens	ASCL2	ENSG00000183734	bHLH	ENSP00000332293;	430
Homo_sapiens	HEY1	ENSG00000164683	bHLH	ENSP00000429705;	23462
Homo_sapiens	EBF3	ENSG00000108001	COE	ENSP00000347463;	253738
Homo_sapiens	XBP1	ENSG00000100219	TF_bZIP	ENSP00000216037;	7494
Homo_sapiens	ZNF562	ENSG00000171466	zf-C2H2	ENSP00000464716;	54811
Homo_sapiens	PROP1	ENSG00000175325	Homeobox	ENSP00000311290;	5626
Homo_sapiens	CDX4	ENSG00000131264	Homeobox	ENSP00000362613;	1046
Homo_sapiens	SOX10	ENSG00000100146	HMG	ENSP00000354130;	6663
Homo_sapiens	BORCS8-MEF2B	ENSG00000064489	SRF	ENSP00000390762;	4207
Homo_sapiens	ZNF211	ENSG00000121417	zf-C2H2	ENSP00000240731;	10520
Homo_sapiens	ZNF266	ENSG00000174652	zf-C2H2	ENSP00000466714;	10781
Homo_sapiens	ZNF580	ENSG00000213015	zf-C2H2	ENSP00000446126;	51157
Homo_sapiens	OVOL3	ENSG00000105261	zf-C2H2	ENSP00000487603;	728361
Homo_sapiens	ZNF391	ENSG00000124613	zf-C2H2	ENSP00000419498;	346157
Homo_sapiens	ATOH1	ENSG00000172238	bHLH	ENSP00000302216;	474
Homo_sapiens	ATF5	ENSG00000169136	TF_bZIP	ENSP00000470633;	22809
Homo_sapiens	MYB	ENSG00000118513	MYB	ENSP00000432948;	4602
Homo_sapiens	ALX3	ENSG00000156150	Homeobox	ENSP00000358807;	257
Homo_sapiens	SP2	ENSG00000167182	zf-C2H2	ENSP00000365931;	6668
Homo_sapiens	THAP2	ENSG00000173451	THAP	ENSP00000310796;	83591
Homo_sapiens	GATA2	ENSG00000179348	zf-GATA	ENSP00000417074;	2624
Homo_sapiens	CDX2	ENSG00000165556	Homeobox	ENSP00000370408;	1045
Homo_sapiens	OLIG2	ENSG00000205927	bHLH	ENSP00000371794;	10215
Homo_sapiens	SIM1	ENSG00000112246	bHLH	ENSP00000358210;	6492
Homo_sapiens	ZNF445	ENSG00000185219	zf-C2H2	ENSP00000413073;	353274
Homo_sapiens	YBX2	ENSG00000006047	CSD	ENSP00000007699;	51087
Homo_sapiens	ZBTB10	ENSG00000205189	ZBTB	ENSP00000368384;	65986
Homo_sapiens	ZIK1	ENSG00000171649	zf-C2H2	ENSP00000472867;	284307
Homo_sapiens	ZNF611	ENSG00000213020	zf-C2H2	ENSP00000443505;	81856
Homo_sapiens	DLX2	ENSG00000115844	Homeobox	ENSP00000234198;	1746
Homo_sapiens	RREB1	ENSG00000124782	zf-C2H2	ENSP00000420519;	6239
Homo_sapiens	GATA1	ENSG00000102145	zf-GATA	ENSP00000365853;	2623
Homo_sapiens	BHLHA15	ENSG00000180535	bHLH	ENSP00000326391;	168620
Homo_sapiens	SOX21	ENSG00000125285	HMG	ENSP00000366144;	11166
Homo_sapiens	MAFA	ENSG00000182759	TF_bZIP	ENSP00000328364;	389692
Homo_sapiens	PITX1	ENSG00000069011	Homeobox	ENSP00000451199;	5307
Homo_sapiens	ZNF286B	ENSG00000249459	zf-C2H2	ENSP00000461413;	729288
Homo_sapiens	TGIF2LX	ENSG00000153779	Homeobox	ENSP00000453704;	90316
Homo_sapiens	SATB1	ENSG00000182568	CUT	ENSP00000399518;	6304
Homo_sapiens	SIM2	ENSG00000159263	bHLH	ENSP00000290399;	6493
Homo_sapiens	EN1	ENSG00000163064	Homeobox	ENSP00000295206;	2019
Homo_sapiens	ZNF845	ENSG00000213799	zf-C2H2	ENSP00000388311;	91664
Homo_sapiens	DRGX	ENSG00000165606	Homeobox	ENSP00000401653;	644168
Homo_sapiens	MAX	ENSG00000125952	bHLH	ENSP00000452197;	4149
Homo_sapiens	ZNF696	ENSG00000185730	zf-C2H2	ENSP00000427857;	79943
Homo_sapiens	ZNF521	ENSG00000198795	zf-C2H2	ENSP00000463000;	25925
Homo_sapiens	ZFP62	ENSG00000196670	zf-C2H2	ENSP00000423820;	643836
Homo_sapiens	GLI3	ENSG00000106571	zf-C2H2	ENSP00000379258;	2737
Homo_sapiens	ZBTB8A	ENSG00000160062	ZBTB	ENSP00000317561;	653121
Homo_sapiens	ZNF791	ENSG00000173875	zf-C2H2	ENSP00000342974;	163049

Homo_sapiens	ZFP42	ENSG00000179059	zf-C2H2	ENSP00000483363;	132625
Homo_sapiens	TGIF1	ENSG00000177426	Homeobox	ENSP00000339631;	7050
Homo_sapiens	ZNF557	ENSG00000130544	zf-C2H2	ENSP00000404065;	79230
Homo_sapiens	MEIS3	ENSG00000105419	Homeobox	ENSP00000454073;	56917
Homo_sapiens	ZNF565	ENSG00000196357	zf-C2H2	ENSP00000306869;	147929
Homo_sapiens	AC002310.5	ENSG00000261459	zf-C2H2	ENSP00000454241;	-
Homo_sapiens	DLX1	ENSG00000144355	Homeobox	ENSP00000354478;	1745
Homo_sapiens	OLIG1	ENSG00000184221	bHLH	ENSP00000371785;	116448
Homo_sapiens	GCFC2	ENSG00000005436	GCFC	ENSP00000318690;	6936
Homo_sapiens	ZNF124	ENSG00000196418	zf-C2H2	ENSP00000440365;	7678
Homo_sapiens	ZBTB5	ENSG00000168795	ZBTB	ENSP00000307604;	9925
Homo_sapiens	ZNF554	ENSG00000172006	zf-C2H2	ENSP00000321132;	115196
Homo_sapiens	ZBTB38	ENSG00000177311	ZBTB	ENSP00000406955;	253461
Homo_sapiens	ZNF600	ENSG00000189190	zf-C2H2	ENSP00000344791;	162966
Homo_sapiens	BSX	ENSG00000188909	Homeobox	ENSP00000344285;	390259
Homo_sapiens	BHLHE41	ENSG00000123095	bHLH	ENSP00000242728;	79365
Homo_sapiens	ZSCAN23	ENSG00000187987	zf-C2H2	ENSP00000289788;	222696
Homo_sapiens	HOXA1	ENSG00000105991	Homeobox	ENSP00000494260;	3198
Homo_sapiens	MLX	ENSG00000108788	bHLH	ENSP00000464697;	6945
Homo_sapiens	TSC22D1	ENSG00000102804	TSC22	ENSP00000481585;	8848
Homo_sapiens	EGR4	ENSG00000135625	zf-C2H2	ENSP00000445626;	1961
Homo_sapiens	DUXA	ENSG00000258873	Homeobox	ENSP00000452398;	503835
Homo_sapiens	ZNF493	ENSG00000196268	zf-C2H2	ENSP00000376110;	284443
Homo_sapiens	CREBZF	ENSG00000137504	TF_bZIP	ENSP00000434281;	58487
Homo_sapiens	PAX1	ENSG00000125813	PAX	ENSP00000481334;	5075
Homo_sapiens	THAP11	ENSG00000168286	THAP	ENSP00000304689;	57215
Homo_sapiens	ARID4A	ENSG00000032219	ARID	ENSP00000344556;	5926
Homo_sapiens	ZSCAN22	ENSG00000182318	zf-C2H2	ENSP00000332433;	342945
Homo_sapiens	ZNF729	ENSG00000196350	zf-C2H2	ENSP00000469582;	100287226
Homo_sapiens	ZNF221	ENSG00000159905	zf-C2H2	ENSP00000467367;	7638
Homo_sapiens	FOXN1	ENSG00000109101	Fork_head	ENSP00000464645;	8456
Homo_sapiens	MSGN1	ENSG00000151379	bHLH	ENSP00000281047;	343930
Homo_sapiens	OTX2	ENSG00000165588	TF_Otx	ENSP00000451272;	5015
Homo_sapiens	TCF7L1	ENSG00000152284	HMG	ENSP00000282111;	83439
Homo_sapiens	THAP6	ENSG00000174796	THAP	ENSP00000422402;	152815
Homo_sapiens	IRF2	ENSG00000168310	IRF	ENSP00000425037;	3660
Homo_sapiens	TFAP2D	ENSG00000008197	AP-2	ENSP00000008391;	83741
Homo_sapiens	ZNF239	ENSG00000196793	zf-C2H2	ENSP00000363569;	8187
Homo_sapiens	EBF1	ENSG00000164330	COE	ENSP00000477809;	1879
Homo_sapiens	GBX1	ENSG00000164900	Homeobox	ENSP00000297537;	2636
Homo_sapiens	REST	ENSG00000084093	zf-C2H2	ENSP00000311816;	5978
Homo_sapiens	CSDE1	ENSG00000009307	CSD	ENSP00000261443;	7812
Homo_sapiens	ZNF641	ENSG00000167528	zf-C2H2	ENSP00000437832;	121274
Homo_sapiens	ZNF90	ENSG00000213988	zf-C2H2	ENSP00000410466;	7643
Homo_sapiens	FOXN3	ENSG00000053254	Fork_head	ENSP00000451135;	1112
Homo_sapiens	ZNF385A	ENSG00000161642	zf-C2H2	ENSP00000338927;	25946
Homo_sapiens	ZNF727	ENSG00000214652	zf-C2H2	ENSP00000485448;	442319
Homo_sapiens	ZNF257	ENSG00000197134	zf-C2H2	ENSP00000470209;	113835
Homo_sapiens	C11orf95	ENSG00000188070	zf-BED	ENSP00000482180;	65998
Homo_sapiens	ZNF98	ENSG00000197360	zf-C2H2	ENSP00000350418;	148198
Homo_sapiens	PPARD	ENSG00000112033	THR-like	ENSP00000353916;	5467
Homo_sapiens	ZNF223	ENSG00000178386	zf-C2H2	ENSP00000467647;	7766
Homo_sapiens	ZNF561	ENSG00000171469	zf-C2H2	ENSP00000393074;	93134
Homo_sapiens	CDX1	ENSG00000113722	Homeobox	ENSP00000477928;	1044
Homo_sapiens	ZBTB3	ENSG00000185670	ZBTB	ENSP00000378286;	79842
Homo_sapiens	TADA2B	ENSG00000173011	MYB	ENSP00000308022;	93624
Homo_sapiens	LHX2	ENSG00000106689	Homeobox	ENSP00000394978;	9355
Homo_sapiens	AC005324.4	ENSG00000255104	zf-C2H2	ENSP00000458062;	-

Homo_sapiens	MEIS2	ENSG00000134138	Homeobox	ENSP00000453793;	4212
Homo_sapiens	MLXIPL	ENSG00000009950	bHLH	ENSP00000392636;	51085
Homo_sapiens	ZNF274	ENSG00000171606	zf-C2H2	ENSP00000484810;	10782
Homo_sapiens	HOXB2	ENSG00000173917	Homeobox	ENSP00000331741;	3212
Homo_sapiens	ZNF816	ENSG00000180257	zf-C2H2	ENSP00000350295;	125893
Homo_sapiens	GTF3A	ENSG00000122034	zf-C2H2	ENSP00000389655;	2971
Homo_sapiens	NKX2-4	ENSG00000125816	Homeobox	ENSP00000345147;	644524
Homo_sapiens	ZNF134	ENSG00000213762	zf-C2H2	ENSP00000379464;	7693
Homo_sapiens	ETV2	ENSG00000105672	ETS	ENSP00000368312;	2116
Homo_sapiens	POU2F1	ENSG00000143190	Pou	ENSP00000414660;	5451
Homo_sapiens	SALL1	ENSG00000103449	zf-C2H2	ENSP00000251020;	6299
Homo_sapiens	ZNF136	ENSG00000196646	zf-C2H2	ENSP00000344162;	7695
Homo_sapiens	SP140L	ENSG00000185404	SAND	ENSP00000397911;	93349
Homo_sapiens	ZNF780B	ENSG00000128000	zf-C2H2	ENSP00000221355;	163131
Homo_sapiens	IRF5	ENSG00000128604	IRF	ENSP00000419950;	3663
Homo_sapiens	ZNF443	ENSG00000180855	zf-C2H2	ENSP00000301547;	10224
Homo_sapiens	ETV1	ENSG00000006468	ETS	ENSP00000385686;	2115
Homo_sapiens	HMG20B	ENSG00000064961	HMG	ENSP00000328269;	10362
Homo_sapiens	PGR	ENSG00000082175	ESR-like	ENSP00000481227;	5241
Homo_sapiens	MYBL2	ENSG00000101057	MYB	ENSP00000380072;	4605
Homo_sapiens	EGR2	ENSG00000122877	zf-C2H2	ENSP00000242480;	1959
Homo_sapiens	ZNF397	ENSG00000186812	zf-C2H2	ENSP00000331577;	84307
Homo_sapiens	NFATC2	ENSG00000101096	RHD	ENSP00000396471;	4773
Homo_sapiens	OTX1	ENSG00000115507	TF_Otx	ENSP00000355631;	5013
Homo_sapiens	CREM	ENSG00000095794	TF_bZIP	ENSP00000417807;	1390
Homo_sapiens	FOXO3	ENSG00000118689	Fork_head	ENSP00000339527;	2309
Homo_sapiens	ZBTB6	ENSG00000186130	ZBTB	ENSP00000362763;	10773
Homo_sapiens	ZNF433	ENSG00000197647	zf-C2H2	ENSP00000448099;	163059
Homo_sapiens	CREB1	ENSG00000118260	TF_bZIP	ENSP00000236995;	1385
Homo_sapiens	POU3F4	ENSG00000196767	Pou	ENSP00000495996;	5456
Homo_sapiens	ZNF672	ENSG00000171161	zf-C2H2	ENSP00000426199;	79894
Homo_sapiens	ZNF329	ENSG00000181894	zf-C2H2	ENSP00000470008;	79673
Homo_sapiens	SCRT1	ENSG00000261678	zf-C2H2	ENSP00000455711;	83482
Homo_sapiens	ZNF140	ENSG00000196387	zf-C2H2	ENSP00000445411;	7699
Homo_sapiens	ZBED6	ENSG00000257315	zf-BED	ENSP00000447879;	100381270
Homo_sapiens	ZNF765	ENSG00000196417	zf-C2H2	ENSP00000379689;	91661
Homo_sapiens	CRX	ENSG00000105392	TF_Otx	ENSP00000221996;	1406
Homo_sapiens	ZNF853	ENSG00000236609	zf-C2H2	ENSP00000455585;	54753
Homo_sapiens	BAZ2B	ENSG00000123636	MBD	ENSP00000339670;	29994
Homo_sapiens	ZNF182	ENSG00000147118	zf-C2H2	ENSP00000366142;	7569
Homo_sapiens	ZNF467	ENSG00000181444	zf-C2H2	ENSP00000304769;	168544
Homo_sapiens	ZNF253	ENSG00000256771	zf-C2H2	ENSP00000467235;	56242
Homo_sapiens	PRDM10	ENSG00000170325	zf-C2H2	ENSP00000432237;	56980
Homo_sapiens	ZNF333	ENSG00000160961	zf-C2H2	ENSP00000292530;	84449
Homo_sapiens	PRDM1	ENSG00000057657	zf-C2H2	ENSP00000358092;	639
Homo_sapiens	ZIM3	ENSG00000141946	zf-C2H2	ENSP00000269834;	114026
Homo_sapiens	GATA4	ENSG00000136574	zf-GATA	ENSP00000435043;	2626
Homo_sapiens	GLIS2	ENSG00000126603	zf-C2H2	ENSP00000395547;	84662
Homo_sapiens	ZNF180	ENSG00000167384	zf-C2H2	ENSP00000221327;	7733
Homo_sapiens	ZNF366	ENSG00000178175	zf-C2H2	ENSP00000313158;	167465
Homo_sapiens	SOX18	ENSG00000203883	HMG	ENSP00000341815;	54345
Homo_sapiens	ZFP1	ENSG00000184517	zf-C2H2	ENSP00000377080;	162239
Homo_sapiens	ZNF517	ENSG00000197363	zf-C2H2	ENSP00000432025;	340385
Homo_sapiens	HOXD10	ENSG00000128710	Homeobox	ENSP00000249501;	3236
Homo_sapiens	ZNF112	ENSG00000062370	zf-C2H2	ENSP00000337081;	7771
Homo_sapiens	CCDC88A	ENSG00000115355	TF_bZIP	ENSP00000480931;	55704
Homo_sapiens	ZNF628	ENSG00000197483	zf-C2H2	ENSP00000469591;	89887
Homo_sapiens	ZNF829	ENSG00000185869	zf-C2H2	ENSP00000429266;	374899

Homo_sapiens	TADA2A	ENSG00000276234	MYB	ENSP00000484884;	6871
Homo_sapiens	ASCL3	ENSG00000176009	bHLH	ENSP00000435770;	56676
Homo_sapiens	ZNF688	ENSG00000229809	zf-C2H2	ENSP00000223459;	146542
Homo_sapiens	ZNF784	ENSG00000179922	zf-C2H2	ENSP00000320096;	147808
Homo_sapiens	MYOD1	ENSG00000129152	bHLH	ENSP00000250003;	4654
Homo_sapiens	SMAD5	ENSG00000113658	MH1	ENSP00000422954;	4090
Homo_sapiens	GSX1	ENSG00000169840	Homeobox	ENSP00000304331;	219409
Homo_sapiens	DMBX1	ENSG00000197587	Homeobox	ENSP00000361024;	127343
Homo_sapiens	ZNF419	ENSG00000105136	zf-C2H2	ENSP00000390916;	79744
Homo_sapiens	SP110	ENSG00000135899	SAND	ENSP00000375902;	3431
Homo_sapiens	SALL3	ENSG00000256463	zf-C2H2	ENSP00000461451;	27164
Homo_sapiens	BBX	ENSG00000114439	HMG	ENSP00000385530;	56987
Homo_sapiens	FEZF2	ENSG00000153266	zf-C2H2	ENSP00000418804;	55079
Homo_sapiens	EBF2	ENSG00000221818	COE	ENSP00000386178;	64641
Homo_sapiens	HMGA2	ENSG00000149948	HMGA	ENSP00000346658;	8091
Homo_sapiens	DACH1	ENSG00000276644	DACH	ENSP00000482245;	1602
Homo_sapiens	SETDB1	ENSG00000143379	MBD	ENSP00000432348;	9869
Homo_sapiens	VAX2	ENSG00000116035	Homeobox	ENSP00000405114;	25806
Homo_sapiens	MEF2D	ENSG00000116604	SRF	ENSP00000477413;	4209
Homo_sapiens	ZNF273	ENSG00000198039	zf-C2H2	ENSP00000418719;	10793
Homo_sapiens	ZNF287	ENSG00000141040	zf-C2H2	ENSP00000379168;	57336
Homo_sapiens	ZNF37A	ENSG00000075407	zf-C2H2	ENSP00000329141;	7587
Homo_sapiens	RAX	ENSG00000134438	Homeobox	ENSP00000334813;	30062
Homo_sapiens	OSR2	ENSG00000164920	zf-C2H2	ENSP00000429910;	116039
Homo_sapiens	ZNF763	ENSG00000197054	zf-C2H2	ENSP00000402017;	284390
Homo_sapiens	TSHZ3	ENSG00000121297	zf-C2H2	ENSP00000240587;	57616
Homo_sapiens	ZNF555	ENSG00000186300	zf-C2H2	ENSP00000467893;	148254
Homo_sapiens	HOXC10	ENSG00000180818	Homeobox	ENSP00000307321;	3226
Homo_sapiens	TOX	ENSG00000198846	HMG	ENSP00000354842;	9760
Homo_sapiens	KLF8	ENSG00000102349	zf-C2H2	ENSP00000417303;	11279
Homo_sapiens	ZNF235	ENSG00000159917	zf-C2H2	ENSP00000291182;	9310
Homo_sapiens	ZNF746	ENSG00000181220	zf-C2H2	ENSP00000395007;	155061
Homo_sapiens	VAX1	ENSG00000148704	Homeobox	ENSP00000277905;	11023
Homo_sapiens	BARX2	ENSG00000043039	Homeobox	ENSP00000281437;	8538
Homo_sapiens	ZNF311	ENSG00000197935	zf-C2H2	ENSP00000366384;	282890
Homo_sapiens	RBPJ	ENSG00000168214	CSL	ENSP00000423703;	3516
Homo_sapiens	PDX1	ENSG00000139515	Homeobox	ENSP00000370421;	3651
Homo_sapiens	ZXDB	ENSG00000198455	zf-C2H2	ENSP00000364023;	158586
Homo_sapiens	ZNF528	ENSG00000167555	zf-C2H2	ENSP00000353652;	84436
Homo_sapiens	BATF3	ENSG00000123685	TF_bZIP	ENSP00000243440;	55509
Homo_sapiens	HOXC12	ENSG00000123407	Homeobox	ENSP00000243103;	3228
Homo_sapiens	SMAD1	ENSG00000170365	MH1	ENSP00000426568;	4086
Homo_sapiens	ZFP91	ENSG00000186660	zf-C2H2	ENSP00000339030;	80829
Homo_sapiens	HMX2	ENSG00000188816	Homeobox	ENSP00000341108;	3167
Homo_sapiens	ZNF416	ENSG00000083817	zf-C2H2	ENSP00000196489;	55659
Homo_sapiens	ZNF776	ENSG00000152443	zf-C2H2	ENSP00000321812;	284309
Homo_sapiens	SPDEF	ENSG00000124664	ETS	ENSP00000363149;	25803
Homo_sapiens	ARID3C	ENSG00000205143	ARID	ENSP00000368189;	138715
Homo_sapiens	ZNF417	ENSG00000173480	zf-C2H2	ENSP00000472272;	147687
Homo_sapiens	FOXO1	ENSG00000150907	Fork_head	ENSP00000368880;	2308
Homo_sapiens	ZNF709	ENSG00000242852	zf-C2H2	ENSP00000380840;	163051
Homo_sapiens	FOXH1	ENSG00000160973	Fork_head	ENSP00000366534;	8928
Homo_sapiens	ZNF80	ENSG00000174255	zf-C2H2	ENSP00000417192;	7634
Homo_sapiens	ZNF296	ENSG00000170684	zf-C2H2	ENSP00000302770;	162979
Homo_sapiens	ZFX	ENSG00000005889	zf-C2H2	ENSP00000438233;	7543
Homo_sapiens	SP4	ENSG00000105866	zf-C2H2	ENSP00000222584;	6671
Homo_sapiens	ID1	ENSG00000125968	bHLH	ENSP00000365280;	3397
Homo_sapiens	ZNF701	ENSG00000167562	zf-C2H2	ENSP00000301093;	55762

Homo_sapiens	CEBPB	ENSG00000172216	TF_bZIP	ENSP00000305422;	1051
Homo_sapiens	ZNF66	ENSG00000160229	zf-C2H2	ENSP00000461425;	7617
Homo_sapiens	TULP2	ENSG00000104804	Tub	ENSP00000429131;	7288
Homo_sapiens	RFX1	ENSG00000132005	RFX	ENSP00000254325;	5989
Homo_sapiens	ZNF724	ENSG00000196081	zf-C2H2	ENSP00000413411;	440519
Homo_sapiens	GRHL2	ENSG00000083307	CP2	ENSP00000379260;	79977
Homo_sapiens	ZNF879	ENSG00000234284	zf-C2H2	ENSP00000414887;	345462
Homo_sapiens	TEAD3	ENSG00000007866	TEA	ENSP00000345772;	7005
Homo_sapiens	ZNF541	ENSG00000118156	zf-C2H2	ENSP00000313258;	84215
Homo_sapiens	ZNF610	ENSG00000167554	zf-C2H2	ENSP00000324441;	162963
Homo_sapiens	ELK4	ENSG00000158711	ETS	ENSP00000289703;	2005
Homo_sapiens	TERF1	ENSG00000147601	MYB	ENSP00000276603;	7013
Homo_sapiens	RXRG	ENSG00000143171	RXR-like	ENSP00000482458;	6258
Homo_sapiens	USF2	ENSG00000105698	bHLH	ENSP00000368429;	7392
Homo_sapiens	ZNF35	ENSG00000169981	zf-C2H2	ENSP00000379368;	7584
Homo_sapiens	FOXO4	ENSG00000184481	Fork_head	ENSP00000363377;	4303
Homo_sapiens	RFX2	ENSG00000087903	RFX	ENSP00000306335;	5990
Homo_sapiens	CTCFL	ENSG00000124092	zf-C2H2	ENSP00000243914;	140690
Homo_sapiens	AFF1	ENSG00000172493	AF-4	ENSP00000425755;	4299
Homo_sapiens	ZNF775	ENSG00000196456	zf-C2H2	ENSP00000417483;	285971
Homo_sapiens	ELF2	ENSG00000109381	ETS	ENSP00000377782;	1998
Homo_sapiens	ZNF32	ENSG00000169740	zf-C2H2	ENSP00000363556;	7580
Homo_sapiens	LHX5	ENSG00000089116	Homeobox	ENSP00000261731;	64211
Homo_sapiens	SOHLH1	ENSG00000165643	bHLH	ENSP00000298466;	402381
Homo_sapiens	NSD2	ENSG00000109685	HMG	ENSP00000372348;	7468
Homo_sapiens	HMGB4	ENSG00000176256	HMG	ENSP00000429214;	127540
Homo_sapiens	ZBTB44	ENSG00000196323	ZBTB	ENSP00000433457;	29068
Homo_sapiens	ZNF444	ENSG00000167685	zf-C2H2	ENSP00000468069;	55311
Homo_sapiens	NKX2-5	ENSG00000183072	Homeobox	ENSP00000327758;	1482
Homo_sapiens	ARID5B	ENSG00000150347	ARID	ENSP00000308862;	84159
Homo_sapiens	JDP2	ENSG00000140044	TF_bZIP	ENSP00000399587;	122953
Homo_sapiens	FOS	ENSG00000170345	TF_bZIP	ENSP00000451786;	2353
Homo_sapiens	BARX1	ENSG00000131668	Homeobox	ENSP00000253968;	56033
Homo_sapiens	LIN28B	ENSG00000187772	CSD	ENSP00000489735;	389421
Homo_sapiens	LHX3	ENSG00000107187	Homeobox	ENSP00000483080;	8022
Homo_sapiens	NRF1	ENSG00000106459	Nrf1	ENSP00000376924;	4899
Homo_sapiens	HOXC13	ENSG00000123364	Homeobox	ENSP00000243056;	3229
Homo_sapiens	FOXS1	ENSG00000179772	Fork_head	ENSP00000365145;	2307
Homo_sapiens	DMTF1	ENSG00000135164	MYB	ENSP00000463638;	9988
Homo_sapiens	ISL1	ENSG00000016082	Homeobox	ENSP00000230658;	3670
Homo_sapiens	STAT3	ENSG00000168610	STAT	ENSP00000373923;	6774
Homo_sapiens	ETV6	ENSG00000139083	ETS	ENSP00000379658;	2120
Homo_sapiens	IRX3	ENSG00000177508	Homeobox	ENSP00000331608;	79191
Homo_sapiens	ZNF627	ENSG00000198551	zf-C2H2	ENSP00000354414;	199692
Homo_sapiens	ZKSCAN5	ENSG00000196652	zf-C2H2	ENSP00000377725;	23660
Homo_sapiens	NFATC4	ENSG00000100968	RHD	ENSP00000451284;	4776
Homo_sapiens	ZNF212	ENSG00000170260	zf-C2H2	ENSP00000338572;	7988
Homo_sapiens	KLF5	ENSG00000102554	zf-C2H2	ENSP00000366915;	688
Homo_sapiens	ZNF572	ENSG00000180938	zf-C2H2	ENSP00000319305;	137209
Homo_sapiens	HES1	ENSG00000114315	bHLH	ENSP00000232424;	3280
Homo_sapiens	ZNF343	ENSG00000088876	zf-C2H2	ENSP00000278772;	79175
Homo_sapiens	ZNF91	ENSG00000167232	zf-C2H2	ENSP00000300619;	7644
Homo_sapiens	THAP7	ENSG00000184436	THAP	ENSP00000382084;	80764
Homo_sapiens	GTF2IRD2B	ENSG00000174428	GTF2I	ENSP00000480524;	389524
Homo_sapiens	ONECUT1	ENSG00000169856	CUT	ENSP00000476168;	3175
Homo_sapiens	ZNF79	ENSG00000196152	zf-C2H2	ENSP00000438418;	7633
Homo_sapiens	ZSCAN5C	ENSG00000204532	zf-C2H2	ENSP00000435234;	649137
Homo_sapiens	TRERF1	ENSG00000124496	zf-C2H2	ENSP00000346285;	55809

Homo_sapiens	BATF	ENSG00000156127	TF_bZIP	ENSP00000450486;	10538
Homo_sapiens	LHX9	ENSG00000143355	Homeobox	ENSP00000356360;	56956
Homo_sapiens	TOX4	ENSG00000092203	HMG	ENSP00000393080;	9878
Homo_sapiens	REL	ENSG00000162924	RHD	ENSP00000496299;	5966
Homo_sapiens	HOXD11	ENSG00000128713	Homeobox	ENSP00000249504;	3237
Homo_sapiens	ZBTB34	ENSG00000177125	ZBTB	ENSP00000362551;	403341
Homo_sapiens	ATF6B	ENSG00000213676	TF_bZIP	ENSP00000364349;	1388
Homo_sapiens	FOXD4L6	ENSG00000273514	Fork_head	ENSP00000484875;	653404
Homo_sapiens	ELK3	ENSG00000111145	ETS	ENSP00000447857;	2004
Homo_sapiens	ZNF559	ENSG00000188321	zf-C2H2	ENSP00000468153;	84527
Homo_sapiens	GSC2	ENSG00000063515	Homeobox	ENSP00000086933;	2928
Homo_sapiens	ONECUT3	ENSG00000205922	CUT	ENSP00000371786;	390874
Homo_sapiens	ARNT	ENSG00000143437	bHLH	ENSP00000346372;	405
Homo_sapiens	ETV4	ENSG00000175832	ETS	ENSP00000465718;	2118
Homo_sapiens	ZNF792	ENSG00000180884	zf-C2H2	ENSP00000385099;	126375
Homo_sapiens	IRF1	ENSG00000125347	IRF	ENSP00000480887;	3659
Homo_sapiens	NFATC3	ENSG00000072736	RHD	ENSP00000456120;	4775
Homo_sapiens	PAX2	ENSG00000075891	PAX	ENSP00000396259;	5076
Homo_sapiens	ZNF222	ENSG00000159885	zf-C2H2	ENSP00000187879;	7673
Homo_sapiens	KLF4	ENSG00000136826	zf-C2H2	ENSP00000363804;	9314
Homo_sapiens	TSC22D3	ENSG00000157514	TSC22	ENSP00000361466;	1831
Homo_sapiens	ZNF229	ENSG00000278318	zf-C2H2	ENSP00000479884;	7772
Homo_sapiens	TFEC	ENSG00000105967	bHLH	ENSP00000318676;	22797
Homo_sapiens	ZNF668	ENSG00000167394	zf-C2H2	ENSP00000440149;	79759
Homo_sapiens	HOXD1	ENSG00000128645	Homeobox	ENSP00000328598;	3231
Homo_sapiens	ASCL1	ENSG00000139352	bHLH	ENSP00000266744;	429
Homo_sapiens	RCOR3	ENSG00000117625	MYB	ENSP00000355972;	55758
Homo_sapiens	ZNF790	ENSG00000197863	zf-C2H2	ENSP00000480834;	388536
Homo_sapiens	ZNF605	ENSG00000196458	zf-C2H2	ENSP00000353314;	100289635
Homo_sapiens	POU4F3	ENSG00000091010	Pou	ENSP00000230732;	5459
Homo_sapiens	ESRRA	ENSG00000173153	ESR-like	ENSP00000441970;	2101
Homo_sapiens	GLIS3	ENSG00000107249	zf-C2H2	ENSP00000371398;	169792
Homo_sapiens	ZNF519	ENSG00000175322	zf-C2H2	ENSP00000464872;	162655
Homo_sapiens	ZNF354A	ENSG00000169131	zf-C2H2	ENSP00000337122;	6940
Homo_sapiens	ZNF214	ENSG00000149050	zf-C2H2	ENSP00000445373;	7761
Homo_sapiens	AC019117.3	ENSG00000283321	bHLH	ENSP00000490530;	-
Homo_sapiens	ZFAT	ENSG00000066827	zf-C2H2	ENSP00000429930;	57623
Homo_sapiens	ZKSCAN4	ENSG00000187626	zf-C2H2	ENSP00000366509;	387032
Homo_sapiens	AC008770.2	ENSG00000267179	zf-C2H2	ENSP00000467286;	-
Homo_sapiens	FOXA1	ENSG00000129514	Fork_head	ENSP00000250448;	3169
Homo_sapiens	ZNF658	ENSG00000274349	zf-C2H2	ENSP00000479295;	26149
Homo_sapiens	PITX3	ENSG00000107859	Homeobox	ENSP00000359019;	5309
Homo_sapiens	ZNF496	ENSG00000162714	zf-C2H2	ENSP00000294753;	84838
Homo_sapiens	ZNF248	ENSG00000198105	zf-C2H2	ENSP00000349882;	57209
Homo_sapiens	KLF10	ENSG00000155090	zf-C2H2	ENSP00000379222;	7071
Homo_sapiens	BCL6	ENSG00000113916	ZBTB	ENSP00000413122;	604
Homo_sapiens	HKR1	ENSG00000181666	zf-C2H2	ENSP00000438261;	284459
Homo_sapiens	TCF7L2	ENSG00000148737	HMG	ENSP00000435694;	6934
Homo_sapiens	MAEL	ENSG00000143194	HMG	ENSP00000356846;	84944
Homo_sapiens	NR1H4	ENSG00000012504	THR-like	ENSP00000315442;	9971
Homo_sapiens	POU5F1B	ENSG00000212993	Pou	ENSP00000495779;	5462
Homo_sapiens	ZNF316	ENSG00000205903	zf-C2H2	ENSP00000477706;	100131017
Homo_sapiens	POU2F2	ENSG00000028277	Pou	ENSP00000452930;	5452
Homo_sapiens	ZNF432	ENSG00000256087	zf-C2H2	ENSP00000221315;	9668
Homo_sapiens	HSF5	ENSG00000176160	HSF	ENSP00000313243;	124535
Homo_sapiens	ZNF382	ENSG00000161298	zf-C2H2	ENSP00000389722;	84911
Homo_sapiens	ZNF507	ENSG00000168813	zf-C2H2	ENSP00000441549;	22847
Homo_sapiens	MYCL	ENSG00000116990	bHLH	ENSP00000380494;	4610

Homo_sapiens	SNAI1	ENSG00000124216	zf-C2H2	ENSP00000244050;	6615
Homo_sapiens	NKX6-3	ENSG00000165066	Homeobox	ENSP00000428361;	157848
Homo_sapiens	SREBF2	ENSG00000198911	bHLH	ENSP00000395728;	6721
Homo_sapiens	ZNF347	ENSG00000197937	zf-C2H2	ENSP00000471712;	84671
Homo_sapiens	ZNF281	ENSG00000162702	zf-C2H2	ENSP00000294740;	23528
Homo_sapiens	BNC2	ENSG00000173068	zf-C2H2	ENSP00000370047;	54796
Homo_sapiens	HOXA10	ENSG00000253293	Homeobox	ENSP00000379633;	3206
Homo_sapiens	SOX4	ENSG00000124766	HMG	ENSP00000244745;	6659
Homo_sapiens	SPI1	ENSG00000066336	ETS	ENSP00000227163;	6688
Homo_sapiens	ZFP90	ENSG00000184939	zf-C2H2	ENSP00000460547;	146198
Homo_sapiens	ZNF23	ENSG00000167377	zf-C2H2	ENSP00000377171;	7571
Homo_sapiens	SOX11	ENSG00000176887	HMG	ENSP00000322568;	6664
Homo_sapiens	MIS18BP1	ENSG00000129534	MYB	ENSP00000309790;	55320
Homo_sapiens	HLX	ENSG00000136630	Homeobox	ENSP00000408248;	3142
Homo_sapiens	ZNF85	ENSG00000105750	zf-C2H2	ENSP00000471588;	7639
Homo_sapiens	ZNF799	ENSG00000196466	zf-C2H2	ENSP00000415278;	90576
Homo_sapiens	MEF2C	ENSG00000081189	SRF	ENSP00000422390;	4208
Homo_sapiens	PRDM16	ENSG00000142611	zf-C2H2	ENSP00000426975;	63976
Homo_sapiens	ZNF408	ENSG00000175213	zf-C2H2	ENSP00000309606;	79797
Homo_sapiens	ZNF200	ENSG00000010539	zf-C2H2	ENSP00000395723;	7752
Homo_sapiens	ZNF883	ENSG00000285447	zf-C2H2	ENSP00000490059;	169834
Homo_sapiens	ZNF526	ENSG00000167625	zf-C2H2	ENSP00000301215;	116115
Homo_sapiens	DBP	ENSG00000105516	TF_bZIP	ENSP00000469426;	1628
Homo_sapiens	ZNF473	ENSG00000142528	zf-C2H2	ENSP00000375697;	25888
Homo_sapiens	ZNF551	ENSG00000204519	zf-C2H2	ENSP00000472674;	90233
Homo_sapiens	IKZF2	ENSG00000030419	zf-C2H2	ENSP00000342876;	22807
Homo_sapiens	E4F1	ENSG00000167967	zf-C2H2	ENSP00000301727;	1877
Homo_sapiens	OTP	ENSG00000171540	Homeobox	ENSP00000302814;	23440
Homo_sapiens	ZNF800	ENSG00000048405	zf-C2H2	ENSP00000376989;	168850
Homo_sapiens	FERD3L	ENSG00000146618	bHLH	ENSP00000275461;	222894
Homo_sapiens	ZNF865	ENSG00000261221	zf-C2H2	ENSP00000457715;	100507290
Homo_sapiens	ZNF707	ENSG00000181135	zf-C2H2	ENSP00000436212;	101928160
Homo_sapiens	ZNF606	ENSG00000166704	zf-C2H2	ENSP00000343617;	80095
Homo_sapiens	SOX8	ENSG00000005513	HMG	ENSP00000293894;	30812
Homo_sapiens	GCM1	ENSG00000137270	GCM	ENSP00000259803;	8521
Homo_sapiens	BCL6B	ENSG00000161940	ZBTB	ENSP00000445010;	255877
Homo_sapiens	HEYL	ENSG00000163909	bHLH	ENSP00000361943;	26508
Homo_sapiens	SALL4	ENSG00000101115	zf-C2H2	ENSP00000379319;	57167
Homo_sapiens	ZNF18	ENSG00000154957	zf-C2H2	ENSP00000462383;	7566
Homo_sapiens	ZSCAN5B	ENSG00000197213	zf-C2H2	ENSP00000466072;	342933
Homo_sapiens	MTA1	ENSG00000182979	zf-GATA	ENSP00000394106;	9112
Homo_sapiens	NR6A1	ENSG00000148200	GCNF-like	ENSP00000420587;	2649
Homo_sapiens	JUN	ENSG00000177606	TF_bZIP	ENSP00000360266;	3725
Homo_sapiens	ZNF141	ENSG00000131127	zf-C2H2	ENSP00000240499;	7700
Homo_sapiens	NFX1	ENSG00000086102	zf-NF-X1	ENSP00000368856;	4799
Homo_sapiens	ARX	ENSG00000004848	Homeobox	ENSP00000368332;	170302
Homo_sapiens	PEG3	ENSG00000198300	zf-C2H2	ENSP00000326581;	5178
Homo_sapiens	RARB	ENSG00000077092	THR-like	ENSP00000332296;	5915
Homo_sapiens	NCOR2	ENSG00000196498	MYB	ENSP00000405367;	9612
Homo_sapiens	UBTFL1	ENSG00000255009	HMG	ENSP00000485108;	642623
Homo_sapiens	ZNF331	ENSG00000130844	zf-C2H2	ENSP00000393817;	55422
Homo_sapiens	ZNF778	ENSG00000170100	zf-C2H2	ENSP00000305203;	197320
Homo_sapiens	NRL	ENSG00000129535	TF_bZIP	ENSP00000380193;	4901
Homo_sapiens	MYOG	ENSG00000122180	bHLH	ENSP00000241651;	4656
Homo_sapiens	NOTO	ENSG00000214513	Homeobox	ENSP00000381486;	344022
Homo_sapiens	ZNF205	ENSG00000122386	zf-C2H2	ENSP00000371627;	7755
Homo_sapiens	LEF1	ENSG00000138795	HMG	ENSP00000369284;	51176
Homo_sapiens	ZNF529	ENSG00000186020	zf-C2H2	ENSP00000465578;	57711

Homo_sapiens	HOXA2	ENSG00000105996	Homeobox	ENSP00000222718;	3199
Homo_sapiens	ZNF148	ENSG00000163848	zf-C2H2	ENSP00000420448;	7707
Homo_sapiens	SMARCC1	ENSG00000173473	MYB	ENSP00000254480;	6599
Homo_sapiens	ZNF322	ENSG00000181315	zf-C2H2	ENSP00000478899;	79692
Homo_sapiens	TAL2	ENSG00000186051	bHLH	ENSP00000334547;	6887
Homo_sapiens	EMX2	ENSG00000170370	Homeobox	ENSP00000450962;	2018
Homo_sapiens	KLF2	ENSG00000127528	zf-C2H2	ENSP00000248071;	10365
Homo_sapiens	ZBTB22	ENSG00000236104	ZBTB	ENSP00000407545;	9278
Homo_sapiens	ZNF550	ENSG00000251369	zf-C2H2	ENSP00000422344;	162972
Homo_sapiens	ZFP3	ENSG00000180787	zf-C2H2	ENSP00000320347;	124961
Homo_sapiens	ZNF597	ENSG00000167981	zf-C2H2	ENSP00000301744;	146434
Homo_sapiens	PBX4	ENSG00000105717	Homeobox	ENSP00000251203;	80714
Homo_sapiens	ZNF652	ENSG00000198740	zf-C2H2	ENSP00000354686;	22834
Homo_sapiens	CSDC2	ENSG00000172346	CSD	ENSP00000417127;	27254
Homo_sapiens	TPRX1	ENSG00000178928	Homeobox	ENSP00000438832;	284355
Homo_sapiens	ZFHX3	ENSG00000140836	Homeobox	ENSP00000493252;	463
Homo_sapiens	ZNF358	ENSG00000198816	zf-C2H2	ENSP00000472777;	140467
Homo_sapiens	FOXD1	ENSG00000251493	Fork_head	ENSP00000481581;	2297
Homo_sapiens	STAT2	ENSG00000170581	STAT	ENSP00000315768;	6773
Homo_sapiens	ZNF431	ENSG00000196705	zf-C2H2	ENSP00000308578;	170959
Homo_sapiens	SREBF1	ENSG00000072310	bHLH	ENSP00000411516;	6720
Homo_sapiens	ZNF69	ENSG00000198429	zf-C2H2	ENSP00000402985;	7620
Homo_sapiens	FOXB2	ENSG00000204612	Fork_head	ENSP00000365898;	442425
Homo_sapiens	MIER1	ENSG00000198160	MYB	ENSP00000360053;	57708
Homo_sapiens	LRRFIP2	ENSG00000093167	LRRFIP	ENSP00000338727;	9209
Homo_sapiens	GATA6	ENSG00000141448	zf-GATA	ENSP00000269216;	2627
Homo_sapiens	HIVEP2	ENSG00000010818	zf-C2H2	ENSP00000356576;	3097
Homo_sapiens	ZNF100	ENSG00000197020	zf-C2H2	ENSP00000445201;	163227
Homo_sapiens	SOHLH2	ENSG00000120669	bHLH	ENSP00000369210;	54937
Homo_sapiens	ZKSCAN8	ENSG00000198315	zf-C2H2	ENSP00000402948;	7745
Homo_sapiens	HOXC9	ENSG00000180806	Homeobox	ENSP00000423861;	3225
Homo_sapiens	SP9	ENSG00000217236	zf-C2H2	ENSP00000378418;	100131390
Homo_sapiens	ZNF684	ENSG00000117010	zf-C2H2	ENSP00000361784;	127396
Homo_sapiens	ZNF484	ENSG00000127081	zf-C2H2	ENSP00000364646;	83744
Homo_sapiens	ZNF570	ENSG00000171827	zf-C2H2	ENSP00000331540;	148268
Homo_sapiens	ZNF251	ENSG00000198169	zf-C2H2	ENSP00000292562;	90987
Homo_sapiens	NR1H3	ENSG00000025434	THR-like	ENSP00000384745;	10062
Homo_sapiens	ZIC3	ENSG00000156925	zf-C2H2	ENSP00000359638;	7547
Homo_sapiens	FEV	ENSG00000163497	ETS	ENSP00000295727;	54738
Homo_sapiens	NFYB	ENSG00000120837	NF-YB	ENSP00000448250;	4801
Homo_sapiens	ZNF677	ENSG00000197928	zf-C2H2	ENSP00000334394;	342926
Homo_sapiens	HOPX	ENSG00000171476	Homeobox	ENSP00000396275;	84525
Homo_sapiens	ZNF460	ENSG00000197714	zf-C2H2	ENSP00000446167;	10794
Homo_sapiens	ARID3B	ENSG00000179361	ARID	ENSP00000455668;	10620
Homo_sapiens	ZNF581	ENSG00000171425	zf-C2H2	ENSP00000466564;	51545
Homo_sapiens	GLMP	ENSG00000198715	NCU-G1	ENSP00000483691;	112770
Homo_sapiens	ZNF649	ENSG00000198093	zf-C2H2	ENSP00000347043;	65251
Homo_sapiens	NKX1-1	ENSG00000235608	Homeobox	ENSP00000407978;	54729
Homo_sapiens	ZNF469	ENSG00000225614	zf-C2H2	ENSP00000402343;	84627
Homo_sapiens	VEZF1	ENSG00000136451	zf-C2H2	ENSP00000462337;	7716
Homo_sapiens	ZNF518A	ENSG00000177853	zf-C2H2	ENSP00000480280;	9849
Homo_sapiens	TFDP1	ENSG00000198176	E2F	ENSP00000364519;	7027
Homo_sapiens	RELA	ENSG00000173039	RHD	ENSP00000436545;	5970
Homo_sapiens	CREB3L3	ENSG00000060566	TF_bZIP	ENSP00000469355;	84699
Homo_sapiens	GZF1	ENSG00000125812	ZBTB	ENSP00000366250;	64412
Homo_sapiens	ZNF19	ENSG00000157429	zf-C2H2	ENSP00000462810;	7567
Homo_sapiens	SAMD11	ENSG00000187634	SAND	ENSP00000411579;	148398
Homo_sapiens	RUNX2	ENSG00000124813	Runt	ENSP00000496517;	860

Homo_sapiens	HSF2	ENSG00000025156	HSF	ENSP00000357440;	3298
Homo_sapiens	CARHSP1	ENSG00000153048	CSD	ENSP00000478055;	23589
Homo_sapiens	TFCP2L1	ENSG00000115112	CP2	ENSP00000263707;	29842
Homo_sapiens	TSHZ1	ENSG00000179981	zf-C2H2	ENSP00000464391;	10194
Homo_sapiens	ZNF234	ENSG00000263002	zf-C2H2	ENSP00000465011;	10780
Homo_sapiens	ZNF43	ENSG00000198521	zf-C2H2	ENSP00000350085;	7594
Homo_sapiens	HIF3A	ENSG00000124440	bHLH	ENSP00000432809;	64344
Homo_sapiens	FOXE3	ENSG00000186790	Fork_head	ENSP00000334472;	2301
Homo_sapiens	POU5F2	ENSG00000248483	Pou	ENSP00000489796;	134187
Homo_sapiens	NOBOX	ENSG00000106410	Homeobox	ENSP00000496732;	135935
Homo_sapiens	FOXR2	ENSG00000189299	Fork_head	ENSP00000427329;	139628
Homo_sapiens	ID4	ENSG00000172201	bHLH	ENSP00000367972;	3400
Homo_sapiens	ZNF93	ENSG00000184635	zf-C2H2	ENSP00000467553;	81931
Homo_sapiens	PTF1A	ENSG00000168267	bHLH	ENSP00000365687;	256297
Homo_sapiens	ZNF625	ENSG00000257591	zf-C2H2	ENSP00000394380;	90589
Homo_sapiens	PAX6	ENSG00000007372	PAX	ENSP00000492316;	5080
Homo_sapiens	ZNF267	ENSG00000185947	zf-C2H2	ENSP00000300870;	10308
Homo_sapiens	PAX7	ENSG00000009709	PAX	ENSP00000383502;	5081
Homo_sapiens	BHLHE23	ENSG00000125533	bHLH	ENSP00000480998;	128408
Homo_sapiens	GRHL3	ENSG00000158055	CP2	ENSP00000348333;	57822
Homo_sapiens	ZNF512	ENSG00000243943	zf-C2H2	ENSP00000347648;	84450
Homo_sapiens	ZFP2	ENSG00000198939	zf-C2H2	ENSP00000430531;	80108
Homo_sapiens	ZNF787	ENSG00000142409	zf-C2H2	ENSP00000478557;	126208
Homo_sapiens	GMEB1	ENSG00000162419	SAND	ENSP00000355186;	10691
Homo_sapiens	ZNF700	ENSG00000196757	zf-C2H2	ENSP00000479449;	90592
Homo_sapiens	SIX5	ENSG00000177045	Homeobox	ENSP00000494267;	147912
Homo_sapiens	HOXD8	ENSG00000175879	Homeobox	ENSP00000406045;	3234
Homo_sapiens	EBF4	ENSG00000088881	COE	ENSP00000345030;	57593
Homo_sapiens	ZNF692	ENSG00000171163	zf-C2H2	ENSP00000305483;	55657
Homo_sapiens	MYT1	ENSG00000196132	zf-C2HC	ENSP00000353269;	4661
Homo_sapiens	CPHXL	ENSG00000283755	Homeobox	ENSP00000491599;	105371346
Homo_sapiens	ZNF615	ENSG00000197619	zf-C2H2	ENSP00000365906;	284370
Homo_sapiens	NR2F1	ENSG00000175745	RXR-like	ENSP00000481517;	7025
Homo_sapiens	IRF7	ENSG00000185507	IRF	ENSP00000433903;	3665
Homo_sapiens	ZNF117	ENSG00000152926	zf-C2H2	ENSP00000479944;	109504726
Homo_sapiens	ZNF579	ENSG00000218891	zf-C2H2	ENSP00000320188;	163033
Homo_sapiens	ZNF556	ENSG00000172000	zf-C2H2	ENSP00000467366;	80032
Homo_sapiens	ZNF777	ENSG00000196453	zf-C2H2	ENSP00000247930;	27153
Homo_sapiens	FOXE1	ENSG00000178919	Fork_head	ENSP00000364265;	2304
Homo_sapiens	ZNF680	ENSG00000173041	zf-C2H2	ENSP00000309330;	340252
Homo_sapiens	ZIC4	ENSG00000174963	zf-C2H2	ENSP00000417855;	84107
Homo_sapiens	NFYC	ENSG00000066136	NF-YC	ENSP00000436710;	4802
Homo_sapiens	PRDM15	ENSG00000141956	zf-C2H2	ENSP00000408592;	63977
Homo_sapiens	ZNF468	ENSG00000204604	zf-C2H2	ENSP00000375660;	162967
Homo_sapiens	ID2	ENSG00000115738	bHLH	ENSP00000385465;	3398
Homo_sapiens	ZSCAN5A	ENSG00000131848	zf-C2H2	ENSP00000466445;	79149
Homo_sapiens	ISL2	ENSG00000159556	Homeobox	ENSP00000290759;	64843
Homo_sapiens	ZNF710	ENSG00000140548	zf-C2H2	ENSP00000268154;	374655
Homo_sapiens	ZIC5	ENSG00000139800	zf-C2H2	ENSP00000267294;	85416
Homo_sapiens	ZBED4	ENSG00000100426	zf-BED	ENSP00000216268;	9889
Homo_sapiens	ZNF679	ENSG00000197123	zf-C2H2	ENSP00000416809;	168417
Homo_sapiens	HMBOX1	ENSG00000147421	Homeobox	ENSP00000380516;	79618
Homo_sapiens	RFX5	ENSG00000143390	RFX	ENSP00000376502;	5993
Homo_sapiens	ZNF687	ENSG00000143373	zf-C2H2	ENSP00000398821;	57592
Homo_sapiens	ZNF773	ENSG00000152439	zf-C2H2	ENSP00000282292;	374928
Homo_sapiens	HOXB7	ENSG00000260027	Homeobox	ENSP00000239165;	3217
Homo_sapiens	ZNF470	ENSG00000197016	zf-C2H2	ENSP00000333223;	388566
Homo_sapiens	HHEX	ENSG00000152804	Homeobox	ENSP00000450017;	3087

Homo_sapiens	ANHX	ENSG00000227059	Homeobox	ENSP00000439513;	647589
Homo_sapiens	L3MBTL1	ENSG00000185513	zf-C2HC	ENSP00000402107;	26013
Homo_sapiens	ASCL4	ENSG00000187855	bHLH	ENSP00000345420;	121549
Homo_sapiens	ZNF480	ENSG00000198464	zf-C2H2	ENSP00000334164;	147657
Homo_sapiens	FOXI3	ENSG00000214336	Fork_head	ENSP00000478384;	344167
Homo_sapiens	ZFP57	ENSG00000204644	zf-C2H2	ENSP00000366078;	346171
Homo_sapiens	RFX8	ENSG00000196460	RFX	ENSP00000494216;	731220
Homo_sapiens	GLI4	ENSG00000250571	zf-C2H2	ENSP00000430987;	2738
Homo_sapiens	MBD3	ENSG00000071655	MBD	ENSP00000412302;	53615
Homo_sapiens	ZNF732	ENSG00000186777	zf-C2H2	ENSP00000478210;	654254
Homo_sapiens	TCF12	ENSG00000140262	bHLH	ENSP00000444696;	6938
Homo_sapiens	ELK1	ENSG00000126767	ETS	ENSP00000345585;	2002
Homo_sapiens	DBX1	ENSG00000109851	Homeobox	ENSP00000436881;	120237
Homo_sapiens	GFI1	ENSG00000162676	zf-C2H2	ENSP00000399719;	2672
Homo_sapiens	ZNF726	ENSG00000213967	zf-C2H2	ENSP00000471516;	730087
Homo_sapiens	SIX3	ENSG00000138083	Homeobox	ENSP00000260653;	6496
Homo_sapiens	ZSCAN12	ENSG00000158691	zf-C2H2	ENSP00000380039;	9753
Homo_sapiens	BATF2	ENSG00000168062	TF_bZIP	ENSP00000301887;	116071
Homo_sapiens	NR5A2	ENSG00000116833	SF-like	ENSP00000236914;	2494
Homo_sapiens	ZEB2	ENSG00000169554	zf-C2H2	ENSP00000454157;	9839
Homo_sapiens	GTF2I	ENSG00000263001	GTF2I	ENSP00000477837;	2969
Homo_sapiens	ZNF568	ENSG00000198453	zf-C2H2	ENSP00000466901;	374900
Homo_sapiens	ZNF217	ENSG00000171940	zf-C2H2	ENSP00000360526;	7764
Homo_sapiens	CDC5L	ENSG00000096401	MYB	ENSP00000360532;	988
Homo_sapiens	TSC22D2	ENSG00000196428	TSC22	ENSP00000354543;	9819
Homo_sapiens	PIAS3	ENSG00000131788	zf-MIZ	ENSP00000358304;	10401
Homo_sapiens	IRX5	ENSG00000176842	Homeobox	ENSP00000378132;	10265
Homo_sapiens	ERF	ENSG00000105722	ETS	ENSP00000388173;	2077
Homo_sapiens	ZFP37	ENSG00000136866	zf-C2H2	ENSP00000452552;	7539
Homo_sapiens	ETV3	ENSG00000117036	ETS	ENSP00000357175;	2117
Homo_sapiens	TFE3	ENSG00000068323	bHLH	ENSP00000314129;	7030
Homo_sapiens	CTCF	ENSG00000102974	zf-C2H2	ENSP00000495218;	10664
Homo_sapiens	EGR1	ENSG00000120738	zf-C2H2	ENSP00000239938;	1958
Homo_sapiens	TFDP3	ENSG00000183434	E2F	ENSP00000385461;	51270
Homo_sapiens	E2F2	ENSG00000007968	E2F	ENSP00000355249;	1870
Homo_sapiens	ZFP36L2	ENSG00000152518	zf-CCCH	ENSP00000282388;	678
Homo_sapiens	NFIC	ENSG00000141905	CTF/NFI	ENSP00000342194;	4782
Homo_sapiens	LCOR	ENSG00000196233	HTH	ENSP00000348298;	84458
Homo_sapiens	ZNF614	ENSG00000142556	zf-C2H2	ENSP00000270649;	80110
Homo_sapiens	RFX7	ENSG00000181827	RFX	ENSP00000453376;	64864
Homo_sapiens	ZBTB7A	ENSG00000178951	ZBTB	ENSP00000471865;	51341
Homo_sapiens	ZNF717	ENSG00000227124	zf-C2H2	ENSP00000419377;	100131827
Homo_sapiens	ZNF34	ENSG00000196378	zf-C2H2	ENSP00000434049;	80778
Homo_sapiens	NR4A2	ENSG00000153234	NGFIB-like	ENSP00000386747;	4929
Homo_sapiens	MEF2A	ENSG00000068305	SRF	ENSP00000452989;	4205
Homo_sapiens	ZNF367	ENSG00000165244	zf-C2H2	ENSP00000364405;	195828
Homo_sapiens	RCOR1	ENSG00000089902	MYB	ENSP00000262241;	23186
Homo_sapiens	ZNF264	ENSG00000083844	zf-C2H2	ENSP00000263095;	9422
Homo_sapiens	ZNF441	ENSG00000197044	zf-C2H2	ENSP00000350576;	126068
Homo_sapiens	TWIST1	ENSG00000122691	bHLH	ENSP00000242261;	7291
Homo_sapiens	AFF4	ENSG00000072364	AF-4	ENSP00000265343;	27125
Homo_sapiens	STAT5A	ENSG00000126561	STAT	ENSP00000465437;	6776
Homo_sapiens	ZNF888	ENSG00000213793	zf-C2H2	ENSP00000491567;	388559
Homo_sapiens	AC023509.3	ENSG00000267281	TF_bZIP	ENSP00000466174;	-
Homo_sapiens	ZNF805	ENSG00000204524	zf-C2H2	ENSP00000412999;	390980
Homo_sapiens	ZHX3	ENSG00000174306	Homeobox	ENSP00000443783;	23051
Homo_sapiens	ZNF584	ENSG00000171574	zf-C2H2	ENSP00000471105;	201514
Homo_sapiens	PRRX1	ENSG00000116132	Homeobox	ENSP00000450762;	5396

Homo_sapiens	HOXA3	ENSG00000105997	Homeobox	ENSP00000379640;	3200
Homo_sapiens	E2F5	ENSG00000133740	E2F	ENSP00000398124;	1875
Homo_sapiens	KLF17	ENSG00000171872	zf-C2H2	ENSP00000361373;	128209
Homo_sapiens	RHOXF1	ENSG00000101883	Homeobox	ENSP00000217999;	158800
Homo_sapiens	NKX2-3	ENSG00000119919	Homeobox	ENSP00000479692;	159296
Homo_sapiens	ZNF691	ENSG00000164011	zf-C2H2	ENSP00000361585;	51058
Homo_sapiens	ZSCAN31	ENSG00000235109	zf-C2H2	ENSP00000391235;	64288
Homo_sapiens	ZNF337	ENSG00000130684	zf-C2H2	ENSP00000252979;	26152
Homo_sapiens	ZNF429	ENSG00000197013	zf-C2H2	ENSP00000351280;	353088
Homo_sapiens	YY1	ENSG00000100811	zf-C2H2	ENSP00000262238;	7528
Homo_sapiens	ZNF76	ENSG00000065029	zf-C2H2	ENSP00000419106;	7629
Homo_sapiens	AC020909.1	ENSG00000142539	ETS	ENSP00000473233;	-
Homo_sapiens	ZSCAN2	ENSG00000176371	zf-C2H2	ENSP00000351257;	54993
Homo_sapiens	ZNF12	ENSG00000164631	zf-C2H2	ENSP00000384405;	7559
Homo_sapiens	DNAJC1	ENSG00000136770	MYB	ENSP00000366179;	64215
Homo_sapiens	ZNF585A	ENSG00000196967	zf-C2H2	ENSP00000375998;	199704
Homo_sapiens	ZNF385B	ENSG00000144331	zf-C2H2	ENSP00000386845;	151126
Homo_sapiens	FOXA2	ENSG00000125798	Fork_head	ENSP00000366319;	3170
Homo_sapiens	ZSCAN9	ENSG00000137185	zf-C2H2	ENSP00000252207;	7746
Homo_sapiens	ZNF814	ENSG00000204514	zf-C2H2	ENSP00000480123;	730051
Homo_sapiens	ZNF697	ENSG00000143067	zf-C2H2	ENSP00000396857;	90874
Homo_sapiens	ZNF462	ENSG00000148143	zf-C2H2	ENSP00000405837;	58499
Homo_sapiens	ZNF618	ENSG00000157657	zf-C2H2	ENSP00000363241;	114991
Homo_sapiens	CREB3L2	ENSG00000182158	TF_bZIP	ENSP00000329140;	64764
Homo_sapiens	ZNF827	ENSG00000151612	zf-C2H2	ENSP00000423130;	152485
Homo_sapiens	ZNF77	ENSG00000175691	zf-C2H2	ENSP00000319053;	58492
Homo_sapiens	NEUROG2	ENSG00000178403	bHLH	ENSP00000317333;	63973
Homo_sapiens	MSC	ENSG00000178860	bHLH	ENSP00000321445;	9242
Homo_sapiens	NEUROD1	ENSG00000162992	bHLH	ENSP00000295108;	4760
Homo_sapiens	ZBTB12	ENSG00000204366	ZBTB	ENSP00000364677;	221527
Homo_sapiens	ZNF629	ENSG00000102870	zf-C2H2	ENSP00000262525;	23361
Homo_sapiens	ATOH7	ENSG00000179774	bHLH	ENSP00000362777;	220202
Homo_sapiens	KLF7	ENSG00000118263	zf-C2H2	ENSP00000387510;	8609
Homo_sapiens	ZBTB48	ENSG00000204859	ZBTB	ENSP00000466390;	3104
Homo_sapiens	MESP2	ENSG00000188095	bHLH	ENSP00000342392;	145873
Homo_sapiens	FOXK1	ENSG00000164916	Fork_head	ENSP00000328720;	221937
Homo_sapiens	ZBTB41	ENSG00000177888	ZBTB	ENSP00000356375;	360023
Homo_sapiens	NR2C2	ENSG00000177463	RXR-like	ENSP00000388387;	7182
Homo_sapiens	ZNF558	ENSG00000167785	zf-C2H2	ENSP00000301475;	148156
Homo_sapiens	RFX4	ENSG00000111783	RFX	ENSP00000444163;	5992
Homo_sapiens	SMARCC2	ENSG00000139613	MYB	ENSP00000449396;	6601
Homo_sapiens	PLAGL1	ENSG00000118495	zf-C2H2	ENSP00000356544;	5325
Homo_sapiens	ZBTB7B	ENSG00000160685	ZBTB	ENSP00000438647;	51043
Homo_sapiens	ZNF425	ENSG00000204947	zf-C2H2	ENSP00000367300;	155054
Homo_sapiens	HOXB4	ENSG00000182742	Homeobox	ENSP00000328928;	3214
Homo_sapiens	ZNF500	ENSG00000103199	zf-C2H2	ENSP00000464747;	26048
Homo_sapiens	FOXL2	ENSG00000183770	Fork_head	ENSP00000333188;	668
Homo_sapiens	PHOX2B	ENSG00000109132	Homeobox	ENSP00000226382;	8929
Homo_sapiens	ISX	ENSG00000175329	Homeobox	ENSP00000386037;	91464
Homo_sapiens	ZBTB21	ENSG00000173276	ZBTB	ENSP00000381512;	49854
Homo_sapiens	ZNF582	ENSG00000018869	zf-C2H2	ENSP00000483414;	147948
Homo_sapiens	SP100	ENSG00000067066	SAND	ENSP00000343023;	6672
Homo_sapiens	ZSCAN21	ENSG00000166529	zf-C2H2	ENSP00000292450;	7589
Homo_sapiens	STAT6	ENSG00000166888	STAT	ENSP00000438451;	6778
Homo_sapiens	FOXC2	ENSG00000176692	Fork_head	ENSP00000326371;	2303
Homo_sapiens	TCF3	ENSG00000071564	bHLH	ENSP00000467508;	6929
Homo_sapiens	LHX1	ENSG00000273706	Homeobox	ENSP00000477829;	3975
Homo_sapiens	ID3	ENSG00000117318	bHLH	ENSP00000363689;	3399

Homo_sapiens	ARID5A	ENSG00000196843	ARID	ENSP00000350078;	10865
Homo_sapiens	PAX3	ENSG00000135903	PAX	ENSP00000386750;	5077
Homo_sapiens	DEAF1	ENSG00000177030	SAND	ENSP00000371846;	10522
Homo_sapiens	ZNF44	ENSG00000197857	zf-C2H2	ENSP00000377008;	51710
Homo_sapiens	KLF1	ENSG00000105610	zf-C2H2	ENSP00000264834;	10661
Homo_sapiens	GATAD2B	ENSG00000143614	zf-GATA	ENSP00000489595;	57459
Homo_sapiens	SIX1	ENSG00000126778	Homeobox	ENSP00000494686;	6495
Homo_sapiens	ONECUT2	ENSG00000119547	CUT	ENSP00000419185;	9480
Homo_sapiens	ZFY	ENSG00000067646	zf-C2H2	ENSP00000372525;	7544
Homo_sapiens	ATMIN	ENSG00000166454	zf-C2H2	ENSP00000464427;	23300
Homo_sapiens	NFIA	ENSG00000162599	CTF/NFI	ENSP00000360233;	4774
Homo_sapiens	FOXI2	ENSG00000186766	Fork_head	ENSP00000373572;	399823
Homo_sapiens	TFCP2	ENSG00000135457	CP2	ENSP00000449280;	7024
Homo_sapiens	MBD4	ENSG00000129071	MBD	ENSP00000394080;	8930
Homo_sapiens	ZIC1	ENSG00000152977	zf-C2H2	ENSP00000419664;	7545
Homo_sapiens	POU6F1	ENSG00000184271	Pou	ENSP00000330190;	5463
Homo_sapiens	FIGLA	ENSG00000183733	bHLH	ENSP00000333097;	344018
Homo_sapiens	TFAP2E	ENSG00000116819	AP-2	ENSP00000362332;	339488
Homo_sapiens	ZNF213	ENSG00000085644	zf-C2H2	ENSP00000380087;	7760
Homo_sapiens	ZNF17	ENSG00000186272	zf-C2H2	ENSP00000302455;	7565
Homo_sapiens	HAND1	ENSG00000113196	bHLH	ENSP00000231121;	9421
Homo_sapiens	HSFX1	ENSG00000171116	HSF	ENSP00000359444;	100506164
Homo_sapiens	FOXC1	ENSG00000054598	Fork_head	ENSP00000493906;	2296
Homo_sapiens	PAX9	ENSG00000198807	PAX	ENSP00000355245;	5083
Homo_sapiens	ZNF28	ENSG00000198538	zf-C2H2	ENSP00000375661;	7576
Homo_sapiens	MNT	ENSG00000070444	bHLH	ENSP00000174618;	4335
Homo_sapiens	NEUROD2	ENSG00000171532	bHLH	ENSP00000306754;	4761
Homo_sapiens	ZNF133	ENSG00000125846	zf-C2H2	ENSP00000346090;	7692
Homo_sapiens	BNC1	ENSG00000169594	zf-C2H2	ENSP00000456727;	646
Homo_sapiens	PRDM9	ENSG00000164256	zf-C2H2	ENSP00000296682;	56979
Homo_sapiens	HNF1A	ENSG00000135100	Homeobox	ENSP00000443112;	6927
Homo_sapiens	ZNF653	ENSG00000161914	zf-C2H2	ENSP00000293771;	115950
Homo_sapiens	UNCX	ENSG00000164853	Homeobox	ENSP00000314480;	340260
Homo_sapiens	TGIF2	ENSG00000118707	Homeobox	ENSP00000362979;	60436
Homo_sapiens	ZSCAN32	ENSG00000140987	zf-C2H2	ENSP00000483210;	54925
Homo_sapiens	ZFHX4	ENSG00000091656	Homeobox	ENSP00000430848;	79776
Homo_sapiens	ZFP69	ENSG00000187815	zf-C2H2	ENSP00000361791;	339559
Homo_sapiens	ETV7	ENSG00000010030	ETS	ENSP00000484485;	51513
Homo_sapiens	TLX1	ENSG00000107807	Homeobox	ENSP00000359215;	3195
Homo_sapiens	ZNF747	ENSG00000169955	zf-C2H2	ENSP00000457274;	65988
Homo_sapiens	ATF7	ENSG00000170653	TF_bZIP	ENSP00000387406;	11016
Homo_sapiens	ZNF74	ENSG00000185252	zf-C2H2	ENSP00000385855;	7625
Homo_sapiens	ETV3L	ENSG00000253831	ETS	ENSP00000430271;	440695
Homo_sapiens	FIZ1	ENSG00000179943	zf-C2H2	ENSP00000468342;	84922
Homo_sapiens	ZNF177	ENSG00000188629	zf-C2H2	ENSP00000468531;	7730
Homo_sapiens	ZKSCAN1	ENSG00000106261	zf-C2H2	ENSP00000443508;	7586
Homo_sapiens	HOXA7	ENSG00000122592	Homeobox	ENSP00000242159;	3204
Homo_sapiens	GATA5	ENSG00000130700	zf-GATA	ENSP00000252997;	140628
Homo_sapiens	THAP3	ENSG00000041988	THAP	ENSP00000311537;	90326
Homo_sapiens	TFEB	ENSG00000112561	bHLH	ENSP00000412551;	7942
Homo_sapiens	SOX3	ENSG00000134595	HMG	ENSP00000359567;	6658
Homo_sapiens	MYSM1	ENSG00000162601	MYB	ENSP00000418734;	114803
Homo_sapiens	HEY2	ENSG00000135547	bHLH	ENSP00000357349;	23493
Homo_sapiens	ZNF84	ENSG00000198040	zf-C2H2	ENSP00000376133;	7637
Homo_sapiens	NCOA1	ENSG00000084676	bHLH	ENSP00000288599;	8648
Homo_sapiens	SUB1	ENSG00000113387	PC4	ENSP00000265073;	10923
Homo_sapiens	ZNF723	ENSG00000268696	zf-C2H2	ENSP00000494306;	646864
Homo_sapiens	SOX13	ENSG00000143842	HMG	ENSP00000356172;	9580

Homo_sapiens	ZBTB37	ENSG00000185278	ZBTB	ENSP00000415293;	84614
Homo_sapiens	MSX1	ENSG00000163132	Homeobox	ENSP00000372170;	4487
Homo_sapiens	ZNF564	ENSG00000249709	zf-C2H2	ENSP00000340004;	163050
Homo_sapiens	NKX2-1	ENSG00000136352	Homeobox	ENSP00000346879;	7080
Homo_sapiens	ZNF292	ENSG00000188994	zf-C2H2	ENSP00000342847;	23036
Homo_sapiens	ZNF749	ENSG00000186230	zf-C2H2	ENSP00000333980;	388567
Homo_sapiens	LHX4	ENSG00000121454	Homeobox	ENSP00000263726;	89884
Homo_sapiens	HES2	ENSG00000069812	bHLH	ENSP00000367065;	54626
Homo_sapiens	HLF	ENSG00000108924	TF_bZIP	ENSP00000226067;	3131
Homo_sapiens	IRF9	ENSG00000213928	IRF	ENSP00000453974;	10379
Homo_sapiens	PPARG	ENSG00000132170	THR-like	ENSP00000495840;	5468
Homo_sapiens	SHOX2	ENSG00000168779	Homeobox	ENSP00000419362;	6474
Homo_sapiens	ZNF277	ENSG00000198839	zf-C2H2	ENSP00000354501;	11179
Homo_sapiens	ZNF878	ENSG00000257446	zf-C2H2	ENSP00000447931;	729747
Homo_sapiens	ARID1B	ENSG00000049618	ARID	ENSP00000344546;	57492
Homo_sapiens	ZNF426	ENSG00000130818	zf-C2H2	ENSP00000468100;	79088
Homo_sapiens	DLX4	ENSG00000108813	Homeobox	ENSP00000240306;	1748
Homo_sapiens	ZNF33B	ENSG00000196693	zf-C2H2	ENSP00000481265;	7582
Homo_sapiens	ZNF639	ENSG00000121864	zf-C2H2	ENSP00000419650;	51193
Homo_sapiens	BARHL2	ENSG00000143032	Homeobox	ENSP00000359474;	343472
Homo_sapiens	ZNF83	ENSG00000167766	zf-C2H2	ENSP00000472619;	55769
Homo_sapiens	HAND2	ENSG00000164107	bHLH	ENSP00000352565;	9464
Homo_sapiens	ZBTB42	ENSG00000179627	ZBTB	ENSP00000450673;	100128927
Homo_sapiens	ARNTL2	ENSG00000029153	bHLH	ENSP00000379238;	56938
Homo_sapiens	ZNF320	ENSG00000182986	zf-C2H2	ENSP00000473091;	162967
Homo_sapiens	ZNF10	ENSG00000256223	zf-C2H2	ENSP00000248211;	7556
Homo_sapiens	TUB	ENSG00000166402	Tub	ENSP00000299506;	7275
Homo_sapiens	ZNF107	ENSG00000196247	zf-C2H2	ENSP00000343443;	51427
Homo_sapiens	ZFP36L1	ENSG00000185650	zf-CCCH	ENSP00000388402;	677
Homo_sapiens	ZNF713	ENSG00000178665	zf-C2H2	ENSP00000487818;	349075
Homo_sapiens	ARID2	ENSG00000189079	ARID	ENSP00000397307;	196528
Homo_sapiens	ATF4	ENSG00000128272	TF_bZIP	ENSP00000336790;	468
Homo_sapiens	KMT2C	ENSG00000055609	HMG	ENSP00000347325;	58508
Homo_sapiens	ZNF783	ENSG00000204946	zf-C2H2	ENSP00000410890;	100289678
Homo_sapiens	HIVEP1	ENSG00000095951	zf-C2H2	ENSP00000486543;	3096
Homo_sapiens	MGA	ENSG00000174197	T-box	ENSP00000219905;	23269
Homo_sapiens	ZNF560	ENSG00000198028	zf-C2H2	ENSP00000301480;	147741
Homo_sapiens	MSX2	ENSG00000120149	Homeobox	ENSP00000239243;	4488
Homo_sapiens	ZNF174	ENSG00000103343	zf-C2H2	ENSP00000268655;	7727
Homo_sapiens	TRPS1	ENSG00000104447	zf-GATA	ENSP00000428680;	7227
Homo_sapiens	ZNF616	ENSG00000204611	zf-C2H2	ENSP00000471000;	90317
Homo_sapiens	DNAJC2	ENSG00000105821	MYB	ENSP00000368565;	27000
Homo_sapiens	ATF3	ENSG00000162772	TF_bZIP	ENSP00000355954;	467
Homo_sapiens	HOXB3	ENSG00000120093	Homeobox	ENSP00000418035;	3213
Homo_sapiens	ZNF101	ENSG00000181896	zf-C2H2	ENSP00000468049;	94039
Homo_sapiens	ZNF583	ENSG00000198440	zf-C2H2	ENSP00000291598;	147949
Homo_sapiens	ZNF880	ENSG00000221923	zf-C2H2	ENSP00000406318;	400713
Homo_sapiens	ELF4	ENSG00000102034	ETS	ENSP00000478297;	2000
Homo_sapiens	ZHX2	ENSG00000178764	Homeobox	ENSP00000314709;	22882
Homo_sapiens	GSC	ENSG00000133937	Homeobox	ENSP00000238558;	145258
Homo_sapiens	ZNF71	ENSG00000197951	zf-C2H2	ENSP00000328245;	58491
Homo_sapiens	HBP1	ENSG00000105856	HMG	ENSP00000418738;	26959
Homo_sapiens	HOXB8	ENSG00000120068	Homeobox	ENSP00000460659;	3218
Homo_sapiens	ZNF302	ENSG00000089335	zf-C2H2	ENSP00000396379;	55900
Homo_sapiens	ZFP41	ENSG00000181638	zf-C2H2	ENSP00000327427;	286128
Homo_sapiens	TBX20	ENSG00000164532	T-box	ENSP00000386170;	57057
Homo_sapiens	NEUROG1	ENSG00000181965	bHLH	ENSP00000317580;	4762
Homo_sapiens	DUX4	ENSG00000260596	Homeobox	ENSP00000458065;	100288687

Homo_sapiens	PKNOX2	ENSG00000165495	Homeobox	ENSP00000298282;	63876
Homo_sapiens	SMARCA1	ENSG00000102038	MYB	ENSP00000360162;	6594
Homo_sapiens	ZSCAN18	ENSG00000121413	zf-C2H2	ENSP00000412253;	65982
Homo_sapiens	ZNF334	ENSG00000198185	zf-C2H2	ENSP00000485779;	55713
Homo_sapiens	ZNF219	ENSG00000165804	zf-C2H2	ENSP00000450609;	51222
Homo_sapiens	THRA	ENSG00000126351	THR-like	ENSP00000264637;	7067
Homo_sapiens	ZIM2	ENSG00000269699	zf-C2H2	ENSP00000470326;	23619
Homo_sapiens	TCF24	ENSG00000261787	bHLH	ENSP00000455444;	100129654
Homo_sapiens	ZNF181	ENSG00000197841	zf-C2H2	ENSP00000420727;	339318
Homo_sapiens	ALX4	ENSG00000052850	Homeobox	ENSP00000332744;	60529
Homo_sapiens	HDX	ENSG00000165259	Homeobox	ENSP00000297977;	139324
Homo_sapiens	ZNF530	ENSG00000183647	zf-C2H2	ENSP00000332861;	348327
Homo_sapiens	GMEB2	ENSG00000101216	SAND	ENSP00000359094;	26205
Homo_sapiens	SMAD9	ENSG00000120693	MH1	ENSP00000382216;	4093
Homo_sapiens	HOXC11	ENSG00000123388	Homeobox	ENSP00000446680;	3227
Homo_sapiens	ZNF502	ENSG00000196653	zf-C2H2	ENSP00000296091;	91392
Homo_sapiens	ZNF114	ENSG00000178150	zf-C2H2	ENSP00000469998;	163071
Homo_sapiens	TBX4	ENSG00000121075	T-box	ENSP00000495714;	9496
Homo_sapiens	E2F6	ENSG00000169016	E2F	ENSP00000446315;	1876
Homo_sapiens	FOXD4L4	ENSG00000184659	Fork_head	ENSP00000366630;	349334
Homo_sapiens	ZNF233	ENSG00000159915	zf-C2H2	ENSP00000375820;	353355
Homo_sapiens	ZNF230	ENSG00000159882	zf-C2H2	ENSP00000409318;	7773
Homo_sapiens	ZNF594	ENSG00000180626	zf-C2H2	ENSP00000382513;	84622
Homo_sapiens	TULP1	ENSG00000112041	Tub	ENSP00000477534;	7287
Homo_sapiens	HOXB9	ENSG00000170689	Homeobox	ENSP00000309439;	3219
Homo_sapiens	SSRP1	ENSG00000149136	HMG	ENSP00000489564;	6749
Homo_sapiens	DLX3	ENSG00000064195	Homeobox	ENSP00000449976;	1747
Homo_sapiens	ZBTB1	ENSG00000126804	ZBTB	ENSP00000451000;	22890
Homo_sapiens	AHR	ENSG00000106546	bHLH	ENSP00000436466;	196
Homo_sapiens	ZNF660	ENSG00000144792	zf-C2H2	ENSP00000324605;	285349
Homo_sapiens	CSRNP2	ENSG00000110925	CSRNP_N	ENSP00000228515;	81566
Homo_sapiens	HIVEP3	ENSG00000127124	zf-C2H2	ENSP00000361665;	59269
Homo_sapiens	FOXJ3	ENSG00000198815	Fork_head	ENSP00000393408;	22887
Homo_sapiens	PRDM8	ENSG00000152784	zf-C2H2	ENSP00000406998;	56978
Homo_sapiens	RORC	ENSG00000143365	THR-like	ENSP00000327025;	6097
Homo_sapiens	CEBPG	ENSG00000153879	TF_bZIP	ENSP00000284000;	1054
Homo_sapiens	BACH1	ENSG00000156273	TF_bZIP	ENSP00000416569;	100379661
Homo_sapiens	ZNF705B	ENSG00000215356	zf-C2H2	ENSP00000382987;	100132396
Homo_sapiens	ZNF319	ENSG00000166188	zf-C2H2	ENSP00000299237;	57567
Homo_sapiens	FOXR1	ENSG00000176302	Fork_head	ENSP00000314806;	283150
Homo_sapiens	ZNF41	ENSG00000147124	zf-C2H2	ENSP00000315173;	7592
Homo_sapiens	YBX1	ENSG00000065978	CSD	ENSP00000361626;	4904
Homo_sapiens	SATB2	ENSG00000119042	CUT	ENSP00000388764;	23314
Homo_sapiens	ZSCAN1	ENSG00000152467	zf-C2H2	ENSP00000282326;	284312
Homo_sapiens	ZNF571	ENSG00000180479	zf-C2H2	ENSP00000351594;	51276
Homo_sapiens	NKX2-8	ENSG00000136327	Homeobox	ENSP00000258829;	26257
Homo_sapiens	ZNF3	ENSG00000166526	zf-C2H2	ENSP00000299667;	7551
Homo_sapiens	TEAD2	ENSG00000074219	TEA	ENSP00000366419;	8463
Homo_sapiens	NR5A1	ENSG00000136931	SF-like	ENSP00000483309;	2516
Homo_sapiens	ZNF485	ENSG00000198298	zf-C2H2	ENSP00000363558;	220992
Homo_sapiens	NR2F2	ENSG00000185551	RXR-like	ENSP00000377721;	7026
Homo_sapiens	ZNF491	ENSG00000177599	zf-C2H2	ENSP00000313443;	126069
Homo_sapiens	SP6	ENSG00000189120	zf-C2H2	ENSP00000340799;	80320
Homo_sapiens	ZNF439	ENSG00000171291	zf-C2H2	ENSP00000395632;	90594
Homo_sapiens	KLF14	ENSG00000266265	zf-C2H2	ENSP00000463287;	136259
Homo_sapiens	IKZF1	ENSG00000185811	zf-C2H2	ENSP00000413025;	10320
Homo_sapiens	UBP1	ENSG00000153560	CP2	ENSP00000395558;	7342
Homo_sapiens	DUXB	ENSG00000282757	Homeobox	ENSP00000491301;	100033411

Homo_sapiens	FOXA3	ENSG00000170608	Fork_head	ENSP00000304004;	3171
Homo_sapiens	ZBTB26	ENSG00000171448	ZBTB	ENSP00000362760;	57684
Homo_sapiens	ZNF215	ENSG00000149054	zf-C2H2	ENSP00000393202;	7762
Homo_sapiens	ZNF284	ENSG00000186026	zf-C2H2	ENSP00000411032;	342909
Homo_sapiens	ZNF667	ENSG00000198046	zf-C2H2	ENSP00000439402;	63934
Homo_sapiens	ZKSCAN2	ENSG00000155592	zf-C2H2	ENSP00000331626;	342357
Homo_sapiens	THAP9	ENSG00000168152	THAP	ENSP00000305533;	79725
Homo_sapiens	TCF21	ENSG00000118526	bHLH	ENSP00000237316;	6943
Homo_sapiens	ZNF197	ENSG00000186448	zf-C2H2	ENSP00000345809;	10168
Homo_sapiens	ZNF549	ENSG00000121406	zf-C2H2	ENSP00000365407;	256051
Homo_sapiens	PROX1	ENSG00000117707	HPD	ENSP00000420283;	5629
Homo_sapiens	TCFL5	ENSG00000101190	bHLH	ENSP00000217162;	10732
Homo_sapiens	FOSL2	ENSG00000075426	TF_bZIP	ENSP00000264716;	2355
Homo_sapiens	E2F3	ENSG00000112242	E2F	ENSP00000443418;	1871
Homo_sapiens	BAZ2A	ENSG00000076108	MBD	ENSP00000368754;	11176
Homo_sapiens	HMGB3	ENSG00000029993	HMG	ENSP00000410354;	3149
Homo_sapiens	ZNF599	ENSG00000153896	zf-C2H2	ENSP00000333802;	148103
Homo_sapiens	ZNF492	ENSG00000229676	zf-C2H2	ENSP00000413660;	57615
Homo_sapiens	ZNF232	ENSG00000167840	zf-C2H2	ENSP00000250076;	7775
Homo_sapiens	MIER3	ENSG00000155545	MYB	ENSP00000386584;	166968
Homo_sapiens	GLI1	ENSG00000111087	zf-C2H2	ENSP00000436671;	2735
Homo_sapiens	ZBTB24	ENSG00000112365	ZBTB	ENSP00000230122;	9841
Homo_sapiens	ZNF532	ENSG00000074657	zf-C2H2	ENSP00000468532;	55205
Homo_sapiens	ZNF644	ENSG00000122482	zf-C2H2	ENSP00000482748;	84146
Homo_sapiens	HOXD3	ENSG00000128652	Homeobox	ENSP00000386498;	3232
Homo_sapiens	UBTF	ENSG00000108312	HMG	ENSP00000345297;	7343
Homo_sapiens	ZNF410	ENSG00000119725	zf-C2H2	ENSP00000334170;	57862
Homo_sapiens	SP140	ENSG00000079263	SAND	ENSP00000393618;	11262
Homo_sapiens	ZNF92	ENSG00000146757	zf-C2H2	ENSP00000400495;	168374
Homo_sapiens	HINFP	ENSG00000172273	zf-C2H2	ENSP00000318085;	25988
Homo_sapiens	LHX8	ENSG00000162624	Homeobox	ENSP00000294638;	431707
Homo_sapiens	AC025287.4	ENSG00000284484	Homeobox	ENSP00000491197;	-
Homo_sapiens	ZNF20	ENSG00000132010	zf-C2H2	ENSP00000335437;	7568
Homo_sapiens	ZNF418	ENSG00000196724	zf-C2H2	ENSP00000379451;	147686
Homo_sapiens	ZBTB14	ENSG00000198081	ZBTB	ENSP00000349503;	7541
Homo_sapiens	MLXIP	ENSG00000175727	bHLH	ENSP00000445891;	22877
Homo_sapiens	CREB3L4	ENSG00000143578	TF_bZIP	ENSP00000357592;	148327
Homo_sapiens	SCX	ENSG00000260428	bHLH	ENSP00000476384;	642658
Homo_sapiens	NANOGP8	ENSG00000255192	Homeobox	ENSP00000487045;	388112
Homo_sapiens	ZNF548	ENSG00000188785	zf-C2H2	ENSP00000379482;	147694
Homo_sapiens	L3MBTL4	ENSG00000154655	zf-C2HC	ENSP00000318543;	91133
Homo_sapiens	ZNF655	ENSG00000197343	zf-C2H2	ENSP00000252713;	79027
Homo_sapiens	AC118549	ENSG00000036549	MYB	ENSP00000359837;	26009
Homo_sapiens	TBX10	ENSG00000167800	T-box	ENSP00000335191;	347853
Homo_sapiens	ZNF587	ENSG00000198466	zf-C2H2	ENSP00000345479;	84914
Homo_sapiens	AC012531.3	ENSG00000273049	Homeobox	ENSP00000476742;	-
Homo_sapiens	ELF1	ENSG00000120690	ETS	ENSP00000489586;	1997
Homo_sapiens	AC073612.1	ENSG00000258064	THAP	ENSP00000454911;	-
Homo_sapiens	LIN28A	ENSG00000131914	CSD	ENSP00000254231;	79727
Homo_sapiens	HMGXB4	ENSG00000100281	HMG	ENSP00000216106;	10042
Homo_sapiens	ZNF396	ENSG00000186496	zf-C2H2	ENSP00000466500;	252884
Homo_sapiens	NR2E1	ENSG00000112333	RXR-like	ENSP00000357982;	7101
Homo_sapiens	ZNF823	ENSG00000197933	zf-C2H2	ENSP00000340683;	55552
Homo_sapiens	STAT4	ENSG00000138378	STAT	ENSP00000376134;	6775
Homo_sapiens	ZNF626	ENSG00000188171	zf-C2H2	ENSP00000484232;	199777
Homo_sapiens	AC105001.2	ENSG00000258724	HMG	ENSP00000451145;	-
Homo_sapiens	TEF	ENSG00000167074	TF_bZIP	ENSP00000266304;	7008
Homo_sapiens	PPARA	ENSG00000186951	THR-like	ENSP00000385523;	5465

Homo_sapiens	ZNF8	ENSG00000278129	zf-C2H2	ENSP00000477716;	7554
Homo_sapiens	ZNF501	ENSG00000186446	zf-C2H2	ENSP00000379363;	115560
Homo_sapiens	ZNF454	ENSG00000178187	zf-C2H2	ENSP00000326249;	285676
Homo_sapiens	PRDM2	ENSG00000116731	zf-C2H2	ENSP00000312352;	7799
Homo_sapiens	ETS1	ENSG00000134954	ETS	ENSP00000441430;	2113
Homo_sapiens	PRDM6	ENSG00000061455	zf-C2H2	ENSP00000384725;	93166
Homo_sapiens	ZBED3	ENSG00000132846	zf-BED	ENSP00000427487;	84327
Homo_sapiens	ZNF354C	ENSG00000177932	zf-C2H2	ENSP00000324064;	30832
Homo_sapiens	ESX1	ENSG00000123576	Homeobox	ENSP00000361669;	80712
Homo_sapiens	HOXB6	ENSG00000108511	Homeobox	ENSP00000420009;	3216
Homo_sapiens	NFKB1	ENSG00000109320	RHD	ENSP00000226574;	4790
Homo_sapiens	TULP3	ENSG00000078246	Tub	ENSP00000380321;	7289
Homo_sapiens	RARG	ENSG00000172819	THR-like	ENSP00000343698;	5916
Homo_sapiens	ZNF705G	ENSG00000215372	zf-C2H2	ENSP00000383020;	100131980
Homo_sapiens	OLIG3	ENSG00000177468	bHLH	ENSP00000356708;	167826
Homo_sapiens	ZNF821	ENSG00000102984	zf-C2H2	ENSP00000458112;	55565
Homo_sapiens	HNF4A	ENSG00000101076	RXR-like	ENSP00000315180;	3172
Homo_sapiens	TCF7	ENSG00000081059	HMG	ENSP00000378472;	6932
Homo_sapiens	SMAD4	ENSG00000141646	MH1	ENSP00000381452;	4089
Homo_sapiens	DMRTC2	ENSG00000142025	DM	ENSP00000470553;	63946
Homo_sapiens	ZBED5	ENSG00000236287	zf-BED	ENSP00000398106;	58486
Homo_sapiens	NEUROG3	ENSG00000122859	bHLH	ENSP00000242462;	50674
Homo_sapiens	ESR2	ENSG00000140009	ESR-like	ENSP00000450488;	2100
Homo_sapiens	ZNF683	ENSG00000176083	zf-C2H2	ENSP00000388792;	257101
Homo_sapiens	ZEB1	ENSG00000148516	zf-C2H2	ENSP00000452787;	6935
Homo_sapiens	NPAS3	ENSG00000151322	bHLH	ENSP00000319610;	64067
Homo_sapiens	ZNF785	ENSG00000197162	zf-C2H2	ENSP00000420340;	146540
Homo_sapiens	HOXA4	ENSG00000197576	Homeobox	ENSP00000448015;	3201
Homo_sapiens	ZNF831	ENSG00000124203	zf-C2H2	ENSP00000360069;	128611
Homo_sapiens	HOXB5	ENSG00000120075	Homeobox	ENSP00000239151;	3215
Homo_sapiens	HMGXB3	ENSG00000113716	HMG	ENSP00000422231;	22993
Homo_sapiens	ZNF227	ENSG00000131115	zf-C2H2	ENSP00000375823;	7770
Homo_sapiens	ZNF446	ENSG00000083838	zf-C2H2	ENSP00000472219;	55663
Homo_sapiens	PAXBP1	ENSG00000159086	GCFC	ENSP00000290178;	94104
Homo_sapiens	HSFX2	ENSG00000268738	HSF	ENSP00000469223;	100130086
Homo_sapiens	ARID4B	ENSG00000054267	ARID	ENSP00000391497;	51742
Homo_sapiens	ZNF157	ENSG00000147117	zf-C2H2	ENSP00000366273;	7712
Homo_sapiens	MXD4	ENSG00000123933	bHLH	ENSP00000337889;	10608
Homo_sapiens	LRRFIP1	ENSG00000124831	LRRFIP	ENSP00000375857;	9208
Homo_sapiens	ZFP30	ENSG00000120784	zf-C2H2	ENSP00000343581;	22835
Homo_sapiens	ELF3	ENSG00000163435	ETS	ENSP00000356253;	1999
Homo_sapiens	INSM2	ENSG00000168348	zf-C2H2	ENSP00000306523;	84684
Homo_sapiens	HMGA1	ENSG00000137309	HMGA	ENSP00000385693;	3159
Homo_sapiens	MITF	ENSG00000187098	bHLH	ENSP00000418845;	4286
Homo_sapiens	MXI1	ENSG00000119950	bHLH	ENSP00000358625;	4601
Homo_sapiens	NR4A1	ENSG00000123358	NGFIB-like	ENSP00000353427;	3164
Homo_sapiens	ZNF585B	ENSG00000245680	zf-C2H2	ENSP00000436774;	92285
Homo_sapiens	TBX21	ENSG00000073861	T-box	ENSP00000177694;	30009
Homo_sapiens	TFAP2C	ENSG00000087510	AP-2	ENSP00000201031;	7022
Homo_sapiens	HMG20A	ENSG00000140382	HMG	ENSP00000452864;	10363
Homo_sapiens	ZNF770	ENSG00000198146	zf-C2H2	ENSP00000453474;	54989
Homo_sapiens	KLF6	ENSG00000067082	zf-C2H2	ENSP00000419923;	1316
Homo_sapiens	GLI2	ENSG00000074047	zf-C2H2	ENSP00000354586;	2736
Homo_sapiens	SIX4	ENSG00000100625	Homeobox	ENSP00000450761;	51804
Homo_sapiens	ZNF813	ENSG00000198346	zf-C2H2	ENSP00000379684;	126017
Homo_sapiens	ZNF7	ENSG00000147789	zf-C2H2	ENSP00000432724;	7553
Homo_sapiens	FOXK2	ENSG00000141568	Fork_head	ENSP00000335677;	3607
Homo_sapiens	ZNF577	ENSG00000161551	zf-C2H2	ENSP00000491349;	84765

Homo_sapiens	RHOXF2B	ENSG00000203989	Homeobox	ENSP00000360455;	727940
Homo_sapiens	ZNF623	ENSG00000183309	zf-C2H2	ENSP00000435232;	9831
Homo_sapiens	USF3	ENSG00000176542	bHLH	ENSP00000420721;	205717
Homo_sapiens	SOX12	ENSG00000177732	HMG	ENSP00000347646;	6666
Homo_sapiens	HSF4	ENSG00000102878	HSF	ENSP00000427832;	3299
Homo_sapiens	ZNF705E	ENSG00000214534	zf-C2H2	ENSP00000492790;	100131539
Homo_sapiens	GCM2	ENSG00000124827	GCM	ENSP00000368805;	9247
Homo_sapiens	E2F4	ENSG00000205250	E2F	ENSP00000458082;	1874
Homo_sapiens	FOXP1	ENSG00000114861	Fork_head	ENSP00000482847;	27086
Homo_sapiens	FOXF1	ENSG00000103241	Fork_head	ENSP00000262426;	2294
Homo_sapiens	DMRT1	ENSG00000137090	DM	ENSP00000371711;	1761
Homo_sapiens	ZNF518B	ENSG00000178163	zf-C2H2	ENSP00000317614;	85460
Homo_sapiens	ZNF436	ENSG00000125945	zf-C2H2	ENSP00000313582;	80818
Homo_sapiens	NHLH1	ENSG00000171786	bHLH	ENSP00000302189;	4807
Homo_sapiens	ZBTB33	ENSG00000177485	ZBTB	ENSP00000450969;	10009
Homo_sapiens	SP8	ENSG00000164651	zf-C2H2	ENSP00000408792;	221833
Homo_sapiens	NR1D2	ENSG00000174738	THR-like	ENSP00000373283;	9975
Homo_sapiens	FLI1	ENSG00000151702	ETS	ENSP00000281428;	2313
Homo_sapiens	REPIN1	ENSG00000214022	zf-C2H2	ENSP00000428562;	29803
Homo_sapiens	SNAI2	ENSG00000019549	zf-C2H2	ENSP00000494171;	6591
Homo_sapiens	TFAP2A	ENSG00000137203	AP-2	ENSP00000419961;	7020
Homo_sapiens	ETS2	ENSG00000157557	ETS	ENSP00000354194;	2114
Homo_sapiens	ZNF735	ENSG00000223614	zf-C2H2	ENSP00000485547;	730291
Homo_sapiens	HOXC5	ENSG00000172789	Homeobox	ENSP00000309336;	3222
Homo_sapiens	SOX9	ENSG00000125398	HMG	ENSP00000495527;	6662
Homo_sapiens	NR2C1	ENSG00000120798	RXR-like	ENSP00000376813;	7181
Homo_sapiens	NFYA	ENSG00000001167	NF-YA	ENSP00000229418;	4800
Homo_sapiens	NKX3-2	ENSG00000109705	Homeobox	ENSP00000371875;	579
Homo_sapiens	TTF1	ENSG00000125482	MYB	ENSP00000481441;	7270
Homo_sapiens	NR4A3	ENSG00000119508	NGFIB-like	ENSP00000333122;	8013
Homo_sapiens	ZNF768	ENSG00000169957	zf-C2H2	ENSP00000369777;	79724
Homo_sapiens	SETDB2	ENSG00000136169	MBD	ENSP00000346175;	83852
Homo_sapiens	FOXI1	ENSG00000168269	Fork_head	ENSP00000415483;	2299
Homo_sapiens	ZNF574	ENSG00000105732	zf-C2H2	ENSP00000351939;	64763
Homo_sapiens	FOXL1	ENSG00000176678	Fork_head	ENSP00000326272;	2300
Homo_sapiens	ZNF527	ENSG00000189164	zf-C2H2	ENSP00000390179;	84503
Homo_sapiens	CIC	ENSG00000079432	HMG	ENSP00000160740;	23152
Homo_sapiens	HES6	ENSG00000144485	bHLH	ENSP00000387155;	55502
Homo_sapiens	NKX2-6	ENSG00000180053	Homeobox	ENSP00000320089;	137814
Homo_sapiens	NR1D1	ENSG00000126368	THR-like	ENSP00000246672;	9572
Homo_sapiens	ZNF121	ENSG00000197961	zf-C2H2	ENSP00000468643;	7675
Homo_sapiens	ZBTB7C	ENSG00000184828	ZBTB	ENSP00000468254;	201501
Homo_sapiens	ZNF619	ENSG00000177873	zf-C2H2	ENSP00000398024;	285267
Homo_sapiens	SOX2	ENSG00000181449	HMG	ENSP00000323588;	6657
Homo_sapiens	ZNF131	ENSG00000172262	ZBTB	ENSP00000423945;	7690
Homo_sapiens	E2F1	ENSG00000101412	E2F	ENSP00000345571;	1869
Homo_sapiens	ZNF678	ENSG00000181450	zf-C2H2	ENSP00000344828;	339500
Homo_sapiens	ZSCAN25	ENSG00000197037	zf-C2H2	ENSP00000262941;	221785
Homo_sapiens	THAP8	ENSG00000161277	THAP	ENSP00000292894;	199745
Homo_sapiens	ZNF596	ENSG00000172748	zf-C2H2	ENSP00000310033;	169270
Homo_sapiens	ZNF622	ENSG00000173545	zf-C2H2	ENSP00000310042;	90441
Homo_sapiens	ZBTB2	ENSG00000181472	ZBTB	ENSP00000323183;	57621
Homo_sapiens	ZSCAN26	ENSG00000197062	zf-C2H2	ENSP00000485228;	7741
Homo_sapiens	MYF6	ENSG00000111046	bHLH	ENSP00000228641;	4618
Homo_sapiens	ZNF236	ENSG00000130856	zf-C2H2	ENSP00000463787;	7776
Homo_sapiens	ZNF589	ENSG00000164048	zf-C2H2	ENSP00000404592;	51385
Homo_sapiens	TWIST2	ENSG00000233608	bHLH	ENSP00000405176;	117581
Homo_sapiens	PATZ1	ENSG00000100105	ZBTB	ENSP00000337520;	23598

Homo_sapiens	LBX1	ENSG00000138136	Homeobox	ENSP00000359212;	10660
Homo_sapiens	ZBTB40	ENSG00000184677	ZBTB	ENSP00000384527;	9923
Homo_sapiens	ZSCAN16	ENSG00000196812	zf-C2H2	ENSP00000366527;	80345
Homo_sapiens	ZNF202	ENSG00000166261	zf-C2H2	ENSP00000433881;	7753
Homo_sapiens	ZNF782	ENSG00000196597	zf-C2H2	ENSP00000419397;	158431
Homo_sapiens	HSFX3	ENSG00000283697	HSF	ENSP00000490928;	101928917
Homo_sapiens	ZNF721	ENSG00000182903	zf-C2H2	ENSP00000340524;	170960
Homo_sapiens	ZNF676	ENSG00000196109	zf-C2H2	ENSP00000380310;	163223
Homo_sapiens	ZXDC	ENSG00000070476	zf-C2H2	ENSP00000374359;	79364
Homo_sapiens	ZNF576	ENSG00000124444	zf-C2H2	ENSP00000435934;	79177
Homo_sapiens	POU3F1	ENSG00000185668	Pou	ENSP00000362103;	5453
Homo_sapiens	IRF6	ENSG00000117595	IRF	ENSP00000355988;	3664
Homo_sapiens	OSR1	ENSG00000143867	zf-C2H2	ENSP00000272223;	130497
Homo_sapiens	PRDM14	ENSG00000147596	zf-C2H2	ENSP00000276594;	63978
Homo_sapiens	ZNF586	ENSG00000083828	zf-C2H2	ENSP00000375583;	54807
Homo_sapiens	TBX19	ENSG00000143178	T-box	ENSP00000356795;	9095
Homo_sapiens	FOXN2	ENSG00000170802	Fork_head	ENSP00000388486;	3344
Homo_sapiens	EVX2	ENSG00000174279	Homeobox	ENSP00000312385;	344191
Homo_sapiens	ZBED1	ENSG00000214717	zf-BED	ENSP00000370621;	9189
Homo_sapiens	IRX6	ENSG00000159387	Homeobox	ENSP00000290552;	79190
Homo_sapiens	PBX2	ENSG00000204304	Homeobox	ENSP00000364190;	5089
Homo_sapiens	CLOCK	ENSG00000134852	bHLH	ENSP00000396649;	9575
Homo_sapiens	TAL1	ENSG00000162367	bHLH	ENSP00000294339;	6886
Homo_sapiens	HELT	ENSG00000187821	bHLH	ENSP00000422140;	391723
Homo_sapiens	DLX5	ENSG00000105880	Homeobox	ENSP00000222598;	1749
Homo_sapiens	GTF2IRD2	ENSG00000196275	GTF2I	ENSP00000406723;	84163
Homo_sapiens	HMGB1	ENSG00000189403	HMG	ENSP00000369904;	3146
Homo_sapiens	HMX1	ENSG00000215612	Homeobox	ENSP00000383516;	3166
Homo_sapiens	GBX2	ENSG00000168505	Homeobox	ENSP00000302251;	2637
Homo_sapiens	NFIX	ENSG00000008441	CTF/NFI	ENSP00000465094;	4784
Homo_sapiens	ZNF646	ENSG00000167395	zf-C2H2	ENSP00000391271;	9726
Homo_sapiens	ZNF479	ENSG00000185177	zf-C2H2	ENSP00000333776;	90827
Homo_sapiens	AC073111.3	ENSG00000284041	zf-C2H2	ENSP00000419336;	-
Homo_sapiens	EVX1	ENSG00000106038	Homeobox	ENSP00000419266;	2128
Homo_sapiens	MZF1	ENSG00000099326	zf-C2H2	ENSP00000469493;	7593
Homo_sapiens	RUNX3	ENSG00000020633	Runt	ENSP00000308051;	864
Homo_sapiens	HOXD12	ENSG00000170178	Homeobox	ENSP00000385586;	3238
Homo_sapiens	JUND	ENSG00000130522	TF_bZIP	ENSP00000252818;	3727
Homo_sapiens	RXRB	ENSG00000204231	RXR-like	ENSP00000363817;	6257
Homo_sapiens	ZNF208	ENSG00000160321	zf-C2H2	ENSP00000380315;	7757
Homo_sapiens	ZNF383	ENSG00000188283	zf-C2H2	ENSP00000464871;	163087
Homo_sapiens	ESRRB	ENSG00000119715	ESR-like	ENSP00000370270;	2103
Homo_sapiens	ZNF891	ENSG00000214029	zf-C2H2	ENSP00000437590;	101060200
Homo_sapiens	ZNF699	ENSG00000196110	zf-C2H2	ENSP00000311596;	374879
Homo_sapiens	NR2E3	ENSG00000278570	RXR-like	ENSP00000482504;	10002
Homo_sapiens	ZNF335	ENSG00000198026	zf-C2H2	ENSP00000325326;	63925
Homo_sapiens	STAT1	ENSG00000115415	STAT	ENSP00000386244;	6772
Homo_sapiens	GATAD2A	ENSG00000167491	zf-GATA	ENSP00000351552;	54815
Homo_sapiens	ZFPM1	ENSG00000179588	zf-C2H2	ENSP00000326630;	161882
Homo_sapiens	NFE2L2	ENSG00000116044	TF_bZIP	ENSP00000380252;	4780
Homo_sapiens	ZNF276	ENSG00000158805	zf-C2H2	ENSP00000415836;	92822
Homo_sapiens	ESRRG	ENSG00000196482	ESR-like	ENSP00000352077;	2104
Homo_sapiens	ZNF835	ENSG00000127903	zf-C2H2	ENSP00000444747;	90485
Homo_sapiens	TP53	ENSG00000141510	P53	ENSP00000425104;	7157
Homo_sapiens	ZNF514	ENSG00000144026	zf-C2H2	ENSP00000295208;	84874
Homo_sapiens	ZFP82	ENSG00000181007	zf-C2H2	ENSP00000431265;	284406
Homo_sapiens	ZNF728	ENSG00000269067	zf-C2H2	ENSP00000471593;	388523
Homo_sapiens	PBX1	ENSG00000185630	Homeobox	ENSP00000453188;	5087

Homo_sapiens	NR1I3	ENSG00000143257	THR-like	ENSP00000421374;	9970
Homo_sapiens	ZNF780A	ENSG00000197782	zf-C2H2	ENSP00000472189;	284323
Homo_sapiens	NPAS2	ENSG00000170485	bHLH	ENSP00000388528;	4862
Homo_sapiens	ZNF154	ENSG00000179909	zf-C2H2	ENSP00000469633;	7710
Homo_sapiens	RERE	ENSG00000142599	zf-GATA	ENSP00000366684;	473
Homo_sapiens	NFATC1	ENSG00000131196	RHD	ENSP00000466489;	4772
Homo_sapiens	SALL2	ENSG00000165821	zf-C2H2	ENSP00000483562;	6297
Homo_sapiens	ATF6	ENSG00000118217	TF_bZIP	ENSP00000356919;	22926
Homo_sapiens	PBX3	ENSG00000167081	Homeobox	ENSP00000362588;	5090
Homo_sapiens	JARID2	ENSG00000008083	ARID	ENSP00000341280;	3720
Homo_sapiens	PKNOX1	ENSG00000160199	Homeobox	ENSP00000402243;	5316
Homo_sapiens	ELF5	ENSG00000135374	ETS	ENSP00000484521;	2001
Homo_sapiens	ZNF714	ENSG00000160352	zf-C2H2	ENSP00000478345;	148206
Homo_sapiens	NFIB	ENSG00000147862	CTF/NFI	ENSP00000475362;	4781
Homo_sapiens	NR0B1	ENSG00000169297	Miscellaneous	ENSP00000368246;	190
Homo_sapiens	ZNF664	ENSG00000179195	zf-C2H2	ENSP00000441405;	144348
Homo_sapiens	DACH2	ENSG00000126733	DACH	ENSP00000420896;	117154
Homo_sapiens	SOX15	ENSG00000129194	HMG	ENSP00000458286;	6665
Homo_sapiens	RBAK	ENSG00000146587	zf-C2H2	ENSP00000275423;	57786
Homo_sapiens	ZNF14	ENSG00000105708	zf-C2H2	ENSP00000340514;	7561
Homo_sapiens	CDIP1	ENSG00000089486	zf-LITAF-like	ENSP00000382508;	29965
Homo_sapiens	VSX1	ENSG00000100987	Homeobox	ENSP00000386612;	30813
Homo_sapiens	HOXD13	ENSG00000128714	Homeobox	ENSP00000376322;	3239
Homo_sapiens	ZNF423	ENSG00000102935	zf-C2H2	ENSP00000455426;	23090
Homo_sapiens	ZNF552	ENSG00000178935	zf-C2H2	ENSP00000375582;	79818
Homo_sapiens	ZNF730	ENSG00000183850	zf-C2H2	ENSP00000472959;	100129543
Homo_sapiens	ZNF781	ENSG00000196381	zf-C2H2	ENSP00000351391;	163115
Homo_sapiens	AC010616.1	ENSG00000268041	ETS	ENSP00000491574;	390937
Homo_sapiens	IRX1	ENSG00000170549	Homeobox	ENSP00000305244;	79192
Homo_sapiens	ARID1A	ENSG00000117713	ARID	ENSP00000478955;	8289
Homo_sapiens	ZNF716	ENSG00000182111	zf-C2H2	ENSP00000394248;	441234
Homo_sapiens	PRDM12	ENSG00000130711	zf-C2H2	ENSP00000253008;	59335
Homo_sapiens	TSHZ2	ENSG00000182463	zf-C2H2	ENSP00000360552;	128553
Homo_sapiens	KLF13	ENSG00000169926	zf-C2H2	ENSP00000452609;	51621
Homo_sapiens	FOXO6	ENSG00000204060	Fork_head	ENSP00000493184;	-
Homo_sapiens	IRX2	ENSG00000170561	Homeobox	ENSP00000372056;	153572
Homo_sapiens	MYBL1	ENSG00000185697	MYB	ENSP00000429633;	4603
Homo_sapiens	CEBPA	ENSG00000245848	TF_bZIP	ENSP00000427514;	1050
Homo_sapiens	ZNF407	ENSG00000215421	zf-C2H2	ENSP00000310359;	55628
Homo_sapiens	MIXL1	ENSG00000185155	Homeobox	ENSP00000355775;	83881
Homo_sapiens	MEIS1	ENSG00000143995	Homeobox	ENSP00000454209;	4211
Homo_sapiens	ZNF671	ENSG00000083814	zf-C2H2	ENSP00000321848;	79891
Homo_sapiens	AC138696.1	ENSG00000264668	zf-C2H2	ENSP00000428966;	-
Homo_sapiens	ZNF630	ENSG00000221994	zf-C2H2	ENSP00000354683;	57232
Homo_sapiens	ZNF524	ENSG00000171443	zf-C2H2	ENSP00000301073;	147807
Homo_sapiens	MEF2B	ENSG00000213999	SRF	ENSP00000386480;	100271849
Homo_sapiens	ZNF662	ENSG00000182983	zf-C2H2	ENSP00000329264;	389114
Homo_sapiens	ZNF534	ENSG00000198633	zf-C2H2	ENSP00000391358;	147658
Homo_sapiens	PRDM5	ENSG00000138738	zf-C2H2	ENSP00000404832;	11107
Homo_sapiens	TOX2	ENSG00000124191	HMG	ENSP00000390278;	84969
Homo_sapiens	ZNF415	ENSG00000170954	zf-C2H2	ENSP00000395055;	55786
Homo_sapiens	ZBTB20	ENSG00000181722	ZBTB	ENSP00000420324;	26137
Homo_sapiens	ZNF740	ENSG00000139651	zf-C2H2	ENSP00000409463;	283337
Homo_sapiens	SPIC	ENSG00000166211	ETS	ENSP00000448580;	121599
Homo_sapiens	TBX15	ENSG00000092607	T-box	ENSP00000207157;	6913
Homo_sapiens	ZNF766	ENSG00000196214	zf-C2H2	ENSP00000409652;	90321
Homo_sapiens	ZNF25	ENSG00000175395	zf-C2H2	ENSP00000302222;	219749
Homo_sapiens	PMS1	ENSG00000064933	HMG	ENSP00000401064;	5378

Homo_sapiens	MYC	ENSG00000136997	bHLH	ENSP00000367207;	4609
Homo_sapiens	SIX6	ENSG00000184302	Homeobox	ENSP00000328596;	4990
Homo_sapiens	POU2F3	ENSG00000137709	Pou	ENSP00000441687;	25833
Homo_sapiens	EHF	ENSG00000135373	ETS	ENSP00000433508;	26298
Homo_sapiens	ZNF544	ENSG00000198131	zf-C2H2	ENSP00000469635;	27300
Homo_sapiens	NANOGNB	ENSG00000205857	Homeobox	ENSP00000492127;	360030
Homo_sapiens	ZBTB43	ENSG00000169155	ZBTB	ENSP00000362563;	23099
Homo_sapiens	ZNF536	ENSG00000198597	zf-C2H2	ENSP00000465771;	9745
Homo_sapiens	ZNF440	ENSG00000171295	zf-C2H2	ENSP00000393489;	126070
Homo_sapiens	RORB	ENSG00000198963	THR-like	ENSP00000366093;	6096
Homo_sapiens	ZNF844	ENSG00000223547	zf-C2H2	ENSP00000448588;	284391
Homo_sapiens	ZNF263	ENSG00000006194	zf-C2H2	ENSP00000461146;	10127
Homo_sapiens	ZNF846	ENSG00000196605	zf-C2H2	ENSP00000467891;	100505555
Homo_sapiens	MTA2	ENSG00000149480	zf-GATA	ENSP00000278823;	9219
Homo_sapiens	CBFB	ENSG00000067955	CBF	ENSP00000415151;	865
Homo_sapiens	NPAS1	ENSG00000130751	bHLH	ENSP00000405290;	4861
Homo_sapiens	AC022167.5	ENSG00000283516	zf-LITAF-like	ENSP00000490446;	-
Homo_sapiens	ZNF57	ENSG00000171970	zf-C2H2	ENSP00000478776;	126295
Homo_sapiens	EN2	ENSG00000164778	Homeobox	ENSP00000297375;	2020
Homo_sapiens	ZFPM2	ENSG00000169946	zf-C2H2	ENSP00000428720;	23414
Homo_sapiens	HESX1	ENSG00000163666	Homeobox	ENSP00000295934;	8820
Homo_sapiens	SP3	ENSG00000172845	zf-C2H2	ENSP00000492253;	6670
Homo_sapiens	E2F8	ENSG00000129173	E2F	ENSP00000481103;	79733
Homo_sapiens	ZNF563	ENSG00000188868	zf-C2H2	ENSP00000469879;	147837
Homo_sapiens	MAFK	ENSG00000198517	TF_bZIP	ENSP00000385437;	7975
Homo_sapiens	ZNF569	ENSG00000196437	zf-C2H2	ENSP00000325018;	148266
Homo_sapiens	ZNF300	ENSG00000145908	zf-C2H2	ENSP00000397178;	91975
Homo_sapiens	HES7	ENSG00000179111	bHLH	ENSP00000314774;	84667
Homo_sapiens	NR1I2	ENSG00000144852	THR-like	ENSP00000336528;	8856
Homo_sapiens	SOX7	ENSG00000171056	HMG	ENSP00000301921;	83595
Homo_sapiens	ZBTB39	ENSG00000166860	ZBTB	ENSP00000300101;	9880
Homo_sapiens	ZNF398	ENSG00000197024	zf-C2H2	ENSP00000389972;	57541
Homo_sapiens	ZNF420	ENSG00000197050	zf-C2H2	ENSP00000338770;	147923
Homo_sapiens	NCOR1	ENSG00000141027	MYB	ENSP00000379189;	9611
Homo_sapiens	SHOX	ENSG00000185960	Homeobox	ENSP00000370987;	6473
Homo_sapiens	CEBPE	ENSG00000092067	TF_bZIP	ENSP00000206513;	1053
Homo_sapiens	LITAF	ENSG00000189067	zf-LITAF-like	ENSP00000461813;	9516
Homo_sapiens	SEBOX	ENSG00000274529	Homeobox	ENSP00000444503;	645832
Homo_sapiens	ZBTB11	ENSG00000066422	ZBTB	ENSP00000326200;	27107
Homo_sapiens	FOXP2	ENSG00000128573	Fork_head	ENSP00000489229;	93986
Homo_sapiens	TLX2	ENSG00000115297	Homeobox	ENSP00000233638;	3196
Homo_sapiens	TOX3	ENSG00000103460	HMG	ENSP00000219746;	27324
Homo_sapiens	NR3C2	ENSG00000151623	ESR-like	ENSP00000423510;	4306
Homo_sapiens	POU5F1	ENSG00000204531	Pou	ENSP00000484778;	5460
Homo_sapiens	ZNF573	ENSG00000189144	zf-C2H2	ENSP00000349861;	126231
Homo_sapiens	ZNF350	ENSG00000256683	zf-C2H2	ENSP00000243644;	59348
Homo_sapiens	ZNF324	ENSG00000083812	zf-C2H2	ENSP00000471778;	25799
Homo_sapiens	ZBTB32	ENSG00000011590	ZBTB	ENSP00000262630;	27033
Homo_sapiens	ZNF394	ENSG00000160908	zf-C2H2	ENSP00000337363;	84124
Homo_sapiens	FOXD4L5	ENSG00000204779	Fork_head	ENSP00000366637;	653427
Homo_sapiens	AHRR	ENSG00000063438	bHLH	ENSP00000428893;	57491
Homo_sapiens	PRDM4	ENSG00000110851	zf-C2H2	ENSP00000228437;	11108
Homo_sapiens	GFI1B	ENSG00000165702	zf-C2H2	ENSP00000361195;	8328
Homo_sapiens	ZNF341	ENSG00000131061	zf-C2H2	ENSP00000344308;	84905
Homo_sapiens	KLF15	ENSG00000163884	zf-C2H2	ENSP00000296233;	28999
Homo_sapiens	ZMIZ1	ENSG00000108175	zf-MIZ	ENSP00000401558;	57178
Homo_sapiens	ZSCAN4	ENSG00000180532	zf-C2H2	ENSP00000480210;	201516
Homo_sapiens	ZNF850	ENSG00000267041	zf-C2H2	ENSP00000464976;	342892

Homo_sapiens	ZNF256	ENSG00000152454	zf-C2H2	ENSP00000282308;	10172
Homo_sapiens	ZBTB46	ENSG00000130584	ZBTB	ENSP00000303102;	140685
Homo_sapiens	HSFY1	ENSG00000172468	HSF	ENSP00000342302;	86614
Homo_sapiens	HSFY2	ENSG00000169953	HSF	ENSP00000372303;	159119
Homo_sapiens	HOXC8	ENSG00000037965	Homeobox	ENSP00000040584;	3224
Homo_sapiens	ZNF33A	ENSG00000189180	zf-C2H2	ENSP00000485869;	7581
Homo_sapiens	ARNTL	ENSG00000133794	bHLH	ENSP00000431488;	406
Homo_sapiens	RLF	ENSG00000117000	zf-C2H2	ENSP00000361857;	6018
Homo_sapiens	SOX1	ENSG00000182968	HMG	ENSP00000330218;	6656
Homo_sapiens	DMRT3	ENSG00000064218	DM	ENSP00000190165;	58524
Homo_sapiens	ZNF624	ENSG00000197566	zf-C2H2	ENSP00000310472;	57547
Homo_sapiens	NPAS4	ENSG00000174576	bHLH	ENSP00000492526;	266743
Homo_sapiens	ZSCAN30	ENSG00000186814	zf-C2H2	ENSP00000329738;	100101467
Homo_sapiens	GLIS1	ENSG00000174332	zf-C2H2	ENSP00000486112;	148979
Homo_sapiens	ZNF146	ENSG00000167635	zf-C2H2	ENSP00000400391;	7705
Homo_sapiens	FOXM1	ENSG00000111206	Fork_head	ENSP00000342307;	2305
Homo_sapiens	AC092329.3	ENSG00000283201	zf-C2H2	ENSP00000478939;	-
Homo_sapiens	SIX2	ENSG00000170577	Homeobox	ENSP00000304502;	10736
Homo_sapiens	KLF18	ENSG00000283039	zf-C2H2	ENSP00000489024;	105378952
Homo_sapiens	MESP1	ENSG00000166823	bHLH	ENSP00000300057;	55897
Homo_sapiens	BHLHE40	ENSG00000134107	bHLH	ENSP00000256495;	8553
Homo_sapiens	ZNF483	ENSG00000173258	zf-C2H2	ENSP00000311679;	158399
Homo_sapiens	HES3	ENSG00000173673	bHLH	ENSP00000367130;	390992
Homo_sapiens	RUNX1	ENSG00000159216	Runt	ENSP00000388189;	100506403
Homo_sapiens	ZNF430	ENSG00000118620	zf-C2H2	ENSP00000261560;	80264
Homo_sapiens	MYNN	ENSG00000085274	ZBTB	ENSP00000326240;	55892
Homo_sapiens	HSFX4	ENSG00000283463	HSF	ENSP00000489814;	101927685
Homo_sapiens	ZNF711	ENSG00000147180	zf-C2H2	ENSP00000276123;	7552
Homo_sapiens	TBX5	ENSG00000089225	T-box	ENSP00000384152;	6910
Homo_sapiens	POU6F2	ENSG00000106536	Pou	ENSP00000430514;	11281
Homo_sapiens	RXRA	ENSG00000186350	RXR-like	ENSP00000419692;	6256
Homo_sapiens	WDHD1	ENSG00000198554	HMG	ENSP00000399349;	11169
Homo_sapiens	LBX2	ENSG00000179528	Homeobox	ENSP00000366789;	85474
Homo_sapiens	ZNF764	ENSG00000169951	zf-C2H2	ENSP00000252797;	92595
Homo_sapiens	RFX6	ENSG00000185002	RFX	ENSP00000332208;	222546
Homo_sapiens	SOX17	ENSG00000164736	HMG	ENSP00000297316;	64321
Homo_sapiens	ZFP91-CNTF	ENSG00000255073	zf-C2H2	ENSP00000455911;	-
Homo_sapiens	ZHX1	ENSG00000165156	Homeobox	ENSP00000297857;	11244
Homo_sapiens	ZNF48	ENSG00000180035	zf-C2H2	ENSP00000324056;	197407
Homo_sapiens	SP7	ENSG00000170374	zf-C2H2	ENSP00000441367;	121340
Homo_sapiens	CSRNP1	ENSG00000144655	CSRNP_N	ENSP00000273153;	64651
Homo_sapiens	DLX6	ENSG00000006377	Homeobox	ENSP00000451635;	1750
Homo_sapiens	HSF1	ENSG00000185122	HSF	ENSP00000383590;	3297
Homo_sapiens	ERG	ENSG00000157554	ETS	ENSP00000288319;	2078
Homo_sapiens	MAF	ENSG00000178573	TF_bZIP	ENSP00000327048;	4094
Homo_sapiens	ZNF404	ENSG00000176222	zf-C2H2	ENSP00000319479;	342908
Homo_sapiens	AL033529.1	ENSG00000254553	ZBTB	ENSP00000455300;	-
Homo_sapiens	ZNF275	ENSG00000063587	zf-C2H2	ENSP00000359271;	105373378
Homo_sapiens	RFX3	ENSG00000080298	RFX	ENSP00000351574;	5991
Homo_sapiens	MAZ	ENSG00000103495	zf-C2H2	ENSP00000458201;	4150
Homo_sapiens	IKZF5	ENSG00000095574	zf-C2H2	ENSP00000478056;	64376
Homo_sapiens	KLF9	ENSG00000119138	zf-C2H2	ENSP00000366330;	687
Homo_sapiens	ZNF665	ENSG00000197497	zf-C2H2	ENSP00000469154;	79788
Homo_sapiens	ZNF682	ENSG00000197124	zf-C2H2	ENSP00000470718;	91120
Homo_sapiens	ZNF566	ENSG00000186017	zf-C2H2	ENSP00000465343;	84924
Homo_sapiens	FOXB1	ENSG00000171956	Fork_head	ENSP00000379369;	27023
Homo_sapiens	DBX2	ENSG00000185610	Homeobox	ENSP00000331470;	440097
Homo_sapiens	FOXG1	ENSG00000176165	Fork_head	ENSP00000339004;	2290

Homo_sapiens	JUNB	ENSG00000171223	TF_bZIP	ENSP00000303315;	3726
Homo_sapiens	DPRX	ENSG00000204595	Homeobox	ENSP00000365838;	503834
Homo_sapiens	MAFF	ENSG00000185022	TF_bZIP	ENSP00000416493;	23764
Homo_sapiens	SRY	ENSG00000184895	HMG	ENSP00000372547;	6736
Homo_sapiens	FOXP4	ENSG00000137166	Fork_head	ENSP00000362154;	116113
Homo_sapiens	MYRF	ENSG00000124920	NDT80/PhoG	ENSP00000265460;	745
Homo_sapiens	AFF2	ENSG00000155966	AF-4	ENSP00000286437;	2334
Homo_sapiens	OVOL2	ENSG00000125850	zf-C2H2	ENSP00000278780;	58495
Homo_sapiens	TGIF2LY	ENSG00000176679	Homeobox	ENSP00000318502;	90655
Homo_sapiens	ZSCAN29	ENSG00000140265	zf-C2H2	ENSP00000456883;	146050
Homo_sapiens	ZNF852	ENSG00000178917	zf-C2H2	ENSP00000389841;	285346
Homo_sapiens	TCF23	ENSG00000163792	bHLH	ENSP00000296096;	150921
Homo_sapiens	FOSB	ENSG00000125740	TF_bZIP	ENSP00000466530;	2354
Homo_sapiens	BHMG1	ENSG00000237452	HMG	ENSP00000402674;	388553
Homo_sapiens	NKX2-2	ENSG00000125820	Homeobox	ENSP00000366347;	4821
Homo_sapiens	POU3F2	ENSG00000184486	Pou	ENSP00000329170;	5454
Homo_sapiens	NR2F6	ENSG00000160113	RXR-like	ENSP00000291442;	2063
Homo_sapiens	BCL11A	ENSG00000119866	zf-C2H2	ENSP00000496168;	53335
Homo_sapiens	AC115220.1	ENSG00000241149	zf-C2H2	ENSP00000492202;	-
Homo_sapiens	ZNF268	ENSG00000090612	zf-C2H2	ENSP00000444412;	10795
Homo_sapiens	TULP4	ENSG00000130338	Tub	ENSP00000356064;	56995
Homo_sapiens	ASCL5	ENSG00000232237	bHLH	ENSP00000469019;	647219
Homo_sapiens	HIC1	ENSG00000177374	ZBTB	ENSP00000314080;	3090
Homo_sapiens	ZBTB45	ENSG00000119574	ZBTB	ENSP00000346603;	84878
Homo_sapiens	ZNF836	ENSG00000196267	zf-C2H2	ENSP00000325038;	162962
Homo_sapiens	ZNF670	ENSG00000277462	zf-C2H2	ENSP00000355459;	93474
Homo_sapiens	ZFHX2	ENSG00000136367	Homeobox	ENSP00000413418;	85446
Homo_sapiens	FOXF2	ENSG00000137273	Fork_head	ENSP00000259806;	2295
Homo_sapiens	SMARCE1	ENSG00000073584	HMG	ENSP00000495857;	6605
Homo_sapiens	ZNF789	ENSG00000198556	zf-C2H2	ENSP00000331927;	285989
Homo_sapiens	MYT1L	ENSG00000186487	zf-C2HC	ENSP00000384219;	23040
Homo_sapiens	ZNF24	ENSG00000172466	zf-C2H2	ENSP00000382015;	7572
Homo_sapiens	TBX3	ENSG00000135111	T-box	ENSP00000257567;	6926
Homo_sapiens	NEUROD4	ENSG00000123307	bHLH	ENSP00000242994;	58158
Homo_sapiens	AR	ENSG00000169083	ESR-like	ENSP00000484033;	367
Homo_sapiens	MBD2	ENSG00000134046	MBD	ENSP00000381435;	8932
Homo_sapiens	ZNF189	ENSG00000136870	zf-C2H2	ENSP00000259395;	7743
Homo_sapiens	PHOX2A	ENSG00000165462	Homeobox	ENSP00000298231;	401
Homo_sapiens	ZFP64	ENSG00000020256	zf-C2H2	ENSP00000344615;	55734
Homo_sapiens	SMAD6	ENSG00000137834	MH1	ENSP00000452955;	4091
Homo_sapiens	THAP10	ENSG00000129028	THAP	ENSP00000249861;	56906
Homo_sapiens	AC073111.5	ENSG00000284691	zf-C2H2	ENSP00000492887;	-
Homo_sapiens	FOXD4L3	ENSG00000187559	Fork_head	ENSP00000341961;	286380
Homo_sapiens	TP73	ENSG00000078900	P53	ENSP00000367537;	7161
Homo_sapiens	ZNF587B	ENSG00000269343	zf-C2H2	ENSP00000472004;	100293516
Homo_sapiens	HOXB13	ENSG00000159184	Homeobox	ENSP00000290295;	10481
Homo_sapiens	BHLHA9	ENSG00000205899	bHLH	ENSP00000375248;	727857
Homo_sapiens	ZNF184	ENSG00000096654	zf-C2H2	ENSP00000366636;	7738
Homo_sapiens	ZNF471	ENSG00000196263	zf-C2H2	ENSP00000309161;	57573
Homo_sapiens	HOXA5	ENSG00000106004	Homeobox	ENSP00000222726;	3202
Homo_sapiens	ZNF362	ENSG00000160094	zf-C2H2	ENSP00000446335;	149076
Homo_sapiens	ZBTB17	ENSG00000116809	ZBTB	ENSP00000438529;	7709
Homo_sapiens	ZNF160	ENSG00000170949	zf-C2H2	ENSP00000470961;	90338
Homo_sapiens	GABPA	ENSG00000154727	ETS	ENSP00000346886;	2551
Homo_sapiens	ZNF142	ENSG00000115568	zf-C2H2	ENSP00000408643;	7701
Homo_sapiens	ZNF771	ENSG00000179965	zf-C2H2	ENSP00000323945;	51333
Homo_sapiens	THAP12	ENSG00000137492	THAP	ENSP00000433966;	5612
Homo_sapiens	HMX3	ENSG00000188620	Homeobox	ENSP00000350549;	340784

Homo_sapiens	ZNF736	ENSG00000234444	zf-C2H2	ENSP00000347210;	728927
Homo_sapiens	ZFP14	ENSG00000142065	zf-C2H2	ENSP00000270001;	57677
Homo_sapiens	RORA	ENSG00000069667	THR-like	ENSP00000402971;	6095
Homo_sapiens	PAX4	ENSG00000106331	PAX	ENSP00000491782;	5078
Homo_sapiens	ZBTB4	ENSG00000174282	ZBTB	ENSP00000307858;	57659
Homo_sapiens	HOXC4	ENSG00000198353	Homeobox	ENSP00000305973;	3221
Homo_sapiens	CREB5	ENSG00000146592	TF_bZIP	ENSP00000379593;	9586
Homo_sapiens	POU4F1	ENSG00000152192	Pou	ENSP00000366413;	5457
Homo_sapiens	KLF12	ENSG00000118922	zf-C2H2	ENSP00000366897;	11278
Homo_sapiens	ZNF345	ENSG00000251247	zf-C2H2	ENSP00000491547;	25850
Homo_sapiens	TEAD1	ENSG00000187079	TEA	ENSP00000334754;	7003
Homo_sapiens	LMX1B	ENSG00000136944	Homeobox	ENSP00000347684;	4010
Homo_sapiens	PIAS1	ENSG00000033800	zf-MIZ	ENSP00000249636;	8554
Homo_sapiens	NR1H2	ENSG00000131408	THR-like	ENSP00000472526;	7376
Homo_sapiens	ZNF324B	ENSG00000249471	zf-C2H2	ENSP00000438930;	388569
Homo_sapiens	MYCN	ENSG00000134323	bHLH	ENSP00000281043;	4613
Homo_sapiens	ZNF175	ENSG00000105497	zf-C2H2	ENSP00000262259;	7728
Homo_sapiens	VENTX	ENSG00000151650	Homeobox	ENSP00000357556;	27287
Homo_sapiens	ZNF559-ZNF177	ENSG00000270011	zf-C2H2	ENSP00000445323;	100529215
Homo_sapiens	VDR	ENSG00000111424	THR-like	ENSP00000229022;	7421
Homo_sapiens	ZNF546	ENSG00000187187	zf-C2H2	ENSP00000469540;	339327
Homo_sapiens	AFF3	ENSG00000144218	AF-4	ENSP00000395068;	3899
Homo_sapiens	MBD1	ENSG00000141644	MBD	ENSP00000381502;	4152
Homo_sapiens	KLF16	ENSG00000129911	zf-C2H2	ENSP00000483701;	83855
Homo_sapiens	ZNF737	ENSG00000237440	zf-C2H2	ENSP00000471995;	100129842
Homo_sapiens	ZNF169	ENSG00000175787	zf-C2H2	ENSP00000378792;	169841
Homo_sapiens	ZNF695	ENSG00000197472	zf-C2H2	ENSP00000341236;	57116
Homo_sapiens	SP5	ENSG00000204335	zf-C2H2	ENSP00000364430;	389058
Homo_sapiens	CAMTA2	ENSG00000108509	CG-1	ENSP00000459519;	23125
Homo_sapiens	SOX6	ENSG00000110693	HMG	ENSP00000324948;	55553
Homo_sapiens	CAMTA1	ENSG00000171735	CG-1	ENSP00000306522;	23261
Homo_sapiens	DDIT3	ENSG00000175197	TF_bZIP	ENSP00000494844;	1649
Homo_sapiens	ZNF525	ENSG00000203326	zf-C2H2	ENSP00000419136;	170958
Homo_sapiens	LEUTX	ENSG00000213921	Homeobox	ENSP00000380053;	342900
Homo_sapiens	AC092835.1	ENSG00000233757	zf-C2H2	ENSP00000478941;	-
Homo_sapiens	ZKSCAN7	ENSG00000196345	zf-C2H2	ENSP00000405034;	55888
Homo_sapiens	ZNF285	ENSG00000267508	zf-C2H2	ENSP00000483662;	26974
Homo_sapiens	RCOR2	ENSG00000167771	MYB	ENSP00000301459;	283248
Homo_sapiens	ARGFX	ENSG00000186103	Homeobox	ENSP00000335578;	503582
Homo_sapiens	ZNF30	ENSG00000168661	zf-C2H2	ENSP00000403441;	90075
Homo_sapiens	MNX1	ENSG00000130675	Homeobox	ENSP00000438552;	3110
Homo_sapiens	MYF5	ENSG00000111049	bHLH	ENSP00000228644;	4617
Homo_sapiens	ZNF354B	ENSG00000178338	zf-C2H2	ENSP00000327143;	117608
Homo_sapiens	NKX3-1	ENSG00000167034	Homeobox	ENSP00000370253;	4824
Homo_sapiens	KLF3	ENSG00000109787	zf-C2H2	ENSP00000261438;	51274
Homo_sapiens	FOXD4L1	ENSG00000184492	Fork_head	ENSP00000302756;	200350
Homo_sapiens	PITX2	ENSG00000164093	Homeobox	ENSP00000484909;	5308
Homo_sapiens	ZNF772	ENSG00000197128	zf-C2H2	ENSP00000395967;	400720
Homo_sapiens	ZBTB16	ENSG00000109906	ZBTB	ENSP00000376721;	7704
Homo_sapiens	ZNF575	ENSG00000176472	zf-C2H2	ENSP00000472578;	284346
Homo_sapiens	ZNF620	ENSG00000177842	zf-C2H2	ENSP00000322265;	253639
Homo_sapiens	ZNF761	ENSG00000160336	zf-C2H2	ENSP00000481272;	388561
Homo_sapiens	ZNF793	ENSG00000188227	zf-C2H2	ENSP00000487183;	390927
Homo_sapiens	ZNF254	ENSG00000213096	zf-C2H2	ENSP00000349494;	9534
Homo_sapiens	TFAP2B	ENSG00000008196	AP-2	ENSP00000377265;	7021
Homo_sapiens	SNAPC4	ENSG00000165684	MYB	ENSP00000298532;	6621
Homo_sapiens	ZNF675	ENSG00000197372	zf-C2H2	ENSP00000352836;	171392
Homo_sapiens	ZNF860	ENSG00000197385	zf-C2H2	ENSP00000373274;	344787

Homo_sapiens	FOXD3	ENSG00000187140	Fork_head	ENSP00000360157;	27022
Homo_sapiens	ZNF132	ENSG00000131849	zf-C2H2	ENSP00000254166;	7691
Homo_sapiens	NFE2L3	ENSG00000050344	TF_bZIP	ENSP00000056233;	9603
Homo_sapiens	ZNF510	ENSG00000081386	zf-C2H2	ENSP00000223428;	22869
Homo_sapiens	HOXC6	ENSG00000197757	Homeobox	ENSP00000243108;	3223
Homo_sapiens	THRB	ENSG00000151090	THR-like	ENSP00000493709;	7068
Homo_sapiens	ZNF774	ENSG00000196391	zf-C2H2	ENSP00000346348;	342132
Homo_sapiens	ZFP28	ENSG00000196867	zf-C2H2	ENSP00000301318;	140612
Homo_sapiens	NFE2L1	ENSG00000082641	TF_bZIP	ENSP00000464446;	4779
Homo_sapiens	HOXD4	ENSG00000170166	Homeobox	ENSP00000302548;	3233
Homo_sapiens	ZNF681	ENSG00000196172	zf-C2H2	ENSP00000384000;	148213
Homo_sapiens	NFIL3	ENSG00000165030	TF_bZIP	ENSP00000297689;	4783
Homo_sapiens	FOXP3	ENSG00000049768	Fork_head	ENSP00000365380;	50943
Homo_sapiens	CUX2	ENSG00000111249	CUT	ENSP00000261726;	23316
Homo_sapiens	CREB3	ENSG00000107175	TF_bZIP	ENSP00000342136;	10488
Homo_sapiens	ARNT2	ENSG00000172379	bHLH	ENSP00000453792;	9915
Homo_sapiens	MTA3	ENSG00000057935	zf-GATA	ENSP00000385045;	57504
Homo_sapiens	AEBP2	ENSG00000139154	zf-C2H2	ENSP00000354267;	121536
Homo_sapiens	TEAD4	ENSG00000197905	TEA	ENSP00000444528;	7004
Homo_sapiens	ZNF250	ENSG00000196150	zf-C2H2	ENSP00000292579;	58500
Homo_sapiens	FOXD2	ENSG00000186564	Fork_head	ENSP00000335493;	2306
Homo_sapiens	JAZF1	ENSG00000153814	zf-C2H2	ENSP00000283928;	221895
Homo_sapiens	MYRFL	ENSG00000166268	NDT80/PhoG	ENSP00000449598;	196446
Homo_sapiens	THAP1	ENSG00000131931	THAP	ENSP00000254250;	55145
Homo_sapiens	ZNF578	ENSG00000258405	zf-C2H2	ENSP00000459216;	147660
Homo_sapiens	ZNF461	ENSG00000197808	zf-C2H2	ENSP00000479057;	92283
Homo_sapiens	IKZF3	ENSG00000161405	zf-C2H2	ENSP00000420463;	22806
Homo_sapiens	FOXJ2	ENSG00000065970	Fork_head	ENSP00000403411;	55810
Homo_sapiens	AC187653.1	ENSG00000248767	Fork_head	ENSP00000492766;	100288524
Homo_sapiens	ZNF788	ENSG00000214189	zf-C2H2	ENSP00000380866;	-
Homo_sapiens	ZNF708	ENSG00000182141	zf-C2H2	ENSP00000469961;	7562
Homo_sapiens	TERB1	ENSG00000249961	MYB	ENSP00000462883;	283847
Homo_sapiens	ZFP92	ENSG00000189420	zf-C2H2	ENSP00000462054;	139735
Homo_sapiens	IRF8	ENSG00000140968	IRF	ENSP00000455784;	3394
Homo_sapiens	ZNF705D	ENSG00000215343	zf-C2H2	ENSP00000445477;	728957
Homo_sapiens	MXD3	ENSG00000213347	bHLH	ENSP00000425029;	83463
Homo_sapiens	ZNF506	ENSG00000081665	zf-C2H2	ENSP00000440625;	440515
Homo_sapiens	RHOXF2	ENSG00000131721	Homeobox	ENSP00000360441;	84528
Homo_sapiens	NHLH2	ENSG00000177551	bHLH	ENSP00000322087;	4808
Homo_sapiens	STAT5B	ENSG00000173757	STAT	ENSP00000293328;	6777
Homo_sapiens	ZNF490	ENSG00000188033	zf-C2H2	ENSP00000311521;	57474
Homo_sapiens	ZNF516	ENSG00000101493	zf-C2H2	ENSP00000478712;	9658
Homo_sapiens	NFKB2	ENSG00000077150	RHD	ENSP00000410256;	4791
Homo_sapiens	ZNF99	ENSG00000213973	zf-C2H2	ENSP00000380293;	7652
Homo_sapiens	ESR1	ENSG00000091831	ESR-like	ENSP00000384064;	2099
Homo_sapiens	DMRTA2	ENSG00000142700	DM	ENSP00000383909;	63950
Homo_sapiens	INSM1	ENSG00000173404	zf-C2H2	ENSP00000312631;	3642
Homo_sapiens	SOX5	ENSG00000134532	HMG	ENSP00000439832;	6660
Homo_sapiens	TBX18	ENSG00000112837	T-box	ENSP00000358677;	9096
Homo_sapiens	HNF4G	ENSG00000164749	RXR-like	ENSP00000346339;	3174
Homo_sapiens	ATF1	ENSG00000123268	TF_bZIP	ENSP00000262053;	466
Homo_sapiens	SCRT2	ENSG00000215397	zf-C2H2	ENSP00000246104;	85508
Homo_sapiens	NKX1-2	ENSG00000229544	Homeobox	ENSP00000451945;	390010
Homo_sapiens	ZNF384	ENSG00000126746	zf-C2H2	ENSP00000473311;	171017
Homo_sapiens	PLAGL2	ENSG00000126003	zf-C2H2	ENSP00000246229;	5326
Homo_sapiens	POU4F2	ENSG00000151615	Pou	ENSP00000281321;	5458
Homo_sapiens	NANOG	ENSG00000111704	Homeobox	ENSP00000435288;	79923
Homo_sapiens	ZNF81	ENSG00000197779	zf-C2H2	ENSP00000341151;	347344

Homo_sapiens	ZNF497	ENSG00000174586	zf-C2H2	ENSP00000311183;	162968
Homo_sapiens	NR0B2	ENSG00000131910	Miscellaneous	ENSP00000254227;	8431
Homo_sapiens	AC010487.3	ENSG00000283088	zf-C2H2	ENSP00000489045;	-
Homo_sapiens	AC004080.3	ENSG00000257184	Homeobox	ENSP00000421799;	-
Homo_sapiens	ZNF135	ENSG00000176293	zf-C2H2	ENSP00000321406;	7694
Homo_sapiens	RELB	ENSG00000104856	RHD	ENSP00000423287;	5971
Homo_sapiens	GTF2IRD1	ENSG00000006704	GTF2I	ENSP00000265755;	9569
Homo_sapiens	CUX1	ENSG00000257923	CUT	ENSP00000451558;	1523
Homo_sapiens	ZNF207	ENSG00000010244	Others	-	7756
Homo_sapiens	LTF	ENSG00000012223	Others	-	4057
Homo_sapiens	PRDM11	ENSG00000019485	Others	-	56981
Homo_sapiens	BCLAF1	ENSG00000029363	Others	-	9774
Homo_sapiens	TFB1M	ENSG00000029639	Others	-	51106
Homo_sapiens	ZNF280C	ENSG00000056277	Others	-	55609
Homo_sapiens	PARP12	ENSG00000059378	Others	-	64761
Homo_sapiens	GPBP1	ENSG00000062194	Others	-	65056
Homo_sapiens	RFXANK	ENSG00000064490	Others	-	8625
Homo_sapiens	MLLT10	ENSG00000078403	Others	-	8028
Homo_sapiens	KHSRP	ENSG00000088247	Others	-	8570
Homo_sapiens	HIF1A	ENSG00000100644	Others	-	3091
Homo_sapiens	ADNP2	ENSG00000101544	Others	-	22850
Homo_sapiens	CENPT	ENSG00000102901	Others	-	80152
Homo_sapiens	CAPN15	ENSG00000103326	Others	-	6650
Homo_sapiens	GABPB1	ENSG00000104064	Others	-	2553
Homo_sapiens	MYEF2	ENSG00000104177	Others	-	50804
Homo_sapiens	TAX1BP1	ENSG00000106052	Others	-	8887
Homo_sapiens	AKNA	ENSG00000106948	Others	-	80709
Homo_sapiens	CREBL2	ENSG00000111269	Others	-	1389
Homo_sapiens	CENPA	ENSG00000115163	Others	-	1058
Homo_sapiens	CEBPZ	ENSG00000115816	Others	-	10153
Homo_sapiens	PLEK	ENSG00000115956	Others	-	5341
Homo_sapiens	EPAS1	ENSG00000116016	Others	-	2034
Homo_sapiens	SFPQ	ENSG00000116560	Others	-	6421
Homo_sapiens	GON4L	ENSG00000116580	Others	-	54856
Homo_sapiens	PHTF1	ENSG00000116793	Others	-	10745
Homo_sapiens	BLZF1	ENSG00000117475	Others	-	8548
Homo_sapiens	ZNF706	ENSG00000120963	Others	-	51123
Homo_sapiens	KIAA1549	ENSG00000122778	Others	-	57670
Homo_sapiens	ZNFX1	ENSG00000124201	Others	-	57169
Homo_sapiens	SLC2A4RG	ENSG00000125520	Others	-	56731
Homo_sapiens	RBCK1	ENSG00000125826	Others	-	10616
Homo_sapiens	YEATS4	ENSG00000127337	Others	-	8089
Homo_sapiens	CASZ1	ENSG00000130940	Others	-	54897
Homo_sapiens	CC2D1A	ENSG00000132024	Others	-	54862
Homo_sapiens	ZNF414	ENSG00000133250	Others	-	84330
Homo_sapiens	XPA	ENSG00000136936	Others	-	7507
Homo_sapiens	TCF19	ENSG00000137310	Others	-	6941
Homo_sapiens	ZNF280D	ENSG00000137871	Others	-	54816
Homo_sapiens	PREB	ENSG00000138073	Others	-	10113
Homo_sapiens	SMARCAL1	ENSG00000138375	Others	-	50485
Homo_sapiens	CARF	ENSG00000138380	Others	-	79800
Homo_sapiens	TCF25	ENSG00000141002	Others	-	22980
Homo_sapiens	ZNF750	ENSG00000141579	Others	-	79755
Homo_sapiens	GABPB2	ENSG00000143458	Others	-	126626
Homo_sapiens	TMF1	ENSG00000144747	Others	-	7110
Homo_sapiens	LYAR	ENSG00000145220	Others	-	55646
Homo_sapiens	PURB	ENSG00000146676	Others	-	5814
Homo_sapiens	CIZ1	ENSG00000148337	Others	-	25792

Homo_sapiens	ANKRD30A	ENSG00000148513	Others	-	91074
Homo_sapiens	THYN1	ENSG00000151500	Others	-	29087
Homo_sapiens	SETBP1	ENSG00000152217	Others	-	26040
Homo_sapiens	AHCTF1	ENSG00000153207	Others	-	25909
Homo_sapiens	ELMSAN1	ENSG00000156030	Others	-	91748
Homo_sapiens	GATAD1	ENSG00000157259	Others	-	57798
Homo_sapiens	SON	ENSG00000159140	Others	-	6651
Homo_sapiens	GPBP1L1	ENSG00000159592	Others	-	60313
Homo_sapiens	ZNF326	ENSG00000162664	Others	-	284695
Homo_sapiens	SPZ1	ENSG00000164299	Others	-	84654
Homo_sapiens	FAM170A	ENSG00000164334	Others	-	340069
Homo_sapiens	CREBRF	ENSG00000164463	Others	-	153222
Homo_sapiens	ZNF704	ENSG00000164684	Others	-	619279
Homo_sapiens	ZNF503	ENSG00000165655	Others	-	84858
Homo_sapiens	RAG1	ENSG00000166349	Others	-	5896
Homo_sapiens	PHB	ENSG00000167085	Others	-	5245
Homo_sapiens	TET2	ENSG00000168769	Others	-	54790
Homo_sapiens	ZNF608	ENSG00000168916	Others	-	57507
Homo_sapiens	ZNF280A	ENSG00000169548	Others	-	129025
Homo_sapiens	CENPX	ENSG00000169689	Others	-	201254
Homo_sapiens	CNBP	ENSG00000169714	Others	-	7555
Homo_sapiens	NFRKB	ENSG00000170322	Others	-	4798
Homo_sapiens	ZNF318	ENSG00000171467	Others	-	24149
Homo_sapiens	PURG	ENSG00000172733	Others	-	29942
Homo_sapiens	CENPS	ENSG00000175279	Others	-	378708
Homo_sapiens	MAF1	ENSG00000179632	Others	-	84232
Homo_sapiens	ZNF609	ENSG00000180357	Others	-	23060
Homo_sapiens	DMRTC1B	ENSG00000184911	Others	-	728656
Homo_sapiens	PURA	ENSG00000185129	Others	-	5813
Homo_sapiens	NKRF	ENSG00000186416	Others	-	55922
Homo_sapiens	ZNF395	ENSG00000186918	Others	-	55893
Homo_sapiens	PLSCR1	ENSG00000188313	Others	-	5359
Homo_sapiens	ZGPAT	ENSG00000197114	Others	-	84619
Homo_sapiens	ZNF720	ENSG00000197302	Others	-	107983990
Homo_sapiens	ZNF511	ENSG00000198546	Others	-	118472
Homo_sapiens	L3MBTL3	ENSG00000198945	Others	-	84456
Homo_sapiens	CPEB1	ENSG00000214575	Others	-	64506
Homo_sapiens	ZNF487	ENSG00000243660	Others	-	642819
Homo_sapiens	NME2	ENSG00000243678	Others	-	4831
Homo_sapiens	ZNF488	ENSG00000265763	Others	-	118738
Homo_sapiens	DMRTC1	ENSG00000269502	Others	-	63947
Homo_sapiens	ZNF280B	ENSG00000275004	Others	-	140883

Supplementary Table S2

	logFC	AveExpr	t	P.Value	adj.P.Val	B
UBE2C	3.41201759	5.69188515	13.1558921	2.09E-33	1.04E-30	65.0950591
KRT7	2.99528215	7.77560607	4.62730069	4.93E-06	6.61E-05	3.12567825
MYBL2	2.98696919	4.7399194	9.79880447	1.41E-20	1.70E-18	35.8790683
CDC20	2.90691209	4.98535065	10.7978791	3.47E-24	6.28E-22	44.0853203
MMP11	2.87817019	3.53364566	6.10194629	2.36E-09	6.05E-08	10.5090196
TK1	2.83528457	5.40374817	11.8790387	2.65E-28	7.46E-26	53.4632032
KRT14	2.82330608	4.00942061	3.31270123	0.00100291	0.00744715	-1.8904316
TPX2	2.78243086	4.64698273	10.5052365	4.16E-23	6.56E-21	41.6326979
SPP1	2.77415327	4.683812	5.54872524	5.07E-08	1.01E-06	7.53232612
TOP2A	2.60362192	4.46344767	10.0003031	2.74E-21	3.62E-19	37.4952084
CTA-384D8.3	2.59271794	3.59122075	4.23199221	2.84E-05	0.00031835	1.45590268
KRT18	2.53765367	7.80134447	7.39945039	7.36E-13	3.24E-11	18.3936627
CST6	2.53684035	3.61715955	5.06915002	5.97E-07	9.76E-06	5.15061659
BIRC5	2.41413664	3.94495541	10.1326329	9.26E-22	1.31E-19	38.5676133
CST1	2.39745323	2.48820586	4.53989961	7.34E-06	9.45E-05	2.74482932
ZWINT	2.38578128	4.21119272	11.097946	2.62E-25	5.41E-23	46.6396248
AURKB	2.38156219	3.74042219	10.3293248	1.81E-22	2.71E-20	40.177389
CDK1	2.3808824	3.73424012	11.7185635	1.11E-27	2.89E-25	52.0417095
CCNB1	2.30963398	4.57278224	10.0582046	1.71E-21	2.31E-19	37.9633797
ASF1B	2.30527388	3.89071965	10.992479	6.53E-25	1.31E-22	45.7374004
SERINC2	2.30324382	6.72402727	6.54334255	1.73E-10	5.39E-09	13.0533079
KLHDC7B	2.27314281	3.34597977	4.07088421	5.58E-05	0.00058625	0.81462697
KIF2C	2.27087414	3.55176954	10.597372	1.91E-23	3.14E-21	42.4006788
CDCA8	2.26464366	3.56337012	10.5027292	4.25E-23	6.68E-21	41.6118531
NUSAP1	2.25172744	4.00001124	9.66955673	3.99E-20	4.53E-18	34.853336
ISG15	2.22431253	6.86239597	6.34699854	5.63E-10	1.58E-08	11.9034099
PRSS8	2.22427748	4.31630934	5.9673207	5.08E-09	1.23E-07	9.76256505
SPINT1	2.17960335	6.39139929	7.63739071	1.48E-13	7.22E-12	19.9684247
EPCAM	2.17727153	5.35004048	6.08046491	2.67E-09	6.78E-08	10.388974
RRM2	2.17022243	3.93334992	8.44489009	4.85E-16	3.35E-14	25.5875399
SFN	2.15805738	8.39886302	5.00617118	8.15E-07	1.30E-05	4.85193701
FOXM1	2.15701092	3.39883057	8.55717199	2.12E-16	1.56E-14	26.4010892
CCNB2	2.15426701	3.73599765	9.862037	8.46E-21	1.05E-18	36.3840189
S100A14	2.14455983	6.32715958	3.73715183	0.00021151	0.00191944	-0.44021046
TROAP	2.1327216	2.85833564	10.54932	2.87E-23	4.66E-21	41.9996611
KRT19	2.12948103	9.58676784	4.36695568	1.58E-05	0.0001888	2.01069627
HIST1H1C	2.12658207	6.16201933	6.33677257	5.98E-10	1.67E-08	11.8443118
PYCR1	2.12563648	3.82934531	6.67329301	7.81E-11	2.56E-09	13.8300827
CDT1	2.12522507	3.31397669	10.0198333	2.34E-21	3.12E-19	37.6529371
KIF20A	2.12020545	3.1928401	9.81370304	1.25E-20	1.52E-18	35.9978588
AURKA	2.11408281	3.39357519	10.1173373	1.05E-21	1.47E-19	38.4432163
KIFC1	2.11352645	3.68551018	9.42122581	2.87E-19	2.96E-17	32.9071051
MELK	2.09260053	3.09147729	8.59225683	1.63E-16	1.22E-14	26.6568545
HIST1H2BD	2.09082011	4.13344145	7.34996317	1.02E-12	4.41E-11	18.070954
PAFAH1B3	2.08690356	5.42538381	9.68901913	3.42E-20	3.93E-18	35.0072398
APOC1	2.08316513	4.36178864	6.1326947	1.98E-09	5.11E-08	10.68147
CA9	2.07335664	2.75317949	4.19382711	3.34E-05	0.0003689	1.30191817
HIST3H2A	2.06457129	4.02809672	7.8327977	3.84E-14	2.04E-12	21.2898638
RECQL4	2.0573617	3.3910884	10.2516012	3.46E-22	5.07E-20	39.5390523
CKS2	2.045763	5.91629931	9.68563095	3.51E-20	4.01E-18	34.9804327
TMEM132A	2.04255287	3.39448731	9.28675554	8.25E-19	8.01E-17	31.8670222
UBE2T	2.03949576	4.28411362	10.5267647	3.47E-23	5.54E-21	41.811792
PLK1	2.03867454	3.28639667	8.94265086	1.17E-17	9.78E-16	29.251018
CEP55	2.02949613	3.26927572	9.21060471	1.49E-18	1.39E-16	31.2824048
MKI67	2.02582861	3.18431458	9.22851647	1.30E-18	1.22E-16	31.4196277
CDCA5	2.02385925	3.26088908	8.9170647	1.42E-17	1.18E-15	29.0591744
HMGB3	2.00558731	4.52578864	10.5418133	3.06E-23	4.94E-21	41.9371098

C4orf48	2.005197	3.33754435	7.21232127	2.54E-12	1.03E-10	17.1822261
CCNA2	1.99954465	3.5273234	9.08207796	4.03E-18	3.49E-16	30.3029877
IQGAP3	1.99179777	2.67272213	9.54658033	1.06E-19	1.16E-17	33.8854554
LSR	1.98404166	6.45499072	7.20572545	2.65E-12	1.07E-10	17.1399668
PTTG1	1.9828727	4.17919299	8.5427951	2.36E-16	1.72E-14	26.296496
KIF18B	1.97502167	2.52160182	9.95908861	3.84E-21	4.98E-19	37.1629793
SAPCD2	1.94937662	2.85269191	8.0675537	7.38E-15	4.41E-13	22.9102117
CDH3	1.9368922	3.84567192	4.48355359	9.45E-06	0.00011867	2.50279583
SNORD104	1.93070685	4.46366753	6.97706793	1.16E-11	4.30E-10	15.6937823
NUF2	1.9306937	2.69914794	8.76092209	4.64E-17	3.63E-15	27.8966147
TACSTD2	1.92946247	8.11063097	4.87603991	1.53E-06	2.30E-05	4.24531481
ETV4	1.92859548	3.01040846	6.55809805	1.58E-10	4.96E-09	13.1408826
TACC3	1.92733815	3.80973568	9.46359689	2.06E-19	2.17E-17	33.2368573
HN1	1.92305579	5.93808036	10.6949728	8.35E-24	1.45E-21	43.2184477
NEK2	1.91845068	2.72794147	9.3336896	5.71E-19	5.66E-17	32.2289245
SPAG5	1.90415472	3.18324464	9.70537924	2.99E-20	3.48E-18	35.1367639
RAC3	1.89853858	2.98851185	7.54481038	2.77E-13	1.29E-11	19.3511767
SDC1	1.89390571	8.14095091	5.13275	4.35E-07	7.29E-06	5.45559536
HJURP	1.89074704	2.66231666	10.0936576	1.28E-21	1.77E-19	38.2508589
ST14	1.8896653	5.94149269	6.95231167	1.36E-11	4.98E-10	15.5394203
CDC45	1.88791547	2.88258688	9.32473656	6.13E-19	6.06E-17	32.1597959
LAMC2	1.88596128	4.06600146	3.98723559	7.87E-05	0.0007973	0.4907473
STMN1	1.88349492	5.32496986	7.89791313	2.44E-14	1.34E-12	21.7357523
KIF4A	1.88009359	2.765584	9.1580435	2.24E-18	2.01E-16	30.8807574
CENPA	1.87454026	2.51307973	8.77763645	4.09E-17	3.23E-15	28.0203844
ESM1	1.87417861	2.05435366	6.72121385	5.81E-11	1.93E-09	14.1196511
KRT16	1.87382735	4.58879711	2.6143939	0.00925578	0.04814837	-3.91290693
AP1M2	1.86949612	5.2515032	6.42369191	3.56E-10	1.04E-08	12.3491421
E2F1	1.85959409	3.54443081	7.34399534	1.06E-12	4.57E-11	18.0321506
CASP14	1.85897303	2.21544267	3.1403308	0.00180525	0.01228042	-2.4320597
CDKN2A	1.8464782	2.50419111	3.67808119	0.00026511	0.00234457	-0.65187669
MMP1	1.8447656	3.72922231	3.29401181	0.00107023	0.00787297	-1.95048823
NCAPH	1.84405071	2.79740559	8.96154129	1.02E-17	8.53E-16	29.392898
GJB2	1.83952836	5.14219576	3.5329967	0.00045586	0.00377051	-1.15830047
VGLL1	1.82762242	4.37864676	3.53004273	0.00046083	0.00380679	-1.16841208
LAD1	1.81687594	6.22003246	5.27409762	2.13E-07	3.79E-06	6.14538471
HIST1H2AE	1.81636601	2.47848491	5.66290719	2.74E-08	5.79E-07	8.12689649
TRIP13	1.81483794	2.98287871	7.7537145	6.65E-14	3.38E-12	20.752041
AGRN	1.80933809	5.37552354	8.87263112	2.00E-17	1.64E-15	28.7269076
COL7A1	1.80820583	3.71752267	4.85851754	1.67E-06	2.48E-05	4.16472169
CDC6	1.80570193	2.89472716	9.46083431	2.10E-19	2.20E-17	33.2153282
KIAA0101	1.8047584	3.01728652	9.22878575	1.30E-18	1.22E-16	31.421692
MCM2	1.80434762	4.03000423	7.95541743	1.63E-14	9.19E-13	22.1318012
CENPF	1.80135448	2.82025226	8.41021114	6.25E-16	4.23E-14	25.3378137
IGFL1	1.79744427	3.07707714	2.74741247	0.00626193	0.03501726	-3.56301138
DLGAP5	1.79367755	2.76039632	8.19425535	2.99E-15	1.87E-13	23.7993209
H2AFX	1.78681303	5.61297606	9.53237446	1.19E-19	1.30E-17	33.7741624
CLIC3	1.78676916	4.01407917	3.55020611	0.00042787	0.00356939	-1.09923298
SCD	1.78636782	5.68022843	5.26921073	2.18E-07	3.88E-06	6.12126156
IFI6	1.7859501	7.26083927	3.91456625	0.00010544	0.00103517	0.21444448
C15orf48	1.78456333	3.67973333	4.04094358	6.32E-05	0.00065414	0.69798418
FAM83H	1.7836104	5.13332032	8.0047249	1.15E-14	6.66E-13	22.4730876
CDH1	1.77810428	5.95014884	5.0366188	7.01E-07	1.13E-05	4.99592252
CCNE1	1.77203	3.15456851	7.35352233	9.99E-13	4.32E-11	18.0941076
KRT17	1.76836343	8.36299855	2.77125288	0.00582893	0.03296528	-3.4985296
UHRF1	1.76825077	2.4710297	9.59211067	7.41E-20	8.20E-18	34.2428728
LMNB1	1.76812022	4.11934182	8.37957653	7.81E-16	5.23E-14	25.1178213
PABPC1L	1.76322093	2.99394909	7.32906789	1.18E-12	5.02E-11	17.9351977

RAB25	1.76258948	6.2043699	4.87515137	1.54E-06	2.31E-05	4.2412218
FXYD3	1.76106793	6.88042788	3.89624398	0.00011344	0.00110462	0.1455256
CENPM	1.75786825	3.09768676	8.95471603	1.07E-17	8.95E-16	29.3416121
HIST1H2BH	1.7552093	2.23099744	5.41203219	1.04E-07	1.96E-06	6.83433052
SNORD99	1.75495501	3.22039247	7.72560784	8.07E-14	4.04E-12	20.5618824
MAL2	1.75484725	5.70067211	4.6876607	3.73E-06	5.13E-05	3.3925262
MARCKSL1	1.75424122	6.93987682	6.71355799	6.09E-11	2.02E-09	14.0732771
MIR4653	1.74628549	2.75661451	6.99612902	1.03E-11	3.83E-10	15.81293
GRB7	1.74092877	4.16202048	5.77128973	1.52E-08	3.36E-07	8.70088158
SPC24	1.74032515	2.8253812	9.11289389	3.18E-18	2.78E-16	30.5369743
PKP3	1.74007399	4.90980427	6.06797504	2.87E-09	7.24E-08	10.3193394
PVRL4	1.73805055	5.39048467	4.51029907	8.38E-06	0.00010665	2.61733834
ANLN	1.73328115	3.2115664	6.83775326	2.80E-11	9.77E-10	14.8308157
RASSF7	1.73197608	4.57622298	7.59396792	1.99E-13	9.47E-12	19.6782054
PRC1	1.72719543	3.28680361	8.25694362	1.90E-15	1.22E-13	24.2429468
COL10A1	1.72685084	1.72432755	4.37041315	1.56E-05	0.00018638	2.02511821
C19orf33	1.72384122	6.75079408	4.1449272	4.10E-05	0.00044483	1.1064992
CTD-2510F5.	1.72307611	2.88144797	6.69255543	6.94E-11	2.29E-09	13.9462772
KPNA2	1.72295558	5.54558526	7.93389532	1.90E-14	1.06E-12	21.9833228
MEX3A	1.71830784	2.44082528	5.73901437	1.81E-08	3.95E-07	8.52897984
GINS1	1.715451	2.74579964	9.19762031	1.65E-18	1.52E-16	31.1830417
HMGA1	1.71238062	6.9974225	7.21565098	2.48E-12	1.01E-10	17.2035709
SOX4	1.70838328	4.9751251	6.73301913	5.40E-11	1.80E-09	14.191243
PLAU	1.70684499	5.32835488	4.51723825	8.13E-06	0.00010375	2.64715778
MDK	1.69697787	6.72464671	5.2566787	2.33E-07	4.11E-06	6.05948933
IER5L	1.6947148	3.25359932	8.19800192	2.91E-15	1.82E-13	23.8257653
PODXL2	1.68874383	3.97047693	4.66950139	4.05E-06	5.54E-05	3.31191683
GGH	1.68835338	3.64747038	6.32043169	6.59E-10	1.83E-08	11.7500378
HILPDA	1.68622962	4.16249659	6.09957913	2.39E-09	6.12E-08	10.4957737
GJB6	1.68323204	4.2092857	3.40507932	0.00072423	0.00562455	-1.58885126
SLC39A4	1.67918779	3.13262496	8.17752222	3.37E-15	2.10E-13	23.6813203
C1QTNF6	1.67717302	2.74681776	6.52212537	1.97E-10	6.07E-09	12.9276653
CXCL10	1.67454649	3.70143421	3.02978812	0.00259643	0.01678824	-2.76486999
KIF11	1.67439903	3.04650143	8.5001988	3.23E-16	2.30E-14	25.9873335
PRR11	1.66981997	2.7080168	7.99766563	1.21E-14	6.96E-13	22.4241307
SKA3	1.66364123	2.39393104	9.6882481	3.44E-20	3.95E-18	35.001139
BUB1B	1.66310888	2.48393428	8.76046227	4.66E-17	3.63E-15	27.8932121
GTSE1	1.6616768	2.30521071	9.34905406	5.06E-19	5.04E-17	32.3476589
CD24	1.66056337	6.75697305	4.06552146	5.71E-05	0.00059766	0.79367619
FER1L4	1.65862991	3.61191303	3.40954425	0.00071279	0.00555788	-1.57407585
NDC80	1.65794048	2.74888279	7.92681777	1.99E-14	1.11E-12	21.9345607
TYMS	1.65565162	3.96284547	6.78928145	3.80E-11	1.30E-09	14.53383
FEN1	1.64702981	4.44487123	7.89334655	2.52E-14	1.38E-12	21.7043923
SQLE	1.64576628	4.10349767	7.23476461	2.19E-12	9.03E-11	17.3262461
ESRP1	1.63914569	4.70936791	5.89223779	7.75E-09	1.80E-07	9.35236671
PKMYT1	1.63803925	2.39588726	8.57482756	1.86E-16	1.38E-14	26.5297047
TTK	1.63727086	2.26844463	8.90639489	1.55E-17	1.28E-15	28.9792837
CDCA3	1.63632424	2.34067549	9.28443161	8.40E-19	8.13E-17	31.849134
SKA1	1.63305751	2.3351431	8.82076587	2.96E-17	2.38E-15	28.3405101
GATA3	1.63247475	5.40780509	3.31840399	0.00098317	0.00731728	-1.87204209
EIF4EBP1	1.62440814	5.77869568	7.09792097	5.34E-12	2.07E-10	16.4535636
DHCR24	1.62437442	5.65028288	4.77933122	2.43E-06	3.48E-05	3.80375001
RNASEH2A	1.62230208	4.36256456	9.75214011	2.06E-20	2.43E-18	35.5077371
YDJC	1.61561173	4.25993009	9.48169076	1.78E-19	1.89E-17	33.3779659
HIST1H2BK	1.61501001	5.50615822	5.00339204	8.26E-07	1.31E-05	4.83883315
NCAPG	1.61408739	2.36915118	8.42519314	5.60E-16	3.81E-14	25.4456106
BUB1	1.61293623	2.64520794	8.50828204	3.04E-16	2.18E-14	26.0459173
SLC52A2	1.61103822	5.09899024	11.3038335	4.36E-26	9.67E-24	48.414419

PBK	1.60866929	2.67478278	7.3483521	1.03E-12	4.46E-11	18.0604763
NME1	1.60583981	4.57252755	10.9206456	1.21E-24	2.35E-22	45.1256355
SNORD14E	1.60511187	2.35996309	5.27891745	2.08E-07	3.71E-06	6.16919603
PPP1R14BP3	1.6050794	5.52590015	9.1312684	2.76E-18	2.43E-16	30.6767461
HMMR	1.6035817	2.39701261	8.01165288	1.10E-14	6.36E-13	22.5211648
CBLC	1.60207647	4.88851776	4.59843736	5.62E-06	7.44E-05	2.99917977
CENPU	1.59543512	3.04802622	7.98449137	1.33E-14	7.58E-13	22.3328509
FAM64A	1.59527891	2.24648285	7.19810831	2.78E-12	1.12E-10	17.0912016
RHPN1	1.59510935	2.917166	5.3285495	1.61E-07	2.93E-06	6.41550011
GRIN2D	1.59419738	1.91632838	5.0179279	7.69E-07	1.23E-05	4.90744218
PSORS1C2	1.58909685	2.03285002	3.04645824	0.00245962	0.01603863	-2.71541178
ULBP2	1.58585418	2.23416671	6.07309648	2.78E-09	7.04E-08	10.3478784
SLC5A6	1.58123409	3.66680319	8.20883574	2.69E-15	1.70E-13	23.9022832
IGSF9	1.57973398	2.78175943	5.5928917	4.00E-08	8.15E-07	7.76107239
UBE2S	1.57624657	4.08760374	7.82824054	3.97E-14	2.10E-12	21.2587609
MEST	1.57262312	3.17138807	4.54545234	7.15E-06	9.25E-05	2.7688295
TLCD1	1.57126577	3.83349475	6.63178727	1.01E-10	3.26E-09	13.5806347
RCC1	1.57069546	4.51769721	10.7089494	7.42E-24	1.30E-21	43.3359072
CKS1B	1.56633258	3.90561701	8.02151622	1.02E-14	5.98E-13	22.5896651
C19orf48	1.56361077	4.67474058	9.41586487	3.00E-19	3.07E-17	32.8654525
KIF23	1.56255574	2.45992331	8.46511938	4.18E-16	2.92E-14	25.7335504
PCNA	1.55898425	6.6358789	8.00792689	1.13E-14	6.52E-13	22.4953042
PPP1R14B	1.55577377	6.22784037	10.0644905	1.62E-21	2.21E-19	38.0143054
GINS2	1.55455591	2.79926634	8.2904751	1.49E-15	9.65E-14	24.4812415
U47924.27	1.55454565	3.97099427	4.65918549	4.25E-06	5.79E-05	3.26625015
CDKN3	1.55325842	2.83858268	7.11307934	4.84E-12	1.89E-10	16.5495878
FAM83H-AS	1.5511262	3.89145736	5.47081907	7.66E-08	1.48E-06	7.13266248
EVPL	1.54340614	4.82171849	4.45180775	1.09E-05	0.00013482	2.3676427
FBXL6	1.54300839	3.42769687	10.3443009	1.60E-22	2.40E-20	40.3007181
TTYH3	1.54185612	4.43511096	9.05219623	5.07E-18	4.34E-16	30.0766046
ECT2	1.53887439	3.04050054	7.26523956	1.79E-12	7.53E-11	17.5223635
POC1A	1.5374829	3.09451337	8.45113446	4.63E-16	3.21E-14	25.6325839
KDF1	1.53650925	3.93308916	6.83231122	2.90E-11	1.01E-09	14.797388
MIR4477B	1.53523677	3.02763988	5.82860596	1.11E-08	2.51E-07	9.00818073
SKP2	1.5349609	3.51757671	7.73436601	7.60E-14	3.84E-12	20.6210811
PSMG3	1.53481695	4.73187822	10.7783159	4.11E-24	7.36E-22	43.9201579
PAQR4	1.53303974	2.51671529	7.46974329	4.60E-13	2.08E-11	18.8549117
EFNA4	1.53062967	3.91458715	8.78653528	3.83E-17	3.03E-15	28.0863467
KRT8	1.52715276	7.9509705	3.97097158	8.40E-05	0.00084548	0.42849851
RAD51	1.52580816	2.45567386	9.37206747	4.23E-19	4.23E-17	32.5257433
FAM110A	1.52421127	4.02992696	9.03211145	5.92E-18	5.05E-16	29.9247262
DHCR7	1.52373393	4.11466963	7.68752079	1.05E-13	5.20E-12	20.3050304
C16orf59	1.52172547	2.0437409	9.39296706	3.59E-19	3.64E-17	32.6877191
MCM4	1.52126455	4.38330609	7.78204539	5.46E-14	2.83E-12	20.9442415
MFSD3	1.52073224	3.77910467	8.23186247	2.28E-15	1.45E-13	24.0651613
MAGEA3	1.51975122	1.87630064	2.90597703	0.0038522	0.02338514	-3.12405695
EZH2	1.51697349	2.77206348	8.02951266	9.67E-15	5.68E-13	22.6452454
HIST1H2BJ	1.5140573	2.07437969	5.27283199	2.14E-07	3.81E-06	6.13913527
SPC25	1.51298883	2.35353536	8.09651874	6.01E-15	3.63E-13	23.1125769
TMC6	1.51006085	3.66187549	8.44143191	4.97E-16	3.42E-14	25.5626044
PDIA4	1.50877151	6.55288052	9.24346135	1.16E-18	1.10E-16	31.5342567
EFNA1	1.50697663	5.08771461	5.79395955	1.34E-08	2.99E-07	8.82211547
SYNE4	1.50005585	2.41113795	5.10927575	4.89E-07	8.13E-06	5.34263872
S100A11	1.49939878	10.6769907	6.50352848	2.20E-10	6.72E-09	12.8178136
HIST1H2BG	1.4980427	1.9287166	4.88248065	1.48E-06	2.24E-05	4.27500379
RAD54L	1.48906766	2.10023763	8.48990675	3.48E-16	2.45E-14	25.9127982
KIFC2	1.48538474	3.20656182	5.69529554	2.30E-08	4.91E-07	8.29744541
HIST1H3D	1.48269777	1.87960738	5.72261496	1.98E-08	4.29E-07	8.44195103

TYMP	1.48186373	4.75863427	3.76575496	0.0001894	0.0017426	-0.33658319
RAD51AP1	1.4781889	2.43197009	7.31312918	1.31E-12	5.55E-11	17.8318454
MAGEA6	1.47808323	1.71094866	3.00150055	0.00284466	0.01811835	-2.848201
TSTD1	1.47781129	5.27463366	5.3741246	1.27E-07	2.36E-06	6.64344517
ADAM8	1.47405265	3.53070975	5.24210153	2.51E-07	4.40E-06	5.98779869
RHOV	1.47360752	4.95626737	3.92836759	9.98E-05	0.00098497	0.26655653
LRRC45	1.47329309	3.58062865	9.26342443	9.89E-19	9.50E-17	31.6875678
OCIAD2	1.47113311	4.84987122	8.02373487	1.01E-14	5.90E-13	22.605082
SPAG4	1.47075403	3.04018065	5.48733768	7.02E-08	1.37E-06	7.21699488
NXPH4	1.46471553	1.66820991	4.52821185	7.73E-06	9.91E-05	2.69439913
TINAGL1	1.46332462	5.73895878	4.23664636	2.78E-05	0.00031299	1.47476848
JUP	1.45634376	7.33286888	5.55773523	4.83E-08	9.71E-07	7.57886335
FAM111B	1.44977125	2.1400243	6.5440142	1.72E-10	5.37E-09	13.0572907
ORC6	1.44965762	2.0787163	8.68900613	7.95E-17	6.09E-15	27.3659468
CHMP4C	1.44887946	3.77917396	6.24030145	1.06E-09	2.86E-08	11.2906714
CKAP2L	1.44873336	1.94907582	7.71165169	8.88E-14	4.44E-12	20.4676537
HIST1H3H	1.44528857	2.07383126	4.75968574	2.66E-06	3.79E-05	3.71501984
RCC2	1.4452635	5.96843372	11.3669666	2.50E-26	5.69E-24	48.9621507
FANCI	1.4447881	2.85552571	9.14330101	2.51E-18	2.24E-16	30.7683783
RMI2	1.44240203	3.20319226	6.70624097	6.37E-11	2.11E-09	14.0289955
SHMT2	1.44128454	4.77609471	9.67873623	3.71E-20	4.23E-18	34.9259006
HIST1H4I	1.44028524	2.98476485	5.63071384	3.26E-08	6.76E-07	7.95820287
FSCN1	1.43713517	5.80104167	4.25484647	2.57E-05	0.00029185	1.54872618
PLA2G2F	1.43625586	2.68922426	2.87832877	0.00419934	0.02510268	-3.2023013
PSPHP1	1.435937	1.85174189	2.66152833	0.00807311	0.04296526	-3.79084345
SAC3D1	1.43576258	3.31027027	8.12792199	4.80E-15	2.92E-13	23.3325758
TNNT1	1.4347333	1.63793747	3.97132416	8.39E-05	0.00084457	0.42984548
UBALD2	1.4346103	5.9425674	8.17126728	3.52E-15	2.18E-13	23.6372561
STAP2	1.43317167	4.64606548	5.72076121	2.00E-08	4.33E-07	8.43212691
CLDN7	1.4317118	5.5456466	4.50188859	8.71E-06	0.00011032	2.58125217
IFI27	1.4311838	5.178232	2.9058479	0.00385376	0.02339217	-3.12442406
MAPK13	1.42874173	4.08119557	7.40257981	7.21E-13	3.18E-11	18.414126
CENPW	1.42829668	4.3505957	5.96062163	5.28E-09	1.27E-07	9.72578768
CDCA4	1.42120367	3.70669276	7.90257117	2.36E-14	1.30E-12	21.7677542
CNKSR1	1.42049254	3.49302133	6.57054416	1.47E-10	4.61E-09	13.2148759
SMIM22	1.41959571	4.20659535	3.4187301	0.00068978	0.00540447	-1.54362027
TIMELESS	1.41951021	3.4203677	8.52435266	2.70E-16	1.96E-14	26.1625073
WDR34	1.41944994	5.07414423	6.5569601	1.59E-10	4.98E-09	13.134123
CHI3L1	1.41850048	2.90207524	2.96320921	0.00321534	0.02007205	-2.95980791
HGH1	1.4169772	4.00038267	10.9183404	1.24E-24	2.38E-22	45.1060403
PCAT6	1.41252328	2.88099584	6.17943867	1.51E-09	3.98E-08	10.9450187
DTL	1.40993954	2.1569477	7.99195365	1.26E-14	7.21E-13	22.3845407
CHTF18	1.40924226	2.61770448	8.78759734	3.80E-17	3.01E-15	28.0942223
MIR25	1.40769446	2.68828351	5.76205282	1.60E-08	3.51E-07	8.65160072
HOXB7	1.40074785	4.07551675	6.17611716	1.54E-09	4.05E-08	10.9262364
MDFI	1.40061969	4.0843067	4.34738253	1.73E-05	0.00020395	1.9292486
FAM83A	1.39702896	3.08881673	2.8086255	0.00520445	0.03002391	-3.39636599
APOBEC3B	1.39005927	2.9158717	4.39725272	1.39E-05	0.00016743	2.13742717
TONSL	1.3886326	2.5933305	9.23721581	1.21E-18	1.15E-16	31.4863376
MFAP2	1.38501824	3.61014402	4.16780193	3.73E-05	0.00040791	1.19765079
EPN3	1.38501483	3.6900074	4.41343817	1.29E-05	0.00015712	2.20545772
RP11-783K1	1.38406223	2.46954771	6.18424471	1.47E-09	3.88E-08	10.9722106
TRIB3	1.38166361	3.11854309	5.42227466	9.88E-08	1.87E-06	6.8861074
LPAR2	1.38118117	3.66437308	7.44695333	5.36E-13	2.40E-11	18.705001
CBX2	1.37869324	1.99759802	5.11905826	4.66E-07	7.77E-06	5.38965595
CYB561	1.37663761	4.52636853	8.98360947	8.58E-18	7.26E-16	29.5589029
FASN	1.37252192	5.27233835	6.08707522	2.57E-09	6.55E-08	10.4258769
SPINT2	1.36924975	6.85836774	5.2391781	2.54E-07	4.45E-06	5.97344229

COMTD1	1.36864879	3.71509216	6.48414017	2.48E-10	7.47E-09	12.7035604
OXLD1	1.36679324	4.23491199	9.07174586	4.37E-18	3.76E-16	30.2246552
RP13-463N1	1.36470201	1.51259691	4.16808745	3.72E-05	0.00040757	1.19879145
HIST1H2BC	1.36462016	2.06226709	4.71140551	3.34E-06	4.65E-05	3.49835502
NMB	1.36049184	3.7934381	5.93048772	6.26E-09	1.48E-07	9.56078701
SNHG1	1.35605931	3.87922741	8.49739566	3.30E-16	2.34E-14	25.9670267
PPP1R14C	1.35519425	1.97891695	3.43742138	0.00064509	0.00509603	-1.48141018
DSP	1.35206133	4.85371384	3.15504207	0.00171864	0.01178463	-2.38690981
MOGS	1.35084157	5.02074525	11.7354158	9.58E-28	2.52E-25	52.1905278
BCL2L12	1.35009153	3.70294896	8.81822711	3.01E-17	2.42E-15	28.3216363
MAD2L1	1.34900956	2.42071439	7.24682627	2.02E-12	8.38E-11	17.4037904
TMEM238	1.34892932	2.79420908	5.5670059	4.60E-08	9.28E-07	7.62681509
ITGB6	1.34880246	4.00124817	3.78012488	0.00017913	0.00165622	-0.28424302
LIG1	1.3468843	3.3513747	9.86444758	8.30E-21	1.03E-18	36.4033091
FCRLB	1.34408869	2.07385244	3.77744117	0.00018101	0.00167198	-0.29403218
CDCP1	1.34256128	3.57057951	5.22236937	2.77E-07	4.81E-06	5.89103438
OIP5	1.34144728	2.03258408	7.7317757	7.73E-14	3.90E-12	20.6035673
F11R	1.34141987	5.65022472	5.94101001	5.90E-09	1.41E-07	9.61832225
SLC50A1	1.34112479	5.00287224	7.69281141	1.01E-13	5.03E-12	20.3406522
EBP	1.34077417	4.80260298	8.34188344	1.03E-15	6.76E-14	24.8479293
SDF2L1	1.33745713	4.68387009	7.45055017	5.23E-13	2.35E-11	18.7286374
S1PR5	1.336646	2.28028834	4.65149866	4.41E-06	5.98E-05	3.23228117
MMP9	1.33648932	3.06545303	2.7972782	0.00538732	0.03089573	-3.42752495
DEPDC1B	1.33644235	1.88278738	7.81750705	4.27E-14	2.25E-12	21.1855578
VAMP8	1.33570557	7.28653551	7.0849862	5.80E-12	2.24E-10	16.371753
MMP13	1.33216409	1.93722626	2.94080651	0.00345218	0.02129108	-3.0244671
COL11A1	1.33166812	1.38538059	3.85014402	0.00013618	0.00129946	-0.02654639
KIF22	1.3316136	4.34068441	7.99696081	1.22E-14	6.99E-13	22.4192445
ORC1	1.33144967	1.9938178	7.57487562	2.26E-13	1.07E-11	19.5509986
B3GNT3	1.33063667	4.51550471	3.46373043	0.00058675	0.00469293	-1.3933025
DUS1L	1.32921947	4.67185912	9.50950599	1.43E-19	1.54E-17	33.5952293
PLEK2	1.32807319	3.9284953	4.26532569	2.46E-05	0.00028	1.5914414
PALM3	1.32641798	2.52161956	3.0213915	0.00266795	0.01717652	-2.78968334
MIR647	1.32607725	2.70536847	5.56745129	4.59E-08	9.26E-07	7.62912059
RACGAP1	1.32251643	3.40060182	6.61701043	1.10E-10	3.55E-09	13.4921313
NFE2L3	1.32228149	3.03852503	5.33474191	1.56E-07	2.85E-06	6.44637206
HIST2H2BE	1.32093006	3.62225443	4.55793258	6.76E-06	8.79E-05	2.82286905
SLC29A2	1.32030377	2.54631852	5.82129565	1.15E-08	2.60E-07	8.96884275
SERPINA1	1.3197249	2.66577739	3.08129602	0.00219483	0.01453935	-2.61121402
STRA13	1.31942353	5.16757894	8.42039214	5.80E-16	3.95E-14	25.4110521
EXO1	1.31520887	1.85480452	7.80260928	4.74E-14	2.48E-12	21.0840786
RFC4	1.3145919	3.31617086	7.35572909	9.85E-13	4.27E-11	18.1084677
SLC12A8	1.31261363	1.96638545	6.61176653	1.14E-10	3.65E-09	13.4607624
UNC13D	1.3122717	3.23097677	4.39808604	1.38E-05	0.00016685	2.1409242
GRHL2	1.31179948	3.66787213	5.27679866	2.10E-07	3.74E-06	6.15872625
RBBP8NL	1.30907269	2.3245344	4.40324257	1.35E-05	0.00016357	2.16257709
PPP1R13L	1.30795783	4.45087875	5.69772325	2.27E-08	4.85E-07	8.31026276
NUP210	1.30695654	3.16672771	4.35112122	1.70E-05	0.00020094	1.94478017
FZD2	1.30668382	2.37783306	5.63030854	3.27E-08	6.77E-07	7.95608439
PFKFB4	1.30184387	1.94369831	7.19664671	2.81E-12	1.13E-10	17.0818491
BOP1	1.30149463	4.63773992	7.85283102	3.34E-14	1.79E-12	21.4267522
IRF5	1.30102611	3.07823902	5.72246019	1.98E-08	4.29E-07	8.44113069
ABRACL	1.29958953	5.36906626	7.21849247	2.43E-12	9.94E-11	17.2217921
ZDHHC12	1.29835888	4.52947904	7.83949173	3.67E-14	1.96E-12	21.3355753
ALDH3B2	1.29833439	3.65596607	3.22533725	0.00135531	0.00962445	-2.16839244
GGCT	1.29774965	5.43696648	7.58028664	2.18E-13	1.03E-11	19.587026
DSG2	1.29688992	4.57298539	4.54700712	7.10E-06	9.19E-05	2.77555437
POLD1	1.29271478	3.24302881	8.81449264	3.10E-17	2.48E-15	28.2938801

CAPG	1.29204243	6.61581333	5.103498	5.04E-07	8.35E-06	5.31490669
KCNG1	1.29100093	2.15472057	3.34529634	0.00089483	0.00675103	-1.78491864
FABP6	1.29080558	2.60424355	3.10306282	0.00204298	0.01367456	-2.54553581
RP11-927P21	1.29011411	2.58600208	5.06779731	6.01E-07	9.82E-06	5.14416658
FUT3	1.28819236	2.74110537	3.49966373	0.000515	0.00419257	-1.27193854
STXBP2	1.28787673	3.83169492	8.20537922	2.76E-15	1.74E-13	23.8778623
MCM10	1.28655144	1.81214994	7.15431616	3.70E-12	1.47E-10	16.811626
ELMO3	1.28578377	4.0517405	4.62442036	4.99E-06	6.68E-05	3.11302256
AC006262.5	1.28524963	1.47755289	3.47467427	0.00056396	0.00453366	-1.35646518
CXCL11	1.28251563	1.94523806	2.87951589	0.00418387	0.02503418	-3.19895652
ALG3	1.28157284	4.43159261	10.8308859	2.62E-24	4.82E-22	44.3643656
SNRPB	1.2811723	7.69021648	8.94090832	1.19E-17	9.90E-16	29.2379406
MYCL	1.28050386	3.85044388	3.03830467	0.00252569	0.01640531	-2.73963488
FERMT1	1.2802768	3.54206716	4.97395524	9.54E-07	1.50E-05	4.70043385
DTYMK	1.27985742	3.95642271	8.45130675	4.62E-16	3.21E-14	25.6338271
DNMT3B	1.27904547	2.03263065	5.91004638	7.02E-09	1.65E-07	9.44926187
TRAF4	1.27904263	5.07458524	5.96627026	5.11E-09	1.24E-07	9.75679588
ASPM	1.27826994	1.75900865	7.00696809	9.58E-12	3.59E-10	15.880798
TCF19	1.27054261	3.52133377	5.41598313	1.02E-07	1.93E-06	6.8542929
CALR	1.26923946	8.68012274	10.1742014	6.57E-22	9.43E-20	38.9062608
MEN1	1.26815077	3.88713191	11.842088	3.69E-28	1.02E-25	53.1350313
LLGL2	1.26743247	3.76209504	5.1045115	5.01E-07	8.31E-06	5.31976929
CDCA7	1.26533228	2.4300262	5.29845374	1.88E-07	3.38E-06	6.26590605
SLC35A2	1.26517702	4.15744645	8.39027644	7.23E-16	4.86E-14	25.1945941
SHCBP1	1.26270888	2.12311165	7.01174994	9.29E-12	3.49E-10	15.9107657
TMEM160	1.26207389	3.76363303	6.68283852	7.37E-11	2.42E-09	13.8876291
SBK1	1.26197165	1.79524039	3.82202156	0.00015211	0.00143431	-0.13057805
PSAT1	1.26106864	3.780597	4.85888654	1.66E-06	2.48E-05	4.16641618
RP11-329L6.	1.26070154	2.14063362	6.21150243	1.25E-09	3.34E-08	11.1267639
P3H4	1.25830486	3.35673942	6.04714709	3.23E-09	8.08E-08	10.2034854
TBX1	1.25820086	2.2421235	3.22256399	0.00136818	0.00970404	-2.17710021
AUNIP	1.25592275	1.83378963	7.75655559	6.52E-14	3.33E-12	20.7712917
KIF15	1.25551505	1.8651413	7.29956833	1.43E-12	6.04E-11	17.7440495
PSRC1	1.25454373	2.34820394	7.25796104	1.88E-12	7.84E-11	17.4754652
CDC25C	1.25365562	1.70199007	8.30678206	1.33E-15	8.62E-14	24.59738
ARHGAP11A	1.25238159	2.20143142	7.35403302	9.96E-13	4.31E-11	18.0974306
HIST1H2AD	1.25213582	1.38600815	5.08672359	5.47E-07	9.01E-06	5.23455026
SGOL1	1.25187885	1.68667745	7.79950603	4.84E-14	2.54E-12	21.0629584
C17orf53	1.25175581	2.01904916	8.59761907	1.57E-16	1.18E-14	26.6960096
ESRP2	1.25133854	3.91033045	4.47396336	9.87E-06	0.00012342	2.46187474
RP3-523K23.	1.24854605	3.2160762	4.83245741	1.89E-06	2.77E-05	4.04533973
SLC26A6	1.2463748	2.13936105	8.42869232	5.46E-16	3.72E-14	25.4708072
MIS18A	1.24623171	3.6414706	7.91830351	2.12E-14	1.18E-12	21.875943
CKAP2	1.24506507	3.20754333	7.04960603	7.29E-12	2.77E-10	16.1485793
MTFR2	1.24474278	1.8169714	8.48189293	3.69E-16	2.60E-14	25.8548063
MTHFD1L	1.24460287	2.90685801	7.11890656	4.66E-12	1.82E-10	16.5865445
DDX39A	1.2427325	4.69313374	9.28674969	8.25E-19	8.01E-17	31.8669771
KNSTRN	1.24218896	2.70030097	7.97860248	1.38E-14	7.88E-13	22.2920848
CDC25A	1.24015963	2.04269547	7.57834286	2.21E-13	1.05E-11	19.5740818
DEPDC1	1.23877145	1.76190844	6.86789297	2.32E-11	8.24E-10	15.0163343
RP11-480I12.	1.2385696	1.85012405	4.84614371	1.77E-06	2.61E-05	4.10796529
KRTCAP3	1.23829463	4.16135875	3.27407885	0.00114664	0.00834465	-2.01418509
RP11-532F12	1.23762697	3.41821597	5.094703	5.26E-07	8.68E-06	5.27274578
HIST1H1PS1	1.23585675	1.40887404	4.91736402	1.26E-06	1.92E-05	4.43640875
SLC25A39	1.2357065	5.8845699	9.86901214	8.00E-21	1.00E-18	36.4398443
NUDT8	1.23474504	2.96523184	5.92359873	6.50E-09	1.54E-07	9.52316517
PRSS22	1.23405729	3.91949721	3.69561288	0.000248	0.00221202	-0.5893857
KAT2A	1.23047186	4.67652549	8.08198306	6.66E-15	4.00E-13	23.0109565

ATAD2	1.2297874	3.02515346	6.35072332	5.51E-10	1.55E-08	11.9249558
CCNF	1.22844049	2.55612863	8.41177799	6.18E-16	4.18E-14	25.3490809
PPP1R35	1.22806394	4.25906891	7.89499592	2.49E-14	1.36E-12	21.7157174
TMEM206	1.22780759	2.55809736	8.90836915	1.52E-17	1.26E-15	28.9940611
GALE	1.22476976	4.15652281	6.82395763	3.06E-11	1.06E-09	14.7461177
POLR2H	1.22383629	4.49438662	10.8828046	1.68E-24	3.18E-22	44.8042681
OAS3	1.22260824	3.82059363	4.66833967	4.08E-06	5.57E-05	3.30676956
TSTA3	1.22070637	4.96781418	8.0246385	1.00E-14	5.87E-13	22.6113621
SYNGR2	1.21896064	5.99085543	7.54595514	2.75E-13	1.29E-11	19.358774
SNHG12	1.21641943	2.95399291	7.74738565	6.94E-14	3.53E-12	20.7091773
CDCA2	1.21274058	1.71909444	7.22581769	2.32E-12	9.52E-11	17.2687914
OAS1	1.2125994	4.34958689	4.26988822	2.41E-05	0.00027521	1.61006928
LMNB2	1.21232866	4.57275143	7.07818926	6.06E-12	2.33E-10	16.3288104
NUDT1	1.2122017	3.73575083	7.57872524	2.20E-13	1.04E-11	19.576628
MBOAT7	1.21017581	5.31805316	6.37935537	4.65E-10	1.33E-08	12.0909255
INHBA	1.20889873	1.99188928	3.74301889	0.00020679	0.00188388	-0.41901479
RP11-50C13.	1.2074554	2.76275123	4.61478589	5.22E-06	6.95E-05	3.07074208
CCDC167	1.20636727	4.86746107	7.45369353	5.12E-13	2.30E-11	18.7493009
POP7	1.20594725	5.22394558	9.57051584	8.80E-20	9.66E-18	34.0732149
RP6-65G23.3	1.20585444	2.31150205	6.39627513	4.20E-10	1.21E-08	12.1892927
CENPH	1.20419608	2.74976341	7.61629718	1.71E-13	8.28E-12	19.8272877
TMSB10	1.20254262	11.2492347	5.38395692	1.21E-07	2.25E-06	6.69284393
PROM2	1.20155744	4.79286799	3.07220632	0.00226127	0.01491512	-2.63851004
RHBDF2	1.20089845	2.94392781	7.56415471	2.43E-13	1.14E-11	19.4796751
C1orf233	1.1990952	3.02946572	4.60467509	5.46E-06	7.25E-05	3.02645703
ISYNA1	1.19892519	4.62727499	3.67173452	0.00027157	0.002394	-0.6744304
PLXNA1	1.1981396	3.63307915	6.78781695	3.84E-11	1.31E-09	14.5248835
DBNDD1	1.19736684	2.29557562	4.82375003	1.97E-06	2.87E-05	4.00557921
MRPL12	1.1969183	5.15537313	7.30794546	1.35E-12	5.74E-11	17.79827
TMUB1	1.19576024	4.96776843	8.77900379	4.05E-17	3.20E-15	28.0305167
PLK4	1.19562535	1.96610624	8.19328619	3.01E-15	1.88E-13	23.7924816
PYCRL	1.19359071	3.03969831	7.86495914	3.07E-14	1.65E-12	21.5097508
MIR205HG	1.19291333	4.11854887	2.89524916	0.00398366	0.02405565	-3.15450211
TMEM74B	1.19242167	1.61320196	4.83243086	1.89E-06	2.77E-05	4.0452184
STEAP3	1.19080628	3.76189449	5.2111927	2.93E-07	5.06E-06	5.83636755
MCM7	1.19053834	5.35371476	7.23234927	2.22E-12	9.15E-11	17.31073
PRRG2	1.18838614	3.1808538	5.53430184	5.47E-08	1.09E-06	7.45796419
EPHA1	1.18675554	3.33665758	4.68372609	3.80E-06	5.22E-05	3.37503652
RP3-416H24.	1.18554915	2.8143828	3.13766918	0.00182134	0.0123793	-2.44020688
BAIAP2L1	1.18485507	3.95127939	6.38160328	4.58E-10	1.31E-08	12.1039819
YIF1B	1.18428202	3.92806049	7.53521411	2.96E-13	1.37E-11	19.2875248
RTKN	1.18185291	2.98315613	5.26959918	2.18E-07	3.87E-06	6.12317834
HIST1H2AC	1.18152143	4.27129927	4.11687034	4.61E-05	0.0004946	0.99532953
ITPR3	1.18055258	3.17616575	5.33958141	1.52E-07	2.78E-06	6.47052095
BID	1.17969903	3.73301677	7.86796312	3.01E-14	1.62E-12	21.5303232
DONSON	1.17965974	2.81765712	7.06726211	6.51E-12	2.50E-10	16.2598415
IGFBP3	1.17927112	6.9630687	2.6518981	0.00830309	0.04398804	-3.81595426
PCK2	1.17819799	3.85651976	6.68834087	7.12E-11	2.34E-09	13.920831
ITGB4	1.17746505	6.01215578	3.60906899	0.00034385	0.0029481	-0.89515653
ACTL6A	1.17698669	4.26952642	8.28918383	1.51E-15	9.73E-14	24.4720521
MRPS12	1.17454954	4.67294091	7.18906377	2.95E-12	1.19E-10	17.0333505
EPS8L2	1.17400592	4.557508	5.01648736	7.74E-07	1.24E-05	4.90063497
FANCD2	1.17316703	2.1176386	7.89941497	2.41E-14	1.33E-12	21.7460688
DSN1	1.17128393	3.46253548	7.63486394	1.50E-13	7.34E-12	19.9515025
CHAF1B	1.17015195	2.13317954	6.92490361	1.62E-11	5.85E-10	15.3690327
SLC1A6	1.17004334	1.19272269	2.95077077	0.00334494	0.02076785	-2.99576617
SEZ6L2	1.1691057	3.03123704	3.53132053	0.00045867	0.00379058	-1.16403909
B4GALNT4	1.16868892	1.76667881	3.39927014	0.00073937	0.00572537	-1.60804766

TRAIP	1.16850167	2.01430372	8.25641882	1.91E-15	1.22E-13	24.2392228
LYPLA2	1.16836663	5.81793769	8.57609422	1.84E-16	1.37E-14	26.538939
AP1S1	1.16654762	5.46803354	8.4578574	4.41E-16	3.07E-14	25.6811065
LY6E	1.16578401	6.52576399	3.08638436	0.00215843	0.01432909	-2.59590026
RP11-295G2(	1.16506218	2.66303047	5.92608614	6.41E-09	1.52E-07	9.53674506
MIF	1.1636419	5.71906667	6.28281019	8.23E-10	2.26E-08	11.5337578
GPR56	1.16312539	4.63630954	4.97684383	9.40E-07	1.48E-05	4.71398263
CEP131	1.16206245	3.24277644	7.28864711	1.54E-12	6.48E-11	17.6734351
B4GALT3	1.1606602	4.35774775	6.61571258	1.11E-10	3.57E-09	13.4843657
CDC7	1.16018247	2.22738206	6.8232088	3.07E-11	1.06E-09	14.7415242
NUDT5	1.15894943	3.90133715	8.56015836	2.07E-16	1.53E-14	26.4228309
CCDC137	1.15866178	4.24804666	9.47220401	1.92E-19	2.03E-17	33.3039597
DPP3	1.15730235	4.32426445	9.12881072	2.81E-18	2.47E-16	30.65804
C21orf58	1.15631021	1.57979257	7.17482559	3.24E-12	1.30E-10	16.9423949
CTSV	1.15517365	1.58686979	3.78219156	0.0001777	0.00164505	-0.27670016
WDR72	1.15510544	2.06433224	3.74472143	0.00020544	0.00187419	-0.41285825
PFDN2	1.15496667	6.82358378	6.33167323	6.17E-10	1.72E-08	11.814871
MROH6	1.15127241	2.59498771	4.47173133	9.97E-06	0.00012439	2.45236221
MANF	1.15125316	5.45782486	7.82935618	3.94E-14	2.09E-12	21.266374
PROSER2	1.15102397	2.51248762	4.90089819	1.36E-06	2.06E-05	4.36009375
SLC9A3R1	1.15020976	5.0256759	4.7134425	3.31E-06	4.61E-05	3.50745619
SLC19A1	1.14944402	1.95327191	7.75894754	6.41E-14	3.27E-12	20.787503
MCM5	1.14876158	3.72453355	6.81666803	3.20E-11	1.10E-09	14.7014187
ARHGAP39	1.14847609	2.07860133	8.92139508	1.38E-17	1.14E-15	29.0916169
TINCR	1.14811721	2.32584524	3.62705081	0.00032145	0.00277395	-0.83218456
NCAPD2	1.1480728	4.21176583	6.20936801	1.27E-09	3.38E-08	11.1146412
KIAA1522	1.14761106	5.51560785	5.10554706	4.98E-07	8.27E-06	5.32473862
KLC3	1.14541806	1.54437809	4.60949576	5.34E-06	7.10E-05	3.04756051
MIIP	1.14507781	3.87269324	7.99820305	1.21E-14	6.95E-13	22.4278567
HOMER3	1.14417356	3.9440431	5.93823626	5.99E-09	1.43E-07	9.60314721
MGME1	1.14403582	3.81373	9.15885492	2.23E-18	2.01E-16	30.8869462
SLC16A3	1.14193427	3.89951116	4.26914714	2.42E-05	0.00027601	1.60704233
ARHGEF19	1.14162039	3.49097537	4.86291384	1.63E-06	2.44E-05	4.18491783
PQLC2	1.14070146	3.23406047	10.0935178	1.28E-21	1.77E-19	38.2497243
STIL	1.14063319	1.61272533	7.7742785	5.77E-14	2.98E-12	20.8914975
SLC39A11	1.13831468	3.40835305	7.21421573	2.50E-12	1.02E-10	17.1943694
AC098973.2	1.13756977	1.77634429	2.99487497	0.00290585	0.01842173	-2.86761073
TREM2	1.13629665	2.51007096	3.76056042	0.00019325	0.00177269	-0.3554576
FLAD1	1.13573084	3.99558095	9.20990958	1.50E-18	1.39E-16	31.277083
ESPL1	1.13513495	1.93467232	6.38911377	4.38E-10	1.26E-08	12.1476321
LSM4	1.13503809	5.29888103	9.30213018	7.31E-19	7.18E-17	31.9854414
IGSF8	1.13468873	4.91036568	6.35739078	5.29E-10	1.49E-08	11.9635496
RANBP1	1.13427611	4.43577999	7.68953811	1.03E-13	5.13E-12	20.3186109
MIEN1	1.1340663	4.83446062	5.65193568	2.91E-08	6.10E-07	8.06931277
CCNL2	1.13251146	4.5306724	5.43510356	9.24E-08	1.76E-06	6.95107917
PFDN6	1.13194971	4.12843262	8.44170042	4.96E-16	3.42E-14	25.5645403
MRPS26	1.13143863	5.94400178	7.95802999	1.60E-14	9.05E-13	22.1498452
GPRIN1	1.12978274	1.49093505	5.51336202	6.12E-08	1.20E-06	7.35030397
HES2	1.12905597	1.8577934	2.92789563	0.00359582	0.02204882	-3.0615168
E2F8	1.12520488	2.01167576	5.56870181	4.55E-08	9.20E-07	7.63559452
PSME2	1.1250984	5.56335297	6.01038647	3.98E-09	9.81E-08	9.99982503
RP1-86C11.7	1.12501289	1.43627675	4.90547181	1.33E-06	2.02E-05	4.38126841
CHAC1	1.1245837	1.69770499	5.71378687	2.08E-08	4.48E-07	8.3951902
PDXK	1.12432894	4.03730542	7.0456907	7.47E-12	2.84E-10	16.1239361
GALNT6	1.12263052	1.96955596	4.69873429	3.54E-06	4.89E-05	3.44182043
SNX10	1.12251304	2.18228026	5.06107944	6.22E-07	1.01E-05	5.11215665
TUBG1	1.12200468	4.77891129	8.06495263	7.52E-15	4.49E-13	22.8920653
PVRL1	1.12136119	5.00664299	3.52880494	0.00046293	0.00382196	-1.17264678

CHEK1	1.12040897	2.10982379	7.50291581	3.68E-13	1.68E-11	19.0737455
P4HB	1.11996949	7.72894837	8.82889069	2.78E-17	2.25E-15	28.4009372
REEP4	1.11912378	4.85552423	6.47692131	2.59E-10	7.75E-09	12.6610919
CLSTN3	1.11846732	3.64664611	6.15428916	1.74E-09	4.56E-08	10.8030146
MAPK15	1.11809332	1.52079198	4.65024082	4.43E-06	6.01E-05	3.22672744
UQCC3	1.11784982	3.65566719	7.21066725	2.56E-12	1.04E-10	17.171626
MIR7111	1.11769922	1.55477712	6.07581238	2.74E-09	6.94E-08	10.3630207
IRF6	1.11718732	5.21102553	3.42271116	0.00068002	0.00533377	-1.53039702
UNG	1.11585094	4.67740522	8.24542438	2.07E-15	1.32E-13	24.1612451
RGS19	1.11460555	3.47731181	7.25117579	1.96E-12	8.16E-11	17.4317782
RFC2	1.11420357	4.29660868	8.07386503	7.06E-15	4.23E-13	22.9542607
TOMM34	1.11351188	5.35855525	6.23549859	1.09E-09	2.93E-08	11.2632924
AC016735.2	1.11350759	1.72724666	3.09895523	0.00207087	0.01383748	-2.5579637
C9orf142	1.11213854	4.89537071	6.556862	1.59E-10	4.98E-09	13.1335404
TMEM97	1.11197722	4.78462089	2.81925871	0.00503821	0.02925611	-3.36705756
NCAPG2	1.11155278	2.4461044	6.25603328	9.63E-10	2.61E-08	11.3804742
GPT2	1.11147532	2.87563371	5.17392469	3.54E-07	6.01E-06	5.65482873
CENPE	1.11089597	1.72621333	7.05933642	6.85E-12	2.62E-10	16.2098696
RP1-34B20.4	1.11024288	1.22890451	4.56231542	6.63E-06	8.64E-05	2.84187864
RP11-303E16	1.11017726	3.36663241	6.4065032	3.95E-10	1.14E-08	12.2488601
SNRPF	1.11003511	4.53859436	7.6070896	1.82E-13	8.76E-12	19.7657727
EIF2AK1	1.10919787	5.14340321	10.366488	1.33E-22	2.01E-20	40.4836245
FANCG	1.10801014	3.09724848	7.12309015	4.53E-12	1.78E-10	16.6130918
AC019129.2	1.10799351	1.62132652	3.55924377	0.00041383	0.0034666	-1.06810491
GMNN	1.10796849	3.93408526	5.77595363	1.48E-08	3.28E-07	8.72579008
IGFL1P1	1.10794159	1.30942975	3.29107072	0.0010812	0.00794066	-1.95990975
FANCA	1.10755881	1.62428108	7.81065101	4.48E-14	2.36E-12	21.1388385
RP11-109M1	1.10731006	1.47441802	2.9289168	0.00358426	0.02199876	-3.05859211
HMGB2	1.10637324	5.58541366	5.04549481	6.71E-07	1.09E-05	5.03804258
TMEM184A	1.1063724	2.94104836	3.7044698	0.00023975	0.00214734	-0.55770967
PARP12	1.10578554	3.26514278	5.79334081	1.34E-08	3.00E-07	8.8188012
PTK6	1.10459756	4.26930204	2.98817409	0.00296897	0.01874859	-2.88719922
ARL6IP1	1.104156	6.21555155	6.50933315	2.13E-10	6.51E-09	12.8520742
DARS2	1.10367582	3.28888892	6.8168615	3.20E-11	1.10E-09	14.7026046
KIAA0907	1.10366524	3.26613907	6.94265103	1.44E-11	5.26E-10	15.479302
GALNT14	1.10237363	2.20065223	3.66506046	0.00027853	0.00244732	-0.69810813
TARBP2	1.1014116	3.28913392	9.59009949	7.53E-20	8.30E-18	34.2270618
EME1	1.10095321	1.39352252	7.79701257	4.93E-14	2.58E-12	21.0459929
THEM6	1.10033408	4.62568489	3.85783996	0.00013211	0.00126387	0.00204662
ZNF692	1.09936129	3.33150549	5.89598769	7.59E-09	1.77E-07	9.372749
C1orf53	1.09928588	2.2083562	6.43723935	3.29E-10	9.65E-09	12.428336
CASP2	1.09873131	2.97111555	9.37761185	4.05E-19	4.07E-17	32.5686902
PRR36	1.0983413	1.50272851	3.70287191	0.00024122	0.00215924	-0.56342965
CHAF1A	1.09731869	3.43457943	7.36875038	9.03E-13	3.93E-11	18.1932694
DSCC1	1.09716871	2.16200764	6.32444811	6.44E-10	1.79E-08	11.7731907
DUSP23	1.09646684	5.49422127	4.86178312	1.64E-06	2.45E-05	4.17972187
HES4	1.09615902	3.88306873	3.64957783	0.00029532	0.002572	-0.75288046
CTD-2537I9.	1.09538085	2.01268003	5.47606996	7.45E-08	1.44E-06	7.15944593
ATAD3A	1.09441289	3.90822023	7.8673716	3.02E-14	1.63E-12	21.5262718
CENPK	1.09387122	1.6123945	7.26233155	1.83E-12	7.64E-11	17.5036217
TAGLN2	1.09332953	8.5470993	5.31497412	1.73E-07	3.12E-06	6.3479305
BLOC1S3	1.09316538	3.19501699	8.63658351	1.18E-16	8.92E-15	26.9810425
MIR621	1.09315003	3.4048716	5.23850601	2.55E-07	4.46E-06	5.97014281
TOMM40	1.09253316	4.88378608	7.98544409	1.32E-14	7.53E-13	22.3394482
ATP5J2	1.09194513	5.77942891	8.5720666	1.90E-16	1.41E-14	26.5095795
FKBPL	1.09084831	3.13990515	7.93028446	1.95E-14	1.09E-12	21.9584411
SREBF1	1.0904303	4.3754413	4.78074981	2.41E-06	3.46E-05	3.81016987
MRM1	1.09042204	2.97538045	7.54082345	2.85E-13	1.33E-11	19.324724

PPAP2C	1.08934023	3.56101466	3.89097697	0.00011584	0.00112484	0.12576955
ARHGAP40	1.08900932	2.04633036	3.5213289	0.00047579	0.00391744	-1.19819365
MYEOV	1.08858173	1.83158753	2.68068655	0.00763255	0.04112223	-3.7406267
BRMS1	1.08800017	4.85043679	7.78847062	5.23E-14	2.72E-12	20.9879042
ROMO1	1.08725472	6.81208241	6.59241078	1.28E-10	4.09E-09	13.3451518
KNTC1	1.08669863	1.94524927	7.58811208	2.07E-13	9.83E-12	19.6391637
PPP1CA	1.08485922	6.45220601	8.58432116	1.73E-16	1.29E-14	26.5989398
LPCAT1	1.08451759	4.09603813	4.45748048	1.06E-05	0.00013176	2.39172934
NR2F6	1.08416885	5.05176533	5.90159074	7.36E-09	1.72E-07	9.40322445
ERBB3	1.08349812	4.17743135	3.49630377	0.00052134	0.00423477	-1.28333686
LAMTOR2	1.08264518	5.35962334	7.33800879	1.11E-12	4.75E-11	17.9932499
BAX	1.08245451	5.0744508	8.51331563	2.93E-16	2.11E-14	26.0824186
EXOSC4	1.08205296	4.49913558	6.71557621	6.01E-11	2.00E-09	14.0854979
SPTBN2	1.08160815	2.53131511	4.68328461	3.80E-06	5.23E-05	3.37307492
TMC4	1.08151887	4.66366887	3.03713002	0.00253534	0.01645518	-2.74311948
SP6	1.08018945	2.89379184	3.16246489	0.00167641	0.01154252	-2.36405228
PDRG1	1.07944796	4.00664996	7.43128464	5.95E-13	2.66E-11	18.6021377
NR2C2AP	1.07880401	4.21173767	8.10554572	5.63E-15	3.42E-13	23.1757526
MYH14	1.07856598	4.27730239	2.89051526	0.00404296	0.02433572	-3.16790225
PERP	1.07837721	7.05728061	3.47685576	0.00055952	0.00450044	-1.3491091
COASY	1.07824304	4.67192651	9.69347166	3.30E-20	3.81E-18	35.042477
ABHD12	1.07735829	5.24564346	5.48239425	7.21E-08	1.40E-06	7.19173407
CTD-2021H9	1.0765001	1.5607768	3.02223855	0.00266066	0.01714278	-2.78718316
KDELR3	1.07634302	3.43651251	3.87999062	0.00012101	0.00116825	0.08464083
LYPD6B	1.07617954	3.03319966	3.46709611	0.00057965	0.00464443	-1.38198521
PSMB3	1.07604486	7.04120011	7.63235865	1.53E-13	7.46E-12	19.9347283
RPS6KA1	1.07590829	3.45174731	6.50230652	2.22E-10	6.76E-09	12.8106045
C10orf35	1.0754861	3.17124404	5.46058529	8.08E-08	1.55E-06	7.08052677
CCNO	1.07214577	2.43249793	4.47251543	9.93E-06	0.00012411	2.45570345
KIAA1524	1.07116931	1.91674684	6.62359569	1.06E-10	3.41E-09	13.5315528
PYCARD	1.07089365	4.32242899	4.35365484	1.68E-05	0.00019889	1.95531246
TFAP2A	1.06973765	2.38167561	3.99619599	7.59E-05	0.00077079	0.52514314
HOXB6	1.06954476	1.98073807	3.58883145	0.00037082	0.00314943	-0.96567594
INCENP	1.06925659	2.88990115	6.09077298	2.52E-09	6.42E-08	10.4465348
RSRP1	1.06888602	3.08911719	5.82126889	1.15E-08	2.60E-07	8.96869883
TFAP2C	1.06793505	3.10657251	4.37317851	1.54E-05	0.00018447	2.03666071
MAFG-AS1	1.06784345	1.79349229	5.57574077	4.39E-08	8.88E-07	7.67205859
SLC35F2	1.06767166	2.72564074	5.38090167	1.23E-07	2.28E-06	6.67748556
PPP1R16A	1.06750415	2.72667992	6.8426874	2.72E-11	9.51E-10	14.861142
MYO19	1.06684003	2.34367761	8.3074532	1.32E-15	8.58E-14	24.6021634
GAPDHP1	1.0649602	2.4846257	2.77415827	0.00577805	0.03272671	-3.49063458
RP11-465B2	1.06384171	2.54442561	3.25961275	0.00120523	0.00870592	-2.06018212
ATP13A2	1.0634931	3.86614613	8.07977555	6.77E-15	4.06E-13	22.9955352
DDX11	1.06346433	2.38074971	7.61030293	1.78E-13	8.59E-12	19.7872342
HENMT1	1.06325933	3.04542219	5.84272603	1.02E-08	2.33E-07	9.08428216
CKLF	1.06305014	3.33202136	7.26454341	1.80E-12	7.55E-11	17.5178763
TNFAIP2	1.0628005	6.23561668	2.99958232	0.00286225	0.01820669	-2.85382471
GALNT3	1.06084724	3.21992638	4.27054529	2.41E-05	0.00027454	1.61275344
LSM7	1.05915245	5.13646447	6.8761768	2.20E-11	7.83E-10	15.067438
CASC9	1.05873347	2.31378488	3.58333174	0.00037848	0.00320306	-0.98477566
TNFRSF25	1.0585759	2.49214047	5.91646923	6.77E-09	1.59E-07	9.4842689
DTX4	1.05826808	3.70681405	3.64144297	0.00030451	0.00264225	-0.78157165
TCF3	1.0580517	4.22971034	7.9884229	1.29E-14	7.38E-13	22.3600795
ATP6V0B	1.05787287	5.40833501	8.26079466	1.85E-15	1.19E-13	24.2702791
SLC37A4	1.05749593	2.58618391	7.8978605	2.44E-14	1.34E-12	21.7353908
KCNN4	1.05704174	4.18620001	2.88990363	0.00405068	0.02436781	-3.16963205
HIST1H4E	1.05613939	1.28587243	3.8482818	0.00013719	0.00130733	-0.03345721
SOX9	1.05562797	2.79081951	2.86910653	0.00432132	0.02570386	-3.22824018

HOXB5	1.05513075	1.79814584	3.68929281	0.00025404	0.00225974	-0.61194547
RP11-54H7.4	1.05487872	1.08227035	2.87924701	0.00418737	0.02505255	-3.19971421
ZNF488	1.05448236	1.521706	3.78070922	0.00017873	0.00165337	-0.28211074
RP11-12G12.	1.05380395	3.23355153	5.75920321	1.62E-08	3.56E-07	8.63641106
COA6	1.05336934	4.33440785	8.05524106	8.06E-15	4.79E-13	22.8243502
CTD-2583A1	1.05298217	2.3629756	6.35398159	5.40E-10	1.52E-08	11.9438118
RHBG	1.05258364	1.46329054	3.15377765	0.00172593	0.01182986	-2.39079831
SLC2A6	1.05223393	2.52359111	3.9414936	9.46E-05	0.00094075	0.31627682
RP11-764K9.	1.05203141	2.51596313	4.77195158	2.51E-06	3.59E-05	3.77038087
MRGBP	1.05201531	3.58521843	8.78941446	3.74E-17	2.97E-15	28.1076984
FBXO6	1.05185428	3.61548891	6.19975985	1.34E-09	3.56E-08	11.0601131
NT5DC2	1.05178327	4.37868185	5.01980752	7.62E-07	1.22E-05	4.91632684
AUP1	1.05125601	6.20297202	9.38534736	3.81E-19	3.85E-17	32.6286376
HIP1R	1.05021312	3.59634799	5.96242885	5.23E-09	1.26E-07	9.73570574
BRI3BP	1.04984572	2.41874161	7.06493184	6.60E-12	2.53E-10	16.2451444
CCDC58	1.04980719	3.57100581	8.87148522	2.01E-17	1.65E-15	28.7183538
SNHG3	1.04976531	3.20434585	6.25451993	9.72E-10	2.63E-08	11.3718272
PCGF2	1.04973005	4.11338527	6.4399265	3.23E-10	9.51E-09	12.4440605
GPR87	1.04933352	3.9816615	2.9169163	0.00372223	0.02270474	-3.09290046
CTD-2538C1	1.04895961	2.40150035	3.67428153	0.00026896	0.00237432	-0.66538366
CLN6	1.04672885	3.80400593	7.76118979	6.31E-14	3.23E-12	20.8027033
TMEM139	1.04635667	1.78751228	3.04568837	0.00246579	0.01606988	-2.71770159
CBX3	1.04581103	5.53239416	9.14337596	2.51E-18	2.24E-16	30.7689494
ITPA	1.04489668	5.08224302	8.13765742	4.48E-15	2.75E-13	23.4009047
RPN1	1.04423597	6.66393575	9.31319921	6.71E-19	6.59E-17	32.0707778
PPP4C	1.04413003	5.88676671	8.12932431	4.75E-15	2.90E-13	23.3424144
MND1	1.04310527	1.97262645	6.31119769	6.96E-10	1.93E-08	11.696854
UNC93B1	1.04295401	4.41882292	5.04321763	6.79E-07	1.10E-05	5.02723022
MGAT4B	1.04271648	4.57197815	7.53527723	2.96E-13	1.37E-11	19.2879433
MANEAL	1.04264497	2.48830555	4.03991007	6.34E-05	0.00065657	0.69397207
ADCK5	1.04251166	2.93904111	6.80836352	3.37E-11	1.16E-09	14.6505431
PDIA3	1.04203998	7.06772783	8.44362114	4.89E-16	3.38E-14	25.5783892
XRCC2	1.04181288	1.36217237	7.88793585	2.62E-14	1.42E-12	21.667253
OLR1	1.04103402	1.97857051	2.67618897	0.00773399	0.04156519	-3.75244685
PPAPDC1A	1.04100086	1.15570608	3.73133704	0.0002163	0.0019592	-0.46118663
MFSD10	1.04031218	5.33137413	6.44242708	3.19E-10	9.38E-09	12.4586981
TMEM223	1.04021457	3.42633284	8.50436365	3.13E-16	2.24E-14	26.0175136
SMYD2	1.03995274	3.38819614	7.61630259	1.71E-13	8.28E-12	19.8273239
CNPY2	1.03993648	3.60555426	7.90247965	2.36E-14	1.30E-12	21.7671253
CTA-384D8.	1.03988196	1.50953746	3.43549879	0.00064956	0.00512648	-1.48782392
RFC5	1.03907271	3.09556028	7.61027992	1.78E-13	8.59E-12	19.7870805
CH17-360D5.	1.03857575	2.06719698	4.36537255	1.60E-05	0.00018995	2.00409615
RIPPLY3	1.03817369	1.56928513	4.25245202	2.60E-05	0.00029435	1.53897948
HCAR1	1.03772667	1.84152725	3.7281158	0.00021899	0.00198053	-0.4727937
RP3-406A7.7	1.03761542	2.78444415	3.88563822	0.00011833	0.00114536	0.10576978
SMPDL3B	1.03741361	1.83497647	3.90446576	0.00010978	0.00107347	0.17641448
EPS8L1	1.03585473	3.35589548	3.25655148	0.00121798	0.00878606	-2.06989105
MAD2L2	1.03581398	3.5958427	5.64454334	3.03E-08	6.31E-07	8.03056833
NAA40	1.03481928	2.82517486	8.36041573	8.98E-16	5.96E-14	24.9805162
KIF14	1.03397699	1.40910211	6.60764359	1.17E-10	3.73E-09	13.4361133
ARRDC1	1.03307427	4.17652988	6.06572093	2.90E-09	7.32E-08	10.306785
MREG	1.03278776	2.81123849	5.6439716	3.04E-08	6.33E-07	8.02757356
IRF7	1.03273146	3.67124389	3.7800717	0.00017917	0.0016563	-0.28443708
DDR1	1.03219372	5.17409728	4.59023625	5.84E-06	7.70E-05	2.96336763
CTA-384D8.	1.03192664	2.87882108	5.10450592	5.01E-07	8.31E-06	5.3197425
SLC25A10	1.03145493	2.55481394	5.3432567	1.49E-07	2.73E-06	6.48887327
ETV7	1.03111107	2.63273323	4.05935863	5.86E-05	0.00061129	0.76963127
ZMYND19	1.03108485	3.74193641	7.60476619	1.85E-13	8.88E-12	19.750259

DNAJB11	1.03094781	4.06947336	8.76794489	4.40E-17	3.44E-15	27.9485986
PTK7	1.03047103	3.78922367	4.57563273	6.24E-06	8.19E-05	2.89974112
IFIT3	1.03033805	3.58161033	2.74815193	0.00624807	0.03495316	-3.56101944
WDR4	1.0299953	3.07251574	7.91494763	2.17E-14	1.20E-12	21.8528518
NDC1	1.02971148	3.30542727	7.51258396	3.45E-13	1.58E-11	19.1376645
AGTRAP	1.02726389	4.57729415	5.74222088	1.78E-08	3.89E-07	8.54602116
PGP	1.02722522	3.35159819	7.51832444	3.32E-13	1.52E-11	19.1756462
PNKP	1.02690315	3.70267777	7.79401249	5.03E-14	2.63E-12	21.0255857
MRPL14	1.02678245	5.99229516	7.07553904	6.17E-12	2.37E-10	16.3120753
CYP4F23P	1.02675866	1.84487553	2.69924942	0.00722643	0.03931848	-3.69163839
TRAF2	1.02668348	3.33849063	7.2583567	1.87E-12	7.82E-11	17.4780136
SMUG1	1.02649883	3.12982144	9.13930932	2.59E-18	2.31E-16	30.7379714
MICB	1.02641136	1.8158224	4.52977795	7.68E-06	9.85E-05	2.70114966
DDOST	1.02571587	6.84337121	8.26759672	1.76E-15	1.13E-13	24.3185785
RAD9A	1.02548155	2.92850876	6.46169689	2.84E-10	8.43E-09	12.5716538
VPS9D1-AS1	1.02372479	1.98217346	4.27955662	2.32E-05	0.00026544	1.64960368
CDC42BPG	1.02359664	3.36336522	4.67181355	4.01E-06	5.49E-05	3.32216487
CBX8	1.02351245	1.95149723	7.71218311	8.85E-14	4.42E-12	20.4712394
CASP6	1.02332253	3.75203848	7.00129749	9.94E-12	3.71E-10	15.8452816
HSBP1L1	1.02189304	3.05492954	5.82788244	1.11E-08	2.52E-07	9.00428547
CCT5	1.02144335	5.46376535	5.82799138	1.11E-08	2.51E-07	9.00487195
IGF2BP2	1.02103991	1.99714575	2.78547671	0.00558367	0.03181995	-3.45980215
FCHO1	1.01932887	1.81746514	4.84226111	1.80E-06	2.66E-05	4.09018324
CSTB	1.01915238	7.62181148	3.83827718	0.0001427	0.00135413	-0.07053142
CA2	1.01909812	2.60223226	2.69068504	0.00741132	0.0401899	-3.71428077
FAM96A	1.01909421	3.90926518	9.43382298	2.60E-19	2.70E-17	33.0050416
SIRT7	1.01894549	3.04017884	7.68784686	1.05E-13	5.19E-12	20.3072254
NAT14	1.01873457	3.30652139	4.98831486	8.89E-07	1.40E-05	4.76785598
CDH24	1.01856633	2.26556673	5.51275007	6.14E-08	1.21E-06	7.34716298
RP11-670E13	1.01853394	2.35550999	4.36526421	1.60E-05	0.00018996	2.00364455
CXADR	1.01739567	3.80256436	3.28519186	0.00110344	0.00808061	-1.97871819
GSS	1.01722792	5.5201186	7.94310555	1.78E-14	1.00E-12	22.0468266
CYBA	1.01686498	5.29935014	3.99556338	7.61E-05	0.00077264	0.52271241
AP1G2	1.01650466	3.36621625	5.37575307	1.26E-07	2.34E-06	6.65162133
TSEN54	1.01626458	3.9373763	7.95544879	1.63E-14	9.19E-13	22.1320178
SLC25A22	1.01526685	3.15210944	7.20940034	2.58E-12	1.05E-10	17.163508
CAMSAP3	1.01418887	3.05238214	4.28552255	2.26E-05	0.00025917	1.67403947
ECE2	1.0134034	1.69011205	7.86679045	3.03E-14	1.63E-12	21.5222917
RPA3	1.01276805	3.23578853	6.91490793	1.72E-11	6.21E-10	15.307026
FBXW9	1.01269471	2.98556167	8.34222833	1.03E-15	6.75E-14	24.8503949
PLEKHJ1	1.01204065	3.90209533	7.04260684	7.62E-12	2.89E-10	16.1045339
ENTPD6	1.01139862	4.1007204	7.54919108	2.69E-13	1.26E-11	19.3802544
MARVELD3	1.01130857	2.00855273	5.91370655	6.87E-09	1.62E-07	9.46920725
TPM3	1.01122849	5.5115274	7.36112289	9.50E-13	4.13E-11	18.143581
AP2S1	1.01053578	5.94055919	6.91200628	1.76E-11	6.32E-10	15.2890394
PIF1	1.00977225	1.53086568	7.00238049	9.87E-12	3.69E-10	15.8520629
RUVBL1	1.0077824	3.50538333	7.42972371	6.01E-13	2.68E-11	18.5918995
EDEM2	1.00749244	4.53317972	7.99378093	1.24E-14	7.13E-13	22.3972034
TUBB	1.00585542	8.12859995	6.59542158	1.26E-10	4.01E-09	13.363117
AATBC	1.00535874	1.88028869	3.08994562	0.00213329	0.01418312	-2.58516801
ACYP1	1.00473703	2.5938072	7.22273389	2.37E-12	9.69E-11	17.2490009
MYDGF	1.00465656	5.91853868	7.37789102	8.50E-13	3.71E-11	18.2528674
MFI2-AS1	1.00430468	1.8263659	5.43279449	9.35E-08	1.78E-06	6.93937504
MIR210HG	1.00377997	2.20940622	4.34281275	1.76E-05	0.00020767	1.91028103
LINC01518	1.00320743	1.08622867	3.12633924	0.00189133	0.01278265	-2.47481385
ERBB2	1.00259603	5.09141748	3.17648454	0.00159925	0.01108448	-2.32074095
UCK2	1.00229453	2.99580327	6.40492899	3.99E-10	1.15E-08	12.2396869
METTL7B	1.00217713	1.48277687	3.48795226	0.00053743	0.00434609	-1.31162369

POLE2	1.00209833	1.6885146	7.22155917	2.39E-12	9.75E-11	17.2414638
POLR2G	1.00201718	5.18687418	8.51009564	3.00E-16	2.16E-14	26.059067
ENO1	1.00161163	8.53271051	5.73674078	1.83E-08	3.99E-07	8.51690155
KIF18A	1.0002719	1.42685059	6.53606342	1.81E-10	5.61E-09	13.0101652
DBI	1.00018061	5.84351232	5.3979574	1.12E-07	2.11E-06	6.76331983
NAT9	1.0001367	3.44856134	8.51407699	2.91E-16	2.10E-14	26.0879409

Supplementary Table S3

	logFC	AveExpr	t	P.Value	adj.P.Val	B
KITLG	-1.000106989	1.866386203	-3.970794439	8.41E-05	0.000845941	0.427821835
MYH3	-1.000778882	0.654330481	-6.253693503	9.77E-10	2.64E-08	11.36710601
COLCA1	-1.002344931	1.207337165	-3.43507543	0.000650545	0.005133581	-1.489235796
SH3D19	-1.003536628	2.659421452	-6.744064063	5.04E-11	1.69E-09	14.25831556
PTGER4	-1.003692238	2.139118564	-4.071754555	5.56E-05	0.00058467	0.818029568
PRSS23	-1.003717409	3.120703858	-4.002265259	7.40E-05	0.000754081	0.548481598
GPM6B	-1.003884406	0.86989705	-7.597287256	1.94E-13	9.28E-12	19.70034604
MPEG1	-1.003891424	1.958956584	-3.640738762	0.000305324	0.002647301	-0.784052507
EPB41L2	-1.003954675	1.862882345	-5.529117721	5.62E-08	1.12E-06	7.43127759
INPP5A	-1.004648596	3.10199096	-6.961096622	1.28E-11	4.73E-10	15.59414695
MEG3	-1.006374094	0.888234072	-5.207397177	2.99E-07	5.14E-06	5.817826463
CYS1	-1.008979474	0.758603188	-6.500607344	2.24E-10	6.83E-09	12.80058181
PNRC1	-1.009215285	4.512708946	-5.946565285	5.71E-09	1.37E-07	9.648732994
FSTL1	-1.009281788	4.543430295	-3.638132894	0.000308334	0.002670626	-0.793228861
ZFP36L1	-1.010867072	6.171919074	-5.286072892	2.00E-07	3.58E-06	6.204581107
PYGB	-1.011496188	5.141796079	-5.018524544	7.67E-07	1.23E-05	4.910262102
MAP3K8	-1.012310996	2.645810549	-5.433021828	9.34E-08	1.77E-06	6.940527186
GABARAPL1	-1.012865752	3.68272068	-5.591610021	4.03E-08	8.20E-07	7.754412281
JDP2	-1.013035006	2.087119333	-5.444762924	8.78E-08	1.67E-06	7.000086954
RP11-514D23.3	-1.013322836	0.437620814	-10.42054904	8.47E-23	1.30E-20	40.93026914
INHBB	-1.016949362	1.707701062	-4.536211366	7.46E-06	9.59E-05	2.728902596
MEF2D	-1.018211752	3.236746255	-9.462900006	2.07E-19	2.17E-17	33.23142601
TSPAN11	-1.019344967	0.820341512	-6.673848034	7.79E-11	2.55E-09	13.83342689
MITF	-1.019400447	0.920008314	-7.44426329	5.46E-13	2.44E-11	18.68732935
AR	-1.02087991	0.966052001	-4.572260848	6.33E-06	8.30E-05	2.885076155
STK40	-1.021666591	3.233252063	-7.547580327	2.72E-13	1.27E-11	19.36956121
ARRDC4	-1.021745488	2.297380656	-5.063743927	6.13E-07	1.00E-05	5.124848148
STEAP4	-1.022011578	1.215583334	-4.285983826	2.25E-05	0.000258702	1.675930095
ROR1	-1.022364142	0.457448928	-9.18398942	1.83E-18	1.68E-16	31.07883189
GHR	-1.023558225	0.408398198	-9.2689309	9.48E-19	9.15E-17	31.72989464
TBL1X	-1.026047231	2.461365301	-5.715305791	2.06E-08	4.45E-07	8.403231238
SCN4B	-1.026698407	0.567120018	-9.072213571	4.35E-18	3.76E-16	30.2281998
TLE2	-1.02718075	3.373143056	-2.947108594	0.003383995	0.020956867	-3.006325487
LEPR	-1.028155294	0.709451886	-9.821244652	1.18E-20	1.44E-18	36.05803339
PLEKHO2	-1.029249549	3.192093548	-5.648467413	2.97E-08	6.19E-07	8.051129587
MICU3	-1.029298172	0.308999824	-14.16633446	1.35E-37	9.87E-35	74.64857636
KLRB1	-1.029550757	1.005300042	-5.729036909	1.91E-08	4.15E-07	8.476005799
NFKBIZ	-1.029934182	2.556970997	-4.634088945	4.77E-06	6.42E-05	3.155532874
RBP1	-1.030640273	2.263530207	-3.053095308	0.002407017	0.015746613	-2.695648096
PTPLA	-1.031136875	1.082162435	-5.570107408	4.52E-08	9.14E-07	7.642872793
UGCG	-1.031352636	3.877394525	-5.921981305	6.56E-09	1.55E-07	9.514337547
AHNAK2	-1.031770498	1.579346892	-3.078916256	0.002212051	0.014638446	-2.618367806
NCOA7	-1.03296022	2.738293857	-4.773831482	2.49E-06	3.56E-05	3.778876989
LINC00641	-1.03345129	0.925619106	-9.784376774	1.59E-20	1.89E-18	35.76414058
GNA14	-1.033701026	1.247850305	-4.5071195	8.50E-06	0.000108064	2.603688809
FKBP5	-1.033896906	2.236075219	-3.932757564	9.80E-05	0.000970068	0.283168253
ALDH1L1	-1.035845375	1.631542424	-3.222911093	0.001366558	0.009693749	-2.176010736
RP11-798K23.5	-1.036659528	1.141135033	-6.002691601	4.16E-09	1.02E-07	9.957326487
WNT9A	-1.037716522	1.368751199	-5.253839731	2.36E-07	4.16E-06	6.045513551
NEURL1B	-1.039492354	2.28063979	-4.826095623	1.94E-06	2.84E-05	4.016283578
C1QTNF2	-1.041549225	0.621663469	-9.390760744	3.65E-19	3.69E-17	32.67060854
RP11-102K13.5	-1.041654254	0.202285499	-8.85082181	2.36E-17	1.91E-15	28.56423789
LRIG1	-1.041735981	1.652083185	-4.041546303	6.30E-05	0.000652703	0.700324411
DYNC1I1	-1.042091872	1.162557973	-5.255528246	2.34E-07	4.13E-06	6.053825028
TMEM220	-1.04227284	0.610091048	-10.96603094	8.21E-25	1.60E-22	45.51189707
FAM46C	-1.04462024	1.594688598	-5.269270467	2.18E-07	3.88E-06	6.121556303
TUB	-1.045827415	0.732387638	-7.430512187	5.98E-13	2.67E-11	18.59707093
FYN	-1.046804434	2.126755351	-5.152356297	3.94E-07	6.66E-06	5.550289914
PBXIP1	-1.047040794	5.339444052	-5.989886085	4.47E-09	1.09E-07	9.886703787
CPEB4	-1.047371296	1.667437944	-7.589030221	2.05E-13	9.78E-12	19.6452835
CDKN1C	-1.047548054	2.874535591	-3.597718449	0.000358741	0.003061807	-0.934754394
AC002398.12	-1.047736702	0.185487225	-12.80214004	5.71E-32	2.45E-29	61.81886289
TTLL7	-1.048163184	0.766215441	-7.681074799	1.10E-13	5.43E-12	20.26165466
MPP7	-1.048712988	2.155048112	-4.942582339	1.11E-06	1.72E-05	4.553731831
NPR2	-1.05036083	1.333788298	-7.748592086	6.89E-14	3.50E-12	20.71734613
MEIS2	-1.050499239	1.31874562	-7.205676542	2.65E-12	1.07E-10	17.13965361
BCL2	-1.050834934	1.080142868	-7.361154135	9.50E-13	4.13E-11	18.14378447
TMEM246	-1.052116909	1.314821398	-4.710229459	3.36E-06	4.67E-05	3.493102125
LDB3	-1.053235558	0.34339145	-10.53692998	3.18E-23	5.14E-21	41.89643235

AL031587.1	-1.053546606	3.150395773	-4.468465693	1.01E-05	0.000126105	2.43845241
PITX2	-1.054500734	1.000565718	-5.80832504	1.24E-08	2.78E-07	8.899149246
TXNIP	-1.054714227	6.708401372	-3.762732419	0.00019163	0.001760063	-0.347568584
PROS1	-1.055817584	1.903089704	-5.031255631	7.20E-07	1.16E-05	4.970504091
NFIC	-1.055935621	3.177719314	-6.578243346	1.40E-10	4.43E-09	13.26070554
LINC01133	-1.059080755	1.447475987	-2.971904172	0.003127486	0.019607484	-2.9345855
FAM110D	-1.059322168	0.961746204	-7.858359213	3.22E-14	1.72E-12	21.4645725
LRRC4B	-1.060258494	0.557430309	-7.771551479	5.88E-14	3.03E-12	20.8729881
REEP2	-1.06030927	0.965601688	-5.525355303	5.74E-08	1.13E-06	7.411923126
ZFPM2	-1.060753383	0.53581358	-9.365827352	4.44E-19	4.43E-17	32.47742702
CHRM3	-1.06096854	0.461813318	-8.370427031	8.35E-16	5.56E-14	25.05222855
PRKAG2	-1.062373145	1.901202987	-8.132635005	4.64E-15	2.84E-13	23.365647
NT5DC3	-1.062566916	1.177517923	-7.34583951	1.05E-12	4.52E-11	18.04413894
CXCR4	-1.063334403	3.790108691	-3.513219473	0.000490128	0.004016439	-1.225847167
FAM180A	-1.063976861	0.37189411	-9.869397342	7.97E-21	9.99E-19	36.442928
AC114498.1	-1.064446505	2.12535057	-3.487016866	0.000539257	0.004358475	-1.314787932
NRP2	-1.065031677	1.705995481	-4.436225628	1.17E-05	0.000143236	2.30162411
LAMA4	-1.065446144	2.459226898	-4.546631904	7.12E-06	9.20E-05	2.773931272
DAAM2	-1.065617491	0.897307938	-7.251697709	1.96E-12	8.14E-11	17.43513743
ITGB1BP2	-1.067320004	0.70586074	-9.368788387	4.34E-19	4.34E-17	32.50035121
PAM	-1.067751179	3.129054161	-4.946072182	1.09E-06	1.69E-05	4.570009735
RP11-703I16.1	-1.067870748	1.294972519	-6.367573089	4.98E-10	1.41E-08	12.02255328
MUC21	-1.068315705	0.303704516	-5.01578481	7.77E-07	1.24E-05	4.897315722
RP11-401P9.4	-1.068510582	0.62502669	-6.984732513	1.10E-11	4.11E-10	15.74166127
HSPB2	-1.068677035	0.560007446	-9.376082795	4.10E-19	4.11E-17	32.55684444
UTRN	-1.068701448	1.709068653	-6.34980167	5.54E-10	1.56E-08	11.91962361
GPC3	-1.072383028	1.824525722	-3.109945177	0.001997011	0.013402241	-2.524677353
CD93	-1.073363854	2.857991783	-4.626349509	4.95E-06	6.64E-05	3.121498141
ITGA1	-1.07405927	1.588118483	-6.076644935	2.73E-09	6.92E-08	10.36766376
PER3	-1.074703615	1.498852006	-6.26755109	9.00E-10	2.45E-08	11.44634094
RND1	-1.074758053	1.120866486	-6.179403066	1.51E-09	3.98E-08	10.94481735
SOWAHC	-1.075202853	3.444447341	-4.695933407	3.59E-06	4.95E-05	3.429342364
LATS2	-1.075275521	2.098058384	-6.709359046	6.25E-11	2.07E-09	14.0478609
TMTC1	-1.07532792	0.807298509	-6.283647653	8.19E-10	2.25E-08	11.53856063
LDLR	-1.075854222	3.017135108	-3.913762901	0.000105777	0.001037982	0.211416392
TNNT2	-1.076023119	0.638784158	-6.517783627	2.02E-10	6.21E-09	12.90199567
PARD3B	-1.076050517	0.732846595	-9.381340879	3.93E-19	3.96E-17	32.59758477
PARVA	-1.076610668	3.00395582	-6.773243132	4.20E-11	1.43E-09	14.43593726
KLHL13	-1.077635596	0.654934925	-7.7900491	5.17E-14	2.70E-12	20.99863489
EPM2A	-1.079836673	0.841851241	-11.30981389	4.13E-26	9.21E-24	48.46623391
CDC42EP3	-1.082116337	2.296172955	-5.433352821	9.33E-08	1.77E-06	6.942204705
NCKAP1L	-1.083963115	1.274581347	-4.797129593	2.23E-06	3.23E-05	3.884420812
CACNA1C	-1.08523936	0.573635553	-8.416241656	5.98E-16	4.06E-14	25.3811874
PPP1R12A	-1.086856027	2.598790657	-8.027230079	9.82E-15	5.77E-13	22.62937586
CLMP	-1.087061663	1.914449136	-3.677090487	0.000266108	0.002352343	-0.655399684
RGN	-1.087680015	0.47561093	-8.499095939	3.25E-16	2.32E-14	25.9793435
CDO1	-1.089732774	0.51193222	-6.840247018	2.76E-11	9.63E-10	14.84614073
TBX5	-1.090912047	0.451760969	-9.323799565	6.17E-19	6.10E-17	32.15256371
SLC25A4	-1.091768467	2.645869318	-6.978192812	1.15E-11	4.27E-10	15.70080652
LAMB2	-1.092088709	4.357735128	-4.91815701	1.25E-06	1.91E-05	4.440089833
CBX6	-1.094324326	2.847701559	-4.747031177	2.82E-06	4.00E-05	3.658038496
FAM50B	-1.09510195	1.55252326	-4.613429696	5.25E-06	6.99E-05	3.064796906
MAPRE2	-1.098418349	2.190577138	-5.82916807	1.10E-08	2.50E-07	9.011207296
SGCB	-1.099183792	2.65060041	-5.759374061	1.62E-08	3.56E-07	8.637321609
ANGPTL7	-1.099590867	0.185224592	-12.66549934	2.03E-31	8.45E-29	60.56386446
DLC1	-1.101771717	1.440704921	-6.595384037	1.26E-10	4.01E-09	13.36289297
PECAM1	-1.102964146	3.488543624	-4.744495665	2.86E-06	4.03E-05	3.646637921
ARHGEF26	-1.105449507	1.168683046	-6.314123868	6.84E-10	1.89E-08	11.71370055
COL21A1	-1.105709573	0.462293701	-8.472997802	3.94E-16	2.77E-14	25.79048226
CTSF	-1.105756781	3.707937531	-4.589820544	5.85E-06	7.72E-05	2.961553881
CYYR1	-1.106079932	1.733377624	-6.824263516	3.05E-11	1.06E-09	14.74799418
ABL1	-1.107037866	3.761111788	-7.601195503	1.89E-13	9.06E-12	19.72642429
IGSF10	-1.108034881	0.229547326	-11.71066878	1.19E-27	3.09E-25	51.97203053
TMEM47	-1.111732959	3.115655217	-3.516878995	0.00048361	0.003974179	-1.213375477
FOXN3	-1.111893398	2.417113578	-7.802653441	4.74E-14	2.48E-12	21.0843792
MYCT1	-1.113605309	1.297125294	-7.389968274	7.84E-13	3.43E-11	18.33169992
ADRB3	-1.114700875	0.220480919	-12.14289519	2.44E-29	7.88E-27	55.82123018
ZEB2	-1.114736321	0.887384678	-8.309439605	1.30E-15	8.47E-14	24.61632267
WEE1	-1.115035798	2.768394826	-6.462061238	2.83E-10	8.42E-09	12.57379216
PDE7B	-1.116226224	0.925276822	-7.040635146	7.72E-12	2.93E-10	16.09213236

GAS1	-1.117097434	1.831895731	-3.283145997	0.00111128	0.008126793	-1.985256091
HSPG2	-1.117792804	3.238666222	-4.474429775	9.85E-06	0.000123239	2.463863081
ARHGEF37	-1.118266391	1.409526439	-6.108923039	2.27E-09	5.82E-08	10.54808455
C1orf21	-1.118731646	2.440076618	-6.527537245	1.91E-10	5.88E-09	12.95968131
LRCH2	-1.118854921	0.630173891	-8.38821291	7.34E-16	4.92E-14	25.17978261
S100B	-1.119083152	1.47953914	-4.535192915	7.49E-06	9.62E-05	2.724506749
PTPRN2	-1.119585385	0.870093759	-6.214663149	1.23E-09	3.29E-08	11.14472207
SPRY2	-1.119912084	2.34241924	-4.947286388	1.09E-06	1.69E-05	4.575675634
MORN5	-1.121604069	0.175666248	-12.18908238	1.60E-29	5.29E-27	56.23658207
OAT	-1.124195672	3.458846121	-3.424867158	0.000674796	0.005298458	-1.523229713
ODF3L1	-1.125846501	0.433281629	-11.33600738	3.29E-26	7.38E-24	48.6933507
WNT5B	-1.125873211	1.656262791	-3.979216487	8.13E-05	0.000821674	0.460025535
SOX7	-1.125902325	1.572444946	-4.272436319	2.39E-05	0.000272741	1.62048056
CHRDL2	-1.126992398	1.415262118	-3.180059707	0.001580111	0.010968723	-2.309666842
EHD2	-1.12726649	4.627151728	-3.944561898	9.35E-05	0.000931268	0.327921513
CDKN1A	-1.128008965	6.079818962	-4.32385091	1.91E-05	0.0002236	1.831772069
PTH1R	-1.12886355	0.499815359	-10.63495882	1.39E-23	2.34E-21	42.71509542
DUSP8	-1.129509701	1.105549514	-7.076714998	6.12E-12	2.35E-10	16.31950037
ATOH8	-1.12955501	1.140702674	-4.199410761	3.26E-05	0.00036096	1.324366376
CRNN	-1.129865128	0.243933035	-4.427821643	1.21E-05	0.000148146	2.266105527
PNMA1	-1.130661576	3.465370744	-4.775859833	2.47E-06	3.53E-05	3.788047384
CD79B	-1.132370149	1.276922894	-4.146472376	4.08E-05	0.000442199	1.112641856
FMOD	-1.133062022	3.02616016	-3.45313342	0.000609626	0.004850674	-1.428867728
LDB2	-1.134024453	1.274290013	-7.824468977	4.07E-14	2.15E-12	21.23303011
HIPK3	-1.135125382	3.061831377	-7.613980233	1.73E-13	8.40E-12	19.81180309
LRRC32	-1.135621271	2.612207736	-4.339769266	1.78E-05	0.000210113	1.897658728
ATP8B2	-1.137329869	1.613521959	-5.526718374	5.70E-08	1.13E-06	7.418933659
ADAMTSL4	-1.137348573	2.009300892	-3.71100313	0.00023384	0.002098877	-0.534298218
NAP1L2	-1.137642321	0.789420853	-8.078204929	6.84E-15	4.10E-13	22.98456508
PLEKHO1	-1.137685786	3.058745945	-4.796630886	2.24E-06	3.23E-05	3.882156772
CACNB2	-1.138207009	0.485666532	-10.16385187	7.16E-22	1.02E-19	38.82186742
RP11-617F23.1	-1.1382845	1.039672656	-8.443588945	4.89E-16	3.38E-14	25.57815705
MT-ND6	-1.138740516	10.37017663	-3.330756762	0.000941626	0.007052172	-1.832105522
RGCC	-1.139583699	3.774367587	-5.318109386	1.70E-07	3.08E-06	6.363522485
OXER1	-1.143490471	0.96702127	-7.653751337	1.32E-13	6.50E-12	20.07809739
CDC42EP2	-1.144622019	2.914997793	-5.355202239	1.40E-07	2.58E-06	6.548598691
RCSD1	-1.146447723	1.290601087	-5.768991675	1.54E-08	3.39E-07	8.688614677
RP11-404P21.9	-1.147319564	0.746392525	-7.189733174	2.94E-12	1.18E-10	17.03763025
FAM46A	-1.147618984	2.307268762	-6.534970355	1.82E-10	5.64E-09	13.00369014
OSR1	-1.148508129	1.921665459	-3.735774835	0.000212638	0.001928742	-0.445180589
PCDH18	-1.148852896	1.042939939	-7.194175741	2.85E-12	1.15E-10	17.06604096
SCUBE2	-1.149248605	2.328579504	-2.627218948	0.008919511	0.04671123	-3.879903088
TMEM132C	-1.149258266	0.156302799	-16.70987812	1.47E-48	3.74E-45	99.66915626
ZBTB16	-1.151201861	0.2693638	-12.12196542	2.95E-29	9.42E-27	55.63326332
KIAA0513	-1.152328103	1.493948085	-7.404145705	7.13E-13	3.15E-11	18.4243679
NRN1	-1.153991249	1.506453198	-4.307550011	2.05E-05	0.00023793	1.764531783
MIR24-2	-1.153994406	0.364738191	-8.63415187	1.20E-16	9.07E-15	26.96322814
PPP1R15A	-1.156787592	5.386755012	-5.768414228	1.54E-08	3.40E-07	8.685532949
CPEB2	-1.157400912	1.42558559	-8.723833164	6.13E-17	4.73E-15	27.62255593
TCEAL1	-1.157630379	3.533712681	-6.65410442	8.79E-11	2.86E-09	13.71460314
ENPP2	-1.15797788	1.74970226	-4.703664685	3.46E-06	4.80E-05	3.463801848
TBX4	-1.158602492	0.561423378	-6.791862246	3.74E-11	1.28E-09	14.54959972
CTSK	-1.158724428	4.683293	-2.985901715	0.002990661	0.018865141	-2.89383243
LGALS4	-1.159027309	1.379689371	-2.70822036	0.007037226	0.03849377	-3.667846572
SEMA3G	-1.160747335	1.244540356	-7.695808572	9.90E-14	4.93E-12	20.36084022
RBMS3	-1.163001387	0.686933012	-9.499850345	1.54E-19	1.66E-17	33.51976274
SEMA3E	-1.165089349	0.543166238	-8.832250539	2.71E-17	2.19E-15	28.42593682
TRPA1	-1.165197716	0.741346315	-5.656494204	2.84E-08	5.96E-07	8.093226419
NGFR	-1.166080981	1.18567002	-4.149458285	4.03E-05	0.000437342	1.124517995
SERPINE2	-1.166285633	1.682646155	-3.920109244	0.000103125	0.001014513	0.235353607
FBN1	-1.166294906	1.946156427	-4.076960285	5.45E-05	0.000573356	0.838395354
PBX1	-1.166633665	2.275084701	-5.646864804	2.99E-08	6.24E-07	8.042730795
COL16A1	-1.16782382	2.759385272	-3.629028579	0.000319072	0.002753826	-0.825240513
GALNT15	-1.168891187	0.610745019	-7.541758767	2.83E-13	1.32E-11	19.33092871
SERPING1	-1.17059027	5.362325638	-3.102367366	0.002047674	0.013699727	-2.547641077
STOM	-1.171155094	5.141816224	-3.974384612	8.29E-05	0.000836039	0.441541971
ARL4D	-1.171655788	3.876712182	-3.663916297	0.000279738	0.002456096	-0.702163228
MEIS1	-1.171941689	1.396764127	-8.560128267	2.07E-16	1.53E-14	26.42261175
RUSC2	-1.175017497	2.163535013	-6.48079695	2.53E-10	7.61E-09	12.68388744
RECK	-1.176302811	0.957369303	-8.973640661	9.26E-18	7.80E-16	29.48387949

HAND2-AS1	-1.176794284	0.206035309	-13.91096415	1.59E-36	1.07E-33	72.20875145
SYNE1	-1.178464287	0.642206918	-11.8120142	4.83E-28	1.31E-25	52.8683139
KCNJ8	-1.178916383	1.55841378	-5.453703133	8.38E-08	1.61E-06	7.045513423
CRISP3	-1.179541237	1.019299351	-3.245082448	0.001266867	0.009084813	-2.106188278
OSBPL10	-1.180512247	1.507593143	-7.531907092	3.02E-13	1.40E-11	19.26560376
ILK	-1.180609016	1.80262756	-8.064117749	7.56E-15	4.51E-13	22.8862416
ETS2	-1.181553817	5.478912207	-4.922840108	1.22E-06	1.88E-05	4.461839658
LSP1	-1.182278952	3.291202421	-3.309482734	0.001014217	0.007516766	-1.900796916
ATP1B2	-1.183024556	0.554128723	-11.45745648	1.13E-26	2.67E-24	49.75004525
CACNA2D1	-1.184073719	0.824313284	-6.640830373	9.54E-11	3.09E-09	13.63487588
JUND	-1.184420227	6.40442784	-6.005580351	4.09E-09	1.00E-07	9.973275586
ADRA2A	-1.186080227	0.949619847	-6.368896729	4.94E-10	1.40E-08	12.03022912
NFIB	-1.186126196	2.032773785	-5.984921801	4.60E-09	1.12E-07	9.859359874
MSX1	-1.186529841	1.420875716	-5.448297189	8.62E-08	1.65E-06	7.018037315
SCN7A	-1.187669494	0.183130736	-14.11972771	2.12E-37	1.53E-34	74.20209828
FAM149A	-1.188163716	0.859141953	-7.330705105	1.16E-12	4.97E-11	17.94582382
NAP1L5	-1.188803171	1.586187175	-8.180546446	3.30E-15	2.06E-13	23.70263392
DOK6	-1.18902661	0.296348759	-11.64961579	2.06E-27	5.22E-25	51.43398691
COL6A3	-1.189235049	3.997365084	-3.005977767	0.002803973	0.017898278	-2.835061672
THRA	-1.189972971	2.236554479	-7.344261141	1.06E-12	4.57E-11	18.03387831
PDLIM7	-1.191275568	4.009211268	-4.794678806	2.26E-06	3.26E-05	3.873296694
KIAA1462	-1.19170765	1.828568094	-5.287916771	1.98E-07	3.55E-06	6.21370626
NECAB1	-1.191710016	0.46368709	-10.12026689	1.03E-21	1.44E-19	38.46703352
LIF	-1.194344091	2.156052188	-4.102669319	4.90E-05	0.000521194	0.939326487
APCDD1	-1.194695629	2.528756775	-4.310063548	2.03E-05	0.000235588	1.77488481
SLC22A3	-1.195677882	0.926084963	-5.596632076	3.92E-08	8.00E-07	7.780516352
STC1	-1.199691937	2.691918846	-4.291881387	2.20E-05	0.000252999	1.700118915
PLCD4	-1.200060728	0.661931162	-13.02116639	7.39E-33	3.54E-30	63.84281954
EML1	-1.201318469	1.149940885	-7.155292503	3.68E-12	1.46E-10	16.81784455
TEAD1	-1.201936758	2.618695726	-6.922402383	1.64E-11	5.94E-10	15.35351002
NBEA	-1.20289786	0.554511832	-9.245891161	1.13E-18	1.08E-16	31.55290524
TNFSF12	-1.203884581	3.156487207	-5.982816264	4.66E-09	1.13E-07	9.847768091
SAMD4A	-1.205127944	1.047624262	-8.243518585	2.10E-15	1.34E-13	24.14773596
MEF2C	-1.206847114	1.10207629	-8.501263135	3.20E-16	2.29E-14	25.99504509
FBXO32	-1.207043803	2.913884776	-4.514845077	8.21E-06	0.00010476	2.636868993
LRFN5	-1.207397212	0.299731105	-11.1679634	1.43E-25	3.02E-23	47.24120214
NFASC	-1.208787694	0.547121577	-10.96778095	8.08E-25	1.58E-22	45.52680882
TRIB1	-1.209190316	4.561970596	-5.509631607	6.24E-08	1.22E-06	7.331161443
FXYD1	-1.212484905	0.326992667	-14.85582308	1.63E-40	1.53E-37	81.31175484
VCL	-1.214169581	4.136409024	-6.696147827	6.78E-11	2.24E-09	13.96797719
ANK2	-1.215249472	0.374678039	-11.57424677	4.02E-27	9.94E-25	50.77177603
PPP1R3B	-1.216964089	2.620076197	-6.165784193	1.63E-09	4.28E-08	10.86786012
PLA2G4A	-1.217519081	2.321776768	-4.884640442	1.47E-06	2.22E-05	4.28496734
AKT3	-1.219230594	1.575743178	-5.808810689	1.23E-08	2.78E-07	8.901756341
KIT	-1.223008675	1.289317784	-4.460739592	1.05E-05	0.000130028	2.405580305
GPC6	-1.223372826	1.159348396	-5.345132282	1.48E-07	2.71E-06	6.498243105
SRGN	-1.229441175	5.198109508	-3.240398781	0.001287348	0.009207933	-2.120976128
AMOTL1	-1.230476203	2.487667884	-5.636660691	3.16E-08	6.57E-07	7.989302183
NFATC4	-1.237280568	1.890835064	-6.50178815	2.23E-10	6.78E-09	12.80754663
GLIPR2	-1.238109138	2.562711283	-4.563014186	6.61E-06	8.61E-05	2.844910918
DMPK	-1.238448836	3.217082137	-7.236309205	2.17E-12	8.95E-11	17.33617061
C20orf166-AS1	-1.24386922	0.207965873	-13.79975817	4.62E-36	2.93E-33	71.15140199
ITGA9	-1.24840907	1.053695391	-8.214024095	2.59E-15	1.64E-13	23.93895385
CSDC2	-1.249832474	0.884830985	-5.816169875	1.18E-08	2.67E-07	8.941285175
LPPR4	-1.250124877	0.461787126	-10.37429121	1.25E-22	1.89E-20	40.54800879
TMEM88	-1.250197994	2.059640762	-6.690975842	7.00E-11	2.31E-09	13.93673864
AEBP1	-1.252379744	4.885370874	-2.704739139	0.00711011	0.038812888	-3.677088164
NPY6R	-1.254504919	0.17818666	-12.65665937	2.20E-31	9.11E-29	60.48287962
SH3BGRL	-1.255013453	5.080514633	-5.611052744	3.63E-08	7.45E-07	7.855585614
PLA2G5	-1.256917408	0.637657862	-7.601373199	1.89E-13	9.06E-12	19.72761023
KCNK3	-1.258385982	0.503352449	-7.957478588	1.61E-14	9.07E-13	22.14603647
PITX1	-1.259338219	3.339753178	-3.786368637	0.000174836	0.00162189	-0.261443069
RND3	-1.261046302	4.208550386	-5.039519386	6.91E-07	1.12E-05	5.009679665
SGCG	-1.261317289	0.213178257	-13.94384408	1.16E-36	7.95E-34	72.52197919
ROR2	-1.262661434	1.380442542	-5.202838259	3.06E-07	5.25E-06	5.795571926
CCDC3	-1.265259463	2.300602286	-5.748264962	1.72E-08	3.77E-07	8.578165142
STARD13	-1.265985678	1.223287439	-8.453224484	4.56E-16	3.17E-14	25.64766564
PPM1L	-1.266096203	1.432141136	-7.428669384	6.06E-13	2.70E-11	18.58498503
CREB3L1	-1.266924534	2.613615078	-4.039823607	6.35E-05	0.000656687	0.69363645
IGFBP2	-1.267464513	3.158641883	-3.253253807	0.001231856	0.008867512	-2.080340009

TLN1	-1.268294127	4.858001759	-7.286608529	1.56E-12	6.56E-11	17.66026314
PLSCR4	-1.269739708	1.439979258	-6.858322938	2.46E-11	8.70E-10	14.95735726
MPZ	-1.270598176	0.93214798	-9.496232587	1.59E-19	1.70E-17	33.49149989
CCL14	-1.270921235	0.315288908	-13.09578596	3.67E-33	1.80E-30	64.53571641
ARID5B	-1.271542009	2.968883844	-6.946802696	1.41E-11	5.14E-10	15.5051297
FOLR2	-1.271723206	2.473640701	-3.770810876	0.000185726	0.001712572	-0.318189069
ID2	-1.274859142	4.043051151	-4.417926561	1.27E-05	0.0001541	2.224363681
SGCD	-1.274943096	0.532340171	-9.46015986	2.11E-19	2.21E-17	33.21007276
SCARA3	-1.277757616	2.836899932	-3.993321588	7.67E-05	0.000779044	0.514101518
GNAZ	-1.278284603	0.771441789	-7.381011583	8.32E-13	3.64E-11	18.2732269
SELP	-1.279476106	1.140131513	-5.790186964	1.37E-08	3.05E-07	8.801912277
SMIM10	-1.28108647	1.873050582	-6.398205247	4.15E-10	1.20E-08	12.20052748
CPE	-1.281636822	2.851154358	-4.322078716	1.93E-05	0.000225012	1.824450602
PPP1R1B	-1.281982559	1.466566299	-3.334959527	0.00092787	0.006960751	-1.818485864
CD55	-1.284033522	4.355152509	-4.964987626	9.96E-07	1.56E-05	4.658416281
TBX20	-1.285414841	0.317154854	-10.61242586	1.68E-23	2.79E-21	42.52652789
RGAG4	-1.286212165	0.848280464	-8.022118124	1.02E-14	5.97E-13	22.59384728
FGF10	-1.286444305	0.222222902	-14.11470993	2.23E-37	1.59E-34	74.15406088
PDE4D	-1.287155541	1.163296785	-10.02948041	2.16E-21	2.89E-19	37.73091812
ACKR3	-1.287803399	4.251037366	-3.895023874	0.00011399	0.00110926	0.140946887
ARID5A	-1.291319338	2.975162426	-6.842392936	2.72E-11	9.52E-10	14.85933172
HAND1	-1.291559916	0.282478379	-8.957624893	1.05E-17	8.78E-16	29.36346639
CTD-3252C9.4	-1.293170946	3.519850244	-5.114553435	4.77E-07	7.93E-06	5.367994738
KCTD12	-1.293314591	3.089735136	-5.177441236	3.48E-07	5.91E-06	5.671909415
C1orf95	-1.293348531	0.318993147	-9.797690969	1.42E-20	1.71E-18	35.87019458
PDE4B	-1.297076146	0.976353914	-7.865600023	3.06E-14	1.65E-12	21.51413936
CRY2	-1.298856924	2.339338068	-11.48132026	9.14E-27	2.20E-24	49.95837513
PDE1A	-1.299886869	0.557324059	-10.97659085	7.49E-25	1.48E-22	45.60189744
RP11-753H16.3	-1.300743644	0.294743848	-10.23559658	3.95E-22	5.73E-20	39.40796706
TPSD1	-1.301015331	0.549784124	-7.87559703	2.85E-14	1.55E-12	21.5826296
TGFB3	-1.301067311	2.096454844	-4.998741051	8.45E-07	1.34E-05	4.816917912
TNFAIP3	-1.302702573	3.288456013	-4.430952437	1.19E-05	0.000146319	2.279330337
FYCO1	-1.303088455	2.625980931	-8.201383788	2.84E-15	1.78E-13	23.84964317
NTN1	-1.303494813	1.000740698	-5.996701427	4.30E-09	1.05E-07	9.924274709
KANK1	-1.30361304	2.408314058	-6.616309869	1.11E-10	3.56E-09	13.4879394
NCALD	-1.306165288	1.011726333	-8.508635414	3.03E-16	2.18E-14	26.04847935
JAZF1	-1.306506635	1.641343739	-7.560595513	2.49E-13	1.17E-11	19.45601359
LINC00675	-1.306641895	1.621260336	-3.578042377	0.000385991	0.00326007	-1.003118883
CPXM1	-1.307537871	2.843655092	-3.40649253	0.000720586	0.005603738	-1.584176638
ASPA	-1.308109663	0.318601719	-15.07195507	1.94E-41	2.05E-38	83.4212601
BVES	-1.309816846	0.793974235	-7.421029088	6.37E-13	2.83E-11	18.53490128
LIFR	-1.310185245	1.02008511	-7.369466879	8.99E-13	3.91E-11	18.19793901
RARRES2	-1.310523597	4.162276861	-3.359537964	0.00085109	0.00646534	-1.738509742
CDIP1	-1.31113146	2.072269112	-5.439665058	9.02E-08	1.72E-06	6.97421297
CSPG4	-1.312070633	2.217959395	-4.790555796	2.30E-06	3.32E-05	3.854593866
TSPYL2	-1.316650145	2.634876484	-8.098771946	5.91E-15	3.58E-13	23.12834119
NDNF	-1.318806195	0.496696668	-8.88090289	1.88E-17	1.54E-15	28.78867635
NES	-1.321572405	2.81102464	-5.033719335	7.11E-07	1.15E-05	4.982177686
ACOX2	-1.324360776	0.562181686	-10.80506163	3.27E-24	5.93E-22	44.14600165
CD69	-1.324379783	1.331883678	-5.260985613	2.28E-07	4.03E-06	6.080704173
ARHGAP6	-1.324936091	0.730973302	-7.610742401	1.77E-13	8.58E-12	19.79016994
RP11-6O2.3	-1.327149398	0.307763501	-13.20625868	1.30E-33	6.77E-31	65.56459087
P2RY14	-1.327834085	0.546509018	-11.91393109	1.93E-28	5.61E-26	53.77356226
ADH1C	-1.330822893	1.315288047	-3.3941911	0.000752843	0.005819708	-1.624805873
TGFBR2	-1.331220395	3.994501569	-6.177767484	1.52E-09	4.02E-08	10.93556755
GNAO1	-1.332395641	0.451777159	-9.844787141	9.73E-21	1.20E-18	36.24606602
DAPL1	-1.33386199	1.012467828	-3.904350768	0.00010983	0.001073781	0.175982028
EMP3	-1.337146065	3.641919535	-4.011394479	7.13E-05	0.000729328	0.583648477
AXL	-1.338250983	2.783962903	-4.306371907	2.06E-05	0.00023891	1.759681182
RBP7	-1.339462042	1.950104281	-5.113002973	4.80E-07	7.99E-06	5.360543324
ADARB1	-1.34098351	1.66417087	-6.845289906	2.67E-11	9.39E-10	14.87714471
CLEC10A	-1.341436733	1.020865689	-6.424894299	3.54E-10	1.03E-08	12.35616534
PHYHD1	-1.341511373	1.321179168	-5.690717964	2.36E-08	5.02E-07	8.273290398
SRF	-1.34310841	4.111002805	-10.99625723	6.32E-25	1.27E-22	45.76963898
RASSF3	-1.343457213	3.25539703	-7.329148446	1.17E-12	5.02E-11	17.93572045
AFF3	-1.344022772	0.261519174	-13.46232334	1.15E-34	6.67E-32	67.96304416
PDLIM4	-1.344573372	2.415455673	-4.365294071	1.60E-05	0.000189956	2.003769009
RNF122	-1.346267161	2.53572781	-7.789417543	5.19E-14	2.70E-12	20.99434129
RPS6KA2	-1.34663867	1.965789121	-7.865187385	3.07E-14	1.65E-12	21.51131374
KLF6	-1.347508617	4.957231172	-6.543448583	1.73E-10	5.39E-09	13.05393667

GFRA3	-1.348241566	0.72753735	-7.056152002	6.99E-12	2.66E-10	16.18980405
RASGRP2	-1.348600511	0.793109613	-8.319712225	1.21E-15	7.89E-14	24.68958562
ODC1	-1.348740014	4.58538079	-4.903240342	1.34E-06	2.04E-05	4.370935095
DKK1	-1.351296131	2.718749279	-2.903652018	0.00388035	0.023519359	-3.130664407
SSPN	-1.355386896	1.802321182	-7.717141517	8.55E-14	4.28E-12	20.50470443
SYT11	-1.35557555	1.571547368	-6.51084802	2.11E-10	6.47E-09	12.86101944
MMP2	-1.356111954	5.668428941	-3.462422809	0.000589526	0.004710637	-1.397696652
THSD4	-1.358274222	1.133907187	-9.266923626	9.63E-19	9.26E-17	31.71446331
DPYSL2	-1.358813913	2.624318656	-5.926642922	6.39E-09	1.51E-07	9.539785415
VIM	-1.360313697	5.940089285	-4.173228714	3.64E-05	0.000399658	1.219343353
DCHS1	-1.360861863	1.284356959	-7.57140126	2.31E-13	1.09E-11	19.52787616
TMEM100	-1.361076976	0.437220571	-10.82762812	2.69E-24	4.93E-22	44.33680224
PALM	-1.362705336	1.594302003	-5.215134709	2.87E-07	4.96E-06	5.855636765
LYNX1	-1.364490465	1.57897626	-4.899224797	1.37E-06	2.08E-05	4.352350766
MCAM	-1.366032247	3.57188168	-5.907702774	7.11E-09	1.67E-07	9.436496313
TACC1	-1.367750885	3.003933089	-5.609644547	3.66E-08	7.49E-07	7.848247665
EMCN	-1.368001122	1.208369744	-8.373198175	8.19E-16	5.47E-14	25.07208948
ACTA2-AS1	-1.368123815	0.558753086	-9.686114319	3.50E-20	4.00E-18	34.98425678
TSHZ3	-1.371849221	1.246379624	-7.145294426	3.93E-12	1.55E-10	16.75419602
FOSL1	-1.372651585	3.857487757	-3.848128309	0.000137271	0.001307814	-0.034026668
NPR1	-1.372947885	1.156142289	-7.598359561	1.93E-13	9.23E-12	19.70750011
HEPH	-1.374644958	1.324023131	-6.27559638	8.59E-10	2.35E-08	11.49240911
C3orf70	-1.374748305	0.911576056	-8.048714594	8.44E-15	5.01E-13	22.77887719
SYNPO	-1.374771971	2.720434556	-6.5747147	1.43E-10	4.51E-09	13.23969574
WLS	-1.375974814	3.770811622	-5.031851637	7.18E-07	1.16E-05	4.97332764
RP11-887P2.5	-1.376431339	0.195034912	-14.8909894	1.15E-40	1.12E-37	81.65434909
PJA2	-1.376910887	3.675545256	-8.821472839	2.94E-17	2.37E-15	28.34576653
ITPKB	-1.377494431	2.634292415	-9.747805592	2.13E-20	2.51E-18	35.47330206
NFIL3	-1.377575993	3.804957401	-6.366292061	5.02E-10	1.42E-08	12.01512579
TACC2	-1.380920865	1.855568575	-8.644097999	1.11E-16	8.47E-15	27.03611641
EPHX2	-1.38486487	1.554634045	-6.743507949	5.06E-11	1.70E-09	14.25493632
CPQ	-1.385077448	2.775797892	-5.971454714	4.97E-09	1.20E-07	9.785277833
CXCL14	-1.38764979	3.617042337	-2.867603117	0.004341505	0.025800249	-3.232461157
PDGFD	-1.388104884	1.384307991	-7.255166937	1.91E-12	7.97E-11	17.45747142
MEOX1	-1.38903834	0.775564741	-8.452318855	4.59E-16	3.19E-14	25.64113023
CFH	-1.389375725	2.896817883	-4.657622297	4.28E-06	5.82E-05	3.25933811
DNAJB4	-1.389862755	2.292194255	-8.298865979	1.40E-15	9.10E-14	24.54098102
DENND2A	-1.391911189	1.243698867	-8.011612384	1.10E-14	6.36E-13	22.5208837
LPAR1	-1.392258954	2.086301331	-7.023382593	8.63E-12	3.26E-10	15.98373479
CYP27A1	-1.39368514	2.292344072	-5.031404774	7.20E-07	1.16E-05	4.97121062
JUNB	-1.39528268	7.503652273	-6.434274333	3.35E-10	9.80E-09	12.41099178
CAP2	-1.395370679	1.599663012	-6.809647532	3.35E-11	1.15E-09	14.65840603
RRAD	-1.397938629	2.353621566	-3.425964733	0.000672149	0.005279801	-1.51957934
COL6A1	-1.398482082	5.730598077	-3.548831542	0.000430047	0.003583946	-1.10396082
CNRIP1	-1.399419368	1.28946775	-7.819713634	4.21E-14	2.22E-12	21.20060078
MMRN1	-1.399849666	0.518761455	-9.932761388	4.76E-21	6.11E-19	36.9512013
RSPO3	-1.402158162	0.705769231	-7.639588618	1.46E-13	7.12E-12	19.98314793
FAM189A2	-1.403360165	0.738351904	-10.57775846	2.26E-23	3.70E-21	42.23686585
GFRA1	-1.404511742	0.347349477	-12.47928528	1.13E-30	4.25E-28	58.86334761
CD200	-1.406250349	1.806719645	-5.960552745	5.28E-09	1.27E-07	9.725409674
RGS1	-1.407656673	3.077354085	-4.093014971	5.10E-05	0.00054055	0.901355732
PRKCB	-1.408407628	0.767603112	-8.852289284	2.33E-17	1.89E-15	28.57517474
PTX3	-1.409276546	1.078207991	-4.918679986	1.25E-06	1.91E-05	4.442517787
RP11-554A11.4	-1.409480635	0.555916347	-11.10241186	2.52E-25	5.24E-23	46.6779328
AHNAK	-1.410131908	5.051467441	-5.686682253	2.41E-08	5.13E-07	8.252008527
PRKG1	-1.412098965	0.740111864	-10.09298573	1.28E-21	1.77E-19	38.2454055
LMCD1	-1.415213613	1.884054517	-5.927397474	6.37E-09	1.51E-07	9.54390612
SGCE	-1.416040396	2.48430499	-5.044679496	6.74E-07	1.09E-05	5.034170862
ABLIM1	-1.416158865	3.261687151	-6.511611113	2.10E-10	6.44E-09	12.86552613
ANGPTL2	-1.416576752	3.248460224	-4.615616734	5.20E-06	6.93E-05	3.074385088
TMEM119	-1.425608409	2.221342412	-4.817969613	2.02E-06	2.95E-05	3.979219548
DSTN	-1.425685983	6.588615313	-9.376048421	4.10E-19	4.11E-17	32.55657815
FAIM2	-1.426076535	0.310452767	-13.68851944	1.34E-35	8.05E-33	70.09695572
LUM	-1.426248874	5.80827435	-3.195137125	0.001501684	0.010489149	-2.262833819
PCDH7	-1.429085303	1.393758794	-5.501287114	6.52E-08	1.28E-06	7.288382558
EBF1	-1.430281015	0.808570245	-10.30593286	2.20E-22	3.26E-20	39.98496964
IL6ST	-1.431496794	3.090867229	-7.532364552	3.02E-13	1.40E-11	19.26863566
AARD	-1.433940158	0.310135336	-10.50917234	4.02E-23	6.37E-21	41.66542426
NCS1	-1.439098128	3.173372141	-6.821725298	3.10E-11	1.07E-09	14.73242521
RBPMS	-1.440934297	3.009149342	-6.574214252	1.43E-10	4.52E-09	13.23671678

LINC00865	-1.441388612	1.19366683	-8.611657707	1.42E-16	1.07E-14	26.79860092
PRDM6	-1.445903244	0.558391601	-11.65193795	2.02E-27	5.14E-25	51.45442515
LGI4	-1.446063579	0.852770348	-10.59952555	1.88E-23	3.10E-21	42.41867568
C1R	-1.446950926	5.069089697	-4.061025989	5.82E-05	0.000607536	0.776133321
TSC22D3	-1.447352077	4.185880314	-6.069189889	2.85E-09	7.19E-08	10.32610728
MAFF	-1.447869553	3.401231526	-6.688183922	7.13E-11	2.34E-09	13.91988369
ATP2B4	-1.448829019	3.553785524	-6.111038678	2.24E-09	5.75E-08	10.55993805
PRICKLE2	-1.450019509	1.185260483	-9.810191885	1.29E-20	1.56E-18	35.9698531
NXPH3	-1.45282058	0.683306882	-9.592866973	7.37E-20	8.17E-18	34.24881914
MTURN	-1.453530106	2.261604263	-8.580204234	1.79E-16	1.33E-14	26.56890913
OMD	-1.457652954	0.479880346	-9.424978416	2.79E-19	2.89E-17	32.93627076
GRASP	-1.458240347	1.800887529	-7.859520009	3.19E-14	1.71E-12	21.47251642
EDNRA	-1.459531448	1.665581914	-6.829776018	2.95E-11	1.02E-09	14.78182286
MT1M	-1.45984163	1.274388723	-4.797541456	2.23E-06	3.22E-05	3.886290762
INMT	-1.460500516	1.030871468	-8.707212036	6.94E-17	5.33E-15	27.50000067
RAB9B	-1.460765286	0.628366784	-10.85291581	2.17E-24	4.06E-22	44.55087799
RERGL	-1.460942607	0.342214889	-14.65889054	1.12E-39	9.63E-37	79.39795662
RHOJ	-1.461052355	1.496870242	-8.431100105	5.36E-16	3.66E-14	25.48814935
GSTM5	-1.463166274	0.686008084	-8.345325697	1.00E-15	6.62E-14	24.87254057
MIR4697HG	-1.46376571	0.400847413	-11.26206826	6.28E-26	1.37E-23	48.05296867
WWTR1	-1.468198185	2.716973136	-7.894357954	2.50E-14	1.37E-12	21.71133677
ADAMTS4	-1.469639386	1.687785808	-5.92547142	6.44E-09	1.52E-07	9.533388564
RANBP3L	-1.471554368	0.303279434	-12.30665317	5.50E-30	1.94E-27	57.29726486
RP11-553L6.5	-1.471803899	2.416192133	-8.356010159	9.28E-16	6.14E-14	24.94897806
FAM43A	-1.474940168	2.000443869	-6.982529828	1.12E-11	4.16E-10	15.72789729
STON1	-1.475442796	1.1024855	-9.209155132	1.51E-18	1.40E-16	31.27130731
ADAMTSL3	-1.476453228	0.280879455	-16.3586685	5.12E-47	1.11E-43	96.15145077
HIF3A	-1.477714473	0.42384126	-9.710667233	2.87E-20	3.35E-18	35.17865892
AC053503.12	-1.480231254	0.262302899	-11.45631582	1.14E-26	2.68E-24	49.74009305
ISLR	-1.480652147	3.696790897	-3.151759926	0.001737622	0.011899427	-2.397000389
ACACB	-1.481067711	0.855106554	-11.85577428	3.26E-28	9.06E-26	53.256524
WISP2	-1.481726131	0.877956136	-6.170394601	1.59E-09	4.18E-08	10.89389664
PDZD4	-1.486369918	0.635792143	-9.2334579	1.25E-18	1.18E-16	31.45751538
KLHL41	-1.486503165	0.287490191	-14.69881524	7.59E-40	6.71E-37	79.78528626
CSGALNACT1	-1.487885121	1.38189804	-10.17084161	6.76E-22	9.65E-20	38.87885846
BDKRB1	-1.490628423	0.815194316	-9.070235882	4.42E-18	3.80E-16	30.21321233
SSC5D	-1.492274552	1.252908987	-6.478981801	2.56E-10	7.67E-09	12.67320978
SGK1	-1.495461082	2.957349579	-4.991648663	8.75E-07	1.38E-05	4.783533766
BOC	-1.496135147	0.833421387	-8.047716919	8.50E-15	5.04E-13	22.77192831
SPEG	-1.496231051	0.755938487	-8.571317827	1.91E-16	1.41E-14	26.50412243
SOBP	-1.496614229	0.641381438	-11.92238893	1.79E-28	5.23E-26	53.84886079
TIPARP	-1.49676903	3.074627078	-7.373350853	8.76E-13	3.82E-11	18.22325788
OLFM1	-1.49903917	0.636995178	-9.320899621	6.31E-19	6.23E-17	32.1301834
TPPP3	-1.502168526	2.265657462	-5.455339128	8.31E-08	1.59E-06	7.053833156
TUBB6	-1.503417533	3.844450744	-4.063070339	5.77E-05	0.000602975	0.78410885
NDN	-1.503689982	2.793453828	-5.08116539	5.63E-07	9.23E-06	5.207975772
CLIC4	-1.505384154	4.538308506	-5.042285129	6.82E-07	1.10E-05	5.022803826
LHFP	-1.505924909	3.133126385	-6.152708981	1.76E-09	4.60E-08	10.79410845
NFIA	-1.513809192	1.880472378	-8.674849832	8.84E-17	6.76E-15	27.26184629
GAS7	-1.514900608	1.284975857	-7.283724672	1.59E-12	6.68E-11	17.64163446
FGF2	-1.515554206	0.639133855	-10.1606489	7.35E-22	1.04E-19	38.7957598
SLMAP	-1.516950838	2.358438847	-9.776283697	1.69E-20	2.01E-18	35.69971975
PDGFRA	-1.51829842	1.577570495	-6.814844758	3.24E-11	1.11E-09	14.69024458
RNF150	-1.519331243	0.541755209	-11.48157305	9.12E-27	2.20E-24	49.96058326
RERG	-1.520644803	0.930532734	-9.129537125	2.80E-18	2.46E-16	30.66356849
SLC9A9	-1.521010968	1.354599141	-8.752468734	4.94E-17	3.84E-15	27.83407992
CCL19	-1.522513852	2.123429891	-3.26881383	0.001167656	0.008475413	-2.030948394
ARMCX1	-1.522785763	2.033896589	-6.099590505	2.39E-09	6.12E-08	10.4958373
PER2	-1.52435437	1.748303689	-10.99157727	6.58E-25	1.31E-22	45.7297068
FBXL22	-1.524681941	0.698146476	-10.66388096	1.09E-23	1.85E-21	42.95746926
PRIMA1	-1.524799602	0.447085046	-12.3749481	2.94E-30	1.06E-27	57.9156047
S1PR1	-1.526806246	2.167774781	-7.123728849	4.52E-12	1.77E-10	16.6171458
KCNE4	-1.527551245	1.15546318	-7.304449664	1.38E-12	5.86E-11	17.77563777
GREM2	-1.527863147	0.422224212	-11.98826244	9.90E-29	2.99E-26	54.43622469
PELI2	-1.528652284	1.050529363	-9.400018086	3.39E-19	3.46E-17	32.74241917
TIMP2	-1.529670018	4.714768907	-4.151284209	4.00E-05	0.000434326	1.131784299
RAB23	-1.53299554	1.537892951	-8.015555062	1.07E-14	6.22E-13	22.5482578
HBA2	-1.533351284	2.327896923	-4.624654263	4.99E-06	6.68E-05	3.114050039
TUBA1A	-1.534009914	4.725340749	-4.725427846	3.13E-06	4.37E-05	3.561077609
CLEC3A	-1.534323587	0.268505485	-9.864791627	8.27E-21	1.03E-18	36.40606256

TSC22D1	-1.535839192	4.302640605	-8.176446283	3.39E-15	2.11E-13	23.67373892
NNAT	-1.536618983	1.565696729	-3.583844338	0.00037776	0.003198419	-0.982996656
OLFML1	-1.538115334	1.144240383	-9.107300591	3.32E-18	2.89E-16	30.49446461
AGTR1	-1.53845666	0.433107948	-11.09955471	2.59E-25	5.35E-23	46.65342316
MYC	-1.538500587	4.622503242	-4.584638766	5.99E-06	7.88E-05	2.93895808
C8orf88	-1.540585646	1.00484394	-6.84483194	2.68E-11	9.40E-10	14.87432835
EVA1C	-1.545166354	1.717512427	-6.74333508	5.06E-11	1.70E-09	14.25388593
ABCA8	-1.549129205	0.400045074	-13.76766288	6.28E-36	3.90E-33	70.84683321
APBB1	-1.549395913	1.562443582	-7.318961202	1.26E-12	5.35E-11	17.86964209
HAS1	-1.550001918	0.573266788	-7.597870481	1.93E-13	9.26E-12	19.70423703
GNAL	-1.552459393	0.77054295	-11.45181078	1.19E-26	2.78E-24	49.70079182
SELM	-1.552668647	3.589351097	-4.947043022	1.09E-06	1.69E-05	4.574539908
NACC2	-1.555068998	2.038245189	-9.423517134	2.82E-19	2.91E-17	32.92491262
EPHA7	-1.556524889	0.575821198	-9.818134004	1.21E-20	1.47E-18	36.03320996
F3	-1.557639613	3.590496594	-3.557922519	0.000415855	0.003481574	-1.072660307
TWIST2	-1.558427388	0.976697984	-7.372343081	8.82E-13	3.84E-11	18.21668742
FBLN1	-1.562642664	6.002241507	-3.709196715	0.000235461	0.002112457	-0.540775173
MXRA7	-1.567294841	2.611393832	-8.038838673	9.05E-15	5.34E-13	22.71011851
SLIT2	-1.567771605	0.676708914	-10.39270893	1.07E-22	1.63E-20	40.70008637
CYP1B1	-1.569428073	1.563559238	-4.96411148	1.00E-06	1.57E-05	4.654314738
SLC2A3	-1.570367048	2.560478184	-5.253999465	2.36E-07	4.16E-06	6.046299716
CRYM	-1.571080809	0.728863227	-8.062489025	7.65E-15	4.56E-13	22.8748818
ADAMTS8	-1.57337477	0.514010168	-11.27159327	5.78E-26	1.27E-23	48.13533798
FCER1A	-1.576260388	0.929842086	-7.901923714	2.37E-14	1.31E-12	21.7633052
EDNRB	-1.576332771	1.434129445	-7.523914592	3.19E-13	1.47E-11	19.21265462
HSPA2	-1.576546375	1.973703887	-6.906481669	1.82E-11	6.52E-10	15.25481035
SELENBP1	-1.58026853	3.008387236	-4.541035442	7.30E-06	9.41E-05	2.749736485
FAXDC2	-1.583569319	0.877989286	-12.13890743	2.53E-29	8.12E-27	55.78540468
C2CD4B	-1.587761451	0.916476509	-7.932316149	1.92E-14	1.07E-12	21.97244001
AKR1B10	-1.589288772	2.543319077	-2.645487052	0.008459427	0.044706787	-3.832622245
SLC25A23	-1.594020011	2.859503638	-7.212077134	2.54E-12	1.03E-10	17.18066138
PDE5A	-1.596610078	1.172286556	-9.963287349	3.71E-21	4.82E-19	37.1967864
CD248	-1.596884066	3.606916612	-5.135397347	4.29E-07	7.20E-06	5.468362905
BMP5	-1.60059174	0.546135195	-9.628018259	5.56E-20	6.25E-18	34.52552114
SH3BGR	-1.600777819	1.685557842	-9.451591987	2.26E-19	2.35E-17	33.14333149
NR2F1	-1.608578521	1.902874759	-6.93923598	1.48E-11	5.37E-10	15.45806591
EPHA3	-1.60925307	0.855481077	-9.964214382	3.69E-21	4.79E-19	37.2042518
PLP1	-1.610029755	0.223538499	-19.86852216	1.25E-62	2.44E-58	131.7860579
RBM24	-1.610895926	0.396071612	-13.17732264	1.71E-33	8.82E-31	65.29474954
BAG2	-1.612202129	1.533847474	-8.323049602	1.18E-15	7.71E-14	24.71340135
ALDH1B1	-1.613372473	3.865094114	-6.563292957	1.53E-10	4.81E-09	13.17175288
AF131217.1	-1.618415685	0.271219367	-16.38861403	3.79E-47	8.50E-44	96.45075703
FBXL7	-1.618846993	1.120736037	-9.921341728	5.23E-21	6.65E-19	36.85944908
GLP2R	-1.618948661	0.207627424	-16.87178035	2.86E-49	7.94E-46	101.295906
CYTL1	-1.619196228	0.915241086	-8.03894293	9.04E-15	5.34E-13	22.71084405
CYGB	-1.62082242	2.750806958	-6.85103485	2.58E-11	9.08E-10	14.91248724
MIR22HG	-1.626091229	2.805375195	-8.15200857	4.04E-15	2.50E-13	23.50173809
SEPP1	-1.626906744	2.186728956	-5.462919388	7.98E-08	1.54E-06	7.09241029
PTGFR	-1.628687107	0.496516921	-11.72978762	1.01E-27	2.64E-25	52.14081472
SVEP1	-1.630098244	0.735874969	-13.35282488	3.26E-34	1.79E-31	66.93512609
AREG	-1.632998571	3.097662334	-3.351770637	0.000874691	0.006614501	-1.76384415
C1S	-1.634215104	4.643976595	-3.935320038	9.70E-05	0.000961604	0.292872656
ADAMTS9-AS1	-1.634332876	0.214214356	-17.78790956	2.52E-53	8.64E-50	110.5527397
VSTM4	-1.635279235	1.031016231	-11.04085122	4.30E-25	8.72E-23	46.15061329
GAS6	-1.637115389	3.542345366	-5.051924063	6.50E-07	1.06E-05	5.06859292
GPIHBP1	-1.637483983	0.646238923	-11.37611263	2.31E-26	5.29E-24	49.04163502
DUSP2	-1.643578932	3.485791784	-4.299743433	2.12E-05	0.000245276	1.732412475
MIR568	-1.644933755	1.730856159	-8.084855504	6.53E-15	3.93E-13	23.03102741
FIGF	-1.645515924	0.478661133	-12.63054151	2.80E-31	1.14E-28	60.24375703
GPR183	-1.648317519	2.198562897	-5.852566396	9.68E-09	2.21E-07	9.137410363
GNG11	-1.650558607	2.586808258	-7.755478808	6.57E-14	3.35E-12	20.76399499
ITPR1	-1.650656047	1.334821938	-9.593087389	7.35E-20	8.17E-18	34.25055218
GPR133	-1.651124713	0.353985794	-14.08550408	2.95E-37	2.08E-34	73.87458184
SDC2	-1.653843485	3.026748752	-6.002483753	4.16E-09	1.02E-07	9.956179185
NR3C2	-1.655931689	0.640870592	-11.64118105	2.22E-27	5.58E-25	51.35976717
SERPINF1	-1.661559442	4.311942621	-4.455907853	1.07E-05	0.000132632	2.385049109
COLEC12	-1.667710173	1.163920877	-7.010093595	9.39E-12	3.52E-10	15.90038366
ID4	-1.667919495	2.777286259	-4.73944168	2.93E-06	4.12E-05	3.62392971
TGFB1I1	-1.670721933	2.573602537	-6.951362304	1.37E-11	5.01E-10	15.53350944
KCNH2	-1.671690508	0.689777503	-8.519516614	2.80E-16	2.03E-14	26.12740613

PRKAR2B	-1.673269465	1.507279114	-7.578824782	2.20E-13	1.04E-11	19.57729085
KCNMA1	-1.675615838	0.541135908	-12.04436121	5.96E-29	1.83E-26	54.93768616
GPRASP1	-1.677659033	0.852826785	-12.3420885	3.97E-30	1.42E-27	57.61789443
FNBP1	-1.678461559	2.82171641	-9.188975513	1.77E-18	1.62E-16	31.11693922
DMD	-1.679544696	0.61608569	-11.06187234	3.59E-25	7.34E-23	46.33049572
DTNA	-1.683060979	0.580721308	-11.1988107	1.09E-25	2.34E-23	47.50689044
FZD7	-1.685226222	2.62821969	-7.732595239	7.69E-14	3.88E-12	20.6091079
MYZAP	-1.694252929	1.886172524	-7.145061146	3.93E-12	1.55E-10	16.75271178
MAP1A	-1.696707563	1.046560316	-8.899975783	1.62E-17	1.34E-15	28.93125188
KCND3	-1.700027721	0.716670711	-10.97010847	7.92E-25	1.56E-22	45.54664349
LAMA2	-1.70078335	1.234985968	-9.645313574	4.85E-20	5.47E-18	34.66190337
PKIG	-1.702795748	3.841445449	-7.768856803	5.99E-14	3.08E-12	20.85470296
CELF2	-1.704081353	1.074522051	-10.04858661	1.85E-21	2.49E-19	37.88549707
ALDH1A1	-1.706801146	2.509464403	-3.964051647	8.64E-05	0.00086634	0.402084825
CD34	-1.713208265	2.266245453	-9.454823564	2.20E-19	2.30E-17	33.16849993
HBB	-1.717345395	2.945370253	-4.450654434	1.09E-05	0.000135338	2.362749082
MIR221	-1.717380841	0.756562513	-9.56810689	8.97E-20	9.83E-18	34.05430443
PLCB4	-1.71769638	0.800586567	-10.14626346	8.28E-22	1.17E-19	38.67856502
HAAO	-1.717762995	1.352565471	-10.1724485	6.67E-22	9.54E-20	38.89196365
PDE2A	-1.720118323	0.921802861	-12.10432589	3.46E-29	1.08E-26	55.47496738
C16orf45	-1.726921745	1.919048746	-7.731088803	7.77E-14	3.91E-12	20.59892369
MBNL1-AS1	-1.728120035	0.654994286	-12.23004999	1.11E-29	3.75E-27	56.60562732
TMEM252	-1.728763065	0.247933264	-15.01354794	3.44E-41	3.59E-38	82.85027625
CRTAC1	-1.731161913	1.566514774	-3.485071047	0.000543084	0.00438515	-1.321367648
CX3CL1	-1.732454295	2.323918892	-5.42641708	9.67E-08	1.83E-06	6.907072022
NFIX	-1.733658229	2.667446675	-7.993162709	1.25E-14	7.15E-13	22.39291905
BDKRB2	-1.736515406	1.608348741	-8.861267969	2.18E-17	1.77E-15	28.64211864
TNS2	-1.742268417	2.355378373	-10.0135702	2.46E-21	3.26E-19	37.60233461
ARHGEF25	-1.743114146	2.157941625	-7.519527288	3.29E-13	1.51E-11	19.18360764
CHRM2	-1.743524554	0.299779205	-13.82617013	3.58E-36	2.32E-33	71.40223947
SVIL	-1.745110945	3.281171809	-7.332090421	1.15E-12	4.93E-11	17.95481648
WBSCR17	-1.745575488	0.531567147	-11.17908047	1.30E-25	2.75E-23	47.33690783
LPP	-1.748495864	2.510201133	-9.396499105	3.49E-19	3.54E-17	32.71511643
TSPAN18	-1.752680461	1.499515674	-8.227160524	2.36E-15	1.50E-13	24.03187553
ZEB1	-1.754440876	1.44102647	-9.197907554	1.65E-18	1.52E-16	31.18523884
DUSP5	-1.754973637	4.484008914	-5.566954069	4.60E-08	9.28E-07	7.62654682
F13A1	-1.757569572	1.979011701	-5.364251358	1.34E-07	2.47E-06	6.593920084
CAV1	-1.758511176	4.501115806	-4.473541129	9.89E-06	0.000123597	2.460074946
SOX17	-1.764658111	0.980941272	-11.96305791	1.24E-28	3.70E-26	54.2112987
GATA5	-1.765014634	0.447177296	-10.91328124	1.29E-24	2.48E-22	45.06304427
XPNPEP2	-1.766802788	0.378513424	-12.59075609	4.04E-31	1.62E-28	59.87992988
JAM2	-1.76758352	0.964060482	-12.28534613	6.68E-30	2.33E-27	57.10468164
LMO3	-1.768248061	0.600464877	-9.79124258	1.50E-20	1.80E-18	35.8188187
AF001548.6	-1.768884753	0.294093354	-15.20957486	4.97E-42	5.80E-39	84.76922257
DNAJB5	-1.774746733	1.441042191	-9.197995141	1.65E-18	1.52E-16	31.1859088
CGNL1	-1.77497991	0.837473567	-11.82124422	4.44E-28	1.21E-25	52.95013643
SELE	-1.775002733	1.178582711	-6.386134005	4.46E-10	1.28E-08	12.13030896
GNG7	-1.775292507	0.809112314	-12.47762393	1.15E-30	4.29E-28	58.84822798
C1QTNF7	-1.775591542	0.436506918	-18.123253	8.09E-55	4.11E-51	113.9594529
TMEM35	-1.785662386	0.723564949	-8.286011462	1.54E-15	9.95E-14	24.44948006
BCHE	-1.786717383	0.608677102	-9.233344472	1.25E-18	1.18E-16	31.45664553
RCAN1	-1.791612309	2.723540718	-7.975086092	1.42E-14	8.06E-13	22.267753
ANTXR2	-1.794700101	2.269641579	-7.899625389	2.41E-14	1.33E-12	21.74751433
WFDC1	-1.796410813	1.129619173	-10.51324978	3.89E-23	6.18E-21	41.69933576
ALDH2	-1.799694162	2.31336167	-6.397603962	4.17E-10	1.20E-08	12.19702721
COL4A6	-1.805802148	1.899890143	-5.963265635	5.20E-09	1.26E-07	9.740298869
RP11-498E2.9	-1.807502308	0.585732244	-11.19391241	1.14E-25	2.43E-23	47.46467483
CCL21	-1.807994316	2.42634846	-3.690114109	0.000253249	0.002254723	-0.609015848
TNFAIP8L3	-1.810004959	1.210317791	-8.79851328	3.50E-17	2.79E-15	28.17520617
CMA1	-1.811210171	0.50258157	-9.257606074	1.04E-18	9.92E-17	31.64286176
ANGPTL1	-1.815484381	0.617725706	-9.352124217	4.94E-19	4.93E-17	32.3714
CCND2	-1.82354804	2.330296066	-6.357873244	5.28E-10	1.49E-08	11.96634364
LAMC3	-1.823908773	1.313417563	-9.622655279	5.81E-20	6.51E-18	34.48326319
TSPAN2	-1.824276774	1.695402818	-6.960342538	1.29E-11	4.75E-10	15.58944716
RASL11A	-1.826066374	1.96481955	-7.642748491	1.42E-13	6.98E-12	20.00432076
LRRN4CL	-1.82757627	0.904841713	-11.51650612	6.70E-27	1.62E-24	50.26596037
EGR2	-1.827998466	1.558376128	-7.765049539	6.15E-14	3.16E-12	20.8288763
MIR143	-1.831139348	0.338727636	-12.83346279	4.26E-32	1.87E-29	62.10739044
SPRY1	-1.834296486	2.927217963	-8.602806994	1.51E-16	1.14E-14	26.73390811
REEP1	-1.835575692	0.578040647	-10.31651816	2.02E-22	3.00E-20	40.07201102

SHH	-1.835887795	1.409627653	-4.53619425	7.46E-06	9.59E-05	2.728828715
BHMT2	-1.839202077	0.455626707	-15.38781797	8.49E-43	1.10E-39	86.52034406
RP11-1100L3.8	-1.840712875	0.788182549	-11.9830189	1.04E-28	3.11E-26	54.389412
MGLL	-1.841880735	2.050631366	-8.014670719	1.07E-14	6.24E-13	22.54211692
PCP4L1	-1.84303444	2.865127303	-3.675763279	0.000267452	0.002362081	-0.660117918
BIN1	-1.844772136	2.081028854	-7.203346789	2.69E-12	1.09E-10	17.12473424
RBFOX3	-1.851243352	0.25555757	-14.79202656	3.04E-40	2.78E-37	80.69088986
GADD45B	-1.852147708	4.215020403	-6.721304372	5.80E-11	1.93E-09	14.12019965
DIXDC1	-1.853053403	1.107196331	-11.26621645	6.06E-26	1.32E-23	48.08883632
NEGR1	-1.863492703	0.462376421	-14.86775266	1.45E-40	1.38E-37	81.42794583
PTRF	-1.863856828	5.501758978	-5.418642657	1.01E-07	1.90E-06	6.867737453
MEDAG	-1.86399296	1.574065193	-6.61554386	1.11E-10	3.57E-09	13.48335629
PRAC1	-1.86851045	0.461578616	-7.861476965	3.15E-14	1.69E-12	21.48591086
TCEAL7	-1.869418731	1.044187978	-10.60027347	1.87E-23	3.08E-21	42.42492656
COL6A2	-1.871921087	6.037347581	-4.448810106	1.10E-05	0.000136251	2.354925849
IER3	-1.873240335	5.496807283	-6.049436021	3.19E-09	7.99E-08	10.21620106
THBS1	-1.877796517	4.587488573	-5.320232466	1.68E-07	3.05E-06	6.374085331
PGM5P4	-1.879175864	0.25395465	-17.98450789	3.36E-54	1.40E-50	112.5489509
JUN	-1.88014467	5.779068383	-6.89031123	2.01E-11	7.18E-10	15.15474807
ITGA5	-1.883469239	3.868124552	-5.901036245	7.38E-09	1.72E-07	9.400207426
GPR124	-1.886072383	2.097472971	-7.833607942	3.82E-14	2.03E-12	21.29539512
PHYHIP	-1.887515397	0.806288799	-10.44309069	7.01E-23	1.09E-20	41.11691073
pk	-1.8897221	2.046856301	-9.34585549	5.19E-19	5.16E-17	32.32293018
CXCL2	-1.890102495	1.845845774	-5.512563848	6.14E-08	1.21E-06	7.346207203
PDZRN4	-1.890225408	0.360403947	-13.16372792	1.94E-33	9.76E-31	65.16805792
MT1A	-1.895385679	1.117256522	-6.26967291	8.89E-10	2.43E-08	11.45848594
HSD17B6	-1.899065844	1.459646192	-8.589276772	1.67E-16	1.25E-14	26.63510153
MIR27A	-1.901641499	0.624796444	-10.04720789	1.87E-21	2.52E-19	37.87433643
FGF7	-1.905699898	1.022053814	-8.198989821	2.89E-15	1.81E-13	23.83273971
VIT	-1.911949918	0.283486837	-14.99858428	3.99E-41	4.09E-38	82.70410034
TP53INP2	-1.913683639	3.162632489	-9.158086025	2.24E-18	2.01E-16	30.88108173
C5orf66-AS1	-1.919531115	0.600692018	-11.91222798	1.96E-28	5.65E-26	53.75840299
CBX7	-1.919953426	1.984483496	-11.57648169	3.94E-27	9.79E-25	50.79138063
DDR2	-1.925833864	1.348478324	-8.894690627	1.69E-17	1.39E-15	28.89172278
DPYSL3	-1.927239928	3.480657176	-5.236607756	2.58E-07	4.50E-06	5.960825653
KIAA1644	-1.927292844	0.535107916	-12.41923505	1.96E-30	7.15E-28	58.31743216
SLC25A25	-1.929199254	2.264245158	-11.22391903	8.76E-26	1.89E-23	47.72344217
FILIP1	-1.931800048	0.575426364	-13.42023233	1.72E-34	9.84E-32	67.56751506
SLC24A3	-1.932668545	1.471414608	-8.501119595	3.21E-16	2.29E-14	25.99400503
TGFBR3	-1.932881445	2.252171692	-7.62667443	1.59E-13	7.75E-12	19.89668501
PARM1	-1.935945518	2.544089727	-6.428998978	3.45E-10	1.01E-08	12.38014916
RP11-867G23.10	-1.945429601	0.393950846	-17.41511992	1.13E-51	3.49E-48	106.7762519
IGFBP6	-1.955395858	3.852867662	-4.832336215	1.89E-06	2.77E-05	4.044785891
LYVE1	-1.962193892	0.892023463	-9.12241439	2.95E-18	2.59E-16	30.60937155
CH25H	-1.966841049	1.350170096	-8.815501485	3.08E-17	2.47E-15	28.30137746
CLCA4	-1.967838707	2.183791973	-3.64316581	0.000302545	0.002627889	-0.775500304
FERMT2	-1.968396105	1.995063309	-8.494481716	3.37E-16	2.37E-14	25.94592235
TSPAN7	-1.969066628	1.631277791	-6.405441117	3.98E-10	1.15E-08	12.24267094
AOX1	-1.970916129	0.566274481	-12.54979399	5.90E-31	2.27E-28	59.50588702
HBEGF	-1.971552407	3.198233024	-6.927605519	1.59E-11	5.75E-10	15.38580586
FGFR1	-1.975894763	1.747387135	-7.781341287	5.49E-14	2.85E-12	20.93945838
DACT3	-1.982891719	0.985876744	-9.889343678	6.78E-21	8.51E-19	36.60270827
MYOM1	-1.986606098	0.536430646	-14.39234998	1.51E-38	1.21E-35	76.82103413
CLDN5	-1.99083184	1.90090441	-8.070607187	7.22E-15	4.32E-13	22.93151993
APOLD1	-1.991483729	2.026798949	-9.847353261	9.53E-21	1.18E-18	36.26657855
GATA6	-1.994976245	1.185621318	-10.53396948	3.26E-23	5.25E-21	41.87177713
GYPC	-1.99632916	1.982988873	-7.728139987	7.93E-14	3.98E-12	20.57899263
PPAP2B	-2.000832892	3.18993857	-10.01427813	2.45E-21	3.26E-19	37.60805329
RP11-64B16.2	-2.001158416	1.118636309	-9.730642069	2.44E-20	2.87E-18	35.33704386
CFL2	-2.002779924	1.727311662	-10.50972705	4.00E-23	6.35E-21	41.67003724
HAND2	-2.003634744	0.717658666	-10.44023471	7.18E-23	1.11E-20	41.09325045
RASD1	-2.008117521	1.948210371	-6.639474484	9.62E-11	3.12E-09	13.62673934
RP11-166D19.1	-2.014199086	0.92282187	-11.02496797	4.93E-25	9.93E-23	46.01482207
CPXM2	-2.021947781	1.617596252	-6.949530898	1.38E-11	5.06E-10	15.52210869
PKDCC	-2.025541484	1.20075647	-7.241602483	2.09E-12	8.66E-11	17.37019435
TCEAL2	-2.032359992	0.561161979	-10.67030221	1.03E-23	1.76E-21	43.01133213
RHOB	-2.036736291	6.411152885	-9.119717616	3.02E-18	2.64E-16	30.58885918
CRISPLD2	-2.043640863	2.702193774	-7.16841389	3.38E-12	1.35E-10	16.90148217
JPH2	-2.047990687	1.214440697	-8.144511055	4.27E-15	2.62E-13	23.44904322
ITGA7	-2.051037022	1.719747574	-8.172947967	3.48E-15	2.16E-13	23.64909362

PER1	-2.064549508	2.780809073	-9.414296208	3.03E-19	3.11E-17	32.85326748
PLIN4	-2.06623944	2.084709645	-6.672541794	7.85E-11	2.57E-09	13.82555669
GPX3	-2.068451832	3.986582396	-5.244243447	2.48E-07	4.35E-06	5.998321717
KANK2	-2.07809101	3.155976886	-9.132459181	2.73E-18	2.41E-16	30.68581065
SBSPON	-2.079329911	1.232373232	-8.4174153	5.93E-16	4.03E-14	25.38963125
PMP22	-2.083610819	3.794368938	-6.34756862	5.61E-10	1.58E-08	11.90670689
RGS5	-2.086365158	2.608243799	-8.008965985	1.12E-14	6.48E-13	22.50251525
IL33	-2.08748132	1.861686034	-6.012157003	3.94E-09	9.72E-08	10.00961011
EFEMP1	-2.087527447	2.80310667	-4.728686663	3.08E-06	4.31E-05	3.575678476
JAM3	-2.091017622	1.879579584	-9.642229301	4.97E-20	5.59E-18	34.63757086
MIR23A	-2.093510928	1.054323467	-9.317176547	6.50E-19	6.40E-17	32.10145732
TACR2	-2.10124133	0.68028022	-10.70425745	7.72E-24	1.35E-21	43.29646625
SORBS2	-2.103438033	0.966311779	-11.38556472	2.13E-26	4.91E-24	49.12381457
CPED1	-2.103582731	0.754923005	-12.9482466	1.46E-32	6.72E-30	63.16734069
MFAP5	-2.112260432	1.378388721	-6.459067797	2.88E-10	8.56E-09	12.55622624
CYBRD1	-2.112621485	3.024697777	-7.161600421	3.53E-12	1.41E-10	16.85803714
FBLN5	-2.112989347	2.14064888	-8.637138254	1.17E-16	8.89E-15	26.9851071
PID1	-2.115477006	0.921364957	-12.45607138	1.40E-30	5.17E-28	58.65216609
ASB5	-2.118267814	0.368946026	-12.58030449	4.45E-31	1.75E-28	59.78443905
C3	-2.124913842	4.242049897	-4.637050083	4.71E-06	6.34E-05	3.168568284
HLF	-2.126780386	0.366242972	-20.37633493	6.59E-65	1.92E-60	136.9884345
ASB2	-2.127044706	0.904152595	-11.36608203	2.52E-26	5.71E-24	48.95446534
TMOD1	-2.127680446	0.778820708	-11.90147081	2.16E-28	6.16E-26	53.66267908
POPDC2	-2.13395481	1.27187214	-9.189843369	1.75E-18	1.61E-16	31.12357342
ZCCHC24	-2.13605866	2.127612103	-9.268367101	9.52E-19	9.17E-17	31.7255601
CADM3	-2.139028829	0.522596112	-11.07419206	3.22E-25	6.62E-23	46.43600588
PDZRN3	-2.140774777	1.252765435	-9.691030502	3.36E-20	3.88E-18	35.02315648
ANXA6	-2.146872095	3.63810078	-6.749726964	4.86E-11	1.64E-09	14.29273903
ELN	-2.164220606	2.23844533	-6.448337107	3.07E-10	9.09E-09	12.49331201
PYGM	-2.166732518	0.470179857	-15.795291	1.46E-44	2.30E-41	90.5444443
CPA3	-2.173386153	1.793262407	-7.114753149	4.79E-12	1.87E-10	16.56020074
CALD1	-2.174035147	4.016863835	-6.709419667	6.25E-11	2.07E-09	14.04822775
CNTN1	-2.178001288	0.993298888	-8.247607999	2.03E-15	1.30E-13	24.17672636
NCAM1	-2.182370438	0.554442921	-11.4584507	1.12E-26	2.66E-24	49.75872028
RAI2	-2.185204002	1.490344501	-10.628204	1.47E-23	2.47E-21	42.6585433
EMILIN1	-2.192734723	3.772996198	-5.700429049	2.24E-08	4.79E-07	8.324553788
NEXN	-2.196529536	1.645976431	-9.2192718	1.40E-18	1.30E-16	31.34878167
AC053503.6	-2.202482729	0.609901017	-9.739128258	2.28E-20	2.69E-18	35.40439522
GSN	-2.20461669	5.018035452	-9.676038788	3.79E-20	4.31E-18	34.9045726
AKAP12	-2.20477142	2.151661677	-7.919202174	2.10E-14	1.17E-12	21.88212777
ABI3BP	-2.207883224	0.877385515	-12.11669904	3.10E-29	9.83E-27	55.58599152
ADAM33	-2.207952691	0.833717278	-12.10142789	3.56E-29	1.10E-26	55.4489716
C8orf4	-2.21238281	4.765209601	-5.371629733	1.29E-07	2.38E-06	6.630923185
HPSE2	-2.219153273	0.61649783	-10.83056608	2.63E-24	4.82E-22	44.36165941
SOCS3	-2.224100566	5.181313989	-7.085092614	5.80E-12	2.24E-10	16.37242555
PRUNE2	-2.225596635	0.706670001	-10.41920081	8.56E-23	1.32E-20	40.91911356
CSF3	-2.22826826	1.007261988	-6.629639104	1.02E-10	3.30E-09	13.56775867
OLFML3	-2.236093351	2.842404557	-6.395525686	4.22E-10	1.21E-08	12.18493102
CTSG	-2.236896665	0.903235711	-8.90087102	1.61E-17	1.33E-15	28.93794919
PODN	-2.237888906	2.222201131	-7.0868485	5.73E-12	2.22E-10	16.38352453
CLIP3	-2.237926796	2.032015302	-8.351125076	9.61E-16	6.36E-14	24.91402109
BTG2	-2.241995518	6.173827269	-6.847574481	2.64E-11	9.27E-10	14.89119642
ADCY5	-2.24241971	0.794955369	-11.65247071	2.01E-27	5.14E-25	51.45911445
CCL2	-2.244777044	3.008501953	-6.433126921	3.37E-10	9.86E-09	12.40428161
TPPP	-2.244921566	0.807196272	-13.89830566	1.79E-36	1.19E-33	72.08823448
MAP1B	-2.249607643	1.591578006	-9.069491363	4.44E-18	3.82E-16	30.20757073
MAMDC2	-2.254486405	0.891900858	-10.81512924	3.00E-24	5.47E-22	44.23109586
KLF9	-2.258392868	2.421385235	-9.709234037	2.90E-20	3.38E-18	35.16730273
FILIP1L	-2.260408763	2.440151189	-8.543721196	2.34E-16	1.71E-14	26.30322966
MYOC	-2.273261799	0.243971329	-17.23407667	7.18E-51	2.10E-47	104.9468013
PAMR1	-2.277227756	1.532415072	-11.77980686	6.44E-28	1.72E-25	52.58305357
SMTN	-2.279897934	3.158266696	-10.83421705	2.55E-24	4.72E-22	44.39255438
F10	-2.289459945	0.638571335	-17.84910695	1.34E-53	4.91E-50	111.1738038
CCDC69	-2.289602446	2.791935273	-9.921307208	5.23E-21	6.65E-19	36.85917182
EMP1	-2.291059708	3.809265871	-7.57157911	2.31E-13	1.09E-11	19.52905958
MRVI1	-2.310857091	1.680477915	-9.780543178	1.64E-20	1.95E-18	35.733621
FAM46B	-2.313887645	1.662248083	-7.834986534	3.78E-14	2.01E-12	21.30480746
KLF4	-2.318664707	3.369327736	-8.643547283	1.12E-16	8.49E-15	27.03207906
CXCL12	-2.322239472	2.004652621	-7.515388134	3.38E-13	1.55E-11	19.15621545
PTGS2	-2.324009766	2.99189498	-5.992872283	4.40E-09	1.07E-07	9.903161356

TPSB2	-2.325203293	2.126995425	-7.263348537	1.81E-12	7.60E-11	17.51017536
AP000892.6	-2.327660258	0.999016837	-10.66604505	1.07E-23	1.82E-21	42.97562001
SOD3	-2.331226439	3.313680406	-6.32390419	6.46E-10	1.80E-08	11.77005456
COX7A1	-2.331806638	2.407611715	-9.477038358	1.85E-19	1.96E-17	33.34166645
LTBP4	-2.353800523	3.186145628	-10.09341656	1.28E-21	1.77E-19	38.24890267
PALLD	-2.35669046	3.551663209	-8.13267585	4.64E-15	2.84E-13	23.36593367
RASL12	-2.362982448	1.763676177	-9.952417059	4.06E-21	5.24E-19	37.10927998
APOD	-2.365286552	2.952427835	-4.875755076	1.53E-06	2.31E-05	4.244002668
ITGA8	-2.384120245	0.969941129	-14.68843428	8.40E-40	7.32E-37	79.68454258
FAM129A	-2.393744627	2.430824834	-8.401757129	6.65E-16	4.49E-14	25.27704675
PSD	-2.39787515	1.11697337	-10.89807016	1.47E-24	2.81E-22	44.93383652
TPSAB1	-2.404470802	2.094988444	-7.64879201	1.37E-13	6.72E-12	20.04483401
PPP1R14A	-2.405146855	2.392908005	-8.730665427	5.82E-17	4.52E-15	27.67298048
TPM1	-2.411259432	3.745766519	-8.549395443	2.25E-16	1.65E-14	26.34449867
CSRP1	-2.414268026	4.493773938	-10.68927938	8.77E-24	1.52E-21	43.17062596
AQP1	-2.415445977	4.283776457	-9.419228918	2.92E-19	3.00E-17	32.89158816
CACNA1H	-2.415599528	1.381734734	-10.35410461	1.48E-22	2.22E-20	40.38150947
FLNA	-2.424352481	6.125495403	-6.983599052	1.11E-11	4.14E-10	15.73457815
CKB	-2.425380208	4.315421645	-6.649186164	9.06E-11	2.94E-09	13.68504781
MYOCD	-2.42674777	0.518216338	-15.40714088	7.01E-43	9.51E-40	86.7105255
RP11-394O4.5	-2.430570157	1.541642578	-8.727119955	5.98E-17	4.62E-15	27.6468102
CSRNP1	-2.432388194	3.590373814	-11.63874385	2.27E-27	5.68E-25	51.33832666
LIMS2	-2.433827837	1.620670498	-10.86127246	2.02E-24	3.79E-22	44.62168407
TCF21	-2.442742989	0.757952224	-16.68960113	1.81E-48	4.40E-45	99.46563888
IGFBP5	-2.454991598	4.443617462	-5.545883858	5.14E-08	1.03E-06	7.517663736
ITM2A	-2.457701984	2.026734754	-9.235767248	1.23E-18	1.16E-16	31.4752266
MATN2	-2.459221527	2.34644755	-8.226784084	2.36E-15	1.50E-13	24.02921125
KCNMB1	-2.479345363	1.037194575	-11.15600335	1.58E-25	3.34E-23	47.1382973
PLA2G2A	-2.480358798	3.458506688	-4.21773581	3.02E-05	0.000336612	1.398232396
NR4A2	-2.483721982	2.152095713	-10.68183726	9.34E-24	1.60E-21	43.10813761
SLC2A4	-2.48721707	0.548813195	-14.61754399	1.68E-39	1.42E-36	78.99719351
SGCA	-2.492966791	0.945895554	-10.62031081	1.57E-23	2.63E-21	42.59248693
MGP	-2.498432536	4.833066588	-5.545730364	5.15E-08	1.03E-06	7.516871843
A2M	-2.50050512	5.634064895	-7.906970443	2.29E-14	1.27E-12	21.79799123
MSRB3	-2.504763509	1.975053136	-8.790740377	3.71E-17	2.95E-15	28.1175329
CILP	-2.50753217	1.155780939	-7.471625341	4.54E-13	2.06E-11	18.86730741
RAMP1	-2.507662666	2.767365354	-6.339349689	5.89E-10	1.65E-08	11.85919812
FBLN2	-2.520218987	3.107063289	-6.845763526	2.67E-11	9.37E-10	14.88005749
MYADM	-2.542202891	4.0891404	-7.618814785	1.68E-13	8.17E-12	19.8441175
CLU	-2.552931254	4.963201057	-5.552568884	4.96E-08	9.96E-07	7.552170841
CCDC80	-2.554769649	2.186422579	-7.459563724	4.92E-13	2.22E-11	18.78790782
RBPMS2	-2.555771355	1.795331301	-9.097459212	3.58E-18	3.12E-16	30.41971157
SPON1	-2.560582828	2.129831422	-7.77830553	5.61E-14	2.90E-12	20.91883966
SLIT3	-2.570855772	1.521416457	-11.43944638	1.32E-26	3.08E-24	49.5929687
FXYD6	-2.573978789	1.443874368	-9.454392703	2.21E-19	2.30E-17	33.16514393
CHRDL1	-2.595038705	0.801631432	-10.52962182	3.39E-23	5.43E-21	41.83557691
TNXB	-2.595091798	0.641530935	-15.68462004	4.42E-44	6.46E-41	89.44872378
ITIH5	-2.602672469	1.134670191	-13.47587981	1.01E-34	5.92E-32	68.09053953
RCAN2	-2.605735268	1.78202142	-11.93673589	1.57E-28	4.62E-26	53.97664972
PDLIM3	-2.611715612	1.858852232	-8.434854911	5.22E-16	3.57E-14	25.51520045
HSPB7	-2.615813984	1.223820653	-8.59685501	1.58E-16	1.18E-14	26.69042935
TPM2	-2.629239209	5.169832558	-7.012477305	9.25E-12	3.48E-10	15.91532555
SFRP1	-2.64356928	1.320898291	-8.3857584	7.47E-16	5.01E-14	25.16216822
PCOLCE2	-2.648051128	0.927695085	-11.901383	2.16E-28	6.16E-26	53.6618979
ZFP36	-2.677550711	6.73371758	-9.290116382	8.03E-19	7.86E-17	31.89289713
PPP1R12B	-2.677800954	1.722033845	-12.08524441	4.12E-29	1.27E-26	55.30385733
PTGDS	-2.720481208	2.922598799	-6.558751873	1.58E-10	4.95E-09	13.14476675
FENDRR	-2.732875915	0.945842099	-13.77000697	6.14E-36	3.85E-33	70.86906838
PLAC9	-2.752440435	1.736754747	-11.79817776	5.46E-28	1.48E-25	52.74571644
COL14A1	-2.753622993	1.975859525	-10.11908252	1.04E-21	1.45E-19	38.45740432
KLF2	-2.754207794	2.820128864	-11.10878252	2.39E-25	4.98E-23	46.73259483
FOXF1	-2.766225141	1.867072811	-11.64116653	2.22E-27	5.58E-25	51.35963945
MAOB	-2.768026078	1.518097937	-9.186620168	1.80E-18	1.65E-16	31.09893625
FABP4	-2.773657811	3.1464568	-4.363210275	1.61E-05	0.000191418	1.995085047
MRGPRF	-2.848647245	2.026741366	-9.813151304	1.26E-20	1.53E-18	35.99345757
EGR3	-2.84929627	1.276036919	-12.90818605	2.13E-32	9.62E-30	62.7969431
SRPX	-2.858002457	2.393900629	-8.374578677	8.10E-16	5.42E-14	25.08198537
CTC-296K1.4	-2.85868433	0.624394719	-13.53986901	5.52E-35	3.26E-32	68.69302951
IL6	-2.871593657	1.638363641	-8.185180449	3.19E-15	1.99E-13	23.73530373
P2RX1	-2.873275217	0.878163007	-11.75822578	7.81E-28	2.07E-25	52.39213023

FGL2	-2.887808286	2.031529348	-10.0547673	1.76E-21	2.37E-19	37.93554069
ATF3	-2.894557157	3.780238685	-8.143566347	4.29E-15	2.64E-13	23.44240602
GEM	-2.915539759	2.332012556	-9.499417788	1.55E-19	1.66E-17	33.51638313
CTGF	-2.917300851	5.166828498	-7.116875104	4.72E-12	1.85E-10	16.57365809
FAM107A	-2.923388315	0.842090541	-16.55212296	7.27E-48	1.70E-44	98.08712957
RGS2	-2.934023291	3.893252327	-8.859022674	2.21E-17	1.80E-15	28.62537364
ATP1A2	-2.948957504	0.490418964	-15.85234352	8.28E-45	1.38E-41	91.11007535
C2orf40	-2.95479639	0.592208643	-15.18374125	6.41E-42	7.07E-39	84.51591219
SMOC2	-2.977765257	2.32771378	-8.834951565	2.66E-17	2.15E-15	28.44603905
CRYAB	-2.986935936	2.352595283	-9.137473825	2.63E-18	2.33E-16	30.72399232
SFRP2	-2.987239783	4.003975361	-4.522238882	7.94E-06	0.000101638	2.668672594
PTGIS	-3.003823143	1.902770778	-7.851628913	3.37E-14	1.80E-12	21.41853083
DCN	-3.014210966	3.596078987	-7.404238809	7.13E-13	3.15E-11	18.42497691
PLN	-3.032370874	1.534306601	-8.773227186	4.23E-17	3.32E-15	27.98771795
NR4A3	-3.037451325	1.177736914	-13.39172716	2.25E-34	1.26E-31	67.29993451
AOC3	-3.054537863	2.487500005	-9.965843173	3.64E-21	4.75E-19	37.21736952
CES1	-3.087902868	1.85688785	-6.476881783	2.59E-10	7.75E-09	12.66085943
CYR61	-3.095690468	5.452860661	-8.496179145	3.33E-16	2.35E-14	25.95821546
MYLK	-3.101843696	2.011639077	-10.27791035	2.78E-22	4.09E-20	39.7548032
C11orf96	-3.107650828	3.258411448	-9.543219971	1.09E-19	1.19E-17	33.85911969
PRELP	-3.126842992	1.729082657	-10.11194751	1.10E-21	1.53E-19	38.39940943
SORBS1	-3.132217448	1.673065863	-10.31029437	2.13E-22	3.15E-20	40.0208272
C16orf89	-3.154573303	0.610827585	-18.88240451	3.30E-58	2.75E-54	121.6980467
LINC01082	-3.154961731	0.961690009	-16.10564927	6.53E-46	1.23E-42	93.62749083
CTC-296K1.3	-3.156672087	0.828948607	-13.24450363	9.06E-34	4.81E-31	65.92161811
SPARCL1	-3.166352822	4.59030219	-10.01365491	2.46E-21	3.26E-19	37.60301891
ACKR1	-3.181804678	2.116679663	-8.362581768	8.84E-16	5.87E-14	24.99602668
CASQ2	-3.183685164	0.952342615	-10.7174048	6.90E-24	1.21E-21	43.40700866
FOS	-3.19269383	6.292509469	-8.70881408	6.86E-17	5.28E-15	27.5118062
HSPB8	-3.20908326	3.554488346	-7.696830359	9.83E-14	4.90E-12	20.36772406
TNS1	-3.213376529	2.499909974	-10.49114048	4.68E-23	7.33E-21	41.51554854
DUSP1	-3.268846791	6.138565839	-9.510780942	1.41E-19	1.53E-17	33.60519777
ADAMTS1	-3.29019114	2.857215813	-11.38382204	2.16E-26	4.96E-24	49.10866045
OGN	-3.293781556	0.725694673	-14.43356726	1.01E-38	8.32E-36	77.21848878
EGR1	-3.300361329	5.468037348	-9.46073562	2.10E-19	2.20E-17	33.21455917
TAGLN	-3.31423293	5.485185691	-7.474309488	4.46E-13	2.02E-11	18.88499008
ACTA2	-3.371749446	5.763277469	-8.167903767	3.61E-15	2.23E-13	23.61357123
PTGS1	-3.382094655	2.153486999	-9.459796293	2.12E-19	2.21E-17	33.20723988
SDPR	-3.402933008	1.779577523	-12.87385731	2.93E-32	1.31E-29	62.47993781
PGM5-AS1	-3.435193171	0.591722861	-15.07378704	1.90E-41	2.05E-38	83.43918007
MYL9	-3.466115942	5.889213881	-8.45562395	4.48E-16	3.12E-14	25.6649836
PDK4	-3.570661116	2.179026689	-11.46029904	1.10E-26	2.62E-24	49.77484876
DPT	-3.695470812	1.759580477	-9.616869486	6.08E-20	6.80E-18	34.43769056
SCARA5	-3.760991268	0.695064267	-19.74874173	4.32E-62	5.05E-58	130.5593832
MFAP4	-3.805716065	3.920850358	-8.801109857	3.43E-17	2.74E-15	28.19448005
C7	-3.830862834	1.245566547	-11.35474542	2.79E-26	6.28E-24	48.85599519
ADH1B	-3.847621583	0.800349637	-15.89182969	5.58E-45	9.57E-42	91.50185106
PGM5	-3.870763221	1.251287901	-13.07600667	4.42E-33	2.13E-30	64.35188798
FHL1	-3.876247111	2.191294431	-11.04379352	4.19E-25	8.53E-23	46.17577982
FLNC	-3.882433477	1.856569966	-10.50061112	4.32E-23	6.79E-21	41.59424702
NR4A1	-3.889159436	3.082770523	-12.01809383	7.56E-29	2.30E-26	54.7027417
PCP4	-3.907196759	1.682131771	-8.436984458	5.14E-16	3.52E-14	25.53054636
CLEC3B	-3.958376422	1.616404298	-17.64774207	1.05E-52	3.42E-49	109.1313881
SYNPO2	-4.017361495	1.66752581	-12.10452987	3.46E-29	1.08E-26	55.47679719
FOSB	-4.074912047	3.506525709	-9.590432298	7.51E-20	8.29E-18	34.22967806
ACTC1	-4.163797761	1.402960214	-9.592717199	7.38E-20	8.17E-18	34.24764155
LMOD1	-4.207963664	2.481478635	-10.52668129	3.47E-23	5.54E-21	41.81109796
CFD	-4.229717944	3.567121323	-12.19622125	1.50E-29	5.02E-27	56.30084792
SYNM	-4.322808213	1.882727156	-11.8815279	2.59E-28	7.33E-26	53.48532873
ACTG2	-4.868656851	4.050553015	-8.926073803	1.33E-17	1.11E-15	29.12668135
CNN1	-5.043359839	3.350814329	-9.729907201	2.46E-20	2.88E-18	35.33121327
HSPB6	-5.070281528	2.275511792	-12.15467874	2.19E-29	7.16E-27	55.92712513
PI16	-5.29308973	0.860198074	-18.63743732	4.11E-57	2.66E-53	119.1974943
MYH11	-5.548364503	2.946500346	-10.62226017	1.55E-23	2.59E-21	42.60879811
DES	-6.058681878	4.138784333	-7.997416175	1.21E-14	6.97E-13	22.42240127

Supplementary Table S4

Gene
HLF
TCF21
AFF3
NR4A3
EGR3
ZBTB16
NR4A1
SOX17
PRDM6
NR3C2
FOXF1
CSRNP1
KLF2
SRF
GATA5
NR4A2
TBX20
HMGB3
GATA6
HAND2
EBF1
MYBL2
HIF3A
KLF9
FOSB
MEF2D
EGR1
ZFPM2
TBX5
ZEB1
HAND1
CENPA
FOS
NFIA
KLF4
MEIS1
FOXM1
MEF2C
MEOX1
ZEB2
TSC22D1
ATF3
NFIX
TCF3
FOXN3
EGR2
JAZF1
MITF
TUB
TWIST2
THRA
E2F1
HMGA1
MEIS2
TSHZ3
ARID5B
NR2F1

TEAD1
JUN
ARID5A
TBX4
SOX4
MAFF
NFIC
ETV4
KLF6
NFATC4
JUNB
NFIL3
HOXB7
TSC22D3
JUND
NFIB
NR2F6
ZNF692
CSDC2
PITX2
PARP12
IRF5
PBX1
E2F8
MSX1
JDP2
CDIP1
TCF19
NFE2L3
ZFP36L1
GRHL2
HMGB2
ETS2
SREBF1
ID4
MYC
AR
ID2
TFAP2C
SOX7
ATOH8
ETV7
CREB3L1
TFAP2A
FOSL1
PITX1
ZNF488
IRF7
OSR1
HOXB5
HES4
HOXB6
IRF6
GATA3
TBX1
SP6
MYCL
HES2

SOX9

Supplementary Table S5

gene	KM.Pvalue	HR	HR.95L	HR.95H	coxPvalue
NFIA	0.00052983	1.24774802	1.02089044	1.52501684	0.03062543
EGR2	0.00086847	1.21606925	1.04430364	1.41608664	0.01180433
CSDC2	0.03341661	1.18841672	1.0209911	1.38329736	0.02587385
MYC	0.00441424	1.12852106	1.00907799	1.26210243	0.03415038
ID2	0.02582234	0.83564424	0.73559758	0.94929797	0.00578548
ETV7	8.67E-06	0.77394341	0.67182928	0.89157828	0.00038577
PITX1	0.02408171	1.11473651	1.00405353	1.23762075	0.04177204
HOXB5	0.00551152	0.77656823	0.67208786	0.89729075	0.00060361
HES4	0.00903485	0.85755488	0.76319043	0.963587	0.009778
HOXB6	0.01578521	0.82041648	0.71185153	0.94553876	0.00627175
GATA3	0.02396519	0.90683608	0.84233547	0.97627573	0.00938324
TBX1	0.00317948	0.85084648	0.77329905	0.93617047	0.00092402
SP6	0.01643687	0.85184172	0.76325411	0.95071132	0.00420811

Supplementary Table S6

id	HR	HR.95L	HR.95H	pvalue
age	1.034145192	1.017462595	1.051101322	5.20E-05
gender	0.836555185	0.597360941	1.171527179	0.298976559
pathologic_stage	1.786622656	1.451989749	2.198376757	4.15E-08
pathologic_t	1.716259328	1.368824022	2.151880763	2.86E-06
pathologic_m	1.186406933	1.015673049	1.385841057	0.031073257
pathologic_n	1.218743707	1.093316548	1.358560085	0.000356955
ETV7	0.963250309	0.939008344	0.988118118	0.003988259

Supplementary Table S7

id	HR	HR.95L	HR.95H	pvalue
age	1.032082299	1.01508778	1.049361338	0.000193219
pathologic_stage	1.25938642	0.961731613	1.649165041	0.093671518
pathologic_t	1.479192444	1.114648582	1.962959736	0.006692214
pathologic_m	1.188906879	1.013452975	1.394736215	0.033670267
pathologic_n	1.206125359	1.051946254	1.382901812	0.007238297
ETV7	0.971290655	0.947953524	0.995202309	0.0188979

Supplementary Table S8

	logFC	AveExpr	t	P.Value	adj.P.Val	B
ETV7	1.749772046	2.678614052	27.47174172	1.08E-94	6.33E-90	205.4113409
PSMB8	1.328317517	5.539403664	15.45528694	1.02E-42	2.98E-38	85.93208743
RTP4	1.413862703	2.869373662	13.79428799	8.90E-36	1.73E-31	70.00463227
IFI35	1.217763071	4.420968973	12.95099938	2.34E-32	1.95E-28	62.16394835
PSMB9	1.739924186	3.79682187	12.80668413	8.82E-32	6.44E-28	60.84216007
TAP1	1.533151009	4.912530527	12.65924075	3.40E-31	2.12E-27	59.49823619
IRF1	1.148894666	3.405502923	12.65214517	3.63E-31	2.12E-27	59.43373043
HLA-F	1.588142799	3.922234477	12.59805735	5.95E-31	2.89E-27	58.94253687
APOL3	1.125780966	2.417882433	12.56966817	7.70E-31	3.40E-27	58.68509161
BATF2	1.344060432	1.780182756	12.52093254	1.20E-30	4.67E-27	58.2437327
HLA-A	1.439018508	8.518930621	12.4719486	1.87E-30	6.84E-27	57.80089091
B2M	1.197326367	9.025079023	12.25756425	1.30E-29	3.73E-26	55.87195077
UBE2L6	1.254700538	5.336784083	12.25431695	1.34E-29	3.73E-26	55.84285019
HLA-B	1.474209435	8.884945599	12.14978609	3.43E-29	9.11E-26	54.90800563
TAP2	1.033733952	3.082742232	12.12124543	4.43E-29	1.13E-25	54.6534077
HCP5	1.46071386	3.252270451	11.68196488	2.20E-27	4.94E-24	50.77108515
HLA-C	1.074021251	8.70003431	11.38781058	2.89E-26	6.02E-23	48.21122539
GBP4	1.27990766	2.990958746	10.9740628	1.02E-24	1.86E-21	44.66834974
UBD	1.727614985	1.921418352	10.95451307	1.21E-24	2.13E-21	44.5026855
OASL	1.257458407	2.473418608	10.88340804	2.21E-24	3.69E-21	43.90150051
CXCL11	1.781598109	2.002305496	10.51153661	5.06E-23	7.38E-20	40.79295113
HLA-H	1.149872835	4.889010592	10.39754352	1.30E-22	1.77E-19	39.85237305
IFIT3	1.477729382	3.627456749	10.31187753	2.65E-22	3.52E-19	39.14944172
IFI44	1.456355946	3.963265916	10.17510372	8.15E-22	1.06E-18	38.03422709
OR2I1P	1.509587989	1.707161933	10.12844278	1.19E-21	1.52E-18	37.65578589
SAMD9L	1.043165366	1.994661364	10.09800073	1.53E-21	1.82E-18	37.40944668
TRIM22	1.12368215	2.807012781	10.04904668	2.28E-21	2.61E-18	37.01423923
GBP1	1.334970622	3.67563619	10.00565444	3.24E-21	3.64E-18	36.66489924
HLA-DMA	1.16910447	4.376872537	9.969427539	4.35E-21	4.62E-18	36.37394571
AC092580.4	1.098182697	1.464995921	9.943053836	5.38E-21	5.61E-18	36.16253026
IFI44L	1.182740946	1.86886036	9.924513054	6.25E-21	6.40E-18	36.01410862
LAMP3	1.023491842	2.326823955	9.616428342	7.33E-20	7.14E-17	33.57291299
IDO1	1.674346886	2.087584825	9.60644812	7.94E-20	7.60E-17	33.49463525
CD74	1.481370247	8.201741802	9.566887306	1.08E-19	1.01E-16	33.18485274
AIM2	1.609943787	2.470992566	9.547220544	1.27E-19	1.16E-16	33.03115204
OAS2	1.209762624	3.711025018	9.516749758	1.61E-19	1.45E-16	32.79341116
CTA-384D8.35	1.103221747	1.555808551	9.349897772	5.94E-19	4.93E-16	31.5002076
GNLY	1.161436122	1.493568173	9.294977883	9.10E-19	7.09E-16	31.07777016
CASP1	1.019589515	2.57671255	9.191343775	2.03E-18	1.52E-15	30.28504305
CXCL10	1.973039439	3.775945644	9.158861703	2.60E-18	1.92E-15	30.03777626
WARS	1.229298574	4.697364037	9.080555139	4.74E-18	3.37E-15	29.44404753
STAT1	1.052289791	5.188311788	8.893779484	1.96E-17	1.27E-14	28.04161294
TNFSF10	1.284594455	4.834056743	8.874044096	2.27E-17	1.46E-14	27.89456985
GZMH	1.061456453	1.46788775	8.81550147	3.52E-17	2.19E-14	27.45968444
GBP5	1.226012661	1.484701858	8.801819466	3.90E-17	2.40E-14	27.35832875
NKG7	1.266884935	2.470888951	8.694908747	8.66E-17	4.86E-14	26.57003833
APOL1	1.270029814	6.443354069	8.639980641	1.30E-16	7.16E-14	26.16760371
GZMA	1.30104792	2.277712452	8.630190997	1.40E-16	7.63E-14	26.09606364
BST2	1.460348275	6.73855428	8.548859981	2.55E-16	1.33E-13	25.50388929
HLA-DQB1	1.310570832	3.692461587	8.272410724	1.90E-15	8.92E-13	23.52046001
CD2	1.048203307	2.178992456	8.245539442	2.30E-15	1.06E-12	23.330129
GZMB	1.251268005	2.118614492	8.219696575	2.76E-15	1.26E-12	23.14749913
MX1	1.066745478	3.719905379	8.160927813	4.20E-15	1.86E-12	22.73371211
ISG15	1.120802833	6.961370064	8.085046412	7.20E-15	3.07E-12	22.2025957
HLA-DRB1	1.412337854	7.128450159	8.014447702	1.18E-14	4.84E-12	21.7116779
HLA-DRB5	1.455113537	5.327326045	7.990639594	1.40E-14	5.60E-12	21.54683019
CD3D	1.022961728	2.298591372	7.978491926	1.52E-14	6.05E-12	21.46285716

CXCL9	1.55708421	2.83400403	7.687197179	1.14E-13	3.97E-11	19.4774235
IFI27	1.513116988	5.241914651	7.663941355	1.34E-13	4.57E-11	19.32127651
HLA-DPA1	1.254814991	4.151252323	7.659463818	1.38E-13	4.68E-11	19.29125349
RARRES3	1.370987427	4.395298565	7.627133746	1.72E-13	5.76E-11	19.07486178
HLA-DRA	1.371065061	7.654804898	7.590606495	2.20E-13	7.30E-11	18.83120338
CCL5	1.383657018	3.970407058	7.571692946	2.50E-13	8.20E-11	18.70538421
IL2RG	1.051234579	2.723889904	7.366124617	9.87E-13	2.94E-10	17.35322093
IFI16	1.004169365	4.228530367	7.193162099	3.07E-12	8.37E-10	16.23761025
IFITM1	1.164264569	5.715766023	7.143303437	4.24E-12	1.11E-09	15.91982479
HLA-DPB1	1.147900051	5.15818674	7.14152805	4.29E-12	1.12E-09	15.90854059
HLA-DQA1	1.112652935	2.916819658	7.105546981	5.41E-12	1.39E-09	15.68031828
KLHDC7B	1.595714174	3.447126636	7.0588815	7.30E-12	1.82E-09	15.38566499
TYMP	1.113816999	4.824572005	7.046305369	7.91E-12	1.95E-09	15.30651671
SECTM1	1.043089404	2.719903416	6.986173414	1.16E-11	2.81E-09	14.92960284
IFI6	1.24597877	7.340307772	6.700014781	6.97E-11	1.52E-08	13.17099
PDZK1IP1	1.419947702	2.982252561	6.6390924	1.01E-10	2.17E-08	12.8041685
HLA-DRB6	1.019086564	3.416528309	6.272737133	9.09E-10	1.66E-07	10.65572211
LAMB3	1.166010585	5.286262677	6.238523526	1.11E-09	2.00E-07	10.46018082
SAA1	1.41600332	2.654930863	6.048062623	3.33E-09	5.38E-07	9.387850504
CTA-384D8.31	1.496002497	3.706587592	5.926902493	6.59E-09	9.89E-07	8.72014756
KRT20	-1.651014337	3.849272968	-5.111245432	4.94E-07	4.44E-05	4.527055269
PTN	-1.187229059	3.467783696	-4.940954515	1.14E-06	9.03E-05	3.719953799
COL17A1	1.052893569	2.930380651	4.84201851	1.83E-06	0.000132701	3.262179777
SLPI	1.253477216	6.10662035	4.642403218	4.65E-06	0.000289119	2.363762761
S100A2	1.340524778	6.890815914	4.557765834	6.85E-06	0.000394335	1.993093726
TAC3	-1.020517525	1.387124891	-4.452689084	1.10E-05	0.000575002	1.541488142
CASP14	1.074722252	2.298160438	4.32014166	1.96E-05	0.000906287	0.985465445
KRT17	1.034247792	8.441684512	4.032005215	6.60E-05	0.002344174	-0.170126098
IGF2	-1.315859273	4.783349661	-3.964475176	8.69E-05	0.002884411	-0.430331139
UPK2	-1.110485535	5.791721532	-3.239613774	0.0012953	0.021795005	-2.963902709

Supplementary Table S9

BP

ONTOLOG	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
BP	GO:0034341	response to interfe	26/77	199/18670	1.42E-32	2.16E-29	1.62E-29	IRF1/HLA-F	26
BP	GO:0071346	cellular response t	23/77	180/18670	1.58E-28	1.20E-25	9.03E-26	IRF1/HLA-F	23
BP	GO:0060333	interferon-gamma	19/77	91/18670	6.44E-28	3.26E-25	2.45E-25	IRF1/HLA-F	19
BP	GO:0060337	type I interferon si	18/77	95/18670	1.23E-25	3.72E-23	2.80E-23	PSMB8/IFI3	18
BP	GO:0071357	cellular response t	18/77	95/18670	1.23E-25	3.72E-23	2.80E-23	PSMB8/IFI3	18
BP	GO:0034340	response to type I	18/77	99/18670	2.74E-25	6.93E-23	5.21E-23	PSMB8/IFI3	18
BP	GO:0002478	antigen processing	19/77	175/18670	3.42E-22	7.42E-20	5.58E-20	PSMB8/PSM	19
BP	GO:0019884	antigen processing	19/77	182/18670	7.35E-22	1.40E-19	1.05E-19	PSMB8/PSM	19
BP	GO:0048002	antigen processing	19/77	189/18670	1.53E-21	2.58E-19	1.94E-19	PSMB8/PSM	19
BP	GO:0019882	antigen processing	19/77	226/18670	4.80E-20	7.28E-18	5.47E-18	PSMB8/PSM	19
BP	GO:0009615	response to virus	21/77	323/18670	8.67E-20	1.20E-17	9.00E-18	RTP4/IRF1/	21
BP	GO:0051607	defense response t	19/77	238/18670	1.29E-19	1.63E-17	1.22E-17	RTP4/IRF1/	19
BP	GO:0019883	antigen processing	9/77	22/18670	1.01E-16	1.18E-14	8.90E-15	TAP1/HLA-	9
BP	GO:0002483	antigen processing	8/77	15/18670	3.62E-16	3.66E-14	2.75E-14	TAP1/HLA-	8
BP	GO:0019885	antigen processing	8/77	15/18670	3.62E-16	3.66E-14	2.75E-14	TAP1/HLA-	8
BP	GO:0002475	antigen processing	7/77	16/18670	1.70E-13	1.62E-11	1.22E-11	HLA-F/HLA	7
BP	GO:0002479	antigen processing	10/77	75/18670	5.20E-13	4.64E-11	3.49E-11	PSMB8/PSM	10
BP	GO:0042590	antigen processing	10/77	79/18670	8.91E-13	7.52E-11	5.65E-11	PSMB8/PSM	10
BP	GO:0002474	antigen processing	10/77	96/18670	6.60E-12	5.27E-10	3.96E-10	PSMB8/PSM	10
BP	GO:1903900	regulation of viral	11/77	149/18670	2.45E-11	1.86E-09	1.40E-09	OASL/LAM	11
BP	GO:0050792	regulation of viral	12/77	208/18670	5.18E-11	3.75E-09	2.82E-09	OASL/LAM	12
BP	GO:0045071	negative regulatio	8/77	59/18670	1.08E-10	7.29E-09	5.48E-09	OASL/BST2	8
BP	GO:0043903	regulation of inter	12/77	222/18670	1.10E-10	7.29E-09	5.48E-09	OASL/LAM	12
BP	GO:0045069	regulation of viral	9/77	95/18670	1.88E-10	1.19E-08	8.96E-09	OASL/BST2	9
BP	GO:0019886	antigen processing	9/77	98/18670	2.50E-10	1.52E-08	1.14E-08	HLA-DMA/	9
BP	GO:0002495	antigen processing	9/77	101/18670	3.28E-10	1.85E-08	1.39E-08	HLA-DMA/	9
BP	GO:0048525	negative regulatio	9/77	101/18670	3.28E-10	1.85E-08	1.39E-08	OASL/STAT	9
BP	GO:0002504	antigen processing	9/77	102/18670	3.59E-10	1.95E-08	1.46E-08	HLA-DMA/	9
BP	GO:0050852	T cell receptor sig	11/77	202/18670	6.49E-10	3.40E-08	2.55E-08	PSMB8/PSM	11
BP	GO:0001916	positive regulatio	6/77	26/18670	8.70E-10	4.40E-08	3.31E-08	HLA-F/HLA	6
BP	GO:0035456	response to interfe	6/77	28/18670	1.41E-09	6.93E-08	5.21E-08	IRF1/AIM2/	6
BP	GO:0019079	viral genome repli	9/77	122/18670	1.79E-09	8.49E-08	6.38E-08	OASL/BST2	9
BP	GO:1903901	negative regulatio	8/77	85/18670	2.15E-09	9.89E-08	7.43E-08	OASL/BST2	8
BP	GO:0001914	regulation of T cel	6/77	33/18670	4.09E-09	1.83E-07	1.37E-07	HLA-F/HLA	6
BP	GO:0001819	positive regulatio	14/77	464/18670	5.67E-09	2.46E-07	1.85E-07	IRF1/HLA-F	14
BP	GO:0001906	cell killing	9/77	168/18670	2.98E-08	1.26E-06	9.45E-07	HLA-F/HLA	9
BP	GO:0002711	positive regulatio	6/77	48/18670	4.32E-08	1.77E-06	1.33E-06	HLA-F/HLA	6
BP	GO:0001913	T cell mediated cy	6/77	49/18670	4.90E-08	1.96E-06	1.47E-06	HLA-F/HLA	6
BP	GO:0050851	antigen receptor-	11/77	316/18670	6.79E-08	2.64E-06	1.99E-06	PSMB8/PSM	11
BP	GO:0019058	viral life cycle	11/77	328/18670	9.90E-08	3.76E-06	2.82E-06	OASL/LAM	11
BP	GO:0001912	positive regulatio	6/77	56/18670	1.11E-07	4.12E-06	3.10E-06	HLA-F/HLA	6
BP	GO:0001909	leukocyte mediate	7/77	107/18670	2.88E-07	1.04E-05	7.83E-06	HLA-F/HLA	7
BP	GO:0031343	positive regulatio	6/77	68/18670	3.61E-07	1.27E-05	9.57E-06	HLA-F/HLA	6
BP	GO:0002709	regulation of T cel	6/77	70/18670	4.29E-07	1.48E-05	1.11E-05	HLA-F/HLA	6
BP	GO:0043122	regulation of I-kap	9/77	237/18670	5.60E-07	1.89E-05	1.42E-05	APOL3/UB	9
BP	GO:0001910	regulation of leuk	6/77	78/18670	8.19E-07	2.70E-05	2.03E-05	HLA-F/HLA	6
BP	GO:0043123	positive regulatio	8/77	183/18670	8.64E-07	2.79E-05	2.10E-05	APOL3/UB	8
BP	GO:0035458	cellular response t	4/77	20/18670	1.23E-06	3.90E-05	2.93E-05	IRF1/AIM2/	4
BP	GO:0035455	response to interfe	4/77	21/18670	1.52E-06	4.70E-05	3.53E-05	IFIT3/LAM	4
BP	GO:0007249	I-kappaB kinase/	9/77	269/18670	1.61E-06	4.88E-05	3.66E-05	APOL3/UB	9
BP	GO:0031341	regulation of cell	6/77	98/18670	3.15E-06	9.36E-05	7.04E-05	HLA-F/HLA	6
BP	GO:0002824	positive regulatio	6/77	100/18670	3.54E-06	0.000101	7.60E-05	HLA-F/HLA	6
BP	GO:0002429	immune response-	11/77	473/18670	3.64E-06	0.000101	7.60E-05	PSMB8/PSM	11
BP	GO:0002757	immune response-	11/77	473/18670	3.64E-06	0.000101	7.60E-05	PSMB8/PSM	11
BP	GO:0070663	regulation of leuk	8/77	222/18670	3.66E-06	0.000101	7.60E-05	IRF1/IDO1/	8
BP	GO:0002819	regulation of adap	7/77	160/18670	4.33E-06	0.000117	8.82E-05	IRF1/HLA-F	7
BP	GO:0030593	neutrophil chemot	6/77	104/18670	4.45E-06	0.000117	8.83E-05	CXCL11/C	6
BP	GO:0045088	regulation of innat	9/77	305/18670	4.49E-06	0.000117	8.83E-05	PSMB8/PSM	9
BP	GO:0002708	positive regulatio	6/77	105/18670	4.70E-06	0.000119	8.94E-05	HLA-F/HLA	6
BP	GO:0002821	positive regulatio	6/77	105/18670	4.70E-06	0.000119	8.94E-05	HLA-F/HLA	6
BP	GO:0002456	T cell mediated i	6/77	106/18670	4.97E-06	0.000124	9.29E-05	HLA-F/HLA	6
BP	GO:1990266	neutrophil migrati	6/77	118/18670	9.22E-06	0.000226	0.00017	CXCL11/C	6
BP	GO:0052548	regulation of endo	10/77	425/18670	9.46E-06	0.000228	0.00017	PSMB8/PSM	10
BP	GO:0071621	granulocyte chem	6/77	123/18670	1.17E-05	0.000278	0.00021	CXCL11/C	6
BP	GO:0002449	lymphocyte media	9/77	352/18670	1.42E-05	0.000331	0.00025	HLA-F/HLA	9
BP	GO:0052547	regulation of pepti	10/77	452/18670	1.61E-05	0.000371	0.00028	PSMB8/PSM	10
BP	GO:0002697	regulation of imm	10/77	462/18670	1.95E-05	0.000441	0.00033	HLA-F/HLA	10
BP	GO:0042110	T cell activation	10/77	464/18670	2.02E-05	0.000451	0.00034	IRF1/B2M/	10
BP	GO:0002705	positive regulatio	6/77	136/18670	2.07E-05	0.000456	0.00034	HLA-F/HLA	6

BP	GO:0002703	regulation of leuk	7/77	205/18670	2.18E-05	0.000467	0.00035	HLA-F/HLA	7
BP	GO:0019835	cytolysis	4/77	40/18670	2.18E-05	0.000467	0.00035	GZMH/APO	4
BP	GO:0070665	positive regulatio	6/77	139/18670	2.35E-05	0.000495	0.00037	CD74/BST2/	6
BP	GO:0050670	regulation of lymp	7/77	208/18670	2.39E-05	0.000498	0.00037	IRF1/IDO1/	7
BP	GO:0032944	regulation of mon	7/77	209/18670	2.47E-05	0.000506	0.00038	IRF1/IDO1/	7
BP	GO:0097530	granulocyte migra	6/77	141/18670	2.55E-05	0.000515	0.00039	CXCL11/CD	6
BP	GO:0045089	positive regulatio	7/77	214/18670	2.87E-05	0.000574	0.00043	PSMB8/PS	7
BP	GO:0002822	regulation of adap	6/77	145/18670	2.98E-05	0.000588	0.00044	HLA-F/HLA	6
BP	GO:0070661	leukocyte prolifer	8/77	298/18670	3.11E-05	0.000605	0.00045	IRF1/IDO1/	8
BP	GO:0002699	positive regulatio	7/77	219/18670	3.33E-05	0.000639	0.00048	HLA-F/HLA	7
BP	GO:0002706	regulation of lymp	6/77	149/18670	3.47E-05	0.000659	0.0005	HLA-F/HLA	6
BP	GO:0030595	leukocyte chemot	7/77	224/18670	3.84E-05	0.000717	0.00054	CXCL11/CD	7
BP	GO:0002831	regulation of resp	9/77	400/18670	3.87E-05	0.000717	0.00054	PSMB8/PS	9
BP	GO:0034612	response to tumor	8/77	312/18670	4.30E-05	0.000787	0.00059	PSMB8/PS	8
BP	GO:0042129	regulation of T ce	6/77	156/18670	4.49E-05	0.000804	0.0006	IRF1/IDO1/	6
BP	GO:0050863	regulation of T ce	8/77	314/18670	4.50E-05	0.000804	0.0006	IRF1/IDO1/	8
BP	GO:2000116	regulation of cyst	7/77	239/18670	5.79E-05	0.001023	0.00077	PSMB9/LA	7
BP	GO:0050663	cytokine secretion	7/77	240/18670	5.95E-05	0.001038	0.00078	GBP1/AIM2	7
BP	GO:0002833	positive regulatio	7/77	249/18670	7.50E-05	0.001293	0.00097	PSMB8/PS	7
BP	GO:0002237	response to molec	8/77	343/18670	8.36E-05	0.001425	0.00107	B2M/CXCL	8
BP	GO:0032069	regulation of nucl	3/77	22/18670	9.82E-05	0.001656	0.00124	OASL/OAS	3
BP	GO:0032732	positive regulatio	4/77	59/18670	0.0001025	0.001709	0.00128	AIM2/CASP	4
BP	GO:0042098	T cell proliferatio	6/77	184/18670	0.0001121	0.00184	0.00138	IRF1/IDO1/	6
BP	GO:0032612	interleukin-1 prod	5/77	115/18670	0.0001127	0.00184	0.00138	AIM2/CASP	5
BP	GO:0050701	interleukin-1 secr	4/77	61/18670	0.0001168	0.001886	0.00142	AIM2/CASP	4
BP	GO:0002460	adaptive immune	8/77	361/18670	0.0001191	0.001902	0.00143	HLA-F/HLA	8
BP	GO:0046651	lymphocyte prolif	7/77	272/18670	0.00013	0.002055	0.00154	IRF1/IDO1/	7
BP	GO:0032943	mononuclear cell	7/77	274/18670	0.000136	0.002128	0.0016	IRF1/IDO1/	7
BP	GO:0048247	lymphocyte chem	4/77	64/18670	0.0001408	0.002182	0.00164	CXCL11/C	4
BP	GO:1903706	regulation of hem	9/77	475/18670	0.0001441	0.00221	0.00166	PSMB8/PS	9
BP	GO:0019730	antimicrobial hum	5/77	122/18670	0.0001489	0.00226	0.0017	CXCL11/G	5
BP	GO:0051249	regulation of lymp	9/77	485/18670	0.0001685	0.002532	0.0019	IRF1/HLA-	9
BP	GO:0032479	regulation of type	5/77	126/18670	0.0001732	0.002577	0.00194	IRF1/UBE2	5
BP	GO:0031349	positive regulatio	8/77	384/18670	0.0001818	0.002679	0.00201	PSMB8/PS	8
BP	GO:0032606	type I interferon p	5/77	128/18670	0.0001864	0.002721	0.00205	IRF1/UBE2	5
BP	GO:0071356	cellular response t	7/77	291/18670	0.0001969	0.002847	0.00214	PSMB8/PS	7
BP	GO:0050671	positive regulatio	5/77	130/18670	0.0002004	0.00287	0.00216	CD74/HLA-	5
BP	GO:0001773	myeloid dendritic	3/77	28/18670	0.0002052	0.002884	0.00217	BATF2/UB	3
BP	GO:0010818	T cell chemotaxis	3/77	28/18670	0.0002052	0.002884	0.00217	CXCL11/C	3
BP	GO:0032946	positive regulatio	5/77	131/18670	0.0002077	0.002892	0.00217	CD74/HLA-	5
BP	GO:0070229	negative regulatio	3/77	29/18670	0.0002281	0.003146	0.00236	IDO1/CD74/	3
BP	GO:0097529	myeloid leukocyt	6/77	210/18670	0.00023	0.003146	0.00236	CXCL11/CD	6
BP	GO:0061844	antimicrobial hum	4/77	73/18670	0.0002346	0.00318	0.00239	CXCL11/G	4
BP	GO:0060326	cell chemotaxis	7/77	304/18670	0.000257	0.003423	0.00257	CXCL11/CD	7
BP	GO:1903037	regulation of leuk	7/77	304/18670	0.000257	0.003423	0.00257	IRF1/IDO1/	7
BP	GO:0002718	regulation of cytol	4/77	84/18670	0.0004019	0.005305	0.00399	HLA-F/B2M	4
BP	GO:0032496	response to lipopo	7/77	330/18670	0.0004216	0.005517	0.00415	CXCL11/ID	7
BP	GO:0002690	positive regulatio	4/77	87/18670	0.0004593	0.005959	0.00448	CD74/CXCL	4
BP	GO:0007159	leukocyte cell-cell	7/77	337/18670	0.0004779	0.006119	0.0046	IRF1/IDO1/	7
BP	GO:0070098	chemokine-media	4/77	88/18670	0.0004797	0.006119	0.0046	CXCL11/C	4
BP	GO:0050716	positive regulatio	3/77	38/18670	0.0005129	0.006488	0.00488	AIM2/CASP	3
BP	GO:0051281	positive regulatio	3/77	40/18670	0.0005971	0.007491	0.00563	CXCL11/C	3
BP	GO:0033209	tumor necrosis fac	5/77	167/18670	0.0006338	0.007887	0.00593	PSMB8/PS	5
BP	GO:0042102	positive regulatio	4/77	95/18670	0.0006408	0.007909	0.00594	HLA-DPA1/	4
BP	GO:1990868	response to chem	4/77	97/18670	0.0006931	0.008417	0.00633	CXCL11/C	4
BP	GO:1990869	cellular response t	4/77	97/18670	0.0006931	0.008417	0.00633	CXCL11/C	4
BP	GO:0071104	response to interl	2/77	10/18670	0.0007395	0.008909	0.0067	STAT1/IL2	2
BP	GO:0032611	interleukin-1 beta	4/77	101/18670	0.0008067	0.009567	0.00719	AIM2/CASP	4
BP	GO:0032649	regulation of inter	4/77	101/18670	0.0008067	0.009567	0.00719	CD2/ISG15/	4
BP	GO:0002367	cytokine producti	4/77	102/18670	0.000837	0.009849	0.0074	HLA-F/B2M	4
BP	GO:0032652	regulation of inter	4/77	103/18670	0.0008681	0.010137	0.00762	AIM2/CASP	4
BP	GO:0045646	regulation of eryt	3/77	47/18670	0.0009599	0.011039	0.0083	B2M/STAT1	3
BP	GO:2000107	negative regulatio	3/77	47/18670	0.0009599	0.011039	0.0083	IDO1/CD74/	3
BP	GO:0002696	positive regulatio	7/77	380/18670	0.0009691	0.011061	0.00831	HLA-F/CD7	7
BP	GO:0050900	leukocyte migrati	8/77	499/18670	0.0010294	0.011662	0.00877	CXCL11/CD	8
BP	GO:0002791	regulation of pept	8/77	500/18670	0.0010427	0.011725	0.00881	GBP1/CD74	8
BP	GO:0031581	hemidesmosome	2/77	12/18670	0.0010788	0.012042	0.00905	LAMB3/CO	2
BP	GO:0072676	lymphocyte migra	4/77	111/18670	0.0011471	0.01271	0.00955	CXCL11/C	4
BP	GO:0050867	positive regulatio	7/77	394/18670	0.0011949	0.013144	0.00988	HLA-F/CD7	7
BP	GO:0032609	interferon-gamma	4/77	113/18670	0.0012256	0.013385	0.01006	CD2/ISG15/	4

BP	GO:0002688	regulation of leuk	4/77	114/18670	0.0012662	0.01369	0.01029	CD74/CXCL	4
BP	GO:0045059	positive thymic T	2/77	13/18670	0.0012716	0.01369	0.01029	CD74/CD3D	2
BP	GO:0032731	positive regulatio	3/77	52/18670	0.0012891	0.01378	0.01036	AIM2/CASP	3
BP	GO:0022407	regulation of cell-	7/77	402/18670	0.0013413	0.014069	0.01058	IRF1/IDO1/	7
BP	GO:0045785	positive regulatio	7/77	403/18670	0.0013606	0.014069	0.01058	CD74/HLA-	7
BP	GO:0050702	interleukin-1 beta	3/77	53/18670	0.0013624	0.014069	0.01058	AIM2/CASP	3
BP	GO:0050704	regulation of inter	3/77	53/18670	0.0013624	0.014069	0.01058	AIM2/CASP	3
BP	GO:0070228	regulation of lymp	3/77	53/18670	0.0013624	0.014069	0.01058	IDO1/CD74/	3
BP	GO:0001818	negative regulatio	6/77	296/18670	0.001394	0.014298	0.01075	HLA-F/UBE	6
BP	GO:0002720	positive regulatio	3/77	54/18670	0.0014383	0.014555	0.01094	HLA-F/B2M	3
BP	GO:0010524	positive regulatio	3/77	54/18670	0.0014383	0.014555	0.01094	CXCL11/CX	3
BP	GO:0070234	positive regulatio	2/77	14/18670	0.0014795	0.014815	0.01114	IDO1/CCL5	2
BP	GO:0050870	positive regulatio	5/77	202/18670	0.0014834	0.014815	0.01114	CD74/HLA-	5
BP	GO:0071222	cellular response t	5/77	205/18670	0.0015829	0.015705	0.0118	CXCL11/CA	5
BP	GO:0030099	myeloid cell differ	7/77	416/18670	0.0016312	0.016079	0.01209	BATF2/B2M	7
BP	GO:0051928	positive regulatio	4/77	123/18670	0.0016753	0.016407	0.01233	CXCL11/CX	4
BP	GO:0009612	response to mecha	5/77	210/18670	0.0017594	0.017012	0.01279	IRF1/CASP1	5
BP	GO:0050707	regulation of cytol	5/77	210/18670	0.0017594	0.017012	0.01279	GBP1/AIM2	5
BP	GO:0071219	cellular response t	5/77	212/18670	0.001834	0.01762	0.01324	CXCL11/CA	5
BP	GO:0002687	positive regulatio	4/77	128/18670	0.0019384	0.018412	0.01384	CD74/CXCL	4
BP	GO:0002830	positive regulatio	2/77	16/18670	0.0019406	0.018412	0.01384	IDO1/CD74	2
BP	GO:1903039	positive regulatio	5/77	218/18670	0.0020714	0.019531	0.01468	CD74/HLA-	5
BP	GO:0002683	negative regulatio	7/77	435/18670	0.0021002	0.01968	0.01479	IRF1/HLA-F	7
BP	GO:0010819	regulation of T cel	2/77	17/18670	0.0021935	0.020428	0.01536	CXCL10/CC	2
BP	GO:0050921	positive regulatio	4/77	135/18670	0.0023528	0.021778	0.01637	CD74/CXCL	4
BP	GO:0032729	positive regulatio	3/77	65/18670	0.0024519	0.021976	0.01652	CD2/HLA-D	3
BP	GO:0072678	T cell migration	3/77	65/18670	0.0024519	0.021976	0.01652	CXCL11/CX	3
BP	GO:0043011	myeloid dendritic	2/77	18/18670	0.0024611	0.021976	0.01652	BATF2/UBD	2
BP	GO:0070230	positive regulatio	2/77	18/18670	0.0024611	0.021976	0.01652	IDO1/CCL5	2
BP	GO:0070233	negative regulatio	2/77	18/18670	0.0024611	0.021976	0.01652	IDO1/CCL5	2
BP	GO:0090026	positive regulatio	2/77	18/18670	0.0024611	0.021976	0.01652	CXCL10/CC	2
BP	GO:0051251	positive regulatio	6/77	334/18670	0.0025594	0.02272	0.01708	HLA-F/CD7	6
BP	GO:0002700	regulation of prod	4/77	139/18670	0.0026152	0.022947	0.01725	HLA-F/B2M	4
BP	GO:0050715	positive regulatio	4/77	139/18670	0.0026152	0.022947	0.01725	AIM2/CASP	4
BP	GO:0002544	chronic inflammat	2/77	19/18670	0.0027433	0.023933	0.01799	IDO1/CCL5	2
BP	GO:0050918	positive chemotax	3/77	68/18670	0.0027884	0.024187	0.01818	CXCL10/CC	3
BP	GO:0002218	activation of innat	4/77	142/18670	0.0028247	0.024363	0.01831	PSMB8/PSM	4
BP	GO:0070227	lymphocyte apopt	3/77	69/18670	0.0029066	0.024893	0.01871	IDO1/CD74/	3
BP	GO:0071216	cellular response t	5/77	236/18670	0.002919	0.024893	0.01871	CXCL11/CA	5
BP	GO:0051346	negative regulatio	7/77	463/18670	0.0029749	0.025228	0.01896	LAMP3/GZM	7
BP	GO:0033077	T cell differentiati	3/77	70/18670	0.0030278	0.025534	0.01919	B2M/CD74/	3
BP	GO:0051250	negative regulatio	4/77	146/18670	0.0031215	0.026147	0.01965	IRF1/HLA-F	4
BP	GO:0030217	T cell differentiati	5/77	240/18670	0.003137	0.026147	0.01965	IRF1/B2M/C	5
BP	GO:1904427	positive regulatio	3/77	71/18670	0.0031521	0.026147	0.01965	CXCL11/CX	3
BP	GO:0050708	regulation of prote	7/77	472/18670	0.0033084	0.027257	0.02049	GBP1/AIM2	7
BP	GO:0045061	thymic T cell sele	2/77	21/18670	0.0033511	0.027257	0.02049	CD74/CD3D	2
BP	GO:1901739	regulation of myol	2/77	21/18670	0.0033511	0.027257	0.02049	CXCL10/CX	2
BP	GO:2001056	positive regulatio	4/77	149/18670	0.0033577	0.027257	0.02049	AIM2/CASP	4
BP	GO:0006959	humoral immune	6/77	356/18670	0.0035051	0.028302	0.02127	CXCL11/GN	6
BP	GO:0072643	interferon-gamma	2/77	22/18670	0.0036764	0.029528	0.0222	CD2/ISG15	2
BP	GO:0010951	negative regulatio	5/77	250/18670	0.0037333	0.029827	0.02242	LAMP3/BST	5
BP	GO:0061025	membrane fusion	4/77	154/18670	0.0037779	0.030025	0.02257	TAP1/TAP2/	4
BP	GO:0032481	positive regulatio	3/77	77/18670	0.0039635	0.031337	0.02356	IRF1/STAT1	3
BP	GO:0010499	proteasomal ubiqu	2/77	23/18670	0.0040158	0.031423	0.02362	PSMB8/PSM	2
BP	GO:0045109	intermediate filam	2/77	23/18670	0.0040158	0.031423	0.02362	KRT20/KRT	2
BP	GO:0022409	positive regulatio	5/77	255/18670	0.0040602	0.031607	0.02376	CD74/HLA-	5
BP	GO:0042832	defense response t	2/77	24/18670	0.0043692	0.033667	0.02531	BATF2/GBP	2
BP	GO:0071677	positive regulatio	2/77	24/18670	0.0043692	0.033667	0.02531	CXCL10/CC	2
BP	GO:0010466	negative regulatio	5/77	262/18670	0.0045516	0.034896	0.02623	LAMP3/BST	5
BP	GO:0051279	regulation of relea	3/77	82/18670	0.0047285	0.035594	0.02676	CXCL11/CX	3
BP	GO:0001562	response to protoz	2/77	25/18670	0.0047365	0.035594	0.02676	BATF2/GBP	2
BP	GO:0002719	negative regulatio	2/77	25/18670	0.0047365	0.035594	0.02676	HLA-F/BST	2
BP	GO:0090025	regulation of mon	2/77	25/18670	0.0047365	0.035594	0.02676	CXCL10/CC	2
BP	GO:2000106	regulation of leuk	3/77	83/18670	0.0048914	0.036577	0.02749	IDO1/CD74/	3
BP	GO:0002230	positive regulatio	2/77	26/18670	0.0051176	0.037895	0.02848	AIM2/STAT	2
BP	GO:0010996	response to audito	2/77	26/18670	0.0051176	0.037895	0.02848	CXCL10/PT	2
BP	GO:0051100	negative regulatio	4/77	169/18670	0.0052496	0.038684	0.02908	B2M/GZMA	4
BP	GO:1901623	regulation of lymp	2/77	27/18670	0.0055123	0.040423	0.03039	CXCL10/CC	2
BP	GO:0051262	protein tetrameriz	4/77	172/18670	0.005584	0.040753	0.03063	B2M/CD74/	4
BP	GO:2000108	positive regulatio	2/77	28/18670	0.0059205	0.042883	0.03223	IDO1/CCL5	2

BP	GO:0002695	negative regulatio	4/77	175/18670	0.0059324	0.042883	0.03223	IRF1/HLA-F	4
BP	GO:0032651	regulation of inter	3/77	90/18670	0.0061269	0.043871	0.03298	AIM2/CASP	3
BP	GO:0045778	positive regulatio	3/77	90/18670	0.0061269	0.043871	0.03298	ISG15/IFITM	3
BP	GO:0001959	regulation of cytol	4/77	177/18670	0.0061726	0.043991	0.03307	CD74/CASP	4
BP	GO:0010950	positive regulatio	4/77	178/18670	0.0062951	0.044571	0.0335	AIM2/CASP	4
BP	GO:0045639	positive regulatio	3/77	91/18670	0.0063172	0.044571	0.0335	CD74/STAT	3
BP	GO:0060142	regulation of sync	2/77	29/18670	0.0063422	0.044571	0.0335	CXCL10/CX	2
BP	GO:0071347	cellular response t	4/77	179/18670	0.0064192	0.044905	0.03375	PSMB8/PSM	4
BP	GO:2000117	negative regulatio	3/77	92/18670	0.006511	0.045259	0.03402	LAMP3/IFI1	3
BP	GO:1905330	regulation of mor	4/77	180/18670	0.0065449	0.045259	0.03402	PSMB8/PSM	4
BP	GO:0002440	production of mol	5/77	286/18670	0.0065592	0.045259	0.03402	HLA-F/B2M	5
BP	GO:0002828	regulation of type	2/77	30/18670	0.0067771	0.046341	0.03483	IDO1/CD74	2
BP	GO:0046596	regulation of viral	2/77	30/18670	0.0067771	0.046341	0.03483	CD74/IFITM	2
BP	GO:0006906	vesicle fusion	3/77	94/18670	0.0069092	0.047032	0.03535	TAP1/TAP2	3
BP	GO:0002702	positive regulatio	3/77	95/18670	0.0071136	0.048207	0.03624	HLA-F/B2M	3
BP	GO:0002724	regulation of T cel	2/77	31/18670	0.0072253	0.048317	0.03632	HLA-F/B2M	2
BP	GO:0045648	positive regulatio	2/77	31/18670	0.0072253	0.048317	0.03632	STAT1/ISG1	2
BP	GO:2000406	positive regulatio	2/77	31/18670	0.0072253	0.048317	0.03632	CXCL10/CC	2

CC

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
CC	GO:0042611	MHC protein	15/79	25/19717	8.49E-31	1.07E-28	5.90E-29	HLA-F/HLA-	15
CC	GO:0071556	integral comp	13/79	29/19717	1.57E-24	6.57E-23	3.62E-23	HLA-F/HLA-	13
CC	GO:0098553	lumenal side	13/79	29/19717	1.57E-24	6.57E-23	3.62E-23	HLA-F/HLA-	13
CC	GO:0098576	lumenal side	13/79	34/19717	2.11E-23	6.64E-22	3.66E-22	HLA-F/HLA-	13
CC	GO:0012507	ER to Golgi t	14/79	62/19717	2.04E-21	5.13E-20	2.83E-20	HLA-F/HLA-	14
CC	GO:0030176	integral comp	16/79	150/19717	7.95E-19	1.67E-17	9.21E-18	TAP1/HLA-F	16
CC	GO:0030134	COPII-coated	14/79	93/19717	9.44E-19	1.70E-17	9.37E-18	HLA-F/HLA-	14
CC	GO:0042613	MHC class II	9/79	16/19717	1.86E-18	2.61E-17	1.44E-17	HLA-DMA/C	9
CC	GO:0031227	intrinsic com	16/79	158/19717	1.86E-18	2.61E-17	1.44E-17	TAP1/HLA-F	16
CC	GO:0030666	endocytic ves	16/79	167/19717	4.59E-18	5.79E-17	3.19E-17	TAP1/HLA-F	16
CC	GO:0030660	Golgi-associa	14/79	114/19717	1.86E-17	2.13E-16	1.18E-16	HLA-F/HLA-	14
CC	GO:0030139	endocytic ves	18/79	303/19717	1.63E-16	1.71E-15	9.45E-16	TAP1/HLA-F	18
CC	GO:0030662	coated vesicle	15/79	182/19717	5.41E-16	5.24E-15	2.89E-15	HLA-F/HLA-	15
CC	GO:0005798	Golgi-associa	14/79	178/19717	1.06E-14	9.58E-14	5.28E-14	HLA-F/HLA-	14
CC	GO:0030658	transport ves	14/79	208/19717	9.27E-14	7.79E-13	4.29E-13	HLA-F/HLA-	14
CC	GO:0030135	coated vesicle	15/79	289/19717	5.01E-13	3.94E-12	2.17E-12	HLA-F/HLA-	15
CC	GO:0031301	integral comp	16/79	350/19717	5.41E-13	4.01E-12	2.21E-12	TAP1/HLA-F	16
CC	GO:0031300	intrinsic com	16/79	381/19717	1.97E-12	1.38E-11	7.60E-12	TAP1/HLA-F	16
CC	GO:0030669	clathrin-coate	8/79	44/19717	7.28E-12	4.83E-11	2.66E-11	CD74/HLA-D	8
CC	GO:0045334	clathrin-coate	8/79	63/19717	1.50E-10	9.43E-10	5.20E-10	CD74/HLA-D	8
CC	GO:0030133	transport ves	14/79	392/19717	4.61E-10	2.77E-09	1.53E-09	HLA-F/HLA-	14
CC	GO:0010008	endosome me	15/79	479/19717	6.32E-10	3.62E-09	2.00E-09	HLA-F/HLA-	15
CC	GO:0030670	phagocytic ve	8/79	76/19717	6.99E-10	3.83E-09	2.11E-09	TAP1/HLA-F	8
CC	GO:0030665	clathrin-coate	9/79	115/19717	8.32E-10	4.37E-09	2.41E-09	CD74/HLA-D	9
CC	GO:0005765	lysosomal me	13/79	354/19717	1.47E-09	7.36E-09	4.06E-09	HLA-F/HLA-	13
CC	GO:0098852	lytic vacuole	13/79	355/19717	1.52E-09	7.36E-09	4.06E-09	HLA-F/HLA-	13
CC	GO:0045335	phagocytic ve	9/79	132/19717	2.84E-09	1.33E-08	7.31E-09	TAP1/HLA-F	9
CC	GO:0032588	trans-Golgi n	8/79	92/19717	3.28E-09	1.48E-08	8.14E-09	CD74/HLA-D	8
CC	GO:0005774	vacuolar mem	13/79	412/19717	9.07E-09	3.94E-08	2.17E-08	HLA-F/HLA-	13
CC	GO:0009897	external side	12/79	393/19717	5.12E-08	2.15E-07	1.18E-07	HLA-F/HLA-	12
CC	GO:0030136	clathrin-coate	9/79	188/19717	6.23E-08	2.53E-07	1.40E-07	CD74/HLA-D	9
CC	GO:0055038	recycling end	6/79	81/19717	8.72E-07	3.43E-06	1.89E-06	HLA-F/HLA-	6
CC	GO:0005802	trans-Golgi n	8/79	236/19717	4.70E-06	1.79E-05	9.89E-06	CD74/HLA-D	8
CC	GO:0031901	early endoson	6/79	149/19717	2.97E-05	0.00011	6.07E-05	HLA-F/HLA-	6
CC	GO:0005770	late endosome	7/79	256/19717	7.49E-05	0.000263	0.000145	HLA-DMA/L	7
CC	GO:0055037	recycling end	6/79	176/19717	7.53E-05	0.000263	0.000145	HLA-F/HLA-	6
CC	GO:0005769	early endoson	8/79	350/19717	7.93E-05	0.00027	0.000149	HLA-F/HLA-	8
CC	GO:0098791	Golgi apparat	8/79	359/19717	9.46E-05	0.000314	0.000173	CD74/HLA-D	8
CC	GO:0031984	organelle sub	8/79	380/19717	0.00014	0.000452	0.000249	CD74/HLA-D	8
CC	GO:0031902	late endosome	5/79	134/19717	0.0002026	0.000638	0.000352	HLA-DMA/L	5
CC	GO:0019774	proteasome c	2/79	11/19717	0.0008516	0.002617	0.001443	PSMB8/PSM	2
CC	GO:0061702	inflammasom	2/79	14/19717	0.0013981	0.004194	0.002313	AIM2/CASP1	2
CC	GO:0005839	proteasome c	2/79	20/19717	0.002874	0.00823	0.004538	PSMB8/PSM	2
CC	GO:0071682	endocytic ves	2/79	20/19717	0.002874	0.00823	0.004538	GNLY/SAA1	2
CC	GO:0034364	high-density	2/79	26/19717	0.0048402	0.013553	0.007473	APOL1/SAA	2
CC	GO:0005604	basement me	3/79	95/19717	0.0065778	0.018017	0.009934	LAMB3/PTN	3
CC	GO:0001772	immunologic	2/79	36/19717	0.009143	0.024511	0.013515	GZMA/GZM	2
CC	GO:0034358	plasma lipopr	2/79	37/19717	0.0096406	0.02479	0.013669	APOL1/SAA	2
CC	GO:1990777	lipoprotein pa	2/79	37/19717	0.0096406	0.02479	0.013669	APOL1/SAA	2
CC	GO:0032994	protein-lipid	2/79	39/19717	0.010671	0.026891	0.014827	APOL1/SAA	2
CC	GO:0005771	multivesicula	2/79	51/19717	0.0178024	0.043983	0.024251	CD74/BST2	2

MF

ONTOLOGY	ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
MF	GO:0042605	peptide antige	13/75	31/17696	9.23E-24	1.58E-21	1.13E-21	TAP1/HLA-F	13
MF	GO:0003823	antigen bindi	13/75	160/17696	1.29E-13	1.10E-11	7.85E-12	TAP1/HLA-F	13
MF	GO:0042277	peptide bindi	14/75	295/17696	2.12E-11	1.21E-09	8.63E-10	TAP1/HLA-F	14
MF	GO:0033218	amide bindin	14/75	356/17696	2.55E-10	1.01E-08	7.23E-09	TAP1/HLA-F	14
MF	GO:0032395	MHC class II	5/75	10/17696	2.96E-10	1.01E-08	7.23E-09	HLA-DQB1/	5
MF	GO:0023026	MHC class II	4/75	16/17696	5.21E-07	1.49E-05	1.06E-05	HLA-DMA/C	4
MF	GO:0140375	immune recep	7/75	128/17696	1.16E-06	2.83E-05	2.02E-05	CD74/HLA-D	7
MF	GO:0023023	MHC protein	4/75	25/17696	3.52E-06	7.52E-05	5.37E-05	HLA-DMA/C	4
MF	GO:0042379	chemokine re	5/75	66/17696	8.73E-06	0.000166	0.00012	CXCL11/CX	5
MF	GO:0045236	CXCR chemo	3/75	11/17696	1.18E-05	0.000201	0.00014	CXCL11/CX	3
MF	GO:0042287	MHC protein	4/75	40/17696	2.42E-05	0.000377	0.00027	TAP1/TAP2/	4
MF	GO:0048018	receptor ligan	10/75	482/17696	3.48E-05	0.000495	0.00035	CXCL11/CX	10
MF	GO:0030546	signaling rece	10/75	487/17696	3.79E-05	0.000499	0.00036	CXCL11/CX	10
MF	GO:0008009	chemokine ac	4/75	49/17696	5.46E-05	0.000667	0.00048	CXCL11/CX	4
MF	GO:0001664	G protein-cou	7/75	280/17696	0.000183	0.002081	0.00149	RTP4/CXCL	7
MF	GO:0005125	cytokine activ	6/75	220/17696	0.00034	0.003633	0.00259	CXCL11/CX	6
MF	GO:0042056	chemoattracta	3/75	38/17696	0.000554	0.005577	0.00398	CXCL10/CC	3
MF	GO:0005126	cytokine rece	6/75	286/17696	0.001338	0.012715	0.00908	CXCL11/CX	6
MF	GO:0097153	cysteine-type	2/75	15/17696	0.001796	0.016161	0.01154	CASP1/CAS	2
MF	GO:0004175	endopeptidas	7/75	427/17696	0.002194	0.018761	0.0134	PSMB8/PSM	7
MF	GO:0042288	MHC class I	2/75	20/17696	0.003205	0.026099	0.01864	TAP1/TAP2	2
MF	GO:0004298	threonine-typ	2/75	21/17696	0.003533	0.026266	0.01876	PSMB8/PSM	2
MF	GO:0070003	threonine-typ	2/75	21/17696	0.003533	0.026266	0.01876	PSMB8/PSM	2
MF	GO:0030247	polysaccharid	2/75	25/17696	0.004992	0.035568	0.0254	HLA-DRB1/	2
MF	GO:0008201	heparin bindi	4/75	169/17696	0.005764	0.039428	0.02815	CXCL11/CX	4

Supplementary Table S10

ID	Description	GeneRatio	BgRatio	pvalue	p.adjust	qvalue	geneID	Count
hsa04612	Antigen processing and	16/55	78/8081	2.47E-20	2.35E-18	1.22E-18	TAP1/HLA-	16
hsa05330	Allograft rejection	13/55	38/8081	6.98E-20	3.32E-18	1.73E-18	HLA-F/HLA	13
hsa05332	Graft-versus-host diseas	13/55	42/8081	3.23E-19	1.02E-17	5.32E-18	HLA-F/HLA	13
hsa04940	Type I diabetes mellitus	13/55	43/8081	4.60E-19	1.09E-17	5.69E-18	HLA-F/HLA	13
hsa05169	Epstein-Barr virus infect	20/55	202/8081	8.28E-19	1.57E-17	8.20E-18	TAP1/HLA-	20
hsa05320	Autoimmune thyroid dis	13/55	53/8081	1.01E-17	1.60E-16	8.32E-17	HLA-F/HLA	13
hsa05416	Viral myocarditis	12/55	60/8081	3.02E-15	4.09E-14	2.13E-14	HLA-F/HLA	12
hsa05164	Influenza A	15/55	171/8081	2.35E-13	2.79E-12	1.45E-12	HLA-DMA/	15
hsa04145	Phagosome	14/55	152/8081	8.51E-13	8.99E-12	4.68E-12	TAP1/HLA-	14
hsa05166	Human T-cell leukemia	15/55	219/8081	8.83E-12	8.39E-11	4.37E-11	HLA-F/HLA	15
hsa05321	Inflammatory bowel dise	10/55	65/8081	1.22E-11	9.93E-11	5.17E-11	HLA-DMA/	10
hsa04514	Cell adhesion molecules	13/55	149/8081	1.25E-11	9.93E-11	5.17E-11	HLA-F/HLA	13
hsa04658	Th1 and Th2 cell differe	11/55	92/8081	1.79E-11	1.29E-10	6.70E-11	HLA-DMA/	11
hsa05310	Asthma	8/55	31/8081	1.90E-11	1.29E-10	6.70E-11	HLA-DMA/	8
hsa05168	Herpes simplex virus 1 i	20/55	498/8081	2.87E-11	1.82E-10	9.46E-11	TAP1/HLA-	20
hsa04659	Th17 cell differentiation	11/55	107/8081	9.58E-11	5.69E-10	2.96E-10	HLA-DMA/	11
hsa05150	Staphylococcus aureus i	10/55	96/8081	6.54E-10	3.65E-09	1.90E-09	HLA-DMA/	10
hsa04640	Hematopoietic cell linea	10/55	99/8081	8.90E-10	4.69E-09	2.44E-09	HLA-DMA/	10
hsa04672	Intestinal immune netwo	8/55	49/8081	9.87E-10	4.94E-09	2.57E-09	HLA-DMA/	8
hsa05140	Leishmaniasis	9/55	77/8081	1.79E-09	8.51E-09	4.43E-09	HLA-DMA/	9
hsa05145	Toxoplasmosis	10/55	112/8081	3.02E-09	1.37E-08	7.12E-09	HLA-DMA/	10
hsa05323	Rheumatoid arthritis	9/55	93/8081	9.84E-09	4.25E-08	2.21E-08	HLA-DMA/	9
hsa05152	Tuberculosis	10/55	180/8081	2.88E-07	1.19E-06	6.19E-07	HLA-DMA/	10
hsa04621	NOD-like receptor signa	9/55	181/8081	3.04E-06	1.20E-05	6.27E-06	GBP4/GBP1	9
hsa05322	Systemic lupus erythema	8/55	136/8081	3.28E-06	1.24E-05	6.48E-06	HLA-DMA/	8
hsa05170	Human immunodeficien	9/55	212/8081	1.11E-05	4.05E-05	2.11E-05	TAP1/HLA-	9
hsa04061	Viral protein interaction	6/55	100/8081	5.48E-05	0.0001929	0.0001	CXCL11/CX	6
hsa05165	Human papillomavirus i	10/55	331/8081	6.55E-05	0.0002224	0.000116	IRF1/HLA-F	10
hsa05340	Primary immunodeficier	4/55	38/8081	0.0001194	0.0003911	0.000204	TAP1/TAP2/	4
hsa05163	Human cytomegalovirus	8/55	225/8081	0.0001256	0.0003977	0.000207	TAP1/HLA-	8
hsa04620	Toll-like receptor signali	5/55	104/8081	0.0006692	0.0020508	0.001068	CXCL11/CX	5
hsa04623	Cytosolic DNA-sensing	4/55	63/8081	0.0008495	0.002522	0.001313	AIM2/CASP	4
hsa04650	Natural killer cell media	5/55	131/8081	0.001885	0.0054265	0.002826	HLA-A/HLA	5
hsa05162	Measles	5/55	139/8081	0.0024442	0.0068295	0.003557	OAS2/STAT	5
hsa05171	Coronavirus disease - C	6/55	232/8081	0.0046964	0.0127474	0.006639	OAS2/CASP	6
hsa04062	Chemokine signaling pa	5/55	192/8081	0.00956	0.0250703	0.013056	CXCL11/CX	5
hsa05167	Kaposi sarcoma-associat	5/55	193/8081	0.0097642	0.0250703	0.013056	HLA-F/HLA	5
hsa04060	Cytokine-cytokine recep	6/55	295/8081	0.0145206	0.0363015	0.018905	CXCL11/CX	6

Supplementary Table S11
HIGH-ETV7

NAME	GS follo	GS DETA	SIZE	ES	NES	NOM p-	FDR q-val	FWER p-v	RANK A	LEADING EDG
GO_HEART	GO_HEART_	Details ...	33	-0.6801	-2.1359	0	0.095677	0.061	8882	tags=52%, list=1
GO_POSITI	GO_POSITI	Details ...	38	-0.6171	-2.1261	0	0.058888	0.072	12788	tags=53%, list=2
GO_SMOOT	GO_SMOOT	Details ...	24	-0.746	-2.0563	0	0.14334	0.173	7471	tags=58%, list=1
GO_CARDI	GO_CARDI	Details ...	73	-0.5774	-2.0543	0	0.111961	0.175	9208	tags=47%, list=1
GO_CARDI	GO_CARDI	Details ...	127	-0.5299	-2.0539	0	0.089712	0.175	12749	tags=48%, list=2
GO_VENTR	GO_VENTR	Details ...	72	-0.5606	-1.9996	0	0.170851	0.301	12749	tags=50%, list=2
GO_AORTA	GO_AORTA_	Details ...	35	-0.6539	-1.9865	0	0.181701	0.345	8882	tags=49%, list=1
GO_VENTR	GO_VENTR	Details ...	16	-0.7194	-1.9807	0	0.171366	0.36	8882	tags=50%, list=1
GO_CARDI	GO_CARDI	Details ...	127	-0.5187	-1.9764	0	0.162129	0.371	12788	tags=48%, list=2
GO_ENDOC	GO_ENDOC	Details ...	45	-0.641	-1.9692	0	0.160401	0.388	13311	tags=62%, list=2
GO_REGUL	GO_REGUL	Details ...	34	-0.6043	-1.965	0	0.154823	0.401	7643	tags=47%, list=1
GO_POSITI	GO_POSITI	Details ...	52	-0.5502	-1.9555	0	0.161212	0.432	12950	tags=48%, list=2
GO_CARDI	GO_CARDI	Details ...	74	-0.5518	-1.9406	0	0.179121	0.473	15844	tags=58%, list=2
GO_CARDI	GO_CARDI	Details ...	169	-0.4954	-1.9205	0	0.1993	0.53	12788	tags=45%, list=2
GO_VENTR	GO_VENTR	Details ...	43	-0.583	-1.9154	0	0.186481	0.545	12664	tags=53%, list=2
GO_POSITI	GO_POSITI	Details ...	61	-0.5145	-1.9056	0	0.200393	0.579	6716	tags=34%, list=1
GO_SYNAP	GO_SYNAP	Details ...	16	-0.7738	-1.9001	0	0.193154	0.589	9188	tags=75%, list=1
GO_STERO	GO_STERO	Details ...	20	-0.6676	-1.8815	0	0.227893	0.637	8941	tags=40%, list=1
GO_CARDI	GO_CARDI	Details ...	110	-0.5122	-1.875	0	0.23483	0.655	12788	tags=45%, list=2
GO_ENDOC	GO_ENDOC	Details ...	35	-0.6373	-1.8728	0	0.229994	0.657	13311	tags=60%, list=2
GO_GAMM	GO_GAMM	Details ...	26	-0.6494	-1.8661	0	0.219056	0.666	12500	tags=65%, list=2
GO_VENTR	GO_VENTR	Details ...	55	-0.531	-1.8652	0	0.212414	0.667	9208	tags=42%, list=1
GO_MESEN	GO_MESEN	Details ...	52	-0.6044	-1.8577	0	0.215545	0.685	13311	tags=62%, list=2
GO_TRABE	GO_TRABE	Details ...	48	-0.55	-1.8515	0	0.208678	0.697	8882	tags=46%, list=1
GO_LATER	GO_LATER	Details ...	15	-0.6554	-1.8474	0	0.194019	0.705	1087	tags=40%, list=2
GO_CARDI	GO_CARDI	Details ...	20	-0.6248	-1.8417	0	0.201133	0.718	8882	tags=50%, list=1
GO_ORGAN	GO_ORGAN_INDUCT		24	-0.6365	-1.835	0	0.194407	0.74	11983	tags=54%, list=2
GO_FIBRO	GO_FIBROBLAST_GR		115	-0.4726	-1.8308	0	0.193739	0.748	9127	tags=37%, list=1
GO_CELL_	GO_CELL_SURFACE_		33	-0.5979	-1.8272	0	0.192085	0.757	11983	tags=48%, list=2
GO_HINDB	GO_HINDBRAIN_MO		42	-0.5574	-1.7899	0	0.233857	0.83	11744	tags=50%, list=2
GO_HEART	GO_HEART_MORPHO		252	-0.4438	-1.7673	0	0.228275	0.866	12817	tags=42%, list=2
GO_SPECIF	GO_SPECIFICATION_		133	-0.4334	-1.7112	0	0.268296	0.935	15533	tags=46%, list=2
GO_REGUL	GO_REGULATION_O		77	-0.5009	-1.7546	0.0019	0.246566	0.877	8997	tags=38%, list=1
GO_RESPO	GO_RESPONSE_TO_F		150	-0.4152	-1.6615	0.0019	0.296147	0.97	9127	tags=33%, list=1
GO_SULFU	GO_SULFU	Details ...	15	-0.678	-1.836	0.0019	0.19727	0.738	7021	tags=40%, list=1
GO_CONVE	GO_CONVE	Details ...	15	-0.6675	-1.8392	0.002	0.195507	0.725	11983	tags=53%, list=2
GO_PDZ_D	GO_PDZ_DOMAIN_B		82	-0.4908	-1.7985	0.002	0.227175	0.809	10885	tags=46%, list=1
GO_ENDOC	GO_ENDOCRINE_HO		45	-0.4919	-1.6933	0.002	0.285436	0.951	14012	tags=42%, list=2
GO_DIGEST	GO_DIGESTIVE_TRA		49	-0.5509	-1.8286	0.002	0.193367	0.752	12111	tags=51%, list=2
GO_REGUL	GO_REGUL	Details ...	57	-0.5184	-1.8551	0.002	0.207934	0.692	8230	tags=39%, list=1
GO_NEGAT	GO_NEGAT	Details ...	19	-0.6637	-1.8695	0.002	0.220189	0.66	4615	tags=42%, list=8
GO_ANIMA	GO_ANIMAL_ORGAN		65	-0.4933	-1.7686	0.002	0.235579	0.863	11983	tags=48%, list=2
GO_SPECIF	GO_SPECIF	Details ...	36	-0.5854	-1.8712	0.002	0.224902	0.658	11983	tags=50%, list=2
GO_ATRIO	GO_ATRIOVENTRICU		25	-0.6272	-1.8127	0.002	0.214023	0.787	12664	tags=64%, list=2
GO_REGUL	GO_REGULATION_O		93	-0.4876	-1.7216	0.002	0.265799	0.925	10004	tags=43%, list=1
GO_CARDI	GO_CARDIAC_MUSC		63	-0.4897	-1.7424	0.0021	0.266048	0.898	12664	tags=46%, list=2
GO_AORTA	GO_AORTA_DEVELO		60	-0.5397	-1.7382	0.0021	0.2561	0.904	8882	tags=40%, list=1
GO_ARTER	GO_ARTER	Details ...	74	-0.5366	-1.8489	0.0021	0.201336	0.702	15325	tags=51%, list=2
GO_REGUL	GO_REGUL	Details ...	38	-0.5885	-1.8478	0.0021	0.198626	0.703	11983	tags=50%, list=2
GO_ENDOC	GO_ENDOC	Details ...	24	-0.6882	-1.8411	0.0021	0.196917	0.719	8882	tags=54%, list=1
GO_DENDR	GO_DENDRITE_MEM		43	-0.5942	-1.7789	0.0021	0.227658	0.846	12500	tags=65%, list=2
GO_HEART	GO_HEART_FORMAT		31	-0.5588	-1.7687	0.0021	0.238845	0.863	11983	tags=52%, list=2
GO_GABA_	GO_GABA_	Details ...	22	-0.7053	-1.9017	0.0021	0.199603	0.587	12825	tags=73%, list=2
GO_GABA_	GO_GABA_	Details ...	20	-0.7341	-1.9375	0.0022	0.171831	0.477	12825	tags=80%, list=2
GO_WNT_A	GO_WNT_A	Details ...	15	-0.7217	-1.9173	0.0022	0.193319	0.54	12292	tags=73%, list=2
GO_POSITI	GO_POSITIVE_REGU		74	-0.4924	-1.7391	0.0038	0.257303	0.904	9553	tags=38%, list=1
GO_REGUL	GO_REGULATION_O		153	-0.4506	-1.6888	0.0039	0.2862	0.953	10004	tags=38%, list=1

GO_MODUI	GO_MODULATION_O	45	-0.591	-1.8327	0.0039	0.194695	0.743	8229	tags=49%, list=1
GO_CARDI	GO_CARDIAC_MUSC	228	-0.4207	-1.6979	0.0039	0.282111	0.946	12976	tags=41%, list=2
GO_DIGEST	GO_DIGESTIVE_SYST	145	-0.4284	-1.6318	0.004	0.312793	0.983	12111	tags=37%, list=2
GO_REGUL	GO_REGULATION_OI	64	-0.45	-1.6374	0.0041	0.319673	0.981	15082	tags=50%, list=2
GO_ROOF_	GO_ROOF_OF_MOUT	90	-0.49	-1.7858	0.0041	0.234935	0.835	14543	tags=49%, list=2
GO_OUTFL	GO_OUTFLOW_TRAC	80	-0.5121	-1.7826	0.0041	0.234632	0.841	16390	tags=58%, list=2
GO_DENDR	GO_DENDR Details ...	15	-0.6735	-1.8651	0.0041	0.205078	0.668	12388	tags=73%, list=2
GO_COCHL	GO_COCHLEA_DEVE	51	-0.5053	-1.7684	0.0041	0.23248	0.863	11028	tags=43%, list=1
GO_CGMP_	GO_CGMP_METABOI	15	-0.6779	-1.7508	0.0042	0.252474	0.88	2051	tags=47%, list=4
GO_AXIS_E	GO_AXIS_ELONGATI	30	-0.6015	-1.7882	0.0042	0.233735	0.832	11983	tags=50%, list=2
GO_CALCIU	GO_CALCIUM_DEPEI	43	-0.5852	-1.8064	0.0043	0.214348	0.799	4441	tags=40%, list=8
GO_REGUL	GO_REGULATION_OI	29	-0.5145	-1.6349	0.0043	0.317368	0.982	20825	tags=69%, list=3
GO_TRABE	GO_TRABECULA_FOI	25	-0.6007	-1.7683	0.0043	0.22932	0.863	8882	tags=48%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.642	-1.7424	0.0057	0.262619	0.898	15514	tags=60%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	48	-0.493	-1.7408	0.0058	0.256503	0.9	3722	tags=33%, list=6
GO_NEGAT	GO_NEGATIVE_REGU	34	-0.5648	-1.8268	0.0059	0.188771	0.757	8229	tags=44%, list=1
GO_CARDI	GO_CARDIAC_ATRIU	34	-0.5342	-1.7324	0.0059	0.260933	0.915	17220	tags=56%, list=2
GO_HEART	GO_HEART_VALVE_I	60	-0.565	-1.8074	0.0059	0.220867	0.798	11808	tags=58%, list=2
GO_NEPHR	GO_NEPHRIC_DUCT_	16	-0.6321	-1.7956	0.0059	0.229161	0.813	15942	tags=75%, list=2
GO_AXIS_S	GO_AXIS_SPECIFICA	87	-0.4587	-1.7176	0.006	0.266782	0.928	14390	tags=49%, list=2
GO_ATRIAI	GO_ATRIAL_SEPTUM	21	-0.5714	-1.701	0.006	0.276907	0.943	15184	tags=57%, list=2
GO_CORTIC	GO_CORTIC Details ...	15	-0.6926	-1.8569	0.006	0.210484	0.686	7396	tags=40%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	45	-0.4973	-1.7414	0.006	0.258239	0.9	8426	tags=36%, list=1
GO_CARDI	GO_CARDIAC_MUSC	67	-0.4841	-1.7943	0.006	0.227776	0.815	11823	tags=40%, list=2
GO_CALCIU	GO_CALCIUM_ION_T	17	-0.619	-1.76	0.0061	0.241507	0.874	11495	tags=35%, list=2
GO_REGUL	GO_REGULATION_OI	17	-0.6018	-1.7304	0.0061	0.262749	0.916	6841	tags=35%, list=1
GO_OUTFL	GO_OUTFL Details ...	27	-0.6291	-1.8508	0.0061	0.203708	0.697	15844	tags=70%, list=2
GO_PARAX	GO_PARAXIAL_MES	18	-0.6327	-1.781	0.0062	0.23079	0.845	11983	tags=72%, list=2
GO_EMBRY	GO_EMBRYONIC_AP	123	-0.4707	-1.6815	0.0062	0.284407	0.958	8585	tags=39%, list=1
GO_CELLU	GO_CELLULAR_RESI	21	-0.6027	-1.7701	0.0062	0.239303	0.86	806	tags=24%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.6051	-1.677	0.0063	0.279086	0.961	8230	tags=40%, list=1
GO_HOMOI	GO_HOMOPHILIC_CE	164	-0.5014	-1.8074	0.0064	0.216451	0.798	12572	tags=48%, list=2
GO_WNT_P	GO_WNT_PROTEIN_I	30	-0.6261	-1.7821	0.0064	0.232098	0.843	12292	tags=63%, list=2
GO_TRACH	GO_TRACHEA_DEVE	19	-0.6283	-1.757	0.0075	0.244656	0.875	6505	tags=53%, list=1
GO_REGUL	GO_REGULATION_OI	86	-0.4491	-1.7228	0.0076	0.265901	0.925	12950	tags=40%, list=2
GO_DOPAM	GO_DOPAMINERGIC_	36	-0.5597	-1.7847	0.0076	0.233731	0.838	13955	tags=58%, list=2
GO_DENDR	GO_DENDRITE_MORI	143	-0.4489	-1.6505	0.0079	0.308306	0.976	10004	tags=38%, list=1
GO_REGUL	GO_REGULATION_OI	24	-0.5207	-1.6918	0.0079	0.283822	0.952	6841	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	32	-0.5006	-1.6573	0.008	0.302435	0.973	7654	tags=31%, list=1
GO_MESEN	GO_MESENCHYME_I	286	-0.416	-1.6368	0.008	0.31719	0.981	11983	tags=42%, list=2
GO_HEART	GO_HEART_FIELD_SI	17	-0.6184	-1.7415	0.0082	0.261318	0.899	11983	tags=59%, list=2
GO_CGMP_	GO_CGMP_MEDIATE	27	-0.5741	-1.7216	0.0083	0.263013	0.925	4174	tags=44%, list=7
GO_CORON	GO_CORONARY_VAS	17	-0.64	-1.721	0.0084	0.261434	0.925	8882	tags=53%, list=1
GO_REGUL	GO_REGULATION_OI	41	-0.518	-1.7116	0.0085	0.270248	0.935	12788	tags=44%, list=2
GO_HEART	GO_HEART_GROWTH	112	-0.4297	-1.6774	0.0095	0.2849	0.961	12950	tags=39%, list=2
GO_UROGE	GO_UROGENITAL_SY	328	-0.399	-1.6481	0.0096	0.311945	0.977	8254	tags=30%, list=1
GO_EMBRY	GO_EMBRYONIC_DI	57	-0.4844	-1.7029	0.0097	0.277421	0.941	17220	tags=54%, list=2
GO_POSITI	GO_POSITIVE_REGUI	63	-0.449	-1.6343	0.0098	0.316807	0.982	13702	tags=46%, list=2
GO_POSITI	GO_POSITIVE_REGUI	25	-0.5377	-1.7121	0.0098	0.274478	0.934	7790	tags=44%, list=1
GO_POSITI	GO_POSITIVE_REGUI	38	-0.5358	-1.7481	0.0098	0.255694	0.887	8876	tags=39%, list=1
GO_POSITI	GO_POSITIVE_REGUI	27	-0.5235	-1.6748	0.0098	0.277639	0.963	16249	tags=52%, list=2
GO_REGUL	GO_REGULATION_OI	44	-0.4834	-1.5901	0.01	0.360667	0.993	15424	tags=45%, list=2
GO_DEVEL	GO_DEVELOPMENTA	36	-0.5199	-1.6888	0.0101	0.283722	0.953	11983	tags=47%, list=2
GO_NEURO	GO_NEURON_PROJE	59	-0.5371	-1.664	0.0101	0.292454	0.97	13008	tags=58%, list=2
GO_ARTER	GO_ARTERY_DEVEL	101	-0.479	-1.7058	0.0101	0.275843	0.939	10490	tags=38%, list=1
GO_SODIUI	GO_SODIUM_ION_TR	174	-0.3677	-1.5024	0.0101	0.374713	0.999	11031	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGUI	17	-0.6051	-1.7245	0.0102	0.264603	0.922	4975	tags=47%, list=9
GO_CARDI	GO_CARDIAC_ATRIU	28	-0.5579	-1.7025	0.0102	0.275639	0.941	17220	tags=61%, list=2

GO_MATIN	GO_MATING_BEHAV	23	-0.5307	-1.6938	0.0102	0.287106	0.951	7870	tags=35%, list=1
GO_FACE_I	GO_FACE_DEVELOPI	48	-0.5156	-1.7121	0.0102	0.271734	0.934	10943	tags=46%, list=1
GO_SYMPA	GO_SYMPATHETIC_N	21	-0.6084	-1.6771	0.0103	0.281119	0.961	7998	tags=52%, list=1
GO_REGUL	GO_REGULATION_OI	115	-0.4143	-1.6335	0.0115	0.316891	0.982	13702	tags=42%, list=2
GO_POSITI	GO_POSITIVE_REGUI	83	-0.4408	-1.6527	0.0116	0.307354	0.975	12950	tags=41%, list=2
GO_RESPIR	GO_RESPIRATORY_S	201	-0.4137	-1.5958	0.0117	0.357493	0.992	10951	tags=36%, list=1
GO_RETINA	GO_RETINA_DEVELC	147	-0.4471	-1.6772	0.0118	0.283072	0.961	15415	tags=49%, list=2
GO_HEAD_	GO_HEAD_MORPHOG	36	-0.5434	-1.7174	0.0118	0.264449	0.928	17220	tags=61%, list=2
GO_REGUL	GO_REGULATION_OI	101	-0.436	-1.6758	0.0119	0.277536	0.961	12950	tags=40%, list=2
GO_RESPIR	GO_RESPIRATORY_S	32	-0.5173	-1.6209	0.0119	0.324505	0.985	16720	tags=69%, list=2
GO_BETA_(	GO_BETA_CATENIN_	84	-0.503	-1.7806	0.012	0.227891	0.845	8878	tags=38%, list=1
GO_PHOSPI	GO_PHOSPHATASE_I	45	-0.4349	-1.5872	0.0121	0.362569	0.993	12823	tags=47%, list=2
GO_NEURO	GO_NEUROMUSCULA	76	-0.4719	-1.6335	0.0121	0.314964	0.982	10655	tags=46%, list=1
GO_EMBRY	GO_EMBRYONIC_PLA	24	-0.5259	-1.6382	0.0123	0.319739	0.98	10234	tags=50%, list=1
GO_MUSCL	GO_MUSCLE_ORGAN	83	-0.4621	-1.6764	0.0125	0.278386	0.961	10943	tags=42%, list=1
GO_CELL_N	GO_CELL_MIGRATIO	18	-0.6241	-1.7377	0.0126	0.254365	0.905	15503	tags=56%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	116	-0.4878	-1.5721	0.0127	0.372215	0.993	15009	tags=54%, list=2
GO_POSITI	GO_POSITIVE_REGUI	43	-0.5075	-1.6301	0.0135	0.313147	0.983	8907	tags=37%, list=1
GO_POSITI	GO_POSITIVE_REGUI	108	-0.3967	-1.5495	0.0136	0.37951	0.995	15514	tags=46%, list=2
GO_REGUL	GO_REGULATION_OI	44	-0.4935	-1.63	0.0136	0.311661	0.983	12067	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	27	-0.5322	-1.6928	0.0137	0.283929	0.952	8229	tags=37%, list=1
GO_EMBRY	GO_EMBRYONIC_FO	32	-0.5161	-1.6364	0.0138	0.316016	0.981	8338	tags=50%, list=1
GO_EMBRY	GO_EMBRYONIC_DIG	18	-0.6458	-1.7786	0.0139	0.224678	0.847	4739	tags=44%, list=8
GO_MESEN	GO_MESENCHYMAL_	44	-0.5281	-1.7258	0.014	0.264606	0.92	10943	tags=52%, list=1
GO_SMOOT	GO_SMOOTH_MUSCI	68	-0.4953	-1.6673	0.014	0.288944	0.969	9318	tags=37%, list=1
GO_REGUL	GO_REGULATION_OI	105	-0.442	-1.6184	0.0141	0.32706	0.986	11448	tags=42%, list=2
GO_REGUL	GO_REGULATION_OI	34	-0.5269	-1.6194	0.0142	0.326285	0.986	7155	tags=38%, list=1
GO_MORPH	GO_MORPHOGENESI	25	-0.527	-1.6398	0.0143	0.319974	0.98	18351	tags=64%, list=3
GO_SODIUI	GO_SODIUM_ION_TR	240	-0.3382	-1.4221	0.0143	0.385582	1	11099	tags=31%, list=1
GO_POSTS	GO_POSTSYNAPTIC_	275	-0.4513	-1.6157	0.0143	0.328052	0.989	15009	tags=52%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	34	-0.5496	-1.5925	0.0143	0.361946	0.993	6442	tags=41%, list=1
GO_SYNAP	GO_SYNAPTIC_TRAN	47	-0.5372	-1.6836	0.0143	0.286265	0.955	12500	tags=51%, list=2
GO_SPINAI	GO_SPINAL_CORD_D	109	-0.4704	-1.5881	0.0144	0.362022	0.993	17220	tags=54%, list=2
GO_EMBRY	GO_EMBRYONIC_HII	29	-0.5592	-1.6887	0.0144	0.281409	0.953	8585	tags=52%, list=1
GO_POSTS	GO_POSTSYNAPTIC_	90	-0.4907	-1.5833	0.0149	0.359687	0.993	13214	tags=51%, list=2
GO_DENDR	GO_DENDRITIC_SPIN	101	-0.4523	-1.6152	0.0151	0.32559	0.989	10263	tags=38%, list=1
GO_SODIUI	GO_SODIUM_ION_TR	152	-0.3711	-1.4906	0.0154	0.371473	0.999	16280	tags=44%, list=2
GO_NEURO	GO_NEURON_TO_NE	358	-0.4123	-1.6453	0.0156	0.312745	0.978	13214	tags=43%, list=2
GO_RNAI_E	GO_RNAI_EFFECTOR	16	-0.6902	-1.6876	0.016	0.281546	0.953	4956	tags=44%, list=8
GO_TRANS	GO_TRANSMEMBRAI	79	-0.4885	-1.7035	0.0161	0.27862	0.941	13311	tags=49%, list=2
GO_TRANS	GO_TRANSMEMBRAI	61	-0.4735	-1.6231	0.0162	0.321097	0.985	13245	tags=49%, list=2
GO_PERICA	GO_PERICARDIUM_D	20	-0.5699	-1.6964	0.0162	0.283191	0.947	11652	tags=65%, list=2
GO_METEN	GO_METENCEPHALO	110	-0.4563	-1.6418	0.0164	0.316966	0.98	11744	tags=44%, list=2
GO_CELL_I	GO_CELL_PROLIFER.	28	-0.5518	-1.6101	0.0164	0.329333	0.989	15207	tags=61%, list=2
GO_SECON	GO_SECONDARY_PA	24	-0.5656	-1.6561	0.0165	0.303069	0.974	12664	tags=63%, list=2
GO_HINDLI	GO_HINDLIMB_MOR	37	-0.5268	-1.6328	0.0168	0.312615	0.982	8585	tags=49%, list=1
GO_MIDBR	GO_MIDBRAIN_DOPA	17	-0.6031	-1.7267	0.0174	0.265512	0.919	10943	tags=53%, list=1
GO_HINDBI	GO_HINDBRAIN_DEV	152	-0.4252	-1.5774	0.0177	0.36581	0.993	12566	tags=42%, list=2
GO_RESPOI	GO_RESPONSE_TO_P	24	-0.5437	-1.6811	0.0178	0.282889	0.959	3744	tags=33%, list=6
GO_BODY_	GO_BODY_MORPHOG	49	-0.5211	-1.7101	0.0178	0.268443	0.937	8248	tags=39%, list=1
GO_POSITI	GO_POSITIVE_REGUI	26	-0.5912	-1.7369	0.0179	0.252992	0.905	9318	tags=42%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	309	-0.3924	-1.563	0.0179	0.376859	0.994	8823	tags=35%, list=1
GO_CLATH	GO_CLATHRIN_COAT	71	-0.4355	-1.5789	0.0179	0.365406	0.993	12509	tags=51%, list=2
GO_MAINT	GO_MAINTENANCE_	34	-0.5409	-1.6776	0.018	0.286673	0.961	7372	tags=41%, list=1
GO_CARDI	GO_CARDIAC_MUSC	124	-0.3991	-1.5307	0.018	0.388098	0.996	12950	tags=39%, list=2
GO_VASCU	GO_VASCULAR_ASS	46	-0.5352	-1.6904	0.0185	0.284758	0.953	9318	tags=35%, list=1
GO_REGUL	GO_REGULATION_OI	21	-0.6021	-1.6791	0.0185	0.285247	0.959	3847	tags=43%, list=7
GO_POSTS	GO_POSTSYNAPTIC_	21	-0.6394	-1.633	0.0186	0.314217	0.982	6442	tags=52%, list=1

GO_ORGAN	GO_ORGAN_GROWT	188	-0.4021	-1.6143	0.0187	0.325959	0.989	13328	tags=39%, list=2
GO_PROTE	GO_PROTEIN_DNA_C	18	-0.6365	-1.6819	0.0191	0.285637	0.958	3233	tags=39%, list=6
GO_TRANS	GO_TRANSLATION_F	26	-0.5795	-1.6824	0.0195	0.286854	0.957	5527	tags=38%, list=9
GO_STERO	GO_STEROL_BIOSYN	79	-0.4673	-1.5851	0.0197	0.364205	0.993	4065	tags=23%, list=7
GO_CEREB	GO_CEREBELLAR_C	31	-0.5569	-1.6857	0.0198	0.283636	0.953	11744	tags=52%, list=2
GO_METAN	GO_METANEPHROS_	91	-0.4628	-1.6558	0.02	0.301572	0.975	9318	tags=40%, list=1
GO_CYCLI	GO_CYCLIC_NUCLE	25	-0.5466	-1.6435	0.0201	0.314872	0.978	3593	tags=32%, list=6
GO_SOLUT	GO_SOLUTE_CATION	98	-0.3774	-1.4726	0.0201	0.376564	0.999	16260	tags=46%, list=2
GO_CARDI	GO_CARDIOCYTE_DI	154	-0.3988	-1.5578	0.0202	0.379201	0.995	18260	tags=49%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	73	-0.4477	-1.5613	0.0203	0.378072	0.995	11596	tags=41%, list=2
GO_PHOTO	GO_PHOTORECEPTO	16	-0.6205	-1.6701	0.0214	0.28439	0.966	18221	tags=63%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	330	-0.3711	-1.5224	0.0216	0.37683	0.997	8823	tags=34%, list=1
GO_REGUL	GO_REGULATION_O	249	-0.3839	-1.5608	0.0217	0.377816	0.995	13802	tags=40%, list=2
GO_RESPO	GO_RESPONSE_TO_E	164	-0.4014	-1.5542	0.0217	0.381876	0.995	14016	tags=42%, list=2
GO_MESON	GO_MESONEPHROS_	103	-0.4365	-1.6385	0.0217	0.321175	0.98	8585	tags=34%, list=1
GO_CELLU	GO_CELLULAR_RESP	26	-0.5298	-1.6316	0.0222	0.311404	0.983	1071	tags=23%, list=2
GO_NEURO	GO_NEUROTRANSMI	19	-0.5524	-1.5846	0.0223	0.361706	0.993	17190	tags=68%, list=2
GO_SECRE	GO_SECRETORY_GR	15	-0.6648	-1.6288	0.0224	0.312399	0.983	5721	tags=47%, list=1
GO_CELL_	GO_CELL_BODY_ME	31	-0.5585	-1.6079	0.0226	0.332873	0.99	14731	tags=68%, list=2
GO_SPINAL	GO_SPINAL_CORD_P	24	-0.5745	-1.5807	0.0226	0.362632	0.993	16549	tags=63%, list=2
GO_REGUL	GO_REGULATION_O	47	-0.5132	-1.6746	0.0227	0.276026	0.963	9869	tags=40%, list=1
GO_CAME	GO_CAMERA_TYPE_	329	-0.3625	-1.4993	0.0228	0.368564	0.999	15683	tags=43%, list=2
GO_EPITHE	GO_EPITHELIAL_TU	132	-0.413	-1.5783	0.0228	0.365246	0.993	10943	tags=39%, list=1
GO_EMBRY	GO_EMBRYONIC_PA	69	-0.426	-1.5847	0.023	0.363291	0.993	12828	tags=43%, list=2
GO_POSIT	GO_POSITIVE_REGU	48	-0.454	-1.5844	0.0236	0.360437	0.993	18362	tags=52%, list=3
GO_KIDNE	GO_KIDNEY_EPITHE	142	-0.4243	-1.6244	0.024	0.319798	0.985	7643	tags=32%, list=1
GO_PEPTID	GO_PEPTIDE_HORM	50	-0.4687	-1.5649	0.0242	0.376976	0.994	20263	tags=62%, list=3
GO_RESPO	GO_RESPONSE_TO_	36	-0.4759	-1.5428	0.0242	0.37839	0.996	8443	tags=33%, list=1
GO_WNT_S	GO_WNT_SIGNALIN	38	-0.4995	-1.6133	0.0243	0.326815	0.989	12463	tags=53%, list=2
GO_ADULT	GO_ADULT_BEHAVI	135	-0.445	-1.5853	0.0245	0.365517	0.993	15699	tags=50%, list=2
GO_COPI_	GO_COPI_COATED_V	27	-0.6025	-1.729	0.0249	0.263145	0.916	7711	tags=37%, list=1
GO_REGUL	GO_REGULATION_O	33	-0.5048	-1.6372	0.0258	0.318085	0.981	5634	tags=39%, list=1
GO_PLACE	GO_PLACENTA_BLO	34	-0.4513	-1.5407	0.0262	0.380603	0.996	10185	tags=44%, list=1
GO_SCHW	GO_SCHWANN_CELL	38	-0.4962	-1.6472	0.0262	0.312183	0.977	15394	tags=50%, list=2
GO_APPEN	GO_APPENDAGE_MO	145	-0.4343	-1.5684	0.0264	0.375026	0.994	8807	tags=37%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	28	-0.4974	-1.5531	0.0264	0.381506	0.995	8426	tags=39%, list=1
GO_CELLU	GO_CELLULAR_RESP	16	-0.5868	-1.6156	0.0265	0.326286	0.989	3347	tags=38%, list=6
GO_SOMITI	GO_SOMITE_DEVEL	88	-0.4226	-1.5587	0.0265	0.378348	0.995	6069	tags=28%, list=1
GO_PANCR	GO_PANCREAS_DEV	78	-0.4425	-1.5103	0.0268	0.37477	0.999	11638	tags=45%, list=2
GO_CELL_	GO_CELL_CELL_ADH	270	-0.3962	-1.538	0.0271	0.382841	0.996	12572	tags=40%, list=2
GO_OVULA	GO_OVULATION_CY	47	-0.453	-1.5473	0.0274	0.380378	0.996	20688	tags=62%, list=3
GO_NEURA	GO_NEURAL_TUBE_	161	-0.4123	-1.547	0.0276	0.379553	0.996	10943	tags=38%, list=1
GO_REGUL	GO_REGULATION_O	347	-0.3549	-1.4692	0.0276	0.376559	0.999	13369	tags=37%, list=2
GO_MORPH	GO_MORPHOGENESI	16	-0.5837	-1.5714	0.0282	0.372458	0.993	7643	tags=50%, list=1
GO_VASCU	GO_VASCULOGENES	81	-0.4784	-1.6597	0.0283	0.298575	0.971	10247	tags=44%, list=1
GO_SMAD_	GO_SMAD_PROTEIN_	76	-0.4179	-1.5315	0.0284	0.390527	0.996	18362	tags=53%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	21	-0.5206	-1.5681	0.0286	0.373968	0.994	8882	tags=48%, list=1
GO_DENDR	GO_DENDRITE_DEV	244	-0.418	-1.5886	0.0287	0.362631	0.993	10263	tags=37%, list=1
GO_POSIT	GO_POSITIVE_REGU	372	-0.3857	-1.5142	0.0288	0.375148	0.999	12629	tags=38%, list=2
GO_POSIT	GO_POSITIVE_REGU	28	-0.4718	-1.5288	0.029	0.384363	0.997	10307	tags=39%, list=1
GO_EMBRY	GO_EMBRYONIC_AX	38	-0.4416	-1.5123	0.0291	0.37611	0.999	13642	tags=45%, list=2
GO_INTRIN	GO_INTRINSIC_COM	120	-0.4771	-1.5412	0.0295	0.380746	0.996	14870	tags=52%, list=2
GO_ADHER	GO_ADHERENS_JUN	61	-0.4666	-1.5948	0.0296	0.357948	0.992	11122	tags=39%, list=1
GO_CALCI	GO_CALCIUM_CHAN	63	-0.4547	-1.5463	0.0296	0.379993	0.996	10331	tags=37%, list=1
GO_REGUL	GO_REGULATION_O	52	-0.5011	-1.583	0.0296	0.35848	0.993	10263	tags=50%, list=1
GO_PEROX	GO_PEROXISOME_P	21	-0.5168	-1.6068	0.0297	0.333779	0.99	9464	tags=43%, list=1
GO_BETA_	GO_BETA_CATENIN_	21	-0.5482	-1.6124	0.0298	0.327325	0.989	10834	tags=48%, list=1
GO_SEGME	GO_SEGMENTATION	99	-0.3861	-1.4803	0.0298	0.373199	0.999	15942	tags=44%, list=2

GO_VENTR	GO_VENTRICULAR_S	32	-0.4956	-1.5252	0.0298	0.375494	0.997	7111	tags=31%, list=1
GO_MAINT	GO_MAINTENANCE_	163	-0.4096	-1.5441	0.0299	0.382495	0.996	8726	tags=31%, list=1
GO_CHROM	GO_CHROMATIN_DIS	18	-0.6266	-1.617	0.0301	0.328693	0.987	3233	tags=39%, list=6
GO_NUCLE	GO_NUCLEUS_LOCA	28	-0.5757	-1.6102	0.0309	0.330886	0.989	6486	tags=39%, list=1
GO_TRANS	GO_TRANSPORTER_	324	-0.4115	-1.5319	0.0312	0.392375	0.996	14144	tags=42%, list=2
GO_NEURO	GO_NEUROMUSCUL	49	-0.4583	-1.5518	0.0315	0.378383	0.995	10655	tags=43%, list=1
GO_POSITI	GO_POSITIVE_REGU	185	-0.3816	-1.5053	0.0316	0.374772	0.999	13067	tags=38%, list=2
GO_MESOD	GO_MESODERMAL_	35	-0.4666	-1.5271	0.0323	0.377535	0.997	5704	tags=31%, list=1
GO_DENDR	GO_DENDRITIC_SPIN	61	-0.4538	-1.5428	0.0324	0.381283	0.996	9869	tags=34%, list=1
GO_NEURO	GO_NEURON_RECOG	50	-0.4769	-1.5906	0.0324	0.362842	0.993	8082	tags=34%, list=1
GO_FRIZZL	GO_FRIZZLED_BINDI	38	-0.4639	-1.517	0.0324	0.379938	0.998	11983	tags=42%, list=2
GO_MESON	GO_MESONEPHRIC_	66	-0.4314	-1.529	0.0327	0.386541	0.996	5634	tags=29%, list=1
GO_PRESY	GO_PRESYNAPTIC_M	15	-0.6198	-1.5562	0.0329	0.381544	0.995	6730	tags=40%, list=1
GO_INTRIN	GO_INTRINSIC_COM	163	-0.4531	-1.5	0.0331	0.36916	0.999	11122	tags=43%, list=1
GO_EXCIT	GO_EXCITATORY_SY	26	-0.5277	-1.5285	0.0332	0.382209	0.997	6442	tags=42%, list=1
GO_RIBOS	GO_RIBOSOMAL_SM	17	-0.6188	-1.6646	0.0332	0.293132	0.97	5882	tags=24%, list=1
GO_EPITHE	GO_EPITHELIAL_TO_	148	-0.4151	-1.5761	0.0333	0.36732	0.993	12664	tags=42%, list=2
GO_REGUL	GO_REGULATION_O	50	-0.5124	-1.6165	0.0333	0.327977	0.987	4065	tags=26%, list=7
GO_INTRIN	GO_INTRINSIC_COM	52	-0.4845	-1.5084	0.0333	0.37218	0.999	14870	tags=52%, list=2
GO_NEURO	GO_NEUROTROPHIN_	39	-0.4614	-1.5059	0.0335	0.374604	0.999	7373	tags=38%, list=1
GO_SYNAP	GO_SYNAPSE_ORGA	422	-0.3813	-1.5008	0.0336	0.373816	0.999	11448	tags=37%, list=2
GO_MONO	GO_MONOVALENT_I	361	-0.3371	-1.4204	0.0337	0.384857	1	15786	tags=40%, list=2
GO_REGUL	GO_REGULATION_O	188	-0.4179	-1.5264	0.0341	0.377724	0.997	9188	tags=39%, list=1
GO_SOMIT	GO_SOMITOGENESIS	69	-0.4144	-1.508	0.0341	0.371905	0.999	6069	tags=28%, list=1
GO_REPRO	GO_REPRODUCTIVE_	30	-0.4604	-1.5601	0.0343	0.378045	0.995	7870	tags=30%, list=1
GO_SENSO	GO_SENSORY_SYSTE	391	-0.3485	-1.4389	0.0346	0.382381	1	15699	tags=44%, list=2
GO_SCHWA	GO_SCHWANN_CELL	30	-0.4949	-1.5709	0.0346	0.371963	0.993	15394	tags=53%, list=2
GO_POSITI	GO_POSITIVE_REGU	40	-0.4682	-1.5118	0.0348	0.375911	0.999	13631	tags=43%, list=2
GO_REGUL	GO_REGULATION_O	18	-0.5795	-1.5917	0.0349	0.361865	0.993	9771	tags=50%, list=1
GO_SCHAF	GO_SCHAFFER_COLI	83	-0.4225	-1.5003	0.0351	0.371716	0.999	14369	tags=42%, list=2
GO_INTRIN	GO_INTRINSIC_COM	75	-0.4842	-1.4908	0.0357	0.371938	0.999	11028	tags=45%, list=1
GO_REGUL	GO_REGULATION_O	36	-0.4625	-1.5088	0.0359	0.37372	0.999	15888	tags=53%, list=2
GO_DORSA	GO_DORSAL_VENTR	92	-0.4179	-1.4916	0.0359	0.371296	0.999	17220	tags=49%, list=2
GO_REGUL	GO_REGULATION_O	65	-0.4121	-1.463	0.0359	0.383785	0.999	12950	tags=37%, list=2
GO_REGUL	GO_REGULATION_O	32	-0.4806	-1.553	0.0359	0.380316	0.995	15514	tags=44%, list=2
GO_CARDI	GO_CARDIAC_MYOF	19	-0.5787	-1.5644	0.0361	0.376372	0.994	17984	tags=68%, list=3
GO_CYCLI	GO_CYCLIC_NUCLE	20	-0.5597	-1.5479	0.0362	0.380407	0.996	19084	tags=75%, list=3
GO_EMBRY	GO_EMBRYONIC_CA	28	-0.5154	-1.5736	0.0363	0.370075	0.993	13841	tags=54%, list=2
GO_RECEP	GO_RECEPTOR_INTE	113	-0.3934	-1.457	0.0363	0.386055	1	8230	tags=35%, list=1
GO_MORPH	GO_MORPHOGENESI	150	-0.3888	-1.5194	0.0365	0.376702	0.998	10943	tags=37%, list=1
GO_STEM_	GO_STEM_CELL_PRO	126	-0.3823	-1.4691	0.0368	0.375916	0.999	11374	tags=33%, list=1
GO_CATEN	GO_CATENIN_COMP	31	-0.5346	-1.5904	0.0369	0.361601	0.993	5308	tags=32%, list=9
GO_NEGAT	GO_NEGATIVE_REGU	23	-0.5081	-1.5517	0.0373	0.377142	0.995	22837	tags=70%, list=3
GO_ARF_P	GO_ARF_PROTEIN_S	18	-0.5521	-1.5981	0.0373	0.353334	0.992	12242	tags=61%, list=2
GO_CORON	GO_CORONARY_VAS	49	-0.5091	-1.6253	0.0375	0.319585	0.985	10888	tags=39%, list=1
GO_RESPO	GO_RESPONSE_TO_C	47	-0.424	-1.4765	0.0375	0.378663	0.999	6841	tags=28%, list=1
GO_EMBRY	GO_EMBRYONIC_EY	37	-0.478	-1.5271	0.0376	0.378846	0.997	10943	tags=46%, list=1
GO_METAL	GO_METAL_ION_TR	426	-0.3486	-1.4233	0.0377	0.385554	1	16280	tags=44%, list=2
GO_PULMO	GO_PULMONARY_V	17	-0.6237	-1.5528	0.0381	0.377614	0.995	15184	tags=65%, list=2
GO_MATIN	GO_MATING	41	-0.4088	-1.4234	0.0382	0.386168	1	9389	tags=32%, list=1
GO_NEURO	GO_NEURON_PROJE	91	-0.4086	-1.4892	0.0382	0.370398	0.999	10114	tags=35%, list=1
GO_PERIPH	GO_PERIPHERAL_NE	74	-0.4062	-1.4828	0.0382	0.373657	0.999	8858	tags=35%, list=1
GO_CARDI	GO_CARDIAC_CELL_	88	-0.4114	-1.4897	0.0383	0.371408	0.999	12950	tags=39%, list=2
GO_GAMM	GO_GAMMA_AMINO	16	-0.5455	-1.5256	0.0384	0.375802	0.997	15095	tags=75%, list=2
GO_ANTER	GO_ANTERIOR_POST	51	-0.4309	-1.5118	0.0386	0.373611	0.999	17335	tags=55%, list=3
GO_CARDI	GO_CARDIAC_COND	146	-0.4104	-1.4946	0.0387	0.37066	0.999	16182	tags=45%, list=2
GO_FOREB	GO_FOREBRAIN_NEU	26	-0.515	-1.5555	0.039	0.381846	0.995	11013	tags=50%, list=1
GO_BONE_	GO_BONE_MORPHO	92	-0.4374	-1.4949	0.039	0.372163	0.999	16214	tags=54%, list=2

GO_FOREB	GO_FOREBRAIN_DEV	384	-0.385	-1.4746	0.0394	0.377876	0.999	15429	tags=45%, list=2
GO_MESEN	GO_MESENCHYMAL_	225	-0.3979	-1.5546	0.0396	0.382532	0.995	11983	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	23	-0.538	-1.521	0.0396	0.376594	0.997	19852	tags=74%, list=3
GO_REGUL	GO_REGULATION_OI	105	-0.3798	-1.4168	0.0396	0.384233	1	13991	tags=41%, list=2
GO_NEURA	GO_NEURAL_CREST_	89	-0.3974	-1.4761	0.0401	0.37846	0.999	15503	tags=48%, list=2
GO_CATIOI	GO_CATION_CHANN	216	-0.4279	-1.4988	0.0409	0.368579	0.999	15172	tags=44%, list=2
GO_CRANI	GO_CRANIOFACIAL_	17	-0.5953	-1.5656	0.0412	0.376641	0.994	11834	tags=59%, list=2
GO_PHARY	GO_PHARYNGEAL_S	25	-0.5129	-1.5259	0.0412	0.37643	0.997	15096	tags=48%, list=2
GO_CHEMC	GO_CHEMOSENSORY	17	-0.5547	-1.5198	0.0413	0.376896	0.998	8980	tags=47%, list=1
GO_RNA_P	GO_RNA_POLYMERA	55	-0.4505	-1.5134	0.0413	0.374718	0.999	5294	tags=27%, list=9
GO_PATTEI	GO_PATTERN_SPECI	452	-0.3474	-1.4356	0.0413	0.383824	1	17224	tags=44%, list=2
GO_RENAL	GO_RENAL_TUBULE_	95	-0.3892	-1.4612	0.0413	0.384978	0.999	13137	tags=40%, list=2
GO_SOLUT	GO_SOLUTE_SODIUM	72	-0.3816	-1.4069	0.0414	0.382752	1	18772	tags=50%, list=3
GO_RENAL	GO_RENAL_WATER_	37	-0.4654	-1.5369	0.0415	0.38396	0.996	15488	tags=51%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	219	-0.3797	-1.4952	0.0415	0.374587	0.999	8823	tags=35%, list=1
GO_MULTI	GO_MULTICELLULAI	53	-0.4019	-1.4761	0.0416	0.377564	0.999	12152	tags=40%, list=2
GO_CELL_	GO_CELL_MIGRATIO	15	-0.5884	-1.495	0.0417	0.372927	0.999	1749	tags=33%, list=3
GO_CARTII	GO_CARTILAGE_DEV	186	-0.4235	-1.5534	0.0417	0.38255	0.995	8947	tags=32%, list=1
GO_REGUL	GO_REGULATION_OI	96	-0.4242	-1.5431	0.0419	0.381986	0.996	8211	tags=34%, list=1
GO_PHOTO	GO_PHOTORECEPTO	40	-0.4993	-1.5145	0.0419	0.37563	0.999	18301	tags=50%, list=3
GO_NEPHR	GO_NEPHRON_DEVE	143	-0.3999	-1.5037	0.042	0.374113	0.999	12175	tags=39%, list=2
GO_SYNAP	GO_SYNAPSE_ASSEN	176	-0.4015	-1.4806	0.0421	0.373555	0.999	11122	tags=38%, list=1
GO_POSTS	GO_POSTSYNAPSE_A	31	-0.5509	-1.5437	0.0422	0.381952	0.996	10943	tags=52%, list=1
GO_POSITI	GO_POSITIVE_REGUI	35	-0.4804	-1.5012	0.0425	0.374105	0.999	13137	tags=43%, list=2
GO_RESPIR	GO_RESPIRATORY_C	66	-0.3995	-1.4208	0.0428	0.385527	1	9188	tags=35%, list=1
GO_RETIN	GO_RETINA_VASCUI	18	-0.6418	-1.6469	0.0428	0.31084	0.977	14838	tags=67%, list=2
GO_REGUL	GO_REGULATION_OI	280	-0.3381	-1.3726	0.0428	0.395377	1	14188	tags=40%, list=2
GO_NEURC	GO_NEURON_PROJEC	59	-0.4266	-1.5156	0.0434	0.37939	0.998	15514	tags=44%, list=2
GO_ADULT	GO_ADULT_LOCOMC	74	-0.4268	-1.4833	0.0436	0.373603	0.999	15699	tags=54%, list=2
GO_DEVEL	GO_DEVELOPMENTA	233	-0.3881	-1.4916	0.0437	0.372188	0.999	8067	tags=30%, list=1
GO_SYNAP	GO_SYNAPTIC_MEM	380	-0.4048	-1.4715	0.0437	0.376345	0.999	13280	tags=45%, list=2
GO_REGUL	GO_REGULATION_OI	127	-0.3856	-1.4487	0.0438	0.384876	1	5887	tags=24%, list=1
GO_ACTIVI	GO_ACTIVE_ION_TR	228	-0.3293	-1.3869	0.0438	0.391148	1	15786	tags=40%, list=2
GO_TRANS	GO_TRANSFERASE_	21	-0.5319	-1.5442	0.044	0.383781	0.996	7085	tags=33%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	130	-0.388	-1.482	0.0442	0.374365	0.999	17271	tags=45%, list=3
GO_MIDBR	GO_MIDBRAIN_DEVI	88	-0.3999	-1.4699	0.0443	0.375855	0.999	13941	tags=41%, list=2
GO_POSTS	GO_POSTSYNAPSE_C	171	-0.3875	-1.5094	0.0444	0.37352	0.999	11448	tags=36%, list=2
GO_ESTABI	GO_ESTABLISHMENT	25	-0.5343	-1.5232	0.0446	0.377578	0.997	5615	tags=40%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	85	-0.3763	-1.4487	0.0446	0.38239	1	13913	tags=39%, list=2
GO_POSITI	GO_POSITIVE_REGUI	33	-0.4591	-1.474	0.0448	0.377376	0.999	8409	tags=30%, list=1
GO_REGUL	GO_REGULATION_OI	142	-0.4428	-1.4994	0.0454	0.369539	0.999	16853	tags=54%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	32	-0.4805	-1.5394	0.0455	0.382493	0.996	4614	tags=34%, list=8
GO_INTRA	GO_INTRASPECIES_I	52	-0.4489	-1.4813	0.0455	0.375021	0.999	15769	tags=48%, list=2
GO_REGUL	GO_REGULATION_OI	67	-0.394	-1.4469	0.0456	0.381044	1	8409	tags=28%, list=1
GO_REGUL	GO_REGULATION_OI	47	-0.4459	-1.4894	0.0458	0.371073	0.999	8907	tags=38%, list=1
GO_SULFU	GO_SULFUR_AMINO_	16	-0.58	-1.5318	0.0459	0.391051	0.996	2548	tags=31%, list=4
GO_CYCLI	GO_CYCLIC_NUCLEC	38	-0.4794	-1.5297	0.0459	0.387693	0.996	17430	tags=58%, list=3
GO_REGUL	GO_REGULATION_OI	45	-0.4745	-1.5333	0.046	0.390429	0.996	11645	tags=44%, list=2
GO_NEPHR	GO_NEPHRON_EPITH	110	-0.3854	-1.45	0.046	0.388036	1	13137	tags=38%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.5455	-1.5146	0.046	0.376688	0.999	8426	tags=47%, list=1
GO_REGUL	GO_REGULATION_OI	17	-0.5904	-1.5481	0.0463	0.381577	0.996	18511	tags=76%, list=3
GO_TELEN	GO_TELENCEPHALO	252	-0.3832	-1.4543	0.0465	0.389536	1	15888	tags=43%, list=2
GO_DYNEII	GO_DYNEIN_LIGHT_	27	-0.4692	-1.5034	0.0467	0.373516	0.999	13484	tags=56%, list=2
GO_REGUL	GO_REGULATION_OI	303	-0.3707	-1.476	0.0469	0.376874	0.999	12518	tags=38%, list=2
GO_REGUL	GO_REGULATION_OI	18	-0.5438	-1.539	0.047	0.381963	0.996	10943	tags=44%, list=1
GO_EPHRII	GO_EPHRIN_RECEPT	19	-0.5665	-1.5759	0.0474	0.366214	0.993	9789	tags=47%, list=1
GO_REGUL	GO_REGULATION_OI	143	-0.3681	-1.4057	0.0474	0.383133	1	9573	tags=35%, list=1
GO_REGUL	GO_REGULATION_OI	15	-0.5916	-1.5136	0.0476	0.375346	0.999	5887	tags=40%, list=1

GO_TRANS	GO_TRANSMEMBRA	18	-0.5585	-1.562	0.0477	0.377881	0.994	9810	tags=44%, list=1
GO_POTAS	GO_POTASSIUM_ION	240	-0.3596	-1.4025	0.0479	0.38275	1	15498	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REG	25	-0.5086	-1.5529	0.0482	0.378897	0.995	17119	tags=60%, list=2
GO_INTRO	GO_INTRONIC_TRAN	16	-0.5571	-1.5285	0.0482	0.380879	0.997	19979	tags=69%, list=3
GO_REGUL	GO_REGULATION_O	26	-0.4895	-1.5068	0.0484	0.373599	0.999	10731	tags=42%, list=1
GO_CGMP_	GO_CGMP_BINDING	15	-0.5348	-1.4863	0.0484	0.372729	0.999	19825	tags=67%, list=3
GO_NEGAT	GO_NEGATIVE_REG	23	-0.4912	-1.5102	0.0486	0.373752	0.999	22382	tags=65%, list=3
GO_COPI_C	GO_COPI_COATED_	17	-0.6707	-1.651	0.0488	0.309333	0.976	10811	tags=59%, list=1
GO_ECTOD	GO_ECTODERM_DE	22	-0.4755	-1.481	0.0491	0.373749	0.999	2934	tags=32%, list=5
GO_MICRO	GO_MICROTUBULE_	77	-0.4783	-1.5597	0.0492	0.377525	0.995	14495	tags=51%, list=2
GO_REGUL	GO_REGULATION_O	66	-0.4635	-1.5235	0.0495	0.378113	0.997	7894	tags=36%, list=1
GO_CALCI	GO_CALCIUM_ION_	80	-0.3877	-1.4417	0.0497	0.380407	1	14054	tags=41%, list=2
GO_NBAF_	GO_NBAF_COMPLEX	15	-0.6704	-1.5841	0.0499	0.359415	0.993	12635	tags=67%, list=2
GO_NEGAT	GO_NEGATIVE_REG	41	-0.4245	-1.4594	0.0502	0.38442	1	9340	tags=34%, list=1
GO_BETA_	GO_BETA_CATENIN_	30	-0.5507	-1.5662	0.0503	0.376976	0.994	9740	tags=43%, list=1
GO_ATP_D	GO_ATP_DEPENDEN	18	-0.5382	-1.528	0.0503	0.380718	0.997	13484	tags=56%, list=2
GO_CEREB	GO_CEREBELLAR_P	25	-0.5338	-1.5496	0.0504	0.380833	0.995	11744	tags=56%, list=2
GO_REGUL	GO_REGULATION_O	20	-0.4843	-1.4905	0.0507	0.370511	0.999	5704	tags=25%, list=1
GO_ACTIN_	GO_ACTIN_MEDIAT	120	-0.4123	-1.4714	0.0507	0.375572	0.999	11874	tags=37%, list=2
GO_AXON	GO_AXONAL_GROW	28	-0.4946	-1.5218	0.0508	0.375883	0.997	12361	tags=57%, list=2
GO_LUNG_	GO_LUNG_MORPHO	52	-0.4457	-1.5286	0.0508	0.383311	0.997	8585	tags=37%, list=1
GO_NEURA	GO_NEURAL_TUBE_	105	-0.418	-1.531	0.0511	0.390217	0.996	10943	tags=39%, list=1
GO_POSIT	GO_POSITIVE_REGU	82	-0.3316	-1.342	0.0511	0.408383	1	7119	tags=26%, list=1
GO_CARD	GO_CARDIAC_MUSC	54	-0.4443	-1.4715	0.0515	0.377278	0.999	10232	tags=39%, list=1
GO_SULFU	GO_SULFUR_COMPO	56	-0.4306	-1.4672	0.0519	0.37813	0.999	13771	tags=43%, list=2
GO_REGUL	GO_REGULATION_O	65	-0.4333	-1.4787	0.0522	0.374828	0.999	4065	tags=22%, list=7
GO_KIDNE	GO_KIDNEY_MORPH	94	-0.3752	-1.4277	0.0522	0.390861	1	7643	tags=29%, list=1
GO_CARBO	GO_CARBOXY_LYAS	33	-0.4872	-1.5158	0.0525	0.380011	0.998	10225	tags=39%, list=1
GO_POSIT	GO_POSITIVE_REGU	15	-0.5346	-1.5221	0.0526	0.37643	0.997	5842	tags=40%, list=1
GO_CHLOR	GO_CHLORIDE_CHA	49	-0.452	-1.5098	0.0527	0.373612	0.999	12825	tags=49%, list=2
GO_ESTRO	GO_ESTROGEN_REC	39	-0.4396	-1.4343	0.0532	0.384227	1	8274	tags=38%, list=1
GO_LOCO	GO_LOCOMOTORY_	193	-0.3802	-1.4657	0.0533	0.379727	0.999	11233	tags=38%, list=1
GO_CELL_	GO_CELL_FATE_CO	34	-0.4488	-1.4591	0.0535	0.384196	1	10888	tags=44%, list=1
GO_REGUL	GO_REGULATION_O	43	-0.4026	-1.4236	0.0536	0.387155	1	10307	tags=35%, list=1
GO_CELL_	GO_CELL_DIFFEREN	57	-0.4429	-1.47	0.0536	0.376694	0.999	9318	tags=37%, list=1
GO_POSIT	GO_POSITIVE_REGU	282	-0.369	-1.4487	0.0536	0.384081	1	10105	tags=32%, list=1
GO_AMINO	GO_AMINO_ACID_C	19	-0.5155	-1.4846	0.0537	0.371608	0.999	15413	tags=58%, list=2
GO_ENDOC	GO_ENDOCRINE_PR	81	-0.4007	-1.4445	0.0539	0.379522	1	15424	tags=40%, list=2
GO_MODIF	GO_MODIFICATION_	24	-0.5353	-1.526	0.0544	0.377365	0.997	5959	tags=38%, list=1
GO_EXPOR	GO_EXPORT_ACROS	60	-0.4165	-1.4745	0.0545	0.377288	0.999	14054	tags=45%, list=2
GO_NEGAT	GO_NEGATIVE_REG	15	-0.5543	-1.5226	0.0547	0.377768	0.997	7826	tags=47%, list=1
GO_CILIU	GO_CILIUM_OR_FLA	115	-0.3776	-1.4462	0.0547	0.380933	1	16638	tags=43%, list=2
GO_LIGAN	GO_LIGAND_GATED_	19	-0.6288	-1.5639	0.0549	0.375897	0.994	12500	tags=68%, list=2
GO_HMG_	GO_HMG_BOX_DOM	16	-0.5455	-1.5002	0.055	0.36976	0.999	8839	tags=44%, list=1
GO_COLLE	GO_COLLECTING_D	15	-0.5533	-1.519	0.055	0.376265	0.998	7640	tags=40%, list=1
GO_TRANS	GO_TRANSMEMBRA	23	-0.5035	-1.4948	0.0551	0.371423	0.999	7643	tags=39%, list=1
GO_CENTR	GO_CENTRAL_NERV	192	-0.4167	-1.5048	0.0551	0.372675	0.999	15429	tags=48%, list=2
GO_LUNG_	GO_LUNG_ALVEOLU	41	-0.4767	-1.5289	0.0552	0.385472	0.997	10888	tags=44%, list=1
GO_VITAM	GO_VITAMIN_TRAN	40	-0.4318	-1.4536	0.0553	0.389075	1	14640	tags=40%, list=2
GO_TUBE_	GO_TUBE_FORMATI	149	-0.384	-1.4973	0.0557	0.370929	0.999	10943	tags=36%, list=1
GO_BRANC	GO_BRANCHING_M	155	-0.3721	-1.4439	0.0557	0.379033	1	9208	tags=33%, list=1
GO_MEMB	GO_MEMBRANE_DE	23	-0.5418	-1.5053	0.0561	0.373817	0.999	20619	tags=70%, list=3
GO_FEEDI	GO_FEEDING_BEHA	105	-0.3887	-1.4154	0.0562	0.384766	1	16390	tags=42%, list=2
GO_INHIBI	GO_INHIBITORY_EX	15	-0.6619	-1.57	0.0563	0.372443	0.994	12500	tags=73%, list=2
GO_MEMB	GO_MEMBRANE_DE	37	-0.4955	-1.4935	0.0564	0.371092	0.999	16280	tags=54%, list=2
GO_EMBRY	GO_EMBRYONIC_HE	80	-0.3897	-1.4487	0.0565	0.383224	1	12794	tags=39%, list=2
GO_REGUL	GO_REGULATION_O	72	-0.4098	-1.4431	0.0566	0.379025	1	10140	tags=33%, list=1
GO_POSIT	GO_POSITIVE_REGU	85	-0.3733	-1.4073	0.0566	0.382764	1	11153	tags=32%, list=1

GO_REGUL	GO_REGULATION_O	16	-0.627	-1.5295	0.0568	0.386844	0.996	10105	tags=56%, list=1
GO_VITAM	GO_VITAMIN_TRANS	29	-0.4714	-1.4622	0.0568	0.383761	0.999	14640	tags=45%, list=2
GO_MYELI	GO_MYELIN_ASSEM	21	-0.5278	-1.5118	0.0569	0.374785	0.999	13008	tags=57%, list=2
GO_POST_	GO_POST_EMBRYON	83	-0.3794	-1.4336	0.0569	0.384136	1	5942	tags=25%, list=1
GO_SYNTA	GO_SYNTAXIN_1_BI	26	-0.5412	-1.5204	0.0572	0.376827	0.997	16853	tags=73%, list=2
GO_MANG	GO_MANGANESE_IO	15	-0.5209	-1.4472	0.0574	0.383078	1	15610	tags=53%, list=2
GO_POSITI	GO_POSITIVE_REGU	43	-0.4604	-1.5003	0.0574	0.372726	0.999	16573	tags=49%, list=2
GO_REGUL	GO_REGULATION_O	46	-0.409	-1.4457	0.0577	0.380976	1	7861	tags=30%, list=1
GO_LYSOS	GO_LYSOSOMAL_PR	15	-0.5449	-1.5302	0.0577	0.387903	0.996	3754	tags=33%, list=6
GO_LONG_	GO_LONG_TERM_SY	86	-0.4001	-1.4536	0.058	0.388309	1	8907	tags=36%, list=1
GO_PATHW	GO_PATHWAY_REST	65	-0.4139	-1.4793	0.058	0.374575	0.999	18362	tags=51%, list=3
GO_VITAM	GO_VITAMIN_B6_BI	48	-0.4125	-1.4477	0.0585	0.383698	1	6471	tags=27%, list=1
GO_REGUL	GO_REGULATION_O	301	-0.3471	-1.414	0.0585	0.384134	1	12067	tags=34%, list=2
GO_TRIPA	GO_TRIPARTITE_RE	15	-0.5036	-1.451	0.0591	0.389456	1	12828	tags=53%, list=2
GO_MESOD	GO_MESODERM_MO	75	-0.3805	-1.4165	0.0591	0.383992	1	10951	tags=37%, list=1
GO_REGUL	GO_REGULATION_O	76	-0.3886	-1.3934	0.0591	0.387511	1	13137	tags=38%, list=2
GO_GLOME	GO_GLOMERULUS_D	64	-0.4765	-1.5279	0.0592	0.379726	0.997	11652	tags=41%, list=2
GO_POSITI	GO_POSITIVE_REGU	154	-0.3687	-1.441	0.0593	0.381197	1	9996	tags=32%, list=1
GO_REGUL	GO_REGULATION_O	23	-0.5162	-1.4951	0.0594	0.373725	0.999	7790	tags=43%, list=1
GO_MODIF	GO_MODIFICATION_	18	-0.5639	-1.5013	0.0595	0.374817	0.999	1449	tags=28%, list=2
GO_NEGAT	GO_NEGATIVE_REG	59	-0.3704	-1.3792	0.0596	0.394962	1	18325	tags=49%, list=3
GO_NEURA	GO_NEURAL_RETIN	72	-0.4093	-1.4374	0.0598	0.384894	1	15415	tags=46%, list=2
GO_NUCLE	GO_NUCLEAR_TRAN	31	-0.4979	-1.5015	0.0599	0.375632	0.999	12332	tags=39%, list=2
GO_REGUL	GO_REGULATION_O	89	-0.4084	-1.4602	0.06	0.383421	0.999	14016	tags=44%, list=2
GO_NEURO	GO_NEUROBLAST_D	15	-0.5701	-1.5275	0.0604	0.379314	0.997	10477	tags=53%, list=1
GO_EXCIT	GO_EXCITATORY_SY	52	-0.4835	-1.515	0.0604	0.378197	0.999	10885	tags=50%, list=1
GO_DENDR	GO_DENDRITIC_SHA	37	-0.4607	-1.455	0.0607	0.388765	1	16473	tags=59%, list=2
GO_NEURO	GO_NEUROTRANSMI	111	-0.3992	-1.3912	0.0611	0.388255	1	14144	tags=41%, list=2
GO_REGUL	GO_REGULATION_O	140	-0.33	-1.3484	0.0613	0.407119	1	11011	tags=32%, list=1
GO_REGUL	GO_REGULATION_O	25	-0.5888	-1.4406	0.0615	0.380502	1	8836	tags=56%, list=1
GO_FOREL	GO_FORELIMB_MOR	40	-0.4591	-1.4855	0.0615	0.3715	0.999	8338	tags=43%, list=1
GO_CARDI	GO_CARDIAC_MUSC	72	-0.4156	-1.4367	0.0615	0.385474	1	11874	tags=38%, list=2
GO_PEPTID	GO_PEPTIDYL_LYSI	21	-0.5537	-1.5049	0.0615	0.373543	0.999	11713	tags=57%, list=2
GO_ACTIV	GO_ACTIVATION_OF	34	-0.4219	-1.4151	0.0619	0.383429	1	12950	tags=44%, list=2
GO_GROW	GO_GROWTH_HORM	15	-0.5608	-1.4861	0.0621	0.371116	0.999	15233	tags=53%, list=2
GO_NEGAT	GO_NEGATIVE_REG	25	-0.5007	-1.4712	0.0621	0.374947	0.999	8290	tags=48%, list=1
GO_MORPH	GO_MORPHOGENESI	201	-0.3661	-1.4357	0.0625	0.384466	1	11180	tags=35%, list=1
GO_NEPHR	GO_NEPHRON_MOR	77	-0.3849	-1.4097	0.0625	0.383255	1	5634	tags=27%, list=1
GO_RESPO	GO_RESPONSE_TO_P	21	-0.5406	-1.5428	0.0626	0.379788	0.996	10708	tags=43%, list=1
GO_RIBON	GO_RIBONUCLEOTI	31	-0.428	-1.4196	0.0628	0.38349	1	3557	tags=29%, list=6
GO_MULTI	GO_MULTICELLULA	204	-0.3795	-1.416	0.0629	0.384353	1	12152	tags=36%, list=2
GO_LABYR	GO_LABYRINTHINE_	48	-0.3946	-1.4019	0.0633	0.383377	1	10234	tags=40%, list=1
GO_MUSCL	GO_MUSCLE_TISSUE	401	-0.3446	-1.3971	0.0634	0.385164	1	11823	tags=34%, list=2
GO_CELL_	GO_CELL_MIGRATIO	15	-0.5459	-1.488	0.0634	0.371032	0.999	14016	tags=60%, list=2
GO_ATP_D	GO_ATP_DEPENDEN	34	-0.5199	-1.5146	0.0637	0.377856	0.999	14495	tags=56%, list=2
GO_CONNE	GO_CONNECTIVE_TI	248	-0.389	-1.4753	0.0637	0.377439	0.999	12749	tags=38%, list=2
GO_VOLTA	GO_VOLTAGE_GATE	43	-0.4724	-1.4505	0.0637	0.387798	1	19511	tags=58%, list=3
GO_POSITI	GO_POSITIVE_REGU	36	-0.4401	-1.4886	0.0638	0.370722	0.999	5634	tags=31%, list=1
GO_REGUL	GO_REGULATION_O	193	-0.3661	-1.4111	0.0638	0.385139	1	9235	tags=32%, list=1
GO_STRIA	GO_STRIATED_MUS	81	-0.384	-1.445	0.0641	0.379912	1	9641	tags=33%, list=1
GO_INHIBI	GO_INHIBITORY_SY	17	-0.5879	-1.5309	0.0641	0.389078	0.996	13278	tags=59%, list=2
GO_LYSIN	GO_LYSINE_N_MET	49	-0.4994	-1.5151	0.0643	0.379201	0.999	12102	tags=43%, list=2
GO_BRAIN_	GO_BRAIN_MORPHO	34	-0.4679	-1.469	0.0644	0.375159	0.999	10943	tags=29%, list=1
GO_ATPAS	GO_ATPASE_DEPEN	24	-0.4809	-1.461	0.0646	0.384542	0.999	13692	tags=54%, list=2
GO_MULTI	GO_MULTICELLULA	146	-0.3508	-1.3982	0.0646	0.386283	1	8409	tags=27%, list=1
GO_ISOPRE	GO_ISOPRENOID_BI	27	-0.5028	-1.4878	0.0648	0.37044	0.999	14556	tags=52%, list=2
GO_INTRIN	GO_INTRINSIC_COM	82	-0.4441	-1.4494	0.0649	0.38763	1	20073	tags=62%, list=3
GO_REGUL	GO_REGULATION_O	25	-0.4928	-1.4604	0.066	0.384053	0.999	8024	tags=48%, list=1

GO_POSITI	GO_POSITIVE_REGU	21	-0.504	-1.4496	0.0661	0.387963	1	15503	tags=62%, list=2
GO_EPITHE	GO_EPITHELIAL_TU	330	-0.3251	-1.3616	0.0661	0.396974	1	12794	tags=36%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	113	-0.3366	-1.3492	0.0664	0.40662	1	9340	tags=30%, list=1
GO_DEVEL	GO_DEVELOPMENT	233	-0.3597	-1.4053	0.0668	0.38273	1	13067	tags=37%, list=2
GO_REGUL	GO_REGULATION_O	56	-0.395	-1.4106	0.0668	0.384805	1	8265	tags=27%, list=1
GO_EMBRY	GO_EMBRYO_IMPLA	55	-0.3774	-1.4092	0.0671	0.383574	1	9127	tags=33%, list=1
GO_SPERM	GO_SPERM_MOTILIT	89	-0.3677	-1.3896	0.0672	0.39021	1	15680	tags=42%, list=2
GO_CELL_	GO_CELL_PROLIFER	18	-0.5418	-1.4862	0.0674	0.371899	0.999	15096	tags=50%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	28	-0.4693	-1.4523	0.0675	0.388328	1	7280	tags=36%, list=1
GO_AORTI	GO_AORTIC_VALVE_	32	-0.5374	-1.5168	0.0675	0.379001	0.998	11808	tags=59%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	19	-0.5139	-1.4606	0.0677	0.384498	0.999	9127	tags=32%, list=1
GO_GASTR	GO_GASTRULATION_	26	-0.4845	-1.4738	0.0679	0.376752	0.999	20508	tags=73%, list=3
GO_GLUTA	GO_GLUTAMATE_SE	44	-0.4431	-1.4473	0.0679	0.383545	1	16390	tags=55%, list=2
GO_CELL_	GO_CELL_CELL_CO	70	-0.3954	-1.4138	0.0681	0.383897	1	8909	tags=36%, list=1
GO_HEMO	GO_HEMOGLOBIN_M	15	-0.4966	-1.4406	0.0682	0.381258	1	19350	tags=60%, list=3
GO_APPEN	GO_APPENDAGE_DE	176	-0.3824	-1.4342	0.0683	0.383527	1	8807	tags=32%, list=1
GO_FIBRO	GO_FIBROBLAST_GR	25	-0.5702	-1.5085	0.0683	0.373294	0.999	12526	tags=56%, list=2
GO_PROTE	GO_PROTEIN_KINAS	50	-0.4425	-1.4934	0.0684	0.370324	0.999	8881	tags=42%, list=1
GO_CEREB	GO_CEREBELLAR_C	47	-0.489	-1.5359	0.0685	0.385196	0.996	11744	tags=47%, list=2
GO_POST_	GO_POST_ANAL_TAI	18	-0.5004	-1.5003	0.0688	0.370641	0.999	6069	tags=33%, list=1
GO_CELLU	GO_CELLULAR_COM	108	-0.4114	-1.4513	0.069	0.389672	1	13249	tags=41%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	40	-0.4504	-1.4488	0.069	0.385481	1	8836	tags=38%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	52	-0.4068	-1.4324	0.069	0.38571	1	8882	tags=42%, list=1
GO_CARDI	GO_CARDIAC_MUSC	73	-0.403	-1.3876	0.0692	0.391757	1	10232	tags=34%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	38	-0.4211	-1.4037	0.0693	0.381763	1	5704	tags=29%, list=1
GO_GLUTA	GO_GLUTAMATERGI	351	-0.3705	-1.4054	0.0696	0.383122	1	11851	tags=39%, list=2
GO_NEURO	GO_NEUROTRANSMI	18	-0.5081	-1.4654	0.0698	0.379589	0.999	18087	tags=56%, list=3
GO_REGUL	GO_REGULATION_O	55	-0.3844	-1.3715	0.0703	0.395797	1	10655	tags=36%, list=1
GO_REGUL	GO_REGULATION_O	65	-0.3723	-1.3631	0.0703	0.396308	1	10655	tags=35%, list=1
GO_POTAS	GO_POTASSIUM_ION	29	-0.4507	-1.3854	0.0707	0.392298	1	15498	tags=59%, list=2
GO_POSITI	GO_POSITIVE_REGU	19	-0.5221	-1.4562	0.0713	0.387069	1	6062	tags=32%, list=1
GO_REGUL	GO_REGULATION_O	445	-0.3654	-1.4151	0.0714	0.383964	1	9470	tags=32%, list=1
GO_AUTON	GO_AUTONOMIC_NE	47	-0.4302	-1.4102	0.0714	0.384342	1	9908	tags=38%, list=1
GO_NEURA	GO_NEURAL_TUBE_	41	-0.4696	-1.5004	0.0716	0.373541	0.999	8640	tags=34%, list=1
GO_POSITI	GO_POSITIVE_REGU	33	-0.4362	-1.4215	0.0717	0.385421	1	13311	tags=45%, list=2
GO_TRANS	GO_TRANSLATION_P	18	-0.6051	-1.4727	0.0719	0.378255	0.999	5882	tags=39%, list=1
GO_ESTAB	GO_ESTABLISHMENT	15	-0.5506	-1.4932	0.0721	0.369596	0.999	10943	tags=47%, list=1
GO_PROTE	GO_PROTEIN_LOCAL	101	-0.4049	-1.4426	0.0724	0.379412	1	8159	tags=32%, list=1
GO_EAR_D	GO_EAR_DEVELOPM	218	-0.3625	-1.3433	0.0738	0.407105	1	16463	tags=45%, list=2
GO_LIPOPR	GO_LIPOPROTEIN_L	18	-0.4756	-1.4469	0.074	0.38187	1	7351	tags=28%, list=1
GO_ORGAN	GO_ORGANIC_ACID_	30	-0.4371	-1.3846	0.0741	0.392047	1	16260	tags=50%, list=2
GO_REGUL	GO_REGULATION_O	39	-0.4094	-1.3891	0.0744	0.390008	1	6939	tags=28%, list=1
GO_CELL_	GO_CELL_PROLIFER	16	-0.5151	-1.4293	0.0746	0.390698	1	8815	tags=38%, list=1
GO_OSTEO	GO_OSTEOBLAST_DI	220	-0.3476	-1.4201	0.0746	0.383872	1	12059	tags=37%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	62	-0.3558	-1.3616	0.0746	0.396455	1	7285	tags=27%, list=1
GO_PHOSP	GO_PHOSPHATASE_	96	-0.3448	-1.398	0.075	0.386003	1	15207	tags=42%, list=2
GO_NEURO	GO_NEUROTRANSMI	30	-0.4309	-1.3936	0.0757	0.38771	1	19243	tags=50%, list=3
GO_RESPO	GO_RESPONSE_TO_P	32	-0.4444	-1.4274	0.0757	0.390816	1	3744	tags=25%, list=6
GO_ENERG	GO_ENERGY_RESER	81	-0.3552	-1.3572	0.0758	0.399142	1	13436	tags=40%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	150	-0.3468	-1.363	0.076	0.395489	1	8823	tags=33%, list=1
GO_RESPO	GO_RESPONSE_TO_V	15	-0.5425	-1.4489	0.0761	0.386283	1	7165	tags=27%, list=1
GO_CELL_	GO_CELL_CELL_JUN	143	-0.351	-1.3822	0.0762	0.391423	1	12361	tags=36%, list=2
GO_DIENC	GO_DIENCEPHALON_	74	-0.396	-1.3753	0.0768	0.396681	1	20089	tags=55%, list=3
GO_MAMM	GO_MAMMARY_GLA	17	-0.4696	-1.4234	0.0769	0.386786	1	6439	tags=35%, list=1
GO_NUCLE	GO_NUCLEAR_MIGR	23	-0.5572	-1.4668	0.0771	0.378295	0.999	14756	tags=57%, list=2
GO_NEURO	GO_NEUROTRANSMI	51	-0.4875	-1.422	0.0771	0.385076	1	23857	tags=76%, list=4
GO_SODIU	GO_SODIUM_ION_H	52	-0.3909	-1.3606	0.0774	0.396723	1	14980	tags=44%, list=2
GO_PHOSP	GO_PHOSPHATIDIC_	49	-0.3676	-1.3495	0.0775	0.406651	1	10781	tags=33%, list=1

GO_NITRIC	GO_NITRIC_OXIDE_M	27	-0.4808	-1.408	0.0779	0.382723	1	3576	tags=26%, list=6
GO_REGUL	GO_REGULATION_OF	26	-0.4708	-1.4224	0.078	0.385836	1	12067	tags=38%, list=2
GO_ACTION	GO_ACTION_POTENT	136	-0.3718	-1.3798	0.078	0.394985	1	10232	tags=33%, list=1
GO_MESOD	GO_MESODERM_DEV	131	-0.3254	-1.323	0.0781	0.409346	1	10951	tags=34%, list=1
GO_ION_TR	GO_ION_TRANSMEM	33	-0.439	-1.4066	0.0786	0.382805	1	12241	tags=48%, list=2
GO_POSITI	GO_POSITIVE_REGUL	27	-0.5002	-1.4717	0.0787	0.377673	0.999	8426	tags=33%, list=1
GO_CELL_C	GO_CELL_CELL_JUN	199	-0.3354	-1.3591	0.0788	0.397882	1	13008	tags=36%, list=2
GO_SENSO	GO_SENSORY_ORGA	265	-0.3325	-1.3371	0.0788	0.407252	1	14688	tags=40%, list=2
GO_EMBRY	GO_EMBRYONIC_OR	299	-0.3386	-1.363	0.079	0.395989	1	12111	tags=33%, list=2
GO_PRESY	GO_PRESYNAPSE_OF	53	-0.4379	-1.4186	0.0792	0.383418	1	10943	tags=42%, list=1
GO_RESPO	GO_RESPONSE_TO_N	52	-0.4446	-1.4529	0.0793	0.38892	1	7870	tags=38%, list=1
GO_CELL_I	GO_CELL_DIFFERENT	57	-0.4249	-1.3971	0.0797	0.384563	1	16459	tags=44%, list=2
GO_SMOOT	GO_SMOOTHENED_S	135	-0.403	-1.4471	0.0806	0.382305	1	10490	tags=35%, list=1
GO_CELL_J	GO_CELL_JUNCTION	422	-0.3298	-1.3638	0.081	0.397257	1	11122	tags=33%, list=1
GO_EMBRY	GO_EMBRYONIC_CA	39	-0.4535	-1.4626	0.0811	0.383896	0.999	10943	tags=46%, list=1
GO_TRANS	GO_TRANSMEMBRAI	353	-0.3239	-1.3551	0.0812	0.400012	1	12361	tags=34%, list=2
GO_PERIKA	GO_PERIKARYON	153	-0.3915	-1.4173	0.0813	0.38473	1	17048	tags=52%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	176	-0.3419	-1.3609	0.0813	0.396661	1	17271	tags=44%, list=3
GO_NEURO	GO_NEURON_PROJEC	37	-0.4273	-1.4432	0.0815	0.379714	1	11227	tags=49%, list=1
GO_9PLUS2	GO_9PLUS2_MOTILE_	105	-0.3483	-1.3594	0.0817	0.397908	1	15284	tags=38%, list=2
GO_BASEM	GO_BASEMENT_MEM	102	-0.4546	-1.4942	0.0818	0.370542	0.999	6867	tags=38%, list=1
GO_REGUL	GO_REGULATION_OF	184	-0.3681	-1.3926	0.0824	0.38852	1	11792	tags=35%, list=2
GO_T_TUBU	GO_T_TUBULE	52	-0.4269	-1.413	0.0828	0.384159	1	8909	tags=40%, list=1
GO_POSITI	GO_POSITIVE_REGUL	20	-0.5216	-1.4246	0.0832	0.389044	1	7379	tags=35%, list=1
GO_CHEMI	GO_CHEMICAL_SYNA	110	-0.4163	-1.412	0.0833	0.384729	1	10937	tags=39%, list=1
GO_TAU_PI	GO_TAU_PROTEIN_B	45	-0.4442	-1.4184	0.0835	0.383064	1	6486	tags=31%, list=1
GO_EPITHE	GO_EPITHELIAL_CEL	47	-0.4426	-1.4082	0.0838	0.383732	1	6716	tags=32%, list=1
GO_POSITI	GO_POSITIVE_REGUL	17	-0.5645	-1.4509	0.0841	0.388884	1	7201	tags=41%, list=1
GO_POSITI	GO_POSITIVE_REGUL	40	-0.4291	-1.4186	0.0843	0.384105	1	12950	tags=38%, list=2
GO_NEURO	GO_NEURON_SPINE	175	-0.3541	-1.3307	0.0845	0.408975	1	15095	tags=47%, list=2
GO_NEURO	GO_NEURONAL_STEI	23	-0.4977	-1.4099	0.0845	0.383596	1	8726	tags=30%, list=1
GO_REGUL	GO_REGULATION_OF	16	-0.5696	-1.4571	0.0847	0.386921	1	16720	tags=69%, list=2
GO_REGUL	GO_REGULATION_OF	431	-0.3405	-1.3482	0.0848	0.406854	1	11031	tags=33%, list=1
GO_EMBRY	GO_EMBRYONIC_SK	15	-0.5167	-1.417	0.0849	0.384518	1	8338	tags=47%, list=1
GO_COCHL	GO_COCHLEA_MORP	24	-0.4634	-1.4286	0.0849	0.390509	1	10943	tags=38%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	44	-0.4027	-1.3961	0.0851	0.385246	1	10299	tags=34%, list=1
GO_REGUL	GO_REGULATION_OF	165	-0.2927	-1.2499	0.0853	0.429732	1	11816	tags=29%, list=2
GO_ATRIAL	GO_ATRIAL_CARDIA	20	-0.5158	-1.4323	0.0855	0.385091	1	15888	tags=65%, list=2
GO_CYCLA	GO_CYCLASE_ACTIV	18	-0.5184	-1.4273	0.0855	0.390249	1	23618	tags=83%, list=4
GO_POSITI	GO_POSITIVE_REGUL	71	-0.3619	-1.3544	0.0855	0.400308	1	11011	tags=31%, list=1
GO_REGUL	GO_REGULATION_OF	34	-0.3963	-1.3241	0.0856	0.411509	1	21540	tags=62%, list=3
GO_CUL3_I	GO_CUL3_RING_UBIQ	36	-0.4528	-1.4243	0.0861	0.388813	1	3635	tags=25%, list=6
GO_DIVALI	GO_DIVALENT_INOR	161	-0.3459	-1.3404	0.0862	0.407291	1	16273	tags=44%, list=2
GO_REGUL	GO_REGULATION_OF	171	-0.3348	-1.3202	0.0862	0.408888	1	8089	tags=29%, list=1
GO_POSITI	GO_POSITIVE_REGUL	25	-0.4715	-1.4525	0.0864	0.388668	1	4739	tags=36%, list=8
GO_POSITI	GO_POSITIVE_REGUL	28	-0.5246	-1.4448	0.0866	0.379715	1	7648	tags=43%, list=1
GO_NEURO	GO_NEUROMUSCULA	50	-0.4548	-1.3892	0.0867	0.390439	1	16273	tags=60%, list=2
GO_VOLTA	GO_VOLTAGE_GATE	138	-0.4182	-1.3992	0.0869	0.38615	1	19616	tags=55%, list=3
GO_REGUL	GO_REGULATION_OF	154	-0.3512	-1.3632	0.087	0.396835	1	11361	tags=34%, list=1
GO_EPITHE	GO_EPITHELIAL_TO_	17	-0.5906	-1.481	0.0871	0.374561	0.999	8882	tags=41%, list=1
GO_9PLUS0	GO_9PLUS0_NON_MO	132	-0.3447	-1.324	0.0876	0.411203	1	19648	tags=47%, list=3
GO_AXON_	GO_AXON_EXTENSIO	122	-0.3914	-1.3881	0.0876	0.39126	1	15894	tags=47%, list=2
GO_GLUTA	GO_GLUTAMINE_ME	21	-0.52	-1.4247	0.0877	0.389612	1	13876	tags=57%, list=2
GO_CEREB	GO_CEREBELLAR_CO	23	-0.5217	-1.459	0.0878	0.383576	1	13615	tags=52%, list=2
GO_NEURO	GO_NEURON_CELL_C	17	-0.5662	-1.4494	0.0888	0.386871	1	9300	tags=53%, list=1
GO_NEURO	GO_NEUROPEPTIDE_	105	-0.3691	-1.3416	0.0888	0.408069	1	15095	tags=43%, list=2
GO_MOTOR	GO_MOTOR_ACTIVIT	132	-0.3951	-1.4045	0.0888	0.383573	1	14648	tags=44%, list=2
GO_EMBRY	GO_EMBRYONIC_OR	447	-0.3181	-1.3381	0.0888	0.407406	1	10951	tags=31%, list=1

GO_BLAST	GO_BLASTODERM_S	19	-0.4315	-1.3349	0.0889	0.406741	1	12828	tags=47%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	30	-0.4768	-1.3791	0.0894	0.393949	1	17412	tags=43%, list=3
GO_VENTR	GO_VENTRAL_SPINA	49	-0.4377	-1.4008	0.0898	0.384771	1	7336	tags=29%, list=1
GO_SMOO	GO_SMOOTH_MUSC	108	-0.4214	-1.4133	0.0898	0.384144	1	10853	tags=42%, list=1
GO_REPLA	GO_REPLACEMENT_	28	-0.4923	-1.436	0.0898	0.38535	1	10188	tags=43%, list=1
GO_REGUL	GO_REGULATION_O	82	-0.4182	-1.4344	0.0899	0.385454	1	13137	tags=41%, list=2
GO_ADREN	GO_ADRENERGIC_R	19	-0.489	-1.4453	0.09	0.380258	1	7522	tags=37%, list=1
GO_BRANC	GO_BRANCHING_IN	36	-0.4977	-1.5109	0.0904	0.37464	0.999	9208	tags=44%, list=1
GO_BASOL	GO_BASOLATERAL_	244	-0.3065	-1.2835	0.0904	0.421631	1	10205	tags=30%, list=1
GO_LOCO	GO_LOCOMOTOR_R	15	-0.4991	-1.3977	0.0906	0.385963	1	10462	tags=47%, list=1
GO_ZINC_I	GO_ZINC_ION_TRAN	27	-0.4941	-1.4439	0.0907	0.379839	1	16073	tags=56%, list=2
GO_PROST	GO_PROSTATE_GLA	49	-0.3855	-1.3543	0.0907	0.399829	1	7643	tags=29%, list=1
GO_VITAM	GO_VITAMIN_TRAN	17	-0.5002	-1.3965	0.0907	0.384993	1	14640	tags=47%, list=2
GO_BONE_	GO_BONE_GROWTH	31	-0.4565	-1.4253	0.0911	0.390438	1	14016	tags=48%, list=2
GO_MUSCL	GO_MUSCLE_CELL_	372	-0.3331	-1.3447	0.0914	0.407115	1	11823	tags=33%, list=2
GO_SEMI_	GO_SEMI_LUNAR_V	37	-0.5055	-1.4537	0.0917	0.389715	1	11808	tags=54%, list=2
GO_NEGAT	GO_NEGATIVE_CHE	47	-0.4056	-1.3842	0.0918	0.39165	1	11227	tags=40%, list=1
GO_BRANC	GO_BRANCH_ELONG	19	-0.5119	-1.4209	0.092	0.386047	1	10943	tags=42%, list=1
GO_SKELE	GO_SKELETAL_SYST	222	-0.3525	-1.3588	0.092	0.397313	1	16549	tags=46%, list=2
GO_CELLU	GO_CELLULAR_AMI	81	-0.3598	-1.3313	0.0923	0.409498	1	7085	tags=23%, list=1
GO_LABYR	GO_LABYRINTHINE_	20	-0.4797	-1.4238	0.0925	0.388303	1	10234	tags=45%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	134	-0.348	-1.3486	0.0927	0.407131	1	16193	tags=41%, list=2
GO_NEURO	GO_NEURON_PROJE	281	-0.3579	-1.366	0.0927	0.398715	1	11227	tags=35%, list=1
GO_CEREB	GO_CEREBRAL_COR	29	-0.4613	-1.4113	0.093	0.385576	1	18320	tags=55%, list=3
GO_LEARN	GO_LEARNING	141	-0.3815	-1.3678	0.093	0.397925	1	9704	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGU	84	-0.3773	-1.4039	0.0931	0.382084	1	12976	tags=40%, list=2
GO_REGUL	GO_REGULATION_O	49	-0.4188	-1.399	0.0932	0.385931	1	7579	tags=33%, list=1
GO_INTER	GO_INTERCALATED_	51	-0.4104	-1.3742	0.0933	0.397743	1	8909	tags=37%, list=1
GO_NEURO	GO_NEUROTROPHIN	33	-0.4169	-1.3564	0.0936	0.399713	1	7373	tags=36%, list=1
GO_POSITI	GO_POSITIVE_REGU	21	-0.4435	-1.3787	0.0938	0.394131	1	3630	tags=24%, list=6
GO_CELLU	GO_CELLULAR_RES	91	-0.3606	-1.3359	0.0938	0.406921	1	10151	tags=27%, list=1
GO_REGUL	GO_REGULATION_O	21	-0.4646	-1.3925	0.094	0.388205	1	13442	tags=43%, list=2
GO_RECEP	GO_RECEPTOR_SER	28	-0.4354	-1.3939	0.0941	0.387855	1	7643	tags=32%, list=1
GO_OXIDA	GO_OXIDATIVE_DEM	19	-0.5183	-1.4262	0.0945	0.390251	1	943	tags=21%, list=2
GO_TRIGL	GO_TRIGLYCERIDE_	29	-0.4119	-1.3402	0.0947	0.407112	1	9980	tags=34%, list=1
GO_POSITI	GO_POSITIVE_REGU	38	-0.4044	-1.3549	0.0947	0.399787	1	20632	tags=55%, list=3
GO_NEURO	GO_NEURON_PROJE	170	-0.362	-1.3459	0.0947	0.406825	1	12077	tags=36%, list=2
GO_CELLU	GO_CELLULAR_SOD	18	-0.5066	-1.4263	0.0948	0.390676	1	14054	tags=61%, list=2
GO_POSITI	GO_POSITIVE_REGU	34	-0.4219	-1.3915	0.0949	0.388922	1	4645	tags=24%, list=8
GO_REGUL	GO_REGULATION_O	17	-0.4765	-1.3791	0.0949	0.394466	1	13378	tags=65%, list=2
GO_CHLOR	GO_CHLORIDE_TRA	101	-0.3515	-1.3186	0.0951	0.407272	1	17190	tags=51%, list=2
GO_OVULA	GO_OVULATION_CY	69	-0.3696	-1.3264	0.0954	0.410544	1	12962	tags=38%, list=2
GO_POTAS	GO_POTASSIUM_CH	95	-0.4296	-1.3854	0.0955	0.391773	1	20230	tags=57%, list=3
GO_REGIO	GO_REGIONALIZATI	353	-0.3268	-1.3214	0.0956	0.409439	1	17335	tags=43%, list=3
GO_REGUL	GO_REGULATION_O	109	-0.3698	-1.3746	0.096	0.397402	1	13067	tags=38%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	50	-0.4209	-1.3858	0.0962	0.392316	1	18948	tags=50%, list=3
GO_CHON	GO_CHONDROCYTE_	100	-0.4073	-1.4145	0.0963	0.383952	1	16573	tags=46%, list=2
GO_SODIU	GO_SODIUM_CHANN	26	-0.479	-1.3716	0.0963	0.396291	1	18109	tags=58%, list=3
GO_CEREB	GO_CEREBRAL_COR	40	-0.4376	-1.4043	0.0965	0.382509	1	18320	tags=52%, list=3
GO_ACTIN_	GO_ACTIN_FILAMEN	150	-0.3794	-1.3831	0.0966	0.390252	1	11874	tags=35%, list=2
GO_GABA_	GO_GABA_ERGIC_SY	72	-0.4583	-1.4081	0.097	0.383219	1	18359	tags=57%, list=3
GO_MUSCL	GO_MUSCLE_CELL_	19	-0.4834	-1.3578	0.0976	0.398606	1	20687	tags=53%, list=3
GO_IN_UTE	GO_IN_UTERO_EMB	378	-0.3064	-1.3232	0.0977	0.410161	1	10444	tags=30%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	22	-0.4556	-1.4041	0.0981	0.382221	1	9340	tags=36%, list=1
GO_NOTCH	GO_NOTCH_BINDIN	22	-0.5085	-1.4127	0.0986	0.384093	1	7175	tags=41%, list=1
GO_LIPID_	GO_LIPID_EXPORT_	38	-0.4028	-1.338	0.0986	0.40714	1	9864	tags=32%, list=1
GO_CARDI	GO_CARDIAC_EPITH	32	-0.4913	-1.4453	0.0987	0.380984	1	17220	tags=53%, list=2
GO_METAN	GO_METANEPHRIC_	16	-0.5762	-1.427	0.0988	0.390047	1	11652	tags=50%, list=2

GO_CENTR	GO_CENTRAL_NERV	82	-0.3998	-1.3915	0.0988	0.388321	1	18325	tags=54%, list=3
GO_SEROT	GO_SEROTONIN_RE	34	-0.4244	-1.3481	0.099	0.406459	1	20978	tags=53%, list=3
GO_REGUL	GO_REGULATION_O	17	-0.5152	-1.4226	0.099	0.386192	1	11448	tags=53%, list=2
GO_CRANI	GO_CRANIAL_SKELE	68	-0.398	-1.3731	0.0992	0.396225	1	9854	tags=37%, list=1
GO_CARBO	GO_CARBOHYDRAT	112	-0.3426	-1.3085	0.0992	0.410638	1	11745	tags=34%, list=2
GO_HIPPO	GO_HIPPOCAMPUS_I	80	-0.3853	-1.3306	0.0994	0.408645	1	15403	tags=43%, list=2
GO_MAIN_	GO_MAIN_AXON	68	-0.4617	-1.4088	0.0996	0.383161	1	14688	tags=56%, list=2
GO_ARF_G	GO_ARF_GUANYL_N	18	-0.4904	-1.4241	0.0996	0.388422	1	12242	tags=56%, list=2
GO_ERYTH	GO_ERYTHROCYTE_	33	-0.3988	-1.3293	0.0996	0.409548	1	5294	tags=21%, list=9
GO_DISTA	GO_DISTAL_AXON	301	-0.3735	-1.374	0.1	0.397536	1	16005	tags=46%, list=2
GO_REGUL	GO_REGULATION_O	231	-0.3546	-1.3448	0.1	0.407517	1	11448	tags=36%, list=2
GO_ESTAB	GO_ESTABLISHMEN	17	-0.5065	-1.4111	0.1004	0.384505	1	10943	tags=41%, list=1
GO_POTAS	GO_POTASSIUM_ION	155	-0.3753	-1.336	0.1006	0.407246	1	15498	tags=43%, list=2
GO_ENDOC	GO_ENDOCHONDRA	54	-0.428	-1.387	0.1014	0.392201	1	16214	tags=50%, list=2
GO_REGUL	GO_REGULATION_O	25	-0.4373	-1.3646	0.1014	0.397398	1	5634	tags=32%, list=1
GO_POSITI	GO_POSITIVE_REGU	378	-0.3242	-1.3276	0.1015	0.410244	1	10105	tags=30%, list=1
GO_LONG_	GO_LONG_TERM_SY	31	-0.4185	-1.3277	0.1016	0.410513	1	11596	tags=45%, list=2
GO_CELL_I	GO_CELL_DIFFEREN	22	-0.5187	-1.4203	0.1017	0.384357	1	13955	tags=55%, list=2
GO_RESPO	GO_RESPONSE_TO_C	17	-0.4888	-1.373	0.1018	0.395912	1	16182	tags=59%, list=2
GO_ANTER	GO_ANTERIOR_POST	218	-0.3253	-1.3018	0.102	0.415803	1	17335	tags=43%, list=3
GO_NEGAT	GO_NEGATIVE_REG	16	-0.5269	-1.4237	0.102	0.387807	1	11360	tags=31%, list=1
GO_EPITHE	GO_EPITHELIAL_CEL	35	-0.4121	-1.3732	0.1022	0.396537	1	10272	tags=43%, list=1
GO_PALLIU	GO_PALLIUM_DEVEI	166	-0.3648	-1.3405	0.1023	0.407545	1	15403	tags=41%, list=2
GO_AXON_	GO_AXON_INITIAL_	17	-0.5814	-1.4362	0.1025	0.38577	1	19825	tags=76%, list=3
GO_CAVEO	GO_CAVEOLA	76	-0.3944	-1.4029	0.1026	0.382699	1	9810	tags=39%, list=1
GO_SECON	GO_SECONDARY_AC	234	-0.2854	-1.2341	0.1027	0.435886	1	16401	tags=38%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	65	-0.4489	-1.3661	0.1027	0.399077	1	19125	tags=58%, list=3
GO_ANATO	GO_ANATOMICAL_S	18	-0.4985	-1.4075	0.1028	0.382923	1	10523	tags=50%, list=1
GO_G_PRO	GO_G_PROTEIN_COU	50	-0.3965	-1.3305	0.1031	0.408222	1	19125	tags=50%, list=3
GO_EMBRY	GO_EMBRYONIC_HE	70	-0.3638	-1.3384	0.1032	0.407934	1	12794	tags=36%, list=2
GO_NODE_	GO_NODE_OF_RANV	15	-0.5824	-1.4358	0.1036	0.384931	1	11099	tags=53%, list=1
GO_NEGAT	GO_NEGATIVE_REG	100	-0.3425	-1.3134	0.1038	0.407589	1	15394	tags=40%, list=2
GO_NEURO	GO_NEURON_MIGRA	159	-0.3836	-1.3257	0.1042	0.410947	1	20062	tags=58%, list=3
GO_NEGAT	GO_NEGATIVE_REG	33	-0.4237	-1.3735	0.1043	0.396568	1	8907	tags=33%, list=1
GO_NON_M	GO_NON_MOTILE_CI	157	-0.3457	-1.3197	0.1043	0.407705	1	19648	tags=48%, list=3
GO_FOREB	GO_FOREBRAIN_CEL	56	-0.4183	-1.385	0.1047	0.391971	1	18325	tags=52%, list=3
GO_OLFAC	GO_OLFACTORY_LO	33	-0.4658	-1.3758	0.1048	0.396179	1	15403	tags=58%, list=2
GO_IONOTI	GO_IONOTROPIC_GL	28	-0.4424	-1.3713	0.105	0.39558	1	15082	tags=50%, list=2
GO_PROTE	GO_PROTEIN_LOCAL	58	-0.4692	-1.4506	0.1051	0.388569	1	22739	tags=72%, list=3
GO_NEURO	GO_NEUROTRANSMI	21	-0.4775	-1.378	0.1051	0.394266	1	8287	tags=43%, list=1
GO_EAR_M	GO_EAR_MORPHOGE	121	-0.3618	-1.318	0.1051	0.407455	1	11779	tags=34%, list=2
GO_INTRA_	GO_INTRA_GOLGI_V	33	-0.4858	-1.439	0.1052	0.383067	1	13882	tags=52%, list=2
GO_LENS_I	GO_LENS_DEVELOP	81	-0.3436	-1.3077	0.1055	0.411281	1	10943	tags=32%, list=1
GO_EPITHE	GO_EPITHELIAL_TU	29	-0.4476	-1.4153	0.1055	0.384397	1	6907	tags=34%, list=1
GO_GASTR	GO_GASTRULATION	185	-0.3444	-1.3511	0.1059	0.403981	1	10951	tags=34%, list=1
GO_CELL_	GO_CELL_CELL_SIG	32	-0.4577	-1.3994	0.106	0.386922	1	15888	tags=53%, list=2
GO_LYSINE	GO_LYSINE_ACETYL	22	-0.5561	-1.4344	0.1061	0.384713	1	4511	tags=41%, list=8
GO_STEM_	GO_STEM_CELL_DIV	44	-0.4036	-1.3694	0.1061	0.397606	1	6459	tags=30%, list=1
GO_REGUL	GO_REGULATION_O	112	-0.4578	-1.4854	0.1066	0.370817	0.999	9389	tags=39%, list=1
GO_RETIN	GO_RETINAL_BINDI	17	-0.505	-1.3589	0.1069	0.397721	1	14556	tags=53%, list=2
GO_MICRO	GO_MICROTUBULE_	92	-0.4035	-1.4089	0.1069	0.383592	1	22421	tags=59%, list=3
GO_TONGU	GO_TONGUE_DEVEL	23	-0.4791	-1.4199	0.1071	0.383584	1	7885	tags=39%, list=1
GO_NEGAT	GO_NEGATIVE_REG	40	-0.3733	-1.3163	0.1071	0.408885	1	21386	tags=63%, list=3
GO_TERPE	GO_TERPENOID_BIO	15	-0.5223	-1.3942	0.1072	0.387896	1	14556	tags=47%, list=2
GO_NEURO	GO_NEUROTRANSMI	50	-0.4622	-1.3676	0.1074	0.397746	1	16720	tags=56%, list=2
GO_NOTOC	GO_NOTOCHORD_DE	19	-0.4662	-1.3921	0.1078	0.388227	1	14539	tags=53%, list=2
GO_REGUL	GO_REGULATION_O	178	-0.3311	-1.326	0.1081	0.410937	1	11792	tags=33%, list=2
GO_REFLE	GO_REFLEX	18	-0.5263	-1.3706	0.1083	0.395863	1	18132	tags=61%, list=3

GO_PROTE	GO_PROTEIN_METH	77	-0.4357	-1.4258	0.1085	0.390179	1	12102	tags=36%, list=2
GO_POSITI	GO_POSITIVE_REGU	208	-0.3213	-1.3386	0.1087	0.408071	1	8635	tags=27%, list=1
GO_DEVEL	GO_DEVELOPMENT_	105	-0.3299	-1.2942	0.1088	0.418131	1	12664	tags=35%, list=2
GO_SPECT	GO_SPECTRIN_BIND	28	-0.456	-1.3762	0.1088	0.396037	1	3453	tags=29%, list=6
GO_EUCHR	GO_EUCHROMATIN	33	-0.4793	-1.4293	0.1092	0.389924	1	6062	tags=30%, list=1
GO_NEGAT	GO_NEGATIVE_REG	69	-0.3641	-1.3335	0.1094	0.407309	1	16473	tags=46%, list=2
GO_VENTR	GO_VENTRICULAR_	36	-0.4187	-1.3554	0.1095	0.400039	1	10004	tags=36%, list=1
GO_CARBO	GO_CARBOHYDRAT	35	-0.4055	-1.341	0.1098	0.407743	1	19217	tags=51%, list=3
GO_NEGAT	GO_NEGATIVE_REG	30	-0.4217	-1.3679	0.1098	0.39836	1	7754	tags=43%, list=1
GO_NEGAT	GO_NEGATIVE_REG	28	-0.4032	-1.3436	0.1098	0.40704	1	11227	tags=46%, list=1
GO_NEGAT	GO_NEGATIVE_REG	124	-0.3217	-1.2775	0.1098	0.42643	1	15394	tags=40%, list=2
GO_MOTIL	GO_MOTILE_CILIUM	177	-0.3373	-1.3569	0.1105	0.39932	1	19501	tags=45%, list=3
GO_POSITI	GO_POSITIVE_REGU	46	-0.3927	-1.3358	0.1105	0.406507	1	15888	tags=50%, list=2
GO_NEURA	GO_NEURAL_CREST_	56	-0.3857	-1.3691	0.1107	0.397606	1	15503	tags=50%, list=2
GO_NEGAT	GO_NEGATIVE_REG	34	-0.438	-1.3653	0.1109	0.3973	1	7826	tags=38%, list=1
GO_CELL_	GO_CELL_FATE_SPE	100	-0.3874	-1.3646	0.1116	0.396925	1	16459	tags=44%, list=2
GO_MAGN	GO_MAGNESIUM_IO	17	-0.5161	-1.3988	0.1116	0.385657	1	8736	tags=47%, list=1
GO_NEGAT	GO_NEGATIVE_REG	23	-0.4867	-1.3903	0.1118	0.389483	1	6062	tags=30%, list=1
GO_REGUL	GO_REGULATION_O	114	-0.3235	-1.306	0.1122	0.414087	1	10136	tags=31%, list=1
GO_RESPO	GO_RESPONSE_TO_F	16	-0.4739	-1.3665	0.1122	0.398846	1	4712	tags=31%, list=8
GO_COLLA	GO_COLLATERAL_S	26	-0.4424	-1.3634	0.1122	0.396953	1	7870	tags=31%, list=1
GO_POSITI	GO_POSITIVE_REGU	85	-0.3788	-1.3418	0.1124	0.408324	1	9996	tags=33%, list=1
GO_AXONE	GO_AXONEME_ASSE	61	-0.436	-1.4281	0.1126	0.390913	1	15680	tags=51%, list=2
GO_VOLTA	GO_VOLTAGE_GATE	17	-0.5259	-1.3464	0.1127	0.408239	1	16280	tags=65%, list=2
GO_REGUL	GO_REGULATION_O	46	-0.4239	-1.3653	0.1129	0.397741	1	6421	tags=30%, list=1
GO_MICRO	GO_MICROTUBULE_	21	-0.5127	-1.4105	0.1129	0.384253	1	7501	tags=33%, list=1
GO_MOTIL	GO_MOTILE_CILIUM	22	-0.5194	-1.4251	0.1132	0.390102	1	11488	tags=45%, list=2
GO_REGUL	GO_REGULATION_O	74	-0.3384	-1.2794	0.1133	0.425151	1	8426	tags=27%, list=1
GO_MUSCL	GO_MUSCLE_ORGA	393	-0.3309	-1.322	0.1133	0.409397	1	9340	tags=30%, list=1
GO_MEMB	GO_MEMBRANE_RE	47	-0.4096	-1.3415	0.1134	0.407106	1	15888	tags=51%, list=2
GO_MICRO	GO_MICROTUBULE_	351	-0.3577	-1.3838	0.1135	0.390677	1	15680	tags=40%, list=2
GO_EMBRY	GO_EMBRYONIC_DI	34	-0.468	-1.396	0.1137	0.384827	1	5708	tags=32%, list=1
GO_SULFU	GO_SULFUR_COMPO	244	-0.3223	-1.3164	0.1139	0.409255	1	14201	tags=36%, list=2
GO_DNA_M	GO_DNA_METHYLA	20	-0.4876	-1.3562	0.1141	0.399463	1	16537	tags=40%, list=2
GO_REGUL	GO_REGULATION_O	24	-0.4339	-1.3462	0.1141	0.40752	1	6239	tags=29%, list=1
GO_REGUL	GO_REGULATION_O	24	-0.4349	-1.3465	0.1143	0.40845	1	3694	tags=29%, list=6
GO_POSITI	GO_POSITIVE_REGU	171	-0.3576	-1.3342	0.1146	0.406992	1	8907	tags=31%, list=1
GO_POSITI	GO_POSITIVE_REGU	265	-0.3108	-1.2868	0.115	0.419031	1	11099	tags=31%, list=1
GO_ZINC_	GO_ZINC_ION_TRAN	21	-0.5051	-1.4063	0.1152	0.382617	1	16073	tags=62%, list=2
GO_NEGAT	GO_NEGATIVE_REG	89	-0.3561	-1.32	0.1156	0.408263	1	16743	tags=45%, list=2
GO_VENTR	GO_VENTRAL_SPINA	17	-0.5103	-1.3388	0.1161	0.408178	1	16459	tags=53%, list=2
GO_CELLU	GO_CELLULAR_RES	22	-0.4637	-1.3721	0.1166	0.395848	1	3347	tags=27%, list=6
GO_REGUL	GO_REGULATION_O	56	-0.3596	-1.2943	0.1168	0.418594	1	5634	tags=27%, list=1
GO_VOLTA	GO_VOLTAGE_GATE	87	-0.4238	-1.3557	0.1169	0.399934	1	20230	tags=59%, list=3
GO_RNA_P	GO_RNA_POLYMER	61	-0.4219	-1.3835	0.117	0.390573	1	12598	tags=34%, list=2
GO_REGUL	GO_REGULATION_O	26	-0.4646	-1.3993	0.1171	0.386545	1	7826	tags=35%, list=1
GO_VOCAL	GO_VOCALIZATION_	19	-0.4931	-1.3729	0.1172	0.39543	1	9854	tags=47%, list=1
GO_CILIAR	GO_CILIARY_MEMB	72	-0.3656	-1.3239	0.1172	0.410403	1	10493	tags=32%, list=1
GO_SARCO	GO_SARCOLEMMA	132	-0.3887	-1.384	0.1176	0.390821	1	8909	tags=35%, list=1
GO_MEMO	GO_MEMORY	118	-0.3508	-1.3125	0.1178	0.407439	1	9340	tags=35%, list=1
GO_STRUC	GO_STRUCTURAL_C	18	-0.4967	-1.3685	0.1182	0.398333	1	8159	tags=44%, list=1
GO_ACETY	GO_ACETYL_COA_M	38	-0.4326	-1.3658	0.1183	0.398563	1	3955	tags=21%, list=7
GO_REGUL	GO_REGULATION_O	16	-0.5337	-1.3792	0.1186	0.395434	1	18541	tags=63%, list=3
GO_REGUL	GO_REGULATION_O	27	-0.4723	-1.4043	0.1186	0.383138	1	12743	tags=48%, list=2
GO_CEREB	GO_CEREBELLAR_P	15	-0.5223	-1.3974	0.119	0.385234	1	11744	tags=53%, list=2
GO_NEURO	GO_NEUROPEPTIDE_	26	-0.431	-1.3201	0.1193	0.408442	1	19821	tags=69%, list=3
GO_REGUL	GO_REGULATION_O	25	-0.4461	-1.3655	0.1197	0.398089	1	18362	tags=60%, list=3
GO_SULFU	GO_SULFUR_AMINO_	38	-0.3965	-1.3383	0.1198	0.40751	1	3723	tags=18%, list=6

GO_NEGAT	GO_NEGATIVE_REGU	16	-0.4584	-1.3049	0.1202	0.414667	1	5277	tags=25%, list=9
GO_LUNG_	GO_LUNG_EPITHELIU	37	-0.3864	-1.3007	0.1204	0.415164	1	17156	tags=46%, list=2
GO_NEURA	GO_NEURAL_PRECU	149	-0.358	-1.3177	0.1206	0.40755	1	11374	tags=34%, list=1
GO_HEART	GO_HEART_PROCESS	290	-0.3268	-1.3008	0.1208	0.415961	1	12152	tags=33%, list=2
GO_CILIAR	GO_CILIARY_PLASM	113	-0.4055	-1.3834	0.121	0.390275	1	12242	tags=38%, list=2
GO_RENAL	GO_RENAL_SYSTEM_	28	-0.5542	-1.4727	0.1214	0.377461	0.999	9318	tags=57%, list=1
GO_AXOLE	GO_AXOLEMMA	15	-0.5679	-1.3842	0.1215	0.39107	1	20089	tags=73%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	37	-0.4338	-1.3679	0.1215	0.398916	1	6847	tags=30%, list=1
GO_CILIUM	GO_CILIUM_MOVEM	143	-0.3485	-1.329	0.1216	0.409209	1	16638	tags=39%, list=2
GO_NEURO	GO_NEUROTRANSMI	225	-0.3646	-1.354	0.122	0.400047	1	10331	tags=35%, list=1
GO_VOLTA	GO_VOLTAGE_GATE	41	-0.4302	-1.3346	0.122	0.406778	1	10331	tags=37%, list=1
GO_POSITI	GO_POSITIVE_REGU	20	-0.542	-1.4248	0.122	0.38997	1	9721	tags=50%, list=1
GO_REGUL	GO_REGULATION_OI	79	-0.4284	-1.4101	0.1221	0.383769	1	5882	tags=27%, list=1
GO_SPERM	GO_SPERM_PRINCIP	23	-0.4253	-1.3255	0.1223	0.410848	1	26388	tags=65%, list=4
GO_REGUL	GO_REGULATION_OI	50	-0.3678	-1.2921	0.1223	0.418008	1	13631	tags=46%, list=2
GO_SOLUT	GO_SOLUTE_PROTO	19	-0.4419	-1.3293	0.1227	0.409041	1	15610	tags=53%, list=2
GO_RETIN	GO_RETINA_LAYER_	25	-0.4679	-1.3975	0.1228	0.385588	1	12111	tags=44%, list=2
GO_TRANS	GO_TRANSMISSION_	72	-0.3969	-1.3155	0.1232	0.408438	1	11099	tags=38%, list=1
GO_POTAS	GO_POTASSIUM_CH	52	-0.3659	-1.2896	0.1233	0.417595	1	15888	tags=44%, list=2
GO_MESOD	GO_MESODERMAL_	18	-0.4874	-1.3425	0.1234	0.408138	1	9208	tags=33%, list=1
GO_EXCRE	GO_EXCRETION	64	-0.3651	-1.2841	0.1235	0.420876	1	13846	tags=39%, list=2
GO_VITAM	GO_VITAMIN_BINDI	135	-0.3161	-1.256	0.1235	0.42468	1	12094	tags=30%, list=2
GO_SEROT	GO_SEROTONIN_RE	39	-0.3866	-1.2673	0.1238	0.428257	1	14144	tags=38%, list=2
GO_CARBO	GO_CARBOHYDRAT	145	-0.3221	-1.2754	0.124	0.425499	1	11745	tags=32%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	73	-0.3609	-1.311	0.1241	0.408801	1	12556	tags=38%, list=2
GO_GOLGI_	GO_GOLGI_LUMEN	101	-0.3667	-1.2792	0.1245	0.42461	1	13137	tags=35%, list=2
GO_REGUL	GO_REGULATION_OI	84	-0.3501	-1.2991	0.1252	0.417644	1	13913	tags=37%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	20	-0.499	-1.3869	0.1253	0.390601	1	6417	tags=35%, list=1
GO_ANION	GO_ANION_TRANSM	311	-0.2968	-1.2514	0.1253	0.428957	1	15498	tags=37%, list=2
GO_ENDOC	GO_ENDOCRINE_SYS	125	-0.329	-1.2598	0.1257	0.424781	1	15534	tags=43%, list=2
GO_SOMAT	GO_SOMATIC_STEM_	75	-0.3382	-1.2675	0.1257	0.429042	1	7643	tags=24%, list=1
GO_DYNEI	GO_DYNEIN_COMPL	53	-0.4149	-1.3708	0.126	0.395927	1	12302	tags=45%, list=2
GO_INTRA	GO_INTRAMOLECUL	25	-0.461	-1.3513	0.126	0.404111	1	8903	tags=32%, list=1
GO_RETIN	GO_RETINA_MORPH	59	-0.3693	-1.3033	0.1263	0.415457	1	7640	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.5786	-1.4204	0.1265	0.385594	1	8399	tags=33%, list=1
GO_REGUL	GO_REGULATION_OI	98	-0.3404	-1.3085	0.1267	0.410241	1	4326	tags=20%, list=7
GO_REGUL	GO_REGULATION_OI	29	-0.4256	-1.3274	0.1268	0.410138	1	18653	tags=55%, list=3
GO_MULTI_	GO_MULTI_MULTICE	222	-0.2831	-1.2227	0.127	0.441841	1	9408	tags=28%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	96	-0.3356	-1.2866	0.127	0.41854	1	8823	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	147	-0.3233	-1.2855	0.1274	0.419178	1	6421	tags=24%, list=1
GO_REGUL	GO_REGULATION_OI	49	-0.3703	-1.3096	0.1274	0.409919	1	6716	tags=27%, list=1
GO_SKELE	GO_SKELETAL_SYST	499	-0.3165	-1.2968	0.1277	0.417804	1	14646	tags=37%, list=2
GO_NOREP	GO_NOREPINEPHRIN	25	-0.4253	-1.2953	0.1277	0.418866	1	5221	tags=24%, list=9
GO_ERYTH	GO_ERYTHROCYTE_	15	-0.4658	-1.3357	0.1279	0.405747	1	3629	tags=27%, list=6
GO_SUGAR	GO_SUGAR_TRANSM	23	-0.4244	-1.3141	0.128	0.407863	1	20436	tags=61%, list=3
GO_CELLU	GO_CELLULAR_RESI	66	-0.3418	-1.2658	0.1289	0.426203	1	14822	tags=44%, list=2
GO_PROTE	GO_PROTEIN_KINAS	26	-0.4628	-1.3869	0.129	0.391752	1	5615	tags=42%, list=1
GO_ORGAN	GO_ORGANIC_HYDR	262	-0.2816	-1.2161	0.1292	0.442757	1	9450	tags=24%, list=1
GO_LATER	GO_LATERAL_PLASM	64	-0.3809	-1.3226	0.1293	0.409286	1	9790	tags=28%, list=1
GO_POSITI	GO_POSITIVE_REGU	20	-0.4587	-1.3204	0.1293	0.409365	1	9318	tags=40%, list=1
GO_POTAS	GO_POTASSIUM_CH	119	-0.392	-1.3219	0.1294	0.40912	1	19152	tags=52%, list=3
GO_CATEC	GO_CATECHOLAMIN	55	-0.4271	-1.3358	0.1296	0.406127	1	11361	tags=38%, list=1
GO_SITE_O	GO_SITE_OF_POLARI	185	-0.3585	-1.3234	0.1298	0.410268	1	12361	tags=39%, list=2
GO_SYNAP	GO_SYNAPTIC_TRAN	94	-0.4163	-1.3738	0.13	0.397305	1	13615	tags=43%, list=2
GO_PEPTID	GO_PEPTIDYL_ARGI	15	-0.5275	-1.3452	0.1306	0.407644	1	13934	tags=40%, list=2
GO_RHYTH	GO_RHYTHMIC_PRO	301	-0.3173	-1.273	0.1306	0.42466	1	12274	tags=33%, list=2
GO_HORM	GO_HORMONE_BIND	82	-0.3482	-1.2711	0.1309	0.425033	1	13742	tags=37%, list=2
GO_POSITI	GO_POSITIVE_REGU	97	-0.3488	-1.275	0.1312	0.424565	1	9235	tags=34%, list=1

GO_E_BOX_	GO_E_BOX_BINDING	50	-0.4084	-1.3243	0.1313	0.412056	1	13688	tags=48%, list=2
GO_CELL_(	GO_CELL_COMMUNI	56	-0.3858	-1.304	0.1313	0.415033	1	10232	tags=32%, list=1
GO_PROTEI	GO_PROTEIN_CATAE	19	-0.4312	-1.3273	0.1316	0.409765	1	3754	tags=26%, list=6
GO_SARCO	GO_SARCOPLASMIC_	38	-0.4122	-1.3197	0.1317	0.408176	1	13692	tags=39%, list=2
GO_REGUL	GO_REGULATION_OI	47	-0.4167	-1.3638	0.1318	0.396794	1	8426	tags=34%, list=1
GO_ANATC	GO_ANATOMICAL_S	17	-0.4564	-1.3142	0.1319	0.407972	1	8489	tags=47%, list=1
GO_REGUL	GO_REGULATION_OI	36	-0.4442	-1.3377	0.132	0.407183	1	10834	tags=42%, list=1
GO_KERAT	GO_KERATAN_SULF	28	-0.4721	-1.381	0.1322	0.393183	1	8113	tags=36%, list=1
GO_INTRA(	GO_INTRACELLULAI	16	-0.4529	-1.309	0.1331	0.410255	1	5852	tags=44%, list=1
GO_CATIOI	GO_CATION_CHANNI	313	-0.3365	-1.2613	0.1335	0.424052	1	15543	tags=41%, list=2
GO_NOREP	GO_NOREPINEPHRIN	17	-0.473	-1.3184	0.1336	0.407171	1	3846	tags=24%, list=7
GO_NEURC	GO_NEURON_FATE_(	66	-0.4249	-1.322	0.1336	0.409776	1	16670	tags=45%, list=2
GO_DYNEII	GO_DYNEIN_INTERM	29	-0.4113	-1.3189	0.1338	0.407184	1	13484	tags=48%, list=2
GO_POSITI	GO_POSITIVE_REGUI	36	-0.4339	-1.3229	0.1343	0.409078	1	18447	tags=53%, list=3
GO_URETE	GO_URETER_DEVEL(	18	-0.4515	-1.2946	0.1344	0.418754	1	10881	tags=33%, list=1
GO_INNER_	GO_INNER_EAR_MOI	101	-0.3715	-1.29	0.1345	0.417852	1	11779	tags=34%, list=2
GO_GATED	GO_GATED_CHANNE	334	-0.3361	-1.2732	0.1348	0.425092	1	15543	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	177	-0.344	-1.2694	0.1349	0.426891	1	13991	tags=40%, list=2
GO_REGUL	GO_REGULATION_OI	65	-0.385	-1.3202	0.1352	0.409344	1	17571	tags=46%, list=3
GO_REGUL	GO_REGULATION_OI	32	-0.375	-1.273	0.1354	0.425007	1	5959	tags=25%, list=1
GO_NEURC	GO_NEUROBLAST_PI	60	-0.3952	-1.315	0.1355	0.408954	1	11374	tags=37%, list=1
GO_ATPASI	GO_ATPASE_COUPLI	57	-0.3847	-1.3134	0.1356	0.407202	1	12270	tags=40%, list=2
GO_BICARI	GO_BICARBONATE_T	43	-0.389	-1.2967	0.1358	0.417617	1	6264	tags=23%, list=1
GO_OSSIFI(	GO_OSSIFICATION	394	-0.32	-1.3105	0.1358	0.409229	1	10490	tags=32%, list=1
GO_POSITI	GO_POSITIVE_REGUI	60	-0.3683	-1.3031	0.1358	0.415287	1	16475	tags=40%, list=2
GO_REGUL	GO_REGULATION_OI	115	-0.3433	-1.2956	0.1358	0.418722	1	9901	tags=35%, list=1
GO_VOLTA	GO_VOLTAGE_GATE	195	-0.3566	-1.2793	0.1364	0.42498	1	19152	tags=48%, list=3
GO_DELAY	GO_DELAYED_RECT	32	-0.4528	-1.2895	0.1365	0.417401	1	15057	tags=47%, list=2
GO_REGUL	GO_REGULATION_OI	296	-0.3292	-1.2876	0.1365	0.419227	1	12152	tags=34%, list=2
GO_POSITI	GO_POSITIVE_REGUI	18	-0.53	-1.3769	0.137	0.395799	1	11596	tags=44%, list=2
GO_DETEC	GO_DETECTION_OF_	139	-0.3183	-1.2296	0.1372	0.43765	1	18221	tags=42%, list=3
GO_MYOSI	GO_MYOSIN_II_COM	20	-0.5045	-1.3444	0.1376	0.406587	1	12596	tags=45%, list=2
GO_REGUL	GO_REGULATION_OI	104	-0.3339	-1.2881	0.138	0.419249	1	11328	tags=32%, list=1
GO_DOPAM	GO_DOPAMINE_TRAI	48	-0.4251	-1.346	0.1382	0.407357	1	9243	tags=38%, list=1
GO_CATIOI	GO_CATION_TRANSI	18	-0.4647	-1.2898	0.1383	0.417801	1	13692	tags=56%, list=2
GO_MAINT	GO_MAINTENANCE_	16	-0.5332	-1.3782	0.1385	0.394532	1	16473	tags=63%, list=2
GO_CELL_\	GO_CELL_VOLUME_	30	-0.3857	-1.2907	0.1387	0.416962	1	7472	tags=30%, list=1
GO_POSITI	GO_POSITIVE_REGUI	42	-0.4182	-1.3209	0.1389	0.409533	1	13067	tags=40%, list=2
GO_REGUL	GO_REGULATION_OI	231	-0.3509	-1.3194	0.1393	0.407207	1	10331	tags=34%, list=1
GO_TRANS	GO_TRANSMITTER_(	60	-0.421	-1.3145	0.1393	0.408397	1	14794	tags=50%, list=2
GO_REGUL	GO_REGULATION_OI	19	-0.4351	-1.2918	0.1394	0.4181	1	11233	tags=42%, list=1
GO_REGUL	GO_REGULATION_OI	76	-0.4579	-1.4196	0.1398	0.382788	1	10263	tags=41%, list=1
GO_PROTEI	GO_PROTEIN_LOCAL	83	-0.4012	-1.3399	0.1399	0.407082	1	8830	tags=34%, list=1
GO_NCRNA	GO_NCRNA_EXPORT	36	-0.5761	-1.4493	0.14	0.386124	1	9700	tags=47%, list=1
GO_REGUL	GO_REGULATION_OI	74	-0.3357	-1.2662	0.1403	0.425878	1	9635	tags=27%, list=1
GO_ENSHE	GO_ENSHEATHMENT	138	-0.319	-1.2724	0.1404	0.424359	1	8858	tags=29%, list=1
GO_INORG	GO_INORGANIC_ANI	143	-0.3151	-1.2587	0.1406	0.42508	1	7452	tags=26%, list=1
GO_HEXOS	GO_HEXOSE_TRANSI	19	-0.4267	-1.2771	0.1409	0.425894	1	8827	tags=37%, list=1
GO_PROTO	GO_PROTON_EXPOR	17	-0.4646	-1.302	0.1415	0.415972	1	12241	tags=47%, list=2
GO_SPINAL	GO_SPINAL_CORD_M	35	-0.4246	-1.2879	0.1416	0.419227	1	16413	tags=46%, list=2
GO_REGUL	GO_REGULATION_OI	129	-0.3274	-1.2648	0.142	0.425945	1	16894	tags=44%, list=2
GO_NOSE_I	GO_NOSE_DEVELOPI	15	-0.5588	-1.3362	0.1426	0.4074	1	9043	tags=47%, list=1
GO_CYTOP	GO_CYTOPLASMIC_S	72	-0.4322	-1.3653	0.1426	0.396715	1	9901	tags=36%, list=1
GO_CALCIU	GO_CALCIUM_ION_II	21	-0.4245	-1.2822	0.1429	0.42299	1	14054	tags=48%, list=2
GO_ANTIP(	GO_ANTIPORTER_AC	82	-0.3319	-1.2486	0.1429	0.429947	1	15374	tags=37%, list=2
GO_REGUL	GO_REGULATION_OI	30	-0.3871	-1.2775	0.1431	0.426143	1	12398	tags=37%, list=2
GO_REGUL	GO_REGULATORY_R	41	-0.4447	-1.3139	0.1434	0.407158	1	9576	tags=39%, list=1
GO_RESPOI	GO_RESPONSE_TO_M	22	-0.4384	-1.3269	0.1434	0.410153	1	9901	tags=41%, list=1

GO_NEGAT	GO_NEGATIVE_REGU	104	-0.3184	-1.2597	0.1437	0.424473	1	7285	tags=24%, list=1
GO_GLUCO	GO_GLUCOSE_IMPOI	71	-0.3566	-1.2645	0.1449	0.425341	1	15413	tags=42%, list=2
GO_MEIOTI	GO_MEIOTIC_CHROM	22	-0.5009	-1.3623	0.145	0.396095	1	15158	tags=50%, list=2
GO_FATTY_	GO_FATTY_ACYL_CC	29	-0.4157	-1.3307	0.1454	0.409437	1	12285	tags=41%, list=2
GO_CELLU	GO_CELLULAR_COM	57	-0.3488	-1.2577	0.146	0.424712	1	11439	tags=37%, list=2
GO_CALYX	GO_CALYX_OF_HELI	23	-0.4921	-1.3239	0.1466	0.410822	1	18541	tags=61%, list=3
GO_NEURO	GO_NEUROMUSCULA	104	-0.3763	-1.2745	0.1468	0.424981	1	16273	tags=49%, list=2
GO_REGUL	GO_REGULATION_OI	486	-0.311	-1.2722	0.147	0.423833	1	12556	tags=35%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	25	-0.4201	-1.2941	0.1473	0.41787	1	18576	tags=48%, list=3
GO_TRNA_	GO_TRNA_TRANSPOI	35	-0.5759	-1.4468	0.1477	0.380407	1	9700	tags=46%, list=1
GO_HIGH_I	GO_HIGH_DENSITY_	16	-0.4819	-1.3312	0.1479	0.409223	1	6746	tags=31%, list=1
GO_EXTRA	GO_EXTRACELLULA	74	-0.3847	-1.2666	0.1482	0.426942	1	15363	tags=50%, list=2
GO_POSITI	GO_POSITIVE_REGUI	22	-0.4558	-1.33	0.1486	0.408806	1	4305	tags=32%, list=7
GO_REGUL	GO_REGULATION_OI	99	-0.3396	-1.2603	0.1491	0.424611	1	8907	tags=30%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	33	-0.3793	-1.2655	0.1492	0.425547	1	9340	tags=30%, list=1
GO_FEMAL	GO_FEMALE_SEX_DI	119	-0.3061	-1.2193	0.15	0.44108	1	13841	tags=38%, list=2
GO_CALMC	GO_CALMODULIN_B	199	-0.3233	-1.2733	0.1504	0.425512	1	10444	tags=32%, list=1
GO_DETEC	GO_DETECTION_OF_	43	-0.3949	-1.2437	0.1505	0.432177	1	10920	tags=33%, list=1
GO_POTAS	GO_POTASSIUM_ION	18	-0.4579	-1.3027	0.1509	0.4156	1	20717	tags=67%, list=3
GO_POSITI	GO_POSITIVE_REGUI	16	-0.486	-1.3366	0.1511	0.407666	1	8997	tags=50%, list=1
GO_TELEN	GO_TELENCEPHALO	22	-0.4477	-1.3156	0.1511	0.409221	1	17193	tags=55%, list=2
GO_REGUL	GO_REGULATION_OI	40	-0.4052	-1.3119	0.1512	0.407587	1	20444	tags=52%, list=3
GO_NEURO	GO_NEUROMUSCULA	23	-0.4571	-1.2929	0.1512	0.417935	1	12506	tags=52%, list=2
GO_DENDR	GO_DENDRITE_SELF	16	-0.4878	-1.2965	0.1513	0.417525	1	12923	tags=38%, list=2
GO_GAP_JU	GO_GAP_JUNCTION	31	-0.3814	-1.2643	0.1517	0.42442	1	6854	tags=29%, list=1
GO_STRIAT	GO_STRIATED_MUSC	21	-0.4754	-1.3395	0.1519	0.407485	1	6864	tags=29%, list=1
GO_FORMA	GO_FORMATION_OF_	124	-0.3621	-1.3416	0.1522	0.407635	1	10951	tags=37%, list=1
GO_PROTO	GO_PROTON_TRANS	137	-0.3029	-1.2388	0.1523	0.433434	1	10114	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	183	-0.3057	-1.242	0.1527	0.432371	1	8823	tags=30%, list=1
GO_C_ACY	GO_C_ACYLTRANSFI	20	-0.4666	-1.2913	0.1529	0.418216	1	12175	tags=40%, list=2
GO_NEPHR	GO_NEPHRON_TUBU	18	-0.4363	-1.286	0.1529	0.419016	1	5439	tags=28%, list=9
GO_PLASM	GO_PLASMA_MEMBI	200	-0.3551	-1.309	0.1532	0.410632	1	17119	tags=43%, list=2
GO_VOLTA	GO_VOLTAGE_GATE	23	-0.4771	-1.306	0.1534	0.413662	1	20619	tags=65%, list=3
GO_POSITI	GO_POSITIVE_REGUI	26	-0.4338	-1.3156	0.1534	0.408832	1	15233	tags=58%, list=2
GO_BITTER	GO_BITTER_TASTE_I	20	-0.5866	-1.3844	0.1535	0.391879	1	13202	tags=60%, list=2
GO_WALKI	GO_WALKING_BEHA	29	-0.4573	-1.3132	0.1538	0.407191	1	18325	tags=59%, list=3
GO_MUSCL	GO_MUSCLE_FILAMI	39	-0.4313	-1.3025	0.154	0.415448	1	11765	tags=38%, list=2
GO_REGUL	GO_REGULATION_OI	15	-0.5176	-1.3445	0.1543	0.406987	1	4573	tags=27%, list=8
GO_REGUL	GO_REGULATION_OI	117	-0.3868	-1.3373	0.1543	0.407331	1	10263	tags=35%, list=1
GO_SYNAP	GO_SYNAPTIC_CLEF	16	-0.4914	-1.3437	0.1545	0.407327	1	7648	tags=38%, list=1
GO_REGUL	GO_REGULATION_OI	58	-0.3699	-1.267	0.1549	0.427017	1	15413	tags=43%, list=2
GO_TROPH	GO_TROPHOBLAST_(	16	-0.4336	-1.2848	0.155	0.419914	1	9127	tags=38%, list=1
GO_CELLU	GO_CELLULAR_RESI	140	-0.2998	-1.2232	0.1551	0.442876	1	11903	tags=31%, list=2
GO_AXONE	GO_AXONEMAL_DYI	29	-0.4727	-1.3518	0.1552	0.403739	1	11864	tags=48%, list=2
GO_ESTABI	GO_ESTABLISHMENT	21	-0.405	-1.2728	0.1552	0.424137	1	13615	tags=43%, list=2
GO_REGUL	GO_REGULATION_OI	78	-0.3961	-1.2736	0.1553	0.425743	1	15315	tags=49%, list=2
GO_MODIF	GO_MODIFIED_AMIN	27	-0.4063	-1.2736	0.1555	0.425308	1	7781	tags=30%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	232	-0.3032	-1.2328	0.1556	0.435113	1	7482	tags=22%, list=1
GO_POSITI	GO_POSITIVE_REGUI	111	-0.3437	-1.2927	0.1558	0.417754	1	11210	tags=32%, list=1
GO_VOLTA	GO_VOLTAGE_GATE	17	-0.4922	-1.3314	0.1561	0.40989	1	2399	tags=18%, list=4
GO_ANION_	GO_ANION_TRANSM	353	-0.2761	-1.2024	0.1561	0.449371	1	15498	tags=35%, list=2
GO_EXTRA	GO_EXTRACELLULA	22	-0.533	-1.3736	0.1562	0.397108	1	13904	tags=55%, list=2
GO_HEPAR	GO_HEPARIN_BINDII	158	-0.3715	-1.3147	0.1563	0.408535	1	8308	tags=30%, list=1
GO_GLYCO	GO_GLYCOGEN_BIOS	45	-0.3567	-1.2297	0.1563	0.437911	1	20825	tags=58%, list=3
GO_REGUL	GO_REGULATION_OI	100	-0.3578	-1.2728	0.1564	0.424447	1	10943	tags=37%, list=1
GO_NEURO	GO_NEURONAL_ACT	34	-0.4227	-1.2642	0.1564	0.424218	1	11031	tags=41%, list=1
GO_MALE_	GO_MALE_GENITALI	23	-0.4358	-1.2912	0.1566	0.417391	1	11652	tags=39%, list=2
GO_REPRO	GO_REPRODUCTIVE_	443	-0.2735	-1.2123	0.1567	0.445521	1	11903	tags=31%, list=2

GO_ESTABL	GO_ESTABLISHMENT	137	-0.3467	-1.2969	0.1568	0.418229		1	12361	tags=35%, list=2
GO_REGUL	GO_REGULATION_OF	52	-0.3715	-1.2407	0.1569	0.43257		1	15864	tags=40%, list=2
GO_STRIAT	GO_STRIATED_MUSC	283	-0.3096	-1.245	0.157	0.433055		1	11823	tags=33%, list=2
GO_STRIAT	GO_STRIATED_MUSC	171	-0.3276	-1.2663	0.1575	0.426965		1	11874	tags=33%, list=2
GO_REGUL	GO_REGULATION_OF	80	-0.3846	-1.3336	0.1576	0.407632		1	7793	tags=30%, list=1
GO_INHIBIT	GO_INHIBITORY_POS	16	-0.5428	-1.3211	0.1578	0.409512		1	18875	tags=63%, list=3
GO_GLOME	GO_GLOMERULAR_E	20	-0.4524	-1.2857	0.1579	0.419257		1	26429	tags=65%, list=4
GO_DETECT	GO_DETECTION_OF_	62	-0.3298	-1.2202	0.1582	0.44221		1	18221	tags=42%, list=3
GO_REGUL	GO_REGULATION_OF	23	-0.3975	-1.2627	0.1582	0.424031		1	20059	tags=61%, list=3
GO_REGUL	GO_REGULATION_OF	34	-0.4592	-1.3148	0.1587	0.408773		1	9243	tags=41%, list=1
GO_TUBUL	GO_TUBULIN_BINDI	348	-0.3539	-1.2981	0.1587	0.418275		1	14612	tags=39%, list=2
GO_ACTIVA	GO_ACTIVATION_OF	18	-0.4756	-1.3406	0.1588	0.407904		1	17430	tags=56%, list=3
GO_SARCO	GO_SARCOPLASM	77	-0.3755	-1.3143	0.1588	0.408356		1	14545	tags=43%, list=2
GO_CARDIA	GO_CARDIAC_MUSC	135	-0.3326	-1.2466	0.1592	0.432427		1	10232	tags=31%, list=1
GO_REGUL	GO_REGULATION_OF	47	-0.3671	-1.2494	0.1594	0.429404		1	12168	tags=43%, list=2
GO_SYNAPT	GO_SYNAPTIC_TRAN	30	-0.3908	-1.2574	0.1596	0.423383		1	8287	tags=30%, list=1
GO_REGUL	GO_REGULATION_OF	167	-0.3185	-1.2599	0.1596	0.424998		1	9577	tags=27%, list=1
GO_CELL_F	GO_CELL_FATE_DET	42	-0.3963	-1.2608	0.1602	0.424227		1	7885	tags=33%, list=1
GO_MUSCL	GO_MUSCLE_HYPER	106	-0.3394	-1.2566	0.1603	0.424316		1	12950	tags=34%, list=2
GO_PROTEI	GO_PROTEIN_MEMB	20	-0.4111	-1.2513	0.1608	0.428799		1	13008	tags=45%, list=2
GO_TRANS	GO_TRANSFORMING	23	-0.5143	-1.3463	0.1608	0.407734		1	17271	tags=52%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	101	-0.3031	-1.2227	0.161	0.442146		1	11087	tags=28%, list=1
GO_MICRO	GO_MICROTUBULE_	20	-0.5337	-1.3602	0.1612	0.396851		1	6486	tags=30%, list=1
GO_POSITI	GO_POSITIVE_REGU	50	-0.4206	-1.333	0.1615	0.407153		1	12664	tags=44%, list=2
GO_TRIGLY	GO_TRIGLYCERIDE_	38	-0.3848	-1.2445	0.1619	0.432636		1	5875	tags=24%, list=1
GO_DNA_P	GO_DNA_PACKAGIN	23	-0.5168	-1.3769	0.1619	0.395179		1	13109	tags=43%, list=2
GO_MUSCL	GO_MUSCLE_CONTR	353	-0.353	-1.3131	0.1619	0.406873		1	11874	tags=37%, list=2
GO_LIMBIC	GO_LIMBIC_SYSTEM	108	-0.3442	-1.2449	0.1622	0.432781		1	15403	tags=37%, list=2
GO_PHENO	GO_PHENOTYPIC_SW	15	-0.5291	-1.3044	0.1624	0.414697		1	13862	tags=47%, list=2
GO_REGUL	GO_REGULATION_OF	72	-0.3714	-1.3013	0.1625	0.415805		1	9654	tags=32%, list=1
GO_NEURO	GO_NEUROTRANSMI	31	-0.4028	-1.2613	0.1626	0.423732		1	18325	tags=48%, list=3
GO_ACIDIC	GO_ACIDIC_AMINO_	70	-0.3512	-1.2463	0.1626	0.432242		1	16390	tags=46%, list=2
GO_STEROI	GO_STEROID_HORM	78	-0.3457	-1.2662	0.1627	0.426288		1	8314	tags=33%, list=1
GO_COPII_	GO_COPII_COATED_	15	-0.5549	-1.3615	0.1632	0.396052		1	15233	tags=60%, list=2
GO_CELL_F	GO_CELL_PROJECTIO	335	-0.2865	-1.2123	0.1632	0.445856		1	13067	tags=34%, list=2
GO_GLYCO	GO_GLYCOPROTEIN_	19	-0.5129	-1.3655	0.1633	0.398655		1	5834	tags=42%, list=1
GO_ORGAN	GO_ORGANIC_HYDR	256	-0.2854	-1.2106	0.1633	0.446338		1	7361	tags=20%, list=1
GO_VESICL	GO_VESICLE_MEDIA	217	-0.3747	-1.3241	0.1636	0.411876		1	9535	tags=34%, list=1
GO_CORTIC	GO_CORTICAL_ACTI	79	-0.3342	-1.2408	0.1638	0.432761		1	11765	tags=32%, list=2
GO_ASSOC	GO_ASSOCIATIVE_LI	75	-0.365	-1.2671	0.1638	0.427218		1	11028	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGU	21	-0.4202	-1.2618	0.164	0.42433		1	5439	tags=29%, list=9
GO_RESPO	GO_RESPONSE_TO_V	19	-0.4431	-1.2576	0.1641	0.424106		1	14804	tags=58%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	49	-0.3452	-1.2501	0.1641	0.429798		1	6476	tags=24%, list=1
GO_AMINE_	GO_AMINE_TRANSPO	96	-0.3614	-1.2485	0.1643	0.42983		1	19324	tags=49%, list=3
GO_EYE_M	GO_EYE_MORPHOGE	154	-0.3105	-1.2367	0.1644	0.43346		1	14688	tags=41%, list=2
GO_PASSIV	GO_PASSIVE_TRANS	457	-0.2992	-1.204	0.1646	0.448836		1	15397	tags=38%, list=2
GO_BASIC_	GO_BASIC_AMINO_A	17	-0.4617	-1.2946	0.165	0.419189		1	6516	tags=24%, list=1
GO_CYTOP	GO_CYTOPLASMIC_	243	-0.3412	-1.2866	0.165	0.418822		1	9173	tags=28%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	154	-0.3175	-1.2621	0.1651	0.424276		1	12756	tags=34%, list=2
GO_REGUL	GO_REGULATION_OF	217	-0.303	-1.249	0.1651	0.429764		1	6486	tags=24%, list=1
GO_DOPAM	GO_DOPAMINE_REC	17	-0.4557	-1.2947	0.1657	0.41964		1	12151	tags=41%, list=2
GO_POSITI	GO_POSITIVE_REGU	171	-0.3191	-1.2631	0.1657	0.424039		1	10045	tags=33%, list=1
GO_PRESY	GO_PRESYNAPTIC_E	62	-0.3627	-1.2647	0.1657	0.425694		1	7560	tags=32%, list=1
GO_COGNI	GO_COGNITION	293	-0.3091	-1.2298	0.1657	0.438066		1	9854	tags=32%, list=1
GO_REGUL	GO_REGULATION_OF	88	-0.3322	-1.2418	0.166	0.432023		1	11099	tags=33%, list=1
GO_PRESY	GO_PRESYNAPTIC_M	154	-0.3787	-1.297	0.1667	0.418383		1	12388	tags=42%, list=2
GO_REGUL	GO_REGULATION_OF	38	-0.4087	-1.2751	0.1667	0.424828		1	20619	tags=58%, list=3
GO_VASCU	GO_VASCULAR_PRO	189	-0.3299	-1.2399	0.1667	0.432476		1	11664	tags=34%, list=2

GO_HORM	GO_HORMONE_TRA	315	-0.2813	-1.1972	0.1667	0.451869	1	12664	tags=32%, list=2
GO_GLUTA	GO_GLUTAMINE_FA	71	-0.3351	-1.2255	0.167	0.439715	1	14421	tags=38%, list=2
GO_CELLU	GO_CELLULAR_RES	81	-0.3448	-1.2378	0.167	0.433082	1	10943	tags=30%, list=1
GO_SYNAP	GO_SYNAPTIC_MEM	28	-0.4526	-1.316	0.1673	0.409002	1	11122	tags=43%, list=1
GO_ENDOT	GO_ENDOTHELIUM_	132	-0.3764	-1.3366	0.1674	0.407193	1	9208	tags=35%, list=1
GO_OOCYT	GO_OOCYTE_DIFFER	48	-0.3503	-1.2268	0.1676	0.439307	1	8476	tags=27%, list=1
GO_RETRO	GO_RETROGRADE_A	20	-0.5001	-1.3097	0.1676	0.410238	1	4046	tags=30%, list=7
GO_INTRA	GO_INTRACELLULA	54	-0.3878	-1.2941	0.1677	0.417503	1	9654	tags=31%, list=1
GO_SMOOT	GO_SMOOTH_ENDO	34	-0.3739	-1.2382	0.1677	0.433254	1	8265	tags=26%, list=1
GO_TYPE_	GO_TYPE_B_PANCR	20	-0.4625	-1.3007	0.1677	0.415545	1	10943	tags=45%, list=1
GO_CELL_	GO_CELL_DIFFEREN	26	-0.4514	-1.2921	0.1677	0.418399	1	9318	tags=46%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.4808	-1.3452	0.168	0.40725	1	2766	tags=28%, list=5
GO_MUSCL	GO_MUSCLE_CELL_	177	-0.3338	-1.2542	0.168	0.425865	1	11808	tags=32%, list=2
GO_MYOSI	GO_MYOSIN_FILAM	22	-0.4778	-1.3016	0.1683	0.415868	1	12387	tags=41%, list=2
GO_MICRO	GO_MICROTUBULE_	185	-0.353	-1.2892	0.1686	0.417579	1	15533	tags=42%, list=2
GO_REGUL	GO_REGULATION_O	41	-0.4049	-1.2764	0.1687	0.425061	1	14070	tags=44%, list=2
GO_MICRO	GO_MICROTUBULE_	74	-0.3816	-1.3038	0.1696	0.414973	1	6486	tags=27%, list=1
GO_AMINO	GO_AMINOGLYCAN_	66	-0.3715	-1.2799	0.1696	0.425118	1	13771	tags=45%, list=2
GO_ACTIVI	GO_ACTIVIN_RECEP	44	-0.3669	-1.2579	0.1697	0.425326	1	14016	tags=36%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.4759	-1.2913	0.1702	0.417758	1	3653	tags=27%, list=6
GO_CATIO	GO_CATION_CHLOR	17	-0.4364	-1.2419	0.1703	0.432223	1	17190	tags=59%, list=2
GO_AMPA_	GO_AMPA_GLUTAM	26	-0.4982	-1.2978	0.1704	0.417966	1	13473	tags=50%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	16	-0.543	-1.3193	0.1711	0.407009	1	10347	tags=38%, list=1
GO_INSULI	GO_INSULIN_RECEP	23	-0.4308	-1.2699	0.1711	0.426761	1	12950	tags=43%, list=2
GO_PRESY	GO_PRESYNAPTIC_A	74	-0.4289	-1.3285	0.1712	0.409534	1	11596	tags=45%, list=2
GO_REGUL	GO_REGULATION_O	44	-0.3721	-1.2624	0.1713	0.424036	1	11227	tags=39%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	27	-0.4425	-1.291	0.1714	0.416964	1	17571	tags=52%, list=3
GO_FOCAL	GO_FOCAL_ADHESI	83	-0.3844	-1.3246	0.1715	0.412089	1	8218	tags=33%, list=1
GO_ALDEH	GO_ALDEHYDE_BIO	15	-0.4395	-1.2794	0.1715	0.425543	1	14980	tags=47%, list=2
GO_AMINO	GO_AMINO_ACID_S	15	-0.4723	-1.2985	0.1715	0.417962	1	15413	tags=53%, list=2
GO_EUKAR	GO_EUKARYOTIC_T	17	-0.556	-1.3641	0.1719	0.397311	1	4823	tags=29%, list=8
GO_EXTRA	GO_EXTRACELLULA	166	-0.4452	-1.3675	0.1721	0.397269	1	14616	tags=49%, list=2
GO_INSULI	GO_INSULIN_SECRE	62	-0.3135	-1.2092	0.1722	0.446746	1	9702	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	21	-0.4984	-1.3049	0.1723	0.414245	1	13862	tags=33%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	28	-0.432	-1.2761	0.1726	0.425066	1	6062	tags=25%, list=1
GO_MIRNA	GO_MIRNA_BINDIN	29	-0.4914	-1.3334	0.173	0.406924	1	9370	tags=41%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	37	-0.42	-1.2868	0.173	0.419461	1	12274	tags=43%, list=2
GO_CARBO	GO_CARBON_CARB	49	-0.375	-1.2575	0.1733	0.424007	1	10225	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	27	-0.4011	-1.2654	0.1736	0.42535	1	12664	tags=37%, list=2
GO_OOGE	GO_OOGENESIS	82	-0.3191	-1.2185	0.1736	0.440635	1	8726	tags=24%, list=1
GO_TIGHT_	GO_TIGHT_JUNCTIO	125	-0.3336	-1.2759	0.1743	0.424995	1	5649	tags=23%, list=1
GO_CYCLI	GO_CYCLIC_NUCLE	36	-0.3733	-1.2386	0.1744	0.432894	1	20068	tags=53%, list=3
GO_ODONT	GO_ODONTOGENESI	129	-0.3349	-1.2671	0.1751	0.428026	1	8585	tags=31%, list=1
GO_REGUL	GO_REGULATION_O	35	-0.3918	-1.231	0.1751	0.437538	1	17921	tags=51%, list=3
GO_RENAL	GO_RENAL_SYSTEM_	123	-0.3214	-1.2273	0.1753	0.43997	1	11922	tags=32%, list=2
GO_RESPO	GO_RESPONSE_TO_A	69	-0.3276	-1.2159	0.1753	0.442415	1	10013	tags=32%, list=1
GO_LENS_	GO_LENS_MORPHOG	20	-0.4322	-1.2662	0.1758	0.426669	1	8997	tags=40%, list=1
GO_MONO	GO_MONOAMINE_T	82	-0.3658	-1.2438	0.1759	0.43278	1	11361	tags=35%, list=1
GO_MRNA_	GO_MRNA_SPLICE_S	48	-0.452	-1.2939	0.1765	0.416927	1	12984	tags=46%, list=2
GO_MEGA	GO_MEGAKARYOCY	16	-0.4724	-1.2765	0.1765	0.425273	1	8217	tags=38%, list=1
GO_MESEN	GO_MESENCHYMAL_	20	-0.4427	-1.2812	0.1767	0.424079	1	5634	tags=40%, list=1
GO_PHOTO	GO_PHOTORECEPTO	111	-0.3242	-1.2295	0.1777	0.437164	1	19648	tags=45%, list=3
GO_2_OXO	GO_2_OXOGLUTARA	43	-0.3808	-1.2656	0.1779	0.425837	1	12094	tags=35%, list=2
GO_REGUL	GO_REGULATION_O	124	-0.3228	-1.2408	0.1783	0.43306	1	12950	tags=38%, list=2
GO_CATEC	GO_CATECHOLAMIN	21	-0.4149	-1.2337	0.1786	0.436224	1	5221	tags=24%, list=9
GO_MODIF	GO_MODIFIED_AMIN	20	-0.4426	-1.2874	0.1788	0.419141	1	7781	tags=35%, list=1
GO_DORSA	GO_DORSAL_SPINAL	22	-0.4983	-1.2645	0.1789	0.425658	1	19979	tags=64%, list=3
GO_RESOL	GO_RESOLUTION_O	15	-0.4976	-1.2977	0.1789	0.417568	1	15158	tags=47%, list=2

GO_REGUL	GO_REGULATION_OI	131	-0.2979	-1.2091	0.1789	0.446589	1	11233	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	36	-0.4043	-1.277	0.1796	0.425526	1	9654	tags=36%, list=1
GO_REGUL	GO_REGULATION_OI	478	-0.2902	-1.1844	0.18	0.458083	1	15397	tags=40%, list=2
GO_AXON_	GO_AXON_CYTOPLA	57	-0.3807	-1.2754	0.1802	0.425173	1	4046	tags=23%, list=7
GO_IMPOR	GO_IMPORT_ACROSS	156	-0.3044	-1.2021	0.1807	0.448878	1	15498	tags=37%, list=2
GO_ION_CI	GO_ION_CHANNEL_I	115	-0.3227	-1.212	0.1807	0.445571	1	6828	tags=24%, list=1
GO_SYNAP	GO_SYNAPTIC_VESI	74	-0.3548	-1.2587	0.181	0.425389	1	9535	tags=34%, list=1
GO_POLY_	GO_POLY_A_BINDIN	23	-0.4698	-1.2978	0.1811	0.418367	1	10103	tags=30%, list=1
GO_MAGNI	GO_MAGNESIUM_IOI	16	-0.4921	-1.3013	0.1814	0.415529	1	8736	tags=44%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	74	-0.3567	-1.2675	0.1815	0.428752	1	7971	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	338	-0.2955	-1.1934	0.1816	0.452642	1	12141	tags=35%, list=2
GO_MITOC	GO_MITOCHONDRIO	16	-0.455	-1.2712	0.1818	0.425275	1	18814	tags=56%, list=3
GO_CONNE	GO_CONNECTIVE_TI	20	-0.4527	-1.2671	0.1818	0.42763	1	9470	tags=35%, list=1
GO_CELLU	GO_CELLULAR_GLU	70	-0.3262	-1.2227	0.1818	0.442502	1	15406	tags=43%, list=2
GO_POSITI	GO_POSITIVE_REGUI	49	-0.4221	-1.2911	0.182	0.417158	1	7830	tags=39%, list=1
GO_SENSO	GO_SENSORY_PERCI	217	-0.2874	-1.1811	0.182	0.460516	1	18301	tags=39%, list=3
GO_SODIU	GO_SODIUM_CHANN	44	-0.3889	-1.2445	0.1822	0.432274	1	11031	tags=34%, list=1
GO_ACROS	GO_ACROSOME_ASS	15	-0.4518	-1.2696	0.1825	0.426975	1	13249	tags=33%, list=2
GO_RESPO	GO_RESPONSE_TO_R	107	-0.2993	-1.1929	0.1828	0.452711	1	4739	tags=20%, list=8
GO_CEREB	GO_CEREBRAL_COR	112	-0.3472	-1.2463	0.183	0.432626	1	15403	tags=39%, list=2
GO_PITUIT	GO_PITUITARY_GLA	42	-0.3715	-1.2066	0.1834	0.446669	1	19979	tags=60%, list=3
GO_POSITI	GO_POSITIVE_REGUI	28	-0.3945	-1.2634	0.1839	0.423943	1	6716	tags=29%, list=1
GO_MICRO	GO_MICROTUBULE_	252	-0.3553	-1.2779	0.184	0.426179	1	14612	tags=39%, list=2
GO_SYNAP	GO_SYNAPTONEMAI	40	-0.4121	-1.2639	0.1842	0.42383	1	17563	tags=48%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	30	-0.3757	-1.2218	0.1847	0.441899	1	19088	tags=53%, list=3
GO_RESPO	GO_RESPONSE_TO_A	234	-0.2776	-1.179	0.1848	0.46108	1	10151	tags=26%, list=1
GO_ANION	GO_ANION_CATION_	22	-0.4214	-1.24	0.185	0.43297	1	17190	tags=59%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	31	-0.376	-1.2313	0.185	0.437412	1	13442	tags=35%, list=2
GO_MATER	GO_MATERNAL_PLA	36	-0.3408	-1.189	0.1858	0.455519	1	12819	tags=39%, list=2
GO_SWI_SN	GO_SWI_SNF_COMPI	17	-0.5231	-1.3169	0.1859	0.408747	1	13852	tags=59%, list=2
GO_DNA_M	GO_DNA_METHYLAT	70	-0.3899	-1.2673	0.1859	0.428673	1	16537	tags=37%, list=2
GO_BONE_	GO_BONE_DEVELOP	195	-0.3367	-1.255	0.186	0.425652	1	16573	tags=43%, list=2
GO_REGUL	GO_REGULATION_OI	18	-0.4561	-1.264	0.186	0.424152	1	18362	tags=44%, list=3
GO_MYOFI	GO_MYOFILAMENT	25	-0.4502	-1.2988	0.1862	0.41788	1	6864	tags=28%, list=1
GO_TRANS	GO_TRANSCYTOSIS	20	-0.4156	-1.2443	0.1864	0.432198	1	3754	tags=35%, list=6
GO_COENZ	GO_COENZYME_A_M	15	-0.4898	-1.323	0.1869	0.40984	1	643	tags=20%, list=1
GO_CYTOS	GO_CYTOSKELETON	196	-0.3504	-1.2723	0.187	0.424164	1	8418	tags=29%, list=1
GO_GLUTA	GO_GLUTAMATE_RE	101	-0.3926	-1.2381	0.1872	0.433073	1	13257	tags=46%, list=2
GO_ENTER	GO_ENTEROENDOCR	27	-0.4399	-1.2807	0.1878	0.424439	1	11638	tags=44%, list=2
GO_POSITI	GO_POSITIVE_REGUI	72	-0.3326	-1.2205	0.1878	0.442287	1	9470	tags=31%, list=1
GO_MAMM	GO_MAMMARY_GLA	140	-0.2837	-1.2038	0.1879	0.448668	1	6873	tags=24%, list=1
GO_TRANS	GO_TRANSLATION_F	16	-0.5156	-1.314	0.1886	0.40752	1	5527	tags=31%, list=9
GO_NEGAT	GO_NEGATIVE_REGU	60	-0.329	-1.2011	0.1887	0.448543	1	12950	tags=33%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	17	-0.4526	-1.2636	0.189	0.424007	1	11765	tags=35%, list=2
GO_CELLU	GO_CELLULAR_RESI	57	-0.3392	-1.2195	0.1891	0.440979	1	11248	tags=32%, list=1
GO_POSTS	GO_POSTSYNAPTIC_	15	-0.4468	-1.2437	0.1899	0.432511	1	8907	tags=40%, list=1
GO_REGUL	GO_REGULATION_OI	78	-0.4225	-1.3205	0.1902	0.409632	1	9389	tags=36%, list=1
GO_REGUL	GO_REGULATION_OI	64	-0.387	-1.2645	0.1902	0.424946	1	10614	tags=41%, list=1
GO_BICARI	GO_BICARBONATE_T	21	-0.4359	-1.2295	0.1902	0.437446	1	2930	tags=19%, list=5
GO_NEGAT	GO_NEGATIVE_REGU	51	-0.3361	-1.2104	0.1908	0.446373	1	12398	tags=37%, list=2
GO_ORGAN	GO_ORGANELLE_TR	82	-0.3754	-1.2686	0.191	0.427457	1	13484	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	33	-0.412	-1.2656	0.1911	0.426097	1	14514	tags=42%, list=2
GO_POSITI	GO_POSITIVE_REGUI	25	-0.3972	-1.2432	0.1912	0.432745	1	11248	tags=40%, list=1
GO_REGUL	GO_REGULATION_OI	81	-0.3359	-1.2214	0.1918	0.441794	1	12556	tags=35%, list=2
GO_CORTI	GO_CORTICAL_CYTO	105	-0.3252	-1.2272	0.1919	0.439716	1	11099	tags=30%, list=1
GO_KINESI	GO_KINESIN_COMPL	50	-0.4383	-1.3122	0.1923	0.407613	1	14495	tags=46%, list=2
GO_CELL_I	GO_CELL_FATE_COM	274	-0.3029	-1.207	0.1923	0.446284	1	15429	tags=43%, list=2
GO_MUSCL	GO_MUSCLE_ADAPT	123	-0.3048	-1.1834	0.193	0.458166	1	11495	tags=32%, list=2

GO_CYTOS	GO_CYTOSKELETAL_	22	-0.4364	-1.2504	0.1932	0.430001	1	13008	tags=45%, list=2
GO_CELL_(	GO_CELL_COMMUNI	31	-0.423	-1.2644	0.1932	0.424704	1	15184	tags=42%, list=2
GO_GLOMI	GO_GLOMERULAR_E	23	-0.4287	-1.2367	0.1933	0.43316	1	11652	tags=30%, list=2
GO_POSITI	GO_POSITIVE_REGUI	17	-0.4342	-1.2421	0.1936	0.433074	1	18926	tags=59%, list=3
GO_POSITI	GO_POSITIVE_REGUI	63	-0.3436	-1.222	0.1937	0.442705	1	10299	tags=33%, list=1
GO_REGUL	GO_REGULATION_OI	46	-0.342	-1.2177	0.1937	0.441613	1	5697	tags=28%, list=1
GO_REGUL	GO_REGULATION_OI	15	-0.4955	-1.2782	0.1938	0.426013	1	9127	tags=40%, list=1
GO_POSITI	GO_POSITIVE_REGUI	32	-0.4536	-1.2589	0.194	0.425436	1	6290	tags=31%, list=1
GO_LUNG_	GO_LUNG_CELL_DIF	23	-0.4087	-1.2238	0.194	0.442124	1	3835	tags=22%, list=7
GO_POSITI	GO_POSITIVE_REGUI	38	-0.3687	-1.2202	0.194	0.441844	1	10299	tags=47%, list=1
GO_N_MET	GO_N_METHYLTRAN	84	-0.3864	-1.2817	0.1946	0.423502	1	12102	tags=35%, list=2
GO_POSITI	GO_POSITIVE_REGUI	41	-0.4224	-1.2768	0.1953	0.4255	1	7690	tags=37%, list=1
GO_CHEMC	GO_CHEMOREPELLE	28	-0.3664	-1.2276	0.1954	0.439816	1	3046	tags=25%, list=5
GO_CYTOS	GO_CYTOSOLIC_TRA	153	-0.3452	-1.2767	0.1956	0.425219	1	6767	tags=27%, list=1
GO_SIGNAI	GO_SIGNAL_TRANSD	19	-0.4425	-1.2263	0.1957	0.439925	1	15534	tags=58%, list=2
GO_ANION	GO_ANION_CHANNE	86	-0.321	-1.2013	0.196	0.448771	1	12825	tags=38%, list=2
GO_RENAL	GO_RENAL_SODIUM_	23	-0.4319	-1.2203	0.1962	0.442338	1	3514	tags=22%, list=6
GO_NEURC	GO_NEUROTRANSMI	171	-0.3634	-1.2774	0.1964	0.425829	1	11615	tags=38%, list=2
GO_REGUL	GO_REGULATION_OI	100	-0.3026	-1.1942	0.1965	0.452414	1	13258	tags=30%, list=2
GO_SKELE	GO_SKELETAL_MUS(	41	-0.3468	-1.2081	0.1965	0.446111	1	11239	tags=37%, list=1
GO_DENTA	GO_DENTATE_GYRU	16	-0.491	-1.2516	0.1969	0.429406	1	15403	tags=56%, list=2
GO_PLACEI	GO_PLACENTA_DEV	155	-0.2841	-1.1865	0.1969	0.455792	1	10234	tags=30%, list=1
GO_PEPTID	GO_PEPTIDYL_THRE	122	-0.3409	-1.233	0.1969	0.435457	1	12361	tags=34%, list=2
GO_MUSCI	GO_MUSCLE_MYOSI	15	-0.544	-1.2931	0.1972	0.417932	1	7538	tags=40%, list=1
GO_EXTRA	GO_EXTRACELLULA	41	-0.5107	-1.3236	0.1972	0.410395	1	14539	tags=56%, list=2
GO_CYCLI(	GO_CYCLIC_NUCLE(	199	-0.3232	-1.2231	0.1972	0.442583	1	20038	tags=55%, list=3
GO_PHOTO	GO_PHOTORECEPTO	23	-0.3881	-1.1785	0.1973	0.460115	1	14353	tags=35%, list=2
GO_ATP_DI	GO_ATP_DEPENDEN	16	-0.5715	-1.3477	0.1977	0.406608	1	24050	tags=94%, list=4
GO_POSITI	GO_POSITIVE_REGUI	18	-0.4492	-1.2392	0.1977	0.432898	1	10263	tags=33%, list=1
GO_NEURC	GO_NEUROTRANSMI	22	-0.4226	-1.2426	0.1984	0.432934	1	24735	tags=77%, list=4
GO_MUSCI	GO_MUSCLE_SYSTEI	456	-0.3245	-1.2549	0.1984	0.425372	1	11874	tags=35%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	29	-0.432	-1.2802	0.1984	0.424909	1	19665	tags=55%, list=3
GO_NUCLE	GO_NUCLEAR_RECE	98	-0.3299	-1.2446	0.1985	0.432818	1	8314	tags=32%, list=1
GO_ACTIN_	GO_ACTIN_MONOMI	25	-0.4076	-1.2428	0.1992	0.433007	1	4062	tags=32%, list=7
GO_PHOSPI	GO_PHOSPHORUS_O	19	-0.4391	-1.2336	0.1992	0.435585	1	19084	tags=63%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	43	-0.3403	-1.2015	0.1996	0.449143	1	15514	tags=44%, list=2
GO_REGUL	GO_REGULATION_OI	72	-0.3965	-1.2628	0.2	0.424251	1	13615	tags=39%, list=2
GO_CIS_GC	GO_CIS_GOLGI_NET	68	-0.3443	-1.2246	0.2	0.441126	1	12821	tags=31%, list=2
GO_POSITI	GO_POSITIVE_REGUI	127	-0.3075	-1.1992	0.2	0.450778	1	10045	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	39	-0.3735	-1.2371	0.2004	0.43359	1	13442	tags=36%, list=2
GO_DORSA	GO_DORSAL_VENTR	24	-0.4447	-1.2666	0.2004	0.427288	1	10490	tags=38%, list=1
GO_CARBC	GO_CARBOHYDRATI	16	-0.4589	-1.2617	0.2008	0.424208	1	19217	tags=69%, list=3
GO_METAN	GO_METANEPHRIC_I	40	-0.416	-1.2739	0.2008	0.425581	1	7640	tags=35%, list=1
GO_ACTOM	GO_ACTOMYOSIN_S	196	-0.3218	-1.2279	0.2012	0.439498	1	10120	tags=30%, list=1
GO_TRANS	GO_TRANSFORMING	24	-0.4034	-1.2336	0.2016	0.43595	1	4335	tags=25%, list=7
GO_EPHRIN	GO_EPHRIN_RECEPT	27	-0.3996	-1.2495	0.2024	0.429532	1	3198	tags=26%, list=5
GO_CAMEF	GO_CAMERA_TYPE_	123	-0.3033	-1.1873	0.2028	0.456128	1	14688	tags=38%, list=2
GO_LEADIN	GO_LEADING_EDGE_	169	-0.311	-1.2005	0.2036	0.449154	1	13067	tags=40%, list=2
GO_GLANE	GO_GLANDULAR_EP	25	-0.4197	-1.2387	0.2041	0.433204	1	6208	tags=32%, list=1
GO_NEURC	GO_NEURON_PROJE(	146	-0.3574	-1.2415	0.2044	0.43217	1	15388	tags=42%, list=2
GO_MYOFI	GO_MYOFIBRIL_ASS	66	-0.3943	-1.2552	0.2045	0.425634	1	10120	tags=35%, list=1
GO_REGUL	GO_REGULATION_OI	25	-0.4322	-1.258	0.2046	0.42584	1	11448	tags=44%, list=2
GO_AXONA	GO_AXONAL_TRANS	58	-0.375	-1.2574	0.2047	0.423747	1	4046	tags=22%, list=7
GO_ACTIVA	GO_ACTIVATION_OF	106	-0.3086	-1.2078	0.205	0.445871	1	7306	tags=25%, list=1
GO_MICRO	GO_MICROTUBULE_	157	-0.3546	-1.2753	0.2051	0.424798	1	14495	tags=39%, list=2
GO_CELLU	GO_CELLULAR_GLU(	148	-0.2853	-1.1736	0.2051	0.460382	1	11903	tags=30%, list=2
GO_REGUL	GO_REGULATION_OI	113	-0.2916	-1.1686	0.2053	0.462906	1	14094	tags=36%, list=2
GO_MICRO	GO_MICROTUBULE_I	33	-0.4413	-1.2616	0.2055	0.423953	1	8726	tags=30%, list=1

GO_GROWT	GO_GROWTH_FACTO	129	-0.3577	-1.2528	0.2056	0.428018	1	8236	tags=30%, list=1
GO_DEMET	GO_DEMETHYLASE_	36	-0.4327	-1.2334	0.2058	0.43506	1	13642	tags=47%, list=2
GO_RESPO	GO_RESPONSE_TO_S	35	-0.3705	-1.2268	0.2062	0.439597	1	3694	tags=23%, list=6
GO_TRANS	GO_TRANSPORT_AL	157	-0.353	-1.258	0.2063	0.425504	1	8418	tags=29%, list=1
GO_RESPO	GO_RESPONSE_TO_F	22	-0.3859	-1.2127	0.2064	0.445527	1	4301	tags=32%, list=7
GO_N_GLY	GO_N_GLYCAN_PRO	18	-0.4429	-1.2094	0.2066	0.446779	1	9966	tags=44%, list=1
GO_APICAI	GO_APICAL_JUNCTI	137	-0.3197	-1.2269	0.2068	0.439938	1	2948	tags=18%, list=5
GO_SARCO	GO_SARCOMERE_OR	44	-0.3792	-1.2217	0.207	0.441681	1	10120	tags=32%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	27	-0.4049	-1.2258	0.207	0.439664	1	18325	tags=52%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	16	-0.4587	-1.2309	0.2071	0.437375	1	7111	tags=38%, list=1
GO_RIBOSI	GO_RIBOSE_PHOSPH	389	-0.2733	-1.1771	0.2072	0.457942	1	9901	tags=26%, list=1
GO_WATEF	GO_WATER_HOMEO	79	-0.3168	-1.1797	0.2073	0.460488	1	15488	tags=38%, list=2
GO_POSITI	GO_POSITIVE_REGU	25	-0.367	-1.1985	0.2079	0.451355	1	10444	tags=32%, list=1
GO_REGUL	GO_REGULATION_OI	16	-0.4285	-1.2196	0.208	0.44127	1	8815	tags=50%, list=1
GO_NEURO	GO_NEUROPEPTIDE_	44	-0.3788	-1.1949	0.2084	0.453525	1	19614	tags=57%, list=3
GO_VASCU	GO_VASCULAR_ASS	25	-0.4505	-1.2459	0.2087	0.432543	1	11664	tags=48%, list=2
GO_PROTEI	GO_PROTEIN_MANN	20	-0.446	-1.2564	0.209	0.42441	1	22092	tags=65%, list=3
GO_REGUL	GO_REGULATION_OI	89	-0.3422	-1.1939	0.209	0.452585	1	10366	tags=40%, list=1
GO_INORG	GO_INORGANIC_ION	97	-0.3062	-1.1745	0.2093	0.459429	1	14248	tags=36%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	41	-0.3631	-1.213	0.2093	0.445732	1	2766	tags=20%, list=5
GO_RECEP	GO_RECEPTOR_LOC	55	-0.3997	-1.2546	0.2096	0.425675	1	7952	tags=33%, list=1
GO_REGUL	GO_REGULATION_OI	19	-0.4115	-1.222	0.2099	0.442365	1	6700	tags=26%, list=1
GO_XENOB	GO_XENOBIOTIC_TR	27	-0.3999	-1.2145	0.2102	0.443813	1	4349	tags=22%, list=7
GO_REGUL	GO_REGULATION_OI	18	-0.4674	-1.2525	0.2104	0.4283	1	3968	tags=22%, list=7
GO_UTERU	GO_UTERUS_DEVEL	21	-0.4184	-1.2085	0.2104	0.44644	1	13941	tags=38%, list=2
GO_NUCLE	GO_NUCLEOSOME_B	53	-0.4611	-1.3196	0.2108	0.407289	1	4301	tags=28%, list=7
GO_NEGAT	GO_NEGATIVE_REGU	20	-0.4224	-1.2374	0.2112	0.433434	1	6429	tags=30%, list=1
GO_REGUL	GO_REGULATION_OI	72	-0.3477	-1.1954	0.2113	0.452966	1	10366	tags=42%, list=1
GO_OTIC_V	GO_OTIC_VESICLE_I	15	-0.4813	-1.2393	0.2114	0.433279	1	14539	tags=60%, list=2
GO_EMBRY	GO_EMBRYONIC_PL	88	-0.3101	-1.191	0.2114	0.452908	1	10234	tags=34%, list=1
GO_ISOPRE	GO_ISOPRENOID_ME	143	-0.297	-1.1728	0.2116	0.459797	1	14868	tags=35%, list=2
GO_RAC_G	GO_RAC_GUANYL_N	19	-0.4398	-1.2359	0.2123	0.433731	1	7772	tags=37%, list=1
GO_LEFT_F	GO_LEFT_RIGHT_PA	22	-0.4116	-1.219	0.2127	0.440838	1	14390	tags=45%, list=2
GO_REGUL	GO_REGULATION_OI	100	-0.3102	-1.1794	0.2136	0.460746	1	11087	tags=29%, list=1
GO_LIGANI	GO_LIGAND_GATED_	139	-0.3268	-1.1921	0.2138	0.452436	1	14144	tags=38%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	16	-0.4776	-1.2578	0.214	0.425089	1	7372	tags=44%, list=1
GO_RETIN	GO_RETINOL_BINDI	16	-0.4391	-1.2098	0.215	0.447024	1	14556	tags=50%, list=2
GO_RESPO	GO_RESPONSE_TO_A	103	-0.2971	-1.1691	0.2151	0.462968	1	8399	tags=23%, list=1
GO_POSITI	GO_POSITIVE_REGU	49	-0.3573	-1.2023	0.2153	0.448886	1	16434	tags=39%, list=2
GO_CARTII	GO_CARTILAGE_DEV	29	-0.393	-1.199	0.2154	0.450829	1	16214	tags=48%, list=2
GO_EXOCY	GO_EXOCYTIC_VESI	216	-0.3109	-1.208	0.2158	0.446033	1	11013	tags=34%, list=1
GO_DRUG_	GO_DRUG_BINDING	101	-0.2964	-1.1591	0.2158	0.470019	1	10550	tags=30%, list=1
GO_REGUL	GO_REGULATION_OI	101	-0.3217	-1.1776	0.216	0.459058	1	20619	tags=49%, list=3
GO_CELL_N	GO_CELL_MIGRATIO	100	-0.3236	-1.1984	0.2161	0.450855	1	15403	tags=32%, list=2
GO_CILIAR	GO_CILIARY_BASE	31	-0.4089	-1.2424	0.2162	0.432924	1	18128	tags=55%, list=3
GO_REGUL	GO_REGULATION_OI	20	-0.3827	-1.1799	0.2162	0.4606	1	11652	tags=35%, list=2
GO_DNA_M	GO_DNA_METHYLAT	18	-0.4968	-1.2692	0.2162	0.426836	1	6893	tags=33%, list=1
GO_EUKAR	GO_EUKARYOTIC_48	15	-0.5701	-1.3057	0.2164	0.41366	1	4823	tags=33%, list=8
GO_BASIC_	GO_BASIC_AMINO_A	15	-0.4448	-1.2147	0.2165	0.443735	1	6516	tags=20%, list=1
GO_SIN3_T	GO_SIN3_TYPE_COM	15	-0.5312	-1.2826	0.2166	0.422676	1	8882	tags=47%, list=1
GO_VASCU	GO_VASCULAR_ASS	37	-0.3793	-1.2097	0.218	0.446906	1	12067	tags=32%, list=2
GO_REGUL	GO_REGULATION_OI	199	-0.2839	-1.1727	0.2182	0.459564	1	9901	tags=30%, list=1
GO_FATTY_	GO_FATTY_ACYL_C	38	-0.3613	-1.1917	0.2182	0.452348	1	12285	tags=37%, list=2
GO_INOSIT	GO_INOSITOL_PHOSI	55	-0.3426	-1.2078	0.2184	0.445607	1	13788	tags=45%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	19	-0.4025	-1.2053	0.2186	0.447457	1	18653	tags=42%, list=3
GO_HORM	GO_HORMONE_ACTI	118	-0.3096	-1.1285	0.2187	0.485538	1	18828	tags=40%, list=3
GO_PROTEI	GO_PROTEIN_DEME	26	-0.4833	-1.287	0.2188	0.419609	1	13642	tags=54%, list=2
GO_SULFUI	GO_SULFUR_COMPO	187	-0.2846	-1.1755	0.2189	0.459815	1	9865	tags=25%, list=1

GO_NEGAT	GO_NEGATIVE_REGU	19	-0.4377	-1.211	0.2191	0.446489	1	9318	tags=32%, list=1
GO_FOREB	GO_FOREBRAIN_GEN	61	-0.3702	-1.2025	0.2198	0.449952	1	15403	tags=49%, list=2
GO_POSITI	GO_POSITIVE_REGU	83	-0.3179	-1.1947	0.2198	0.452578	1	7870	tags=30%, list=1
GO_GLUTA	GO_GLUTAMATE_RE	46	-0.3625	-1.2032	0.22	0.449538	1	15082	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	261	-0.2686	-1.1376	0.2201	0.481501	1	12664	tags=31%, list=2
GO_PHOSPI	GO_PHOSPHATIDYLI	18	-0.5038	-1.2945	0.2202	0.418467	1	9535	tags=44%, list=1
GO_HYALU	GO_HYALURONIC_A	22	-0.4485	-1.2342	0.2208	0.436027	1	13904	tags=59%, list=2
GO_HISTON	GO_HISTONE_H3_AC	58	-0.3877	-1.245	0.2214	0.433728	1	7417	tags=31%, list=1
GO_RESPOI	GO_RESPONSE_TO_M	19	-0.3844	-1.1787	0.2216	0.460587	1	22566	tags=58%, list=3
GO_REGUL	GO_REGULATION_OI	82	-0.3207	-1.1827	0.222	0.458513	1	4326	tags=21%, list=7
GO_POSITI	GO_POSITIVE_REGUI	37	-0.3633	-1.1802	0.2225	0.460373	1	17429	tags=46%, list=3
GO_CALCIU	GO_CALCIUM_ION_T	133	-0.3116	-1.1731	0.2227	0.459887	1	11394	tags=32%, list=2
GO_DETEC	GO_DETECTION_OF_	74	-0.2955	-1.1403	0.2235	0.480682	1	18221	tags=41%, list=3
GO_REGUL	GO_REGULATION_OI	248	-0.3058	-1.1945	0.2236	0.452478	1	11186	tags=31%, list=1
GO_GLYCO	GO_GLYCOSAMINOC	219	-0.3322	-1.2024	0.224	0.449051	1	14201	tags=38%, list=2
GO_REGUL	GO_REGULATION_OI	33	-0.3903	-1.2421	0.2241	0.432686	1	6954	tags=21%, list=1
GO_REGUL	GO_REGULATION_OI	46	-0.3564	-1.2084	0.2243	0.445967	1	16180	tags=37%, list=2
GO_RESPOI	GO_RESPONSE_TO_T	258	-0.2976	-1.1959	0.2248	0.453471	1	12361	tags=33%, list=2
GO_RESPOI	GO_RESPONSE_TO_E	139	-0.283	-1.1509	0.2254	0.476927	1	11596	tags=31%, list=2
GO_CENTR	GO_CENTRAL_NERV	36	-0.3975	-1.2159	0.2257	0.442761	1	19852	tags=58%, list=3
GO_POSITI	GO_POSITIVE_REGUI	22	-0.4316	-1.2059	0.2257	0.446743	1	1512	tags=14%, list=3
GO_AMINO	GO_AMINO_ACID_TR	152	-0.3036	-1.1784	0.226	0.460067	1	9188	tags=27%, list=1
GO_TRANS	GO_TRANSLATION_F	134	-0.3461	-1.2166	0.2261	0.442531	1	5882	tags=21%, list=1
GO_EPITHE	GO_EPITHELIAL_CEL	116	-0.3094	-1.1868	0.2267	0.455832	1	3722	tags=22%, list=6
GO_APOLIF	GO_APOLIPOPROTEI	17	-0.4252	-1.1925	0.227	0.452426	1	10013	tags=35%, list=1
GO_CARDI	GO_CARDIAC_MUSC	39	-0.3611	-1.1872	0.2276	0.455819	1	15888	tags=46%, list=2
GO_HSP90_	GO_HSP90_PROTEIN_	41	-0.3559	-1.2155	0.2277	0.442677	1	8021	tags=34%, list=1
GO_VASCU	GO_VASCULAR_WOU	21	-0.4437	-1.2515	0.2279	0.429109	1	4750	tags=29%, list=8
GO_REGUL	GO_REGULATION_OI	86	-0.3296	-1.1929	0.2285	0.452361	1	11374	tags=31%, list=1
GO_PHOSPI	GO_PHOSPHATIDYLI	29	-0.4313	-1.2577	0.2295	0.424326	1	9535	tags=38%, list=1
GO_RESPOI	GO_RESPONSE_TO_L	23	-0.4041	-1.2042	0.2297	0.449058	1	8635	tags=30%, list=1
GO_SERINE	GO_SERINE_FAMILY_	37	-0.3736	-1.1948	0.23	0.452989	1	10956	tags=32%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	107	-0.3467	-1.2211	0.2302	0.441949	1	10363	tags=33%, list=1
GO_REGUL	GO_REGULATION_OI	166	-0.3208	-1.1982	0.2308	0.450879	1	11808	tags=34%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.4203	-1.1949	0.2308	0.453172	1	15942	tags=53%, list=2
GO_GLUTA	GO_GLUTAMINE_FAI	27	-0.3785	-1.1944	0.2312	0.452412	1	10225	tags=30%, list=1
GO_RESPOI	GO_RESPONSE_TO_D	27	-0.3587	-1.1666	0.2314	0.464995	1	20508	tags=56%, list=3
GO_ORGAN	GO_ORGANIC_ACID_	148	-0.2988	-1.1652	0.2319	0.465603	1	9901	tags=25%, list=1
GO_OXIDO	GO_OXIDOREDUCTA	159	-0.2698	-1.1353	0.2322	0.481953	1	12188	tags=25%, list=2
GO_EMBRY	GO_EMBRYONIC_CR	48	-0.3656	-1.211	0.2323	0.446702	1	9208	tags=35%, list=1
GO_RESPOI	GO_RESPONSE_TO_A	125	-0.2985	-1.1749	0.2326	0.459147	1	8989	tags=27%, list=1
GO_PROTEI	GO_PROTEIN_DEMET	30	-0.4343	-1.2401	0.2329	0.433316	1	13642	tags=50%, list=2
GO_ANKYF	GO_ANKYRIN_BINDI	20	-0.4182	-1.2015	0.2331	0.448792	1	18920	tags=65%, list=3
GO_IONOTI	GO_IONOTROPIC_GL	26	-0.4121	-1.1934	0.2331	0.452309	1	23732	tags=69%, list=4
GO_CHONI	GO_CHONDROCYTE_	28	-0.4297	-1.2206	0.2339	0.44247	1	9810	tags=39%, list=1
GO_HISTON	GO_HISTONE_METH	54	-0.4067	-1.2345	0.2344	0.435886	1	11713	tags=35%, list=2
GO_PHOSPI	GO_PHOSPHOLIPID_I	32	-0.4118	-1.233	0.2345	0.435124	1	9535	tags=34%, list=1
GO_REGUL	GO_REGULATION_OI	42	-0.333	-1.1761	0.2354	0.458931	1	21540	tags=60%, list=3
GO_ORGAN	GO_ORGANIC_ACID_	161	-0.2776	-1.1276	0.2355	0.48557	1	9176	tags=23%, list=1
GO_REGUL	GO_REGULATION_OI	70	-0.3203	-1.1518	0.2359	0.476023	1	12323	tags=37%, list=2
GO_COLLA	GO_COLLAGEN_TRIM	87	-0.4117	-1.2503	0.2361	0.429829	1	14539	tags=45%, list=2
GO_PLASM	GO_PLASMA_MEMBI	107	-0.3191	-1.1789	0.2361	0.460772	1	8343	tags=32%, list=1
GO_DICARI	GO_DICARBOXYLIC_	97	-0.3123	-1.1655	0.2361	0.465725	1	16390	tags=41%, list=2
GO_EPITHE	GO_EPITHELIAL_CEL	215	-0.2749	-1.1405	0.2363	0.480644	1	11075	tags=28%, list=1
GO_GLOMI	GO_GLOMERULAR_M	16	-0.5029	-1.2362	0.2364	0.433641	1	11652	tags=63%, list=2
GO_NOTCH	GO_NOTCH_SIGNALI	187	-0.2716	-1.1415	0.2364	0.479803	1	13258	tags=30%, list=2
GO_RNA_P	GO_RNA_POLYMERA	78	-0.3479	-1.206	0.2364	0.446897	1	12598	tags=32%, list=2
GO_AMEBC	GO_AMEBOIDAL_TY	467	-0.2672	-1.1457	0.2364	0.479392	1	9908	tags=27%, list=1

GO_REGUL	GO_REGULATION_O	24	-0.4355	-1.2109	0.2368	0.446282	1	6893	tags=33%, list=1
GO_ADREN	GO_ADRENAL_GLAN	24	-0.3732	-1.16	0.2373	0.469997	1	13841	tags=42%, list=2
GO_PEPTID	GO_PEPTIDYL_LYSI	43	-0.4107	-1.2227	0.2373	0.442865	1	15665	tags=49%, list=2
GO_POTAS	GO_POTASSIUM_ION	48	-0.3409	-1.1572	0.2373	0.471419	1	10114	tags=29%, list=1
GO_ANIMA	GO_ANIMAL_ORGAN	24	-0.3852	-1.1627	0.2378	0.467302	1	17571	tags=50%, list=3
GO_TASTE_	GO_TASTE_RECEPT	26	-0.4939	-1.2497	0.2379	0.429643	1	13202	tags=54%, list=2
GO_CERAM	GO_CERAMIDE_BIN	15	-0.4142	-1.2012	0.2379	0.448569	1	16638	tags=60%, list=2
GO_NEGAT	GO_NEGATIVE_REG	63	-0.3321	-1.1947	0.238	0.4528	1	10299	tags=32%, list=1
GO_DENDR	GO_DENDRITE_CYT	34	-0.3833	-1.2132	0.2383	0.445627	1	23782	tags=68%, list=4
GO_EMBRY	GO_EMBRYONIC_HE	23	-0.3822	-1.1867	0.2386	0.45577	1	10083	tags=39%, list=1
GO_POSITI	GO_POSITIVE_REGU	29	-0.4267	-1.2334	0.2387	0.435439	1	6476	tags=34%, list=1
GO_CELL_	GO_CELL_COMMUNI	24	-0.4118	-1.1921	0.2387	0.452692	1	10114	tags=33%, list=1
GO_TAU_P	GO_TAU_PROTEIN_K	22	-0.4476	-1.2474	0.2388	0.431447	1	3847	tags=27%, list=7
GO_ALPHA	GO_ALPHA_AMINO_	64	-0.3322	-1.1731	0.2388	0.460183	1	7085	tags=22%, list=1
GO_MAMM	GO_MAMMARY_GLA	71	-0.2878	-1.1574	0.2389	0.471608	1	6450	tags=27%, list=1
GO_PHOTO	GO_PHOTORECEPTO	85	-0.2962	-1.1469	0.2392	0.479471	1	19521	tags=41%, list=3
GO_NADP_	GO_NADP_BINDING	53	-0.3406	-1.1925	0.2395	0.452715	1	6576	tags=23%, list=1
GO_POSITI	GO_POSITIVE_REGU	25	-0.4207	-1.2199	0.2402	0.441949	1	10863	tags=40%, list=1
GO_SPERM	GO_SPERM_MIDPIEC	28	-0.3592	-1.1506	0.2402	0.476833	1	6841	tags=25%, list=1
GO_SIALYI	GO_SIALYLATION	20	-0.4332	-1.1898	0.2403	0.454741	1	9966	tags=35%, list=1
GO_PHOTO	GO_PHOTORECEPTO	57	-0.3545	-1.1655	0.2405	0.466031	1	15415	tags=42%, list=2
GO_2_OXO	GO_2_OXOGLUTARA	15	-0.4966	-1.2399	0.2406	0.432834	1	11385	tags=33%, list=1
GO_CHRO	GO_CHROMOSOME_	61	-0.3785	-1.209	0.2406	0.446258	1	17563	tags=46%, list=3
GO_POSITI	GO_POSITIVE_REGU	20	-0.4646	-1.245	0.241	0.433386	1	25975	tags=65%, list=4
GO_POSITI	GO_POSITIVE_REGU	81	-0.379	-1.2096	0.241	0.4467	1	7830	tags=32%, list=1
GO_NEGAT	GO_NEGATIVE_REG	35	-0.3462	-1.1682	0.241	0.463218	1	12997	tags=46%, list=2
GO_REGUL	GO_REGULATION_O	367	-0.2723	-1.1539	0.2411	0.474589	1	8997	tags=26%, list=1
GO_CARDI	GO_CARDIOBLAST_	18	-0.4417	-1.2086	0.2411	0.446708	1	15096	tags=50%, list=2
GO_HISTO	GO_HISTONE_METH	17	-0.4818	-1.226	0.2412	0.439719	1	10083	tags=35%, list=1
GO_PROTE	GO_PROTEOGLYCAN	64	-0.3693	-1.2041	0.2413	0.448979	1	13771	tags=39%, list=2
GO_PROTE	GO_PROTEIN_DEPOL	108	-0.3236	-1.17	0.2414	0.462417	1	12556	tags=32%, list=2
GO_GLIAL_	GO_GLIAL_CELL_DI	228	-0.2811	-1.1336	0.2417	0.48237	1	8692	tags=24%, list=1
GO_URONI	GO_URONIC_ACID_	23	-0.4475	-1.2219	0.2417	0.442161	1	7161	tags=26%, list=1
GO_ENDOP	GO_ENDOPLASMIC_	204	-0.3121	-1.1858	0.2418	0.455891	1	8051	tags=25%, list=1
GO_PROTE	GO_PROTEIN_METH	163	-0.3682	-1.2367	0.2422	0.43383	1	19156	tags=49%, list=3
GO_AXONE	GO_AXONEMAL_DY	20	-0.4224	-1.1835	0.2422	0.458305	1	11500	tags=40%, list=2
GO_VENTR	GO_VENTRICULAR_	17	-0.4158	-1.1777	0.2424	0.459607	1	8882	tags=29%, list=1
GO_NEGAT	GO_NEGATIVE_REG	59	-0.3266	-1.1808	0.2426	0.46067	1	11099	tags=32%, list=1
GO_MRNA_	GO_MRNA_5_SPLICE	23	-0.556	-1.294	0.2432	0.417172	1	12984	tags=65%, list=2
GO_CELLU	GO_CELLULAR_RES	26	-0.4063	-1.1879	0.2434	0.456391	1	22993	tags=62%, list=3
GO_SYMPO	GO_SYMPORTER_AC	142	-0.2669	-1.1172	0.2436	0.489667	1	16401	tags=39%, list=2
GO_MICRO	GO_MICROTUBULE_	112	-0.3535	-1.219	0.2436	0.441211	1	7793	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REG	23	-0.3823	-1.1593	0.2437	0.470059	1	17571	tags=48%, list=3
GO_RESPO	GO_RESPONSE_TO_	200	-0.2717	-1.1418	0.2438	0.479986	1	12041	tags=29%, list=2
GO_ENDON	GO_ENDONUCLEASE	36	-0.4021	-1.2129	0.2442	0.445465	1	5361	tags=25%, list=9
GO_THIOE	GO_THIOESTER_BIO	50	-0.3546	-1.1975	0.2444	0.451711	1	15930	tags=40%, list=2
GO_REGUL	GO_REGULATION_O	168	-0.2758	-1.1487	0.2447	0.477527	1	11628	tags=30%, list=2
GO_STRUC	GO_STRUCTURAL_C	27	-0.516	-1.2918	0.2449	0.417686	1	10044	tags=44%, list=1
GO_VENTR	GO_VENTRICULAR_	28	-0.3931	-1.1822	0.245	0.459062	1	15184	tags=43%, list=2
GO_POSITI	GO_POSITIVE_REGU	30	-0.3694	-1.1863	0.2452	0.455387	1	18362	tags=57%, list=3
GO_FIBRO	GO_FIBROBLAST_GR	23	-0.3776	-1.1877	0.2454	0.456046	1	7101	tags=26%, list=1
GO_UBIQU	GO_UBIQUITIN_CON	30	-0.3814	-1.1961	0.2455	0.453427	1	11621	tags=40%, list=2
GO_REGUL	GO_REGULATION_O	15	-0.4558	-1.2072	0.2458	0.446289	1	6442	tags=40%, list=1
GO_RESPO	GO_RESPONSE_TO_	145	-0.289	-1.1387	0.2461	0.480193	1	11239	tags=28%, list=1
GO_MEIOT	GO_MEIOTIC_CHRO	80	-0.3688	-1.2199	0.2467	0.441599	1	21601	tags=54%, list=3
GO_NEGAT	GO_NEGATIVE_REG	26	-0.4086	-1.1863	0.2475	0.455708	1	15864	tags=42%, list=2
GO_CELLU	GO_CELLULAR_RES	71	-0.3404	-1.1985	0.2481	0.451077	1	8635	tags=31%, list=1
GO_POSITI	GO_POSITIVE_REGU	15	-0.4583	-1.192	0.2485	0.452156	1	14514	tags=47%, list=2

GO_SEX_DI	GO_SEX_DIFFERENT	276	-0.2693	-1.1387	0.249	0.480453	1	13995	tags=33%, list=2
GO_PLATEI	GO_PLATELET_MORI	21	-0.3836	-1.1732	0.2495	0.460412	1	6716	tags=33%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	29	-0.3516	-1.16	0.2495	0.469813	1	11233	tags=28%, list=1
GO_MUSCL	GO_MUSCLE_HYPER	31	-0.3563	-1.1671	0.25	0.464549	1	11495	tags=32%, list=2
GO_VASCU	GO_VASCULAR_END	48	-0.3308	-1.1608	0.25	0.469387	1	11210	tags=25%, list=1
GO_HISTON	GO_HISTONE_METHY	132	-0.3709	-1.2114	0.2505	0.446372	1	16651	tags=45%, list=2
GO_ODONT	GO_ODONTOGENESIS	89	-0.3258	-1.1773	0.2515	0.458943	1	10299	tags=34%, list=1
GO_FOREB	GO_FOREBRAIN_NEU	51	-0.3718	-1.171	0.2515	0.461386	1	15008	tags=49%, list=2
GO_MUSCL	GO_MUSCLE_CELL_I	239	-0.293	-1.1661	0.252	0.465596	1	9340	tags=28%, list=1
GO_MITOC	GO_MITOCHONDRIO	45	-0.3623	-1.1804	0.2524	0.460215	1	5615	tags=24%, list=1
GO_RESPOI	GO_RESPONSE_TO_E	75	-0.2926	-1.1255	0.2524	0.486766	1	4349	tags=20%, list=7
GO_PEPTID	GO_PEPTIDYL_LYSIN	113	-0.373	-1.2017	0.2524	0.44913	1	16445	tags=48%, list=2
GO_REGUL	GO_REGULATION_OI	32	-0.3304	-1.1412	0.2524	0.480011	1	8094	tags=22%, list=1
GO_EYE_PI	GO_EYE_PHOTORECI	35	-0.345	-1.1556	0.2526	0.472608	1	17875	tags=51%, list=3
GO_ENDOT	GO_ENDOTHELIAL_C	191	-0.2968	-1.1782	0.253	0.460107	1	11210	tags=30%, list=1
GO_AXONA	GO_AXONAL_FASCIC	23	-0.3974	-1.1767	0.2534	0.458241	1	8082	tags=30%, list=1
GO_REGUL	GO_REGULATION_OI	25	-0.4229	-1.2166	0.2535	0.442901	1	10660	tags=36%, list=1
GO_EPHRIN	GO_EPHRIN_RECEPT	87	-0.3087	-1.1541	0.2542	0.474634	1	6457	tags=24%, list=1
GO_REGUL	GO_REGULATION_OI	232	-0.3286	-1.1955	0.2545	0.453165	1	8019	tags=28%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	152	-0.2843	-1.1241	0.2552	0.487577	1	18325	tags=41%, list=3
GO_RAC_G	GO_RAC_GTPASE_BI	69	-0.3382	-1.1776	0.2559	0.459367	1	10477	tags=35%, list=1
GO_CILIAR	GO_CILIARY_TRANS	63	-0.3938	-1.2167	0.2564	0.443044	1	18128	tags=48%, list=3
GO_MICRO	GO_MICROTUBULE_(	29	-0.444	-1.2301	0.2568	0.437954	1	9173	tags=34%, list=1
GO_ACTIVI	GO_ACTIVE_TRANSM	341	-0.2545	-1.1119	0.2569	0.491483	1	15786	tags=36%, list=2
GO_ESTABI	GO_ESTABLISHMENT	214	-0.2969	-1.1639	0.2572	0.466068	1	12361	tags=35%, list=2
GO_INSULI	GO_INSULIN_RECEPT	141	-0.2861	-1.135	0.2572	0.481877	1	12270	tags=31%, list=2
GO_HETER	GO_HETEROPHILIC_(	42	-0.3775	-1.184	0.2573	0.45849	1	10254	tags=38%, list=1
GO_REGUL	GO_REGULATION_OI	353	-0.2737	-1.1422	0.2574	0.479611	1	8997	tags=26%, list=1
GO_CELL_A	GO_CELL_AGGREGAT	23	-0.4255	-1.1699	0.2577	0.462198	1	4391	tags=26%, list=8
GO_REGUL	GO_REGULATION_OI	41	-0.3429	-1.152	0.2578	0.475873	1	15919	tags=41%, list=2
GO_CELLU	GO_CELLULAR_RESI	201	-0.2838	-1.1361	0.2581	0.482057	1	10247	tags=28%, list=1
GO_NEURO	GO_NEURON_PROJE(	26	-0.3857	-1.1839	0.2581	0.458301	1	11034	tags=50%, list=1
GO_ISOPRE	GO_ISOPRENOID_BIN	37	-0.3357	-1.1172	0.2586	0.489446	1	20680	tags=49%, list=3
GO_CILIAR	GO_CILIARY_TIP	45	-0.4086	-1.2262	0.259	0.439678	1	8248	tags=36%, list=1
GO_PHOTO	GO_PHOTORECEPTO	47	-0.326	-1.1375	0.2592	0.48133	1	18128	tags=49%, list=3
GO_TRANS	GO_TRANSFERASE_A	248	-0.2891	-1.1574	0.2597	0.471336	1	12756	tags=31%, list=2
GO_CELL_(	GO_CELL_CELL_JUN(	476	-0.2689	-1.1426	0.2597	0.480882	1	8997	tags=25%, list=1
GO_TERPEI	GO_TERPENOID_MET	124	-0.2898	-1.1277	0.2597	0.485735	1	14868	tags=33%, list=2
GO_ALPHA	GO_ALPHA_TUBULIN	36	-0.3655	-1.1806	0.2604	0.460689	1	17190	tags=42%, list=2
GO_PHYSI(	GO_PHYSIOLOGICAL	37	-0.3475	-1.1647	0.2608	0.466098	1	12950	tags=35%, list=2
GO_REGUL	GO_REGULATION_OI	208	-0.2721	-1.1245	0.261	0.487253	1	11448	tags=29%, list=2
GO_REGUL	GO_REGULATION_OI	15	-0.4469	-1.1873	0.2621	0.456366	1	10781	tags=40%, list=1
GO_VESICI	GO_VESICLE_COAT	54	-0.3572	-1.1805	0.2628	0.460367	1	11813	tags=37%, list=2
GO_REGUL	GO_REGULATION_OI	16	-0.453	-1.1889	0.2629	0.455209	1	6442	tags=38%, list=1
GO_STRIAT	GO_STRIATED_MUSC	59	-0.322	-1.1448	0.2632	0.479553	1	10263	tags=31%, list=1
GO_POSITI	GO_POSITIVE_REGUI	25	-0.3922	-1.1416	0.2635	0.479999	1	15047	tags=52%, list=2
GO_FILOPC	GO_FILOPODIUM_AS	58	-0.3112	-1.1465	0.2641	0.479439	1	8956	tags=28%, list=1
GO_ENDOR	GO_ENDORIBONUCL	30	-0.4098	-1.1911	0.2647	0.453044	1	5361	tags=27%, list=9
GO_INORG	GO_INORGANIC_ANI	120	-0.2871	-1.1188	0.2652	0.48942	1	15498	tags=43%, list=2
GO_MICRO	GO_MICROTUBULE_I	23	-0.4534	-1.2186	0.2653	0.440756	1	7579	tags=30%, list=1
GO_TRANS	GO_TRANSFORMING	202	-0.2869	-1.1462	0.2653	0.479516	1	18362	tags=44%, list=3
GO_OVULA	GO_OVULATION	21	-0.4145	-1.1744	0.2655	0.459222	1	8274	tags=38%, list=1
GO_CIRCAI	GO_CIRCADIAN_RHY	215	-0.3001	-1.1533	0.2655	0.474636	1	12274	tags=32%, list=2
GO_RESPOI	GO_RESPONSE_TO_C	226	-0.2647	-1.1157	0.2655	0.489607	1	10951	tags=27%, list=1
GO_NEURO	GO_NEURON_CELLU	32	-0.3824	-1.1688	0.2657	0.462918	1	18541	tags=59%, list=3
GO_LONG_	GO_LONG_CHAIN_FA	17	-0.4016	-1.1636	0.2661	0.466376	1	15873	tags=41%, list=2
GO_REGIOI	GO_REGION_OF_CYT	25	-0.4097	-1.1937	0.2663	0.452446	1	18541	tags=40%, list=3
GO_OXYGE	GO_OXYGEN_BINDIN	36	-0.3487	-1.1496	0.2664	0.477225	1	7577	tags=19%, list=1

GO_REGUL	GO_REGULATION_O	388	-0.2702	-1.1261	0.267	0.486826	1	8997	tags=26%, list=1
GO_STERO	GO_STEROID_BIOSY	193	-0.2722	-1.1315	0.2671	0.483421	1	4766	tags=16%, list=8
GO_REGUL	GO_REGULATION_O	204	-0.2637	-1.1105	0.2672	0.493112	1	4326	tags=16%, list=7
GO_HIPPO_	GO_HIPPO_SIGNALIN	44	-0.3958	-1.1958	0.2673	0.453042	1	13328	tags=45%, list=2
GO_RESPO	GO_RESPONSE_TO_F	36	-0.3676	-1.1605	0.2673	0.469498	1	7165	tags=31%, list=1
GO_ACYLG	GO_ACYLGLYCEROL	22	-0.3846	-1.1594	0.2676	0.470232	1	10468	tags=27%, list=1
GO_HISTO	GO_HISTONE_LYSIN	39	-0.4309	-1.2302	0.2676	0.438174	1	11713	tags=38%, list=2
GO_KERAT	GO_KERATINOCYTE_	19	-0.4306	-1.1682	0.2676	0.462944	1	9367	tags=37%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	24	-0.4285	-1.1832	0.2681	0.458116	1	12885	tags=42%, list=2
GO_REGUL	GO_REGULATION_O	34	-0.3555	-1.1494	0.2681	0.477331	1	13913	tags=38%, list=2
GO_PHOTO	GO_PHOTORECEPTO	37	-0.3879	-1.1751	0.2682	0.45935	1	18128	tags=51%, list=3
GO_POSITI	GO_POSITIVE_REGU	15	-0.4498	-1.1779	0.2685	0.459548	1	9377	tags=47%, list=1
GO_POSITI	GO_POSITIVE_REGU	20	-0.4071	-1.1388	0.2687	0.480699	1	15095	tags=45%, list=2
GO_IMPOR	GO_IMPORT_INTO_C	227	-0.276	-1.1146	0.2687	0.490837	1	8452	tags=24%, list=1
GO_APICA	GO_APICAL_JUNCTI	81	-0.3192	-1.1632	0.2688	0.466709	1	14513	tags=40%, list=2
GO_ADHER	GO_ADHERENS_JUN	157	-0.2862	-1.1447	0.2692	0.479494	1	12361	tags=31%, list=2
GO_PHOTO	GO_PHOTORECEPTO	62	-0.3036	-1.1171	0.2694	0.489019	1	18128	tags=45%, list=3
GO_ENDOT	GO_ENDOTHELIAL_	67	-0.3449	-1.1789	0.2695	0.460456	1	3722	tags=24%, list=6
GO_REGUL	GO_REGULATION_O	39	-0.351	-1.1462	0.2695	0.479204	1	13913	tags=38%, list=2
GO_SPLICE	GO_SPLICEOSOMAL_	27	-0.4968	-1.2196	0.2697	0.441604	1	9759	tags=44%, list=1
GO_FLUID_	GO_FLUID_TRANSPO	28	-0.3724	-1.1537	0.27	0.47425	1	12152	tags=32%, list=2
GO_CELLU	GO_CELLULAR_GLU	18	-0.475	-1.2024	0.2702	0.449699	1	7161	tags=28%, list=1
GO_REGUL	GO_REGULATION_O	136	-0.2844	-1.1427	0.2702	0.480967	1	10136	tags=27%, list=1
GO_ION_G	GO_ION_GATED_CH	42	-0.3504	-1.153	0.2702	0.474844	1	9297	tags=33%, list=1
GO_SIALY	GO_SIALYLTRANSFE	21	-0.412	-1.1492	0.2703	0.477287	1	9966	tags=33%, list=1
GO_SOLUT	GO_SOLUTE_CATION	32	-0.337	-1.1356	0.2703	0.482092	1	3579	tags=19%, list=6
GO_RESPO	GO_RESPONSE_TO_I	29	-0.3318	-1.1367	0.2706	0.482303	1	4301	tags=24%, list=7
GO_NEGAT	GO_NEGATIVE_REGU	21	-0.3815	-1.1471	0.2707	0.479432	1	11087	tags=43%, list=1
GO_CELLU	GO_CELLULAR_RES	21	-0.381	-1.14	0.271	0.480478	1	7165	tags=29%, list=1
GO_REGUL	GO_REGULATION_O	19	-0.4387	-1.2026	0.2711	0.4502	1	12415	tags=42%, list=2
GO_WATER	GO_WATER_TRANSP	21	-0.3959	-1.1703	0.2714	0.462282	1	11581	tags=29%, list=2
GO_FORM	GO_FORMATION_OF_	16	-0.5044	-1.2163	0.2715	0.442655	1	4823	tags=31%, list=8
GO_NEURO	GO_NEUROPEPTIDE_	33	-0.345	-1.1201	0.2717	0.490039	1	3611	tags=18%, list=6
GO_SPLICE	GO_SPLICEOSOMAL_	78	-0.3741	-1.1837	0.2717	0.458225	1	12984	tags=37%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	86	-0.3272	-1.1203	0.2718	0.490258	1	10853	tags=33%, list=1
GO_REGUL	GO_REGULATION_O	140	-0.2639	-1.104	0.272	0.494833	1	9806	tags=28%, list=1
GO_GENIT	GO_GENITALIA_DEV	47	-0.3472	-1.1614	0.2724	0.468854	1	13941	tags=43%, list=2
GO_CLATH	GO_CLATHRIN_BIND	64	-0.3119	-1.1352	0.2725	0.481732	1	12130	tags=36%, list=2
GO_CELLU	GO_CELLULAR_PRO	350	-0.2657	-1.1069	0.2727	0.494009	1	13279	tags=29%, list=2
GO_MICRO	GO_MICROTUBULE_	44	-0.3975	-1.1893	0.2729	0.455232	1	7793	tags=30%, list=1
GO_ORGAN	GO_ORGANIC_ACID_	346	-0.2538	-1.098	0.2733	0.497943	1	9188	tags=23%, list=1
GO_ANDRO	GO_ANDROGEN_REC	28	-0.3678	-1.1627	0.2736	0.46704	1	4536	tags=29%, list=8
GO_CARBO	GO_CARBOHYDRAT	235	-0.2604	-1.1048	0.2736	0.494751	1	12527	tags=29%, list=2
GO_COSTA	GO_COSTAMERE	19	-0.4731	-1.2084	0.2737	0.446295	1	8533	tags=47%, list=1
GO_REGUL	GO_REGULATION_O	23	-0.3768	-1.1537	0.2738	0.47458	1	18131	tags=57%, list=3
GO_NUCLE	GO_NUCLEOSIDE_TR	339	-0.2752	-1.1504	0.2738	0.476788	1	11448	tags=30%, list=2
GO_POSITI	GO_POSITIVE_REGU	23	-0.4368	-1.1958	0.274	0.453269	1	19653	tags=61%, list=3
GO_N_TER	GO_N_TERMINAL_P	16	-0.4276	-1.1814	0.2741	0.460272	1	8564	tags=38%, list=1
GO_REGUL	GO_REGULATION_O	201	-0.2881	-1.1409	0.2744	0.480341	1	10490	tags=32%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.401	-1.1643	0.2746	0.466166	1	8726	tags=33%, list=1
GO_ACTIVI	GO_ACTIVIN_BINDIN	15	-0.4432	-1.1752	0.2752	0.459668	1	6239	tags=27%, list=1
GO_ALCOH	GO_ALCOHOL_BIOS	163	-0.2887	-1.1394	0.2752	0.480638	1	6020	tags=19%, list=1
GO_REGUL	GO_REGULATION_O	24	-0.3901	-1.1344	0.2761	0.481864	1	3514	tags=21%, list=6
GO_EPIDE	GO_EPIDERMIS_MO	32	-0.3829	-1.1434	0.2764	0.480363	1	5708	tags=25%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	82	-0.3244	-1.1713	0.2765	0.461381	1	7095	tags=26%, list=1
GO_TISSUE	GO_TISSUE_MIGRAT	362	-0.269	-1.1202	0.2766	0.490064	1	10485	tags=28%, list=1
GO_ANTER	GO_ANTEROGRADE_	47	-0.3528	-1.1729	0.2768	0.459892	1	15315	tags=40%, list=2
GO_ANDRO	GO_ANDROGEN_REC	42	-0.3575	-1.1436	0.2768	0.480308	1	8314	tags=31%, list=1

GO_POSITI	GO_POSITIVE_REGUI	27	-0.4258	-1.178	0.2769	0.459719	1	19653	tags=59%, list=3
GO_NON_M	GO_NON_MOTILE_CI	52	-0.404	-1.2188	0.2771	0.440716	1	20204	tags=46%, list=3
GO_MIRNA	GO_MIRNA_MEDIATI	97	-0.3465	-1.171	0.2773	0.461652	1	15529	tags=33%, list=2
GO_ENDOD	GO_ENDODERM_DEV	78	-0.3377	-1.1575	0.2773	0.471845	1	11075	tags=36%, list=1
GO_RESPOI	GO_RESPONSE_TO_E	40	-0.3229	-1.1283	0.2778	0.485154	1	11013	tags=33%, list=1
GO_GLAND	GO_GLANDULAR_EP	47	-0.3389	-1.1389	0.278	0.481115	1	11638	tags=36%, list=2
GO_METAN	GO_METANEPHROS_	33	-0.3544	-1.1209	0.2784	0.489787	1	7165	tags=30%, list=1
GO_GTPASI	GO_GTPASE_REGUL	300	-0.2825	-1.151	0.2784	0.477102	1	10059	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	291	-0.2676	-1.113	0.2787	0.490823	1	9810	tags=26%, list=1
GO_REGUL	GO_REGULATION_OI	39	-0.3324	-1.1281	0.2788	0.485194	1	10511	tags=33%, list=1
GO_CELLU	GO_CELLULAR_RESI	44	-0.3263	-1.1259	0.2794	0.486671	1	10781	tags=34%, list=1
GO_BHLH_	GO_BHLH_TRANSCR	29	-0.3534	-1.1394	0.2812	0.480924	1	7826	tags=34%, list=1
GO_POSITI	GO_POSITIVE_REGUI	16	-0.434	-1.1718	0.2813	0.460882	1	18299	tags=63%, list=3
GO_MICRO	GO_MICROTUBULE	418	-0.3107	-1.175	0.2814	0.459173	1	12302	tags=31%, list=2
GO_NEURO	GO_NEURON_FATE_	34	-0.4464	-1.1776	0.2814	0.458813	1	16459	tags=47%, list=2
GO_BIOMIN	GO_BIOMINERALIZA	156	-0.295	-1.1041	0.2816	0.495032	1	14054	tags=42%, list=2
GO_SYNAP	GO_SYNAPTIC_VESI	119	-0.3611	-1.187	0.2816	0.455984	1	11615	tags=37%, list=2
GO_REGUL	GO_REGULATION_OI	23	-0.3897	-1.1568	0.2819	0.471754	1	10185	tags=30%, list=1
GO_FEAR_I	GO_FEAR_RESPONSE	41	-0.3519	-1.1498	0.2823	0.477281	1	15403	tags=39%, list=2
GO_PENTO	GO_PENTOSE_METAI	15	-0.4708	-1.1772	0.2823	0.458469	1	10883	tags=33%, list=1
GO_SCAFF	GO_SCAFFOLD_PROT	60	-0.3162	-1.1324	0.2823	0.482903	1	12320	tags=33%, list=2
GO_NUCLE	GO_NUCLEOSIDE_BI	131	-0.2893	-1.1198	0.2832	0.48927	1	15930	tags=35%, list=2
GO_OXIDO	GO_OXIDOREDUCTA	35	-0.3538	-1.1353	0.2837	0.482182	1	3257	tags=17%, list=6
GO_PRESYI	GO_PRESYNAPTIC_A	15	-0.489	-1.1753	0.284	0.459826	1	19869	tags=60%, list=3
GO_ENDOC	GO_ENDOCRINE_PAI	45	-0.3566	-1.1643	0.284	0.466436	1	12398	tags=42%, list=2
GO_NUCLE	GO_NUCLEAR_EUCH	25	-0.4022	-1.1548	0.2843	0.473714	1	12819	tags=36%, list=2
GO_MEMBI	GO_MEMBRANE_DEI	88	-0.3201	-1.1256	0.2846	0.486828	1	11031	tags=33%, list=1
GO_HORM	GO_HORMONE_MED	195	-0.2813	-1.1159	0.2846	0.489762	1	10247	tags=28%, list=1
GO_SOLUT	GO_SOLUTE_PROTOI	20	-0.375	-1.1366	0.2849	0.482237	1	1420	tags=15%, list=2
GO_HOMOI	GO_HOMOLOGOUS_	53	-0.3452	-1.1343	0.2849	0.481755	1	12772	tags=32%, list=2
GO_POSITI	GO_POSITIVE_REGUI	23	-0.383	-1.121	0.2849	0.489892	1	554	tags=17%, list=1
GO_POSITI	GO_POSITIVE_REGUI	67	-0.2987	-1.1026	0.2851	0.495208	1	3180	tags=19%, list=5
GO_BILE_A	GO_BILE_ACID_BIOS	37	-0.3264	-1.1175	0.2852	0.490196	1	9049	tags=27%, list=1
GO_POSITI	GO_POSITIVE_REGUI	61	-0.3438	-1.1424	0.2854	0.480563	1	10254	tags=36%, list=1
GO_SODIUI	GO_SODIUM_ION_EX	15	-0.4135	-1.1389	0.286	0.48092	1	14054	tags=53%, list=2
GO_REGUL	GO_REGULATION_OI	113	-0.2992	-1.1223	0.2863	0.488576	1	6421	tags=21%, list=1
GO_REGUL	GO_REGULATION_OI	50	-0.3166	-1.1132	0.2863	0.491723	1	12168	tags=38%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	17	-0.3988	-1.1357	0.2863	0.482128	1	19483	tags=53%, list=3
GO_PHOSPI	GO_PHOSPHATIDYLI	31	-0.3947	-1.1735	0.2871	0.460272	1	9535	tags=35%, list=1
GO_UBIQUI	GO_UBIQUITIN_LIKE	36	-0.3528	-1.1566	0.2877	0.471064	1	11621	tags=36%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.4171	-1.1334	0.2882	0.482313	1	8426	tags=44%, list=1
GO_CELL_I	GO_CELL_LEADING_	411	-0.2739	-1.12	0.2884	0.48974	1	10885	tags=30%, list=1
GO_REGUL	GO_REGULATION_OI	53	-0.307	-1.1169	0.2885	0.488931	1	5855	tags=23%, list=1
GO_NUCLE	GO_NUCLEAR_LOCA	26	-0.4479	-1.1999	0.2886	0.449859	1	10044	tags=38%, list=1
GO_SUBPA	GO_SUBPALLIUM_DI	24	-0.4034	-1.1508	0.2888	0.476801	1	24085	tags=63%, list=4
GO_NEGAT	GO_NEGATIVE_REGU	39	-0.3428	-1.1236	0.289	0.487813	1	15095	tags=36%, list=2
GO_RETRO	GO_RETROGRADE_T	83	-0.3184	-1.1462	0.2891	0.478897	1	6767	tags=25%, list=1
GO_RETIN	GO_RETINOIC_ACID_	27	-0.3572	-1.1179	0.2891	0.490347	1	10781	tags=41%, list=1
GO_REGUL	GO_REGULATION_OI	24	-0.3955	-1.166	0.2899	0.465386	1	19968	tags=46%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.3975	-1.1383	0.2899	0.480502	1	11000	tags=39%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.3892	-1.1206	0.2903	0.490085	1	9806	tags=47%, list=1
GO_PULMO	GO_PULMONARY_V	21	-0.4422	-1.1879	0.2904	0.456733	1	15184	tags=57%, list=2
GO_G_PRO	GO_G_PROTEIN_COU	17	-0.386	-1.1158	0.2906	0.489667	1	6730	tags=29%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	73	-0.3136	-1.1145	0.2907	0.490793	1	12556	tags=32%, list=2
GO_POSITI	GO_POSITIVE_REGUI	15	-0.4414	-1.1429	0.2908	0.480916	1	9641	tags=33%, list=1
GO_AXO_D	GO_AXO_DENDRITIC	69	-0.3507	-1.1879	0.2913	0.456157	1	15315	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	29	-0.3911	-1.1476	0.2916	0.478762	1	6260	tags=28%, list=1
GO_PROTEI	GO_PROTEIN_LOCAI	46	-0.3601	-1.1425	0.2916	0.480702	1	7952	tags=30%, list=1

GO_NEPHR	GO_NEPHRON_TUBU	15	-0.4153	-1.1449	0.2917	0.479861	1	6716	tags=40%, list=1
GO_CHANN	GO_CHANNEL_REGU	144	-0.2902	-1.1066	0.292	0.494204	1	6828	tags=22%, list=1
GO_MELAN	GO_MELANOCYTE_D	25	-0.4	-1.1291	0.2941	0.485515	1	11664	tags=40%, list=2
GO_MYELI	GO_MYELIN_SHEAT	46	-0.3297	-1.1261	0.2943	0.486512	1	4017	tags=22%, list=7
GO_NADPL	GO_NADPLUS_KINAS	17	-0.3818	-1.131	0.2946	0.483369	1	9222	tags=35%, list=1
GO_DEVEL	GO_DEVELOPMENT_	226	-0.2585	-1.0965	0.2947	0.498538	1	12116	tags=30%, list=2
GO_EPITHE	GO_EPITHELIAL_CEL	441	-0.2505	-1.1001	0.2949	0.497214	1	11210	tags=28%, list=1
GO_SMALL	GO_SMALL_SUBUNIT	34	-0.4243	-1.161	0.2952	0.469225	1	12741	tags=41%, list=2
GO_ESTAB	GO_ESTABLISHMENT	47	-0.3151	-1.1226	0.2955	0.488408	1	13615	tags=34%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	26	-0.4079	-1.1771	0.2956	0.458224	1	18369	tags=35%, list=3
GO_PLATE	GO_PLATELET_DERI	59	-0.3533	-1.1642	0.2957	0.465971	1	8101	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.3842	-1.1287	0.2957	0.485473	1	8426	tags=40%, list=1
GO_REGUL	GO_REGULATION_O	28	-0.4343	-1.1772	0.2959	0.45878	1	12664	tags=50%, list=2
GO_DEFINI	GO_DEFINITIVE_HEM	21	-0.3831	-1.1322	0.2967	0.482534	1	5294	tags=29%, list=9
GO_ACETY	GO_ACETYL_COA_B	22	-0.4073	-1.1567	0.2969	0.471209	1	15930	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	16	-0.4342	-1.1597	0.2972	0.469934	1	10431	tags=44%, list=1
GO_ESTAB	GO_ESTABLISHMENT	45	-0.3607	-1.1467	0.2976	0.479391	1	7372	tags=29%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	37	-0.3748	-1.1453	0.2977	0.479326	1	7103	tags=24%, list=1
GO_EXOCR	GO_EXOCRINE_SYST	51	-0.3104	-1.1121	0.2978	0.491442	1	19965	tags=45%, list=3
GO_SYNTA	GO_SYNTAXIN_BIND	78	-0.3282	-1.1324	0.2981	0.483089	1	8341	tags=28%, list=1
GO_RESPO	GO_RESPONSE_TO_P	16	-0.4276	-1.1522	0.2984	0.475944	1	15919	tags=50%, list=2
GO_REGUL	GO_REGULATION_O	202	-0.2688	-1.1073	0.2985	0.494202	1	10299	tags=27%, list=1
GO_POSITI	GO_POSITIVE_REGU	15	-0.4192	-1.135	0.2998	0.481571	1	18362	tags=67%, list=3
GO_METAN	GO_METANEPHRIC_	26	-0.383	-1.133	0.3	0.482474	1	7165	tags=35%, list=1
GO_LYASE_	GO_LYASE_ACTIVIT	171	-0.2795	-1.1034	0.3002	0.494684	1	10225	tags=25%, list=1
GO_GLYCO	GO_GLYCOPROTEIN_	329	-0.2677	-1.107	0.3002	0.494237	1	13066	tags=29%, list=2
GO_PHOSP	GO_PHOSPHORIC_DI	89	-0.2867	-1.0969	0.3002	0.498206	1	14223	tags=36%, list=2
GO_STRUC	GO_STRUCTURAL_C	43	-0.3893	-1.1422	0.3006	0.479819	1	12596	tags=44%, list=2
GO_TRANS	GO_TRANSLATION_I	50	-0.3862	-1.1689	0.301	0.463073	1	5882	tags=22%, list=1
GO_INWAR	GO_INWARD_RECTIF	22	-0.381	-1.1174	0.3015	0.490013	1	8265	tags=27%, list=1
GO_REGUL	GO_REGULATION_O	26	-0.3542	-1.1138	0.3017	0.491324	1	22139	tags=65%, list=3
GO_REGUL	GO_REGULATION_O	32	-0.3588	-1.1198	0.3018	0.489578	1	694	tags=16%, list=1
GO_METAL	GO_METALLOENDO	104	-0.303	-1.1245	0.3024	0.487535	1	11456	tags=30%, list=2
GO_SYNAP	GO_SYNAPTIC_VESI	55	-0.3555	-1.1492	0.3028	0.477025	1	9535	tags=38%, list=1
GO_NUCLE	GO_NUCLEAR_HORM	141	-0.2963	-1.119	0.3029	0.489594	1	8416	tags=30%, list=1
GO_ALPHA	GO_ALPHA_ACTININ	27	-0.3952	-1.1322	0.303	0.48281	1	18359	tags=59%, list=3
GO_NADPH	GO_NADPH_BINDING	16	-0.4102	-1.1442	0.303	0.480054	1	8553	tags=31%, list=1
GO_REGUL	GO_REGULATION_O	93	-0.2962	-1.1181	0.3034	0.490375	1	3722	tags=20%, list=6
GO_REGUL	GO_REGULATION_O	178	-0.2863	-1.1054	0.3037	0.49458	1	9641	tags=28%, list=1
GO_REGUL	GO_REGULATION_O	19	-0.37	-1.1229	0.3038	0.488072	1	10943	tags=32%, list=1
GO_SPIND	GO_SPINDLE_MIDZO	36	-0.4294	-1.2063	0.3039	0.446771	1	13727	tags=36%, list=2
GO_CELLU	GO_CELLULAR_RES	96	-0.2966	-1.1032	0.3039	0.494876	1	6062	tags=19%, list=1
GO_REGUL	GO_REGULATION_O	50	-0.312	-1.0965	0.3043	0.498268	1	16781	tags=38%, list=2
GO_APICA	GO_APICAL_PART_O	421	-0.2552	-1.0757	0.3047	0.511363	1	9810	tags=24%, list=1
GO_EXPLO	GO_EXPLORATION_	25	-0.3679	-1.1149	0.3049	0.490585	1	17607	tags=52%, list=3
GO_GROW	GO_GROWTH_FACT	156	-0.2961	-1.0964	0.3054	0.498253	1	12526	tags=35%, list=2
GO_RESPO	GO_RESPONSE_TO_E	122	-0.2624	-1.0735	0.3055	0.513023	1	9793	tags=25%, list=1
GO_ORGAN	GO_ORGANELLE_IN	15	-0.4202	-1.1333	0.3062	0.482227	1	5751	tags=27%, list=1
GO_ATPAS	GO_ATPASE_BINDIN	84	-0.2731	-1.0765	0.3062	0.510556	1	9306	tags=25%, list=1
GO_COMPL	GO_COMPLEX_OF_C	21	-0.5057	-1.1654	0.3071	0.465486	1	14539	tags=57%, list=2
GO_POSITI	GO_POSITIVE_REGU	64	-0.3227	-1.1271	0.3072	0.48602	1	10462	tags=36%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	36	-0.3381	-1.1285	0.3074	0.485293	1	3347	tags=22%, list=6
GO_KERAT	GO_KERATAN_SULF	33	-0.3776	-1.1423	0.3078	0.480111	1	8113	tags=30%, list=1
GO_FEMAL	GO_FEMALE_GAMET	131	-0.2712	-1.0919	0.3084	0.501034	1	8726	tags=22%, list=1
GO_ACETY	GO_ACETYLTRANSF	103	-0.3307	-1.1583	0.3084	0.470666	1	9645	tags=29%, list=1
GO_VISUA	GO_VISUAL_BEHAVI	52	-0.3225	-1.0998	0.3086	0.496257	1	9704	tags=29%, list=1
GO_CELL_J	GO_CELL_JUNCTION	30	-0.3614	-1.1219	0.3091	0.488931	1	18638	tags=53%, list=3
GO_SENSO	GO_SENSORY_PERC	99	-0.3121	-1.1131	0.3091	0.491396	1	15154	tags=42%, list=2

GO_REGUL	GO_REGULATION_OI	31	-0.3336	-1.09	0.3102	0.501565	1	17429	tags=45%, list=3
GO_POSITI	GO_POSITIVE_REGUI	37	-0.388	-1.1455	0.3102	0.479378	1	16562	tags=41%, list=2
GO_PROTEI	GO_PROTEIN_STABII	179	-0.2708	-1.0976	0.3105	0.497942	1	8168	tags=23%, list=1
GO_RESPOI	GO_RESPONSE_TO_P	147	-0.2737	-1.0811	0.3106	0.506969	1	10013	tags=28%, list=1
GO_I_BANI	GO_I_BAND	139	-0.34	-1.1586	0.3106	0.470578	1	14188	tags=40%, list=2
GO_POSITI	GO_POSITIVE_REGUI	90	-0.2999	-1.1162	0.3109	0.489542	1	10299	tags=33%, list=1
GO_GERM_	GO_GERM_CELL_DE	253	-0.2661	-1.0852	0.3109	0.505008	1	13279	tags=30%, list=2
GO_N_TERI	GO_N_TERMINAL_PF	28	-0.3756	-1.1365	0.3111	0.482032	1	10505	tags=36%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	46	-0.3005	-1.0879	0.3112	0.50206	1	9653	tags=30%, list=1
GO_CAMP_	GO_CAMP_METABOI	22	-0.3774	-1.113	0.3115	0.491112	1	17430	tags=45%, list=3
GO_REGUL	GO_REGULATION_OI	15	-0.4352	-1.1481	0.3124	0.478191	1	2535	tags=27%, list=4
GO_ESTABI	GO_ESTABLISHMENT	15	-0.3858	-1.1075	0.3124	0.494483	1	13615	tags=40%, list=2
GO_REGUL	GO_REGULATION_OI	15	-0.4011	-1.1176	0.3125	0.490275	1	9340	tags=33%, list=1
GO_90S_PR	GO_90S_PRERIBOSOI	26	-0.4474	-1.1568	0.3126	0.471422	1	3054	tags=23%, list=5
GO_NEGAT	GO_NEGATIVE_REGU	66	-0.3033	-1.0999	0.3135	0.496252	1	22995	tags=59%, list=3
GO_EXTRA	GO_EXTRACELLULA	31	-0.3629	-1.0958	0.3141	0.498352	1	13011	tags=39%, list=2
GO_POSITI	GO_POSITIVE_REGUI	33	-0.3583	-1.1198	0.3145	0.489791	1	7579	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	39	-0.3314	-1.1002	0.3146	0.497409	1	6429	tags=28%, list=1
GO_EXTRA	GO_EXTRACELLULA	44	-0.4192	-1.1785	0.3149	0.460425	1	10198	tags=41%, list=1
GO_POSITI	GO_POSITIVE_REGUI	43	-0.3268	-1.104	0.315	0.494638	1	3501	tags=19%, list=6
GO_RECEP	GO_RECEPTOR_CLUS	55	-0.3325	-1.1265	0.3153	0.486778	1	8836	tags=33%, list=1
GO_CELL_	GO_CELL_CORTEX_F	42	-0.3433	-1.1082	0.3156	0.494617	1	11439	tags=36%, list=2
GO_NEURO	GO_NEUROTRANSMI	41	-0.3309	-1.0933	0.3158	0.500075	1	8909	tags=29%, list=1
GO_BASAL	GO_BASAL_TRANSCI	71	-0.3325	-1.1499	0.3161	0.477489	1	12067	tags=30%, list=2
GO_CHLOR	GO_CHLORIDE_TRAI	110	-0.2823	-1.08	0.3167	0.507064	1	13975	tags=39%, list=2
GO_NEURO	GO_NEURON_PROJE	87	-0.312	-1.119	0.3172	0.489428	1	5721	tags=21%, list=1
GO_CELL_	GO_CELL_CELL_ADH	26	-0.3477	-1.1075	0.3172	0.494274	1	21835	tags=54%, list=3
GO_REGUL	GO_REGULATION_OI	284	-0.2598	-1.0954	0.3173	0.498493	1	8171	tags=23%, list=1
GO_PROTEI	GO_PROTEIN_LOCAL	65	-0.2966	-1.0802	0.3175	0.507082	1	11983	tags=38%, list=2
GO_PLATEI	GO_PLATELET_ALPH	17	-0.4177	-1.1196	0.3176	0.488919	1	9024	tags=35%, list=1
GO_MULTI	GO_MULTICELLULAI	76	-0.3064	-1.0995	0.3179	0.496187	1	15514	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	24	-0.3613	-1.1345	0.3179	0.482104	1	3119	tags=29%, list=5
GO_HISTOI	GO_HISTONE_H3_K4_	53	-0.404	-1.1697	0.3181	0.462247	1	17788	tags=51%, list=3
GO_REGUL	GO_REGULATION_OI	30	-0.3504	-1.1092	0.3182	0.494351	1	9127	tags=33%, list=1
GO_CALCII	GO_CALCINEURIN_N	47	-0.3125	-1.096	0.3183	0.498313	1	13788	tags=40%, list=2
GO_ENDOT	GO_ENDOTHELIAL_C	62	-0.3411	-1.1288	0.3185	0.485706	1	8947	tags=34%, list=1
GO_STEROI	GO_STEROID_HORM	135	-0.2916	-1.0975	0.3185	0.497492	1	10247	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	31	-0.353	-1.1082	0.3194	0.494922	1	12168	tags=45%, list=2
GO_REGUL	GO_REGULATION_OI	15	-0.4208	-1.123	0.3196	0.488277	1	20576	tags=53%, list=3
GO_THIOES	GO_THIOESTER_MET	98	-0.294	-1.0887	0.32	0.501734	1	15930	tags=35%, list=2
GO_HIPPO	GO_HIPPOCAMPAL_I	32	-0.3722	-1.1106	0.3207	0.4931	1	19653	tags=53%, list=3
GO_REGUL	GO_REGULATION_OI	20	-0.3465	-1.0956	0.3207	0.498339	1	8635	tags=30%, list=1
GO_SIGNAI	GO_SIGNAL_SEQUEN	47	-0.3686	-1.14	0.3208	0.480259	1	10044	tags=32%, list=1
GO_O_ACY	GO_O_ACYLTRANSFI	47	-0.3152	-1.0915	0.3209	0.500777	1	13412	tags=32%, list=2
GO_PROTEI	GO_PROTEIN_C_TER	186	-0.2767	-1.1063	0.3214	0.493967	1	6085	tags=22%, list=1
GO_BONE_	GO_BONE_MINERAL	112	-0.2983	-1.0843	0.3216	0.505311	1	14054	tags=43%, list=2
GO_REGUL	GO_REGULATION_OI	365	-0.2653	-1.0727	0.3218	0.514162	1	8941	tags=29%, list=1
GO_POSITI	GO_POSITIVE_REGUI	45	-0.3235	-1.0931	0.3219	0.499836	1	10299	tags=42%, list=1
GO_RESPOI	GO_RESPONSE_TO_D	87	-0.2827	-1.0649	0.3219	0.519177	1	19410	tags=46%, list=3
GO_REGUL	GO_REGULATION_OI	19	-0.4233	-1.1176	0.3221	0.490578	1	6893	tags=37%, list=1
GO_MUSCL	GO_MUSCLE_CELL_I	103	-0.3037	-1.1046	0.3232	0.494812	1	8635	tags=24%, list=1
GO_GLIAL_	GO_GLIAL_CELL_MI	53	-0.316	-1.0976	0.3233	0.497721	1	6187	tags=23%, list=1
GO_INSULI	GO_INSULIN_LIKE_G	35	-0.3278	-1.0845	0.3235	0.50533	1	12950	tags=34%, list=2
GO_MANN	GO_MANNOSYLTRAI	28	-0.3644	-1.1212	0.3237	0.490004	1	15915	tags=43%, list=2
GO_MUSCL	GO_MUSCLE_FIBER_	56	-0.3245	-1.0952	0.3241	0.498551	1	9641	tags=30%, list=1
GO_MRNA_	GO_MRNA_CIS_SPLI	52	-0.3781	-1.1293	0.3242	0.485414	1	12984	tags=42%, list=2
GO_GLUCU	GO_GLUCURONOSYI	30	-0.3591	-1.1076	0.3244	0.494666	1	12247	tags=37%, list=2
GO_MEGAI	GO_MEGAKARYOCY	70	-0.3217	-1.1091	0.3245	0.494155	1	10083	tags=33%, list=1

GO_REGUL	GO_REGULATION_O	101	-0.2956	-1.0904	0.3245	0.50154	1	8907	tags=28%, list=1
GO_NEUTR	GO_NEUTRAL_LIPID_	48	-0.3243	-1.0803	0.3245	0.507207	1	13220	tags=33%, list=2
GO_INORG	GO_INORGANIC_ANI	170	-0.2588	-1.0618	0.3248	0.519336	1	10550	tags=27%, list=1
GO_PROTE	GO_PROTEIN_KINAS	30	-0.3345	-1.0916	0.325	0.500902	1	13378	tags=47%, list=2
GO_PHOSP	GO_PHOSPHOPROTE	85	-0.2939	-1.0835	0.3251	0.505876	1	7287	tags=28%, list=1
GO_REGUL	GO_REGULATION_O	228	-0.2602	-1.0824	0.3252	0.506702	1	9450	tags=25%, list=1
GO_RESPO	GO_RESPONSE_TO_S	340	-0.244	-1.063	0.3258	0.518913	1	10247	tags=25%, list=1
GO_SYNAP	GO_SYNAPSE_MATU	25	-0.4211	-1.1309	0.3261	0.483229	1	11013	tags=40%, list=1
GO_POTAS	GO_POTASSIUM_ION	16	-0.3805	-1.0884	0.3262	0.502074	1	15374	tags=38%, list=2
GO_REGUL	GO_REGULATION_O	17	-0.4621	-1.1311	0.3267	0.483571	1	7430	tags=35%, list=1
GO_HISTO	GO_HISTONE_H3_K9_	48	-0.3713	-1.1301	0.3269	0.484227	1	15678	tags=46%, list=2
GO_AMINO	GO_AMINO_ACID_T	80	-0.3012	-1.0888	0.3272	0.501973	1	4015	tags=18%, list=7
GO_CHRO	GO_CHROMATIN_DN	89	-0.3417	-1.1231	0.3275	0.488388	1	5294	tags=24%, list=9
GO_POSIT	GO_POSITIVE_REGU	24	-0.3842	-1.0945	0.3281	0.498538	1	14609	tags=46%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	21	-0.3526	-1.0894	0.3281	0.501497	1	7754	tags=38%, list=1
GO_SEMAP	GO_SEMAPHORIN_R	23	-0.3462	-1.0921	0.3286	0.500869	1	3046	tags=26%, list=5
GO_REGUL	GO_REGULATION_O	93	-0.2876	-1.0793	0.33	0.507448	1	16570	tags=39%, list=2
GO_AMINO	GO_AMINO_SUGAR_	39	-0.3384	-1.1018	0.3301	0.496302	1	8437	tags=28%, list=1
GO_INTRA	GO_INTRACELLULA	112	-0.2979	-1.0995	0.3302	0.496455	1	9654	tags=28%, list=1
GO_STRES	GO_STRESS_FIBER_	104	-0.294	-1.1	0.3302	0.49703	1	9937	tags=29%, list=1
GO_REGUL	GO_REGULATION_O	64	-0.3824	-1.1312	0.3306	0.483607	1	7870	tags=36%, list=1
GO_THYM	GO_THYMUS_DEVEL	46	-0.3259	-1.1097	0.3307	0.493745	1	8398	tags=24%, list=1
GO_SODIU	GO_SODIUM_CHANN	40	-0.329	-1.1078	0.3313	0.494729	1	10004	tags=30%, list=1
GO_SPANN	GO_SPANNING_COM	19	-0.3956	-1.1016	0.3314	0.49613	1	13679	tags=37%, list=2
GO_HISTO	GO_HISTONE_H3_K9_	37	-0.3923	-1.1403	0.3314	0.480426	1	21001	tags=59%, list=3
GO_POSIT	GO_POSITIVE_REGU	110	-0.3275	-1.1144	0.332	0.490602	1	16983	tags=37%, list=2
GO_MIDDL	GO_MIDDLE_EAR_M	20	-0.3669	-1.0888	0.332	0.502259	1	17220	tags=50%, list=2
GO_C2H2_	GO_C2H2_ZINC_FIN	15	-0.413	-1.1172	0.332	0.489144	1	11652	tags=40%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	18	-0.4279	-1.1358	0.3321	0.482304	1	18541	tags=44%, list=3
GO_COLLA	GO_COLLAGEN_FIB	55	-0.4471	-1.178	0.3327	0.460061	1	16983	tags=53%, list=2
GO_REGUL	GO_REGULATION_O	23	-0.3653	-1.1058	0.3333	0.494089	1	8887	tags=30%, list=1
GO_LONG_	GO_LONG_CHAIN_F	23	-0.3588	-1.1037	0.3333	0.494552	1	12285	tags=35%, list=2
GO_REGUL	GO_REGULATION_O	35	-0.3266	-1.1014	0.3333	0.496153	1	12629	tags=37%, list=2
GO_CELL_	GO_CELL_GROWTH	475	-0.258	-1.0961	0.3333	0.498464	1	13067	tags=32%, list=2
GO_REGUL	GO_REGULATION_O	35	-0.3197	-1.0847	0.3333	0.505227	1	13788	tags=43%, list=2
GO_ARGIN	GO_ARGININE_MET	20	-0.3634	-1.0752	0.3333	0.511789	1	3576	tags=20%, list=6
GO_CELL_	GO_CELL_CORTEX	285	-0.2551	-1.0647	0.334	0.519333	1	11780	tags=30%, list=2
GO_TRANS	GO_TRANSCRIPTION	260	-0.292	-1.1066	0.334	0.493727	1	12828	tags=34%, list=2
GO_GLIOG	GO_GLIOGENESIS	303	-0.2624	-1.0723	0.334	0.514587	1	12629	tags=29%, list=2
GO_PHOSP	GO_PHOSPHATIDYLI	27	-0.3378	-1.0896	0.3346	0.502085	1	5751	tags=26%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	52	-0.3614	-1.1341	0.3346	0.481776	1	6879	tags=29%, list=1
GO_INSULI	GO_INSULIN_LIKE_G	16	-0.3823	-1.0948	0.3353	0.498394	1	12950	tags=50%, list=2
GO_CCR4_	GO_CCR4_NOT_COM	15	-0.4462	-1.1173	0.3353	0.489895	1	7128	tags=33%, list=1
GO_CALCI	GO_CALCIUM_ION_R	63	-0.3364	-1.1086	0.3354	0.49481	1	11615	tags=37%, list=2
GO_CALCI	GO_CALCIUM_CHAN	45	-0.3469	-1.1016	0.3361	0.496378	1	6290	tags=22%, list=1
GO_REGUL	GO_REGULATION_O	314	-0.2765	-1.0948	0.3365	0.498639	1	10612	tags=31%, list=1
GO_PEPTID	GO_PEPTIDE_HORM	251	-0.2515	-1.0484	0.3367	0.526526	1	12629	tags=31%, list=2
GO_GLUTA	GO_GLUTAMATE_RE	27	-0.4351	-1.1439	0.3368	0.480194	1	23732	tags=70%, list=4
GO_IONOT	GO_IONOTROPIC_GL	19	-0.4439	-1.1241	0.3369	0.487336	1	23732	tags=74%, list=4
GO_ASTRO	GO_ASTROCYTE_DIF	82	-0.299	-1.079	0.3373	0.507403	1	8426	tags=28%, list=1
GO_PHOTO	GO_PHOTOTRANSDU	58	-0.2863	-1.0658	0.3373	0.518999	1	18221	tags=40%, list=3
GO_MITOC	GO_MITOCHONDRIA	39	-0.3271	-1.1	0.3384	0.496489	1	3119	tags=28%, list=5
GO_NUCLE	GO_NUCLEOSIDE_BI	64	-0.3165	-1.1038	0.3387	0.49471	1	17293	tags=41%, list=3
GO_LYMPH	GO_LYMPH_VESSEL_	26	-0.3627	-1.0739	0.339	0.513167	1	14543	tags=46%, list=2
GO_RESPO	GO_RESPONSE_TO_F	89	-0.2752	-1.0667	0.3391	0.518729	1	11248	tags=25%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.3936	-1.0942	0.3393	0.498773	1	10004	tags=33%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	47	-0.3087	-1.0741	0.3393	0.513014	1	15325	tags=30%, list=2
GO_POSIT	GO_POSITIVE_REGU	105	-0.2916	-1.0672	0.3397	0.518366	1	9641	tags=28%, list=1

GO_STEROI	GO_STEROL_METAB	164	-0.265	-1.0748	0.3404	0.512179	1	4065	tags=14%, list=7
GO_PROTO	GO_PROTON_TRANS	108	-0.2681	-1.0641	0.3408	0.518619	1	12508	tags=29%, list=2
GO_LABYR	GO_LABYRINTHINE_	20	-0.3639	-1.0911	0.3414	0.501149	1	10185	tags=40%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	26	-0.37	-1.0895	0.3415	0.501905	1	10431	tags=35%, list=1
GO_ENDOD	GO_ENDODEOXYRIB	17	-0.407	-1.108	0.3431	0.494521	1	10581	tags=29%, list=1
GO_PROTEI	GO_PROTEIN_O_LINI	96	-0.289	-1.0645	0.3433	0.518943	1	6384	tags=19%, list=1
GO_CILIUM	GO_CILIUM_ORGANI	367	-0.3081	-1.1084	0.3434	0.494753	1	13011	tags=32%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	94	-0.2625	-1.0697	0.3435	0.516767	1	12318	tags=26%, list=2
GO_ION_CI	GO_ION_CHANNEL_I	130	-0.2776	-1.0714	0.3436	0.515744	1	15356	tags=38%, list=2
GO_ENDOD	GO_ENDODERMAL_C	15	-0.3949	-1.0879	0.3437	0.502302	1	10888	tags=47%, list=1
GO_MYOSI	GO_MYOSIN_BINDIN	71	-0.2808	-1.0632	0.3439	0.519223	1	9192	tags=28%, list=1
GO_ORGAN	GO_ORGANIC_HYDR	48	-0.2995	-1.0608	0.3443	0.51844	1	7107	tags=23%, list=1
GO_HISTON	GO_HISTONE_H4_AC	70	-0.3618	-1.1362	0.3444	0.482157	1	18074	tags=49%, list=3
GO_RAL_G	GO_RAL_GTPASE_BI	15	-0.4016	-1.1066	0.345	0.493919	1	15888	tags=47%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	249	-0.246	-1.0544	0.3457	0.521801	1	13311	tags=32%, list=2
GO_ORGAN	GO_ORGANISM_EME	28	-0.3251	-1.0859	0.3458	0.504283	1	7793	tags=36%, list=1
GO_RHYTH	GO_RHYTHMIC_BEH	50	-0.3027	-1.0797	0.3459	0.507277	1	7968	tags=24%, list=1
GO_VESICI	GO_VESICLE_CARGC	27	-0.3799	-1.111	0.3463	0.492784	1	15233	tags=44%, list=2
GO_HORM(	GO_HORMONE_RECI	174	-0.2733	-1.0701	0.347	0.5169	1	8416	tags=28%, list=1
GO_AMINO	GO_AMINO_ACID_TF	89	-0.2948	-1.066	0.3472	0.51911	1	9176	tags=24%, list=1
GO_OXIDO	GO_OXIDOREDUCTA	43	-0.3266	-1.0791	0.3478	0.507614	1	13276	tags=30%, list=2
GO_P53_BII	GO_P53_BINDING	64	-0.3515	-1.1104	0.349	0.492877	1	15621	tags=42%, list=2
GO_CELLU	GO_CELLULAR_RESI	70	-0.2879	-1.0556	0.3504	0.521476	1	7789	tags=27%, list=1
GO_VENOU	GO_VENOUS_BLOOD	15	-0.4124	-1.1131	0.3515	0.491562	1	1087	tags=20%, list=2
GO_REGUL	GO_REGULATION_OI	88	-0.3489	-1.1168	0.3517	0.488852	1	9771	tags=34%, list=1
GO_DEVEL	GO_DEVELOPMENTA	274	-0.2621	-1.0649	0.3518	0.519453	1	11099	tags=27%, list=1
GO_RRNA_	GO_RRNA_TRANSCR	28	-0.4132	-1.1423	0.3519	0.480401	1	13219	tags=39%, list=2
GO_PROTEI	GO_PROTEIN_TRANS	67	-0.3604	-1.1127	0.3523	0.491001	1	12749	tags=39%, list=2
GO_ESTABI	GO_ESTABLISHMENT	16	-0.4084	-1.103	0.3526	0.49476	1	2297	tags=25%, list=4
GO_METAN	GO_METANEPHRIC_I	16	-0.4186	-1.0977	0.3534	0.498121	1	5634	tags=38%, list=1
GO_METAL	GO_METALLOAMINC	21	-0.3466	-1.0705	0.3537	0.51672	1	3016	tags=24%, list=5
GO_EATIN(	GO_EATING_BEHAVI	33	-0.3372	-1.1049	0.354	0.494817	1	17571	tags=42%, list=3
GO_NEURO	GO_NEUROMUSCUL	16	-0.4055	-1.0907	0.354	0.501313	1	7714	tags=44%, list=1
GO_PROTEI	GO_PROTEIN_DEMAI	19	-0.3835	-1.0693	0.3543	0.517068	1	11143	tags=42%, list=1
GO_REGUL	GO_REGULATION_OI	15	-0.4145	-1.1073	0.3544	0.493907	1	7372	tags=40%, list=1
GO_FATTY_	GO_FATTY_ACID_DE	99	-0.2553	-1.0572	0.3545	0.520568	1	12285	tags=29%, list=2
GO_POSITI	GO_POSITIVE_REGUI	47	-0.3333	-1.0865	0.3555	0.50358	1	9318	tags=30%, list=1
GO_IRE1_M	GO_IRE1_MEDIATED	65	-0.3118	-1.0815	0.3556	0.506913	1	7176	tags=23%, list=1
GO_TERTIA	GO_TERTIARY_ALCC	20	-0.3723	-1.0704	0.3566	0.516623	1	22074	tags=65%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	186	-0.2543	-1.0504	0.3569	0.523544	1	6461	tags=22%, list=1
GO_GANGL	GO_GANGLION_DEV	16	-0.4716	-1.1245	0.3573	0.487797	1	7998	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	49	-0.3132	-1.0763	0.3573	0.510573	1	12059	tags=37%, list=2
GO_BONE_	GO_BONE_MATURAT	20	-0.3736	-1.0842	0.358	0.505225	1	17571	tags=50%, list=3
GO_INTEGI	GO_INTEGRAL_COMI	34	-0.362	-1.083	0.358	0.50634	1	14389	tags=44%, list=2
GO_DNA_B	GO_DNA_BINDING_T	333	-0.2746	-1.0811	0.358	0.50726	1	9390	tags=26%, list=1
GO_R_SMA	GO_R_SMAD_BINDIN	23	-0.3577	-1.0821	0.3583	0.506865	1	15946	tags=43%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	32	-0.3844	-1.0933	0.3587	0.499824	1	8399	tags=25%, list=1
GO_REGUL	GO_REGULATION_OI	150	-0.2724	-1.0633	0.3591	0.519267	1	9901	tags=28%, list=1
GO_POSITI	GO_POSITIVE_REGUI	40	-0.3607	-1.1003	0.3594	0.4974	1	15109	tags=38%, list=2
GO_PEPTID	GO_PEPTIDE_LYSINE	56	-0.3813	-1.1062	0.3595	0.493752	1	12756	tags=34%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	387	-0.2782	-1.0894	0.3596	0.501718	1	11099	tags=29%, list=1
GO_VASCU	GO_VASCULAR_END	48	-0.3192	-1.0641	0.3597	0.518845	1	10523	tags=35%, list=1
GO_PURINI	GO_PURINE_CONTAI	430	-0.2441	-1.0561	0.36	0.521089	1	9901	tags=25%, list=1
GO_POSITI	GO_POSITIVE_REGUI	37	-0.3173	-1.0765	0.3602	0.510812	1	10660	tags=32%, list=1
GO_INSULI	GO_INSULIN_SECRE	207	-0.2506	-1.0425	0.3602	0.529397	1	12629	tags=32%, list=2
GO_ORGAN	GO_ORGANIC_ACID_	219	-0.2534	-1.0517	0.3603	0.523573	1	12405	tags=30%, list=2
GO_REGUL	GO_REGULATION_OI	183	-0.2751	-1.0573	0.3608	0.52126	1	10614	tags=28%, list=1
GO_DIOXY	GO_DIOXYGENASE_	88	-0.2782	-1.0643	0.3609	0.518778	1	12725	tags=31%, list=2

GO_REGUL	GO_REGULATION_OI	20	-0.3685	-1.0877	0.3614	0.501973	1	8997	tags=30%, list=1
GO_POSITI	GO_POSITIVE_REGU	20	-0.393	-1.0811	0.3615	0.506753	1	2889	tags=25%, list=5
GO_SPHINC	GO_SPHINGOLIPID_E	24	-0.3546	-1.0857	0.3618	0.504368	1	2672	tags=25%, list=5
GO_POSITI	GO_POSITIVE_REGU	99	-0.2814	-1.0573	0.3619	0.521046	1	13137	tags=36%, list=2
GO_INTERN	GO_INTERMEDIATE_	50	-0.3164	-1.0553	0.362	0.521067	1	7970	tags=26%, list=1
GO_ENDOP	GO_ENDOPLASMIC_I	17	-0.4143	-1.0993	0.3624	0.496117	1	11595	tags=29%, list=2
GO_PRE_M	GO_PRE_MRNA_BINI	57	-0.3734	-1.101	0.3626	0.496545	1	12984	tags=42%, list=2
GO_CATION	GO_CATION_CATION	26	-0.3209	-1.0461	0.3627	0.528001	1	15374	tags=42%, list=2
GO_GLYCO	GO_GLYCOSYLATIOI	253	-0.258	-1.0456	0.3631	0.528282	1	12832	tags=28%, list=2
GO_INTERN	GO_INTERMEDIATE_	15	-0.3795	-1.0804	0.3634	0.507364	1	13136	tags=47%, list=2
GO_CAMP_	GO_CAMP_BINDING	23	-0.3541	-1.0623	0.3636	0.518777	1	20068	tags=48%, list=3
GO_REGUL	GO_REGULATION_OI	40	-0.3893	-1.0949	0.3638	0.49876	1	10276	tags=33%, list=1
GO_LYSOPI	GO_LYSOPHOSPHOL	18	-0.3654	-1.0756	0.3642	0.511334	1	646	tags=17%, list=1
GO_PEPTID	GO_PEPTIDE_N_ACE	63	-0.3716	-1.1125	0.3642	0.491046	1	12756	tags=35%, list=2
GO_PRE_M	GO_PRE_MRNA_5_SP	18	-0.5452	-1.1251	0.3642	0.487179	1	12984	tags=72%, list=2
GO_BLOOD	GO_BLOOD_VESSEL_	55	-0.3008	-1.045	0.3649	0.528807	1	15325	tags=31%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	30	-0.3218	-1.07	0.3655	0.516686	1	7971	tags=27%, list=1
GO_GOLGI_	GO_GOLGI_CISTERN	91	-0.2709	-1.0651	0.3656	0.519791	1	8047	tags=20%, list=1
GO_LIVER_	GO_LIVER_REGENER	32	-0.3272	-1.0632	0.3658	0.518999	1	3652	tags=19%, list=6
GO_CENTR	GO_CENTRAL_NERV	26	-0.3804	-1.1	0.3661	0.496737	1	11108	tags=38%, list=1
GO_POSITI	GO_POSITIVE_REGU	40	-0.3029	-1.0608	0.3663	0.518919	1	7119	tags=28%, list=1
GO_POSITI	GO_POSITIVE_REGU	59	-0.299	-1.0511	0.3665	0.52435	1	9470	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	184	-0.3181	-1.1051	0.3667	0.494711	1	10581	tags=32%, list=1
GO_NLS_BI	GO_NLS_BEARING_P	20	-0.4246	-1.1197	0.3667	0.488997	1	14625	tags=45%, list=2
GO_ATPASI	GO_ATPASE_COMPLI	76	-0.3661	-1.1045	0.3673	0.49462	1	8390	tags=28%, list=1
GO_ADREN	GO_ADRENERGIC_RI	31	-0.3525	-1.0816	0.368	0.50709	1	19410	tags=45%, list=3
GO_REGUL	GO_REGULATION_OI	35	-0.348	-1.0565	0.3682	0.521204	1	9470	tags=29%, list=1
GO_SERINE	GO_SERINE_FAMILY_	17	-0.426	-1.069	0.3685	0.516781	1	6471	tags=29%, list=1
GO_ACTIN_	GO_ACTIN_BINDING	425	-0.2603	-1.0315	0.3685	0.537633	1	11800	tags=31%, list=2
GO_PROTEI	GO_PROTEIN_LOCAL	330	-0.2507	-1.0612	0.3696	0.519709	1	9188	tags=24%, list=1
GO_PIRNA_	GO_PIRNA_METABOI	18	-0.3922	-1.0591	0.3697	0.519561	1	16537	tags=33%, list=2
GO_REGUL	GO_REGULATION_OI	126	-0.2678	-1.0554	0.37	0.521255	1	10299	tags=26%, list=1
GO_REGUL	GO_REGULATION_OI	25	-0.3494	-1.0575	0.3702	0.521138	1	9127	tags=36%, list=1
GO_FORMA	GO_FORMATION_OF_	15	-0.443	-1.0929	0.3704	0.499824	1	11005	tags=47%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	20	-0.3431	-1.0523	0.3715	0.523078	1	9806	tags=35%, list=1
GO_GLIAL_	GO_GLIAL_CELL_DE	120	-0.2604	-1.0395	0.3716	0.532011	1	12426	tags=30%, list=2
GO_GOLGI_	GO_GOLGI_TO_END	15	-0.4194	-1.0882	0.3719	0.502029	1	15530	tags=53%, list=2
GO_ORGAN	GO_ORGANIC_ANION	231	-0.2492	-1.043	0.3723	0.52916	1	9711	tags=22%, list=1
GO_MICRO	GO_MICROVILLUS_A	17	-0.3772	-1.0638	0.373	0.518853	1	8740	tags=35%, list=1
GO_CYTOP	GO_CYTOPLASMIC_	62	-0.3266	-1.0876	0.3733	0.501868	1	4421	tags=21%, list=8
GO_VESICL	GO_VESICLE_TETHE	66	-0.3078	-1.0562	0.374	0.521224	1	5773	tags=24%, list=1
GO_HEPAR	GO_HEPARAN_SULF	26	-0.3565	-1.0738	0.3748	0.513116	1	17308	tags=50%, list=3
GO_POSITI	GO_POSITIVE_REGU	37	-0.3399	-1.078	0.375	0.508885	1	11248	tags=32%, list=1
GO_REGUL	GO_REGULATION_OI	16	-0.4127	-1.0677	0.375	0.517722	1	8882	tags=50%, list=1
GO_REGUL	GO_REGULATION_OI	46	-0.3092	-1.0593	0.3752	0.519829	1	3829	tags=20%, list=7
GO_COLUM	GO_COLUMNAR_CUI	116	-0.2842	-1.0506	0.3752	0.524082	1	12934	tags=32%, list=2
GO_REGUL	GO_REGULATION_OI	48	-0.3472	-1.091	0.376	0.501158	1	6594	tags=27%, list=1
GO_PEPTID	GO_PEPTIDYL_GLUT	30	-0.3453	-1.0609	0.377	0.51916	1	13631	tags=37%, list=2
GO_POSITI	GO_POSITIVE_REGU	76	-0.2857	-1.0446	0.3776	0.528636	1	10045	tags=29%, list=1
GO_SODIUI	GO_SODIUM_ION_IM	19	-0.3632	-1.0504	0.378	0.523792	1	4750	tags=21%, list=8
GO_REGUL	GO_REGULATION_OI	84	-0.2883	-1.0475	0.3786	0.52669	1	11210	tags=24%, list=1
GO_REGUL	GO_REGULATION_OI	85	-0.296	-1.0601	0.3788	0.519342	1	7103	tags=20%, list=1
GO_STRESS	GO_STRESS_GRANUI	23	-0.4078	-1.1136	0.3789	0.491371	1	14298	tags=43%, list=2
GO_REGUL	GO_REGULATION_OI	22	-0.4122	-1.0986	0.3789	0.497205	1	19156	tags=59%, list=3
GO_REGUL	GO_REGULATION_OI	20	-0.3675	-1.0395	0.379	0.532254	1	8022	tags=35%, list=1
GO_DYNEII	GO_DYNEIN_COMPL	20	-0.411	-1.0901	0.3794	0.50177	1	9173	tags=30%, list=1
GO_NUCLE	GO_NUCLEOTIDE_DI	17	-0.3737	-1.057	0.3796	0.520669	1	2118	tags=18%, list=4
GO_CYTOP	GO_CYTOPLASMIC_I	21	-0.3832	-1.0692	0.3797	0.51695	1	7336	tags=38%, list=1

GO_RESPO	GO_RESPONSE_TO_F	161	-0.286	-1.0541	0.38	0.521671	1	10263	tags=29%, list=1
GO_CELLU	GO_CELLULAR_RESF	23	-0.3582	-1.0692	0.3801	0.516711	1	4065	tags=22%, list=7
GO_STRUC	GO_STRUCTURAL_C	101	-0.2801	-1.0426	0.3802	0.529548	1	12035	tags=35%, list=2
GO_POSITI	GO_POSITIVE_REGU	96	-0.2716	-1.0449	0.3803	0.528576	1	8956	tags=26%, list=1
GO_PSEUD	GO_PSEUDOPODIUM	18	-0.3606	-1.0572	0.3807	0.520788	1	14188	tags=50%, list=2
GO_EPIDEF	GO_EPIDERMAL_GR	33	-0.3388	-1.0669	0.381	0.518582	1	2867	tags=18%, list=5
GO_GLUTA	GO_GLUTAMINE_FAI	16	-0.366	-1.0588	0.3823	0.51985	1	5161	tags=25%, list=9
GO_ACTIN_	GO_ACTIN_CYTOSKE	486	-0.2491	-1.028	0.3825	0.540998	1	8907	tags=26%, list=1
GO_REGUL	GO_REGULATION_OI	36	-0.3224	-1.0584	0.3826	0.520221	1	3829	tags=19%, list=7
GO_TRANS	GO_TRANSLATION_F	105	-0.3076	-1.0545	0.383	0.521836	1	5882	tags=17%, list=1
GO_CONTR	GO_CONTRACTILE_F	236	-0.3046	-1.084	0.3832	0.505303	1	14372	tags=36%, list=2
GO_INTRA	GO_INTRACELLULAI	43	-0.3202	-1.0612	0.3839	0.519438	1	11233	tags=30%, list=1
GO_GLAND	GO_GLAND_DEVELO	441	-0.2324	-1.0372	0.3839	0.533682	1	8692	tags=22%, list=1
GO_GROW	GO_GROWTH_PLATE	19	-0.356	-1.0414	0.3846	0.530745	1	15844	tags=42%, list=2
GO_REGUL	GO_REGULATION_OI	65	-0.3191	-1.0531	0.3849	0.522539	1	10511	tags=34%, list=1
GO_SMAD_	GO_SMAD_BINDING	79	-0.3043	-1.0344	0.3853	0.536391	1	15946	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	194	-0.2646	-1.0308	0.3854	0.538069	1	11813	tags=28%, list=2
GO_NUCLE	GO_NUCLEOSOMAL_	24	-0.4466	-1.1263	0.3855	0.486815	1	4301	tags=29%, list=7
GO_CELL_	GO_CELL_MATRIX_A	227	-0.2784	-1.048	0.3855	0.526138	1	5834	tags=22%, list=1
GO_DIACY	GO_DIACYLGLYCER	24	-0.3457	-1.0522	0.3855	0.522959	1	10468	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGU	37	-0.3711	-1.0735	0.386	0.513253	1	14474	tags=43%, list=2
GO_POSITI	GO_POSITIVE_REGU	40	-0.3211	-1.0398	0.3868	0.53201	1	5634	tags=23%, list=1
GO_REGUL	GO_REGULATION_OI	77	-0.2867	-1.0339	0.3868	0.536725	1	7567	tags=26%, list=1
GO_PHOSP	GO_PHOSPHATIDYLS	20	-0.3528	-1.0483	0.3869	0.526414	1	8929	tags=35%, list=1
GO_REGUL	GO_REGULATION_OI	74	-0.2981	-1.0665	0.387	0.518808	1	6429	tags=22%, list=1
GO_L_ALPI	GO_L_ALPHA_AMIN	59	-0.3101	-1.0388	0.3871	0.532668	1	9176	tags=25%, list=1
GO_CLATH	GO_CLATHRIN_DEPE	45	-0.3222	-1.0623	0.3872	0.519236	1	11328	tags=33%, list=1
GO_SMOOT	GO_SMOOTH_MUSCI	90	-0.2925	-1.0532	0.3874	0.52272	1	9996	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	16	-0.3872	-1.0689	0.3876	0.516617	1	18948	tags=50%, list=3
GO_PHENO	GO_PHENOL_CONTA	45	-0.2927	-1.0304	0.3881	0.538279	1	7111	tags=22%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	131	-0.3421	-1.0847	0.3886	0.505474	1	6879	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	86	-0.2994	-1.0593	0.3894	0.520088	1	14094	tags=41%, list=2
GO_PROTE	GO_PROTEIN_SUMO	80	-0.3365	-1.0714	0.39	0.515531	1	10731	tags=33%, list=1
GO_RESPO	GO_RESPONSE_TO_A	28	-0.3426	-1.0549	0.3902	0.521561	1	14538	tags=50%, list=2
GO_CELLU	GO_CELLULAR_RESF	72	-0.3046	-1.0459	0.3902	0.528003	1	9450	tags=29%, list=1
GO_ALTER	GO_ALTERNATIVE_M	87	-0.3563	-1.0592	0.3903	0.519741	1	12613	tags=36%, list=2
GO_GLYCO	GO_GLYCOLIPID_BIN	25	-0.3533	-1.0437	0.3904	0.529061	1	2672	tags=20%, list=5
GO_NEGAT	GO_NEGATIVE_REGU	41	-0.3085	-1.0509	0.3912	0.524338	1	6700	tags=27%, list=1
GO_PREPU	GO_PREPULSE_INHII	15	-0.4421	-1.0811	0.3913	0.506494	1	29412	tags=93%, list=5
GO_PCG_PI	GO_PCG_PROTEIN_C	46	-0.3663	-1.0611	0.3916	0.519374	1	7569	tags=37%, list=1
GO_SAGA_	GO_SAGA_TYPE_CON	27	-0.3855	-1.0794	0.3919	0.507536	1	15421	tags=44%, list=2
GO_RESPO	GO_RESPONSE_TO_T	225	-0.2587	-1.044	0.3921	0.529027	1	10263	tags=26%, list=1
GO_MITOC	GO_MITOCHONDRIA	24	-0.3346	-1.0576	0.3922	0.521361	1	3579	tags=17%, list=6
GO_ADENY	GO_ADENYLATE_CY	86	-0.3022	-1.0507	0.3924	0.524108	1	12323	tags=33%, list=2
GO_REGUL	GO_REGULATION_OI	63	-0.2787	-1.021	0.3928	0.545753	1	17921	tags=40%, list=3
GO_PROTE	GO_PROTEIN_CONTA	283	-0.3075	-1.0623	0.393	0.519017	1	9869	tags=28%, list=1
GO_REGUL	GO_REGULATION_OI	25	-0.3359	-1.0437	0.3933	0.529295	1	6429	tags=24%, list=1
GO_PROTE	GO_PROTEIN_DEGLY	26	-0.3512	-1.0524	0.3934	0.523166	1	11143	tags=38%, list=1
GO_POSITI	GO_POSITIVE_REGU	52	-0.2863	-1.0413	0.3934	0.530643	1	12756	tags=29%, list=2
GO_DEMET	GO_DEMETHYLATIO	69	-0.3155	-1.0563	0.3941	0.521312	1	14019	tags=39%, list=2
GO_SPINDI	GO_SPINDLE_LOCAL	49	-0.3683	-1.0608	0.3941	0.518722	1	10477	tags=33%, list=1
GO_EMBRY	GO_EMBRYONIC_SK	97	-0.2916	-1.0505	0.3944	0.524025	1	9208	tags=29%, list=1
GO_MANN	GO_MANNOSYLATIO	33	-0.3468	-1.0817	0.3948	0.507256	1	22092	tags=58%, list=3
GO_APICAI	GO_APICAL_PLASMA	351	-0.2427	-1.0268	0.3949	0.541351	1	9810	tags=23%, list=1
GO_CILIAR	GO_CILIARY_BASAL	140	-0.3152	-1.0682	0.3956	0.517195	1	18128	tags=41%, list=3
GO_POSITI	GO_POSITIVE_REGU	72	-0.2675	-1.0202	0.3957	0.545098	1	8426	tags=22%, list=1
GO_INOSIT	GO_INOSITOL_LIPID	194	-0.2599	-1.0274	0.3958	0.541138	1	7815	tags=23%, list=1
GO_P_BOD	GO_P_BODY_ASSEM	19	-0.3943	-1.0661	0.3968	0.519166	1	13484	tags=53%, list=2

GO_PROTEI	GO_PROTEIN_LOCAL	29	-0.388	-1.0699	0.3976	0.516717	1	9146	tags=34%, list=1
GO_POSITI	GO_POSITIVE_REGUI	25	-0.3375	-1.0486	0.398	0.526572	1	5232	tags=20%, list=9
GO_REGUL	GO_REGULATION_OI	53	-0.3176	-1.0645	0.3981	0.518779	1	10083	tags=34%, list=1
GO_DNA_D	GO_DNA_DEPENDEN	105	-0.3751	-1.0825	0.3984	0.506791	1	9177	tags=29%, list=1
GO_PROTEI	GO_PROTEIN_ACETY	91	-0.3432	-1.0775	0.3985	0.509424	1	15855	tags=42%, list=2
GO_AMMO	GO_AMMONIUM_ION	25	-0.3478	-1.0431	0.3988	0.529223	1	22025	tags=52%, list=3
GO_ACTIN_	GO_ACTIN_FILAMEN	154	-0.2639	-1.0273	0.3989	0.541099	1	9937	tags=28%, list=1
GO_PEPTID	GO_PEPTIDYL_LYSIN	170	-0.3058	-1.0542	0.3992	0.521832	1	12883	tags=32%, list=2
GO_GLYCO	GO_GLYCOPROTEIN_	398	-0.24	-1.0105	0.3996	0.55105	1	13066	tags=28%, list=2
GO_POSITI	GO_POSITIVE_REGUI	23	-0.3531	-1.0646	0.4	0.519163	1	13631	tags=48%, list=2
GO_PROSTA	GO_PROSTATE_GLAN	28	-0.3302	-1.031	0.4	0.538268	1	7643	tags=29%, list=1
GO_CELLU	GO_CELLULAR_CARI	85	-0.2653	-1.0237	0.4008	0.545654	1	20106	tags=46%, list=3
GO_PROTEI	GO_PROTEIN_ACETY	200	-0.2981	-1.063	0.4012	0.518738	1	12883	tags=33%, list=2
GO_REGUL	GO_REGULATION_OI	22	-0.3653	-1.0446	0.4012	0.528847	1	19084	tags=55%, list=3
GO_REGUL	GO_REGULATION_OI	493	-0.249	-1.047	0.4015	0.527171	1	8481	tags=22%, list=1
GO_HISTON	GO_HISTONE_H2A_A	17	-0.4289	-1.0828	0.4016	0.506522	1	23608	tags=71%, list=4
GO_DECIDI	GO_DECIDUALIZATI	25	-0.3236	-1.0307	0.4016	0.537962	1	12819	tags=40%, list=2
GO_ACTIN_	GO_ACTIN_FILAMEN	53	-0.3037	-1.0261	0.4019	0.54188	1	12556	tags=32%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	304	-0.2552	-1.0386	0.4019	0.53275	1	7095	tags=20%, list=1
GO_TRANS	GO_TRANSFERASE_A	202	-0.283	-1.0336	0.4031	0.53645	1	16653	tags=37%, list=2
GO_SUBSTA	GO_SUBSTANTIA_NI	40	-0.3218	-1.0371	0.4031	0.533682	1	12976	tags=38%, list=2
GO_DICARI	GO_DICARBOXYLIC_	39	-0.3076	-1.0258	0.4035	0.542162	1	9176	tags=28%, list=1
GO_INTRA	GO_INTRACILIARY_T	27	-0.4099	-1.0916	0.4035	0.501161	1	8248	tags=30%, list=1
GO_VESICI	GO_VESICLE_LOCAL	222	-0.2741	-1.0361	0.4036	0.535064	1	6170	tags=21%, list=1
GO_LYMPH	GO_LYMPH_VESSEL_	20	-0.3766	-1.0398	0.4038	0.532278	1	13596	tags=50%, list=2
GO_METHY	GO_METHYLATED_H	68	-0.3499	-1.0434	0.4039	0.52922	1	16569	tags=43%, list=2
GO_REGUL	GO_REGULATION_OI	416	-0.231	-1.0174	0.4042	0.546938	1	9049	tags=22%, list=1
GO_MEIOTI	GO_MEIOTIC_CELL_	236	-0.3008	-1.0629	0.4043	0.518633	1	17789	tags=39%, list=3
GO_MEMBI	GO_MEMBRANE_REI	29	-0.327	-1.022	0.4043	0.546633	1	3440	tags=21%, list=6
GO_POSITI	GO_POSITIVE_REGUI	51	-0.2952	-1.0441	0.4054	0.529062	1	9222	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	27	-0.3713	-1.045	0.4062	0.529015	1	15487	tags=44%, list=2
GO_CELL_S	GO_CELL_SUBSTRAT	102	-0.316	-1.0611	0.4071	0.519107	1	8218	tags=29%, list=1
GO_POSITI	GO_POSITIVE_REGUI	31	-0.3128	-1.0214	0.4079	0.54653	1	13311	tags=32%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	58	-0.2685	-1.0205	0.4082	0.545118	1	11823	tags=24%, list=2
GO_POSTS	GO_POSTSYNAPTIC_	21	-0.3394	-1.02	0.409	0.545145	1	11765	tags=33%, list=2
GO_PEPTID	GO_PEPTIDYL_LYSIN	382	-0.2926	-1.0554	0.4093	0.521489	1	13852	tags=34%, list=2
GO_EYE_PI	GO_EYE_PHOTORECI	46	-0.2852	-1.0128	0.4097	0.54953	1	17875	tags=43%, list=3
GO_MRNA_	GO_MRNA_3_UTR_BI	115	-0.2926	-1.0316	0.41	0.537879	1	16716	tags=33%, list=2
GO_REGUL	GO_REGULATION_OI	28	-0.361	-1.0294	0.41	0.539391	1	9858	tags=36%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	22	-0.3323	-1.021	0.4102	0.545484	1	6746	tags=18%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.3835	-1.0525	0.4103	0.523279	1	8740	tags=27%, list=1
GO_POSITI	GO_POSITIVE_REGUI	30	-0.3264	-1.0296	0.4113	0.539235	1	12130	tags=30%, list=2
GO_POSITI	GO_POSITIVE_REGUI	16	-0.3968	-1.0269	0.4115	0.54133	1	17806	tags=56%, list=3
GO_SALIVA	GO_SALIVARY_GLAN	39	-0.2999	-1.0115	0.4132	0.550936	1	19965	tags=46%, list=3
GO_CELLU	GO_CELLULAR_RESI	120	-0.302	-1.0222	0.4136	0.546428	1	10263	tags=32%, list=1
GO_RNA_SI	GO_RNA_SPLICING_	15	-0.4221	-1.0596	0.4138	0.519785	1	1292	tags=13%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	39	-0.298	-1.0278	0.4139	0.540627	1	8882	tags=28%, list=1
GO_POSITI	GO_POSITIVE_REGUI	88	-0.2939	-1.0224	0.4144	0.546456	1	9573	tags=31%, list=1
GO_REGUL	GO_REGULATION_OI	23	-0.3948	-1.0382	0.4145	0.532734	1	14054	tags=43%, list=2
GO_REGUL	GO_REGULATION_OI	28	-0.3566	-1.0326	0.4148	0.536717	1	12474	tags=39%, list=2
GO_REGUL	GO_REGULATION_OI	123	-0.2764	-1.0179	0.415	0.546242	1	4258	tags=19%, list=7
GO_ADIPOS	GO_ADIPOSE_TISSUI	41	-0.3074	-1.0385	0.4154	0.532625	1	13607	tags=37%, list=2
GO_RETINO	GO_RETINOIC_ACID_	20	-0.3438	-1.0193	0.4155	0.54587	1	11709	tags=30%, list=2
GO_DETEC	GO_DETECTION_OF_	28	-0.358	-1.0168	0.4157	0.546974	1	24987	tags=57%, list=4
GO_RIBONI	GO_RIBONUCLEOPRO	226	-0.292	-1.032	0.4159	0.537455	1	14074	tags=33%, list=2
GO_DETEC	GO_DETECTION_OF_	19	-0.3383	-1.0287	0.4159	0.539921	1	19521	tags=42%, list=3
GO_RETRO	GO_RETROGRADE_V	85	-0.3088	-1.038	0.4162	0.532784	1	15233	tags=36%, list=2
GO_RESPOI	GO_RESPONSE_TO_X	31	-0.3187	-1.0079	0.4165	0.553074	1	9146	tags=29%, list=1

GO_KINESI	GO_KINESIN_BINDIN	41	-0.3495	-1.0432	0.4165	0.529386		1	15530	tags=41%, list=2
GO_SYNAP	GO_SYNAPTIC_VESI	101	-0.312	-1.0329	0.4174	0.536762		1	13475	tags=41%, list=2
GO_ACETY	GO_ACETYLGALACT	45	-0.3097	-1.0149	0.4182	0.549006		1	13406	tags=33%, list=2
GO_MICRO	GO_MICROVILLUS_C	25	-0.3787	-1.0337	0.4185	0.536528		1	9629	tags=36%, list=1
GO_N_ACY	GO_N_ACYLTRANSF	98	-0.3045	-1.048	0.4194	0.526365		1	12756	tags=33%, list=2
GO_LONG_	GO_LONG_TERM_ME	34	-0.3255	-1.0066	0.4204	0.553365		1	7944	tags=29%, list=1
GO_CHROM	GO_CHROMOSOME_	91	-0.3513	-1.0688	0.4208	0.516424		1	17523	tags=41%, list=3
GO_STRIAT	GO_STRIATED_MUS	54	-0.2837	-1.0168	0.4209	0.54678		1	11495	tags=33%, list=2
GO_SNARE	GO_SNARE_BINDING	114	-0.2798	-1.0184	0.4211	0.545931		1	8423	tags=28%, list=1
GO_DENDR	GO_DENDRITE_EXTE	35	-0.3461	-1.0213	0.4216	0.546382		1	10105	tags=31%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	60	-0.3593	-1.056	0.4221	0.521041		1	11360	tags=33%, list=1
GO_COLLA	GO_COLLAGEN_ACT	15	-0.4046	-1.0332	0.4225	0.536496		1	8211	tags=40%, list=1
GO_PROLIN	GO_PROLINE_RICH_	17	-0.3649	-1.0338	0.4226	0.536551		1	8997	tags=41%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	34	-0.369	-1.0613	0.4226	0.519898		1	13631	tags=38%, list=2
GO_REGUL	GO_REGULATION_OI	175	-0.2454	-1.0135	0.4233	0.549516		1	8956	tags=23%, list=1
GO_INTRA	GO_INTRACILIARY_	52	-0.3651	-1.065	0.4235	0.519576		1	8248	tags=31%, list=1
GO_PROTEI	GO_PROTEIN_O_LIN	15	-0.3988	-1.0464	0.4235	0.527999		1	22092	tags=60%, list=3
GO_SULFU	GO_SULFUR_COMPO	355	-0.2351	-1.0134	0.4235	0.549245		1	10936	tags=23%, list=1
GO_NEURA	GO_NEURAL_NUCLE	59	-0.3067	-1.0152	0.4237	0.548831		1	14256	tags=37%, list=2
GO_AMINO	GO_AMINOGLYCAN_	115	-0.2796	-0.9996	0.4241	0.560297		1	14148	tags=35%, list=2
GO_CORTI	GO_CORTICAL_ACTI	38	-0.3406	-1.0464	0.4242	0.527758		1	4264	tags=21%, list=7
GO_EMBRY	GO_EMBRYONIC_SK	129	-0.2724	-1.0185	0.4243	0.546093		1	8585	tags=25%, list=1
GO_HYDRO	GO_HYDRO_LYASE_	51	-0.3101	-1.0351	0.4244	0.536199		1	7353	tags=20%, list=1
GO_REGUL	GO_REGULATION_OI	32	-0.3206	-1.0123	0.4245	0.549849		1	16781	tags=38%, list=2
GO_PSEUD	GO_PSEUDOPODIUM	16	-0.3579	-1.0403	0.4248	0.532014		1	8364	tags=38%, list=1
GO_POSITI	GO_POSITIVE_REGU	165	-0.2869	-1.031	0.4248	0.538087		1	19953	tags=39%, list=3
GO_MEIOTI	GO_MEIOTIC_CELL_	177	-0.2928	-1.0232	0.4253	0.54611		1	21000	tags=45%, list=3
GO_CYTOP	GO_CYTOPLASMIC_	34	-0.3643	-1.0208	0.4253	0.545253		1	9370	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	59	-0.3387	-1.0204	0.4258	0.545097		1	14474	tags=37%, list=2
GO_ENDOT	GO_ENDOTHELIAL_	31	-0.3221	-1.0186	0.4259	0.546184		1	7026	tags=29%, list=1
GO_BETA_	GO_BETA_TUBULIN_	37	-0.3148	-1.0081	0.4263	0.552956		1	18442	tags=46%, list=3
GO_COLLA	GO_COLLAGEN_CON	422	-0.3074	-1.0482	0.4265	0.526248		1	14616	tags=40%, list=2
GO_VIRAL_	GO_VIRAL_RNA_GEN	33	-0.336	-1.0343	0.4269	0.536429		1	5779	tags=24%, list=1
GO_ESTABI	GO_ESTABLISHMENT	35	-0.392	-1.0541	0.4269	0.521489		1	10477	tags=34%, list=1
GO_L_AMII	GO_L_AMINO_ACID_	70	-0.2916	-1.0109	0.4271	0.550912		1	15413	tags=36%, list=2
GO_SECON	GO_SECOND_MESSE	427	-0.2542	-1.0107	0.4272	0.550933		1	11534	tags=32%, list=2
GO_NUCLE	GO_NUCLEAR_RECE	54	-0.3116	-1.0219	0.4272	0.546499		1	15151	tags=43%, list=2
GO_PROTEI	GO_PROTEIN_HYDR	25	-0.3587	-1.0328	0.4274	0.536641		1	12094	tags=32%, list=2
GO_GAMM	GO_GAMMA_TUBULI	28	-0.3395	-1.0509	0.4277	0.524135		1	5942	tags=21%, list=1
GO_ASYMM	GO_ASYMMETRIC_C	20	-0.3604	-1.0292	0.428	0.539343		1	18797	tags=60%, list=3
GO_ACROS	GO_ACROSOMAL_VE	111	-0.2445	-1.0092	0.4286	0.552939		1	10889	tags=24%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	32	-0.3303	-1.0214	0.4288	0.546695		1	6552	tags=25%, list=1
GO_PHOSPI	GO_PHOSPHATASE_	15	-0.388	-1.0333	0.4294	0.536571		1	10299	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	143	-0.2759	-1.0032	0.4298	0.558476		1	10853	tags=29%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	43	-0.3319	-1.035	0.4302	0.536007		1	6062	tags=26%, list=1
GO_REGUL	GO_REGULATION_OI	89	-0.3143	-1.0264	0.4303	0.541621		1	15493	tags=34%, list=2
GO_LYMPH	GO_LYMPHANGIOGE	15	-0.4154	-1.0352	0.4303	0.536356		1	13596	tags=53%, list=2
GO_ASTRO	GO_ASTROCYTE_PR	18	-0.3991	-1.0392	0.4306	0.532245		1	18447	tags=50%, list=3
GO_GOLGI_	GO_GOLGI_ORGANIZ	148	-0.2693	-1.0007	0.431	0.559692		1	13249	tags=30%, list=2
GO_REGUL	GO_REGULATION_OI	155	-0.3104	-1.0197	0.4316	0.545481		1	12743	tags=30%, list=2
GO_PROTEI	GO_PROTEIN_ACYLA	244	-0.2711	-1.0001	0.4316	0.55991		1	12883	tags=31%, list=2
GO_ANATO	GO_ANATOMICAL_S	223	-0.2416	-1.0029	0.4322	0.558208		1	11099	tags=25%, list=1
GO_POSITI	GO_POSITIVE_REGU	31	-0.3252	-1.0224	0.4324	0.546735		1	4975	tags=26%, list=9
GO_NEGAT	GO_NEGATIVE_REGU	58	-0.2772	-1.0082	0.4327	0.552993		1	17923	tags=41%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	145	-0.2731	-1.0163	0.4329	0.547323		1	12974	tags=36%, list=2
GO_TRANS	GO_TRANSEPITHELI	26	-0.346	-1.0114	0.4333	0.55079		1	17128	tags=50%, list=2
GO_PROTE	GO_PROTEOGLYCAN	88	-0.2938	-1.0032	0.4333	0.558213		1	14654	tags=38%, list=2
GO_THYRO	GO_THYROID_HORM	26	-0.3245	-1.0072	0.4337	0.553088		1	12434	tags=42%, list=2

GO_BASAL_	GO_BASAL_PART_OF	68	-0.2913	-1.0141	0.4337	0.549427	1	9810	tags=26%, list=1
GO_TELOM	GO_TELOMERASE_R	19	-0.4421	-1.0656	0.4339	0.519162	1	27032	tags=79%, list=4
GO_POSITI	GO_POSITIVE_REGU	17	-0.3674	-1.0003	0.4344	0.560113	1	7991	tags=24%, list=1
GO_REGUL	GO_REGULATION_OF	166	-0.2444	-0.9986	0.4348	0.560488	1	8426	tags=22%, list=1
GO_FEMAL	GO_FEMALE_MEIOTI	28	-0.363	-1.0213	0.4349	0.545876	1	20799	tags=50%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	384	-0.2343	-0.9937	0.4354	0.565607	1	15704	tags=33%, list=2
GO_CHOND	GO_CHONDROITIN_S	31	-0.3595	-1.0228	0.436	0.546354	1	19019	tags=52%, list=3
GO_LOW_D	GO_LOW_DENSITY_L	16	-0.3761	-1.0173	0.4361	0.546728	1	6746	tags=31%, list=1
GO_COPUL	GO_COPULATION	20	-0.3411	-1.013	0.4366	0.54954	1	6239	tags=25%, list=1
GO_RAB_G	GO_RAB_GTPASE_BI	168	-0.2529	-0.9805	0.4371	0.578323	1	7878	tags=23%, list=1
GO_NUCLE	GO_NUCLEAR_PERIP	130	-0.2987	-1.018	0.4377	0.546347	1	12268	tags=36%, list=2
GO_GLIAL_	GO_GLIAL_CELL_PR	50	-0.283	-1.0074	0.4381	0.553251	1	12629	tags=36%, list=2
GO_RENAL	GO_RENAL_VESICLE	20	-0.3613	-0.9919	0.4381	0.566875	1	5634	tags=30%, list=1
GO_PHOSP	GO_PHOSPHATIDYLI	152	-0.2615	-0.9992	0.4391	0.560372	1	7771	tags=24%, list=1
GO_TELOM	GO_TELOMERE_CAP	38	-0.3469	-1.0346	0.4392	0.536355	1	6594	tags=29%, list=1
GO_FOREB	GO_FOREBRAIN_REG	23	-0.3469	-1.0169	0.4392	0.547212	1	10299	tags=35%, list=1
GO_REGUL	GO_REGULATION_OF	18	-0.4262	-1.0423	0.4393	0.529478	1	6091	tags=33%, list=1
GO_EXTRIN	GO_EXTRINSIC_COM	168	-0.259	-1.0141	0.4393	0.549268	1	9326	tags=26%, list=1
GO_REGUL	GO_REGULATION_OF	106	-0.2923	-1.0111	0.4401	0.55077	1	9810	tags=27%, list=1
GO_OXIDO	GO_OXIDOREDUCTA	45	-0.2984	-1.0136	0.4401	0.549591	1	3386	tags=13%, list=6
GO_NEGAT	GO_NEGATIVE_REGU	27	-0.343	-0.9986	0.4406	0.560223	1	9880	tags=37%, list=1
GO_RESPO	GO_RESPONSE_TO_P	439	-0.2258	-0.9802	0.4407	0.578222	1	9208	tags=23%, list=1
GO_MALE_	GO_MALE_SEX_DIFF	161	-0.2456	-1.007	0.4412	0.553224	1	11808	tags=29%, list=2
GO_GENET	GO_GENETIC_IMPRIN	26	-0.3511	-1.0215	0.4419	0.54681	1	16435	tags=46%, list=2
GO_NUCLE	GO_NUCLEAR_MATR	108	-0.3016	-1.0187	0.4427	0.546365	1	12268	tags=36%, list=2
GO_POSITI	GO_POSITIVE_REGU	33	-0.3697	-1.0279	0.4429	0.540811	1	16562	tags=45%, list=2
GO_PRC1_C	GO_PRC1_COMPLEX	15	-0.3915	-1.038	0.4436	0.532656	1	5223	tags=33%, list=9
GO_CATEC	GO_CATECHOLAMIN	52	-0.2733	-0.9881	0.4442	0.571663	1	8976	tags=23%, list=1
GO_CLATH	GO_CLATHRIN_COAT	16	-0.3456	-1.0146	0.4449	0.549119	1	11018	tags=44%, list=1
GO_CELLU	GO_CELLULAR_AMI	121	-0.2628	-1.0083	0.4449	0.553194	1	7085	tags=18%, list=1
GO_RNA_D	GO_RNA_DESTABILI	34	-0.3508	-1.021	0.4451	0.545205	1	5380	tags=32%, list=9
GO_EPITHE	GO_EPITHELIAL_STR	26	-0.319	-0.998	0.4456	0.560739	1	17625	tags=35%, list=3
GO_VESICL	GO_VESICLE_CYTOS	72	-0.3063	-1.0207	0.4458	0.545107	1	6170	tags=22%, list=1
GO_AMINO	GO_AMINOGLYCAN_	170	-0.2547	-0.9744	0.4458	0.580037	1	14148	tags=35%, list=2
GO_ENDOP	GO_ENDOPLASMIC_I	299	-0.2673	-0.9799	0.446	0.57789	1	13850	tags=36%, list=2
GO_POSITI	GO_POSITIVE_REGU	23	-0.3405	-0.9921	0.4462	0.566937	1	8836	tags=26%, list=1
GO_REGUL	GO_REGULATION_OF	117	-0.264	-1.0088	0.4463	0.553122	1	9901	tags=28%, list=1
GO_N_ACE	GO_N_ACETYLTRAN	82	-0.3091	-1.0213	0.4464	0.546126	1	9645	tags=28%, list=1
GO_METAL	GO_METALLOCARBO	29	-0.3173	-0.9798	0.4472	0.577902	1	25053	tags=66%, list=4
GO_INSULI	GO_INSULIN_LIKE_G	23	-0.3561	-1.0126	0.4478	0.549617	1	22384	tags=61%, list=3
GO_BRANC	GO_BRANCHING_INV	23	-0.3405	-0.9992	0.4479	0.560595	1	9996	tags=35%, list=1
GO_RESPO	GO_RESPONSE_TO_H	19	-0.3592	-0.9946	0.4483	0.564362	1	18609	tags=53%, list=3
GO_MYOBL	GO_MYOBLAST_PRO	27	-0.322	-0.9978	0.4499	0.560812	1	12950	tags=41%, list=2
GO_REGUL	GO_REGULATION_OF	39	-0.321	-0.999	0.4509	0.560185	1	8426	tags=31%, list=1
GO_POLYS	GO_POLYSACCHARI	108	-0.2579	-0.9922	0.4509	0.56753	1	14094	tags=35%, list=2
GO_INTRIN	GO_INTRINSIC_COM	47	-0.3314	-1.0075	0.4512	0.553432	1	14389	tags=43%, list=2
GO_FAT_CI	GO_FAT_CELL_DIFF	229	-0.2348	-0.9852	0.4513	0.574185	1	11011	tags=27%, list=1
GO_ACYL_	GO_ACYL_COA_BIND	22	-0.3454	-0.9858	0.4517	0.573746	1	1159	tags=14%, list=2
GO_POSITI	GO_POSITIVE_REGU	297	-0.2701	-1.0086	0.4526	0.553094	1	18914	tags=41%, list=3
GO_POSITI	GO_POSITIVE_REGU	15	-0.3704	-0.9968	0.4527	0.562349	1	7026	tags=40%, list=1
GO_POLYS	GO_POLYSACCHARI	25	-0.3171	-0.9911	0.4533	0.567768	1	14094	tags=44%, list=2
GO_REGUL	GO_REGULATION_OF	98	-0.3193	-1.0232	0.4535	0.545887	1	7154	tags=28%, list=1
GO_NEUTR	GO_NEUTROPHIL_HO	16	-0.3863	-1.0139	0.4537	0.549366	1	359	tags=13%, list=1
GO_CILIAR	GO_CILIARY_BASAL_	94	-0.3385	-1.0212	0.4538	0.545612	1	8595	tags=26%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	20	-0.3388	-1.007	0.454	0.552967	1	9127	tags=40%, list=1
GO_CALCIU	GO_CALCIUM_ACTIV	25	-0.3375	-1.0031	0.454	0.558008	1	11874	tags=32%, list=2
GO_CIRCA	GO_CIRCADIAN_REG	64	-0.2885	-0.9921	0.454	0.567094	1	11334	tags=38%, list=1
GO_HISTO	GO_HISTONE_BINDI	230	-0.3131	-1.0191	0.4549	0.54595	1	6879	tags=25%, list=1

GO_HEPAT	GO_HEPATICOBILIA	144	-0.251	-0.9996	0.4552	0.560552	1	11335	tags=28%, list=1
GO_PROTE	GO_PROTEIN_SERIN	75	-0.2739	-1.0074	0.4554	0.55298	1	11153	tags=32%, list=1
GO_REGUL	GO_REGULATION_OI	27	-0.3783	-1.0161	0.4554	0.547448	1	7690	tags=33%, list=1
GO_COPII_	GO_COPII_VESICLE_	15	-0.3908	-0.9954	0.4554	0.563267	1	11751	tags=33%, list=2
GO_TERMI	GO_TERMINAL_BOU	56	-0.3232	-1.0057	0.4555	0.554565	1	16853	tags=46%, list=2
GO_AMINO	GO_AMINO_ACID_IM	44	-0.3109	-0.9926	0.456	0.566997	1	8909	tags=27%, list=1
GO_POSITI	GO_POSITIVE_REGU	51	-0.3078	-0.9985	0.457	0.560169	1	8726	tags=27%, list=1
GO_OSTEO	GO_OSTEOBLAST_DI	19	-0.3394	-1.0143	0.4571	0.549449	1	16015	tags=53%, list=2
GO_SPROU	GO_SPROUTING_AN	186	-0.2461	-0.9699	0.4572	0.583735	1	9208	tags=20%, list=1
GO_ALPHA	GO_ALPHA_AMINO_	190	-0.2473	-0.996	0.4575	0.562783	1	10956	tags=24%, list=1
GO_POSITI	GO_POSITIVE_REGU	23	-0.3511	-1.0013	0.4586	0.559487	1	9901	tags=39%, list=1
GO_GUANY	GO_GUANYL_NUCLE	210	-0.2508	-0.9815	0.4587	0.577155	1	7772	tags=20%, list=1
GO_INTER	GO_INTERCELLULA	70	-0.278	-0.9803	0.4588	0.578359	1	11877	tags=29%, list=2
GO_SEMAP	GO_SEMAPHORIN_PI	40	-0.2952	-1.0028	0.4588	0.558039	1	7998	tags=30%, list=1
GO_REGEN	GO_REGENERATION	196	-0.2437	-0.9885	0.4589	0.571241	1	8707	tags=23%, list=1
GO_GAS_T	GO_GAS_TRANSPOR	20	-0.3644	-1.0003	0.4592	0.559857	1	4675	tags=20%, list=8
GO_LOCAL	GO_LOCALIZATION_	95	-0.2765	-0.9866	0.4597	0.573175	1	8836	tags=29%, list=1
GO_FERRO	GO_FERROUS_IRON_	26	-0.3147	-0.9964	0.4602	0.562729	1	13270	tags=35%, list=2
GO_REGUL	GO_REGULATION_OI	63	-0.3285	-1.0008	0.4605	0.559896	1	15678	tags=46%, list=2
GO_HYPER	GO_HYPEROSMOTIC	28	-0.3042	-0.9992	0.4611	0.560141	1	10608	tags=32%, list=1
GO_CALCI	GO_CALCIUM_ION_R	23	-0.3931	-1.0091	0.4612	0.552809	1	19869	tags=52%, list=3
GO_BLAST	GO_BLASTOCYST_GI	20	-0.3752	-1.0016	0.4612	0.559311	1	12950	tags=35%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	49	-0.2873	-1.0132	0.4617	0.549439	1	13913	tags=31%, list=2
GO_PHOSP	GO_PHOSPHOLIPID_	263	-0.2338	-0.9763	0.4618	0.579516	1	9956	tags=24%, list=1
GO_ENTER	GO_ENTERIC_NERVO	15	-0.4077	-1.0037	0.4627	0.557918	1	13955	tags=47%, list=2
GO_CELLU	GO_CELLULAR_HYP	15	-0.3567	-0.9841	0.4644	0.57467	1	13811	tags=40%, list=2
GO_BLOOD	GO_BLOOD_VESSEL_	183	-0.2417	-0.9807	0.4647	0.578203	1	11823	tags=26%, list=2
GO_DNA_M	GO_DNA_METHYLAT	94	-0.2895	-0.9908	0.4656	0.568078	1	16537	tags=35%, list=2
GO_PHOSP	GO_PHOSPHATIDYLI	16	-0.3741	-1.0086	0.466	0.552981	1	8398	tags=38%, list=1
GO_PHOSP	GO_PHOSPHATIDYLI	27	-0.3189	-0.9873	0.4668	0.572536	1	2684	tags=19%, list=5
GO_CELLU	GO_CELLULAR_RESI	22	-0.3296	-0.9801	0.467	0.578071	1	5278	tags=18%, list=9
GO_RESPO	GO_RESPONSE_TO_K	199	-0.235	-0.9852	0.4671	0.574424	1	5228	tags=16%, list=9
GO_RAC_P	GO_RAC_PROTEIN_S	37	-0.3051	-0.9958	0.4678	0.562919	1	8997	tags=35%, list=1
GO_MITOT	GO_MITOTIC_SPIND	127	-0.2996	-0.9737	0.468	0.580185	1	11553	tags=27%, list=2
GO_SOLUT	GO_SOLUTE_ANION_	28	-0.3251	-0.9962	0.4692	0.562806	1	16343	tags=39%, list=2
GO_PROXI	GO_PROXIMAL_DIST	33	-0.3335	-0.9792	0.4697	0.578378	1	8254	tags=30%, list=1
GO_REGUL	GO_REGULATION_OI	23	-0.3706	-1.0012	0.4701	0.559424	1	1712	tags=17%, list=3
GO_CHAPE	GO_CHAPERONE_CO	25	-0.3486	-0.9725	0.4701	0.580799	1	18833	tags=48%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	34	-0.295	-0.9835	0.4702	0.575288	1	13129	tags=24%, list=2
GO_CELLU	GO_CELLULAR_MON	113	-0.2581	-0.9776	0.4704	0.578569	1	10114	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	39	-0.2993	-0.9719	0.4706	0.581455	1	16193	tags=38%, list=2
GO_AMYL	GO_AMYLOID_PREC	18	-0.3321	-0.9933	0.4707	0.566186	1	5855	tags=22%, list=1
GO_METHY	GO_METHYLATION	333	-0.2727	-0.9899	0.4709	0.569436	1	16653	tags=37%, list=2
GO_PRIMA	GO_PRIMARY_ALCO	94	-0.2588	-0.9824	0.4712	0.57637	1	15827	tags=33%, list=2
GO_EXTRA	GO_EXTRACELLULA	387	-0.2924	-0.9777	0.4715	0.578894	1	10359	tags=31%, list=1
GO_SPHIN	GO_SPHINGOID_MET	18	-0.3509	-0.9874	0.4717	0.572626	1	5845	tags=22%, list=1
GO_REGUL	GO_REGULATION_OI	42	-0.3205	-0.9781	0.4717	0.578835	1	14502	tags=45%, list=2
GO_REGUL	GO_REGULATION_OI	56	-0.2888	-0.9843	0.4734	0.574968	1	6438	tags=23%, list=1
GO_ENDOP	GO_ENDOPLASMIC_	120	-0.2601	-0.9831	0.4734	0.575576	1	7176	tags=20%, list=1
GO_PRERIE	GO_PRERIBOSOME	72	-0.3383	-0.9727	0.4739	0.580695	1	3469	tags=18%, list=6
GO_RNA_P	GO_RNA_POLYADEN	42	-0.3453	-0.9897	0.4744	0.569443	1	7870	tags=29%, list=1
GO_POSITI	GO_POSITIVE_REGU	65	-0.2862	-0.9873	0.4749	0.572333	1	9647	tags=20%, list=1
GO_HOMOI	GO_HOMOLOGOUS_	42	-0.3034	-0.9686	0.475	0.584156	1	17563	tags=38%, list=3
GO_SEROT	GO_SEROTONIN_TRA	21	-0.342	-0.9692	0.4752	0.584088	1	9389	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGU	36	-0.3125	-0.983	0.4754	0.575474	1	6753	tags=19%, list=1
GO_MITOT	GO_MITOTIC_CYTOK	71	-0.3108	-0.984	0.4759	0.574587	1	8593	tags=24%, list=1
GO_RESPO	GO_RESPONSE_TO_E	45	-0.298	-0.9753	0.476	0.579757	1	8211	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	25	-0.367	-1.0113	0.4762	0.550675	1	3475	tags=20%, list=6

GO_DETER	GO_DETERMINATION	16	-0.3646	-0.9912	0.4765	0.567865	1	18070	tags=56%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	248	-0.2486	-0.9791	0.4771	0.578265	1	6622	tags=20%, list=1
GO_G_PRO	GO_G_PROTEIN_COU	241	-0.2542	-0.9766	0.4776	0.579189	1	20489	tags=49%, list=3
GO_REGUL	GO_REGULATION_O	24	-0.3614	-0.9922	0.4782	0.567305	1	10105	tags=33%, list=1
GO_REGUL	GO_REGULATION_O	16	-0.4408	-1.0402	0.4782	0.531991	1	5865	tags=31%, list=1
GO_PROTE	GO_PROTEIN_HETER	22	-0.3337	-0.974	0.4782	0.580157	1	8456	tags=32%, list=1
GO_MRNA_	GO_MRNA_5_UTR_B	26	-0.3491	-0.9792	0.4784	0.578617	1	6459	tags=23%, list=1
GO_G_PRO	GO_G_PROTEIN_COU	15	-0.3891	-1.0025	0.4787	0.558234	1	16646	tags=53%, list=2
GO_PHOSP	GO_PHOSPHATIDYL	18	-0.3394	-0.9714	0.481	0.582033	1	8929	tags=33%, list=1
GO_MECH	GO_MECHANOSENS	15	-0.3733	-0.979	0.4813	0.57806	1	20089	tags=67%, list=3
GO_TRANS	GO_TRANSCRIPTION	481	-0.2512	-0.9768	0.4816	0.579113	1	8870	tags=23%, list=1
GO_GLUCO	GO_GLUCOSAMINE_	24	-0.322	-0.9753	0.4818	0.579253	1	8437	tags=29%, list=1
GO_REGUL	GO_REGULATION_O	128	-0.2377	-0.9801	0.4826	0.577916	1	7458	tags=18%, list=1
GO_PHOSP	GO_PHOSPHATIDYLI	179	-0.2399	-0.9681	0.4826	0.584137	1	9535	tags=24%, list=1
GO_COVAL	GO_COVALENT_CHR	460	-0.2735	-0.9822	0.4828	0.576341	1	12756	tags=31%, list=2
GO_POSIT	GO_POSITIVE_REGU	20	-0.3409	-0.9774	0.4831	0.578622	1	17171	tags=40%, list=2
GO_REGUL	GO_REGULATION_O	40	-0.2889	-0.9863	0.4832	0.57349	1	7461	tags=23%, list=1
GO_ADAPT	GO_ADAPTATION_O	21	-0.3192	-0.9746	0.4833	0.579973	1	6745	tags=29%, list=1
GO_M_BAN	GO_M_BAND	25	-0.3171	-0.9698	0.4837	0.583674	1	6954	tags=24%, list=1
GO_MANN	GO_MANNOSIDASE_	15	-0.3702	-0.9669	0.4839	0.584675	1	6183	tags=33%, list=1
GO_PROTE	GO_PROTEIN_DEPHO	316	-0.2311	-0.9678	0.4859	0.583867	1	10136	tags=25%, list=1
GO_REGUL	GO_REGULATION_O	211	-0.2459	-0.9575	0.4862	0.593026	1	11638	tags=29%, list=2
GO_ACETY	GO_ACETYL_COA_B	16	-0.3671	-0.9753	0.4866	0.579487	1	15930	tags=38%, list=2
GO_START	GO_STARTLE_RESPO	27	-0.3446	-0.9756	0.4868	0.579516	1	18325	tags=48%, list=3
GO_RNA_B	GO_RNA_BINDING_I	259	-0.2715	-1.0016	0.4871	0.559586	1	23672	tags=33%, list=4
GO_UDP_N	GO_UDP_N_ACETYL	16	-0.3716	-0.974	0.4873	0.58036	1	10761	tags=44%, list=1
GO_S_ADE	GO_S_ADENOSYLME	138	-0.2792	-0.9609	0.4875	0.589368	1	14041	tags=33%, list=2
GO_NEURO	GO_NEUROTRANSMI	46	-0.3362	-0.9858	0.4876	0.573929	1	6136	tags=28%, list=1
GO_PROTE	GO_PROTEIN_SERIN	422	-0.241	-0.9662	0.4876	0.585282	1	8398	tags=23%, list=1
GO_MUCO	GO_MUCOPOLYSAC	111	-0.2786	-0.9752	0.4881	0.579209	1	13893	tags=35%, list=2
GO_METHY	GO_METHYL_CPG_B	24	-0.3462	-0.9817	0.4884	0.576921	1	2333	tags=13%, list=4
GO_MITOC	GO_MITOCHONDRIA	81	-0.2581	-0.9547	0.4885	0.595894	1	10643	tags=26%, list=1
GO_TRANS	GO_TRANSITION_ME	37	-0.3042	-0.9628	0.4886	0.588309	1	16073	tags=46%, list=2
GO_REGUL	GO_REGULATION_O	30	-0.3129	-0.9614	0.4892	0.589118	1	8024	tags=27%, list=1
GO_HETER	GO_HETEROTRIMER	33	-0.3295	-0.9845	0.4897	0.575133	1	13655	tags=45%, list=2
GO_PHASIC	GO_PHASIC_SMOOT	21	-0.338	-0.9692	0.4906	0.583958	1	15363	tags=43%, list=2
GO_RHO_G	GO_RHO_GUANYL_N	60	-0.2955	-0.9732	0.4908	0.580451	1	10477	tags=35%, list=1
GO_POSIT	GO_POSITIVE_REGU	231	-0.2497	-0.9381	0.4909	0.610773	1	10943	tags=28%, list=1
GO_NEURO	GO_NEUROEPITHELI	54	-0.2981	-0.969	0.4912	0.583978	1	16442	tags=41%, list=2
GO_CELLU	GO_CELLULAR_RES	220	-0.2317	-0.9597	0.4917	0.590966	1	10177	tags=24%, list=1
GO_POSIT	GO_POSITIVE_REGU	27	-0.3207	-0.9602	0.4919	0.590386	1	21115	tags=44%, list=3
GO_MEIOS	GO_MEIOSIS_I_CELL	112	-0.282	-0.9559	0.4935	0.59476	1	6091	tags=18%, list=1
GO_MEMB	GO_MEMBRANE_CO	91	-0.2698	-0.9615	0.494	0.5892	1	12519	tags=32%, list=2
GO_PROTE	GO_PROTEIN_KINAS	52	-0.2645	-0.9842	0.4945	0.574893	1	5779	tags=21%, list=1
GO_INTRIN	GO_INTRINSIC_COM	18	-0.3602	-0.9695	0.4949	0.584002	1	21094	tags=61%, list=3
GO_G_PRO	GO_G_PROTEIN_BET	19	-0.3652	-0.9776	0.495	0.578845	1	13655	tags=53%, list=2
GO_GOLGI_	GO_GOLGI_VESICLE_	365	-0.249	-0.9761	0.495	0.579154	1	13249	tags=30%, list=2
GO_ANGIO	GO_ANGIOGENESIS_	30	-0.3256	-0.9545	0.495	0.595944	1	4750	tags=23%, list=8
GO_MICRO	GO_MICROTUBULE_	29	-0.3291	-0.9571	0.4951	0.593331	1	7579	tags=24%, list=1
GO_REGUL	GO_REGULATION_O	61	-0.2819	-0.9778	0.4952	0.579066	1	12883	tags=31%, list=2
GO_CAJAL_	GO_CAJAL_BODY	75	-0.3136	-0.9787	0.4952	0.578094	1	19578	tags=60%, list=3
GO_REGUL	GO_REGULATION_O	58	-0.2791	-0.9673	0.496	0.584546	1	6746	tags=21%, list=1
GO_REGUL	GO_REGULATION_O	66	-0.3313	-0.9623	0.4961	0.588592	1	17523	tags=41%, list=3
GO_REGUL	GO_REGULATION_O	80	-0.263	-0.9626	0.4969	0.588337	1	16570	tags=36%, list=2
GO_L_AMI	GO_L_AMINO_ACID_	57	-0.2865	-0.9699	0.497	0.58395	1	13965	tags=32%, list=2
GO_ARACH	GO_ARACHIDONIC_	31	-0.294	-0.973	0.498	0.580568	1	16012	tags=39%, list=2
GO_LENS_	GO_LENS_FIBER_CE	35	-0.2952	-0.9787	0.498	0.578299	1	15683	tags=43%, list=2
GO_ACTIV	GO_ACTIVATION_OF	38	-0.299	-0.967	0.499	0.584785	1	15488	tags=42%, list=2

GO_REGUL	GO_REGULATION_OI	120	-0.267	-0.9615	0.501	0.589441	1	14094	tags=34%, list=2
GO_CLATH	GO_CLATHRIN_COA	45	-0.2838	-0.9657	0.501	0.585827	1	12519	tags=33%, list=2
GO_SYNAP	GO_SYNAPTIC_VESI	20	-0.384	-0.9762	0.501	0.579307	1	16005	tags=50%, list=2
GO_MAMM	GO_MAMMARY_GLA	32	-0.2858	-0.9573	0.501	0.593102	1	8067	tags=31%, list=1
GO_NUCLE	GO_NUCLEOSOME_C	108	-0.318	-0.9758	0.5019	0.579555	1	7540	tags=24%, list=1
GO_OUTER	GO_OUTER_DYNEIN_	17	-0.3515	-0.952	0.5019	0.598357	1	22421	tags=59%, list=3
GO_POSITI	GO_POSITIVE_REGUI	201	-0.2483	-0.9773	0.502	0.578554	1	15413	tags=39%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	15	-0.3609	-0.9618	0.5029	0.58926	1	2895	tags=20%, list=5
GO_PROTEI	GO_PROTEIN_TARGE	40	-0.295	-0.9291	0.5029	0.620245	1	15946	tags=38%, list=2
GO_WW_D	GO_WW_DOMAIN_BI	30	-0.306	-0.9634	0.503	0.587801	1	13846	tags=40%, list=2
GO_OXYGE	GO_OXYGEN_TRANS	15	-0.3731	-0.9486	0.503	0.6017	1	4675	tags=20%, list=8
GO_MITOTI	GO_MITOTIC_DNA_II	104	-0.2842	-0.9414	0.503	0.609471	1	8824	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	18	-0.333	-0.964	0.5039	0.587779	1	5959	tags=22%, list=1
GO_PHENO	GO_PHENOL_CONTA	107	-0.2394	-0.9653	0.504	0.586045	1	12434	tags=29%, list=2
GO_RNA_PI	GO_RNA_PHOSPHOD	80	-0.2714	-0.9583	0.5047	0.592533	1	5896	tags=16%, list=1
GO_REGUL	GO_REGULATION_OI	17	-0.389	-0.9684	0.5048	0.584166	1	3895	tags=24%, list=7
GO_FIBROI	GO_FIBROBLAST_MI	44	-0.2897	-0.951	0.5048	0.598222	1	14514	tags=41%, list=2
GO_POSITI	GO_POSITIVE_REGUI	24	-0.3243	-0.9541	0.5048	0.596244	1	4975	tags=29%, list=9
GO_PHOSPI	GO_PHOSPHOLIPASE	100	-0.2478	-0.964	0.5049	0.58761	1	9182	tags=26%, list=1
GO_POSITI	GO_POSITIVE_REGUI	15	-0.4302	-0.9843	0.5058	0.57514	1	26594	tags=73%, list=4
GO_POSITI	GO_POSITIVE_REGUI	22	-0.325	-0.9645	0.5059	0.587088	1	10511	tags=36%, list=1
GO_SUMO_	GO_SUMO_TRANSFE	19	-0.3346	-0.9553	0.5067	0.595401	1	7426	tags=21%, list=1
GO_RAB_G	GO_RAB_GUANYL_N	32	-0.3104	-0.9269	0.5068	0.621654	1	7749	tags=22%, list=1
GO_SEGME	GO_SEGMENT_SPECI	16	-0.3411	-0.9549	0.5068	0.595678	1	5536	tags=25%, list=9
GO_TELOM	GO_TELOMERIC_DN	35	-0.3465	-0.9664	0.5075	0.58528	1	9146	tags=29%, list=1
GO_INTRA	GO_INTRACILIARY_	40	-0.3452	-0.9678	0.508	0.584136	1	18904	tags=52%, list=3
GO_ACETY	GO_ACETYLCHOLINI	22	-0.3321	-0.9412	0.5082	0.609022	1	22111	tags=64%, list=3
GO_REGUL	GO_REGULATION_OI	113	-0.3023	-0.9378	0.5095	0.610821	1	12743	tags=29%, list=2
GO_ESTABI	GO_ESTABLISHMEN	36	-0.3389	-0.9578	0.5097	0.592863	1	10477	tags=31%, list=1
GO_REGUL	GO_REGULATION_OI	27	-0.3065	-0.9395	0.5104	0.60924	1	6054	tags=26%, list=1
GO_STRIAT	GO_STRIATUM_DEVI	18	-0.3531	-0.9735	0.5118	0.580202	1	22617	tags=50%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	44	-0.3654	-0.9634	0.512	0.588062	1	11360	tags=36%, list=1
GO_DENSE	GO_DENSE_CORE_GI	27	-0.3602	-0.9524	0.5125	0.598107	1	13742	tags=44%, list=2
GO_ESTABI	GO_ESTABLISHMEN	417	-0.2437	-0.9414	0.5132	0.609741	1	6630	tags=20%, list=1
GO_SENSOI	GO_SENSORY_PERCI	166	-0.28	-0.9703	0.5139	0.583547	1	16160	tags=37%, list=2
GO_MEMBI	GO_MEMBRANE_REI	17	-0.3426	-0.9419	0.5144	0.610456	1	2848	tags=18%, list=5
GO_NUCLE	GO_NUCLEAR_OUTE	27	-0.292	-0.9519	0.5145	0.598271	1	18929	tags=37%, list=3
GO_CRISTA	GO_CRISTAE_FORMA	18	-0.3279	-0.9454	0.515	0.606257	1	4162	tags=22%, list=7
GO_GLYCII	GO_GLYCINE_METAI	15	-0.3602	-0.9537	0.5154	0.596761	1	16964	tags=47%, list=2
GO_RETRO	GO_RETROMER_CON	20	-0.3562	-0.9413	0.5154	0.609114	1	6486	tags=25%, list=1
GO_POSITI	GO_POSITIVE_REGUI	389	-0.2512	-0.9569	0.5158	0.59329	1	11153	tags=25%, list=1
GO_NUCLE	GO_NUCLEAR_PORE	83	-0.2943	-0.9297	0.5159	0.620196	1	10044	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	15	-0.3591	-0.9681	0.5161	0.584352	1	17557	tags=47%, list=3
GO_PRERIE	GO_PRERIBOSOME_I	23	-0.3784	-0.9399	0.5163	0.609744	1	3469	tags=22%, list=6
GO_BILE_A	GO_BILE_ACID_MET	48	-0.2665	-0.951	0.5164	0.598494	1	9049	tags=23%, list=1
GO_REGUL	GO_REGULATION_OI	36	-0.3301	-0.9688	0.5172	0.584024	1	13742	tags=42%, list=2
GO_HORMO	GO_HORMONE_MET	215	-0.2261	-0.9632	0.5172	0.587771	1	15827	tags=32%, list=2
GO_MIRNA	GO_MIRNA_METABO	26	-0.3486	-0.9579	0.5174	0.592913	1	5380	tags=23%, list=9
GO_NEGAT	GO_NEGATIVE_REGU	38	-0.2849	-0.9738	0.5176	0.580251	1	8882	tags=26%, list=1
GO_NEURO	GO_NEUROTRANSMI	27	-0.3661	-0.9656	0.5176	0.585714	1	10511	tags=41%, list=1
GO_MORPH	GO_MORPHOGENESI	55	-0.2836	-0.9511	0.518	0.598759	1	4326	tags=20%, list=7
GO_ADENY	GO_ADENYLATE_CY	125	-0.2666	-0.951	0.5181	0.598592	1	20038	tags=54%, list=3
GO_PRONU	GO_PRONUCLEUS	15	-0.4154	-0.9613	0.5198	0.58893	1	2606	tags=20%, list=4
GO_HETER	GO_HETEROCHROM	49	-0.3121	-0.9638	0.522	0.587532	1	6893	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	25	-0.3118	-0.9453	0.5224	0.606108	1	17429	tags=44%, list=3
GO_CHROM	GO_CHROMATIN_AS	143	-0.2933	-0.9243	0.5242	0.62424	1	4155	tags=19%, list=7
GO_NEGAT	GO_NEGATIVE_REGU	65	-0.2565	-0.9369	0.5251	0.611854	1	3334	tags=17%, list=6
GO_REGUL	GO_REGULATION_OI	16	-0.3183	-0.9421	0.5252	0.610441	1	23440	tags=56%, list=4

GO_APICOI	GO_APICOLATERAL_	19	-0.3268	-0.9589	0.5268	0.591781	1	8956	tags=26%, list=1
GO_HISTON	GO_HISTONE_H4_K5_	16	-0.4083	-0.9721	0.5273	0.58139	1	10844	tags=38%, list=1
GO_POLYS.	GO_POLYSACCHARII	77	-0.2555	-0.9416	0.5278	0.610404	1	20825	tags=49%, list=3
GO_RESPOI	GO_RESPONSE_TO_M	19	-0.3187	-0.9427	0.5279	0.609669	1	19889	tags=47%, list=3
GO_SISTER	GO_SISTER_CHROMA	54	-0.3353	-0.9595	0.5284	0.590993	1	20697	tags=56%, list=3
GO_REGUL	GO_REGULATION_OI	24	-0.3228	-0.9416	0.5286	0.61014	1	9919	tags=25%, list=1
GO_REGUL	GO_REGULATION_OI	101	-0.3253	-0.9451	0.5286	0.60632	1	17523	tags=43%, list=3
GO_GLIAL_	GO_GLIAL_CELL_PR	33	-0.3235	-0.9392	0.5288	0.609424	1	16357	tags=45%, list=2
GO_ENDOR	GO_ENDORIBONUCL	29	-0.3437	-0.9402	0.5289	0.609607	1	5361	tags=21%, list=9
GO_NEURO	GO_NEURON_DEATH	27	-0.3074	-0.9415	0.5291	0.609828	1	11000	tags=33%, list=1
GO_ENDOD	GO_ENDODERM_FOR	54	-0.3017	-0.9353	0.5305	0.613426	1	10951	tags=33%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.3131	-0.911	0.5309	0.63537	1	7458	tags=33%, list=1
GO_RESPOI	GO_RESPONSE_TO_IS	31	-0.2928	-0.9364	0.531	0.612248	1	7944	tags=19%, list=1
GO_VESICI	GO_VESICLE_MEDIA	41	-0.281	-0.9246	0.531	0.623916	1	5006	tags=20%, list=9
GO_POSITI	GO_POSITIVE_REGUI	25	-0.3425	-0.9681	0.5314	0.58396	1	5634	tags=28%, list=1
GO_INTRA(	GO_INTRACILIARY_T	19	-0.371	-0.9553	0.5315	0.595593	1	5992	tags=21%, list=1
GO_POSITI	GO_POSITIVE_REGUI	33	-0.2883	-0.9411	0.5315	0.608871	1	15621	tags=39%, list=2
GO_MATUF	GO_MATURATION_O	15	-0.4062	-0.9478	0.5315	0.602858	1	23194	tags=73%, list=4
GO_REGUL	GO_REGULATION_OI	75	-0.2692	-0.9523	0.5322	0.598144	1	12883	tags=31%, list=2
GO_ESTABI	GO_ESTABLISHMENT	23	-0.3605	-0.9429	0.5322	0.609648	1	10459	tags=30%, list=1
GO_DIOL_E	GO_DIOL_BIOSYNTH	22	-0.3217	-0.9413	0.5336	0.609328	1	6020	tags=23%, list=1
GO_POSITI	GO_POSITIVE_REGUI	23	-0.3623	-0.9306	0.5342	0.619104	1	16562	tags=39%, list=2
GO_PEPTID	GO_PEPTIDYL_SERIN	326	-0.2312	-0.9379	0.5352	0.610809	1	12398	tags=29%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	19	-0.3768	-0.9534	0.5355	0.596965	1	8687	tags=37%, list=1
GO_CELLU	GO_CELLULAR_POLY	23	-0.3091	-0.9399	0.5356	0.609358	1	14094	tags=43%, list=2
GO_CULLIN	GO_CULLIN_RING_U	156	-0.2499	-0.9293	0.5363	0.620025	1	6450	tags=19%, list=1
GO_SPERM	GO_SPERMATID_NU(	19	-0.3417	-0.923	0.5363	0.625454	1	11656	tags=37%, list=2
GO_REGUL	GO_REGULATION_OI	26	-0.3269	-0.9512	0.5364	0.598971	1	12233	tags=38%, list=2
GO_MAMM	GO_MAMMARY_GLA	45	-0.2687	-0.9533	0.5365	0.596876	1	6450	tags=27%, list=1
GO_ENDON	GO_ENDONUCLEASE	42	-0.3014	-0.9191	0.537	0.628155	1	10581	tags=24%, list=1
GO_POSITI	GO_POSITIVE_REGUI	69	-0.2833	-0.9345	0.5373	0.614034	1	9573	tags=26%, list=1
GO_ORGAN	GO_ORGANIC_CATIC	49	-0.2702	-0.9287	0.5377	0.620312	1	9389	tags=27%, list=1
GO_TRANS	GO_TRANSCRIPTION	29	-0.2788	-0.9254	0.5377	0.623396	1	8815	tags=24%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	37	-0.3757	-0.9463	0.5391	0.605071	1	11360	tags=35%, list=1
GO_POSITI	GO_POSITIVE_REGUI	23	-0.3078	-0.9407	0.5411	0.609013	1	10511	tags=35%, list=1
GO_REGUL	GO_REGULATION_OI	60	-0.2807	-0.9178	0.5412	0.628917	1	11664	tags=33%, list=2
GO_RNA_P(	GO_RNA_POLYMERA	18	-0.3402	-0.9287	0.5413	0.62017	1	10889	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGUI	162	-0.2404	-0.9335	0.5413	0.614998	1	10105	tags=25%, list=1
GO_APICAI	GO_APICAL_DENDRI	18	-0.3432	-0.9358	0.5417	0.612692	1	10937	tags=28%, list=1
GO_POLY_I	GO_POLY_PURINE_T	29	-0.328	-0.9418	0.5417	0.610406	1	10103	tags=24%, list=1
GO_ENDOD	GO_ENDODERMAL_(	45	-0.307	-0.9124	0.5423	0.634518	1	10888	tags=36%, list=1
GO_MITOC	GO_MITOCHONDRIA	16	-0.3589	-0.9398	0.5424	0.608953	1	8465	tags=31%, list=1
GO_RETINA	GO_RETINAL_GANGI	20	-0.3422	-0.9212	0.5431	0.627722	1	5001	tags=20%, list=9
GO_REGUL	GO_REGULATION_OI	151	-0.2952	-0.9211	0.5434	0.627701	1	16716	tags=36%, list=2
GO_ACTINI	GO_ACTININ_BINDIN	36	-0.306	-0.9199	0.5438	0.627843	1	12326	tags=39%, list=2
GO_AUDIT(	GO_AUDITORY_RECI	19	-0.3473	-0.9399	0.5444	0.609605	1	1855	tags=16%, list=3
GO_ETHAN	GO_ETHANOL_META	22	-0.3226	-0.9276	0.5445	0.621466	1	15748	tags=41%, list=2
GO_VESICI	GO_VESICLE_TRANS	46	-0.2969	-0.9336	0.5446	0.614956	1	6170	tags=22%, list=1
GO_SECON	GO_SECONDARY_ME	59	-0.2586	-0.9416	0.5448	0.609908	1	15827	tags=32%, list=2
GO_MONO	GO_MONOVALENT_I	158	-0.2402	-0.9384	0.5451	0.61041	1	10114	tags=24%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	30	-0.2818	-0.9296	0.5453	0.619928	1	10299	tags=27%, list=1
GO_REGUL	GO_REGULATION_OI	94	-0.2402	-0.9515	0.5456	0.598629	1	20825	tags=49%, list=3
GO_CHONI	GO_CHONDROITIN_S	43	-0.308	-0.9262	0.5456	0.622553	1	19068	tags=51%, list=3
GO_POSITI	GO_POSITIVE_REGUI	58	-0.2665	-0.9366	0.5462	0.612048	1	9790	tags=24%, list=1
GO_AXON_	GO_AXON_ENSHEAT	23	-0.3009	-0.9375	0.5464	0.611019	1	11233	tags=26%, list=1
GO_A_BAN	GO_A_BAND	37	-0.2905	-0.9175	0.5465	0.629051	1	6954	tags=22%, list=1
GO_RELAX	GO_RELAXATION_OI	30	-0.3135	-0.9317	0.547	0.617434	1	14054	tags=43%, list=2
GO_TRNA_	GO_TRNA_METHYLT	32	-0.3115	-0.895	0.5472	0.653225	1	16653	tags=44%, list=2

GO_POSITI	GO_POSITIVE_REGU	16	-0.3183	-0.9198	0.5476	0.627764	1	3630	tags=19%, list=6
GO_NEUTR	GO_NEUTRAL_LIPID_	135	-0.2376	-0.9407	0.5479	0.609202	1	10468	tags=22%, list=1
GO_NEURO	GO_NEURON_MATU	46	-0.2799	-0.9275	0.5482	0.621445	1	11099	tags=33%, list=1
GO_ASPAR	GO_ASPARTATE_FAM	21	-0.3299	-0.9361	0.5491	0.612458	1	3280	tags=14%, list=6
GO_NUCLE	GO_NUCLEAR_MEM	282	-0.2349	-0.9205	0.5491	0.627954	1	9389	tags=24%, list=1
GO_MITOT	GO_MITOTIC_SPIND	111	-0.3018	-0.9187	0.5504	0.628464	1	8019	tags=22%, list=1
GO_NEGAT	GO_NEGATIVE_REG	78	-0.2697	-0.9496	0.5509	0.600369	1	2658	tags=13%, list=5
GO_REGUL	GO_REGULATION_O	17	-0.3154	-0.9234	0.5509	0.624929	1	5959	tags=24%, list=1
GO_SPIND	GO_SPINDLE_ORGA	174	-0.2786	-0.911	0.5521	0.635868	1	8019	tags=22%, list=1
GO_RESPO	GO_RESPONSE_TO_P	30	-0.2978	-0.9288	0.5535	0.620512	1	15363	tags=43%, list=2
GO_PEPTID	GO_PEPTIDE_RECEP	151	-0.2511	-0.92	0.5542	0.627929	1	13464	tags=36%, list=2
GO_MICRO	GO_MICROTUBULE_	137	-0.3027	-0.9206	0.5542	0.627978	1	8171	tags=23%, list=1
GO_RETIN	GO_RETINOIC_ACID_	33	-0.305	-0.924	0.5545	0.624479	1	11335	tags=30%, list=1
GO_REGUL	GO_REGULATION_O	185	-0.2392	-0.9184	0.5547	0.628288	1	9173	tags=23%, list=1
GO_VESIC	GO_VESICLE_TARGE	92	-0.2669	-0.9132	0.5551	0.633907	1	15968	tags=36%, list=2
GO_NEGAT	GO_NEGATIVE_REG	86	-0.2447	-0.9251	0.5551	0.623649	1	15632	tags=28%, list=2
GO_SPIND	GO_SPINDLE	351	-0.2563	-0.8886	0.5553	0.659942	1	12046	tags=26%, list=2
GO_ACYL_	GO_ACYL_COA_LIG	16	-0.3567	-0.9449	0.5558	0.606381	1	8465	tags=19%, list=1
GO_RESPO	GO_RESPONSE_TO_S	27	-0.2783	-0.9297	0.5562	0.620038	1	16894	tags=37%, list=2
GO_RESPO	GO_RESPONSE_TO_A	34	-0.2778	-0.9398	0.5564	0.609101	1	16041	tags=41%, list=2
GO_POLAR	GO_POLARIZED_EPI	22	-0.2981	-0.9274	0.5579	0.62133	1	13615	tags=32%, list=2
GO_FAD_B	GO_FAD_BINDING	32	-0.2772	-0.9256	0.5583	0.623221	1	9494	tags=25%, list=1
GO_POSITI	GO_POSITIVE_REGU	15	-0.3483	-0.911	0.5584	0.6356	1	9858	tags=27%, list=1
GO_PROTE	GO_PROTEIN_CONTA	32	-0.3193	-0.9192	0.5589	0.628385	1	6746	tags=22%, list=1
GO_SEX_D	GO_SEX_DETERMIN	24	-0.3057	-0.9347	0.5592	0.614149	1	11652	tags=33%, list=2
GO_3_PHO	GO_3_PHOSPHOADE	23	-0.2941	-0.9135	0.5595	0.633714	1	15354	tags=39%, list=2
GO_NEGAT	GO_NEGATIVE_REG	32	-0.2988	-0.9203	0.5605	0.627759	1	24245	tags=66%, list=4
GO_RESPO	GO_RESPONSE_TO_A	47	-0.2597	-0.9466	0.5607	0.604801	1	8929	tags=28%, list=1
GO_POSITI	GO_POSITIVE_REGU	36	-0.3012	-0.892	0.5613	0.656161	1	6594	tags=22%, list=1
GO_LAMEL	GO_LAMELLIPODIU	67	-0.263	-0.9219	0.5618	0.626911	1	4975	tags=19%, list=9
GO_COLLA	GO_COLLAGEN_BIO	52	-0.2892	-0.8885	0.562	0.659916	1	10863	tags=29%, list=1
GO_REGUL	GO_REGULATION_O	62	-0.2591	-0.9249	0.5631	0.623737	1	8882	tags=26%, list=1
GO_BASEM	GO_BASEMENT_ME	15	-0.3586	-0.8932	0.564	0.654719	1	7550	tags=40%, list=1
GO_REGUL	GO_REGULATION_O	47	-0.286	-0.8967	0.5643	0.652383	1	10863	tags=28%, list=1
GO_LAMEL	GO_LAMELLIPODIU	17	-0.3214	-0.9269	0.5645	0.621857	1	8823	tags=24%, list=1
GO_ALCOH	GO_ALCOHOL_BIND	86	-0.2425	-0.9347	0.5645	0.613974	1	14556	tags=34%, list=2
GO_CHRO	GO_CHROMATIN_RE	182	-0.2698	-0.8984	0.5651	0.651255	1	6893	tags=20%, list=1
GO_REGUL	GO_REGULATION_O	22	-0.357	-0.9136	0.5656	0.633906	1	12756	tags=36%, list=2
GO_CENTR	GO_CENTRIOLE_ASS	38	-0.3257	-0.8897	0.5665	0.658795	1	12794	tags=34%, list=2
GO_ANOIK	GO_ANOIKIS	33	-0.28	-0.9156	0.5666	0.63141	1	9443	tags=30%, list=1
GO_OLIGO	GO_OLIGODENDROC	103	-0.2403	-0.9341	0.5667	0.614496	1	8082	tags=20%, list=1
GO_FLAVO	GO_FLAVONOID_ME	16	-0.3499	-0.8919	0.5668	0.656135	1	12725	tags=38%, list=2
GO_CONDE	GO_CONDENSED_NU	94	-0.286	-0.8933	0.5672	0.655151	1	13830	tags=34%, list=2
GO_INNER_	GO_INNER_EAR_REC	40	-0.2975	-0.9219	0.5677	0.627134	1	16160	tags=38%, list=2
GO_REVER	GO_REVERSE_CHOL	20	-0.3334	-0.921	0.5678	0.627667	1	6746	tags=15%, list=1
GO_CYTOS	GO_CYTOSKELETON	85	-0.2744	-0.9004	0.5679	0.648852	1	8593	tags=22%, list=1
GO_PHOSP	GO_PHOSPHOLIPID_	19	-0.303	-0.9146	0.5681	0.632397	1	24757	tags=63%, list=4
GO_ATP_D	GO_ATP_DEPENDEN	72	-0.3015	-0.8761	0.5684	0.6741	1	8549	tags=24%, list=1
GO_HISTO	GO_HISTONE_DEAC	75	-0.2834	-0.8982	0.5697	0.651376	1	8882	tags=25%, list=1
GO_PODOS	GO_PODOSOME	29	-0.3104	-0.8952	0.57	0.653142	1	10477	tags=34%, list=1
GO_NUCLE	GO_NUCLEOCYTOPL	29	-0.3683	-0.9171	0.5706	0.629281	1	8809	tags=34%, list=1
GO_NEGAT	GO_NEGATIVE_REG	15	-0.3384	-0.9278	0.5706	0.621429	1	24735	tags=53%, list=4
GO_METAP	GO_METAPHASE_AN	60	-0.3166	-0.8932	0.5706	0.65491	1	17523	tags=40%, list=3
GO_POSITI	GO_POSITIVE_REGU	19	-0.3209	-0.9132	0.5709	0.633651	1	20441	tags=47%, list=3
GO_RESPO	GO_RESPONSE_TO_	106	-0.2394	-0.9197	0.5714	0.627671	1	9204	tags=23%, list=1
GO_BASAL	GO_BASAL_PLASMA	50	-0.2687	-0.9187	0.572	0.628192	1	9810	tags=26%, list=1
GO_C21_ST	GO_C21_STEROID_H	24	-0.2872	-0.9299	0.5729	0.620183	1	5959	tags=21%, list=1
GO_INCLU	GO_INCLUSION_BOD	76	-0.2482	-0.9105	0.573	0.635924	1	7861	tags=22%, list=1

GO_NUCLE	GO_NUCLEAR_UBIQU	42	-0.2859	-0.8758	0.5731	0.673864	1	5398	tags=19%, list=9
GO_ANION_	GO_ANION_HOMEOS	61	-0.2675	-0.9146	0.5734	0.632657	1	15534	tags=38%, list=2
GO_ENTRY	GO_ENTRY_OF_BACT	15	-0.359	-0.8975	0.574	0.651462	1	441	tags=13%, list=1
GO_POSITI	GO_POSITIVE_REGUI	43	-0.2606	-0.9174	0.575	0.629028	1	6208	tags=19%, list=1
GO_NUCLE	GO_NUCLEAR_TRAN	72	-0.2539	-0.8943	0.575	0.653957	1	7449	tags=19%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	25	-0.3012	-0.9162	0.5752	0.630583	1	12168	tags=40%, list=2
GO_U1_SNI	GO_U1_SNRNP	33	-0.3231	-0.9039	0.5755	0.644295	1	7422	tags=27%, list=1
GO_MITOTI	GO_MITOTIC_DNA_R	15	-0.3914	-0.9014	0.5764	0.647951	1	5672	tags=20%, list=1
GO_HEPAR	GO_HEPARAN_SULFA	32	-0.2987	-0.915	0.5766	0.632229	1	3026	tags=16%, list=5
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.3344	-0.8737	0.5767	0.675791	1	2649	tags=17%, list=5
GO_RNA_P	GO_RNA_POLYMERA	46	-0.2822	-0.8878	0.5768	0.660027	1	5662	tags=24%, list=1
GO_L_ASC	GO_L_ASCORBIC_AC	20	-0.3305	-0.8956	0.5775	0.653188	1	12094	tags=35%, list=2
GO_REGUL	GO_REGULATION_OI	15	-0.3312	-0.8966	0.5781	0.652357	1	3910	tags=20%, list=7
GO_EPOXY	GO_EPOXYGENASE_	20	-0.3316	-0.9047	0.5787	0.643176	1	16530	tags=45%, list=2
GO_ESTABI	GO_ESTABLISHMENT	18	-0.3631	-0.8976	0.5792	0.651625	1	8398	tags=28%, list=1
GO_NUCLE	GO_NUCLEAR_IMPOI	19	-0.3606	-0.8925	0.5796	0.655613	1	8809	tags=37%, list=1
GO_REGUL	GO_REGULATION_OI	16	-0.3548	-0.9006	0.5799	0.648796	1	15919	tags=50%, list=2
GO_SKIN_E	GO_SKIN_EPIDERMIS	90	-0.2541	-0.8962	0.5813	0.652704	1	8635	tags=21%, list=1
GO_PEPTID	GO_PEPTIDYL_ARGII	27	-0.2918	-0.9114	0.5814	0.63581	1	10781	tags=22%, list=1
GO_H4_HIS	GO_H4_HISTONE_AC	44	-0.3077	-0.8937	0.5819	0.654629	1	18074	tags=45%, list=3
GO_CLEAV	GO_CLEAVAGE_FUR	50	-0.2692	-0.8855	0.5825	0.662916	1	11638	tags=32%, list=2
GO_HISTON	GO_HISTONE_H3_K4_	18	-0.3737	-0.9077	0.5838	0.638916	1	17788	tags=44%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	119	-0.2314	-0.9189	0.5845	0.628359	1	15632	tags=29%, list=2
GO_POSITI	GO_POSITIVE_REGUI	35	-0.2787	-0.91	0.5848	0.63589	1	11621	tags=23%, list=2
GO_DNA_H	GO_DNA_HELICASE_	75	-0.3072	-0.8832	0.5848	0.666232	1	9177	tags=24%, list=1
GO_ENDON	GO_ENDONUCLEOLY	16	-0.366	-0.8819	0.5849	0.667436	1	2603	tags=19%, list=4
GO_TRANS	GO_TRANSFERASE_A	18	-0.3187	-0.8952	0.585	0.653408	1	5103	tags=22%, list=9
GO_REGUL	GO_REGULATION_OI	46	-0.2759	-0.8787	0.5858	0.671518	1	12598	tags=30%, list=2
GO_RESPOI	GO_RESPONSE_TO_A	33	-0.2788	-0.8945	0.5859	0.653763	1	7648	tags=21%, list=1
GO_REGUL	GO_REGULATION_OI	171	-0.2338	-0.8879	0.586	0.660146	1	9141	tags=23%, list=1
GO_TELOM	GO_TELOMERE_MAI	78	-0.273	-0.8656	0.586	0.682952	1	6594	tags=19%, list=1
GO_REGUL	GO_REGULATION_OI	51	-0.3185	-0.8725	0.5861	0.676904	1	8399	tags=24%, list=1
GO_RNA_P	GO_RNA_POLYMERA	43	-0.2903	-0.8833	0.5878	0.666408	1	7398	tags=26%, list=1
GO_DNA_D	GO_DNA_DEMETHYI	27	-0.2982	-0.8962	0.5883	0.652482	1	943	tags=15%, list=2
GO_CELLU	GO_CELLULAR_RESI	18	-0.3063	-0.9113	0.5889	0.635724	1	19375	tags=50%, list=3
GO_MONOS	GO_MONOSACCHARI	286	-0.2124	-0.906	0.5893	0.641187	1	9806	tags=21%, list=1
GO_RAN_G	GO_RAN_GTPASE_BI	41	-0.2859	-0.8648	0.5893	0.683851	1	9626	tags=24%, list=1
GO_COLUM	GO_COLUMNAR_CUI	60	-0.2661	-0.9099	0.5894	0.63586	1	6208	tags=18%, list=1
GO_CONNE	GO_CONNEXIN_COM	21	-0.3037	-0.9102	0.5905	0.636139	1	6854	tags=29%, list=1
GO_GAP_JU	GO_GAP_JUNCTION_	21	-0.3037	-0.9102	0.5905	0.635865	1	6854	tags=29%, list=1
GO_CARBO	GO_CARBOHYDRATI	21	-0.3075	-0.8917	0.5924	0.656111	1	15701	tags=38%, list=2
GO_RNA_IN	GO_RNA_INTERFERE	17	-0.3575	-0.8773	0.5934	0.673346	1	5902	tags=24%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	43	-0.2566	-0.9125	0.5935	0.634583	1	10490	tags=28%, list=1
GO_MONO	GO_MONOCARBOXY	171	-0.2221	-0.9321	0.5941	0.617131	1	16401	tags=34%, list=2
GO_PROTEI	GO_PROTEIN_OXIDA	15	-0.3378	-0.8997	0.5949	0.649827	1	6746	tags=27%, list=1
GO_STERE	GO_STEREOCILIUM_	18	-0.3376	-0.9097	0.5953	0.635858	1	15397	tags=50%, list=2
GO_CLATH	GO_CLATHRIN_COAT	16	-0.3329	-0.8992	0.5969	0.65041	1	11018	tags=44%, list=1
GO_PHOSPI	GO_PHOSPHATIDYLI	17	-0.3071	-0.8978	0.5972	0.65155	1	24285	tags=59%, list=4
GO_CENTR	GO_CENTROSOME_D	66	-0.2898	-0.8567	0.598	0.691629	1	12794	tags=36%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	51	-0.2673	-0.9236	0.5985	0.62496	1	6745	tags=24%, list=1
GO_CYTOK	GO_CYTOKINESIS	156	-0.252	-0.8823	0.5988	0.66696	1	11646	tags=24%, list=2
GO_FOUR_	GO_FOUR_WAY_JUN	17	-0.3842	-0.8792	0.5992	0.670882	1	12831	tags=41%, list=2
GO_REGUL	GO_REGULATION_OI	15	-0.3505	-0.9094	0.6008	0.636246	1	6429	tags=20%, list=1
GO_HYDRO	GO_HYDROGEN_PER	32	-0.2824	-0.9024	0.6015	0.646642	1	4675	tags=16%, list=8
GO_REGUL	GO_REGULATION_OI	50	-0.2522	-0.8992	0.6029	0.650232	1	12398	tags=32%, list=2
GO_MICRO	GO_MICROTUBULE_	132	-0.2591	-0.8356	0.6035	0.717421	1	14975	tags=34%, list=2
GO_DIOL_M	GO_DIOL_METABOLI	25	-0.2877	-0.8702	0.604	0.679331	1	6020	tags=20%, list=1
GO_CELL_M	GO_CELL_MATURAT	170	-0.2243	-0.9204	0.6045	0.627871	1	10220	tags=22%, list=1

GO_TRANS	GO_TRANSLATION_	80	-0.2708	-0.8866	0.6055	0.661625	1	5882	tags=16%, list=1
GO_POSTSY	GO_POSTSYNAPTIC_	20	-0.3316	-0.901	0.6057	0.648305	1	10511	tags=40%, list=1
GO_NEGAT	GO_NEGATIVE_REG	19	-0.3029	-0.8828	0.606	0.666694	1	12168	tags=42%, list=2
GO_HISTO	GO_HISTONE_DEAC	112	-0.2366	-0.8794	0.606	0.670726	1	8882	tags=21%, list=1
GO_CONDE	GO_CONDENSED_CH	205	-0.2766	-0.8535	0.6062	0.695466	1	17779	tags=38%, list=3
GO_POSITI	GO_POSITIVE_REGU	37	-0.2872	-0.8685	0.6068	0.681223	1	8067	tags=27%, list=1
GO_SMALL	GO_SMALL_NUCLEA	95	-0.2783	-0.8749	0.607	0.67421	1	12984	tags=31%, list=2
GO_ORGAN	GO_ORGANOPHOSP	129	-0.2204	-0.898	0.6072	0.651396	1	10619	tags=26%, list=1
GO_SPERM	GO_SPERMATID_DI	152	-0.2335	-0.9073	0.6074	0.639369	1	15236	tags=32%, list=2
GO_STERO	GO_STEROID_META	326	-0.2117	-0.918	0.6081	0.628713	1	5277	tags=14%, list=9
GO_POLY_	GO_POLY_PYRIMIDI	29	-0.2905	-0.8556	0.6081	0.692261	1	9657	tags=28%, list=1
GO_DERM	GO_DERMATAN_SU	16	-0.3389	-0.8955	0.6096	0.653182	1	13771	tags=38%, list=2
GO_TOXIN_	GO_TOXIN_METABO	15	-0.3336	-0.9022	0.6099	0.646664	1	14838	tags=33%, list=2
GO_POSITI	GO_POSITIVE_REGU	38	-0.2703	-0.8971	0.6107	0.652016	1	15095	tags=34%, list=2
GO_PERICE	GO_PERICENTRIOLA	21	-0.3371	-0.8782	0.611	0.672092	1	14756	tags=43%, list=2
GO_REGUL	GO_REGULATION_O	42	-0.2657	-0.9068	0.6115	0.639894	1	12745	tags=33%, list=2
GO_DNA_D	GO_DNA_DOUBLE_S	24	-0.328	-0.8771	0.6118	0.672821	1	11005	tags=33%, list=1
GO_POSITI	GO_POSITIVE_REGU	50	-0.2607	-0.8766	0.6126	0.673484	1	3729	tags=14%, list=6
GO_VESICL	GO_VESICLE_TARGE	73	-0.265	-0.8835	0.6133	0.666317	1	15552	tags=37%, list=2
GO_PYRUV	GO_PYRUVATE_MET	148	-0.2373	-0.8753	0.6142	0.673805	1	9901	tags=24%, list=1
GO_GROOM	GO_GROOMING_BEH	19	-0.3148	-0.887	0.6143	0.661153	1	7522	tags=32%, list=1
GO_DESMO	GO_DESMOSOME	25	-0.3226	-0.8351	0.6147	0.717707	1	5139	tags=16%, list=9
GO_POSITI	GO_POSITIVE_REGU	18	-0.3437	-0.8557	0.6148	0.69268	1	12664	tags=44%, list=2
GO_PHOSP	GO_PHOSPHOLIPASE	103	-0.2506	-0.8892	0.6148	0.659355	1	18325	tags=46%, list=3
GO_ESTAB	GO_ESTABLISHMEN	52	-0.2562	-0.8694	0.6151	0.680204	1	18948	tags=40%, list=3
GO_DNA_R	GO_DNA_REPAIR_CO	38	-0.2873	-0.8574	0.6155	0.69156	1	10439	tags=24%, list=1
GO_REGUL	GO_REGULATION_O	37	-0.2756	-0.8888	0.6175	0.659968	1	4975	tags=22%, list=9
GO_MICRO	GO_MICROBODY	130	-0.2304	-0.8589	0.6218	0.690587	1	11448	tags=28%, list=2
GO_PROTE	GO_PROTEIN_ACTIV	28	-0.3312	-0.8677	0.6218	0.681265	1	9751	tags=29%, list=1
GO_COPII_	GO_COPII_COATED_	72	-0.2556	-0.8727	0.6225	0.676992	1	15552	tags=35%, list=2
GO_ATPAS	GO_ATPASE_ACTIVI	407	-0.2343	-0.8411	0.6228	0.710295	1	11510	tags=28%, list=2
GO_UBIQU	GO_UBIQUITIN_PRO	18	-0.3101	-0.8713	0.6233	0.678153	1	7307	tags=28%, list=1
GO_REGUL	GO_REGULATION_O	17	-0.3194	-0.8773	0.624	0.673093	1	12320	tags=41%, list=2
GO_VITAM	GO_VITAMIN_D_REC	15	-0.3624	-0.8759	0.6245	0.674231	1	11914	tags=33%, list=2
GO_REGUL	GO_REGULATION_O	36	-0.2762	-0.8677	0.6245	0.681673	1	2086	tags=14%, list=4
GO_MYOTU	GO_MYOTUBE_CELL	31	-0.2801	-0.8696	0.625	0.680054	1	5030	tags=19%, list=9
GO_REGUL	GO_REGULATION_O	23	-0.3053	-0.8507	0.6252	0.698492	1	8088	tags=26%, list=1
GO_TRANS	GO_TRANSCRIPTION	61	-0.2744	-0.868	0.6257	0.681749	1	13219	tags=30%, list=2
GO_NEGAT	GO_NEGATIVE_REG	57	-0.2502	-0.9119	0.626	0.635219	1	8089	tags=23%, list=1
GO_STERO	GO_STEROID_HYDR	38	-0.2724	-0.8915	0.6262	0.656219	1	16530	tags=34%, list=2
GO_PEPTID	GO_PEPTIDYL_ASPA	31	-0.2731	-0.8369	0.6263	0.715678	1	12796	tags=32%, list=2
GO_MRNA_	GO_MRNA_3_END_P	96	-0.2755	-0.8322	0.6264	0.720932	1	7870	tags=22%, list=1
GO_MITOC	GO_MITOCHONDRIA	24	-0.2953	-0.8685	0.627	0.681464	1	1656	tags=17%, list=3
GO_DNA_D	GO_DNA_DEALKYLA	33	-0.2739	-0.8758	0.6272	0.674116	1	943	tags=12%, list=2
GO_LIGASE	GO_LIGASE_ACTIVIT	22	-0.3252	-0.8455	0.6274	0.70416	1	15754	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REG	77	-0.2417	-0.8631	0.6286	0.685715	1	10490	tags=29%, list=1
GO_RNA_D	GO_RNA_DEPENDEN	68	-0.2613	-0.8153	0.6286	0.740379	1	6594	tags=19%, list=1
GO_RETIN	GO_RETINOL_META	47	-0.2551	-0.868	0.6292	0.681564	1	15748	tags=32%, list=2
GO_OLIGO	GO_OLIGODENDROC	47	-0.2458	-0.8899	0.6294	0.658711	1	9077	tags=21%, list=1
GO_REGUL	GO_REGULATION_O	184	-0.2405	-0.8424	0.6297	0.70842	1	16983	tags=36%, list=2
GO_POSITI	GO_POSITIVE_REGU	26	-0.2832	-0.8558	0.6298	0.692817	1	11005	tags=31%, list=1
GO_CLATH	GO_CLATHRIN_ADA	24	-0.2885	-0.8653	0.6317	0.683321	1	11018	tags=29%, list=1
GO_CARBO	GO_CARBON_OXYG	66	-0.2545	-0.8773	0.6337	0.672926	1	9927	tags=21%, list=1
GO_ESTAB	GO_ESTABLISHMEN	198	-0.2503	-0.8136	0.6351	0.742961	1	10044	tags=24%, list=1
GO_POSTSY	GO_POSTSYNAPTIC_	16	-0.3188	-0.8814	0.6357	0.668119	1	28358	tags=69%, list=4
GO_INTRA	GO_INTRACELLULA	24	-0.2786	-0.8708	0.6358	0.678829	1	11233	tags=25%, list=1
GO_PROTE	GO_PROTEIN_LOCA	33	-0.2994	-0.8354	0.6364	0.71749	1	27350	tags=67%, list=4
GO_ACROS	GO_ACROSOME_REA	38	-0.2728	-0.8861	0.6365	0.662154	1	19501	tags=58%, list=3

GO_RESPOI	GO_RESPONSE_TO_L	97	-0.23	-0.8384	0.6387	0.713914	1	11709	tags=31%, list=2
GO_RETINC	GO_RETINOL_DEHYI	20	-0.3089	-0.8664	0.6389	0.681821	1	21629	tags=55%, list=3
GO_REGUL	GO_REGULATION_OI	15	-0.3133	-0.8283	0.6392	0.723541	1	3308	tags=20%, list=6
GO_GOLGI_	GO_GOLGI_CISTERN	115	-0.2224	-0.888	0.6393	0.660252	1	9923	tags=22%, list=1
GO_PYROP	GO_PYROPHOSPHAT	30	-0.2876	-0.8525	0.6394	0.696823	1	12270	tags=33%, list=2
GO_REGUL	GO_REGULATION_OI	80	-0.2768	-0.8111	0.6397	0.746196	1	18666	tags=41%, list=3
GO_POLYPI	GO_POLYPEPTIDE_N	18	-0.3079	-0.8544	0.6399	0.694127	1	17072	tags=44%, list=2
GO_BRANC	GO_BRANCHED_CHA	25	-0.2968	-0.8505	0.6402	0.698383	1	12830	tags=32%, list=2
GO_REGUL	GO_REGULATION_OI	19	-0.3261	-0.8704	0.6408	0.679281	1	24735	tags=47%, list=4
GO_WOUNI	GO_WOUND_HEALIN	18	-0.3258	-0.8569	0.6409	0.691665	1	4213	tags=22%, list=7
GO_NEGAT	GO_NEGATIVE_REGU	61	-0.2479	-0.8828	0.6416	0.666416	1	13913	tags=30%, list=2
GO_TRANS	GO_TRANSLATION_I	32	-0.2915	-0.8587	0.6419	0.690126	1	6272	tags=22%, list=1
GO_REGUL	GO_REGULATION_OI	23	-0.3085	-0.8481	0.642	0.701452	1	6438	tags=26%, list=1
GO_RNA_SI	GO_RNA_SPLICING	471	-0.2377	-0.8295	0.6423	0.722851	1	12984	tags=27%, list=2
GO_RNA_P	GO_RNA_POLYMERA	159	-0.2423	-0.8521	0.6424	0.697325	1	12664	tags=30%, list=2
GO_RECEP	GO_RECEPTOR_ANT	32	-0.2781	-0.8606	0.6433	0.688722	1	12885	tags=34%, list=2
GO_ACYLG	GO_ACYLGLYCEROL	38	-0.2814	-0.8576	0.6433	0.691631	1	16012	tags=42%, list=2
GO_PIGMEI	GO_PIGMENT_CELL_	35	-0.2839	-0.8674	0.644	0.681418	1	13068	tags=34%, list=2
GO_UDP_G	GO_UDP_GLYCOSYL	136	-0.2211	-0.8884	0.644	0.65978	1	13687	tags=29%, list=2
GO_G_PRO	GO_G_PROTEIN_COU	18	-0.3053	-0.8714	0.6441	0.678241	1	14538	tags=50%, list=2
GO_POSITI	GO_POSITIVE_REGUI	26	-0.3115	-0.8285	0.6453	0.723472	1	9845	tags=31%, list=1
GO_REGUL	GO_REGULATION_OI	19	-0.3271	-0.8184	0.6456	0.736655	1	5865	tags=26%, list=1
GO_MRNA_	GO_MRNA_EXPORT_	111	-0.282	-0.8297	0.6464	0.723076	1	12883	tags=28%, list=2
GO_ORGAN	GO_ORGANIC_CATIC	24	-0.2841	-0.8619	0.6472	0.687498	1	4341	tags=21%, list=7
GO_BARBE	GO_BARBED_END_A	21	-0.2874	-0.8492	0.6475	0.70004	1	12556	tags=33%, list=2
GO_MOLTII	GO_MOLTING_CYCLI	110	-0.2502	-0.8727	0.6485	0.676808	1	8635	tags=21%, list=1
GO_RELAX	GO_RELAXATION_OI	16	-0.3403	-0.8599	0.6491	0.689423	1	16241	tags=56%, list=2
GO_POSITI	GO_POSITIVE_REGUI	48	-0.2608	-0.8456	0.6492	0.704299	1	6874	tags=21%, list=1
GO_NUCLE	GO_NUCLEOBASE_C	256	-0.2394	-0.8248	0.6497	0.727659	1	9700	tags=24%, list=1
GO_INNER	GO_INNERVATION	26	-0.2967	-0.8467	0.6498	0.703146	1	20398	tags=54%, list=3
GO_HISTOI	GO_HISTONE_DEUBI	22	-0.3011	-0.8252	0.6503	0.727605	1	11768	tags=32%, list=2
GO_PEPTID	GO_PEPTIDYL_L_CY	23	-0.2802	-0.8322	0.651	0.721383	1	7566	tags=22%, list=1
GO_PROTEI	GO_PROTEIN_SERINI	38	-0.2772	-0.8512	0.6515	0.698277	1	8409	tags=24%, list=1
GO_CHONE	GO_CHONDROITIN_S	26	-0.3092	-0.8277	0.652	0.724292	1	19019	tags=46%, list=3
GO_APOPT	GO_APOPTOTIC_DNA	25	-0.2814	-0.8556	0.6525	0.692446	1	23801	tags=48%, list=4
GO_DENDR	GO_DENDRITIC_SPIN	20	-0.2916	-0.8724	0.6526	0.676818	1	11239	tags=35%, list=1
GO_PROTEI	GO_PROTEIN_PHOSP	31	-0.278	-0.842	0.654	0.708912	1	9654	tags=29%, list=1
GO_FMN_B	GO_FMN_BINDING	16	-0.3064	-0.8615	0.6552	0.687903	1	12725	tags=31%, list=2
GO_POSITI	GO_POSITIVE_REGUI	17	-0.3143	-0.8602	0.6555	0.6892	1	6594	tags=29%, list=1
GO_HISTOI	GO_HISTONE_H3_K9_	16	-0.3225	-0.8315	0.6566	0.720661	1	15348	tags=50%, list=2
GO_FLEMM	GO_FLEMMING_BOD	31	-0.2842	-0.8318	0.6575	0.720652	1	11768	tags=26%, list=2
GO_REGUL	GO_REGULATION_OI	48	-0.2506	-0.8573	0.6577	0.691507	1	4975	tags=19%, list=9
GO_TRANS	GO_TRANSCRIPTION	47	-0.2714	-0.8251	0.6586	0.727387	1	13069	tags=34%, list=2
GO_CAMEF	GO_CAMERA_TYPE_	26	-0.2743	-0.8677	0.6587	0.681426	1	782	tags=12%, list=1
GO_CALMC	GO_CALMODULIN_D	28	-0.2674	-0.8672	0.6588	0.681526	1	12445	tags=32%, list=2
GO_AMINO	GO_AMINO_ACID_BI	17	-0.3064	-0.823	0.659	0.729028	1	1186	tags=12%, list=2
GO_ESTROI	GO_ESTROUS_CYCLI	15	-0.3143	-0.8666	0.659	0.681725	1	694	tags=13%, list=1
GO_PRODU	GO_PRODUCTION_OI	51	-0.2783	-0.8488	0.659	0.700487	1	5902	tags=20%, list=1
GO_TRANS	GO_TRANSMEMBRAI	17	-0.2968	-0.8351	0.66	0.717439	1	13713	tags=41%, list=2
GO_FILOPC	GO_FILOPODIUM	101	-0.2363	-0.864	0.6603	0.684524	1	11800	tags=33%, list=2
GO_REGUL	GO_REGULATION_OI	34	-0.2763	-0.8804	0.6612	0.66925	1	15095	tags=44%, list=2
GO_DNA_C	GO_DNA_CATABOLI	32	-0.2683	-0.8588	0.6621	0.690327	1	23801	tags=44%, list=4
GO_PROTEI	GO_PROTEIN_KINAS	27	-0.2743	-0.8755	0.6623	0.674073	1	15209	tags=41%, list=2
GO_LIGANI	GO_LIGAND_GATED_	108	-0.2406	-0.861	0.6626	0.688287	1	20230	tags=43%, list=3
GO_POSITI	GO_POSITIVE_REGUI	18	-0.3107	-0.8319	0.6634	0.721134	1	8835	tags=33%, list=1
GO_RNA_E	GO_RNA_EXPORT_FI	142	-0.2671	-0.7954	0.6641	0.765972	1	12883	tags=27%, list=2
GO_PHOSPI	GO_PHOSPHOTRANS	18	-0.2962	-0.8263	0.6646	0.726127	1	17839	tags=44%, list=3
GO_CYTOP	GO_CYTOPLASMIC_S	23	-0.2736	-0.8466	0.6648	0.702734	1	15888	tags=48%, list=2

GO_COLLA	GO_COLLAGEN_BINI	68	-0.2957	-0.8174	0.6653	0.737445	1	17625	tags=51%, list=3
GO_ATTAC	GO_ATTACHMENT_C	30	-0.3093	-0.7656	0.668	0.800695	1	22531	tags=53%, list=3
GO_REGUL	GO_REGULATION_OI	44	-0.2515	-0.8647	0.668	0.683683	1	10468	tags=25%, list=1
GO_REGUL	GO_REGULATION_OI	47	-0.2685	-0.8611	0.6686	0.688483	1	8338	tags=28%, list=1
GO_TRANS	GO_TRANSLATIONAI	190	-0.2405	-0.79	0.6687	0.772832	1	7176	tags=16%, list=1
GO_MEMBI	GO_MEMBRANE_DO	178	-0.2298	-0.8044	0.6693	0.75409	1	9326	tags=23%, list=1
GO_ALKAL	GO_ALKALI_METAL_	17	-0.3129	-0.85	0.6699	0.699046	1	12175	tags=41%, list=2
GO_POSITI	GO_POSITIVE_REGUI	20	-0.2939	-0.851	0.6706	0.698296	1	6062	tags=20%, list=1
GO_REGUL	GO_REGULATION_OI	16	-0.3404	-0.8425	0.6714	0.708785	1	10198	tags=31%, list=1
GO_NUCLE	GO_NUCLEOBASE_C	54	-0.2511	-0.8596	0.6715	0.689788	1	10619	tags=30%, list=1
GO_PRESYI	GO_PRESYNAPTIC_A	30	-0.2817	-0.8237	0.672	0.728708	1	11596	tags=37%, list=2
GO_PROTEI	GO_PROTEIN_KINAS	36	-0.2617	-0.8731	0.6725	0.676571	1	16853	tags=42%, list=2
GO_MITOC	GO_MITOCHONDRIA	23	-0.2826	-0.8366	0.6729	0.7159	1	3579	tags=13%, list=6
GO_ORGAN	GO_ORGANELLE_FIS	438	-0.219	-0.7839	0.6732	0.780696	1	18914	tags=37%, list=3
GO_INHIBI	GO_INHIBITORY_SYI	16	-0.3277	-0.8305	0.6754	0.722073	1	10943	tags=44%, list=1
GO_POSITI	GO_POSITIVE_REGUI	38	-0.2674	-0.8373	0.6759	0.715226	1	8067	tags=24%, list=1
GO_VACUC	GO_VACUOLAR_PRO	17	-0.3088	-0.8323	0.676	0.72159	1	12270	tags=35%, list=2
GO_HOMOI	GO_HOMOLOGOUS_I	52	-0.2563	-0.8056	0.6778	0.753706	1	8562	tags=21%, list=1
GO_CUL4_I	GO_CUL4_RING_E3_	33	-0.2693	-0.8008	0.6789	0.759081	1	9307	tags=24%, list=1
GO_PROTO	GO_PROTON_TRANS	31	-0.2723	-0.8233	0.679	0.729164	1	12270	tags=29%, list=2
GO_REGUL	GO_REGULATION_OI	26	-0.2894	-0.8466	0.6792	0.702954	1	17984	tags=42%, list=3
GO_TRANS	GO_TRANSCRIPTION	46	-0.258	-0.8106	0.6801	0.746822	1	8088	tags=24%, list=1
GO_MECHA	GO_MECHANORECEI	62	-0.2827	-0.8753	0.6824	0.67402	1	16442	tags=42%, list=2
GO_SPLEEI	GO_SPLEEN_DEVELC	34	-0.2629	-0.8506	0.6832	0.698395	1	5380	tags=21%, list=9
GO_ENDOR	GO_ENDORIBONUCL	63	-0.2336	-0.8167	0.6842	0.738531	1	15983	tags=30%, list=2
GO_PROTEI	GO_PROTEIN_LOCAI	42	-0.2491	-0.8347	0.6848	0.717816	1	18948	tags=36%, list=3
GO_KINET	GO_KINETOCHORE	128	-0.2667	-0.7559	0.685	0.810201	1	11646	tags=27%, list=2
GO_POSITI	GO_POSITIVE_REGUI	19	-0.288	-0.8468	0.6857	0.70323	1	12506	tags=42%, list=2
GO_RIBONI	GO_RIBONUCLEOPR	455	-0.229	-0.7882	0.6865	0.775357	1	9172	tags=20%, list=1
GO_METAL	GO_METALLOENDOI	16	-0.308	-0.8043	0.6868	0.753971	1	12162	tags=44%, list=2
GO_REGUL	GO_REGULATION_OI	141	-0.2148	-0.8479	0.6875	0.701537	1	11813	tags=21%, list=2
GO_REGUL	GO_REGULATION_OI	39	-0.273	-0.8254	0.6881	0.727453	1	15184	tags=31%, list=2
GO_CELLU	GO_CELLULAR_RESI	62	-0.2424	-0.867	0.6886	0.681395	1	8947	tags=23%, list=1
GO_CELLU	GO_CELLULAR_RESI	15	-0.3046	-0.8056	0.6892	0.75343	1	20646	tags=53%, list=3
GO_DNA_C	GO_DNA_CONFORM	273	-0.2352	-0.7568	0.6892	0.809972	1	9177	tags=21%, list=1
GO_PROTEI	GO_PROTEIN_LIPID_	54	-0.2493	-0.8374	0.6902	0.715321	1	6746	tags=19%, list=1
GO_HISTOI	GO_HISTONE_METH	76	-0.2624	-0.7754	0.6911	0.790043	1	16569	tags=41%, list=2
GO_NUCLE	GO_NUCLEAR_CHRO	251	-0.2305	-0.7466	0.6919	0.819849	1	17836	tags=33%, list=3
GO_LYMPH	GO_LYMPHOID_PRO	20	-0.2757	-0.8233	0.6923	0.728879	1	5634	tags=20%, list=1
GO_MITOC	GO_MITOCHONDRIA	15	-0.3192	-0.7662	0.6923	0.800219	1	17399	tags=47%, list=3
GO_DNA_B	GO_DNA_BINDING_E	18	-0.2959	-0.8156	0.6926	0.740077	1	12817	tags=33%, list=2
GO_MONO	GO_MONOOXYGENA	101	-0.2239	-0.8744	0.6932	0.674815	1	12725	tags=23%, list=2
GO_PROTEI	GO_PROTEIN_DNA_C	110	-0.2398	-0.7953	0.6935	0.765846	1	3322	tags=13%, list=6
GO_PROTEI	GO_PROTEIN_DNA_C	206	-0.2374	-0.7646	0.6941	0.801522	1	4155	tags=14%, list=7
GO_ACTIN_	GO_ACTIN_BASED_C	212	-0.2231	-0.8645	0.6944	0.683845	1	11800	tags=29%, list=2
GO_POSITI	GO_POSITIVE_REGUI	30	-0.2874	-0.7637	0.6946	0.802434	1	7870	tags=20%, list=1
GO_DNA_P	GO_DNA_POLYMERA	20	-0.3163	-0.7982	0.6946	0.761465	1	5902	tags=25%, list=1
GO_CEREB	GO_CEREBRAL_COR	25	-0.2911	-0.8286	0.6959	0.723877	1	19175	tags=56%, list=3
GO_MITOTI	GO_MITOTIC_CELL_	161	-0.234	-0.776	0.6969	0.789929	1	8824	tags=22%, list=1
GO_NCRNA	GO_NCRNA_TRANSC	101	-0.2428	-0.7721	0.6969	0.793517	1	7201	tags=19%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	17	-0.2913	-0.841	0.6978	0.710102	1	7567	tags=29%, list=1
GO_REGUL	GO_REGULATION_OI	58	-0.252	-0.7543	0.6988	0.810906	1	14495	tags=36%, list=2
GO_LIPID_I	GO_LIPID_DROPLET_	26	-0.2544	-0.8408	0.6994	0.710222	1	8620	tags=23%, list=1
GO_GOLGI_	GO_GOLGI_STACK	146	-0.2057	-0.8319	0.6994	0.72088	1	9923	tags=21%, list=1
GO_REGUL	GO_REGULATION_OI	54	-0.2423	-0.8304	0.7002	0.72206	1	20646	tags=41%, list=3
GO_MICRO	GO_MICROFILAMEN	29	-0.2854	-0.8078	0.7006	0.750576	1	11314	tags=28%, list=1
GO_MLL1_	GO_MLL1_2_COMPLI	29	-0.2913	-0.7844	0.7006	0.780356	1	10844	tags=31%, list=1
GO_RECEP	GO_RECEPTOR_INHI	40	-0.2608	-0.845	0.7016	0.704733	1	12885	tags=33%, list=2

GO_POSITI	GO_POSITIVE_REGU	15	-0.2993	-0.829	0.702	0.723356	1	3289	tags=13%, list=6
GO_INTEG	GO_INTEGRATOR_CO	25	-0.3107	-0.8046	0.7036	0.754299	1	15517	tags=24%, list=2
GO_BLOOD	GO_BLOOD_COAGU	18	-0.3187	-0.7915	0.7043	0.77092	1	9751	tags=28%, list=1
GO_CHRO	GO_CHROMOSOME_	310	-0.2215	-0.7234	0.7052	0.842967	1	17836	tags=33%, list=3
GO_PEPTID	GO_PEPTIDYL_CYST	49	-0.2285	-0.8296	0.7056	0.72288	1	7566	tags=18%, list=1
GO_CORE_	GO_CORE_PROMOTE	42	-0.2635	-0.8091	0.7061	0.748511	1	7201	tags=21%, list=1
GO_HAIR_	GO_HAIR_CELL_DIF	43	-0.3069	-0.857	0.7068	0.691692	1	16442	tags=42%, list=2
GO_TOXIN_	GO_TOXIN_TRANSP	41	-0.2448	-0.8285	0.707	0.72374	1	10198	tags=24%, list=1
GO_SNORN	GO_SNORNA_BINDI	30	-0.2796	-0.7559	0.7086	0.81043	1	9146	tags=23%, list=1
GO_POSITI	GO_POSITIVE_REGU	15	-0.2889	-0.8006	0.7087	0.758793	1	21972	tags=60%, list=3
GO_CENTR	GO_CENTRIOLE	131	-0.2445	-0.7775	0.709	0.788949	1	6486	tags=18%, list=1
GO_PYRIM	GO_PYRIMIDINE_RI	16	-0.2826	-0.7807	0.711	0.784504	1	8153	tags=25%, list=1
GO_CHRO	GO_CHROMOSOME_	183	-0.2539	-0.7285	0.7112	0.837706	1	17779	tags=38%, list=3
GO_RNA_L	GO_RNA_LOCALIZA	231	-0.232	-0.7506	0.7115	0.814763	1	9014	tags=21%, list=1
GO_CONDE	GO_CONDENSED_CH	111	-0.2511	-0.7029	0.7123	0.864922	1	11646	tags=26%, list=2
GO_ALCOH	GO_ALCOHOL_DEHY	21	-0.2925	-0.7934	0.7132	0.768165	1	27057	tags=67%, list=4
GO_HISTO	GO_HISTONE_H4_K1	21	-0.3031	-0.7708	0.7135	0.79477	1	16590	tags=43%, list=2
GO_PARAL	GO_PARALLEL_FIBE	16	-0.3087	-0.8182	0.7137	0.736462	1	10254	tags=31%, list=1
GO_TRAPP_	GO_TRAPP_COMPLE	15	-0.2914	-0.8126	0.7146	0.743974	1	4704	tags=20%, list=8
GO_PSEUD	GO_PSEUDOURIDINE	18	-0.2842	-0.7546	0.7151	0.810818	1	4290	tags=17%, list=7
GO_ZINC_I	GO_ZINC_ION_HOME	38	-0.2648	-0.799	0.7154	0.760552	1	14248	tags=37%, list=2
GO_GOLGI_	GO_GOLGI_VESICLE_	80	-0.2383	-0.8048	0.7154	0.754307	1	15552	tags=34%, list=2
GO_FERTIL	GO_FERTILIZATION	184	-0.2072	-0.8812	0.7156	0.668081	1	11099	tags=23%, list=1
GO_PHOSP	GO_PHOSPHOLIPID_	44	-0.235	-0.833	0.7157	0.720523	1	14517	tags=34%, list=2
GO_INNER_	GO_INNER_EAR_AU	34	-0.2895	-0.8272	0.7165	0.724834	1	16442	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REG	26	-0.2953	-0.7421	0.7171	0.824528	1	5527	tags=15%, list=9
GO_REGUL	GO_REGULATION_O	29	-0.2733	-0.8007	0.7171	0.758906	1	10347	tags=24%, list=1
GO_CATAL	GO_CATALYTIC_AC	99	-0.2304	-0.7646	0.7173	0.80182	1	15754	tags=32%, list=2
GO_REGUL	GO_REGULATION_O	77	-0.2468	-0.7716	0.7176	0.793676	1	6594	tags=21%, list=1
GO_FILOPO	GO_FILOPODIUM_TI	17	-0.2907	-0.7994	0.7176	0.760196	1	3074	tags=18%, list=5
GO_REGUL	GO_REGULATION_O	108	-0.237	-0.7438	0.7179	0.823556	1	8769	tags=21%, list=1
GO_ODORA	GO_ODORANT_BIND	101	-0.2722	-0.8582	0.719	0.690732	1	21322	tags=35%, list=3
GO_AMINO	GO_AMINO_ACID_BI	55	-0.2373	-0.8316	0.7194	0.720812	1	10550	tags=25%, list=1
GO_REGUL	GO_REGULATION_O	94	-0.236	-0.8401	0.7197	0.711113	1	17322	tags=34%, list=3
GO_TRANS	GO_TRANSFERASE_	70	-0.224	-0.8424	0.7202	0.708689	1	15562	tags=33%, list=2
GO_POSITI	GO_POSITIVE_REGU	39	-0.2631	-0.7671	0.7208	0.799456	1	15678	tags=41%, list=2
GO_NEGAT	GO_NEGATIVE_REG	80	-0.2554	-0.7674	0.7209	0.799213	1	12278	tags=26%, list=2
GO_NEGAT	GO_NEGATIVE_REG	16	-0.2857	-0.8046	0.721	0.754029	1	5704	tags=25%, list=1
GO_CATAL	GO_CATALYTIC_AC	200	-0.23	-0.7597	0.7218	0.806495	1	9242	tags=21%, list=1
GO_REPLIC	GO_REPLICATION_F	31	-0.2775	-0.7522	0.7221	0.813365	1	12831	tags=42%, list=2
GO_REGUL	GO_REGULATION_O	333	-0.2186	-0.7615	0.7247	0.804422	1	7417	tags=19%, list=1
GO_HISTO	GO_HISTONE_MRNA_	22	-0.2805	-0.7667	0.7248	0.799718	1	14433	tags=36%, list=2
GO_HELICA	GO_HELICASE_ACTI	156	-0.2378	-0.7363	0.7248	0.829406	1	9177	tags=25%, list=1
GO_GLUCO	GO_GLUCOCORTICO	19	-0.2763	-0.8238	0.726	0.728827	1	22074	tags=58%, list=3
GO_POLY_	GO_POLY_A_PLUS_M	21	-0.2938	-0.8014	0.7271	0.758209	1	18666	tags=38%, list=3
GO_CARBO	GO_CARBOHYDRAT	208	-0.2007	-0.8562	0.7283	0.692291	1	9806	tags=20%, list=1
GO_ALDO_	GO_ALDO_KETO_RE	27	-0.2573	-0.7742	0.7295	0.7905	1	27057	tags=63%, list=4
GO_SPINDL	GO_SPINDLE_ASSEM	109	-0.2314	-0.7428	0.7296	0.824571	1	9173	tags=18%, list=1
GO_INTER	GO_INTERMEDIATE_	25	-0.2758	-0.8041	0.7308	0.753971	1	11611	tags=32%, list=2
GO_SM_LI	GO_SM_LIKE_PROTE	107	-0.2486	-0.7938	0.7318	0.767853	1	12984	tags=28%, list=2
GO_RACEM	GO_RACEMASE_AN	16	-0.2686	-0.8063	0.7319	0.752823	1	9659	tags=25%, list=1
GO_TERMI	GO_TERMINATION_	35	-0.2761	-0.7424	0.7328	0.824354	1	7203	tags=20%, list=1
GO_MYOSI	GO_MYOSIN_COMPL	57	-0.2497	-0.8135	0.7328	0.742842	1	14648	tags=33%, list=2
GO_PROTE	GO_PROTEIN_LOCAL	21	-0.2776	-0.7317	0.7345	0.833871	1	17062	tags=38%, list=2
GO_GLYCE	GO_GLYCEROLIPID_	74	-0.2337	-0.8589	0.7346	0.690316	1	10220	tags=23%, list=1
GO_PHOSP	GO_PHOSPHATIDYLI	16	-0.2971	-0.7767	0.7368	0.789911	1	17096	tags=38%, list=2
GO_REGUL	GO_REGULATION_O	38	-0.2542	-0.7596	0.7369	0.806348	1	9173	tags=26%, list=1
GO_DNA_G	GO_DNA_GEOMETRI	113	-0.2476	-0.7367	0.7371	0.829346	1	9177	tags=21%, list=1

GO_RNA_S	GO_RNA_SPLICING_	381	-0.2133	-0.7177	0.7371	0.847728	1	12984	tags=26%, list=2
GO_EPITHE	GO_EPITHELIAL_CEL	15	-0.3071	-0.7474	0.738	0.818864	1	16442	tags=47%, list=2
GO_PROTE	GO_PROTEIN_N_LIN	73	-0.2245	-0.761	0.7381	0.80488	1	14906	tags=29%, list=2
GO_MRNA_	GO_MRNA_TRANSPC	148	-0.2392	-0.7394	0.7383	0.827192	1	12883	tags=26%, list=2
GO_SPLICE	GO_SPLICEOSOMAL_	54	-0.2572	-0.7721	0.7388	0.793796	1	9759	tags=26%, list=1
GO_PROTE	GO_PROTEIN_LOCAL	57	-0.2418	-0.7511	0.7391	0.814761	1	15772	tags=32%, list=2
GO_TRIGLY	GO_TRIGLYCERIDE_	107	-0.2197	-0.824	0.7395	0.728723	1	10468	tags=20%, list=1
GO_CYCLIN	GO_CYCLIN_DEPEND	29	-0.2445	-0.779	0.7396	0.787098	1	19997	tags=48%, list=3
GO_CELL_I	GO_CELL_DIVISION_	58	-0.2364	-0.7908	0.7402	0.771737	1	11638	tags=28%, list=2
GO_H4_H2	GO_H4_H2A_HISTON	21	-0.2863	-0.7701	0.7402	0.795658	1	23608	tags=67%, list=4
GO_MITOT	GO_MITOTIC_NUCLE	266	-0.2023	-0.6795	0.7424	0.8899	1	19968	tags=37%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	59	-0.2476	-0.7567	0.7432	0.809831	1	12278	tags=27%, list=2
GO_PROTE	GO_PROTEIN_HETER	15	-0.2992	-0.7826	0.7441	0.782299	1	13986	tags=40%, list=2
GO_MATUR	GO_MATURATION_O	25	-0.292	-0.7379	0.7441	0.829029	1	3054	tags=16%, list=5
GO_TRANS	GO_TRANSCRIPTION	405	-0.2041	-0.7748	0.7443	0.790476	1	13705	tags=28%, list=2
GO_RNA_3_	GO_RNA_3_END_PRC	145	-0.2339	-0.7272	0.7452	0.838929	1	17509	tags=33%, list=3
GO_MITOT	GO_MITOTIC_G2_DN	21	-0.2728	-0.7406	0.7454	0.825574	1	18290	tags=48%, list=3
GO_PRERIE	GO_PRERIBOSOME_	15	-0.3129	-0.7348	0.7457	0.830818	1	1885	tags=13%, list=3
GO_SINGLE	GO_SINGLE_FERTILI	153	-0.2089	-0.8672	0.7462	0.681355	1	10831	tags=23%, list=1
GO_POSITI	GO_POSITIVE_REGU	15	-0.3043	-0.7848	0.7465	0.78002	1	19965	tags=60%, list=3
GO_LIPOPR	GO_LIPOPROTEIN_P	25	-0.2733	-0.7856	0.7466	0.778872	1	6746	tags=20%, list=1
GO_INTRA_	GO_INTRA_S_DNA_D	15	-0.2882	-0.7229	0.7466	0.842885	1	4348	tags=20%, list=7
GO_PROTE	GO_PROTEIN_TRANS	35	-0.2461	-0.7554	0.7475	0.810417	1	10643	tags=26%, list=1
GO_NUCLE	GO_NUCLEOBASE_B	18	-0.3069	-0.7418	0.7485	0.824684	1	13876	tags=39%, list=2
GO_REGUL	GO_REGULATION_O	15	-0.3013	-0.8054	0.751	0.753495	1	16390	tags=47%, list=2
GO_PROTE	GO_PROTEIN_PHOSP	15	-0.2733	-0.7785	0.7516	0.787661	1	17654	tags=47%, list=3
GO_MITOT	GO_MITOTIC_SPIND	61	-0.2436	-0.7066	0.752	0.860761	1	8019	tags=16%, list=1
GO_U5_SN	GO_U5_SNRNP	22	-0.3009	-0.7765	0.752	0.789889	1	8662	tags=27%, list=1
GO_ARACH	GO_ARACHIDONIC_	16	-0.3015	-0.7581	0.7524	0.808446	1	16530	tags=44%, list=2
GO_ACID_	GO_ACID_THIOL_LIC	30	-0.2397	-0.7764	0.7529	0.789535	1	2881	tags=10%, list=5
GO_CHON	GO_CHONDROCYTE_	17	-0.2833	-0.7661	0.7531	0.800093	1	9810	tags=24%, list=1
GO_OLIGO	GO_OLIGOSACCHAR	21	-0.272	-0.7243	0.7535	0.842258	1	15915	tags=33%, list=2
GO_VESICI	GO_VESICLE_DOCKI	44	-0.2388	-0.7835	0.7553	0.781019	1	17970	tags=45%, list=3
GO_NUCLE	GO_NUCLEAR_EXPO	202	-0.2227	-0.7257	0.7558	0.840922	1	10044	tags=23%, list=1
GO_DNA_S	GO_DNA_SECONDAR	33	-0.2632	-0.7181	0.7564	0.847858	1	12831	tags=36%, list=2
GO_GDP_D	GO_GDP_DISSOCIAT	16	-0.2842	-0.7549	0.7571	0.810605	1	4769	tags=19%, list=8
GO_METHY	GO_METHYLTRANSF	102	-0.2372	-0.722	0.7578	0.843609	1	16569	tags=39%, list=2
GO_RESPO	GO_RESPONSE_TO_A	47	-0.2382	-0.8105	0.7578	0.746619	1	7789	tags=19%, list=1
GO_OUTER	GO_OUTER_MITOCH	21	-0.2878	-0.7363	0.7612	0.82971	1	17033	tags=38%, list=2
GO_LONG_	GO_LONG_CHAIN_F	73	-0.2232	-0.8322	0.7621	0.721138	1	16156	tags=33%, list=2
GO_MONO	GO_MONOCARBOXY	59	-0.229	-0.8518	0.7626	0.697491	1	7107	tags=19%, list=1
GO_POSITI	GO_POSITIVE_REGU	23	-0.2664	-0.7639	0.7646	0.802295	1	2644	tags=13%, list=5
GO_PROTE	GO_PROTEIN_QUALI	28	-0.2494	-0.7743	0.7648	0.791018	1	15109	tags=32%, list=2
GO_NURD_	GO_NURD_COMPLEX	15	-0.302	-0.7158	0.7648	0.848916	1	6622	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	18	-0.2624	-0.7627	0.7655	0.803119	1	6677	tags=17%, list=1
GO_SISTER	GO_SISTER_CHROM	187	-0.2025	-0.6275	0.7666	0.930279	1	20886	tags=40%, list=3
GO_CHRON	GO_CHROMOSOMAL	314	-0.2157	-0.6657	0.7669	0.901264	1	11713	tags=25%, list=2
GO_3_5_DN	GO_3_5_DNA_HELIC	18	-0.2944	-0.6902	0.767	0.879163	1	8399	tags=22%, list=1
GO_RNA_S	GO_RNA_STABILIZA	49	-0.2547	-0.7369	0.7701	0.829381	1	14561	tags=29%, list=2
GO_MONO	GO_MONOVALENT_I	26	-0.2691	-0.7947	0.771	0.766557	1	9880	tags=35%, list=1
GO_CENTR	GO_CENTROSOME_S	15	-0.3016	-0.71	0.7722	0.856371	1	23739	tags=60%, list=4
GO_FATTY_	GO_FATTY_ACID_BE	73	-0.2248	-0.7651	0.7763	0.801279	1	9927	tags=22%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	29	-0.2445	-0.7871	0.7776	0.776619	1	8823	tags=21%, list=1
GO_GOLGI_	GO_GOLGI_CIS_CIST	29	-0.2461	-0.7623	0.7815	0.80342	1	4642	tags=10%, list=8
GO_BRUSH	GO_BRUSH_BORDER	58	-0.2373	-0.7931	0.782	0.768426	1	24481	tags=52%, list=4
GO_OLIGO	GO_OLIGOSACCHAR	15	-0.3228	-0.7511	0.7822	0.814525	1	8442	tags=33%, list=1
GO_CYCLIN	GO_CYCLIN_BINDIN	29	-0.2427	-0.7598	0.7826	0.806531	1	17539	tags=41%, list=3
GO_SULFA	GO_SULFATION	18	-0.2676	-0.757	0.7826	0.809858	1	14920	tags=33%, list=2

GO_SPINDL	GO_SPINDLE_POLE	160	-0.2108	-0.6868	0.7829	0.88199	1	11153	tags=21%, list=1
GO_HEMAT	GO_HEMATOPOIETIC	26	-0.2506	-0.7782	0.7849	0.788052	1	10943	tags=23%, list=1
GO_POSITI	GO_POSITIVE_REGU	23	-0.2442	-0.7874	0.785	0.776419	1	21972	tags=52%, list=3
GO_NUCLE	GO_NUCLEOSOME_A	71	-0.2437	-0.7007	0.7864	0.866844	1	8867	tags=21%, list=1
GO_PROTE	GO_PROTEIN_LIPID_	34	-0.2509	-0.7634	0.7864	0.802487	1	16638	tags=35%, list=2
GO_POSITI	GO_POSITIVE_REGU	35	-0.2398	-0.734	0.7865	0.831357	1	17193	tags=37%, list=2
GO_REGUL	GO_REGULATION_OI	33	-0.2407	-0.7718	0.7871	0.793607	1	8941	tags=24%, list=1
GO_REGUL	GO_REGULATION_OI	23	-0.2518	-0.7327	0.7879	0.832773	1	9118	tags=22%, list=1
GO_PHOTO	GO_PHOTOTRANSDU	34	-0.2397	-0.8099	0.7881	0.747361	1	2640	tags=12%, list=5
GO_SMALL	GO_SMALL_NUCLEO	29	-0.2672	-0.7253	0.7885	0.841139	1	9800	tags=28%, list=1
GO_RESPIR	GO_RESPIRATORY_C	19	-0.2847	-0.7001	0.7889	0.867349	1	9949	tags=32%, list=1
GO_MITOTI	GO_MITOTIC_G2_M_	29	-0.2487	-0.6873	0.7894	0.881714	1	18515	tags=41%, list=3
GO_REGUL	GO_REGULATION_OI	16	-0.2663	-0.7479	0.7901	0.818758	1	10444	tags=25%, list=1
GO_DNA_M	GO_DNA_MODIFICAT	116	-0.2118	-0.7566	0.7902	0.809572	1	16537	tags=31%, list=2
GO_RESPO	GO_RESPONSE_TO_L	23	-0.2621	-0.7757	0.7905	0.790168	1	26232	tags=65%, list=4
GO_ACID_S	GO_ACID_SECRETIO	43	-0.2316	-0.8182	0.7918	0.736697	1	8032	tags=23%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	22	-0.2789	-0.6659	0.7923	0.901347	1	5527	tags=14%, list=9
GO_ER_NU	GO_ER_NUCLEUS_SI	50	-0.227	-0.7475	0.7926	0.818979	1	4873	tags=16%, list=8
GO_TRNA_	GO_TRNA_METHYLA	37	-0.2495	-0.7359	0.7938	0.829303	1	16653	tags=38%, list=2
GO_EXCIT	GO_EXCITATORY_EX	30	-0.2592	-0.7811	0.7946	0.784252	1	16720	tags=47%, list=2
GO_TRNA_	GO_TRNA_MODIFIC	83	-0.2141	-0.7012	0.7951	0.866532	1	16653	tags=31%, list=2
GO_LIPID_	GO_LIPID_OXIDATIO	110	-0.2058	-0.7629	0.7957	0.803076	1	13129	tags=25%, list=2
GO_PROTE	GO_PROTEIN_TARGE	22	-0.2429	-0.7024	0.7965	0.865296	1	15043	tags=32%, list=2
GO_REGUL	GO_REGULATION_OI	28	-0.2545	-0.8129	0.7972	0.743658	1	20196	tags=50%, list=3
GO_REGUL	GO_REGULATION_OI	17	-0.2573	-0.7156	0.7977	0.849013	1	9118	tags=24%, list=1
GO_G_PRO	GO_G_PROTEIN_COU	15	-0.2938	-0.7193	0.7984	0.846674	1	16241	tags=27%, list=2
GO_REGUL	GO_REGULATION_OI	37	-0.2337	-0.7195	0.7984	0.846737	1	12024	tags=27%, list=2
GO_PARAS	GO_PARASYMPATHE	19	-0.263	-0.7697	0.7996	0.796004	1	14543	tags=42%, list=2
GO_POSITI	GO_POSITIVE_REGU	68	-0.2121	-0.7755	0.8008	0.79022	1	18604	tags=35%, list=3
GO_NEGAT	GO_NEGATIVE_REGU	22	-0.2728	-0.7683	0.8019	0.797974	1	20847	tags=36%, list=3
GO_SPINDL	GO_SPINDLE_MICRO	64	-0.2303	-0.6526	0.8028	0.910967	1	22327	tags=39%, list=3
GO_MITOC	GO_MITOCHONDRIA	23	-0.2606	-0.7231	0.8049	0.842866	1	1196	tags=13%, list=2
GO_REGUL	GO_REGULATION_OI	25	-0.2522	-0.7432	0.8053	0.824262	1	24735	tags=48%, list=4
GO_MRNA_	GO_MRNA_CLEAVAC	18	-0.291	-0.7195	0.8059	0.846974	1	20353	tags=39%, list=3
GO_INTERM	GO_INTERMEMBRAN	41	-0.2256	-0.7765	0.8079	0.789701	1	10316	tags=22%, list=1
GO_POSITI	GO_POSITIVE_REGU	41	-0.2343	-0.7996	0.8083	0.760215	1	12950	tags=34%, list=2
GO_C21_ST	GO_C21_STEROID_H	38	-0.2246	-0.7819	0.8091	0.783233	1	7872	tags=18%, list=1
GO_SENSO	GO_SENSORY_PERCI	446	-0.2223	-0.7984	0.8092	0.761462	1	27389	tags=47%, list=4
GO_ERBB2_	GO_ERBB2_SIGNALI	31	-0.2226	-0.7374	0.8123	0.829449	1	19903	tags=39%, list=3
GO_REGUL	GO_REGULATION_OI	46	-0.2309	-0.6771	0.8127	0.892191	1	7890	tags=22%, list=1
GO_NEGAT	GO_NEGATIVE_REGU	31	-0.2671	-0.6763	0.8127	0.892801	1	7690	tags=19%, list=1
GO_SULFO	GO_SULFOTRANSFEI	52	-0.2246	-0.7752	0.8134	0.790017	1	15562	tags=33%, list=2
GO_LYSOP	GO_LYSOPHOSPHOL	25	-0.2449	-0.7511	0.8135	0.814255	1	21985	tags=52%, list=3
GO_AU_RI	GO_AU_RICH_ELEMI	27	-0.2492	-0.7161	0.814	0.84917	1	16310	tags=44%, list=2
GO_MITOTI	GO_MITOTIC_SPINDI	30	-0.2492	-0.6728	0.8151	0.895933	1	9173	tags=23%, list=1
GO_REGUL	GO_REGULATION_OI	49	-0.2337	-0.7227	0.8152	0.842843	1	17322	tags=37%, list=3
GO_REGUL	GO_REGULATION_OI	19	-0.2497	-0.7425	0.8193	0.824499	1	5730	tags=21%, list=1
GO_ZYMO	GO_ZYMOGEN_GRAI	15	-0.2748	-0.7374	0.8195	0.829262	1	17970	tags=47%, list=3
GO_HISTO	GO_HISTONE_H3_DE	20	-0.2547	-0.7191	0.8205	0.846671	1	6062	tags=20%, list=1
GO_PHOSP	GO_PHOSPHATIDYL	38	-0.2291	-0.7842	0.8209	0.780462	1	11054	tags=24%, list=1
GO_POSITI	GO_POSITIVE_REGU	33	-0.2391	-0.753	0.8227	0.812424	1	12065	tags=30%, list=2
GO_DNA_T	GO_DNA_TEMPLATE	74	-0.2168	-0.6463	0.8295	0.916151	1	7203	tags=16%, list=1
GO_OLFAC	GO_OLFACTORY_RE	421	-0.2231	-0.7743	0.8307	0.790777	1	27336	tags=47%, list=4
GO_PROTE	GO_PROTEIN_TRANS	59	-0.2103	-0.7288	0.8333	0.837965	1	16133	tags=31%, list=2
GO_CHROM	GO_CHROMOCENTEI	15	-0.278	-0.6715	0.8333	0.896833	1	4311	tags=20%, list=7
GO_GENER	GO_GENERAL_TRAN	44	-0.2169	-0.671	0.8343	0.89679	1	10622	tags=23%, list=1
GO_CYTOP	GO_CYTOPLASMIC_	70	-0.2095	-0.7178	0.8353	0.847889	1	14125	tags=26%, list=2
GO_SULFU	GO_SULFUR_COMPO	42	-0.2325	-0.7537	0.8356	0.811651	1	7781	tags=19%, list=1

GO_DOSAG	GO_DOSAGE_COMPE	17	-0.26	-0.6579	0.8369	0.906973	1	26262	tags=59%, list=4
GO_MRNA_	GO_MRNA_CLEAVAG	22	-0.2591	-0.6619	0.8376	0.904171	1	21770	tags=41%, list=3
GO_MAINT	GO_MAINTENANCE_	19	-0.2574	-0.7425	0.8377	0.824736	1	10518	tags=21%, list=1
GO_CARBO	GO_CARBOHYDRATE	22	-0.24	-0.7277	0.839	0.838571	1	8443	tags=23%, list=1
GO_REGUL	GO_REGULATION_OF	48	-0.2222	-0.7559	0.8391	0.809929	1	19410	tags=38%, list=3
GO_ESTRO	GO_ESTROGEN_MET	32	-0.2354	-0.7154	0.8406	0.84891	1	11913	tags=25%, list=2
GO_BRUSH	GO_BRUSH_BORDER	106	-0.2152	-0.7409	0.8437	0.825308	1	13050	tags=25%, list=2
GO_NEGAT	GO_NEGATIVE_REGU	26	-0.236	-0.7338	0.8444	0.831442	1	17153	tags=38%, list=2
GO_INTRA	GO_INTRACELLULAR	29	-0.235	-0.736	0.8449	0.829474	1	20068	tags=41%, list=3
GO_MALE_	GO_MALE_SEX_DETE	15	-0.2626	-0.7234	0.8454	0.842695	1	10388	tags=27%, list=1
GO_CELLU	GO_CELLULAR_HOR	132	-0.1985	-0.7892	0.8473	0.773952	1	15827	tags=30%, list=2
GO_RETINA	GO_RETINAL_METAB	15	-0.2662	-0.703	0.8477	0.865009	1	15827	tags=33%, list=2
GO_ICOSAN	GO_ICOSANOID_REC	15	-0.2629	-0.6986	0.8479	0.868828	1	4644	tags=20%, list=8
GO_NEURO	GO_NEUROPEPTIDE_	30	-0.2587	-0.7415	0.8494	0.824718	1	18674	tags=30%, list=3
GO_PROTEI	GO_PROTEIN_LOCAL	74	-0.2132	-0.6124	0.8499	0.94118	1	10459	tags=23%, list=1
GO_QUATE	GO_QUATERNARY_A	28	-0.2421	-0.7465	0.8521	0.819688	1	19238	tags=43%, list=3
GO_RHODO	GO_RHODOPSIN_ME	29	-0.2346	-0.755	0.8528	0.810728	1	2042	tags=10%, list=3
GO_TBP_CL	GO_TBP_CLASS_PRO	26	-0.2369	-0.6716	0.8539	0.89707	1	10197	tags=23%, list=1
GO_TRIGLY	GO_TRIGLYCERIDE_	41	-0.2224	-0.7287	0.856	0.837698	1	1653	tags=7%, list=3%
GO_CHROM	GO_CHROMOSOME_	32	-0.2226	-0.6097	0.8563	0.942202	1	21505	tags=34%, list=3
GO_SIGNAL	GO_SIGNALING_REC	32	-0.2267	-0.6848	0.86	0.884207	1	4232	tags=13%, list=7
GO_REGUL	GO_REGULATION_OF	40	-0.2138	-0.6899	0.8607	0.879239	1	20646	tags=45%, list=3
GO_MITOTI	GO_MITOTIC_CHROM	15	-0.2567	-0.5941	0.8615	0.951751	1	23311	tags=40%, list=4
GO_TELOM	GO_TELOMERASE_H	21	-0.2465	-0.6357	0.8621	0.923822	1	8833	tags=19%, list=1
GO_BINDIN	GO_BINDING_OF_SPE	43	-0.2124	-0.7341	0.8635	0.831462	1	24643	tags=49%, list=4
GO_VASCU	GO_VASCULAR_END	63	-0.2049	-0.7371	0.8657	0.829383	1	18245	tags=35%, list=3
GO_RIBOS	GO_RIBOSOMAL_LA	29	-0.2307	-0.5912	0.869	0.95298	1	16922	tags=34%, list=2
GO_ARACH	GO_ARACHIDONIC_	20	-0.2509	-0.6701	0.8715	0.89749	1	16530	tags=40%, list=2
GO_STEROI	GO_STEROID_HORM	26	-0.231	-0.7241	0.8717	0.842329	1	20810	tags=50%, list=3
GO_MALE_	GO_MALE_MEIOTIC_	45	-0.2242	-0.7169	0.8725	0.848349	1	9845	tags=22%, list=1
GO_STABIL	GO_STABILIZATION_	17	-0.2616	-0.7159	0.8735	0.849171	1	20717	tags=47%, list=3
GO_GLYCO	GO_GLYCOSIDE_MET	21	-0.2367	-0.6715	0.8753	0.896564	1	4812	tags=14%, list=8
GO_STRUC	GO_STRUCTURAL_C	23	-0.2436	-0.7039	0.8767	0.864194	1	22190	tags=43%, list=3
GO_CYTOC	GO_CYTOCHROME_C	33	-0.2216	-0.5933	0.8768	0.951919	1	11858	tags=27%, list=2
GO_MITOC	GO_MITOCHONDRIA	42	-0.2092	-0.6114	0.8783	0.941661	1	20105	tags=38%, list=3
GO_RRNA_	GO_RRNA_CONTAIN	15	-0.2478	-0.6147	0.8819	0.939983	1	18453	tags=47%, list=3
GO_PROTEI	GO_PROTEIN_LOCAL	18	-0.2349	-0.6677	0.8825	0.899557	1	8830	tags=22%, list=1
GO_POSITI	GO_POSITIVE_REGU	67	-0.1997	-0.6742	0.8838	0.894689	1	14975	tags=28%, list=2
GO_CELL_I	GO_CELL_DEATH_IN	33	-0.2178	-0.6986	0.8844	0.869028	1	20847	tags=36%, list=3
GO_SEQUE	GO_SEQUESTERING_	17	-0.2249	-0.6444	0.8845	0.917054	1	9653	tags=24%, list=1
GO_PROTEI	GO_PROTEIN_PHOSP	18	-0.2367	-0.6648	0.8948	0.901642	1	14849	tags=33%, list=2
GO_RESPO	GO_RESPONSE_TO_M	18	-0.2463	-0.6792	0.8953	0.88984	1	7373	tags=22%, list=1
GO_CHANN	GO_CHANNEL_INHIB	37	-0.2078	-0.6824	0.896	0.886525	1	6828	tags=16%, list=1
GO_INNER_	GO_INNER_EAR_REC	27	-0.2482	-0.689	0.8967	0.880158	1	18458	tags=37%, list=3
GO_ANCHO	GO_ANCHORED_COM	19	-0.24	-0.6554	0.8983	0.908972	1	1000	tags=11%, list=2
GO_REGUL	GO_REGULATION_OF	51	-0.1976	-0.6599	0.9022	0.905668	1	4751	tags=12%, list=8
GO_PRIMA	GO_PRIMARY_ALCO	16	-0.2345	-0.6508	0.9028	0.912203	1	14920	tags=31%, list=2
GO_SECON	GO_SECONDARY_ME	24	-0.2239	-0.7174	0.9029	0.847884	1	18645	tags=42%, list=3
GO_ACETY	GO_ACETYLCHOLINE	16	-0.2589	-0.6578	0.9059	0.906748	1	14794	tags=38%, list=2
GO_CENTR	GO_CENTROMERE_C	37	-0.2011	-0.5043	0.9082	0.986492	1	8549	tags=16%, list=1
GO_DRUG_	GO_DRUG_CATABOL	26	-0.2258	-0.6611	0.9091	0.904697	1	19093	tags=38%, list=3
GO_SYNAP	GO_SYNAPTIC_TRAN	26	-0.2207	-0.6653	0.9113	0.901318	1	6123	tags=15%, list=1
GO_LAMEL	GO_LAMELLIPODIUM	22	-0.2184	-0.5993	0.9122	0.949146	1	11877	tags=27%, list=2
GO_MEMBI	GO_MEMBRANE_DIS	16	-0.2349	-0.5791	0.9122	0.960107	1	22327	tags=38%, list=3
GO_SENSO	GO_SENSORY_PERCE	23	-0.2344	-0.6847	0.9153	0.88403	1	19156	tags=39%, list=3
GO_SKIN_I	GO_SKIN_DEVELOPM	420	-0.2073	-0.6884	0.9198	0.880567	1	16432	tags=33%, list=2
GO_POSITI	GO_POSITIVE_REGU	30	-0.1992	-0.5249	0.9202	0.981482	1	18223	tags=33%, list=3
GO_TRANS	GO_TRANSCRIPTION	36	-0.2074	-0.6143	0.921	0.939951	1	13219	tags=25%, list=2

GO_HEPAT	GO_HEPATOCYTE_D	15	-0.2501	-0.6454	0.9229	0.916696	1	11335	tags=27%, list=1
GO_NEGAT	GO_NEGATIVE_REG	78	-0.1821	-0.6935	0.9258	0.875233	1	11813	tags=19%, list=2
GO_KERAT	GO_KERATIN_FILAM	94	-0.2793	-0.6622	0.9269	0.904088	1	22704	tags=55%, list=3
GO_LOW_	GO_LOW_DENSITY_	17	-0.2323	-0.6078	0.9273	0.94329	1	18948	tags=35%, list=3
GO_DETEC	GO_DETECTION_OF_	23	-0.2287	-0.6537	0.9302	0.910426	1	19156	tags=48%, list=3
GO_ACETY	GO_ACETYLCHOLIN	16	-0.2457	-0.6244	0.9315	0.932647	1	8287	tags=25%, list=1
GO_NEGAT	GO_NEGATIVE_REG	21	-0.2104	-0.6382	0.9341	0.922398	1	6062	tags=10%, list=1
GO_CELLU	GO_CELLULAR_COM	36	-0.1916	-0.6423	0.9342	0.918874	1	22533	tags=44%, list=3
GO_PHOTO	GO_PHOTORECEPTO	17	-0.2153	-0.6197	0.9368	0.936295	1	14223	tags=24%, list=2
GO_INTRIN	GO_INTRINSIC_COM	64	-0.1834	-0.6497	0.938	0.913057	1	10565	tags=19%, list=1
GO_DETEC	GO_DETECTION_OF_	24	-0.2306	-0.6692	0.9382	0.898127	1	7971	tags=21%, list=1
GO_INO80_	GO_INO80_TYPE_CO	25	-0.1941	-0.5361	0.94	0.978781	1	6344	tags=12%, list=1
GO_REGUL	GO_REGULATION_O	23	-0.2113	-0.6379	0.9409	0.92209	1	24735	tags=39%, list=4
GO_POSITI	GO_POSITIVE_REGU	54	-0.1884	-0.6381	0.9415	0.92225	1	18604	tags=33%, list=3
GO_FATTY_	GO_FATTY_ACID_LI	22	-0.2131	-0.6279	0.9472	0.930199	1	2881	tags=9%, list=5%
GO_EPITHE	GO_EPITHELIAL_CE	15	-0.2211	-0.6108	0.9519	0.941707	1	9937	tags=20%, list=1
GO_CELLU	GO_CELLULAR_ALD	62	-0.1845	-0.6589	0.9525	0.906463	1	15827	tags=26%, list=2
GO_EPIDER	GO_EPIDERMAL_CE	358	-0.2119	-0.6589	0.9543	0.90617	1	16442	tags=35%, list=2
GO_NEGAT	GO_NEGATIVE_REG	37	-0.1985	-0.653	0.9572	0.910846	1	13692	tags=27%, list=2
GO_GLUCO	GO_GLUCOSYLTRAN	16	-0.2033	-0.5618	0.9582	0.968273	1	22571	tags=44%, list=3
GO_POTAS	GO_POTASSIUM_ION	16	-0.2237	-0.5979	0.9603	0.949764	1	20717	tags=50%, list=3
GO_GLUCO	GO_GLUCOCORTICO	26	-0.2008	-0.6334	0.9608	0.925586	1	22074	tags=46%, list=3
GO_CATEC	GO_CATECHOLAMIN	17	-0.2117	-0.5978	0.9685	0.94951	1	18325	tags=35%, list=3
GO_DRUG_	GO_DRUG_METABO	46	-0.1913	-0.6519	0.9734	0.911388	1	19093	tags=35%, list=3
GO_REGUL	GO_REGULATION_O	18	-0.2067	-0.526	0.9754	0.981487	1	27396	tags=61%, list=4
GO_REGUL	GO_REGULATION_O	25	-0.1915	-0.5131	0.9791	0.984655	1	1992	tags=8%, list=3%
GO_LONG_	GO_LONG_CHAIN_F	33	-0.1714	-0.5741	0.9861	0.96259	1	27131	tags=52%, list=4
GO_KERAT	GO_KERATINIZATIO	223	-0.2249	-0.5738	0.9865	0.962372	1	22704	tags=49%, list=3
GO_POSITI	GO_POSITIVE_REGU	15	-0.1832	-0.4832	0.9867	0.990684	1	2375	tags=7%, list=4%
GO_INTERM	GO_INTERMEDIATE_	239	-0.2558	-0.6745	0.988	0.894575	1	19653	tags=48%, list=3
GO_SPERM	GO_SPERM_EGG_RE	60	-0.1757	-0.6453	0.9885	0.916481	1	10826	tags=18%, list=1
GO_KERAT	GO_KERATINOCYTE_	301	-0.1833	-0.5344	0.9981	0.979031	1	16432	tags=33%, list=2

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LOW-ETV7

NAME	GS follow	GS DETAII	SIZE	ES	NES	NOM p	FDR q-v	FWER p-	RANK	LEADING EDGE
GO RESPON	GO RESPONS	Details ...	195	0.8	2.717	0	0	0	4226	tags=57%, list=7%, sign
GO TUMOR	GO TUMOR N	Details ...	167	0.71	2.664	0	0	0	7722	tags=55%, list=13%, sig
GO RESPON	GO RESPONS	Details ...	337	0.68	2.649	0	0	0	3967	tags=41%, list=7%, sign
GO DEFENS	GO DEFENSE	Details ...	248	0.72	2.642	0	0	0	4091	tags=44%, list=7%, sign
GO INTERFE	GO INTERFER	Details ...	89	0.88	2.635	0	0	0	2184	tags=63%, list=4%, sign
GO RESPON	GO RESPONS	Details ...	98	0.83	2.635	0	0	0	2184	tags=48%, list=4%, sign
GO T CELL I	GO T CELL R	Details ...	200	0.75	2.614	0	0	0	2512	tags=45%, list=4%, sign
GO NEGATI	GO NEGATIV	Details ...	100	0.76	2.561	0	0	0	1638	tags=39%, list=3%, sign
GO NEGATI	GO NEGATIV	Details ...	157	0.7	2.547	0	0	0	4992	tags=45%, list=9%, sign
GO REGULA	GO REGULAT	Details ...	397	0.66	2.519	0	0	0	5145	tags=41%, list=9%, sign
GO LEUKOC	GO LEUKOCY	Details ...	106	0.75	2.51	0	0	0	4639	tags=54%, list=8%, sign
GO CELL KI	GO CELL KIL	Details ...	168	0.71	2.508	0	0	0	7298	tags=55%, list=12%, sig
GO REGULA	GO REGULAT	Details ...	300	0.68	2.504	0	0	0	5145	tags=44%, list=9%, sign
GO RESPON	GO RESPONS	Details ...	27	0.85	2.503	0	0	0	3436	tags=56%, list=6%, sign
GO NEGATI	GO NEGATIV	Details ...	82	0.76	2.501	0	0	0	1638	tags=41%, list=3%, sign
GO T CELL N	GO T CELL M	Details ...	102	0.73	2.493	0	0	0	4639	tags=46%, list=8%, sign
GO NATURA	GO NATURAL	Details ...	84	0.71	2.49	0	0	0	3951	tags=44%, list=7%, sign
GO REGULA	GO REGULAT	Details ...	90	0.8	2.487	0	0	0	5312	tags=61%, list=9%, sign
GO NEGATI	GO NEGATIV	Details ...	150	0.69	2.484	0	0	0	3062	tags=38%, list=5%, sign
GO ANTIGE	GO ANTIGEN	Details ...	99	0.8	2.473	0	0	0	2352	tags=48%, list=4%, sign
GO NEGATI	GO NEGATIV	Details ...	133	0.67	2.471	0	0	0	4797	tags=38%, list=8%, sign
GO NEGATI	GO NEGATIV	Details ...	45	0.74	2.471	0	0	0	2916	tags=38%, list=5%, sign
GO PHAGOC	GO PHAGOCY	Details ...	75	0.76	2.47	0	0	0	3436	tags=51%, list=6%, sign
GO REGULA	GO REGULAT	Details ...	146	0.72	2.468	0	0	0	4639	tags=50%, list=8%, sign
GO PROGRA	GO PROGRAM	Details ...	49	0.73	2.461	0	0	0	6083	tags=55%, list=10%, sig
GO NEGATI	GO NEGATIV	Details ...	61	0.74	2.457	0	0	0	4992	tags=51%, list=9%, sign
GO RESPON	GO RESPONS	Details ...	308	0.6	2.452	0	0	0	6375	tags=42%, list=11%, sig
GO POSITIV	GO POSITIVE	Details ...	26	0.85	2.45	0	0	0	2307	tags=54%, list=4%, sign
GO REGULA	GO REGULAT	Details ...	151	0.67	2.449	0	0	0	5636	tags=42%, list=10%, sig
GO POSITIV	GO POSITIVE	Details ...	245	0.66	2.449	0	0	0	5145	tags=42%, list=9%, sign
GO POSITIV	GO POSITIVE	Details ...	208	0.67	2.443	0	0	0	5145	tags=44%, list=9%, sign
GO NEGATI	GO NEGATIV	Details ...	94	0.69	2.442	0	0	0	4992	tags=45%, list=9%, sign
GO NECROT	GO NECROTI	Details ...	61	0.67	2.442	0	0	0	6795	tags=49%, list=12%, sig
GO NEGATI	GO NEGATIV	Details ...	42	0.81	2.442	0	0	0	4639	tags=60%, list=8%, sign
GO T CELL A	GO T CELL A	Details ...	109	0.7	2.437	0	0	0	3951	tags=44%, list=7%, sign
GO ANTIGE	GO ANTIGEN	Details ...	80	0.85	2.434	0	0	0	2352	tags=54%, list=4%, sign
GO NEGATI	GO NEGATIV	Details ...	61	0.68	2.431	0	0	0	5319	tags=48%, list=9%, sign
GO REGULA	GO REGULAT	Details ...	37	0.79	2.421	0	0	0	2307	tags=46%, list=4%, sign
GO ANTIGE	GO ANTIGEN	Details ...	228	0.7	2.42	0	0	0	3517	tags=39%, list=6%, sign
GO REGULA	GO REGULAT	Details ...	160	0.69	2.416	0	0	0	4639	tags=44%, list=8%, sign
GO INTERFE	GO INTERFERON GAMM		112	0.74	2.415	0	0	0	6299	tags=59%, list=11%, sig
GO T CELL I	GO T CELL PROLIFERAT		191	0.68	2.415	0	0	0	3062	tags=38%, list=5%, sign
GO NEGATI	GO NEGATIVE REGULAT		48	0.75	2.411	0	0	0	4639	tags=54%, list=8%, sign
GO POSITIV	GO POSITIVE REGULATI		374	0.61	2.408	0	0	0	6109	tags=42%, list=10%, sig
GO ANTIGE	GO ANTIGEN RECEPTOR		306	0.72	2.405	0	0	0	6103	tags=51%, list=10%, sig
GO REGULA	GO REGULATION OF DE		71	0.72	2.404	0	0	0	3254	tags=41%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULAT		57	0.79	2.404	0	0	0	1550	tags=49%, list=3%, sign
GO ACTIVA	GO ACTIVATION OF CYS		84	0.62	2.401	0	0	0	6948	tags=51%, list=12%, sig
GO REGULA	GO REGULATION OF T C		71	0.73	2.398	0	0	0	4639	tags=45%, list=8%, sign
GO REGULA	GO REGULATION OF LE		202	0.68	2.396	0	0	0	4977	tags=49%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI		98	0.73	2.396	0	0	0	4152	tags=50%, list=7%, sign
GO ANTIGE	GO ANTIGEN PROCESSI		190	0.72	2.395	0	0	0	3473	tags=41%, list=6%, sign
GO MYD88 I	GO MYD88 INDEPENDEN		34	0.78	2.363	0	######	0.001	6083	tags=74%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI		59	0.82	2.363	0	######	0.001	3623	tags=58%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULAT		52	0.77	2.365	0	######	0.001	4639	tags=58%, list=8%, sign
GO INTERLE	GO INTERLEUKIN 10 PR		61	0.73	2.368	0	######	0.001	5312	tags=51%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT		44	0.76	2.37	0	######	0.001	952	tags=36%, list=2%, sign

GO REGULA	GO REGULATION OF AL	96	0.71	2.37	0	######	0.001	3033	tags=41%, list=5%, sign
GO T CELL	GO T CELL MEDIATED C	42	0.81	2.378	0	######	0.001	4639	tags=60%, list=8%, sign
GO REGULA	GO REGULATION OF LE	73	0.8	2.388	0	######	0.001	4977	tags=62%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	93	0.67	2.389	0	######	0.001	4977	tags=45%, list=9%, sign
GO NATURA	GO NATURAL KILLER C	65	0.8	2.389	0	######	0.001	4152	tags=65%, list=7%, sign
GO REGULA	GO REGULATION OF IM	452	0.66	2.342	0	######	0.001	6328	tags=48%, list=11%, sig
GO NEGATI	GO NEGATIVE REGULA	121	0.66	2.342	0	######	0.001	5890	tags=44%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	64	0.77	2.343	0	######	0.001	3594	tags=53%, list=6%, sign
GO REGULA	GO REGULATION OF RE	190	0.6	2.343	0	######	0.001	7722	tags=43%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULA	54	0.67	2.343	0	######	0.001	2916	tags=31%, list=5%, sign
GO REGULA	GO REGULATION OF PR	136	0.63	2.348	0	######	0.001	4977	tags=40%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	100	0.74	2.348	0	######	0.001	3033	tags=42%, list=5%, sign
GO NIK NF	GO NIK NF KAPPAB SIG	181	0.62	2.349	0	######	0.001	5095	tags=38%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULA	83	0.67	2.35	0	######	0.001	3062	tags=41%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	130	0.68	2.352	0	######	0.001	2648	tags=43%, list=5%, sign
GO ALPHA	GO ALPHA BETA T CELL	145	0.68	2.341	0	######	0.001	5785	tags=47%, list=10%, sig
GO TUMOR	GO TUMOR NECROSIS F	46	0.72	2.341	0	######	0.001	7035	tags=61%, list=12%, sig
GO REGULA	GO REGULATION OF NA	44	0.86	2.333	0	######	0.001	4639	tags=82%, list=8%, sign
GO T CELL	GO T CELL ACTIVATION	475	0.62	2.336	0	######	0.001	5856	tags=43%, list=10%, sig
GO T CELL	GO T CELL DIFFERENTI	71	0.71	2.337	0	######	0.001	3678	tags=46%, list=6%, sign
GO REGULA	GO REGULATION OF T C	325	0.64	2.337	0	######	0.001	3340	tags=37%, list=6%, sign
GO MODUL	GO MODULATION BY SY	44	0.74	2.337	0	######	0.001	6795	tags=52%, list=12%, sig
GO LYMPH	GO LYMPHOCYTE MEDI	345	0.73	2.331	0	######	0.001	7314	tags=60%, list=13%, sig
GO NUCLEO	GO NUCLEOSIDE CATAB	31	0.74	2.332	0	######	0.001	9155	tags=65%, list=16%, sig
GO REGULA	GO REGULATION OF T C	32	0.77	2.333	0	######	0.001	2050	tags=41%, list=4%, sign
GO CD4 POS	GO CD4 POSITIVE ALPH	96	0.66	2.327	0	######	0.002	3062	tags=40%, list=5%, sign
GO PROTEIN	GO PROTEIN ADP RIBOS	32	0.72	2.328	0	######	0.002	3915	tags=47%, list=7%, sign
GO NEGATI	GO NEGATIVE REGULA	436	0.6	2.329	0	######	0.002	6384	tags=39%, list=11%, sig
GO REGULA	GO REGULATION OF VI	37	0.77	2.33	0	######	0.002	1764	tags=41%, list=3%, sign
GO REGULA	GO REGULATION OF NA	34	0.79	2.321	0	######	0.003	3033	tags=50%, list=5%, sign
GO REGULA	GO REGULATION OF TU	57	0.65	2.323	0	######	0.003	7722	tags=54%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	159	0.62	2.324	0	######	0.003	7035	tags=51%, list=12%, sig
GO POSITIV	GO POSITIVE REGULATI	54	0.72	2.325	0	######	0.003	2315	tags=43%, list=4%, sign
GO IMMUN	GO IMMUNE RESPONSE	496	0.66	2.325	0	######	0.003	6131	tags=46%, list=11%, sig
GO RESPON	GO RESPONSE TO INTE	206	0.6	2.304	0	######	0.004	5368	tags=36%, list=9%, sign
GO REGULA	GO REGULATION OF CD	62	0.68	2.307	0	######	0.004	2916	tags=37%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	213	0.64	2.308	0	######	0.004	3075	tags=37%, list=5%, sign
GO T CELL	GO T CELL APOPTOTIC	49	0.68	2.31	0	######	0.004	3621	tags=47%, list=6%, sign
GO REGULA	GO REGULATION OF LE	236	0.64	2.311	0	######	0.004	3062	tags=36%, list=5%, sign
GO INTERL	GO INTERLEUKIN 17 PR	43	0.73	2.312	0	######	0.004	7273	tags=51%, list=12%, sig
GO PHAGO	GO PHAGOCYTIC VESIC	138	0.64	2.314	0	######	0.004	4392	tags=41%, list=8%, sign
GO POSITIV	GO POSITIVE REGULATI	450	0.6	2.298	0	######	0.005	4977	tags=39%, list=9%, sign
GO REGULA	GO REGULATION OF CY	82	0.68	2.299	0	######	0.005	2315	tags=37%, list=4%, sign
GO POSITIV	GO POSITIVE REGULATI	48	0.75	2.3	0	######	0.005	3033	tags=40%, list=5%, sign
GO ALPHA	GO ALPHA BETA T CELL	35	0.78	2.3	0	######	0.005	5312	tags=54%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULA	39	0.7	2.297	0	######	0.006	2916	tags=36%, list=5%, sign
GO REGULA	GO REGULATION OF T C	42	0.75	2.291	0	######	0.006	5319	tags=60%, list=9%, sign
GO REGULA	GO REGULATION OF T C	148	0.64	2.292	0	######	0.006	3623	tags=37%, list=6%, sign
GO LYMPH	GO LYMPHOCYTE APOP	73	0.64	2.297	0	######	0.006	3621	tags=40%, list=6%, sign
GO ALPHA	GO ALPHA BETA T CELL	63	0.69	2.285	0	######	0.006	2916	tags=43%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	102	0.69	2.285	0	######	0.006	4152	tags=40%, list=7%, sign
GO RESPIRA	GO RESPIRATORY BURS	34	0.79	2.285	0	######	0.006	6750	tags=65%, list=12%, sig
GO T CELL	GO T CELL CYTOKINE P	43	0.71	2.288	0	######	0.006	3436	tags=40%, list=6%, sign
GO RESPON	GO RESPONSE TO INTE	28	0.79	2.262	0	######	0.008	1015	tags=46%, list=2%, sign
GO REGULA	GO REGULATION OF T C	33	0.81	2.271	0	######	0.008	4639	tags=55%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULA	23	0.85	2.28	0	######	0.007	5319	tags=70%, list=9%, sign
GO REGULA	GO REGULATION OF CD	48	0.72	2.263	0	######	0.008	2916	tags=40%, list=5%, sign
GO LEUKOC	GO LEUKOCYTE PROLIF	309	0.61	2.271	0	######	0.008	5596	tags=38%, list=10%, sig

GO INTERLE	GO INTERLEUKIN 1 MEI	103	0.67	2.283	0	######	0.007	7814	tags=49%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	232	0.66	2.264	0	######	0.008	3188	tags=40%, list=5%, sign
GO REGULA	GO REGULATION OF VII	95	0.67	2.272	0	######	0.008	3263	tags=37%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	20	0.83	2.279	0	######	0.008	3033	tags=55%, list=5%, sign
GO ADAPTI	GO ADAPTIVE IMMUNE	349	0.71	2.264	0	######	0.008	7314	tags=57%, list=13%, sig
GO INNATE	GO INNATE IMMUNE RE	116	0.66	2.272	0	######	0.008	6872	tags=45%, list=12%, sig
GO REGULA	GO REGULATION OF SY	225	0.6	2.266	0	######	0.008	6065	tags=39%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULA	31	0.81	2.276	0	######	0.008	5319	tags=58%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULA	201	0.62	2.267	0	######	0.008	3331	tags=34%, list=6%, sign
GO LYMPHO	GO LYMPHOCYTE ACTI	181	0.63	2.277	0	######	0.008	4039	tags=37%, list=7%, sign
GO POSITIV	GO POSITIVE REGULATI	149	0.66	2.261	0	######	0.008	3033	tags=37%, list=5%, sign
GO ACTIVA	GO ACTIVATION OF INN	140	0.64	2.262	0	######	0.008	5312	tags=39%, list=9%, sign
GO LEUKOC	GO LEUKOCYTE CELL C	358	0.62	2.259	0	######	0.008	5319	tags=41%, list=9%, sign
GO THREON	GO THREONINE TYPE PI	31	0.81	2.26	0	######	0.008	3035	tags=48%, list=5%, sign
GO LUMEN	GO LUMENAL SIDE OF M	33	0.87	2.26	0	######	0.008	2478	tags=61%, list=4%, sign
GO PATTER	GO PATTERN RECOGNIT	194	0.61	2.257	0	######	0.01	7299	tags=46%, list=13%, sig
GO TRANSF	GO TRANSFERASE ACTI	44	0.62	2.257	0	######	0.01	4201	tags=34%, list=7%, sign
GO POSITIV	GO POSITIVE REGULATI	186	0.58	2.254	0	######	0.01	6083	tags=41%, list=10%, sig
GO REGULA	GO REGULATION OF RE	25	0.76	2.258	0	######	0.01	3625	tags=48%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULA	27	0.71	2.255	0	######	0.01	1638	tags=33%, list=3%, sign
GO POSITIV	GO POSITIVE REGULATI	54	0.66	2.255	0	######	0.01	6083	tags=46%, list=10%, sig
GO RESPON	GO RESPONSE TO INTEI	50	0.68	2.253	0	######	0.01	4625	tags=36%, list=8%, sign
GO I KAPPA	GO I KAPPAB KINASE N	282	0.55	2.251	0	######	0.011	4977	tags=37%, list=9%, sign
GO TYPE 2 I	GO TYPE 2 IMMUNE RES	39	0.69	2.246	0	######	0.013	3678	tags=41%, list=6%, sign
GO CYTOKI	GO CYTOKINE PRODUC	102	0.63	2.246	0	######	0.013	2315	tags=33%, list=4%, sign
GO CD4 POS	GO CD4 POSITIVE ALPH	78	0.67	2.247	0	######	0.013	3062	tags=41%, list=5%, sign
GO INTERLE	GO INTERLEUKIN 12 PR	57	0.7	2.247	0	######	0.013	6386	tags=49%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	195	0.53	2.239	0	######	0.015	7430	tags=40%, list=13%, sig
GO LATE EN	GO LATE ENDOSOME M	129	0.57	2.239	0	######	0.015	5939	tags=41%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	147	0.54	2.24	0	######	0.015	7430	tags=41%, list=13%, sig
GO RECYCL	GO RECYCLING ENDOS	83	0.6	2.237	0	######	0.015	5164	tags=37%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	274	0.62	2.242	0	######	0.015	3188	tags=35%, list=5%, sign
GO ENDOCY	GO ENDOCYTIC VESICL	160	0.62	2.236	0	######	0.015	4152	tags=35%, list=7%, sign
GO INTERLE	GO INTERLEUKIN 4 PRO	35	0.77	2.233	0	######	0.015	2987	tags=54%, list=5%, sign
GO VIRAL R	GO VIRAL RELEASE FRO	34	0.71	2.233	0	######	0.015	6065	tags=47%, list=10%, sig
GO T CELL I	GO T CELL DIFFERENTI	251	0.61	2.229	0	######	0.015	3678	tags=37%, list=6%, sign
GO REGULA	GO REGULATION OF TY	31	0.72	2.227	0	######	0.015	4795	tags=48%, list=8%, sign
GO DEFENS	GO DEFENSE RESPONSE	90	0.62	2.227	0	######	0.015	8635	tags=46%, list=15%, sig
GO PYRIMI	GO PYRIMIDINE NUCLE	34	0.69	2.227	0	######	0.015	9155	tags=62%, list=16%, sig
GO NEGATI	GO NEGATIVE REGULA	258	0.54	2.216	0	######	0.015	4992	tags=31%, list=9%, sign
GO REGULA	GO REGULATION OF LY	489	0.61	2.219	0	######	0.015	5919	tags=43%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULA	186	0.56	2.222	0	######	0.015	5416	tags=33%, list=9%, sign
GO TOLL LI	GO TOLL LIKE RECEPTO	150	0.62	2.219	0	######	0.015	7299	tags=49%, list=13%, sig
GO MHC PR	GO MHC PROTEIN BIND	36	0.88	2.22	0	######	0.015	1764	tags=64%, list=3%, sign
GO REGULA	GO REGULATION OF PR	26	0.75	2.214	0	######	0.015	1937	tags=42%, list=3%, sign
GO REGULA	GO REGULATION OF LY	179	0.61	2.211	0	######	0.015	3623	tags=34%, list=6%, sign
GO CELLUL	GO CELLULAR RESPONS	218	0.61	2.205	0	######	0.016	6064	tags=41%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	335	0.64	2.206	0	######	0.016	6083	tags=47%, list=10%, sig
GO CYTOKI	GO CYTOKINE RECEPTO	260	0.57	2.209	0	######	0.016	6389	tags=37%, list=11%, sig
GO TYPE I I	GO TYPE I INTERFERON	121	0.63	2.206	0	######	0.016	3678	tags=35%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULA	24	0.85	2.202	0	######	0.018	5089	tags=67%, list=9%, sign
GO THREON	GO THREONINE TYPE EI	21	0.91	2.202	0	######	0.018	2770	tags=67%, list=5%, sign
GO REGULA	GO REGULATORY T CEL	34	0.76	2.204	0	######	0.017	4152	tags=47%, list=7%, sign
GO POSITIV	GO POSITIVE REGULATI	28	0.87	2.2	0	######	0.018	3033	tags=82%, list=5%, sign
GO ALPHA I	GO ALPHA BETA T CELI	106	0.65	2.203	0	######	0.018	3062	tags=37%, list=5%, sign
GO PYRIMI	GO PYRIMIDINE NUCLE	23	0.74	2.19	0	######	0.021	10152	tags=70%, list=17%, sig
GO NEGATI	GO NEGATIVE REGULA	357	0.51	2.191	0	######	0.021	5947	tags=30%, list=10%, sig
GO REGULA	GO REGULATION OF AL	64	0.67	2.189	0	######	0.021	2916	tags=36%, list=5%, sign

GO TUMOR	GO TUMOR NECROSIS F	30	0.76	2.193	0	######	0.02	6975	tags=67%, list=12%, sig
GO CELLUL	GO CELLULAR DEFENSI	52	0.76	2.192	0	######	0.021	4317	tags=56%, list=7%, sign
GO POSITIV	GO POSITIVE REGULATI	63	0.71	2.189	0	######	0.021	3033	tags=41%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	26	0.83	2.194	0	######	0.02	3033	tags=46%, list=5%, sign
GO REGULA	GO REGULATION OF CE	430	0.56	2.188	0	######	0.021	5416	tags=35%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	30	0.76	2.189	0	######	0.021	2916	tags=43%, list=5%, sign
GO REGULA	GO REGULATION OF CY	234	0.51	2.187	0	######	0.021	7829	tags=38%, list=13%, sig
GO NLRP3 I	GO NLRP3 INFLAMMAS	16	0.77	2.187	0	######	0.021	2198	tags=44%, list=4%, sign
GO REGULA	GO REGULATION OF LY	56	0.65	2.187	0	######	0.021	3621	tags=41%, list=6%, sign
GO REGULA	GO REGULATION OF HE	464	0.53	2.184	0	######	0.024	6389	tags=35%, list=11%, sig
GO REGULA	GO REGULATION OF PA	93	0.61	2.183	0	######	0.025	6065	tags=41%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	56	0.68	2.183	0	######	0.026	2052	tags=34%, list=4%, sign
GO MYELOI	GO MYELOID DENDRITI	29	0.79	2.183	0	######	0.026	3953	tags=55%, list=7%, sign
GO ER TO G	GO ER TO GOLGI TRANS	59	0.72	2.18	0	######	0.027	2619	tags=37%, list=4%, sign
GO NADPLU	GO NADPLUS ADP RIBO	24	0.71	2.181	0	######	0.027	3915	tags=42%, list=7%, sign
GO IMMUN	GO IMMUNE RECEPTOR	132	0.68	2.181	0	######	0.027	4457	tags=49%, list=8%, sign
GO ACTIVA	GO ACTIVATED T CELL	46	0.63	2.179	0	######	0.028	2711	tags=33%, list=5%, sign
GO CELLUL	GO CELLULAR RESPONS	240	0.59	2.175	0	######	0.028	6064	tags=39%, list=10%, sig
GO IMMUN	GO IMMUNE RESPONSE	19	0.81	2.176	0	######	0.028	4639	tags=68%, list=8%, sign
GO POSITIV	GO POSITIVE REGULATI	394	0.63	2.174	0	######	0.029	6083	tags=46%, list=10%, sig
GO T HELPE	GO T HELPER 1 TYPE IM	44	0.73	2.177	0	######	0.028	3678	tags=50%, list=6%, sign
GO GLYCOS	GO GLYCOSYL COMPOU	41	0.65	2.176	0	######	0.028	9155	tags=56%, list=16%, sig
GO ANTIGE	GO ANTIGEN PROCESSI	24	0.91	2.168	0	######	0.03	856	tags=58%, list=1%, sign
GO POSITIV	GO POSITIVE REGULATI	104	0.63	2.168	0	######	0.03	3623	tags=37%, list=6%, sign
GO IMMUN	GO IMMUNOGLOBULIN	21	0.8	2.167	0	######	0.03	2354	tags=43%, list=4%, sign
GO MHC CL	GO MHC CLASS I PROTE	19	0.88	2.17	0	######	0.03	1536	tags=58%, list=3%, sign
GO MHC PR	GO MHC PROTEIN COM	24	0.88	2.169	0	######	0.03	1586	tags=67%, list=3%, sign
GO PRODUC	GO PRODUCTION OF M	296	0.64	2.168	0	######	0.03	6737	tags=48%, list=12%, sig
GO INTERL	GO INTERLEUKIN 1 PRO	117	0.62	2.165	0	######	0.032	5216	tags=42%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	71	0.61	2.161	0	######	0.033	3273	tags=30%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	57	0.72	2.16	0	######	0.034	5926	tags=58%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULA	17	0.89	2.161	0	######	0.033	4639	tags=82%, list=8%, sign
GO INTERL	GO INTERLEUKIN 1 BET	103	0.63	2.162	0	######	0.032	5216	tags=43%, list=9%, sign
GO PEPTIDE	GO PEPTIDE ANTIGEN B	30	0.94	2.159	0	######	0.034	1461	tags=70%, list=3%, sign
GO SCF DEP	GO SCF DEPENDENT PR	91	0.64	2.159	0	######	0.034	3078	tags=32%, list=5%, sign
GO CELLUL	GO CELLULAR RESPONS	60	0.62	2.157	0	######	0.038	4792	tags=35%, list=8%, sign
GO CELLUL	GO CELLULAR METABO	32	0.66	2.157	0	######	0.038	8789	tags=56%, list=15%, sig
GO T HELPE	GO T HELPER 17 TYPE I	31	0.74	2.156	0	######	0.04	2916	tags=45%, list=5%, sign
GO REGULA	GO REGULATION OF LE	287	0.56	2.155	0	######	0.044	6389	tags=38%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	23	0.88	2.153	0	######	0.044	3033	tags=83%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	36	0.73	2.152	0	######	0.045	2916	tags=42%, list=5%, sign
GO REGULA	GO REGULATION OF T H	36	0.71	2.15	0	######	0.046	2916	tags=39%, list=5%, sign
GO LUMEN	GO LUMENAL SIDE OF E	27	0.9	2.15	0	######	0.046	2478	tags=70%, list=4%, sign
GO POSITIV	GO POSITIVE T CELL SE	36	0.81	2.15	0	######	0.046	4279	tags=64%, list=7%, sign
GO RESPON	GO RESPONSE TO TUM	25	0.72	2.146	0	######	0.051	4639	tags=56%, list=8%, sign
GO CYSTEI	GO CYSTEINE TYPE EN	15	0.84	2.147	0	######	0.051	597	tags=53%, list=1%, sign
GO NEGATI	GO NEGATIVE REGULA	22	0.75	2.147	0	######	0.051	5143	tags=50%, list=9%, sign
GO REGULA	GO REGULATION OF TR	75	0.66	2.144	0	######	0.053	6103	tags=43%, list=10%, sig
GO DEFENS	GO DEFENSE RESPONSE	318	0.6	2.14	0	######	0.058	8773	tags=48%, list=15%, sig
GO POSITIV	GO POSITIVE REGULATI	24	0.81	2.141	0	######	0.058	2512	tags=63%, list=4%, sign
GO INTERF	GO INTERFERON BETA	49	0.65	2.138	0	######	0.06	3254	tags=37%, list=6%, sign
GO LYMPH	GO LYMPHOCYTE COST	58	0.7	2.136	0	######	0.062	2552	tags=43%, list=4%, sign
GO POSITIV	GO POSITIVE REGULATI	158	0.59	2.136	0	######	0.063	5416	tags=37%, list=9%, sign
GO PROTEA	GO PROTEASOMAL UBI	22	0.86	2.134	0	######	0.065	2770	tags=64%, list=5%, sign
GO TOLERA	GO TOLERANCE INDUCT	24	0.85	2.135	0	######	0.065	937	tags=54%, list=2%, sign
GO VIRAL G	GO VIRAL GENOME REF	121	0.6	2.133	0	######	0.065	3263	tags=31%, list=6%, sign
GO CELLUL	GO CELLULAR RESPONS	20	0.77	2.133	0	######	0.068	2122	tags=55%, list=4%, sign
GO POSITIV	GO POSITIVE REGULATI	92	0.65	2.132	0	######	0.068	4795	tags=43%, list=8%, sign

GO NEGATI	GO NEGATIVE REGULA	30	0.68	2.13	0	######	0.069	2916	tags=33%, list=5%, sign
GO REGULA	GO REGULATION OF CD	17	0.83	2.13	0	######	0.069	2916	tags=59%, list=5%, sign
GO REGULA	GO REGULATION OF TO	72	0.63	2.129	0	######	0.069	7299	tags=47%, list=13%, sig
GO T CELL	GO T CELL RECEPTOR C	125	0.87	2.13	0	######	0.069	3220	tags=77%, list=6%, sign
GO FC RECE	GO FC RECEPTOR SIGN	239	0.63	2.128	0	######	0.069	6131	tags=45%, list=11%, sig
GO MOVEM	GO MOVEMENT IN HOS	165	0.54	2.128	0	######	0.069	7367	tags=38%, list=13%, sig
GO RESPON	GO RESPONSE TO MOLE	348	0.54	2.126	0	######	0.07	6161	tags=36%, list=11%, sig
GO TUMOR	GO TUMOR NECROSIS F	178	0.58	2.123	0	######	0.071	4795	tags=36%, list=8%, sign
GO RESPON	GO RESPONSE TO INTEF	20	0.81	2.122	0	######	0.074	1015	tags=50%, list=2%, sign
GO NEGATI	GO NEGATIVE REGULA	20	0.87	2.121	0	######	0.077	4639	tags=75%, list=8%, sign
GO REGULA	GO REGULATION OF T C	34	0.67	2.121	0	######	0.077	3621	tags=47%, list=6%, sign
GO POSITIV	GO POSITIVE REGULAT	20	0.74	2.119	0	######	0.081	2050	tags=40%, list=4%, sign
GO NEGATI	GO NEGATIVE REGULA	36	0.65	2.118	0	######	0.082	5890	tags=42%, list=10%, sig
GO POSITIV	GO POSITIVE REGULAT	35	0.68	2.119	0	######	0.081	5926	tags=51%, list=10%, sig
GO NUCLEO	GO NUCLEOSIDE SALVA	15	0.8	2.117	0	######	0.082	8789	tags=73%, list=15%, sig
GO INTERA	GO INTERACTION WITH	208	0.53	2.117	0	######	0.082	7367	tags=37%, list=13%, sig
GO FC EPSI	GO FC EPSILON RECEPT	168	0.66	2.116	0	######	0.084	7851	tags=52%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULA	89	0.55	2.113	0	######	0.085	7080	tags=43%, list=12%, sig
GO LEUKOC	GO LEUKOCYTE APOPT	107	0.58	2.113	0	######	0.085	5081	tags=38%, list=9%, sign
GO CD8 POS	GO CD8 POSITIVE ALPH	26	0.77	2.108	0	######	0.089	2916	tags=46%, list=5%, sign
GO REGULA	GO REGULATION OF NE	38	0.61	2.106	0	######	0.09	1937	tags=29%, list=3%, sign
GO TERTIAR	GO TERTIARY GRANUL	55	0.62	2.107	0	######	0.09	4842	tags=44%, list=8%, sign
GO NUCLEO	GO NUCLEOBASE CONT	48	0.59	2.103	0	0.001	0.091	9289	tags=52%, list=16%, sig
GO POSITIV	GO POSITIVE REGULAT	152	0.56	2.103	0	0.001	0.091	6027	tags=38%, list=10%, sig
GO REGULA	GO REGULATION OF IM	61	0.62	2.103	0	0.001	0.091	5890	tags=41%, list=10%, sig
GO T CELL	GO T CELL SELECTION	49	0.74	2.1	0	0.001	0.096	7430	tags=67%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULA	31	0.64	2.1	0	0.001	0.096	3621	tags=42%, list=6%, sign
GO INTRINS	GO INTRINSIC COMPON	154	0.57	2.099	0	0.0011	0.098	5351	tags=31%, list=9%, sign
GO B CELL	GO B CELL MEDIATED I	210	0.72	2.097	0	0.0011	0.102	7314	tags=60%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULA	36	0.66	2.095	0	0.0011	0.102	8426	tags=56%, list=14%, sig
GO REGULA	GO REGULATION OF CY	17	0.75	2.094	0	0.0011	0.104	2630	tags=41%, list=5%, sign
GO PLASMA	GO PLASMA MEMBRAN	291	0.64	2.095	0	0.0011	0.103	3254	tags=44%, list=6%, sign
GO TYROSI	GO TYROSINE PHOSPHO	89	0.58	2.092	0	0.0011	0.109	3273	tags=28%, list=6%, sign
GO POSITIV	GO POSITIVE REGULAT	68	0.66	2.089	0	0.0011	0.112	5307	tags=46%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULA	19	0.79	2.089	0	0.0012	0.114	5785	tags=63%, list=10%, sig
GO REGULA	GO REGULATION OF B C	49	0.65	2.088	0	0.0012	0.115	7243	tags=49%, list=12%, sig
GO CHEMO	GO CHEMOKINE RECEP	63	0.69	2.082	0	0.0013	0.126	4110	tags=40%, list=7%, sign
GO VIRAL L	GO VIRAL LIFE CYCLE	330	0.53	2.081	0	0.0013	0.127	6485	tags=34%, list=11%, sig
GO LYMPH	GO LYMPHOCYTE CHEM	63	0.67	2.08	0	0.0013	0.127	4110	tags=46%, list=7%, sign
GO POSITIV	GO POSITIVE REGULAT	18	0.81	2.078	0	0.0013	0.127	6605	tags=67%, list=11%, sig
GO ENDOPE	GO ENDOPEPTIDASE CO	68	0.72	2.074	0	0.0014	0.134	3994	tags=38%, list=7%, sign
GO CYTOPL	GO CYTOPLASMIC PAT	63	0.59	2.074	0	0.0014	0.134	7270	tags=43%, list=12%, sig
GO REGULA	GO REGULATION OF AN	67	0.68	2.073	0	0.0014	0.137	5319	tags=43%, list=9%, sign
GO INFLAM	GO INFLAMMASOME CO	16	0.81	2.073	0	0.0014	0.135	2238	tags=50%, list=4%, sign
GO IMMUN	GO IMMUNOGLOBULIN	202	0.66	2.072	0	0.0014	0.137	6737	tags=51%, list=12%, sig
GO POSITIV	GO POSITIVE REGULAT	39	0.64	2.073	0	0.0014	0.137	4039	tags=41%, list=7%, sign
GO ZYMOG	GO ZYMOGEN ACTIVAT	55	0.63	2.07	0	0.0015	0.143	8621	tags=45%, list=15%, sig
GO REGULA	GO REGULATION OF DN	111	0.6	2.069	0	0.0015	0.147	7705	tags=42%, list=13%, sig
GO REGULA	GO REGULATION OF HY	20	0.64	2.066	0	0.0015	0.15	7462	tags=50%, list=13%, sig
GO REGULA	GO REGULATION OF T H	22	0.73	2.065	0	0.0015	0.15	2916	tags=41%, list=5%, sign
GO HUMOR	GO HUMORAL IMMUNE	352	0.62	2.065	0	0.0016	0.15	8001	tags=48%, list=14%, sig
GO T CELL	GO T CELL HOMEOSTAS	38	0.65	2.064	0	0.0016	0.154	6691	tags=55%, list=11%, sig
GO POSITIV	GO POSITIVE REGULAT	16	0.77	2.063	0	0.0016	0.156	2043	tags=50%, list=3%, sign
GO LYMPH	GO LYMPHOCYTE DIFF	364	0.55	2.062	0	0.0016	0.158	4279	tags=32%, list=7%, sign
GO CD4 POS	GO CD4 POSITIVE ALPH	23	0.69	2.063	0	0.0016	0.158	3033	tags=39%, list=5%, sign
GO TOLL LI	GO TOLL LIKE RECEPTO	20	0.74	2.061	0	0.0016	0.159	7273	tags=70%, list=12%, sig
GO ENTRY I	GO ENTRY INTO HOST	143	0.54	2.056	0	0.0018	0.168	7367	tags=38%, list=13%, sig
GO RIBONU	GO RIBONUCLEOSIDE C	21	0.7	2.055	0	0.0018	0.169	8764	tags=57%, list=15%, sig

GO PROTEA	GO PROTEASOME CORE	20	0.89	2.052	0	0.0018	0.172	2770	tags=70%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	37	0.65	2.049	0	0.0019	0.184	6795	tags=49%, list=12%, sig
GO CLATHR	GO CLATHRIN COATED	57	0.62	2.048	0	0.0019	0.187	3159	tags=32%, list=5%, sign
GO INTERLI	GO INTERLEUKIN 8 PRO	101	0.54	2.047	0	0.002	0.19	6083	tags=35%, list=10%, sig
GO CYTOKI	GO CYTOKINE SECRETI	128	0.58	2.04	0	0.0021	0.202	5312	tags=41%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	42	0.62	2.036	0	0.0022	0.208	1939	tags=31%, list=3%, sign
GO NEGATI	GO NEGATIVE REGULA	48	0.61	2.036	0	0.0022	0.209	6299	tags=48%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	37	0.67	2.037	0	0.0022	0.208	5312	tags=46%, list=9%, sign
GO T CELL I	GO T CELL LINEAGE CO	28	0.7	2.034	0	0.0023	0.218	7430	tags=64%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULA	18	0.75	2.034	0	0.0023	0.218	1638	tags=33%, list=3%, sign
GO ACTIVA	GO ACTIVATION OF CY	15	0.76	2.031	0	0.0023	0.222	7263	tags=60%, list=12%, sig
GO REGULA	GO REGULATION OF RE	16	0.75	2.03	0	0.0024	0.224	6665	tags=63%, list=11%, sig
GO MYELOI	GO MYELOID DENDRITI	18	0.75	2.028	0	0.0024	0.229	3897	tags=50%, list=7%, sign
GO ANAPHA	GO ANAPHASE PROMOT	82	0.69	2.025	0	0.0025	0.236	7798	tags=48%, list=13%, sig
GO ENDOSC	GO ENDOSOME MEMBR	484	0.48	2.025	0	0.0025	0.236	4686	tags=29%, list=8%, sign
GO ANTIGEI	GO ANTIGEN BINDING	152	0.8	2.023	0	0.0025	0.237	6303	tags=64%, list=11%, sig
GO INTERLI	GO INTERLEUKIN 6 PRO	165	0.56	2.024	0	0.0025	0.237	6299	tags=38%, list=11%, sig
GO EOSINOI	GO EOSINOPHIL MIGRA	22	0.79	2.024	0	0.0025	0.237	3400	tags=50%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULA	18	0.78	2.022	0	0.0025	0.239	1718	tags=33%, list=3%, sign
GO PEPTIDE	GO PEPTIDE TRANSMEM	30	0.64	2.022	0	0.0025	0.239	2875	tags=23%, list=5%, sign
GO T HELPE	GO T HELPER 2 CELL DI	15	0.72	2.022	0	0.0025	0.239	2043	tags=40%, list=3%, sign
GO REGULA	GO REGULATION OF LE	85	0.58	2.02	0	0.0026	0.247	3621	tags=35%, list=6%, sign
GO EXTRINS	GO EXTRINSIC APOPTO	226	0.49	2.018	0	0.0026	0.25	6800	tags=35%, list=12%, sig
GO POSITIV	GO POSITIVE REGULATI	202	0.53	2.015	0	0.0028	0.256	5416	tags=33%, list=9%, sign
GO CYTOPL	GO CYTOPLASMIC PATT	28	0.65	2.012	0	0.0028	0.262	7270	tags=46%, list=12%, sig
GO MHC CL	GO MHC CLASS II PROTI	16	0.86	2.011	0	0.0029	0.266	3139	tags=63%, list=5%, sign
GO I KAPPA	GO I KAPPAB PHOSPHOI	20	0.72	2.009	0	0.0029	0.27	6845	tags=55%, list=12%, sig
GO REGULA	GO REGULATION OF TO	16	0.84	2.008	0	0.003	0.273	937	tags=56%, list=2%, sign
GO CHEMOI	GO CHEMOKINE ACTIVI	47	0.72	2.007	0	0.003	0.273	4110	tags=45%, list=7%, sign
GO REGULA	GO REGULATION OF INI	412	0.48	2.005	0	0.0031	0.276	5619	tags=32%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULA	52	0.58	2.005	0	0.0031	0.276	4374	tags=38%, list=7%, sign
GO REGULA	GO REGULATION OF B C	176	0.65	2.004	0	0.0031	0.278	7877	tags=54%, list=13%, sig
GO REGULA	GO REGULATION OF NII	116	0.53	2.003	0	0.0032	0.279	4938	tags=34%, list=8%, sign
GO EOSINOI	GO EOSINOPHIL CHEMC	18	0.84	2	0	0.0032	0.286	3400	tags=50%, list=6%, sign
GO REGULA	GO REGULATION OF SY	28	0.72	1.997	0	0.0034	0.294	3679	tags=43%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULA	15	0.73	1.995	0	0.0035	0.303	4795	tags=40%, list=8%, sign
GO RECEPT	GO RECEPTOR SIGNALI	174	0.5	1.994	0	0.0035	0.305	4938	tags=28%, list=8%, sign
GO ANTIMI	GO ANTIMICROBIAL HU	66	0.63	1.993	0	0.0035	0.309	8971	tags=50%, list=15%, sig
GO CELLUL	GO CELLULAR RESPONS	20	0.7	1.992	0	0.0035	0.312	3698	tags=45%, list=6%, sign
GO REGULA	GO REGULATION OF MY	20	0.74	1.99	0	0.0036	0.316	3679	tags=45%, list=6%, sign
GO ANTIGEI	GO ANTIGEN PROCESSII	17	0.94	1.988	0	0.0037	0.326	856	tags=76%, list=1%, sign
GO REGULA	GO REGULATION OF PEI	450	0.46	1.985	0	0.0038	0.329	7829	tags=34%, list=13%, sig
GO NATURA	GO NATURAL KILLER C	31	0.64	1.983	0	0.0039	0.331	3951	tags=35%, list=7%, sign
GO NEGATI	GO NEGATIVE REGULA	25	0.66	1.98	0	0.004	0.338	2916	tags=32%, list=5%, sign
GO PRODUC	GO PRODUCTION OF MC	90	0.53	1.977	0	0.0041	0.344	6027	tags=38%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	18	0.72	1.977	0	0.0041	0.347	3340	tags=50%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	21	0.8	1.972	0	0.0043	0.36	2361	tags=48%, list=4%, sign
GO AMINE M	GO AMINE METABOLIC	138	0.51	1.972	0	0.0044	0.36	6782	tags=33%, list=12%, sig
GO POSITIV	GO POSITIVE REGULATI	356	0.45	1.97	0	0.0044	0.365	7430	tags=34%, list=13%, sig
GO TOLL LI	GO TOLL LIKE RECEPTC	25	0.67	1.967	0	0.0045	0.367	3930	tags=40%, list=7%, sign
GO NEGATI	GO NEGATIVE REGULA	21	0.69	1.963	0	0.0047	0.378	5947	tags=38%, list=10%, sig
GO CHEMOI	GO CHEMOKINE C X C M	15	0.7	1.963	0	0.0047	0.378	7614	tags=47%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	93	0.55	1.959	0	0.0049	0.384	4938	tags=32%, list=8%, sign
GO ANTIMI	GO ANTIMICROBIAL HU	125	0.56	1.957	0	0.0049	0.386	10480	tags=46%, list=18%, sig
GO NEGATI	GO NEGATIVE REGULA	19	0.7	1.955	0	0.005	0.391	6083	tags=63%, list=10%, sig
GO HUMOR	GO HUMORAL IMMUNE	142	0.76	1.953	0	0.0051	0.397	7872	tags=66%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	71	0.56	1.951	0	0.0052	0.4	6196	tags=41%, list=11%, sig
GO ENDOCY	GO ENDOCYTIC VESICL	308	0.49	1.947	0	0.0054	0.415	4795	tags=30%, list=8%, sign

GO MHC PR	GO MHC PROTEIN COMI	23	0.96	1.947	0	0.0054	0.415	1500	tags=96%, list=3%, sign
GO CYTOKI	GO CYTOKINE PRODUCT	67	0.55	1.945	0	0.0055	0.419	5216	tags=36%, list=9%, sign
GO ACTIVAT	GO ACTIVATION OF NF	17	0.71	1.946	0	0.0055	0.419	3003	tags=41%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	177	0.46	1.941	0	0.0057	0.428	7615	tags=39%, list=13%, sig
GO FICOLIN	GO FICOLIN 1 RICH GRA	124	0.53	1.933	0	0.0062	0.45	4842	tags=38%, list=8%, sign
GO POSITIV	GO POSITIVE REGULATI	267	0.48	1.933	0	0.0062	0.452	7243	tags=39%, list=12%, sig
GO ACTIVAT	GO ACTIVATION OF JAN	15	0.74	1.933	0	0.0062	0.452	3483	tags=47%, list=6%, sign
GO RESPON	GO RESPONSE TO INTEF	35	0.58	1.929	0	0.0065	0.462	3678	tags=31%, list=6%, sign
GO EARLY E	GO EARLY ENDOSOME	152	0.5	1.924	0	0.0068	0.479	3740	tags=23%, list=6%, sign
GO B CELL A	GO B CELL APOPTOTIC	26	0.61	1.921	0	0.0069	0.486	2630	tags=31%, list=5%, sign
GO DEOXYR	GO DEOXYRIBONUCLEO	15	0.75	1.91	0	0.0078	0.508	7852	tags=60%, list=13%, sig
GO KILLING	GO KILLING OF CELLS O	63	0.57	1.901	0	0.0085	0.535	8971	tags=46%, list=15%, sig
GO LATE EN	GO LATE ENDOSOME	263	0.45	1.886	0	0.0097	0.571	5939	tags=30%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULAT	83	0.47	1.886	0	0.0097	0.571	7662	tags=34%, list=13%, sig
GO REGULA	GO REGULATION OF MY	122	0.5	1.873	0	0.0111	0.616	6389	tags=34%, list=11%, sig
GO HYDROL	GO HYDROLASE ACTIVI	34	0.57	1.87	0	0.0113	0.622	4524	tags=35%, list=8%, sign
GO REGULA	GO REGULATION OF DN	444	0.43	1.862	0	0.0125	0.643	7243	tags=34%, list=12%, sig
GO CYSTEIN	GO CYSTEINE TYPE ENI	41	0.55	1.859	0	0.0127	0.651	6860	tags=39%, list=12%, sig
GO REGULA	GO REGULATION OF RE	151	0.46	1.856	0	0.0131	0.662	4938	tags=27%, list=8%, sign
GO PEPTIDA	GO PEPTIDASE ACTIVAT	18	0.6	1.842	0	0.0148	0.698	5115	tags=44%, list=9%, sign
GO DEAMIN	GO DEAMINASE ACTIVI	30	0.58	1.841	0	0.015	0.702	4524	tags=37%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULAT	92	0.48	1.839	0	0.0152	0.703	7829	tags=34%, list=13%, sig
GO CELLUL	GO CELLULAR KETONE	253	0.44	1.839	0	0.0152	0.705	6795	tags=32%, list=12%, sig
GO POSITIV	GO POSITIVE REGULATI	26	0.57	1.836	0	0.0155	0.712	6083	tags=35%, list=10%, sig
GO CYSTEIN	GO CYSTEINE TYPE PEP	137	0.48	1.835	0	0.0155	0.713	6375	tags=28%, list=11%, sig
GO PEPTIDE	GO PEPTIDE BINDING	299	0.44	1.835	0	0.0156	0.715	4903	tags=25%, list=8%, sign
GO VESICLE	GO VESICLE LUMEN	322	0.46	1.828	0	0.0164	0.723	6500	tags=34%, list=11%, sig
GO REGULA	GO REGULATION OF CE	187	0.45	1.826	0	0.0165	0.728	6795	tags=30%, list=12%, sig
GO INTRINS	GO INTRINSIC COMPON	377	0.44	1.821	0	0.0172	0.739	6323	tags=28%, list=11%, sig
GO RECYCL	GO RECYCLING ENDOSO	180	0.44	1.812	0	0.0187	0.762	6267	tags=31%, list=11%, sig
GO MULTIV	GO MULTIVESICULAR E	59	0.49	1.771	0	0.0261	0.845	4279	tags=29%, list=7%, sign
GO ENDOPE	GO ENDOPEPTIDASE AC	430	0.39	1.733	0	0.0347	0.904	6588	tags=26%, list=11%, sig
GO NAD BIO	GO NAD BIOSYNTHETIC	27	0.51	1.645	0	0.0614	0.979	4542	tags=30%, list=8%, sign
GO REGULA	GO REGULATION OF HU	132	0.67	1.899	0.002	0.0087	0.541	7314	tags=55%, list=13%, sig
GO PHAGOC	GO PHAGOCYTOSIS	362	0.58	1.958	0.002	0.0049	0.385	6328	tags=44%, list=11%, sig
GO NEUTRO	GO NEUTROPHIL CHEMO	98	0.61	1.981	0.002	0.004	0.335	6161	tags=42%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	132	0.65	1.892	0.002	0.0093	0.559	7877	tags=56%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	33	0.64	1.898	0.002	0.0087	0.546	5416	tags=45%, list=9%, sign
GO DENDRI	GO DENDRITIC CELL DI	44	0.7	2.098	0.002	0.0011	0.1	6299	tags=55%, list=11%, sig
GO CD4 POS	GO CD4 POSITIVE OR CI	22	0.75	2.012	0.002	0.0028	0.261	7133	tags=68%, list=12%, sig
GO POSITIV	GO POSITIVE REGULATI	221	0.44	1.848	0.002	0.0141	0.681	5820	tags=29%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULAT	23	0.64	1.968	0.002	0.0044	0.366	5319	tags=48%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	16	0.72	1.836	0.002	0.0154	0.71	5045	tags=44%, list=9%, sign
GO FC RECE	GO FC RECEPTOR MEDI	143	0.64	1.898	0.002	0.0087	0.545	6719	tags=52%, list=12%, sig
GO NEUTRO	GO NEUTROPHIL MIGRA	117	0.61	1.996	0.002	0.0034	0.299	5820	tags=43%, list=10%, sig
GO PROTEIN	GO PROTEIN ADP RIBOS	16	0.76	1.979	0.002	0.004	0.339	3915	tags=50%, list=7%, sign
GO REGULA	GO REGULATION OF MO	22	0.71	2.037	0.002	0.0022	0.208	2052	tags=32%, list=4%, sign
GO COPII CO	GO COPII COATED ER TO	91	0.62	2.018	0.002	0.0026	0.25	4459	tags=34%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULAT	22	0.68	2.012	0.002	0.0028	0.263	725	tags=27%, list=1%, sign
GO CYTOKI	GO CYTOKINE ACTIVIT	232	0.49	1.848	0.002	0.0141	0.681	6195	tags=30%, list=11%, sig
GO NEGATI	GO NEGATIVE REGULAT	175	0.39	1.702	0.002	0.043	0.937	7080	tags=30%, list=12%, sig
GO NEGATI	GO NEGATIVE REGULAT	76	0.52	1.83	0.002	0.0161	0.721	5546	tags=32%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	104	0.56	2.137	0.002	######	0.062	3263	tags=28%, list=6%, sign
GO INFLAM	GO INFLAMMATORY RE	63	0.59	1.925	0.002	0.0067	0.474	7314	tags=40%, list=13%, sig
GO REGULA	GO REGULATION OF PE	423	0.38	1.683	0.002	0.0477	0.956	4629	tags=23%, list=8%, sign
GO REGULA	GO REGULATION OF CE	80	0.64	2.07	0.002	0.0015	0.143	6782	tags=44%, list=12%, sig
GO MACROI	GO MACROPHAGE ACTI	97	0.63	2.064	0.002	0.0016	0.154	5312	tags=43%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	22	0.69	1.955	0.002	0.005	0.393	2043	tags=32%, list=3%, sign

GO SUPERO	GO SUPEROXIDE ANION	35	0.6	1.883	0.002	0.01	0.586	6444	tags=51%, list=11%, sig
GO CHEMOI	GO CHEMOKINE BIOSYI	16	0.65	1.801	0.002	0.0204	0.79	5876	tags=50%, list=10%, sig
GO INTERLI	GO INTERLEUKIN 2 PRO	54	0.64	2.042	0.002	0.0021	0.198	3436	tags=37%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	60	0.6	2.015	0.002	0.0028	0.256	5312	tags=37%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	24	0.68	1.988	0.002	0.0037	0.325	5785	tags=46%, list=10%, sig
GO CLATHR	GO CLATHRIN COATED	38	0.67	1.948	0.002	0.0053	0.415	4653	tags=42%, list=8%, sign
GO IMMUN	GO IMMUNOLOGICAL S	38	0.67	1.928	0.002	0.0065	0.467	3379	tags=45%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	58	0.54	1.79	0.002	0.0221	0.811	3238	tags=29%, list=6%, sign
GO PEPTIDA	GO PEPTIDASE REGULA	221	0.41	1.595	0.002	0.0825	0.992	7209	tags=29%, list=12%, sig
GO LEUKOC	GO LEUKOCYTE ACTIV	48	0.73	2.137	0.002	######	0.062	4938	tags=52%, list=8%, sign
GO REGULA	GO REGULATION OF LE	46	0.61	1.982	0.002	0.0039	0.335	6769	tags=54%, list=12%, sig
GO INTERLI	GO INTERLEUKIN 13 PR	21	0.67	1.973	0.002	0.0043	0.357	4359	tags=48%, list=7%, sign
GO MYD88 I	GO MYD88 DEPENDENT	36	0.68	2.069	0.002	0.0015	0.147	8635	tags=61%, list=15%, sig
GO CYTOKI	GO CYTOKINE RECEPTC	97	0.61	1.972	0.002	0.0043	0.358	8001	tags=53%, list=14%, sig
GO LIPOPOI	GO LIPOPOLYSACCHAR	58	0.59	1.945	0.002	0.0055	0.419	5876	tags=47%, list=10%, sig
GO MIDBOD	GO MIDBODY ABSCISSI	17	0.69	1.938	0.002	0.0059	0.437	5636	tags=47%, list=10%, sig
GO ANTIGEI	GO ANTIGEN PROCESSII	100	0.57	1.914	0.002	0.0074	0.5	4390	tags=32%, list=8%, sign
GO REGULA	GO REGULATION OF ISC	31	0.6	1.899	0.002	0.0086	0.539	3991	tags=39%, list=7%, sign
GO SPECIFI	GO SPECIFIC GRANULE	62	0.56	1.897	0.002	0.0089	0.549	4998	tags=39%, list=9%, sign
GO REGULA	GO REGULATION OF CE	63	0.71	2.091	0.002	0.0011	0.11	3994	tags=40%, list=7%, sign
GO REGULA	GO REGULATION OF PH	95	0.62	2.056	0.002	0.0018	0.167	5312	tags=44%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	143	0.5	2	0.002	0.0032	0.284	6384	tags=31%, list=11%, sig
GO INTRINS	GO INTRINSIC APOPTOT	101	0.47	1.8	0.002	0.0203	0.79	7681	tags=40%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	47	0.67	2.098	0.002	0.0011	0.102	2916	tags=36%, list=5%, sign
GO TERTIAI	GO TERTIARY GRANULI	160	0.56	2.048	0.002	0.0019	0.185	4859	tags=39%, list=8%, sign
GO SPECIFI	GO SPECIFIC GRANULE	158	0.52	1.949	0.002	0.0053	0.405	4998	tags=37%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	30	0.54	1.9	0.002	0.0086	0.536	5045	tags=43%, list=9%, sign
GO INTERFI	GO INTERFERON ALPHA	27	0.68	1.96	0.002	0.0048	0.383	1068	tags=30%, list=2%, sign
GO MACROI	GO MACROPHAGE CHEI	40	0.6	1.939	0.002	0.0058	0.434	4317	tags=38%, list=7%, sign
GO NEGATI	GO NEGATIVE REGULAT	21	0.67	1.891	0.002	0.0093	0.562	2916	tags=33%, list=5%, sign
GO OXIDOR	GO OXIDOREDUCTASE	19	0.67	1.821	0.002	0.0172	0.739	8581	tags=58%, list=15%, sig
GO NEGATI	GO NEGATIVE REGULAT	292	0.43	1.828	0.002	0.0164	0.723	6069	tags=27%, list=10%, sig
GO LYMPH	GO LYMPHOCYTE MIGR	113	0.61	1.979	0.002	0.004	0.339	6434	tags=47%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	21	0.66	1.98	0.002	0.004	0.339	5838	tags=33%, list=10%, sig
GO CELLUL	GO CELLULAR RESPONS	15	0.76	1.965	0.002	0.0046	0.372	2122	tags=53%, list=4%, sign
GO TRANS (	GO TRANS GOLGI NETW	86	0.52	1.923	0.002	0.0068	0.479	4952	tags=30%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULAT	17	0.69	1.872	0.002	0.0112	0.618	2916	tags=35%, list=5%, sign
GO REGULA	GO REGULATION OF HE	86	0.59	1.967	0.002	0.0045	0.369	3131	tags=27%, list=5%, sign
GO B CELL	GO B CELL ACTIVATION	307	0.57	1.928	0.002	0.0065	0.467	7939	tags=45%, list=14%, sig
GO CELLUL	GO CELLULAR MODIFIE	48	0.55	1.88	0.002	0.0103	0.593	5400	tags=33%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	15	0.78	2.053	0.002	0.0018	0.172	6065	tags=53%, list=10%, sig
GO INFLAM	GO INFLAMMATORY CE	21	0.68	1.949	0.002	0.0053	0.406	4795	tags=43%, list=8%, sign
GO REACTI	GO REACTIVE OXYGEN	274	0.41	1.722	0.002	0.0374	0.918	5619	tags=28%, list=10%, sig
GO TUMOR	GO TUMOR NECROSIS F	47	0.58	1.888	0.002	0.0096	0.569	4124	tags=32%, list=7%, sign
GO REGULA	GO REGULATION OF RE	15	0.75	1.949	0.002	0.0053	0.411	4639	tags=60%, list=8%, sign
GO KILLING	GO KILLING OF CELLS I	28	0.61	1.768	0.002	0.0266	0.85	10123	tags=50%, list=17%, sig
GO POSITIV	GO POSITIVE REGULATI	30	0.66	2.014	0.002	0.0028	0.259	2002	tags=33%, list=3%, sign
GO DEOXYI	GO DEOXYRIBONUCLE	17	0.71	1.922	0.002	0.0069	0.482	2242	tags=35%, list=4%, sign
GO REGULA	GO REGULATION OF HE	73	0.63	1.994	0.002	0.0035	0.305	3131	tags=32%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	37	0.66	1.925	0.002	0.0067	0.475	6093	tags=51%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULAT	41	0.58	1.868	0.002	0.0117	0.632	3003	tags=32%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	79	0.51	1.831	0.002	0.0161	0.721	4938	tags=34%, list=8%, sign
GO CYSTEII	GO CYSTEINE TYPE ENI	114	0.47	1.768	0.002	0.0266	0.85	6375	tags=26%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	86	0.6	1.995	0.002	0.0035	0.304	5312	tags=42%, list=9%, sign
GO PEPTIDA	GO PEPTIDASE ACTIVAT	37	0.6	1.979	0.002	0.004	0.339	5115	tags=35%, list=9%, sign
GO NADPLU	GO NADPLUS NUCLEOS	16	0.71	1.841	0.002	0.0149	0.702	3466	tags=50%, list=6%, sign
GO RESPON	GO RESPONSE TO DSRN	51	0.54	1.823	0.002	0.0169	0.735	8377	tags=47%, list=14%, sig
GO NEGATI	GO NEGATIVE REGULAT	422	0.43	1.861	0.002	0.0125	0.645	4992	tags=24%, list=9%, sign

GO REGULA	GO REGULATION OF RE	191	0.42	1.732	0.002	0.0349	0.905	5619	tags=30%, list=10%, sig
GO CYTOKI	GO CYTOKINE METABO	73	0.57	1.943	0.002	0.0056	0.424	2705	tags=32%, list=5%, sign
GO NUCLE	GO NUCLEOSIDE META	99	0.49	1.871	0.002	0.0112	0.619	10245	tags=48%, list=18%, sig
GO POSITIV	GO POSITIVE REGULAT	21	0.63	1.764	0.002	0.0274	0.859	10532	tags=62%, list=18%, sig
GO POSITIV	GO POSITIVE REGULAT	54	0.51	1.722	0.002	0.0374	0.918	6444	tags=39%, list=11%, sig
GO NEGATI	GO NEGATIVE REGULA	43	0.59	1.93	0.002	0.0064	0.46	7299	tags=47%, list=13%, sig
GO REGULA	GO REGULATION OF RE	47	0.54	1.873	0.002	0.0111	0.616	7601	tags=43%, list=13%, sig
GO INTRINS	GO INTRINSIC APOPTO	280	0.42	1.717	0.002	0.0386	0.926	7681	tags=35%, list=13%, sig
GO INTRINS	GO INTRINSIC APOPTO	44	0.55	1.881	0.004	0.0102	0.592	7681	tags=48%, list=13%, sig
GO REGULA	GO REGULATION OF T	27	0.71	1.928	0.004	0.0065	0.467	3436	tags=44%, list=6%, sign
GO CCR CH	GO CCR CHEMOKINE R	41	0.71	2.002	0.004	0.0032	0.281	4110	tags=46%, list=7%, sign
GO T CELL	GO T CELL CHEMOTAXI	28	0.68	1.949	0.004	0.0053	0.411	2542	tags=36%, list=4%, sign
GO DEATH	GO DEATH RECEPTOR	19	0.64	1.904	0.004	0.0083	0.521	6375	tags=53%, list=11%, sig
GO T HELPE	GO T HELPER 1 CELL D	19	0.67	1.859	0.004	0.0128	0.652	1318	tags=42%, list=2%, sign
GO GOLGI A	GO GOLGI ASSOCIATED	107	0.55	1.957	0.004	0.0049	0.386	4459	tags=30%, list=8%, sign
GO REGULA	GO REGULATION OF LY	27	0.67	1.98	0.004	0.004	0.339	3483	tags=44%, list=6%, sign
GO VIRION	GO VIRION ASSEMBLY	40	0.54	1.793	0.004	0.0215	0.802	5777	tags=45%, list=10%, sig
GO ANTIBA	GO ANTIBACTERIAL HU	49	0.6	1.802	0.004	0.0201	0.78	9849	tags=45%, list=17%, sig
GO HEPATO	GO HEPATOCYTE GRO	16	0.6	1.744	0.004	0.0319	0.89	6471	tags=50%, list=11%, sig
GO ENDOS	GO ENDOSOME ORGAN	75	0.51	1.85	0.004	0.0139	0.676	7629	tags=43%, list=13%, sig
GO THYMO	GO THYMOCYTE APOPT	17	0.63	1.85	0.004	0.0139	0.677	2894	tags=41%, list=5%, sign
GO REGULA	GO REGULATION OF TY	35	0.61	1.97	0.004	0.0044	0.365	1735	tags=29%, list=3%, sign
GO EXTERN	GO EXTERNAL SIDE OF	401	0.58	1.978	0.004	0.0041	0.343	3878	tags=34%, list=7%, sign
GO POSITIV	GO POSITIVE REGULAT	26	0.67	1.856	0.004	0.0131	0.661	2361	tags=35%, list=4%, sign
GO REGULA	GO REGULATION OF DE	29	0.65	1.943	0.004	0.0056	0.424	3967	tags=38%, list=7%, sign
GO GLIAL C	GO GLIAL CELL ACTIVA	58	0.63	1.937	0.004	0.0059	0.439	4938	tags=45%, list=8%, sign
GO POSITIV	GO POSITIVE REGULAT	24	0.68	1.932	0.004	0.0062	0.453	6795	tags=54%, list=12%, sig
GO T HELPE	GO T HELPER CELL LIN	16	0.76	1.901	0.004	0.0086	0.535	6605	tags=69%, list=11%, sig
GO POSITIV	GO POSITIVE REGULAT	28	0.56	1.851	0.004	0.0138	0.674	3623	tags=32%, list=6%, sign
GO AMIDE	GO AMIDE TRANSMEM	49	0.48	1.694	0.004	0.0449	0.948	4959	tags=22%, list=8%, sign
GO DEFENS	GO DEFENSE RESPONS	78	0.49	1.752	0.004	0.0299	0.872	8971	tags=37%, list=15%, sig
GO POSITIV	GO POSITIVE REGULAT	37	0.62	1.876	0.004	0.0107	0.606	3483	tags=38%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULA	54	0.5	1.826	0.004	0.0165	0.728	7903	tags=44%, list=14%, sig
GO POSITIV	GO POSITIVE REGULAT	60	0.52	1.846	0.004	0.0144	0.689	5636	tags=35%, list=10%, sig
GO POSITIV	GO POSITIVE REGULAT	102	0.48	1.811	0.004	0.0187	0.762	5546	tags=37%, list=9%, sign
GO AMIDE	GO AMIDE BINDING	368	0.4	1.699	0.004	0.0436	0.94	4903	tags=23%, list=8%, sign
GO IMMUN	GO IMMUNOGLOBULIN	55	0.59	1.892	0.004	0.0092	0.559	4039	tags=35%, list=7%, sign
GO POSITIV	GO POSITIVE REGULAT	21	0.6	1.84	0.004	0.0151	0.703	4852	tags=38%, list=8%, sign
GO NON ME	GO NON MEMBRANE SP	46	0.56	1.829	0.004	0.0163	0.723	7949	tags=46%, list=14%, sig
GO T CELL	GO T CELL DIFFERENT	75	0.51	1.83	0.004	0.0161	0.721	2519	tags=28%, list=4%, sign
GO PEPTID	GO PEPTIDASE COMPLE	90	0.63	2.004	0.004	0.0031	0.278	2770	tags=28%, list=5%, sign
GO TRANSL	GO TRANSLESION SYNT	39	0.68	1.97	0.004	0.0044	0.365	9018	tags=56%, list=15%, sig
GO PURINE	GO PURINE CONTAININ	15	0.7	1.909	0.004	0.0079	0.512	8546	tags=67%, list=15%, sig
GO POSITIV	GO POSITIVE REGULAT	25	0.65	1.975	0.004	0.0042	0.349	2359	tags=44%, list=4%, sign
GO MACRO	GO MACROPHAGE ACTI	15	0.74	1.855	0.004	0.0132	0.662	2086	tags=53%, list=4%, sign
GO MACRO	GO MACROPHAGE DIFF	47	0.61	1.885	0.004	0.0099	0.578	2629	tags=32%, list=5%, sign
GO LYMPH	GO LYMPHOCYTE HOM	62	0.64	2.033	0.004	0.0023	0.218	6691	tags=47%, list=11%, sig
GO HYDRO	GO HYDROLASE ACTIV	34	0.52	1.737	0.004	0.0337	0.898	5989	tags=41%, list=10%, sig
GO SUPERO	GO SUPEROXIDE META	73	0.48	1.733	0.004	0.0348	0.903	6665	tags=37%, list=11%, sig
GO RELEAS	GO RELEASE OF CYTOC	58	0.53	1.918	0.004	0.0071	0.491	6251	tags=38%, list=11%, sig
GO DETECT	GO DETECTION OF EXT	24	0.73	1.874	0.004	0.011	0.611	2983	tags=42%, list=5%, sign
GO HEMAT	GO HEMATOPOIETIC ST	87	0.58	1.985	0.004	0.0038	0.328	5095	tags=33%, list=9%, sign
GO PYRIMI	GO PYRIMIDINE CONTA	38	0.51	1.777	0.004	0.0249	0.833	10152	tags=55%, list=17%, sig
GO COMPLE	GO COMPLEMENT ACTI	165	0.66	1.801	0.006	0.0202	0.789	7872	tags=58%, list=13%, sig
GO NUCLE	GO NUCLEOTIDE BINDI	36	0.57	1.837	0.006	0.0155	0.709	10512	tags=58%, list=18%, sig
GO CHEMO	GO CHEMOKINE PRODU	93	0.53	1.963	0.006	0.0047	0.378	5876	tags=34%, list=10%, sig
GO SECRET	GO SECRETORY GRANU	296	0.46	1.84	0.006	0.0151	0.703	7668	tags=36%, list=13%, sig
GO POSITIV	GO POSITIVE REGULAT	138	0.54	1.92	0.006	0.007	0.488	6386	tags=42%, list=11%, sig

GO CXCR CI	GO CXCR CHEMOKINE I	17	0.79	1.908	0.006	0.008	0.516	2542	tags=35%, list=4%, sign
GO POSITIV	GO POSITIVE REGULATI	67	0.6	2.011	0.006	0.0029	0.265	5619	tags=43%, list=10%, sig
GO LEUKOC	GO LEUKOCYTE CHEMC	222	0.53	1.925	0.006	0.0067	0.473	6386	tags=36%, list=11%, sig
GO NUCLEO	GO NUCLEOTIDE RECEF	21	0.69	1.826	0.006	0.0166	0.728	6701	tags=52%, list=11%, sig
GO IMMUNC	GO IMMUNOGLOBULIN	148	0.77	1.8	0.006	0.0204	0.79	8081	tags=69%, list=14%, sig
GO REGULA	GO REGULATION OF B C	20	0.59	1.764	0.006	0.0273	0.856	2630	tags=30%, list=5%, sign
GO REGULA	GO REGULATION OF AN	20	0.76	1.885	0.006	0.0098	0.575	5785	tags=65%, list=10%, sig
GO REGULA	GO REGULATION OF MY	57	0.57	1.884	0.006	0.0099	0.58	3331	tags=37%, list=6%, sign
GO ENDOSC	GO ENDOSOME LUMEN	35	0.53	1.74	0.006	0.0329	0.893	8253	tags=37%, list=14%, sig
GO CYSTEIN	GO CYSTEINE TYPE ENI	59	0.49	1.699	0.006	0.0437	0.94	6860	tags=37%, list=12%, sig
GO REGULA	GO REGULATION OF LEI	120	0.54	1.946	0.006	0.0054	0.416	6386	tags=39%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	20	0.68	1.849	0.006	0.014	0.681	1068	tags=30%, list=2%, sign
GO ESCRT C	GO ESCRT COMPLEX	27	0.58	1.808	0.006	0.0192	0.769	5636	tags=44%, list=10%, sig
GO PHAGOC	GO PHAGOCYTIC CUP	25	0.64	1.901	0.006	0.0085	0.532	5939	tags=52%, list=10%, sig
GO REGULA	GO REGULATION OF LEI	206	0.52	1.914	0.006	0.0074	0.499	6434	tags=39%, list=11%, sig
GO T CELL I	GO T CELL MIGRATION	65	0.63	1.922	0.006	0.0069	0.483	2846	tags=35%, list=5%, sign
GO RESPON	GO RESPONSE TO UV C	16	0.64	1.817	0.006	0.0178	0.746	2111	tags=31%, list=4%, sign
GO RESPON	GO RESPONSE TO FUNG	54	0.56	1.773	0.006	0.0255	0.84	7298	tags=43%, list=12%, sig
GO REGULA	GO REGULATION OF MA	42	0.62	1.956	0.006	0.0049	0.387	7814	tags=52%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	419	0.5	1.921	0.006	0.0069	0.486	3623	tags=28%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	34	0.6	1.874	0.006	0.011	0.614	2290	tags=38%, list=4%, sign
GO CELLUL	GO CELLULAR RESPONS	78	0.53	1.871	0.006	0.0112	0.619	6506	tags=38%, list=11%, sig
GO MACROI	GO MACROPHAGE MIGF	54	0.6	1.937	0.006	0.0059	0.441	8001	tags=50%, list=14%, sig
GO EXTRINS	GO EXTRINSIC APOPTO	87	0.48	1.831	0.006	0.016	0.721	3003	tags=26%, list=5%, sign
GO COATED	GO COATED VESICLE M	177	0.49	1.821	0.006	0.0172	0.74	4653	tags=27%, list=8%, sign
GO POSITIV	GO POSITIVE REGULATI	29	0.64	1.9	0.006	0.0086	0.538	3340	tags=41%, list=6%, sign
GO INTERLI	GO INTERLEUKIN 7 MEI	17	0.69	1.805	0.006	0.0197	0.777	2519	tags=47%, list=4%, sign
GO PINOCY	GO PINOCYTOSIS	22	0.58	1.788	0.006	0.0224	0.814	8857	tags=59%, list=15%, sig
GO GLYCOS	GO GLYCOSYL COMPOU	124	0.43	1.689	0.006	0.0462	0.952	8789	tags=39%, list=15%, sig
GO DEOXYI	GO DEOXYRIBONUCLEC	34	0.62	1.887	0.006	0.0096	0.569	7852	tags=53%, list=13%, sig
GO REGULA	GO REGULATION OF EX	61	0.52	1.793	0.006	0.0216	0.802	3003	tags=28%, list=5%, sign
GO RESPON	GO RESPONSE TO INTEF	55	0.49	1.642	0.006	0.0622	0.979	1386	tags=20%, list=2%, sign
GO PROTEIN	GO PROTEIN MODIFICA	288	0.5	1.83	0.006	0.0161	0.721	6166	tags=29%, list=11%, sig
GO INTRINS	GO INTRINSIC APOPTOT	59	0.5	1.815	0.006	0.0181	0.75	6471	tags=34%, list=11%, sig
GO NUCLEO	GO NUCLEOSIDE TRIPH	87	0.43	1.656	0.007	0.0577	0.973	8789	tags=40%, list=15%, sig
GO T HELPE	GO T HELPER 2 CELL CY	15	0.62	1.76	0.007	0.0282	0.863	2043	tags=27%, list=3%, sign
GO REGULA	GO REGULATION OF MA	55	0.59	1.92	0.008	0.0069	0.487	5104	tags=36%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	41	0.59	1.858	0.008	0.0128	0.653	2361	tags=32%, list=4%, sign
GO ORGAN (	GO ORGAN OR TISSUE S	32	0.56	1.665	0.008	0.0545	0.969	8589	tags=50%, list=15%, sig
GO NITRIC (	GO NITRIC OXIDE SYNT	19	0.65	1.796	0.008	0.0211	0.796	2266	tags=32%, list=4%, sign
GO REGULA	GO REGULATION OF MI	19	0.7	1.807	0.008	0.0195	0.775	4352	tags=47%, list=7%, sign
GO REGULA	GO REGULATION OF NE	41	0.58	1.789	0.008	0.0222	0.812	5045	tags=39%, list=9%, sign
GO GRANUI	GO GRANULOCYTE MIG	143	0.57	1.969	0.008	0.0044	0.366	6386	tags=41%, list=11%, sig
GO CHRONI	GO CHRONIC INFLAMM	20	0.67	1.791	0.008	0.0218	0.808	9938	tags=65%, list=17%, sig
GO MYELOI	GO MYELOID LEUKOCY	208	0.47	1.831	0.008	0.016	0.721	6389	tags=34%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	93	0.54	1.907	0.008	0.008	0.516	6386	tags=42%, list=11%, sig
GO GRANUI	GO GRANULOCYTE CHE	120	0.57	1.903	0.008	0.0083	0.527	6386	tags=39%, list=11%, sig
GO NEUROI	GO NEUROINFLAMMAT	75	0.58	1.9	0.008	0.0086	0.536	5045	tags=41%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULA	188	0.42	1.714	0.008	0.0397	0.929	5619	tags=27%, list=10%, sig
GO NEGATI	GO NEGATIVE REGULA	25	0.56	1.692	0.008	0.0454	0.951	5416	tags=44%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULA	32	0.63	1.884	0.008	0.0099	0.58	4359	tags=38%, list=7%, sign
GO MYELOI	GO MYELOID LEUKOCY	211	0.53	1.904	0.008	0.0083	0.521	6161	tags=37%, list=11%, sig
GO CLATHR	GO CLATHRIN COATED	115	0.48	1.786	0.008	0.0227	0.818	3159	tags=24%, list=5%, sign
GO VIRAL B	GO VIRAL BUDDING	26	0.58	1.751	0.008	0.0301	0.875	5636	tags=42%, list=10%, sig
GO OXIDOR	GO OXIDOREDUCTASE	108	0.5	1.816	0.008	0.018	0.747	8955	tags=48%, list=15%, sig
GO NEGATI	GO NEGATIVE REGULA	102	0.61	1.938	0.008	0.0059	0.437	6103	tags=33%, list=10%, sig
GO INTERLI	GO INTERLEUKIN 1 REC	16	0.69	1.706	0.008	0.0421	0.932	6836	tags=56%, list=12%, sig
GO PROTEIN	GO PROTEIN POLYUBIQ	332	0.46	1.805	0.008	0.0196	0.778	6850	tags=30%, list=12%, sig

GO THYMIC	GO THYMIC T CELL SEL	22	0.7	1.89	0.008	0.0094	0.565	3953	tags=55%, list=7%, sign
GO MHC CL	GO MHC CLASS II BIOSY	16	0.73	1.836	0.008	0.0155	0.71	3436	tags=44%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	22	0.63	1.77	0.008	0.0262	0.846	4938	tags=50%, list=8%, sign
GO RIG I SIC	GO RIG I SIGNALING PA	23	0.57	1.69	0.008	0.0459	0.952	1144	tags=22%, list=2%, sign
GO ACUTE I	GO ACUTE INFLAMMAT	110	0.5	1.8	0.008	0.0204	0.79	8635	tags=41%, list=15%, sig
GO BLOC C	GO BLOC COMPLEX	19	0.63	1.827	0.009	0.0165	0.728	8714	tags=63%, list=15%, sig
GO REGULA	GO REGULATION OF MY	232	0.42	1.685	0.009	0.0471	0.955	6389	tags=29%, list=11%, sig
GO MYELOI	GO MYELOID CELL DIFF	396	0.41	1.701	0.009	0.0432	0.939	6389	tags=28%, list=11%, sig
GO NEGATI	GO NEGATIVE REGULAT	16	0.61	1.7	0.009	0.0435	0.94	1338	tags=25%, list=2%, sign
GO NATURA	GO NATURAL KILLER C	22	0.58	1.67	0.009	0.0524	0.968	2396	tags=27%, list=4%, sign
GO HYDRO	GO HYDROGEN PEROXI	16	0.62	1.766	0.009	0.0269	0.851	4738	tags=50%, list=8%, sign
GO REGULA	GO REGULATION OF AP	401	0.38	1.631	0.009	0.0671	0.984	7681	tags=31%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	393	0.38	1.627	0.009	0.0688	0.985	5494	tags=25%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	16	0.71	1.819	0.01	0.0175	0.744	2748	tags=44%, list=5%, sign
GO TRANSP	GO TRANSPORT VESICL	200	0.44	1.684	0.01	0.0476	0.956	5698	tags=26%, list=10%, sig
GO REGULA	GO REGULATION OF INF	32	0.69	1.875	0.01	0.0109	0.611	7314	tags=50%, list=13%, sig
GO IRON IO	GO IRON ION TRANSME	18	0.59	1.706	0.01	0.0421	0.932	6306	tags=44%, list=11%, sig
GO FAT SOL	GO FAT SOLUBLE VITAM	15	0.66	1.792	0.01	0.0217	0.806	5219	tags=47%, list=9%, sign
GO MULTIV	GO MULTIVESICULAR B	31	0.58	1.823	0.01	0.017	0.735	3932	tags=39%, list=7%, sign
GO REGULA	GO REGULATION OF VI	19	0.58	1.725	0.01	0.0368	0.916	2002	tags=26%, list=3%, sign
GO REGULA	GO REGULATION OF B C	62	0.58	1.825	0.01	0.0167	0.732	2802	tags=32%, list=5%, sign
GO POSTRE	GO POSTREPLICATION I	49	0.62	1.848	0.01	0.0141	0.681	9018	tags=51%, list=15%, sig
GO NEGATI	GO NEGATIVE REGULAT	15	0.67	1.746	0.01	0.0314	0.885	1735	tags=33%, list=3%, sign
GO REGULA	GO REGULATION OF OS	66	0.49	1.71	0.01	0.0408	0.93	6716	tags=39%, list=12%, sig
GO REGULA	GO REGULATION OF SU	37	0.52	1.737	0.01	0.0337	0.896	6444	tags=38%, list=11%, sig
GO MEMBR	GO MEMBRANE RAFT O	25	0.6	1.836	0.01	0.0155	0.712	8159	tags=68%, list=14%, sig
GO POSITIV	GO POSITIVE REGULATI	25	0.67	1.845	0.01	0.0144	0.69	8001	tags=60%, list=14%, sig
GO CD8 POS	GO CD8 POSITIVE ALPH	15	0.69	1.73	0.01	0.0352	0.91	6975	tags=47%, list=12%, sig
GO NUCLEO	GO NUCLEOBASE CONT	102	0.42	1.659	0.01	0.0563	0.973	8966	tags=38%, list=15%, sig
GO POSITIV	GO POSITIVE REGULATI	26	0.67	1.814	0.01	0.0183	0.752	4124	tags=42%, list=7%, sign
GO POSITIV	GO POSITIVE REGULATI	31	0.54	1.667	0.011	0.0534	0.969	5619	tags=32%, list=10%, sig
GO DNA DA	GO DNA DAMAGE RESP	18	0.55	1.622	0.011	0.0706	0.987	4763	tags=28%, list=8%, sign
GO REGULA	GO REGULATION OF LY	62	0.57	1.848	0.011	0.0141	0.681	8773	tags=48%, list=15%, sig
GO PHOSPH	GO PHOSPHATIDYLINOS	29	0.56	1.77	0.011	0.0262	0.847	8059	tags=52%, list=14%, sig
GO ENDOPL	GO ENDOPLASMIC RETI	23	0.56	1.758	0.011	0.0286	0.865	7829	tags=39%, list=13%, sig
GO APOPTO	GO APOPTOTIC MITOCH	120	0.44	1.713	0.011	0.04	0.929	7601	tags=37%, list=13%, sig
GO HYDROL	GO HYDROLASE ACTIVI	119	0.4	1.627	0.011	0.0688	0.985	6396	tags=28%, list=11%, sig
GO HEMATO	GO HEMATOPOIETIC PR	170	0.43	1.679	0.011	0.0494	0.961	7843	tags=32%, list=13%, sig
GO DETECT	GO DETECTION OF OTH	19	0.73	1.806	0.011	0.0195	0.775	2198	tags=37%, list=4%, sign
GO RIBONU	GO RIBONUCLEOSIDE M	69	0.44	1.682	0.011	0.0479	0.957	8764	tags=41%, list=15%, sig
GO NEGATI	GO NEGATIVE REGULAT	356	0.35	1.48	0.011	0.1439	0.999	7829	tags=27%, list=13%, sig
GO PIGMEN	GO PIGMENT GRANULE	26	0.55	1.731	0.011	0.0352	0.909	7458	tags=35%, list=13%, sig
GO ESTABL	GO ESTABLISHMENT OF	24	0.55	1.686	0.011	0.047	0.955	6036	tags=29%, list=10%, sig
GO LAMELL	GO LAMELLAR BODY	17	0.66	1.648	0.012	0.0603	0.977	4659	tags=29%, list=8%, sign
GO MONOC	GO MONOCYTE CHEMO	64	0.59	1.799	0.012	0.0206	0.79	5097	tags=41%, list=9%, sign
GO IMMUN	GO IMMUNOGLOBULIN	62	0.79	1.733	0.012	0.0347	0.903	7872	tags=74%, list=13%, sig
GO OXIDOR	GO OXIDOREDUCTASE	55	0.51	1.792	0.012	0.0216	0.804	6732	tags=38%, list=12%, sig
GO INTRINS	GO INTRINSIC APOPTOT	76	0.48	1.756	0.012	0.0289	0.868	7681	tags=41%, list=13%, sig
GO VIRAL B	GO VIRAL BUDDING VIA	21	0.6	1.704	0.012	0.0425	0.936	5636	tags=48%, list=10%, sig
GO MONON	GO MONONUCLEAR CEL	38	0.52	1.73	0.012	0.0353	0.91	2629	tags=26%, list=5%, sign
GO LIPOPO	GO LIPOPOLYSACCHAR	31	0.61	1.788	0.012	0.0224	0.813	4094	tags=42%, list=7%, sign
GO PYRIDIN	GO PYRIDINE CONTAIN	33	0.47	1.565	0.012	0.0969	0.996	8909	tags=39%, list=15%, sig
GO REGULA	GO REGULATION OF B C	29	0.61	1.763	0.012	0.0275	0.86	7576	tags=48%, list=13%, sig
GO CYTOLY	GO CYTOLYSIS	29	0.62	1.765	0.012	0.0272	0.855	6482	tags=45%, list=11%, sig
GO HYDRO	GO HYDROGEN PEROXI	56	0.41	1.508	0.013	0.1269	0.999	4738	tags=25%, list=8%, sign
GO REGULA	GO REGULATION OF MA	29	0.58	1.805	0.013	0.0197	0.778	10492	tags=55%, list=18%, sig
GO PURINE	GO PURINE NUCLEOSID	65	0.43	1.642	0.013	0.0624	0.981	8753	tags=43%, list=15%, sig
GO GRANUL	GO GRANULOCYTE MA	16	0.64	1.72	0.013	0.0379	0.922	5312	tags=50%, list=9%, sign

GO INTERLI	GO INTERLEUKIN 6 MEI	34	0.54	1.675	0.013	0.0504	0.965	1386	tags=21%, list=2%, sign
GO COPPER	GO COPPER ION HOMEC	17	0.59	1.644	0.013	0.0614	0.979	2308	tags=35%, list=4%, sign
GO RESPON	GO RESPONSE TO INTEF	28	0.56	1.703	0.013	0.0427	0.936	2988	tags=36%, list=5%, sign
GO REGULA	GO REGULATION OF NU	22	0.6	1.722	0.013	0.0375	0.918	4960	tags=36%, list=8%, sign
GO RESPON	GO RESPONSE TO CADM	64	0.45	1.61	0.013	0.0761	0.989	5332	tags=25%, list=9%, sign
GO MYELOI	GO MYELOID CELL APO	32	0.55	1.73	0.013	0.0353	0.911	4795	tags=31%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULAT	22	0.57	1.698	0.013	0.044	0.941	2481	tags=27%, list=4%, sign
GO IMMUN(	GO IMMUNOGLOBULIN	66	0.77	1.733	0.014	0.0348	0.903	7872	tags=71%, list=13%, sig
GO SERINE	GO SERINE HYDROLASI	186	0.36	1.473	0.014	0.1478	0.999	8238	tags=30%, list=14%, sig
GO CELL CH	GO CELL CHEMOTAXIS	298	0.47	1.804	0.014	0.0198	0.779	6386	tags=33%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	26	0.61	1.768	0.014	0.0266	0.85	4352	tags=31%, list=7%, sign
GO ENDOPE	GO ENDOPEPTIDASE RE	187	0.4	1.54	0.014	0.1086	0.999	7209	tags=28%, list=12%, sig
GO POSITIV	GO POSITIVE REGULATI	25	0.65	1.808	0.014	0.0193	0.77	10492	tags=76%, list=18%, sig
GO B CELL	GO B CELL ACTIVATION	74	0.54	1.75	0.014	0.0302	0.876	5416	tags=34%, list=9%, sign
GO LATE EN	GO LATE ENDOSOME TO	24	0.59	1.765	0.014	0.0272	0.855	5636	tags=38%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	30	0.62	1.827	0.014	0.0163	0.723	2542	tags=33%, list=4%, sign
GO REGULA	GO REGULATION OF AM	40	0.46	1.628	0.014	0.0685	0.985	6375	tags=38%, list=11%, sig
GO REGULA	GO REGULATION OF PEI	259	0.41	1.66	0.014	0.0561	0.972	7314	tags=31%, list=13%, sig
GO MAINTE	GO MAINTENANCE OF F	23	0.56	1.726	0.015	0.0365	0.916	7037	tags=39%, list=12%, sig
GO REGULA	GO REGULATION OF EX	160	0.44	1.693	0.015	0.0451	0.949	3039	tags=22%, list=5%, sign
GO PEPTIDY	GO PEPTIDYL TYROSINI	41	0.5	1.651	0.015	0.0594	0.977	7843	tags=41%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	58	0.41	1.588	0.015	0.0855	0.994	6828	tags=36%, list=12%, sig
GO MODUL	GO MODULATION BY H(	29	0.57	1.693	0.015	0.0451	0.949	5615	tags=34%, list=10%, sig
GO INTRINS	GO INTRINSIC APOPTOT	42	0.52	1.662	0.016	0.0555	0.972	9734	tags=45%, list=17%, sig
GO RESPON	GO RESPONSE TO CHEM	94	0.57	1.8	0.016	0.0203	0.79	4110	tags=34%, list=7%, sign
GO MEMBR	GO MEMBRANE INVAGI	129	0.59	1.747	0.016	0.031	0.883	8121	tags=57%, list=14%, sig
GO CYSTEIN	GO CYSTEINE TYPE ENI	25	0.52	1.593	0.016	0.083	0.993	7800	tags=40%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULAT	18	0.63	1.716	0.016	0.039	0.927	2846	tags=39%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	100	0.44	1.651	0.016	0.0595	0.977	5416	tags=28%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	16	0.66	1.727	0.016	0.0361	0.915	1644	tags=31%, list=3%, sign
GO B CELL I	GO B CELL PROLIFERAT	97	0.54	1.783	0.016	0.0235	0.822	5364	tags=34%, list=9%, sign
GO TUMOR	GO TUMOR NECROSIS F	41	0.59	1.814	0.016	0.0183	0.751	8001	tags=46%, list=14%, sig
GO UBIQUIT	GO UBIQUITIN BINDING	72	0.48	1.704	0.016	0.0424	0.936	2742	tags=24%, list=5%, sign
GO LEUKOC	GO LEUKOCYTE HOMEC	86	0.55	1.842	0.016	0.0149	0.7	8001	tags=45%, list=14%, sig
GO MITOCH	GO MITOCHONDRIAL CY	21	0.65	1.721	0.017	0.0375	0.919	10686	tags=62%, list=18%, sig
GO NEGATI	GO NEGATIVE REGULAT	264	0.37	1.516	0.017	0.1225	0.999	7829	tags=28%, list=13%, sig
GO DETECT	GO DETECTION OF BIOT	36	0.62	1.779	0.017	0.0244	0.827	5546	tags=44%, list=9%, sign
GO VACUOI	GO VACUOLAR MEMBR	403	0.43	1.769	0.017	0.0263	0.849	7659	tags=34%, list=13%, sig
GO MEMBR	GO MEMBRANE FUSION	156	0.41	1.619	0.017	0.0722	0.988	6323	tags=29%, list=11%, sig
GO AMYLOI	GO AMYLOID FIBRIL FC	18	0.58	1.683	0.017	0.0476	0.956	6008	tags=33%, list=10%, sig
GO SNAP RE	GO SNAP RECEPTOR AC	36	0.51	1.692	0.017	0.0452	0.949	6323	tags=42%, list=11%, sig
GO APOPTO	GO APOPTOTIC PROCES	25	0.54	1.687	0.018	0.0467	0.954	3131	tags=32%, list=5%, sign
GO GOLGI A	GO GOLGI ASSOCIATED	175	0.46	1.721	0.018	0.0375	0.918	4459	tags=24%, list=8%, sign
GO TERTIAF	GO TERTIARY GRANULI	71	0.55	1.811	0.018	0.0188	0.763	4639	tags=41%, list=8%, sign
GO POSITIV	GO POSITIVE REGULATI	193	0.42	1.662	0.018	0.0554	0.972	6471	tags=28%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	28	0.53	1.696	0.018	0.0446	0.946	6161	tags=36%, list=11%, sig
GO OSTEOC	GO OSTEOCLAST DIFFE	96	0.46	1.627	0.018	0.0687	0.985	7877	tags=42%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	366	0.34	1.487	0.018	0.1403	0.999	4124	tags=20%, list=7%, sign
GO DNA SYI	GO DNA SYNTHESIS INV	49	0.59	1.76	0.019	0.0283	0.864	9018	tags=47%, list=15%, sig
GO VITAMII	GO VITAMIN BIOSYNTH	21	0.55	1.635	0.019	0.0656	0.982	5219	tags=33%, list=9%, sign
GO ACTIVA	GO ACTIVATION OF MA	151	0.38	1.54	0.019	0.1087	0.999	8568	tags=36%, list=15%, sig
GO HOMEOS	GO HOMEOSTASIS OF N	251	0.4	1.645	0.019	0.0613	0.979	6691	tags=28%, list=11%, sig
GO NEGATI	GO NEGATIVE REGULAT	33	0.51	1.609	0.019	0.0765	0.989	4694	tags=27%, list=8%, sign
GO NUCLEO	GO NUCLEOSIDE PHOSF	71	0.4	1.546	0.019	0.105	0.998	10440	tags=45%, list=18%, sig
GO PROTEII	GO PROTEIN MATURATI	277	0.33	1.448	0.019	0.162	0.999	8256	tags=27%, list=14%, sig
GO POSITIV	GO POSITIVE REGULATI	25	0.6	1.723	0.02	0.0374	0.918	8559	tags=56%, list=15%, sig
GO IRON IOI	GO IRON ION TRANSPOI	77	0.43	1.643	0.02	0.0621	0.979	9251	tags=40%, list=16%, sig
GO LYMPH	GO LYMPH NODE DEVE	17	0.65	1.777	0.02	0.0248	0.832	7717	tags=53%, list=13%, sig

GO POSITIV	GO POSITIVE REGULATI	51	0.5	1.684	0.02	0.0476	0.956	7972	tags=45%, list=14%, sig
GO POSITIV	GO POSITIVE REGULATI	57	0.45	1.618	0.02	0.0721	0.988	4938	tags=33%, list=8%, sign
GO LATE EN	GO LATE ENDOSOME T	17	0.59	1.677	0.02	0.05	0.963	3870	tags=35%, list=7%, sign
GO REGULA	GO REGULATION OF TR	22	0.55	1.613	0.02	0.0746	0.988	1169	tags=23%, list=2%, sign
GO SIGNAL	GO SIGNAL TRANSDUCT	74	0.44	1.598	0.02	0.081	0.992	7662	tags=34%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	85	0.4	1.554	0.021	0.1014	0.996	8753	tags=39%, list=15%, sig
GO REGULA	GO REGULATION OF T C	42	0.56	1.762	0.021	0.0276	0.86	2846	tags=31%, list=5%, sign
GO B CELL	GO B CELL RECEPTOR S	121	0.68	1.776	0.021	0.0249	0.833	7872	tags=56%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULAT	81	0.41	1.578	0.021	0.0903	0.996	6716	tags=32%, list=12%, sig
GO PURINE	GO PURINE CONTAININ	49	0.45	1.604	0.021	0.0783	0.992	2599	tags=24%, list=4%, sign
GO PYRIMI	GO PYRIMIDINE CONTA	81	0.43	1.612	0.021	0.0749	0.989	9155	tags=41%, list=16%, sig
GO NEGATI	GO NEGATIVE REGULAT	60	0.42	1.553	0.021	0.1016	0.996	7614	tags=32%, list=13%, sig
GO HEXOSE	GO HEXOSE CATABOLI	54	0.49	1.657	0.021	0.0574	0.973	4282	tags=30%, list=7%, sign
GO ENDOLY	GO ENDOLYSOSOME	20	0.62	1.714	0.021	0.0394	0.928	4279	tags=40%, list=7%, sign
GO ORGAN	GO ORGANELLE MEMB	100	0.45	1.645	0.021	0.0614	0.979	6267	tags=33%, list=11%, sig
GO FIBROB	GO FIBROBLAST PROLI	83	0.41	1.562	0.021	0.0984	0.996	6729	tags=34%, list=12%, sig
GO B CELL	GO B CELL HOMEOSTAS	29	0.63	1.749	0.022	0.0306	0.879	2630	tags=28%, list=5%, sign
GO REGULA	GO REGULATION OF ST	117	0.49	1.704	0.022	0.0425	0.936	4080	tags=26%, list=7%, sign
GO CARD D	GO CARD DOMAIN BIND	15	0.65	1.739	0.022	0.0332	0.894	1465	tags=33%, list=3%, sign
GO RESPON	GO RESPONSE TO MUR	18	0.61	1.695	0.023	0.0447	0.946	11765	tags=67%, list=20%, sig
GO INTESTI	GO INTESTINAL EPITHE	15	0.62	1.643	0.023	0.0622	0.979	8888	tags=47%, list=15%, sig
GO CELL CE	GO CELL CELL ADHESI	16	0.69	1.701	0.023	0.0432	0.939	3663	tags=38%, list=6%, sign
GO PROTEA	GO PROTEASOME ACCE	24	0.72	1.759	0.023	0.0282	0.864	2348	tags=33%, list=4%, sign
GO CELLUL	GO CELLULAR MODIFIE	184	0.34	1.432	0.023	0.1725	0.999	8059	tags=31%, list=14%, sig
GO POSITIV	GO POSITIVE REGULATI	19	0.65	1.711	0.024	0.0404	0.929	9845	tags=68%, list=17%, sig
GO NEGATI	GO NEGATIVE REGULAT	16	0.59	1.69	0.024	0.046	0.952	5785	tags=31%, list=10%, sig
GO REGULA	GO REGULATION OF INT	159	0.37	1.528	0.024	0.1155	0.999	7829	tags=31%, list=13%, sig
GO PHOSPH	GO PHOSPHATIDYLINOS	76	0.38	1.467	0.024	0.1511	0.999	4380	tags=25%, list=8%, sign
GO DISULFI	GO DISULFIDE OXIDOR	38	0.52	1.687	0.024	0.0469	0.955	6732	tags=39%, list=12%, sig
GO AMYLOI	GO AMYLOID PRECURS	50	0.42	1.566	0.024	0.0965	0.996	6375	tags=32%, list=11%, sig
GO CELLUL	GO CELLULAR PIGMENT	52	0.46	1.664	0.024	0.0548	0.969	9027	tags=40%, list=15%, sig
GO POSITIV	GO POSITIVE REGULATI	90	0.4	1.539	0.024	0.1087	0.999	2824	tags=21%, list=5%, sign
GO MAP KIN	GO MAP KINASE KINAS	22	0.57	1.693	0.025	0.0451	0.949	5542	tags=36%, list=9%, sign
GO SOMATI	GO SOMATIC DIVERSIFI	60	0.5	1.649	0.025	0.0603	0.977	4441	tags=30%, list=8%, sign
GO ACUTE	GO ACUTE PHASE RESP	47	0.55	1.638	0.025	0.0641	0.982	9190	tags=49%, list=16%, sig
GO POSITIV	GO POSITIVE REGULATI	37	0.49	1.648	0.025	0.0605	0.977	2630	tags=24%, list=5%, sign
GO INTERA	GO INTERACTION WITH	92	0.43	1.572	0.025	0.0937	0.996	7298	tags=32%, list=12%, sig
GO VACUOL	GO VACUOLAR ACIDIFI	23	0.55	1.634	0.025	0.0659	0.983	8159	tags=52%, list=14%, sig
GO INNATE	GO INNATE IMMUNE RE	17	0.63	1.548	0.026	0.1043	0.998	8589	tags=53%, list=15%, sig
GO PROTEI	GO PROTEIN INSERTION	61	0.45	1.578	0.026	0.0904	0.996	7432	tags=36%, list=13%, sig
GO REGULA	GO REGULATION OF PE	23	0.57	1.591	0.026	0.084	0.994	10532	tags=48%, list=18%, sig
GO REGULA	GO REGULATION OF MI	44	0.48	1.578	0.026	0.0902	0.996	9259	tags=52%, list=16%, sig
GO ACTIVA	GO ACTIVATION OF JUN	37	0.47	1.56	0.026	0.099	0.996	6471	tags=41%, list=11%, sig
GO CYTOPL	GO CYTOPLASMIC SIDE	15	0.56	1.574	0.026	0.0924	0.996	7383	tags=60%, list=13%, sig
GO MULTIV	GO MULTIVESICULAR B	39	0.5	1.701	0.026	0.0433	0.939	5636	tags=41%, list=10%, sig
GO REGULA	GO REGULATION OF MA	42	0.53	1.692	0.027	0.0455	0.951	3075	tags=36%, list=5%, sign
GO REGULA	GO REGULATION OF RE	27	0.51	1.591	0.027	0.0841	0.994	5785	tags=33%, list=10%, sig
GO MITOTIC	GO MITOTIC CYTOKINE	23	0.57	1.661	0.027	0.0559	0.972	7430	tags=39%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	21	0.59	1.688	0.028	0.0467	0.954	3483	tags=38%, list=6%, sign
GO CELLUL	GO CELLULAR OXIDANT	96	0.39	1.518	0.028	0.1208	0.999	5400	tags=26%, list=9%, sign
GO NUCLEO	GO NUCLEOTIDE EXCIS	29	0.57	1.691	0.028	0.0455	0.951	8544	tags=45%, list=15%, sig
GO PHOSPH	GO PHOSPHATIDYLINOS	19	0.59	1.677	0.028	0.0498	0.962	3076	tags=37%, list=5%, sign
GO NEGATI	GO NEGATIVE REGULAT	204	0.33	1.404	0.028	0.1931	0.999	7003	tags=25%, list=12%, sig
GO REGULA	GO REGULATION OF MY	52	0.47	1.607	0.028	0.0772	0.991	5416	tags=37%, list=9%, sign
GO PURINE	GO PURINERGIC NUCLE	32	0.58	1.698	0.029	0.0439	0.941	6701	tags=44%, list=11%, sig
GO BENZEN	GO BENZENE CONTAINI	23	0.51	1.539	0.029	0.1088	0.999	5608	tags=35%, list=10%, sig
GO SECOND	GO SECONDARY LYSOS	16	0.63	1.607	0.029	0.0771	0.991	8159	tags=56%, list=14%, sig
GO PROTEI	GO PROTEIN K63 LINKE	56	0.46	1.635	0.029	0.0655	0.982	8055	tags=39%, list=14%, sig

GO POSITIV	GO POSITIVE REGULATI	23	0.56	1.588	0.029	0.0856	0.994	8593	tags=43%, list=15%, sig
GO SOMATI	GO SOMATIC RECOMBII	50	0.52	1.67	0.03	0.0524	0.968	3991	tags=30%, list=7%, sign
GO PYRIMII	GO PYRIMIDINE CONTA	38	0.51	1.684	0.03	0.0474	0.955	7852	tags=37%, list=13%, sig
GO TOLL LII	GO TOLL LIKE RECEPTC	39	0.53	1.645	0.03	0.0614	0.979	5939	tags=49%, list=10%, sig
GO POSITIV	GO POSITIVE REGULATI	27	0.54	1.562	0.03	0.0982	0.996	6389	tags=41%, list=11%, sig
GO CYTOPL	GO CYTOPLASMIC SIDE	184	0.37	1.517	0.03	0.1213	0.999	7643	tags=34%, list=13%, sig
GO MEMBR	GO MEMBRANE PROTEI	60	0.47	1.645	0.03	0.0614	0.979	6075	tags=35%, list=10%, sig
GO MODUL	GO MODULATION OF PF	112	0.43	1.564	0.03	0.0974	0.996	7298	tags=34%, list=12%, sig
GO NEGATI	GO NEGATIVE REGULAT	39	0.47	1.536	0.03	0.111	0.999	5216	tags=26%, list=9%, sign
GO REGULA	GO REGULATION OF ME	85	0.41	1.531	0.03	0.113	0.999	9399	tags=40%, list=16%, sig
GO MONON	GO MONONUCLEAR CEI	91	0.54	1.736	0.03	0.0341	0.899	5097	tags=38%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	119	0.35	1.417	0.03	0.1837	0.999	4977	tags=21%, list=9%, sign
GO ACUTE I	GO ACUTE INFLAMMAT	23	0.6	1.694	0.03	0.0451	0.949	7243	tags=43%, list=12%, sig
GO CD40 SI	GO CD40 SIGNALING PA	15	0.62	1.653	0.03	0.0585	0.974	2354	tags=40%, list=4%, sign
GO NEGATI	GO NEGATIVE REGULAT	19	0.59	1.587	0.03	0.0855	0.994	6181	tags=32%, list=11%, sig
GO RESPON	GO RESPONSE TO GAMI	53	0.45	1.605	0.031	0.0778	0.991	3397	tags=25%, list=6%, sign
GO NEGATI	GO NEGATIVE REGULAT	51	0.44	1.558	0.031	0.0996	0.996	6716	tags=33%, list=12%, sig
GO REGULA	GO REGULATION OF PR	24	0.53	1.595	0.031	0.0825	0.993	5482	tags=29%, list=9%, sign
GO NEGATI	GO NEGATIVE REGULAT	38	0.47	1.555	0.031	0.1013	0.996	2711	tags=24%, list=5%, sign
GO DEOXYF	GO DEOXYRIBOSE PHOS	20	0.59	1.656	0.031	0.0577	0.973	6751	tags=50%, list=12%, sig
GO NEGATI	GO NEGATIVE REGULAT	21	0.48	1.548	0.032	0.1044	0.998	9091	tags=43%, list=16%, sig
GO FICOLIN	GO FICOLIN 1 RICH GRA	57	0.52	1.677	0.032	0.0498	0.961	8559	tags=47%, list=15%, sig
GO POSITIV	GO POSITIVE REGULATI	30	0.52	1.656	0.032	0.0576	0.973	6161	tags=37%, list=11%, sig
GO COATED	GO COATED VESICLE	290	0.41	1.63	0.032	0.0678	0.985	4653	tags=22%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULAT	20	0.61	1.655	0.032	0.0579	0.974	2489	tags=40%, list=4%, sign
GO LRR DOI	GO LRR DOMAIN BINDII	16	0.58	1.62	0.033	0.0718	0.987	3028	tags=31%, list=5%, sign
GO SPECIFI	GO SPECIFIC GRANULE	89	0.48	1.702	0.033	0.0431	0.937	4639	tags=35%, list=8%, sign
GO REGULA	GO REGULATION OF CH	223	0.4	1.585	0.033	0.0863	0.994	6386	tags=32%, list=11%, sig
GO CYTOKI	GO CYTOKINE BINDING	134	0.51	1.655	0.033	0.0579	0.974	8001	tags=37%, list=14%, sig
GO REGULA	GO REGULATION OF MA	23	0.56	1.609	0.033	0.0763	0.989	6083	tags=35%, list=10%, sig
GO IMMUN	GO IMMUNOGLOBULIN	23	0.67	1.651	0.033	0.0593	0.977	4939	tags=43%, list=8%, sign
GO NEGATI	GO NEGATIVE REGULAT	106	0.42	1.563	0.033	0.0981	0.996	3003	tags=20%, list=5%, sign
GO PHAGOC	GO PHAGOCYTOSIS REC	74	0.7	1.675	0.034	0.0505	0.966	7872	tags=64%, list=13%, sig
GO DEFENS	GO DEFENSE RESPONSE	41	0.52	1.544	0.034	0.1064	0.998	7298	tags=39%, list=12%, sig
GO SIGNALI	GO SIGNALING RECEPT	41	0.47	1.568	0.034	0.0958	0.996	2179	tags=29%, list=4%, sign
GO NEGATI	GO NEGATIVE REGULAT	102	0.38	1.487	0.034	0.1404	0.999	7843	tags=36%, list=13%, sig
GO HETERO	GO HETEROTYPIC CELL	62	0.47	1.599	0.034	0.0805	0.992	7662	tags=34%, list=13%, sig
GO PROTEII	GO PROTEIN TRIMERIZ	17	0.55	1.556	0.034	0.1008	0.996	4152	tags=29%, list=7%, sign
GO TRANS	GO TRANS GOLGI NETW	225	0.39	1.587	0.034	0.0857	0.994	4982	tags=24%, list=9%, sign
GO REGULA	GO REGULATION OF MC	181	0.4	1.559	0.034	0.0992	0.996	3994	tags=21%, list=7%, sign
GO PROTEII	GO PROTEIN PROCESSII	213	0.35	1.449	0.035	0.1619	0.999	8256	tags=28%, list=14%, sig
GO SIGNALI	GO SIGNALING ADAPTC	67	0.44	1.597	0.035	0.0817	0.992	2179	tags=25%, list=4%, sign
GO NEGATI	GO NEGATIVE REGULAT	27	0.49	1.622	0.035	0.0707	0.987	7903	tags=56%, list=14%, sig
GO REGULA	GO REGULATION OF SPI	17	0.53	1.569	0.035	0.0951	0.996	6670	tags=47%, list=11%, sig
GO PHAGOL	GO PHAGOLYSOSOME A	15	0.54	1.554	0.035	0.1015	0.996	11162	tags=73%, list=19%, sig
GO RESPON	GO RESPONSE TO OXID	446	0.32	1.43	0.035	0.1736	0.999	5802	tags=22%, list=10%, sig
GO CLATHR	GO CLATHRIN COATED	190	0.38	1.51	0.036	0.1262	0.999	4653	tags=22%, list=8%, sign
GO FOAM C	GO FOAM CELL DIFFERI	37	0.5	1.61	0.037	0.076	0.989	2748	tags=22%, list=5%, sign
GO ORGAN	GO ORGANOPHOSPHAT	141	0.34	1.414	0.037	0.185	0.999	8569	tags=32%, list=15%, sig
GO POSITIV	GO POSITIVE REGULATI	34	0.5	1.604	0.037	0.0781	0.991	7432	tags=47%, list=13%, sig
GO PEPTIDY	GO PEPTIDYL TYROSINI	373	0.36	1.487	0.037	0.1403	0.999	7949	tags=30%, list=14%, sig
GO MAST CI	GO MAST CELL ACTIVA	59	0.53	1.695	0.037	0.0448	0.946	3188	tags=36%, list=5%, sign
GO DENDRI	GO DENDRITIC CELL CH	24	0.6	1.646	0.037	0.0611	0.977	8001	tags=50%, list=14%, sig
GO REGULA	GO REGULATION OF OX	114	0.36	1.434	0.038	0.171	0.999	7462	tags=29%, list=13%, sig
GO REGULA	GO REGULATION OF NE	41	0.54	1.695	0.038	0.0447	0.946	6161	tags=39%, list=11%, sig
GO LYSOSO	GO LYSOSOME LOCALI	71	0.44	1.59	0.038	0.0847	0.994	7851	tags=45%, list=13%, sig
GO AZUROP	GO AZUROPHIL GRANU	150	0.43	1.624	0.038	0.07	0.986	9621	tags=43%, list=16%, sig
GO REGULA	GO REGULATION OF HE	26	0.53	1.602	0.038	0.0792	0.992	7662	tags=42%, list=13%, sig

GO POSITIV	GO POSITIVE REGULATI	149	0.42	1.568	0.038	0.0958	0.996	5416	tags=26%, list=9%, sign
GO VESICLE	GO VESICLE ORGANIZA	326	0.38	1.561	0.038	0.0989	0.996	4727	tags=25%, list=8%, sign
GO EARLY I	GO EARLY ENDOSOME	359	0.38	1.558	0.038	0.0995	0.996	4527	tags=21%, list=8%, sign
GO MATURI	GO MATURE B CELL DIF	22	0.59	1.542	0.038	0.1077	0.999	8719	tags=50%, list=15%, sig
GO POSITIV	GO POSITIVE REGULATI	23	0.51	1.548	0.039	0.1046	0.998	11877	tags=57%, list=20%, sig
GO POSITIV	GO POSITIVE REGULATI	20	0.51	1.529	0.039	0.1144	0.999	2807	tags=25%, list=5%, sign
GO UNSATU	GO UNSATURATED FAT	116	0.36	1.465	0.039	0.1525	0.999	7814	tags=29%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	17	0.55	1.595	0.039	0.0825	0.993	7615	tags=53%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULAT	16	0.6	1.577	0.039	0.0908	0.996	2873	tags=25%, list=5%, sign
GO ENDOPL	GO ENDOPLASMIC RETI	72	0.48	1.62	0.039	0.0717	0.987	2856	tags=24%, list=5%, sign
GO UBIQUIT	GO UBIQUITIN LIKE PRO	90	0.43	1.558	0.04	0.0995	0.996	2742	tags=20%, list=5%, sign
GO RESPON	GO RESPONSE TO HYDR	18	0.5	1.496	0.04	0.135	0.999	1641	tags=28%, list=3%, sign
GO ERROR I	GO ERROR FREE TRANS	21	0.63	1.603	0.04	0.0789	0.992	9018	tags=52%, list=15%, sig
GO RESPON	GO RESPONSE TO OXYG	387	0.33	1.439	0.041	0.1677	0.999	6166	tags=23%, list=11%, sig
GO IRON IOI	GO IRON ION HOMEOST	84	0.38	1.478	0.041	0.1449	0.999	4769	tags=23%, list=8%, sign
GO CELLUL	GO CELLULAR SENESCE	75	0.43	1.535	0.041	0.1113	0.999	4893	tags=23%, list=8%, sign
GO SYNCYT	GO SYNCYTIUM FORMA	55	0.48	1.539	0.041	0.1087	0.999	3679	tags=25%, list=6%, sign
GO POSITIV	GO POSITIVE REGULATI	141	0.44	1.611	0.041	0.0755	0.989	6386	tags=38%, list=11%, sig
GO SOMATI	GO SOMATIC DIVERSIFI	70	0.47	1.563	0.041	0.0979	0.996	4441	tags=27%, list=8%, sign
GO MORPHO	GO MORPHOGENESIS OI	144	0.42	1.545	0.042	0.1059	0.998	5095	tags=24%, list=9%, sign
GO MODULA	GO MODULATION BY HO	17	0.58	1.601	0.042	0.0793	0.992	5615	tags=35%, list=10%, sig
GO RRNA CA	GO RRNA CATABOLIC P	20	0.56	1.624	0.042	0.07	0.986	11964	tags=55%, list=20%, sig
GO REPLISO	GO REPLISOME	26	0.63	1.645	0.042	0.0615	0.979	6794	tags=46%, list=12%, sig
GO POST TR	GO POST TRANSLATION	356	0.36	1.486	0.042	0.1408	0.999	4674	tags=21%, list=8%, sign
GO PROTEA	GO PROTEASE BINDING	133	0.41	1.521	0.042	0.1199	0.999	6375	tags=34%, list=11%, sig
GO MYELOI	GO MYELOID CELL HOM	150	0.37	1.493	0.042	0.137	0.999	5377	tags=23%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	64	0.41	1.461	0.043	0.1541	0.999	9259	tags=42%, list=16%, sig
GO POSITIV	GO POSITIVE REGULATI	46	0.47	1.547	0.043	0.1046	0.998	2198	tags=28%, list=4%, sign
GO B CELL I	GO B CELL DIFFERENTI	135	0.44	1.549	0.044	0.1037	0.998	9075	tags=38%, list=16%, sig
GO ANTIOX	GO ANTIOXIDANT ACTI	79	0.41	1.505	0.045	0.1289	0.999	5400	tags=28%, list=9%, sign
GO POSITIV	GO POSITIVE REGULATI	19	0.54	1.555	0.045	0.1009	0.996	2052	tags=26%, list=4%, sign
GO ICOSAN	GO ICOSANOID METABO	121	0.35	1.426	0.045	0.1762	0.999	7814	tags=29%, list=13%, sig
GO GLYCOS	GO GLYCOSYL COMPOU	40	0.5	1.627	0.045	0.0689	0.985	7852	tags=38%, list=13%, sig
GO HYDROI	GO HYDROLASE ACTIVI	126	0.36	1.453	0.045	0.1593	0.999	6465	tags=32%, list=11%, sig
GO REGULA	GO REGULATION OF SU	22	0.57	1.603	0.045	0.0789	0.992	6444	tags=50%, list=11%, sig
GO UBIQUIT	GO UBIQUITIN LIKE PRO	307	0.4	1.577	0.045	0.0909	0.996	4306	tags=23%, list=7%, sign
GO POSITIV	GO POSITIVE REGULATI	80	0.43	1.534	0.045	0.1115	0.999	6506	tags=31%, list=11%, sig
GO MONOSA	GO MONOSACCHARIDE	64	0.43	1.482	0.045	0.1429	0.999	4282	tags=25%, list=7%, sign
GO MYOBLA	GO MYOBLAST FUSION	40	0.49	1.552	0.045	0.1022	0.996	3679	tags=25%, list=6%, sign
GO REGULA	GO REGULATION OF CA	97	0.42	1.534	0.046	0.1114	0.999	2723	tags=21%, list=5%, sign
GO POSITIV	GO POSITIVE REGULATI	20	0.61	1.624	0.046	0.07	0.986	3436	tags=35%, list=6%, sign
GO DETOXII	GO DETOXIFICATION	129	0.35	1.423	0.046	0.1786	0.999	6151	tags=24%, list=11%, sig
GO PATTERI	GO PATTERN RECOGNIT	23	0.61	1.62	0.046	0.0718	0.987	4795	tags=43%, list=8%, sign
GO PROTEIN	GO PROTEIN HOMOTETI	59	0.4	1.458	0.047	0.1562	0.999	7756	tags=27%, list=13%, sig
GO REGULA	GO REGULATION OF DE	19	0.51	1.508	0.047	0.1269	0.999	4977	tags=32%, list=9%, sign
GO BLOOD I	GO BLOOD MICROPART	146	0.48	1.562	0.047	0.0983	0.996	7462	tags=36%, list=13%, sig
GO POSITIV	GO POSITIVE REGULATI	17	0.55	1.559	0.047	0.0992	0.996	8900	tags=47%, list=15%, sig
GO ESTABLI	GO ESTABLISHMENT OI	123	0.45	1.579	0.047	0.0899	0.996	4089	tags=24%, list=7%, sign
GO AZUROP	GO AZUROPHIL GRANU	56	0.49	1.592	0.047	0.0838	0.994	4415	tags=30%, list=8%, sign
GO REGULA	GO REGULATION OF ER	49	0.44	1.508	0.047	0.1269	0.999	6297	tags=29%, list=11%, sig
GO POSITIV	GO POSITIVE REGULATI	127	0.43	1.608	0.047	0.0766	0.989	4469	tags=24%, list=8%, sign
GO P38MAPI	GO P38MAPK CASCADE	51	0.41	1.446	0.048	0.1627	0.999	6093	tags=35%, list=10%, sig
GO PHOSPH	GO PHOSPHATIDYLINOS	38	0.46	1.498	0.048	0.1339	0.999	8059	tags=42%, list=14%, sig
GO POSITIV	GO POSITIVE REGULATI	35	0.49	1.49	0.048	0.1387	0.999	3679	tags=20%, list=6%, sign
GO CELL RE	GO CELL REDOX HOME	55	0.45	1.535	0.048	0.1112	0.999	5126	tags=29%, list=9%, sign
GO PYRIMII	GO PYRIMIDINE DEOXY	18	0.6	1.58	0.049	0.0893	0.996	7756	tags=56%, list=13%, sig
GO NEGATI	GO NEGATIVE REGULAT	36	0.47	1.478	0.049	0.145	0.999	2875	tags=25%, list=5%, sign
GO NUCLEO	GO NUCLEOSIDE TRIPH	61	0.4	1.482	0.049	0.1427	0.999	8789	tags=39%, list=15%, sig

GO EXTRAC	GO EXTRACELLULAR V	21	0.5	1.551	0.05	0.103	0.997	5938	tags=33%, list=10%, sig
GO REACTI\	GO REACTIVE OXYGEN	122	0.37	1.469	0.05	0.1499	0.999	3483	tags=24%, list=6%, sign

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Supplementary Table S12
HIGH-ETV7

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KEGG_BAS	KEGG_BA	Details ...	55	-0.58	-1.97	0.002	0.05303	0.046	11983	tags=55%, list=21%, signal=69%
KEGG_HEI	KEGG_HI	Details ...	56	-0.51	-1.79	0.006	0.20421	0.241	12159	tags=50%, list=21%, signal=63%
KEGG_MEI	KEGG_MI	Details ...	101	-0.42	-1.59	0.022	0.72224	0.653	10983	tags=36%, list=19%, signal=44%
KEGG_WN	KEGG_W	Details ...	150	-0.41	-1.58	0.024	0.58769	0.667	12664	tags=41%, list=22%, signal=53%
KEGG_TGI	KEGG_TC	Details ...	85	-0.4	-1.47	0.069	0.74151	0.82	10951	tags=39%, list=19%, signal=48%
KEGG_GLY	KEGG_GI	Details ...	31	-0.48	-1.49	0.073	0.8036	0.795	9508	tags=32%, list=16%, signal=39%
KEGG_THY	KEGG_TH	Details ...	29	-0.42	-1.36	0.098	0.76568	0.92	3454	tags=24%, list=6%, signal=26%
KEGG_TAS	KEGG_TA	Details ...	51	-0.43	-1.38	0.099	0.79558	0.913	13846	tags=49%, list=24%, signal=64%
KEGG_GLY	KEGG_GI	Details ...	43	-0.36	-1.33	0.101	0.69017	0.945	10468	tags=33%, list=18%, signal=40%
KEGG_TER	KEGG_TE	Details ...	15	-0.57	-1.44	0.107	0.73815	0.855	14002	tags=60%, list=24%, signal=79%
KEGG_CYS	KEGG_CY	Details ...	34	-0.42	-1.34	0.108	0.78905	0.941	2713	tags=24%, list=5%, signal=25%
KEGG_ADI	KEGG_AI	Details ...	68	-0.4	-1.38	0.121	0.85938	0.901	12976	tags=43%, list=22%, signal=55%
KEGG_NEU	KEGG_NI	Details ...	271	-0.33	-1.26	0.14	0.66414	0.973	16803	tags=47%, list=29%, signal=65%
KEGG_CAI	KEGG_CA	Details ...	177	-0.34	-1.27	0.151	0.75093	0.971	16796	tags=48%, list=29%, signal=67%
KEGG_AXO	KEGG_AX	Details ...	128	-0.33	-1.27	0.151	0.67795	0.971	11441	tags=37%, list=20%, signal=46%
KEGG_VAS	KEGG_VA	Details ...	112	-0.35	-1.27	0.173	0.71534	0.971	10983	tags=37%, list=19%, signal=45%
KEGG_ARI	KEGG_AI	Details ...	74	-0.41	-1.31	0.178	0.69452	0.956	5081	tags=30%, list=9%, signal=33%
KEGG_STE	KEGG_ST	Details ...	17	-0.52	-1.33	0.184	0.72927	0.943	3808	tags=35%, list=7%, signal=38%
KEGG_CAI	KEGG_CA	Details ...	78	-0.36	-1.22	0.193	0.67633	0.98	10114	tags=35%, list=17%, signal=42%
KEGG_DIL	KEGG_DI	Details ...	90	-0.38	-1.26	0.216	0.62984	0.973	8375	tags=34%, list=14%, signal=40%
KEGG_TIG	KEGG_TI	Details ...	129	-0.3	-1.16	0.216	0.6966	0.994	14188	tags=36%, list=24%, signal=48%
KEGG_HYI	KEGG_HY	Details ...	83	-0.38	-1.25	0.221	0.62664	0.974	9937	tags=37%, list=17%, signal=45%
KEGG_GAI	KEGG_GA	Details ...	88	-0.33	-1.18	0.239	0.69933	0.988	13078	tags=35%, list=22%, signal=45%
KEGG_NIT	KEGG_NI	Details ...	23	-0.38	-1.17	0.249	0.71056	0.993	8749	tags=30%, list=15%, signal=36%
KEGG_ENI	KEGG_EN	Details ...	52	-0.35	-1.19	0.256	0.71435	0.987	7373	tags=25%, list=13%, signal=29%
KEGG_VAS	KEGG_VA	Details ...	44	-0.34	-1.15	0.275	0.70916	0.996	14782	tags=39%, list=25%, signal=52%
KEGG_MEI	KEGG_MI	Details ...	71	-0.33	-1.13	0.276	0.72375	0.996	11361	tags=37%, list=19%, signal=45%
KEGG_LON	KEGG_LC	Details ...	68	-0.3	-1.11	0.279	0.71052	0.997	13078	tags=40%, list=22%, signal=51%
KEGG_RNA	KEGG_RN	Details ...	29	-0.4	-1.13	0.329	0.70202	0.996	7398	tags=34%, list=13%, signal=39%
KEGG_PRC	KEGG_PR	Details ...	89	-0.29	-1.08	0.338	0.69489	0.999	2978	tags=17%, list=5%, signal=18%
KEGG_ECM	KEGG_EC	Details ...	84	-0.36	-1.1	0.343	0.71284	0.997	5853	tags=31%, list=10%, signal=34%
KEGG_VAI	KEGG_VA	Details ...	43	-0.35	-1.08	0.349	0.7127	0.999	13739	tags=40%, list=24%, signal=52%
KEGG_SEL	KEGG_SE	Details ...	24	-0.38	-1.1	0.356	0.70687	0.997	1725	tags=17%, list=3%, signal=17%
KEGG_FAT	KEGG_FA	Details ...	42	-0.33	-1.08	0.36	0.69075	1	9927	tags=26%, list=17%, signal=32%
KEGG_REN	KEGG_RE	Details ...	17	-0.4	-1.07	0.368	0.66127	1	1992	tags=18%, list=3%, signal=18%
KEGG_ALF	KEGG_AI	Details ...	19	-0.37	-1.07	0.368	0.6795	1	8929	tags=32%, list=15%, signal=37%
KEGG_LON	KEGG_LC	Details ...	70	-0.29	-1.04	0.381	0.69626	1	14094	tags=39%, list=24%, signal=51%
KEGG_BUT	KEGG_BU	Details ...	34	-0.32	-1.04	0.395	0.70103	1	13739	tags=35%, list=24%, signal=46%
KEGG_ALA	KEGG_AI	Details ...	30	-0.32	-1.02	0.41	0.69777	1	10761	tags=37%, list=18%, signal=45%
KEGG_INS	KEGG_INSULIN_SI		137	-0.25	-1.01	0.421	0.70997	1	12445	tags=27%, list=21%, signal=34%
KEGG_REC	KEGG_REGULATIC		212	-0.27	-1.01	0.422	0.69781	1	12596	tags=37%, list=22%, signal=47%
KEGG_PRC	KEGG_PR	Details ...	32	-0.34	-1.02	0.425	0.70964	1	12175	tags=28%, list=21%, signal=36%
KEGG_COI	KEGG_COLORECT		62	-0.28	-0.98	0.457	0.71236	1	7373	tags=23%, list=13%, signal=26%
KEGG_MA	KEGG_MATURITY		25	-0.4	-0.99	0.467	0.71104	1	20436	tags=56%, list=35%, signal=86%
KEGG_PRC	KEGG_PROXIMAL		23	-0.33	-0.98	0.472	0.69988	1	10114	tags=30%, list=17%, signal=37%
KEGG_N_C	KEGG_N_GLYCAN		46	-0.31	-0.96	0.483	0.70577	1	8949	tags=26%, list=15%, signal=31%
KEGG_FOC	KEGG_FOCAL_AD		197	-0.28	-0.96	0.489	0.69583	1	14616	tags=39%, list=25%, signal=51%
KEGG_PEN	KEGG_PENTOSE_		28	-0.33	-0.95	0.495	0.69723	1	7161	tags=21%, list=12%, signal=24%
KEGG_GLY	KEGG_GLYCEROP		72	-0.25	-0.97	0.498	0.70235	1	9719	tags=24%, list=17%, signal=28%
KEGG_ETH	KEGG_ETHER_LIP		30	-0.28	-0.94	0.506	0.70127	1	9494	tags=23%, list=16%, signal=28%
KEGG_BIO	KEGG_BIOSYNTHI		20	-0.35	-0.94	0.541	0.68942	1	8137	tags=25%, list=14%, signal=29%
KEGG_ALI	KEGG_ALDOSTER		42	-0.29	-0.94	0.552	0.68205	1	13846	tags=38%, list=24%, signal=50%
KEGG_CEI	KEGG_CELL_CYCI		124	-0.27	-0.85	0.588	0.78302	1	6335	tags=21%, list=11%, signal=23%
KEGG_OOC	KEGG_OOCYTE_M		111	-0.25	-0.88	0.598	0.76009	1	10983	tags=24%, list=19%, signal=30%
KEGG_RET	KEGG_RETINOL_M		64	-0.26	-0.88	0.625	0.7717	1	12457	tags=30%, list=21%, signal=38%
KEGG_GLY	KEGG_GLYCOSAM		26	-0.28	-0.88	0.628	0.77349	1	14148	tags=42%, list=24%, signal=56%
KEGG_PRI	KEGG_PRIMARY_		16	-0.32	-0.84	0.654	0.79428	1	3897	tags=19%, list=7%, signal=20%

KEGG_BET	KEGG_BETA_ALA	22	-0.28	-0.86	0.655	0.78172	1	10225	tags=32%, list=18%, signal=39%
KEGG_PRO	KEGG_PROGESTE	85	-0.23	-0.82	0.682	0.80926	1	7944	tags=21%, list=14%, signal=24%
KEGG_AM	KEGG_AMINOACY	22	-0.28	-0.78	0.692	0.80953	1	15754	tags=36%, list=27%, signal=50%
KEGG_VIB	KEGG_VIBRIO_CH	53	-0.25	-0.83	0.703	0.78874	1	12270	tags=26%, list=21%, signal=33%
KEGG_DRU	KEGG_DRUG_MET	71	-0.23	-0.81	0.713	0.79332	1	12457	tags=24%, list=21%, signal=30%
KEGG_LYS	KEGG_LYSINE_DE	39	-0.26	-0.8	0.718	0.79555	1	15507	tags=33%, list=27%, signal=45%
KEGG_ASC	KEGG_ASCORBAT	25	-0.27	-0.79	0.721	0.80873	1	7161	tags=20%, list=12%, signal=23%
KEGG_BAS	KEGG_BASAL_TR	35	-0.24	-0.73	0.746	0.85078	1	8359	tags=20%, list=14%, signal=23%
KEGG_O_G	KEGG_O_GLYCAN	29	-0.26	-0.77	0.778	0.81067	1	6278	tags=21%, list=11%, signal=23%
KEGG_GLY	KEGG_GLYCOSAM	15	-0.28	-0.74	0.787	0.84923	1	6384	tags=20%, list=11%, signal=22%
KEGG_OLF	KEGG_OLFACTOR	387	-0.23	-0.81	0.788	0.7986	1	25693	tags=44%, list=44%, signal=78%
KEGG_MET	KEGG_METABOLI	69	-0.21	-0.71	0.843	0.85804	1	16652	tags=30%, list=29%, signal=43%
KEGG_GLY	KEGG_GLYCOSAM	22	-0.23	-0.62	0.871	0.93712	1	13687	tags=32%, list=23%, signal=42%
KEGG_PPA	KEGG_PPAR_SIGN	69	-0.2	-0.72	0.882	0.85736	1	16885	tags=32%, list=29%, signal=45%
KEGG_TYR	KEGG_TYROSINE_	40	-0.2	-0.66	0.953	0.90538	1	21853	tags=40%, list=37%, signal=64%
KEGG_STE	KEGG_STEROID_H	55	-0.17	-0.59	0.987	0.94646	1	21547	tags=40%, list=37%, signal=63%

LOW-ETV7

NAME	GS f	GS DETAI	SIZE	ES	NES	NOM p	FDR q-val	FWER p	RANK A	LEADING EDGE
KEGG_R	KEGG_R	Details ...	69	0.7394	2.5376	0	0	0	5113	tags=46%, list=9%, signal=51%
KEGG_T	KEGG_T	Details ...	102	0.6917	2.4542	0	0	0	5230	tags=45%, list=9%, signal=49%
KEGG_A	KEGG_A	Details ...	81	0.8407	2.4412	0	0	0	1969	tags=48%, list=3%, signal=50%
KEGG_N	KEGG_N	Details ...	132	0.6877	2.3568	0	0	0	4152	tags=44%, list=7%, signal=47%
KEGG_C	KEGG_C	Details ...	53	0.6957	2.3341	0	0	0	4772	tags=43%, list=8%, signal=47%
KEGG_L	KEGG_L	Details ...	70	0.7787	2.3015	0	0	0	5416	tags=54%, list=9%, signal=60%
KEGG_A	KEGG_A	Details ...	50	0.8365	2.2788	0	0	0	1416	tags=48%, list=2%, signal=49%
KEGG_T	KEGG_T	Details ...	41	0.8633	2.1907	0	2.04E-04	0.002	1416	tags=61%, list=2%, signal=62%
KEGG_J	KEGG_J	Details ...	155	0.592	2.1886	0	1.81E-04	0.002	3951	tags=35%, list=7%, signal=37%
KEGG_G	KEGG_G	Details ...	37	0.9237	2.1668	0	3.76E-04	0.005	1416	tags=68%, list=2%, signal=69%
KEGG_N	KEGG_N	Details ...	61	0.6433	2.1321	0	6.07E-04	0.007	4938	tags=39%, list=8%, signal=43%
KEGG_I	KEGG_I	Details ...	46	0.8277	2.131	0	5.56E-04	0.007	1479	tags=50%, list=3%, signal=51%
KEGG_P	KEGG_P	Details ...	35	0.8694	2.1239	0	5.14E-04	0.007	2519	tags=63%, list=4%, signal=66%
KEGG_P	KEGG_P	Details ...	45	0.8184	2.1067	0	4.77E-04	0.007	2770	tags=47%, list=5%, signal=49%
KEGG_V	KEGG_V	Details ...	68	0.7075	2.0924	0	6.13E-04	0.009	1499	tags=40%, list=3%, signal=41%
KEGG_A	KEGG_A	Details ...	35	0.9048	2.0896	0	5.75E-04	0.009	1416	tags=71%, list=2%, signal=73%
KEGG_C	KEGG_C	Details ...	262	0.6056	2.078	0	6.88E-04	0.01	4938	tags=38%, list=8%, signal=42%
KEGG_A	KEGG_A	Details ...	28	0.833	2.0584	0	8.11E-04	0.013	2354	tags=54%, list=4%, signal=56%
KEGG_A	KEGG_A	Details ...	87	0.564	2.049	0	0.001024	0.016	7295	tags=41%, list=12%, signal=47%
KEGG_S	KEGG_S	Details ...	55	0.7761	2.0476	0	9.72E-04	0.016	4993	tags=58%, list=9%, signal=64%
KEGG_C	KEGG_C	Details ...	128	0.6082	1.965	0	0.003656	0.055	2424	tags=33%, list=4%, signal=34%
KEGG_T	KEGG_T	Details ...	107	0.5798	1.974	0.002	0.00337	0.052	2962	tags=34%, list=5%, signal=35%
KEGG_S	KEGG_S	Details ...	38	0.5253	1.7411	0.002	0.037199	0.349	6323	tags=42%, list=11%, signal=47%
KEGG_B	KEGG_B	Details ...	41	0.4665	1.6264	0.0061	0.071072	0.561	4779	tags=29%, list=8%, signal=32%
KEGG_H	KEGG_H	Details ...	85	0.6379	1.8874	0.0061	0.009901	0.121	6871	tags=41%, list=12%, signal=47%
KEGG_E	KEGG_E	Details ...	179	0.3949	1.6193	0.0062	0.070835	0.575	4152	tags=22%, list=7%, signal=24%
KEGG_A	KEGG_A	Details ...	53	0.4677	1.6904	0.0062	0.051639	0.439	3679	tags=28%, list=6%, signal=30%
KEGG_P	KEGG_P	Details ...	69	0.4749	1.707	0.008	0.046557	0.408	5416	tags=32%, list=9%, signal=35%
KEGG_C	KEGG_C	Details ...	185	0.5026	1.8164	0.0119	0.019633	0.21	4110	tags=30%, list=7%, signal=32%
KEGG_A	KEGG_A	Details ...	67	0.4803	1.7095	0.0127	0.047067	0.4	4938	tags=25%, list=8%, signal=28%
KEGG_A	KEGG_A	Details ...	57	0.4664	1.6575	0.0173	0.06029	0.509	4779	tags=32%, list=8%, signal=34%
KEGG_R	KEGG_R	Details ...	34	0.5204	1.6616	0.0179	0.060155	0.498	10204	tags=38%, list=17%, signal=46%
KEGG_P	KEGG_P	Details ...	66	0.4639	1.6804	0.0195	0.053874	0.459	7460	tags=38%, list=13%, signal=43%
KEGG_L	KEGG_L	Details ...	121	0.5155	1.7594	0.0204	0.033567	0.318	8480	tags=48%, list=15%, signal=56%
KEGG_P	KEGG_P	Details ...	98	0.4734	1.6441	0.0213	0.064283	0.534	9339	tags=48%, list=16%, signal=57%
KEGG_F	KEGG_F	Details ...	79	0.4188	1.5818	0.0267	0.086035	0.629	3679	tags=27%, list=6%, signal=28%
KEGG_N	KEGG_N	Details ...	24	0.4585	1.4983	0.0368	0.132922	0.756	13070	tags=54%, list=22%, signal=70%
KEGG_B	KEGG_B	Details ...	75	0.5096	1.6259	0.0435	0.069279	0.561	5312	tags=31%, list=9%, signal=34%
KEGG_N	KEGG_N	Details ...	44	0.5645	1.6102	0.0438	0.073587	0.588	9018	tags=45%, list=15%, signal=54%
KEGG_D	KEGG_DRUG_ME		51	0.41	1.4066	0.0631	0.205037	0.879	10228	tags=39%, list=18%, signal=48%
KEGG_E	KEGG_EPITHELIA		68	0.3931	1.4265	0.0707	0.189534	0.857	7659	tags=34%, list=13%, signal=39%
KEGG_A	KEGG_ABC_TRAN		44	0.4087	1.3775	0.071	0.211885	0.905	2599	tags=14%, list=4%, signal=14%
KEGG_F	KEGG_FC_GAMM		93	0.3907	1.452	0.0782	0.168368	0.828	5312	tags=32%, list=9%, signal=35%
KEGG_P	KEGG_PANTOTHE		16	0.4875	1.3982	0.0811	0.204622	0.887	5260	tags=44%, list=9%, signal=48%
KEGG_D	KEGG_D	Details ...	36	0.647	1.5374	0.0853	0.108318	0.695	9659	tags=64%, list=17%, signal=77%
KEGG_G	KEGG_GALACTOS		26	0.442	1.3508	0.099	0.230996	0.928	7247	tags=38%, list=12%, signal=44%
KEGG_A	KEGG_ALZHEIME		152	0.3581	1.3977	0.1066	0.200529	0.887	6375	tags=32%, list=11%, signal=36%
KEGG_C	KEGG_COMPLEM		69	0.4625	1.399	0.1377	0.208358	0.886	7209	tags=36%, list=12%, signal=41%
KEGG_S	KEGG_SMALL_CE		84	0.3825	1.3679	0.1389	0.217411	0.917	4893	tags=25%, list=8%, signal=27%
KEGG_B	KEGG_BASE_EXC		34	0.4945	1.3973	0.14	0.19669	0.889	8950	tags=53%, list=15%, signal=62%
KEGG_V	KEGG_VEGF_SIG		76	0.3093	1.2198	0.1772	0.339008	0.982	3740	tags=22%, list=6%, signal=24%
KEGG_N	KEGG_NON_SMA		54	0.3484	1.2151	0.188	0.333643	0.983	5194	tags=24%, list=9%, signal=26%
KEGG_N	KEGG_NEUROTR		125	0.323	1.2325	0.1952	0.353451	0.978	3679	tags=18%, list=6%, signal=20%
KEGG_P	KEGG_PEROXISO		78	0.352	1.2296	0.2065	0.35091	0.98	7807	tags=31%, list=13%, signal=35%
KEGG_C	KEGG_CHRONIC_		73	0.3363	1.2255	0.2102	0.343847	0.98	5416	tags=26%, list=9%, signal=29%
KEGG_O	KEGG_OTHER_GL		16	0.4972	1.2602	0.2162	0.329655	0.974	8380	tags=50%, list=14%, signal=58%
KEGG_A	KEGG_ARGININE_		53	0.3261	1.1719	0.2237	0.356609	0.992	3608	tags=19%, list=6%, signal=20%

KEGG_A	KEGG_AMINO_SU	43	0.3811	1.2222	0.2283	0.34227	0.981	3815	tags=28%, list=7%, signal=30%
KEGG_G	KEGG_GLYCOSA	21	0.4386	1.2359	0.2305	0.35566	0.978	2583	tags=33%, list=4%, signal=35%
KEGG_G	KEGG_GLUTATHI	49	0.348	1.2022	0.2341	0.345267	0.986	6970	tags=29%, list=12%, signal=32%
KEGG_G	KEGG_GLYCOSP	26	0.3747	1.1878	0.2377	0.353601	0.989	4615	tags=19%, list=8%, signal=21%
KEGG_H	KEGG_HUNTINGT	167	0.3224	1.2172	0.2379	0.336581	0.983	5427	tags=27%, list=9%, signal=30%
KEGG_L	KEGG_LEUKOCY	115	0.3317	1.1774	0.2451	0.355289	0.992	8107	tags=35%, list=14%, signal=40%
KEGG_M	KEGG_MISMATC	23	0.5333	1.2709	0.251	0.321072	0.97	9018	tags=43%, list=15%, signal=51%
KEGG_P	KEGG_PARKINSO	113	0.3731	1.2295	0.2531	0.344741	0.98	5427	tags=28%, list=9%, signal=31%
KEGG_G	KEGG_GLYCOSP	15	0.455	1.1988	0.2551	0.344585	0.986	4888	tags=27%, list=8%, signal=29%
KEGG_D	KEGG_DORSO_VE	24	0.3976	1.1779	0.2651	0.360145	0.992	2282	tags=8%, list=4%, signal=9%
KEGG_A	KEGG_ARACHIDO	58	0.3075	1.1246	0.2725	0.399014	0.995	8244	tags=31%, list=14%, signal=36%
KEGG_T	KEGG_TRYPTOPH	39	0.3418	1.1246	0.2806	0.404691	0.995	6419	tags=23%, list=11%, signal=26%
KEGG_N	KEGG_NOTCH_SI	47	0.3125	1.1051	0.2916	0.420731	0.996	5143	tags=23%, list=9%, signal=26%
KEGG_U	KEGG_UBIQUITIN	130	0.3133	1.1277	0.3057	0.406363	0.995	6666	tags=20%, list=11%, signal=23%
KEGG_O	KEGG_OXIDATIV	115	0.3576	1.1444	0.3144	0.389029	0.994	9341	tags=43%, list=16%, signal=51%
KEGG_M	KEGG_MTOR_SIG	51	0.3071	1.0992	0.3156	0.423348	0.996	5619	tags=24%, list=10%, signal=26%
KEGG_P	KEGG_PATHWAY	322	0.2668	1.0943	0.3288	0.424847	0.996	6436	tags=21%, list=11%, signal=23%
KEGG_F	KEGG_FRUCTOSE	33	0.3345	1.0773	0.334	0.431541	0.998	5318	tags=24%, list=9%, signal=27%
KEGG_G	KEGG_GLYCOLYS	62	0.3122	1.0749	0.3373	0.429558	0.998	4426	tags=19%, list=8%, signal=21%
KEGG_M	KEGG_MAPK_SIG	266	0.2571	1.0556	0.3387	0.451136	0.999	6872	tags=22%, list=12%, signal=25%
KEGG_P	KEGG_PRION_DIS	35	0.3444	1.0835	0.3707	0.428877	0.997	7814	tags=29%, list=13%, signal=33%
KEGG_P	KEGG_PHENYLAL	17	0.3655	1.054	0.3768	0.447627	0.999	181	tags=6%, list=0%, signal=6%
KEGG_P	KEGG_PHOSPHAT	76	0.2861	1.033	0.3829	0.466592	0.999	5659	tags=20%, list=10%, signal=22%
KEGG_O	KEGG_ONE_CARB	17	0.4098	1.0836	0.3919	0.434583	0.997	9467	tags=41%, list=16%, signal=49%
KEGG_R	KEGG_RENAL_CE	66	0.3001	1.0382	0.4044	0.464795	0.999	5822	tags=24%, list=10%, signal=27%
KEGG_P	KEGG_PURINE_M	154	0.2544	0.9892	0.4561	0.527215	0.999	8661	tags=32%, list=15%, signal=37%
KEGG_G	KEGG_GLYOXYL	16	0.3689	0.9764	0.4646	0.528011	0.999	12323	tags=50%, list=21%, signal=63%
KEGG_S	KEGG_SPLICEOS	126	0.3223	0.9783	0.4656	0.531249	0.999	11437	tags=33%, list=20%, signal=40%
KEGG_E	KEGG_ERBB_SIG	86	0.2645	0.9879	0.4672	0.52283	0.999	5194	tags=19%, list=9%, signal=20%
KEGG_G	KEGG_GNRH_SIG	101	0.2425	0.9733	0.4835	0.526375	0.999	8278	tags=25%, list=14%, signal=29%
KEGG_P	KEGG_PATHOGE	56	0.2785	0.9432	0.5108	0.550449	0.999	5537	tags=27%, list=9%, signal=30%
KEGG_T	KEGG_TYPE_II_D	47	0.2758	0.948	0.5245	0.555092	0.999	5619	tags=21%, list=10%, signal=24%
KEGG_G	KEGG_GLIOMA	65	0.265	0.947	0.534	0.550309	0.999	5346	tags=18%, list=9%, signal=20%
KEGG_P	KEGG_PORPHYR	40	0.2837	0.9299	0.5405	0.564787	0.999	4216	tags=18%, list=7%, signal=19%
KEGG_R	KEGG_RIBOSOME	88	0.4374	0.9531	0.5775	0.552912	0.999	11521	tags=45%, list=20%, signal=57%
KEGG_P	KEGG_PROTEIN_	23	0.312	0.8814	0.5849	0.626644	1	10237	tags=35%, list=18%, signal=42%
KEGG_S	KEGG_SPHINGOL	36	0.2718	0.8874	0.5965	0.624103	1	4766	tags=25%, list=8%, signal=27%
KEGG_P	KEGG_PENTOSE_	27	0.2855	0.8512	0.649	0.670163	1	3816	tags=19%, list=7%, signal=20%
KEGG_P	KEGG_PYRUVATE	40	0.2721	0.8461	0.6586	0.671998	1	11307	tags=38%, list=19%, signal=46%
KEGG_S	KEGG_STARCH_A	52	0.2446	0.8449	0.6816	0.666834	1	10144	tags=33%, list=17%, signal=40%
KEGG_H	KEGG_HOMOLOG	26	0.2894	0.753	0.6929	0.790617	1	6781	tags=27%, list=12%, signal=30%
KEGG_L	KEGG_LINOLEIC_	29	0.2666	0.8197	0.7064	0.699062	1	8059	tags=31%, list=14%, signal=36%
KEGG_I	KEGG_INOSITOL_	54	0.2301	0.7987	0.7079	0.726346	1	3391	tags=13%, list=6%, signal=14%
KEGG_R	KEGG_RNA_DEG	56	0.2251	0.7143	0.7945	0.839877	1	4005	tags=14%, list=7%, signal=15%
KEGG_C	KEGG_CITRATE_	31	0.2432	0.645	0.8168	0.897515	1	11160	tags=35%, list=19%, signal=44%
KEGG_G	KEGG_GLYCOSY	25	0.2278	0.6621	0.8819	0.888242	1	11700	tags=40%, list=20%, signal=50%
KEGG_H	KEGG_HISTIDINE_	28	0.2106	0.6727	0.899	0.884859	1	3608	tags=11%, list=6%, signal=11%

Supplementary Table S13

id	StromalScore	ImmuneScore	ESTIMATEScore
TCGA-ZF-AA51-01A-21R-A39I-07	32.78758553	1444.819214	1477.6068
TCGA-BT-A42C-01A-11R-A23N-07	-1816.216696	-483.7612023	-2299.977898
TCGA-G2-A3IB-01A-11R-A20F-07	-1518.143937	-225.0357511	-1743.179688
TCGA-2F-A9KW-01A-11R-A38B-07	-48.54229396	356.7002633	308.1579693
TCGA-XF-AAME-01A-12R-A42T-07	1578.90321	2416.129621	3995.032831
TCGA-XF-AAN0-01A-11R-A42T-07	-478.6836735	905.2061996	426.5225261
TCGA-CF-A47W-01A-11R-A23W-07	-1716.804659	-427.4608438	-2144.265503
TCGA-DK-A1A7-01A-11R-A13Y-07	-1140.910945	14.5936377	-1126.317308
TCGA-PQ-A6FN-01A-11R-A31N-07	-581.3200502	695.3542011	114.0341509
TCGA-XF-AAMY-01A-11R-A42T-07	160.4655591	170.5982823	331.0638414
TCGA-G2-AA3F-01A-12R-A42T-07	-1186.437579	-504.1818732	-1690.619452
TCGA-FJ-A871-01A-11R-A352-07	-855.7657065	-553.759908	-1409.525614
TCGA-GC-A3RB-01A-12R-A220-07	-1391.079424	-236.0362272	-1627.115651
TCGA-UY-A9PF-01A-11R-A38B-07	-492.9209929	439.8202686	-53.1007243
TCGA-YC-A89H-01A-11R-A36F-07	-696.6120188	326.9249216	-369.6870972
TCGA-DK-A6AW-01A-11R-A30C-07	-1173.620338	-350.3122251	-1523.932563
TCGA-FD-A43N-01A-11R-A23W-07	-70.3616635	321.5900412	251.2283777
TCGA-UY-A8OD-01A-11R-A36F-07	535.1499961	957.2512666	1492.401263
TCGA-2F-A9KT-01A-11R-A38B-07	-992.4049851	-140.5560666	-1132.961052
TCGA-CU-A0YR-01A-12R-A10U-07	100.2806991	1292.605424	1392.886123
TCGA-4Z-AA84-01A-11R-A39I-07	-1061.160717	-394.0577722	-1455.218489
TCGA-CF-A27C-01A-11R-A16R-07	-2243.149142	-473.6248049	-2716.773947
TCGA-ZF-AA5N-01A-11R-A42T-07	-1576.902874	-206.0772239	-1782.980098
TCGA-DK-AA6U-01A-11R-A39I-07	-1946.190087	-454.0905119	-2400.280599
TCGA-GD-A3OS-01A-12R-A220-07	-388.7079012	-97.09982404	-485.8077253
TCGA-4Z-AA82-01A-11R-A39I-07	-209.9392227	316.0597709	106.1205482
TCGA-DK-AA76-01A-11R-A39I-07	-1893.2902	-1172.424071	-3065.714271
TCGA-DK-A3IL-01A-11R-A20F-07	-818.9546252	-309.9665023	-1128.921127
TCGA-ZF-A9R1-01A-11R-A39I-07	-1266.521024	-193.0916174	-1459.612642
TCGA-XF-A9SH-01A-11R-A39I-07	-938.7449668	94.17531933	-844.5696475
TCGA-C4-A0F7-01A-11R-A084-07	-1010.934687	-503.9408277	-1514.875514
TCGA-C4-A0F0-01A-12R-A10U-07	-226.5068584	824.9287192	598.4218607
TCGA-DK-A3WX-01A-22R-A22U-07	83.46013378	1462.896289	1546.356422
TCGA-BT-A2LA-01A-11R-A18C-07	-1464.130769	-1513.818931	-2977.9497
TCGA-4Z-AA87-01A-11R-A39I-07	-872.3538145	670.1355676	-202.2182469
TCGA-BT-A2LB-01A-11R-A18C-07	204.2524299	1000.185237	1204.437667
TCGA-DK-A2I6-01A-12R-A18C-07	-1006.766968	-242.5377144	-1249.304683
TCGA-BT-A20W-01A-21R-A14Y-07	-653.8803137	576.592141	-77.28817278
TCGA-FD-A5BX-01A-11R-A26T-07	775.9310027	1853.73093	2629.661933
TCGA-FJ-A3Z7-01A-12R-A23N-07	110.5601186	322.5521122	433.1122307
TCGA-E7-A7PW-01A-11R-A352-07	-1959.356768	-179.0879645	-2138.444732
TCGA-4Z-AA7S-01A-11R-A39I-07	-1447.857701	-662.0392345	-2109.896935
TCGA-CF-A3MH-01A-11R-A20F-07	-2027.983214	-153.7949789	-2181.778193
TCGA-FD-A6TG-01A-11R-A32O-07	540.0878306	831.4355355	1371.523366
TCGA-DK-A6AV-01A-12R-A30C-07	-1054.822791	291.8651778	-762.9576129
TCGA-DK-A1A3-01A-11R-A13Y-07	198.295734	647.8116132	846.1073472
TCGA-GC-A3RD-01A-12R-A22U-07	-1229.620182	-152.1366199	-1381.756801
TCGA-BT-A20R-01A-12R-A16R-07	853.666859	565.4212595	1419.088119
TCGA-XF-A9T0-01A-11R-A39I-07	-256.927916	613.0123839	356.0844679
TCGA-YF-AA3M-01A-11R-A42T-07	-1580.181137	-145.5690255	-1725.750163
TCGA-FD-A62O-01A-11R-A30C-07	-911.152237	-472.2078529	-1383.36009
TCGA-BL-A3JM-01A-12R-A21D-07	-596.2249657	-225.9493769	-822.1743426
TCGA-FJ-A3ZF-01A-11R-A23N-07	-1923.981545	-1086.243591	-3010.225135
TCGA-K4-AAQO-01A-11R-A38B-07	438.9785152	820.0172589	1258.995774
TCGA-XF-AAMJ-01A-11R-A42T-07	1228.824521	590.482679	1819.3072
TCGA-G2-A2EC-01A-11R-A180-07	361.7462563	953.5753123	1315.321569
TCGA-CU-A0YN-01A-21R-A10U-07	-126.2738067	912.9617221	786.6879155

TCGA-FD-A5BZ-01A-11R-A28M-07	1044.086987	114.9040768	1158.991064
TCGA-UY-A9PE-01A-11R-A38B-07	-570.4405076	-302.1433496	-872.5838573
TCGA-BT-A2LD-01A-12R-A20F-07	-666.3928008	182.4357063	-483.9570945
TCGA-UY-A9PD-01A-11R-A38B-07	-302.7679125	-89.78217376	-392.5500863
TCGA-CU-A5W6-01A-11R-A28M-07	-1014.502831	131.0137774	-883.4890535
TCGA-CF-A3MF-01A-12R-A21D-07	-1360.903018	-318.9058452	-1679.808863
TCGA-CF-A47T-01A-11R-A23W-07	-1362.24037	-583.3195482	-1945.559918
TCGA-YC-A8S6-01A-31R-A38B-07	601.02009	1310.698215	1911.718305
TCGA-DK-AA6T-01A-11R-A39I-07	-167.0789988	2176.911384	2009.832385
TCGA-BT-A20N-01A-11R-A14Y-07	-1085.321534	-733.3445574	-1818.666091
TCGA-C4-A0F6-01A-11R-A10U-07	-405.7798152	69.03659456	-336.7432207
TCGA-FD-A3B6-01A-21R-A20F-07	-238.7557348	1723.945563	1485.189829
TCGA-XF-A9T2-01A-11R-A42T-07	-192.3304104	-125.504888	-317.8352984
TCGA-GC-A3OO-01A-11R-A22U-07	-50.91724238	384.1812845	333.2640421
TCGA-FD-A3SN-01A-12R-A22U-07	-332.1015498	277.9910893	-54.11046043
TCGA-ZF-A9R2-01A-11R-A39I-07	-2523.807661	-812.8730472	-3336.680708
TCGA-E7-A4IJ-01A-31R-A26T-07	-1415.960934	502.3874337	-913.5735004
TCGA-H4-A2HO-01A-11R-A180-07	-854.6917222	517.1168972	-337.574825
TCGA-XF-AAN3-01A-11R-A42T-07	253.5486609	731.8099038	985.3585646
TCGA-XF-AAMH-01A-11R-A42T-07	-941.0822289	-654.4744663	-1595.556695
TCGA-XF-A9ST-01A-11R-A42T-07	-1532.276709	-943.9025576	-2476.179267
TCGA-GU-A42R-01A-11R-A23N-07	-1671.688448	-712.150787	-2383.839235
TCGA-R3-A69X-01A-22R-A30C-07	475.0582581	1277.384239	1752.442497
TCGA-FD-A6TF-01A-52R-A32O-07	445.7657454	405.8761549	851.6419003
TCGA-XF-AAMR-01A-31R-A42T-07	568.425506	559.6323707	1128.057877
TCGA-DK-A3IQ-01A-31R-A32Y-07	1788.15184	359.371394	2147.523234
TCGA-E7-A4XJ-01A-11R-A26T-07	-1435.63348	-529.1924223	-1964.825902
TCGA-4Z-AA7M-01A-11R-A39I-07	-1117.078008	-201.8104095	-1318.888418
TCGA-ZF-AA56-01A-31R-A39I-07	-214.6232854	1024.735281	810.1119953
TCGA-XF-A8HH-01A-11R-A38B-07	208.4458413	274.5703945	483.0162358
TCGA-C4-A0EZ-01A-21R-A24X-07	-1369.738353	-1194.460849	-2564.199202
TCGA-FD-A62P-01A-32R-A30C-07	128.5319136	1162.745729	1291.277643
TCGA-GU-A42Q-01A-11R-A23W-07	-1500.810052	-551.5190562	-2052.329108
TCGA-GD-A3OQ-01A-32R-A220-07	-1232.185027	-127.7196991	-1359.904726
TCGA-BT-A20U-01A-11R-A14Y-07	-382.5827482	199.1047669	-183.4779812
TCGA-XF-A9SW-01A-11R-A42T-07	1487.841307	1133.862423	2621.70373
TCGA-ZF-A9RC-01A-11R-A38B-07	-9.625174738	-284.4898875	-294.1150622
TCGA-E7-A6MD-01A-41R-A352-07	29.90544266	1081.904457	1111.809899
TCGA-E5-A4TZ-01A-11R-A31N-07	-2067.906824	-317.3408843	-2385.247709
TCGA-BT-A0YX-01A-11R-A10U-07	-579.917691	955.6813362	375.7636453
TCGA-FT-A3EE-01A-11R-A206-07	-1111.13526	-284.8973122	-1396.032573
TCGA-ZF-A9RL-01A-11R-A38B-07	-2280.334192	-960.0256762	-3240.359869
TCGA-ZF-A9R9-01A-11R-A38B-07	752.5509131	519.0648935	1271.615807
TCGA-ZF-A9RE-01A-11R-A38B-07	-2084.600796	-382.3380309	-2466.938827
TCGA-CF-A5U8-01A-11R-A28M-07	-1834.582029	-519.9362869	-2354.518316
TCGA-XF-AAMW-01A-11R-A42T-07	-479.1744084	808.3740612	329.1996528
TCGA-GU-A767-01A-11R-A32O-07	-411.9720135	-151.5376607	-563.5096742
TCGA-SY-A9G0-01A-12R-A38B-07	1125.940816	675.7224522	1801.663269
TCGA-GV-A40G-01A-11R-A23N-07	-1904.050598	-719.6521703	-2623.702768
TCGA-ZF-AA4R-01A-11R-A38B-07	142.3784664	-166.9331611	-24.55469468
TCGA-K4-A3WV-01A-11R-A22U-07	-1432.971567	-898.8744651	-2331.846033
TCGA-G2-A3VY-01A-11R-A22U-07	-2141.305525	-1052.268306	-3193.573831
TCGA-XF-AAN8-01A-11R-A42T-07	2173.232609	2220.757388	4393.989998
TCGA-K4-A3WU-01B-11R-A23N-07	159.6359884	1563.817383	1723.453372
TCGA-FD-A3SJ-01A-12R-A22U-07	-241.1800793	-37.37734681	-278.5574261
TCGA-FD-A3B5-01A-11R-A20F-07	-827.669585	-300.3755513	-1128.045136
TCGA-4Z-AA80-01A-11R-A39I-07	-1797.747274	-519.8471313	-2317.594405
TCGA-G2-A3IE-01A-11R-A20F-07	-1417.870033	-173.5491115	-1591.419145

TCGA-XF-A8HG-01A-11R-A36F-07	-1718.539812	-537.1999557	-2255.739767
TCGA-K4-A83P-01A-11R-A352-07	1135.523307	2564.842421	3700.365728
TCGA-GD-A2C5-01A-12R-A180-07	-231.137795	1.799243369	-229.3385517
TCGA-XF-AAMX-01A-11R-A42T-07	-424.7911888	-297.7370873	-722.5282762
TCGA-DK-A1AE-01A-11R-A13Y-07	-1303.741983	-411.3217483	-1715.063731
TCGA-FJ-A3ZE-01A-11R-A23N-07	-2127.572862	-1083.612839	-3211.185701
TCGA-DK-A2I1-01A-11R-A180-07	797.1507132	1228.090061	2025.240774
TCGA-FD-A5BR-01A-11R-A26T-07	-182.6517508	1038.227009	855.575258
TCGA-DK-A1AF-01A-11R-A13Y-07	1249.508009	1761.440866	3010.948874
TCGA-LT-A5Z6-01A-11R-A28M-07	-1882.686355	29.5367305	-1853.149624
TCGA-K4-A4AB-01B-12R-A28M-07	142.4038111	527.8312289	670.23504
TCGA-G2-A2EO-01A-11R-A180-07	453.7178217	1415.61875	1869.336572
TCGA-GV-A3JZ-01A-11R-A21D-07	-403.8390167	78.82385838	-325.0151583
TCGA-XF-A9SV-01A-21R-A42T-07	143.7136967	-104.6311617	39.08253496
TCGA-FD-A6TH-01A-11R-A32O-07	-6.917396765	118.6160187	111.6986219
TCGA-DK-AA6W-01A-12R-A39I-07	-1255.623448	-112.2454485	-1367.868896
TCGA-DK-A3X1-01A-12R-A22U-07	-574.1578472	74.44436244	-499.7134848
TCGA-XF-AAMG-01A-11R-A42T-07	-197.7613322	-66.20829109	-263.9696233
TCGA-UY-A78N-01A-12R-A33J-07	-1236.422921	-942.8949187	-2179.31784
TCGA-DK-AA75-01A-11R-A39I-07	-1972.59542	-796.1124949	-2768.707915
TCGA-ZF-AA5P-01A-11R-A39I-07	729.3630128	922.5889047	1651.951917
TCGA-FD-A3SL-01A-21R-A22U-07	1147.831214	726.9441881	1874.775402
TCGA-XF-AAN7-01A-11R-A42T-07	-171.193373	10.51867845	-160.6746946
TCGA-DK-A3IM-01A-11R-A20F-07	-1830.555732	-695.9575307	-2526.513262
TCGA-FD-A3SS-01A-12R-A22U-07	-1028.806074	-464.6981206	-1493.504195
TCGA-4Z-AA7N-01A-11R-A39I-07	827.6745637	2635.708844	3463.383407
TCGA-HQ-A2OE-01A-11R-A206-07	-1835.818542	-440.5767062	-2276.395248
TCGA-UY-A8OC-01A-11R-A36F-07	343.0170832	302.6127004	645.6297836
TCGA-GV-A3JV-01A-11R-A220-07	-217.5467589	602.62852	385.0817611
TCGA-KQ-A41S-01A-12R-A33J-07	333.8836771	262.8166139	596.700291
TCGA-DK-A2HX-01A-12R-A18C-07	991.3564904	253.722966	1245.079456
TCGA-CF-A8HY-01A-11R-A36F-07	-1698.927477	-142.2891317	-1841.216609
TCGA-BT-A0S7-01A-11R-A10U-07	-526.6595009	-122.6401389	-649.2996398
TCGA-GU-A42P-01A-11R-A23W-07	-1997.738307	-1036.828308	-3034.566615
TCGA-FD-A3NA-01A-11R-A21D-07	-371.7782667	672.1949436	300.4166769
TCGA-XF-A9SL-01A-11R-A39I-07	1104.762651	2056.881516	3161.644167
TCGA-ZF-AA54-01A-11R-A39I-07	852.3590577	1768.691196	2621.050254
TCGA-ZF-AA4N-01A-11R-A38B-07	-825.1804995	777.6069411	-47.57355842
TCGA-BT-A20X-01A-11R-A16R-07	-263.7677593	419.6619824	155.8942231
TCGA-GV-A3JW-01A-11R-A20F-07	-1625.82104	-1052.891038	-2678.712078
TCGA-FD-A6TI-01A-11R-A32O-07	-757.3087017	-73.43860388	-830.7473056
TCGA-FD-A3SP-01A-31R-A22U-07	1721.496654	1948.137055	3669.633709
TCGA-E7-A97Q-01A-11R-A38B-07	-191.4426117	267.3977259	75.95511422
TCGA-GV-A3QG-01A-11R-A220-07	1355.165006	2745.437968	4100.602975
TCGA-ZF-AA52-01A-12R-A39I-07	824.4039566	1057.351027	1881.754984
TCGA-CF-A9FL-01A-11R-A38B-07	-406.2534876	-26.95832667	-433.2118142
TCGA-G2-AA3D-01A-11R-A39I-07	-2172.978646	-396.9958516	-2569.974497
TCGA-DK-A2I2-01A-11R-A180-07	224.6640859	1605.855233	1830.519319
TCGA-FD-A62S-01A-11R-A30C-07	1251.034062	1439.004175	2690.038238
TCGA-MV-A51V-01A-11R-A26T-07	-1296.676001	-614.729522	-1911.405523
TCGA-DK-A3X2-01A-11R-A22U-07	-1883.308754	-1012.314809	-2895.623562
TCGA-DK-A1AD-01A-11R-A13Y-07	-377.5006652	270.698277	-106.8023881
TCGA-K4-A5RI-01A-11R-A28M-07	-624.4263477	218.7532106	-405.6731372
TCGA-GV-A3QF-01A-31R-A22U-07	-1773.780482	-487.8241834	-2261.604665
TCGA-E7-A7DV-01A-11R-A33J-07	568.209344	2127.30066	2695.510004
TCGA-HQ-A2OF-01A-11R-A26T-07	-1767.350566	-973.7110747	-2741.061641
TCGA-DK-AA6P-01A-11R-A39I-07	-1680.012178	-850.9457257	-2530.957903
TCGA-CF-A47Y-01A-11R-A23W-07	-1708.484958	-439.0111195	-2147.496077

TCGA-G2-A2EL-01A-12R-A18C-07	-2124.970789	-1658.358265	-3783.329054
TCGA-K4-A6MB-01A-11R-A31N-07	-457.1787123	-245.4388237	-702.617536
TCGA-CU-A3KJ-01A-11R-A21D-07	-1059.523645	400.9905439	-658.5331013
TCGA-E7-A85H-01A-11R-A352-07	-588.2514974	572.298086	-15.95341146
TCGA-G2-AA3C-01A-21R-A39I-07	-37.48969662	2038.93435	2001.444653
TCGA-DK-A3IN-01A-11R-A20F-07	465.616211	1027.236029	1492.85224
TCGA-FJ-A3Z9-01A-11R-A26T-07	-2017.966953	-786.2358303	-2804.202783
TCGA-DK-A1AC-01A-11R-A13Y-07	-22.76497704	943.8747838	921.1098068
TCGA-C4-A0F1-01A-11R-A034-07	-412.7782617	275.0028923	-137.7753693
TCGA-E7-A5KE-01A-11R-A28M-07	-2261.04139	-1028.366253	-3289.407643
TCGA-ZF-A9RM-01A-11R-A38B-07	-2588.148024	-922.9273562	-3511.07538
TCGA-CU-A72E-01A-12R-A33J-07	-186.6435857	266.4353444	79.79175873
TCGA-E7-A3Y1-01A-11R-A22U-07	-1339.211405	-158.9554072	-1498.166812
TCGA-FD-A5BV-01A-11R-A26T-07	-1126.249514	-514.0468952	-1640.296409
TCGA-UY-A78M-01A-21R-A352-07	-344.521255	-288.7816628	-633.3029178
TCGA-4Z-AA7R-01A-11R-A39I-07	-1004.307293	-722.8728613	-1727.180154
TCGA-FD-A3SM-01A-11R-A22U-07	136.8667851	-63.02683872	73.83994641
TCGA-BL-A5ZZ-01A-31R-A30C-07	959.5110654	1240.12303	2199.634095
TCGA-CF-A1HS-01A-11R-A13Y-07	-687.9632531	599.1528819	-88.81037127
TCGA-XF-AAMT-01A-11R-A42T-07	861.5669208	1019.31705	1880.883971
TCGA-XF-A9SU-01A-31R-A39I-07	424.4102853	935.8789488	1360.289234
TCGA-UY-A78L-01A-12R-A33J-07	-283.35069	184.7672186	-98.5834714
TCGA-S5-A6DX-01A-11R-A31N-07	306.3621256	1893.493591	2199.855717
TCGA-XF-A8HI-01A-11R-A38B-07	-1606.874392	-23.16932086	-1630.043713
TCGA-G2-A2EK-01A-22R-A18C-07	-960.0274924	307.2632962	-652.7641962
TCGA-H4-A2HQ-01A-11R-A180-07	-1815.266986	-390.6468364	-2205.913823
TCGA-XF-A9SP-01A-11R-A39I-07	935.2435017	823.3006988	1758.544201
TCGA-DK-A3IK-01A-32R-A21D-07	-437.8304164	-57.91427346	-495.7446898
TCGA-BL-A13J-01A-11R-A277-07	313.7952719	-98.3449596	215.4503123
TCGA-BL-A0C8-01A-11R-A277-07	-523.2953681	-161.1414728	-684.4368409
TCGA-BL-A13I-01A-11R-A277-07	801.5887458	2090.466539	2892.055285
TCGA-CF-A47X-01A-31R-A23W-07	-1848.82024	-663.0271473	-2511.847387
TCGA-2F-A9KP-01A-11R-A38B-07	-1709.896998	-741.1543763	-2451.051374
TCGA-DK-A3IT-01A-31R-A20F-07	-81.53021808	495.4069134	413.8766953
TCGA-FD-A43P-01A-31R-A23W-07	-317.5126138	1974.137375	1656.624761
TCGA-DK-A3IV-01A-22R-A21D-07	-1572.831352	1264.139589	-308.6917635
TCGA-GU-A762-01A-11R-A33J-07	402.0133415	2424.909083	2826.922424
TCGA-GC-A3I6-01A-11R-A20F-07	-537.0423196	845.8469502	308.8046306
TCGA-FD-A6TA-01A-12R-A33J-07	523.898597	1256.301763	1780.20036
TCGA-FD-A3SR-01A-11R-A22U-07	341.0635199	981.2454676	1322.308988
TCGA-GU-AATP-01A-11R-A39I-07	511.8350025	729.421091	1241.256094
TCGA-DK-AA6X-01A-12R-A42T-07	-609.4335956	860.3999819	250.9663863
TCGA-XF-A9T3-01A-11R-A42T-07	492.7313344	1010.732116	1503.463451
TCGA-DK-A3WW-01A-22R-A23N-07	-503.2795337	1984.798444	1481.51891
TCGA-K4-A3WS-01A-11R-A22U-07	1151.375337	1231.980508	2383.355845
TCGA-UY-A9PA-01A-11R-A38B-07	-1715.101731	809.5126444	-905.5890863
TCGA-ZF-A9RN-01A-11R-A42T-07	-1208.53587	1068.752541	-139.7833294
TCGA-XF-AAMQ-01A-11R-A42T-07	-743.6207282	1138.105582	394.4848539
TCGA-CF-A1HR-01A-11R-A13Y-07	-861.159498	358.8656037	-502.2938943
TCGA-E7-A3X6-01A-12R-A22U-07	-676.5265375	1082.542682	406.0161441
TCGA-GC-A3BM-01A-11R-A22U-07	-1575.717898	-69.24486766	-1644.962766
TCGA-GV-A6ZA-01A-12R-A33J-07	-1425.267806	362.6185483	-1062.649258
TCGA-G2-A2EJ-01A-11R-A180-07	-1373.677426	382.4072563	-991.2701697
TCGA-BT-A20Q-01A-11R-A14Y-07	411.1787277	1045.015366	1456.194094
TCGA-SY-A9G5-01A-11R-A38B-07	770.7190819	1712.124038	2482.84312
TCGA-4Z-AA7Q-01A-11R-A39I-07	-563.8149181	1814.351433	1250.536515
TCGA-FD-A5BT-01A-11R-A26T-07	1476.900148	2406.39686	3883.297008
TCGA-E7-A6MF-01A-12R-A32O-07	-1915.665027	-335.4330596	-2251.098087

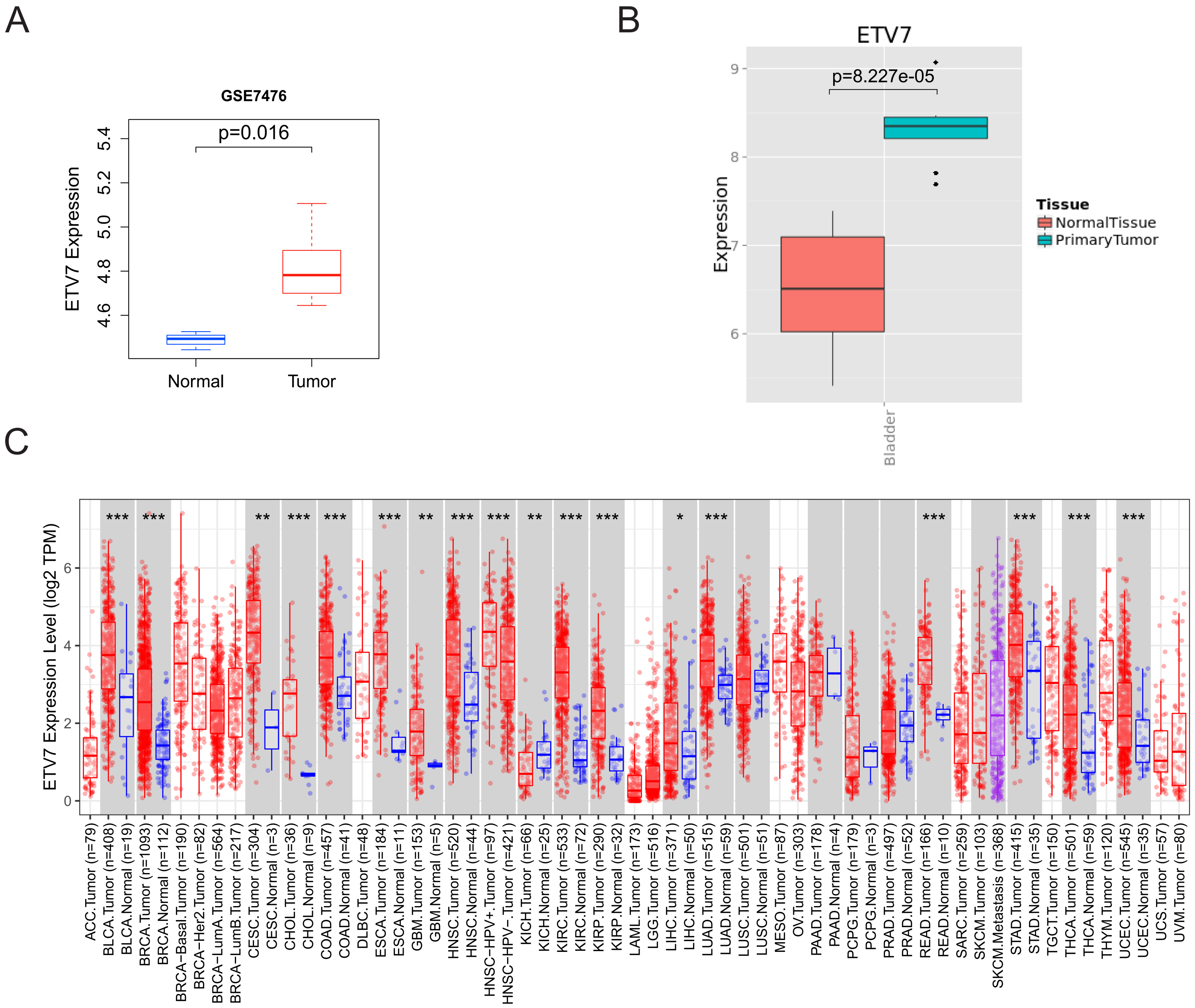
TCGA-FT-A61P-01A-11R-A30C-07	644.0366851	1189.782331	1833.819016
TCGA-DK-AA77-01A-11R-A39I-07	-1499.781866	474.0717997	-1025.710066
TCGA-BT-A20O-01A-21R-A14Y-07	1019.523722	3151.039523	4170.563245
TCGA-XF-A9SZ-01A-11R-A39I-07	618.9346292	820.4232616	1439.357891
TCGA-E7-A678-01A-11R-A30C-07	-1978.549287	-36.27803697	-2014.827324
TCGA-FD-A5BU-01A-31R-A26T-07	468.3143181	1326.942104	1795.256423
TCGA-FD-A3N5-01A-11R-A21D-07	-969.2172299	328.8625387	-640.3546912
TCGA-ZF-AA5H-01A-11R-A39I-07	-231.0234485	1297.840865	1066.817417
TCGA-YF-AA3L-01A-11R-A38B-07	-1372.501922	-170.2256283	-1542.727551
TCGA-XF-A8HB-01A-11R-A36F-07	-2002.990837	-439.7866781	-2442.777515
TCGA-ZF-AA4X-01A-11R-A38B-07	-2533.601785	-415.0545048	-2948.656289
TCGA-BT-A20P-01A-11R-A14Y-07	-1572.721914	-435.4062115	-2008.128125
TCGA-CF-A8HX-01A-11R-A36F-07	-1670.945487	-533.7359621	-2204.681449
TCGA-PQ-A6FI-01A-11R-A31N-07	-1267.741531	437.6005744	-830.1409566
TCGA-DK-A6B2-01A-11R-A30C-07	609.0382062	1286.128871	1895.167077
TCGA-4Z-AA86-01A-11R-A39I-07	638.1567973	1888.156489	2526.313286
TCGA-5N-A9KI-01A-31R-A42T-07	-48.34767329	719.9197549	671.5720816
TCGA-GU-AATO-01A-11R-A39I-07	-142.5775717	1144.076157	1001.498585
TCGA-CF-A9FH-01A-11R-A38B-07	-2008.774173	-301.9735391	-2310.747712
TCGA-4Z-AA7O-01A-31R-A39I-07	-668.3140391	624.4774728	-43.83656624
TCGA-GV-A3QI-01A-11R-A220-07	-1923.958005	-1225.787417	-3149.745422
TCGA-GD-A6C6-01A-21R-A31N-07	-1109.785263	121.3666558	-988.4186073
TCGA-4Z-AA7Y-01A-11R-A39I-07	-1795.928912	-528.5197698	-2324.448681
TCGA-CU-A0YO-01A-11R-A10U-07	-370.7622481	858.9446806	488.1824325
TCGA-CF-A5UA-01A-11R-A28M-07	-1631.416187	-274.0619484	-1905.478136
TCGA-GU-A763-01A-11R-A32O-07	-2043.548404	-94.22525745	-2137.773661
TCGA-FD-A3B7-01A-31R-A20F-07	1307.473753	2178.621502	3486.095255
TCGA-FD-A5C0-01A-11R-A28M-07	-478.6449067	169.6606306	-308.9842761
TCGA-FD-A5BS-01A-21R-A26T-07	1676.875644	3222.838941	4899.714585
TCGA-GV-A40E-01A-12R-A23N-07	-649.5693633	378.9344242	-270.6349391
TCGA-G2-AA3B-01A-11R-A39I-07	-1802.724911	265.3575045	-1537.367407
TCGA-K4-A54R-01A-11R-A26T-07	229.7982701	1383.333752	1613.132022
TCGA-DK-A1AA-01A-11R-A13Y-07	-1496.805699	26.4058372	-1470.399862
TCGA-DK-AA6R-01A-11R-A42T-07	-955.068776	162.063047	-793.005729
TCGA-BT-A3PH-01A-11R-A220-07	-1053.160723	-435.3754732	-1488.536196
TCGA-DK-A3IS-01A-21R-A21D-07	-1903.05477	-224.8047015	-2127.859471
TCGA-XF-A9SJ-01A-11R-A39I-07	167.0876112	1410.224228	1577.311839
TCGA-CF-A7I0-01A-22R-A352-07	-505.7188032	53.7238252	-451.994978
TCGA-GC-A3YS-01A-11R-A23N-07	457.5273144	925.7018167	1383.229131
TCGA-UY-A78O-01A-12R-A33J-07	-940.4286026	-76.3763374	-1016.80494
TCGA-E7-A6ME-01A-22R-A32O-07	-1676.948414	170.375103	-1506.573311
TCGA-XF-AAN5-01A-11R-A42T-07	-633.4749981	1476.43372	842.9587216
TCGA-ZF-AA4T-01A-11R-A38B-07	-1841.793029	-429.0312969	-2270.824326
TCGA-FD-A6TE-01A-12R-A33J-07	-1997.023821	-138.1366701	-2135.160492
TCGA-FD-A6TB-01A-12R-A33J-07	463.5365261	2001.234907	2464.771433
TCGA-FD-A3B8-01A-31R-A20F-07	1684.673792	2749.287768	4433.961561
TCGA-XF-A9SY-01A-21R-A42T-07	574.6123891	2118.849622	2693.462011
TCGA-CF-A9FF-01A-11R-A38B-07	-671.0588926	427.4448425	-243.61405
TCGA-DK-A6B5-01A-11R-A31N-07	-997.0761807	761.5287405	-235.5474402
TCGA-GC-A3RC-01A-11R-A22U-07	-453.8394384	1424.27857	970.4391312
TCGA-GV-A3QK-01B-11R-A23N-07	-1312.556734	886.6372722	-425.919462
TCGA-GU-A764-01A-11R-A352-07	258.2604641	1446.796261	1705.056725
TCGA-DK-A6B6-01A-11R-A30C-07	-1527.169061	765.2468446	-761.9222167
TCGA-5N-A9KM-01A-11R-A42T-07	-114.2816029	865.7125958	751.4309929
TCGA-XF-A8HF-01A-11R-A36F-07	-220.5700229	450.473264	229.9032411
TCGA-ZF-AA4U-01A-11R-A38B-07	-2331.30795	-325.5973252	-2656.905276
TCGA-XF-A9T6-01A-11R-A42T-07	-1275.929362	274.9708245	-1000.958538
TCGA-CF-A47V-01A-11R-A23W-07	-885.9062731	359.3802344	-526.5260387

TCGA-XF-A9SI-01A-11R-A39I-07	701.3164857	2861.25513	3562.571615
TCGA-BT-A42F-01A-11R-A23W-07	-263.0806128	2080.801078	1817.720466
TCGA-ZF-A9RF-01A-11R-A38B-07	-820.6767404	1900.256751	1079.58001
TCGA-KQ-A41N-01A-11R-A33J-07	-1310.12826	-798.2579723	-2108.386232
TCGA-FD-A3B3-01A-12R-A206-07	728.4621731	2018.206635	2746.668808
TCGA-ZF-A9R4-01A-11R-A38B-07	-1667.657169	144.2200828	-1523.437086
TCGA-GV-A3QH-01A-11R-A220-07	-2315.126991	-796.1678231	-3111.294814
TCGA-DK-A6B1-01A-12R-A30C-07	-1285.21522	-450.0220625	-1735.237282
TCGA-BT-A3PJ-01A-21R-A220-07	-690.013622	1040.838577	350.8249553
TCGA-ZF-A9R7-01A-11R-A38B-07	-1030.289194	2039.911953	1009.622759
TCGA-FD-A3SO-01A-11R-A22U-07	376.3905814	1008.022168	1384.41275
TCGA-E7-A97P-01A-11R-A38B-07	85.41712198	1758.170782	1843.587904
TCGA-4Z-AA81-01A-11R-A39I-07	-1339.501233	794.196638	-545.3045952
TCGA-2F-A9KQ-01A-11R-A38B-07	-1267.917662	-622.5833127	-1890.500975
TCGA-FD-A43Y-01A-21R-A26T-07	25.24793983	811.3713864	836.6193262
TCGA-S5-AA26-01A-11R-A38B-07	-1965.669533	-651.4471161	-2617.116649
TCGA-BT-A42E-01A-11R-A23W-07	-553.8595471	1714.42268	1160.563133
TCGA-FD-A43X-01A-11R-A23W-07	-1872.637832	-561.1370293	-2433.774861
TCGA-BT-A20T-01A-11R-A14Y-07	-61.98117668	758.9264427	696.945266
TCGA-E7-A7DU-01A-11R-A32O-07	-1609.985081	-233.9700033	-1843.955085
TCGA-DK-A3WY-01A-11R-A22U-07	861.6143521	3106.438631	3968.052983
TCGA-G2-A2EF-01A-12R-A18C-07	-728.9693036	1674.273404	945.3041006
TCGA-BT-A20V-01A-11R-A14Y-07	-1678.36541	461.7712266	-1216.594184
TCGA-GU-AATQ-01A-11R-A39I-07	-1143.554395	130.1087361	-1013.445659
TCGA-CU-A3QU-01A-11R-A22U-07	-2122.563116	-443.7451121	-2566.308229
TCGA-GD-A3OP-01A-21R-A220-07	-4.885339164	306.2879674	301.4026282
TCGA-KQ-A41P-01A-12R-A33J-07	-113.0210206	511.7070521	398.6860315
TCGA-UY-A9PH-01A-11R-A38B-07	195.566241	2037.051923	2232.618164
TCGA-FD-A5BY-01A-31R-A28M-07	-221.1067779	422.4666339	201.3598559
TCGA-GC-A6I3-01A-11R-A31N-07	-266.297353	1655.925947	1389.628594
TCGA-ZF-A9R0-01A-11R-A38B-07	-653.2427849	352.8323174	-300.4104675
TCGA-FD-A43S-01A-21R-A23W-07	789.0673245	2299.092267	3088.159592
TCGA-DK-A6B0-01A-11R-A31N-07	-1823.490888	-271.5698067	-2095.060694
TCGA-KQ-A41Q-01A-11R-A33J-07	-1488.340056	-466.7211157	-1955.061172
TCGA-GC-A4ZW-01A-11R-A26T-07	-1748.249737	-605.5915716	-2353.841309
TCGA-DK-AA74-01A-11R-A39I-07	1437.047766	2409.08864	3846.136406
TCGA-DK-A1AG-01A-11R-A13Y-07	-1836.599059	150.1596338	-1686.439426
TCGA-UY-A78K-01A-11R-A33J-07	-581.1620123	1809.74824	1228.586227
TCGA-CF-A3MG-01A-11R-A20F-07	-2232.594209	-659.3294039	-2891.923613
TCGA-DK-A1A6-01A-11R-A13Y-07	-511.8082838	952.039678	440.2313942
TCGA-E7-A541-01A-11R-A26T-07	-879.8186074	1257.309063	377.4904555
TCGA-XF-A8HE-01A-11R-A36F-07	-299.5006307	1338.901558	1039.400927
TCGA-DK-AA6Q-01A-11R-A39I-07	-1597.07376	1100.98942	-496.0843402
TCGA-GC-A3WC-01A-31R-A22U-07	-226.1007212	1770.137538	1544.036817
TCGA-K4-A4AC-01A-21R-A26T-07	-581.9779849	970.3238015	388.3458166
TCGA-K4-A5RH-01A-11R-A30C-07	909.439295	2532.638723	3442.078018
TCGA-FD-A5C1-01A-11R-A28M-07	669.1189458	1824.191966	2493.310912
TCGA-2F-A9KO-01A-11R-A38B-07	-161.8736535	1493.746541	1331.872887
TCGA-XF-A9T8-01A-11R-A39I-07	332.4904965	2014.121867	2346.612363
TCGA-CU-A3YL-01A-11R-A22U-07	-1022.911338	-156.5561219	-1179.46746
TCGA-E7-A7XN-01A-11R-A352-07	-973.6604474	1940.965514	967.3050663
TCGA-4Z-AA7W-01A-11R-A39I-07	-120.2389766	2503.076128	2382.837152
TCGA-FD-A43U-01A-11R-A23W-07	1011.250719	2322.557889	3333.808608
TCGA-ZF-A9R3-01A-11R-A38B-07	-1250.781485	213.0911189	-1037.690366
TCGA-4Z-AA89-01A-11R-A39I-07	-2259.354207	-109.1984497	-2368.552657
TCGA-XF-AAN2-01A-11R-A42T-07	-975.3213791	930.8740714	-44.44730766
TCGA-GU-A766-01A-11R-A32O-07	195.0621659	2466.897305	2661.95947
TCGA-FD-A6TD-01A-51R-A33J-07	248.8665104	1641.192188	1890.058699

TCGA-FD-A3B4-01A-12R-A206-07	133.3733211	1361.332141	1494.705462
TCGA-DK-A1AB-01A-11R-A13Y-07	916.5544277	983.9636554	1900.518083
TCGA-UY-A9PB-01A-11R-A38B-07	742.0603299	1956.712288	2698.772618
TCGA-XF-AAML-01A-11R-A42T-07	-2047.822511	202.3436944	-1845.478817
TCGA-ZF-AA58-01A-12R-A42T-07	805.6731736	2438.800865	3244.474039
TCGA-YC-A9TC-01A-22R-A39I-07	-993.9997731	-219.0162723	-1213.016045
TCGA-K4-A6FZ-01A-11R-A31N-07	-986.3385852	906.9215332	-79.41705203
TCGA-KQ-A41R-01A-21R-A352-07	-1385.798899	-409.5779862	-1795.376885
TCGA-DK-AA6M-01A-11R-A39I-07	-61.36532586	1635.813719	1574.448393
TCGA-K4-A5RJ-01A-11R-A28M-07	430.9058846	2851.186287	3282.092172
TCGA-HQ-A5ND-01A-11R-A26T-07	-1768.411829	-161.6735963	-1930.085425
TCGA-BT-A3PK-01A-21R-A220-07	292.6698977	996.6827945	1289.352692
TCGA-FD-A3N6-01A-11R-A21D-07	-1115.554824	282.5503169	-833.0045073
TCGA-UY-A78P-01A-12R-A36F-07	145.8544856	2022.382299	2168.236785
TCGA-CF-A9FM-01A-11R-A38B-07	-1596.205833	186.8179386	-1409.387894
TCGA-ZF-A9RD-01A-11R-A42T-07	-252.8536021	1869.219779	1616.366177
TCGA-E5-A2PC-01A-11R-A206-07	-1609.003846	428.8184961	-1180.18535
TCGA-GD-A76B-01A-11R-A32O-07	-790.3707292	1389.137916	598.7671868
TCGA-GC-A6I1-01A-12R-A31N-07	-226.3933988	2385.615733	2159.222334
TCGA-XF-A9SK-01A-11R-A42T-07	753.839608	1232.181322	1986.02093
TCGA-FD-A3SQ-01A-21R-A22U-07	826.3206792	874.748291	1701.06897
TCGA-XF-AAN1-01A-31R-A42T-07	-1533.309465	-179.8087465	-1713.118212
TCGA-CF-A3MI-01A-11R-A20F-07	-1083.354352	305.0378533	-778.316499
TCGA-XF-AAMZ-01A-11R-A42T-07	-1040.171478	277.0433006	-763.1281777
TCGA-DK-AA6L-01A-11R-A39I-07	-996.4174984	806.9454933	-189.4720052
TCGA-XF-A9T4-01A-11R-A39I-07	-766.355213	633.6415239	-132.7136891
TCGA-UY-A8OB-01A-12R-A42T-07	-1353.194513	559.3032572	-793.8912562
TCGA-ZF-A9R5-01A-12R-A42T-07	-1815.834321	-129.4551807	-1945.289502
TCGA-DK-AA6S-01A-21R-A39I-07	782.7296813	1143.21047	1925.940151
TCGA-E7-A8O8-01A-11R-A36F-07	-1496.13599	-257.3871474	-1753.523137
TCGA-XF-A9SM-01A-11R-A42T-07	634.4185294	2503.287899	3137.706429
TCGA-XF-A8HC-01A-11R-A36F-07	-2107.396829	-1006.849264	-3114.246093
TCGA-ZF-AA4W-01A-12R-A38B-07	-1370.094795	-28.20276328	-1398.297558
TCGA-LC-A66R-01A-41R-A30C-07	-318.2627684	1546.1339	1227.871132
TCGA-E7-A8O7-01A-11R-A36F-07	-1388.360374	619.6363924	-768.7239817
TCGA-LT-A8JT-01A-11R-A36F-07	-1556.331424	130.824802	-1425.506622
TCGA-G2-A2ES-01A-11R-A180-07	-68.42878294	858.0730644	789.6442814
TCGA-XF-AAN4-01A-11R-A42T-07	1656.09277	2083.460102	3739.552872
TCGA-4Z-AA83-01A-11R-A39I-07	-892.8526444	433.9900057	-458.8626387
TCGA-ZF-AA4V-01A-11R-A38B-07	-501.210461	835.9013809	334.6909199
TCGA-ZF-AA53-01A-11R-A39I-07	627.4177166	1716.30379	2343.721506
TCGA-2F-A9KR-01A-11R-A38B-07	-1517.31536	-265.5124642	-1782.827825
TCGA-E5-A4U1-01A-11R-A31N-07	-2138.538263	-1004.774796	-3143.313059
TCGA-FD-A6TC-01A-21R-A33J-07	275.8638956	92.00264738	367.866543
TCGA-DK-A2I4-01A-11R-A21D-07	1185.889107	2810.607313	3996.49642
TCGA-E7-A519-01A-11R-A26T-07	-862.9036785	1295.520672	432.616994
TCGA-DK-A3IU-01A-11R-A20F-07	907.4536714	2780.344056	3687.797727
TCGA-FD-A62N-01A-11R-A30C-07	1349.404838	3059.573389	4408.978227
TCGA-BT-A20J-01A-11R-A14Y-07	-349.6230465	1808.946079	1459.323032
TCGA-DK-AA71-01A-31R-A39I-07	-1331.309229	-277.1844743	-1608.493703
TCGA-KQ-A41O-01A-12R-A352-07	-2613.724799	-1515.696098	-4129.420897
TCGA-E7-A677-01A-11R-A30C-07	-1148.375527	130.352718	-1018.022809
TCGA-DK-A1A5-01A-11R-A13Y-07	318.5220176	370.5145254	689.0365431
TCGA-HQ-A5NE-01A-12R-A28M-07	-476.961112	355.1763586	-121.7847534
TCGA-CF-A47S-01A-11R-A23W-07	-1566.93325	225.0535836	-1341.879666
TCGA-FD-A6TK-01A-42R-A33J-07	899.7378973	1612.090718	2511.828615
TCGA-E7-A5KF-01A-11R-A28M-07	-2486.722808	-588.0182852	-3074.741093
TCGA-XF-A9T5-01A-11R-A42T-07	63.12894021	2157.275735	2220.404675

TCGA-XF-A9SX-01A-21R-A39I-07	957.0337531	1915.062531	2872.096284
TCGA-XF-A8HD-01A-11R-A36F-07	-290.1865231	1430.546284	1140.359761
TCGA-GV-A3JX-01A-11R-A20F-07	-1347.360869	611.0888419	-736.2720272

Figure S1


A
GSE7476
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ETV7 Expression
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4.8
5.0
5.2
5.4
Normal
Tumor
B
ETV7
p=8.227e-05
Expression
6
7
8
9
Bladder
Tissue
NormalTissue
PrimaryTumor
C
ETV7 Expression Level (log2 TPM)
0
2
4
6
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ACC.Tumor (n=79)
BLCA.Tumor (n=408)
BLCA.Normal (n=19)
BRCA.Tumor (n=1093)
BRCA.Normal (n=112)
BRCA−Basal.Tumor (n=190)
BRCA−Her2.Tumor (n=82)
BRCA−LumA.Tumor (n=564)
BRCA−LumB.Tumor (n=217)
CESC.Tumor (n=304)
CESC.Normal (n=3)
CHOL.Tumor (n=36)
CHOL.Normal (n=9)
COAD.Tumor (n=457)
COAD.Normal (n=41)
DLBC.Tumor (n=48)
ESCA.Tumor (n=184)
ESCA.Normal (n=11)
GBM.Tumor (n=153)
GBM.Normal (n=5)
HNSC.Tumor (n=520)
HNSC.Normal (n=44)
HNSC−HPV+.Tumor (n=97)
HNSC−HPV−.Tumor (n=421)
KICH.Tumor (n=66)
KICH.Normal (n=25)
KIRC.Tumor (n=533)
KIRC.Normal (n=72)
KIRP.Tumor (n=290)
KIRP.Normal (n=32)
LAML.Tumor (n=173)
LGG.Tumor (n=516)
LIHC.Tumor (n=371)
LIHC.Normal (n=50)
LUAD.Tumor (n=515)
LUAD.Normal (n=59)
LUSC.Tumor (n=501)
LUSC.Normal (n=51)
MESO.Tumor (n=87)
OV.Tumor (n=303)
PAAD.Tumor (n=178)
PAAD.Normal (n=4)
PCPG.Tumor (n=179)
PCPG.Normal (n=3)
PRAD.Tumor (n=497)
PRAD.Normal (n=52)
READ.Tumor (n=166)
READ.Normal (n=10)
SARC.Tumor (n=259)
SKCM.Tumor (n=103)
SKCM.Metastasis (n=368)
STAD.Tumor (n=415)
STAD.Normal (n=35)
TGCT.Tumor (n=150)
THCA.Tumor (n=501)
THCA.Normal (n=59)
THYM.Tumor (n=120)
UCEC.Tumor (n=545)
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UCS.Tumor (n=57)
UVM.Tumor (n=80)