

GSE set #	ID	adj.P.Val	P.Value	t	Gene.Symbol
2871	AF020212_	9.5E-06	1.33E-10	8.235159	Dnm1l
2871	rc_AI63951	9.5E-06	2.23E-10	8.081836	
2871	rc_AI1721E	2.57E-05	9.06E-10	-7.67066	Psmb4
2871	AFFX-BioB-	0.000026	1.22E-09	-7.58256	
2871	rc_AA8008	2.98E-05	1.75E-09	-7.47808	Prickle2
2871	rc_AI6392E	4.69E-05	3.31E-09	7.292805	Dock8
2871	rc_AA8595	5.64E-05	4.65E-09	-7.19464	Arhgef7
2871	X93352_at	7.52E-05	7.08E-09	-7.07244	Rpl10a
2871	rc_AA8756	7.69E-05	8.14E-09	-7.03201	Ina
2871	M33025_s_	0.000374	4.40E-08	-6.54413	Ptms
2871	rc_AI14504	0.00045	6.22E-08	-6.44412	Mapk8ip2
2871	rc_AA7997	0.00045	6.38E-08	-6.43674	Polr2i
2871	rc_AA9247	0.00045	6.89E-08	-6.41487	Mt3
2871	rc_AI17882	0.000505	9.61E-08	6.318706	Eif4ebp1
2871	rc_AA8586	0.000505	1.04E-07	-6.29545	Lztr1
2871	rc_AI22854	0.000505	1.06E-07	-6.29035	S100a1
2871	M27207mf	0.000505	1.10E-07	6.280866	Col1a1
2871	rc_H33491	0.000505	1.10E-07	6.279312	Ebp
2871	U83880UTI	0.000505	1.13E-07	6.271728	Gpd2
2871	rc_AI0138E	0.000505	1.36E-07	6.217925	Hibadh
2871	M73808mf	0.000505	1.45E-07	-6.20015	Phkg2
2871	rc_AA8938	0.000505	1.45E-07	-6.19969	
2871	D25224_at	0.000505	1.47E-07	-6.19567	Rpsa
2871	D89655_at	0.000505	1.50E-07	-6.19034	Scarb1
2871	D49653_s_	0.000505	1.54E-07	6.181884	Lep
2871	rc_AA8922	0.000505	1.55E-07	-6.18132	Mgst3
2871	AB017188_	0.000532	1.69E-07	-6.15534	Psm4
2871	rc_H33461	0.000565	1.90E-07	6.12206	Oxr1
2871	rc_AA9579	0.000565	1.96E-07	6.113201	
2871	L14323_at	0.000565	1.99E-07	6.107677	Plcb1
2871	X62671cds	0.000585	2.14E-07	-6.08784	Fau
2871	rc_AI00881	0.000746	2.89E-07	6.000456	Cy5
2871	AF055884_	0.000746	2.92E-07	-5.99676	Deaf1
2871	AF100421_	0.000746	3.01E-07	-5.9885	Mtdh
2871	D00189_at	0.000746	3.07E-07	-5.98238	Atp1a3
2871	rc_AA8497	0.000795	3.37E-07	-5.95606	Psm1
2871	D10262_at	0.000833	3.63E-07	-5.93449	Chka
2871	U75405UTI	0.000834	3.78E-07	5.922158	Col1a1
2871	rc_AA8927	0.000834	3.82E-07	-5.91896	LOC301124
2871	AF007107_	0.000902	4.24E-07	-5.88873	Cy5a
96	33387_at	0.000668	6.45E-09	-18.5397	GAS7
96	35817_at	0.001521	3.51E-08	-15.4941	MBP
96	32243_g_a	0.001521	5.49E-08	-14.7724	CRYAB
96	40567_at	0.001521	6.95E-08	-14.4032	TUBA1A
96	34407_at	0.001649	1.04E-07	13.79605	RARRES2
96	33917_at	0.001649	1.12E-07	-13.6905	EPB41L1

96 39178_at	0.001521	7.35E-08	-16.3926	RTN1
96 32623_at	0.002027	1.70E-07	-13.085	GABBR1
96 40422_at	0.002027	1.76E-07	13.03089	IGFBP2
96 40607_at	0.002433	2.41E-07	-12.5972	DPYSL2
96 37406_at	0.002433	2.59E-07	-12.5009	MAPRE2
96 33835_at	0.002841	3.30E-07	-12.176	TSPYL4
96 32260_at	0.003074	4.16E-07	-11.8707	PEA15
96 35778_at	0.003112	4.60E-07	-11.7397	KIF5C
96 32076_at	0.003112	5.43E-07	-11.5299	RCAN2
96 36536_at	0.003112	5.81E-07	-11.4446	SCHIP1
96 38044_at	0.003112	6.32E-07	-11.34	FAM107A
96 39385_at	0.003112	5.85E-07	12.81128	ANPEP
96 38408_at	0.003403	7.48E-07	-11.1312	TSPAN7
96 691_g_at	0.003403	7.57E-07	11.11716	P4HB
96 36939_at	0.002894	3.64E-07	-15.814	GPM6A
96 35742_at	0.004005	9.29E-07	-10.868	C16orf45
96 39760_at	0.004126	1.08E-06	-10.6929	QKI
96 36152_at	0.004126	1.08E-06	-10.6922	GDI1
96 41416_at	0.004205	1.14E-06	11.82358	FGL1
96 36666_at	0.004725	1.32E-06	10.44976	P4HB
96 32254_at	0.005188	1.61E-06	-10.225	VAMP2
96 38800_at	0.005188	1.65E-06	-10.1939	STMN2
96 36567_at	0.005011	1.50E-06	-11.4329	SLC17A7
96 37182_at	0.005455	1.81E-06	-10.09	SYP
96 40075_at	0.005455	1.85E-06	-10.0706	SYT1
96 39756_g_a	0.005806	2.04E-06	9.960928	XBP1
96 41288_at	0.005806	2.08E-06	-9.93809	CALM1 /CALM2 /CALM3
96 39331_at	0.005806	2.13E-06	-9.90903	TUBB2A
96 32715_at	0.005838	2.20E-06	9.87419	VAMP8
96 362_at	0.005944	2.30E-06	-9.82624	PRKCZ
96 38630_at	0.005011	1.47E-06	-13.1177	LASS6
96 35174_i_at	0.006537	2.59E-06	-9.69505	EEF1A2
96 35599_at	0.006547	2.68E-06	9.65951	GNMT
96 33942_s_a	0.006547	2.86E-06	-9.58607	STXBP1
96 38406_f_at	0.006547	2.88E-06	-9.57914	PTGDS
96 296_at	0.006547	2.90E-06	-9.57348	TUBB2A
96 38810_at	0.006547	2.91E-06	-9.56812	HDAC5
96 36159_s_a	0.006547	2.97E-06	-9.54558	PRNP
96 40193_at	0.007668	3.66E-06	-9.32462	ENO2
96 40653_at	0.007668	3.67E-06	-9.3209	RGS7
96 38797_at	0.007668	3.71E-06	9.311241	SLC39A14
96 37921_at	0.008094	4.11E-06	-9.20391	NPTX1
96 40825_at	0.008094	4.12E-06	-9.20013	MAPRE3
96 37365_at	0.008094	4.15E-06	-9.19343	DNAJB2
96 34767_at	0.008272	4.32E-06	-9.1514	MOAP1
96 39755_at	0.008406	4.83E-06	9.03459	XBP1
96 32607_at	0.008406	4.85E-06	-9.03071	BASP1

96	38855_s_a	0.008406	4.86E-06	-9.0284	OLFM1
96	925_at	0.008406	4.88E-06	9.02584	IFI30
96	40862_i_at	0.008812	5.20E-06	-8.96057	CKB
96	41629_at	0.008406	4.70E-06	11.20857	TM4SF4
96	40568_at	0.008994	5.39E-06	-8.9231	ATP6V1B2
96	39175_at	0.003112	5.53E-07	-18.2475	PFKP
96	40753_at	0.009343	5.69E-06	-8.86819	SNCB
96	32138_at	0.009345	5.78E-06	-8.85208	DNM1
96	35670_at	0.003112	6.24E-07	-17.9176	ATP1A3
96	1305_s_at	0.008406	4.61E-06	11.2392	CYP4F2 /// CYP4F3
96	40165_at	0.00971	6.10E-06	-8.7977	TSPYL2
4692	920252	0.000362	1.72E-09	-44.1824	Mest
4692	434767	0.008825	1.18E-07	23.38013	
4692	395082	0.008825	2.08E-07	21.44224	
4692	932079	0.008825	3.01E-07	20.27519	Ucp1
4692	552459	0.008825	3.21E-07	27.06012	Csn3
4692	372851	0.008825	3.58E-07	19.74737	Apol7c
4692	926942	0.008825	3.99E-07	-19.4269	Lipf
4692	884776	0.008825	4.02E-07	25.99746	Klk1
4692	498083	0.008825	4.36E-07	19.16774	Cd79b
4692	453230	0.008825	4.40E-07	19.14105	Cd3d
4692	520081	0.008825	5.21E-07	18.65379	Cd19
4692	568122	0.008825	6.40E-07	-18.0779	Bpifb6
4692	913882	0.008825	6.67E-07	17.96527	Fcrl1
4692	523646	0.008825	7.27E-07	17.72702	
4692	721976	0.008825	8.36E-07	17.35327	
4692	717215	0.008825	8.68E-07	-17.2555	Sfrp5
4692	517377	0.008825	8.95E-07	17.17593	Btla
4692	925254	0.008825	9.00E-07	17.1615	Cd8b1
4692	928212	0.008825	9.88E-07	16.9184	
4692	918751	0.008825	9.90E-07	16.9131	Siglech
4692	654956	0.008825	1.03E-06	16.8088	
4692	517553	0.008825	1.03E-06	-16.8024	Cyp8b1
4692	387643	0.008825	1.11E-06	16.61592	Tbc1d10c
4692	587497	0.008825	1.12E-06	16.59005	
4692	301218	0.008825	1.16E-06	16.51516	
4692	421942	0.008825	1.16E-06	16.50258	
4692	573645	0.008825	1.20E-06	16.42979	Gimap3
4692	801472	0.008825	1.26E-06	16.30018	Ccr6
4692	880995	0.008825	1.27E-06	16.28084	Cd72
4692	819976	0.008825	1.30E-06	16.22695	
4692	797351	0.008825	1.32E-06	16.18913	
4692	607840	0.008825	1.38E-06	-16.0714	Lbp
4692	508185	0.008825	1.40E-06	16.03654	Ccl19
4692	834755	0.008825	1.43E-06	15.99413	Pyhin1
4692	876665	0.009416	1.57E-06	15.76589	Ccr7
4697	703036	0.0111	5.91E-07	-14.6746	Gh

4697	414508	0.7308	7.80E-05	-8.41568	Cga
4697	922742	0.737	1.18E-04	-7.08172	Prl
4697	351994	0.8453	6.30E-04	10.40948	
4697	576185	0.8453	6.59E-04	10.28535	Wasf2
4697	359219	0.8453	7.44E-04	5.794825	
4697	578302	0.8453	7.76E-04	9.836459	Prss22
4697	836606	0.8453	8.05E-04	15.86033	
4697	925379	0.8453	8.21E-04	9.687803	Akr1c12///Akr1c13
4697	731647	0.8453	8.59E-04	15.49426	
4697	481010	0.8453	9.52E-04	9.304993	Tm4sf4
4697	503258	0.8453	1.10E-03	14.1507	
4697	740245	0.8453	1.11E-03	14.13459	Olfr715
4697	394882	0.8453	1.15E-03	13.92921	Arap3
4697	642951	0.8453	1.21E-03	13.69892	
4697	433383	0.8453	1.26E-03	8.623701	
4697	496299	0.8453	1.34E-03	8.468667	
4697	455292	0.8453	1.43E-03	12.89714	
4697	345648	0.8453	1.43E-03	12.88002	Plin4
4697	628023	0.8453	1.48E-03	12.70949	Ceacam12
4697	722499	0.8453	1.60E-03	12.37138	
4697	514577	0.8453	1.72E-03	12.04201	
4697	889516	0.8453	1.90E-03	7.691509	
4697	802117	0.8453	2.01E-03	11.39398	
4697	423363	0.8453	2.16E-03	11.08435	Olfr1388
4697	726960	0.8453	2.20E-03	7.384923	Hoxb8///Hoxb7
4697	537148	0.8453	2.25E-03	7.336838	
4697	919710	0.8453	2.27E-03	7.318424	Krtcap3
4697	774769	0.8453	2.33E-03	-4.72408	Pitpnc1
4697	927625	0.8453	2.37E-03	10.72571	Spint1
4697	570967	0.8453	2.37E-03	7.230971	
4697	861602	0.8453	2.49E-03	10.53339	Crisp3
4697	809745	0.8453	2.58E-03	7.063346	
4697	765100	0.8453	2.60E-03	-7.04612	
4697	706854	0.8453	2.62E-03	10.33537	Add1
4697	551762	0.8453	2.72E-03	10.19112	
4697	555166	0.8453	3.04E-03	9.782792	
4697	468073	0.8453	3.11E-03	-4.21629	Ncs1
4697	391299	0.8453	3.13E-03	9.678432	
4697	431194	0.8453	3.14E-03	6.682255	Syvn1
4697	686764	0.8453	3.15E-03	9.66561	Fan1
4697	637912	0.8453	3.17E-03	9.640178	H2-Ab1
4697	643417	0.8453	3.61E-03	9.191686	
4697	431239	0.8453	3.63E-03	6.417459	Cyp1a1
4697	739801	0.8453	3.66E-03	9.145989	
4697	761765	0.8453	3.75E-03	9.065753	
4697	887284	0.8453	3.77E-03	4.666326	Neurod4
4697	579707	0.8453	3.80E-03	9.020696	Mbnl3

4697	711970	0.8453	4.07E-03	8.795212
4697	501592	0.8453	4.10E-03	6.198191 Zbtb1
4697	742371	0.8453	4.11E-03	8.763966
4697	743542	0.8453	4.34E-03	8.586383
4697	904044	0.8453	4.44E-03	-4.17661 U2af2
4697	734984	0.8453	4.59E-03	-3.93035
4697	910186	0.8453	4.70E-03	5.961607 Ly6g6d
4697	440799	0.8453	4.98E-03	5.863956 Slc2a1
4697	768318	0.8453	5.01E-03	4.077644 Usp46
4697	687305	0.8453	5.08E-03	8.104154
4697	321657	0.8453	5.22E-03	8.020458
4697	452741	0.8453	5.24E-03	5.77894 Nalcn
4697	875485	0.8453	5.30E-03	7.974875
4697	381228	0.8453	5.33E-03	5.750843
4697	602022	0.8453	5.45E-03	17.005 Zbtb3
4697	577870	0.8453	5.65E-03	5.65209 Man2a1
4697	507838	0.8453	5.73E-03	7.751222
4697	816158	0.8453	5.92E-03	7.655486 Stard6
4697	797753	0.8453	6.05E-03	16.03346 Csprs
4697	603454	0.8453	6.10E-03	7.572942
4697	805171	0.8453	6.15E-03	7.548369
4697	437867	0.8453	6.24E-03	7.506692
4697	869937	0.8453	6.27E-03	15.71386
4697	671029	0.8453	6.30E-03	3.894729
4697	387960	0.8453	6.43E-03	15.49212
4697	875178	0.8453	6.53E-03	15.3674 Slco2a1
4697	529442	0.8453	6.56E-03	7.370013
4697	918411	0.8453	6.63E-03	4.574189 Ankzf1
4697	426365	0.8453	6.80E-03	7.272155
4697	866377	0.8453	6.81E-03	-3.64774 Rph3a
4697	444707	0.8453	6.92E-03	7.223912 Wnt10a
4697	710433	0.8453	6.94E-03	14.84083
4697	462644	0.8453	7.11E-03	5.28696
4697	677543	0.8453	7.23E-03	-3.60664
4697	753535	0.8453	7.24E-03	7.103013
4697	890829	0.8453	7.28E-03	7.087737
4697	646322	0.8453	7.46E-03	-3.58444
4697	357505	0.8453	7.48E-03	-7.01567 Hdlbp
4697	789627	0.8453	7.63E-03	-3.74421 Caln1
4697	742280	0.8453	7.75E-03	-3.9886 Cln3
4697	633863	0.8453	7.85E-03	6.892396 2310057N15Rik
4697	601927	0.8453	7.90E-03	6.874536 Klk7
4697	429546	0.8453	8.15E-03	13.56918
4697	905687	0.8453	8.25E-03	6.763077
4697	897303	0.8453	8.35E-03	13.38357
4697	475137	0.8453	8.47E-03	13.27317 Hrasls5
4697	864285	0.8453	8.47E-03	6.696009 Tmem65

4697	504508	0.8453	8.52E-03	13.2332	Olfr657///Olfr504
4697	589372	0.8453	8.52E-03	13.22645	Dip2b
4697	461975	0.8453	8.59E-03	6.661009	
4697	313790	0.8453	8.67E-03	6.64035	
4697	924680	0.8453	8.70E-03	4.982374	Col14a1
4697	436792	0.8453	8.71E-03	3.884086	Prpf38b
4697	627556	0.8453	8.80E-03	12.99014	
4697	381663	0.8453	8.85E-03	6.588466	Oprl1
4697	921686	0.8453	8.86E-03	3.628744	Spg7
4697	738869	0.8453	8.87E-03	6.58296	Grlf1
4697	580113	0.8453	8.88E-03	4.953056	
4697	519165	0.8453	8.99E-03	6.548694	Bpifa3
2392	1427660_x	0.000387	7.60E-10	35.64727	Gm10883 /
2392	1427455_x	0.002221	1.11E-08	25.10947	Gm10883 /
2392	1452417_x	0.002221	1.31E-08	24.58184	Gm10883 /
2392	1428720_s	0.009057	8.20E-08	19.31265	2010309G21Rik
2392	1425295_a	0.009057	8.89E-08	19.10708	Ear11
2392	1425519_a	0.016287	1.92E-07	17.25857	Cd74
2392	1452463_x	0.016465	2.31E-07	16.83847	Gm10883
2392	1427329_a	0.016465	2.75E-07	16.45434	Igh-6
2392	1424305_a	0.016465	2.91E-07	16.33073	Igj
2392	1425324_x	0.016766	3.29E-07	16.06485	Igh-6
2392	1447918_x	0.017884	3.86E-07	15.72661	Igl-V1
2392	1452557_a	0.018799	4.43E-07	15.44229	
2392	1438858_x	0.021354	5.53E-07	14.99313	H2-Aa
2392	1435290_x	0.021354	6.27E-07	14.74097	H2-Aa
2392	1427351_s	0.021354	6.56E-07	14.65271	Igh-6
2392	1456693_a	0.021354	6.94E-07	-14.5424	LOC100504413
2392	1425451_s	0.021354	7.18E-07	14.47809	Chi3l3 /// Chi3l4
2392	1425151_a	0.021354	7.55E-07	14.38126	Noxo1
2392	1443783_x	0.027963	1.04E-06	13.77039	H2-Aa
2392	1422386_a	0.030002	1.18E-06	13.54716	Olfr64
2392	1452431_s	0.034451	1.44E-06	13.19171	H2-Aa
2392	1452393_a	0.034451	1.49E-06	13.12788	Akna
2392	1419684_a	0.041091	1.86E-06	12.74283	Ccl8
2392	1427756_x	0.043094	2.11E-06	12.52465	Igh-6
2392	1451721_a	0.043094	2.12E-06	12.5192	H2-Ab1
3293	X60769mR	0.0949	1.12E-06	19.73167	Cebpb
3293	X17053mR	0.2617	6.16E-06	16.47086	Ccl2
3293	X63594cds	0.3119	1.1E-05	15.424	Nfkbia
3293	rc_AA8919	0.5432	2.56E-05	13.95903	LOC100365106
3293	X96437mR	0.6704	3.94E-05	13.22917	Ier3
3293	X61381cds	0.7225	0.000051	12.80364	Ifitm3
3293	D11445exc	0.7284	6E-05	12.53801	Cxcl1
3293	U22414_at	0.7655	7.51E-05	12.17301	Ccl3
3293	M32062_a	0.7655	8.11E-05	12.05072	LOC498276///Fcgr2a
3293	rc_AA8932	0.7933	0.000104	11.65785	Plin2

3293	X57523_g_	0.7933	0.000111	11.554	Tap1
3293	L18948_at	0.7933	0.000121	11.41297	S100a9
3293	M61875_s_	0.7933	0.000144	11.13711	Cd44
3293	rc_AI16932	0.7933	0.000148	11.09675	Timp1
3293	rc_AI16932	0.7933	0.000149	11.09116	Timp1
3293	D28557_s_	0.7933	0.000158	10.99757	Ybx3
3293	M14656_a	0.7933	0.000159	10.98994	Spp1
3293	J02962_at	1	0.000244	10.32751	Lgals3
3293	M34253_g_	1	0.000276	10.14373	Irf1
3293	X13044_at	1	0.00028	10.12136	Cd74
3293	rc_AA9448	1	0.000282	10.11153	Rap1b
3293	Y07704_g_	1	0.000287	10.08245	Rsad2
3293	rc_AA8927	1	0.000295	10.03984	
3293	rc_AA8188	1	0.000318	9.93058	Srgn
3293	M24026_f_	1	0.000325	9.895678	RT1-CE12
3293	L32591mRl	1	0.000353	9.773429	Gadd45a
3293	X17053cds	1	0.00036	9.743878	Ccl2
3293	M86389cd:	1	0.000369	9.706979	Hspb1
3293	rc_AA8927	1	0.000375	9.684939	Lyz2
3293	M11794cd:	1	0.0004	9.587694	Mt1a
3293	rc_AI1759E	1	0.000434	9.466105	Jun
3293	rc_AA8751	1	0.000444	9.4336	
3293	M65149_a	1	0.000455	9.397779	Cebpd
3293	rc_AA8923	1	0.000461	9.375997	Tuba1c
3293	U92081mR	1	0.000476	9.329486	Pdpr
3293	M97656_s_	1	0.00049	9.288221	Sstr1
3293	J05122_at	1	0.000507	9.23654	Tspo
3293	M32062_g_	1	0.000508	9.234172	Fcgr2a
3293	rc_AI1025E	1	0.000524	9.189888	Mt1a
3293	rc_AI07153	1	0.000573	9.059433	Olr1
3293	rc_AI17961	1	0.00063	8.920815	Hmox1
3293	J03627_at	1	0.00069	8.789253	S100a10
3293	AF083269_	1	0.000718	8.731736	Arpc1b
3293	M15562_g_	1	0.000721	8.726889	RT1-Da
3293	X13044_g_	1	0.000721	8.726757	Cd74
3293	L13039_s_:	1	0.000732	8.705222	Anxa2
3293	rc_AA7993	1	0.000741	8.686901	Plek
3293	rc_AI1702E	1	0.000805	8.568954	B2m
3293	L14782_s_:	1	0.000864	8.467791	Lyn
3293	X14254cds	1	0.00088	8.441683	Cd74
3293	X73371_at	1	0.000889	8.426975	Fcgr2b///Fcgr2a
3293	rc_AA8927	1	0.000944	8.340947	Rgs1
3293	U75404UTl	1	0.000946	8.339193	Akap12
3293	M24067_a	1	0.00098	8.288734	Serpine1
3293	U07619_at	1	0.000981	8.287469	F3
3293	AF030089L	1	0.001054	8.18546	Dcll1
3293	S61865_s_:	1	0.001056	8.182953	Sdc1

3293 rc_AA8006	1	0.001066	8.169595	Zfp36
3293 rc_AA9443	1	0.001096	8.129784	Arf6
3293 M92074_g	1	0.001111	8.110825	Tnni3
3293 D90035_s	1	0.001168	8.040681	Ppp3ca
3293 M94919mf	1	0.001262	7.932791	Hbb-b1
3293 rc_AA9465	1	0.001427	7.760848	Lcn2
3293 M29866_s	1	0.001467	7.722195	C3
3293 M31018_f	1	0.001541	7.654075	Rt1.aa///RT1-EC2
3293 rc_AA8934	1	0.00171	7.510634	Rap1b
3293 rc_AA8939	1	0.001738	7.488359	
3293 S77528cde	1	0.001783	7.452768	Cebpb
3293 S49491_s	1	0.001867	7.389517	Penk
3293 X05834_at	1	0.002083	7.239804	Fn1
3293 rc_AI6391C	1	0.00213	7.20964	Rab33b
3293 M37394_at	1	0.002139	7.203876	Egfr
3293 Z75029_s	1	0.002197	7.167421	Hspa1a
3293 rc_AI6394C	1	0.002213	7.157482	
3293 rc_AA9570	1	0.002221	7.152805	S100a8
3293 M98820_at	1	0.002282	7.115663	Il1b
3293 X52477_at	1	0.00234	7.082029	C3
3293 S56464mRI	1	0.002351	7.075365	
3293 rc_AI17645	1	0.002362	7.069138	Mt2A
3293 rc_AI1719E	1	0.002389	7.053617	Anxa1
3293 D15069_s	1	0.002392	7.052042	Adm
3293 rc_AI16975	1	0.0024	7.047259	Errfi1
3293 rc_AA9444	1	0.002654	6.911526	Cnn3
3293 D45187_s	1	0.002701	6.887755	Ctse
3293 Z54212_at	1	0.002735	6.871302	Emp1
3293 AF033355	1	0.002791	6.843988	Pip4k2b
3293 U77777_s	1	0.002826	6.826891	Il18
3293 M74488cd	1	0.002858	6.811841	Camk4
3293 D00913_g	1	0.002859	6.811454	Icam1
3293 AB022209	1	0.002894	6.795049	Hnrnpf
3293 D38065exc	1	0.002929	6.779223	Ugt1a1
3293 M94918mf	1	0.00293	6.778662	Hbb
3293 S75960_s	1	0.00313	6.690366	Umod
3293 rc_AA8750	1	0.003155	6.679743	
3293 M63282_at	1	0.003205	6.658381	Atf3
3293 M15562_at	1	0.003348	6.600476	RT1-Da
3293 X59864mR	1	0.003415	6.57406	H19
3293 rc_AI17897	1	0.003552	6.521808	LOC287167
3293 M63122_at	1	0.003585	6.509396	Tnfrsf1a
3293 X76489cde	1	0.003593	6.506408	Cd9
3293 U53184_at	1	0.003652	6.484937	Litaf
3293 rc_AA9986	1	0.003771	6.442253	Hspb1
3293 rc_AI1456E	1	0.003777	6.440259	Slc16a1
3293 rc_AI0443E	1	0.00381	6.428718	Hmgb2

3293 M86341_g	1	0.00385	6.414974	Adprh
3293 U95178_s	1	0.003901	6.397644	Dab2
3293 AF074608n	1	0.003925	6.389413	RT1-EC2
3293 AF022083_	1	0.003965	6.376001	Gnb1
3293 AF037272_	1	0.00415	6.315847	Wfdc1
3293 M96630_a	1	0.004355	6.252423	Sec61a1
3293 U09540_g	1	0.00437	6.247877	Cyp1b1
3293 rc_AA8751	1	0.00448	6.215062	
3293 rc_AI00883	1	0.004502	6.208825	Hmgb2
3293 rc_AI63923	1	0.004519	6.203899	Phf7
3293 rc_AI04503	1	0.0046	6.180634	Cebpd
3293 L32591mRI	1	0.004638	6.169634	Gadd45a
3293 rc_AA8943	1	0.00468	6.157907	Rbpj
3293 D86297_at	1	0.004743	6.140341	Alas2
3293 rc_AI17716	1	0.004976	6.077653	Nfe2l2
3293 rc_AA8186	1	0.005	6.071389	Hspa1b///Hspa1a
3293 J04943_at	1	0.005219	6.015668	Npm1
3293 rc_AA9458	1	0.005262	6.004887	Jun
3293 AF035963_	1	0.005277	6.001083	Havcr1
3293 M15191_s	1	0.005405	5.969937	Tac1
3293 AJ222813_	1	0.005508	5.94541	Il18
3293 rc_AI01416	1	0.005608	5.922096	lfrd1
3293 M58364_a	1	0.00564	5.914812	Gch1
3293 U17035_s	1	0.005658	5.910677	Cxcl10
3293 X76489cds	1	0.005708	5.899225	Cd9
3293 rc_AI17659	1	0.00572	5.896507	Ctsl1
3293 D10693_at	1	0.005742	5.891542	Hnmt
3293 M24604_a	1	0.005746	5.890462	Pcna
3293 M23697_a	1	0.0058	5.878355	Plat
3293 M63333exc	1	0.005841	5.869368	Camk4
3293 Y12319cds	1	0.006017	5.830991	Atxn3
3293 X12355_s	1	0.006038	5.826309	Pdia3
3293 rc_AA8936	1	0.006106	5.812006	Pxn
3293 S66184_s	1	0.006285	5.774614	Lox
3293 U41453_at	1	0.006397	5.751833	Akap12
3293 X54617mR	1	0.006425	5.746276	Myl12a
3293 rc_AI1011C	1	0.006697	5.692857	Vamp2
3293 S74141_s	1	0.006846	5.66443	Hck
3293 AF028784c	1	0.006866	5.660831	Gfap
3293 AF028784n	1	0.00688	5.658209	Gfap
3293 K03039mR	1	0.006922	5.650292	Ptpcr
3293 rc_AA8940	1	0.007125	5.61328	Capg
3293 L06040_s	1	0.00728	5.585717	Alox15
3293 U09407_at	1	0.007351	5.573192	Hint1
3293 D26393exc	1	0.007543	5.540207	Hk2
3293 J02722cds	1	0.007785	5.499822	Hmox1
3293 X61654_at	1	0.007799	5.497579	Cd63

3293 rc_H31550	1	0.007914	5.478893	Cpeb1
3293 M14050_s	1	0.007945	5.473905	Hspa5
3293 AA848563_	1	0.008185	5.435989	Hspa1b///Hspa1a
3293 rc_AI6393E	1	0.008208	5.43245	LOC100360017
3293 rc_AI63914	1	0.008241	5.427229	Mdfic
3293 M26744_a	1	0.008325	5.414451	Il6
3293 X67788_at	1	0.008435	5.397765	Ezr
3293 X71127_at	1	0.008487	5.389931	C1qb
3293 J03624_at	1	0.008489	5.389645	Gal
3293 L12383_at	1	0.008506	5.387109	Arf4
3293 X71127_g	1	0.008511	5.386329	C1qb
3293 D88666_at	1	0.008539	5.38207	Pla1a
3293 rc_AI1773E	1	0.008603	5.372634	Itgb1
3293 L26268_g	1	0.008963	5.320558	Btg1
3293 rc_AI14544	1	0.008985	5.317515	Ppp1r9a
3293 M58587_a	1	0.009036	5.31037	Il6r
3293 U36899_at	1	0.009113	5.299522	Vom1r102
3293 Y00766_at	1	0.009142	5.295542	Scn3a
3293 D88534_s	1	0.009387	5.262047	Pnlip
3293 U27558_at	1	0.009587	5.2355	Kcnj10
3293 AF087943_	1	0.009756	5.213414	Cd14
6514 1423795_a	3.68E-13	7.22E-19	6.92E+01	Sfpq
6514 1416332_a	2.76E-10	1.09E-15	5.20E+01	Cirbp
6514 1442051_a	1.38E-09	8.14E-15	4.77E+01	Hist2h3c1
6514 1422660_a	1.46E-09	1.15E-14	4.70E+01	Rbm3
6514 1452091_a	2.33E-09	2.29E-14	4.56E+01	Rbm28
6514 1435854_a	5.53E-09	6.51E-14	4.35E+01	Opalin
6514 1427464_s	6.11E-09	8.40E-14	4.30E+01	Hspa5
6514 1425993_a	1.50E-08	2.36E-13	4.10E+01	Hsph1
6514 1424638_a	3.36E-08	5.94E-13	3.92E+01	Cdkn1a
6514 1454725_a	1.42E-07	2.79E-12	3.64E+01	Tra2a
6514 1417574_a	1.61E-07	3.47E-12	3.60E+01	Cxcl12
6514 1416749_a	1.66E-07	3.92E-12	3.58E+01	Htra1
6514 1436094_a	3.05E-07	7.79E-12	3.45E+01	Vgf
6514 1420093_s	3.13E-07	8.61E-12	3.44E+01	Hnrpd1
6514 1451566_a	3.93E-07	1.16E-11	3.38E+01	Zfp810
6514 1416354_a	8.52E-07	2.68E-11	3.24E+01	RbmX
6514 1448654_a	9.60E-07	3.21E-11	3.21E+01	Mtch2
6514 1439630_x	1.12E-06	3.96E-11	3.17E+01	Sbsn
6514 1423796_a	1.23E-06	4.58E-11	3.15E+01	Sfpq
6514 1441075_a	1.28E-06	5.03E-11	3.13E+01	Nostrin
6514 1454014_a	1.94E-06	7.98E-11	3.05E+01	Mkks
6514 1429862_a	2.03E-06	8.78E-11	3.04E+01	Pla2g4e
6514 1428470_a	2.88E-06	1.30E-10	2.97E+01	Exoc2
6514 1426722_a	3.53E-06	1.66E-10	2.93E+01	Slc38a2
6514 1442077_a	4.83E-06	2.45E-10	2.87E+01	2310076G05Rik
6514 1448454_a	4.83E-06	2.46E-10	2.86E+01	Srsf6

6514	1417303_a	6.37E-06	3.38E-10	2.81E+01	Mvd
6514	1460645_a	8.39E-06	4.61E-10	2.76E+01	Chordc1
6514	1452318_a	9.49E-06	5.53E-10	2.73E+01	Hspa1b
6514	1451047_a	9.49E-06	5.59E-10	2.73E+01	Itm2a
6514	1417606_a	1.00E-05	6.10E-10	2.72E+01	Calr
6514	1452170_a	1.05E-05	6.61E-10	2.70E+01	Chpf2
6514	1428112_a	1.08E-05	6.99E-10	2.70E+01	Manf
6514	1435158_a	1.14E-05	7.59E-10	2.68E+01	Rbm12b1
6514	1438211_s	1.63E-05	1.12E-09	2.62E+01	Dbp
6514	1416064_a	1.63E-05	1.15E-09	2.62E+01	Hspa5
6514	1455039_a	2.09E-05	1.51E-09	2.57E+01	Sin3b
6514	1415889_a	2.21E-05	1.65E-09	2.56E+01	Hsp90b1
6514	1448930_a	2.31E-05	1.77E-09	2.55E+01	3010026O09Rik
6514	1420772_a	2.62E-05	2.06E-09	2.52E+01	Tsc22d3
6514	1454711_a	3.24E-05	2.65E-09	2.48E+01	Trio
6514	1429169_a	3.24E-05	2.71E-09	2.48E+01	Rbm3
6514	1434557_a	3.24E-05	2.74E-09	2.48E+01	Hip1
6514	1445669_a	3.26E-05	2.82E-09	2.48E+01	Spry4
6514	1424182_a	3.89E-05	3.44E-09	2.44E+01	Acat1
6514	1417706_a	3.92E-05	3.54E-09	2.44E+01	Naglu
6514	1434817_s	4.09E-05	3.78E-09	2.43E+01	Rprd2
6514	1452052_s	4.29E-05	4.05E-09	2.42E+01	Eif3j1
6514	1426100_a	4.38E-05	4.22E-09	2.41E+01	Tk2
6514	1452754_a	4.61E-05	4.52E-09	2.40E+01	Creld2
6514	1457984_a	4.71E-05	4.72E-09	2.40E+01	Crh
6514	1437223_s	4.75E-05	4.85E-09	2.39E+01	Xbp1
6514	1448484_a	4.85E-05	5.04E-09	2.38E+01	Amd1
6514	1426913_a	5.09E-05	5.40E-09	2.37E+01	Lss
6514	1434618_a	5.39E-05	5.82E-09	2.36E+01	Crebzf
6514	1455444_a	5.46E-05	6.05E-09	2.36E+01	Gabra2
6514	1448471_a	5.46E-05	6.11E-09	2.36E+01	Ctla2a
6514	1424355_a	6.64E-05	7.56E-09	2.32E+01	Sin3b
6514	1427127_x	6.90E-05	7.99E-09	2.31E+01	Hspa1b
6514	1449039_a	7.54E-05	8.89E-09	2.30E+01	Hnrpd1
6514	1448130_a	7.70E-05	9.23E-09	2.29E+01	Fdft1
6514	1427126_a	7.89E-05	9.60E-09	2.29E+01	Hspa1b
6514	1428834_a	9.83E-05	1.22E-08	2.25E+01	Dusp4
6514	1442570_a	1.02E-04	1.30E-08	2.24E+01	
6514	1418174_a	1.02E-04	1.30E-08	2.24E+01	Dbp
6514	1426380_a	1.14E-04	1.48E-08	2.22E+01	Eif4b
6514	1424434_a	1.17E-04	1.53E-08	2.22E+01	Mettl22
6514	1455003_a	1.22E-04	1.63E-08	2.21E+01	Thap1
6514	1435119_a	1.32E-04	1.79E-08	2.19E+01	Gm19439
6514	1424235_a	1.39E-04	1.90E-08	2.18E+01	Ormdl2
6514	1448663_s	1.48E-04	2.07E-08	2.17E+01	Mvd
6514	1428052_a	1.48E-04	2.09E-08	2.17E+01	Zmym1
6514	1428233_a	1.70E-04	2.45E-08	2.15E+01	Cpsf6

6514	1438251_x	1.70E-04	2.48E-08	2.14E+01	Htra1
6514	1435437_a	1.70E-04	2.50E-08	2.14E+01	Setd7
6514	1420886_a	1.85E-04	2.76E-08	2.13E+01	Xbp1
6514	1434637_x	2.04E-04	3.09E-08	2.11E+01	Sin3b
6514	1455339_a	2.34E-04	3.58E-08	2.09E+01	Fkbp15
6514	1435188_a	2.44E-04	3.83E-08	2.08E+01	Gm129
6514	1430798_x	2.44E-04	3.84E-08	2.08E+01	Mrpl15
6514	1436045_a	2.47E-04	3.92E-08	2.08E+01	Tsga10
6514	1417146_a	2.56E-04	4.12E-08	2.07E+01	Mri1
6514	1416041_a	2.68E-04	4.37E-08	2.06E+01	Sgk1
6514	1416155_a	2.69E-04	4.44E-08	2.06E+01	Hmgb3
6514	1428584_a	2.77E-04	4.62E-08	2.05E+01	Haghl
6514	1448705_a	3.03E-04	5.11E-08	2.04E+01	Zbtb22
6514	1451190_a	3.26E-04	5.56E-08	2.03E+01	Sbk1
6514	1415886_a	3.35E-04	5.84E-08	2.02E+01	Sh2d3c
6514	1424033_a	3.35E-04	5.90E-08	2.02E+01	Srsf7
6514	1423723_s	3.35E-04	5.91E-08	2.02E+01	Tardbp
6514	1416811_s	3.69E-04	6.60E-08	2.00E+01	Ctla2b///Ctla2a
6514	1438635_x	3.70E-04	6.69E-08	2.00E+01	B930041F14Rik
6514	1423151_a	4.28E-04	7.82E-08	1.98E+01	Dnajb11
6514	1424068_a	4.30E-04	7.94E-08	1.97E+01	Tcta
6514	1438851_x	4.32E-04	8.15E-08	1.97E+01	Cldn1
6514	1423946_a	4.32E-04	8.18E-08	1.97E+01	Pdlim2
6514	1424481_s	4.32E-04	8.31E-08	1.97E+01	Armcx5
6514	1423667_a	4.32E-04	8.35E-08	1.97E+01	Mat2a
6514	1418902_a	4.32E-04	8.39E-08	1.97E+01	Chid1
6514	1445342_a	4.54E-04	8.91E-08	1.96E+01	
6514	1423797_a	5.06E-04	1.00E-07	1.94E+01	Aacs
6514	1435137_s	6.34E-04	1.27E-07	1.91E+01	E430024C06Rik
6514	1422943_a	6.37E-04	1.29E-07	1.91E+01	Hspb1
6514	1435902_a	6.89E-04	1.41E-07	1.89E+01	Nudt18
6514	1456170_x	7.33E-04	1.51E-07	1.88E+01	Calr
6514	1424251_a	7.36E-04	1.53E-07	1.88E+01	Hnrpd1
6514	1447223_a	7.36E-04	1.55E-07	1.88E+01	
6514	1428202_a	7.65E-04	1.62E-07	1.87E+01	Fam3a
6514	1435286_a	7.70E-04	1.65E-07	1.87E+01	Epha5
6514	1434223_a	7.70E-04	1.66E-07	1.87E+01	Oscp1
6514	1420011_s	7.73E-04	1.68E-07	1.87E+01	Xbp1
6514	1428725_a	7.82E-04	1.72E-07	1.86E+01	Pias2
6514	1452257_a	8.14E-04	1.80E-07	1.86E+01	Bdh1
6514	1428747_a	8.80E-04	1.97E-07	1.84E+01	Trnau1ap
6514	1455047_a	8.99E-04	2.03E-07	1.84E+01	Fbxo3
6514	1452094_a	9.90E-04	2.25E-07	1.83E+01	P4ha1
6514	1436209_a	1.02E-03	2.35E-07	1.82E+01	Dnajc16
6514	1455868_a	1.05E-03	2.45E-07	1.81E+01	Tubgcp2
6514	1426441_a	1.05E-03	2.45E-07	1.81E+01	Slc11a2
6514	1416609_a	1.07E-03	2.53E-07	1.81E+01	BC004004

6514	1416591_a	1.10E-03	2.61E-07	1.81E+01	Rab34
6514	1433446_a	1.28E-03	3.06E-07	1.78E+01	Hmgcs1
6514	1420365_a	1.31E-03	3.16E-07	1.78E+01	Hnrnpa2b1
6514	1459897_a	1.36E-03	3.30E-07	1.77E+01	Sbsn
6514	1416146_a	1.39E-03	3.42E-07	1.77E+01	Hspa4
6514	1416129_a	1.49E-03	3.67E-07	1.76E+01	Errfi1
6514	1425281_a	1.49E-03	3.76E-07	1.75E+01	Tsc22d3
6514	1455007_s	1.49E-03	3.76E-07	1.75E+01	Gpt2
6514	1435105_a	1.49E-03	3.77E-07	1.75E+01	Rnf208
6514	1418382_a	1.49E-03	3.83E-07	1.75E+01	Apcdd1
6514	1424591_a	1.49E-03	3.84E-07	1.75E+01	Caap1
6514	1460240_a	1.49E-03	3.85E-07	1.75E+01	Hnrnpc
6514	1417000_a	1.55E-03	4.04E-07	1.74E+01	Abtb1
6514	1435357_a	1.63E-03	4.30E-07	1.74E+01	D4Wsu53e
6514	1435880_a	1.66E-03	4.40E-07	1.73E+01	Ankrd50
6514	1437464_a	1.82E-03	4.86E-07	1.72E+01	Spata7
6514	1423608_a	1.84E-03	4.96E-07	1.72E+01	Itm2a
6514	1448351_a	1.92E-03	5.20E-07	1.71E+01	Coro1b
6514	1416461_a	1.94E-03	5.33E-07	1.71E+01	Gm20253///Caprin1
6514	1426312_a	1.94E-03	5.34E-07	1.71E+01	Bre
6514	1418706_a	1.95E-03	5.40E-07	1.70E+01	Slc38a3
6514	1450713_a	1.95E-03	5.44E-07	1.70E+01	Cspg5
6514	1448319_a	2.13E-03	5.97E-07	1.69E+01	Akr1b3
6514	1447930_a	2.26E-03	6.40E-07	1.68E+01	Baz1a
6514	1422155_a	2.29E-03	6.51E-07	1.68E+01	Hist2h3c2
6514	1435248_a	2.38E-03	6.84E-07	1.67E+01	Btaf1
6514	1424058_a	2.38E-03	6.88E-07	1.67E+01	Prrc1
6514	1452176_a	2.67E-03	7.77E-07	1.65E+01	Nup153
6514	1428958_a	2.68E-03	7.83E-07	1.65E+01	Paqr8
6514	1423474_a	2.68E-03	7.88E-07	1.65E+01	Top1
6514	1419914_s	2.73E-03	8.10E-07	1.65E+01	Nus1
6514	1417394_a	2.83E-03	8.50E-07	1.64E+01	Klf4
6514	1424074_a	2.83E-03	8.51E-07	1.64E+01	Btf3l4
6514	1451495_a	3.08E-03	9.30E-07	1.63E+01	Wac
6514	1433890_a	3.11E-03	9.47E-07	1.63E+01	Bag6
6514	1418700_a	3.11E-03	9.53E-07	1.63E+01	Lias
6514	1440867_a	3.18E-03	9.85E-07	1.62E+01	Spry4
6514	1454645_a	3.18E-03	9.87E-07	1.62E+01	Mgrn1
6514	1435826_a	3.76E-03	1.17E-06	1.60E+01	Rad18
6514	1449121_a	3.78E-03	1.19E-06	1.60E+01	Srsf10
6514	1460672_a	3.98E-03	1.26E-06	1.59E+01	2410002F23Rik
6514	1437334_x	4.02E-03	1.28E-06	1.59E+01	Parn
6514	1435374_a	4.03E-03	1.29E-06	1.58E+01	Cdyl2
6514	1436081_a	4.11E-03	1.32E-06	1.58E+01	Zfp414
6514	1434865_a	4.19E-03	1.36E-06	1.58E+01	Exoc7
6514	1425422_a	4.24E-03	1.38E-06	1.58E+01	Parn
6514	1424461_a	4.28E-03	1.40E-06	1.57E+01	Dctn2

6514	1424285_s	4.56E-03	1.51E-06	1.56E+01	Arl6ip4
6514	1455187_a	4.83E-03	1.60E-06	1.56E+01	Zbtb40
6514	1436790_a	4.99E-03	1.66E-06	1.55E+01	Sox11
6514	1428223_a	4.99E-03	1.68E-06	1.55E+01	Mfsd2a
6514	1452661_a	5.08E-03	1.72E-06	1.55E+01	Tfr3
6514	1418408_a	5.29E-03	1.80E-06	1.54E+01	Zfand1
6514	1460243_a	5.31E-03	1.81E-06	1.54E+01	Sptlc2
6514	1438075_a	5.39E-03	1.85E-06	1.54E+01	Fem1c
6514	1437151_a	5.57E-03	1.92E-06	1.53E+01	Usp22
6514	1448497_a	5.60E-03	1.95E-06	1.53E+01	Ercc3
6514	1428755_a	5.60E-03	1.96E-06	1.53E+01	Creb1
6514	1452980_a	5.98E-03	2.10E-06	1.52E+01	2810468N07Rik
6514	1434309_a	6.35E-03	2.25E-06	1.51E+01	Fntb
6514	1420500_a	6.35E-03	2.26E-06	1.51E+01	Dnajc1
6514	1456763_a	6.38E-03	2.28E-06	1.51E+01	Mpr1p
6514	1452247_a	6.50E-03	2.34E-06	1.50E+01	Fxr1
6514	1428917_a	6.64E-03	2.40E-06	1.50E+01	Stx17
6514	1433806_x	6.67E-03	2.42E-06	1.50E+01	Calr
6514	1448446_a	6.95E-03	2.54E-06	1.49E+01	Deaf1
6514	1426040_a	7.14E-03	2.62E-06	1.49E+01	Odf2
6514	1449184_a	7.19E-03	2.65E-06	1.49E+01	Pglyrp1
6514	1423375_a	7.23E-03	2.68E-06	1.49E+01	Cir1
6514	1435369_a	7.38E-03	2.75E-06	1.48E+01	Fastkd5
6514	1457316_a	7.40E-03	2.78E-06	1.48E+01	Map6
6514	1426402_a	7.49E-03	2.82E-06	1.48E+01	Syncrin1
6514	1433700_a	7.49E-03	2.84E-06	1.48E+01	Gskip
6514	1424369_a	7.50E-03	2.86E-06	1.48E+01	Psmf1
6514	1436843_a	7.84E-03	3.00E-06	1.47E+01	Rbm12b2
6514	1447851_x	8.05E-03	3.10E-06	1.47E+01	Atp10a
6514	1428147_a	9.00E-03	3.49E-06	1.45E+01	Coro7
6514	1455105_a	9.00E-03	3.50E-06	1.45E+01	Ptpn12
6514	1438786_a	9.29E-03	3.63E-06	1.45E+01	2610021A01Rik
6514	1450674_a	9.46E-03	3.71E-06	1.44E+01	Cdk5
8700	1382553_a	0.102	4.77E-06	6.947697	Rfx3
8700	1380567_a	0.102	8.14E-06	-6.63261	
8700	1371303_a	0.102	9.84E-06	6.522384	Tdh
8700	1397039_a	0.123	1.91E-05	6.143221	
8700	1381166_a	0.123	1.99E-05	6.122652	
8700	1392329_a	0.181	3.49E-05	5.810787	Homez
8700	1370074_a	0.202	6.31E-05	-5.48995	Baiap2
8700	1370281_a	0.202	7.31E-05	-5.41184	Fabp5
8700	1369787_a	0.202	7.67E-05	5.386206	Cckar
8700	1368312_a	0.202	9.46E-05	-5.27516	Oxt
8700	1392172_a	0.202	9.51E-05	-5.2723	Ccl9
8700	1394593_a	0.202	9.64E-05	5.265458	
8700	1369049_a	0.202	9.67E-05	-5.26355	Rere
8700	1389695_a	0.202	9.69E-05	-5.26247	Fam20c

8700 1367768_a	0.202	9.72E-05	-5.26071	Lxn
8700 1368187_a	0.205	0.000106	-5.21741	Gpnmb
8700 1376321_a	0.213	0.000116	-5.16605	Piezo1
8700 1387819_a	0.225	0.00013	-5.10729	Cela1
8700 1383500_a	0.236	0.000144	-5.05558	Rrbp1
8700 1371731_a	0.239	0.000158	5.008648	Copg2
8700 1397007_a	0.239	0.000177	4.949498	
8700 1378531_a	0.239	0.00018	4.938675	
8700 1367660_a	0.239	0.00019	-4.91203	Fabp3
8700 1371487_a	0.239	0.000202	-4.88031	Sh3bgrl3
8700 1370355_a	0.239	0.000212	-4.85489	Scd1
8700 1385126_a	0.239	0.000228	4.817838	Magi2
8700 1390918_a	0.239	0.00024	-4.79278	Grtp1
8700 1391395_a	0.239	0.00027	4.732196	Ddx50
8700 1374626_a	0.239	0.000272	-4.72797	Lrg1
8700 1368930_a	0.239	0.000277	-4.71945	Kcnn4
8700 1377599_a	0.239	0.000284	-4.70628	
8700 1368037_a	0.239	0.000289	4.698307	LOC100360507///Cbr1
8700 1386877_a	0.239	0.0003	-4.67916	Ap2s1
8700 1386879_a	0.239	0.0003	-4.67792	Lgals3
8700 1374272_a	0.239	0.000301	4.676216	LOC679383
8700 1367712_a	0.239	0.000303	-4.67334	Timp1
8700 1391591_a	0.239	0.000304	4.672076	Zfp275
8700 1387581_a	0.239	0.00031	4.661992	Rassf9
8700 1373471_a	0.239	0.000311	-4.66118	Rnf166
8700 1391948_a	0.239	0.000318	4.649661	Bcl11b
8700 1371237_a	0.239	0.000321	-4.64469	Mt1a
8700 1384703_a	0.239	0.000339	4.617291	
8700 1369560_a	0.239	0.000349	-4.60142	Gpd1
8700 1387951_a	0.239	0.000351	4.598645	Cd55
8700 1394218_s	0.239	0.000355	4.593235	Zfpm2
8700 1390270_a	0.239	0.000373	4.568986	
8700 1367932_a	0.239	0.000388	-4.5489	Hmgcs1
8700 1393915_a	0.239	0.000403	-4.52939	Lpcat3
8700 1386287_a	0.239	0.000416	-4.51293	Slain2
8700 1394636_a	0.239	0.000418	4.510662	
8700 1375316_a	0.239	0.000418	4.510495	
8700 1370902_a	0.239	0.000424	-4.50391	Akr1b8
8700 1379932_a	0.239	0.000425	4.502753	Clcn4
8700 1387967_a	0.239	0.000427	-4.50091	Spink1
8700 1390383_a	0.239	0.000428	-4.49968	Plin2
8700 1390449_a	0.239	0.000437	4.488411	
8700 1375517_a	0.239	0.000442	-4.48247	Tp53inp2
8700 1370032_a	0.239	0.000452	4.471321	Slc9a3r1
8700 1381116_a	0.239	0.000454	4.469798	
8700 1378353_a	0.239	0.000461	4.462328	Setdb1
8700 1384298_a	0.245	0.000495	-4.42591	Myo1f

8700 1387834_a	0.245	0.000508	-4.41295	Matk
8700 1367609_a	0.245	0.000525	-4.39698	Mif
8700 1385036_a	0.245	0.000544	4.379371	Sncaip
8700 1381489_a	0.245	0.000554	4.369592	
8700 1387148_a	0.245	0.000564	4.360592	Gprasp1
8700 1371816_a	0.245	0.000573	4.353332	Zcchc3
8700 1391252_a	0.245	0.000573	-4.35325	Rnf41
8700 1383768_a	0.245	0.000573	4.352682	Elavl2
8700 1369788_s	0.245	0.000576	4.349991	Jun
8700 1372590_a	0.245	0.000577	-4.34968	C1qtnf1
8700 1393812_a	0.245	0.000581	4.345754	
8700 1389251_a	0.245	0.000593	-4.33618	Nudt7
8700 1374274_a	0.245	0.000623	4.311434	
8700 1392415_a	0.245	0.000637	4.300502	
8700 1369310_a	0.245	0.000647	-4.29221	Basp1
8700 1396712_a	0.245	0.000657	4.284501	
8700 1367850_a	0.245	0.000694	-4.25765	LOC100362543
8700 1367969_a	0.245	0.000709	-4.2471	Prdx6
8700 1379650_a	0.245	0.000725	4.235921	Pdzd8
8700 1377922_a	0.245	0.00073	4.232279	Zfp507
8700 1383658_a	0.245	0.000732	-4.23129	Laptm5
8700 1386859_a	0.245	0.000745	-4.2221	Tkt
8700 1382488_a	0.245	0.000749	4.219807	Ankef1
8700 1371325_a	0.245	0.000762	-4.21111	Ctsa
8700 1376456_a	0.245	0.000768	4.207241	Nmnat2
8700 1373889_a	0.245	0.000776	-4.20197	LOC363715
8700 1376786_a	0.245	0.000781	4.198744	Neo1
8700 1367633_a	0.245	0.000782	-4.19838	Glul
8700 1370377_a	0.245	0.000785	-4.1962	Cyp2d5///Cyp2d1
8700 1397800_a	0.245	0.000791	4.192715	
8700 1368671_a	0.245	0.000798	-4.18787	Srpx
8700 1388485_a	0.245	0.000799	-4.18768	Cxcl14
8700 1395390_a	0.245	0.000804	4.184549	
8700 1367632_a	0.245	0.000812	-4.17965	Glul
8700 1382435_a	0.245	0.000831	-4.16835	Fzr1
8700 1373175_a	0.245	0.00084	-4.16264	Plbd1
8700 1391153_a	0.245	0.000846	4.159386	
8700 1392857_a	0.245	0.000856	4.153363	Zscan20
8700 1374377_a	0.245	0.00086	4.151094	Ppp1r13l
8700 1375961_a	0.245	0.000863	4.149581	Frzb
8700 1377552_a	0.245	0.000863	4.149321	Zfpm1
8700 1369931_a	0.245	0.000883	-4.13806	Pkm
8700 1383131_a	0.245	0.000892	-4.1332	Itgb2
8700 1369385_a	0.245	0.000895	4.131418	Afap1
8700 1388116_a	0.245	0.000899	-4.12888	Col1a1
8700 1391951_a	0.245	0.000905	4.125985	
8700 1380428_a	0.245	0.000906	4.125334	

8700	1398537_a	0.245	0.000914	-4.12096	Amfr
8700	1395554_a	0.245	0.000926	4.114413	
8700	1386991_a	0.245	0.000929	-4.11272	Bad
8700	1380738_a	0.245	0.000932	4.111461	
8700	1385313_a	0.245	0.000935	4.109527	Pogk
8700	1391566_a	0.245	0.000941	4.106393	
8700	1382882_x	0.245	0.000944	4.104895	
8700	1391039_a	0.245	0.000965	4.094083	
8700	1371757_s	0.245	0.000987	4.083036	LOC683313
8700	1398838_a	0.245	0.000988	-4.08233	Rab7a
8700	1371402_a	0.245	0.000993	-4.08012	Atp6v1b2
8700	1367677_a	0.245	0.000993	-4.08004	Prdx5
19185	ILMN_2717	0.00133	5.17E-08	10.58453	Pim3
19185	ILMN_123E	0.00179	1.87E-07	9.530893	Gbp2b
19185	ILMN_125C	0.00179	2.09E-07	-9.44431	B930041F14Rik
19185	ILMN_1231	0.00236	3.71E-07	9.00473	Cyp4f14
19185	ILMN_276E	0.00236	4.59E-07	-8.84474	Col6a1
19185	ILMN_267Z	0.00255	6.18E-07	-8.62536	Ccdc120
19185	ILMN_270E	0.00255	7.16E-07	-8.51757	Cdkn1c
19185	ILMN_264Z	0.00255	9.56E-07	8.310266	Rnase4
19185	ILMN_313E	0.00255	9.77E-07	-8.29474	Mfge8
19185	ILMN_287E	0.00255	9.90E-07	8.284847	Ang
19185	ILMN_310Z	0.00345	1.55E-06	7.971238	Coq10b
19185	ILMN_269E	0.00345	1.75E-06	7.888096	Npr2
19185	ILMN_125E	0.00345	1.81E-06	7.86543	Cyp2d13
19185	ILMN_266Z	0.00345	1.88E-06	7.836874	Hist1h4h
19185	ILMN_2771	0.00441	2.58E-06	-7.62404	Mfge8
19185	ILMN_3031	0.00534	3.32E-06	7.454122	Coq10b
19185	ILMN_243Z	0.00651	4.31E-06	7.283505	Tmem30a
19185	ILMN_260E	0.00651	4.56E-06	-7.24607	Slc6a8
19185	ILMN_122E	0.00661	4.89E-06	7.200546	Ugt2b1
19185	ILMN_276C	0.00664	5.17E-06	7.164918	Cxcl13
19185	ILMN_125E	0.00666	5.44E-06	-7.13105	Col6a1
19185	ILMN_271E	0.00711	6.09E-06	7.059425	Hist1h2bh
19185	ILMN_123Z	0.0075	6.83E-06	-6.98612	Rbm3
19185	ILMN_125E	0.0075	7.01E-06	6.969443	Wnt2
19185	ILMN_259Z	0.00755	7.57E-06	6.920036	Mup4
19185	ILMN_315E	0.00755	7.63E-06	6.915013	Cyp2c67
19185	ILMN_293C	0.00756	8.21E-06	6.869003	Igfbp2
19185	ILMN_264Z	0.00756	8.24E-06	-6.86641	Emp1
19185	ILMN_297E	0.00756	8.65E-06	-6.8361	Rps6ka1
19185	ILMN_265Z	0.00756	8.82E-06	6.823563	Hist1h2bj
19185	ILMN_268Z	0.00822	1.03E-05	6.727628	Elovl3
19185	ILMN_262Z	0.00822	1.05E-05	6.713226	Apol9b
19185	ILMN_264E	0.00822	1.06E-05	-6.71123	Arrdc4
19185	ILMN_290C	0.00881	1.17E-05	-6.64998	Rorc
19185	ILMN_125E	0.00962	1.31E-05	6.577718	Nudt7

39375	1427351_s	0.0197	4.36E-07	11.13447	Ighm
39375	1441219_a	0.0382	1.69E-06	9.654656	
39375	1438108_a	0.0557	3.71E-06	-8.8757	Plekhm3
39375	1447462_a	0.0934	8.28E-06	-8.12914	D7Wsu130e
39375	1419579_a	0.1183	1.55E-05	7.579565	Slc7a12
39375	1430161_a	0.1183	1.57E-05	7.567581	Dlst
39375	1455445_a	0.1285	2.00E-05	-7.36755	Cbln3
39375	1457814_a	0.188	3.91E-05	6.82004	
39375	1459159_a	0.188	3.96E-05	6.809493	Ccdc6
39375	1432897_a	0.188	4.26E-05	6.752486	4930435N07Rik
39375	1439993_a	0.188	5.26E-05	6.588525	
39375	1424098_a	0.188	5.40E-05	-6.56769	Elov17
39375	1433293_a	0.188	5.79E-05	6.514153	Sdha
39375	1443637_a	0.188	5.92E-05	6.497413	Slc25a42
39375	1420380_a	0.188	6.25E-05	-6.45517	Ccl2
39375	1450511_a	0.1953	6.93E-05	6.376988	Musk
39375	1443138_a	0.2152	8.27E-05	6.243604	
39375	1439679_a	0.2152	8.59E-05	6.215384	Cct3
39375	1433369_a	0.2218	1.03E-04	6.08113	8430401P03Rik
39375	1457210_a	0.2218	1.04E-04	6.075841	1700092E19Rik
39375	1436725_a	0.2218	1.08E-04	-6.04885	Arhgef39
39375	1430960_a	0.2218	1.12E-04	-6.01815	4933440J02Rik
39375	1447529_a	0.2218	1.23E-04	-5.95365	
39375	1454145_a	0.2218	1.25E-04	-5.93844	Pla2r1
39375	1419793_a	0.2218	1.29E-04	5.914907	D5Ertd615e
39375	1425567_a	0.2218	1.35E-04	-5.88295	Anxa5
39375	1445706_x	0.2218	1.36E-04	5.879134	Mettl2
39375	1458149_a	0.2218	1.38E-04	5.869155	
39375	1441202_a	0.2228	1.43E-04	-5.84074	
39375	1431608_a	0.2389	1.65E-04	5.740486	Als2
39375	1444671_a	0.2389	1.68E-04	5.725144	Rasal2
39375	1419776_a	0.2389	1.70E-04	-5.71838	
39375	1441147_a	0.2389	1.75E-04	5.698785	D3Ertd229e
39375	1441627_a	0.2425	1.83E-04	5.665401	
39375	1435271_a	0.2425	1.88E-04	5.646617	Irf3
39375	1418792_a	0.2429	1.98E-04	5.610609	Sh3gl2
39375	1444806_a	0.2429	1.99E-04	5.606312	
929	98990_at	0.00102	9.18E-08	-16.6665	Bcar1
929	96993_at	0.00197	3.55E-07	10.38824	Pax5
929	98416_at	0.00262	8.55E-07	9.543666	Traf2
929	94805_f_at	0.00262	9.47E-07	9.44898	Hist1h
929	160778_at	0.00361	1.75E-06	8.895415	Uhmk1
929	161627_r_	0.00361	1.96E-06	8.798954	Prkd2
929	99928_at	0.00363	2.62E-06	-8.54583	Map1b
929	160664_at	0.00363	2.62E-06	8.545394	Frmd8
929	160744_r_	0.00471	4.09E-06	8.711054	Ctrl
929	101508_at	0.00471	4.50E-06	-8.09441	Khdrbs1

929	103926_at	0.00471	4.76E-06	8.047659	Eif4g1
929	162484_r_	0.00471	5.37E-06	7.950162	Tmed1
929	162231_r_	0.00471	5.53E-06	7.926796	Mesdc2
929	161145_f_	0.01127	1.52E-05	-7.13852	Atp5d
929	161271_r_	0.01127	1.57E-05	7.116406	
929	101312_at	0.01127	1.63E-05	7.485894	Grin2b
929	AFFX-b-Act	0.01182	1.89E-05	6.978795	Actb
929	100947_at	0.01182	1.95E-05	6.954187	
929	103227_at	0.01182	2.03E-05	13.60691	Ugt2b34
929	93712_at	0.01239	2.24E-05	6.852711	Ccnt1
929	161705_r_	0.01376	2.66E-05	6.727575	
929	95880_s_a	0.01376	2.73E-05	7.061336	C79130
929	161366_r_	0.01799	4.00E-05	6.760082	Cdh15
929	162399_f_	0.01799	4.00E-05	-6.43598	Atxn2
929	102231_at	0.01799	4.06E-05	6.425373	Creb3l1
929	AFFX-b-Act	0.01816	4.27E-05	6.391337	Actb
929	93493_at	0.01816	4.57E-05	-6.34277	Ddx5
929	92968_at	0.01816	4.69E-05	6.324479	Arf5
929	160851_r_	0.01816	5.00E-05	6.587742	Cox8b
929	101492_at	0.01816	5.17E-05	-6.25738	Pin1
929	161149_r_	0.01816	5.24E-05	6.248215	Slc23a3
929	162479_f_	0.01816	5.39E-05	-6.22934	
929	93835_at	0.01816	5.54E-05	-6.20974	Fuca1
929	103994_at	0.01816	5.92E-05	6.163699	Ago2
929	96070_at	0.01816	5.99E-05	-6.15608	Pfn1
929	161563_r_	0.01816	6.11E-05	6.143117	
929	99397_at	0.01816	6.24E-05	6.127903	Ercc2
929	162080_f_	0.01816	6.39E-05	-6.11182	Kctd17
929	96924_at	0.01816	6.52E-05	-6.09808	Wdr82
929	160585_at	0.01816	6.56E-05	-6.09391	Rpf2
929	96020_at	0.01917	7.45E-05	-6.00831	C1qb
929	93004_r_at	0.01917	7.48E-05	6.005134	BC018242
929	161348_r_	0.01917	7.54E-05	5.999875	Pdim1
929	99486_at	0.01917	7.72E-05	5.983583	Cenpb
929	102247_at	0.01917	7.80E-05	5.977269	Ubr1
929	103501_at	0.02052	8.53E-05	5.916817	Pura
929	92592_at	0.02144	9.11E-05	5.873163	Gpd1
929	101665_at	0.02167	9.40E-05	5.852216	Nr5a1
929	AFFX-18SR1	0.02175	9.75E-05	5.827991	
929	161678_at	0.02175	9.83E-05	5.822488	Inpp5d
929	93917_at	0.02454	1.14E-04	-5.97686	Tnfsf12
929	94804_at	0.02454	1.15E-04	5.716963	Pbx1
929	161357_r_	0.02485	1.19E-04	5.696208	Gstm2
2870	1389554_a	6.16E-06	1.84E-11	814.9337	
2870	1382205_a	6.16E-06	3.63E-11	702.7191	
2870	1390838_a	8.15E-06	7.20E-11	604.8326	
2870	1385638_a	1.54E-05	1.82E-10	493.8453	

2870	1369751_a	2.33E-05	3.42E-10	429.8427	thyrotropin	Trhr
2870	1367851_a	5.07E-05	9.73E-10	341.785	prostaglandin synthase	Ptgds
2870	1367949_a	5.07E-05	1.11E-09	331.9962	proenkephalin	Penk
2870	1373957_a	5.07E-05	1.19E-09	326.7376	reelin	Reln
2870	1374503_a	7.84E-05	2.08E-09	289.2824	pre-B-cell leukemia	Pbx3
2870	1384392_a	0.000143	4.22E-09	247.3914	cytochrome c	Cyp26b1
2870	1385031_a	0.000181	5.96E-09	229.2882		
2870	1378997_a	0.000181	6.38E-09	225.8625	Eph receptor	Ephb6
2870	1385143_a	0.000224	9.11E-09	208.7681	similar to RGD1561963	
2870	1368256_a	0.000224	9.25E-09	208.0744	serine protease	Serpini1
2870	1379902_a	0.000686	3.03E-08	159.9809		
2870	1375984_a	0.000739	4.05E-08	149.9438	zinc finger protein	Zfx4
2870	1369562_a	0.000739	4.07E-08	149.8073	hippocalcin	Hpcal1
2870	1376749_a	0.000739	4.24E-08	148.4294	osteoglycin	Ogn
2870	1388170_a	0.000739	4.34E-08	147.6915	potassium channel	Kctd1
2870	1387131_a	0.000739	4.46E-08	146.7743	serine protease	Serpini1
2870	1372179_a	0.000739	4.57E-08	146.0153	hippocalcin	Hpcal1
2870	1377853_a	0.00083	5.47E-08	140.278	teashirt zinc finger	Tshz3
2870	1392416_a	0.00083	5.84E-08	138.2551		
2870	1374934_a	0.00083	5.98E-08	137.505		
2870	1391071_a	0.00083	6.11E-08	136.8604		
2870	1367555_a	0.00087	6.66E-08	134.2362	albumin	Alb
2870	1384158_a	0.000978	7.94E-08	129.0592		
2870	1370063_a	0.000978	8.29E-08	127.8468	nuclear receptor	Nr2f2
2870	1368059_a	0.000978	8.64E-08	126.6558	crystallin, r	Crym
2870	1378128_a	0.000978	8.89E-08	125.8605		
2870	1374818_a	0.000978	8.98E-08	125.5749	neurexophorin	Nxph3
2870	1370432_a	0.000978	9.26E-08	124.7151	POU class 3	Pou3f1
2870	1372626_a	0.000978	9.50E-08	124.0074	tumor protein	Tpd5211
2870	1367648_a	0.001134	1.14E-07	119.1554	insulin-like growth factor	Igf2
2870	1395431_a	0.001136	1.17E-07	118.279		
2870	1378163_a	0.001136	1.20E-07	117.6017	gremlin 2, r	Grem2
2870	1367598_a	0.001191	1.33E-07	115.002	transthyretin	Ttr
2870	1368534_a	0.001191	1.34E-07	114.8922	adrenergic, Adra1d	
2870	1376645_a	0.001191	1.37E-07	114.3073	similar to RGD1307396	
2870	1371922_a	0.001219	1.44E-07	113.0137	Carbonic anhydrase	Car12
2870	1369093_a	0.001219	1.54E-07	111.3583	reelin	Reln
2870	1368883_a	0.001219	1.55E-07	111.1913	nephroblastin	Nov
2870	1387004_a	0.001219	1.56E-07	110.9679	neuroblastin	Nbl1
2870	1368395_a	0.001219	1.58E-07	110.6681	glypican 3	Gpc3
2870	1385285_a	0.00127	1.68E-07	109.107		
2870	1387907_a	0.001524	2.11E-07	103.7376	inositol 1,4	Itpr1
2870	1367845_a	0.001524	2.11E-07	103.7178	neurofilament	Nefm
2870	1387854_a	0.001595	2.25E-07	102.1768	collagen, ty	Col1a2
2870	1389120_a	0.001877	2.79E-07	97.40126	potassium channel	Kcnc3
2870	1376734_a	0.001877	2.79E-07	97.39491		
2870	1388936_a	0.001877	2.82E-07	97.17368	cadherin 11	Cdh11

2870	1398616_a	0.001932	2.96E-07	96.11827	adaptor-rel	Ap1s2
2870	1370558_a	0.001974	3.08E-07	95.24754	potassium	Kcnc2
2870	1373648_a	0.001979	3.15E-07	94.78869	similar to P	LOC681849
2870	1391146_a	0.002075	3.36E-07	93.40018	cadherin 1	Cdh11
2870	1369999_a	0.002103	3.47E-07	92.73591	neuronatin	Nnat
2870	1367887_a	0.002123	3.56E-07	92.17622	lecithin chc	Lcat
2870	1388968_a	0.002271	3.88E-07	90.43119	metallophc	Mpped1
2870	1376909_a	0.002285	3.97E-07	89.9585	RAS-like, fa	Ras10a
2870	1383573_a	0.002363	4.21E-07	88.74209	teashirt zin	Tshz1
2870	1395052_a	0.002363	4.29E-07	88.40693		
2870	1368478_a	0.002363	4.31E-07	88.2847	dopamine	Drd1a
2870	1373098_a	0.002494	4.72E-07	86.49136	breast carc	Bcas1
2870	1382138_a	0.002494	4.74E-07	86.42412	Notch-regu	Nrarp
2870	1367691_a	0.002494	4.77E-07	86.28532	protein kin	Prkcdbp
2870	1383895_a	0.002795	5.43E-07	83.79756	dynein ligh	Dynlrb2
2870	1376319_a	0.002853	5.63E-07	83.13116	sema domæ	Sema3c
2870	1389181_a	0.002948	5.90E-07	82.23569		
2870	1383353_a	0.003036	6.24E-07	81.20057		
2870	1386962_a	0.003036	6.26E-07	81.15574	phospholip	Plcb4
2870	1392867_a	0.003146	6.58E-07	80.24702		
2870	1383010_a	0.003204	6.79E-07	79.66302		
2870	1384308_a	0.003284	7.06E-07	78.97103	Meis home	Meis1
2870	1384225_a	0.003302	7.20E-07	78.60277		
2870	1380306_a	0.003302	7.37E-07	78.18876		
2870	1368542_a	0.003302	7.39E-07	78.15268	zinc finger	Zfp423
2870	1375647_a	0.00336	7.62E-07	77.6185		
2870	1372755_a	0.003381	7.79E-07	77.21777	mal, T-cell	Mal2
2870	1379594_a	0.003381	7.86E-07	77.05737		
2870	1388718_a	0.003654	8.60E-07	75.49549	tropomodul	Tmod1
2870	1371861_a	0.004095	9.76E-07	73.35646		
2870	1383644_a	0.004304	1.05E-06	72.20802		
2870	1390317_a	0.004304	1.07E-06	71.80617	similar to R	RGD1561849
2870	1389998_a	0.004304	1.08E-06	71.6724	Nuclear rec	Nr2f2
2870	1383205_a	0.004304	1.10E-06	71.45714	dapper, an	Dact2
2870	1384869_a	0.004304	1.10E-06	71.37029	epoxide hy	Ephx4
2870	1389186_a	0.004304	1.10E-06	71.35742		
2870	1369625_a	0.004672	1.22E-06	69.70514	aquaporin	Aqp1
2870	1376362_a	0.004672	1.22E-06	69.67304	neuronal p	Nptxr
2870	1392077_a	0.004705	1.28E-06	68.97086	metallophc	Mpped2
2870	1372208_a	0.004705	1.29E-06	68.84109	protein phc	Ppp1r1b
2870	1369047_a	0.004705	1.29E-06	68.83365	sulfotransf	Sult1d1
2870	1384863_a	0.004705	1.30E-06	68.72739	copine VII	Cpne7
2870	1384112_a	0.004705	1.32E-06	68.54487	5' nucleotic	Nt5e
2870	1385598_a	0.004705	1.33E-06	68.4052		
2870	1390539_a	0.004705	1.33E-06	68.36946		
2870	1377640_a	0.004922	1.41E-06	67.5098		
2870	1370434_a	0.005064	1.47E-06	66.77124	myelin-ass	Mobp

2870	1388753_a	0.005064	1.48E-06	66.73912	sulfatase 2 Sulf2
2870	1377404_a	0.005064	1.49E-06	66.60904	stanniocalc Stc1
2870	1383699_a	0.005087	1.51E-06	66.38669	Ras-like wit Rit2
2870	1370312_a	0.005295	1.59E-06	65.63505	spondin 1, Spon1
2870	1384226_a	0.005313	1.61E-06	65.43677	
2870	1394786_a	0.005373	1.66E-06	64.99919	sortilin-rela Sorl1
2870	1368144_a	0.005373	1.66E-06	64.98253	regulator o Rgs2
2870	1375658_a	0.005592	1.77E-06	64.07157	
2870	1390923_a	0.005592	1.78E-06	63.93196	oxysterol b Osbpl1a
2870	1372110_a	0.005592	1.79E-06	63.84455	
2870	1368443_a	0.005592	1.81E-06	63.70159	N-terminal Necab2
2870	1391919_a	0.005592	1.82E-06	63.64359	transcriptic Tcerg1l
2870	1387725_a	0.005592	1.86E-06	63.35791	gulonolactr Gulo
2870	1393478_a	0.005592	1.87E-06	63.27415	
2870	1391605_a	0.005592	1.88E-06	63.20169	
2870	1395436_a	0.005592	1.88E-06	63.19003	
2870	1390958_a	0.005875	2.01E-06	62.22248	hypothetic LOC690333
2870	1398305_a	0.005875	2.01E-06	62.20378	synaptotag Syt17
2870	1386922_a	0.005875	2.02E-06	62.10714	carbonic ar Car2
2870	1368587_a	0.006179	2.15E-06	61.27284	apolipopro Apoc1
2870	1383218_a	0.006228	2.18E-06	61.04416	
2870	1375377_a	0.006308	2.23E-06	60.74782	immunoglc lgsf3
2870	1367768_a	0.00631	2.25E-06	60.62846	latexin Lxn
2870	1393263_a	0.006474	2.37E-06	59.92308	
2870	1382626_a	0.006474	2.37E-06	59.90677	
2870	1374168_a	0.006474	2.38E-06	59.85329	
2870	1370959_a	0.006474	2.38E-06	59.82368	collagen, ty Col3a1
2870	1370228_a	0.006509	2.41E-06	59.6398	transferrin Tf
2870	1398622_a	0.006603	2.47E-06	59.33635	Cysteine ric Crim1
2870	1381133_a	0.006681	2.52E-06	59.06852	
2870	1393084_a	0.006695	2.54E-06	58.93494	HRAS-like s Hrasls
2870	1370410_a	0.006824	2.61E-06	58.57303	immunoglc lgsf1
2870	1382981_a	0.007051	2.72E-06	58.03098	Abelson he Ahi1
2870	1380696_a	0.007105	2.76E-06	57.82806	family with Fam102b
2870	1389586_a	0.007214	2.82E-06	57.52671	
2870	1385130_a	0.007357	2.90E-06	57.16755	Fez family ; Fezf2
2870	1384254_a	0.007839	3.12E-06	56.2412	OTU domai Otud1
2870	1382114_a	0.008156	3.27E-06	55.61551	tousled-like Tlk1
2870	1384025_a	0.008156	3.29E-06	55.54018	
2870	1373386_a	0.008191	3.33E-06	55.39313	gap junctio Gjb2
2870	1387811_a	0.008197	3.35E-06	55.29068	angiotensir Agt
2870	1373416_a	0.008287	3.42E-06	55.06027	Fibronectir Fndc3b
2870	1392613_a	0.00846	3.51E-06	54.70807	
2870	1372027_a	0.008493	3.58E-06	54.48227	
2870	1386348_a	0.008493	3.58E-06	54.48151	
2870	1383422_a	0.008505	3.61E-06	54.37706	BEN domai Bend5
2870	1396771_a	0.008859	3.78E-06	53.78017	

2870	1370048_a	0.008946	3.85E-06	53.56326	lysophosph Lpar1
2870	1375043_a	0.008946	3.90E-06	53.4063	FBJ osteos Fos
2870	1374280_a	0.008946	3.92E-06	53.33394	cerebellin 2 Cbln2
2870	1374046_a	0.008946	3.95E-06	53.2332	heparan su Hs3st2
2870	1367563_a	0.008946	3.96E-06	53.2208	secreted pr Sparc
2870	1374546_a	0.008946	3.99E-06	53.12704	
2870	1391032_a	0.008946	4.00E-06	53.07797	seizure rel Sez6
2870	1398689_a	0.00905	4.08E-06	52.85588	unc-79 hon Unc79
2870	1380222_a	0.009064	4.11E-06	52.75658	
2870	1395474_a	0.00914	4.17E-06	52.57579	
2870	1376667_a	0.009227	4.24E-06	52.38291	cytochrom Cyp26b1
2870	1396366_a	0.009242	4.27E-06	52.2858	
2870	1373487_a	0.009467	4.42E-06	51.88572	
2870	1389937_a	0.009467	4.43E-06	51.84275	
2870	1398263_a	0.009471	4.46E-06	51.76298	spectrin re Syne1
2870	1390828_a	0.009647	4.57E-06	51.46849	neuropepti Npy1r
2870	1391765_a	0.009796	4.67E-06	51.21177	leucine ricl Lrrc48
2870	1376893_a	0.009951	4.78E-06	50.95356	neurensin : Nrsn1
2870	1370841_a	0.00999	4.82E-06	50.83516	growth hor Gh1