Supplementary Material

Identification of Potential Prognostic Long Non-Coding RNA Biomarkers for Predicting Survival in Patients with Hepatocellular Carcinoma

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Table S1. DELs identified using the edgeR package.

Table S2. DELs identified using the DESeq package.

Table S3. The univariate survival analysis results of the 827 overlapping DELs.

Table S4. Coexpression analysis results of the 13 DELs and lncRNA-correlated PCGs.

Table S5. GO term enrichment results of lncRNA-correlated PCGs of 13 prognostic DELs.

Table S6. GSEA results between patients with low and high risk score in HCC using c5 reference gene sets.

Table S7. GSEA results between patients with low and high risk score in HCC using c2 reference gene sets.

Table S1. DELs identified using the edgeR package.

ID	logFC	logCPM	PValue	FDR
SFTA1P	5,442900617	5,391468759	3,47E-47	2,41E-43
AC008556.1	-2,135894321	6,609700422	1,25E-45	4,34E-42
AC016999.1	-2,912513529	3,992014151	7,76E-42	1,80E-38
LINC01093	-3,602648462	10,15931385	3,18E-41	5,51E-38
AL391845.2	4,056411278	4,996932279	6,21E-40	8,61E-37
AC092171.2	2,506685269	10,27988982	9,21E-40	1,06E-36
CAPN10-AS1	2,172878799	7,28206146	1,25E-39	1,11E-36
AC132192.2	2,203270497	7,085450171	1,28E-39	1,11E-36
AL359715.4	-1,677220459	7,502678075	1,58E-39	1,22E-36
AC004477.1	2,563456734	6,300015904	1,94E-39	1,35E-36
AF165147.1	-2,568903568	5,371481726	2,55E-38	1,61E-35
AC138356.1	-2,420149261	6,911608238	3,82E-37	2,21E-34
AL357055.3	-1,600997144	5,728321952	2,65E-36	1,42E-33
AC008741.2	1,778327605	7,173419197	2,87E-35	1,42E-32
CDKN2B-AS1	3,375137213	6,706276165	4,61E-34	2,13E-31
DDX11-AS1	2,655050181	5,992199939	5,56E-34	2,41E-31
AC010719.1	2,663363194	7,55536535	2,54E-33	9,97E-31
LINC00907	-2,988553248	5,995397872	2,59E-33	9,97E-31
AC092119.2	2,251819398	6,06037648	4,61E-33	1,68E-30
HAGLROS	4,798236517	5,156127113	2,91E-32	1,01E-29
LINC01089	1,526391077	9,272962416	2,09E-31	6,91E-29
FENDRR	-2,805604966	5,642085516	5,68E-31	1,79E-28
AC092171.4	2,337049714	5,331594133	1,53E-30	4,62E-28
AL353708.3	2,296963369	5,739391237	1,98E-30	5,73E-28
HAGLR	6,121958799	9,714084497	3,36E-30	9,32E-28
AC010776.2	-3,602511304	3,465446174	8,50E-30	2,27E-27
B4GALT1-AS1	-1,525471515	7,801873307	1,25E-29	3,22E-27
AC239868.2	2,000086721	9,568590165	1,63E-29	4,04E-27
HOTTIP	7,140636784	7,635250117	3,19E-29	7,63E-27
AC055713.1	1,185360743	7,968383646	4,74E-29	1,10E-26
AC009831.1	-1,209987703	6,509388332	8,97E-29	2,01E-26
LINC01311	1,938553895	6,383223348	1,20E-28	2,61E-26
C17orf82	2,820343148	6,40054423	2,20E-28	4,62E-26
AC026369.3	-2,682576481	4,477250952	3,81E-28	7,76E-26
AC010280.2	-2,719275916	6,567720653	4,76E-28	9,44E-26
AL162431.2	2,227643998	6,676016563	6,22E-28	1,20E-25
AC008080.1	-2,23390826	3,263473784	9,18E-28	1,72E-25
AC100810.1	-1,178159457	10,00917304	1,26E-27	2,30E-25
AC005332.8	1,505644158	9,233889772	1,29E-27	2,30E-25
MYLK-AS1	2,007133047	6,455840258	1,82E-27	3,12E-25
DNAJC9-AS1	1,625898736	6,421797364	1,84E-27	3,12E-25
AL355488.2	1,758176611	8,339613835	3,32E-27	5,48E-25
AL606489.1	2,972822635	5,747351864	3,47E-27	5,60E-25
LINC02475	6,313156081	6,361298909	8,94E-27	1,39E-24
LINC00261	-1,477079762	14,42026694	9,00E-27	1,39E-24
AC107396.1	-4,39468261	4,350341289	9,94E-27	1,50E-24
AL121906.2	2,643912785	6,009170089	1,54E-26	2,28E-24

AC016773.1	2,362107324	5,867898964	2,03E-26	2,93E-24
AC129507.1	-1,88928484	5,778283683	2,39E-26	3,38E-24
AL021453.1	1,497220068	8,445316272	2,95E-26	4,09E-24
MAFG-AS1	2,769128146	8,363951784	4,80E-26	6,52E-24
RUSC1-AS1	1,710763523	9,454279158	6,80E-26	9,08E-24
AL023803.2	2,864894557	5,597974974	7,25E-26	9,49E-24
LINC01704	3,664046119	4,010058111	1,05E-25	1,35E-23
AC024937.3	2,007172975	6,148956607	1,36E-25	1,72E-23
HTR2A-AS1	-2,361777068	3,467404501	1,46E-25	1,81E-23
AL137060.1	2,489456103	4,945273187	1,79E-25	2,18E-23
TMEM220-AS1	-1,524686161	9,652418212	2,15E-25	2,58E-23
LENG8-AS1	1,389887146	7,078135525	2,84E-25	3,33E-23
HCG25	1,611603583	6,309256016	3,78E-25	4,37E-23
LINC02163	7,205073945	6,213721842	3,97E-25	4,52E-23
CRNDE	3,221278872	8,79324542	7,68E-25	8,60E-23
SNHG1	1,443833821	11,41168436	9,79E-25	1,07E-22
AC010973.2	1,652200873	6,60479227	9,90E-25	1,07E-22
AC107375.1	1,345921407	7,65637132	1,36E-24	1,45E-22
AC102953.2	1,935107237	7,597627547	1,83E-24	1,92E-22
AC009159.3	-1,415123694	7,29554069	2,19E-24	2,27E-22
ZNF252P-AS1	1,970011898	5,63493374	2,98E-24	3,04E-22
PTGES2-AS1	3,315349118	4,914093432	4,08E-24	4,10E-22
AC074327.1	5,896660486	8,798727439	7,44E-24	7,38E-22
AC004080.2	6,486126794	5,348271602	9,43E-24	9,21E-22
AL133367.1	2,023733626	6,758992363	1,15E-23	1,11E-21
AC092155.1	-2,964704841	4,090917624	1,18E-23	1,12E-21
AC109322.1	1,868989933	7,961333134	1,23E-23	1,16E-21
AC110285.6	3,350929996	5,294463126	1,26E-23	1,17E-21
AC018809.1	2,313185778	4,856626002	1,32E-23	1,21E-21
MIR3945HG	-1,964144136	4,494209162	1,37E-23	1,23E-21
LINC01537	-1,633405934	5,571648267	3,35E-23	2,98E-21
AC024361.1	2,051078197	5,681379013	3,42E-23	3,00E-21
AL161740.1	-1,739389277	6,038459196	3,52E-23	3,05E-21
AC015908.3	-1,507075259	8,285639693	4,95E-23	4,24E-21
AL161668.3	-2,042600891	8,233333692	6,21E-23	5,25E-21
AC110995.1	-1,719602744	5,436437884	1,34E-22	1,12E-20
BACE1-AS	1,151708634	8,12452977	1,58E-22	1,30E-20
LINC02202	2,565295057	5,180847516	1,63E-22	1,33E-20
AL136162.1	2,006775935	5,718365934	1,72E-22	1,38E-20
AC099508.2	-2,540482034	6,080341745	2,11E-22	1,68E-20
AC006960.2	-4,022232871	3,670192919	2,21E-22	1,74E-20
AL451050.2	2,136873125	4,988720992	3,07E-22	2,40E-20
ST8SIA6-AS1	5,560289977	9,00497327	3,88E-22	2,99E-20
AL359076.1	-1,058427491	7,090493022	5,83E-22	4,40E-20
AC116049.2	4,92091054	5,440578265	5,84E-22	4,40E-20
LINC01767	-1,787497531	9,786977667	6,59E-22	4,92E-20
TMEM26-AS1	-2,011477928	3,472713927	6,97E-22	5,15E-20
AP003774.3	-1,914562569	3,686479781	9,11E-22	6,65E-20
LINC01818	-2,667585047	4,30202127	9,78E-22	7,07E-20
AC004160.1	-2,494015706	7,099984227	1,06E-21	7,58E-20

AL136084.3	3,934944488	4,211956641	1,33E-21	9,35E-20
GAS5	1,74123909	13,91155661	1,88E-21	1,30E-19
DLG5-AS1	2,151611566	6,461525275	2,04E-21	1,40E-19
AL731569.1	1,329249586	6,591293315	2,18E-21	1,48E-19
AC011294.1	4,304478619	7,085730811	2,49E-21	1,68E-19
AC105137.3	1,917269185	4,760732792	3,73E-21	2,49E-19
HID1-AS1	-1,67454407	4,485027268	3,90E-21	2,57E-19
LINC01419	10,98225205	10,59497695	4,87E-21	3,19E-19
AL139089.1	1,545559709	5,818195204	5,21E-21	3,38E-19
AC016027.1	-1,025710608	7,27298246	5,34E-21	3,43E-19
AL513320.1	1,934422329	4,875826191	5,42E-21	3,45E-19
FOXD2-AS1	1,973980494	8,867924263	6,51E-21	4,11E-19
AC010201.2	1,929025196	5,721698519	6,85E-21	4,28E-19
AC100849.1	-1,872782127	3,68352156	7,33E-21	4,54E-19
AL590235.1	2,180867609	6,132471772	8,35E-21	5,10E-19
AC084033.3	1,519815948	8,294150527	8,37E-21	5,10E-19
LINC00685	1,943927911	5,624136265	9,11E-21	5,49E-19
U73166.1	2,006593163	6,031558896	1,12E-20	6,65E-19
AL451074.2	1,893503937	5,453792441	2,29E-20	1,34E-18
AC132872.2	2,31592942	4,64351416	2,30E-20	1,34E-18
LINC02241	8,750619455	7,703907982	2,58E-20	1,48E-18
AC011921.1	2,140927896	4,481725569	2,78E-20	1,58E-18
LINC00355	7,197708316	6,189992273	3,22E-20	1,82E-18
RNF139-AS1	1,332754889	7,14535752	3,31E-20	1,85E-18
AC116025.2	3,036715525	4,488089711	3,34E-20	1,85E-18
AC012409.1	-1,810681791	6,884933297	3,96E-20	2,18E-18
LEF1-AS1	3,683993596	4,655531831	4,28E-20	2,34E-18
AC015468.1	-2,975721523	3,306774393	4,93E-20	2,67E-18
AC079789.1	-2,650034212	3,211464143	5,14E-20	2,77E-18
MIR4435-2HG	1,673432924	11,08443213	5,28E-20	2,82E-18
AC245100.6	7,689878098	7,381559724	5,54E-20	2,93E-18
AC079174.2	1,612796833	6,10943753	8,69E-20	4,57E-18
LINC01703	2,250266239	6,809226745	8,99E-20	4,69E-18
GNG12-AS1	-1,43636695	6,238105572	9,96E-20	5,16E-18
NPSR1-AS1	6,281757522	7,246457885	1,14E-19	5,86E-18
KCNMB2-AS1	4,487036693	7,218708605	1,26E-19	6,43E-18
AFAP1-AS1	7,109688254	10,03120244	1,32E-19	6,66E-18
DUXAP8	2,995894526	7,721397712	1,39E-19	6,94E-18
CCDC18-AS1	1,228190995	9,214322253	1,39E-19	6,94E-18
AC139100.2	1,92163465	6,362816585	1,48E-19	7,26E-18
LINC02476	7,665217212	7,026422433	1,54E-19	7,52E-18
AP001469.3	1,852393196	6,966861282	1,56E-19	7,56E-18
AC004816.1	1,887852578	6,487075526	1,73E-19	8,34E-18
TMPO-AS1	1,532546603	8,902156932	2,16E-19	1,03E-17
LINC00853	2,197376014	7,537339547	2,23E-19	1,06E-17
AC023908.3	1,912526466	5,00518308	2,31E-19	1,09E-17
PVT1	2,188943423	9,289911703	2,75E-19	1,29E-17
AC026362.1	1,304159459	5,536867753	2,93E-19	1,36E-17
AL136987.1	4,810742794	6,116883458	3,49E-19	1,61E-17
FGF14-AS2	-1,387674665	8,069951836	4,09E-19	1,88E-17

MELTF-AS1	2,181513133	6,995768723	4,13E-19	1,88E-17
STAM-AS1	2,066738737	4,810801342	4,68E-19	2,12E-17
LINC01138	1,426115122	9,017313898	4,87E-19	2,19E-17
LINC01532	5,5616188	5,254285384	5,42E-19	2,42E-17
AC020978.5	-1,869598004	7,764696309	6,26E-19	2,78E-17
TDRKH-AS1	1,636477493	5,652692387	6,45E-19	2,85E-17
FEZF1-AS1	5,378131561	7,206125286	6,91E-19	3,03E-17
AC017083.2	1,781386089	4,734266387	7,91E-19	3,45E-17
SNHG20	1,02099093	8,971841334	9,28E-19	4,02E-17
AC105384.1	-2,131835492	3,341703314	9,51E-19	4,10E-17
AL365181.3	3,540102671	10,78074372	1,00E-18	4,29E-17
AC009148.1	1,985616384	4,494287037	1,23E-18	5,23E-17
CDKN2A-AS1	4,081712186	3,747401648	1,29E-18	5,47E-17
AC010864.1	1,473189846	5,238828354	1,34E-18	5,61E-17
HOXA11-AS	5,599254903	5,164293749	1,34E-18	5,61E-17
AC073352.1	2,354131028	4,089734533	1,70E-18	7,07E-17
AL512652.1	2,661951728	3,808050096	1,76E-18	7,28E-17
GUSBP11	1,697904481	7,353364431	1,79E-18	7,33E-17
LINC00205	1,426447569	7,873506393	1,95E-18	7,98E-17
AC099850.3	2,593509105	6,382704025	2,31E-18	9,39E-17
AL121832.3	2,073076702	5,573731552	2,35E-18	9,46E-17
AC087392.1	-2,575228131	7,114274446	2,36E-18	9,46E-17
AC009690.2	1,175409668	7,071259554	2,48E-18	9,90E-17
AC004540.2	-2,448212975	6,754854888	2,55E-18	1,01E-16
AC068858.1	3,240792923	4,171000206	2,75E-18	1,09E-16
AC097641.3	1,631679163	4,556141932	3,80E-18	1,49E-16
AL445524.1	2,07476085	10,76091367	4,14E-18	1,61E-16
SNHG7	1,433467913	11,79356402	4,28E-18	1,66E-16
AL590666.2	3,110258756	7,943795933	5,03E-18	1,94E-16
AC016550.2	5,546265858	4,564270504	5,10E-18	1,95E-16
AL512791.2	-1,135397993	5,701820213	5,28E-18	2,01E-16
TM4SF19-AS1	1,764520222	5,466840581	5,64E-18	2,14E-16
PRKAR2A-AS1	1,436297649	7,555635319	6,02E-18	2,27E-16
AL355303.1	3,256785283	5,270876147	7,06E-18	2,65E-16
SNHG25	2,115182582	7,43106807	8,07E-18	3,01E-16
LINC00528	1,536463126	7,449359549	8,23E-18	3,05E-16
AC114316.2	4,039600128	5,084331179	8,95E-18	3,30E-16
AL078581.1	-1,225242309	5,071641503	9,42E-18	3,46E-16
AL121899.1	2,114662563	7,402568372	9,89E-18	3,61E-16
AC009005.1	2,074574792	7,258198487	1,01E-17	3,67E-16
AC079061.1	-2,296009718	7,774794276	1,02E-17	3,70E-16
TFAP2A-AS1	3,791608798	5,849434579	1,08E-17	3,87E-16
CELSR3-AS1	2,082844415	4,840887489	1,08E-17	3,87E-16
AC048341.3	1,467134487	6,069032008	1,11E-17	3,94E-16
MAFA-AS1	7,227037975	6,247048265	1,12E-17	3,95E-16
AL359878.1	2,248186538	4,722570059	1,18E-17	4,15E-16
SNHG4	2,284225127	6,722879948	1,19E-17	4,15E-16
AC232271.1	1,248362593	6,856174957	1,35E-17	4,71E-16
AC111000.4	2,342440612	8,613799374	1,48E-17	5,14E-16
AC024230.1	5,579561935	4,964176714	1,67E-17	5,75E-16

LINC01004	1,237548718	6,90567492	1,72E-17	5,91E-16
AC099520.1	5,437363299	4,263726882	1,79E-17	6,13E-16
AC011462.4	1,778998976	5,020038737	2,09E-17	7,09E-16
AC034229.4	2,423157607	4,318058254	2,09E-17	7,09E-16
AC078778.1	1,890369405	5,537547404	2,13E-17	7,16E-16
AC090227.2	-2,661173911	3,850160875	2,25E-17	7,54E-16
AC025171.2	1,414548301	7,34841862	2,50E-17	8,33E-16
AL158212.3	1,429105209	7,640691128	3,05E-17	1,01E-15
LINC01451	3,076393761	8,931586848	3,26E-17	1,07E-15
AC016737.1	1,942018447	4,904695516	3,32E-17	1,09E-15
AL117379.1	1,449798821	5,784326357	3,39E-17	1,10E-15
AC003102.1	1,399202937	7,045173503	3,40E-17	1,10E-15
AC090502.1	7,785744055	7,917433159	3,47E-17	1,12E-15
AC069544.1	1,203344294	6,305982057	3,54E-17	1,14E-15
AC092384.2	-2,455851158	6,987993206	3,69E-17	1,18E-15
AC091987.1	5,659260158	4,660076096	3,85E-17	1,22E-15
FP671120.4	-1,78456333	6,433846571	4,13E-17	1,30E-15
AC013731.1	1,767877194	5,222464848	4,14E-17	1,30E-15
WARS2-IT1	-2,0037032	4,14582662	4,68E-17	1,46E-15
AL139412.1	2,233054778	6,325805926	5,48E-17	1,70E-15
AC105118.1	7,332091483	6,392910013	5,52E-17	1,71E-15
CYTOR	1,774563662	10,80564124	5,61E-17	1,73E-15
DHRS4-AS1	-1,035112133	11,70304522	5,69E-17	1,75E-15
AP001178.3	2,895303482	4,10884619	5,93E-17	1,81E-15
AL022322.1	1,718992532	6,431128552	5,97E-17	1,82E-15
AC026740.1	2,454182187	7,054174275	6,48E-17	1,96E-15
AC245128.3	-2,109944686	4,530295089	6,72E-17	2,03E-15
LINC01863	-2,447817721	4,328565582	7,35E-17	2,21E-15
HAO2-IT1	-2,321952487	4,571979553	7,58E-17	2,27E-15
LINC01121	4,095131264	4,945161276	7,68E-17	2,29E-15
ASMTL-AS1	1,411421887	8,838693094	8,14E-17	2,41E-15
HRAT92	2,811352031	7,084448623	8,33E-17	2,46E-15
HAND2-AS1	-2,422273467	7,684874057	9,10E-17	2,67E-15
AC110285.2	1,943317352	8,148591117	9,15E-17	2,68E-15
AL157832.2	-2,039539484	3,953484258	9,79E-17	2,85E-15
AL024498.1	1,81079949	4,448784177	1,00E-16	2,91E-15
AC120114.2	1,004269922	7,538469196	1,06E-16	3,07E-15
AC019131.2	-1,030004155	7,158579639	1,10E-16	3,17E-15
LINC01970	2,869289445	5,116392687	1,13E-16	3,23E-15
AC005332.1	1,751675695	4,401813274	1,13E-16	3,23E-15
AC099676.1	1,384540902	7,300184413	1,17E-16	3,33E-15
STAU2-AS1	2,260934028	4,8125525	1,18E-16	3,35E-15
AC073842.2	2,104212055	4,67351364	1,27E-16	3,59E-15
AC012615.1	1,147262844	8,156430758	1,40E-16	3,93E-15
AL392089.1	-2,008128607	3,633864122	1,45E-16	4,07E-15
ZFPM2-AS1	3,982593062	8,640837743	1,56E-16	4,34E-15
AC009831.4	-1,821845596	3,216093182	1,70E-16	4,72E-15
LINC01679	-1,427606703	6,344997521	1,76E-16	4,85E-15
AP003352.1	1,241512051	8,597571673	1,76E-16	4,85E-15
AC023355.1	1,938178168	5,03603598	1,83E-16	5,01E-15

AL021707.2	1,449944999	6,782642331	1,85E-16	5,05E-15
AP000553.1	2,776615328	4,250725725	1,90E-16	5,16E-15
LINC02428	-2,110721887	9,595126564	1,98E-16	5,38E-15
AC099778.1	1,117316939	6,099642432	2,07E-16	5,60E-15
PRR7-AS1	2,479840207	4,690710652	2,36E-16	6,35E-15
AC009509.4	-1,298970623	4,890290174	2,50E-16	6,71E-15
U91324.1	-1,478758615	7,804607517	2,58E-16	6,88E-15
AC112484.4	2,012603031	6,425496946	2,77E-16	7,36E-15
AC011005.4	2,398671675	4,967543699	2,91E-16	7,70E-15
AL133215.2	2,366554475	4,649511312	3,01E-16	7,94E-15
AC007364.1	-1,329273839	6,098666502	3,11E-16	8,17E-15
STEAP3-AS1	-1,539195998	4,96475787	3,12E-16	8,18E-15
LINC00628	2,61110319	4,475617818	3,40E-16	8,87E-15
TMEM147-AS1	1,063346542	8,664669682	3,43E-16	8,91E-15
AC005041.2	1,531034327	6,079387838	3,52E-16	9,11E-15
AC092809.2	-1,792278634	5,032954235	3,78E-16	9,75E-15
AL445228.2	2,827528128	4,428987052	3,79E-16	9,75E-15
AL731897.1	7,175311195	5,681221066	3,96E-16	1,01E-14
LINC00894	1,425787098	7,258236122	4,04E-16	1,03E-14
F11-AS1	-1,320147146	9,999832823	4,32E-16	1,10E-14
AC126118.1	1,871514472	4,49622873	4,71E-16	1,19E-14
SNHG3	1,519320629	10,63144664	5,13E-16	1,29E-14
IBA57-AS1	1,991524622	4,196247068	5,23E-16	1,31E-14
FLJ31104	1,925691759	5,828998306	5,69E-16	1,42E-14
LINC00665	2,686488275	10,17659746	5,70E-16	1,42E-14
AC093609.1	-1,641610087	5,319402074	6,49E-16	1,61E-14
LINC01833	7,18903392	6,580945635	6,62E-16	1,64E-14
AF127577.4	-1,000653514	8,862777107	6,73E-16	1,66E-14
AC103706.1	1,622897251	6,887795462	6,73E-16	1,66E-14
LINC01116	3,181844176	6,767014739	7,36E-16	1,81E-14
AP002954.1	-1,833412857	4,290781269	7,47E-16	1,82E-14
MAGI2-AS3	-1,781091653	10,65838243	8,05E-16	1,96E-14
AC009137.2	-1,288500891	4,564094264	8,75E-16	2,12E-14
NCOA7-AS1	-2,331939804	4,068824295	9,37E-16	2,27E-14
AC124242.1	-1,313683581	5,740594339	1,01E-15	2,43E-14
AP001412.1	1,700966905	4,427689912	1,01E-15	2,43E-14
AL035461.2	1,605791359	7,049260653	1,05E-15	2,51E-14
AC117386.2	4,880224501	5,89661148	1,22E-15	2,92E-14
AL365181.2	3,530175141	8,460351133	1,31E-15	3,10E-14
LINC01535	3,287370699	5,693433365	1,35E-15	3,19E-14
AC011445.2	2,347369569	5,989215003	1,40E-15	3,30E-14
AC091057.3	2,15455155	4,534768032	1,41E-15	3,32E-14
AL138828.1	4,225102767	7,973961139	1,43E-15	3,34E-14
AC006252.1	1,851049459	4,696549179	1,45E-15	3,38E-14
LINC00511	3,188109999	9,112126539	1,51E-15	3,51E-14
AC096642.1	1,594702205	5,500710228	1,56E-15	3,63E-14
AL031186.1	1,431795506	5,056423275	1,93E-15	4,47E-14
LINC01980	7,024457806	7,572901148	1,97E-15	4,54E-14
AC068987.1	2,126645789	4,669233892	2,22E-15	5,11E-14
AC022306.2	1,254114516	6,748632068	2,24E-15	5,11E-14

FIRRE	3,046661081	5,326920921	2,40E-15	5,47E-14
AC108748.1	-1,732823084	4,662986013	2,42E-15	5,48E-14
TMCC1-AS1	1,462553473	7,326763787	2,49E-15	5,63E-14
AC010331.1	1,539898911	5,616919656	2,50E-15	5,64E-14
AC093895.1	4,980335596	5,538964414	2,53E-15	5,69E-14
AC233280.1	2,155999019	4,54005548	2,67E-15	5,99E-14
STK24-AS1	1,61112147	5,399037737	2,79E-15	6,23E-14
AC132872.1	1,068638446	8,159669966	2,85E-15	6,33E-14
LINC01287	8,449068906	10,12333714	3,27E-15	7,26E-14
AP000347.2	1,600531421	6,026507812	3,29E-15	7,26E-14
LINC01224	4,450295143	6,581658188	3,58E-15	7,88E-14
Z97832.2	1,49730943	5,659370051	3,74E-15	8,21E-14
SNHG12	1,110348646	9,533067811	3,83E-15	8,37E-14
AC010280.1	-2,24747102	4,128114606	3,96E-15	8,64E-14
AC004263.2	1,965057301	4,678024602	4,25E-15	9,25E-14
AC005089.1	1,667461292	6,875229007	4,64E-15	1,01E-13
AC078909.2	2,775051806	4,338336217	4,85E-15	1,04E-13
AC119424.1	-1,801097818	5,595992535	4,98E-15	1,07E-13
HOXD-AS2	3,905408661	5,19056176	5,02E-15	1,07E-13
LINC01194	7,079060856	6,063087315	5,18E-15	1,11E-13
AC005785.1	1,339751665	6,175858779	5,30E-15	1,13E-13
LINC01235	2,944179922	6,168693197	5,58E-15	1,18E-13
TEX41	3,096745382	8,143497743	5,88E-15	1,24E-13
AC006538.1	2,204024214	5,682577245	6,04E-15	1,27E-13
AL355388.2	2,336985364	5,06433378	6,07E-15	1,28E-13
AC092535.4	1,804250313	8,306508252	6,30E-15	1,32E-13
AC005393.1	1,995764719	4,566773839	6,53E-15	1,36E-13
AC106822.1	-1,960684119	5,024071657	6,75E-15	1,41E-13
AC127024.5	1,357421983	5,734957287	6,94E-15	1,44E-13
AP006623.1	1,442713718	6,259873183	7,30E-15	1,51E-13
AC036176.1	-1,079313599	8,547561164	7,36E-15	1,52E-13
LINC02466	5,277993313	4,159152188	7,85E-15	1,61E-13
AC022007.1	1,162692467	7,469327334	7,86E-15	1,61E-13
AL592424.1	1,830227052	6,564423869	8,03E-15	1,64E-13
FP236383.2	-4,469272551	3,855221243	8,27E-15	1,69E-13
AL358072.1	1,545722067	4,285427109	8,37E-15	1,70E-13
AP003469.2	3,809092844	4,969071679	8,41E-15	1,71E-13
RBMS3-AS3	-1,703726939	3,76841553	8,63E-15	1,75E-13
LINC01611	6,199704938	5,078903483	8,66E-15	1,75E-13
AC008875.1	2,280956152	4,127749773	9,07E-15	1,82E-13
AC087741.1	1,167185137	8,810609088	9,44E-15	1,89E-13
LINC00482	1,612963656	9,066685532	9,79E-15	1,96E-13
AL078590.3	-1,642581044	5,950723161	9,84E-15	1,96E-13
AC021491.2	2,932670323	3,715969242	1,02E-14	2,03E-13
LINC01426	2,750322827	8,45800901	1,13E-14	2,23E-13
AC124016.1	1,248576009	5,246820377	1,22E-14	2,40E-13
AC107419.1	4,388636237	4,920905628	1,31E-14	2,59E-13
RASGRF2-AS1	2,775300117	3,544089691	1,34E-14	2,63E-13
AP003469.4	1,374978502	9,209723306	1,35E-14	2,64E-13
FLVCR1-AS1	1,506594156	8,790088676	1,42E-14	2,78E-13

AL731563.3	1,067300838	6,159665321	1,47E-14	2,86E-13
AL121658.1	1,631290969	4,667338126	1,52E-14	2,95E-13
AP000253.1	-1,381039745	4,947183569	1,83E-14	3,55E-13
LINC00893	1,295561482	6,982809259	2,00E-14	3,86E-13
AC104590.1	2,169803636	4,048397832	2,07E-14	3,99E-13
AL731684.1	4,825936636	5,021643962	2,28E-14	4,39E-13
AP001453.3	1,218135418	6,034502984	2,45E-14	4,70E-13
AL358613.2	-2,176523909	3,635001386	2,82E-14	5,39E-13
LINC00942	7,03786952	8,844689173	2,86E-14	5,45E-13
AC016394.1	1,304713809	6,668396229	2,88E-14	5,48E-13
MIR2052HG	4,47382595	4,843520466	2,94E-14	5,57E-13
AC022211.2	1,378500696	6,727018185	2,96E-14	5,60E-13
AL162413.1	6,563812506	5,933327884	3,08E-14	5,80E-13
LINC02365	4,332032931	8,805657124	3,11E-14	5,84E-13
AC000067.1	2,864857821	3,3835569	3,19E-14	5,98E-13
AC139100.1	1,863272937	6,635990655	3,32E-14	6,20E-13
AC129507.2	-1,347233412	7,276834676	3,32E-14	6,20E-13
AC104170.1	-1,215743676	5,682322365	3,48E-14	6,48E-13
ATP2A1-AS1	2,131559977	5,354330714	3,57E-14	6,63E-13
LINC01234	5,587622	7,880684633	3,93E-14	7,27E-13
AC239809.3	3,588324896	7,118699434	4,02E-14	7,41E-13
AL163953.1	3,578159515	5,313726716	4,04E-14	7,43E-13
LINC00221	7,583755205	8,629224014	4,19E-14	7,69E-13
AL359313.1	5,602380776	5,301524227	4,36E-14	7,98E-13
AC073195.1	1,181350592	5,513885572	4,57E-14	8,35E-13
AC073111.1	2,375008764	3,656091488	4,65E-14	8,46E-13
AC010300.1	1,513021824	6,156862177	4,76E-14	8,65E-13
AC005670.1	2,569106525	3,722865457	4,89E-14	8,85E-13
PCAT6	1,500276945	7,877363785	5,06E-14	9,15E-13
NOVA1-AS1	5,699524803	5,305379046	5,31E-14	9,58E-13
LINC00310	-1,237318906	4,893013895	5,57E-14	1,00E-12
AP006621.2	1,897826687	5,909413797	5,96E-14	1,07E-12
AL160006.1	1,154852073	8,786510685	5,97E-14	1,07E-12
AL358075.2	2,518574967	4,113026733	5,99E-14	1,07E-12
AC245060.6	1,573646786	6,369596319	6,13E-14	1,09E-12
AC090809.1	6,542338694	5,363819177	6,15E-14	1,09E-12
AC105202.1	-1,914680347	7,193954768	6,26E-14	1,11E-12
AC141002.1	2,006301085	4,168596976	6,53E-14	1,15E-12
AP000593.3	5,132889644	6,778251315	6,76E-14	1,19E-12
AC079466.1	6,151438276	11,28018292	7,10E-14	1,24E-12
AL117329.1	5,233739214	4,72700771	7,39E-14	1,29E-12
AC114401.1	4,280373718	4,58398335	7,46E-14	1,30E-12
AC080129.2	1,839284239	5,518715891	7,61E-14	1,32E-12
AC010894.3	4,488584173	6,56612371	8,38E-14	1,45E-12
LINC01355	1,139978446	8,111753269	8,72E-14	1,51E-12
AC011337.1	1,482341126	4,71267817	8,84E-14	1,52E-12
AL021807.1	2,15090756	5,581930487	8,87E-14	1,52E-12
AC074212.1	1,259319141	7,744833474	9,19E-14	1,57E-12
AC104794.4	-1,500834994	3,919143017	9,29E-14	1,59E-12
AC025176.1	2,716960621	3,876993463	9,51E-14	1,62E-12

LUCAT1	3,925870288	7,679773184	9,54E-14	1,62E-12
AL035563.1	1,289645982	5,813855747	1,02E-13	1,73E-12
AC078993.1	4,206805243	7,024797543	1,04E-13	1,76E-12
LINC01186	2,560309916	6,050331431	1,08E-13	1,82E-12
ELF3-AS1	1,56271763	8,262452854	1,11E-13	1,86E-12
DCST1-AS1	1,345008154	7,703124245	1,21E-13	2,03E-12
AC011503.1	4,588696513	5,780320851	1,31E-13	2,18E-12
FBXL19-AS1	1,446411881	7,44002635	1,33E-13	2,21E-12
AC063948.1	1,489878741	4,528714418	1,36E-13	2,25E-12
MINCR	1,364045933	9,244806954	1,50E-13	2,48E-12
AL139123.1	1,628470796	4,215809363	1,60E-13	2,64E-12
AC008764.8	1,110568668	5,819672986	1,65E-13	2,71E-12
AC145285.7	1,119402734	5,528203174	1,70E-13	2,79E-12
AC245884.8	1,288816007	5,567228188	1,81E-13	2,95E-12
LINC01424	1,951959346	4,027306307	1,86E-13	3,04E-12
LINC01762	2,343210165	4,977988864	1,87E-13	3,04E-12
PCDH9-AS2	-3,219713616	4,850478245	1,96E-13	3,19E-12
AL133410.1	1,645930665	5,074558245	1,98E-13	3,21E-12
AC145343.1	1,613062118	6,110251083	2,03E-13	3,29E-12
AL133410.3	1,321515654	6,641752216	2,07E-13	3,33E-12
AL450992.2	1,461391793	8,304223334	2,08E-13	3,35E-12
AC090192.2	5,22480861	4,996981032	2,17E-13	3,48E-12
LINC02313	3,306386014	4,832952501	2,26E-13	3,62E-12
AC138696.2	1,358637544	6,295383554	2,26E-13	3,62E-12
LINC02367	1,928739118	5,437008333	2,33E-13	3,72E-12
AP003419.4	1,900305086	4,953155517	3,01E-13	4,79E-12
AC012146.1	1,418864203	8,600949401	3,02E-13	4,79E-12
GAPLINC	2,935523027	7,016543719	3,05E-13	4,83E-12
DNM3OS	-1,411071953	6,993772882	3,15E-13	4,97E-12
AC106900.2	4,187837384	4,704900886	3,16E-13	4,98E-12
LINC02335	5,478457957	4,817321271	3,21E-13	5,05E-12
SERTAD4-AS1	2,831992648	6,435685246	3,26E-13	5,11E-12
AC012236.1	2,373271695	7,807526028	3,34E-13	5,24E-12
C2orf48	2,183019533	5,344169405	3,49E-13	5,45E-12
AC011498.7	1,600170663	4,396487533	3,73E-13	5,82E-12
LINC00906	5,280480024	4,591289613	3,93E-13	6,11E-12
AC007639.1	4,093469974	5,806403914	3,98E-13	6,18E-12
AC087294.1	1,549304865	4,236629613	4,18E-13	6,47E-12
AC024600.1	-1,920226235	4,478968067	4,25E-13	6,57E-12
AL591848.2	3,077690207	3,898310764	4,27E-13	6,57E-12
LINC02377	6,138959782	5,563881524	4,27E-13	6,57E-12
AL355802.3	1,447765491	5,528776562	4,28E-13	6,57E-12
AP002807.1	1,457647083	7,001724914	4,44E-13	6,80E-12
FAM3D-AS1	-1,750924736	3,722206716	4,61E-13	7,05E-12
AC106820.3	1,514481471	5,671473088	4,67E-13	7,12E-12
AC079766.1	-1,17710747	4,622116609	4,73E-13	7,20E-12
AC013553.3	2,20662846	3,818941384	4,90E-13	7,43E-12
AL139095.4	-1,227724623	3,678211341	4,99E-13	7,57E-12
AC012613.2	-1,857566508	3,65004137	5,09E-13	7,69E-12
MIR194-2HG	1,237660787	7,795317257	5,29E-13	7,98E-12

TSPEAR-AS2	2,576242465	8,411526543	5,34E-13	8,03E-12
AC098820.1	1,345497447	6,105358736	5,72E-13	8,59E-12
AC025031.1	-1,424807095	4,074200185	5,98E-13	8,96E-12
AL391056.1	3,944965498	7,495090969	7,12E-13	1,06E-11
AC097515.1	3,554368993	4,08718599	7,23E-13	1,07E-11
AC012313.9	1,497855726	5,340076827	7,42E-13	1,10E-11
AC008610.1	1,51174193	5,74217724	7,84E-13	1,16E-11
LINC01572	2,012990703	4,880470748	8,06E-13	1,19E-11
AC096564.1	-1,408682214	4,961109065	8,20E-13	1,21E-11
LINC02152	3,89393949	4,067505921	8,39E-13	1,23E-11
ZMIZ1-AS1	1,674954227	7,032410583	8,63E-13	1,26E-11
AL035401.1	4,425081594	4,087998134	8,75E-13	1,28E-11
AC131391.1	4,729748469	3,972641029	9,02E-13	1,31E-11
LINC01612	-3,151449742	5,9491878	9,16E-13	1,33E-11
MIR600HG	1,330868961	8,2590439	9,29E-13	1,35E-11
AP006216.2	-1,631799533	6,571759162	9,80E-13	1,42E-11
LINC02275	-2,212091024	6,007799079	9,92E-13	1,43E-11
AL160314.2	1,404491372	4,688471803	1,00E-12	1,44E-11
HCG27	1,092063256	7,035931595	1,01E-12	1,46E-11
AC109460.1	1,135919796	4,946433627	1,08E-12	1,56E-11
AL359921.2	1,084273504	6,964386024	1,12E-12	1,61E-11
AC004160.2	-2,196590639	4,66785088	1,15E-12	1,65E-11
AC087388.1	1,122764985	6,155990238	1,16E-12	1,65E-11
LINC01136	2,347693375	5,152882403	1,21E-12	1,71E-11
AC109460.3	1,0970147	5,943710331	1,39E-12	1,96E-11
AC084018.1	1,431192878	6,329151402	1,39E-12	1,96E-11
CTD-2201I18.1	1,679054965	6,509282718	1,40E-12	1,96E-11
AC109830.1	5,186477753	4,321380076	1,40E-12	1,96E-11
AC002128.1	1,259948267	5,347617149	1,41E-12	1,96E-11
AC112178.1	5,868488015	5,231210497	1,42E-12	1,97E-11
AC145423.3	1,627100712	4,129697263	1,45E-12	2,02E-11
AC023090.1	4,912913435	5,336798518	1,49E-12	2,07E-11
AL139023.1	5,131584592	4,91606461	1,54E-12	2,13E-11
AL136537.2	6,12738418	5,228152459	1,57E-12	2,16E-11
DNM1P35	1,790068524	6,17085548	1,67E-12	2,29E-11
PRC1-AS1	1,709433457	4,153804378	1,71E-12	2,35E-11
AL355987.4	2,096564921	7,053943869	1,85E-12	2,54E-11
LINC01748	4,912801948	5,600635328	1,86E-12	2,54E-11
LINC01667	7,495286448	7,4838537	1,97E-12	2,69E-11
AC005264.1	1,703978946	3,888044648	2,06E-12	2,79E-11
HEXA-AS1	1,608936138	5,448809647	2,08E-12	2,82E-11
AC007773.1	1,507521005	6,443898243	2,14E-12	2,89E-11
AL031722.1	-1,209001745	5,232449376	2,14E-12	2,89E-11
LINC02323	3,765108276	5,07913072	2,32E-12	3,13E-11
LINC01389	1,647896854	5,885481074	2,36E-12	3,18E-11
AL589765.6	2,022538104	3,845634822	2,50E-12	3,35E-11
AL121772.1	1,929863024	5,23896149	2,52E-12	3,38E-11
AC021321.1	1,679260451	4,428388672	2,54E-12	3,39E-11
AC011468.1	1,192549165	6,683768905	2,72E-12	3,64E-11
LINC01126	1,641775333	5,3243507	2,85E-12	3,79E-11

U47924.3	1,947019768	3,975182706	2,91E-12	3,87E-11
AC092910.3	1,132327981	6,014550022	2,92E-12	3,88E-11
SLC9A3-AS1	1,964945473	10,62473635	3,03E-12	4,00E-11
LINC01372	1,173391717	5,377408351	3,14E-12	4,14E-11
FLJ12825	2,593999246	4,625419626	3,16E-12	4,17E-11
AL390728.6	1,146939465	9,209236543	3,24E-12	4,25E-11
AC002116.2	1,315128213	5,380810779	3,32E-12	4,35E-11
AC016877.3	4,361365599	4,075465447	3,32E-12	4,35E-11
KIAA1614-AS1	2,085647917	4,1143464	3,43E-12	4,48E-11
MORF4L2-AS1	1,135749546	5,394862875	3,46E-12	4,51E-11
AC015922.4	-1,123453454	6,408448925	3,54E-12	4,61E-11
AC092957.1	5,495575272	4,868396102	3,57E-12	4,64E-11
AL135999.1	1,158883781	8,02341912	3,62E-12	4,70E-11
AL080317.3	1,172191941	7,298826625	4,00E-12	5,17E-11
AC027796.4	1,554768911	6,001570811	4,21E-12	5,43E-11
AC009065.4	1,019183398	6,328941952	4,25E-12	5,47E-11
AC007277.1	3,7129755	5,672267888	4,31E-12	5,53E-11
LINC01775	2,587775604	3,377065001	4,31E-12	5,53E-11
LINC02388	-1,88658826	4,901012941	4,33E-12	5,55E-11
Z99289.1	-1,754953034	4,526894723	4,50E-12	5,74E-11
AC018648.1	1,779136644	3,938481061	4,51E-12	5,74E-11
AL590705.1	2,298258739	6,031608486	4,51E-12	5,74E-11
AL031673.1	1,084130793	6,835090067	4,64E-12	5,90E-11
AC092123.2	1,090965841	7,661371097	4,81E-12	6,08E-11
LINC01468	4,314113312	3,550460698	4,90E-12	6,18E-11
AL049830.3	2,86685948	4,386828095	4,93E-12	6,21E-11
AC007298.2	-1,730306972	6,553185771	4,96E-12	6,24E-11
AC010201.1	1,901544552	4,057481404	5,10E-12	6,40E-11
AC018755.4	-1,720207888	5,240975654	5,16E-12	6,46E-11
AC105105.3	-1,217643727	8,142388549	5,43E-12	6,79E-11
AC090164.2	2,436441677	5,648604981	5,52E-12	6,88E-11
AL591895.1	1,040089868	8,789416841	5,64E-12	7,03E-11
KDM4A-AS1	1,045451934	6,737034903	5,66E-12	7,04E-11
STPG3-AS1	1,716677166	7,416354185	6,07E-12	7,53E-11
AC087521.1	-1,536619831	4,640303537	6,08E-12	7,54E-11
AC025254.1	6,813611384	5,368615623	6,21E-12	7,68E-11
AC106820.5	1,951567448	4,556526811	6,22E-12	7,68E-11
AC008870.2	1,045517796	5,454238526	6,36E-12	7,84E-11
GSEC	1,201976956	7,949983212	6,56E-12	8,07E-11
AC022424.1	5,371378225	6,357275184	6,57E-12	8,07E-11
SSTR5-AS1	6,281201043	9,490398455	6,59E-12	8,08E-11
AC020658.4	3,248784035	3,30237594	6,67E-12	8,16E-11
LINC02404	6,526496795	6,593595671	6,86E-12	8,38E-11
AC007319.1	-1,094979606	6,570511039	7,05E-12	8,60E-11
AL118511.2	3,210979407	4,519402907	7,15E-12	8,71E-11
AL357060.1	3,235223613	5,983341748	7,28E-12	8,84E-11
BBOX1-AS1	4,553561607	5,685682605	7,36E-12	8,92E-11
AC003988.1	-2,208211124	3,171544947	7,43E-12	8,99E-11
LINC01607	1,738216185	5,853210994	7,62E-12	9,21E-11
HCG23	-1,613475882	3,522900883	7,89E-12	9,52E-11

AC010333.1	4,148494844	4,267524469	8,28E-12	9,94E-11
LINC01943	1,61762383	6,168350085	8,28E-12	9,94E-11
CYP4A22-AS1	1,782198737	4,384274921	8,34E-12	1,00E-10
AC110799.1	3,234309082	3,191133084	9,16E-12	1,10E-10
LINC02156	-1,883353434	4,381481914	9,33E-12	1,11E-10
LINC01524	4,068004369	4,188261167	9,49E-12	1,13E-10
SPATA3-AS1	2,571552267	4,529936201	9,49E-12	1,13E-10
AC093515.1	4,954907935	3,947662843	9,74E-12	1,15E-10
RMST	3,551865891	5,80422708	1,00E-11	1,19E-10
LINC01608	6,360113481	6,517178167	1,11E-11	1,31E-10
LINC00607	2,377864633	7,468325641	1,11E-11	1,31E-10
SOCS2-AS1	-1,249910394	8,155180847	1,14E-11	1,34E-10
LINC01480	3,390758938	7,522439991	1,14E-11	1,34E-10
AC091182.1	2,124926375	6,079310085	1,15E-11	1,35E-10
AC091588.3	-1,369757187	4,146526228	1,15E-11	1,35E-10
AP001995.2	2,902249668	3,164988437	1,20E-11	1,41E-10
AC105219.1	1,254390799	5,331946689	1,21E-11	1,42E-10
AC025171.4	1,447977777	5,531780591	1,22E-11	1,43E-10
AL391095.2	-1,392847442	9,371058032	1,23E-11	1,43E-10
ZFHX2-AS1	1,012959133	6,353590761	1,24E-11	1,44E-10
LINC01979	-1,738442872	6,327853309	1,24E-11	1,44E-10
AL157778.1	5,530864695	4,773783542	1,26E-11	1,46E-10
AC106771.1	5,335613492	4,436494928	1,28E-11	1,48E-10
AC211476.2	1,679531049	3,819141122	1,29E-11	1,49E-10
AL139286.2	1,784277368	4,167588576	1,32E-11	1,52E-10
PART1	6,936358182	7,778421119	1,32E-11	1,52E-10
AC100803.3	1,899027502	5,391043876	1,35E-11	1,55E-10
RPL34-AS1	-1,136380768	4,457475233	1,37E-11	1,56E-10
AC010333.2	3,904808573	4,271220826	1,37E-11	1,57E-10
AC008549.1	-1,777051388	10,40086206	1,41E-11	1,60E-10
AL589182.1	4,563741407	3,702473114	1,42E-11	1,61E-10
AP000525.1	2,498075146	4,667146684	1,43E-11	1,62E-10
AC115619.1	-1,172190169	12,85900411	1,44E-11	1,63E-10
AC090559.1	-1,308266321	6,118007238	1,51E-11	1,70E-10
AL031665.2	1,136415338	5,13842651	1,52E-11	1,71E-10
AC005387.2	1,721113036	3,824622989	1,56E-11	1,76E-10
AC245595.1	2,232021497	5,158210558	1,63E-11	1,84E-10
AP002360.4	1,589685534	4,877694492	1,75E-11	1,96E-10
AC068987.4	1,784086486	8,726183867	1,89E-11	2,12E-10
AL139130.1	3,456230281	4,432521231	1,90E-11	2,12E-10
AC103740.1	-1,48362268	9,181950171	1,91E-11	2,13E-10
AC069277.1	4,910144932	5,085517329	1,92E-11	2,14E-10
LINC02027	-2,308701761	7,923708188	1,94E-11	2,16E-10
AC010595.1	5,17906803	4,651696406	2,04E-11	2,27E-10
AL137026.2	4,27702764	4,510177692	2,05E-11	2,27E-10
AC122710.1	5,587203265	4,798621306	2,06E-11	2,28E-10
AL031123.2	1,223122824	7,044980627	2,06E-11	2,28E-10
AP002478.1	5,090544659	4,829939418	2,08E-11	2,29E-10
RHPN1-AS1	1,361810592	6,874986862	2,11E-11	2,33E-10
CASC20	5,653179228	5,256709858	2,14E-11	2,36E-10

AL359513.1	1,437123929	5,502206274	2,20E-11	2,42E-10
LINC00491	5,582752693	4,586261253	2,28E-11	2,49E-10
SMIM25	-1,331705589	7,936292456	2,28E-11	2,49E-10
BX649601.1	1,711994141	5,383822345	2,28E-11	2,49E-10
AC011489.1	1,017518314	5,057403126	2,30E-11	2,51E-10
AC069224.1	1,193989975	6,05239722	2,33E-11	2,54E-10
AL031055.1	-1,055009097	5,97294082	2,34E-11	2,54E-10
Z98882.1	1,298975484	6,255915497	2,43E-11	2,63E-10
LINC01108	2,817269182	5,688830872	2,43E-11	2,63E-10
SNHG6	1,180615783	12,8199886	2,46E-11	2,66E-10
CEP83-AS1	1,283925301	4,933846241	2,47E-11	2,67E-10
AC108463.2	1,520662645	4,227400592	2,48E-11	2,67E-10
Z99755.3	2,878985231	5,595006676	2,55E-11	2,74E-10
AL138762.1	1,20156924	5,235206548	2,56E-11	2,75E-10
PLA2G4C-AS1	1,557102856	4,683816595	2,56E-11	2,75E-10
AL353801.3	1,489458609	4,39338076	2,59E-11	2,77E-10
AL109615.3	3,061921045	7,586422876	2,63E-11	2,81E-10
AC092117.1	1,349021769	6,291807578	2,65E-11	2,83E-10
CCDC26	-2,019885886	3,369855708	2,70E-11	2,87E-10
LINC01719	1,467921347	7,430056908	2,76E-11	2,94E-10
AL008729.1	1,218239208	5,934553634	2,84E-11	3,01E-10
AC023302.1	2,383148366	3,447097009	2,84E-11	3,01E-10
AC074138.1	1,764232014	4,1040865	2,87E-11	3,04E-10
AC027801.1	1,253862153	6,537295337	2,96E-11	3,13E-10
AC104809.1	-2,540413451	9,217842466	3,00E-11	3,17E-10
AL121772.3	1,496248797	4,623370224	3,02E-11	3,19E-10
AF279873.3	6,579849504	6,040525735	3,28E-11	3,45E-10
MIR548XHG	6,447964621	5,541417178	3,30E-11	3,46E-10
AL008582.1	1,62921363	4,245397854	3,37E-11	3,53E-10
LINC00683	-2,143107142	4,359998416	3,50E-11	3,66E-10
AL357079.1	1,259906003	4,951162854	3,58E-11	3,73E-10
HM13-AS1	-1,05400144	5,337553221	3,62E-11	3,77E-10
AC113404.1	2,835840976	5,334429401	3,63E-11	3,77E-10
LINC02438	3,316280718	4,395901453	3,70E-11	3,84E-10
AC113383.1	2,98502166	3,863835395	3,75E-11	3,89E-10
LINC02153	-2,547152948	3,659651881	3,78E-11	3,92E-10
HOXC-AS1	5,520493207	4,317997082	4,01E-11	4,14E-10
AC092667.1	2,074425086	5,239055425	4,10E-11	4,22E-10
LINC00106	1,319624458	6,93849855	4,25E-11	4,37E-10
AL512770.1	1,092640278	5,851845878	4,43E-11	4,55E-10
AC112484.2	1,451102943	5,868373362	4,48E-11	4,59E-10
AC108751.4	1,628709868	5,81222948	4,59E-11	4,70E-10
AL355574.1	1,226231736	5,34716167	4,66E-11	4,76E-10
AC234772.2	2,991796618	3,469052977	4,76E-11	4,84E-10
SLC12A5-AS1	2,280575874	5,798188318	4,77E-11	4,84E-10
AC019193.3	-1,407125223	3,406045733	4,77E-11	4,84E-10
AL021328.1	-2,262430621	7,128987537	4,85E-11	4,92E-10
AC099343.2	1,26204676	4,882284208	4,87E-11	4,93E-10
C9orf163	1,236967997	5,545977305	4,90E-11	4,95E-10
AC099568.2	1,294453978	5,527726066	5,24E-11	5,29E-10

AC015802.4	1,141018238	5,286409991	5,27E-11	5,31E-10
LINC00624	2,66243989	7,241936766	5,41E-11	5,42E-10
LINC01197	-1,067079133	7,319168546	5,42E-11	5,43E-10
FAM99A	-1,993015762	11,23664253	5,66E-11	5,65E-10
AC100872.1	2,813839417	4,373789938	6,09E-11	6,05E-10
DLX6-AS1	5,282261477	6,238385295	6,19E-11	6,14E-10
AC239803.1	1,58120682	5,396453624	6,30E-11	6,25E-10
AL513327.3	2,109768678	3,467265633	6,38E-11	6,31E-10
AC097521.2	5,419258604	4,452820614	6,42E-11	6,34E-10
AC012617.1	2,237498996	4,511480533	6,55E-11	6,47E-10
LINC02037	-1,515113891	8,278306775	6,66E-11	6,56E-10
AC036108.2	2,187635118	6,043994321	6,72E-11	6,61E-10
VIPR1-AS1	-1,429511067	4,006818471	6,77E-11	6,65E-10
AC016710.1	6,208699545	5,119087853	6,91E-11	6,78E-10
AP005230.1	3,790655216	4,215187525	7,06E-11	6,90E-10
AP005057.1	3,235926333	5,071302123	7,06E-11	6,90E-10
HYI-AS1	1,235868815	5,266441592	7,09E-11	6,91E-10
AC092171.3	1,081153481	8,145519214	7,23E-11	7,04E-10
AL158063.1	1,442982143	4,206849403	7,30E-11	7,10E-10
LINC01977	2,754612521	5,331676948	7,63E-11	7,41E-10
AC027601.2	1,594033579	4,101348191	7,90E-11	7,65E-10
AC145207.8	2,487220244	5,228234087	7,94E-11	7,67E-10
LINC02159	4,475932642	5,556905084	8,00E-11	7,72E-10
AC112493.1	3,636840932	4,578758897	8,04E-11	7,75E-10
LINC00944	2,628205383	6,709695251	8,32E-11	8,00E-10
AL033527.3	2,619964261	4,016423036	8,35E-11	8,02E-10
HOXA-AS3	3,618987985	4,127342378	8,37E-11	8,03E-10
AC092171.5	1,090262334	7,563624472	8,40E-11	8,05E-10
AC008750.3	2,612404004	4,218314235	8,55E-11	8,18E-10
AC005150.1	7,88520773	6,804886409	8,80E-11	8,41E-10
AC112907.3	1,076695532	5,389195882	8,87E-11	8,46E-10
AC015813.1	1,098657577	9,137439859	9,07E-11	8,63E-10
FP325330.3	3,788431446	3,433730472	9,88E-11	9,39E-10
AC105411.1	2,856872892	6,997352668	1,01E-10	9,57E-10
AC017002.3	1,894955216	4,154352694	1,04E-10	9,83E-10
MGC27382	-1,203979462	6,741374519	1,10E-10	1,04E-09
AC012676.1	1,283319325	6,328506633	1,10E-10	1,04E-09
AC010542.5	1,054456768	5,522486859	1,10E-10	1,04E-09
AC244153.1	-1,07030103	5,5350244	1,15E-10	1,08E-09
AC010615.2	2,353163519	6,35989839	1,16E-10	1,09E-09
RNF157-AS1	2,488018978	6,602198889	1,16E-10	1,09E-09
AC007128.1	4,696910387	4,133117806	1,17E-10	1,09E-09
AC069222.1	1,584857576	4,21111586	1,18E-10	1,10E-09
AC008735.2	1,213748178	6,758394605	1,23E-10	1,15E-09
AL133264.2	-1,642078602	3,173050434	1,27E-10	1,18E-09
LINC01269	3,481817799	4,672230894	1,30E-10	1,20E-09
AC004076.2	1,259773968	5,632187537	1,33E-10	1,24E-09
AC108062.1	1,066233442	7,398192528	1,33E-10	1,24E-09
AC024581.1	3,244544929	3,671502691	1,35E-10	1,25E-09
AC078942.1	-1,901052491	3,4690309	1,36E-10	1,25E-09

AL139220.2	1,834709322	5,268528242	1,40E-10	1,29E-09
MIS18A-AS1	1,47550176	4,09065123	1,43E-10	1,31E-09
AC239803.4	2,452577443	4,655959934	1,47E-10	1,35E-09
LINC01549	3,252091752	7,618247931	1,58E-10	1,45E-09
LINC01842	3,135749445	3,75133821	1,58E-10	1,45E-09
IGF2BP2-AS1	3,203529959	5,067183126	1,59E-10	1,46E-09
AL590652.1	2,330033953	4,291397028	1,64E-10	1,50E-09
AC023590.1	-1,105192071	4,224635561	1,67E-10	1,52E-09
AC089983.1	3,647109268	3,505634933	1,67E-10	1,52E-09
AC008250.2	-1,393687474	4,362353649	1,71E-10	1,55E-09
AC068389.2	2,309050891	3,263370066	1,72E-10	1,56E-09
CLRN1-AS1	-2,060644794	4,799648282	1,74E-10	1,59E-09
AP000526.1	3,285686373	3,323285978	1,82E-10	1,65E-09
AC007099.1	4,785015902	6,708700265	1,84E-10	1,67E-09
AC025171.5	1,39195873	4,898402218	1,85E-10	1,67E-09
AC007611.1	1,065211877	5,869167615	1,85E-10	1,67E-09
AL592211.1	1,845837285	3,934750427	1,85E-10	1,67E-09
AC073611.1	1,040314946	6,024674935	1,85E-10	1,67E-09
AC009275.1	2,24367529	6,776420587	1,87E-10	1,69E-09
AC069208.1	-1,391296165	4,708898819	1,91E-10	1,71E-09
AP003390.1	1,98458585	4,177792863	1,93E-10	1,73E-09
MIR663AHG	6,080212439	5,554171331	1,93E-10	1,73E-09
AC068831.3	1,112070413	4,721520546	1,93E-10	1,73E-09
AC007292.1	1,014561449	6,665082648	1,99E-10	1,78E-09
WDFY3-AS2	-1,068728494	6,997932323	2,02E-10	1,81E-09
Z95331.1	1,018476839	6,002965548	2,12E-10	1,89E-09
LINC00664	2,622714565	5,025053564	2,12E-10	1,89E-09
HNF4A-AS1	-1,413956815	9,878557318	2,15E-10	1,91E-09
AC005224.3	-1,489536051	4,688381681	2,17E-10	1,93E-09
AC013275.1	2,471649926	7,91594036	2,20E-10	1,95E-09
LINC00896	1,942189346	7,447829062	2,27E-10	2,01E-09
AL513211.1	2,095960318	3,985134424	2,28E-10	2,02E-09
AC073529.1	1,276697133	5,013944638	2,46E-10	2,17E-09
LINC01901	4,245166354	3,945135648	2,48E-10	2,18E-09
AC011481.1	1,347706332	4,379207068	2,48E-10	2,18E-09
TSPEAR-AS1	2,021204239	8,065048529	2,52E-10	2,21E-09
AL365226.2	5,506055315	5,245168342	2,52E-10	2,21E-09
LINC01666	3,740752485	4,800072946	2,54E-10	2,22E-09
AC092757.3	1,931014046	4,150422699	2,66E-10	2,32E-09
AL133325.3	3,7232754	3,644196987	2,67E-10	2,33E-09
AC092115.3	3,358033011	4,509326487	2,69E-10	2,34E-09
AC006249.1	-1,142437843	4,187331606	2,75E-10	2,39E-09
LINC01019	6,383541246	5,91245874	2,86E-10	2,48E-09
LINC02362	-1,410073706	10,2354457	2,87E-10	2,48E-09
AC107959.3	2,07553446	5,880746802	2,87E-10	2,48E-09
AC010735.1	2,452579745	3,944411681	2,89E-10	2,50E-09
FAM99B	-1,813063943	8,472194822	2,95E-10	2,55E-09
AC096536.1	-1,099552785	5,336393266	2,97E-10	2,56E-09
AC109588.1	6,173761464	5,321209736	2,97E-10	2,56E-09
LINC01446	4,414969914	6,405784829	2,99E-10	2,57E-09

AL033384.2	2,229024205	3,667336892	3,04E-10	2,62E-09
TLX1NB	3,046848095	3,603441541	3,13E-10	2,69E-09
AC010999.2	1,620344994	3,900146023	3,18E-10	2,72E-09
RNF144A-AS1	2,609339261	6,03173315	3,19E-10	2,73E-09
AC022154.1	1,343734328	4,333624218	3,19E-10	2,73E-09
AL353708.1	1,025626862	5,84046345	3,30E-10	2,82E-09
AC026469.1	-1,485228404	5,644735946	3,36E-10	2,87E-09
BPESC1	3,475408148	3,407520595	3,43E-10	2,92E-09
AL031600.1	1,539301601	4,932475642	3,45E-10	2,93E-09
HOXC-AS2	3,767463426	4,372427547	3,45E-10	2,93E-09
AL512306.2	1,473721183	6,682133889	3,48E-10	2,95E-09
AC005381.1	4,915674865	4,931341487	3,52E-10	2,98E-09
AL928654.2	1,044937673	7,244335353	3,61E-10	3,06E-09
AC012645.4	1,469742935	4,159504006	3,63E-10	3,07E-09
AL021392.1	1,897366232	5,295201455	3,75E-10	3,16E-09
AC010336.2	-1,308925628	6,035914658	3,76E-10	3,17E-09
LRP4-AS1	1,913348142	4,015237166	3,79E-10	3,19E-09
LINC01134	1,141302417	7,468697495	3,87E-10	3,26E-09
AC020765.2	1,051275215	5,817852491	3,95E-10	3,32E-09
AC120498.9	1,640804937	3,809020521	3,97E-10	3,33E-09
AP006222.1	1,695810942	5,243374253	4,02E-10	3,37E-09
FALEC	1,653781753	4,014956545	4,10E-10	3,44E-09
MIR99AHG	-1,044230238	8,853377885	4,17E-10	3,48E-09
BX649632.1	1,350990381	4,38410706	4,18E-10	3,49E-09
LINC00622	1,43068367	5,727766313	4,48E-10	3,73E-09
AL391832.1	2,539307257	5,610319052	4,51E-10	3,75E-09
WFDC21P	2,667997669	8,018531851	4,59E-10	3,82E-09
AL669831.5	1,052673973	5,691120887	4,62E-10	3,83E-09
PP7080	1,255993229	10,58973859	4,71E-10	3,90E-09
COLCA1	1,775616395	8,6456852	4,94E-10	4,09E-09
AC130343.2	-1,16910846	4,38676681	4,96E-10	4,10E-09
AC011632.1	5,472789936	5,733561904	5,07E-10	4,19E-09
LINC01615	2,788915415	4,730658427	5,22E-10	4,31E-09
AC010931.2	3,033828243	4,177035657	5,23E-10	4,31E-09
ARHGEF26-AS1	-1,090585454	6,555899057	5,45E-10	4,48E-09
DEPDC1-AS1	3,145441051	3,351306113	5,70E-10	4,67E-09
AC034213.1	3,802899085	5,321735067	5,72E-10	4,69E-09
AL445434.1	5,383459661	4,932880206	5,73E-10	4,69E-09
AP003181.1	3,780531671	3,298420018	5,79E-10	4,73E-09
AC013400.1	1,820606628	3,546964467	5,82E-10	4,75E-09
LINC00173	1,89466365	4,759159178	5,83E-10	4,75E-09
MNX1-AS1	6,321612744	6,047908007	6,03E-10	4,91E-09
LINC00485	2,249765015	3,695482605	6,12E-10	4,97E-09
AL645608.1	-1,699453693	6,756739699	6,14E-10	4,98E-09
AC090709.1	3,650438422	3,238740549	6,25E-10	5,06E-09
AC020928.1	2,789439582	4,955589927	6,28E-10	5,09E-09
LINC01630	5,004984284	5,16267573	6,32E-10	5,11E-09
AL596223.2	2,59429663	4,061216117	6,47E-10	5,23E-09
AC011933.3	2,237345464	3,291217943	6,63E-10	5,35E-09
FAM87A	3,02329836	4,946907085	6,68E-10	5,39E-09

AC090510.2	1,195609649	4,042762135	6,96E-10	5,60E-09
AC020594.1	1,290492697	4,653989241	7,15E-10	5,74E-09
AL109976.1	2,069356477	5,346614999	7,26E-10	5,82E-09
AC018553.1	2,560099707	6,860481503	7,33E-10	5,85E-09
MCCC1-AS1	1,313933754	5,022426996	7,37E-10	5,88E-09
AP006285.2	-1,750105683	5,366062108	7,44E-10	5,92E-09
AL133370.1	4,418052876	4,919292763	7,57E-10	6,02E-09
AC093788.1	1,037093468	5,327133615	7,58E-10	6,02E-09
LINC00885	-1,960721197	7,154599748	7,95E-10	6,29E-09
AC009121.2	1,793774188	4,240115704	8,31E-10	6,58E-09
AC022296.3	2,309934611	3,600863872	8,34E-10	6,59E-09
TMEM132D-AS1	7,310292144	6,721615214	8,67E-10	6,84E-09
AL670729.1	2,441735228	4,02182938	8,68E-10	6,84E-09
AC096637.2	2,354207184	3,609996008	9,32E-10	7,31E-09
AC112206.2	-1,73129692	9,567067446	9,60E-10	7,53E-09
AC073655.2	1,034232103	5,397312889	9,79E-10	7,67E-09
AC016722.3	1,539835945	4,528136764	1,03E-09	8,03E-09
AC005618.1	1,795325048	5,054143489	1,04E-09	8,08E-09
LINC01238	1,548700638	5,003771654	1,04E-09	8,08E-09
LINC01431	1,094121944	5,884469936	1,06E-09	8,28E-09
SLC7A11-AS1	3,615934629	4,411321748	1,08E-09	8,43E-09
AC092954.1	3,792739702	3,299999365	1,13E-09	8,77E-09
BAALC-AS1	1,487357792	6,460993409	1,15E-09	8,93E-09
MAPT-IT1	2,423597334	4,286476392	1,16E-09	9,00E-09
DGCR9	1,960860386	6,069666855	1,16E-09	9,00E-09
LINC01929	3,20400063	5,48341072	1,17E-09	9,03E-09
AC026250.1	1,384421669	5,860639031	1,17E-09	9,06E-09
AP001107.5	-1,349527709	4,083251241	1,24E-09	9,54E-09
AL357033.2	-2,129435818	3,989636277	1,26E-09	9,70E-09
LINC01714	-1,491821177	5,212349356	1,29E-09	9,92E-09
AC091133.3	3,488668388	4,175606981	1,29E-09	9,92E-09
ATP6V0E2-AS1	1,185327576	7,046115344	1,30E-09	9,98E-09
ZNF385D-AS1	5,346896068	4,215013172	1,31E-09	1,00E-08
AC129507.3	-1,067736421	5,990659349	1,32E-09	1,01E-08
AC242426.3	1,004246014	8,773236098	1,36E-09	1,03E-08
AC009121.1	2,446651019	3,427879059	1,36E-09	1,03E-08
LINC02293	4,041088149	3,584444298	1,39E-09	1,06E-08
AF196972.1	1,177662772	4,956616784	1,41E-09	1,07E-08
AC092625.1	4,807627506	3,851224337	1,42E-09	1,08E-08
AP002360.3	2,105856624	3,317717929	1,46E-09	1,11E-08
AC099518.2	1,975084723	3,641463199	1,46E-09	1,11E-08
AC011611.3	-1,649143977	3,474036944	1,47E-09	1,12E-08
AC092683.1	1,693304243	4,399185094	1,48E-09	1,12E-08
AC020907.1	1,893215381	7,036364872	1,53E-09	1,15E-08
AC005858.1	5,057119685	6,480640541	1,59E-09	1,20E-08
AL450998.2	2,245590005	3,825415803	1,65E-09	1,24E-08
LINC00346	1,622010637	8,388927697	1,67E-09	1,26E-08
AP000842.3	2,90899504	3,162647271	1,68E-09	1,26E-08
AC106820.2	1,882256197	4,023381802	1,69E-09	1,27E-08
AC114811.2	3,518827927	5,27522946	1,69E-09	1,27E-08

AC104118.1	1,05171153	5,846012429	1,70E-09	1,27E-08
AL133467.4	4,469933804	4,155256977	1,70E-09	1,27E-08
PCAT18	-1,623877385	4,255501258	1,70E-09	1,27E-08
AP001432.1	1,61432966	4,195605861	1,71E-09	1,27E-08
LINC01341	1,271995247	8,079317919	1,82E-09	1,35E-08
AC011603.2	1,750982859	4,717651818	1,85E-09	1,38E-08
AC013451.2	2,96862496	3,912904353	1,94E-09	1,44E-08
AC108002.1	1,466776538	5,736479368	1,97E-09	1,46E-08
AC004923.4	1,315760717	4,582517882	1,98E-09	1,47E-08
B3GALT5-AS1	-2,325739721	4,235579682	2,00E-09	1,48E-08
AC079907.1	1,412083363	4,185430417	2,04E-09	1,50E-08
AP001830.1	1,038786616	7,161241171	2,04E-09	1,50E-08
AP003716.1	-1,532417087	9,946747839	2,04E-09	1,50E-08
AC114485.1	5,835895763	4,568284259	2,08E-09	1,53E-08
FAM212B-AS1	1,956378578	3,909870198	2,10E-09	1,54E-08
AP003174.1	1,949186121	5,046359137	2,13E-09	1,56E-08
LINC00648	5,120139636	6,168612461	2,15E-09	1,57E-08
AC005722.3	4,741679687	4,1785367	2,16E-09	1,58E-08
AC139769.2	4,492186055	5,623075562	2,22E-09	1,62E-08
AL360219.1	-1,063128397	5,146211259	2,25E-09	1,63E-08
AC019257.1	-1,825293734	5,054718291	2,25E-09	1,63E-08
NALT1	1,161281812	6,833931947	2,26E-09	1,65E-08
AC108136.1	2,612422339	5,31499406	2,29E-09	1,66E-08
LINC00941	2,518562084	5,693173893	2,29E-09	1,66E-08
AC073263.1	2,124044996	4,487284517	2,33E-09	1,69E-08
AC010997.5	1,998723735	3,645298511	2,41E-09	1,74E-08
LINC00862	1,602710453	6,163818013	2,54E-09	1,83E-08
LINC01747	1,891631714	3,408072413	2,56E-09	1,85E-08
AL161729.4	1,92869256	3,802821814	2,57E-09	1,86E-08
LINC01436	3,38634708	7,63217779	2,62E-09	1,89E-08
AC245060.5	1,082929503	6,480994532	2,62E-09	1,89E-08
AC010148.1	1,58608274	5,440457602	2,63E-09	1,89E-08
FAM230C	5,869539082	5,082142076	2,68E-09	1,92E-08
ADGRD1-AS1	6,063586588	5,343766521	2,68E-09	1,92E-08
AC006483.2	2,104226146	3,800307473	2,68E-09	1,92E-08
AL121721.1	4,555372714	4,156674301	2,71E-09	1,94E-08
LINC01117	2,705182178	3,804926584	2,74E-09	1,96E-08
AC012629.2	-1,262938629	3,623609009	2,80E-09	2,00E-08
AC234582.1	1,059685697	5,647397921	2,82E-09	2,01E-08
AC097634.1	1,579281644	4,331626477	2,92E-09	2,07E-08
LINC01021	2,217595291	7,743150422	2,93E-09	2,08E-08
Z84485.1	1,211906994	6,036116025	2,94E-09	2,08E-08
AL662844.3	1,316311841	4,239612432	3,04E-09	2,15E-08
AP001065.2	-1,202007079	8,237593447	3,04E-09	2,15E-08
AC008991.2	4,594979037	3,719333759	3,10E-09	2,18E-08
AC080013.3	1,430474849	4,157765992	3,13E-09	2,20E-08
AC114489.1	4,463652806	3,782565125	3,22E-09	2,27E-08
AC021079.1	4,823918251	3,85979129	3,31E-09	2,33E-08
LINC01297	4,291368289	3,909016308	3,32E-09	2,33E-08
LINC00383	4,673072904	4,145588503	3,36E-09	2,36E-08

AL117355.1	4,990013227	5,0058947	3,37E-09	2,36E-08
AC110285.1	1,778273945	4,328752086	3,41E-09	2,39E-08
AL391244.2	1,791112234	4,475182486	3,51E-09	2,45E-08
CASC8	3,341846699	5,011786036	3,61E-09	2,52E-08
AC020907.4	1,549980843	4,701183684	3,79E-09	2,64E-08
LINC02327	4,425879576	4,679898078	3,82E-09	2,66E-08
AL513217.1	2,256857458	3,866271274	4,08E-09	2,83E-08
AL035252.3	1,513836063	6,406210256	4,13E-09	2,86E-08
AC108134.2	1,203223617	5,910987748	4,17E-09	2,89E-08
AC245100.1	2,130320301	3,584629606	4,22E-09	2,92E-08
LINC01091	1,780093732	6,354642918	4,38E-09	3,03E-08
AL121583.1	1,22315553	4,644948557	4,60E-09	3,18E-08
LINC02413	5,09279684	5,749607102	4,66E-09	3,21E-08
AC124067.4	2,908140605	6,956505575	4,67E-09	3,22E-08
LINC01702	-1,579702422	10,1031441	4,72E-09	3,25E-08
AC004870.2	6,065303275	4,9725644	4,79E-09	3,29E-08
AL158212.2	1,390706027	3,893234325	4,90E-09	3,36E-08
CR381653.1	1,184138361	5,583649593	4,91E-09	3,36E-08
AP000561.1	3,303890577	3,321909272	4,93E-09	3,37E-08
AC125603.2	2,92128179	5,587421495	4,93E-09	3,37E-08
AC026254.5	1,47596369	4,363590207	4,94E-09	3,37E-08
AC099552.1	6,497715789	5,09540598	4,94E-09	3,37E-08
LINC01730	1,741826789	4,586858668	5,02E-09	3,42E-08
C3orf67-AS1	2,524777332	3,91980266	5,04E-09	3,43E-08
LINC02188	3,5197435	6,385606907	5,06E-09	3,44E-08
AC016717.2	5,908595897	6,444066838	5,13E-09	3,48E-08
AL109811.1	1,209012537	4,261859816	5,15E-09	3,49E-08
AC090921.1	4,623372012	5,816883789	5,21E-09	3,53E-08
AC125603.1	4,014410093	4,20807332	5,22E-09	3,54E-08
AL161669.3	1,164134036	7,144948051	5,48E-09	3,71E-08
AC020915.3	1,317170608	4,53027816	5,49E-09	3,71E-08
LINC02043	2,166907001	3,977179461	5,51E-09	3,72E-08
AL590079.1	-1,713055338	4,908041285	5,64E-09	3,81E-08
AC084864.1	3,074533231	3,303769964	5,72E-09	3,86E-08
LINC02082	3,860307614	4,054266861	5,83E-09	3,92E-08
AC006065.4	5,785768932	5,930227461	5,87E-09	3,95E-08
AC133644.2	2,314845772	5,013077663	5,93E-09	3,98E-08
C1orf220	1,135321294	6,591408882	5,94E-09	3,99E-08
AL138974.1	4,059006612	3,933025608	6,37E-09	4,27E-08
UPK1A-AS1	3,136876834	5,21065362	6,62E-09	4,43E-08
SATB2-AS1	1,585620912	5,224038287	6,82E-09	4,56E-08
AL359851.1	2,484498386	3,211442609	7,03E-09	4,69E-08
C10orf91	4,455264614	6,160964046	7,10E-09	4,73E-08
MIR9-3HG	2,730029116	7,95976727	7,12E-09	4,74E-08
AL359541.1	-1,129196671	4,129980745	7,19E-09	4,78E-08
AC104088.1	3,841299217	4,107692308	7,36E-09	4,89E-08
LINC01711	3,638219489	3,605035696	7,56E-09	5,02E-08
AC005165.1	3,476592378	6,21377478	7,59E-09	5,04E-08
AC007687.1	2,281599164	3,254832067	7,70E-09	5,10E-08
AL139275.2	4,907814857	3,91153561	7,91E-09	5,23E-08

FAM85B	-1,471228573	3,798091421	7,92E-09	5,24E-08
AC010969.1	-1,925533549	6,095428553	8,00E-09	5,28E-08
AL139289.1	1,091997937	5,129415584	8,08E-09	5,33E-08
AC010247.2	2,590398912	7,477925737	8,15E-09	5,37E-08
AC141928.1	2,470950493	6,387215608	8,22E-09	5,41E-08
LINC00399	-1,509113899	4,171044537	8,47E-09	5,56E-08
LINC01956	4,681118288	5,40271853	8,67E-09	5,68E-08
AP003900.1	4,613275155	3,743884858	8,85E-09	5,80E-08
AC079315.1	1,299200376	6,966317827	9,21E-09	6,03E-08
AC105053.1	-1,621685491	3,268442606	9,28E-09	6,06E-08
AP000350.5	1,307458179	4,307102999	9,39E-09	6,13E-08
AL356512.1	1,086862661	5,282484753	9,45E-09	6,16E-08
AC021092.1	1,813934205	4,367551183	9,60E-09	6,25E-08
AP000997.2	2,668604561	4,094876707	9,77E-09	6,35E-08
AC092809.4	1,165771448	4,771776456	1,02E-08	6,61E-08
AC104534.1	1,914989095	5,965042093	1,02E-08	6,62E-08
AC092378.1	-1,341065341	3,738122387	1,02E-08	6,64E-08
AC108752.1	5,989651426	5,148741905	1,03E-08	6,70E-08
DSCR9	1,356120613	4,037517073	1,04E-08	6,70E-08
AL445647.1	3,597056357	4,305150287	1,04E-08	6,72E-08
UCKL1-AS1	1,251166103	5,457047365	1,07E-08	6,93E-08
AC022306.3	1,191604991	4,748609453	1,08E-08	6,97E-08
AC007405.1	1,082999024	5,604315977	1,08E-08	6,97E-08
TRPC7-AS1	3,518130558	3,775574989	1,08E-08	6,97E-08
AC097461.1	1,053989403	6,218151564	1,09E-08	7,01E-08
AC006557.1	2,073069244	3,342825132	1,10E-08	7,07E-08
AP001453.2	1,262993141	6,638397776	1,12E-08	7,20E-08
PTPRVP	1,127371271	5,007451864	1,16E-08	7,43E-08
AC010132.4	1,18885684	4,063145724	1,18E-08	7,55E-08
TTC39A-AS1	2,245217535	4,67032858	1,20E-08	7,62E-08
EXTL3-AS1	1,068368594	5,655373611	1,20E-08	7,62E-08
AC118754.1	-1,245040547	4,795042301	1,20E-08	7,66E-08
AP006284.1	1,163766226	7,857236816	1,23E-08	7,79E-08
LINC00519	2,930042739	3,802400974	1,23E-08	7,84E-08
AC068675.1	2,545937039	3,495080466	1,26E-08	8,02E-08
FGF14-IT1	-1,875908403	3,23884285	1,27E-08	8,04E-08
AC006449.5	1,093287389	5,553275705	1,28E-08	8,12E-08
AC011466.3	1,699680352	3,458357721	1,29E-08	8,15E-08
AC103808.3	3,585104117	3,675764779	1,33E-08	8,43E-08
AC090409.1	1,358739229	4,677622679	1,40E-08	8,87E-08
AC005725.1	3,125922354	3,151717998	1,41E-08	8,92E-08
AC010643.1	2,137193161	7,702462439	1,42E-08	8,92E-08
TDRG1	4,653337559	3,75994551	1,45E-08	9,14E-08
PKP4-AS1	1,332493208	4,356968751	1,46E-08	9,21E-08
AC139887.1	1,174855572	4,847324089	1,50E-08	9,41E-08
LINC01509	3,220666672	3,192221361	1,50E-08	9,41E-08
LINC01725	-1,027250339	6,673230959	1,51E-08	9,43E-08
AC124067.2	2,071802091	4,4016987	1,52E-08	9,50E-08
SOX9-AS1	1,666733836	9,926265517	1,55E-08	9,67E-08
LINC01315	1,256597801	6,780842442	1,57E-08	9,82E-08

AC037487.1	1,516872489	3,946554998	1,59E-08	9,92E-08
AC015922.3	-1,222344823	5,156131922	1,59E-08	9,92E-08
AC016590.1	1,981168147	3,910425643	1,60E-08	9,95E-08
SLC12A9-AS1	1,540152397	4,923826629	1,65E-08	1,03E-07
AC002378.1	3,044947513	3,31707369	1,66E-08	1,03E-07
MIR325HG	2,585292194	5,962127707	1,71E-08	1,06E-07
AC027682.4	1,406919653	3,891153481	1,77E-08	1,10E-07
KCNQ1OT1	1,077468168	8,322547221	1,78E-08	1,10E-07
AC079760.2	2,985060375	4,528520754	1,79E-08	1,11E-07
AC006504.8	1,015534461	5,970324279	1,79E-08	1,11E-07
AL359710.1	-1,090418791	3,766544998	1,84E-08	1,14E-07
AL080317.2	1,074915531	5,792528737	1,87E-08	1,15E-07
AC010973.1	1,693628045	3,53550743	1,90E-08	1,17E-07
U52111.1	1,491064806	4,195703716	1,90E-08	1,17E-07
AP002761.4	1,312421172	8,340735994	1,91E-08	1,18E-07
AC008060.1	5,23705597	4,47720432	1,96E-08	1,21E-07
TYMSOS	1,132514906	8,534155604	1,97E-08	1,21E-07
AC002091.1	-1,169432442	4,178620856	1,98E-08	1,21E-07
AL049795.1	1,34533188	3,995571509	1,99E-08	1,22E-07
AC007406.2	2,183318764	6,352869995	2,00E-08	1,23E-07
AL354704.1	4,372081725	3,603415426	2,07E-08	1,27E-07
AL442128.2	1,227209121	4,349709276	2,12E-08	1,30E-07
LINC02058	4,528044205	3,679063442	2,12E-08	1,30E-07
LINC00114	2,803424377	4,480934146	2,14E-08	1,31E-07
LINC01151	2,07659304	7,79018566	2,20E-08	1,34E-07
AC106038.1	1,720440998	3,807756942	2,21E-08	1,35E-07
AC120498.4	1,141406607	7,485160877	2,21E-08	1,35E-07
ELFN1-AS1	3,327159045	6,723070243	2,22E-08	1,35E-07
AP001767.3	1,318233861	4,533356547	2,31E-08	1,41E-07
AC090772.3	1,54342909	5,700069613	2,32E-08	1,41E-07
LINC01697	4,658524549	6,119388256	2,33E-08	1,41E-07
AC011773.4	2,017112336	3,485576921	2,37E-08	1,44E-07
AL031709.1	1,356289563	3,967356901	2,38E-08	1,44E-07
LINC01694	2,738284252	6,370622008	2,39E-08	1,45E-07
LINC01792	4,092601976	4,1705298	2,42E-08	1,47E-07
AL163952.1	2,9291824	4,795096763	2,44E-08	1,47E-07
AC099684.1	-1,231322686	7,037184377	2,46E-08	1,49E-07
AC092296.3	-1,18767545	4,025549515	2,48E-08	1,50E-07
AC025016.1	4,681294993	4,443567868	2,49E-08	1,50E-07
AC099792.1	2,970613625	4,244410573	2,50E-08	1,50E-07
AC087627.1	2,084595906	3,580800147	2,52E-08	1,52E-07
DDX39B-AS1	1,329319196	4,224230607	2,57E-08	1,55E-07
AL139246.3	1,303805886	5,119930437	2,61E-08	1,57E-07
AL118505.1	2,39601909	5,064091834	2,62E-08	1,57E-07
LINC01625	-1,702110368	6,152181462	2,62E-08	1,57E-07
AC137630.3	1,367016869	4,569006664	2,63E-08	1,58E-07
AL022324.3	3,05176475	3,318889729	2,67E-08	1,60E-07
AL008721.2	1,121139246	6,080653271	2,69E-08	1,61E-07
CASC15	1,797905686	7,3091468	2,73E-08	1,63E-07
AC121338.2	1,503241741	6,20887147	2,83E-08	1,69E-07

AC131009.1	1,191001341	5,004978653	2,84E-08	1,69E-07
PLCE1-AS1	3,333693626	3,961040761	2,92E-08	1,73E-07
LINC-ROR	3,456044061	4,503865447	2,94E-08	1,75E-07
TBX2-AS1	1,381283874	6,911955013	2,95E-08	1,75E-07
LINC02267	4,831560814	4,449158437	2,96E-08	1,76E-07
AC010327.4	1,022556684	6,125186153	2,98E-08	1,76E-07
FP700125.1	-1,309835895	11,1773062	2,98E-08	1,76E-07
AC008060.4	5,778286935	4,504046914	3,00E-08	1,77E-07
AC139491.2	1,845630767	7,716606124	3,00E-08	1,77E-07
AL591845.1	1,126014275	6,639904092	3,05E-08	1,80E-07
AL390067.1	1,299850382	3,78417435	3,06E-08	1,81E-07
AL451069.3	4,029415061	4,943423579	3,09E-08	1,82E-07
AC145423.2	1,45923776	4,299174707	3,15E-08	1,85E-07
AC006946.2	3,236363092	4,316145229	3,15E-08	1,85E-07
AC087742.2	1,554292139	3,861851935	3,15E-08	1,85E-07
AC074135.1	3,131544701	4,293287672	3,20E-08	1,88E-07
AC010307.4	3,441157374	3,290853479	3,25E-08	1,91E-07
SACS-AS1	6,435526779	5,869835552	3,29E-08	1,92E-07
AC127496.1	1,283972444	4,35334152	3,29E-08	1,92E-07
OVAAL	4,792902393	4,653640598	3,30E-08	1,92E-07
AL162582.1	3,231294389	7,026161616	3,36E-08	1,96E-07
TCL6	2,615797268	5,76608887	3,38E-08	1,97E-07
AL139042.1	4,756834553	4,037063246	3,38E-08	1,97E-07
LINC01876	1,803335096	5,505825097	3,38E-08	1,97E-07
AC243836.1	-1,004590524	6,447289797	3,41E-08	1,98E-07
LINC00702	1,251143454	6,499264439	3,42E-08	1,98E-07
AC025575.2	3,118995277	5,08767859	3,42E-08	1,99E-07
LINC02253	4,54798555	5,214332202	3,46E-08	2,00E-07
ADAMTS9-AS2	-1,118651765	5,168447456	3,46E-08	2,01E-07
AL139289.2	1,04381438	5,614337891	3,51E-08	2,03E-07
AL358473.1	2,389547475	3,541987636	3,52E-08	2,04E-07
AC093249.2	1,474066469	3,840139589	3,54E-08	2,04E-07
Z97192.2	2,343394087	5,933175179	3,55E-08	2,05E-07
AC062015.1	6,162979514	5,028041828	3,59E-08	2,07E-07
AL954650.1	5,510895725	4,588717331	3,59E-08	2,07E-07
AL359881.1	3,003665317	4,261904129	3,63E-08	2,08E-07
AC009093.5	-1,506360296	5,827883173	3,68E-08	2,11E-07
AC011352.1	3,136184549	3,360566152	3,72E-08	2,13E-07
AL161891.1	1,096563324	6,593544964	3,79E-08	2,17E-07
PSORS1C3	1,75437553	6,141692413	3,82E-08	2,18E-07
AL513218.1	1,124839942	4,192708181	3,86E-08	2,20E-07
AC010463.3	1,299727806	3,885161515	3,86E-08	2,20E-07
LINC01507	-2,411644607	3,492198819	3,87E-08	2,21E-07
AC011815.1	1,118907174	6,408559951	3,90E-08	2,22E-07
AL354707.1	-1,117300294	9,436557773	3,98E-08	2,26E-07
AC068580.1	1,284573598	5,084428816	3,98E-08	2,26E-07
AC007785.3	1,664048129	3,368158739	4,10E-08	2,33E-07
DLGAP1-AS2	1,005801256	7,407894504	4,14E-08	2,35E-07
AC116914.2	1,017107266	4,528656022	4,18E-08	2,37E-07
AC068620.3	1,04342755	4,365092804	4,29E-08	2,43E-07

AL110115.2	1,436419565	3,626168505	4,32E-08	2,44E-07
AL365361.1	-1,167099381	7,000190997	4,42E-08	2,49E-07
ADAMTS9-AS1	-1,104328312	5,683538694	4,53E-08	2,55E-07
AC097478.1	3,420922186	6,115442118	4,54E-08	2,55E-07
LINC02109	3,684423766	4,960462646	4,57E-08	2,57E-07
AC004832.5	-1,029286466	6,34131161	4,73E-08	2,65E-07
LINC01637	1,203127627	6,175050419	4,76E-08	2,67E-07
AL133467.1	-1,068263162	5,872908282	4,83E-08	2,71E-07
LINC01605	3,155932478	4,59380537	4,85E-08	2,71E-07
CCDC13-AS1	2,087574574	6,058956456	5,03E-08	2,80E-07
LINC01731	3,792917333	3,601531378	5,05E-08	2,81E-07
AL121790.1	-1,422497927	3,660860798	5,10E-08	2,84E-07
AC002384.1	4,433144396	4,3213673	5,19E-08	2,88E-07
AL031705.1	1,608949921	3,465082068	5,21E-08	2,90E-07
AL109754.1	2,798902809	4,091358926	5,23E-08	2,90E-07
FLJ36000	4,666301859	3,765884744	5,24E-08	2,91E-07
AC025171.3	1,676630607	3,716526629	5,33E-08	2,95E-07
LINC00308	3,162156934	3,049323017	5,55E-08	3,07E-07
AC008109.1	2,919732342	6,400998142	5,79E-08	3,20E-07
LINC00488	3,456498744	5,798358306	6,03E-08	3,33E-07
DSCR4-IT1	4,897508596	3,910863682	6,11E-08	3,37E-07
FAM83C-AS1	1,337959546	4,156723614	6,15E-08	3,39E-07
AC113145.1	5,442995182	4,260803035	6,20E-08	3,41E-07
AGAP1-IT1	-1,314451036	7,036232718	6,21E-08	3,41E-07
LINC00244	1,616846498	3,586033497	6,49E-08	3,56E-07
BX322234.2	3,248559576	3,478294642	6,52E-08	3,57E-07
AC034102.5	1,73741523	3,338386772	6,61E-08	3,61E-07
MIR217HG	3,534461308	5,203167121	6,71E-08	3,66E-07
BHLHE40-AS1	1,652308627	7,145528536	6,78E-08	3,70E-07
AL158211.3	2,179693367	3,166510625	6,80E-08	3,71E-07
SAMMSON	3,545319274	3,482975555	6,83E-08	3,72E-07
AC083809.1	4,042950555	7,452703865	6,84E-08	3,72E-07
AC016575.1	1,493187859	3,892011217	6,94E-08	3,77E-07
AL450306.1	1,413396214	4,520876382	7,15E-08	3,89E-07
LINC00645	3,797229538	3,459597784	7,20E-08	3,90E-07
AL117350.1	1,470061263	3,719253982	7,30E-08	3,95E-07
AC020934.1	2,792258288	3,436444519	7,42E-08	4,01E-07
AL161645.1	-1,46496811	6,695940622	7,78E-08	4,20E-07
AC068189.1	2,13321238	3,505742369	7,90E-08	4,26E-07
AC012640.1	2,342993266	3,832680203	8,01E-08	4,32E-07
LINC02050	3,787901755	3,458622028	8,21E-08	4,42E-07
AL160408.4	4,758439096	3,810372112	8,25E-08	4,44E-07
LINC00689	3,377012012	6,149221896	8,33E-08	4,47E-07
AL161772.1	2,174900977	5,102183246	8,48E-08	4,55E-07
AL445488.1	1,914562211	3,409581562	8,51E-08	4,56E-07
HCG20	1,830801013	4,973203977	8,69E-08	4,65E-07
LINC01139	3,596419998	7,17695469	8,72E-08	4,66E-07
LINC01675	2,334369336	4,280408862	8,87E-08	4,73E-07
TM4SF1-AS1	1,384206646	5,32698915	9,12E-08	4,86E-07
LINC02259	-1,041410424	4,561926565	9,17E-08	4,88E-07

LINC01192	3,417705139	3,724156965	9,37E-08	4,98E-07
LINC00316	3,004733713	3,517851603	9,38E-08	4,99E-07
AL117335.1	1,413507024	5,786846603	9,73E-08	5,16E-07
AC025580.3	1,330653373	4,688902523	9,79E-08	5,19E-07
AC061975.6	5,154264019	5,832134719	9,98E-08	5,27E-07
AL355601.1	3,423032226	3,572581028	9,98E-08	5,27E-07
LINC00879	5,600797971	4,96705943	1,01E-07	5,33E-07
PRR34-AS1	1,108236423	8,93979052	1,01E-07	5,33E-07
AC092747.1	-1,585214338	3,151138845	1,01E-07	5,33E-07
AC025279.1	-1,052838352	5,657290231	1,02E-07	5,35E-07
AC010624.2	4,18480169	4,569321794	1,02E-07	5,37E-07
AC010536.1	1,008921428	5,350321266	1,06E-07	5,58E-07
AC096577.1	-2,753857694	4,087964641	1,07E-07	5,61E-07
AC090826.2	1,674557362	4,588692012	1,08E-07	5,66E-07
AC084125.4	1,100885787	5,141375858	1,08E-07	5,66E-07
AC007998.3	1,288041344	4,974892688	1,10E-07	5,74E-07
AL445483.1	2,185432321	5,483269563	1,11E-07	5,78E-07
LINC02055	3,200352939	6,91884395	1,12E-07	5,87E-07
AC018467.1	-1,161602252	8,135361983	1,14E-07	5,96E-07
AL139041.1	1,398593139	3,532747244	1,17E-07	6,10E-07
AC092490.1	2,977784808	7,72108158	1,18E-07	6,17E-07
AC009271.1	3,934910347	4,215501398	1,19E-07	6,18E-07
AL136379.1	1,991911856	3,285177301	1,20E-07	6,23E-07
AC007663.3	1,132591707	4,707568135	1,20E-07	6,26E-07
AP001107.4	1,285069011	4,066275641	1,21E-07	6,28E-07
AC024941.2	1,966311027	3,834401843	1,21E-07	6,29E-07
AL354928.1	1,265997815	3,945462285	1,24E-07	6,40E-07
AL160290.2	2,801044373	3,353421077	1,26E-07	6,53E-07
AC020922.4	2,661344091	3,075808544	1,28E-07	6,62E-07
AL133467.2	3,663932858	4,12339067	1,28E-07	6,63E-07
AC099791.2	1,825510046	3,498103888	1,30E-07	6,73E-07
AL583810.1	1,119695833	4,318826731	1,33E-07	6,84E-07
LINC00501	2,793135971	4,176658379	1,40E-07	7,24E-07
AC002351.1	3,685092935	3,844128665	1,41E-07	7,24E-07
LINC00856	3,202632961	4,1513021	1,41E-07	7,24E-07
AC011944.1	2,396810044	4,547318019	1,44E-07	7,42E-07
PTPRG-AS1	1,568059893	5,281955137	1,47E-07	7,56E-07
AC026356.2	1,235117598	4,519510534	1,49E-07	7,63E-07
PKIA-AS1	3,573988499	3,999615451	1,51E-07	7,73E-07
CASC22	3,072940682	4,699795904	1,55E-07	7,96E-07
AP000472.1	-1,506753503	3,551102704	1,58E-07	8,09E-07
AL354760.1	1,075905002	4,524470672	1,61E-07	8,24E-07
AC026368.1	1,857760642	4,44091249	1,61E-07	8,24E-07
AL137230.1	1,247025036	5,493072589	1,63E-07	8,29E-07
AL354872.2	-1,145120944	9,587370438	1,68E-07	8,53E-07
AC016405.3	1,260785649	6,664613844	1,70E-07	8,65E-07
LINC01018	-1,576882222	12,86688728	1,70E-07	8,65E-07
AC009292.1	2,507493711	3,428421019	1,70E-07	8,65E-07
LINC01511	4,626689581	4,237771715	1,70E-07	8,65E-07
AP001628.1	1,423383825	3,653780711	1,71E-07	8,68E-07

AC008443.3	3,268225209	3,513511265	1,72E-07	8,73E-07
AC011461.1	1,191255571	4,120124841	1,73E-07	8,74E-07
AL513534.1	1,053330542	7,116232048	1,73E-07	8,76E-07
AL355803.1	1,41748901	4,508747172	1,75E-07	8,87E-07
FP236383.3	-3,193481424	4,016005432	1,77E-07	8,93E-07
AP000997.1	2,132327971	3,841607685	1,77E-07	8,93E-07
AC022031.2	4,325012583	4,056278024	1,77E-07	8,94E-07
AC127024.4	1,100918096	4,09022084	1,78E-07	8,95E-07
AC004253.1	1,031193688	4,791577194	1,79E-07	9,01E-07
LINC02119	5,103605913	6,254717183	1,80E-07	9,03E-07
IGFL2-AS1	4,063430079	4,742196816	1,80E-07	9,03E-07
AL353148.1	-1,676265311	3,336205426	1,82E-07	9,16E-07
LINC00494	3,241666666	6,829549342	1,84E-07	9,23E-07
AP000977.1	-1,117848324	3,775853809	1,87E-07	9,35E-07
DLX2-AS1	3,637074346	3,362512365	1,87E-07	9,36E-07
AL512328.1	2,217241781	3,21114856	1,91E-07	9,54E-07
AC106881.1	-1,120697209	4,322949031	1,96E-07	9,78E-07
AL353807.2	1,385894579	3,656261095	1,97E-07	9,81E-07
AC134312.6	-1,499611626	3,587272237	1,98E-07	9,86E-07
AC087741.2	1,062454785	5,05112984	1,99E-07	9,90E-07
AC003985.2	6,299307097	6,104961972	2,05E-07	1,02E-06
LINC01474	2,099857315	7,748062882	2,05E-07	1,02E-06
AC078850.1	2,107741455	3,909394522	2,09E-07	1,04E-06
AC046158.1	-1,380706944	3,946679332	2,12E-07	1,05E-06
ZNF32-AS2	1,019896295	5,201360452	2,16E-07	1,07E-06
AC104667.1	1,583987654	4,410568614	2,17E-07	1,07E-06
AC040970.1	1,771158689	6,075666127	2,18E-07	1,08E-06
AL645608.9	1,920968139	5,136589192	2,21E-07	1,09E-06
AL355102.4	1,939986239	7,736864182	2,23E-07	1,10E-06
AC063977.6	-1,221663528	3,913927015	2,27E-07	1,12E-06
CTB-178M22.2	1,644375875	4,338360428	2,29E-07	1,12E-06
AL591501.1	4,243742589	3,528082316	2,29E-07	1,13E-06
AL117339.4	1,178249893	4,663864011	2,34E-07	1,15E-06
LINC00880	1,89497929	5,861736797	2,36E-07	1,16E-06
AC127024.6	1,162523187	4,071385425	2,51E-07	1,23E-06
AL035045.1	3,32232215	4,018300365	2,52E-07	1,23E-06
AC073896.5	2,038832148	3,157666779	2,56E-07	1,25E-06
AC126407.1	2,754658866	3,10436656	2,57E-07	1,25E-06
AC016395.1	-1,201531127	5,502350554	2,61E-07	1,27E-06
LINC02041	2,71962605	5,136974554	2,67E-07	1,30E-06
AC007036.1	2,254151509	3,850352182	2,69E-07	1,31E-06
AC253576.2	1,184616644	4,343654069	2,73E-07	1,33E-06
AC084757.3	1,69189781	3,697840288	2,75E-07	1,34E-06
AL110292.1	3,414942164	3,632546198	2,86E-07	1,39E-06
AL583808.1	3,948256096	3,699005905	2,89E-07	1,41E-06
AP003559.1	1,823863457	4,544350606	2,94E-07	1,43E-06
AC011676.1	2,311669244	3,389367693	2,94E-07	1,43E-06
AC018529.1	-1,291556303	3,822693018	2,95E-07	1,43E-06
AC008991.1	4,256697745	3,862645757	2,97E-07	1,44E-06
SERHL	1,028133306	5,581177354	2,98E-07	1,44E-06

HCG9	1,533698801	4,460875315	3,08E-07	1,49E-06
AP000569.1	2,158838004	3,616353198	3,10E-07	1,50E-06
Z82246.1	2,078516514	6,378776156	3,17E-07	1,53E-06
AC116025.1	-1,302664077	5,738526736	3,21E-07	1,55E-06
LINC02200	4,639279363	5,986428346	3,29E-07	1,58E-06
CASC9	3,180306408	8,694065558	3,30E-07	1,59E-06
AC010618.2	1,175766649	3,96878276	3,38E-07	1,62E-06
AC090358.1	4,952617222	3,953445259	3,44E-07	1,65E-06
AL391427.1	1,229289791	6,491904164	3,44E-07	1,65E-06
LINC02158	3,256007011	9,23539135	3,47E-07	1,66E-06
AC024243.1	1,505507014	3,415013419	3,47E-07	1,66E-06
AC010528.1	3,27261527	3,089125608	3,54E-07	1,69E-06
AC025048.4	1,036308866	4,824790827	3,55E-07	1,70E-06
LINC01448	3,968748687	4,432310987	3,57E-07	1,70E-06
AL356123.1	1,328421852	6,808584921	3,61E-07	1,72E-06
AC087564.1	-1,577323345	3,573060298	3,62E-07	1,72E-06
Z98257.1	1,452078426	8,09115616	3,64E-07	1,73E-06
AC022809.1	1,478136691	4,498628459	3,65E-07	1,74E-06
AC006305.1	2,964215873	5,498025446	3,68E-07	1,75E-06
AL645939.5	2,043344934	3,855686915	3,71E-07	1,76E-06
AP003119.1	1,499851191	6,12852039	3,77E-07	1,79E-06
AL353801.1	1,871174285	3,499537882	3,82E-07	1,81E-06
AL035446.1	2,37111087	6,548477144	3,83E-07	1,81E-06
AC018638.7	1,037648588	5,901673504	3,93E-07	1,86E-06
LINC00839	1,683114434	6,512354592	3,95E-07	1,87E-06
AC133919.2	1,614966356	5,895150584	3,98E-07	1,88E-06
AL591686.1	5,826381567	5,044069087	4,02E-07	1,90E-06
AL626787.1	-1,204892888	4,502066998	4,08E-07	1,92E-06
AL445209.1	3,171435991	3,859450807	4,08E-07	1,92E-06
AL139349.1	1,112081676	5,10244018	4,13E-07	1,94E-06
AL139385.1	-1,376162267	7,939331568	4,19E-07	1,97E-06
AL451074.6	2,461073618	4,65103266	4,35E-07	2,04E-06
AP001619.1	1,801565527	3,156348258	4,37E-07	2,05E-06
AC048337.1	1,87380124	3,422138869	4,41E-07	2,07E-06
LINC00958	4,095179367	5,821019975	4,42E-07	2,07E-06
AC007750.1	1,921774656	4,096539181	4,43E-07	2,07E-06
BSN-AS2	1,432902975	4,753001897	4,48E-07	2,09E-06
AC079380.1	2,366591842	3,40744189	4,56E-07	2,13E-06
AL450322.1	2,926614864	3,078635507	4,68E-07	2,18E-06
AC023906.5	2,203896716	6,101601919	4,70E-07	2,19E-06
AP000695.2	1,581249762	5,035557202	4,71E-07	2,19E-06
MEOX2-AS1	3,049823946	4,987671893	4,78E-07	2,22E-06
CERNA1	1,578040816	6,600413953	4,80E-07	2,23E-06
AL158839.1	2,464746575	3,591634493	4,89E-07	2,27E-06
AC138150.2	1,117136059	5,811063713	4,92E-07	2,28E-06
AP000346.1	1,447234117	3,676870292	4,93E-07	2,28E-06
AL162632.3	1,161025941	3,903927542	4,96E-07	2,30E-06
ERVMER61-1	4,413535032	4,499322917	5,04E-07	2,33E-06
LINC00898	3,305250063	3,567802704	5,09E-07	2,35E-06
AC104777.1	-1,422717473	3,396693428	5,10E-07	2,35E-06

AC025259.3	-1,096359014	4,892472398	5,15E-07	2,38E-06
AC139887.4	1,267766089	4,385874231	5,17E-07	2,38E-06
AC244197.2	1,375229523	4,793768489	5,18E-07	2,38E-06
AC008892.1	2,316580437	3,267903107	5,27E-07	2,43E-06
PRRT3-AS1	1,180567706	7,159688654	5,29E-07	2,43E-06
AL512598.1	1,575308575	4,760969774	5,36E-07	2,46E-06
SOX21-AS1	3,489024476	4,704435548	5,39E-07	2,47E-06
AL162726.4	3,312232727	3,10115559	5,41E-07	2,48E-06
LINC00887	1,979815686	6,043689407	5,43E-07	2,49E-06
AC019294.2	1,161668958	4,169496351	5,49E-07	2,51E-06
AC011352.3	2,549744733	3,479819209	5,65E-07	2,58E-06
ZNF793-AS1	1,583088663	6,502754609	5,67E-07	2,59E-06
LINC01164	4,27051105	4,642297605	5,80E-07	2,64E-06
LINC02416	2,427578594	3,414919206	5,82E-07	2,65E-06
AC107973.1	4,629153215	3,741517794	5,84E-07	2,66E-06
LINC02208	2,236427508	3,121568302	5,85E-07	2,66E-06
AC006064.3	1,418774726	3,69098125	5,88E-07	2,67E-06
LINC01589	2,996742195	5,315354122	6,00E-07	2,73E-06
LINC00635	3,217368973	3,613598242	6,09E-07	2,76E-06
AP005328.1	3,17113965	3,303759916	6,10E-07	2,76E-06
AL355810.1	2,00230547	3,145696586	6,16E-07	2,79E-06
LINC01992	4,418568517	3,958039436	6,24E-07	2,82E-06
AL358394.1	4,966110681	4,169172381	6,25E-07	2,82E-06
AC025265.1	1,043225944	6,315126458	6,31E-07	2,85E-06
AC006460.1	1,908597311	4,065099471	6,34E-07	2,86E-06
LINC01681	2,957711057	5,474015844	6,39E-07	2,88E-06
AC138965.2	3,518240861	3,295962344	6,40E-07	2,88E-06
AC093730.1	3,641192546	3,244163847	6,48E-07	2,91E-06
AL359551.1	3,600387318	4,243546039	6,59E-07	2,96E-06
PTPRD-AS1	-1,202252908	5,278315055	6,61E-07	2,97E-06
LINC00535	1,528849616	7,212238719	6,68E-07	3,00E-06
LINC01550	-1,224327133	5,39658601	6,76E-07	3,03E-06
HOXA-AS2	1,246715368	8,163408421	6,82E-07	3,06E-06
AC006012.1	1,947607795	3,385344412	6,90E-07	3,08E-06
AC005519.2	1,003438923	5,318199299	6,90E-07	3,08E-06
AC016708.1	1,528098164	4,444189103	6,97E-07	3,11E-06
LINC01831	-1,571868067	8,360693475	7,11E-07	3,16E-06
AC009065.1	2,088066943	3,404808297	7,12E-07	3,17E-06
LGALS8-AS1	1,126092877	5,559001934	7,25E-07	3,23E-06
AL359636.2	2,360324363	3,233300767	7,39E-07	3,28E-06
GDNF-AS1	2,358458356	6,717433309	7,42E-07	3,29E-06
LINC01267	2,733337584	3,176498564	7,42E-07	3,29E-06
AC025271.4	1,057538718	5,624510259	7,57E-07	3,35E-06
C1QTNF1-AS1	2,177529284	6,159078202	7,63E-07	3,38E-06
AL513329.1	1,06634282	4,461973721	7,72E-07	3,41E-06
AC011447.3	1,387604417	4,982228459	7,76E-07	3,43E-06
AC091133.2	4,084878316	3,582284734	7,82E-07	3,45E-06
EGLN3-AS1	3,951174378	3,382869291	7,87E-07	3,47E-06
GTF3C2-AS1	1,040364595	4,366417383	7,97E-07	3,51E-06
AC073321.1	-1,568700658	4,598988048	7,98E-07	3,51E-06

AL353622.2	1,508623764	3,393961303	7,98E-07	3,51E-06
AL078604.2	1,451130918	5,940982299	8,00E-07	3,52E-06
AC025265.3	2,875512987	3,335179174	8,01E-07	3,52E-06
C1orf229	1,214577504	6,055115237	8,03E-07	3,53E-06
AC092757.2	1,493136728	4,158871639	8,06E-07	3,53E-06
AL121672.1	1,316641835	4,266772819	8,06E-07	3,53E-06
AC107393.2	4,343358709	4,665381979	8,08E-07	3,54E-06
LINC02307	3,630302012	3,233547197	8,09E-07	3,54E-06
LINC01353	1,473435919	4,462835656	8,11E-07	3,55E-06
LINC01952	1,671196802	3,734133827	8,11E-07	3,55E-06
LINC02473	2,915383696	3,260920199	8,14E-07	3,56E-06
AC008738.2	1,227503197	4,804031186	8,18E-07	3,57E-06
AC127070.2	1,167306416	4,546351126	8,18E-07	3,57E-06
AP001437.1	1,112587194	4,2392882	8,26E-07	3,60E-06
AL133255.1	1,797417853	3,150865512	8,35E-07	3,64E-06
AL445673.1	1,818226628	4,573428092	8,64E-07	3,75E-06
AC068987.3	1,832401822	3,664404073	8,67E-07	3,76E-06
AC108058.1	-1,180290409	3,802913159	8,74E-07	3,79E-06
AL049539.1	1,501273962	3,565897908	8,74E-07	3,79E-06
AL035701.1	1,35750586	5,301229081	8,98E-07	3,89E-06
AC108865.1	3,784468102	4,311026733	9,08E-07	3,93E-06
DGCR10	1,820621668	3,783966825	9,14E-07	3,96E-06
AC111182.1	1,591422497	5,602656414	9,28E-07	4,01E-06
AC012213.3	1,132235696	4,369763343	9,32E-07	4,02E-06
AC010457.1	3,014577071	4,591392425	9,33E-07	4,02E-06
AL732292.2	1,245249801	4,291711744	9,34E-07	4,03E-06
AC011754.1	4,491915771	3,662333832	9,43E-07	4,06E-06
AP001972.4	4,147608099	4,97397967	9,43E-07	4,06E-06
LINC01948	1,588679283	4,525937747	9,48E-07	4,08E-06
AC012073.1	1,062618025	6,266716411	9,51E-07	4,09E-06
LINC01338	3,226313094	3,538360268	9,65E-07	4,15E-06
AC007743.1	1,351273598	4,90451096	9,75E-07	4,19E-06
AC007128.2	3,226354691	3,20304635	9,76E-07	4,19E-06
AC110285.5	1,56333058	3,487689154	9,80E-07	4,20E-06
AC024560.3	1,1842278	3,795702671	1,01E-06	4,33E-06
AL357153.1	2,787309197	3,506845293	1,07E-06	4,58E-06
LINC01598	2,146254694	3,261967986	1,08E-06	4,58E-06
AC027682.5	2,064859286	3,111553646	1,08E-06	4,58E-06
AC100791.2	2,600900635	3,199809786	1,08E-06	4,58E-06
AL138760.1	3,014270275	3,386976721	1,08E-06	4,59E-06
AL022158.1	4,667439683	4,074947763	1,08E-06	4,60E-06
FER1L6-AS2	3,800024729	3,597609324	1,10E-06	4,67E-06
AL353150.1	1,361072902	6,098396252	1,10E-06	4,69E-06
L29074.1	1,969879451	3,13337807	1,13E-06	4,78E-06
GPR1-AS	4,836745065	5,787837538	1,13E-06	4,80E-06
AC040173.1	2,810733038	4,738217438	1,16E-06	4,91E-06
U62317.1	2,333341307	4,473063067	1,17E-06	4,94E-06
AC008622.2	1,4202859	4,567531254	1,21E-06	5,12E-06
AL513318.2	3,268973649	5,549375426	1,22E-06	5,14E-06
AP000844.2	4,432590025	4,599406099	1,22E-06	5,14E-06

AC107398.3	2,654616198	4,038409732	1,23E-06	5,19E-06
AL390115.1	2,129181239	3,133408729	1,23E-06	5,19E-06
AC008105.1	1,269358176	5,136458846	1,24E-06	5,21E-06
HDAC11-AS1	1,633677441	3,25920286	1,25E-06	5,25E-06
LINC02154	3,349160905	4,196985657	1,25E-06	5,27E-06
AL158071.3	1,437502953	4,359249041	1,26E-06	5,29E-06
AL133279.1	-1,224347047	3,934227493	1,29E-06	5,42E-06
AC026992.2	2,177920832	4,666924027	1,30E-06	5,43E-06
AC079239.1	4,199958336	3,837571411	1,32E-06	5,52E-06
AP004147.1	2,899503954	4,025195016	1,33E-06	5,54E-06
AC011815.2	1,173403821	4,73309208	1,33E-06	5,56E-06
AL355596.1	3,251737339	3,894735047	1,34E-06	5,58E-06
AC087273.1	-1,07255023	4,968896394	1,37E-06	5,71E-06
AC022098.2	3,432320921	4,503918988	1,38E-06	5,75E-06
AC064807.2	2,327855888	4,75357523	1,39E-06	5,79E-06
LINC01231	4,93345363	3,916790177	1,40E-06	5,84E-06
AL450384.1	-1,068369867	4,558613487	1,42E-06	5,88E-06
AC126696.3	1,847355835	3,4012355	1,43E-06	5,94E-06
KRTAP5-AS1	1,742051226	5,882344913	1,44E-06	5,99E-06
AC027117.2	-1,101269682	9,494915669	1,45E-06	6,00E-06
LINC01085	3,500380315	3,91710939	1,46E-06	6,05E-06
AL450322.2	2,498647373	3,674605526	1,46E-06	6,05E-06
AC126175.1	4,121142038	4,353309996	1,47E-06	6,06E-06
AC024560.1	1,538789087	4,903474949	1,49E-06	6,15E-06
AC112251.1	3,248328993	7,718054712	1,51E-06	6,21E-06
AL118511.1	1,083452197	4,435714896	1,51E-06	6,22E-06
AL133215.1	1,58593267	3,757938709	1,52E-06	6,26E-06
GATA2-AS1	1,467647639	6,883081446	1,52E-06	6,27E-06
AC004877.1	1,227953298	4,022635284	1,53E-06	6,30E-06
VAC14-AS1	1,548226532	7,480343891	1,53E-06	6,30E-06
AC005363.2	1,57692618	3,404418249	1,54E-06	6,31E-06
AL355482.1	1,755754771	6,907254402	1,54E-06	6,31E-06
AC006213.3	1,736658536	4,87154457	1,55E-06	6,37E-06
UTAT33	1,061251467	4,089780623	1,56E-06	6,41E-06
AC114812.2	2,24312661	3,135929532	1,57E-06	6,42E-06
AC009686.2	1,148718351	5,730325244	1,57E-06	6,43E-06
C10orf71-AS1	3,771948627	3,27802459	1,58E-06	6,47E-06
AC129492.2	3,268326267	3,20169258	1,58E-06	6,47E-06
WASIR2	2,000454232	3,651397774	1,59E-06	6,50E-06
AC134682.1	1,438611428	5,108502921	1,60E-06	6,52E-06
UBE2Q1-AS1	1,188430203	4,047147258	1,62E-06	6,59E-06
AC100803.1	2,922522186	3,66446316	1,62E-06	6,62E-06
AL035661.1	-1,355259314	9,037589154	1,64E-06	6,67E-06
AL355607.1	1,755548513	3,912081734	1,64E-06	6,68E-06
AC034228.1	5,045874929	4,535123606	1,66E-06	6,75E-06
AC024563.1	3,342863943	3,579740405	1,66E-06	6,75E-06
LINC02421	1,870770487	3,530568123	1,67E-06	6,77E-06
LINC02298	1,636912547	6,754381891	1,68E-06	6,80E-06
AP001363.2	1,157218381	4,077613114	1,68E-06	6,80E-06
AL138966.2	1,274765567	3,778303512	1,69E-06	6,83E-06

AL021707.4	1,314158452	3,543948787	1,71E-06	6,91E-06
EHD4-AS1	1,183268131	3,916117821	1,71E-06	6,93E-06
AL583810.2	1,479827553	3,789256828	1,75E-06	7,06E-06
AC073324.2	1,95807436	3,335921915	1,78E-06	7,20E-06
AL121601.1	1,077822371	4,484402982	1,79E-06	7,21E-06
AC006206.2	3,438147454	5,257611684	1,80E-06	7,27E-06
AL359878.2	1,387756271	3,645715246	1,81E-06	7,29E-06
AC138904.1	1,961240449	4,299198838	1,82E-06	7,33E-06
AC108517.1	4,523717829	3,676166165	1,83E-06	7,34E-06
AC136188.1	4,232418809	3,716588089	1,83E-06	7,35E-06
AC092598.1	3,499414254	4,406743376	1,87E-06	7,50E-06
AC007402.1	4,703087232	3,993795488	1,87E-06	7,52E-06
LINC01649	3,385930283	3,352701449	1,89E-06	7,58E-06
AC007991.3	-1,695961442	3,49782356	1,89E-06	7,59E-06
AC006064.1	1,284212353	3,389630144	1,90E-06	7,59E-06
TRIM31-AS1	1,822518498	3,745469753	1,90E-06	7,61E-06
LINC02099	1,529921267	3,765448339	1,91E-06	7,63E-06
LINC01301	1,033243353	6,213628203	1,92E-06	7,69E-06
AC008742.1	1,68512607	3,83657569	1,94E-06	7,76E-06
AC116337.3	1,352089982	4,145905657	1,96E-06	7,83E-06
AC109460.2	1,023657697	5,414063465	1,97E-06	7,86E-06
AC253536.6	1,235435961	7,185741248	1,98E-06	7,88E-06
AC002091.2	-1,100326753	3,552702873	1,98E-06	7,88E-06
AC107294.1	-1,237904106	3,191422338	1,99E-06	7,90E-06
AC097512.1	3,508914071	4,421760198	2,01E-06	8,00E-06
LINC00189	1,934693265	6,443784052	2,02E-06	8,04E-06
AC005324.5	1,609873728	3,950867039	2,03E-06	8,06E-06
AP000812.1	-1,034723699	3,729271575	2,04E-06	8,08E-06
AL132655.2	2,373556036	3,736727375	2,05E-06	8,14E-06
AC108868.2	4,529073261	3,697398657	2,08E-06	8,22E-06
LINC00616	4,007083747	3,676461375	2,08E-06	8,24E-06
AP000892.2	1,09732388	4,252036056	2,08E-06	8,24E-06
LINC00668	3,450136116	6,091719841	2,09E-06	8,24E-06
AC015912.3	1,104226532	6,044071206	2,13E-06	8,42E-06
AC102953.1	1,139211323	4,355841152	2,15E-06	8,48E-06
AC068790.3	1,248239994	3,690753285	2,15E-06	8,48E-06
AL080248.1	-1,091296532	7,949936031	2,15E-06	8,48E-06
AC007495.1	-1,446089253	5,521278871	2,18E-06	8,59E-06
AC069061.2	5,014510419	4,178459027	2,19E-06	8,60E-06
AL033384.1	1,891220481	4,667023531	2,19E-06	8,62E-06
LINC01096	3,685349384	3,399575925	2,21E-06	8,68E-06
AC040934.1	1,240377	3,445408531	2,22E-06	8,72E-06
AC012485.2	1,36821247	4,366800132	2,23E-06	8,76E-06
ZNF32-AS1	1,017669526	4,124522649	2,24E-06	8,77E-06
AL121782.1	1,273795227	3,539268502	2,26E-06	8,85E-06
AL138900.2	4,15493003	3,648961782	2,28E-06	8,91E-06
AL035427.1	1,698772456	3,20447727	2,31E-06	9,05E-06
AC108463.3	1,602093895	3,822968555	2,32E-06	9,08E-06
ERVH48-1	2,602590807	6,109596148	2,33E-06	9,10E-06
AC012625.1	2,884316013	3,586525481	2,42E-06	9,45E-06

LINC01967	3,152780195	3,429436809	2,44E-06	9,52E-06
AL592466.1	3,655973084	3,246468591	2,46E-06	9,58E-06
AL590004.4	1,658811868	7,768701698	2,47E-06	9,59E-06
AP000851.2	-1,849250476	6,647453437	2,49E-06	9,68E-06
LINC00239	1,918055877	5,911429963	2,51E-06	9,75E-06
AC034236.3	1,566964861	3,143876914	2,51E-06	9,75E-06
LINC02384	2,018898952	9,039791096	2,54E-06	9,87E-06
Z94160.1	2,375742449	3,12439134	2,54E-06	9,88E-06
AL356417.2	2,043523956	3,467670317	2,55E-06	9,89E-06
LBX1-AS1	3,753270705	3,287211273	2,62E-06	1,01E-05
AC008735.1	1,108080906	4,149839115	2,64E-06	1,02E-05
AC004221.1	2,223911725	3,302109621	2,75E-06	1,06E-05
AC243773.2	4,647691891	3,760539371	2,75E-06	1,06E-05
AC100812.1	1,376979816	3,559651562	2,78E-06	1,07E-05
AC008825.1	3,097446317	3,147328667	2,79E-06	1,07E-05
AC037198.3	-1,327902338	4,263333202	2,89E-06	1,11E-05
CU104787.1	3,854975162	3,504702471	2,90E-06	1,11E-05
AC122685.1	4,207933112	4,085796506	2,92E-06	1,12E-05
LINC01559	3,742733709	6,742145437	2,94E-06	1,13E-05
LINC00922	3,29825007	3,439783426	2,96E-06	1,13E-05
AC113355.1	4,274270046	3,561091509	3,17E-06	1,21E-05
AL355385.1	1,003813354	3,859150959	3,18E-06	1,21E-05
AL031665.1	2,077419394	3,622521245	3,25E-06	1,24E-05
AL445070.1	3,411891273	3,149978815	3,25E-06	1,24E-05
AC010890.1	-1,203450132	3,812216274	3,27E-06	1,24E-05
AC125421.1	2,823608811	3,308430246	3,27E-06	1,24E-05
HULC	1,27492238	14,30587154	3,35E-06	1,27E-05
AC004253.2	2,067438061	3,375086061	3,41E-06	1,30E-05
AC011503.2	1,178714548	6,940013491	3,42E-06	1,30E-05
AC090241.3	1,279541386	3,745958785	3,43E-06	1,30E-05
AC109439.2	3,284104844	3,64031701	3,43E-06	1,30E-05
AC010547.2	-2,083483239	6,295970778	3,48E-06	1,32E-05
C5orf66	1,373525748	7,101357726	3,61E-06	1,36E-05
AL160400.1	-1,008417526	4,442050729	3,61E-06	1,36E-05
AC011330.2	1,101490084	3,981289476	3,65E-06	1,37E-05
SMC2-AS1	1,126922941	4,233778128	3,65E-06	1,37E-05
AC103858.1	-1,028448437	3,373960413	3,69E-06	1,39E-05
ZIM2-AS1	2,0753818	4,887930098	3,72E-06	1,40E-05
LINC01793	4,25603563	4,771149235	3,74E-06	1,41E-05
AL109933.1	-1,280478207	4,031505863	3,77E-06	1,42E-05
AC010336.1	1,031035277	3,910447838	3,79E-06	1,42E-05
AC132938.5	1,097927364	4,149154657	3,81E-06	1,43E-05
KLF7-IT1	-1,215925879	3,196025113	3,85E-06	1,44E-05
LINC00479	1,433171366	5,173008853	3,86E-06	1,44E-05
SRGAP3-AS2	3,525252399	3,651806931	3,89E-06	1,45E-05
AC091230.1	3,249868625	3,212583555	3,91E-06	1,46E-05
PWRN1	-1,650134951	4,092045934	3,94E-06	1,47E-05
AP001646.3	-1,124435322	3,377387716	3,94E-06	1,47E-05
AP003171.1	4,882030122	4,490374117	4,02E-06	1,50E-05
AC011840.1	4,675277057	4,731094369	4,04E-06	1,51E-05

LINC00858	3,32177309	3,900732355	4,07E-06	1,51E-05
AC007064.2	2,452598091	3,367294982	4,27E-06	1,59E-05
AC005534.1	1,010914221	4,670096773	4,30E-06	1,60E-05
AC009097.2	2,077791531	3,63502052	4,32E-06	1,61E-05
AL445190.1	-1,164620001	3,17782944	4,35E-06	1,62E-05
LINC01754	1,859929098	4,698986999	4,41E-06	1,64E-05
AC112219.2	1,282438041	4,315187086	4,41E-06	1,64E-05
AL157823.2	1,344666119	4,016450206	4,47E-06	1,66E-05
LINC00844	-1,518153134	10,83507322	4,47E-06	1,66E-05
AF254983.1	3,46244398	3,287340654	4,55E-06	1,69E-05
AC026320.1	3,867115594	3,350332314	4,56E-06	1,69E-05
AC008870.4	1,343134707	3,337725862	4,58E-06	1,69E-05
AL122125.1	1,144508285	4,326240092	4,61E-06	1,70E-05
AC092159.2	1,80925333	4,148945269	4,62E-06	1,71E-05
AC074044.1	1,261894558	3,624523157	4,63E-06	1,71E-05
AC122694.1	3,075923382	3,369256882	4,71E-06	1,74E-05
EGFR-AS1	2,304066805	8,283432302	4,73E-06	1,74E-05
AC103770.1	4,026776265	4,993348418	4,76E-06	1,75E-05
AC126323.3	3,03347544	3,236667593	4,80E-06	1,77E-05
AL583785.1	1,56093165	3,778604521	4,83E-06	1,77E-05
AC067930.3	1,21154486	4,306701878	4,90E-06	1,80E-05
AC144833.1	4,405284889	5,24506069	4,91E-06	1,80E-05
AC004080.1	3,214451781	3,197565411	4,91E-06	1,80E-05
AC104041.1	2,831930592	4,005514374	4,92E-06	1,81E-05
AC008759.3	-1,010393677	4,253149807	4,97E-06	1,82E-05
PRKG1-AS1	2,634961322	3,914609819	4,98E-06	1,82E-05
AL138781.1	1,038363106	5,416771808	5,07E-06	1,85E-05
AP000757.2	2,851976742	5,462663782	5,11E-06	1,87E-05
AL160291.1	1,444790222	3,193025229	5,11E-06	1,87E-05
LINC01012	2,023334143	4,034580276	5,11E-06	1,87E-05
AC079062.1	3,378210858	8,220326656	5,21E-06	1,90E-05
AC006387.1	-1,129342524	3,184952819	5,29E-06	1,93E-05
AC103808.6	3,012720704	3,289607288	5,34E-06	1,94E-05
AL135744.1	1,122921049	3,623993358	5,35E-06	1,95E-05
EVX1-AS	3,138090774	3,046398201	5,37E-06	1,95E-05
AC018742.1	-1,238979425	4,14575986	5,38E-06	1,96E-05
C8orf87	3,971165239	3,39261885	5,46E-06	1,98E-05
AC006042.1	1,13817363	5,508013384	5,55E-06	2,02E-05
AC145207.7	2,426765941	3,132559208	5,71E-06	2,07E-05
AL807757.2	1,295545384	5,131184852	5,74E-06	2,08E-05
LINC00601	4,31934369	4,265425951	5,75E-06	2,08E-05
AC106744.1	3,779265293	3,306562602	5,82E-06	2,10E-05
LINC01361	3,412362561	4,970945871	5,83E-06	2,11E-05
FZD10-AS1	1,548210404	5,317240212	5,86E-06	2,12E-05
AC019155.3	4,027507228	3,42589922	5,89E-06	2,12E-05
AC018638.6	1,276306016	4,865213794	5,97E-06	2,15E-05
AC005753.1	1,399048272	3,374846342	5,98E-06	2,16E-05
LINC00513	1,258346307	7,160178709	6,03E-06	2,17E-05
AC138646.1	2,905670164	3,062152827	6,06E-06	2,18E-05
AC068506.1	1,92737257	6,142554913	6,09E-06	2,19E-05

ZNF571-AS1	1,154037326	5,182038474	6,10E-06	2,19E-05
AC026495.1	1,857582163	4,31002776	6,11E-06	2,20E-05
AC007278.1	-1,236160223	3,703920157	6,12E-06	2,20E-05
AC073655.1	1,901022361	3,394325167	6,18E-06	2,22E-05
AL356740.3	3,025327282	3,976188749	6,21E-06	2,23E-05
AC104134.1	2,505126429	4,053257404	6,31E-06	2,26E-05
AC010422.4	1,074792928	3,998777214	6,36E-06	2,28E-05
AL136528.1	2,151198683	5,022670268	6,37E-06	2,28E-05
LINC01033	2,123795142	3,089974042	6,44E-06	2,30E-05
DSG1-AS1	2,82968265	3,276776949	6,45E-06	2,30E-05
AL035706.1	-1,234062336	4,113082149	6,52E-06	2,33E-05
AC084782.2	2,393863083	3,186566525	6,53E-06	2,33E-05
AC004943.1	1,126656833	4,044883656	6,60E-06	2,35E-05
LINC00160	3,162707711	3,656090542	6,64E-06	2,36E-05
LINC01297	3,806881044	3,852438576	6,65E-06	2,37E-05
HHIP-AS1	-1,42942541	6,371622807	6,70E-06	2,38E-05
AL356215.1	2,090069309	4,057819177	6,71E-06	2,38E-05
LINC01482	-1,02146006	6,127980728	6,93E-06	2,46E-05
LINC01819	3,412295783	5,653423665	7,02E-06	2,49E-05
AC105460.2	-1,393341607	3,289335819	7,18E-06	2,54E-05
AC134407.1	1,509272883	3,089905549	7,21E-06	2,55E-05
AC093702.1	3,285408118	3,231295204	7,22E-06	2,55E-05
AP005717.1	1,012398228	4,274595697	7,24E-06	2,56E-05
AL355075.4	-1,485422043	3,552617198	7,35E-06	2,59E-05
LINC01645	-1,036317327	3,499288891	7,40E-06	2,61E-05
DLGAP1-AS5	6,067892554	7,383712643	7,41E-06	2,61E-05
AL359924.1	5,263596637	4,124826717	7,47E-06	2,63E-05
AC017002.2	1,822534528	3,50016042	7,52E-06	2,65E-05
AL359881.3	2,802635263	3,677862977	7,56E-06	2,66E-05
AC138761.4	3,499176144	3,740520017	7,58E-06	2,67E-05
LINC02334	2,381082413	4,84865797	7,59E-06	2,67E-05
LINC00184	1,71090022	3,370745575	7,65E-06	2,69E-05
AC105446.1	2,135472272	4,913662796	7,71E-06	2,71E-05
AC048383.1	2,363796657	3,311723583	7,84E-06	2,75E-05
AC116021.2	3,490352611	4,044393844	7,85E-06	2,75E-05
LINC02469	4,0736485	3,404631035	8,05E-06	2,82E-05
AL121652.1	1,456419479	3,163589292	8,06E-06	2,82E-05
AC244517.1	1,858418182	4,424618617	8,17E-06	2,86E-05
AC005993.1	3,169442306	3,27692981	8,26E-06	2,89E-05
AC024257.3	1,488659142	3,984848245	8,37E-06	2,92E-05
LINC01843	1,107571487	9,015968345	8,47E-06	2,96E-05
AC090912.3	1,524696347	3,15196104	8,51E-06	2,97E-05
AC006205.2	2,082228585	8,980671212	8,60E-06	3,00E-05
LINC02046	3,932832009	3,725096838	8,75E-06	3,04E-05
LINC01257	3,485991487	3,791498012	8,84E-06	3,07E-05
AC008655.2	1,115776417	3,518587651	8,89E-06	3,09E-05
AP001099.1	2,478169002	3,774452145	8,95E-06	3,10E-05
AC007114.2	1,350942739	4,628254576	9,09E-06	3,15E-05
LINC02204	1,683765549	3,649339008	9,09E-06	3,15E-05
LINC01483	2,450409233	3,618176314	9,16E-06	3,17E-05

AL356966.1	1,222894669	4,856683521	9,28E-06	3,21E-05
AC005537.1	2,692816114	4,596407799	9,36E-06	3,23E-05
AL445426.1	-1,274427181	3,30980238	9,43E-06	3,26E-05
AC105999.2	4,156093373	3,505225009	9,56E-06	3,30E-05
AC006548.3	1,583345983	4,941227141	9,57E-06	3,30E-05
AC068025.1	1,22362792	4,00738833	9,57E-06	3,30E-05
AP001596.1	1,772020345	3,644997	9,66E-06	3,32E-05
LINC00322	2,756974277	3,922143318	9,72E-06	3,34E-05
AP000919.2	-1,024949609	3,662142171	9,75E-06	3,35E-05
PICSAR	3,923863435	4,381856571	9,81E-06	3,37E-05
AC092916.1	3,699163517	3,270201578	1,00E-05	3,43E-05
AC027279.2	1,36023447	4,409018155	1,02E-05	3,48E-05
AC092447.5	2,943350369	3,98805457	1,03E-05	3,51E-05
AC105339.2	1,191744801	3,631449515	1,04E-05	3,54E-05
AC010547.1	1,088431611	3,560986368	1,04E-05	3,55E-05
AC009902.2	1,561033789	3,508734948	1,05E-05	3,57E-05
Z82249.1	6,026202338	5,187328926	1,05E-05	3,57E-05
AC036214.1	1,513699318	3,591383583	1,05E-05	3,58E-05
AC067930.5	1,284819696	4,756132015	1,06E-05	3,59E-05
AC007966.1	1,591079076	4,29684719	1,06E-05	3,61E-05
LINC00640	1,77038852	3,929950836	1,07E-05	3,64E-05
AP005271.1	3,139559901	3,624048275	1,08E-05	3,67E-05
AP000696.1	4,22128424	3,695089997	1,09E-05	3,70E-05
AC109779.1	2,972603392	3,900365218	1,10E-05	3,71E-05
LINC02127	1,267049045	4,762810447	1,13E-05	3,81E-05
LINC01518	3,841107663	4,167204913	1,14E-05	3,84E-05
AC016586.1	1,098697651	3,848579054	1,14E-05	3,84E-05
AC243965.2	1,110760923	4,753612485	1,18E-05	3,96E-05
AC068756.1	2,924789334	4,390725384	1,19E-05	4,01E-05
AC119150.1	1,762125948	5,46976003	1,20E-05	4,04E-05
AC131902.1	4,64697251	4,180644621	1,21E-05	4,09E-05
CLDN10-AS1	4,179579913	3,945014798	1,22E-05	4,11E-05
AC096759.2	2,93884554	3,086054681	1,23E-05	4,14E-05
AC090618.1	-1,022081261	3,732694943	1,24E-05	4,17E-05
AC114488.1	1,764592909	4,823910159	1,25E-05	4,18E-05
AC008592.5	-1,200296357	5,590063555	1,27E-05	4,24E-05
LINC01060	2,905895901	3,880442925	1,31E-05	4,37E-05
AL355297.3	1,115908354	3,777982061	1,32E-05	4,40E-05
AL356310.1	1,910948159	4,10253953	1,32E-05	4,42E-05
SMILR	1,762729011	4,89359066	1,33E-05	4,44E-05
AL355472.4	1,710624545	3,77241823	1,34E-05	4,46E-05
LINC02003	2,473519936	3,085203464	1,35E-05	4,49E-05
AC073323.1	4,016806726	3,560941196	1,36E-05	4,51E-05
AC012074.1	1,08856511	4,17214955	1,36E-05	4,53E-05
AC022150.4	1,483141397	5,949133625	1,37E-05	4,56E-05
AC069234.5	1,120356037	4,038711217	1,38E-05	4,57E-05
GPC6-AS1	2,316742604	3,685947013	1,38E-05	4,58E-05
AC011247.1	1,11316774	4,647288371	1,40E-05	4,63E-05
AC011374.1	-1,18851573	3,245261434	1,41E-05	4,68E-05
AL353693.1	-1,409128426	3,643285234	1,42E-05	4,71E-05

AL133372.2	3,336649677	3,337365552	1,43E-05	4,72E-05
ST7-OT4	1,193296612	4,09187606	1,45E-05	4,79E-05
AC108676.1	1,370664709	5,607994565	1,48E-05	4,88E-05
AL161752.1	2,235937225	3,27216416	1,50E-05	4,93E-05
LINC01029	4,531493198	3,914566896	1,50E-05	4,93E-05
AL031717.1	1,166102422	3,669063355	1,50E-05	4,95E-05
AC026355.1	2,080409903	3,937424635	1,51E-05	4,98E-05
ZNF350-AS1	1,140841545	4,047918337	1,52E-05	4,99E-05
AC011365.1	-1,022396991	5,038346102	1,52E-05	5,00E-05
AC096729.1	3,50209513	3,191136366	1,53E-05	5,01E-05
AL355472.3	1,947815651	3,053825279	1,53E-05	5,03E-05
AC092447.8	4,720356695	4,036976674	1,54E-05	5,03E-05
AC093458.1	1,57834953	3,243902757	1,54E-05	5,04E-05
MRPL23-AS1	2,478903188	5,947650787	1,54E-05	5,05E-05
AC005329.1	1,286621506	6,367238266	1,56E-05	5,10E-05
CCDC144NL-AS1	1,403934542	7,739650275	1,58E-05	5,15E-05
AL359881.2	2,393168508	3,959325644	1,58E-05	5,16E-05
LINC02105	3,155968633	3,159941807	1,59E-05	5,18E-05
AC131532.1	2,823280384	4,387618612	1,59E-05	5,19E-05
AP003062.1	4,323981663	3,742851234	1,59E-05	5,19E-05
AC027117.1	1,121558629	6,059291081	1,61E-05	5,24E-05
AC244090.2	1,603419444	3,527232857	1,61E-05	5,24E-05
AC125611.4	1,767453145	3,09413908	1,62E-05	5,27E-05
LINC00351	3,429487344	3,159672208	1,62E-05	5,28E-05
AL121970.1	2,869964474	3,227104902	1,63E-05	5,31E-05
AC087855.2	3,078991734	3,028724447	1,64E-05	5,32E-05
AC022098.3	1,097856922	4,20020481	1,64E-05	5,33E-05
LINC02274	-1,346912531	3,541995566	1,65E-05	5,36E-05
AC007923.1	4,65822008	4,007652563	1,65E-05	5,36E-05
AC092343.1	3,327597103	3,550143859	1,66E-05	5,36E-05
AC105219.4	1,804314708	3,969641969	1,66E-05	5,39E-05
LINC01647	2,902822166	3,414164227	1,67E-05	5,41E-05
LINC01804	3,877696175	3,60228164	1,68E-05	5,43E-05
USP2-AS1	1,114535581	7,792702354	1,69E-05	5,45E-05
AC008567.3	1,030969498	5,487261355	1,69E-05	5,45E-05
AC079160.1	3,431856109	3,533215724	1,70E-05	5,49E-05
AC096708.4	1,797722967	3,099800202	1,72E-05	5,55E-05
AC078820.1	1,844625454	3,157997406	1,72E-05	5,56E-05
AL160408.1	2,144253408	4,820908157	1,72E-05	5,56E-05
AC015961.2	1,110350708	4,244800251	1,74E-05	5,61E-05
AC025580.1	2,202970039	4,373272458	1,74E-05	5,61E-05
AL365356.4	1,304943097	4,654489238	1,75E-05	5,62E-05
AC027237.2	1,125693104	3,473615409	1,75E-05	5,64E-05
AC239585.2	2,752069917	3,86334571	1,79E-05	5,74E-05
AC015660.4	1,333474306	4,280424971	1,80E-05	5,78E-05
AC009118.2	1,072826931	3,66230774	1,80E-05	5,78E-05
AC008033.3	1,981164146	5,695708831	1,81E-05	5,81E-05
AC027682.1	1,006576232	3,755020147	1,81E-05	5,81E-05
AC020656.2	1,361677688	7,869259741	1,83E-05	5,85E-05
AC126283.1	1,204798815	3,461908765	1,86E-05	5,95E-05

AC099786.2	4,273295713	3,528373174	1,87E-05	5,97E-05
FLJ16779	3,210865666	4,513889853	1,89E-05	6,03E-05
AC148476.1	2,224405087	5,250151482	1,89E-05	6,05E-05
AC084757.2	1,359506718	3,260598061	1,91E-05	6,09E-05
NDST1-AS1	1,418311389	5,981736563	1,91E-05	6,09E-05
AL021391.1	2,254521934	3,070118687	1,91E-05	6,09E-05
AC009108.3	1,036559302	4,912105379	1,91E-05	6,10E-05
LINC01508	3,872914956	5,432646936	1,92E-05	6,12E-05
KC877982.1	5,765045312	5,813070287	1,94E-05	6,19E-05
AC106795.2	-1,230931291	6,539223886	1,97E-05	6,25E-05
LINC00632	2,927516528	4,843504761	2,00E-05	6,35E-05
FMR1-IT1	1,050922328	4,30621239	2,02E-05	6,40E-05
AC092171.1	1,121835533	3,36680171	2,03E-05	6,42E-05
AC010149.1	1,652383832	3,729495634	2,04E-05	6,46E-05
U91319.1	-1,248549943	7,978818164	2,06E-05	6,51E-05
AL136985.2	1,110666637	3,596501862	2,09E-05	6,60E-05
C5orf66-AS1	3,302571295	3,231061453	2,18E-05	6,87E-05
AC009955.3	1,501841953	3,1813267	2,20E-05	6,94E-05
AC078860.1	2,192168347	3,35122351	2,21E-05	6,96E-05
SEMA3B-AS1	1,065409514	6,052844431	2,24E-05	7,06E-05
AC007608.3	1,239501606	5,914535132	2,25E-05	7,08E-05
AC106892.1	4,621135886	4,214853907	2,25E-05	7,08E-05
AC027088.3	2,711256387	3,091559126	2,32E-05	7,28E-05
AC124290.1	3,689933539	3,263620314	2,33E-05	7,30E-05
AL356124.1	1,618911505	3,087768987	2,36E-05	7,40E-05
AL592043.1	3,183971204	3,061350619	2,37E-05	7,41E-05
AC087525.1	2,200285528	3,680631978	2,39E-05	7,46E-05
AC011306.1	2,080561185	3,063648534	2,40E-05	7,50E-05
AC027688.1	1,196367358	5,577335829	2,41E-05	7,52E-05
AC135279.3	-1,059933151	3,129208575	2,43E-05	7,59E-05
AC239803.2	1,851156048	4,096085209	2,45E-05	7,65E-05
AC093627.7	1,37108647	4,536560519	2,45E-05	7,65E-05
AC087222.1	1,213826308	4,015966263	2,45E-05	7,65E-05
AC138393.3	1,201894686	3,921594019	2,46E-05	7,67E-05
UBXN10-AS1	1,34063303	5,444630978	2,47E-05	7,69E-05
AL445238.1	2,402990999	3,38335597	2,48E-05	7,71E-05
LINC02212	4,214457491	5,109556615	2,52E-05	7,82E-05
LINC01479	2,666963701	3,345805743	2,54E-05	7,89E-05
AL513548.3	1,708608379	3,098052703	2,58E-05	8,01E-05
AP005205.2	2,437385868	3,366632299	2,58E-05	8,01E-05
AC099518.1	1,241975196	3,944365473	2,60E-05	8,05E-05
AC104009.1	2,467919664	3,147053047	2,68E-05	8,31E-05
AC079465.1	-1,026222009	4,21073817	2,69E-05	8,34E-05
LINC01397	2,211454591	3,177987268	2,70E-05	8,36E-05
AC226118.1	2,119191856	3,744712625	2,71E-05	8,39E-05
AC002454.1	1,505228831	4,005816005	2,72E-05	8,39E-05
AC010255.1	2,770681803	3,39327039	2,77E-05	8,56E-05
MIR137HG	3,214912446	3,427626623	2,78E-05	8,56E-05
AC012313.4	1,824997589	3,303283653	2,78E-05	8,56E-05
AC234917.1	1,129099745	3,947541101	2,78E-05	8,58E-05

AL713998.1	4,782660218	5,035458104	2,79E-05	8,60E-05
LINC02407	1,622564578	4,082241949	2,80E-05	8,63E-05
AC090116.1	2,38254478	3,485147083	2,86E-05	8,80E-05
LINC01594	2,232948155	3,061194044	2,87E-05	8,82E-05
LINC02434	3,408564721	3,520717938	2,88E-05	8,85E-05
AL138737.1	2,597102439	4,362531225	2,89E-05	8,88E-05
LINC02228	3,038238977	4,547178797	2,90E-05	8,91E-05
AC022034.2	1,781468639	6,06440849	2,91E-05	8,93E-05
ZBTB46-AS1	3,13676203	3,487754164	2,93E-05	8,96E-05
AC091173.1	2,873000765	3,052416437	2,93E-05	8,98E-05
AC113346.1	2,916816768	3,057416649	2,94E-05	9,01E-05
AC131902.2	4,439751316	4,152066258	2,95E-05	9,01E-05
IL21-AS1	2,530329281	4,655015264	2,97E-05	9,09E-05
AC023347.1	2,885749248	3,809550518	2,98E-05	9,11E-05
AC105219.2	1,970584205	3,082848645	3,02E-05	9,22E-05
AC090568.2	3,472172099	4,650775526	3,04E-05	9,28E-05
AC007848.1	2,697556091	3,704074175	3,06E-05	9,34E-05
LINC00402	-1,145101224	5,611979086	3,09E-05	9,41E-05
AC099066.2	1,458869685	5,330572977	3,10E-05	9,43E-05
LINC02097	1,290940893	3,825760823	3,11E-05	9,45E-05
AC005699.1	1,966162511	3,090121412	3,13E-05	9,52E-05
AP001599.1	3,417734113	3,152816811	3,14E-05	9,54E-05
LINC00200	3,889640512	4,948440172	3,14E-05	9,55E-05
AC008125.1	-1,104784	4,078676001	3,29E-05	9,97E-05
FLJ31356	1,504942945	4,47709579	3,31E-05	0,0001003
GLIS2-AS1	1,153795747	6,391860097	3,33E-05	0,0001009
AL365259.1	-1,058015645	6,192327713	3,39E-05	0,0001024
AC246817.2	-1,326233366	3,131328799	3,41E-05	0,0001029
AC097358.2	2,190224989	3,041217741	3,46E-05	0,0001043
AC009646.2	5,850926384	5,583490484	3,46E-05	0,0001045
AL121929.2	1,431450867	4,217266877	3,49E-05	0,0001052
AC092794.2	1,193095043	3,281929105	3,50E-05	0,0001054
UNC5B-AS1	1,635437919	3,682801814	3,50E-05	0,0001054
AC104793.1	4,392465786	3,858636736	3,52E-05	0,0001059
AC009902.3	1,453834457	3,432451759	3,54E-05	0,0001065
AL033381.2	2,491750637	3,674469948	3,56E-05	0,000107
AL354984.1	2,08661681	3,527673983	3,58E-05	0,0001073
CALML3-AS1	1,335987737	6,239291963	3,60E-05	0,0001079
ACTN1-AS1	1,120359315	3,745498463	3,65E-05	0,0001095
MYHAS	2,465869973	3,506061204	3,66E-05	0,0001096
AP003064.2	1,833193458	4,020086095	3,66E-05	0,0001098
AC111149.2	1,735523465	6,465720488	3,68E-05	0,0001101
AP001469.2	1,111968133	3,648955644	3,71E-05	0,0001109
AC092756.1	-1,074797944	3,261503594	3,72E-05	0,0001112
AC110760.4	2,591105589	4,778863059	3,74E-05	0,0001118
LINC01036	3,419353728	3,428248266	3,75E-05	0,000112
AC011816.2	1,236378518	3,139937294	3,80E-05	0,0001135
AC010907.2	2,063914296	4,558738281	3,82E-05	0,0001138
AC004596.1	1,094527588	3,749108194	3,85E-05	0,0001149
LINC01124	1,107444141	9,896609668	3,90E-05	0,0001162

SCHLAP1	3,555727923	3,454822409	3,99E-05	0,0001187
AC080038.2	1,556300489	3,412651216	4,01E-05	0,0001191
AC243772.2	1,430770299	4,184610133	4,02E-05	0,0001196
AL078587.1	1,289564845	3,718557591	4,07E-05	0,000121
LINC01632	3,332832464	4,509072042	4,11E-05	0,0001219
LINC02477	2,595082416	3,588791367	4,13E-05	0,0001225
AL138960.1	2,004359516	3,294911639	4,14E-05	0,0001228
AC006273.1	1,410760336	4,786360475	4,20E-05	0,0001244
AC022784.1	1,084625347	6,757706222	4,23E-05	0,0001253
AL033380.1	1,897251202	3,759372601	4,25E-05	0,0001258
AC005884.1	-1,069023348	3,203967808	4,28E-05	0,0001265
AC020637.1	3,063439218	3,486171043	4,31E-05	0,0001274
AL356364.1	3,308550176	3,73895391	4,40E-05	0,0001299
AC114803.1	2,61707072	3,057498805	4,41E-05	0,0001301
AC018558.1	2,998644574	3,002796729	4,41E-05	0,0001302
AC110048.2	1,221567539	3,72782943	4,50E-05	0,0001325
AL365295.1	1,08575733	5,215685435	4,61E-05	0,0001353
AC079089.1	1,75262387	3,708442364	4,62E-05	0,0001356
STXBP5-AS1	1,002889933	6,014852365	4,64E-05	0,0001361
KIZ-AS1	1,07585724	3,821270139	4,66E-05	0,0001365
AL121672.3	1,294923902	3,329792688	4,77E-05	0,0001397
AC016738.1	1,06115702	5,090403888	4,78E-05	0,0001399
AL049836.1	2,117549483	3,188701559	4,82E-05	0,0001411
AC092167.1	1,796715951	3,50193464	4,84E-05	0,0001415
AL356056.2	1,080024945	5,544522846	4,89E-05	0,0001428
LHFPL3-AS2	2,211168322	6,995710493	4,91E-05	0,0001432
AL121845.4	1,068490241	6,417788808	4,92E-05	0,0001436
OVOL1-AS1	2,401861865	5,987824625	4,93E-05	0,0001437
AC009414.2	1,088115573	7,212386008	4,93E-05	0,0001437
Z82214.2	2,614134163	3,181627917	4,94E-05	0,000144
ERVH-1	2,070131813	3,164444232	5,01E-05	0,000146
AC012360.1	1,07647224	3,677235489	5,15E-05	0,00015
MNX1-AS2	2,801797556	3,835263464	5,20E-05	0,0001511
AL080312.2	1,799820105	3,375654662	5,20E-05	0,0001511
AC022092.1	1,950720896	3,393863733	5,20E-05	0,0001511
DOCK9-AS1	-1,056905388	3,295197085	5,23E-05	0,0001519
LINC02389	2,011454029	3,173572557	5,24E-05	0,0001521
AC005256.1	2,96402157	3,254661619	5,30E-05	0,0001536
AC023301.1	2,096140766	3,295191612	5,32E-05	0,0001539
AC125608.1	4,113459775	4,325462521	5,34E-05	0,0001545
AC097717.1	1,230698719	3,529946463	5,34E-05	0,0001545
AC023824.6	3,765669263	3,714260149	5,37E-05	0,0001553
AC012339.1	3,140570848	3,055075966	5,41E-05	0,0001562
LINC01556	1,709752012	4,169660032	5,42E-05	0,0001565
MEG3	1,606820046	12,1927992	5,48E-05	0,0001582
LINC02427	1,233675626	3,955962037	5,49E-05	0,0001584
AC108865.2	3,027215049	3,558992475	5,50E-05	0,0001585
AL049543.1	1,705471415	3,446692832	5,53E-05	0,0001592
AL121890.2	1,149922141	3,136181057	5,55E-05	0,0001597
AC022784.6	-1,062282963	9,428967228	5,55E-05	0,0001597

LINC01073	-1,013863898	3,727029192	5,57E-05	0,0001602
AC022148.1	1,797791861	3,670889654	5,61E-05	0,000161
LINC01510	2,109317642	4,56330402	5,67E-05	0,0001627
AC117402.1	1,304426075	5,117588535	5,76E-05	0,0001654
AL450263.1	1,522789341	3,951011053	5,84E-05	0,0001674
AC105046.1	-1,13966558	3,576722809	5,91E-05	0,0001692
AC073370.1	1,568521876	3,56273638	5,97E-05	0,0001708
AC092652.1	3,473791109	3,432024274	5,97E-05	0,0001708
AC097478.3	2,686957931	3,077044203	6,03E-05	0,0001723
AL606468.1	1,662947411	3,333714968	6,06E-05	0,0001731
AC135371.1	3,850705199	3,671414635	6,12E-05	0,0001745
AL773572.1	5,08776075	4,670853658	6,12E-05	0,0001747
AC131934.1	1,155285292	3,357828316	6,22E-05	0,0001771
LINC01854	3,157678442	3,365130999	6,26E-05	0,0001781
AP000808.1	1,655652273	8,797098413	6,29E-05	0,0001786
AC129507.4	-1,006375057	3,300286435	6,35E-05	0,0001802
LINC01460	1,942238697	3,307813676	6,37E-05	0,0001807
AC022146.2	1,278129718	3,450121973	6,40E-05	0,0001814
C8orf37-AS1	1,18104955	4,614457802	6,49E-05	0,0001837
AL117328.2	1,127212814	3,350371972	6,53E-05	0,0001849
AC034111.1	1,443783947	3,076756954	6,56E-05	0,0001855
LINC01788	3,356316264	3,130025015	6,57E-05	0,0001857
AC093821.1	2,685579538	3,31164345	6,62E-05	0,0001871
AL354977.1	1,680478367	3,157162498	6,65E-05	0,0001879
AC064875.1	1,088263798	4,129524327	6,85E-05	0,0001933
AL157931.1	2,888807496	3,241841284	6,91E-05	0,0001949
AC008514.1	1,834759573	4,323255043	6,91E-05	0,0001949
PLBD1-AS1	-1,06848425	5,137414374	6,94E-05	0,0001956
AC079298.3	2,613768856	3,134004208	6,99E-05	0,0001967
AC008738.6	1,30946511	3,609399909	7,02E-05	0,0001975
BLACAT1	2,329950266	4,22703839	7,03E-05	0,0001978
AC019183.1	1,880617577	3,502553875	7,08E-05	0,000199
AL023803.3	1,124588819	3,62388234	7,10E-05	0,0001995
LINC01579	2,685580716	4,128150619	7,11E-05	0,0001998
AC011453.1	2,230688477	3,98149152	7,24E-05	0,0002033
AL356056.1	1,940179619	3,687652092	7,25E-05	0,0002035
AC126773.2	1,779611083	3,315535478	7,38E-05	0,0002068
AC096711.3	1,95195386	4,489460187	7,40E-05	0,0002071
AL627309.1	1,968495588	4,085197603	7,43E-05	0,0002079
LINC01832	1,809126775	3,065309102	7,45E-05	0,0002084
AC060834.2	3,8658687	3,863683707	7,48E-05	0,000209
LINC02269	3,873211909	4,180263105	7,57E-05	0,0002111
AL391832.3	1,147320203	3,909336216	7,58E-05	0,0002112
MYOSLID	1,662877062	3,68337046	7,59E-05	0,0002114
LINC02185	1,435370951	3,91875831	7,60E-05	0,0002116
FOCAD-AS1	1,12272005	3,410713295	7,69E-05	0,0002138
Z97056.1	1,38714335	7,595815426	7,69E-05	0,000214
AC024601.1	2,053311621	3,463118308	7,74E-05	0,000215
AC008554.1	2,0346819	4,448176293	7,74E-05	0,0002151
AC079305.1	1,174390605	5,398585741	7,81E-05	0,000217

AC025154.2	2,526409651	3,553668094	7,91E-05	0,0002194
AL512413.1	1,517241107	3,9660081	7,92E-05	0,0002195
LINC02242	2,03065083	3,481627656	7,93E-05	0,0002197
AC005091.1	1,247863851	3,136104291	7,96E-05	0,0002204
AC010880.1	3,83396321	3,451392719	7,97E-05	0,0002207
AC087289.1	1,115494258	3,485006747	7,98E-05	0,0002208
AC087273.2	1,702826272	5,480260305	7,99E-05	0,000221
AL162431.1	1,670885176	3,113984525	8,04E-05	0,0002223
AP000808.2	1,063688751	4,128976045	8,14E-05	0,0002249
AL355340.1	1,151293394	3,164126592	8,24E-05	0,0002274
AC017048.3	2,220258062	3,121674321	8,27E-05	0,000228
AC027288.3	1,54557961	4,776372024	8,27E-05	0,000228
AL359397.1	1,34057296	3,290080862	8,32E-05	0,0002293
AL592071.1	1,490867717	3,505173622	8,37E-05	0,0002306
WT1-AS	2,393012712	5,451707331	8,49E-05	0,0002332
AC097478.2	2,537794	3,213500154	8,50E-05	0,0002333
AC108474.1	2,727635345	3,183581048	8,58E-05	0,0002355
AP001610.1	-1,105477413	3,709067295	8,82E-05	0,0002412
AL121992.1	1,008748987	3,649971084	8,82E-05	0,0002413
U95743.1	2,648768502	3,465887426	8,84E-05	0,0002417
AC106744.2	3,170111716	3,064721041	8,90E-05	0,0002432
LINC01933	1,585145244	3,450889329	9,00E-05	0,0002456
AC096711.1	2,078993104	3,690658461	9,04E-05	0,0002468
LINC01193	3,363986315	3,261641017	9,19E-05	0,0002506
Z97192.3	1,277860662	4,19968894	9,22E-05	0,0002513
AL157834.1	1,244294343	3,602911738	9,34E-05	0,0002544
LINC00462	2,646669447	3,381911448	9,36E-05	0,0002548
Z82188.2	1,142150523	3,451860848	9,52E-05	0,0002588
AL137802.2	1,030217921	4,259342402	9,55E-05	0,0002594
AC005329.3	1,311146926	3,22137605	9,56E-05	0,0002596
MIR181A2HG	1,116939969	4,64170676	9,60E-05	0,0002607
AC008403.3	1,508155841	3,582391793	9,79E-05	0,0002653
LINC01208	2,069626442	3,733606047	9,92E-05	0,0002686
AC132938.1	1,220933371	4,60049358	9,94E-05	0,000269
AC007938.3	1,103109385	5,461967103	9,98E-05	0,0002698
AC130469.1	1,165216247	3,790552725	0,000100041	0,0002703
AC068790.7	1,113136203	3,54776783	0,000101328	0,0002734
AC132807.2	2,438150197	4,362431829	0,000102012	0,0002748
AC004839.1	1,192383589	3,366846176	0,000102661	0,0002764
LINC00578	1,617139348	4,090237591	0,000103068	0,0002774
FMR1-AS1	1,077071227	4,135828535	0,000103199	0,0002776
LINC01914	1,517825685	4,844294236	0,000103838	0,0002791
PGM5P3-AS1	1,789426654	3,349558801	0,000104162	0,0002798
AC139749.1	2,179312544	7,005592244	0,000104185	0,0002798
AL354719.2	1,29463291	7,746661271	0,000104414	0,0002802
AC010317.1	1,290918294	4,328683318	0,000106621	0,0002858
AL928921.1	1,145755924	7,226817622	0,000107273	0,0002875
AC015849.5	1,088564407	6,552936903	0,000109613	0,0002928
AC106786.1	1,543138068	4,097047186	0,000111417	0,0002973
AF127577.3	3,492122157	4,004044765	0,000111622	0,0002977

LINC00460	3,061088143	4,11584185	0,000112848	0,0003007
AL353803.1	1,960644717	3,199650627	0,000113228	0,0003016
AC023824.1	3,502929954	3,349573793	0,000114426	0,0003045
LINC02315	2,170388265	5,966574701	0,000115515	0,0003073
AC108868.1	3,589092022	4,253829958	0,000116342	0,0003094
AL157714.2	2,622056049	3,496959343	0,000116817	0,0003105
MIR3681HG	1,566073421	4,744766652	0,000116976	0,0003107
MIR4300HG	2,563909766	3,344603002	0,000117848	0,0003128
AC026523.1	2,95381937	4,026323539	0,000123177	0,0003259
AC104971.4	2,23138525	4,583530463	0,000125292	0,0003313
LINC01996	3,048389754	3,258469545	0,000126299	0,0003337
AL512306.3	1,161181812	3,847836397	0,000127481	0,0003363
AC080037.1	2,397634076	4,011048182	0,000128587	0,0003391
LINC00473	2,670840095	6,211265031	0,000131488	0,0003463
AC237221.1	1,712006665	7,319483145	0,000133782	0,000352
AC061975.1	1,651566139	3,350446066	0,000134548	0,0003539
LINC01203	3,700132685	3,55840957	0,000135513	0,0003563
ITFG1-AS1	1,047421711	3,451719796	0,000138702	0,0003635
LINC02054	2,773608268	4,603410705	0,00013968	0,000366
AL442067.1	1,207394162	3,383968989	0,000142101	0,0003719
LINC01807	2,023284471	4,823115365	0,000142196	0,000372
AC078778.2	1,257977124	3,238674387	0,000144395	0,0003775
AC106895.1	3,148549453	3,273696737	0,000145084	0,0003789
AC005307.1	3,045586628	3,246431433	0,000145089	0,0003789
RAMP2-AS1	1,061295896	7,221859716	0,000145397	0,0003795
LINC01048	3,094665067	3,239158044	0,000145766	0,0003802
AL138924.1	1,369700399	3,362336507	0,00014694	0,0003831
AC005696.4	1,768863402	3,676693153	0,000147058	0,0003833
AC022167.4	-1,128406975	5,599357552	0,000148189	0,0003861
AC092336.1	4,039229016	3,967946721	0,00014868	0,0003871
FARP1-AS1	1,421572126	3,167067182	0,000149726	0,0003896
LOXL1-AS1	1,263948468	6,742308618	0,000150656	0,0003919
AP000345.3	1,009820206	4,938948191	0,000151965	0,000395
AC021351.1	3,154505006	3,174842966	0,000153055	0,0003977
LINC01249	3,434490226	4,045690826	0,000154395	0,000401
LINC01022	3,251552966	3,350544629	0,00015568	0,0004039
SNAP25-AS1	1,230997838	8,265608965	0,000156731	0,0004062
BX284668.6	1,068735395	3,581263167	0,000158709	0,0004104
AP000688.2	2,21728649	4,512442122	0,000159731	0,0004126
TGFB2-AS1	1,447787575	4,795465315	0,00016313	0,0004209
AL357078.3	1,036359894	3,42810212	0,000163877	0,0004227
AL138885.3	3,515223022	3,212958293	0,000164059	0,000423
LINC00272	2,40933407	3,495412173	0,000165574	0,0004266
LINC00982	1,346134668	6,998913629	0,000165576	0,0004266
LHFPL3-AS1	2,498430407	3,396847588	0,000166379	0,0004285
AP000785.1	-1,249393134	3,44000938	0,000169076	0,0004348
AL121832.1	3,072872035	3,12735051	0,000170542	0,0004382
AP005229.1	3,456595076	3,183852302	0,000172376	0,0004426
LINC01951	3,432622133	3,270024201	0,000176603	0,0004528
AC114284.1	1,262948733	3,595115402	0,00017778	0,0004556

AC016205.1	1,660925822	7,066331819	0,000178393	0,000457
AC022211.1	1,194857515	3,35564669	0,000178622	0,0004575
AC005730.2	2,152724126	4,111030534	0,000179865	0,0004603
LINC01976	2,54670654	3,111315721	0,000180801	0,0004624
AC130456.3	2,145209645	4,413095737	0,000181588	0,0004642
AL451069.1	1,884622354	4,502721154	0,000182535	0,0004663
LINC01230	3,534594132	3,721807917	0,000183298	0,0004681
SLC6A1-AS1	1,05434345	5,520006692	0,000184387	0,0004707
LINC00551	-1,436003243	3,303852568	0,000184532	0,0004709
AC004835.1	2,051943655	3,179953964	0,000185378	0,0004728
AC025162.2	1,051198164	3,383791731	0,000187782	0,0004786
AC097065.2	1,485050994	3,426840904	0,000188672	0,0004807
HOTAIR	3,131327231	3,444647671	0,000188903	0,000481
AL157904.1	1,267234882	3,201568478	0,000189297	0,0004818
EPHA5-AS1	3,527419811	3,587041663	0,000190198	0,0004839
AC061975.7	-1,685269246	4,558444671	0,000192862	0,0004903
AC128689.1	2,601574858	3,501492285	0,000193031	0,0004906
AL159972.1	-1,058550979	3,18433946	0,000193265	0,000491
AL139002.1	2,44987161	3,968664495	0,000193702	0,0004919
KCCAT198	2,056728447	3,366731408	0,0001956	0,0004962
AC010737.1	-1,214331157	3,503905017	0,00019573	0,0004962
AL033381.1	2,051235884	3,507426044	0,000195742	0,0004962
AL117338.1	2,460529852	3,220875655	0,000196816	0,0004985
BX119904.2	3,304358688	3,261933317	0,000197267	0,0004995
AC087380.1	2,097792875	4,60150748	0,000199668	0,000505
DSCR10	2,812652227	3,149662951	0,000202429	0,0005113
LINC01037	2,777946547	3,124097254	0,00020274	0,0005119
AC100827.4	1,225021391	3,315666313	0,000204591	0,000516
HOXC-AS3	2,806599351	3,121479188	0,000204681	0,000516
AC010524.1	1,379009991	3,272597386	0,000204882	0,0005163
AC090337.1	1,294372202	3,474854115	0,000205408	0,0005175
RHOXF1-AS1	1,249428416	6,099372233	0,000207537	0,0005225
FAM225B	1,320415147	3,819103655	0,00020778	0,0005229
RUNDC3A-AS1	1,154785397	4,04539961	0,000208623	0,0005248
HOXC13-AS	3,07490191	3,218081995	0,000209075	0,0005258
AC008906.2	1,078562266	3,523888239	0,000211898	0,0005327
LINC02091	1,253812168	3,484204516	0,000212039	0,0005328
AP001626.1	1,700642739	4,513732522	0,00021233	0,0005334
AC104574.2	1,945936534	4,097571083	0,00022096	0,000554
AL353747.3	2,162695534	4,283557619	0,000221692	0,0005555
AL021937.1	1,075864679	3,593922764	0,000224659	0,0005619
AC092143.4	1,031524308	3,327554043	0,000225892	0,0005644
LAMP5-AS1	3,450625253	3,305965083	0,000226877	0,0005666
LINC01088	1,399721404	4,129904315	0,000228098	0,0005695
AL121974.1	2,953181049	5,204088765	0,000230463	0,0005747
DIO3OS	-1,167206595	8,666903304	0,000230527	0,0005747
LINC01978	1,123067814	4,958545181	0,00023385	0,0005828
AL139246.4	1,78969548	3,551558399	0,00023407	0,0005831
AC156455.1	1,020586571	6,27363586	0,000239136	0,0005951
AC010967.1	1,60864645	3,674518201	0,000240321	0,0005978

AC032011.1	1,100665807	3,178805715	0,000241837	0,0006012
AC112236.1	1,772955053	3,654391968	0,000243143	0,000604
SRGAP3-AS4	2,524707215	3,385408523	0,000245919	0,0006104
AC012414.5	-1,021433474	3,295332481	0,000246783	0,0006122
LINC02280	1,537831422	3,466370009	0,000246799	0,0006122
LINC02125	2,343666341	3,470955015	0,000247929	0,0006148
AL157700.1	1,008972724	4,169704474	0,0002484	0,0006157
LINC02211	2,332296922	4,396954186	0,000252833	0,000626
AC093151.2	1,796491473	3,479889697	0,000253655	0,0006276
DNAJB5-AS1	1,261260625	3,691494649	0,000254233	0,0006288
LINC01836	1,043803166	6,560615662	0,000261095	0,0006453
LINC01738	3,044578329	3,966005608	0,000261367	0,0006458
AC004988.1	1,274134848	4,121559779	0,000261972	0,000647
AC006213.5	1,015263796	4,244977339	0,000262975	0,0006493
AC044781.1	1,663896017	3,136871224	0,000264063	0,0006515
AP003680.1	1,069524831	3,539093449	0,000269706	0,0006645
LINC00593	1,753805291	4,07415187	0,000270105	0,0006652
AL596223.1	1,551466663	3,258785016	0,000272445	0,0006705
AC016831.5	1,214523273	4,17180068	0,000274201	0,0006744
AL354714.1	1,496557159	3,672316476	0,000275908	0,0006782
AC100826.1	1,656135123	4,778238278	0,000275969	0,0006782
LINC01281	1,783073237	3,434245809	0,000276238	0,0006787
AC009312.1	3,865622402	3,854349102	0,00027813	0,0006831
AF274855.1	3,722880326	3,599168052	0,000279801	0,0006867
LINC02247	3,64741292	4,662159986	0,000285221	0,000699
AL138720.1	1,762301704	3,423327848	0,000286487	0,0007014
C20orf166-AS1	1,952383647	4,562166455	0,00028751	0,0007036
AC004000.1	1,247624851	3,413122776	0,000287918	0,0007044
AL049646.1	2,315118064	3,355346792	0,000289314	0,0007075
LINC02381	1,155348551	8,560723024	0,000291006	0,0007114
AC126323.6	1,932830663	3,623492975	0,00029384	0,0007181
AC004775.1	1,038461028	3,651795107	0,000294717	0,0007197
LINC02345	1,275566848	4,18521476	0,000295031	0,0007202
MSC-AS1	1,171725347	9,018654692	0,000297427	0,0007258
AC010789.1	2,773583773	3,294628077	0,000297609	0,000726
AC120498.10	1,76163057	4,645814497	0,000298525	0,000728
AC010536.3	1,266049249	3,103436277	0,000299844	0,0007307
AC012640.3	-1,005105962	4,114563262	0,00030176	0,0007351
AP003717.1	1,603156077	3,04292666	0,000302494	0,0007366
AC110285.3	2,680460873	3,408727941	0,00030266	0,0007368
AC090503.1	2,421643426	3,317200163	0,000305544	0,0007428
AL669970.1	2,693914564	3,152329041	0,000306241	0,0007442
AC009264.1	2,531991396	3,737631982	0,000306403	0,0007443
AL160162.1	2,786063112	3,526180556	0,000307641	0,0007468
AC069228.1	2,86498734	3,331962134	0,000308022	0,0007474
AC018814.1	2,67128052	3,015228914	0,000308086	0,0007474
AL391069.4	1,146414472	3,281664193	0,000309338	0,0007497
ROR1-AS1	2,145612148	3,704881816	0,000310795	0,0007526
AL355916.1	1,422303923	4,786284445	0,000312084	0,0007552
AC079906.1	1,184282026	3,267122875	0,000313498	0,0007584

AC007614.4	1,393565406	3,631252725	0,000314422	0,0007604
AC092801.1	2,67284014	3,37732172	0,000316583	0,000765
LINC02257	1,901012243	3,671508226	0,000323891	0,0007812
LINC00504	1,073287515	6,415721056	0,000327866	0,0007898
AC023983.2	1,423713188	3,397256094	0,000329369	0,000793
AC020571.1	1,4532029	5,099351598	0,000329392	0,000793
AC048344.4	1,203811591	3,530521315	0,000330076	0,0007943
AC090673.1	1,719864708	3,371364033	0,000331052	0,0007961
AL445493.2	1,707636356	4,182468187	0,000337373	0,0008102
AL159169.3	1,087359335	3,177231654	0,00034585	0,0008297
LINC01477	4,32720804	3,951144191	0,000354096	0,0008483
BX322559.1	4,134962583	4,277820385	0,000361297	0,0008644
AL078612.2	2,147613101	3,346357848	0,000362414	0,0008667
SPACA6P-AS	1,676934515	3,097377553	0,000373015	0,0008903
AC131097.1	1,701910569	4,602984166	0,00037388	0,0008913
CSTF3-AS1	1,004323864	3,641498358	0,000380221	0,0009053
AC087857.1	2,720875954	3,282519964	0,000382065	0,0009094
LINC02393	3,226079772	3,207948426	0,000382832	0,0009102
AC079336.2	1,138550639	3,136095655	0,000383756	0,0009121
AC002094.4	1,11917293	3,208184482	0,000384758	0,0009139
LINC01993	1,560009538	4,716458727	0,000385449	0,0009152
LINC01143	2,330953856	3,195882132	0,00039212	0,0009298
CASC11	1,127051791	3,383828217	0,0003932	0,0009317
LINC02038	1,323694563	4,981127201	0,000396477	0,0009385
LINC01750	-1,003762287	6,647594983	0,000397712	0,0009411
PLUT	2,213355174	4,209214106	0,00039945	0,0009449
AC064836.2	1,167341311	3,164936729	0,000401374	0,0009488
AL080314.1	1,346557516	3,367110182	0,000409293	0,0009652
AC040174.2	2,706861851	3,395293796	0,000412301	0,0009713
AC106799.2	2,439113871	3,014186086	0,000418934	0,0009859
AP005328.2	2,047998591	3,265177407	0,000419923	0,0009876
AF186192.3	1,509930667	3,500557709	0,000428437	0,0010066
AC005540.1	1,100145798	3,521466666	0,000436326	0,0010229
AC007614.3	1,018617581	4,168351917	0,000437495	0,0010248
AC004231.1	1,606091535	4,662101366	0,000438923	0,0010274
AC079209.1	1,185306039	6,22522682	0,000447207	0,0010461
LINC01777	2,840564955	3,389356312	0,000449889	0,0010517
C7orf71	1,897360288	3,216724754	0,000452686	0,0010578
AC005841.1	1,384046295	3,247068727	0,000457346	0,001068
MIMT1	1,852231796	4,014394211	0,000457819	0,0010688
LINC01827	1,534596176	3,112403187	0,00045896	0,0010711
LINC02008	2,713832218	3,271787194	0,00046063	0,0010735
LINC01727	-1,419214035	5,718508226	0,000461322	0,0010748
Z93403.1	2,122327724	3,164201564	0,000463679	0,0010796
AC012103.1	2,935485275	3,305849353	0,000463693	0,0010796
AC011287.1	2,099379229	3,499939602	0,000468689	0,0010897
PCAT29	1,135295302	6,025130545	0,00046941	0,001091
NAV2-AS3	1,61709025	3,343136413	0,000470319	0,0010928
LINC01152	1,347674709	6,596475906	0,000473177	0,0010983
AC021393.1	3,652468351	3,263307058	0,000473752	0,0010993

AC026992.1	1,441017449	3,388764962	0,000476012	0,0011042
CR559946.2	1,055906394	3,362897831	0,000477979	0,0011076
DISC1FP1	-1,21808085	4,305684305	0,000481874	0,0011159
LINC01886	2,925582602	3,271816907	0,000489336	0,0011317
AL590822.1	1,008111784	4,317829408	0,000493953	0,001142
AC003092.1	2,887713726	3,05963347	0,000494327	0,0011425
AC244517.2	2,222133891	3,194845758	0,000494833	0,0011432
LINC02195	1,18636087	3,848148537	0,000495808	0,0011451
AP005233.1	2,959437122	3,19274672	0,000496298	0,0011459
AL354824.2	1,435150731	3,303510918	0,000496649	0,0011463
AC117382.2	1,229603136	3,244819665	0,000498916	0,0011506
AC112495.1	-1,546351839	3,252074995	0,000501449	0,0011556
AP005229.2	3,363630895	3,153604513	0,000501495	0,0011556
AC115837.2	3,260033636	3,419804922	0,000502331	0,0011571
AP000924.1	1,42475875	6,221786536	0,000503542	0,0011595
LINC01726	-1,417116935	3,614638364	0,000504655	0,0011617
AC090541.1	2,846651092	3,584209957	0,000506805	0,0011662
AC124287.1	1,155110971	3,284447297	0,000507028	0,0011664
AL122058.1	2,873862701	3,085497577	0,000507817	0,0011678
PPP4R1-AS1	1,009190465	3,62795793	0,000510555	0,0011737
AC019185.2	1,821015854	3,242325315	0,000511098	0,0011746
CASC16	1,503084718	3,486273431	0,000521826	0,0011988
AC105105.4	1,582457215	3,401156027	0,000525039	0,0012046
C1orf147	1,062288952	3,598064067	0,000529772	0,0012148
GACAT3	2,618086462	3,234294559	0,000529816	0,0012148
AC019117.1	1,066925871	6,723369188	0,000534618	0,0012242
AC026336.3	4,137917373	4,782284503	0,000535942	0,0012268
AC090774.4	2,652543548	3,474842637	0,000538105	0,0012313
FRY-AS1	1,065758464	3,927822588	0,000542405	0,0012403
CU634019.6	1,088786585	3,460103922	0,000544672	0,0012451
LINC02128	-1,059852084	6,589795498	0,000549205	0,0012538
LINC02408	1,785994924	3,148516049	0,000556615	0,0012694
LUARIS	1,199273105	4,174097587	0,000557263	0,0012701
AL133396.2	1,167788895	3,157303123	0,000561241	0,0012784
AL138749.1	-1,75059416	4,491690094	0,000569691	0,0012955
AL121890.4	1,050641646	3,194971451	0,000574252	0,0013046
AC062004.1	-1,08759092	4,136691217	0,000577985	0,0013118
LINC01517	2,352736068	3,229705075	0,00058164	0,0013196
MEG9	1,676986024	5,948638522	0,000584352	0,0013253
AL008733.1	2,294740371	3,287644032	0,000587767	0,0013322
AC079385.3	1,045352436	3,707150631	0,000592907	0,0013434
AC113361.1	1,104527839	3,463771286	0,000605001	0,0013673
AC119428.2	-1,019910092	3,216161909	0,000611313	0,0013802
AC005746.3	1,446439464	3,100185095	0,000627286	0,0014144
AP003086.2	1,056632044	3,203720323	0,000628089	0,0014158
AC211433.1	1,030482952	3,497606969	0,000628307	0,0014158
AC007376.2	1,086795815	3,241116808	0,000633978	0,0014276
TESC-AS1	1,657489665	4,734995929	0,00063462	0,0014286
LINGO1-AS1	2,223119039	3,571709808	0,00064162	0,0014439
MIR7-3HG	1,893612582	3,887823799	0,000644356	0,0014496

ABHD11-AS1	1,23993351	4,779704079	0,000646661	0,0014538
AC107871.2	1,181165524	3,479838268	0,000651312	0,0014638
LINC02268	-1,058605766	3,73915573	0,000660197	0,0014814
LY86-AS1	1,841696424	5,027801144	0,000663568	0,0014885
LINC00336	1,791608066	3,342884463	0,000667386	0,0014961
LINC01170	1,878696444	3,210047292	0,000668028	0,0014966
BVES-AS1	1,413357537	3,177014279	0,000672746	0,0015066
AL359694.2	1,41106144	3,225895174	0,000674895	0,0015105
AL355482.2	1,875679334	3,054031968	0,000680206	0,0015219
AL121852.1	1,012650896	3,119952324	0,000683127	0,0015279
BX470209.1	1,816475911	4,593239938	0,000700511	0,0015648
LMO7-AS1	1,079631829	4,792374374	0,00070233	0,0015683
AP000424.2	1,30667902	4,427794823	0,000710327	0,0015839
AC025524.2	1,960043769	3,132915562	0,000711669	0,0015857
AL353803.2	1,611323811	3,483202723	0,000711713	0,0015857
AC040174.1	2,522661508	4,06008172	0,000712339	0,0015866
AC068790.5	1,007502585	3,434860601	0,000712688	0,0015869
NFIA-AS2	1,213353598	3,800927295	0,000718202	0,0015981
MIR202HG	2,403565505	3,286967592	0,000718444	0,0015981
LINC00470	1,42228733	7,28687163	0,000720643	0,001602
TH2LCRR	1,095455329	4,117776739	0,000722797	0,0016063
AL136129.1	1,553579746	4,393235822	0,000723702	0,0016072
AC005304.2	-1,207290248	4,698308864	0,000726855	0,0016131
AC068831.8	1,317122026	3,131543325	0,000731128	0,0016201
LINC00327	1,323728375	4,097985133	0,000739028	0,0016371
AC004466.3	1,157605	3,2843634	0,000751082	0,0016622
AL031674.1	2,010988559	3,300323575	0,000757184	0,001673
AC004593.1	1,115892959	5,372837672	0,000758148	0,0016746
LINC01665	2,577106487	3,031671088	0,000759895	0,001678
AL121895.2	1,181861542	3,971741621	0,000761684	0,0016814
RAPGEF4-AS1	1,172563505	3,742040879	0,00076794	0,0016936
AC010487.2	1,206483709	3,699445651	0,000775981	0,0017091
AC016723.1	1,591337249	4,993360119	0,000778194	0,0017135
AC073342.1	1,047801618	3,08474568	0,000797621	0,001754
BARX1-AS1	2,414752833	3,092327571	0,000800648	0,0017601
AC110618.1	1,097671356	3,519040583	0,000802195	0,0017624
AC005487.1	1,298651274	3,249419587	0,000804434	0,0017648
LINC01090	2,169722981	3,085361814	0,000806591	0,0017687
AC106799.3	2,195282923	3,16099341	0,000816216	0,0017881
AL157896.1	1,405663643	3,845213759	0,000827136	0,0018109
VLDLR-AS1	1,287739199	5,067971171	0,000829728	0,0018154
AC136475.3	1,161213487	9,129429867	0,000840247	0,0018367
LINC00323	1,569540363	4,199365779	0,000854036	0,0018651
AC145146.2	1,572970873	3,147817775	0,000854759	0,0018661
AL390778.2	-1,836737517	4,951237348	0,000862169	0,0018816
AL391813.2	2,434825182	3,199765638	0,00086552	0,0018878
LINC02444	2,059864907	3,052715998	0,000874598	0,0019051
LINC01580	2,631234369	3,256802222	0,000874838	0,0019051
AC245407.1	1,782007928	3,438755191	0,000880554	0,0019147
AC004466.2	1,24799636	3,183159362	0,000880632	0,0019147

AC104072.1	3,228487183	4,606214615	0,000892259	0,0019394
CELF2-AS1	1,798894578	4,308767756	0,000910115	0,0019751
AC092131.1	2,446349453	3,023219511	0,000917027	0,0019889
IGF2-AS	1,879866532	7,843048341	0,000917838	0,00199
LINC00304	1,248327107	4,065593103	0,000935674	0,0020274
LINC01671	1,162268924	7,277424293	0,000941209	0,0020387
AC009084.1	1,424680511	3,210964548	0,000942127	0,0020401
LINC02011	1,575501369	3,078812723	0,000942775	0,0020409
SNAP47-AS1	1,131815632	3,104828496	0,000944206	0,0020427
AC073072.1	1,340756097	3,219272022	0,000945684	0,0020452
AL442125.2	1,075701842	3,558463489	0,000979252	0,0021146
AL136172.1	1,038649848	3,325372111	0,000988025	0,0021328
AC078880.3	1,926278363	3,990236146	0,000989772	0,0021353
LINC00392	2,940321559	3,012502086	0,000995874	0,0021471
AC245884.9	1,959105967	4,032638192	0,0009981	0,0021506
PRICKLE2-AS3	1,582694976	3,096435448	0,001005977	0,0021648
AC008568.1	3,12274384	3,560338464	0,001006929	0,0021662
AC005821.1	1,584342632	3,126891917	0,001008525	0,002169
LINC02087	2,459875353	3,229225166	0,001020765	0,0021933
LINC00412	1,038689979	3,165451886	0,001029623	0,0022109
AC121247.1	1,100286699	4,126430506	0,001032879	0,0022166
AC105105.5	2,229845342	3,417376064	0,00103377	0,0022178
ARAP1-AS1	1,964215097	3,316635601	0,001057336	0,0022648
AL158166.1	1,132975786	3,69016715	0,001059904	0,0022689
AL356108.1	1,304980741	3,522152276	0,001068215	0,002286
AC027228.2	1,079595859	4,426200932	0,001102344	0,0023547
AL157401.1	2,487930113	3,010441041	0,001108456	0,0023663
AC007255.1	1,33766753	4,107362067	0,001109645	0,0023681
AC013565.1	1,588702044	3,178381539	0,001117875	0,0023842
LINC00582	-1,109590193	3,396472112	0,001119641	0,0023872
AC015660.2	1,586370209	3,785158109	0,00112096	0,0023893
AJ009632.2	1,267519837	7,450047843	0,001128842	0,0024054
AL109807.1	3,148070599	3,168648899	0,00113061	0,0024084
AC103702.2	1,963617746	4,499431678	0,0011527	0,0024517
LINC01705	1,422906199	5,312772443	0,001225612	0,0025964
AL929236.1	1,232228709	3,159948749	0,001230004	0,0026043
AL121757.1	1,657653043	3,492407496	0,001230889	0,0026052
AC087235.1	2,395537256	3,041377303	0,001235658	0,0026129
LINC01358	1,644757414	4,128092397	0,001239804	0,0026201
AC138466.1	1,834129515	3,40526058	0,001258141	0,0026548
AC124312.3	1,203982713	4,734864976	0,001261201	0,0026596
AC006111.3	1,413241765	3,060448237	0,001271321	0,0026794
AP003472.1	1,401248205	3,095146136	0,001280005	0,0026954
AC022028.2	1,885969542	3,417160031	0,001283448	0,0027008
AC002480.4	2,996315368	3,543776785	0,001285415	0,0027041
GRM5-AS1	2,265887857	3,151230092	0,001300304	0,0027338
AC131009.2	1,040489862	5,526653392	0,001312169	0,0027562
AL160286.2	1,619106703	3,21813436	0,001319988	0,0027718
AC008667.1	1,112319526	3,262898906	0,001322252	0,0027757
AC006504.7	-1,610393455	3,164818041	0,001326569	0,0027823

AC092198.1	1,397745024	3,874673214	0,001346245	0,0028193
RFPL1S	1,133077536	5,983702404	0,001353525	0,0028337
AC013652.1	1,095881456	5,882322444	0,001355654	0,0028373
AC015849.1	1,034592573	3,435098118	0,001372884	0,0028725
AC138305.1	2,605024167	3,072717464	0,001377368	0,0028801
LINC01568	3,349645122	3,364992522	0,001383164	0,0028914
AL136529.1	2,641761667	3,064286214	0,001385729	0,0028958
LINC00229	3,089442764	3,225765686	0,001411153	0,0029466
LINC01551	2,690618296	3,455820553	0,001424743	0,0029729
AC008659.1	1,814088096	3,497709657	0,001425538	0,0029737
AC012379.1	-1,148027158	5,800957455	0,00143276	0,002986
LINC02137	2,025526001	3,699851321	0,001446311	0,0030134
AL583722.3	-1,029923203	3,547475664	0,001476275	0,0030693
IL12A-AS1	1,425069887	3,439412005	0,001477467	0,0030709
AP002852.2	1,67039221	3,3680802	0,001482149	0,0030793
AL033527.2	1,053041467	3,63944102	0,001482542	0,0030793
LINC01370	-1,215380763	9,348659266	0,001500142	0,0031121
LINC01829	1,484067623	3,462376227	0,00151122	0,0031326
AL596330.1	1,967542628	4,133010803	0,001516869	0,0031424
UBE2E1-AS1	1,184328703	3,078724449	0,001517603	0,003143
AC114912.1	2,134592904	3,539391668	0,001544211	0,0031934
AL023583.1	1,007656644	4,99545808	0,001565745	0,0032302
TMEM72-AS1	1,012202706	3,996199302	0,001566978	0,0032318
AC064853.1	2,386065945	3,886368868	0,001571028	0,0032392
LINC01693	1,839357033	3,232274732	0,001577036	0,0032487
AC093772.1	2,358933538	3,132474195	0,001591886	0,0032763
AC020922.3	1,162459851	3,209499991	0,001600106	0,0032903
AC018521.7	1,070253074	3,261421658	0,001607578	0,0033037
AC016642.1	2,228780546	3,173679988	0,001614032	0,003315
AC099786.1	3,099723764	3,159199388	0,001615052	0,0033161
AC078906.1	1,469775674	3,470528761	0,00162566	0,0033359
AC104823.1	2,380117383	3,195897275	0,001643498	0,0033706
AC015660.3	1,406022639	3,43973401	0,001651655	0,0033843
AC091182.2	1,971692297	3,146189727	0,00165755	0,0033936
AL589947.1	2,496381731	3,178760869	0,001666744	0,0034102
LINC01014	2,395703828	4,37782342	0,001670481	0,0034158
AP005264.3	2,065213754	3,25592448	0,001708043	0,0034885
AC128709.1	1,032102911	3,96689387	0,001712245	0,003496
AC027348.1	1,202011388	3,250003407	0,001713736	0,0034981
LINC01105	2,603883751	3,75683232	0,001714281	0,0034981
MIR646HG	1,137720064	5,809075085	0,001722828	0,0035145
AP001476.1	1,639565843	4,183543096	0,001725198	0,0035183
CAMTA1-IT1	2,101338621	3,301866496	0,001741947	0,0035472
ZBTB40-IT1	1,140859243	3,089379564	0,001742402	0,0035472
AC073476.3	1,01072419	3,540385091	0,001760828	0,0035826
AL359636.1	1,470954873	3,267034986	0,001785852	0,0036324
AC239584.1	1,937912801	3,09790914	0,001797713	0,0036555
AL450992.1	1,000405124	3,211078049	0,001798877	0,0036568
LINC02160	-1,481014216	4,967357301	0,001825841	0,0037062
LINC01402	1,028255438	3,179819979	0,001829201	0,0037108

AC004975.2	1,343125266	3,191023947	0,001848511	0,0037445
MEG8	1,860197465	4,804128094	0,001852149	0,0037486
AC007552.2	1,130085562	3,213346236	0,001858149	0,0037596
LINC00967	1,710332308	3,786956272	0,001864931	0,0037723
AC097059.1	1,259462366	3,566150831	0,001879559	0,0037996
AC147651.1	2,340985919	5,968167339	0,001887586	0,0038137
AC133919.1	1,098102802	3,258461279	0,00189247	0,0038224
AP000439.1	2,945641384	3,80979207	0,001895167	0,0038267
AL117190.1	1,669004522	4,91911828	0,00190204	0,0038384
AC096734.1	1,771379302	3,40078845	0,001909881	0,0038531
AC026310.2	2,293534006	3,127728297	0,001911676	0,0038556
LINC00520	1,640985434	3,43149517	0,001937625	0,0038977
AC109361.2	1,524545519	3,235181183	0,001942798	0,0039059
AP000679.1	1,252325387	3,327557745	0,001965122	0,0039473
AL365181.4	1,973389296	3,340799443	0,001966554	0,003949
LINC00923	1,391928387	5,304362711	0,002014585	0,0040385
LINC01204	1,844494779	3,106506737	0,002038015	0,0040796
AC120042.2	1,042324647	3,485214909	0,002039769	0,0040819
AC083967.1	2,789151379	3,351686585	0,002048179	0,0040975
Z84468.1	2,600396772	3,377520398	0,002057392	0,0041124
LINC00567	1,762841756	3,347915961	0,002062349	0,0041199
AL365275.1	1,048575966	3,754203157	0,002071528	0,0041359
AC017076.1	1,556843109	3,809986783	0,002130315	0,0042459
LINC02470	1,724900523	3,420197931	0,002283857	0,0045363
AP001011.1	1,945905028	3,133003169	0,002291062	0,004548
LINC01896	2,661261022	3,173566385	0,002300467	0,0045615
AC005695.1	1,070549237	4,096814416	0,002368836	0,004685
AP003396.3	1,149339893	3,304768991	0,002371332	0,004688
LINC00332	1,991098501	4,326967954	0,002373663	0,0046886
AC109479.1	1,020187266	4,171407301	0,002421163	0,0047762
FOXCUT	1,692118849	3,190556226	0,002453754	0,0048337
AC005498.2	1,005496281	3,962071198	0,002473697	0,0048674
AC097460.1	1,09859442	3,225520504	0,002504025	0,0049218
AP002754.1	1,930037515	3,114299331	0,002548527	0,0050018
LINC01585	1,100377263	3,101261541	0,002555789	0,0050119
AP000897.2	1,669386541	3,097278412	0,002609981	0,0051109
CU639417.6	1,296161452	3,992163082	0,002653619	0,0051905
LINC00993	2,638276433	3,794348531	0,002670702	0,0052181
AL162293.1	1,397913396	5,40152203	0,002698836	0,0052663
AC019080.4	1,341945393	3,099547368	0,002699174	0,0052663
AC008752.2	1,085602659	3,177609318	0,002714587	0,0052934
AC254629.1	1,055652775	5,303702781	0,002756088	0,0053713
HHATL-AS1	1,428256331	3,853610682	0,002782853	0,0054179
AC022639.1	2,11229866	3,120519908	0,002939018	0,0056974
AC092691.1	2,089581323	3,502395992	0,002966684	0,0057462
AL357992.1	1,385856413	3,117957095	0,002967838	0,0057467
AC073283.2	1,347567241	5,093731954	0,002999164	0,0057962
LINC01598	2,73743151	3,019576587	0,003007329	0,0058103
AC090825.1	1,005157012	4,969661995	0,003042619	0,0058752
AC092112.1	1,29449287	3,84082992	0,0030483	0,0058846

AC008434.1	1,081539087	3,159662679	0,00304917	0,0058846
AL353747.4	1,540109742	3,527930951	0,003070821	0,0059214
NRG1-IT1	1,755273028	3,120653402	0,003074935	0,0059261
AC002480.2	1,045073857	4,391980103	0,00307883	0,005927
AL450468.2	1,412213302	3,190559216	0,003082025	0,0059304
AC116609.1	2,115828985	3,123922153	0,003082313	0,0059304
AC015574.1	2,614927645	3,283406871	0,003092879	0,0059442
AL021154.1	1,114865107	3,452125905	0,003106257	0,0059649
AC021683.2	1,364480545	3,50218399	0,003121273	0,0059904
AC083805.1	1,375397083	3,084007677	0,003123536	0,0059931
AL365436.2	1,007948725	3,118226264	0,003261481	0,0062371
AL591468.1	-1,036805471	3,346154914	0,003277533	0,0062626
NCAM1-AS1	1,410939071	3,890133679	0,003309211	0,0063212
AC017033.1	1,805733186	3,086520783	0,003393574	0,0064594
AC011445.1	1,072748895	3,889141487	0,003438464	0,0065377
AP000757.1	1,030814863	5,731578433	0,003521225	0,0066731
AC027288.1	1,670841106	3,704166275	0,003632875	0,0068734
AP005233.2	1,840630581	4,38786506	0,003671819	0,0069452
ZNF385D-AS2	3,513246662	3,578399853	0,003695036	0,0069872
AC128685.1	2,325966828	3,036320544	0,003797078	0,0071763
AC138649.1	1,044091886	4,504835244	0,003883027	0,0073228
AC027013.1	1,580255212	3,105510534	0,003910164	0,0073679
OXCT1-AS1	1,190365342	3,588973516	0,003912653	0,0073706
AL161630.1	-1,050829937	4,952662676	0,004008453	0,0075306
AL161431.1	2,869865359	5,921681588	0,004022816	0,0075535
AC010904.2	1,091995581	3,14577228	0,004029881	0,0075627
LINC01954	1,300576065	3,8820179	0,004040392	0,0075783
AC131956.2	1,216861708	3,306779883	0,004055422	0,0076024
AL450003.2	1,377342481	3,393514325	0,004085866	0,0076553
HCG22	1,098923566	3,214340972	0,004114222	0,0077002
AL133297.2	1,553925992	3,375864826	0,004226612	0,0078871
AF121898.1	2,105355847	3,104936361	0,004291311	0,0079971
AC091544.5	1,044081984	4,017653955	0,004347472	0,0080926
AC129492.1	1,218814089	4,281319148	0,004348403	0,0080926
LINC01158	2,509188921	3,014015965	0,004378235	0,0081394
LINC01638	1,182006441	4,011925434	0,004392087	0,0081542
Z97200.1	1,256964778	3,232388092	0,004456912	0,0082613
AC127496.5	1,033110622	4,429548323	0,004469545	0,008279
AC124312.4	1,232821711	3,290895888	0,004470045	0,008279
AC090907.2	1,245034088	3,601575694	0,004504514	0,0083384
LINC02232	2,362640035	4,7278591	0,004514804	0,0083552
AJ239322.1	1,972176514	2,96530297	0,004569812	0,0084503
LINC02081	1,185237683	3,760302167	0,004586477	0,0084788
AC128707.1	1,285374847	4,204934228	0,004626813	0,0085488
EMX2OS	1,251289148	4,072486492	0,004690762	0,0086555
AP001505.1	2,118655364	3,010862075	0,004725988	0,0087112
MIR200CHG	2,188669076	3,933954545	0,004750053	0,0087509
AL355312.3	1,625735415	3,008638843	0,004992349	0,0091608
AC106754.1	2,025365633	4,161051214	0,005012747	0,0091909
AJ011931.1	2,326822682	3,088598927	0,005144563	0,0094077

AC098617.1	1,388943718	4,280459912	0,005163267	0,0094395
LINC01587	1,389436045	5,953248348	0,005227704	0,0095431
AC027281.1	-1,209205294	3,30180659	0,005228214	0,0095431
AL139246.1	1,159675106	3,570531467	0,005255454	0,0095878
AC008440.3	1,02505387	3,391814348	0,005340455	0,0097326
AC124861.1	1,148030818	3,241086417	0,005459511	0,0099261
AC084855.2	1,040083627	3,947400769	0,005547202	0,0100803
AC104248.1	1,296806617	3,254889214	0,005622683	0,0102121
AL591178.1	1,245073217	3,099040482	0,005629675	0,0102194
AC092574.2	1,270373205	3,089841498	0,005703325	0,0103423
LINC01882	1,338380884	4,356434182	0,005757142	0,0104372
LINC01324	2,267838513	3,07466361	0,005805346	0,0105163
LINC01639	-1,030176497	6,29921993	0,005848423	0,0105814
AC010127.1	1,339715134	5,318789677	0,005848905	0,0105814
PCAT2	1,07122209	3,860036215	0,00588494	0,01063
AC098864.1	2,117108309	3,832699527	0,005912668	0,0106773
AC106798.1	1,336677919	4,376171221	0,005981162	0,0107897
SPINT1-AS1	1,082283558	7,365974783	0,006115295	0,0110145
LINC01634	1,07598691	3,456046003	0,006176773	0,0111195
LINC01293	1,400005609	3,423526008	0,006208199	0,0111645
AC024901.1	1,568888891	4,254567998	0,006213564	0,0111712
LINC00930	1,254658972	3,752296479	0,006497582	0,0116396
AC027130.1	1,271292761	3,473778696	0,006560015	0,0117454
AC002401.4	1,269458333	3,454411062	0,006595526	0,0118029
AL137186.1	1,105544364	3,52831862	0,006674412	0,0119317
LINC00113	2,572815098	3,348289708	0,00670213	0,0119782
AL021940.1	1,492926407	4,680958536	0,006747527	0,0120469
AL590428.1	1,031878971	3,278786019	0,00685386	0,0122224
AC104135.1	1,091964444	3,268101855	0,006861204	0,0122247
LINC01541	2,475427828	3,251078589	0,007027594	0,0124955
LINC00676	-1,12268544	3,475005054	0,007089706	0,0125963
FAM182A	1,106995229	4,058499129	0,007097321	0,0126066
AC007663.2	1,078340497	5,146229459	0,007193714	0,0127549
AC074033.2	1,527671891	3,117960363	0,007209395	0,0127765
AC108860.2	1,633742538	4,795812105	0,007209571	0,0127765
AC009163.6	1,584579044	3,515090283	0,007277761	0,0128875
AC005550.3	1,721071334	7,569238209	0,007355086	0,0130111
POU6F2-AS2	1,997852364	3,46849766	0,007423066	0,0131247
AC079360.1	1,025653801	6,500993428	0,007454302	0,0131732
LINC01087	1,672134316	3,831599319	0,007481768	0,0132157
AL157395.1	1,091366138	3,209433803	0,007482147	0,0132157
AL122019.1	1,499214835	4,019652412	0,007514144	0,0132688
AL356804.1	1,396905426	3,240585705	0,007522785	0,0132773
AL032821.1	1,176717512	3,109726861	0,007581464	0,0133741
AL137798.1	1,070087385	6,608422577	0,007671372	0,0135155
AL008723.3	1,058907244	3,952196426	0,007820105	0,0137496
AP003355.2	1,564493644	3,463050407	0,007827529	0,0137592
FOXD3-AS1	1,742644471	3,991869315	0,007944251	0,0139467
AC022509.1	1,585680406	3,33502326	0,007993703	0,0140157
LINC02182	1,522080894	3,502134899	0,008025672	0,0140647

PCA3	-1,351930793	3,564291496	0,008042192	0,0140871
LINC01198	2,269479057	3,275719743	0,008121258	0,0142107
LINC01133	1,144881848	4,768114766	0,008254533	0,0144184
AC138819.1	1,167583967	3,397858348	0,008394073	0,01464
AC023154.1	1,208459578	4,681389897	0,008401619	0,0146458
DPP10-AS1	2,373609938	6,565361996	0,008521735	0,0148403
LINC01182	1,116358955	5,573649841	0,008797751	0,0152712
BX664718.1	2,461982244	3,243293771	0,00882214	0,015302
AL157834.2	1,276758692	3,315927663	0,008875898	0,0153876
AC109927.1	1,549627903	3,580121715	0,008916271	0,0154498
AC069148.1	1,148821207	3,346856556	0,008924917	0,0154578
APCDD1L-AS1	1,190574174	3,807336005	0,008957291	0,0155015
AC006058.3	2,09190406	3,342342334	0,009110855	0,0157477
AP001180.4	1,02990249	3,092117517	0,009257691	0,0159696
AL513283.1	1,11916151	3,306811914	0,009393269	0,0161713
LINC01659	1,424077759	3,942732442	0,00946223	0,0162618
AP002957.1	1,71585578	3,253085835	0,009550085	0,0163966
AC090152.1	1,02105713	7,524880289	0,009711629	0,0166574
AC097652.1	1,408194522	4,206212138	0,010610239	0,0180603
FGF13-AS1	1,139510604	3,54760233	0,010673697	0,0181594
LINC00237	2,096743605	3,599110873	0,010709086	0,0182107
AL162574.2	1,090502485	3,267555256	0,010819535	0,0183805
LINC02398	1,467058119	3,536858389	0,010890709	0,0184791
AC137894.1	1,033038882	3,133244644	0,011060154	0,0187525
LINC00484	1,348599318	3,415252366	0,011256999	0,019049
AC107926.1	1,353002157	3,085374619	0,011355882	0,0191976
AC110741.1	1,684320948	4,345524701	0,011381149	0,0192357
AL049836.2	2,371160317	4,717719819	0,01156806	0,0195183
AL772337.2	1,577260142	3,267629561	0,011658584	0,0196615
BX470209.2	1,381397604	4,856856627	0,01241038	0,0207878
AL050338.2	1,212695298	3,43807953	0,012420969	0,0208006
MUC19	1,256050834	3,790171806	0,012667082	0,0211718
AL138881.1	1,192634096	3,353635814	0,012683983	0,021195
AC233266.2	1,180233129	3,993278055	0,012688998	0,0211982
AC074237.1	1,775957075	3,270848507	0,013018101	0,021701
AC022509.3	1,011105544	3,950849329	0,013050237	0,0217493
SLCO4A1-AS1	1,470598177	5,55842428	0,013911189	0,0230458
PCAT14	1,430947692	4,857373062	0,014182505	0,0234561
AC005006.1	1,496494542	3,331518348	0,014398171	0,0237731
LINC01115	1,493618713	3,206195183	0,014546023	0,0240001
AC006372.1	1,84440491	3,235926523	0,015620676	0,0256088
LINC02450	1,097053771	3,37861597	0,015688659	0,0257085
AC068700.1	1,203166006	3,1976461	0,016148143	0,0263862
AL049629.1	1,27236448	5,005599476	0,01618837	0,0264457
AL353593.3	1,232421213	3,181839124	0,016252524	0,026538
AC021683.1	1,114934521	3,640037762	0,016271192	0,0265622
LINC00970	1,508813319	3,165084495	0,016628627	0,0270884
FARSA-AS1	1,150214589	3,285387034	0,016807035	0,0273533
LINC00443	1,468999799	3,181158764	0,017250496	0,0280093
BANCR	1,037543879	3,092901938	0,018152701	0,0293369

AP003393.1	1,028402163	3,806446035	0,018321264	0,0295956
AL358394.2	1,384130949	3,186401529	0,018634019	0,0300448
AL138789.1	1,08511682	3,068294272	0,018704392	0,0301303
SPANXA2-OT1	1,588577128	3,216056622	0,018888836	0,0303851
LINC01924	1,474139764	3,333400519	0,019295104	0,0309811
AL359853.1	1,198609169	4,32936354	0,019561767	0,031373
CHRM3-AS1	1,518709253	4,046636772	0,01957935	0,0313867
CU639417.5	1,254570458	3,085915957	0,020004543	0,0320165
AC069360.1	1,121546942	3,433416212	0,020189862	0,0322907
LINC00524	1,492124138	4,673532542	0,021291622	0,033881
AL358334.2	1,129606544	4,741510112	0,021321355	0,0339206
AL590438.1	1,273602855	3,577131275	0,021403282	0,0340353
AC010478.1	1,62685438	3,165605071	0,022328794	0,0353128
AL355607.2	1,061882946	3,574753314	0,022611323	0,0357189
AC106795.3	1,751203207	3,875039159	0,02301134	0,0362929
TLR8-AS1	1,689879885	3,062742714	0,023122045	0,036451
AC015722.2	1,73496139	3,879209356	0,023807226	0,0374291
AC007608.1	1,108944147	4,502776684	0,025007827	0,0391216
AP000943.2	1,429827851	3,272398166	0,025354769	0,039584
AC007952.2	1,07727958	3,887974341	0,025410722	0,0396446
AC090503.2	1,343776343	3,715757454	0,025970725	0,0404365
AC128709.2	1,161878884	3,393578615	0,026686645	0,0414396
AC073174.1	-1,272205709	4,697498337	0,027462535	0,0425682
AC093001.1	-1,204313972	4,580144826	0,028246007	0,0436558
AC004853.1	1,202582234	3,194728855	0,029343572	0,045171
AL161908.1	1,488483264	3,16311365	0,029849374	0,0458276
LINC01115	1,690280871	3,155438058	0,030704174	0,0470463
AC005291.2	1,400031125	3,192165526	0,030958659	0,0473734
GCSAML-AS1	1,110355651	4,038903397	0,032019336	0,0488672

Table S2. DELs identified using the DESeq package.

id	baseMean	baseMeanA	baseMeanB	foldChange	log2FoldChange	pval	FDR
LINC01093	387,7061719	2060,357802	164,0896438	0,079641334	-3,650338804	1,36E-49	9,42E-46
ST8SIA6-AS1	160,5274056	4,118704838	181,4376597	44,05211512	5,461139385	8,64E-32	3,00E-28
AC107396.1	5,071664776	32,54549172	1,398693259	0,042976559	-4,5403062	1,61E-24	3,72E-21
LINC02476	39,21064551	0,108630276	44,43818765	409,0773699	8,676229919	3,41E-24	5,91E-21
LINC02241	62,76467021	0,066517117	71,14677624	1069,601026	10,06285704	2,74E-21	3,71E-18
LINC00221	125,0509956	0,662353918	141,6804932	213,9045143	7,740823119	3,21E-21	3,71E-18
LINC02428	253,5940767	811,3144243	179,0325329	0,220669728	-2,180039367	5,15E-21	5,10E-18
AC074327.1	140,8068856	2,751798233	159,263448	57,87613573	5,854896694	1,66E-20	1,44E-17
LINC01980	59,6520262	0,425398359	67,57002457	158,8394105	7,311425101	1,36E-19	1,05E-16
AC090502.1	76,36906969	0,291660917	86,53984626	296,7138934	8,212928671	2,89E-19	2,00E-16
FAM99A	792,9834158	2424,044611	574,9271063	0,237176784	-2,075965293	2,39E-18	1,50E-15
LINC02163	21,41872201	0,053599929	24,27502175	452,8927989	8,82302579	7,60E-18	4,39E-15
LINC00355	21,22585041	0,047620083	24,05716463	505,1894774	8,980680779	8,48E-18	4,53E-15
LINC01194	19,54035969	0,045161858	22,14666956	490,3843793	8,937769214	5,17E-17	2,43E-14
MAGI2-AS3	528,2226453	1472,005087	402,0485221	0,273129846	-1,872341125	5,26E-17	2,43E-14
LINC02027	78,8460896	274,4846304	52,69120446	0,191964134	-2,381091305	6,64E-17	2,88E-14
AC008549.1	427,3147189	1221,11195	321,1920944	0,263032472	-1,926687181	1,13E-16	4,60E-14
AL731897.1	14,70045194	0	16,66575301	Inf	Inf	3,54E-16	1,37E-13
LINC02475	24,43203516	0,223910103	27,66841551	123,5693038	6,949176593	5,12E-16	1,87E-13
AC087392.1	44,39309349	173,5713648	27,12327113	0,156265817	-2,67792587	6,07E-16	2,11E-13
LINC01767	286,5515511	804,4169572	217,318208	0,270156175	-1,888134438	8,71E-16	2,88E-13
HOTTIP	61,72968188	0,390172983	69,93015098	179,2285834	7,485656927	9,26E-16	2,92E-13
AL365181.3	559,791237	57,12483987	626,992627	10,97583168	3,456258357	1,88E-15	5,66E-13
AC010280.2	29,85453561	122,2051184	17,50820101	0,143268967	-2,803201953	2,10E-14	6,08E-12
AC004160.1	44,12036662	165,3612674	27,91169005	0,168792187	-2,566679964	2,78E-14	7,73E-12
AL161668.3	95,71228372	302,0365758	68,12882222	0,225564808	-2,148386095	5,84E-14	1,56E-11
CRNDE	138,9772833	17,77269869	155,1811047	8,731431701	3,126218233	9,00E-14	2,31E-11
PCDH9-AS2	7,832361986	37,80149403	3,82579353	0,101207469	-3,304612333	1,93E-13	4,69E-11
KCNMB2-AS1	44,97775266	2,282957507	50,68561297	22,20173298	4,472600387	1,96E-13	4,69E-11
HAGLR	268,5183054	4,461859172	303,8199693	68,0926846	6,089427908	3,57E-13	8,26E-11
AC092171.2	395,5805284	81,63844219	437,5513955	5,359624507	2,42213193	3,88E-13	8,68E-11
AC004080.2	11,11935759	0,029665935	12,60193668	424,794863	8,73062251	5,42E-13	1,15E-10
AC090809.1	11,17025222	0,01985937	12,66094646	637,5301189	9,316349691	5,48E-13	1,15E-10
LINC01018	2464,018024	6187,375437	1966,242969	0,317783039	-1,65388597	5,69E-13	1,16E-10
AC092384.2	40,1243296	149,3934412	25,5161596	0,170798392	-2,549633699	7,32E-13	1,45E-10
AC138356.1	38,12619923	140,0773709	24,49636344	0,174877379	-2,515584414	7,61E-13	1,47E-10
LINC01833	28,77738903	0,118113231	32,60884301	276,081203	8,108948855	7,84E-13	1,47E-10
LINC00907	19,80467914	88,47881622	10,62364477	0,120069924	-3,058053271	8,66E-13	1,58E-10
LINC02377	13,26633295	0,096098082	15,02705954	156,3721065	7,288839379	9,38E-13	1,67E-10
LINC01287	356,0779219	1,081446409	403,5373437	373,1459465	8,543596204	1,11E-12	1,93E-10
AC025254.1	11,26795248	0	12,77436324	Inf	Inf	1,60E-12	2,71E-10
LINC02404	29,08641834	0,263093383	32,93980403	125,2019477	6,968113196	3,37E-12	5,56E-10
AL136537.2	10,23981194	0,046660622	11,6025327	248,6579115	7,958018524	3,56E-12	5,74E-10
NPSR1-AS1	46,27790041	0,594501576	52,38530668	88,11634615	6,461337768	4,44E-12	7,00E-10
FENDRR	15,24085382	62,98983421	8,857300297	0,140614758	-2,830180076	5,35E-12	8,25E-10
AC016710.1	9,098738668	0,027509126	10,31146989	374,8381555	8,550124005	7,11E-12	1,07E-09
LINC01611	9,016802405	0,021449212	10,21938973	476,4459277	8,89616868	9,21E-12	1,36E-09
LINC00665	371,3323607	68,07877546	411,8742838	6,049966102	2,596927059	1,04E-11	1,50E-09
AC004540.2	34,40746607	125,8625479	22,18085084	0,176230747	-2,504462441	1,34E-11	1,88E-09
AP003716.1	313,9235601	795,2660852	249,5729551	0,313823209	-1,671976042	1,35E-11	1,88E-09
LINC01608	27,71672803	0,281923965	31,38448259	111,322507	6,798601494	1,48E-11	2,01E-09
LINC01224	28,60706713	1,434300539	32,23978994	22,47770887	4,490423085	1,70E-11	2,26E-09
AC010776.2	1,914700567	10,53714686	0,761967106	0,072312469	-3,789611754	1,79E-11	2,34E-09
TMEM220-AS1	261,7696199	647,8554942	210,1538613	0,324383853	-1,624226088	2,18E-11	2,80E-09
MIR548XHG	13,01847687	0,056272787	14,75139185	262,1407734	8,034197958	2,57E-11	3,24E-09
TEX41	89,68734694	12,47745733	100,0095247	8,015216725	3,00274153	2,92E-11	3,62E-09
AC112178.1	10,11694149	0,097252951	11,45647205	117,8007656	6,880205105	3,04E-11	3,70E-09
NOVA1-AS1	10,6536853	0,155659492	12,05716468	77,45858944	6,275353324	3,09E-11	3,70E-09
AL021328.1	44,77086939	154,5036426	30,10071254	0,194822025	-2,359771308	3,69E-11	4,34E-09
AC099508.2	20,57386286	78,75174218	12,7960715	0,162486202	-2,621610881	3,91E-11	4,52E-09
LINC00261	7167,117955	17372,21667	5802,799945	0,334027606	-1,581960755	5,64E-11	6,41E-09
LINC01446	25,3241311	1,352405745	28,52890722	21,094932	4,398824532	6,03E-11	6,74E-09
FEZF1-AS1	46,36431216	1,146242084	52,4095087	45,72289696	5,514844909	6,66E-11	7,33E-09
AL136987.1	20,37884981	0,771169453	23,00019745	29,82508885	4,898454531	8,18E-11	8,86E-09
LINC01612	18,67246461	89,38594313	9,218791008	0,103134684	-3,277398504	1,03E-10	1,10E-08

CASC20	10,29992073	0,117484387	11,66120901	99,2575214	6,633104524	1,26E-10	1,32E-08
AC109588.1	11,02513252	0,061299016	12,49088566	203,7697568	7,670796135	1,53E-10	1,59E-08
AL590666.2	77,57580569	10,4481934	86,55008541	8,283736923	3,050281737	1,76E-10	1,79E-08
LINC01532	10,25984752	0,1431318	11,61234962	81,13046598	6,34217187	2,11E-10	2,12E-08
SFTA1P	11,66820209	0,189772442	13,20275151	69,57148964	6,120424306	2,22E-10	2,20E-08
FAM99B	116,3692888	324,7087798	88,51641571	0,272602471	-1,875129456	2,58E-10	2,52E-08
AC093895.1	13,22550281	0,414384134	14,93821921	36,04920648	5,171895598	3,52E-10	3,39E-08
HNF4A-AS1	303,2738491	713,4595795	248,4361846	0,348213398	-1,521956381	3,84E-10	3,65E-08
MAFG-AS1	102,2468261	17,92775502	113,5194291	6,332049329	2,662672495	3,97E-10	3,72E-08
AC011294.1	42,84327957	2,320854399	48,26071609	20,79437474	4,3781214	4,76E-10	4,40E-08
AC024230.1	8,134077112	0,077533923	9,211155078	118,8016129	6,892410613	5,64E-10	5,15E-08
AC115619.1	2419,285718	5001,667551	2074,047505	0,414671204	-1,26996023	5,85E-10	5,27E-08
LINC01748	13,80164455	0,41122039	15,59180821	37,91594137	5,244732637	6,25E-10	5,56E-08
AL162413.1	17,93963923	0,089936247	20,32596316	226,0041288	7,820205319	6,88E-10	6,04E-08
AC104809.1	194,0183922	759,0073792	118,4851052	0,15610534	-2,679408203	7,24E-10	6,28E-08
AC091987.1	6,218173078	0,025387566	7,04608558	277,5408119	8,116556123	7,87E-10	6,74E-08
DUXAP8	66,84750052	9,674454217	74,49095591	7,699757965	2,944813097	9,41E-10	7,96E-08
ZFPM2-AS1	127,267771	9,442419732	143,0198233	15,14652254	3,920914701	1,04E-09	8,65E-08
AC103740.1	190,1286077	455,0755713	154,7078907	0,339960878	-1,556559362	1,07E-09	8,82E-08
AL157778.1	6,789698316	0,055521425	7,689989344	138,5048979	7,113793184	1,20E-09	9,80E-08
LINC00491	5,911164107	0,021017416	6,698616873	318,7174293	8,316134106	1,27E-09	1,03E-07
AC092957.1	7,514220794	0,06977857	8,50946708	121,9495764	6,930140937	1,35E-09	1,08E-07
FP700125.1	767,7975102	1687,748499	644,80941	0,382053019	-1,388155233	1,40E-09	1,10E-07
AC016550.2	5,762777417	0,020769825	6,53042549	314,4189002	8,296544133	1,86E-09	1,45E-07
LINC02335	7,158059158	0,058350436	8,107218078	138,9401466	7,118319715	1,91E-09	1,47E-07
AC116049.2	11,89947951	0,347655356	13,44384102	38,67002424	5,273143763	2,74E-09	2,09E-07
AC020978.5	69,96864124	202,8172877	52,208127	0,25741458	-1,957834323	2,94E-09	2,22E-07
AF165147.1	11,97616058	46,69346373	7,334809892	0,157084296	-2,670389133	3,21E-09	2,39E-07
F11-AS1	335,1243523	739,3565382	281,0826162	0,380171949	-1,395276008	4,00E-09	2,95E-07
AC069277.1	9,055016267	0,245064325	10,23281733	41,75563833	5,383899115	4,09E-09	2,99E-07
AL117329.1	6,670174522	0,095136496	7,549190301	79,35114961	6,310179219	4,22E-09	3,05E-07
AC117386.2	17,43485457	0,576580085	19,68863459	34,14726783	5,093698246	4,33E-09	3,10E-07
LINC02362	396,143035	916,4023683	326,5896482	0,35638237	-1,488502124	4,60E-09	3,25E-07
CASC9	130,9065038	17,41795003	146,0787704	8,38667984	3,068099782	4,68E-09	3,28E-07
AC097521.2	5,211130102	0,020053769	5,905124264	294,4645531	8,201950166	4,72E-09	3,28E-07
AC099520.1	4,315074741	0	4,89195639	Inf	Inf	4,86E-09	3,34E-07
LINC01019	17,60270405	0,118389814	19,94017921	168,4281654	7,395989603	5,15E-09	3,50E-07
LINC01831	105,6979488	266,9979749	84,13377422	0,315110159	-1,66607183	5,49E-09	3,70E-07
AC026369.3	5,712127191	22,91766015	3,41192225	0,148877426	-2,747803078	5,54E-09	3,70E-07
LINC02365	139,0441693	8,361247027	156,5151482	18,71911542	4,226440356	5,59E-09	3,70E-07
PVT1	201,5115148	51,31353694	221,5914584	4,318382079	2,110490895	5,74E-09	3,76E-07
AL139023.1	7,739256111	0,150203681	8,753835312	58,27976537	5,864923164	5,91E-09	3,83E-07
AC106771.1	5,020947228	0,033957311	5,68765711	167,4943338	7,387968481	6,66E-09	4,28E-07
AL117355.1	8,441351955	0,197654511	9,543450543	48,28349467	5,593458194	7,70E-09	4,90E-07
AC092155.1	3,86917325	17,75555731	2,012704793	0,113356329	-3,141063154	8,04E-09	5,07E-07
AC010595.1	6,240227541	0,080206781	7,063759728	88,06935844	6,460568251	8,83E-09	5,52E-07
LINC02466	3,90647711	0	4,428733408	Inf	Inf	9,00E-09	5,58E-07
LINC00648	21,26177319	0,640529868	24,0186239	37,49805452	5,228743842	1,10E-08	6,74E-07
AC245100.6	52,03240246	0,178621137	58,96472617	330,1105755	8,366805548	1,19E-08	7,25E-07
HAND2-AS1	68,91344173	242,9593495	45,64527225	0,187872055	-2,412177606	1,22E-08	7,32E-07
AC008556.1	30,67451328	99,67199812	21,4502506	0,215208394	-2,216193748	1,22E-08	7,32E-07
LINC01234	73,28068355	1,671436082	82,85411236	49,57061371	5,631413215	1,31E-08	7,77E-07
AC109830.1	4,464213115	0,029665935	5,057067016	170,4671389	7,413349846	1,45E-08	8,55E-07
AC105202.1	46,72737032	138,5909394	34,44614451	0,248545429	-2,008418523	1,79E-08	1,04E-06
AC010894.3	28,23449159	1,385806031	31,82388805	22,964172	4,521312861	2,05E-08	1,19E-06
AC239868.2	242,0820944	69,95331755	265,0939629	3,789583857	1,922039431	2,23E-08	1,28E-06
AC112251.1	64,82649689	7,882441974	72,43933846	9,189961525	3,200058821	2,25E-08	1,28E-06
AL391095.2	217,706728	502,6999387	179,6060314	0,35728278	-1,484861715	2,61E-08	1,46E-06
AC015908.3	100,4312072	246,2265461	80,93985169	0,328721062	-1,605064199	2,62E-08	1,46E-06
CYTOR	579,2562094	195,9730379	630,4972751	3,217265405	1,685834954	2,63E-08	1,46E-06
AC112206.2	246,5979438	675,7430898	189,2255981	0,280025946	-1,836367587	2,81E-08	1,55E-06
AC079061.1	71,07395183	247,8988831	47,43425514	0,191345175	-2,385750574	3,06E-08	1,67E-06
LINC02055	36,37432728	4,77510988	40,59882158	8,502175364	3,087832016	3,26E-08	1,77E-06
AC122710.1	6,905068573	0,05537949	7,820802408	141,2220023	7,141821067	3,32E-08	1,79E-06
MNX1-AS1	19,32606002	0,160650295	21,88828057	136,2479947	7,090091187	3,58E-08	1,91E-06
LINC02037	100,3872379	245,7885989	80,94855328	0,329342181	-1,602340795	3,81E-08	2,02E-06
AC011632.1	14,79970396	0,319733809	16,73552884	52,34206827	5,709899028	3,98E-08	2,08E-06

LINC01818	4,794321065	19,38027838	2,844326772	0,146763979	-2,76843017	3,99E-08	2,08E-06
LINC01702	359,2936304	909,415793	285,7478868	0,314210385	-1,670197229	4,57E-08	2,37E-06
AC016999.1	3,496978925	15,74075597	1,860110336	0,118171601	-3,081044724	5,19E-08	2,67E-06
CDKN2B-AS1	31,81206676	3,393439596	35,61134847	10,49417485	3,391516828	5,25E-08	2,67E-06
LINC01419	487,137234	0,155393544	552,2417581	3553,826909	11,7951577	5,27E-08	2,67E-06
LINC02267	5,06287389	0,122585741	5,72334022	46,68846607	5,544994285	5,64E-08	2,84E-06
MIR4435-2HG	703,5251144	254,6338549	763,5373148	2,998569515	1,584274419	5,75E-08	2,87E-06
AF279873.3	19,05953761	0,124267741	21,5909908	173,7457417	7,440833809	6,47E-08	3,21E-06
ZNF385D-AS1	4,059675059	0	4,602412366	Inf	Inf	6,53E-08	3,21E-06
AC093515.1	3,090785136	0	3,503991705	Inf	Inf	6,93E-08	3,39E-06
LINC00844	583,9704413	1466,449501	465,9919574	0,31776884	-1,653950431	8,25E-08	4,00E-06
LINC02275	19,3316061	65,47624854	13,16253626	0,201027648	-2,31453416	9,79E-08	4,69E-06
GAS5	4917,44311	1711,064233	5346,103388	3,124431734	1,643593819	9,80E-08	4,69E-06
LINC00885	46,15808561	138,5189959	33,81037033	0,24408472	-2,034546111	1,02E-07	4,85E-06
LINC01426	111,7550169	19,76665386	124,0529263	6,275868804	2,649815193	1,09E-07	5,14E-06
AC114485.1	5,804105524	0	6,58005546	Inf	Inf	1,16E-07	5,42E-06
HAGLROS	9,66368205	0,303170671	10,91508731	36,00311096	5,170049667	1,36E-07	6,32E-06
TFAP2A-AS1	16,80892327	1,320775495	18,87953127	14,29427737	3,837365783	1,38E-07	6,38E-06
AL359715.4	57,64012783	152,740428	44,92618396	0,294134202	-1,765453542	1,39E-07	6,38E-06
AFAP1-AS1	346,7155272	2,836798293	392,6886193	138,4266976	7,112978404	1,45E-07	6,63E-06
AC012409.1	36,63060501	104,1246348	27,607339	0,265137439	-1,915187693	1,75E-07	7,95E-06
U91324.1	71,08519507	171,1249164	57,71090077	0,337244289	-1,568134082	1,78E-07	8,02E-06
AC010719.1	57,92687101	10,68462737	64,24267898	6,012626997	2,587995461	1,95E-07	8,71E-06
FOXD2-AS1	150,0256613	43,79899811	164,2270869	3,749562637	1,906722324	2,08E-07	9,24E-06
AL365181.2	110,6129451	11,23609475	123,8986203	11,02684011	3,462947522	2,09E-07	9,24E-06
B4GALT1-AS1	71,07208295	175,0998985	57,16462097	0,326468613	-1,6149838	2,14E-07	9,38E-06
AC100810.1	335,0347936	692,5575222	287,2376374	0,414749141	-1,269689102	2,28E-07	9,96E-06
AC092625.1	2,704097605	0	3,06560798	Inf	Inf	2,45E-07	1,06E-05
LUCAT1	63,5247946	4,937082264	71,35737646	14,4533497	3,853331985	2,57E-07	1,10E-05
FAM230C	9,087015665	0,07065144	10,29241195	145,678728	7,18664642	2,57E-07	1,10E-05
LINC02327	6,334379087	0,233291376	7,150032525	30,64850766	4,937744922	2,69E-07	1,14E-05
LINC00383	3,737083263	0,064557251	4,228062676	65,49322673	6,033273807	2,78E-07	1,17E-05
MIR2052HG	7,11556796	0,272434822	8,030425331	29,47650113	4,881493381	2,85E-07	1,19E-05
AC007128.1	3,770028496	0,048225606	4,267595728	88,49231898	6,467480331	2,86E-07	1,19E-05
AC107419.1	7,768798554	0,309903984	8,765976972	28,28610613	4,822021684	2,88E-07	1,19E-05
LINC01863	4,828135504	18,20261432	3,040103577	0,167014667	-2,581953288	3,05E-07	1,26E-05
AC012236.1	71,86714802	16,13984758	79,31732187	4,914378621	2,297009012	3,25E-07	1,33E-05
LINC01667	58,01330025	0,252939385	65,73527363	259,8854807	8,021732225	3,42E-07	1,39E-05
TSPEAR-AS2	106,2222815	21,18042926	117,5915131	5,551894706	2,472980207	3,56E-07	1,45E-05
HRAT92	42,25990531	6,91001235	46,98582682	6,79967335	2,765465442	3,75E-07	1,51E-05
AC023090.1	11,11567797	0,308524171	12,56048462	40,71150921	5,347364799	4,49E-07	1,80E-05
DHRS4-AS1	1082,027433	2070,921137	949,8223926	0,458647302	-1,124542941	4,67E-07	1,86E-05
DLX6-AS1	21,69014277	0,599906854	24,50969303	40,85583098	5,352470091	4,70E-07	1,86E-05
LINC01956	11,78157604	0,44702681	13,29689011	29,7451737	4,894583698	4,73E-07	1,86E-05
AC131391.1	3,116103556	0,020053769	3,530013955	176,0274527	7,459656634	4,99E-07	1,96E-05
AC090227.2	3,025992524	12,38507449	1,774778357	0,143299773	-2,802891775	5,27E-07	2,05E-05
AC015468.1	1,46709767	6,835377485	0,749413203	0,109637427	-3,189187713	5,30E-07	2,05E-05
AP003900.1	2,402475351	0	2,723661895	Inf	Inf	5,48E-07	2,11E-05
AC079466.1	809,607249	13,62971377	916,021358	67,20767389	6,070554067	5,56E-07	2,13E-05
AC021079.1	2,81336827	0	3,189487023	Inf	Inf	5,61E-07	2,14E-05
AL133467.4	3,865109256	0,090863895	4,369687513	48,09047113	5,587679155	5,79E-07	2,20E-05
AC114316.2	9,067801415	0,584600863	10,20191914	17,45108464	4,125244802	6,36E-07	2,40E-05
SSTR5-AS1	229,6171664	3,499215001	259,846839	74,25860912	6,214486388	6,76E-07	2,54E-05
AL035661.1	173,0160167	386,4303318	144,4846911	0,373895834	-1,419291699	1,04E-06	3,89E-05
LINC01121	8,000622451	0,431198947	9,012577465	20,90120472	4,385514194	1,08E-06	3,99E-05
RUSC1-AS1	224,517655	78,79749332	243,99896	3,096532006	1,630653358	1,13E-06	4,17E-05
LINC01146	689,8960966	1264,054267	613,1369829	0,485055902	-1,043777068	1,14E-06	4,18E-05
LINC00511	174,7306275	23,02049395	195,012731	8,471266142	3,082577615	1,17E-06	4,29E-05
AL391845.2	8,468956579	0,492042016	9,535389007	19,37921701	4,276438377	1,25E-06	4,55E-05
LINC02153	2,361076035	9,214864112	1,444794207	0,156789529	-2,673098878	1,27E-06	4,58E-05
AC022031.2	3,396677059	0,095369985	3,838028272	40,2435658	5,330686236	1,49E-06	5,36E-05
AL035401.1	3,529126717	0,072196247	3,991283197	55,28380453	5,788784998	1,54E-06	5,50E-05
AC004160.2	6,621547719	22,18996831	4,540208068	0,204606334	-2,289077287	1,71E-06	6,08E-05
SNHG1	878,7354046	369,9230053	946,7584527	2,559339212	1,355771373	1,78E-06	6,31E-05
AC007298.2	29,39766753	79,01836625	22,76388428	0,288083459	-1,795441268	1,85E-06	6,47E-05
AC016877.3	3,504562789	0,102423345	3,959394265	38,65714648	5,272663242	1,85E-06	6,47E-05
SNHG3	507,3441087	203,333373	547,9872552	2,695018763	1,430295317	1,90E-06	6,64E-05

AC124067.4	37,36982404	6,012451381	41,56198616	6,912652349	2,789239371	2,15E-06	7,45E-05
AC106900.2	6,57149154	0,273714029	7,413440405	27,08461975	4,759401931	2,16E-06	7,45E-05
NCOA7-AS1	3,723365478	13,36463635	2,434425521	0,182154266	-2,456767314	2,17E-06	7,45E-05
AC114401.1	5,779837182	0,223720666	6,522633508	29,15525693	4,865684131	2,20E-06	7,53E-05
AC010643.1	64,55361786	17,50518795	70,84351491	4,0470011	2,016853241	2,22E-06	7,54E-05
AL645608.1	33,84729059	89,81888698	26,36445685	0,293529098	-1,76842457	2,37E-06	8,00E-05
SNHG7	1130,028096	480,9625303	1216,801567	2,529930068	1,339097506	2,38E-06	8,00E-05
RMST	16,0789985	1,527989907	18,0243205	11,79609919	3,560237954	2,47E-06	8,27E-05
AL354704.1	2,041853322	0	2,314828365	Inf	Inf	2,74E-06	9,15E-05
AC027117.2	237,8603378	463,016474	207,7592501	0,448708117	-1,156150814	2,78E-06	9,23E-05
AL139042.1	3,323682252	0,029665935	3,764058766	126,8815157	6,987338101	2,79E-06	9,23E-05
HAO2-IT1	6,208255571	22,15944288	4,075743899	0,183928085	-2,442786303	2,85E-06	9,36E-05
AC129507.1	16,51713544	47,75417793	12,34106024	0,258428912	-1,952160614	2,95E-06	9,66E-05
AC006960.2	2,592129038	15,91077704	0,811561123	0,051007007	-4,293160729	2,98E-06	9,71E-05
FGF14-AS2	85,62598881	198,0856687	70,59127224	0,356367387	-1,488562779	3,06E-06	9,91E-05
AP003469.2	8,251682297	0,547082746	9,281708975	16,9658229	4,084559502	3,31E-06	0,00010689
LINC02323	9,013141263	0,681228064	10,1270334	14,8658488	3,893929935	3,54E-06	0,000113854
AC010333.1	4,258387004	0,176438154	4,804102091	27,22824963	4,767032337	3,58E-06	0,000114354
AP001065.2	96,91134479	202,1707351	82,83923379	0,409748888	-1,287188062	3,79E-06	0,000120755
LINC01901	3,012463952	0,062189107	3,406885722	54,78267609	5,775647837	4,20E-06	0,000133079
HOXD-AS2	9,85463608	0,642885766	11,0861535	17,24435988	4,108052671	4,38E-06	0,000138072
AC006206.2	10,40744239	1,002746722	11,66475464	11,63280257	3,540126806	4,49E-06	0,000140934
HOXC-AS1	4,578922748	0	5,191078196	Inf	Inf	4,75E-06	0,000148365
AC068987.4	134,026776	45,31508977	145,8866271	3,219382945	1,686784195	4,88E-06	0,000151488
B3GALT5-AS1	4,559264936	15,78698418	3,058232952	0,19371863	-2,367965387	4,89E-06	0,000151488
LINC00683	5,072196702	16,34669313	3,564911083	0,218081483	-2,197060816	4,95E-06	0,000152651
LINC02109	8,020808101	0,628962447	9,00902276	14,32362585	3,840324834	5,02E-06	0,00015404
LINC01535	14,71775657	1,671783178	16,46187066	9,846893349	3,299668633	5,16E-06	0,000157811
AC008109.1	25,32581974	3,809893526	28,20228047	7,402380216	2,88798924	5,23E-06	0,000159272
AC018553.1	34,96318714	7,115933141	38,68608206	5,43654378	2,442689766	5,28E-06	0,000160008
AP000851.2	31,19270651	90,51169478	23,26236049	0,257009446	-1,960106713	5,67E-06	0,000170902
AL357060.1	18,7845243	2,165104095	21,00637192	9,702245708	3,278318716	5,85E-06	0,000175693
DSCR4-IT1	2,901283057	0	3,289155123	Inf	Inf	5,92E-06	0,000176984
MIR217HG	10,10896937	0,910183197	11,33875362	12,4576609	3,638961302	6,20E-06	0,00018466
AC009271.1	4,05788305	0,207532529	4,572635794	22,03334493	4,461616625	6,23E-06	0,000184751
LINC01666	6,979703355	0,551979787	7,839024688	14,20165171	3,827986826	6,45E-06	0,000190535
C17orf82	24,69473187	4,205413594	27,43394554	6,523483345	2,705642526	6,78E-06	0,000199346
LINC01524	3,861607328	0,15898776	4,356609944	27,40217203	4,776218348	6,94E-06	0,000203124
LINC02058	2,207644747	0	2,502784419	Inf	Inf	7,04E-06	0,000205222
LINC01021	67,61927548	16,78969464	74,41467399	4,432163634	2,148011146	7,08E-06	0,00020543
CLRN1-AS1	7,194662088	23,09555189	5,068874681	0,219474066	-2,18787762	7,89E-06	0,000227974
SMIM25	80,99182423	175,9859139	68,29207962	0,388054237	-1,365669786	8,07E-06	0,000232382
LINC01468	1,96623954	0	2,229105789	Inf	Inf	8,21E-06	0,000235239
AC010280.1	3,987767801	13,7205525	2,686593376	0,195807959	-2,35248869	8,27E-06	0,000236252
AL163953.1	10,24625633	0,902188643	11,49546324	12,74175122	3,67149167	8,38E-06	0,000238407
AL354707.1	225,5269378	452,1471823	195,2301136	0,431784431	-1,211616872	9,41E-06	0,000266616
AC110285.2	87,61021329	26,54386095	95,77416414	3,608147448	1,851258296	1,03E-05	0,000289399
AL591501.1	1,775021594	0	2,012323946	Inf	Inf	1,04E-05	0,000293074
U91319.1	81,49611328	172,0473257	69,39033622	0,403321214	-1,309998805	1,05E-05	0,000294719
AP006216.2	29,1794343	75,35710637	23,00594873	0,305292358	-1,711736616	1,08E-05	0,000299852
AC010333.2	4,301152565	0,240252251	4,844053677	20,16236543	4,333592999	1,11E-05	0,000306104
AC092535.4	99,75341652	33,23699677	108,645986	3,268826807	1,70877294	1,11E-05	0,000306104
AL136084.3	4,262955482	0,220581928	4,803379755	21,77594424	4,444663372	1,12E-05	0,000309574
AL138974.1	3,010690716	0,086123101	3,401675692	39,49783089	5,303701522	1,22E-05	0,000334883
AC111000.4	126,5234196	28,66037745	139,606714	4,871070322	2,284238811	1,23E-05	0,000335961
LINC01370	216,166974	447,1497768	185,2869202	0,414373281	-1,270997114	1,26E-05	0,000344037
LINC00482	169,0132931	64,49963827	182,9857068	2,837003613	1,504367988	1,29E-05	0,000348569
LINC01235	21,21283903	3,189856221	23,62232871	7,405452494	2,888587891	1,31E-05	0,000352325
LEF1-AS1	6,208056198	0,480336474	6,973794129	14,51856044	3,859826507	1,37E-05	0,000369285
AC112493.1	5,770780422	0,449161171	6,482226846	14,43185044	3,851184388	1,48E-05	0,00039481
LINC01625	21,52305463	57,75461138	16,67926362	0,288795357	-1,791880546	1,48E-05	0,00039481
AC110285.6	10,59074309	1,073105872	11,86315448	11,05497117	3,466623358	1,50E-05	0,000399278
CDKN2A-AS1	2,415889055	0,07520231	2,72881509	36,2863199	5,181353843	1,51E-05	0,000399278
LINC01451	157,6859617	21,86707796	175,8435665	8,041475263	3,007460198	1,51E-05	0,000399278
AL589182.1	2,268953767	0	2,572289832	Inf	Inf	1,53E-05	0,000402194
LINC00853	56,21807929	14,58240629	61,78434573	4,236910185	2,083012546	1,58E-05	0,000412634
AC106822.1	8,901435407	26,93615757	6,490376295	0,240954051	-2,053170036	1,62E-05	0,000420536

TSPEAR-AS1	83,68091537	24,19647048	91,63338126	3,787055692	1,921076638	1,62E-05	0,000420536
LINC02152	3,550515564	0,155214797	4,004432779	25,79929784	4,689259896	1,64E-05	0,000424237
AL355303.1	10,71860655	1,201973777	11,99088365	9,975994384	3,318460653	1,65E-05	0,000425225
AC009159.3	49,10144874	115,0252618	40,28810476	0,350254406	-1,513524895	1,74E-05	0,000445894
AP005230.1	4,08634034	0,204307667	4,605328665	22,54114465	4,494488873	1,75E-05	0,000447106
HOXC-AS2	4,866638266	0,293169296	5,478064599	18,68566961	4,223860359	1,78E-05	0,000454956
AL445647.1	4,49812768	0,347078157	5,053080825	14,55891339	3,863830778	1,86E-05	0,000471346
AL161740.1	20,0921267	54,26375255	15,52372753	0,286079137	-1,805513803	1,86E-05	0,000471346
AL606489.1	15,47798981	2,193688222	17,25396595	7,865277199	2,975497612	1,97E-05	0,000498104
AL133467.2	3,733004706	0,237627344	4,200301145	17,67600086	4,143720002	2,00E-05	0,000502342
LINC02293	1,975475187	0,026606852	2,236019082	84,03921954	6,392990859	2,01E-05	0,000504389
LINC01151	68,23807074	19,110033	74,80599022	3,914487758	1,968823532	2,13E-05	0,000532042
AC025016.1	5,185973614	0,119166094	5,863354298	49,20320942	5,620680518	2,22E-05	0,000550169
LINC01681	12,58004723	1,830448095	14,01715942	7,657774867	2,936925247	2,23E-05	0,000550169
AC099850.3	25,11564896	4,744171706	27,83910848	5,868065114	2,55288488	2,23E-05	0,000550169
AC079789.1	1,261586465	5,215337185	0,733010166	0,14054895	-2,830855418	2,25E-05	0,000553767
DNM3OS	41,1329172	92,5253504	34,26227105	0,370301446	-1,433227912	2,37E-05	0,00057985
LINC00944	32,00101638	5,928881856	35,48659586	5,985377465	2,581442233	2,46E-05	0,000601418
CAPN10-AS1	48,25347035	12,13392798	53,08228618	4,374699296	2,129183854	2,47E-05	0,00060251
AC245128.3	5,942471697	19,09601606	4,183976462	0,21910206	-2,190325044	2,48E-05	0,000602788
AL355488.2	103,0769283	34,6722111	112,2219439	3,236653804	1,694503061	2,55E-05	0,00061643
AC005332.8	190,9295674	77,5966604	206,0810256	2,655797615	1,40914521	2,57E-05	0,00061661
AC074250.2	275,0559442	503,7289798	244,4846827	0,485349647	-1,042903651	2,57E-05	0,00061661
HOXA11-AS	10,14316793	0,121264442	11,4829946	94,69383147	6,565198544	2,58E-05	0,00061661
SOCS2-AS1	92,23577957	196,7468063	78,26371718	0,397789009	-1,329924679	2,69E-05	0,000642041
FLJ36000	2,515597599	0	2,851907438	Inf	Inf	2,70E-05	0,000642196
AL078590.3	18,76698964	48,44964705	14,79871993	0,305445361	-1,711013765	2,72E-05	0,000644892
HOXA-AS3	3,851758259	0,304600672	4,325977187	14,20212619	3,828035026	2,78E-05	0,000657095
AC006305.1	12,69851337	1,847000136	14,14925044	7,660665617	2,93746975	2,90E-05	0,000681557
AC119424.1	14,02994783	39,68190385	10,60054195	0,267137937	-1,904343221	3,08E-05	0,000721509
FIRRE	11,07550454	1,469013321	12,35979481	8,413671018	3,072735409	3,18E-05	0,000740069
BBOX1-AS1	14,57321762	0,616563379	16,43908049	26,66243416	4,736736593	3,18E-05	0,000740069
LINC01089	197,9507348	77,99362078	213,9877821	2,743657494	1,456100393	3,19E-05	0,000740069
AC022424.1	24,32368448	0,607780151	27,49425993	45,23717971	5,499437083	3,50E-05	0,000809897
AL445524.1	562,570839	155,1358412	617,0407585	3,977422328	1,991833758	3,58E-05	0,000825362
AC105105.3	90,92319138	191,9348781	77,41895519	0,403360535	-1,309858157	3,64E-05	0,000835978
PTGES2-AS1	7,685553305	0,790198922	8,607392126	10,8926903	3,445288412	3,66E-05	0,000837182
AL357033.2	3,42725662	11,2676108	2,379080928	0,211143335	-2,243705384	3,68E-05	0,000840973
AC109322.1	78,18264792	24,785582	85,3212931	3,44237602	1,783404695	3,73E-05	0,000847672
AC018755.4	10,83024654	29,03165747	8,396902828	0,289232636	-1,789697743	3,78E-05	0,000856579
AC018467.1	90,68110273	184,4661241	78,14299826	0,423617066	-1,239167384	3,87E-05	0,000874901
AL359313.1	10,89706084	0,148917389	12,33397842	82,82429918	6,371982186	3,96E-05	0,00089303
MELTF-AS1	39,49319403	10,09345915	43,42363986	4,302156397	2,105059972	4,04E-05	0,000905556
AL354872.2	250,3862726	508,6084525	215,8645908	0,424421949	-1,236428827	4,05E-05	0,000905556
AP005057.1	8,9537693	0,995184031	10,01775129	10,06622994	3,331451554	4,06E-05	0,000905556
LINC02313	7,466540122	0,744084874	8,365264085	11,24235202	3,49087199	4,13E-05	0,00091735
TMPO-AS1	151,3868003	60,43088539	163,546682	2,706342642	1,436344506	4,15E-05	0,000919058
HTR2A-AS1	1,830809901	6,75218244	1,172872396	0,173702711	-2,525307824	4,31E-05	0,000952501
AC129507.2	48,53906174	110,1219662	40,30605312	0,366012836	-1,450033852	4,33E-05	0,000953464
AL121899.1	51,82105268	14,1001576	56,86395309	4,032859399	2,011803109	4,34E-05	0,000953464
MIR99AHG	149,2339717	286,4380176	130,8911848	0,456961635	-1,129855048	4,50E-05	0,000985267
LINC01979	25,2176504	67,97395072	19,50156747	0,286897661	-1,801391889	4,54E-05	0,000990833
AC004477.1	23,16621746	4,455359091	25,66766911	5,761077521	2,526338671	4,59E-05	0,00099853
AL137026.2	5,369575774	0,200023847	6,060692342	30,29984897	4,921238698	4,63E-05	0,001004201
AC019257.1	9,068413187	25,9203271	6,81548352	0,262939719	-1,927196007	4,70E-05	0,001015134
SNHG4	32,3476352	7,630397848	35,65207869	4,672374809	2,224156009	4,71E-05	0,001015134
LINC01108	14,54451514	2,472080222	16,15847703	6,53638862	2,708493761	4,74E-05	0,001018219
Z99755.3	13,64118475	2,03295319	15,19308737	7,473407376	2,901766166	4,86E-05	0,00104155
AL731684.1	8,784788006	0,228694505	9,928650774	43,4144702	5,440104073	4,94E-05	0,001048783
AC102953.2	60,73249816	18,12908108	66,42814215	3,664175909	1,873488766	4,94E-05	0,001048783
AC008991.2	2,323522804	0	2,634154195	Inf	Inf	4,94E-05	0,001048783
AC110995.1	12,60331864	33,78717411	9,771252402	0,289200049	-1,789860299	4,98E-05	0,001054211
LINC00896	54,73314709	16,51793018	59,8421333	3,622859079	1,857128689	5,15E-05	0,001086997
AC009005.1	47,5070874	13,01417355	52,11843951	4,004744466	2,00171019	5,24E-05	0,001101171
AC132192.2	41,33270222	10,24062091	45,48939758	4,442054635	2,151227138	5,40E-05	0,001132335
LINC01537	13,8564365	35,47706248	10,96597848	0,309100521	-1,693852011	5,53E-05	0,001154736
AC097515.1	3,56552536	0,237416101	4,010459753	16,89211365	4,078277954	5,62E-05	0,001170612

AC091133.2	1,865108032	0,01985937	2,111799029	106,3376653	6,732508886	5,67E-05	0,001178654
AL358613.2	2,189428575	7,560182279	1,471413374	0,194626706	-2,36121841	6,04E-05	0,001247255
LINC02388	8,15905022	23,73444526	6,076778155	0,256032028	-1,965603801	6,08E-05	0,001250964
AL139130.1	4,856921525	0,458963045	5,444883888	11,86344729	3,568451385	6,19E-05	0,001269192
AC036176.1	118,8034379	236,5430814	103,0628439	0,435704326	-1,198578657	6,20E-05	0,001269192
LINC01704	3,35283783	0,187482939	3,776013618	20,14057188	4,332032744	6,25E-05	0,00127635
AC009275.1	34,42964514	8,188800025	37,93777951	4,632886308	2,211911279	6,40E-05	0,001301618
AC004870.2	8,622907125	0,022747789	9,772661047	429,6092786	8,746881342	6,82E-05	0,001383302
WARS2-IT1	4,136516842	12,64502829	2,999015311	0,237169522	-2,076009472	6,88E-05	0,001392251
AC078993.1	37,97290994	2,540539816	42,70985782	16,81133181	4,071362116	6,96E-05	0,00140327
AC022784.6	224,8256136	437,5734325	196,3833918	0,448800995	-1,155852221	7,05E-05	0,001416327
DDX11-AS1	18,42247233	3,249442029	20,45095232	6,293681235	2,65390411	7,08E-05	0,001416327
AL445434.1	7,844473114	0,102104942	8,879549072	86,96492981	6,44236182	7,08E-05	0,001416327
AL583808.1	2,21521198	0,07065144	2,501917934	35,41212924	5,146171687	7,20E-05	0,001434829
LINC01703	33,68641242	8,381712405	37,06939371	4,422651592	2,144911594	7,56E-05	0,001499297
AL161645.1	31,7321853	77,46016732	25,61881872	0,330735391	-1,596250663	7,56E-05	0,001499297
AC107973.1	2,401362609	0	2,722400391	Inf	Inf	7,66E-05	0,001513127
AC010615.2	24,66348913	5,499362266	27,22553817	4,950671888	2,307624336	8,04E-05	0,001584983
AC092115.3	5,513193172	0,525416796	6,180008196	11,76210628	3,556074527	8,15E-05	0,001602074
AC090358.1	2,960650184	0	3,356459033	Inf	Inf	8,32E-05	0,001631505
AC139491.2	67,67671542	20,84248882	73,93797566	3,547463852	1,826787983	8,41E-05	0,001643624
AP002478.1	7,015155763	0,123945988	7,936440492	64,03144342	6,000708627	8,62E-05	0,001680032
AL121906.2	18,88842876	3,412302869	20,95742955	6,141726087	2,618644171	8,74E-05	0,001698258
LINC00645	1,677372958	0,032732891	1,897244624	57,96141251	5,857020849	9,01E-05	0,001746317
LINC00879	7,993411847	0,069459903	9,052763711	130,3307854	7,026034093	9,40E-05	0,001815952
AL023803.2	13,5671154	2,010896869	15,1120644	7,51508674	2,909789756	9,57E-05	0,001844188
LINC02438	4,828946432	0,456507937	5,413497033	11,85849488	3,567849005	9,67E-05	0,001858963
AC091133.3	3,843796562	0,305446302	4,316838041	14,13288692	3,82098429	9,85E-05	0,001887145
AL157832.2	3,216892849	10,27036899	2,273914754	0,221405361	-2,17523794	9,90E-05	0,001891971
MIR3945HG	5,767988631	17,4150831	4,210890441	0,241795598	-2,048140112	0,000100384	0,001912095
AL080248.1	77,60942253	154,6454201	67,31049238	0,43525694	-1,200060793	0,000100593	0,001912095
LINC00942	146,8894199	1,243394936	166,3608137	133,7956339	7,063887228	0,000102903	0,001950663
AC034213.1	11,26421626	0,773215232	12,66675651	16,38192831	4,034033281	0,000104207	0,001969986
LINC00668	19,94547079	2,042841701	22,3388704	10,93519404	3,450906916	0,000105194	0,001983246
AC092490.1	66,47429252	9,723846364	74,06125057	7,616456266	2,929119906	0,000107287	0,002017237
TCL6	15,70010243	2,857855569	17,41698036	6,094422875	2,607489608	0,000110927	0,002077012
AC079062.1	92,89934794	10,17838696	103,9582999	10,21363212	3,352424096	0,000111065	0,002077012
LINC02253	10,19095983	0,414319622	11,49799729	27,75151521	4,794494639	0,000114109	0,002128186
LINC02050	1,607691261	0,033958271	1,818083373	53,53874985	5,742511547	0,000119443	0,002221478
FP325330.3	1,628170137	0,020053769	1,843158956	91,91084792	6,522163243	0,000120032	0,002221478
AC103808.3	2,22859729	0,095477591	2,513773721	26,32841592	4,718548817	0,000120071	0,002221478
LINC00906	5,887792558	0,072749081	6,665204788	91,61909316	6,517576378	0,000122107	0,002253139
LINC02156	5,115498319	14,77027324	3,824753009	0,258949374	-1,949258024	0,000126204	0,002316441
LINC01138	164,7121312	70,43296339	177,316298	2,517518637	1,332002459	0,000126206	0,002316441
AL118511.2	5,635810272	0,632696501	6,30467575	9,964771005	3,316836652	0,000130686	0,002389976
AL392089.1	2,282556805	6,970312815	1,655851456	0,237557696	-2,073650146	0,000130901	0,002389976
AC092809.2	9,099358712	25,73048397	6,875946244	0,267229573	-1,903848422	0,000131317	0,002391278
AC006946.2	4,463338573	0,427550802	5,002882392	11,70125835	3,54859178	0,000132112	0,002396811
AL163952.1	7,183134201	1,015417128	8,007695307	7,886114075	2,97931458	0,000132312	0,002396811
LINC01679	25,35999132	58,52118491	20,92667666	0,357591472	-1,483615763	0,000133006	0,002403118
AL355102.4	67,92872531	20,18535974	74,31152819	3,681456717	1,88027674	0,000134956	0,002432008
FLVCR1-AS1	139,3557084	56,43143908	150,4418407	2,665922456	1,414634817	0,000137892	0,002478484
DIO3OS	131,1850647	264,9374408	113,303731	0,427662208	-1,225456371	0,000141797	0,002542078
AC090192.2	8,562349038	0,16620731	9,684827878	58,26956652	5,864670673	0,00014465	0,002586544
LINC01977	11,27419261	1,828841044	12,53694015	6,855128384	2,777183685	0,000150889	0,002691181
AC024600.1	5,53361519	16,61911055	4,051597093	0,243791452	-2,036280553	0,000152068	0,002705243
AC074135.1	4,431640397	0,482913915	4,959545007	10,27003956	3,360369834	0,000152772	0,002710828
LINC02041	9,628306271	1,621608656	10,69872039	6,597596991	2,721940655	0,000156595	0,002771576
LINC01192	2,355517989	0,161845716	2,648789683	16,36614023	4,032642214	0,000160563	0,002834578
AC113404.1	10,81922039	1,719386032	12,03577579	7,000042782	2,807363739	0,000163362	0,002876672
AC104088.1	3,409925758	0,178268842	3,841965452	21,55152531	4,429718074	0,000165675	0,002910002
AC092954.1	1,31889677	0	1,495219868	Inf	Inf	0,000166315	0,002913868
AC089983.1	1,783369984	0,060383112	2,013715822	33,34899049	5,059571185	0,000169693	0,002965574
AP003181.1	1,265132616	0	1,434267993	Inf	Inf	0,000175029	0,003051141
SAMMSON	1,71641809	0,07662145	1,935642239	25,26240695	4,658920198	0,00017698	0,003077407
RNF157-AS1	28,81624824	6,067484551	31,8575268	5,250532826	2,392463835	0,000177778	0,003083564
AC079760.2	5,537333648	0,721661343	6,181140106	8,565153401	3,098479085	0,000183372	0,003171771

AC105384.1	1,522622489	5,009444376	1,056469831	0,210895611	-2,245399026	0,000184004	0,003171771
AL954650.1	5,661579598	0,035167527	6,413773725	182,3777319	7,510785779	0,000184235	0,003171771
AL162431.2	30,44414243	7,522962272	33,50847132	4,454159161	2,155153111	0,000185215	0,003180741
AC010547.2	24,21136877	77,24749987	17,12097691	0,221637942	-2,173723218	0,000185698	0,003181171
AF127577.4	149,5553836	282,5725375	131,7723416	0,466331027	-1,100573673	0,000187169	0,00319669
AGAP1-IT1	41,54392297	92,22882282	34,76786684	0,376973985	-1,40746313	0,000187526	0,00319669
LINC00858	2,878260564	0,240911708	3,230847309	13,41091859	3,745336154	0,00019209	0,003260619
LINC01507	1,95303225	7,391841719	1,225918684	0,165847529	-2,592070577	0,000192216	0,003260619
AL110292.1	2,131678514	0,141972246	2,397682026	16,88838557	4,077959516	0,000195752	0,003312503
AP006285.2	11,85899776	32,68790977	9,074383859	0,277606734	-1,848885533	0,000198974	0,003351421
LINC01186	18,92107917	3,670971477	20,95986362	5,709623121	2,51339552	0,000199018	0,003351421
LINC02015	181,3857968	333,4978802	161,0499567	0,482911485	-1,050169318	0,000203789	0,00342345
AC141928.1	24,1338226	5,158011911	26,67069569	5,170731698	2,370368447	0,000209439	0,003501416
AC090340.1	102,0944095	193,5778561	89,8640022	0,464226663	-1,107098708	0,00021151	0,003527533
AL357055.3	15,50191558	39,96046489	12,23205605	0,306103948	-1,707906445	0,000215912	0,003585333
ELF3-AS1	97,92300068	37,86917839	105,9515865	2,797831668	1,484309165	0,000216036	0,003585333
AP002954.1	4,71939717	13,42588552	3,555428139	0,264818893	-1,916922043	0,000216526	0,003585333
MIR325HG	17,59077327	3,425114921	19,48457787	5,688736967	2,508108376	0,000219781	0,003630575
LINC01518	3,828475521	0,238978045	4,308354862	18,02824546	4,172187093	0,000221322	0,003647345
AP003469.4	188,73541	82,93753116	202,8795115	2,446172543	1,290526169	0,000222298	0,003654751
AC093609.1	11,36671496	29,58335118	8,931335781	0,301904126	-1,727837621	0,000224083	0,00367538
AL133325.3	2,114729384	0,075797989	2,387313795	31,49574069	4,977084834	0,000229875	0,003759354
AC068756.1	4,847387594	0,672134587	5,405576499	8,042401934	3,007626439	0,000230286	0,003759354
LINC00346	108,1627255	40,04374637	117,2695409	2,928535703	1,550179483	0,000232847	0,00379223
MINCR	191,6910818	85,36680336	205,9055575	2,412009697	1,270235707	0,000237779	0,003863496
GNG12-AS1	22,89441639	54,01971425	18,73328031	0,346785994	-1,527882462	0,000240139	0,003887916
ASMTL-AS1	146,6054265	62,52385762	157,846278	2,524576761	1,336041544	0,000240403	0,003887916
AC113145.1	4,093715038	0	4,641003144	Inf	Inf	0,000243355	0,003926502
AL590079.1	8,156215765	22,07929818	6,294841111	0,285101504	-1,810452446	0,000246025	0,003960376
AC068858.1	3,996505985	0,332197948	4,486386739	13,50516091	3,755438924	0,000252817	0,004060295
AC020907.1	41,017877	12,78937631	44,79174073	3,502261537	1,808286823	0,000253636	0,004064035
AL133370.1	8,043186149	0,297123063	9,07875608	30,55554145	4,933362141	0,000260682	0,004167311
AP003774.3	2,421886353	7,224902235	1,779771931	0,246338549	-2,021285687	0,000263942	0,004209716
AL021453.1	109,4312045	44,57207188	118,1022115	2,649690861	1,405824051	0,000268341	0,004270065
AL365361.1	41,10082044	82,35174089	35,5859915	0,432121909	-1,210489715	0,000271207	0,004305798
AC005722.3	3,698383738	0,058513903	4,184997353	71,52141803	6,160303436	0,000272923	0,004316114
AC011503.1	15,49868374	0,656314708	17,48295767	26,63807081	4,735417698	0,000273101	0,004316114
AL513318.2	13,04527603	1,520681681	14,58599719	9,591749134	3,261793926	0,000281887	0,00444484
AC008080.1	1,299530126	4,607612035	0,857273187	0,186055853	-2,42619232	0,000282738	0,004448161
HS1BP3-IT1	177,3891093	320,601062	158,2431263	0,493582664	-1,01863637	0,000287327	0,004501934
AC108748.1	6,47294645	17,7119317	4,970408315	0,280624858	-1,833285286	0,000287454	0,004501934
AC116025.2	5,283168	0,606907296	5,908336543	9,735154913	3,283203936	0,000294708	0,004605152
LINC01793	6,688394236	0,312369966	7,540803898	24,14061762	4,593390682	0,000300164	0,004675738
AL138828.1	81,9946618	4,928436257	92,29763313	18,72756962	4,22709178	0,000300574	0,004675738
SLC7A11-AS1	4,927125558	0,361467743	5,537507619	15,31950702	3,937297967	0,000320273	0,004971037
AC084033.3	98,54268723	39,46697533	106,4405097	2,696951282	1,431329461	0,000323441	0,005009011
HULC	6335,873612	3079,950648	6771,15743	2,198462964	1,136495229	0,000325655	0,005032058
AC009093.5	16,84875289	41,4533899	13,55936292	0,327099013	-1,612200689	0,000331076	0,005097733
AC099684.1	41,24761116	88,28700903	34,95892161	0,395969033	-1,336540486	0,000342969	0,005258183
AC005150.1	35,37819922	0,04495141	40,10189545	892,116515	9,801088336	0,000343681	0,005258183
AC090709.1	1,186681009	0	1,345328203	Inf	Inf	0,000344078	0,005258183
AC024563.1	1,957057606	0,130842398	2,201204024	16,82332372	4,072390856	0,000346186	0,005278769
AC099792.1	4,312570286	0,551763359	4,815351961	8,727205029	3,125519691	0,000347688	0,005290041
LINC00664	8,631601263	1,49045073	9,586300532	6,4318131	2,685225484	0,000350113	0,005315287
LINC00898	1,906969373	0,130097938	2,144519031	16,48388174	4,042984113	0,000351816	0,005329478
AC131532.1	4,755301983	0,72118444	5,29462251	7,341565096	2,876087654	0,000357088	0,005397559
AL139412.1	23,72171922	5,743089171	26,12527939	4,548994211	2,185547599	0,000362171	0,00546249
AL133367.1	33,16011969	9,25061792	36,35657714	3,930178228	1,974594738	0,000371196	0,005586457
AC012146.1	121,3785229	52,73405645	130,5555906	2,475735784	1,307857355	0,000374314	0,005621192
AC010931.2	4,159090063	0,476627439	4,651397901	9,758980539	3,286730446	0,000381085	0,005710508
AL590705.1	18,80068254	4,480806661	20,71510445	4,62307482	2,208852711	0,000398638	0,005947858
AC109439.2	2,127743114	0,148329674	2,392370579	16,12873891	4,011561735	0,000399676	0,00595054
AL355601.1	1,968213257	0,09331371	2,218868277	23,77858807	4,571591148	0,000402526	0,005980135
DLG5-AS1	26,01587386	6,873984611	28,57494997	4,156970314	2,055532445	0,00040915	0,006065559
AC011445.2	18,37313268	4,186396239	20,2697552	4,841814784	2,275547892	0,000414073	0,006125452
LINC02307	1,152244435	0	1,306287808	Inf	Inf	0,000423724	0,006233275
AC026740.1	41,92598904	8,578349411	46,38422963	5,407127573	2,434862395	0,000423957	0,006233275

AL450992.2	100,5361987	41,96628185	108,3664015	2,582225461	1,368614972	0,000424057	0,006233275
SNHG6	2330,140942	1164,840534	2485,929766	2,134137415	1,093653073	0,000427533	0,006260752
AC013275.1	77,02813492	16,05123568	85,18012679	5,306764444	2,407832512	0,000427731	0,006260752
AC090164.2	14,43640706	3,005685315	15,96457842	5,311460364	2,409108579	0,000435314	0,00635833
AC110760.4	7,005325561	1,318374851	7,765613089	5,89029219	2,558339201	0,000440312	0,006417821
AC005537.1	5,832235934	0,999041581	6,478384911	6,484599878	2,697017558	0,000450707	0,00655557
AC003988.1	1,096430461	3,91618013	0,71945858	0,183714374	-2,444463589	0,000456058	0,006619516
AC026320.1	1,325113071	0	1,502267225	Inf	Inf	0,000460325	0,00666751
AC016773.1	17,01212064	3,647741671	18,79880232	5,153545404	2,365565282	0,000463902	0,006705322
SNHG25	53,49511717	14,30500265	58,73443729	4,105866929	2,03768687	0,000466354	0,006726751
AL445209.1	2,794687391	0,259761335	3,133581249	12,06330901	3,592553793	0,000482155	0,006940232
SLC9A3-AS1	511,8492846	150,3255688	560,1813321	3,726454099	1,897803489	0,00048403	0,006952791
LINC02202	10,08744563	1,833784575	11,19087626	6,102612275	2,609426933	0,000508449	0,007288468
AL592466.1	1,164108874	0	1,319738402	Inf	Inf	0,000513819	0,007350254
AC024581.1	2,205178815	0,167994718	2,47752963	14,74766382	3,88241453	0,000519027	0,007409484
TMEM26-AS1	1,857817702	5,852020149	1,323833417	0,226218192	-2,144213143	0,000526876	0,007506093
AC092119.2	19,57530996	4,52482764	21,58740652	4,7708793	2,254255187	0,000528232	0,007509987
FER1L6-AS2	1,996071099	0,060405896	2,25484987	37,32830738	5,222198187	0,000535209	0,007593623
AL049830.3	4,898487832	0,678415595	5,462668612	8,052097644	3,009364667	0,000540075	0,007647018
IGF2BP2-AS1	8,898149606	1,00774849	9,953016065	9,876488198	3,303998151	0,000559896	0,00790393
LINC02028	123,236234	222,263682	109,9972704	0,494895385	-1,014804507	0,000560498	0,00790393
LINC01197	51,4035874	97,91229	45,18584641	0,461493102	-1,115619012	0,000566906	0,007974759
BPESC1	1,537605339	0,047559386	1,736809343	36,51875033	5,190565492	0,000567819	0,007974759
MIR663AHG	13,1719361	0,116033078	14,91737768	128,5614238	7,006314002	0,000572292	0,008021338
AC008741.2	44,77923776	14,74498412	48,79451231	3,309227864	1,726494635	0,000573696	0,008024807
AP001469.3	37,76646807	12,11860206	41,19532717	3,399346474	1,765257414	0,000580051	0,008097366
Z99289.1	5,924914646	16,2557964	4,543780722	0,279517571	-1,838989119	0,00058576	0,008160654
AC108136.1	10,80420227	1,968345994	11,98546648	6,089105531	2,606230317	0,000590549	0,008210884
LINC01448	4,860587465	0,279873926	5,472982323	19,55517044	4,289478205	0,000595639	0,008262263
AC090559.1	21,43629581	46,30889349	18,11108222	0,39109296	-1,354416529	0,000596626	0,008262263
AL359881.1	4,285503651	0,482462848	4,793931566	9,936374558	3,312719558	0,000608912	0,008415598
AC026469.1	14,99170927	35,30852511	12,27555742	0,347665539	-1,524228022	0,000620542	0,00855928
STPG3-AS1	52,013311	18,55079118	56,4869099	3,044986565	1,606435863	0,000628616	0,008653452
DLX2-AS1	1,431780188	0,024974856	1,619855767	64,85946262	6,019245166	0,000639035	0,00877946
AC092447.5	3,16109092	0,369033889	3,534360577	9,577333364	3,259624019	0,000644472	0,008836652
LINC02315	17,82211527	4,639374199	19,58451381	4,22136973	2,077711194	0,000645849	0,008838066
AC107393.2	6,257911537	0,244987595	7,061778374	28,82504467	4,849250938	0,000652417	0,008908076
AC007639.1	15,70636003	1,023062588	17,66936771	17,27105254	4,110284102	0,000653533	0,008908076
AL445228.2	5,020426163	0,723882796	5,594830356	7,728917427	2,950266353	0,000657555	0,008945331
TRPC7-AS1	2,53894881	0,160359407	2,856942046	17,8158681	4,155090877	0,000659149	0,008949467
AL022323.1	87,47011865	162,9745374	77,37594502	0,474773215	-1,074689551	0,000661983	0,008970387
AL590235.1	20,55774049	5,110060281	22,62293838	4,427137281	2,146374111	0,000665753	0,009003893
LINC01842	2,510759035	0,211582889	2,818135525	13,31929791	3,735446131	0,000668695	0,009026079
ADGRD1-AS1	10,87792554	0,068073841	12,32309288	181,025379	7,500048161	0,000689877	0,009272679
AP001178.3	3,660348283	0,459473985	4,088272654	8,897723885	3,153436329	0,000690128	0,009272679
AC007495.1	13,35949197	31,62678987	10,91733985	0,345192791	-1,534525761	0,000691226	0,009272679
LINC02082	3,563572759	0,172754523	4,016890705	23,25201469	4,53928382	0,00069231	0,009272679
AC078909.2	4,646353274	0,720181271	5,171242579	7,180473562	2,844078995	0,000699246	0,0093447
LINC01697	20,90518771	0,860195044	23,58499957	27,41819979	4,777061945	0,000700381	0,0093447
AC100872.1	4,789747928	0,668743421	5,340684359	7,98614864	2,997499924	0,000709453	0,009447571
ERVMER61-1	5,325963258	0,177995608	6,014194227	33,78844164	5,078457908	0,000719137	0,009558186
GUSBP11	51,36275516	17,91458495	55,83443567	3,116702722	1,640020554	0,00072635	0,009617207
AP004147.1	3,363679325	0,465703479	3,751109251	8,054715968	3,009833716	0,000728789	0,009631121
AL591848.2	2,954656939	0,282903593	3,311843216	11,7066142	3,549251973	0,000732455	0,009653604
AF254983.1	1,246900978	0,01985937	1,410943974	71,04676437	6,150697042	0,00073405	0,009653604
CCDC18-AS1	191,2235559	92,06918795	204,4794874	2,220932887	1,151165798	0,000734665	0,009653604
AC008443.3	1,760499512	0,107088474	1,981543768	18,50380066	4,209749724	0,000743035	0,009745137
AC007406.2	23,6323106	6,127890621	25,9724737	4,238403605	2,083520976	0,000764781	0,010011422
MYLK-AS1	26,24605048	7,525625757	28,74878105	3,820118351	1,933617335	0,000768001	0,01003463
VAC14-AS1	56,37710916	22,40754172	60,91849518	2,718660348	1,442895922	0,000802861	0,010431177
AL353708.3	15,06775815	3,401380392	16,62743432	4,888437165	2,289373309	0,000826148	0,010713676
AC100849.1	2,429546455	7,221384817	1,788926353	0,247726218	-2,013181529	0,00084025	0,010876216
AC097512.1	4,870265513	0,384196164	5,470007405	14,23753778	3,831627765	0,000844723	0,010913763
LINC01297	2,974201228	0,067914621	3,362742218	49,51426013	5,629772177	0,000852202	0,010989917
UPK1A-AS1	9,944543024	1,201292034	11,11342685	9,251228288	3,209644925	0,000858343	0,011048573
AC013451.2	2,907928447	0,349915675	3,249908764	9,287691272	3,215320017	0,000860895	0,011060905
SLC12A5-AS1	16,09296043	3,767504236	17,74074869	4,708886196	2,235385856	0,000865778	0,011103084

HID1-AS1	5,631480609	14,92083782	4,389587933	0,294191786	-1,765171127	0,000880588	0,01127218
PCAT6	73,33143823	29,88313079	79,14003549	2,648318078	1,405076408	0,000894462	0,011428692
LINC01338	1,753043556	0,157962691	1,966289661	12,44781058	3,637820107	0,000903202	0,011519148
AC104041.1	3,201990231	0,450226907	3,569873029	7,929053055	2,987148579	0,000906163	0,01153571
AC007364.1	20,78399897	46,09949109	17,39957489	0,377435292	-1,405698766	0,000914359	0,011618723
AC006538.1	14,82886371	3,68482885	16,31870794	4,428620325	2,146857317	0,000922733	0,011703692
AC040173.1	6,711112109	1,08374092	7,463434461	6,886733098	2,783819765	0,000927258	0,011739632
SOX9-AS1	308,8213796	113,7647882	334,898464	2,943779612	1,557669667	0,000944502	0,011936161
AC010307.4	1,243484805	0,037658108	1,404691583	37,30117267	5,221149081	0,000949356	0,011975691
PWRN1	3,805996421	9,871652146	2,99507988	0,303402089	-1,720697077	0,000961879	0,012111649
AC138761.4	2,350591464	0,137557713	2,646451591	19,23884554	4,265950325	0,000964406	0,012121459
AC036108.2	19,59315015	5,042600113	21,53841085	4,271290676	2,094672082	0,000967744	0,012141424
AC112484.4	25,79431176	7,224072177	28,27696411	3,914269323	1,968743025	0,000979664	0,012264454
LINC02159	13,4555942	0,593350423	15,17514551	25,57535131	4,676682152	0,000981086	0,012264454
AP000553.1	4,166448153	0,618142598	4,640820554	7,50768604	2,90836832	0,000989709	0,012350003
LINC01096	1,505532039	0,023224516	1,703701493	73,35788904	6,196880219	0,000998225	0,01243391
AC023347.1	2,597835962	0,304302342	2,904458104	9,544645903	3,254691676	0,001019815	0,012680068
LINC00488	15,72581853	1,648689989	17,60778759	10,67986565	3,416821593	0,001027135	0,012748238
AC024937.3	21,22099751	5,917167603	23,26696408	3,93211172	1,975304312	0,001039445	0,012877976
BX322234.2	1,701507765	0,088663848	1,91712861	21,6224385	4,434457329	0,00104358	0,012906165
AP002761.4	101,5251858	47,14507338	108,7952543	2,307669636	1,206436704	0,001047937	0,012936993
AC092171.4	11,03269231	2,485423364	12,17537533	4,898712833	2,292402722	0,001053924	0,012987793
ZMIZ1-AS1	40,94513656	14,60480682	44,46657101	3,044653145	1,606277882	0,001062314	0,013047863
AC004816.1	26,82617624	8,427542478	29,28588663	3,475020946	1,797021674	0,00106256	0,013047863
AL137060.1	7,889258967	1,60201895	8,729799077	5,449248322	2,446057236	0,001095543	0,013429114
U73166.1	19,12980381	5,68052468	20,92783578	3,684137815	1,88132703	0,001110801	0,013592129
AC078942.1	1,772927908	5,412956253	1,286293103	0,237632274	-2,073197307	0,001120823	0,013690617
AC139100.1	29,95138537	9,603352278	32,67171065	3,402115189	1,766431989	0,001126029	0,013730031
AP000525.1	6,292518918	1,244900719	6,967334186	5,596698661	2,484576072	0,001139363	0,013868249
AC005224.3	6,643375481	16,33545995	5,347642263	0,327364046	-1,611032213	0,001144617	0,013892765
LINC01714	10,29080256	25,10944725	8,309700328	0,330939198	-1,595361915	0,001145382	0,013892765
PCAT18	4,495583377	11,57706467	3,548861279	0,306542408	-1,705841421	0,001163771	0,014091172
RBMS3-AS3	2,658603135	7,047848922	2,07180557	0,293962824	-1,76629438	0,001173014	0,014178345
FAM3D-AS1	2,484303586	6,988852671	1,882091142	0,269299015	-1,892719141	0,001182438	0,014267405
COLCA1	127,8077394	42,90991215	139,1577164	3,243020304	1,697338056	0,001195164	0,014370966
AL592494.1	63,00924728	117,1956577	55,76507476	0,475828848	-1,071485355	0,001201361	0,01442049
AC107959.3	17,24972469	4,652676186	18,93382209	4,069447632	2,024832983	0,00122454	0,014673332
MGC27382	33,522432	69,59845979	28,69943363	0,41235731	-1,278033113	0,001253985	0,014992605
SERTAD4-AS1	25,31043125	4,309657855	28,11802127	6,524420781	2,705849829	0,001255506	0,014992605
LINC01311	24,74446216	7,443579093	27,05741444	3,635000597	1,861955601	0,001265268	0,015083212
AC113383.1	2,894164302	0,306823178	3,240065522	10,56004158	3,40054361	0,001280852	0,015242792
AP000526.1	1,331302842	0,057369871	1,501614737	26,17427433	4,710077635	0,001295923	0,015335327
MIR600HG	97,38483298	43,83685559	104,5436535	2,38483468	1,25388926	0,001296301	0,015335327
LINC01136	9,591521411	2,184068929	10,58182254	4,845003931	2,276497836	0,001297244	0,015335327
MAFA-AS1	23,59936473	0,059962699	26,74634361	446,0496914	8,80106063	0,001297469	0,015335327
FLJ12825	6,100366489	1,061817135	6,773969344	6,379600705	2,673466129	0,001330572	0,015624578
AC021491.2	2,326470163	0,299447748	2,597462465	8,674175989	3,116726714	0,001330949	0,015624578
AL355482.1	36,30349203	12,6035796	39,47192952	3,13180309	1,646993507	0,001342069	0,01570961
AC012613.2	2,367917438	7,056492147	1,741102638	0,246737699	-2,018949932	0,001342721	0,01570961
LINC01257	2,624928782	0,177298252	2,952152115	16,65076829	4,057516842	0,00134705	0,01573373
AC023824.6	2,301017865	0,088675045	2,596785621	29,28428885	4,872054955	0,00135401	0,015778754
LINC00205	73,28041165	31,0858478	78,92139612	2,538820772	1,344158552	0,001355454	0,015778754
LINC02200	18,42845897	0,792091724	20,78626208	26,24224121	4,713819033	0,001363057	0,015838113
SPATA3-AS1	5,553710963	0,989581309	6,163888725	6,228784506	2,638950661	0,001365118	0,015838113
AC019131.2	44,54523	85,64713405	39,05032304	0,455944305	-1,133070488	0,001368702	0,015853182
AC011005.4	8,176000672	1,73902321	9,036559156	5,19634189	2,377496355	0,001399936	0,016160992
LINC00628	5,250952276	0,931224317	5,828456014	6,258917331	2,645913121	0,001426363	0,016438717
AC073321.1	6,178919901	15,58204129	4,921818112	0,315864784	-1,662620994	0,001432236	0,016479029
AL390728.6	191,1891264	96,353859	203,867638	2,115822243	1,081218427	0,001464485	0,016822177
AL118505.1	8,58958227	1,879239744	9,486686886	5,048151475	2,335755201	0,001468667	0,016842331
LINC01967	1,577472998	0,088785618	1,776495375	20,00881927	4,322564131	0,001484366	0,016994274
AC106795.2	28,84062107	60,8008854	24,56785846	0,404070735	-1,307320227	0,001489869	0,017029182
AC139100.2	24,79804043	7,357361544	27,12968199	3,687419984	1,882611744	0,001497406	0,017071739
AC093702.1	1,173738279	0,035167527	1,32595362	37,70392038	5,236642635	0,001498514	0,017071739
AP005328.1	1,304128944	0,082858967	1,467400331	17,70961418	4,146460877	0,001518734	0,017273731
AC132807.2	4,678509203	0,996900373	5,170702897	5,186779981	2,374839173	0,001522644	0,01728986
AL021807.1	13,52290976	3,414576984	14,87429115	4,356115331	2,123042151	0,001539065	0,017447771

C1QTNF1-AS1	21,80988312	5,326305978	24,01356991	4,508484869	2,17264268	0,001580839	0,017892104
PRR7-AS1	6,555005757	1,222121929	7,26795814	5,946999204	2,572161883	0,001608729	0,018178114
LINC02384	170,8870011	47,79196162	187,3435572	3,919980492	1,970846475	0,001641711	0,018520633
AC005089.1	36,34915196	13,17528953	39,44726191	2,99403378	1,582090498	0,001644625	0,018523385
STEAP3-AS1	8,604077277	21,2695149	6,910836953	0,324917469	-1,621854782	0,001678495	0,018874229
AC097478.1	20,64224373	2,151756494	23,11423401	10,74203055	3,425194825	0,001699807	0,019062358
SNHG12	240,1195249	124,2051523	255,6160988	2,05801526	1,04125368	0,001701882	0,019062358
AL121832.3	13,50473861	3,729770261	14,81155256	3,971170212	1,989564199	0,001706216	0,019062358
C2orf48	11,17228609	2,759775099	12,29695333	4,455780958	2,155678313	0,001709785	0,019071525
AC011352.1	1,433938711	0,083083201	1,614534367	19,43274151	4,280417541	0,001732113	0,019289561
AC011840.1	6,35862239	0,198114155	7,182219748	36,25293581	5,180025926	0,001758177	0,01954845
AC010336.2	19,41468242	43,87517713	16,1445628	0,367965758	-1,442356577	0,001782454	0,019786664
LINC01116	33,81934831	4,171768284	37,78292853	9,056813791	3,179003596	0,001791231	0,019852329
AP000997.2	3,580692362	0,565642472	3,983773898	7,042918625	2,816173414	0,001810056	0,020028979
LINC00607	56,87541995	12,73579746	62,77643899	4,929132955	2,301333896	0,001815178	0,020045057
DGCR9	19,81790268	5,815133259	21,68993068	3,729911201	1,899141284	0,001817489	0,020045057
CASC15	50,80043903	16,31390498	55,41093823	3,396546584	1,764068641	0,001820177	0,020045057
TLX1NB	1,971464069	0,157127439	2,214022441	14,09061624	3,816662803	0,001825086	0,020067268
AC087521.1	6,565046278	15,99016511	5,305003654	0,331766659	-1,591759186	0,001830249	0,020092191
LINC01762	8,15088302	1,867336392	8,990929361	4,814841826	2,267488404	0,00183784	0,020143654
AC009831.1	27,80565148	59,2856764	23,597092	0,398023493	-1,329074508	0,001841808	0,020155308
ZBTB46-AS1	1,661047446	0,13263014	1,865381311	14,06453546	3,813989997	0,001846173	0,020171257
AC124242.1	15,60876328	34,64760783	13,06346321	0,377037955	-1,407218333	0,00185459	0,020231358
CU104787.1	1,694203206	0,037658108	1,915666454	50,86996039	5,668742066	0,001912361	0,020828819
AC008060.1	5,538704636	0,044496349	6,27322446	140,9829023	7,1393764	0,001946322	0,02116405
AC008750.3	4,085935937	0,713920158	4,536740185	6,354688453	2,667821397	0,00194924	0,02116405
LINC00351	0,930962969	0	1,055423259	Inf	Inf	0,001956566	0,021210402
AC106744.1	1,1977186	0	1,357841408	Inf	Inf	0,001972855	0,021335834
AP000561.1	1,300772405	0,045199472	1,468629749	32,49218821	5,022021001	0,001974287	0,021335834
LINC00689	21,39901276	2,328263762	23,94857814	10,28602452	3,362613592	0,001994432	0,02152001
AC020658.4	1,287525716	0,051747503	1,452736707	28,07356142	4,811140191	0,001997944	0,021524437
LINC00941	15,37354717	3,003910659	17,0272419	5,668358293	2,502930953	0,002002476	0,021539815
AC061975.6	16,66832316	0,425048312	18,83988397	44,32410016	5,470019438	0,002028912	0,021790386
AL121721.1	3,886185345	0,069018028	4,396501831	63,70077444	5,993239007	0,002057341	0,022061559
DEPDC1-AS1	1,391195709	0,077302864	1,566849833	20,2689751	4,341201235	0,002063012	0,022088239
LINC01719	53,24743507	22,32741243	57,38112794	2,569985579	1,361760264	0,002067891	0,022106356
AC024361.1	14,65951848	4,022251192	16,08161304	3,998162292	1,999337035	0,002098581	0,022380717
AC005993.1	1,264101307	0,051747503	1,426180692	27,56037695	4,784523715	0,002102943	0,022380717
AL359076.1	43,00172091	82,73401775	37,68991652	0,455555255	-1,134302045	0,002103233	0,022380717
AC239585.2	2,76145202	0,405001148	3,076485559	7,596239115	2,925285319	0,002108909	0,022406754
AL035461.2	40,63768241	15,28706692	44,02680213	2,880003232	1,526070431	0,0021128	0,022413768
EGFR-AS1	94,02180171	23,07502258	103,5066652	4,485658243	2,165319707	0,002127213	0,022532222
AC007128.2	1,107457268	0,03532572	1,250790363	35,40735639	5,145977227	0,002178879	0,023044306
AL596223.2	3,584209608	0,539182486	3,991298796	7,402500826	2,888012746	0,002197472	0,023205567
AL592424.1	28,0551158	9,142234113	30,58357592	3,345306578	1,742138432	0,00220316	0,023230281
AP003352.1	123,1363957	59,33504813	131,6659876	2,219025547	1,149926277	0,002214069	0,023309879
AC025176.1	2,843093508	0,36478071	3,174418748	8,702265948	3,121391107	0,002235005	0,023494643
AC015813.1	182,7014488	94,69177492	194,467448	2,05368891	1,03821766	0,00225597	0,023679155
AC092916.1	1,247110356	0	1,413836339	Inf	Inf	0,002300713	0,024072841
AL355388.2	8,940044595	1,862380558	9,886256364	5,308397536	2,408276415	0,002304601	0,024072841
AC007991.3	1,915546022	5,102493553	1,489483518	0,291912866	-1,776390295	0,002307356	0,024072841
FBXL19-AS1	54,50285001	22,6878805	58,75618818	2,589761004	1,372818965	0,002343106	0,024409112
AC016027.1	48,09752174	92,86522119	42,11253518	0,453480158	-1,140888668	0,002376169	0,024696439
AP001781.2	69,03996937	127,2358461	61,25977194	0,481466299	-1,054493277	0,002377806	0,024696439
AC010969.1	21,34484548	63,27596288	15,73908113	0,248737126	-2,00730624	0,002392481	0,024737118
Z82246.1	24,31330818	6,947866315	26,63489131	3,833535377	1,938675494	0,002392731	0,024737118
AC234772.2	1,690424007	0,15868578	1,895201845	11,94311078	3,578106755	0,002393166	0,024737118
LINC01117	2,631899491	0,371065755	2,934149991	7,907358605	2,983195853	0,002395985	0,024737118
AC011899.2	49,28329996	90,45379873	43,77922258	0,483995401	-1,046934756	0,002466498	0,02542729
FP671120.4	26,71908213	75,31362885	20,22248498	0,268510299	-1,896950671	0,002490037	0,025631868
AL133215.2	6,100211114	1,3465682	6,735724873	5,002141647	2,322545911	0,002505	0,025747686
PART1	67,54620558	0,574584938	76,4996308	133,1389421	7,0567888	0,002543131	0,02604919
AL160408.4	2,751789418	0	3,119675704	Inf	Inf	0,002543265	0,02604919
AC111149.2	27,46655261	9,1845965	29,91066439	3,256611696	1,703371709	0,002545597	0,02604919
AL022322.1	26,41944964	9,086348542	28,73670915	3,16262457	1,661122306	0,002606174	0,0266298
ATP2A1-AS1	11,31496904	2,873705239	12,44348025	4,330117118	2,114406046	0,002619024	0,026721745
AC007277.1	13,73244877	1,190022999	15,40924366	12,94869399	3,694734689	0,002649549	0,026951035

LINC01091	24,41743498	8,168677605	26,58972875	3,25508363	1,70269461	0,002657035	0,026951035
AC068506.1	21,00999202	6,232631194	22,98557502	3,687940824	1,882815507	0,002681005	0,027154468
AC145207.8	10,11226251	1,971250515	11,2006331	5,681993745	2,506397243	0,002690381	0,027209712
AC245595.1	9,646008297	2,259197146	10,63354989	4,706782635	2,234741229	0,002716249	0,027373043
LINC00528	54,37626896	21,27792353	58,80118145	2,763483071	1,466487775	0,002718137	0,027373043
AL033527.3	3,292018536	0,472367986	3,668977165	7,767201153	2,957394829	0,002720036	0,027373043
LINC00114	5,406468572	0,792778622	6,023272041	7,597672126	2,925557455	0,002722456	0,027373043
AC105118.1	26,04947447	0,082858967	29,52094713	356,2794508	8,476865465	0,002726257	0,027373043
FAM87A	8,27553191	1,050815365	9,241403106	8,794507021	3,136602709	0,002738435	0,027455582
WDFY3-AS2	40,21032307	77,63648198	35,20682589	0,453483015	-1,14087958	0,002762166	0,02765355
LINC00501	3,942408837	0,59225953	4,390289761	7,412780272	2,890014748	0,002777967	0,027771662
AL158212.3	62,69327227	26,15431896	67,57815908	2,583824079	1,369507846	0,002789237	0,027844211
AL445070.1	0,9800673	0	1,11109234	Inf	Inf	0,002801679	0,027928226
AC087741.1	142,9605182	71,70922603	152,486092	2,126450116	1,088447011	0,002851601	0,02831026
AL359878.1	6,620995768	1,55882895	7,297756038	4,681563065	2,226990293	0,002852244	0,02831026
AC079239.1	2,610975393	0,05381668	2,952841531	54,86851856	5,777906719	0,002872862	0,028474165
AC129492.2	1,083356062	0,023933994	1,224990029	51,18201452	5,677565028	0,002877431	0,028478768
GAPLINC	40,05917111	6,122487913	44,59616084	7,283993284	2,864729592	0,002883351	0,028496711
AC114810.1	47,79320002	89,6969151	42,19109907	0,470374026	-1,088119698	0,002912941	0,028748202
AC108517.1	2,299342704	0	2,606741461	Inf	Inf	0,002943938	0,029012846
PRKAR2A-AS1	57,68930998	24,62119596	62,11018083	2,522630539	1,334928927	0,002966351	0,02919226
TTC39A-AS1	6,445858341	1,524071402	7,103851247	4,661101335	2,220670878	0,002975455	0,02924038
AC012625.1	2,034533233	0,234140761	2,275227414	9,717348681	3,280562737	0,002982901	0,029272086
LINC01509	1,095842223	0,037658108	1,237310688	32,85642213	5,038103483	0,002996922	0,029368139
AC002378.1	1,387107736	0,087269944	1,560882842	17,88568638	4,160733579	0,003003549	0,029391571
LINC02119	21,27283267	0,657960002	24,02883169	36,52020127	5,190622811	0,003014505	0,029457236
AC015922.4	26,35507471	51,98198841	22,92901673	0,441095415	-1,180837332	0,003033105	0,029597299
AC011611.3	1,795950941	4,794885217	1,395023899	0,290939999	-1,781206442	0,00305159	0,029735862
AC007848.1	2,315886624	0,283537552	2,587591045	9,126096443	3,1899979	0,003072577	0,029898373
AC110799.1	1,086983586	0,022922288	1,22923777	53,62631185	5,74486913	0,003091111	0,030036596
AC010528.1	0,884692853	0	1,002967298	Inf	Inf	0,003097449	0,030056082
AC018809.1	7,458055868	1,543063222	8,248830285	5,345750042	2,418392381	0,003114573	0,03018004
AL138760.1	1,434665443	0,106660739	1,612206178	15,11527284	3,917935116	0,003138093	0,030365534
AL136162.1	14,53667629	4,188966677	15,92005993	3,800474235	1,926179454	0,003146082	0,030385776
LINC02128	29,64548654	57,17193855	25,96547958	0,454164757	-1,138712337	0,003148944	0,030385776
AL162726.4	0,887175795	0	1,005782185	Inf	Inf	0,00316224	0,03044071
AL512652.1	2,608873097	0,353074421	2,91045046	8,243164303	3,043198251	0,003163412	0,03044071
LINC01992	3,134158523	0,051994418	3,546212548	68,20371695	6,09177846	0,003176217	0,030521599
AL358075.2	3,612276518	0,6666413	4,006078018	6,009345686	2,587207915	0,003188201	0,030594381
LINC02298	33,02889403	12,20510198	35,81282345	2,934250243	1,552991914	0,003215619	0,030814866
AC096564.1	8,37392367	19,85240114	6,839367859	0,344510864	-1,537378618	0,003221178	0,03082556
AC004080.1	1,044266838	0,03532572	1,179152014	33,37941901	5,060886939	0,003245254	0,031013186
LINC01549	57,63882398	7,492875428	64,34282779	8,587201057	3,102187971	0,003275785	0,031242818
TMCC1-AS1	49,39374476	20,59719252	53,24355121	2,584990705	1,370159093	0,003278289	0,031242818
AL160006.1	138,562796	70,89968715	147,6086662	2,081936777	1,057926258	0,003308584	0,031488278
PRKG1-AS1	2,845137536	0,468266472	3,162901048	6,754489677	2,755846773	0,003314035	0,03149695
AP006621.2	17,49338598	5,309793679	19,12220848	3,601309135	1,848521445	0,003365548	0,031942784
AC010201.2	15,09246594	4,468168342	16,51282658	3,695659009	1,885831648	0,00338044	0,031997883
AC010973.2	29,64099244	10,75927335	32,16528644	2,989540779	1,57992389	0,003382349	0,031997883
AC034229.4	4,494400077	0,849056264	4,981745506	5,867391499	2,552719258	0,00338519	0,031997883
AC132872.2	6,094774338	1,3408421	6,730326776	5,019477516	2,3275372	0,00340264	0,032075434
MAPT-IT1	4,354357947	0,814005411	4,82766711	5,930755554	2,56821591	0,003430654	0,03229563
GPR1-AS	15,79985598	0,550140334	17,83858802	32,42552293	5,019057936	0,003449533	0,03242935
STAU2-AS1	7,191008401	1,658809054	7,930607244	4,780904242	2,25728351	0,003507374	0,032928499
MNX1-AS2	2,753534109	0,338289038	3,076427835	9,094080756	3,184927815	0,003530606	0,033101817
AC008991.1	2,79241206	0,059662782	3,157752872	52,92667821	5,725923205	0,003561382	0,033345303
AL022324.3	1,298059934	0,088259903	1,459797906	16,5397633	4,047866683	0,003569744	0,033378548
DNM1P35	21,00953854	7,118754364	22,86659525	3,21216242	1,683544843	0,00357908	0,033420799
AL359551.1	4,177577899	0,281520817	4,698441145	16,6894981	4,060868665	0,003609334	0,033658012
CASC22	6,472928457	0,771961807	7,235089774	9,372341618	3,228409541	0,003619304	0,033705684
AC084864.1	1,325992398	0,059847738	1,495263074	24,98445441	4,642958809	0,003634959	0,033806092
AC092667.1	10,25619277	2,725852576	11,26292274	4,131889904	2,046801813	0,003667322	0,034061423
AC092598.1	4,949711191	0,406207291	5,557131499	13,68053116	3,774052341	0,00373224	0,034571803
LINC00635	2,037833008	0,133807992	2,292381807	17,13187511	4,09861116	0,003757219	0,034679807
AC103808.6	1,243730927	0,068097131	1,400901221	20,57210347	4,36261741	0,003763887	0,034679807
AC107375.1	62,81324674	28,17783739	67,44364906	2,393499832	1,259121705	0,003763894	0,034679807
ARHGEF26-AS1	28,85775538	56,69981655	25,13555469	0,443309277	-1,17361454	0,003773956	0,034726398

TMEM132D-AS1	31,52344396	0,121018404	35,7216292	295,17518	8,205427606	0,003786705	0,034797566
FLJ31104	16,37938986	4,8289463	17,9235668	3,711693129	1,892077438	0,003797519	0,034850779
AC007319.1	29,37449535	57,48219623	25,61678132	0,445647227	-1,166025968	0,003844396	0,03518789
AC124290.1	1,220072555	0	1,383183859	Inf	Inf	0,00385037	0,035196139
AC093730.1	1,153036451	0	1,307185709	Inf	Inf	0,003859862	0,035236481
AC025031.1	3,767294199	8,654931212	3,113866791	0,359779496	-1,474815125	0,003896195	0,035467912
AC114489.1	2,623231495	0,018242897	2,971492003	162,8848783	7,347708865	0,00390055	0,035467912
AC116025.1	15,44209322	34,59969966	12,88091589	0,372284038	-1,425524336	0,003916592	0,03556717
AC026992.2	6,259849109	1,493401252	6,897074758	4,618366797	2,207382758	0,003941036	0,035742362
AL590652.1	4,371039452	0,941266295	4,829565275	5,13092342	2,359218493	0,003971691	0,03597336
AL121992.3	47,5808917	85,51198894	42,5098894	0,497121982	-1,008328197	0,003981088	0,036011457
AP000253.1	8,205222023	19,039954	6,756728443	0,354871049	-1,494633215	0,003989538	0,036040904
AL355987.4	40,48610595	10,89791056	44,44174705	4,07800622	2,027863976	0,003996088	0,036053134
AC138965.2	1,238518067	0,018242897	1,401656458	76,83299885	6,263654159	0,004006666	0,036101623
AL353148.1	1,437936788	3,97253867	1,099086269	0,276671006	-1,853756633	0,004025439	0,036223732
LINC01675	4,419616151	0,939316004	4,88489692	5,200483009	2,378645624	0,004038818	0,036297046
AC087564.1	2,057914439	5,292408524	1,625495443	0,307137183	-1,703044917	0,004067938	0,036511451
AC103706.1	36,35756992	13,35972938	39,43214753	2,951567836	1,5614815	0,004095762	0,036666317
AC020656.2	71,94965609	32,25526377	77,25639303	2,395156139	1,260119707	0,004111303	0,036758018
DCST1-AS1	64,13573639	29,19190745	68,80737127	2,357070068	1,236994646	0,004125258	0,036835314
VIPR1-AS1	3,500464937	8,096366457	2,8860396	0,356461088	-1,488183495	0,004187583	0,037266042
LINC00494	35,81419357	4,261389987	40,03248282	9,394231211	3,231775102	0,004188031	0,037266042
AL160162.1	1,763319925	0,199554488	1,972379475	9,883914363	3,305082511	0,00418961	0,037266042
AL670729.1	3,333525874	0,589170612	3,700418289	6,280724483	2,650930984	0,004234345	0,037614914
AL592043.1	0,83386654	0	0,945346023	Inf	Inf	0,004239675	0,037614914
PSORS1C3	20,93856759	7,059111375	22,79410987	3,229033891	1,691102583	0,004262891	0,037772589
LINC01341	85,96324757	39,68054475	92,15077469	2,32231627	1,215564462	0,004273453	0,037817876
AF111167.2	68,10317192	123,5710621	60,68767858	0,491115619	-1,025865391	0,004282347	0,037848312
AC005165.1	20,7709719	2,280825125	23,24291666	10,19057375	3,349163376	0,004300319	0,037958798
RASGRF2-AS1	1,902797489	0,194194874	2,131220298	10,97464757	3,456102705	0,004335021	0,038167985
AP000593.3	31,71953709	1,051621058	35,81952587	34,06124819	5,090059399	0,004343769	0,038196539
AC239809.3	42,40567974	4,199231037	47,51349374	11,31480819	3,500140223	0,004356955	0,038263994
C3orf67-AS1	2,988405319	0,500318092	3,321037301	6,637851706	2,730716399	0,004371373	0,038342077
AL451050.2	8,150045819	2,093609893	8,959729766	4,279560292	2,097462573	0,004413415	0,038661961
AC025265.3	1,415363695	0,131589691	1,586991236	12,06014867	3,592175787	0,004455197	0,038978761
TYMSOS	115,959333	61,5725941	123,2302874	2,001382095	1,000996626	0,004488974	0,039224815
AC025171.2	50,89051906	21,59698236	54,80676728	2,537704869	1,343524296	0,004513158	0,039383766
AL035446.1	28,02461798	6,363018258	30,92055378	4,859416164	2,280782991	0,004518518	0,039383766
AC010735.1	3,043495053	0,542078094	3,377909085	6,231406736	2,639557887	0,00457672	0,039841011
AC040970.1	20,02179091	6,702031025	21,80250747	3,253119449	1,701823796	0,004589159	0,039899233
LINC01807	7,333378209	1,962100143	8,051463512	4,103492648	2,036852369	0,004602839	0,039968083
LINC02477	2,075606302	0,295807564	2,31354731	7,821122886	2,967375751	0,004656645	0,040334333
AL109754.1	3,649244854	0,46755394	4,074604602	8,714726272	3,12345535	0,004743674	0,040934837
AP001107.5	3,748897602	8,295705329	3,141035606	0,378633941	-1,401124352	0,004776772	0,041169245
AC016395.1	13,09214454	27,31156379	11,19115266	0,409758766	-1,287153283	0,004808563	0,041391821
AC122694.1	1,469526726	0,123788291	1,649438282	13,3246713	3,736028039	0,004855585	0,041693128
PRR34-AS1	155,8104806	81,49776613	165,7453355	2,033740841	1,024135849	0,004882216	0,041869979
LINC00399	4,097837572	10,16689405	3,286466385	0,323251759	-1,629269875	0,004894974	0,041927568
AC020934.1	1,581332452	0,185829024	1,767897081	9,513568149	3,249986538	0,004918894	0,041986489
ZNF252P-AS1	13,98597577	3,84665295	15,34150021	3,988272508	1,995763989	0,004918906	0,041986489
AC005670.1	2,322265917	0,366714883	2,583703221	7,045536853	2,816709641	0,004920008	0,041986489
LINC00402	14,01541959	28,28699858	12,10745449	0,428021886	-1,224243527	0,004928252	0,042005174
AC008825.1	0,960355644	0,028413684	1,084946815	38,18395499	5,254894636	0,004934318	0,042005271
Z97192.2	18,17278812	4,034133162	20,06298263	4,973306985	2,314205486	0,004947756	0,042058656
AL451074.2	12,11888585	3,842222618	13,22539162	3,44212008	1,783297427	0,004952713	0,042058656
LINC00308	0,815486792	0	0,924509091	Inf	Inf	0,004973369	0,042182437
AC069208.1	6,815823252	15,75121381	5,621252323	0,356877406	-1,486499528	0,004982747	0,042210378
AC005381.1	8,037764622	0,184074391	9,087723209	49,36983987	5,625558061	0,00499213	0,042238294
AC104794.4	3,146952976	7,679827642	2,540953689	0,33086077	-1,595703852	0,005006179	0,042281342
AC104170.1	14,95279922	31,50226468	12,74030384	0,404425014	-1,306055862	0,00501132	0,042281342
AL139275.2	2,957965217	0	3,353415112	Inf	Inf	0,00501979	0,042281342
AC012617.1	5,476897862	1,195283003	6,049306265	5,060982419	2,339417463	0,005030459	0,042281342
C5orf66-AS1	1,147040211	0,029665935	1,296421799	43,70068936	5,449584133	0,005031771	0,042281342
LINC01854	1,428185752	0,070620301	1,609678459	22,79342379	4,510545743	0,005033783	0,042281342
AC000067.1	1,520168868	0,107942394	1,708969199	15,8322336	3,984792899	0,005087441	0,042680371
LINC00894	47,6820013	19,9715156	51,38661169	2,572995095	1,363448707	0,005095123	0,042693193
LINC00365	39,39103275	72,6116374	34,94977544	0,481324712	-1,0549176	0,005139395	0,043012211

LINC00685	13,89223902	4,00267899	15,21437271	3,801047436	1,92639703	0,005148485	0,043036371
AC009831.4	1,200898519	3,578207672	0,88307644	0,246792954	-2,018626891	0,005171623	0,043177759
SACS-AS1	16,80625994	0,109653641	19,03842655	173,6232954	7,43981672	0,005182994	0,043220687
LINC01727	15,42485835	36,83807362	12,56212903	0,34100939	-1,552116627	0,005258743	0,043747189
AC099676.1	49,27284767	21,31513842	53,01050934	2,486988744	1,314399978	0,00528184	0,04388671
FAM85B	2,724989989	6,659565027	2,198977283	0,330198335	-1,59859525	0,005293758	0,043917838
AC055713.1	78,89817235	39,57325837	84,15551379	2,1265753	1,08853194	0,005298246	0,043917838
AP002807.1	40,39493627	16,22119316	43,62672011	2,689488971	1,427332073	0,005327448	0,044103565
AL021392.1	10,82441062	3,332968334	11,82594034	3,548170627	1,827075389	0,005333366	0,044103565
AC005725.1	0,992475007	0,031787768	1,12090913	35,26227817	5,14005378	0,005346729	0,044161431
AL121772.1	10,39526232	3,04140182	11,37839875	3,74116918	1,903489208	0,005359827	0,044181709
ZNF793-AS1	27,03779101	10,43051319	29,25801532	2,805040825	1,488021768	0,00536192	0,044181709
AC062015.1	8,169071088	0,01985937	9,258537895	466,2050176	8,864820722	0,005370741	0,044201896
HOXA-AS2	89,23369046	43,45345437	95,35404288	2,194394997	1,133823238	0,005391366	0,04431907
LINC01572	7,668909159	2,137250271	8,408435749	3,934230755	1,976081579	0,005447617	0,044728481
GATA2-AS1	37,28454534	15,09063836	40,25164521	2,667325546	1,415393916	0,005462815	0,044800249
AL359881.2	3,125207935	0,616578581	3,460586191	5,612563102	2,48865976	0,005548208	0,045397499
AC104134.1	3,519207524	0,614269422	3,907568233	6,361326303	2,669327591	0,005548729	0,045397499
AL162377.1	41,21985491	76,15493576	36,54938956	0,479934612	-1,059090233	0,005576588	0,045571691
AP000472.1	1,97697263	4,95246615	1,579179379	0,318867274	-1,648972059	0,00558405	0,045578988
AC073352.1	3,546807938	0,692938736	3,928341254	5,669103272	2,50312055	0,005644092	0,046014936
LINC02367	12,11240782	3,591262389	13,25159839	3,689955497	1,883603416	0,005671544	0,046184476
AL450322.2	2,232877263	0,379415001	2,480666335	6,538134574	2,708879072	0,005710451	0,046446783
AC012339.1	0,768594222	0	0,87134746	Inf	Inf	0,005750319	0,046716292
LINC02413	14,2726258	0,430937576	16,12311887	37,41404739	5,225508138	0,005839225	0,047268457
LINC00535	46,02062065	18,22958235	49,7360001	2,728312648	1,448008978	0,005850526	0,047268457
AC008250.2	4,880711253	11,39948065	4,009218019	0,351701814	-1,50757532	0,00585193	0,047268457
AC074212.1	66,88663694	31,87901585	71,56680019	2,244950112	1,166683385	0,005851944	0,047268457
AL512791.2	15,07813817	30,3957167	13,03033355	0,428689795	-1,221994022	0,005866087	0,047268457
AL132655.2	2,422602775	0,475303259	2,682936935	5,644684491	2,496892944	0,005870213	0,047268457
AC009509.4	7,919784937	17,33978182	6,660427066	0,384112507	-1,380399155	0,005872546	0,047268457
HCG23	1,946087846	5,119161655	1,521880118	0,297290889	-1,750052847	0,005872789	0,047268457
GDNF-AS1	32,03304162	7,30507544	35,33891945	4,837584463	2,274286851	0,005950583	0,047839102
AC068987.1	6,309572989	1,601616386	6,938978951	4,332484989	2,115194751	0,005976205	0,047989478
FGF14-IT1	1,296492999	3,936048982	0,943611183	0,23973563	-2,060483753	0,006035511	0,048409682
AC078778.1	13,09435339	3,885948844	14,32542352	3,686467346	1,882238978	0,006157234	0,049320454
AC008875.1	3,722563927	0,797921034	4,113558966	5,155345942	2,366069241	0,00616328	0,049320454
AL136528.1	8,608851478	2,166373293	9,470145353	4,371428222	2,12810471	0,006197424	0,049536554
FP236383.2	3,066785443	20,62837295	0,718979627	0,034853918	-4,842535333	0,006206188	0,049549517
AC011754.1	2,095710211	0	2,375885373	Inf	Inf	0,006254789	0,049880143

Table S3. The univariate survival analysis results of the 827 overlapping DELs.

ID	HR	z	pvalue
TMCC1-AS1	1,561787105	5,414009	6,16E-08
AP002478.1	1,243018248	4,905161	9,34E-07
AC015908.3	0,77868509	-4,88684	1,02E-06
AL592043.1	1,434065392	4,860423	1,17E-06
AC090192.2	1,208639649	4,640166	3,48E-06
AP001065.2	0,826485649	-4,46559	7,98E-06
LINC02313	1,213965664	4,321122	1,55E-05
AC079239.1	1,261913617	4,254367	2,10E-05
TMEM220-AS1	0,811857625	-4,16253	3,15E-05
ERVMER61-1	1,196984064	4,126015	3,69E-05
AC009005.1	1,304236177	4,120153	3,79E-05
AC114489.1	1,233780519	4,112789	3,91E-05
SNHG3	1,387923403	4,038766	5,37E-05
AL591501.1	1,261076973	3,987915	6,67E-05
DDX11-AS1	1,401173852	3,94852	7,86E-05
FLJ36000	1,229364544	3,937979	8,22E-05
AL160162.1	1,249463716	3,914925	9,04E-05
DEPDC1-AS1	1,359333413	3,849806	0,000118212
AC025176.1	1,312159247	3,836284	0,00012491
ZFPM2-AS1	1,127802513	3,773632	0,000160888
AC089983.1	1,284593543	3,72154	0,000198011
LINC00402	0,823916878	-3,71017	0,000207121
LINC01138	1,407414414	3,70008	0,000215532
AC012339.1	1,34299105	3,695671	0,000219307
AP001469.3	1,330564031	3,675688	0,000237209
AC099850.3	1,227833808	3,672546	0,000240146
AP003469.2	1,181616219	3,655603	0,000256578
MAFG-AS1	1,224445198	3,654037	0,000258149
LINC00501	1,23576094	3,646006	0,000266348
SOCS2-AS1	0,818713182	-3,60996	0,00030624
AC007128.1	1,189115449	3,585394	0,000336569
AP000526.1	1,32032699	3,548434	0,00038753
F11-AS1	0,854904737	-3,54172	0,00039752
FIRRE	1,193076928	3,510751	0,000446842
LINC01224	1,130728602	3,503147	0,000459796
AC004816.1	1,299894776	3,497295	0,000470002
LINC02362	0,869577567	-3,43255	0,000597931
AL592466.1	1,262443499	3,395288	0,000685565
MIR663AHG	1,129567751	3,391227	0,000695805
AC093609.1	0,798913877	-3,38901	0,000701455
AL121721.1	1,191765586	3,385311	0,000710976
FOXD2-AS1	1,264964864	3,380682	0,00072306
AC124067.4	1,119317264	3,372249	0,00074557
AC107959.3	1,182695452	3,367925	0,000757362
CYTOR	1,251471489	3,351915	0,000802546
AC034229.4	1,312273589	3,338846	0,000841272
LINC00668	1,118310096	3,31581	0,000913781

AC115619.1	0,884626447	-3,28922	0,001004671
HTR2A-AS1	0,691884276	-3,28588	0,001016646
TMEM132D-AS1	1,117326661	3,283695	0,001024558
AC122710.1	1,147022439	3,275117	0,001056182
LINC00942	1,089760009	3,272088	0,001067563
AC093515.1	1,175655618	3,258684	0,001119301
DUXAP8	1,155482394	3,25172	0,001147088
BX322234.2	1,226319536	3,250415	0,001152369
AC010280.2	0,853379693	-3,24754	0,001164073
AL133215.2	1,26056104	3,232806	0,001225808
SNHG4	1,227625516	3,220769	0,001278469
AC116025.2	1,252946963	3,214795	0,001305376
AL021453.1	1,38330009	3,200248	0,001373096
PRR7-AS1	1,226812646	3,195722	0,001394812
AL359878.1	1,278018619	3,180078	0,001472352
AL136084.3	0,802570724	-3,17748	0,001485587
AC084033.3	1,321291712	3,176283	0,001491756
LINC01116	1,159831939	3,162382	0,001564841
AL359313.1	1,140024962	3,155763	0,001600787
LINC02293	1,221851754	3,11356	0,00184845
AL450322.2	1,213690421	3,108258	0,00188194
AC040970.1	1,152919259	3,076218	0,002096448
AL355303.1	1,179695152	3,072691	0,002121384
NOVA1-AS1	1,127901935	3,071043	0,002133123
DLX2-AS1	1,227444947	3,068585	0,002150754
LINC01748	1,11564119	3,034114	0,00241243
AL355987.4	1,198127146	3,019638	0,002530773
LINC01967	1,223642209	3,01794	0,002544994
AC011632.1	1,109599921	3,007711	0,002632232
AC025016.1	1,144396769	3,006836	0,002639819
LINC01537	0,812222664	-3,00664	0,002641482
LINC01018	0,937871822	-2,97881	0,002893675
LUCAT1	1,104946607	2,9749	0,002930841
CASC9	1,075668251	2,971633	0,002962207
LINC01234	1,084230399	2,948742	0,003190697
AC019257.1	0,857766178	-2,93541	0,003331049
AC100872.1	1,179491099	2,934165	0,003344463
LINC00205	1,316907144	2,932321	0,003364388
AL445434.1	1,136516568	2,928386	0,003407269
AL163952.1	1,144107817	2,922345	0,003474064
AL445228.2	1,198976613	2,906149	0,003659077
FER1L6-AS2	1,174458515	2,895438	0,003786304
LINC01136	1,171005071	2,892526	0,003821575
AC092115.3	1,147687011	2,876447	0,004021798
AC009275.1	1,125645944	2,873785	0,004055847
AC109588.1	1,107659914	2,870525	0,00409791
AC079061.1	0,892605318	-2,84223	0,004479983
MYLK-AS1	1,268386023	2,831123	0,004638487
AL365361.1	0,870575827	-2,80731	0,004995638
LINC01096	1,192626535	2,803087	0,0050616

AC005332.8	1,334541175	2,800491	0,005102494
AL161668.3	0,88421809	-2,74741	0,006006845
DCST1-AS1	1,228320544	2,741186	0,006121781
PCAT6	1,201629191	2,729671	0,006339748
CASC15	1,136610553	2,701933	0,006893769
FAM99A	0,934893146	-2,68929	0,007160384
MIR4435-2HG	1,23972435	2,686113	0,007228857
AL136537.2	1,104722399	2,683017	0,007296126
LINC01532	1,124435673	2,669388	0,007598968
AC006946.2	1,140175699	2,664948	0,007700019
LINC00346	1,153488846	2,664652	0,007706793
AC007128.2	1,207298597	2,658776	0,007842499
AC026320.1	1,203094814	2,656906	0,007886145
AC099508.2	0,889940338	-2,65559	0,007916953
LINC01793	1,117827131	2,647088	0,008118824
AP000525.1	1,16171141	2,612141	0,008997707
AC109439.2	1,168603842	2,610284	0,009046699
AL451074.2	1,256802942	2,60489	0,009190366
AP003900.1	1,151871769	2,597454	0,009391779
AL133467.2	1,135393425	2,592891	0,009517294
AP003716.1	0,916663848	-2,5913	0,009561443
LINC01093	0,918561961	-2,57901	0,009908374
MIR99AHG	0,872835941	-2,56642	0,010275398
LINC01518	1,134564271	2,559084	0,010494823
ADGRD1-AS1	1,112018635	2,550881	0,010745088
LINC00491	1,112712516	2,549122	0,010799456
AL133370.1	1,125595573	2,544478	0,010944108
AP003181.1	1,205432189	2,543981	0,010959699
GPR1-AS	1,105084391	2,524725	0,011578877
FAM99B	0,923273065	-2,52423	0,011595235
SNHG1	1,326310192	2,516165	0,011863971
AC093895.1	1,09787452	2,515846	0,011874694
AP003469.4	1,198879035	2,51291	0,011973992
AC245595.1	1,152232767	2,503696	0,012290342
AL133467.4	1,124371496	2,500434	0,01240414
AL355488.2	1,262964487	2,484027	0,012990598
AC109830.1	1,125520822	2,476077	0,013283511
AC079466.1	1,055317698	2,47536	0,013310192
AC020658.4	1,233183673	2,474677	0,013335681
MELTF-AS1	1,169076265	2,470827	0,013480106
AC131391.1	1,148747818	2,465079	0,01369832
AC106822.1	0,871837628	-2,46488	0,013705943
B4GALT1-AS1	0,823747076	-2,46144	0,013838019
AC012146.1	1,187273377	2,452546	0,014184923
AP005230.1	1,139963384	2,443306	0,01455339
SNHG12	1,312144741	2,441618	0,014621608
AC092171.2	1,203841894	2,439198	0,014719884
AC074135.1	1,125715364	2,437345	0,014795572
AF254983.1	1,170871731	2,437107	0,014805304
AP001107.5	0,820431597	-2,43601	0,014850082

LINC02475	1,099836433	2,432944	0,014976615
SAMMSON	1,173854954	2,429941	0,015101278
CDKN2B-AS1	1,161264398	2,428992	0,015140876
AC073352.1	1,230016874	2,428603	0,015157112
AC025265.3	1,192801994	2,422224	0,015425852
LINC01667	1,067959009	2,404761	0,016183049
AL354872.2	0,898971363	-2,39194	0,016759554
AL391095.2	0,899410062	-2,3895	0,0168714
AP005328.1	1,191148178	2,373186	0,017635399
LINC00879	1,105179002	2,364428	0,018057949
LINC00648	1,077213996	2,354979	0,018523752
LINC01992	1,137441975	2,342744	0,019142523
FAM230C	1,09509948	2,332562	0,019671155
AC132807.2	1,116072118	2,327211	0,019954021
AC023347.1	1,134657341	2,324986	0,020072703
AL078590.3	0,870430241	-2,32314	0,020171394
PART1	1,07354687	2,313615	0,020688844
AC091987.1	1,109695426	2,310525	0,020859091
AC016877.3	1,134251827	2,308613	0,020965082
DSCR4-IT1	1,129738456	2,298882	0,021511664
LINC00858	1,128936902	2,278208	0,022714202
AC006305.1	1,092773098	2,27693	0,022790406
AL359076.1	0,799354709	-2,27589	0,022852319
AL035461.2	1,190804555	2,273602	0,022989914
HULC	0,929227768	-2,27348	0,022997248
AC004160.1	0,915293492	-2,27236	0,023064877
AL137026.2	1,122952296	2,266277	0,023434458
AC092667.1	1,128495928	2,264302	0,02355555
TCL6	1,093684115	2,262782	0,023649145
AC005381.1	1,104044818	2,262605	0,023660057
AC007364.1	0,848553438	-2,26219	0,023685882
SERTAD4-AS1	0,87869538	-2,25503	0,024131597
ATP2A1-AS1	1,145634307	2,249066	0,024508285
AL139042.1	1,125228415	2,246602	0,024665499
AL138974.1	1,128434266	2,245806	0,024716451
AC016395.1	0,891005986	-2,24391	0,024838499
AC002378.1	1,196365261	2,241035	0,0250238
LINC02253	1,091356556	2,236868	0,025294946
AC078778.1	1,192563584	2,230897	0,025687981
AC004160.2	0,883076395	-2,23087	0,025689424
AL355388.2	1,147887433	2,227785	0,025894872
AL606489.1	1,155575052	2,220689	0,026372005
LINC00628	1,159796528	2,217042	0,026620189
AC023090.1	1,089893762	2,214455	0,026797491
AC016710.1	1,089336608	2,203323	0,027571964
TSPEAR-AS1	0,923082751	-2,19271	0,028328537
LINC02466	1,117965407	2,187775	0,028685985
VIPR1-AS1	0,838556583	-2,18573	0,028835357
BBOX1-AS1	1,091555644	2,175717	0,02957646
AC092384.2	0,915962818	-2,17459	0,029660742

LINC00511	1,080599991	2,172216	0,029839408
AL161645.1	0,920877574	-2,17091	0,02993767
AC114485.1	1,099793412	2,166188	0,030296802
LINC01194	1,071226542	2,166001	0,030311147
AL022324.3	1,165281947	2,16373	0,030485111
SLC7A11-AS1	1,116481064	2,15643	0,031050112
LINC01703	1,128993035	2,153886	0,031249089
AC010973.2	1,256153514	2,150932	0,031481572
AC007639.1	1,087667435	2,149005	0,031633973
AC008875.1	1,188262032	2,132996	0,032925071
AC138356.1	0,893690277	-2,13077	0,03310814
LINC00664	1,109824874	2,130467	0,03313307
AL161740.1	0,883498141	-2,12981	0,033187218
HAO2-IT1	0,876009673	-2,12966	0,033199353
LINC02152	1,134177087	2,128228	0,033318198
AL589182.1	1,133570313	2,125582	0,033538043
HOXA-AS3	1,124588008	2,120065	0,034000548
AC020978.5	0,907308111	-2,11664	0,034290497
AC022784.6	0,933238296	-2,1161	0,034336533
AC093730.1	1,177479155	2,114237	0,034495046
AC010280.1	0,863648215	-2,11163	0,034718285
AL035661.1	0,935264248	-2,10745	0,035078393
CASC20	1,080618923	2,106298	0,035178464
AL590079.1	0,895008351	-2,09738	0,035960178
AC011352.1	1,187399512	2,094794	0,036189317
AL162431.2	1,180124933	2,09389	0,03626978
LINC02327	1,095279713	2,092716	0,036374495
AL117355.1	1,08696998	2,091283	0,036502741
AF279873.3	1,072839489	2,090639	0,036560394
AC116025.1	0,904939122	-2,08707	0,036881718
CLRN1-AS1	0,873158875	-2,0741	0,038070355
AC132872.2	1,177173539	2,068895	0,038555905
LINC00221	1,0483128	2,067819	0,038657025
AC069277.1	1,088752614	2,064677	0,038953533
AC112251.1	1,05555906	2,056194	0,039763845
AL139412.1	1,125400747	2,054156	0,039960631
CU104787.1	1,130039193	2,052391	0,040131723
LINC01833	1,066608712	2,051294	0,040238349
AC010894.3	1,073380169	2,050832	0,040283316
AL121832.3	1,162862399	2,045242	0,040831
AC245100.6	1,063584239	2,039128	0,041437257
AC068506.1	1,084506287	2,026239	0,042740318
AC107396.1	0,77691773	-2,02334	0,043038145
AC006206.2	1,079368227	2,014331	0,043974786
AC110760.4	1,093362808	2,01282	0,044133563
AC024361.1	1,198522584	2,012019	0,044217919
SPATA3-AS1	1,129181418	2,009701	0,044462867
AC005993.1	1,146211623	2,009502	0,044483888
AC009271.1	1,104246369	2,006429	0,044810477
ELF3-AS1	1,137212634	2,003654	0,045107186

LINC00261	0,911779621	-1,99695	0,045830578
AL390728.6	1,184959527	1,994564	0,046090407
LINC02159	1,088535379	1,993801	0,046173832
AC009159.3	0,859109011	-1,99082	0,046501197
LINC02377	1,070732538	1,990339	0,046553606
AC011503.1	1,082255719	1,985521	0,047086506
BPESC1	1,145346773	1,984587	0,047190416
FP325330.3	1,148481938	1,98127	0,047561042
AC116049.2	1,087783978	1,980756	0,047618694
MINCR	1,15290503	1,980668	0,047628567
AC024230.1	1,090696812	1,979042	0,04781133
AL139023.1	1,086905803	1,976046	0,048149565
AL021392.1	1,126941528	1,971936	0,048616861
LINC02082	1,106372305	1,971447	0,048672743
AC026992.2	1,100087723	1,968772	0,048979305
AC010615.2	1,089561585	1,955616	0,050510453
AC018467.1	0,926406288	-1,94872	0,051329284
DIO3OS	0,942964674	-1,94552	0,051712798
AC068756.1	1,096428177	1,943035	0,05201191
LINC00383	1,105741516	1,938229	0,052595335
AC008109.1	1,068598134	1,938183	0,052600932
NPSR1-AS1	1,06270759	1,936654	0,052787671
LINC02058	1,11848644	1,930713	0,053518563
LINC01370	1,046740123	1,927587	0,053906575
AC036176.1	0,8659762	-1,91993	0,054866136
MAFA-AS1	1,071955636	1,917006	0,055237189
AC008750.3	1,121541197	1,912621	0,055796616
HOXC-AS1	1,093778453	1,910939	0,056012478
AC004477.1	1,182143582	1,910797	0,056030725
AC104794.4	1,175412482	1,910184	0,056109571
AC091133.2	1,129554952	1,905227	0,056750559
LINC02055	1,060698856	1,904784	0,056808095
AL117329.1	1,087660863	1,900634	0,057350002
AC131532.1	1,093965873	1,898325	0,057653248
PRKAR2A-AS1	1,17675529	1,89511	0,058077844
AC010333.1	1,104105509	1,888593	0,058946362
LINC01446	1,061429491	1,888467	0,058963334
UPK1A-AS1	1,08041444	1,885693	0,059336292
AC008549.1	0,945007455	-1,88428	0,059526768
AC122694.1	1,154557249	1,877603	0,060435472
LINC01311	1,191138581	1,873907	0,060943289
AL033527.3	1,131678252	1,868357	0,061712323
CDKN2A-AS1	1,143141049	1,864784	0,062211707
AC010336.2	0,907578295	-1,86398	0,062324691
AC009831.1	0,829329638	-1,85889	0,063042437
RASGRF2-AS1	0,836463351	-1,85708	0,063300363
AC012625.1	1,133415527	1,855981	0,063456207
AC006538.1	1,121357326	1,853383	0,063827481
PWRN1	0,873988444	-1,84332	0,065282805
AC012409.1	0,909551856	-1,84297	0,065332746

LINC00844	0,955387106	-1,8372	0,066180796
AC019131.2	0,839495089	-1,83534	0,066455479
AL590652.1	1,121081108	1,827828	0,067575377
LINC00665	1,07987713	1,826912	0,067713021
AC084864.1	1,14779834	1,826209	0,067818846
AL731897.1	1,064454838	1,818408	0,069001787
AC022424.1	1,063523358	1,817447	0,069148623
AL590705.1	1,091489473	1,816055	0,069361867
AP000997.2	0,887024821	-1,81395	0,069684706
STPG3-AS1	0,902934685	-1,81137	0,07008421
AC109322.1	1,147765632	1,808787	0,070484039
LINC01287	1,038170578	1,808336	0,070554167
AC097512.1	1,092573599	1,803875	0,071250911
AL136162.1	1,168055587	1,803276	0,07134482
LINC02037	0,938843495	-1,801	0,071703522
AP006285.2	0,912918007	-1,79803	0,072172136
AL158212.3	1,171945962	1,787396	0,073873438
AC010595.1	1,078142531	1,786032	0,074093997
AL121772.1	1,120554912	1,783403	0,07452078
AC026740.1	1,099550773	1,777223	0,075531613
LINC01549	0,93399842	-1,76926	0,076849909
LINC01572	1,124573799	1,764766	0,077603144
LINC02041	1,076170287	1,76395	0,077740337
AL591848.2	1,118428026	1,761681	0,078123132
AL157778.1	1,076497316	1,761669	0,078125285
STEAP3-AS1	0,892812631	-1,75763	0,078809995
AL445524.1	1,113652686	1,756532	0,078997675
SNHG7	1,168612026	1,745292	0,080933982
AC106771.1	1,080054454	1,744569	0,081059923
C2orf48	1,10542365	1,742412	0,081436427
LINC00685	1,158776518	1,72018	0,085399652
AC099684.1	0,922714557	-1,71479	0,08638449
AC105118.1	1,065522899	1,713067	0,086700282
WARS2-IT1	0,878909476	-1,71139	0,087009734
AC025171.2	1,153718364	1,707429	0,087742302
LINC01762	1,105154451	1,706542	0,087907232
SNHG6	1,138318277	1,698449	0,089423071
LINC00885	0,940757423	-1,6966	0,08977228
AC145207.8	1,100281814	1,695467	0,089986809
AC129492.2	1,138621099	1,694431	0,0901835
GUSBP11	1,139775532	1,686274	0,091743001
AC112206.2	0,946285331	-1,67959	0,093037969
AL357033.2	0,881054708	-1,67921	0,09311142
AP000553.1	1,127555331	1,677998	0,093347452
AC104809.1	0,951692516	-1,66973	0,094973009
DLG5-AS1	1,119871943	1,666619	0,095590257
LINC02335	1,072142504	1,666182	0,09567718
AL035401.1	1,091179491	1,66463	0,095986567
AC102953.2	1,147287182	1,659218	0,097071772
LINC00941	1,080399553	1,658874	0,097141112

MIR548XHG	1,062297936	1,655784	0,097765662
FBXL19-AS1	1,132544388	1,651365	0,098664069
KCNMB2-AS1	1,059701955	1,65058	0,098824343
LINC02404	1,050131606	1,624777	0,104210165
AC112493.1	1,079735237	1,619392	0,105362928
HAGLR	1,055522783	1,606125	0,108246407
LINC01980	1,043055545	1,606095	0,108253099
LINC01666	1,076188851	1,603165	0,108898327
AC007848.1	1,101915574	1,601357	0,109297826
HOXA11-AS	1,074709227	1,599267	0,109761321
AL136987.1	1,063144316	1,596041	0,110479577
AC096564.1	0,902037256	-1,59077	0,111661688
LINC01019	1,053547239	1,586557	0,11261305
LINC01197	0,905073392	-1,58307	0,113404823
SOX9-AS1	1,071830735	1,575069	0,115240602
AC092625.1	1,085804984	1,572329	0,115874225
AC079789.1	0,832183113	-1,5631	0,118028982
AL731684.1	1,076055672	1,557961	0,119242573
AL080248.1	0,94362736	-1,55661	0,119561954
AL109754.1	1,092788242	1,548694	0,121455267
AC007495.1	0,933831162	-1,5431	0,12280634
AL353708.3	1,145956792	1,534779	0,124838143
AC087392.1	0,939887192	-1,52766	0,126596296
AC092535.4	1,097073586	1,527248	0,12669938
AC092957.1	1,066045408	1,524117	0,127479585
HOXC-AS2	1,081112419	1,52388	0,127538758
LINC02163	1,054360089	1,523557	0,127619411
AL451050.2	1,162600923	1,520136	0,128476861
AC013275.1	1,058536912	1,517519	0,129135681
AC008825.1	1,129983468	1,517361	0,129175552
AC007991.3	0,87147242	-1,51554	0,129635672
AC099676.1	1,146224223	1,513793	0,130078343
ZNF252P-AS1	1,152373533	1,511656	0,13062149
TFAP2A-AS1	1,069668133	1,508525	0,131420107
AC010735.1	0,897740408	-1,50685	0,131848956
AC025254.1	1,057081309	1,500585	0,133462883
AL137060.1	1,134117113	1,498865	0,133908635
AL513318.2	1,060115259	1,4952	0,134862369
AC107419.1	1,066882416	1,485913	0,137302179
FGF14-AS2	1,100319164	1,482808	0,138125339
AC090502.1	1,038796599	1,48231	0,138257865
LINC02438	1,080288015	1,475237	0,140148916
AC004870.2	1,066204647	1,475185	0,140162787
AC005537.1	1,0699321	1,474879	0,140245049
AC010333.2	1,080127705	1,469553	0,141682825
TEX41	1,055254687	1,468123	0,142070877
FGF14-IT1	1,138939129	1,46541	0,142809135
MIR3945HG	0,894246451	-1,46111	0,143984894
HAGLROS	1,089316452	1,460004	0,144289109
Z99289.1	0,909181561	-1,45408	0,145925062

GAS5	1,116612809	1,45405	0,145932394
AC026369.3	0,901892442	-1,45311	0,146193583
AL590235.1	1,096255689	1,451329	0,146688147
LINC01625	0,941854279	-1,45031	0,146973175
MGC27382	0,924994462	-1,44969	0,147145948
AC078942.1	0,868085949	-1,44692	0,147918844
HNF4A-AS1	0,952770352	-1,44672	0,147976076
AC068987.4	1,076479404	1,441549	0,149429737
AC009093.5	0,934285293	-1,43708	0,150695162
AC239868.2	1,127768202	1,434005	0,151570707
LINC01297	1,079440667	1,424538	0,154290842
SLC9A3-AS1	1,074736727	1,421827	0,155076507
LINC00645	1,101332326	1,415883	0,156809853
AC013451.2	1,093470183	1,415003	0,157067483
LINC01807	1,063532466	1,414631	0,157176678
AC099520.1	1,075578185	1,411904	0,157978267
SACS-AS1	1,064512566	1,411697	0,158039234
AC007406.2	1,060219683	1,40448	0,160176034
AC022031.2	1,074055235	1,404272	0,160238011
LINC02109	1,059166885	1,401913	0,160941257
LINC00689	1,049244394	1,397839	0,16216136
DHRS4-AS1	0,893833375	-1,3974	0,162292171
LINC01901	1,08567669	1,396434	0,162583846
AL354704.1	1,087987223	1,3917	0,164013295
AC015468.1	0,857835216	-1,39028	0,164442445
AC090809.1	1,053192283	1,387436	0,165308944
AC024937.3	1,131042819	1,385807	0,165805897
MNX1-AS2	0,915077317	-1,37532	0,1690311
TTC39A-AS1	1,075670854	1,37463	0,169246226
AC103740.1	0,951667013	-1,37064	0,170488021
LINC01702	0,957221807	-1,36902	0,170992884
LINC02428	0,960499615	-1,36778	0,171380304
SMIM25	1,078566993	1,367651	0,171421467
HID1-AS1	0,903663869	-1,3648	0,172317299
RUSC1-AS1	1,136276064	1,364763	0,172327518
GDNF-AS1	0,950899546	-1,36345	0,172739829
TSPEAR-AS2	0,952302737	-1,35847	0,174313221
LINC01697	1,050415981	1,354384	0,175613987
LINC01021	0,955480698	-1,3539	0,175767194
AC008250.2	0,912686635	-1,34762	0,177781686
AC021079.1	1,079526606	1,342005	0,179594222
AC008443.3	1,088788283	1,341647	0,179710374
AL110292.1	1,0862189	1,339099	0,180538333
AC097515.1	1,079574201	1,338782	0,180641745
AC025031.1	0,900077209	-1,33856	0,180713811
LINC01608	1,041929137	1,335057	0,181857756
LINC02476	1,039737923	1,333517	0,182362184
AC015922.4	0,906861878	-1,32669	0,184610521
LINC01818	0,914150097	-1,32277	0,185911007
AL160006.1	1,135741394	1,315857	0,188222125

AC012617.1	1,084670441	1,315307	0,188406803
AC097521.2	1,063194526	1,314473	0,188686947
AC138761.4	1,083712221	1,309195	0,190468292
AP000593.3	1,051031549	1,30902	0,190527462
CRNDE	1,061040171	1,302209	0,192845066
ZNF793-AS1	1,061492711	1,301429	0,193111573
HOXD-AS2	1,060531329	1,291477	0,196538295
LINC00488	1,04951893	1,28604	0,198428973
LINC02367	1,090865	1,280017	0,200539027
AC003988.1	0,866306253	-1,26882	0,204504527
AC026469.1	0,92924408	-1,25929	0,207926217
LINC00308	1,118235211	1,257372	0,208618836
SLC12A5-AS1	1,066548422	1,255795	0,20919042
AC010643.1	1,045393746	1,255449	0,209315686
MIR2052HG	1,062614867	1,254523	0,2096521
LINC01091	1,06973552	1,254257	0,209748747
AC092916.1	1,1012048	1,249302	0,211554553
AC034213.1	1,05201942	1,247214	0,212319108
LINC02050	1,09393523	1,234058	0,21718144
AC010307.4	1,106652709	1,233785	0,217283029
AC092171.4	1,119019695	1,232428	0,217789194
C5orf66-AS1	0,903587447	-1,23173	0,218049611
LINC01257	1,075654681	1,230676	0,218444251
AC100810.1	0,878478263	-1,22991	0,21873095
AL163953.1	1,061143053	1,217147	0,223548222
MAPT-IT1	0,925545604	-1,21548	0,224182741
LINC02202	0,91940729	-1,21516	0,224304638
AL357060.1	0,952275756	-1,21355	0,224917786
LINC00944	1,050006646	1,207133	0,227381104
AC020934.1	1,090010202	1,204657	0,228335829
AC011754.1	0,902408427	-1,19585	0,231754798
AC129507.1	0,924888711	-1,19303	0,23285697
MIR325HG	0,953054832	-1,19231	0,233139021
LINC00399	0,918574591	-1,19096	0,233670275
AC024600.1	0,930805647	-1,18872	0,234550737
Z97192.2	1,050686358	1,182832	0,236875595
AC092447.5	1,065199629	1,182476	0,237016841
AC107973.1	1,070364897	1,18216	0,237142072
AC107393.2	1,056333126	1,178882	0,238445186
AC112178.1	1,045859694	1,175888	0,239639648
LINC02323	1,05151338	1,169019	0,242396
AC097478.1	1,044184153	1,166599	0,243372424
FEZF1-AS1	1,039353455	1,163079	0,244797654
LINC02307	1,086422562	1,148842	0,250621177
VAC14-AS1	1,050257468	1,146402	0,251628887
AC023824.6	1,069291137	1,14505	0,252188562
LINC00853	1,071898568	1,1418	0,253537352
AC092490.1	1,033170075	1,134509	0,256581183
FLJ31104	1,086162939	1,133551	0,256983083
U91319.1	0,964422755	-1,13018	0,25839855

AL023803.2	1,075379645	1,127703	0,259445267
AL133325.3	1,081700039	1,114539	0,265048008
AP001178.3	1,083500315	1,113419	0,265528709
AL512652.1	1,104376966	1,112266	0,26602386
AC139100.1	0,935200672	-1,1012	0,270809164
LINC01235	1,05247125	1,101	0,27089665
B3GALT5-AS1	1,071653506	1,085895	0,277525297
AC078909.2	1,074232911	1,083484	0,27859377
AFAP1-AS1	1,027806376	1,082255	0,279139343
DLX6-AS1	1,039520926	1,078045	0,281013866
PTGES2-AS1	1,071143822	1,071172	0,284092295
PRR34-AS1	1,071712767	1,069394	0,284892288
GAPLINC	0,952223296	-1,06825	0,28540771
LINC00607	1,051115088	1,065442	0,286675819
AL670729.1	1,068598348	1,060772	0,288793522
AC124242.1	0,928046557	-1,05543	0,29123045
DNM3OS	0,942866639	-1,04978	0,293821169
AC005224.3	0,93584631	-1,04486	0,296087772
CASC22	0,94731993	-1,0414	0,297691345
AC005165.1	0,95576434	-1,04105	0,297852635
AL035446.1	1,03890846	1,031217	0,302438946
AC010776.2	0,887189365	-1,02695	0,304445191
STAU2-AS1	1,080043446	1,025808	0,304982195
AC010547.2	1,040090697	1,025426	0,305162148
PVT1	1,062091991	1,015317	0,30995481
LINC01507	1,08956494	1,009147	0,312904048
AC079062.1	1,027092044	1,008496	0,313216325
AL354707.1	1,042914632	1,00455	0,315113536
AC104170.1	0,935364875	-1,00215	0,316268991
LINC02388	0,946992168	-0,99599	0,319256795
TLX1NB	1,073677756	0,993958	0,320243086
AC007319.1	1,064719602	0,984892	0,324677318
FLVCR1-AS1	1,072232168	0,984399	0,324919154
AL355482.1	0,963494021	-0,98173	0,326231363
COLCA1	1,04784151	0,981577	0,326308371
LINC01854	1,074691745	0,981428	0,326381968
AC092809.2	0,941556167	-0,97894	0,327610789
AL583808.1	1,065320316	0,977115	0,328512356
AC011840.1	1,044602636	0,97269	0,330707392
DGCR9	0,952671868	-0,97174	0,331178551
AL162413.1	0,963374699	-0,96829	0,33290017
AC110285.2	0,938496123	-0,96824	0,332924611
HAND2-AS1	0,965839622	-0,96515	0,334469196
AC129507.2	0,950973199	-0,9628	0,335648938
AC005089.1	0,936246874	-0,96056	0,336771657
AL590666.2	1,038218183	0,958286	0,337918675
AC107375.1	1,121821213	0,95772	0,338204043
TMPO-AS1	1,079226492	0,950661	0,341776333
AC239809.3	1,039058251	0,950366	0,341926399
RNF157-AS1	1,040279987	0,949832	0,342197768

AL133367.1	1,082710513	0,949345	0,342444964
LINC01681	1,037647154	0,943593	0,345377912
LINC01419	1,018749499	0,917833	0,358706072
LINC00907	0,950313024	-0,91736	0,35895274
LINC02477	0,93618401	-0,91187	0,361836919
AC011294.1	1,035155043	0,910066	0,362787788
HOTTIP	1,030213471	0,905251	0,365332491
LINC01341	0,944998132	-0,89261	0,372064658
AL355601.1	1,059230492	0,889085	0,373957462
AF127577.4	0,924993934	-0,88655	0,375320476
LINC01117	1,063147198	0,883534	0,376947641
AL355102.4	1,030854645	0,87553	0,381285721
LINC02298	1,03583812	0,862227	0,388562604
AL136528.1	0,959763044	-0,85857	0,39057586
AC124290.1	1,064660715	0,856891	0,391505302
AC108748.1	0,949309567	-0,8567	0,391609867
LINC02267	1,042399319	0,85383	0,39319938
ZMIZ1-AS1	1,054295845	0,846519	0,397263075
LINC01611	1,033421476	0,841088	0,400298761
PRKG1-AS1	1,051717295	0,83934	0,401278458
AL365181.3	1,028271219	0,836492	0,402878022
AC114316.2	1,041623683	0,831638	0,405613058
AC105384.1	0,916118165	-0,82902	0,407091637
RBMS3-AS3	0,932857031	-0,82888	0,407169974
AL645608.1	0,964537747	-0,82764	0,407876876
LINC00896	1,03571481	0,823917	0,409986745
AL391845.2	1,057337316	0,822901	0,410564321
AC091133.3	1,045249818	0,822641	0,410712318
AL121906.2	1,057107907	0,821412	0,411411497
ZNF385D-AS1	1,042499715	0,820845	0,411734467
AP002761.4	1,047281918	0,817932	0,41339623
AC009509.4	0,9360432	-0,81776	0,413496137
AP000472.1	0,931909219	-0,81095	0,417396116
AC114401.1	1,042979631	0,808576	0,418759196
AL358075.2	1,061550895	0,806107	0,42018143
AL445209.1	1,047030476	0,803616	0,421618914
AP003352.1	1,078005103	0,800227	0,42357951
AGAP1-IT1	1,035512013	0,795056	0,426580728
FENDRR	0,960128771	-0,78993	0,429568364
TMEM26-AS1	1,078550237	0,786341	0,431667761
AP006621.2	0,95597828	-0,78277	0,433760486
AC099792.1	1,042496782	0,781848	0,434303835
LINC01767	0,962844148	-0,7792	0,435863618
LINC00351	1,074134833	0,775834	0,437847266
AC087741.1	1,075717491	0,77478	0,438469941
AC079760.2	1,040615682	0,771522	0,440397436
AC087521.1	0,950598553	-0,76327	0,445300993
AC103808.6	1,058819155	0,762549	0,445732332
AC106744.1	1,059712218	0,760811	0,446769689
ARHGEF26-AS1	0,954069898	-0,75996	0,447281003

NCOA7-AS1	0,948450449	-0,75698	0,449063212
AL592424.1	1,050179876	0,75389	0,450915196
AL139130.1	0,956863564	-0,75189	0,452115672
AL160408.4	1,048882133	0,748551	0,454128078
LINC01979	1,035500665	0,745909	0,455722664
CAPN10-AS1	1,076988733	0,739789	0,459428234
AC018755.4	0,962529683	-0,73786	0,460597907
AC139491.2	1,031301571	0,736486	0,461434775
MAGI2-AS3	0,96993307	-0,73272	0,463727225
LINC00494	1,026809488	0,731491	0,464479455
LINC02275	0,970512486	-0,71782	0,472870277
AC068858.1	0,951343789	-0,71712	0,473302466
GATA2-AS1	0,965293596	-0,71707	0,47333095
AC132192.2	1,072971713	0,716306	0,473802512
LINC02200	0,973321074	-0,70804	0,478919756
AC062015.1	0,959868585	-0,70798	0,478958268
TYMSOS	1,049653574	0,706566	0,479836289
AC004080.1	1,060716898	0,701796	0,48280623
AC104088.1	1,038845101	0,698319	0,484977521
LINC00535	0,969628308	-0,69824	0,485025269
AL954650.1	1,036296541	0,697321	0,485602013
LINC00355	1,02363756	0,691661	0,489150472
AP002954.1	1,049398026	0,686849	0,492178044
AC015813.1	1,056052366	0,677887	0,497843445
AC111149.2	1,025036812	0,677331	0,498196067
LINC02365	1,019041791	0,676142	0,498950369
LINC02413	1,030829638	0,675345	0,499456698
AC112484.4	1,04565701	0,674912	0,499731541
AC027117.2	0,972578285	-0,67362	0,500551768
AP000253.1	0,957171231	-0,672	0,501585728
AC000067.1	0,940925905	-0,66666	0,504989322
HCG23	1,0622287	0,665572	0,505684402
LINC01524	0,963057557	-0,66533	0,505837395
LINC00898	1,044607982	0,664269	0,50651825
AC110995.1	0,954202727	-0,66277	0,507477417
AC009831.4	1,080519938	0,66015	0,509157531
AC055713.1	1,097117675	0,659653	0,509476584
CCDC18-AS1	1,072788065	0,659176	0,509782552
AC090559.1	1,039192001	0,650211	0,515556005
AL021328.1	0,978679442	-0,64893	0,516383042
PCAT18	0,959488044	-0,64731	0,517432901
AC068987.1	1,045822654	0,641	0,521522427
AP003774.3	0,944571927	-0,64032	0,521967243
AC106900.2	1,031593474	0,64014	0,522081507
AP006216.2	0,972441499	-0,63196	0,527409766
AC119424.1	0,968577433	-0,63037	0,52845537
AL162726.4	1,055854602	0,630151	0,528596044
ST8SIA6-AS1	1,01647863	0,629287	0,529161038
C1QTNF1-AS1	1,023412659	0,621141	0,534507157
AL353148.1	0,939006113	-0,60887	0,542612263

AC007298.2	0,974301195	-0,60786	0,543279368
FP700125.1	0,979073695	-0,60785	0,54328568
LINC01535	1,027633183	0,604284	0,54565493
AC004540.2	0,973694322	-0,60121	0,547697223
LINC02027	1,018386631	0,599495	0,548842806
LEF1-AS1	1,035182873	0,598158	0,549734763
AL365181.2	1,020923059	0,596371	0,550927624
AL138828.1	1,021194955	0,594442	0,552216847
LINC02119	1,021780142	0,590509	0,554849473
AC005670.1	0,953035297	-0,58879	0,556001219
U91324.1	0,969010407	-0,58504	0,558517761
AC092954.1	1,043519966	0,579457	0,562281054
LINC01977	1,027222706	0,578008	0,563258612
AL359881.1	0,96782584	-0,5681	0,5699701
AC108517.1	0,955699316	-0,56437	0,572500321
AC245128.3	0,964497924	-0,5618	0,574251292
AC012613.2	0,953525702	-0,55985	0,57558145
MNX1-AS1	0,981119537	-0,5531	0,58019564
AP002807.1	1,042228967	0,551825	0,581067972
AP004147.1	1,032116184	0,549412	0,582722609
AC010201.2	1,046865706	0,542664	0,58736102
AC113383.1	1,037614407	0,539936	0,589240948
AL121899.1	1,027732942	0,532749	0,594207177
AC005150.1	1,018164293	0,526562	0,598498046
LINC00635	1,038258935	0,523408	0,600690025
AL359551.1	0,972171933	-0,5193	0,603552185
AC020656.2	0,980264902	-0,5142	0,607109643
AC138965.2	1,041820905	0,509477	0,610418052
ASMTL-AS1	0,956891575	-0,50395	0,614294817
LINC01121	1,024638957	0,502591	0,615252095
AC104041.1	1,029378969	0,501949	0,615703623
HOXA-AS2	0,97307363	-0,49393	0,621356281
AL445070.1	1,039728135	0,478777	0,632097518
AC040173.1	1,022856009	0,474084	0,635439686
LINC01704	0,964787376	-0,47246	0,636599559
EGFR-AS1	0,985725599	-0,46327	0,643173208
C17orf82	1,031668016	0,46326	0,643177999
AC008556.1	1,038517837	0,460681	0,645027517
GNG12-AS1	0,972441944	-0,46012	0,645432597
AC021491.2	1,035381887	0,447462	0,654541655
LINC01451	0,982287279	-0,44724	0,654705223
AC110285.6	1,027754258	0,445784	0,655753225
AC024563.1	0,969587041	-0,44369	0,657264021
AL357055.3	0,959689786	-0,44101	0,659206419
AC090164.2	0,978062801	-0,43727	0,661914541
AP000561.1	0,962269288	-0,43681	0,662250121
AC105105.3	0,977732194	-0,43652	0,662456579
AC073321.1	1,024385203	0,432649	0,66526995
AC090227.2	0,9672075	-0,42978	0,667354557
AC005722.3	1,025857006	0,4292	0,667777941

AC008080.1	1,047145438	0,427011	0,669371606
WDFY3-AS2	1,029282869	0,414922	0,678199122
AC008060.1	0,979513713	-0,40928	0,682337834
LINC01426	1,014753284	0,406612	0,684292945
AC239585.2	1,023763706	0,405474	0,685128919
HRAT92	1,017961171	0,382598	0,702017648
AC113145.1	0,978082669	-0,3817	0,702681816
AF165147.1	0,976174768	-0,38137	0,702931666
AC061975.6	1,015525265	0,377262	0,705979004
SFTA1P	0,977597216	-0,37557	0,707235856
LINC01468	1,02515578	0,374084	0,708341814
AL022322.1	0,97288614	-0,37324	0,708969422
SSTR5-AS1	1,00881104	0,372646	0,709411924
AL021807.1	0,978700592	-0,37264	0,709412975
LINC01192	1,021884784	0,368646	0,712391874
AL359715.4	0,974245155	-0,36751	0,713237384
AC011005.4	0,977287667	-0,36741	0,71331445
AC069208.1	0,978181716	-0,3548	0,722739066
LINC01831	0,989491287	-0,35102	0,725570601
AC074212.1	1,03063619	0,346141	0,729236539
AC113404.1	1,016532935	0,343004	0,731595107
TRPC7-AS1	1,022824959	0,339195	0,73446252
AC016773.1	1,029196487	0,338292	0,735143031
AC087564.1	1,025194713	0,336122	0,7367791
AC092119.2	0,969760536	-0,33555	0,737213921
LINC01956	1,012651698	0,3343	0,738152943
LINC02241	1,008995238	0,332875	0,73922836
C3orf67-AS1	0,978810895	-0,33283	0,739262345
AC117386.2	1,012404021	0,330216	0,741236412
AC074327.1	1,009271205	0,319463	0,749375737
AC016999.1	1,028138935	0,318502	0,750104291
AC036108.2	1,016176585	0,315469	0,752405414
LINC01186	1,014931836	0,313831	0,753649547
MIR600HG	1,024115031	0,310931	0,755853176
AC010528.1	1,027095105	0,308799	0,757474311
U73166.1	0,977682429	-0,3081	0,758004748
AL445647.1	0,98443218	-0,29875	0,765133296
MIR217HG	1,012223352	0,298742	0,765137191
AC090358.1	1,017549921	0,297831	0,76583202
AC010969.1	1,012874626	0,295155	0,76787572
AC103808.3	1,018359389	0,294607	0,768294468
AC104134.1	0,983126954	-0,29356	0,769096239
AC139100.2	1,020681558	0,291814	0,770429176
AL132655.2	1,020017955	0,29027	0,771609932
LINC01675	1,017094836	0,289036	0,772553451
LINC01727	1,012508248	0,288651	0,772848094
AC106795.2	0,98818919	-0,28676	0,774296466
AC092155.1	0,979787623	-0,28663	0,774392874
AC093702.1	1,02116183	0,277424	0,781454258
AC018553.1	1,010383337	0,271914	0,785688383

LINC00482	1,019125943	0,267828	0,788831966
AL157832.2	1,020133337	0,267557	0,789039982
AC008741.2	0,970350919	-0,26723	0,789295298
AC105202.1	0,989454301	-0,26505	0,790967351
AC018809.1	1,023290621	0,264457	0,791427555
AC016550.2	1,012643319	0,260583	0,794413893
AC006960.2	0,972985795	-0,25485	0,798835485
AC110799.1	1,02310298	0,253981	0,799510456
SNHG25	1,017519683	0,253577	0,799822486
AP005057.1	1,011643828	0,25314	0,800160128
AC090709.1	1,02059082	0,250085	0,802521637
ZBTB46-AS1	1,01666102	0,241087	0,809487359
AL596223.2	1,015775167	0,240765	0,80973719
AC078993.1	1,008562096	0,238387	0,811581028
LINC01448	1,013035532	0,23541	0,813890815
LINC00528	0,983438461	-0,21959	0,826192482
LINC01108	0,990479591	-0,21891	0,826722209
LINC02315	1,007621342	0,21619	0,828839544
LINC01612	1,009534791	0,210881	0,832980019
AC141928.1	1,008707186	0,20861	0,834752371
FP671120.4	0,986760961	-0,20721	0,835842325
LINC01842	1,014253809	0,205273	0,837358863
LINC00894	1,01586015	0,202011	0,839908163
LINC01089	0,978365432	-0,1936	0,84649043
AL359881.2	1,011938767	0,193268	0,846748765
AL512791.2	0,982414171	-0,19315	0,84684433
AC234772.2	1,015437976	0,189637	0,849593472
FP236383.2	0,971737207	-0,18836	0,850597221
FAM3D-AS1	1,01453329	0,18713	0,851558672
LINC01719	1,011219586	0,186066	0,85239266
LINC01679	0,988508053	-0,18201	0,855575162
AC007277.1	1,008055559	0,172641	0,862933756
AL118511.2	1,008738032	0,164339	0,869464174
PSORS1C3	0,992011619	-0,16418	0,869590544
LINC01151	1,00572552	0,163378	0,87022078
FAM87A	0,99188059	-0,16218	0,871161797
Z82246.1	0,993412359	-0,16101	0,872082977
LINC01863	0,99026689	-0,14723	0,882953287
AC004080.2	1,00608513	0,146311	0,883676017
AC100849.1	1,013679934	0,145978	0,883938945
LINC00683	1,009176971	0,144359	0,885216948
AC010719.1	0,99054499	-0,13982	0,888804773
DNM1P35	0,991858892	-0,13939	0,889140472
AC005725.1	1,013081933	0,137452	0,890673379
AP000851.2	1,004518085	0,13483	0,892745969
AC016027.1	1,014348002	0,134251	0,893203989
AC020907.1	1,00584807	0,132336	0,894718182
LINC00114	0,993124383	-0,1294	0,897038028
AL138760.1	1,009873398	0,12885	0,897476249
LINC00906	0,993302124	-0,12803	0,898126288

PCDH9-AS2	0,992693416	-0,12009	0,904408732
AL049830.3	1,007129031	0,119958	0,904516345
AL118505.1	1,005649961	0,119795	0,904645892
LINC01714	0,993340563	-0,11912	0,905183963
AC103706.1	1,00786623	0,109344	0,91292937
AC111000.4	0,995501962	-0,08898	0,929100743
AC024581.1	0,994097368	-0,08565	0,931748063
LINC02156	0,99480661	-0,08365	0,933338412
LINC02153	0,993989362	-0,08054	0,935804224
LINC01509	1,006677079	0,080419	0,935904097
AL450992.2	0,995133872	-0,07588	0,939516134
RMST	1,002475331	0,06103	0,951335396
Z99755.3	1,002554856	0,054135	0,956827478
LINC01338	1,003632265	0,050154	0,959999422
AC008991.1	0,996658219	-0,04907	0,960861551
AC010931.2	1,00242997	0,040004	0,968089714
AC092598.1	0,998295787	-0,03337	0,973378719
FAM85B	1,002541914	0,032091	0,974399659
AL392089.1	0,997749835	-0,02677	0,978646973
AL139275.2	1,001340589	0,021872	0,982549735
LINC02384	1,000563262	0,018496	0,985242988
IGF2BP2-AS1	1,000788265	0,017558	0,985991217
AC008991.2	1,001251938	0,017419	0,986102322
AC108136.1	0,999280616	-0,0159	0,987315221
FLJ12825	1,000821828	0,014352	0,988549273
AC011445.2	1,000771863	0,013215	0,989456362
LINC02128	0,999638865	-0,00928	0,992596019
AC012236.1	1,00033587	0,007788	0,993785925
AC011611.3	0,999522421	-0,00514	0,99590022
AL358613.2	1,000189182	0,002188	0,998254306

Table S4. Coexpression analysis results of the 13 DELs and lncRNA-correlated PCGs.

LncRNA	Gene	Cor	corMean	corSd	pValue
AC009005.1	PTTG1	0,512	0,007698439	0,144046753	0,00046359
AC009005.1	PA2G4	0,511	0,007698439	0,144046753	0,000475814
AC009005.1	RFXANK	0,505	0,007698439	0,144046753	0,000555701
AC009005.1	JPT1	0,504	0,007698439	0,144046753	0,000570173
AC009005.1	RASSF7	0,491	0,007698439	0,144046753	0,000793158
AC009005.1	B3GNTL1	0,488	0,007698439	0,144046753	0,000855006
AC009005.1	PUSL1	0,487	0,007698439	0,144046753	0,000876596
AC009005.1	SNRPA	0,479	0,007698439	0,144046753	0,001068405
AC009005.1	TLCD1	0,477	0,007698439	0,144046753	0,00112208
AC009005.1	CENPM	0,476	0,007698439	0,144046753	0,001149842
AC009005.1	C9orf142	0,471	0,007698439	0,144046753	0,001298425
AC009005.1	CCDC137	0,471	0,007698439	0,144046753	0,001298425
AC009005.1	SCNM1	0,467	0,007698439	0,144046753	0,001429839
AC009005.1	SAC3D1	0,464	0,007698439	0,144046753	0,001536329
AC009005.1	PIGU	0,463	0,007698439	0,144046753	0,001573418
AC009005.1	UBE2S	0,462	0,007698439	0,144046753	0,00161133
AC009005.1	HMGA1	0,457	0,007698439	0,144046753	0,001813816
AC009005.1	NME6	0,455	0,007698439	0,144046753	0,001901166
AC009005.1	NUDT1	0,454	0,007698439	0,144046753	0,001946274
AC009005.1	PSMG3	0,454	0,007698439	0,144046753	0,001946274
AC009005.1	NME1	0,452	0,007698439	0,144046753	0,002039453
AC009005.1	SNRPB	0,449	0,007698439	0,144046753	0,002186915
AC009005.1	TCOF1	0,445	0,007698439	0,144046753	0,00239874
AC009005.1	EEF1E1	0,444	0,007698439	0,144046753	0,002454552
AC009005.1	TSEN54	0,443	0,007698439	0,144046753	0,00251155
AC009005.1	C16orf59	0,443	0,007698439	0,144046753	0,00251155
AC009005.1	DAZAP1	0,443	0,007698439	0,144046753	0,00251155
AC009005.1	NT5C	0,442	0,007698439	0,144046753	0,002569757
AC009005.1	NR2C2AP	0,44	0,007698439	0,144046753	0,002689887
AC009005.1	SYNE4	0,439	0,007698439	0,144046753	0,002751857
AC009005.1	CAGE1	0,438	0,007698439	0,144046753	0,002815129
AC009005.1	ZNF408	0,438	0,007698439	0,144046753	0,002815129
AC009005.1	RNASEH2A	0,434	0,007698439	0,144046753	0,003081721
AC009005.1	PPAN	0,434	0,007698439	0,144046753	0,003081721
AC009005.1	CHTOP	0,433	0,007698439	0,144046753	0,003151871
AC009005.1	CKLF	0,432	0,007698439	0,144046753	0,003223474
AC009005.1	DTYMK	0,432	0,007698439	0,144046753	0,003223474
AC009005.1	ZNF692	0,431	0,007698439	0,144046753	0,003296556
AC009005.1	LSM4	0,431	0,007698439	0,144046753	0,003296556
AC009005.1	WDR62	0,43	0,007698439	0,144046753	0,003371145
AC009005.1	BIRC5	0,428	0,007698439	0,144046753	0,003524951
AC009005.1	CD320	0,427	0,007698439	0,144046753	0,003604224
AC009005.1	ARL16	0,426	0,007698439	0,144046753	0,003685116
AC009005.1	ANAPC7	0,424	0,007698439	0,144046753	0,00385187
AC009005.1	FDX2	0,424	0,007698439	0,144046753	0,00385187
AC009005.1	IQCD	0,423	0,007698439	0,144046753	0,003937792
AC009005.1	MCRS1	0,422	0,007698439	0,144046753	0,004025451

AC009005.1	PGP	0,419	0,007698439	0,144046753	0,004299162
AC009005.1	SAMD1	0,419	0,007698439	0,144046753	0,004299162
AC009005.1	BRMS1	0,416	0,007698439	0,144046753	0,004589642
AC009005.1	NOC4L	0,415	0,007698439	0,144046753	0,004690349
AC009005.1	SIRT6	0,414	0,007698439	0,144046753	0,004793052
AC009005.1	NCAPH2	0,414	0,007698439	0,144046753	0,004793052
AC009005.1	ZNF695	0,413	0,007698439	0,144046753	0,004897786
AC009005.1	PUS1	0,412	0,007698439	0,144046753	0,005004586
AC009005.1	OXLD1	0,411	0,007698439	0,144046753	0,005113487
AC009005.1	TRMU	0,411	0,007698439	0,144046753	0,005113487
AC009005.1	NABP2	0,411	0,007698439	0,144046753	0,005113487
AC009005.1	TROAP	0,41	0,007698439	0,144046753	0,005224525
AC009005.1	HDAC11	0,41	0,007698439	0,144046753	0,005224525
AC009005.1	PPP1R14B	0,409	0,007698439	0,144046753	0,005337738
AC009005.1	ZNF670-ZNF695	0,409	0,007698439	0,144046753	0,005337738
AC009005.1	SFN	0,409	0,007698439	0,144046753	0,005337738
AC009005.1	MYBL2	0,408	0,007698439	0,144046753	0,005453161
AC009005.1	TRMT1	0,408	0,007698439	0,144046753	0,005453161
AC009005.1	SURF2	0,407	0,007698439	0,144046753	0,005570833
AC009005.1	KRTAP5-7	0,407	0,007698439	0,144046753	0,005570833
AC009005.1	SNRPF	0,406	0,007698439	0,144046753	0,005690791
AC009005.1	POP7	0,406	0,007698439	0,144046753	0,005690791
AC009005.1	PAFAH1B3	0,406	0,007698439	0,144046753	0,005690791
AC009005.1	GIT1	0,406	0,007698439	0,144046753	0,005690791
AC009005.1	POLA2	0,404	0,007698439	0,144046753	0,005937721
AC009005.1	TBC1D30	0,403	0,007698439	0,144046753	0,006064771
AC009005.1	SSR2	0,402	0,007698439	0,144046753	0,006194266
AC009005.1	ANKRD13D	0,402	0,007698439	0,144046753	0,006194266
AC009005.1	GTF3C6	0,402	0,007698439	0,144046753	0,006194266
AC009005.1	SNRNP35	0,402	0,007698439	0,144046753	0,006194266
AC009005.1	RECQL4	0,402	0,007698439	0,144046753	0,006194266
AC009005.1	CLIC1	0,4	0,007698439	0,144046753	0,006460748
AC009005.1	SNRPD1	0,4	0,007698439	0,144046753	0,006460748
AC012339.1	VCX3A	0,639	0,006728646	0,095046633	2,89E-11
AC012339.1	CXorf67	0,609	0,006728646	0,095046633	2,35E-10
AC012339.1	KLK15	0,581	0,006728646	0,095046633	1,52E-09
AC012339.1	SOHLH1	0,579	0,006728646	0,095046633	1,73E-09
AC012339.1	RHOXF2B	0,577	0,006728646	0,095046633	1,97E-09
AC012339.1	FOXR2	0,577	0,006728646	0,095046633	1,97E-09
AC012339.1	OTX2	0,569	0,006728646	0,095046633	3,30E-09
AC012339.1	PYY	0,566	0,006728646	0,095046633	4,00E-09
AC012339.1	CRH	0,561	0,006728646	0,095046633	5,49E-09
AC012339.1	VCX2	0,554	0,006728646	0,095046633	8,52E-09
AC012339.1	NPAP1	0,551	0,006728646	0,095046633	1,03E-08
AC012339.1	MAGEA9	0,543	0,006728646	0,095046633	1,68E-08
AC012339.1	PCDH8	0,543	0,006728646	0,095046633	1,68E-08
AC012339.1	RBMXL2	0,539	0,006728646	0,095046633	2,14E-08
AC012339.1	CETN1	0,535	0,006728646	0,095046633	2,73E-08
AC012339.1	TP53TG3D	0,534	0,006728646	0,095046633	2,90E-08
AC012339.1	HOXD13	0,533	0,006728646	0,095046633	3,08E-08

AC012339.1	OR2C3	0,528	0,006728646	0,095046633	4,15E-08
AC012339.1	TUBA3C	0,52	0,006728646	0,095046633	6,66E-08
AC012339.1	HOXC12	0,514	0,006728646	0,095046633	9,45E-08
AC012339.1	PRB3	0,512	0,006728646	0,095046633	1,06E-07
AC012339.1	SLC1A6	0,506	0,006728646	0,095046633	1,50E-07
AC012339.1	PRDM13	0,501	0,006728646	0,095046633	1,99E-07
AC012339.1	ACTN3	0,499	0,006728646	0,095046633	2,23E-07
AC012339.1	KRTAP19-5	0,499	0,006728646	0,095046633	2,23E-07
AC012339.1	RBM46	0,491	0,006728646	0,095046633	3,49E-07
AC012339.1	ISL1	0,49	0,006728646	0,095046633	3,68E-07
AC012339.1	ADAM18	0,487	0,006728646	0,095046633	4,35E-07
AC012339.1	CT55	0,472	0,006728646	0,095046633	9,82E-07
AC012339.1	VCX3B	0,47	0,006728646	0,095046633	1,09E-06
AC012339.1	MAGEC2	0,469	0,006728646	0,095046633	1,15E-06
AC012339.1	VSX2	0,462	0,006728646	0,095046633	1,67E-06
AC012339.1	UPK1B	0,461	0,006728646	0,095046633	1,76E-06
AC012339.1	LDHAL6A	0,458	0,006728646	0,095046633	2,06E-06
AC012339.1	SLC27A6	0,457	0,006728646	0,095046633	2,17E-06
AC012339.1	VAX1	0,456	0,006728646	0,095046633	2,28E-06
AC012339.1	MAGEC1	0,454	0,006728646	0,095046633	2,53E-06
AC012339.1	HRASLS	0,45	0,006728646	0,095046633	3,11E-06
AC012339.1	GPAT2	0,449	0,006728646	0,095046633	3,27E-06
AC012339.1	H1FNT	0,444	0,006728646	0,095046633	4,21E-06
AC012339.1	SRRM4	0,438	0,006728646	0,095046633	5,69E-06
AC012339.1	NLRP4	0,438	0,006728646	0,095046633	5,69E-06
AC012339.1	TPTE	0,436	0,006728646	0,095046633	6,29E-06
AC012339.1	GAGE1	0,435	0,006728646	0,095046633	6,61E-06
AC012339.1	GPRC5D	0,434	0,006728646	0,095046633	6,94E-06
AC012339.1	AQP10	0,431	0,006728646	0,095046633	8,05E-06
AC012339.1	ZFP42	0,429	0,006728646	0,095046633	8,88E-06
AC012339.1	CST8	0,427	0,006728646	0,095046633	9,79E-06
AC012339.1	AC068775.1	0,427	0,006728646	0,095046633	9,79E-06
AC012339.1	KRTAP20-4	0,424	0,006728646	0,095046633	1,13E-05
AC012339.1	CPNE4	0,424	0,006728646	0,095046633	1,13E-05
AC012339.1	FAM181B	0,423	0,006728646	0,095046633	1,19E-05
AC012339.1	H2BFWT	0,423	0,006728646	0,095046633	1,19E-05
AC012339.1	FGF11	0,42	0,006728646	0,095046633	1,37E-05
AC012339.1	ZNF492	0,42	0,006728646	0,095046633	1,37E-05
AC012339.1	YBX2	0,419	0,006728646	0,095046633	1,44E-05
AC012339.1	PLAC1	0,414	0,006728646	0,095046633	1,83E-05
AC012339.1	GRK7	0,413	0,006728646	0,095046633	1,92E-05
AC012339.1	CNR1	0,409	0,006728646	0,095046633	2,31E-05
AC012339.1	NAA11	0,407	0,006728646	0,095046633	2,54E-05
AC012339.1	TULP1	0,406	0,006728646	0,095046633	2,66E-05
AC012339.1	ZNF98	0,406	0,006728646	0,095046633	2,66E-05
AC012339.1	GLB1L3	0,403	0,006728646	0,095046633	3,06E-05
AC012339.1	CDCA8	0,401	0,006728646	0,095046633	3,35E-05
AC012339.1	PRPH2	0,4	0,006728646	0,095046633	3,51E-05
AC012339.1	RTN4RL2	0,4	0,006728646	0,095046633	3,51E-05
AC012339.1	KLK5	0,4	0,006728646	0,095046633	3,51E-05

AC015908.3	TMEM220	0,592	-0,028465946	0,154708082	6,06E-05
AC015908.3	ZNF18	0,567	-0,028465946	0,154708082	0,000118618
AC015908.3	SHPK	0,562	-0,028465946	0,154708082	0,000135278
AC015908.3	CYB5D2	0,556	-0,028465946	0,154708082	0,00015818
AC015908.3	ASGR2	0,537	-0,028465946	0,154708082	0,000257131
AC015908.3	KLKB1	0,534	-0,028465946	0,154708082	0,00027727
AC015908.3	SERPINF2	0,533	-0,028465946	0,154708082	0,000284305
AC015908.3	CLYBL	0,523	-0,028465946	0,154708082	0,00036447
AC015908.3	SIRT3	0,521	-0,028465946	0,154708082	0,000382852
AC015908.3	PEBP1	0,521	-0,028465946	0,154708082	0,000382852
AC015908.3	DHRS4L2	0,519	-0,028465946	0,154708082	0,000402098
AC015908.3	BDH1	0,518	-0,028465946	0,154708082	0,000412056
AC015908.3	ZSWIM7	0,516	-0,028465946	0,154708082	0,000432668
AC015908.3	SPRYD4	0,51	-0,028465946	0,154708082	0,000500425
AC015908.3	IVD	0,502	-0,028465946	0,154708082	0,000606215
AC015908.3	HAO1	0,5	-0,028465946	0,154708082	0,000635737
AC015908.3	TMEM256	0,498	-0,028465946	0,154708082	0,000666592
AC015908.3	SLC27A5	0,495	-0,028465946	0,154708082	0,000715494
AC015908.3	AMBP	0,493	-0,028465946	0,154708082	0,000749926
AC015908.3	ASGR1	0,493	-0,028465946	0,154708082	0,000749926
AC015908.3	ENO3	0,492	-0,028465946	0,154708082	0,000767713
AC015908.3	SERPINA4	0,489	-0,028465946	0,154708082	0,000823451
AC015908.3	MGST2	0,487	-0,028465946	0,154708082	0,000862671
AC015908.3	ACADVL	0,481	-0,028465946	0,154708082	0,000990966
AC015908.3	SCO1	0,48	-0,028465946	0,154708082	0,001013993
AC015908.3	RNASE4	0,48	-0,028465946	0,154708082	0,001013993
AC015908.3	AFM	0,479	-0,028465946	0,154708082	0,001037514
AC015908.3	MRPL46	0,479	-0,028465946	0,154708082	0,001037514
AC015908.3	SARDH	0,479	-0,028465946	0,154708082	0,001037514
AC015908.3	PROC	0,478	-0,028465946	0,154708082	0,001061539
AC015908.3	GLYAT	0,478	-0,028465946	0,154708082	0,001061539
AC015908.3	TTR	0,475	-0,028465946	0,154708082	0,001136736
AC015908.3	ADPRM	0,472	-0,028465946	0,154708082	0,001216832
AC015908.3	PON1	0,472	-0,028465946	0,154708082	0,001216832
AC015908.3	AGXT	0,472	-0,028465946	0,154708082	0,001216832
AC015908.3	PCK2	0,47	-0,028465946	0,154708082	0,001273092
AC015908.3	F2	0,47	-0,028465946	0,154708082	0,001273092
AC015908.3	ITIH1	0,466	-0,028465946	0,154708082	0,001392881
AC015908.3	GCDH	0,466	-0,028465946	0,154708082	0,001392881
AC015908.3	HPX	0,464	-0,028465946	0,154708082	0,001456596
AC015908.3	ADI1	0,462	-0,028465946	0,154708082	0,001522989
AC015908.3	GLYATL1	0,461	-0,028465946	0,154708082	0,00155722
AC015908.3	GSTA1	0,46	-0,028465946	0,154708082	0,001592158
AC015908.3	AZGP1	0,459	-0,028465946	0,154708082	0,001627817
AC015908.3	NDUFV2	0,459	-0,028465946	0,154708082	0,001627817
AC015908.3	APOC3	0,459	-0,028465946	0,154708082	0,001627817
AC015908.3	HMGCL	0,459	-0,028465946	0,154708082	0,001627817
AC015908.3	HINT2	0,457	-0,028465946	0,154708082	0,001701349
AC015908.3	PON3	0,456	-0,028465946	0,154708082	0,00173925
AC015908.3	DHRS1	0,455	-0,028465946	0,154708082	0,001777926

AC015908.3	LDHD		0,454	-0,028465946	0,154708082	0,001817391
AC015908.3		02. Mrz	0,449	-0,028465946	0,154708082	0,002027066
AC015908.3	MED11		0,448	-0,028465946	0,154708082	0,002071576
AC015908.3	PEX11G		0,448	-0,028465946	0,154708082	0,002071576
AC015908.3	CCS		0,447	-0,028465946	0,154708082	0,002116982
AC015908.3	MRPL16		0,443	-0,028465946	0,154708082	0,002307879
AC015908.3	HMGCS2		0,443	-0,028465946	0,154708082	0,002307879
AC015908.3	APOC1		0,442	-0,028465946	0,154708082	0,002358006
AC015908.3	NIT2		0,442	-0,028465946	0,154708082	0,002358006
AC015908.3	ALDH2		0,441	-0,028465946	0,154708082	0,002409127
AC015908.3	GLRX5		0,441	-0,028465946	0,154708082	0,002409127
AC015908.3	KNG1		0,44	-0,028465946	0,154708082	0,002461261
AC015908.3	UBB		0,437	-0,028465946	0,154708082	0,002623918
AC015908.3	CCDC152		0,436	-0,028465946	0,154708082	0,002680284
AC015908.3	SUCLG2		0,435	-0,028465946	0,154708082	0,002737754
AC015908.3	PCCB		0,434	-0,028465946	0,154708082	0,002796347
AC015908.3	QDPR		0,433	-0,028465946	0,154708082	0,002856084
AC015908.3	SEPSECS		0,433	-0,028465946	0,154708082	0,002856084
AC015908.3	TAPT1		0,432	-0,028465946	0,154708082	0,002916984
AC015908.3	DHRS12		0,431	-0,028465946	0,154708082	0,002979066
AC015908.3	GSTO1		0,43	-0,028465946	0,154708082	0,003042352
AC015908.3	CYP4A11		0,43	-0,028465946	0,154708082	0,003042352
AC015908.3	SLC13A5		0,429	-0,028465946	0,154708082	0,003106862
AC015908.3	MTMR10		0,429	-0,028465946	0,154708082	0,003106862
AC015908.3	MLXIPL		0,429	-0,028465946	0,154708082	0,003106862
AC015908.3	MMAA		0,429	-0,028465946	0,154708082	0,003106862
AC015908.3	NDUFB1		0,428	-0,028465946	0,154708082	0,003172617
AC015908.3	MASP1		0,428	-0,028465946	0,154708082	0,003172617
AC015908.3	HGD		0,427	-0,028465946	0,154708082	0,003239638
AC015908.3	ACSM2A		0,427	-0,028465946	0,154708082	0,003239638
AC015908.3	MPDU1		0,425	-0,028465946	0,154708082	0,003377564
AC015908.3	CTAGE5		0,425	-0,028465946	0,154708082	0,003377564
AC015908.3	CLUH		0,424	-0,028465946	0,154708082	0,003448513
AC015908.3	COQ5		0,423	-0,028465946	0,154708082	0,003520817
AC015908.3	ETFBKMT		0,423	-0,028465946	0,154708082	0,003520817
AC015908.3	ECHS1		0,422	-0,028465946	0,154708082	0,003594497
AC015908.3	C4BPB		0,422	-0,028465946	0,154708082	0,003594497
AC015908.3	TST		0,421	-0,028465946	0,154708082	0,003669577
AC015908.3	MCEE		0,421	-0,028465946	0,154708082	0,003669577
AC015908.3	GSTZ1		0,42	-0,028465946	0,154708082	0,00374608
AC015908.3	DNAJC30		0,42	-0,028465946	0,154708082	0,00374608
AC015908.3	RBP4		0,42	-0,028465946	0,154708082	0,00374608
AC015908.3	MGMT		0,419	-0,028465946	0,154708082	0,00382403
AC015908.3	PUS3		0,419	-0,028465946	0,154708082	0,00382403
AC015908.3	NDUFAF1		0,419	-0,028465946	0,154708082	0,00382403
AC015908.3	ASPDH		0,418	-0,028465946	0,154708082	0,003903451
AC015908.3	FTCD		0,418	-0,028465946	0,154708082	0,003903451
AC015908.3	PROZ		0,418	-0,028465946	0,154708082	0,003903451
AC015908.3	MST1		0,418	-0,028465946	0,154708082	0,003903451
AC015908.3	OTC		0,418	-0,028465946	0,154708082	0,003903451

AC015908.3	NDUFC2	0,417	-0,028465946	0,154708082	0,003984367
AC015908.3	C14orf28	0,417	-0,028465946	0,154708082	0,003984367
AC015908.3	DHRS4	0,417	-0,028465946	0,154708082	0,003984367
AC015908.3	PXMP2	0,415	-0,028465946	0,154708082	0,004150786
AC015908.3	ETFB	0,415	-0,028465946	0,154708082	0,004150786
AC015908.3	EPHX2	0,415	-0,028465946	0,154708082	0,004150786
AC015908.3	ECHDC2	0,415	-0,028465946	0,154708082	0,004150786
AC015908.3	HSD17B6	0,415	-0,028465946	0,154708082	0,004150786
AC015908.3	C3	0,413	-0,028465946	0,154708082	0,004323487
AC015908.3	ST3GAL6	0,413	-0,028465946	0,154708082	0,004323487
AC015908.3	SERPINA6	0,411	-0,028465946	0,154708082	0,004502677
AC015908.3	SERPINA10	0,41	-0,028465946	0,154708082	0,004594773
AC015908.3	ECI2	0,409	-0,028465946	0,154708082	0,00468857
AC015908.3	RNF167	0,409	-0,028465946	0,154708082	0,00468857
AC015908.3	MSRA	0,408	-0,028465946	0,154708082	0,004784098
AC015908.3	GRHPR	0,408	-0,028465946	0,154708082	0,004784098
AC015908.3	SLC37A4	0,408	-0,028465946	0,154708082	0,004784098
AC015908.3	SLC43A1	0,407	-0,028465946	0,154708082	0,004881384
AC015908.3	APOH	0,406	-0,028465946	0,154708082	0,004980457
AC015908.3	RAB17	0,406	-0,028465946	0,154708082	0,004980457
AC015908.3	CYP27A1	0,405	-0,028465946	0,154708082	0,005081344
AC015908.3	DHRS3	0,405	-0,028465946	0,154708082	0,005081344
AC015908.3	SAT2	0,405	-0,028465946	0,154708082	0,005081344
AC015908.3	MLYCD	0,405	-0,028465946	0,154708082	0,005081344
AC015908.3	RPL36AL	0,405	-0,028465946	0,154708082	0,005081344
AC015908.3	MTMR2	-0,461	-0,028465946	0,154708082	0,005177019
AC015908.3	PBLD	0,404	-0,028465946	0,154708082	0,005184074
AC015908.3	ALB	0,403	-0,028465946	0,154708082	0,005288678
AC015908.3	SRR	0,403	-0,028465946	0,154708082	0,005288678
AC015908.3	CLU	0,402	-0,028465946	0,154708082	0,005395185
AC015908.3	HDHD3	0,401	-0,028465946	0,154708082	0,005503624
AC015908.3	SERPINC1	0,4	-0,028465946	0,154708082	0,005614027
AC015908.3	MRPL54	0,4	-0,028465946	0,154708082	0,005614027
AC015908.3	RCC2	-0,448	-0,028465946	0,154708082	0,006692329
AC015908.3	SPATS2	-0,424	-0,028465946	0,154708082	0,010568621
AC015908.3	TUBA1B	-0,421	-0,028465946	0,154708082	0,011172513
AC015908.3	CBX1	-0,419	-0,028465946	0,154708082	0,011591948
AC015908.3	MAPRE1	-0,412	-0,028465946	0,154708082	0,013172094
AC015908.3	YEATS2	-0,41	-0,028465946	0,154708082	0,013657236
AC015908.3	HMGN4	-0,41	-0,028465946	0,154708082	0,013657236
AC015908.3	BUB1	-0,409	-0,028465946	0,154708082	0,013905674
AC015908.3	ZNF207	-0,409	-0,028465946	0,154708082	0,013905674
AC015908.3	KIF2A	-0,409	-0,028465946	0,154708082	0,013905674
AC015908.3	NDE1	-0,405	-0,028465946	0,154708082	0,014939774
AC015908.3	PSMC3IP	-0,405	-0,028465946	0,154708082	0,014939774
AC089983.1	LRRC25	0,605	0,011587284	0,08659626	7,25E-12
AC089983.1	STC2	0,546	0,011587284	0,08659626	6,77E-10
AC089983.1	CYP11B2	0,545	0,011587284	0,08659626	7,29E-10
AC089983.1	SHANK1	0,517	0,011587284	0,08659626	5,33E-09
AC089983.1	CYP1B1	0,515	0,011587284	0,08659626	6,12E-09

AC089983.1	TREML4	0,488	0,011587284	0,08659626	3,76E-08
AC089983.1	TXNRD1	0,463	0,011587284	0,08659626	1,86E-07
AC089983.1	XAGE2	0,463	0,011587284	0,08659626	1,86E-07
AC089983.1	AC083902.2	0,463	0,011587284	0,08659626	1,86E-07
AC089983.1	DPPA2	0,452	0,011587284	0,08659626	3,66E-07
AC089983.1	ATP2B3	0,45	0,011587284	0,08659626	4,13E-07
AC089983.1	AHRR	0,449	0,011587284	0,08659626	4,39E-07
AC089983.1	XKR4	0,445	0,011587284	0,08659626	5,59E-07
AC089983.1	KRT4	0,445	0,011587284	0,08659626	5,59E-07
AC089983.1	ALDH3A1	0,444	0,011587284	0,08659626	5,93E-07
AC089983.1	C4orf26	0,437	0,011587284	0,08659626	8,99E-07
AC089983.1	NBPF6	0,434	0,011587284	0,08659626	1,07E-06
AC089983.1	DSC3	0,432	0,011587284	0,08659626	1,20E-06
AC089983.1	SPTSSB	0,425	0,011587284	0,08659626	1,81E-06
AC089983.1	RNF103-CHMP3	0,423	0,011587284	0,08659626	2,02E-06
AC089983.1	PSG9	0,421	0,011587284	0,08659626	2,27E-06
AC089983.1	MB21D2	0,411	0,011587284	0,08659626	3,98E-06
AC089983.1	EID3	0,409	0,011587284	0,08659626	4,45E-06
AC089983.1	NTNG2	0,406	0,011587284	0,08659626	5,25E-06
AC089983.1	SRXN1	0,401	0,011587284	0,08659626	6,90E-06
AC093609.1	APOLD1	0,431	-0,007985688	0,103063581	2,05E-05
AC124067.4	CYB5B	0,444	0,006028284	0,098004347	7,86E-06
AC124067.4	NKD1	0,427	0,006028284	0,098004347	1,74E-05
AC124067.4	RNF43	0,426	0,006028284	0,098004347	1,83E-05
AC124067.4	TCF7	0,422	0,006028284	0,098004347	2,19E-05
AC124067.4	NPL	0,42	0,006028284	0,098004347	2,40E-05
AC124067.4	PHYHIPL	0,407	0,006028284	0,098004347	4,29E-05
AC124067.4	ZNF703	0,401	0,006028284	0,098004347	5,57E-05
AL592043.1	MAGEA4	0,529	0,008147528	0,078406754	3,07E-11
AL592043.1	PRDM9	0,484	0,008147528	0,078406754	1,29E-09
AL592043.1	FSTL5	0,462	0,008147528	0,078406754	7,10E-09
AL592043.1	DGKK	0,416	0,008147528	0,078406754	1,97E-07
AL592466.1	PKIB	0,491	0,00315426	0,098086643	6,57E-07
AL592466.1	NPAS1	0,487	0,00315426	0,098086643	8,10E-07
AL592466.1	CARD18	0,48	0,00315426	0,098086643	1,17E-06
AL592466.1	NME6	0,458	0,00315426	0,098086643	3,53E-06
AL592466.1	CKLF	0,447	0,00315426	0,098086643	6,04E-06
AL592466.1	MCEMP1	0,419	0,00315426	0,098086643	2,24E-05
AL592466.1	HMX2	0,418	0,00315426	0,098086643	2,34E-05
AL592466.1	MRTO4	0,415	0,00315426	0,098086643	2,68E-05
AL592466.1	POC1A	0,415	0,00315426	0,098086643	2,68E-05
AL592466.1	DGAT2L6	0,414	0,00315426	0,098086643	2,81E-05
AL592466.1	HIF3A	0,412	0,00315426	0,098086643	3,07E-05
AL592466.1	MAGEC3	0,412	0,00315426	0,098086643	3,07E-05
AL592466.1	DUSP13	0,411	0,00315426	0,098086643	3,21E-05
AL592466.1	KRTAP19-5	0,411	0,00315426	0,098086643	3,21E-05
AL592466.1	RPRML	0,405	0,00315426	0,098086643	4,19E-05
AL592466.1	CDC20	0,403	0,00315426	0,098086643	4,57E-05
AL592466.1	PFKFB4	0,401	0,00315426	0,098086643	4,99E-05
F11-AS1	F11	0,931	-0,016086718	0,162090441	5,13E-09

F11-AS1	ABHD18	0,652	-0,016086718	0,162090441	3,76E-05
F11-AS1	LARP1B	0,638	-0,016086718	0,162090441	5,45E-05
F11-AS1	CYP4V2	0,635	-0,016086718	0,162090441	5,90E-05
F11-AS1	TMEM192	0,615	-0,016086718	0,162090441	9,88E-05
F11-AS1	KLKB1	0,593	-0,016086718	0,162090441	0,000171485
F11-AS1	CBR4	0,585	-0,016086718	0,162090441	0,000208621
F11-AS1	CYP4F3	0,571	-0,016086718	0,162090441	0,000292368
F11-AS1	MFSD8	0,571	-0,016086718	0,162090441	0,000292368
F11-AS1	KIAA0922	0,57	-0,016086718	0,162090441	0,000299421
F11-AS1	SORBS2	0,565	-0,016086718	0,162090441	0,000337138
F11-AS1	ANXA10	0,546	-0,016086718	0,162090441	0,000524864
F11-AS1	SLC35D1	0,543	-0,016086718	0,162090441	0,000562194
F11-AS1	ABAT	0,543	-0,016086718	0,162090441	0,000562194
F11-AS1	ALDH6A1	0,543	-0,016086718	0,162090441	0,000562194
F11-AS1	ACSL1	0,541	-0,016086718	0,162090441	0,000588439
F11-AS1	SLC38A4	0,538	-0,016086718	0,162090441	0,000629951
F11-AS1	RAPGEF2	0,536	-0,016086718	0,162090441	0,000659122
F11-AS1	TMEM184C	0,53	-0,016086718	0,162090441	0,000754346
F11-AS1	EHHADH	0,527	-0,016086718	0,162090441	0,00080661
F11-AS1	C8A	0,524	-0,016086718	0,162090441	0,000862216
F11-AS1	ACOX1	0,523	-0,016086718	0,162090441	0,000881528
F11-AS1	EDEM1	0,514	-0,016086718	0,162090441	0,00107428
F11-AS1	XDH	0,511	-0,016086718	0,162090441	0,001146741
F11-AS1	CTSO	0,507	-0,016086718	0,162090441	0,001250392
F11-AS1	DBT	0,507	-0,016086718	0,162090441	0,001250392
F11-AS1	C6	0,504	-0,016086718	0,162090441	0,001333734
F11-AS1	GTF2IRD2	0,502	-0,016086718	0,162090441	0,001392111
F11-AS1	SEPSECS	0,496	-0,016086718	0,162090441	0,001581674
F11-AS1	ABCC6	0,496	-0,016086718	0,162090441	0,001581674
F11-AS1	MMACHC	0,495	-0,016086718	0,162090441	0,001615487
F11-AS1	PDLIM5	0,494	-0,016086718	0,162090441	0,001649964
F11-AS1	ETFDH	0,493	-0,016086718	0,162090441	0,001685117
F11-AS1	SETD7	0,493	-0,016086718	0,162090441	0,001685117
F11-AS1	IVD	0,493	-0,016086718	0,162090441	0,001685117
F11-AS1	AGXT	0,491	-0,016086718	0,162090441	0,001757498
F11-AS1	KLHL8	0,49	-0,016086718	0,162090441	0,001794751
F11-AS1	GLYATL1	0,49	-0,016086718	0,162090441	0,001794751
F11-AS1	MMAA	0,488	-0,016086718	0,162090441	0,001871442
F11-AS1	DDI2	0,487	-0,016086718	0,162090441	0,001910907
F11-AS1	TFR2	0,486	-0,016086718	0,162090441	0,001951134
F11-AS1	ZNF680	0,484	-0,016086718	0,162090441	0,00203393
F11-AS1	F13B	0,482	-0,016086718	0,162090441	0,002119939
F11-AS1	HSD17B6	0,48	-0,016086718	0,162090441	0,002209271
F11-AS1	SLC22A25	0,479	-0,016086718	0,162090441	0,00225522
F11-AS1	TRAPPC11	0,479	-0,016086718	0,162090441	0,00225522
F11-AS1	KNG1	0,478	-0,016086718	0,162090441	0,002302042
F11-AS1	TAT	0,477	-0,016086718	0,162090441	0,002349753
F11-AS1	SLC25A4	0,474	-0,016086718	0,162090441	0,002498371
F11-AS1	PPID	0,473	-0,016086718	0,162090441	0,00254979
F11-AS1	SCP2	0,473	-0,016086718	0,162090441	0,00254979

F11-AS1	MCFD2	0,473	-0,016086718	0,162090441	0,00254979
F11-AS1	PBLD	0,473	-0,016086718	0,162090441	0,00254979
F11-AS1	PCYOX1	0,471	-0,016086718	0,162090441	0,002655542
F11-AS1	CENPC	0,471	-0,016086718	0,162090441	0,002655542
F11-AS1	ETFBKMT	0,471	-0,016086718	0,162090441	0,002655542
F11-AS1	C1RL	0,469	-0,016086718	0,162090441	0,002765289
F11-AS1	PLG	0,468	-0,016086718	0,162090441	0,002821703
F11-AS1	BCKDHB	0,468	-0,016086718	0,162090441	0,002821703
F11-AS1	STARD5	0,467	-0,016086718	0,162090441	0,002879165
F11-AS1	GLS2	0,467	-0,016086718	0,162090441	0,002879165
F11-AS1	TAPT1	0,466	-0,016086718	0,162090441	0,002937693
F11-AS1	METTL7A	0,465	-0,016086718	0,162090441	0,002997306
F11-AS1	MASP1	0,465	-0,016086718	0,162090441	0,002997306
F11-AS1	SLC10A7	0,464	-0,016086718	0,162090441	0,00305802
F11-AS1	GC	0,463	-0,016086718	0,162090441	0,003119853
F11-AS1	SMIM14	0,463	-0,016086718	0,162090441	0,003119853
F11-AS1	COX18	0,462	-0,016086718	0,162090441	0,003182825
F11-AS1	USP38	0,462	-0,016086718	0,162090441	0,003182825
F11-AS1	SLC6A1	0,461	-0,016086718	0,162090441	0,003246952
F11-AS1	MIP	0,461	-0,016086718	0,162090441	0,003246952
F11-AS1	ALDH2	0,461	-0,016086718	0,162090441	0,003246952
F11-AS1	MFAP3L	0,46	-0,016086718	0,162090441	0,003312255
F11-AS1	FAM149A	0,46	-0,016086718	0,162090441	0,003312255
F11-AS1	SARDH	0,46	-0,016086718	0,162090441	0,003312255
F11-AS1	SLC31A1	0,46	-0,016086718	0,162090441	0,003312255
F11-AS1	PAN2	0,459	-0,016086718	0,162090441	0,003378752
F11-AS1	ECHDC2	0,458	-0,016086718	0,162090441	0,003446463
F11-AS1	PRMT9	0,458	-0,016086718	0,162090441	0,003446463
F11-AS1	LONP2	0,458	-0,016086718	0,162090441	0,003446463
F11-AS1	CCDC158	0,457	-0,016086718	0,162090441	0,003515406
F11-AS1	GYS2	0,457	-0,016086718	0,162090441	0,003515406
F11-AS1	AC011498.5	0,457	-0,016086718	0,162090441	0,003515406
F11-AS1	MLYCD	0,457	-0,016086718	0,162090441	0,003515406
F11-AS1	TNRC6A	0,456	-0,016086718	0,162090441	0,003585602
F11-AS1	EHBP1	0,454	-0,016086718	0,162090441	0,003729832
F11-AS1	ALDH7A1	0,453	-0,016086718	0,162090441	0,003803907
F11-AS1	MYO1B	0,453	-0,016086718	0,162090441	0,003803907
F11-AS1	SYNJ2BP	0,453	-0,016086718	0,162090441	0,003803907
F11-AS1	CERS5	-0,485	-0,016086718	0,162090441	0,00381689
F11-AS1	C1S	0,451	-0,016086718	0,162090441	0,003956082
F11-AS1	CYP2C8	0,45	-0,016086718	0,162090441	0,004034224
F11-AS1	AKR1D1	0,45	-0,016086718	0,162090441	0,004034224
F11-AS1	GNE	0,45	-0,016086718	0,162090441	0,004034224
F11-AS1	AADAT	0,449	-0,016086718	0,162090441	0,004113765
F11-AS1	C11orf54	0,449	-0,016086718	0,162090441	0,004113765
F11-AS1	NR3C2	0,448	-0,016086718	0,162090441	0,004194726
F11-AS1	DCAF11	0,447	-0,016086718	0,162090441	0,00427713
F11-AS1	ETNPPL	0,447	-0,016086718	0,162090441	0,00427713
F11-AS1	PPM1A	0,447	-0,016086718	0,162090441	0,00427713
F11-AS1	PPARA	0,447	-0,016086718	0,162090441	0,00427713

F11-AS1	CFHR4	0,445	-0,016086718	0,162090441	0,004446357
F11-AS1	RBL2	0,444	-0,016086718	0,162090441	0,004533225
F11-AS1	ACSM2A	0,441	-0,016086718	0,162090441	0,004803134
F11-AS1	GHR	0,439	-0,016086718	0,162090441	0,004991066
F11-AS1	HORMAD2	0,439	-0,016086718	0,162090441	0,004991066
F11-AS1	EPB41L5	0,439	-0,016086718	0,162090441	0,004991066
F11-AS1	NLRP14	0,439	-0,016086718	0,162090441	0,004991066
F11-AS1	EGFR	0,438	-0,016086718	0,162090441	0,005087503
F11-AS1	OSBP	0,438	-0,016086718	0,162090441	0,005087503
F11-AS1	PCSK6	0,437	-0,016086718	0,162090441	0,005185622
F11-AS1	02. Mrz	0,437	-0,016086718	0,162090441	0,005185622
F11-AS1	ACAD8	0,435	-0,016086718	0,162090441	0,005387005
F11-AS1	PLA2G12A	0,435	-0,016086718	0,162090441	0,005387005
F11-AS1	FBXW7	0,435	-0,016086718	0,162090441	0,005387005
F11-AS1	AS3MT	0,433	-0,016086718	0,162090441	0,005595424
F11-AS1	CAT	0,432	-0,016086718	0,162090441	0,005702338
F11-AS1	SLC25A15	0,431	-0,016086718	0,162090441	0,00581109
F11-AS1	METTL14	0,431	-0,016086718	0,162090441	0,00581109
F11-AS1	DNAJC25	0,43	-0,016086718	0,162090441	0,00592171
F11-AS1	GCDH	0,43	-0,016086718	0,162090441	0,00592171
F11-AS1	PANK1	0,429	-0,016086718	0,162090441	0,006034223
F11-AS1	SEC24B	0,429	-0,016086718	0,162090441	0,006034223
F11-AS1	DMGDH	0,428	-0,016086718	0,162090441	0,006148659
F11-AS1	DNAJC16	0,428	-0,016086718	0,162090441	0,006148659
F11-AS1	CFI	0,428	-0,016086718	0,162090441	0,006148659
F11-AS1	PGRMC1	0,428	-0,016086718	0,162090441	0,006148659
F11-AS1	GTF2IRD2B	0,427	-0,016086718	0,162090441	0,006265045
F11-AS1	CPEB3	0,427	-0,016086718	0,162090441	0,006265045
F11-AS1	SERPIND1	0,427	-0,016086718	0,162090441	0,006265045
F11-AS1	L2HGDH	0,426	-0,016086718	0,162090441	0,006383411
F11-AS1	SERPING1	0,424	-0,016086718	0,162090441	0,006626198
F11-AS1	SLCO1B1	0,423	-0,016086718	0,162090441	0,006750678
F11-AS1	SLCO2B1	0,423	-0,016086718	0,162090441	0,006750678
F11-AS1	SEL1L	0,422	-0,016086718	0,162090441	0,006877256
F11-AS1	IRF2	0,422	-0,016086718	0,162090441	0,006877256
F11-AS1	ENTPD5	0,422	-0,016086718	0,162090441	0,006877256
F11-AS1	PAH	0,422	-0,016086718	0,162090441	0,006877256
F11-AS1	AMOTL1	0,422	-0,016086718	0,162090441	0,006877256
F11-AS1	ACADM	0,421	-0,016086718	0,162090441	0,007005962
F11-AS1	INSR	0,42	-0,016086718	0,162090441	0,007136828
F11-AS1	CPB2	0,42	-0,016086718	0,162090441	0,007136828
F11-AS1	SPCS3	0,419	-0,016086718	0,162090441	0,007269883
F11-AS1	FAM214A	0,419	-0,016086718	0,162090441	0,007269883
F11-AS1	SIK2	0,419	-0,016086718	0,162090441	0,007269883
F11-AS1	ALAD	0,419	-0,016086718	0,162090441	0,007269883
F11-AS1	SIAE	0,418	-0,016086718	0,162090441	0,00740516
F11-AS1	MTHFD1	0,418	-0,016086718	0,162090441	0,00740516
F11-AS1	PUS10	0,418	-0,016086718	0,162090441	0,00740516
F11-AS1	SDHD	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	C8B	0,417	-0,016086718	0,162090441	0,007542691

F11-AS1	PRKAG2	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	PGM1	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	PEX13	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	LDHD	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	PROZ	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	PLIN5	0,417	-0,016086718	0,162090441	0,007542691
F11-AS1	LRP6	0,416	-0,016086718	0,162090441	0,007682508
F11-AS1	KLHL2	0,415	-0,016086718	0,162090441	0,007824643
F11-AS1	VWA8	0,415	-0,016086718	0,162090441	0,007824643
F11-AS1	CFAP57	0,413	-0,016086718	0,162090441	0,008116
F11-AS1	ACAT1	0,413	-0,016086718	0,162090441	0,008116
F11-AS1	SAR1B	0,413	-0,016086718	0,162090441	0,008116
F11-AS1	CPED1	0,413	-0,016086718	0,162090441	0,008116
F11-AS1	SYT2	0,412	-0,016086718	0,162090441	0,00826529
F11-AS1	TMEM56	0,412	-0,016086718	0,162090441	0,00826529
F11-AS1	ITCH	0,412	-0,016086718	0,162090441	0,00826529
F11-AS1	NR3C1	0,412	-0,016086718	0,162090441	0,00826529
F11-AS1	SFXN1	0,411	-0,016086718	0,162090441	0,008417031
F11-AS1	PCK1	0,411	-0,016086718	0,162090441	0,008417031
F11-AS1	SLC41A2	0,411	-0,016086718	0,162090441	0,008417031
F11-AS1	SH3D19	0,41	-0,016086718	0,162090441	0,00857126
F11-AS1	ACAD11	0,41	-0,016086718	0,162090441	0,00857126
F11-AS1	C3	0,409	-0,016086718	0,162090441	0,00872801
F11-AS1	ARHGAP36	0,409	-0,016086718	0,162090441	0,00872801
F11-AS1	TIGD2	0,409	-0,016086718	0,162090441	0,00872801
F11-AS1	ABCA9	0,409	-0,016086718	0,162090441	0,00872801
F11-AS1	HAO1	0,408	-0,016086718	0,162090441	0,008887317
F11-AS1	ZFYVE28	0,408	-0,016086718	0,162090441	0,008887317
F11-AS1	SORL1	0,407	-0,016086718	0,162090441	0,009049216
F11-AS1	MPDZ	0,407	-0,016086718	0,162090441	0,009049216
F11-AS1	CPN2	0,406	-0,016086718	0,162090441	0,009213744
F11-AS1	SMAD1	0,406	-0,016086718	0,162090441	0,009213744
F11-AS1	NUDT12	0,406	-0,016086718	0,162090441	0,009213744
F11-AS1	ATP8A1	0,406	-0,016086718	0,162090441	0,009213744
F11-AS1	SEC24D	0,405	-0,016086718	0,162090441	0,009380935
F11-AS1	RAB33B	0,405	-0,016086718	0,162090441	0,009380935
F11-AS1	SUOX	0,405	-0,016086718	0,162090441	0,009380935
F11-AS1	LPA	0,405	-0,016086718	0,162090441	0,009380935
F11-AS1	UGT2B10	0,405	-0,016086718	0,162090441	0,009380935
F11-AS1	AL132639.3	0,404	-0,016086718	0,162090441	0,009550828
F11-AS1	MCEE	0,404	-0,016086718	0,162090441	0,009550828
F11-AS1	ST3GAL6	0,404	-0,016086718	0,162090441	0,009550828
F11-AS1	MCCC2	0,403	-0,016086718	0,162090441	0,00972346
F11-AS1	ENPEP	0,403	-0,016086718	0,162090441	0,00972346
F11-AS1	ASPRV1	0,403	-0,016086718	0,162090441	0,00972346
F11-AS1	ALDH9A1	0,402	-0,016086718	0,162090441	0,009898867
F11-AS1	PDXDC1	0,402	-0,016086718	0,162090441	0,009898867
F11-AS1	APOL6	0,402	-0,016086718	0,162090441	0,009898867
F11-AS1	FHL3	-0,434	-0,016086718	0,162090441	0,009929574
F11-AS1	ANGPTL3	0,401	-0,016086718	0,162090441	0,010077088

F11-AS1	ACACB	0,401	-0,016086718	0,162090441	0,010077088
F11-AS1	MUT	0,401	-0,016086718	0,162090441	0,010077088
F11-AS1	AASS	0,4	-0,016086718	0,162090441	0,01025816
F11-AS1	PIGV	0,4	-0,016086718	0,162090441	0,01025816
F11-AS1	THAP9	0,4	-0,016086718	0,162090441	0,01025816
F11-AS1	CNDP1	0,4	-0,016086718	0,162090441	0,01025816
F11-AS1	MTHFD1L	-0,424	-0,016086718	0,162090441	0,011850058
F11-AS1	SNRPB	-0,423	-0,016086718	0,162090441	0,012059144
F11-AS1	CMTM7	-0,421	-0,016086718	0,162090441	0,012487151
F11-AS1	HMGA1	-0,421	-0,016086718	0,162090441	0,012487151
F11-AS1	NAP1L1	-0,42	-0,016086718	0,162090441	0,012706156
F11-AS1	SMYD5	-0,42	-0,016086718	0,162090441	0,012706156
F11-AS1	TPD52L2	-0,418	-0,016086718	0,162090441	0,01315439
F11-AS1	YWHAZ	-0,416	-0,016086718	0,162090441	0,013616549
F11-AS1	RCC2	-0,415	-0,016086718	0,162090441	0,013852963
F11-AS1	TCF3	-0,413	-0,016086718	0,162090441	0,014336687
F11-AS1	ANXA2	-0,411	-0,016086718	0,162090441	0,01483525
F11-AS1	IKBKE	-0,409	-0,016086718	0,162090441	0,015349027
F11-AS1	CLIC1	-0,408	-0,016086718	0,162090441	0,015611741
F11-AS1	ATIC	-0,405	-0,016086718	0,162090441	0,01642377
F11-AS1	MPZL1	-0,402	-0,016086718	0,162090441	0,01727267
FLJ36000	HOXA9	0,486	0,000300882	0,074095001	5,56E-11
FLJ36000	MMP3	0,458	0,000300882	0,074095001	6,53E-10
FLJ36000	TSPY10	0,452	0,000300882	0,074095001	1,09E-09
FLJ36000	TSPY3	0,442	0,000300882	0,074095001	2,50E-09
FLJ36000	DUSP26	0,43	0,000300882	0,074095001	6,66E-09
FLJ36000	CT45A10	0,424	0,000300882	0,074095001	1,08E-08
FLJ36000	SAGE1	0,421	0,000300882	0,074095001	1,36E-08
FLJ36000	MAGEB10	0,42	0,000300882	0,074095001	1,48E-08
FLJ36000	SPATA17	0,405	0,000300882	0,074095001	4,71E-08
FLJ36000	CCL13	0,402	0,000300882	0,074095001	5,91E-08
FOXD2-AS1	FOXD2	0,677	0,003094128	0,13850604	1,14E-06
FOXD2-AS1	E2F2	0,483	0,003094128	0,13850604	0,000530481
FOXD2-AS1	TRAIP	0,475	0,003094128	0,13850604	0,000656537
FOXD2-AS1	AUNIP	0,475	0,003094128	0,13850604	0,000656537
FOXD2-AS1	CDT1	0,472	0,003094128	0,13850604	0,000710605
FOXD2-AS1	CDC25B	0,464	0,003094128	0,13850604	0,000875676
FOXD2-AS1	CEP131	0,456	0,003094128	0,13850604	0,001075719
FOXD2-AS1	CENPM	0,455	0,003094128	0,13850604	0,0011035
FOXD2-AS1	CDC20	0,455	0,003094128	0,13850604	0,0011035
FOXD2-AS1	BIRC5	0,446	0,003094128	0,13850604	0,001385106
FOXD2-AS1	WDR34	0,445	0,003094128	0,13850604	0,001420185
FOXD2-AS1	NASP	0,444	0,003094128	0,13850604	0,001456081
FOXD2-AS1	PKMYT1	0,439	0,003094128	0,13850604	0,001648435
FOXD2-AS1	KIF2C	0,436	0,003094128	0,13850604	0,001774802
FOXD2-AS1	RMI2	0,431	0,003094128	0,13850604	0,002005353
FOXD2-AS1	TSEN54	0,428	0,003094128	0,13850604	0,002156563
FOXD2-AS1	FAM72D	0,427	0,003094128	0,13850604	0,002209244
FOXD2-AS1	C16orf59	0,427	0,003094128	0,13850604	0,002209244
FOXD2-AS1	GINS2	0,425	0,003094128	0,13850604	0,002318161

FOXD2-AS1	CDC45	0,422	0,003094128	0,13850604	0,00249078
FOXD2-AS1	FAM110A	0,422	0,003094128	0,13850604	0,00249078
FOXD2-AS1	CDCA8	0,421	0,003094128	0,13850604	0,002550883
FOXD2-AS1	ACD	0,42	0,003094128	0,13850604	0,00261231
FOXD2-AS1	RAD54L	0,42	0,003094128	0,13850604	0,00261231
FOXD2-AS1	PTTG1	0,419	0,003094128	0,13850604	0,002675086
FOXD2-AS1	CCNF	0,419	0,003094128	0,13850604	0,002675086
FOXD2-AS1	PHF19	0,417	0,003094128	0,13850604	0,002804792
FOXD2-AS1	RFC4	0,417	0,003094128	0,13850604	0,002804792
FOXD2-AS1	CCDC137	0,417	0,003094128	0,13850604	0,002804792
FOXD2-AS1	NABP2	0,417	0,003094128	0,13850604	0,002804792
FOXD2-AS1	TROAP	0,414	0,003094128	0,13850604	0,003010145
FOXD2-AS1	USP47	-0,407	0,003094128	0,13850604	0,00306802
FOXD2-AS1	CDCA5	0,413	0,003094128	0,13850604	0,003081586
FOXD2-AS1	RNASEH2A	0,412	0,003094128	0,13850604	0,00315457
FOXD2-AS1	TGFBR2	-0,405	0,003094128	0,13850604	0,003214969
FOXD2-AS1	CENPA	0,407	0,003094128	0,13850604	0,003543679
FOXD2-AS1	ARMC7	0,405	0,003094128	0,13850604	0,00371119
FOXD2-AS1	ALYREF	0,405	0,003094128	0,13850604	0,00371119
FOXD2-AS1	SPC24	0,402	0,003094128	0,13850604	0,00397598
FOXD2-AS1	PRELID2	0,4	0,003094128	0,13850604	0,004161917
FOXD2-AS1	PIF1	0,4	0,003094128	0,13850604	0,004161917
MIR663AHG	ATP1A2	0,766	0,001194366	0,07294387	1,01E-25
MIR663AHG	CPA6	0,694	0,001194366	0,07294387	2,14E-21
MIR663AHG	TCEAL2	0,691	0,001194366	0,07294387	3,18E-21
MIR663AHG	PRKN	0,52	0,001194366	0,07294387	1,14E-12
MIR663AHG	MYBPH	0,509	0,001194366	0,07294387	3,36E-12
MIR663AHG	CCK	0,507	0,001194366	0,07294387	4,09E-12
MIR663AHG	HS3ST4	0,427	0,001194366	0,07294387	5,30E-09
MIR663AHG	DKK4	0,404	0,001194366	0,07294387	3,35E-08
TMCC1-AS1	CDC123	0,582	0,021888901	0,131591826	2,08E-05
TMCC1-AS1	RUVBL1	0,571	0,021888901	0,131591826	3,01E-05
TMCC1-AS1	NOP56	0,569	0,021888901	0,131591826	3,22E-05
TMCC1-AS1	SSB	0,551	0,021888901	0,131591826	5,80E-05
TMCC1-AS1	WDR77	0,549	0,021888901	0,131591826	6,18E-05
TMCC1-AS1	DCAF13	0,541	0,021888901	0,131591826	7,98E-05
TMCC1-AS1	ATIC	0,531	0,021888901	0,131591826	0,000109343
TMCC1-AS1	ADSL	0,529	0,021888901	0,131591826	0,000116362
TMCC1-AS1	CCT4	0,527	0,021888901	0,131591826	0,000123804
TMCC1-AS1	NUDCD1	0,527	0,021888901	0,131591826	0,000123804
TMCC1-AS1	CMSS1	0,521	0,021888901	0,131591826	0,000148914
TMCC1-AS1	BZW2	0,517	0,021888901	0,131591826	0,000168239
TMCC1-AS1	TKT	0,514	0,021888901	0,131591826	0,000184256
TMCC1-AS1	PANX3	0,505	0,021888901	0,131591826	0,000241334
TMCC1-AS1	CD3EAP	0,502	0,021888901	0,131591826	0,000263789
TMCC1-AS1	METTL8	0,501	0,021888901	0,131591826	0,000271699
TMCC1-AS1	CCR3	0,497	0,021888901	0,131591826	0,000305618
TMCC1-AS1	FARSB	0,497	0,021888901	0,131591826	0,000305618
TMCC1-AS1	NUP37	0,496	0,021888901	0,131591826	0,000314697
TMCC1-AS1	TTC27	0,493	0,021888901	0,131591826	0,000343471

TMCC1-AS1	MRTO4	0,49	0,021888901	0,131591826	0,000374692
TMCC1-AS1	DSCC1	0,484	0,021888901	0,131591826	0,000445249
TMCC1-AS1	NCL	0,483	0,021888901	0,131591826	0,000458151
TMCC1-AS1	WDR75	0,479	0,021888901	0,131591826	0,000513326
TMCC1-AS1	LYAR	0,477	0,021888901	0,131591826	0,000543181
TMCC1-AS1	FAM136A	0,476	0,021888901	0,131591826	0,000558707
TMCC1-AS1	SMYD5	0,473	0,021888901	0,131591826	0,000607802
TMCC1-AS1	KDM1A	0,47	0,021888901	0,131591826	0,000660887
TMCC1-AS1	FBL	0,468	0,021888901	0,131591826	0,000698639
TMCC1-AS1	PNO1	0,468	0,021888901	0,131591826	0,000698639
TMCC1-AS1	G6PD	0,462	0,021888901	0,131591826	0,00082426
TMCC1-AS1	WDCP	0,461	0,021888901	0,131591826	0,00084713
TMCC1-AS1	CCT2	0,46	0,021888901	0,131591826	0,000870588
TMCC1-AS1	UBE3D	0,459	0,021888901	0,131591826	0,000894647
TMCC1-AS1	THOC5	0,459	0,021888901	0,131591826	0,000894647
TMCC1-AS1	PLBD1	0,459	0,021888901	0,131591826	0,000894647
TMCC1-AS1	CCDC77	0,458	0,021888901	0,131591826	0,000919321
TMCC1-AS1	RRP12	0,453	0,021888901	0,131591826	0,001052425
TMCC1-AS1	RPL5	0,45	0,021888901	0,131591826	0,001140626
TMCC1-AS1	METTL12	0,45	0,021888901	0,131591826	0,001140626
TMCC1-AS1	WDR12	0,445	0,021888901	0,131591826	0,001302948
TMCC1-AS1	INTS13	0,445	0,021888901	0,131591826	0,001302948
TMCC1-AS1	TPD52L2	0,443	0,021888901	0,131591826	0,001373651
TMCC1-AS1	IMPDH2	0,443	0,021888901	0,131591826	0,001373651
TMCC1-AS1	NIFK	0,443	0,021888901	0,131591826	0,001373651
TMCC1-AS1	CSE1L	0,442	0,021888901	0,131591826	0,001410314
TMCC1-AS1	PYCR1	0,44	0,021888901	0,131591826	0,001486361
TMCC1-AS1	CKS2	0,439	0,021888901	0,131591826	0,001525785
TMCC1-AS1	PRMT1	0,439	0,021888901	0,131591826	0,001525785
TMCC1-AS1	AKR1C1	0,439	0,021888901	0,131591826	0,001525785
TMCC1-AS1	FBXO46	0,439	0,021888901	0,131591826	0,001525785
TMCC1-AS1	CCT7	0,438	0,021888901	0,131591826	0,00156617
TMCC1-AS1	YBX1	0,438	0,021888901	0,131591826	0,00156617
TMCC1-AS1	NAP1L1	0,437	0,021888901	0,131591826	0,001607538
TMCC1-AS1	TWNK	0,437	0,021888901	0,131591826	0,001607538
TMCC1-AS1	XPO5	0,436	0,021888901	0,131591826	0,001649909
TMCC1-AS1	METTL6	0,434	0,021888901	0,131591826	0,00173775
TMCC1-AS1	QPCTL	0,434	0,021888901	0,131591826	0,00173775
TMCC1-AS1	RCC1	0,433	0,021888901	0,131591826	0,001783265
TMCC1-AS1	CDC25A	0,433	0,021888901	0,131591826	0,001783265
TMCC1-AS1	PDCD2	0,431	0,021888901	0,131591826	0,001877598
TMCC1-AS1	TRIM28	0,431	0,021888901	0,131591826	0,001877598
TMCC1-AS1	MTHFD1L	0,43	0,021888901	0,131591826	0,001926464
TMCC1-AS1	SUV39H2	0,43	0,021888901	0,131591826	0,001926464
TMCC1-AS1	CCT5	0,429	0,021888901	0,131591826	0,001976496
TMCC1-AS1	GNL3	0,427	0,021888901	0,131591826	0,002080155
TMCC1-AS1	SNRPD2	0,425	0,021888901	0,131591826	0,002188779
TMCC1-AS1	UTP4	0,425	0,021888901	0,131591826	0,002188779
TMCC1-AS1	FAM24B	0,425	0,021888901	0,131591826	0,002188779
TMCC1-AS1	NPM1	0,424	0,021888901	0,131591826	0,002245019

TMCC1-AS1	NME6	0,423	0,021888901	0,131591826	0,00230258
TMCC1-AS1	ARHGAP39	0,423	0,021888901	0,131591826	0,00230258
TMCC1-AS1	TAF9	0,422	0,021888901	0,131591826	0,00236149
TMCC1-AS1	DPH2	0,422	0,021888901	0,131591826	0,00236149
TMCC1-AS1	NUP93	0,422	0,021888901	0,131591826	0,00236149
TMCC1-AS1	STIP1	0,421	0,021888901	0,131591826	0,002421777
TMCC1-AS1	RBM45	0,421	0,021888901	0,131591826	0,002421777
TMCC1-AS1	UBA2	0,42	0,021888901	0,131591826	0,00248347
TMCC1-AS1	NCBP2	0,419	0,021888901	0,131591826	0,002546598
TMCC1-AS1	GEMIN7	0,418	0,021888901	0,131591826	0,002611189
TMCC1-AS1	ZNF239	0,418	0,021888901	0,131591826	0,002611189
TMCC1-AS1	HDAC2	0,417	0,021888901	0,131591826	0,002677276
TMCC1-AS1	E2F5	0,417	0,021888901	0,131591826	0,002677276
TMCC1-AS1	RPL17	0,417	0,021888901	0,131591826	0,002677276
TMCC1-AS1	PFN2	0,417	0,021888901	0,131591826	0,002677276
TMCC1-AS1	SET	0,416	0,021888901	0,131591826	0,002744888
TMCC1-AS1	TOMM40	0,416	0,021888901	0,131591826	0,002744888
TMCC1-AS1	CPSF3	0,415	0,021888901	0,131591826	0,002814056
TMCC1-AS1	REXO4	0,415	0,021888901	0,131591826	0,002814056
TMCC1-AS1	CCNB1	0,415	0,021888901	0,131591826	0,002814056
TMCC1-AS1	EIF3H	0,415	0,021888901	0,131591826	0,002814056
TMCC1-AS1	TSEN2	0,414	0,021888901	0,131591826	0,002884812
TMCC1-AS1	RRP9	0,414	0,021888901	0,131591826	0,002884812
TMCC1-AS1	CLIC1	0,412	0,021888901	0,131591826	0,003031219
TMCC1-AS1	IARS	0,412	0,021888901	0,131591826	0,003031219
TMCC1-AS1	GYG1	0,411	0,021888901	0,131591826	0,003106935
TMCC1-AS1	ZNF589	0,41	0,021888901	0,131591826	0,003184373
TMCC1-AS1	IGF2BP1	0,41	0,021888901	0,131591826	0,003184373
TMCC1-AS1	EXOSC3	0,41	0,021888901	0,131591826	0,003184373
TMCC1-AS1	HSPD1	0,409	0,021888901	0,131591826	0,003263565
TMCC1-AS1	AKR1C3	0,409	0,021888901	0,131591826	0,003263565
TMCC1-AS1	POLR1A	0,408	0,021888901	0,131591826	0,003344548
TMCC1-AS1	UCK2	0,406	0,021888901	0,131591826	0,003512028
TMCC1-AS1	SLC10A4	0,406	0,021888901	0,131591826	0,003512028
TMCC1-AS1	FXR1	0,406	0,021888901	0,131591826	0,003512028
TMCC1-AS1	RAN	0,405	0,021888901	0,131591826	0,003598598
TMCC1-AS1	RPS8	0,404	0,021888901	0,131591826	0,003687105
TMCC1-AS1	GTF3C3	0,403	0,021888901	0,131591826	0,003777587
TMCC1-AS1	ANKLE1	0,402	0,021888901	0,131591826	0,003870082
TMCC1-AS1	PABPC1	0,401	0,021888901	0,131591826	0,00396463

Table S5. GO term enrichment results of lncRNA-correlated PCGs of 13 prognostic DELs.

Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enrichment	Bonferroni	Benjamini	FDR
GOTERM_BP_FAT	GO:0055114~oxidation reduction	66	0,859375	6,98E-14	ASPDH, ACOX1, EHHADH, CYP11B2, LDHD, NDUFAF1, MTHFD1, AKR1C3, KDM1A, MSRA, CAT, ACAD8, SARDH, IMPDH2, AKR1C1, SUOX, ALDH6A1, ACADM, LDHAL6A, QDPR, NDUFC2, CBR4, CYB5B, GRHPR, HAO1, ACADVL, DHRS1, PYCR1, DHRS3, ALDH7A1, G6PD, DHRS4, CYP27A1, TXNRD1, PCYOX1, AKR1D1, ALDH9A1, SRXN1, XDH, CYP1B1, DHRS4L2, AASS, PAH, NDUFB1, ALDH3A1, IVD, ETFDH, DMGDH, HSD17B6, CCS, BDH1, ETFB, GCDH, DHRS12, CYP2C8, BCKDHB, HGD, CYP4V2, ADI1, CYP4A11, L2HGDH, SDHD, NDUFV2, ALDH2, CYP4F3, ACAD11	501	639	13528	2,788938555	1,74E-10	1,74E-10	1,23E-10
GOTERM_CC_FAT	GO:0005739~mitochondrion	90	1,171875	2,67E-13	ACOX1, NIT2, EHHADH, CYP11B2, LDHD, HINT2, ECHDC2, GPAT2, AGXT, CLYBL, NDUFAF1, MTHFD1L, GLYATL1, MTHFD1, MCCC2, MCEE, GSTZ1, CAT, ACAD8, COX18, SARDH, HMGCL, GHR, AADAT, SUOX, ALDH6A1, ACADM, SLC25A4, SUCLG2, OTC, ACSM2A, NDUFC2, CBR4, CYB5B, SYNJ2BP, TAT, COQ5, ACADVL, DHRS1, PYCR1, ALDH7A1, DHRS4, CYP27A1, PEBP1, ABAT, PCCB, MRPL46, GLRX5, YWHAZ, CLU, AASS, ECHS1, FAM136A, SFXN1, NR3C1, ACAT1, NDUFB1, GLS2, MUT, ACSL1, IVD, MRPL16, ETFDH, MRPL54, DMGDH, BDH1, ETFB, SCO1, GCDH, TRMU, BCKDHB, TOMM40, PCK2, SIRT3, MMAA, TST, METTL12, DBT, GLYAT, ANXA10, HMGCS2, L2HGDH, MLYCD, SDHD, NDUFV2, HDHD3, ALDH2, HSPD1, SLC25A15, SCP2	471	1087	12782	2,246936874	1,05E-10	1,05E-10	3,71E-10
GOTERM_MF_FAT	GO:0048037~cofactor binding	38	0,49479167	4,56E-13	XDH, ASPDH, ACOX1, EHHADH, LDHD, PAH, AGXT, PDXDC1, KDM1A, IVD, ALB, SRR, ETFDH, DMGDH, ACAD8, CAT, SARDH, INSR, HMGCL, AADAT, GCDH, SUOX, ALDH6A1, ACADM, SIRT6, BIRC5, CBR4, GRHPR, TAT, SIRT3, ACADVL, HAO1, DBT, G6PD, NDUFV2, ABAT, TXNRD1, ACAD11	484	249	12983	4,093680507	3,85E-10	3,85E-10	7,05E-10
GOTERM_CC_FAT	GO:0031974~membrane-enclosed lumen	128	1,66666667	4,72E-13	NCBP2, SNRPD1, SNRPD2, PKMYT1, CCT2, CBX1, AGXT, KDM1A, WDR75, CDCA8, PGRMC1, HMGCL, GNL3, MCRS1, RBL2, SUCLG2, RAN, ACSM2A, MLXIPL, MED11, SERPING1, HDAC11, RRP9, MRTO4, PA2G4, RFC4, RCC2, SERPINF2, HRASLS, SNRPB, ABAT, ANAPC7, SNRPF, PCCB, DSCC1, CLU, IGF2BP1, ACAT1, DAZAP1, PPAN, MUT, ACD, ALB, IVD, NPM1, ENTPD5, HOXA9, RPL5, TAF9, TCF3, GCDH, TSEN54, NOC4L, SSB, CDC20, SMAD1, FXR1, TST, CCT5, HDAC2, HMGCS2, ALDH2, HSPD1, POP7, E2F2, ZNF18, E2F5, LYAR, TCOF1, PRKAG2, ZNF207, CDT1, DCAF13, MCCC2, CDC45, LONP2, ZNF680, CAT, TSEN2, SARDH, SUOX, ACADM, OTC, POLR1A, EXOSC3, CBR4, NCL, HMGA1, VCX3A, ACADVL, CD3EAP, VCX3B, CYP27A1, UBB, RUVBL1, CPSF3, MGMT, ECHS1, NR3C1, POLA2, GLS2, SET, REXO4, MRPL16, GTF3C6, WDR12, DMGDH, PCSK6, GEMIN7, BDH1, ETFB, GTF3C3, RRP12, BCKDHB, PNO1, TRIM28, BIRC5, SIRT6, VSX2, CDC25A, FBL, PCK1, SIRT3, CDC25B, CCNB1, DBT, SH3D19, NOP56	471	1856	12782	1,8715865	1,86E-10	9,28E-11	6,57E-10
GOTERM_CC_FAT	GO:0043233~organelle lumen	125	1,62760417	1,38E-12	NCBP2, SNRPD1, SNRPD2, PKMYT1, CCT2, CBX1, AGXT, KDM1A, WDR75, CDCA8, PGRMC1, HMGCL, GNL3, MCRS1, RBL2, SUCLG2, RAN, ACSM2A, MLXIPL, MED11, SERPING1, HDAC11, RRP9, MRTO4, PA2G4, RFC4, RCC2, SERPINF2, SNRPB, ABAT, ANAPC7, SNRPF, PCCB, DSCC1, CLU, IGF2BP1, ACAT1, DAZAP1, PPAN, MUT, ACD, ALB, IVD, NPM1, ENTPD5, HOXA9, RPL5, TAF9, TCF3, GCDH, TSEN54, NOC4L, SSB, CDC20, SMAD1, FXR1, TST, CCT5, HDAC2, HMGCS2, ALDH2, HSPD1, POP7, E2F2, ZNF18, E2F5, LYAR, TCOF1, PRKAG2, ZNF207, CDT1, MCCC2, DCAF13, CDC45, LONP2, ZNF680, TSEN2, SARDH, ACADM, OTC, POLR1A, EXOSC3, CBR4, NCL, HMGA1, VCX3A, ACADVL, CD3EAP, VCX3B, CYP27A1, UBB, RUVBL1, CPSF3, MGMT, ECHS1, NR3C1, POLA2, GLS2, SET, REXO4, MRPL16, GTF3C6, WDR12, DMGDH, PCSK6, GEMIN7, BDH1, ETFB, GTF3C3, RRP12, BCKDHB, PNO1, TRIM28, BIRC5, SIRT6, VSX2, CDC25A, FBL, PCK1, SIRT3, CDC25B, CCNB1, DBT, SH3D19, NOP56	471	1820	12782	1,863873918	5,42E-10	1,81E-10	1,92E-09
GOTERM_CC_FAT	GO:0070013~intracellular organelle lumen	121	1,57552083	7,46E-12	NCBP2, SNRPD1, SNRPD2, PKMYT1, CCT2, CBX1, AGXT, KDM1A, WDR75, CDCA8, PGRMC1, HMGCL, GNL3, MCRS1, RBL2, SUCLG2, RAN, ACSM2A, MLXIPL, MED11, HDAC11, RRP9, MRTO4, PA2G4, RFC4, RCC2, SNRPB, ABAT, ANAPC7, SNRPF, PCCB, DSCC1, IGF2BP1, ACAT1, DAZAP1, PPAN, MUT, ACD, IVD, NPM1, ENTPD5, HOXA9, RPL5, TAF9, TCF3, GCDH, TSEN54, NOC4L, SSB, CDC20, SMAD1, FXR1, TST, CCT5, HDAC2, HMGCS2, ALDH2, HSPD1, POP7, E2F2, ZNF18, E2F5, LYAR, TCOF1, PRKAG2, ZNF207, CDT1, MCCC2, DCAF13, CDC45, LONP2, ZNF680, TSEN2, SARDH, ACADM, OTC, POLR1A, EXOSC3, CBR4, NCL, HMGA1, VCX3A, ACADVL, CD3EAP, VCX3B, CYP27A1, UBB, RUVBL1, CPSF3, MGMT, ECHS1, NR3C1, POLA2, GLS2, SET, REXO4, MRPL16, GTF3C6, WDR12, DMGDH, PCSK6, GEMIN7, BDH1, ETFB, GTF3C3, RRP12, PNO1, TRIM28, BCKDHB, BIRC5, SIRT6, VSX2, FBL, CDC25A, PCK1, SIRT3, CDC25B, CCNB1, DBT, SH3D19, NOP56	471	1779	12782	1,845811419	2,93E-09	7,33E-10	1,04E-08
GOTERM_BP_FAT	GO:0016054~organic acid catabolic process	23	0,29947917	8,73E-11	ACOX1, ALDH6A1, ACADM, EHHADH, BCKDHB, AASS, ECHS1, HGD, PAH, TAT, HAO1, ACADVL, MTHFD1, MCCC2, ETFDH, PON1, DMGDH, GSTZ1, PEX13, ACAD8, AKR1D1, SARDH, PON3	501	111	13528	5,595008182	2,18E-07	1,09E-07	1,54E-07
GOTERM_BP_FAT	GO:0046395~carboxylic acid catabolic process	23	0,29947917	8,73E-11	ACOX1, ALDH6A1, ACADM, EHHADH, BCKDHB, AASS, ECHS1, HGD, PAH, TAT, HAO1, ACADVL, MTHFD1, MCCC2, ETFDH, PON1, DMGDH, GSTZ1, PEX13, ACAD8, AKR1D1, SARDH, PON3	501	111	13528	5,595008182	2,18E-07	1,09E-07	1,54E-07
GOTERM_MF_FAT	GO:0050662~coenzyme binding	29	0,37760417	1,32E-10	XDH, ASPDH, ACOX1, EHHADH, LDHD, KDM1A, IVD, ETFDH, DMGDH, ACAD8, CAT, INSR, SARDH, HMGCL, SUOX, ALDH6A1, GCDH, ACADM, SIRT6, CBR4, GRHPR, SIRT3, HAO1, ACADVL, DBT, G6PD, NDUFV2, TXNRD1, ACAD11	484	181	12983	4,297828866	1,11E-07	5,55E-08	2,03E-07
GOTERM_CC_FAT	GO:0005759~mitochondrial matrix	31	0,40364583	1,10E-09	ECHS1, NR3C1, AGXT, ACAT1, GLS2, MCCC2, MUT, IVD, MRPL16, DMGDH, BDH1, SARDH, ETFB, HMGCL, GCDH, ACADM, SUCLG2, OTC, ACSM2A, BCKDHB, CBR4, SIRT3, ACADVL, TST, DBT, HMGCS2, CYP27A1, ALDH2, ABAT, HSPD1, PCCB	471	227	12782	3,706071064	4,31E-07	8,62E-08	1,53E-06
GOTERM_CC_FAT	GO:0031980~mitochondrial lumen	31	0,40364583	1,10E-09	ECHS1, NR3C1, AGXT, ACAT1, GLS2, MCCC2, MUT, IVD, MRPL16, DMGDH, BDH1, SARDH, ETFB, HMGCL, GCDH, ACADM, SUCLG2, OTC, ACSM2A, BCKDHB, CBR4, SIRT3, ACADVL, TST, DBT, HMGCS2, CYP27A1, ALDH2, ABAT, HSPD1, PCCB	471	227	12782	3,706071064	4,31E-07	8,62E-08	1,53E-06
GOTERM_CC_FAT	GO:0044429~mitochondrial part	54	0,703125	1,78E-09	CYP11B2, LDHD, GPAT2, AGXT, NDUFAF1, MCCC2, CAT, COX18, SARDH, HMGCL, SUOX, ACADM, SLC25A4, SUCLG2, OTC, ACSM2A, NDUFC2, CBR4, SYNJ2BP, CYB5B, ACADVL, DHRS1, CYP27A1, ABAT, PEBP1, PCCB, ECHS1, SFXN1, NR3C1, ACAT1, NDUFB1, GLS2, MUT, ACSL1, IVD, MRPL16, ETFDH, DMGDH, BDH1, ETFB, SCO1, GCDH, BCKDHB, TOMM40, SIRT3, TST, DBT, HMGCS2, L2HGDH, NDUFV2, SDHD, ALDH2, HSPD1, SLC25A15	471	595	12782	2,462944923	6,99E-07	1,16E-07	2,47E-06
GOTERM_MF_FAT	GO:0009055~electron carrier activity	30	0,390625	3,25E-09	XDH, ACOX1, GLRX5, CYP1B1, CYP11B2, AASS, KDM1A, IVD, ETFDH, HSD17B6, DMGDH, ACAD8, ETFB, SUOX, GCDH, ACADM, CYP2C8, QDPR, CYP4V2, HAO1, ACADVL, CYP4A11, DHRS3, CYP27A1, NDUFV2, SDHD, ALDH2, TXNRD1, CYP4F3, ACAD11	484	221	12983	3,641318574	2,74E-06	9,14E-07	5,03E-06
GOTERM_BP_FAT	GO:0051605~protein maturation by peptide bond cleavage	17	0,22135417	8,46E-08	F11, MASP1, C3, C6, CLU, C4BPB, SERPING1, C1S, C8A, C8B, KLKB1, C1RL, SPCS3, APOH, CFI, PCSK6, ASPRV1	501	86	13528	5,337603862	2,11E-04	7,03E-05	1,49E-04
GOTERM_BP_FAT	GO:0051604~protein maturation	19	0,24739583	5,19E-07	F11, MASP1, C3, C6, CLU, C4BPB, SERPING1, C1S, C8A, C8B, LONP2, KLKB1, APOH, C1RL, SPCS3, HSPD1, CFI, PCSK6, ASPRV1	501	122	13528	4,205228886	0,001294567	3,24E-04	9,16E-04
GOTERM_BP_FAT	GO:0006958~complement activation, classical pathway	10	0,13020833	6,20E-07	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, CFI	501	29	13528	9,311033106	0,001544741	3,09E-04	0,001092807
GOTERM_BP_FAT	GO:0016485~protein processing	18	0,234375	7,13E-07	F11, MASP1, C3, C6, CLU, C4BPB, SERPING1, C1S, C8A, C8B, LONP2, KLKB1, C1RL, SPCS3, APOH, CFI, PCSK6, ASPRV1	501	112	13528	4,339606501	0,001777793	2,97E-04	0,001257822
GOTERM_BP_FAT	GO:0030195~negative regulation of blood coagulation	9	0,1171875	9,89E-07	F11, KNG1, KLKB1, F2, APOH, CPB2, PLG, PROC, ANXA2	501	23	13528	10,56599844	0,002464349	3,52E-04	0,00174417
GOTERM_CC_FAT	GO:0042579~microbody	17	0,22135417	1,02E-06	XDH, ACOX1, NUDT12, EHHADH, EPHX2, AGXT, PEX11G, HAO1, LONP2, ACSL1, DHRS4, MLYCD, PXMP2, PEX13, CAT, ACAD11, SCP2	471	103	12782	4,479088079	4,01E-04	5,72E-05	0,001418247
GOTERM_CC_FAT	GO:0005777~peroxisome	17	0,22135417	1,02E-06	XDH, ACOX1, NUDT12, EHHADH, EPHX2, AGXT, PEX11G, HAO1, LONP2, ACSL1, DHRS4, MLYCD, PXMP2, PEX13, CAT, ACAD11, SCP2	471	103	12782	4,479088079	4,01E-04	5,72E-05	0,001418247
GOTERM_BP_FAT	GO:0006631~fatty acid metabolic process	24	0,3125	1,15E-06	ACOX1, PPARA, ACADM, EHHADH, ACSM2A, PRKAG2, EPHX2, ECHDC2, ECHS1, ACACB, HAO1, ACADVL, AKR1C3, CYP4A11, ACSL1, MLYCD, ETFDH, SLC27A6, CYP4F3, PEX13, ANGPTL3, SLC27A5, MGST2, GHR	501	198	13528	3,272969213	0,002859623	3,58E-04	0,002024327
GOTERM_BP_FAT	GO:0002455~humoral immune response mediated by circulating immunoglobulin	10	0,13020833	1,17E-06	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, CFI	501	31	13528	8,710321293	0,002908773	3,24E-04	0,002059171
GOTERM_BP_FAT	GO:0048285~organelle fission	26	0,33854167	1,26E-06	PKMYT1, CETN1, PTTG1, RCC1, PEX11G, SPC24, KIF2C, CDCA8, NDE1, SAC3D1, BUB1, NUP37, CDCA5, RAN, CCNF, BIRC5, CDC20, CDC25A, CDC25B, CCNB1, RCC2, RUVBL1, ANAPC7, MAPRE1, HORMAD2, DSCC1	501	229	13528	3,065728804	0,003148478	3,15E-04	0,002229128
GOTERM_BP_FAT	GO:0000279~M phase	32	0,41666667	1,72E-06	ZFP42, PKMYT1, CETN1, PTTG1, RCC1, SPC24, KIF2C, CDCA8, NDE1, DUSP13, SAC3D1, PSMC3IP, BUB1, NUP37, CDCA5, RAN, CCNF, BIRC5, CDC20, RAD54L, CDC25A, SUV39H2, CDC25B, CCNB1, PRDM9, RCC2, CKS2, HORMAD2, RUVBL1, ANAPC7, MAPRE1, DSCC1	501	329	13528	2,626333958	0,00428768	3,91E-04	0,003037408
GOTERM_BP_FAT	GO:0007067~mitosis	25	0,32552083	2,09E-06	RAN, CCNF, PKMYT1, CDC20, CETN1, BIRC5, PTTG1, RCC1, CDC25A, CDC25B, SPC24, CCNB1, KIF2C, NDE1, CDCA8, RCC2, SAC3D1, BUB1, NUP37, HORMAD2, MAPRE1, ANAPC7, RUVBL1, CDCA5, DSCC1	501	220	13528	3,068408637	0,005190202	4,34E-04	0,003678412
GOTERM_BP_FAT	GO:0000280~nuclear division	25	0,32552083	2,09E-06	RAN, CCNF, PKMYT1, CDC20, CETN1, BIRC5, PTTG1, RCC1, CDC25A, CDC25B, SPC24, CCNB1, KIF2C, NDE1, CDCA8, RCC2, SAC3D1, BUB1, NUP37, HORMAD2, MAPRE1, ANAPC7, RUVBL1, CDCA5, DSCC1	501	220	13528	3,068408637	0,005190202	4,34E-04	0,003678412
GOTERM_MF_FAT	GO:0050660~FAD binding	14	0,18229167	2,12E-06	ACADVL, XDH, KDM1A, ACOX1, GCDH, ACADM, IVD, LDHD, ETFDH, DMGDH, TXNRD1, ACAD8, ACAD11, SARDH	484	72	12983	5,215851699	0,001784701	4,46E-04	0,003274949

GOTERM_CC_FAT	GO:0031981~nuclear lumen	88	1,14583333	2,18E-06	NCBP2, E2F2, ZNF18, E2F5, LYAR, TCOF1, PRKAG2, SNRPD1, SNRPD2, PKMYT1, CCT2, CBX1, CDT1, ZNF207, KDM1A, WDR75, DCAF13, CDC45, CDCA8, PGRMC1, ZNF680, TSEN2, GNL3, MCRS1, RBL2, RAN, MLXIPL, POLR1A, MED11, EXOSC3, RRP9, HDAC11, NCL, HMGA1, MRTO4, CD3EAP, VCX3A, PA2G4, VCX3B, RFC4, RCC2, SNRPB, UBB, RUVBL1, ANAPC7, CPSF3, SNRPF, DSCC1, MGMT, IGF2BP1, NR3C1, POLA2, DAZAP1, PPAN, ACD, SET, REXO4, NPM1, GTF3C6, WDR12, HOXA9, TAF9, RPL5, TCF3, GEMIN7, GTF3C3, TSEN54, RRP12, NOC4L, TRIM28, PNO1, SIRT6, SSB, CDC20, BIRC5, SMAD1, VSX2, FBL, CDC25A, FXR1, PCK1, CDC25B, CCNB1, CCT5, HDAC2, NOP56, SH3D19, POP7	471	1450	12782	1,64699612	8,57E-04	1,07E-04	0,003036565
GOTERM_BP_FAT	GO:0006956~complement activation	11	0,14322917	2,20E-06	C8A, C8B, MASP1, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, CFI	501	42	13528	7,071951335	0,005484266	4,23E-04	0,003887392
GOTERM_BP_FAT	GO:0002541~activation of plasma proteins involved in acute inflammatory response	11	0,14322917	2,78E-06	C8A, C8B, MASP1, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, CFI	501	43	13528	6,907487351	0,006907547	4,95E-04	0,00489973
GOTERM_BP_FAT	GO:0050819~negative regulation of coagulation	9	0,1171875	2,86E-06	F11, KNG1, KLKB1, F2, APOH, CPB2, PLG, PROC, ANXA2	501	26	13528	9,346844772	0,007102171	4,75E-04	0,005038272
GOTERM_BP_FAT	GO:0000087~M phase of mitotic cell cycle	25	0,32552083	2,88E-06	RAN, CCNF, PKMYT1, CDC20, CETN1, BIRC5, PTTG1, RCC1, CDC25A, CDC25B, SPC24, CCNB1, KIF2C, NDE1, CDCA8, RCC2, SAC3D1, BUB1, NUP37, HORMAD2, MAPRE1, ANAPC7, RUVBL1, CDCA5, DSCC1	501	224	13528	3,013615626	0,007151994	4,49E-04	0,005073743
GOTERM_BP_FAT	GO:0002526~acute inflammatory response	16	0,20833333	2,88E-06	YWHAZ, MASP1, C3, C6, CLU, EPHX2, C4BPB, SERPING1, C1S, C8A, C8B, SERPINF2, KLKB1, F2, C1RL, CFI	501	98	13528	4,408489144	0,00716315	4,23E-04	0,005081685
GOTERM_BP_FAT	GO:0030193~regulation of blood coagulation	10	0,13020833	4,62E-06	F11, KNG1, SERPINF2, KLKB1, F2, APOH, CPB2, PLG, PROC, ANXA2	501	36	13528	7,500554447	0,01146817	6,41E-04	0,008153298
GOTERM_MF_FAT	GO:0003995~acyl-CoA dehydrogenase activity	7	0,09114583	9,66E-06	ACADVL, ACOX1, GCDH, ACADM, IVD, ACAD8, ACAD11	484	15	12983	12,51804408	0,008110524	0,001627393	0,014929386
GOTERM_BP_FAT	GO:0022403~cell cycle phase	35	0,45572917	1,14E-05	ZFP42, PKMYT1, CETN1, PTTG1, RCC1, SPC24, KIF2C, CDCA8, NDE1, DUSP13, SAC3D1, CDC123, PSMC3IP, BUB1, NUP37, CDCA5, TCF3, EGFR, RAN, CCNF, CDC20, BIRC5, RAD54L, CDC25A, SUV39H2, CDC25B, CCNB1, PRDM9, RCC2, CKS2, HORMAD2, RUVBL1, ANAPC7, MAPRE1, DSCC1	501	414	13528	2,28277744	0,028000632	0,001493627	0,020073879
GOTERM_BP_FAT	GO:0050818~regulation of coagulation	10	0,13020833	1,46E-05	F11, KNG1, SERPINF2, KLKB1, F2, APOH, CPB2, PLG, PROC, ANXA2	501	41	13528	6,585852685	0,03575175	0,001818669	0,025732243
GOTERM_BP_FAT	GO:0008202~steroid metabolic process	22	0,28645833	1,90E-05	GC, OSBP, CYP1B1, CYP11B2, PRKAG2, SORL1, APOC1, NR3C1, STARD5, G6PD, CYP27A1, HMGCS2, SERPINA6, APOC3, CRH, HSD17B6, CAT, ANGPTL3, AKR1D1, SCP2, AKR1C1, SLC27A5	501	202	13528	2,940811446	0,046235774	0,002251689	0,033457928
GOTERM_BP_FAT	GO:0007596~blood coagulation	15	0,1953125	2,22E-05	F11, KNG1, MST1, C4BPB, SERPING1, PLG, PROC, F13B, LPA, KLKB1, PROZ, F2, SERPINC1, APOH, SERPIND1	501	102	13528	3,970881766	0,053963	0,002518351	0,039206297
GOTERM_BP_FAT	GO:0050817~coagulation	15	0,1953125	2,22E-05	F11, KNG1, MST1, C4BPB, SERPING1, PLG, PROC, F13B, LPA, KLKB1, PROZ, F2, SERPINC1, APOH, SERPIND1	501	102	13528	3,970881766	0,053963	0,002518351	0,039206297
GOTERM_BP_FAT	GO:0016064~immunoglobulin mediated immune response	11	0,14322917	2,41E-05	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	54	13528	5,500406594	0,058284952	0,002607575	0,042441809
GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	26	0,33854167	2,59E-05	SERPINA10, C3, PRKAG2, APOC1, SFN, PTTG1, LPA, SET, SERPINA6, ITIH1, APOC3, SERPINA4, SERPINC1, ANGPTL3, PPP1R14B, KNG1, PKIB, BIRC5, SERPING1, ANXA2, AMBP, CST8, SERPINF2, CARD18, PEBP1, SERPIND1	484	270	12983	2,58308846	0,021618673	0,003636004	0,040062458
GOTERM_BP_FAT	GO:0042060~wound healing	21	0,2734375	2,69E-05	F11, KNG1, PPARA, SERPINA10, TGFBR2, MST1, C4BPB, SERPING1, SMAD1, PLG, PROC, F13B, CCNB1, LPA, KLKB1, F2, PROZ, APOH, SERPINC1, ENO3, SERPIND1	501	191	13528	2,968805844	0,064901937	0,00279209	0,047424115
GOTERM_BP_FAT	GO:0009611~response to wounding	40	0,52083333	3,18E-05	PPARA, YWHAZ, SERPINA10, MASP1, C3, C6, CLU, MST1, C1S, F13B, LPA, KLKB1, PROZ, SERPINC1, APOH, ENO3, RTN4RL2, CFI, ITCH, F11, KNG1, TGFBR2, EPHX2, C4BPB, SERPING1, SMAD1, PLG, PROC, C8A, CCNB1, C8B, CCL13, SERPINF2, CCR3, CARD18, F2, CRH, C1RL, PEBP1, SERPIND1	501	530	13528	2,037886491	0,07622086	0,003166267	0,056028497
GOTERM_BP_FAT	GO:0019724~B cell mediated immunity	11	0,14322917	3,35E-05	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	56	13528	5,303963502	0,080224394	0,0032112	0,059096973
GOTERM_BP_FAT	GO:0009063~cellular amino acid catabolic process	12	0,15625	3,58E-05	MTHFD1, ALDH6A1, MCCC2, BCKDHB, HGD, GSTZ1, AASS, DMGDH, PAH, ACAD8, TAT, SARDH	501	68	13528	4,765058119	0,085490861	0,003304447	0,063153673
GOTERM_BP_FAT	GO:0007599~hemostasis	15	0,1953125	4,27E-05	F11, KNG1, MST1, C4BPB, SERPING1, PLG, PROC, F13B, LPA, KLKB1, PROZ, F2, SERPINC1, APOH, SERPIND1	501	108	13528	3,750277223	0,100993059	0,003795085	0,075230879
GOTERM_BP_FAT	GO:0019439~aromatic compound catabolic process	7	0,09114583	6,16E-05	EPHX2, PON1, HGD, GSTZ1, PAH, TAT, PON3	501	20	13528	9,450698603	0,142464421	0,005285726	0,108585471
GOTERM_BP_FAT	GO:0050878~regulation of body fluid levels	17	0,22135417	6,49E-05	F11, KNG1, CYP11B2, MST1, C4BPB, SERPING1, PLG, PROC, ANXA2, F13B, LPA, KLKB1, F2, PROZ, SERPINC1, APOH, SERPIND1	501	141	13528	3,255559802	0,149458959	0,005381554	0,114368487
GOTERM_CC_FAT	GO:0005740~mitochondrial envelope	33	0,4296875	7,52E-05	CYP11B2, LDHD, SFXN1, GPAT2, ACAT1, NDUFAF1, NDUFB1, ACSL1, ETFDH, CAT, COX18, BDH1, HMGCL, SCO1, GCDH, SUOX, SLC25A4, OTC, NDUFC2, TOMM40, SYNJ2BP, CYB5B, DHRS1, TST, ACADVL, CYP27A1, HMGCS2, L2HGDH, NDUFV2, SDHD, PEBP1, HSPD1, SLC25A15	471	419	12782	2,137360716	0,029140611	0,003280566	0,104636019
GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	16	0,20833333	8,83E-05	SUOX, CYP1B1, CYP11B2, CYP2C8, CYB5B, CYP4V2, AMBP, CYP4A11, MUT, CYP27A1, MMACHC, PGRMC1, SDHD, CYP4F3, CAT, CYB5D2	484	129	12983	3,327054904	0,071764853	0,010582208	0,136440811
GOTERM_MF_FAT	GO:0031406~carboxylic acid binding	17	0,22135417	8,99E-05	ALDH6A1, OTC, FTCD, APOC1, PAH, ACACB, AGXT, TAT, PCK1, DBT, AZGP1, ALB, SRR, DMGDH, INSR, AKR1C1, HMGCL	484	144	12983	3,166767103	0,072962679	0,009425481	0,138804968
GOTERM_CC_FAT	GO:0031967~organelle envelope	43	0,55989583	9,49E-05	CYP11B2, LDHD, NUP93, SFXN1, GPAT2, ANKLE1, NDUFAF1, ACAT1, NDUFB1, ACSL1, CSE1L, ETFDH, NUP37, CAT, COX18, BDH1, HMGCL, SCO1, GCDH, SUOX, SLC25A4, RAN, OTC, NDUFC2, TOMM40, CLIC1, CYB5B, SMAD1, SYNJ2BP, H2BFWT, DHRS1, TST, ACADVL, RNF43, CYP27A1, HMGCS2, L2HGDH, HRASLS, SDHD, NDUFV2, PEBP1, HSPD1, SLC25A15	471	620	12782	1,882151907	0,03661518	0,003723286	0,131963324
GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	17	0,22135417	9,76E-05	KNG1, SERPINA10, C3, SERPING1, BIRC5, PTTG1, AMBP, CST8, LPA, SERPINA6, ITIH1, SERPINF2, CARD18, SERPINA4, SERPINC1, PEBP1, SERPIND1	484	145	12983	3,14492733	0,079007773	0,009103167	0,150782151
GOTERM_CC_FAT	GO:0031975~envelope	43	0,55989583	1,01E-04	CYP11B2, LDHD, NUP93, SFXN1, GPAT2, ANKLE1, NDUFAF1, ACAT1, NDUFB1, ACSL1, CSE1L, ETFDH, NUP37, CAT, COX18, BDH1, HMGCL, SCO1, GCDH, SUOX, SLC25A4, RAN, OTC, NDUFC2, TOMM40, CLIC1, CYB5B, SMAD1, SYNJ2BP, H2BFWT, DHRS1, TST, ACADVL, RNF43, CYP27A1, HMGCS2, L2HGDH, HRASLS, SDHD, NDUFV2, PEBP1, HSPD1, SLC25A15	471	622	12782	1,876099972	0,03905309	0,003614915	0,140920657
GOTERM_BP_FAT	GO:0000278~mitotic cell cycle	30	0,390625	1,15E-04	PKMYT1, CETN1, PTTG1, RCC1, SPC24, KIF2C, CDCA8, NDE1, SAC3D1, CENPA, CDC123, BUB1, NUP37, CDCA5, TCF3, EGFR, RAN, CCNF, BIRC5, CDC20, CDC25A, CDC25B, CCNB1, RCC2, HORMAD2, RUVBL1, ANAPC7, UBB, MAPRE1, DSCC1	501	370	13528	2,189351028	0,250168552	0,009244323	0,203312811
GOTERM_BP_FAT	GO:0009310~amine catabolic process	12	0,15625	1,30E-04	MTHFD1, ALDH6A1, MCCC2, BCKDHB, HGD, GSTZ1, AASS, DMGDH, PAH, ACAD8, TAT, SARDH	501	78	13528	4,154153232	0,277545589	0,010107973	0,229548231
GOTERM_CC_FAT	GO:0031966~mitochondrial membrane	31	0,40364583	1,33E-04	CYP11B2, LDHD, SFXN1, GPAT2, ACAT1, NDUFAF1, NDUFB1, ACSL1, ETFDH, COX18, BDH1, HMGCL, SCO1, GCDH, SLC25A4, OTC, NDUFC2, TOMM40, SYNJ2BP, CYB5B, DHRS1, TST, ACADVL, HMGCS2, CYP27A1, L2HGDH, NDUFV2, SDHD, PEBP1, HSPD1, SLC25A15	471	394	12782	2,135223684	0,050956574	0,004348909	0,184973524
GOTERM_MF_FAT	GO:0008289~lipid binding	34	0,44270833	1,59E-04	GC, PPARA, RBP4, OSBP, CYP11B2, SYT2, APOC1, NR3C2, NR3C1, YBX2, AZGP1, PFN2, STARD5, ALB, SERPINA6, PGRMC1, APOC3, APOH, RAPGEF2, AKR1C1, HMGCL, ALDH6A1, OTC, PIGU, APOLD1, DGKK, ANXA2, ANXA10, ZFYVE28, PON1, PEBP1, APOL6, AKR1D1, SCP2	484	450	12983	2,026730946	0,125321544	0,013300648	0,245189835
GOTERM_CC_FAT	GO:0005743~mitochondrial inner membrane	26	0,33854167	1,63E-04	CYP11B2, LDHD, SFXN1, ACAT1, NDUFAF1, NDUFB1, ETFDH, COX18, BDH1, HMGCL, SCO1, GCDH, SLC25A4, OTC, NDUFC2, CYB5B, DHRS1, ACADVL, TST, HMGCS2, CYP27A1, L2HGDH, NDUFV2, SDHD, HSPD1, SLC25A15	471	306	12782	2,305843498	0,062135875	0,004922475	0,226834348
GOTERM_CC_FAT	GO:0005829~cytosol	75	0,9765625	1,74E-04	NCBP2, RPL17, ALAD, PDLIM5, DTYMK, PRKAG2, SNRPD1, SNRPD2, CCT2, PTTG1, STARD5, NDE1, GSTZ1, CAT, INSR, IMPDH2, AKR1C1, NT5C, AADAT, SUOX, RAN, CLIC1, HMGA1, G6PD, PANK1, NME1, AS3MT, PGM1, ZFYVE28, FARSB, SNRPB, ADSL, TXNRD1, MAPRE1, UBB, ANAPC7, SNRPF, AKR1D1, ALDH9A1, SRXN1, XDH, PFKFB4, GNE, NR3C1, ALDH3A1, IARS, ACSL1, SET, EIF3H, NPM1, GYS2, ENO3, RPL5, UCK2, PABPC1, GEMIN7, TGFBR2, EPHX2, CDC20, BIRC5, TKT, GYG1, SMAD1, ACACB, RPS8, PCK1, CDC25B, CCT7, CCNB1, CCT5, CCT4, MLYCD, EEF1E1, HSPD1, SH3D19	471	1330	12782	1,530338585	0,066280328	0,004886524	0,242475628
GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	17	0,22135417	1,84E-04	KNG1, SERPINA10, C3, SERPING1, BIRC5, PTTG1, AMBP, CST8, LPA, SERPINA6, ITIH1, SERPINF2, CARD18, SERPINA4, SERPINC1, PEBP1, SERPIND1	484	153	12983	2,980486685	0,143612536	0,013994998	0,283833454
GOTERM_BP_FAT	GO:0034470~ncRNA processing	19	0,24739583	1,98E-04	TRMU, PUS3, TSEN54, PUS1, PUSL1, PUS10, EXOSC3, SSB, TRMT1, RRP9, SMAD1, FBL, DCAF13, PA2G4, WDR12, RPL5, NOP56, TSEN2, POP7	501	187	13528	2,743518311	0,389852915	0,014859857	0,348635798
GOTERM_BP_FAT	GO:0051917~regulation of fibrinolysis	5	0,06510417	2,00E-04	F11, SERPINF2, KLKB1, APOH, PLG	501	9	13528	15,00110889	0,393415052	0,014595685	0,35276034

GOTERM_CC_FAT	GO:0019866~organelle inner membrane	27	0,3515625	2,06E-04	CYP11B2, LDHD, SFXN1, ACAT1, NDUFAF1, NDUFB1, ETFDH, COX18, BDH1, HMGCL, SCO1, GCDH, SLC25A4, OTC, NDUFC2, SMAD1, CYB5B, DHRS1, ACADVL, TST, HMGCS2, CYP27A1, L2HGDH, NDUFV2, SDHD, HSPD1, SLC25A15	471	329	12782	2,227131048	0,077934075	0,005394633	0,28681877
GOTERM_BP_FAT	GO:0010876~lipid localization	17	0,22135417	2,31E-04	RBP4, PPARA, OSBP, SORL1, CLU, APOC1, APOLD1, STARD5, LPA, APOC3, APOH, SLC27A6, ANGPTL3, APOL6, SCP2, AKR1C1, ATP8A1	501	157	13528	2,923783007	0,438432992	0,016351248	0,407064482
GOTERM_BP_FAT	GO:0002449~lymphocyte mediated immunity	11	0,14322917	2,35E-04	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	70	13528	4,243170801	0,443815314	0,016163908	0,413844427
GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	17	0,22135417	2,67E-04	F11, KNG1, PPARA, CCK, MASP1, C3, TGFBR2, SERPING1, PLG, PROC, ANXA2, SERPINF2, KLKB1, F2, SERPINC1, APOH, CPB2	501	159	13528	2,887005862	0,486843462	0,01787014	0,470511514
GOTERM_BP_FAT	GO:0022402~cell cycle process	39	0,5078125	2,69E-04	ZFP42, PKMYT1, CETN1, PTTG1, RCC1, SPC24, KIF2C, CDCA8, NDE1, DUSP13, SAC3D1, CENPA, CDC123, NPM1, PSMC3IP, BUB1, NUP37, TCF3, CDCA5, EGFR, RAN, CCNF, CDC20, BIRC5, RAD54L, CDC25A, SUV39H2, CDC25B, CCNB1, PA2G4, PRDM9, RCC2, CKS2, HORMAD2, MAPRE1, RUVBL1, ANAPC7, UBB, DSCC1	501	565	13528	1,863854592	0,488777	0,017501599	0,473167483
GOTERM_BP_FAT	GO:0009062~fatty acid catabolic process	8	0,10416667	2,97E-04	HAO1, ACADVL, ACOX1, ACADM, EHHADH, ETFDH, ECHS1, PEX13	501	36	13528	6,000443557	0,523244175	0,018814369	0,522264151
GOTERM_BP_FAT	GO:0006869~lipid transport	16	0,20833333	3,06E-04	RBP4, PPARA, OSBP, SORL1, CLU, APOC1, APOLD1, STARD5, LPA, APOC3, APOH, SLC27A6, APOL6, SCP2, AKR1C1, ATP8A1	501	145	13528	2,979530594	0,533697493	0,018892278	0,537852849
GOTERM_BP_FAT	GO:0002443~leukocyte mediated immunity	12	0,15625	3,14E-04	C8A, C8B, YWHAZ, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	86	13528	3,767720373	0,543446121	0,018941448	0,552706582
GOTERM_CC_FAT	GO:0005730~nucleolus	45	0,5859375	3,23E-04	ZNF18, LYAR, TCOF1, IGF2BP1, CCT2, NR3C1, DAZAP1, ZNF207, DCAF13, PPAN, WDR75, CDCA8, REXO4, ZNF680, PGRMC1, NPM1, WDR12, RPL5, TSEN2, GNL3, TSEN54, MCRS1, RRP12, NOC4L, PNO1, POLR1A, EXOSC3, SSB, BIRC5, RRP9, VSX2, NCL, FBL, MRTO4, FXR1, PCK1, VCX3A, CD3EAP, PA2G4, CCT5, VCX3B, RCC2, SH3D19, NOP56, POP7	471	698	12782	1,749584801	0,119199863	0,007901402	0,44830558
GOTERM_CC_FAT	GO:0044452~nucleolar part	7	0,09114583	3,67E-04	CD3EAP, NPM1, POLR1A, WDR12, NOP56, FBL, POP7	471	27	12782	7,035778879	0,13423414	0,008443025	0,508959443
GOTERM_CC_FAT	GO:0005615~extracellular space	44	0,57291667	4,14E-04	GC, RBP4, CCK, MASP1, C3, C6, CLU, SORL1, APOC1, SFN, MMP3, TTR, SERPINA6, ALB, KLKB1, APOC3, CKLF, SERPINC1, APOH, CFI, PCSK6, ANGPTL3, GHR, F11, KNG1, EGFR, KLK5, SERPING1, PLG, C8A, C8B, AFM, CCL13, SERPINF2, HPX, F2, C1RL, PON1, PEBP1, CMTM7, PCYOX1, HSPD1, CPB2, PON3	471	685	12782	1,743171076	0,150072074	0,00899286	0,573964477
GOTERM_BP_FAT	GO:0008033~tRNA processing	11	0,14322917	4,64E-04	TRMU, PUS3, TSEN54, PUS1, PUSL1, PUS10, TRMT1, SSB, TSEN2, FBL, POP7	501	76	13528	3,908183633	0,686060637	0,027207671	0,81563204
GOTERM_BP_FAT	GO:0006081~cellular aldehyde metabolic process	7	0,09114583	4,66E-04	HAO1, RBP4, ALDH7A1, GRHPR, AGXT, ALDH9A1, ALDH3A1	501	28	13528	6,750499002	0,687077906	0,02665689	0,817907596
GOTERM_BP_FAT	GO:0000387~spliceosomal snRNP biogenesis	7	0,09114583	4,66E-04	NCBP2, WDR77, SNRPD1, SNRPB, SNRPD2, SNRPF, GEMIN7	501	28	13528	6,750499002	0,687077906	0,02665689	0,817907596
GOTERM_CC_FAT	GO:0044427~chromosomal part	29	0,37760417	4,94E-04	H1FNT, CBX1, POLA2, RCC1, HMGN4, SPC24, KIF2C, CDCA8, NDE1, ACD, CENPA, TIGD2, BUB1, NUP37, CDCA5, CENPM, RBL2, RAN, PIF1, TRIM28, SIRT6, BIRC5, H2BFWT, HMGA1, SUV39H2, RFC4, HDAC2, RCC2, DSCC1	471	386	12782	2,038865604	0,176578352	0,010173521	0,685416729
GOTERM_BP_FAT	GO:0034440~lipid oxidation	8	0,10416667	4,97E-04	HAO1, ACADVL, ACOX1, ACADM, EHHADH, ETFDH, ECHS1, PEX13	501	39	13528	5,538870976	0,710712627	0,027795811	0,872953295
GOTERM_BP_FAT	GO:0019395~fatty acid oxidation	8	0,10416667	4,97E-04	HAO1, ACADVL, ACOX1, ACADM, EHHADH, ETFDH, ECHS1, PEX13	501	39	13528	5,538870976	0,710712627	0,027795811	0,872953295
GOTERM_BP_FAT	GO:0002250~adaptive immune response	11	0,14322917	5,16E-04	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	77	13528	3,857428001	0,724291784	0,028225387	0,906636576
GOTERM_BP_FAT	GO:0002460~adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	11	0,14322917	5,16E-04	C8A, C8B, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	77	13528	3,857428001	0,724291784	0,028225387	0,906636576
GOTERM_MF_FAT	GO:0020037~heme binding	14	0,18229167	5,59E-04	SUOX, CYP1B1, CYP11B2, CYP2C8, CYB5B, CYP4V2, AMBP, CYP4A11, CYP27A1, PGRMC1, SDHD, CYP4F3, CAT, CYB5D2	484	121	12983	3,103647292	0,376105942	0,03855177	0,861223898
GOTERM_MF_FAT	GO:0005496~steroid binding	10	0,13020833	5,65E-04	GC, OSBP, SERPINA6, PGRMC1, CYP11B2, APOC3, NR3C2, NR3C1, AKR1D1, AKR1C1	484	64	12983	4,191309401	0,37892303	0,035975415	0,869449273
GOTERM_MF_FAT	GO:0016645~oxidoreductase activity, acting on the CH-NH group of donors	7	0,09114583	5,88E-04	MTHFD1, PYCR1, ETFDH, QDPR, AASS, DMGDH, SARDH	484	29	12983	6,474850385	0,391108295	0,034816244	0,905455041
GOTERM_BP_FAT	GO:0051301~cell division	24	0,3125	6,20E-04	RBP4, RAN, CCNF, BIRC5, CDC20, CETN1, PTTG1, RCC1, CDC25A, CDC25B, SPC24, CCNB1, NDE1, CDCA8, RCC2, SAC3D1, CDC123, CKS2, BUB1, NUP37, RUVBL1, ANAPC7, MAPRE1, CDCA5	501	295	13528	2,196772557	0,78719649	0,033079333	1,087878091
GOTERM_MF_FAT	GO:0004252~serine-type endopeptidase activity	16	0,20833333	6,21E-04	F11, MASP1, KLK5, MST1, C1S, PLG, PROC, LPA, LONP2, KLKB1, F2, PROZ, C1RL, CFI, PCSK6, KLK15	484	154	12983	2,786948589	0,407754927	0,03431957	0,955803872
GOTERM_CC_FAT	GO:0000775~chromosome, centromeric region	14	0,18229167	6,34E-04	CENPM, BIRC5, CBX1, SUV39H2, SPC24, KIF2C, NDE1, CDCA8, RCC2, CENPA, TIGD2, BUB1, NUP37, DSCC1	471	124	12782	3,063968221	0,220485498	0,012376967	0,877882437
GOTERM_BP_FAT	GO:0006959~humoral immune response	11	0,14322917	6,35E-04	C8A, C8B, MASP1, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, CFI	501	79	13528	3,759771596	0,794940969	0,033149947	1,11379515
GOTERM_BP_FAT	GO:0002253~activation of immune response	12	0,15625	6,80E-04	C8A, C8B, MASP1, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, HSPD1, CFI	501	94	13528	3,44706332	0,81694162	0,034755616	1,19309719
GOTERM_CC_FAT	GO:0030529~ribonucleoprotein complex	35	0,45572917	6,98E-04	RPL17, SNRPD1, SNRPD2, IGF2BP1, YBX1, YBX2, DCAF13, MRPL16, NPM1, MRPL54, WDR12, LSM4, RPL5, TAF9, PABPC1, SNRNP35, TNRC6A, GEMIN7, RPL36AL, NOC4L, SSB, RRP9, NCL, RPS8, FBL, FXR1, PA2G4, RBMXL2, SNRPB, SNRPA, NOP56, UBB, SNRPF, MRPL46, POP7	471	515	12782	1,844330386	0,240071658	0,012987832	0,967134446
GOTERM_BP_FAT	GO:0042730~fibrinolysis	5	0,06510417	7,20E-04	KLKB1, F2, CPB2, PLG, ANXA2	501	12	13528	11,25083167	0,834328524	0,036023869	1,262777826
GOTERM_BP_FAT	GO:0034660~ncRNA metabolic process	20	0,26041667	9,10E-04	TRMU, PUS3, TSEN54, PUS1, PUSL1, PUS10, EXOSC3, SSB, TRMT1, RRP9, FBL, IARS, DCAF13, PA2G4, FARSB, WDR12, RPL5, NOP56, TSEN2, POP7	501	230	13528	2,347999653	0,896896378	0,044423461	1,593250413
GOTERM_BP_FAT	GO:0051186~cofactor metabolic process	18	0,234375	9,23E-04	GSTA1, ASPDH, ALAD, SUCLG2, FTCD, MTHFD1L, COQ5, AMBP, MTHFD1, DBT, GLYAT, G6PD, PANK1, HPX, MLYCD, MCEE, SDHD, HMGCL	501	195	13528	2,492491939	0,900042191	0,0441526	1,614803142
GOTERM_BP_FAT	GO:0006559~L-phenylalanine catabolic process	4	0,05208333	9,23E-04	HGD, GSTZ1, PAH, TAT	501	6	13528	18,00133067	0,900231523	0,043357057	1,616121699
GOTERM_BP_FAT	GO:0006558~L-phenylalanine metabolic process	4	0,05208333	9,23E-04	HGD, GSTZ1, PAH, TAT	501	6	13528	18,00133067	0,900231523	0,043357057	1,616121699
GOTERM_BP_FAT	GO:0022613~ribonucleoprotein complex biogenesis	17	0,22135417	0,00105149	NCBP2, SNRPD1, SNRPD2, EXOSC3, RRP9, FBL, MRTO4, DCAF13, PA2G4, WDR77, NPM1, SNRPB, WDR12, RPL5, NOP56, SNRPF, GEMIN7	501	180	13528	2,550188512	0,927548505	0,048318867	1,838375544
GOTERM_MF_FAT	GO:0019842~vitamin binding	14	0,18229167	0,00110222	GC, AADAT, RBP4, FTCD, ACACB, AGXT, TAT, PDXDC1, MUT, MMACHC, ALB, SRR, DMGDH, ABAT	484	130	12983	2,888779402	0,605321748	0,05644939	1,690043346
GOTERM_BP_FAT	GO:0010565~regulation of cellular ketone metabolic process	9	0,1171875	0,0011051	PPARA, ACSL1, MLYCD, PRKAG2, APOC3, MLXIPL, APOC1, NR3C1, ACACB	501	57	13528	4,263473054	0,936629568	0,049805054	1,931258493
GOTERM_BP_FAT	GO:0051241~negative regulation of multicellular organismal process	16	0,20833333	0,00111821	KNG1, F11, RBP4, SLC6A1, TGFBR2, APOC1, ATP1A2, PLG, PROC, ANXA2, KLKB1, F2, APOC3, APOH, CRH, CPB2	501	164	13528	2,634341074	0,938670681	0,049488003	1,953952197
GOTERM_BP_FAT	GO:0006399~tRNA metabolic process	13	0,16927083	0,00138781	TSEN54, PUS3, TRMU, PUS1, PUSL1, PUS10, TRMT1, SSB, FBL, IARS, FARSB, TSEN2, POP7	501	118	13528	2,97479617	0,968726384	0,059999293	2,419622036

GOTERM_BP_FAT	GO:0034754~cellular hormone metabolic process	9	0,1171875	0,00139052	RBP4, DHRS3, CYP1B1, SERPINA6, CYP11B2, CRH, HSD17B6, NR3C1, AKR1D1	501	59	13528	4,118948544	0,968937845	0,059090351	2,424301884
GOTERM_CC_FAT	GO:0005832~chaperonin-containing T-complex	4	0,05208333	0,00154791	CCT7, CCT5, CCT4, CCT2	471	7	12782	15,507431	0,455997225	0,027293386	2,132100671
GOTERM_CC_FAT	GO:0030532~small nuclear ribonucleoprotein complex	6	0,078125	0,00156627	SNRPD1, SNRPB, LSM4, SNRPD2, RRP9, SNRPF	471	24	12782	6,784501062	0,459914032	0,026428276	2,157132225
GOTERM_CC_FAT	GO:0032994~protein-lipid complex	7	0,09114583	0,00156776	SORL1, CLU, APOC3, PON1, APOH, APOC1, PCYOX1	471	35	12782	5,427600849	0,460231353	0,02536504	2,159167824
GOTERM_CC_FAT	GO:0034358~plasma lipoprotein particle	7	0,09114583	0,00156776	SORL1, CLU, APOC3, PON1, APOH, APOC1, PCYOX1	471	35	12782	5,427600849	0,460231353	0,02536504	2,159167824
GOTERM_BP_FAT	GO:0006732~coenzyme metabolic process	15	0,1953125	0,00161058	GSTA1, ASPDH, SUCLG2, FTCD, MTHFD1L, COQ5, MTHFD1, DBT, GLYAT, G6PD, MLYCD, PANK1, MCEE, SDHD, HMGCL	501	153	13528	2,647254511	0,982076189	0,066989073	2,802835798
GOTERM_CC_FAT	GO:0005694~chromosome	31	0,40364583	0,00170245	H1FNT, CBX1, POLA2, RCC1, HMGN4, SPC24, KIF2C, CDCA8, NDE1, ACD, CENPA, TIGD2, BUB1, NUP37, CDCA5, CENPM, RBL2, RAN, PIF1, TRIM28, SIRT6, BIRC5, H2BFWT, HMGA1, SUV39H2, PRDM9, RFC4, HDAC2, RCC2, SETD7, DSCC1	471	460	12782	1,828865504	0,488104319	0,02642983	2,342633255
GOTERM_CC_FAT	GO:0042598~vesicular fraction	20	0,26041667	0,00170652	CYP1B1, CYP2C8, SYT2, ATP1A2, CYB5B, PLG, AMBP, MIP, CYP4A11, ACSL1, NME1, PGRMC1, SPCS3, PON1, HSD17B6, CYP4F3, UGT2B10, INSR, PON3, MGST2	471	244	12782	2,224426578	0,488923644	0,025486376	2,348170827
GOTERM_BP_FAT	GO:0031329~regulation of cellular catabolic process	9	0,1171875	0,00173158	PPARA, MLYCD, PRKAG2, APOC3, MLXIPL, APOC1, TAF9, SH3D19, INSR	501	61	13528	3,98390105	0,986753724	0,070667594	3,010396639
GOTERM_BP_FAT	GO:0044242~cellular lipid catabolic process	10	0,13020833	0,00188948	HAO1, ACADVL, ACOX1, ACADM, EHHADH, APOC3, ETFDH, ECHS1, PEX13, ANGPTL3	501	76	13528	3,552894212	0,991073278	0,075632075	3,280608936
GOTERM_BP_FAT	GO:0016042~lipid catabolic process	16	0,20833333	0,00190828	ACOX1, ACADM, EHHADH, PLBD1, ECHS1, ACADVL, HAO1, AZGP1, PLA2G12A, APOC3, ETFDH, PAFAH1B3, HSD17B6, PEX13, ANGPTL3, AKR1D1	501	173	13528	2,497294428	0,99148311	0,075152385	3,312736359
GOTERM_BP_FAT	GO:0019217~regulation of fatty acid metabolic process	8	0,10416667	0,00201958	PPARA, ACSL1, MLYCD, PRKAG2, APOC3, MLXIPL, APOC1, ACACB	501	49	13528	4,408489144	0,993551695	0,078132557	3,502715928
GOTERM_MF_FAT	GO:0000166~nucleotide binding	109	1,41927083	0,00214897	NCBP2, LDHD, DTYMK, PKMYT1, CCT2, MTHFD1L, KDM1A, ATP2B3, SAR1B, INSR, GNL3, EGFR, RAN, SUCLG2, ACSM2A, ARL16, NME6, RFC4, NME1, RAB17, SNRPA, PCCB, SRXN1, XDH, ABCA9, PFKFB4, GNE, IGF2BP1, DAZAP1, IVD, SRR, TAF9, SNRNP35, PABPC1, RECQL4, GCDH, MYO1B, PIF1, TGFBR2, SSB, ACACB, RAD54L, RAB33B, MMAA, CCT7, IKBKE, CCT5, CCT4, UBA2, NDUFV2, RBMXL2, GRK7, HSPD1, ACAD11, ASPDH, ACOX1, CPEB3, PRKAG2, MTHFD1, MCCC2, KIF2C, LONP2, CAT, ACAD8, TUBA1B, SARDH, SIK2, KIF2A, NT5C, NLRP4, ACADM, RBM46, RBM45, CBR4, GRHPR, NCL, ACADVL, HAO1, DHRS3, G6PD, PANK1, FARSB, SLC27A6, PEBP1, TXNRD1, RUVBL1, UBE2S, SLC27A5, H1FNT, CETN1, SHPK, IARS, ACSL1, BUB1, ETFDH, TUBA3C, DMGDH, UCK2, TNRC6A, TRMU, DGKK, SIRT6, ATP1A2, PCK2, SIRT3, PCK1, NLRP14, ABCC6, ATP8A1	484	2245	12983	1,302386387	0,836922895	0,10118528	3,270269504
GOTERM_BP_FAT	GO:0006396~RNA processing	35	0,45572917	0,00216888	NCBP2, PUS3, PUS1, PUSL1, PUS10, SNRPD1, SNRPD2, TRMT1, YBX1, DCAF13, PPAN, WDR77, WDR12, LSM4, RPL5, SCNM1, PABPC1, SNRNP35, TSEN2, GEMIN7, TSEN54, TRMU, RNASE4, EXOSC3, SSB, RRP9, SMAD1, FBL, PA2G4, SNRPB, SNRPA, NOP56, SNRPF, CPSF3, POP7	501	547	13528	1,727732834	0,995560581	0,082394578	3,757016636
GOTERM_BP_FAT	GO:0009081~branched chain family amino acid metabolic process	5	0,06510417	0,00235425	ALDH6A1, MCCC2, BCKDHB, ACAD8, GHR	501	16	13528	8,438123752	0,997207367	0,08779181	4,071862754
GOTERM_CC_FAT	GO:0005654~nucleoplasm	50	0,65104167	0,00240779	NCBP2, E2F2, E2F5, PRKAG2, SNRPD1, SNRPD2, PKMYT1, CBX1, CDT1, KDM1A, CDC45, GNL3, MCRS1, RBL2, RAN, POLR1A, MLXIPL, MED11, HDAC11, HMGA1, NCL, CD3EAP, RFC4, SNRPB, ANAPC7, RUVBL1, UBB, SNRPF, CPSF3, DSCC1, MGMT, POLA2, SET, ACD, NPM1, GTF3C6, HOXA9, WDR12, TAF9, GEMIN7, TCF3, GTF3C3, TRIM28, SIRT6, CDC20, SMAD1, CDC25A, CDC25B, CCNB1, HDAC2	471	882	12782	1,538435615	0,612253069	0,034480497	3,298192409
GOTERM_MF_FAT	GO:0004029~aldehyde dehydrogenase (NAD) activity	4	0,05208333	0,00249147	ALDH7A1, ALDH2, ALDH9A1, ALDH3A1	484	8	12983	13,41219008	0,877901649	0,110262991	3,782139341
GOTERM_MF_FAT	GO:0008236~serine-type peptidase activity	16	0,20833333	0,00267242	F11, MASP1, KLK5, MST1, C1S, PLG, PROC, LPA, LONP2, KLKB1, F2, PROZ, C1RL, CFI, PCSK6, KLK15	484	178	12983	2,41118024	0,89521748	0,11195238	4,051557024
GOTERM_BP_FAT	GO:0009894~regulation of catabolic process	11	0,14322917	0,00284739	PPARA, MLYCD, PRKAG2, APOC3, MLXIPL, APOC1, TAF9, ITCH, SH3D19, ANGPTL3, INSR	501	96	13528	3,093978709	0,999186667	0,10367468	4,904743476
GOTERM_BP_FAT	GO:0051262~protein tetramerization	7	0,09114583	0,00285945	MTMR2, SRR, AASS, ADSL, CBR4, CAT, INSR	501	39	13528	4,846512104	0,999210837	0,102597287	4,9250201
GOTERM_CC_FAT	GO:0005792~microsome	19	0,24739583	0,00293187	CYP1B1, CYP2C8, ATP1A2, CYB5B, PLG, AMBP, MIP, CYP4A11, ACSL1, NME1, PGRMC1, PON1, SPCS3, HSD17B6, CYP4F3, UGT2B10, INSR, PON3, MGST2	471	237	12782	2,175620594	0,684600975	0,040373671	4,002564393
GOTERM_MF_FAT	GO:0017171~serine hydrolase activity	16	0,20833333	0,00297458	F11, MASP1, KLK5, MST1, C1S, PLG, PROC, LPA, LONP2, KLKB1, F2, PROZ, C1RL, CFI, PCSK6, KLK15	484	180	12983	2,384389348	0,918838025	0,118001939	4,499857048
GOTERM_BP_FAT	GO:0006091~generation of precursor metabolites and energy	23	0,29947917	0,00301106	ACOX1, SLC25A4, SUCLG2, LDHAL6A, PRKAG2, NDUFC2, CYB5B, GYG1, ISL1, NDUFAF1, NDUFB1, PCK1, ACADVL, SDHD, PGM1, NDUFV2, ETFDH, ENO3, GYS2, TXNRD1, CAT, ETFB, SCO1	501	313	13528	1,984172231	0,999459995	0,106221669	5,179661855
GOTERM_BP_FAT	GO:0007049~cell cycle	45	0,5859375	0,00303978	E2F2, DTYMK, ZFP42, PKMYT1, CETN1, PTTG1, RCC1, CDT1, SPC24, KIF2C, CDCA8, CDC45, NDE1, DUSP13, SAC3D1, CENPA, CDC123, NPM1, PSMC3IP, BUB1, NUP37, TCF3, CDCA5, EGFR, RBL2, RAN, NASP, CCNF, CDC20, BIRC5, RAD54L, CDC25A, SUV39H2, CDC25B, CCNB1, PA2G4, PRDM9, RCC2, CKS2, HORMAD2, MAPRE1, UBB, RUVBL1, ANAPC7, DSCC1	501	776	13528	1,565837397	0,999497441	0,105690081	5,227819634
GOTERM_BP_FAT	GO:0006635~fatty acid beta-oxidation	6	0,078125	0,00328364	ACADVL, ACOX1, ACADM, EHHADH, ETFDH, ECHS1	501	28	13528	5,786142002	0,999727031	0,112129823	5,635839784
GOTERM_BP_FAT	GO:0034621~cellular macromolecular complex subunit organization	25	0,32552083	0,00353034	NCBP2, TSPY3, NASP, NAP1L1, SNRPD1, SNRPD2, SMAD1, H2BFWT, HMGA1, TSPY10, KIF2C, SET, CSE1L, CENPA, NPM1, WDR77, TUBA3C, SNRPB, PEX13, HSPD1, SNRPF, COX18, TUBA1B, GEMIN7, SCO1	501	357	13528	1,890896079	0,999852811	0,118432941	6,046943016
GOTERM_BP_FAT	GO:0006570~tyrosine metabolic process	4	0,05208333	0,00356856	HGD, GSTZ1, PAH, TAT	501	9	13528	12,00088711	0,999866241	0,118055656	6,110463817
GOTERM_BP_FAT	GO:0002252~immune effector process	13	0,16927083	0,00403524	YWHAZ, MASP1, C3, C6, CLU, C4BPB, SERPING1, C1S, C8A, C8B, C1RL, HSPD1, CFI	501	134	13528	2,619596628	0,999958436	0,130741733	6,8830076
GOTERM_CC_FAT	GO:0031090~organelle membrane	58	0,75520833	0,0046196	ACOX1, SEC24B, SYT2, CYP11B2, LDHD, GPAT2, PEX11G, NDUFAF1, SLC35D1, ST3GAL6, CAT, COX18, SEC24D, INSR, HMGCL, EGFR, SLC25A4, OTC, PIGV, NDUFC2, PIGU, CYB5B, SYNJ2BP, H2BFWT, ACADVL, DHRS1, CYP27A1, ZFYVE28, PEBP1, SLC27A5, CYP1B1, SLC37A4, SFXN1, ACAT1, EDEM1, NDUFB1, MTMR2, ACSL1, MPDU1, ETFDH, PEX13, BDH1, SCO1, GCDH, CYP2C8, TOMM40, SMAD1, TST, CYP4A11, HMGCS2, L2HGDH, NDUFV2, SDHD, SPCS3, CYP4F3, HSPD1, SLC25A15, SSR2	471	1096	12782	1,436135261	0,837927153	0,060820445	6,238681758
GOTERM_BP_FAT	GO:0006954~inflammatory response	23	0,29947917	0,0047104	KNG1, YWHAZ, MASP1, C3, C6, CLU, EPHX2, C4BPB, SERPING1, SMAD1, C1S, C8A, C8B, CCL13, SERPINF2, CCR3, CARD18, KLKB1, F2, CRH, C1RL, CFI, ITCH	501	325	13528	1,910910487	0,999992346	0,149025335	7,990077028
GOTERM_BP_FAT	GO:0016053~organic acid biosynthetic process	14	0,18229167	0,00494591	OTC, PRKAG2, PAH, ACACB, AGXT, ADI1, MTHFD1, PYCR1, SLC35D1, MLYCD, SRR, GSTO1, AKR1D1, MGST2	501	155	13528	2,438889962	0,999995759	0,153945289	8,373312695
GOTERM_BP_FAT	GO:0046394~carboxylic acid biosynthetic process	14	0,18229167	0,00494591	OTC, PRKAG2, PAH, ACACB, AGXT, ADI1, MTHFD1, PYCR1, SLC35D1, MLYCD, SRR, GSTO1, AKR1D1, MGST2	501	155	13528	2,438889962	0,999995759	0,153945289	8,373312695
GOTERM_BP_FAT	GO:0008211~glucocorticoid metabolic process	4	0,05208333	0,00495901	SERPINA6, CYP11B2, CRH, NR3C1	501	10	13528	10,8007984	0,999995896	0,152428421	8,394571913

GOTERM_BP_FAT	GO:0030194~positive regulation of blood coagulation	4	0,05208333	0,00495901	SERPINF2, F2, APOH, PLG	501	10	13528	10,8007984	0,999995896	0,152428421	8,394571913
GOTERM_BP_FAT	GO:0065003~macromolecular complex assembly	39	0,5078125	0,00505742	NCBP2, E2F2, TSPY3, SLC6A1, APOC1, NAP1L1, SNRPD1, AASS, SNRPD2, NDUFAF1, TSPY10, MTMR2, SET, CSE1L, CENPA, NPM1, APOC3, WDR77, SRR, TUBA3C, PEX13, TAF9, CAT, COX18, TUBA1B, GEMIN7, INSR, AKR1C1, SCO1, OTC, CBR4, SMAD1, H2BFWT, HMGA1, SNRPB, PEBP1, ADSL, HSPD1, SNRPF	501	665	13528	1,583575706	0,999996793	0,153335837	8,554242191
GOTERM_BP_FAT	GO:0043933~macromolecular complex subunit organization	41	0,53385417	0,00519271	NCBP2, E2F2, TSPY3, SLC6A1, APOC1, NAP1L1, SNRPD1, AASS, SNRPD2, NDUFAF1, TSPY10, MTMR2, KIF2C, SET, CSE1L, CENPA, NPM1, APOC3, WDR77, SRR, TUBA3C, PEX13, TAF9, CAT, COX18, TUBA1B, GEMIN7, INSR, AKR1C1, SCO1, NASP, OTC, CBR4, SMAD1, H2BFWT, HMGA1, SNRPB, PEBP1, ADSL, HSPD1, SNRPF	501	710	13528	1,559270192	0,999997716	0,155233921	8,773289771
GOTERM_CC_FAT	GO:0005732~small nucleolar ribonucleoprotein complex	5	0,06510417	0,00547156	NOC4L, SNRPB, RRP9, NOP56, FBL	471	20	12782	6,784501062	0,88423916	0,069352127	7,349015723
GOTERM_CC_FAT	GO:0000267~cell fraction	57	0,7421875	0,00549228	SLC13A5, SLC6A1, SYT2, PDLIM5, PKMYT1, PGP, SLC1A6, PGRMC1, ITCH, INSR, MPDZ, CYB5B, CLIC1, AMBP, PSG9, NME1, AS3MT, F2, FARSB, PEBP1, ABAT, ADAM18, UGT2B10, YWHAZ, CYP1B1, PPM1A, MIP, IARS, ACSL1, SRR, HSD17B6, ENO3, GYS2, PEX13, CCS, PCSK6, CYP2C8, EPHX2, TOMM40, ATP1A2, GYG1, SHANK1, PLG, ANXA2, PCK1, CYP4A11, SLCO1B1, CRH, PON1, LRP6, DSC3, SPCS3, CYP4F3, PYY, PON3, ABCC6, MGST2	471	1083	12782	1,428316013	0,885182749	0,06743814	7,375856085
GOTERM_BP_FAT	GO:0042445~hormone metabolic process	11	0,14322917	0,00580365	RBP4, DHRS3, CYP1B1, SERPINA6, CYP11B2, CRH, HSD17B6, NR3C1, PCSK6, AKR1D1, ALDH9A1	501	106	13528	2,802093925	0,999999507	0,169878529	9,756381045
GOTERM_BP_FAT	GO:0009083~branched chain family amino acid catabolic process	4	0,05208333	0,00663317	ALDH6A1, MCCC2, BCKDHB, ACAD8	501	11	13528	9,818907639	0,999999939	0,18956847	11,07519212
GOTERM_MF_FAT	GO:0003723~RNA binding	41	0,53385417	0,00684129	NCBP2, PUS3, PUS1, CPEB3, XPO5, PUSL1, SNRPD1, IGF2BP1, LARP1B, TRMT1, YBX1, DAZAP1, YBX2, MRPL16, NPM1, SEPSECS, LSM4, RPL5, PABPC1, SNRNP35, TNRC6A, TRMU, RBM46, RBM45, PNO1, EXOSC3, SSB, RRP9, RNASEH2A, NCL, FBL, FXR1, PA2G4, ZNF239, FARSB, RBMXL2, SNRPB, SNRPA, NOP56, SNRPF, CPSF3	484	718	12983	1,531754299	0,996932916	0,240862806	10,06649581
GOTERM_MF_FAT	GO:0042803~protein homodimerization activity	23	0,29947917	0,00691686	MASP1, EPHX2, MLXIPL, PAH, BIRC5, ACTN3, TPD52L2, AGXT, MTHFD1L, AMBP, MTMR2, ASGR1, G6PD, NPM1, SRR, PON1, ABAT, ENO3, GYS2, CAT, TCF3, PON3, GHR	484	334	12983	1,847187856	0,997123464	0,233531909	10,17219163
GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	10	0,13020833	0,00714659	AMBP, SERPINA10, ITIH1, SERPINA6, SERPINF2, SERPINA4, SERPINC1, PEBP1, SERPING1, SERPIND1	484	92	12983	2,915693496	0,997633172	0,231164659	10,49282386
GOTERM_BP_FAT	GO:0034622~cellular macromolecular complex assembly	22	0,28645833	0,00747404	NCBP2, TSPY3, SNRPD1, NAP1L1, SNRPD2, SMAD1, H2BFWT, TSPY10, SET, CSE1L, CENPA, WDR77, NPM1, SNRPB, TUBA3C, PEX13, HSPD1, SNRPF, COX18, TUBA1B, GEMIN7, SCO1	501	318	13528	1,868062617	0,999999993	0,208616125	12,39349182
GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	13	0,16927083	0,00752848	MASP1, C3, C6, CLU, C4BPB, SERPING1, C1S, C8A, C8B, HPX, C1RL, HSPD1, CFI	501	145	13528	2,420868608	0,999999994	0,207666588	12,47819577
GOTERM_CC_FAT	GO:0031305~integral to mitochondrial inner membrane	3	0,0390625	0,0077059	L2HGDH, ETFDH, COX18	471	4	12782	20,35350318	0,952172217	0,090631288	10,20325048
GOTERM_BP_FAT	GO:0031639~plasminogen activation	3	0,0390625	0,00778457	F11, KLKB1, APOH	501	4	13528	20,25149701	0,999999997	0,211629049	12,87565318
GOTERM_BP_FAT	GO:0051919~positive regulation of fibrinolysis	3	0,0390625	0,00778457	F11, KLKB1, PLG	501	4	13528	20,25149701	0,999999997	0,211629049	12,87565318
GOTERM_CC_FAT	GO:0043232~intracellular non-membrane-bounded organelle	118	1,53645833	0,00811725	FAM110A, RPL17, PDLIM5, CCT2, CBX1, HMGN4, KLHL2, WDR75, CDCA8, PGRMC1, TIGD2, NUP37, CDCA5, RPL36AL, GNL3, MCRS1, RBL2, RAN, MPDZ, ACTN3, RRP9, H2BFWT, MRTO4, PA2G4, PRDM9, RFC4, RCC2, NME1, MRPL46, DSCC1, GNE, IGF2BP1, RCC1, DAZAP1, SPC24, PPAN, PFN2, ACD, SAC3D1, NPM1, MRPL54, GYS2, RPL5, GIT1, TSEN54, NOC4L, MYO1B, PIF1, SSB, CDC20, SHANK1, RPS8, FXR1, SUV39H2, CCT5, HDAC2, KRTAP19-5, ACAD11, POP7, ZNF18, LYAR, TCOF1, ZNF207, KIF2C, DCAF13, CDC45, NDE1, ZNF680, ZNF492, TSEN2, TUBA1B, KIF2A, POLR1A, EXOSC3, NCL, HMGA1, VCX3A, ACADVL, CD3EAP, KRTAP5-7, G6PD, VCX3B, EPB41L5, PEBP1, UBB, MAPRE1, RUVBL1, ZNF98, ALDH9A1, YWHAZ, H1FNT, FHL3, CETN1, NR3C1, POLA2, REXO4, CENPA, SORBS2, MRPL16, MYBPH, BUB1, TUBA3C, WDR12, KRT4, CENPM, RRP12, PNO1, TRIM28, BIRC5, SIRT6, VSX2, FBL, PCK1, CDC25B, CCNB1, DBT, SETD7, SH3D19, NOP56	471	2596	12782	1,233545648	0,959363892	0,092501697	10,71974526
GOTERM_CC_FAT	GO:0043228~non-membrane-bounded organelle	118	1,53645833	0,00811725	FAM110A, RPL17, PDLIM5, CCT2, CBX1, HMGN4, KLHL2, WDR75, CDCA8, PGRMC1, TIGD2, NUP37, CDCA5, RPL36AL, GNL3, MCRS1, RBL2, RAN, MPDZ, ACTN3, RRP9, H2BFWT, MRTO4, PA2G4, PRDM9, RFC4, RCC2, NME1, MRPL46, DSCC1, GNE, IGF2BP1, RCC1, DAZAP1, SPC24, PPAN, PFN2, ACD, SAC3D1, NPM1, MRPL54, GYS2, RPL5, GIT1, TSEN54, NOC4L, MYO1B, PIF1, SSB, CDC20, SHANK1, RPS8, FXR1, SUV39H2, CCT5, HDAC2, KRTAP19-5, ACAD11, POP7, ZNF18, LYAR, TCOF1, ZNF207, KIF2C, DCAF13, CDC45, NDE1, ZNF680, ZNF492, TSEN2, TUBA1B, KIF2A, POLR1A, EXOSC3, NCL, HMGA1, VCX3A, ACADVL, CD3EAP, KRTAP5-7, G6PD, VCX3B, EPB41L5, PEBP1, UBB, MAPRE1, RUVBL1, ZNF98, ALDH9A1, YWHAZ, H1FNT, FHL3, CETN1, NR3C1, POLA2, REXO4, CENPA, SORBS2, MRPL16, MYBPH, BUB1, TUBA3C, WDR12, KRT4, CENPM, RRP12, PNO1, TRIM28, BIRC5, SIRT6, VSX2, FBL, PCK1, CDC25B, CCNB1, DBT, SETD7, SH3D19, NOP56	471	2596	12782	1,233545648	0,959363892	0,092501697	10,71974526
GOTERM_CC_FAT	GO:0032592~integral to mitochondrial membrane	4	0,05208333	0,00848072	L2HGDH, ETFDH, TOMM40, COX18	471	12	12782	9,046001415	0,964815041	0,093754641	11,17382347
GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	11	0,14322917	0,0084847	PPARA, ACSL1, RBL2, MLYCD, PRKAG2, APOC3, MLXIPL, APOC1, NR3C1, ACACB, ANGPTL3	501	112	13528	2,651981751	0,999999999	0,225966544	13,95357435
GOTERM_BP_FAT	GO:0009074~aromatic amino acid family catabolic process	4	0,05208333	0,00860413	HGD, GSTZ1, PAH, TAT	501	12	13528	9,000665336	1	0,226375704	14,13619509
GOTERM_BP_FAT	GO:0007031~peroxisome organization	5	0,06510417	0,00933627	LONP2, PEX13, PEX11G, AGXT, SCP2	501	23	13528	5,869999132	1	0,240681848	15,24772014
GOTERM_MF_FAT	GO:0016620~oxidoreductase activity, acting on the aldehyde or oxo group of donors, NAD or NADP as acceptor	5	0,06510417	0,00954567	ALDH6A1, ALDH7A1, ALDH2, ALDH9A1, ALDH3A1	484	23	12983	5,831386992	0,999692075	0,286021361	13,77782033
GOTERM_BP_FAT	GO:0050820~positive regulation of coagulation	4	0,05208333	0,01088231	SERPINF2, F2, APOH, PLG	501	13	13528	8,308306464	1	0,271992603	17,55044679
GOTERM_BP_FAT	GO:0008652~cellular amino acid biosynthetic process	7	0,09114583	0,01088725	MTHFD1, ADI1, PYCR1, OTC, SRR, PAH, AGXT	501	51	13528	3,706156315	1	0,26943597	17,55770317
GOTERM_MF_FAT	GO:0005506~iron ion binding	21	0,2734375	0,0112989	XDH, SUOX, CYP1B1, CYP2C8, CYP11B2, HGD, PAH, SFXN1, CYP4V2, CYB5B, AMBP, CYP4A11, CYP27A1, HPX, PGRMC1, SDHD, NDUFV2, ETFDH, CYP4F3, CAT, CYB5D2	484	308	12983	1,828935011	0,999930847	0,31830146	16,10677824
GOTERM_BP_FAT	GO:0016125~sterol metabolic process	10	0,13020833	0,01235898	G6PD, CYP27A1, HMGCS2, PRKAG2, SORL1, APOC3, APOC1, CAT, ANGPTL3, AKR1D1	501	101	13528	2,673464951	1	0,297133597	19,69463117
GOTERM_CC_FAT	GO:0034364~high-density lipoprotein particle	5	0,06510417	0,01236212	CLU, APOC3, PON1, APOH, APOC1	471	25	12782	5,427600849	0,992467985	0,130358376	15,89098421
GOTERM_CC_FAT	GO:0031304~intrinsic to mitochondrial inner membrane	3	0,0390625	0,01253156	L2HGDH, ETFDH, COX18	471	5	12782	16,28280255	0,992959117	0,128611418	16,09151188
GOTERM_BP_FAT	GO:0051005~negative regulation of lipoprotein lipase activity	3	0,0390625	0,0126578	APOC3, APOC1, ANGPTL3	501	5	13528	16,2011976	1	0,30030447	20,1220873

GOTERM_BP_FAT	GO:0006572~tyrosine catabolic process	3	0,0390625	0,0126578	HGD, GSTZ1, TAT	501	5	13528	16,2011976	1	0,30030447	20,1220873
GOTERM_MF_FAT	GO:0016833~oxo-acid-lyase activity	3	0,0390625	0,01281714	NPL, CLYBL, HMGCL	484	5	12983	16,0946281	0,999981069	0,341807231	18,07591108
GOTERM_MF_FAT	GO:0005343~organic acid:sodium symporter activity	5	0,06510417	0,01286292	SLC13A5, SLC6A1, SLC1A6, SLC10A7, SLC10A4	484	25	12983	5,364876033	0,999981794	0,33249881	18,13459984
GOTERM_BP_FAT	GO:0006694~steroid biosynthetic process	9	0,1171875	0,01314792	STARD5, G6PD, HMGCS2, CYP11B2, PRKAG2, CRH, HSD17B6, AKR1D1, SCP2	501	85	13528	2,859034871	1	0,307125831	20,81854123
GOTERM_BP_FAT	GO:0022618~ribonucleoprotein complex assembly	8	0,10416667	0,01351011	NCBP2, NPM1, WDR77, SNRPD1, SNRPB, SNRPD2, SNRPF, GEMIN7	501	69	13528	3,130666204	1	0,311293122	21,32952966
GOTERM_BP_FAT	GO:0034637~cellular carbohydrate biosynthetic process	8	0,10416667	0,01351011	RBP4, G6PD, GNE, PGM1, GYS2, GYG1, PCK2, PCK1	501	69	13528	3,130666204	1	0,311293122	21,32952966
GOTERM_BP_FAT	GO:0030258~lipid modification	8	0,10416667	0,01351011	HAO1, ACADVL, ACOX1, ACADM, EHHADH, ETFDH, ECHS1, PEX13	501	69	13528	3,130666204	1	0,311293122	21,32952966
GOTERM_MF_FAT	GO:0016667~oxidoreductase activity, acting on sulfur group of donors	6	0,078125	0,01416072	SUOX, MSRA, GLRX5, TXNRD1, PCYOX1, SRXN1	484	39	12983	4,126827718	0,999993994	0,349091524	19,78236625
GOTERM_BP_FAT	GO:0014070~response to organic cyclic substance	11	0,14322917	0,01417223	LONP2, ACSL1, HDAC2, SLC6A1, TGFBR2, SRR, ALDH2, ABAT, PEBP1, TAT, GHR	501	121	13528	2,45472691	1	0,320972819	22,25562208
GOTERM_CC_FAT	GO:0044454~nuclear chromosome part	11	0,14322917	0,01443991	H1FNT, ACD, HDAC2, PIF1, TRIM28, BUB1, SIRT6, POLA2, CBX1, RCC1, SUV39H2	471	122	12782	2,446869235	0,996707988	0,143150867	18,31957065
GOTERM_BP_FAT	GO:0050994~regulation of lipid catabolic process	5	0,06510417	0,01444892	PPARA, MLYCD, APOC3, APOC1, ANGPTL3	501	26	13528	5,19269154	1	0,323256349	22,63957643
GOTERM_MF_FAT	GO:0033293~monocarboxylic acid binding	7	0,09114583	0,0146544	AZGP1, ALDH6A1, ALB, APOC1, ACACB, AKR1C1, HMGCL	484	54	12983	3,477234466	0,999996063	0,348931397	20,40098186
GOTERM_MF_FAT	GO:0030170~pyridoxal phosphate binding	7	0,09114583	0,0146544	AADAT, ALB, SRR, ABAT, AGXT, TAT, PDXDC1	484	54	12983	3,477234466	0,999996063	0,348931397	20,40098186
GOTERM_MF_FAT	GO:0070279~vitamin B6 binding	7	0,09114583	0,0146544	AADAT, ALB, SRR, ABAT, AGXT, TAT, PDXDC1	484	54	12983	3,477234466	0,999996063	0,348931397	20,40098186
GOTERM_BP_FAT	GO:0031667~response to nutrient levels	15	0,1953125	0,01475161	RBP4, SUOX, PPARA, CCK, STC2, TGFBR2, BCKDHB, CLIC1, ACSL1, HMGCS2, ALB, SERPINC1, INSR, TNRC6A, GHR	501	197	13528	2,055989544	1	0,325957443	23,0575523
GOTERM_MF_FAT	GO:0016866~intramolecular transferase activity	5	0,06510417	0,01476498	MUT, PUS3, PUS1, PUSL1, PGM1	484	26	12983	5,158534647	0,999996418	0,341630808	20,53894077
GOTERM_CC_FAT	GO:0000790~nuclear chromatin	7	0,09114583	0,01513083	H1FNT, HDAC2, TRIM28, SIRT6, CBX1, RCC1, SUV39H2	471	55	12782	3,453927813	0,997500991	0,145877414	19,11260395
GOTERM_BP_FAT	GO:0032269~negative regulation of cellular protein metabolic process	14	0,18229167	0,01628507	MASP1, IGF2BP1, CDC20, SERPING1, YBX2, SET, G6PD, PON1, PEBP1, TAF9, UBB, ANAPC7, TNRC6A, INSR	501	180	13528	2,100155245	1	0,350282932	25,14255149
GOTERM_BP_FAT	GO:0043489~RNA stabilization	4	0,05208333	0,01639005	IGF2BP1, PABPC1, YBX1, YBX2	501	15	13528	7,200532269	1	0,349165658	25,28332214
GOTERM_MF_FAT	GO:0004033~aldo-keto reductase activity	4	0,05208333	0,01667556	AKR1C3, AKR1D1, AKR1C1, ALDH3A1	484	15	12983	7,153168044	0,999999303	0,367003982	22,88743045
GOTERM_MF_FAT	GO:0055102~lipase inhibitor activity	4	0,05208333	0,01667556	APOC3, APOC1, ANGPTL3, ANXA2	484	15	12983	7,153168044	0,999999303	0,367003982	22,88743045
GOTERM_BP_FAT	GO:0009991~response to extracellular stimulus	16	0,20833333	0,01671715	RBP4, SUOX, PPARA, CCK, STC2, BCKDHB, TGFBR2, CLIC1, ASGR1, ACSL1, HMGCS2, ALB, SERPINC1, INSR, TNRC6A, GHR	501	220	13528	1,963781528	1	0,351846312	25,72033858
GOTERM_MF_FAT	GO:0016877~ligase activity, forming carbon-sulfur bonds	5	0,06510417	0,01683565	ACSL1, SUCLG2, ACSM2A, SLC27A6, SLC27A5	484	27	12983	4,967477808	0,999999392	0,360641612	23,08124044
GOTERM_BP_FAT	GO:0032268~regulation of cellular protein metabolic process	28	0,36458333	0,01718996	NCBP2, CCK, MASP1, PRKAG2, IGF2BP1, YBX2, SET, EIF3H, KLKB1, SEPSECS, TAF9, INSR, TNRC6A, GHR, EGFR, SERPING1, CDC20, CCNB1, PA2G4, HDAC2, G6PD, HPX, F2, PON1, PEBP1, SH3D19, ANAPC7, UBB	501	474	13528	1,595054617	1	0,356895192	26,34776842
GOTERM_BP_FAT	GO:0016051~carbohydrate biosynthetic process	10	0,13020833	0,01750928	RBP4, G6PD, SLC35D1, GNE, PGM1, MPDU1, GYS2, GYG1, PCK2, PCK1	501	107	13528	2,523551029	1	0,359289784	26,76867849
GOTERM_BP_FAT	GO:0015980~energy derivation by oxidation of organic compounds	12	0,15625	0,01786475	ACADVL, SUCLG2, NDUFV2, PRKAG2, SDHD, NDUFC2, GYS2, CAT, GYG1, NDUFAF1, NDUFB1, PCK1	501	144	13528	2,250166334	1	0,362215589	27,23457945
GOTERM_BP_FAT	GO:0044271~nitrogen compound biosynthetic process	21	0,2734375	0,018112	ASPDH, ALAD, OTC, PRKAG2, DTYMK, QDPR, PAH, ATP1A2, AGXT, NME6, MTHFD1, ADI1, PYCR1, ATP2B3, NME1, ATIC, SRR, ADSL, SLC25A15, IMPDH2, ATP8A1	501	325	13528	1,744744357	1	0,363341275	27,5569814
GOTERM_BP_FAT	GO:0046487~glyoxylate metabolic process	3	0,0390625	0,01852501	HAO1, GRHPR, AGXT	501	6	13528	13,500998	1	0,367064027	28,09253867
GOTERM_BP_FAT	GO:0070613~regulation of protein processing	3	0,0390625	0,01852501	MASP1, KLKB1, SERPING1	501	6	13528	13,500998	1	0,367064027	28,09253867
GOTERM_BP_FAT	GO:0051918~negative regulation of fibrinolysis	3	0,0390625	0,01852501	SERPINF2, APOH, PLG	501	6	13528	13,500998	1	0,367064027	28,09253867
GOTERM_BP_FAT	GO:0010953~regulation of protein maturation by peptide bond cleavage	3	0,0390625	0,01852501	MASP1, KLKB1, SERPING1	501	6	13528	13,500998	1	0,367064027	28,09253867
GOTERM_BP_FAT	GO:0006090~pyruvate metabolic process	6	0,078125	0,01864321	RBP4, PGM1, SRR, PCK2, AGXT, PCK1	501	42	13528	3,857428001	1	0,366099169	28,24511892
GOTERM_BP_FAT	GO:0046320~regulation of fatty acid oxidation	5	0,06510417	0,01867733	PPARA, ACSL1, MLYCD, PRKAG2, ACACB	501	28	13528	4,821785001	1	0,363845296	28,28910279
GOTERM_BP_FAT	GO:0006508~proteolysis	53	0,69010417	0,01912935	QPCTL, CNDP1, MASP1, ENPEP, MMP3, DDI2, LONP2, LPA, PROZ, APOH, ITCH, CFI, KLK15, F11, PAN2, SERPING1, PROC, C8A, C8B, CTSO, CARD18, F2, ADAM18, ANAPC7, PCYOX1, UBB, UBE2S, ASPRV1, C3, C6, TFR2, CLU, MST1, C1S, EDEM1, FBXW7, KLKB1, USP38, RNF167, PCSK6, FBXO46, CPA6, KLK5, CDC20, C4BPB, PLG, CCNB1, RNF43, UBA2, C1RL, SPCS3, USP47, CPB2	501	1054	13528	1,357785378	1	0,368055519	28,86946601
GOTERM_CC_FAT	GO:0000777~condensed chromosome kinetochore	7	0,09114583	0,01927971	SPC24, KIF2C, NDE1, CENPM, CENPA, BUB1, NUP37	471	58	12782	3,275276375	0,999524392	0,178133555	23,72636525

GOTERM_BP_FAT	GO:0006637~acyl-CoA metabolic process	4	0,05208333	0,01962909	DBT, GLYAT, MLYCD, HMGCL	501	16	13528	6,750499002	1	0,372881047	29,50592231
GOTERM_MF_FAT	GO:0001883~purine nucleoside binding	76	0,98958333	0,01973447	ACOX1, LDHD, DTYMK, PRKAG2, PKMYT1, CCT2, MTHFD1L, MTHFD1, KDM1A, KIF2C, MCCC2, ATP2B3, LONP2, ACAD8, SARDH, INSR, SIK2, KIF2A, EGFR, NLRP4, ACADM, SUCLG2, ACSM2A, NME6, ACADVL, RFC4, PANK1, NME1, FARSB, PEBP1, TXNRD1, RUVBL1, PCCB, UBE2S, SLC27A5, SRXN1, XDH, H1FNT, ABCA9, PFKFB4, GNE, CETN1, SHPK, IARS, ACSL1, IVD, BUB1, ETFDH, SRR, DMGDH, TAF9, UCK2, SNRNP35, RECQL4, GCDH, TRMU, MYO1B, PIF1, TGFBR2, DGKK, ATP1A2, ACACB, RAD54L, PCK1, MMAA, CCT7, IKBKE, CCT5, CCT4, UBA2, GRK7, NLRP14, HSPD1, ACAD11, ABCC6, ATP8A1	484	1601	12983	1,273362206	0,99999995	0,399003812	26,51271606
GOTERM_CC_FAT	GO:0044438~microbody part	6	0,078125	0,02006092	ACOX1, LONP2, ACSL1, PEX13, CAT, PEX11G	471	43	12782	3,786698267	0,999652274	0,180533999	24,56730186
GOTERM_CC_FAT	GO:0044439~peroxisomal part	6	0,078125	0,02006092	ACOX1, LONP2, ACSL1, PEX13, CAT, PEX11G	471	43	12782	3,786698267	0,999652274	0,180533999	24,56730186
GOTERM_MF_FAT	GO:0030554~adenyl nucleotide binding	75	0,9765625	0,0201397	ACOX1, LDHD, DTYMK, PRKAG2, PKMYT1, CCT2, MTHFD1L, MTHFD1, KDM1A, KIF2C, MCCC2, ATP2B3, LONP2, ACAD8, SARDH, INSR, SIK2, KIF2A, EGFR, NLRP4, ACADM, SUCLG2, ACSM2A, NME6, ACADVL, RFC4, PANK1, NME1, FARSB, PEBP1, TXNRD1, RUVBL1, PCCB, UBE2S, SLC27A5, SRXN1, XDH, H1FNT, ABCA9, PFKFB4, GNE, CETN1, SHPK, IARS, ACSL1, IVD, BUB1, ETFDH, SRR, DMGDH, TAF9, UCK2, SNRNP35, RECQL4, GCDH, TRMU, MYO1B, PIF1, TGFBR2, DGKK, ATP1A2, ACACB, RAD54L, MMAA, CCT7, IKBKE, CCT5, CCT4, UBA2, GRK7, NLRP14, HSPD1, ACAD11, ABCC6, ATP8A1	484	1577	12983	1,27573146	0,999999964	0,396158158	26,98084051
GOTERM_BP_FAT	GO:0008203~cholesterol metabolic process	9	0,1171875	0,02037669	G6PD, CYP27A1, HMGCS2, SORL1, APOC3, APOC1, CAT, ANGPTL3, AKR1D1	501	92	13528	2,641499609	1	0,381245295	30,44804148
GOTERM_MF_FAT	GO:0016831~carboxy-lyase activity	5	0,06510417	0,02149872	MLYCD, BCKDHB, PCK2, PCK1, PDXDC1	484	29	12983	4,624893132	0,999999989	0,407532548	28,53050331
GOTERM_BP_FAT	GO:0034728~nucleosome organization	9	0,1171875	0,02160164	TSPY3, SET, CENPA, NASP, NPM1, NAP1L1, H2BFWT, HMGA1, TSPY10	501	93	13528	2,613096388	1	0,396196755	31,96608286
GOTERM_BP_FAT	GO:0051248~negative regulation of protein metabolic process	14	0,18229167	0,02161012	MASP1, IGF2BP1, CDC20, SERPING1, YBX2, SET, G6PD, PON1, PEBP1, TAF9, UBB, ANAPC7, TNRC6A, INSR	501	187	13528	2,021539808	1	0,393515869	31,97647884
GOTERM_BP_FAT	GO:0051276~chromosome organization	28	0,36458333	0,022271	TSPY3, H1FNT, NAP1L1, CBX1, NR3C1, PTTG1, TSPY10, KDM1A, CDCA8, ACD, SET, CENPA, NPM1, TAF9, CDCA5, RBL2, NASP, HDAC11, H2BFWT, HMGA1, RAD54L, SUV39H2, PRDM9, HDAC2, SETD7, RUVBL1, NCAPH2, DSCC1	501	485	13528	1,55887812	1	0,400018628	32,78232667
GOTERM_CC_FAT	GO:0005625~soluble fraction	20	0,26041667	0,02227317	YWHAZ, EPHX2, CLIC1, GYG1, PCK1, ANXA2, IARS, ACSL1, NME1, F2, AS3MT, CRH, SRR, FARSB, PEBP1, GYS2, CCS, PYY, PCSK6, INSR	471	313	12782	1,734057779	0,999856949	0,194192172	26,9022203
GOTERM_MF_FAT	GO:0042802~identical protein binding	35	0,45572917	0,02298899	TSPY3, ALAD, PFKFB4, MASP1, PAH, AMOTL1, AGXT, MTHFD1L, TSPY10, ASGR1, MTMR2, NDE1, NPM1, SRR, ENO3, GYS2, CAT, ZNF408, TCF3, GHR, EGFR, MLXIPL, EPHX2, BIRC5, ACTN3, TPD52L2, SMAD1, CCT7, AMBP, G6PD, NME1, ALDH2, PON1, ABAT, PON3	484	640	12983	1,46695829	0,999999997	0,419931916	30,19443255
GOTERM_MF_FAT	GO:0001882~nucleoside binding	76	0,98958333	0,02314607	ACOX1, LDHD, DTYMK, PRKAG2, PKMYT1, CCT2, MTHFD1L, MTHFD1, KDM1A, KIF2C, MCCC2, ATP2B3, LONP2, ACAD8, SARDH, INSR, SIK2, KIF2A, EGFR, NLRP4, ACADM, SUCLG2, ACSM2A, NME6, ACADVL, RFC4, PANK1, NME1, FARSB, PEBP1, TXNRD1, RUVBL1, PCCB, UBE2S, SLC27A5, SRXN1, XDH, H1FNT, ABCA9, PFKFB4, GNE, CETN1, SHPK, IARS, ACSL1, IVD, BUB1, ETFDH, SRR, DMGDH, TAF9, UCK2, SNRNP35, RECQL4, GCDH, TRMU, MYO1B, PIF1, TGFBR2, DGKK, ATP1A2, ACACB, RAD54L, PCK1, MMAA, CCT7, IKBKE, CCT5, CCT4, UBA2, GRK7, NLRP14, HSPD1, ACAD11, ABCC6, ATP8A1	484	1612	12983	1,26467301	0,999999997	0,413483196	30,36768872
GOTERM_BP_FAT	GO:0051004~regulation of lipoprotein lipase activity	4	0,05208333	0,02319468	APOC3, APOH, APOC1, ANGPTL3	501	17	13528	6,353410825	1	0,409921329	33,89355692
GOTERM_MF_FAT	GO:0016597~amino acid binding	7	0,09114583	0,02361071	OTC, SRR, FTCD, DMGDH, PAH, AGXT, TAT	484	60	12983	3,129511019	0,999999998	0,411434827	30,87783714
GOTERM_BP_FAT	GO:0010817~regulation of hormone levels	12	0,15625	0,02444446	RBP4, DHRS3, YWHAZ, CYP1B1, SERPINA6, CYP11B2, CRH, HSD17B6, NR3C1, PCSK6, AKR1D1, ALDH9A1	501	151	13528	2,145853987	1	0,423805527	35,36953156
GOTERM_BP_FAT	GO:0009636~response to toxin	7	0,09114583	0,02470323	GLYAT, SLC6A1, EPHX2, PON1, PEBP1, AQP10, AKR1C1	501	61	13528	3,098589706	1	0,424369092	35,67122118
GOTERM_CC_FAT	GO:0005579~membrane attack complex	3	0,0390625	0,0250606	C8A, C8B, C6	471	7	12782	11,63057325	0,999953419	0,211390417	29,74871297
GOTERM_BP_FAT	GO:0060192~negative regulation of lipase activity	3	0,0390625	0,02530636	APOC3, APOC1, ANGPTL3	501	7	13528	11,572284	1	0,429351976	36,36925265
GOTERM_MF_FAT	GO:0016885~ligase activity, forming carbon-carbon bonds	3	0,0390625	0,02561684	MCCC2, ACACB, PCCB	484	7	12983	11,49616293	1	0,429323925	33,04055421
GOTERM_CC_FAT	GO:0005626~insoluble fraction	43	0,55989583	0,02576802	CYP1B1, SLC13A5, SLC6A1, PDLIM5, SYT2, PPM1A, PKMYT1, MIP, PGP, ACSL1, PGRMC1, SLC1A6, GYS2, ENO3, HSD17B6, PEX13, ITCH, INSR, MPDZ, CYP2C8, TOMM40, CLIC1, ATP1A2, CYB5B, SHANK1, PLG, AMBP, CYP4A11, PSG9, NME1, SLCO1B1, DSC3, SPCS3, LRP6, PON1, ABAT, PEBP1, ADAM18, CYP4F3, UGT2B10, PON3, ABCC6, MGST2	471	839	12782	1,39086315	0,99996498	0,2122663	30,4545785
GOTERM_CC_FAT	GO:0031903~microbody membrane	5	0,06510417	0,02588445	ACOX1, ACSL1, PEX13, CAT, PEX11G	471	31	12782	4,377097459	0,999966587	0,208828128	30,57011594
GOTERM_CC_FAT	GO:0005778~peroxisomal membrane	5	0,06510417	0,02588445	ACOX1, ACSL1, PEX13, CAT, PEX11G	471	31	12782	4,377097459	0,999966587	0,208828128	30,57011594
GOTERM_BP_FAT	GO:0009303~rRNA transcription	4	0,05208333	0,02708704	CD3EAP, TCOF1, GTF3C6, GTF3C3	501	18	13528	6,000443557	1	0,448865716	38,38864953
GOTERM_MF_FAT	GO:0016646~oxidoreductase activity, acting on the CH-NH group of donors, NAD or NADP as acceptor	4	0,05208333	0,02754473	MTHFD1, PYCR1, QDPR, AASS	484	18	12983	5,96097337	1	0,444923844	35,05915385
GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	16	0,20833333	0,02925291	MASP1, C3, C6, CLU, C4BPB, SERPING1, C1S, C8A, C8B, HPX, EEF1E1, C1RL, CRH, TAF9, HSPD1, CFI	501	236	13528	1,830643797	1	0,471956171	40,76341411
GOTERM_BP_FAT	GO:0006323~DNA packaging	10	0,13020833	0,02931906	TSPY3, H1FNT, SET, CENPA, NPM1, NAP1L1, NCAPH2, H2BFWT, CDCA5, TSPY10	501	117	13528	2,307862907	1	0,46983734	40,83457422
GOTERM_BP_FAT	GO:0002684~positive regulation of immune system process	16	0,20833333	0,0311988	MASP1, C3, C6, TGFBR2, CLU, C4BPB, SERPING1, C1S, C8A, C8B, HPX, C1RL, HSPD1, CFI, ITCH, TCF3	501	238	13528	1,815260236	1	0,488383093	42,82310363
GOTERM_BP_FAT	GO:0007098~centrosome cycle	4	0,05208333	0,03130485	NDE1, SAC3D1, NPM1, CETN1	501	19	13528	5,684630739	1	0,486673221	42,9333921
GOTERM_BP_FAT	GO:0009072~aromatic amino acid family metabolic process	4	0,05208333	0,03130485	HGD, GSTZ1, PAH, TAT	501	19	13528	5,684630739	1	0,486673221	42,9333921
GOTERM_BP_FAT	GO:0045087~innate immune response	11	0,14322917	0,03203416	C8A, C8B, MASP1, C3, C6, CLU, C1RL, C4BPB, SERPING1, C1S, CFI	501	138	13528	2,152333015	1	0,49183296	43,68642354
GOTERM_CC_FAT	GO:0034366~spherical high-density lipoprotein particle	3	0,0390625	0,03261104	CLU, APOC3, PON1	471	8	12782	10,17675159	0,999997806	0,251399936	36,95077523
GOTERM_CC_FAT	GO:0000785~chromatin	14	0,18229167	0,0335256	H1FNT, HDAC2, RBL2, CENPA, RAN, TRIM28, SIRT6, CBX1, RCC1, H2BFWT, HMGN4, HMGA1, DSCC1, SUV39H2	471	200	12782	1,899660297	0,999998487	0,252735886	37,77498875
GOTERM_BP_FAT	GO:0008283~cell proliferation	25	0,32552083	0,03376545	EGFR, TSPY3, RBP4, NASP, DTYMK, ENPEP, SFN, TRAIP, CDC25A, TSPY10, KIF2C, KDM1A, PA2G4, NDE1, CSE1L, CKLF, BUB1, CKS2, WDR12, IRF2, TXNRD1, MAPRE1, HSPD1, PYY, IMPDH2	501	436	13528	1,548279588	1	0,50750152	45,43667073
GOTERM_BP_FAT	GO:0006639~acylglycerol metabolic process	6	0,078125	0,03392935	APOC3, APOH, APOC1, DGKK, CAT, PCK1	501	49	13528	3,306366858	1	0,506349638	45,59967908
GOTERM_BP_FAT	GO:0009896~positive regulation of catabolic process	6	0,078125	0,03392935	PPARA, MLXIPL, ITCH, SH3D19, ANGPTL3, INSR	501	49	13528	3,306366858	1	0,506349638	45,59967908

GOTERM_CC_FAT	GO:0000779~condensed chromosome, centromeric region	7	0,09114583	0,03395546	SPC24, KIF2C, NDE1, CENPM, CENPA, BUB1, NUP37	471	66	12782	2,878273178	0,99999873	0,250881276	38,15891691
GOTERM_CC_FAT	GO:0005624~membrane fraction	41	0,53385417	0,03421237	CYP1B1, SLC6A1, PDLIM5, SYT2, PPM1A, PKMYT1, MIP, PGP, ACSL1, PGRMC1, SLC1A6, ENO3, HSD17B6, PEX13, ITCH, INSR, MPDZ, CYP2C8, TOMM40, CLIC1, ATP1A2, CYB5B, SHANK1, PLG, AMBP, CYP4A11, PSG9, NME1, SLCO1B1, DSC3, SPCS3, LRP6, PON1, ABAT, PEBP1, ADAM18, CYP4F3, UGT2B10, PON3, ABCC6, MGST2	471	809	12782	1,37535003	0,999998856	0,247998994	38,38732673
GOTERM_CC_FAT	GO:0034361~very-low-density lipoprotein particle	4	0,05208333	0,03537293	APOC3, APOH, APOC1, PCYOX1	471	20	12782	5,427600849	0,999999287	0,250871388	39,40940673
GOTERM_CC_FAT	GO:0034385~triglyceride-rich lipoprotein particle	4	0,05208333	0,03537293	APOC3, APOH, APOC1, PCYOX1	471	20	12782	5,427600849	0,999999287	0,250871388	39,40940673
GOTERM_MF_FAT	GO:0004540~ribonuclease activity	7	0,09114583	0,03565245	PAN2, AZGP1, RNASE4, EXOSC3, TSEN2, RNASEH2A, POP7	484	66	12983	2,845010018	1	0,525946795	42,9414712
GOTERM_MF_FAT	GO:0004364~glutathione transferase activity	4	0,05208333	0,03643878	GSTA1, GSTZ1, GSTO1, MGST2	484	20	12983	5,364876033	1	0,525282976	43,65633011
GOTERM_BP_FAT	GO:0005996~monosaccharide metabolic process	15	0,1953125	0,03644624	RBP4, PFKFB4, GNE, LDHAL6A, SLC37A4, PRKAG2, GYG1, PCK2, PCK1, G6PD, SLC35D1, PGM1, ST3GAL6, GYS2, ENO3	501	222	13528	1,82445919	1	0,529097653	48,04590045
GOTERM_BP_FAT	GO:0006638~neutral lipid metabolic process	6	0,078125	0,03659851	APOC3, APOH, APOC1, DGKK, CAT, PCK1	501	50	13528	3,240239521	1	0,527733088	48,19051015
GOTERM_CC_FAT	GO:0000228~nuclear chromosome	12	0,15625	0,0368695	H1FNT, ACD, HDAC2, PIF1, TRIM28, BUB1, SIRT6, BIRC5, POLA2, CBX1, RCC1, SUV39H2	471	162	12782	2,010222537	0,999999613	0,25567063	40,70418906
GOTERM_BP_FAT	GO:0042254~ribosome biogenesis	10	0,13020833	0,03694143	DCAF13, PA2G4, NPM1, WDR12, EXOSC3, RPL5, RRP9, NOP56, FBL, MRTO4	501	122	13528	2,213278361	1	0,528254365	48,51480557
GOTERM_BP_FAT	GO:0044270~nitrogen compound catabolic process	7	0,09114583	0,03698829	AMBP, TST, ASPDH, ALDH6A1, NUDT1, NT5C, ABCC6	501	67	13528	2,821104061	1	0,525890047	48,55896958
GOTERM_CC_FAT	GO:0005813~centrosome	15	0,1953125	0,03738314	FAM110A, CETN1, BIRC5, PCK1, CDC25B, CCNB1, NDE1, CDC45, G6PD, SAC3D1, NME1, NPM1, MAPRE1, RUVBL1, KIF2A	471	224	12782	1,81727707	0,999999686	0,254419842	41,14261443
GOTERM_CC_FAT	GO:0031301~integral to organelle membrane	10	0,13020833	0,03752102	SLC35D1, L2HGDH, SLC37A4, ST3GAL6, ETFDH, PIGU, TOMM40, PEX13, COX18, EDEM1	471	123	12782	2,206341809	0,999999703	0,251009677	41,2597916
GOTERM_MF_FAT	GO:0008233~peptidase activity	31	0,40364583	0,03796341	CNDP1, MASP1, QPCTL, TFR2, MST1, ENPEP, C1S, MMP3, DDI2, LPA, LONP2, KLKB1, PROZ, USP38, CFI, PCSK6, KLK15, F11, CPA6, KLK5, PLG, PROC, CTSO, CARD18, F2, SPCS3, USP47, C1RL, ADAM18, CPB2, ASPRV1	484	574	12983	1,448703458	1	0,531750905	45,01858531
GOTERM_BP_FAT	GO:0006662~glycerol ether metabolic process	6	0,078125	0,03939321	APOC3, APOH, APOC1, DGKK, CAT, PCK1	501	51	13528	3,176705413	1	0,545956277	50,7782156
GOTERM_BP_FAT	GO:0002673~regulation of acute inflammatory response	4	0,05208333	0,04070493	MASP1, C3, KLKB1, SERPING1	501	21	13528	5,143237335	1	0,555154557	51,95028335
GOTERM_MF_FAT	GO:0004175~endopeptidase activity	22	0,28645833	0,04102357	F11, MASP1, KLK5, MST1, C1S, MMP3, PLG, PROC, DDI2, LPA, LONP2, CARD18, CTSO, KLKB1, F2, PROZ, C1RL, ADAM18, CFI, PCSK6, KLK15, ASPRV1	484	375	12983	1,57369697	1	0,55181585	47,66036869
GOTERM_BP_FAT	GO:0006979~response to oxidative stress	12	0,15625	0,04106216	EGFR, PYCR1, MSRA, G6PD, NUDT1, CLU, ETFDH, DGKK, PEBP1, CAT, TAT, SRXN1	501	164	13528	1,975755805	1	0,555565575	52,26488687
GOTERM_BP_FAT	GO:0031638~zymogen activation	3	0,0390625	0,04131454	F11, KLKB1, APOH	501	9	13528	9,000665336	1	0,555038063	52,48598276
GOTERM_MF_FAT	GO:0008483~transaminase activity	4	0,05208333	0,04137173	AADAT, ABAT, AGXT, TAT	484	21	12983	5,109405746	1	0,54684406	47,95328467
GOTERM_MF_FAT	GO:0000049~tRNA binding	4	0,05208333	0,04137173	TRMU, XPO5, SEPSECS, SSB	484	21	12983	5,109405746	1	0,54684406	47,95328467
GOTERM_MF_FAT	GO:0016840~carbon-nitrogen lyase activity	3	0,0390625	0,04180837	SRR, FTCD, ADSL	484	9	12983	8,941460055	1	0,542812277	48,31847906
GOTERM_BP_FAT	GO:0009108~coenzyme biosynthetic process	7	0,09114583	0,04181715	MTHFD1, ASPDH, DBT, MLYCD, PANK1, MTHFD1L, COQ5	501	69	13528	2,739332928	1	0,556728497	52,92341099
GOTERM_BP_FAT	GO:0031099~regeneration	7	0,09114583	0,04181715	CCNB1, SERPINA10, ATIC, APOH, ENO3, RTN4RL2, PLG	501	69	13528	2,739332928	1	0,556728497	52,92341099
GOTERM_MF_FAT	GO:0050661~NADP or NADPH binding	5	0,06510417	0,04357142	ASPDH, G6PD, TXNRD1, CBR4, CAT	484	36	12983	3,725608356	1	0,550240098	49,76881088
GOTERM_CC_FAT	GO:0005819~spindle	11	0,14322917	0,04477392	CDCA8, NDE1, RCC2, SAC3D1, NPM1, BUB1, BIRC5, CETN1, CDC20, CBX1, MAPRE1	471	147	12782	2,030735012	0,999999985	0,287991167	47,12715356
GOTERM_BP_FAT	GO:0030162~regulation of proteolysis	6	0,078125	0,04536273	HDAC2, MASP1, KLKB1, TAF9, SERPING1, SH3D19	501	53	13528	3,056829737	1	0,584170814	55,90297929
GOTERM_BP_FAT	GO:0018904~organic ether metabolic process	6	0,078125	0,04536273	APOC3, APOH, APOC1, DGKK, CAT, PCK1	501	53	13528	3,056829737	1	0,584170814	55,90297929
GOTERM_BP_FAT	GO:0006333~chromatin assembly or disassembly	10	0,13020833	0,04581925	TSPY3, SET, CENPA, NPM1, NAP1L1, CBX1, H2BFWT, HMGA1, TSPY10, SUV39H2	501	127	13528	2,126141418	1	0,585157519	56,27343481
GOTERM_BP_FAT	GO:0043488~regulation of mRNA stability	4	0,05208333	0,04587831	IGF2BP1, PABPC1, YBX1, YBX2	501	22	13528	4,90945382	1	0,582905578	56,32113853
GOTERM_BP_FAT	GO:0006476~protein amino acid deacetylation	4	0,05208333	0,04587831	HDAC2, SIRT6, HDAC11, SIRT3	501	22	13528	4,90945382	1	0,582905578	56,32113853
GOTERM_BP_FAT	GO:0046942~carboxylic acid transport	11	0,14322917	0,04613771	MIP, PPARA, SLC38A4, SLC13A5, SLC25A4, SLC6A1, SLC1A6, AGXT, SLC43A1, SLC25A15, AKR1C1	501	147	13528	2,020557524	1	0,582299527	56,53011013
GOTERM_BP_FAT	GO:0046364~monosaccharide biosynthetic process	5	0,06510417	0,04654665	RBP4, G6PD, PGM1, PCK2, PCK1	501	37	13528	3,648918379	1	0,582903787	56,85762813
GOTERM_CC_FAT	GO:0005815~microtubule organizing center	16	0,20833333	0,04715067	FAM110A, CETN1, BIRC5, PCK1, CDC25B, CCNB1, NDE1, CDC45, G6PD, SAC3D1, NME1, NPM1, BUB1, MAPRE1, RUVBL1, KIF2A	471	253	12782	1,716237423	0,999999994	0,296372147	48,92827579
GOTERM_MF_FAT	GO:0004869~cysteine-type endopeptidase inhibitor activity	5	0,06510417	0,04747238	KNG1, CST8, CARD18, BIRC5, PTTG1	484	37	12983	3,624916239	1	0,574364852	52,8436356
GOTERM_BP_FAT	GO:0015849~organic acid transport	11	0,14322917	0,04792752	MIP, PPARA, SLC38A4, SLC13A5, SLC25A4, SLC6A1, SLC1A6, AGXT, SLC43A1, SLC25A15, AKR1C1	501	148	13528	2,006905109	1	0,591167796	57,94645761
GOTERM_BP_FAT	GO:0043279~response to alkaloid	6	0,078125	0,0485388	HDAC2, SLC6A1, SRR, ALDH2, ABAT, GHR	501	54	13528	3,000221779	1	0,59325989	58,42013474

Table S6. GSEA results between patients with low and high risk score in HCC using c5 reference gene sets.

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
GO_MONOOXYGENASE_ACTIVITY	GO_MONOOXYGENASE_ACTIVITY	Details ...	91	-0,64725167	-2,2339163	0	0,01850588	0,015	2682	tags=52%, list=15%, signal=61%
GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	GO_MONOCARBOXYLIC_ACID_CATABOLIC_PROCESS	Details ...	95	-0,76393163	-2,2128446	0	0,01910473	0,026	1294	tags=60%, list=7%, signal=64%
GO_ORGANIC_ACID_CATABOLIC_PROCESS	GO_ORGANIC_ACID_CATABOLIC_PROCESS	Details ...	199	-0,69650483	-2,1954443	0	0,01682339	0,029	2373	tags=63%, list=13%, signal=72%
GO_LIPID_OXIDATION	GO_LIPID_OXIDATION	Details ...	70	-0,7244144	-2,1836228	0	0,0145474	0,031	1475	tags=53%, list=8%, signal=57%
GO_SMALL_MOLECULE_CATABOLIC_PROCESS	GO_SMALL_MOLECULE_CATABOLIC_PROCESS	Details ...	313	-0,5922846	-2,1785884	0	0,01253337	0,033	2441	tags=50%, list=14%, signal=57%
GO_ACYLGLYCEROL_HOMEOSTASIS	GO_ACYLGLYCEROL_HOMEOSTASIS	Details ...	28	-0,77552307	-2,1676342	0	0,01281307	0,038	1266	tags=54%, list=7%, signal=58%
GO_PROTEIN_ACTIVATION_CASCADE	GO_PROTEIN_ACTIVATION_CASCADE	Details ...	68	-0,76253724	-2,1669734	0	0,01108546	0,039	1411	tags=56%, list=8%, signal=60%
GO_FATTY_ACID_CATABOLIC_PROCESS	GO_FATTY_ACID_CATABOLIC_PROCESS	Details ...	73	-0,75551295	-2,165033	0	0,01011865	0,042	1475	tags=59%, list=8%, signal=64%
GO_POSITIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	Details ...	23	-0,70050496	-2,1517339	0	0,01217316	0,055	1364	tags=30%, list=8%, signal=33%
GO_FATTY_ACID_BETA_OXIDATION	GO_FATTY_ACID_BETA_OXIDATION	Details ...	51	-0,75201035	-2,1321826	0	0,01744607	0,082	1294	tags=57%, list=7%, signal=61%
GO_PROTEIN_LIPID_COMPLEX	GO_PROTEIN_LIPID_COMPLEX	Details ...	39	-0,71502864	-2,130173	0	0,01655827	0,084	2400	tags=62%, list=14%, signal=71%
GO_FATTY_ACID_METABOLIC_PROCESS	GO_FATTY_ACID_METABOLIC_PROCESS	Details ...	280	-0,5314531	-2,1206534	0	0,01784658	0,094	2483	tags=41%, list=14%, signal=47%
GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	GO_CELLULAR_AMINO_ACID_CATABOLIC_PROCESS	Details ...	107	-0,69132376	-2,1089823	0	0,01982443	0,108	2441	tags=68%, list=14%, signal=79%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_REDUCED_FLAVIN_OR_FLAVOPROTEIN_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	Details ...	25	-0,76700807	-2,0982666	0	0,02219645	0,123	2263	tags=60%, list=13%, signal=69%
GO_TETRAPYRROLE_BINDING	GO_TETRAPYRROLE_BINDING	Details ...	126	-0,54693145	-2,0964603	0	0,02138869	0,128	2682	tags=40%, list=15%, signal=47%
GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	GO_MONOCARBOXYLIC_ACID_METABOLIC_PROCESS	Details ...	477	-0,50842535	-2,0903687	0	0,02225787	0,139	2762	tags=41%, list=16%, signal=48%
GO_COMPLEMENT_ACTIVATION	GO_COMPLEMENT_ACTIVATION	Details ...	46	-0,7581798	-2,0812724	0	0,02501534	0,163	1411	tags=52%, list=8%, signal=57%
GO_REGULATION_OF_CHOLESTEROL_METABOLIC_PROCESS	GO_REGULATION_OF_CHOLESTEROL_METABOLIC_PROCESS	Details ...	22	-0,7402332	-2,0667927	0	0,02982108	0,2	1364	tags=45%, list=8%, signal=49%
GO_PYRIDOXAL_PHOSPHATE_BINDING	GO_PYRIDOXAL_PHOSPHATE_BINDING	Details ...	42	-0,69297236	-2,0660295	0	0,02828914	0,201	3031	tags=67%, list=17%, signal=80%
GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE	Details ...	26	-0,79809	-2,0649266	0	0,02710226	0,202	1798	tags=65%, list=10%, signal=73%
GO_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	GO_ORGANIC_HYDROXY_COMPOUND_CATABOLIC_PROCESS	Details ...	71	-0,5461234	-2,0633392	0,00195313	0,0263302	0,206	2682	tags=46%, list=15%, signal=55%
GO_ANDROGEN_METABOLIC_PROCESS	GO_ANDROGEN_METABOLIC_PROCESS	Details ...	30	-0,66304314	-2,0591185	0	0,02640564	0,217	1873	tags=43%, list=11%, signal=48%
GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	GO_ALPHA_AMINO_ACID_CATABOLIC_PROCESS	Details ...	90	-0,68360925	-2,0535429	0,00200803	0,02807486	0,237	2441	tags=67%, list=14%, signal=77%
GO_STEROID_HYDROXYLASE_ACTIVITY	GO_STEROID_HYDROXYLASE_ACTIVITY	Details ...	30	-0,7292214	-2,049613	0	0,0285771	0,247	2682	tags=67%, list=15%, signal=78%
GO_BENZENE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_BENZENE_CONTAINING_COMPOUND_METABOLIC_PROCESS	Details ...	22	-0,72456264	-2,0485537	0	0,02786365	0,249	1975	tags=45%, list=11%, signal=51%
GO_REGULATION_OF_PROTEIN_MATURATION	GO_REGULATION_OF_PROTEIN_MATURATION	Details ...	76	-0,59423524	-2,0432937	0	0,02854943	0,26	2417	tags=43%, list=14%, signal=50%
GO_LIPID_HOMEOSTASIS	GO_LIPID_HOMEOSTASIS	Details ...	105	-0,56605726	-2,040697	0	0,0284505	0,271	1737	tags=40%, list=10%, signal=44%
GO_OXYGEN_BINDING	GO_OXYGEN_BINDING	Details ...	44	-0,673479	-2,039156	0	0,02812789	0,275	2303	tags=48%, list=13%, signal=55%
GO_SULFUR_COMPOUND_BINDING	GO_SULFUR_COMPOUND_BINDING	Details ...	222	-0,5012744	-2,0320785	0	0,02933644	0,291	2975	tags=38%, list=17%, signal=45%
GO_STEROID_METABOLIC_PROCESS	GO_STEROID_METABOLIC_PROCESS	Details ...	227	-0,5137845	-2,0318122	0,00197239	0,02841153	0,291	1873	tags=33%, list=11%, signal=37%
GO_POSITIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	Details ...	32	-0,6376851	-2,0275838	0	0,02903715	0,306	1294	tags=38%, list=7%, signal=40%
GO_CELLULAR_LIPID_CATABOLIC_PROCESS	GO_CELLULAR_LIPID_CATABOLIC_PROCESS	Details ...	146	-0,5586912	-2,02324	0	0,02998673	0,315	2410	tags=46%, list=14%, signal=53%
GO_COFACTOR_BINDING	GO_COFACTOR_BINDING	Details ...	245	-0,55063194	-2,0229442	0	0,02926724	0,316	2644	tags=49%, list=15%, signal=57%
GO_2_OXOGLUTARATE_METABOLIC_PROCESS	GO_2_OXOGLUTARATE_METABOLIC_PROCESS	Details ...	19	-0,8030974	-2,0224195	0	0,02881737	0,321	2644	tags=79%, list=15%, signal=93%
GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	GO_ORGANONITROGEN_COMPOUND_CATABOLIC_PROCESS	Details ...	322	-0,48551187	-2,0113807	0	0,03222359	0,355	2736	tags=42%, list=15%, signal=49%
GO_VESICLE_LUMEN	GO_VESICLE_LUMEN	Details ...	102	-0,55837	-2,0049307	0,00196464	0,03489634	0,383	3072	tags=50%, list=17%, signal=60%
GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	GO_RESPONSE_TO_XENOBIOTIC_STIMULUS	Details ...	101	-0,58690315	-2,0047896	0	0,03403035	0,383	2345	tags=48%, list=13%, signal=54%
GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	GO_BRANCHED_CHAIN_AMINO_ACID_METABOLIC_PROCESS	Details ...	23	-0,8154927	-2,002992	0	0,03385229	0,387	2352	tags=87%, list=13%, signal=100%
GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING	GO_FLAVIN_ADENINE_DINUCLEOTIDE_BINDING	Details ...	73	-0,6085079	-1,999715	0	0,03475875	0,398	1899	tags=48%, list=11%, signal=53%
GO_STEROL_TRANSPORT	GO_STEROL_TRANSPORT	Details ...	49	-0,569209	-1,9970477	0	0,03482107	0,406	1477	tags=35%, list=8%, signal=38%
GO_BLOOD_MICROPARTICLE	GO_BLOOD_MICROPARTICLE	Details ...	113	-0,5777138	-1,9928979	0	0,03553536	0,418	1411	tags=39%, list=8%, signal=42%
GO_ACYL_COA_DEHYDROGENASE_ACTIVITY	GO_ACYL_COA_DEHYDROGENASE_ACTIVITY	Details ...	17	-0,8532674	-1,9906337	0	0,03561897	0,429	1180	tags=71%, list=7%, signal=76%
GO_BILE_ACID_METABOLIC_PROCESS	GO_BILE_ACID_METABOLIC_PROCESS	Details ...	35	-0,6726724	-1,9899396	0,00410678	0,03505693	0,431	1580	tags=51%, list=9%, signal=56%
GO_MICROBODY	GO_MICROBODY	Details ...	125	-0,587952	-1,9897792	0	0,03429188	0,431	2826	tags=51%, list=16%, signal=61%
GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	GO_REGULATION_OF_HUMORAL_IMMUNE_RESPONSE	Details ...	47	-0,6361168	-1,9819348	0,00596422	0,03703229	0,456	2417	tags=43%, list=14%, signal=49%
GO_MICROBODY_PART	GO_MICROBODY_PART	Details ...	92	-0,6210376	-1,9817057	0	0,03630292	0,456	2826	tags=54%, list=16%, signal=64%
GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_INDOLE_CONTAINING_COMPOUND_METABOLIC_PROCESS	Details ...	24	-0,6312164	-1,9790218	0	0,03651165	0,461	3367	tags=58%, list=19%, signal=72%
GO_SECRETORY_GRANULE_LUMEN	GO_SECRETORY_GRANULE_LUMEN	Details ...	81	-0,56199	-1,9762166	0	0,03694793	0,469	3072	tags=49%, list=17%, signal=60%
GO_BLOOD_COAGULATION_FIBRIN_CLOT_FORMATION	GO_BLOOD_COAGULATION_FIBRIN_CLOT_FORMATION	Details ...	24	-0,7710755	-1,9753087	0	0,03683236	0,47	1894	tags=67%, list=11%, signal=75%
GO_FATTY_ACYL_COA_BINDING	GO_FATTY_ACYL_COA_BINDING	Details ...	31	-0,7322581	-1,9716842	0	0,03788658	0,485	1212	tags=61%, list=7%, signal=66%

GO_CATECHOLAMINE_METABOLIC_PROCESS	GO_CATECHOLAMINE_METABOLIC_PROCESS	Details ...	39	-0,5567574	-1,9709811	0	0,0374672	0,489	1828	tags=36%, list=10%, signal=40%
GO_REGULATION_OF_STEROID_METABOLIC_PROCESS	GO_REGULATION_OF_STEROID_METABOLIC_PROCESS	Details ...	73	-0,5059383	-1,9697281	0	0,03727556	0,493	1364	tags=26%, list=8%, signal=28%
GO_REVERSE_CHOLESTEROL_TRANSPORT	GO_REVERSE_CHOLESTEROL_TRANSPORT	Details ...	17	-0,7687011	-1,9679462	0	0,03750481	0,499	1477	tags=53%, list=8%, signal=58%
GO_LIPID_CATABOLIC_PROCESS	GO_LIPID_CATABOLIC_PROCESS	Details ...	233	-0,47538042	-1,9616017	0	0,04021562	0,523	1990	tags=34%, list=11%, signal=38%
GO_IRON_ION_BINDING	GO_IRON_ION_BINDING	Details ...	145	-0,49499094	-1,9606515	0	0,03984975	0,525	2804	tags=40%, list=16%, signal=47%
GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	GO_REGULATION_OF_LIPOPROTEIN_LIPASE_ACTIVITY	Details ...	15	-0,79908955	-1,9605287	0	0,03922771	0,527	1219	tags=60%, list=7%, signal=64%
GO_GLUCAN_METABOLIC_PROCESS	GO_GLUCAN_METABOLIC_PROCESS	Details ...	56	-0,5397104	-1,9595233	0	0,03882796	0,528	1280	tags=30%, list=7%, signal=33%
GO_STEROID_BINDING	GO_STEROID_BINDING	Details ...	88	-0,46814862	-1,9551784	0	0,04055278	0,54	2241	tags=32%, list=13%, signal=36%
GO_ARACHIDONIC_ACID_MONOOXYGENASE_ACTIVITY	GO_ARACHIDONIC_ACID_MONOOXYGENASE_ACTIVITY	Details ...	15	-0,85052043	-1,9542285	0	0,04041125	0,545	2263	tags=87%, list=13%, signal=99%
GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	GO_PRIMARY_ALCOHOL_METABOLIC_PROCESS	Details ...	46	-0,60863495	-1,9536359	0,00391389	0,040263	0,548	2159	tags=46%, list=12%, signal=52%
GO_BILE_ACID_AND_BILE_SALT_TRANSPORT	GO_BILE_ACID_AND_BILE_SALT_TRANSPORT	Details ...	29	-0,6515906	-1,9513642	0,00207469	0,04064262	0,556	1521	tags=48%, list=9%, signal=53%
GO_REGULATION_OF_PROTEIN_ACTIVATION_CASCADE	GO_REGULATION_OF_PROTEIN_ACTIVATION_CASCADE	Details ...	34	-0,7480471	-1,9511274	0,00408998	0,04009021	0,556	2417	tags=62%, list=14%, signal=71%
GO_REGULATION_OF_FATTY_ACID_OXIDATION	GO_REGULATION_OF_FATTY_ACID_OXIDATION	Details ...	27	-0,6462782	-1,9456749	0,00411523	0,04231639	0,574	1597	tags=48%, list=9%, signal=53%
GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	GO_HUMORAL_IMMUNE_RESPONSE_MEDIATED_BY_CIRCULATING_IMMUNOGLOBULIN	Details ...	38	-0,68730855	-1,9448819	0,0122449	0,04195672	0,575	1223	tags=42%, list=7%, signal=45%
GO_DRUG_METABOLIC_PROCESS	GO_DRUG_METABOLIC_PROCESS	Details ...	38	-0,6562659	-1,9442074	0,00208333	0,04169502	0,576	1901	tags=58%, list=11%, signal=65%
GO_EPOXYGENASE_P450_PATHWAY	GO_EPOXYGENASE_P450_PATHWAY	Details ...	18	-0,8327286	-1,9436226	0	0,04131101	0,577	2263	tags=78%, list=13%, signal=89%
GO_VITAMIN_BINDING	GO_VITAMIN_BINDING	Details ...	70	-0,5162863	-1,9389296	0	0,04279309	0,592	3044	tags=46%, list=17%, signal=55%
GO_NEGATIVE_REGULATION_OF_WOUND_HEALING	GO_NEGATIVE_REGULATION_OF_WOUND_HEALING	Details ...	58	-0,5688087	-1,938656	0	0,04227182	0,592	1844	tags=43%, list=10%, signal=48%
GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	GO_BLOOD_COAGULATION_INTRINSIC_PATHWAY	Details ...	17	-0,8047923	-1,9385667	0	0,04165919	0,592	887	tags=65%, list=5%, signal=68%
GO_BILE_ACID_BIOSYNTHETIC_PROCESS	GO_BILE_ACID_BIOSYNTHETIC_PROCESS	Details ...	20	-0,7755732	-1,9375606	0,00204918	0,04150002	0,592	1580	tags=65%, list=9%, signal=71%
GO_MICROBODY_LUMEN	GO_MICROBODY_LUMEN	Details ...	45	-0,6975984	-1,936968	0,00204499	0,04114826	0,594	2762	tags=62%, list=16%, signal=74%
GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	GO_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	Details ...	33	-0,63109	-1,9351121	0,00203666	0,04152201	0,603	2623	tags=48%, list=15%, signal=57%
GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_REMODELING	GO_HIGH_DENSITY_LIPOPROTEIN_PARTICLE_REMODELING	Details ...	15	-0,7766948	-1,9347178	0	0,04106272	0,604	1477	tags=53%, list=8%, signal=58%
GO_COENZYME_BINDING	GO_COENZYME_BINDING	Details ...	172	-0,5353736	-1,9324707	0,00394477	0,0416062	0,617	1740	tags=40%, list=10%, signal=43%
GO_POSITIVE_REGULATION_OF_PROTEIN_MATURATION	GO_POSITIVE_REGULATION_OF_PROTEIN_MATURATION	Details ...	16	-0,7261733	-1,9305393	0	0,04209302	0,62	2385	tags=56%, list=14%, signal=65%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN	Details ...	141	-0,47918147	-1,9283249	0,00194932	0,04237021	0,63	2738	tags=39%, list=15%, signal=46%
GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	GO_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	Details ...	27	-0,62434715	-1,9263738	0	0,04286051	0,636	2465	tags=41%, list=14%, signal=47%
GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	GO_ORGANIC_HYDROXY_COMPOUND_METABOLIC_PROCESS	Details ...	464	-0,41999725	-1,9216862	0	0,04455196	0,651	2687	tags=32%, list=15%, signal=37%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_NAD_P_H_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PAIRED_DONORS_WITH_INCORPORATION_OR_REDUCTION_OF_MOLECULAR_OXYGEN_NAD_P_H_AS_ONE_DONOR_AND_INCORPORATION_OF_ONE_ATOM_OF_OXYGEN	Details ...	36	-0,6714395	-1,9216734	0,0020202	0,04398801	0,651	1580	tags=53%, list=9%, signal=58%
GO_GLYOXYLATE_METABOLIC_PROCESS	GO_GLYOXYLATE_METABOLIC_PROCESS	Details ...	28	-0,72777784	-1,9176809	0	0,04546981	0,662	2694	tags=68%, list=15%, signal=80%
GO_TRIGLYCERIDE_RICH_LIPOPROTEIN_PARTICLE	GO_TRIGLYCERIDE_RICH_LIPOPROTEIN_PARTICLE	Details ...	19	-0,72229445	-1,9160188	0	0,04568736	0,667	1364	tags=47%, list=8%, signal=51%
GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE	GO_FATTY_ACID_BETA_OXIDATION_USING_ACYL_COA_DEHYDROGENASE	Details ...	18	-0,8426442	-1,9141173	0	0,04590538	0,669	1180	tags=72%, list=7%, signal=77%
GO_STEROL_TRANSPORTER_ACTIVITY	GO_STEROL_TRANSPORTER_ACTIVITY	Details ...	17	-0,6945631	-1,9117035	0	0,04647711	0,676	1364	tags=53%, list=8%, signal=57%
GO_STEROID_CATABOLIC_PROCESS	GO_STEROID_CATABOLIC_PROCESS	Details ...	24	-0,6155727	-1,9116141	0,00203666	0,04598664	0,676	1791	tags=46%, list=10%, signal=51%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS	Details ...	56	-0,64276344	-1,9114913	0,0059761	0,04549256	0,676	2452	tags=54%, list=14%, signal=62%
GO_IRON_ION_HOMEOSTASIS	GO_IRON_ION_HOMEOSTASIS	Details ...	65	-0,5175793	-1,9074801	0,002	0,04728421	0,692	3702	tags=52%, list=21%, signal=66%
GO_NEGATIVE_REGULATION_OF_COAGULATION	GO_NEGATIVE_REGULATION_OF_COAGULATION	Details ...	48	-0,5983845	-1,9059997	0,00195695	0,04760283	0,698	1816	tags=48%, list=10%, signal=53%
GO_MACROMOLECULAR_COMPLEX_REMODELING	GO_MACROMOLECULAR_COMPLEX_REMODELING	Details ...	24	-0,6794892	-1,9054792	0,00199601	0,04734677	0,7	1477	tags=42%, list=8%, signal=45%
GO_POSITIVE_REGULATION_OF_WOUND_HEALING	GO_POSITIVE_REGULATION_OF_WOUND_HEALING	Details ...	45	-0,54431427	-1,9028826	0,0020284	0,04809185	0,707	2975	tags=44%, list=17%, signal=53%
GO_ENERGY_RESERVE_METABOLIC_PROCESS	GO_ENERGY_RESERVE_METABOLIC_PROCESS	Details ...	66	-0,5064369	-1,8987234	0	0,05007699	0,721	2602	tags=35%, list=15%, signal=41%
GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	GO_ALPHA_AMINO_ACID_METABOLIC_PROCESS	Details ...	213	-0,501136	-1,8982041	0,00404858	0,04993778	0,723	2373	tags=42%, list=13%, signal=48%
GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	GO_ORGANIC_ACID_BIOSYNTHETIC_PROCESS	Details ...	248	-0,44619268	-1,8974739	0	0,04978792	0,727	2682	tags=38%, list=15%, signal=44%
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_DIFFERENTIATION	Details ...	15	-0,6695542	-1,8960267	0,00411523	0,05001893	0,731	3192	tags=53%, list=18%, signal=65%
GO_ALDEHYDE_DEHYDROGENASE_NAD_ACTIVITY	GO_ALDEHYDE_DEHYDROGENASE_NAD_ACTIVITY	Details ...	19	-0,7262572	-1,8957406	0,00206186	0,04965481	0,733	2159	tags=58%, list=12%, signal=66%
GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	Details ...	122	-0,44488233	-1,8903457	0	0,05246965	0,748	1639	tags=27%, list=9%, signal=30%
GO_PLATELET_DEGRANULATION	GO_PLATELET_DEGRANULATION	Details ...	103	-0,5054994	-1,8861799	0,00194932	0,05426304	0,755	2975	tags=41%, list=17%, signal=49%
GO_LIVER_REGENERATION	GO_LIVER_REGENERATION	Details ...	19	-0,63174254	-1,8856959	0,0021097	0,05401395	0,756	1639	tags=47%, list=9%, signal=52%
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	Details ...	31	-0,594789	-1,8848194	0,00201207	0,05397792	0,758	2975	tags=45%, list=17%, signal=54%
GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	GO_ORGANIC_HYDROXY_COMPOUND_TRANSPORT	Details ...	148	-0,44766673	-1,8827698	0	0,05449998	0,763	1735	tags=30%, list=10%, signal=33%
GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	GO_CELLULAR_CARBOHYDRATE_CATABOLIC_PROCESS	Details ...	31	-0,54394305	-1,8825331	0,00403226	0,05407605	0,763	1314	tags=35%, list=7%, signal=38%

GO_NEGATIVE_REGULATION_OF_LIPASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_LIPASE_ACTIVITY	Details ...	15	-0,6606955	-1,8816273	0	0,05405796	0,765	941	tags=47%, list=5%, signal=49%
GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS	GO_DICARBOXYLIC_ACID_METABOLIC_PROCESS	Details ...	97	-0,539	-1,8749225	0,00395257	0,05728421	0,784	2849	tags=48%, list=16%, signal=57%
GO_AMINO_ACID_BETAINE_METABOLIC_PROCESS	GO_AMINO_ACID_BETAINE_METABOLIC_PROCESS	Details ...	18	-0,7674527	-1,8739604	0,00209205	0,05728946	0,786	2762	tags=83%, list=16%, signal=99%
GO_HYDRO_LYASE_ACTIVITY	GO_HYDRO_LYASE_ACTIVITY	Details ...	42	-0,58687574	-1,8688825	0,00206612	0,05981439	0,806	2067	tags=48%, list=12%, signal=54%
GO_MONOCARBOXYLIC_ACID_TRANSPORT	GO_MONOCARBOXYLIC_ACID_TRANSPORT	Details ...	114	-0,47020394	-1,8616612	0	0,06406587	0,817	3604	tags=46%, list=20%, signal=57%
GO_BASAL_PLASMA_MEMBRANE	GO_BASAL_PLASMA_MEMBRANE	Details ...	31	-0,58996654	-1,860667	0,00387597	0,06416673	0,819	1916	tags=29%, list=11%, signal=33%
GO_CELLULAR_HORMONE_METABOLIC_PROCESS	GO_CELLULAR_HORMONE_METABOLIC_PROCESS	Details ...	100	-0,4956057	-1,859022	0,00199203	0,06476727	0,825	2159	tags=32%, list=12%, signal=36%
GO_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	GO_POSITIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	Details ...	62	-0,47880775	-1,8574194	0	0,06525222	0,829	1633	tags=29%, list=9%, signal=32%
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_NITROGENOUS_GROUPS	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_NITROGENOUS_GROUPS	Details ...	18	-0,71023256	-1,8535339	0,004	0,06726842	0,836	2373	tags=67%, list=13%, signal=77%
GO_REGULATION_OF_COAGULATION	GO_REGULATION_OF_COAGULATION	Details ...	86	-0,50291145	-1,8465102	0,0039604	0,07159423	0,855	2451	tags=40%, list=14%, signal=46%
GO_SIGNAL_PEPTIDE_PROCESSING	GO_SIGNAL_PEPTIDE_PROCESSING	Details ...	23	-0,6630223	-1,8457985	0,00604839	0,07141288	0,855	2050	tags=52%, list=12%, signal=59%
GO_AMINE_CATABOLIC_PROCESS	GO_AMINE_CATABOLIC_PROCESS	Details ...	20	-0,7020396	-1,8455808	0	0,07095297	0,855	2388	tags=70%, list=14%, signal=81%
GO_POSITIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	Details ...	25	-0,5857494	-1,8419329	0,00399202	0,07302118	0,86	1990	tags=44%, list=11%, signal=50%
GO_ALCOHOL_CATABOLIC_PROCESS	GO_ALCOHOL_CATABOLIC_PROCESS	Details ...	57	-0,474049	-1,8405263	0,00394477	0,07343855	0,865	2410	tags=39%, list=14%, signal=45%
GO_REGULATION_OF_STEROL_TRANSPORT	GO_REGULATION_OF_STEROL_TRANSPORT	Details ...	38	-0,55839413	-1,8394755	0,00396825	0,07344633	0,867	1495	tags=37%, list=8%, signal=40%
GO_POLYSACCHARIDE_BINDING	GO_POLYSACCHARIDE_BINDING	Details ...	20	-0,61036575	-1,8330517	0,00589391	0,07772277	0,875	2289	tags=50%, list=13%, signal=57%
GO_STEROID_BIOSYNTHETIC_PROCESS	GO_STEROID_BIOSYNTHETIC_PROCESS	Details ...	107	-0,50659555	-1,8304715	0,00604839	0,07923202	0,883	1627	tags=32%, list=9%, signal=35%
GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	GO_SULFUR_AMINO_ACID_METABOLIC_PROCESS	Details ...	40	-0,557247	-1,8266537	0,00396825	0,081836	0,891	1563	tags=38%, list=9%, signal=41%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS	Details ...	43	-0,6018674	-1,8235689	0,00399202	0,08366089	0,898	2441	tags=51%, list=14%, signal=59%
GO_ENDOTHELIUM_DEVELOPMENT	GO_ENDOTHELIUM_DEVELOPMENT	Details ...	88	-0,4970302	-1,8233801	0,01162791	0,08308778	0,898	2840	tags=40%, list=16%, signal=47%
GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	GO_REGULATION_OF_LIPID_CATABOLIC_PROCESS	Details ...	51	-0,5046747	-1,8212367	0,00409836	0,08393434	0,901	2265	tags=37%, list=13%, signal=43%
GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	GO_POSITIVE_REGULATION_OF_STEROL_TRANSPORT	Details ...	17	-0,6313739	-1,8204528	0,00193424	0,08383671	0,901	3412	tags=53%, list=19%, signal=66%
GO_AROMATIC_AMINO_ACID_FAMILY_METABOLIC_PROCESS	GO_AROMATIC_AMINO_ACID_FAMILY_METABOLIC_PROCESS	Details ...	27	-0,6365514	-1,8193406	0,00596422	0,08408084	0,903	1975	tags=56%, list=11%, signal=62%
GO_BROWN_FAT_CELL_DIFFERENTIATION	GO_BROWN_FAT_CELL_DIFFERENTIATION	Details ...	27	-0,5729959	-1,8192885	0	0,0834606	0,903	3645	tags=56%, list=21%, signal=70%
GO_LIPID_MODIFICATION	GO_LIPID_MODIFICATION	Details ...	195	-0,4250519	-1,8184413	0	0,08348152	0,904	1687	tags=26%, list=10%, signal=28%
GO_QUINONE_BINDING	GO_QUINONE_BINDING	Details ...	15	-0,69184345	-1,8165408	0,002	0,08439871	0,908	2463	tags=53%, list=14%, signal=62%
GO_POSITIVE_REGULATION_OF_COAGULATION	GO_POSITIVE_REGULATION_OF_COAGULATION	Details ...	24	-0,6308925	-1,8148237	0,00826446	0,0850656	0,909	3482	tags=67%, list=20%, signal=83%
GO_LYASE_ACTIVITY	GO_LYASE_ACTIVITY	Details ...	160	-0,45479304	-1,812963	0	0,085873	0,913	2763	tags=41%, list=16%, signal=48%
GO_REGULATION_OF_WOUND_HEALING	GO_REGULATION_OF_WOUND_HEALING	Details ...	121	-0,46007746	-1,81288	0	0,08525825	0,914	2451	tags=34%, list=14%, signal=39%
GO_DOPAMINE_METABOLIC_PROCESS	GO_DOPAMINE_METABOLIC_PROCESS	Details ...	23	-0,5789056	-1,8119771	0	0,08538821	0,915	1827	tags=35%, list=10%, signal=39%
GO_RETINOL_DEHYDROGENASE_ACTIVITY	GO_RETINOL_DEHYDROGENASE_ACTIVITY	Details ...	17	-0,6651796	-1,8116729	0,00377359	0,0850056	0,916	247	tags=35%, list=1%, signal=36%
GO_POSITIVE_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_TRIGLYCERIDE_METABOLIC_PROCESS	Details ...	20	-0,6817104	-1,8104653	0,00609756	0,08556841	0,917	2623	tags=55%, list=15%, signal=65%
GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_TRIGLYCERIDE_BIOSYNTHETIC_PROCESS	Details ...	17	-0,66994005	-1,8087813	0,01207244	0,08625191	0,92	2623	tags=53%, list=15%, signal=62%
GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	GO_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	Details ...	87	-0,47480303	-1,8083172	0,00194932	0,0859657	0,921	2449	tags=39%, list=14%, signal=45%
GO_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	Details ...	35	-0,5535544	-1,8082396	0,00835073	0,08537901	0,922	1212	tags=34%, list=7%, signal=37%
GO_CELLULAR_RESPONSE_TO_PH	GO_CELLULAR_RESPONSE_TO_PH	Details ...	15	-0,6284256	-1,8080517	0	0,08487389	0,922	2594	tags=53%, list=15%, signal=62%
GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	GO_STEROID_HORMONE_RECEPTOR_ACTIVITY	Details ...	58	-0,47505412	-1,8070428	0	0,08507907	0,923	2726	tags=38%, list=15%, signal=45%
GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	GO_SMALL_MOLECULE_BIOSYNTHETIC_PROCESS	Details ...	412	-0,41897294	-1,8048432	0,002	0,0863853	0,925	2504	tags=33%, list=14%, signal=38%
GO_LIPID_LOCALIZATION	GO_LIPID_LOCALIZATION	Details ...	251	-0,42159757	-1,8037466	0	0,08664539	0,927	3536	tags=40%, list=20%, signal=49%
GO_PLATELET_ALPHA_GRANULE	GO_PLATELET_ALPHA_GRANULE	Details ...	74	-0,5063972	-1,8002372	0,01764706	0,08865079	0,931	2975	tags=39%, list=17%, signal=47%
GO_HORMONE_METABOLIC_PROCESS	GO_HORMONE_METABOLIC_PROCESS	Details ...	156	-0,44072866	-1,7998334	0	0,0883358	0,931	4217	tags=41%, list=24%, signal=53%
GO_COPPER_ION_HOMEOSTASIS	GO_COPPER_ION_HOMEOSTASIS	Details ...	16	-0,59567106	-1,799367	0,00784314	0,0881116	0,931	3060	tags=50%, list=17%, signal=60%
GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	GO_ENERGY_DERIVATION_BY_OXIDATION_OF_ORGANIC_COMPOUNDS	Details ...	204	-0,5399454	-1,7989155	0,01622718	0,08792199	0,932	2766	tags=42%, list=16%, signal=49%
GO_FIBRINOLYSIS	GO_FIBRINOLYSIS	Details ...	21	-0,69292724	-1,7985109	0,00613497	0,08764146	0,932	2285	tags=67%, list=13%, signal=76%
GO_POLYSACCHARIDE_METABOLIC_PROCESS	GO_POLYSACCHARIDE_METABOLIC_PROCESS	Details ...	76	-0,45927575	-1,7969018	0,01048218	0,08845878	0,933	1596	tags=24%, list=9%, signal=26%
GO_ACID_THIOL_LIGASE_ACTIVITY	GO_ACID_THIOL_LIGASE_ACTIVITY	Details ...	19	-0,671552	-1,7968425	0,014	0,08790939	0,933	2221	tags=63%, list=13%, signal=72%
GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	Details ...	32	-0,52757454	-1,7953011	0,00199601	0,08874272	0,935	2081	tags=34%, list=12%, signal=39%
GO_FERROUS_IRON_BINDING	GO_FERROUS_IRON_BINDING	Details ...	22	-0,60287666	-1,7946297	0,00603622	0,08868232	0,935	2738	tags=45%, list=15%, signal=54%
GO_PLATELET_ALPHA_GRANULE_LUMEN	GO_PLATELET_ALPHA_GRANULE_LUMEN	Details ...	54	-0,5364289	-1,7939306	0,01581028	0,08860435	0,937	3598	tags=52%, list=20%, signal=65%
GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	GO_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	Details ...	44	-0,51018703	-1,7938521	0,00863931	0,08809668	0,937	1877	tags=36%, list=11%, signal=41%
GO_RESPONSE_TO_GLUCAGON	GO_RESPONSE_TO_GLUCAGON	Details ...	46	-0,4907027	-1,793	0,0019685	0,08814389	0,938	2802	tags=33%, list=16%, signal=39%
GO_RHYTHMIC_BEHAVIOR	GO_RHYTHMIC_BEHAVIOR	Details ...	15	-0,6241152	-1,792781	0,00571429	0,08771134	0,938	1726	tags=33%, list=10%, signal=37%
GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_LIPASE_ACTIVITY	Details ...	64	-0,46813923	-1,7923957	0,00204918	0,08746151	0,939	1947	tags=31%, list=11%, signal=35%

GO_NEUTRAL_LIPID_METABOLIC_PROCESS	GO_NEUTRAL_LIPID_METABOLIC_PROCESS	Details ...	77	-0,47656634	-1,7919419	0,0020202	0,08717705	0,939	1990	tags=38%, list=11%, signal=42%
GO_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	Details ...	122	-0,42015442	-1,7914983	0	0,08699817	0,939	1814	tags=26%, list=10%, signal=29%
GO_TRIGLYCERIDE_LIPASE_ACTIVITY	GO_TRIGLYCERIDE_LIPASE_ACTIVITY	Details ...	17	-0,6831773	-1,7899749	0,00609756	0,08749538	0,939	3809	tags=65%, list=22%, signal=82%
GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	GO_CELLULAR_AMINO_ACID_METABOLIC_PROCESS	Details ...	314	-0,45118284	-1,7897297	0,0101626	0,08721232	0,939	2373	tags=38%, list=13%, signal=43%
GO_REGULATION_OF_LIPASE_ACTIVITY	GO_REGULATION_OF_LIPASE_ACTIVITY	Details ...	81	-0,45739278	-1,7888359	0,00205339	0,08754694	0,94	1947	tags=31%, list=11%, signal=35%
GO_RESPONSE_TO_CAMP	GO_RESPONSE_TO_CAMP	Details ...	101	-0,4469512	-1,7869376	0	0,08860859	0,941	1880	tags=27%, list=11%, signal=30%
GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	GO_CATECHOLAMINE_BIOSYNTHETIC_PROCESS	Details ...	18	-0,6178347	-1,7853948	0,00773694	0,08934176	0,942	2542	tags=39%, list=14%, signal=45%
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	Details ...	37	-0,5135373	-1,7846259	0,00996016	0,08948581	0,944	3788	tags=49%, list=21%, signal=62%
GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	GO_SERINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	Details ...	39	-0,60855484	-1,7816324	0,02376238	0,09133664	0,948	3421	tags=56%, list=19%, signal=70%
GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	GO_REGULATION_OF_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	Details ...	80	-0,44305333	-1,7778456	0,00835073	0,09394229	0,95	2726	tags=36%, list=15%, signal=43%
GO_HEPARIN_BINDING	GO_HEPARIN_BINDING	Details ...	148	-0,46375543	-1,7763042	0,01338432	0,0947625	0,953	2975	tags=33%, list=17%, signal=39%
GO_ORGANIC_HYDROXY_COMPOUND_BIOSYNTHETIC_PROCESS	GO_ORGANIC_HYDROXY_COMPOUND_BIOSYNTHETIC_PROCESS	Details ...	169	-0,4297717	-1,7722924	0,00199203	0,09740865	0,955	2687	tags=31%, list=15%, signal=36%
GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	Details ...	17	-0,6082977	-1,7679873	0,00806452	0,10087777	0,958	1661	tags=47%, list=9%, signal=52%
GO_MICROBODY_MEMBRANE	GO_MICROBODY_MEMBRANE	Details ...	57	-0,52680844	-1,7669498	0,01397206	0,10132378	0,96	2826	tags=47%, list=16%, signal=56%
GO_2_IRON_2_SULFUR_CLUSTER_BINDING	GO_2_IRON_2_SULFUR_CLUSTER_BINDING	Details ...	20	-0,7153084	-1,7636684	0,00417537	0,1035068	0,961	2607	tags=60%, list=15%, signal=70%
GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	GO_MONOCARBOXYLIC_ACID_BIOSYNTHETIC_PROCESS	Details ...	157	-0,42328498	-1,7632381	0,00411523	0,10323986	0,961	2682	tags=34%, list=15%, signal=40%
GO_MUSCLE_HYPERTROPHY	GO_MUSCLE_HYPERTROPHY	Details ...	27	-0,54194015	-1,763184	0,00587084	0,10265528	0,961	1412	tags=37%, list=8%, signal=40%
GO_RESPONSE_TO_GROWTH_HORMONE	GO_RESPONSE_TO_GROWTH_HORMONE	Details ...	27	-0,55373055	-1,761642	0,00421941	0,10333195	0,964	1115	tags=33%, list=6%, signal=36%
GO_STEROL_METABOLIC_PROCESS	GO_STEROL_METABOLIC_PROCESS	Details ...	117	-0,48564547	-1,7600948	0,00606061	0,10408144	0,964	1581	tags=28%, list=9%, signal=31%
GO_AMINE_METABOLIC_PROCESS	GO_AMINE_METABOLIC_PROCESS	Details ...	124	-0,39750946	-1,7593795	0	0,10411583	0,965	2410	tags=32%, list=14%, signal=37%
GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	GO_REGULATION_OF_LIPID_METABOLIC_PROCESS	Details ...	266	-0,38416108	-1,7587813	0	0,10402779	0,966	2785	tags=30%, list=16%, signal=36%
GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	GO_NEGATIVE_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	Details ...	30	-0,51804906	-1,7582363	0,01153846	0,10399349	0,966	3951	tags=47%, list=22%, signal=60%
GO_HORMONE_BINDING	GO_HORMONE_BINDING	Details ...	54	-0,48749548	-1,7567884	0,00204499	0,10458715	0,967	1750	tags=31%, list=10%, signal=35%
GO_PLATELET_DENSE_GRANULE	GO_PLATELET_DENSE_GRANULE	Details ...	19	-0,61336046	-1,7534741	0,015625	0,10706806	0,968	1976	tags=53%, list=11%, signal=59%
GO_ELECTRON_CARRIER_ACTIVITY	GO_ELECTRON_CARRIER_ACTIVITY	Details ...	108	-0,5484259	-1,7532752	0,02615694	0,10667446	0,968	2402	tags=43%, list=14%, signal=49%
GO_TRANSCRIPTION_FACTOR_ACTIVITY_DIRECT_LIGAND_REGULATED_SEQUENCE_SPECIFIC_DNA_BINDING	GO_TRANSCRIPTION_FACTOR_ACTIVITY_DIRECT_LIGAND_REGULATED_SEQUENCE_SPECIFIC_DNA_BINDING	Details ...	46	-0,4890155	-1,7513381	0,00585938	0,10806712	0,969	2726	tags=39%, list=15%, signal=46%
GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK	GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK	Details ...	25	-0,540097	-1,7504162	0,01149425	0,10831621	0,969	2594	tags=44%, list=15%, signal=52%
GO_CGMP_METABOLIC_PROCESS	GO_CGMP_METABOLIC_PROCESS	Details ...	22	-0,578251	-1,747544	0,00984252	0,11032745	0,971	3799	tags=45%, list=22%, signal=58%
GO_STEROL_HOMEOSTASIS	GO_STEROL_HOMEOSTASIS	Details ...	55	-0,5002029	-1,7467674	0,01006036	0,11059474	0,972	1631	tags=33%, list=9%, signal=36%
GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	GO_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	Details ...	71	-0,50905335	-1,7456037	0,01984127	0,11104169	0,973	2417	tags=34%, list=14%, signal=39%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_CH_OH_GROUP_OF_DONORS	Details ...	129	-0,48741078	-1,7440922	0,00798403	0,11193463	0,973	2080	tags=36%, list=12%, signal=41%
GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	GO_CELLULAR_AMINO_ACID_BIOSYNTHETIC_PROCESS	Details ...	86	-0,47433913	-1,7340412	0,02173913	0,12121582	0,977	1697	tags=37%, list=10%, signal=41%
GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	GO_ASPARTATE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	Details ...	16	-0,70233417	-1,7331643	0,00988142	0,12143245	0,978	1605	tags=69%, list=9%, signal=76%
GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	GO_ARACHIDONIC_ACID_METABOLIC_PROCESS	Details ...	49	-0,48642308	-1,73052	0,01006036	0,12347131	0,979	2410	tags=41%, list=14%, signal=47%
GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	GO_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	Details ...	109	-0,43756226	-1,7252631	0,00796813	0,12839681	0,98	3550	tags=36%, list=20%, signal=45%
GO_MITOCHONDRIAL_MATRIX	GO_MITOCHONDRIAL_MATRIX	Details ...	385	-0,50749093	-1,7217401	0,02443992	0,13141319	0,983	2463	tags=38%, list=14%, signal=43%
GO_INDOLALKYLAMINE_METABOLIC_PROCESS	GO_INDOLALKYLAMINE_METABOLIC_PROCESS	Details ...	16	-0,60591704	-1,7215823	0,02321083	0,13090277	0,983	1975	tags=44%, list=11%, signal=49%
GO_CELLULAR_RESPONSE_TO_ESTRADIOL_STIMULUS	GO_CELLULAR_RESPONSE_TO_ESTRADIOL_STIMULUS	Details ...	27	-0,5057837	-1,7210566	0,00986193	0,13080184	0,985	1412	tags=33%, list=8%, signal=36%
GO_ENDOTHELIAL_CELL_DIFFERENTIATION	GO_ENDOTHELIAL_CELL_DIFFERENTIATION	Details ...	70	-0,4748727	-1,720914	0,01926782	0,13022353	0,985	3854	tags=46%, list=22%, signal=58%
GO_LIPID_TRANSPORTER_ACTIVITY	GO_LIPID_TRANSPORTER_ACTIVITY	Details ...	103	-0,42982048	-1,7195137	0,00389105	0,13107307	0,985	3604	tags=43%, list=20%, signal=53%
GO_CELLULAR_MODIFIED_AMINO_ACID_CATABOLIC_PROCESS	GO_CELLULAR_MODIFIED_AMINO_ACID_CATABOLIC_PROCESS	Details ...	16	-0,6263035	-1,7192994	0,01375246	0,13065599	0,985	2067	tags=44%, list=12%, signal=50%
GO_SODIUM_INDEPENDENT_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_SODIUM_INDEPENDENT_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	Details ...	20	-0,57042	-1,7192327	0,0101833	0,13005482	0,985	2588	tags=45%, list=15%, signal=53%
GO_NITROGEN_CYCLE_METABOLIC_PROCESS	GO_NITROGEN_CYCLE_METABOLIC_PROCESS	Details ...	15	-0,6777852	-1,7181299	0,02718447	0,1305443	0,985	2325	tags=67%, list=13%, signal=77%
GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	GO_NEGATIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	Details ...	74	-0,46154147	-1,7181296	0,0139165	0,12988165	0,985	3202	tags=34%, list=18%, signal=41%
GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	GO_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	Details ...	91	-0,44252685	-1,7130827	0,00203666	0,13437547	0,987	3552	tags=41%, list=20%, signal=51%
GO_RESPONSE_TO_INTERLEUKIN_6	GO_RESPONSE_TO_INTERLEUKIN_6	Details ...	26	-0,5459248	-1,712032	0,01089325	0,13499953	0,988	3976	tags=58%, list=23%, signal=74%
GO_CELLULAR_KETONE_METABOLIC_PROCESS	GO_CELLULAR_KETONE_METABOLIC_PROCESS	Details ...	62	-0,52648354	-1,7119527	0,02079002	0,13442837	0,988	2352	tags=40%, list=13%, signal=46%
GO_ISOPRENOID_METABOLIC_PROCESS	GO_ISOPRENOID_METABOLIC_PROCESS		119	-0,42901736	-1,7109425	0,0019305	0,13483039	0,988	2159	tags=31%, list=12%, signal=35%
GO_CELLULAR_IRON_ION_HOMEOSTASIS	GO_CELLULAR_IRON_ION_HOMEOSTASIS		43	-0,50051355	-1,710027	0,01214575	0,13509826	0,989	3702	tags=51%, list=21%, signal=65%
GO_UNSATURATED_FATTY_ACID_METABOLIC_PROCESS	GO_UNSATURATED_FATTY_ACID_METABOLIC_PROCESS		102	-0,41977084	-1,709942	0,00398406	0,13450657	0,989	2449	tags=33%, list=14%, signal=38%
GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM	GO_MORPHOGENESIS_OF_AN_ENDOTHELIUM		16	-0,6021874	-1,7094703	0,01629328	0,13441202	0,989	2783	tags=50%, list=16%, signal=59%
GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	GO_ASPARTATE_FAMILY_AMINO_ACID_METABOLIC_PROCESS		51	-0,52709776	-1,7094414	0,01377953	0,13379826	0,989	1605	tags=41%, list=9%, signal=45%

GO_POSITIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_NUCLEOSIDE_METABOLIC_PROCESS	21	-0,56256986	-1,7084038	0,02719665	0,13426037	0,989	1506	tags=38%, list=9%, signal=42%
GO_TERPENOID_METABOLIC_PROCESS	GO_TERPENOID_METABOLIC_PROCESS	100	-0,43062425	-1,7079554	0,00587084	0,13423747	0,989	2159	tags=32%, list=12%, signal=36%
GO_VITAMIN_METABOLIC_PROCESS	GO_VITAMIN_METABOLIC_PROCESS	112	-0,44093686	-1,7071509	0,00384615	0,13452159	0,989	3044	tags=38%, list=17%, signal=45%
GO_BASAL_PART_OF_CELL	GO_BASAL_PART_OF_CELL	48	-0,5010099	-1,7065052	0,01553398	0,13463809	0,99	1325	tags=23%, list=8%, signal=25%
GO_HUMORAL_IMMUNE_RESPONSE	GO_HUMORAL_IMMUNE_RESPONSE	128	-0,46937856	-1,7050369	0,01574803	0,13559905	0,99	1411	tags=23%, list=8%, signal=24%
GO_POSITIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	GO_POSITIVE_REGULATION_OF_FATTY_ACID_BIOSYNTHETIC_PROCESS	17	-0,5955206	-1,702651	0,02105263	0,13743462	0,991	1212	tags=29%, list=7%, signal=32%
GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	GO_CELLULAR_CARBOHYDRATE_METABOLIC_PROCESS	133	-0,39724636	-1,7025129	0,01237113	0,13690451	0,991	2644	tags=31%, list=15%, signal=36%
GO_CARBON_CARBON_LYASE_ACTIVITY	GO_CARBON_CARBON_LYASE_ACTIVITY	47	-0,5171985	-1,7015898	0,00798403	0,137173	0,991	2628	tags=45%, list=15%, signal=52%
GO_AEROBIC_RESPIRATION	GO_AEROBIC_RESPIRATION	49	-0,60699254	-1,7000617	0,02024292	0,13817148	0,991	2751	tags=51%, list=16%, signal=60%
GO_TRANSLATION_REPRESSOR_ACTIVITY	GO_TRANSLATION_REPRESSOR_ACTIVITY	20	-0,5774243	-1,6996834	0,02380952	0,13796939	0,991	3447	tags=70%, list=20%, signal=87%
GO_VASODILATION	GO_VASODILATION	25	-0,5308907	-1,6983069	0,01720841	0,13886447	0,991	2445	tags=44%, list=14%, signal=51%
GO_SULFUR_COMPOUND_METABOLIC_PROCESS	GO_SULFUR_COMPOUND_METABOLIC_PROCESS	340	-0,38135087	-1,6974909	0,00205339	0,13913631	0,991	2523	tags=31%, list=14%, signal=35%
GO_AROMATIC_AMINO_ACID_FAMILY_CATABOLIC_PROCESS	GO_AROMATIC_AMINO_ACID_FAMILY_CATABOLIC_PROCESS	19	-0,7061217	-1,6973675	0,01832994	0,13862525	0,992	1975	tags=74%, list=11%, signal=83%
GO_TRANSITION_METAL_ION_HOMEOSTASIS	GO_TRANSITION_METAL_ION_HOMEOSTASIS	101	-0,42396468	-1,6969337	0,00215517	0,13861324	0,992	3702	tags=46%, list=21%, signal=57%
GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_PTERIDINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	34	-0,5305593	-1,6964186	0,02244898	0,1385664	0,992	1178	tags=35%, list=7%, signal=38%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	144	-0,4224124	-1,6957104	0,02165354	0,13864152	0,992	2969	tags=33%, list=17%, signal=40%
GO_POSITIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	GO_POSITIVE_REGULATION_OF_MUSCLE_HYPERTROPHY	22	-0,5391094	-1,6897722	0,01612903	0,14461395	0,992	1412	tags=32%, list=8%, signal=35%
GO_REACTIVE_NITROGEN_SPECIES_METABOLIC_PROCESS	GO_REACTIVE_NITROGEN_SPECIES_METABOLIC_PROCESS	17	-0,6211433	-1,6890011	0,01956947	0,14473909	0,992	3263	tags=65%, list=18%, signal=79%
GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_PHENOL_CONTAINING_COMPOUND_METABOLIC_PROCESS	76	-0,44544923	-1,6864215	0,00195695	0,14684883	0,993	2848	tags=33%, list=16%, signal=39%
GO_ENDOTHELIAL_CELL_DEVELOPMENT	GO_ENDOTHELIAL_CELL_DEVELOPMENT	44	-0,49126416	-1,6858774	0,02165354	0,14682724	0,993	2840	tags=36%, list=16%, signal=43%
GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	GO_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	95	-0,43252683	-1,6842171	0,01052632	0,14809622	0,994	3932	tags=45%, list=22%, signal=58%
GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_GLUCOSE_METABOLIC_PROCESS	33	-0,5052631	-1,6837255	0,00833333	0,14796181	0,994	3110	tags=48%, list=18%, signal=59%
GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	GO_REGULATION_OF_CARBOHYDRATE_CATABOLIC_PROCESS	38	-0,46843058	-1,6836767	0,01449275	0,14739282	0,994	1540	tags=29%, list=9%, signal=32%
GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	GO_NEGATIVE_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	26	-0,57031924	-1,6832129	0,02362205	0,14727679	0,994	2081	tags=35%, list=12%, signal=39%
GO_RETINOL_METABOLIC_PROCESS	GO_RETINOL_METABOLIC_PROCESS	28	-0,5482961	-1,6819626	0,01694915	0,14810507	0,994	2623	tags=39%, list=15%, signal=46%
GO_POLYSACCHARIDE_CATABOLIC_PROCESS	GO_POLYSACCHARIDE_CATABOLIC_PROCESS	24	-0,5369757	-1,6809835	0,01996008	0,14857297	0,994	1280	tags=29%, list=7%, signal=31%
GO_ALCOHOL_METABOLIC_PROCESS	GO_ALCOHOL_METABOLIC_PROCESS	336	-0,36380595	-1,6790677	0,00198807	0,15007664	0,994	1706	tags=23%, list=10%, signal=25%
GO_GLYCINE_METABOLIC_PROCESS	GO_GLYCINE_METABOLIC_PROCESS	15	-0,6984688	-1,6764872	0,02191235	0,15251519	0,994	2694	tags=60%, list=15%, signal=71%
GO_AMMONIUM_ION_METABOLIC_PROCESS	GO_AMMONIUM_ION_METABOLIC_PROCESS	161	-0,36470643	-1,6758723	0	0,15255415	0,994	1827	tags=26%, list=10%, signal=29%
GO_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	GO_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	32	-0,4894461	-1,6752589	0,01437372	0,15254661	0,995	1540	tags=34%, list=9%, signal=38%
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	34	-0,52453	-1,6751524	0,00988142	0,15202154	0,995	2081	tags=29%, list=12%, signal=33%
GO_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	GO_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	33	-0,47521088	-1,6704907	0,01646091	0,15684637	0,995	3110	tags=45%, list=18%, signal=55%
GO_SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	GO_SERINE_TYPE_ENDOPEPTIDASE_INHIBITOR_ACTIVITY	80	-0,44047898	-1,6682085	0,01178782	0,15891327	0,997	1844	tags=24%, list=10%, signal=26%
GO_ORGANIC_ACID_BINDING	GO_ORGANIC_ACID_BINDING	196	-0,37158	-1,6681983	0,00192678	0,15825908	0,997	3031	tags=34%, list=17%, signal=40%
GO_RESPONSE_TO_PH	GO_RESPONSE_TO_PH	36	-0,4956629	-1,664615	0,01035197	0,16177766	0,997	1994	tags=36%, list=11%, signal=41%
GO_POSITIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_GLYCOGEN_METABOLIC_PROCESS	16	-0,5644429	-1,6614658	0,02579365	0,164991	0,997	3788	tags=56%, list=21%, signal=72%
GO_POSITIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	45	-0,4463877	-1,6601232	0,02008032	0,16593935	0,997	1364	tags=22%, list=8%, signal=24%
GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_BINDING	GO_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_BINDING	15	-0,5877879	-1,6600273	0,02254098	0,16538385	0,997	1412	tags=33%, list=8%, signal=36%
GO_PHOSPHATIDYLCHOLINE_BINDING	GO_PHOSPHATIDYLCHOLINE_BINDING	18	-0,53233737	-1,6594524	0,02061856	0,16551913	0,997	1837	tags=39%, list=10%, signal=43%
GO_GLUCAN_BIOSYNTHETIC_PROCESS	GO_GLUCAN_BIOSYNTHETIC_PROCESS	25	-0,5464365	-1,6586037	0,02997859	0,16582724	0,997	3110	tags=36%, list=18%, signal=44%
GO_FATTY_ACID_TRANSPORT	GO_FATTY_ACID_TRANSPORT	52	-0,4673875	-1,6579881	0,01207244	0,16595098	0,997	3496	tags=44%, list=20%, signal=55%
GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	GO_GLUTATHIONE_DERIVATIVE_METABOLIC_PROCESS	21	-0,6276175	-1,6573375	0,04125737	0,16615216	0,998	3807	tags=62%, list=22%, signal=79%
GO_PROTEIN_HOMOTETRAMERIZATION	GO_PROTEIN_HOMOTETRAMERIZATION	58	-0,44536257	-1,6551657	0,02976191	0,1681184	0,999	1914	tags=36%, list=11%, signal=40%
GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	GO_CELLULAR_ALDEHYDE_METABOLIC_PROCESS	79	-0,50686955	-1,6551499	0,02777778	0,16745903	0,999	2694	tags=47%, list=15%, signal=55%
GO_REGULATION_OF_GLUCOSE_IMPORT	GO_REGULATION_OF_GLUCOSE_IMPORT	56	-0,4388923	-1,6549548	0,00785855	0,16708423	0,999	1633	tags=30%, list=9%, signal=33%
GO_WATER_SOLUBLE_VITAMIN_METABOLIC_PROCESS	GO_WATER_SOLUBLE_VITAMIN_METABOLIC_PROCESS	82	-0,4467212	-1,6496606	0,01153846	0,17287831	0,999	3010	tags=38%, list=17%, signal=45%
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_6	GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_6	22	-0,5440883	-1,6482248	0,01898734	0,17385578	0,999	3976	tags=59%, list=23%, signal=76%
GO_SODIUM_INDEPENDENT_ORGANIC_ANION_TRANSPORT	GO_SODIUM_INDEPENDENT_ORGANIC_ANION_TRANSPORT	22	-0,531431	-1,6478391	0,01489362	0,17362905	1	2588	tags=41%, list=15%, signal=48%
GO_ADRENERGIC_RECEPTOR_SIGNALING_PATHWAY	GO_ADRENERGIC_RECEPTOR_SIGNALING_PATHWAY	16	-0,6117831	-1,6467565	0,01160542	0,17426276	1	2204	tags=44%, list=12%, signal=50%
GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	21	-0,52117795	-1,6467077	0,01832994	0,17362899	1	1364	tags=29%, list=8%, signal=31%
GO_RENAL_SYSTEM_PROCESS	GO_RENAL_SYSTEM_PROCESS	96	-0,42622256	-1,6463706	0,01356589	0,17351945	1	2692	tags=29%, list=15%, signal=34%
GO_TRIGLYCERIDE_CATABOLIC_PROCESS	GO_TRIGLYCERIDE_CATABOLIC_PROCESS	19	-0,62061	-1,6438967	0,02880658	0,17612548	1	1990	tags=47%, list=11%, signal=53%
GO_NEGATIVE_REGULATION_OF_JNK_CASCADE	GO_NEGATIVE_REGULATION_OF_JNK_CASCADE	32	-0,47253343	-1,6401535	0,01318268	0,18053557	1	3815	tags=47%, list=22%, signal=60%
GO_ARGININE_METABOLIC_PROCESS	GO_ARGININE_METABOLIC_PROCESS	17	-0,61864173	-1,6379684	0,03495146	0,18269397	1	2627	tags=65%, list=15%, signal=76%

GO_HEPATICOBILIARY_SYSTEM_DEVELOPMENT	GO_HEPATICOBILIARY_SYSTEM_DEVELOPMENT	125	-0,38367218	-1,6342793	0,00595238	0,18656373	1	2372	tags=27%, list=13%, signal=31%
GO_RESPONSE_TO_ZINC_ION	GO_RESPONSE_TO_ZINC_ION	52	-0,4701628	-1,6341414	0,03483607	0,18607324	1	4247	tags=50%, list=24%, signal=66%
GO_THIOESTER_METABOLIC_PROCESS	GO_THIOESTER_METABOLIC_PROCESS	76	-0,4776514	-1,6341168	0,03815261	0,18539391	1	2623	tags=42%, list=15%, signal=49%
GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS	GO_TRICARBOXYLIC_ACID_METABOLIC_PROCESS	36	-0,5864198	-1,6315395	0,05338809	0,18809757	1	2718	tags=53%, list=15%, signal=62%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_OH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	109	-0,45812282	-1,6311059	0,03024194	0,18790825	1	2080	tags=33%, list=12%, signal=37%
GO_NAD_BINDING	GO_NAD_BINDING	52	-0,4899246	-1,6306435	0,03012048	0,18779352	1	2885	tags=42%, list=16%, signal=50%
GO_FATTY_ACID_DERIVATIVE_METABOLIC_PROCESS	GO_FATTY_ACID_DERIVATIVE_METABOLIC_PROCESS	90	-0,40943164	-1,6293763	0,01004016	0,1886479	1	2410	tags=31%, list=14%, signal=36%
GO_RESPONSE_TO_CORTICOSTEROID	GO_RESPONSE_TO_CORTICOSTEROID	166	-0,36316538	-1,6256592	0,00389864	0,19311161	1	2126	tags=25%, list=12%, signal=28%
GO_GLUTAMATE_METABOLIC_PROCESS	GO_GLUTAMATE_METABOLIC_PROCESS	28	-0,54897624	-1,6229343	0,03320313	0,1961604	1	4216	tags=71%, list=24%, signal=94%
GO_CELLULAR_RESPIRATION	GO_CELLULAR_RESPIRATION	136	-0,5590691	-1,6223464	0,06813628	0,19622461	1	3915	tags=54%, list=22%, signal=69%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_INCORPORATION_OF_MOLECULAR_OXYGEN	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_SINGLE_DONORS_WITH_INCORPORATION_OF_MOLECULAR_OXYGEN	26	-0,48479536	-1,6182499	0,02091255	0,20108818	1	2213	tags=35%, list=13%, signal=40%
GO_PEROXISOME_ORGANIZATION	GO_PEROXISOME_ORGANIZATION	33	-0,54268247	-1,6170484	0,05882353	0,20204972	1	2826	tags=52%, list=16%, signal=61%
GO_RESPONSE_TO_STARVATION	GO_RESPONSE_TO_STARVATION	144	-0,36817124	-1,6154977	0,00613497	0,20353267	1	2712	tags=28%, list=15%, signal=33%
GO_POSITIVE_REGULATION_OF_LIPID_STORAGE	GO_POSITIVE_REGULATION_OF_LIPID_STORAGE	19	-0,5343505	-1,6134063	0,02923977	0,2057618	1	1651	tags=37%, list=9%, signal=41%
GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	GO_GENERATION_OF_PRECURSOR_METABOLITES_AND_ENERGY	273	-0,45242143	-1,6128287	0,04115227	0,2058699	1	2766	tags=37%, list=16%, signal=43%
GO_PLASMA_LIPOPROTEIN_PARTICLE_CLEARANCE	GO_PLASMA_LIPOPROTEIN_PARTICLE_CLEARANCE	21	-0,5767078	-1,6126926	0,043222	0,20529863	1	2623	tags=48%, list=15%, signal=56%
GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	GO_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	85	-0,3886115	-1,6109467	0,00821355	0,20693025	1	3786	tags=34%, list=21%, signal=43%
GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	GO_CELLULAR_MODIFIED_AMINO_ACID_METABOLIC_PROCESS	205	-0,3742802	-1,6101831	0,00798403	0,20727922	1	2612	tags=31%, list=15%, signal=36%
GO_NEGATIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	GO_NEGATIVE_REGULATION_OF_LIPID_BIOSYNTHETIC_PROCESS	42	-0,42552698	-1,6099986	0,01026694	0,20689824	1	4068	tags=45%, list=23%, signal=59%
GO_VASCULOGENESIS	GO_VASCULOGENESIS	57	-0,48048282	-1,6087662	0,02923977	0,20791782	1	2769	tags=37%, list=16%, signal=44%
GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	GO_NEUTRAL_LIPID_CATABOLIC_PROCESS	24	-0,5673424	-1,6084939	0,02505219	0,20754936	1	1990	tags=46%, list=11%, signal=52%
GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	GO_REGULATION_OF_MUSCLE_CELL_APOPTOTIC_PROCESS	42	-0,4274763	-1,6059272	0,02290076	0,2105114	1	4458	tags=52%, list=25%, signal=70%
GO_RENAL_WATER_HOMEOSTASIS	GO_RENAL_WATER_HOMEOSTASIS	32	-0,49609238	-1,6012529	0,02231237	0,21664247	1	4327	tags=41%, list=24%, signal=54%
GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_MONOOXYGENASE_ACTIVITY	28	-0,47998366	-1,5990559	0,02105263	0,21917036	1	1364	tags=25%, list=8%, signal=27%
GO_RESPONSE_TO_AMINO_ACID	GO_RESPONSE_TO_AMINO_ACID	102	-0,3814269	-1,597549	0,01014199	0,2207485	1	3061	tags=32%, list=17%, signal=39%
GO_RESPONSE_TO_METAL_ION	GO_RESPONSE_TO_METAL_ION	313	-0,33011445	-1,5965482	0	0,2216897	1	2126	tags=24%, list=12%, signal=27%
GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	GO_POSITIVE_REGULATION_OF_GLUCOSE_TRANSPORT	39	-0,4548297	-1,5941837	0,01158301	0,22458988	1	2081	tags=36%, list=12%, signal=41%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_HEME_GROUP_OF_DONORS	24	-0,63384235	-1,5941339	0,05454546	0,22387922	1	3851	tags=54%, list=22%, signal=69%
GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	GO_REGULATION_OF_FATTY_ACID_BETA_OXIDATION	15	-0,57371783	-1,5928425	0,04132231	0,22509438	1	3110	tags=53%, list=18%, signal=65%
GO_ONE_CARBON_METABOLIC_PROCESS	GO_ONE_CARBON_METABOLIC_PROCESS	34	-0,4810951	-1,5910903	0,02822581	0,22678854	1	1826	tags=29%, list=10%, signal=33%
GO_MAMMARY_GLAND_EPITHELIAL_CELL_DIFFERENTIATION	GO_MAMMARY_GLAND_EPITHELIAL_CELL_DIFFERENTIATION	15	-0,543894	-1,5907137	0,03006012	0,22669023	1	3110	tags=47%, list=18%, signal=57%
GO_FMN_BINDING	GO_FMN_BINDING	15	-0,59120685	-1,5887033	0,04024145	0,22907303	1	2627	tags=67%, list=15%, signal=78%
GO_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	GO_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	95	-0,42239735	-1,5865391	0,03162056	0,23169927	1	3540	tags=36%, list=20%, signal=45%
GO_CYTOCHROME_COMPLEX_ASSEMBLY	GO_CYTOCHROME_COMPLEX_ASSEMBLY	15	-0,64136386	-1,5865002	0,04024145	0,2309859	1	2314	tags=33%, list=13%, signal=38%
GO_NITRIC_OXIDE_METABOLIC_PROCESS	GO_NITRIC_OXIDE_METABOLIC_PROCESS	15	-0,60035735	-1,5862535	0,03333334	0,23059048	1	3263	tags=67%, list=18%, signal=82%
GO_COFACTOR_METABOLIC_PROCESS	GO_COFACTOR_METABOLIC_PROCESS	316	-0,41688752	-1,5859573	0,04848485	0,23020464	1	2452	tags=34%, list=14%, signal=39%
GO_RESPONSE_TO_TRANSITION_METAL_NANOPARTICLE	GO_RESPONSE_TO_TRANSITION_METAL_NANOPARTICLE	139	-0,36514422	-1,5841962	0,00601202	0,23235314	1	3862	tags=37%, list=22%, signal=48%
GO_REGULATION_OF_LIPID_STORAGE	GO_REGULATION_OF_LIPID_STORAGE	40	-0,45484912	-1,5809495	0,02514507	0,23662089	1	3809	tags=45%, list=22%, signal=57%
GO_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	GO_REGULATION_OF_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	18	-0,5340725	-1,5809097	0,04065041	0,23588252	1	2480	tags=39%, list=14%, signal=45%
GO_REGULATION_OF_RESPONSE_TO_WOUNDING	GO_REGULATION_OF_RESPONSE_TO_WOUNDING	388	-0,36856687	-1,5806352	0,03278688	0,23544474	1	2975	tags=28%, list=17%, signal=33%
GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	77	-0,39053234	-1,5804418	0,01386139	0,23499613	1	3555	tags=38%, list=20%, signal=47%
GO_BILE_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_BILE_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	-0,5935729	-1,5801374	0,02636917	0,23470424	1	3604	tags=60%, list=20%, signal=75%
GO_REGULATION_OF_P38MAPK_CASCADE	GO_REGULATION_OF_P38MAPK_CASCADE	25	-0,47828054	-1,5792907	0,02079002	0,23539542	1	1322	tags=24%, list=7%, signal=26%
GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_MONOCARBOXYLIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	42	-0,45151526	-1,579082	0,03	0,23493427	1	3604	tags=48%, list=20%, signal=60%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_ALDEHYDE_OR_OXO_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	33	-0,5170088	-1,5790644	0,05128205	0,2341794	1	2441	tags=42%, list=14%, signal=49%
GO_MONOCARBOXYLIC_ACID_BINDING	GO_MONOCARBOXYLIC_ACID_BINDING	63	-0,41282108	-1,5784302	0,02615694	0,23435381	1	2946	tags=40%, list=17%, signal=47%
GO_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	GO_NEGATIVE_REGULATION_OF_PROTEIN_MATURATION	33	-0,4609647	-1,5758052	0,03048781	0,23762557	1	2975	tags=36%, list=17%, signal=44%
GO_GLUCOCORTICOID_METABOLIC_PROCESS	GO_GLUCOCORTICOID_METABOLIC_PROCESS	15	-0,5712929	-1,5755792	0,01976285	0,23723099	1	1375	tags=27%, list=8%, signal=29%
GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	65	-0,39535147	-1,5746889	0,02119461	0,23777178	1	1633	tags=26%, list=9%, signal=29%
GO_NADP_BINDING	GO_NADP_BINDING	41	-0,48186168	-1,574597	0,0362173	0,23717442	1	3352	tags=51%, list=19%, signal=63%
GO_COENZYME_METABOLIC_PROCESS	GO_COENZYME_METABOLIC_PROCESS	247	-0,40660712	-1,5731041	0,04426559	0,23863812	1	2449	tags=34%, list=14%, signal=38%
GO_CARBOXYLIC_ESTER_HYDROLASE_ACTIVITY	GO_CARBOXYLIC_ESTER_HYDROLASE_ACTIVITY	120	-0,3754274	-1,5727592	0,01980198	0,2384003	1	1750	tags=24%, list=10%, signal=27%

GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	GO_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	84	-0,4149836	-1,5722549	0,02822581	0,23846391	1	2736	tags=33%, list=15%, signal=39%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS	25	-0,5161963	-1,5709274	0,0392562	0,23988356	1	1899	tags=44%, list=11%, signal=49%
GO_C21_STEROID_HORMONE_METABOLIC_PROCESS	GO_C21_STEROID_HORMONE_METABOLIC_PROCESS	22	-0,51916414	-1,5703151	0,03909465	0,24014333	1	788	tags=27%, list=4%, signal=29%
GO_GLYCOSAMINOGLYCAN_BINDING	GO_GLYCOSAMINOGLYCAN_BINDING	190	-0,41032383	-1,5691063	0,03846154	0,24109893	1	2975	tags=31%, list=17%, signal=36%
GO_RESPONSE_TO_MUSCLE_ACTIVITY	GO_RESPONSE_TO_MUSCLE_ACTIVITY	16	-0,52856654	-1,5667483	0,04065041	0,24426813	1	788	tags=25%, list=4%, signal=26%
GO_LONG_TERM_SYNAPTIC_DEPRESSION	GO_LONG_TERM_SYNAPTIC_DEPRESSION	15	-0,53195834	-1,5659595	0,02811245	0,24460022	1	1472	tags=27%, list=8%, signal=29%
GO_REGULATION_OF_GLUCOSE_IMPORT_IN_RESPONSE_TO_INSULIN_STIMULUS	GO_REGULATION_OF_GLUCOSE_IMPORT_IN_RESPONSE_TO_INSULIN_STIMULUS	16	-0,5129495	-1,5648525	0,03792415	0,24561016	1	1602	tags=38%, list=9%, signal=41%
GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	GO_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	153	-0,36225706	-1,5621741	0,01010101	0,24919036	1	1687	tags=24%, list=10%, signal=27%
GO_CYCLASE_ACTIVITY	GO_CYCLASE_ACTIVITY	19	-0,57257164	-1,5621369	0,05040323	0,24845947	1	4964	tags=53%, list=28%, signal=73%
GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	GO_PHOSPHATIDYLINOSITOL_3_KINASE_BINDING	28	-0,4832066	-1,5599562	0,04198473	0,25109386	1	1288	tags=25%, list=7%, signal=27%
GO_HISTONE_ACETYLTRANSFERASE_BINDING	GO_HISTONE_ACETYLTRANSFERASE_BINDING	28	-0,47208485	-1,5588834	0,03256705	0,25209305	1	2969	tags=43%, list=17%, signal=51%
GO_NEGATIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	GO_NEGATIVE_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	49	-0,4196096	-1,5585916	0,02765958	0,25180674	1	3412	tags=39%, list=19%, signal=48%
GO_HEART_GROWTH	GO_HEART_GROWTH	24	-0,50244766	-1,5584192	0,04008016	0,2512849	1	2715	tags=38%, list=15%, signal=44%
GO_CARBOHYDRATE_HOMEOSTASIS	GO_CARBOHYDRATE_HOMEOSTASIS	156	-0,35312787	-1,5559046	0,01046025	0,25459114	1	3110	tags=29%, list=18%, signal=35%
GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	GO_RESPONSE_TO_PURINE_CONTAINING_COMPOUND	154	-0,35497597	-1,5554627	0,01359223	0,25463116	1	1687	tags=23%, list=10%, signal=25%
GO_COFACTOR_CATABOLIC_PROCESS	GO_COFACTOR_CATABOLIC_PROCESS	20	-0,58768106	-1,5554094	0,05498982	0,2539226	1	2736	tags=50%, list=15%, signal=59%
GO_PHOSPHOLIPID_TRANSPORT	GO_PHOSPHOLIPID_TRANSPORT	54	-0,42342645	-1,5546379	0,03187251	0,25448298	1	2265	tags=31%, list=13%, signal=36%
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_CATABOLIC_PROCESS	15	-0,5628448	-1,5538017	0,04573805	0,25507697	1	1506	tags=40%, list=9%, signal=44%
GO_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	GO_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	21	-0,48838112	-1,5514	0,03896104	0,25822225	1	3951	tags=52%, list=22%, signal=67%
GO_VERY_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	GO_VERY_LONG_CHAIN_FATTY_ACID_METABOLIC_PROCESS	25	-0,5211066	-1,5457339	0,04844961	0,2669389	1	2449	tags=44%, list=14%, signal=51%
GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	144	-0,34312984	-1,54475	0,02539063	0,267848	1	1395	tags=19%, list=8%, signal=21%
GO_LEUKOTRIENE_METABOLIC_PROCESS	GO_LEUKOTRIENE_METABOLIC_PROCESS	29	-0,468496	-1,5446918	0,02277433	0,2671451	1	1133	tags=28%, list=6%, signal=29%
GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	GO_REGULATION_OF_VASCULATURE_DEVELOPMENT	221	-0,38346168	-1,5433421	0,02805611	0,26869196	1	3540	tags=33%, list=20%, signal=40%
GO_PROTEIN_LIPID_COMPLEX_BINDING	GO_PROTEIN_LIPID_COMPLEX_BINDING	24	-0,4875767	-1,5428438	0,05823293	0,2687127	1	1366	tags=33%, list=8%, signal=36%
GO_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	GO_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	54	-0,43877202	-1,5423728	0,028463	0,26873854	1	4442	tags=44%, list=25%, signal=59%
GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	GO_LIGASE_ACTIVITY_FORMING_CARBON_SULFUR_BONDS	39	-0,45179453	-1,541751	0,04508197	0,26901403	1	2221	tags=38%, list=13%, signal=44%
GO_GLUTAMINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	GO_GLUTAMINE_FAMILY_AMINO_ACID_METABOLIC_PROCESS	63	-0,43681353	-1,5395223	0,05633803	0,27201778	1	2849	tags=44%, list=16%, signal=53%
GO_NEGATIVE_REGULATION_OF_LIPID_TRANSPORT	GO_NEGATIVE_REGULATION_OF_LIPID_TRANSPORT	26	-0,48620868	-1,5395024	0,05498982	0,27123442	1	1364	tags=31%, list=8%, signal=33%
GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	23	-0,4775587	-1,5393968	0,05343511	0,2706404	1	3679	tags=39%, list=21%, signal=49%
GO_ENDOTHELIAL_CELL_PROLIFERATION	GO_ENDOTHELIAL_CELL_PROLIFERATION	23	-0,4876523	-1,5384443	0,0446602	0,27159706	1	2712	tags=30%, list=15%, signal=36%
GO_PYRIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	GO_PYRIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	18	-0,5666012	-1,5369673	0,06300813	0,2732626	1	2298	tags=39%, list=13%, signal=45%
GO_ACUTE_PHASE_RESPONSE	GO_ACUTE_PHASE_RESPONSE	41	-0,5187178	-1,5362169	0,07017544	0,2736668	1	3976	tags=56%, list=23%, signal=72%
GO_ADIPOSE_TISSUE_DEVELOPMENT	GO_ADIPOSE_TISSUE_DEVELOPMENT	30	-0,47525924	-1,5336281	0,03883495	0,27720514	1	3003	tags=37%, list=17%, signal=44%
GO_REGULATION_OF_URINE_VOLUME	GO_REGULATION_OF_URINE_VOLUME	20	-0,5128742	-1,5336221	0,03875969	0,27641013	1	1687	tags=30%, list=10%, signal=33%
GO_STEROL_BINDING	GO_STEROL_BINDING	42	-0,39904374	-1,5314565	0,01724138	0,2794655	1	1364	tags=24%, list=8%, signal=26%
GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	GO_ALPHA_AMINO_ACID_BIOSYNTHETIC_PROCESS	72	-0,43188617	-1,5312202	0,06160164	0,27909556	1	2067	tags=36%, list=12%, signal=41%
GO_ETHANOLAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_ETHANOLAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	82	-0,34906408	-1,5300245	0,01512287	0,28030416	1	1611	tags=22%, list=9%, signal=24%
GO_COPPER_ION_TRANSPORT	GO_COPPER_ION_TRANSPORT	20	-0,50658333	-1,5290253	0,06262627	0,28126606	1	3060	tags=50%, list=17%, signal=60%
GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	56	-0,41092613	-1,5258075	0,02294455	0,28603867	1	2939	tags=29%, list=17%, signal=34%
GO_ORGAN_REGENERATION	GO_ORGAN_REGENERATION	81	-0,36374545	-1,5253365	0,01984127	0,28612182	1	1639	tags=27%, list=9%, signal=30%
GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_STEROID_BIOSYNTHETIC_PROCESS	48	-0,39740837	-1,5251305	0,01405623	0,28564304	1	3547	tags=31%, list=20%, signal=39%
GO_CYTOCHROME_COMPLEX	GO_CYTOCHROME_COMPLEX	20	-0,63235533	-1,5228748	0,07370518	0,2887021	1	3811	tags=60%, list=22%, signal=76%
GO_ALCOHOL_BINDING	GO_ALCOHOL_BINDING	93	-0,34904918	-1,5228679	0,01174168	0,28790608	1	972	tags=18%, list=6%, signal=19%
GO_RESPONSE_TO_ORGANOPHOSPHORUS	GO_RESPONSE_TO_ORGANOPHOSPHORUS	136	-0,35511678	-1,5223067	0,02217742	0,28809568	1	3236	tags=31%, list=18%, signal=38%
GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	GO_NUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	37	-0,46976647	-1,5221819	0,06175299	0,2875053	1	1847	tags=41%, list=10%, signal=45%
GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	GO_REGULATION_OF_ENDOTHELIAL_CELL_APOPTOTIC_PROCESS	38	-0,46925247	-1,5210006	0,04330709	0,2886911	1	2081	tags=29%, list=12%, signal=33%
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIATED_BY_A_CHEMICAL_SIGNAL	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_MEDIATED_BY_A_CHEMICAL_SIGNAL	42	-0,45481205	-1,520583	0,02918288	0,2885857	1	5881	tags=57%, list=33%, signal=85%
GO_CELLULAR_RESPONSE_TO_ESTROGEN_STIMULUS	GO_CELLULAR_RESPONSE_TO_ESTROGEN_STIMULUS	37	-0,4140385	-1,5202867	0,03094778	0,28830266	1	1412	tags=27%, list=8%, signal=29%
GO_REGULATION_OF_GLUCONEOGENESIS	GO_REGULATION_OF_GLUCONEOGENESIS	32	-0,46985886	-1,5199443	0,03092784	0,28802752	1	3932	tags=47%, list=22%, signal=60%
GO_CARBOXY_LYASE_ACTIVITY	GO_CARBOXY_LYASE_ACTIVITY	32	-0,47656876	-1,5197134	0,04609219	0,28759825	1	1240	tags=31%, list=7%, signal=34%
GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	GO_VASCULAR_PROCESS_IN_CIRCULATORY_SYSTEM	157	-0,3781933	-1,5189127	0,02857143	0,28821018	1	3192	tags=30%, list=18%, signal=36%
GO_FOLIC_ACID_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_FOLIC_ACID_CONTAINING_COMPOUND_METABOLIC_PROCESS	27	-0,47608665	-1,5182185	0,06613226	0,2885804	1	1178	tags=30%, list=7%, signal=32%

GO_RESPONSE_TO_ACIDIC_PH	GO_RESPONSE_TO_ACIDIC_PH	17	-0,5082526	-1,5177945	0,04098361	0,28859177	1	1994	tags=41%, list=11%, signal=46%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	30	-0,4814651	-1,5159396	0,05283757	0,29107937	1	3794	tags=40%, list=21%, signal=51%
GO_CELLULAR_RESPONSE_TO_LITHIUM_ION	GO_CELLULAR_RESPONSE_TO_LITHIUM_ION	16	-0,5021558	-1,5158314	0,04807692	0,29046977	1	1779	tags=38%, list=10%, signal=42%
GO_FATTY_ACID_LIGASE_ACTIVITY	GO_FATTY_ACID_LIGASE_ACTIVITY	16	-0,5324205	-1,5136844	0,04887984	0,29351023	1	3437	tags=50%, list=19%, signal=62%
GO_ELECTRON_TRANSPORT_CHAIN	GO_ELECTRON_TRANSPORT_CHAIN	91	-0,5597955	-1,5108134	0,140625	0,2975924	1	3915	tags=56%, list=22%, signal=72%
GO_PEPTIDE_HORMONE_BINDING	GO_PEPTIDE_HORMONE_BINDING	30	-0,4736623	-1,5101476	0,04417671	0,29790938	1	1534	tags=30%, list=9%, signal=33%
GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	GO_ESTABLISHMENT_OF_ENDOTHELIAL_BARRIER	29	-0,4950037	-1,5097803	0,06387226	0,2977701	1	2840	tags=34%, list=16%, signal=41%
GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK_BY_PHOTOPERIOD	GO_ENTRAINMENT_OF_CIRCADIAN_CLOCK_BY_PHOTOPERIOD	18	-0,5032341	-1,5097756	0,06746032	0,29697627	1	1380	tags=28%, list=8%, signal=30%
GO_SERINE_HYDROLASE_ACTIVITY	GO_SERINE_HYDROLASE_ACTIVITY	198	-0,35921285	-1,5089736	0,01593626	0,29755107	1	3178	tags=27%, list=18%, signal=33%
GO_CAMP_METABOLIC_PROCESS	GO_CAMP_METABOLIC_PROCESS	32	-0,4925443	-1,5088319	0,06321839	0,29703274	1	4645	tags=56%, list=26%, signal=76%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_ACTIVITY	17	-0,56390005	-1,5084318	0,0704501	0,2969313	1	2712	tags=47%, list=15%, signal=56%
GO_CHOLESTEROL_EFFLUX	GO_CHOLESTEROL_EFFLUX	26	-0,49250317	-1,507515	0,05870445	0,2978332	1	1364	tags=31%, list=8%, signal=33%
GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO_CELLULAR_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	49	-0,40371186	-1,5065016	0,04831933	0,29879332	1	2503	tags=24%, list=14%, signal=28%
GO_ENDOCYTIC_VESICLE_LUMEN	GO_ENDOCYTIC_VESICLE_LUMEN	17	-0,5734462	-1,5056112	0,07142858	0,2996065	1	2913	tags=53%, list=16%, signal=63%
GO_PROTEIN_LIPID_COMPLEX_SUBUNIT_ORGANIZATION	GO_PROTEIN_LIPID_COMPLEX_SUBUNIT_ORGANIZATION	36	-0,47283834	-1,5044609	0,06425703	0,30083564	1	1707	tags=31%, list=10%, signal=34%
GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	GO_LONG_CHAIN_FATTY_ACID_TRANSPORT	38	-0,43891475	-1,5042493	0,0407332	0,30039462	1	3496	tags=42%, list=20%, signal=52%
GO_RESPONSE_TO_ETHANOL	GO_RESPONSE_TO_ETHANOL	126	-0,35070953	-1,5039779	0,00626305	0,30005834	1	2971	tags=31%, list=17%, signal=37%
GO_LIPID_STORAGE	GO_LIPID_STORAGE	26	-0,4465143	-1,5030254	0,03326403	0,30110535	1	2623	tags=38%, list=15%, signal=45%
GO_REGULATION_OF_ENERGY_HOMEOSTASIS	GO_REGULATION_OF_ENERGY_HOMEOSTASIS	17	-0,51010036	-1,5011485	0,06090373	0,30360222	1	2281	tags=35%, list=13%, signal=40%
GO_THIOLESTER_HYDROLASE_ACTIVITY	GO_THIOLESTER_HYDROLASE_ACTIVITY	32	-0,49635866	-1,5011119	0,08401639	0,30289388	1	1659	tags=34%, list=9%, signal=38%
GO_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	GO_CELLULAR_TRANSITION_METAL_ION_HOMEOSTASIS	74	-0,38960776	-1,5005814	0,04291846	0,3030997	1	3128	tags=39%, list=18%, signal=47%
GO_POSITIVE_T_CELL_SELECTION	GO_POSITIVE_T_CELL_SELECTION	20	-0,5689966	-1,5002152	0,10386965	0,30296493	1	4209	tags=50%, list=24%, signal=66%
GO_NONRIBOSOMAL_PEPTIDE_BIOSYNTHETIC_PROCESS	GO_NONRIBOSOMAL_PEPTIDE_BIOSYNTHETIC_PROCESS	16	-0,5247218	-1,4986575	0,06679764	0,30489457	1	2845	tags=44%, list=16%, signal=52%
GO_ISOPRENOID_BINDING	GO_ISOPRENOID_BINDING	37	-0,43809772	-1,4938277	0,06262627	0,31261063	1	3044	tags=41%, list=17%, signal=49%
GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	GO_NEGATIVE_REGULATION_OF_MITOCHONDRION_ORGANIZATION	35	-0,4318537	-1,4935919	0,06212425	0,31223264	1	3552	tags=40%, list=20%, signal=50%
GO_REGULATION_OF_PLASMA_LIPOPROTEIN_PARTICLE_LEVELS	GO_REGULATION_OF_PLASMA_LIPOPROTEIN_PARTICLE_LEVELS	45	-0,44769552	-1,4925327	0,05443548	0,3133437	1	3612	tags=42%, list=20%, signal=53%
GO_RESPONSE_TO_TOXIC_SUBSTANCE	GO_RESPONSE_TO_TOXIC_SUBSTANCE	227	-0,31530416	-1,4923209	0,00594059	0,31293106	1	2832	tags=27%, list=16%, signal=32%
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE	79	-0,38306767	-1,491873	0,02996255	0,3129692	1	3679	tags=30%, list=21%, signal=38%
GO_RESPIRATORY_CHAIN	GO_RESPIRATORY_CHAIN	77	-0,5970965	-1,4889631	0,1391129	0,3176445	1	3915	tags=58%, list=22%, signal=75%
GO_COENZYME_BIOSYNTHETIC_PROCESS	GO_COENZYME_BIOSYNTHETIC_PROCESS	114	-0,41564697	-1,4874083	0,09108911	0,31975627	1	2449	tags=36%, list=14%, signal=41%
GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	GO_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	183	-0,3428936	-1,4844054	0,01568628	0,3246217	1	3227	tags=28%, list=18%, signal=34%
GO_DRUG_TRANSMEMBRANE_TRANSPORT	GO_DRUG_TRANSMEMBRANE_TRANSPORT	19	-0,54585826	-1,4841344	0,07858546	0,32429013	1	2286	tags=37%, list=13%, signal=42%
GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_VASCULATURE_DEVELOPMENT	129	-0,39510933	-1,4839334	0,0583501	0,3239086	1	3507	tags=34%, list=20%, signal=42%
GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	GO_CELLULAR_RESPONSE_TO_GLUCAGON_STIMULUS	36	-0,44130987	-1,4822507	0,06470589	0,32614794	1	2802	tags=31%, list=16%, signal=36%
GO_HEME_METABOLIC_PROCESS	GO_HEME_METABOLIC_PROCESS	29	-0,5186498	-1,482174	0,0929293	0,32548594	1	2736	tags=41%, list=15%, signal=49%
GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_PORPHYRIN_CONTAINING_COMPOUND_METABOLIC_PROCESS	36	-0,49999642	-1,4813493	0,0775348	0,32623312	1	3963	tags=50%, list=22%, signal=64%
GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_BINDING	15	-0,54000956	-1,4809453	0,08484849	0,32615966	1	3558	tags=53%, list=20%, signal=67%
GO_TEMPERATURE_HOMEOSTASIS	GO_TEMPERATURE_HOMEOSTASIS	22	-0,49123695	-1,4804963	0,06391753	0,32622695	1	2509	tags=41%, list=14%, signal=48%
GO_REGULATION_OF_VASOCONSTRICTION	GO_REGULATION_OF_VASOCONSTRICTION	64	-0,42254013	-1,4798522	0,06346154	0,32667214	1	3322	tags=36%, list=19%, signal=44%
GO_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	GO_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	23	-0,4847556	-1,4796083	0,06589147	0,32634127	1	3263	tags=48%, list=18%, signal=59%
GO_SECONDARY_METABOLIC_PROCESS	GO_SECONDARY_METABOLIC_PROCESS	47	-0,43626922	-1,478091	0,04716981	0,3283847	1	2687	tags=34%, list=15%, signal=40%
GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	GO_POLYSACCHARIDE_BIOSYNTHETIC_PROCESS	41	-0,41078702	-1,4778162	0,06567796	0,32801977	1	5538	tags=46%, list=31%, signal=67%
GO_COPPER_ION_BINDING	GO_COPPER_ION_BINDING	51	-0,40200907	-1,47708	0,04356436	0,32848722	1	3060	tags=33%, list=17%, signal=40%
GO_RESPONSE_TO_EXTRACELLULAR_STIMULUS	GO_RESPONSE_TO_EXTRACELLULAR_STIMULUS	411	-0,29588333	-1,4758283	0,00425532	0,3299279	1	2759	tags=25%, list=16%, signal=29%
GO_ACUTE_INFLAMMATORY_RESPONSE	GO_ACUTE_INFLAMMATORY_RESPONSE	69	-0,41497645	-1,4755849	0,05042017	0,32961378	1	3976	tags=42%, list=23%, signal=54%
GO_NADH_DEHYDROGENASE_COMPLEX	GO_NADH_DEHYDROGENASE_COMPLEX	42	-0,6399025	-1,4727632	0,14314115	0,3341592	1	5353	tags=79%, list=30%, signal=112%
GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	GO_REGULATION_OF_COFACTOR_METABOLIC_PROCESS	46	-0,4309435	-1,4727261	0,06047516	0,33341613	1	1605	tags=28%, list=9%, signal=31%
GO_FAT_SOLUBLE_VITAMIN_METABOLIC_PROCESS	GO_FAT_SOLUBLE_VITAMIN_METABOLIC_PROCESS	30	-0,43544576	-1,4702661	0,04970179	0,33729354	1	1878	tags=30%, list=11%, signal=34%
GO_COFACTOR_BIOSYNTHETIC_PROCESS	GO_COFACTOR_BIOSYNTHETIC_PROCESS	153	-0,40810406	-1,4697728	0,09696969	0,33747563	1	2332	tags=33%, list=13%, signal=38%
GO_OXIDOREDUCTASE_COMPLEX	GO_OXIDOREDUCTASE_COMPLEX	89	-0,49879864	-1,469654	0,13034624	0,33688733	1	3946	tags=56%, list=22%, signal=72%
GO_B_CELL_MEDIATED_IMMUNITY	GO_B_CELL_MEDIATED_IMMUNITY	68	-0,44357455	-1,4686553	0,10147992	0,3380145	1	1223	tags=25%, list=7%, signal=27%
GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	GO_SECONDARY_METABOLITE_BIOSYNTHETIC_PROCESS	19	-0,5407037	-1,4673824	0,06653992	0,33959767	1	3678	tags=47%, list=21%, signal=60%
GO_PHOTOPERIODISM	GO_PHOTOPERIODISM	23	-0,4497267	-1,4666262	0,06769826	0,34022686	1	1622	tags=26%, list=9%, signal=29%

GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	GO_REGULATION_OF_POSITIVE_CHEMOTAXIS	22	-0,49831733	-1,4666133	0,09179688	0,33942866	1	921	tags=27%, list=5%, signal=29%
GO_NEGATIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_STEROID_METABOLIC_PROCESS	23	-0,45669174	-1,4656887	0,06818182	0,3404025	1	3891	tags=39%, list=22%, signal=50%
GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_MIGRATION	64	-0,3990523	-1,4656206	0,06586827	0,33971095	1	3192	tags=30%, list=18%, signal=36%
GO_ORGANOPHOSPHATE_ESTER_TRANSPORT	GO_ORGANOPHOSPHATE_ESTER_TRANSPORT	84	-0,36350888	-1,4653536	0,03448276	0,33939767	1	2418	tags=30%, list=14%, signal=34%
GO_ORGANIC_ANION_TRANSPORT	GO_ORGANIC_ANION_TRANSPORT	360	-0,30606815	-1,464682	0,01646091	0,33986112	1	3555	tags=33%, list=20%, signal=40%
GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	GO_CARBOHYDRATE_BIOSYNTHETIC_PROCESS	117	-0,35507867	-1,4646473	0,04637097	0,33911848	1	2503	tags=30%, list=14%, signal=35%
GO_RESPONSE_TO_INORGANIC_SUBSTANCE	GO_RESPONSE_TO_INORGANIC_SUBSTANCE	456	-0,2920812	-1,4618582	0,00806452	0,34375638	1	3060	tags=28%, list=17%, signal=33%
GO_HEART_TRABECULA_MORPHOGENESIS	GO_HEART_TRABECULA_MORPHOGENESIS	24	-0,46465355	-1,4606293	0,07088123	0,34534147	1	3202	tags=42%, list=18%, signal=51%
GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	GO_TETRAHYDROFOLATE_METABOLIC_PROCESS	19	-0,50568974	-1,4603701	0,08817636	0,3450418	1	1178	tags=37%, list=7%, signal=39%
GO_DRUG_TRANSPORT	GO_DRUG_TRANSPORT	25	-0,48209548	-1,4597026	0,07677165	0,3456375	1	2286	tags=32%, list=13%, signal=37%
GO_ORGANIC_ACID_TRANSPORT	GO_ORGANIC_ACID_TRANSPORT	245	-0,32123286	-1,4587106	0,02272727	0,3468368	1	3539	tags=34%, list=20%, signal=42%
GO_SULFUR_AMINO_ACID_BIOSYNTHETIC_PROCESS	GO_SULFUR_AMINO_ACID_BIOSYNTHETIC_PROCESS	19	-0,5336767	-1,4575384	0,10580913	0,34831548	1	2067	tags=37%, list=12%, signal=42%
GO_ENDOCRINE_PROCESS	GO_ENDOCRINE_PROCESS	42	-0,4278863	-1,4574059	0,04397706	0,34774438	1	5167	tags=45%, list=29%, signal=64%
GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	84	-0,3528923	-1,4558188	0,04453441	0,3499468	1	3110	tags=29%, list=18%, signal=35%
GO_HORMONE_BIOSYNTHETIC_PROCESS	GO_HORMONE_BIOSYNTHETIC_PROCESS	46	-0,4128917	-1,454098	0,06841046	0,3524619	1	1627	tags=22%, list=9%, signal=24%
GO_CARBON_OXYGEN_LYASE_ACTIVITY	GO_CARBON_OXYGEN_LYASE_ACTIVITY	62	-0,40774807	-1,4539853	0,05613306	0,35188234	1	3141	tags=47%, list=18%, signal=57%
GO_SMOOTH_MUSCLE_CONTRACTION	GO_SMOOTH_MUSCLE_CONTRACTION	45	-0,43098235	-1,4537864	0,07014028	0,35145298	1	5654	tags=58%, list=32%, signal=85%
GO_BETA_AMYLOID_BINDING	GO_BETA_AMYLOID_BINDING	33	-0,4072823	-1,4534495	0,05788423	0,35128105	1	3439	tags=42%, list=19%, signal=53%
GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	GO_NEGATIVE_REGULATION_OF_HEMOPOIESIS	117	-0,34093797	-1,4528335	0,04791667	0,35173503	1	3507	tags=32%, list=20%, signal=39%
GO_QUATERNARY_AMMONIUM_GROUP_TRANSPORT	GO_QUATERNARY_AMMONIUM_GROUP_TRANSPORT	18	-0,5204037	-1,4525449	0,07039338	0,35145128	1	3386	tags=61%, list=19%, signal=76%
GO_PROTEIN_MATURATION	GO_PROTEIN_MATURATION	250	-0,31167528	-1,452512	0,02282158	0,35071066	1	3265	tags=30%, list=18%, signal=36%
GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	GO_RENAL_SYSTEM_VASCULATURE_DEVELOPMENT	19	-0,5852382	-1,4522103	0,12770137	0,35047388	1	2311	tags=37%, list=13%, signal=42%
GO_NEGATIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_LIPID_METABOLIC_PROCESS	76	-0,35321587	-1,4516866	0,03144654	0,35070333	1	3350	tags=34%, list=19%, signal=42%
GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_ACTIVITY	47	-0,39364293	-1,4511601	0,05295316	0,35091722	1	3785	tags=36%, list=21%, signal=46%
GO_REGULATION_OF_LIPID_TRANSPORT	GO_REGULATION_OF_LIPID_TRANSPORT	92	-0,3471132	-1,4511354	0,03174603	0,35016394	1	1540	tags=20%, list=9%, signal=21%
GO_VITAMIN_TRANSPORT	GO_VITAMIN_TRANSPORT	29	-0,41972017	-1,4507782	0,05327869	0,35007146	1	2573	tags=31%, list=15%, signal=36%
GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	GO_CD4_POSITIVE_ALPHA_BETA_T_CELL_ACTIVATION	32	-0,42965218	-1,450509	0,08910891	0,3497661	1	4193	tags=47%, list=24%, signal=61%
GO_REGULATION_OF_INFLAMMATORY_RESPONSE	GO_REGULATION_OF_INFLAMMATORY_RESPONSE	274	-0,3470482	-1,4502387	0,06339468	0,34948418	1	3695	tags=31%, list=21%, signal=39%
GO_TRABECULA_FORMATION	GO_TRABECULA_FORMATION	22	-0,4999193	-1,4475206	0,0859375	0,35379842	1	1053	tags=27%, list=6%, signal=29%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_CH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	24	-0,5025981	-1,4463421	0,11340206	0,35519478	1	2452	tags=46%, list=14%, signal=53%
GO_RESPONSE_TO_EPINEPHRINE	GO_RESPONSE_TO_EPINEPHRINE	16	-0,54134303	-1,4461871	0,07485604	0,35468742	1	4442	tags=50%, list=25%, signal=67%
GO_TETRAPYRROLE_METABOLIC_PROCESS	GO_TETRAPYRROLE_METABOLIC_PROCESS	56	-0,44433406	-1,4448577	0,0724346	0,3565166	1	2736	tags=36%, list=15%, signal=42%
GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	GO_MONOSACCHARIDE_BIOSYNTHETIC_PROCESS	52	-0,4470651	-1,4438716	0,11270492	0,35761893	1	2454	tags=46%, list=14%, signal=53%
GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_PHOSPHATASE_ACTIVITY	27	-0,44680017	-1,4413805	0,06903353	0,36162665	1	1445	tags=26%, list=8%, signal=28%
GO_PEPTIDASE_INHIBITOR_ACTIVITY	GO_PEPTIDASE_INHIBITOR_ACTIVITY	152	-0,334239	-1,4413531	0,03180914	0,36088714	1	1844	tags=18%, list=10%, signal=20%
GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	GO_SULFUR_COMPOUND_BIOSYNTHETIC_PROCESS	192	-0,32524818	-1,4411719	0,02976191	0,36041248	1	2504	tags=26%, list=14%, signal=30%
GO_REGULATED_EXOCYTOSIS	GO_REGULATED_EXOCYTOSIS	211	-0,33700085	-1,440053	0,05108055	0,3618481	1	2977	tags=27%, list=17%, signal=33%
GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	GO_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	24	-0,45140842	-1,4383196	0,08350731	0,3643529	1	2904	tags=38%, list=16%, signal=45%
GO_CAMP_BINDING	GO_CAMP_BINDING	21	-0,48832622	-1,4381955	0,07572816	0,3637799	1	2132	tags=24%, list=12%, signal=27%
GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	GO_PURINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	47	-0,3814872	-1,4360002	0,08219178	0,36710823	1	2982	tags=34%, list=17%, signal=41%
GO_REGULATION_OF_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	GO_REGULATION_OF_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	18	-0,4939655	-1,4345216	0,07915058	0,369462	1	4409	tags=56%, list=25%, signal=74%
GO_GLYCEROLIPID_CATABOLIC_PROCESS	GO_GLYCEROLIPID_CATABOLIC_PROCESS	35	-0,42852026	-1,4333214	0,08401639	0,37089017	1	2410	tags=37%, list=14%, signal=43%
GO_PEPTIDYL_GLUTAMIC_ACID_MODIFICATION	GO_PEPTIDYL_GLUTAMIC_ACID_MODIFICATION	26	-0,43037206	-1,4326683	0,06910569	0,37137604	1	1894	tags=38%, list=11%, signal=43%
GO_INSULIN_RECEPTOR_BINDING	GO_INSULIN_RECEPTOR_BINDING	31	-0,42621833	-1,4323992	0,06225681	0,3710758	1	3032	tags=42%, list=17%, signal=51%
GO_REGULATION_OF_BLOOD_PRESSURE	GO_REGULATION_OF_BLOOD_PRESSURE	158	-0,34322363	-1,4323958	0,02906977	0,37028003	1	2958	tags=29%, list=17%, signal=35%
GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_ORGANIC_HYDROXY_COMPOUND_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	58	-0,386243	-1,4309868	0,03629032	0,37237334	1	4372	tags=47%, list=25%, signal=62%
GO_PRE_AUTOPHAGOSOMAL_STRUCTURE_MEMBRANE	GO_PRE_AUTOPHAGOSOMAL_STRUCTURE_MEMBRANE	15	-0,51567286	-1,4308145	0,1030303	0,37197042	1	5022	tags=60%, list=28%, signal=84%
GO_RESPONSE_TO_ISCHEMIA	GO_RESPONSE_TO_ISCHEMIA	28	-0,44050997	-1,43074	0,07484408	0,37129682	1	3688	tags=46%, list=21%, signal=59%
GO_TRANSCRIPTION_COFACTOR_BINDING	GO_TRANSCRIPTION_COFACTOR_BINDING	24	-0,47696036	-1,4305736	0,10588235	0,37080812	1	2726	tags=29%, list=15%, signal=34%
GO_INNATE_IMMUNE_RESPONSE_IN_MUCOSA	GO_INNATE_IMMUNE_RESPONSE_IN_MUCOSA	17	-0,544689	-1,428713	0,11020408	0,37374377	1	6407	tags=71%, list=36%, signal=111%
GO_RESPONSE_TO_DRUG	GO_RESPONSE_TO_DRUG	419	-0,2959047	-1,428673	0,01364522	0,37300035	1	2126	tags=21%, list=12%, signal=24%
GO_RESPONSE_TO_IRON_ION	GO_RESPONSE_TO_IRON_ION	35	-0,4056362	-1,4279076	0,07212476	0,373726	1	2723	tags=29%, list=15%, signal=34%

GO_STRIATED_MUSCLE_ADAPTATION	GO_STRIATED_MUSCLE_ADAPTATION	21	-0,46696112	-1,4263172	0,07321773	0,3760052	1	3685	tags=52%, list=21%, signal=66%
GO_REGULATION_OF_SUPEROXIDE_METABOLIC_PROCESS	GO_REGULATION_OF_SUPEROXIDE_METABOLIC_PROCESS	22	-0,42620656	-1,4257377	0,08442777	0,37643692	1	1178	tags=23%, list=7%, signal=24%
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_THE_RELEASE_OF_SEQUESTERED_CALCIUM_ION	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_REGULATION_OF_THE_RELEASE_OF_SEQUESTERED_CALCIUM_ION	19	-0,50751656	-1,4253074	0,08267716	0,37641072	1	3787	tags=47%, list=21%, signal=60%
GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN	GO_MITOCHONDRIAL_ELECTRON_TRANSPORT_CYTOCHROME_C_TO_OXYGEN	16	-0,6535106	-1,4250762	0,14371258	0,37605864	1	3811	tags=56%, list=22%, signal=72%
GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	GO_CELLULAR_MODIFIED_AMINO_ACID_BIOSYNTHETIC_PROCESS	49	-0,41156816	-1,424824	0,08722109	0,37581283	1	3301	tags=41%, list=19%, signal=50%
GO_ANION_HOMEOSTASIS	GO_ANION_HOMEOSTASIS	39	-0,40348333	-1,4245856	0,06183369	0,37543437	1	3350	tags=44%, list=19%, signal=54%
GO_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_NITRIC_OXIDE_BIOSYNTHETIC_PROCESS	51	-0,38830438	-1,4237725	0,1026694	0,37628075	1	3110	tags=29%, list=18%, signal=36%
GO_REGULATION_OF_MUSCLE_HYPERTROPHY	GO_REGULATION_OF_MUSCLE_HYPERTROPHY	36	-0,39803496	-1,4227599	0,06346154	0,3775545	1	1412	tags=25%, list=8%, signal=27%
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	56	-0,36523655	-1,422253	0,04106776	0,37778896	1	1687	tags=25%, list=10%, signal=28%
GO_REGULATION_OF_HORMONE_LEVELS	GO_REGULATION_OF_HORMONE_LEVELS	450	-0,28912804	-1,4222406	0,00603622	0,37701952	1	3106	tags=24%, list=18%, signal=29%
GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	GO_SMOOTH_MUSCLE_TISSUE_DEVELOPMENT	18	-0,50952166	-1,4201105	0,10912699	0,38062558	1	427	tags=22%, list=2%, signal=23%
GO_RESPONSE_TO_LITHIUM_ION	GO_RESPONSE_TO_LITHIUM_ION	26	-0,43080777	-1,4192191	0,06626506	0,381644	1	2846	tags=35%, list=16%, signal=41%
GO_RESPONSE_TO_CARBOHYDRATE	GO_RESPONSE_TO_CARBOHYDRATE	160	-0,31609523	-1,4187297	0,02892562	0,38180587	1	3154	tags=28%, list=18%, signal=34%
GO_AMINO_ACID_BINDING	GO_AMINO_ACID_BINDING	101	-0,3375821	-1,4185363	0,04	0,38138914	1	3457	tags=33%, list=20%, signal=40%
GO_RESPONSE_TO_FATTY_ACID	GO_RESPONSE_TO_FATTY_ACID	81	-0,3408979	-1,418346	0,04391218	0,3810096	1	1294	tags=23%, list=7%, signal=25%
GO_ORGAN_GROWTH	GO_ORGAN_GROWTH	66	-0,39844626	-1,4179082	0,06809338	0,3810706	1	2715	tags=29%, list=15%, signal=34%
GO_CELLULAR_RESPONSE_TO_CAMP	GO_CELLULAR_RESPONSE_TO_CAMP	49	-0,4046924	-1,4178014	0,076	0,3804879	1	1687	tags=22%, list=10%, signal=25%
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HORMONE	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_HORMONE	33	-0,4463487	-1,4172623	0,06177606	0,38075083	1	5881	tags=58%, list=33%, signal=86%
GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	GO_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	55	-0,39876655	-1,4163318	0,06072874	0,38184664	1	2975	tags=31%, list=17%, signal=37%
GO_PYRUVATE_METABOLIC_PROCESS	GO_PYRUVATE_METABOLIC_PROCESS	59	-0,40780258	-1,4159251	0,10123967	0,38182703	1	1605	tags=27%, list=9%, signal=30%
GO_REGULATION_OF_MONOOXYGENASE_ACTIVITY	GO_REGULATION_OF_MONOOXYGENASE_ACTIVITY	58	-0,36791277	-1,4157581	0,06066536	0,38140056	1	3786	tags=34%, list=21%, signal=44%
GO_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	GO_RESPONSE_TO_ARSENIC_CONTAINING_SUBSTANCE	29	-0,4161133	-1,4140359	0,06930693	0,38404098	1	2845	tags=31%, list=16%, signal=37%
GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	GO_POSITIVE_REGULATION_OF_BLOOD_PRESSURE	34	-0,41057476	-1,4125814	0,05465587	0,38624868	1	2569	tags=29%, list=15%, signal=34%
GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	GO_INNER_MITOCHONDRIAL_MEMBRANE_PROTEIN_COMPLEX	100	-0,55479234	-1,4123853	0,1996008	0,38580638	1	4432	tags=55%, list=25%, signal=73%
GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_BLOOD_VOLUME	GO_RENAL_SYSTEM_PROCESS_INVOLVED_IN_REGULATION_OF_BLOOD_VOLUME	17	-0,48196903	-1,4100738	0,08461539	0,38960966	1	2648	tags=35%, list=15%, signal=41%
GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO_ADENYLATE_CYCLASE_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	53	-0,40645704	-1,4096198	0,06090373	0,38971046	1	2802	tags=32%, list=16%, signal=38%
GO_CELLULAR_GLUCOSE_HOMEOSTASIS	GO_CELLULAR_GLUCOSE_HOMEOSTASIS	70	-0,3411068	-1,4094524	0,05394191	0,3892597	1	1693	tags=20%, list=10%, signal=22%
GO_REGULATION_OF_CATECHOLAMINE_METABOLIC_PROCESS	GO_REGULATION_OF_CATECHOLAMINE_METABOLIC_PROCESS	15	-0,5095384	-1,4079524	0,10061602	0,39139593	1	4107	tags=47%, list=23%, signal=61%
GO_PROTEIN_DEGLYCOSYLATION	GO_PROTEIN_DEGLYCOSYLATION	21	-0,49106348	-1,4062369	0,13692947	0,39412463	1	2480	tags=38%, list=14%, signal=44%
GO_ORGANELLE_INNER_MEMBRANE	GO_ORGANELLE_INNER_MEMBRANE	481	-0,40632066	-1,4055097	0,14345114	0,39478606	1	3976	tags=41%, list=23%, signal=52%
GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSPORT	GO_NEGATIVE_REGULATION_OF_GLUCOSE_TRANSPORT	16	-0,49123025	-1,4049231	0,09503239	0,3951436	1	2573	tags=38%, list=15%, signal=44%
GO_POSITIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	28	-0,4445142	-1,4029491	0,09475806	0,39836374	1	3073	tags=39%, list=17%, signal=47%
GO_RESPONSE_TO_ALCOHOL	GO_RESPONSE_TO_ALCOHOL	345	-0,2964184	-1,4026436	0,01829268	0,39821	1	2176	tags=23%, list=12%, signal=26%
GO_REGULATION_OF_POLYSACCHARIDE_METABOLIC_PROCESS	GO_REGULATION_OF_POLYSACCHARIDE_METABOLIC_PROCESS	41	-0,3736694	-1,4022486	0,0761523	0,39819252	1	3110	tags=37%, list=18%, signal=44%
GO_MANNOSE_BINDING	GO_MANNOSE_BINDING	18	-0,46813473	-1,4018153	0,09716599	0,3983162	1	2109	tags=33%, list=12%, signal=38%
GO_SECRETORY_GRANULE	GO_SECRETORY_GRANULE	321	-0,30653507	-1,401606	0,03366337	0,39797044	1	2977	tags=27%, list=17%, signal=32%
GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	GO_ASPARTATE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	22	-0,49247903	-1,4013033	0,1352459	0,39778554	1	1369	tags=36%, list=8%, signal=39%
GO_COFACTOR_TRANSPORT	GO_COFACTOR_TRANSPORT	26	-0,42000058	-1,4012367	0,1108742	0,39709917	1	2523	tags=31%, list=14%, signal=36%
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_ASSEMBLY	63	-0,5578393	-1,4011799	0,18787879	0,3964176	1	5394	tags=68%, list=31%, signal=98%
GO_INTRACELLULAR_LIPID_TRANSPORT	GO_INTRACELLULAR_LIPID_TRANSPORT	20	-0,4670632	-1,4004103	0,10462777	0,39725608	1	3227	tags=50%, list=18%, signal=61%
GO_RETROGRADE_TRANSPORT_VESICLE_RECYCLING_WITHIN_GOLGI	GO_RETROGRADE_TRANSPORT_VESICLE_RECYCLING_WITHIN_GOLGI	21	-0,4958192	-1,3992571	0,12678936	0,39879587	1	3002	tags=52%, list=17%, signal=63%
GO_PURINE_RIBONUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	GO_PURINE_RIBONUCLEOSIDE_BISPHOSPHATE_METABOLIC_PROCESS	20	-0,45398936	-1,399133	0,09839357	0,39824852	1	1847	tags=45%, list=10%, signal=50%
GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_LIPID_CATABOLIC_PROCESS	20	-0,4531308	-1,3988326	0,08464567	0,3981255	1	1770	tags=30%, list=10%, signal=33%
GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	GO_MITOCHONDRIAL_RESPIRATORY_CHAIN_COMPLEX_I_BIOGENESIS	51	-0,5920041	-1,3970547	0,18275154	0,40088367	1	5394	tags=75%, list=31%, signal=107%
GO_VITAMIN_TRANSPORTER_ACTIVITY	GO_VITAMIN_TRANSPORTER_ACTIVITY	20	-0,43330508	-1,3969567	0,08008213	0,400291	1	2573	tags=35%, list=15%, signal=41%
GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	GO_3_5_CYCLIC_AMP_PHOSPHODIESTERASE_ACTIVITY	15	-0,55137557	-1,3969284	0,13931298	0,399578	1	4442	tags=73%, list=25%, signal=98%
GO_EXCRETION	GO_EXCRETION	42	-0,40736586	-1,3950995	0,07017544	0,4024492	1	1735	tags=24%, list=10%, signal=26%
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	50	-0,37584618	-1,3948257	0,08847737	0,40220356	1	3236	tags=34%, list=18%, signal=42%
GO_DEFINITIVE_HEMOPOIESIS	GO_DEFINITIVE_HEMOPOIESIS	16	-0,52329504	-1,3929459	0,13671875	0,40523955	1	3041	tags=44%, list=17%, signal=53%
GO_REGULATION_OF_MUSCLE_ADAPTATION	GO_REGULATION_OF_MUSCLE_ADAPTATION	60	-0,3616757	-1,3924643	0,07156673	0,40538564	1	1412	tags=20%, list=8%, signal=22%
GO_DETOXIFICATION	GO_DETOXIFICATION	68	-0,38602984	-1,3916693	0,09036145	0,40616632	1	2832	tags=32%, list=16%, signal=38%
GO_METHIONINE_METABOLIC_PROCESS	GO_METHIONINE_METABOLIC_PROCESS	18	-0,4911615	-1,3897113	0,12783505	0,40944228	1	1369	tags=33%, list=8%, signal=36%

GO_PEPTIDE_HORMONE_PROCESSING	GO_PEPTIDE_HORMONE_PROCESSING	28	-0,43777573	-1,3895974	0,10139165	0,40890324	1	5597	tags=57%, list=32%, signal=84%
GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RENIN_ANGIOTENSIN	GO_REGULATION_OF_SYSTEMIC_ARTERIAL_BLOOD_PRESSURE_BY_RENIN_ANGIOTENSIN	21	-0,48533502	-1,3894649	0,11368015	0,4083923	1	5060	tags=52%, list=29%, signal=73%
GO_NEUROTRANSMITTER_METABOLIC_PROCESS	GO_NEUROTRANSMITTER_METABOLIC_PROCESS	24	-0,44429335	-1,3891672	0,07471264	0,40825647	1	650	tags=21%, list=4%, signal=22%
GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	GO_TRANSLATION_REGULATOR_ACTIVITY_NUCLEIC_ACID_BINDING	16	-0,48406425	-1,3884121	0,10192308	0,40905786	1	3447	tags=56%, list=20%, signal=70%
GO_MULTIVESICULAR_BODY	GO_MULTIVESICULAR_BODY	35	-0,3870633	-1,3873341	0,05858586	0,4104728	1	2271	tags=31%, list=13%, signal=36%
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	17	-0,5054023	-1,3873225	0,10153256	0,4096996	1	4988	tags=53%, list=28%, signal=74%
GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	GO_RIBONUCLEOTIDE_CATABOLIC_PROCESS	28	-0,4232905	-1,3857862	0,1223301	0,4121314	1	2982	tags=36%, list=17%, signal=43%
GO_RESPONSE_TO_ESTRADIOL	GO_RESPONSE_TO_ESTRADIOL	142	-0,31597543	-1,3849659	0,05598456	0,4129585	1	1875	tags=22%, list=11%, signal=24%
GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_NUCLEOTIDE_METABOLIC_PROCESS	114	-0,33163393	-1,3843979	0,05436893	0,41325328	1	3355	tags=29%, list=19%, signal=36%
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STARVATION	GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STARVATION	24	-0,42102253	-1,383694	0,11507937	0,4138849	1	2288	tags=29%, list=13%, signal=33%
GO_WATER_HOMEOSTASIS	GO_WATER_HOMEOSTASIS	65	-0,36247876	-1,3831877	0,06309751	0,41416278	1	4327	tags=40%, list=24%, signal=53%
GO_NECROPTOTIC_PROCESS	GO_NECROPTOTIC_PROCESS	21	-0,45266613	-1,3830448	0,10874201	0,41363314	1	4684	tags=57%, list=27%, signal=78%
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSPORT	33	-0,4127298	-1,3801736	0,08232932	0,41878945	1	4465	tags=48%, list=25%, signal=65%
GO_REFLEX	GO_REFLEX	18	-0,47690186	-1,3795751	0,10153256	0,41920963	1	2260	tags=28%, list=13%, signal=32%
GO_ACETYL_COA_METABOLIC_PROCESS	GO_ACETYL_COA_METABOLIC_PROCESS	23	-0,5082317	-1,3795702	0,14979757	0,41844112	1	1975	tags=43%, list=11%, signal=49%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	19	-0,55082035	-1,378037	0,186	0,42088956	1	3553	tags=63%, list=20%, signal=79%
GO_GROWTH_FACTOR_BINDING	GO_GROWTH_FACTOR_BINDING	121	-0,37850896	-1,377288	0,13163064	0,42160475	1	3061	tags=29%, list=17%, signal=35%
GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	GO_TETRAPYRROLE_BIOSYNTHETIC_PROCESS	27	-0,48486727	-1,3757609	0,14851485	0,42396292	1	4768	tags=59%, list=27%, signal=81%
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	110	-0,32823366	-1,3755487	0,08134921	0,4235476	1	2321	tags=25%, list=13%, signal=29%
GO_PEPTIDASE_REGULATOR_ACTIVITY	GO_PEPTIDASE_REGULATOR_ACTIVITY	187	-0,30551875	-1,3753215	0,05263158	0,42322344	1	2168	tags=19%, list=12%, signal=22%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	252	-0,31180948	-1,3749908	0,07370518	0,4231539	1	2975	tags=25%, list=17%, signal=30%
GO_NEGATIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	GO_NEGATIVE_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	40	-0,38148558	-1,3749263	0,08778626	0,42249152	1	3110	tags=35%, list=18%, signal=42%
GO_ACTININ_BINDING	GO_ACTININ_BINDING	27	-0,4330756	-1,3724812	0,13372093	0,42686978	1	3547	tags=44%, list=20%, signal=56%
GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	GO_REGULATION_OF_RENAL_SYSTEM_PROCESS	36	-0,4157997	-1,3715988	0,08187135	0,4279391	1	4296	tags=42%, list=24%, signal=55%
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_LINEAR_AMIDES	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS_IN_LINEAR_AMIDES	83	-0,31885013	-1,3688542	0,0562249	0,4327746	1	1898	tags=28%, list=11%, signal=31%
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL_BY_SARCOPLASMIC_RETICULUM	GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL_BY_SARCOPLASMIC_RETICULUM	24	-0,4895674	-1,3685423	0,11787819	0,43264621	1	3794	tags=46%, list=21%, signal=58%
GO_OXIDATIVE_PHOSPHORYLATION	GO_OXIDATIVE_PHOSPHORYLATION	79	-0,5490197	-1,3674488	0,23015873	0,43417072	1	3915	tags=54%, list=22%, signal=70%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_A_SULFUR_GROUP_OF_DONORS	42	-0,40489435	-1,3666377	0,13867188	0,43514204	1	1730	tags=29%, list=10%, signal=32%
GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	GO_SULFUR_COMPOUND_CATABOLIC_PROCESS	38	-0,40181312	-1,3662026	0,12475634	0,4353397	1	1007	tags=24%, list=6%, signal=25%
GO_SERTOLI_CELL_DIFFERENTIATION	GO_SERTOLI_CELL_DIFFERENTIATION	17	-0,4625483	-1,3657762	0,09218437	0,4353787	1	3003	tags=47%, list=17%, signal=57%
GO_HEMOSTASIS	GO_HEMOSTASIS	285	-0,314563	-1,3645155	0,10123967	0,4371839	1	2737	tags=26%, list=15%, signal=30%
GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS	GO_HYDROLASE_ACTIVITY_ACTING_ON_CARBON_NITROGEN_BUT_NOT_PEPTIDE_BONDS	138	-0,29737025	-1,3631228	0,02819957	0,43934172	1	2166	tags=25%, list=12%, signal=28%
GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_PURINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	373	-0,33201864	-1,3629351	0,11983471	0,4390068	1	3217	tags=31%, list=18%, signal=38%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_WOUNDING	153	-0,34769386	-1,3621638	0,1206544	0,4398215	1	2194	tags=21%, list=12%, signal=24%
GO_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	GO_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	22	-0,4663155	-1,3615538	0,13250518	0,44037428	1	1364	tags=27%, list=8%, signal=30%
GO_MONOSACCHARIDE_BINDING	GO_MONOSACCHARIDE_BINDING	65	-0,3610726	-1,3613837	0,0955414	0,43994302	1	2213	tags=29%, list=13%, signal=33%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_OF_DONORS	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH2_GROUP_OF_DONORS	18	-0,47507873	-1,3605878	0,09453782	0,4408957	1	2239	tags=39%, list=13%, signal=44%
GO_PHOSPHATIDYLCHOLINE_METABOLIC_PROCESS	GO_PHOSPHATIDYLCHOLINE_METABOLIC_PROCESS	61	-0,33525527	-1,3603991	0,06457926	0,44049364	1	1465	tags=20%, list=8%, signal=21%
GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	GO_ORGANOPHOSPHATE_CATABOLIC_PROCESS	110	-0,30863255	-1,3595526	0,06748466	0,44165674	1	2674	tags=29%, list=15%, signal=34%
GO_CAMP_BIOSYNTHETIC_PROCESS	GO_CAMP_BIOSYNTHETIC_PROCESS	16	-0,50943923	-1,3589792	0,138833	0,4420803	1	4964	tags=56%, list=28%, signal=78%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	35	-0,392775	-1,3589658	0,11752137	0,44131324	1	3788	tags=34%, list=21%, signal=44%
GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	GO_S_ADENOSYLMETHIONINE_METABOLIC_PROCESS	18	-0,46590087	-1,3570087	0,15944882	0,44462258	1	1389	tags=33%, list=8%, signal=36%
GO_CIRCULATORY_SYSTEM_PROCESS	GO_CIRCULATORY_SYSTEM_PROCESS	346	-0,31600416	-1,3569674	0,07524753	0,44392624	1	3545	tags=29%, list=20%, signal=35%
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	51	-0,39379945	-1,356142	0,13865547	0,44496438	1	1947	tags=27%, list=11%, signal=31%
GO_CELLULAR_RESPONSE_TO_FLUID_SHEAR_STRESS	GO_CELLULAR_RESPONSE_TO_FLUID_SHEAR_STRESS	18	-0,4695678	-1,3558027	0,11389961	0,44487593	1	2081	tags=39%, list=12%, signal=44%
GO_EPITHELIAL_CELL_PROLIFERATION	GO_EPITHELIAL_CELL_PROLIFERATION	86	-0,35814962	-1,3556162	0,08366534	0,44450507	1	1870	tags=22%, list=11%, signal=25%
GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	GO_REGULATION_OF_BMP_SIGNALING_PATHWAY	74	-0,37937483	-1,3552463	0,11153119	0,44452247	1	2829	tags=31%, list=16%, signal=37%
GO_CYCLIC_NUCLEOTIDE_BINDING	GO_CYCLIC_NUCLEOTIDE_BINDING	32	-0,4050091	-1,3548487	0,10364683	0,44459975	1	4486	tags=38%, list=25%, signal=50%
GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS	GO_DICARBOXYLIC_ACID_CATABOLIC_PROCESS	16	-0,48834398	-1,3547152	0,12704918	0,44408235	1	4125	tags=56%, list=23%, signal=73%
GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	GO_OXIDOREDUCTASE_ACTIVITY_OXIDIZING_METAL_IONS	17	-0,48188365	-1,3545134	0,1417004	0,44375694	1	2432	tags=41%, list=14%, signal=48%
GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	GO_UBIQUITIN_LIKE_PROTEIN_CONJUGATING_ENZYME_BINDING	32	-0,38464677	-1,351965	0,11594203	0,4482923	1	2726	tags=38%, list=15%, signal=44%

GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	GO_POSITIVE_REGULATION_OF_ENDOTHELIAL_CELL_PROLIFERATION	67	-0,37082794	-1,3511468	0,152	0,4492567	1	3424	tags=31%, list=19%, signal=39%
GO_CYTOLYSIS	GO_CYTOLYSIS	23	-0,46290657	-1,3507019	0,17327766	0,44945875	1	920	tags=26%, list=5%, signal=27%
GO_WATER_TRANSPORT	GO_WATER_TRANSPORT	18	-0,47246224	-1,3482543	0,12350598	0,45383793	1	4327	tags=50%, list=24%, signal=66%
GO_MYOSIN_II_COMPLEX	GO_MYOSIN_II_COMPLEX	24	-0,44884434	-1,3479594	0,12423626	0,45363653	1	3750	tags=42%, list=21%, signal=53%
GO_PROTEIN_LIPID_COMPLEX_ASSEMBLY	GO_PROTEIN_LIPID_COMPLEX_ASSEMBLY	21	-0,46186805	-1,346043	0,15461847	0,45710185	1	3291	tags=48%, list=19%, signal=58%
GO_EXTRACELLULAR_MATRIX_ASSEMBLY	GO_EXTRACELLULAR_MATRIX_ASSEMBLY	16	-0,53322864	-1,3449047	0,14453125	0,45873433	1	2546	tags=44%, list=14%, signal=51%
GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	GO_REGULATION_OF_FAT_CELL_DIFFERENTIATION	100	-0,32934764	-1,3440782	0,08458646	0,4597399	1	3412	tags=31%, list=19%, signal=38%
GO_MICROVILLUS	GO_MICROVILLUS	70	-0,3444355	-1,3439542	0,09	0,45922828	1	4416	tags=36%, list=25%, signal=47%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H_QUINONE_OR_SIMILAR_COMPOUND_AS_ACCEPTOR	51	-0,54318655	-1,3429618	0,23673469	0,46060133	1	3915	tags=59%, list=22%, signal=75%
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT1_PROTEIN	GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT1_PROTEIN	15	-0,4940319	-1,3422531	0,15105163	0,46127617	1	3311	tags=33%, list=19%, signal=41%
GO_LIPID_DIGESTION	GO_LIPID_DIGESTION	19	-0,44304457	-1,3407476	0,09126984	0,46384495	1	2265	tags=32%, list=13%, signal=36%
GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	GO_PHENOL_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	33	-0,43409562	-1,3405039	0,10396975	0,46355698	1	3678	tags=33%, list=21%, signal=42%
GO_STEROID_DEHYDROGENASE_ACTIVITY	GO_STEROID_DEHYDROGENASE_ACTIVITY	27	-0,45853242	-1,339679	0,13690476	0,46452323	1	2080	tags=33%, list=12%, signal=38%
GO_ALDITOL_METABOLIC_PROCESS	GO_ALDITOL_METABOLIC_PROCESS	18	-0,4712036	-1,3388541	0,14910537	0,46559653	1	3470	tags=50%, list=20%, signal=62%
GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	GO_ACTIVATION_OF_PHOSPHOLIPASE_C_ACTIVITY	26	-0,45341983	-1,3385956	0,1764706	0,4653965	1	2630	tags=38%, list=15%, signal=45%
GO_COENZYME_A_METABOLIC_PROCESS	GO_COENZYME_A_METABOLIC_PROCESS	17	-0,5057559	-1,3377773	0,17519686	0,46640685	1	503	tags=29%, list=3%, signal=30%
GO_E_BOX_BINDING	GO_E_BOX_BINDING	27	-0,4313756	-1,3367269	0,12922466	0,46783626	1	2856	tags=37%, list=16%, signal=44%
GO_CARBOHYDRATE_BINDING	GO_CARBOHYDRATE_BINDING	244	-0,32423463	-1,3352742	0,10860656	0,47025174	1	3089	tags=27%, list=17%, signal=32%
GO_BLOOD_VESSEL_MORPHOGENESIS	GO_BLOOD_VESSEL_MORPHOGENESIS	352	-0,33839408	-1,3346957	0,13786408	0,47076294	1	3217	tags=29%, list=18%, signal=35%
GO_REGULATION_OF_HYDROGEN_PEROXIDE_INDUCED_CELL_DEATH	GO_REGULATION_OF_HYDROGEN_PEROXIDE_INDUCED_CELL_DEATH	17	-0,44674197	-1,3337148	0,13025211	0,4721445	1	2081	tags=35%, list=12%, signal=40%
GO_ALPHA_ACTININ_BINDING	GO_ALPHA_ACTININ_BINDING	20	-0,45703858	-1,3327414	0,17227723	0,47342253	1	2701	tags=40%, list=15%, signal=47%
GO_RESPONSE_TO_PEPTIDE	GO_RESPONSE_TO_PEPTIDE	375	-0,27628744	-1,3324252	0,07258064	0,4733048	1	2726	tags=23%, list=15%, signal=27%
GO_POSITIVE_REGULATION_OF_VASODILATION	GO_POSITIVE_REGULATION_OF_VASODILATION	31	-0,4029067	-1,3317438	0,0995935	0,47410747	1	3540	tags=32%, list=20%, signal=40%
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	30	-0,3794993	-1,3309703	0,10660981	0,47508055	1	1687	tags=27%, list=10%, signal=29%
GO_LYMPH_VESSEL_DEVELOPMENT	GO_LYMPH_VESSEL_DEVELOPMENT	20	-0,50053304	-1,3306845	0,16666667	0,47489673	1	3078	tags=50%, list=17%, signal=60%
GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	GO_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	160	-0,3279274	-1,3294059	0,11952192	0,47693613	1	3236	tags=28%, list=18%, signal=33%
GO_MODIFIED_AMINO_ACID_TRANSPORT	GO_MODIFIED_AMINO_ACID_TRANSPORT	26	-0,42027825	-1,3292476	0,12262157	0,47644144	1	2523	tags=27%, list=14%, signal=31%
GO_REGULATION_OF_BODY_FLUID_LEVELS	GO_REGULATION_OF_BODY_FLUID_LEVELS	467	-0,29355305	-1,328422	0,07628866	0,4774398	1	3192	tags=27%, list=18%, signal=32%
GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	GO_NEGATIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	95	-0,34046432	-1,3281162	0,11445783	0,47731757	1	2969	tags=23%, list=17%, signal=28%
GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	GO_POSITIVE_REGULATION_OF_CIRCADIAN_RHYTHM	18	-0,44334027	-1,3272743	0,10707457	0,47836903	1	960	tags=17%, list=5%, signal=18%
GO_REGULATION_OF_ANION_TRANSPORT	GO_REGULATION_OF_ANION_TRANSPORT	130	-0,29916504	-1,326221	0,05521473	0,47994977	1	3497	tags=30%, list=20%, signal=37%
GO_TRABECULA_MORPHOGENESIS	GO_TRABECULA_MORPHOGENESIS	37	-0,39210138	-1,3230022	0,1330724	0,48643205	1	1053	tags=19%, list=6%, signal=20%
GO_COA_HYDROLASE_ACTIVITY	GO_COA_HYDROLASE_ACTIVITY	20	-0,4634957	-1,3229877	0,1714876	0,48565668	1	2332	tags=40%, list=13%, signal=46%
GO_REGULATION_OF_AMINO_ACID_TRANSPORT	GO_REGULATION_OF_AMINO_ACID_TRANSPORT	25	-0,41759408	-1,322631	0,11428572	0,48570603	1	5013	tags=52%, list=28%, signal=73%
GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	GO_POSITIVE_REGULATION_OF_VASOCONSTRICTION	34	-0,42512926	-1,3210248	0,15717092	0,48859048	1	3110	tags=35%, list=18%, signal=43%
GO_OVULATION	GO_OVULATION	17	-0,48293844	-1,3196311	0,16260162	0,490852	1	1693	tags=24%, list=10%, signal=26%
GO_CELL_VOLUME_HOMEOSTASIS	GO_CELL_VOLUME_HOMEOSTASIS	26	-0,41370204	-1,3194056	0,13939394	0,49054214	1	4988	tags=58%, list=28%, signal=80%
GO_REGULATION_OF_ARF_PROTEIN_SIGNAL_TRANSDUCTION	GO_REGULATION_OF_ARF_PROTEIN_SIGNAL_TRANSDUCTION	15	-0,4684354	-1,3187048	0,14784394	0,4913898	1	725	tags=20%, list=4%, signal=21%
GO_MODULATION_BY_HOST_OF_VIRAL_PROCESS	GO_MODULATION_BY_HOST_OF_VIRAL_PROCESS	17	-0,4469678	-1,3178121	0,13333334	0,49258018	1	1364	tags=24%, list=8%, signal=25%
GO_RESPONSE_TO_CALCIUM_ION	GO_RESPONSE_TO_CALCIUM_ION	109	-0,3046778	-1,3168428	0,07884616	0,49396393	1	2975	tags=31%, list=17%, signal=37%
GO_RESPONSE_TO_STEROL	GO_RESPONSE_TO_STEROL	23	-0,41568646	-1,3161523	0,14428858	0,49463245	1	3413	tags=39%, list=19%, signal=48%
GO_GLUCOSE_METABOLIC_PROCESS	GO_GLUCOSE_METABOLIC_PROCESS	113	-0,3276879	-1,3161368	0,12215321	0,49387223	1	3110	tags=32%, list=18%, signal=38%
GO_RESPONSE_TO_ESTROGEN	GO_RESPONSE_TO_ESTROGEN	211	-0,28447905	-1,315235	0,04518664	0,49503776	1	1875	tags=19%, list=11%, signal=21%
GO_CELLULAR_RESPONSE_TO_LEPTIN_STIMULUS	GO_CELLULAR_RESPONSE_TO_LEPTIN_STIMULUS	16	-0,4520526	-1,3151947	0,1459566	0,49432647	1	4874	tags=56%, list=28%, signal=78%
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	19	-0,45377117	-1,3139758	0,16283526	0,49618125	1	4672	tags=58%, list=26%, signal=79%
GO_URONIC_ACID_METABOLIC_PROCESS	GO_URONIC_ACID_METABOLIC_PROCESS	27	-0,46082237	-1,313281	0,17979798	0,49692556	1	825	tags=26%, list=5%, signal=27%
GO_MITOCHONDRIAL_PROTEIN_COMPLEX	GO_MITOCHONDRIAL_PROTEIN_COMPLEX	127	-0,47212812	-1,3118085	0,26494023	0,49945435	1	4432	tags=51%, list=25%, signal=68%
GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	GO_POSITIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	31	-0,40881196	-1,3115834	0,14722754	0,49914786	1	2818	tags=35%, list=16%, signal=42%
GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	GO_ADAPTIVE_IMMUNE_RESPONSE_BASED_ON_SOMATIC_RECOMBINATION_OF_IMMUNE_RECEPTORS_BUILT_FROM_IMMUNOGLOBULIN_SUPERFAMILY_DOMAINS	122	-0,35323668	-1,3106788	0,18511066	0,5003343	1	1223	tags=18%, list=7%, signal=19%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_NAD_P_H	88	-0,41762143	-1,3093812	0,21588595	0,5024334	1	3946	tags=49%, list=22%, signal=63%
GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO_PHOSPHOLIPASE_C_ACTIVATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	70	-0,358014	-1,3086966	0,12109375	0,5031511	1	3427	tags=36%, list=19%, signal=44%

GO_RESPONSE_TO_CADMIUM_ION	GO_RESPONSE_TO_CADMIUM_ION	39	-0,39709172	-1,3085765	0,1871345	0,5026294	1	2913	tags=44%, list=16%, signal=52%
GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	63	-0,3366989	-1,3081248	0,13855422	0,5028784	1	3110	tags=25%, list=18%, signal=31%
GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	GO_POSITIVE_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	58	-0,37098303	-1,3065805	0,15019763	0,505399	1	5320	tags=48%, list=30%, signal=69%
GO_METAL_CLUSTER_BINDING	GO_METAL_CLUSTER_BINDING	60	-0,3863378	-1,3047044	0,18436874	0,5088769	1	3379	tags=47%, list=19%, signal=58%
GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	GO_NEGATIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	88	-0,3379555	-1,3046849	0,14285715	0,5081151	1	3547	tags=32%, list=20%, signal=40%
GO_RESPONSE_TO_ACID_CHEMICAL	GO_RESPONSE_TO_ACID_CHEMICAL	296	-0,27074853	-1,3046213	0,06813628	0,5074437	1	2802	tags=24%, list=16%, signal=28%
GO_RESPONSE_TO_STEROID_HORMONE	GO_RESPONSE_TO_STEROID_HORMONE	473	-0,26085842	-1,3043196	0,0368932	0,5072839	1	2126	tags=20%, list=12%, signal=22%
GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS	GO_CELLULAR_RESPONSE_TO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_STIMULUS	29	-0,42280185	-1,3039054	0,18837675	0,507449	1	3936	tags=45%, list=22%, signal=58%
GO_PROTEIN_TETRAMERIZATION	GO_PROTEIN_TETRAMERIZATION	124	-0,30522534	-1,3037083	0,14020619	0,50706804	1	1914	tags=25%, list=11%, signal=28%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_PEROXIDE_AS_ACCEPTOR	39	-0,40772912	-1,3029032	0,15983607	0,50802684	1	2832	tags=33%, list=16%, signal=40%
GO_RESPONSE_TO_VITAMIN_E	GO_RESPONSE_TO_VITAMIN_E	15	-0,46762726	-1,3026912	0,15682282	0,50767434	1	2627	tags=27%, list=15%, signal=31%
GO_ALCOHOL_BIOSYNTHETIC_PROCESS	GO_ALCOHOL_BIOSYNTHETIC_PROCESS	106	-0,3252716	-1,3019725	0,14227642	0,5085213	1	1581	tags=19%, list=9%, signal=21%
GO_CARBOHYDRATE_TRANSPORTER_ACTIVITY	GO_CARBOHYDRATE_TRANSPORTER_ACTIVITY	41	-0,3555319	-1,3017439	0,10891089	0,5082626	1	3752	tags=41%, list=21%, signal=53%
GO_ZYMOGEN_ACTIVATION	GO_ZYMOGEN_ACTIVATION	108	-0,2977006	-1,3016721	0,08677686	0,50763184	1	2285	tags=25%, list=13%, signal=29%
GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_METABOLIC_PROCESS	38	-0,3645484	-1,3006537	0,14990138	0,50896776	1	1056	tags=21%, list=6%, signal=22%
GO_ANGIOGENESIS	GO_ANGIOGENESIS	282	-0,33862236	-1,3005991	0,15187377	0,50828743	1	3217	tags=29%, list=18%, signal=35%
GO_QUINONE_METABOLIC_PROCESS	GO_QUINONE_METABOLIC_PROCESS	28	-0,4728693	-1,2999107	0,22129436	0,5090468	1	2100	tags=39%, list=12%, signal=45%
GO_RESPONSE_TO_NUTRIENT	GO_RESPONSE_TO_NUTRIENT	183	-0,27360153	-1,2989227	0,05189621	0,51051736	1	1761	tags=19%, list=10%, signal=20%
GO_CELLULAR_RESPONSE_TO_DRUG	GO_CELLULAR_RESPONSE_TO_DRUG	66	-0,3271135	-1,2964177	0,11089109	0,51529664	1	1491	tags=18%, list=8%, signal=20%
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	35	-0,4366052	-1,2962619	0,18421052	0,5149039	1	1648	tags=23%, list=9%, signal=25%
GO_REGULATION_OF_ORGAN_GROWTH	GO_REGULATION_OF_ORGAN_GROWTH	70	-0,3201339	-1,2949171	0,11368015	0,51709217	1	2195	tags=24%, list=12%, signal=28%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	26	-0,38991046	-1,2947024	0,14814815	0,51674926	1	4510	tags=50%, list=26%, signal=67%
GO_RESPONSE_TO_HYDROGEN_PEROXIDE	GO_RESPONSE_TO_HYDROGEN_PEROXIDE	107	-0,30472362	-1,2939032	0,11646587	0,5177545	1	3057	tags=33%, list=17%, signal=39%
GO_CELLULAR_RESPONSE_TO_STARVATION	GO_CELLULAR_RESPONSE_TO_STARVATION	108	-0,3007176	-1,2930355	0,10515873	0,51892966	1	2712	tags=25%, list=15%, signal=29%
GO_FATTY_ACYL_COA_METABOLIC_PROCESS	GO_FATTY_ACYL_COA_METABOLIC_PROCESS	48	-0,36627293	-1,29267	0,18379447	0,5189069	1	2623	tags=33%, list=15%, signal=39%
GO_PEROXISOMAL_TRANSPORT	GO_PEROXISOMAL_TRANSPORT	18	-0,48165876	-1,2921742	0,21802935	0,5192852	1	2826	tags=50%, list=16%, signal=59%
GO_AMMONIUM_TRANSMEMBRANE_TRANSPORT	GO_AMMONIUM_TRANSMEMBRANE_TRANSPORT	24	-0,41370893	-1,2908083	0,1734694	0,5216871	1	3444	tags=46%, list=19%, signal=57%
GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	GO_PROTEIN_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	19	-0,46837428	-1,2897117	0,21556886	0,52348256	1	547	tags=26%, list=3%, signal=27%
GO_INORGANIC_ION_IMPORT_INTO_CELL	GO_INORGANIC_ION_IMPORT_INTO_CELL	15	-0,4428301	-1,2892095	0,16634052	0,52381444	1	1915	tags=33%, list=11%, signal=37%
GO_NEGATIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	GO_NEGATIVE_REGULATION_OF_STRESS_FIBER_ASSEMBLY	16	-0,45317835	-1,2887506	0,18640776	0,52410704	1	1830	tags=31%, list=10%, signal=35%
GO_VASCULATURE_DEVELOPMENT	GO_VASCULATURE_DEVELOPMENT	452	-0,31882408	-1,2881905	0,17884615	0,52463293	1	3250	tags=28%, list=18%, signal=34%
GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COMMITMENT	GO_REGULATION_OF_TRANSCRIPTION_INVOLVED_IN_CELL_FATE_COMMITMENT	20	-0,41771188	-1,2865677	0,14574899	0,527555	1	1374	tags=25%, list=8%, signal=27%
GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_HYDROLASE_ACTIVITY	358	-0,2545224	-1,2862314	0,0513347	0,5276107	1	2627	tags=19%, list=15%, signal=22%
GO_POSITIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	46	-0,34997725	-1,2861682	0,12548262	0,52694076	1	1547	tags=20%, list=9%, signal=21%
GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	GO_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	24	-0,43934464	-1,2857822	0,19615385	0,52704054	1	3155	tags=46%, list=18%, signal=56%
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_SIGNAL_TRANSDUCTION	411	-0,2629421	-1,285053	0,10060363	0,52782565	1	2785	tags=24%, list=16%, signal=27%
GO_GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	GO_GLUTAMINE_FAMILY_AMINO_ACID_CATABOLIC_PROCESS	24	-0,43094823	-1,2849346	0,18	0,52733254	1	2627	tags=50%, list=15%, signal=59%
GO_CELLULAR_RESPONSE_TO_ALCOHOL	GO_CELLULAR_RESPONSE_TO_ALCOHOL	107	-0,3072826	-1,2848074	0,10060363	0,52684236	1	2124	tags=24%, list=12%, signal=27%
GO_NEGATIVE_REGULATION_OF_RECEPTOR_ACTIVITY	GO_NEGATIVE_REGULATION_OF_RECEPTOR_ACTIVITY	29	-0,37727144	-1,2838951	0,1311787	0,5280814	1	3794	tags=34%, list=21%, signal=44%
GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	GO_REGULATION_OF_CAMP_MEDIATED_SIGNALING	21	-0,40815175	-1,2834629	0,16633664	0,52829707	1	3608	tags=29%, list=20%, signal=36%
GO_MONOSACCHARIDE_METABOLIC_PROCESS	GO_MONOSACCHARIDE_METABOLIC_PROCESS	191	-0,29362983	-1,2832261	0,13671875	0,5280135	1	3110	tags=29%, list=18%, signal=35%
GO_REGULATION_OF_RENAL_SODIUM_EXCRETION	GO_REGULATION_OF_RENAL_SODIUM_EXCRETION	22	-0,41750222	-1,2824932	0,13562752	0,5288281	1	4296	tags=36%, list=24%, signal=48%
GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	GO_NEGATIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	18	-0,4336736	-1,2809402	0,15400411	0,5315509	1	3381	tags=39%, list=19%, signal=48%
GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	GO_NEGATIVE_REGULATION_OF_BLOOD_PRESSURE	41	-0,35711884	-1,2800424	0,13359529	0,53280544	1	3886	tags=41%, list=22%, signal=53%
GO_COMPLEMENT_BINDING	GO_COMPLEMENT_BINDING	19	-0,48334378	-1,2796509	0,23293173	0,5328448	1	3533	tags=37%, list=20%, signal=46%
GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	GO_CYCLIC_NUCLEOTIDE_BIOSYNTHETIC_PROCESS	32	-0,40056273	-1,2794293	0,17029703	0,5325636	1	2692	tags=25%, list=15%, signal=29%
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_AXONOGENESIS	26	-0,4184334	-1,278727	0,1417004	0,5333414	1	3780	tags=42%, list=21%, signal=54%
GO_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEIN_CATABOLIC_PROCESS	GO_MISFOLDED_OR_INCOMPLETELY_SYNTHESIZED_PROTEIN_CATABOLIC_PROCESS	15	-0,49169728	-1,277772	0,22929937	0,53470105	1	3330	tags=40%, list=19%, signal=49%
GO_T_CELL_SELECTION	GO_T_CELL_SELECTION	35	-0,44936818	-1,2774072	0,2480315	0,53476584	1	4916	tags=46%, list=28%, signal=63%
GO_ALPHA_TUBULIN_BINDING	GO_ALPHA_TUBULIN_BINDING	22	-0,38877055	-1,277059	0,16829745	0,53476626	1	2022	tags=27%, list=11%, signal=31%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	54	-0,36044225	-1,2766687	0,14428858	0,5348174	1	3951	tags=35%, list=22%, signal=45%
GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	GO_NEGATIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_APOPTOTIC_PROCESS	17	-0,42514297	-1,2739667	0,15879017	0,54029566	1	3951	tags=41%, list=22%, signal=53%

GO_POSITIVE_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	GO_POSITIVE_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	16	-0,45666152	-1,273795	0,1846473	0,5398932	1	2365	tags=38%, list=13%, signal=43%
GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	GO_POSITIVE_REGULATION_OF_REACTIVE_OXYGEN_SPECIES_BIOSYNTHETIC_PROCESS	47	-0,3420368	-1,273535	0,14712153	0,5396982	1	3110	tags=28%, list=18%, signal=33%
GO_ENZYME_INHIBITOR_ACTIVITY	GO_ENZYME_INHIBITOR_ACTIVITY	334	-0,25455534	-1,2733891	0,05952381	0,5392552	1	1907	tags=17%, list=11%, signal=18%
GO_CALCIUM_INDEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	GO_CALCIUM_INDEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	19	-0,42762554	-1,2719053	0,17680608	0,5419665	1	5309	tags=58%, list=30%, signal=83%
GO_MUSCLE_ADAPTATION	GO_MUSCLE_ADAPTATION	27	-0,380307	-1,2716316	0,14147286	0,54182017	1	3685	tags=41%, list=21%, signal=51%
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	60	-0,3464689	-1,2710576	0,14705883	0,54237854	1	4322	tags=38%, list=24%, signal=51%
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_PROLIFERATION	99	-0,32819095	-1,2707632	0,15384616	0,5422921	1	4322	tags=36%, list=24%, signal=48%
GO_CARBOHYDRATE_CATABOLIC_PROCESS	GO_CARBOHYDRATE_CATABOLIC_PROCESS	104	-0,3150993	-1,2694839	0,16973415	0,54439676	1	2602	tags=28%, list=15%, signal=33%
GO_FAT_CELL_DIFFERENTIATION	GO_FAT_CELL_DIFFERENTIATION	99	-0,30856943	-1,2689844	0,1364562	0,5447476	1	3645	tags=32%, list=21%, signal=40%
GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	GO_PTERIDINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	16	-0,48084766	-1,267457	0,21338913	0,5474205	1	1888	tags=44%, list=11%, signal=49%
GO_RESPONSE_TO_MUSCLE_STRETCH	GO_RESPONSE_TO_MUSCLE_STRETCH	17	-0,43663698	-1,2671705	0,19477911	0,5472992	1	3547	tags=35%, list=20%, signal=44%
GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	GO_POSITIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	32	-0,36808896	-1,2669309	0,18181819	0,54705966	1	3232	tags=41%, list=18%, signal=50%
GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	GO_ALPHA_BETA_T_CELL_DIFFERENTIATION	43	-0,40473914	-1,2669154	0,23469388	0,54628813	1	4209	tags=44%, list=24%, signal=58%
GO_SECOND_MESSENGER_MEDIATED_SIGNALING	GO_SECOND_MESSENGER_MEDIATED_SIGNALING	150	-0,31606036	-1,2654133	0,15667312	0,5490963	1	2692	tags=24%, list=15%, signal=28%
GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	GO_ORGANIC_ACID_SODIUM_SYMPORTER_ACTIVITY	30	-0,38155162	-1,2645974	0,14669421	0,55011314	1	1382	tags=30%, list=8%, signal=32%
GO_GLYCOPROTEIN_BINDING	GO_GLYCOPROTEIN_BINDING	98	-0,32004356	-1,2642031	0,1553398	0,55020237	1	2975	tags=30%, list=17%, signal=35%
GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	GO_CYCLIC_NUCLEOTIDE_CATABOLIC_PROCESS	17	-0,46238804	-1,263979	0,21212122	0,5499088	1	4442	tags=59%, list=25%, signal=79%
GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	GO_NUCLEOSIDE_PHOSPHATE_CATABOLIC_PROCESS	67	-0,3169024	-1,2631977	0,14375	0,55092293	1	3141	tags=33%, list=18%, signal=40%
GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	GO_CELLULAR_RESPONSE_TO_CARBOHYDRATE_STIMULUS	70	-0,31134328	-1,262865	0,11458334	0,5508686	1	1745	tags=20%, list=10%, signal=22%
GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	GO_POSITIVE_REGULATION_OF_ANION_TRANSPORT	55	-0,32554877	-1,261133	0,12398374	0,5540197	1	2194	tags=22%, list=12%, signal=25%
GO_WOUND_HEALING	GO_WOUND_HEALING	431	-0,28463668	-1,2609133	0,15071283	0,5536934	1	2737	tags=24%, list=15%, signal=28%
GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	GO_CYCLIC_NUCLEOTIDE_MEDIATED_SIGNALING	44	-0,3673865	-1,2606051	0,18903592	0,5536592	1	2692	tags=30%, list=15%, signal=35%
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT5_PROTEIN	16	-0,43982658	-1,2605135	0,18307087	0,55305743	1	3311	tags=38%, list=19%, signal=46%
GO_LIPASE_INHIBITOR_ACTIVITY	GO_LIPASE_INHIBITOR_ACTIVITY	15	-0,45411018	-1,2604115	0,16242662	0,55250067	1	854	tags=27%, list=5%, signal=28%
GO_RESPONSE_TO_ANTIBIOTIC	GO_RESPONSE_TO_ANTIBIOTIC	44	-0,3492133	-1,2602189	0,1663158	0,55213994	1	2971	tags=25%, list=17%, signal=30%
GO_CIRCADIAN_RHYTHM	GO_CIRCADIAN_RHYTHM	125	-0,30362007	-1,259908	0,15280464	0,5520875	1	3412	tags=33%, list=19%, signal=40%
GO_RESPONSE_TO_LEPTIN	GO_RESPONSE_TO_LEPTIN	20	-0,41460964	-1,2592989	0,15936255	0,5526803	1	4902	tags=50%, list=28%, signal=69%
GO_RESPONSE_TO_ACTIVITY	GO_RESPONSE_TO_ACTIVITY	64	-0,3300028	-1,2582299	0,14	0,5544368	1	1790	tags=20%, list=10%, signal=23%
GO_GLUTATHIONE_PEROXIDASE_ACTIVITY	GO_GLUTATHIONE_PEROXIDASE_ACTIVITY	15	-0,4853439	-1,2579077	0,2248996	0,5544141	1	2832	tags=47%, list=16%, signal=56%
GO_PORE_COMPLEX	GO_PORE_COMPLEX	17	-0,45352077	-1,2577133	0,20558882	0,55405104	1	920	tags=35%, list=5%, signal=37%
GO_EXOCYTOSIS	GO_EXOCYTOSIS	294	-0,27102795	-1,2571241	0,11394892	0,55466056	1	3151	tags=24%, list=18%, signal=29%
GO_SIALYLATION	GO_SIALYLATION	20	-0,41377738	-1,2567163	0,16122448	0,5548442	1	2435	tags=30%, list=14%, signal=35%
GO_APICAL_PLASMA_MEMBRANE	GO_APICAL_PLASMA_MEMBRANE	273	-0,27934316	-1,2562137	0,12475634	0,5553127	1	4553	tags=37%, list=26%, signal=49%
GO_EPITHELIAL_STRUCTURE_MAINTENANCE	GO_EPITHELIAL_STRUCTURE_MAINTENANCE	20	-0,39077896	-1,2561319	0,1627451	0,5547158	1	178	tags=15%, list=1%, signal=15%
GO_SECRETORY_GRANULE_MEMBRANE	GO_SECRETORY_GRANULE_MEMBRANE	73	-0,31671435	-1,2561098	0,12790698	0,55398595	1	2977	tags=26%, list=17%, signal=31%
GO_NEGATIVE_REGULATION_OF_ORGAN_GROWTH	GO_NEGATIVE_REGULATION_OF_ORGAN_GROWTH	20	-0,40657383	-1,2551484	0,17408907	0,5553914	1	1937	tags=30%, list=11%, signal=34%
GO_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_PEPTIDASE_ACTIVITY	218	-0,26907977	-1,2547535	0,10843374	0,55544096	1	1844	tags=16%, list=10%, signal=18%
GO_MUSCLE_SYSTEM_PROCESS	GO_MUSCLE_SYSTEM_PROCESS	270	-0,30259702	-1,252611	0,14117648	0,55966884	1	3819	tags=31%, list=22%, signal=39%
GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	GO_REGULATION_OF_ESTABLISHMENT_OR_MAINTENANCE_OF_CELL_POLARITY	20	-0,44133267	-1,2525989	0,19132149	0,5589113	1	2385	tags=35%, list=14%, signal=40%
GO_PHOSPHOLIPASE_BINDING	GO_PHOSPHOLIPASE_BINDING	18	-0,39533746	-1,2519023	0,17460318	0,5597975	1	1830	tags=28%, list=10%, signal=31%
GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	GO_CELLULAR_RESPONSE_TO_GROWTH_HORMONE_STIMULUS	17	-0,43384457	-1,2517186	0,2053942	0,559464	1	349	tags=18%, list=2%, signal=18%
GO_AUTOPHAGOSOME_ORGANIZATION	GO_AUTOPHAGOSOME_ORGANIZATION	39	-0,3709233	-1,2513416	0,17561984	0,5595917	1	4710	tags=44%, list=27%, signal=59%
GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_LYASE_ACTIVITY	53	-0,3399171	-1,2510523	0,13680154	0,5594799	1	2692	tags=26%, list=15%, signal=31%
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	26	-0,38721812	-1,2509551	0,18072289	0,5589305	1	2810	tags=31%, list=16%, signal=37%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	75	-0,32186902	-1,250774	0,20404041	0,5585482	1	3467	tags=28%, list=20%, signal=35%
GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	GO_OXIDOREDUCTASE_ACTIVITY_ACTING_ON_THE_CH_NH_GROUP_OF_DONORS_NAD_OR_NADP_AS_ACCEPTOR	16	-0,4222883	-1,2504908	0,21782178	0,5584558	1	1501	tags=31%, list=8%, signal=34%
GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	GO_NEGATIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	115	-0,3235575	-1,2504503	0,18644068	0,5577678	1	1688	tags=17%, list=10%, signal=19%
GO_AMIDE_BINDING	GO_AMIDE_BINDING	238	-0,2604167	-1,2483947	0,09267242	0,56194717	1	2957	tags=24%, list=17%, signal=28%
GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY	GO_ACTIVATION_OF_ADENYLATE_CYCLASE_ACTIVITY	36	-0,37219423	-1,2483857	0,16438356	0,56119883	1	2692	tags=28%, list=15%, signal=33%
GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	GO_NEGATIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	23	-0,39436483	-1,2474883	0,18518518	0,56259274	1	2975	tags=35%, list=17%, signal=42%
GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	GO_REGULATION_OF_CELLULAR_KETONE_METABOLIC_PROCESS	167	-0,31082517	-1,2462718	0,16736402	0,5646173	1	1294	tags=17%, list=7%, signal=19%

GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	GO_NUCLEOBASE_CONTAINING_SMALL_MOLECULE_METABOLIC_PROCESS	495	-0,29242525	-1,2462138	0,1865828	0,5639732	1	2766	tags=26%, list=16%, signal=30%
GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	GO_POSITIVE_REGULATION_OF_BLOOD_CIRCULATION	91	-0,32198808	-1,2460607	0,14428858	0,56358474	1	3202	tags=27%, list=18%, signal=33%
GO_EPITHELIAL_CELL_MORPHOGENESIS	GO_EPITHELIAL_CELL_MORPHOGENESIS	42	-0,34891093	-1,2428302	0,152	0,57046324	1	3769	tags=29%, list=21%, signal=36%
GO_PROTEIN_HOMOOLIGOMERIZATION	GO_PROTEIN_HOMOOLIGOMERIZATION	234	-0,25207293	-1,2417377	0,09940358	0,5723407	1	3316	tags=28%, list=19%, signal=34%
GO_NEURON_PROJECTION_REGENERATION	GO_NEURON_PROJECTION_REGENERATION	31	-0,36333773	-1,2415857	0,20235756	0,57194155	1	3010	tags=35%, list=17%, signal=43%
GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_OXIDOREDUCTASE_ACTIVITY	23	-0,38366333	-1,2404664	0,16595745	0,5737624	1	1794	tags=22%, list=10%, signal=24%
GO_AMMONIUM_TRANSPORT	GO_AMMONIUM_TRANSPORT	55	-0,32599127	-1,23974	0,13894325	0,57475156	1	3926	tags=40%, list=22%, signal=51%
GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	GO_ALDO_KETO_REDUCTASE_NADP_ACTIVITY	25	-0,43160954	-1,239217	0,25	0,57515764	1	2078	tags=32%, list=12%, signal=36%
GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	GO_POSITIVE_REGULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	21	-0,4170739	-1,2386367	0,20286885	0,5756801	1	2048	tags=24%, list=12%, signal=27%
GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	46	-0,32642856	-1,2369794	0,1611002	0,5789138	1	1633	tags=17%, list=9%, signal=19%
GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	GO_NEGATIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	51	-0,3319674	-1,2368817	0,18813907	0,57833236	1	3030	tags=27%, list=17%, signal=33%
GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	GO_REGULATION_OF_DENDRITIC_SPINE_MORPHOGENESIS	30	-0,35723668	-1,2359477	0,19253439	0,57982266	1	2097	tags=30%, list=12%, signal=34%
GO_FOLIC_ACID_METABOLIC_PROCESS	GO_FOLIC_ACID_METABOLIC_PROCESS	17	-0,40679684	-1,2351526	0,23155738	0,5809235	1	698	tags=18%, list=4%, signal=18%
GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	GO_CELLULAR_RESPONSE_TO_INORGANIC_SUBSTANCE	142	-0,28022268	-1,2329628	0,11919192	0,58555347	1	2852	tags=29%, list=16%, signal=34%
GO_GOLGI_LUMEN	GO_GOLGI_LUMEN	83	-0,3265072	-1,2325591	0,16795367	0,5857123	1	2057	tags=22%, list=12%, signal=24%
GO_ACTIVATION_OF_PROTEIN_KINASE_B_ACTIVITY	GO_ACTIVATION_OF_PROTEIN_KINASE_B_ACTIVITY	21	-0,3854628	-1,2323512	0,200409	0,5854347	1	1491	tags=29%, list=8%, signal=31%
GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	GO_NEGATIVE_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	16	-0,43668446	-1,2321892	0,21991701	0,5850723	1	1983	tags=31%, list=11%, signal=35%
GO_REGULATION_OF_ERAD_PATHWAY	GO_REGULATION_OF_ERAD_PATHWAY	26	-0,37371692	-1,2312362	0,20247933	0,5864766	1	2480	tags=27%, list=14%, signal=31%
GO_REGULATION_OF_CELLULAR_RESPIRATION	GO_REGULATION_OF_CELLULAR_RESPIRATION	22	-0,39248618	-1,2308655	0,18825911	0,5865508	1	2369	tags=32%, list=13%, signal=37%
GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	23	-0,36043096	-1,229831	0,18548387	0,5882869	1	3507	tags=43%, list=20%, signal=54%
GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	GO_GLYCOSYL_COMPOUND_CATABOLIC_PROCESS	37	-0,35662907	-1,2295657	0,2	0,58810914	1	2042	tags=22%, list=12%, signal=24%
GO_PHOSPHATIDYLETHANOLAMINE_METABOLIC_PROCESS	GO_PHOSPHATIDYLETHANOLAMINE_METABOLIC_PROCESS	16	-0,4164697	-1,2291032	0,20116054	0,58842015	1	4984	tags=63%, list=28%, signal=87%
GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	GO_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	22	-0,37804368	-1,2288097	0,2109375	0,58837503	1	4344	tags=36%, list=25%, signal=48%
GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	GO_POSITIVE_REGULATION_OF_ORGANIC_ACID_TRANSPORT	29	-0,3687231	-1,2272935	0,20594059	0,59116995	1	1720	tags=21%, list=10%, signal=23%
GO_HEXOSE_METABOLIC_PROCESS	GO_HEXOSE_METABOLIC_PROCESS	148	-0,2853454	-1,226731	0,17444219	0,59172153	1	3527	tags=32%, list=20%, signal=39%
GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	40	-0,36611193	-1,2253116	0,17706238	0,5943081	1	4409	tags=48%, list=25%, signal=63%
GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	GO_G_PROTEIN_BETA_GAMMA_SUBUNIT_COMPLEX_BINDING	19	-0,40162656	-1,2250662	0,21181263	0,59414023	1	2820	tags=32%, list=16%, signal=38%
GO_POSITIVE_REGULATION_OF_AUTOPHAGY	GO_POSITIVE_REGULATION_OF_AUTOPHAGY	74	-0,31282473	-1,2245703	0,18864097	0,59450704	1	1639	tags=19%, list=9%, signal=21%
GO_VENOUS_BLOOD_VESSEL_DEVELOPMENT	GO_VENOUS_BLOOD_VESSEL_DEVELOPMENT	15	-0,48578647	-1,2238253	0,256917	0,5955141	1	3187	tags=53%, list=18%, signal=65%
GO_SECRETORY_VESICLE	GO_SECRETORY_VESICLE	425	-0,25932747	-1,223767	0,11067194	0,5948556	1	3012	tags=24%, list=17%, signal=28%
GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	GO_GLUTATHIONE_TRANSFERASE_ACTIVITY	32	-0,393553	-1,2229671	0,2019802	0,5959674	1	3807	tags=47%, list=22%, signal=60%
GO_VASOCONSTRICTION	GO_VASOCONSTRICTION	27	-0,39027143	-1,2224195	0,21272366	0,5964968	1	5881	tags=52%, list=33%, signal=78%
GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	42	-0,33324057	-1,2223166	0,196	0,5959684	1	1364	tags=17%, list=8%, signal=18%
GO_REGULATION_OF_CHOLESTEROL_EFFLUX	GO_REGULATION_OF_CHOLESTEROL_EFFLUX	20	-0,4117301	-1,2218709	0,19535783	0,59628546	1	3412	tags=40%, list=19%, signal=50%
GO_MITOCHONDRIAL_MEMBRANE_PART	GO_MITOCHONDRIAL_MEMBRANE_PART	156	-0,40978098	-1,220643	0,30645162	0,5983635	1	3956	tags=43%, list=22%, signal=55%
GO_ENDOPEPTIDASE_ACTIVITY	GO_ENDOPEPTIDASE_ACTIVITY	377	-0,25462115	-1,2202432	0,10365854	0,59850615	1	2776	tags=20%, list=16%, signal=24%
GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	GO_CYCLIC_NUCLEOTIDE_PHOSPHODIESTERASE_ACTIVITY	24	-0,4157451	-1,2202071	0,23856859	0,597812	1	4501	tags=54%, list=25%, signal=73%
GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS	17	-0,4103469	-1,21877	0,22924902	0,6003969	1	3693	tags=47%, list=21%, signal=59%
GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	GO_NEGATIVE_REGULATION_OF_ION_TRANSPORT	119	-0,29922813	-1,2179912	0,17281553	0,6014527	1	4322	tags=37%, list=24%, signal=49%
GO_SPROUTING_ANGIOGENESIS	GO_SPROUTING_ANGIOGENESIS	43	-0,3733302	-1,2179234	0,24752475	0,6007991	1	1840	tags=28%, list=10%, signal=31%
GO_CALCIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	GO_CALCIUM_ACTIVATED_POTASSIUM_CHANNEL_ACTIVITY	15	-0,43229097	-1,2174548	0,22574258	0,6011579	1	2013	tags=33%, list=11%, signal=38%
GO_EPITHELIAL_CELL_DEVELOPMENT	GO_EPITHELIAL_CELL_DEVELOPMENT	178	-0,28822362	-1,2156541	0,16858238	0,6047163	1	2848	tags=25%, list=16%, signal=29%
GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	GO_NEGATIVE_REGULATION_OF_PHOSPHORYLATION	400	-0,2430577	-1,2151092	0,12623274	0,60522527	1	3428	tags=27%, list=19%, signal=33%
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_GROWTH_FACTOR_STIMULUS	217	-0,296398	-1,2137914	0,19455253	0,6075941	1	2829	tags=23%, list=16%, signal=27%
GO_RESPONSE_TO_MONOAMINE	GO_RESPONSE_TO_MONOAMINE	34	-0,3727727	-1,2127639	0,20703125	0,6093229	1	2802	tags=29%, list=16%, signal=35%
GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHANNEL_ACTIVITY	GO_REGULATION_OF_RYANODINE_SENSITIVE_CALCIUM_RELEASE_CHANNEL_ACTIVITY	26	-0,41457158	-1,2122102	0,23228346	0,60986835	1	3966	tags=50%, list=22%, signal=64%
GO_PLATELET_MORPHOGENESIS	GO_PLATELET_MORPHOGENESIS	18	-0,4021923	-1,2119623	0,22244489	0,6096687	1	720	tags=17%, list=4%, signal=17%
GO_STRIATUM_DEVELOPMENT	GO_STRIATUM_DEVELOPMENT	16	-0,4190117	-1,2116953	0,23293173	0,60954094	1	5185	tags=63%, list=29%, signal=88%
GO_ANION_TRANSPORT	GO_ANION_TRANSPORT	473	-0,24519615	-1,2110425	0,11181434	0,6103042	1	3555	tags=29%, list=20%, signal=35%
GO_CELL_SUBSTRATE_ADHERENS_JUNCTION_ASSEMBLY	GO_CELL_SUBSTRATE_ADHERENS_JUNCTION_ASSEMBLY	23	-0,39122686	-1,2108347	0,22011386	0,6100353	1	2994	tags=39%, list=17%, signal=47%
GO_R_SMAD_BINDING	GO_R_SMAD_BINDING	21	-0,4001329	-1,2105987	0,22941177	0,60982054	1	2829	tags=38%, list=16%, signal=45%
GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	GO_HYDROGEN_PEROXIDE_METABOLIC_PROCESS	30	-0,38579735	-1,2101651	0,22851562	0,6100605	1	2804	tags=30%, list=16%, signal=36%

GO_REGULATION_OF_IMMUNOGLOBULIN_SECRETION	GO_REGULATION_OF_IMMUNOGLOBULIN_SECRETION	15	-0,41264933	-1,2097387	0,21940929	0,6102642	1	2734	tags=27%, list=15%, signal=32%
GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	GO_POSITIVE_REGULATION_OF_LIPID_TRANSPORT	50	-0,3167267	-1,2091007	0,17490494	0,6109939	1	1495	tags=16%, list=8%, signal=17%
GO_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	GO_REGULATION_OF_MULTICELLULAR_ORGANISM_GROWTH	57	-0,31445852	-1,2079391	0,19305019	0,6129789	1	5328	tags=46%, list=30%, signal=65%
GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	GO_REGULATION_OF_ORGANIC_ACID_TRANSPORT	48	-0,32486853	-1,2071079	0,18864097	0,6141608	1	4322	tags=38%, list=24%, signal=50%
GO_APOLIPOPROTEIN_BINDING	GO_APOLIPOPROTEIN_BINDING	15	-0,44002447	-1,2060765	0,23732251	0,61580175	1	1193	tags=33%, list=7%, signal=36%
GO_GAP_JUNCTION	GO_GAP_JUNCTION	26	-0,383907	-1,2045746	0,22047244	0,6186517	1	3812	tags=42%, list=22%, signal=54%
GO_CELLULAR_RESPONSE_TO_STEROID_HORMONE_STIMULUS	GO_CELLULAR_RESPONSE_TO_STEROID_HORMONE_STIMULUS	204	-0,2581922	-1,2030815	0,13948919	0,6214731	1	2484	tags=22%, list=14%, signal=25%
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	66	-0,33096948	-1,2030541	0,19762845	0,6207457	1	4442	tags=36%, list=25%, signal=48%
GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	GO_POSITIVE_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	45	-0,333807	-1,202683	0,214	0,62087387	1	4458	tags=49%, list=25%, signal=65%
GO_RESPONSE_TO_DIETARY_EXCESS	GO_RESPONSE_TO_DIETARY_EXCESS	16	-0,43785322	-1,2023056	0,250478	0,6210046	1	3242	tags=44%, list=18%, signal=54%
GO_REGULATION_OF_BONE_DEVELOPMENT	GO_REGULATION_OF_BONE_DEVELOPMENT	16	-0,42631632	-1,2022158	0,2430279	0,62042946	1	1297	tags=19%, list=7%, signal=20%
GO_STEROL_BIOSYNTHETIC_PROCESS	GO_STEROL_BIOSYNTHETIC_PROCESS	41	-0,4108138	-1,2012529	0,2927835	0,62205034	1	1581	tags=24%, list=9%, signal=27%
GO_CELLULAR_RESPONSE_TO_PEPTIDE	GO_CELLULAR_RESPONSE_TO_PEPTIDE	253	-0,2549837	-1,201163	0,148	0,6214429	1	2692	tags=24%, list=15%, signal=28%
GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	GO_NEGATIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	18	-0,42149538	-1,1999826	0,26043737	0,6235658	1	1830	tags=28%, list=10%, signal=31%
GO_FATTY_ACID_BINDING	GO_FATTY_ACID_BINDING	29	-0,3678791	-1,1998358	0,23076923	0,6231729	1	1706	tags=28%, list=10%, signal=30%
GO_MUSCLE_CONTRACTION	GO_MUSCLE_CONTRACTION	223	-0,2938515	-1,1995094	0,18972331	0,6231333	1	4597	tags=36%, list=26%, signal=48%
GO_INSULIN_LIKE_GROWTH_FACTOR_BINDING	GO_INSULIN_LIKE_GROWTH_FACTOR_BINDING	25	-0,4161315	-1,1989926	0,26129666	0,6236037	1	2676	tags=36%, list=15%, signal=42%
GO_POSITIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	GO_POSITIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	72	-0,30359155	-1,1983237	0,1845238	0,6244558	1	3794	tags=31%, list=21%, signal=39%
GO_LYMPHOCYTE_MEDIATED_IMMUNITY	GO_LYMPHOCYTE_MEDIATED_IMMUNITY	113	-0,32239193	-1,1973705	0,24796748	0,62601715	1	1223	tags=17%, list=7%, signal=18%
GO_CAMP_MEDIATED_SIGNALING	GO_CAMP_MEDIATED_SIGNALING	35	-0,36224034	-1,1972355	0,234714	0,6255563	1	2692	tags=29%, list=15%, signal=34%
GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	GO_CELLULAR_RESPONSE_TO_AMINO_ACID_STIMULUS	46	-0,34931806	-1,1953899	0,25675675	0,62924016	1	3506	tags=33%, list=20%, signal=41%
GO_GLYCEROLIPID_METABOLIC_PROCESS	GO_GLYCEROLIPID_METABOLIC_PROCESS	336	-0,24206856	-1,195375	0,11545988	0,62849545	1	2442	tags=20%, list=14%, signal=23%
GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	GO_REGULATION_OF_PHOSPHOLIPASE_ACTIVITY	62	-0,3441439	-1,1949286	0,27160493	0,6287935	1	1947	tags=24%, list=11%, signal=27%
GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	GO_CELL_MIGRATION_INVOLVED_IN_SPROUTING_ANGIOGENESIS	15	-0,4398679	-1,1948119	0,25443786	0,6283062	1	2904	tags=40%, list=16%, signal=48%
GO_DORSAL_SPINAL_CORD_DEVELOPMENT	GO_DORSAL_SPINAL_CORD_DEVELOPMENT	16	-0,41891378	-1,1942023	0,2188755	0,6290191	1	1134	tags=19%, list=6%, signal=20%
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	18	-0,38202208	-1,1927052	0,23925234	0,6318283	1	1658	tags=22%, list=9%, signal=24%
GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_BMP_SIGNALING_PATHWAY	40	-0,36462227	-1,1925176	0,2581262	0,63148624	1	2829	tags=28%, list=16%, signal=33%
GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	GO_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	59	-0,29832506	-1,1923275	0,21616162	0,63116467	1	2081	tags=22%, list=12%, signal=25%
GO_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	GO_REGULATION_OF_ENDOTHELIAL_CELL_CHEMOTAXIS	16	-0,40189087	-1,1921306	0,2334004	0,6308768	1	329	tags=13%, list=2%, signal=13%
GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	GO_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	133	-0,30127195	-1,1919844	0,2059925	0,63050187	1	3434	tags=27%, list=19%, signal=33%
GO_RESPONSE_TO_CORTICOSTERONE	GO_RESPONSE_TO_CORTICOSTERONE	26	-0,3772685	-1,1909163	0,19169961	0,6321854	1	2126	tags=23%, list=12%, signal=26%
GO_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS_VIA_THE_MULTIVESICULAR_BODY_SORTING_PATHWAY	GO_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS_VIA_THE_MULTIVESICULAR_BODY_SORTING_PATHWAY	16	-0,42673376	-1,1908686	0,25303644	0,6315248	1	2673	tags=44%, list=15%, signal=52%
GO_RESPONSE_TO_BMP	GO_RESPONSE_TO_BMP	88	-0,31588304	-1,1899061	0,23506744	0,6331312	1	3183	tags=27%, list=18%, signal=33%
GO_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	GO_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	273	-0,2658967	-1,1890122	0,2007722	0,63452643	1	3110	tags=25%, list=18%, signal=30%
GO_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS	GO_PHOSPHATIDYLCHOLINE_BIOSYNTHETIC_PROCESS	25	-0,34264374	-1,1888711	0,20467836	0,6340751	1	1465	tags=20%, list=8%, signal=22%
GO_ENDOPLASMIC_RETICULUM_LUMEN	GO_ENDOPLASMIC_RETICULUM_LUMEN	191	-0,28545216	-1,1887871	0,21616162	0,63350606	1	3061	tags=24%, list=17%, signal=28%
GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	GO_NEGATIVE_REGULATION_OF_DEFENSE_RESPONSE	130	-0,29307005	-1,1880672	0,2188755	0,6345124	1	3412	tags=26%, list=19%, signal=32%
GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	GO_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	35	-0,38610965	-1,1876808	0,2548638	0,6347151	1	2664	tags=34%, list=15%, signal=40%
GO_COFACTOR_TRANSPORTER_ACTIVITY	GO_COFACTOR_TRANSPORTER_ACTIVITY	21	-0,39005157	-1,1876593	0,2489796	0,6339978	1	2006	tags=24%, list=11%, signal=27%
GO_MYOFIBRIL_ASSEMBLY	GO_MYOFIBRIL_ASSEMBLY	45	-0,34190115	-1,1875827	0,21626984	0,6334174	1	4046	tags=42%, list=23%, signal=55%
GO_CELLULAR_RESPONSE_TO_CORTICOSTEROID_STIMULUS	GO_CELLULAR_RESPONSE_TO_CORTICOSTEROID_STIMULUS	53	-0,30492988	-1,187557	0,20507812	0,6327165	1	2124	tags=25%, list=12%, signal=28%
GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	GO_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	37	-0,35925353	-1,1867496	0,2601626	0,63391715	1	1223	tags=19%, list=7%, signal=20%
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_MIGRATION	100	-0,311833	-1,1842556	0,22244489	0,639234	1	3192	tags=26%, list=18%, signal=32%
GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	GO_PHOSPHOLIPID_TRANSPORTER_ACTIVITY	45	-0,33489972	-1,1838831	0,23214285	0,6394084	1	3536	tags=36%, list=20%, signal=44%
GO_NEGATIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_FATTY_ACID_METABOLIC_PROCESS	28	-0,38491186	-1,182071	0,24946696	0,64312476	1	3891	tags=54%, list=22%, signal=69%
GO_PROTEIN_ADP_RIBOSYLATION	GO_PROTEIN_ADP_RIBOSYLATION	19	-0,38158715	-1,1819974	0,23240939	0,64253116	1	1873	tags=26%, list=11%, signal=29%
GO_REGULATION_OF_VASODILATION	GO_REGULATION_OF_VASODILATION	46	-0,31911767	-1,181917	0,20477137	0,6419835	1	3540	tags=26%, list=20%, signal=33%
GO_PIGMENT_METABOLIC_PROCESS	GO_PIGMENT_METABOLIC_PROCESS	61	-0,3297269	-1,181827	0,27125505	0,6414133	1	2736	tags=30%, list=15%, signal=35%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_KINASE_ACTIVITY	81	-0,3517209	-1,1812334	0,26877472	0,64216715	1	2933	tags=28%, list=17%, signal=34%
GO_THYROID_HORMONE_METABOLIC_PROCESS	GO_THYROID_HORMONE_METABOLIC_PROCESS	15	-0,41010854	-1,1812227	0,26418787	0,6414124	1	1501	tags=27%, list=8%, signal=29%
GO_REGULATION_OF_INSULIN_RECEPTOR_SIGNALING_PATHWAY	GO_REGULATION_OF_INSULIN_RECEPTOR_SIGNALING_PATHWAY	41	-0,32744142	-1,1803775	0,21030928	0,6426275	1	1687	tags=22%, list=10%, signal=24%
GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_GTPASE_ACTIVITY	41	-0,30869547	-1,1802524	0,22067595	0,6421868	1	2569	tags=24%, list=15%, signal=28%
GO_GLUTATHIONE_METABOLIC_PROCESS	GO_GLUTATHIONE_METABOLIC_PROCESS	56	-0,34039235	-1,1789994	0,253493	0,64448434	1	2845	tags=30%, list=16%, signal=36%

GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	GO_REGULATION_OF_PHOSPHOLIPASE_C_ACTIVITY	38	-0,38875636	-1,1785264	0,3043478	0,6448922	1	1947	tags=29%, list=11%, signal=32%
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	15	-0,4178993	-1,1785252	0,246	0,6441186	1	4232	tags=60%, list=24%, signal=79%
GO_AMMONIUM_ION_BINDING	GO_AMMONIUM_ION_BINDING	62	-0,31306896	-1,1783124	0,18012422	0,6438865	1	2075	tags=21%, list=12%, signal=24%
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CALCIUM_ION_SIGNALING	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION_BY_CALCIUM_ION_SIGNALING	23	-0,4019102	-1,1782423	0,2485323	0,6432852	1	3787	tags=39%, list=21%, signal=50%
GO_CIS_GOLGI_NETWORK	GO_CIS_GOLGI_NETWORK	38	-0,3485463	-1,178	0,24485597	0,6430636	1	2798	tags=34%, list=16%, signal=41%
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_INNER_MEMBRANE	16	-0,44144145	-1,177257	0,3089431	0,6440904	1	2851	tags=31%, list=16%, signal=37%
GO_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA	GO_REGULATION_OF_RESPONSE_TO_INTERFERON_GAMMA	22	-0,38955986	-1,177194	0,2652174	0,64349097	1	2173	tags=27%, list=12%, signal=31%
GO_LUNG_CELL_DIFFERENTIATION	GO_LUNG_CELL_DIFFERENTIATION	25	-0,37512618	-1,17706	0,2715105	0,64303565	1	1323	tags=24%, list=7%, signal=26%
GO_HEME_BIOSYNTHETIC_PROCESS	GO_HEME_BIOSYNTHETIC_PROCESS	20	-0,44463268	-1,1759498	0,30801687	0,6450279	1	4768	tags=55%, list=27%, signal=75%
GO_NECROTIC_CELL_DEATH	GO_NECROTIC_CELL_DEATH	28	-0,35358945	-1,1757246	0,23529412	0,64481145	1	4684	tags=54%, list=27%, signal=73%
GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	GO_REGULATION_OF_ERK1_AND_ERK2_CASCADE	224	-0,27984187	-1,1754702	0,2128514	0,6446961	1	3916	tags=27%, list=22%, signal=34%
GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	GO_CELLULAR_RESPONSE_TO_CALCIUM_ION	45	-0,3257216	-1,1745219	0,21305183	0,64618355	1	2728	tags=36%, list=15%, signal=42%
GO_CONNEXON_COMPLEX	GO_CONNEXON_COMPLEX	16	-0,43612048	-1,1741371	0,26796117	0,64634645	1	3729	tags=38%, list=21%, signal=47%
GO_POSITIVE_REGULATION_OF_BEHAVIOR	GO_POSITIVE_REGULATION_OF_BEHAVIOR	21	-0,3866352	-1,1732899	0,22289157	0,64766866	1	1472	tags=19%, list=8%, signal=21%
GO_RESPONSE_TO_DEXAMETHASONE	GO_RESPONSE_TO_DEXAMETHASONE	32	-0,32906368	-1,1726937	0,21073559	0,6484254	1	2124	tags=28%, list=12%, signal=32%
GO_FLAVONOID_METABOLIC_PROCESS	GO_FLAVONOID_METABOLIC_PROCESS	28	-0,3903614	-1,1706773	0,29960316	0,65267634	1	1901	tags=29%, list=11%, signal=32%
GO_REGULATION_OF_HEART_GROWTH	GO_REGULATION_OF_HEART_GROWTH	41	-0,3330101	-1,1705896	0,2407045	0,6521071	1	1597	tags=22%, list=9%, signal=24%
GO_LIPOPROTEIN_METABOLIC_PROCESS	GO_LIPOPROTEIN_METABOLIC_PROCESS	120	-0,27805927	-1,1702805	0,22920893	0,65205216	1	3400	tags=28%, list=19%, signal=34%
GO_ACID_SECRETION	GO_ACID_SECRETION	62	-0,31359613	-1,1696525	0,23395444	0,6528876	1	1697	tags=21%, list=10%, signal=23%
GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	GO_REGULATION_OF_NEUROTRANSMITTER_RECEPTOR_ACTIVITY	26	-0,3934692	-1,1694684	0,25742576	0,6525665	1	1488	tags=19%, list=8%, signal=21%
GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	GO_REGULATION_OF_MUSCLE_SYSTEM_PROCESS	185	-0,28074875	-1,1691265	0,19455253	0,652644	1	4445	tags=37%, list=25%, signal=49%
GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	GO_POSITIVE_REGULATION_OF_CELL_MATRIX_ADHESION	40	-0,3295874	-1,1682354	0,23952095	0,6540352	1	3137	tags=30%, list=18%, signal=36%
GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	GO_NEGATIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	34	-0,3593776	-1,1675913	0,25838265	0,6548594	1	1295	tags=21%, list=7%, signal=22%
GO_TRANSLATION_REGULATOR_ACTIVITY	GO_TRANSLATION_REGULATOR_ACTIVITY	32	-0,34726232	-1,1670326	0,2524851	0,655508	1	3447	tags=47%, list=20%, signal=58%
GO_ANION_CATION_SYMPORTER_ACTIVITY	GO_ANION_CATION_SYMPORTER_ACTIVITY	53	-0,30958378	-1,166976	0,21689059	0,65489274	1	2142	tags=26%, list=12%, signal=30%
GO_PROTEIN_KINASE_A_BINDING	GO_PROTEIN_KINASE_A_BINDING	39	-0,31961125	-1,1661896	0,24809161	0,6560601	1	2834	tags=26%, list=16%, signal=30%
GO_KETONE_BIOSYNTHETIC_PROCESS	GO_KETONE_BIOSYNTHETIC_PROCESS	22	-0,40787935	-1,1650621	0,2760736	0,65807843	1	2100	tags=32%, list=12%, signal=36%
GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	GO_HORMONE_MEDIATED_SIGNALING_PATHWAY	148	-0,26717922	-1,1650255	0,2194617	0,6573889	1	2726	tags=24%, list=15%, signal=29%
GO_GABA_RECEPTOR_BINDING	GO_GABA_RECEPTOR_BINDING	15	-0,3983331	-1,1645768	0,26050422	0,657764	1	2677	tags=27%, list=15%, signal=31%
GO_NEGATIVE_REGULATION_OF_TOR_SIGNALING	GO_NEGATIVE_REGULATION_OF_TOR_SIGNALING	30	-0,33865553	-1,1639478	0,26987448	0,6585765	1	3588	tags=37%, list=20%, signal=46%
GO_CARDIAC_SEPTUM_MORPHOGENESIS	GO_CARDIAC_SEPTUM_MORPHOGENESIS	47	-0,34376115	-1,1637422	0,27572817	0,6583178	1	3211	tags=40%, list=18%, signal=49%
GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	GO_SMOOTH_MUSCLE_CELL_DIFFERENTIATION	30	-0,3812748	-1,1636553	0,2704762	0,657766	1	2065	tags=27%, list=12%, signal=30%
GO_APICAL_PART_OF_CELL	GO_APICAL_PART_OF_CELL	337	-0,25363675	-1,160436	0,21386139	0,6648755	1	4481	tags=35%, list=25%, signal=46%
GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	53	-0,30637974	-1,1602722	0,25335893	0,66451186	1	3202	tags=34%, list=18%, signal=41%
GO_SYMPORTER_ACTIVITY	GO_SYMPORTER_ACTIVITY	137	-0,26298895	-1,1598388	0,18436874	0,6648428	1	3280	tags=30%, list=19%, signal=36%
GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	GO_POSITIVE_REGULATION_OF_ORGAN_GROWTH	36	-0,323268	-1,1596663	0,21787709	0,66450894	1	3202	tags=33%, list=18%, signal=41%
GO_STEROID_HORMONE_MEDIATED_SIGNALING_PATHWAY	GO_STEROID_HORMONE_MEDIATED_SIGNALING_PATHWAY	120	-0,2723057	-1,1588098	0,25409836	0,6658482	1	2726	tags=25%, list=15%, signal=29%
GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	GO_POSITIVE_REGULATION_OF_ION_TRANSPORT	225	-0,253857	-1,1587936	0,171875	0,66511506	1	3951	tags=30%, list=22%, signal=38%
GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	GO_POSITIVE_REGULATION_OF_AMINE_TRANSPORT	29	-0,3554738	-1,1586919	0,24351297	0,6645855	1	1720	tags=21%, list=10%, signal=23%
GO_REGULATION_OF_MITOCHONDRIAL_DEPOLARIZATION	GO_REGULATION_OF_MITOCHONDRIAL_DEPOLARIZATION	17	-0,3854039	-1,1585137	0,27755904	0,6642605	1	3192	tags=41%, list=18%, signal=50%
GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	GO_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	67	-0,32899734	-1,1581745	0,29504952	0,6643916	1	2975	tags=31%, list=17%, signal=38%
GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	GO_NEGATIVE_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	17	-0,39337578	-1,1573	0,27868852	0,66576153	1	1495	tags=18%, list=8%, signal=19%
GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	GO_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	31	-0,35487095	-1,1570039	0,2730845	0,66577953	1	920	tags=19%, list=5%, signal=20%
GO_METALLO_SULFUR_CLUSTER_ASSEMBLY	GO_METALLO_SULFUR_CLUSTER_ASSEMBLY	18	-0,44286278	-1,156643	0,32083333	0,6659086	1	3606	tags=44%, list=20%, signal=56%
GO_CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	GO_CIRCADIAN_REGULATION_OF_GENE_EXPRESSION	50	-0,31968182	-1,1556939	0,2951807	0,66748667	1	1622	tags=24%, list=9%, signal=26%
GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	GO_CELL_DIFFERENTIATION_IN_HINDBRAIN	19	-0,3946586	-1,1556444	0,29032257	0,6668319	1	2875	tags=32%, list=16%, signal=38%
GO_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	GO_ACTIVIN_RECEPTOR_SIGNALING_PATHWAY	21	-0,39711702	-1,1554673	0,26937985	0,66649085	1	2712	tags=33%, list=15%, signal=39%
GO_G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	GO_G_PROTEIN_COUPLED_AMINE_RECEPTOR_ACTIVITY	32	-0,36138722	-1,1545184	0,26052105	0,66803175	1	3425	tags=34%, list=19%, signal=43%
GO_RECEPTOR_SERINE_THREONINE_KINASE_BINDING	GO_RECEPTOR_SERINE_THREONINE_KINASE_BINDING	15	-0,41353917	-1,1533338	0,26639345	0,6701687	1	3413	tags=33%, list=19%, signal=41%
GO_NEGATIVE_REGULATION_OF_STAT_CASCADE	GO_NEGATIVE_REGULATION_OF_STAT_CASCADE	41	-0,3256313	-1,1530294	0,2815534	0,6702041	1	2543	tags=27%, list=14%, signal=31%
GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	43	-0,33223504	-1,1521589	0,24902724	0,6716239	1	2692	tags=23%, list=15%, signal=27%
GO_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	GO_NEGATIVE_REGULATION_OF_ANION_TRANSPORT	32	-0,35208866	-1,1516874	0,24554455	0,67198694	1	3381	tags=31%, list=19%, signal=39%

GO_POLYOL_BIOSYNTHETIC_PROCESS	GO_POLYOL_BIOSYNTHETIC_PROCESS	26	-0,34553483	-1,1516113	0,25502008	0,6714176	1	2349	tags=27%, list=13%, signal=31%
GO_RESPONSE_TO_INSULIN	GO_RESPONSE_TO_INSULIN	194	-0,25609612	-1,1511418	0,23387097	0,67178863	1	3412	tags=28%, list=19%, signal=34%
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_SULFUR_CONTAINING_GROUPS	63	-0,29883358	-1,1506295	0,25447315	0,6722652	1	2504	tags=24%, list=14%, signal=28%
GO_PYRIMIDINE_NUCLEOSIDE_CATABOLIC_PROCESS	GO_PYRIMIDINE_NUCLEOSIDE_CATABOLIC_PROCESS	18	-0,39523247	-1,1505829	0,31578946	0,6716103	1	1479	tags=17%, list=8%, signal=18%
GO_REGULATION_OF_CAMP_METABOLIC_PROCESS	GO_REGULATION_OF_CAMP_METABOLIC_PROCESS	111	-0,29871684	-1,1501895	0,24952015	0,67188925	1	3227	tags=23%, list=18%, signal=28%
GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	GO_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	204	-0,31304285	-1,149911	0,29025844	0,67178404	1	3137	tags=26%, list=18%, signal=31%
GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	GO_REGULATION_OF_MEMBRANE_REPOLARIZATION	28	-0,37348655	-1,1487404	0,29025844	0,6739109	1	4597	tags=43%, list=26%, signal=58%
GO_NEGATIVE_REGULATION_OF_MAPK_CASCADE	GO_NEGATIVE_REGULATION_OF_MAPK_CASCADE	140	-0,25385976	-1,147121	0,22011386	0,6771943	1	3110	tags=25%, list=18%, signal=30%
GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	GO_VENTRICULAR_SEPTUM_MORPHOGENESIS	27	-0,36789975	-1,1469551	0,30408162	0,67684513	1	4420	tags=56%, list=25%, signal=74%
GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	GO_REGULATION_OF_DENDRITE_MORPHOGENESIS	72	-0,28263333	-1,146673	0,23895583	0,67676586	1	3232	tags=29%, list=18%, signal=36%
GO_RETINOIC_ACID_BINDING	GO_RETINOIC_ACID_BINDING	23	-0,37212119	-1,146465	0,2917505	0,67653316	1	2867	tags=39%, list=16%, signal=47%
GO_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING	GO_TRANSFORMING_GROWTH_FACTOR_BETA_BINDING	16	-0,4439013	-1,1460406	0,32064128	0,6767842	1	1840	tags=31%, list=10%, signal=35%
GO_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	GO_REGULATION_OF_INCLUSION_BODY_ASSEMBLY	15	-0,4107764	-1,1460346	0,32079208	0,6760442	1	1366	tags=20%, list=8%, signal=22%
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	134	-0,27256888	-1,1459482	0,21181263	0,67549205	1	3095	tags=29%, list=18%, signal=35%
GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	93	-0,2947201	-1,1455433	0,22846442	0,6757044	1	3355	tags=27%, list=19%, signal=33%
GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_FAT_CELL_DIFFERENTIATION	40	-0,3217838	-1,1446184	0,25378788	0,6771641	1	3412	tags=35%, list=19%, signal=43%
GO_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	GO_REGULATION_OF_INSULIN_LIKE_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	19	-0,38922942	-1,1445934	0,27897838	0,6764802	1	4761	tags=53%, list=27%, signal=72%
GO_CELL_MATRIX_ADHESION	GO_CELL_MATRIX_ADHESION	115	-0,30125567	-1,1442078	0,26615968	0,676703	1	3105	tags=28%, list=18%, signal=34%
GO_NEUTRAL_LIPID_BIOSYNTHETIC_PROCESS	GO_NEUTRAL_LIPID_BIOSYNTHETIC_PROCESS	27	-0,3439717	-1,142856	0,28323698	0,6793039	1	1184	tags=22%, list=7%, signal=24%
GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	GO_SMAD_PROTEIN_SIGNAL_TRANSDUCTION	53	-0,31034696	-1,1426023	0,26534653	0,6792429	1	3599	tags=32%, list=20%, signal=40%
GO_ALPHA_BETA_T_CELL_ACTIVATION	GO_ALPHA_BETA_T_CELL_ACTIVATION	51	-0,35084343	-1,1415187	0,33811477	0,68105733	1	4209	tags=39%, list=24%, signal=51%
GO_RESPONSE_TO_OSMOTIC_STRESS	GO_RESPONSE_TO_OSMOTIC_STRESS	61	-0,28847915	-1,1403846	0,23232323	0,68308276	1	1489	tags=18%, list=8%, signal=20%
GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	GO_INTERMEDIATE_FILAMENT_BASED_PROCESS	37	-0,32267213	-1,1402156	0,27920792	0,6827517	1	3516	tags=30%, list=20%, signal=37%
GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	GO_ORGANIC_CYCLIC_COMPOUND_CATABOLIC_PROCESS	406	-0,2701132	-1,1401917	0,31462926	0,682063	1	1975	tags=18%, list=11%, signal=20%
GO_GLOMERULUS_DEVELOPMENT	GO_GLOMERULUS_DEVELOPMENT	49	-0,363555	-1,1401157	0,29981026	0,68150127	1	2664	tags=33%, list=15%, signal=38%
GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	GO_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	22	-0,377216	-1,1399596	0,30753967	0,6810918	1	4502	tags=36%, list=25%, signal=49%
GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	GO_GLYCOSYL_COMPOUND_METABOLIC_PROCESS	343	-0,28564063	-1,1399544	0,31687242	0,68034977	1	2766	tags=27%, list=16%, signal=31%
GO_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	GO_POSITIVE_REGULATION_OF_CELL_SUBSTRATE_ADHESION	93	-0,3017257	-1,1371237	0,28654972	0,68665373	1	2910	tags=26%, list=16%, signal=31%
GO_CORECEPTOR_ACTIVITY	GO_CORECEPTOR_ACTIVITY	34	-0,37147477	-1,1361523	0,32115385	0,6883045	1	2884	tags=29%, list=16%, signal=35%
GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	GO_NEGATIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	33	-0,3508151	-1,1352133	0,28320312	0,6898334	1	4232	tags=42%, list=24%, signal=56%
GO_DIOXYGENASE_ACTIVITY	GO_DIOXYGENASE_ACTIVITY	78	-0,26745728	-1,1352038	0,27091634	0,6890922	1	3410	tags=31%, list=19%, signal=38%
GO_REGULATION_OF_LYASE_ACTIVITY	GO_REGULATION_OF_LYASE_ACTIVITY	76	-0,29632288	-1,1341981	0,24810606	0,6908505	1	2820	tags=24%, list=16%, signal=28%
GO_REGULATION_OF_PLATELET_ACTIVATION	GO_REGULATION_OF_PLATELET_ACTIVATION	30	-0,363328	-1,1333773	0,3059548	0,69213563	1	4209	tags=47%, list=24%, signal=61%
GO_RESPONSE_TO_KETONE	GO_RESPONSE_TO_KETONE	178	-0,24979591	-1,1333649	0,22529644	0,6914141	1	2126	tags=20%, list=12%, signal=23%
GO_MANGANESE_ION_BINDING	GO_MANGANESE_ION_BINDING	43	-0,31504402	-1,133222	0,272541	0,6910043	1	3892	tags=40%, list=22%, signal=51%
GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	GO_RECEPTOR_MEDIATED_ENDOCYTOSIS	199	-0,26272377	-1,1327773	0,26789367	0,6913444	1	2979	tags=26%, list=17%, signal=30%
GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	GO_REGULATION_OF_LIPID_KINASE_ACTIVITY	47	-0,33190632	-1,1324728	0,282	0,69136125	1	3936	tags=40%, list=22%, signal=52%
GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	GO_REGULATION_OF_ASTROCYTE_DIFFERENTIATION	27	-0,34263566	-1,1324513	0,29313928	0,69065744	1	2663	tags=30%, list=15%, signal=35%
GO_LEUKOTRIENE_BIOSYNTHETIC_PROCESS	GO_LEUKOTRIENE_BIOSYNTHETIC_PROCESS	19	-0,39211422	-1,1316837	0,3094737	0,6918066	1	851	tags=21%, list=5%, signal=22%
GO_POSITIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	GO_POSITIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	90	-0,28116947	-1,1313723	0,249501	0,6918351	1	4409	tags=33%, list=25%, signal=44%
GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	GO_INTRAMOLECULAR_TRANSFERASE_ACTIVITY	26	-0,35475454	-1,1309073	0,30952382	0,69222546	1	298	tags=15%, list=2%, signal=16%
GO_CALCIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	GO_CALCIUM_DEPENDENT_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	26	-0,41197896	-1,1307651	0,3464567	0,69181234	1	3565	tags=31%, list=20%, signal=38%
GO_APOPTOTIC_CELL_CLEARANCE	GO_APOPTOTIC_CELL_CLEARANCE	27	-0,33857828	-1,1303333	0,29718876	0,6921058	1	4709	tags=52%, list=27%, signal=71%
GO_PHOSPHOLIPID_CATABOLIC_PROCESS	GO_PHOSPHOLIPID_CATABOLIC_PROCESS	29	-0,32434788	-1,130124	0,27416173	0,69185114	1	2410	tags=31%, list=14%, signal=36%
GO_AMINO_ACID_IMPORT	GO_AMINO_ACID_IMPORT	15	-0,40963224	-1,1280681	0,32271764	0,6960496	1	2999	tags=40%, list=17%, signal=48%
GO_CARDIAC_CHAMBER_MORPHOGENESIS	GO_CARDIAC_CHAMBER_MORPHOGENESIS	99	-0,3016653	-1,1279507	0,28235295	0,6955758	1	3211	tags=30%, list=18%, signal=37%
GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	79	-0,27994844	-1,12739	0,25099602	0,69626427	1	4232	tags=37%, list=24%, signal=48%
GO_METALLOEXOPEPTIDASE_ACTIVITY	GO_METALLOEXOPEPTIDASE_ACTIVITY	48	-0,308121	-1,1267744	0,28367347	0,6970755	1	2889	tags=27%, list=16%, signal=32%
GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	15	-0,40372568	-1,1265792	0,32283464	0,696818	1	2664	tags=33%, list=15%, signal=39%
GO_REGULATION_OF_SYSTEM_PROCESS	GO_REGULATION_OF_SYSTEM_PROCESS	472	-0,25488308	-1,1258935	0,25515947	0,6977339	1	3898	tags=28%, list=22%, signal=35%
GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	GO_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	53	-0,29344094	-1,125497	0,2952756	0,6980018	1	1638	tags=23%, list=9%, signal=25%
GO_BONE_MINERALIZATION	GO_BONE_MINERALIZATION	38	-0,3240612	-1,1250194	0,27091634	0,69846296	1	2038	tags=24%, list=12%, signal=27%
GO_SODIUM_ION_HOMEOSTASIS	GO_SODIUM_ION_HOMEOSTASIS	29	-0,34997362	-1,1245879	0,26060605	0,6988189	1	4465	tags=38%, list=25%, signal=51%

GO_RESPONSE_TO_LEAD_ION	GO_RESPONSE_TO_LEAD_ION	19	-0,37489605	-1,1237702	0,3049505	0,7000772	1	3246	tags=42%, list=18%, signal=52%
GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	GO_NEGATIVE_REGULATION_OF_IMMUNE_RESPONSE	111	-0,29867086	-1,122525	0,32443532	0,7023933	1	2969	tags=20%, list=17%, signal=24%
GO_ORGANIC_CATION_TRANSPORT	GO_ORGANIC_CATION_TRANSPORT	19	-0,38707334	-1,1219025	0,3128964	0,7032353	1	3926	tags=42%, list=22%, signal=54%
GO_INNER_EAR_RECEPTOR_CELL_DEVELOPMENT	GO_INNER_EAR_RECEPTOR_CELL_DEVELOPMENT	33	-0,32561162	-1,1207833	0,27977315	0,70527595	1	2108	tags=30%, list=12%, signal=34%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	17	-0,37249878	-1,1204906	0,33333334	0,7052333	1	2081	tags=29%, list=12%, signal=33%
GO_EPITHELIAL_CELL_FATE_COMMITMENT	GO_EPITHELIAL_CELL_FATE_COMMITMENT	15	-0,4135504	-1,1196187	0,32827324	0,706572	1	3507	tags=40%, list=20%, signal=50%
GO_RESPIRATORY_GASEOUS_EXCHANGE	GO_RESPIRATORY_GASEOUS_EXCHANGE	47	-0,29698405	-1,1190156	0,28189301	0,70733136	1	2636	tags=21%, list=15%, signal=25%
GO_RESPONSE_TO_OXIDATIVE_STRESS	GO_RESPONSE_TO_OXIDATIVE_STRESS	335	-0,22738095	-1,1184977	0,22134387	0,7079197	1	3151	tags=26%, list=18%, signal=31%
GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	GO_HETEROPHILIC_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_CELL_ADHESION_MOLECULES	37	-0,3178442	-1,1184642	0,2891089	0,7072596	1	3878	tags=30%, list=22%, signal=38%
GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	GO_PROTON_TRANSPORTING_ATP_SYNTHASE_COMPLEX	22	-0,50213784	-1,1184161	0,40079364	0,7066359	1	4649	tags=55%, list=26%, signal=74%
GO_MITOCHONDRION_LOCALIZATION	GO_MITOCHONDRION_LOCALIZATION	33	-0,31484175	-1,1184132	0,29098362	0,7058954	1	1638	tags=24%, list=9%, signal=27%
GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	GO_VOLTAGE_GATED_SODIUM_CHANNEL_ACTIVITY	18	-0,40512842	-1,1178479	0,2945892	0,7065348	1	416	tags=11%, list=2%, signal=11%
GO_RESPONSE_TO_MAGNESIUM_ION	GO_RESPONSE_TO_MAGNESIUM_ION	22	-0,35858777	-1,1173034	0,28456914	0,707121	1	3344	tags=36%, list=19%, signal=45%
GO_NEGATIVE_REGULATION_OF_TRANSPORT	GO_NEGATIVE_REGULATION_OF_TRANSPORT	424	-0,23121433	-1,1163819	0,23809524	0,70869213	1	3886	tags=27%, list=22%, signal=33%
GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	GO_POSITIVE_REGULATION_OF_ENDOCYTOSIS	111	-0,27425125	-1,115865	0,27875245	0,70920223	1	3529	tags=29%, list=20%, signal=36%
GO_FLUID_TRANSPORT	GO_FLUID_TRANSPORT	25	-0,35148448	-1,1155653	0,32741618	0,70918447	1	4329	tags=44%, list=25%, signal=58%
GO_EXOPEPTIDASE_ACTIVITY	GO_EXOPEPTIDASE_ACTIVITY	98	-0,26175416	-1,1154319	0,2514735	0,7087435	1	2889	tags=24%, list=16%, signal=29%
GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	GO_CELLULAR_RESPONSE_TO_EXTRACELLULAR_STIMULUS	177	-0,24619484	-1,115362	0,27959183	0,7081644	1	2712	tags=21%, list=15%, signal=25%
GO_CYTOKINE_BINDING	GO_CYTOKINE_BINDING	86	-0,31771675	-1,1146382	0,3149284	0,7092929	1	3328	tags=29%, list=19%, signal=36%
GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_ORGANIC_ANION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	169	-0,2483395	-1,1143963	0,25462013	0,70911545	1	3140	tags=28%, list=18%, signal=33%
GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	GO_REGULATION_OF_MACROPHAGE_CHEMOTAXIS	16	-0,43041256	-1,1139089	0,3507014	0,7095419	1	2975	tags=31%, list=17%, signal=38%
GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	GO_REGULATION_OF_ADENYLATE_CYCLASE_ACTIVITY	63	-0,30734593	-1,1135964	0,28927204	0,7095626	1	2820	tags=22%, list=16%, signal=26%
GO_RESPONSE_TO_GONADOTROPIN	GO_RESPONSE_TO_GONADOTROPIN	24	-0,3408597	-1,1127924	0,3190184	0,7108615	1	1627	tags=25%, list=9%, signal=27%
GO_PROTEIN_KINASE_A_REGULATORY_SUBUNIT_BINDING	GO_PROTEIN_KINASE_A_REGULATORY_SUBUNIT_BINDING	16	-0,40581164	-1,1114118	0,33530572	0,71362054	1	2716	tags=25%, list=15%, signal=30%
GO_ARTERY_MORPHOGENESIS	GO_ARTERY_MORPHOGENESIS	51	-0,33696103	-1,111078	0,3254902	0,7137101	1	4271	tags=39%, list=24%, signal=52%
GO_POSITIVE_REGULATION_OF_CELL_KILLING	GO_POSITIVE_REGULATION_OF_CELL_KILLING	37	-0,38074538	-1,1110505	0,34808853	0,71303487	1	3553	tags=41%, list=20%, signal=51%
GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	GO_REGULATION_OF_POTASSIUM_ION_TRANSPORT	80	-0,29396945	-1,1108706	0,2784091	0,7127401	1	4409	tags=38%, list=25%, signal=50%
GO_CALCIUM_MEDIATED_SIGNALING	GO_CALCIUM_MEDIATED_SIGNALING	83	-0,2975945	-1,1099803	0,3233533	0,7141941	1	2462	tags=22%, list=14%, signal=25%
GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	GO_REGULATION_OF_EXTRACELLULAR_MATRIX_ORGANIZATION	26	-0,34599137	-1,1097152	0,336	0,7141174	1	1244	tags=19%, list=7%, signal=21%
GO_REGULATION_OF_PEPTIDASE_ACTIVITY	GO_REGULATION_OF_PEPTIDASE_ACTIVITY	359	-0,22452542	-1,1095817	0,23640168	0,71372294	1	2192	tags=17%, list=12%, signal=19%
GO_SULFATION	GO_SULFATION	16	-0,37495273	-1,1085577	0,30192307	0,71554977	1	2504	tags=31%, list=14%, signal=36%
GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_CAMP_METABOLIC_PROCESS	76	-0,29496872	-1,1059417	0,28764477	0,7213358	1	3227	tags=24%, list=18%, signal=29%
GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	GO_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	74	-0,31487915	-1,1058536	0,30876493	0,7207913	1	4270	tags=39%, list=24%, signal=51%
GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_CARBOHYDRATE_METABOLIC_PROCESS	47	-0,29109722	-1,1054701	0,3130252	0,72110385	1	3976	tags=38%, list=23%, signal=49%
GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	GO_METALLOCARBOXYPEPTIDASE_ACTIVITY	25	-0,3645297	-1,1036222	0,3046875	0,7251057	1	2889	tags=28%, list=16%, signal=33%
GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	GO_PYRIMIDINE_NUCLEOBASE_METABOLIC_PROCESS	19	-0,36045107	-1,1036149	0,31434184	0,72437245	1	656	tags=21%, list=4%, signal=22%
GO_DRUG_TRANSPORTER_ACTIVITY	GO_DRUG_TRANSPORTER_ACTIVITY	20	-0,37008065	-1,1034075	0,311412	0,72413456	1	2286	tags=30%, list=13%, signal=34%
GO_RESPONSE_TO_MINERALOCORTICOID	GO_RESPONSE_TO_MINERALOCORTICOID	34	-0,32992426	-1,1026825	0,31991953	0,725239	1	2126	tags=24%, list=12%, signal=27%
GO_KIDNEY_EPITHELIUM_DEVELOPMENT	GO_KIDNEY_EPITHELIUM_DEVELOPMENT	123	-0,29805386	-1,1023473	0,30392158	0,72536147	1	2829	tags=24%, list=16%, signal=29%
GO_EXPLORATION_BEHAVIOR	GO_EXPLORATION_BEHAVIOR	22	-0,3537553	-1,1019936	0,28985506	0,72547823	1	2987	tags=32%, list=17%, signal=38%
GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	98	-0,28779092	-1,1013114	0,31835207	0,72645646	1	1688	tags=16%, list=10%, signal=18%
GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_ENDOPLASMIC_RETICULUM_STRESS_INDUCED_INTRINSIC_APOPTOTIC_SIGNALING_PATHWAY	16	-0,36845082	-1,1007481	0,3241107	0,72707725	1	1893	tags=31%, list=11%, signal=35%
GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	GO_FATTY_ACID_BIOSYNTHETIC_PROCESS	101	-0,26379144	-1,1004921	0,28031808	0,72697186	1	2651	tags=25%, list=15%, signal=29%
GO_REGULATION_OF_DOPAMINE_SECRETION	GO_REGULATION_OF_DOPAMINE_SECRETION	19	-0,37818104	-1,0999577	0,32064128	0,7275704	1	2075	tags=21%, list=12%, signal=24%
GO_TRANSMISSION_OF_NERVE_IMPULSE	GO_TRANSMISSION_OF_NERVE_IMPULSE	48	-0,33604825	-1,0997823	0,34237996	0,72720766	1	3390	tags=27%, list=19%, signal=33%
GO_SODIUM_CHANNEL_COMPLEX	GO_SODIUM_CHANNEL_COMPLEX	16	-0,43185553	-1,0992497	0,3233533	0,72782654	1	416	tags=13%, list=2%, signal=13%
GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	GO_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA	142	-0,26853687	-1,0981199	0,31609195	0,7299553	1	2829	tags=23%, list=16%, signal=27%
GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	GO_CENTRAL_NERVOUS_SYSTEM_PROJECTION_NEURON_AXONOGENESIS	22	-0,37448397	-1,0972893	0,36526945	0,73131573	1	3780	tags=41%, list=21%, signal=52%
GO_RESPONSE_TO_FLUID_SHEAR_STRESS	GO_RESPONSE_TO_FLUID_SHEAR_STRESS	33	-0,34560403	-1,096917	0,33020636	0,73154974	1	4271	tags=45%, list=24%, signal=60%
GO_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	GO_REGULATION_OF_PHOSPHOPROTEIN_PHOSPHATASE_ACTIVITY	56	-0,28338948	-1,0960455	0,326	0,7330217	1	1568	tags=18%, list=9%, signal=20%
GO_PHASIC_SMOOTH_MUSCLE_CONTRACTION	GO_PHASIC_SMOOTH_MUSCLE_CONTRACTION	16	-0,38879076	-1,095682	0,34530938	0,73317605	1	5513	tags=63%, list=31%, signal=91%

GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	77	-0,27480945	-1,0956279	0,30478087	0,7325652	1	3507	tags=27%, list=20%, signal=34%
GO_LATE_ENDOSOME	GO_LATE_ENDOSOME	196	-0,24376535	-1,0945923	0,30346233	0,73442566	1	3075	tags=28%, list=17%, signal=33%
GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	GO_NEGATIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	33	-0,3439039	-1,09453	0,3266533	0,73383504	1	2969	tags=24%, list=17%, signal=29%
GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	GO_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	29	-0,35913742	-1,0935504	0,34050882	0,7356198	1	2969	tags=28%, list=17%, signal=33%
GO_CARBOHYDRATE_TRANSPORT	GO_CARBOHYDRATE_TRANSPORT	89	-0,2566721	-1,0934682	0,3306288	0,73509	1	3854	tags=34%, list=22%, signal=43%
GO_REGULATION_OF_EXCRETION	GO_REGULATION_OF_EXCRETION	27	-0,33865574	-1,0924033	0,31762296	0,7370096	1	4296	tags=33%, list=24%, signal=44%
GO_RESPONSE_TO_COPPER_ION	GO_RESPONSE_TO_COPPER_ION	26	-0,31986305	-1,0921253	0,334004	0,7369482	1	1107	tags=19%, list=6%, signal=20%
GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	GO_REGULATION_OF_MEMBRANE_PROTEIN_ECTODOMAIN_PROTEOLYSIS	20	-0,37028867	-1,0914863	0,35528943	0,73779446	1	2959	tags=30%, list=17%, signal=36%
GO_BASOLATERAL_PLASMA_MEMBRANE	GO_BASOLATERAL_PLASMA_MEMBRANE	205	-0,25308818	-1,0912572	0,29622266	0,73764163	1	3095	tags=23%, list=18%, signal=27%
GO_MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_MONOSACCHARIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	20	-0,34208375	-1,0903255	0,34225622	0,7392641	1	3455	tags=40%, list=20%, signal=50%
GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	22	-0,3650709	-1,0896783	0,35742188	0,7401685	1	1880	tags=23%, list=11%, signal=25%
GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_CATABOLIC_PROCESS	381	-0,22131057	-1,0892909	0,31376517	0,740411	1	2014	tags=18%, list=11%, signal=20%
GO_REGULATION_OF_HEAT_GENERATION	GO_REGULATION_OF_HEAT_GENERATION	15	-0,40106356	-1,0877562	0,3483366	0,74355	1	308	tags=13%, list=2%, signal=14%
GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	GO_HETEROTRIMERIC_G_PROTEIN_COMPLEX	29	-0,3389601	-1,0872201	0,3562753	0,7441793	1	565	tags=14%, list=3%, signal=14%
GO_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	GO_REGULATION_OF_HETEROTYPIC_CELL_CELL_ADHESION	18	-0,3914151	-1,0866251	0,36738703	0,74494714	1	1608	tags=28%, list=9%, signal=31%
GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	GO_REGULATION_OF_SKELETAL_MUSCLE_TISSUE_DEVELOPMENT	44	-0,2893746	-1,0862314	0,33532935	0,74514306	1	3599	tags=34%, list=20%, signal=43%
GO_REGENERATION	GO_REGENERATION	152	-0,2539172	-1,0856006	0,29563493	0,74599314	1	3010	tags=27%, list=17%, signal=32%
GO_PDZ_DOMAIN_BINDING	GO_PDZ_DOMAIN_BINDING	88	-0,25737643	-1,0851529	0,3372549	0,74639297	1	3386	tags=28%, list=19%, signal=35%
GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	GO_GLOMERULAR_EPITHELIUM_DEVELOPMENT	19	-0,38627568	-1,0850143	0,35887095	0,74601775	1	3155	tags=42%, list=18%, signal=51%
GO_LUNG_EPITHELIUM_DEVELOPMENT	GO_LUNG_EPITHELIUM_DEVELOPMENT	34	-0,31962547	-1,0845717	0,34117648	0,74638784	1	1688	tags=24%, list=10%, signal=26%
GO_CELLULAR_RESPONSE_TO_HYDROGEN_PEROXIDE	GO_CELLULAR_RESPONSE_TO_HYDROGEN_PEROXIDE	60	-0,27236262	-1,0845195	0,3043478	0,7457971	1	2081	tags=25%, list=12%, signal=28%
GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	GO_NEGATIVE_REGULATION_OF_PLATELET_ACTIVATION	17	-0,39309475	-1,0844288	0,35856575	0,74528366	1	3192	tags=41%, list=18%, signal=50%
GO_GLAND_DEVELOPMENT	GO_GLAND_DEVELOPMENT	377	-0,22695519	-1,0842822	0,27875245	0,74490774	1	2875	tags=21%, list=16%, signal=24%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	182	-0,25224534	-1,0838566	0,33590734	0,7452553	1	3183	tags=26%, list=18%, signal=31%
GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	GO_RESPONSE_TO_REACTIVE_OXYGEN_SPECIES	185	-0,23968741	-1,0837024	0,3006135	0,74489176	1	3137	tags=26%, list=18%, signal=32%
GO_SIDE_OF_MEMBRANE	GO_SIDE_OF_MEMBRANE	387	-0,26704416	-1,0835254	0,34226805	0,7445991	1	3082	tags=24%, list=17%, signal=28%
GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	GO_GLUTAMINE_FAMILY_AMINO_ACID_BIOSYNTHETIC_PROCESS	19	-0,3630735	-1,0833813	0,3583815	0,74423236	1	2049	tags=37%, list=12%, signal=42%
GO_NAD_ADP_RIBOSYLTRANSFERASE_ACTIVITY	GO_NAD_ADP_RIBOSYLTRANSFERASE_ACTIVITY	25	-0,3390932	-1,0826744	0,3443299	0,74528146	1	2123	tags=24%, list=12%, signal=27%
GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	GO_LOW_DENSITY_LIPOPROTEIN_PARTICLE_RECEPTOR_BINDING	17	-0,3894783	-1,0826235	0,38311687	0,74468166	1	1364	tags=24%, list=8%, signal=25%
GO_FATTY_ACID_DERIVATIVE_TRANSPORT	GO_FATTY_ACID_DERIVATIVE_TRANSPORT	18	-0,3764521	-1,0818024	0,3365949	0,74602133	1	3322	tags=28%, list=19%, signal=34%
GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	GO_MONOVALENT_INORGANIC_CATION_TRANSPORT	394	-0,2294877	-1,0812635	0,298	0,7466024	1	4272	tags=31%, list=24%, signal=40%
GO_SOLUTE_SODIUM_SYMPORTER_ACTIVITY	GO_SOLUTE_SODIUM_SYMPORTER_ACTIVITY	50	-0,28893167	-1,0803899	0,32264528	0,74803406	1	1615	tags=20%, list=9%, signal=22%
GO_REGULATION_OF_JNK_CASCADE	GO_REGULATION_OF_JNK_CASCADE	154	-0,24915425	-1,080191	0,322	0,747812	1	3137	tags=26%, list=18%, signal=31%
GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS	GO_OXIDOREDUCTION_COENZYME_METABOLIC_PROCESS	96	-0,30321488	-1,0801342	0,3478261	0,7472173	1	2441	tags=27%, list=14%, signal=31%
GO_HEART_MORPHOGENESIS	GO_HEART_MORPHOGENESIS	204	-0,26382783	-1,0775877	0,3295238	0,7529051	1	3211	tags=27%, list=18%, signal=33%
GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	GO_ACTOMYOSIN_STRUCTURE_ORGANIZATION	73	-0,28068575	-1,0765052	0,35140562	0,75496525	1	4046	tags=38%, list=23%, signal=50%
GO_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	GO_REGULATION_OF_DIGESTIVE_SYSTEM_PROCESS	34	-0,3179536	-1,0763627	0,32515338	0,7546241	1	1336	tags=18%, list=8%, signal=19%
GO_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS	GO_HYDROGEN_PEROXIDE_CATABOLIC_PROCESS	20	-0,3852881	-1,0758759	0,3547718	0,755147	1	2804	tags=30%, list=16%, signal=36%
GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORT	GO_ORGANIC_ACID_TRANSMEMBRANE_TRANSPORT	96	-0,26736087	-1,0756211	0,33401638	0,75502855	1	2742	tags=27%, list=16%, signal=32%
GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	GO_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	72	-0,2808346	-1,0755109	0,35329342	0,7545642	1	2117	tags=19%, list=12%, signal=22%
GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	59	-0,30073595	-1,0749127	0,3475728	0,7554115	1	4409	tags=39%, list=25%, signal=52%
GO_GANGLIOSIDE_BIOSYNTHETIC_PROCESS	GO_GANGLIOSIDE_BIOSYNTHETIC_PROCESS	17	-0,36940876	-1,0737722	0,34	0,75766635	1	2435	tags=29%, list=14%, signal=34%
GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	GO_MULTICELLULAR_ORGANISMAL_HOMEOSTASIS	242	-0,23172092	-1,0730962	0,3231939	0,7586014	1	2999	tags=21%, list=17%, signal=26%
GO_NEGATIVE_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_HEMATOPOIETIC_PROGENITOR_CELL_DIFFERENTIATION	20	-0,37288684	-1,0729167	0,38235295	0,75834215	1	3370	tags=40%, list=19%, signal=49%
GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	GO_RETINA_VASCULATURE_DEVELOPMENT_IN_CAMERA_TYPE_EYE	16	-0,42883074	-1,0728091	0,41468254	0,7578689	1	3910	tags=50%, list=22%, signal=64%
GO_BETA_CATENIN_BINDING	GO_BETA_CATENIN_BINDING	79	-0,2886383	-1,0716422	0,35589942	0,76011735	1	1827	tags=19%, list=10%, signal=21%
GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	GO_POSITIVE_REGULATION_OF_B_CELL_MEDIATED_IMMUNITY	22	-0,36737308	-1,0713664	0,36561266	0,76010025	1	1129	tags=18%, list=6%, signal=19%
GO_SEX_DETERMINATION	GO_SEX_DETERMINATION	19	-0,348629	-1,0698687	0,34516767	0,7632265	1	1814	tags=26%, list=10%, signal=29%
GO_PROTEASE_BINDING	GO_PROTEASE_BINDING	98	-0,26367015	-1,0687162	0,34836066	0,76542944	1	2937	tags=26%, list=17%, signal=30%
GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	GO_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	25	-0,34460407	-1,0685438	0,36779323	0,765117	1	5052	tags=48%, list=29%, signal=67%
GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	GO_DISULFIDE_OXIDOREDUCTASE_ACTIVITY	26	-0,36461595	-1,068516	0,39285713	0,76444906	1	547	tags=19%, list=3%, signal=20%
GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	GO_POSITIVE_REGULATION_OF_ERK1_AND_ERK2_CASCADE	158	-0,2713081	-1,0683774	0,364	0,76404274	1	3916	tags=27%, list=22%, signal=34%
GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	GO_REGULATION_OF_MITOCHONDRIAL_MEMBRANE_POTENTIAL	52	-0,26926523	-1,0683471	0,35353535	0,76338434	1	1056	tags=19%, list=6%, signal=20%

GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	GO_POTASSIUM_CHANNEL_REGULATOR_ACTIVITY	43	-0,28551874	-1,0683317	0,3465909	0,762701	1	4465	tags=35%, list=25%, signal=47%
GO_MYOSIN_COMPLEX	GO_MYOSIN_COMPLEX	65	-0,28213277	-1,0680106	0,31697342	0,7627472	1	3750	tags=28%, list=21%, signal=35%
GO_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	GO_POSITIVE_REGULATION_OF_CELL_JUNCTION_ASSEMBLY	24	-0,3222475	-1,068003	0,375	0,76203555	1	922	tags=17%, list=5%, signal=18%
GO_QUATERNARY_AMMONIUM_GROUP_BINDING	GO_QUATERNARY_AMMONIUM_GROUP_BINDING	45	-0,2905108	-1,0677059	0,352	0,76210266	1	2075	tags=20%, list=12%, signal=23%
GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS	GO_NEGATIVE_REGULATION_OF_PROTEOLYSIS	298	-0,21619767	-1,0662236	0,31111112	0,7651705	1	1844	tags=15%, list=10%, signal=17%
GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_DENDRITIC_SPINE_DEVELOPMENT	33	-0,30591145	-1,0660561	0,35470942	0,7648368	1	2097	tags=24%, list=12%, signal=27%
GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	GO_POSITIVE_REGULATION_OF_DEPHOSPHORYLATION	44	-0,28583062	-1,065898	0,34710744	0,764484	1	1445	tags=20%, list=8%, signal=22%
GO_HORMONE_TRANSPORT	GO_HORMONE_TRANSPORT	69	-0,26872343	-1,065897	0,326	0,7637562	1	1812	tags=17%, list=10%, signal=19%
GO_REGULATION_OF_CIRCADIAN_RHYTHM	GO_REGULATION_OF_CIRCADIAN_RHYTHM	94	-0,26896596	-1,0656279	0,36272544	0,76367706	1	2856	tags=27%, list=16%, signal=32%
GO_LONG_TERM_MEMORY	GO_LONG_TERM_MEMORY	28	-0,33266744	-1,064718	0,33661416	0,76531494	1	3411	tags=29%, list=19%, signal=35%
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_PRODUCTION	26	-0,33683404	-1,0643598	0,38372093	0,7654737	1	920	tags=19%, list=5%, signal=20%
GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	GO_ORGANOPHOSPHATE_BIOSYNTHETIC_PROCESS	420	-0,20885424	-1,0631256	0,32163742	0,76793164	1	1725	tags=15%, list=10%, signal=16%
GO_REGULATION_OF_NEURON_PROJECTION_REGENERATION	GO_REGULATION_OF_NEURON_PROJECTION_REGENERATION	20	-0,35027605	-1,0620823	0,39053255	0,7699009	1	1455	tags=20%, list=8%, signal=22%
GO_BRANCH_ELONGATION_OF_AN_EPITHELIUM	GO_BRANCH_ELONGATION_OF_AN_EPITHELIUM	17	-0,37323534	-1,0619752	0,37037036	0,7694677	1	1295	tags=18%, list=7%, signal=19%
GO_ENDOTHELIAL_CELL_MIGRATION	GO_ENDOTHELIAL_CELL_MIGRATION	55	-0,2933023	-1,0617702	0,3507014	0,7692641	1	2904	tags=24%, list=16%, signal=28%
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	30	-0,32593924	-1,0609913	0,3654224	0,770546	1	4232	tags=43%, list=24%, signal=57%
GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	GO_ASPARTIC_TYPE_PEPTIDASE_ACTIVITY	21	-0,32463494	-1,0604198	0,3778234	0,77133614	1	3679	tags=33%, list=21%, signal=42%
GO_ESTROGEN_METABOLIC_PROCESS	GO_ESTROGEN_METABOLIC_PROCESS	23	-0,3557769	-1,0601097	0,38794726	0,77142084	1	1873	tags=22%, list=11%, signal=24%
GO_RESPONSE_TO_THYROID_HORMONE	GO_RESPONSE_TO_THYROID_HORMONE	21	-0,3370004	-1,0597075	0,38253638	0,77171934	1	628	tags=19%, list=4%, signal=20%
GO_RESPONSE_TO_IMMOBILIZATION_STRESS	GO_RESPONSE_TO_IMMOBILIZATION_STRESS	22	-0,33747238	-1,0579484	0,36023623	0,77553266	1	3842	tags=36%, list=22%, signal=46%
GO_BIOMINERAL_TISSUE_DEVELOPMENT	GO_BIOMINERAL_TISSUE_DEVELOPMENT	67	-0,27569622	-1,0577829	0,34246576	0,7752585	1	3742	tags=31%, list=21%, signal=40%
GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	GO_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	138	-0,24337566	-1,0569766	0,36511156	0,776543	1	2329	tags=22%, list=13%, signal=26%
GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	GO_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	28	-0,3311485	-1,0569397	0,4054581	0,7759069	1	3612	tags=36%, list=20%, signal=45%
GO_EMBRYONIC_DIGESTIVE_TRACT_MORPHOGENESIS	GO_EMBRYONIC_DIGESTIVE_TRACT_MORPHOGENESIS	17	-0,37923142	-1,0553098	0,38019803	0,77922827	1	1810	tags=29%, list=10%, signal=33%
GO_TISSUE_MIGRATION	GO_TISSUE_MIGRATION	80	-0,2761481	-1,0542455	0,37349397	0,78114486	1	2917	tags=25%, list=17%, signal=30%
GO_INFLAMMATORY_RESPONSE	GO_INFLAMMATORY_RESPONSE	422	-0,25385168	-1,0540075	0,38193017	0,78100884	1	3137	tags=23%, list=18%, signal=27%
GO_EXTRACELLULAR_MATRIX	GO_EXTRACELLULAR_MATRIX	396	-0,27985296	-1,0531683	0,3680154	0,7824255	1	3873	tags=30%, list=22%, signal=38%
GO_PHAGOCYTOSIS_RECOGNITION	GO_PHAGOCYTOSIS_RECOGNITION	15	-0,38476938	-1,052742	0,39263803	0,78275	1	778	tags=20%, list=4%, signal=21%
GO_INOSITOL_PHOSPHATE_MEDIATED_SIGNALING	GO_INOSITOL_PHOSPHATE_MEDIATED_SIGNALING	16	-0,37908536	-1,0525402	0,39148074	0,78249913	1	1669	tags=25%, list=9%, signal=28%
GO_CELLULAR_RESPONSE_TO_FATTY_ACID	GO_CELLULAR_RESPONSE_TO_FATTY_ACID	50	-0,269597	-1,0524043	0,374502	0,7821403	1	1294	tags=22%, list=7%, signal=24%
GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	GO_ACTIVATION_OF_PROTEIN_KINASE_A_ACTIVITY	16	-0,37447172	-1,0519087	0,3988212	0,78271544	1	2692	tags=25%, list=15%, signal=29%
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	29	-0,31220984	-1,0518552	0,3785851	0,78211397	1	3695	tags=41%, list=21%, signal=52%
GO_ENDOCARDIAL_CUSHION_FORMATION	GO_ENDOCARDIAL_CUSHION_FORMATION	15	-0,40701544	-1,0515951	0,40726578	0,7820904	1	3187	tags=40%, list=18%, signal=49%
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	39	-0,32707378	-1,0515205	0,4	0,78155774	1	3936	tags=38%, list=22%, signal=49%
GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	GO_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	69	-0,272398	-1,0514143	0,36673346	0,7811361	1	4046	tags=38%, list=23%, signal=49%
GO_CELLULAR_EXTRAVASATION	GO_CELLULAR_EXTRAVASATION	24	-0,36971217	-1,0508943	0,37449393	0,78178805	1	2971	tags=29%, list=17%, signal=35%
GO_POSITIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	GO_POSITIVE_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	21	-0,32771006	-1,0502393	0,3732535	0,78266066	1	922	tags=19%, list=5%, signal=20%
GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	GO_NUCLEOSIDE_TRIPHOSPHATE_METABOLIC_PROCESS	213	-0,3073378	-1,0501747	0,4375	0,7821036	1	3462	tags=33%, list=20%, signal=41%
GO_EPITHELIAL_CELL_DIFFERENTIATION	GO_EPITHELIAL_CELL_DIFFERENTIATION	445	-0,2263313	-1,0499896	0,37258688	0,781827	1	2848	tags=22%, list=16%, signal=26%
GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	GO_SERINE_TYPE_EXOPEPTIDASE_ACTIVITY	18	-0,36938727	-1,0488513	0,3939394	0,78403634	1	2131	tags=28%, list=12%, signal=32%
GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	GO_NEGATIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	32	-0,29902944	-1,0478837	0,3972056	0,7857437	1	3599	tags=28%, list=20%, signal=35%
GO_LYMPHOCYTE_MIGRATION	GO_LYMPHOCYTE_MIGRATION	47	-0,36280587	-1,0475745	0,41041666	0,78585124	1	4244	tags=36%, list=24%, signal=47%
GO_LEUKOCYTE_MEDIATED_IMMUNITY	GO_LEUKOCYTE_MEDIATED_IMMUNITY	154	-0,27129248	-1,0472841	0,37860084	0,78589636	1	1223	tags=14%, list=7%, signal=15%
GO_AXO_DENDRITIC_TRANSPORT	GO_AXO_DENDRITIC_TRANSPORT	33	-0,30090022	-1,0471191	0,4039604	0,78556436	1	1611	tags=24%, list=9%, signal=27%
GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	GO_PYRIMIDINE_CONTAINING_COMPOUND_CATABOLIC_PROCESS	29	-0,2979101	-1,047105	0,35234216	0,7848774	1	1842	tags=17%, list=10%, signal=19%
GO_REGULATION_OF_TRANSPORTER_ACTIVITY	GO_REGULATION_OF_TRANSPORTER_ACTIVITY	183	-0,24968769	-1,0464542	0,34516767	0,78582495	1	4465	tags=34%, list=25%, signal=46%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_EXTERNAL_STIMULUS	280	-0,2490502	-1,0461056	0,3697479	0,7859787	1	1699	tags=14%, list=10%, signal=15%
GO_UROGENITAL_SYSTEM_DEVELOPMENT	GO_UROGENITAL_SYSTEM_DEVELOPMENT	292	-0,24531518	-1,0451608	0,37807184	0,78773713	1	2875	tags=22%, list=16%, signal=26%
GO_CEREBELLAR_CORTEX_FORMATION	GO_CEREBELLAR_CORTEX_FORMATION	21	-0,34909517	-1,0451359	0,40246406	0,78708094	1	4919	tags=48%, list=28%, signal=66%
GO_NEURON_MATURATION	GO_NEURON_MATURATION	30	-0,3194792	-1,0449821	0,36144578	0,78673595	1	2050	tags=20%, list=12%, signal=23%
GO_LIPASE_ACTIVITY	GO_LIPASE_ACTIVITY	109	-0,24660455	-1,0445405	0,3528265	0,78713477	1	3809	tags=31%, list=22%, signal=40%
GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	GO_POSITIVE_REGULATION_OF_INTERLEUKIN_4_PRODUCTION	22	-0,3694334	-1,0438486	0,39960238	0,7881805	1	2969	tags=27%, list=17%, signal=33%
GO_NITRIC_OXIDE_MEDIATED_SIGNAL_TRANSDUCTION	GO_NITRIC_OXIDE_MEDIATED_SIGNAL_TRANSDUCTION	18	-0,34789833	-1,0429515	0,40697673	0,7897418	1	2627	tags=22%, list=15%, signal=26%

GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	GO_REGULATION_OF_CELL_SUBSTRATE_ADHESION	163	-0,26461205	-1,0426638	0,38910505	0,7897507	1	2975	tags=25%, list=17%, signal=30%
GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX	GO_PHOSPHATIDYLINOSITOL_3_KINASE_COMPLEX	19	-0,37480256	-1,0425531	0,3995984	0,78930634	1	5321	tags=53%, list=30%, signal=75%
GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	GO_REGULATION_OF_EXECUTION_PHASE_OF_APOPTOSIS	24	-0,30911875	-1,0417618	0,398	0,79058754	1	956	tags=17%, list=5%, signal=18%
GO_BASEMENT_MEMBRANE	GO_BASEMENT_MEMBRANE	88	-0,29929137	-1,0414897	0,37904763	0,7905421	1	3873	tags=34%, list=22%, signal=43%
GO_TRANSCRIPTIONALLY_ACTIVE_CHROMATIN	GO_TRANSCRIPTIONALLY_ACTIVE_CHROMATIN	16	-0,3522542	-1,0414684	0,3760504	0,7898787	1	3148	tags=38%, list=18%, signal=46%
GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_KINASE_ACTIVITY	239	-0,2089691	-1,0406728	0,3761996	0,7911753	1	3509	tags=26%, list=20%, signal=32%
GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_T_CELL_DIFFERENTIATION	28	-0,3110723	-1,0401316	0,41563785	0,7918794	1	3788	tags=29%, list=21%, signal=36%
GO_NEGATIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	GO_NEGATIVE_REGULATION_OF_DENDRITE_MORPHOGENESIS	15	-0,36365762	-1,0391626	0,39156628	0,79364675	1	4746	tags=40%, list=27%, signal=55%
GO_GTP_METABOLIC_PROCESS	GO_GTP_METABOLIC_PROCESS	21	-0,33846438	-1,0390372	0,4003984	0,7932617	1	2278	tags=33%, list=13%, signal=38%
GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	GO_NEGATIVE_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	40	-0,33127663	-1,0381998	0,41304347	0,7946712	1	3412	tags=28%, list=19%, signal=34%
GO_NEGATIVE_REGULATION_OF_LIPID_STORAGE	GO_NEGATIVE_REGULATION_OF_LIPID_STORAGE	17	-0,3495903	-1,0371652	0,3895349	0,7965633	1	4942	tags=47%, list=28%, signal=65%
GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	GO_VENTRICULAR_CARDIAC_MUSCLE_CELL_DIFFERENTIATION	18	-0,35132506	-1,0369811	0,4060606	0,79631263	1	3202	tags=56%, list=18%, signal=68%
GO_POSITIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_DENDRITE_DEVELOPMENT	62	-0,2663552	-1,0365703	0,39130434	0,79666984	1	3232	tags=31%, list=18%, signal=37%
GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	GO_DOPAMINE_RECEPTOR_SIGNALING_PATHWAY	25	-0,31710157	-1,0365605	0,40118578	0,7959708	1	2802	tags=24%, list=16%, signal=28%
GO_HINDBRAIN_MORPHOGENESIS	GO_HINDBRAIN_MORPHOGENESIS	37	-0,30198032	-1,0365082	0,39078155	0,79539174	1	4919	tags=49%, list=28%, signal=67%
GO_NEGATIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	GO_NEGATIVE_REGULATION_OF_TRANSPORTER_ACTIVITY	60	-0,2763441	-1,0362872	0,39534885	0,7952379	1	4232	tags=38%, list=24%, signal=50%
GO_COBALAMIN_METABOLIC_PROCESS	GO_COBALAMIN_METABOLIC_PROCESS	20	-0,37824336	-1,0360045	0,4011628	0,7952159	1	3010	tags=35%, list=17%, signal=42%
GO_REGULATION_OF_THYMOCYTE_AGGREGATION	GO_REGULATION_OF_THYMOCYTE_AGGREGATION	25	-0,32116094	-1,0345604	0,39789474	0,798157	1	3467	tags=36%, list=20%, signal=45%
GO_PROTEIN_OLIGOMERIZATION	GO_PROTEIN_OLIGOMERIZATION	402	-0,20181827	-1,0342748	0,36864406	0,79812115	1	3265	tags=25%, list=18%, signal=30%
GO_CELLULAR_RESPONSE_TO_DEXAMETHASONE_STIMULUS	GO_CELLULAR_RESPONSE_TO_DEXAMETHASONE_STIMULUS	26	-0,31148618	-1,0342345	0,39714867	0,7974932	1	3030	tags=35%, list=17%, signal=42%
GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	GO_MUSCLE_CELL_CELLULAR_HOMEOSTASIS	16	-0,3513382	-1,0341197	0,41344196	0,7970526	1	2685	tags=38%, list=15%, signal=44%
GO_PERIKARYON	GO_PERIKARYON	94	-0,25247324	-1,0338161	0,3875502	0,79713964	1	3072	tags=24%, list=17%, signal=29%
GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	GO_CELLULAR_RESPONSE_TO_NITROGEN_COMPOUND	465	-0,21758544	-1,033762	0,3802817	0,7965579	1	3425	tags=26%, list=19%, signal=31%
GO_ACTIN_BASED_CELL_PROJECTION	GO_ACTIN_BASED_CELL_PROJECTION	167	-0,23304391	-1,0330168	0,38326848	0,7976848	1	2192	tags=18%, list=12%, signal=20%
GO_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	GO_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	35	-0,31926894	-1,0319439	0,3992016	0,7996711	1	3202	tags=31%, list=18%, signal=38%
GO_REGULATION_OF_PEPTIDE_SECRETION	GO_REGULATION_OF_PEPTIDE_SECRETION	193	-0,22087231	-1,0317818	0,37747034	0,79934573	1	2856	tags=21%, list=16%, signal=24%
GO_MODULATION_OF_GROWTH_OF_SYMBIONT_INVOLVED_IN_INTERACTION_WITH_HOST	GO_MODULATION_OF_GROWTH_OF_SYMBIONT_INVOLVED_IN_INTERACTION_WITH_HOST	16	-0,38518503	-1,0314214	0,42454728	0,79954	1	3311	tags=31%, list=19%, signal=38%
GO_INTRACELLULAR_RECEPTOR_SIGNALING_PATHWAY	GO_INTRACELLULAR_RECEPTOR_SIGNALING_PATHWAY	160	-0,2346844	-1,0308589	0,38877755	0,8001518	1	2726	tags=23%, list=15%, signal=27%
GO_IMMUNOGLOBULIN_BINDING	GO_IMMUNOGLOBULIN_BINDING	19	-0,39511943	-1,0307796	0,42331287	0,7996271	1	2759	tags=37%, list=16%, signal=44%
GO_GLUTAMATE_RECEPTOR_BINDING	GO_GLUTAMATE_RECEPTOR_BINDING	36	-0,29336923	-1,0307404	0,40466926	0,79900765	1	3411	tags=31%, list=19%, signal=38%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_6_PRODUCTION	31	-0,33431742	-1,0301809	0,4020408	0,79966444	1	2969	tags=23%, list=17%, signal=27%
GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	107	-0,2735323	-1,0297635	0,412731	0,80001944	1	5062	tags=37%, list=29%, signal=52%
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_BINDING	48	-0,30138543	-1,0292901	0,39363816	0,80057454	1	3599	tags=27%, list=20%, signal=34%
GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	GO_POSITIVE_REGULATION_OF_RECEPTOR_INTERNALIZATION	23	-0,32264072	-1,029046	0,4055118	0,800484	1	2704	tags=30%, list=15%, signal=36%
GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	GO_NEGATIVE_REGULATION_OF_IMMUNE_SYSTEM_PROCESS	345	-0,24040492	-1,0289898	0,3787234	0,7998894	1	3507	tags=24%, list=20%, signal=29%
GO_CARGO_RECEPTOR_ACTIVITY	GO_CARGO_RECEPTOR_ACTIVITY	60	-0,28151324	-1,0283467	0,40325865	0,800794	1	2451	tags=23%, list=14%, signal=27%
GO_COLLAGEN_BINDING	GO_COLLAGEN_BINDING	59	-0,32610053	-1,0282695	0,41992188	0,8002673	1	3156	tags=32%, list=18%, signal=39%
GO_SMAD_BINDING	GO_SMAD_BINDING	69	-0,29396343	-1,0280782	0,4169884	0,80008525	1	3208	tags=30%, list=18%, signal=37%
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_PROLIFERATION	29	-0,32747132	-1,0277365	0,44067797	0,8002822	1	1138	tags=21%, list=6%, signal=22%
GO_SODIUM_ION_TRANSPORT	GO_SODIUM_ION_TRANSPORT	130	-0,24527884	-1,0276875	0,392	0,79970485	1	4261	tags=30%, list=24%, signal=39%
GO_CORTICAL_ACTIN_CYTOSKELETON	GO_CORTICAL_ACTIN_CYTOSKELETON	57	-0,28766316	-1,0274942	0,408	0,7995115	1	2656	tags=26%, list=15%, signal=31%
GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	GO_LIGASE_ACTIVITY_FORMING_CARBON_NITROGEN_BONDS	51	-0,27036977	-1,0273944	0,39219713	0,799038	1	2259	tags=27%, list=13%, signal=31%
GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	GO_REGULATION_OF_ACTIN_CYTOSKELETON_REORGANIZATION	31	-0,32135645	-1,026568	0,41563785	0,80046064	1	2569	tags=29%, list=15%, signal=34%
GO_INNER_EAR_RECEPTOR_STEREOCILIUM_ORGANIZATION	GO_INNER_EAR_RECEPTOR_STEREOCILIUM_ORGANIZATION	19	-0,33688566	-1,0265573	0,42031872	0,7997844	1	2108	tags=37%, list=12%, signal=42%
GO_PEPTIDE_ANTIGEN_BINDING	GO_PEPTIDE_ANTIGEN_BINDING	26	-0,38951862	-1,0263877	0,4392157	0,7995093	1	877	tags=12%, list=5%, signal=12%
GO_REGULATION_OF_MULTICELLULAR_ORGANISMAL_METABOLIC_PROCESS	GO_REGULATION_OF_MULTICELLULAR_ORGANISMAL_METABOLIC_PROCESS	34	-0,30753082	-1,0257812	0,42105263	0,8003565	1	3030	tags=26%, list=17%, signal=32%
GO_4_IRON_4_SULFUR_CLUSTER_BINDING	GO_4_IRON_4_SULFUR_CLUSTER_BINDING	40	-0,3058784	-1,025659	0,4180328	0,79999125	1	3740	tags=50%, list=21%, signal=63%
GO_SECRETION_BY_CELL	GO_SECRETION_BY_CELL	456	-0,21922848	-1,0252126	0,35403726	0,80041444	1	3151	tags=21%, list=18%, signal=25%
GO_OSTEOBLAST_DEVELOPMENT	GO_OSTEOBLAST_DEVELOPMENT	18	-0,3461072	-1,0245221	0,41422594	0,8014809	1	1295	tags=17%, list=7%, signal=18%
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	46	-0,30101684	-1,0239929	0,40471512	0,80211437	1	3794	tags=30%, list=21%, signal=39%
GO_REGULATION_OF_CELL_MATURATION	GO_REGULATION_OF_CELL_MATURATION	18	-0,32774377	-1,0236382	0,43460765	0,8023468	1	2598	tags=28%, list=15%, signal=33%
GO_ADHERENS_JUNCTION_ASSEMBLY	GO_ADHERENS_JUNCTION_ASSEMBLY	33	-0,3168589	-1,0229244	0,4139265	0,80345446	1	2994	tags=30%, list=17%, signal=36%
GO_SMOOTH_ENDOPLASMIC_RETICULUM	GO_SMOOTH_ENDOPLASMIC_RETICULUM	33	-0,30702507	-1,0223104	0,42578125	0,8043927	1	3151	tags=24%, list=18%, signal=29%

GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	GO_REGULATION_OF_NATURAL_KILLER_CELL_MEDIATED_IMMUNITY	33	-0,3697833	-1,0216283	0,44512194	0,80549157	1	3553	tags=39%, list=20%, signal=49%
GO_RECEPTOR_INTERNALIZATION	GO_RECEPTOR_INTERNALIZATION	44	-0,30397758	-1,021624	0,42650104	0,80480313	1	3251	tags=27%, list=18%, signal=33%
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ACYL_GROUPS	226	-0,21660432	-1,0209731	0,40836653	0,8057733	1	1107	tags=12%, list=6%, signal=12%
GO_TRANSITION_METAL_ION_TRANSPORT	GO_TRANSITION_METAL_ION_TRANSPORT	101	-0,23996466	-1,0208355	0,40408164	0,80538327	1	3128	tags=29%, list=18%, signal=35%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	64	-0,30425957	-1,0192951	0,42454728	0,8085548	1	3553	tags=33%, list=20%, signal=41%
GO_POSITIVE_REGULATION_OF_HEART_GROWTH	GO_POSITIVE_REGULATION_OF_HEART_GROWTH	27	-0,3134858	-1,0188718	0,4296875	0,80896324	1	3997	tags=41%, list=23%, signal=53%
GO_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	GO_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	50	-0,27744544	-1,01812	0,39803922	0,8101685	1	3110	tags=24%, list=18%, signal=29%
GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	GO_CELLULAR_RESPONSE_TO_EXTERNAL_STIMULUS	251	-0,22005084	-1,0172409	0,3991684	0,8117354	1	2712	tags=20%, list=15%, signal=23%
GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO_NEGATIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	40	-0,30738455	-1,0172029	0,41897234	0,8111342	1	1533	tags=15%, list=9%, signal=16%
GO_RESPONSE_TO_WATER	GO_RESPONSE_TO_WATER	17	-0,3341343	-1,0171373	0,42322835	0,81059027	1	557	tags=12%, list=3%, signal=12%
GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_POSITIVE_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	16	-0,35804775	-1,0167352	0,42629483	0,8109128	1	4406	tags=44%, list=25%, signal=58%
GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	GO_INWARD_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	21	-0,33165216	-1,0163803	0,43159923	0,8110883	1	324	tags=10%, list=2%, signal=10%
GO_REGULATION_OF_STAT_CASCADE	GO_REGULATION_OF_STAT_CASCADE	115	-0,25193837	-1,0162126	0,45661157	0,810818	1	2108	tags=19%, list=12%, signal=22%
GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	GO_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	58	-0,2732826	-1,0160224	0,434	0,8106119	1	4068	tags=38%, list=23%, signal=49%
GO_MULTICELLULAR_ORGANISMAL_WATER_HOMEOSTASIS	GO_MULTICELLULAR_ORGANISMAL_WATER_HOMEOSTASIS	54	-0,2795379	-1,0155778	0,4185606	0,8110086	1	4327	tags=33%, list=24%, signal=44%
GO_ACIDIC_AMINO_ACID_TRANSPORT	GO_ACIDIC_AMINO_ACID_TRANSPORT	20	-0,33200938	-1,0149462	0,43451142	0,8118968	1	3381	tags=35%, list=19%, signal=43%
GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	GO_REGULATION_OF_LONG_TERM_NEURONAL_SYNAPTIC_PLASTICITY	23	-0,3237866	-1,0147501	0,41682974	0,8116834	1	3346	tags=22%, list=19%, signal=27%
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_PROLIFERATION	148	-0,24379009	-1,0147325	0,4311741	0,81102604	1	3110	tags=22%, list=18%, signal=27%
GO_REGULATION_OF_BLOOD_CIRCULATION	GO_REGULATION_OF_BLOOD_CIRCULATION	278	-0,24588409	-1,0147231	0,42722118	0,810354	1	4442	tags=32%, list=25%, signal=42%
GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	GO_REGULATION_OF_PROTEIN_AUTOPHOSPHORYLATION	35	-0,31734872	-1,0143026	0,4288618	0,8107178	1	3412	tags=29%, list=19%, signal=35%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT	100	-0,2596177	-1,014067	0,4279919	0,8105957	1	3951	tags=32%, list=22%, signal=41%
GO_ISOMERASE_ACTIVITY	GO_ISOMERASE_ACTIVITY	143	-0,23507985	-1,0135441	0,44791666	0,8112267	1	1081	tags=12%, list=6%, signal=13%
GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	GO_REGULATION_OF_CARTILAGE_DEVELOPMENT	58	-0,30635914	-1,0129364	0,44040403	0,81202424	1	3073	tags=29%, list=17%, signal=35%
GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	GO_NEGATIVE_REGULATION_OF_TRANSLATIONAL_INITIATION	20	-0,3255423	-1,0127898	0,43531826	0,81171876	1	3201	tags=30%, list=18%, signal=37%
GO_MONOSACCHARIDE_TRANSPORT	GO_MONOSACCHARIDE_TRANSPORT	53	-0,26261923	-1,0124524	0,43849206	0,81191355	1	3854	tags=32%, list=22%, signal=41%
GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	GO_CARDIAC_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	24	-0,3357332	-1,0121818	0,43554688	0,81193036	1	3202	tags=29%, list=18%, signal=36%
GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	GO_RETINOIC_ACID_RECEPTOR_SIGNALING_PATHWAY	17	-0,3333352	-1,0120013	0,41509435	0,8116855	1	4659	tags=47%, list=26%, signal=64%
GO_INACTIVATION_OF_MAPK_ACTIVITY	GO_INACTIVATION_OF_MAPK_ACTIVITY	25	-0,29483014	-1,0109948	0,43371212	0,8135522	1	2900	tags=24%, list=16%, signal=29%
GO_ANTIMICROBIAL_HUMORAL_RESPONSE	GO_ANTIMICROBIAL_HUMORAL_RESPONSE	38	-0,326898	-1,0099175	0,4448819	0,8155309	1	5889	tags=45%, list=33%, signal=67%
GO_NEGATIVE_REGULATION_OF_LOCOMOTION	GO_NEGATIVE_REGULATION_OF_LOCOMOTION	248	-0,2372037	-1,0098511	0,43452382	0,8150014	1	2975	tags=20%, list=17%, signal=23%
GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	340	-0,2119584	-1,0097343	0,42137095	0,8145948	1	3310	tags=25%, list=19%, signal=30%
GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_SECONDARY_ACTIVE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	222	-0,21988265	-1,009245	0,4186508	0,81517196	1	3280	tags=26%, list=19%, signal=32%
GO_MELANOCYTE_DIFFERENTIATION	GO_MELANOCYTE_DIFFERENTIATION	16	-0,3709198	-1,0089335	0,44990548	0,81525636	1	5473	tags=63%, list=31%, signal=90%
GO_REGULATION_OF_AMINE_TRANSPORT	GO_REGULATION_OF_AMINE_TRANSPORT	66	-0,26900712	-1,0081481	0,43625498	0,8165679	1	2075	tags=18%, list=12%, signal=21%
GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	GO_POSITIVE_REGULATION_OF_SUBSTRATE_ADHESION_DEPENDENT_CELL_SPREADING	26	-0,30571955	-1,0077268	0,45086706	0,81692636	1	1636	tags=19%, list=9%, signal=21%
GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY	GO_INSULIN_RECEPTOR_SIGNALING_PATHWAY	76	-0,24909279	-1,0072731	0,43292683	0,81734073	1	2329	tags=22%, list=13%, signal=26%
GO_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	GO_REGULATION_OF_SYNAPTIC_VESICLE_TRANSPORT	28	-0,29484937	-1,0069219	0,41516966	0,8175031	1	1638	tags=21%, list=9%, signal=24%
GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_NEGATIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	19	-0,34242344	-1,0067915	0,42239687	0,8171487	1	5059	tags=58%, list=29%, signal=81%
GO_SARCOPLASMIC_RETICULUM_MEMBRANE	GO_SARCOPLASMIC_RETICULUM_MEMBRANE	34	-0,31566772	-1,0059413	0,4372549	0,81862587	1	4409	tags=41%, list=25%, signal=55%
GO_DRUG_BINDING	GO_DRUG_BINDING	104	-0,23034362	-1,0058591	0,44	0,8181599	1	3324	tags=25%, list=19%, signal=31%
GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	GO_POSITIVE_REGULATION_OF_LIPID_KINASE_ACTIVITY	32	-0,31745496	-1,005208	0,45346534	0,8190942	1	3936	tags=41%, list=22%, signal=52%
GO_REGULATION_OF_CALCINEURIN_NFAT_SIGNALING_CASCADE	GO_REGULATION_OF_CALCINEURIN_NFAT_SIGNALING_CASCADE	16	-0,3417946	-1,0052041	0,45833334	0,81841224	1	1412	tags=19%, list=8%, signal=20%
GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	GO_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	132	-0,24542627	-1,0051888	0,4417178	0,8177544	1	4046	tags=34%, list=23%, signal=44%
GO_RESPONSE_TO_NITRIC_OXIDE	GO_RESPONSE_TO_NITRIC_OXIDE	21	-0,31576332	-1,0045265	0,44246033	0,8187285	1	3529	tags=38%, list=20%, signal=48%
GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	GO_STRIATED_MUSCLE_CELL_DIFFERENTIATION	157	-0,23311415	-1,0033802	0,424	0,82090604	1	4046	tags=32%, list=23%, signal=42%
GO_EXTRACELLULAR_MATRIX_COMPONENT	GO_EXTRACELLULAR_MATRIX_COMPONENT	120	-0,29287976	-1,0023676	0,42095238	0,82278514	1	4061	tags=33%, list=23%, signal=43%
GO_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_SUGAR_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	31	-0,2878767	-1,0020025	0,4459725	0,82305366	1	3455	tags=35%, list=20%, signal=44%
GO_AUTOPHAGOSOME_MEMBRANE	GO_AUTOPHAGOSOME_MEMBRANE	27	-0,30128285	-1,001814	0,45415777	0,82285523	1	4710	tags=37%, list=27%, signal=50%
GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_COUPLED_TO_CYCLIC_NUCLEOTIDE_SECOND_MESSENGER	GO_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY_COUPLED_TO_CYCLIC_NUCLEOTIDE_SECOND_MESSENGER	137	-0,25627565	-1,0011164	0,45755693	0,8238874	1	2971	tags=23%, list=17%, signal=27%
GO_GAS_TRANSPORT	GO_GAS_TRANSPORT	17	-0,43380335	-1,000968	0,47679326	0,8235595	1	5061	tags=53%, list=29%, signal=74%
GO_NUCLEOBASE_METABOLIC_PROCESS	GO_NUCLEOBASE_METABOLIC_PROCESS	37	-0,29066417	-1,000166	0,46520874	0,82485676	1	2020	tags=24%, list=11%, signal=27%
GO_NEGATIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	GO_NEGATIVE_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	57	-0,27039644	-0,9999833	0,44401544	0,8246521	1	5062	tags=47%, list=29%, signal=66%

GO_IRON_ION_TRANSPORT	GO_IRON_ION_TRANSPORT	52	-0,27150902	-0,999787	0,43326488	0,8244493	1	2451	tags=25%, list=14%, signal=29%
GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	GO_STRUCTURAL_CONSTITUENT_OF_MUSCLE	39	-0,29796445	-0,9993985	0,4490196	0,8247625	1	3750	tags=36%, list=21%, signal=45%
GO_PEPTIDE_HORMONE_RECEPTOR_BINDING	GO_PEPTIDE_HORMONE_RECEPTOR_BINDING	15	-0,35785672	-0,9992053	0,4390244	0,82457817	1	1941	tags=20%, list=11%, signal=22%
GO_SCAVENGER_RECEPTOR_ACTIVITY	GO_SCAVENGER_RECEPTOR_ACTIVITY	39	-0,31031895	-0,9984062	0,44827586	0,82593155	1	2451	tags=23%, list=14%, signal=27%
GO_OUTFLOW_TRACT_MORPHOGENESIS	GO_OUTFLOW_TRACT_MORPHOGENESIS	55	-0,29632682	-0,9977204	0,42610365	0,8270258	1	3211	tags=38%, list=18%, signal=47%
GO_CATION_SUGAR_SYMPORTER_ACTIVITY	GO_CATION_SUGAR_SYMPORTER_ACTIVITY	15	-0,34905645	-0,9967561	0,4607646	0,8287924	1	3248	tags=47%, list=18%, signal=57%
GO_ADHERENS_JUNCTION_ORGANIZATION	GO_ADHERENS_JUNCTION_ORGANIZATION	65	-0,26811543	-0,9967076	0,47976878	0,82822156	1	3530	tags=29%, list=20%, signal=36%
GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	GO_MULTICELLULAR_ORGANISMAL_RESPONSE_TO_STRESS	64	-0,2579536	-0,9949933	0,468	0,831809	1	3154	tags=23%, list=18%, signal=28%
GO_LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_BINDING	GO_LIGAND_DEPENDENT_NUCLEAR_RECEPTOR_BINDING	23	-0,3256677	-0,9946792	0,4612326	0,83189255	1	1540	tags=22%, list=9%, signal=24%
GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	GO_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	47	-0,28688774	-0,9946464	0,44981414	0,83128947	1	1658	tags=19%, list=9%, signal=21%
GO_PHOSPHOLIPID_BINDING	GO_PHOSPHOLIPID_BINDING	338	-0,21384692	-0,9946182	0,45238096	0,83068055	1	1894	tags=14%, list=11%, signal=16%
GO_SARCOLEMMA	GO_SARCOLEMMA	121	-0,26218542	-0,9940226	0,44847327	0,83147323	1	3192	tags=25%, list=18%, signal=30%
GO_ARTERY_DEVELOPMENT	GO_ARTERY_DEVELOPMENT	75	-0,28883958	-0,9926642	0,46230158	0,83422774	1	3250	tags=29%, list=18%, signal=36%
GO_CELLULAR_RESPONSE_TO_REACTIVE_NITROGEN_SPECIES	GO_CELLULAR_RESPONSE_TO_REACTIVE_NITROGEN_SPECIES	19	-0,3320694	-0,9923281	0,454	0,83437407	1	1129	tags=21%, list=6%, signal=22%
GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	GO_T_CELL_DIFFERENTIATION_INVOLVED_IN_IMMUNE_RESPONSE	28	-0,32546172	-0,9917033	0,45030427	0,8352185	1	4193	tags=43%, list=24%, signal=56%
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_MEMBRANE_REPOLARIZATION	19	-0,34195173	-0,9915656	0,44930416	0,8348878	1	4597	tags=42%, list=26%, signal=57%
GO_MULTICELLULAR_ORGANISMAL_SIGNALING	GO_MULTICELLULAR_ORGANISMAL_SIGNALING	116	-0,26744425	-0,9905828	0,4481409	0,8366864	1	4437	tags=33%, list=25%, signal=43%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_10_PRODUCTION	16	-0,37730032	-0,9905224	0,4661191	0,8361404	1	3507	tags=31%, list=20%, signal=39%
GO_CELL_SUBSTRATE_ADHESION	GO_CELL_SUBSTRATE_ADHESION	160	-0,2549083	-0,9905065	0,45574388	0,83548886	1	2994	tags=26%, list=17%, signal=31%
GO_CORE_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	GO_CORE_PROMOTER_SEQUENCE_SPECIFIC_DNA_BINDING	97	-0,24880956	-0,9904153	0,46732673	0,83503497	1	3003	tags=28%, list=17%, signal=33%
GO_THYMIC_T_CELL_SELECTION	GO_THYMIC_T_CELL_SELECTION	19	-0,38762107	-0,9897741	0,47010309	0,8359912	1	4910	tags=32%, list=28%, signal=44%
GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	GO_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	55	-0,29326037	-0,9894682	0,46613547	0,8361003	1	3188	tags=29%, list=18%, signal=35%
GO_APOPTOTIC_DNA_FRAGMENTATION	GO_APOPTOTIC_DNA_FRAGMENTATION	15	-0,34318364	-0,9891014	0,48490945	0,8363457	1	977	tags=20%, list=6%, signal=21%
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_INSULIN_STIMULUS	21	-0,31582418	-0,9881006	0,4624506	0,8381148	1	5408	tags=62%, list=31%, signal=89%
GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	GO_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	399	-0,22316073	-0,987308	0,45656565	0,8393965	1	2971	tags=21%, list=17%, signal=24%
GO_T_TUBULE	GO_T_TUBULE	44	-0,30180582	-0,9860696	0,4581749	0,8418945	1	3102	tags=25%, list=18%, signal=30%
GO_CARBOHYDRATE_KINASE_ACTIVITY	GO_CARBOHYDRATE_KINASE_ACTIVITY	19	-0,32934126	-0,9859811	0,47070706	0,8414575	1	1150	tags=21%, list=7%, signal=22%
GO_ISOPRENOID_BIOSYNTHETIC_PROCESS	GO_ISOPRENOID_BIOSYNTHETIC_PROCESS	23	-0,34294927	-0,9858164	0,48906562	0,8412016	1	1403	tags=17%, list=8%, signal=19%
GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	GO_CARBOHYDRATE_DERIVATIVE_CATABOLIC_PROCESS	161	-0,22088121	-0,9855315	0,46893787	0,84122646	1	2132	tags=19%, list=12%, signal=21%
GO_RESPONSE_TO_OXYGEN_LEVELS	GO_RESPONSE_TO_OXYGEN_LEVELS	300	-0,21717393	-0,985171	0,44941634	0,84144944	1	3019	tags=22%, list=17%, signal=26%
GO_SOLUTE_CATION_SYMPORTER_ACTIVITY	GO_SOLUTE_CATION_SYMPORTER_ACTIVITY	97	-0,23396674	-0,9849046	0,47034764	0,8413983	1	3248	tags=28%, list=18%, signal=34%
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	122	-0,23717676	-0,9849028	0,46558705	0,8407177	1	3951	tags=29%, list=22%, signal=37%
GO_ACTIN_FILAMENT_POLYMERIZATION	GO_ACTIN_FILAMENT_POLYMERIZATION	21	-0,30899715	-0,9845464	0,46183953	0,84094733	1	4407	tags=43%, list=25%, signal=57%
GO_DNA_CATABOLIC_PROCESS	GO_DNA_CATABOLIC_PROCESS	26	-0,27761427	-0,9840905	0,4748491	0,84141713	1	977	tags=15%, list=6%, signal=16%
GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	GO_PLASMA_MEMBRANE_PROTEIN_COMPLEX	473	-0,21664669	-0,9840112	0,4484127	0,8409488	1	2820	tags=18%, list=16%, signal=21%
GO_GLUTAMATE_SECRETION	GO_GLUTAMATE_SECRETION	27	-0,30686793	-0,9839886	0,49896908	0,84032416	1	1697	tags=22%, list=10%, signal=25%
GO_FILAMENTOUS_ACTIN	GO_FILAMENTOUS_ACTIN	19	-0,33022964	-0,9839045	0,4725051	0,83986187	1	1290	tags=21%, list=7%, signal=23%
GO_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	GO_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	57	-0,2720736	-0,9830316	0,45961538	0,84134054	1	3599	tags=26%, list=20%, signal=33%
GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	GO_NUCLEOTIDE_SUGAR_BIOSYNTHETIC_PROCESS	19	-0,32501093	-0,9825321	0,4968153	0,8419448	1	1096	tags=21%, list=6%, signal=22%
GO_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	GO_REGULATION_OF_MUSCLE_TISSUE_DEVELOPMENT	96	-0,24276753	-0,981948	0,47069943	0,8427573	1	3997	tags=33%, list=23%, signal=43%
GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	GO_CELLULAR_RESPONSE_TO_ORGANIC_CYCLIC_COMPOUND	438	-0,20538867	-0,9809992	0,49411765	0,8444249	1	2802	tags=20%, list=16%, signal=24%
GO_DIGESTION	GO_DIGESTION	115	-0,24684425	-0,9808376	0,4913958	0,8441198	1	1477	tags=13%, list=8%, signal=14%
GO_ORGANELLE_ENVELOPE_LUMEN	GO_ORGANELLE_ENVELOPE_LUMEN	73	-0,2760263	-0,9794027	0,4948025	0,84706485	1	2062	tags=19%, list=12%, signal=22%
GO_RESPONSE_TO_TEMPERATURE_STIMULUS	GO_RESPONSE_TO_TEMPERATURE_STIMULUS	138	-0,22521375	-0,9776145	0,47758284	0,8509507	1	3154	tags=23%, list=18%, signal=28%
GO_CELL_PROJECTION_CYTOPLASM	GO_CELL_PROJECTION_CYTOPLASM	47	-0,25490865	-0,9775658	0,47261664	0,85037446	1	1638	tags=21%, list=9%, signal=23%
GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER	GO_TRANSCRIPTION_INITIATION_FROM_RNA_POLYMERASE_II_PROMOTER	150	-0,21740268	-0,9774802	0,5194274	0,84993434	1	2241	tags=19%, list=13%, signal=21%
GO_REGULATION_OF_HAIR_CYCLE	GO_REGULATION_OF_HAIR_CYCLE	22	-0,3190302	-0,9766923	0,48526523	0,85127413	1	2856	tags=23%, list=16%, signal=27%
GO_CHANNEL_INHIBITOR_ACTIVITY	GO_CHANNEL_INHIBITOR_ACTIVITY	33	-0,25865352	-0,9766201	0,4882353	0,85078	1	2701	tags=24%, list=15%, signal=29%
GO_AMINOPEPTIDASE_ACTIVITY	GO_AMINOPEPTIDASE_ACTIVITY	40	-0,2591602	-0,9765263	0,4882227	0,85031414	1	2859	tags=25%, list=16%, signal=30%
GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	GO_CELLULAR_RESPONSE_TO_ACID_CHEMICAL	160	-0,22416918	-0,9759457	0,47440946	0,85109615	1	1547	tags=15%, list=9%, signal=16%
GO_REGULATION_OF_SULFUR_METABOLIC_PROCESS	GO_REGULATION_OF_SULFUR_METABOLIC_PROCESS	19	-0,34333652	-0,9755081	0,49800798	0,8515365	1	4538	tags=47%, list=26%, signal=64%
GO_RESPONSE_TO_VITAMIN	GO_RESPONSE_TO_VITAMIN	95	-0,23066454	-0,9753789	0,47953215	0,8511753	1	3344	tags=26%, list=19%, signal=32%
GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	GO_REGULATION_OF_HEART_RATE_BY_CARDIAC_CONDUCTION	29	-0,32079244	-0,9751992	0,486	0,8509648	1	4123	tags=38%, list=23%, signal=49%

GO_RESPONSE_TO_FOOD	GO_RESPONSE_TO_FOOD	16	-0,3360422	-0,9747059	0,51028806	0,85156006	1	1472	tags=25%, list=8%, signal=27%
GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	GO_NEGATIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	16	-0,34077686	-0,9746624	0,48766604	0,85099095	1	1138	tags=19%, list=6%, signal=20%
GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	GO_PEPTIDYL_TYROSINE_AUTOPHOSPHORYLATION	39	-0,30464587	-0,9741849	0,47	0,85150474	1	2630	tags=23%, list=15%, signal=27%
GO_CONNECTIVE_TISSUE_DEVELOPMENT	GO_CONNECTIVE_TISSUE_DEVELOPMENT	183	-0,25201946	-0,9733176	0,48242188	0,85306805	1	2785	tags=21%, list=16%, signal=25%
GO_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO_ADENYLATE_CYCLASE_MODULATING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	117	-0,25111625	-0,972813	0,4857143	0,85371417	1	2932	tags=22%, list=17%, signal=26%
GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	GO_CELLULAR_RESPONSE_TO_TOXIC_SUBSTANCE	24	-0,2987628	-0,9725763	0,5009901	0,85361516	1	1799	tags=17%, list=10%, signal=19%
GO_CHEMOATTRACTANT_ACTIVITY	GO_CHEMOATTRACTANT_ACTIVITY	26	-0,2961558	-0,9722723	0,513834	0,85372823	1	2810	tags=31%, list=16%, signal=37%
GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	GO_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	115	-0,27103397	-0,9721438	0,45061728	0,85335994	1	3548	tags=25%, list=20%, signal=31%
GO_CHANNEL_REGULATOR_ACTIVITY	GO_CHANNEL_REGULATOR_ACTIVITY	118	-0,22314093	-0,9721261	0,51434034	0,852732	1	2701	tags=19%, list=15%, signal=23%
GO_POST_EMBRYONIC_DEVELOPMENT	GO_POST_EMBRYONIC_DEVELOPMENT	84	-0,2505111	-0,9716854	0,48757172	0,8531341	1	2672	tags=21%, list=15%, signal=25%
GO_REGULATION_OF_VASCULAR_PERMEABILITY	GO_REGULATION_OF_VASCULAR_PERMEABILITY	30	-0,29432687	-0,9716634	0,49340865	0,85253024	1	1560	tags=13%, list=9%, signal=15%
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_TRANSPORT	136	-0,22385918	-0,9713711	0,4810379	0,85256875	1	2627	tags=19%, list=15%, signal=22%
GO_RECEPTOR_COMPLEX	GO_RECEPTOR_COMPLEX	310	-0,21910132	-0,9711459	0,4834308	0,8524533	1	2923	tags=20%, list=17%, signal=24%
GO_MUSCLE_TISSUE_DEVELOPMENT	GO_MUSCLE_TISSUE_DEVELOPMENT	253	-0,22329926	-0,9703592	0,49011856	0,853749	1	3910	tags=30%, list=22%, signal=38%
GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	26	-0,29722875	-0,9702194	0,506	0,85343313	1	3424	tags=35%, list=19%, signal=43%
GO_PROTEIN_LOCALIZATION_TO_LYSOSOME	GO_PROTEIN_LOCALIZATION_TO_LYSOSOME	17	-0,36351678	-0,9696764	0,49484536	0,85413027	1	2544	tags=41%, list=14%, signal=48%
GO_DENDRITE_CYTOPLASM	GO_DENDRITE_CYTOPLASM	15	-0,32152584	-0,9685299	0,5175781	0,8562832	1	2078	tags=27%, list=12%, signal=30%
GO_CARBOHYDRATE_PHOSPHORYLATION	GO_CARBOHYDRATE_PHOSPHORYLATION	20	-0,31999502	-0,9684854	0,5237113	0,8557196	1	1150	tags=20%, list=7%, signal=21%
GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	GO_POSITIVE_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	21	-0,30383462	-0,9684535	0,48906562	0,8551243	1	2627	tags=19%, list=15%, signal=22%
GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	GO_CYTOPLASMIC_SIDE_OF_MEMBRANE	164	-0,23143403	-0,9679723	0,4959514	0,8557082	1	3030	tags=23%, list=17%, signal=27%
GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	GO_NEGATIVE_REGULATION_OF_CELL_ADHESION	209	-0,23145394	-0,9679176	0,47835052	0,85516125	1	1907	tags=16%, list=11%, signal=18%
GO_MUSCLE_CELL_DEVELOPMENT	GO_MUSCLE_CELL_DEVELOPMENT	114	-0,23451716	-0,9677641	0,5040816	0,8548588	1	4046	tags=35%, list=23%, signal=45%
GO_POLYOL_TRANSPORT	GO_POLYOL_TRANSPORT	16	-0,33235267	-0,9671423	0,47780126	0,855765	1	2600	tags=38%, list=15%, signal=44%
GO_REGULATION_OF_HEART_RATE	GO_REGULATION_OF_HEART_RATE	80	-0,26171035	-0,9668784	0,49215686	0,8557568	1	4409	tags=31%, list=25%, signal=41%
GO_CONTRACTILE_FIBER	GO_CONTRACTILE_FIBER	199	-0,23757802	-0,9668412	0,49900597	0,8551761	1	3334	tags=26%, list=19%, signal=31%
GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	GO_ORGANELLAR_SMALL_RIBOSOMAL_SUBUNIT	25	-0,40898415	-0,9667288	0,5273834	0,8547838	1	5904	tags=56%, list=33%, signal=84%
GO_RECYCLING_ENDOSOME	GO_RECYCLING_ENDOSOME	115	-0,2195247	-0,9665052	0,5	0,8546583	1	1736	tags=16%, list=10%, signal=17%
GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	GO_REGULATION_OF_CATION_CHANNEL_ACTIVITY	84	-0,2577669	-0,9662115	0,5188119	0,8547745	1	4442	tags=37%, list=25%, signal=49%
GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	GO_NUCLEOSIDE_MONOPHOSPHATE_METABOLIC_PROCESS	227	-0,2676139	-0,9660755	0,48367348	0,8544508	1	3915	tags=34%, list=22%, signal=43%
GO_REGULATION_OF_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	GO_REGULATION_OF_SKELETAL_MUSCLE_CELL_DIFFERENTIATION	15	-0,33157972	-0,9654381	0,49704143	0,85539716	1	3599	tags=47%, list=20%, signal=59%
GO_SINGLE_ORGANISM_MEMBRANE_BUDDING	GO_SINGLE_ORGANISM_MEMBRANE_BUDDING	71	-0,26011693	-0,9653248	0,47928995	0,85503453	1	5031	tags=46%, list=28%, signal=65%
GO_AMELOGENESIS	GO_AMELOGENESIS	18	-0,3106769	-0,9653204	0,5049702	0,85438097	1	3078	tags=33%, list=17%, signal=40%
GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	GO_REGULATION_OF_PHOSPHATIDYLINOSITOL_3_KINASE_SIGNALING	132	-0,24585055	-0,9652069	0,5	0,8540258	1	2273	tags=17%, list=13%, signal=19%
GO_MUSCLE_CELL_PROLIFERATION	GO_MUSCLE_CELL_PROLIFERATION	18	-0,32632613	-0,9649217	0,4844358	0,85410464	1	2715	tags=28%, list=15%, signal=33%
GO_REGULATION_OF_ION_HOMEOSTASIS	GO_REGULATION_OF_ION_HOMEOSTASIS	187	-0,23311162	-0,9648891	0,5234216	0,8535201	1	4340	tags=34%, list=25%, signal=44%
GO_NEGATIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	GO_NEGATIVE_REGULATION_OF_CYCLIC_NUCLEOTIDE_METABOLIC_PROCESS	37	-0,29461303	-0,9636337	0,5105162	0,8559415	1	3434	tags=22%, list=19%, signal=27%
GO_MUSCLE_MYOSIN_COMPLEX	GO_MUSCLE_MYOSIN_COMPLEX	18	-0,3531828	-0,9629143	0,5	0,8571183	1	3750	tags=39%, list=21%, signal=49%
GO_PROSTATE_GLAND_DEVELOPMENT	GO_PROSTATE_GLAND_DEVELOPMENT	41	-0,27111873	-0,9624011	0,52208835	0,857729	1	1580	tags=17%, list=9%, signal=19%
GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	GO_BHLH_TRANSCRIPTION_FACTOR_BINDING	26	-0,30737454	-0,9623973	0,5126706	0,8570758	1	797	tags=15%, list=5%, signal=16%
GO_KINASE_INHIBITOR_ACTIVITY	GO_KINASE_INHIBITOR_ACTIVITY	83	-0,22562018	-0,9619075	0,50481695	0,8576824	1	2225	tags=20%, list=13%, signal=23%
GO_REGULATION_OF_CELL_MATRIX_ADHESION	GO_REGULATION_OF_CELL_MATRIX_ADHESION	87	-0,2580608	-0,9618329	0,5038023	0,85722685	1	3137	tags=28%, list=18%, signal=33%
GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_MEMBRANE	GO_EXTRINSIC_COMPONENT_OF_CYTOPLASMIC_SIDE_OF_PLASMA_MEMBRANE	94	-0,25894535	-0,961799	0,5073069	0,8566592	1	3030	tags=23%, list=17%, signal=28%
GO_ORGAN_MATURATION	GO_ORGAN_MATURATION	17	-0,34081706	-0,9615294	0,5072165	0,8567161	1	5503	tags=47%, list=31%, signal=68%
GO_POSITIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	GO_POSITIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	16	-0,3408868	-0,9613718	0,50503016	0,8564399	1	4252	tags=50%, list=24%, signal=66%
GO_CARDIAC_MUSCLE_CELL_CONTRACTION	GO_CARDIAC_MUSCLE_CELL_CONTRACTION	27	-0,32408845	-0,9601653	0,49425286	0,8587806	1	4974	tags=44%, list=28%, signal=62%
GO_ACTIN_FILAMENT_BUNDLE	GO_ACTIN_FILAMENT_BUNDLE	49	-0,2855363	-0,9596426	0,47440946	0,8594051	1	2517	tags=22%, list=14%, signal=26%
GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	GO_NEGATIVE_REGULATION_OF_CELLULAR_PROTEIN_LOCALIZATION	130	-0,21187207	-0,9589361	0,5263158	0,8605188	1	2860	tags=19%, list=16%, signal=23%
GO_RETINOIC_ACID_METABOLIC_PROCESS	GO_RETINOIC_ACID_METABOLIC_PROCESS	21	-0,3116595	-0,9588739	0,507874	0,86000794	1	1901	tags=19%, list=11%, signal=21%
GO_REGULATION_OF_METANEPHROS_DEVELOPMENT	GO_REGULATION_OF_METANEPHROS_DEVELOPMENT	23	-0,32640052	-0,9584218	0,4950884	0,8604437	1	6259	tags=52%, list=35%, signal=81%
GO_CARDIOCYTE_DIFFERENTIATION	GO_CARDIOCYTE_DIFFERENTIATION	89	-0,245337	-0,9582142	0,5200803	0,86024404	1	3328	tags=29%, list=19%, signal=36%
GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	GO_REGULATION_OF_RHO_PROTEIN_SIGNAL_TRANSDUCTION	105	-0,2509776	-0,9566733	0,5096525	0,8634436	1	2193	tags=18%, list=12%, signal=21%

GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	GO_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	196	-0,2278904	-0,9566096	0,5112782	0,8629297	1	2829	tags=20%, list=16%, signal=23%
GO_NEGATIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	GO_NEGATIVE_REGULATION_OF_CYTOPLASMIC_TRANSPORT	113	-0,22029802	-0,9561485	0,5223577	0,8633338	1	2627	tags=19%, list=15%, signal=22%
GO_RESPONSE_TO_INTERLEUKIN_4	GO_RESPONSE_TO_INTERLEUKIN_4	29	-0,28524363	-0,9561371	0,4947589	0,8627081	1	2352	tags=28%, list=13%, signal=32%
GO_COLLAGEN_TRIMER	GO_COLLAGEN_TRIMER	83	-0,29964042	-0,9551662	0,5179283	0,86435944	1	4566	tags=35%, list=26%, signal=47%
GO_POSITIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	GO_POSITIVE_REGULATION_OF_CATION_CHANNEL_ACTIVITY	36	-0,28100374	-0,9551395	0,53501946	0,86375546	1	4409	tags=36%, list=25%, signal=48%
GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	GO_PROTEIN_TRANSMEMBRANE_TRANSPORT	49	-0,29556397	-0,9544526	0,5297741	0,8647955	1	2826	tags=24%, list=16%, signal=29%
GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	119	-0,23326325	-0,9528009	0,5310621	0,86826634	1	3894	tags=31%, list=22%, signal=40%
GO_HYDROGEN_TRANSPORT	GO_HYDROGEN_TRANSPORT	127	-0,2565969	-0,9527813	0,50509167	0,8676436	1	3851	tags=30%, list=22%, signal=38%
GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_GLIAL_CELL_DIFFERENTIATION	25	-0,30177036	-0,9522878	0,5249501	0,8682333	1	4138	tags=36%, list=23%, signal=47%
GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	GO_REGULATION_OF_CARDIAC_MUSCLE_CONTRACTION	64	-0,2565636	-0,9518616	0,5132383	0,868686	1	4442	tags=39%, list=25%, signal=52%
GO_REGULATION_OF_CGMP_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_CGMP_BIOSYNTHETIC_PROCESS	19	-0,321621	-0,9508918	0,53992397	0,8704065	1	2627	tags=37%, list=15%, signal=43%
GO_CARBOXYPEPTIDASE_ACTIVITY	GO_CARBOXYPEPTIDASE_ACTIVITY	37	-0,2775335	-0,9508493	0,5135659	0,8698422	1	2889	tags=27%, list=16%, signal=32%
GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	GO_POSITIVE_REGULATION_OF_ACUTE_INFLAMMATORY_RESPONSE	28	-0,31395137	-0,950745	0,49601594	0,86944485	1	887	tags=14%, list=5%, signal=15%
GO_REGULATION_OF_TOLERANCE_INDUCTION	GO_REGULATION_OF_TOLERANCE_INDUCTION	17	-0,3531166	-0,9506316	0,50206614	0,869086	1	1322	tags=18%, list=7%, signal=19%
GO_MEMBRANE_MICRODOMAIN	GO_MEMBRANE_MICRODOMAIN	278	-0,22562346	-0,9505894	0,49803922	0,86853117	1	3301	tags=24%, list=19%, signal=30%
GO_MODIFIED_AMINO_ACID_BINDING	GO_MODIFIED_AMINO_ACID_BINDING	62	-0,24820083	-0,9503885	0,53294575	0,86839014	1	3807	tags=29%, list=22%, signal=37%
GO_SODIUM_CHANNEL_REGULATOR_ACTIVITY	GO_SODIUM_CHANNEL_REGULATOR_ACTIVITY	30	-0,26809746	-0,9503819	0,53294575	0,8677533	1	4597	tags=43%, list=26%, signal=58%
GO_EMBRYONIC_DIGESTIVE_TRACT_DEVELOPMENT	GO_EMBRYONIC_DIGESTIVE_TRACT_DEVELOPMENT	32	-0,29419184	-0,9495894	0,5019763	0,8690663	1	1810	tags=22%, list=10%, signal=24%
GO_REGULATION_OF_DENDRITE_DEVELOPMENT	GO_REGULATION_OF_DENDRITE_DEVELOPMENT	115	-0,22262174	-0,9493712	0,5246548	0,8689363	1	3232	tags=27%, list=18%, signal=33%
GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	GO_REGULATION_OF_MEMBRANE_DEPOLARIZATION	37	-0,280563	-0,9491471	0,5319149	0,868833	1	4271	tags=41%, list=24%, signal=53%
GO_NEGATIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	64	-0,25813273	-0,948657	0,48956355	0,86935824	1	2829	tags=20%, list=16%, signal=24%
GO_POSITIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	19	-0,32085696	-0,948027	0,5071283	0,87023133	1	2782	tags=26%, list=16%, signal=31%
GO_PROLINE_RICH_REGION_BINDING	GO_PROLINE_RICH_REGION_BINDING	18	-0,29989466	-0,9476378	0,5206612	0,8705635	1	2460	tags=28%, list=14%, signal=32%
GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	GO_EXTRINSIC_COMPONENT_OF_PLASMA_MEMBRANE	129	-0,23710428	-0,9475235	0,5216495	0,8701729	1	3030	tags=22%, list=17%, signal=26%
GO_EPITHELIAL_TUBE_BRANCHING_INVOLVED_IN_LUNG_MORPHOGENESIS	GO_EPITHELIAL_TUBE_BRANCHING_INVOLVED_IN_LUNG_MORPHOGENESIS	25	-0,31401116	-0,9475067	0,512476	0,8695595	1	1810	tags=16%, list=10%, signal=18%
GO_LYSOPHOSPHOLIPASE_ACTIVITY	GO_LYSOPHOSPHOLIPASE_ACTIVITY	19	-0,31129768	-0,9474312	0,5331992	0,8690939	1	1107	tags=16%, list=6%, signal=17%
GO_REGULATION_OF_PEPTIDE_TRANSPORT	GO_REGULATION_OF_PEPTIDE_TRANSPORT	239	-0,19872236	-0,9470713	0,5793651	0,8693655	1	2922	tags=20%, list=17%, signal=23%
GO_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	GO_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	114	-0,22994578	-0,947047	0,5303327	0,8687787	1	5291	tags=40%, list=30%, signal=57%
GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	GO_ANCHORED_COMPONENT_OF_PLASMA_MEMBRANE	38	-0,27341053	-0,9467425	0,511579	0,8688819	1	2417	tags=24%, list=14%, signal=27%
GO_PHOSPHOLIPASE_A2_ACTIVITY	GO_PHOSPHOLIPASE_A2_ACTIVITY	29	-0,27774534	-0,9465914	0,5125725	0,86862165	1	1676	tags=17%, list=9%, signal=19%
GO_MAGNESIUM_ION_BINDING	GO_MAGNESIUM_ION_BINDING	187	-0,20146984	-0,9464862	0,554	0,8682145	1	2992	tags=22%, list=17%, signal=27%
GO_RESPIRATORY_SYSTEM_DEVELOPMENT	GO_RESPIRATORY_SYSTEM_DEVELOPMENT	192	-0,22257057	-0,9463169	0,5222222	0,86801654	1	2735	tags=21%, list=15%, signal=25%
GO_REGULATION_OF_CORTICOSTEROID_HORMONE_SECRETION	GO_REGULATION_OF_CORTICOSTEROID_HORMONE_SECRETION	15	-0,34538242	-0,9460021	0,5188119	0,8681377	1	11570	tags=100%, list=65%, signal=290%
GO_POLYOL_METABOLIC_PROCESS	GO_POLYOL_METABOLIC_PROCESS	93	-0,21851435	-0,9458877	0,5650485	0,8677566	1	2662	tags=22%, list=15%, signal=25%
GO_ER_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	GO_ER_TO_GOLGI_VESICLE_MEDIATED_TRANSPORT	161	-0,23686574	-0,9457775	0,5294118	0,86738276	1	2994	tags=24%, list=17%, signal=29%
GO_ER_NUCLEUS_SIGNALING_PATHWAY	GO_ER_NUCLEUS_SIGNALING_PATHWAY	31	-0,2922562	-0,9457048	0,48336595	0,866899	1	3891	tags=35%, list=22%, signal=45%
GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	GO_OLIGOSACCHARIDE_METABOLIC_PROCESS	60	-0,24240367	-0,9455544	0,54564315	0,86664265	1	2544	tags=25%, list=14%, signal=29%
GO_ENDOPLASMIC_RETICULUM_TO_CYTOSOL_TRANSPORT	GO_ENDOPLASMIC_RETICULUM_TO_CYTOSOL_TRANSPORT	21	-0,3258326	-0,9444304	0,53722334	0,86879605	1	3794	tags=38%, list=21%, signal=48%
GO_EARLY_ENDOSOME	GO_EARLY_ENDOSOME	277	-0,20378783	-0,9426264	0,55711424	0,8725734	1	3175	tags=23%, list=18%, signal=28%
GO_SARCOPLASM	GO_SARCOPLASM	64	-0,27037224	-0,9422398	0,5473888	0,8728592	1	4409	tags=39%, list=25%, signal=52%
GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	GO_REGULATION_OF_ADHERENS_JUNCTION_ORGANIZATION	49	-0,27654925	-0,94222	0,5009488	0,8722474	1	2365	tags=27%, list=13%, signal=31%
GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	GO_CEREBELLAR_PURKINJE_CELL_LAYER_DEVELOPMENT	22	-0,30546805	-0,9421837	0,5368217	0,8716892	1	3507	tags=36%, list=20%, signal=45%
GO_14_3_3_PROTEIN_BINDING	GO_14_3_3_PROTEIN_BINDING	19	-0,3201052	-0,9418603	0,5472441	0,8718688	1	3110	tags=26%, list=18%, signal=32%
GO_FEMALE_GENITALIA_DEVELOPMENT	GO_FEMALE_GENITALIA_DEVELOPMENT	16	-0,31288835	-0,9404985	0,5201613	0,87444526	1	2366	tags=31%, list=13%, signal=36%
GO_PROTEINACEOUS_EXTRACELLULAR_MATRIX	GO_PROTEINACEOUS_EXTRACELLULAR_MATRIX	329	-0,25357738	-0,9404843	0,5240848	0,873831	1	4061	tags=30%, list=23%, signal=38%
GO_THIOESTER_BIOSYNTHETIC_PROCESS	GO_THIOESTER_BIOSYNTHETIC_PROCESS	48	-0,27657533	-0,9401381	0,52208835	0,87406707	1	2449	tags=27%, list=14%, signal=31%
GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	GO_POSITIVE_REGULATION_OF_ACTIN_FILAMENT_BUNDLE_ASSEMBLY	45	-0,26553616	-0,9394848	0,5212355	0,8750307	1	1173	tags=16%, list=7%, signal=17%
GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	17	-0,3293976	-0,9393169	0,554	0,8747951	1	3774	tags=47%, list=21%, signal=60%
GO_ATP_BIOSYNTHETIC_PROCESS	GO_ATP_BIOSYNTHETIC_PROCESS	31	-0,3478827	-0,939023	0,5387674	0,8748827	1	3754	tags=32%, list=21%, signal=41%
GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	GO_NEGATIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	58	-0,2506662	-0,938372	0,56031126	0,8757983	1	4350	tags=31%, list=25%, signal=41%
GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	GO_CHLORIDE_CHANNEL_REGULATOR_ACTIVITY	16	-0,31025696	-0,9381903	0,552	0,87560767	1	2529	tags=31%, list=14%, signal=36%
GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	GO_METANEPHRIC_EPITHELIUM_DEVELOPMENT	19	-0,32357907	-0,9381645	0,53722334	0,87502474	1	3672	tags=32%, list=21%, signal=40%
GO_LOCOMOTORY_BEHAVIOR	GO_LOCOMOTORY_BEHAVIOR	165	-0,22017659	-0,9379092	0,57253385	0,875011	1	2113	tags=15%, list=12%, signal=17%

GO_REGULATION_OF_METAL_ION_TRANSPORT	GO_REGULATION_OF_METAL_ION_TRANSPORT	305	-0,21686578	-0,9378418	0,5511811	0,8745459	1	4465	tags=31%, list=25%, signal=41%
GO_ALCOHOL_DEHYDROGENASE_NADP_ACTIVITY	GO_ALCOHOL_DEHYDROGENASE_NADP_ACTIVITY	16	-0,35304007	-0,9377736	0,5423387	0,87407935	1	1616	tags=25%, list=9%, signal=27%
GO_NEGATIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	GO_NEGATIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	17	-0,30269727	-0,9377565	0,5373737	0,87348104	1	3547	tags=29%, list=20%, signal=37%
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	126	-0,23647305	-0,9373004	0,5690722	0,87392724	1	1882	tags=15%, list=11%, signal=17%
GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_ORGANELLE_MEMBRANE	242	-0,21203792	-0,9372775	0,5456389	0,8733478	1	3012	tags=21%, list=17%, signal=25%
GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	GO_REGULATION_OF_GLYCOPROTEIN_METABOLIC_PROCESS	39	-0,25797445	-0,9367374	0,5582329	0,87408197	1	3774	tags=38%, list=21%, signal=49%
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_ALKYL_OR_ARYL_OTHER_THAN_METHYL_GROUPS	60	-0,25278592	-0,9364315	0,5668016	0,8741796	1	3807	tags=37%, list=22%, signal=47%
GO_AXON_CYTOPLASM	GO_AXON_CYTOPLASM	29	-0,2735637	-0,9356778	0,53754944	0,87545836	1	1611	tags=24%, list=9%, signal=27%
GO_NUCLEOPHAGY	GO_NUCLEOPHAGY	17	-0,32749572	-0,9353836	0,5452632	0,8755339	1	2008	tags=24%, list=11%, signal=27%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_ACTIVITY	64	-0,2832294	-0,935335	0,53216374	0,8750016	1	3171	tags=25%, list=18%, signal=30%
GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION	GO_MESENCHYMAL_TO_EPITHELIAL_TRANSITION	15	-0,33936575	-0,9351131	0,5471311	0,87493235	1	2769	tags=27%, list=16%, signal=32%
GO_POTASSIUM_ION_IMPORT	GO_POTASSIUM_ION_IMPORT	28	-0,2958002	-0,9337909	0,56565654	0,87750095	1	759	tags=11%, list=4%, signal=11%
GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	GO_NEGATIVE_REGULATION_OF_GLIOGENESIS	36	-0,27053732	-0,9337065	0,56646216	0,8770506	1	4138	tags=33%, list=23%, signal=43%
GO_COMPLEX_OF_COLLAGEN_TRIMERS	GO_COMPLEX_OF_COLLAGEN_TRIMERS	23	-0,3647545	-0,93099	0,5220729	0,88309556	1	4500	tags=39%, list=25%, signal=52%
GO_REGULATION_OF_MUSCLE_CONTRACTION	GO_REGULATION_OF_MUSCLE_CONTRACTION	139	-0,23936976	-0,9307522	0,5673077	0,8830495	1	4442	tags=36%, list=25%, signal=48%
GO_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	GO_REGULATION_OF_INTRACELLULAR_STEROID_HORMONE_RECEPTOR_SIGNALING_PATHWAY	55	-0,24219114	-0,9306844	0,5728347	0,8825687	1	3786	tags=35%, list=21%, signal=44%
GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	GO_CELLULAR_METABOLIC_COMPOUND_SALVAGE	35	-0,2668891	-0,9299006	0,5407098	0,8839435	1	2020	tags=23%, list=11%, signal=26%
GO_CELL_FATE_DETERMINATION	GO_CELL_FATE_DETERMINATION	41	-0,28326297	-0,9284917	0,54579437	0,8867308	1	3670	tags=27%, list=21%, signal=34%
GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	GO_TRANSFORMING_GROWTH_FACTOR_BETA_RECEPTOR_SIGNALING_PATHWAY	94	-0,2323124	-0,9281853	0,5423077	0,88684404	1	3183	tags=24%, list=18%, signal=30%
GO_CALCIUM_DEPENDENT_PROTEIN_BINDING	GO_CALCIUM_DEPENDENT_PROTEIN_BINDING	58	-0,24919212	-0,9279453	0,5731463	0,88680243	1	1509	tags=17%, list=9%, signal=19%
GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	GO_POSITIVE_REGULATION_OF_RESPONSE_TO_BIOTIC_STIMULUS	36	-0,2650427	-0,9279189	0,5146771	0,88623077	1	3530	tags=33%, list=20%, signal=42%
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT	193	-0,22639234	-0,927765	0,54043394	0,8859873	1	3966	tags=28%, list=22%, signal=36%
GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	GO_PURINE_CONTAINING_COMPOUND_BIOSYNTHETIC_PROCESS	129	-0,22071075	-0,9275558	0,5441767	0,8858592	1	1769	tags=16%, list=10%, signal=17%
GO_GTP_RHO_BINDING	GO_GTP_RHO_BINDING	16	-0,31177583	-0,9275256	0,5467197	0,8852755	1	1570	tags=19%, list=9%, signal=21%
GO_SIGNALING_ADAPTOR_ACTIVITY	GO_SIGNALING_ADAPTOR_ACTIVITY	72	-0,25023216	-0,9270665	0,5564202	0,88577247	1	3689	tags=32%, list=21%, signal=40%
GO_PLATELET_ACTIVATION	GO_PLATELET_ACTIVATION	139	-0,24876466	-0,9265279	0,5125523	0,88644564	1	3110	tags=24%, list=18%, signal=29%
GO_REGULATION_OF_PLASMA_MEMBRANE_ORGANIZATION	GO_REGULATION_OF_PLASMA_MEMBRANE_ORGANIZATION	71	-0,23243047	-0,9265021	0,52871287	0,88587636	1	2391	tags=18%, list=14%, signal=21%
GO_MATERNAL_PLACENTA_DEVELOPMENT	GO_MATERNAL_PLACENTA_DEVELOPMENT	29	-0,27075058	-0,9262636	0,55776894	0,88579756	1	4252	tags=38%, list=24%, signal=50%
GO_PHOSPHATE_ION_TRANSPORT	GO_PHOSPHATE_ION_TRANSPORT	18	-0,30739534	-0,9258565	0,5570866	0,8861659	1	2142	tags=28%, list=12%, signal=32%
GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	97	-0,2350014	-0,925856	0,5325444	0,8855262	1	3550	tags=25%, list=20%, signal=31%
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_GOLGI	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_GOLGI	17	-0,3433239	-0,9254536	0,51282054	0,8858685	1	3002	tags=41%, list=17%, signal=50%
GO_CALCIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	GO_CALCIUM_ACTIVATED_CATION_CHANNEL_ACTIVITY	24	-0,28768757	-0,9254247	0,58914727	0,885311	1	2013	tags=25%, list=11%, signal=28%
GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS	GO_TRANSFERASE_ACTIVITY_TRANSFERRING_PENTOSYL_GROUPS	48	-0,23592047	-0,9252099	0,5520833	0,8852207	1	2298	tags=21%, list=13%, signal=24%
GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	GO_NEGATIVE_REGULATION_OF_PRODUCTION_OF_MOLECULAR_MEDIATOR_OF_IMMUNE_RESPONSE	26	-0,28354943	-0,9247944	0,5487078	0,88556033	1	894	tags=12%, list=5%, signal=12%
GO_CORTICAL_CYTOSKELETON	GO_CORTICAL_CYTOSKELETON	78	-0,254216	-0,9243499	0,5350701	0,8860021	1	2391	tags=22%, list=14%, signal=25%
GO_REGULATION_OF_ENDOCYTOSIS	GO_REGULATION_OF_ENDOCYTOSIS	194	-0,20716266	-0,9238017	0,582	0,8866494	1	3708	tags=26%, list=21%, signal=32%
GO_PEPTIDE_CATABOLIC_PROCESS	GO_PEPTIDE_CATABOLIC_PROCESS	22	-0,2841576	-0,9235646	0,5954357	0,88659775	1	3265	tags=32%, list=18%, signal=39%
GO_DIGESTIVE_SYSTEM_DEVELOPMENT	GO_DIGESTIVE_SYSTEM_DEVELOPMENT	140	-0,2283148	-0,9230289	0,5766283	0,88725173	1	2141	tags=19%, list=12%, signal=21%
GO_BONE_RESORPTION	GO_BONE_RESORPTION	20	-0,31472376	-0,9230135	0,5410156	0,8866577	1	1639	tags=20%, list=9%, signal=22%
GO_MUSCLE_CELL_DIFFERENTIATION	GO_MUSCLE_CELL_DIFFERENTIATION	218	-0,21327907	-0,9219899	0,5800781	0,88840234	1	3202	tags=24%, list=18%, signal=29%
GO_NEGATIVE_REGULATION_OF_CATECHOLAMINE_SECRETION	GO_NEGATIVE_REGULATION_OF_CATECHOLAMINE_SECRETION	16	-0,3327569	-0,9219494	0,5833333	0,8878842	1	559	tags=13%, list=3%, signal=13%
GO_PLASMA_MEMBRANE_ORGANIZATION	GO_PLASMA_MEMBRANE_ORGANIZATION	199	-0,20562947	-0,9218611	0,5772994	0,8874648	1	3526	tags=24%, list=20%, signal=29%
GO_PHOSPHATASE_COMPLEX	GO_PHOSPHATASE_COMPLEX	42	-0,27280876	-0,9217763	0,5632653	0,8870446	1	3334	tags=31%, list=19%, signal=38%
GO_UTERUS_DEVELOPMENT	GO_UTERUS_DEVELOPMENT	18	-0,31541765	-0,9216459	0,5445545	0,88671184	1	795	tags=17%, list=5%, signal=17%
GO_BETA_TUBULIN_BINDING	GO_BETA_TUBULIN_BINDING	35	-0,25839013	-0,9212391	0,55130786	0,8871185	1	2677	tags=26%, list=15%, signal=30%
GO_ORGAN_OR_TISSUE_SPECIFIC_IMMUNE_RESPONSE	GO_ORGAN_OR_TISSUE_SPECIFIC_IMMUNE_RESPONSE	25	-0,308362	-0,9211984	0,54285717	0,88656557	1	5377	tags=48%, list=30%, signal=69%
GO_RESPONSE_TO_BACTERIUM	GO_RESPONSE_TO_BACTERIUM	440	-0,21069038	-0,9203528	0,54545456	0,88793045	1	3353	tags=23%, list=19%, signal=27%
GO_DIVALENT_INORGANIC_CATION_TRANSPORT	GO_DIVALENT_INORGANIC_CATION_TRANSPORT	245	-0,2106817	-0,9202811	0,6130952	0,8874821	1	4066	tags=29%, list=23%, signal=38%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_ENDOPLASMIC_RETICULUM_STRESS	34	-0,2643274	-0,9196821	0,54325956	0,8882542	1	2480	tags=24%, list=14%, signal=27%
GO_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_INTERFERON_GAMMA_BIOSYNTHETIC_PROCESS	15	-0,3332511	-0,9187287	0,53169733	0,8899588	1	4739	tags=47%, list=27%, signal=64%
GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	GO_RESPONSE_TO_ISOQUINOLINE_ALKALOID	27	-0,29145274	-0,9183555	0,597166	0,8903034	1	1472	tags=19%, list=8%, signal=20%

GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DEVELOPMENT	69	-0,25959113	-0,9175381	0,5597609	0,89172155	1	3780	tags=32%, list=21%, signal=40%
GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	GO_DIVALENT_INORGANIC_CATION_HOMEOSTASIS	313	-0,21442139	-0,9174103	0,58316636	0,8914198	1	4066	tags=28%, list=23%, signal=35%
GO_INTESTINAL_ABSORPTION	GO_INTESTINAL_ABSORPTION	26	-0,277388	-0,9165632	0,5917603	0,89287645	1	2569	tags=23%, list=15%, signal=27%
GO_RESPONSE_TO_AMINE	GO_RESPONSE_TO_AMINE	47	-0,2412798	-0,9165341	0,6146045	0,8923068	1	2778	tags=28%, list=16%, signal=33%
GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	GO_NEGATIVE_REGULATION_OF_ALPHA_BETA_T_CELL_ACTIVATION	21	-0,29450595	-0,9161181	0,5672878	0,89267284	1	3788	tags=29%, list=21%, signal=36%
GO_DEMETHYLATION	GO_DEMETHYLATION	50	-0,26182687	-0,9156445	0,5612648	0,8931575	1	3410	tags=30%, list=19%, signal=37%
GO_CELLULAR_RESPONSE_TO_CADMIUM_ION	GO_CELLULAR_RESPONSE_TO_CADMIUM_ION	15	-0,3739834	-0,9150195	0,546371	0,8941051	1	4247	tags=60%, list=24%, signal=79%
GO_MUSCLE_ORGAN_DEVELOPMENT	GO_MUSCLE_ORGAN_DEVELOPMENT	253	-0,21179451	-0,9148563	0,58429116	0,8938529	1	3876	tags=29%, list=22%, signal=37%
GO_ADRENERGIC_RECEPTOR_BINDING	GO_ADRENERGIC_RECEPTOR_BINDING	17	-0,3179337	-0,9145504	0,5766129	0,89397436	1	5062	tags=47%, list=29%, signal=66%
GO_REGULATION_OF_FATTY_ACID_TRANSPORT	GO_REGULATION_OF_FATTY_ACID_TRANSPORT	26	-0,2788573	-0,9140533	0,56969696	0,8945353	1	1540	tags=15%, list=9%, signal=17%
GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	GO_NEGATIVE_REGULATION_OF_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION	193	-0,19641298	-0,9134206	0,59876543	0,89547276	1	2480	tags=15%, list=14%, signal=17%
GO_APICAL_JUNCTION_COMPLEX	GO_APICAL_JUNCTION_COMPLEX	118	-0,22985345	-0,9132418	0,54924244	0,8952802	1	3165	tags=25%, list=18%, signal=30%
GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	GO_REGULATION_OF_TYPE_2_IMMUNE_RESPONSE	23	-0,30560434	-0,9127548	0,5478615	0,89581543	1	3377	tags=26%, list=19%, signal=32%
GO_ADAPTIVE_IMMUNE_RESPONSE	GO_ADAPTIVE_IMMUNE_RESPONSE	229	-0,2627504	-0,9124754	0,51829267	0,89586544	1	1234	tags=13%, list=7%, signal=14%
GO_NEURON_DEATH	GO_NEURON_DEATH	44	-0,25163358	-0,9122374	0,6041237	0,89585114	1	3151	tags=25%, list=18%, signal=30%
GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_MONOVALENT_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	330	-0,20314221	-0,9122157	0,6422925	0,8952801	1	3622	tags=23%, list=21%, signal=28%
GO_RHYTHMIC_PROCESS	GO_RHYTHMIC_PROCESS	272	-0,20495579	-0,9120511	0,6101695	0,8949991	1	2917	tags=22%, list=17%, signal=26%
GO_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	GO_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	100	-0,24968277	-0,9115983	0,5699797	0,89544284	1	4066	tags=32%, list=23%, signal=41%
GO_HEPARAN_SULFATE_PROTEOGLYCAN_BINDING	GO_HEPARAN_SULFATE_PROTEOGLYCAN_BINDING	18	-0,31623632	-0,9106736	0,58800775	0,8970353	1	1107	tags=17%, list=6%, signal=18%
GO_MUSCLE_STRUCTURE_DEVELOPMENT	GO_MUSCLE_STRUCTURE_DEVELOPMENT	401	-0,20584622	-0,9105058	0,5861386	0,8967973	1	3910	tags=29%, list=22%, signal=36%
GO_GDP_BINDING	GO_GDP_BINDING	48	-0,26438564	-0,9101697	0,5569106	0,8969592	1	1463	tags=19%, list=8%, signal=20%
GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	GO_GLYCOSPHINGOLIPID_BIOSYNTHETIC_PROCESS	23	-0,2883091	-0,9100805	0,5731463	0,89654905	1	1407	tags=17%, list=8%, signal=19%
GO_ADULT_BEHAVIOR	GO_ADULT_BEHAVIOR	125	-0,21736693	-0,9100719	0,627907	0,8959398	1	2999	tags=20%, list=17%, signal=24%
GO_CELLULAR_GLUCURONIDATION	GO_CELLULAR_GLUCURONIDATION	22	-0,32503167	-0,9099388	0,53968257	0,8956473	1	825	tags=18%, list=5%, signal=19%
GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	GO_REGULATION_OF_CATION_TRANSMEMBRANE_TRANSPORT	195	-0,21802989	-0,9095953	0,609901	0,8958592	1	4442	tags=31%, list=25%, signal=41%
GO_LENS_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	GO_LENS_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	15	-0,32564694	-0,9092723	0,5694444	0,89597124	1	3517	tags=27%, list=20%, signal=33%
GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	GO_CARDIAC_MUSCLE_TISSUE_MORPHOGENESIS	52	-0,2573097	-0,9092023	0,60587	0,8955219	1	4326	tags=35%, list=24%, signal=46%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	80	-0,26349297	-0,909074	0,5102041	0,89519376	1	3553	tags=30%, list=20%, signal=37%
GO_PIGMENT_BIOSYNTHETIC_PROCESS	GO_PIGMENT_BIOSYNTHETIC_PROCESS	46	-0,26692957	-0,9085962	0,5755102	0,89577025	1	4834	tags=43%, list=27%, signal=60%
GO_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	GO_INTRA_GOLGI_VESICLE_MEDIATED_TRANSPORT	44	-0,27381527	-0,9085132	0,5672878	0,89529926	1	2634	tags=32%, list=15%, signal=37%
GO_RESPONSE_TO_GROWTH_FACTOR	GO_RESPONSE_TO_GROWTH_FACTOR	456	-0,20120388	-0,9084518	0,6149312	0,89483124	1	3183	tags=21%, list=18%, signal=24%
GO_REGULATION_OF_HORMONE_SECRETION	GO_REGULATION_OF_HORMONE_SECRETION	245	-0,19649716	-0,9083989	0,68326694	0,8943396	1	2932	tags=19%, list=17%, signal=22%
GO_CALCIUM_ION_TRANSPORT	GO_CALCIUM_ION_TRANSPORT	201	-0,21904846	-0,9080089	0,61290324	0,89464086	1	4066	tags=29%, list=23%, signal=37%
GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	GO_POSITIVE_REGULATION_OF_NATURAL_KILLER_CELL_ACTIVATION	17	-0,31193477	-0,9079987	0,5652174	0,8940416	1	5052	tags=53%, list=29%, signal=74%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_12_PRODUCTION	15	-0,3773371	-0,9076879	0,55991733	0,89416945	1	11006	tags=100%, list=62%, signal=265%
GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CELL_DIFFERENTIATION	46	-0,24143636	-0,9073266	0,59921414	0,8944121	1	1763	tags=17%, list=10%, signal=19%
GO_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	GO_REGULATION_OF_VOLTAGE_GATED_CALCIUM_CHANNEL_ACTIVITY	24	-0,27689147	-0,9072712	0,5960396	0,89392835	1	3172	tags=25%, list=18%, signal=30%
GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	29	-0,2846674	-0,907029	0,58449304	0,8938727	1	1658	tags=21%, list=9%, signal=23%
GO_CELLULAR_RESPONSE_TO_ANTIBIOTIC	GO_CELLULAR_RESPONSE_TO_ANTIBIOTIC	16	-0,31473452	-0,906466	0,58185405	0,8946015	1	1648	tags=13%, list=9%, signal=14%
GO_SH3_SH2_ADAPTOR_ACTIVITY	GO_SH3_SH2_ADAPTOR_ACTIVITY	51	-0,26098323	-0,9059342	0,56614786	0,8952826	1	1862	tags=22%, list=11%, signal=24%
GO_VESICLE_COATING	GO_VESICLE_COATING	73	-0,24170233	-0,9052841	0,55193484	0,8962226	1	5031	tags=45%, list=28%, signal=63%
GO_INTEGRIN_BINDING	GO_INTEGRIN_BINDING	100	-0,25010923	-0,9051638	0,5654762	0,8958776	1	2975	tags=22%, list=17%, signal=26%
GO_GENITALIA_DEVELOPMENT	GO_GENITALIA_DEVELOPMENT	41	-0,24867707	-0,9049473	0,61077845	0,89575434	1	1627	tags=17%, list=9%, signal=19%
GO_PRE_AUTOPHAGOSOMAL_STRUCTURE	GO_PRE_AUTOPHAGOSOMAL_STRUCTURE	28	-0,29407546	-0,9048902	0,59026366	0,89527345	1	4619	tags=46%, list=26%, signal=63%
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_IMPORT	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_IMPORT	22	-0,30492565	-0,9046096	0,56978965	0,89536375	1	3794	tags=32%, list=21%, signal=40%
GO_AMINE_BIOSYNTHETIC_PROCESS	GO_AMINE_BIOSYNTHETIC_PROCESS	19	-0,30216995	-0,9033908	0,5714286	0,8976837	1	2166	tags=32%, list=12%, signal=36%
GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	GO_POSITIVE_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	27	-0,27880877	-0,9032804	0,5780933	0,8973396	1	1129	tags=11%, list=6%, signal=12%
GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	GO_REGULATION_OF_IMMUNOGLOBULIN_PRODUCTION	43	-0,24540484	-0,9032165	0,570297	0,8968696	1	1590	tags=14%, list=9%, signal=15%
GO_CELL_ADHESION_MOLECULE_BINDING	GO_CELL_ADHESION_MOLECULE_BINDING	175	-0,23023105	-0,903177	0,57425743	0,89633995	1	3548	tags=24%, list=20%, signal=30%
GO_PLASMA_MEMBRANE_RAFT	GO_PLASMA_MEMBRANE_RAFT	82	-0,2386238	-0,902444	0,5863454	0,89748263	1	2769	tags=26%, list=16%, signal=30%
GO_MONOAMINE_TRANSPORT	GO_MONOAMINE_TRANSPORT	21	-0,2955043	-0,9023005	0,6027944	0,8971939	1	3786	tags=33%, list=21%, signal=42%
GO_AXONAL_GROWTH_CONE	GO_AXONAL_GROWTH_CONE	19	-0,30533987	-0,9014751	0,5888889	0,89851767	1	3092	tags=32%, list=18%, signal=38%
GO_ORGAN_FORMATION	GO_ORGAN_FORMATION	33	-0,2748309	-0,9008005	0,6186613	0,8995225	1	1295	tags=15%, list=7%, signal=16%

GO_BINDING_BRIDGING	GO_BINDING_BRIDGING	169	-0,21090214	-0,9006985	0,5849421	0,8991852	1	1862	tags=16%, list=11%, signal=18%
GO_RESPONSE_TO_COLD	GO_RESPONSE_TO_COLD	40	-0,25744408	-0,9005317	0,60714287	0,8989699	1	2119	tags=23%, list=12%, signal=26%
GO_NEPHRON_EPITHELIUM_DEVELOPMENT	GO_NEPHRON_EPITHELIUM_DEVELOPMENT	91	-0,24833192	-0,900242	0,59356135	0,8990524	1	3155	tags=24%, list=18%, signal=29%
GO_GOLGI_TO_VACUOLE_TRANSPORT	GO_GOLGI_TO_VACUOLE_TRANSPORT	25	-0,30089992	-0,8993991	0,5740741	0,9004225	1	3024	tags=32%, list=17%, signal=39%
GO_ACTOMYOSIN	GO_ACTOMYOSIN	56	-0,2604609	-0,8989555	0,5885827	0,90084654	1	1028	tags=14%, list=6%, signal=15%
GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	GO_CELL_SUBSTRATE_JUNCTION_ASSEMBLY	40	-0,27044547	-0,8987799	0,5646388	0,90065175	1	3514	tags=33%, list=20%, signal=40%
GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	GO_POSITIVE_REGULATION_OF_PEPTIDE_SECRETION	84	-0,21441065	-0,8986776	0,7106796	0,9002759	1	1941	tags=14%, list=11%, signal=16%
GO_PEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	GO_PEPTIDASE_ACTIVATOR_ACTIVITY_INVOLVED_IN_APOPTOTIC_PROCESS	19	-0,28465968	-0,8984602	0,61554193	0,900175	1	2168	tags=26%, list=12%, signal=30%
GO_CELLULAR_RESPONSE_TO_LIPID	GO_CELLULAR_RESPONSE_TO_LIPID	432	-0,18286683	-0,8978372	0,64356434	0,9010824	1	3354	tags=23%, list=19%, signal=27%
GO_PURINE_NUCLEOBASE_METABOLIC_PROCESS	GO_PURINE_NUCLEOBASE_METABOLIC_PROCESS	19	-0,2967772	-0,8975069	0,5796813	0,90127516	1	2020	tags=26%, list=11%, signal=30%
GO_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_INORGANIC_CATION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	482	-0,19055967	-0,8969742	0,6926148	0,9019136	1	3341	tags=22%, list=19%, signal=27%
GO_VIRAL_GENOME_REPLICATION	GO_VIRAL_GENOME_REPLICATION	19	-0,28239346	-0,896924	0,5878525	0,9014333	1	1491	tags=16%, list=8%, signal=17%
GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	GO_RESPONSE_TO_INCREASED_OXYGEN_LEVELS	23	-0,27012902	-0,8968308	0,59325397	0,9010246	1	557	tags=13%, list=3%, signal=13%
GO_PROTEIN_LOCALIZATION_TO_VACUOLE	GO_PROTEIN_LOCALIZATION_TO_VACUOLE	42	-0,28117514	-0,8964952	0,55668014	0,9011947	1	3175	tags=33%, list=18%, signal=41%
GO_CELL_CORTEX_PART	GO_CELL_CORTEX_PART	109	-0,22906703	-0,8963149	0,5683168	0,9010133	1	2462	tags=20%, list=14%, signal=23%
GO_NEGATIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	GO_NEGATIVE_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	17	-0,31580272	-0,895952	0,6137255	0,9012433	1	4852	tags=41%, list=27%, signal=57%
GO_MONOSACCHARIDE_CATABOLIC_PROCESS	GO_MONOSACCHARIDE_CATABOLIC_PROCESS	54	-0,251048	-0,8955645	0,59791666	0,9015725	1	1433	tags=17%, list=8%, signal=18%
GO_GLYCEROLIPID_BIOSYNTHETIC_PROCESS	GO_GLYCEROLIPID_BIOSYNTHETIC_PROCESS	200	-0,18714178	-0,8953891	0,70708954	0,90140647	1	2442	tags=17%, list=14%, signal=20%
GO_LYSOSOMAL_TRANSPORT	GO_LYSOSOMAL_TRANSPORT	65	-0,24283701	-0,8952143	0,5976331	0,9012011	1	3028	tags=29%, list=17%, signal=35%
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DAMAGE_RECOGNITION	23	-0,31177494	-0,8951986	0,5995935	0,9006286	1	2654	tags=30%, list=15%, signal=36%
GO_RESPONSE_TO_COCAINE	GO_RESPONSE_TO_COCAINE	43	-0,24299744	-0,895085	0,62919134	0,90029407	1	1472	tags=16%, list=8%, signal=18%
GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	GO_REGULATION_OF_POSTSYNAPTIC_MEMBRANE_POTENTIAL	50	-0,25830305	-0,8946543	0,610998	0,9007092	1	2075	tags=14%, list=12%, signal=16%
GO_DETECTION_OF_CHEMICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION_OF_TASTE	GO_DETECTION_OF_CHEMICAL_STIMULUS_INVOLVED_IN_SENSORY_PERCEPTION_OF_TASTE	22	-0,29971486	-0,8935038	0,5945946	0,90290195	1	2606	tags=18%, list=15%, signal=21%
GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	GO_POSITIVE_REGULATION_OF_PROTEIN_KINASE_B_SIGNALING	79	-0,23329537	-0,8933657	0,61478597	0,90264535	1	5291	tags=43%, list=30%, signal=61%
GO_VIRUS_RECEPTOR_ACTIVITY	GO_VIRUS_RECEPTOR_ACTIVITY	64	-0,2359927	-0,8931139	0,5964912	0,9026431	1	3782	tags=31%, list=21%, signal=40%
GO_TRACHEA_DEVELOPMENT	GO_TRACHEA_DEVELOPMENT	20	-0,29399577	-0,8924798	0,6	0,90349483	1	3791	tags=40%, list=21%, signal=51%
GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	GO_EXTRACELLULAR_STRUCTURE_ORGANIZATION	292	-0,24846	-0,8924397	0,56772906	0,90298647	1	3156	tags=23%, list=18%, signal=28%
GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	GO_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	69	-0,26086923	-0,8918071	0,6119096	0,9038782	1	3966	tags=30%, list=22%, signal=39%
GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	168	-0,20555201	-0,8916943	0,62575454	0,9034966	1	3800	tags=26%, list=22%, signal=32%
GO_BRUSH_BORDER_MEMBRANE	GO_BRUSH_BORDER_MEMBRANE	55	-0,22841054	-0,8914098	0,6502058	0,90356725	1	3386	tags=25%, list=19%, signal=31%
GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	GO_NEGATIVE_REGULATION_OF_CELL_CELL_ADHESION	127	-0,22611472	-0,8902649	0,56666666	0,90570205	1	3192	tags=23%, list=18%, signal=28%
GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	GO_ENDOSOME_TO_LYSOSOME_TRANSPORT	40	-0,2538596	-0,8896518	0,59152216	0,9065448	1	4158	tags=35%, list=24%, signal=46%
GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	GO_ACTIVATION_OF_CYSTEINE_TYPE_ENDOPEPTIDASE_ACTIVITY	92	-0,20610017	-0,8889649	0,6498952	0,90754914	1	2192	tags=20%, list=12%, signal=22%
GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	GO_POSITIVE_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	24	-0,26881376	-0,8888852	0,60612243	0,90713817	1	5473	tags=54%, list=31%, signal=78%
GO_INTRINSIC_COMPONENT_OF_GOLGI_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_GOLGI_MEMBRANE	52	-0,23984128	-0,8883712	0,6234568	0,907702	1	1846	tags=13%, list=10%, signal=15%
GO_NUCLEAR_NUCLEOSOME	GO_NUCLEAR_NUCLEOSOME	28	-0,34588706	-0,8877986	0,5694444	0,9084255	1	6015	tags=46%, list=34%, signal=70%
GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_NEURAL_PRECURSOR_CELL_PROLIFERATION	21	-0,28484568	-0,8877439	0,6044177	0,9079479	1	574	tags=10%, list=3%, signal=10%
GO_LYMPHOCYTE_CHEMOTAXIS	GO_LYMPHOCYTE_CHEMOTAXIS	36	-0,3106872	-0,8874614	0,56082475	0,9080142	1	4244	tags=33%, list=24%, signal=44%
GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	GO_MITOCHONDRIAL_ATP_SYNTHESIS_COUPLED_PROTON_TRANSPORT	17	-0,40972888	-0,8869081	0,59491193	0,9087714	1	3754	tags=41%, list=21%, signal=52%
GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	GO_REGULATION_OF_CYTOSOLIC_CALCIUM_ION_CONCENTRATION	188	-0,22595342	-0,8862761	0,62096775	0,9097	1	4066	tags=27%, list=23%, signal=35%
GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	GO_POSITIVE_REGULATION_OF_SEQUESTERING_OF_CALCIUM_ION	16	-0,32858124	-0,8857061	0,6083499	0,91041243	1	1542	tags=19%, list=9%, signal=21%
GO_ORGANELLAR_RIBOSOME	GO_ORGANELLAR_RIBOSOME	67	-0,33601484	-0,885543	0,58739835	0,91017854	1	2755	tags=22%, list=16%, signal=26%
GO_LABYRINTHINE_LAYER_BLOOD_VESSEL_DEVELOPMENT	GO_LABYRINTHINE_LAYER_BLOOD_VESSEL_DEVELOPMENT	17	-0,2985292	-0,8852324	0,6277228	0,9102612	1	3997	tags=35%, list=23%, signal=46%
GO_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVITY	GO_REGULATION_OF_PROTEIN_HOMODIMERIZATION_ACTIVITY	22	-0,26229852	-0,8849478	0,6587771	0,9103013	1	4746	tags=41%, list=27%, signal=56%
GO_REGULATION_OF_HORMONE_METABOLIC_PROCESS	GO_REGULATION_OF_HORMONE_METABOLIC_PROCESS	26	-0,26550972	-0,884544	0,64705884	0,9106636	1	628	tags=12%, list=4%, signal=12%
GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO_POSITIVE_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	36	-0,2740161	-0,8844387	0,6027668	0,91031003	1	3854	tags=33%, list=22%, signal=43%
GO_DNA_CATABOLIC_PROCESS_ENDONUCLEOLYTIC	GO_DNA_CATABOLIC_PROCESS_ENDONUCLEOLYTIC	18	-0,2947577	-0,8838821	0,6204082	0,91099113	1	977	tags=17%, list=6%, signal=18%
GO_REGULATION_OF_ICOSANOID_SECRETION	GO_REGULATION_OF_ICOSANOID_SECRETION	20	-0,28675765	-0,8838481	0,63723606	0,9104661	1	244	tags=10%, list=1%, signal=10%
GO_POSITIVE_CHEMOTAXIS	GO_POSITIVE_CHEMOTAXIS	35	-0,24599123	-0,8835975	0,6507937	0,9104697	1	2810	tags=23%, list=16%, signal=27%
GO_NEUROTRANSMITTER_TRANSPORTER_ACTIVITY	GO_NEUROTRANSMITTER_TRANSPORTER_ACTIVITY	24	-0,28937203	-0,8831989	0,62033194	0,9108604	1	1227	tags=17%, list=7%, signal=18%
GO_MULTI_MULTICELLULAR_ORGANISM_PROCESS	GO_MULTI_MULTICELLULAR_ORGANISM_PROCESS	193	-0,19918083	-0,8830728	0,69155204	0,9105504	1	3900	tags=26%, list=22%, signal=34%
GO_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	GO_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	34	-0,26806006	-0,8824633	0,6320939	0,9113169	1	4757	tags=41%, list=27%, signal=56%

GO_NUCLEOTIDE_TRANSPORT	GO_NUCLEOTIDE_TRANSPORT	24	-0,2634011	-0,8823733	0,602	0,9109347	1	3555	tags=33%, list=20%, signal=42%
GO_MONOCYTE_DIFFERENTIATION	GO_MONOCYTE_DIFFERENTIATION	16	-0,31213024	-0,8822755	0,59582543	0,9105716	1	2668	tags=25%, list=15%, signal=29%
GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	GO_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	106	-0,25332472	-0,8822033	0,55279505	0,91013414	1	3553	tags=25%, list=20%, signal=32%
GO_NEGATIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	GO_NEGATIVE_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	16	-0,3252305	-0,8814751	0,5862069	0,91124016	1	3707	tags=44%, list=21%, signal=55%
GO_IMPORT_INTO_CELL	GO_IMPORT_INTO_CELL	36	-0,25113574	-0,8805378	0,6344538	0,9127567	1	2175	tags=19%, list=12%, signal=22%
GO_MECHANORECEPTOR_DIFFERENTIATION	GO_MECHANORECEPTOR_DIFFERENTIATION	48	-0,25026906	-0,8793074	0,6463878	0,9149975	1	2108	tags=23%, list=12%, signal=26%
GO_BONE_REMODELING	GO_BONE_REMODELING	34	-0,26697442	-0,8791772	0,63432837	0,91471493	1	1639	tags=15%, list=9%, signal=16%
GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	GO_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_SURFACE	26	-0,25863117	-0,8790615	0,6277228	0,9143783	1	2656	tags=27%, list=15%, signal=32%
GO_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	GO_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	49	-0,22909756	-0,8790268	0,6738703	0,9138621	1	1870	tags=14%, list=11%, signal=16%
GO_CELL_BODY	GO_CELL_BODY	471	-0,1832391	-0,8785712	0,7651822	0,9143446	1	3155	tags=21%, list=18%, signal=25%
GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	GO_MOVEMENT_IN_ENVIRONMENT_OF_OTHER_ORGANISM_INVOLVED_IN_SYMBIOTIC_INTERACTION	80	-0,22584955	-0,87825	0,61689585	0,91453004	1	3782	tags=29%, list=21%, signal=36%
GO_POSITIVE_REGULATION_OF_STAT_CASCADE	GO_POSITIVE_REGULATION_OF_STAT_CASCADE	63	-0,24877433	-0,8781264	0,61569417	0,9142136	1	2108	tags=17%, list=12%, signal=20%
GO_POSITIVE_REGULATION_OF_LOCOMOTION	GO_POSITIVE_REGULATION_OF_LOCOMOTION	395	-0,20800284	-0,8770336	0,6089613	0,916204	1	3192	tags=20%, list=18%, signal=24%
GO_LIPID_PARTICLE	GO_LIPID_PARTICLE	60	-0,23741691	-0,8767178	0,65163934	0,9163453	1	2623	tags=23%, list=15%, signal=27%
GO_O_ACYLTRANSFERASE_ACTIVITY	GO_O_ACYLTRANSFERASE_ACTIVITY	44	-0,22966987	-0,8763472	0,6633065	0,9165937	1	2762	tags=20%, list=16%, signal=24%
GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	GO_REGULATION_OF_STRESS_ACTIVATED_PROTEIN_KINASE_SIGNALING_CASCADE	191	-0,19737515	-0,876178	0,68503934	0,9163784	1	3137	tags=23%, list=18%, signal=27%
GO_HEART_VALVE_DEVELOPMENT	GO_HEART_VALVE_DEVELOPMENT	32	-0,29655245	-0,8760789	0,6035503	0,9160099	1	3202	tags=34%, list=18%, signal=42%
GO_ATPASE_BINDING	GO_ATPASE_BINDING	71	-0,21398175	-0,8760696	0,704501	0,9154288	1	4676	tags=34%, list=26%, signal=46%
GO_AMINO_SUGAR_METABOLIC_PROCESS	GO_AMINO_SUGAR_METABOLIC_PROCESS	39	-0,24091902	-0,8758637	0,6745562	0,915286	1	1997	tags=21%, list=11%, signal=23%
GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	GO_ENDOCARDIAL_CUSHION_DEVELOPMENT	32	-0,28703782	-0,8751981	0,576699	0,9162679	1	3187	tags=28%, list=18%, signal=34%
GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	GO_REGULATION_OF_CELLULAR_RESPONSE_TO_TRANSFORMING_GROWTH_FACTOR_BETA_STIMULUS	94	-0,22501425	-0,8741503	0,61657035	0,9181005	1	2975	tags=20%, list=17%, signal=24%
GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	GO_POSITIVE_REGULATION_OF_EPITHELIAL_CELL_APOPTOTIC_PROCESS	21	-0,26600352	-0,8740896	0,63723606	0,91764593	1	3482	tags=33%, list=20%, signal=41%
GO_NEGATIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	GO_NEGATIVE_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	16	-0,32329145	-0,8732209	0,5942029	0,9190199	1	4558	tags=38%, list=26%, signal=50%
GO_RESPONSE_TO_PAIN	GO_RESPONSE_TO_PAIN	28	-0,2782315	-0,8721609	0,654224	0,9208801	1	1210	tags=14%, list=7%, signal=15%
GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	GO_MITOCHONDRIAL_TRANSMEMBRANE_TRANSPORT	52	-0,3007181	-0,872016	0,6057495	0,9206179	1	3310	tags=29%, list=19%, signal=35%
GO_GUANYL_NUCLEOTIDE_BINDING	GO_GUANYL_NUCLEOTIDE_BINDING	349	-0,17916569	-0,8718452	0,68367344	0,92042166	1	2820	tags=19%, list=16%, signal=22%
GO_MUSCLE_ORGAN_MORPHOGENESIS	GO_MUSCLE_ORGAN_MORPHOGENESIS	67	-0,23739585	-0,8716111	0,674	0,9203594	1	4326	tags=33%, list=24%, signal=43%
GO_MESONEPHROS_DEVELOPMENT	GO_MESONEPHROS_DEVELOPMENT	90	-0,24011229	-0,870881	0,6292585	0,9214148	1	2829	tags=19%, list=16%, signal=22%
GO_CYTOPLASMIC_REGION	GO_CYTOPLASMIC_REGION	267	-0,1930977	-0,8707088	0,6646943	0,92120665	1	2462	tags=19%, list=14%, signal=22%
GO_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	GO_REGULATION_OF_RECEPTOR_MEDIATED_ENDOCYTOSIS	76	-0,20878938	-0,8704785	0,6686508	0,92112505	1	3708	tags=32%, list=21%, signal=40%
GO_INOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	GO_INOSITOL_PHOSPHATE_PHOSPHATASE_ACTIVITY	20	-0,2892858	-0,8703796	0,6484375	0,9207523	1	3305	tags=35%, list=19%, signal=43%
GO_PERICARDIUM_DEVELOPMENT	GO_PERICARDIUM_DEVELOPMENT	17	-0,3043447	-0,8703426	0,61657035	0,9202459	1	3187	tags=29%, list=18%, signal=36%
GO_REGULATION_OF_PHAGOCYTOSIS	GO_REGULATION_OF_PHAGOCYTOSIS	66	-0,2406655	-0,8702799	0,62851405	0,9197983	1	3482	tags=24%, list=20%, signal=30%
GO_EMBRYONIC_HEMOPOIESIS	GO_EMBRYONIC_HEMOPOIESIS	18	-0,30154255	-0,8699459	0,5831622	0,91999626	1	757	tags=17%, list=4%, signal=17%
GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	GO_PROTEIN_SERINE_THREONINE_PHOSPHATASE_ACTIVITY	62	-0,21237926	-0,8697985	0,68473893	0,9197314	1	3406	tags=26%, list=19%, signal=32%
GO_CELLULAR_RESPONSE_TO_KETONE	GO_CELLULAR_RESPONSE_TO_KETONE	71	-0,2205484	-0,8695766	0,68774706	0,9196578	1	3110	tags=25%, list=18%, signal=31%
GO_CARDIAC_CHAMBER_DEVELOPMENT	GO_CARDIAC_CHAMBER_DEVELOPMENT	138	-0,22291805	-0,8694352	0,6464844	0,9193864	1	3211	tags=26%, list=18%, signal=32%
GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO_T_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	42	-0,27025968	-0,8694069	0,5748988	0,9188542	1	4193	tags=36%, list=24%, signal=47%
GO_A_BAND	GO_A_BAND	32	-0,2638768	-0,869365	0,6582031	0,9183496	1	3685	tags=31%, list=21%, signal=39%
GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	GO_NEGATIVE_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	31	-0,29659066	-0,8678414	0,59137577	0,92119044	1	4911	tags=42%, list=28%, signal=58%
GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	GO_REGULATION_OF_LONG_TERM_SYNAPTIC_POTENTIATION	19	-0,29707885	-0,8676074	0,6449704	0,92114997	1	2704	tags=21%, list=15%, signal=25%
GO_DETECTION_OF_TEMPERATURE_STIMULUS	GO_DETECTION_OF_TEMPERATURE_STIMULUS	16	-0,2957372	-0,8674388	0,62049335	0,9209825	1	5901	tags=63%, list=33%, signal=94%
GO_NOTCH_SIGNALING_PATHWAY	GO_NOTCH_SIGNALING_PATHWAY	110	-0,20695567	-0,867314	0,68503934	0,9206739	1	3894	tags=26%, list=22%, signal=34%
GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	211	-0,21635751	-0,8663524	0,593047	0,9222433	1	3550	tags=23%, list=20%, signal=29%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	26	-0,2700522	-0,8662641	0,62729126	0,9218341	1	847	tags=15%, list=5%, signal=16%
GO_INTERFERON_GAMMA_PRODUCTION	GO_INTERFERON_GAMMA_PRODUCTION	15	-0,3332164	-0,8658332	0,607438	0,9222025	1	3311	tags=27%, list=19%, signal=33%
GO_PROTEIN_PHOSPHATASE_TYPE_2A_COMPLEX	GO_PROTEIN_PHOSPHATASE_TYPE_2A_COMPLEX	19	-0,28232512	-0,8657137	0,6416185	0,92185223	1	3334	tags=32%, list=19%, signal=39%
GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	GO_ARF_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	23	-0,2787676	-0,8654518	0,64166665	0,9218328	1	725	tags=13%, list=4%, signal=14%
GO_LABYRINTHINE_LAYER_DEVELOPMENT	GO_LABYRINTHINE_LAYER_DEVELOPMENT	42	-0,2532054	-0,8652296	0,61849713	0,92177755	1	4047	tags=36%, list=23%, signal=46%
GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	GO_ORGANELLAR_LARGE_RIBOSOMAL_SUBUNIT	30	-0,34291068	-0,8649612	0,5836735	0,9217854	1	636	tags=13%, list=4%, signal=14%
GO_CARDIAC_CELL_DEVELOPMENT	GO_CARDIAC_CELL_DEVELOPMENT	45	-0,24943899	-0,8647741	0,6511156	0,9216099	1	4046	tags=40%, list=23%, signal=52%
GO_LOCALIZATION_WITHIN_MEMBRANE	GO_LOCALIZATION_WITHIN_MEMBRANE	120	-0,19557361	-0,863765	0,69311064	0,92331433	1	5031	tags=37%, list=28%, signal=51%

GO_AORTA_MORPHOGENESIS	GO_AORTA_MORPHOGENESIS	22	-0,28106266	-0,8635175	0,61969113	0,92328846	1	3202	tags=32%, list=18%, signal=39%
GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	GO_NUCLEOTIDE_SUGAR_METABOLIC_PROCESS	33	-0,25197753	-0,8627433	0,6673866	0,92449725	1	1096	tags=15%, list=6%, signal=16%
GO_NEUROTRANSMITTER_SODIUM_SYMPORTER_ACTIVITY	GO_NEUROTRANSMITTER_SODIUM_SYMPORTER_ACTIVITY	19	-0,29075977	-0,8625215	0,6447106	0,92441887	1	1227	tags=16%, list=7%, signal=17%
GO_ION_CHANNEL_BINDING	GO_ION_CHANNEL_BINDING	104	-0,21005982	-0,8613896	0,6897233	0,926461	1	1638	tags=14%, list=9%, signal=16%
GO_DICARBOXYLIC_ACID_TRANSPORT	GO_DICARBOXYLIC_ACID_TRANSPORT	69	-0,20807968	-0,861217	0,7134146	0,9262643	1	1751	tags=16%, list=10%, signal=18%
GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	GO_MULTICELLULAR_ORGANISMAL_MOVEMENT	40	-0,23916839	-0,8611712	0,67975205	0,9257768	1	4725	tags=35%, list=27%, signal=48%
GO_WALKING_BEHAVIOR	GO_WALKING_BEHAVIOR	28	-0,2656596	-0,8606337	0,672549	0,9263892	1	2113	tags=18%, list=12%, signal=20%
GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	GO_POSITIVE_REGULATION_OF_RELEASE_OF_SEQUESTERED_CALCIUM_ION_INTO_CYTOSOL	35	-0,2659339	-0,8604637	0,6621359	0,92617196	1	3951	tags=34%, list=22%, signal=44%
GO_AU_RICH_ELEMENT_BINDING	GO_AU_RICH_ELEMENT_BINDING	21	-0,26853883	-0,8604075	0,6308594	0,9257205	1	2320	tags=24%, list=13%, signal=27%
GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	GO_POSITIVE_REGULATION_OF_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	16	-0,29883024	-0,8599562	0,6221766	0,9261981	1	1539	tags=19%, list=9%, signal=21%
GO_RESPONSE_TO_AMPHETAMINE	GO_RESPONSE_TO_AMPHETAMINE	29	-0,26722315	-0,8599398	0,68199235	0,9256443	1	2778	tags=28%, list=16%, signal=33%
GO_RESPONSE_TO_ALKALOID	GO_RESPONSE_TO_ALKALOID	130	-0,20461254	-0,859889	0,7590361	0,92517805	1	2751	tags=21%, list=16%, signal=24%
GO_RNA_POLYMERASE_BINDING	GO_RNA_POLYMERASE_BINDING	32	-0,24899638	-0,8594133	0,6166008	0,9257096	1	4532	tags=34%, list=26%, signal=46%
GO_T_CELL_DIFFERENTIATION	GO_T_CELL_DIFFERENTIATION	119	-0,24831349	-0,8591071	0,5777778	0,92580074	1	4209	tags=34%, list=24%, signal=44%
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	28	-0,2891842	-0,8589122	0,65451056	0,9256433	1	5062	tags=39%, list=29%, signal=55%
GO_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	GO_NEGATIVE_REGULATION_OF_NUCLEOCYTOPLASMIC_TRANSPORT	69	-0,21533038	-0,8588543	0,6563107	0,9251872	1	1670	tags=13%, list=9%, signal=14%
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC_BINDING	GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_CORE_PROMOTER_PROXIMAL_REGION_SEQUENCE_SPECIFIC_BINDING	99	-0,21045415	-0,8586147	0,68101764	0,92515606	1	2785	tags=20%, list=16%, signal=24%
GO_DIGESTIVE_SYSTEM_PROCESS	GO_DIGESTIVE_SYSTEM_PROCESS	57	-0,22037573	-0,8585004	0,75	0,92482597	1	3390	tags=23%, list=19%, signal=28%
GO_REGULATION_OF_SODIUM_ION_TRANSPORT	GO_REGULATION_OF_SODIUM_ION_TRANSPORT	73	-0,2160674	-0,8583123	0,7039848	0,92467225	1	4597	tags=34%, list=26%, signal=46%
GO_WIDE_PORE_CHANNEL_ACTIVITY	GO_WIDE_PORE_CHANNEL_ACTIVITY	21	-0,2634639	-0,8577858	0,64143425	0,9253263	1	2787	tags=29%, list=16%, signal=34%
GO_PROTEIN_HOMOTRIMERIZATION	GO_PROTEIN_HOMOTRIMERIZATION	19	-0,26559693	-0,8571195	0,67596567	0,9262889	1	3050	tags=26%, list=17%, signal=32%
GO_CELL_REDOX_HOMEOSTASIS	GO_CELL_REDOX_HOMEOSTASIS	60	-0,23462388	-0,8569582	0,64426875	0,9260538	1	2845	tags=25%, list=16%, signal=30%
GO_LUNG_MORPHOGENESIS	GO_LUNG_MORPHOGENESIS	45	-0,24326585	-0,8568355	0,6827458	0,9257365	1	1923	tags=16%, list=11%, signal=17%
GO_REGULATION_OF_MACROPHAGE_ACTIVATION	GO_REGULATION_OF_MACROPHAGE_ACTIVATION	23	-0,2769707	-0,8564484	0,6792035	0,9260324	1	2975	tags=22%, list=17%, signal=26%
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_DOPAMINERGIC	16	-0,28637248	-0,8561408	0,66927594	0,92614055	1	1472	tags=19%, list=8%, signal=20%
GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	GO_NEGATIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	19	-0,3082966	-0,8556759	0,67404425	0,9266271	1	3794	tags=37%, list=21%, signal=47%
GO_LYMPH_NODE_DEVELOPMENT	GO_LYMPH_NODE_DEVELOPMENT	17	-0,3009262	-0,8556352	0,6485944	0,92613596	1	5336	tags=53%, list=30%, signal=76%
GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	GO_ACTIN_POLYMERIZATION_OR_DEPOLYMERIZATION	34	-0,24915549	-0,8547556	0,6809816	0,9275066	1	2391	tags=24%, list=14%, signal=27%
GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	GO_ATPASE_ACTIVITY_COUPLED_TO_MOVEMENT_OF_SUBSTANCES	117	-0,20564994	-0,8545428	0,6993988	0,92741007	1	3497	tags=25%, list=20%, signal=31%
GO_NEPHRON_DEVELOPMENT	GO_NEPHRON_DEVELOPMENT	113	-0,23469156	-0,8544375	0,65234375	0,9270722	1	2818	tags=21%, list=16%, signal=25%
GO_I_BAND	GO_I_BAND	116	-0,22829525	-0,8535512	0,6606786	0,92848665	1	4445	tags=35%, list=25%, signal=47%
GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	GO_POSITIVE_REGULATION_OF_ALCOHOL_BIOSYNTHETIC_PROCESS	20	-0,29281497	-0,8533563	0,6400778	0,9283505	1	532	tags=10%, list=3%, signal=10%
GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	GO_REGULATION_OF_BIOMINERAL_TISSUE_DEVELOPMENT	68	-0,24075815	-0,8527135	0,6686047	0,92922574	1	3801	tags=28%, list=22%, signal=35%
GO_BRUSH_BORDER	GO_BRUSH_BORDER	102	-0,20250426	-0,8518261	0,72032195	0,9306368	1	3534	tags=24%, list=20%, signal=29%
GO_ANCHORED_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	GO_ANCHORED_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	19	-0,30896342	-0,8515965	0,625	0,9306175	1	2417	tags=26%, list=14%, signal=30%
GO_POSITIVE_REGULATION_OF_EXOCYTOSIS	GO_POSITIVE_REGULATION_OF_EXOCYTOSIS	77	-0,20625477	-0,8513269	0,73100615	0,9306537	1	3069	tags=25%, list=17%, signal=30%
GO_TRANSITION_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_TRANSITION_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	39	-0,23153543	-0,8510791	0,68367344	0,9306204	1	3341	tags=36%, list=19%, signal=44%
GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	GO_REGULATION_OF_ANATOMICAL_STRUCTURE_SIZE	447	-0,18672359	-0,850959	0,7137014	0,93031424	1	3192	tags=21%, list=18%, signal=25%
GO_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	GO_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	56	-0,23308794	-0,8507751	0,6627219	0,9301216	1	3202	tags=27%, list=18%, signal=33%
GO_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_PROTEIN_TYROSINE_KINASE_ACTIVITY	19	-0,2760608	-0,8499105	0,66459626	0,9315319	1	4594	tags=42%, list=26%, signal=57%
GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	GO_NEGATIVE_REGULATION_OF_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	20	-0,2683869	-0,8497052	0,6506986	0,93140435	1	1402	tags=15%, list=8%, signal=16%
GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	GO_NEGATIVE_REGULATION_OF_INTRACELLULAR_PROTEIN_TRANSPORT	91	-0,19796094	-0,8494688	0,7418033	0,9313421	1	2480	tags=16%, list=14%, signal=19%
GO_BODY_FLUID_SECRETION	GO_BODY_FLUID_SECRETION	64	-0,21457224	-0,8489472	0,7346535	0,9319217	1	5141	tags=42%, list=29%, signal=59%
GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	GO_POSITIVE_REGULATION_OF_TRANSMEMBRANE_RECEPTOR_PROTEIN_SERINE_THREONINE_KINASE_SIGNALING_PATHWAY	97	-0,21373716	-0,8488669	0,69921875	0,93151295	1	2267	tags=18%, list=13%, signal=20%
GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	GO_REGULATION_OF_T_HELPER_CELL_DIFFERENTIATION	25	-0,28215906	-0,8483524	0,6239496	0,9321017	1	3529	tags=28%, list=20%, signal=35%
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION	37	-0,2552275	-0,848042	0,72015655	0,93220586	1	4902	tags=43%, list=28%, signal=60%
GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	GO_POSITIVE_REGULATION_OF_PATHWAY_RESTRICTED_SMAD_PROTEIN_PHOSPHORYLATION	46	-0,2384442	-0,8478913	0,6917148	0,9320025	1	3599	tags=26%, list=20%, signal=33%
GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	GO_POSITIVE_REGULATION_OF_PHAGOCYTOSIS	45	-0,24468423	-0,8476408	0,6759443	0,9320082	1	3482	tags=24%, list=20%, signal=30%
GO_PROTEOGLYCAN_BINDING	GO_PROTEOGLYCAN_BINDING	28	-0,27598047	-0,8471299	0,68218625	0,932546	1	1107	tags=14%, list=6%, signal=15%
GO_THYMOCYTE_AGGREGATION	GO_THYMOCYTE_AGGREGATION	44	-0,25777614	-0,846461	0,6334012	0,933477	1	3137	tags=25%, list=18%, signal=30%

GO_GLIAL_CELL_DEVELOPMENT	GO_GLIAL_CELL_DEVELOPMENT	73	-0,20484181	-0,8462105	0,76152307	0,9333832	1	3619	tags=26%, list=20%, signal=33%
GO_OVULATION_CYCLE	GO_OVULATION_CYCLE	103	-0,20963216	-0,8461641	0,73295456	0,93290263	1	1374	tags=13%, list=8%, signal=14%
GO_CXCR_CHEMOKINE_RECEPTOR_BINDING	GO_CXCR_CHEMOKINE_RECEPTOR_BINDING	15	-0,331207	-0,8452227	0,6216216	0,934484	1	1092	tags=20%, list=6%, signal=21%
GO_RECEPTOR_METABOLIC_PROCESS	GO_RECEPTOR_METABOLIC_PROCESS	75	-0,2220122	-0,8450778	0,6890244	0,93421435	1	2889	tags=20%, list=16%, signal=24%
GO_AMINOGLYCAN_CATABOLIC_PROCESS	GO_AMINOGLYCAN_CATABOLIC_PROCESS	63	-0,22377703	-0,8449187	0,670412	0,9340276	1	1726	tags=17%, list=10%, signal=19%
GO_NAD_METABOLIC_PROCESS	GO_NAD_METABOLIC_PROCESS	48	-0,26262	-0,8444182	0,6152263	0,93452406	1	2718	tags=25%, list=15%, signal=29%
GO_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	GO_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	20	-0,2764704	-0,8428354	0,6897233	0,9374719	1	4232	tags=45%, list=24%, signal=59%
GO_CALCIUM_CHANNEL_REGULATOR_ACTIVITY	GO_CALCIUM_CHANNEL_REGULATOR_ACTIVITY	34	-0,23785852	-0,8424574	0,72	0,9377219	1	2529	tags=18%, list=14%, signal=21%
GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	GO_HYDROGEN_ION_TRANSMEMBRANE_TRANSPORT	97	-0,24818511	-0,8424536	0,6015936	0,9371521	1	3851	tags=29%, list=22%, signal=37%
GO_BEHAVIOR	GO_BEHAVIOR	467	-0,18249644	-0,8424345	0,8326693	0,9366148	1	2999	tags=19%, list=17%, signal=22%
GO_SARCOMERE_ORGANIZATION	GO_SARCOMERE_ORGANIZATION	26	-0,2575689	-0,8423377	0,704501	0,9362579	1	2685	tags=27%, list=15%, signal=32%
GO_MYELOID_CELL_HOMEOSTASIS	GO_MYELOID_CELL_HOMEOSTASIS	84	-0,20439115	-0,8419476	0,7020408	0,93654746	1	1262	tags=12%, list=7%, signal=13%
GO_ORGANELLE_MEMBRANE_FUSION	GO_ORGANELLE_MEMBRANE_FUSION	91	-0,1991989	-0,8417527	0,7386831	0,93640536	1	3528	tags=25%, list=20%, signal=31%
GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	GO_REGULATION_OF_NITRIC_OXIDE_SYNTHASE_BIOSYNTHETIC_PROCESS	18	-0,2936023	-0,8416209	0,6292585	0,9361614	1	3548	tags=33%, list=20%, signal=42%
GO_PEPTIDASE_ACTIVATOR_ACTIVITY	GO_PEPTIDASE_ACTIVATOR_ACTIVITY	36	-0,22448868	-0,8415104	0,7160494	0,93582267	1	2168	tags=19%, list=12%, signal=22%
GO_VESICLE_TARGETING	GO_VESICLE_TARGETING	75	-0,22470422	-0,8413611	0,67479676	0,93555933	1	5078	tags=45%, list=29%, signal=63%
GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	GO_MODULATION_OF_EXCITATORY_POSTSYNAPTIC_POTENTIAL	29	-0,2549521	-0,8412135	0,6990099	0,93532526	1	2048	tags=21%, list=12%, signal=23%
GO_PLACENTA_BLOOD_VESSEL_DEVELOPMENT	GO_PLACENTA_BLOOD_VESSEL_DEVELOPMENT	27	-0,26464862	-0,841002	0,6640471	0,9351964	1	4047	tags=33%, list=23%, signal=43%
GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	55	-0,24326804	-0,8407825	0,6421471	0,9351002	1	5291	tags=38%, list=30%, signal=54%
GO_REGULATION_OF_HEMOPOIESIS	GO_REGULATION_OF_HEMOPOIESIS	289	-0,19448306	-0,8398699	0,6659836	0,93649334	1	3550	tags=23%, list=20%, signal=28%
GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	GO_POSITIVE_REGULATION_OF_SYNAPTIC_TRANSMISSION	107	-0,21617314	-0,8393936	0,778865	0,936962	1	2048	tags=16%, list=12%, signal=18%
GO_POSITIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	GO_POSITIVE_REGULATION_OF_PROTEIN_EXPORT_FROM_NUCLEUS	19	-0,2729341	-0,8392421	0,66797644	0,93673366	1	2794	tags=32%, list=16%, signal=37%
GO_MYOSIN_FILAMENT	GO_MYOSIN_FILAMENT	22	-0,28595003	-0,8390774	0,69631237	0,93652505	1	4695	tags=36%, list=27%, signal=49%
GO_PHOSPHOLIPASE_ACTIVITY	GO_PHOSPHOLIPASE_ACTIVITY	89	-0,20146935	-0,8381809	0,76023394	0,9379588	1	3612	tags=26%, list=20%, signal=32%
GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS	GO_REGULATION_OF_MRNA_CATABOLIC_PROCESS	24	-0,26762396	-0,838088	0,6743738	0,93760973	1	3403	tags=33%, list=19%, signal=41%
GO_BONE_DEVELOPMENT	GO_BONE_DEVELOPMENT	147	-0,21655817	-0,8380621	0,6646943	0,9370926	1	2917	tags=22%, list=17%, signal=26%
GO_MAMMARY_GLAND_DEVELOPMENT	GO_MAMMARY_GLAND_DEVELOPMENT	112	-0,19908433	-0,8377689	0,74313724	0,93717456	1	2366	tags=17%, list=13%, signal=19%
GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	GO_REGULATION_OF_NOTCH_SIGNALING_PATHWAY	63	-0,21854319	-0,8376778	0,7242063	0,9368096	1	4260	tags=35%, list=24%, signal=46%
GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	GO_POSITIVE_REGULATION_OF_ADAPTIVE_IMMUNE_RESPONSE	68	-0,24409913	-0,8371005	0,61167	0,9374725	1	3548	tags=28%, list=20%, signal=35%
GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	GO_RHO_PROTEIN_SIGNAL_TRANSDUCTION	46	-0,2281846	-0,8356136	0,65225565	0,9401757	1	2242	tags=17%, list=13%, signal=20%
GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	GO_EXTRINSIC_COMPONENT_OF_MEMBRANE	236	-0,19867426	-0,8353474	0,6912065	0,9402317	1	2820	tags=19%, list=16%, signal=22%
GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	GO_REGULATION_OF_RAS_PROTEIN_SIGNAL_TRANSDUCTION	178	-0,2065452	-0,8346772	0,67578125	0,94109845	1	2193	tags=16%, list=12%, signal=18%
GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	GO_NEGATIVE_REGULATION_OF_EPITHELIAL_TO_MESENCHYMAL_TRANSITION	22	-0,27854738	-0,8328994	0,71	0,94443125	1	546	tags=9%, list=3%, signal=9%
GO_HEART_DEVELOPMENT	GO_HEART_DEVELOPMENT	441	-0,1913043	-0,8322535	0,7202268	0,9453436	1	3211	tags=23%, list=18%, signal=27%
GO_DEVELOPMENTAL_CELL_GROWTH	GO_DEVELOPMENTAL_CELL_GROWTH	71	-0,22870724	-0,8317374	0,6890595	0,9459103	1	1200	tags=13%, list=7%, signal=14%
GO_POSITIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_ERYTHROCYTE_DIFFERENTIATION	23	-0,25893646	-0,8314707	0,718	0,94593227	1	647	tags=13%, list=4%, signal=14%
GO_ACTIN_FILAMENT_BASED_MOVEMENT	GO_ACTIN_FILAMENT_BASED_MOVEMENT	89	-0,22224134	-0,8312547	0,74509805	0,94585186	1	4326	tags=34%, list=24%, signal=44%
GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	GO_NEGATIVE_REGULATION_OF_NEURON_DEATH	160	-0,19394211	-0,8309606	0,75096524	0,945891	1	3151	tags=22%, list=18%, signal=26%
GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	GO_POSITIVE_REGULATION_OF_MAPK_CASCADE	442	-0,18431228	-0,8304575	0,75301206	0,9463838	1	3151	tags=19%, list=18%, signal=23%
GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_EXTERNAL_SIDE_OF_PLASMA_MEMBRANE	24	-0,2787411	-0,8299579	0,68774706	0,94692194	1	2417	tags=25%, list=14%, signal=29%
GO_MAMMARY_GLAND_LOBULE_DEVELOPMENT	GO_MAMMARY_GLAND_LOBULE_DEVELOPMENT	16	-0,2828327	-0,8292825	0,67537314	0,9478198	1	1810	tags=19%, list=10%, signal=21%
GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	GO_RESPONSE_TO_MOLECULE_OF_BACTERIAL_ORIGIN	310	-0,1977836	-0,8292559	0,720339	0,9473066	1	3311	tags=22%, list=19%, signal=27%
GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	76	-0,20583816	-0,8288058	0,7375746	0,9476361	1	3078	tags=24%, list=17%, signal=29%
GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_MITOCHONDRIAL_MEMBRANE	43	-0,24737939	-0,8287581	0,654	0,94716555	1	2851	tags=23%, list=16%, signal=28%
GO_REGULATION_OF_RECEPTOR_ACTIVITY	GO_REGULATION_OF_RECEPTOR_ACTIVITY	109	-0,20653754	-0,8284789	0,75435203	0,947238	1	3794	tags=26%, list=21%, signal=33%
GO_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_MODIFIED_AMINO_ACID_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16	-0,2854678	-0,8277558	0,6706827	0,9482044	1	679	tags=13%, list=4%, signal=13%
GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	GO_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	121	-0,226877	-0,8272237	0,627907	0,9488314	1	3529	tags=24%, list=20%, signal=30%
GO_PROTEIN_INSERTION_INTO_MEMBRANE	GO_PROTEIN_INSERTION_INTO_MEMBRANE	20	-0,2737889	-0,826918	0,6726547	0,9489255	1	1395	tags=15%, list=8%, signal=16%
GO_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	GO_AUDITORY_RECEPTOR_CELL_DIFFERENTIATION	27	-0,25156116	-0,826732	0,7059925	0,94875866	1	2108	tags=26%, list=12%, signal=29%
GO_REGULATION_OF_CARDIAC_CONDUCTION	GO_REGULATION_OF_CARDIAC_CONDUCTION	65	-0,23129386	-0,826508	0,7407407	0,9486969	1	3880	tags=29%, list=22%, signal=37%
GO_L_ALPHA_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	GO_L_ALPHA_AMINO_ACID_TRANSMEMBRANE_TRANSPORT	30	-0,25243673	-0,8264098	0,7243461	0,948328	1	2325	tags=27%, list=13%, signal=31%
GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	GO_PHOSPHATIDYLINOSITOL_3_4_5_TRISPHOSPHATE_BINDING	32	-0,25601965	-0,825868	0,6845361	0,9489666	1	1041	tags=13%, list=6%, signal=13%
GO_ATRIOVENTRICULAR_VALVE_DEVELOPMENT	GO_ATRIOVENTRICULAR_VALVE_DEVELOPMENT	19	-0,29500082	-0,8256142	0,6590476	0,9489403	1	3202	tags=37%, list=18%, signal=45%

GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_MULTICELLULAR_ORGANISMAL_METABOLIC_PROCESS	19	-0,28475362	-0,825573	0,66462165	0,9484757	1	2971	tags=26%, list=17%, signal=32%
GO_NEGATIVE_REGULATION_OF_SECRETION	GO_NEGATIVE_REGULATION_OF_SECRETION	180	-0,19532722	-0,8248563	0,7873684	0,9494615	1	3413	tags=18%, list=19%, signal=22%
GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	GO_INNER_MITOCHONDRIAL_MEMBRANE_ORGANIZATION	16	-0,32039142	-0,8246916	0,66799206	0,9492511	1	4850	tags=38%, list=27%, signal=52%
GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	GO_REGULATION_OF_INFLAMMATORY_RESPONSE_TO_ANTIGENIC_STIMULUS	17	-0,30480638	-0,8246579	0,6507937	0,94874763	1	3311	tags=29%, list=19%, signal=36%
GO_MALE_GENITALIA_DEVELOPMENT	GO_MALE_GENITALIA_DEVELOPMENT	20	-0,26364428	-0,824101	0,6802444	0,9493516	1	4309	tags=35%, list=24%, signal=46%
GO_SINGLE_ORGANISM_BEHAVIOR	GO_SINGLE_ORGANISM_BEHAVIOR	354	-0,18369491	-0,8237148	0,83693516	0,9495741	1	2999	tags=19%, list=17%, signal=23%
GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT	GO_ENDOPLASMIC_RETICULUM_GOLGI_INTERMEDIATE_COMPARTMENT	96	-0,20725654	-0,8235457	0,6991701	0,9493523	1	3788	tags=29%, list=21%, signal=37%
GO_PROTEIN_KINASE_COMPLEX	GO_PROTEIN_KINASE_COMPLEX	88	-0,2070381	-0,8233972	0,70422536	0,9490955	1	3055	tags=20%, list=17%, signal=25%
GO_NUCLEOID	GO_NUCLEOID	39	-0,27241963	-0,8232165	0,6577869	0,9489303	1	3217	tags=33%, list=18%, signal=41%
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	16	-0,2857283	-0,8229798	0,72336066	0,9488474	1	4409	tags=38%, list=25%, signal=50%
GO_AXIS_ELONGATION	GO_AXIS_ELONGATION	27	-0,26267278	-0,8229268	0,6920078	0,94839615	1	1295	tags=15%, list=7%, signal=16%
GO_MAINTENANCE_OF_LOCATION	GO_MAINTENANCE_OF_LOCATION	134	-0,18399325	-0,8225824	0,78512394	0,9485508	1	3110	tags=22%, list=18%, signal=27%
GO_REGULATION_OF_HEART_CONTRACTION	GO_REGULATION_OF_HEART_CONTRACTION	208	-0,20299895	-0,8224191	0,7741935	0,94832236	1	4442	tags=30%, list=25%, signal=39%
GO_REGULATION_OF_CELL_SHAPE	GO_REGULATION_OF_CELL_SHAPE	134	-0,20409912	-0,8222129	0,694165	0,9481754	1	2097	tags=15%, list=12%, signal=17%
GO_ADP_METABOLIC_PROCESS	GO_ADP_METABOLIC_PROCESS	43	-0,25257775	-0,8220906	0,6473029	0,9478871	1	761	tags=14%, list=4%, signal=15%
GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_ACTIVE_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	166	-0,18803234	-0,8217174	0,83095723	0,94813985	1	3310	tags=24%, list=19%, signal=29%
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	28	-0,26681778	-0,8212614	0,68650794	0,9485575	1	2204	tags=21%, list=12%, signal=24%
GO_RESPONSE_TO_HEAT	GO_RESPONSE_TO_HEAT	85	-0,20303209	-0,8208132	0,7665996	0,9488919	1	3154	tags=22%, list=18%, signal=27%
GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	GO_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	76	-0,22089374	-0,8202251	0,77603143	0,94959617	1	4442	tags=34%, list=25%, signal=46%
GO_AUTOPHAGY	GO_AUTOPHAGY	362	-0,16772708	-0,8199116	0,8109756	0,9497184	1	4063	tags=29%, list=23%, signal=37%
GO_ADRENAL_GLAND_DEVELOPMENT	GO_ADRENAL_GLAND_DEVELOPMENT	23	-0,25781375	-0,8196965	0,7509881	0,9496266	1	1074	tags=13%, list=6%, signal=14%
GO_REPRODUCTIVE_BEHAVIOR	GO_REPRODUCTIVE_BEHAVIOR	27	-0,2436376	-0,8195439	0,75247526	0,94939524	1	2280	tags=22%, list=13%, signal=25%
GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_ABSENCE_OF_LIGAND	GO_REGULATION_OF_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_IN_ABSENCE_OF_LIGAND	45	-0,22396995	-0,8190883	0,7521008	0,94983804	1	3854	tags=24%, list=22%, signal=31%
GO_PROTEIN_BINDING_INVOLVED_IN_CELL_ADHESION	GO_PROTEIN_BINDING_INVOLVED_IN_CELL_ADHESION	17	-0,2873012	-0,8187202	0,6794355	0,9501065	1	2578	tags=29%, list=15%, signal=34%
GO_ACTIN_MEDIATED_CELL_CONTRACTION	GO_ACTIN_MEDIATED_CELL_CONTRACTION	70	-0,23113038	-0,8183819	0,75595236	0,9502296	1	4326	tags=34%, list=24%, signal=45%
GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	GO_POSTSYNAPTIC_MEMBRANE_ORGANIZATION	25	-0,24697897	-0,8182942	0,72064775	0,9498502	1	2725	tags=20%, list=15%, signal=24%
GO_REGULATION_OF_SYNAPTIC_PLASTICITY	GO_REGULATION_OF_SYNAPTIC_PLASTICITY	136	-0,19392858	-0,818143	0,80588233	0,94960403	1	3411	tags=22%, list=19%, signal=27%
GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	GO_REGULATION_OF_MYOBLAST_DIFFERENTIATION	41	-0,232678	-0,8176525	0,7364185	0,9500505	1	3600	tags=34%, list=20%, signal=43%
GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_METAL_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	382	-0,18512496	-0,8167337	0,84063745	0,95139647	1	3189	tags=21%, list=18%, signal=25%
GO_IMMUNE_EFFECTOR_PROCESS	GO_IMMUNE_EFFECTOR_PROCESS	424	-0,19793336	-0,8166294	0,6585366	0,9510621	1	2923	tags=18%, list=17%, signal=22%
GO_STAT_CASCADE	GO_STAT_CASCADE	43	-0,24089041	-0,8161004	0,6876268	0,9516263	1	4308	tags=33%, list=24%, signal=43%
GO_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS	GO_MONOVALENT_INORGANIC_ANION_HOMEOSTASIS	18	-0,26274303	-0,8160064	0,70920503	0,95127195	1	4276	tags=39%, list=24%, signal=51%
GO_CLUSTER_OF_ACTIN_BASED_CELL_PROJECTIONS	GO_CLUSTER_OF_ACTIN_BASED_CELL_PROJECTIONS	132	-0,18500587	-0,8154486	0,82510287	0,9518642	1	2164	tags=15%, list=12%, signal=17%
GO_DEFENSE_RESPONSE_TO_BACTERIUM	GO_DEFENSE_RESPONSE_TO_BACTERIUM	162	-0,206631	-0,8151963	0,75449103	0,9518509	1	2949	tags=20%, list=17%, signal=23%
GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	GO_RAS_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	218	-0,19526492	-0,8149074	0,7229602	0,9518898	1	4157	tags=27%, list=24%, signal=35%
GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	GO_REGULATION_OF_VESICLE_MEDIATED_TRANSPORT	440	-0,16966258	-0,8144274	0,808	0,95234734	1	3069	tags=20%, list=17%, signal=23%
GO_ENDOCYTIC_VESICLE	GO_ENDOCYTIC_VESICLE	247	-0,18578283	-0,8143038	0,7798354	0,9520561	1	3346	tags=21%, list=19%, signal=25%
GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	GO_HYDROLASE_ACTIVITY_HYDROLYZING_O_GLYCOSYL_COMPOUNDS	82	-0,2066814	-0,8138866	0,7344064	0,9523422	1	2585	tags=20%, list=15%, signal=23%
GO_TISSUE_REMODELING	GO_TISSUE_REMODELING	83	-0,23278828	-0,8138313	0,70414203	0,95191574	1	2783	tags=19%, list=16%, signal=23%
GO_DISRUPTION_OF_CELLS_OF_OTHER_ORGANISM	GO_DISRUPTION_OF_CELLS_OF_OTHER_ORGANISM	22	-0,3189199	-0,8129599	0,71428573	0,95317954	1	5602	tags=55%, list=32%, signal=80%
GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	GO_G_PROTEIN_COUPLED_RECEPTOR_BINDING	230	-0,18373382	-0,8129137	0,8486708	0,952715	1	2971	tags=17%, list=17%, signal=21%
GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	GO_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	34	-0,2564635	-0,8126269	0,7181996	0,9527712	1	4597	tags=38%, list=26%, signal=52%
GO_ER_TO_GOLGI_TRANSPORT_VESICLE	GO_ER_TO_GOLGI_TRANSPORT_VESICLE	67	-0,23726396	-0,8126225	0,6895075	0,9522233	1	4979	tags=36%, list=28%, signal=50%
GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	GO_POSITIVE_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	34	-0,25665453	-0,81055	0,71031743	0,9560182	1	4916	tags=44%, list=28%, signal=61%
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GABAERGIC	28	-0,26101092	-0,81041	0,74556214	0,955749	1	2778	tags=21%, list=16%, signal=25%
GO_NUCLEUS_LOCALIZATION	GO_NUCLEUS_LOCALIZATION	19	-0,272108	-0,8099987	0,7070707	0,95601535	1	4013	tags=42%, list=23%, signal=54%
GO_REGULATION_OF_PHOSPHATASE_ACTIVITY	GO_REGULATION_OF_PHOSPHATASE_ACTIVITY	112	-0,1854127	-0,8099695	0,8015873	0,95551866	1	1568	tags=13%, list=9%, signal=14%
GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	GO_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	193	-0,1797658	-0,8098293	0,7804878	0,95521545	1	2241	tags=16%, list=13%, signal=18%
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT_PROTEIN	61	-0,23019445	-0,8096401	0,70987654	0,955044	1	2108	tags=16%, list=12%, signal=19%
GO_CELL_CORTEX	GO_CELL_CORTEX	223	-0,18661322	-0,809404	0,7619048	0,9549684	1	2462	tags=18%, list=14%, signal=21%
GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	GO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	288	-0,18589976	-0,808714	0,7581574	0,9558396	1	4157	tags=26%, list=24%, signal=34%
GO_HEART_PROCESS	GO_HEART_PROCESS	80	-0,22486836	-0,8080228	0,7446394	0,9567143	1	4406	tags=30%, list=25%, signal=40%

GO_PHOSPHATASE_REGULATOR_ACTIVITY	GO_PHOSPHATASE_REGULATOR_ACTIVITY	80	-0,19860598	-0,8077474	0,807393	0,95672756	1	1568	tags=14%, list=9%, signal=15%
GO_NEUROEPITHELIAL_CELL_DIFFERENTIATION	GO_NEUROEPITHELIAL_CELL_DIFFERENTIATION	58	-0,21753274	-0,8073524	0,79017013	0,95696485	1	2917	tags=24%, list=17%, signal=29%
GO_PHOSPHOLIPID_METABOLIC_PROCESS	GO_PHOSPHOLIPID_METABOLIC_PROCESS	336	-0,16347104	-0,8072851	0,9054054	0,9565436	1	2442	tags=15%, list=14%, signal=17%
GO_PROSTATE_GLAND_MORPHOGENESIS	GO_PROSTATE_GLAND_MORPHOGENESIS	23	-0,2690552	-0,8071876	0,71794873	0,956194	1	1580	tags=13%, list=9%, signal=14%
GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	GO_NEGATIVE_REGULATION_OF_CARTILAGE_DEVELOPMENT	23	-0,28631726	-0,8064916	0,70980394	0,95706326	1	4843	tags=39%, list=27%, signal=54%
GO_PROTEIN_KINASE_B_SIGNALING	GO_PROTEIN_KINASE_B_SIGNALING	34	-0,2319805	-0,8062746	0,73100615	0,9569343	1	5728	tags=50%, list=32%, signal=74%
GO_COPULATION	GO_COPULATION	16	-0,28662026	-0,8062195	0,7675781	0,95648485	1	5491	tags=44%, list=31%, signal=63%
GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	GO_REGULATION_OF_G_PROTEIN_COUPLED_RECEPTOR_PROTEIN_SIGNALING_PATHWAY	115	-0,19128117	-0,8057437	0,8003992	0,9568998	1	1941	tags=14%, list=11%, signal=16%
GO_ENSHEATHMENT_OF_NEURONS	GO_ENSHEATHMENT_OF_NEURONS	87	-0,20927875	-0,805708	0,792	0,9564179	1	4358	tags=32%, list=25%, signal=43%
GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	GO_CYTOSOLIC_CALCIUM_ION_TRANSPORT	52	-0,24434742	-0,8055394	0,7232704	0,95620674	1	4066	tags=35%, list=23%, signal=45%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	GO_REGULATION_OF_LEUKOCYTE_MEDIATED_CYTOTOXICITY	51	-0,2674284	-0,8051806	0,6460905	0,956397	1	3553	tags=31%, list=20%, signal=39%
GO_METANEPHROS_DEVELOPMENT	GO_METANEPHROS_DEVELOPMENT	78	-0,22453322	-0,8048969	0,73767257	0,9564304	1	3003	tags=22%, list=17%, signal=26%
GO_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	GO_PROTEIN_LOCALIZATION_TO_CELL_PERIPHERY	148	-0,18896398	-0,8048301	0,796371	0,9560196	1	3526	tags=22%, list=20%, signal=28%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	GO_NEGATIVE_REGULATION_OF_CYTOKINE_SECRETION	39	-0,24058604	-0,804605	0,694	0,9559455	1	1491	tags=10%, list=8%, signal=11%
GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	GO_POSITIVE_REGULATION_OF_STRIATED_MUSCLE_CONTRACTION	15	-0,27197382	-0,8044412	0,75	0,9557262	1	2889	tags=27%, list=16%, signal=32%
GO_POSITIVE_REGULATION_OF_GROWTH	GO_POSITIVE_REGULATION_OF_GROWTH	223	-0,1746072	-0,8040549	0,8639847	0,955989	1	3202	tags=19%, list=18%, signal=23%
GO_MEMBRANE_PROTEIN_INTRACELLULAR_DOMAIN_PROTEOLYSIS	GO_MEMBRANE_PROTEIN_INTRACELLULAR_DOMAIN_PROTEOLYSIS	16	-0,27017713	-0,8038016	0,7050505	0,95596653	1	3745	tags=38%, list=21%, signal=48%
GO_PHOSPHATIDYLSERINE_METABOLIC_PROCESS	GO_PHOSPHATIDYLSERINE_METABOLIC_PROCESS	27	-0,23191762	-0,8036388	0,776699	0,9557462	1	1221	tags=15%, list=7%, signal=16%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_IMPORT	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_IMPORT	50	-0,23767973	-0,8035716	0,74552685	0,9553318	1	3951	tags=32%, list=22%, signal=41%
GO_ANATOMICAL_STRUCTURE_MATURATION	GO_ANATOMICAL_STRUCTURE_MATURATION	38	-0,23872112	-0,8029136	0,71568626	0,95610076	1	1840	tags=13%, list=10%, signal=15%
GO_NEURON_MIGRATION	GO_NEURON_MIGRATION	101	-0,21608101	-0,8015787	0,77735126	0,95815945	1	3187	tags=24%, list=18%, signal=29%
GO_FIBROBLAST_GROWTH_FACTOR_BINDING	GO_FIBROBLAST_GROWTH_FACTOR_BINDING	23	-0,25098595	-0,8015696	0,71779144	0,9576309	1	3964	tags=30%, list=22%, signal=39%
GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT	GO_ENERGY_COUPLED_PROTON_TRANSPORT_DOWN_ELECTROCHEMICAL_GRADIENT	23	-0,3293563	-0,8014939	0,6527778	0,9572185	1	3754	tags=30%, list=21%, signal=39%
GO_ASTROCYTE_DIFFERENTIATION	GO_ASTROCYTE_DIFFERENTIATION	38	-0,2211837	-0,8013133	0,7854251	0,9570206	1	3976	tags=34%, list=23%, signal=44%
GO_MACROPHAGE_ACTIVATION	GO_MACROPHAGE_ACTIVATION	30	-0,27103657	-0,8011134	0,6955603	0,9568729	1	4961	tags=43%, list=28%, signal=60%
GO_INTERACTION_WITH_HOST	GO_INTERACTION_WITH_HOST	126	-0,18893237	-0,800505	0,79253113	0,95754576	1	3782	tags=28%, list=21%, signal=35%
GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	GO_REGULATION_OF_GRANULOCYTE_CHEMOTAXIS	36	-0,2687538	-0,8004837	0,6902287	0,9570309	1	4344	tags=33%, list=25%, signal=44%
GO_ACTIN_FILAMENT	GO_ACTIN_FILAMENT	67	-0,2171915	-0,8000791	0,7295597	0,9572891	1	685	tags=9%, list=4%, signal=9%
GO_ERYTHROCYTE_HOMEOSTASIS	GO_ERYTHROCYTE_HOMEOSTASIS	69	-0,19823477	-0,8000514	0,76553106	0,95679206	1	1262	tags=12%, list=7%, signal=12%
GO_ASYMMETRIC_PROTEIN_LOCALIZATION	GO_ASYMMETRIC_PROTEIN_LOCALIZATION	18	-0,27707475	-0,7991939	0,7305389	0,95798695	1	4702	tags=50%, list=27%, signal=68%
GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	GO_CELL_COMMUNICATION_BY_ELECTRICAL_COUPLING	15	-0,30174515	-0,7983471	0,73427993	0,9591555	1	4406	tags=40%, list=25%, signal=53%
GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	GO_NEGATIVE_REGULATION_OF_LYMPHOCYTE_MEDIATED_IMMUNITY	33	-0,2527232	-0,7975322	0,69184893	0,9602485	1	1223	tags=12%, list=7%, signal=13%
GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	GO_SENSORY_PERCEPTION_OF_LIGHT_STIMULUS	177	-0,17615308	-0,7974579	0,8946322	0,9598453	1	3228	tags=18%, list=18%, signal=22%
GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	GO_NEGATIVE_REGULATION_OF_EXOCYTOSIS	26	-0,25860685	-0,796673	0,7165049	0,96084684	1	2057	tags=15%, list=12%, signal=17%
GO_OLIGODENDROCYTE_DEVELOPMENT	GO_OLIGODENDROCYTE_DEVELOPMENT	32	-0,22812426	-0,7960259	0,7739307	0,9616325	1	2663	tags=22%, list=15%, signal=26%
GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	GO_MAINTENANCE_OF_PROTEIN_LOCALIZATION_IN_ORGANELLE	29	-0,22818021	-0,795148	0,77935225	0,96289253	1	3110	tags=28%, list=18%, signal=33%
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FACTOR_IMPORT_INTO_NUCLEUS	49	-0,22508079	-0,7948819	0,7227926	0,9628727	1	4447	tags=41%, list=25%, signal=54%
GO_CARDIAC_SEPTUM_DEVELOPMENT	GO_CARDIAC_SEPTUM_DEVELOPMENT	82	-0,21444541	-0,7945465	0,70703125	0,96300393	1	3211	tags=29%, list=18%, signal=36%
GO_PEPTIDE_RECEPTOR_ACTIVITY	GO_PEPTIDE_RECEPTOR_ACTIVITY	105	-0,21015917	-0,7935145	0,78149605	0,9645431	1	3464	tags=24%, list=20%, signal=29%
GO_AXON_REGENERATION	GO_AXON_REGENERATION	22	-0,2572656	-0,7925996	0,72637796	0,96581006	1	3010	tags=32%, list=17%, signal=38%
GO_GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	GO_GLYCEROPHOSPHOLIPID_METABOLIC_PROCESS	283	-0,16201243	-0,7923914	0,9318182	0,96567285	1	2442	tags=16%, list=14%, signal=18%
GO_ALCOHOL_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_ALCOHOL_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	22	-0,25788537	-0,792311	0,79029125	0,9652853	1	4595	tags=41%, list=26%, signal=55%
GO_INTRINSIC_COMPONENT_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	GO_INTRINSIC_COMPONENT_OF_ENDOPLASMIC_RETICULUM_MEMBRANE	116	-0,20185877	-0,7919452	0,72895277	0,9654789	1	2623	tags=19%, list=15%, signal=22%
GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESS	GO_KERATAN_SULFATE_BIOSYNTHETIC_PROCESS	26	-0,2460634	-0,7919212	0,7619048	0,96498615	1	2022	tags=19%, list=11%, signal=22%
GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	GO_CELLULAR_RESPONSE_TO_INTERLEUKIN_1	82	-0,20319873	-0,7918771	0,7426778	0,96451133	1	2971	tags=20%, list=17%, signal=23%
GO_REGULATION_OF_EXOCYTOSIS	GO_REGULATION_OF_EXOCYTOSIS	175	-0,17695835	-0,7911773	0,8356998	0,96532446	1	3069	tags=19%, list=17%, signal=23%
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	44	-0,21643284	-0,7910655	0,8007737	0,9650028	1	4974	tags=39%, list=28%, signal=54%
GO_NEGATIVE_REGULATION_OF_GROWTH	GO_NEGATIVE_REGULATION_OF_GROWTH	229	-0,17017215	-0,789133	0,89669424	0,9683365	1	2852	tags=18%, list=16%, signal=22%
GO_CHEMOKINE_ACTIVITY	GO_CHEMOKINE_ACTIVITY	44	-0,2643184	-0,7887354	0,7035491	0,9685877	1	3916	tags=30%, list=22%, signal=38%
GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	GO_REGULATION_OF_I_KAPPAB_KINASE_NF_KAPPAB_SIGNALING	228	-0,17351176	-0,7868477	0,828866	0,971748	1	3412	tags=23%, list=19%, signal=28%
GO_SINGLE_ORGANISM_MEMBRANE_FUSION	GO_SINGLE_ORGANISM_MEMBRANE_FUSION	115	-0,1790327	-0,7862307	0,85835093	0,97246814	1	3528	tags=24%, list=20%, signal=30%
GO_CELL_FATE_COMMITMENT	GO_CELL_FATE_COMMITMENT	209	-0,1883845	-0,7861748	0,85142857	0,9720324	1	4079	tags=28%, list=23%, signal=36%

GO_RESPONSE_TO_PROSTAGLANDIN	GO_RESPONSE_TO_PROSTAGLANDIN	34	-0,23482838	-0,7860319	0,7833002	0,97176963	1	1003	tags=15%, list=6%, signal=16%
GO_REGULATION_OF_CALCIUM_ION_IMPORT	GO_REGULATION_OF_CALCIUM_ION_IMPORT	93	-0,21204294	-0,7852593	0,7984032	0,972722	1	3966	tags=28%, list=22%, signal=36%
GO_REGULATION_OF_CGMP_METABOLIC_PROCESS	GO_REGULATION_OF_CGMP_METABOLIC_PROCESS	25	-0,2552858	-0,7844417	0,7589641	0,9738289	1	3355	tags=36%, list=19%, signal=44%
GO_POSITIVE_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_MACROPHAGE_DERIVED_FOAM_CELL_DIFFERENTIATION	15	-0,28727624	-0,7839542	0,7281947	0,97428435	1	3612	tags=33%, list=20%, signal=42%
GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	GO_PLASMA_MEMBRANE_RECEPTOR_COMPLEX	165	-0,18973088	-0,7839355	0,82	0,97378236	1	2923	tags=19%, list=17%, signal=22%
GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	GO_POSITIVE_REGULATION_OF_MUSCLE_CONTRACTION	42	-0,22465698	-0,7837433	0,794971	0,97361887	1	2204	tags=19%, list=12%, signal=22%
GO_RESPONSE_TO_PROGESTERONE	GO_RESPONSE_TO_PROGESTERONE	47	-0,22904213	-0,7837255	0,77530366	0,9730992	1	4047	tags=34%, list=23%, signal=44%
GO_REGULATION_OF_TISSUE_REMODELING	GO_REGULATION_OF_TISSUE_REMODELING	55	-0,2197092	-0,7835943	0,7903226	0,9728224	1	819	tags=9%, list=5%, signal=10%
GO_GLIAL_CELL_DIFFERENTIATION	GO_GLIAL_CELL_DIFFERENTIATION	129	-0,1822023	-0,7828972	0,8691406	0,9736039	1	3976	tags=26%, list=23%, signal=34%
GO_REGULATION_OF_ACTION_POTENTIAL	GO_REGULATION_OF_ACTION_POTENTIAL	36	-0,23521335	-0,7824687	0,8257426	0,9738431	1	4409	tags=36%, list=25%, signal=48%
GO_PROTEIN_K63_LINKED_DEUBIQUITINATION	GO_PROTEIN_K63_LINKED_DEUBIQUITINATION	22	-0,2550417	-0,7819299	0,7169043	0,9743376	1	3209	tags=27%, list=18%, signal=33%
GO_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	GO_N_ACETYLGLUCOSAMINE_METABOLIC_PROCESS	15	-0,2786824	-0,7817894	0,74951077	0,9740761	1	1997	tags=27%, list=11%, signal=30%
GO_REGULATION_OF_OSSIFICATION	GO_REGULATION_OF_OSSIFICATION	167	-0,20056453	-0,7807766	0,8111332	0,9754214	1	4578	tags=31%, list=26%, signal=41%
GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	GO_REGULATION_OF_OXIDATIVE_STRESS_INDUCED_CELL_DEATH	42	-0,20794998	-0,7804088	0,8052209	0,975563	1	2081	tags=19%, list=12%, signal=22%
GO_ACTIVATION_OF_IMMUNE_RESPONSE	GO_ACTIVATION_OF_IMMUNE_RESPONSE	384	-0,19051626	-0,7803322	0,70464134	0,97517216	1	2403	tags=15%, list=14%, signal=17%
GO_ACTIVATION_OF_MAPKK_ACTIVITY	GO_ACTIVATION_OF_MAPKK_ACTIVITY	48	-0,22685868	-0,7802253	0,7574553	0,9748566	1	3151	tags=25%, list=18%, signal=30%
GO_NUCLEAR_OUTER_MEMBRANE	GO_NUCLEAR_OUTER_MEMBRANE	18	-0,24487624	-0,7799512	0,78210115	0,9748345	1	3819	tags=33%, list=22%, signal=42%
GO_ASTROCYTE_DEVELOPMENT	GO_ASTROCYTE_DEVELOPMENT	19	-0,25021946	-0,7798279	0,7740586	0,9745256	1	3507	tags=32%, list=20%, signal=39%
GO_MEMBRANE_FUSION	GO_MEMBRANE_FUSION	140	-0,17358543	-0,7798092	0,8625	0,9740143	1	3528	tags=24%, list=20%, signal=29%
GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	GO_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	42	-0,24353258	-0,7794552	0,757874	0,9740942	1	2223	tags=19%, list=13%, signal=22%
GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	GO_NEGATIVE_REGULATION_OF_CELL_ACTIVATION	145	-0,2093213	-0,7791298	0,6967742	0,97418624	1	2969	tags=18%, list=17%, signal=21%
GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS	GO_LIPOPROTEIN_BIOSYNTHETIC_PROCESS	82	-0,19350581	-0,779003	0,80658436	0,9738857	1	3400	tags=22%, list=19%, signal=27%
GO_LACTATION	GO_LACTATION	37	-0,21458413	-0,7787906	0,79324055	0,9737195	1	5328	tags=46%, list=30%, signal=66%
GO_GLUCOSAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	GO_GLUCOSAMINE_CONTAINING_COMPOUND_METABOLIC_PROCESS	25	-0,2385817	-0,778572	0,7678917	0,97358173	1	1997	tags=20%, list=11%, signal=23%
GO_RENAL_TUBULE_DEVELOPMENT	GO_RENAL_TUBULE_DEVELOPMENT	76	-0,21770278	-0,7776197	0,7764706	0,974851	1	3672	tags=24%, list=21%, signal=30%
GO_ACROSOMAL_VESICLE	GO_ACROSOMAL_VESICLE	72	-0,18434997	-0,7775073	0,8773006	0,97454315	1	2233	tags=17%, list=13%, signal=19%
GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	GO_POSITIVE_REGULATION_OF_FILOPODIUM_ASSEMBLY	23	-0,24925667	-0,7774774	0,77867204	0,97404987	1	3137	tags=30%, list=18%, signal=37%
GO_PEPTIDE_CROSS_LINKING	GO_PEPTIDE_CROSS_LINKING	31	-0,27310878	-0,7773552	0,7601547	0,97373646	1	12850	tags=100%, list=73%, signal=366%
GO_MATING	GO_MATING	34	-0,21943617	-0,7772967	0,85714287	0,97330874	1	2338	tags=18%, list=13%, signal=20%
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CONTRACTION	15	-0,2939516	-0,7771164	0,74067163	0,97310907	1	4252	tags=47%, list=24%, signal=61%
GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	GO_CHEMOKINE_MEDIATED_SIGNALING_PATHWAY	65	-0,25232625	-0,7771155	0,6755102	0,97257036	1	3529	tags=22%, list=20%, signal=27%
GO_SYNTAXIN_1_BINDING	GO_SYNTAXIN_1_BINDING	18	-0,24536112	-0,7769867	0,784	0,972271	1	1638	tags=17%, list=9%, signal=18%
GO_MEMORY	GO_MEMORY	93	-0,19673172	-0,776829	0,8828125	0,972045	1	3411	tags=23%, list=19%, signal=28%
GO_PERIPHERAL_NERVOUS_SYSTEM_AXON_ENSHEATHMENT	GO_PERIPHERAL_NERVOUS_SYSTEM_AXON_ENSHEATHMENT	21	-0,2505141	-0,7765971	0,7571702	0,97194207	1	4237	tags=33%, list=24%, signal=44%
GO_METALLOPEPTIDASE_ACTIVITY	GO_METALLOPEPTIDASE_ACTIVITY	172	-0,17881359	-0,7753578	0,8774704	0,97365785	1	3282	tags=22%, list=19%, signal=27%
GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	GO_RIBONUCLEOSIDE_CATABOLIC_PROCESS	23	-0,24672712	-0,774829	0,7413442	0,97410405	1	1769	tags=13%, list=10%, signal=14%
GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	GO_DEVELOPMENTAL_GROWTH_INVOLVED_IN_MORPHOGENESIS	99	-0,21230759	-0,7747509	0,7614504	0,9737199	1	1295	tags=12%, list=7%, signal=13%
GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	GO_PLATELET_DERIVED_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	34	-0,25942025	-0,7742333	0,7210626	0,97417045	1	2285	tags=21%, list=13%, signal=24%
GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_MYOBLAST_DIFFERENTIATION	22	-0,2558118	-0,7735416	0,74459726	0,97493976	1	3600	tags=36%, list=20%, signal=46%
GO_TRANSLATIONAL_TERMINATION	GO_TRANSLATIONAL_TERMINATION	91	-0,27994752	-0,7732118	0,64908725	0,9750655	1	2160	tags=16%, list=12%, signal=19%
GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	GO_NEGATIVE_REGULATION_OF_TYPE_I_INTERFERON_PRODUCTION	38	-0,22514668	-0,7731489	0,753876	0,9746525	1	3304	tags=29%, list=19%, signal=36%
GO_REGULATION_OF_CELLULAR_EXTRAVASATION	GO_REGULATION_OF_CELLULAR_EXTRAVASATION	22	-0,28242442	-0,7718686	0,72619045	0,9764829	1	2971	tags=27%, list=17%, signal=33%
GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	GO_POSITIVE_REGULATION_OF_IMMUNE_EFFECTOR_PROCESS	146	-0,2021166	-0,7717099	0,6938776	0,97624546	1	3553	tags=24%, list=20%, signal=30%
GO_MONOCYTE_CHEMOTAXIS	GO_MONOCYTE_CHEMOTAXIS	39	-0,25367883	-0,7709187	0,7046843	0,97715276	1	5783	tags=51%, list=33%, signal=76%
GO_PHOSPHATIDYLSERINE_ACYL_CHAIN_REMODELING	GO_PHOSPHATIDYLSERINE_ACYL_CHAIN_REMODELING	16	-0,26400986	-0,7708995	0,7573385	0,9766463	1	570	tags=13%, list=3%, signal=13%
GO_GLUCOSYLTRANSFERASE_ACTIVITY	GO_GLUCOSYLTRANSFERASE_ACTIVITY	16	-0,262719	-0,7708745	0,7475149	0,9761522	1	1660	tags=19%, list=9%, signal=21%
GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	GO_REGULATION_OF_RELEASE_OF_CYTOCHROME_C_FROM_MITOCHONDRIA	42	-0,21506687	-0,7704523	0,7802419	0,9763982	1	1983	tags=19%, list=11%, signal=21%
GO_POSITIVE_REGULATION_OF_SECRETION	GO_POSITIVE_REGULATION_OF_SECRETION	344	-0,1651214	-0,7704046	0,9292929	0,97594374	1	2256	tags=14%, list=13%, signal=16%
GO_ERAD_PATHWAY	GO_ERAD_PATHWAY	70	-0,2247001	-0,7702208	0,7258065	0,97575086	1	3330	tags=27%, list=19%, signal=33%
GO_RESPONSE_TO_RETINOIC_ACID	GO_RESPONSE_TO_RETINOIC_ACID	98	-0,18244174	-0,7691683	0,888668	0,977098	1	4858	tags=35%, list=28%, signal=48%
GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	GO_POSITIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	38	-0,23844804	-0,7691084	0,75396824	0,97666293	1	3854	tags=34%, list=22%, signal=44%
GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	GO_REGULATION_OF_TRANSMEMBRANE_TRANSPORT	389	-0,17121378	-0,7690741	0,91812867	0,97618437	1	4462	tags=28%, list=25%, signal=36%
GO_ENDOCYTOSIS	GO_ENDOCYTOSIS	458	-0,1706313	-0,7689318	0,8343685	0,975892	1	3013	tags=20%, list=17%, signal=23%

GO_POSITIVE_REGULATION_OF_HEART_RATE	GO_POSITIVE_REGULATION_OF_HEART_RATE	22	-0,24343897	-0,7685835	0,8032454	0,9759972	1	2119	tags=14%, list=12%, signal=15%
GO_FIBRIL_ORGANIZATION	GO_FIBRIL_ORGANIZATION	19	-0,28915814	-0,7677727	0,7263582	0,97692305	1	2546	tags=26%, list=14%, signal=31%
GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	GO_POST_GOLGI_VESICLE_MEDIATED_TRANSPORT	81	-0,19978502	-0,7676147	0,75306123	0,97664666	1	3024	tags=21%, list=17%, signal=25%
GO_REGULATION_OF_PROTEIN_OLIGOMERIZATION	GO_REGULATION_OF_PROTEIN_OLIGOMERIZATION	29	-0,22504176	-0,7670077	0,832998	0,97720635	1	3265	tags=28%, list=18%, signal=34%
GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	GO_SKELETAL_MUSCLE_ORGAN_DEVELOPMENT	121	-0,1893582	-0,7666903	0,8922764	0,9772639	1	2772	tags=21%, list=16%, signal=25%
GO_FEAR_RESPONSE	GO_FEAR_RESPONSE	27	-0,22640762	-0,7664226	0,8470825	0,97719705	1	2710	tags=22%, list=15%, signal=26%
GO_RESPONSE_TO_TYPE_I_INTERFERON	GO_RESPONSE_TO_TYPE_I_INTERFERON	53	-0,27414662	-0,7651269	0,6806084	0,9789715	1	4932	tags=45%, list=28%, signal=63%
GO_REGULATION_OF_CELL_GROWTH	GO_REGULATION_OF_CELL_GROWTH	375	-0,15744607	-0,7650562	0,94831014	0,9785636	1	2170	tags=14%, list=12%, signal=16%
GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	GO_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_INFLAMMATORY_RESPONSE	16	-0,27233878	-0,7647863	0,7768763	0,9784886	1	55	tags=6%, list=0%, signal=6%
GO_RNA_DESTABILIZATION	GO_RNA_DESTABILIZATION	15	-0,289059	-0,7636919	0,7665289	0,97984636	1	2861	tags=33%, list=16%, signal=40%
GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	GO_POSITIVE_REGULATION_OF_PHOSPHOLIPID_METABOLIC_PROCESS	40	-0,22684817	-0,763153	0,81666666	0,98024493	1	3936	tags=35%, list=22%, signal=45%
GO_CEREBELLAR_CORTEX_MORPHOGENESIS	GO_CEREBELLAR_CORTEX_MORPHOGENESIS	29	-0,23564532	-0,7630867	0,82304525	0,97982216	1	4919	tags=45%, list=28%, signal=62%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION	193	-0,18455027	-0,7623507	0,8074534	0,9805708	1	3906	tags=23%, list=22%, signal=30%
GO_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	GO_PHOSPHATIDYLINOSITOL_KINASE_ACTIVITY	47	-0,22560367	-0,762323	0,82941175	0,9800899	1	2110	tags=15%, list=12%, signal=17%
GO_REGULATION_OF_MEMBRANE_POTENTIAL	GO_REGULATION_OF_MEMBRANE_POTENTIAL	319	-0,16838384	-0,7622573	0,96237624	0,9796751	1	3255	tags=21%, list=18%, signal=25%
GO_EMBRYONIC_PATTERN_SPECIFICATION	GO_EMBRYONIC_PATTERN_SPECIFICATION	56	-0,21657477	-0,7620476	0,8293173	0,9794952	1	3092	tags=23%, list=18%, signal=28%
GO_POSITIVE_REGULATION_OF_OSSIFICATION	GO_POSITIVE_REGULATION_OF_OSSIFICATION	81	-0,2051459	-0,7617562	0,8220503	0,979457	1	1778	tags=15%, list=10%, signal=16%
GO_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	GO_REGULATION_OF_AUTOPHAGOSOME_ASSEMBLY	34	-0,22112046	-0,7616581	0,78340083	0,97910744	1	5807	tags=44%, list=33%, signal=66%
GO_REGULATION_OF_PROTEIN_SECRETION	GO_REGULATION_OF_PROTEIN_SECRETION	360	-0,16444875	-0,7611309	0,88819873	0,97950315	1	2856	tags=17%, list=16%, signal=20%
GO_VIRION_ASSEMBLY	GO_VIRION_ASSEMBLY	36	-0,21796611	-0,760704	0,76152307	0,9797413	1	4041	tags=33%, list=23%, signal=43%
GO_RESPONSE_TO_MECHANICAL_STIMULUS	GO_RESPONSE_TO_MECHANICAL_STIMULUS	203	-0,17667608	-0,7605892	0,89387757	0,9794375	1	2971	tags=19%, list=17%, signal=22%
GO_RESPONSE_TO_NICOTINE	GO_RESPONSE_TO_NICOTINE	50	-0,22302917	-0,7604641	0,87966806	0,979129	1	2726	tags=20%, list=15%, signal=24%
GO_SODIUM_CHANNEL_ACTIVITY	GO_SODIUM_CHANNEL_ACTIVITY	30	-0,2422196	-0,7601975	0,82828283	0,97905695	1	416	tags=7%, list=2%, signal=7%
GO_ER_TO_GOLGI_TRANSPORT_VESICLE_MEMBRANE	GO_ER_TO_GOLGI_TRANSPORT_VESICLE_MEMBRANE	51	-0,23973568	-0,7600889	0,72727275	0,97872835	1	2968	tags=22%, list=17%, signal=26%
GO_REGULATION_OF_CATECHOLAMINE_SECRETION	GO_REGULATION_OF_CATECHOLAMINE_SECRETION	38	-0,22848663	-0,7597644	0,8156863	0,9787591	1	1056	tags=11%, list=6%, signal=11%
GO_ATP_GENERATION_FROM_ADP	GO_ATP_GENERATION_FROM_ADP	35	-0,2458956	-0,7592458	0,74788135	0,97914654	1	761	tags=14%, list=4%, signal=15%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	GO_NEGATIVE_REGULATION_OF_CYTOKINE_BIOSYNTHETIC_PROCESS	27	-0,22546044	-0,7590216	0,8032129	0,9789714	1	3906	tags=30%, list=22%, signal=38%
GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	GO_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	148	-0,21009555	-0,7585697	0,70445347	0,9791999	1	3553	tags=22%, list=20%, signal=28%
GO_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_BINDING	GO_PHOSPHATIDYLINOSITOL_4_PHOSPHATE_BINDING	19	-0,25038698	-0,758307	0,77120316	0,9791456	1	719	tags=11%, list=4%, signal=11%
GO_MITOCHONDRIAL_TRANSLATION	GO_MITOCHONDRIAL_TRANSLATION	104	-0,26895362	-0,7582129	0,66530615	0,9787738	1	4929	tags=37%, list=28%, signal=50%
GO_PROTEIN_N_LINKED_GLYCOSYLATION	GO_PROTEIN_N_LINKED_GLYCOSYLATION	73	-0,19905739	-0,7577142	0,80404043	0,9791351	1	2544	tags=21%, list=14%, signal=24%
GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	GO_PROTEIN_LOCALIZATION_TO_MITOCHONDRION	62	-0,22303544	-0,7573667	0,7581967	0,9791987	1	1638	tags=13%, list=9%, signal=14%
GO_CELL_CELL_JUNCTION	GO_CELL_CELL_JUNCTION	357	-0,17684159	-0,757171	0,85742974	0,9790051	1	4058	tags=27%, list=23%, signal=34%
GO_ATPASE_COMPLEX	GO_ATPASE_COMPLEX	22	-0,24272037	-0,7570891	0,8333333	0,9786239	1	1948	tags=18%, list=11%, signal=20%
GO_MYOSIN_BINDING	GO_MYOSIN_BINDING	58	-0,19770174	-0,7563152	0,8836735	0,9794805	1	2385	tags=17%, list=14%, signal=20%
GO_GLYCOPROTEIN_COMPLEX	GO_GLYCOPROTEIN_COMPLEX	20	-0,25873268	-0,7561459	0,79041916	0,9792445	1	2503	tags=20%, list=14%, signal=23%
GO_MITOCHONDRIAL_TRANSPORT	GO_MITOCHONDRIAL_TRANSPORT	160	-0,19215396	-0,7555541	0,7938144	0,97977316	1	3310	tags=24%, list=19%, signal=29%
GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	GO_MONOVALENT_INORGANIC_CATION_HOMEOSTASIS	119	-0,1816563	-0,7552883	0,9048626	0,9796884	1	4465	tags=32%, list=25%, signal=42%
GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	GO_EXTRINSIC_APOPTOTIC_SIGNALING_PATHWAY_VIA_DEATH_DOMAIN_RECEPTORS	38	-0,20307346	-0,7542048	0,830303	0,9810462	1	2677	tags=16%, list=15%, signal=19%
GO_METANEPHRIC_NEPHRON_DEVELOPMENT	GO_METANEPHRIC_NEPHRON_DEVELOPMENT	31	-0,23758574	-0,7541192	0,7745665	0,980662	1	3003	tags=26%, list=17%, signal=31%
GO_MAMMARY_GLAND_EPITHELIUM_DEVELOPMENT	GO_MAMMARY_GLAND_EPITHELIUM_DEVELOPMENT	52	-0,20304802	-0,7536926	0,85655737	0,98088175	1	1810	tags=13%, list=10%, signal=15%
GO_ACTION_POTENTIAL	GO_ACTION_POTENTIAL	87	-0,19712989	-0,7535798	0,8644401	0,9805607	1	3167	tags=22%, list=18%, signal=26%
GO_REGULATION_OF_VACUOLE_ORGANIZATION	GO_REGULATION_OF_VACUOLE_ORGANIZATION	40	-0,2139799	-0,7534918	0,8060606	0,9801986	1	5807	tags=45%, list=33%, signal=67%
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_IN_RESPONSE_TO_STRESS	63	-0,19105335	-0,7533121	0,84351146	0,9799932	1	2939	tags=24%, list=17%, signal=28%
GO_TRANSLATIONAL_ELONGATION	GO_TRANSLATIONAL_ELONGATION	108	-0,26048785	-0,7529871	0,67346936	0,98002326	1	4195	tags=30%, list=24%, signal=39%
GO_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	GO_REGULATION_OF_NEUROTRANSMITTER_TRANSPORT	57	-0,20452575	-0,7523783	0,8809035	0,98052186	1	2737	tags=19%, list=15%, signal=23%
GO_BODY_MORPHOGENESIS	GO_BODY_MORPHOGENESIS	43	-0,2233536	-0,7522909	0,80278885	0,98013335	1	1873	tags=16%, list=11%, signal=18%
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION_INVOLVED_IN_CELLULAR_RESPONSE_TO_GLUCOSE_STIMULUS	25	-0,23516068	-0,7520288	0,8623482	0,9800531	1	1363	tags=12%, list=8%, signal=13%
GO_REGULATION_OF_CELL_ACTIVATION	GO_REGULATION_OF_CELL_ACTIVATION	434	-0,18960914	-0,751192	0,71836734	0,9809597	1	3137	tags=20%, list=18%, signal=23%
GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	GO_ENDOCARDIAL_CUSHION_MORPHOGENESIS	22	-0,26874384	-0,751058	0,7675781	0,98067033	1	3187	tags=27%, list=18%, signal=33%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MEDIATED_IMMUNITY	44	-0,23453696	-0,7503313	0,75944334	0,981387	1	2112	tags=14%, list=12%, signal=15%
GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	GO_POSITIVE_REGULATION_OF_INFLAMMATORY_RESPONSE	107	-0,20934194	-0,7500252	0,77272725	0,98136693	1	3657	tags=21%, list=21%, signal=27%

GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_VACUOLE	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_VACUOLE	30	-0,24700066	-0,748926	0,7388664	0,9827106	1	2899	tags=30%, list=16%, signal=36%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_MIGRATION	30	-0,2523237	-0,7489171	0,76938367	0,9821985	1	3082	tags=27%, list=17%, signal=32%
GO_PATTERNING_OF_BLOOD_VESSELS	GO_PATTERNING_OF_BLOOD_VESSELS	32	-0,2444738	-0,7488199	0,78669274	0,9818226	1	1295	tags=16%, list=7%, signal=17%
GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	GO_POSITIVE_REGULATION_OF_CELLULAR_COMPONENT_BIOGENESIS	368	-0,15888621	-0,7465121	0,9389764	0,98527217	1	3175	tags=20%, list=18%, signal=24%
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_ACTIVATING_TRANSCRIPTION_FACTOR_BINDING	51	-0,21029568	-0,7458973	0,85404336	0,98574626	1	2856	tags=25%, list=16%, signal=30%
GO_MYOBLAST_DIFFERENTIATION	GO_MYOBLAST_DIFFERENTIATION	33	-0,21043131	-0,744184	0,8509434	0,9880426	1	2078	tags=18%, list=12%, signal=21%
GO_HEAD_MORPHOGENESIS	GO_HEAD_MORPHOGENESIS	35	-0,23244731	-0,7440535	0,7923387	0,98775524	1	1873	tags=17%, list=11%, signal=19%
GO_CATION_CHANNEL_COMPLEX	GO_CATION_CHANNEL_COMPLEX	149	-0,19016875	-0,743227	0,8925781	0,98855585	1	4442	tags=28%, list=25%, signal=36%
GO_CARDIAC_CONDUCTION	GO_CARDIAC_CONDUCTION	77	-0,21448879	-0,7430009	0,8424125	0,98838013	1	4437	tags=31%, list=25%, signal=41%
GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	GO_CELLULAR_RESPONSE_TO_MECHANICAL_STIMULUS	78	-0,19341001	-0,7425135	0,8242678	0,9886517	1	1537	tags=12%, list=9%, signal=13%
GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	GO_REGULATION_OF_ACTIN_FILAMENT_BASED_PROCESS	294	-0,17385438	-0,7420162	0,87349397	0,9889323	1	3236	tags=21%, list=18%, signal=25%
GO_MEGAKARYOCYTE_DEVELOPMENT	GO_MEGAKARYOCYTE_DEVELOPMENT	15	-0,27327734	-0,741868	0,76878613	0,9886494	1	2917	tags=27%, list=17%, signal=32%
GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_T_CELL_PROLIFERATION	47	-0,21003237	-0,7409078	0,779798	0,9896684	1	2969	tags=21%, list=17%, signal=26%
GO_POSITIVE_REGULATION_OF_HORMONE_SECRETION	GO_POSITIVE_REGULATION_OF_HORMONE_SECRETION	110	-0,17439605	-0,7408391	0,9559387	0,9892635	1	2818	tags=15%, list=16%, signal=18%
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BINDING	29	-0,21709265	-0,7403477	0,8326772	0,989546	1	4371	tags=31%, list=25%, signal=41%
GO_CCR_CHEMOKINE_RECEPTOR_BINDING	GO_CCR_CHEMOKINE_RECEPTOR_BINDING	33	-0,2544073	-0,7402472	0,725	0,9891729	1	4244	tags=33%, list=24%, signal=44%
GO_ER_ASSOCIATED_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	GO_ER_ASSOCIATED_UBIQUITIN_DEPENDENT_PROTEIN_CATABOLIC_PROCESS	59	-0,21919525	-0,740177	0,7683168	0,98877937	1	3768	tags=31%, list=21%, signal=39%
GO_REGULATION_OF_GASTRULATION	GO_REGULATION_OF_GASTRULATION	32	-0,21812695	-0,739866	0,8429119	0,9887851	1	1608	tags=16%, list=9%, signal=17%
GO_VESICLE_ORGANIZATION	GO_VESICLE_ORGANIZATION	264	-0,15917256	-0,7395666	0,9159836	0,9887494	1	3644	tags=25%, list=21%, signal=31%
GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	GO_PHOSPHATIDYLINOSITOL_3_4_BISPHOSPHATE_BINDING	18	-0,25572395	-0,7391347	0,8121086	0,98892725	1	1876	tags=17%, list=11%, signal=19%
GO_THIOL_DEPENDENT_UBIQUITIN_SPECIFIC_PROTEASE_ACTIVITY	GO_THIOL_DEPENDENT_UBIQUITIN_SPECIFIC_PROTEASE_ACTIVITY	68	-0,19872344	-0,7375239	0,76969695	0,99096954	1	2589	tags=18%, list=15%, signal=21%
GO_ENDOCYTIC_VESICLE_MEMBRANE	GO_ENDOCYTIC_VESICLE_MEMBRANE	146	-0,179043	-0,7364049	0,85979384	0,9922222	1	3346	tags=18%, list=19%, signal=22%
GO_AUTOPHAGOSOME	GO_AUTOPHAGOSOME	76	-0,18417072	-0,7363436	0,8496994	0,9917914	1	2677	tags=17%, list=15%, signal=20%
GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	GO_POSITIVE_REGULATION_OF_DEVELOPMENTAL_GROWTH	146	-0,17209466	-0,7361266	0,9147287	0,9916259	1	4291	tags=28%, list=24%, signal=37%
GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	GO_CELL_CELL_SIGNALING_INVOLVED_IN_CARDIAC_CONDUCTION	20	-0,26989776	-0,7358559	0,7894737	0,99152464	1	2701	tags=25%, list=15%, signal=29%
GO_HIPPO_SIGNALING	GO_HIPPO_SIGNALING	27	-0,2522643	-0,7355195	0,7558594	0,9915421	1	2554	tags=26%, list=14%, signal=30%
GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	GO_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	86	-0,20329024	-0,7341648	0,842	0,99317294	1	3966	tags=29%, list=22%, signal=37%
GO_CELLULAR_RESPONSE_TO_NITRIC_OXIDE	GO_CELLULAR_RESPONSE_TO_NITRIC_OXIDE	15	-0,2516898	-0,7341192	0,82941175	0,9927211	1	956	tags=13%, list=5%, signal=14%
GO_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	GO_REGULATION_OF_INTERLEUKIN_5_PRODUCTION	16	-0,25971913	-0,7339715	0,8329897	0,9924474	1	2969	tags=31%, list=17%, signal=38%
GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_STEM_CELL_DIFFERENTIATION	41	-0,21359225	-0,7338108	0,8424125	0,9921951	1	3879	tags=27%, list=22%, signal=34%
GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	GO_PHOSPHATIDYLINOSITOL_3_KINASE_ACTIVITY	68	-0,20957872	-0,7336517	0,864	0,99192995	1	5321	tags=40%, list=30%, signal=57%
GO_POSITIVE_REGULATION_OF_TISSUE_REMODELING	GO_POSITIVE_REGULATION_OF_TISSUE_REMODELING	21	-0,25269955	-0,7334818	0,7741273	0,99168736	1	2022	tags=19%, list=11%, signal=21%
GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	GO_CARBOHYDRATE_TRANSMEMBRANE_TRANSPORT	23	-0,22324193	-0,7330309	0,85071576	0,99189234	1	3455	tags=30%, list=20%, signal=38%
GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	GO_VASCULAR_ENDOTHELIAL_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	72	-0,20118031	-0,7308868	0,8097166	0,99473906	1	2971	tags=19%, list=17%, signal=23%
GO_ESTROUS_CYCLE	GO_ESTROUS_CYCLE	18	-0,26031125	-0,7302323	0,8296146	0,9952233	1	1639	tags=17%, list=9%, signal=18%
GO_CHONDROCYTE_DIFFERENTIATION	GO_CHONDROCYTE_DIFFERENTIATION	58	-0,21904325	-0,7300112	0,83396226	0,9950538	1	2149	tags=17%, list=12%, signal=20%
GO_NEURON_APOPTOTIC_PROCESS	GO_NEURON_APOPTOTIC_PROCESS	33	-0,20553923	-0,7292618	0,8489796	0,99571776	1	4196	tags=33%, list=24%, signal=44%
GO_LONG_TERM_SYNAPTIC_POTENTIATION	GO_LONG_TERM_SYNAPTIC_POTENTIATION	39	-0,21562192	-0,7290651	0,9101796	0,9955038	1	1472	tags=13%, list=8%, signal=14%
GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_REGULATION_OF_SODIUM_ION_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	34	-0,20793965	-0,7270105	0,8699809	0,9981652	1	4974	tags=38%, list=28%, signal=53%
GO_CELL_FATE_COMMITMENT_INVOLVED_IN_FORMATION_OF_PRIMARY_GERM_LAYER	GO_CELL_FATE_COMMITMENT_INVOLVED_IN_FORMATION_OF_PRIMARY_GERM_LAYER	27	-0,21468578	-0,7268934	0,8687873	0,99781126	1	2715	tags=19%, list=15%, signal=22%
GO_CHEMOKINE_RECEPTOR_BINDING	GO_CHEMOKINE_RECEPTOR_BINDING	53	-0,22827253	-0,7267792	0,78691983	0,99744326	1	3976	tags=30%, list=23%, signal=39%
GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	GO_POSITIVE_REGULATION_OF_PROTEIN_DEPOLYMERIZATION	16	-0,25242224	-0,7267121	0,83092785	0,99703217	1	13211	tags=100%, list=75%, signal=396%
GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	GO_VENTRICULAR_CARDIAC_MUSCLE_TISSUE_DEVELOPMENT	43	-0,2102438	-0,7264942	0,9039666	0,9968159	1	4326	tags=30%, list=24%, signal=40%
GO_REGULATION_OF_CELL_KILLING	GO_REGULATION_OF_CELL_KILLING	60	-0,23525052	-0,725999	0,7287449	0,9970278	1	3553	tags=28%, list=20%, signal=35%
GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	GO_CELL_COMMUNICATION_INVOLVED_IN_CARDIAC_CONDUCTION	35	-0,22681783	-0,7259329	0,834	0,99660414	1	3880	tags=31%, list=22%, signal=40%
GO_SULFOTRANSFERASE_ACTIVITY	GO_SULFOTRANSFERASE_ACTIVITY	49	-0,20173422	-0,7252174	0,8796844	0,9971612	1	1847	tags=16%, list=10%, signal=18%
GO_POSITIVE_REGULATION_OF_CELL_ADHESION	GO_POSITIVE_REGULATION_OF_CELL_ADHESION	353	-0,1795082	-0,7247726	0,7903226	0,9973022	1	3529	tags=22%, list=20%, signal=26%
GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	58	-0,20239976	-0,7245733	0,85214007	0,997086	1	2923	tags=21%, list=17%, signal=25%
GO_REGULATION_OF_NEUTROPHIL_CHEMOTAXIS	GO_REGULATION_OF_NEUTROPHIL_CHEMOTAXIS	25	-0,25442865	-0,7245544	0,78483605	0,9966036	1	4344	tags=32%, list=25%, signal=42%
GO_MUCOPOLYSACCHARIDE_METABOLIC_PROCESS	GO_MUCOPOLYSACCHARIDE_METABOLIC_PROCESS	104	-0,1800404	-0,7245289	0,877907	0,99613273	1	1596	tags=13%, list=9%, signal=14%
GO_MODULATION_OF_SYNAPTIC_TRANSMISSION	GO_MODULATION_OF_SYNAPTIC_TRANSMISSION	283	-0,16438453	-0,7244998	0,9664694	0,99565727	1	3154	tags=19%, list=18%, signal=22%
GO_ATRIOVENTRICULAR_VALVE_MORPHOGENESIS	GO_ATRIOVENTRICULAR_VALVE_MORPHOGENESIS	16	-0,26727784	-0,7242573	0,7964775	0,9954826	1	3202	tags=31%, list=18%, signal=38%

GO_OLIGODENDROCYTE_DIFFERENTIATION	GO_OLIGODENDROCYTE_DIFFERENTIATION	57	-0,19494122	-0,723766	0,8727634	0,9957208	1	3854	tags=26%, list=22%, signal=34%
GO_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_CHONDROCYTE_DIFFERENTIATION	17	-0,27041563	-0,7233303	0,82	0,9958608	1	2145	tags=18%, list=12%, signal=20%
GO_CYTOKINE_RECEPTOR_BINDING	GO_CYTOKINE_RECEPTOR_BINDING	227	-0,17431293	-0,7225555	0,9038855	0,99651295	1	2971	tags=18%, list=17%, signal=21%
GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	GO_T_HELPER_1_TYPE_IMMUNE_RESPONSE	18	-0,26392964	-0,7219231	0,7427983	0,9968915	1	4193	tags=33%, list=24%, signal=44%
GO_CYTOKINE_RECEPTOR_ACTIVITY	GO_CYTOKINE_RECEPTOR_ACTIVITY	84	-0,21317849	-0,7219004	0,7796258	0,99640894	1	3311	tags=21%, list=19%, signal=26%
GO_NEGATIVE_REGULATION_OF_OSSIFICATION	GO_NEGATIVE_REGULATION_OF_OSSIFICATION	61	-0,21042894	-0,7218285	0,83935744	0,99599355	1	4115	tags=26%, list=23%, signal=34%
GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	GO_NEGATIVE_REGULATION_OF_PEPTIDE_SECRETION	44	-0,2002698	-0,7213558	0,91568625	0,9961785	1	1288	tags=9%, list=7%, signal=10%
GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	GO_POSITIVE_REGULATION_OF_MESENCHYMAL_CELL_PROLIFERATION	27	-0,22388051	-0,7209249	0,85171103	0,99625957	1	4757	tags=41%, list=27%, signal=56%
GO_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_MAP_KINASE_ACTIVITY	71	-0,17745444	-0,720859	0,9238477	0,99583226	1	2900	tags=20%, list=16%, signal=23%
GO_VESICLE_MEDIATED_TRANSPORT_BETWEEN_ENDOSOMAL_COMPARTMENTS	GO_VESICLE_MEDIATED_TRANSPORT_BETWEEN_ENDOSOMAL_COMPARTMENTS	19	-0,22912806	-0,7196901	0,822314	0,99703383	1	4587	tags=42%, list=26%, signal=57%
GO_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	GO_REGULATION_OF_LEUKOCYTE_APOPTOTIC_PROCESS	75	-0,20814733	-0,7189542	0,8054968	0,99756706	1	1491	tags=15%, list=8%, signal=16%
GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	GO_NEGATIVE_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	92	-0,19197045	-0,7187764	0,80368096	0,9972916	1	2969	tags=18%, list=17%, signal=22%
GO_POSITIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	GO_POSITIVE_REGULATION_OF_VIRAL_RELEASE_FROM_HOST_CELL	15	-0,25827408	-0,7185591	0,8146718	0,9970817	1	3008	tags=27%, list=17%, signal=32%
GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	GO_POSITIVE_REGULATION_OF_CHEMOTAXIS	116	-0,19799061	-0,718487	0,8148148	0,99667346	1	3910	tags=22%, list=22%, signal=29%
GO_CALCIUM_CHANNEL_COMPLEX	GO_CALCIUM_CHANNEL_COMPLEX	53	-0,20652248	-0,7181568	0,8957916	0,9966414	1	4442	tags=34%, list=25%, signal=45%
GO_NUCLEOSIDE_TRANSPORT	GO_NUCLEOSIDE_TRANSPORT	15	-0,24683172	-0,7179771	0,805383	0,99638873	1	1657	tags=20%, list=9%, signal=22%
GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	GO_POSITIVE_REGULATION_OF_PROTEIN_TARGETING_TO_MEMBRANE	15	-0,25230527	-0,7179346	0,8518519	0,99593896	1	4232	tags=47%, list=24%, signal=61%
GO_POTASSIUM_CHANNEL_ACTIVITY	GO_POTASSIUM_CHANNEL_ACTIVITY	105	-0,18289135	-0,7163883	0,934334	0,9977283	1	2701	tags=15%, list=15%, signal=18%
GO_EXOCYST	GO_EXOCYST	15	-0,25920063	-0,7156572	0,8172888	0,9982436	1	3075	tags=27%, list=17%, signal=32%
GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY	GO_UBIQUITIN_LIKE_PROTEIN_SPECIFIC_PROTEASE_ACTIVITY	91	-0,18665077	-0,715615	0,82459676	0,99779147	1	2589	tags=18%, list=15%, signal=20%
GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	GO_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	49	-0,21856017	-0,7152938	0,8263359	0,9977366	1	4242	tags=31%, list=24%, signal=40%
GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	GO_NEGATIVE_REGULATION_OF_LYASE_ACTIVITY	25	-0,22517371	-0,7150599	0,88950276	0,99756235	1	3959	tags=24%, list=22%, signal=31%
GO_DEVELOPMENTAL_PIGMENTATION	GO_DEVELOPMENTAL_PIGMENTATION	35	-0,23255031	-0,7150227	0,84774435	0,99711215	1	4210	tags=37%, list=24%, signal=49%
GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	GO_REGULATION_OF_SMALL_GTPASE_MEDIATED_SIGNAL_TRANSDUCTION	271	-0,17045255	-0,7149	0,87140113	0,9967773	1	1533	tags=11%, list=9%, signal=12%
GO_REGULATION_OF_EXOSOMAL_SECRETION	GO_REGULATION_OF_EXOSOMAL_SECRETION	17	-0,23710684	-0,7145084	0,83168316	0,996808	1	3008	tags=29%, list=17%, signal=35%
GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	GO_POSITIVE_REGULATION_OF_INSULIN_SECRETION	60	-0,17912397	-0,7144532	0,9489195	0,99637985	1	2794	tags=17%, list=16%, signal=20%
GO_MYELOID_CELL_DIFFERENTIATION	GO_MYELOID_CELL_DIFFERENTIATION	180	-0,16961934	-0,7142544	0,9072165	0,9961606	1	968	tags=9%, list=5%, signal=9%
GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	45	-0,20032382	-0,7142398	0,8473896	0,9956745	1	2619	tags=18%, list=15%, signal=21%
GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	GO_CENTRAL_NERVOUS_SYSTEM_NEURON_DIFFERENTIATION	157	-0,17924273	-0,714045	0,95686275	0,9954444	1	3780	tags=26%, list=21%, signal=33%
GO_RUFFLE_ORGANIZATION	GO_RUFFLE_ORGANIZATION	20	-0,23770784	-0,7131375	0,81338745	0,99627894	1	3175	tags=25%, list=18%, signal=30%
GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	GO_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	107	-0,19082801	-0,7126743	0,86507934	0,99641967	1	2715	tags=17%, list=15%, signal=20%
GO_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	GO_REGULATION_OF_CALCIUM_ION_DEPENDENT_EXOCYTOSIS	76	-0,17713664	-0,7124025	0,91468257	0,99630827	1	3069	tags=20%, list=17%, signal=24%
GO_PANCREAS_DEVELOPMENT	GO_PANCREAS_DEVELOPMENT	68	-0,19009523	-0,7118651	0,91085273	0,9965617	1	3994	tags=29%, list=23%, signal=38%
GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	20	-0,24682637	-0,7117609	0,78163266	0,9961958	1	4895	tags=35%, list=28%, signal=48%
GO_REGULATION_OF_CELL_CELL_ADHESION	GO_REGULATION_OF_CELL_CELL_ADHESION	353	-0,17598407	-0,7117193	0,7959596	0,9957526	1	3353	tags=20%, list=19%, signal=25%
GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	GO_PHOSPHOLIPID_TRANSLOCATING_ATPASE_ACTIVITY	16	-0,26555732	-0,7113593	0,824	0,99574393	1	1936	tags=19%, list=11%, signal=21%
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY	50	-0,19729544	-0,7111342	0,87246966	0,9955569	1	2713	tags=18%, list=15%, signal=21%
GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	GO_REGULATION_OF_NEUROTRANSMITTER_LEVELS	177	-0,16080165	-0,7108903	0,9843137	0,99538773	1	2072	tags=12%, list=12%, signal=14%
GO_MICROFILAMENT_MOTOR_ACTIVITY	GO_MICROFILAMENT_MOTOR_ACTIVITY	21	-0,24191467	-0,7094452	0,8556485	0,99684435	1	3136	tags=24%, list=18%, signal=29%
GO_SENSORY_PERCEPTION_OF_TEMPERATURE_STIMULUS	GO_SENSORY_PERCEPTION_OF_TEMPERATURE_STIMULUS	19	-0,2357531	-0,7081364	0,8787879	0,99821925	1	5901	tags=58%, list=33%, signal=87%
GO_CEREBELLAR_CORTEX_DEVELOPMENT	GO_CEREBELLAR_CORTEX_DEVELOPMENT	44	-0,1971293	-0,7078567	0,93503934	0,99807733	1	3136	tags=25%, list=18%, signal=30%
GO_FACE_DEVELOPMENT	GO_FACE_DEVELOPMENT	48	-0,20252125	-0,7077652	0,8562874	0,99770725	1	1873	tags=15%, list=11%, signal=16%
GO_FOREBRAIN_GENERATION_OF_NEURONS	GO_FOREBRAIN_GENERATION_OF_NEURONS	62	-0,19539961	-0,7070099	0,9261364	0,9982031	1	3709	tags=29%, list=21%, signal=37%
GO_REGULATION_OF_SPROUTING_ANGIOGENESIS	GO_REGULATION_OF_SPROUTING_ANGIOGENESIS	27	-0,21913046	-0,7069313	0,8635438	0,99780494	1	4252	tags=33%, list=24%, signal=44%
GO_ADULT_LOCOMOTORY_BEHAVIOR	GO_ADULT_LOCOMOTORY_BEHAVIOR	76	-0,18228072	-0,7065313	0,95542634	0,997834	1	2113	tags=13%, list=12%, signal=15%
GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_BINDING	GO_TRANSCRIPTION_FACTOR_ACTIVITY_RNA_POLYMERASE_II_DISTAL_ENHANCER_SEQUENCE_SPECIFIC_BINDING	79	-0,18077064	-0,7063424	0,9132948	0,99758285	1	4487	tags=35%, list=25%, signal=47%
GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	GO_RESPONSE_TO_TUMOR_NECROSIS_FACTOR	220	-0,16120751	-0,7048342	0,9270833	0,9991338	1	1700	tags=10%, list=10%, signal=11%
GO_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	GO_RESPONSE_TO_TOPOLOGICALLY_INCORRECT_PROTEIN	153	-0,17471333	-0,7047395	0,89183676	0,9987683	1	2326	tags=16%, list=13%, signal=19%
GO_POTASSIUM_CHANNEL_COMPLEX	GO_POTASSIUM_CHANNEL_COMPLEX	82	-0,1861388	-0,7046255	0,9435798	0,9984164	1	2701	tags=16%, list=15%, signal=19%
GO_LEUKOCYTE_MIGRATION	GO_LEUKOCYTE_MIGRATION	250	-0,18470734	-0,7041889	0,82194614	0,9985417	1	2971	tags=18%, list=17%, signal=21%
GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	GO_REGULATION_OF_ALPHA_BETA_T_CELL_DIFFERENTIATION	45	-0,21692796	-0,704167	0,7690722	0,9980683	1	3788	tags=27%, list=21%, signal=34%
GO_REPLACEMENT_OSSIFICATION	GO_REPLACEMENT_OSSIFICATION	25	-0,23822187	-0,7039865	0,82149714	0,9977921	1	2149	tags=16%, list=12%, signal=18%
GO_NEGATIVE_REGULATION_OF_PROTEIN_SECRETION	GO_NEGATIVE_REGULATION_OF_PROTEIN_SECRETION	95	-0,17164846	-0,7033749	0,9271255	0,9980923	1	1491	tags=8%, list=8%, signal=9%

GO_PHOTOTRANSDUCTION_VISIBLE_LIGHT	GO_PHOTOTRANSDUCTION_VISIBLE_LIGHT	18	-0,23378424	-0,7029146	0,86326534	0,9982055	1	2594	tags=22%, list=15%, signal=26%
GO_CELL_JUNCTION_ASSEMBLY	GO_CELL_JUNCTION_ASSEMBLY	125	-0,18000504	-0,7029059	0,85714287	0,99771386	1	2994	tags=21%, list=17%, signal=25%
GO_LENS_FIBER_CELL_DIFFERENTIATION	GO_LENS_FIBER_CELL_DIFFERENTIATION	22	-0,22145148	-0,7017147	0,88588005	0,998804	1	2223	tags=18%, list=13%, signal=21%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_TYROSINE_KINASE_SIGNALING_PATHWAY	482	-0,15459244	-0,701374	0,9665272	0,99878174	1	2759	tags=17%, list=16%, signal=19%
GO_VENTRICULAR_SEPTUM_DEVELOPMENT	GO_VENTRICULAR_SEPTUM_DEVELOPMENT	53	-0,20283893	-0,7002518	0,83466136	0,9997838	1	3202	tags=28%, list=18%, signal=34%
GO_FILOPODIUM	GO_FILOPODIUM	88	-0,17636049	-0,7000155	0,92673266	0,99958473	1	2097	tags=16%, list=12%, signal=18%
GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	GO_NEGATIVE_REGULATION_OF_INTERLEUKIN_1_PRODUCTION	16	-0,2639136	-0,6995945	0,78015566	0,99962044	1	3030	tags=19%, list=17%, signal=23%
GO_POTASSIUM_ION_TRANSPORT	GO_POTASSIUM_ION_TRANSPORT	136	-0,17300096	-0,699303	0,96387833	0,9994728	1	2701	tags=16%, list=15%, signal=19%
GO_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	GO_REGULATION_OF_TRANSFORMING_GROWTH_FACTOR_BETA_PRODUCTION	25	-0,23038895	-0,6992016	0,87866926	0,9990938	1	4252	tags=40%, list=24%, signal=53%
GO_FOREBRAIN_CELL_MIGRATION	GO_FOREBRAIN_CELL_MIGRATION	58	-0,19697043	-0,6988851	0,9082218	0,99898744	1	2524	tags=21%, list=14%, signal=24%
GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_CELL_DEVELOPMENT	443	-0,15493421	-0,6985244	0,98245615	0,9989557	1	3049	tags=19%, list=17%, signal=22%
GO_REGULATION_OF_RHODOPSIN_MEDIATED_SIGNALING_PATHWAY	GO_REGULATION_OF_RHODOPSIN_MEDIATED_SIGNALING_PATHWAY	24	-0,20884535	-0,6978951	0,86904764	0,9992804	1	1545	tags=13%, list=9%, signal=14%
GO_MAGNESIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_MAGNESIUM_ION_TRANSMEMBRANE_TRANSPORT	16	-0,2633641	-0,6970701	0,80594057	0,99987996	1	2983	tags=31%, list=17%, signal=38%
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_FOLD	GO_MORPHOGENESIS_OF_AN_EPITHELIAL_FOLD	15	-0,2542424	-0,6966978	0,9082031	0,999848	1	1395	tags=13%, list=8%, signal=14%
GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	GO_NEGATIVE_REGULATION_OF_SIGNAL_TRANSDUCTION_IN_ABSENCE_OF_LIGAND	31	-0,20393056	-0,6965017	0,89378756	0,99958766	1	4244	tags=26%, list=24%, signal=34%
GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	GO_NEGATIVE_REGULATION_OF_CALCIUM_MEDIATED_SIGNALING	18	-0,2640615	-0,6963241	0,8169014	0,9993068	1	4725	tags=39%, list=27%, signal=53%
GO_PREASSEMBLY_OF_GPI_ANCHOR_IN_ER_MEMBRANE	GO_PREASSEMBLY_OF_GPI_ANCHOR_IN_ER_MEMBRANE	15	-0,25857568	-0,6961102	0,80658436	0,9991082	1	2158	tags=20%, list=12%, signal=23%
GO_OVULATION_CYCLE_PROCESS	GO_OVULATION_CYCLE_PROCESS	79	-0,17328204	-0,6957179	0,97196263	0,9991161	1	2917	tags=19%, list=17%, signal=23%
GO_ADENYLYLTRANSFERASE_ACTIVITY	GO_ADENYLYLTRANSFERASE_ACTIVITY	23	-0,22735573	-0,6949555	0,84031934	0,9996251	1	4494	tags=35%, list=25%, signal=47%
GO_CELL_CELL_ADHERENS_JUNCTION	GO_CELL_CELL_ADHERENS_JUNCTION	50	-0,19357401	-0,6948057	0,9010101	0,9993249	1	4271	tags=30%, list=24%, signal=39%
GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS	GO_PHOSPHATIDYLINOSITOL_3_PHOSPHATE_BIOSYNTHETIC_PROCESS	47	-0,21356682	-0,694779	0,9076305	0,9988558	1	2147	tags=15%, list=12%, signal=17%
GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	GO_POSITIVE_REGULATION_OF_CALCIUM_ION_TRANSPORT_INTO_CYTOSOL	48	-0,19832937	-0,694325	0,8996063	0,9989334	1	3951	tags=31%, list=22%, signal=40%
GO_CARDIAC_ATRIUM_DEVELOPMENT	GO_CARDIAC_ATRIUM_DEVELOPMENT	29	-0,22429754	-0,6943233	0,83908045	0,9984404	1	3202	tags=31%, list=18%, signal=38%
GO_SKELETAL_MUSCLE_CONTRACTION	GO_SKELETAL_MUSCLE_CONTRACTION	31	-0,2087763	-0,6935492	0,9227557	0,99896324	1	4451	tags=32%, list=25%, signal=43%
GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSPORT	37	-0,20235693	-0,69336	0,90873784	0,998707	1	4409	tags=32%, list=25%, signal=43%
GO_DENDRITIC_CELL_CHEMOTAXIS	GO_DENDRITIC_CELL_CHEMOTAXIS	16	-0,28868246	-0,6930072	0,79012346	0,99864644	1	3788	tags=31%, list=21%, signal=40%
GO_CARDIAC_MYOFIBRIL_ASSEMBLY	GO_CARDIAC_MYOFIBRIL_ASSEMBLY	15	-0,25569615	-0,6923319	0,875502	0,99895656	1	4046	tags=40%, list=23%, signal=52%
GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	GO_DEFENSE_RESPONSE_TO_OTHER_ORGANISM	398	-0,15602012	-0,6921247	0,95983934	0,9987223	1	4637	tags=30%, list=26%, signal=40%
GO_NEGATIVE_REGULATION_OF_AUTOPHAGY	GO_NEGATIVE_REGULATION_OF_AUTOPHAGY	51	-0,1780788	-0,6917468	0,9133065	0,9987197	1	3330	tags=24%, list=19%, signal=29%
GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_SODIUM_ION_TRANSMEMBRANE_TRANSPORT	81	-0,1884883	-0,6914161	0,95679015	0,998649	1	2142	tags=12%, list=12%, signal=14%
GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	GO_REGULATION_OF_SYNAPTIC_TRANSMISSION_GLUTAMATERGIC	48	-0,20220453	-0,6913365	0,93203884	0,9982576	1	2299	tags=17%, list=13%, signal=19%
GO_TRANSPORT_VESICLE_MEMBRANE	GO_TRANSPORT_VESICLE_MEMBRANE	140	-0,16301982	-0,6889841	0,9591002	1	1	3012	tags=18%, list=17%, signal=21%
GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	GO_CELL_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	189	-0,17846853	-0,6884123	0,8704062	1	1	3878	tags=23%, list=22%, signal=29%
GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_INVOLVED_IN_CELLULAR_RESPONSE_TO_CHEMICAL_STIMULUS	GO_POSITIVE_REGULATION_OF_TRANSCRIPTION_FROM_RNA_POLYMERASE_II_PROMOTER_INVOLVED_IN_CELLULAR_RESPONSE_TO_CHEMICAL_STIMULUS	25	-0,2126079	-0,6881992	0,8853755	1	1	2818	tags=24%, list=16%, signal=29%
GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	GO_REGULATION_OF_MONONUCLEAR_CELL_MIGRATION	15	-0,27823386	-0,6881931	0,7991803	1	1	6288	tags=60%, list=36%, signal=93%
GO_EXTRACELLULAR_MATRIX_DISASSEMBLY	GO_EXTRACELLULAR_MATRIX_DISASSEMBLY	71	-0,2055831	-0,6878387	0,91050583	1	1	3106	tags=23%, list=18%, signal=27%
GO_SENSORY_PERCEPTION	GO_SENSORY_PERCEPTION	446	-0,14468817	-0,6874489	1	1	1	3266	tags=17%, list=18%, signal=20%
GO_CARDIAC_VENTRICLE_DEVELOPMENT	GO_CARDIAC_VENTRICLE_DEVELOPMENT	102	-0,18413202	-0,6872915	0,9271653	0,9998485	1	3202	tags=24%, list=18%, signal=29%
GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	GO_PROTEIN_EXIT_FROM_ENDOPLASMIC_RETICULUM	18	-0,26286605	-0,685831	0,7944112	1	1	3768	tags=39%, list=21%, signal=49%
GO_REGULATION_OF_STEROID_HORMONE_SECRETION	GO_REGULATION_OF_STEROID_HORMONE_SECRETION	20	-0,22744337	-0,6857508	0,93762994	1	1	11570	tags=95%, list=65%, signal=275%
GO_HINDBRAIN_DEVELOPMENT	GO_HINDBRAIN_DEVELOPMENT	130	-0,16741681	-0,6843341	0,974359	1	1	2875	tags=19%, list=16%, signal=23%
GO_REGULATION_OF_TOR_SIGNALING	GO_REGULATION_OF_TOR_SIGNALING	63	-0,17450236	-0,6841559	0,935743	1	1	3588	tags=25%, list=20%, signal=32%
GO_SKELETAL_SYSTEM_DEVELOPMENT	GO_SKELETAL_SYSTEM_DEVELOPMENT	427	-0,16128215	-0,6841084	0,95922333	1	1	2793	tags=18%, list=16%, signal=20%
GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	GO_HOMEOSTASIS_OF_NUMBER_OF_CELLS	167	-0,1608082	-0,683227	0,9450317	1	1	4919	tags=35%, list=28%, signal=48%
GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_NEURON_DIFFERENTIATION	290	-0,15632746	-0,6827092	0,9785156	1	1	3171	tags=19%, list=18%, signal=22%
GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	GO_REGULATION_OF_T_CELL_APOPTOTIC_PROCESS	31	-0,22011535	-0,6826606	0,83613443	1	1	960	tags=10%, list=5%, signal=10%
GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	GO_REGULATION_OF_T_HELPER_1_TYPE_IMMUNE_RESPONSE	21	-0,24923079	-0,6824248	0,7979592	1	1	3529	tags=24%, list=20%, signal=30%
GO_REGULATION_OF_JUN_KINASE_ACTIVITY	GO_REGULATION_OF_JUN_KINASE_ACTIVITY	77	-0,1767	-0,6815077	0,9304175	1	1	2961	tags=23%, list=17%, signal=28%
GO_PROTEIN_TARGETING_TO_PLASMA_MEMBRANE	GO_PROTEIN_TARGETING_TO_PLASMA_MEMBRANE	22	-0,24677373	-0,6810501	0,8452611	1	1	3069	tags=27%, list=17%, signal=33%
GO_PEPTIDYL_TYROSINE_MODIFICATION	GO_PEPTIDYL_TYROSINE_MODIFICATION	181	-0,16675399	-0,6807692	0,9437751	1	1	4843	tags=33%, list=27%, signal=45%
GO_REGULATION_OF_STEM_CELL_POPULATION_MAINTENANCE	GO_REGULATION_OF_STEM_CELL_POPULATION_MAINTENANCE	17	-0,24026704	-0,6807389	0,86336637	1	1	1138	tags=12%, list=6%, signal=13%
GO_CALCIUM_ION_IMPORT	GO_CALCIUM_ION_IMPORT	61	-0,18684304	-0,6804404	0,92433536	1	1	5713	tags=48%, list=32%, signal=70%

GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	GO_DEFENSE_RESPONSE_TO_GRAM_POSITIVE_BACTERIUM	65	-0,18525186	-0,6802264	0,9424603	1	1	3303	tags=22%, list=19%, signal=26%
GO_CATION_CATION_ANTIPORTER_ACTIVITY	GO_CATION_CATION_ANTIPORTER_ACTIVITY	23	-0,22396605	-0,6801673	0,9259259	1	1	2286	tags=17%, list=13%, signal=20%
GO_REGULATION_OF_B_CELL_DIFFERENTIATION	GO_REGULATION_OF_B_CELL_DIFFERENTIATION	21	-0,25551948	-0,6789223	0,772	1	1	4209	tags=29%, list=24%, signal=37%
GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	GO_ACTIN_FILAMENT_BUNDLE_ORGANIZATION	44	-0,1872116	-0,6780238	0,892	1	1	2674	tags=18%, list=15%, signal=21%
GO_MEMBRANE_BUDDING	GO_MEMBRANE_BUDDING	111	-0,16651392	-0,676774	0,9109731	1	1	5031	tags=40%, list=28%, signal=55%
GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	GO_PROTEIN_TYROSINE_KINASE_ACTIVITY	172	-0,16465512	-0,67637	0,96626985	1	1	4635	tags=31%, list=26%, signal=42%
GO_SUBPALLIUM_DEVELOPMENT	GO_SUBPALLIUM_DEVELOPMENT	21	-0,22378914	-0,674628	0,8913934	1	1	5185	tags=48%, list=29%, signal=67%
GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	GO_REGULATION_OF_VIRAL_ENTRY_INTO_HOST_CELL	25	-0,21866806	-0,6737165	0,8782435	1	1	4148	tags=32%, list=23%, signal=42%
GO_PROTEIN_TARGETING_TO_MITOCHONDRION	GO_PROTEIN_TARGETING_TO_MITOCHONDRION	46	-0,22225243	-0,6734644	0,798768	1	1	842	tags=9%, list=5%, signal=9%
GO_MESENCHYME_MORPHOGENESIS	GO_MESENCHYME_MORPHOGENESIS	38	-0,21097884	-0,6733541	0,8747554	1	1	4744	tags=34%, list=27%, signal=47%
GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	GO_REGULATION_OF_MUSCLE_CELL_DIFFERENTIATION	140	-0,15582249	-0,6732631	0,9765166	1	1	3250	tags=23%, list=18%, signal=28%
GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_REGULATORY_REGION_SEQUENCE_SPECIFIC_BINDING	GO_TRANSCRIPTIONAL_REPRESSOR_ACTIVITY_RNA_POLYMERASE_II_TRANSCRIPTION_REGULATORY_REGION_SEQUENCE_SPECIFIC_BINDING	155	-0,16269754	-0,6731076	0,9685658	1	1	2791	tags=17%, list=16%, signal=20%
GO_NODE_OF_RANVIER	GO_NODE_OF_RANVIER	15	-0,23761114	-0,6729881	0,90457255	1	1	484	tags=7%, list=3%, signal=7%
GO_CELLULAR_SODIUM_ION_HOMEOSTASIS	GO_CELLULAR_SODIUM_ION_HOMEOSTASIS	19	-0,22292836	-0,6726845	0,8960499	1	1	4465	tags=37%, list=25%, signal=49%
GO_DIENCEPHALON_DEVELOPMENT	GO_DIENCEPHALON_DEVELOPMENT	70	-0,18121085	-0,6715293	0,9672447	1	1	2875	tags=21%, list=16%, signal=25%
GO_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	GO_REGULATION_OF_MACROPHAGE_DIFFERENTIATION	20	-0,2214585	-0,6714135	0,89314514	1	1	3413	tags=25%, list=19%, signal=31%
GO_BONE_GROWTH	GO_BONE_GROWTH	20	-0,25871548	-0,6711738	0,8767677	1	1	4843	tags=35%, list=27%, signal=48%
GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	GO_FATTY_ACID_DERIVATIVE_BIOSYNTHETIC_PROCESS	41	-0,1936225	-0,6706479	0,91434264	1	1	3192	tags=22%, list=18%, signal=27%
GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_MYELOID_LEUKOCYTE_DIFFERENTIATION	41	-0,19866043	-0,670328	0,89349115	1	1	3413	tags=22%, list=19%, signal=27%
GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	GO_CELLULAR_PROTEIN_COMPLEX_DISASSEMBLY	119	-0,20952718	-0,6701189	0,75670105	1	1	2755	tags=20%, list=16%, signal=24%
GO_SCHWANN_CELL_DEVELOPMENT	GO_SCHWANN_CELL_DEVELOPMENT	25	-0,20630416	-0,6695255	0,8925144	1	1	4237	tags=32%, list=24%, signal=42%
GO_SYNAPTIC_TRANSMISSION_CHOLINERGIC	GO_SYNAPTIC_TRANSMISSION_CHOLINERGIC	34	-0,20730118	-0,668897	0,9229249	1	1	3425	tags=26%, list=19%, signal=33%
GO_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	GO_REGULATION_OF_INTERFERON_GAMMA_PRODUCTION	89	-0,20159061	-0,6688746	0,7962963	1	1	4911	tags=36%, list=28%, signal=50%
GO_REGULATION_OF_BEHAVIOR	GO_REGULATION_OF_BEHAVIOR	55	-0,18741772	-0,6674384	0,95218295	1	1	847	tags=9%, list=5%, signal=10%
GO_MEMBRANE_BIOGENESIS	GO_MEMBRANE_BIOGENESIS	29	-0,19522537	-0,667118	0,9072165	1	1	5011	tags=41%, list=28%, signal=58%
GO_EMBRYONIC_HEART_TUBE_MORPHOGENESIS	GO_EMBRYONIC_HEART_TUBE_MORPHOGENESIS	59	-0,1848839	-0,6667235	0,93773586	1	1	3187	tags=24%, list=18%, signal=29%
GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	GO_NUCLEOTIDE_EXCISION_REPAIR_DNA_DUPLEX_UNWINDING	22	-0,21787041	-0,6661484	0,8557505	1	1	2654	tags=27%, list=15%, signal=32%
GO_SYNAPSE_ORGANIZATION	GO_SYNAPSE_ORGANIZATION	141	-0,16732395	-0,6659201	0,95284873	1	1	5073	tags=30%, list=29%, signal=42%
GO_COGNITION	GO_COGNITION	231	-0,15624912	-0,6658555	0,9859438	1	1	2999	tags=18%, list=17%, signal=21%
GO_LEUKOCYTE_DIFFERENTIATION	GO_LEUKOCYTE_DIFFERENTIATION	266	-0,17603503	-0,664955	0,845679	1	1	4213	tags=29%, list=24%, signal=37%
GO_AMEBOIDAL_TYPE_CELL_MIGRATION	GO_AMEBOIDAL_TYPE_CELL_MIGRATION	148	-0,16400403	-0,664924	0,9519038	1	1	3078	tags=21%, list=17%, signal=25%
GO_MITOCHONDRION_MORPHOGENESIS	GO_MITOCHONDRION_MORPHOGENESIS	19	-0,22832194	-0,664552	0,86270493	1	1	3830	tags=37%, list=22%, signal=47%
GO_ACETYLCHOLINE_RECEPTOR_ACTIVITY	GO_ACETYLCHOLINE_RECEPTOR_ACTIVITY	28	-0,21659733	-0,664326	0,9387352	1	1	3425	tags=29%, list=19%, signal=35%
GO_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	GO_GOLGI_TO_PLASMA_MEMBRANE_PROTEIN_TRANSPORT	26	-0,1972753	-0,6638045	0,91382766	1	1	5638	tags=46%, list=32%, signal=68%
GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO_LYMPHOCYTE_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	79	-0,18419619	-0,6637973	0,8722555	1	1	4213	tags=32%, list=24%, signal=41%
GO_MATURE_B_CELL_DIFFERENTIATION	GO_MATURE_B_CELL_DIFFERENTIATION	17	-0,23880506	-0,6636438	0,8888889	1	1	4213	tags=29%, list=24%, signal=39%
GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_TRANSPOSING_S_S_BONDS	GO_INTRAMOLECULAR_OXIDOREDUCTASE_ACTIVITY_TRANSPOSING_S_S_BONDS	20	-0,2317095	-0,663107	0,8629857	1	1	2713	tags=20%, list=15%, signal=24%
GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	GO_NEGATIVE_REGULATION_OF_NEURON_APOPTOTIC_PROCESS	127	-0,162954	-0,6629553	0,97900766	1	1	2971	tags=19%, list=17%, signal=23%
GO_LYMPHOCYTE_DIFFERENTIATION	GO_LYMPHOCYTE_DIFFERENTIATION	186	-0,18421075	-0,6629437	0,8145161	1	1	4213	tags=29%, list=24%, signal=38%
GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	GO_ESTABLISHMENT_OF_PROTEIN_LOCALIZATION_TO_PLASMA_MEMBRANE	88	-0,1654586	-0,6619564	0,95201534	1	1	4874	tags=34%, list=28%, signal=47%
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_CONTRACTION	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_CONTRACTION	27	-0,20917895	-0,6608141	0,9116466	1	1	4442	tags=37%, list=25%, signal=49%
GO_BLOOD_VESSEL_REMODELING	GO_BLOOD_VESSEL_REMODELING	31	-0,21578522	-0,6607101	0,872549	1	1	2783	tags=19%, list=16%, signal=23%
GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	GO_POSITIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	30	-0,21749389	-0,6600363	0,88293654	1	1	3910	tags=27%, list=22%, signal=34%
GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	GO_RETINA_MORPHOGENESIS_IN_CAMERA_TYPE_EYE	43	-0,19411029	-0,6595333	0,94262296	1	1	3674	tags=23%, list=21%, signal=29%
GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	GO_SIGNAL_TRANSDUCTION_BY_PROTEIN_PHOSPHORYLATION	389	-0,13420433	-0,6587372	0,994012	1	1	3547	tags=20%, list=20%, signal=24%
GO_PROTEIN_K48_LINKED_DEUBIQUITINATION	GO_PROTEIN_K48_LINKED_DEUBIQUITINATION	19	-0,22836472	-0,6584792	0,8530021	1	1	5129	tags=42%, list=29%, signal=59%
GO_NEURON_PROJECTION_EXTENSION	GO_NEURON_PROJECTION_EXTENSION	48	-0,192636	-0,6566092	0,91634244	1	1	1200	tags=10%, list=7%, signal=11%
GO_AMIDE_TRANSPORT	GO_AMIDE_TRANSPORT	87	-0,15503313	-0,6563665	0,98214287	1	1	3584	tags=22%, list=20%, signal=27%
GO_MULTICELLULAR_ORGANISM_METABOLIC_PROCESS	GO_MULTICELLULAR_ORGANISM_METABOLIC_PROCESS	84	-0,19650723	-0,6560932	0,88735175	1	1	3242	tags=21%, list=18%, signal=26%
GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	GO_PROTEIN_PHOSPHORYLATED_AMINO_ACID_BINDING	24	-0,20535448	-0,6560481	0,8863636	1	1	4941	tags=46%, list=28%, signal=64%
GO_MULTI_ORGANISM_BEHAVIOR	GO_MULTI_ORGANISM_BEHAVIOR	70	-0,16545896	-0,6559129	0,97604793	1	1	3078	tags=19%, list=17%, signal=22%
GO_DEFENSE_RESPONSE_TO_VIRUS	GO_DEFENSE_RESPONSE_TO_VIRUS	139	-0,17199393	-0,6552427	0,86512524	1	1	4978	tags=36%, list=28%, signal=50%

GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_POSITIVE_REGULATION_OF_POTASSIUM_ION_TRANSMEMBRANE_TRANSPORT	26	-0,20133299	-0,6544233	0,9466403	1	1	4409	tags=31%, list=25%, signal=41%
GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	GO_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	119	-0,15971698	-0,654173	0,96257794	1	1	2254	tags=14%, list=13%, signal=16%
GO_REGULATION_OF_ENDOCRINE_PROCESS	GO_REGULATION_OF_ENDOCRINE_PROCESS	47	-0,1781133	-0,6518518	0,9593496	1	1	14528	tags=100%, list=82%, signal=562%
GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	GO_CHONDROITIN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	42	-0,18773583	-0,6516845	0,9508841	1	1	4090	tags=26%, list=23%, signal=34%
GO_GLIOGENESIS	GO_GLIOGENESIS	166	-0,15041342	-0,6515417	0,97868216	1	1	1611	tags=11%, list=9%, signal=12%
GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	GO_PERIPHERAL_NERVOUS_SYSTEM_DEVELOPMENT	64	-0,17193265	-0,6504657	0,95238096	1	1	4358	tags=31%, list=25%, signal=41%
GO_KIDNEY_MESENCHYME_DEVELOPMENT	GO_KIDNEY_MESENCHYME_DEVELOPMENT	17	-0,22989102	-0,6490502	0,889336	1	1	2818	tags=24%, list=16%, signal=28%
GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	GO_REGULATION_OF_STEM_CELL_DIFFERENTIATION	107	-0,17074706	-0,6484053	0,9357977	1	1	2834	tags=19%, list=16%, signal=22%
GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	GO_EMBRYONIC_HEART_TUBE_DEVELOPMENT	69	-0,17653674	-0,6481422	0,9550781	1	1	3187	tags=22%, list=18%, signal=26%
GO_SUPEROXIDE_METABOLIC_PROCESS	GO_SUPEROXIDE_METABOLIC_PROCESS	29	-0,19819449	-0,6479627	0,94129556	1	1	945	tags=10%, list=5%, signal=11%
GO_MAIN_AXON	GO_MAIN_AXON	57	-0,174381	-0,6479319	0,9587426	1	1	2771	tags=16%, list=16%, signal=19%
GO_VACUOLE_ORGANIZATION	GO_VACUOLE_ORGANIZATION	156	-0,14884757	-0,6473645	0,9756098	1	1	3275	tags=20%, list=19%, signal=24%
GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	GO_REGULATION_OF_TUMOR_NECROSIS_FACTOR_SUPERFAMILY_CYTOKINE_PRODUCTION	97	-0,18193704	-0,6467196	0,88372093	1	1	3550	tags=24%, list=20%, signal=30%
GO_STRIATED_MUSCLE_CONTRACTION	GO_STRIATED_MUSCLE_CONTRACTION	92	-0,16713616	-0,6461598	0,9776876	1	1	4451	tags=28%, list=25%, signal=38%
GO_CATION_CHANNEL_ACTIVITY	GO_CATION_CHANNEL_ACTIVITY	263	-0,1553339	-0,6458716	0,99201596	1	1	3572	tags=20%, list=20%, signal=25%
GO_REGULATION_OF_THE_FORCE_OF_HEART_CONTRACTION	GO_REGULATION_OF_THE_FORCE_OF_HEART_CONTRACTION	27	-0,21219383	-0,6454585	0,9586777	1	1	3675	tags=22%, list=21%, signal=28%
GO_ADAPTATION_OF_SIGNALING_PATHWAY	GO_ADAPTATION_OF_SIGNALING_PATHWAY	18	-0,21599029	-0,6452428	0,90981966	1	1	1639	tags=17%, list=9%, signal=18%
GO_NEURONAL_ACTION_POTENTIAL	GO_NEURONAL_ACTION_POTENTIAL	25	-0,22980335	-0,6447338	0,91182363	1	1	3154	tags=24%, list=18%, signal=29%
GO_CELL_CHEMOTAXIS	GO_CELL_CHEMOTAXIS	156	-0,18006423	-0,6442335	0,89855075	1	1	3916	tags=25%, list=22%, signal=32%
GO_ACROSOMAL_MEMBRANE	GO_ACROSOMAL_MEMBRANE	18	-0,21043016	-0,6420724	0,93359375	1	1	2233	tags=17%, list=13%, signal=19%
GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	GO_POSITIVE_REGULATION_OF_NEURON_PROJECTION_DEVELOPMENT	224	-0,14880118	-0,6413049	0,98613864	1	1	3232	tags=18%, list=18%, signal=22%
GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	GO_REGULATION_OF_DEVELOPMENTAL_GROWTH	270	-0,1452275	-0,6413041	0,9961759	1	1	2769	tags=16%, list=16%, signal=18%
GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	GO_REGULATION_OF_CELLULAR_AMINE_METABOLIC_PROCESS	85	-0,18884872	-0,6411412	0,87090164	1	1	2265	tags=15%, list=13%, signal=17%
GO_POSITIVE_REGULATION_OF_HEART_CONTRACTION	GO_POSITIVE_REGULATION_OF_HEART_CONTRACTION	35	-0,18261655	-0,64098	0,9554656	1	1	3202	tags=20%, list=18%, signal=24%
GO_FEEDING_BEHAVIOR	GO_FEEDING_BEHAVIOR	75	-0,17721102	-0,6406514	0,99230766	1	1	2932	tags=17%, list=17%, signal=21%
GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	GO_REGULATION_OF_CARDIAC_MUSCLE_CELL_ACTION_POTENTIAL	18	-0,22153562	-0,6406414	0,9251968	1	1	5345	tags=50%, list=30%, signal=72%
GO_MUSCLE_FIBER_DEVELOPMENT	GO_MUSCLE_FIBER_DEVELOPMENT	38	-0,17662074	-0,639666	0,96545106	1	1	3782	tags=29%, list=21%, signal=37%
GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	GO_PHOSPHATIDYLINOSITOL_BIOSYNTHETIC_PROCESS	117	-0,1533484	-0,6394678	0,98418975	1	1	2442	tags=16%, list=14%, signal=19%
GO_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	GO_REGULATION_OF_GRANULOCYTE_DIFFERENTIATION	15	-0,22147308	-0,6385672	0,9029703	1	1	13757	tags=100%, list=78%, signal=452%
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX	46	-0,21574372	-0,6363185	0,8181818	1	1	4676	tags=35%, list=26%, signal=47%
GO_LEUKOCYTE_DEGRANULATION	GO_LEUKOCYTE_DEGRANULATION	29	-0,21013835	-0,6356418	0,89858013	1	1	13960	tags=100%, list=79%, signal=476%
GO_LYTIC_VACUOLE_ORGANIZATION	GO_LYTIC_VACUOLE_ORGANIZATION	50	-0,16627996	-0,6351594	0,94409937	1	1	3227	tags=22%, list=18%, signal=27%
GO_PLATELET_AGGREGATION	GO_PLATELET_AGGREGATION	38	-0,20197825	-0,6349491	0,90020365	1	1	2511	tags=18%, list=14%, signal=21%
GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	GO_TRANSMEMBRANE_RECEPTOR_PROTEIN_PHOSPHATASE_ACTIVITY	17	-0,23314786	-0,6333208	0,9158513	1	1	106	tags=6%, list=1%, signal=6%
GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	GO_REGULATION_OF_LYMPHOCYTE_MIGRATION	36	-0,21188249	-0,6332617	0,86530614	1	1	3082	tags=22%, list=17%, signal=27%
GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	GO_NEGATIVE_REGULATION_OF_SMOOTH_MUSCLE_CELL_MIGRATION	16	-0,2493714	-0,6325891	0,87649405	1	1	4242	tags=31%, list=24%, signal=41%
GO_CYTOKINE_PRODUCTION	GO_CYTOKINE_PRODUCTION	112	-0,17193978	-0,6325033	0,91735536	1	1	3894	tags=25%, list=22%, signal=32%
GO_ENDODERM_FORMATION	GO_ENDODERM_FORMATION	49	-0,18989931	-0,6318301	0,9230769	1	1	917	tags=10%, list=5%, signal=11%
GO_PRENYLTRANSFERASE_ACTIVITY	GO_PRENYLTRANSFERASE_ACTIVITY	15	-0,22310105	-0,6309031	0,92622954	1	1	3805	tags=33%, list=22%, signal=42%
GO_GROWTH_FACTOR_ACTIVITY	GO_GROWTH_FACTOR_ACTIVITY	144	-0,15952814	-0,6299132	0,9921414	1	1	1139	tags=8%, list=6%, signal=9%
GO_OSSIFICATION	GO_OSSIFICATION	241	-0,15278997	-0,6286455	0,996124	1	1	3246	tags=19%, list=18%, signal=23%
GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	GO_REGULATION_OF_HOMOTYPIC_CELL_CELL_ADHESION	283	-0,16498294	-0,6276082	0,8783505	1	1	3353	tags=20%, list=19%, signal=24%
GO_MYOSIN_V_BINDING	GO_MYOSIN_V_BINDING	17	-0,21742953	-0,6272467	0,9009709	1	1	1124	tags=12%, list=6%, signal=13%
GO_INOSITOL_LIPID_MEDIATED_SIGNALING	GO_INOSITOL_LIPID_MEDIATED_SIGNALING	113	-0,16008282	-0,6265641	0,9781746	1	1	4645	tags=30%, list=26%, signal=41%
GO_B_CELL_PROLIFERATION	GO_B_CELL_PROLIFERATION	19	-0,26062414	-0,6262472	0,8326613	1	1	2922	tags=32%, list=17%, signal=38%
GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	GO_NEGATIVE_REGULATION_OF_INNATE_IMMUNE_RESPONSE	36	-0,19585203	-0,6262453	0,9323467	1	1	1145	tags=8%, list=6%, signal=9%
GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	GO_PURINERGIC_NUCLEOTIDE_RECEPTOR_SIGNALING_PATHWAY	22	-0,217155	-0,6249966	0,932	1	1	3959	tags=36%, list=22%, signal=47%
GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_OSTEOCLAST_DIFFERENTIATION	22	-0,2202438	-0,6247936	0,8997996	1	1	6259	tags=55%, list=35%, signal=84%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_CYTOKINE_STIMULUS	40	-0,18047997	-0,6237598	0,96311474	1	1	6361	tags=60%, list=36%, signal=94%
GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	GO_MEMBRANE_DEPOLARIZATION_DURING_ACTION_POTENTIAL	37	-0,19325764	-0,6235266	0,94827586	1	1	1787	tags=11%, list=10%, signal=12%
GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	GO_NEGATIVE_REGULATION_OF_AMINE_TRANSPORT	25	-0,21410874	-0,6223958	0,9593496	1	1	559	tags=8%, list=3%, signal=8%
GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	GO_GLANDULAR_EPITHELIAL_CELL_DEVELOPMENT	17	-0,22145745	-0,6218268	0,9171717	1	1	4796	tags=41%, list=27%, signal=56%
GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	GO_NEGATIVE_REGULATION_OF_T_CELL_RECEPTOR_SIGNALING_PATHWAY	16	-0,22159897	-0,6214641	0,9153226	1	1	13755	tags=100%, list=78%, signal=451%

GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	GO_NEGATIVE_REGULATION_OF_B_CELL_ACTIVATION	30	-0,20185696	-0,6208507	0,8953975	1	1	894	tags=10%, list=5%, signal=11%
GO_REGULATION_OF_T_CELL_DIFFERENTIATION	GO_REGULATION_OF_T_CELL_DIFFERENTIATION	97	-0,16711633	-0,6198865	0,89387757	1	1	3529	tags=22%, list=20%, signal=27%
GO_RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	GO_RHO_GUANYL_NUCLEOTIDE_EXCHANGE_FACTOR_ACTIVITY	75	-0,17814387	-0,619347	0,9142857	1	1	4237	tags=29%, list=24%, signal=38%
GO_LUNG_ALVEOLUS_DEVELOPMENT	GO_LUNG_ALVEOLUS_DEVELOPMENT	40	-0,19085604	-0,618768	0,9359699	1	1	4068	tags=28%, list=23%, signal=36%
GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	GO_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	489	-0,14546323	-0,61657	1	1	1	3236	tags=18%, list=18%, signal=22%
GO_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	GO_ANDROGEN_RECEPTOR_SIGNALING_PATHWAY	40	-0,17991927	-0,6164467	0,9161677	1	1	1747	tags=15%, list=10%, signal=17%
GO_CALCIUM_ION_IMPORT_INTO_CYTOSOL	GO_CALCIUM_ION_IMPORT_INTO_CYTOSOL	41	-0,18912517	-0,6156836	0,942029	1	1	5700	tags=51%, list=32%, signal=75%
GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	GO_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	92	-0,18129642	-0,6155201	0,9389474	1	1	3529	tags=22%, list=20%, signal=27%
GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	GO_G_PROTEIN_COUPLED_RECEPTOR_ACTIVITY	343	-0,14716206	-0,6152293	0,9859438	1	1	3911	tags=22%, list=22%, signal=28%
GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	GO_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	31	-0,17919746	-0,6151464	0,957115	1	1	6517	tags=52%, list=37%, signal=82%
GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	GO_REGULATION_OF_DEFENSE_RESPONSE_TO_VIRUS_BY_VIRUS	29	-0,20540452	-0,6148818	0,9035433	1	1	2808	tags=17%, list=16%, signal=20%
GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	GO_NEGATIVE_REGULATION_OF_RESPONSE_TO_OXIDATIVE_STRESS	32	-0,17287832	-0,6131751	0,96606785	1	1	2081	tags=16%, list=12%, signal=18%
GO_LEUKOCYTE_HOMEOSTASIS	GO_LEUKOCYTE_HOMEOSTASIS	60	-0,17281601	-0,6126041	0,94887525	1	1	5336	tags=40%, list=30%, signal=57%
GO_SINGLE_ORGANISM_CELL_ADHESION	GO_SINGLE_ORGANISM_CELL_ADHESION	425	-0,14940467	-0,6107675	0,96385545	1	1	4096	tags=24%, list=23%, signal=31%
GO_CYTOKINE_ACTIVITY	GO_CYTOKINE_ACTIVITY	177	-0,16015777	-0,6094791	0,98770493	1	1	4024	tags=24%, list=23%, signal=31%
GO_CADHERIN_BINDING	GO_CADHERIN_BINDING	28	-0,19370249	-0,6092702	0,93653846	1	1	4232	tags=36%, list=24%, signal=47%
GO_PROTEIN_SECRETION	GO_PROTEIN_SECRETION	106	-0,14715153	-0,6069813	0,99147123	1	1	4008	tags=24%, list=23%, signal=30%
GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	GO_REGULATION_OF_SYNAPSE_STRUCTURE_OR_ACTIVITY	216	-0,14147288	-0,6062319	0,9980159	1	1	3154	tags=18%, list=18%, signal=21%
GO_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	GO_BRANCHING_INVOLVED_IN_URETERIC_BUD_MORPHOGENESIS	44	-0,18084009	-0,6047942	0,9609375	1	1	2818	tags=16%, list=16%, signal=19%
GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	GO_NEGATIVE_REGULATION_OF_OSTEOBLAST_DIFFERENTIATION	37	-0,19182356	-0,6047443	0,9458918	1	1	4796	tags=27%, list=27%, signal=37%
GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	GO_CALCIUM_ION_TRANSMEMBRANE_TRANSPORT	144	-0,15051389	-0,6038994	0,9979839	1	1	4066	tags=26%, list=23%, signal=34%
GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	GO_CELLULAR_RESPONSE_TO_RETINOIC_ACID	59	-0,16211767	-0,6032075	0,97415507	1	1	4962	tags=32%, list=28%, signal=45%
GO_LIPID_TRANSLOCATION	GO_LIPID_TRANSLOCATION	21	-0,20882705	-0,6021119	0,9305556	1	1	3682	tags=29%, list=21%, signal=36%
GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	GO_MORPHOGENESIS_OF_AN_EPITHELIAL_SHEET	40	-0,17996918	-0,6020765	0,96259844	1	1	3187	tags=23%, list=18%, signal=27%
GO_POTASSIUM_ION_HOMEOSTASIS	GO_POTASSIUM_ION_HOMEOSTASIS	18	-0,21315466	-0,6017033	0,96516395	1	1	4406	tags=33%, list=25%, signal=44%
GO_VENTRAL_SPINAL_CORD_INTERNEURON_DIFFERENTIATION	GO_VENTRAL_SPINAL_CORD_INTERNEURON_DIFFERENTIATION	16	-0,22320563	-0,601516	0,973025	1	1	4591	tags=38%, list=26%, signal=51%
GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_CELL_MORPHOGENESIS_INVOLVED_IN_DIFFERENTIATION	158	-0,14522856	-0,6008517	0,984252	1	1	3049	tags=18%, list=17%, signal=21%
GO_FOREBRAIN_NEURON_DEVELOPMENT	GO_FOREBRAIN_NEURON_DEVELOPMENT	34	-0,18662557	-0,600381	0,986692	1	1	3709	tags=29%, list=21%, signal=37%
GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	GO_NEGATIVE_REGULATION_OF_MULTI_ORGANISM_PROCESS	137	-0,1482571	-0,5998592	0,97637796	1	1	4853	tags=31%, list=27%, signal=43%
GO_NEURAL_TUBE_PATTERNING	GO_NEURAL_TUBE_PATTERNING	32	-0,18518026	-0,5982376	0,97669905	1	1	3445	tags=22%, list=20%, signal=27%
GO_AMIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	GO_AMIDE_TRANSMEMBRANE_TRANSPORTER_ACTIVITY	18	-0,20360912	-0,5979324	0,9578313	1	1	1720	tags=17%, list=10%, signal=18%
GO_REGULATION_OF_CIRCADIAN_SLEEP_WAKE_CYCLE	GO_REGULATION_OF_CIRCADIAN_SLEEP_WAKE_CYCLE	20	-0,20278253	-0,5977846	0,95652175	1	1	1472	tags=10%, list=8%, signal=11%
GO_NITRIC_OXIDE_SYNTHASE_BINDING	GO_NITRIC_OXIDE_SYNTHASE_BINDING	18	-0,20096235	-0,5976911	0,9611452	1	1	4597	tags=28%, list=26%, signal=38%
GO_RESPONSE_TO_INTERFERON_ALPHA	GO_RESPONSE_TO_INTERFERON_ALPHA	20	-0,22918522	-0,5949689	0,8910891	1	1	4852	tags=45%, list=27%, signal=62%
GO_LEUKOCYTE_CELL_CELL_ADHESION	GO_LEUKOCYTE_CELL_CELL_ADHESION	230	-0,16063489	-0,5945821	0,8913934	1	1	4075	tags=25%, list=23%, signal=32%
GO_CARDIAC_VENTRICLE_MORPHOGENESIS	GO_CARDIAC_VENTRICLE_MORPHOGENESIS	59	-0,17396133	-0,5945493	0,9863281	1	1	4420	tags=29%, list=25%, signal=38%
GO_EXCITATORY_POSTSYNAPTIC_POTENTIAL	GO_EXCITATORY_POSTSYNAPTIC_POTENTIAL	25	-0,18807547	-0,5934659	0,9688716	1	1	1639	tags=12%, list=9%, signal=13%
GO_POSITIVE_REGULATION_OF_CELL_GROWTH	GO_POSITIVE_REGULATION_OF_CELL_GROWTH	141	-0,13541217	-0,5928255	1	1	1	4296	tags=24%, list=24%, signal=32%
GO_DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	GO_DEFENSE_RESPONSE_TO_GRAM_NEGATIVE_BACTERIUM	41	-0,1769569	-0,5925038	0,979716	1	1	3311	tags=22%, list=19%, signal=27%
GO_LEUKOCYTE_CHEMOTAXIS	GO_LEUKOCYTE_CHEMOTAXIS	112	-0,17264889	-0,5918395	0,9498956	1	1	3916	tags=24%, list=22%, signal=31%
GO_ENDOCRINE_PANCREAS_DEVELOPMENT	GO_ENDOCRINE_PANCREAS_DEVELOPMENT	39	-0,1728125	-0,590838	0,96606785	1	1	3951	tags=28%, list=22%, signal=36%
GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	GO_POSITIVE_REGULATION_OF_AXON_EXTENSION	35	-0,18227756	-0,5902099	0,9476744	1	1	4234	tags=29%, list=24%, signal=38%
GO_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	GO_REGULATION_OF_ACTIN_FILAMENT_DEPOLYMERIZATION	43	-0,16833614	-0,5881771	0,9589322	1	1	2819	tags=19%, list=16%, signal=22%
GO_NOTCH_RECEPTOR_PROCESSING	GO_NOTCH_RECEPTOR_PROCESSING	16	-0,22359885	-0,5880501	0,9203187	1	1	3507	tags=31%, list=20%, signal=39%
GO_CARTILAGE_DEVELOPMENT	GO_CARTILAGE_DEVELOPMENT	138	-0,15883341	-0,5869174	0,9862205	1	1	2785	tags=17%, list=16%, signal=20%
GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	GO_POSITIVE_REGULATION_OF_CELL_ACTIVATION	273	-0,15671173	-0,5864742	0,8848485	1	1	3137	tags=19%, list=18%, signal=23%
GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	GO_NEGATIVE_REGULATION_OF_MUSCLE_CONTRACTION	21	-0,20449479	-0,5842662	0,9496124	1	1	4252	tags=33%, list=24%, signal=44%
GO_AORTA_DEVELOPMENT	GO_AORTA_DEVELOPMENT	41	-0,17448449	-0,5840451	0,9680639	1	1	3910	tags=29%, list=22%, signal=38%
GO_PHAGOCYTIC_VESICLE_MEMBRANE	GO_PHAGOCYTIC_VESICLE_MEMBRANE	56	-0,1595207	-0,5795273	0,9652352	1	1	14857	tags=100%, list=84%, signal=627%
GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	GO_REGULATION_OF_TYROSINE_PHOSPHORYLATION_OF_STAT3_PROTEIN	41	-0,17429912	-0,5789161	0,972549	1	1	4916	tags=37%, list=28%, signal=51%
GO_AXONEME_PART	GO_AXONEME_PART	20	-0,19506942	-0,578536	0,9585799	1	1	14224	tags=100%, list=81%, signal=513%
GO_RRNA_BINDING	GO_RRNA_BINDING	55	-0,20414363	-0,5771704	0,8249497	1	1	752	tags=9%, list=4%, signal=9%
GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	GO_CYTOKINE_MEDIATED_SIGNALING_PATHWAY	413	-0,13775262	-0,5770495	0,9857724	1	1	3531	tags=19%, list=20%, signal=23%

GO_RNA_POLYMERASE_II_CORE_BINDING	GO_RNA_POLYMERASE_II_CORE_BINDING	15	-0,21094508	-0,5770009	0,93439364	1	1	4287	tags=33%, list=24%, signal=44%
GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	GO_POSITIVE_REGULATION_OF_PROTEIN_COMPLEX_DISASSEMBLY	22	-0,17763858	-0,5761681	0,9747899	1	1	4626	tags=32%, list=26%, signal=43%
GO_INTERMEDIATE_FILAMENT_ORGANIZATION	GO_INTERMEDIATE_FILAMENT_ORGANIZATION	17	-0,20202993	-0,5755637	0,956	1	1	3516	tags=29%, list=20%, signal=37%
GO_DERMATAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	GO_DERMATAN_SULFATE_PROTEOGLYCAN_METABOLIC_PROCESS	16	-0,21295545	-0,5747383	0,939834	1	1	3509	tags=25%, list=20%, signal=31%
GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	GO_CELL_SURFACE_RECEPTOR_SIGNALING_PATHWAY_INVOLVED_IN_HEART_DEVELOPMENT	15	-0,21649514	-0,5737015	0,94650203	1	1	3202	tags=27%, list=18%, signal=33%
GO_NEUROTRANSMITTER_BINDING	GO_NEUROTRANSMITTER_BINDING	28	-0,18266824	-0,5734195	0,97485495	1	1	3266	tags=21%, list=18%, signal=26%
GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	GO_POSITIVE_REGULATION_OF_CELL_CELL_ADHESION	226	-0,15152207	-0,5729463	0,9402391	1	1	4963	tags=32%, list=28%, signal=44%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_DIFFERENTIATION	119	-0,15671948	-0,5714234	0,9608247	1	1	2969	tags=18%, list=17%, signal=21%
GO_ANTIGEN_BINDING	GO_ANTIGEN_BINDING	76	-0,16855806	-0,5700017	0,9315069	1	1	900	tags=8%, list=5%, signal=8%
GO_LYMPHOCYTE_COSTIMULATION	GO_LYMPHOCYTE_COSTIMULATION	72	-0,18404606	-0,5683167	0,8742138	1	1	3232	tags=21%, list=18%, signal=25%
GO_TRANSPORTER_COMPLEX	GO_TRANSPORTER_COMPLEX	286	-0,13089107	-0,5680151	1	1	1	2751	tags=14%, list=16%, signal=17%
GO_DECIDUALIZATION	GO_DECIDUALIZATION	19	-0,19393453	-0,5677904	0,95740366	1	1	53	tags=5%, list=0%, signal=5%
GO_REGULATION_OF_APPETITE	GO_REGULATION_OF_APPETITE	18	-0,19287992	-0,5675185	0,9900398	1	1	4874	tags=33%, list=28%, signal=46%
GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	GO_ENDOPLASMIC_RETICULUM_ORGANIZATION	36	-0,1731499	-0,5658438	0,96516395	1	1	4404	tags=31%, list=25%, signal=41%
GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	GO_PROTEIN_LOCALIZATION_TO_SYNAPSE	15	-0,20719546	-0,5639034	0,9736842	1	1	14009	tags=100%, list=79%, signal=483%
GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	GO_MULTI_ORGANISM_MEMBRANE_ORGANIZATION	29	-0,1691146	-0,5627753	0,97137016	1	1	3275	tags=28%, list=19%, signal=34%
GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	GO_POSITIVE_REGULATION_OF_MONOCYTE_CHEMOTAXIS	15	-0,21051334	-0,5626701	0,94343436	1	1	3788	tags=27%, list=21%, signal=34%
GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	GO_AUTONOMIC_NERVOUS_SYSTEM_DEVELOPMENT	37	-0,17339402	-0,5623564	0,9866412	1	1	3078	tags=19%, list=17%, signal=23%
GO_NEGATIVE_REGULATION_OF_BLOOD_CIRCULATION	GO_NEGATIVE_REGULATION_OF_BLOOD_CIRCULATION	32	-0,18160821	-0,5618995	0,99385244	1	1	4244	tags=25%, list=24%, signal=33%
GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	GO_REGULATION_OF_LIPOPOLYSACCHARIDE_MEDIATED_SIGNALING_PATHWAY	16	-0,19075148	-0,5591772	0,95951414	1	1	5987	tags=50%, list=34%, signal=76%
GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	GO_HOMOPHILIC_CELL_ADHESION_VIA_PLASMA_MEMBRANE_ADHESION_MOLECULES	145	-0,15980385	-0,5588769	0,9688716	1	1	3674	tags=20%, list=21%, signal=25%
GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	120	-0,15404055	-0,5582721	0,9620758	1	1	4916	tags=33%, list=28%, signal=46%
GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_MYELOID_CELL_DIFFERENTIATION	76	-0,14280201	-0,557026	0,99607074	1	1	2211	tags=13%, list=13%, signal=15%
GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	GO_POSITIVE_REGULATION_OF_NEUROLOGICAL_SYSTEM_PROCESS	19	-0,17714009	-0,5539535	0,96031743	1	1	4061	tags=32%, list=23%, signal=41%
GO_CEREBRAL_CORTEX_NEURON_DIFFERENTIATION	GO_CEREBRAL_CORTEX_NEURON_DIFFERENTIATION	22	-0,17675178	-0,5535184	0,9901575	1	1	3151	tags=23%, list=18%, signal=28%
GO_SCHWANN_CELL_DIFFERENTIATION	GO_SCHWANN_CELL_DIFFERENTIATION	30	-0,16324042	-0,5518125	0,98659	1	1	4358	tags=30%, list=25%, signal=40%
GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	GO_SIGNALING_PATTERN_RECOGNITION_RECEPTOR_ACTIVITY	16	-0,19789222	-0,5508926	0,94959676	1	1	2922	tags=25%, list=17%, signal=30%
GO_EXTRACELLULAR_MATRIX_BINDING	GO_EXTRACELLULAR_MATRIX_BINDING	48	-0,178176	-0,5500686	0,96138996	1	1	2975	tags=21%, list=17%, signal=25%
GO_CHRONIC_INFLAMMATORY_RESPONSE	GO_CHRONIC_INFLAMMATORY_RESPONSE	15	-0,1972238	-0,5498281	0,98454744	1	1	14185	tags=100%, list=80%, signal=507%
GO_PROTEIN_REFOLDING	GO_PROTEIN_REFOLDING	20	-0,2031302	-0,5489639	0,9375	1	1	2723	tags=20%, list=15%, signal=24%
GO_HOMOTYPIC_CELL_CELL_ADHESION	GO_HOMOTYPIC_CELL_CELL_ADHESION	49	-0,159909	-0,548528	0,9698189	1	1	3782	tags=24%, list=21%, signal=31%
GO_REGULATION_OF_CHEMOTAXIS	GO_REGULATION_OF_CHEMOTAXIS	173	-0,1454722	-0,5482205	0,99175256	1	1	3137	tags=16%, list=18%, signal=19%
GO_DENDRITIC_CELL_MIGRATION	GO_DENDRITIC_CELL_MIGRATION	20	-0,2104602	-0,5461954	0,9347826	1	1	5576	tags=40%, list=32%, signal=58%
GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	GO_REGULATION_OF_FIBROBLAST_GROWTH_FACTOR_RECEPTOR_SIGNALING_PATHWAY	24	-0,17555694	-0,5454904	0,9808061	1	1	14569	tags=100%, list=82%, signal=570%
GO_HORMONE_ACTIVITY	GO_HORMONE_ACTIVITY	92	-0,14644149	-0,5447096	1	1	1	3886	tags=21%, list=22%, signal=26%
GO_REGULATION_OF_NEUTROPHIL_MIGRATION	GO_REGULATION_OF_NEUTROPHIL_MIGRATION	30	-0,18660411	-0,5441569	0,962963	1	1	5986	tags=47%, list=34%, signal=70%
GO_IONOTROPIC_GLUTAMATE_RECEPTOR_COMPLEX	GO_IONOTROPIC_GLUTAMATE_RECEPTOR_COMPLEX	41	-0,15747388	-0,5409266	0,98846155	1	1	2576	tags=15%, list=15%, signal=17%
GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	GO_STRUCTURAL_CONSTITUENT_OF_RIBOSOME	200	-0,19272164	-0,5391902	0,8484849	1	1	2556	tags=16%, list=14%, signal=18%
GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	GO_POSITIVE_REGULATION_OF_LEUKOCYTE_CHEMOTAXIS	78	-0,15738466	-0,5373654	0,98755187	1	1	3529	tags=21%, list=20%, signal=26%
GO_DNA_DIRECTED_RNA_POLYMERASE_II_CORE_COMPLEX	GO_DNA_DIRECTED_RNA_POLYMERASE_II_CORE_COMPLEX	16	-0,19063851	-0,5367007	0,97341514	1	1	1644	tags=13%, list=9%, signal=14%
GO_REGULATION_OF_SENSORY_PERCEPTION	GO_REGULATION_OF_SENSORY_PERCEPTION	31	-0,16265549	-0,5366567	0,99230766	1	1	4107	tags=26%, list=23%, signal=34%
GO_LAMELLAR_BODY	GO_LAMELLAR_BODY	19	-0,19660427	-0,5352832	0,97336066	1	1	2636	tags=21%, list=15%, signal=25%
GO_CYTOKINE_SECRETION	GO_CYTOKINE_SECRETION	37	-0,16410273	-0,5351765	0,97689074	1	1	4843	tags=32%, list=27%, signal=45%
GO_ALKALI_METAL_ION_BINDING	GO_ALKALI_METAL_ION_BINDING	18	-0,18310963	-0,5348369	0,98613864	1	1	4734	tags=33%, list=27%, signal=45%
GO_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	GO_REGULATION_OF_NF_KAPPAB_IMPORT_INTO_NUCLEUS	47	-0,1514907	-0,5341858	0,98971194	1	1	4447	tags=28%, list=25%, signal=37%
GO_REGULATION_OF_T_CELL_PROLIFERATION	GO_REGULATION_OF_T_CELL_PROLIFERATION	137	-0,15226167	-0,5314435	0,946281	1	1	3529	tags=19%, list=20%, signal=24%
GO_CORNIFIED_ENVELOPE	GO_CORNIFIED_ENVELOPE	20	-0,21524511	-0,5267835	0,95384616	1	1	13868	tags=100%, list=79%, signal=465%
GO_ANCHORED_COMPONENT_OF_MEMBRANE	GO_ANCHORED_COMPONENT_OF_MEMBRANE	134	-0,1314258	-0,5245162	0,9979757	1	1	2417	tags=13%, list=14%, signal=15%
GO_REGULATION_OF_MAST_CELL_ACTIVATION	GO_REGULATION_OF_MAST_CELL_ACTIVATION	37	-0,16897713	-0,5239064	0,96887964	1	1	2194	tags=14%, list=12%, signal=15%
GO_CLATHRIN_VESICLE_COAT	GO_CLATHRIN_VESICLE_COAT	23	-0,16155222	-0,5236928	0,9856263	1	1	2144	tags=13%, list=12%, signal=15%
GO_CALCIUM_DEPENDENT_PHOSPHOLIPID_BINDING	GO_CALCIUM_DEPENDENT_PHOSPHOLIPID_BINDING	53	-0,14775361	-0,5207573	0,994012	1	1	2254	tags=13%, list=13%, signal=15%
GO_NEGATIVE_REGULATION_OF_HORMONE_SECRETION	GO_NEGATIVE_REGULATION_OF_HORMONE_SECRETION	68	-0,1395335	-0,520061	1	1	1	3413	tags=18%, list=19%, signal=22%

GO_LYSOSOME_LOCALIZATION	GO_LYSOSOME_LOCALIZATION	23	-0,1648032	-0,5163732	0,9841584	1	1	884	tags=9%, list=5%, signal=9%
GO_HMG_BOX_DOMAIN_BINDING	GO_HMG_BOX_DOMAIN_BINDING	17	-0,20829555	-0,5157436	0,96666664	1	1	13990	tags=100%, list=79%, signal=480%
GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	GO_NEGATIVE_REGULATION_OF_LEUKOCYTE_PROLIFERATION	63	-0,15078902	-0,5142147	0,9855372	1	1	1374	tags=10%, list=8%, signal=10%
GO_ENDOSOME_LUMEN	GO_ENDOSOME_LUMEN	23	-0,15780613	-0,5111723	0,9940358	1	1	1013	tags=9%, list=6%, signal=9%
GO_PROTEIN_LOCALIZATION_TO_GOLGI_APPARATUS	GO_PROTEIN_LOCALIZATION_TO_GOLGI_APPARATUS	29	-0,16778973	-0,510999	0,9790795	1	1	3002	tags=24%, list=17%, signal=29%
GO_SOLUTE_CATION_ANTIPORTER_ACTIVITY	GO_SOLUTE_CATION_ANTIPORTER_ACTIVITY	26	-0,15872808	-0,5085269	0,99603176	1	1	2286	tags=15%, list=13%, signal=18%
GO_MYELOID_DENDRITIC_CELL_ACTIVATION	GO_MYELOID_DENDRITIC_CELL_ACTIVATION	24	-0,17464995	-0,5072768	0,97160244	1	1	14585	tags=100%, list=83%, signal=573%
GO_NEUROTROPHIN_SIGNALING_PATHWAY	GO_NEUROTROPHIN_SIGNALING_PATHWAY	23	-0,16682854	-0,5071114	0,99408287	1	1	1040	tags=9%, list=6%, signal=9%
GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	GO_DELAYED_RECTIFIER_POTASSIUM_CHANNEL_ACTIVITY	30	-0,16436265	-0,5066717	0,973384	1	1	3572	tags=20%, list=20%, signal=25%
GO_STRUCTURAL_CONSTITUENT_OF_EYE_LENS	GO_STRUCTURAL_CONSTITUENT_OF_EYE_LENS	15	-0,22614914	-0,5066617	0,9979675	1	1	2336	tags=20%, list=13%, signal=23%
GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	GO_ANTIGEN_PROCESSING_AND_PRESENTATION_OF_ENDOGENOUS_ANTIGEN	17	-0,208672	-0,5062707	0,9447732	1	1	3353	tags=18%, list=19%, signal=22%
GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	GO_REGULATION_OF_NEURONAL_SYNAPTIC_PLASTICITY	45	-0,14460558	-0,5052334	0,997992	1	1	3411	tags=18%, list=19%, signal=22%
GO_MEGAKARYOCYTE_DIFFERENTIATION	GO_MEGAKARYOCYTE_DIFFERENTIATION	19	-0,1788063	-0,5036265	0,9799599	1	1	2917	tags=21%, list=17%, signal=25%
GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	GO_ADENYLATE_CYCLASE_INHIBITING_G_PROTEIN_COUPLED_RECEPTOR_SIGNALING_PATHWAY	60	-0,14059472	-0,5009196	1	1	1	3425	tags=18%, list=19%, signal=23%
GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	GO_REGULATION_OF_EPITHELIAL_CELL_DIFFERENTIATION_INVOLVED_IN_KIDNEY_DEVELOPMENT	15	-0,19570684	-0,500122	0,9901575	1	1	455	tags=7%, list=3%, signal=7%
GO_AXON_EXTENSION	GO_AXON_EXTENSION	33	-0,16175136	-0,499931	0,9883721	1	1	14814	tags=100%, list=84%, signal=618%
GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	GO_REGULATION_OF_LYMPHOCYTE_CHEMOTAXIS	20	-0,18565166	-0,4997327	0,9770833	1	1	3082	tags=20%, list=17%, signal=24%
GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	GO_NEGATIVE_REGULATION_OF_PEPTIDYL_TYROSINE_PHOSPHORYLATION	37	-0,13981302	-0,499128	0,99375	1	1	4594	tags=27%, list=26%, signal=36%
GO_NEUROPEPTIDE_RECEPTOR_BINDING	GO_NEUROPEPTIDE_RECEPTOR_BINDING	24	-0,16185504	-0,4984545	0,9961977	1	1	3174	tags=21%, list=18%, signal=25%
GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	GO_NEGATIVE_REGULATION_OF_HEART_CONTRACTION	18	-0,17631473	-0,4982063	0,9939638	1	1	491	tags=6%, list=3%, signal=6%
GO_DORSAL_VENTRAL_NEURAL_TUBE_PATTERNING	GO_DORSAL_VENTRAL_NEURAL_TUBE_PATTERNING	16	-0,18440126	-0,4932215	0,98971194	1	1	3151	tags=19%, list=18%, signal=23%
GO_LEUKOCYTE_ACTIVATION	GO_LEUKOCYTE_ACTIVATION	381	-0,13015407	-0,493161	0,99389005	1	1	3575	tags=21%, list=20%, signal=25%
GO_DENDRITIC_CELL_DIFFERENTIATION	GO_DENDRITIC_CELL_DIFFERENTIATION	31	-0,16711934	-0,4909584	0,979716	1	1	4145	tags=32%, list=23%, signal=42%
GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	GO_POSITIVE_REGULATION_OF_DNA_TEMPLATED_TRANSCRIPTION_INITIATION	24	-0,14936794	-0,4904722	0,9884393	1	1	15031	tags=100%, list=85%, signal=670%
GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	GO_ENDOCHONDRAL_BONE_MORPHOGENESIS	44	-0,15721595	-0,4899018	0,98797596	1	1	2712	tags=16%, list=15%, signal=19%
GO_NATURAL_KILLER_CELL_ACTIVATION	GO_NATURAL_KILLER_CELL_ACTIVATION	35	-0,17067523	-0,4893211	0,94363254	1	1	4911	tags=43%, list=28%, signal=59%
GO_VACUOLE_FUSION	GO_VACUOLE_FUSION	22	-0,1551257	-0,4886635	0,98624754	1	1	233	tags=5%, list=1%, signal=5%
GO_SYNAPSE_ASSEMBLY	GO_SYNAPSE_ASSEMBLY	67	-0,1347566	-0,4876277	0,99605525	1	1	5011	tags=25%, list=28%, signal=35%
GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	GO_MYELOID_DENDRITIC_CELL_DIFFERENTIATION	18	-0,17459059	-0,4860948	0,98547715	1	1	14585	tags=100%, list=83%, signal=573%
GO_NUCLEAR_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	GO_NUCLEAR_CYCLIN_DEPENDENT_PROTEIN_KINASE_HOLOENZYME_COMPLEX	15	-0,17380337	-0,4846756	0,98035365	1	1	5093	tags=40%, list=29%, signal=56%
GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	GO_POSITIVE_REGULATION_OF_LYMPHOCYTE_DIFFERENTIATION	73	-0,14733368	-0,4823748	0,96875	1	1	2969	tags=18%, list=17%, signal=21%
GO_MHC_PROTEIN_COMPLEX	GO_MHC_PROTEIN_COMPLEX	24	-0,21951182	-0,4821565	0,88235295	1	1	171	tags=4%, list=1%, signal=4%
GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	GO_EMBRYONIC_CAMERA_TYPE_EYE_MORPHOGENESIS	24	-0,1648727	-0,4815081	0,9903101	1	1	1262	tags=8%, list=7%, signal=9%
GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	GO_POSITIVE_REGULATION_OF_T_CELL_PROLIFERATION	90	-0,15079741	-0,4810978	0,9472617	1	1	4963	tags=33%, list=28%, signal=46%
GO_REGULATION_OF_LEUKOCYTE_MIGRATION	GO_REGULATION_OF_LEUKOCYTE_MIGRATION	143	-0,13531421	-0,4803421	0,99793816	1	1	3137	tags=17%, list=18%, signal=20%
GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	GO_REGULATION_OF_LEUKOCYTE_DEGRANULATION	40	-0,14836201	-0,4756435	0,98971194	1	1	2194	tags=13%, list=12%, signal=14%
GO_CHROMATIN_SILENCING_AT_RDNA	GO_CHROMATIN_SILENCING_AT_RDNA	30	-0,17092423	-0,4755439	0,96237624	1	1	4954	tags=33%, list=28%, signal=46%
GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	GO_POSITIVE_REGULATION_OF_NEUTROPHIL_MIGRATION	26	-0,16564815	-0,4739875	0,98556703	1	1	5913	tags=42%, list=33%, signal=64%
GO_CALCIUM_ION_REGULATED_EXOCYTOSIS_OF_NEUROTRANSMITTER	GO_CALCIUM_ION_REGULATED_EXOCYTOSIS_OF_NEUROTRANSMITTER	33	-0,14512727	-0,4720328	0,99801195	1	1	4701	tags=27%, list=27%, signal=37%
GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	GO_G_PROTEIN_COUPLED_CHEMOATTRACTANT_RECEPTOR_ACTIVITY	22	-0,18658958	-0,4677424	0,9576613	1	1	14374	tags=100%, list=81%, signal=536%
GO_MEMBRANE_DEPOLARIZATION	GO_MEMBRANE_DEPOLARIZATION	56	-0,13098188	-0,4665711	1	1	1	4202	tags=23%, list=24%, signal=30%
GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	GO_VOLTAGE_GATED_POTASSIUM_CHANNEL_ACTIVITY	78	-0,12399393	-0,4663314	1	1	1	1246	tags=6%, list=7%, signal=7%
GO_MYELOID_LEUKOCYTE_ACTIVATION	GO_MYELOID_LEUKOCYTE_ACTIVATION	92	-0,13450897	-0,4531125	0,9958592	1	1	5052	tags=34%, list=29%, signal=47%
GO_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	GO_REGULATION_OF_INTERLEUKIN_17_PRODUCTION	19	-0,17151164	-0,4470395	0,9830508	1	1	3627	tags=32%, list=21%, signal=40%
GO_SENSORY_PERCEPTION_OF_PAIN	GO_SENSORY_PERCEPTION_OF_PAIN	69	-0,12830347	-0,4466218	1	1	1	3311	tags=17%, list=19%, signal=21%
GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	GO_NEGATIVE_REGULATION_OF_CYTOKINE_PRODUCTION_INVOLVED_IN_IMMUNE_RESPONSE	19	-0,1502424	-0,445222	0,9980237	1	1	5447	tags=32%, list=31%, signal=46%
GO_ACTIN_MYOSIN_FILAMENT_SLIDING	GO_ACTIN_MYOSIN_FILAMENT_SLIDING	37	-0,13867278	-0,4374088	0,9979798	1	1	4326	tags=30%, list=24%, signal=39%
GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	GO_MYELOID_LEUKOCYTE_MEDIATED_IMMUNITY	42	-0,13063851	-0,4371499	0,9979879	1	1	3455	tags=19%, list=20%, signal=24%
GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	GO_VOLTAGE_GATED_CALCIUM_CHANNEL_COMPLEX	35	-0,14103349	-0,4338705	1	1	1	4442	tags=31%, list=25%, signal=42%
GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	GO_NEGATIVE_REGULATION_OF_REGULATED_SECRETORY_PATHWAY	20	-0,14726777	-0,4332422	1	1	1	1810	tags=10%, list=10%, signal=11%
GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN	GO_PROTON_TRANSPORTING_TWO_SECTOR_ATPASE_COMPLEX_PROTON_TRANSPORTING_DOMAIN	21	-0,1641918	-0,4296501	0,9775051	1	1	14769	tags=100%, list=84%, signal=609%
GO_T_CELL_RECEPTOR_COMPLEX	GO_T_CELL_RECEPTOR_COMPLEX	19	-0,179885	-0,4260422	0,9628866	1	1	4963	tags=42%, list=28%, signal=58%

GO_MHC_PROTEIN_BINDING	GO_MHC_PROTEIN_BINDING	26	-0,16279264	-0,4238095	0,97894734	1	1	3217	tags=23%, list=18%, signal=28%
GO_MYELOID_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	GO_MYELOID_CELL_ACTIVATION_INVOLVED_IN_IMMUNE_RESPONSE	41	-0,1350261	-0,4218451	0,997955	1	1	5052	tags=32%, list=29%, signal=44%
GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	GO_POSITIVE_REGULATION_OF_BLOOD_VESSEL_ENDOTHELIAL_CELL_MIGRATION	25	-0,13503401	-0,4191034	1	1	1	15284	tags=100%, list=87%, signal=741%
GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	GO_REGULATION_OF_LEUKOCYTE_PROLIFERATION	193	-0,11706647	-0,4184085	1	0,9999795	1	2969	tags=14%, list=17%, signal=17%
GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	GO_T_CELL_RECEPTOR_SIGNALING_PATHWAY	138	-0,10754088	-0,4080395	1	1	1	4910	tags=28%, list=28%, signal=39%
GO_RESPONSE_TO_SALT	GO_RESPONSE_TO_SALT	15	-0,15110481	-0,4028981	1	0,9999583	1	14999	tags=100%, list=85%, signal=662%
GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	GO_REGULATION_OF_MONOCYTE_CHEMOTAXIS	20	-0,14450043	-0,3957196	0,99385244	0,99985826	1	3788	tags=20%, list=21%, signal=25%
GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	GO_ANTIGEN_RECEPTOR_MEDIATED_SIGNALING_PATHWAY	168	-0,10157853	-0,3800498	1	1	1	4461	tags=23%, list=25%, signal=31%
GO_NEGATIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	GO_NEGATIVE_REGULATION_OF_KIDNEY_DEVELOPMENT	17	-0,13225295	-0,3600861	1	1	1	15332	tags=100%, list=87%, signal=756%
GO_SMALL_RIBOSOMAL_SUBUNIT	GO_SMALL_RIBOSOMAL_SUBUNIT	66	-0,14131485	-0,352245	0,95445544	0,99978125	1	15179	tags=100%, list=86%, signal=708%
GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	GO_B_CELL_RECEPTOR_SIGNALING_PATHWAY	35	-0,11854792	-0,3135141	0,9959514	0,9997533	1	15576	tags=100%, list=88%, signal=844%

Table S7. GSEA results between patients with low and high risk score in HCC using c2 reference gene sets.

NAME	GS follow link to MSigDB	GS DETAILS	SIZE	ES	NES	NOM p-val	FDR q-val	FWER p-val	RANK AT MAX	LEADING EDGE
KEGG_CELL_CYCLE	KEGG_CELL_CYCLE	Details ...	124	0,6155322	2,1585038	0	0,003869959	0,005	2268	tags=47%, list=13%, signal=53%
KEGG_HOMOLOGOUS_RECOMBINATION	KEGG_HOMOLOGOUS_RECOMBINATION	Details ...	26	0,70383924	1,9720181	0,004016064	0,036262944	0,065	1544	tags=46%, list=9%, signal=50%
KEGG_DNA_REPLICATION	KEGG_DNA_REPLICATION	Details ...	36	0,7249568	1,8371171	0,017964073	0,12880258	0,22	3849	tags=75%, list=22%, signal=96%
KEGG_MISMATCH_REPAIR	KEGG_MISMATCH_REPAIR	Details ...	23	0,6691371	1,7701713	0,01178782	0,1802107	0,344	3849	tags=61%, list=22%, signal=78%
KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	KEGG_PROGESTERONE_MEDIATED_OOCYTE_MATURATION	Details ...	84	0,43977514	1,7545147	0,001988072	0,1630894	0,376	1554	tags=21%, list=9%, signal=23%
KEGG_PYRIMIDINE_METABOLISM	KEGG_PYRIMIDINE_METABOLISM	Details ...	95	0,46432248	1,7509055	0,015180266	0,14221975	0,392	3668	tags=41%, list=21%, signal=52%
KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	KEGG_PATHOGENIC_ESCHERICHIA_COLI_INFECTION	Details ...	55	0,48835197	1,7266618	0,006072875	0,15037675	0,46	3150	tags=40%, list=18%, signal=49%
KEGG_SPLICEOSOME	KEGG_SPLICEOSOME	Details ...	123	0,5127535	1,6983334	0,025948104	0,16811872	0,525	5741	tags=59%, list=32%, signal=87%
KEGG_PURINE_METABOLISM	KEGG_PURINE_METABOLISM	Details ...	151	0,37085232	1,6258548	0,009881423	0,25479984	0,685	3668	tags=33%, list=21%, signal=41%
KEGG_OOCYTE_MEIOSIS	KEGG_OOCYTE_MEIOSIS	Details ...	108	0,37672263	1,5574483	0,032786883	0,35173073	0,819	2750	tags=27%, list=16%, signal=32%
KEGG_BASE_EXCISION_REPAIR	KEGG_BASE_EXCISION_REPAIR	Details ...	33	0,5204019	1,5572145	0,05367793	0,32054177	0,82	4433	tags=58%, list=25%, signal=77%
KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	KEGG_FC_GAMMA_R_MEDIATED_PHAGOCYTOSIS	Details ...	92	0,4149337	1,5403961	0,05811623	0,32406256	0,844	3733	tags=35%, list=21%, signal=44%
KEGG_BLADDER_CANCER	KEGG_BLADDER_CANCER	Details ...	40	0,42111984	1,4880093	0,053359684	0,3988251	0,906	4734	tags=40%, list=27%, signal=55%
KEGG_P53_SIGNALING_PATHWAY	KEGG_P53_SIGNALING_PATHWAY	Details ...	66	0,37484267	1,466628	0,04901961	0,41438103	0,925	2090	tags=23%, list=12%, signal=26%
KEGG_RNA_DEGRADATION	KEGG_RNA_DEGRADATION	Details ...	55	0,39242494	1,3947031	0,11222445	0,5538853	0,965	4766	tags=42%, list=27%, signal=57%
KEGG_NUCLEOTIDE_EXCISION_REPAIR	KEGG_NUCLEOTIDE_EXCISION_REPAIR	Details ...	44	0,41476136	1,3494776	0,1468254	0,6428831	0,977	5018	tags=52%, list=28%, signal=73%
KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	KEGG_UBIQUITIN_MEDIATED_PROTEOLYSIS	Details ...	130	0,3120668	1,28694	0,1605691	0,7883941	0,99	2024	tags=19%, list=11%, signal=22%
KEGG_GAP_JUNCTION	KEGG_GAP_JUNCTION	Details ...	87	0,34347126	1,2825308	0,16194332	0,7564353	0,99	3395	tags=29%, list=19%, signal=35%
KEGG_NON_SMALL_CELL_LUNG_CANCER	KEGG_NON_SMALL_CELL_LUNG_CANCER	Details ...	54	0,33702022	1,2795492	0,15445544	0,7243852	0,991	2921	tags=24%, list=17%, signal=29%
KEGG_N_GLYCAN_BIOSYNTHESIS	KEGG_N_GLYCAN_BIOSYNTHESIS	Details ...	46	0,37061676	1,2321048	0,23564357	0,82178086	0,994	3935	tags=35%, list=22%, signal=45%
KEGG_OTHER_GLYCAN_DEGRADATION	KEGG_OTHER_GLYCAN_DEGRADATION	Details ...	15	0,45322442	1,2116436	0,24752475	0,8421376	0,997	2702	tags=33%, list=15%, signal=39%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_CHONDROITIN_SULFATE	Details ...	22	0,38654673	1,1474564	0,2972973	1	0,999	3834	tags=32%, list=22%, signal=41%
KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	KEGG_AMINOACYL_TRNA_BIOSYNTHESIS	Details ...	41	0,39557242	1,1439517	0,3550864	0,9711358	0,999	3705	tags=41%, list=21%, signal=52%
KEGG_RNA_POLYMERASE	KEGG_RNA_POLYMERASE	Details ...	29	0,40004012	1,1284323	0,32936507	0,9766947	1	3594	tags=31%, list=20%, signal=39%
KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	KEGG_GLYCEROPHOSPHOLIPID_METABOLISM	Details ...	69	0,26271772	1,1064779	0,2777778	1	1	4162	tags=32%, list=24%, signal=42%
KEGG_NOTCH_SIGNALING_PATHWAY	KEGG_NOTCH_SIGNALING_PATHWAY	Details ...	47	0,30593646	1,1044234	0,3044316	0,9725813	1	3704	tags=30%, list=21%, signal=38%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_LACTO_AND_NEOLACTO_SERIES	Details ...	25	0,34087148	1,0978259	0,34607646	0,9559105	1	4858	tags=44%, list=28%, signal=61%
KEGG_PENTOSE_PHOSPHATE_PATHWAY	KEGG_PENTOSE_PHOSPHATE_PATHWAY	Details ...	26	0,35071173	1,0905482	0,35271317	0,9437918	1	738	tags=19%, list=4%, signal=20%
KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	KEGG_GLYCOSAMINOGLYCAN_BIOSYNTHESIS_HEPARAN_SULFATE	Details ...	26	0,34122962	1,0863018	0,3223301	0,92267543	1	4412	tags=38%, list=25%, signal=51%
KEGG_INOSITOL_PHOSPHATE_METABOLISM	KEGG_INOSITOL_PHOSPHATE_METABOLISM	Details ...	54	0,29156476	1,0548661	0,40842104	0,97926956	1	3649	tags=30%, list=21%, signal=37%
KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_NOD_LIKE_RECEPTOR_SIGNALING_PATHWAY	Details ...	60	0,28737354	1,0329949	0,41393444	1	1	6949	tags=50%, list=39%, signal=82%
KEGG_CHRONIC_MYELOID_LEUKEMIA	KEGG_CHRONIC_MYELOID_LEUKEMIA	Details ...	73	0,25847396	1,0170614	0,41535434	1	1	1225	tags=12%, list=7%, signal=13%
KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	KEGG_PHOSPHATIDYLINOSITOL_SIGNALING_SYSTEM	Details ...	76	0,2651341	0,9988607	0,45093945	1	1	2921	tags=24%, list=17%, signal=28%
KEGG_PANCREATIC_CANCER	KEGG_PANCREATIC_CANCER	Details ...	69	0,27465317	0,99551135	0,4625	1	1	1617	tags=13%, list=9%, signal=14%
KEGG_SMALL_CELL_LUNG_CANCER	KEGG_SMALL_CELL_LUNG_CANCER	Details ...	84	0,25896278	0,99076277	0,46666667	1	1	1945	tags=17%, list=11%, signal=19%
KEGG_THYROID_CANCER	KEGG_THYROID_CANCER	Details ...	29	0,29183733	0,98313034	0,47357294	0,99716526	1	4436	tags=31%, list=25%, signal=41%
KEGG_PATHWAYS_IN_CANCER	KEGG_PATHWAYS_IN_CANCER	Details ...	318	0,22552809	0,9824015	0,46058092	0,9721661	1	3947	tags=23%, list=22%, signal=29%
KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	KEGG_CYTOSOLIC_DNA_SENSING_PATHWAY	Details ...	40	0,29171258	0,9771051	0,4939759	0,9601363	1	5021	tags=33%, list=28%, signal=45%
KEGG_VIBRIO_CHOLERAE_INFECTION	KEGG_VIBRIO_CHOLERAE_INFECTION	Details ...	50	0,26464018	0,9669994	0,49015749	0,96074134	1	6101	tags=38%, list=35%, signal=58%
KEGG_GLIOMA	KEGG_GLIOMA	Details ...	65	0,23612846	0,93458056	0,57768923	1	1	1287	tags=12%, list=7%, signal=13%
KEGG_SPHINGOLIPID_METABOLISM	KEGG_SPHINGOLIPID_METABOLISM	Details ...	35	0,2689066	0,9270105	0,528	1	1	5187	tags=37%, list=29%, signal=52%
KEGG_LYSOSOME	KEGG_LYSOSOME	Details ...	119	0,24635006	0,9152191	0,5373444	1	1	3597	tags=25%, list=20%, signal=31%
KEGG_O_GLYCAN_BIOSYNTHESIS	KEGG_O_GLYCAN_BIOSYNTHESIS	Details ...	26	0,31957603	0,9140492	0,58882236	0,9980428	1	5010	tags=38%, list=28%, signal=54%
KEGG_MELANOMA	KEGG_MELANOMA	Details ...	69	0,23984186	0,89470965	0,63821137	1	1	1287	tags=10%, list=7%, signal=11%
KEGG_AXON_GUIDANCE	KEGG_AXON_GUIDANCE	Details ...	126	0,22730005	0,88770586	0,56875	1	1	6358	tags=40%, list=36%, signal=63%
KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	KEGG_GLYCOSYLPHOSPHATIDYLINOSITOL_GPI_ANCHOR_BIOSYNTHESIS	Details ...	24	0,2889382	0,8803324	0,6074074	1	1	5532	tags=46%, list=31%, signal=67%
KEGG_BASAL_CELL_CARCINOMA	KEGG_BASAL_CELL_CARCINOMA	Details ...	54	0,25005826	0,8640582	0,6902834	1	1	4495	tags=24%, list=25%, signal=32%
KEGG_BASAL_TRANSCRIPTION_FACTORS	KEGG_BASAL_TRANSCRIPTION_FACTORS	Details ...	32	0,26158246	0,8622462	0,60655737	1	1	6579	tags=41%, list=37%, signal=65%
KEGG_SELENOAMINO_ACID_METABOLISM	KEGG_SELENOAMINO_ACID_METABOLISM	Details ...	25	0,26322237	0,8532891	0,6369048	1	1	2949	tags=28%, list=17%, signal=34%
KEGG_ENDOCYTOSIS	KEGG_ENDOCYTOSIS	Details ...	174	0,18960148	0,85239756	0,69502074	0,98913974	1	5151	tags=30%, list=29%, signal=43%
KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	KEGG_GLYCOSPHINGOLIPID_BIOSYNTHESIS_GANGLIO_SERIES	Details ...	15	0,2962208	0,84863186	0,6587771	0,97734225	1	3295	tags=27%, list=19%, signal=33%
KEGG_RIBOSOME	KEGG_RIBOSOME	Details ...	87	0,4062507	0,8389416	0,63779527	0,9785362	1	8330	tags=76%, list=47%, signal=143%

KEGG_MTOR_SIGNALING_PATHWAY	KEGG_MTOR_SIGNALING_PATHWAY	Details ...	50	0,21858816	0,83341515	0,71428573	0,97125345	1	5862	tags=36%, list=33%, signal=54%
KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	KEGG_REGULATION_OF_ACTIN_CYTOSKELETON	Details ...	207	0,19870076	0,81905884	0,7393075	0,98270905	1	6372	tags=40%, list=36%, signal=62%
KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	KEGG_SNARE_INTERACTIONS_IN_VESICULAR_TRANSPORT	Details ...	38	0,2182764	0,80118626	0,78336555	0,99912137	1	3046	tags=21%, list=17%, signal=25%
KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	KEGG_ANTIGEN_PROCESSING_AND_PRESENTATION	Details ...	64	0,2729097	0,7767325	0,65625	1	1	7454	tags=48%, list=42%, signal=83%
KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	KEGG_EPITHELIAL_CELL_SIGNALING_IN_HELICOBACTER_PYLORI_INFECTION	Details ...	66	0,19623992	0,77019966	0,7995992	1	1	6570	tags=41%, list=37%, signal=65%
KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	KEGG_AMINO_SUGAR_AND_NUCLEOTIDE_SUGAR_METABOLISM	Details ...	44	0,22427061	0,76172364	0,7972167	1	1	5939	tags=43%, list=34%, signal=65%
KEGG_LEISHMANIA_INFECTION	KEGG_LEISHMANIA_INFECTION	Details ...	68	0,24153586	0,75380605	0,7084189	1	1	4248	tags=29%, list=24%, signal=39%
KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	KEGG_RIG_I_LIKE_RECEPTOR_SIGNALING_PATHWAY	Details ...	52	0,19403042	0,73760027	0,8431772	1	1	3799	tags=21%, list=22%, signal=27%
KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	KEGG_VASOPRESSIN_REGULATED_WATER_REABSORPTION	Details ...	42	0,19331592	0,7050169	0,8548708	1	1	4407	tags=29%, list=25%, signal=38%
KEGG_TYPE_I_DIABETES_MELLITUS	KEGG_TYPE_I_DIABETES_MELLITUS	Details ...	40	0,2661847	0,6914583	0,7401575	1	1	8100	tags=50%, list=46%, signal=92%
KEGG_RENAL_CELL_CARCINOMA	KEGG_RENAL_CELL_CARCINOMA	Details ...	66	0,19213766	0,69041896	0,88582677	1	1	1567	tags=14%, list=9%, signal=15%
KEGG_HEDGEHOG_SIGNALING_PATHWAY	KEGG_HEDGEHOG_SIGNALING_PATHWAY	Details ...	53	0,20092505	0,6886464	0,93402064	1	1	4495	tags=23%, list=25%, signal=30%
KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	KEGG_NEUROTROPHIN_SIGNALING_PATHWAY	Details ...	124	0,16766089	0,68851405	0,9173387	1	1	2921	tags=18%, list=17%, signal=21%
KEGG_COLORECTAL_CANCER	KEGG_COLORECTAL_CANCER	Details ...	62	0,18039545	0,6727387	0,9216102	1	1	973	tags=6%, list=6%, signal=7%
KEGG_PROSTATE_CANCER	KEGG_PROSTATE_CANCER	Details ...	89	0,16743046	0,6726398	0,95051545	1	1	2768	tags=15%, list=16%, signal=17%
KEGG_ERBB_SIGNALING_PATHWAY	KEGG_ERBB_SIGNALING_PATHWAY	Details ...	86	0,16706443	0,6725594	0,9410569	0,9920536	1	4515	tags=26%, list=26%, signal=34%
KEGG_TASTE_TRANSDUCTION	KEGG_TASTE_TRANSDUCTION	Details ...	31	0,2148674	0,6675798	0,910387	0,9836075	1	5901	tags=39%, list=33%, signal=58%
KEGG_RIBOFLAVIN_METABOLISM	KEGG_RIBOFLAVIN_METABOLISM	Details ...	16	0,22421877	0,65676427	0,9034908	0,9816828	1	5185	tags=31%, list=29%, signal=44%
KEGG_PROTEASOME	KEGG_PROTEASOME	Details ...	42	0,25783333	0,6467845	0,77272725	0,9777743	1	7415	tags=48%, list=42%, signal=82%
KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	KEGG_GLYCOSAMINOGLYCAN_DEGRADATION	Details ...	20	0,20937546	0,6220124	0,91902834	0,9865529	1	5179	tags=40%, list=29%, signal=57%
KEGG_WNT_SIGNALING_PATHWAY	KEGG_WNT_SIGNALING_PATHWAY	Details ...	145	0,14015299	0,58276045	0,99793816	1	1	3144	tags=14%, list=18%, signal=17%
KEGG_PRIMARY_IMMUNODEFICIENCY	KEGG_PRIMARY_IMMUNODEFICIENCY	Details ...	34	0,2263321	0,5716892	0,851927	0,9960515	1	2987	tags=18%, list=17%, signal=21%
KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	KEGG_ARRHYTHMOGENIC_RIGHT_VENTRICULAR_CARDIOMYOPATHY_ARVC	Details ...	71	0,15198575	0,5337538	0,9855967	1	1	5324	tags=30%, list=30%, signal=42%
KEGG_OLFACTORY_TRANSDUCTION	KEGG_OLFACTORY_TRANSDUCTION	Details ...	47	0,14665638	0,53211623	1	0,9891365	1	5601	tags=28%, list=32%, signal=40%
KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	KEGG_T_CELL_RECEPTOR_SIGNALING_PATHWAY	Details ...	103	0,13810618	0,501458	0,979716	0,9877316	1	1852	tags=10%, list=10%, signal=11%
KEGG_CARDIAC_MUSCLE_CONTRACTION	KEGG_CARDIAC_MUSCLE_CONTRACTION	Details ...	69	0,13323483	0,44595295	1	0,9879766	1	5751	tags=26%, list=33%, signal=39%