Supplementary Table1A

Qmin was the smallest Q in the six comprisons
null indicates that the Q>=0.1
-1 means downregulated in tumor
1 means upregulated in tumor

			Normal vs IA			Normal vs IB			Normal vs IIA		Normal vs IIB		Normal vs IIIA			Normal vs IIIB			
Refsequer	Total Rar	Qmin	regulatic	Rank	Qvalue	regulatic	Rank	Qvalue	regulatic	Qvalue	regulatic	Qvalue	regulatic	Rank	Qvalue	regulatic	Rank	Qvalue	Symbol
NM_002576	6	1.96E-06	1	0	4.60E-06	1	0	1.96E-06	null	null	null	null	1	3	5.85E-06	1	3	0.094625	PAK1
NM_014448	9	3.26E-06	1	5	6.09E-06	1	0	3.26E-06	null	null	1	6.14E-06	1	0	6.25E-06	null	4	null	ARHGEF16
NM_001136	10	4.26E-06	-1	3	4.26E-06	-1	3	4.38E-06	null	null	-1	5.80E-06	-1	2	5.27E-06	-1	2	0.010202	AGER
NM_005308	10	5.48E-06	-1	3	5.48E-06	-1	3	5.94E-06	-1	7.48E-05	-1	8.23E-06	-1	2	7.57E-06	-1	2	0.013074	GRK5
NM_000442	11	1.66E-06	-1	3	2.61E-06	-1	3	1.66E-06	-1	0.067008	-1	2.02E-06	-1	3	3.42E-06	-1	2	0.010327	PECAM1
NM_001752	11	1.69E-06	-1	3	2.66E-06	-1	3	1.69E-06	-1	3.17E-05	-1	2.06E-06	-1	4	3.52E-06	-1	1	0.017122	CAT
NM_004684	11	1.7E-06	-1	3	2.68E-06	-1	3	1.70E-06	null	null	-1	2.09E-06	-1	3	3.55E-06	-1	2	0.009204	SPARCL1
NM_003734	11	1.89E-06	-1	3	2.93E-06	-1	3	1.89E-06	-1	0.077317	-1	2.34E-06	-1	3	3.96E-06	-1	2	0.010948	AOC3
NM_000552	11	1.92E-06	-1	3	2.98E-06	-1	3	1.92E-06	-1	0.078834	-1	2.37E-06	-1	3	4.04E-06	-1	2	0.010422	VWF
NM_005574	11	1.99E-06	-1	3	3.17E-06	-1	3	1.99E-06	-1	0.08477	-1	2.46E-06	-1	3	4.18E-06	-1	2	0.016332	LMO2
NM_001449	11	2.31E-06	-1	3	3.69E-06	-1	3	2.31E-06	-1	0.085543	-1	2.84E-06	-1	3	4.87E-06	-1	2	0.012035	FHL1
NM_006829	11	2.33E-06	-1	3	3.71E-06	-1	3	2.33E-06	-1	0.097837	null	null	-1	3	4.93E-06	-1	2	0.011249	C10orf116
NM_000873	11	2.46E-06	-1	3	3.98E-06	-1	3	2.46E-06	null	null	-1	3.00E-06	-1	3	5.21E-06	-1	2	0.021281	ICAM2
NM_000304	11	2.46E-06	-1	3	4.00E-06	-1	3	2.46E-06	null	null	-1	3.02E-06	-1	3	5.24E-06	-1	2	0.010202	PMP22
NM_003278	11	2.82E-06	-1	3	4.79E-06	-1	3	2.82E-06	-1	4.84E-05	-1	3.46E-06	-1	3	6.19E-06	-1	2	0.000118	CLEC3B
NM_000668	11	2.84E-06	-1	3	4.81E-06	-1	3	2.84E-06	null	null	-1	3.49E-06	-1	3	6.24E-06	-1	2	0.009252	ADH1B
NM_001025	11	3.24E-06	-1	3	5.6E-06	-1	3	3.24E-06	null	null	-1	3.86E-06	-1	3	7.16E-06	-1	2	0.009761	CD34
NM_001424	11	4.84E-06	-1	3	4.84E-06	-1	3	5.25E-06	-1	0.08597	-1	6.69E-06	-1	3	6.11E-06	-1	2	0.007996	EMP2
NM_001386	11	4.99E-06	-1	3	4.99E-06	-1	3	5.37E-06	-1	0.087117	-1	6.92E-06	-1	3	6.40E-06	-1	2	0.009628	DPYSL2
NM_001753	11	5.25E-06	-1	3	5.25E-06	-1	3	5.61E-06	-1	6.86E-05	-1	7.77E-06	-1	2	7.08E-06	-1	3	0.07378	CAV1
NM_003773	12	1.76E-06	-1	3	2.78E-06	-1	3	1.76E-06	-1	0.071795	-1	2.17E-06	-1	3	3.71E-06	-1	3	0.051036	HYAL2
NM_002404	12	1.96E-06	-1	3	3.09E-06	-1	4	1.96E-06	-1	0.095483	-1	2.41E-06	-1	3	4.14E-06	-1	2	0.010401	MFAP4
NM_005964	12	2.03E-06	-1	3	3.20E-06	-1	3	2.03E-06	null	null	null	null	-1	3	4.22E-06	-1	3	0.022456	MYH10
NM_001146	12	2.1E-06	-1	3	3.31E-06	-1	5	2.1E-06	-1	3.43E-05	-1	2.56E-06	-1	3	4.36E-06	-1	1	0.014558	ANGPT1
NM_004840	12	2.12E-06	-1	3	3.35E-06	-1	3	2.12E-06	null	null	-1	2.59E-06	-1	3	4.43E-06	-1	3	0.022038	ARHGEF6
NM_000115	12	2.16E-06	-1	3	3.40E-06	-1	3	2.16E-06	-1	0.086154	-1	2.65E-06	-1	3	4.50E-06	-1	3	0.012389	EDNRB
NM_004166	12	2.49E-06	-1	3	4.06E-06	-1	3	2.49E-06	null	null	null	null	-1	3	5.35E-06	-1	3	0.024999	CCL14
NM_000820	12	2.56E-06	-1	3	4.18E-06	-1	3	2.56E-06	-1	0.091375	null	null	-1	3	5.52E-06	-1	3	0.030775	GAS6
NM_005795	12	2.61E-06	-1	3	4.22E-06	-1	4	2.61E-06	null	null	-1	3.14E-06	-1	3	5.64E-06	-1	2	0.010088	CALCRL
NM_023037	12	2.73E-06	-1	3	4.47E-06	-1	3	2.73E-06	null	null	-1	3.32E-06	-1	3	5.97E-06	-1	3	0.021313	FRY
NM_000049	12	2.87E-06	-1	3	2.87E-06	-1	3	2.88E-06	null	null	-1	4.12E-06	-1	3	3.79E-06	-1	3	0.054458	ASPA
NM_002084	12	2.95E-06	-1	3	2.95E-06	-1	3	2.99E-06	-1	0.092781	-1	4.24E-06	-1	3	3.93E-06	-1	3	0.014216	GPX3
NM_005512	12	3.09E-06	-1	3	5.35E-06	-1	3	3.09E-06	null	null	-1	3.76E-06	-1	3	6.75E-06	-1	3	0.030853	LRRC32
NM_000698	12	3.51E-06	-1	3	3.51E-06	-1	3	3.68E-06	null	null	-1	5.08E-06	-1	3	4.60E-06	-1	3	0.077521	ALOX5
NM_000216	12	3.84E-06	-1	3	3.84E-06	-1	3	3.96E-06	-1	0.095726	-1	5.42E-06	-1	4	4.85E-06	-1	2	0.010696	KAL1
NM_001860	12	4.8E-06	-1	3	4.80E-06	-1	3	5.20E-06	null	null	-1	6.64E-06	-1	3	6.04E-06	-1	3	0.094571	SLC31A2
NM_014767	12	5.2E-06	-1	3	5.20E-06	-1	3	5.54E-06	-1	0.09727	-1	7.35E-06	-1	3	6.81E-06	-1	3	0.014281	SPOCK2

NM_004484	12	7.34E-06	-1	3	7.34E-06	-1	3	8.75E-06	-1	0.000103	-1	1.19E-05	-1	3	9.60E-06	-1	3	0.012077	GPC3
NM_001442	12	1.78E-05	-1	3	1.78E-05	-1	3	1.85E-05	-1	0.098319	-1	2.84E-05	-1	3	2.07E-05	-1	3	0.009489	FABP4
NM_001795	12	2.5E-05	-1	3	2.5E-05	-1	3	2.77E-05	-1	0.000412	-1	4.57E-05	-1	3	2.83E-05	-1	3	0.010015	CDH5
NM_000517	12	3.84E-05	-1	3	3.84E-05	-1	3	4.14E-05	null	null	-1	5.88E-05	-1	3	4.48E-05	-1	3	0.030495	HBA2
NM_001024	12	4.16E-05	-1	3	4.16E-05	-1	3	4.48E-05	null	null	-1	6.33E-05	-1	3	4.89E-05	-1	3	0.009963	TGFBR2
NM_001460	13	1.8E-06	-1	3	2.81E-06	-1	3	1.80E-06	null	null	-1	2.21E-06	-1	4	4.41E-06	-1	3	0.021362	FMO2
NM_001343	13	1.94E-06	-1	3	3.05E-06	-1	3	1.94E-06	null	null	null	null	-1	3	4.10E-06	null	4	null	DAB2
NM_001233	13	2.39E-06	-1	3	3.85E-06	-1	3	2.39E-06	-1	0.089345	-1	2.93E-06	-1	3	5.05E-06	null	4	null	CAV2
NM_003380	13	2.87E-06	-1	3	4.96E-06	-1	3	2.87E-06	null	null	-1	3.55E-06	-1	3	6.33E-06	null	4	null	VIM
NM_000118	13	2.89E-06	-1	3	5.02E-06	-1	3	2.89E-06	-1	0.090011	-1	3.58E-06	-1	4	6.38E-06	-1	3	0.036157	ENG
NM_001089	13	2.97E-06	-1	3	5.18E-06	-1	3	2.97E-06	null	null	-1	3.64E-06	-1	4	2.99E-05	-1	3	0.010336	ABCA3
NM_000361	13	3.12E-06	-1	3	5.42E-06	-1	4	3.12E-06	-1	0.094222	-1	3.79E-06	-1	3	6.80E-06	-1	3	0.038974	THBD
NM_000062	13	4.62E-06	-1	3	4.62E-06	-1	3	4.89E-06	null	null	-1	6.14E-06	-1	4	5.85E-06	-1	3	0.050187	SERPING1
NM_000459	13	9.42E-06	-1	3	9.42E-06	-1	3	1.08E-05	-1	0.000165	-1	1.47E-05	-1	4	3.05E-05	-1	3	0.018369	TEK
NM_005277	14	2.07E-06	-1	3	3.27E-06	-1	3	2.07E-06	-1	0.085804	-1	2.53E-06	-1	5	4.29E-06	-1	3	0.01324	GPM6A
NM_004106	14	2.22E-06	-1	3	3.56E-06	-1	3	2.22E-06	null	null	null	null	-1	4	4.7E-06	null	4	null	FCER1G
NM_005641	14	2.29E-06	1	7	8.05E-06	1	0	2.29E-06	null	null	null	null	1	3	2.77E-05	null	4	null	TAF6
NM_003713	14	2.88E-06	-1	3	4.99E-06	-1	3	2.88E-06	null	null	-1	3.56E-06	-1	6	2.44E-05	-1	2	0.01268	PPAP2B
NM_001067	14	3.24E-06	1	4	5.11E-05	1	0	3.24E-06	null	null	null	null	1	7	5.98E-05	1	3	0.083378	TOP2A
NM_001444	14	3.26E-06	-1	3	3.26E-06	-1	3	3.36E-06	-1	0.083766	-1	4.7E-06	-1	4	4.23E-06	null	4	null	FABP5
NM_000784	14	6.84E-06	-1	3	6.84E-06	-1	3	7.92E-06	null	null	-1	1.06E-05	-1	4	8.96E-06	null	4	null	CYP27A1
NM_003638	14	7.03E-06	-1	5	7.03E-06	-1	3	8.18E-06	null	null	-1	1.11E-05	-1	3	9.27E-06	-1	3	0.061157	ITGA8
NM_001001	14	1.35E-05	-1	3	1.35E-05	-1	3	1.43E-05	null	null	-1	1.96E-05	-1	5	1.49E-05	-1	3	0.017771	GPM6B
NM_002017	15	1.68E-06	-1	3	2.66E-06	-1	3	1.68E-06	null	null	-1	2.05E-06	-1	5	3.50E-06	null	4	null	FLI1
NM_003128	15	1.8E-06	-1	7	2.82E-06	-1	3	1.80E-06	-1	0.082613	-1	2.21E-06	-1	3	3.81E-06	-1	2	0.011043	SPTBN1
NM_001033	15	1.81E-06	-1	3	2.83E-06	-1	6	1.81E-06	-1	0.0731	-1	2.22E-06	-1	3	3.83E-06	-1	3	0.009777	ADARB1
NM_001870	15	1.82E-06	-1	5	3.44E-06	-1	3	1.82E-06	null	null	-1	2.23E-06	-1	4	4.52E-06	-1	3	0.049748	CPA3
NM_021953	15	1.92E-06	1	8	5.54E-06	1	0	1.92E-06	null	null	null	null	1	3	5.60E-06	null	4	null	FOXM1
NM_014880	15	2.82E-06	-1	3	2.84E-06	-1	5	2.82E-06	null	null	-1	4.04E-06	-1	4	3.71E-06	-1	3	0.030639	CD302
NM_002060	15	2.91E-06	-1	7	5.08E-06	-1	3	2.91E-06	null	null	-1	3.59E-06	-1	3	6.43E-06	-1	2	0.00972	GJA4
NM_003070	15	3.18E-06	-1	5	4.27E-06	-1	3	3.18E-06	null	null	-1	4.47E-06	-1	5	4.07E-06	-1	2	0.000269	SMARCA2
NM_004515	15	3.24E-06	1	0	6.01E-06	1	6	3.24E-06	1	0.000274	1	6.10E-06	1	5	1.87E-05	null	4	null	ILF2
NM_006097	15	3.31E-06	-1	5	0.000166	-1	3	3.31E-06	null	null	-1	3.92E-06	-1	4	0.000269	-1	3	0.052605	MYL9
NM_002543	15	3.75E-06	-1	3	3.75E-06	-1	3	3.93E-06	null	null	-1	5.38E-06	-1	6	0.003464	-1	3	0.067067	OLR1
NM_001854	15	3.76E-06	1	0	5.09E-06	1	8	3.76E-06	null	null	1	5.35E-06	1	5	1.58E-05	1	2	8.96E-05	COL11A1
NM_006307	15	4.09E-06	-1	3	4.09E-06	-1	3	4.23E-06	null	null	-1	5.52E-06	-1	5	1.04E-05	null	4	null	SRPX
NM_000313	15	4.46E-06	-1	3	4.46E-06	-1	3	4.62E-06	null	null	-1	6.01E-06	-1	6	0.015235	-1	3	0.049767	PROS1
NM_000491	15	6.4E-06	-1	3	6.40E-06	-1	5	7.56E-06	null	null	-1	9.8E-06	-1	3	8.40E-06	null	4	null	C1QB
NM_005037	15	1.39E-05	-1	3	1.39E-05	-1	3	1.51E-05	null	null	-1	2.17E-05	-1	5	2.08E-05	null	4	null	PPARG
NM_000587	15	3.56E-05	-1	3	3.56E-05	-1	6	3.84E-05	null	null	-1	5.49E-05	-1	3	3.84E-05	-1	3	0.026391	C7
NM_021102	16	1.85E-06	1	7	1.13E-05	1	0	1.85E-06	null	null	1	2.75E-06	1	5	1.43E-05	null	4	null	SPINT2
NM_000527	16	1.88E-06	-1	3	2.90E-06	-1	5	1.88E-06	-1	0.088354	-1	2.33E-06	-1	5	5.67E-06	-1	3	0.054867	LDLR
NM_002444	16	1.93E-06	-1	3	2.99E-06	-1	3	1.93E-06	null	null	-1	2.38E-06	-1	6	0.013883	null	4	null	MSN
NM_007161	16	2.44E-06	-1	5	7.68E-06	-1	3	2.44E-06	null	null	-1	2.99E-06	-1	4	1.22E-05	null	4	null	LST1
NM_001801	16	2.53E-06	-1	3	4.14E-06	-1	7	2.53E-06	null	null	-1	3.06E-06	-1	3	5.42E-06	-1	3	0.010292	CDO1
NM_000507	16	2.54E-06	-1	5	8.75E-06	-1	3	2.54E-06	null	null	-1	3.07E-06	-1	4	5.45E-06	null	4	null	FBP1
NM_003277	16	3.26E-06	-1	7	6.80E-06	-1	3	3.26E-06	null	null	-1	4.57E-06	-1	4	8.76E-06	-1	2	0.000165	CLDN5

NM_001885	16	3.34E-06	-1	7	4.44E-06	-1	3	3.34E-06	null	null	-1	4.68E-06	-1	3	4.20E-06	-1	3	0.035961	CRYAB
NM_000906	16	3.38E-06	-1	7	7.04E-06	-1	3	3.38E-06	-1	5.49E-05	-1	4.76E-06	-1	3	4.30E-06	-1	3	0.009492	NPR1
NM_001629	16	4.19E-06	-1	5	4.19E-06	-1	3	4.30E-06	null	null	-1	5.68E-06	-1	5	6.40E-06	-1	3	0.085119	ALOX5AP
NM_021136	16	6.24E-06	-1	5	1.35E-05	-1	3	6.24E-06	null	null	-1	8.58E-06	-1	5	1.72E-05	-1	3	0.047452	RTN1
NM_003243	16	3.12E-05	-1	3	3.12E-05	-1	3	3.33E-05	-1	0.099509	-1	5.15E-05	-1	7	0.000137	-1	3	0.013152	TGFBR3
NM_004816	17	2.28E-06	-1	5	3.64E-06	-1	5	2.28E-06	-1	0.083761	-1	2.8E-06	-1	6	4.81E-06	-1	1	0.009524	C9orf61
NM_004099	17	2.81E-06	-1	6	4.73E-06	-1	6	2.81E-06	-1	0.095726	-1	3.42E-06	-1	3	6.14E-06	-1	2	0.012778	STOM
NM_002432	17	3.07E-06	-1	5	6.28E-06	-1	3	3.07E-06	null	null	-1	4.36E-06	-1	5	8.32E-06	null	4	null	MNDA
NM_015245	17	5.42E-06	-1	3	5.42E-06	-1	3	5.87E-06	null	null	-1	8.07E-06	-1	8	0.025364	-1	3	0.02727	ANKS1A
NM_002101	17	7.56E-06	-1	7	7.56E-06	-1	3	8.91E-06	null	null	-1	1.23E-05	-1	3	9.96E-06	null	4	null	GYPC
NM_001957	18	1.85E-06	-1	3	2.85E-06	-1	3	1.85E-06	null	null	-1	2.29E-06	-1	9	0.05383	-1	3	0.090641	EDNRA
NM_000416	18	2.34E-06	-1	5	6.32E-06	-1	3	2.34E-06	null	null	-1	2.86E-06	-1	7	0.016493	-1	3	0.056786	IFNGR1
NM_000518	18	2.68E-06	-1	6	4.38E-06	-1	6	2.68E-06	null	null	-1	3.25E-06	-1	3	5.80E-06	-1	3	0.017986	HBB
NM_001928	18	3.17E-06	-1	6	5.49E-06	-1	6	3.17E-06	-1	0.095214	-1	3.81E-06	-1	3	6.86E-06	-1	3	0.010867	CFD
NM_004394	18	3.35E-06	1	9	0.034486	1	0	3.35E-06	null	null	1	4.79E-06	1	5	1.40E-05	null	4	null	DAP
NM_005587	18	3.54E-06	-1	3	3.54E-06	-1	3	3.75E-06	null	null	-1	5.11E-06	-1	9	0.048144	-1	3	0.038814	MEF2A
NM_006009	18	3.64E-06	-1	7	3.64E-06	-1	4	3.84E-06	null	null	-1	5.31E-06	-1	3	4.76E-06	null	4	null	TUBA1A
NM_001945	18	4.16E-06	-1	5	7.55E-06	-1	5	4.16E-06	null	null	null	null	-1	5	9.8E-06	-1	3	0.024974	HBEGF
NM_002573	18	1.34E-05	1	5	2.63E-05	1	6	1.34E-05	null	null	1	2.42E-05	1	4	2.83E-05	1	3	0.083348	PAFAH1B3
NM_006832	18	1.73E-05	-1	6	4.12E-05	-1	7	2.35E-05	null	null	-1	2.42E-05	-1	3	1.73E-05	-1	2	0.009537	FERMT2
NM_000582	18	2.22E-05	1	4	4.57E-05	1	6	2.22E-05	null	null	1	3.05E-05	1	5	3.59E-05	1	3	0.068206	SPP1
NM_003127	19	2.64E-06	-1	7	1.08E-05	-1	6	2.64E-06	-1	0.0996	-1	3.20E-06	-1	3	5.68E-06	-1	3	0.04878	SPTAN1
NM_003137	19	2.76E-06	1	6	4.99E-06	1	6	2.76E-06	1	0.000206	1	5.28E-06	1	4	5.22E-06	1	3	0.063619	SRPK1
NM_002131	19	2.84E-06	1	6	6.64E-06	1	6	2.84E-06	1	0.000118	1	4.2E-06	1	4	1.23E-05	1	3	0.03561	HMGA1
NM_004349	19	3.3E-06	-1	5	3.30E-06	-1	4	3.43E-06	null	null	null	null	-1	6	9.15E-06	null	4	null	RUNX1T1
NM_000430	19	4.16E-06	-1	3	4.16E-06	-1	8	4.76E-06	null	null	-1	5.64E-06	-1	5	6.24E-06	-1	3	0.053446	PAFAH1B1
NM_002298	19	5.8E-06	-1	7	5.80E-06	-1	3	6.48E-06	null	null	null	null	-1	5	0.002638	null	4	null	LCP1
NM_006201	19	6.48E-06	1	8	1.28E-05	1	0	6.48E-06	null	null	null	null	1	7	0.017044	null	4	null	PCTK1
NM_004624	19	6.86E-06	-1	5	1.16E-05	-1	5	6.86E-06	null	null	-1	7.69E-06	-1	7	1.50E-05	-1	2	0.043341	VIPR1
NM_004603	19	7.16E-06	1	3	1.13E-05	1	8	7.16E-06	null	null	1	9.15E-06	1	5	1.08E-05	1	3	0.040342	STX1A
NM_000237	19	8.49E-06	-1	6	1.47E-05	-1	5	8.49E-06	-1	9.15E-05	-1	9.05E-06	-1	5	1.87E-05	-1	3	0.012835	LPL
NM_004051	19	1.06E-05	1	6	1.61E-05	1	3	1.06E-05	null	null	null	null	1	6	8.51E-05	null	4	null	BDH1
NM_002185	19	1.72E-05	-1	9	0.03819	-1	3	1.72E-05	null	null	-1	2.57E-05	-1	3	1.92E-05	null	4	null	IL7R
NM_000175	19	1.75E-05	1	5	3.92E-05	1	5	1.75E-05	null	null	1	2.29E-05	1	6	2.69E-05	1	3	0.087805	GPI
NM_002619	20	1.72E-06	-1	5	3.08E-06	-1	5	1.72E-06	null	null	-1	2.12E-06	-1	6	0.009859	null	4	null	PF4
NM_000433	20	1.9E-06	-1	6	2.94E-06	-1	5	1.90E-06	null	null	null	null	-1	5	3.98E-06	null	4	null	NCF2
NM_000717	20	2.24E-06	-1	7	3.58E-06	-1	3	2.24E-06	-1	0.082051	-1	2.75E-06	-1	7	4.73E-06	-1	3	0.034745	CA4
NM_001608	20	2.25E-06	-1	5	3.59E-06	-1	7	2.25E-06	null	null	-1	2.78E-06	-1	6	0.002499	-1	2	0.030967	ACADL
NM_000132	20	3.17E-06	-1	3	4.24E-06	-1	7	1.14E-05	null	null	-1	3.17E-06	-1	6	0.006766	null	4	null	F8
NM_006456	20	3.76E-06	-1	6	0.005774	-1	5	3.76E-06	null	null	null	null	-1	5	4.04E-06	null	4	null	ST6GALNAC
NM_000898	20	4.12E-06	-1	5	4.12E-06	-1	7	9.98E-06	null	null	null	null	-1	5	5.38E-06	-1	3	0.009994	MAOB
NM_005726	20	4.14E-06	1	6	7.45E-06	1	6	4.14E-06	null	null	1	6.92E-06	1	4	7.57E-06	null	4	null	TSFM
NM_001650	20	6.8E-06	-1	5	1.14E-05	-1	5	6.80E-06	null	null	-1	7.62E-06	-1	7	6.98E-06	-1	3	0.018949	AQP4
NM_001615	20	1.51E-05	-1	7	1.51E-05	-1	3	1.66E-05	null	null	-1	2.49E-05	-1	7	1.85E-05	-1	3	0.08485	ACTG2
NM_006416	20	1.72E-05	-1	3	1.72E-05	-1	8	0.038487	null	null	-1	2.74E-05	-1	6	0.00867	-1	3	0.034497	SLC35A1
NM_004053	20	4.14E-05	1	6	8.23E-05	1	6	4.14E-05	null	null	1	0.000118	1	5	0.000108	1	3	0.068705	BYSL
NM_005424	21	1.73E-06	-1	7	2.71E-06	-1	5	1.73E-06	-1	0.070535	-1	2.12E-06	-1	7	3.61E-06	-1	2	0.018948	TIE1

NM_000954	21	1.78E-06	-1	9	0.017204	-1	6	1.78E-06	null	null	null	null	-1	3	3.78E-06	-1	3	0.05743	PTGDS
NM_001223	21	1.91E-06	-1	5	2.96E-06	-1	3	1.91E-06	null	null	-1	2.35E-06	-1	9	0.027191	null	4	null	CASP1
NM_004944	21	1.93E-06	-1	7	3.02E-06	-1	7	1.93E-06	null	null	-1	2.39E-06	-1	3	4.08E-06	null	4	null	DNASE1L3
NM_001007	21	1.96E-06	-1	5	3.11E-06	-1	3	1.96E-06	null	null	null	null	-1	9	0.044769	null	4	null	SDCBP
NM_021978	21	2.59E-06	1	4	6.10E-06	1	6	2.59E-06	null	null	null	null	1	7	1.18E-05	null	4	null	ST14
NM_000779	21	2.67E-06	-1	3	3.43E-06	-1	8	6.11E-06	null	null	-1	2.67E-06	-1	7	7.37E-06	-1	3	0.023208	CYP4B1
NM_005729	21	3.31E-06	1	10	0.092363	1	0	3.31E-06	null	null	null	null	1	7	0.000125	null	4	null	PPIF
NM_002105	21	3.68E-06	1	8	1.42E-05	1	0	3.68E-06	null	null	1	6.64E-06	1	9	0.027641	null	4	null	H2AFX
NM_003064	21	4.27E-06	-1	6	0.011319	-1	8	0.050076	null	null	-1	4.73E-06	-1	4	4.27E-06	-1	3	0.030589	SLPI
NM_005997	21	4.57E-06	1	8	1.02E-05	1	3	4.57E-06	null	null	1	6.43E-06	1	6	0.016973	null	4	null	VPS72
NM_001005	21	4.76E-06	1	5	8.75E-06	1	6	4.76E-06	null	null	null	null	1	6	8.67E-06	null	4	null	ERBB2
NM_007019	21	5.32E-06	1	6	1.38E-05	1	6	5.32E-06	null	null	null	null	1	5	9.27E-06	null	4	null	UBE2C
NM_000141	21	6.25E-06	-1	7	6.89E-06	-1	6	0.013905	null	null	-1	6.75E-06	-1	5	6.25E-06	-1	3	0.085214	FGFR2
NM_000902	21	2.27E-05	-1	3	2.27E-05	-1	3	2.44E-05	null	null	-1	3.43E-05	null	11	null	null	4	null	MME
NM_001237	21	3.16E-05	1	10	0.059192	1	0	3.16E-05	null	null	null	null	1	8	0.000228	1	3	0.08434	CCNA2
NM_019102	22	1.67E-06	-1	5	2.62E-06	-1	6	1.67E-06	null	null	-1	2.03E-06	-1	8	3.43E-06	-1	3	0.007693	HOXA5
NM_000190	22	1.9E-06	1	6	4.45E-06	1	6	1.90E-06	null	null	1	2.85E-06	1	6	5.54E-06	null	4	null	HMBS
NM_002916	22	1.91E-06	1	5	4.47E-06	1	6	1.91E-06	null	null	1	2.88E-06	1	7	0.017142	null	4	null	RFC4
NM_002110	22	2.07E-06	-1	7	3.25E-06	-1	3	2.07E-06	null	null	null	null	-1	8	0.051362	null	4	null	HCK
NM_002466	22	2.11E-06	1	8	2.75E-05	1	0	2.11E-06	null	null	null	null	1	10	0.044647	null	4	null	MYBL2
NM_002056	22	2.12E-06	1	6	5.02E-06	1	6	2.12E-06	null	null	1	3.15E-06	1	6	6.89E-06	null	4	null	GFPT1
NM_004295	22	2.19E-06	1	5	5.21E-06	1	3	2.19E-06	1	0.09145	1	3.24E-06	1	10	1.08E-05	null	4	null	TRAF4
NM_014634	22	2.47E-06	-1	7	4.02E-06	-1	7	2.47E-06	-1	3.92E-05	-1	3.03E-06	-1	5	5.28E-06	-1	3	0.089656	PPM1F
NM_003966	22	2.75E-06	-1	7	4.60E-06	-1	6	2.75E-06	null	null	-1	3.35E-06	-1	6	0.013276	-1	3	0.009364	SEMA5A
NM_002011	22	2.8E-06	-1	7	4.7E-06	-1	8	2.8E-06	-1	4.57E-05	-1	3.40E-06	-1	5	6.10E-06	-1	2	0.024887	FGFR4
NM_006302	22	2.91E-06	1	7	8.85E-06	1	0	2.91E-06	null	null	1	5.76E-06	null	11	null	null	4	null	GCS1
NM_033554	22	3.28E-06	-1	6	3.28E-06	-1	8	3.42E-06	null	null	null	null	-1	4	4.34E-06	null	4	null	HLA-DPA1
NM_001070	22	3.32E-06	1	8	8.82E-06	1	6	3.32E-06	null	null	1	6.24E-06	1	4	6.48E-06	null	4	null	TUBG1
NM_006332	22	3.35E-06	-1	7	3.35E-06	-1	6	0.015564	null	null	null	null	-1	5	0.005302	null	4	null	IFI30
NM_001025	22	4.34E-06	1	8	1.11E-05	1	6	4.34E-06	null	null	1	7.22E-06	1	5	8.03E-06	1	3	0.044253	IRAK1
NM_007312	22	4.6E-06	-1	6	0.011647	-1	7	4.60E-06	null	null	-1	5.45E-06	-1	7	1.03E-05	-1	2	0.018183	HYAL1
NM_005213	22	4.87E-06	-1	3	4.87E-06	-1	9	0.082118	null	null	null	null	-1	6	0.007536	null	4	null	CSTA
NM_002720	22	7.37E-06	1	9	0.039667	1	0	7.37E-06	null	null	1	1.18E-05	1	9	0.046377	null	4	null	PPP4C
NM_000928	22	7.47E-06	-1	7	1.58E-05	-1	7	7.47E-06	null	null	-1	9.57E-06	-1	5	2.01E-05	-1	3	0.044751	PLA2G1B
NM_001878	22	8.4E-06	1	6	1.39E-05	1	8	8.4E-06	null	null	1	1.08E-05	1	4	1.31E-05	null	4	null	CRABP2
NM_000096	22	1.03E-05	1	4	2.08E-05	1	6	1.03E-05	null	null	1	1.79E-05	1	8	0.032833	null	4	null	CP
NM_000362	22	1.47E-05	-1	9	0.036941	-1	3	1.47E-05	null	null	null	null	-1	7	1.54E-05	-1	3	0.070733	TIMP3
NM_002612	22	3.58E-05	-1	5	6.33E-05	-1	7	3.58E-05	null	null	-1	3.58E-05	-1	6	9.15E-05	null	4	null	PDK4
NM_001400	23	1.71E-06	-1	7	2.69E-06	-1	7	1.71E-06	null	null	-1	2.11E-06	-1	8	3.56E-06	-1	1	0.010477	S1PR1
NM_004480	23	1.89E-06	1	6	4.43E-06	1	6	1.89E-06	null	null	1	2.83E-06	1	9	0.073339	1	2	0.000108	FUT8
NM_004446	23	1.92E-06	1	7	4.50E-06	1	6	1.92E-06	null	null	1	2.89E-06	1	6	9.05E-06	null	4	null	EPRS
NM_003311	23	1.99E-06	1	6	4.7E-06	1	6	1.99E-06	null	null	1	2.97E-06	1	8	6.18E-06	1	3	0.056755	PHLDA2
NM_001030	23	2.03E-06	1	4	9.12E-06	1	4	2.03E-06	null	null	null	null	null	11	null	null	4	null	GRB7
NM_000248	23	2.09E-06	-1	8	0.029564	-1	7	2.09E-06	null	null	-1	2.55E-06	-1	4	5.98E-06	null	4	null	MITF
NM_004962	23	2.17E-06	-1	7	3.42E-06	-1	6	2.17E-06	-1	0.095719	-1	2.66E-06	-1	7	4.55E-06	-1	3	0.077337	GDF10
NM_005437	23	2.21E-06	-1	3	3.52E-06	-1	7	2.21E-06	null	null	-1	2.72E-06	-1	10	0.086671	-1	3	0.048995	NCOA4
NM_004456	23	2.48E-06	1	4	1.06E-05	1	6	2.48E-06	null	null	1	3.71E-06	1	9	0.042358	null	4	null	EZH2

NM_00563(	23	2.56E-06	-1	7	4.2E-06	-1	7	2.56E-06	null	null	-1	3.08E-06	-1	6	0.006808	-1	3	0.084882	SLCO2A1
NM_00385(	23	2.61E-06	-1	5	5.09E-06	null	11	null	null	null	-1	2.61E-06	-1	3	4.45E-06	null	4	null	IL1RL1
NM_00178(	23	3.17E-06	1	8	4.16E-05	1	6	3.17E-06	null	null	null	null	1	6	4.89E-05	1	3	0.081802	CDC2
NM_00301(	23	3.32E-06	-1	7	5.72E-06	-1	7	3.32E-06	-1	5.15E-05	-1	3.94E-06	-1	6	7.35E-06	-1	3	0.000137	SFTPC
NM_00132	23	3.66E-06	1	6	6.65E-06	1	6	3.66E-06	null	null	1	6.59E-06	1	8	6.81E-06	1	3	0.086503	CSTF2
NM_00142	23	4.02E-06	-1	7	4.02E-06	-1	5	4.16E-06	null	null	null	null	-1	7	6.09E-06	null	4	null	EMP3
NM_00519	23	6.33E-06	1	4	1.43E-05	1	8	6.33E-06	null	null	null	null	1	7	1.20E-05	null	4	null	CDKN3
NM_00535	23	6.48E-06	-1	8	0.03522	-1	7	6.48E-06	null	null	-1	7.22E-06	-1	5	7.92E-06	-1	3	0.018727	JUND
NM_00040	23	9.96E-06	1	6	2E-05	1	6	9.96E-06	null	null	1	1.75E-05	1	8	2.07E-05	1	3	0.086073	GALE
NM_00335	23	1.85E-05	-1	8	1.85E-05	-1	6	1.92E-05	null	null	-1	2.94E-05	-1	5	2.94E-05	null	4	null	SCGB1A1
NM_00186	23	1.92E-05	-1	7	1.92E-05	-1	7	1.99E-05	-1	0.088294	-1	3.05E-05	-1	7	2.24E-05	-1	2	0.011474	COX7A1
NM_00194	23	2.69E-05	1	5	4.99E-05	1	6	2.69E-05	null	null	1	6.86E-05	1	8	0.000137	null	4	null	DSG2
NM_00272	23	2.77E-05	-1	5	2.77E-05	-1	5	3.12E-05	null	null	null	null	-1	9	0.027979	null	4	null	SRGN
NM_00541	23	7.68E-05	1	6	0.000137	1	6	7.68E-05	null	null	1	0.000165	1	7	0.000179	null	4	null	SHMT2
NM_00162	23	0.005646	-1	6	0.005646	-1	7	0.022025	null	null	null	null	-1	6	0.006201	null	4	null	AIF1
NM_00323	23	0.005964	-1	6	0.005964	-1	7	0.034983	null	null	null	null	-1	6	0.01456	null	4	null	TFRC
NM_00239	24	1.68E-06	-1	7	2.64E-06	-1	7	1.68E-06	-1	0.068144	null	null	-1	7	3.47E-06	-1	3	0.014151	MEIS1
NM_00007	24	1.71E-06	-1	9	0.04913	-1	8	1.71E-06	null	null	-1	2.1E-06	-1	4	4.01E-06	-1	3	0.009661	CDKN1C
NM_001451	24	1.87E-06	-1	7	2.87E-06	-1	7	1.87E-06	-1	0.075859	-1	2.31E-06	-1	8	3.92E-06	-1	2	0.009798	FOXF1
NM_000821	24	1.96E-06	1	6	4.57E-06	1	6	1.96E-06	null	null	null	null	1	8	5.78E-06	null	4	null	GGCX
NM_00201	24	1.96E-06	-1	7	0.022328	-1	8	1.96E-06	null	null	-1	2.42E-06	-1	5	5.43E-06	null	4	null	FOXO1
NM_00241	24	1.96E-06	1	7	4.62E-06	1	7	1.96E-06	null	null	1	2.93E-06	1	7	5.91E-06	1	3	0.035982	MIF
NM_00623	24	2.01E-06	1	7	4.79E-06	1	7	2.01E-06	null	null	1	3.03E-06	1	7	6.40E-06	1	3	0.081552	POLR2H
NM_00690	24	2.18E-06	1	7	5.18E-06	1	7	2.18E-06	null	null	1	3.23E-06	1	7	7.37E-06	1	3	0.051317	PYCR1
NM_00331	24	2.36E-06	1	6	5.6E-06	1	6	2.36E-06	null	null	1	3.52E-06	1	8	8.82E-06	null	4	null	TSTA3
NM_01473	24	2.41E-06	-1	7	3.90E-06	-1	7	2.41E-06	null	null	-1	2.96E-06	-1	7	5.15E-06	-1	3	0.020685	RASSF2
NM_00203(	24	2.48E-06	-1	7	4.04E-06	-1	7	2.48E-06	null	null	-1	3.04E-06	-1	7	5.31E-06	-1	3	0.054841	DARC
NM_00102	24	2.55E-06	1	6	5.97E-06	1	3	2.55E-06	null	null	1	3.81E-06	null	11	null	null	4	null	CEACAM1
NM_00628(	24	2.73E-06	1	8	1.56E-05	1	3	2.73E-06	null	null	null	null	1	9	0.090167	null	4	null	TFDP2
NM_01213	24	2.8E-06	null	11	null	-1	6	2.80E-06	null	null	-1	4.00E-06	-1	3	3.68E-06	null	4	null	LMOD1
NM_01329	24	2.81E-06	1	9	3.40E-05	1	6	2.81E-06	null	null	null	null	1	5	3.42E-05	null	4	null	SAC3D1
NM_00167	24	2.99E-06	1	5	5.37E-06	1	8	2.99E-06	null	null	1	5.84E-06	1	7	5.49E-06	null	4	null	ASNS
NM_18150	24	3.03E-06	-1	6	5.24E-06	-1	6	3.03E-06	null	null	-1	3.68E-06	-1	8	3.59E-05	null	4	null	PIK3R1
NM_00423	24	3.07E-06	-1	7	5.28E-06	-1	7	3.07E-06	null	null	-1	3.72E-06	-1	7	0.016072	-1	3	0.017628	KLF4
NM_00066	24	3.18E-06	-1	7	3.18E-06	-1	7	3.28E-06	null	null	-1	4.60E-06	-1	7	4.14E-06	-1	3	0.027354	ADH1A
NM_00154	24	3.22E-06	-1	10	0.09817	-1	7	3.22E-06	null	null	null	null	-1	3	7.04E-06	null	4	null	NDST1
NM_02110	24	3.47E-06	-1	6	3.47E-06	-1	7	6.01E-06	null	null	null	null	-1	7	0.043228	null	4	null	TMSB4X
NM_00133	24	3.5E-06	-1	7	4.84E-06	-1	7	0.033112	null	null	-1	3.50E-06	-1	6	0.014434	null	4	null	CTSO
NM_00067(	24	3.87E-06	1	6	6.84E-06	1	6	3.87E-06	null	null	null	null	1	8	7.08E-06	null	4	null	ADORA2B
NM_001981	24	3.98E-06	-1	5	5.07E-06	-1	6	3.98E-06	null	null	null	null	-1	9	0.049328	null	4	null	EPS15
NM_01771	24	4.12E-06	-1	7	4.12E-06	-1	7	4.26E-06	null	null	-1	5.6E-06	-1	7	5.12E-06	-1	3	0.02045	SNRK
NM_01214	24	4.68E-06	1	7	1.20E-05	1	6	4.68E-06	null	null	1	7.48E-06	1	7	8.40E-06	null	4	null	DTYMK
NM_00328(	24	4.71E-06	-1	7	4.71E-06	-1	7	5.09E-06	-1	0.084854	-1	6.28E-06	-1	7	5.91E-06	-1	3	0.009268	TNNC1
NM_01910	24	5.14E-06	-1	7	5.14E-06	-1	7	5.48E-06	null	null	-1	7.28E-06	-1	7	6.72E-06	-1	3	0.012266	TNXB
NM_00676	24	5.67E-06	-1	7	5.67E-06	-1	5	6.16E-06	null	null	null	null	-1	8	0.026227	null	4	null	LAPTM5
NM_01653	24	6.19E-06	-1	8	1.07E-05	-1	7	6.19E-06	null	null	-1	7.04E-06	-1	5	6.56E-06	null	4	null	SKIP
NM_00102	24	6.74E-06	-1	7	6.74E-06	-1	7	7.68E-06	null	null	-1	1.03E-05	-1	7	8.67E-06	-1	3	0.012696	CD97

NM_003200	24	7.55E-06	1	7	1.61E-05	1	8	7.55E-06	null	null	1	9.68E-06	1	5	2.63E-05	null	4	null	TCF3
NM_001620	24	8.67E-06	-1	7	1.52E-05	-1	7	8.67E-06	-1	0.089062	-1	9.25E-06	-1	7	1.91E-05	-1	3	0.079482	AHNAK
NM_001066	24	8.76E-06	-1	6	0.014329	-1	7	8.76E-06	null	null	-1	9.35E-06	-1	7	1.96E-05	null	4	null	TNFRSF1B
NM_007005	24	1.01E-05	-1	7	2.22E-05	-1	6	1.01E-05	null	null	-1	1.40E-05	-1	8	0.023255	-1	3	0.084472	TLE4
NM_003486	24	1.73E-05	1	8	3.56E-05	1	6	1.73E-05	null	null	1	3.58E-05	1	6	9.98E-05	null	4	null	SLC7A5
NM_014701	24	2.56E-05	-1	7	6.86E-05	-1	5	2.56E-05	-1	0.000274	-1	3.74E-05	-1	9	0.055952	-1	3	0.026179	KIAA0256
NM_003152	25	1.77E-06	-1	7	2.79E-06	-1	7	1.77E-06	null	null	-1	2.17E-06	-1	8	3.76E-06	-1	3	0.078015	STAT5A
NM_002667	25	1.79E-06	-1	7	3.33E-06	-1	3	1.79E-06	null	null	null	null	null	11	null	null	4	null	PLN
NM_001611	25	1.9E-06	-1	7	2.95E-06	-1	7	1.90E-06	null	null	-1	2.35E-06	-1	7	4.00E-06	null	4	null	ACP5
NM_002837	25	1.91E-06	-1	7	2.97E-06	-1	9	1.91E-06	-1	3.29E-05	-1	2.36E-06	-1	7	4.02E-06	-1	2	0.009642	PTPRB
NM_005585	25	2.03E-06	-1	7	3.22E-06	-1	7	2.03E-06	null	null	-1	2.49E-06	-1	7	4.24E-06	null	4	null	SMAD6
NM_000055	25	2.06E-06	-1	7	3.24E-06	-1	5	2.06E-06	null	null	-1	2.52E-06	null	11	null	-1	2	0.024002	BCHE
NM_004512	25	2.09E-06	-1	9	3.29E-06	-1	6	2.09E-06	null	null	-1	2.56E-06	-1	7	4.33E-06	-1	3	0.022459	IL11RA
NM_005203	25	2.2E-06	-1	7	3.50E-06	-1	7	2.20E-06	null	null	-1	2.71E-06	-1	7	4.62E-06	null	4	null	COL13A1
NM_000163	25	2.26E-06	-1	7	3.61E-06	-1	7	2.26E-06	null	null	null	null	-1	9	0.033374	-1	2	0.051212	GHR
NM_006295	25	2.35E-06	1	8	8.91E-06	1	6	2.35E-06	null	null	1	3.50E-06	1	7	2.94E-05	null	4	null	VARS
NM_003005	25	2.38E-06	-1	9	3.81E-06	-1	7	2.38E-06	null	null	-1	2.91E-06	-1	7	5.02E-06	-1	2	0.012425	SELP
NM_004048	25	2.44E-06	-1	5	7.45E-06	-1	7	2.44E-06	null	null	null	null	-1	9	0.086783	null	4	null	B2M
NM_000224	25	2.58E-06	1	8	1.73E-05	1	6	2.58E-06	null	null	null	null	1	7	1.14E-05	null	4	null	KRT18
NM_005465	25	2.77E-06	-1	7	3.76E-06	-1	7	2.77E-06	null	null	null	null	-1	7	3.63E-06	null	4	null	AKT3
NM_014742	25	3.22E-06	1	8	5.38E-05	1	6	3.22E-06	null	null	null	null	1	7	5.38E-05	null	4	null	TM9SF4
NM_020529	25	3.29E-06	-1	3	5.68E-06	-1	7	3.29E-06	null	null	null	null	null	11	null	null	4	null	NFKBIA
NM_016292	25	3.36E-06	1	7	7.48E-06	1	6	3.36E-06	1	0.000165	1	4.81E-06	1	9	0.072745	1	3	0.083014	TRAP1
NM_004237	25	3.47E-06	1	9	2.23E-05	1	5	3.47E-06	null	null	null	null	1	7	5.96E-05	null	4	null	TRIP13
NM_005558	25	4.48E-06	1	6	8.18E-06	1	6	4.48E-06	null	null	null	null	1	9	0.021653	null	4	null	LAD1
NM_004568	25	7.04E-06	-1	9	0.034671	-1	9	7.04E-06	null	null	-1	8.15E-06	-1	3	7.47E-06	null	4	null	SERPINB6
NM_015925	25	8.27E-06	1	7	1.72E-05	1	7	8.27E-06	null	null	1	1.42E-05	1	7	1.54E-05	null	4	null	LSR
NM_004107	25	1E-05	-1	10	0.086437	-1	7	1.00E-05	null	null	-1	1.08E-05	-1	5	2.17E-05	-1	3	0.018836	FCGRT
NM_006270	25	1.16E-05	-1	7	1.16E-05	-1	7	1.28E-05	-1	0.000206	-1	1.75E-05	-1	7	1.38E-05	null	4	null	RRAS
NM_002815	25	1.42E-05	1	10	0.072223	null	11	null	null	null	null	null	1	0	1.42E-05	null	4	null	PSMD11
NM_002505	25	1.72E-05	1	4	3.57E-05	1	8	1.72E-05	null	null	null	null	1	9	0.036197	null	4	null	NFYA
NM_021067	25	1.79E-05	1	6	4.12E-05	1	6	1.79E-05	null	null	1	2.35E-05	1	9	0.055152	null	4	null	GINS1
NM_006646	25	7.68E-05	-1	9	0.035092	-1	7	0.021938	null	null	null	null	-1	5	7.68E-05	null	4	null	WASF3
NM_005965	26	1.76E-06	-1	9	3.20E-06	-1	7	1.76E-06	null	null	null	null	-1	7	3.72E-06	-1	3	0.034343	
NM_002230	26	1.88E-06	1	8	5.25E-06	1	6	1.88E-06	null	null	1	2.81E-06	1	8	0.034707	null	4	null	JUP
NM_014268	26	1.95E-06	-1	8	3.07E-06	-1	8	1.95E-06	null	null	-1	2.41E-06	-1	7	4.12E-06	-1	3	0.095393	MAPRE2
NM_001337	26	2.44E-06	-1	8	0.05597	-1	9	0.077853	null	null	-1	2.44E-06	-1	5	6.74E-06	null	4	null	CX3CR1
NM_014780	26	2.5E-06	1	7	5.92E-06	1	9	2.50E-06	null	null	1	3.76E-06	1	6	3.33E-05	null	4	null	CUL7
NM_003093	26	2.73E-06	1	6	6.48E-06	1	6	2.73E-06	null	null	null	null	null	11	null	1	3	0.089352	SNRPC
NM_000877	26	2.82E-06	-1	7	2.82E-06	-1	7	2.87E-06	null	null	null	null	-1	8	0.029958	null	4	null	IL1R1
NM_002487	26	3.06E-06	-1	10	0.098228	-1	6	3.06E-06	null	null	null	null	-1	7	5.54E-05	-1	3	0.021181	NDN
NM_005940	26	3.53E-06	1	8	7.92E-06	1	6	3.53E-06	null	null	1	5.05E-06	1	10	1.47E-05	1	2	0.000412	MMP11
NM_006406	26	4.38E-06	1	8	9.8E-06	1	6	4.38E-06	null	null	null	null	1	8	2.06E-05	null	4	null	PRDX4
NM_001430	26	4.43E-06	-1	7	7.84E-06	-1	7	4.43E-06	null	null	-1	5.24E-06	-1	8	0.026404	null	4	null	EPAS1
NM_004126	26	4.94E-06	-1	7	4.94E-06	-1	9	5.38E-06	null	null	-1	6.86E-06	-1	7	6.33E-06	-1	3	0.013615	GNG11
NM_005148	26	5.04E-06	1	6	7.13E-06	1	6	5.04E-06	null	null	null	null	null	11	null	1	3	0.087543	UNC119
NM_002121	26	5.74E-06	-1	9	0.036578	-1	7	5.74E-06	null	null	-1	7.92E-06	-1	7	0.034388	-1	3	0.099464	HLA-DPB1

NM_021958	26	6.16E-06	-1	7	6.16E-06	-1	7	7.27E-06	null	null	null	null	-1	9	8.27E-06	-1	3	0.074358	HLX
NM_002691	26	7.45E-06	1	6	1.02E-05	1	5	7.45E-06	null	null	null	null	null	11	null	null	4	null	POLD1
NM_002037	26	7.68E-06	null	11	null	-1	8	7.77E-06	null	null	-1	8.67E-06	-1	3	7.68E-06	null	4	null	FYN
NM_014578	26	9.44E-06	1	10	1.92E-05	1	6	9.44E-06	null	null	1	1.72E-05	1	6	1.79E-05	null	4	null	RHOD
NM_015150	26	1.58E-05	-1	8	0.039173	-1	8	0.048888	null	null	-1	2.35E-05	-1	7	1.58E-05	-1	3	0.009225	RFTN1
NM_004356	26	2.01E-05	-1	7	0.021293	-1	9	2.01E-05	null	null	-1	2.06E-05	-1	7	5.15E-05	-1	3	0.036271	CD81
NM_032638	26	2.22E-05	-1	8	0.059742	-1	7	2.22E-05	null	null	-1	2.22E-05	-1	8	0.021366	-1	3	0.01435	GATA2
NM_004994	26	2.57E-05	1	8	0.000102	1	10	2.57E-05	null	null	1	3.74E-05	1	4	6.85E-05	null	4	null	MMP9
NM_003258	26	2.66E-05	null	11	null	1	8	2.66E-05	null	null	null	null	1	3	4.14E-05	null	4	null	TK1
NM_001032	26	3.59E-05	1	9	7.13E-05	1	6	3.59E-05	null	null	null	null	1	7	7.68E-05	null	4	null	SLC35A2
NM_000918	26	5.38E-05	1	6	0.000108	1	6	5.38E-05	null	null	null	null	1	10	0.060461	null	4	null	P4HB
NM_001295	26	0.00025	-1	7	0.029494	-1	8	0.050077	null	null	null	null	-1	7	0.00025	null	4	null	CCR1
NM_001937	26	0.009861	-1	9	0.066884	-1	7	0.033344	null	null	null	null	-1	6	0.009861	null	4	null	DPT
NM_000690	27	1.63E-06	-1	7	2.58E-06	-1	7	1.63E-06	null	null	-1	1.98E-06	null	11	null	-1	2	0.009746	ALDH2
NM_001206	27	1.73E-06	-1	7	2.73E-06	-1	7	1.73E-06	null	null	-1	2.14E-06	-1	10	0.015405	-1	3	0.011808	KLF9
NM_003189	27	1.86E-06	-1	7	2.86E-06	-1	7	1.86E-06	null	null	-1	2.30E-06	-1	10	0.041642	-1	3	0.011939	TAL1
NM_004632	27	1.98E-06	1	7	4.68E-06	1	7	1.98E-06	null	null	1	2.95E-06	1	9	9.46E-06	null	4	null	DAP3
NM_002290	27	2E-06	-1	7	3.18E-06	-1	7	2.00E-06	null	null	null	null	-1	10	0.015252	-1	3	0.061576	LAMA4
NM_005516	27	2.01E-06	-1	7	3.19E-06	-1	7	2.01E-06	-1	0.093251	-1	2.47E-06	-1	9	4.2E-06	null	4	null	HLA-E
NM_020992	27	2.26E-06	-1	9	3.63E-06	-1	9	2.26E-06	null	null	-1	2.79E-06	-1	7	4.79E-06	-1	2	0.009915	PDLIM1
NM_001032	27	2.32E-06	-1	6	0.022051	-1	7	2.32E-06	null	null	null	null	-1	10	0.068842	null	4	null	KLF10
NM_003824	27	2.44E-06	1	10	0.082755	1	6	2.44E-06	null	null	null	null	1	7	2.28E-05	null	4	null	FADD
NM_002738	27	2.51E-06	null	11	null	-1	8	4.84E-06	null	null	-1	2.51E-06	-1	4	5.78E-06	null	4	null	PRKCB1
NM_000426	27	2.53E-06	-1	7	0.021398	-1	5	2.53E-06	null	null	null	null	null	11	null	null	4	null	LAMA2
NM_004341	27	2.57E-06	1	6	6.05E-06	1	9	2.57E-06	null	null	1	3.88E-06	1	8	1.12E-05	null	4	null	CAD
NM_004078	27	2.61E-06	-1	9	9.78E-06	-1	7	2.61E-06	null	null	-1	3.13E-06	-1	8	1.20E-05	-1	3	0.014218	CSRP1
NM_006389	27	2.72E-06	1	7	4.94E-06	1	7	2.72E-06	null	null	1	5.18E-06	1	9	1.50E-05	null	4	null	HYOU1
NM_001087	27	2.77E-06	1	6	1.66E-05	1	6	2.77E-06	null	null	1	4.10E-06	null	11	null	null	4	null	AAMP
NM_175617	27	2.79E-06	-1	5	4.68E-06	-1	7	2.79E-06	null	null	-1	3.39E-06	null	11	null	null	4	null	MT1E
NM_000269	27	2.86E-06	1	8	6.69E-06	1	8	2.86E-06	null	null	1	4.22E-06	1	7	1.85E-05	null	4	null	NME1
NM_001803	27	2.88E-06	-1	9	2.88E-06	-1	7	2.91E-06	null	null	-1	4.14E-06	-1	7	3.81E-06	null	4	null	CD52
NM_006670	27	2.89E-06	1	9	8.76E-06	1	6	2.89E-06	null	null	1	5.72E-06	1	8	1.72E-05	null	4	null	TPBG
NM_000903	27	2.95E-06	1	9	2.27E-05	1	7	2.95E-06	null	null	1	4.38E-06	1	7	1.27E-05	null	4	null	NQO1
NM_001546	27	2.95E-06	-1	9	0.082625	-1	8	2.95E-06	null	null	-1	4.2E-06	-1	8	0.023099	-1	2	0.068463	ID4
NM_006074	27	3.16E-06	-1	7	4.23E-06	-1	7	3.16E-06	null	null	null	null	-1	9	0.028309	null	4	null	TRIM22
NM_000598	27	3.36E-06	1	7	6.24E-06	1	7	3.36E-06	null	null	null	null	1	9	6.56E-06	null	4	null	IGFBP3
NM_000689	27	3.44E-06	-1	9	0.07325	null	11	null	null	null	null	null	-1	3	3.44E-06	null	4	null	ALDH1A1
NM_005935	27	4.55E-06	-1	3	4.55E-06	-1	9	0.048355	null	null	null	null	null	11	null	null	4	null	AFF1
NM_001159	27	4.71E-06	-1	9	6.25E-06	-1	7	4.71E-06	null	null	null	null	-1	8	5.60E-06	-1	3	0.068357	AOX1
NM_001017	27	5.05E-06	-1	5	5.05E-06	-1	7	0.039309	null	null	null	null	null	11	null	null	4	null	SC4MOL
NM_000493	27	5.12E-06	1	7	9.42E-06	1	7	5.12E-06	null	null	1	7.84E-06	1	9	2.49E-05	null	4	null	COL10A1
NM_025207	27	5.17E-06	1	8	1.31E-05	1	6	5.17E-06	null	null	1	7.99E-06	1	9	0.025844	null	4	null	FLAD1
NM_000725	27	5.66E-06	1	8	1.49E-05	1	4	5.66E-06	null	null	null	null	null	11	null	null	4	null	CACNB3
NM_002354	27	5.85E-06	1	7	1.08E-05	1	7	5.85E-06	null	null	1	8.67E-06	1	9	3.05E-05	null	4	null	TACSTD1
NM_004460	27	7.16E-06	null	11	null	1	9	9.38E-06	null	null	1	7.16E-06	1	3	2.01E-05	null	4	null	FAP
NM_001005	27	9.6E-06	1	6	1.47E-05	1	9	9.60E-06	null	null	null	null	1	8	4.16E-05	null	4	null	ERBB3
NM_002436	27	1.22E-05	-1	7	1.58E-05	-1	7	1.22E-05	null	null	null	null	-1	9	0.042026	null	4	null	MPP1

NM_019111	27	1.31E-05	-1	8	1.31E-05	-1	8	1.39E-05	null	null	null	null	-1	7	2E-05	null	4	null	HLA-DRA
NM_006115	27	2.07E-05	1	10	0.03834	1	4	2.07E-05	null	null	null	null	1	9	9.78E-05	null	4	null	PRAME
NM_002332	27	2.57E-05	null	11	null	-1	5	2.57E-05	null	null	null	null	-1	7	0.016425	null	4	null	LRP1
NM_001109	27	3.56E-05	null	11	null	1	3	3.56E-05	null	null	null	null	1	9	0.060807	null	4	null	ADAM8
NM_020470	27	3.84E-05	1	9	0.073407	1	6	3.84E-05	null	null	1	0.000103	1	8	8.96E-05	null	4	null	YIF1A
NM_002428	27	6.24E-05	1	9	8.32E-05	1	6	6.24E-05	null	null	null	null	1	8	0.000206	null	4	null	MMP15
NM_001012	27	0.000108	1	7	0.000206	1	7	0.000108	null	null	1	0.000274	1	9	0.000269	null	4	null	MDK
NM_006495	27	0.011774	-1	10	0.082618	-1	6	0.011774	null	null	null	null	-1	7	0.043809	null	4	null	EVI2B
NM_002221	28	1.64E-06	-1	9	2.85E-06	-1	7	1.64E-06	null	null	null	null	-1	9	3.73E-06	-1	3	0.099709	ITPKB
NM_000061	28	1.65E-06	-1	10	0.027051	-1	7	1.65E-06	null	null	-1	2.01E-06	-1	7	3.36E-06	null	4	null	BTK
NM_005994	28	1.66E-06	-1	10	2.60E-06	-1	8	1.66E-06	-1	2.94E-05	-1	2.01E-06	-1	8	3.39E-06	-1	2	0.01422	TBX2
NM_005552	28	1.7E-06	-1	9	0.031242	-1	8	1.70E-06	null	null	-1	2.09E-06	-1	8	3.53E-06	-1	3	0.097351	KLC1
NM_004332	28	1.88E-06	1	5	4.38E-06	1	8	1.88E-06	null	null	null	null	null	11	null	null	4	null	BPHL
NM_004360	28	1.97E-06	1	8	4.65E-06	1	8	1.97E-06	null	null	1	2.94E-06	1	8	9.35E-06	null	4	null	CDH1
NM_001679	28	2.01E-06	-1	7	4.50E-06	-1	8	2.01E-06	null	null	null	null	-1	9	0.058135	null	4	null	ATP1B3
NM_000532	28	2.05E-06	1	6	9.27E-06	1	9	2.05E-06	null	null	null	null	1	9	0.065919	null	4	null	PCCB
NM_002273	28	2.17E-06	1	9	0.05461	1	6	2.17E-06	null	null	null	null	1	9	0.06869	null	4	null	KRT8
NM_004449	28	2.18E-06	-1	8	3.44E-06	-1	8	2.18E-06	null	null	-1	2.69E-06	-1	9	0.022024	-1	3	0.085244	ERG
NM_001299	28	2.27E-06	-1	9	0.033974	-1	6	2.27E-06	null	null	null	null	-1	9	0.024778	null	4	null	CNN1
NM_006303	28	2.28E-06	1	9	0.084495	1	6	2.28E-06	null	null	1	3.39E-06	1	9	0.062287	null	4	null	JTV1
NM_004363	28	2.31E-06	1	6	5.49E-06	1	8	2.31E-06	null	null	1	3.43E-06	1	10	0.09801	null	4	null	CEACAM5
NM_005318	28	2.34E-06	1	8	5.56E-06	1	8	2.34E-06	null	null	1	3.49E-06	1	8	1.11E-05	null	4	null	H1F0
NM_000139	28	2.59E-06	-1	9	9.24E-06	-1	9	2.59E-06	null	null	-1	3.11E-06	-1	7	5.6E-06	-1	3	0.078031	MS4A2
NM_004557	28	2.66E-06	-1	8	4.31E-06	-1	9	2.66E-06	-1	4.33E-05	-1	3.22E-06	-1	8	5.72E-06	-1	3	0.053768	NOTCH4
NM_000075	28	2.69E-06	1	9	7.99E-06	1	6	2.69E-06	null	null	null	null	1	9	0.087115	null	4	null	CDK4
NM_002046	28	2.8E-06	1	9	6.59E-06	1	7	2.8E-06	null	null	1	4.14E-06	1	9	1.58E-05	1	3	0.000269	GAPDH
NM_006744	28	2.94E-06	-1	7	3.88E-06	null	11	null	null	null	-1	2.94E-06	-1	7	1.11E-05	-1	3	0.051544	RBP4
NM_002949	28	3.13E-06	1	7	7.10E-06	1	7	3.13E-06	null	null	1	4.62E-06	1	10	0.080438	null	4	null	MRPL12
NM_006103	28	3.18E-06	1	8	4.54E-05	1	5	3.18E-06	null	null	null	null	null	11	null	null	4	null	WFDC2
NM_000398	28	3.35E-06	-1	9	5.80E-06	-1	9	3.35E-06	-1	0.096447	-1	3.98E-06	-1	7	3.66E-06	-1	3	0.097106	CYB5R3
NM_005814	28	3.43E-06	null	11	null	-1	7	3.43E-06	null	null	null	null	-1	6	0.004808	null	4	null	GPA33
NM_002072	28	3.47E-06	-1	9	3.47E-06	-1	7	3.66E-06	-1	5.88E-05	-1	4.9E-06	-1	9	4.56E-06	-1	3	0.011348	GNAQ
NM_015027	28	3.81E-06	1	8	8.49E-06	1	8	3.81E-06	null	null	1	5.49E-06	1	8	1.61E-05	null	4	null	PDXDC1
NM_002375	28	4.38E-06	-1	7	7.77E-06	-1	8	4.38E-06	null	null	-1	5.21E-06	-1	9	0.041648	null	4	null	MAP4
NM_000760	28	4.47E-06	null	11	null	null	11	null	null	null	null	null	-1	3	4.47E-06	-1	3	0.024271	CSF3R
NM_005914	28	4.72E-06	1	8	1.22E-05	1	8	4.72E-06	null	null	null	null	1	8	8.54E-06	null	4	null	MCM4
NM_001799	28	6.53E-06	null	11	null	1	9	6.53E-06	null	null	null	null	1	4	1.01E-05	null	4	null	CDK7
NM_000320	28	7.68E-06	-1	7	1.65E-05	-1	8	7.68E-06	null	null	null	null	-1	10	0.089791	-1	3	0.061444	QDPR
NM_006845	28	8.67E-06	1	8	2.94E-05	1	6	8.67E-06	null	null	1	1.55E-05	null	11	null	1	3	0.054064	KIF2C
NM_002627	28	9.27E-06	1	8	2.69E-05	1	10	9.27E-06	null	null	1	1.68E-05	1	7	1.73E-05	1	3	0.064577	PFKP
NM_003294	28	1.19E-05	-1	9	1.19E-05	-1	9	1.31E-05	null	null	-1	1.83E-05	-1	7	1.42E-05	-1	3	0.01918	TPSAB1
NM_005181	28	1.25E-05	-1	7	0.029452	-1	8	1.25E-05	null	null	null	null	-1	9	0.058791	null	4	null	CA3
NM_002194	28	1.55E-05	null	11	null	-1	7	1.55E-05	null	null	-1	1.55E-05	-1	7	3.43E-05	-1	3	0.021508	INPP1
NM_004429	28	2.29E-05	-1	9	0.051719	-1	10	0.094323	null	null	-1	2.29E-05	-1	5	5.49E-05	null	4	null	EFNB1
NM_001759	28	2.34E-05	null	11	null	-1	7	2.34E-05	null	null	null	null	-1	7	2.56E-05	-1	3	0.099756	CCND2
NM_005257	28	4.14E-05	-1	8	5.38E-05	null	11	null	null	null	null	null	-1	5	4.14E-05	null	4	null	GATA6
NM_006751	28	0.017816	-1	7	0.028027	-1	6	0.017816	null	null	null	null	null	11	null	null	4	null	SSFA2

NM_002468	28	0.02854	-1	10	0.098243	-1	7	0.038666	null	null	null	null	-1	7	0.02854	null	4	null	MYD88
NM_000887	29	1.77E-06	null	11	null	-1	7	1.77E-06	null	null	null	null	-1	7	3.74E-06	null	4	null	ITGAX
NM_001452	29	1.79E-06	null	11	null	-1	7	1.79E-06	-1	0.096979	-1	2.20E-06	-1	7	3.79E-06	null	4	null	FOXF2
NM_004496	29	1.82E-06	1	8	0.025684	1	8	1.82E-06	null	null	1	2.72E-06	1	9	0.032135	null	4	null	FOXA1
NM_014941	29	1.83E-06	1	9	1.09E-05	1	7	1.83E-06	null	null	1	2.73E-06	1	9	1.37E-05	null	4	null	MORC2
NM_000228	29	1.87E-06	1	9	5.14E-06	1	7	1.87E-06	null	null	null	null	1	9	5.38E-06	null	4	null	LAMB3
NM_002167	29	2.02E-06	-1	9	0.027582	-1	8	2.02E-06	null	null	null	null	-1	9	0.029864	-1	3	0.035811	ID3
NM_000609	29	2.02E-06	null	11	null	-1	3	2.02E-06	null	null	null	null	null	11	null	null	4	null	CXCL12
NM_002447	29	2.08E-06	null	11	null	1	6	2.08E-06	null	null	1	3.12E-06	1	8	1.03E-05	null	4	null	MST1R
NM_016343	29	2.11E-06	1	10	0.04907	1	6	2.11E-06	null	null	1	3.14E-06	1	10	0.053969	1	3	0.069834	CENPF
NM_003104	29	2.14E-06	1	9	6.93E-06	1	7	2.14E-06	null	null	1	3.18E-06	1	9	7.17E-06	null	4	null	SORD
NM_000149	29	2.2E-06	1	9	5.24E-06	1	7	2.20E-06	null	null	1	3.25E-06	1	9	7.47E-06	null	4	null	FUT3
NM_001031	29	2.29E-06	-1	10	0.046517	-1	7	2.29E-06	null	null	-1	2.81E-06	-1	10	0.039289	-1	2	0.013243	
NM_001257	29	2.37E-06	-1	9	3.79E-06	-1	7	2.37E-06	null	null	null	null	-1	9	0.039704	null	4	null	CDH13
NM_003528	29	2.61E-06	1	9	0.043528	1	6	2.61E-06	null	null	null	null	1	10	0.098601	null	4	null	HIST2H2BE
NM_021078	29	2.83E-06	1	9	1.78E-05	1	7	2.83E-06	null	null	1	4.18E-06	1	10	0.066218	1	3	0.037764	GCN5L2
NM_002245	29	2.87E-06	1	9	6.75E-06	1	8	2.87E-06	null	null	1	4.29E-06	1	8	1.92E-05	null	4	null	KCNK1
NM_003102	29	2.98E-06	null	11	null	-1	7	2.98E-06	null	null	-1	3.66E-06	-1	7	6.53E-06	null	4	null	SOD3
NM_001238	29	2.99E-06	1	7	6.98E-06	1	7	2.99E-06	null	null	null	null	null	11	null	null	4	null	CCNE1
NM_001197	29	3.15E-06	1	9	3.84E-05	1	7	3.15E-06	null	null	null	null	1	9	4.48E-05	null	4	null	BIK
NM_002618	29	3.34E-06	null	11	null	1	6	3.34E-06	null	null	null	null	1	8	2.01E-05	null	4	null	PEX13
NM_000414	29	3.43E-06	-1	7	0.037648	-1	10	0.0878	null	null	-1	3.43E-06	-1	8	0.047776	null	4	null	HSD17B4
NM_002445	29	3.49E-06	-1	7	3.49E-06	-1	9	4.14E-06	null	null	-1	5.05E-06	-1	9	9.68E-06	null	4	null	MSR1
NM_005216	29	3.5E-06	1	9	0.061569	1	8	3.50E-06	null	null	null	null	1	9	0.035615	1	3	0.084731	DDOST
NM_006198	29	3.55E-06	1	9	0.061252	1	5	3.55E-06	null	null	1	5.08E-06	null	11	null	null	4	null	PCP4
NM_001014	29	3.71E-06	null	11	null	-1	3	3.71E-06	null	null	null	null	null	11	null	null	4	null	DDR2
NM_002455	29	4.12E-06	1	7	9.15E-06	1	7	4.12E-06	null	null	null	null	null	11	null	null	4	null	MTX1
NM_002276	29	5.91E-06	1	9	0.04023	1	8	5.91E-06	null	null	1	9.46E-06	1	8	1.10E-05	null	4	null	KRT19
NM_003107	29	7.08E-06	1	9	1.96E-05	1	7	7.08E-06	null	null	1	1.11E-05	1	9	4.33E-05	null	4	null	SOX4
NM_006709	29	7.23E-06	1	8	9.78E-06	1	8	7.23E-06	null	null	1	8.15E-06	1	9	0.083445	null	4	null	EHMT2
NM_015327	29	9.68E-06	1	7	2.22E-05	1	7	9.68E-06	null	null	null	null	null	11	null	null	4	null	SMG5
NM_004289	29	1.07E-05	1	7	2.57E-05	1	7	1.07E-05	null	null	1	1.33E-05	null	11	null	null	4	null	NFE2L3
NM_014734	29	1.23E-05	-1	8	0.031975	-1	6	1.23E-05	null	null	null	null	null	11	null	null	4	null	KIAA0247
NM_004968	29	1.28E-05	1	9	0.038159	1	5	1.28E-05	null	null	1	2.22E-05	null	11	null	null	4	null	ICA1
NM_006547	29	1.49E-05	1	8	2.01E-05	1	8	1.49E-05	null	null	null	null	1	9	0.065522	null	4	null	IGF2BP3
NM_002266	29	1.54E-05	null	11	null	1	8	1.54E-05	null	null	null	null	1	7	3.16E-05	1	3	0.084675	KPNA2
NM_002658	29	1.96E-05	1	9	5.27E-05	null	11	null	null	null	1	1.96E-05	1	5	4.03E-05	null	4	null	PLAU
NM_004482	29	2.34E-05	null	11	null	1	6	2.34E-05	null	null	null	null	1	8	0.033	null	4	null	GALNT3
NM_001322	29	3.36E-05	1	9	6.24E-05	1	7	3.36E-05	null	null	null	null	1	10	0.044239	1	3	0.057488	CST2
NM_002588	29	3.74E-05	null	11	null	-1	8	3.74E-05	null	null	-1	3.92E-05	-1	7	0.000103	-1	3	0.026217	PCDHGC3
NM_004417	29	6.86E-05	-1	9	0.036063	-1	7	7.48E-05	null	null	-1	6.86E-05	-1	10	0.093589	-1	3	0.027753	DUSP1
NM_000067	29	8.32E-05	-1	7	8.32E-05	null	11	null	null	null	null	null	-1	8	0.021721	-1	3	0.061585	CA2
NM_007276	29	0.000137	1	10	0.000274	1	9	0.000137	null	null	null	null	1	6	0.015337	null	4	null	CBX3
NM_001280	29	0.000179	-1	10	0.075607	-1	8	0.000179	null	null	null	null	-1	8	0.000179	-1	3	0.035839	CIRBP
NM_000239	29	0.010327	-1	10	0.084111	-1	6	0.010327	null	null	null	null	-1	9	0.066663	null	4	null	LYZ
NM_001029	29	0.016997	1	9	0.097842	1	10	0.071061	null	null	null	null	1	7	0.016997	1	3	0.082921	KIAA0101
NM_000856	29	0.019712	null	11	null	-1	6	0.019712	null	null	null	null	-1	8	0.027247	null	4	null	GUCY1A3

NM_000397	29	0.024488	-1	6	0.024488	-1	8	0.034989	null	null	null	null	null	11	null	null	4	null	CYBB
NM_014708	29	0.026212	1	8	0.040104	1	10	0.066734	null	null	null	null	1	8	0.026212	1	3	0.091235	KNTC1
NM_006682	29	0.029359	-1	6	0.029359	-1	8	0.049726	null	null	null	null	null	11	null	null	4	null	FGL2
NM_004832	29	0.031986	-1	7	0.043793	-1	7	0.031986	null	null	null	null	null	11	null	null	4	null	GSTO1
NM_012383	29	0.034138	-1	8	0.034138	-1	8	0.044011	null	null	null	null	-1	9	0.041409	null	4	null	OSTF1
NM_002009	30	1.64E-06	null	11	null	-1	5	1.64E-06	null	null	null	null	null	11	null	-1	3	0.097544	FGF7
NM_005064	30	1.83E-06	-1	9	0.054478	-1	7	1.83E-06	null	null	null	null	-1	10	0.089021	null	4	null	CCL23
NM_001009	30	1.84E-06	1	9	4.29E-06	1	7	1.84E-06	null	null	1	2.73E-06	1	10	0.060828	null	4	null	SMPDL3B
NM_000666	30	1.85E-06	1	9	0.056989	1	6	1.85E-06	null	null	null	null	null	11	null	null	4	null	ACY1
NM_003523	30	1.94E-06	1	9	4.55E-06	1	10	1.94E-06	null	null	1	2.91E-06	1	7	5.66E-06	null	4	null	HIST1H2BE
NM_004154	30	1.94E-06	null	11	null	1	10	1.94E-06	null	null	1	2.92E-06	1	5	4.25E-05	null	4	null	P2RY6
NM_001545	30	2E-06	1	9	4.73E-06	1	7	2.00E-06	null	null	null	null	1	10	0.075646	null	4	null	ICT1
NM_001006	30	2.04E-06	-1	9	0.036709	-1	9	2.04E-06	null	null	null	null	-1	8	5.72E-06	null	4	null	IHPK1
NM_005234	30	2.08E-06	1	9	4.96E-06	1	6	2.08E-06	null	null	null	null	null	11	null	null	4	null	NR2F6
NM_001290	30	2.11E-06	-1	9	3.32E-06	-1	9	2.11E-06	-1	0.08041	-1	2.57E-06	-1	9	4.38E-06	-1	3	0.095726	LDB2
NM_001018	30	2.14E-06	-1	9	3.37E-06	-1	9	2.14E-06	-1	0.08494	-1	2.61E-06	-1	9	0.011863	-1	3	0.094609	ZBTB16
NM_005854	30	2.22E-06	-1	9	3.53E-06	-1	9	2.22E-06	-1	3.74E-05	-1	2.73E-06	-1	9	4.65E-06	-1	3	0.098061	RAMP2
NM_004935	30	2.33E-06	1	8	8.46E-06	1	9	2.33E-06	null	null	null	null	1	10	0.096529	1	3	0.0714	CDK5
NM_001001	30	2.8E-06	-1	7	2.80E-06	-1	8	0.035888	null	null	null	null	null	11	null	null	4	null	ATP2B1
NM_001826	30	2.83E-06	1	9	0.041982	1	8	2.83E-06	null	null	null	null	1	9	0.04861	null	4	null	CKS1B
NM_002518	30	2.98E-06	1	7	4.76E-06	1	9	4.09E-06	null	null	1	2.98E-06	1	10	0.075644	null	4	null	NPAS2
NM_002222	30	3.1E-06	-1	9	3.10E-06	-1	7	3.20E-06	null	null	-1	4.50E-06	null	11	null	-1	3	0.061008	ITPR1
NM_004168	30	3.12E-06	1	10	0.088991	1	5	3.12E-06	null	null	null	null	null	11	null	null	4	null	SDHA
NM_006516	30	3.16E-06	1	10	7.79E-06	1	10	3.16E-06	null	null	null	null	1	8	5.98E-06	1	2	0.000134	SLC2A1
NM_014762	30	3.19E-06	-1	6	0.010531	-1	9	0.042479	null	null	-1	3.19E-06	null	11	null	null	4	null	DHCR24
NM_000576	30	3.24E-06	-1	7	3.24E-06	-1	8	0.040698	null	null	null	null	null	11	null	null	4	null	IL1B
NM_013291	30	3.32E-06	1	10	0.055028	1	5	5.48E-06	null	null	1	3.32E-06	null	11	null	null	4	null	CPSF1
NM_003345	30	3.33E-06	null	11	null	1	6	3.33E-06	null	null	null	null	1	9	0.074646	null	4	null	UBE2I
NM_005980	30	3.35E-06	1	6	5.38E-06	1	10	0.076125	null	null	1	3.35E-06	1	10	0.070118	null	4	null	S100P
NM_000213	30	3.45E-06	1	10	6.40E-06	1	6	3.45E-06	null	null	null	null	1	10	0.091774	null	4	null	ITGB4
NM_003855	30	3.59E-06	-1	10	0.067883	-1	9	3.59E-06	null	null	-1	4.31E-06	-1	7	8.15E-06	null	4	null	IL18R1
NM_006290	30	3.63E-06	-1	8	0.033922	-1	7	3.63E-06	null	null	null	null	null	11	null	null	4	null	TNFAIP3
NM_015278	30	3.69E-06	-1	9	6.38E-06	-1	9	3.69E-06	null	null	-1	4.38E-06	-1	9	8.4E-06	-1	3	0.095483	SASH1
NM_002703	30	4.23E-06	1	10	0.080376	1	6	4.23E-06	null	null	null	null	null	11	null	1	3	0.094288	PPAT
NM_002810	30	4.41E-06	1	9	1.13E-05	1	7	4.41E-06	null	null	1	7.28E-06	1	10	0.068265	null	4	null	PSMD4
NM_001008	30	4.5E-06	null	11	null	1	10	0.084701	null	null	1	4.50E-06	1	5	4.89E-05	null	4	null	CKAP5
NM_005621	30	4.87E-06	-1	8	0.029495	-1	7	0.034111	null	null	-1	4.87E-06	null	11	null	null	4	null	S100A12
NM_002621	30	5.18E-06	-1	9	8.95E-06	-1	9	5.18E-06	null	null	-1	5.97E-06	-1	8	1.13E-05	null	4	null	CFP
NM_004414	30	5.42E-06	-1	10	0.095859	-1	9	5.42E-06	null	null	null	null	-1	7	1.14E-05	null	4	null	RCAN1
NM_001155	30	6.01E-06	-1	10	6.01E-06	-1	8	7.03E-06	null	null	null	null	-1	8	0.018761	null	4	null	ANXA6
NM_002794	30	6.04E-06	1	10	0.085775	1	9	0.058399	null	null	null	null	1	7	6.04E-06	null	4	null	PSMB2
NM_012072	30	6.33E-06	-1	9	0.034575	-1	9	0.05047	null	null	-1	6.33E-06	-1	10	0.052392	-1	2	0.000206	CD93
NM_006014	30	6.38E-06	1	7	1.40E-05	1	10	6.38E-06	null	null	1	8.4E-06	1	10	0.084442	1	3	0.089165	LAGE3
NM_000611	30	6.48E-06	-1	5	6.48E-06	-1	10	0.095434	null	null	-1	9.92E-06	null	11	null	null	4	null	CD59
NM_001003	30	6.64E-06	null	11	null	null	11	null	null	null	null	null	-1	5	6.64E-06	-1	3	0.062749	MGLL
NM_007256	30	7.16E-06	-1	9	1.27E-05	-1	9	7.16E-06	null	null	null	null	-1	9	1.58E-05	-1	3	0.093881	SLCO2B1
NM_001916	30	7.79E-06	1	9	0.05965	1	8	7.79E-06	null	null	null	null	1	9	0.049288	null	4	null	CYC1

NM_003149	30	8.6E-06	-1	9	1.87E-05	-1	7	8.60E-06	null	null	-1	1.16E-05	-1	10	0.036488	null	4	null	STAC
NM_003006	30	8.91E-06	-1	9	8.91E-06	-1	9	1.03E-05	null	null	null	null	-1	8	1.12E-05	null	4	null	SELPLG
NM_000578	30	1.11E-05	-1	9	1.91E-05	-1	9	1.11E-05	null	null	-1	1.18E-05	-1	9	2.35E-05	-1	3	0.076699	SLC11A1
NM_003132	30	1.14E-05	1	8	2.15E-05	1	10	0.093838	null	null	1	1.14E-05	1	9	0.049309	1	3	0.088649	SRM
NM_002246	30	1.42E-05	-1	9	2.29E-05	-1	9	1.42E-05	null	null	-1	1.44E-05	-1	9	2.94E-05	-1	3	0.09145	KCNK3
NM_001091	30	1.65E-05	1	8	1.72E-05	1	7	1.65E-05	null	null	null	null	null	11	null	null	4	null	ABP1
NM_005904	30	1.96E-05	-1	9	0.026573	-1	7	1.96E-05	null	null	-1	2.01E-05	null	11	null	-1	3	0.041661	SMAD7
NM_004178	30	5.98E-05	1	8	0.000134	1	7	5.98E-05	null	null	null	null	null	11	null	null	4	null	TARBP2
NM_014847	30	6.24E-05	1	9	0.031637	1	10	0.099042	null	null	null	null	1	7	6.24E-05	null	4	null	UBAP2L
NM_002135	30	0.028947	null	11	null	-1	8	0.045882	null	null	null	null	-1	7	0.028947	null	4	null	NR4A1
NM_000560	30	0.035159	-1	9	0.07711	-1	8	0.035159	null	null	null	null	-1	9	0.062687	null	4	null	CD53
NM_002165	31	1.69E-06	null	11	null	-1	7	1.69E-06	-1	0.069319	null	null	null	11	null	-1	2	0.014598	ID1
NM_001901	31	1.75E-06	-1	9	0.059292	-1	7	1.75E-06	null	null	null	null	null	11	null	null	4	null	CTGF
NM_001025	31	1.75E-06	-1	8	2.77E-06	-1	8	1.75E-06	null	null	null	null	null	11	null	null	4	null	CHN1
NM_004628	31	1.76E-06	-1	9	0.029614	-1	7	1.76E-06	null	null	null	null	null	11	null	null	4	null	XPC
NM_002209	31	1.81E-06	-1	10	0.03747	-1	7	1.81E-06	null	null	-1	2.22E-06	-1	10	0.022937	null	4	null	ITGAL
NM_000819	31	1.84E-06	1	10	0.09174	1	10	1.84E-06	null	null	null	null	1	7	5.27E-06	null	4	null	GART
NM_004044	31	1.85E-06	1	9	4.31E-06	1	9	1.85E-06	null	null	1	2.74E-06	1	9	5.32E-06	null	4	null	ATIC
NM_001015	31	1.88E-06	-1	8	2.88E-06	-1	8	1.88E-06	null	null	-1	2.31E-06	null	11	null	null	4	null	TSC22D3
NM_004867	31	1.89E-06	-1	9	2.91E-06	-1	9	1.89E-06	-1	0.083761	-1	2.33E-06	-1	9	3.94E-06	null	4	null	ITM2A
NM_004781	31	1.98E-06	-1	9	3.13E-06	-1	9	1.98E-06	null	null	-1	2.44E-06	-1	10	0.075767	-1	3	0.030236	VAMP3
NM_005103	31	1.99E-06	-1	9	3.15E-06	-1	9	1.99E-06	null	null	-1	2.46E-06	-1	9	4.16E-06	null	4	null	FEZ1
NM_021052	31	2.03E-06	1	9	6.32E-06	1	7	2.03E-06	null	null	1	3.05E-06	null	11	null	null	4	null	HIST1H2AE
NM_004318	31	2.07E-06	1	10	0.088123	1	8	2.07E-06	null	null	null	null	1	9	0.046952	null	4	null	ASPH
NM_003808	31	2.08E-06	-1	9	3.28E-06	-1	9	2.08E-06	null	null	-1	2.54E-06	-1	9	4.31E-06	null	4	null	TNFSF13
NM_003362	31	2.09E-06	null	11	null	1	5	2.09E-06	null	null	null	null	null	11	null	null	4	null	UNG
NM_006094	31	2.11E-06	-1	10	3.33E-06	-1	9	2.11E-06	-1	3.58E-05	-1	2.58E-06	-1	9	4.40E-06	-1	3	0.000103	DLC1
NM_002704	31	2.15E-06	null	11	null	-1	7	2.15E-06	null	null	null	null	-1	9	0.034399	null	4	null	PPBP
NM_002124	31	2.19E-06	-1	9	2.8E-06	-1	9	0.052544	null	null	-1	2.19E-06	-1	9	0.051512	null	4	null	HLA-DRB1
NM_001954	31	2.2E-06	1	8	5.28E-06	1	8	2.20E-06	null	null	null	null	null	11	null	null	4	null	DDR1
NM_012073	31	2.22E-06	null	11	null	1	8	2.22E-06	null	null	null	null	1	9	0.026672	1	3	0.085976	CCT5
NM_006280	31	2.24E-06	1	9	5.31E-06	1	10	2.24E-06	null	null	1	3.29E-06	1	8	1.1E-05	null	4	null	SSR4
NM_000960	31	2.24E-06	null	11	null	-1	7	2.24E-06	null	null	-1	2.77E-06	-1	9	4.76E-06	null	4	null	PTGIR
NM_002198	31	2.27E-06	-1	9	0.045163	-1	7	2.27E-06	null	null	null	null	null	11	null	null	4	null	IRF1
NM_004615	31	2.27E-06	-1	10	0.076964	-1	9	0.076601	-1	0.074454	-1	2.27E-06	-1	10	0.057539	-1	2	0.094816	TSPAN7
NM_001723	31	2.3E-06	-1	9	3.66E-06	-1	9	2.30E-06	-1	0.087402	-1	2.82E-06	-1	9	4.84E-06	null	4	null	DST
NM_001618	31	2.32E-06	1	9	5.52E-06	1	9	2.32E-06	null	null	1	3.44E-06	1	9	8.27E-06	null	4	null	PARP1
NM_001407	31	2.33E-06	1	9	1.65E-05	1	7	2.33E-06	null	null	null	null	null	11	null	null	4	null	CELSR3
NM_001018	31	2.36E-06	-1	9	3.78E-06	-1	9	2.36E-06	null	null	-1	2.88E-06	-1	9	4.99E-06	null	4	null	PODXL
NM_005831	31	2.49E-06	-1	7	4.10E-06	-1	9	2.49E-06	null	null	-1	3.05E-06	null	11	null	null	4	null	CALCOCO2
NM_005139	31	2.63E-06	-1	7	4.27E-06	-1	9	2.63E-06	null	null	-1	3.18E-06	null	11	null	null	4	null	ANXA3
NM_033439	31	2.72E-06	-1	9	4.45E-06	-1	10	2.72E-06	null	null	-1	3.31E-06	-1	9	5.92E-06	-1	3	0.090011	IL33
NM_004787	31	2.73E-06	-1	9	4.50E-06	-1	9	2.73E-06	null	null	-1	3.33E-06	-1	9	6.01E-06	null	4	null	SLIT2
NM_014033	31	2.76E-06	-1	9	4.62E-06	-1	9	2.76E-06	null	null	-1	3.36E-06	-1	9	6.05E-06	null	4	null	METTL7A
NM_001017	31	2.94E-06	-1	9	5.11E-06	-1	9	2.94E-06	null	null	-1	3.61E-06	-1	9	6.48E-06	null	4	null	RP1-21018
NM_003779	31	3.11E-06	1	9	7.04E-06	1	7	3.11E-06	1	0.000137	1	4.57E-06	null	11	null	null	4	null	B4GALT3
NM_000389	31	3.12E-06	-1	7	3.12E-06	-1	9	0.037603	null	null	null	null	null	11	null	null	4	null	CDKN1A

NM_002923	31	3.14E-06	-1	9	5.54E-05	-1	7	3.14E-06	null	null	null	null	null	11	null	null	4	null	RGS2
NM_003332	31	3.2E-06	-1	9	5.52E-06	-1	9	3.20E-06	null	null	-1	3.83E-06	-1	9	6.98E-06	null	4	null	TYROBP
NM_003917	31	3.23E-06	1	10	0.079765	1	7	3.23E-06	null	null	null	null	1	10	0.000114	null	4	null	AP1G2
NM_000135	31	3.43E-06	1	10	0.089595	1	6	3.43E-06	null	null	null	null	null	11	null	null	4	null	FANCA
NM_003810	31	3.44E-06	-1	7	4.76E-06	null	11	null	null	null	-1	3.44E-06	-1	9	0.067674	null	4	null	TNFSF10
NM_014795	31	3.46E-06	-1	9	6.05E-06	-1	9	3.46E-06	null	null	null	null	-1	9	7.84E-06	null	4	null	ZEB2
NM_007111	31	3.52E-06	1	10	0.084123	1	6	3.52E-06	null	null	null	null	null	11	null	null	4	null	TFDP1
NM_031966	31	3.56E-06	1	9	9.44E-06	1	9	3.56E-06	null	null	null	null	1	9	6.72E-06	null	4	null	CCNB1
NM_006702	31	3.56E-06	-1	9	6.19E-06	-1	9	3.56E-06	null	null	-1	4.27E-06	-1	9	8.07E-06	null	4	null	PNPLA6
NM_001015	31	3.61E-06	-1	9	6.24E-06	-1	9	3.61E-06	null	null	-1	4.33E-06	-1	9	8.23E-06	null	4	null	PAPSS2
NM_005566	31	3.66E-06	null	11	null	1	10	0.099419	null	null	1	3.66E-06	1	6	9.78E-06	null	4	null	LDHA
NM_002961	31	3.72E-06	-1	7	3.72E-06	-1	9	3.93E-06	null	null	null	null	null	11	null	null	4	null	S100A4
NM_006468	31	3.83E-06	1	8	1.19E-05	1	8	8.32E-06	null	null	1	3.83E-06	null	11	null	null	4	null	POLR3C
NM_007168	31	3.85E-06	-1	9	6.64E-06	-1	9	3.85E-06	null	null	-1	4.52E-06	-1	9	8.67E-06	null	4	null	ABCA8
NM_005480	31	3.95E-06	1	7	5.08E-06	1	9	3.95E-06	null	null	null	null	null	11	null	null	4	null	TROAP
NM_000095	31	3.96E-06	1	8	6.24E-06	null	11	null	null	null	1	3.96E-06	1	8	1.25E-05	null	4	null	COMP
NM_002250	31	4E-06	1	9	8.95E-06	1	7	4.00E-06	null	null	1	5.80E-06	null	11	null	null	4	null	KCNN4
NM_000072	31	4.01E-06	-1	9	5.12E-06	-1	9	4.01E-06	null	null	null	null	-1	9	4.80E-06	null	4	null	CD36
NM_012302	31	4.12E-06	-1	9	7.42E-06	-1	9	4.12E-06	-1	0.096227	-1	4.99E-06	-1	9	9.57E-06	null	4	null	LPHN2
NM_003099	31	4.33E-06	-1	7	4.33E-06	null	11	null	null	null	null	null	-1	9	0.061609	null	4	null	SNX1
NM_006373	31	4.36E-06	-1	9	0.050051	-1	7	4.36E-06	null	null	-1	5.18E-06	null	11	null	null	4	null	VAT1
NM_001872	31	4.45E-06	null	11	null	null	11	null	null	null	-1	4.45E-06	-1	7	8.58E-06	-1	2	0.008024	CPB2
NM_006775	31	4.84E-06	-1	9	8.49E-06	-1	9	4.84E-06	null	null	-1	5.72E-06	-1	9	1.07E-05	null	4	null	QKI
NM_002848	31	4.89E-06	-1	9	0.068719	-1	7	4.89E-06	null	null	null	null	null	11	null	null	4	null	PTPRO
NM_004526	31	5.03E-06	1	9	1.31E-05	1	9	5.03E-06	null	null	null	null	1	9	8.96E-06	null	4	null	MCM2
NM_003275	31	5.52E-06	-1	9	9.25E-06	-1	9	5.52E-06	null	null	null	null	-1	10	0.040257	-1	3	0.050044	TMOD1
NM_006770	31	5.64E-06	-1	9	9.68E-06	-1	9	5.64E-06	null	null	-1	6.48E-06	-1	9	1.21E-05	null	4	null	MARCO
NM_001042	31	5.98E-06	-1	9	7.91E-06	-1	9	5.98E-06	null	null	null	null	-1	9	7.27E-06	null	4	null	FGR
NM_014764	31	6.01E-06	-1	10	0.095194	-1	7	6.01E-06	null	null	null	null	null	11	null	-1	3	0.063111	DAZAP2
NM_002616	31	6.1E-06	-1	10	1.04E-05	-1	7	6.10E-06	null	null	-1	6.98E-06	-1	10	1.33E-05	null	4	null	PER1
NM_001086	31	6.24E-06	-1	7	6.24E-06	null	11	null	null	null	null	null	-1	9	0.069941	null	4	null	AADAC
NM_001002	31	6.57E-06	-1	7	6.57E-06	null	11	null	null	null	null	null	-1	9	9.98E-06	null	4	null	FMO3
NM_001081	31	6.72E-06	-1	9	8.82E-06	-1	9	6.72E-06	null	null	null	null	-1	9	7.91E-06	null	4	null	P2RY14
NM_003870	31	7.23E-06	-1	5	7.23E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	IQGAP1
NM_001045	31	7.28E-06	-1	9	1.31E-05	-1	9	7.28E-06	null	null	-1	8.32E-06	-1	9	1.65E-05	null	4	null	SLC6A4
NM_014873	31	7.77E-06	1	10	7.77E-06	null	11	null	null	null	null	null	1	6	0.000255	null	4	null	LPGAT1
NM_001085	31	7.79E-06	-1	9	9.96E-06	-1	9	7.79E-06	null	null	null	null	-1	9	8.54E-06	null	4	null	SEPP1
NM_005855	31	7.92E-06	null	11	null	1	7	7.92E-06	null	null	null	null	1	9	2.74E-05	null	4	null	RAMP1
NM_002151	31	8.15E-06	1	10	0.093754	1	6	8.15E-06	null	null	null	null	null	11	null	null	4	null	HPN
NM_000034	31	8.15E-06	1	10	1.75E-05	1	10	8.15E-06	null	null	1	1.06E-05	1	7	1.22E-05	null	4	null	ALDOA
NM_014791	31	8.32E-06	1	10	1.83E-05	1	10	8.32E-06	null	null	1	1.07E-05	1	9	1.28E-05	1	2	0.000179	MELK
NM_006475	31	8.58E-06	null	11	null	null	11	null	null	null	1	8.58E-06	1	5	2.84E-05	null	4	null	POSTN
NM_015239	31	8.58E-06	-1	9	1.50E-05	-1	9	8.58E-06	null	null	-1	9.15E-06	-1	10	0.055966	-1	3	0.094924	AGTPBP1
NM_001428	31	8.76E-06	1	9	1.91E-05	1	10	8.76E-06	null	null	null	null	1	9	1.38E-05	1	3	0.084221	ENO1
NM_004359	31	9.12E-06	1	10	0.088962	1	10	0.047071	null	null	null	null	1	7	9.12E-06	null	4	null	CDC34
NM_000192	31	9.92E-06	null	11	null	-1	5	9.92E-06	null	null	null	null	null	11	null	null	4	null	TBX5
NM_005319	31	1.02E-05	1	8	2.13E-05	null	11	null	null	null	1	1.02E-05	1	8	0.029844	null	4	null	HIST1H1C

NM_001305	31	1.03E-05	1	7	2.42E-05	1	10	1.03E-05	null	null	1	1.27E-05	1	10	5.15E-05	null	4	null	CLDN4
NM_000178	31	1.05E-05	1	10	4.89E-05	1	6	1.05E-05	null	null	null	null	null	11	null	null	4	null	GSS
NM_002292	31	1.07E-05	null	11	null	-1	8	1.07E-05	null	null	null	null	-1	9	0.044283	-1	3	0.03786	LAMB2
NM_001254	31	1.17E-05	1	9	0.071336	1	10	1.17E-05	null	null	null	null	1	8	4.28E-05	null	4	null	CDC6
NM_001311	31	1.19E-05	-1	8	1.49E-05	-1	8	1.19E-05	null	null	null	null	null	11	null	null	4	null	CRIP1
NM_001002	31	1.25E-05	-1	9	2.01E-05	-1	9	1.25E-05	null	null	-1	1.33E-05	-1	9	2.66E-05	null	4	null	CLDN18
NM_000685	31	1.35E-05	-1	9	2.06E-05	-1	10	0.048483	null	null	-1	1.35E-05	-1	9	2.74E-05	-1	3	0.014083	AGTR1
NM_002754	31	1.47E-05	1	9	3.58E-05	1	7	1.47E-05	null	null	1	2.06E-05	null	11	null	null	4	null	MAPK13
NM_003798	31	1.47E-05	-1	9	2.42E-05	-1	9	1.47E-05	null	null	-1	1.50E-05	-1	9	3.17E-05	null	4	null	CTNNAL1
NM_004514	31	1.49E-05	1	8	2.34E-05	null	11	null	null	null	null	null	1	8	1.49E-05	null	4	null	FOXK2
NM_004747	31	1.58E-05	null	11	null	1	7	1.58E-05	null	null	1	2.17E-05	1	9	7.48E-05	null	4	null	DLG5
NM_031442	31	1.65E-05	-1	9	2.74E-05	-1	9	1.65E-05	null	null	null	null	-1	9	3.92E-05	null	4	null	TMEM47
NM_000090	31	2.08E-05	null	11	null	1	10	2.08E-05	null	null	null	null	1	6	3.80E-05	null	4	null	COL3A1
NM_004663	31	2.38E-05	-1	7	2.38E-05	-1	10	0.048113	null	null	null	null	-1	10	0.062912	null	4	null	RAB11A
NM_012232	31	2.66E-05	-1	9	4.33E-05	-1	9	2.66E-05	null	null	-1	2.66E-05	-1	9	6.86E-05	null	4	null	PTRF
NM_001974	31	0.000108	null	11	null	null	11	null	null	null	null	null	-1	5	0.000108	null	4	null	EMR1
NM_016083	31	0.008114	-1	10	0.079607	null	11	null	null	null	null	null	-1	6	0.008114	null	4	null	CNR1
NM_005952	31	0.024577	-1	8	0.024577	-1	8	0.041186	null	null	null	null	null	11	null	null	4	null	MT1X
NM_002964	31	0.025531	-1	10	0.058727	-1	8	0.044253	null	null	null	null	-1	9	0.025531	null	4	null	S100A8
NM_006022	31	0.050161	-1	9	0.050161	-1	8	0.065128	null	null	null	null	null	11	null	-1	3	0.097349	TSC22D1
NM_001003	32	1.63E-06	null	11	null	-1	7	1.63E-06	null	null	-1	2.00E-06	null	11	null	-1	3	0.078747	ABLIM1
NM_002183	32	1.64E-06	-1	9	2.59E-06	-1	9	1.64E-06	null	null	-1	2.00E-06	-1	10	0.034459	null	4	null	IL3RA
NM_006766	32	1.73E-06	null	11	null	-1	9	1.73E-06	null	null	null	null	-1	9	3.58E-06	-1	3	0.034542	MYST3
NM_182487	32	1.84E-06	-1	10	0.083814	-1	9	1.84E-06	null	null	null	null	-1	10	0.02636	-1	3	0.091927	OLFML2A
NM_012112	32	1.88E-06	1	9	4.40E-06	1	10	1.88E-06	null	null	1	2.82E-06	1	9	1.49E-05	null	4	null	TPX2
NM_002149	32	1.95E-06	-1	8	3.08E-06	-1	9	1.95E-06	null	null	null	null	null	11	null	null	4	null	HPCAL1
NM_015993	32	2.13E-06	-1	9	2.72E-06	-1	10	0.097594	null	null	-1	2.13E-06	-1	9	3.63E-06	null	4	null	PLLP
NM_002971	32	2.15E-06	null	11	null	-1	8	2.15E-06	null	null	-1	2.63E-06	-1	10	0.057955	-1	3	0.068301	SATB1
NM_002637	32	2.27E-06	1	10	0.055413	1	9	2.27E-06	null	null	1	3.37E-06	1	10	0.081203	1	3	0.082761	PHKA1
NM_000542	32	2.28E-06	-1	10	0.049615	-1	9	0.051921	null	null	-1	2.28E-06	-1	10	0.084186	-1	3	0.012168	SFTPB
NM_000251	32	2.35E-06	null	11	null	1	6	2.35E-06	null	null	null	null	null	11	null	null	4	null	MSH2
NM_018407	32	2.39E-06	1	7	5.72E-06	1	10	2.39E-06	null	null	1	3.59E-06	null	11	null	null	4	null	LAPTM4B
NM_002205	32	2.39E-06	-1	9	3.86E-06	-1	9	2.39E-06	null	null	null	null	-1	10	0.067951	null	4	null	ITGA5
NM_004915	32	2.4E-06	-1	10	0.035228	-1	9	2.4E-06	null	null	-1	2.95E-06	-1	9	5.08E-06	null	4	null	ABCG1
NM_005031	32	2.42E-06	-1	9	3.92E-06	-1	9	2.42E-06	-1	0.098711	-1	2.97E-06	-1	10	5.18E-06	null	4	null	FXYD1
NM_001015	32	2.49E-06	1	9	0.039864	1	8	2.49E-06	null	null	null	null	null	11	null	null	4	null	RAE1
NM_004956	32	2.49E-06	null	11	null	-1	10	0.098613	null	null	-1	2.49E-06	-1	7	4.27E-06	null	4	null	ETV1
NM_002168	32	2.53E-06	1	9	0.038899	1	9	2.53E-06	null	null	null	null	1	10	0.056085	null	4	null	IDH2
NM_014957	32	2.69E-06	-1	9	4.40E-06	-1	10	2.69E-06	-1	0.088688	-1	3.27E-06	-1	9	5.84E-06	null	4	null	DENND3
NM_005204	32	2.74E-06	-1	9	4.57E-06	-1	8	2.74E-06	null	null	null	null	null	11	null	null	4	null	MAP3K8
NM_001024	32	2.8E-06	1	9	5.04E-06	1	9	2.80E-06	null	null	null	null	1	10	0.095364	null	4	null	
NM_003693	32	2.83E-06	-1	9	3.84E-06	-1	9	2.83E-06	null	null	null	null	-1	10	0.040014	null	4	null	SCARF1
NM_006120	32	2.85E-06	-1	10	0.053762	null	11	null	null	null	-1	2.85E-06	-1	7	4.9E-06	null	4	null	HLA-DMA
NM_002725	32	2.93E-06	-1	9	0.032293	-1	8	2.93E-06	null	null	null	null	null	11	null	null	4	null	PRELP
NM_006801	32	2.94E-06	null	11	null	1	6	2.94E-06	null	null	null	null	null	11	null	null	4	null	KDELR1
NM_052851	32	2.96E-06	-1	9	5.15E-06	-1	9	2.96E-06	null	null	-1	3.63E-06	-1	10	0.028957	null	4	null	STARD13
NM_001081	32	2.97E-06	1	9	1.49E-05	1	10	2.97E-06	null	null	null	null	1	9	5.43E-06	null	4	null	PRKDC

NM_014254	32	2.97E-06	1	7	6.92E-06	1	10	2.97E-06	null	null	null	null	null	11	null	null	4	null	TMEM5
NM_000901	32	2.98E-06	-1	9	0.05118	null	11	null	null	null	-1	2.98E-06	-1	8	0.014629	null	4	null	NR3C2
NM_015472	32	3.02E-06	-1	9	5.21E-06	-1	9	3.02E-06	null	null	null	null	-1	10	0.032403	null	4	null	WWTR1
NM_004052	32	3.08E-06	null	11	null	1	7	3.08E-06	null	null	null	null	1	10	0.073023	null	4	null	BNIP3
NM_000929	32	3.19E-06	null	11	null	-1	7	3.19E-06	null	null	null	null	-1	10	0.091482	null	4	null	PLA2G5
NM_003045	32	3.56E-06	1	8	5.68E-06	null	11	null	null	null	1	3.56E-06	1	9	0.06649	null	4	null	SLC7A1
NM_004683	32	3.59E-06	null	11	null	null	11	null	null	null	null	null	-1	7	3.59E-06	-1	3	0.097687	RGN
NM_001039	32	3.63E-06	null	11	null	-1	9	3.63E-06	null	null	null	null	-1	8	0.000342	null	4	null	EFEMP1
NM_004964	32	3.63E-06	1	9	0.042022	1	8	3.63E-06	null	null	null	null	null	11	null	null	4	null	HDAC1
NM_000900	32	3.87E-06	null	11	null	-1	7	3.87E-06	null	null	null	null	-1	10	0.06317	null	4	null	MGP
NM_005009	32	3.88E-06	1	10	0.084537	1	9	3.88E-06	null	null	1	5.68E-06	1	9	0.047768	null	4	null	NME4
NM_015035	32	4E-06	-1	9	7.16E-06	-1	9	4.00E-06	null	null	-1	4.81E-06	-1	10	0.065443	null	4	null	ZHX3
NM_003633	32	4.02E-06	1	10	0.070949	1	7	4.02E-06	null	null	null	null	null	11	null	null	4	null	ENC1
NM_024551	32	4.1E-06	-1	9	7.35E-06	-1	10	4.10E-06	null	null	-1	4.96E-06	-1	9	9.46E-06	null	4	null	ADIPOR2
NM_002001	32	4.16E-06	-1	9	4.16E-06	null	11	null	null	null	null	null	-1	9	1.43E-05	-1	3	0.022433	FCER1A
NM_005232	32	4.27E-06	1	6	4.27E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	EPHA1
NM_005953	32	4.29E-06	-1	7	4.29E-06	-1	10	0.07712	null	null	null	null	null	11	null	null	4	null	MT2A
NM_144998	32	4.42E-06	1	7	6.48E-06	1	10	4.42E-06	null	null	null	null	null	11	null	null	4	null	STRA13
NM_002452	32	4.55E-06	null	11	null	1	10	4.55E-06	null	null	null	null	1	7	6.64E-06	null	4	null	NUDT1
NM_001681	32	4.6E-06	null	11	null	1	8	1.49E-05	null	null	1	4.60E-06	1	9	0.043779	null	4	null	ATP2A2
NM_002003	32	5.45E-06	-1	9	5.45E-06	-1	10	0.042504	null	null	null	null	-1	9	8.32E-05	null	4	null	FCN1
NM_001255	32	5.72E-06	null	11	null	1	7	5.72E-06	null	null	null	null	1	10	0.049655	null	4	null	CDC20
NM_001130	32	5.76E-06	null	11	null	-1	10	0.052952	null	null	null	null	-1	7	5.76E-06	null	4	null	AES
NM_001040	32	5.78E-06	-1	9	7.57E-06	-1	9	5.78E-06	null	null	null	null	-1	10	0.039072	null	4	null	CD68
NM_012474	32	6.11E-06	null	11	null	1	10	6.11E-06	null	null	null	null	1	8	1.17E-05	1	3	0.086483	UCK2
NM_001177	32	6.24E-06	null	11	null	1	8	6.24E-06	null	null	1	8.23E-06	1	9	0.034623	null	4	null	ARL1
NM_005030	32	6.25E-06	1	10	0.081048	1	8	6.25E-06	null	null	null	null	1	10	0.077852	null	4	null	PLK1
NM_001253	32	6.33E-06	1	10	8.54E-06	null	11	null	null	null	null	null	1	7	6.33E-06	null	4	null	CDC5L
NM_002822	32	6.33E-06	1	10	1.82E-05	1	10	6.33E-06	null	null	1	8.32E-06	1	8	2.74E-05	null	4	null	TWF1
NM_021144	32	6.33E-06	null	11	null	-1	7	6.33E-06	null	null	null	null	null	11	null	-1	3	0.079473	PSIP1
NM_000177	32	6.65E-06	-1	9	6.65E-06	-1	9	9.46E-06	null	null	-1	1.02E-05	-1	10	0.067728	null	4	null	GSN
NM_024650	32	6.98E-06	1	9	1.47E-05	1	10	6.98E-06	null	null	1	8.76E-06	1	9	3.17E-05	null	4	null	C11orf80
NM_004378	32	7.47E-06	null	11	null	1	6	7.47E-06	null	null	null	null	null	11	null	null	4	null	CRABP1
NM_012333	32	7.56E-06	1	9	8.94E-05	1	10	7.56E-06	null	null	null	null	1	9	9.96E-06	null	4	null	MYCBP
NM_001001	32	7.68E-06	1	9	0.055084	null	11	null	null	null	null	null	1	8	7.68E-06	null	4	null	RUNX1
NM_004390	32	7.84E-06	-1	9	0.04986	null	11	null	null	null	-1	7.84E-06	-1	8	0.018261	null	4	null	CTSH
NM_003491	32	8.15E-06	null	11	null	1	10	0.068916	null	null	null	null	1	7	8.15E-06	null	4	null	ARD1A
NM_002526	32	8.49E-06	null	11	null	1	6	8.49E-06	null	null	null	null	null	11	null	null	4	null	NT5E
NM_000393	32	9.05E-06	null	11	null	1	10	1.27E-05	null	null	1	9.05E-06	1	7	0.018277	null	4	null	COL5A2
NM_002599	32	9.35E-06	-1	9	1.72E-05	-1	10	9.35E-06	null	null	null	null	-1	10	0.040145	-1	3	0.077487	PDE2A
NM_014613	32	9.8E-06	1	7	2.29E-05	1	10	9.8E-06	null	null	1	1.23E-05	null	11	null	null	4	null	UBXD8
NM_006868	32	1.04E-05	-1	10	0.081515	-1	7	1.04E-05	null	null	null	null	null	11	null	null	4	null	RAB31
NM_005195	32	1.11E-05	-1	9	1.11E-05	-1	10	0.048668	null	null	-1	1.72E-05	-1	10	0.074766	-1	3	0.062751	CEBPD
NM_002229	32	1.16E-05	null	11	null	-1	6	1.16E-05	null	null	null	null	null	11	null	null	4	null	JUNB
NM_004946	32	1.19E-05	-1	10	0.067858	-1	7	1.19E-05	null	null	-1	1.25E-05	null	11	null	null	4	null	DOCK2
NM_006472	32	1.21E-05	-1	9	0.043407	-1	8	1.21E-05	null	null	-1	1.29E-05	null	11	null	null	4	null	TXNIP
NM_015009	32	1.35E-05	-1	9	2.17E-05	-1	9	1.35E-05	null	null	null	null	-1	10	0.068564	null	4	null	PDZRN3

NM_001025	32	1.37E-05	null	11	null	-1	10	0.04704	null	null	null	null	-1	9	1.37E-05	-1	2	0.01214	CES1
NM_005542	32	1.52E-05	-1	9	2.57E-05	-1	9	1.52E-05	null	null	null	null	-1	10	0.07268	null	4	null	INSIG1
NM_001048	32	1.63E-05	1	9	1.99E-05	1	10	1.90E-05	null	null	null	null	1	9	1.63E-05	null	4	null	RCC1
NM_003916	32	1.79E-05	-1	9	3.17E-05	-1	9	1.83E-05	null	null	-1	1.79E-05	-1	10	0.0337	null	4	null	AP1S2
NM_002028	32	2.55E-05	1	9	2.55E-05	null	11	null	null	null	null	null	1	8	0.0446	null	4	null	FNTB
NM_001572	32	2.83E-05	1	8	2.83E-05	null	11	null	null	null	null	null	1	9	0.06814	null	4	null	IRF7
NM_017514	32	3.25E-05	1	9	3.25E-05	1	9	0.026559	null	null	null	null	null	11	null	1	3	0.087198	PLXNA3
NM_014669	32	3.84E-05	1	10	0.082991	null	11	null	null	null	null	null	1	7	3.84E-05	null	4	null	NUP93
NM_007357	32	5.27E-05	1	8	0.000114	1	9	5.27E-05	null	null	null	null	null	11	null	null	4	null	COG2
NM_001116	32	7.48E-05	-1	9	0.000137	-1	9	8.23E-05	null	null	-1	7.48E-05	-1	10	0.047612	null	4	null	ADCY9
NM_002845	32	9.98E-05	-1	9	9.98E-05	-1	9	0.000274	null	null	-1	0.000412	null	11	null	-1	3	0.008636	PTPRM
NM_016441	32	0.000103	-1	9	0.000206	-1	9	0.000118	-1	0.092416	-1	0.000103	-1	10	0.033341	null	4	null	CRIM1
NM_005990	32	0.000206	-1	9	0.000274	-1	9	0.000206	null	null	-1	0.000206	-1	10	0.032484	null	4	null	STK10
NM_006243	32	0.012554	-1	8	0.039521	null	11	null	null	null	null	null	-1	10	0.094744	-1	3	0.012554	PPP2R5A
NM_006633	32	0.01464	null	11	null	null	11	null	null	null	null	null	-1	6	0.01464	null	4	null	IQGAP2
NM_006364	32	0.016124	null	11	null	null	11	null	null	null	null	null	1	6	0.016124	null	4	null	SEC23A
NM_021107	32	0.024955	1	9	0.024955	1	10	0.025987	null	null	null	null	1	9	0.069074	null	4	null	MRPS12
NM_018999	32	0.029672	-1	8	0.029672	-1	9	0.071486	null	null	null	null	null	11	null	null	4	null	KIAA1128
NM_005384	32	0.053799	-1	8	0.053799	-1	9	0.065976	null	null	null	null	null	11	null	null	4	null	NFIL3
NM_003206	33	1.67E-06	-1	10	2.63E-06	-1	10	1.67E-06	-1	3.05E-05	-1	2.04E-06	-1	10	3.46E-06	-1	3	0.079352	TCF21
NM_005358	33	1.7E-06	-1	10	0.051269	-1	9	1.70E-06	null	null	-1	2.07E-06	-1	10	0.041581	null	4	null	LMO7
NM_001003	33	1.72E-06	null	11	null	-1	7	1.72E-06	null	null	-1	2.11E-06	null	11	null	null	4	null	TARP
NM_001017	33	1.82E-06	1	10	1.06E-05	1	10	1.82E-06	null	null	null	null	1	9	8.95E-06	null	4	null	PRR5
NM_000789	33	1.83E-06	-1	10	2.84E-06	-1	10	1.83E-06	null	null	-1	2.26E-06	-1	10	3.90E-06	-1	3	0.097194	ACE
NM_007351	33	1.83E-06	-1	10	0.027433	-1	9	1.83E-06	null	null	null	null	-1	10	0.047601	null	4	null	MMRN1
NM_014686	33	1.92E-06	null	11	null	-1	9	1.92E-06	null	null	null	null	-1	9	4.06E-06	null	4	null	KIAA0355
NM_001008	33	1.97E-06	-1	9	3.12E-06	-1	9	1.97E-06	null	null	-1	2.43E-06	null	11	null	null	4	null	
NM_005859	33	1.99E-06	null	11	null	null	11	null	null	null	-1	1.99E-06	-1	7	3.35E-06	null	4	null	PURA
NM_015261	33	2.02E-06	1	10	0.0695	1	10	2.02E-06	null	null	null	null	1	9	0.041268	null	4	null	NCAPD3
NM_001032	33	2.06E-06	1	9	4.9E-06	1	9	2.06E-06	null	null	1	3.09E-06	null	11	null	null	4	null	TFAP2A
NM_000450	33	2.08E-06	null	11	null	-1	7	2.08E-06	null	null	null	null	null	11	null	null	4	null	SELL
NM_003019	33	2.08E-06	-1	9	2.67E-06	null	11	null	null	null	-1	2.08E-06	-1	10	0.084133	-1	3	0.087402	SFTPD
NM_015140	33	2.09E-06	null	11	null	1	10	2.09E-06	null	null	1	3.13E-06	1	9	0.044972	1	3	0.082953	TTLL12
NM_001005	33	2.15E-06	null	11	null	-1	10	0.056097	null	null	-1	2.15E-06	-1	9	3.68E-06	-1	3	0.082613	CACNA2D2
NM_005443	33	2.2E-06	null	11	null	-1	9	2.20E-06	null	null	null	null	-1	9	4.60E-06	null	4	null	PAPSS1
NM_003094	33	2.25E-06	1	10	5.35E-06	1	10	2.25E-06	null	null	1	3.33E-06	1	9	0.089092	null	4	null	SNRPE
NM_020379	33	2.29E-06	-1	10	0.049481	-1	9	2.29E-06	null	null	null	null	-1	10	0.039839	null	4	null	MAN1C1
NM_015213	33	2.33E-06	-1	9	3.72E-06	-1	9	2.33E-06	null	null	null	null	null	11	null	null	4	null	RAB6IP1
NM_006946	33	2.39E-06	null	11	null	1	7	2.39E-06	null	null	1	3.61E-06	null	11	null	null	4	null	SPTBN2
NM_003877	33	2.43E-06	-1	9	3.94E-06	-1	9	2.43E-06	null	null	null	null	null	11	null	null	4	null	SOCS2
NM_012307	33	2.45E-06	-1	9	3.96E-06	-1	9	2.45E-06	null	null	null	null	null	11	null	null	4	null	EPB41L3
NM_001306	33	2.49E-06	1	9	5.88E-06	1	10	2.49E-06	null	null	1	3.72E-06	1	10	1.13E-05	null	4	null	CLDN3
NM_003056	33	2.5E-06	-1	9	8.46E-06	-1	9	2.50E-06	null	null	null	null	null	11	null	null	4	null	
NM_000376	33	2.53E-06	null	11	null	1	10	2.53E-06	null	null	1	3.78E-06	1	8	1.05E-05	null	4	null	VDR
NM_000350	33	2.6E-06	1	10	1.25E-05	1	9	2.60E-06	null	null	null	null	1	10	0.091884	null	4	null	ABCA4
NM_006005	33	2.67E-06	-1	9	4.36E-06	-1	9	2.67E-06	-1	0.0935	-1	3.24E-06	null	11	null	null	4	null	WFS1
NM_023009	33	2.68E-06	1	10	6.38E-06	1	10	2.68E-06	null	null	1	4.00E-06	1	10	1.21E-05	1	3	0.000206	MARCKSL1

NM_001423	33	2.7E-06	-1	9	2.70E-06	-1	9	3.15E-06	null	null	null	null	null	11	null	null	4	null	EMP1
NM_002496	33	2.7E-06	null	11	null	1	9	2.70E-06	null	null	1	4.02E-06	1	9	0.040425	null	4	null	NDUFS8
NM_021137	33	2.77E-06	-1	10	0.075378	-1	9	2.77E-06	-1	0.096639	-1	3.37E-06	-1	10	0.074885	null	4	null	TNFAIP1
NM_003124	33	2.79E-06	null	11	null	1	7	2.79E-06	null	null	null	null	null	11	null	null	4	null	SPR
NM_020755	33	2.83E-06	-1	10	0.034553	-1	9	2.83E-06	null	null	-1	3.47E-06	-1	10	0.022255	null	4	null	SERINC1
NM_006310	33	2.88E-06	null	11	null	1	9	2.88E-06	null	null	1	5.64E-06	1	9	1.68E-05	null	4	null	NPEPPS
NM_000631	33	2.95E-06	null	11	null	-1	7	2.95E-06	null	null	null	null	null	11	null	null	4	null	NCF4
NM_005393	33	2.98E-06	null	11	null	1	8	2.98E-06	null	null	1	4.47E-06	1	10	0.097788	null	4	null	PLXNB3
NM_005380	33	2.99E-06	null	11	null	-1	7	2.99E-06	null	null	null	null	null	11	null	null	4	null	NBL1
NM_000311	33	3.01E-06	-1	9	3.01E-06	-1	9	3.12E-06	null	null	null	null	null	11	null	null	4	null	PRNP
NM_001349	33	3.04E-06	null	11	null	1	10	3.04E-06	null	null	null	null	1	8	5.27E-05	null	4	null	DARS
NM_004244	33	3.04E-06	-1	7	3.04E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	CD163
NM_017526	33	3.06E-06	-1	9	3.06E-06	-1	9	3.74E-06	null	null	-1	4.43E-06	null	11	null	null	4	null	LEPR
NM_006329	33	3.08E-06	-1	10	5.31E-06	-1	10	3.08E-06	null	null	-1	3.74E-06	-1	10	6.69E-06	-1	3	0.085884	FBLN5
NM_001718	33	3.11E-06	null	11	null	-1	7	3.11E-06	null	null	null	null	null	11	null	null	4	null	BMP6
NM_004330	33	3.23E-06	-1	7	3.23E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	BNIP2
NM_001455	33	3.28E-06	null	11	null	-1	9	3.28E-06	null	null	-1	3.90E-06	-1	9	7.28E-06	null	4	null	FOXO3
NM_020215	33	3.37E-06	-1	10	5.84E-06	-1	10	3.37E-06	-1	0.098061	-1	4.02E-06	-1	10	7.55E-06	-1	3	0.095726	
NM_003583	33	3.42E-06	null	11	null	1	8	4.52E-06	null	null	1	3.42E-06	1	10	0.099519	null	4	null	DYRK2
NM_006815	33	3.46E-06	null	11	null	1	9	3.46E-06	null	null	1	4.93E-06	1	9	1.44E-05	null	4	null	TMED2
NM_014705	33	3.49E-06	-1	10	6.10E-06	-1	10	3.49E-06	null	null	-1	4.18E-06	-1	10	7.92E-06	-1	3	0.093251	DOCK4
NM_003407	33	3.5E-06	-1	10	0.043259	-1	9	3.50E-06	null	null	null	null	null	11	null	-1	3	0.022494	ZFP36
NM_080284	33	3.52E-06	-1	10	0.031509	-1	9	3.52E-06	null	null	-1	4.22E-06	-1	10	0.033974	null	4	null	ABCA6
NM_002048	33	3.59E-06	null	11	null	-1	7	3.59E-06	null	null	null	null	null	11	null	null	4	null	GAS1
NM_015201	33	3.64E-06	1	9	1.42E-05	1	10	0.062096	null	null	1	3.64E-06	1	10	0.066016	null	4	null	BOP1
NM_006984	33	3.71E-06	1	10	0.08866	1	8	3.71E-06	null	null	null	null	null	11	null	null	4	null	CLDN10
NM_006111	33	3.78E-06	-1	9	3.78E-06	-1	10	0.061644	null	null	null	null	-1	10	0.047283	null	4	null	MYO5B
NM_014629	33	3.86E-06	-1	9	6.69E-06	-1	9	3.86E-06	-1	0.094231	-1	4.55E-06	null	11	null	null	4	null	ARHGEF10
NM_005975	33	3.93E-06	null	11	null	1	7	3.93E-06	null	null	null	null	null	11	null	null	4	null	PTK6
NM_004596	33	4.2E-06	null	11	null	1	7	4.20E-06	null	null	null	null	null	11	null	null	4	null	SNRPA
NM_004574	33	4.31E-06	-1	10	0.081256	-1	9	4.31E-06	null	null	null	null	-1	10	0.041988	null	4	null	SEPT4
NM_006000	33	4.36E-06	null	11	null	1	10	4.36E-06	null	null	null	null	1	8	1.71E-05	null	4	null	TUBA4A
NM_000600	33	4.54E-06	-1	9	4.54E-06	-1	9	4.75E-06	null	null	null	null	null	11	null	null	4	null	IL6
NM_002927	33	4.55E-06	null	11	null	-1	9	4.55E-06	null	null	null	null	-1	9	1.02E-05	null	4	null	RGS13
NM_004127	33	4.56E-06	null	11	null	1	7	4.56E-06	null	null	null	null	null	11	null	null	4	null	GPS1
NM_003974	33	4.62E-06	-1	10	0.048497	-1	9	4.62E-06	null	null	null	null	-1	10	0.095072	null	4	null	DOK2
NM_005629	33	4.7E-06	1	8	7.28E-06	1	10	0.091577	null	null	1	4.7E-06	null	11	null	null	4	null	SLC6A8
NM_024989	33	4.9E-06	null	11	null	-1	9	4.9E-06	null	null	-1	5.76E-06	-1	9	1.08E-05	null	4	null	PGAP1
NM_007208	33	4.93E-06	null	11	null	1	9	4.93E-06	null	null	1	6.86E-06	1	9	2.11E-05	null	4	null	MRPL3
NM_000089	33	4.99E-06	null	11	null	null	11	null	null	null	1	4.99E-06	1	7	0.016685	null	4	null	COL1A2
NM_000395	33	5.05E-06	-1	10	0.067672	-1	8	5.05E-06	null	null	null	null	null	11	null	null	4	null	CSF2RB
NM_002882	33	5.17E-06	null	11	null	1	10	0.091671	null	null	null	null	1	9	5.17E-06	1	3	0.056464	RANBP1
NM_030794	33	5.24E-06	-1	10	0.083382	-1	9	5.24E-06	null	null	null	null	-1	10	0.056664	null	4	null	TDRD3
NM_004093	33	5.35E-06	-1	8	7.92E-06	null	11	null	null	null	-1	5.35E-06	-1	10	0.095196	null	4	null	EFNB2
NM_014232	33	5.45E-06	null	11	null	-1	8	5.45E-06	null	null	-1	6.05E-06	-1	10	0.07568	null	4	null	VAMP2
NM_005856	33	5.6E-06	-1	10	9.57E-06	-1	10	5.6E-06	-1	0.097577	-1	6.43E-06	-1	10	1.19E-05	-1	3	0.000412	RAMP3
NM_004481	33	6.01E-06	null	11	null	1	7	6.01E-06	null	null	null	null	null	11	null	null	4	null	GALNT2

NM_003944	33	6.1E-06	null	11	null	null	11	null	null	null	-1	6.10E-06	-1	9	0.051065	-1	2	0.022632	SELENBP1
NM_003321	33	6.19E-06	1	10	1.35E-05	1	10	6.19E-06	null	null	1	8.07E-06	1	9	2.57E-05	null	4	null	TUFM
NM_006931	33	6.33E-06	-1	7	6.33E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	SLC2A3
NM_000071	33	6.64E-06	1	9	1.04E-05	1	9	6.64E-06	null	null	null	null	null	11	null	null	4	null	CBS
NM_000229	33	6.75E-06	-1	10	1.13E-05	-1	10	6.75E-06	null	null	-1	7.55E-06	-1	9	1.47E-05	null	4	null	LCAT
NM_006002	33	6.75E-06	null	11	null	1	9	6.75E-06	null	null	null	null	1	9	0.065487	null	4	null	UCHL3
NM_012151	33	6.81E-06	null	11	null	1	10	6.81E-06	null	null	null	null	1	9	1.34E-05	1	3	0.062162	F8A1
NM_001008	33	7.04E-06	1	10	1.52E-05	1	10	7.04E-06	null	null	1	8.85E-06	1	9	3.29E-05	null	4	null	CCT3
NM_003665	33	7.48E-06	-1	10	1.33E-05	-1	10	7.48E-06	null	null	-1	8.49E-06	-1	10	1.68E-05	-1	3	0.091637	FCN3
NM_006393	33	7.69E-06	-1	9	1.37E-05	-1	9	7.69E-06	null	null	null	null	null	11	null	null	4	null	NEBL
NM_001005	33	7.84E-06	1	9	0.067345	1	9	7.84E-06	null	null	null	null	null	11	null	null	4	null	MTIF2
NM_001393	33	7.99E-06	-1	10	0.098519	-1	9	7.99E-06	null	null	null	null	-1	10	0.068232	null	4	null	ECM2
NM_005715	33	7.99E-06	-1	9	1.19E-05	-1	10	0.076574	null	null	-1	7.99E-06	-1	10	0.054631	null	4	null	UST
NM_001996	33	8.07E-06	-1	9	1.42E-05	-1	9	8.07E-06	null	null	null	null	null	11	null	null	4	null	FBLN1
NM_000024	33	8.23E-06	null	11	null	-1	9	8.23E-06	null	null	-1	8.95E-06	-1	10	1.83E-05	-1	3	0.029644	ADRB2
NM_020796	33	8.32E-06	-1	10	0.065756	-1	9	8.32E-06	null	null	null	null	-1	10	0.04501	null	4	null	SEMA6A
NM_001498	33	8.58E-06	null	11	null	1	10	8.58E-06	null	null	1	1.1E-05	1	9	0.041519	1	3	0.082372	GCLC
NM_002797	33	9.01E-06	null	11	null	1	9	9.01E-06	null	null	null	null	1	9	0.047365	null	4	null	PSMB5
NM_006834	33	9.27E-06	-1	7	9.27E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	RAB32
NM_005127	33	9.35E-06	-1	7	9.35E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	CLEC2B
NM_003131	33	9.6E-06	-1	9	9.60E-06	-1	9	0.059927	null	null	null	null	null	11	null	null	4	null	SRF
NM_001958	33	1.01E-05	1	10	3.16E-05	1	10	1.01E-05	null	null	null	null	1	9	2.15E-05	null	4	null	EEF1A2
NM_003039	33	1.1E-05	1	8	1.10E-05	null	11	null	null	null	null	null	1	10	0.09939	null	4	null	SLC2A5
NM_006813	33	1.17E-05	null	11	null	-1	7	1.17E-05	null	null	null	null	null	11	null	null	4	null	PNRC1
NM_002906	33	1.23E-05	-1	7	1.23E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	RDX
NM_007033	33	1.25E-05	null	11	null	1	9	1.25E-05	null	null	null	null	1	10	0.059492	1	3	0.089551	RER1
NM_001984	33	1.29E-05	null	11	null	-1	8	1.29E-05	null	null	null	null	null	11	null	-1	3	0.0476	ESD
NM_024574	33	1.31E-05	-1	10	0.034805	-1	10	0.086732	null	null	-1	1.31E-05	-1	9	2.57E-05	null	4	null	C4orf31
NM_016929	33	1.33E-05	-1	10	2.11E-05	-1	10	1.33E-05	-1	0.000118	-1	1.37E-05	-1	10	2.84E-05	-1	3	0.095311	CLIC5
NM_015143	33	1.42E-05	null	11	null	1	9	1.42E-05	null	null	1	1.91E-05	1	9	0.066373	null	4	null	METAP1
NM_002112	33	1.87E-05	null	11	null	-1	9	1.87E-05	null	null	-1	1.91E-05	-1	9	4.84E-05	null	4	null	HDC
NM_005805	33	1.96E-05	null	11	null	null	11	null	null	null	null	null	1	7	1.96E-05	null	4	null	PSMD14
NM_017510	33	1.99E-05	1	10	0.065713	null	11	null	null	null	null	null	1	8	1.99E-05	null	4	null	TMED9
NM_003319	33	2.11E-05	-1	9	3.74E-05	null	11	null	null	null	-1	2.11E-05	-1	10	0.075669	-1	3	0.032768	TTN
NM_003608	33	2.17E-05	-1	10	0.053256	-1	9	2.17E-05	null	null	null	null	-1	10	0.047715	null	4	null	GPR65
NM_001419	33	2.24E-05	null	11	null	null	11	null	null	null	null	null	1	7	2.24E-05	null	4	null	ELAVL1
NM_000247	33	2.29E-05	-1	10	0.051556	-1	8	2.29E-05	null	null	null	null	null	11	null	null	4	null	MICA
NM_001033	33	3E-05	1	9	5.67E-05	1	9	3.00E-05	null	null	null	null	null	11	null	null	4	null	NOL1
NM_001007	33	3.36E-05	null	11	null	-1	9	4.57E-05	null	null	-1	4.84E-05	-1	9	3.36E-05	null	4	null	ARHGAP25
NM_005754	33	3.36E-05	null	11	null	null	11	null	null	null	null	null	1	7	3.36E-05	null	4	null	G3BP1
NM_000316	33	3.43E-05	-1	8	3.43E-05	-1	10	0.0599	null	null	null	null	null	11	null	null	4	null	PTHR1
NM_003743	33	3.92E-05	null	11	null	-1	7	3.92E-05	null	null	null	null	null	11	null	null	4	null	NCOA1
NM_003090	33	7.29E-05	null	11	null	null	11	null	null	null	null	null	1	7	7.29E-05	null	4	null	SNRPA1
NM_004856	33	8.56E-05	null	11	null	1	10	0.047261	null	null	null	null	1	8	8.56E-05	null	4	null	KIF23
NM_005371	33	8.96E-05	1	10	0.097469	1	8	8.96E-05	null	null	null	null	null	11	null	null	4	null	METTL1
NM_015141	33	0.021343	null	11	null	null	11	null	null	null	null	null	-1	8	0.021343	-1	3	0.061239	GPD1L
NM_001554	33	0.021805	null	11	null	-1	7	0.021805	null	null	null	null	null	11	null	null	4	null	CYR61

NM_002061	33	0.026532	null	11	null	1	9	0.063957	null	null	null	null	1	9	0.026532	null	4	null	GCLM
NM_000478	33	0.030267	-1	9	0.075853	null	11	null	null	null	null	null	-1	9	0.030267	null	4	null	ALPL
NM_004730	33	0.03088	-1	9	0.03088	-1	9	0.049574	null	null	null	null	null	11	null	null	4	null	ETF1
NM_001005	33	0.035724	-1	9	0.035724	-1	10	0.054655	null	null	null	null	-1	10	0.062844	null	4	null	FPR2
NM_002838	33	0.038799	-1	10	0.098296	-1	8	0.038799	null	null	null	null	null	11	null	null	4	null	PTPRC
NM_000110	33	0.039506	-1	7	0.039506	null	11	null	null	null	null	null	null	11	null	null	4	null	DPYD
NM_006200	33	0.041905	-1	10	0.095011	-1	10	0.094788	null	null	null	null	-1	9	0.041905	null	4	null	PCSK5
NM_000869	33	0.044907	null	11	null	1	10	0.047318	null	null	null	null	1	9	0.044907	1	3	0.096025	HTR3A
NM_004050	33	0.044988	-1	9	0.044988	-1	9	0.060383	null	null	null	null	null	11	null	null	4	null	BCL2L2
NM_002122	33	0.047986	-1	10	0.063794	-1	8	0.047986	null	null	null	null	null	11	null	null	4	null	HLA-DQA1
NM_000574	33	0.048412	-1	8	0.048412	null	11	null	null	null	null	null	-1	10	0.093864	null	4	null	CD55
NM_001693	33	0.049001	-1	9	0.076812	-1	9	0.049001	null	null	null	null	null	11	null	null	4	null	ATP6V1B2
NM_006763	33	0.054143	null	11	null	-1	10	0.060048	null	null	null	null	-1	9	0.054143	-1	3	0.077753	BTG2
NM_014845	33	0.057884	null	11	null	-1	9	0.057884	null	null	null	null	-1	9	0.078447	null	4	null	FIG4
NM_000803	33	0.058921	null	11	null	-1	9	0.072509	null	null	null	null	-1	9	0.058921	null	4	null	FOLR2
NM_152280	33	0.059308	-1	9	0.059308	-1	9	0.066275	null	null	null	null	null	11	null	null	4	null	SYT11
NM_005848	33	0.059928	-1	9	0.096275	-1	9	0.059928	null	null	null	null	null	11	null	null	4	null	DENND4A
NM_001008	33	0.063502	-1	10	0.063502	-1	10	0.085887	null	null	null	null	-1	10	0.091205	-1	3	0.097548	EML1
NM_005768	34	1.65E-06	null	11	null	-1	10	1.65E-06	null	null	null	null	-1	9	3.37E-06	null	4	null	MBOAT5
NM_015079	34	1.66E-06	-1	10	2.61E-06	-1	10	1.66E-06	-1	0.081813	-1	2.02E-06	-1	10	3.40E-06	null	4	null	TBC1D2B
NM_001003	34	1.74E-06	-1	10	2.74E-06	-1	10	1.74E-06	-1	0.092299	-1	2.14E-06	-1	10	3.66E-06	null	4	null	BICD2
NM_145234	34	1.74E-06	-1	10	2.75E-06	-1	10	1.74E-06	null	null	-1	2.15E-06	-1	10	3.69E-06	null	4	null	CHRDL1
NM_005924	34	1.81E-06	null	11	null	-1	10	1.81E-06	null	null	null	null	-1	10	0.063722	-1	3	0.078989	MEOX2
NM_001770	34	1.83E-06	1	10	0.078462	1	9	1.83E-06	null	null	null	null	null	11	null	null	4	null	CD19
NM_001558	34	1.84E-06	null	11	null	-1	9	1.84E-06	null	null	null	null	-1	10	0.066101	null	4	null	IL10RA
NM_013372	34	1.86E-06	1	9	4.33E-06	1	10	1.86E-06	null	null	null	null	null	11	null	null	4	null	GREM1
NM_005085	34	1.87E-06	null	11	null	-1	8	1.87E-06	null	null	null	null	null	11	null	null	4	null	NUP214
NM_021117	34	1.88E-06	null	11	null	-1	9	1.88E-06	null	null	-1	2.32E-06	-1	10	0.044108	null	4	null	CRY2
NM_005956	34	1.91E-06	null	11	null	1	10	1.91E-06	null	null	1	2.87E-06	1	9	0.046477	null	4	null	MTHFD1
NM_015622	34	1.93E-06	1	9	4.52E-06	1	10	1.93E-06	null	null	null	null	null	11	null	null	4	null	C7orf28A
NM_022154	34	1.98E-06	-1	10	3.14E-06	-1	10	1.98E-06	null	null	-1	2.45E-06	null	11	null	-1	3	0.09317	SLC39A8
NM_000550	34	1.99E-06	null	11	null	-1	8	2.85E-06	null	null	-1	1.99E-06	null	11	null	null	4	null	TYRP1
NM_002653	34	2E-06	null	11	null	1	9	2.00E-06	null	null	1	2.99E-06	1	10	0.07817	null	4	null	PITX1
NM_021111	34	2E-06	-1	10	0.095685	-1	9	2.00E-06	null	null	null	null	null	11	null	null	4	null	RECK
NM_003634	34	2.02E-06	1	10	4.81E-06	1	10	2.02E-06	null	null	1	3.04E-06	1	10	9.8E-06	null	4	null	NIPSNAP1
NM_007259	34	2.04E-06	1	10	4.84E-06	1	9	2.04E-06	null	null	1	3.06E-06	null	11	null	null	4	null	VPS45
NM_004911	34	2.04E-06	1	10	4.87E-06	1	10	2.04E-06	null	null	1	3.07E-06	1	10	1.00E-05	null	4	null	PDIA4
NM_006510	34	2.07E-06	1	10	4.93E-06	1	10	2.07E-06	1	0.000103	1	3.11E-06	1	10	1.02E-05	null	4	null	TRIM27
NM_001431	34	2.12E-06	-1	9	3.36E-06	-1	10	2.12E-06	null	null	-1	2.60E-06	null	11	null	null	4	null	EPB41L2
NM_003600	34	2.13E-06	1	9	5.05E-06	1	10	2.13E-06	null	null	1	3.17E-06	null	11	null	null	4	null	AURKA
NM_003620	34	2.14E-06	-1	10	3.39E-06	-1	9	2.14E-06	null	null	-1	2.62E-06	null	11	null	null	4	null	PPM1D
NM_014292	34	2.17E-06	null	11	null	-1	10	2.17E-06	null	null	null	null	-1	9	4.52E-06	null	4	null	CBX6
NM_015169	34	2.17E-06	1	10	0.067538	1	10	2.17E-06	null	null	1	3.22E-06	1	10	0.044014	null	4	null	RRS1
NM_007191	34	2.18E-06	-1	10	0.093474	null	11	null	null	null	-1	2.18E-06	-1	10	0.03269	-1	3	0.091413	WIF1
NM_000687	34	2.21E-06	null	11	null	1	10	2.21E-06	null	null	null	null	1	9	0.083089	null	4	null	AHCY
NM_012323	34	2.23E-06	-1	10	0.063382	-1	9	2.23E-06	null	null	null	null	null	11	null	null	4	null	MAFF
NM_005567	34	2.26E-06	1	9	0.066191	1	10	2.26E-06	null	null	null	null	null	11	null	null	4	null	LGALS3BP

NM_002314	34	2.38E-06	null	11	null	1	8	2.38E-06	null	null	null	null	null	11	null	null	4	null	LIMK1
NM_014461	34	2.39E-06	-1	9	3.00E-06	null	11	null	null	null	-1	2.39E-06	-1	10	0.033278	null	4	null	CNTN6
NM_003373	34	2.41E-06	-1	10	0.060237	-1	9	2.41E-06	null	null	null	null	null	11	null	null	4	null	VCL
NM_004327	34	2.51E-06	null	11	null	1	8	2.51E-06	null	null	null	null	null	11	null	null	4	null	BCR
NM_000328	34	2.52E-06	null	11	null	-1	9	2.52E-06	null	null	null	null	-1	10	0.042834	null	4	null	RPGR
NM_001031	34	2.56E-06	1	10	6.01E-06	1	10	2.56E-06	null	null	1	3.85E-06	1	10	1.16E-05	null	4	null	BOLA2
NM_018224	34	2.62E-06	1	9	6.19E-06	1	10	2.62E-06	null	null	null	null	null	11	null	null	4	null	C7orf44
NM_004827	34	2.66E-06	-1	10	0.039347	-1	9	2.66E-06	null	null	-1	3.23E-06	null	11	null	null	4	null	ABCG2
NM_004877	34	2.7E-06	-1	10	4.43E-06	-1	10	2.70E-06	null	null	-1	3.28E-06	-1	10	5.88E-06	null	4	null	GMFG
NM_015464	34	2.73E-06	-1	10	3.55E-06	null	11	null	null	null	-1	2.73E-06	-1	10	4.68E-06	-1	3	0.094228	SOSTDC1
NM_001001	34	2.74E-06	null	11	null	-1	10	0.070961	null	null	-1	2.74E-06	null	11	null	-1	2	0.078213	ATP2B4
NM_002960	34	2.78E-06	-1	9	4.65E-06	-1	10	2.78E-06	null	null	null	null	null	11	null	null	4	null	S100A3
NM_001025	34	2.85E-06	1	9	1.63E-05	1	10	2.85E-06	null	null	null	null	null	11	null	null	4	null	ADAR
NM_002568	34	2.85E-06	null	11	null	1	10	2.85E-06	null	null	null	null	1	9	0.049528	null	4	null	PABPC1
NM_016322	34	2.85E-06	-1	10	4.9E-06	-1	10	2.85E-06	null	null	-1	3.52E-06	null	11	null	-1	3	0.095766	RAB14
NM_001018	34	2.86E-06	-1	10	4.93E-06	-1	10	2.86E-06	null	null	-1	3.53E-06	-1	10	6.28E-06	null	4	null	SH3BP5
NM_000895	34	2.9E-06	-1	9	0.061395	null	11	null	null	null	-1	2.90E-06	null	11	null	-1	3	0.059939	LTA4H
NM_003725	34	2.92E-06	-1	9	3.83E-06	null	11	null	-1	0.087402	-1	2.92E-06	-1	10	0.029641	null	4	null	HSD17B6
NM_080593	34	2.93E-06	1	10	6.86E-06	1	10	2.93E-06	null	null	1	4.36E-06	1	10	1.25E-05	null	4	null	HIST1H2BK
NM_006618	34	3.14E-06	1	9	9.78E-05	1	10	3.14E-06	null	null	null	null	null	11	null	null	4	null	JARID1B
NM_007268	34	3.23E-06	-1	10	5.56E-06	-1	10	3.23E-06	null	null	-1	3.85E-06	-1	10	7.10E-06	null	4	null	VSIG4
NM_012248	34	3.27E-06	null	11	null	1	10	3.27E-06	null	null	null	null	1	9	1.35E-05	null	4	null	SEPHS2
NM_177424	34	3.27E-06	-1	10	5.64E-06	-1	10	3.27E-06	-1	0.091375	-1	3.88E-06	-1	10	7.22E-06	null	4	null	STX12
NM_000047	34	3.28E-06	1	10	0.072163	1	9	3.28E-06	null	null	null	null	null	11	null	null	4	null	ARSE
NM_007183	34	3.29E-06	1	10	7.42E-06	1	10	3.29E-06	null	null	1	4.76E-06	1	10	1.37E-05	null	4	null	PKP3
NM_006283	34	3.4E-06	-1	10	5.97E-06	-1	10	3.40E-06	null	null	-1	4.10E-06	-1	10	7.62E-06	null	4	null	TACC1
NM_003122	34	3.4E-06	null	11	null	1	8	3.40E-06	null	null	null	null	null	11	null	null	4	null	SPINK1
NM_006819	34	3.44E-06	1	10	7.69E-06	1	9	3.44E-06	null	null	null	null	null	11	null	null	4	null	STIP1
NM_005982	34	3.47E-06	1	10	0.042494	1	9	3.47E-06	null	null	null	null	null	11	null	null	4	null	SIX1
NM_007021	34	3.47E-06	-1	10	0.043315	-1	9	3.47E-06	null	null	-1	4.16E-06	null	11	null	null	4	null	C10orf10
NM_001001	34	3.54E-06	null	11	null	-1	8	3.54E-06	null	null	null	null	null	11	null	null	4	null	TAGLN
NM_001641	34	3.58E-06	null	11	null	1	10	3.58E-06	null	null	null	null	1	9	0.077664	null	4	null	APEX1
NM_006136	34	3.59E-06	null	11	null	-1	9	3.59E-06	null	null	null	null	-1	10	5.48E-06	null	4	null	CAPZA2
NM_018993	34	3.68E-06	null	11	null	-1	8	3.68E-06	null	null	null	null	null	11	null	null	4	null	RIN2
NM_004469	34	3.72E-06	-1	10	6.48E-06	-1	10	3.72E-06	null	null	-1	4.40E-06	-1	10	8.49E-06	null	4	null	FIGF
NM_001736	34	3.79E-06	-1	10	4.80E-06	-1	10	3.79E-06	null	null	null	null	-1	10	4.64E-06	null	4	null	C5AR1
NM_014637	34	3.79E-06	null	11	null	1	10	3.79E-06	null	null	1	5.38E-06	1	9	0.046121	null	4	null	MTFR1
NM_018060	34	3.85E-06	1	10	8.58E-06	1	10	3.85E-06	null	null	1	5.56E-06	1	10	1.65E-05	null	4	null	IARS2
NM_001007	34	3.86E-06	1	9	8.67E-06	1	10	3.86E-06	null	null	1	5.6E-06	null	11	null	null	4	null	ALG8
NM_004442	34	3.86E-06	null	11	null	null	11	null	null	null	1	3.86E-06	1	9	0.080953	1	3	0.081581	EPHB2
NM_003257	34	3.87E-06	-1	8	3.87E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	TJP1
NM_207517	34	3.92E-06	-1	10	6.92E-06	-1	10	3.92E-06	-1	0.086863	-1	4.65E-06	null	11	null	-1	3	0.09727	ADAMTSL3
NM_003437	34	3.95E-06	null	11	null	-1	10	0.060701	null	null	null	null	-1	9	3.95E-06	null	4	null	ZNF136
NM_014330	34	4.04E-06	-1	10	7.28E-06	-1	10	4.04E-06	null	null	null	null	-1	10	9.35E-06	null	4	null	PPP1R15A
NM_000184	34	4.08E-06	-1	9	4.08E-06	-1	10	0.067301	null	null	null	null	null	11	null	null	4	null	HBG2
NM_001010	34	4.08E-06	null	11	null	-1	9	4.08E-06	null	null	-1	4.93E-06	-1	10	0.043674	null	4	null	ZYX
NM_014467	34	4.14E-06	1	10	9.25E-06	1	10	4.14E-06	null	null	1	6.01E-06	1	10	1.79E-05	null	4	null	SRPX2

NM_015654	34	4.16E-06	1	10	9.35E-06	1	10	4.16E-06	null	null	1	6.05E-06	1	10	1.83E-05	null	4	null	NAT9
NM_006277	34	4.2E-06	-1	8	4.20E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	ITSN2
NM_004811	34	4.22E-06	null	11	null	-1	9	4.22E-06	null	null	null	null	-1	10	0.092448	null	4	null	LPXN
NM_001079	34	4.27E-06	null	11	null	1	10	4.27E-06	null	null	null	null	1	9	7.91E-06	null	4	null	PAICS
NM_002399	34	4.4E-06	-1	10	0.081438	-1	9	4.40E-06	null	null	null	null	null	11	null	null	4	null	MEIS2
NM_002871	34	4.45E-06	null	11	null	1	8	4.45E-06	null	null	null	null	null	11	null	null	4	null	RABIF
NM_00103	34	4.57E-06	null	11	null	-1	10	0.094011	null	null	null	null	-1	9	4.57E-06	null	4	null	NLRP1
NM_001061	34	4.65E-06	null	11	null	-1	8	4.65E-06	null	null	null	null	null	11	null	null	4	null	TBXAS1
NM_02040	34	4.68E-06	null	11	null	-1	9	4.68E-06	null	null	-1	5.49E-06	-1	10	0.036795	null	4	null	PCDH9
NM_001154	34	4.75E-06	-1	9	4.75E-06	-1	10	0.059433	null	null	null	null	null	11	null	null	4	null	ANXA5
NM_006729	34	4.84E-06	-1	10	7.22E-06	null	11	null	null	null	-1	4.84E-06	-1	10	9.25E-06	-1	3	0.096447	DIAPH2
NM_003636	34	4.87E-06	null	11	null	-1	8	4.87E-06	null	null	null	null	null	11	null	null	4	null	KCNAB2
NM_004638	34	4.87E-06	1	9	5.54E-05	1	10	3.33E-05	null	null	1	4.87E-06	null	11	null	null	4	null	
NM_033416	34	4.9E-06	1	9	1.06E-05	1	10	4.9E-06	null	null	1	6.80E-06	null	11	null	null	4	null	IMP4
NM_003139	34	4.98E-06	null	11	null	1	9	4.98E-06	null	null	null	null	1	10	0.077505	null	4	null	SRPR
NM_001704	34	5.08E-06	-1	10	0.051749	-1	9	5.08E-06	null	null	null	null	null	11	null	null	4	null	BAI3
NM_004990	34	5.31E-06	null	11	null	1	10	0.070851	null	null	1	5.31E-06	1	9	1.55E-05	null	4	null	MARS
NM_00103	34	5.42E-06	1	8	8.4E-06	null	11	null	null	null	1	5.42E-06	null	11	null	null	4	null	TRAF5
NM_001015	34	5.42E-06	null	11	null	1	8	5.42E-06	null	null	null	null	null	11	null	null	4	null	MPG
NM_001761	34	5.48E-06	1	10	5.48E-06	1	9	0.064254	null	null	null	null	null	11	null	null	4	null	CCNF
NM_024536	34	5.49E-06	1	10	1.16E-05	1	10	5.49E-06	null	null	null	null	1	10	2.35E-05	null	4	null	CHPF
NM_015530	34	5.52E-06	1	10	1.18E-05	1	10	5.52E-06	null	null	1	7.35E-06	1	10	2.42E-05	null	4	null	GORASP2
NM_001040	34	5.54E-06	null	11	null	-1	9	5.54E-06	null	null	null	null	-1	10	0.021389	null	4	null	CD83
NM_005475	34	5.68E-06	-1	10	9.8E-06	-1	10	5.68E-06	null	null	-1	6.53E-06	-1	10	1.23E-05	null	4	null	SH2B3
NM_000802	34	5.84E-06	null	11	null	null	11	null	null	null	-1	5.84E-06	-1	9	0.0355	-1	3	0.049886	FOLR1
NM_152295	34	5.88E-06	null	11	null	null	11	null	null	null	1	5.88E-06	1	8	0.044569	null	4	null	TARS
NM_003027	34	5.97E-06	null	11	null	-1	8	5.97E-06	null	null	null	null	null	11	null	null	4	null	SH3GL3
NM_002166	34	6.14E-06	-1	10	1.06E-05	-1	10	6.14E-06	null	null	null	null	-1	10	1.35E-05	null	4	null	ID2
NM_001031	34	6.19E-06	null	11	null	-1	8	0.083928	null	null	-1	6.19E-06	null	11	null	null	4	null	RUNX3
NM_014251	34	6.28E-06	null	11	null	1	10	6.28E-06	null	null	null	null	1	10	0.080553	1	3	0.06384	SLC25A13
NM_001015	34	6.32E-06	1	10	8.60E-06	1	9	6.32E-06	null	null	null	null	null	11	null	null	4	null	LLGL2
NM_031412	34	6.43E-06	null	11	null	-1	9	6.43E-06	null	null	-1	7.16E-06	-1	10	0.099339	null	4	null	GABARAPL1
NM_018151	34	6.56E-06	null	11	null	1	9	6.56E-06	null	null	null	null	1	10	0.066134	null	4	null	RIF1
NM_001018	34	6.64E-06	null	11	null	-1	10	6.64E-06	null	null	null	null	-1	9	1.44E-05	null	4	null	SORBS3
NM_002070	34	6.69E-06	null	11	null	-1	9	6.69E-06	null	null	-1	7.48E-06	-1	10	0.018703	null	4	null	GNAI2
NM_013301	34	6.74E-06	1	9	9.24E-06	1	10	6.74E-06	null	null	null	null	null	11	null	null	4	null	CCDC106
NM_001980	34	6.75E-06	-1	9	6.75E-06	-1	10	0.045134	null	null	null	null	null	11	null	null	4	null	STX2
NM_001071	34	6.78E-06	null	11	null	1	9	6.78E-06	null	null	null	null	1	10	0.099332	null	4	null	TYMS
NM_002473	34	7.23E-06	null	11	null	-1	8	7.23E-06	null	null	null	null	null	11	null	null	4	null	MYH9
NM_018840	34	7.27E-06	1	10	2.24E-05	1	10	7.27E-06	null	null	null	null	1	10	1.45E-05	null	4	null	C20orf24
NM_020143	34	7.35E-06	null	11	null	1	8	7.35E-06	null	null	null	null	null	11	null	null	4	null	PNO1
NM_003712	34	7.69E-06	1	10	1.65E-05	1	10	7.69E-06	null	null	1	9.92E-06	1	10	3.74E-05	null	4	null	PPAP2C
NM_005850	34	7.77E-06	1	9	1.68E-05	1	10	7.77E-06	null	null	1	1.00E-05	null	11	null	null	4	null	SF3B4
XM_166132	34	7.92E-06	-1	10	1.40E-05	-1	10	7.92E-06	-1	0.090339	-1	8.76E-06	-1	10	1.79E-05	null	4	null	
NM_005834	34	8.23E-06	1	9	1.79E-05	1	10	8.23E-06	null	null	null	null	null	11	null	null	4	null	TIMM17B
NM_005040	34	8.32E-06	-1	10	0.067799	-1	9	8.32E-06	null	null	null	null	null	11	null	null	4	null	PRCP
NM_005915	34	8.49E-06	null	11	null	null	11	null	null	null	1	8.49E-06	1	8	0.044304	null	4	null	MCM6

NM_004766	34	9.05E-06	1	10	2.06E-05	1	9	9.05E-06	null	null	1	1.13E-05	null	11	null	null	4	null	COPB2
NM_015361	34	9.44E-06	null	11	null	null	11	null	null	null	null	null	1	8	9.44E-06	null	4	null	R3HDM1
NM_014255	34	9.57E-06	1	10	2.17E-05	1	10	9.57E-06	null	null	1	1.21E-05	1	10	4.84E-05	null	4	null	CNPY2
NM_006403	34	9.78E-06	null	11	null	null	11	null	null	null	-1	1.21E-05	-1	9	9.78E-06	-1	3	0.085213	NEDD9
NM_002891	34	1E-05	-1	9	0.048818	null	11	null	null	null	-1	1.00E-05	-1	10	0.077608	null	4	null	RASGRF1
NM_005564	34	1.04E-05	1	8	1.04E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	LCN2
NM_000421	34	1.04E-05	null	11	null	1	9	1.04E-05	null	null	null	null	1	10	0.080942	null	4	null	KRT10
NM_138444	34	1.06E-05	-1	10	1.83E-05	-1	10	1.06E-05	null	null	-1	1.13E-05	-1	10	2.29E-05	null	4	null	KCTD12
NM_003626	34	1.16E-05	1	10	1.16E-05	null	11	null	null	null	null	null	1	9	0.071097	null	4	null	PPFIA1
NM_017896	34	1.25E-05	1	10	2.98E-05	1	10	1.25E-05	null	null	null	null	1	10	2.45E-05	null	4	null	C20orf11
NM_030806	34	1.27E-05	-1	10	0.059982	-1	10	0.060383	null	null	-1	1.27E-05	-1	10	0.030265	null	4	null	C1orf21
NM_002624	34	1.28E-05	-1	8	1.28E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	PFDN5
NM_001467	34	1.29E-05	1	10	3.65E-05	1	10	1.29E-05	null	null	1	1.58E-05	1	10	6.33E-05	null	4	null	SLC37A4
NM_001781	34	1.31E-05	-1	10	0.071645	-1	9	1.31E-05	null	null	null	null	null	11	null	null	4	null	CD69
NM_000014	34	1.31E-05	-1	10	1.68E-05	-1	10	1.31E-05	null	null	null	null	-1	10	1.34E-05	null	4	null	A2M
NM_006230	34	1.38E-05	null	11	null	1	8	1.38E-05	null	null	null	null	null	11	null	null	4	null	POLD2
NM_006234	34	1.46E-05	1	9	2.22E-05	1	10	1.46E-05	null	null	null	null	null	11	null	null	4	null	POLR2J
NM_007363	34	1.46E-05	null	11	null	null	11	null	null	null	null	null	1	8	1.46E-05	null	4	null	NONO
NM_001031	34	1.5E-05	-1	10	2.49E-05	-1	10	1.50E-05	null	null	-1	1.52E-05	-1	10	3.29E-05	null	4	null	C10orf72
NM_007286	34	1.58E-05	-1	10	2.66E-05	-1	10	1.58E-05	null	null	-1	1.58E-05	-1	10	3.58E-05	null	4	null	SYNPO
NM_001010	34	1.61E-05	-1	8	1.61E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	RAP1A
NM_012090	34	1.65E-05	-1	10	2.84E-05	-1	10	1.68E-05	-1	0.098865	-1	1.65E-05	-1	10	4.12E-05	null	4	null	MACF1
NM_002821	34	1.76E-05	1	8	1.76E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	PTK7
NM_000413	34	1.78E-05	1	10	3.12E-05	1	9	1.78E-05	null	null	null	null	null	11	null	null	4	null	HSD17B1
NM_004735	34	1.87E-05	-1	9	3.29E-05	null	11	null	null	null	-1	1.87E-05	-1	10	0.037644	null	4	null	LRRFIP1
NM_007235	34	1.87E-05	1	9	6.38E-05	1	10	1.87E-05	null	null	1	2.49E-05	null	11	null	null	4	null	XPOT
NM_001080	34	2E-05	1	9	4.47E-05	1	10	2E-05	null	null	null	null	null	11	null	null	4	null	ALDH5A1
NM_006335	34	2.17E-05	null	11	null	1	8	2.17E-05	null	null	null	null	null	11	null	null	4	null	TIMM17A
NM_006442	34	2.21E-05	null	11	null	null	11	null	null	null	null	null	1	8	2.21E-05	null	4	null	DRAP1
NM_000129	34	2.27E-05	-1	10	0.07081	-1	9	2.27E-05	null	null	null	null	null	11	null	null	4	null	F13A1
NM_000274	34	2.66E-05	null	11	null	null	11	null	null	null	null	null	1	8	2.66E-05	null	4	null	OAT
NM_001001	34	2.75E-05	null	11	null	1	8	2.75E-05	null	null	null	null	null	11	null	null	4	null	RORC
NM_005100	34	2.94E-05	-1	8	2.94E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	AKAP12
NM_021063	34	3.05E-05	1	9	5.49E-05	1	10	3.05E-05	null	null	1	4.84E-05	null	11	null	null	4	null	HIST1H2BD
NM_000535	34	3.17E-05	1	9	5.88E-05	1	10	3.17E-05	null	null	null	null	null	11	null	null	4	null	PMS2
NM_000961	34	3.17E-05	null	11	null	-1	8	3.17E-05	null	null	null	null	null	11	null	null	4	null	PTGIS
NM_004815	34	3.29E-05	-1	9	5.49E-05	-1	10	3.29E-05	null	null	-1	3.29E-05	null	11	null	null	4	null	ARHGAP29
NM_030920	34	3.92E-05	1	9	6.33E-05	1	10	3.92E-05	null	null	null	null	null	11	null	null	4	null	ANP32E
NM_004443	34	4.25E-05	null	11	null	1	9	4.25E-05	null	null	null	null	1	10	0.000128	null	4	null	EPHB3
NM_006712	34	4.25E-05	1	9	4.25E-05	1	10	0.075328	null	null	null	null	null	11	null	null	4	null	FASTK
NM_015621	34	4.33E-05	-1	10	0.049144	-1	9	4.33E-05	null	null	null	null	null	11	null	null	4	null	CCDC69
NM_005483	34	4.47E-05	null	11	null	null	11	null	null	null	null	null	1	8	4.47E-05	null	4	null	CHAF1A
NM_012286	34	4.57E-05	null	11	null	null	11	null	null	null	null	null	1	8	4.57E-05	null	4	null	MORF4L2
NM_001039	34	5.38E-05	-1	9	7.68E-05	-1	10	5.38E-05	null	null	null	null	null	11	null	null	4	null	SEC14L1
NM_003569	34	5.49E-05	-1	10	0.068445	-1	9	5.49E-05	null	null	null	null	null	11	null	null	4	null	STX7
NM_015170	34	6.33E-05	1	10	9.15E-05	1	10	6.33E-05	null	null	1	0.000137	1	10	0.000412	null	4	null	SULF1
NM_015319	34	8.23E-05	-1	10	0.000165	-1	10	0.000103	null	null	-1	8.23E-05	-1	10	0.096597	null	4	null	TENC1

NM_00178	34	0.000128	1	8	0.000128	null	11	null	null	null	null	null	null	11	null	null	4	null	CD79A
NM_00565	34	0.000137	null	11	null	-1	9	0.000165	null	null	-1	0.000137	-1	10	0.088116	null	4	null	NR2F1
NM_00652	34	0.000274	1	10	0.071266	1	10	0.000274	null	null	null	null	1	10	0.077243	null	4	null	ZNF217
NM_00100	34	0.000412	-1	10	0.000412	-1	10	0.000412	null	null	null	null	-1	10	0.000412	null	4	null	MRC1L1
NM_00439	34	0.022878	-1	10	0.08939	-1	10	0.072963	null	null	null	null	-1	10	0.022878	null	4	null	DACH1
NM_01684	34	0.031584	null	11	null	null	11	null	null	null	null	null	-1	8	0.031584	null	4	null	SHC3
NM_00527	34	0.032551	-1	10	0.050271	-1	10	0.050949	null	null	null	null	-1	10	0.032551	null	4	null	GPD1
NM_00039	34	0.035292	null	11	null	-1	8	0.035292	null	null	null	null	null	11	null	null	4	null	EGR2
NM_00030	34	0.039221	null	11	null	null	11	null	null	null	null	null	1	8	0.039221	null	4	null	PLOD1
NM_00616	34	0.041366	-1	8	0.041366	null	11	null	null	null	null	null	null	11	null	null	4	null	NFE2L2
NM_00166	34	0.041457	-1	9	0.041457	null	11	null	null	null	null	null	-1	10	0.055035	null	4	null	RHOA
NM_01838	34	0.042058	-1	10	0.076818	-1	10	0.0839	null	null	null	null	-1	10	0.042058	null	4	null	GIMAP5
NM_01421	34	0.042316	null	11	null	null	11	null	null	null	null	null	-1	8	0.042316	null	4	null	ITPK1
NM_000851	34	0.04395	null	11	null	-1	10	0.082524	null	null	null	null	-1	9	0.04395	null	4	null	GSTM5
NM_00326	34	0.04804	null	11	null	null	11	null	null	null	null	null	-1	9	0.04804	-1	3	0.084311	TLE2
NM_00293	34	0.04817	-1	10	0.095655	-1	9	0.04817	null	null	null	null	null	11	null	null	4	null	RNH1
NM_17801	34	0.049211	null	11	null	null	11	null	null	null	null	null	1	8	0.049211	null	4	null	TUBB
NM_00006	34	0.049673	null	11	null	-1	8	0.049673	null	null	null	null	null	11	null	null	4	null	C2
NM_00192	34	0.053067	-1	10	0.075475	-1	10	0.053067	null	null	null	null	null	11	null	-1	3	0.062997	DES
NM_00673	34	0.053275	null	11	null	1	10	0.093395	null	null	null	null	1	9	0.053275	null	4	null	MCM5
NM_00171	34	0.054412	1	9	0.054412	1	10	0.09887	null	null	null	null	null	11	null	null	4	null	CFB
NM_00100	34	0.056028	-1	9	0.056028	-1	10	0.076726	-1	0.097262	null	null	null	11	null	null	4	null	PPP2CB
NM_00355	34	0.056366	1	9	0.056366	null	11	null	null	null	null	null	1	10	0.087662	null	4	null	PIP5K1A
NM_00102	34	0.058687	null	11	null	null	11	null	null	null	null	null	-1	8	0.058687	null	4	null	CUGBP2
NM_00407	34	0.059746	null	11	null	-1	8	0.059746	null	null	null	null	null	11	null	null	4	null	CTSS
NM_00240	34	0.060108	-1	10	0.086019	-1	10	0.060108	null	null	null	null	-1	10	0.088722	null	4	null	MGAT1
NM_00227	34	0.06238	null	11	null	null	11	null	null	null	null	null	-1	8	0.06238	null	4	null	KRT4
NM_00310	34	0.06487	-1	10	0.06487	-1	10	0.08462	null	null	null	null	-1	10	0.090442	null	4	null	SNX2
NM_00010	34	0.065187	null	11	null	-1	8	0.065187	null	null	null	null	null	11	null	null	4	null	DMD
NM_001001	34	0.066203	1	9	0.066203	null	11	null	null	null	null	null	null	11	null	1	3	0.09109	STX16
NM_00445	34	0.08167	null	11	null	-1	9	0.08167	null	null	null	null	null	11	null	-1	3	0.094938	ETV5
NM_01223	35	1.65E-06	null	11	null	-1	9	1.65E-06	null	null	null	null	null	11	null	null	4	null	RYBP
NM_01545	35	1.67E-06	null	11	null	-1	9	1.67E-06	null	null	-1	2.03E-06	null	11	null	null	4	null	MTMR9
NM_01483	35	1.68E-06	null	11	null	-1	9	1.68E-06	null	null	null	null	null	11	null	null	4	null	LPPR4
NM_14471	35	1.74E-06	-1	10	2.76E-06	-1	10	1.74E-06	null	null	null	null	null	11	null	null	4	null	SEPT10
NM_014391	35	1.77E-06	null	11	null	-1	9	1.77E-06	null	null	null	null	null	11	null	null	4	null	ANKRD1
NM_00493	35	1.79E-06	null	11	null	-1	10	1.79E-06	null	null	null	null	null	11	null	-1	3	0.06364	DAPK1
NM_00568	35	1.82E-06	null	11	null	-1	10	1.82E-06	null	null	-1	2.25E-06	-1	10	3.85E-06	null	4	null	SOX13
NM_00586	35	1.83E-06	null	11	null	1	10	1.83E-06	null	null	null	null	null	11	null	1	3	0.094396	BET1
NM_00561	35	1.9E-06	1	10	0.083523	1	10	1.90E-06	null	null	null	null	null	11	null	null	4	null	RBBP4
NM_00299	35	1.91E-06	null	11	null	-1	9	1.91E-06	null	null	null	null	null	11	null	null	4	null	CX3CL1
NM_01506	35	1.94E-06	-1	10	3.06E-06	-1	10	1.94E-06	null	null	-1	2.4E-06	null	11	null	null	4	null	ZNF423
NM_00388	35	1.97E-06	null	11	null	-1	9	1.97E-06	null	null	null	null	null	11	null	null	4	null	ALDH1A2
NM_00100	35	2.01E-06	null	11	null	1	10	2.01E-06	null	null	1	3.02E-06	1	10	9.57E-06	null	4	null	MAGED1
NM_00380	35	2.05E-06	-1	10	2.65E-06	null	11	null	null	null	-1	2.05E-06	-1	10	3.49E-06	null	4	null	TNFSF13
NM_00679	35	2.05E-06	null	11	null	-1	9	2.05E-06	null	null	null	null	null	11	null	null	4	null	EHD1
NM_00258	35	2.06E-06	null	11	null	-1	9	2.06E-06	null	null	null	null	null	11	null	null	4	null	PBX1

NM_003655	35	2.1E-06	1	10	4.99E-06	1	10	2.1E-06	null	null	null	null	null	11	null	null	4	null	CBX4
NM_007066	35	2.13E-06	-1	10	2.73E-06	null	11	null	null	null	-1	2.13E-06	-1	10	3.64E-06	null	4	null	PKIG
NM_015285	35	2.13E-06	null	11	null	-1	9	2.13E-06	null	null	null	null	null	11	null	null	4	null	WDR7
NM_015187	35	2.15E-06	null	11	null	1	10	2.15E-06	null	null	1	3.19E-06	1	10	1.06E-05	null	4	null	KIAA0746
NM_001018	35	2.15E-06	1	10	5.11E-06	1	10	2.15E-06	null	null	null	null	null	11	null	null	4	null	HAX1
NM_015073	35	2.16E-06	1	10	5.15E-06	1	10	2.16E-06	null	null	1	3.20E-06	null	11	null	null	4	null	SIPA1L3
NM_003982	35	2.19E-06	-1	10	3.46E-06	-1	10	2.19E-06	null	null	null	null	null	11	null	null	4	null	SLC7A7
NM_006764	35	2.21E-06	null	11	null	1	9	2.21E-06	null	null	null	null	null	11	null	null	4	null	IFRD2
NM_002840	35	2.24E-06	null	11	null	1	9	2.24E-06	null	null	null	null	null	11	null	null	4	null	PTPRF
NM_004095	35	2.29E-06	1	10	5.42E-06	1	10	2.29E-06	null	null	null	null	null	11	null	null	4	null	EIF4EBP1
NM_001001	35	2.31E-06	1	10	5.45E-06	1	10	2.31E-06	null	null	null	null	null	11	null	null	4	null	ATP1B1
NM_175709	35	2.31E-06	-1	10	3.68E-06	-1	10	2.31E-06	null	null	-1	2.83E-06	null	11	null	null	4	null	CBX7
NM_003644	35	2.35E-06	-1	10	3.76E-06	-1	10	2.35E-06	null	null	null	null	null	11	null	null	4	null	GAS7
NM_002533	35	2.37E-06	1	10	5.64E-06	1	10	2.37E-06	null	null	1	3.53E-06	null	11	null	null	4	null	NVL
NM_001404	35	2.41E-06	null	11	null	1	10	2.41E-06	null	null	null	null	1	10	0.096732	null	4	null	EEF1G
NM_005227	35	2.46E-06	1	10	5.80E-06	1	10	2.46E-06	null	null	1	3.69E-06	null	11	null	null	4	null	EFNA4
NM_003946	35	2.52E-06	null	11	null	1	10	2.52E-06	null	null	null	null	1	10	1.14E-05	null	4	null	NOL3
NM_153367	35	2.55E-06	null	11	null	-1	10	2.55E-06	null	null	null	null	-1	10	5.49E-06	null	4	null	C10orf56
NM_001760	35	2.57E-06	null	11	null	-1	9	2.57E-06	null	null	null	null	null	11	null	null	4	null	CCND3
NM_014256	35	2.61E-06	1	10	6.14E-06	1	10	2.61E-06	null	null	1	3.90E-06	null	11	null	null	4	null	B3GNT3
NM_001541	35	2.62E-06	null	11	null	-1	9	2.62E-06	null	null	-1	3.15E-06	null	11	null	null	4	null	HSPB2
NM_005342	35	2.66E-06	1	10	6.28E-06	1	10	2.66E-06	null	null	null	null	null	11	null	null	4	null	HMGB3
NM_031420	35	2.67E-06	1	10	6.33E-06	1	10	2.67E-06	null	null	null	null	null	11	null	null	4	null	MRPL9
NM_001040	35	2.68E-06	null	11	null	1	10	2.68E-06	null	null	null	null	1	10	5.12E-06	null	4	null	HIST2H2AA
NM_002947	35	2.69E-06	null	11	null	1	9	2.69E-06	null	null	null	null	null	11	null	null	4	null	RPA3
NM_006334	35	2.7E-06	-1	9	3.49E-06	null	11	null	null	null	-1	2.70E-06	null	11	null	null	4	null	OLFM1
NM_001047	35	2.7E-06	1	10	1.15E-05	1	10	2.70E-06	null	null	null	null	null	11	null	null	4	null	NET1
NM_003541	35	2.74E-06	1	10	6.53E-06	1	10	2.74E-06	null	null	1	4.06E-06	null	11	null	null	4	null	HIST4H4
NM_012402	35	2.78E-06	null	11	null	1	9	2.78E-06	null	null	1	4.12E-06	null	11	null	null	4	null	ARFIP2
NM_015014	35	2.88E-06	null	11	null	1	10	2.88E-06	null	null	1	4.31E-06	1	10	0.076144	null	4	null	RBM34
NM_000345	35	2.89E-06	null	11	null	-1	9	2.89E-06	null	null	null	null	null	11	null	null	4	null	SNCA
NM_032233	35	2.9E-06	-1	10	0.09089	-1	10	2.90E-06	null	null	null	null	null	11	null	null	4	null	SETD3
NM_004699	35	2.91E-06	null	11	null	1	10	2.91E-06	null	null	1	4.33E-06	1	10	0.081171	null	4	null	FAM50A
NM_007198	35	2.95E-06	null	11	null	-1	9	2.95E-06	null	null	null	null	null	11	null	null	4	null	PROSC
NM_012319	35	3E-06	null	11	null	1	10	0.061713	null	null	1	3.00E-06	1	10	0.033954	null	4	null	SLC39A6
NM_001040	35	3E-06	null	11	null	-1	9	3.00E-06	null	null	null	null	null	11	null	null	4	null	CD37
NM_001029	35	3.03E-06	-1	9	3.03E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	PDE8B
NM_173728	35	3.05E-06	null	11	null	-1	10	3.05E-06	null	null	-1	3.71E-06	-1	10	6.59E-06	null	4	null	ARHGEF15
NM_003381	35	3.06E-06	null	11	null	-1	9	3.06E-06	null	null	null	null	null	11	null	null	4	null	VIP
NM_002427	35	3.07E-06	1	10	0.054953	1	10	3.07E-06	null	null	null	null	null	11	null	null	4	null	MMP13
NM_015293	35	3.11E-06	-1	10	5.38E-06	-1	10	3.11E-06	null	null	-1	3.78E-06	null	11	null	null	4	null	SYNE1
NM_004313	35	3.18E-06	null	11	null	-1	10	3.18E-06	null	null	null	null	-1	10	6.92E-06	null	4	null	ARRB2
NM_012291	35	3.25E-06	null	11	null	1	9	3.25E-06	null	null	null	null	null	11	null	null	4	null	ESPL1
NM_014988	35	3.33E-06	-1	10	5.76E-06	-1	10	3.33E-06	null	null	-1	3.96E-06	null	11	null	null	4	null	LIMCH1
NM_022132	35	3.37E-06	1	10	7.55E-06	1	10	3.37E-06	null	null	null	null	null	11	null	null	4	null	MCCC2
NM_019613	35	3.39E-06	1	10	7.62E-06	1	10	3.39E-06	null	null	1	4.9E-06	null	11	null	null	4	null	WDR45L
NM_002426	35	3.4E-06	1	10	0.089328	null	11	null	null	null	1	3.40E-06	null	11	null	1	3	0.094994	MMP12

NM_002014	35	3.49E-06	null	11	null	1	9	3.49E-06	null	null	null	null	null	11	null	null	4	null	FKBP4
NM_015356	35	3.52E-06	null	11	null	1	9	3.52E-06	null	null	1	5.02E-06	null	11	null	null	4	null	SCRIB
NM_000505	35	3.56E-06	null	11	null	1	9	3.56E-06	null	null	null	null	null	11	null	null	4	null	F12
NM_006471	35	3.62E-06	-1	9	3.62E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	MRCL3
NM_021005	35	3.66E-06	null	11	null	-1	9	3.66E-06	null	null	null	null	null	11	null	null	4	null	NR2F2
NM_003881	35	3.71E-06	-1	10	6.43E-06	-1	10	3.71E-06	null	null	null	null	null	11	null	null	4	null	WISP2
NM_024098	35	3.71E-06	1	10	8.15E-06	1	10	3.71E-06	null	null	null	null	null	11	null	null	4	null	CCDC86
NM_004170	35	3.74E-06	-1	10	3.74E-06	null	11	null	null	null	null	null	-1	10	4.96E-06	null	4	null	SLC1A1
NM_000020	35	3.78E-06	-1	10	6.53E-06	-1	10	3.78E-06	null	null	null	null	null	11	null	null	4	null	ACVRL1
NM_014945	35	3.83E-06	-1	10	6.59E-06	-1	10	3.83E-06	null	null	null	null	null	11	null	null	4	null	ABLIM3
NM_002154	35	3.84E-06	null	11	null	1	10	3.84E-06	null	null	null	null	1	10	6.98E-06	null	4	null	HSPA4
NM_002388	35	4.11E-06	null	11	null	1	9	4.11E-06	null	null	null	null	null	11	null	null	4	null	MCM3
NM_001853	35	4.16E-06	1	10	0.075182	1	10	4.16E-06	null	null	null	null	null	11	null	null	4	null	COL9A3
NM_004445	35	4.24E-06	null	11	null	-1	9	4.24E-06	null	null	null	null	null	11	null	null	4	null	EPHB6
NM_004035	35	4.3E-06	null	11	null	1	9	4.30E-06	null	null	null	null	null	11	null	null	4	null	ACOX1
NM_003344	35	4.33E-06	null	11	null	1	10	4.33E-06	null	null	null	null	1	10	0.0806	null	4	null	UBE2H
NM_002156	35	4.4E-06	null	11	null	null	11	null	null	null	1	4.40E-06	1	9	1.29E-05	null	4	null	HSPD1
NM_001040	35	4.44E-06	null	11	null	-1	10	4.44E-06	null	null	null	null	-1	10	5.32E-06	null	4	null	MYH11
NM_004284	35	4.5E-06	1	10	1.00E-05	1	10	4.50E-06	null	null	null	null	null	11	null	null	4	null	CHD1L
NM_007048	35	4.5E-06	null	11	null	-1	9	4.50E-06	null	null	null	null	null	11	null	null	4	null	BTN3A1
NM_002610	35	4.52E-06	null	11	null	1	9	4.52E-06	null	null	1	6.33E-06	null	11	null	null	4	null	PDK1
NM_001793	35	4.62E-06	null	11	null	1	9	4.62E-06	null	null	1	6.48E-06	null	11	null	null	4	null	CDH3
NM_001047	35	4.64E-06	null	11	null	1	9	4.64E-06	null	null	null	null	null	11	null	null	4	null	SRD5A1
NM_000917	35	4.65E-06	null	11	null	null	11	null	null	null	1	4.65E-06	1	9	0.050563	null	4	null	P4HA1
NM_001085	35	4.68E-06	null	11	null	null	11	null	null	null	null	null	-1	9	4.68E-06	null	4	null	FOXN3
NM_006926	35	4.68E-06	null	11	null	-1	10	4.68E-06	null	null	null	null	-1	10	5.54E-06	null	4	null	SFTPA2B
NM_003430	35	4.72E-06	null	11	null	null	11	null	null	null	null	null	-1	9	4.72E-06	null	4	null	ZNF91
NM_002914	35	4.84E-06	null	11	null	1	10	4.84E-06	null	null	null	null	1	10	0.044243	null	4	null	RFC2
NM_002220	35	4.85E-06	null	11	null	1	9	4.85E-06	null	null	null	null	null	11	null	null	4	null	ITPKA
NM_013230	35	4.87E-06	null	11	null	1	9	4.87E-06	null	null	1	6.75E-06	null	11	null	null	4	null	CD24
NM_006289	35	4.93E-06	null	11	null	-1	10	4.93E-06	null	null	null	null	-1	10	1.1E-05	null	4	null	TLN1
NM_005881	35	4.99E-06	1	10	1.08E-05	1	10	4.99E-06	null	null	1	6.98E-06	null	11	null	null	4	null	BCKDK
NM_015101	35	4.99E-06	-1	10	0.067946	-1	10	4.99E-06	null	null	-1	5.88E-06	null	11	null	null	4	null	GLT25D2
NM_002083	35	5.09E-06	null	11	null	1	9	5.09E-06	null	null	null	null	null	11	null	null	4	null	GPX2
NM_014696	35	5.11E-06	-1	10	8.76E-06	-1	10	5.11E-06	null	null	null	null	null	11	null	null	4	null	GPRIN2
NM_003022	35	5.15E-06	-1	10	8.85E-06	-1	10	5.15E-06	null	null	null	null	null	11	null	null	4	null	SH3BGRL
NM_015871	35	5.18E-06	1	10	1.1E-05	1	10	5.18E-06	null	null	1	7.10E-06	null	11	null	null	4	null	ZNF593
NM_002141	35	5.21E-06	null	11	null	-1	9	5.21E-06	null	null	null	null	null	11	null	null	4	null	HOXA4
NM_005441	35	5.21E-06	null	11	null	1	9	5.21E-06	null	null	null	null	null	11	null	null	4	null	CHAF1B
NM_024298	35	5.22E-06	null	11	null	1	9	5.22E-06	null	null	null	null	null	11	null	null	4	null	MBOAT7
NM_014501	35	5.27E-06	null	11	null	1	9	5.27E-06	null	null	null	null	null	11	null	null	4	null	UBE2S
NM_001014	35	5.35E-06	null	11	null	-1	9	5.35E-06	null	null	null	null	null	11	null	null	4	null	ILK
NM_001008	35	5.56E-06	null	11	null	null	11	null	null	null	null	null	-1	9	5.56E-06	null	4	null	CTDSPL
NM_002417	35	5.6E-06	null	11	null	1	9	5.60E-06	null	null	null	null	null	11	null	null	4	null	MKI67
NM_002596	35	5.61E-06	1	10	7.56E-06	1	10	5.61E-06	null	null	null	null	null	11	null	null	4	null	PCTK3
NM_000365	35	5.72E-06	1	10	1.23E-05	1	10	5.72E-06	null	null	1	7.55E-06	null	11	null	null	4	null	TPI1
NM_001037	35	5.72E-06	null	11	null	-1	9	5.72E-06	null	null	null	null	null	11	null	null	4	null	PDE4B

NM_002654	35	5.72E-06	null	11	null	null	11	null	null	null	null	null	1	9	5.72E-06	null	4	null	PKM2
NM_004494	35	5.84E-06	1	10	1.25E-05	1	10	5.84E-06	1	0.000412	null	null	null	11	null	null	4	null	HDGF
NM_006052	35	5.84E-06	null	11	null	-1	9	5.84E-06	null	null	null	null	null	11	null	null	4	null	DSCR3
NM_004437	35	5.87E-06	1	10	7.92E-06	1	10	5.87E-06	null	null	null	null	null	11	null	null	4	null	EPB41
NM_003247	35	5.92E-06	null	11	null	null	11	null	null	null	1	5.92E-06	1	9	1.75E-05	null	4	null	THBS2
NM_018955	35	5.92E-06	null	11	null	-1	9	5.92E-06	null	null	null	null	null	11	null	null	4	null	UBB
NM_005807	35	6.09E-06	null	11	null	-1	9	6.09E-06	null	null	null	null	null	11	null	null	4	null	
NM_006694	35	6.14E-06	1	10	1.33E-05	1	10	6.14E-06	null	null	null	null	null	11	null	null	4	null	JTB
NM_002234	35	6.24E-06	null	11	null	-1	9	6.24E-06	null	null	null	null	null	11	null	null	4	null	KCNA5
NM_000240	35	6.38E-06	null	11	null	null	11	null	-1	0.089335	-1	6.38E-06	null	11	null	-1	2	0.000274	MAOA
NM_014398	35	6.38E-06	-1	10	1.08E-05	-1	10	6.38E-06	-1	0.098534	-1	7.10E-06	null	11	null	null	4	null	LAMP3
NM_000234	35	6.4E-06	null	11	null	1	9	6.40E-06	null	null	null	null	null	11	null	null	4	null	LIG1
NM_004900	35	6.64E-06	null	11	null	1	9	6.64E-06	null	null	null	null	null	11	null	null	4	null	APOBEC3B
NM_001080	35	6.71E-06	null	11	null	1	10	6.71E-06	null	null	null	null	1	10	1.34E-05	null	4	null	DNA2
NM_006142	35	6.72E-06	null	11	null	1	10	6.72E-06	null	null	null	null	1	10	0.051775	null	4	null	SFN
NM_001034	35	6.8E-06	null	11	null	1	10	6.80E-06	null	null	null	null	1	10	0.072558	null	4	null	RRM2
NM_022551	35	6.86E-06	1	10	1.42E-05	1	10	6.86E-06	null	null	null	null	null	11	null	null	4	null	RPS18
NM_001291	35	6.93E-06	null	11	null	1	9	6.93E-06	null	null	1	7.92E-06	null	11	null	null	4	null	
NM_005368	35	6.98E-06	null	11	null	1	9	6.98E-06	null	null	null	null	null	11	null	null	4	null	MB
NM_001033	35	7.08E-06	-1	9	7.08E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	GLUL
NM_013272	35	7.1E-06	-1	10	1.25E-05	-1	10	7.10E-06	null	null	null	null	null	11	null	null	4	null	SLCO3A1
NM_000665	35	7.13E-06	1	10	9.60E-06	1	10	7.13E-06	null	null	null	null	null	11	null	null	4	null	ACHE
NM_001042	35	7.27E-06	null	11	null	null	11	null	null	null	null	null	1	9	7.27E-06	null	4	null	NCBP2
NM_003786	35	7.28E-06	1	10	1.55E-05	1	10	7.28E-06	null	null	1	9.35E-06	null	11	null	null	4	null	ABCC3
NM_001033	35	7.42E-06	null	11	null	1	9	7.42E-06	null	null	null	null	null	11	null	null	4	null	
NM_014413	35	7.61E-06	1	10	1.96E-05	1	10	7.61E-06	null	null	null	null	null	11	null	null	4	null	EIF2AK1
NM_004346	35	7.68E-06	null	11	null	1	9	7.68E-06	null	null	null	null	null	11	null	null	4	null	CASP3
NM_014298	35	7.77E-06	1	9	1.27E-05	null	11	null	null	null	1	7.77E-06	null	11	null	null	4	null	QPRT
NM_001931	35	7.79E-06	null	11	null	null	11	null	null	null	null	null	1	9	7.79E-06	null	4	null	DLAT
NM_005096	35	7.92E-06	null	11	null	1	9	7.92E-06	null	null	null	null	null	11	null	null	4	null	ZMYM3
NM_003659	35	8.03E-06	null	11	null	1	9	8.03E-06	null	null	null	null	null	11	null	null	4	null	AGPS
NM_020713	35	8.35E-06	1	10	2.14E-05	1	10	8.35E-06	null	null	null	null	null	11	null	null	4	null	ZNF512B
NM_017760	35	8.45E-06	null	11	null	1	10	8.45E-06	null	null	null	null	1	10	1.76E-05	null	4	null	NCAPG2
NM_000261	35	8.95E-06	null	11	null	-1	9	8.95E-06	null	null	null	null	null	11	null	null	4	null	MYOC
NM_006929	35	9.07E-06	null	11	null	1	9	9.07E-06	null	null	1	1.03E-05	null	11	null	null	4	null	SKIV2L
NM_003522	35	9.15E-06	null	11	null	1	10	9.15E-06	null	null	1	1.16E-05	1	10	4.57E-05	null	4	null	HIST1H2BF
NM_014260	35	9.51E-06	1	10	2.36E-05	1	10	9.51E-06	null	null	null	null	null	11	null	null	4	null	PFDN6
NM_014377	35	9.6E-06	1	10	1.45E-05	null	11	null	null	null	null	null	1	10	9.60E-06	null	4	null	ZRF1
NM_016147	35	9.65E-06	1	10	2.45E-05	1	10	9.65E-06	null	null	null	null	null	11	null	null	4	null	PPME1
NM_015292	35	9.68E-06	null	11	null	-1	9	9.68E-06	null	null	-1	1.04E-05	null	11	null	null	4	null	FAM62A
NM_003143	35	9.92E-06	null	11	null	null	11	null	null	null	null	null	1	9	9.92E-06	null	4	null	SSBP1
NM_144570	35	9.92E-06	null	11	null	1	10	9.92E-06	null	null	null	null	1	10	3.11E-05	null	4	null	HN1L
NM_004689	35	1E-05	null	11	null	1	9	1.00E-05	null	null	null	null	null	11	null	null	4	null	MTA1
NM_004520	35	1E-05	1	10	2.35E-05	1	10	1.00E-05	null	null	null	null	null	11	null	null	4	null	KIF2A
NM_002441	35	1.02E-05	1	10	0.07292	1	10	1.02E-05	null	null	1	1.25E-05	null	11	null	null	4	null	MSH5
NM_005801	35	1.02E-05	null	11	null	-1	9	1.02E-05	null	null	-1	1.1E-05	null	11	null	null	4	null	EIF1
NM_002729	35	1.03E-05	null	11	null	-1	9	1.03E-05	null	null	null	null	null	11	null	null	4	null	HHEX

NM_002556	35	1.03E-05	null	11	null	null	11	null	null	null	null	null	1	9	1.03E-05	null	4	null	OSBP
NM_005853	35	1.04E-05	1	10	0.094785	1	10	1.04E-05	null	null	null	null	null	11	null	null	4	null	IRX5
NM_018265	35	1.05E-05	1	10	2.54E-05	1	10	1.05E-05	null	null	null	null	null	11	null	null	4	null	C1orf106
NM_001247	35	1.06E-05	1	10	2.49E-05	1	10	1.06E-05	null	null	1	1.31E-05	null	11	null	null	4	null	ENTPD6
NM_032737	35	1.1E-05	null	11	null	1	9	1.10E-05	null	null	null	null	null	11	null	null	4	null	LMNB2
NM_000303	35	1.11E-05	1	10	2.66E-05	1	10	1.11E-05	null	null	1	1.40E-05	null	11	null	null	4	null	PMM2
NM_004850	35	1.18E-05	null	11	null	-1	9	1.18E-05	null	null	null	null	null	11	null	null	4	null	ROCK2
NM_014175	35	1.18E-05	1	10	2.85E-05	1	10	1.18E-05	null	null	null	null	null	11	null	null	4	null	MRPL15
NM_002670	35	1.19E-05	null	11	null	null	11	null	null	null	null	null	1	9	1.19E-05	null	4	null	PLS1
NM_006855	35	1.19E-05	1	10	2.84E-05	1	10	1.19E-05	null	null	1	1.44E-05	null	11	null	null	4	null	KDELR3
NM_001813	35	1.22E-05	null	11	null	1	10	1.22E-05	null	null	null	null	1	10	2.36E-05	null	4	null	CENPE
NM_000747	35	1.25E-05	null	11	null	1	9	1.25E-05	null	null	null	null	null	11	null	null	4	null	CHRNB1
NM_015149	35	1.27E-05	null	11	null	-1	9	1.27E-05	null	null	null	null	null	11	null	null	4	null	RGL1
NM_003222	35	1.33E-05	null	11	null	null	11	null	null	null	null	null	1	9	1.33E-05	null	4	null	TFAP2C
NM_003076	35	1.37E-05	1	9	1.37E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	SMARCD1
NM_014623	35	1.4E-05	1	10	3.29E-05	1	10	1.40E-05	null	null	1	1.83E-05	null	11	null	null	4	null	MEA1
NM_004203	35	1.42E-05	null	11	null	1	9	1.42E-05	null	null	null	null	null	11	null	null	4	null	PKMYT1
NM_002421	35	1.44E-05	1	10	3.43E-05	1	10	1.44E-05	null	null	1	2.01E-05	null	11	null	null	4	null	MMP1
NM_001895	35	1.5E-05	null	11	null	1	9	1.50E-05	null	null	null	null	null	11	null	null	4	null	CSNK2A1
NM_006181	35	1.5E-05	1	9	1.50E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	NTN2L
NM_014452	35	1.52E-05	1	10	3.74E-05	1	10	1.52E-05	null	null	1	2.11E-05	null	11	null	null	4	null	TNFRSF21
NM_007212	35	1.58E-05	1	9	1.58E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	RNF2
NM_003953	35	1.58E-05	1	9	1.58E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	MPZL1
NM_004833	35	1.6E-05	1	9	1.60E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	AIM2
NM_002067	35	1.61E-05	null	11	null	-1	10	1.61E-05	null	null	-1	1.61E-05	-1	10	3.74E-05	null	4	null	GNA11
NM_000091	35	1.68E-05	null	11	null	null	11	null	null	null	null	null	-1	9	1.68E-05	null	4	null	COL4A3
NM_000817	35	1.68E-05	null	11	null	1	9	1.68E-05	null	null	null	null	null	11	null	null	4	null	GAD1
NM_198474	35	1.72E-05	-1	10	2.94E-05	-1	10	1.72E-05	null	null	null	null	null	11	null	null	4	null	OLFML1
NM_002263	35	1.76E-05	null	11	null	1	9	1.76E-05	null	null	null	null	null	11	null	null	4	null	KIFC1
NM_007370	35	1.79E-05	null	11	null	1	10	1.79E-05	null	null	null	null	1	10	0.081257	null	4	null	RFC5
NM_005245	35	1.85E-05	null	11	null	null	11	null	null	null	null	null	1	9	1.85E-05	null	4	null	FAT
NM_000935	35	1.87E-05	null	11	null	null	11	null	null	null	1	1.87E-05	1	9	0.079936	null	4	null	PLOD2
NM_003512	35	2.01E-05	null	11	null	1	10	2.01E-05	null	null	1	2.84E-05	1	10	0.0763	null	4	null	HIST1H2AC
NM_018944	35	2.01E-05	1	10	4.57E-05	1	10	2.01E-05	null	null	null	null	null	11	null	null	4	null	C21orf45
NM_007114	35	2.07E-05	1	9	2.07E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	TMF1
NM_000146	35	2.15E-05	null	11	null	null	11	null	null	null	null	null	-1	9	2.15E-05	null	4	null	FTL
NM_174930	35	2.17E-05	1	10	2.17E-05	1	10	0.06802	null	null	null	null	null	11	null	null	4	null	PMS2L5
NM_002592	35	2.35E-05	null	11	null	1	10	2.35E-05	null	null	null	null	1	10	0.097162	null	4	null	PCNA
NM_020892	35	2.42E-05	null	11	null	1	10	2.42E-05	null	null	1	3.43E-05	1	10	9.15E-05	null	4	null	DTX2
NM_006106	35	2.44E-05	null	11	null	null	11	null	null	null	null	null	1	9	2.44E-05	null	4	null	YAP1
NM_001950	35	2.5E-05	1	9	2.5E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	E2F4
NM_005634	35	2.55E-05	null	11	null	1	9	2.55E-05	null	null	null	null	null	11	null	null	4	null	SOX3
NM_014750	35	2.63E-05	null	11	null	1	10	2.63E-05	null	null	null	null	1	10	0.099689	null	4	null	DLGAP5
NM_001008	35	2.74E-05	1	10	4.84E-05	1	10	2.74E-05	null	null	1	3.92E-05	null	11	null	null	4	null	DSP
NM_000347	35	2.94E-05	1	9	2.94E-05	null	11	null	null	null	1	2.94E-05	null	11	null	null	4	null	SPTB
NM_006408	35	2.94E-05	1	10	5.15E-05	1	10	2.94E-05	null	null	1	4.57E-05	null	11	null	null	4	null	AGR2
NM_017802	35	3.11E-05	null	11	null	1	10	3.11E-05	null	null	null	null	1	10	6.23E-05	null	4	null	HEATR2

NM_001039	35	3.16E-05	null	11	null	-1	10	3.16E-05	null	null	null	null	-1	10	3.16E-05	null	4	null	
NM_004298	35	3.43E-05	null	11	null	1	10	3.43E-05	null	null	1	5.49E-05	1	10	0.000118	null	4	null	NUP155
NM_014239	35	3.6E-05	null	11	null	1	10	3.60E-05	null	null	null	null	1	10	0.093288	null	4	null	EIF2B2
NM_002874	35	3.92E-05	null	11	null	null	11	null	null	null	null	null	1	9	3.92E-05	null	4	null	RAD23B
NM_000029	35	3.97E-05	1	9	3.97E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	AGT
NM_000715	35	4.33E-05	null	11	null	-1	9	0.049271	null	null	-1	4.33E-05	null	11	null	null	4	null	C4BPA
NM_005242	35	4.48E-05	1	9	4.48E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	F2RL1
NM_001852	35	4.64E-05	null	11	null	1	9	4.64E-05	null	null	null	null	null	11	null	null	4	null	COL9A2
NM_001232	35	4.84E-05	null	11	null	-1	9	4.84E-05	null	null	null	null	null	11	null	null	4	null	CASQ2
NM_003318	35	4.89E-05	null	11	null	1	9	4.89E-05	null	null	null	null	null	11	null	null	4	null	TTK
NM_004399	35	5.15E-05	null	11	null	1	9	0.036942	null	null	1	5.15E-05	null	11	null	null	4	null	DDX11
NM_032283	35	5.15E-05	null	11	null	1	10	5.15E-05	null	null	1	9.15E-05	1	10	0.000165	null	4	null	ZDHHC18
NM_006087	35	5.67E-05	1	10	0.000255	1	10	5.67E-05	null	null	null	null	null	11	null	null	4	null	TUBB4
NM_001003	35	5.71E-05	null	11	null	null	11	null	null	null	null	null	1	9	5.71E-05	null	4	null	HMG2L1
NM_018116	35	5.71E-05	1	10	0.000137	1	10	5.71E-05	null	null	null	null	null	11	null	null	4	null	MSTO1
NM_001039	35	6.72E-05	null	11	null	1	10	6.72E-05	null	null	null	null	1	10	0.000134	null	4	null	FHL2
NM_004701	35	6.86E-05	1	10	0.000103	1	10	6.86E-05	null	null	null	null	null	11	null	null	4	null	CCNB2
NM_021220	35	7.29E-05	1	9	7.29E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	OVOL2
NM_004326	35	7.48E-05	1	9	7.48E-05	null	11	null	null	null	1	7.48E-05	null	11	null	null	4	null	BCL9
NM_004804	35	0.000103	1	10	0.000165	1	10	0.000103	null	null	1	0.000206	null	11	null	null	4	null	CIAO1
NM_003729	35	0.000137	null	11	null	null	11	null	null	null	null	null	1	9	0.000137	null	4	null	RTCD1
NM_006398	35	0.00017	1	9	0.00017	null	11	null	null	null	null	null	null	11	null	null	4	null	UBD
NM_001500	35	0.000206	1	10	0.000412	1	10	0.000206	null	null	null	null	null	11	null	null	4	null	GMDS
NM_001839	35	0.00025	null	11	null	-1	9	0.00025	null	null	null	null	null	11	null	null	4	null	CNN3
NM_004508	35	0.025393	-1	9	0.025393	null	11	null	null	null	null	null	null	11	null	null	4	null	IDI1
NM_002897	35	0.026096	null	11	null	-1	10	0.056185	null	null	null	null	-1	10	0.026096	null	4	null	RBMS1
NM_002825	35	0.026433	null	11	null	null	11	null	null	null	null	null	-1	10	0.026433	-1	3	0.060918	PTN
NM_002405	35	0.026435	-1	10	0.026435	null	11	null	null	null	null	null	-1	10	0.063832	null	4	null	MFNG
NM_000637	35	0.027127	null	11	null	null	11	null	null	null	null	null	1	9	0.027127	null	4	null	GSR
NM_001567	35	0.030216	null	11	null	1	9	0.030216	null	null	null	null	null	11	null	null	4	null	INPPL1
NM_001064	35	0.033142	null	11	null	null	11	null	null	null	null	null	1	9	0.033142	null	4	null	TKT
NM_004969	35	0.033249	null	11	null	null	11	null	null	null	null	null	1	9	0.033249	null	4	null	IDE
NM_005665	35	0.034878	-1	10	0.034878	-1	10	0.059834	null	null	null	null	null	11	null	null	4	null	EVI5
NM_000570	35	0.035352	-1	10	0.035352	-1	10	0.088738	null	null	null	null	null	11	null	null	4	null	FCGR3B
NM_001005	35	0.037312	null	11	null	null	11	null	null	null	null	null	1	10	0.037312	1	3	0.080229	AK3L1
NM_001613	35	0.039164	null	11	null	-1	9	0.039164	null	null	null	null	null	11	null	null	4	null	ACTA2
NM_015148	35	0.039229	1	9	0.039229	null	11	null	null	null	null	null	null	11	null	null	4	null	PASK
NM_000060	35	0.039471	null	11	null	null	11	null	null	null	null	null	-1	9	0.039471	null	4	null	BTD
NM_001079	35	0.03982	-1	10	0.03982	-1	10	0.070339	null	null	null	null	null	11	null	null	4	null	N4BP2L1
NM_005949	35	0.04207	-1	9	0.04207	null	11	null	null	null	null	null	null	11	null	null	4	null	MT1F
NM_000495	35	0.042077	null	11	null	-1	10	0.091855	null	null	null	null	null	11	null	-1	3	0.042077	COL4A5
NM_002889	35	0.042241	null	11	null	-1	9	0.042241	null	null	null	null	null	11	null	null	4	null	RARRES2
NM_004523	35	0.043347	null	11	null	1	10	0.07089	null	null	null	null	1	10	0.043347	null	4	null	KIF11
NM_006710	35	0.044695	null	11	null	null	11	null	null	null	null	null	1	9	0.044695	null	4	null	COPS8
NM_001006	35	0.045483	null	11	null	-1	9	0.045483	null	null	null	null	null	11	null	null	4	null	RPS6KA1
NM_014683	35	0.048065	null	11	null	-1	10	0.091867	null	null	null	null	-1	10	0.048065	null	4	null	ULK2
NM_001002	35	0.048628	-1	9	0.048628	null	11	null	null	null	null	null	null	11	null	null	4	null	ANXA2

NM_004334	35	0.049259	null	11	null	-1	9	0.049259	null	null	null	null	null	11	null	null	4	null	BST1
NM_198098	35	0.049522	-1	10	0.049522	-1	10	0.085807	null	null	null	null	null	11	null	null	4	null	AQP1
NM_006288	35	0.049659	null	11	null	null	11	null	null	null	null	null	1	9	0.049659	null	4	null	THY1
NM_001006	35	0.049747	null	11	null	-1	9	0.049747	null	null	null	null	null	11	null	null	4	null	TCEAL1
NM_006981	35	0.049747	null	11	null	-1	9	0.049747	null	null	null	null	null	11	null	null	4	null	NR4A3
NM_004342	35	0.049843	null	11	null	-1	9	0.049843	null	null	null	null	null	11	null	null	4	null	CALD1
NM_020980	35	0.052365	-1	10	0.052365	-1	10	0.070469	null	null	null	null	null	11	null	null	4	null	AQP9
NM_004941	35	0.052635	null	11	null	null	11	null	null	null	null	null	1	9	0.052635	null	4	null	DHX8
NM_006304	35	0.05267	null	11	null	null	11	null	null	null	null	null	1	9	0.05267	null	4	null	SHFM1
NM_004430	35	0.055299	null	11	null	-1	9	0.055299	null	null	null	null	null	11	null	null	4	null	EGR3
NM_022107	35	0.055907	null	11	null	null	11	null	null	null	null	null	-1	9	0.055907	null	4	null	GPSM3
NM_014235	35	0.055997	null	11	null	null	11	null	null	null	null	null	1	9	0.055997	null	4	null	UBL4A
NM_002306	35	0.057422	-1	9	0.057422	null	11	null	null	null	null	null	null	11	null	null	4	null	LGALS3
NM_000702	35	0.058119	null	11	null	-1	9	0.058119	null	null	null	null	null	11	null	null	4	null	ATP1A2
NM_000927	35	0.058718	null	11	null	null	11	null	null	null	null	null	-1	9	0.058718	null	4	null	ABCB1
NM_001006	35	0.058764	-1	10	0.094331	-1	10	0.058764	null	null	null	null	null	11	null	null	4	null	PDPN
NM_002862	35	0.058772	null	11	null	1	10	0.058772	null	null	null	null	1	10	0.087358	null	4	null	PYGB
NM_001011	35	0.058821	-1	10	0.058821	-1	10	0.087542	null	null	null	null	null	11	null	null	4	null	DSTN
NM_002311	35	0.059546	null	11	null	1	9	0.059546	null	null	null	null	null	11	null	null	4	null	LIG3
NM_004073	35	0.060678	null	11	null	-1	9	0.060678	null	null	null	null	null	11	null	null	4	null	PLK3
NM_002047	35	0.062376	null	11	null	null	11	null	null	null	null	null	1	9	0.062376	null	4	null	GARS
NM_000695	35	0.062484	null	11	null	1	10	0.062484	null	null	null	null	1	10	0.09045	null	4	null	ALDH3B2
NM_006433	35	0.063355	-1	9	0.063355	null	11	null	null	null	null	null	null	11	null	null	4	null	GNLY
NM_006431	35	0.063378	null	11	null	null	11	null	null	null	null	null	1	9	0.063378	null	4	null	CCT2
NM_000317	35	0.066164	null	11	null	null	11	null	null	null	null	null	1	9	0.066164	null	4	null	PTS
NM_004385	35	0.066567	null	11	null	null	11	null	null	null	null	null	1	9	0.066567	null	4	null	VCAN
NM_000297	35	0.066707	-1	10	0.066707	-1	10	0.092133	null	null	null	null	null	11	null	null	4	null	PKD2
NM_001012	35	0.067295	null	11	null	-1	10	0.067295	null	null	null	null	-1	10	0.090844	null	4	null	
NM_006184	35	0.068218	null	11	null	null	11	null	null	null	null	null	-1	9	0.068218	null	4	null	NUCB1
NM_015135	35	0.06967	null	11	null	null	11	null	null	null	null	null	1	9	0.06967	null	4	null	NUP205
NM_005072	35	0.070023	null	11	null	-1	9	0.070023	null	null	null	null	null	11	null	null	4	null	SLC12A4
NM_000610	35	0.071587	-1	10	0.071587	-1	10	0.072087	null	null	null	null	null	11	null	null	4	null	CD44
NM_002358	35	0.071856	null	11	null	null	11	null	null	null	null	null	1	9	0.071856	null	4	null	MAD2L1
NM_001964	35	0.074772	null	11	null	-1	9	0.074772	null	null	null	null	null	11	null	null	4	null	EGR1
NM_014763	35	0.075501	null	11	null	null	11	null	null	null	null	null	1	9	0.075501	null	4	null	MRPL19
NM_002115	35	0.075832	-1	10	0.096436	-1	10	0.075832	null	null	null	null	null	11	null	null	4	null	HK3
NM_001977	35	0.076082	null	11	null	-1	9	0.076082	null	null	null	null	null	11	null	null	4	null	ENPEP
NM_001009	35	0.076212	null	11	null	null	11	null	null	null	null	null	1	9	0.076212	null	4	null	CCT6A
NM_004613	35	0.076467	-1	9	0.076467	null	11	null	null	null	null	null	null	11	null	null	4	null	TGM2
NM_001645	35	0.080777	-1	10	0.09485	null	11	null	null	null	null	null	-1	10	0.080777	null	4	null	APOC1
NM_021974	35	0.08301	1	10	0.08301	null	11	null	null	null	null	null	1	10	0.089499	null	4	null	POLR2F
NM_006207	35	0.084116	1	10	0.096356	null	11	null	null	null	null	null	1	10	0.084116	null	4	null	PDGFRL
NM_007002	35	0.084135	null	11	null	null	11	null	null	null	null	null	1	9	0.084135	null	4	null	ADRM1
NM_015060	35	0.088613	1	10	0.088613	null	11	null	null	null	null	null	1	10	0.09542	null	4	null	KIAA0241
NM_001033	35	0.088839	-1	10	0.094558	-1	10	0.088839	null	null	null	null	null	11	null	null	4	null	CYFIP1
NM_002123	35	0.091274	-1	10	0.09909	null	11	null	null	null	null	null	-1	10	0.091274	null	4	null	HLA-DQB1
NM_025201	36	1.69E-06	null	11	null	-1	10	1.69E-06	null	null	null	null	null	11	null	null	4	null	PLEKHO2

NM_015898	36	1.72E-06	null	11	null	-1	10	1.72E-06	null	null	null	null	null	11	null	null	4	null	ZBTB7A
NM_006257	36	1.78E-06	null	11	null	-1	10	1.78E-06	null	null	-1	2.20E-06	null	11	null	null	4	null	PRKCQ
NM_005837	36	1.81E-06	null	11	null	1	10	1.81E-06	null	null	null	null	null	11	null	null	4	null	POP7
NM_002864	36	1.85E-06	null	11	null	-1	10	1.85E-06	null	null	-1	2.29E-06	null	11	null	null	4	null	A2M
NM_013279	36	1.85E-06	null	11	null	-1	10	1.85E-06	null	null	null	null	null	11	null	null	4	null	C11orf9
NM_004808	36	1.86E-06	null	11	null	-1	10	1.86E-06	null	null	null	null	null	11	null	null	4	null	NMT2
NM_003283	36	1.86E-06	null	11	null	1	10	1.86E-06	null	null	1	2.76E-06	null	11	null	null	4	null	TNNT1
NM_013233	36	1.87E-06	null	11	null	1	10	1.87E-06	null	null	1	2.77E-06	null	11	null	null	4	null	STK39
NM_006451	36	1.89E-06	null	11	null	1	10	1.89E-06	null	null	1	2.84E-06	null	11	null	null	4	null	PAIP1
NM_003145	36	1.91E-06	null	11	null	1	10	1.91E-06	null	null	null	null	null	11	null	null	4	null	SSR2
NM_002952	36	1.93E-06	null	11	null	1	10	1.93E-06	null	null	null	null	null	11	null	null	4	null	RPS2
NM_002157	36	1.95E-06	null	11	null	1	10	1.95E-06	null	null	null	null	null	11	null	null	4	null	HSPE1
NM_002431	36	1.95E-06	null	11	null	1	10	1.95E-06	null	null	null	null	null	11	null	null	4	null	MNAT1
NM_006443	36	1.97E-06	null	11	null	1	10	1.97E-06	null	null	null	null	null	11	null	null	4	null	C6orf108
NM_000070	36	1.98E-06	null	11	null	null	11	null	null	null	-1	1.98E-06	-1	10	0.031364	null	4	null	CAPN3
NM_003525	36	1.98E-06	null	11	null	1	10	1.98E-06	null	null	1	2.96E-06	null	11	null	null	4	null	HIST1H2BI
NM_181581	36	1.99E-06	null	11	null	1	10	1.99E-06	null	null	null	null	null	11	null	null	4	null	DUS4L
NM_031899	36	2.04E-06	null	11	null	-1	10	2.04E-06	null	null	null	null	null	11	null	null	4	null	GORASP1
NM_006932	36	2.05E-06	null	11	null	-1	10	2.05E-06	null	null	null	null	null	11	null	null	4	null	SMTN
NM_024051	36	2.05E-06	null	11	null	1	10	2.05E-06	null	null	1	3.08E-06	null	11	null	null	4	null	C7orf24
NM_002707	36	2.06E-06	null	11	null	1	10	2.06E-06	null	null	null	null	null	11	null	null	4	null	PPM1G
NM_138342	36	2.12E-06	null	11	null	1	10	2.12E-06	null	null	null	null	null	11	null	null	4	null	GLB1L2
NM_002894	36	2.13E-06	null	11	null	1	10	2.13E-06	null	null	null	null	null	11	null	null	4	null	RBBP8
NM_004420	36	2.13E-06	null	11	null	-1	10	2.13E-06	null	null	null	null	null	11	null	null	4	null	DUSP8
NM_003071	36	2.14E-06	null	11	null	1	10	2.14E-06	null	null	null	null	null	11	null	null	4	null	HLTF
NM_001289	36	2.16E-06	-1	10	0.056327	null	11	null	null	null	-1	2.16E-06	null	11	null	null	4	null	CLIC2
NM_005206	36	2.18E-06	null	11	null	-1	10	2.18E-06	null	null	-1	2.68E-06	null	11	null	null	4	null	CRK
NM_017439	36	2.18E-06	-1	10	0.072278	null	11	null	null	null	-1	2.18E-06	null	11	null	null	4	null	tcag7.131
NM_000480	36	2.18E-06	null	11	null	1	10	2.18E-06	null	null	null	null	null	11	null	null	4	null	AMPD3
NM_001008	36	2.21E-06	null	11	null	-1	10	2.21E-06	null	null	null	null	null	11	null	null	4	null	OPTN
NM_001032	36	2.22E-06	null	11	null	1	10	2.22E-06	null	null	null	null	null	11	null	null	4	null	SPINT1
NM_006419	36	2.23E-06	null	11	null	1	10	2.23E-06	null	null	1	3.28E-06	null	11	null	null	4	null	CXCL13
NM_183373	36	2.26E-06	null	11	null	null	11	null	-1	0.083761	-1	2.26E-06	-1	10	3.86E-06	null	4	null	C6orf145
NM_003074	36	2.26E-06	null	11	null	1	10	2.26E-06	null	null	null	null	null	11	null	null	4	null	SMARCC1
NM_001005	36	2.27E-06	null	11	null	1	10	2.27E-06	null	null	1	3.36E-06	null	11	null	null	4	null	B4GALT2
NM_004217	36	2.3E-06	null	11	null	1	10	2.30E-06	null	null	null	null	null	11	null	null	4	null	AURKB
NM_198471	36	2.35E-06	null	11	null	-1	10	2.35E-06	null	null	-1	2.87E-06	null	11	null	null	4	null	KANK3
NM_020898	36	2.37E-06	null	11	null	-1	10	2.37E-06	null	null	-1	2.89E-06	null	11	null	null	4	null	CALCOCO1
NM_021095	36	2.37E-06	null	11	null	1	10	2.37E-06	null	null	null	null	null	11	null	null	4	null	SLC5A6
NM_001469	36	2.4E-06	null	11	null	1	10	2.4E-06	null	null	null	null	null	11	null	null	4	null	XRCC6
NM_002275	36	2.41E-06	null	11	null	1	10	2.41E-06	null	null	null	null	null	11	null	null	4	null	KRT15
NM_003096	36	2.42E-06	null	11	null	1	10	2.42E-06	null	null	null	null	null	11	null	null	4	null	SNRPG
NM_002842	36	2.43E-06	null	11	null	1	10	2.43E-06	null	null	null	null	null	11	null	null	4	null	PTPRH
NM_001005	36	2.44E-06	null	11	null	1	10	2.44E-06	null	null	1	3.68E-06	null	11	null	null	4	null	CHEK2
NM_005682	36	2.45E-06	null	11	null	1	10	2.45E-06	null	null	null	null	null	11	null	null	4	null	GPR56
NM_001015	36	2.46E-06	null	11	null	1	10	2.46E-06	null	null	null	null	null	11	null	null	4	null	CKMT1B
NM_003161	36	2.47E-06	null	11	null	1	10	2.47E-06	null	null	null	null	null	11	null	null	4	null	RPS6KB1

NM_006887	36	2.51E-06	null	11	null	-1	10	2.51E-06	null	null	null	null	null	11	null	null	4	null	ZFP36L2
NM_012120	36	2.54E-06	null	11	null	1	10	2.54E-06	null	null	1	3.79E-06	null	11	null	null	4	null	CD2AP
NM_004450	36	2.56E-06	null	11	null	1	10	2.56E-06	null	null	null	null	null	11	null	null	4	null	ERH
NM_144617	36	2.58E-06	null	11	null	-1	10	2.58E-06	null	null	-1	3.09E-06	null	11	null	null	4	null	HSPB6
NM_004271	36	2.6E-06	null	11	null	-1	10	2.60E-06	null	null	-1	3.12E-06	null	11	null	null	4	null	LY86
NM_005336	36	2.63E-06	null	11	null	1	10	2.63E-06	null	null	1	3.92E-06	null	11	null	null	4	null	HDLBP
NM_002773	36	2.64E-06	null	11	null	1	10	2.64E-06	null	null	null	null	null	11	null	null	4	null	PRSS8
NM_000296	36	2.65E-06	null	11	null	-1	10	2.65E-06	null	null	null	null	null	11	null	null	4	null	PKD1
NM_005486	36	2.65E-06	null	11	null	1	10	2.65E-06	null	null	1	3.94E-06	null	11	null	null	4	null	TOM1L1
NM_001007	36	2.66E-06	null	11	null	null	11	null	null	null	-1	2.66E-06	-1	10	0.05608	null	4	null	NTRK2
NM_015599	36	2.66E-06	null	11	null	1	10	2.66E-06	null	null	1	3.98E-06	null	11	null	null	4	null	PGM3
NM_005302	36	2.71E-06	null	11	null	null	11	null	null	null	1	2.71E-06	1	10	0.065636	null	4	null	GPR37
NM_015113	36	2.71E-06	null	11	null	-1	10	2.71E-06	null	null	-1	3.29E-06	null	11	null	null	4	null	ZZEF1
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NM_052969	36	2.72E-06	null	11	null	1	10	2.72E-06	null	null	null	null	null	11	null	null	4	null	RPL39L
NM_006947	36	2.74E-06	null	11	null	1	10	2.74E-06	null	null	null	null	null	11	null	null	4	null	SRP72
NM_014949	36	2.75E-06	null	11	null	1	10	2.75E-06	null	null	1	4.08E-06	null	11	null	null	4	null	KIAA0907
NM_015415	36	2.76E-06	null	11	null	1	10	2.76E-06	null	null	null	null	null	11	null	null	4	null	BRP44
NM_006681	36	2.79E-06	null	11	null	1	10	2.79E-06	null	null	null	null	null	11	null	null	4	null	NMU
NM_003536	36	2.82E-06	null	11	null	1	10	2.82E-06	null	null	1	4.16E-06	null	11	null	null	4	null	HIST1H3H
NM_003401	36	2.86E-06	null	11	null	1	10	2.86E-06	null	null	null	null	null	11	null	null	4	null	XRCC4
NM_004336	36	2.89E-06	null	11	null	1	10	2.89E-06	null	null	null	null	null	11	null	null	4	null	BUB1
NM_007008	36	2.89E-06	-1	10	2.89E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	RTN4
NM_000245	36	2.9E-06	null	11	null	1	10	2.90E-06	null	null	null	null	null	11	null	null	4	null	MET
NM_004483	36	2.92E-06	null	11	null	1	10	2.92E-06	null	null	null	null	null	11	null	null	4	null	GCSH
NM_006108	36	2.92E-06	null	11	null	-1	10	2.92E-06	null	null	null	null	null	11	null	null	4	null	SPON1
NM_012296	36	2.92E-06	-1	10	2.92E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	GAB2
NM_021127	36	2.96E-06	null	11	null	1	10	2.96E-06	null	null	1	4.45E-06	null	11	null	null	4	null	PMAIP1
NM_000267	36	3E-06	null	11	null	1	10	3.00E-06	null	null	null	null	null	11	null	null	4	null	NF1
NM_004972	36	3E-06	null	11	null	-1	10	3.00E-06	null	null	null	null	null	11	null	null	4	null	JAK2
NM_004805	36	3.02E-06	null	11	null	1	10	3.02E-06	null	null	null	null	null	11	null	null	4	null	POLR2D
NM_001106	36	3.02E-06	null	11	null	1	10	3.02E-06	null	null	null	null	null	11	null	null	4	null	ACVR2B
NM_003504	36	3.03E-06	null	11	null	1	10	3.03E-06	null	null	null	null	null	11	null	null	4	null	CDC45L
NM_001001	36	3.04E-06	null	11	null	-1	10	3.04E-06	null	null	null	null	null	11	null	null	4	null	FARP1
NM_014014	36	3.05E-06	null	11	null	1	10	3.05E-06	null	null	null	null	null	11	null	null	4	null	ASCC3L1
NM_003201	36	3.06E-06	null	11	null	1	10	3.06E-06	null	null	null	null	null	11	null	null	4	null	TFAM
NM_004499	36	3.07E-06	null	11	null	1	10	3.07E-06	null	null	1	4.52E-06	null	11	null	null	4	null	HNRNPAB
NM_002634	36	3.09E-06	null	11	null	1	10	3.09E-06	null	null	null	null	null	11	null	null	4	null	PHB
NM_000485	36	3.09E-06	null	11	null	1	10	3.09E-06	null	null	null	null	null	11	null	null	4	null	APRT
NM_012398	36	3.13E-06	null	11	null	-1	10	3.13E-06	null	null	null	null	null	11	null	null	4	null	PIP5K1C
NM_013943	36	3.15E-06	null	11	null	-1	10	3.15E-06	null	null	null	null	null	11	null	null	4	null	CLIC4
NM_014481	36	3.19E-06	null	11	null	1	10	3.19E-06	null	null	null	null	null	11	null	null	4	null	APEX2
NM_001024	36	3.2E-06	null	11	null	1	10	3.20E-06	null	null	null	null	null	11	null	null	4	null	SC5DL
NM_018416	36	3.25E-06	null	11	null	-1	10	3.25E-06	null	null	null	null	null	11	null	null	4	null	FOXJ2
NM_020474	36	3.27E-06	null	11	null	null	11	null	null	null	1	3.27E-06	1	10	0.076352	null	4	null	GALNT1
XM_371891	36	3.28E-06	null	11	null	1	10	3.28E-06	null	null	1	4.73E-06	null	11	null	null	4	null	
NM_015577	36	3.32E-06	null	11	null	1	10	3.32E-06	null	null	null	null	null	11	null	null	4	null	RAI14

NM_002608	36	3.39E-06	null	11	null	-1	10	3.39E-06	null	null	-1	4.06E-06	null	11	null	null	4	null	PDGFB
NM_012393	36	3.4E-06	null	11	null	1	10	3.40E-06	null	null	null	null	null	11	null	null	4	null	PFAS
NM_004965	36	3.42E-06	null	11	null	1	10	3.42E-06	null	null	null	null	null	11	null	null	4	null	HMGN1
NM_052940	36	3.43E-06	null	11	null	1	10	3.43E-06	null	null	null	null	null	11	null	null	4	null	LRRC42
NM_001692	36	3.47E-06	null	11	null	1	10	3.47E-06	null	null	null	null	null	11	null	null	4	null	ATP6V1B1
NM_003133	36	3.49E-06	null	11	null	1	10	3.49E-06	null	null	null	null	null	11	null	null	4	null	SRP9
NM_020338	36	3.55E-06	null	11	null	-1	10	3.55E-06	null	null	null	null	null	11	null	null	4	null	ZMIZ1
NM_013285	36	3.58E-06	null	11	null	1	10	0.098661	null	null	1	3.58E-06	null	11	null	null	4	null	GNL2
NM_014959	36	3.58E-06	null	11	null	-1	10	3.58E-06	null	null	-1	4.29E-06	null	11	null	null	4	null	CARD8
NM_018356	36	3.59E-06	null	11	null	1	10	3.59E-06	null	null	null	null	null	11	null	null	4	null	C5orf22
NM_006993	36	3.61E-06	null	11	null	1	10	3.61E-06	null	null	1	5.11E-06	null	11	null	null	4	null	NPM3
NM_006330	36	3.64E-06	null	11	null	1	10	3.64E-06	null	null	1	5.15E-06	null	11	null	null	4	null	LYPLA1
NM_006256	36	3.67E-06	-1	10	3.67E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	PKN2
NM_005600	36	3.68E-06	null	11	null	1	10	3.68E-06	null	null	1	5.21E-06	null	11	null	null	4	null	NIT1
NM_000143	36	3.69E-06	null	11	null	1	10	3.69E-06	null	null	1	5.24E-06	null	11	null	null	4	null	FH
NM_014887	36	3.73E-06	null	11	null	-1	10	3.73E-06	null	null	null	null	null	11	null	null	4	null	N4BP2L2
NM_006421	36	3.74E-06	null	11	null	1	10	3.74E-06	null	null	null	null	null	11	null	null	4	null	ARFGEF1
NM_002532	36	3.78E-06	null	11	null	1	10	3.78E-06	null	null	null	null	null	11	null	null	4	null	NUP88
NM_020730	36	3.81E-06	null	11	null	1	10	3.81E-06	null	null	null	null	null	11	null	null	4	null	DLG3
NM_022119	36	3.83E-06	null	11	null	1	10	3.83E-06	null	null	1	5.52E-06	null	11	null	null	4	null	PRSS22
NM_001017	36	3.88E-06	null	11	null	null	11	null	null	null	null	null	-1	10	3.88E-06	null	4	null	SFRS14
NM_015704	36	3.92E-06	null	11	null	1	10	3.92E-06	null	null	null	null	null	11	null	null	4	null	FAM152B
NM_012294	36	3.93E-06	-1	10	3.93E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	RAPGEF5
NM_032673	36	3.96E-06	null	11	null	1	10	3.96E-06	null	null	null	null	null	11	null	null	4	null	PCGF1
NM_002294	36	3.96E-06	null	11	null	1	10	3.96E-06	null	null	null	null	null	11	null	null	4	null	PHKG2
NM_003144	36	3.98E-06	null	11	null	1	10	3.98E-06	null	null	null	null	null	11	null	null	4	null	SSR1
NM_006396	36	4.04E-06	null	11	null	1	10	4.04E-06	null	null	null	null	null	11	null	null	4	null	SSSCA1
NM_057735	36	4.06E-06	null	11	null	1	10	4.06E-06	null	null	null	null	null	11	null	null	4	null	
NM_001517	36	4.08E-06	null	11	null	1	10	4.08E-06	null	null	null	null	null	11	null	null	4	null	GTF2H4
NM_016134	36	4.08E-06	null	11	null	-1	10	0.075519	null	null	-1	4.08E-06	null	11	null	null	4	null	PGCP
NM_015271	36	4.1E-06	null	11	null	1	10	4.10E-06	null	null	null	null	null	11	null	null	4	null	TRIM2
NM_000077	36	4.17E-06	null	11	null	1	10	4.17E-06	null	null	null	null	null	11	null	null	4	null	CDKN2A
NM_001293	36	4.18E-06	null	11	null	1	10	4.18E-06	null	null	null	null	null	11	null	null	4	null	CLNS1A
NM_015057	36	4.18E-06	null	11	null	-1	10	4.18E-06	null	null	null	null	null	11	null	null	4	null	MYCBP2
NM_001304	36	4.24E-06	null	11	null	null	11	null	null	null	1	4.24E-06	1	10	0.049193	null	4	null	CPD
NM_017751	36	4.24E-06	null	11	null	1	10	4.24E-06	null	null	1	6.19E-06	null	11	null	null	4	null	SMPD4
NM_007364	36	4.27E-06	null	11	null	1	10	4.27E-06	null	null	1	6.28E-06	null	11	null	null	4	null	TMED3
NM_004875	36	4.31E-06	null	11	null	1	10	4.31E-06	null	null	null	null	null	11	null	null	4	null	POLR1C
NM_003706	36	4.33E-06	null	11	null	-1	10	4.33E-06	null	null	-1	5.15E-06	null	11	null	null	4	null	PLA2G4C
NM_015005	36	4.36E-06	1	10	4.36E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	KIAA0284
NM_022735	36	4.43E-06	null	11	null	null	11	null	null	null	1	4.43E-06	1	10	1.31E-05	null	4	null	ACBD3
NM_006321	36	4.45E-06	null	11	null	-1	10	4.45E-06	null	null	null	null	null	11	null	null	4	null	ARIH2
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NM_012304	36	4.52E-06	-1	10	4.52E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	FBXL7
NM_006190	36	4.6E-06	null	11	null	1	10	4.60E-06	null	null	null	null	null	11	null	null	4	null	ORC2L
NM_003902	36	4.65E-06	null	11	null	1	10	4.65E-06	null	null	1	6.53E-06	null	11	null	null	4	null	FUBP1
NM_005452	36	4.7E-06	null	11	null	1	10	4.7E-06	null	null	null	null	null	11	null	null	4	null	WDR46

NM_001006	36	4.79E-06	null	11	null	1	10	4.79E-06	null	null	null	null	null	11	null	null	4	null	MTX2
NM_002206	36	4.81E-06	null	11	null	-1	10	4.81E-06	null	null	null	null	null	11	null	null	4	null	ITGA7
NM_016155	36	4.99E-06	null	11	null	1	10	4.99E-06	null	null	null	null	null	11	null	null	4	null	MMP17
NM_001007	36	5.02E-06	null	11	null	1	10	5.02E-06	null	null	null	null	null	11	null	null	4	null	SMARCB1
NM_006888	36	5.02E-06	null	11	null	-1	10	5.02E-06	null	null	-1	5.92E-06	null	11	null	null	4	null	CALM1
NM_002212	36	5.05E-06	null	11	null	1	10	5.05E-06	null	null	null	null	null	11	null	null	4	null	EIF6
NM_003360	36	5.07E-06	null	11	null	1	10	5.07E-06	null	null	null	null	null	11	null	null	4	null	UGT8
NM_013974	36	5.11E-06	null	11	null	null	11	null	null	null	null	null	-1	10	5.11E-06	null	4	null	DDAH2
NM_018473	36	5.11E-06	null	11	null	1	10	5.11E-06	null	null	null	null	null	11	null	null	4	null	THEM2
NM_019026	36	5.15E-06	null	11	null	1	10	5.15E-06	null	null	1	7.04E-06	null	11	null	null	4	null	TMCO1
NM_005223	36	5.2E-06	1	10	5.20E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	DNASE1
NM_001032	36	5.28E-06	null	11	null	1	10	5.28E-06	null	null	null	null	null	11	null	null	4	null	PQBP1
NM_002371	36	5.28E-06	null	11	null	null	11	null	null	null	-1	5.28E-06	null	11	null	-1	3	0.086185	MAL
NM_018121	36	5.28E-06	null	11	null	-1	10	5.28E-06	null	null	null	null	null	11	null	null	4	null	C10orf6
NM_001226	36	5.31E-06	null	11	null	1	10	5.31E-06	null	null	null	null	null	11	null	null	4	null	CASP6
NM_080916	36	5.38E-06	null	11	null	1	10	5.38E-06	null	null	null	null	null	11	null	null	4	null	DGUOK
NM_006455	36	5.43E-06	null	11	null	1	10	5.43E-06	null	null	null	null	null	11	null	null	4	null	SC65
NM_014291	36	5.45E-06	null	11	null	1	10	5.45E-06	null	null	null	null	null	11	null	null	4	null	GCAT
NM_001042	36	5.54E-06	null	11	null	1	10	5.54E-06	null	null	null	null	null	11	null	null	4	null	CENPA
NM_001024	36	5.56E-06	null	11	null	1	10	5.56E-06	null	null	null	null	null	11	null	null	4	null	RPS21
NM_000031	36	5.67E-06	null	11	null	1	10	5.67E-06	null	null	null	null	null	11	null	null	4	null	ALAD
NM_014731	36	5.68E-06	null	11	null	1	10	5.68E-06	null	null	null	null	null	11	null	null	4	null	ProSAPiP1
NM_014485	36	5.72E-06	null	11	null	-1	10	5.72E-06	null	null	-1	6.59E-06	null	11	null	null	4	null	PGDS
NM_012432	36	5.76E-06	1	10	5.76E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	SETDB1
NM_015132	36	5.76E-06	null	11	null	1	10	5.76E-06	null	null	null	null	null	11	null	null	4	null	SNX13
NM_005006	36	5.8E-06	null	11	null	1	10	5.80E-06	null	null	1	7.62E-06	null	11	null	null	4	null	NDUFS1
NM_014428	36	5.84E-06	1	10	5.84E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	TJP3
NM_001119	36	5.88E-06	null	11	null	-1	10	5.88E-06	-1	6.33E-05	-1	6.80E-06	null	11	null	null	4	null	ADD1
NM_002210	36	5.88E-06	null	11	null	1	10	5.88E-06	null	null	1	7.69E-06	null	11	null	null	4	null	ITGAV
NM_001991	36	5.92E-06	-1	10	5.92E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	EZH1
NM_004503	36	5.97E-06	1	10	0.090566	null	11	null	null	null	1	5.97E-06	null	11	null	null	4	null	HOXC6
NM_003342	36	6.05E-06	null	11	null	1	10	6.05E-06	null	null	null	null	null	11	null	null	4	null	UBE2G1
NM_014393	36	6.1E-06	null	11	null	1	10	6.10E-06	null	null	null	null	null	11	null	null	4	null	STAU2
NM_001039	36	6.11E-06	null	11	null	null	11	null	null	null	null	null	1	10	6.11E-06	null	4	null	PRMT5
NM_015234	36	6.24E-06	null	11	null	null	11	null	-1	0.087949	-1	6.24E-06	-1	10	1.16E-05	null	4	null	GPR116
NM_000765	36	6.28E-06	null	11	null	-1	10	6.28E-06	null	null	null	null	null	11	null	null	4	null	CYP3A7
NM_002692	36	6.43E-06	null	11	null	1	10	6.43E-06	null	null	null	null	null	11	null	null	4	null	POLE2
XM_371575	36	6.43E-06	1	10	6.43E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	
NM_001307	36	6.48E-06	null	11	null	1	10	6.48E-06	null	null	null	null	null	11	null	null	4	null	CLDN7
NM_003098	36	6.57E-06	1	10	6.57E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	SNTA1
NM_017528	36	6.8E-06	1	10	6.80E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	WBSCR22
NM_006854	36	6.89E-06	null	11	null	1	10	6.89E-06	null	null	null	null	null	11	null	null	4	null	KDELR2
NM_022073	36	6.99E-06	null	11	null	1	10	6.99E-06	null	null	null	null	null	11	null	null	4	null	EGLN3
NM_001668	36	7.03E-06	1	10	7.03E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	ARNT
NM_024056	36	7.1E-06	null	11	null	1	10	7.10E-06	null	null	1	8.95E-06	null	11	null	null	4	null	TMEM106C
XM_037557	36	7.16E-06	1	10	7.16E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	TBC1D30
NM_005788	36	7.22E-06	null	11	null	1	10	7.22E-06	null	null	1	9.25E-06	null	11	null	null	4	null	PRMT3

NM_014265	36	7.22E-06	1	10	7.22E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	ADAM28
NM_006638	36	7.35E-06	1	10	7.35E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	RPP40
NM_021727	36	7.35E-06	null	11	null	-1	10	7.35E-06	null	null	null	null	null	11	null	null	4	null	FADS3
NM_001003	36	7.42E-06	null	11	null	-1	10	7.42E-06	null	null	-1	8.4E-06	null	11	null	null	4	null	PARVB
NM_001605	36	7.42E-06	null	11	null	null	11	null	null	null	1	7.42E-06	1	10	0.077736	null	4	null	AARS
NM_014016	36	7.42E-06	null	11	null	-1	10	0.094576	null	null	-1	7.42E-06	null	11	null	null	4	null	SACM1L
NM_014283	36	7.48E-06	null	11	null	1	10	7.48E-06	null	null	1	9.57E-06	null	11	null	null	4	null	C1orf9
NM_024745	36	7.53E-06	null	11	null	1	10	7.53E-06	null	null	null	null	null	11	null	null	4	null	SHCBP1
NM_002419	36	7.55E-06	null	11	null	-1	10	7.55E-06	null	null	null	null	null	11	null	null	4	null	MAP3K11
NM_005762	36	7.57E-06	null	11	null	1	10	7.57E-06	null	null	null	null	null	11	null	null	4	null	TRIM28
NM_001011	36	7.62E-06	null	11	null	1	10	7.62E-06	null	null	null	null	null	11	null	null	4	null	RPS7
NM_018063	36	7.69E-06	null	11	null	1	10	7.69E-06	null	null	null	null	null	11	null	null	4	null	HELLS
NM_004132	36	7.8E-06	1	10	7.80E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	HABP2
NM_001949	36	7.84E-06	1	10	7.84E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	E2F3
NM_022369	36	7.87E-06	null	11	null	1	10	7.87E-06	null	null	null	null	null	11	null	null	4	null	STRA6
NM_001363	36	8.07E-06	null	11	null	1	10	8.07E-06	null	null	1	1.04E-05	null	11	null	null	4	null	DKC1
NM_003335	36	8.15E-06	null	11	null	-1	10	8.15E-06	null	null	-1	8.85E-06	null	11	null	null	4	null	UBA7
NM_014745	36	8.4E-06	null	11	null	-1	10	8.4E-06	null	null	null	null	null	11	null	null	4	null	
NM_016426	36	8.51E-06	null	11	null	1	10	8.51E-06	null	null	null	null	null	11	null	null	4	null	GTSE1
NM_002094	36	8.67E-06	null	11	null	1	10	8.67E-06	null	null	null	null	null	11	null	null	4	null	GSPT1
NM_003656	36	8.67E-06	-1	10	8.67E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	CAMK1
NM_021064	36	8.82E-06	null	11	null	1	10	8.82E-06	null	null	null	null	null	11	null	null	4	null	HIST1H2AG
NM_002555	36	8.85E-06	null	11	null	1	10	8.85E-06	null	null	null	null	null	11	null	null	4	null	SLC22A18
NM_015506	36	8.89E-06	null	11	null	1	10	8.89E-06	null	null	null	null	null	11	null	null	4	null	MMACHC
NM_014710	36	9.05E-06	null	11	null	-1	10	9.05E-06	null	null	null	null	null	11	null	null	4	null	GPRASP1
NM_017729	36	9.13E-06	null	11	null	1	10	9.13E-06	null	null	null	null	null	11	null	null	4	null	EPS8L1
NM_006255	36	9.15E-06	null	11	null	-1	10	9.15E-06	null	null	-1	9.68E-06	null	11	null	null	4	null	PRKCH
NM_001528	36	9.24E-06	null	11	null	1	10	9.24E-06	null	null	null	null	null	11	null	null	4	null	HGFAC
NM_006004	36	9.25E-06	null	11	null	1	10	9.25E-06	null	null	null	null	null	11	null	null	4	null	UQCRH
NM_003254	36	9.25E-06	null	11	null	1	10	9.25E-06	null	null	null	null	null	11	null	null	4	null	TIMP1
NM_033450	36	9.28E-06	null	11	null	1	10	9.28E-06	null	null	null	null	null	11	null	null	4	null	ABCC10
NM_002690	36	9.46E-06	1	10	9.46E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	POLB
NM_001017	36	9.6E-06	null	11	null	1	10	9.60E-06	null	null	null	null	null	11	null	null	4	null	ALDH18A1
NM_002403	36	9.78E-06	null	11	null	1	10	9.78E-06	null	null	null	null	null	11	null	null	4	null	MFAP2
NM_006836	36	9.78E-06	null	11	null	1	10	9.78E-06	null	null	null	null	null	11	null	null	4	null	GCN1L1
NM_000187	36	9.8E-06	null	11	null	null	11	null	null	null	1	9.8E-06	1	10	0.080986	null	4	null	HGD
NM_004405	36	9.98E-06	1	10	9.98E-06	null	11	null	null	null	null	null	null	11	null	null	4	null	DLX2
NM_001042	36	1.01E-05	null	11	null	1	10	1.01E-05	null	null	null	null	null	11	null	null	4	null	RRBP1
NM_014661	36	1.07E-05	null	11	null	-1	10	0.098594	null	null	-1	1.07E-05	null	11	null	null	4	null	FAM53B
NM_018077	36	1.07E-05	null	11	null	1	10	1.07E-05	null	null	null	null	null	11	null	null	4	null	RBM28
NM_006933	36	1.08E-05	1	10	1.08E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	MRPS6
NM_014326	36	1.08E-05	null	11	null	-1	10	1.08E-05	null	null	-1	1.14E-05	null	11	null	null	4	null	DAPK2
NM_020312	36	1.08E-05	null	11	null	1	10	1.08E-05	null	null	null	null	null	11	null	null	4	null	COQ9
NM_015550	36	1.09E-05	null	11	null	1	10	1.09E-05	null	null	null	null	null	11	null	null	4	null	OSBPL3
NM_004553	36	1.1E-05	null	11	null	1	10	1.1E-05	null	null	1	1.37E-05	null	11	null	null	4	null	NDUFS6
NM_004933	36	1.11E-05	1	10	1.11E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	CDH15
NM_025155	36	1.12E-05	null	11	null	1	10	1.12E-05	null	null	null	null	null	11	null	null	4	null	PAAF1

NM_002475	36	1.14E-05	null	11	null	1	10	1.14E-05	null	null	null	null	null	11	null	null	4	null	MYL6B
NM_006399	36	1.14E-05	null	11	null	1	10	1.14E-05	null	null	null	null	null	11	null	null	4	null	BATF
NM_004252	36	1.18E-05	null	11	null	1	10	1.18E-05	null	null	null	null	null	11	null	null	4	null	SLC9A3R1
NM_001347	36	1.19E-05	null	11	null	1	10	1.19E-05	null	null	null	null	null	11	null	null	4	null	DGKQ
NM_000356	36	1.19E-05	1	10	0.048075	null	11	null	null	null	1	1.19E-05	null	11	null	null	4	null	TCOF1
NM_015966	36	1.19E-05	1	10	1.19E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	ERGIC3
NM_001007	36	1.21E-05	null	11	null	1	10	1.21E-05	null	null	1	1.47E-05	null	11	null	null	4	null	
NM_004645	36	1.22E-05	null	11	null	1	10	1.22E-05	null	null	null	null	null	11	null	null	4	null	COIL
NM_007145	36	1.23E-05	null	11	null	1	10	1.23E-05	null	null	1	1.52E-05	null	11	null	null	4	null	ZNF146
NM_001443	36	1.23E-05	1	10	1.23E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	FABP1
NM_002651	36	1.28E-05	1	10	1.28E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	PI4KB
NM_203463	36	1.29E-05	null	11	null	null	11	null	null	null	1	1.29E-05	1	10	3.26E-05	null	4	null	LASS6
NM_005674	36	1.31E-05	null	11	null	1	10	1.31E-05	null	null	1	1.61E-05	null	11	null	null	4	null	ZNF239
NM_014727	36	1.31E-05	1	10	1.31E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	MLL4
NM_003185	36	1.31E-05	null	11	null	1	10	1.31E-05	null	null	null	null	null	11	null	null	4	null	TAF4
NM_002052	36	1.31E-05	1	10	1.31E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	GATA4
NM_001033	36	1.32E-05	null	11	null	1	10	1.32E-05	null	null	null	null	null	11	null	null	4	null	RRM1
NM_002257	36	1.35E-05	1	10	1.35E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	KLK1
NM_004617	36	1.37E-05	1	10	1.37E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	TM4SF4
NM_005392	36	1.4E-05	null	11	null	-1	10	1.40E-05	-1	0.000137	-1	1.42E-05	null	11	null	null	4	null	PHF2
NM_014050	36	1.4E-05	null	11	null	null	11	null	null	null	null	null	1	10	1.40E-05	null	4	null	MRPL42
NM_024712	36	1.4E-05	null	11	null	1	10	1.40E-05	null	null	null	null	null	11	null	null	4	null	ELMO3
NM_001048	36	1.42E-05	null	11	null	null	11	null	null	null	null	null	1	10	1.42E-05	null	4	null	STIL
NM_003922	36	1.42E-05	null	11	null	-1	10	1.42E-05	null	null	null	null	null	11	null	null	4	null	HERC1
NM_001030	36	1.43E-05	1	10	1.43E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	KLK3
NM_018334	36	1.44E-05	-1	10	1.44E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	LRRN3
NM_001042	36	1.45E-05	null	11	null	1	10	1.45E-05	null	null	null	null	null	11	null	null	4	null	COASY
NM_002972	36	1.5E-05	null	11	null	1	10	1.50E-05	null	null	null	null	null	11	null	null	4	null	SBF1
NM_014715	36	1.52E-05	null	11	null	null	11	null	null	null	null	null	1	10	1.52E-05	null	4	null	RICS
NM_020664	36	1.52E-05	null	11	null	1	10	1.52E-05	null	null	null	null	null	11	null	null	4	null	DECR2
NM_020438	36	1.55E-05	1	10	1.55E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	DOLPP1
NM_000997	36	1.55E-05	null	11	null	1	10	1.55E-05	null	null	null	null	null	11	null	null	4	null	RPL37
NM_017864	36	1.56E-05	1	10	1.56E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	INTS8
NM_017906	36	1.56E-05	null	11	null	1	10	1.56E-05	null	null	null	null	null	11	null	null	4	null	PAK1IP1
NM_000832	36	1.61E-05	null	11	null	1	10	1.61E-05	null	null	null	null	null	11	null	null	4	null	GRIN1
NM_001625	36	1.61E-05	null	11	null	1	10	1.61E-05	null	null	null	null	null	11	null	null	4	null	AK2
NM_000511	36	1.63E-05	null	11	null	1	10	1.63E-05	null	null	null	null	null	11	null	null	4	null	FUT2
NM_006828	36	1.67E-05	null	11	null	1	10	1.67E-05	null	null	null	null	null	11	null	null	4	null	ASCC3
NM_012223	36	1.68E-05	null	11	null	-1	10	0.097527	null	null	-1	1.68E-05	null	11	null	null	4	null	MYO1B
NM_014479	36	1.68E-05	null	11	null	1	10	1.68E-05	null	null	null	null	null	11	null	null	4	null	ADAMDEC1
NM_024728	36	1.71E-05	1	10	1.71E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	C7orf10
NM_015559	36	1.75E-05	null	11	null	-1	10	1.75E-05	null	null	null	null	null	11	null	null	4	null	SETBP1
NM_006978	36	1.8E-05	null	11	null	null	11	null	null	null	null	null	1	10	1.80E-05	null	4	null	RNF113A
NM_001040	36	1.9E-05	null	11	null	null	11	null	null	null	null	null	1	10	1.90E-05	null	4	null	TMEM70
NM_006463	36	1.91E-05	null	11	null	1	10	1.91E-05	null	null	1	2.57E-05	null	11	null	null	4	null	STAMBP
NM_004502	36	1.96E-05	null	11	null	1	10	1.96E-05	null	null	null	null	null	11	null	null	4	null	HOXB7
NM_014206	36	1.96E-05	null	11	null	null	11	null	null	null	null	null	1	10	1.96E-05	null	4	null	C11orf10

NM_017570	36	1.96E-05	null	11	null	1	10	1.96E-05	null	null	1	2.74E-05	null	11	null	null	4	null	OPLAH
NM_006479	36	2.06E-05	null	11	null	1	10	2.06E-05	null	null	null	null	null	11	null	null	4	null	RAD51AP1
NM_016310	36	2.08E-05	null	11	null	null	11	null	null	null	null	null	1	10	2.08E-05	null	4	null	POLR3K
NM_001123	36	2.11E-05	null	11	null	1	10	2.11E-05	null	null	null	null	null	11	null	null	4	null	ADK
NM_170662	36	2.21E-05	null	11	null	1	10	2.21E-05	null	null	null	null	null	11	null	null	4	null	CBLB
NM_000434	36	2.22E-05	null	11	null	1	10	2.22E-05	null	null	null	null	null	11	null	null	4	null	NEU1
NM_017515	36	2.24E-05	null	11	null	1	10	2.24E-05	null	null	null	null	null	11	null	null	4	null	SLC35F2
NM_001040	36	2.28E-05	null	11	null	1	10	2.28E-05	null	null	null	null	null	11	null	null	4	null	SLC26A6
NM_024096	36	2.28E-05	1	10	2.28E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	XTP3TPA
NM_005663	36	2.29E-05	null	11	null	1	10	2.29E-05	null	null	null	null	null	11	null	null	4	null	WHSC2
NM_000375	36	2.32E-05	1	10	2.32E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	UROS
NM_001079	36	2.34E-05	null	11	null	null	11	null	null	null	null	null	1	10	2.34E-05	null	4	null	CUL4B
NM_022754	36	2.36E-05	null	11	null	1	10	2.36E-05	null	null	null	null	null	11	null	null	4	null	SFXN1
NM_003075	36	2.38E-05	1	10	2.38E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	SMARCC2
NM_005550	36	2.43E-05	null	11	null	1	10	2.43E-05	null	null	null	null	null	11	null	null	4	null	KIFC3
NM_001001	36	2.54E-05	null	11	null	null	11	null	null	null	null	null	1	10	2.54E-05	null	4	null	ZDHHC13
NM_000088	36	2.66E-05	null	11	null	null	11	null	null	null	1	2.66E-05	1	10	0.05564	null	4	null	COL1A1
NM_000056	36	2.77E-05	1	10	2.77E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	BCKDHB
NM_015421	36	2.84E-05	null	11	null	1	10	2.84E-05	null	null	1	4.33E-05	null	11	null	null	4	null	TMEM186
NM_024092	36	2.84E-05	null	11	null	-1	10	2.84E-05	null	null	null	null	null	11	null	null	4	null	TMEM109
NM_001211	36	2.85E-05	null	11	null	null	11	null	null	null	null	null	1	10	2.85E-05	null	4	null	BUB1B
NM_001975	36	2.85E-05	null	11	null	1	10	2.85E-05	null	null	null	null	null	11	null	null	4	null	ENO2
NM_033540	36	2.98E-05	null	11	null	null	11	null	null	null	null	null	1	10	2.98E-05	null	4	null	MFN1
NM_001018	36	2.99E-05	null	11	null	null	11	null	null	null	null	null	1	10	2.99E-05	null	4	null	BRCC3
NM_005787	36	2.99E-05	null	11	null	1	10	2.99E-05	null	null	null	null	null	11	null	null	4	null	ALG3
NM_002795	36	3.11E-05	1	10	3.11E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	PSMB3
NM_014281	36	3.17E-05	null	11	null	1	10	0.057788	null	null	1	3.17E-05	null	11	null	null	4	null	PUF60
NM_181672	36	3.57E-05	null	11	null	null	11	null	null	null	null	null	1	10	3.57E-05	null	4	null	OGT
NM_014328	36	3.58E-05	null	11	null	1	10	3.58E-05	null	null	1	5.88E-05	null	11	null	null	4	null	RUSC1
NM_016049	36	3.6E-05	null	11	null	null	11	null	null	null	null	null	1	10	3.60E-05	null	4	null	FAM158A
NM_004208	36	3.74E-05	null	11	null	1	10	3.74E-05	null	null	null	null	null	11	null	null	4	null	AIFM1
NM_005646	36	3.84E-05	null	11	null	1	10	3.84E-05	null	null	null	null	null	11	null	null	4	null	TARBP1
NM_001042	36	4.03E-05	null	11	null	1	10	4.03E-05	null	null	null	null	null	11	null	null	4	null	PARP2
NM_004998	36	4.48E-05	null	11	null	1	10	4.48E-05	null	null	null	null	null	11	null	null	4	null	MYO1E
NM_018490	36	4.57E-05	null	11	null	1	10	4.57E-05	null	null	null	null	null	11	null	null	4	null	LGR4
NM_001083	36	4.89E-05	null	11	null	-1	10	4.89E-05	null	null	null	null	null	11	null	null	4	null	TCF4
NM_002689	36	4.89E-05	null	11	null	1	10	4.89E-05	null	null	null	null	null	11	null	null	4	null	POLA2
NM_014820	36	5.49E-05	null	11	null	null	11	null	null	null	null	null	1	10	5.49E-05	null	4	null	TOMM70A
NM_006080	36	6.72E-05	1	10	6.72E-05	null	11	null	null	null	null	null	null	11	null	null	4	null	SEMA3A
NM_004169	36	7.48E-05	null	11	null	1	10	7.48E-05	null	null	null	null	null	11	null	null	4	null	SHMT1
NM_002103	36	7.61E-05	null	11	null	1	10	7.61E-05	null	null	null	null	null	11	null	null	4	null	GYS1
NM_015675	36	9.15E-05	null	11	null	-1	10	9.15E-05	null	null	null	null	null	11	null	null	4	null	GADD45B
NM_017763	36	9.78E-05	null	11	null	1	10	9.78E-05	null	null	null	null	null	11	null	null	4	null	RNF43
NM_015277	36	0.000118	null	11	null	-1	10	0.000137	null	null	-1	0.000118	null	11	null	null	4	null	NEDD4L
NM_001013	36	0.000165	null	11	null	1	10	0.000165	null	null	1	0.000412	null	11	null	null	4	null	CXorf40B
NM_022085	36	0.000228	1	10	0.000228	null	11	null	null	null	null	null	null	11	null	null	4	null	TXNDC5
NM_025107	36	0.000228	null	11	null	null	11	null	null	null	null	null	-1	10	0.000228	null	4	null	MYCT1

NM_001037	36	0.000269	null	11	null	1	10	0.000269	null	null	null	null	null	11	null	null	4	null	EIF3B
NM_152341	36	0.000274	null	11	null	null	11	null	null	null	null	null	null	11	null	1	3	0.000274	PAQR4
NM_004687	36	0.000342	null	11	null	1	10	0.000342	null	null	null	null	null	11	null	null	4	null	MTMR4
NM_006284	36	0.000342	1	10	0.000342	null	11	null	null	null	null	null	null	11	null	null	4	null	TAF10
NM_024116	36	0.000342	null	11	null	null	11	null	null	null	null	null	1	10	0.000342	null	4	null	JOSD3
NM_006528	36	0.000412	null	11	null	1	10	0.000412	null	null	null	null	null	11	null	null	4	null	TFPI2
NM_006176	36	0.022574	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.022574	NRGN
NM_006210	36	0.027053	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.027053	PEG3
NM_005730	36	0.029094	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.029094	CTDSP2
NM_030797	36	0.034312	-1	10	0.034312	null	11	null	null	null	null	null	null	11	null	null	4	null	FAM49A
NM_005742	36	0.037593	null	11	null	null	11	null	null	null	null	null	1	10	0.037593	null	4	null	PDIA6
NM_014725	36	0.040704	null	11	null	-1	10	0.040704	null	null	null	null	null	11	null	null	4	null	STARD8
NM_004153	36	0.041174	null	11	null	null	11	null	null	null	null	null	1	10	0.041174	null	4	null	ORC1L
NM_000112	36	0.041833	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.041833	SLC26A2
NM_003768	36	0.042022	null	11	null	-1	10	0.042022	null	null	null	null	null	11	null	null	4	null	PEA15
NM_001092	36	0.045832	null	11	null	null	11	null	null	null	null	null	-1	10	0.045832	null	4	null	ABR
NM_002630	36	0.045918	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.045918	PGC
NM_001005	36	0.047397	null	11	null	null	11	null	null	null	null	null	-1	10	0.047397	null	4	null	CPM
NM_015198	36	0.047821	-1	10	0.047821	null	11	null	null	null	null	null	null	11	null	null	4	null	COBL
NM_006732	36	0.047986	null	11	null	-1	10	0.047986	null	null	null	null	null	11	null	null	4	null	FOSB
NM_003629	36	0.048747	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.048747	PIK3R3
NM_015296	36	0.048843	-1	10	0.048843	null	11	null	null	null	null	null	null	11	null	null	4	null	DOCK9
NM_007282	36	0.048927	-1	10	0.048927	null	11	null	null	null	null	null	null	11	null	null	4	null	RNF13
NM_004049	36	0.048988	-1	10	0.048988	null	11	null	null	null	null	null	null	11	null	null	4	null	BCL2A1
NM_012256	36	0.049346	1	10	0.049346	null	11	null	null	null	null	null	null	11	null	null	4	null	ZNF212
NM_000210	36	0.050313	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.050313	ITGA6
NM_002998	36	0.050336	-1	10	0.050336	null	11	null	null	null	null	null	null	11	null	null	4	null	SDC2
NM_022912	36	0.050364	-1	10	0.050364	null	11	null	null	null	null	null	null	11	null	null	4	null	REEP1
NM_006750	36	0.050994	-1	10	0.050994	null	11	null	null	null	null	null	null	11	null	null	4	null	SNTB2
NM_001032	36	0.051321	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.051321	STXBP1
NM_015714	36	0.051474	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.051474	G0S2
NM_015045	36	0.052354	-1	10	0.052354	null	11	null	null	null	null	null	null	11	null	null	4	null	WAPAL
NM_002937	36	0.053481	null	11	null	null	11	null	null	null	null	null	-1	10	0.053481	null	4	null	ANG
NM_006673	36	0.053637	null	11	null	-1	10	0.053637	null	null	null	null	null	11	null	null	4	null	
NM_006258	36	0.053828	null	11	null	-1	10	0.053828	null	null	null	null	null	11	null	null	4	null	PRKG1
NM_004762	36	0.054712	null	11	null	-1	10	0.054712	null	null	null	null	null	11	null	null	4	null	PSCD1
NM_021244	36	0.055627	-1	10	0.055627	null	11	null	null	null	null	null	null	11	null	null	4	null	RRAGD
NM_002881	36	0.056962	-1	10	0.056962	null	11	null	-1	0.082775	null	null	null	11	null	null	4	null	RALB
NM_001017	36	0.059188	null	11	null	null	11	null	null	null	null	null	-1	10	0.059188	null	4	null	INPP5D
NM_001003	36	0.060497	null	11	null	null	11	null	null	null	null	null	1	10	0.060497	null	4	null	MAD2L1BP
NM_004685	36	0.060799	null	11	null	-1	10	0.060799	null	null	null	null	null	11	null	null	4	null	MTMR6
NM_005590	36	0.062877	null	11	null	1	10	0.062877	null	null	null	null	null	11	null	null	4	null	MRE11A
NM_030971	36	0.064048	null	11	null	-1	10	0.064048	null	null	null	null	null	11	null	null	4	null	SFXN3
NM_001540	36	0.064684	null	11	null	null	11	null	null	null	null	null	null	11	null	1	3	0.064684	HSPB1
NM_006793	36	0.065078	null	11	null	null	11	null	null	null	null	null	1	10	0.065078	null	4	null	PRDX3
NM_017534	36	0.065721	null	11	null	-1	10	0.065721	null	null	null	null	null	11	null	null	4	null	MYH2
NM_001032	36	0.06575	-1	10	0.06575	null	11	null	null	null	null	null	null	11	null	null	4	null	TFPI

NM_015049	36	0.067779	null	11	null	null	11	null	null	null	null	null	-1	10	0.067779	null	4	null	TRAK2
NM_003899	36	0.0679	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.0679	ARHGEF7
NM_002865	36	0.067951	null	11	null	null	11	null	null	null	null	null	1	10	0.067951	null	4	null	RAB2A
NM_004573	36	0.068346	null	11	null	null	11	null	null	null	null	null	-1	10	0.068346	null	4	null	PLCB2
NM_005842	36	0.068387	null	11	null	null	11	null	null	null	null	null	-1	10	0.068387	null	4	null	SPRY2
NM_002933	36	0.068543	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.068543	RNASE1
NM_000714	36	0.068895	-1	10	0.068895	null	11	null	null	null	null	null	null	11	null	null	4	null	TSPO
NM_014670	36	0.069065	null	11	null	null	11	null	null	null	null	null	1	10	0.069065	null	4	null	BZW1
NM_004137	36	0.070352	null	11	null	-1	10	0.070352	null	null	null	null	null	11	null	null	4	null	KCNMB1
NM_002010	36	0.070657	null	11	null	null	11	null	null	null	null	null	-1	10	0.070657	null	4	null	FGF9
NM_000380	36	0.071273	-1	10	0.071273	null	11	null	null	null	null	null	null	11	null	null	4	null	XPA
NM_005539	36	0.071881	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.071881	INPP5A
NM_005335	36	0.072291	null	11	null	-1	10	0.072291	null	null	null	null	null	11	null	null	4	null	HCLS1
NM_006875	36	0.072425	1	10	0.072425	null	11	null	null	null	null	null	null	11	null	null	4	null	PIM2
NM_006866	36	0.072494	null	11	null	null	11	null	null	null	null	null	-1	10	0.072494	null	4	null	LILRA2
NM_001045	36	0.073572	null	11	null	-1	10	0.073572	null	null	null	null	null	11	null	null	4	null	SLA
NM_005266	36	0.073985	null	11	null	-1	10	0.073985	null	null	null	null	null	11	null	null	4	null	GJA5
NM_003684	36	0.075629	null	11	null	-1	10	0.075629	null	null	null	null	null	11	null	null	4	null	MKNK1
NM_005436	36	0.075715	null	11	null	null	11	null	null	null	null	null	1	10	0.075715	null	4	null	CCDC6
NM_004907	36	0.075991	null	11	null	-1	10	0.075991	null	null	null	null	null	11	null	null	4	null	IER2
NM_001379	36	0.077531	null	11	null	1	10	0.077531	null	null	null	null	null	11	null	null	4	null	DNMT1
NM_001287	36	0.077601	null	11	null	1	10	0.077601	null	null	null	null	null	11	null	null	4	null	CLCN7
NM_000156	36	0.077985	null	11	null	1	10	0.077985	null	null	null	null	null	11	null	null	4	null	GAMT
NM_002353	36	0.079035	null	11	null	null	11	null	null	null	null	null	1	10	0.079035	null	4	null	TACSTD2
NM_024420	36	0.079381	null	11	null	null	11	null	null	null	null	null	1	10	0.079381	null	4	null	PLA2G4A
NM_000153	36	0.079452	-1	10	0.079452	null	11	null	null	null	null	null	null	11	null	null	4	null	GALC
NM_007317	36	0.079483	1	10	0.079483	null	11	null	null	null	null	null	null	11	null	null	4	null	KIF22
NM_003403	36	0.079808	null	11	null	null	11	null	null	null	null	null	1	10	0.079808	null	4	null	YY1
NM_003097	36	0.080039	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.080039	SNRPN
NM_005922	36	0.080173	null	11	null	-1	10	0.080173	null	null	null	null	null	11	null	null	4	null	MAP3K4
NM_001009	36	0.080267	-1	10	0.080267	null	11	null	null	null	null	null	null	11	null	null	4	null	MFAP3L
NM_006086	36	0.08081	null	11	null	null	11	null	null	null	null	null	1	10	0.08081	null	4	null	TUBB3
NM_015878	36	0.08083	null	11	null	null	11	null	null	null	null	null	1	10	0.08083	null	4	null	AZIN1
NM_001914	36	0.080963	null	11	null	-1	10	0.080963	null	null	null	null	null	11	null	null	4	null	CYB5A
NM_001025	36	0.081178	-1	10	0.081178	null	11	null	null	null	null	null	null	11	null	null	4	null	NDEL1
NM_002628	36	0.081191	null	11	null	null	11	null	null	null	null	null	1	10	0.081191	null	4	null	PFN2
NM_012290	36	0.081254	null	11	null	null	11	null	null	null	null	null	1	10	0.081254	null	4	null	TLK1
NM_004691	36	0.082092	null	11	null	-1	10	0.082092	null	null	null	null	null	11	null	null	4	null	ATP6V0D1
NM_000291	36	0.082536	null	11	null	null	11	null	null	null	null	null	1	10	0.082536	null	4	null	PGK1
NM_000782	36	0.082539	null	11	null	null	11	null	null	null	null	null	1	10	0.082539	null	4	null	CYP24A1
NM_033133	36	0.083037	1	10	0.083037	null	11	null	null	null	null	null	null	11	null	null	4	null	CNP
NM_001012	36	0.08336	null	11	null	1	10	0.08336	null	null	null	null	null	11	null	null	4	null	U2AF2
NM_021960	36	0.083726	null	11	null	-1	10	0.083726	null	null	null	null	null	11	null	null	4	null	MCL1
NM_003622	36	0.083728	-1	10	0.083728	null	11	null	null	null	null	null	null	11	null	null	4	null	PPFIBP1
NM_003878	36	0.084306	null	11	null	null	11	null	null	null	null	null	1	10	0.084306	null	4	null	GGH
NM_002380	36	0.084355	null	11	null	null	11	null	null	null	null	null	-1	10	0.084355	null	4	null	MATN2
NM_002803	36	0.084424	null	11	null	null	11	null	null	null	null	null	1	10	0.084424	null	4	null	PSMC2

NM_005596	36	0.085248	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.085248	NFIB
NM_014991	36	0.085315	-1	10	0.085315	null	11	null	null	null	null	null	null	11	null	null	4	null	WDFY3
NM_003300	36	0.085776	1	10	0.085776	null	11	null	null	null	null	null	null	11	null	null	4	null	TRAF3
NM_014301	36	0.085853	-1	10	0.085853	null	11	null	null	null	null	null	null	11	null	null	4	null	ISCU
NM_002355	36	0.086171	-1	10	0.086171	null	11	null	null	null	null	null	null	11	null	null	4	null	M6PR
NM_005347	36	0.086204	null	11	null	null	11	null	null	null	null	null	1	10	0.086204	null	4	null	HSPA5
NM_001456	36	0.087029	null	11	null	-1	10	0.087029	null	null	null	null	null	11	null	null	4	null	FLNA
NM_003551	36	0.087031	null	11	null	-1	10	0.087031	null	null	null	null	null	11	null	null	4	null	NME5
NM_005611	36	0.087469	null	11	null	-1	10	0.087469	null	null	null	null	null	11	null	null	4	null	RBL2
NM_000231	36	0.087525	null	11	null	-1	10	0.087525	null	null	null	null	null	11	null	null	4	null	SGCG
NM_004240	36	0.087947	null	11	null	-1	10	0.087947	null	null	null	null	null	11	null	null	4	null	TRIP10
NM_002938	36	0.088268	null	11	null	null	11	null	null	null	null	null	1	10	0.088268	null	4	null	RNF4
NM_000675	36	0.089468	null	11	null	null	11	null	null	null	null	null	-1	10	0.089468	null	4	null	ADORA2A
NM_000884	36	0.090115	null	11	null	null	11	null	null	null	null	null	1	10	0.090115	null	4	null	IMPDH2
NM_000093	36	0.090374	null	11	null	null	11	null	null	null	null	null	1	10	0.090374	null	4	null	COL5A1
NM_006377	36	0.090392	null	11	null	null	11	null	null	null	null	null	-1	10	0.090392	null	4	null	UNC13B
NM_000107	36	0.090407	null	11	null	null	11	null	null	null	null	null	-1	10	0.090407	null	4	null	DDB2
NM_004953	36	0.090557	null	11	null	null	11	null	null	null	null	null	1	10	0.090557	null	4	null	EIF4G1
NM_012198	36	0.090631	-1	10	0.090631	null	11	null	null	null	null	null	null	11	null	null	4	null	GCA
NM_006816	36	0.090833	null	11	null	1	10	0.090833	null	null	null	null	null	11	null	null	4	null	LMAN2
NM_004302	36	0.09093	1	10	0.09093	null	11	null	null	null	null	null	null	11	null	null	4	null	ACVR1B
NM_001897	36	0.090985	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.090985	CSPG4
NM_006570	36	0.091186	-1	10	0.091186	null	11	null	null	null	null	null	null	11	null	null	4	null	RRAGA
NM_003020	36	0.09146	null	11	null	null	11	null	null	null	null	null	1	10	0.09146	null	4	null	SCG5
NM_005444	36	0.091626	1	10	0.091626	null	11	null	null	null	null	null	null	11	null	null	4	null	RQCD1
NM_003762	36	0.091767	null	11	null	-1	10	0.091767	null	null	null	null	null	11	null	null	4	null	VAMP4
NM_000982	36	0.092771	null	11	null	-1	10	0.092771	null	null	null	null	null	11	null	null	4	null	RPL21
NM_001039	36	0.093353	-1	10	0.093353	null	11	null	null	null	null	null	null	11	null	null	4	null	ELMO1
NM_001030	36	0.093647	null	11	null	null	11	null	null	null	null	null	-1	10	0.093647	null	4	null	SPN
NM_015850	36	0.093846	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.093846	FGFR1
NM_001835	36	0.094049	null	11	null	null	11	null	null	null	null	null	null	11	null	1	3	0.094049	
NM_005930	36	0.094109	null	11	null	null	11	null	null	null	null	null	1	10	0.094109	null	4	null	CTAGE5
NM_032632	36	0.094441	null	11	null	1	10	0.094441	null	null	null	null	null	11	null	null	4	null	PAPOLA
NM_004094	36	0.094475	null	11	null	null	11	null	null	null	null	null	null	11	null	1	3	0.094475	EIF2S1
NM_006711	36	0.09506	null	11	null	null	11	null	null	null	null	null	1	10	0.09506	null	4	null	RNPS1
NM_002742	36	0.095098	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.095098	PRKD1
NM_006435	36	0.096321	-1	10	0.096321	null	11	null	null	null	null	null	null	11	null	null	4	null	IFITM2
NM_002811	36	0.096483	null	11	null	null	11	null	null	null	null	null	1	10	0.096483	null	4	null	PSMD7
NM_000418	36	0.09663	null	11	null	-1	10	0.09663	null	null	null	null	null	11	null	null	4	null	IL4R
NM_000791	36	0.097066	null	11	null	1	10	0.097066	null	null	null	null	null	11	null	null	4	null	DHFR
NM_000325	36	0.097157	null	11	null	1	10	0.097157	null	null	null	null	null	11	null	null	4	null	PITX2
NM_014875	36	0.097187	null	11	null	null	11	null	null	null	null	null	1	10	0.097187	null	4	null	KIF14
NM_000336	36	0.097687	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.097687	SCNN1B
NM_005239	36	0.097745	-1	10	0.097745	null	11	null	null	null	null	null	null	11	null	null	4	null	ETS2
NM_004862	36	0.09795	null	11	null	-1	10	0.09795	null	null	null	null	null	11	null	null	4	null	LITAF
NM_000066	36	0.098273	null	11	null	-1	10	0.098273	null	null	null	null	null	11	null	null	4	null	C8B
NM_000194	36	0.098385	null	11	null	null	11	null	null	null	null	null	1	10	0.098385	null	4	null	HPRT1

NM_004598	36	0.098403	1	10	0.098403	null	11	null	null	null	null	null	null	11	null	null	4	null	SPOCK1
NM_005186	36	0.098535	null	11	null	null	11	null	null	null	null	null	1	10	0.098535	null	4	null	CAPN1
NM_003797	36	0.098561	null	11	null	null	11	null	null	null	null	null	1	10	0.098561	null	4	null	EED
NM_003680	36	0.098615	null	11	null	1	10	0.098615	null	null	null	null	null	11	null	null	4	null	YARS
NM_001831	36	0.098971	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.098971	CLU
NM_007294	36	0.099294	null	11	null	1	10	0.099294	null	null	null	null	null	11	null	null	4	null	BRCA1
NM_001018	36	0.09967	null	11	null	null	11	null	null	null	null	null	1	10	0.09967	null	4	null	LRP8
NM_006842	36	0.099675	null	11	null	null	11	null	null	null	null	null	1	10	0.099675	null	4	null	SF3B2
NM_001017	36	0.099958	null	11	null	null	11	null	null	null	null	null	null	11	null	-1	3	0.099958	SULT1A3
NM_004555	37	2.04E-06	null	11	null	null	11	null	null	null	-1	2.04E-06	null	11	null	null	4	null	NFATC3
NM_003775	37	2.06E-06	null	11	null	null	11	null	null	null	-1	2.06E-06	null	11	null	null	4	null	S1PR4
NM_005187	37	2.07E-06	null	11	null	null	11	null	null	null	-1	2.07E-06	null	11	null	null	4	null	CBFA2T3
NM_001006	37	2.08E-06	null	11	null	null	11	null		-1	0.099668	-1	2.08E-06	null	11	null	null	4	null	RPS6KA2
NM_001010	37	2.24E-06	null	11	null	null	11	null	null	null	-1	2.24E-06	null	11	null	null	4	null	C10orf38
NM_004621	37	2.24E-06	null	11	null	null	11	null	null	null	-1	2.24E-06	null	11	null	null	4	null	TRPC6
NM_000023	37	2.27E-06	null	11	null	null	11	null	null	null	-1	2.27E-06	null	11	null	null	4	null	SGCA
NM_003240	37	2.37E-06	null	11	null	null	11	null	null	null	-1	2.37E-06	null	11	null	null	4	null	LEFTY2
NM_015864	37	2.48E-06	null	11	null	null	11	null	null	null	-1	2.48E-06	null	11	null	null	4	null	C6orf32
NM_015378	37	2.5E-06	null	11	null	null	11	null	null	null	-1	2.50E-06	null	11	null	null	4	null	VPS13D
NM_002337	37	2.53E-06	null	11	null	null	11	null	null	null	-1	2.53E-06	null	11	null	null	4	null	LRPAP1
NM_000565	37	2.64E-06	null	11	null	null	11	null	null	null	-1	2.64E-06	null	11	null	null	4	null	IL6R
NM_001025	37	2.76E-06	null	11	null	null	11	null	null	null	-1	2.76E-06	null	11	null	null	4	null	CHI3L2
NM_005827	37	2.78E-06	null	11	null	null	11	null	null	null	1	2.78E-06	null	11	null	null	4	null	SLC35B1
NM_004824	37	2.79E-06	null	11	null	null	11	null	null	null	1	2.79E-06	null	11	null	null	4	null	CDYL
NM_004532	37	2.8E-06	null	11	null	null	11	null	null	null	1	2.8E-06	null	11	null	null	4	null	MUC4
NM_004470	37	2.86E-06	null	11	null	null	11	null	null	null	1	2.86E-06	null	11	null	null	4	null	FKBP2
NM_014607	37	2.9E-06	null	11	null	null	11	null	null	null	1	2.90E-06	null	11	null	null	4	null	UBXD2
NM_012067	37	3.31E-06	null	11	null	null	11	null	null	null	1	3.31E-06	null	11	null	null	4	null	AKR7A3
NM_003668	37	3.46E-06	null	11	null	null	11	null	null	null	1	3.46E-06	null	11	null	null	4	null	MAPKAPK5
NM_001188	37	3.47E-06	null	11	null	null	11	null	null	null	1	3.47E-06	null	11	null	null	4	null	BAK1
NM_000094	37	3.55E-06	null	11	null	null	11	null	null	null	1	3.55E-06	null	11	null	null	4	null	COL7A1
NM_002639	37	3.63E-06	null	11	null	null	11	null	null	null	1	3.63E-06	null	11	null	null	4	null	SERPINB5
NM_014904	37	3.69E-06	null	11	null	null	11	null	null	null	-1	3.69E-06	null	11	null	null	4	null	RAB11FIP2
NM_003898	37	3.74E-06	null	11	null	null	11	null	null	null	1	3.74E-06	null	11	null	null	4	null	SYNJ2
NM_004995	37	4.27E-06	null	11	null	null	11	null	null	null	1	4.27E-06	null	11	null	null	4	null	MMP14
NM_000474	37	4.55E-06	null	11	null	null	11	null	null	null	1	4.55E-06	null	11	null	null	4	null	TWIST1
NM_024315	37	4.62E-06	null	11	null	null	11	null	null	null	-1	4.62E-06	null	11	null	null	4	null	C7orf23
NM_001033	37	4.68E-06	null	11	null	null	11	null	null	null	1	4.68E-06	null	11	null	null	4	null	TIAL1
NM_003795	37	4.79E-06	null	11	null	null	11	null	null	null	-1	4.79E-06	null	11	null	null	4	null	SNX3
NM_001018	37	4.84E-06	null	11	null	null	11	null	null	null	1	4.84E-06	null	11	null	null	4	null	NME1
NM_015419	37	4.96E-06	null	11	null	null	11	null	null	null	1	4.96E-06	null	11	null	null	4	null	MXRA5
NM_002827	37	5.02E-06	null	11	null	null	11	null	null	null	-1	5.02E-06	null	11	null	null	4	null	PTPN1
NM_006231	37	5.45E-06	null	11	null	null	11	null	null	null	1	5.45E-06	null	11	null	null	4	null	POLE
NM_004723	37	5.56E-06	null	11	null	null	11	null	null	null	-1	5.56E-06	null	11	null	null	4	null	ARHGEF2
NM_006178	37	6.38E-06	null	11	null	null	11	null	null	null	1	6.38E-06	null	11	null	null	4	null	NSF
NM_003969	37	6.69E-06	null	11	null	null	11	null	null	null	1	6.69E-06	null	11	null	null	4	null	UBE2M
NM_133494	37	9.46E-06	null	11	null	null	11	null	null	null	-1	9.46E-06	null	11	null	null	4	null	NEK7

NM_018982	37	1.35E-05	null	11	null	null	11	null	null	null	1	1.35E-05	null	11	null	null	4	null	YIPF1
NM_005052	37	1.5E-05	null	11	null	null	11	null	null	null	1	1.50E-05	null	11	null	null	4	null	RAC3
NM_000692	37	1.65E-05	null	11	null	null	11	null	null	null	1	1.65E-05	null	11	null	null	4	null	ALDH1B1
NM_021999	37	3.17E-05	null	11	null	null	11	null	null	null	-1	3.17E-05	null	11	null	null	4	null	ITM2B
NM_004301	37	3.29E-05	null	11	null	null	11	null	null	null	1	3.29E-05	null	11	null	null	4	null	ACTL6A
NM_001184	37	4.12E-05	null	11	null	null	11	null	null	null	1	4.12E-05	null	11	null	null	4	null	ATR
NM_003979	37	4.12E-05	null	11	null	null	11	null	-1	4.12E-05	null	null	null	11	null	null	4	null	GPRC5A
NM_007106	37	4.12E-05	null	11	null	null	11	null	null	null	-1	4.12E-05	null	11	null	null	4	null	UBL3
NM_015112	37	6.33E-05	null	11	null	null	11	null	null	null	1	6.33E-05	null	11	null	null	4	null	MAST2
NM_003778	37	8.23E-05	null	11	null	null	11	null	null	null	1	8.23E-05	null	11	null	null	4	null	B4GALT4
XM_376350	37	8.23E-05	null	11	null	null	11	null	-1	8.23E-05	null	null	null	11	null	null	4	null	
NM_002957	37	9.15E-05	null	11	null	null	11	null	-1	0.091366	-1	9.15E-05	null	11	null	null	4	null	RXRA
NM_001335	37	0.000165	null	11	null	null	11	null	null	null	-1	0.000165	null	11	null	null	4	null	CTSW
NM_001032	37	0.000274	null	11	null	null	11	null	null	null	-1	0.000274	null	11	null	null	4	null	
NM_006478	37	0.099636	null	11	null	null	11	null	-1	0.099636	null	null	null	11	null	null	4	null	GAS2L1

Supplementary Table1B

	Q<0.1	changed	up	down
	all	1838	918	920
group I	Nor-IA	1004	415	589
	nor-IB	1419	690	729
	nor-I	1602	778	824
group II	Nor-IIA	106	8	98
	nor-IIB	718	303	415
	nor-II	728	304	424
group III	Nor-IIIA	928	413	515
	nor-IIIB	321	62	259
	nor-III	984	425	559

Q<0.05	changed	up	down
all	1651	844	807
Nor-IA	945	398	547
nor-IB	1348	674	674
nor-I	1493	750	743
Nor-IIA	103	8	95
nor-IIB	718	303	415
nor-II	725	304	421
Nor-IIIA	852	363	489
nor-IIIB	298	58	240
nor-III	887	371	516

Q<0.1	II(728)	III(984)
overlap	II	III
I(1602)	647	801
up(778)	261	311
down(824)	386	490
II(728)		507
up(304)		173
down(424)		334

Q<0.05		
overlap	II(725)	III(887)
I(1493)	645	781
up(750)	261	303
down(743)	384	478
II(725)		507
up(304)		173
down		334

Q<0.1	changed	up	down
I-II-III	479	156	323
only I	632	362	271
only II	53	26	27
only III	155	97	58

Q<0.05	changed	up	down
I-II-III	479	156	323
only I	546	342	204
only II	52	26	26
only III	78	51	27

Q<0.01	changed	up	down
I-II-III	479	156	323
only I	504	339	165
only II	52	26	26
only III	52	40	12

Supplementary Table2 All pathways

Pathway	Normal vs	Normal vs	Normal vs	Normal vs	Normal vs	Normal vs	Rank
Hs_2-Tissues-Internal_Organs	8.632	6.741	5.424	5.966	5.922	5.062	0
Hs_Adipogenesis	3.93	2.968	3.138	3.359	2.775	4.004	0
Hs_1-Tissue-Blood_and_Lymph	8.638	6.16	2.583	4.535	6.702	/	1
Hs_2-Tissues-Blood_and_Lymph	6.192	5.84	/	4.442	6.166	3.402	1
Hs_IL-5_NetPath_17	6.048	6.114	/	5.106	5.178	4.192	1
Hs_Complement_and_Coagulatio	5.673	4.175	/	4.042	6.004	3.947	1
Hs_TGF-beta-Receptor_NetPath_	5.339	5.428	/	3.432	4.383	2.822	1
Hs_2-Tissues-Endocrine_and_C	4.963	3.81	/	3.74	4.653	3.937	1
Hs_Circadian_Exercise	4.825	3.027	/	3.572	5.621	4.016	1
Hs_Peptide_GPCRs	4.297	2.135	/	2.674	3.802	3.449	1
Hs_1-Tissue-Internal_Organs	4.034	2.054	/	2.697	3.124	3.485	1
Hs_Prostaglandin_synthesis_re	3.467	4.481	/	2.554	3.699	3.683	1
Hs_Statin_Pathway_PharmGKB	3.244	2.362	/	4.215	3.439	4.179	1
Hs_IL-3_NetPath_15	2.775	2.519	/	2.709	2.037	2.427	1
Hs_Calcium_regulation_in_car	2.701	3.39	/	2.869	2.217	3.311	1
Hs_Focal_adhesion_KEGG	2.355	4.011	/	3.331	5.787	3.706	1
Hs_Eicosanoid_Synthesis	2.322	2.867	/	2.282	2.491	5.242	1
Hs_Glycolysis_Gluconeogenesi	2.088	2.207	/	2.679	3.253	3.688	1
Hs_Oxidative_Stress	/	3.168	/	3.948	3.145	2.21	2
Hs_Glycolysis_and_Gluconeoge	/	2.275	/	2.306	3.153	2.833	2
Hs_Integrin-mediated_cell_ad	/	2.758	/	2.277	2.687	3.477	2
Hs_Matrix_Metalloproteinases	2.982	2.524	/	2.647	1.953	/	2
Hs_Id_NetPath_5	2.76	3.26	/	/	2.04	2.376	2
Hs_Striated_muscle_contracti	2.749	3.122	/	1.986	/	3.968	2
Hs_IL-7_NetPath_19	2.25	3.405	/	3.901	4.01	/	2
Hs_EGFR1_NetPath_4	2.141	2.625	3.038	/	/	2.714	2
Hs_T-Cell-Receptor_NetPath_1	/	3.849	/	3.584	/	2.02	3
Hs_2-Tissues-Muscle_Fat and_	/	/	/	3.846	5.413	2.968	3
Hs_Nuclear_Receptors	/	2.482	/	2.86	2.109	/	3
Hs_Cell_cycle_KEGG	5.372	6.442	/	/	4.649	/	3
Hs_IL-6_NetPath_18	4.018	4.454	/	/	2.985	/	3
Hs_Cell_Cycle-G1_to_S_control	3.026	5.33	/	/	3.301	/	3
Hs_Fatty_Acid_Omega_Oxidatio	2.961	2.156	/	/	2.259	/	3
Hs_Glutamate_metabolism	2.819	3.027	/	/	2.352	/	3
Hs_TGF_Beta_Signaling_Pathwa	2.613	/	/	2.744	/	2.276	3
Hs_Apoptosis	2.586	2.575	/	2.663	/	/	3
Hs_Triacylglyceride_Synthesi	2.519	2.269	/	/	2.704	/	3
Hs_1-Tissue-Muscle_fat_and_c	2.512	2.455	/	/	2.764	/	3
Hs_Ovarian_Infertility_Genes	2.378	3.576	/	/	3.197	/	3
Hs_Fructose_and_mannose_meta	2.25	2.536	/	3.901	/	/	3
Hs_Smooth_muscle_contraction	2.217	2.661	/	2.057	/	/	3
Hs_p38_MAPK_signaling_pathway	/	/	/	2.377	/	2.577	4
Hs_Glycerolipid_metabolism	/	/	/	2.758	/	2.701	4
Hs_Arginine_and_proline_meta	/	/	/	2.094	/	2.904	4
Hs_Tyrosine_metabolism	/	/	/	/	2.107	3.947	4
Hs_Folate_biosynthesis	/	1.986	/	/	2.107	/	4
Hs_Alpha6-Beta4-Integrin_Net	/	2.824	/	/	2.454	/	4
Hs_1-Tissue-Embryonic_Stem_C	/	2.536	/	/	2.983	/	4
Hs_Aminoacyl_tRNA_biosynthesi	/	/	/	2.637	3.414	/	4
Hs_One_carbon_pool_by_folate	/	4.138	/	/	3.552	/	4
Hs_DNA_replication_Reactome	/	4.945	/	/	3.679	/	4
Hs_B_Cell_Receptor_NetPath_1	/	3.214	/	2.116	/	/	4
Hs_IL-2_NetPath_14	/	2.162	/	3.306	/	/	4
Hs_Blood_Clotting_Cascade	2.927	/	/	/	3.117	/	4
Hs_N_Glycans_biosynthesis	2.101	/	/	2.037	/	/	4
Hs_Nucleotide_Metabolism	1.956	1.986	/	/	/	/	4
Hs_Phosphatidylinositol_sign	/	/	/	/	/	2.176	5
Hs_Prostaglandin_and_leukotri	/	/	/	/	/	2.651	5
Hs_G_Protein_Signaling	/	/	/	/	/	2.666	5
Hs_Histidine_metabolism	/	/	/	/	/	2.833	5
Hs_Regulation_of_Actin_Cytos	/	/	/	/	/	3.086	5
Hs_Nucleotide_GPCRs	/	/	/	/	2.003	/	5
Hs_GPCRDB_Class_B_Secretin-li	/	/	/	/	2.108	/	5
Hs_Phospholipid_degradation	/	/	/	/	2.108	/	5
Hs_RNA_transcription_Reactom	/	/	/	/	2.794	/	5
Hs_Inflammatory_Response_Pat	/	/	/	/	3.087	/	5
Hs_Small_ligand_GPCRs	/	/	/	2.411	/	/	5
Hs_O_Glycans_biosynthesis	/	/	/	2.637	/	/	5

Hs_Blood_group_glycolipid_bi	/	/	/	2.698	/	/	5
Hs_Keratan_sulfate_biosynthes	/	/	/	4.058	/	/	5
Hs_Translation_Factors	/	2.036	/	/	/	/	5
Hs_Phenylalanine_metabolism	/	2.06	/	/	/	/	5
Hs_Pyrimidine_metabolism	/	2.072	/	/	/	/	5
Hs_Complement_Activation_Clas	/	2.156	/	/	/	/	5
Hs_Starch_and_sucrose_metabol	/	2.201	/	/	/	/	5
Hs_Fas_Pathway_and_Stress_In	/	2.282	/	/	/	/	5
Hs_Androgen-Receptor_NetPath_	/	2.414	/	/	/	/	5
Hs_Ribosomal_Proteins	/	2.416	/	/	/	/	5
Hs_HSP70_and_Apoptosis	/	2.528	/	/	/	/	5
Hs_MAPK_signaling_pathway_KE	/	2.539	/	/	/	/	5
Hs_Inositol_phosphate_metabol	/	2.552	/	/	/	/	5
Hs_Purine_metabolism	/	2.591	/	/	/	/	5
Hs_D_Arginine_and_D_ornithin	/	2.63	/	/	/	/	5
Hs_Benzoate_degradation_via_	/	2.663	/	/	/	/	5
Hs_Nicotinate_and_nicotinami	/	2.688	/	/	/	/	5
Hs_Hypertrophy_model	/	2.704	/	/	/	/	5
Hs_Sphingoglycolipid_metaboli	/	2.94	/	/	/	/	5
Hs_Kit-Receptor_NetPath_6	/	3.257	/	/	/	/	5
Hs_ACE-Inhibitor_pathway_Pha	3.72	/	/	/	/	/	5
Hs_beta_Alanine_metabolism	2.519	/	/	/	/	/	5
Hs_IL-1_NetPath_13	2.212	/	/	/	/	/	5
Hs_Fatty_Acid_Beta_Oxidation_	2.184	/	/	/	/	/	5

Supplementary Table3 All GOs

1	GO	Normal vs IA	Normal vs IB	Normal vs IIA	Normal vs IIB	Normal vs IIIA	Normal vs IIIB	Rank
2	multicellular organismal process	7.334	7.096	7.341	6.669	6.952	10.309	0
3	coreceptor\, soluble ligand activi	5.328	4.434	17.157	6.381	5.551	9.573	0
4	platelet alpha granule	5.328	4.434	8.52	6.381	5.551	9.573	0
5	endothelin receptor activity	5.328	4.434	8.52	6.381	5.551	9.573	0
6	enzyme linked receptor protein sig	4.464	3.405	5.507	3.462	4.699	9.23	0
7	amine oxidase activity	4.818	3.922	10.741	3.739	3.169	8.95	0
8	regulation of liquid surface tensi	4.818	3.922	5.278	5.856	6.908	8.95	0
9	fibroblast growth factor receptor	3.014	2.377	5.278	3.739	3.169	8.95	0
10	system development	7.92	7.609	7.15	7.1	7.259	8.943	0
11	organ development	7.546	8.741	6.988	7.613	8.211	8.94	0
12	multicellular organismal developme	7.058	7.078	7.254	6.515	7.17	8.867	0
13	anatomical structure development	7.326	6.911	6.289	6.575	6.769	8.151	0
17	response to wounding	8.174	6.629	2.816	5.218	5.832	7.509	0
18	developmental process	7.759	8.469	5.512	7.006	7.218	7.351	0
19	integral to plasma membrane	7.622	5.873	5.03	6.401	6.807	7.206	0
20	response to external stimulus	7.535	5.739	2.233	4.265	5.232	7.191	0
21	intrinsic to plasma membrane	7.476	5.821	4.971	6.279	6.67	7.109	0
22	plasma membrane	10.17	7.824	4.988	8.097	8.055	7.088	0
23	plasma membrane part	9.112	7.037	5.561	6.942	7.899	7.065	0
24	organ morphogenesis	5.074	3.94	7.234	4.835	5.278	7.048	0
25	circulation	3.658	4.087	4.184	3.364	5.096	7.017	0
26	immunoglobulin binding	6.554	3.424	2.957	2.967	4.634	6.844	0
27	cell migration	5.895	5.836	3.092	5.246	4.665	6.812	0
28	respiratory gaseous exchange	4.441	3.933	4.012	3.975	4.714	6.774	0
35	negative regulation of endothelial	3.767	3.135	12.131	4.512	3.925	6.769	0
45	complement factor D activity	3.767	3.135	12.131	4.512	3.925	6.769	0
47	peroxisome proliferator activated	3.767	3.135	12.131	4.512	3.925	6.769	0
52	germ-line stem cell division	3.767	3.135	12.131	4.512	3.925	6.769	0
85	male germ-line stem cell division	3.767	3.135	12.131	4.512	3.925	6.769	0
88	AT DNA binding	3.767	3.135	12.131	4.512	3.925	6.769	0
91	endothelin-B receptor activity	3.767	3.135	12.131	4.512	3.925	6.769	0
100	negative regulation of vasodilatio	3.767	3.135	12.131	4.512	3.925	6.769	0
101	quinone binding	3.767	3.135	12.131	4.512	3.925	6.769	0
102	catalase activity	3.767	3.135	12.131	4.512	3.925	6.769	0
103	transmembrane receptor protein ser	2.782	2.377	6.303	3.506	2.1	6.663	0
111	transmembrane receptor protein tyr	3.89	2.649	2.646	2.136	4.302	6.509	0
112	blood vessel development	5.119	4.872	5.97	4.846	4.98	6.509	0
113	hemoglobin complex	4.582	3.65	3.825	4.07	3.417	6.475	0
114	positive regulation of inflammator	4.582	3.65	3.825	2.491	4.81	6.475	0
115	positive regulation of defense res	4.582	3.65	3.825	2.491	4.81	6.475	0
116	vasculature development	5.606	5.016	5.907	5.103	5.189	6.427	0
118	anatomical structure morphogenesis	5.22	3.856	5.685	4.107	4.519	6.112	0
119	Z disc	4.777	2.876	2.624	4.829	4.021	6.104	0
121	cell proliferation	5.994	7.667	2.773	4.719	6.15	6.064	0

128	regulation of vasodilation	3.014	2.377	10.741	3.739	3.169	5.857	0
129	negative regulation of erythrocyte	3.014	2.377	5.278	3.739	3.169	5.857	0
132	tube development	4.224	3.204	6.721	3.43	2.738	5.761	0
133	anatomical structure formation	4.187	3.624	5.238	4.025	4.305	5.707	0
135	extracellular region part	4.819	3.381	2.965	4.064	5.224	5.631	0
137	localization of cell	5.6	6.703	2.569	5.828	4.555	5.587	0
138	cell motility	5.6	6.703	2.569	5.828	4.555	5.587	0
140	negative regulation of myeloid cel	5.129	3.983	5.097	4.304	3.536	5.529	0
141	gland development	2.931	2.763	2.687	3.469	3.189	5.443	0
142	biological adhesion	6.525	5.7	2.267	6.01	7.294	5.317	0
143	cell adhesion	6.525	5.7	2.267	6.01	7.294	5.317	0
144	angiogenesis	4.036	3.542	5.243	3.394	4.071	5.292	0
151	hyaluronoglucosaminidase activity	2.643	3.45	4.785	3.322	2.789	5.286	0
155	extracellular region	4.618	2.53	2.699	2.992	4.133	5.211	0
156	proteinaceous extracellular matrix	4.739	4.232	3.873	3.863	5.25	5.179	0
157	embryonic development	3.84	4.027	4.462	2.571	3.448	5.168	0
158	branching morphogenesis of a tube	2.961	3.445	4.851	3.387	2.59	5.125	0
159	extracellular matrix	4.665	4.151	3.837	3.802	5.175	5.124	0
160	blood vessel morphogenesis	3.769	3.382	5.583	3.75	4.171	5.078	0
161	carbohydrate binding	3.829	2.668	3.279	3.565	4.561	5.011	0
163	contractile fiber	3.551	3.198	2.458	2.468	2.777	4.996	0
169	morphogenesis of a branching struc	2.755	3.695	4.665	3.187	2.4	4.902	0
170	cell-substrate adhesion	4.401	4.11	3.369	2.788	3.338	4.878	0
172	regulation of biological process	4.3	5.898	3.502	2.483	4.553	4.865	0
173	cell communication	3.773	3.89	3.722	4.073	4.722	4.859	0
174	biological_process	7.717	8.88	3.226	5.946	7.879	4.846	0
179	receptor activity	3.088	2.126	4.389	3.689	4.455	4.744	0
180	biological regulation	4.408	6.132	3.804	2.705	4.94	4.725	0
198	midgut development	2.476	1.992	8.52	3.034	2.595	4.682	0
206	leg morphogenesis	2.476	1.992	8.52	3.034	2.595	4.682	0
207	positive regulation of vasoconstri	2.476	1.992	8.52	3.034	2.595	4.682	0
209	loss of chromatin silencing	2.476	1.992	8.52	3.034	2.595	4.682	0
230	mesonephros development	2.476	1.992	8.52	3.034	2.595	4.682	0
233	asymmetric cell division	2.476	1.992	8.52	3.034	2.595	4.682	0
235	regulation of melanocyte different	2.476	4.434	8.52	6.381	5.551	4.682	0
238	regulation of pigment cell differe	2.476	4.434	8.52	6.381	5.551	4.682	0
244	posterior midgut development	2.476	1.992	8.52	3.034	2.595	4.682	0
245	positive regulation of BMP signali	2.476	1.992	8.52	3.034	2.595	4.682	0
261	cholesterol homeostasis	2.972	2.18	8.835	3.849	3.162	4.599	0
262	myofibril	2.994	2.832	2.723	2.24	2.683	4.57	0
270	wound healing	5.411	3.679	3.859	2.717	3.802	4.471	0
271	transmembrane receptor protein kin	4.889	4.225	6.514	4.266	4.746	4.463	0
272	negative regulation of cell differ	2.983	2.184	3.628	3.147	2.771	4.463	0
273	contractile fiber part	3.409	3.158	2.652	2.774	2.567	4.448	0
274	hormone binding	3.798	2.876	2.624	3.68	6.049	4.426	0
277	heparin binding	3.405	3.348	2.16	4.211	5.174	4.415	0
278	regulation of cell migration	3.879	4.922	5.86	2.092	3.065	4.39	0

279	receptor-mediated endocytosis	4.509	2.2	3.24	3.681	4.16	4.385	0
280	glycosaminoglycan binding	3.725	3.023	3.014	3.764	4.927	4.327	0
281	cell-matrix adhesion	4.231	3.629	2.112	2.459	2.627	4.322	0
282	regulation of body fluids	5.927	4.426	3.734	4.787	3.597	4.302	0
287	signal transducer activity	3.599	2.555	3.338	3.878	4.298	4.261	0
288	molecular transducer activity	3.599	2.555	3.338	3.878	4.298	4.261	0
290	lipid raft	3.704	3.302	8.477	4.84	3.951	4.246	0
291	polysaccharide binding	3.539	2.831	2.918	3.596	4.721	4.177	0
292	spectrin	5.927	4.802	7.897	7.226	2.023	4.169	0
296	cholesterol transport	3.237	2.498	7.897	4.07	3.417	4.169	0
299	sterol transport	3.237	2.498	7.897	4.07	3.417	4.169	0
302	transmembrane receptor protein tyr	4.649	3.709	7.19	4.338	4.978	4.168	0
309	cell differentiation	5.769	6.361	2.344	4.88	4.99	4.098	0
310	cellular developmental process	5.769	6.361	2.344	4.88	4.99	4.098	0
311	signal transduction	3.524	3.555	4.199	3.726	4.528	4.079	0
324	negative regulation of cellular pr	4.907	5.707	5.119	2.203	3.476	3.98	0
328	regulation of developmental proces	4.698	3.925	2.655	2.946	3.567	3.942	0
341	negative regulation of biological	4.977	5.686	4.861	2.074	3.357	3.854	0
347	cell fraction	2.914	3.013	2.67	4.136	3.047	3.816	0
348	regulation of biological quality	3.663	4.317	3.962	3.3	4.094	3.811	0
350	pattern binding	3.074	2.345	2.679	3.174	4.206	3.803	0
356	hemostasis	5.206	3.593	3.116	3.942	3.811	3.75	0
393	regulation of endothelial cell dif	4.197	3.436	6.909	5.082	4.386	3.738	0
406	blood vessel maturation	4.197	3.436	6.909	2.349	1.972	3.738	0
446	retrograde axon cargo transport	4.197	3.436	6.909	5.082	4.386	3.738	0
456	cellular_component	5.435	6.154	3.71	3.89	5.153	3.691	0
464	regulation of myeloid cell differe	4.358	3.175	3.519	3.325	3.953	3.654	0
472	extracellular matrix organization	2.931	2.297	4.337	3.469	3.189	3.574	0
486	complement activation\, alternativ	3.738	3.882	3.241	3.333	2.738	3.483	0
488	calcium ion binding	4.691	3.456	3.083	4.033	4.977	3.48	0
490	regulation of angiogenesis	4.065	2.355	7.213	2.343	3.681	3.445	0
495	skeletal development	3.678	4.12	2.077	3.738	4.117	3.413	0
510	regulation of cell differentiation	3.979	3.125	3.978	3.458	3.692	3.267	0
512	actin cytoskeleton organization an	5.281	5.399	2.259	5.156	4.883	3.239	0
520	blood coagulation	4.621	3.116	3.252	3.142	3.147	3.183	0
594	gut development	3.319	2.501	9.489	2.967	2.399	3.146	0
602	embryonic organ development	2.408	2.231	4.184	2.407	2.604	3.142	0
607	protein-tyrosine kinase activity	3.097	3.43	4.82	4.014	4.136	3.112	0
609	integrin binding	2.961	2.424	3.047	1.989	3.825	3.082	0
611	coagulation	4.455	2.959	3.169	3.016	3.01	3.08	0
620	phosphotransferase activity\, alco	2.794	4.72	2.394	2.863	2.56	3.021	0
622	actin filament-based process	4.887	5.426	2.118	4.804	4.51	3.011	0
630	lysosome	3.658	2.625	3.151	3.364	2.266	2.92	0
631	lytic vacuole	3.658	2.625	3.151	3.364	2.266	2.92	0
633	protein kinase activity	2.791	4.639	2.894	3.521	2.269	2.908	0
639	pigment cell differentiation	1.964	3.044	5.78	5.033	3.162	2.869	0
640	melanocyte differentiation	1.964	3.044	5.78	5.033	3.162	2.869	0

662	negative regulation of endothelial	3.014	2.377	10.741	3.739	3.169	2.763	0
768	vacuole	3.005	2.774	2.82	3.174	2.049	2.5	0
771	cellular component organization an	5.218	6.379	2.155	3.938	5.374	2.475	0
782	cytochrome-b5 reductase activity	2.643	2.04	4.785	3.322	2.789	2.462	0
859	barbed-end actin filament capping	3.056	2.188	4.825	4.009	2.371	2.258	0
864	actin filament capping	3.056	2.188	4.825	4.009	2.371	2.258	0
889	caveolar membrane	3.871	3.074	9.016	4.782	4.066	2.224	0
934	protein dimerization activity	2.472	4.6	2.356	2.376	2.646	2.184	0
938	regulation of actin filament depol	2.934	2.073	4.702	3.875	2.266	2.177	0
940	actin filament depolymerization	2.934	2.073	4.702	3.875	2.266	2.177	0
942	negative regulation of actin filam	2.934	2.073	4.702	3.875	2.266	2.177	0
1000	hydrolase activity\, acting on car	2.101	2.762	4.086	4.395	2.236	2.028	0
15	alcohol dehydrogenase activity\, z	4.197	3.436	/	5.082	4.386	7.731	1
16	icosanoid biosynthetic process	3.515	3.244	/	3.628	2.908	7.567	1
29	platelet alpha granule membrane	3.767	3.135	/	4.512	3.925	6.769	1
30	virion attachment\, binding of hos	3.767	3.135	/	4.512	3.925	6.769	1
31	establishment of mitotic spindle o	3.767	3.135	/	4.512	3.925	6.769	1
33	astral microtubule	3.767	3.135	/	4.512	3.925	6.769	1
37	endothelin-A receptor activity	3.767	3.135	/	4.512	3.925	6.769	1
39	alpha(1\,6)-fucosyltransferase act	3.767	3.135	/	4.512	3.925	6.769	1
41	nitric oxide transport	3.767	3.135	/	4.512	3.925	6.769	1
44	negative regulation of astrocyte d	3.767	3.135	/	4.512	3.925	6.769	1
51	CMP-sialic acid transport	3.767	3.135	/	4.512	3.925	6.769	1
55	phenylpyruvate tautomerase activit	3.767	3.135	/	4.512	3.925	6.769	1
60	CMP-sialic acid transporter activi	3.767	3.135	/	4.512	3.925	6.769	1
62	arachidonate 5-lipoxygenase activi	3.767	3.135	/	4.512	3.925	6.769	1
63	regulation of 1-phosphatidylinosit	3.767	3.135	/	4.512	3.925	6.769	1
65	complement component C1q binding	3.767	3.135	/	4.512	3.925	6.769	1
68	lamellar body	3.767	3.135	/	4.512	3.925	6.769	1
72	positive regulation of 1-phosphati	3.767	3.135	/	4.512	3.925	6.769	1
73	prostaglandin transporter activity	3.767	3.135	/	4.512	3.925	6.769	1
74	glycoprotein 6-alpha-L-fucosyltran	3.767	3.135	/	4.512	3.925	6.769	1
75	prostaglandin transport	3.767	3.135	/	4.512	3.925	6.769	1
76	taurine metabolic process	3.767	3.135	/	4.512	3.925	6.769	1
89	stromelysin 3 activity	3.767	3.135	/	4.512	3.925	6.769	1
90	cysteine dioxygenase activity	3.767	3.135	/	4.512	3.925	6.769	1
92	UDP-glucose\:hexose-1-phosphate ur	3.767	3.135	/	4.512	3.925	6.769	1
93	taurine biosynthetic process	3.767	3.135	/	4.512	3.925	6.769	1
94	aster	3.767	3.135	/	4.512	3.925	6.769	1
96	establishment of spindle orientati	3.767	3.135	/	4.512	3.925	6.769	1
98	glucose-6-phosphate isomerase acti	3.767	3.135	/	4.512	3.925	6.769	1
99	L-cysteine metabolic process	3.767	3.135	/	4.512	3.925	6.769	1
117	response to stress	6.056	8.638	/	4.587	6.755	6.313	1
120	vasodilation	/	2.269	7.466	3.791	3.161	6.096	1
122	icosanoid metabolic process	2.443	2.695	/	2.618	2.654	6.037	1
123	inflammatory response	5.675	4.389	/	4.112	4.689	5.988	1
126	cysteine metabolic process	3.014	5.467	/	3.739	5.039	5.857	1

134	regulation of blood vessel size	/	2.775	4.096	3.204	3.288	5.632	1
136	regulation of multicellular organi	3.762	4.092	/	3.729	4.251	5.628	1
139	insoluble fraction	2.421	3.21	2.364	3.245	/	5.529	1
152	cell surface receptor linked signa	2.396	/	4.342	2.082	3.861	5.276	1
153	response to stimulus	4.826	5.391	/	3.828	5.882	5.232	1
162	regulation of cell proliferation	4.185	4.874	/	3.496	3.987	4.998	1
165	regulation of defense response	3.642	2.67	2.091	/	3.874	4.927	1
166	regulation of inflammatory respons	3.642	2.67	2.091	/	3.874	4.927	1
167	NAD binding	2.818	1.965	2.091	/	3.874	4.927	1
178	respiratory tube development	2.061	/	4.55	3.062	2.868	4.764	1
181	embryonic pattern specification	/	3.081	3.459	2.476	2.501	4.705	1
183	negative regulation of cAMP metabo	2.476	1.992	/	3.034	2.595	4.682	1
184	receptor signaling protein serine/	5.328	4.434	/	6.381	2.595	4.682	1
185	interferon-gamma receptor activity	2.476	1.992	/	3.034	2.595	4.682	1
186	prostaglandin-D synthase activity	2.476	4.434	/	3.034	2.595	4.682	1
188	spermidine synthase activity	2.476	1.992	/	3.034	2.595	4.682	1
191	transforming growth factor beta re	5.328	4.434	/	6.381	2.595	4.682	1
192	development of secondary male sexu	2.476	1.992	/	3.034	2.595	4.682	1
193	long-chain-acyl-CoA dehydrogenase	2.476	1.992	/	3.034	2.595	4.682	1
194	natural killer cell differentiatio	2.476	1.992	/	3.034	2.595	4.682	1
195	development of secondary female se	2.476	1.992	/	3.034	2.595	4.682	1
197	RNA destabilization	5.328	4.434	/	3.034	2.595	4.682	1
202	interferon-gamma binding	2.476	1.992	/	3.034	2.595	4.682	1
208	inositol bisphosphate phosphatase	2.476	4.434	/	6.381	5.551	4.682	1
212	circadian sleep/wake cycle	5.328	4.434	/	3.034	5.551	4.682	1
223	calcitonin gene-related polypeptid	2.476	1.992	/	3.034	2.595	4.682	1
225	glyceraldehyde-3-phosphate dehydro	2.476	1.992	/	3.034	2.595	4.682	1
227	glyceraldehyde-3-phosphate dehydro	2.476	1.992	/	3.034	2.595	4.682	1
228	establishment and/or maintenance o	2.476	4.434	/	6.381	2.595	4.682	1
231	collagen type XI	2.476	1.992	/	3.034	2.595	4.682	1
234	establishment and/or maintenance o	2.476	4.434	/	6.381	2.595	4.682	1
237	transforming growth factor beta re	2.476	4.434	/	3.034	2.595	4.682	1
240	tryptase activity	2.476	1.992	/	3.034	2.595	4.682	1
241	regulation of astrocyte differenti	2.476	1.992	/	3.034	2.595	4.682	1
242	negative regulation of cAMP biosyn	2.476	1.992	/	3.034	2.595	4.682	1
247	phosphorylase kinase regulator act	2.476	1.992	/	3.034	2.595	4.682	1
258	negative regulation of development	3.687	/	3.224	2.585	2.646	4.653	1
259	myofibril assembly	2.972	2.18	/	2.665	5.253	4.599	1
260	striated muscle cell development	2.972	2.18	/	2.665	5.253	4.599	1
263	defense response	5.374	3.784	/	3.601	4.698	4.53	1
264	oxygen and reactive oxygen species	2.633	3.593	/	3.942	4.256	4.485	1
265	positive regulation of cell prolif	2.46	3.618	/	3.977	3.14	4.483	1
266	hindbrain morphogenesis	2.101	/	4.086	2.721	2.236	4.474	1
276	muscle cell development	2.819	2.037	/	2.532	5.035	4.426	1
285	mammary gland development	2.677	/	5.411	2.408	2.862	4.266	1
312	complement activation	2.779	3.696	/	3.771	2.256	4.059	1
315	leukocyte migration	3.492	3.084	/	2.933	2.995	4.059	1

316	activation of plasma proteins duri	2.779	3.696	/	3.771	2.256	4.059	1
317	sarcomere	2.302	/	3.003	2.627	2.525	4.038	1
320	cellular structure morphogenesis	3.004	2.542	2.833	2.122	/	3.99	1
321	cell morphogenesis	3.004	2.542	2.833	2.122	/	3.99	1
325	tube morphogenesis	3.346	2.409	4.625	2.664	/	3.98	1
327	regulation of cell motility	3.871	4.723	5.407	/	2.618	3.965	1
338	rough endoplasmic reticulum	2.987	4.455	/	2.293	3.161	3.908	1
340	cellular process	7.05	8.617	/	6.149	8.15	3.885	1
343	protein complex binding	5.322	4.074	/	3.016	4.808	3.824	1
346	positive regulation of biological	3.056	4.046	/	3.818	3.98	3.821	1
351	myeloid cell differentiation	3.108	4.386	/	2.469	3.413	3.787	1
353	regulation of locomotion	3.629	4.847	5.209	/	2.418	3.778	1
371	establishment of epithelial cell p	4.197	/	6.909	2.349	1.972	3.738	1
384	phosphatidate phosphatase activity	4.197	3.436	/	5.082	4.386	3.738	1
418	circadian behavior	4.197	3.436	/	2.349	4.386	3.738	1
444	ErbB-3 class receptor binding	6.526	5.431	/	2.349	6.799	3.738	1
452	actomyosin structure organization	4.777	4.399	/	4.009	5.939	3.733	1
454	transmembrane receptor activity	3.589	/	3.638	2.674	3.73	3.732	1
474	locomotion	3.351	4.898	4.983	/	2.187	3.562	1
475	alcohol metabolic process	2.868	2.873	/	4.26	3.049	3.56	1
476	protein binding	7.853	8.619	/	5.778	8.014	3.55	1
477	localization	3.29	4.235	/	3.737	3.501	3.544	1
478	immune system process	4.643	4.212	/	3.238	4.455	3.541	1
483	positive regulation of multicellul	2.759	2.878	/	2.668	3.06	3.505	1
489	muscle development	3.036	3.582	3.287	/	2.52	3.467	1
491	extracellular matrix part	2.677	4.184	/	2.116	4.672	3.44	1
496	cell development	4.774	6.141	/	3.697	4.241	3.39	1
497	striated muscle cell differentiati	2.603	/	1.977	3.514	4.443	3.319	1
507	regulation of cellular process	3.094	4.65	3.425	/	3.578	3.288	1
508	response to oxidative stress	2.579	3.265	/	3.124	3.369	3.281	1
513	acute inflammatory response	4.064	3.198	/	2.468	2.777	3.235	1
538	low-density lipoprotein catabolic	3.502	2.817	5.943	/	3.671	3.163	1
604	negative regulation of cell prolif	3.974	3.268	3.042	/	3.835	3.132	1
610	glycolysis	2.366	2.424	/	2.688	3.825	3.082	1
612	membrane fraction	/	2.187	2.252	2.745	2.054	3.07	1
623	protein amino acid phosphorylation	2.297	4.677	/	3.231	2.331	3.001	1
624	axon cargo transport	2.097	/	2.836	2.809	2.252	3.001	1
627	cytoskeleton organization and biog	5.089	6.612	/	3.902	6.114	2.997	1
634	positive regulation of cellular pr	2.239	3.042	/	2.55	3.387	2.897	1
636	phospholipase C activation	1.964	/	2.725	2.665	4.208	2.869	1
637	coreceptor activity	1.964	/	5.78	2.665	2.117	2.869	1
646	skeletal muscle development	2.983	2.592	2.185	/	3.759	2.829	1
663	lipoprotein catabolic process	3.014	2.377	5.278	/	3.169	2.763	1
686	NF-kappaB-inducing kinase activity	3.014	2.377	/	3.739	3.169	2.763	1
705	positive regulation of immune resp	3.351	3.288	/	2.502	3.161	2.756	1
706	positive regulation of immune syst	3.351	3.288	/	2.502	3.161	2.756	1
717	excretion	3.059	3.378	/	2.292	2.168	2.73	1

719	hematopoietin/interferon-class (D2	3.613	2.903	/	3.594	3.894	2.73	1
720	kinase activity	2.726	4.903	/	2.644	3.074	2.719	1
727	molecular_function	2.988	4.683	/	2.676	4.258	2.637	1
733	cortical actin cytoskeleton	3.629	3.534	5.411	4.641	/	2.635	1
734	negative regulation of angiogenesi	2.677	/	5.411	2.408	2.862	2.635	1
742	negative regulation of metabolic p	1.962	3.145	3.275	/	2.659	2.604	1
743	integrin-mediated signaling pathwa	2.329	4.083	/	2.774	2.007	2.596	1
744	hemopoietic or lymphoid organ deve	2.476	3.15	/	2.275	2.003	2.586	1
749	immunoglobulin mediated immune res	3.344	2.63	/	2.092	3.62	2.554	1
750	cell cortex	2.274	3.088	2.618	3.349	/	2.554	1
760	protein transporter activity	3.895	3.28	3.339	/	2.358	2.52	1
766	B cell mediated immunity	3.28	2.565	/	2.045	3.555	2.512	1
767	protein oligomerization	2.75	/	5.799	3.291	2.455	2.512	1
811	pyrimidine nucleotide sugar transp	2.643	2.04	/	3.322	2.789	2.462	1
824	protein amino acid N-linked glycos	5.567	3.642	/	3.245	2.501	2.458	1
825	regulation of RNA metabolic proces	/	3.21	2.364	2.185	2.601	2.434	1
831	transferase activity\, transferrin	2.431	4.827	/	2.376	2.541	2.407	1
833	intramolecular oxidoreductase acti	2.866	2.99	/	2.409	2.428	2.403	1
836	immune system development	2.444	3.245	/	2.334	2.003	2.383	1
840	cell-cell adhesion	3.204	3.188	/	3.555	3.074	2.353	1
846	regulation of immune system proces	2.72	2.588	/	1.998	3.01	2.337	1
847	regulation of immune response	2.72	2.588	/	1.998	3.01	2.337	1
849	cellular biosynthetic process	2.904	4.214	/	2.316	3.173	2.336	1
854	sequence-specific DNA binding	2.066	2.869	/	2.246	1.96	2.278	1
857	transcription cofactor activity	2.903	3.511	2.128	/	2.876	2.269	1
871	cellular component assembly	2.864	4.421	/	2.422	4.57	2.251	1
875	glutamine family amino acid metabo	2.016	3.268	/	2.219	4.16	2.247	1
879	carboxylic acid metabolic process	2.237	3.121	/	3.729	3.942	2.23	1
910	oxidoreductase activity\, acting o	2.347	/	4.399	2.992	2.486	2.224	1
928	organic acid metabolic process	2.208	3.085	/	3.701	3.91	2.212	1
935	protein complex assembly	2.132	3.309	2.676	/	3.886	2.18	1
950	regulation of mononuclear cell pro	2.431	1.983	/	2.751	2.033	2.105	1
951	regulation of lymphocyte prolifera	2.431	1.983	/	2.751	2.033	2.105	1
956	homeostatic process	3.066	4.451	/	2.99	4.015	2.078	1
971	peripheral nervous system developm	2.708	2.553	2.032	/	2.072	2.03	1
993	chylomicron	2.101	/	4.086	2.721	2.236	2.028	1
1026	soluble fraction	2.288	2.22	/	3.395	2.96	1.992	1
1037	RNA polymerase II transcription fa	2.603	/	1.977	2.585	2.802	1.961	1
1067	latrotoxin receptor activity	3.237	2.498	3.825	2.491	2.023	/	1
1090	liver development	3.237	2.498	3.825	2.491	3.417	/	1
1097	caveola	3.237	2.498	7.897	4.07	3.417	/	1
1125	actin cytoskeleton	3.804	5.004	3.52	2.76	2.616	/	1
1142	intercellular junction	4.303	3.755	3.133	4.531	3.647	/	1
1156	regulation of endothelial cell pro	2.987	3.362	7.466	5.288	4.483	/	1
1263	endothelial cell proliferation	2.768	3.109	7.094	4.975	4.198	/	1
1398	cell part	3.711	4.894	2.287	3.504	3.9	/	1
1399	cell	3.706	4.888	2.286	3.5	3.895	/	1

1478	cell junction	3.859	3.935	2.632	3.557	3.314	/	1
1499	chemical homeostasis	3.031	3.388	2.15	2.927	2.866	/	1
1564	negative regulation of cell migrat	2.819	4.552	5.588	2.532	1.992	/	1
1639	structural constituent of cytoskel	3.79	4.311	3.28	4.227	4.114	/	1
1760	cell-cell adherens junction	3.775	4.236	2.153	4.863	3.138	/	1
4801	hemidesmosome	2.476	1.992	8.52	3.034	2.595	/	1
34	cocaine metabolic process	3.767	3.135	/	4.512	/	6.769	2
38	cGMP-stimulated cyclic-nucleotide	3.767	3.135	/	/	3.925	6.769	2
40	circadian sleep/wake cycle\, sleep	3.767	3.135	/	/	3.925	6.769	2
42	aldehyde oxidase activity	3.767	3.135	/	/	3.925	6.769	2
43	positive regulation of keratinocyt	3.767	3.135	/	/	3.925	6.769	2
48	regulation of circadian sleep/wake	3.767	3.135	/	/	3.925	6.769	2
49	circadian sleep/wake cycle process	3.767	3.135	/	/	3.925	6.769	2
50	oxidoreductase activity\, acting o	3.767	3.135	/	/	3.925	6.769	2
53	ventricular system development	3.767	3.135	/	/	3.925	6.769	2
57	6\,7-dihydropteridine reductase ac	3.767	3.135	/	/	3.925	6.769	2
58	dihydrobiopterin metabolic process	3.767	3.135	/	/	3.925	6.769	2
64	arrestin mediated desensitization	/	3.135	/	4.512	3.925	6.769	2
66	beta2-adrenergic receptor activity	/	3.135	/	4.512	3.925	6.769	2
70	fourth ventricle development	3.767	3.135	/	/	3.925	6.769	2
71	inositol-1\,4-bisphosphate 1-phosp	/	3.135	/	4.512	3.925	6.769	2
77	regulation of keratinocyte migrati	3.767	3.135	/	/	3.925	6.769	2
79	acetylcholine receptor activator a	3.767	3.135	/	/	3.925	6.769	2
81	lateral ventricle development	3.767	3.135	/	/	3.925	6.769	2
82	third ventricle development	3.767	3.135	/	/	3.925	6.769	2
83	ventricular cardiac muscle cell de	3.767	3.135	/	/	3.925	6.769	2
95	growth hormone receptor activity	3.767	3.135	/	/	3.925	6.769	2
97	regulation of circadian sleep/wake	3.767	3.135	/	/	3.925	6.769	2
104	cerebellar Purkinje cell layer dev	3.502	2.817	/	/	3.671	6.622	2
107	positive regulation of smooth musc	3.502	2.817	/	/	3.671	6.622	2
108	mitotic G2 checkpoint	3.502	2.817	/	/	3.671	6.622	2
109	leukotriene biosynthetic process	3.138	/	/	2.809	2.252	6.574	2
110	alkene biosynthetic process	3.138	/	/	2.809	2.252	6.574	2
127	IgE binding	6.621	2.377	/	/	5.039	5.857	2
130	glial cell migration	3.014	2.377	/	/	3.169	5.857	2
131	telencephalon development	3.014	2.377	/	/	3.169	5.857	2
146	G2/M transition checkpoint	2.643	2.04	/	/	2.789	5.286	2
147	regulation of smooth muscle cell p	2.643	2.04	/	/	4.496	5.286	2
148	G2/M transition DNA damage checkpo	2.643	2.04	/	/	2.789	5.286	2
154	gas transport	3.518	2.683	/	/	2.56	5.224	2
168	lung development	/	/	2.917	2.51	2.4	4.902	2
171	nervous system development	2.951	/	2.372	/	2.03	4.871	2
187	negative regulation of protein mod	/	1.992	/	3.034	2.595	4.682	2
190	keratinocyte migration	2.476	1.992	/	/	2.595	4.682	2
200	xanthine dehydrogenase activity	2.476	1.992	/	/	2.595	4.682	2
204	IgE receptor activity	5.328	1.992	/	/	5.551	4.682	2
210	polyol catabolic process	2.476	1.992	/	/	5.551	4.682	2

211	glycerol catabolic process	2.476	1.992	/	/	5.551	4.682	2
213	negative regulation of smooth musc	/	1.992	/	3.034	2.595	4.682	2
215	regulation of sodium ion transport	/	1.992	/	3.034	2.595	4.682	2
216	norepinephrine binding	/	1.992	/	3.034	2.595	4.682	2
217	positive regulation of type I hype	5.328	1.992	/	/	5.551	4.682	2
219	regulation of type I hypersensitiv	5.328	1.992	/	/	5.551	4.682	2
226	Hsp70 protein binding	2.476	1.992	/	/	2.595	4.682	2
229	chemical homeostasis within a tiss	2.476	/	/	3.034	2.595	4.682	2
236	receptor activator activity	2.476	1.992	/	/	2.595	4.682	2
239	glutamate binding	/	4.434	/	3.034	2.595	4.682	2
243	oxidoreductase activity\, acting o	2.476	1.992	/	/	2.595	4.682	2
246	glycerol-3-phosphate catabolic pro	2.476	1.992	/	/	5.551	4.682	2
250	surfactant homeostasis	2.476	/	/	3.034	2.595	4.682	2
251	glycerol-3-phosphate dehydrogenase	2.476	1.992	/	/	5.551	4.682	2
252	glutamate-cysteine ligase activity	/	4.434	/	3.034	5.551	4.682	2
253	glutamate-cysteine ligase complex	/	4.434	/	3.034	5.551	4.682	2
256	negative regulation of protein ubi	/	1.992	/	3.034	2.595	4.682	2
268	alcohol dehydrogenase activity	2.101	/	/	2.721	2.236	4.474	2
284	patterning of blood vessels	/	3.534	2.531	2.408	/	4.266	2
294	sequestering of lipid	/	/	3.825	2.491	2.023	4.169	2
295	regulation of nitric oxide biosynt	/	/	3.825	2.491	2.023	4.169	2
297	cyclin-dependent protein kinase ac	3.237	4.802	/	/	4.81	4.169	2
304	G-protein signaling\, coupled to c	/	/	3.399	2.83	2.445	4.145	2
307	pregnancy	2.525	/	2.458	3.07	/	4.116	2
318	transforming growth factor beta re	2.302	/	4.787	2.627	/	4.038	2
319	cAMP-mediated signaling	/	/	3.309	2.705	2.315	4.02	2
322	spindle microtubule	3.324	2.437	/	/	3.536	3.982	2
333	positive regulation of phagocytosi	2.987	/	/	2.293	3.161	3.908	2
336	regulation of phagocytosis	2.987	/	/	2.293	3.161	3.908	2
352	alcohol catabolic process	2.17	/	/	2.153	3.931	3.778	2
357	G-protein signaling\, coupled to c	/	/	2.639	2.65	3.319	3.74	2
358	natriuresis	/	/	6.909	2.349	1.972	3.738	2
375	cholinesterase activity	4.197	3.436	/	2.349	/	3.738	2
379	establishment of mitotic spindle l	/	3.436	/	2.349	1.972	3.738	2
381	regulation of vascular permeabilit	/	/	6.909	2.349	1.972	3.738	2
383	negative regulation of muscle cont	/	3.436	/	2.349	1.972	3.738	2
403	negative regulation of nitric oxid	/	/	6.909	2.349	1.972	3.738	2
427	wound healing\, spreading of epide	4.197	3.436	/	/	1.972	3.738	2
453	humoral immune response	2.122	3.533	/	3.245	/	3.733	2
457	fibrillar collagen	/	3.109	/	6.403	7.98	3.682	2
458	oxygen transporter activity	2.768	3.109	/	2.12	/	3.682	2
460	oxygen transport	2.768	3.109	/	2.12	/	3.682	2
463	regulation of G-protein coupled re	/	2.606	5.529	/	3.265	3.654	2
466	membrane organization and biogenes	3.207	/	/	1.987	2.875	3.624	2
468	cell surface	3.997	2.808	/	/	3.405	3.619	2
469	cyclic-nucleotide-mediated signali	/	/	2.543	2.488	3.127	3.59	2
484	regulation of erythrocyte differen	/	/	3.241	3.333	2.738	3.483	2

511	extracellular space	3.622	/	/	2.675	3.025	3.241	2
514	endocytosis	3.432	1.971	/	/	3.515	3.233	2
515	membrane invagination	3.432	1.971	/	/	3.515	3.233	2
517	axon guidance	2.014	2.029	/	2.143	/	3.218	2
537	sleep	3.502	2.817	/	/	3.671	3.163	2
553	purine base biosynthetic process	3.502	4.544	/	/	3.671	3.163	2
574	rhythmic behavior	3.502	2.817	/	/	3.671	3.163	2
576	peptide hormone binding	3.502	2.817	/	/	3.671	3.163	2
584	retina development in camera-type	3.014	2.377	/	/	3.169	2.763	2
597	low-density lipoprotein binding	2.241	/	2.957	/	2.399	3.146	2
599	ureteric bud branching	3.319	2.501	6.223	/	/	3.146	2
600	negative regulation of multicellul	/	2.231	/	2.407	2.604	3.142	2
614	spindle	3.311	4.648	/	/	5.145	3.063	2
615	cell division	2.753	5.053	/	/	4.305	3.062	2
629	coenzyme binding	2.499	2.795	/	/	3.202	2.996	2
632	receptor binding	2.365	/	2.159	/	2.826	2.917	2
642	hemopoiesis	2.299	2.897	/	/	2.073	2.856	2
649	erythrocyte differentiation	/	3.584	/	2.025	2.177	2.766	2
658	transforming growth factor beta re	3.014	2.377	/	3.739	/	2.763	2
692	retina development in camera-type	3.014	2.377	/	/	3.169	2.763	2
699	substrate-bound cell migration\, c	3.014	3.922	/	/	3.169	2.763	2
701	pyrimidine nucleotide-sugar transp	3.014	2.377	/	/	3.169	2.763	2
702	fascia adherens	3.014	2.377	5.278	/	/	2.763	2
708	fluid secretion	/	2.037	2.624	2.532	/	2.747	2
716	morphogenesis of an epithelium	2.677	/	2.895	/	2.553	2.739	2
728	collagen	/	2.787	/	4.294	4.857	2.636	2
730	sulfur amino acid metabolic proces	/	2.719	/	2.408	2.862	2.635	2
737	collagen metabolic process	3.629	2.719	/	3.524	/	2.635	2
746	M phase of mitotic cell cycle	2.334	4.324	/	/	4.554	2.584	2
753	transmembrane receptor protein tyr	2.545	3.367	2.444	/	/	2.531	2
754	transmembrane receptor protein pho	2.545	3.367	2.444	/	/	2.531	2
755	oxidoreductase activity\, acting o	2.545	3.367	/	2.293	/	2.531	2
765	protein homooligomerization	/	/	5.529	2.546	2.577	2.516	2
770	membrane	3.591	/	3.289	3.738	/	2.491	2
781	IgG binding	4.29	3.45	/	/	2.789	2.462	2
783	nucleotide-sugar transport	2.643	2.04	/	/	2.789	2.462	2
784	galactose metabolic process	2.643	2.04	/	/	2.789	2.462	2
786	LIM domain binding	/	2.04	4.785	/	2.789	2.462	2
803	transmembrane receptor protein ser	2.643	2.04	/	3.322	/	2.462	2
828	activation of immune response	2.113	3.334	/	2.566	/	2.432	2
830	cytokine activity	2.242	/	/	2.394	2.068	2.429	2
844	iron ion transport	/	2.309	2.289	/	2.483	2.343	2
845	multicellular organismal metabolic	2.305	2.309	/	3.118	/	2.343	2
851	cofactor binding	2.119	3.279	/	/	3.431	2.331	2
853	nitrogen compound biosynthetic pro	/	2.539	/	2.976	3.86	2.308	2
858	nitric oxide metabolic process	/	/	2.219	1.989	3.263	2.258	2
860	serine family amino acid metabolic	/	4.399	/	1.989	2.371	2.258	2

865	nitric oxide biosynthetic process	/	/	2.219	1.989	3.263	2.258	2
878	mitotic cell cycle	3.548	5.35	/	/	4.786	2.237	2
924	inositol trisphosphate 3-kinase ac	2.347	3.074	/	/	2.486	2.224	2
925	inositol trisphosphate kinase acti	2.347	3.074	/	/	2.486	2.224	2
927	purine base metabolic process	2.347	4.379	/	/	4.066	2.224	2
941	leukocyte chemotaxis	2.934	2.073	/	/	2.266	2.177	2
944	muscle fiber development	2.76	2.036	/	/	3.54	2.176	2
945	skeletal muscle fiber development	2.76	2.036	/	/	3.54	2.176	2
946	peptide binding	2.389	2.06	/	/	2.037	2.174	2
947	M phase	2.11	4.626	/	/	3.59	2.166	2
948	mitosis	2.137	4.208	/	/	4.367	2.139	2
957	negative regulation of nucleobase\	/	2.738	2	/	2.334	2.077	2
963	transcriptional repressor activity	2.083	2.771	2.097	/	/	2.035	2
966	neural crest cell development	2.708	/	2.032	/	2.072	2.03	2
967	neural crest cell differentiation	2.708	/	2.032	/	2.072	2.03	2
972	pigmentation during development	/	/	4.477	3.628	2.072	2.03	2
981	metalloendopeptidase inhibitor act	2.101	2.762	/	/	2.236	2.028	2
984	mRNA cleavage	2.101	/	/	2.721	2.236	2.028	2
988	nucleotide-sugar transporter activ	2.101	/	/	2.721	2.236	2.028	2
1057	binding	4.362	5.966	/	4.15	5.136	/	2
1058	cytoplasm	4.962	6.976	/	4.151	6.022	/	2
1104	cortical cytoskeleton	3.171	3.538	4.184	4.198	/	/	2
1105	MHC protein complex	6.985	4.191	/	3.303	5.767	/	2
1119	hexose metabolic process	2.731	2.735	/	3.457	3.071	/	2
1122	cytoplasmic part	3.236	4.606	/	3.023	4.276	/	2
1136	monosaccharide metabolic process	2.634	2.625	/	3.364	2.973	/	2
1166	embryonic gut development	2.987	2.269	7.466	2.293	/	/	2
1167	intramolecular oxidoreductase acti	2.987	2.269	/	2.293	4.483	/	2
1192	transcription coactivator activity	/	2.848	2.618	2.81	2.649	/	2
1196	phosphoinositide-mediated signalin	2.014	2.409	/	2.664	4.114	/	2
1199	actin polymerization and/or depoly	2.869	/	2.652	2.141	2.567	/	2
1203	protein metabolic process	2.059	3.756	/	2.978	3.791	/	2
1204	metabolic process	2.074	5.353	/	2.983	4.336	/	2
1231	C-X-C chemokine binding	2.768	2.067	/	3.548	2.937	/	2
1243	establishment of cell polarity	2.768	2.067	3.41	2.12	/	/	2
1249	MHC class II protein complex	7.634	4.151	/	3.548	6.719	/	2
1292	protein depolymerization	2.605	/	3.713	4.395	2.101	/	2
1295	cytoskeleton	3.821	5.646	/	2.289	3.855	/	2
1301	DNA geometric change	2.574	/	3.241	3.333	5.153	/	2
1302	DNA duplex unwinding	2.574	/	3.241	3.333	5.153	/	2
1333	DNA unwinding during replication	2.574	/	3.241	3.333	5.153	/	2
1346	mononuclear cell proliferation	2.471	3.133	/	3.018	2.195	/	2
1347	lymphocyte proliferation	2.471	3.133	/	3.018	2.195	/	2
1384	tubulin binding	2.316	/	2.342	3.451	2.051	/	2
1388	death	3.369	3.84	/	2.543	2.328	/	2
1389	cell death	3.369	3.84	/	2.543	2.328	/	2
1428	cell cortex part	2.22	2.99	3.401	3.168	/	/	2

1438	amino acid biosynthetic process	2.15	2.355	/	2.343	2.357	/	2
1440	immune response	3.763	2.372	/	2.063	3.483	/	2
1453	antigen processing and presentatio	8.347	5.01	/	2.809	7.651	/	2
1497	lipid transporter activity	1.985	/	2.16	1.989	2.232	/	2
1525	glutamine metabolic process	3.981	3.044	/	2.665	3.162	/	2
1535	serine-type endopeptidase inhibito	3.245	1.98	2.089	2.962	/	/	2
1545	apoptosis	3.089	3.233	/	2.405	1.975	/	2
1555	MHC class I protein complex	2.819	2.037	2.624	/	1.992	/	2
1586	macromolecular complex assembly	2.416	4.159	/	2.109	3.938	/	2
1621	microtubule cytoskeleton organizat	2.502	3.989	/	2.705	4.167	/	2
1622	cytokine binding	4.289	3.224	/	3.753	3.704	/	2
1665	negative regulation of cell motili	2.421	3.983	5.097	2.185	/	/	2
1686	calcium-independent cell-cell adhe	3.186	3.818	/	3.118	2.483	/	2
1688	negative regulation of locomotion	2.305	3.818	4.956	2.084	/	/	2
1741	cytoskeletal protein binding	5.193	5.199	/	3.128	2.926	/	2
1745	organelle organization and biogene	3.953	6.317	/	4.224	5.179	/	2
1867	structural molecule activity	2.349	3.936	/	2.52	3.296	/	2
1945	chromatin	3.356	5.005	/	3.578	3.073	/	2
1961	intracellular part	2.584	7.115	/	2.153	4.379	/	2
2080	nucleosome	3.125	4.414	/	5.632	3.386	/	2
2279	negative regulation of megakaryocy	3.767	3.135	/	4.512	3.925	/	2
2403	cholestanetriol 26-monooxygenase a	3.767	3.135	/	4.512	3.925	/	2
2456	thymidylate kinase activity	3.767	3.135	/	4.512	3.925	/	2
2473	dTDP biosynthetic process	3.767	3.135	/	4.512	3.925	/	2
2485	regulation of negative chemotaxis	3.767	3.135	/	4.512	3.925	/	2
2486	positive regulation of negative ch	3.767	3.135	/	4.512	3.925	/	2
2542	rRNA primary transcript binding	3.767	3.135	/	4.512	3.925	/	2
2574	aspartate carbamoyltransferase act	3.767	3.135	/	4.512	3.925	/	2
2576	carbamoyl-phosphate synthase (glut	3.767	3.135	/	4.512	3.925	/	2
2602	dihydroorotase activity	3.767	3.135	/	4.512	3.925	/	2
2621	L-iditol 2-dehydrogenase activity	3.767	3.135	/	4.512	3.925	/	2
2637	GDP-4-dehydro-D-rhamnose reductase	3.767	3.135	/	4.512	3.925	/	2
2638	GDP-L-fucose synthase activity	3.767	3.135	/	4.512	3.925	/	2
2667	sorbitol metabolic process	3.767	3.135	/	4.512	3.925	/	2
2677	exocrine pancreas development	3.767	3.135	/	4.512	3.925	/	2
2794	androgen catabolic process	3.767	/	12.131	4.512	3.925	/	2
2809	phosphoribosylaminoimidazolecarbox	3.767	3.135	/	4.512	3.925	/	2
2810	IMP cyclohydrolase activity	3.767	3.135	/	4.512	3.925	/	2
2824	regulation of striated muscle cell	3.767	3.135	/	4.512	3.925	/	2
2881	pyrimidine nucleoside diphosphate	3.767	3.135	/	4.512	3.925	/	2
2885	dTDP metabolic process	3.767	3.135	/	4.512	3.925	/	2
2886	pyrimidine deoxyribonucleoside dip	3.767	3.135	/	4.512	3.925	/	2
2894	pyrimidine deoxyribonucleoside dip	3.767	3.135	/	4.512	3.925	/	2
3083	induction of negative chemotaxis	3.767	3.135	/	4.512	3.925	/	2
3084	mesoderm migration	3.767	3.135	/	4.512	3.925	/	2
3171	serine transport	3.767	3.135	/	4.512	3.925	/	2
3198	phosphoinositide 3-kinase complex\	3.767	3.135	/	4.512	3.925	/	2

3266	negative regulation of striated mu	3.767	3.135	/	4.512	3.925	/	2
3383	serotonin transport	3.767	3.135	/	4.512	3.925	/	2
3402	serotonin\:sodium symporter activi	3.767	3.135	/	4.512	3.925	/	2
3413	serotonin transporter activity	3.767	3.135	/	4.512	3.925	/	2
3555	NAD(P)H dehydrogenase (quinone) ac	3.767	3.135	/	4.512	3.925	/	2
3585	hydroxymethylbilane synthase activ	3.767	3.135	/	4.512	3.925	/	2
3736	retinoic acid binding	3.767	3.135	/	4.512	3.925	/	2
3759	detection of hormone stimulus	3.767	3.135	/	4.512	3.925	/	2
3760	permease activity	3.767	3.135	/	4.512	3.925	/	2
3761	purine nucleotide transporter acti	3.767	3.135	/	4.512	3.925	/	2
3762	L-tryptophan transporter activity	3.767	3.135	/	4.512	3.925	/	2
3893	L-serine transport	3.767	3.135	/	4.512	3.925	/	2
3926	white fat cell differentiation	3.767	3.135	/	4.512	3.925	/	2
3942	gelatinase B activity	3.767	3.135	/	4.512	3.925	/	2
4291	adherens junction	2.274	4.005	/	2.092	2.511	/	2
4297	valyl-tRNA aminoacylation	2.476	4.434	/	3.034	2.595	/	2
4314	glutamine-fructose-6-phosphate tra	2.476	1.992	/	3.034	2.595	/	2
4355	locomotor rhythm	2.476	1.992	/	3.034	2.595	/	2
4368	positive regulation of isotype swi	2.476	1.992	/	3.034	2.595	/	2
4386	polar microtubule	2.476	1.992	/	3.034	2.595	/	2
4450	establishment of polarity of embry	/	1.992	8.52	3.034	2.595	/	2
4508	insulin binding	2.476	1.992	/	3.034	2.595	/	2
4525	’de novo’ GDP-L-fucose biosynthe	5.328	4.434	/	3.034	2.595	/	2
4531	valine-tRNA ligase activity	2.476	4.434	/	3.034	2.595	/	2
4646	oxidoreductase activity\, oxidizin	2.476	1.992	/	3.034	2.595	/	2
4659	carbamoyl-phosphate synthase activ	2.476	1.992	/	3.034	2.595	/	2
4667	interleukin-7 receptor activity	2.476	1.992	/	3.034	2.595	/	2
4669	phosphatidylcholine-sterol O-acylt	2.476	1.992	/	3.034	2.595	/	2
4674	complement component C1 complex	2.476	1.992	/	3.034	2.595	/	2
4678	protein amino acid esterification	2.476	1.992	/	3.034	2.595	/	2
4688	alditol metabolic process	2.476	1.992	/	3.034	2.595	/	2
4689	hexitol metabolic process	2.476	1.992	/	3.034	2.595	/	2
4742	phosphoinositide phosphorylation	2.476	1.992	/	3.034	2.595	/	2
4747	UDP-activated nucleotide receptor	2.476	4.434	/	3.034	5.551	/	2
4785	interleukin-7 binding	2.476	1.992	/	3.034	2.595	/	2
4808	asparagine biosynthetic process	2.476	1.992	/	3.034	2.595	/	2
4810	L-serine transporter activity	2.476	1.992	/	3.034	2.595	/	2
4817	positive regulation of keratinocyt	2.476	1.992	/	3.034	2.595	/	2
4825	asparagine synthase (glutamine-hyd	2.476	1.992	/	3.034	2.595	/	2
4835	pyrimidine nucleoside diphosphate	2.476	1.992	/	3.034	2.595	/	2
4866	sulfate adenylyltransferase activi	2.476	4.434	/	3.034	5.551	/	2
4903	detection of endogenous stimulus	2.476	1.992	/	3.034	2.595	/	2
4914	nucleotide transporter activity	2.476	1.992	/	3.034	2.595	/	2
4928	asparagine metabolic process	2.476	1.992	/	3.034	2.595	/	2
4937	deoxyribonucleoside diphosphate bi	2.476	1.992	/	3.034	2.595	/	2
4954	protein carrier activity	2.476	1.992	/	3.034	2.595	/	2
4957	wide-spectrum protease inhibitor a	2.476	1.992	/	3.034	2.595	/	2

4972	ferroxidase activity	2.476	1.992	/	3.034	2.595	/	2
4974	carboxyl- and carbamoyltransferase	2.476	1.992	/	3.034	2.595	/	2
4976	isotype switching to IgA isotypes	2.476	1.992	/	3.034	2.595	/	2
4993	regulation of isotype switching to	2.476	1.992	/	3.034	2.595	/	2
5003	aromatic amino acid transporter ac	2.476	1.992	/	3.034	2.595	/	2
5019	interleukin-3 binding	5.328	4.434	/	3.034	2.595	/	2
5061	regulation of megakaryocyte differ	2.476	1.992	/	3.034	2.595	/	2
5095	GDP-L-fucose metabolic process	5.328	4.434	/	3.034	2.595	/	2
5096	fucose biosynthetic process	5.328	4.434	/	3.034	2.595	/	2
5097	L-fucose biosynthetic process	5.328	4.434	/	3.034	2.595	/	2
5098	GDP-L-fucose biosynthetic process	5.328	4.434	/	3.034	2.595	/	2
5129	adenylylsulfate kinase activity	2.476	4.434	/	3.034	5.551	/	2
5133	sulfate adenylyltransferase (ATP)	2.476	4.434	/	3.034	5.551	/	2
5167	transcription initiation from RNA	2.476	1.992	/	3.034	2.595	/	2
5169	RNA polymerase I transcription ter	2.476	1.992	/	3.034	2.595	/	2
5192	prolyl-tRNA aminoacylation	2.476	1.992	/	3.034	2.595	/	2
5193	proline-tRNA ligase activity	2.476	1.992	/	3.034	2.595	/	2
5213	interleukin-3 receptor activity	5.328	4.434	/	3.034	2.595	/	2
5241	UDP-galactose transporter activity	2.476	1.992	/	3.034	2.595	/	2
5288	isoleucine-tRNA ligase activity	2.476	1.992	/	3.034	2.595	/	2
5289	isoleucyl-tRNA aminoacylation	2.476	1.992	/	3.034	2.595	/	2
5697	entrainment of circadian clock	4.197	3.436	/	2.349	1.972	/	2
5757	phospholipase A2 inhibitor activit	4.197	3.436	/	5.082	1.972	/	2
5872	inner cell mass cell proliferation	4.197	3.436	/	2.349	4.386	/	2
5892	nucleotide-sugar biosynthetic proc	6.526	5.431	/	5.082	1.972	/	2
6403	intracellular non-membrane-bound o	2.729	6.301	/	2.176	3.54	/	2
6404	non-membrane-bound organelle	2.729	6.301	/	2.176	3.54	/	2
6713	chromatin assembly or disassembly	2.66	3.82	/	3.672	2.981	/	2
6716	nucleosome assembly	2.814	4.222	/	4.619	3.598	/	2
6914	MHC class II receptor activity	4.29	2.04	/	3.322	4.496	/	2
7207	glycine hydroxymethyltransferase a	3.527	3.984	/	2.721	3.714	/	2
7315	interleukin-1 binding	5.927	3.65	/	4.07	4.81	/	2
7668	desmosome	4.903	3.882	/	6.066	3.945	/	2
7688	chromatin assembly	2.228	3.843	/	3.948	2.964	/	2
7764	pyrimidine nucleoside triphosphate	2.241	2.501	/	2.967	2.399	/	2
7928	intracellular	2.039	6.072	/	2.034	3.716	/	2
7986	translational elongation	2.545	3.367	/	2.293	3.686	/	2
8000	pyrimidine nucleotide biosynthetic	2.421	3.21	/	3.245	3.536	/	2
8208	interleukin receptor activity	2.779	2.473	/	2.933	2.995	/	2
8249	interleukin binding	3.789	3.272	/	3.408	3.352	/	2
8291	protein-DNA complex assembly	2.66	2.866	/	2.8	2.981	/	2
8370	growth factor binding	4.242	4.151	/	2.818	3.028	/	2
14	positive regulation of mesenchymal	/	/	/	2.349	4.386	7.731	3
36	limbic system development	3.767	3.135	/	/	/	6.769	3
46	carbon dioxide transport	3.767	/	/	/	3.925	6.769	3
54	hippocampus development	3.767	3.135	/	/	/	6.769	3
56	macrophage elastase activity	3.767	/	/	4.512	/	6.769	3

59	positive regulation of mitotic cen	/	3.135	/	/	3.925	6.769	3
61	regulation of mitotic centrosome s	/	3.135	/	/	3.925	6.769	3
67	somatic stem cell maintenance	/	3.135	/	/	3.925	6.769	3
78	positive regulation of centrosome	/	3.135	/	/	3.925	6.769	3
80	regulation of centrosome cycle	/	3.135	/	/	3.925	6.769	3
86	folic acid metabolic process	/	/	/	4.512	3.925	6.769	3
87	amidophosphoribosyltransferase act	3.767	3.135	/	/	/	6.769	3
105	cardiac muscle cell development	3.502	/	/	/	3.671	6.622	3
106	cardiac myofibril assembly	3.502	/	/	/	3.671	6.622	3
124	alkene metabolic process	2.677	/	/	2.408	/	5.897	3
125	leukotriene metabolic process	2.677	/	/	2.408	/	5.897	3
145	selenium binding	/	/	/	3.322	2.789	5.286	3
164	oxidoreductase activity\, acting o	2.241	/	6.223	/	/	4.995	3
175	axon guidance receptor activity	/	/	/	2.992	4.066	4.838	3
176	muscle cell proliferation	3.871	/	/	/	4.066	4.838	3
177	smooth muscle cell proliferation	3.871	/	/	/	4.066	4.838	3
182	calmodulin binding	2.958	4.045	/	/	/	4.682	3
189	pyramidal neuron development	2.476	1.992	/	/	/	4.682	3
201	pallium development	2.476	1.992	/	/	/	4.682	3
203	positive regulation of interleukin	2.476	/	/	/	2.595	4.682	3
205	serotonin secretion	2.476	/	/	/	2.595	4.682	3
218	M phase specific microtubule proce	/	1.992	/	/	2.595	4.682	3
220	regulation of interleukin-3 biosyn	2.476	/	/	/	2.595	4.682	3
221	lysine carboxypeptidase activity	/	/	/	3.034	2.595	4.682	3
222	interleukin-3 biosynthetic process	2.476	/	/	/	2.595	4.682	3
224	interleukin-3 production	2.476	/	/	/	2.595	4.682	3
232	serotonin-activated cation-selecti	/	1.992	/	/	2.595	4.682	3
248	forebrain neuron development	2.476	1.992	/	/	/	4.682	3
249	snRNP U1	2.476	4.434	/	/	/	4.682	3
254	receptor signaling protein tyrosin	2.476	1.992	/	/	/	4.682	3
255	pyramidal neuron differentiation	2.476	1.992	/	/	/	4.682	3
257	bone mineralization	/	2.44	/	/	3.623	4.676	3
267	cerebellar cortex development	2.101	/	/	/	2.236	4.474	3
269	midbody	2.101	/	/	/	2.236	4.474	3
283	fatty acid biosynthetic process	2.166	/	/	1.999	/	4.276	3
303	regulation of response to stimulus	2.871	/	/	/	3.089	4.151	3
323	mitotic checkpoint	/	2.437	/	/	3.536	3.982	3
329	developmental maturation	/	/	/	2.106	2.232	3.94	3
330	negative regulation of transcripti	/	3.362	3.603	/	/	3.908	3
331	low-density lipoprotein receptor a	/	/	3.603	2.293	/	3.908	3
332	prostaglandin biosynthetic process	/	4.455	/	2.293	/	3.908	3
334	neuromuscular junction	2.987	2.269	/	/	/	3.908	3
335	lipoprotein receptor activity	/	/	3.603	2.293	/	3.908	3
339	prostanoid biosynthetic process	/	4.455	/	2.293	/	3.908	3
342	carboxypeptidase A activity	/	/	/	3.118	3.395	3.853	3
349	G-protein signaling\, adenylate cy	/	/	/	2.692	2.735	3.807	3
355	cellular carbohydrate catabolic pr	/	/	/	2.935	3.367	3.75	3

360	L-ascorbic acid metabolic process	/	/	/	2.349	1.972	3.738	3
362	positive regulation of immunoglobu	4.197	/	/	/	4.386	3.738	3
363	positive regulation of B cell medi	4.197	/	/	/	4.386	3.738	3
365	virion attachment to host cell sur	/	/	/	2.349	1.972	3.738	3
367	negative regulation of cyclic nucl	/	/	/	2.349	1.972	3.738	3
368	desensitization of G-protein coupl	/	/	/	2.349	1.972	3.738	3
369	negative regulation of nucleotide	/	/	/	2.349	1.972	3.738	3
372	regulation of cAMP biosynthetic pr	/	/	/	2.349	1.972	3.738	3
373	negative regulation of gliogenesis	/	/	/	2.349	1.972	3.738	3
374	cerebellar Purkinje cell different	/	/	/	2.349	1.972	3.738	3
377	diet induced thermogenesis	/	/	/	2.349	1.972	3.738	3
378	norepinephrine-epinephrine vasodil	/	/	/	2.349	1.972	3.738	3
380	beta-adrenergic receptor activity	/	/	/	2.349	1.972	3.738	3
382	development of secondary sexual ch	/	/	/	2.349	1.972	3.738	3
385	regulation of immunoglobulin media	4.197	/	/	/	4.386	3.738	3
387	regulation of B cell mediated immu	4.197	/	/	/	4.386	3.738	3
388	spermidine biosynthetic process	/	/	/	2.349	1.972	3.738	3
389	luteinization	/	/	/	2.349	1.972	3.738	3
390	immunoglobulin receptor activity	4.197	/	/	/	4.386	3.738	3
391	positive regulation of acute infla	4.197	/	/	/	4.386	3.738	3
392	positive regulation of acute infla	4.197	/	/	/	4.386	3.738	3
394	cerebellar Purkinje cell layer for	/	/	/	2.349	1.972	3.738	3
398	interleukin-1 receptor complex	/	/	/	2.349	1.972	3.738	3
399	positive regulation of leukocyte d	4.197	/	/	/	4.386	3.738	3
404	alpha-actinin binding	/	/	/	2.349	1.972	3.738	3
407	6-phosphofructokinase activity	/	/	/	2.349	1.972	3.738	3
408	6-phosphofructokinase complex	/	/	/	2.349	1.972	3.738	3
409	positive regulation of inflammator	4.197	/	/	/	4.386	3.738	3
410	adaptation of signaling pathway	/	/	/	2.349	1.972	3.738	3
411	regulation of mast cell degranulat	4.197	/	/	/	4.386	3.738	3
412	regulation of leukocyte degranulat	4.197	/	/	/	4.386	3.738	3
413	positive regulation of multicellul	/	/	/	2.349	1.972	3.738	3
415	regulation of organismal metabolic	/	/	/	2.349	1.972	3.738	3
416	response to dietary excess	/	/	/	2.349	1.972	3.738	3
419	positive regulation of mast cell d	4.197	/	/	/	4.386	3.738	3
420	cerebellar Purkinje cell layer mor	/	/	/	2.349	1.972	3.738	3
423	calcitonin receptor activity	/	/	/	2.349	1.972	3.738	3
424	peptidyl-dipeptidase A activity	/	/	/	2.349	1.972	3.738	3
425	positive regulation of hypersensit	4.197	/	/	/	4.386	3.738	3
428	negative regulation of cyclic nucl	/	/	/	2.349	1.972	3.738	3
429	response to arsenic	/	/	/	2.349	1.972	3.738	3
430	opsonin binding	/	/	/	2.349	1.972	3.738	3
431	transmembrane receptor protein tyr	/	/	/	2.349	1.972	3.738	3
432	negative regulation of glial cell	/	/	/	2.349	1.972	3.738	3
437	trypsin activity	/	/	/	2.349	1.972	3.738	3
438	male pronucleus	/	3.436	/	/	4.386	3.738	3
440	mitotic centrosome separation	/	3.436	/	/	4.386	3.738	3

442	1-alkyl-2-acetylglycerophosphochol	/	/	/	2.349	1.972	3.738	3
443	positive regulation of long-term n	/	/	/	2.349	1.972	3.738	3
445	peptidyl-dipeptidase activity	/	/	/	2.349	1.972	3.738	3
449	rhythmic synaptic transmission	/	/	/	2.349	1.972	3.738	3
450	progesterone receptor signaling pa	/	/	/	2.349	1.972	3.738	3
455	carboxypeptidase activity	/	/	/	3.408	2.654	3.729	3
465	cell maturation	/	/	/	2.029	2.277	3.646	3
467	axon extension	3.775	2.073	/	/	/	3.621	3
471	secretory granule	/	/	/	4.014	3.859	3.582	3
480	heart morphogenesis	1.994	/	4.586	/	/	3.514	3
481	complement activation\, classical	/	2.67	/	2.781	/	3.514	3
482	carbohydrate catabolic process	/	/	/	2.668	3.06	3.505	3
485	regulation of BMP signaling pathwa	/	/	3.241	1.966	/	3.483	3
487	pteridine and derivative metabolic	/	/	/	1.966	3.945	3.483	3
492	heart development	/	3.097	4.12	/	/	3.432	3
499	humoral immune response mediated b	/	2.44	/	2.585	/	3.319	3
500	metallocarboxypeptidase activity	/	/	/	3.514	2.802	3.319	3
502	calcium ion transporter activity	/	2.683	/	3.141	/	3.305	3
518	fatty acid metabolic process	2.242	/	/	2.603	/	3.2	3
536	cell-substrate junction assembly	/	2.817	/	/	3.671	3.163	3
540	regulation of mitochondrial depola	/	2.817	/	/	3.671	3.163	3
547	centrosome separation	/	2.817	/	/	3.671	3.163	3
549	G2 phase	/	2.817	/	/	3.671	3.163	3
551	female pronucleus	/	2.817	/	/	3.671	3.163	3
552	polarized epithelial cell differen	3.502	/	5.943	/	/	3.163	3
556	positive regulation of exocytosis	3.502	/	/	/	3.671	3.163	3
564	G2 phase of mitotic cell cycle	/	2.817	/	/	3.671	3.163	3
566	elastic fiber assembly	/	2.817	/	/	3.671	3.163	3
569	microfibril	/	2.817	5.943	/	/	3.163	3
571	regulation of inflammatory respons	3.502	/	/	/	5.761	3.163	3
575	regulation of acute inflammatory r	3.502	/	/	/	5.761	3.163	3
580	regulation of acute inflammatory r	3.502	/	/	/	5.761	3.163	3
582	regulation of hypersensitivity	3.502	/	/	/	5.761	3.163	3
585	type I hypersensitivity	3.502	/	/	/	3.671	3.163	3
590	exopeptidase activity	/	/	/	3.1	2.191	3.148	3
591	retinoid binding	2.241	/	/	/	2.399	3.146	3
592	isoprenoid binding	2.241	/	/	/	2.399	3.146	3
601	oxidoreductase activity\, acting o	3.171	2.885	/	/	/	3.142	3
603	regulation of cell size	2.157	/	3.862	/	/	3.134	3
608	blood pressure regulation	/	/	3.047	1.989	/	3.082	3
613	hexose catabolic process	/	/	/	2.283	3.082	3.063	3
618	vesicle-mediated transport	1.991	/	/	/	2.078	3.038	3
619	monosaccharide catabolic process	/	/	/	2.239	3.028	3.022	3
628	multi-organism process	2.88	/	/	3.446	/	2.996	3
641	vasoconstriction	1.964	/	2.725	/	/	2.869	3
645	phagocytosis	2.779	/	/	/	2.995	2.835	3
648	muscle contraction	2.114	4.991	/	/	/	2.787	3

654	mitochondrial depolarization	/	2.377	/	/	3.169	2.763	3
661	negative regulation of G-protein c	/	2.377	/	/	3.169	2.763	3
665	regulation of cell redox homeostas	/	2.377	/	/	3.169	2.763	3
674	embryonic hemopoiesis	/	2.377	/	/	3.169	2.763	3
676	plasminogen activator activity	3.014	/	/	/	3.169	2.763	3
677	negative chemotaxis	4.818	2.377	/	/	/	2.763	3
683	complement binding	3.014	2.377	/	/	/	2.763	3
685	dimethylaniline monooxygenase (N-o	3.014	/	/	/	3.169	2.763	3
688	establishment of apical/basal cell	3.014	/	5.278	/	/	2.763	3
697	fibril	/	2.377	5.278	/	/	2.763	3
707	oxidoreductase activity\, acting o	/	2.037	/	/	1.992	2.747	3
710	kinesin complex	/	2.876	/	/	1.992	2.747	3
711	actin filament bundle	/	2.037	/	/	1.992	2.747	3
713	stress fiber	/	2.037	/	/	1.992	2.747	3
715	carbonate dehydratase activity	/	/	2.624	/	1.992	2.747	3
718	metalloexopeptidase activity	/	/	/	3.594	2.168	2.73	3
722	regulation of muscle contraction	/	3.476	/	/	2.101	2.7	3
726	regulation of cell adhesion	2.386	2.297	/	/	/	2.64	3
745	second-messenger-mediated signalin	/	/	/	2.275	4.593	2.586	3
751	glucose catabolic process	/	/	/	2.092	3.065	2.554	3
774	chaperonin-containing T-complex	/	2.04	/	/	6.203	2.462	3
790	glycogen catabolic process	/	2.04	/	/	2.789	2.462	3
795	hypersensitivity	2.643	/	/	/	4.496	2.462	3
797	acute inflammatory response to ant	2.643	/	/	/	4.496	2.462	3
798	inflammatory response to antigenic	2.643	/	/	/	4.496	2.462	3
801	tetrahydrobiopterin metabolic proc	/	2.04	/	/	2.789	2.462	3
802	oxidoreductase activity\, acting o	/	3.45	/	/	2.789	2.462	3
805	stem cell division	/	/	4.785	3.322	/	2.462	3
810	mast cell mediated immunity	2.643	/	/	/	2.789	2.462	3
816	positive regulation of gene expres	2.643	/	4.785	/	/	2.462	3
817	mast cell degranulation	2.643	/	/	/	2.789	2.462	3
818	regulation of embryonic developmen	2.643	2.04	/	/	/	2.462	3
820	tetrahydrobiopterin biosynthetic p	/	2.04	/	/	2.789	2.462	3
821	electron carrier activity	/	/	2.206	2.324	/	2.462	3
823	epithelial cell differentiation	2.947	/	/	/	2.501	2.458	3
832	integral to membrane	/	/	2.587	2.424	/	2.403	3
835	chordate embryonic development	3.076	2.144	/	/	/	2.397	3
838	intrinsic to membrane	/	/	2.564	2.367	/	2.364	3
839	embryonic development ending in bi	3.009	2.075	/	/	/	2.355	3
841	phosphorus metabolic process	/	4.48	/	2.467	/	2.346	3
842	phosphate metabolic process	/	4.48	/	2.467	/	2.346	3
867	positive regulation of B cell acti	2.196	/	/	1.989	/	2.258	3
868	cytoplasm organization and biogene	2.196	2.188	/	/	/	2.258	3
872	carbohydrate transport	2.639	/	/	/	2.222	2.247	3
880	striated muscle development	/	/	2.488	/	2.63	2.224	3
891	traversing start control point of	2.347	/	/	/	2.486	2.224	3
895	aldehyde dehydrogenase (NAD) activ	2.347	/	/	2.992	/	2.224	3

898	gamma-tubulin binding	2.347	/	/	/	2.486	2.224	3
903	myeloid leukocyte mediated immunit	2.347	/	/	/	2.486	2.224	3
907	glutathione biosynthetic process	/	3.074	/	/	2.486	2.224	3
911	intramolecular oxidoreductase acti	2.347	/	/	2.992	/	2.224	3
926	leukocyte degranulation	2.347	/	/	/	2.486	2.224	3
929	basement membrane	/	2.517	/	/	2.051	2.21	3
930	G-protein signaling\, coupled to I	/	/	2.342	/	2.051	2.21	3
931	endopeptidase inhibitor activity	3.032	/	/	/	2.211	2.202	3
937	protease inhibitor activity	2.995	/	/	/	2.179	2.179	3
949	phosphorylation	/	4.15	/	2.573	/	2.119	3
952	peroxidase activity	/	/	2.091	/	2.166	2.102	3
953	oxidoreductase activity\, acting o	/	/	2.091	/	2.166	2.102	3
960	transition metal ion transport	/	/	/	1.989	2.59	2.06	3
962	transcription regulator activity	2.021	2.4	/	/	/	2.052	3
976	regulation of fatty acid metabolic	2.101	/	4.086	/	/	2.028	3
977	cardiac muscle development	2.101	/	4.086	/	/	2.028	3
978	pituitary gland development	/	/	/	2.721	2.236	2.028	3
982	thyroid gland development	2.101	2.762	/	/	/	2.028	3
1018	diencephalon development	/	/	/	2.721	2.236	2.028	3
1023	in utero embryonic development	2.03	2.592	/	/	/	2.012	3
1028	negative regulation of cellular me	/	2.742	/	/	2.037	1.971	3
1035	monosaccharide transport	2.603	/	/	/	1.982	1.961	3
1040	hexose transport	2.603	/	/	/	1.982	1.961	3
1042	lymphocyte mediated immunity	2.881	2.08	/	/	3.648	/	3
1043	negative regulation of transcripti	/	2.459	2.187	/	2.274	/	3
1045	carbohydrate metabolic process	2.656	2.026	/	3.863	/	/	3
1047	membrane part	2.239	/	2.604	2.616	/	/	3
1050	immune effector process	3.278	2.558	/	/	3.605	/	3
1053	chemokine binding	2.503	/	/	2.494	2.701	/	3
1068	secretory granule membrane	/	3.65	/	5.648	3.417	/	3
1072	cytoplasmic microtubule	/	2.498	/	2.491	2.023	/	3
1077	nucleobase biosynthetic process	4.582	3.65	/	/	3.417	/	3
1083	regulation of mitochondrial membra	/	2.498	/	4.07	2.023	/	3
1107	adaptive immune response based on	3.143	2.274	/	/	2.964	/	3
1108	adaptive immune response	3.143	2.274	/	/	2.964	/	3
1121	adenyl nucleotide binding	/	6.47	/	2.995	4.249	/	3
1123	protein homodimerization activity	/	2.11	3.187	/	1.969	/	3
1132	nitrogen compound metabolic proces	/	2.354	/	3.199	3.894	/	3
1135	protein complex	3.728	6.142	/	/	5.062	/	3
1140	response to chemical stimulus	/	2.641	/	1.98	2.598	/	3
1141	transcription factor binding	2.061	3.355	/	/	2.106	/	3
1143	regulation of cell activation	2.056	/	/	2.705	2.315	/	3
1181	L-fucose metabolic process	2.987	2.269	/	2.293	/	/	3
1187	ureteric bud development	2.967	2.039	4.012	/	/	/	3
1194	GPI anchor binding	2.153	/	3.758	2.135	/	/	3
1205	cellular metabolic process	/	4.945	/	2.851	4.332	/	3
1262	forelimb morphogenesis	/	3.109	3.41	3.548	/	/	3

1321	regulation of RNA stability	/	3.882	/	1.966	2.738	/	3
1336	cell cycle phase	2.688	5.355	/	/	3.385	/	3
1348	cell cycle process	3.119	7.64	/	/	3.943	/	3
1377	cytokine and chemokine mediated si	4.358	3.175	/	/	3.265	/	3
1379	negative regulation of cell organi	2.366	/	3.519	4.104	/	/	3
1383	ATP binding	/	6.342	/	3.017	4.197	/	3
1385	amine biosynthetic process	/	2.091	/	2.283	2.567	/	3
1386	amino acid and derivative metaboli	/	3.073	/	2.866	4.367	/	3
1387	amine metabolic process	/	2.044	/	2.683	3.57	/	3
1441	cell cycle	3.877	8.202	/	/	4.458	/	3
1445	transcription factor complex	2.04	2.121	3.58	/	/	/	3
1449	regulation of actin filament lengt	2.082	/	3.292	2.28	/	/	3
1470	voltage-gated chloride channel act	2.097	2.333	2.836	/	/	/	3
1475	inorganic anion transport	/	2.144	/	3.457	3.786	/	3
1479	external side of plasma membrane	2.983	2.184	/	/	3.265	/	3
1481	transcription from RNA polymerase	2.376	3.278	/	/	1.98	/	3
1491	cellular protein metabolic process	/	3.027	/	2.599	3.33	/	3
1492	primary metabolic process	/	4.808	/	2.757	4.034	/	3
1501	cellular macromolecule metabolic p	/	3.18	/	2.747	3.391	/	3
1510	nucleobase metabolic process	2.972	3.044	/	/	3.162	/	3
1552	collagen catabolic process	2.819	2.037	/	2.532	/	/	3
1556	multicellular organismal protein c	2.819	2.037	/	2.532	/	/	3
1557	multicellular organismal macromole	2.819	2.037	/	2.532	/	/	3
1558	multicellular organismal protein m	2.819	2.037	/	2.532	/	/	3
1559	multicellular organismal macromole	2.819	2.037	/	2.532	/	/	3
1561	protein digestion	2.819	2.037	/	2.532	/	/	3
1578	enzyme inhibitor activity	3.924	2.454	/	/	2.394	/	3
1585	programmed cell death	3.015	3.279	/	2.344	/	/	3
1620	macromolecular complex	2.341	5.063	/	/	3.789	/	3
1642	antigen processing and presentatio	5.547	3.124	/	/	4.709	/	3
1643	microtubule binding	2.119	/	2.877	2.453	/	/	3
1708	purine nucleotide binding	/	5.525	/	2.705	4.265	/	3
1732	regulation of apoptosis	2.859	2.75	/	2.355	/	/	3
1733	copper ion binding	3.476	2.763	/	2.829	/	/	3
1737	catalytic activity	/	4.356	/	2.648	3.037	/	3
1739	regulation of progression through	2.446	6.483	/	/	3.379	/	3
1742	perinuclear region of cytoplasm	2.869	/	2.652	/	2.007	/	3
1766	circadian rhythm	2.092	2.794	/	/	2.266	/	3
1768	regulation of programmed cell deat	2.77	2.647	/	2.281	/	/	3
1771	regulation of cell cycle	2.572	6.557	/	/	3.319	/	3
1774	amino acid metabolic process	/	3.234	/	3.068	4.42	/	3
1830	monosaccharide biosynthetic proces	3.28	2.334	/	2.494	/	/	3
1834	hexose biosynthetic process	3.28	2.334	/	2.494	/	/	3
1835	alcohol biosynthetic process	3.28	2.334	/	2.494	/	/	3
1848	biosynthetic process	2.139	3.441	/	/	2.698	/	3
1851	spindle organization and biogenesi	3.171	6.152	/	/	5.767	/	3
1877	regulation of cellular component o	/	/	3.81	2.818	2.516	/	3

1948	actin binding	4.566	4.669	/	/	2.379	/	3
1962	apical junction complex	3.655	/	/	3.458	2.057	/	3
1965	nucleotide binding	/	4.752	/	2.22	3.808	/	3
1966	interphase of mitotic cell cycle	2.686	3.843	/	/	2.015	/	3
1968	apicolateral plasma membrane	3.549	/	/	3.364	1.973	/	3
1969	interphase	2.639	3.782	/	/	1.973	/	3
1994	macromolecule metabolic process	/	4.369	/	2.086	3.122	/	3
2038	di-\, tri-valent inorganic cation	2.386	2.735	/	/	1.998	/	3
2046	chromosome	/	4.238	/	2.581	2.84	/	3
2048	chromosomal part	/	5.034	/	2.539	3.263	/	3
2066	metal ion homeostasis	2.479	2.735	/	/	2.121	/	3
2099	triose-phosphate isomerase activit	3.767	3.135	/	4.512	/	/	3
2146	plasminogen activation	3.767	3.135	/	4.512	/	/	3
2165	gamma-glutamyl carboxylase activit	3.767	3.135	/	/	3.925	/	3
2190	peptidyl-glutamic acid carboxylati	3.767	3.135	/	/	3.925	/	3
2205	creatine transporter activity	3.767	3.135	/	4.512	/	/	3
2215	thioredoxin peroxidase activity	3.767	3.135	/	/	3.925	/	3
2221	mannosyl-oligosaccharide glucosida	3.767	3.135	/	4.512	/	/	3
2231	histidine family amino acid biosyn	/	3.135	/	4.512	3.925	/	3
2249	nuclear condensin complex	3.767	3.135	/	/	3.925	/	3
2261	GDP-mannose biosynthetic process	3.767	3.135	/	4.512	/	/	3
2339	mRNA cleavage and polyadenylation	3.767	3.135	/	4.512	/	/	3
2370	regulation of type III hypersensit	3.767	3.135	/	/	3.925	/	3
2382	type III hypersensitivity	3.767	3.135	/	/	3.925	/	3
2590	propionyl-CoA carboxylase activity	3.767	3.135	/	/	3.925	/	3
2620	antigen processing and presentatio	3.767	3.135	/	/	3.925	/	3
2670	plasma membrane to endosome transp	3.767	3.135	/	/	3.925	/	3
2722	positive regulation of type III hy	3.767	3.135	/	/	3.925	/	3
2890	UDP-galactose transport	3.767	3.135	/	/	3.925	/	3
2903	A2B adenosine receptor activity\,	3.767	3.135	/	/	3.925	/	3
2935	creatine\:sodium symporter activit	3.767	3.135	/	4.512	/	/	3
3022	histidine biosynthetic process	/	3.135	/	4.512	3.925	/	3
3325	meiosis II	3.767	3.135	/	4.512	/	/	3
3329	phosphoribosylformylglycinamidine	3.767	3.135	/	/	3.925	/	3
3435	phosphoribosylamine-glycine ligase	3.767	3.135	/	/	3.925	/	3
3447	histidine decarboxylase activity	/	3.135	/	4.512	3.925	/	3
3469	phosphoribosylglycinamide formyltr	3.767	3.135	/	/	3.925	/	3
3481	cathepsin H activity	3.767	/	/	4.512	3.925	/	3
3566	vitamin D3 receptor activity	/	3.135	/	4.512	3.925	/	3
3664	initiation of primordial ovarian f	/	3.135	/	4.512	3.925	/	3
3683	meiotic prophase II	3.767	3.135	/	4.512	/	/	3
3702	peptidyl-glutamic acid modificatio	3.767	3.135	/	/	3.925	/	3
3703	protein amino acid carboxylation	3.767	3.135	/	/	3.925	/	3
3847	formation of immunological synapse	3.767	3.135	/	4.512	/	/	3
4306	macrophage colony stimulating fact	/	1.992	/	3.034	2.595	/	3
4315	phagocytic cup	5.328	4.434	/	/	5.551	/	3
4338	interstitial collagenase activity	2.476	1.992	/	3.034	/	/	3

4354	alpha-1\,3-mannosylglycoprotein 2-	2.476	1.992	/	/	2.595	/	3
4364	protein tyrosine phosphatase activ	2.476	1.992	/	/	2.595	/	3
4388	transepithelial chloride transport	/	1.992	/	3.034	2.595	/	3
4394	transferrin receptor activity	2.476	1.992	/	/	2.595	/	3
4405	angiogenin-PRI complex	2.476	1.992	/	/	2.595	/	3
4418	mannose biosynthetic process	2.476	1.992	/	3.034	/	/	3
4460	isocitrate dehydrogenase (NADP+) a	2.476	1.992	/	/	2.595	/	3
4462	glyoxylate cycle	2.476	1.992	/	/	2.595	/	3
4476	establishment of T cell polarity	2.476	4.434	/	3.034	/	/	3
4488	polytene chromosome chromocenter	2.476	1.992	/	/	2.595	/	3
4493	interleukin-1\, Type I\, activatin	2.476	1.992	/	/	2.595	/	3
4496	interleukin-5 receptor binding	2.476	1.992	/	/	2.595	/	3
4504	DNA-dependent protein kinase activ	2.476	1.992	/	/	2.595	/	3
4535	electron transporter\, transferrin	2.476	1.992	/	/	2.595	/	3
4546	mast cell granule	2.476	1.992	/	/	2.595	/	3
4555	GDP-mannose metabolic process	5.328	4.434	/	3.034	/	/	3
4560	methionyl-tRNA aminoacylation	/	1.992	/	3.034	2.595	/	3
4563	methionine-tRNA ligase activity	/	1.992	/	3.034	2.595	/	3
4677	type II hypersensitivity	2.476	1.992	/	/	2.595	/	3
4692	regulation of type IIa hypersensit	2.476	1.992	/	/	2.595	/	3
4694	type IIa hypersensitivity	2.476	1.992	/	/	2.595	/	3
4696	regulation of myeloid leukocyte me	2.476	1.992	/	/	2.595	/	3
4697	positive regulation of myeloid leu	2.476	1.992	/	/	2.595	/	3
4698	positive regulation of type II hyp	2.476	1.992	/	/	2.595	/	3
4699	regulation of type II hypersensiti	2.476	1.992	/	/	2.595	/	3
4733	phosphomannomutase activity	2.476	1.992	/	3.034	/	/	3
4758	negative regulation of fat cell di	2.476	1.992	/	/	2.595	/	3
4832	3-hydroxybutyrate dehydrogenase ac	2.476	1.992	/	/	2.595	/	3
4945	chromocenter	2.476	1.992	/	/	2.595	/	3
4946	polytene chromosome	2.476	1.992	/	/	2.595	/	3
4996	interleukin-1\, Type I\, activatin	2.476	1.992	/	/	2.595	/	3
5057	establishment of lymphocyte polari	2.476	4.434	/	3.034	/	/	3
5079	positive regulation of type IIa hy	2.476	1.992	/	/	2.595	/	3
5149	DNA photolyase activity	/	1.992	/	3.034	2.595	/	3
5183	formate-tetrahydrofolate ligase ac	/	1.992	/	3.034	2.595	/	3
5210	spindle pole body organization and	/	4.434	/	3.034	5.551	/	3
5246	interleukin-5 receptor complex	2.476	1.992	/	/	2.595	/	3
5254	S100 alpha binding	/	1.992	/	3.034	2.595	/	3
5275	cyclin catabolic process	2.476	1.992	/	/	2.595	/	3
5279	positive regulation of mast cell c	2.476	1.992	/	/	2.595	/	3
5327	syndecan binding	2.476	1.992	/	/	2.595	/	3
5397	spindle pole body	/	3.436	/	2.349	1.972	/	3
5399	meiotic spindle organization and b	/	5.431	/	2.349	1.972	/	3
5444	beta-N-acetylglucosaminylglycopept	/	3.436	6.909	5.082	/	/	3
5449	sulfate assimilation	/	3.436	/	2.349	4.386	/	3
5519	nucleoside diphosphate biosyntheti	/	3.436	/	2.349	4.386	/	3
5522	positive T cell selection	4.197	/	/	5.082	1.972	/	3

5572	ubiquitin protein ligase binding	4.197	3.436	/	2.349	/	/	3
5624	uridine nucleotide receptor activi	/	3.436	/	2.349	4.386	/	3
5649	sulfur utilization	/	3.436	/	2.349	4.386	/	3
5655	epidermal growth factor receptor a	4.197	3.436	/	/	4.386	/	3
5661	hormone catabolic process	/	/	6.909	2.349	1.972	/	3
5727	cytoplasmic microtubule organizati	/	/	6.909	2.349	1.972	/	3
5782	positive thymic T cell selection	4.197	/	/	5.082	1.972	/	3
5863	insulin-like growth factor recepto	/	/	6.909	2.349	1.972	/	3
6037	cell ion homeostasis	2.31	2.707	/	/	1.997	/	3
6129	N-acetyllactosamine synthase activ	/	2.817	5.943	6.657	/	/	3
6207	mitotic spindle assembly	3.502	2.817	/	/	3.671	/	3
6264	release of sequestered calcium ion	3.502	2.817	/	/	3.671	/	3
6273	negative regulation of sequesterin	3.502	2.817	/	/	3.671	/	3
6274	regulation of sequestering of calc	3.502	2.817	/	/	3.671	/	3
6348	spindle assembly	3.502	2.817	/	/	3.671	/	3
6419	zymogen granule membrane	/	2.377	/	3.739	3.169	/	3
6422	peptidyl-histidine phosphorylation	3.014	3.922	/	5.856	/	/	3
6585	collagenase activity	4.818	3.922	/	3.739	/	/	3
6628	cyclohydrolase activity	/	2.377	/	3.739	3.169	/	3
6634	cyclin-dependent protein kinase ho	4.818	5.467	/	/	3.169	/	3
6754	regulation of fat cell differentia	2.643	2.04	/	/	2.789	/	3
6755	zymogen granule	/	2.04	/	3.322	2.789	/	3
6793	sequestering of calcium ion	2.643	2.04	/	/	2.789	/	3
6803	hydroxymethyl-\, formyl- and relat	2.643	2.04	/	/	2.789	/	3
6815	AP-1 adaptor complex	2.643	2.04	/	/	2.789	/	3
6849	blastocyst growth	2.643	2.04	/	/	2.789	/	3
6866	tricarboxylic acid cycle enzyme co	2.643	2.04	/	3.322	/	/	3
6869	positive regulation of endothelial	/	2.04	/	3.322	2.789	/	3
6970	peptidyl-histidine modification	2.347	3.074	/	4.782	/	/	3
6973	antigen processing and presentatio	5.396	3.074	/	/	5.646	/	3
6980	antigen processing and presentatio	5.396	3.074	/	/	5.646	/	3
6999	amino acid permease activity	3.871	/	/	2.992	2.486	/	3
7003	antigen processing and presentatio	5.396	3.074	/	/	5.646	/	3
7056	interleukin-1 receptor activity	3.871	/	/	2.992	4.066	/	3
7199	neurotransmitter uptake	2.101	2.762	/	2.721	/	/	3
7225	ephrin receptor binding	2.101	/	/	2.721	2.236	/	3
7258	phospholipase inhibitor activity	4.954	2.762	/	2.721	/	/	3
7363	regulation of mitotic metaphase/an	/	3.65	/	2.491	2.023	/	3
7368	carbon-nitrogen ligase activity\,	/	2.498	/	2.491	2.023	/	3
7377	UTP biosynthetic process	/	2.498	/	2.491	2.023	/	3
7378	UTP metabolic process	/	2.498	/	2.491	2.023	/	3
7379	nucleoside diphosphate kinase acti	/	2.498	/	2.491	2.023	/	3
7461	antigen processing and presentatio	4.263	2.269	/	/	4.483	/	3
7492	leukocyte adhesion	2.987	2.269	/	2.293	/	/	3
7572	nucleotide-sugar metabolic process	2.768	2.067	/	2.12	/	/	3
7633	cortical cytoskeleton organization	3.738	3.882	/	1.966	/	/	3
7872	mitotic spindle organization and b	2.972	4.772	/	/	5.253	/	3

7888	DNA-dependent DNA replication	2.856	3.872	/	/	2.689	/	3
8063	insulin-like growth factor binding	2.196	2.188	2.219	/	/	/	3
8110	antigen processing and presentatio	3.515	/	2.032	/	3.745	/	3
8119	DNA replication initiation	2.603	4.475	/	/	5.263	/	3
8161	DNA packaging	/	2.652	/	2.053	2.351	/	3
8164	pyrimidine nucleotide metabolic pr	/	2.133	/	2.324	2.511	/	3
8194	actin filament binding	2.871	2.57	3.932	/	/	/	3
8201	carbon-carbon lyase activity	/	2.473	/	2.095	2.995	/	3
8389	chromosome organization and biogen	/	3.227	/	2.281	2.044	/	3
69	S-formylglutathione hydrolase acti	/	3.135	/	/	/	6.769	4
84	calmodulin-dependent protein kinas	/	3.135	/	/	/	6.769	4
196	acylglycerol lipase activity	/	/	/	/	2.595	4.682	4
199	t-SNARE activity	2.476	/	/	/	/	4.682	4
275	oxidoreductase activity\, acting o	/	/	5.588	/	/	4.426	4
286	growth cone	/	/	/	/	2.862	4.266	4
293	cerebellum development	/	/	/	/	2.023	4.169	4
298	metencephalon development	/	/	/	/	2.023	4.169	4
300	response to cold	/	/	/	/	2.023	4.169	4
301	adult heart development	/	/	/	/	2.023	4.169	4
305	site of polarized growth	/	/	/	/	2.727	4.119	4
306	fibroblast growth factor receptor	/	/	2.444	/	/	4.119	4
337	macrophage activation	/	/	/	2.293	/	3.908	4
354	growth	/	/	3.314	/	/	3.754	4
359	axon extension involved in axon gu	4.197	/	/	/	/	3.738	4
361	regulation of axon extension invol	4.197	/	/	/	/	3.738	4
364	axon extension involved in develop	/	/	/	/	1.972	3.738	4
366	glycerol-3-phosphate dehydrogenase	/	/	/	/	4.386	3.738	4
370	lipid raft distribution	/	/	/	5.082	/	3.738	4
376	inositol 1\,4\,5-triphosphate-sens	/	/	/	2.349	/	3.738	4
386	lipid raft localization	/	/	/	5.082	/	3.738	4
395	lipid raft polarization	/	/	/	5.082	/	3.738	4
396	structural constituent of myelin s	/	/	/	2.349	/	3.738	4
397	acetylcholine receptor regulator a	/	/	/	/	1.972	3.738	4
400	cerebral cortex neuron differentia	/	/	/	/	1.972	3.738	4
401	tau-protein kinase activity	/	/	/	/	1.972	3.738	4
405	leukotriene-A4 hydrolase activity	/	/	/	2.349	/	3.738	4
414	regulation of circadian rhythm	/	/	/	/	1.972	3.738	4
421	positive regulation of granulocyte	/	/	/	/	1.972	3.738	4
426	epoxide hydrolase activity	/	/	/	2.349	/	3.738	4
433	cytokinesis after mitosis	/	/	/	/	1.972	3.738	4
434	aspartate transport	/	/	/	/	1.972	3.738	4
435	negative regulation of axon extens	4.197	/	/	/	/	3.738	4
436	L-aspartate transporter activity	/	/	/	/	1.972	3.738	4
441	somite specification	/	/	/	/	1.972	3.738	4
451	negative regulation of growth	/	/	4.495	/	/	3.737	4
461	neuron differentiation	2.011	/	/	/	/	3.672	4
473	axon	/	/	/	/	2.06	3.574	4

493	myoblast maturation	/	/	/	/	3.745	3.414	4
494	BMP signaling pathway	/	/	4.477	/	/	3.414	4
498	myoblast development	/	/	/	/	3.623	3.319	4
501	induction of an organ	/	/	3.092	/	/	3.305	4
503	hexosaminidase activity	/	/	3.092	/	/	3.305	4
504	specification of organ identity	/	/	3.092	/	/	3.305	4
505	cell-cell signaling	/	/	/	/	2.047	3.304	4
509	forebrain development	/	2.379	/	/	/	3.281	4
516	neuron development	2.129	/	/	/	/	3.221	4
519	cell growth	/	/	3.919	/	/	3.2	4
521	monocarboxylic acid metabolic proc	/	/	/	2.4	/	3.167	4
534	diuresis	/	/	5.943	/	/	3.163	4
535	dihydropyrimidinase activity	/	/	5.943	/	/	3.163	4
543	ventricular cardiac muscle cell di	/	/	5.943	/	/	3.163	4
546	dopamine catabolic process	/	/	5.943	/	/	3.163	4
550	lipoprotein lipase activity	/	/	5.943	/	/	3.163	4
555	SMAD protein nuclear translocation	/	/	5.943	/	/	3.163	4
557	spindle localization	/	4.544	/	/	/	3.163	4
558	establishment of spindle localizat	/	4.544	/	/	/	3.163	4
559	protease binding	/	/	5.943	/	/	3.163	4
563	plasma membrane repair	/	2.817	/	/	/	3.163	4
568	catecholamine catabolic process	/	/	5.943	/	/	3.163	4
572	cleavage furrow	/	2.817	/	/	/	3.163	4
578	phosphopyruvate hydratase activity	/	2.817	/	/	/	3.163	4
581	phosphopyruvate hydratase complex	/	2.817	/	/	/	3.163	4
586	cell part morphogenesis	1.976	/	/	/	/	3.159	4
587	cell projection morphogenesis	1.976	/	/	/	/	3.159	4
588	cell projection organization and b	1.976	/	/	/	/	3.159	4
589	neurite development	2.112	/	/	/	/	3.154	4
593	cell-cell signaling during cell fa	/	/	2.957	/	/	3.146	4
595	regulation of bone mineralization	/	/	/	/	2.399	3.146	4
596	induction	/	/	2.957	/	/	3.146	4
616	myeloid leukocyte activation	/	/	/	/	2.511	3.06	4
621	central nervous system development	/	/	/	/	2.173	3.016	4
625	calmodulin regulated protein kinas	/	3.226	/	/	/	3.001	4
626	regulation of interleukin-2 biosyn	/	/	/	2.809	/	3.001	4
647	regulation of growth	/	/	3.564	/	/	2.787	4
652	retinoic acid receptor binding	/	/	5.278	/	/	2.763	4
668	centromeric DNA binding	/	2.377	/	/	/	2.763	4
671	aldehyde dehydrogenase [NAD(P)+] a	/	2.377	/	/	/	2.763	4
672	neuron remodeling	/	/	5.278	/	/	2.763	4
679	lipid raft organization and biogen	/	/	/	3.739	/	2.763	4
687	retinoid X receptor binding	/	/	5.278	/	/	2.763	4
693	glycosaminoglycan catabolic proces	/	/	5.278	/	/	2.763	4
695	transmembrane-ephrin receptor acti	/	/	/	3.739	/	2.763	4
696	phosphorylase kinase activity	/	2.377	/	/	/	2.763	4
700	glycerol-3-phosphate metabolic pro	/	/	/	/	3.169	2.763	4

704	aminoglycan catabolic process	/	/	5.278	/	/	2.763	4
712	prostanoid metabolic process	/	3.714	/	/	/	2.747	4
714	prostaglandin metabolic process	/	3.714	/	/	/	2.747	4
721	regulation of adenylate cyclase ac	/	/	/	/	2.819	2.7	4
725	metal ion transporter activity	/	/	/	2.829	/	2.64	4
732	interleukin-2 biosynthetic process	/	/	/	2.408	/	2.635	4
736	interleukin-2 production	/	/	/	2.408	/	2.635	4
739	sugar binding	/	/	/	/	2.212	2.619	4
747	regulation of cyclase activity	/	/	/	/	2.654	2.575	4
748	regulation of lyase activity	/	/	/	/	2.654	2.575	4
756	positive regulation of endocytosis	/	/	/	2.293	/	2.531	4
761	negative regulation of cell size	/	/	3.519	/	/	2.516	4
762	di-\, tri-valent inorganic cation	/	/	/	2.546	/	2.516	4
763	positive regulation of transport	/	/	/	/	2.577	2.516	4
764	negative regulation of cell growth	/	/	3.519	/	/	2.516	4
769	extracellular structure organizati	/	/	2.699	/	/	2.493	4
772	aromatic compound metabolic proces	/	/	/	/	2.187	2.467	4
776	nucleosome disassembly	/	/	4.785	/	/	2.462	4
778	membrane attack complex	/	2.04	/	/	/	2.462	4
779	chromatin disassembly	/	/	4.785	/	/	2.462	4
789	regulation of mRNA processing	/	/	4.785	/	/	2.462	4
794	G-protein coupled receptor kinase	/	/	4.785	/	/	2.462	4
796	proline biosynthetic process	/	2.04	/	/	/	2.462	4
804	phosphatidylinositol biosynthetic	2.643	/	/	/	/	2.462	4
807	heat generation	/	2.04	/	/	/	2.462	4
809	endosome to lysosome transport	/	/	/	/	2.789	2.462	4
814	troponin complex	/	/	4.785	/	/	2.462	4
827	secretin-like receptor activity	2.421	/	/	/	/	2.434	4
834	negative regulation of biosyntheti	2.22	/	/	/	/	2.403	4
843	adenylate cyclase activation	/	/	/	/	2.483	2.343	4
850	metallopeptidase activity	/	/	/	3.666	/	2.331	4
855	reproductive process in a multicel	/	/	/	2.016	/	2.271	4
856	multicellular organism reproductio	/	/	/	2.016	/	2.271	4
862	positive regulation of lyase activ	/	/	/	/	2.371	2.258	4
863	positive regulation of cyclase act	/	/	/	/	2.371	2.258	4
870	positive regulation of adenylate c	/	/	/	/	2.371	2.258	4
876	apical part of cell	/	/	/	/	2.098	2.245	4
877	electron transport	/	/	2.112	/	/	2.244	4
884	glycoprotein binding	/	/	4.399	/	/	2.224	4
887	laminin-1 complex	2.347	/	/	/	/	2.224	4
890	axonal fasciculation	2.347	/	/	/	/	2.224	4
894	guanylate cyclase activity	/	/	4.399	/	/	2.224	4
901	cardiac muscle cell differentiatio	/	/	4.399	/	/	2.224	4
902	regulation of protein binding	/	/	/	2.992	/	2.224	4
904	membrane depolarization	/	/	/	/	2.486	2.224	4
912	lysophospholipase activity	/	/	/	/	2.486	2.224	4
913	adenosine deaminase activity	/	/	4.399	/	/	2.224	4

915	glucan catabolic process	/	/	/	/	2.486	2.224	4
916	polyamine biosynthetic process	/	/	/	/	2.486	2.224	4
922	astrocyte differentiation	2.347	/	/	/	/	2.224	4
923	negative regulation of axon extens	3.871	/	/	/	/	2.224	4
932	myoblast differentiation	/	/	/	/	2.795	2.199	4
936	regulation of cell growth	/	/	3.572	/	/	2.179	4
943	somitogenesis	/	/	/	/	2.266	2.177	4
954	regulation of lipid metabolic proc	/	/	2.091	/	/	2.102	4
955	catecholamine metabolic process	/	/	2.091	/	/	2.102	4
964	glucose transport	/	/	/	/	2.072	2.03	4
965	small nuclear ribonucleoprotein co	/	2.553	/	/	/	2.03	4
968	chemokine receptor activity	/	/	/	/	2.072	2.03	4
970	G-protein chemoattractant receptor	/	/	/	/	2.072	2.03	4
973	phenol metabolic process	/	/	2.032	/	/	2.03	4
985	negative regulation of axonogenesi	3.527	/	/	/	/	2.028	4
987	positive regulation of MAPKKK casc	/	/	/	/	2.236	2.028	4
996	embryonic hindlimb morphogenesis	/	/	4.086	/	/	2.028	4
997	neuromuscular process	/	/	/	2.721	/	2.028	4
998	hydrogen peroxide catabolic proces	/	/	4.086	/	/	2.028	4
1004	cell division site part	/	2.762	/	/	/	2.028	4
1006	imprinting	/	/	/	/	2.236	2.028	4
1010	water channel activity	2.101	/	/	/	/	2.028	4
1011	beta-amyloid binding	2.101	/	/	/	/	2.028	4
1015	laminin complex	2.101	/	/	/	/	2.028	4
1017	cholesterol binding	/	/	4.086	/	/	2.028	4
1019	cell division site	/	2.762	/	/	/	2.028	4
1021	hydrogen peroxide metabolic proces	/	/	4.086	/	/	2.028	4
1031	protein amino acid methylation	/	/	/	/	2.802	1.961	4
1032	heterotrimeric G-protein complex	/	/	1.977	/	/	1.961	4
1038	protein amino acid alkylation	/	/	/	/	2.802	1.961	4
1046	kidney development	2.178	/	4.665	/	/	/	4
1064	positive regulation of transcripti	/	2.098	2.842	/	/	/	4
1071	copper ion transporter activity	/	/	/	2.491	2.023	/	4
1074	copper ion transport	/	/	/	2.491	2.023	/	4
1084	calcium-transporting ATPase activi	/	2.498	/	2.491	/	/	4
1092	glutamate metabolic process	/	2.498	/	/	2.023	/	4
1110	receptor signaling protein activit	3.11	2.773	/	/	/	/	4
1113	cell cycle checkpoint	/	3.455	/	/	2.805	/	4
1120	leukocyte mediated immunity	2.639	/	/	/	3.388	/	4
1127	regulation of mitosis	/	3.378	/	/	4.469	/	4
1144	pronucleus	/	2.269	/	/	4.483	/	4
1161	morphogenesis of a polarized epith	/	/	7.466	2.293	/	/	4
1171	mRNA polyadenylation	/	3.362	/	2.293	/	/	4
1182	water transporter activity	2.987	2.269	/	/	/	/	4
1197	cytoskeletal part	/	3.558	/	/	2.991	/	4
1210	oxidoreductase activity	/	2.205	/	/	2.414	/	4
1211	microtubule cytoskeleton	/	2.995	/	/	3.406	/	4

1230	aromatic compound biosynthetic pro	/	2.067	/	/	2.937	/	4
1236	protein kinase C activity	/	2.067	/	3.548	/	/	4
1242	amino acid binding	/	2.067	/	2.12	/	/	4
1245	RNA polyadenylation	/	3.109	/	2.12	/	/	4
1252	substrate-bound cell migration	/	3.109	/	2.12	/	/	4
1255	phorbol ester receptor activity	/	2.067	/	3.548	/	/	4
1259	pteridine and derivative biosynthe	/	2.067	/	/	2.937	/	4
1261	sulfur amino acid biosynthetic pro	/	2.067	/	2.12	/	/	4
1276	negative regulation of apoptosis	3.456	2.535	/	/	/	/	4
1281	positive regulation of lymphocyte	1.987	/	/	2.025	/	/	4
1282	positive regulation of mononuclear	1.987	/	/	2.025	/	/	4
1283	inositol or phosphatidylinositol p	/	2.38	/	2.025	/	/	4
1288	negative regulation of programmed	3.379	2.454	/	/	/	/	4
1311	tropomyosin binding	/	3.882	/	1.966	/	/	4
1318	negative regulation of adenylate c	/	/	3.241	1.966	/	/	4
1320	negative regulation of lyase activ	/	/	3.241	1.966	/	/	4
1324	intercellular junction assembly	2.574	2.885	/	/	/	/	4
1328	negative regulation of cyclase act	/	/	3.241	1.966	/	/	4
1331	hindlimb morphogenesis	/	/	3.241	3.333	/	/	4
1334	transcriptional activator activity	/	/	/	2.246	2.181	/	4
1340	pigmentation	/	/	3.646	2.692	/	/	4
1345	muscle cell differentiation	1.962	/	/	/	2.195	/	4
1353	metanephros development	2.443	/	3.581	/	/	/	4
1355	anti-apoptosis	3.356	2.259	/	/	/	/	4
1359	memory	2.399	/	/	/	2.56	/	4
1364	endothelial cell differentiation	2.399	/	3.092	/	/	/	4
1368	glucose transporter activity	2.399	/	/	/	2.56	/	4
1376	male sex differentiation	2.366	2.606	/	/	/	/	4
1378	mesenchymal cell development	2.366	2.606	/	/	/	/	4
1390	glucose metabolic process	/	/	/	2.596	2.553	/	4
1394	mesenchymal cell differentiation	2.292	2.52	/	/	/	/	4
1418	hexose transporter activity	3.319	/	/	/	2.399	/	4
1421	monosaccharide transporter activit	3.319	/	/	/	2.399	/	4
1425	sugar transporter activity	2.866	/	/	/	2.428	/	4
1427	regulation of actin polymerization	/	/	3.401	2.409	/	/	4
1435	carbohydrate transporter activity	2.788	/	/	/	2.357	/	4
1446	regulation of anatomical structure	2.082	2.817	/	/	/	/	4
1447	regulation of cell shape	2.082	2.817	/	/	/	/	4
1452	regulation of cell morphogenesis	2.082	2.817	/	/	/	/	4
1462	protein N-terminus binding	/	2.333	2.836	/	/	/	4
1469	sterol binding	/	/	2.836	/	2.252	/	4
1472	cytolysis	2.097	/	/	/	2.252	/	4
1484	taxis	2.324	/	/	/	2.296	/	4
1485	chemotaxis	2.324	/	/	/	2.296	/	4
1493	negative regulation of transcripti	/	2.464	2.16	/	/	/	4
1495	centrosome	/	2.132	/	/	2.722	/	4
1496	negative regulation of enzyme acti	/	2.132	3.593	/	/	/	4

1506	nucleobase\, nucleoside\, nucleoti	/	3.709	/	/	2.795	/	4
1507	receptor signaling protein serine/	/	2.653	/	2.159	/	/	4
1529	sarcolemma	2.972	3.044	/	/	/	/	4
1546	regulation of lymphocyte activatio	/	/	/	2.377	2.057	/	4
1562	centrosome organization and biogen	/	2.037	/	/	3.006	/	4
1566	microtubule organizing center orga	/	2.037	/	/	3.006	/	4
1575	unlocalized protein complex	/	2.876	/	/	1.992	/	4
1588	protein amino acid glycosylation	3.222	/	/	2.075	/	/	4
1592	coated pit	/	/	3.003	/	2.525	/	4
1593	T cell proliferation	/	2.352	/	2.627	/	/	4
1601	tumor necrosis factor receptor bin	/	/	2.531	2.408	/	/	4
1607	multicellular organismal catabolic	2.677	/	/	2.408	/	/	4
1611	phosphate transport	/	/	/	3.274	4.221	/	4
1617	biopolymer glycosylation	3.107	/	/	1.986	/	/	4
1632	fatty acid binding	/	/	5.248	2.293	/	/	4
1634	tumor necrosis factor receptor sup	/	/	2.444	2.293	/	/	4
1645	negative regulation of protein met	1.973	/	/	2.106	/	/	4
1647	microtubule organizing center	/	2.312	/	/	2.191	/	4
1655	neural crest cell migration	2.421	/	2.364	/	/	/	4
1656	digestive process	/	/	2.364	2.185	/	/	4
1660	collagen binding	2.421	/	2.364	/	/	/	4
1662	androgen receptor binding	/	2.437	/	/	2.601	/	4
1669	cellular protein complex disassemb	2.421	/	2.364	/	/	/	4
1677	identical protein binding	/	2.498	/	/	3.484	/	4
1681	negative regulation of protein kin	/	2.495	2.798	/	/	/	4
1682	negative regulation of transferase	/	2.495	2.798	/	/	/	4
1690	macromolecular complex disassembly	2.305	/	2.289	/	/	/	4
1691	protein complex disassembly	2.305	/	2.289	/	/	/	4
1710	anion transport	/	/	/	2.721	2.956	/	4
1712	positive regulation of lymphocyte	/	/	/	2.24	2.113	/	4
1747	response to hypoxia	/	2.073	/	/	3.138	/	4
1779	spindle pole	/	2.67	/	/	3.02	/	4
1790	transferase activity	/	3.276	/	/	2.103	/	4
1802	protein amino acid O-linked glycos	/	/	2.032	/	2.072	/	4
1818	primary neural tube formation	2.603	/	1.977	/	/	/	4
1819	epithelial cell proliferation	/	2.44	/	/	2.802	/	4
1826	phospholipid binding	1.993	/	2.881	/	/	/	4
1845	lyase activity	/	1.973	/	/	2.207	/	4
1854	peptidoglycan metabolic process	2.408	/	/	2.407	/	/	4
1866	microtubule-based process	/	3.459	/	/	3.541	/	4
1870	interspecies interaction between o	2.317	/	/	2.324	/	/	4
1875	symbiosis\, encompassing mutualism	2.317	/	/	2.324	/	/	4
1892	peptidyl-amino acid modification	/	1.971	/	/	2.956	/	4
1908	cytoskeleton-dependent intracellul	/	2.182	/	/	2.051	/	4
1923	establishment of cellular localiza	/	2.071	/	/	2.411	/	4
1941	phosphotransferase activity\, phos	/	2.883	/	/	2.819	/	4
1981	intracellular transport	/	2.361	/	/	2.255	/	4

1984	lipid binding	/	/	2.693	2.522	/	/	4
1991	manganese ion binding	/	/	2.333	2.132	/	/	4
2002	nucleotide biosynthetic process	/	3.388	/	/	3.008	/	4
2006	regulation of cyclin-dependent pro	/	3.897	/	/	2.289	/	4
2011	chloride transport	/	/	3.24	2.219	/	/	4
2016	ion homeostasis	2.215	2.752	/	/	/	/	4
2029	protein heterodimerization activit	/	2.444	/	/	1.995	/	4
2067	intracellular organelle part	/	4.487	/	/	2.646	/	4
2079	organelle part	/	4.51	/	/	2.602	/	4
2126	C-4 methylsterol oxidase activity	3.767	3.135	/	/	/	/	4
2174	protein import into peroxisome mat	/	3.135	/	/	3.925	/	4
2207	hydrolase activity\, acting on car	/	3.135	/	4.512	/	/	4
2217	protein C-terminal methylesterase	3.767	3.135	/	/	/	/	4
2237	platelet-derived growth factor bet	3.767	/	/	/	3.925	/	4
2250	DNA replication proofreading	3.767	3.135	/	/	/	/	4
2278	NACHT domain binding	/	3.135	/	4.512	/	/	4
2291	phosphoribosylaminoimidazolesuccin	/	3.135	/	/	3.925	/	4
2314	phosphoribosylaminoimidazole carbo	/	3.135	/	/	3.925	/	4
2319	phosphoribosylaminoimidazole carbo	/	3.135	/	/	3.925	/	4
2325	nicotinate-nucleotide diphosphoryl	3.767	/	/	4.512	/	/	4
2356	ribosomal small subunit binding	3.767	3.135	/	/	/	/	4
2357	fumarate reductase complex	3.767	3.135	/	/	/	/	4
2363	response to host defenses	3.767	/	/	/	3.925	/	4
2379	glucose 1-phosphate metabolic proc	/	3.135	/	4.512	/	/	4
2380	succinate dehydrogenase complex (u	3.767	3.135	/	/	/	/	4
2384	acetylcholinesterase activity	3.767	3.135	/	/	/	/	4
2388	induction by organism of defense r	3.767	/	/	/	3.925	/	4
2398	serine hydrolase activity	3.767	3.135	/	/	/	/	4
2417	response to defenses of other orga	3.767	/	/	/	3.925	/	4
2427	modulation by organism of defense	3.767	/	/	/	3.925	/	4
2428	positive regulation by symbiont of	3.767	/	/	/	3.925	/	4
2430	positive regulation by organism of	3.767	/	/	/	3.925	/	4
2435	modulation by symbiont of host def	3.767	/	/	/	3.925	/	4
2436	induction of host immune response	3.767	/	/	/	3.925	/	4
2437	induction by symbiont of host defe	3.767	/	/	/	3.925	/	4
2441	negative regulation of synaptic tr	3.767	3.135	/	/	/	/	4
2475	mitotic chromosome movement toward	/	3.135	/	/	3.925	/	4
2480	succinate dehydrogenase complex	3.767	3.135	/	/	/	/	4
2525	phosphoacetylglucosamine mutase ac	/	3.135	/	4.512	/	/	4
2540	negative regulation of hemoglobin	3.767	3.135	/	/	/	/	4
2543	negative regulation of translation	3.767	3.135	/	/	/	/	4
2613	mitochondrial respiratory chain co	3.767	3.135	/	/	/	/	4
2622	glutamate\:sodium symporter activi	3.767	/	/	/	3.925	/	4
2653	regulation of T cell mediated cyto	3.767	3.135	/	/	/	/	4
2673	negative regulation of leukocyte m	3.767	3.135	/	/	/	/	4
2732	triphosphatase activity	/	3.135	/	/	3.925	/	4
2735	purine deoxyribonucleoside triphos	/	3.135	/	/	3.925	/	4

2736	purine deoxyribonucleotide catabol	/	3.135	/	/	3.925	/	4
2737	deoxyribonucleoside triphosphate c	/	3.135	/	/	3.925	/	4
2752	JAK pathway signal transduction ad	3.767	3.135	/	/	/	/	4
2781	purine deoxyribonucleoside triphos	/	3.135	/	/	3.925	/	4
2784	dGTP metabolic process	/	3.135	/	/	3.925	/	4
2791	Pro-X carboxypeptidase activity	3.767	3.135	/	/	/	/	4
2816	negative regulation of membrane po	/	3.135	/	/	3.925	/	4
2844	peptide alpha-N-acetyltransferase	/	3.135	/	/	3.925	/	4
2845	passive induction of host immune r	3.767	/	/	/	3.925	/	4
2856	basic amino acid permease activity	3.767	3.135	/	/	/	/	4
2877	regulation of synaptic transmissio	3.767	3.135	/	/	/	/	4
2911	carboxypeptidase D activity	/	/	/	4.512	3.925	/	4
2943	chromosome movement towards spindl	/	3.135	/	/	3.925	/	4
2952	nitrilase activity	/	3.135	/	4.512	/	/	4
2998	granulocyte macrophage colony-stim	3.767	3.135	/	/	/	/	4
3052	fructose transporter activity	3.767	/	/	/	3.925	/	4
3054	fructose transport	3.767	/	/	/	3.925	/	4
3055	acetoacetic acid metabolic process	/	3.135	/	4.512	/	/	4
3070	monodehydroascorbate reductase (NA	3.767	3.135	/	/	/	/	4
3130	negative regulation of synaptic tr	3.767	3.135	/	/	/	/	4
3132	protein methylesterase activity	3.767	3.135	/	/	/	/	4
3140	3’ -phosphoadenosine 5’ -phosphosu	/	3.135	/	/	3.925	/	4
3151	myosin filament assembly	/	3.135	/	/	3.925	/	4
3153	myosin filament assembly or disass	/	3.135	/	/	3.925	/	4
3165	smooth muscle development	/	3.135	/	/	3.925	/	4
3182	entrainment of circadian clock by	3.767	3.135	/	/	/	/	4
3189	deoxyribonucleoside monophosphate	/	3.135	/	/	3.925	/	4
3194	PCNA complex	/	3.135	/	/	3.925	/	4
3209	pyrimidine deoxyribonucleoside mon	/	3.135	/	/	3.925	/	4
3213	DNA polymerase processivity factor	/	3.135	/	/	3.925	/	4
3216	pyrimidine deoxyribonucleoside mon	/	3.135	/	/	3.925	/	4
3222	dTMP metabolic process	/	3.135	/	/	3.925	/	4
3263	serine-type Pro-X carboxypeptidase	3.767	3.135	/	/	/	/	4
3279	5\,10-methylenetetrahydrofolate-de	/	3.135	/	/	3.925	/	4
3330	dGTP catabolic process	/	3.135	/	/	3.925	/	4
3331	8-oxo-7\,8-dihydroguanine triphosp	/	3.135	/	/	3.925	/	4
3342	negative regulation of T cell medi	3.767	3.135	/	/	/	/	4
3434	succinate-semialdehyde dehydrogena	3.767	3.135	/	/	/	/	4
3497	glutathione synthase activity	3.767	3.135	/	/	/	/	4
3508	fumarate hydratase activity	/	3.135	/	4.512	/	/	4
3515	regulation of hemoglobin biosynthe	3.767	3.135	/	/	/	/	4
3525	alternative-complement-pathway C3/	3.767	3.135	/	/	/	/	4
3542	fumarate metabolic process	/	3.135	/	4.512	/	/	4
3567	N-terminal myristoylation domain b	/	3.135	/	4.512	/	/	4
3602	positive regulation of granulocyte	3.767	/	/	/	3.925	/	4
3604	homogentisate 1\,2-dioxygenase act	/	/	/	4.512	3.925	/	4
3671	collagen type III	/	3.135	/	/	3.925	/	4

3685	cysteine biosynthetic process via	3.767	3.135	/	/	/	/	4
3689	GDP-mannose 4\,6-dehydratase activ	3.767	3.135	/	/	/	/	4
3691	cystathionine beta-synthase activi	3.767	3.135	/	/	/	/	4
3700	cysteine biosynthetic process from	3.767	3.135	/	/	/	/	4
3732	butanoic acid metabolic process	/	3.135	/	4.512	/	/	4
3899	dTMP biosynthetic process	/	3.135	/	/	3.925	/	4
3911	regulation of glutamate-cysteine l	/	3.135	/	/	3.925	/	4
3915	deoxyribonucleoside monophosphate	/	3.135	/	/	3.925	/	4
3918	pyrimidine transport	3.767	3.135	/	/	/	/	4
3920	thymidylate synthase activity	/	3.135	/	/	3.925	/	4
3937	positive regulation of non-apoptot	3.767	3.135	/	/	/	/	4
3992	glutamate-cysteine ligase catalyti	/	3.135	/	/	3.925	/	4
4028	positive regulation of glutamate-c	/	3.135	/	/	3.925	/	4
4045	regulation of granulocyte differen	3.767	/	/	/	3.925	/	4
4201	tRNA (guanine-N7-)-methyltransfera	3.767	3.135	/	/	/	/	4
4207	smooth muscle fiber development	/	3.135	/	/	3.925	/	4
4209	muscle thick filament assembly	/	3.135	/	/	3.925	/	4
4256	5-oxoprolinase (ATP-hydrolyzing) a	/	3.135	/	4.512	/	/	4
4281	cation homeostasis	2.242	2.457	/	/	/	/	4
4321	protein farnesyltransferase activi	2.476	/	/	/	2.595	/	4
4333	internal protein amino acid acetyl	/	1.992	/	/	2.595	/	4
4348	cannabinoid receptor activity	2.476	/	/	/	2.595	/	4
4350	protein amino acid farnesylation	2.476	/	/	/	2.595	/	4
4370	ribonuclease inhibitor activity	2.476	1.992	/	/	/	/	4
4406	respiratory chain complex II	2.476	1.992	/	/	/	/	4
4408	succinate dehydrogenase (ubiquinon	2.476	1.992	/	/	/	/	4
4461	ATPase inhibitor activity	2.476	1.992	/	/	/	/	4
4473	apical junction assembly	2.476	1.992	/	/	/	/	4
4486	activin receptor activity\, type I	2.476	1.992	/	/	/	/	4
4540	thymidine kinase activity	/	1.992	/	/	2.595	/	4
4551	alpha-catenin binding	2.476	1.992	/	/	/	/	4
4556	interleukin-10 receptor activity	/	1.992	/	/	2.595	/	4
4584	gamma-aminobutyric acid metabolic	2.476	1.992	/	/	/	/	4
4643	laminin-1 binding	2.476	1.992	/	/	/	/	4
4647	adenine salvage	/	1.992	/	/	2.595	/	4
4649	adenine metabolic process	/	1.992	/	/	2.595	/	4
4650	cysteine biosynthetic process	2.476	1.992	/	/	/	/	4
4716	positive regulation of ligase acti	/	1.992	/	/	2.595	/	4
4718	cyclin binding	2.476	1.992	/	/	/	/	4
4726	metallocarboxypeptidase D activity	/	/	/	3.034	2.595	/	4
4737	regulation of dephosphorylation	2.476	1.992	/	/	/	/	4
4738	protein phosphatase 2A binding	5.328	4.434	/	/	/	/	4
4745	negative regulation of focal adhes	2.476	1.992	/	/	/	/	4
4753	protein amino acid demethylation	2.476	1.992	/	/	/	/	4
4761	receptor internalization	2.476	1.992	/	/	/	/	4
4762	acetylcholine catabolic process	2.476	1.992	/	/	/	/	4
4763	neurotransmitter receptor biosynth	2.476	1.992	/	/	/	/	4

4764	acetylcholine catabolic process in	2.476	1.992	/	/	/	/	4
4771	negative regulation of cytokine an	2.476	1.992	/	/	/	/	4
4774	mitotic spindle elongation	/	1.992	/	/	2.595	/	4
4799	purine transport	2.476	1.992	/	/	/	/	4
4802	response to mercury ion	2.476	1.992	/	/	/	/	4
4820	pyrimidine transporter activity	2.476	1.992	/	/	/	/	4
4821	nutrient import	2.476	1.992	/	/	/	/	4
4824	gamma-aminobutyric acid catabolic	2.476	1.992	/	/	/	/	4
4827	polyol transport	2.476	1.992	/	/	/	/	4
4830	leucine catabolic process	2.476	1.992	/	/	/	/	4
4831	methylcrotonoyl-CoA carboxylase ac	2.476	1.992	/	/	/	/	4
4856	ribonucleoside diphosphate biosynt	/	1.992	/	/	2.595	/	4
4857	purine nucleoside diphosphate bios	/	1.992	/	/	2.595	/	4
4867	purine ribonucleoside diphosphate	/	1.992	/	/	2.595	/	4
4882	purine base salvage	/	1.992	/	/	2.595	/	4
4907	positive regulation of actin filam	/	1.992	/	/	2.595	/	4
4913	regulation of cytokine and chemoki	2.476	1.992	/	/	/	/	4
4923	purine deoxyribonucleotide metabol	/	1.992	/	/	2.595	/	4
4927	spindle elongation	/	1.992	/	/	2.595	/	4
4930	T cell mediated cytotoxicity	2.476	1.992	/	/	/	/	4
4932	butyrate catabolic process	2.476	1.992	/	/	/	/	4
4955	leucine metabolic process	2.476	1.992	/	/	/	/	4
4960	short-chain fatty acid catabolic p	2.476	1.992	/	/	/	/	4
4965	protein amino acid dealkylation	2.476	1.992	/	/	/	/	4
4970	interleukin-10 binding	/	1.992	/	/	2.595	/	4
4973	neutrophil homeostasis	2.476	1.992	/	/	/	/	4
4975	regulation of translational initia	2.476	1.992	/	/	/	/	4
5009	regulation of focal adhesion forma	2.476	1.992	/	/	/	/	4
5010	negative regulation of transmissio	2.476	1.992	/	/	/	/	4
5020	interleukin-5 binding	2.476	1.992	/	/	/	/	4
5060	oxidoreductase activity\, acting o	2.476	1.992	/	/	/	/	4
5084	detoxification of copper ion	2.476	1.992	/	/	/	/	4
5174	DNA replication-dependent nucleoso	/	1.992	/	/	2.595	/	4
5184	positive regulation of T-helper 2	2.476	1.992	/	/	/	/	4
5186	myoblast migration	2.476	1.992	/	/	/	/	4
5189	interleukin-5 receptor activity	2.476	1.992	/	/	/	/	4
5191	neutrophil apoptosis	2.476	1.992	/	/	/	/	4
5201	double-stranded telomeric DNA bind	/	/	/	3.034	2.595	/	4
5207	positive regulation of cytoskeleto	/	1.992	/	/	2.595	/	4
5209	positive regulation of stress fibe	/	1.992	/	/	2.595	/	4
5263	growth hormone receptor binding	2.476	1.992	/	/	/	/	4
5290	spindle pole centrosome	/	1.992	/	/	2.595	/	4
5297	glycerophospholipid catabolic proc	/	1.992	/	3.034	/	/	4
5300	parathyroid hormone receptor activ	2.476	1.992	/	/	/	/	4
5331	photoperiodism	2.476	1.992	/	/	/	/	4
5342	negative regulation of Notch signa	2.476	1.992	/	/	/	/	4
5345	prolactin receptor binding	2.476	1.992	/	/	/	/	4

5350	positive regulation of mitotic met	/	4.434	/	/	2.595	/	4
5357	lymphangiogenesis	2.476	1.992	/	/	/	/	4
5379	collagen type V	/	/	/	2.349	4.386	/	4
5400	follicle-stimulating hormone recep	/	/	/	2.349	1.972	/	4
5421	dTTP biosynthetic process	/	/	/	2.349	1.972	/	4
5434	peptidyl-proline 4-dioxygenase act	/	/	/	2.349	4.386	/	4
5435	peptidyl-proline hydroxylation	/	/	/	2.349	4.386	/	4
5438	negative regulation of muscle cell	/	/	/	2.349	1.972	/	4
5440	4-hydroxyproline metabolic process	/	/	/	2.349	4.386	/	4
5450	regulation of muscle cell differen	/	/	/	2.349	1.972	/	4
5457	collagen type I	/	/	/	5.082	4.386	/	4
5459	xenobiotic transporter activity	/	/	/	2.349	1.972	/	4
5470	long-term memory	/	/	/	2.349	1.972	/	4
5482	megakaryocyte differentiation	/	/	/	2.349	1.972	/	4
5496	methylenetetrahydrofolate dehydrog	/	/	/	2.349	1.972	/	4
5504	IMP biosynthetic process	/	5.431	/	/	4.386	/	4
5505	IMP metabolic process	/	5.431	/	/	4.386	/	4
5511	pyrimidine deoxyribonucleoside tri	/	/	/	2.349	1.972	/	4
5513	pyrimidine nucleoside triphosphate	/	/	/	2.349	1.972	/	4
5514	deoxyribonucleoside triphosphate b	/	/	/	2.349	1.972	/	4
5515	dTTP metabolic process	/	/	/	2.349	1.972	/	4
5517	water homeostasis	/	3.436	/	2.349	/	/	4
5525	xenobiotic-transporting ATPase act	/	/	/	2.349	1.972	/	4
5577	interleukin-8 binding	/	/	/	2.349	1.972	/	4
5601	regulation of keratinocyte differe	/	/	/	2.349	1.972	/	4
5618	fructose-bisphosphate aldolase act	/	/	/	2.349	1.972	/	4
5646	glutamate-tRNA ligase activity	/	/	/	2.349	1.972	/	4
5648	glutamyl-tRNA aminoacylation	/	/	/	2.349	1.972	/	4
5657	regulation of growth rate	/	/	/	2.349	1.972	/	4
5666	peptidyl-proline hydroxylation to	/	/	/	2.349	4.386	/	4
5672	procollagen-proline 4-dioxygenase	/	/	/	2.349	4.386	/	4
5690	signal recognition particle bindin	/	3.436	/	/	1.972	/	4
5700	threonine-tRNA ligase activity	/	/	/	2.349	1.972	/	4
5701	threonyl-tRNA aminoacylation	/	/	/	2.349	1.972	/	4
5703	protein import into mitochondrial	/	/	/	2.349	1.972	/	4
5704	signal recognition particle recept	/	3.436	/	/	1.972	/	4
5715	sodium ion homeostasis	/	/	/	5.082	1.972	/	4
5735	translocon complex	/	/	/	2.349	1.972	/	4
5738	base-excision repair\, gap-filling	/	3.436	/	/	1.972	/	4
5752	cAMP-dependent protein kinase inhi	/	/	/	2.349	1.972	/	4
5755	’ de novo’ IMP biosynthetic proce	/	5.431	/	/	4.386	/	4
5823	ESC/E(Z) complex	/	/	/	2.349	4.386	/	4
5857	retinal rod cell development	/	/	/	2.349	1.972	/	4
5880	lipid phosphorylation	/	/	/	2.349	1.972	/	4
5898	retinoid-X receptor activity	/	/	6.909	2.349	/	/	4
5904	aminoacylase activity	/	3.436	/	/	1.972	/	4
5924	positive regulation of fat cell di	/	/	/	2.349	1.972	/	4

5949	alanyl-tRNA aminoacylation	/	/	/	2.349	1.972	/	4
5950	alanine-tRNA ligase activity	/	/	/	2.349	1.972	/	4
5972	formyltetrahydrofolate dehydrogena	/	/	/	2.349	1.972	/	4
5977	methylenetetrahydrofolate dehydrog	/	/	/	2.349	1.972	/	4
5986	methenyltetrahydrofolate cyclohydr	/	/	/	2.349	1.972	/	4
6002	vinculin binding	/	3.436	/	/	4.386	/	4
6011	copper\, zinc superoxide dismutase	/	/	/	2.349	1.972	/	4
6014	antral ovarian follicle growth	/	/	/	2.349	1.972	/	4
6036	intracellular organelle	/	4.762	/	/	2.225	/	4
6038	organelle	/	4.745	/	/	2.213	/	4
6067	structural constituent of bone	/	/	/	4.29	5.761	/	4
6112	deoxyribonucleoside diphosphate me	/	2.817	/	/	3.671	/	4
6213	pyrimidine deoxyribonucleotide bio	/	2.817	/	/	3.671	/	4
6256	[pyruvate dehydrogenase (lipoamide	/	2.817	/	4.29	/	/	4
6263	costamere	3.502	4.544	/	/	/	/	4
6310	uropod	/	2.817	/	/	3.671	/	4
6332	Rac GTPase binding	/	2.817	/	4.29	/	/	4
6365	trailing edge	/	2.817	/	/	3.671	/	4
6373	actin filament severing	3.502	2.817	/	/	/	/	4
6386	mRNA stabilization	/	2.817	/	/	3.671	/	4
6392	RNA stabilization	/	2.817	/	/	3.671	/	4
6608	CoA carboxylase activity	3.014	2.377	/	/	/	/	4
6632	eukaryotic translation elongation	/	2.377	/	/	3.169	/	4
6636	negative regulation of cell-matrix	3.014	2.377	/	/	/	/	4
6651	platelet-derived growth factor rec	/	2.377	/	3.739	/	/	4
6670	positive regulation of myeloid leu	3.014	/	/	/	3.169	/	4
6688	deoxyribonucleoside triphosphate m	/	2.377	/	/	3.169	/	4
6737	positive regulation of chemokine b	2.643	2.04	/	/	/	/	4
6759	fatty acid catabolic process	2.643	2.04	/	/	/	/	4
6779	SRP-dependent cotranslational prot	/	2.04	/	/	2.789	/	4
6791	negative regulation of translation	2.643	2.04	/	/	/	/	4
6801	deoxyribonucleotide biosynthetic p	/	2.04	/	/	2.789	/	4
6828	ligase activity\, forming carbon-c	2.643	2.04	/	/	/	/	4
6892	cyclin-dependent protein kinase re	2.643	2.04	/	/	/	/	4
6922	DNA replication factor C complex	/	4.86	/	/	6.203	/	4
6932	cellular defense response	2.76	/	/	/	2.004	/	4
6945	negative regulation of caspase act	/	3.074	/	/	2.486	/	4
6995	rough endoplasmic reticulum membra	/	3.074	/	/	2.486	/	4
7013	positive regulation of tumor necro	2.347	/	/	/	4.066	/	4
7015	ligand-regulated transcription fac	/	/	4.399	2.992	/	/	4
7063	translation termination factor act	2.347	3.074	/	/	/	/	4
7065	translation release factor activit	2.347	3.074	/	/	/	/	4
7115	tumor necrosis factor production	2.101	/	/	/	3.714	/	4
7117	regulation of tumor necrosis facto	2.101	/	/	/	3.714	/	4
7127	tumor necrosis factor biosynthetic	2.101	/	/	/	3.714	/	4
7130	sarcomere organization	/	/	/	2.721	2.236	/	4
7138	regulation of cell-cell adhesion	2.101	2.762	/	/	/	/	4

7143	copper ion homeostasis	3.527	2.762	/	/	/	/	4
7188	sulfation	2.101	/	/	/	2.236	/	4
7190	gamma-tubulin complex	/	/	/	2.721	2.236	/	4
7204	sodium\:potassium-exchanging ATPas	2.101	2.762	/	/	/	/	4
7221	death receptor binding	2.101	/	/	/	2.236	/	4
7230	L-serine metabolic process	2.101	2.762	/	/	/	/	4
7249	protein amino acid sulfation	2.101	/	/	/	2.236	/	4
7276	purine nucleotide biosynthetic pro	/	3.408	/	/	2.277	/	4
7323	tumor necrosis factor binding	/	/	/	2.491	2.023	/	4
7327	ribosome binding	/	3.65	/	/	2.023	/	4
7337	regulation of chemokine biosynthet	3.237	2.498	/	/	/	/	4
7346	thymic T cell selection	/	/	/	2.491	2.023	/	4
7423	CTP biosynthetic process	/	2.269	/	2.293	/	/	4
7425	pyrimidine ribonucleoside triphosp	/	2.269	/	2.293	/	/	4
7437	aspartate family amino acid biosyn	/	/	/	2.293	3.161	/	4
7451	CTP metabolic process	/	2.269	/	2.293	/	/	4
7452	pyrimidine ribonucleoside triphosp	/	2.269	/	2.293	/	/	4
7456	chemokine metabolic process	2.987	2.269	/	/	/	/	4
7464	embryonic forelimb morphogenesis	/	2.269	/	2.293	/	/	4
7465	chemokine production	2.987	2.269	/	/	/	/	4
7470	mitotic metaphase/anaphase transit	/	3.362	/	2.293	/	/	4
7487	skin development	/	2.269	/	2.293	/	/	4
7494	chemokine biosynthetic process	2.987	2.269	/	/	/	/	4
7496	cortical actin cytoskeleton organi	2.987	3.362	/	/	/	/	4
7532	endothelial cell migration	/	2.067	/	2.12	/	/	4
7543	mismatched DNA binding	2.768	3.109	/	/	/	/	4
7550	intermediate filament-based proces	/	/	3.41	2.12	/	/	4
7557	GTP biosynthetic process	/	2.067	/	2.12	/	/	4
7587	GTP metabolic process	/	2.067	/	2.12	/	/	4
7592	nucleoside diphosphate metabolic p	/	2.067	/	/	2.937	/	4
7602	intracellular protein transport	/	2.328	/	/	2.306	/	4
7653	deoxyribonucleotide metabolic proc	/	2.885	/	/	3.945	/	4
7716	purine ribonucleoside monophosphat	/	2.683	/	/	2.56	/	4
7722	regulation of microtubule polymeri	/	/	3.092	3.141	/	/	4
7734	purine nucleoside monophosphate bi	/	2.683	/	/	2.56	/	4
7739	purine ribonucleoside monophosphat	/	2.683	/	/	2.56	/	4
7740	purine nucleoside monophosphate me	/	2.683	/	/	2.56	/	4
7743	T cell differentiation in the thym	2.399	/	/	/	2.56	/	4
7746	purine nucleotide metabolic proces	/	3.723	/	/	2.401	/	4
7826	microtubule polymerization or depo	/	/	2.836	2.809	/	/	4
7874	ribonucleoprotein binding	/	4.772	/	/	2.117	/	4
7887	leading edge	1.973	2.36	/	/	/	/	4
7900	UDP-galactosyltransferase activity	/	/	2.624	2.532	/	/	4
7903	phosphotransferase activity\, nitr	/	2.037	/	2.532	/	/	4
7914	antigen processing and presentatio	/	/	2.624	/	1.992	/	4
7918	apoptotic mitochondrial changes	/	2.037	/	2.532	/	/	4
7954	cell homeostasis	/	3.373	/	/	2.498	/	4

7956	response to endogenous stimulus	/	4.24	/	/	3.145	/	4
7984	maintenance of fidelity during DNA	2.545	2.574	/	/	/	/	4
8012	nucleoside monophosphate biosynthe	/	3.21	/	/	2.601	/	4
8020	nucleoside monophosphate metabolic	/	3.21	/	/	2.601	/	4
8099	carboxy-lyase activity	/	1.965	/	/	2.166	/	4
8118	establishment and/or maintenance o	/	2.349	/	2.139	/	/	4
8148	replication fork	/	4.191	/	/	3.395	/	4
8174	response to DNA damage stimulus	/	4.097	/	/	2.839	/	4
8196	antigen binding	2.146	/	/	/	2.338	/	4
8198	DNA replication	/	6.114	/	/	3.551	/	4
8241	G1/S transition of mitotic cell cy	2.523	2.203	/	/	/	/	4
8293	ruffle	3.033	3.53	/	/	/	/	4
8296	single-stranded DNA binding	/	1.983	/	/	2.033	/	4
8303	tRNA aminoacylation for protein tr	/	/	/	2.688	3.207	/	4
8304	tRNA aminoacylation	/	/	/	2.688	3.207	/	4
8305	amino acid activation	/	/	/	2.688	3.207	/	4
8306	aminoacyl-tRNA ligase activity	/	/	/	2.627	3.136	/	4
8309	ligase activity\, forming aminoacy	/	/	/	2.627	3.136	/	4
8311	ligase activity\, forming carbon-o	/	/	/	2.627	3.136	/	4
8394	cell cycle arrest	/	2.829	3.526	/	/	/	4
8398	chromosome organization and biogen	/	3.262	/	2.175	/	/	4
8422	DNA metabolic process	/	5.768	/	/	3.82	/	4
8438	nucleoside-triphosphatase activity	/	2.312	/	/	2.111	/	4
32	receptor signaling protein tyrosin	/	/	/	/	/	6.769	5
149	salivary gland morphogenesis	/	/	/	/	/	5.286	5
150	gland morphogenesis	/	/	/	/	/	5.286	5
214	phosphatidylinositol 3-kinase regu	/	/	/	/	/	4.682	5
289	hindbrain development	/	/	/	/	/	4.246	5
308	neurogenesis	/	/	/	/	/	4.106	5
313	carboxylesterase activity	/	/	/	/	/	4.059	5
314	serine esterase activity	/	/	/	/	/	4.059	5
326	generation of neurons	/	/	/	/	/	3.977	5
344	organic acid biosynthetic process	/	/	/	/	/	3.823	5
345	carboxylic acid biosynthetic proce	/	/	/	/	/	3.823	5
402	regulation of translation initiati	/	/	/	/	/	3.738	5
417	generation of neurons in the foreb	/	/	/	/	/	3.738	5
422	regulation of translation in respo	/	/	/	/	/	3.738	5
439	atypical protein kinase C activity	/	/	/	/	/	3.738	5
447	axon target recognition	/	/	/	/	/	3.738	5
448	forebrain neuron differentiation	/	/	/	/	/	3.738	5
459	salivary gland development	/	/	/	/	/	3.682	5
462	pattern specification process	/	/	/	/	/	3.669	5
470	carboxylic ester hydrolase activit	/	/	/	/	/	3.59	5
479	cell fate commitment	/	/	/	/	/	3.539	5
506	axonogenesis	/	/	/	/	/	3.29	5
522	ethanol oxidation	/	/	/	/	/	3.163	5
523	regulation of cyclic nucleotide bi	/	/	/	/	/	3.163	5

524	aryl sulfotransferase activity	/	/	/	/	/	3.163	5
525	ether hydrolase activity	/	/	/	/	/	3.163	5
526	kinetochore microtubule	/	/	/	/	/	3.163	5
527	ethanol metabolic process	/	/	/	/	/	3.163	5
528	folic acid transport	/	/	/	/	/	3.163	5
529	ErbB-2 class receptor binding	/	/	/	/	/	3.163	5
530	spermidine metabolic process	/	/	/	/	/	3.163	5
531	cell differentiation in hindbrain	/	/	/	/	/	3.163	5
532	bradykinin receptor activity	/	/	/	/	/	3.163	5
533	cerebellar cortex formation	/	/	/	/	/	3.163	5
539	hemoglobin binding	/	/	/	/	/	3.163	5
541	regulation of nucleotide biosynthe	/	/	/	/	/	3.163	5
542	nuclear envelope lumen	/	/	/	/	/	3.163	5
544	regulation of gliogenesis	/	/	/	/	/	3.163	5
545	regulation of glial cell different	/	/	/	/	/	3.163	5
548	regulation of granulocyte macropha	/	/	/	/	/	3.163	5
554	negative regulation of interleukin	/	/	/	/	/	3.163	5
560	lithium ion binding	/	/	/	/	/	3.163	5
561	nuclear migration	/	/	/	/	/	3.163	5
562	negative regulation of bone minera	/	/	/	/	/	3.163	5
565	neuroblast proliferation (sensu Ve	/	/	/	/	/	3.163	5
567	synaptic vesicle maturation	/	/	/	/	/	3.163	5
570	actinin binding	/	/	/	/	/	3.163	5
573	regulation of cAMP metabolic proce	/	/	/	/	/	3.163	5
577	nerve growth factor receptor signa	/	/	/	/	/	3.163	5
579	pyrroline-5-carboxylate reductase	/	/	/	/	/	3.163	5
583	inositol-1\,4\,5-triphosphate rece	/	/	/	/	/	3.163	5
598	exocrine system development	/	/	/	/	/	3.146	5
605	neurite morphogenesis	/	/	/	/	/	3.112	5
606	neuron morphogenesis during differ	/	/	/	/	/	3.112	5
617	response to temperature stimulus	/	/	/	/	/	3.06	5
635	transmission of nerve impulse	/	/	/	/	/	2.878	5
638	plasma membrane organization and b	/	/	/	/	/	2.869	5
643	cellular morphogenesis during diff	/	/	/	/	/	2.845	5
644	cell fate determination	/	/	/	/	/	2.835	5
650	multicellular organism growth	/	/	/	/	/	2.766	5
651	brain development	/	/	/	/	/	2.765	5
653	alveolus development	/	/	/	/	/	2.763	5
655	dynein binding	/	/	/	/	/	2.763	5
656	uridine kinase activity	/	/	/	/	/	2.763	5
657	vesicle transport along microtubul	/	/	/	/	/	2.763	5
659	stem cell development	/	/	/	/	/	2.763	5
660	macrophage chemotaxis	/	/	/	/	/	2.763	5
664	brown fat cell differentiation	/	/	/	/	/	2.763	5
666	mesodermal cell fate determination	/	/	/	/	/	2.763	5
667	positive regulation of B cell diff	/	/	/	/	/	2.763	5
669	vasoactive intestinal polypeptide	/	/	/	/	/	2.763	5

670	positive regulation of neuron apop	/	/	/	/	/	2.763	5
673	regulation of macrophage activatio	/	/	/	/	/	2.763	5
675	granulocyte macrophage colony-stim	/	/	/	/	/	2.763	5
678	positive regulation of progression	/	/	/	/	/	2.763	5
680	elastase activity	/	/	/	/	/	2.763	5
681	granulocyte macrophage colony-stim	/	/	/	/	/	2.763	5
682	interferon receptor activity	/	/	/	/	/	2.763	5
684	negative regulation of nucleotide	/	/	/	/	/	2.763	5
689	acrosome formation	/	/	/	/	/	2.763	5
690	stem cell maintenance	/	/	/	/	/	2.763	5
691	norepinephrine-epinephrine regulat	/	/	/	/	/	2.763	5
694	interferon binding	/	/	/	/	/	2.763	5
698	eukaryotic translation initiation	/	/	/	/	/	2.763	5
703	positive regulation of bone minera	/	/	/	/	/	2.763	5
709	receptor metabolic process	/	/	/	/	/	2.747	5
723	gliogenesis	/	/	/	/	/	2.7	5
724	activation of MAPK activity	/	/	/	/	/	2.64	5
729	neuroblast proliferation	/	/	/	/	/	2.635	5
731	lysine N-acetyltransferase activit	/	/	/	/	/	2.635	5
735	histone acetyltransferase activity	/	/	/	/	/	2.635	5
738	vesicle docking during exocytosis	/	/	/	/	/	2.635	5
740	MAPKKK cascade	/	/	/	/	/	2.619	5
741	innate immune response	/	/	/	/	/	2.618	5
752	synaptic transmission	/	/	/	/	/	2.539	5
757	membrane docking	/	/	/	/	/	2.531	5
758	vesicle docking	/	/	/	/	/	2.531	5
759	cytosolic part	/	/	/	/	/	2.528	5
773	phosphoinositide 3-kinase regulato	/	/	/	/	/	2.462	5
775	inositol-polyphosphate 5-phosphata	/	/	/	/	/	2.462	5
777	segment specification	/	/	/	/	/	2.462	5
780	inositol trisphosphate phosphatase	/	/	/	/	/	2.462	5
785	stem cell differentiation	/	/	/	/	/	2.462	5
787	positive regulation of calcium-med	/	/	/	/	/	2.462	5
788	GDP-dissociation inhibitor activit	/	/	/	/	/	2.462	5
791	collagen type IV	/	/	/	/	/	2.462	5
792	positive regulation of survival ge	/	/	/	/	/	2.462	5
793	calcium-release channel activity	/	/	/	/	/	2.462	5
799	positive regulation of nitric oxid	/	/	/	/	/	2.462	5
800	chemoattractant activity	/	/	/	/	/	2.462	5
806	drug metabolic process	/	/	/	/	/	2.462	5
808	lipoxygenase activity	/	/	/	/	/	2.462	5
812	regulation of epithelial cell diff	/	/	/	/	/	2.462	5
813	eukaryotic translation initiation	/	/	/	/	/	2.462	5
815	regulation of cyclic nucleotide me	/	/	/	/	/	2.462	5
819	receptor clustering	/	/	/	/	/	2.462	5
822	dendrite	/	/	/	/	/	2.458	5
826	Golgi stack	/	/	/	/	/	2.434	5

829	positive regulation of MAPK activi	/	/	/	/	/	2.432	5
837	digestion	/	/	/	/	/	2.366	5
848	regulation of MAPK activity	/	/	/	/	/	2.337	5
852	exocytosis	/	/	/	/	/	2.308	5
861	positive regulation of peptidyl-ty	/	/	/	/	/	2.258	5
866	tissue homeostasis	/	/	/	/	/	2.258	5
869	multicellular organismal homeostas	/	/	/	/	/	2.258	5
873	cell soma	/	/	/	/	/	2.247	5
874	inner ear morphogenesis	/	/	/	/	/	2.247	5
881	nucleus localization	/	/	/	/	/	2.224	5
882	germ cell migration	/	/	/	/	/	2.224	5
883	angiotensin type II receptor activ	/	/	/	/	/	2.224	5
885	cerebellar cortex morphogenesis	/	/	/	/	/	2.224	5
886	phosphofructokinase activity	/	/	/	/	/	2.224	5
888	N-glycan processing	/	/	/	/	/	2.224	5
892	regulation of protein ubiquitinati	/	/	/	/	/	2.224	5
893	sheet-forming collagen	/	/	/	/	/	2.224	5
896	molybdenum ion binding	/	/	/	/	/	2.224	5
897	amiloride-sensitive sodium channel	/	/	/	/	/	2.224	5
899	hemocyte development	/	/	/	/	/	2.224	5
900	regulation of lipid kinase activit	/	/	/	/	/	2.224	5
905	pepsin A activity	/	/	/	/	/	2.224	5
906	regulation of calcium-mediated sig	/	/	/	/	/	2.224	5
908	cerebellum morphogenesis	/	/	/	/	/	2.224	5
909	ciliary rootlet	/	/	/	/	/	2.224	5
914	mechanosensory behavior	/	/	/	/	/	2.224	5
917	angiotensin receptor activity	/	/	/	/	/	2.224	5
918	hydrolase activity\, acting on eth	/	/	/	/	/	2.224	5
919	positive regulation of ossificatio	/	/	/	/	/	2.224	5
920	phosphopantetheine binding	/	/	/	/	/	2.224	5
921	establishment of nucleus localizat	/	/	/	/	/	2.224	5
933	neuron migration	/	/	/	/	/	2.199	5
939	protein amino acid acetylation	/	/	/	/	/	2.177	5
958	lipid metabolic process	/	/	/	/	/	2.072	5
959	regulation of biosynthetic process	/	/	/	/	/	2.072	5
961	ear morphogenesis	/	/	/	/	/	2.06	5
969	regulation of ossification	/	/	/	/	/	2.03	5
974	positive regulation of activated T	/	/	/	/	/	2.028	5
975	synaptic vesicle endocytosis	/	/	/	/	/	2.028	5
979	L-fucose catabolic process	/	/	/	/	/	2.028	5
980	SNAP receptor activity	/	/	/	/	/	2.028	5
983	regulation of insulin secretion	/	/	/	/	/	2.028	5
986	hemocyte differentiation	/	/	/	/	/	2.028	5
989	negative regulation of body size	/	/	/	/	/	2.028	5
990	regulation of steroid metabolic pr	/	/	/	/	/	2.028	5
991	retinol binding	/	/	/	/	/	2.028	5
992	Golgi to endosome transport	/	/	/	/	/	2.028	5

994	ADP binding	/	/	/	/	/	2.028	5
995	proline metabolic process	/	/	/	/	/	2.028	5
999	epidermal growth factor receptor b	/	/	/	/	/	2.028	5
1001	non-membrane spanning protein tyro	/	/	/	/	/	2.028	5
1002	T cell homeostasis	/	/	/	/	/	2.028	5
1003	mesodermal cell fate commitment	/	/	/	/	/	2.028	5
1005	regulation of nucleotide metabolic	/	/	/	/	/	2.028	5
1007	fucose catabolic process	/	/	/	/	/	2.028	5
1008	nuclear localization sequence bind	/	/	/	/	/	2.028	5
1009	transmembrane receptor protein tyr	/	/	/	/	/	2.028	5
1012	central nervous system neuron deve	/	/	/	/	/	2.028	5
1013	positive regulation of bone remode	/	/	/	/	/	2.028	5
1014	adrenoceptor activity	/	/	/	/	/	2.028	5
1016	regulation of B cell differentiati	/	/	/	/	/	2.028	5
1020	mesodermal cell differentiation	/	/	/	/	/	2.028	5
1022	adenylate kinase activity	/	/	/	/	/	2.028	5
1024	amino acid derivative metabolic pr	/	/	/	/	/	2.012	5
1025	regionalization	/	/	/	/	/	2.005	5
1027	neuron projection	/	/	/	/	/	1.988	5
1029	hydrolase activity\, acting on est	/	/	/	/	/	1.962	5
1030	positive regulation of protein ami	/	/	/	/	/	1.961	5
1033	positive regulation of amino acid	/	/	/	/	/	1.961	5
1034	positive regulation of phosphate m	/	/	/	/	/	1.961	5
1036	DNA damage checkpoint	/	/	/	/	/	1.961	5
1039	positive regulation of phosphoryla	/	/	/	/	/	1.961	5
1041	receptor complex	/	2.885	/	/	/	/	5
1044	positive regulation of metabolic p	/	/	2.064	/	/	/	5
1052	integrin complex	/	2.999	/	/	/	/	5
1055	hydro-lyase activity	2.119	/	/	/	/	/	5
1056	iron ion binding	/	2.728	/	/	/	/	5
1065	positive regulation of lymphocyte	/	/	/	/	2.023	/	5
1069	positive regulation of adaptive im	/	/	/	/	2.023	/	5
1073	positive regulation of leukocyte m	/	/	/	/	2.023	/	5
1075	neurotransmitter catabolic process	/	/	3.825	/	/	/	5
1076	dendritic spine	/	/	/	/	2.023	/	5
1078	L-phenylalanine catabolic process	/	/	/	/	3.417	/	5
1079	positive regulation of adaptive im	/	/	/	/	2.023	/	5
1086	protein kinase C binding	/	/	3.825	/	/	/	5
1087	mast cell activation	/	/	/	/	3.417	/	5
1089	L-phenylalanine metabolic process	/	/	/	/	3.417	/	5
1093	cell aging	/	/	3.825	/	/	/	5
1098	one-carbon compound metabolic proc	/	/	/	/	3.012	/	5
1103	lipoprotein binding	/	/	/	/	2.604	/	5
1114	FAD binding	2.004	/	/	/	/	/	5
1115	chloride ion binding	/	/	4.495	/	/	/	5
1116	anion binding	/	/	4.495	/	/	/	5
1118	magnesium ion binding	/	/	/	2.894	/	/	5

1124	positive regulation of nucleobase\	/	/	2.777	/	/	/	5
1126	urogenital system development	/	/	4.441	/	/	/	5
1128	embryonic appendage morphogenesis	/	/	2.76	/	/	/	5
1129	embryonic limb morphogenesis	/	/	2.76	/	/	/	5
1130	DNA integrity checkpoint	/	2.775	/	/	/	/	5
1131	establishment of organelle localiz	/	2.133	/	/	/	/	5
1133	cytosol	/	/	/	/	3.086	/	5
1134	positive regulation of cellular me	/	/	2.181	/	/	/	5
1138	learning and/or memory	/	/	/	/	2.113	/	5
1148	cGMP biosynthetic process	/	/	3.603	/	/	/	5
1158	regulation of lymphocyte mediated	/	/	/	/	3.161	/	5
1159	histone acetyltransferase complex	/	/	/	2.293	/	/	5
1162	regulation of DNA recombination	/	3.362	/	/	/	/	5
1165	establishment and/or maintenance o	/	/	3.603	/	/	/	5
1169	U2-dependent spliceosome	/	3.362	/	/	/	/	5
1172	regulation of leukocyte mediated i	/	/	/	/	3.161	/	5
1173	bioactive lipid receptor activity	/	/	/	2.293	/	/	5
1174	C-X-C chemokine receptor activity	/	/	/	2.293	/	/	5
1175	lysosphingolipid and lysophosphati	/	/	/	2.293	/	/	5
1176	lipid digestion	/	/	3.603	/	/	/	5
1177	calcium- and calmodulin-dependent	/	2.269	/	/	/	/	5
1179	cholesterol absorption	/	/	3.603	/	/	/	5
1183	positive regulation of interleukin	/	/	/	2.293	/	/	5
1184	regulation of vasoconstriction	/	/	3.603	/	/	/	5
1185	filamentous actin	/	/	/	2.293	/	/	5
1190	basal lamina	/	2.039	/	/	/	/	5
1198	protein serine/threonine kinase ac	/	3.587	/	/	/	/	5
1200	extracellular matrix structural co	/	/	/	/	2.689	/	5
1201	smooth muscle contraction	/	4.433	/	/	/	/	5
1206	appendage development	/	/	2.618	/	/	/	5
1207	appendage morphogenesis	/	/	2.618	/	/	/	5
1208	limb morphogenesis	/	/	2.618	/	/	/	5
1213	endocrine system development	/	/	/	2.095	/	/	5
1220	phosphoprotein phosphatase activit	/	/	2.006	/	/	/	5
1222	behavior	/	/	/	/	2.191	/	5
1225	retinal binding	/	/	/	2.12	/	/	5
1228	positive regulation of lymphocyte	/	/	/	2.12	/	/	5
1234	regulation of mRNA stability	/	3.109	/	/	/	/	5
1247	striated muscle thin filament	/	/	3.41	/	/	/	5
1250	response to hydrogen peroxide	/	/	3.41	/	/	/	5
1251	embryonic digit morphogenesis	/	/	3.41	/	/	/	5
1253	integral to membrane of membrane f	/	/	3.41	/	/	/	5
1254	transforming growth factor beta re	/	2.067	/	/	/	/	5
1256	regulation of exit from mitosis	/	/	/	/	2.937	/	5
1264	biogenic amine catabolic process	/	/	3.41	/	/	/	5
1265	bacterial binding	/	/	/	/	2.937	/	5
1266	myosin binding	/	2.067	/	/	/	/	5

1270	transmembrane receptor protein ser	/	2.067	/	/	/	/	5
1272	cytoplasmic vesicle	/	/	/	2.448	/	/	5
1275	carbon-oxygen lyase activity	/	2.051	/	/	/	/	5
1284	protein serine/threonine phosphata	/	/	3.783	/	/	/	5
1287	transcription factor activity	/	2.23	/	/	/	/	5
1291	antioxidant activity	/	/	/	/	2.819	/	5
1296	vesicle	/	/	/	2.336	/	/	5
1300	nucleoside kinase activity	/	3.882	/	/	/	/	5
1304	localization within membrane	/	/	/	1.966	/	/	5
1305	lipopolysaccharide-mediated signal	2.574	/	/	/	/	/	5
1308	regulation of adaptive immune resp	/	/	/	/	2.738	/	5
1309	regulation of adaptive immune resp	/	/	/	/	2.738	/	5
1312	regulation of immune effector proc	/	/	/	/	2.738	/	5
1316	focal adhesion formation	/	/	3.241	/	/	/	5
1317	aromatic amino acid family catabol	/	/	/	/	2.738	/	5
1325	activated T cell proliferation	/	/	/	1.966	/	/	5
1326	folic acid and derivative metaboli	/	/	/	1.966	/	/	5
1329	plasma membrane fusion	/	/	3.241	/	/	/	5
1344	mesoderm development	/	/	3.971	/	/	/	5
1352	sulfur compound biosynthetic proce	/	2.119	/	/	/	/	5
1358	lipid phosphatase activity	/	/	/	3.141	/	/	5
1360	establishment and/or maintenance o	/	/	3.092	/	/	/	5
1361	chaperone binding	/	/	3.092	/	/	/	5
1363	centrosome cycle	/	/	/	/	2.56	/	5
1365	specific transcriptional repressor	/	/	3.092	/	/	/	5
1370	glutathione metabolic process	/	/	/	/	2.56	/	5
1374	transcriptional repressor complex	/	/	3.092	/	/	/	5
1375	negative regulation of neurogenesi	2.399	/	/	/	/	/	5
1380	sugar porter activity	2.366	/	/	/	/	/	5
1393	structural constituent of muscle	/	2.52	/	/	/	/	5
1395	positive regulation of biosyntheti	2.267	/	/	/	/	/	5
1401	amino acid derivative catabolic pr	/	/	2.957	/	/	/	5
1402	oogenesis	/	/	/	2.967	/	/	5
1403	protein phosphatase type 2C activi	/	/	2.957	/	/	/	5
1404	dopamine metabolic process	/	/	2.957	/	/	/	5
1406	phosphatidylinositol metabolic pro	2.241	/	/	/	/	/	5
1407	intestinal absorption	/	/	2.957	/	/	/	5
1409	fucose metabolic process	2.241	/	/	/	/	/	5
1411	cardiac cell differentiation	/	/	2.957	/	/	/	5
1413	cGMP metabolic process	/	/	2.957	/	/	/	5
1416	mRNA 3’ -end processing	/	2.501	/	/	/	/	5
1420	SNARE binding	/	/	/	/	2.399	/	5
1422	microvillus	/	/	2.957	/	/	/	5
1423	filopodium	2.241	/	/	/	/	/	5
1432	cytoplasmic membrane-bound vesicle	/	/	/	2.065	/	/	5
1434	catabolic process	/	/	/	/	2.291	/	5
1439	cell recognition	2.15	/	/	/	/	/	5

1444	membrane-bound vesicle	/	/	/	1.973	/	/	5
1454	neuron maturation	/	/	2.836	/	/	/	5
1455	regulation of smooth muscle contra	/	3.226	/	/	/	/	5
1456	cartilage condensation	/	2.333	/	/	/	/	5
1457	aromatic compound catabolic proces	/	/	/	/	2.252	/	5
1459	RNA 3’ -end processing	/	2.333	/	/	/	/	5
1460	regulation of axon extension	2.097	/	/	/	/	/	5
1465	response to inorganic substance	/	2.333	/	/	/	/	5
1466	gastrulation (sensu Mammalia)	2.097	/	/	/	/	/	5
1468	PML body	/	/	2.836	/	/	/	5
1471	regulation of exocytosis	/	/	/	/	2.252	/	5
1473	apoptotic protease activator activ	/	/	/	2.809	/	/	5
1474	histone methylation	/	/	/	/	2.252	/	5
1500	enzyme regulator activity	2.621	/	/	/	/	/	5
1503	protein modification process	/	2.828	/	/	/	/	5
1519	negative regulation of mononuclear	/	/	/	/	2.117	/	5
1522	negative regulation of lymphocyte	/	/	/	/	2.117	/	5
1527	response to reactive oxygen specie	/	/	2.725	/	/	/	5
1528	neuron recognition	1.964	/	/	/	/	/	5
1531	tissue development	/	2.56	/	/	/	/	5
1537	cellular carbohydrate metabolic pr	/	/	/	2.523	/	/	5
1539	regulation of catalytic activity	/	/	/	/	1.984	/	5
1547	protease activator activity	/	/	/	2.532	/	/	5
1551	cAMP biosynthetic process	/	/	/	/	1.992	/	5
1560	intercellular junction assembly an	/	2.037	/	/	/	/	5
1567	protein phosphatase type 2A comple	/	/	2.624	/	/	/	5
1572	nuclear speck	/	/	2.624	/	/	/	5
1574	triacylglycerol metabolic process	/	/	2.624	/	/	/	5
1579	negative regulation of transcripti	/	2.664	/	/	/	/	5
1580	regulation of transcription from R	/	2.887	/	/	/	/	5
1596	ligand-dependent nuclear receptor	/	/	2.531	/	/	/	5
1597	glutamate signaling pathway	/	/	2.531	/	/	/	5
1603	response to toxin	2.677	/	/	/	/	/	5
1606	signal sequence binding	/	4.349	/	/	/	/	5
1608	actin filament bundle formation	/	/	/	/	2.862	/	5
1609	regulation of neurotransmitter lev	/	/	/	2.257	/	/	5
1610	transcription corepressor activity	/	2.669	/	/	/	/	5
1615	dioxygenase activity	/	/	/	/	2.462	/	5
1616	oxidoreductase activity\, acting o	/	/	/	/	2.462	/	5
1625	oxidoreductase activity\, acting o	/	/	/	/	2.4	/	5
1631	placenta development	/	/	2.444	/	/	/	5
1635	phosphorus-oxygen lyase activity	/	/	2.444	/	/	/	5
1636	inactivation of MAPK activity	/	/	2.444	/	/	/	5
1637	biopolymer modification	/	2.832	/	/	/	/	5
1648	sex differentiation	/	2.312	/	/	/	/	5
1649	post-translational protein modific	/	2.841	/	/	/	/	5
1650	regulation of a molecular function	/	/	/	/	2.085	/	5

1653	aging	/	/	2.364	/	/	/	5
1663	oxidoreductase activity\, acting o	2.421	/	/	/	/	/	5
1664	cyclase activity	/	/	2.364	/	/	/	5
1666	glutathione transferase activity	/	/	2.364	/	/	/	5
1678	protein amino acid dephosphorylati	/	/	2.4	/	/	/	5
1694	neutral lipid metabolic process	/	/	2.289	/	/	/	5
1696	platelet activation	/	/	2.289	/	/	/	5
1699	acylglycerol metabolic process	/	/	2.289	/	/	/	5
1702	cholesterol biosynthetic process	/	/	2.289	/	/	/	5
1703	oxidoreductase activity\, acting o	/	/	/	/	2.519	/	5
1704	glycoprotein biosynthetic process	2.816	/	/	/	/	/	5
1716	reproductive developmental process	/	2.078	/	/	/	/	5
1718	regulation of pH	/	/	2.219	/	/	/	5
1720	Rho GTPase binding	/	/	/	1.989	/	/	5
1730	fat cell differentiation	/	/	/	/	2.371	/	5
1731	glycerolipid metabolic process	/	/	2.219	/	/	/	5
1734	cellular protein complex assembly	/	/	/	/	2.06	/	5
1748	protein import into nucleus\, tran	/	/	2.153	/	/	/	5
1753	Rho GTPase activator activity	/	/	2.153	/	/	/	5
1756	deaminase activity	/	/	2.153	/	/	/	5
1757	peroxisomal membrane	/	/	2.153	/	/	/	5
1761	intracellular protein transport ac	/	/	2.153	/	/	/	5
1762	microbody membrane	/	/	2.153	/	/	/	5
1763	glycerol ether metabolic process	/	/	2.153	/	/	/	5
1764	regulation of membrane potential	/	2.073	/	/	/	/	5
1769	microtubule-based movement	/	/	/	/	2.753	/	5
1777	peroxisomal part	/	/	2.091	/	/	/	5
1778	male gonad development	1.994	/	/	/	/	/	5
1784	negative regulation of MAPK activi	/	/	2.091	/	/	/	5
1786	microbody part	/	/	2.091	/	/	/	5
1795	oxidoreductase activity\, acting o	/	/	/	/	2.166	/	5
1798	neural tube closure	/	/	2.032	/	/	/	5
1800	hydrolase activity\, acting on car	/	/	2.032	/	/	/	5
1803	cellular catabolic process	/	/	/	/	2.043	/	5
1807	ion binding	/	/	2.019	/	/	/	5
1809	tight junction	2.062	/	/	/	/	/	5
1814	phosphoinositide binding	/	/	2.565	/	/	/	5
1816	cytochrome-c oxidase activity	/	/	1.977	/	/	/	5
1820	heme-copper terminal oxidase activ	/	/	1.977	/	/	/	5
1821	oxidoreductase activity\, acting o	/	/	1.977	/	/	/	5
1822	oxidoreductase activity\, acting o	/	/	1.977	/	/	/	5
1823	positive regulation of cellular bi	2.011	/	/	/	/	/	5
1825	dephosphorylation	/	/	2.117	/	/	/	5
1829	actin filament	2.503	/	/	/	/	/	5
1833	steroid hormone receptor binding	/	2.334	/	/	/	/	5
1840	germ cell development	/	/	/	2.494	/	/	5
1857	basolateral plasma membrane	/	3.005	/	/	/	/	5

1859	glycoprotein metabolic process	2.814	/	/	/	/	/	5
1861	cholesterol metabolic process	/	/	2.342	/	/	/	5
1862	heterocycle metabolic process	/	/	/	/	3.082	/	5
1868	cellular localization	/	/	/	/	2.197	/	5
1873	nucleoside metabolic process	/	3.417	/	/	/	/	5
1883	calcium ion homeostasis	/	2.345	/	/	/	/	5
1891	double-stranded RNA binding	/	/	4.012	/	/	/	5
1894	sulfur metabolic process	/	/	/	/	3.427	/	5
1899	steroid metabolic process	/	/	1.966	/	/	/	5
1903	development of primary male sexual	2.146	/	/	/	/	/	5
1909	Rho guanyl-nucleotide exchange fac	/	/	/	2.07	/	/	5
1911	pigment biosynthetic process	2.065	/	/	/	/	/	5
1917	positive regulation of transcripti	/	/	3.47	/	/	/	5
1918	sterol metabolic process	/	/	2.185	/	/	/	5
1920	vitamin binding	/	/	/	/	1.985	/	5
1928	neural tube formation	1.987	/	/	/	/	/	5
1938	L-amino acid transporter activity	/	/	/	/	2.101	/	5
1952	kinase regulator activity	/	1.98	/	/	/	/	5
1973	establishment and/or maintenance o	/	/	3.519	/	/	/	5
1978	double-stranded DNA binding	/	3.081	/	/	/	/	5
1979	cellular component disassembly	/	3.081	/	/	/	/	5
1985	nucleoplasm	/	/	2.071	/	/	/	5
1988	cartilage development	/	2.436	/	/	/	/	5
2000	Ras guanyl-nucleotide exchange fac	1.973	/	/	/	/	/	5
2009	protein serine/threonine phosphata	/	/	3.24	/	/	/	5
2013	cell redox homeostasis	/	/	/	/	2.222	/	5
2018	isomerase activity	/	/	/	2.38	/	/	5
2055	ATPase activity\, coupled to trans	/	2.281	/	/	/	/	5
2057	nucleoplasm part	/	/	2.549	/	/	/	5
2064	chloride channel activity	/	/	2.877	/	/	/	5
2065	steroid binding	/	/	2.877	/	/	/	5
2092	carbohydrate biosynthetic process	2.082	/	/	/	/	/	5
2094	protein polymerization	/	/	/	/	3.253	/	5
2102	negative regulation of striated mu	/	3.135	/	/	/	/	5
2121	adenosine kinase activity	/	3.135	/	/	/	/	5
2124	reduction of cytosolic calcium ion	/	3.135	/	/	/	/	5
2128	regulation of membrane protein ect	/	3.135	/	/	/	/	5
2131	regulation of translational elonga	/	3.135	/	/	/	/	5
2208	retinal cone cell development	/	/	/	/	3.925	/	5
2211	positive regulation of release of	/	/	/	/	3.925	/	5
2218	synaptic vesicle priming	/	/	/	/	3.925	/	5
2228	uroporphyrinogen-III synthase acti	3.767	/	/	/	/	/	5
2242	hydroxylysine biosynthetic process	/	/	/	/	3.925	/	5
2269	positive regulation of cytolysis	3.767	/	/	/	/	/	5
2275	positive regulation of RNA export	/	/	/	/	3.925	/	5
2285	neurological control of breathing	/	3.135	/	/	/	/	5
2290	positive regulation of neurotransm	/	3.135	/	/	/	/	5

2301	negative regulation of acute infla	/	/	/	/	3.925	/	5
2322	mannose transport	3.767	/	/	/	/	/	5
2331	glycine C-acetyltransferase activi	/	3.135	/	/	/	/	5
2332	mannose transporter activity	3.767	/	/	/	/	/	5
2334	glutamyl aminopeptidase activity	/	3.135	/	/	/	/	5
2351	melanocyte stimulating hormone rec	/	/	/	/	3.925	/	5
2362	angiotensin mediated regulation of	3.767	/	/	/	/	/	5
2387	meiotic metaphase I	/	3.135	/	/	/	/	5
2389	NADPH oxidase complex	/	3.135	/	/	/	/	5
2390	establishment of meiotic spindle l	/	3.135	/	/	/	/	5
2395	glutamate decarboxylase activity	/	3.135	/	/	/	/	5
2400	protein-pyridoxal-5-phosphate link	/	3.135	/	/	/	/	5
2412	glutamate decarboxylation to succi	/	3.135	/	/	/	/	5
2413	inner kinetochore of condensed chr	/	3.135	/	/	/	/	5
2416	inositol tetrakisphosphate 1-kinas	/	/	/	/	3.925	/	5
2424	alkyl hydroperoxide reductase acti	/	/	/	/	3.925	/	5
2425	protein anchor	/	3.135	/	/	/	/	5
2433	steroid hormone receptor complex a	/	3.135	/	/	/	/	5
2462	angiotensin mediated vasoconstrict	3.767	/	/	/	/	/	5
2465	6-pyruvoyltetrahydropterin synthas	/	/	/	/	3.925	/	5
2498	type 2 angiotensin receptor bindin	3.767	/	/	/	/	/	5
2503	type 1 angiotensin receptor bindin	3.767	/	/	/	/	/	5
2508	negative regulation of sister chro	/	3.135	/	/	/	/	5
2510	Rap guanyl-nucleotide exchange fac	3.767	/	/	/	/	/	5
2511	photosynthesis	3.767	/	/	/	/	/	5
2513	phycobilisome	3.767	/	/	/	/	/	5
2526	phosphoribosylformylglycinamidine	/	3.135	/	/	/	/	5
2528	renin-angiotensin regulation of al	3.767	/	/	/	/	/	5
2535	renal response to blood flow durin	3.767	/	/	/	/	/	5
2604	calcium-independent cell-matrix ad	/	3.135	/	/	/	/	5
2628	beta-2 adrenergic receptor binding	/	3.135	/	/	/	/	5
2629	sodium\:hydrogen antiporter regula	/	3.135	/	/	/	/	5
2680	sensory perception of bitter taste	/	/	/	/	3.925	/	5
2707	chromatin remodeling at centromere	/	3.135	/	/	/	/	5
2742	phosphatidylinositol-4\,5-bisphosp	/	/	/	4.512	/	/	5
2749	gamma-glutamyl hydrolase activity	/	/	/	/	3.925	/	5
2755	prostaglandin-I synthase activity	/	3.135	/	/	/	/	5
2773	alkylglycerone-phosphate synthase	/	3.135	/	/	/	/	5
2822	2-hydroxyacylsphingosine 1-beta-ga	/	3.135	/	/	/	/	5
2823	UDP-galactose\:glucosylceramide be	/	3.135	/	/	/	/	5
2832	cathepsin S activity	/	3.135	/	/	/	/	5
2880	A2A adenosine receptor activity\,	/	/	/	/	3.925	/	5
2940	regulation of sister chromatid coh	/	3.135	/	/	/	/	5
2944	N-acetyl-gamma-glutamyl-phosphate	/	3.135	/	/	/	/	5
2948	glutamate 5-kinase activity	/	3.135	/	/	/	/	5
2949	glutamate-5-semialdehyde dehydroge	/	3.135	/	/	/	/	5
2953	regulation of release of sequester	/	/	/	/	3.925	/	5

2962	retina morphogenesis in camera-typ	/	/	/	/	3.925	/	5
2968	regulation of cytolysis	3.767	/	/	/	/	/	5
2971	retinal cone cell differentiation	/	/	/	/	3.925	/	5
2983	activin receptor activity\, type I	/	3.135	/	/	/	/	5
3075	apolipoprotein receptor activity	/	/	/	/	3.925	/	5
3099	glutathione-disulfide reductase ac	/	/	/	/	3.925	/	5
3105	myo-inositol transporter activity	3.767	/	/	/	/	/	5
3157	deoxyribonuclease I activity	3.767	/	/	/	/	/	5
3170	leukocyte adhesive activation	/	3.135	/	/	/	/	5
3173	positive regulation of calcium-ind	/	3.135	/	/	/	/	5
3191	pyruvate kinase activity	/	/	/	/	3.925	/	5
3197	biotinidase activity	/	/	/	/	3.925	/	5
3201	mature ribosome assembly	/	3.135	/	/	/	/	5
3225	interleukin-6 receptor complex	/	/	/	4.512	/	/	5
3262	glycosylceramide catabolic process	3.767	/	/	/	/	/	5
3268	galactolipid catabolic process	3.767	/	/	/	/	/	5
3276	classical-complement-pathway C3/C5	/	3.135	/	/	/	/	5
3277	dihydrolipoyllysine-residue acetyl	/	/	/	/	3.925	/	5
3326	pyruvate dehydrogenase complex	/	/	/	/	3.925	/	5
3328	mitochondrial pyruvate dehydrogena	/	/	/	/	3.925	/	5
3344	deoxyguanosine kinase activity	/	3.135	/	/	/	/	5
3355	septate junction	3.767	/	/	/	/	/	5
3380	apolipoprotein E receptor activity	/	/	/	/	3.925	/	5
3385	actin cap	/	3.135	/	/	/	/	5
3387	2’\,3’-cyclic-nucleotide 3’-pho	3.767	/	/	/	/	/	5
3456	L-serine catabolic process	/	3.135	/	/	/	/	5
3498	positive regulation of catecholami	/	/	/	/	3.925	/	5
3500	guanine metabolic process	/	/	/	/	3.925	/	5
3520	AMP catabolic process	/	3.135	/	/	/	/	5
3523	positive regulation of aldosterone	/	3.135	/	/	/	/	5
3531	adenine phosphoribosyltransferase	/	3.135	/	/	/	/	5
3558	inositol tetrakisphosphate kinase	/	/	/	/	3.925	/	5
3560	ribonucleoside-diphosphate reducta	/	3.135	/	/	/	/	5
3562	hydroxylysine metabolic process	/	/	/	/	3.925	/	5
3569	light-harvesting complex	3.767	/	/	/	/	/	5
3570	thylakoid	3.767	/	/	/	/	/	5
3571	thylakoid part	3.767	/	/	/	/	/	5
3575	chromatophore	3.767	/	/	/	/	/	5
3593	dihydrolipoamide S-acyltransferase	/	/	/	/	3.925	/	5
3595	cyanelle thylakoid	3.767	/	/	/	/	/	5
3597	cyanelle	3.767	/	/	/	/	/	5
3598	plastid	3.767	/	/	/	/	/	5
3599	plastid part	3.767	/	/	/	/	/	5
3600	plastid thylakoid	3.767	/	/	/	/	/	5
3601	plasma membrane-derived thylakoid	3.767	/	/	/	/	/	5
3609	positive regulation of dopamine me	/	/	/	/	3.925	/	5
3612	hypoxanthine metabolic process	/	/	/	/	3.925	/	5

3613	succinate metabolic process	/	3.135	/	/	/	/	5
3618	guanine salvage	/	/	/	/	3.925	/	5
3619	oxidoreductase activity\, acting o	/	/	/	/	3.925	/	5
3635	deoxyribonucleoside catabolic proc	3.767	/	/	/	/	/	5
3636	pyrimidine deoxyribonucleoside cat	3.767	/	/	/	/	/	5
3637	uracil metabolic process	3.767	/	/	/	/	/	5
3638	nucleobase catabolic process	3.767	/	/	/	/	/	5
3643	thymidine metabolic process	3.767	/	/	/	/	/	5
3672	galactosylceramide catabolic proce	3.767	/	/	/	/	/	5
3674	coagulation factor XIIa activity	/	3.135	/	/	/	/	5
3677	collagen type VII	/	/	/	4.512	/	/	5
3684	angiotensin receptor binding	3.767	/	/	/	/	/	5
3694	purine ribonucleoside monophosphat	/	3.135	/	/	/	/	5
3695	purine nucleoside monophosphate ca	/	3.135	/	/	/	/	5
3696	nucleoside monophosphate catabolic	/	3.135	/	/	/	/	5
3697	ribonucleoside monophosphate catab	/	3.135	/	/	/	/	5
3718	regulation of fatty acid biosynthe	3.767	/	/	/	/	/	5
3779	pyrimidine base catabolic process	3.767	/	/	/	/	/	5
3780	thymidine catabolic process	3.767	/	/	/	/	/	5
3781	uracil catabolic process	3.767	/	/	/	/	/	5
3783	dihydropyrimidine dehydrogenase (N	3.767	/	/	/	/	/	5
3794	nitrogen fixation	3.767	/	/	/	/	/	5
3798	ornithine-oxo-acid transaminase ac	/	/	/	/	3.925	/	5
3802	dolichyldiphosphatase activity	3.767	/	/	/	/	/	5
3829	porphobilinogen synthase activity	/	3.135	/	/	/	/	5
3844	insulysin activity	/	/	/	/	3.925	/	5
3863	neural fold formation	3.767	/	/	/	/	/	5
3892	centric heterochromatin formation	/	3.135	/	/	/	/	5
3921	negative regulation of membrane pr	/	3.135	/	/	/	/	5
3978	C-5 sterol desaturase activity	/	3.135	/	/	/	/	5
4083	thromboxane-A synthase activity	/	3.135	/	/	/	/	5
4097	negative regulation of type IV hyp	/	/	/	/	3.925	/	5
4102	pantetheine-phosphate adenylyltran	/	3.135	/	/	/	/	5
4103	dephospho-CoA kinase activity	/	3.135	/	/	/	/	5
4122	negative regulation of acute infla	/	/	/	/	3.925	/	5
4128	myo-inositol\:sodium symporter act	3.767	/	/	/	/	/	5
4132	negative regulation of inflammator	/	/	/	/	3.925	/	5
4140	negative regulation of hypersensit	/	/	/	/	3.925	/	5
4172	regulation of type IV hypersensiti	/	/	/	/	3.925	/	5
4179	type IV hypersensitivity	/	/	/	/	3.925	/	5
4182	regulation of calcium-independent	/	3.135	/	/	/	/	5
4211	positive regulation of hormone bio	/	3.135	/	/	/	/	5
4213	positive regulation of aldosterone	/	3.135	/	/	/	/	5
4220	amino acid kinase activity	/	3.135	/	/	/	/	5
4223	positive regulation of hormone met	/	3.135	/	/	/	/	5
4234	regulation of hormone biosynthetic	/	3.135	/	/	/	/	5
4235	regulation of aldosterone biosynth	/	3.135	/	/	/	/	5

4237	aldosterone biosynthetic process	/	3.135	/	/	/	/	5
4249	negative regulation of translation	/	3.135	/	/	/	/	5
4259	sepiapterin reductase activity	/	3.135	/	/	/	/	5
4273	positive regulation of organ size	3.767	/	/	/	/	/	5
4279	positive regulation of fatty acid	3.767	/	/	/	/	/	5
4286	anion channel activity	/	/	2.652	/	/	/	5
4295	nucleotidyltransferase activity	/	2.011	/	/	/	/	5
4298	glycine biosynthetic process	/	1.992	/	/	/	/	5
4316	dihydrofolate reductase activity	/	1.992	/	/	/	/	5
4343	embryonic heart tube anterior/post	2.476	/	/	/	/	/	5
4344	regulation of aldosterone metaboli	/	1.992	/	/	/	/	5
4366	alpha-ketoacid dehydrogenase activ	2.476	/	/	/	/	/	5
4377	3-methyl-2-oxobutanoate dehydrogen	2.476	/	/	/	/	/	5
4380	adenosine receptor signaling pathw	/	/	/	/	2.595	/	5
4390	oocyte axis determination	/	/	/	3.034	/	/	5
4393	positive regulation of cardioblast	/	1.992	/	/	/	/	5
4398	oxysterol binding	/	/	/	/	2.595	/	5
4400	outer kinetochore of condensed chr	/	/	/	/	2.595	/	5
4411	negative regulation of smooth musc	/	/	/	/	2.595	/	5
4423	beta DNA polymerase activity	2.476	/	/	/	/	/	5
4453	AU-specific RNA binding	/	/	/	3.034	/	/	5
4458	2\,4-dienoyl-CoA reductase (NADPH)	/	1.992	/	/	/	/	5
4469	platelet formation	/	1.992	/	/	/	/	5
4475	regulation of chromatin assembly o	/	/	/	/	2.595	/	5
4485	IMP dehydrogenase activity	/	/	/	/	2.595	/	5
4491	positive regulation of smoothened	/	/	/	/	2.595	/	5
4499	Ral guanyl-nucleotide exchange fac	/	1.992	/	/	/	/	5
4503	galactosylceramidase activity	2.476	/	/	/	/	/	5
4539	alkylbase DNA N-glycosylase activi	/	1.992	/	/	/	/	5
4543	glycogen (starch) synthase activit	/	1.992	/	/	/	/	5
4544	tyrosyl-tRNA aminoacylation	/	1.992	/	/	/	/	5
4545	KDEL sequence binding	/	4.434	/	/	/	/	5
4553	negative transcription elongation	/	1.992	/	/	/	/	5
4569	tyrosine-tRNA ligase activity	/	1.992	/	/	/	/	5
4570	dinucleotide repeat insertion bind	/	1.992	/	/	/	/	5
4572	interleukin-6 receptor activity	/	/	/	3.034	/	/	5
4579	maintenance of DNA repeat elements	/	1.992	/	/	/	/	5
4581	MutSbeta complex	/	1.992	/	/	/	/	5
4598	protein channel activity	/	1.992	/	/	/	/	5
4611	nuclear fragmentation during apopt	/	1.992	/	/	/	/	5
4633	cyclic nucleotide catabolic proces	2.476	/	/	/	/	/	5
4634	adrenergic receptor binding	/	1.992	/	/	/	/	5
4645	pyrimidine nucleoside catabolic pr	2.476	/	/	/	/	/	5
4648	striatum development	/	/	/	/	2.595	/	5
4654	four-way junction DNA binding	/	1.992	/	/	/	/	5
4655	single thymine insertion binding	/	1.992	/	/	/	/	5
4656	MutSalpha complex	/	1.992	/	/	/	/	5

4661	S-acetyltransferase activity	/	/	/	/	2.595	/	5
4680	regulation of organ size	2.476	/	/	/	/	/	5
4681	positive regulation of lipid biosy	2.476	/	/	/	/	/	5
4682	renal blood volume regulation of b	2.476	/	/	/	/	/	5
4683	renin-angiotensin regulation of bl	2.476	/	/	/	/	/	5
4686	interleukin-4 receptor activity	/	1.992	/	/	/	/	5
4717	protein targeting to Golgi	/	1.992	/	/	/	/	5
4749	aryl hydrocarbon receptor nuclear	2.476	/	/	/	/	/	5
4765	iron-sulfur cluster assembly	2.476	/	/	/	/	/	5
4775	N-methyl-D-aspartate selective glu	/	1.992	/	/	/	/	5
4782	sodium-dependent multivitamin tran	/	1.992	/	/	/	/	5
4783	response to ethanol	/	1.992	/	/	/	/	5
4784	olfactory receptor binding	2.476	/	/	/	/	/	5
4787	beta-galactosidase complex	/	1.992	/	/	/	/	5
4793	Golgi to plasma membrane protein t	/	1.992	/	/	/	/	5
4826	platelet activating factor biosynt	/	/	/	/	2.595	/	5
4834	ornithine metabolic process	/	/	/	/	2.595	/	5
4841	myristoyltransferase activity	/	1.992	/	/	/	/	5
4845	nuclear mRNA cis splicing\, via U2	/	4.434	/	/	/	/	5
4846	cis assembly of pre-catalytic spli	/	4.434	/	/	/	/	5
4847	protein myristoylation	/	1.992	/	/	/	/	5
4848	protein amino acid myristoylation	/	1.992	/	/	/	/	5
4874	N-terminal protein lipidation	/	1.992	/	/	/	/	5
4877	ovarian follicle rupture	2.476	/	/	/	/	/	5
4878	oocyte construction	/	/	/	3.034	/	/	5
4879	regulation of cardioblast differen	/	1.992	/	/	/	/	5
4888	nonselective channel activity	/	/	/	3.034	/	/	5
4900	endodeoxyribonuclease activity\, p	2.476	/	/	/	/	/	5
4915	ionotropic glutamate receptor comp	/	1.992	/	/	/	/	5
4922	interleukin-6 binding	/	/	/	3.034	/	/	5
4929	retrograde transport\, vesicle rec	/	1.992	/	/	/	/	5
4938	snRNA transport	/	/	/	/	2.595	/	5
4953	platelet activating factor metabol	/	/	/	/	2.595	/	5
4963	metallo-sulfur cluster assembly	2.476	/	/	/	/	/	5
4968	pyrimidine dimer repair	/	/	/	/	2.595	/	5
4977	dihydroorotate dehydrogenase activ	2.476	/	/	/	/	/	5
4978	dihydroorotate oxidase activity	2.476	/	/	/	/	/	5
4982	brain renin-angiotensin system	2.476	/	/	/	/	/	5
5004	nonprotein amino acid metabolic pr	/	/	/	/	2.595	/	5
5014	interleukin-4 binding	/	1.992	/	/	/	/	5
5018	coagulation factor XIa activity	/	1.992	/	/	/	/	5
5022	ferritin complex	/	/	/	/	2.595	/	5
5024	gastric inhibitory peptide recepto	/	/	/	/	2.595	/	5
5031	carbon-oxygen lyase activity\, act	/	/	/	/	2.595	/	5
5033	uroporphyrinogen III metabolic pro	2.476	/	/	/	/	/	5
5043	aldosterone metabolic process	/	1.992	/	/	/	/	5
5044	regulation of hormone metabolic pr	/	1.992	/	/	/	/	5

5045	positive regulation of steroid met	/	1.992	/	/	/	/	5
5051	negative regulation of leukocyte m	/	/	/	/	2.595	/	5
5052	negative regulation of lymphocyte	/	/	/	/	2.595	/	5
5053	negative regulation of T cell medi	/	/	/	/	2.595	/	5
5054	establishment of blood-nerve barri	2.476	/	/	/	/	/	5
5055	drinking behavior	2.476	/	/	/	/	/	5
5058	astrocyte activation	2.476	/	/	/	/	/	5
5075	biotin metabolic process	/	/	/	/	2.595	/	5
5080	AMP metabolic process	/	1.992	/	/	/	/	5
5082	subpallium development	/	/	/	/	2.595	/	5
5128	dendritic shaft	/	/	/	3.034	/	/	5
5132	homologous chromosome segregation	/	1.992	/	/	/	/	5
5134	maintenance of DNA methylation	/	1.992	/	/	/	/	5
5141	interleukin-8 receptor binding	/	1.992	/	/	/	/	5
5142	snRNA export from nucleus	/	/	/	/	2.595	/	5
5151	glycylpeptide N-tetradecanoyltrans	/	1.992	/	/	/	/	5
5154	N-terminal protein myristoylation	/	1.992	/	/	/	/	5
5171	electron donor activity	/	1.992	/	/	/	/	5
5211	isopentenyl-diphosphate delta-isom	2.476	/	/	/	/	/	5
5222	negative regulation of glucose imp	/	1.992	/	/	/	/	5
5236	uroporphyrinogen III biosynthetic	2.476	/	/	/	/	/	5
5240	nonselective cation channel activi	/	/	/	3.034	/	/	5
5247	single-stranded DNA specific endod	/	1.992	/	/	/	/	5
5252	renin-angiotensin regulation of bo	2.476	/	/	/	/	/	5
5253	cGMP-dependent protein kinase acti	/	1.992	/	/	/	/	5
5256	peptidyl-arginine N-methylation	/	/	/	/	2.595	/	5
5265	negative regulation of activated T	/	1.992	/	/	/	/	5
5296	two-component response regulator a	2.476	/	/	/	/	/	5
5304	RNA-3’ -phosphate cyclase activity	/	/	/	/	2.595	/	5
5341	glutamate catabolic process	/	1.992	/	/	/	/	5
5360	cis assembly of U2-type pre-cataly	/	4.434	/	/	/	/	5
5369	intracellular membrane-bound organ	/	3.456	/	/	/	/	5
5371	membrane-bound organelle	/	3.44	/	/	/	/	5
5376	protein kinase regulator activity	/	2.44	/	/	/	/	5
5385	regulation of mast cell cytokine p	/	/	/	/	1.972	/	5
5389	mast cell cytokine production	/	/	/	/	1.972	/	5
5392	negative regulation of immune effe	/	/	/	/	1.972	/	5
5401	peptide disulfide oxidoreductase a	/	/	/	/	1.972	/	5
5414	regulation of ligase activity	/	/	/	/	1.972	/	5
5416	biotin carboxylase activity	/	/	/	/	1.972	/	5
5426	T cell receptor binding	/	/	/	2.349	/	/	5
5431	perikaryon	/	/	/	/	1.972	/	5
5442	lactose synthase activity	/	/	/	2.349	/	/	5
5468	regulation of phospholipase A2 act	/	/	/	/	1.972	/	5
5469	GMP metabolic process	/	/	/	/	1.972	/	5
5476	alcohol transporter activity	4.197	/	/	/	/	/	5
5480	positive regulation of phospholipa	/	/	/	/	1.972	/	5

5483	trialkylsulfonium hydrolase activi	/	/	/	/	1.972	/	5
5484	snRNP U2	/	/	/	/	1.972	/	5
5485	peptidyl-arginine modification	/	/	/	/	1.972	/	5
5494	regulation of actin filament bundl	/	/	/	/	1.972	/	5
5503	cyclo-ligase activity	/	/	/	/	1.972	/	5
5508	regulation of stress fiber formati	/	/	/	/	1.972	/	5
5536	activation of phospholipase A2	/	/	/	/	1.972	/	5
5548	positive regulation of exit from m	/	/	/	/	1.972	/	5
5553	calcium-independent phospholipase	/	/	/	2.349	/	/	5
5558	nuclear mRNA splicing via U2-type	/	3.436	/	/	/	/	5
5562	platelet activating factor recepto	/	/	/	/	1.972	/	5
5564	transmembrane receptor protein tyr	/	/	/	/	1.972	/	5
5573	dimethylargininase activity	/	/	/	/	4.386	/	5
5576	nickel ion binding	/	/	/	/	1.972	/	5
5586	glycyl-tRNA aminoacylation	/	/	/	/	1.972	/	5
5587	glycine-tRNA ligase activity	/	/	/	/	1.972	/	5
5607	transcription factor TFIIE complex	/	/	/	/	1.972	/	5
5612	regulation of interleukin-10 biosy	/	/	/	/	1.972	/	5
5613	interleukin-10 biosynthetic proces	/	/	/	/	1.972	/	5
5622	glutathione disulfide oxidoreducta	/	/	/	/	1.972	/	5
5627	glyoxylate metabolic process	/	/	/	/	1.972	/	5
5687	platelet-derived growth factor rec	/	/	/	/	1.972	/	5
5694	phosphatase activator activity	/	/	/	/	1.972	/	5
5696	regulation of antiviral response	/	/	/	/	1.972	/	5
5705	response to dsRNA	/	/	/	2.349	/	/	5
5714	polyol transporter activity	4.197	/	/	/	/	/	5
5728	mRNA cleavage factor complex	/	/	/	2.349	/	/	5
5734	negative regulation of fibroblast	/	/	/	/	1.972	/	5
5747	positive regulation of myoblast di	/	/	/	/	1.972	/	5
5758	regulation of RNA export from nucl	/	/	/	/	1.972	/	5
5793	inositol hexakisphosphate kinase a	/	/	/	/	1.972	/	5
5804	phosphoglycerate kinase activity	/	/	/	/	1.972	/	5
5806	sodium channel regulator activity	/	/	/	2.349	/	/	5
5814	regulation of phosphoprotein phosp	/	/	/	/	1.972	/	5
5822	positive regulation of interleukin	/	/	/	/	1.972	/	5
5826	UV protection	/	/	/	/	1.972	/	5
5827	protein farnesylation	/	/	/	/	1.972	/	5
5831	zymogen activation	/	/	/	5.082	/	/	5
5839	GMP biosynthetic process	/	/	/	/	1.972	/	5
5841	peptidyl-arginine methylation	/	/	/	/	1.972	/	5
5862	protein import into peroxisome mat	/	/	/	/	1.972	/	5
5888	chymotrypsin activity	/	/	/	/	1.972	/	5
5899	DNA ligase activity	/	3.436	/	/	/	/	5
5905	C5a anaphylatoxin receptor activit	/	/	/	/	1.972	/	5
5945	pigment granule organization and b	/	/	/	2.349	/	/	5
5946	melanosome organization and biogen	/	/	/	2.349	/	/	5
5954	asialoglycoprotein receptor activi	/	/	/	2.349	/	/	5

5958	pyrimidine nucleoside monophosphat	/	/	/	/	1.972	/	5
5959	pyrimidine nucleoside monophosphat	/	/	/	/	1.972	/	5
6006	MP kinase activity	/	/	/	2.349	/	/	5
6010	collagen type IX	/	3.436	/	/	/	/	5
6016	positive regulation of osteoclast	/	/	/	/	1.972	/	5
6019	hypoxanthine phosphoribosyltransfe	/	/	/	/	1.972	/	5
6021	grooming behavior	/	/	/	/	1.972	/	5
6028	adenosylhomocysteinase activity	/	/	/	/	1.972	/	5
6029	retinal dehydrogenase activity	/	/	/	/	1.972	/	5
6034	purine nucleoside triphosphate cat	/	/	/	/	1.972	/	5
6035	DNA ligase (ATP) activity	/	3.436	/	/	/	/	5
6049	single base insertion or deletion	/	2.817	/	/	/	/	5
6051	' de novo' pyrimidine base biosyn	3.502	/	/	/	/	/	5
6054	procollagen-lysine 5-dioxygenase a	/	/	/	/	3.671	/	5
6072	purine ribonucleoside salvage	/	2.817	/	/	/	/	5
6100	enucleate erythrocyte differentiat	/	2.817	/	/	/	/	5
6114	ribonucleoside-diphosphate reducta	/	2.817	/	/	/	/	5
6123	blastocyst hatching	/	2.817	/	/	/	/	5
6132	DNA insertion or deletion binding	/	2.817	/	/	/	/	5
6176	lymph vessel development	3.502	/	/	/	/	/	5
6177	hatching	/	2.817	/	/	/	/	5
6193	peptidyl-proline modification	/	/	/	/	3.671	/	5
6201	activin receptor activity	/	2.817	/	/	/	/	5
6209	oxidoreductase activity\, acting o	/	2.817	/	/	/	/	5
6215	uracil DNA N-glycosylase activity	/	2.817	/	/	/	/	5
6219	hydrogen-translocating V-type ATPa	/	2.817	/	/	/	/	5
6246	osmoregulation	/	2.817	/	/	/	/	5
6250	deoxynucleoside kinase activity	/	2.817	/	/	/	/	5
6313	nucleoside salvage	/	2.817	/	/	/	/	5
6316	lamin filament	/	2.817	/	/	/	/	5
6319	purine salvage	/	2.817	/	/	/	/	5
6343	snRNP U5	/	2.817	/	/	/	/	5
6355	Rac guanyl-nucleotide exchange fac	/	/	/	4.29	/	/	5
6397	ER retention sequence binding	/	4.544	/	/	/	/	5
6414	peroxiredoxin activity	/	/	/	/	3.169	/	5
6417	thyroid hormone receptor activity	/	2.377	/	/	/	/	5
6425	negative regulation of heart contr	/	3.922	/	/	/	/	5
6437	pyrimidine deoxyribonucleoside met	3.014	/	/	/	/	/	5
6439	deoxyribonucleoside metabolic proc	3.014	/	/	/	/	/	5
6466	contractile ring	/	2.377	/	/	/	/	5
6468	ligase activity\, forming phosphor	/	2.377	/	/	/	/	5
6474	nuclear origin of replication reco	/	2.377	/	/	/	/	5
6475	mitochondrial alpha-ketoglutarate	3.014	/	/	/	/	/	5
6476	DNA replication origin binding	/	2.377	/	/	/	/	5
6483	MutLalpha complex binding	/	2.377	/	/	/	/	5
6506	adenosine receptor activity\, G-pr	/	/	/	/	3.169	/	5
6521	nuclear lamina	/	3.922	/	/	/	/	5

6544	androgen biosynthetic process	/	/	5.278	/	/	/	5
6556	protein phosphatase type 2A activi	/	/	5.278	/	/	/	5
6578	alpha DNA polymerase\:primase comp	/	2.377	/	/	/	/	5
6588	protein-cofactor linkage	/	2.377	/	/	/	/	5
6592	negative regulation of DNA replica	/	2.377	/	/	/	/	5
6599	origin recognition complex	/	2.377	/	/	/	/	5
6624	activin binding	/	2.377	/	/	/	/	5
6635	alpha-ketoglutarate dehydrogenase	3.014	/	/	/	/	/	5
6654	pyrimidine base biosynthetic proce	3.014	/	/	/	/	/	5
6661	ruffle organization and biogenesis	/	2.377	/	/	/	/	5
6662	mitochondrial tricarboxylic acid c	3.014	/	/	/	/	/	5
6682	retinoic acid receptor activity	/	/	5.278	/	/	/	5
6702	DNA replication checkpoint	/	2.377	/	/	/	/	5
6719	purine nucleotide catabolic proces	/	2.04	/	/	/	/	5
6731	endoplasmic reticulum organization	/	/	4.785	/	/	/	5
6736	mitotic spindle checkpoint	/	2.04	/	/	/	/	5
6748	basal plasma membrane	/	/	4.785	/	/	/	5
6761	basal part of cell	/	/	4.785	/	/	/	5
6771	protein retention in ER	/	3.45	/	/	/	/	5
6780	negative regulation of epithelial	/	2.04	/	/	/	/	5
6782	positive regulation of mitosis	/	2.04	/	/	/	/	5
6789	establishment of planar polarity	/	/	4.785	/	/	/	5
6805	negative regulation of I-kappaB ki	/	2.04	/	/	/	/	5
6838	3-chloroallyl aldehyde dehydrogena	/	2.04	/	/	/	/	5
6867	FACIT collagen	/	2.04	/	/	/	/	5
6879	nitric oxide mediated signal trans	/	/	/	/	2.789	/	5
6890	GABA receptor binding	/	/	/	/	2.789	/	5
6891	response to X-ray	/	2.04	/	/	/	/	5
6901	positive transcription elongation	/	2.04	/	/	/	/	5
6903	peptide or protein amino-terminal	/	2.04	/	/	/	/	5
6917	peptidyl-proline dioxygenase activ	/	/	/	/	2.789	/	5
6918	procollagen-proline dioxygenase ac	/	/	/	/	2.789	/	5
6919	histone acetyltransferase binding	/	2.04	/	/	/	/	5
6920	transcription initiation factor ac	/	2.04	/	/	/	/	5
6928	translation activator activity	/	2.04	/	/	/	/	5
6934	steroid biosynthetic process	/	/	2.315	/	/	/	5
6940	regulation of cell-matrix adhesion	2.347	/	/	/	/	/	5
6977	phagocytosis\, engulfment	2.347	/	/	/	/	/	5
6996	recombinational repair	/	/	/	/	2.486	/	5
7010	hydrogen-exporting ATPase activity	/	3.074	/	/	/	/	5
7023	negative regulation of cell-cell a	2.347	/	/	/	/	/	5
7041	embryonic gut morphogenesis	2.347	/	/	/	/	/	5
7066	translational termination	2.347	/	/	/	/	/	5
7077	double-strand break repair via hom	/	/	/	/	2.486	/	5
7086	ventricular cardiac muscle morphog	/	/	4.399	/	/	/	5
7095	pyrimidine deoxyribonucleotide met	/	/	/	/	2.486	/	5
7104	RNA polymerase II transcription fa	/	/	2.822	/	/	/	5

7106	nucleus	/	2.212	/	/	/	/	5
7107	nuclear chromosome part	/	2.291	/	/	/	/	5
7131	arginine catabolic process	/	/	/	/	2.236	/	5
7132	muscle morphogenesis	/	/	4.086	/	/	/	5
7136	purine ribonucleoside metabolic pr	/	2.762	/	/	/	/	5
7142	cadmium ion binding	3.527	/	/	/	/	/	5
7144	purine nucleoside metabolic proces	/	2.762	/	/	/	/	5
7153	mismatch repair complex binding	/	2.762	/	/	/	/	5
7161	synaptic vesicle exocytosis	/	/	/	/	2.236	/	5
7173	protein-glutamine gamma-glutamyltr	2.101	/	/	/	/	/	5
7187	basic amino acid transporter activ	2.101	/	/	/	/	/	5
7200	synaptic vesicle membrane	/	/	/	2.721	/	/	5
7201	establishment of tissue polarity	/	/	4.086	/	/	/	5
7202	embryonic digestive tract morphoge	2.101	/	/	/	/	/	5
7217	lymph node development	/	/	/	2.721	/	/	5
7223	cardiac muscle morphogensis	/	/	4.086	/	/	/	5
7235	insulin-like growth factor recepto	2.101	/	/	/	/	/	5
7247	oocyte development	/	/	/	2.721	/	/	5
7248	histone methyltransferase complex	/	/	/	/	2.236	/	5
7278	protein disulfide isomerase activi	/	/	/	/	3.417	/	5
7284	cyclin-dependent protein kinase in	/	2.498	/	/	/	/	5
7285	negative regulation of cyclin-depe	/	2.498	/	/	/	/	5
7290	neurofilament cytoskeleton	/	/	3.825	/	/	/	5
7293	sequestering of metal ion	/	/	/	/	2.023	/	5
7294	intermediate filament cytoskeleton	/	/	3.825	/	/	/	5
7295	oocyte differentiation	/	/	/	2.491	/	/	5
7303	interferon type I production	/	/	/	/	2.023	/	5
7313	branched chain family amino acid c	3.237	/	/	/	/	/	5
7326	intramolecular oxidoreductase acti	/	/	/	/	3.417	/	5
7334	mannosyl-oligosaccharide 1\,2-alph	/	/	/	/	2.023	/	5
7335	positive regulation of nucleocytop	/	/	/	/	2.023	/	5
7392	cardiac inotropy	/	2.498	/	/	/	/	5
7401	interferon type I biosynthetic pro	/	/	/	/	2.023	/	5
7409	GTPase activity	/	/	/	/	3.401	/	5
7415	peptide antigen binding	/	/	/	2.293	/	/	5
7418	histidine metabolic process	/	/	/	2.293	/	/	5
7421	histidine family amino acid metabo	/	/	/	2.293	/	/	5
7430	sodium\:potassium-exchanging ATPas	/	2.269	/	/	/	/	5
7435	L-amino acid transport	/	/	/	2.293	/	/	5
7441	double-strand break repair via non	/	3.362	/	/	/	/	5
7448	N-terminal protein amino acid modi	/	2.269	/	/	/	/	5
7462	androgen metabolic process	/	/	3.603	/	/	/	5
7463	non-recombinational repair	/	3.362	/	/	/	/	5
7481	eye photoreceptor cell development	/	/	/	/	3.161	/	5
7482	Golgi organization and biogenesis	/	3.362	/	/	/	/	5
7485	pathogenesis	/	/	/	2.293	/	/	5
7489	regulation of microtubule depolyme	/	/	/	2.293	/	/	5

7500	energy coupled proton transport\,	/	2.269	/	/	/	/	5
7515	negative regulation of microtubule	/	/	/	2.293	/	/	5
7523	transcription from RNA polymerase	/	2.269	/	/	/	/	5
7541	ribonucleoside metabolic process	/	2.067	/	/	/	/	5
7545	steroid catabolic process	/	/	3.41	/	/	/	5
7548	microtubule depolymerization	/	/	/	2.12	/	/	5
7559	synaptic transmission\, cholinergi	/	2.067	/	/	/	/	5
7561	photoreceptor cell development	/	/	/	/	2.937	/	5
7576	negative regulation of microtubule	/	/	/	2.12	/	/	5
7577	intramolecular transferase activit	/	/	/	2.12	/	/	5
7579	eye photoreceptor cell differentia	/	/	/	/	2.937	/	5
7593	branched chain family amino acid m	2.768	/	/	/	/	/	5
7604	structure-specific DNA binding	/	2.325	/	/	/	/	5
7607	positive regulation of epithelial	/	/	/	/	2.738	/	5
7621	S phase	/	2.885	/	/	/	/	5
7624	S phase of mitotic cell cycle	/	2.885	/	/	/	/	5
7641	tyrosine metabolic process	/	/	/	1.966	/	/	5
7657	PcG protein complex	/	/	/	/	2.738	/	5
7659	protein phosphatase binding	2.574	/	/	/	/	/	5
7661	signal recognition particle\, endo	/	2.885	/	/	/	/	5
7662	signal recognition particle	/	2.885	/	/	/	/	5
7670	fructose metabolic process	/	/	/	1.966	/	/	5
7675	release of cytochrome c from mitoc	/	/	/	1.966	/	/	5
7677	glycine metabolic process	/	2.885	/	/	/	/	5
7680	photoreceptor cell differentiation	/	/	/	/	2.738	/	5
7694	lysosomal membrane	/	/	3.092	/	/	/	5
7705	MHC class I receptor activity	/	/	3.092	/	/	/	5
7715	protein histidine kinase activity	/	/	/	3.141	/	/	5
7730	DNA fragmentation during apoptosis	/	2.683	/	/	/	/	5
7754	cotranslational protein targeting	/	2.501	/	/	/	/	5
7763	protein targeting to ER	/	2.501	/	/	/	/	5
7766	arginine metabolic process	/	/	/	/	2.399	/	5
7785	aldehyde metabolic process	/	/	/	/	2.399	/	5
7800	neuropeptide signaling pathway	/	/	1.978	/	/	/	5
7801	nucleotide metabolic process	/	2.519	/	/	/	/	5
7807	phospholipid dephosphorylation	/	2.333	/	/	/	/	5
7810	response to nutrient	/	/	/	/	2.252	/	5
7811	urea cycle intermediate metabolic	/	/	/	/	3.332	/	5
7825	positive regulation of myeloid cel	/	/	/	/	2.252	/	5
7844	response to bacterium	2.056	/	/	/	/	/	5
7851	tRNA-pseudouridine synthase activi	/	/	2.725	/	/	/	5
7856	metabotropic glutamate\, GABA-B-li	/	/	2.725	/	/	/	5
7863	tRNA binding	/	/	/	2.665	/	/	5
7867	peptide cross-linking	2.972	/	/	/	/	/	5
7876	phosphatase binding	1.964	/	/	/	/	/	5
7879	L-ascorbic acid binding	/	/	/	/	2.117	/	5
7890	apoptotic nuclear changes	/	2.037	/	/	/	/	5

7909	cell structure disassembly during	/	2.876	/	/	/	/	5
7910	nuclear ubiquitin ligase complex	/	/	/	/	1.992	/	5
7912	vacuolar membrane	/	/	2.624	/	/	/	5
7913	aspartate family amino acid metabo	/	/	/	/	1.992	/	5
7936	amino acid-polyamine transporter a	2.677	/	/	/	/	/	5
7942	calcium-dependent phospholipid bin	2.677	/	/	/	/	/	5
7949	polyamine transporter activity	2.677	/	/	/	/	/	5
7962	translation elongation factor acti	/	/	/	/	2.727	/	5
7974	vacuolar part	/	/	2.444	/	/	/	5
7978	ribonucleoside monophosphate biosy	/	2.574	/	/	/	/	5
7979	ribonucleoside monophosphate metab	/	2.574	/	/	/	/	5
7999	pseudouridine synthase activity	/	/	2.364	/	/	/	5
8015	regulation of epithelial cell prol	/	/	/	/	2.601	/	5
8057	lipid modification	/	2.188	/	/	/	/	5
8075	DNA recombination	/	1.989	/	/	/	/	5
8104	acute-phase response	1.994	/	/	/	/	/	5
8116	translation factor activity\, nucl	/	2.17	/	/	/	/	5
8124	mitotic sister chromatid segregati	/	2.44	/	/	/	/	5
8125	base-excision repair	/	3.797	/	/	/	/	5
8126	mitochondrion	/	2.053	/	/	/	/	5
8127	double-strand break repair	/	2.334	/	/	/	/	5
8136	focal adhesion	/	2.334	/	/	/	/	5
8137	sister chromatid segregation	/	2.334	/	/	/	/	5
8143	galactosyltransferase activity	/	/	/	2.407	/	/	5
8145	ER-Golgi intermediate compartment	/	/	/	/	3.395	/	5
8157	oxidoreductase activity\, acting o	/	/	/	/	2.604	/	5
8186	cell-substrate adherens junction	/	2.039	/	/	/	/	5
8202	scavenger receptor activity	2.065	/	/	/	/	/	5
8205	cell-matrix junction	/	2.473	/	/	/	/	5
8220	intramolecular transferase activit	/	/	/	2.025	/	/	5
8224	transition metal ion homeostasis	1.987	/	/	/	/	/	5
8242	chromatin binding	2.646	/	/	/	/	/	5
8254	nucleobase\, nucleoside\, nucleoti	/	2.325	/	/	/	/	5
8257	DNA-dependent ATPase activity	/	2.038	/	/	/	/	5
8274	negative regulation of progression	/	3.045	/	/	/	/	5
8279	biopolymer metabolic process	/	3.486	/	/	/	/	5
8285	positive regulation of cell differ	/	/	/	/	2.157	/	5
8297	proteasome complex (sensu Eukaryot	/	/	/	/	3.905	/	5
8299	biopolymer biosynthetic process	/	2.424	/	/	/	/	5
8366	purine ribonucleotide biosynthetic	/	2.091	/	/	/	/	5
8384	DNA repair	/	3.476	/	/	/	/	5
8385	purine ribonucleotide metabolic pr	/	2.132	/	/	/	/	5
8392	ribonucleotide biosynthetic proces	/	2.08	/	/	/	/	5
8403	ribonucleotide metabolic process	/	2.029	/	/	/	/	5
8442	pyrophosphatase activity	/	2.23	/	/	/	/	5
8444	hydrolase activity\, acting on aci	/	2.198	/	/	/	/	5
8445	hydrolase activity\, acting on aci	/	2.167	/	/	/	/	5