Table S1

ID	logFC	AveExpr	P.Value	GenbankAccession	GeneSymbol
A_44_P505500	1.607556	11.90701	0.00122	CK358354	
A_43_P12141	1.561647	11.19161	0.001065	NM_021869	Stx7
A_44_P992854	1.324382	11.73082	0.002197	NM_057132	Rhoa
A_44_P196717	1.318426	10.03627	0.004003	XM_344970	Stk32c_predicted
A_44_P113842	1.173214	8.328451	0.000128	NM_022210	Max
A_44_P403482	1.15254	8.621625	0.000569	XM_213493	RGD1311493_predicted
A_44_P248111	1.143281	9.320377	1.87E-05	NM_001047107	Igsf4c_predicted
A_43_P16511	1.072354	9.35087	0.009672	NM_001044300	MGC112715
A_42_P522171	1.030953	9.111699	0.001285	XM_001081512	RGD1307966_predicted
A_44_P223252	1.015676	13.88146	0.009124	NM_031595	Psmc3
A_44_P239105	1.014573	8.624869	0.003369	XM_233341	Zfyve9_predicted
A_44_P563128	1.013565	7.972642	0.00074	XR_007778	
A_44_P864185	0.99365	9.886928	0.004432	AW142955	
A_44_P255954	0.985852	11.34905	0.008416	XM_573223	RGD1566063_predicted
A_44_P548507	0.976934	14.00466	0.003327	NM_032083	Chn1
A_42_P713975	0.96633	14.00655	0.002899	BC082799	LOC499779
A_43_P13247	0.945033	9.21568	0.001365	XM_001070141	Psd
A_44_P187789	0.919478	8.124942	0.001183	XM_001066818	
A_43_P16512	0.917668	12.84756	0.007548	XM_218824	RGD1311021_predicted
A_44_P769703	0.915946	8.731323	0.009651	NM_178096	Nrep
A_44_P210461	0.909428	13.77556	0.005967	NM_017025	Ldha
A_44_P176606	0.891879	7.720083	0.005843	NM_001007235	Itpr1
A_44_P480605	0.877686	13.69188	0.008763	XM_001066230	LOC291543
A_44_P1029397	0.874681	9.78541	0.006524	NM_198134	Bst2
A_44_P463858	0.858747	7.846463	0.000999	NM_133303	Bhlhb3
A_44_P189326	0.845271	12.61675	0.003442	NM_017319	Pdia3
A_43_P10162	0.837812	9.295357	0.0075	XM_224841	Odz3_predicted
A_43_P11622	0.797153	14.22093	0.002926	NM_012925	Cd59
A_44_P552865	0.794559	12.17696	0.008261	XM_221896	LOC304280
A_44_P508264	0.752347	7.640307	0.002071	NM_031762	Cdkn1b
A_44_P424570	0.739812	7.775522	0.002451	XM_235521	Poldip3_predicted
A_43_P12779	0.734704	13.88252	0.006576	NM_053346	Nrn1
A_44_P379976	0.719224	8.728674	0.009711	NM_001024782	Lrrc8
A_44_P797926	0.71717	11.582	0.009305	BG673275	
A_44_P506374	0.709429	8.661933	0.004513	XM_001073596	Nyw1
A_44_P356658	0.709393	8.23732	0.009249	XM_219716	Pdzd4_predicted
A_44_P108421	0.689004	9.564137	0.00606	XM_224350	Fndc3a_predicted
A_43_P16811	0.685518	9.346495	0.008035	NM_001014073	RGD1305486
A_44_P473322	0.680296	7.868224	0.005619	XM_224778	
A_44_P417077	0.679432	8.061647	0.001949	XM_573664	RGD1566234_predicted
A_44_P403410	0.65013	11.05502	0.004235	NM_001079895	Rbm9_predicted
A_44_P714315	0.649504	12.25655	0.006677	CO404950	
A_44_P501483	0.646159	14.38167	0.006042	XR_006667	LOC310385
A_44_P156966	0.642122	9.596286	0.007913	XM_228708	RGD1563226_predicted

A_44_P350794	0.5956	8.367077	0.009356	AA894317	
A_43_P10735	0.590686	11.8257	0.009669	BF555100	RGD1566317_predicted
A_43_P17622	0.586863	9.765676	0.005446	XM_345870	Lass5_predicted
A_42_P704370	0.57628	13.13036	0.008636	NM_023972	Arl6ip5
A_44_P448307	0.576147	14.16514	0.004325	XM_217432	Arpc2_predicted
A_44_P473472	0.569886	10.61491	0.008531	BC091233	RGD1307434_predicted
A_43_P21003	0.560543	10.93669	0.006849	NM_001033892	RGD1306841
A_44_P738831	0.55264	8.290444	0.004326	BE105152	
A_44_P189813	0.551359	9.934035	0.00539	XM_214295	Glt25d1_predicted
A_44_P161220	0.542591	14.16572	0.008859	NM_080482	Dbccr1
A_43_P19892	0.536862	10.33035	0.006277	NM_001014255	Aph1a
A_44_P108680	0.53537	8.102587	0.006747	NM_057116	Ppp2r2c
A_44_P229618	0.527464	8.367113	0.008818	XM_228065	Tmem1_predicted
A_44_P255236	0.525992	9.239359	0.009952	NM_019212	Acta1
A_44_P455065	0.518588	14.18702	0.006125	XM_001077680	RGD1564600_predicted
A_44_P208275	0.511361	8.057972	0.001406	NM_031795	Ugcg
A_43_P15848	0.510606	9.342219	0.007543	M81783	Kcnf1
A_44_P180294	0.507879	8.206421	0.006738	XM_344235	
A_44_P180676	0.507554	7.614493	0.004982	XM_341141	
A_44_P274573	0.507395	9.295892	0.007497	XM_232283	Plxnd1_predicted
A_44_P222865	0.490304	14.40565	0.009316	XR_006686	
A_44_P101023	0.487674	10.99103	0.008547	XM_239335	RGD1564778_predicted
A_44_P194863	0.470415	11.45454	0.005744	XM_220574	Spag7_predicted
A_42_P573610	0.468416	7.658664	0.003621	XM_233544	Eif2c1_predicted
A_44_P142843	0.46753	8.161509	0.009195	XM_001065442	LOC685834
A_42_P707937	0.463584	13.34077	0.006472	NM_080583	Ap2b1
A_44_P549028	0.462526	9.336237	0.005687	XM_001076082	
A_43_P17264	0.458705	8.929598	0.00814	XM_240329	RGD1565549_predicted
A_44_P720473	0.453531	8.555751	0.00795	CA512655	
A_44_P267155	0.448921	7.431128	0.008325	XM_221887	
A_44_P827752	0.443672	7.507669	0.008733		
A_43_P18570	0.433168	7.264582	0.003564	XM_236194	Mll
A_43_P21027	0.433031	8.243299	0.007216	XM_235023	RGD1560606_predicted
A_44_P195291	0.431798	12.51609	0.002861	XM_233382	RGD1560252_predicted
A_43_P23298	0.431665	8.463371	0.003823	XM_001079737	RGD1311730_predicted
A_44_P1005858	0.428954	8.971588	0.009179	CO404131	
A_44_P147980	0.42782	8.163945	0.003669	XM_576503	
A_44_P546901	0.41725	7.567971	0.007509	NM_012502	Ar
A_44_P304493	0.417047	8.166562	0.005191	NM_001024970	RGD1305572
A_43_P21762	0.387674	7.279607	0.007224	NM_001013187	Slc25a30
A_44_P333550	0.370196	7.827262	0.009141	NM_001013986	LOC305076
A_44_P119442	0.36235	11.97699	0.00757	XM_216492	Creb3
A_44_P277126	0.362131	7.823398	0.007942	XM_221369	
A_44_P133226	0.361641	7.62301	0.007063	XM_224852	Stox2
A_42_P601971	0.351093	7.762251	0.004338	XM_220328	Sox30_predicted
A_42_P504240	-0.304158	14.22476	0.007788	XM_237998	

A_44_P637629	-0.337548	12.37837	0.008706	DV727233	
A_42_P771373	-0.352053	15.04484	0.008398	NM_012614	Npy
A_44_P561760	-0.371864	10.60745	0.009932		
A_44_P479766	-0.372905	7.061162	0.008134	BM986564	
A_44_P535706	-0.375911	12.21228	0.007752	XM_216485	
A_42_P626023	-0.381003	10.46022	0.006668	XM_224232	Cenpj_predicted
A_44_P255384	-0.383536	15.24025	0.009335	XM_344225	RGD1562394_predicted
A_42_P570848	-0.388127	9.382288	0.007135	NM_017091	Pcsk1
A_42_P791872	-0.395678	15.20882	0.009108	XM_001061587	LOC682454
A_44_P212695	-0.39929	15.55995	0.00973	XM_212890	
A_42_P549321	-0.402635	15.09135	0.003742		
A_44_P473731	-0.40425	15.44158	0.00932	XM_220717	Abr_predicted
A_44_P762268	-0.405311	13.79055	0.006136		
A_44_P792063	-0.406364	12.72072	0.003616		
A_44_P593331	-0.407158	11.10025	0.00566		
A_44_P501390	-0.410068	12.88181	0.009047	XM_001055728	RGD1561042_predicted
A_44_P884739	-0.411871	14.79085	0.004969	XM_219339	Sez6l2_predicted
A_44_P1043979	-0.416159	15.46051	0.000961	NM_001030052	Ndufs5b
A_44_P161709	-0.418994	15.66453	0.005418	XM_345662	
A_42_P634674	-0.420247	15.27808	0.008207	NM_145783	Cox5a
A_43_P11268	-0.420794	12.19783	0.007261	NM_031762	Cdkn1b
A_44_P525486	-0.440114	10.56008	0.009935	XM_343841	Plxnb3_predicted
A_44_P592613	-0.444442	11.81328	0.008322	XM_576601	RGD1560766_predicted
A_42_P703403	-0.448031	15.45875	0.00121	NM_031974	Clta
A_44_P866539	-0.448651	15.46571	0.003064	AW913986	
A_44_P554867	-0.449101	13.80371	0.006241	AW917688	
A_44_P792470	-0.456522	10.01488	0.00406	DV722661	
A_43_P10505	-0.459756	15.07648	0.009444	XM_226549	Jph3_predicted
A_44_P995316	-0.460859	12.4553	0.007066	XM_343081	Sgpp1
A_44_P1055366	-0.461078	15.4244	0.005917	AW919175	
A_44_P914323	-0.461087	14.00556	0.009917	DV718684	
A_43_P16707	-0.462778	8.462194	0.007004	NM_001004202	Ccl6
A_44_P730454	-0.463051	11.17696	0.009253	XM_341399	Mapk8
A_42_P623151	-0.46981	15.46891	0.002427	NM_031026	Dncli2
A_44_P638345	-0.46998	11.36836	0.009927	NM_001034130	Wasl
A_44_P152635	-0.471578	7.525866	0.00501	NM_021857	Htr1f
A_44_P822928	-0.471616	12.19977	0.000854		
A_44_P156922	-0.473462	15.34944	0.008611	NM_001008312	Serinc3
A_44_P745579	-0.47912	11.5586	0.004111		
A_44_P1031514	-0.480469	12.12573	0.005639	NM_001014054	RGD1307778
A_44_P361202	-0.481728	13.36097	0.003147	CB569688	
A_42_P619248	-0.48445	15.32374	0.005621	XM_001053199	RGD1560511_predicted
A_44_P392886	-0.484852	15.8303	0.002919	CB567353	ND2
A_42_P614711	-0.494634	10.99742	0.003489	BF548552	
A_42_P475623	-0.495946	11.46603	0.007179	NM_053394	Klf5
A_43_P12692	-0.497221	15.00459	0.008597	NM_031814	Git1

A_44_P727480	-0.499614	12.44601	0.005736	AW142602	
A_44_P976007	-0.501242	10.5042	0.007044	DV719080	
A_44_P357478	-0.503165	7.182014	0.007098	CK481254	
A_44_P775118	-0.503898	10.08036	0.002595	NM_001014205	Tmem123
A_44_P372261	-0.505527	7.827664	0.00773	NM_053372	Slpi
A_44_P965429	-0.506297	11.15919	0.009965		
A_44_P393551	-0.507718	15.04609	0.006586	NM_012567	Gja1
A_44_P700333	-0.507758	11.50827	0.001397	CX570601	
A_43_P15460	-0.50937	11.70692	0.008183	NM_053879	Cntn4
A_44_P299247	-0.515458	14.98393	0.00915	NM_012778	Aqp1
A_44_P311334	-0.516913	8.09389	0.007592	L27060	Pde4d
A_44_P996952	-0.517441	9.262775	0.007491	NM_001039454	RGD1561028
A_44_P373681	-0.517613	11.90056	0.008317	BF563424	
A_42_P544321	-0.521129	10.1151	0.007505	AI136185	
A_44_P791696	-0.521548	11.62472	0.003333	DV725758	
A_44_P493603	-0.525791	11.8103	0.007827	DY472377	
A_44_P270700	-0.537381	15.29789	0.002379	BG663460	
A_42_P521814	-0.537861	11.63224	0.009573		
A_44_P640301	-0.54291	13.82233	0.0009	XM_001065707	RGD1566031_predicted
A_42_P525317	-0.54563	11.28367	0.006987	NM_053851	Cacnb2
A_44_P884444	-0.546077	10.18235	0.001586	XM_343782	RGD1563952_predicted
A_44_P650550	-0.558033	11.4954	0.001961	BF289404	
A_43_P11492	-0.559424	7.373786	0.002587	NM_012629	Prl
A_42_P839655	-0.561899	14.45612	0.003112	BF555716	
A_44_P443657	-0.564112	12.11021	0.008022	BI281988	
A_44_P655666	-0.576235	10.32947	0.003753		
A_42_P503281	-0.577323	11.59358	0.002812	NM_053603	Clic5
A_43_P12283	-0.579016	12.80167	0.004402	NM_022668	Mog
A_44_P884766	-0.5965	15.49362	0.000367		
A_44_P702115	-0.601856	10.62476	0.003276		
A_44_P283909	-0.609549	9.066482	0.008587	XM_216079	
A_44_P175677	-0.618299	7.45903	0.001548	XM_001062365	LOC685114
A_44_P386633	-0.630651	13.84789	0.00755	NM_145785	Hdgfrp3
A_44_P956310	-0.631047	7.415374	0.005342	AI171999	
A_42_P621736	-0.6312	15.79036	0.005605	NM_001007604	Rplp1
A_44_P469517	-0.631758	9.924125	0.005796	BF551572	
A_44_P605123	-0.644716	10.78691	0.005895	DV716579	
A_44_P770724	-0.651454	10.89887	0.002755	XM_225941	Dmxl1_predicted
A_44_P1017996	-0.663612	11.77483	0.00737	XM_341470	LOC361188
A_44_P350074	-0.666196	14.75075	0.004962	XM_001075009	LOC686892
A_44_P914438	-0.668649	10.16228	0.009157	NM_080782	Cdkn1a
A_44_P593071	-0.674446	7.774681	0.003372		
A_42_P575140	-0.683968	11.45806	0.009127	AW916021	
A_44_P652899	-0.703191	15.67359	0.004507	NM_178105	Gpm6a
A_44_P793157	-0.711691	9.441904	0.005513		
A_44_P416127	-0.713822	14.78112	0.002027	BG665128	

A_44_P123857	-0.729971	7.392116	0.00623	XM_227855	
A_44_P576019	-0.731695	9.762224	0.009106		
A_44_P556677	-0.742666	12.03146	0.004327	AW525326	
A_44_P531685	-0.774814	15.7317	0.002598	NM_212511	Rpl35
A_42_P484738	-0.777717	10.55331	0.009229	NM_022266	Ctgf
A_44_P976667	-0.778059	11.33574	0.002631		
A_44_P575265	-0.78268	7.162824	0.005089	XM_001059898	
A_44_P341298	-0.801823	10.7338	0.001651	BF396386	
A_44_P684912	-0.868223	11.62549	0.004168		
A_44_P344475	-0.871819	11.22742	0.007204	NM_053522	Rhoq
A_44_P608966	-0.898967	11.02197	0.002516		
A_42_P783113	-0.940675	15.01051	0.008372	XM_215044	
A_44_P728524	-0.948968	8.649392	0.004864	XM_218037	Zfp54_predicted
A_44_P353618	-1.598265	10.41172	0.006037	NM_053587	S100a9
A_44_P1055780	-1.799489	9.625261	0.00237	NM_053822	S100a8

Table S2

ID	logFC	AveExpr	P.Value	GenbankAccession	GeneSymbol
A_44_P255954	1.092079	11.34905	0.004114	XM_573223	RGD1566063_predicted
A_43_P16512	0.958391	12.84756	0.005599	XM_218824	RGD1311021_predicted
A_44_P199211	0.888268	13.1782	0.007	NM_001077641	Plcb1
A_44_P519174	0.865479	10.15332	0.001505	NM_001015027	Crebl2
A_44_P797926	0.827698	11.582	0.003393	BG673275	
A_44_P638014	0.786066	9.362983	0.001642	XM_001067431	Irf6_predicted
A_44_P253196	0.72852	10.6956	0.000407	XM_228114	Arid5b_predicted
A_44_P817120	0.705276	10.23002	0.000413	BF563826	
A_44_P764308	0.70371	12.43124	0.00571		
A_44_P515211	0.702895	9.195753	0.000603	NM_145765	Tnfsf15
A_44_P405203	0.692478	10.26765	0.001054	XM_218664	Hebp2_predicted
A_44_P314492	0.692285	10.13554	0.004549	XM_221672	Tiam1
A_44_P108421	0.689739	9.564137	0.006015	XM_224350	Fndc3a_predicted
A_44_P274573	0.681768	9.295892	0.000701	XM_232283	Plxnd1_predicted
A_44_P525431	0.678326	10.94687	0.001897		
A_43_P11622	0.670731	14.22093	0.009935	NM_012925	Cd59
A_44_P1050433	0.669816	10.15768	0.008041	XM_001078552	LOC691501
A_43_P19994	0.651395	9.365389	0.004094	XM_233485	Rlf_predicted
A_44_P473472	0.649492	10.61491	0.003372	BC091233	RGD1307434_predicted
A_44_P168514	0.64246	9.344473	0.001894	XM_226964	Zfhx4_predicted
A_44_P377645	0.63785	8.537705	0.000763	XM_342774	
A_44_P300612	0.625149	10.59645	0.008106	NM_022850	Dpp6
A_43_P17175	0.624011	8.564087	0.001089	NM_001031642	Serpinb1a
A_43_P17180	0.623162	11.83235	0.002449	NM_001007696	mrpl9
A_44_P323430	0.620476	9.88312	0.008344	NM_138532	Nme7
A_44_P422271	0.600331	10.07162	0.00451	XM_217019	Cerk_predicted
A_44_P525645	0.592939	8.785316	0.008531	XM_220442	
A_44_P175495	0.59217	7.297441	0.003832	NM_182952	Cxcl11
A_44_P163242	0.587393	8.543951	0.00271	NM_138541	Tacstd1
A_44_P102291	0.58478	9.037239	0.001128	XM_341619	Adamts19_predicted
A_43_P10020	0.579306	12.71223	0.009383	NM_012771	Lyz
A_44_P522492	0.577851	8.866765	0.002137	NM_133414	Clcc1
A_44_P348973	0.574847	8.505955	0.006247	NM_001004277	Lypla3
A_44_P160846	0.574796	8.886562	0.000923	NM_182673	Rnasel
A_44_P1027904	0.574744	12.94124	0.003016	XM_213794	Pop5_predicted
A_44_P269425	0.57387	10.3993	0.005824	NM_133415	Efcbp2
A_43_P17880	0.572611	8.703786	0.003833	NM_182953	Nek6
A_44_P440633	0.569351	10.4556	0.0078	NM_031639	Dlgh3
A_44_P255236	0.561685	9.239359	0.006445	NM_019212	Acta1
A_44_P469113	0.561279	9.121905	0.004531	XM_220779	Slfn2_predicted
A_42_P744464	0.559015	8.758601	0.006845	XM_340740	RGD1565449_predicted
A_44_P247219	0.558874	9.764186	0.001307	NM_053699	Cited4
A_42_P453976	0.554018	9.751298	0.000729	XM_219476	Ifitm6_predicted
A_44_P191022	0.553331	11.25682	0.006487	NM_053674	Phyh
A_44_P492629	0.552641	11.97851	0.003115	DV727624	LOC497975
A_43_P10824	0.546754	11.88143	0.00131	NM_001015010	Cib2
A_43_P18186	0.539919	10.43356	0.008235	XM_232226	Pdzrn3_predicted

A_44_P408520	0.539577	10.59062	0.006601	NM_031569	Oprl1
A_44_P189813	0.539428	9.934035	0.006284	XM_214295	Glt25d1_predicted
A_44_P150471	0.535326	12.78451	0.00827	NM_031696	Gpr88
A_43_P12802	0.5329	12.46216	0.00132	NM_053418	Ufd1l
A_44_P445369	0.532457	8.410379	0.004245	XM_001080476	LOC360824
A_44_P114184	0.525917	10.4511	0.003452	NM_022543	Ssg1
A_44_P134634	0.519467	9.390154	0.008789	CB576476	RGD1562272_predicted
A_44_P309523	0.516512	10.28453	0.007552	XM_001076269	LOC501230
A_44_P273449	0.514881	8.7635	0.008173	XM_214953	Perp_predicted
A_44_P823303	0.512983	7.675391	0.004082		
A_44_P729266	0.503142	7.240329	0.001277	XR_005718	LOC300506
A_43_P18294	0.500507	7.598985	0.003877	BC099835	
A_44_P314353	0.499854	9.286162	0.008369	NM_001037765	RGD1306649
A_44_P288241	0.496253	8.737087	0.006619	XM_341029	RGD1307396_predicted
A_44_P167408	0.492468	9.154808	0.007935	AW144014	
A_44_P229051	0.492248	7.852318	0.00518	NM_012748	Epim
A_44_P668388	0.490809	12.07127	0.004134	BC098022	RGD1561494_predicted
A_44_P408108	0.475979	9.272041	0.008532	XM_236649	Nbeal2_predicted
A_44_P189953	0.471873	9.605232	0.008348	NM_031769	Pdxk
A_44_P549028	0.471493	9.336237	0.004959	XM_001076082	
A_42_P839541	0.466727	8.176077	0.008615	NM_001007671	Cyb5d2
A_44_P252756	0.466033	9.749369	0.008365	XM_221874	
A_44_P655158	0.462016	10.96723	0.003263	CO567276	
A_44_P426624	0.46039	9.187297	0.002826	XM_344380	
A_43_P23215	0.456773	10.24316	0.001849	NM_001025737	Smpdl3b
A_44_P299123	0.452931	7.997765	0.006893	XM_215847	Nphp1_predicted
A_44_P456747	0.438792	8.694571	0.005099	AB012231	Nfib
A_44_P237220	0.438141	9.322389	0.003965	XM_214720	
A_44_P148280	0.437942	12.38004	0.007917	NM_053670	Crcp
A_43_P10534	0.434336	11.85153	0.00493	NM_001034108	Mar.02
A_44_P332817	0.430724	12.22793	0.008347	NM_053527	Cdc5l
A_43_P20794	0.418891	8.354658	0.007973	BC091326	Osbpl5
A_44_P483177	0.416901	11.34909	0.006728	NM_001009344	Tbrg1
A_43_P19369	0.414985	8.634819	0.008199	XM_219805	Prkg1_predicted
A_44_P545649	0.410999	7.755706	0.001615	NM_001014093	Parp16
A_44_P111825	0.410741	8.817684	0.006841	NM_001014144	RGD1305679
A_44_P1051765	0.405347	11.08866	0.005446	XM_342984	Thap3_predicted
A_44_P109834	0.401496	7.550092	0.006214	XM_341783	Rdh13_predicted
A_44_P809514	0.398808	7.858837	0.00334		
A_44_P1038400	0.394146	12.34258	0.005052	DV727624	LOC497975
A_43_P10315	0.393843	8.182339	0.009911	XM_341626	Gnal
A_44_P289173	0.390852	9.276699	0.007259	BC097985	Grtp1
A_44_P187300	0.390448	8.451293	0.008284	XM_344202	
A_44_P228903	0.389952	7.646097	0.001145	NM_078621	Ccbp2
A_44_P532500	0.387401	9.399204	0.008349	XM_217354	
A_43_P12267	0.380794	7.482954	0.00323	NM_022623	Fzd4
A_44_P424069	0.380306	7.490027	0.006055	XM_218463	Zfp84_predicted
A_44_P370082	0.379629	12.25524	0.005576	XM_340856	Timm22
A_43_P15129	0.377676	7.558528	0.009304	BF558849	

A_44_P349817	0.373434	7.119817	0.006636	XM_237215	LOC301455
A_44_P1010416	0.365499	8.425505	0.003415	NM_001002853	P2ry13
A_44_P447927	0.362439	7.278709	0.004074		
A_44_P356482	0.359146	7.30241	0.008106		
A_44_P119442	0.353803	11.97699	0.00886	XM_216492	Creb3
A_44_P409539	0.350217	7.44798	0.004442	NM_175869	Plod2
A_44_P407800	0.350096	7.710196	0.001764	XM_225607	
A_43_P17282	0.349379	7.370769	0.00758	XM_219879	Cnnm1_predicted
A_42_P809101	0.345238	10.43971	0.005251	XM_342873	Tctex1d1_predicted
A_44_P468816	0.340427	7.136901	0.008588	XM_001057103	
A_42_P601971	0.333952	7.762251	0.006207	XM_220328	Sox30_predicted
A_44_P398433	0.328459	7.746764	0.00909	XM_224923	Tnks_predicted
A_44_P156846	0.326852	7.465644	0.009923	XM_231139	Lamc3_predicted
A_44_P370774	0.321406	7.045656	0.007011	XM_235183	Irak3_predicted
A_44_P260384	0.313235	7.263999	0.00804	XM_240915	RGD1307915_predicted
A_44_P388709	0.279068	7.125181	0.007876	NM_145767	Prrxl1
A_44_P591036	-0.312213	7.029821	0.008327	XM_001069503	LOC685839
A_43_P11492	-0.341474	7.590819	0.006493	NM_012629	Prl
A_44_P229557	-0.344053	10.42845	0.008754	XM_230513	RGD1561554_predicted
A_44_P518050	-0.364194	11.07642	0.004205	XM_223566	Sf3a1_predicted
A_44_P184865	-0.377312	14.20673	0.007668	NM_031579	Ptp4a1
A_44_P1002407	-0.383112	12.21029	0.009369	AI137378	
A_44_P334736	-0.388138	8.79879	0.002976	NM_012548	Edn1
A_44_P839802	-0.389477	7.467368	0.008537		
A_44_P307646	-0.395441	7.041288	0.007608	BI289723	
A_44_P420046	-0.409126	8.398432	0.009059	NM_021669	Ghrl
A_42_P736812	-0.412467	13.07906	0.004888	NM_134449	Prkcdbp
A_44_P777113	-0.4134	11.74969	0.008401	XM_001068152	LOC684233
A_42_P840867	-0.416389	11.51094	0.005105	XR_008037	RGD1561455_predicted
A_44_P597013	-0.422945	9.936548	0.006715		
A_44_P288443	-0.423627	10.61669	0.00444	XM_344542	Thsd1_predicted
A_43_P13326	-0.425342	9.86345	0.003719	NM_138894	Grasp
A_44_P110334	-0.427016	7.55124	0.004078	XM_236387	RGD1560796_predicted
A_43_P23304	-0.429392	11.02713	0.004137	NM_199397	Panx1
A_44_P428338	-0.437758	7.45371	0.000983	AA817984	
A_44_P1050510	-0.440611	8.275122	0.007818	XM_001075804	LOC686809
A_44_P127962	-0.442185	9.386424	0.006015	NM_181771	Gpr135
A_44_P379645	-0.450221	7.565198	0.004867	AF030090	
A_44_P578593	-0.4523	9.756066	0.004554		
A_43_P18201	-0.452482	11.10478	0.007172	XM_230639	Zfp339_predicted
A_44_P283372	-0.452635	15.04796	0.00478	BC062235	Hnrpa1
A_44_P960490	-0.453901	13.07605	0.005162	XM_573497	
A_44_P171321	-0.460493	12.38677	0.003954	NM_001009671	RGD1359509
A_42_P737455	-0.463557	12.01383	0.00428	AI071866	
A_44_P182739	-0.466768	8.675444	0.009307	XM_217651	Pdzk8_predicted
A_44_P853624	-0.468433	10.94544	0.006035	XM_237855	RGD1308321_predicted
A_44_P650550	-0.475469	11.4954	0.00659	BF289404	
A_44_P745585	-0.483808	11.0584	0.00908	NM_001024309	LOC499749
A_44_P376411	-0.489603	13.76028	0.007865	BF548067	

A_44_P885461	-0.491508	11.36357	0.002118		
A_44_P976153	-0.492456	13.56608	0.002154		
A_44_P792746	-0.494639	12.61698	0.003912		
A_43_P14760	-0.495239	8.143939	0.006653		
A_44_P578847	-0.497309	11.57353	0.005959		
A_44_P1031380	-0.49908	7.921169	0.009759	XM_001077462	
A_44_P808218	-0.499845	10.42192	0.006617	XM_233470	RGD1311937_predicted
A_44_P278659	-0.509675	11.62496	0.001616	AJ517196	
A_44_P988767	-0.510231	9.065142	0.004772	BF564195	
A_42_P475623	-0.519306	11.46603	0.005213	NM_053394	Klf5
A_44_P653818	-0.5195	11.96479	0.002595		
A_44_P254238	-0.519538	12.83616	0.005937	NM_001033670	Bcl2l1
A_44_P635089	-0.520099	14.54726	0.000703	AI030078	
A_44_P724632	-0.522737	10.62241	0.006501	AI176008	
A_44_P1026631	-0.523563	12.89669	0.008387	XM_573823	Akap11
A_44_P840348	-0.530728	11.49232	0.00838		
A_44_P559242	-0.532673	9.055327	0.004592	XM_001065920	
A_42_P570848	-0.544448	9.382288	0.000431	NM_017091	Pcsk1
A_44_P175677	-0.555101	7.45903	0.00369	XM_001062365	LOC685114
A_42_P788810	-0.562441	11.15106	0.008966	AW918709	
A_44_P837846	-0.574638	11.59704	0.005446	DV723320	
A_44_P895064	-0.576006	8.930311	0.00887	XM_341290	RGD1562692_predicted
A_44_P570046	-0.577647	10.78454	0.007289	XM_001067059	LOC314964
A_42_P502759	-0.58777	14.49019	0.00567	XM_343513	Aplp2
A_44_P249774	-0.594975	8.836396	0.009915	BG668003	LOC688621
A_44_P731912	-0.601613	10.58883	0.006816		
A_42_P638620	-0.608517	7.700495	0.003204	NM_130741	Lcn2
A_44_P181718	-0.61556	8.066556	0.003116	BI285476	
A_44_P521587	-0.616852	13.53308	0.00098	XM_224588	Arhgef3_predicted
A_44_P374708	-0.619325	11.886	0.0085	NM_198750	Cry1
A_44_P962074	-0.632751	9.587462	0.006478		
A_44_P551872	-0.637831	8.523936	0.009835	AI555745	
A_42_P556083	-0.641374	11.39813	0.009144	NM_013165	Cckbr
A_44_P492624	-0.643134	9.667534	0.000409	XM_340867	
A_44_P472989	-0.643421	10.67878	0.003461	NM_017232	Ptgs2
A_44_P199107	-0.65155	7.152713	0.003241	XM_345241	RGD1562545_predicted
A_44_P341298	-0.654523	10.7338	0.007667	BF396386	
A_43_P12535	-0.655373	13.32748	0.009243	NM_031135	Klf10
A_43_P14919	-0.660635	12.98223	0.002117	NM_019372	Ppm2c
A_43_P12283	-0.667059	12.80167	0.001419	NM_022668	Mog
A_44_P776423	-0.671757	12.77633	0.001579	NM_001017386	Tmem10
A_44_P559239	-0.692896	8.905563	0.004793	AW921223	
A_44_P1034541	-0.694564	12.09181	0.001515	NM_022602	Pim3
A_44_P254130	-0.701323	10.04192	0.000593	AA875032	
A_44_P337351	-0.707538	13.17046	0.00034	NM_001033883	Cxcl12
A_44_P593071	-0.709574	7.774681	0.002257		
A_44_P221885	-0.71164	11.43124	0.005104	BF565038	
A_44_P589346	-0.723727	11.5605	0.003934	DY471743	
A_42_P762508	-0.757283	9.97503	0.000872	NM_001034199	Nptx2

A_44_P670185	-0.758857	10.81712	0.00219		
A_44_P823528	-0.760627	10.71223	0.000555		
A_42_P681722	-0.767592	10.37324	0.00117	BF554576	
A_44_P870183	-0.771142	10.51029	0.007791		
A_42_P739860	-0.772039	11.50895	0.005963	NM_133578	Dusp5
A_44_P914438	-0.778529	10.16228	0.003109	NM_080782	Cdkn1a
A_44_P219026	-0.785466	10.94052	0.002205	NM_012513	Bdnf
A_44_P732510	-0.804474	8.797511	0.008231	DV722942	
A_44_P307971	-0.824418	12.49927	0.004772	L04739	
A_44_P807565	-0.830688	10.52499	0.002158		
A_44_P1029253	-0.914823	10.58408	0.002969	NM_012757	Mas1
A_44_P378959	-0.933023	11.30108	5.98E-06	AA859348	
A_44_P763434	-0.945217	10.5241	0.005537	XM_576579	RGD1560005_predicted
A_44_P437896	-0.953692	10.65054	1.17E-05	NM_012513	Bdnf
A_44_P303430	-0.964636	12.90879	5.44E-06	AW142654	
A_44_P916210	-0.990373	15.19466	0.001296		
A_44_P522524	-0.9989	9.086332	0.000509	NM_019328	Nr4a2
A_44_P931389	-1.006772	11.03869	0.002907	CA509267	
A_44_P1032732	-1.010129	9.622861	0.006732	NM_031740	B4galt6
A_42_P839593	-1.017323	11.81139	0.002422	AW142999	
A_44_P424723	-1.05196	11.14587	0.005727	NM_021693	Snf1lk
A_42_P484738	-1.143309	10.55331	0.000399	NM_022266	Ctgf
A_44_P512806	-1.18274	7.98503	0.000782	NM_153626	Npas4
A_44_P654444	-1.185412	12.51873	8.56E-06	DQ268830	Nr4a3
A_44_P365379	-1.251433	11.97297	0.000967	NM_001077640	Gadd45g
A_42_P594613	-1.298603	11.44392	0.000322	NM_053883	Dusp6
A_42_P540950	-1.311262	12.17803	0.004526	NM_001009541	Ier2
A_44_P233080	-1.323167	14.34415	9.76E-05	NM_012551	Egr1
A_44_P701809	-1.392299	9.465179	0.000511		
A_44_P591857	-1.393798	11.97394	0.000557		
A_42_P708068	-1.414561	13.68879	5.27E-05	NM_019137	Egr4
A_44_P560710	-1.449866	9.965458	0.000353		
A_44_P495480	-1.508251	10.05032	0.001411	NM_022197	Fos
A_43_P12619	-1.588268	12.07253	0.000459	NM_031628	Nr4a3
A_44_P212803	-1.612143	13.06959	0.002631	AF050659	
A_43_P12125	-1.615114	11.49742	0.003416	NM_021836	Junb
A_44_P218896	-1.65862	9.205401	0.006471	NM_031327	Cyr61
A_44_P398142	-1.690248	12.12949	0.002178	NM_017259	Btg2
A_44_P380835	-1.72043	11.95836	1.00E-05	AB003726	Homer1
A_44_P839581	-1.759771	11.1114	0.000537		
A_42_P682589	-1.881937	13.8678	0.000267	NM_024388	Nr4a1
A_43_P11932	-2.061968	9.928836	0.000533	NM_017352	Nr4a3
A_42_P750683	-2.096022	9.035922	0.000742	NM_031327	Cyr61
A_44_P118724	-2.159492	14.27586	4.76E-05	NM_019361	Arc
A_42_P473594	-2.43313	11.62043	3.64E-06	NM_053633	Egr2

Table S3

ID	logFC	AveExpr	P.Value	GenbankAccession	GeneSymbol
A_44_P839581	1.478474	11.1114	0.002504		
A_44_P157527	1.190031	9.92948	0.000759	BF285469	
A_44_P535706	1.064651	12.24392	0.008651	XM_216485	
A_42_P525886	1.056686	10.01648	0.004039	XM_236253	Crabp1
A_44_P262625	0.984094	10.4371	0.002967	XM_344424	
A_44_P217250	0.951383	10.90076	0.00608	NM_012949	Eno3
A_44_P478637	0.946374	8.477595	0.000206	BI274236	
A_42_P679251	0.920972	10.74394	0.00304	NM_031503	Ascl2
A_44_P931389	0.919886	11.03869	0.005691	CA509267	
A_44_P913689	0.915771	12.44902	0.003316		
A_43_P16887	0.914468	10.50225	0.006547	XM_215059	Eraf_predicted
A_44_P479890	0.912017	9.666256	0.000903	NM_153821	Prrx1
A_42_P793008	0.908714	15.02889	0.007719	NM_130432	Rps13
A_44_P231657	0.907535	10.83999	0.000947	XM_341779	Zfp628_predicted
A_43_P14752	0.898158	10.27264	0.000507	XM_001073940	LOC690274
A_44_P236566	0.897017	9.874991	0.000944	XM_230848	Neurl2_predicted
A_44_P671992	0.894022	11.10745	3.85E-05	XM_575387	RGD1566201_predicted
A_43_P16949	0.846619	9.382546	0.006384	XM_220884	Sgca_predicted
A_43_P11563	0.835843	9.280827	0.00022	NM_012784	Cnr1
A_44_P685508	0.821372	10.87674	0.005479		
A_44_P743576	0.820139	10.21146	0.001612	AW917533	
A_44_P1009948	0.806853	12.19187	0.002096	XM_220532	RGD1304587
A_44_P252855	0.803766	10.96382	0.000453		
A_44_P853254	0.800247	10.52673	0.005443		
A_44_P197290	0.792545	9.481667	0.001253	NM_021760	Col5a3
A_44_P588759	0.792232	10.76386	0.000334	BF563670	
A_44_P543813	0.776085	10.17043	0.005401	XM_228345	Ascc3_predicted
A_44_P974651	0.774859	10.43947	0.000564	XM_575260	RGD1564048_predicted
A_42_P635881	0.773147	11.75922	0.000466	NM_031782	Slc32a1
A_44_P558838	0.769348	9.104969	0.00724	BF417038	
A_44_P413324	0.763004	10.31502	0.00565	BF558477	
A_44_P307308	0.761818	9.460592	0.008579	XM_237568	LOC301725
A_43_P11044	0.760943	11.9497	0.003488	NM_001009632	G0s2
A_44_P409913	0.750951	8.847053	0.008251	XM_341043	
A_44_P685354	0.747361	8.734705	0.001885		
A_42_P596942	0.746022	8.598174	8.19E-05	NM_145682	Filip1
A_42_P568943	0.738116	8.151025	0.007983	XM_217167	RGD1311874_predicted
A_44_P592800	0.732669	10.93803	0.001284		
A_44_P233786	0.73062	14.31421	0.002362	NM_030997	Vgf
A_44_P461587	0.727787	10.34052	0.000607	XM_341847	RGD1311142_predicted
A_44_P808072	0.727337	10.73465	0.007333		
A_43_P11082	0.723487	10.05847	0.003035		
A_44_P304759	0.722884	9.750024	0.003913	XR_007322	RGD1563459_predicted
A_44_P670185	0.715761	10.81712	0.003476		
A_42_P814235	0.715392	9.823875	0.00957	NM_057124	P2ry6
A_44_P848951	0.708819	10.57781	0.002262	AW915522	
A_44_P222447	0.706019	14.60212	0.004094	CF979076	RGD1560394_predicted

A_44_P319238	0.705051	9.700374	0.003076	XM_345977	Cpne4_predicted
A_44_P589674	0.702823	9.794569	0.002936	AI406628	
A_44_P394279	0.701716	14.61949	0.008634	XM_001081777	RGD1560070_predicted
A_43_P19039	0.699688	11.21215	0.001006	XM_342487	RGD1560583_predicted
A_44_P1014527	0.698386	11.80935	0.007188	XM_216189	Alms1_predicted
A_44_P1000100	0.69182	10.41259	0.000131	XM_215666	Trim45_predicted
A_44_P117216	0.691555	9.702736	0.004375	NM_001025007	RGD1310852
A_44_P559239	0.69093	8.905563	0.004893	AW921223	
A_44_P620208	0.688642	11.0855	0.001347	BF549419	
A_44_P868418	0.683253	11.31543	0.002557	AI043758	
A_44_P748361	0.683244	9.811364	0.009237		
A_42_P797638	0.677852	11.19226	0.001471	XM_341839	Wtip_predicted
A_43_P12401	0.677561	9.473038	0.006205	NM_024142	Mepe
A_42_P596050	0.674306	9.845698	0.004973	NM_053572	Pcdh21
A_44_P435158	0.674159	8.895149	0.004429	AW917664	
A_44_P930681	0.673171	11.51947	0.003812	DV723298	
A_44_P882551	0.671501	11.07155	0.007595	XM_001072622	RGD1560871_predicted
A_42_P782490	0.669773	9.828156	0.005585	XM_226464	RGD1560268_predicted
A_44_P640931	0.668623	11.37124	0.001121		
A_44_P1049275	0.666814	10.60548	0.009591	DQ889715	
A_44_P272253	0.66654	9.507764	0.001977	XM_213864	LOC288978
A_44_P507773	0.661387	10.38264	0.009943	BG663014	RGD1565037_predicted
A_44_P971665	0.659826	11.41268	0.003752	AW916050	
A_43_P11476	0.656787	9.86656	0.003993	NM_012590	Inha
A_44_P668572	0.65317	10.08484	0.003757		
A_44_P900576	0.653048	9.196065	0.006286		
A_44_P996952	0.653002	9.262775	0.001239	NM_001039454	RGD1561028
A_44_P376112	0.652891	10.44574	0.00588	X72758	
A_44_P178503	0.652686	9.392082	0.007859	XM_221452	
A_44_P1034937	0.650992	12.38865	0.006503	NM_001011966	Smarcd3
A_44_P296473	0.648189	8.12823	0.003827	AI013718	
A_44_P623694	0.648094	9.491483	0.003318	XM_001067023	LOC688455
A_44_P358028	0.646793	10.30608	0.009916	CO569648	
A_44_P179338	0.646712	8.706902	0.007715	AI603168	Rps15
A_42_P740209	0.643911	10.52559	0.000482	NM_012601	Mpg
A_44_P669323	0.641396	9.487703	0.003317		
A_44_P500295	0.639834	8.53055	0.005152	BI274118	
A_42_P619403	0.638018	10.81318	0.00178	XM_341720	RGD1309879
A_44_P316898	0.636016	11.33567	0.002103	XM_213488	Higd1b_predicted
A_44_P324906	0.635202	11.11406	0.004427	AW142380	
A_43_P11634	0.633438	9.769668	0.004831	NM_012959	Gfra1
A_44_P753353	0.633317	8.537939	0.008049	CO401859	
A_44_P464065	0.632653	9.778917	0.008309	NM_001033687	Ushbp1
A_44_P729931	0.632187	10.18263	0.001685	XM_001061367	LOC682404
A_44_P808566	0.631451	9.344853	0.003337		
A_43_P11350	0.629225	9.91316	0.006281	NM_001009271	Nt5dc2
A_44_P637675	0.627415	11.75785	0.004746		
A_44_P1024315	0.625645	10.69359	0.006978	NM_031321	Slit3
A_42_P560984	0.625403	13.64446	0.000459	XM_574891	RGD1565641_predicted

A_44_P1048140	0.620488	10.50182	0.000329	AI072036	
A_43_P12205	0.619793	10.56946	0.007281	NM_022294	Eltd1
A_42_P558206	0.618407	11.05513	0.005686	AW144330	
A_44_P513232	0.618325	12.10898	0.003182	BC099181	
A_44_P747073	0.618093	8.869727	0.002865		
A_43_P11654	0.616996	11.29558	0.003532	NM_013007	Pnoc
A_44_P1007449	0.6148	11.20815	0.004405	XM_222190	RGD1310159_predicted
A_44_P1026706	0.612765	10.75157	0.003673	XM_001061644	RGD1560433_predicted
A_44_P900390	0.611891	10.72012	0.000772		
A_42_P735417	0.610726	9.364027	0.003617	NM_175756	Fcgr2b
A_44_P284079	0.610166	8.530775	0.005062		
A_44_P839432	0.609938	9.475047	0.003499		
A_44_P747182	0.60653	11.36896	0.005169		
A_44_P376411	0.606227	13.76028	0.001558	BF548067	
A_44_P559242	0.605856	9.055327	0.001664	XM_001065920	
A_42_P694208	0.602707	9.982905	0.00706	XM_216483	RGD1311126_predicted
A_43_P17094	0.602556	11.6708	0.005941	XM_575803	RGD1561916_predicted
A_44_P977637	0.599374	9.003673	0.001018		
A_43_P10036	0.598834	12.94357	0.004326		
A_43_P11441	0.598154	9.32848	0.006699	NM_012510	Atp4b
A_44_P113907	0.59688	10.14031	0.007975	NM_170787	Cmbp
A_42_P620042	0.594377	11.38184	0.009277	NM_032080	Gsk3b
A_43_P14264	0.593121	10.59142	0.003642	NM_053653	Vegfc
A_44_P311963	0.588438	10.50042	0.001069	XM_575939	RGD1560468_predicted
A_44_P420046	0.586908	8.398432	0.000493	NM_021669	Ghrl
A_44_P653264	0.586072	11.61992	0.004981		
A_44_P408050	0.585517	11.32287	0.007527	XM_343189	Ckap4_predicted
A_44_P200522	0.584708	8.435389	0.006355	AI171232	
A_44_P404737	0.584359	8.349892	0.006292	BQ208553	
A_44_P1031380	0.584111	7.921169	0.003226	XM_001077462	
A_43_P22042	0.583503	10.78119	0.009341	NM_001009353	Pla2g7
A_43_P17061	0.582069	10.14337	0.00096	XM_223729	Rnf3_predicted
A_44_P746478	0.581686	10.85794	0.009795		
A_42_P829349	0.580869	12.14343	0.001062	XM_223785	Comtd1_predicted
A_44_P1017035	0.580629	9.27318	0.003502	NM_019214	Slc26a4
A_44_P250575	0.580384	9.39954	0.009085	XM_214236	Nudt15_predicted
A_43_P13381	0.577117	10.26594	0.001837	NM_139326	Pomc
A_44_P1026631	0.577082	12.89669	0.004254	XM_573823	Akap11
A_44_P255837	0.576706	15.01845	0.004168	XR_007349	RGD1561996_predicted
A_44_P215917	0.573202	8.78396	0.009015	XM_344018	RGD1563504_predicted
A_44_P686665	0.566384	9.497307	0.007581		
A_44_P1036170	0.565807	10.90934	0.006795	XM_220770	Nle1_predicted
A_44_P434118	0.565666	8.471229	0.007235	XM_213408	Rhbdl4_predicted
A_42_P695770	0.565462	13.0292	0.000787	XM_214288	
A_42_P686756	0.564589	11.6427	0.008268	BC087706	
A_42_P781585	0.56446	10.69382	0.006588	NM_001037554	Bex4
A_44_P1027971	0.564132	10.09748	0.002595	XM_001068081	LOC688730
A_43_P15659	0.563997	11.5428	0.000662	XM_342062	
A_44_P457599	0.563541	9.073987	0.003797	NM_053832	Foxj1

A_43_P17945	0.56207	9.8905	0.006736	NM_001014006	F12
A_43_P18226	0.561037	9.822439	0.009187	XM_234942	Myo1f_predicted
A_44_P956958	0.560997	10.34486	0.00161	AW143890	
A_42_P747311	0.560893	10.13027	0.008442	NM_057204	Ptpn23
A_44_P533531	0.560063	7.749707	0.003019	AI406723	
A_44_P302265	0.558124	8.517348	0.00574	XM_001065833	
A_44_P1050510	0.55727	8.275122	0.001286	XM_001075804	LOC686809
A_44_P302383	0.557114	15.03616	0.006088	XR_006725	LOC288777
A_44_P273734	0.556905	11.77642	0.00382	BC090336	Man1a_predicted
A_44_P983188	0.555079	9.746672	0.005676	AA818818	
A_44_P128820	0.554639	9.493733	0.000674		
A_42_P454907	0.554121	8.79808	0.001381	NM_053644	Cdh23
A_43_P14870	0.553953	10.69843	0.008927	NM_001013224	Nmnat3
A_42_P771373	0.553627	15.02783	0.001801	NM_012614	Npy
A_44_P454065	0.552253	10.04517	0.00631	NM_019147	Jag1
A_44_P527154	0.552208	10.96466	0.002312	NM_001024282	RGD1564767_predicted
A_42_P550172	0.55146	10.77524	0.008243	XM_001072438	
A_44_P356679	0.550647	10.6521	0.002296	XM_342932	Atpbd1b_predicted
A_44_P186883	0.550626	10.1592	0.004351	NM_173103	Clcnkb
A_44_P731439	0.550347	9.554146	0.002267		
A_44_P1020748	0.549987	11.98345	0.002468	XM_343405	RGD1309779_predicted
A_43_P19791	0.549438	10.00081	0.007721	XM_343063	
A_43_P13996	0.548706	10.46704	0.007236		
A_42_P515028	0.548351	8.802646	0.007597	XM_574162	RGD1564431_predicted
A_44_P527089	0.5474	8.896843	0.004266	M11597	Calca
A_44_P117015	0.546888	14.60943	0.009864	XM_342664	Ndufb2_predicted
A_44_P454847	0.546823	12.30266	0.002103	XM_342460	Ptpmt1
A_42_P502768	0.543328	11.25355	0.009264	XM_001065468	LOC685841
A_44_P974137	0.541887	7.395577	0.0006	AI716115	
A_44_P354018	0.540368	13.14388	0.00538	XM_224779	RGD1559708_predicted
A_43_P16588	0.540157	12.47542	0.0032	XM_342414	Sh2d3c_predicted
A_44_P993027	0.538938	11.5777	0.00983	NM_017060	Hrasls3
A_44_P186860	0.537831	10.31388	0.007414	NM_030867	Nfkbib
A_44_P779143	0.537821	8.487288	0.00418		
A_44_P468661	0.536414	10.48671	0.003267	XM_001067949	LOC688966
A_42_P797965	0.535476	11.00195	0.00189	XM_341902	RGD1306959_predicted
A_44_P728951	0.534878	15.17816	0.006581	NM_031838	Rps2
A_44_P960935	0.5334	11.41158	0.002319		
A_44_P525649	0.533214	11.41392	0.003291		
A_44_P1020608	0.533079	9.273392	0.007964	XM_227821	Ifi44
A_44_P115509	0.532461	8.32335	0.003018	CN542475	Mrpl34
A_44_P901878	0.531861	8.805109	0.001812		
A_44_P389590	0.530125	8.795146	0.006664	XM_236348	Cilp_predicted
A_44_P1034346	0.527902	15.16222	0.002687	NM_001013922	RGD1307752
A_44_P996729	0.524978	9.473439	0.003588	NM_031054	Mmp2
A_44_P792646	0.524628	8.148467	0.006338		
A_44_P187641	0.524616	10.19557	0.009149	XM_342871	RGD1307610_predicted
A_42_P700089	0.52346	11.57458	0.009959	NM_001034157	Bat4
A_44_P791860	0.521772	9.427981	0.001731		

A_42_P501233	0.521734	12.36386	0.003728	NM_024483	Adra1d
A_44_P592844	0.521615	9.250689	0.000598		
A_44_P159613	0.521193	9.600495	0.006964	XM_344763	RGD1306894_predicted
A_43_P14871	0.520827	9.257777	0.002226	NM_021587	Ltbp1
A_44_P792446	0.520423	9.211865	0.009129	XM_235529	Scube1
A_44_P189859	0.517844	8.457089	0.006586	NM_001012094	Zfp297b
A_43_P22700	0.517808	8.510855	0.00613		
A_42_P578953	0.517652	9.465361	0.009175	XM_342416	Ptrh1_predicted
A_44_P210736	0.51718	10.06647	0.009054	XR_007818	RGD1563527_predicted
A_44_P668620	0.516418	10.83056	0.003444	XM_340915	Ccdc43
A_42_P837214	0.516128	9.812712	0.005553	NM_012861	Mgmt
A_44_P164848	0.514671	10.69432	0.007166	AW142951	
A_43_P10498	0.514272	11.03042	0.001276	XM_237039	
A_44_P421333	0.513769	8.574784	0.007005	NM_080778	Nr2f2
A_44_P122206	0.513365	15.15379	0.003959	NM_022541	Timm8b
A_44_P133485	0.512323	12.43585	0.003145	XM_342883	LOC362564
A_44_P337311	0.511511	7.975955	0.001121	XM_342172	Thbs4
A_44_P670043	0.510834	10.45987	0.007806		
A_44_P1026123	0.509573	12.01201	0.008494	XM_341806	
A_44_P978083	0.507157	10.46215	0.00409		
A_42_P737455	0.506634	12.01383	0.002142	AI071866	
A_44_P607632	0.505455	10.97934	0.004712	XM_001079243	LOC691678
A_44_P412236	0.505256	10.44247	0.004168	NM_053730	Stag3
A_44_P976153	0.504629	13.56608	0.001759		
A_44_P853624	0.503794	10.94544	0.003551	XM_237855	RGD1308321_predicted
A_44_P370645	0.503213	13.74896	0.007767	XM_216400	Sec61b_predicted
A_44_P561643	0.502716	8.03752	0.008948		
A_44_P274083	0.502042	11.44706	0.007485	NM_173105	Aqp11
A_44_P263854	0.500949	7.556899	0.002011	AA819299	
A_44_P997787	0.499178	11.68636	0.001984	XM_213799	RGD1562579_predicted
A_44_P215056	0.49916	15.24759	0.00311	NM_001007235	Itpr1
A_42_P621832	0.498006	13.25698	0.002695	XM_215083	RGD1306636_predicted
A_43_P12437	0.496721	9.648658	0.008789	NM_024385	Hhex
A_44_P513360	0.494845	8.485518	0.000889	XM_214152	Cdkn3_predicted
A_43_P14954	0.493343	11.66088	0.004046	XM_233820	Sos1
A_44_P447701	0.492105	10.46227	0.008867		
A_43_P19306	0.491696	10.80629	0.0087	XM_223660	RGD1309501_predicted
A_43_P19265	0.490977	10.98343	0.009847	XM_342507	RGD1562705_predicted
A_44_P330109	0.490805	10.01774	0.00451	NM_040669	Hps1
A_43_P10072	0.490183	10.93163	0.005158	NM_213564	Zbtb9
A_44_P241190	0.48927	10.80101	0.003973	NM_001013199	Sdccag10
A_42_P601961	0.487725	10.03823	0.00844	XM_225203	Susd3_predicted
A_44_P932158	0.487385	9.506271	0.005037		
A_42_P512838	0.487372	12.00659	0.004471	XM_217335	Trem2_predicted
A_44_P562712	0.486028	9.158063	0.005034		
A_44_P409232	0.485898	7.385279	0.003633	NM_031543	Cyp2e1
A_44_P370335	0.48549	11.42783	0.006794	NM_001011911	Lyar
A_44_P597013	0.484512	9.936548	0.002444		
A_44_P713589	0.482311	9.954375	0.008636		

A_44_P591963	0.481999	11.282	0.009105	DV728639	
A_44_P822852	0.480143	13.07186	0.008598	XM_001073919	LOC686393
A_43_P10505	0.479408	15.07648	0.007169	XM_226549	Jph3_predicted
A_44_P428922	0.479017	10.93142	0.009585	XM_341979	
A_42_P824657	0.47757	10.6343	0.002811	XM_214678	RGD1307357_predicted
A_44_P306626	0.476762	11.74221	0.007671	XM_577573	
A_44_P277669	0.47676	9.356253	0.008363	XM_573168	RGD1559961_predicted
A_42_P770330	0.47665	12.22638	0.008628	XM_001062632	LOC684934
A_44_P125145	0.476294	9.924844	0.006945	CF109884	
A_44_P387314	0.476035	8.528691	0.007087		
A_42_P738337	0.475807	13.2805	0.005505	NM_012575	Grin2c
A_43_P16816	0.47557	11.83034	0.009131	NM_001044290	LOC686883
A_44_P1022403	0.474294	13.72272	0.002583	NM_001004204	MGC94190
A_42_P506956	0.473183	10.23541	0.006511	NM_133559	Pcsk4
A_43_P17196	0.473149	10.88791	0.007969	XM_576184	RGD1562114_predicted
A_44_P1058112	0.473068	10.42333	0.002332	NM_001009627	Yars2
A_44_P578250	0.472654	10.84042	0.007706	DV714571	
A_44_P290327	0.471468	10.33899	0.008942	NM_001004234	MGC94881
A_44_P669746	0.471266	9.35851	0.001943	XM_229131	Cova1_predicted
A_44_P776556	0.470685	10.6081	0.007348	XM_342497	Chac1_predicted
A_44_P239176	0.468474	12.48785	0.009179	NM_001008380	RGD1308959
A_43_P14144	0.468252	12.01082	0.002547	XM_222855	Umpk_predicted
A_42_P700150	0.467273	11.80679	0.000671	BP483355	
A_44_P240414	0.466987	11.48117	0.005379	NM_001017537	Tex261
A_42_P515931	0.466948	11.1748	0.009094	XM_220256	
A_44_P225353	0.465362	10.46115	0.008862	NM_001009678	RGD1311458
A_44_P492624	0.465045	9.667534	0.006243	XM_340867	
A_44_P930534	0.464955	9.366294	0.00883	BC092660	RGD1563167_predicted
A_43_P11236	0.463992	12.00416	0.001889	NM_053538	Laptm5
A_44_P281457	0.463175	15.21279	0.006222	XM_001054883	LOC679899
A_44_P792746	0.462911	12.61698	0.006308		
A_43_P10692	0.461194	10.27534	0.009132		
A_44_P859124	0.460771	9.379251	0.006061	CB328239	LOC689165
A_44_P437346	0.460583	8.365901	0.002927	AW435442	
A_44_P368513	0.459819	9.534264	0.003137	BF282682	
A_44_P816687	0.457365	15.08238	0.006713		
A_44_P1008245	0.457175	10.86121	0.004652	XM_216310	Casc1_predicted
A_44_P997737	0.457138	10.4096	0.009265	AA942848	
A_44_P288443	0.456325	10.61669	0.002509	XM_344542	Thsd1_predicted
A_44_P472635	0.454909	7.530146	0.002444	AA900458	
A_44_P938669	0.454871	10.45325	0.007816	BC127463	Ng3
A_44_P496788	0.454063	11.58357	0.008877	NM_001008295	Fip1l1
A_42_P459306	0.453602	15.23919	0.009502	CB314148	RGD1305687_predicted
A_44_P1030801	0.453237	11.43176	0.005632	NM_031749	Gcs1
A_44_P557994	0.451938	15.05147	0.00241	XR_006555	LOC298125
A_44_P142472	0.451815	13.74517	0.002097	XM_214293	RGD1308064_predicted
A_44_P1027866	0.45081	10.85902	0.004562	NM_001011925	Nup93
A_44_P292419	0.449724	7.803599	0.006188	AA944408	
A_44_P1045652	0.449511	10.26325	0.009308	XM_001057185	LOC680266

A_44_P843798	0.448234	10.13852	0.00458	AW144049	
A_42_P792497	0.446787	8.957712	0.00776	NM_023025	Cyp2j4
A_44_P747708	0.445849	8.532038	0.006265		
A_42_P809733	0.445214	10.10656	0.009371	XM_347094	RGD1309410_predicted
A_44_P281216	0.444489	11.03937	0.00685	XM_341975	
A_42_P666843	0.44252	12.14138	0.000614	XM_214296	Pgls_predicted
A_44_P838483	0.439995	12.02493	0.003033		
A_44_P980178	0.439693	9.848248	0.007696		
A_42_P838051	0.439586	10.38087	0.002926	XM_216446	Oma1_predicted
A_44_P211997	0.436673	8.390802	0.00677	BF282863	
A_44_P381177	0.433194	8.439087	0.00677	AA925047	
A_44_P1058421	0.432785	11.85759	0.007566	BC091438	Phf12
A_44_P884119	0.432377	11.39608	0.007537	NM_001014061	LOC312863
A_44_P303883	0.431123	8.470756	0.007266	AI602844	
A_43_P17192	0.430405	11.86591	0.00643		
A_44_P274785	0.427234	11.39347	0.009019	XM_213260	RGD1310922_predicted
A_44_P1004260	0.426859	11.65237	0.009919	XM_231121	Tmem15_predicted
A_44_P147888	0.424227	7.149848	0.009323	AA925444	
A_43_P11580	0.423705	9.696657	0.007139	NM_012833	Abcc2
A_44_P402559	0.422607	7.597691	0.002504	NM_001000910	Olr1598_predicted
A_44_P307646	0.422312	7.041288	0.004813	BI289723	
A_44_P591370	0.421966	13.85891	0.006538		
A_44_P993577	0.42188	10.7227	0.005385	XM_214633	RGD1560538_predicted
A_44_P710192	0.419518	7.395678	0.007925	NM_001033067	Tmem45b
A_44_P251542	0.418155	7.329535	0.00136	NM_001008864	Tessp5
A_44_P1045612	0.416475	9.352711	0.005762	NM_172317	Fxyd3
A_44_P156317	0.413928	15.16467	0.005538	NM_138910	Dad1
A_42_P705083	0.413592	9.636382	0.00501	XM_341621	Il17b
A_44_P638411	0.411681	8.943508	0.009697		
A_44_P1030648	0.41131	11.38167	0.009437	XM_001079792	LOC687694
A_43_P23304	0.410921	11.02713	0.005687	NM_199397	Panx1
A_44_P476237	0.409138	7.158337	0.005359	BF406637	
A_44_P822839	0.408016	12.31907	0.007651		
A_44_P890053	0.407782	7.351377	0.005303	CA505010	
A_44_P899264	0.405945	11.22946	0.007897		
A_44_P421534	0.405341	12.30185	0.00563	NM_017196	Aif1
A_44_P981783	0.402686	9.048275	0.007562		
A_44_P558411	0.39837	12.48958	0.005443	NM_033499	Scrg1
A_42_P802520	0.396592	12.61219	0.008982	NM_172063	Pex14
A_44_P340498	0.396466	12.96412	0.007304	XM_213445	RGD1559720_predicted
A_44_P1050444	0.396311	10.22641	0.007523	NM_001007749	Atp5s
A_44_P229769	0.395256	15.30845	0.006174	NM_031838	Rps2
A_44_P140266	0.39507	8.238868	0.007651	XM_227523	Slc22a15_predicted
A_44_P562685	0.393179	8.369911	0.003369	XM_575917	RGD1564163_predicted
A_44_P810151	0.392701	11.82465	0.003282		
A_43_P14262	0.391785	13.5887	0.006879	XM_001057346	RGD1565310_predicted
A_44_P422602	0.390835	7.556121	0.007543	AI177360	
A_44_P667745	0.387442	13.15201	0.007663	DY311022	
A_44_P475617	0.386967	7.385824	0.004279	XM_238082	RGD1565487_predicted

A_43_P21364	0.383104	8.531841	0.007566	XM_343342	LOC363009
A_44_P399999	0.379395	15.41955	0.009292	NM_053752	Suclg1
A_44_P1002320	0.378477	13.9765	0.006397	BF289377	
A_44_P505188	0.378105	7.591275	0.009527	AI454498	
A_44_P378322	0.375598	9.393646	0.00534	AA858768	
A_44_P290016	0.375006	13.07897	0.009351	BG666843	
A_43_P22494	0.37441	8.369659	0.007185		
A_43_P16530	0.374106	13.06302	0.009245	XM_213733	Pop7_predicted
A_44_P1043668	0.372798	7.238479	0.006893	NM_001014003	RGD1307172
A_44_P1051894	0.368997	9.204886	0.007275	XR_009243	LOC363915
A_44_P1047992	0.367006	7.214531	0.008066	NM_012803	Proc
A_42_P685138	0.366955	11.97115	0.009234	NM_153621	Dab1
A_44_P351239	0.366576	7.624133	0.008737	NM_001000949	Olr179_predicted
A_43_P16804	0.363022	11.4628	0.007236	NM_001007652	Pole3
A_42_P626023	0.358798	10.46022	0.00991	XM_224232	Cenpj_predicted
A_44_P134465	0.350702	8.410751	0.0084	AA963226	
A_44_P257522	0.348981	8.174514	0.007883	XM_574228	Agrp
A_44_P178014	0.346895	7.08938	0.007953	BC079202	RGD1560814_predicted
A_44_P273515	0.339925	12.94672	0.0055	DV723169	
A_44_P108993	0.338519	7.542753	0.006345	BF420718	
A_43_P14576	0.33491	13.26406	0.006177		
A_44_P794680	0.332151	8.579136	0.009291		
A_44_P505488	0.329268	7.348394	0.008895	BI288152	
A_44_P591036	0.30765	7.029821	0.009164	XM_001069503	LOC685839
A_44_P388709	-0.277114	7.125181	0.00825	NM_145767	Prrxl1
A_44_P163408	-0.301364	7.336079	0.007371	NM_031798	Slc12a2
A_44_P370774	-0.30644	7.045656	0.009599	XM_235183	Irak3_predicted
A_44_P300110	-0.31546	8.120294	0.00754	XM_234335	Zfyve26_predicted
A_44_P515461	-0.317648	12.48507	0.00948	NM_171990	Bpnt1
A_44_P228903	-0.319342	7.646097	0.005616	NM_078621	Ccbp2
A_44_P349720	-0.326164	7.517157	0.006523	NM_001039174	LOC654482
A_44_P374795	-0.328038	7.277528	0.009295	XM_232197	Fbln2
A_44_P242252	-0.328341	13.95643	0.008558	NM_031237	Ube2d3
A_44_P557376	-0.334624	7.479056	0.009316	NM_012546	Drd1a
A_43_P18979	-0.337979	8.103409	0.009229	XM_340992	Rabl3_predicted
A_43_P16060	-0.338348	7.375756	0.005639	XM_001065759	Mitf
A_44_P332429	-0.34648	8.812568	0.004876	NM_138900	C1s
A_44_P274526	-0.347421	7.964663	0.002915	XM_230889	RGD1311378_predicted
A_44_P865552	-0.352072	7.495648	0.007668	AW143038	
A_44_P291081	-0.354249	10.2845	0.008309	XM_001054316	Mon2
A_44_P372555	-0.355726	10.97908	0.008972	NM_175764	Jmjd1a
A_44_P604860	-0.355913	8.288109	0.008249	BC098774	
A_44_P150432	-0.356004	7.38676	0.000845	D38557	
A_43_P15352	-0.360573	7.803403	0.006078	NM_080577	Nploc4
A_43_P18495	-0.362158	8.081096	0.009698	NM_001011952	Slc39a8
A_44_P304374	-0.363852	8.110134	0.007795	NM_001012745	Zfp422_predicted
A_44_P187388	-0.371358	7.568589	0.008114	XR_006961	LOC295077
A_44_P464428	-0.371729	7.097096	0.001069	XM_343279	Zfp647_predicted
A_43_P21231	-0.372047	8.054747	0.008386	XM_217594	Suv39h1_predicted

A_42_P703664	-0.372616	8.338728	0.00858	CV118897	Srxn1
A_44_P1010416	-0.372721	8.425505	0.002935	NM_001002853	P2ry13
A_44_P187524	-0.376345	13.29484	0.008423	XM_214690	Aars
A_44_P527635	-0.377348	7.727722	0.0087	NM_001014055	RGD1309682
A_44_P874814	-0.377382	8.871871	0.007677		
A_44_P437973	-0.377777	7.563555	0.005686	NM_020090	Slc24a1
A_44_P412418	-0.37849	7.41379	0.004835	XM_001063618	
A_43_P17282	-0.380701	7.370769	0.004136	XM_219879	Cnnm1_predicted
A_44_P180645	-0.382578	7.562432	0.006521	BC098851	Usp24_predicted
A_44_P333452	-0.385514	7.947414	0.004676	XM_347258	RGD1563309_predicted
A_44_P1000561	-0.386045	8.849037	0.007385	XM_235378	RGD1305781
A_44_P136911	-0.386216	13.38161	0.006216	BC078917	Rnpc2
A_43_P16885	-0.386816	8.04462	0.007478	XM_235169	Mdm2_predicted
A_44_P536125	-0.388142	9.259137	0.006564	NM_053557	Hrmt1l3
A_44_P656668	-0.388242	7.348888	0.009361	CK476135	
A_44_P154721	-0.389698	9.396214	0.006498	XM_220217	Zfp263_predicted
A_44_P116606	-0.392618	7.486812	0.007196	XM_342337	Ank2
A_43_P12267	-0.392704	7.482954	0.002535	NM_022623	Fzd4
A_44_P829047	-0.393483	8.964901	0.006918	CO402576	
A_44_P541431	-0.395296	8.013577	0.009828	NM_001024246	RGD1310794
A_44_P925410	-0.396807	9.196403	0.00307	BF386740	
A_43_P22351	-0.398613	8.784806	0.007162	NM_001024968	RGD1307594
A_43_P19646	-0.399039	7.740829	0.002969	XM_341833	
A_44_P984158	-0.40054	7.913112	0.002939	BI291259	LOC691759
A_43_P11729	-0.401196	7.849259	0.005334	NM_013134	Hmgcr
A_44_P184955	-0.402159	9.922687	0.009914	XM_215006	RGD1307366_predicted
A_44_P374341	-0.402413	11.9804	0.009791	NM_001029897	Strn3
A_44_P395572	-0.402616	7.391226	0.004891	NM_147210	Nr1d2
A_43_P18148	-0.402674	8.9781	0.008113	XM_218963	Arhgef17_predicted
A_44_P333374	-0.402932	7.958977	0.004709	XM_001064905	RGD1560736_predicted
A_44_P998042	-0.405032	7.829167	0.005607	XM_229579	RGD1309621
A_44_P128986	-0.406634	10.13576	0.006003	NM_001034959	LOC619574
A_44_P893828	-0.408401	8.447218	0.009765		
A_42_P584710	-0.409763	7.911257	0.005578	XM_213677	
A_44_P545649	-0.411763	7.755706	0.00159	NM_001014093	Parp16
A_44_P147980	-0.41267	8.163945	0.004793	XM_576503	
A_44_P126027	-0.414711	8.320375	0.002833	NM_019333	Pfkfb4
A_44_P149599	-0.415456	8.959757	0.008602	NM_001079705	RGD1311558_predicted
A_43_P22795	-0.416161	8.343222	0.009128	NM_001037204	Taf1a
A_44_P303716	-0.417343	9.839435	0.004084	XM_345266	Trim33_predicted
A_44_P100609	-0.418309	11.7365	0.008571	XM_001064153	
A_44_P655158	-0.418598	10.96723	0.00669	CO567276	
A_44_P337579	-0.41874	7.77436	0.007229	NM_001008346	RGD1308302
A_43_P16847	-0.419123	7.615653	0.004217	XM_233686	Spsb1_predicted
A_44_P523190	-0.420052	7.857785	0.004025	XM_343095	RGD1311756_predicted
A_44_P683082	-0.422342	8.705595	0.008957		
A_44_P473314	-0.424177	7.958854	0.0092	NM_001013997	RGD1309522
A_44_P729266	-0.425062	7.240329	0.00491	XR_005718	LOC300506
A_44_P357870	-0.425064	10.4228	0.00681	NM_031559	Cpt1a

A_43_P15840	-0.425124	8.202072	0.006167	XM_221874	
A_44_P166464	-0.425388	7.355895	0.005999	XM_235050	Scyl2_predicted
A_43_P15468	-0.426087	7.748036	0.004805	NM_012585	Htr1a
A_44_P549198	-0.426763	7.242243	0.007579	XM_224165	Ift88_predicted
A_44_P520700	-0.426846	10.3449	0.007187	XM_341377	RGD1561742_predicted
A_44_P986848	-0.427928	13.98555	0.004016	XM_341882	Sytl2_predicted
A_44_P206258	-0.430841	10.53316	0.008065	NM_001034146	Usp10
A_44_P123813	-0.43159	7.738666	0.005008	XM_223597	Cobl_predicted
A_44_P258277	-0.432043	11.92776	0.007726	NM_001008507	Dhrs7b
A_44_P304493	-0.432466	8.166562	0.00398	NM_001024970	RGD1305572
A_44_P668388	-0.433567	12.07127	0.009722	BC098022	RGD1561494_predicted
A_44_P1004392	-0.435274	12.93181	0.003053	XM_221455	LOC288109
A_44_P328654	-0.436421	11.70857	0.007688	XM_576882	LOC501474
A_43_P19234	-0.437806	11.46931	0.009135	NM_001034926	LOC310946
A_44_P1026191	-0.438058	10.88975	0.004056	NM_001039338	LOC362156
A_44_P116809	-0.439177	7.470634	0.000991	NM_001014136	Ngly1
A_44_P501242	-0.439216	8.149434	0.006859	XM_215947	Ncoa3
A_44_P327515	-0.440596	8.048777	0.003946	XM_001060307	LOC501515
A_44_P206154	-0.4407	7.880564	0.005502	XM_345231	RGD1307244_predicted
A_43_P10608	-0.442394	12.19876	0.002867	XR_006750	RGD1310444_predicted
A_44_P188869	-0.443051	7.32103	0.003535	AW915311	
A_44_P333550	-0.443265	7.827262	0.002488	NM_001013986	LOC305076
A_44_P360563	-0.443912	7.683515	0.003859	NM_017012	Grm5
A_44_P456747	-0.445211	8.694571	0.00459	AB012231	Nfib
A_43_P12243	-0.445373	13.92915	0.006547	NM_022540	Prdx3
A_44_P134186	-0.445505	12.47747	0.00625	NM_145678	Vps4a
A_44_P377722	-0.446034	12.68135	0.009816	NM_001007651	Peflin
A_44_P183227	-0.446446	9.436279	0.008026	CO394022	
A_44_P545867	-0.446549	8.205647	0.001163	XM_222229	RGD1309359_predicted
A_42_P574960	-0.447813	11.39518	0.001401	XR_009643	
A_44_P682849	-0.448246	8.37393	0.00533	XM_001081465	Rundc1_predicted
A_44_P462285	-0.450382	7.83441	0.00322	XM_342391	Inpp5e
A_44_P170864	-0.450423	10.55487	0.006427	XM_223651	RGD1311920_predicted
A_44_P729342	-0.451904	12.94046	0.007958	XR_009643	
A_44_P124027	-0.452323	8.094798	0.001562	XM_226458	RGD1309394_predicted
A_44_P193644	-0.452453	9.664843	0.00925	XM_001062296	RGD1561065_predicted
A_44_P466608	-0.454116	10.16095	0.008012	XM_238380	Usp5_predicted
A_43_P22288	-0.45513	8.782478	0.008509	XM_001068814	
A_44_P437721	-0.455167	9.310782	0.004106	CO566833	
A_44_P449819	-0.455646	8.385985	0.006492	NM_053851	Cacnb2
A_44_P443493	-0.45642	9.271581	0.007848	NM_001025754	Neil1
A_43_P17816	-0.456669	9.180063	0.00936	NM_199120	Cdv1
A_44_P544297	-0.457127	7.92615	0.004401	NM_001009661	Wbp11
A_44_P114184	-0.457582	10.4511	0.009192	NM_022543	Ssg1
A_44_P485592	-0.457681	12.21972	0.009729	XM_217388	Mrps9
A_44_P257832	-0.458486	8.387939	0.007793	XM_224535	Farp1_predicted
A_44_P174982	-0.458794	10.12484	0.004693	NM_022601	Pnpo
A_43_P10332	-0.460476	7.918233	0.004285	XR_009629	
A_44_P759334	-0.461876	12.22712	0.009711	NM_001011914	Dr1

A_44_P424069	-0.463971	7.490027	0.001269	XM_218463	Zfp84_predicted
A_44_P324034	-0.465472	8.71878	0.006468	XM_235942	RGD1308472_predicted
A_43_P19519	-0.465646	8.376732	0.001694	XM_223781	Vcl_predicted
A_43_P22080	-0.465665	8.304411	0.004401	NM_001012044	Lcp1
A_43_P15916	-0.465861	8.580545	0.006233	XM_342491	
A_44_P249717	-0.465922	7.787938	0.004592	AW144114	
A_43_P10414	-0.466482	9.127477	0.001963	NM_001017445	Ubxd8
A_44_P515792	-0.466818	8.010703	0.008513	XM_341532	Elmo1_predicted
A_44_P260475	-0.467015	10.55382	0.007242	XM_238362	Hdac11_predicted
A_44_P492629	-0.469771	11.97851	0.009798	DV727624	LOC497975
A_44_P412710	-0.469921	10.97259	0.005681	NM_001025423	Adhfe1
A_44_P211111	-0.470244	8.929899	0.007857	XM_236367	RGD1565416_predicted
A_44_P445521	-0.470433	13.10279	0.000946	XM_226843	Rnasen
A_44_P267501	-0.47192	7.687429	0.007344	NM_001017448	RGD1311358
A_44_P520557	-0.472441	9.851848	0.009165	XM_230284	Arhgap1_predicted
A_43_P21150	-0.472475	9.124359	0.007372	XM_345825	Tbc1d15
A_44_P484877	-0.472528	11.40675	0.009604	AF475093	
A_44_P283772	-0.47292	8.297396	0.005855	XM_573876	RGD1561342_predicted
A_44_P345136	-0.473156	8.837558	0.00698	XM_340879	Spag9_predicted
A_44_P625829	-0.474148	8.485355	0.009303		
A_44_P427067	-0.474709	11.6164	0.0082	XM_001076752	
A_43_P13424	-0.474807	9.092693	0.004906	NM_173290	Yy1
A_44_P231655	-0.476392	7.596331	0.007901	XM_222147	Glt1d1_predicted
A_44_P414704	-0.47772	8.234356	0.008052		
A_44_P397851	-0.477779	9.15503	0.007182	NM_053518	Lyst
A_44_P730048	-0.477978	10.56896	0.008411		
A_43_P21938	-0.478192	8.638288	0.008101	XM_220541	Ulk2_predicted
A_44_P381842	-0.479346	8.259924	0.009669	XM_343640	Ptprm
A_44_P1058502	-0.479398	8.486831	0.004314	XM_238162	Ppfia1_predicted
A_44_P463973	-0.479937	10.936	0.006261	NM_001079889	Sephs2
A_44_P126498	-0.479954	8.848829	0.009172	XM_234272	Klhdc1_predicted
A_43_P15409	-0.480053	8.148761	0.006225	NM_023971	Drp2
A_44_P384833	-0.480229	7.833966	0.007021	XM_343166	Mum1_predicted
A_44_P324124	-0.480593	10.55514	0.009972	XM_220595	RGD1563106_predicted
A_44_P350098	-0.480639	8.884507	0.006151	XM_345938	Alg9_predicted
A_44_P107177	-0.481244	7.566365	0.008674	NM_017018	Hrh1
A_42_P645142	-0.483451	11.32202	0.008261	NM_019375	Sep.03
A_44_P356445	-0.483861	7.658623	0.002629	XM_227547	Lrig2_predicted
A_44_P376905	-0.484469	12.72706	0.003147	XM_214994	Spcs2_predicted
A_44_P532020	-0.484935	8.716298	0.008881	XM_219414	RGD1306820_predicted
A_44_P501220	-0.485339	7.802926	0.003192	NM_053951	Mcf2l
A_44_P331109	-0.485528	8.957026	0.006251	XM_220175	
A_44_P105229	-0.485553	10.16727	0.004021	NM_001013157	Nnt
A_44_P664802	-0.485909	12.15639	0.007649	DV728182	
A_44_P136845	-0.486006	12.40366	0.00595	XM_340879	Spag9_predicted
A_44_P397495	-0.487804	12.14965	0.00402	NM_024359	Hif1a
A_44_P311955	-0.488411	8.390355	0.004453	NM_017171	Prkce
A_42_P765031	-0.48852	8.84223	0.007803	XM_346083	
A_44_P480830	-0.489345	8.330588	0.005378	NM_001079943	Zfp426

A_44_P661516	-0.490505	7.975856	0.002516		
A_43_P18324	-0.490957	7.896779	0.0057	NM_207165	Arl10
A_44_P215931	-0.491066	7.225432	0.004447	AI232088	
A_44_P501992	-0.491468	12.71414	0.003475	BC071175	Ero1l
A_44_P693682	-0.49161	10.28309	0.008944		
A_43_P12802	-0.491629	12.46216	0.002589	NM_053418	Ufd1l
A_43_P18343	-0.492117	10.27197	0.005068	XM_001072617	Gga2
A_44_P299123	-0.492405	7.997765	0.003786	XM_215847	Nphp1_predicted
A_44_P301512	-0.492541	11.62567	0.003021	NM_176077	G6pc3
A_42_P612592	-0.495016	7.834775	0.002747	XM_001067905	Saps3_predicted
A_44_P583834	-0.495725	11.18116	0.005538	XM_223597	Cobl_predicted
A_44_P534113	-0.496145	8.15518	0.008216	NM_053866	Plaa
A_44_P409977	-0.496805	8.586221	0.003235	NM_001012742	Wee1
A_44_P403816	-0.497337	10.19456	0.002825	AW142588	
A_44_P1057763	-0.497353	14.89762	0.00726	NM_053576	Prdx6
A_44_P768438	-0.498157	15.05002	0.00177	XM_225314	Vmp_predicted
A_44_P539167	-0.498327	7.569368	0.001016	XR_009059	LOC317276
A_44_P729229	-0.498505	8.042134	0.00752	XR_009322	LOC366863
A_44_P210753	-0.499432	9.573971	0.006112	M22631	Pcca
A_44_P935947	-0.499675	9.102805	0.004718	XM_342684	Hnrpa2b1_predicted
A_44_P303044	-0.499955	8.694465	0.006585	XM_239258	Supt6h
A_44_P555760	-0.50031	7.670131	0.002044	XM_001064688	LOC257646
A_44_P286467	-0.50037	9.413313	0.009875	XM_237056	RGD1309266_predicted
A_44_P388973	-0.501101	14.59061	0.004797	NM_012571	Got1
A_44_P123102	-0.501148	8.015902	0.00321	NM_001039607	LOC294154
A_44_P293438	-0.502716	12.33671	0.00823	XM_340949	RGD1311925_predicted
A_44_P993382	-0.503389	10.06768	0.009282	NM_031121	Ssrp1
A_44_P351490	-0.504828	10.77395	0.000536	NM_031797	Cd82
A_44_P370213	-0.505052	14.71043	0.007415	NM_012749	Ncl
A_43_P16583	-0.505052	11.68119	0.002588	XM_214539	Snx2_predicted
A_44_P400520	-0.505512	11.05271	0.004681	NM_012866	Nfyc
A_44_P133464	-0.511164	8.223828	0.008518		
A_43_P23298	-0.511238	8.463371	0.000938	XM_001079737	RGD1311730_predicted
A_44_P281750	-0.511574	12.76908	0.004393	XM_237790	Poldip2_predicted
A_44_P533572	-0.511838	8.138074	0.003513	AI639343	
A_44_P292900	-0.512225	7.828978	0.007812	XM_219377	LOC309016
A_44_P340180	-0.51227	9.585392	0.00796	XM_341668	Anapc10_predicted
A_44_P1048296	-0.512554	13.82163	0.005698	NM_172023	Osbpl1a
A_44_P238019	-0.513936	9.708293	0.005888	AW143671	
A_43_P21191	-0.513978	8.21006	0.001345	XM_234988	Btbd11_predicted
A_44_P1034030	-0.514586	8.979437	0.008022	XM_220420	Aff4_predicted
A_44_P290424	-0.51475	10.67252	0.004908	NM_080905	Siah1a
A_44_P461678	-0.515057	8.811745	0.002391	XM_574677	RGD1564887_predicted
A_44_P363522	-0.515107	10.42892	0.005067	NM_001031661	B4galt7
A_43_P23210	-0.515252	11.99024	0.00817	NM_001012153	Fmip
A_44_P477633	-0.516537	9.815629	0.007468	NM_174864	Ncstn
A_44_P226906	-0.517049	7.231693	0.004884	NM_147205	St6gal1
A_44_P540279	-0.517501	11.62786	0.00369	AW144704	
A_44_P377698	-0.518017	8.032468	0.004629	XR_006438	LOC303083

A_44_P157009	-0.518179	7.915851	0.008623	XM_232995	Rnf20_predicted
A_44_P445369	-0.518198	8.410379	0.005173	XM_001080476	LOC360824
A_44_P520929	-0.51833	8.270723	0.001288	NM_001007675	C1qtnf1
A_44_P208566	-0.520218	8.194993	0.000909	XM_341567	Plxdc2_predicted
A_44_P301875	-0.521017	8.537786	0.005085	XM_343761	Wdr44
A_43_P10744	-0.521209	11.8158	0.00767	NM_001014212	RGD1309784
A_43_P16724	-0.521403	8.927668	0.008353	NM_001014188	RGD1307688
A_44_P974892	-0.521521	8.218009	0.000906		RGD1560103_predicted
A_43_P18451	-0.521667	10.50442	0.007196	NM_080579	Gpr19
A_44_P342730	-0.521799	9.506206	0.005248	NM_001012275	Arih2_predicted
A_44_P362498	-0.523592	9.057442	0.008193	AW143788	
A_44_P255678	-0.523681	10.04796	0.004349	XM_228777	RGD1564628_predicted
A_43_P13675	-0.524202	9.004544	0.003831	CO570281	
A_44_P150877	-0.525453	9.650493	0.008311	XM_001080836	RGD1560454_predicted
A_44_P109834	-0.526057	7.550092	0.000686	XM_341783	Rdh13_predicted
A_42_P644929	-0.527818	13.23495	0.009106	NM_021579	Nxf1
A_44_P171155	-0.527957	12.38644	0.002943	NM_001014221	LOC363337
A_44_P142843	-0.528222	8.161509	0.003931	XM_001065442	LOC685834
A_43_P17871	-0.529071	9.583896	0.008044	NM_001013186	Bin3
A_44_P940553	-0.529771	14.44724	0.005633	AW143148	
A_43_P21003	-0.529928	10.93669	0.009913	NM_001033892	RGD1306841
A_44_P651694	-0.530167	7.349954	0.003359		
A_44_P776937	-0.530279	8.932346	0.00542	CR754170	
A_44_P227201	-0.530711	8.205059	0.002803	XM_225013	Tubgcp3
A_43_P10797	-0.532261	13.40048	0.001705	BG666794	
A_44_P471691	-0.532338	8.448807	0.000262	XM_223781	Vcl_predicted
A_44_P378225	-0.532628	11.11796	0.003763	NM_001011993	Pycrl
A_44_P315714	-0.535232	9.634824	0.009022	NM_021577	Asl
A_44_P683068	-0.535246	8.540939	0.005211	NM_017032	Pde4d
A_44_P260055	-0.53652	10.82252	0.004399	NM_031043	Gyg1
A_42_P750029	-0.537118	10.17965	0.001934	BF559198	
A_44_P490460	-0.537239	8.583732	0.001709	XM_224518	Tgds_predicted
A_44_P230960	-0.5381	12.36711	0.005794	AW144271	
A_44_P415459	-0.538541	9.588119	0.007499	CB547990	
A_44_P228874	-0.538818	9.251096	0.007028	NM_012815	Gclc
A_44_P516073	-0.539135	9.313478	0.001599	XM_217194	RGD1310552_predicted
A_44_P223808	-0.540022	11.92907	0.003404	XM_225711	
A_44_P170338	-0.540274	7.955337	0.009628	NM_001002815	Ece2
A_44_P485614	-0.540413	8.787416	0.00262		
A_44_P241371	-0.54044	9.019803	0.007357	NM_001013161	Cstf1
A_44_P175543	-0.541018	8.534275	0.005918	NM_001033699	Cox15
A_44_P579630	-0.541041	9.037196	0.009716		
A_44_P515211	-0.541293	9.195753	0.005306	NM_145765	Tnfsf15
A_44_P466183	-0.541305	8.38538	0.006606	NM_133410	Rap2b
A_44_P168778	-0.541812	8.029785	0.008427	XM_233220	LOC313391
A_44_P201601	-0.542679	9.320256	0.006957	XM_216096	
A_44_P180080	-0.54313	13.22102	0.002966	NM_022867	Map1lc3b
A_44_P353927	-0.543168	8.204865	0.002782	XM_341931	RGD1564195_predicted
A_44_P344340	-0.543214	8.425997	0.006536	U78135	Zfoc1

A_44_P310949	-0.543425	11.20006	0.004972	NM_001004283	Eif3s7
A_43_P12473	-0.543679	8.782044	0.000727	NM_031006	Adar
A_44_P207215	-0.543992	8.44599	0.001323	XM_237115	Nck2_predicted
A_44_P281155	-0.544066	7.616002	0.008359	XM_341127	Nek7_predicted
A_44_P323729	-0.544773	7.638288	0.004219	NM_001042621	Pip5k1a_predicted
A_43_P10248	-0.544913	13.09991	0.007402	NM_001014117	Ublcp1
A_44_P147622	-0.545175	10.55648	0.001064	XM_343462	Dnajc13_predicted
A_44_P386375	-0.545382	10.05504	0.004797	NM_053842	Mapk1
A_44_P333232	-0.545453	7.603713	0.001496	XM_342803	
A_44_P265326	-0.545734	8.11399	0.003644	BC087674	Pus3_predicted
A_43_P19260	-0.546023	9.074997	0.004115	XM_001053368	RGD1559803_predicted
A_44_P525101	-0.546161	7.790761	0.001773	XR_006056	
A_44_P534508	-0.546585	8.026102	0.003988	XM_231749	Zfp212
A_44_P447514	-0.546908	9.609403	0.003516	NM_017155	Adora1
A_44_P493688	-0.547009	12.20581	0.001709	NM_001008371	RGD1309216
A_44_P587322	-0.547841	13.30776	0.002382	AW917250	
A_43_P15866	-0.548306	9.016571	0.002132	XM_341686	Ap1g1
A_43_P21374	-0.548726	8.795816	0.003865	NM_001008353	Mkks
A_44_P557474	-0.549682	9.075636	0.006461	NM_053742	Pitpnb
A_44_P191022	-0.549841	11.25682	0.006775	NM_053674	Phyh
A_44_P338068	-0.550111	9.971705	0.002162	NM_001024355	LOC500909
A_44_P331003	-0.551713	8.367306	0.002003	XM_234281	
A_44_P222603	-0.551891	8.122971	0.004433	XM_341580	
A_44_P995544	-0.552105	10.31184	0.006155	NM_001039034	Wdr5
A_44_P241781	-0.552115	9.261364	0.004623	BF558420	
A_44_P228715	-0.552514	9.397023	0.000278	NM_019275	Smad4
A_44_P803129	-0.552556	8.623957	0.002243	AW918772	
A_44_P352104	-0.552676	11.45537	0.00664	XM_216993	Slc25a17_predicted
A_44_P168083	-0.553081	12.95714	0.005519	NM_019381	Tegt
A_44_P443228	-0.554142	10.05594	0.005989	XM_341622	Fech_predicted
A_43_P21031	-0.554515	8.256688	0.002089	XM_232343	Pex5_predicted
A_44_P171128	-0.55544	10.96284	0.00987	XM_232987	Alg2
A_44_P160550	-0.555742	12.55467	0.008317	NM_017116	Capn2
A_44_P349689	-0.555915	13.50737	0.009107	NM_001009831	Spg3a
A_44_P550670	-0.556316	11.92568	0.005809	XM_223611	Tmed4_predicted
A_44_P454426	-0.556338	8.18265	0.002798	AF133906	
A_43_P15280	-0.556496	8.112504	0.001725	NM_019194	Tef
A_43_P21715	-0.557461	8.881928	0.008605	BC091390	RGD1305062
A_44_P147582	-0.558181	7.806964	0.004217	NM_001079936	Rab5b_predicted
A_44_P173345	-0.558596	7.899522	0.002954	XM_342595	Stx16_predicted
A_44_P381483	-0.558686	11.69825	0.003748	XM_213930	
A_44_P167403	-0.558725	9.628788	0.006902	AA875633	
A_44_P191924	-0.559349	10.83352	0.006013	NM_019906	Frap1
A_43_P20321	-0.559792	8.491448	0.000581	XM_228770	Ccdc22_predicted
A_44_P744309	-0.560586	10.48679	0.005371	XM_222534	LOC683847
A_44_P289630	-0.562386	13.30648	0.005131	NM_017261	Gria2
A_44_P1019326	-0.562708	14.64606	0.007105	NM_199372	Eif4a1
A_44_P292479	-0.563031	12.45133	0.007171	NM_053880	Dncic2
A_44_P146833	-0.563782	11.62293	0.007793	M92076	Grm3

A_44_P284462	-0.563948	12.82861	0.003027	NM_031728	Snap91
A_44_P529934	-0.56395	8.644282	0.007049	XM_225661	RGD1566269_predicted
A_43_P16274	-0.564297	11.44811	0.004857	S53987	Chrna7
A_43_P16927	-0.564312	8.495799	0.003682	XM_228073	Pofut2_predicted
A_43_P19892	-0.564842	10.33035	0.004367	NM_001014255	Aph1a
A_44_P147062	-0.564927	9.477962	0.008194	XM_220095	Moxd1
A_42_P627394	-0.564957	13.05839	0.000589	BC089998	
A_44_P299699	-0.565034	9.391809	0.005983	NM_001013896	RGD1309948
A_44_P309513	-0.566123	8.088215	0.003308	NM_001024367	LOC501619
A_44_P207634	-0.566195	14.25058	0.008942	NM_001014148	LOC361309
A_44_P618177	-0.566587	12.8748	0.003863	CF110664	
A_44_P156805	-0.566739	8.099318	0.008471	XM_227475	Pogz_predicted
A_44_P280759	-0.568056	14.37983	0.007818	NM_012992	Npm1
A_44_P212355	-0.56835	9.738948	0.002238	XM_232466	Lrp6_predicted
A_44_P468544	-0.568435	9.993473	0.004454	NM_001013126	Cyb5r1
A_44_P738643	-0.568634	9.591004	0.003566		
A_44_P348973	-0.568895	8.505955	0.006712	NM_001004277	Lypla3
A_44_P261883	-0.569063	11.145	0.008299	NM_134402	Bzw2
A_44_P650648	-0.570226	10.93273	0.000434	BF561546	
A_44_P1060064	-0.570935	9.82548	0.005238	NM_001024883	RGD1310810
A_44_P409866	-0.572035	8.822675	0.003034	NM_013221	Hbp1
A_44_P347771	-0.572246	12.42882	0.002978	CB579735	
A_44_P384688	-0.572632	13.66295	0.002533		
A_44_P356027	-0.572935	12.00952	0.008344	NM_053642	Sc5d
A_44_P249606	-0.573078	7.971547	0.008649	NM_001025718	MGC112830
A_43_P15129	-0.573778	7.558528	0.000289	BF558849	
A_44_P137356	-0.574199	13.12717	0.009568	NM_053523	Herpud1
A_44_P550497	-0.57495	8.939273	0.002301	NM_022684	Bid
A_44_P365765	-0.575656	8.050544	0.005348	XM_224579	Slmap_predicted
A_44_P190115	-0.576073	9.257267	0.002651	XM_235940	Snx19_predicted
A_43_P19005	-0.576291	8.928856	0.008555	XM_574285	RGD1566426_predicted
A_44_P229352	-0.577022	8.451554	0.005411	XM_222717	Rgl1_predicted
A_44_P729514	-0.577376	9.689644	0.009895	XM_573199	RGD1560049_predicted
A_44_P130849	-0.577743	8.230187	0.008975	XM_224627	
A_44_P534249	-0.578016	14.39865	0.009912	NM_001013874	Ociad1
A_44_P707011	-0.578591	8.762253	0.003167	CO393635	
A_42_P747877	-0.57873	10.76747	0.00304	NM_172029	Eif2b1
A_44_P101223	-0.579038	10.35117	0.001145	XM_344744	Gcdh_predicted
A_44_P246311	-0.580416	10.15275	0.006615	NM_001017473	MGC112682
A_44_P548450	-0.580709	10.99874	0.007588	XM_225160	
A_44_P356596	-0.581185	10.9493	0.008387	XM_342783	RGD1304592_predicted
A_44_P368170	-0.581794	8.855102	0.001661	XM_342563	Actr5_predicted
A_44_P987846	-0.581855	11.16986	0.006395	XM_001075075	Dpp8_predicted
A_44_P246554	-0.582001	8.905353	0.003826	CO566833	
A_44_P463557	-0.582634	14.19713	0.004298	NM_013067	Rpn1
A_44_P231583	-0.583034	10.75149	0.007279	NM_032462	Csen
A_44_P130732	-0.583815	8.713516	0.003228	XM_001064066	LOC682999
A_43_P15355	-0.584685	13.54511	0.007016	NM_130755	Cs
A_44_P235090	-0.586284	8.863998	0.005913	XM_234988	Btbd11_predicted

A_44_P271989	-0.586374	11.34059	0.0094	XM_345169	Zfr
A_44_P170070	-0.586507	9.614184	0.004003	XM_236380	Rnf111_predicted
A_44_P810365	-0.586805	9.726458	0.009332	CV104092	
A_44_P382611	-0.587121	10.96644	0.00759	NM_001031651	RGD1304758
A_44_P444039	-0.58729	8.409482	0.006954	XM_215897	
A_44_P637334	-0.587827	10.97686	0.005035		
A_44_P262569	-0.58791	8.076643	0.001623	XM_341961	Tollip_predicted
A_44_P344730	-0.588025	7.880086	0.001613	NM_001009405	Arhgap29
A_44_P103692	-0.589224	10.07171	0.008032	XM_234484	RGD1309059_predicted
A_44_P698466	-0.58941	8.937917	0.008468	XM_001062636	
A_44_P504298	-0.589507	8.821758	0.007981	XM_221077	Cdc42ep4_predicted
A_44_P509129	-0.589766	8.808838	0.009171	BC083806	Tex2
A_42_P744464	-0.590185	8.758601	0.004669	XM_340740	RGD1565449_predicted
A_43_P17175	-0.590299	8.564087	0.001764	NM_001031642	Serpinb1a
A_43_P21386	-0.59044	8.419719	0.004713	CB546740	
A_43_P11905	-0.590826	9.270507	0.006217	NM_017303	Kcnab1
A_44_P471386	-0.591807	13.18609	0.008934	NM_001013107	Dazap2
A_44_P530041	-0.592177	9.105207	0.007566	XM_343804	Hdac8_predicted
A_44_P529718	-0.592568	7.591056	0.00106	XM_341914	RGD1310509_predicted
A_44_P237220	-0.592591	9.322389	0.000271	XM_214720	
A_44_P398587	-0.592826	11.00259	0.006479	XM_343766	Usp9x_predicted
A_44_P292327	-0.593308	11.46625	0.006377	NM_017006	G6pdx
A_44_P782486	-0.593503	7.65762	0.00356	XM_575380	RGD1563612_predicted
A_44_P508462	-0.593522	11.23446	0.009071	NM_131911	Anp32b
A_44_P222011	-0.593914	13.04026	0.005138	NM_017343	Mrlcb
A_44_P312371	-0.594586	12.02887	0.0022	NM_172066	Slc30a4
A_43_P21821	-0.595729	8.545106	0.004644	CB547114	
A_44_P222353	-0.596088	8.508683	0.001984	NM_001040128	RGD1309546_predicted
A_44_P217462	-0.596111	8.18643	0.002077	U78138	
A_43_P13557	-0.597345	13.14417	0.002976	CF110620	
A_44_P226353	-0.598015	11.01006	0.004433	NM_031672	Slc15a2
A_44_P438269	-0.598109	9.857028	0.000911	NM_022585	Azin1
A_44_P1009692	-0.598298	13.31779	0.004267	NM_001025624	Hmgn2
A_43_P12191	-0.598708	12.60738	0.00218	NM_022265	Pdcd4
A_44_P302996	-0.599223	11.48023	0.002285	XM_342171	RGD1562968_predicted
A_44_P461489	-0.599266	8.962531	0.00937	XM_231528	RGD1559440_predicted
A_44_P686863	-0.599609	11.85384	0.001206		
A_43_P18281	-0.599651	8.903045	0.000566	XM_001057305	
A_44_P703930	-0.600012	8.125062	0.002394		
A_44_P955997	-0.600108	11.43887	0.002913	DN932367	
A_44_P327535	-0.6004	8.105457	0.001482	XR_007094	LOC691397
A_44_P1049827	-0.600752	13.66577	0.008886	NM_024128	Nsg1
A_44_P516958	-0.601174	11.62942	0.004807	EF076766	
A_43_P10835	-0.601231	11.4609	0.008636	BP482727	RGD1308816_predicted
A_44_P823303	-0.601517	7.675391	0.001111		
A_44_P186813	-0.602333	8.109993	0.004622	XM_213276	Rars_predicted
A_44_P128711	-0.602335	7.768201	0.008573	XM_217566	Sh3bgrl_predicted
A_43_P18294	-0.60239	7.598985	0.000823	BC099835	
A_44_P326176	-0.602682	9.917051	0.005607	XM_222244	RGD1563628_predicted

A_44_P217909	-0.602949	8.417672	0.002581	XM_228644	Mtmr1_predicted
A_44_P851961	-0.603248	8.122635	0.00924	NM_001009504	Fbxl16
A_44_P325189	-0.603659	13.30424	0.000582	NM_175578	Dscr1l1
A_44_P789739	-0.60378	10.19794	0.002178	NM_001030024	Slc19a2
A_42_P688027	-0.606511	9.303765	0.005323	NM_030999	Crhr1
A_44_P114298	-0.606513	8.87185	0.002852	XM_215693	Hiat1_predicted
A_44_P344096	-0.606913	9.736673	0.009398	NM_138890	Ehd3
A_43_P10536	-0.607958	8.086298	0.007905	XR_007603	
A_44_P917935	-0.607991	8.678929	0.007689		
A_44_P377653	-0.608356	9.62169	0.001543		
A_43_P17872	-0.608383	10.81552	0.006759	CB545618	
A_44_P142318	-0.608411	10.34125	0.006816	XM_222171	Anapc7_predicted
A_44_P400936	-0.608664	12.47592	0.006637	XR_006350	LOC314123
A_44_P735345	-0.6091	7.725892	0.001624	XM_576015	RGD1560812_predicted
A_44_P495832	-0.610195	7.98717	0.001613	XM_343442	Pgm3_predicted
A_44_P356711	-0.610563	7.862104	0.006197	XM_343094	Ttc7b_predicted
A_44_P702685	-0.61115	11.2384	0.006725	CO402564	
A_43_P18909	-0.611317	9.101784	0.006293	XM_236648	Kif9_predicted
A_44_P809536	-0.611648	9.018063	0.002691	AW144200	
A_44_P475932	-0.612343	9.506439	0.008437	NM_001037496	Otud5
A_44_P465188	-0.613837	12.99403	0.006046	NM_053445	Fads1
A_44_P192018	-0.613883	7.703809	0.000494		
A_44_P354806	-0.614498	11.63019	0.005472	NM_172072	Vps45
A_44_P477135	-0.615226	8.68826	0.002682	NM_052801	Vhl
A_44_P513246	-0.615322	8.481193	0.004191	XM_341091	Fbxo21_predicted
A_44_P348983	-0.615971	8.261497	0.007893	XM_340889	Npepps
A_44_P671422	-0.616393	10.93854	0.004166		
A_43_P18993	-0.616672	10.24685	0.007665	XM_216679	Lamb1_predicted
A_44_P261179	-0.616735	9.356162	0.001222	XM_343177	LOC362845
A_44_P384223	-0.617224	12.50624	0.00345	NM_024151	Arf4
A_44_P358664	-0.617255	10.2275	0.009024	XM_223454	Stim2_predicted
A_44_P418824	-0.617423	9.363052	0.001671	NM_053430	Fen1
A_44_P253196	-0.617866	10.6956	0.001838	XM_228114	Arid5b_predicted
A_43_P18795	-0.618039	10.72011	0.008233	NM_001047849	Agpat6
A_44_P108680	-0.618465	8.102587	0.002297	NM_057116	Ppp2r2c
A_44_P396772	-0.619342	10.46003	0.001217	NM_001037363	Lrrn1
A_44_P457129	-0.619549	8.743385	0.006961	XM_227809	LOC310958
A_44_P301812	-0.619841	11.17309	0.004013	NM_001005765	Rap1a
A_44_P183048	-0.620055	10.77672	0.002498	XM_233467	
A_44_P199358	-0.620299	10.4968	0.007816	XM_229162	RGD1561327_predicted
A_43_P12127	-0.620811	14.8234	0.006163	NM_021842	Ensa
A_44_P526729	-0.62244	9.842671	0.006342	NM_031135	Klf10
A_44_P240973	-0.622495	7.998083	0.00086	NM_022264	Kit
A_44_P370761	-0.622587	8.463284	0.003614	XM_236009	Nfrkb_predicted
A_44_P135944	-0.62263	11.26265	0.008567	XM_220178	Adcy9_predicted
A_44_P396198	-0.623268	8.938957	0.00662	NM_001025421	Cugbp1
A_44_P400884	-0.62356	11.45829	0.004356	XM_345073	
A_44_P552986	-0.623801	9.054984	0.002394	NM_001007693	Ttc9c
A_44_P523016	-0.623912	12.37282	0.009372	NM_001024314	LOC499913

A_44_P1024729	-0.623962	9.026463	0.001142	XR_006336	RGD1311429_predicted
A_44_P303777	-0.624011	13.52164	0.00533	AW143533	
A_44_P271625	-0.624662	14.84276	0.002663	NM_053291	Pgk1
A_43_P17160	-0.62594	9.958981	0.00768	NM_001017383	Ppil2
A_44_P469040	-0.62652	8.165212	0.001126	XM_235547	RGD1560783_predicted
A_44_P917437	-0.626641	9.558865	0.002512		
A_44_P548203	-0.626707	12.49294	0.005956	BC087677	Rbm3
A_44_P293124	-0.628186	7.935044	0.009121	NM_001044243	Tasp1_predicted
A_44_P321359	-0.628274	10.01661	0.006258	XM_226455	Zfp612_predicted
A_44_P779609	-0.628795	8.320908	0.001183	NM_001037652	Zdhhc6
A_44_P171183	-0.629303	8.474922	0.00293	NM_001044267	MGC112775
A_43_P13046	-0.629635	9.752248	0.001519	NM_057147	Sec22l2
A_44_P318999	-0.629726	8.872416	0.008478		
A_43_P10386	-0.630223	12.97329	0.000518	CA511607	
A_44_P192548	-0.630339	9.351752	0.001843	XM_343535	Gtpbp2
A_44_P494723	-0.630505	11.4003	0.009436	XM_343716	
A_44_P262192	-0.631249	12.84926	0.009614	NM_182814	Cct4
A_44_P240248	-0.632188	8.634159	0.003151	AB012232	Nfib
A_44_P492268	-0.63219	10.8392	0.006459	XM_212982	
A_44_P403084	-0.632293	9.823149	0.001151	NM_001039044	Cdc42se1
A_44_P461807	-0.632695	8.095919	0.000504	XM_229225	Baz2b_predicted
A_44_P348825	-0.632978	9.691787	0.003731	NM_024150	Arf2
A_44_P398014	-0.633132	12.4155	0.0051	NM_053448	Hdac3
A_44_P527134	-0.63402	14.00775	0.007491	BC081744	Oxr1
A_44_P191962	-0.634064	9.541643	0.005569	NM_001007734	Echdc1
A_43_P19178	-0.634171	8.223944	0.001053	NM_031574	Rasa3
A_44_P400857	-0.634452	12.21639	0.006584	NM_001011926	Fts
A_43_P13362	-0.634717	10.72983	0.006961	NM_139094	Rbm16
A_44_P908874	-0.634786	8.955233	0.003401		
A_44_P112488	-0.635472	8.404066	0.0068	XM_343087	Galntl1
A_44_P454180	-0.635515	8.272513	0.003393	NM_182675	Rab40c
A_44_P288548	-0.63558	9.253557	0.004623	XR_008866	RGD1306534_predicted
A_44_P139291	-0.635986	9.326605	0.001776	XM_001058939	
A_44_P791631	-0.636117	8.807255	0.003104	XM_227139	RGD1565414_predicted
A_44_P473472	-0.636139	10.61491	0.003947	BC091233	RGD1307434_predicted
A_44_P760606	-0.637549	12.68986	0.002205	XR_007237	
A_42_P521902	-0.637726	8.609116	0.000822	NM_001079941	Gtf3c5_predicted
A_44_P345101	-0.637911	10.42344	0.005728	XM_217367	Bai3_predicted
A_44_P178179	-0.638409	11.32229	0.008534	XM_226561	Pgbd5_predicted
A_44_P508750	-0.638435	8.171009	0.004833	XM_001056358	
A_42_P707937	-0.639077	13.34077	0.000445	NM_080583	Ap2b1
A_44_P1007105	-0.63928	13.26468	0.00435	NM_138905	Ppap2b
A_43_P22124	-0.639677	13.337	0.004781	NM_213625	Dnajc7
A_44_P859113	-0.640213	8.953787	0.004534	NM_199463	Ripk5
A_44_P148695	-0.640551	9.640543	0.000911	XM_240915	RGD1307915_predicted
A_43_P12462	-0.641286	8.041492	0.002222	NM_030863	Msn
A_44_P383199	-0.641381	9.791592	0.002582	XM_214649	RGD1308706_predicted
A_44_P267595	-0.641725	10.04405	0.007378	XM_233839	Eml4_predicted
A_44_P323882	-0.641998	9.658085	0.003262	NM_001013073	Btbd9

A_44_P477889	-0.642086	13.29279	0.004444	NM_031783	Nefl
A_44_P523112	-0.643135	11.37171	0.003507	XM_232937	RGD1306148_predicted
A_44_P840751	-0.643651	8.0978	0.00193		
A_43_P11938	-0.643668	7.909169	0.0072	NM_017364	Zfp260
A_44_P340839	-0.643741	8.838773	0.004557	XM_001055446	
A_43_P17983	-0.644983	12.6799	0.006621	XM_342679	Cul1_predicted
A_44_P1054864	-0.645182	11.12162	0.002305	NM_001007662	Arcn1
A_44_P825644	-0.64519	9.057609	0.003705		
A_44_P369701	-0.646083	11.87503	0.003244	NM_001025660	Ei24
A_44_P152395	-0.646432	12.2429	0.008762	NM_001013222	Rnd1
A_44_P365882	-0.646949	10.84827	0.004004	NM_001014046	RGD1308697
A_44_P177678	-0.647221	8.401784	0.007057	CB547239	
A_44_P375613	-0.647271	10.40813	0.006682	NM_001013183	Narfl
A_44_P235336	-0.648526	9.743373	0.001962	NM_001083966	Rev3l
A_44_P438478	-0.648574	14.64021	0.009817	XR_006258	
A_44_P523924	-0.648626	9.63477	0.008841	NM_001007689	Ciapin1
A_44_P449969	-0.648891	8.622949	0.001171	NM_001009258	Chfr
A_43_P17172	-0.648993	7.549533	0.000382	XM_213385	Prpf8
A_44_P514539	-0.649428	12.17488	0.005961	NM_001008324	Eif4b
A_44_P442941	-0.649561	9.201323	0.00355	NM_032067	Ralbp1
A_43_P18744	-0.650106	11.15677	0.002633	NM_001012744	Enpp5
A_44_P443343	-0.650592	7.957523	0.001555	XM_216091	Pdk3
A_44_P137262	-0.650642	10.46178	0.003983	NM_148891	Nmt1
A_44_P366056	-0.6509	9.137319	0.001343	XM_233418	Mmachc_predicted
A_44_P395709	-0.651297	12.14363	0.005458	NM_134366	Rac1
A_44_P422063	-0.651673	8.392712	0.006469	XM_228173	Gopc_predicted
A_43_P17344	-0.652063	8.310589	0.001639	XM_232252	Bcl2l13_predicted
A_44_P555261	-0.652078	8.380619	0.008749	NM_031057	Aldh6a1
A_43_P12591	-0.65239	7.777536	0.000543	NM_031569	Oprl1
A_44_P441434	-0.6525	9.111109	0.003536	NM_131914	Cav2
A_44_P248111	-0.652911	9.320377	0.004791	NM_001047107	Igsf4c_predicted
A_44_P794608	-0.657157	9.089318	0.00904	AI112975	
A_44_P594969	-0.657411	7.785626	0.0006		
A_43_P18497	-0.657706	8.96092	0.001825	NM_001007609	Mfap3
A_43_P13344	-0.657852	8.783735	0.008338	NM_138976	Mfn1
A_44_P272294	-0.658024	7.434132	0.000969	XM_233937	Asxl2_predicted
A_44_P255341	-0.658029	10.7227	0.003693	XM_222661	Ipo9_predicted
A_44_P342314	-0.658159	13.2173	0.009311	NM_001014232	RGD1308373
A_43_P18271	-0.658212	11.17964	0.005555	XM_576264	RGD1564335_predicted
A_44_P466827	-0.658495	9.300238	0.007269	NM_001034835	RGD1309220
A_44_P233867	-0.659003	9.728503	0.003555	NM_172067	Spon1
A_44_P1007438	-0.659371	9.813387	0.004121	NM_001044238	Gdpd1_predicted
A_44_P215210	-0.659582	9.528286	0.00427	XM_342568	Ptprt_predicted
A_44_P166216	-0.659636	14.18189	0.004388	NM_001013059	Ndfip1
A_44_P886861	-0.65992	11.82148	0.002477	NM_001024245	Ccdc32
A_44_P170710	-0.660042	13.38092	0.007866	NM_013060	Id2
A_44_P344397	-0.661307	11.05304	0.007497	NM_001024233	Bles03
A_43_P17012	-0.661735	13.29255	0.003819	NM_001014227	RGD1307010
A_44_P667977	-0.663111	9.045672	0.004604	XR_007894	LOC367705

A_44_P902742	-0.663318	11.53225	0.001062	XM_343576	Als2cr13_predicted
A_42_P826202	-0.663566	8.962978	0.006901	NM_153732	Zfp597
A_44_P147702	-0.663636	8.978381	0.003573	XM_340853	RGD1311017_predicted
A_43_P12487	-0.664083	9.881514	0.001847	NM_031040	Grm7
A_44_P324042	-0.664103	9.089293	0.004246	NM_001034150	Srpr
A_44_P477927	-0.665178	9.91646	0.003267	NM_013225	Cntn6
A_44_P1026688	-0.665491	11.02828	0.006486	NM_001014263	Sypl
A_44_P552977	-0.665722	9.640369	0.003625	NM_001007693	Ttc9c
A_44_P175751	-0.66592	8.42582	0.006218	XR_009314	LOC690211
A_44_P352268	-0.665997	13.87135	0.000486	NM_031821	Plk2
A_44_P241439	-0.666017	12.2453	0.003634	NM_001024789	Nap1l2
A_44_P288691	-0.66628	12.61409	0.008512		
A_44_P475371	-0.666669	9.786368	0.004316	XM_342812	Ccnc
A_44_P334195	-0.666683	11.19342	0.003964	NM_001007624	Qars
A_44_P175461	-0.667045	8.767074	0.001832	XM_239761	RGD1565602_predicted
A_43_P12936	-0.66754	11.16029	0.009331	NM_053801	Sec14l2
A_44_P485453	-0.667632	10.32878	0.008859	XM_001063164	RGD1561943_predicted
A_44_P744519	-0.667916	13.73968	0.00043	NM_012992	Npm1
A_42_P654739	-0.668259	9.014156	0.003873	XM_221888	Rnf6_predicted
A_44_P208880	-0.668399	10.47121	0.006465	NM_001038595	Dnaja3
A_44_P476107	-0.668587	11.31869	0.003496	XM_217278	
A_44_P217590	-0.668667	9.059417	0.000726	NM_053794	Prkwnk1
A_44_P199661	-0.669436	8.687349	0.006699	XM_341464	RGD1563853_predicted
A_44_P632544	-0.669509	7.896681	0.005783	AA944304	
A_44_P231556	-0.669772	7.869283	0.00065	NM_001077589	Rgs16
A_44_P658594	-0.670139	9.191758	0.000253	CO575464	
A_44_P269596	-0.671296	13.26019	0.006176	XM_344976	Psmd13_predicted
A_44_P328302	-0.672591	8.777259	0.002665	XM_213992	Glmn
A_44_P473322	-0.672656	7.868224	0.006082	XM_224778	
A_44_P293944	-0.672671	13.8667	0.007733	NM_001005908	Ghitm
A_44_P775787	-0.673339	11.32534	0.00098	XM_575783	LOC500420
A_44_P281959	-0.673402	8.081822	0.000983	XM_218006	RGD1310304_predicted
A_44_P421391	-0.673725	8.967514	0.008583	NM_198763	Slc1a4
A_44_P414757	-0.674502	9.692538	0.00543	NM_001024770	Sec3l1
A_44_P521893	-0.674632	8.832269	0.00481	BG669130	
A_43_P11734	-0.674874	9.655395	0.008583	NM_013145	Gnai1
A_42_P814410	-0.67517	11.87156	0.007169	NM_212500	Gnl1
A_44_P175681	-0.675396	10.52681	0.00529	NM_001014011	Gramd3
A_44_P492635	-0.67561	14.04256	0.005462	NM_001008281	Psmd3
A_44_P243102	-0.677044	8.408617	0.008294	NM_017007	Gad1
A_44_P172941	-0.67789	9.432247	0.006219	NM_182821	Pxk
A_43_P20530	-0.678095	8.871127	0.006082	XM_231400	Steap2_predicted
A_44_P482200	-0.678514	12.40565	0.003411	XM_222785	Astn1
A_44_P112546	-0.679215	9.419917	0.009026	CO400633	RGD1309873_predicted
A_44_P182555	-0.681208	11.999	0.008571	NM_138509	Mapre1
A_44_P375322	-0.681511	10.1816	0.00845	XM_001074519	Trpc4ap
A_44_P338095	-0.681595	9.584036	0.00481	NM_001013112	Hibch
A_44_P525482	-0.68227	8.987538	0.005143	CB546704	
A_44_P300612	-0.683667	10.59645	0.004338	NM_022850	Dpp6

A_42_P712718	-0.683836	10.9304	0.005702	NM_001004280	RGD1303272
A_43_P19662	-0.683865	8.366867	0.004069	CB547048	
A_44_P121457	-0.683919	12.36108	0.004367	NM_001037778	Dctn5
A_44_P340490	-0.684095	8.01205	0.005384	XM_221232	RGD1310429_predicted
A_44_P104679	-0.684853	9.308212	0.005798	NM_053481	Pik3cb
A_43_P18706	-0.684899	8.990666	0.003995	NM_001012103	Trim32
A_44_P686038	-0.686229	9.953226	0.000504	NM_022198	Clcn4-2
A_44_P509099	-0.686288	11.11681	0.003834	NM_001008382	Cnot8
A_44_P248598	-0.68654	9.140249	4.10E-05	NM_001017459	LOC314859
A_44_P332041	-0.686639	11.95608	0.009963	NM_022385	Arl1
A_44_P525827	-0.686772	12.63864	0.003991	NM_199091	Cct3
A_44_P324066	-0.687064	8.571865	0.004003	XM_001072853	LOC689997
A_44_P149734	-0.687945	9.954353	0.005321	NM_001009657	Hat1
A_44_P466041	-0.688036	10.14526	0.001573	NM_001007682	Thtpa
A_43_P11763	-0.689954	8.225533	0.001545	Z49081	Add1
A_44_P466565	-0.690363	10.13551	0.005187	XM_001058018	RGD1565759_predicted
A_44_P959355	-0.690506	14.41659	0.00172	XR_008469	LOC361963
A_44_P636077	-0.691064	9.295773	0.002041	XM_225093	RGD1308377_predicted
A_44_P192568	-0.691346	9.9763	0.005102	NM_172335	Gm2a
A_44_P321605	-0.691528	14.38762	0.00993	XM_576504	LOC501089
A_44_P715184	-0.692584	8.486267	0.003501	XM_215883	Kif3b_predicted
A_44_P557979	-0.692677	8.67592	0.002177	NM_001012190	Ubap1
A_44_P285741	-0.692747	9.249087	0.009985	NM_031556	Cav
A_44_P128629	-0.693207	10.22845	0.006852	XM_344744	Gcdh_predicted
A_43_P18261	-0.693296	11.92018	0.002116	NM_001008345	Mesdc2
A_44_P356538	-0.693746	10.46584	0.002295	XM_341666	Zfp330_predicted
A_43_P16735	-0.694316	11.01645	0.007446	XM_340886	Nfe2l1_predicted
A_44_P426707	-0.694392	12.88563	0.009882	XM_001053199	RGD1560511_predicted
A_44_P370502	-0.695424	8.655955	0.009894	XM_342445	RGD1561141_predicted
A_44_P516017	-0.695966	10.87721	0.006661	NM_001031648	Efhd2
A_44_P234362	-0.696237	7.659072	0.000406	NM_001007745	Tmem43
A_44_P781559	-0.696443	12.18886	0.006077	XM_233944	Ncoa1_predicted
A_44_P543350	-0.696783	8.474691	0.00037	NM_017063	Kpnb1
A_44_P371823	-0.697464	9.537366	0.006001	XM_242940	
A_44_P471818	-0.697741	9.200884	0.003551	XM_001071384	LOC689616
A_44_P405679	-0.697777	9.039271	0.009317	XM_233609	Rap1ga1
A_43_P16946	-0.697811	9.672708	0.007204	XM_213649	Ifnar1_predicted
A_44_P509473	-0.698504	10.44605	0.005045	NM_139060	Csnk1d
A_44_P503673	-0.699146	9.366485	0.006058	XM_341100	Ulk1
A_44_P386748	-0.702079	13.34473	0.009233	NM_001007616	Wsb2
A_43_P20777	-0.702381	9.632501	0.009165	XM_341474	Nsun2_predicted
A_43_P15781	-0.702694	9.424702	0.009951	BC090029	Jak1
A_44_P345009	-0.704027	10.85685	0.006687	NM_001008526	Bag5
A_43_P16640	-0.704181	11.01546	0.006406	XM_343298	RGD1311547
A_44_P822082	-0.704323	13.25393	0.004761	XR_009104	
A_44_P648671	-0.706766	11.58223	0.006472	XM_001076507	RGD1559498_predicted
A_44_P928907	-0.706901	9.190431	0.000626	XM_574241	RGD1565049_predicted
A_44_P229079	-0.707063	11.94041	0.00343	XM_344434	Rb1
A_44_P510470	-0.707064	8.08123	0.008377	NM_053487	Pex11a

A_44_P278923	-0.707738	10.52196	6.05E-05	XM_224623	Oxnad1_predicted
A_44_P132822	-0.707764	8.916867	0.001035	NM_001005265	Crry
A_44_P110098	-0.708323	10.09779	0.001122	NM_001080783	RGD1311552_predicted
A_44_P260850	-0.708435	9.12765	0.0044	CO394432	
A_44_P206520	-0.709319	10.11567	0.004135	XM_217385	Lman2l_predicted
A_44_P429364	-0.710105	10.76198	0.000908	NM_001012113	Ptdss1
A_44_P135339	-0.710133	14.74068	0.002906	NM_175761	Hspca
A_44_P459851	-0.710349	9.658631	0.001275	XM_340974	Dscr3_predicted
A_44_P442873	-0.710445	13.18986	0.000449	NM_053739	Becn1
A_44_P535400	-0.710756	10.29758	0.00891	AW916612	
A_44_P463996	-0.710903	8.168438	0.000841	XM_344971	Inpp5a_predicted
A_44_P637889	-0.711137	9.731263	0.001241		
A_44_P271368	-0.711859	13.0028	0.00484	AW917142	
A_44_P494644	-0.712484	11.96627	0.006901	NM_001012075	Tspyl4
A_44_P365653	-0.713637	11.76364	0.005634	NM_001014161	LOC361596
A_44_P222779	-0.713943	8.50309	0.000525	XM_342937	RGD1305162_predicted
A_44_P543288	-0.714546	10.03262	0.003176	NM_031704	Stx5a
A_42_P724600	-0.71565	10.02345	0.003976	NM_001006976	Tars
A_44_P281540	-0.715686	8.615028	0.000588	XM_215428	LOC294560
A_44_P329139	-0.715693	8.394615	0.006545	XM_224588	Arhgef3_predicted
A_43_P17974	-0.716595	9.515081	0.005591	XM_341688	Cog4_predicted
A_44_P295151	-0.716847	9.093263	0.000871	XM_224561	Flnb_predicted
A_44_P403209	-0.717596	9.277081	0.005136	NM_001013073	Btbd9
A_43_P19299	-0.718378	7.772278	0.0002	XM_235571	RGD1309983_predicted
A_44_P323430	-0.718496	9.88312	0.002903	NM_138532	Nme7
A_44_P128447	-0.719167	11.31551	0.003131	NM_001007680	Abhd6
A_44_P229618	-0.71918	8.367113	0.000769	XM_228065	Tmem1_predicted
A_44_P187789	-0.719962	8.124942	0.007832	XM_001066818	
A_44_P474509	-0.720164	12.50656	0.001046	CO394478	
A_44_P389212	-0.720654	11.51459	0.007951	NM_001024975	RGD1307336
A_44_P887061	-0.720696	10.08852	0.007313	BC107438	
A_44_P260644	-0.72127	8.407463	0.001474	XM_576264	RGD1564335_predicted
A_44_P437641	-0.721334	9.637998	0.001922	NM_001007702	RGD1359108
A_44_P366177	-0.72167	9.880374	0.004393	DN933141	LOC681352
A_43_P17527	-0.722108	8.781197	0.00568	NM_001024261	Trnt1
A_44_P250983	-0.722291	10.81962	0.000881	XM_001057073	LOC680451
A_44_P124294	-0.722674	9.650509	0.004216	NM_001012003	Orc2l
A_44_P538531	-0.722867	10.08705	0.002979	NM_053742	Pitpnb
A_44_P424092	-0.722882	8.510474	0.006779	NM_001025669	RGD1307161
A_44_P189909	-0.723969	10.66671	0.002177	NM_001025020	RGD1310753
A_44_P607982	-0.724047	8.726039	0.009631		
A_44_P210461	-0.724218	14.11055	0.002096	NM_017025	Ldha
A_44_P227121	-0.725426	9.930826	0.000234	XM_341301	RGD1306755_predicted
A_44_P356322	-0.725778	10.89637	0.001673	XM_219482	
A_44_P126131	-0.726175	8.173707	0.001792	XM_341215	Tbc1d1_predicted
A_44_P827919	-0.726469	9.333749	0.00967		
A_42_P521609	-0.726957	9.608308	0.002166	XM_221635	Morc3_predicted
A_43_P12890	-0.727081	8.909091	0.003676	NM_053665	Akap1
A_44_P126310	-0.72742	12.22158	0.00529	NM_001005537	Ik

A_44_P438442	-0.728064	8.337862	0.006042	XM_001069431	
A_44_P197041	-0.728079	10.51144	0.001425	NM_001035221	Ypel5
A_44_P320894	-0.728496	10.37575	0.003358	NM_013090	Vamp1
A_44_P854406	-0.729	8.456598	0.007527		
A_44_P400112	-0.729177	12.19754	0.006955	CO384551	
A_44_P326124	-0.729686	15.26894	0.002926	XM_001056105	LOC679385
A_44_P154367	-0.730342	9.281083	0.004187	NM_001024744	Cdc16
A_44_P530424	-0.732079	12.73546	0.004615	BC085931	RGD1309459
A_44_P116846	-0.732713	10.5152	8.84E-05	XM_341384	LOC361098
A_44_P250412	-0.733285	9.320603	0.003192	NM_001007713	Tmbim1
A_43_P13047	-0.735128	8.592086	0.003122	NM_057148	Sep.02
A_44_P103160	-0.735662	10.16767	0.001835	XM_342909	Inpp5b
A_43_P11514	-0.736388	11.08872	0.002482	NM_012678	Tpm4
A_44_P119007	-0.736654	11.29753	0.002083	NM_172321	Slc6a15
A_44_P729866	-0.737709	10.44694	0.001265	CA511309	
A_44_P300506	-0.738032	13.37647	0.000788	NM_022399	Calr
A_44_P656856	-0.738458	11.02773	0.008158	CK596682	
A_44_P557962	-0.73918	14.79963	0.00234	XM_232602	
A_44_P520190	-0.739506	8.711355	0.007267	NM_134414	Exoc2
A_44_P443030	-0.739533	10.324	0.005014	XM_223227	Sept6_predicted
A_44_P525645	-0.739723	8.785316	0.001623	XM_220442	
A_44_P550581	-0.739757	8.369567	0.001509	XM_218411	Dmpk_predicted
A_44_P434216	-0.740314	10.10546	0.004603	NM_001012193	Rdh11
A_43_P12932	-0.740654	12.20032	0.002856	NM_053788	Stx1a
A_44_P233736	-0.74102	11.56517	0.004468	NM_001004090	Tspan5
A_44_P489120	-0.741475	10.20944	0.008299	NM_001007701	Tram1
A_44_P440633	-0.741539	10.4556	0.000987	NM_031639	Dlgh3
A_44_P415412	-0.742562	8.633771	0.005222	NM_001004252	Farslb
A_44_P445318	-0.742956	10.76738	0.002692	XM_215985	
A_43_P15432	-0.742965	8.174573	0.003091	NM_053910	Pscd1
A_44_P1015001	-0.743467	8.405712	0.008775	U50842	Nedd4a
A_44_P1014311	-0.743779	8.744107	0.003717	XM_343619	Atg16l1_predicted
A_44_P248484	-0.743898	13.35195	0.003782	XM_001069080	LOC367617
A_44_P312484	-0.743971	10.08945	0.002171	XM_213426	Mtmr4_predicted
A_44_P405793	-0.745803	9.317497	0.000835	XM_244089	Npas2_predicted
A_44_P473754	-0.746888	9.118205	0.001714	XM_221656	Son
A_43_P18072	-0.746961	8.805348	0.001287	NM_001013413	Als2
A_44_P714315	-0.747239	12.25655	0.002346	CO404950	
A_43_P18263	-0.750304	8.603148	0.005633	NM_001025421	Cugbp1
A_44_P760403	-0.750365	11.83512	0.000948		
A_44_P454177	-0.750546	9.564492	0.005748	NM_182675	Rab40c
A_43_P20387	-0.750553	8.592192	0.001522	XM_232614	Arfgef1_predicted
A_44_P853268	-0.751009	8.775023	0.000223	CO393484	
A_43_P16469	-0.751323	10.77797	0.006331	NM_001083313	Chmp1a
A_43_P10226	-0.751437	10.42195	0.009819	XM_236333	Lrrc49_predicted
A_44_P159569	-0.75145	9.190013	0.000607	NM_001039587	Wdr45l_predicted
A_44_P330332	-0.751549	8.728765	0.003646	BC129128	
A_44_P229800	-0.754324	9.060456	0.009386	NM_001011991	Ndrg1
A_43_P15423	-0.754442	9.635179	0.0005	NM_019239	Mgat3

A_44_P806641	-0.754958	11.49879	0.005591	XM_236024	
A_44_P187293	-0.755579	11.71979	0.0067	XM_344175	
A_44_P286719	-0.756576	9.510973	0.004347	XM_224863	Snx25
A_44_P321686	-0.756834	8.771057	0.006453	XM_001060299	
A_44_P270510	-0.757372	8.717218	0.005432	XM_220420	Aff4_predicted
A_44_P203842	-0.757977	8.823596	0.00582	BP485454	RGD1559751_predicted
A_44_P145416	-0.758544	8.271167	0.003876	NM_001007646	Fkbp9
A_44_P775952	-0.759294	12.15302	0.001784		
A_44_P482512	-0.759667	10.47499	0.000794	XM_343513	Aplp2
A_44_P548303	-0.760193	8.571865	0.004889	NM_001009688	Thumpd1
A_44_P375252	-0.760435	9.392698	0.00157	XM_342379	Ehmt1_predicted
A_44_P838313	-0.760683	13.05444	0.001		
A_43_P17880	-0.762673	8.703786	0.000302	NM_182953	Nek6
A_44_P545635	-0.762675	8.296813	0.00081	AY325140	RGD1560766_predicted
A_44_P541378	-0.762945	7.579984	0.000277	NM_001014242	Isoc1
A_44_P475159	-0.762947	13.19762	0.001813	NM_012673	Thy1
A_44_P261818	-0.76305	9.329422	0.004341	BC087666	
A_44_P806713	-0.763825	10.53177	0.0004		
A_44_P1020219	-0.764497	8.876013	0.003207	CO574509	Rundc1_predicted
A_44_P439573	-0.764536	13.61199	0.000165	DV728042	
A_43_P12453	-0.764651	9.151736	0.005921	NM_030839	Syt13
A_44_P253601	-0.765994	8.243451	0.001336	NM_001025009	Josd1
A_44_P203793	-0.766671	11.35587	0.002354	NM_001013912	Mllt11
A_44_P172936	-0.767375	9.619187	0.009972	NM_138613	Zfp179
A_44_P229670	-0.767526	12.75535	0.008309	XM_001075438	LOC686934
A_44_P451014	-0.768482	10.82196	0.006677	NM_017322	Mapk9
A_44_P203665	-0.768518	8.505706	0.004547	XM_223270	Ccng2_predicted
A_44_P550454	-0.768846	7.804654	0.000548		
A_44_P213320	-0.768863	14.2796	0.00708	XM_236873	LOC688956
A_44_P852634	-0.769854	8.744858	0.001617	XR_007953	LOC501135
A_44_P961330	-0.770326	10.5835	0.00473		
A_44_P351789	-0.770822	9.291229	0.005812	XM_341509	Cd83_predicted
A_44_P134405	-0.770887	9.108849	0.004683	NM_031798	Slc12a2
A_44_P545727	-0.771223	10.49515	0.001557	XM_341086	Fln29
A_44_P236656	-0.771271	9.238519	0.001101	XM_343817	Gla
A_44_P832837	-0.771519	9.96242	0.007956	AW143397	
A_44_P230410	-0.771562	12.57756	0.007994	NM_031600	Ptprn2
A_44_P363204	-0.77167	8.892924	0.006836	NM_053824	Csnk2a1
A_44_P274397	-0.771797	10.44541	0.004003	NM_001033700	Lass2
A_43_P17671	-0.772099	8.388576	0.001237	NM_001014186	LOC362304
A_44_P150089	-0.7723	8.616038	0.001656	NM_001013229	Eral1
A_44_P671470	-0.772302	9.103882	0.004433		
A_44_P459301	-0.77262	9.149703	0.007149	XM_219377	LOC309016
A_44_P377645	-0.773449	8.537705	0.000106	XM_342774	
A_44_P287250	-0.773756	11.2841	0.008399	NM_022521	Oat
A_44_P538538	-0.774107	11.86528	0.008686	NM_017357	Hpcal4
A_44_P250030	-0.775557	8.910662	0.009305	NM_013107	Bmp6
A_44_P142562	-0.776339	13.17596	0.003051	NM_001007643	Tmx2
A_44_P215689	-0.77949	12.56723	0.007158	XM_343744	LOC686934

A_44_P725617	-0.779699	12.15481	0.001587	BF548107	
A_44_P138363	-0.779752	11.52163	0.008934	XM_344057	LOC363849
A_44_P184279	-0.78011	11.55638	0.008311	NM_012504	Atp1a1
A_43_P17443	-0.780406	8.247825	9.77E-05	XM_230647	Rin2_predicted
A_44_P157118	-0.781188	9.479825	0.004446	BC089114	Foxred1_predicted
A_44_P159455	-0.782713	8.994728	0.002178	XM_001062352	Ibtk_predicted
A_44_P208711	-0.782766	13.39	0.009113	XM_001075438	
A_44_P290703	-0.782788	15.64819	0.002914	XM_226680	
A_44_P322500	-0.782907	8.670947	0.001796	CK473706	
A_44_P100740	-0.783096	12.38389	0.005403	NM_001024243	Nudt3
A_44_P386515	-0.783243	9.980967	0.006867	NM_001008771	Wdr77
A_44_P322960	-0.783753	12.49027	0.000134	NM_022532	Araf
A_44_P759589	-0.783856	12.06586	0.002218	CF110322	
A_44_P452668	-0.783988	8.976903	0.000605	XM_342731	Sumf1_predicted
A_44_P356468	-0.784919	10.14415	0.002477	XR_007829	RGD1561940_predicted
A_44_P283971	-0.785012	9.049607	0.000234	XM_232972	Zfp189_predicted
A_43_P19994	-0.785178	9.365389	0.000868	XM_233485	Rlf_predicted
A_43_P20118	-0.785793	10.4862	0.008255	BC099746	Suclg2
A_43_P21464	-0.78587	9.177944	0.006099	XM_233220	LOC313391
A_44_P382523	-0.786011	10.81879	0.009434	XM_236376	RGD1311958_predicted
A_44_P344425	-0.786114	9.781851	0.004082	XM_224538	Dock9
A_44_P1039444	-0.786386	8.248205	0.007048	NM_032613	Lasp1
A_44_P326090	-0.786522	11.3645	0.001936	XM_342312	Ahcyl1_predicted
A_44_P425380	-0.786802	12.00819	2.62E-05	NM_001011991	Ndrg1
A_44_P480240	-0.786957	9.61964	0.007872	NM_019182	Rnf4
A_44_P831218	-0.788899	12.51332	0.008455	CK596627	
A_43_P23188	-0.789235	8.984787	0.006612	XM_001053087	LOC678766
A_44_P422271	-0.789537	10.07162	0.000428	XM_217019	Cerk_predicted
A_44_P825629	-0.789986	8.743667	0.004918		
A_44_P966141	-0.790387	10.67786	0.004458	CO399145	
A_44_P501082	-0.790871	10.12628	0.008074	NM_134346	Rap1b
A_44_P367698	-0.791355	8.877036	0.005434	NM_031720	Dio2
A_43_P10511	-0.792255	11.50748	0.00296	XM_342289	
A_44_P340393	-0.792382	10.64778	5.48E-05	XR_009391	RGD1565753_predicted
A_44_P246128	-0.792787	10.07023	0.006945	XM_576696	LOC501281
A_44_P168102	-0.792962	11.70241	0.009798	NM_031729	Ppp5c
A_43_P17837	-0.792995	10.48533	0.004349	XM_215423	Sesn1_predicted
A_43_P18051	-0.793458	9.698695	0.001821	XM_001054856	LOC679203
A_44_P536676	-0.793756	10.54809	0.005142	NM_001013158	B3galt3
A_44_P506374	-0.794243	8.661933	0.001863	XM_001073596	Nyw1
A_44_P553939	-0.794537	10.15677	0.003392	BG667845	
A_44_P149954	-0.794596	9.399586	0.00696	XM_576917	RGD1562289_predicted
A_44_P324452	-0.794638	10.7937	0.004997	NM_001048184	Rragc_predicted
A_44_P1029770	-0.795192	11.5724	0.002588	NM_001025732	Nol5a
A_44_P485246	-0.795505	11.15076	0.000209	XR_006015	LOC296593
A_43_P21256	-0.79594	9.616947	0.007425	NM_001083966	Rev3l
A_44_P764308	-0.796777	12.43124	0.002224		
A_44_P1008284	-0.797081	11.05187	0.000467		
A_44_P500250	-0.797368	10.23157	0.007857	XM_343404	RGD1565253_predicted

A_44_P380157	-0.797475	13.15193	0.004485	XM_001074009	LOC690298
A_44_P539738	-0.798034	8.898049	0.007117	NM_022862	Unc13b
A_44_P268837	-0.800875	14.91321	0.002766	NM_001013923	LOC296318
A_44_P536282	-0.801147	14.54553	0.000242	NM_001013130	Spnb2
A_44_P506464	-0.802365	11.35145	0.003007	XR_005489	LOC316483
A_42_P505280	-0.80242	11.65719	0.002254	NM_001012063	Uble1a
A_43_P16672	-0.802949	11.21939	0.002994	NM_001024800	Txndc1
A_44_P331164	-0.804514	11.57423	0.004321	NM_001013974	RGD1308813
A_44_P218229	-0.805107	12.3132	0.007585	XR_006724	LOC363208
A_44_P806917	-0.805151	8.473763	0.001051		
A_44_P366005	-0.805172	11.03052	0.003555	XR_008061	RGD1560954_predicted
A_44_P387374	-0.805344	9.379108	0.003578	XM_221315	RGD1309443_predicted
A_44_P944991	-0.805734	11.55252	0.000681		
A_44_P335898	-0.805981	9.912098	0.003737	BC097982	
A_44_P871871	-0.807236	9.084835	0.000161		
A_44_P987960	-0.80876	11.55567	0.002189	CO398009	
A_44_P365155	-0.809646	13.55149	0.004859	NM_012583	Hprt
A_44_P410080	-0.810974	9.846895	0.007343	XM_001061719	RGD1563620_predicted
A_43_P13247	-0.810995	9.21568	0.004632	XM_001070141	Psd
A_43_P10441	-0.81137	10.65016	0.002046	XM_217149	RGD1310937_predicted
A_44_P558119	-0.811375	8.498026	0.004495	XM_236476	Elovl4_predicted
A_44_P612824	-0.811468	12.84505	0.006458	NM_183326	Gabra1
A_44_P524981	-0.811837	8.832762	0.005526	NM_024373	Galnt1
A_43_P13175	-0.812151	9.510029	0.003163	NM_133405	Cry2
A_44_P177793	-0.812473	13.2334	0.008377		
A_44_P165692	-0.813438	10.70566	0.00093	NM_001034003	RGD1308874
A_44_P344421	-0.814478	11.30413	0.001612	XM_224538	Dock9
A_44_P590197	-0.815765	12.77303	0.001655	AW915353	
A_44_P419565	-0.817066	8.767756	0.001182	XM_231128	RGD1310887_predicted
A_43_P10318	-0.817311	9.623956	0.009787	XM_001062954	Amfr_predicted
A_44_P375593	-0.817459	8.904718	0.004004	XM_001053401	RGD1305001_predicted
A_42_P658005	-0.817751	10.96039	0.000808	XM_573442	R3hdm1
A_44_P821396	-0.81801	11.14901	0.005183	XM_220013	RGD1564625_predicted
A_44_P297114	-0.818198	9.289671	0.000997	NM_001014226	RGD1308915
A_43_P10712	-0.818306	11.54703	0.000346	CO385963	
A_44_P135148	-0.818866	9.836715	0.005412	NM_130894	Mfn2
A_43_P20941	-0.818953	10.36852	0.003289	NM_001009685	Drg1
A_44_P114774	-0.819684	8.742619	0.003905	XM_343190	RGD1563028_predicted
A_44_P231724	-0.8197	11.55686	0.008186	XR_009038	LOC308950
A_44_P287286	-0.821021	9.32241	0.004277	XM_216910	
A_44_P589989	-0.821357	11.40158	0.006218	CA339579	
A_42_P544887	-0.823142	10.02887	0.004302	NM_031665	Stx6
A_44_P509872	-0.82419	9.224376	0.006955	XM_238280	Stard7_predicted
A_43_P23313	-0.824556	10.73031	0.006603	NM_001006960	MGC94604
A_44_P637687	-0.825702	12.07551	0.004244	XM_001079537	RGD1310754_predicted
A_44_P476598	-0.826362	13.11167	0.00335	XM_575808	
A_44_P471848	-0.82645	9.127431	0.002307	XM_225257	
A_44_P560788	-0.826837	14.22944	0.001736	CO566111	
A_43_P18579	-0.827324	11.47094	0.004409	XM_231162	Fbxw2_predicted

A_44_P507881	-0.827462	10.73166	0.005981	AI502676	
A_44_P550412	-0.827778	8.910014	0.001253	AF375874	Trpm7
A_44_P455174	-0.830207	10.55528	0.000725	NM_001014116	RGD1307381
A_44_P203682	-0.830529	10.79381	0.001988	XM_215113	Ptdss2_predicted
A_44_P671835	-0.830567	8.357442	0.003606		
A_44_P259574	-0.830641	14.92661	0.004778	NM_053290	Pgam1
A_44_P494510	-0.83076	8.47185	0.002851	XM_001068808	
A_44_P166777	-0.831154	8.870917	0.006837	XM_574528	LOC499235
A_44_P920120	-0.831683	10.40844	0.002672	XM_001066536	LOC686098
A_44_P606516	-0.83203	11.17502	0.000829		
A_44_P209817	-0.832416	9.940716	0.000341	BC078744	Cav
A_43_P21088	-0.83259	8.417264	0.002447	XM_229993	RGD1306214_predicted
A_44_P274491	-0.832886	11.54702	0.004151	XM_341645	Large_predicted
A_44_P141513	-0.833535	11.4231	0.003774	NM_001014175	LOC361990
A_44_P123908	-0.833932	9.166325	0.008822	XM_342338	RGD1311435
A_43_P18107	-0.834743	10.78105	0.002496	XR_008372	RGD1307034_predicted
A_44_P432432	-0.835275	9.693417	0.002327	NM_013151	Plat
A_43_P10854	-0.8356	9.558071	0.007977	NM_001011934	Hbs1l
A_44_P124225	-0.835726	11.15481	0.002671	NM_001025701	MGC116373
A_44_P852513	-0.835811	13.01714	0.00087	XR_005712	LOC366544
A_44_P883146	-0.835885	9.733681	0.001575	NM_001007682	Thtpa
A_43_P10831	-0.836254	9.547403	0.00254	NM_001013207	Rnpc2
A_44_P662685	-0.836691	8.319404	0.00219	NM_001025046	LOC500102
A_44_P540542	-0.836969	8.683687	0.004265	XM_001054154	Myef2
A_44_P720404	-0.837213	9.667063	0.004071	XM_231564	RGD1564895_predicted
A_44_P963185	-0.838192	12.09844	0.001448	AB014879	
A_44_P226881	-0.839542	12.48466	0.00757	NM_031079	Pde2a
A_44_P177807	-0.839994	8.88638	0.000103	NM_023090	Epas1
A_44_P511049	-0.840182	10.80784	0.001527	XM_224947	Prosc_predicted
A_44_P974681	-0.840279	10.35346	0.001809	XM_575362	RGD1562992_predicted
A_43_P17622	-0.84034	9.765676	0.000235	XM_345870	Lass5_predicted
A_44_P794598	-0.840375	12.69006	0.003716	NM_198132	Hnrpa3
A_44_P621980	-0.840874	11.64749	0.007824	M31178	
A_44_P163645	-0.841165	12.14695	0.000501	NM_001014135	Wdr1
A_43_P10843	-0.842047	9.483842	0.005797	XM_342312	Ahcyl1_predicted
A_44_P856158	-0.842088	8.219854	0.000446	XM_001058383	RGD1559576_predicted
A_44_P680369	-0.842217	8.724026	0.000689	BF545930	
A_44_P487562	-0.843181	7.793448	0.001154	NM_001039023	Net1
A_43_P15854	-0.843798	9.295432	0.002712	XM_227134	
A_44_P241862	-0.844188	9.094338	0.002739	NM_022615	Top1
A_44_P403415	-0.84445	8.996061	0.001818	XM_343301	Mpped1_predicted
A_44_P543548	-0.844926	9.422296	0.002666	NM_057119	Sfrs10
A_44_P1039760	-0.844948	9.985154	0.009284	NM_001013228	Tcte1l
A_44_P249164	-0.845962	13.33993	0.004086	NM_031028	Gabbr1
A_43_P15265	-0.847874	13.38868	0.000515	NM_017042	Ppp3cb
A_44_P242781	-0.848486	9.029121	0.001246	DY308836	
A_44_P501483	-0.850384	14.38167	0.000633	XR_006667	LOC310385
A_44_P475744	-0.850696	11.65921	0.005254	XM_215524	Tpd52_predicted
A_44_P151399	-0.851778	10.08971	0.003203	NM_198737	Arl6ip1

A_44_P112788	-0.852687	8.668467	0.000613	NM_021850	Bcl2l2
A_42_P693042	-0.85293	10.92209	0.001492	XM_214555	RGD1312005_predicted
A_44_P932876	-0.85312	10.2437	0.005947	NM_001014239	LOC364637
A_42_P713975	-0.853185	14.00655	0.007192	BC082799	LOC499779
A_43_P10213	-0.854676	11.58924	0.003286	XM_232515	Etnk1_predicted
A_44_P323496	-0.857383	9.456808	0.001818	NM_019311	Inpp5d
A_44_P322590	-0.858927	11.83874	0.004295	NM_057211	Klf9
A_44_P243701	-0.859383	12.2999	0.007041	XM_578871	
A_44_P753384	-0.860601	10.44877	0.001563		
A_44_P319042	-0.861633	10.52504	0.000626	XM_231798	Kbtbd2_predicted
A_44_P342586	-0.862131	9.340877	0.002361	NM_001014019	LOC308650
A_44_P425367	-0.86303	13.09488	0.005032	NM_001024332	LOC500282
A_44_P759588	-0.864571	12.31002	0.000475	CF110322	
A_44_P667768	-0.86515	10.03546	0.002647		
A_44_P520324	-0.865344	14.543	0.001973	XM_213911	
A_44_P342657	-0.867773	9.773441	0.0038	XM_233792	Vps13d_predicted
A_44_P534374	-0.867883	9.892686	0.00205	XM_227614	Extl2
A_44_P199420	-0.86915	10.28286	0.002966	XM_235924	RGD1309188_predicted
A_42_P522171	-0.869716	9.111699	0.004987	XM_001081512	RGD1307966_predicted
A_44_P930764	-0.870367	8.618998	0.001655	NM_001013125	Bfar
A_44_P145549	-0.870394	8.732414	0.001413	NM_019182	Rnf4
A_44_P230875	-0.870405	12.33114	0.004182	BF567478	
A_42_P545928	-0.871064	9.551304	0.007959	NM_153730	Klhl12
A_44_P233569	-0.871688	11.89088	0.000435	NM_031770	Gnb5
A_44_P198535	-0.874525	8.467903	0.000164	NM_057103	Akap12
A_44_P975286	-0.875152	9.924327	0.000359	CO403766	
A_44_P944912	-0.876799	10.35114	0.002205		
A_44_P362541	-0.87682	10.72609	0.00118	NM_001013235	Scoc
A_44_P283715	-0.876952	9.429911	0.006233	XM_223664	Ehbp1_predicted
A_44_P219796	-0.879236	13.31127	0.003461	XM_230038	Nckap1
A_44_P102628	-0.880199	12.04884	0.00607	NM_021688	Kcnk1
A_44_P548507	-0.882136	14.00466	0.006965	NM_032083	Chn1
A_44_P471440	-0.882876	9.075809	0.004845	NM_001024765	Nbr1
A_44_P476663	-0.88324	9.22413	0.001022	XM_344277	Asb3_predicted
A_44_P465329	-0.885403	13.18839	0.00018	NM_012798	Mal
A_44_P157167	-0.88618	11.39183	0.001068	NM_001008324	Eif4b
A_43_P17496	-0.887473	9.19712	0.008464	XM_231176	Rbm18_predicted
A_44_P137247	-0.891594	10.70451	0.002241	NM_001025142	Trim35
A_44_P438744	-0.892502	9.47676	0.001538	XM_233718	
A_44_P112050	-0.893598	8.93452	0.002972	XM_573428	RGD1560523_predicted
A_44_P895660	-0.893805	9.179857	0.009931	AW916954	
A_43_P17964	-0.893859	9.14457	0.001186	NM_001007662	Arcn1
A_44_P393929	-0.894308	9.800587	0.002936	NM_001039713	RGD1305121_predicted
A_44_P207721	-0.894337	8.940166	0.006695	XM_222946	Adss_predicted
A_44_P267724	-0.895152	8.893436	0.008978	XM_217022	Kif21a_predicted
A_44_P512255	-0.895159	12.15255	0.006149	NM_017214	Rgs4
A_44_P354208	-0.896039	10.41378	0.007776	XM_232315	Rasgef1a_predicted
A_44_P860400	-0.896072	10.18175	0.002993	CK839443	LOC680003
A_44_P344273	-0.897967	11.44876	0.002233	NM_001034129	Tloc1

A_44_P948202	-0.899553	11.85151	8.66E-05		
A_44_P463759	-0.899619	8.247009	6.28E-05	XM_235609	Prickle1
A_44_P667548	-0.89963	13.34538	0.004697		
A_44_P918128	-0.901601	9.504957	0.002334		
A_44_P233742	-0.902752	10.44578	0.000809	NM_001004090	Tspan5
A_44_P409694	-0.903718	11.87361	0.002481	XM_343604	Serpine2
A_44_P232642	-0.905716	10.50494	0.006499	NM_001008301	Usp14
A_44_P121401	-0.909039	9.597854	0.000594	XM_237998	
A_44_P356078	-0.912182	10.7963	0.000877	NM_017033	Pgm1
A_44_P157604	-0.912277	9.631781	0.005396	DY315019	RGD1565556_predicted
A_44_P745191	-0.913003	11.38851	0.002981	CF978988	Prkacb
A_43_P11416	-0.913741	11.3789	0.004315	XM_225625	Gpr158_predicted
A_44_P158973	-0.914102	9.52898	0.001232	NM_001013046	Rab35
A_43_P21122	-0.916898	11.25123	0.000669	XM_341882	Sytl2_predicted
A_44_P552865	-0.917112	12.17696	0.002942	XM_221896	LOC304280
A_44_P147509	-0.91732	11.89346	0.000271	NM_199412	Cbara1
A_43_P13702	-0.919716	10.92545	0.003644	NM_001025136	Clp1
A_44_P492153	-0.91998	8.651813	0.004016	XM_224271	Mtmr6_predicted
A_43_P10791	-0.921154	10.07704	0.001537	CB547648	
A_43_P12189	-0.922647	11.87634	0.007109	NM_022262	Tsnax
A_44_P526933	-0.922673	11.59775	0.001857	NM_053357	Ctnnb1
A_43_P10856	-0.922774	9.374146	0.006399	XM_001077761	
A_44_P415115	-0.923459	11.48848	0.003641	XM_345660	
A_44_P221077	-0.92647	11.11792	0.007184	NM_001017479	MGC108778
A_44_P505932	-0.927578	9.684475	0.000221	NM_021868	Cttn
A_44_P469394	-0.927674	10.95975	0.000659	NM_022217	Amph1
A_44_P409339	-0.931009	8.033903	0.005822	NM_053357	Ctnnb1
A_44_P621820	-0.933715	11.95108	0.002175	XR_005838	LOC501532
A_44_P349309	-0.936479	10.88574	0.007826	XM_223327	
A_44_P269752	-0.937257	12.53318	0.005391	XM_341581	Rnf125_predicted
A_44_P261326	-0.937683	9.315438	0.003697	XM_342782	Golt1b_predicted
A_44_P278639	-0.938965	9.436573	0.003089	NM_053693	Dmtf1
A_44_P210563	-0.939523	11.39399	0.003864	NM_012578	H1f0
A_44_P443976	-0.939799	8.653178	0.003824	NM_031697	St3gal3
A_44_P868060	-0.940038	9.085655	0.000327	XR_005433	
A_44_P143974	-0.940953	12.80713	0.001732	NM_001013235	Scoc
A_43_P21660	-0.941041	10.4107	0.000164	NM_001007147	Unc84a
A_43_P18787	-0.9414	9.262463	0.002095	XM_342552	Ncoa6
A_44_P115461	-0.942682	9.245119	0.007063	NM_017007	Gad1
A_44_P410062	-0.943971	12.47318	0.001655	XR_005977	LOC290503
A_43_P17406	-0.945546	9.715528	0.001908	NM_001005541	Vps16
A_44_P794770	-0.94696	10.27504	0.004338	NM_133560	Trak2
A_44_P973796	-0.947016	11.59966	0.004459	DY319575	
A_43_P10574	-0.947419	9.88833	0.000371	NM_001012012	Snx11
A_44_P164287	-0.947676	8.473386	0.000485	NM_001013925	Nub1
A_44_P427089	-0.948337	11.95941	0.000863	XM_341008	
A_44_P606344	-0.948971	10.54105	0.003253	XM_343550	RGD1310392_predicted
A_44_P356876	-0.950631	8.529601	8.67E-05	NM_001039002	RGD1304790
A_44_P113842	-0.951642	8.328451	0.001042	NM_022210	Max

A_44_P365516	-0.952073	14.32874	0.00153	BC059146	Tgfb1i4
A_43_P10725	-0.952393	10.57854	0.006304	NM_001012468	Rab18
A_43_P16458	-0.956172	13.35345	0.001088	NM_001011992	Atp6v1c1
A_44_P433334	-0.957339	9.778173	0.001503	NM_001012197	Tra1_predicted
A_44_P466489	-0.957393	10.38779	0.005784	NM_001007642	MGC93920
A_44_P413294	-0.958499	10.65194	0.004919	NM_022864	Cplx1
A_44_P288796	-0.958543	9.77281	0.001562	NM_001013125	Bfar
A_44_P609842	-0.959053	9.079842	0.006878		
A_44_P822078	-0.959623	10.3268	0.002286	XM_576832	LOC501422
A_44_P984248	-0.959633	8.922284	0.000801	XM_222785	Astn1
A_42_P832417	-0.959872	14.31019	0.001339	NM_012686	Vsnl1
A_44_P317520	-0.960089	11.88639	0.000868	BC079339	Atp6ap2
A_44_P286573	-0.96102	9.659496	0.000623	AA955833	
A_43_P11752	-0.964338	10.8451	0.0015	NM_013198	Maob
A_44_P342908	-0.965246	10.98916	0.000306	NM_001012076	Phyhipl
A_43_P17784	-0.966917	10.40971	0.000967	NM_001025722	Cdk10
A_44_P487021	-0.967089	11.75454	0.004192	NM_001002830	Rasl11b
A_44_P698487	-0.967251	11.0701	0.003175	XR_007600	LOC501341
A_44_P776000	-0.967895	12.74713	0.001375	XM_001061754	
A_44_P196757	-0.968211	10.26993	0.002441	XM_224256	Sacs_predicted
A_44_P764653	-0.968498	9.566406	0.000695	CO559017	
A_44_P166396	-0.969982	9.102654	0.000579	XM_216348	RGD1311622_predicted
A_44_P111368	-0.970396	10.00032	0.005783	NM_001037356	MGC125015
A_44_P191903	-0.971317	9.005184	0.000774	NM_053693	Dmtf1
A_44_P625415	-0.971557	14.28528	0.000403	XM_220333	Cyfip2_predicted
A_44_P237886	-0.97168	14.67145	0.009105	NM_031353	Vdac1
A_44_P318891	-0.973557	14.13979	0.004502	XR_007422	RGD1561111_predicted
A_44_P248541	-0.974703	10.35557	0.004283	NM_001014263	Sypl
A_44_P111959	-0.974894	8.187997	3.11E-06	BC087709	Slc15a4
A_44_P187827	-0.975297	10.99753	0.00531	XM_213437	Spop
A_44_P156439	-0.976221	9.753425	0.00196	XM_344861	Trim28
A_44_P193210	-0.979059	10.75687	0.005774	AY724483	LOC690163
A_44_P114023	-0.979827	9.12418	0.002735	NM_001047972	LOC501706
A_44_P501593	-0.981285	9.661811	0.001256	XM_230773	Acss2_predicted
A_44_P555525	-0.983285	11.03448	0.008015	NM_001007625	Epdr2
A_44_P347007	-0.985732	9.112875	0.005147	XM_001058095	
A_44_P290231	-0.991312	15.26656	0.005277	NM_013013	Psap
A_44_P201511	-0.991781	8.903813	0.000151	NM_001012087	Mar.07
A_44_P386840	-0.992813	13.26252	0.003197	NM_001013209	Dnajb6
A_44_P401170	-0.994067	10.95804	0.005615	NM_001025014	Tmem50b
A_44_P328311	-0.995783	13.29344	0.004944	XR_007180	LOC499261
A_44_P149161	-0.99613	10.26854	0.007722	NM_198738	Psat1
A_44_P238710	-0.997814	8.468174	0.000807	XM_218747	Tjp1_predicted
A_43_P10867	-1.00068	9.238465	0.001962	CB547678	
A_44_P239095	-1.001923	11.38682	0.000538	XM_223440	RGD1564407_predicted
A_43_P15490	-1.002544	11.39528	0.000103	NM_134377	Clstn2
A_44_P123898	-1.002823	10.07004	0.003245	XM_341452	
A_44_P214054	-1.004151	11.25551	0.008879	NM_031722	Tmed2
A_44_P162099	-1.004188	9.388554	0.002809	NM_053296	Glrb

A_43_P15623	-1.004336	10.74371	0.001195	NM_053414	Ddx1
A_44_P479520	-1.00546	10.10051	0.003832	XM_341907	Eif4g2_predicted
A_44_P905187	-1.005469	11.47995	0.002067	XM_233231	Dnajc6_predicted
A_44_P170309	-1.006565	8.625744	0.000217	XM_001064372	RGD1562407_predicted
A_44_P950583	-1.008831	9.836371	0.002687	CO396335	
A_44_P500906	-1.010881	9.936269	0.004815	NM_012788	Dlgh1
A_44_P912711	-1.012212	11.21529	0.004315	XM_224429	Pcdh9_predicted
A_44_P929345	-1.012916	10.90634	0.001278	XM_576703	LOC681644
A_44_P426919	-1.013338	12.66231	0.005288	XM_345601	
A_44_P328121	-1.016958	10.3368	0.006076	NM_057207	Sv2b
A_44_P978901	-1.017263	10.12303	0.00224	XM_218747	Tjp1_predicted
A_44_P296084	-1.020161	9.707363	0.000465	CB544459	
A_44_P159296	-1.020721	10.10136	0.007064	NM_001013929	Atp6v1h
A_44_P100991	-1.020722	10.01432	0.001454	XM_220404	RGD1310352
A_44_P519174	-1.021111	10.15332	0.000319	NM_001015027	Crebl2
A_44_P320955	-1.023289	9.428457	0.003607	NM_001012213	Sfxn1
A_44_P231994	-1.023305	9.89084	0.000809	XM_231626	Slc37a3_predicted
A_44_P183241	-1.023585	9.310267	0.005435	XM_221333	Bcl6_predicted
A_43_P16889	-1.025905	10.09083	0.002697	XM_220636	RGD1307929
A_44_P131031	-1.026384	15.044	0.002092	XR_006475	LOC499479
A_44_P428872	-1.027036	8.76117	0.007642	XM_341137	
A_44_P769703	-1.029805	8.731323	0.004312	NM_178096	Nrep
A_42_P843366	-1.030639	9.593706	0.001143	NM_022681	Adnp
A_44_P394401	-1.035642	9.837967	8.60E-05	XM_230531	Disp2_predicted
A_44_P269675	-1.039368	9.460818	0.006258	XM_001065667	LOC685894
A_44_P251692	-1.042788	12.91922	0.00797	NM_019257	Sfrs5
A_43_P15601	-1.043059	9.276099	0.00032	NM_134351	Mat2a
A_44_P118993	-1.045783	9.558989	0.00415	NM_134351	Mat2a
A_44_P108728	-1.052343	9.228743	0.005081	CA512164	
A_44_P356658	-1.052781	8.23732	0.000364	XM_219716	Pdzd4_predicted
A_44_P433568	-1.055139	10.05306	0.008337	XM_341882	Sytl2_predicted
A_44_P420005	-1.060142	10.64892	0.001587	NM_001047897	LOC360618
A_44_P110392	-1.062312	10.29743	0.009783		
A_44_P917564	-1.062494	13.42654	0.000786	NM_001044282	MGC94725
A_44_P790861	-1.062642	8.940687	0.001409		
A_44_P189326	-1.066924	12.61675	0.00045	NM_017319	Pdia3
A_44_P215393	-1.067533	11.4316	0.006142	NM_001025129	RGD1306327
A_44_P109887	-1.069138	12.16077	0.005229	XM_214007	Ccni_predicted
A_42_P509365	-1.069294	12.67278	0.005048	NM_031140	Vim
A_44_P374848	-1.069632	10.04428	0.000273	NM_024139	Chp
A_44_P354008	-1.072481	9.573272	0.001294	XM_224429	Pcdh9_predicted
A_44_P482267	-1.073559	9.237502	0.005217	NM_134382	Elovl5
A_43_P16591	-1.075943	9.78436	0.001714	AY724483	LOC690163
A_44_P461470	-1.077919	9.689354	0.000273	NM_053714	Ank
A_44_P699787	-1.077996	9.30303	0.000781	XM_221369	Senp5_predicted
A_44_P443138	-1.080637	14.64915	0.002534	XM_001054273	RGD1561628_predicted
A_44_P116904	-1.081159	12.77852	0.000733	XM_225314	Vmp_predicted
A_43_P11707	-1.081189	10.4956	0.000904	NM_013090	Vamp1
A_44_P484826	-1.081737	10.2743	0.002837	NM_017276	Gdi2

A_44_P856083	-1.082793	9.886582	0.001193		
A_44_P732939	-1.088751	9.200086	0.008222	XM_220269	
A_44_P828123	-1.088815	11.76102	0.002066	CO393245	
A_44_P687063	-1.094545	8.473641	0.009149		
A_43_P16511	-1.100214	9.35087	0.008189	NM_001044300	MGC112715
A_44_P651866	-1.100887	9.020218	0.000955	XR_009004	RGD1560288_predicted
A_44_P846589	-1.104643	10.63952	0.002532	NM_022229	Hspd1
A_44_P109862	-1.106694	10.03475	2.72E-05	NM_001047085	Ivns1abp_predicted
A_44_P141351	-1.119344	15.11579	0.0025	AY035551	
A_44_P855981	-1.121351	8.017247	0.002263		
A_44_P110158	-1.123021	9.375679	0.000752	XM_232077	Ctnna2_predicted
A_44_P433542	-1.126	9.254163	0.007077	NM_198132	Hnrpa3
A_44_P112641	-1.127383	10.04735	7.45E-05	XM_221214	RGD1304570_predicted
A_44_P108982	-1.131107	11.66852	0.004792	XM_341354	Sucla2_predicted
A_44_P283366	-1.131551	9.4448	0.000311	NM_181081	Myst2
A_44_P379420	-1.132617	14.026	9.91E-05	NM_017088	Gdi1
A_44_P903850	-1.134347	12.62073	0.009738	NM_001042621	Pip5k1a_predicted
A_44_P419757	-1.136875	11.96629	0.000772	XM_346210	
A_44_P187144	-1.144151	10.41503	0.001052	NM_080896	Hnrph1
A_44_P205301	-1.144216	11.84258	0.000678	NM_183402	Grinl1a
A_44_P281435	-1.148942	12.47708	0.000275	NM_001013923	LOC296318
A_44_P206284	-1.150263	8.977071	0.000717	XM_217496	RGD1566215_predicted
A_44_P458704	-1.158889	15.178	0.000227	NM_017073	Glul
A_44_P426808	-1.161242	10.50081	0.000721	NM_001013033	Tspyl
A_42_P828898	-1.169638	9.093417	0.000622	XM_219958	RGD1305793
A_43_P21284	-1.177773	9.659302	0.00667	NM_001012072	Ppp1r3c
A_44_P365598	-1.181633	10.34801	0.000439	NM_001012060	Rnf146
A_44_P554271	-1.182362	9.892054	0.003047	NM_001012235	Impact
A_43_P22174	-1.189049	9.629683	7.01E-05	NM_001014135	Wdr1
A_44_P549445	-1.189998	10.69697	0.001182	NM_130755	Cs
A_44_P149114	-1.190204	13.43588	0.007867	NM_057213	Atp6v1b2
A_43_P12430	-1.191741	9.018875	0.001834	NM_024374	Mtpn
A_43_P11881	-1.195272	14.19091	1.92E-05	NM_017253	Bcat1
A_44_P112597	-1.196669	10.69711	0.001391	XM_220423	Sept8_predicted
A_44_P196717	-1.210552	10.03627	0.007336	XM_344970	Stk32c_predicted
A_44_P496496	-1.216847	9.512697	0.001327	XM_342857	Sh3gl2
A_44_P852695	-1.230847	12.96167	0.002981	XR_007221	LOC367738
A_44_P594455	-1.232739	10.56054	0.002363	XM_341907	Eif4g2_predicted
A_43_P10894	-1.237647	10.40303	0.000796	NM_001025635	Nars
A_44_P409336	-1.242365	13.4477	0.002121	U56261	
A_44_P555389	-1.243916	11.1337	0.005838	NM_138839	Tmem49
A_43_P12816	-1.246149	9.601757	0.006035	U45479	Synj1
A_44_P550364	-1.247556	13.63787	0.00729	NM_080697	Dynll2
A_44_P538779	-1.250005	12.36209	0.003068	NM_001017385	Kdelr1
A_44_P625348	-1.263318	12.04507	0.004999		
A_43_P11613	-1.272921	11.1712	0.007455	NM_012903	Anp32a
A_44_P992854	-1.285168	11.73082	0.002797	NM_057132	Rhoa
A_44_P480605	-1.285189	13.4398	0.003088	XM_001066230	LOC291543
A_44_P243145	-1.291999	10.89005	0.001388	NM_021748	Nsf

A_44_P1040736	-1.294283	14.45449	0.000396	NM_199384	Laptm4a
A_44_P196625	-1.300095	11.39929	0.003723	XM_222253	
A_43_P18282	-1.304967	9.017291	0.000401	XM_341483	RGD1311345
A_44_P858481	-1.31791	9.906794	0.000748		
A_44_P442161	-1.319289	10.07827	0.003586	XM_342405	Ppp2r4_predicted
A_44_P964633	-1.334951	9.974101	0.001176	CO393123	
A_44_P104976	-1.341226	10.14277	0.000192	NM_080583	Ap2b1
A_44_P515029	-1.347381	11.9698	0.004702	XM_215469	Map1b
A_44_P293750	-1.357619	10.95115	0.001441	XM_001066493	Rnf14
A_44_P133044	-1.366986	11.71581	0.008077		
A_44_P338059	-1.370934	9.325555	0.000154	XM_343264	RGD1562665_predicted
A_44_P127156	-1.375902	10.39584	0.00155	M55017	
A_44_P480533	-1.376007	10.07984	0.000659		
A_44_P544023	-1.37978	15.59272	0.00558	NM_001011995	Tuba6
A_44_P902244	-1.382804	10.55446	0.002626	XM_001066493	Rnf14
A_43_P12839	-1.392875	12.20892	0.003602	NM_053531	Sybl1
A_44_P198396	-1.397774	12.74067	0.004725	NM_031841	Scd2
A_44_P958966	-1.414575	12.88172	1.04E-05	XR_005722	LOC360902
A_42_P618436	-1.425871	10.82035	0.00057	XM_235689	RGD1305138_predicted
A_44_P213415	-1.441176	12.31949	0.001576	NM_031353	Vdac1
A_44_P529743	-1.451843	10.57053	0.002358	XM_574587	RGD1562983_predicted
A_44_P107219	-1.469824	12.54211	0.003115	NM_207591	Gltscr2
A_44_P238314	-1.485104	9.641584	0.009513	NM_019621	Dlgh4
A_44_P918103	-1.509247	10.93965	0.002717		
A_44_P177434	-1.512322	12.02379	0.000964	NM_178105	Gpm6a
A_44_P488637	-1.526402	13.0635	0.004916	NM_019351	Timm17a
A_44_P180786	-1.563483	10.31511	0.00123	XM_217372	Plekhb2_predicted
A_44_P217648	-1.66614	11.36677	0.00039	NM_001037217	Mmd2_predicted
A_44_P488022	-1.667428	9.204686	1.12E-05	XM_576451	LOC501039
A_44_P238312	-1.676628	9.563557	0.005752	NM_019621	Dlgh4
A_44_P168842	-1.683993	10.19831	0.000402	XR_006947	LOC300429
A_44_P477322	-1.696866	13.70206	0.000621	NM_031831	Rtn4
A_43_P12141	-1.79599	11.19161	0.000277	NM_021869	Stx7
A_44_P448181	-1.799041	11.6104	0.000186	AY569014	Clstn1
A_43_P18735	-1.800031	10.71494	0.001217	NM_001030030	Cpsf3
A_43_P15367	-1.835326	11.87294	0.001591	NM_139189	Lmbrd1
A_44_P149148	-1.923989	10.84637	0.000345	NM_017309	Ppp3r1

Table S4

Median: 0.00999179436682584 Geo: 0.013098146982064234

Term	Count	%	PValue
GO:0032502~developmental process	29	24.37%	0.0019038
GO:0048513~organ development	17	14.29%	0.00264471
GO:0048468~cell development	16	13.45%	0.00365645
GO:0030154~cell differentiation	19	15.97%	0.00467809
GO:0048869~cellular developmental process	19	15.97%	0.00467809
GO:0048731~system development	19	15.97%	0.00999198
GO:0007275~multicellular organismal development	21	17.65%	0.0146788
GO:0048856~anatomical structure development	20	16.81%	0.02188862
GO:0007399~nervous system development	10	8.40%	0.03763158
GO:0009653~anatomical structure morphogenesis	11	9.24%	0.09039635
GO:0032501~multicellular organismal process	27	22.69%	0.44243405

Median: 0.007011150321556307 Geo: 0.01656665519371505

Term	Count	%	PValue
GO:0065007~biological regulation	36	30.25%	0.00358475
GO:0050789~regulation of biological process	32	26.89%	0.00624207
GO:0050794~regulation of cellular process	29	24.37%	0.00778023
GO:0019222~regulation of metabolic process	13	10.92%	0.43267287

Median: 0.05358450190602306 Geo: 0.03213539348414222

Term	Count	%	PValue
GO:0048468~cell development	16	13.45%	0.00365645
GO:0030154~cell differentiation	19	15.97%	0.00467809
GO:0048869~cellular developmental process	19	15.97%	0.00467809
GO:0016265~death	11	9.24%	0.00950467
GO:0008219~cell death	11	9.24%	0.00950467
GO:0008283~cell proliferation	11	9.24%	0.01140801
GO:0006915~apoptosis	10	8.40%	0.01943025
GO:0012501~programmed cell death	10	8.40%	0.02096655
GO:0048518~positive regulation of biological proce	12	10.08%	0.04580325
GO:0048523~negative regulation of cellular proces	11	9.24%	0.05139072
GO:0048522~positive regulation of cellular process	11	9.24%	0.05577828
GO:0008284~positive regulation of cell proliferatior	5	4.20%	0.05685355
GO:0043065~positive regulation of apoptosis	5	4.20%	0.06626229
GO:0043068~positive regulation of programmed ce	5	4.20%	0.06854287
GO:0048519~negative regulation of biological proc	11	9.24%	0.07541499
GO:0042127~regulation of cell proliferation	7	5.88%	0.08055805
GO:0042981~regulation of apoptosis	7	5.88%	0.09226092
GO:0043067~regulation of programmed cell death	7	5.88%	0.09745399
GO:0043066~negative regulation of apoptosis	4	3.36%	0.147503
GO:0043069~negative regulation of programmed c	4	3.36%	0.15030364

Median: 0.029321235494187657 Geo: 0.038754254726694026

Term	Count	%	PValue
GO:0051179~localization	30	25.21%	7.56E-04
GO:0006810~transport	25	21.01%	0.00354746
GO:0051234~establishment of localization	25	21.01%	0.00574139
GO:0022892~substrate-specific transporter activity	14	11.76%	0.00815607
GO:0022857~transmembrane transporter activity	13	10.92%	0.00963755
GO:0006812~cation transport	9	7.56%	0.00979958
GO:0030001~metal ion transport	8	6.72%	0.01000551
GO:0022891~substrate-specific transmembrane tra	12	10.08%	0.01211268
GO:0015674~di-, tri-valent inorganic cation transpo	5	4.20%	0.01456401
GO:0005215~transporter activity	15	12.61%	0.02445628
GO:0022803~passive transmembrane transporter a	7	5.88%	0.02559288
GO:0015267~channel activity	7	5.88%	0.02559288
GO:0015075~ion transmembrane transporter activi	10	8.40%	0.02773796
GO:0006811~ion transport	10	8.40%	0.02932124
GO:0006816~calcium ion transport	4	3.36%	0.03470812
GO:0046873~metal ion transmembrane transporter	6	5.04%	0.04073964
GO:0008324~cation transmembrane transporter ac	8	6.72%	0.04694332
GO:0022838~substrate specific channel activity	6	5.04%	0.06781793
GO:0022890~inorganic cation transmembrane tran	4	3.36%	0.09697663
GO:0005216~ion channel activity	5	4.20%	0.16194302
GO:0015077~monovalent inorganic cation transme	3	2.52%	0.19009553
GO:0005261~cation channel activity	4	3.36%	0.20972592
GO:0015672~monovalent inorganic cation transpor	4	3.36%	0.27459217
GO:0005244~voltage-gated ion channel activity	3	2.52%	0.27903633
GO:0022832~voltage-gated channel activity	3	2.52%	0.27903633
GO:0022836~gated channel activity	3	2.52%	0.50244347
transport	4	3.36%	0.92879381

Median: 0.05103870428246421 Geo: 0.04066100997140925

Term	Count	%	PValue
gpi-anchor	4	3.36%	0.00498683
GO:0048503~GPI anchor binding	4	3.36%	0.00526782
GO:0035091~phosphoinositide binding	4	3.36%	0.03295023
GO:0008289~lipid binding	6	5.04%	0.0510387
lipoprotein	6	5.04%	0.0603392
GO:0005543~phospholipid binding	4	3.36%	0.08847203
glycoprotein	10	8.40%	0.77916217

Median: 0.06375143382925563 Geo: 0.055121287609943094

Term	Count	%	PValue
GO:0000902~cell morphogenesis	9	7.56%	0.00654198
GO:0032989~cellular structure morphogenesis	9	7.56%	0.00654198
GO:0051674~localization of cell	8	6.72%	0.00843971

GO:0006928~cell motility	8	6.72%	0.00843971
GO:0045664~regulation of neuron differentiation	3	2.52%	0.02142502
GO:0030182~neuron differentiation	6	5.04%	0.03435246
GO:0007399~nervous system development	10	8.40%	0.03763158
GO:0009966~regulation of signal transduction	7	5.88%	0.0550051
GO:0048699~generation of neurons	6	5.04%	0.0551754
GO:0009888~tissue development	6	5.04%	0.06087848
GO:0030030~cell projection organization and bioge	5	4.20%	0.06255205
GO:0032990~cell part morphogenesis	5	4.20%	0.06255205
GO:0048858~cell projection morphogenesis	5	4.20%	0.06255205
GO:0009611~response to wounding	7	5.88%	0.06495082
GO:0022008~neurogenesis	6	5.04%	0.07722863
GO:0048667~neuron morphogenesis during differe	4	3.36%	0.08301481
GO:0048812~neurite morphogenesis	4	3.36%	0.08301481
GO:0050793~regulation of developmental process	5	4.20%	0.0890998
GO:0009653~anatomical structure morphogenesis	11	9.24%	0.09039635
GO:0016477~cell migration	5	4.20%	0.09174819
GO:0040007~growth	5	4.20%	0.09533805
GO:0000904~cellular morphogenesis during differe	4	3.36%	0.10288219
GO:0031175~neurite development	4	3.36%	0.11410047
GO:0048666~neuron development	4	3.36%	0.14890113
GO:0045595~regulation of cell differentiation	3	2.52%	0.29754846
GO:0007243~protein kinase cascade	4	3.36%	0.38887732

Median: 0.06568497554225985 Geo: 0.07576685350125058

Term	Count	%	PValue
GO:0006665~sphingolipid metabolic process	4	3.36%	0.00289589
GO:0046519~sphingoid metabolic process	3	2.52%	0.01366877
GO:0006643~membrane lipid metabolic process	4	3.36%	0.06305875
GO:0005783~endoplasmic reticulum	8	6.72%	0.06568498
GO:0044255~cellular lipid metabolic process	5	4.20%	0.38170379
GO:0008610~lipid biosynthetic process	3	2.52%	0.43645072
GO:0006629~lipid metabolic process	5	4.20%	0.52477172

Median: 0.12698373523485457 Geo: 0.1085747713659542

Term	Count	%	PValue
GO:0030659~cytoplasmic vesicle membrane	4	3.36%	0.00995806
GO:0044433~cytoplasmic vesicle part	4	3.36%	0.01786045
GO:0012506~vesicle membrane	4	3.36%	0.02250049
GO:0006886~intracellular protein transport	7	5.88%	0.03008529
GO:0030662~coated vesicle membrane	3	2.52%	0.03867681
GO:0046907~intracellular transport	9	7.56%	0.04142686
GO:0031982~vesicle	6	5.04%	0.05214339
calcium	6	5.04%	0.0881864
GO:0016023~cytoplasmic membrane-bound vesicle	5	4.20%	0.10152223

GO:0031988~membrane-bound vesicle	5	4.20%	0.10963595
GO:0015031~protein transport	7	5.88%	0.11611726
GO:0031410~cytoplasmic vesicle	5	4.20%	0.12233789
GO:0051649~establishment of cellular localization	9	7.56%	0.12639205
GO:0031090~organelle membrane	8	6.72%	0.12757542
GO:0051641~cellular localization	9	7.56%	0.13266272
GO:0045184~establishment of protein localization	7	5.88%	0.1517592
GO:0022607~cellular component assembly	6	5.04%	0.16807623
GO:0008104~protein localization	7	5.88%	0.18813107
GO:0006461~protein complex assembly	4	3.36%	0.20488479
GO:0033036~macromolecule localization	7	5.88%	0.21509493
GO:0030135~coated vesicle	3	2.52%	0.24447744
GO:0016192~vesicle-mediated transport	5	4.20%	0.27460159
GO:0065003~macromolecular complex assembly	5	4.20%	0.27726166
alternative splicing	7	5.88%	0.28705867
GO:0012505~endomembrane system	4	3.36%	0.49566323
splice variant	6	5.04%	0.50529718

Median: 0.09566593468640966 Geo: 0.12641338012275546

Term	Count	%	PValue
GO:0048514~blood vessel morphogenesis	4	3.36%	0.06705093
GO:0009653~anatomical structure morphogenesis	11	9.24%	0.09039635
GO:0001568~blood vessel development	4	3.36%	0.09097701
GO:0001944~vasculature development	4	3.36%	0.09566593
GO:0001525~angiogenesis	3	2.52%	0.17276244
GO:0009887~organ morphogenesis	5	4.20%	0.23150988
GO:0048646~anatomical structure formation	3	2.52%	0.244505

Median: 0.4181424454299303 Geo: 0.12708631750829097

Term	Count	%	PValue
GO:0051258~protein polymerization	5	4.20%	3.37E-04
GO:0046785~microtubule polymerization	3	2.52%	0.00122634
propeptide:Removed in mature form	5	4.20%	0.00483429
GO:0007010~cytoskeleton organization and biogen	9	7.56%	0.00554424
GO:0051128~regulation of cellular component orga	4	3.36%	0.00739916
GO:0031109~microtubule polymerization or depoly	3	2.52%	0.00960909
GO:0030036~actin cytoskeleton organization and b	5	4.20%	0.0231797
Methylation	4	3.36%	0.02721095
GO:0030029~actin filament-based process	5	4.20%	0.02752056
GO:0006996~organelle organization and biogenesis	11	9.24%	0.04869729
GO:0000226~microtubule cytoskeleton organizatio	3	2.52%	0.07868213
GO:0050793~regulation of developmental process	5	4.20%	0.0890998
GO:0007017~microtubule-based process	4	3.36%	0.11923121
rno04810:Regulation of actin cytoskeleton	4	3.36%	0.30419871

cytoplasm	9	7.56%	0.40296436
GO:0017111~nucleoside-triphosphatase activity	5	4.20%	0.41814245
GO:0016462~pyrophosphatase activity	5	4.20%	0.44739985
GO:0016818~hydrolase activity, acting on acid anh	5	4.20%	0.45292712
GO:0016817~hydrolase activity, acting on acid anh	5	4.20%	0.4598126
GO:0042623~ATPase activity, coupled	3	2.52%	0.51221187
nucleotide-binding	6	5.04%	0.55462111
GO:0016787~hydrolase activity	13	10.92%	0.58971636
GO:0016887~ATPase activity	3	2.52%	0.6078906
atp-binding	4	3.36%	0.72056333
GO:0032553~ribonucleotide binding	6	5.04%	0.96851476
GO:0032555~purine ribonucleotide binding	6	5.04%	0.96851476
GO:0017076~purine nucleotide binding	6	5.04%	0.97692857
GO:0000166~nucleotide binding	7	5.88%	0.97699087
GO:0005524~ATP binding	4	3.36%	0.9859679
GO:0032559~adenyl ribonucleotide binding	4	3.36%	0.98743697
GO:0030554~adenyl nucleotide binding	4	3.36%	0.99120971

Median: 0.22688672366390947 Geo: 0.17317491533194845

Term	Count	%	PValue
GO:0040007~growth	5	4.20%	0.09533805
GO:0016049~cell growth	3	2.52%	0.22688672
GO:0008361~regulation of cell size	3	2.52%	0.24009306

Median: 0.2165902008057497 Geo: 0.19738681531543417

Term	Count	%	PValue
GO:0009611~response to wounding	7	5.88%	0.06495082
GO:0006950~response to stress	10	8.40%	0.16020793
GO:0006954~inflammatory response	4	3.36%	0.27297247
GO:0006952~defense response	4	3.36%	0.53442293

Median: 0.21605817549213288 Geo: 0.19865088907109454

Term	Count	%	PValue
GO:0009888~tissue development	6	5.04%	0.06087848
GO:0001503~ossification	3	2.52%	0.1920233
GO:0031214~biomineral formation	3	2.52%	0.1920233
GO:0046849~bone remodeling	3	2.52%	0.24009306
GO:0048771~tissue remodeling	3	2.52%	0.26881863
GO:0001501~skeletal development	3	2.52%	0.42416269

Median: 0.27889043603661545 Geo: 0.2011624834289807

Term	Count	%	PValue
GO:0044444~cytoplasmic part	27	22.69%	0.03720137
GO:0005737~cytoplasm	33	27.73%	0.05258976
GO:0005622~intracellular	51	42.86%	0.13093863

GO:0043229~intracellular organelle	41	34.45%	0.1348883
GO:0043226~organelle	41	34.45%	0.13808623
GO:0044424~intracellular part	45	37.82%	0.27889044
GO:0043231~intracellular membrane-bound organe	33	27.73%	0.30426919
GO:0043227~membrane-bound organelle	33	27.73%	0.30690129
GO:0005623~cell	75	63.03%	0.37068418
GO:0044464~cell part	74	62.18%	0.54899273
GO:0009987~cellular process	64	53.78%	0.863184

Median: 0.15196001235368436 Geo: 0.20457578861941178

Term	Count	%	PValue
GO:0005783~endoplasmic reticulum	8	6.72%	0.06568498
endoplasmic reticulum	5	4.20%	0.15196001
transmembrane region	10	8.40%	0.85776306

Median: 0.13366383848907484 Geo: 0.22905797793122154

Term	Count	%	PValue
GO:0006935~chemotaxis	3	2.52%	0.13340296
GO:0042330~taxis	3	2.52%	0.13340296
GO:0007610~behavior	5	4.20%	0.13366384
GO:0007626~locomotory behavior	3	2.52%	0.26660663
GO:0042221~response to chemical stimulus	6	5.04%	0.99428592

Median: 0.21635803992904926 Geo: 0.2376488035116084

Term	Count	%	PValue
GO:0005096~GTPase activator activity	3	2.52%	0.18339936
GO:0030234~enzyme regulator activity	7	5.88%	0.20844452
GO:0030695~GTPase regulator activity	4	3.36%	0.22427156
GO:0008047~enzyme activator activity	3	2.52%	0.37203176

Median: 0.22736533800174696 Geo: 0.2824205975609152

Term	Count	%	PValue
GO:0048545~response to steroid hormone stimulus	3	2.52%	0.12540959
GO:0009719~response to endogenous stimulus	5	4.20%	0.20139135
GO:0009725~response to hormone stimulus	3	2.52%	0.25333932
GO:0042221~response to chemical stimulus	6	5.04%	0.99428592

Median: 0.2986929605585694 Geo: 0.2956774482192189

Term	Count	%	PValue
GO:0050790~regulation of catalytic activity	5	4.20%	0.23023173
GO:0065009~regulation of a molecular function	5	4.20%	0.29869296
GO:0051338~regulation of transferase activity	3	2.52%	0.37589317

Median: 0.48319041257918804 Geo: 0.2994837815815022

Term	Count	%	PValue

GO:0007050~cell cycle arrest	3	2.52%	0.03831729
GO:0045786~negative regulation of progression thr	3	2.52%	0.13139359
GO:0000074~regulation of progression through cell	3	2.52%	0.48028099
GO:0051726~regulation of cell cycle	3	2.52%	0.48609983
GO:0022402~cell cycle process	3	2.52%	0.74850836
GO:0007049~cell cycle	3	2.52%	0.82007454

Median: 0.36012413372890034 Geo: 0.34114833908466563

Term	Count	%	PValue
GO:0005615~extracellular space	16	13.45%	0.10473089
GO:0044421~extracellular region part	16	13.45%	0.14825301
GO:0005576~extracellular region	16	13.45%	0.28147749
signal	11	9.24%	0.36012413
disulfide bond	10	8.40%	0.49379321
signal peptide	9	7.56%	0.82725323
Secreted	4	3.36%	0.83645974

Median: 0.41578343518711314 Geo: 0.3415495270682285

Term	Count	%	PValue
GO:0031090~organelle membrane	8	6.72%	0.12757542
GO:0031966~mitochondrial membrane	4	3.36%	0.21886529
GO:0005740~mitochondrial envelope	4	3.36%	0.26119565
GO:0044429~mitochondrial part	4	3.36%	0.38474803
GO:0005743~mitochondrial inner membrane	3	2.52%	0.41578344
GO:0019866~organelle inner membrane	3	2.52%	0.44419225
GO:0031975~envelope	4	3.36%	0.47119996
GO:0031967~organelle envelope	4	3.36%	0.47119996
GO:0005739~mitochondrion	6	5.04%	0.54972855

Median: 0.6692685796256796 Geo: 0.34206884401432364

Term	Count	%	PValue
GO:0005886~plasma membrane	21	17.65%	0.00824633
membrane	23	19.33%	0.04504188
GO:0044459~plasma membrane part	15	12.61%	0.07477456
GO:0005887~integral to plasma membrane	8	6.72%	0.35720236
GO:0016020~membrane	42	35.29%	0.37195217
GO:0031226~intrinsic to plasma membrane	8	6.72%	0.3720425
transmembrane	13	10.92%	0.66010746
GO:0044425~membrane part	32	26.89%	0.6784297
transmembrane protein	3	2.52%	0.77150498
topological domain:Cytoplasmic	8	6.72%	0.85461623
transmembrane region	10	8.40%	0.85776306
GO:0016021~integral to membrane	24	20.17%	0.94918057
GO:0031224~intrinsic to membrane	24	20.17%	0.95202413
topological domain:Extracellular	5	4.20%	0.95580871

Median: 0.6697869754096847 Geo: 0.3551016719532347

Term	Count	%	PValue
GO:0007242~intracellular signaling cascade	14	11.76%	0.0380455
GO:0007154~cell communication	27	22.69%	0.54613563
GO:0007165~signal transduction	22	18.49%	0.79343832
GO:0007166~cell surface receptor linked signal tra	11	9.24%	0.9644815

Median: 0.4580394280214789 Geo: 0.3817041963201787

Term	Count	%	PValue
GO:0003714~transcription corepressor activity	3	2.52%	0.10708232
GO:0016564~transcription repressor activity	3	2.52%	0.33159958
GO:0003712~transcription cofactor activity	3	2.52%	0.45803943
GO:0008134~transcription factor binding	3	2.52%	0.65248975
GO:0030528~transcription regulator activity	7	5.88%	0.76353048

Median: 0.9948670647412782 Geo: 0.38869644747229287

Term	Count	%	PValue
GO:0007267~cell-cell signaling	10	8.40%	0.02010251
GO:0007268~synaptic transmission	6	5.04%	0.08269739
GO:0019226~transmission of nerve impulse	6	5.04%	0.1264984
GO:0003008~system process	9	7.56%	0.96937986
GO:0050877~neurological system process	6	5.04%	0.99486706
GO:0007186~G-protein coupled receptor protein si	5	4.20%	0.99888011
GO:0001584~rhodopsin-like receptor activity	3	2.52%	0.99985866
GO:0004930~G-protein coupled receptor activity	3	2.52%	0.99994731
GO:0004888~transmembrane receptor activity	4	3.36%	0.99995356

Median: 0.7490033588699851 Geo: 0.4160549356873782

Term	Count	%	PValue
GO:0031090~organelle membrane	8	6.72%	0.12757542
GO:0044446~intracellular organelle part	13	10.92%	0.74900336
GO:0044422~organelle part	13	10.92%	0.75370476

Median: 0.4748806082394614 Geo: 0.45696154314135434

Term	Count	%	PValue
GO:0005509~calcium ion binding	7	5.88%	0.30641968
GO:0043167~ion binding	20	16.81%	0.35301025
GO:0046872~metal ion binding	19	15.97%	0.41200894
GO:0043169~cation binding	17	14.29%	0.53775228
GO:0008270~zinc ion binding	9	7.56%	0.58962396
GO:0046914~transition metal ion binding	11	9.24%	0.64433232

Median: 0.6108548056123693 Geo: 0.46366787538666515

Term	Count	%	PValue

GO:0009055~electron carrier activity	4	3.36%	0.16010272
rno00190:Oxidative phosphorylation	3	2.52%	0.29465413
GO:0005739~mitochondrion	6	5.04%	0.54972855
GO:0006091~generation of precursor metabolites a	4	3.36%	0.67198106
GO:0006118~electron transport	3	2.52%	0.72145424
GO:0016491~oxidoreductase activity	5	4.20%	0.79034494

Median: 0.5781882914454173 Geo: 0.4860358594698407

Term	Count	%	PValue
GO:0005856~cytoskeleton	8	6.72%	0.18425912
GO:0043232~intracellular non-membrane-bound or	10	8.40%	0.57818829
GO:0043228~non-membrane-bound organelle	10	8.40%	0.57818829
GO:0044430~cytoskeletal part	4	3.36%	0.64268789
GO:0005198~structural molecule activity	5	4.20%	0.68513139

Median: 0.9423352055185812 Geo: 0.5612926576195539

Term	Count	%	PValue
GO:0006119~oxidative phosphorylation	3	2.52%	0.09294528
GO:0006091~generation of precursor metabolites a	4	3.36%	0.67198106
GO:0016310~phosphorylation	3	2.52%	0.94233521
GO:0006793~phosphorus metabolic process	3	2.52%	0.97292307
GO:0006796~phosphate metabolic process	3	2.52%	0.97292307

Median: 0.9706858737440671 Geo: 0.6755664698446382

Term	Count	%	PValue
rno04012:ErbB signaling pathway	3	2.52%	0.19756883
kinase	3	2.52%	0.74437278
GO:0016301~kinase activity	3	2.52%	0.97068587
GO:0016772~transferase activity, transferring phos	3	2.52%	0.98728428
GO:0016740~transferase activity	4	3.36%	0.99841383

Median: 0.7330494427919996 Geo: 0.689925413309536

Term	Count	%	PValue
Ionic channel	3	2.52%	0.48234063
ion transport	3	2.52%	0.73304944
transport	4	3.36%	0.92879381

Median: 0.7762607275814594 Geo: 0.7381337367173091

Term	Count	%	PValue
GO:0019538~protein metabolic process	20	16.81%	0.51096511
GO:0043170~macromolecule metabolic process	32	26.89%	0.65084492
GO:0044260~cellular macromolecule metabolic pro	17	14.29%	0.72895769
GO:0044238~primary metabolic process	36	30.25%	0.76037186
GO:0044267~cellular protein metabolic process	16	13.45%	0.79214959
GO:0044237~cellular metabolic process	35	29.41%	0.81029799

GO:0008152~metabolic process	39	32.77%	0.85052368
GO:0043283~biopolymer metabolic process	19	15.97%	0.87567903

Median: 0.796723032466517 Geo: 0.7558166759021745

Term	Count	%	PValue
GO:0019222~regulation of metabolic process	13	10.92%	0.43267287
GO:0010468~regulation of gene expression	11	9.24%	0.53827834
GO:0031323~regulation of cellular metabolic proces	11	9.24%	0.62702663
GO:0045449~regulation of transcription	9	7.56%	0.71296839
GO:0006355~regulation of transcription, DNA-depe	8	6.72%	0.74680584
GO:0019219~regulation of nucleobase, nucleoside,	9	7.56%	0.74927528
GO:0030528~transcription regulator activity	7	5.88%	0.76353048
GO:0006350~transcription	9	7.56%	0.77827361
GO:0006351~transcription, DNA-dependent	8	6.72%	0.79672303
GO:0032774~RNA biosynthetic process	8	6.72%	0.79846712
GO:0010467~gene expression	13	10.92%	0.81665599
GO:0006139~nucleobase, nucleoside, nucleotide ar	14	11.76%	0.82572682
GO:0016070~RNA metabolic process	9	7.56%	0.8732745
GO:0043283~biopolymer metabolic process	19	15.97%	0.87567903
GO:0003700~transcription factor activity	4	3.36%	0.89256127
GO:0003677~DNA binding	7	5.88%	0.91650031
GO:0003676~nucleic acid binding	12	10.08%	0.92266281

Median: 0.7346365499807694 Geo: 0.7567949594906387

Term	Count	%	PValue
GO:0006412~translation	4	3.36%	0.6856941
GO:0009058~biosynthetic process	8	6.72%	0.73223591
GO:0009059~macromolecule biosynthetic process	5	4.20%	0.73703719
GO:0044249~cellular biosynthetic process	5	4.20%	0.88642519

Median: 0.8973573679866338 Geo: 0.8617550111058944

Term	Count	%	PValue
zinc-finger	3	2.52%	0.77262736
metal-binding	5	4.20%	0.89735737
zinc	3	2.52%	0.92303026

Median: 0.9736314715800498 Geo: 0.9595490109139895

Term	Count	%	PValue
GO:0043687~post-translational protein modificatior	5	4.20%	0.92717983
GO:0006464~protein modification process	5	4.20%	0.97363147
GO:0043412~biopolymer modification	5	4.20%	0.97868494

Median: 0.9468890540524483 Geo: 0.9630591152749226

Term	Count	%	PValue
GO:0004871~signal transducer activity	14	11.76%	0.94688905

GO:0060089~molecular transducer activity	14	11.76%	0.94688905
GO:0004872~receptor activity	9	7.56%	0.99623236

Table S5

Median: 6.748340700062148E-4 Geo: 6.426805056597486E-4

Term	Count	%	PValue
GO:0032502~developmental process	45	29.61%	4.78E-06
GO:0048869~cellular developmental process	30	19.74%	2.99E-05
GO:0030154~cell differentiation	30	19.74%	2.99E-05
GO:0007275~multicellular organismal development	32	21.05%	5.16E-04
GO:0048731~system development	28	18.42%	6.75E-04
GO:0048856~anatomical structure development	30	19.74%	0.00152982
GO:0048513~organ development	22	14.47%	0.00159909
GO:0009653~anatomical structure morphogenesis	15	9.87%	0.05367044
GO:0032501~multicellular organismal process	43	28.29%	0.09576885

Median: 0.0036852104896518256 Geo: 0.00177884271287579

Term	Count	%	PValue
GO:0042127~regulation of cell proliferation	15	9.87%	8.15E-05
GO:0008283~cell proliferation	18	11.84%	1.21E-04
GO:0008285~negative regulation of cell proliferatior	8	5.26%	0.00304683
GO:0008284~positive regulation of cell proliferation	8	5.26%	0.00432359
GO:0048523~negative regulation of cellular process	16	10.53%	0.01161529
GO:0048519~negative regulation of biological proce	16	10.53%	0.02091638

Median: 0.011553468381934585 Geo: 0.003868567826100308

Term	Count	%	PValue
GO:0032502~developmental process	45	29.61%	4.78E-06
GO:0048869~cellular developmental process	30	19.74%	2.99E-05
GO:0030154~cell differentiation	30	19.74%	2.99E-05
GO:0048468~cell development	23	15.13%	2.67E-04
GO:0008219~cell death	14	9.21%	0.0066416
GO:0016265~death	14	9.21%	0.0066416
GO:0006915~apoptosis	13	8.55%	0.01155347
GO:0012501~programmed cell death	13	8.55%	0.01272079
GO:0042981~regulation of apoptosis	10	6.58%	0.03207116
GO:0043067~regulation of programmed cell death	10	6.58%	0.03482955
GO:0043066~negative regulation of apoptosis	5	3.29%	0.11766584
GO:0043069~negative regulation of programmed ce	5	3.29%	0.12049239
GO:0006916~anti-apoptosis	3	1.97%	0.37109276

Median: 0.011139084952939873 Geo: 0.004790451489712513

Term	Count	%	PValue
GO:0048518~positive regulation of biological proces	26	17.11%	1.34E-06
GO:0032502~developmental process	45	29.61%	4.78E-06
GO:0048522~positive regulation of cellular process	23	15.13%	1.10E-05
GO:0065007~biological regulation	55	36.18%	1.57E-05
GO:0050794~regulation of cellular process	46	30.26%	2.45E-05
Transcription	15	9.87%	1.83E-04
GO:0050789~regulation of biological process	47	30.92%	2.50E-04
Transcription regulation	14	9.21%	5.62E-04
GO:0045941~positive regulation of transcription	10	6.58%	7.67E-04

GO:0045935~positive regulation of nucleobase, nucl	10	6.58%	0.00109242
GO:0031325~positive regulation of cellular metaboli	10	6.58%	0.00394122
dna-binding	13	8.55%	0.00417032
GO:0043283~biopolymer metabolic process	45	29.61%	0.00463287
GO:0006355~regulation of transcription, DNA-depen	22	14.47%	0.00601692
GO:0009893~positive regulation of metabolic proces	10	6.58%	0.00619934
GO:0003677~DNA binding	23	15.13%	0.00621432
nucleus	22	14.47%	0.00675776
GO:0016070~RNA metabolic process	26	17.11%	0.00861611
GO:0006351~transcription, DNA-dependent	22	14.47%	0.01101814
GO:0032774~RNA biosynthetic process	22	14.47%	0.01126003
GO:0003676~nucleic acid binding	32	21.05%	0.01151421
GO:0019219~regulation of nucleobase, nucleoside, r	23	15.13%	0.01208922
GO:0045449~regulation of transcription	22	14.47%	0.01618277
GO:0019222~regulation of metabolic process	25	16.45%	0.01911386
GO:0003700~transcription factor activity	14	9.21%	0.01981277
GO:0030528~transcription regulator activity	18	11.84%	0.02085853
GO:0005634~nucleus	35	23.03%	0.02523932
GO:0006139~nucleobase, nucleoside, nucleotide an	32	21.05%	0.02781943
GO:0006350~transcription	22	14.47%	0.03053968
GO:0010468~regulation of gene expression	22	14.47%	0.03448082
GO:0031323~regulation of cellular metabolic proces	23	15.13%	0.03705001
GO:0045893~positive regulation of transcription, DN	6	3.95%	0.05128254
GO:0045944~positive regulation of transcription fror	5	3.29%	0.06361487
GO:0010467~gene expression	27	17.76%	0.11393444
GO:0006357~regulation of transcription from RNA po	7	4.61%	0.14555294
GO:0016563~transcription activator activity	5	3.29%	0.20323926
GO:0006366~transcription from RNA polymerase II p	7	4.61%	0.30991157
GO:0046983~protein dimerization activity	4	2.63%	0.5722885

Median: 0.00888381322916805 Geo: 0.005713472237800778

Term	Count	%	PValue
GO:0046872~metal ion binding	38	25.00%	9.66E-04
GO:0043167~ion binding	38	25.00%	0.00152226
GO:0046914~transition metal ion binding	26	17.11%	0.00400902
GO:0008270~zinc ion binding	20	13.16%	0.0137586
GO:0043169~cation binding	32	21.05%	0.01799826
metal-binding	18	11.84%	0.02383083

Median: 0.004267893538795904 Geo: 0.005825031646840147

Term	Count	%	PValue
zinc finger	6	3.95%	2.17E-05
DNA binding	7	4.61%	5.82E-04
zinc finger region:C2H2-type 3	4	2.63%	0.00360219
zinc finger region:C2H2-type 2	4	2.63%	0.00403583
zinc finger region:C2H2-type 1	4	2.63%	0.00449996
zinc-finger	9	5.92%	0.07610532
IPR007087:Zinc finger, C2H2-type	5	3.29%	0.10183541
zinc	10	6.58%	0.20726519

Median: 0.00782651025183407 Geo: 0.00761178627655859

Term	Count	%	PValue
GO:0001569~patterning of blood vessels	4	2.63%	2.96E-04
GO:0007389~pattern specification process	7	4.61%	0.00204985
GO:0048646~anatomical structure formation	7	4.61%	0.00218479
GO:0009880~embryonic pattern specification	4	2.63%	0.00361935
GO:0001525~angiogenesis	6	3.95%	0.00412935
GO:0048754~branching morphogenesis of a tube	4	2.63%	0.00484675
GO:0001763~morphogenesis of a branching structur	4	2.63%	0.00669642
GO:0009887~organ morphogenesis	10	6.58%	0.00782651
GO:0048514~blood vessel morphogenesis	6	3.95%	0.01028697
GO:0001568~blood vessel development	6	3.95%	0.01730714
GO:0035295~tube development	6	3.95%	0.0176862
GO:0001944~vasculature development	6	3.95%	0.01885633
GO:0035239~tube morphogenesis	5	3.29%	0.0231404
GO:0009790~embryonic development	7	4.61%	0.044897
GO:0009653~anatomical structure morphogenesis	15	9.87%	0.05367044

Median: 0.05457297922436276 Geo: 0.014620536960131459

Term	Count	%	PValue
zinc finger	6	3.95%	2.17E-05
IPR003070:Orphan nuclear receptor	3	1.97%	2.97E-04
PIRSF002524:probable hormone receptor N10, nucle	3	1.97%	3.95E-04
DNA binding	7	4.61%	5.82E-04
region of interest:Ligand-binding	3	1.97%	0.02103787
IPR001723:Steroid hormone receptor	3	1.97%	0.05028855
zinc finger region:NR C4-type	3	1.97%	0.05111912
DNA-binding region:Nuclear receptor	3	1.97%	0.05111912
IPR001628:Zinc finger, nuclear hormone receptor-typ	3	1.97%	0.05802684
IPR000536:Nuclear hormone receptor, ligand-bindin	3	1.97%	0.05802684
IPR008946:Nuclear hormone receptor, ligand-bindin	3	1.97%	0.05802684
GO:0003707~steroid hormone receptor activity	3	1.97%	0.06048219
SM00430:HOLI	3	1.97%	0.07872766
SM00399:ZnF_C4	3	1.97%	0.07872766
GO:0043565~sequence-specific DNA binding	7	4.61%	0.11289371
GO:0004879~ligand-dependent nuclear receptor act	3	1.97%	0.12910237

Median: 0.027819433619917497 Geo: 0.0306394706702835

Term	Count	%	PValue
GO:0043283~biopolymer metabolic process	45	29.61%	0.00463287
GO:0009987~cellular process	101	66.45%	0.01801886
GO:0044237~cellular metabolic process	64	42.11%	0.02644205
GO:0006139~nucleobase, nucleoside, nucleotide an	32	21.05%	0.02781943
GO:0044238~primary metabolic process	62	40.79%	0.07000976
GO:0008152~metabolic process	68	44.74%	0.0740469
GO:0043170~macromolecule metabolic process	54	35.53%	0.07963106

Median: 0.04353482301401534 Geo: 0.04295313228238676

Term	Count	%	PValue
GO:0019932~second-messenger-mediated signaling	7	4.61%	0.0298774
GO:0007200~G-protein signaling, coupled to IP3 sec	4	2.63%	0.03872718
GO:0043085~positive regulation of catalytic activity	6	3.95%	0.04834246
GO:0048015~phosphoinositide-mediated signaling	4	2.63%	0.06085438

Median: 0.04555127796655499 Geo: 0.04839470743609883

Term	Count	%	PValue
GO:0030335~positive regulation of cell migration	3	1.97%	0.01085114
GO:0040017~positive regulation of locomotion	3	1.97%	0.01842662
GO:0051272~positive regulation of cell motility	3	1.97%	0.01842662
GO:0016477~cell migration	7	4.61%	0.03362988
GO:0006928~cell motility	8	5.26%	0.04555128
GO:0051674~localization of cell	8	5.26%	0.04555128
GO:0030334~regulation of cell migration	3	1.97%	0.10050712
GO:0051270~regulation of cell motility	3	1.97%	0.12495972
GO:0040012~regulation of locomotion	3	1.97%	0.14485459
GO:0040011~locomotion	3	1.97%	0.15065598

Median: 0.04022831394862833 Geo: 0.04844946335952177

Term	Count	%	PValue
GO:0005622~intracellular	77	50.66%	0.00474
GO:0043231~intracellular membrane-bound organel	54	35.53%	0.01200889
GO:0043227~membrane-bound organelle	54	35.53%	0.01229198
GO:0005634~nucleus	35	23.03%	0.02523932
GO:0044424~intracellular part	68	44.74%	0.03572386
GO:0043229~intracellular organelle	59	38.82%	0.04022831
GO:0043226~organelle	59	38.82%	0.0417487
GO:0005737~cytoplasm	42	27.63%	0.11320826
GO:0044464~cell part	105	69.08%	0.23012183
GO:0005623~cell	105	69.08%	0.23111091
GO:0044444~cytoplasmic part	27	17.76%	0.54126325

Median: 0.06545635625828403 Geo: 0.04962889637919206

Term	Count	%	PValue
GO:0050790~regulation of catalytic activity	10	6.58%	0.0077088
GO:0032147~activation of protein kinase activity	4	2.63%	0.0132609
GO:0065009~regulation of a molecular function	10	6.58%	0.01587624
GO:0045859~regulation of protein kinase activity	6	3.95%	0.02954193
GO:0043549~regulation of kinase activity	6	3.95%	0.03284997
GO:0051338~regulation of transferase activity	6	3.95%	0.0369918
GO:0007243~protein kinase cascade	8	5.26%	0.0386475
GO:0043085~positive regulation of catalytic activity	6	3.95%	0.04834246
GO:0006469~negative regulation of protein kinase a	3	1.97%	0.08257025
GO:0033673~negative regulation of kinase activity	3	1.97%	0.08257025
GO:0051348~negative regulation of transferase acti	3	1.97%	0.08758647
GO:0045860~positive regulation of protein kinase ac	4	2.63%	0.0941953
GO:0033674~positive regulation of kinase activity	4	2.63%	0.10092596
GO:0051347~positive regulation of transferase activ	4	2.63%	0.10960265

GO:0051336~regulation of hydrolase activity	4	2.63%	0.12777791
GO:0043086~negative regulation of catalytic activity	3	1.97%	0.15650345

Median: 0.14206229159700978 Geo: 0.07125983280189296

Term	Count	%	PValue
GO:0007242~intracellular signaling cascade	22	14.47%	0.00196264
GO:0007154~cell communication	45	29.61%	0.08178314
GO:0007165~signal transduction	39	25.66%	0.20234145
GO:0007166~cell surface receptor linked signal tran	20	13.16%	0.79394355

Median: 0.10637149401814736 Geo: 0.0849474832216158

Term	Count	%	PValue
GO:0000902~cell morphogenesis	10	6.58%	0.01669842
GO:0032989~cellular structure morphogenesis	10	6.58%	0.01669842
GO:0016477~cell migration	7	4.61%	0.03362988
GO:0006928~cell motility	8	5.26%	0.04555128
GO:0051674~localization of cell	8	5.26%	0.04555128
GO:0030030~cell projection organization and bioger	6	3.95%	0.05990029
GO:0048858~cell projection morphogenesis	6	3.95%	0.05990029
GO:0032990~cell part morphogenesis	6	3.95%	0.05990029
GO:0022008~neurogenesis	7	4.61%	0.10172001
GO:0030182~neuron differentiation	6	3.95%	0.11102298
GO:0016043~cellular component organization and b	26	17.11%	0.11236985
GO:0007409~axonogenesis	4	2.63%	0.13916871
GO:0048699~generation of neurons	6	3.95%	0.1651285
GO:0048812~neurite morphogenesis	4	2.63%	0.1752294
GO:0048667~neuron morphogenesis during differen	4	2.63%	0.1752294
GO:0000904~cellular morphogenesis during differen	4	2.63%	0.21139848
GO:0031175~neurite development	4	2.63%	0.23117678
GO:0048666~neuron development	4	2.63%	0.28990286

Median: 0.09104503852992898 Geo: 0.0908244416758216

Term	Count	%	PValue
GO:0046649~lymphocyte activation	5	3.29%	0.03889336
GO:0042110~T cell activation	4	2.63%	0.05815535
GO:0045321~leukocyte activation	5	3.29%	0.08376054
GO:0002376~immune system process	11	7.24%	0.0842084
GO:0046651~lymphocyte proliferation	3	1.97%	0.09788168
GO:0032943~mononuclear cell proliferation	3	1.97%	0.09788168
GO:0001775~cell activation	5	3.29%	0.1162637
GO:0006955~immune response	7	4.61%	0.26056428

Median: 0.10263827467169256 Geo: 0.1099454504314445

Term	Count	%	PValue
protein phosphatase	4	2.63%	0.01933435
domain:Tyrosine-protein phosphatase	3	1.97%	0.03341908
active site:Phosphocysteine intermediate	3	1.97%	0.04191161
GO:0006470~protein amino acid dephosphorylation	4	2.63%	0.08289082
IPR000387:Protein-tyrosine phosphatase, Tyr-specific	3	1.97%	0.08945855

GO:0042578~phosphoric ester hydrolase activity	6	3.95%	0.09679904
GO:0016311~dephosphorylation	4	2.63%	0.10263827
GO:0016788~hydrolase activity, acting on ester bon	9	5.92%	0.10830484
GO:0004721~phosphoprotein phosphatase activity	4	2.63%	0.11146389
GO:0004725~protein tyrosine phosphatase activity	3	1.97%	0.12631583
GO:0016791~phosphoric monoester hydrolase activi	4	2.63%	0.28627894
GO:0016787~hydrolase activity	18	11.84%	0.49881661
hydrolase	7	4.61%	0.78952711

Median: 0.07802447275373386 Geo: 0.11298829618483724

Term	Count	%	PValue
GO:0048168~regulation of neuronal synaptic plastic	3	1.97%	0.03105792
GO:0007268~synaptic transmission	8	5.26%	0.04555128
GO:0007267~cell-cell signaling	11	7.24%	0.06121429
GO:0048167~regulation of synaptic plasticity	3	1.97%	0.07522256
GO:0019226~transmission of nerve impulse	8	5.26%	0.08082638
GO:0050803~regulation of synapse structure and ac	3	1.97%	0.08758647
GO:0003008~system process	18	11.84%	0.71987716
GO:0050877~neurological system process	15	9.87%	0.80010184

Median: 0.07946974656261849 Geo: 0.12741174769041366

Term	Count	%	PValue
GO:0007049~cell cycle	9	5.92%	0.06925923
cell cycle	5	3.29%	0.07650756
GO:0000074~regulation of progression through cell	6	3.95%	0.07661957
GO:0051726~regulation of cell cycle	6	3.95%	0.07946975
GO:0022402~cell cycle process	8	5.26%	0.08008684
GO:0000278~mitotic cell cycle	4	2.63%	0.32204552
GO:0022403~cell cycle phase	3	1.97%	0.65503475

Median: 0.12910236754218637 Geo: 0.1315662955643494

Term	Count	%	PValue
GO:0004620~phospholipase activity	3	1.97%	0.09416653
GO:0016298~lipase activity	3	1.97%	0.12910237
GO:0004091~carboxylesterase activity	3	1.97%	0.18732821

Median: 0.23450793810192835 Geo: 0.1421944033974187

Term	Count	%	PValue
GO:0042981~regulation of apoptosis	10	6.58%	0.03207116
GO:0043067~regulation of programmed cell death	10	6.58%	0.03482955
GO:0006917~induction of apoptosis	4	2.63%	0.23339623
GO:0012502~induction of programmed cell death	4	2.63%	0.23561965
GO:0043065~positive regulation of apoptosis	4	2.63%	0.36341037
GO:0043068~positive regulation of programmed cel	4	2.63%	0.37027961

Median: 0.21298981099252623 Geo: 0.14655099926417334

Term	Count	%	PValue
GO:0043687~post-translational protein modification	17	11.18%	0.03447465
GO:0043412~biopolymer modification	19	12.50%	0.05642001

GO:0006464~protein modification process	18	11.84%	0.07583392
GO:0043170~macromolecule metabolic process	54	35.53%	0.07963106
GO:0006793~phosphorus metabolic process	11	7.24%	0.21298981
GO:0006796~phosphate metabolic process	11	7.24%	0.21298981
GO:0044260~cellular macromolecule metabolic proc	28	18.42%	0.36408905
GO:0019538~protein metabolic process	29	19.08%	0.38759877
GO:0044267~cellular protein metabolic process	27	17.76%	0.41467928

Median: 0.14499032954436994 Geo: 0.15202648386524137

Term	Count	%	PValue
GO:0040007~growth	6	3.95%	0.09774778
GO:0016049~cell growth	4	2.63%	0.13343014
GO:0008361~regulation of cell size	4	2.63%	0.14499033
GO:0040008~regulation of growth	4	2.63%	0.16699377
GO:0001558~regulation of cell growth	3	1.97%	0.25715566

Median: 0.28092879778048224 Geo: 0.15998774749004374

Term	Count	%	PValue
GO:0035295~tube development	6	3.95%	0.0176862
GO:0045934~negative regulation of nucleobase, nuc	5	3.29%	0.17765547
GO:0031324~negative regulation of cellular metabo	5	3.29%	0.2809288
GO:0016481~negative regulation of transcription	4	2.63%	0.33814868
GO:0009892~negative regulation of metabolic proce	5	3.29%	0.35116929

Median: 0.21679396770072448 Geo: 0.17254682489492937

Term	Count	%	PValue
GO:0007631~feeding behavior	4	2.63%	0.0132609
GO:0019932~second-messenger-mediated signaling	7	4.61%	0.0298774
GO:0006873~cellular ion homeostasis	5	3.29%	0.14107926
GO:0055082~cellular chemical homeostasis	5	3.29%	0.14107926
GO:0007204~elevation of cytosolic calcium ion conc	3	1.97%	0.14485459
GO:0051480~cytosolic calcium ion homeostasis	3	1.97%	0.15357415
GO:0050801~ion homeostasis	5	3.29%	0.17931515
GO:0030005~cellular di-, tri-valent inorganic cation l	4	2.63%	0.18779203
GO:0055066~di-, tri-valent inorganic cation homeost	4	2.63%	0.18779203
GO:0048878~chemical homeostasis	5	3.29%	0.24579591
GO:0030003~cellular cation homeostasis	4	2.63%	0.24679262
GO:0055080~cation homeostasis	4	2.63%	0.24679262
GO:0019725~cellular homeostasis	5	3.29%	0.2753221
GO:0042592~homeostatic process	6	3.95%	0.3060075
GO:0006874~cellular calcium ion homeostasis	3	1.97%	0.31923838
GO:0055074~calcium ion homeostasis	3	1.97%	0.31923838
GO:0006875~cellular metal ion homeostasis	3	1.97%	0.3590126
GO:0055065~metal ion homeostasis	3	1.97%	0.3590126

Median: 0.21687007947550468 Geo: 0.18081047887105914

Term	Count	%	PValue
GO:0002376~immune system process	11	7.24%	0.0842084
GO:0030097~hemopoiesis	4	2.63%	0.19629554

GO:0002521~leukocyte differentiation	3	1.97%	0.21687008
GO:0048534~hemopoietic or lymphoid organ develo	4	2.63%	0.22454334
GO:0002520~immune system development	4	2.63%	0.24007799

Median: 0.1515089135837126 Geo: 0.18575887357629942

Term	Count	%	PValue
GO:0006665~sphingolipid metabolic process	3	1.97%	0.0612205
GO:0006643~membrane lipid metabolic process	4	2.63%	0.13724646
GO:0044255~cellular lipid metabolic process	8	5.26%	0.15150891
GO:0006629~lipid metabolic process	8	5.26%	0.28070626
GO:0008610~lipid biosynthetic process	3	1.97%	0.61895567

Median: 0.31306330276550215 Geo: 0.20213993292493965

Term	Count	%	PValue
GO:0009888~tissue development	8	5.26%	0.03004377
GO:0001501~skeletal development	5	3.29%	0.14566491
GO:0001503~ossification	3	1.97%	0.3130633
GO:0031214~biomineral formation	3	1.97%	0.3130633
GO:0046849~bone remodeling	3	1.97%	0.38009492
GO:0048771~tissue remodeling	3	1.97%	0.41845332

Median: 0.22612678300387035 Geo: 0.20522610538248465

Term	Count	%	PValue
GO:0007626~locomotory behavior	4	2.63%	0.16904168
GO:0006935~chemotaxis	3	1.97%	0.22612678
GO:0042330~taxis	3	1.97%	0.22612678

Median: 0.18718910532733748 Geo: 0.2140013630480883

Term	Count	%	PValue
disulfide bond	18	11.84%	0.09644361
GO:0005576~extracellular region	24	15.79%	0.10978214
GO:0044421~extracellular region part	21	13.82%	0.1520038
GO:0005615~extracellular space	20	13.16%	0.15518646
signal	18	11.84%	0.21919175
glycoprotein	20	13.16%	0.36803111
Secreted	9	5.92%	0.43196977
signal peptide	16	10.53%	0.50542507

Median: 0.28744567816976296 Geo: 0.24435719127448727

Term	Count	%	PValue
IPR007087:Zinc finger, C2H2-type	5	3.29%	0.10183541
IPR013087:Zinc finger, C2H2-type/integrase, DNA-bi	3	1.97%	0.22072902
IPR015880:Zinc finger, C2H2-like	3	1.97%	0.35416233
SM00355:ZnF_C2H2	3	1.97%	0.44785751

Median: 0.35873012641214763 Geo: 0.2739158732596765

Term	Count	%	PValue
GO:0004857~enzyme inhibitor activity	5	3.29%	0.1570748
GO:0004866~endopeptidase inhibitor activity	3	1.97%	0.35873013

GO:0030414~protease inhibitor activity	3	1.97%	0.36473484

Median: 0.25732520791296887 Geo: 0.3070428593235986

Term	Count	%	PValue
GO:0006397~mRNA processing	4	2.63%	0.13533357
GO:0005681~spliceosome	3	1.97%	0.14319607
GO:0016071~mRNA metabolic process	4	2.63%	0.19416055
GO:0006396~RNA processing	5	3.29%	0.21707126
GO:0008380~RNA splicing	3	1.97%	0.29757916
GO:0044428~nuclear part	7	4.61%	0.61839088
GO:0030529~ribonucleoprotein complex	5	3.29%	0.6720952
GO:0003723~RNA binding	4	2.63%	0.78198005

Median: 0.3776840545803085 Geo: 0.35546088644285123

Term	Count	%	PValue
Postsynaptic cell membrane	3	1.97%	0.24967477
cell junction	4	2.63%	0.37768405
synapse	3	1.97%	0.47629076

Median: 0.4350696695030194 Geo: 0.3726779361542909

Term	Count	%	PValue
lipoprotein	6	3.95%	0.25929439
Palmitate	3	1.97%	0.43506967
lipid moiety-binding region:S-palmitoyl cysteine	3	1.97%	0.45882716

Median: 0.6550347493280828 Geo: 0.3930222011751995

Term	Count	%	PValue
GO:0051704~multi-organism process	5	3.29%	0.11907542
GO:0022414~reproductive process	3	1.97%	0.65503475
GO:0000003~reproduction	4	2.63%	0.77833184

Median: 0.5887866746955883 Geo: 0.40006057508686044

Term	Count	%	PValue
GO:0000287~magnesium ion binding	8	5.26%	0.00212904
GO:0016301~kinase activity	12	7.89%	0.09401846
magnesium	5	3.29%	0.11028258
GO:0016772~transferase activity, transferring phosp	12	7.89%	0.20462216
GO:0006793~phosphorus metabolic process	11	7.24%	0.21298981
GO:0006796~phosphate metabolic process	11	7.24%	0.21298981
kinase	7	4.61%	0.24441827
GO:0016773~phosphotransferase activity, alcohol g	9	5.92%	0.27451616
SM00220:S_TKc	6	3.95%	0.28396519
GO:0016740~transferase activity	17	11.18%	0.2851711
IPR002290:Serine/threonine protein kinase	3	1.97%	0.40439199
GO:0004672~protein kinase activity	7	4.61%	0.44285187
binding site:ATP	4	2.63%	0.45273372
IPR000719:Protein kinase, core	4	2.63%	0.5317224
IPR008271:Serine/threonine protein kinase, active si	3	1.97%	0.55142859
Serine/threonine-protein kinase	3	1.97%	0.57400518

GO:0016310~phosphorylation	7	4.61%	0.60356817
GO:0004674~protein serine/threonine kinase activit	5	3.29%	0.61344031
GO:0006468~protein amino acid phosphorylation	6	3.95%	0.62083328
active site:Proton acceptor	4	2.63%	0.66904821
domain:Protein kinase	3	1.97%	0.68221601
nucleotide phosphate-binding region:ATP	4	2.63%	0.68868595
nucleotide-binding	8	5.26%	0.69231599
atp-binding	6	3.95%	0.71410301
GO:0005524~ATP binding	9	5.92%	0.82230441
GO:0032559~adenyl ribonucleotide binding	9	5.92%	0.83617534
GO:0000166~nucleotide binding	13	8.55%	0.84942789
transferase	6	3.95%	0.87435008
GO:0030554~adenyl nucleotide binding	9	5.92%	0.87489505
GO:0032555~purine ribonucleotide binding	10	6.58%	0.90630926
GO:0032553~ribonucleotide binding	10	6.58%	0.90630926
GO:0017076~purine nucleotide binding	10	6.58%	0.93066493

Median: 0.38568296458186957 Geo: 0.4004411400930015

Term	Count	%	PValue
GO:0005764~lysosome	3	1.97%	0.38252226
GO:0000323~lytic vacuole	3	1.97%	0.38568296
GO:0005773~vacuole	3	1.97%	0.43524009

Median: 0.6351311617719959 Geo: 0.4636426277900228

Term	Count	%	PValue
transducer	10	6.58%	0.02538471
g-protein coupled receptor	8	5.26%	0.09168277
GO:0001653~peptide receptor activity	4	2.63%	0.09275957
GO:0042277~peptide binding	5	3.29%	0.09441662
rno04080:Neuroactive ligand-receptor interaction	5	3.29%	0.23679494
membrane	30	19.74%	0.2394147
IPR000276:Rhodopsin-like GPCR superfamily	7	4.61%	0.24170315
G protein-coupled receptor	3	1.97%	0.24587694
GO:0005886~plasma membrane	20	13.16%	0.25253032
glycoprotein	20	13.16%	0.36803111
receptor	12	7.89%	0.40674756
GO:0044459~plasma membrane part	14	9.21%	0.54022955
GO:0005887~integral to plasma membrane	9	5.92%	0.56466453
GO:0031226~intrinsic to plasma membrane	9	5.92%	0.58241564
glycosylation site:N-linked (GlcNAc...)	17	11.18%	0.61271877
transmembrane	21	13.82%	0.6131457
transmembrane protein	5	3.29%	0.65711662
topological domain:Extracellular	11	7.24%	0.6586014
topological domain:Cytoplasmic	13	8.55%	0.72610211
GO:0007186~G-protein coupled receptor protein sig	16	10.53%	0.74139492
GO:0007166~cell surface receptor linked signal tran	20	13.16%	0.79394355
transmembrane region	15	9.87%	0.8266659
GO:0004871~signal transducer activity	20	13.16%	0.92876504
GO:0060089~molecular transducer activity	20	13.16%	0.92876504

GO:0004930~G-protein coupled receptor activity	11	7.24%	0.96003914
GO:0001584~rhodopsin-like receptor activity	9	5.92%	0.9810981
GO:0004888~transmembrane receptor activity	12	7.89%	0.9839537
GO:0004872~receptor activity	15	9.87%	0.98458069
GO:0016020~membrane	41	26.97%	0.9982432
GO:0044425~membrane part	31	20.39%	0.99928109
GO:0016021~integral to membrane	26	17.11%	0.99967323
GO:0031224~intrinsic to membrane	26	17.11%	0.99970986

Median: 0.4708182436304623 Geo: 0.4660174692927841

Term	Count	%	PValue
GO:0030135~coated vesicle	3	1.97%	0.38252226
GO:0016023~cytoplasmic membrane-bound vesicle	4	2.63%	0.45233669
GO:0031988~membrane-bound vesicle	4	2.63%	0.47081824
GO:0031410~cytoplasmic vesicle	4	2.63%	0.49801369
GO:0031982~vesicle	4	2.63%	0.54174871

Median: 0.5977868973943758 Geo: 0.5188412456329615

Term	Count	%	PValue
GO:0006396~RNA processing	5	3.29%	0.21707126
GO:0043233~organelle lumen	8	5.26%	0.25090659
GO:0031974~membrane-enclosed lumen	8	5.26%	0.25090659
rna-binding	3	1.97%	0.45932768
GO:0031981~nuclear lumen	5	3.29%	0.54864712
GO:0005654~nucleoplasm	4	2.63%	0.57718292
GO:0044428~nuclear part	7	4.61%	0.61839088
GO:0030529~ribonucleoprotein complex	5	3.29%	0.6720952
GO:0044451~nucleoplasm part	3	1.97%	0.72030841
GO:0044446~intracellular organelle part	17	11.18%	0.83082855
GO:0044422~organelle part	17	11.18%	0.83519455
GO:0032991~macromolecular complex	15	9.87%	0.92160933

Median: 0.5316807174174902 Geo: 0.5256863931597372

Term	Count	%	PValue
GO:0006954~inflammatory response	4	2.63%	0.47305709
GO:0006950~response to stress	10	6.58%	0.50424836
GO:0006952~defense response	5	3.29%	0.55911307
GO:0009611~response to wounding	5	3.29%	0.57259724

Median: 0.6050691824575416 Geo: 0.5538417602513612

Term	Count	%	PValue
GO:0005739~mitochondrion	9	5.92%	0.38018834
GO:0044429~mitochondrial part	4	2.63%	0.60506918
Mitochondrion	4	2.63%	0.7385047

Median: 0.6203505593051134 Geo: 0.5574080784731396

Term	Count	%	PValue
GO:0005578~proteinaceous extracellular matrix	4	2.63%	0.34465906
GO:0031012~extracellular matrix	4	2.63%	0.36653473

GO:0022610~biological adhesion	4	2.63%	0.87416638
GO:0007155~cell adhesion	4	2.63%	0.87416638

Median: 0.6077307778369707 Geo: 0.6401225395288845

Term	Count	%	PValue
GO:0051179~localization	25	16.45%	0.45835904
GO:0046907~intracellular transport	7	4.61%	0.47664479
GO:0033036~macromolecule localization	7	4.61%	0.50456307
GO:0006605~protein targeting	3	1.97%	0.55097123
GO:0051649~establishment of cellular localization	8	5.26%	0.56384228
GO:0051641~cellular localization	8	5.26%	0.57663052
GO:0008104~protein localization	6	3.95%	0.63883103
GO:0006886~intracellular protein transport	4	2.63%	0.64815115
GO:0045184~establishment of protein localization	5	3.29%	0.7541813
GO:0015031~protein transport	4	2.63%	0.85437133
GO:0051234~establishment of localization	16	10.53%	0.92870858
GO:0006810~transport	14	9.21%	0.96737074

Median: 0.7180410061501701 Geo: 0.6532110505514424

Term	Count	%	PValue
GO:0005506~iron ion binding	4	2.63%	0.40215727
iron	3	1.97%	0.58274416
GO:0016491~oxidoreductase activity	6	3.95%	0.85333785
oxidoreductase	3	1.97%	0.9103727

Median: 0.7898650649158409 Geo: 0.8021733696316998

Term	Count	%	PValue
GO:0006508~proteolysis	6	3.95%	0.73437339
GO:0008233~peptidase activity	5	3.29%	0.78986506
GO:0004175~endopeptidase activity	3	1.97%	0.88988704

Median: 0.970335217397613 Geo: 0.9247462277976668

Term	Count	%	PValue
GO:0008092~cytoskeletal protein binding	3	1.97%	0.79393513
GO:0005856~cytoskeleton	4	2.63%	0.9623272
GO:0043228~non-membrane-bound organelle	8	5.26%	0.97834324
GO:0043232~intracellular non-membrane-bound org	8	5.26%	0.97834324

Median: 0.9839158915997125 Geo: 0.9253029306672969

Term	Count	%	PValue
GO:0015267~channel activity	3	1.97%	0.81163057
GO:0022803~passive transmembrane transporter ac	3	1.97%	0.81163057
GO:0022857~transmembrane transporter activity	4	2.63%	0.9832207
GO:0005215~transporter activity	6	3.95%	0.98461108
GO:0022892~substrate-specific transporter activity	4	2.63%	0.99122499
GO:0022891~substrate-specific transmembrane trar	3	1.97%	0.9928848

Median: 0.9998834069831795 Geo: 0.9976789972437883

Term	Count	%	PValue

GO:0007600~sensory perception	7	4.61%	0.99325095
GO:0007608~sensory perception of smell	3	1.97%	0.99988341
GO:0007606~sensory perception of chemical stimulu	3	1.97%	0.99991743

Table S6

Median: 7.044309624431602E-9 Geo: 1.1045055549475803E-8

Term	Count	%	PValue
GO:0005622~intracellular	501	44.81%	1.21E-19
GO:0044424~intracellular part	453	40.52%	3.90E-14
GO:0005737~cytoplasm	291	26.03%	8.02E-10
GO:0043227~membrane-bound organelle	333	29.79%	1.05E-09
GO:0043231~intracellular membrane-bound	332	29.70%	1.48E-09
GO:0043226~organelle	377	33.72%	7.04E-09
GO:0043229~intracellular organelle	376	33.63%	8.62E-09
GO:0044444~cytoplasmic part	215	19.23%	2.79E-06
GO:0005634~nucleus	184	16.46%	0.005189
GO:0005623~cell	652	58.32%	0.006045
GO:0044464~cell part	651	58.23%	0.009543

Median: 3.542056092261983E-5 Geo: 3.775890795601803E-5

Term	Count	%	PValue
GO:0016192~vesicle-mediated transport	55	4.92%	1.25E-07
GO:0015031~protein transport	64	5.72%	1.64E-07
GO:0045184~establishment of protein localiz	67	5.99%	2.77E-07
GO:0008104~protein localization	69	6.17%	7.17E-07
GO:0033036~macromolecule localization	70	6.26%	1.71E-06
GO:0006886~intracellular protein transport	47	4.20%	3.20E-06
GO:0016043~cellular component organizatio	181	16.19%	6.81E-06
GO:0046907~intracellular transport	64	5.72%	3.54E-05
GO:0051649~establishment of cellular localiz	74	6.62%	2.04E-04
GO:0051641~cellular localization	74	6.62%	2.87E-04
GO:0006810~transport	169	15.12%	5.43E-04
GO:0051234~establishment of localization	174	15.56%	6.17E-04
GO:0051179~localization	194	17.35%	8.66E-04
GO:0032940~secretion by cell	26	2.33%	0.044288
GO:0005215~transporter activity	81	7.25%	0.112579

Median: 0.0011776838916593433 Geo: 6.354060560924282E-4

Term	Count	%	PValue
GO:0031090~organelle membrane	61	5.46%	1.14E-04
GO:0044422~organelle part	153	13.69%	0.001178
GO:0044446~intracellular organelle part	151	13.51%	0.001906

Median: 0.00409552834425737 Geo: 0.0011073699870049756

Term	Count	%	PValue
GO:0016791~phosphoric monoester hydrolas	31	2.77%	5.27E-06
GO:0042578~phosphoric ester hydrolase acti	35	3.13%	2.72E-05
GO:0016788~hydrolase activity, acting on es	56	5.01%	4.15E-05
GO:0016311~dephosphorylation	17	1.52%	0.004096
GO:0004721~phosphoprotein phosphatase a	16	1.43%	0.009877
GO:0006470~protein amino acid dephosphor	14	1.25%	0.022158
GO:0004725~protein tyrosine phosphatase a	6	0.54%	0.383037

Median: 0.003228915351500921 Geo: 0.0014419553823479551

Term	Count	%	PValue
GO:0044238~primary metabolic process	417	37.30%	1.56E-05
GO:0008152~metabolic process	458	40.97%	2.05E-05
GO:0044237~cellular metabolic process	411	36.76%	4.95E-05
GO:0019538~protein metabolic process	218	19.50%	6.51E-04
GO:0043170~macromolecule metabolic proce	348	31.13%	0.002058
GO:0009987~cellular process	658	58.86%	0.002091
GO:0044267~cellular protein metabolic proce	199	17.80%	0.004366
GO:0044260~cellular macromolecule metabo	202	18.07%	0.004398
GO:0043412~biopolymer modification	104	9.30%	0.010652
GO:0006464~protein modification process	101	9.03%	0.011152
GO:0043283~biopolymer metabolic process	239	21.38%	0.015262
GO:0043687~post-translational protein modif	81	7.25%	0.052405

Median: 0.0014458326006580122 Geo: 0.0018374799149451773

Term	Count	%	PValue
GO:0004437~inositol or phosphatidylinositol p	9	0.81%	2.56E-04
GO:0042577~lipid phosphatase activity	5	0.45%	0.001446
GO:0004439~phosphoinositide 5-phosphatase	3	0.27%	0.016744

Median: 0.023947488057755185 Geo: 0.0019884476899413527

Term	Count	%	PValue
GO:0016192~vesicle-mediated transport	55	4.92%	1.25E-07
GO:0048193~Golgi vesicle transport	13	1.16%	0.007169
GO:0045045~secretory pathway	24	2.15%	0.023947
GO:0046903~secretion	33	2.95%	0.032828
GO:0032940~secretion by cell	26	2.33%	0.044288

Median: 0.0016357492368776236 Geo: 0.0032548360076113886

Term	Count	%	PValue
GO:0014069~postsynaptic density	8	0.72%	5.29E-04
GO:0042734~presynaptic membrane	7	0.63%	0.001636
GO:0032279~asymmetric synapse	3	0.27%	0.039821

Median: 0.004086253621505005 Geo: 0.00368195326563183

Term	Count	%	PValue
GO:0006807~nitrogen compound metabolic p	44	3.94%	3.81E-04
GO:0006519~amino acid and derivative meta	38	3.40%	5.58E-04
GO:0009308~amine metabolic process	41	3.67%	7.89E-04
GO:0006520~amino acid metabolic process	27	2.42%	0.007384
GO:0019752~carboxylic acid metabolic proce	41	3.67%	0.044166
GO:0006082~organic acid metabolic process	41	3.67%	0.04559

Median: 0.0024659668666173417 Geo: 0.0038986907006064455

Term	Count	%	PValue
GO:0031988~membrane-bound vesicle	32	2.86%	2.95E-04
GO:0016023~cytoplasmic membrane-bound v	30	2.68%	8.53E-04

GO:0031982~vesicle	32	2.86%	0.001726
GO:0031410~cytoplasmic vesicle	30	2.68%	0.002466
GO:0030135~coated vesicle	17	1.52%	0.008603
GO:0030136~clathrin-coated vesicle	15	1.34%	0.011561
GO:0008021~synaptic vesicle	8	0.72%	0.128535

Median: 0.00569726956942036l Geo: 0.003905295818069365

Term	Count	%	PValue
GO:0012505~endomembrane system	41	3.67%	4.89E-04
GO:0005789~endoplasmic reticulum membra	15	1.34%	0.004224
GO:0042175~nuclear envelope-endoplasmic r	15	1.34%	0.007171
GO:0044432~endoplasmic reticulum part	16	1.43%	0.01569

Median: 0.00580008303153623l Geo: 0.0045423103766470746

Term	Count	%	PValue
GO:0065003~macromolecular complex assen	42	3.76%	0.00193
GO:0022607~cellular component assembly	43	3.85%	0.0058
GO:0006461~protein complex assembly	26	2.33%	0.008372

Median: 0.003102987338819654 Geo: 0.005413943633266698

Term	Count	%	PValue
GO:0000166~nucleotide binding	139	12.43%	4.33E-05
GO:0032553~ribonucleotide binding	114	10.20%	6.94E-04
GO:0032555~purine ribonucleotide binding	114	10.20%	6.94E-04
GO:0017076~purine nucleotide binding	116	10.38%	0.001642
nucleotide-binding	68	6.08%	0.004564
GO:0032559~adenyl ribonucleotide binding	79	7.07%	0.140823
GO:0005524~ATP binding	77	6.89%	0.165516
GO:0030554~adenyl nucleotide binding	81	7.25%	0.202837

Median: 0.004872413994231359 Geo: 0.006380150986284573

Term	Count	%	PValue
GO:0004437~inositol or phosphatidylinositol p	9	0.81%	2.56E-04
SM00128:IPPc	5	0.45%	0.002727
GO:0046030~inositol trisphosphate phosphat	4	0.36%	0.004872
GO:0004445~inositol-polyphosphate 5-phospl	4	0.36%	0.004872
IPR000300:Inositol polyphosphate related pho	4	0.36%	0.011463
IPR005135:Endonuclease/exonuclease/phosph	4	0.36%	0.354689

Median: 0.01031240595268623 Geo: 0.00687033963953285

Term	Count	%	PValue
GO:0007049~cell cycle	50	4.47%	3.48E-04
GO:0007050~cell cycle arrest	10	0.89%	0.002501
GO:0045786~negative regulation of progress	15	1.34%	0.002807
GO:0022402~cell cycle process	39	3.49%	0.008623
GO:0000074~regulation of progression throu	26	2.33%	0.012002
GO:0051726~regulation of cell cycle	26	2.33%	0.013531
GO:0000278~mitotic cell cycle	23	2.06%	0.017947

GO:0022403~cell cycle phase	22	1.97%	0.080816

Median: 0.0028084324789411762　Geo: 0.008228285605659864

Term	Count	%	PValue
GO:0048519~negative regulation of biologica	80	7.16%	0.00239
GO:0048523~negative regulation of cellular p	75	6.71%	0.002808
GO:0009892~negative regulation of metaboli	28	2.50%	0.082998

Median: 0.012960373553618398　Geo: 0.008546649490151655

Term	Count	%	PValue
GO:0006457~protein folding	23	2.06%	0.001451
chaperone	10	0.89%	0.011169
GO:0051082~unfolded protein binding	12	1.07%	0.014752
IPR002423:Chaperonin Cpn60/TCP-1	4	0.36%	0.022313

Median: 0.9967247590148626　Geo: 0.01098528701294567

Term	Count	%	PValue
GO:0007242~intracellular signaling cascade	114	10.20%	1.33E-06
GO:0007154~cell communication	218	19.50%	0.996725
GO:0007165~signal transduction	196	17.53%	0.997839

Median: 0.040660299161142804　Geo: 0.012755242088997738

Term	Count	%	PValue
GO:0016044~membrane organization and bio	29	2.59%	0.001255
GO:0010324~membrane invagination	16	1.43%	0.04066
GO:0006897~endocytosis	16	1.43%	0.04066

Median: 0.10964998236347706　Geo: 0.014021621729689819

Term	Count	%	PValue
GO:0005525~GTP binding	37	3.31%	7.53E-06
GO:0032561~guanyl ribonucleotide binding	37	3.31%	1.26E-05
GO:0019001~guanyl nucleotide binding	37	3.31%	1.46E-05
GTP-binding	26	2.33%	2.21E-04
GO:0003924~GTPase activity	21	1.88%	4.06E-04
IPR005225:Small GTP-binding protein domain	15	1.34%	0.007434
IPR001806:Ras GTPase	15	1.34%	0.007434
nucleotide phosphate-binding region:GTP	14	1.25%	0.023175
lipid moiety-binding region:S-geranylgeranyl c	7	0.63%	0.041332
short sequence motif:Effector region	7	0.63%	0.062708
GO:0017111~nucleoside-triphosphatase activ	37	3.31%	0.10965
GO:0016462~pyrophosphatase activity	38	3.40%	0.122742
GO:0016818~hydrolase activity, acting on aci	38	3.40%	0.12873
GO:0016817~hydrolase activity, acting on aci	38	3.40%	0.139562
prenylation	8	0.72%	0.152535
IPR013753:Ras	9	0.81%	0.152954
PIRSF037165:ras protein	3	0.27%	0.159725
propeptide:Removed in mature form	9	0.81%	0.175615
Methylation	10	0.89%	0.203346

IPR003577:Ras small GTPase, Ras type	3	0.27%	0.297638
SM00173:RAS	3	0.27%	0.305554

Median: 0.01276382284052376 Geo: 0.01838815303424093

Term	Count	%	PValue
GO:0004774~succinate-CoA ligase activity	3	0.27%	0.008688
GO:0016405~CoA-ligase activity	4	0.36%	0.010767
GO:0016878~acid-thiol ligase activity	4	0.36%	0.014761
GO:0016877~ligase activity, forming carbon-s	4	0.36%	0.082806

Median: 0.017439820365672112 Geo: 0.024768054688680787

Term	Count	%	PValue
IPR000504:RNA recognition motif, RNP-1	14	1.25%	0.012923
rna-binding	18	1.61%	0.014434
IPR012677:Nucleotide-binding, alpha-beta pla	14	1.25%	0.01744
SM00360:RRM	16	1.43%	0.042508
GO:0003723~RNA binding	36	3.22%	0.067407

Median: 0.035923506232415525 Geo: 0.0260307834995732

Term	Count	%	PValue
GO:0044271~nitrogen compound biosyntheti	13	1.16%	0.010719
GO:0009309~amine biosynthetic process	10	0.89%	0.035924
GO:0008652~amino acid biosynthetic process	7	0.63%	0.045807

Median: 0.020676498351106368 Geo: 0.02792059126257564

Term	Count	%	PValue
GO:0005794~Golgi apparatus	31	2.77%	0.015073
GO:0044431~Golgi apparatus part	19	1.70%	0.020676
GO:0000139~Golgi membrane	12	1.07%	0.069837

Median: 0.04179945450168271 Geo: 0.02866270308739085

Term	Count	%	PValue
GO:0051020~GTPase binding	11	0.98%	0.005704
GO:0031267~small GTPase binding	9	0.81%	0.0147
GO:0017016~Ras GTPase binding	7	0.63%	0.068898
GO:0017048~Rho GTPase binding	4	0.36%	0.116835

Median: 0.05672383173871821 Geo: 0.03746482697220645

Term	Count	%	PValue
GO:0007264~small GTPase mediated signal t	43	3.85%	9.56E-06
GO:0005083~small GTPase regulator activity	20	1.79%	7.72E-04
GO:0030695~GTPase regulator activity	27	2.42%	0.002797
GO:0005085~guanyl-nucleotide exchange fac	15	1.34%	0.007996
GO:0051056~regulation of small GTPase med	17	1.52%	0.017757
GO:0008047~enzyme activator activity	20	1.79%	0.02122
GO:0005088~Ras guanyl-nucleotide exchang	9	0.81%	0.025163
GO:0007265~Ras protein signal transduction	17	1.52%	0.031174
GO:0030234~enzyme regulator activity	47	4.20%	0.038539

GO:0046578~regulation of Ras protein signal	12	1.07%	0.039714
GO:0007266~Rho protein signal transduction	10	0.89%	0.056724
GO:0009966~regulation of signal transductio	35	3.13%	0.071205
GO:0005089~Rho guanyl-nucleotide exchang	7	0.63%	0.074098
GO:0005096~GTPase activator activity	12	1.07%	0.085486
GO:0035023~regulation of Rho protein signal	7	0.63%	0.112689
IPR011993:Pleckstrin homology-type	12	1.07%	0.182677
IPR001849:Pleckstrin-like	9	0.81%	0.407613
IPR000219:DH	3	0.27%	0.415812
SM00325:RhoGEF	3	0.27%	0.425544
SM00233:PH	9	0.81%	0.488891
domain:PH	3	0.27%	0.801822

Median: 0.05790452203551337 Geo: 0.03831891115558686

Term	Count	%	PValue
GO:0044463~cell projection part	14	1.25%	0.004533
GO:0043198~dendritic shaft	5	0.45%	0.015482
GO:0042995~cell projection	33	2.95%	0.033403
GO:0043197~dendritic spine	5	0.45%	0.082407
GO:0043005~neuron projection	18	1.61%	0.125864
GO:0030425~dendrite	11	0.98%	0.130214

Median: 0.029417122574276287 Geo: 0.03899252756753423

Term	Count	%	PValue
aminoacyl-tRNA synthetase	6	0.54%	0.018385
GO:0043039~tRNA aminoacylation	9	0.81%	0.024262
GO:0006418~tRNA aminoacylation for protei	9	0.81%	0.024262
GO:0043038~amino acid activation	9	0.81%	0.024262
GO:0006399~tRNA metabolic process	12	1.07%	0.029253
GO:0016875~ligase activity, forming carbon-	9	0.81%	0.029581
GO:0016876~ligase activity, forming aminoac	9	0.81%	0.029581
GO:0004812~aminoacyl-tRNA ligase activity	9	0.81%	0.029581
rno00970:Aminoacyl-tRNA biosynthesis	4	0.36%	0.116794
protein biosynthesis	11	0.98%	0.349878

Median: 0.07501409807774695 Geo: 0.04573781156503287

Term	Count	%	PValue
GO:0048193~Golgi vesicle transport	13	1.16%	0.007169
GO:0006888~ER to Golgi vesicle-mediated tr	7	0.63%	0.075014
er-golgi transport	5	0.45%	0.177915

Median: 0.06899050268680867 Geo: 0.046416713865919654

Term	Count	%	PValue
outer membrane	6	0.54%	0.010652
GO:0019867~outer membrane	9	0.81%	0.020773
GO:0005741~mitochondrial outer membrane	6	0.54%	0.068991
GO:0031968~organelle outer membrane	6	0.54%	0.118051
topological domain:Mitochondrial intermembr	4	0.36%	0.119556

Median: 0.06513242583564044 Geo: 0.05036987687278405

Term	Count	%	PValue
GO:0016874~ligase activity	34	3.04%	1.59E-04
GO:0016881~acid-amino acid ligase activity	15	1.34%	0.04563
GO:0019787~small conjugating protein ligas	14	1.25%	0.046039
GO:0016879~ligase activity, forming carbon-	17	1.52%	0.047902
GO:0004842~ubiquitin-protein ligase activity	12	1.07%	0.050809
GO:0008639~small protein conjugating enzy	12	1.07%	0.065132
GO:0006512~ubiquitin cycle	21	1.88%	0.111332
GO:0016567~protein ubiquitination	8	0.72%	0.143279
GO:0000209~protein polyubiquitination	3	0.27%	0.168192
rno04120:Ubiquitin mediated proteolysis	12	1.07%	0.18278
GO:0032446~protein modification by small p	8	0.72%	0.204258

Median: 0.0316532809502792 Geo: 0.05575989202701649

Term	Count	%	PValue
GO:0048468~cell development	89	7.96%	0.005336
GO:0042981~regulation of apoptosis	44	3.94%	0.011114
GO:0043067~regulation of programmed cell	44	3.94%	0.01401
GO:0008219~cell death	56	5.01%	0.014591
GO:0016265~death	56	5.01%	0.014591
GO:0048869~cellular developmental process	110	9.84%	0.021203
GO:0030154~cell differentiation	110	9.84%	0.021203
GO:0006915~apoptosis	52	4.65%	0.028182
GO:0012501~programmed cell death	52	4.65%	0.035124
GO:0043066~negative regulation of apoptosi	18	1.61%	0.138967
GO:0043069~negative regulation of program	18	1.61%	0.146863
GO:0006916~anti-apoptosis	12	1.07%	0.266561
GO:0043065~positive regulation of apoptosis	18	1.61%	0.29451
GO:0043068~positive regulation of programm	18	1.61%	0.311435
GO:0006917~induction of apoptosis	13	1.16%	0.467993
GO:0012502~induction of programmed cell d	13	1.16%	0.475026

Median: 0.1562812317333729 Geo: 0.057707693908155444

Term	Count	%	PValue
GO:0005856~cytoskeleton	60	5.37%	0.002472
GO:0044430~cytoskeletal part	37	3.31%	0.093461
GO:0043232~intracellular non-membrane-bo	88	7.87%	0.219101
GO:0043228~non-membrane-bound organell	88	7.87%	0.219101

Median: 0.06825579194341394 Geo: 0.06084916171997176

Term	Count	%	PValue
IPR006689:ARF/SAR superfamily	5	0.45%	0.041646
IPR006688:ADP-ribosylation factor	4	0.36%	0.066748
SM00177:ARF	4	0.36%	0.069764
PIRSF001711:ADP-ribosylation factor	4	0.36%	0.070693

Median: 0.142736866623424 Geo: 0.0615377040316669

Term	Count	%	PValue
GO:0065007~biological regulation	277	24.78%	1.82E-05
GO:0050789~regulation of biological process	237	21.20%	6.06E-04
GO:0050794~regulation of cellular process	210	18.78%	0.001453
GO:0005634~nucleus	184	16.46%	0.005189
GO:0003676~nucleic acid binding	160	14.31%	0.018851
GO:0019222~regulation of metabolic process	125	11.18%	0.037235
GO:0006139~nucleobase, nucleoside, nucleot	171	15.30%	0.051081
GO:0003677~DNA binding	96	8.59%	0.081483
GO:0031323~regulation of cellular metabolic	115	10.29%	0.098182
GO:0010468~regulation of gene expression	107	9.57%	0.117897
GO:0010467~gene expression	153	13.69%	0.133621
GO:0016070~RNA metabolic process	116	10.38%	0.151853
Transcription regulation	35	3.13%	0.152907
Transcription	35	3.13%	0.176114
GO:0006350~transcription	100	8.94%	0.289473
GO:0045449~regulation of transcription	94	8.41%	0.302651
GO:0019219~regulation of nucleobase, nucle	95	8.50%	0.390213
GO:0006355~regulation of transcription, DNA	84	7.51%	0.393237
GO:0006351~transcription, DNA-dependent	86	7.69%	0.51837
GO:0032774~RNA biosynthetic process	86	7.69%	0.526486
GO:0030528~transcription regulator activity	66	5.90%	0.563567
GO:0003700~transcription factor activity	43	3.85%	0.721366

Median: 0.2068132443128243 Geo: 0.06384945590624247

Term	Count	%	PValue
lipoprotein	35	3.13%	0.004159
lipid moiety-binding region:S-palmitoyl cystei	12	1.07%	0.206813
Palmitate	12	1.07%	0.302654

Median: 0.05902448559063275 Geo: 0.06952667627562897

Term	Count	%	PValue
GO:0008270~zinc ion binding	90	8.05%	0.027333
GO:0043167~ion binding	172	15.38%	0.047907
GO:0046872~metal ion binding	167	14.94%	0.059024
GO:0046914~transition metal ion binding	109	9.75%	0.084958
GO:0043169~cation binding	150	13.42%	0.247418

Median: 0.08069942792163615 Geo: 0.07022645291284828

Term	Count	%	PValue
lipid moiety-binding region:N-myristoyl glycin	9	0.81%	0.01454
myristate	9	0.81%	0.017341
myristylation	6	0.54%	0.018385
blocked amino end	6	0.54%	0.143013
nucleotide binding	6	0.54%	0.406721
P-loop	6	0.54%	0.444845

Median: 0.052526849789520304 Geo: 0.07343970394205135

Term	Count	%	PValue
GO:0006584~catecholamine metabolic proce	6	0.54%	0.019824
GO:0018958~phenol metabolic process	6	0.54%	0.02286
GO:0006576~biogenic amine metabolic proce	10	0.89%	0.022861
GO:0006575~amino acid derivative metabolic	12	1.07%	0.052527
GO:0042133~neurotransmitter metabolic pro	5	0.45%	0.181854
GO:0042417~dopamine metabolic process	3	0.27%	0.297004
GO:0006725~aromatic compound metabolic	10	0.89%	0.392012

Median: 0.08857971092806124 Geo: 0.07428537664101921

Term	Count	%	PValue
rno04130:SNARE interactions in vesicular trar	7	0.63%	0.027406
IPR006012:Syntaxin/epimorphin coiled-coil	4	0.36%	0.046104
domain:t-SNARE coiled-coil homology	4	0.36%	0.053705
IPR006011:Syntaxin, N-terminal	3	0.27%	0.08858
SM00503:SynN	3	0.27%	0.091493
IPR000727:Target SNARE coiled-coil region	4	0.36%	0.147697
SM00397:t_SNARE	4	0.36%	0.153687

Median: 0.062429438292995174 Geo: 0.07578489960391194

Term	Count	%	PValue
lipid moiety-binding region:N-myristoyl glycine	9	0.81%	0.01454
myristate	9	0.81%	0.017341
calcium-binding region:1	8	0.72%	0.019181
domain:EF-hand 3	7	0.63%	0.02202
calcium-binding region:2	7	0.63%	0.046167
IPR002048:Calcium-binding EF-hand	14	1.25%	0.056269
domain:EF-hand 2	9	0.81%	0.057434
domain:EF-hand 4	5	0.45%	0.058266
IPR011992:EF-Hand type	14	1.25%	0.062354
SM00054:EFh	14	1.25%	0.062505
PIRSF002350:calmodulin	4	0.36%	0.070693
domain:EF-hand 1	8	0.72%	0.090052
calcium	30	2.68%	0.152543
calcium-binding region:3	3	0.27%	0.246277
IPR001125:Recoverin	3	0.27%	0.273309
Signal transduction mechanisms / Cytoskeleto	6	0.54%	0.282244
EF hand	4	0.36%	0.294715
calcium binding	5	0.45%	0.346603

Median: 0.08419109283311178 Geo: 0.07865101152463738

Term	Count	%	PValue
GO:0008289~lipid binding	27	2.42%	0.034511
GO:0005543~phospholipid binding	15	1.34%	0.084191
GO:0035091~phosphoinositide binding	10	0.89%	0.167453

Median: 0.06749757640491225 Geo: 0.08163632183901466

Term	Count	%	PValue
GO:0006396~RNA processing	26	2.33%	0.021741
GO:0006397~mRNA processing	16	1.43%	0.027483
mrna processing	10	0.89%	0.03976
GO:0016071~mRNA metabolic process	16	1.43%	0.095236
mrna splicing	6	0.54%	0.279462
GO:0008380~RNA splicing	9	0.81%	0.468157

Median: 0.08367445242528601 Geo: 0.09325118835443283

Term	Count	%	PValue
GO:0019226~transmission of nerve impulse	39	3.49%	0.008986
GO:0007268~synaptic transmission	35	3.13%	0.009379
GO:0007267~cell-cell signaling	49	4.38%	0.083674
GO:0003008~system process	69	6.17%	1
GO:0050877~neurological system process	57	5.10%	1

Median: 0.10197451032252433 Geo: 0.09443930654308128

Term	Count	%	PValue
GO:0008285~negative regulation of cell prolif	22	1.97%	0.021171
GO:0042127~regulation of cell proliferation	37	3.31%	0.101975
GO:0008283~cell proliferation	45	4.03%	0.390141

Median: 0.07380752782690993 Geo: 0.09919375989807463

Term	Count	%	PValue
GO:0006536~glutamate metabolic process	3	0.27%	0.072716
rno00251:Glutamate metabolism	5	0.45%	0.073808
GO:0009064~glutamine family amino acid me	5	0.45%	0.181854

Median: 0.15290711979150115 Geo: 0.10087618409325069

Term	Count	%	PValue
repressor	12	1.07%	0.02792
nucleus	91	8.14%	0.033644
Transcription regulation	35	3.13%	0.152907
Transcription	35	3.13%	0.176114
dna-binding	34	3.04%	0.412953

Median: 0.1309296131274359 Geo: 0.10616709332351958

Term	Count	%	PValue
domain:BAR	3	0.27%	0.057758
IPR004148:BAR	3	0.27%	0.13093
SM00721:BAR	3	0.27%	0.158241

Median: 0.10584057003619658 Geo: 0.10679216096906936

Term	Count	%	PValue
GO:0005100~Rho GTPase activator activity	4	0.36%	0.053969
GO:0005096~GTPase activator activity	12	1.07%	0.085486
GO:0043087~regulation of GTPase activity	7	0.63%	0.105841
gtpase activation	5	0.45%	0.141009

GO:0005099~Ras GTPase activator activity	6	0.54%	0.201724

Median: 0.10189181414834529 Geo: 0.10949812218825965

Term	Count	%	PValue
GO:0019725~cellular homeostasis	29	2.59%	0.014671
GO:0042592~homeostatic process	36	3.22%	0.02805
GO:0006875~cellular metal ion homeostasis	14	1.25%	0.088302
GO:0055065~metal ion homeostasis	14	1.25%	0.088302
GO:0006873~cellular ion homeostasis	20	1.79%	0.091552
GO:0055082~cellular chemical homeostasis	20	1.79%	0.091552
GO:0006874~cellular calcium ion homeostasi	13	1.16%	0.093013
GO:0055074~calcium ion homeostasis	13	1.16%	0.093013
GO:0065008~regulation of biological quality	59	5.28%	0.101892
GO:0050801~ion homeostasis	21	1.88%	0.117543
GO:0030003~cellular cation homeostasis	17	1.52%	0.128115
GO:0055080~cation homeostasis	17	1.52%	0.128115
GO:0048878~chemical homeostasis	22	1.97%	0.204232
GO:0030005~cellular di-, tri-valent inorganic	14	1.25%	0.219321
GO:0055066~di-, tri-valent inorganic cation h	14	1.25%	0.219321
GO:0007204~elevation of cytosolic calcium i	7	0.63%	0.307615
GO:0051480~cytosolic calcium ion homeosta	7	0.63%	0.338314

Median: 0.10842151729013733 Geo: 0.11186370049581089

Term	Count	%	PValue
GO:0032012~regulation of ARF protein signal	3	0.27%	0.108422
GO:0032011~ARF protein signal transduction	3	0.27%	0.108422
GO:0005086~ARF guanyl-nucleotide exchang	3	0.27%	0.119079

Median: 0.1076855020720717 Geo: 0.11547631425780384

Term	Count	%	PValue
rno00510:N-Glycan biosynthesis	8	0.72%	0.013869
GO:0009100~glycoprotein metabolic process	13	1.16%	0.054018
rno01030:Glycan structures - biosynthesis 1	12	1.07%	0.088684
GO:0016757~transferase activity, transferrin	17	1.52%	0.098527
GO:0006486~protein amino acid glycosylatio	10	0.89%	0.107686
GO:0043413~biopolymer glycosylation	10	0.89%	0.118084
GO:0009101~glycoprotein biosynthetic proce	10	0.89%	0.152395
GO:0016758~transferase activity, transferrin	10	0.89%	0.369148
glycosyltransferase	7	0.63%	0.779679

Median: 0.1258641009200506 Geo: 0.11806714660258627

Term	Count	%	PValue
GO:0030424~axon	10	0.89%	0.076941
GO:0043005~neuron projection	18	1.61%	0.125864
GO:0043025~cell soma	10	0.89%	0.169952

Median: 0.1677959048829996 Geo: 0.11965887011097136

Term	Count	%	PValue

GO:0007010~cytoskeleton organization and b	37	3.31%	0.029817
GO:0007015~actin filament organization	7	0.63%	0.092817
GO:0030036~actin cytoskeleton organization	14	1.25%	0.242775
GO:0030029~actin filament-based process	14	1.25%	0.305131

Median: 0.18185380918816363 Geo: 0.12058492068067901

Term	Count	%	PValue
GO:0008652~amino acid biosynthetic process	7	0.63%	0.045807
GO:0009064~glutamine family amino acid me	5	0.45%	0.181854
GO:0009084~glutamine family amino acid bio	3	0.27%	0.210485

Median: 0.13346020508450196 Geo: 0.1210625157076649

Term	Count	%	PValue
GO:0051246~regulation of protein metabolic	22	1.97%	0.040026
GO:0022618~protein-RNA complex assembly	10	0.89%	0.053362
GO:0009889~regulation of biosynthetic proce	16	1.43%	0.060281
GO:0006413~translational initiation	7	0.63%	0.092817
GO:0008135~translation factor activity, nucle	9	0.81%	0.104059
GO:0003743~translation initiation factor activ	6	0.54%	0.129377
GO:0006446~regulation of translational initia	5	0.45%	0.137543
GO:0022613~ribonucleoprotein complex biog	12	1.07%	0.150133
GO:0045182~translation regulator activity	9	0.81%	0.175896
GO:0031326~regulation of cellular biosynthet	12	1.07%	0.207834
initiation factor	4	0.36%	0.277076
GO:0006417~regulation of translation	10	0.89%	0.294521

Median: 0.1803019793844538 Geo: 0.12215092015596596

Term	Count	%	PValue
GO:0051301~cell division	16	1.43%	0.002944
GO:0000278~mitotic cell cycle	23	2.06%	0.017947
GO:0022403~cell cycle phase	22	1.97%	0.080816
cell cycle	15	1.34%	0.121315
cell division	9	0.81%	0.125236
GO:0051329~interphase of mitotic cell cycle	8	0.72%	0.172594
GO:0051325~interphase	8	0.72%	0.180302
GO:0051318~G1 phase	3	0.27%	0.210485
GO:0000279~M phase	15	1.34%	0.249235
GO:0007067~mitosis	11	0.98%	0.302128
mitosis	5	0.45%	0.302678
GO:0000087~M phase of mitotic cell cycle	11	0.98%	0.332362
GO:0000082~G1/S transition of mitotic cell cy	4	0.36%	0.418699

Median: 0.11267688765907659 Geo: 0.1268010744333647

Term	Count	%	PValue
GO:0035258~steroid hormone receptor bindi	5	0.45%	0.025487
GO:0030518~steroid hormone receptor signa	6	0.54%	0.047282
GO:0050681~androgen receptor binding	4	0.36%	0.053969
GO:0003713~transcription coactivator activity	14	1.25%	0.060449

GO:0030522~intracellular receptor-mediated	6	0.54%	0.097158
GO:0030521~androgen receptor signaling pa	4	0.36%	0.128196
GO:0035257~nuclear hormone receptor bindi	6	0.54%	0.211598
GO:0051427~hormone receptor binding	6	0.54%	0.242086
GO:0046966~thyroid hormone receptor bindi	3	0.27%	0.610061
GO:0045944~positive regulation of transcript	10	0.89%	0.702208

Median: 0.10065090511468879 Geo: 0.1276364001100667

Term	Count	%	PValue
pyridoxal phosphate	7	0.63%	0.047012
GO:0008483~transaminase activity	5	0.45%	0.051374
aminotransferase	4	0.36%	0.076229
GO:0016769~transferase activity, transferrin	5	0.45%	0.095855
IPR015421:Pyridoxal phosphate-dependent tr	5	0.45%	0.100651
GO:0019842~vitamin binding	10	0.89%	0.155451
GO:0030170~pyridoxal phosphate binding	5	0.45%	0.256409
binding site:Pyridoxal phosphate (covalent)	4	0.36%	0.258983
GO:0048037~cofactor binding	14	1.25%	0.490306

Median: 0.09004221777709542 Geo: 0.13237772337733444

Term	Count	%	PValue
GO:0048583~regulation of response to stimul	9	0.81%	0.01677
GO:0032107~regulation of response to nutrie	3	0.27%	0.072716
GO:0032104~regulation of response to extrac	3	0.27%	0.072716
GO:0032095~regulation of response to food	3	0.27%	0.072716
GO:0032101~regulation of response to exter	3	0.27%	0.090042
GO:0032094~response to food	3	0.27%	0.127677
GO:0031667~response to nutrient levels	8	0.72%	0.507172
GO:0009991~response to extracellular stimul	8	0.72%	0.552089
GO:0007584~response to nutrient	6	0.54%	0.601449

Median: 0.24146442504751328 Geo: 0.1327707699357756

Term	Count	%	PValue
GO:0032502~developmental process	184	16.46%	0.015368
GO:0048869~cellular developmental process	110	9.84%	0.021203
GO:0030154~cell differentiation	110	9.84%	0.021203
GO:0007275~multicellular organismal develo	131	11.72%	0.100626
GO:0048856~anatomical structure developm	118	10.55%	0.382303
GO:0048731~system development	101	9.03%	0.421206
GO:0048513~organ development	65	5.81%	0.862571
GO:0032501~multicellular organismal proces	185	16.55%	0.999998

Median: 0.17519858930582505 Geo: 0.1329722840960057

Term	Count	%	PValue
GO:0006626~protein targeting to mitochondr	5	0.45%	0.017079
GO:0006839~mitochondrial transport	6	0.54%	0.082855
GO:0007005~mitochondrion organization and	7	0.63%	0.267542
GO:0044455~mitochondrial membrane part	3	0.27%	0.825805

Median: 0.10305094387637022 Geo: 0.1330202062600308

Term	Count	%	PValue
GO:0001937~negative regulation of endothel	3	0.27%	0.090042
GO:0001935~endothelial cell proliferation	4	0.36%	0.103051
GO:0001936~regulation of endothelial cell pr	3	0.27%	0.253662

Median: 0.11990710670990666 Geo: 0.13685778237651414

Term	Count	%	PValue
GO:0007187~G-protein signaling, coupled to	14	1.25%	0.031366
GO:0019935~cyclic-nucleotide-mediated sign	14	1.25%	0.065869
GO:0007188~G-protein signaling, coupled to	11	0.98%	0.066354
GO:0045761~regulation of adenylate cyclase	6	0.54%	0.097158
GO:0051339~regulation of lyase activity	6	0.54%	0.11262
GO:0031279~regulation of cyclase activity	6	0.54%	0.11262
GO:0019933~cAMP-mediated signaling	11	0.98%	0.127194
GO:0007190~adenylate cyclase activation	4	0.36%	0.213759
GO:0051349~positive regulation of lyase acti	4	0.36%	0.244569
GO:0045762~positive regulation of adenylate	4	0.36%	0.244569
GO:0031281~positive regulation of cyclase ac	4	0.36%	0.260231
GO:0007189~G-protein signaling, adenylate	4	0.36%	0.603889

Median: 0.0908459699550602 Geo: 0.13704169444018185

Term	Count	%	PValue
IPR003958:Transcription factor CBF/NF-Y/arch	3	0.27%	0.035936
IPR009072:Histone-fold	4	0.36%	0.090846
Transcription	3	0.27%	0.788366

Median: 0.13734646667265776 Geo: 0.14002507969953631

Term	Count	%	PValue
GO:0005798~Golgi-associated vesicle	8	0.72%	0.034523
GO:0012506~vesicle membrane	11	0.98%	0.037788
IPR008152:Clathrin adaptor, alpha/beta/gam	3	0.27%	0.051649
SM00809:Alpha_adaptinC2	3	0.27%	0.053424
GO:0030659~cytoplasmic vesicle membrane	8	0.72%	0.092881
GO:0030133~transport vesicle	6	0.54%	0.095371
GO:0044433~cytoplasmic vesicle part	9	0.81%	0.109754
GO:0048475~coated membrane	6	0.54%	0.134454
GO:0030117~membrane coat	6	0.54%	0.134454
GO:0030118~clathrin coat	5	0.45%	0.137346
GO:0030140~trans-Golgi network transport v	4	0.36%	0.159338
GO:0030130~clathrin coat of trans-Golgi netw	3	0.27%	0.201342
GO:0030120~vesicle coat	5	0.45%	0.239078
GO:0012510~trans-Golgi network transport v	3	0.27%	0.243116
GO:0030125~clathrin vesicle coat	4	0.36%	0.276901
GO:0030662~coated vesicle membrane	5	0.45%	0.288866
GO:0030665~clathrin coated vesicle membra	4	0.36%	0.307779
GO:0030658~transport vesicle membrane	3	0.27%	0.368185

GO:0030660~Golgi-associated vesicle membr	3	0.27%	0.408313

Median: 0.1361326064824238 Geo: 0.1440097981822845

Term	Count	%	PValue
GO:0002761~regulation of myeloid leukocyte	6	0.54%	0.008587
GO:0002762~negative regulation of myeloid l	4	0.36%	0.016525
GO:0045637~regulation of myeloid cell differe	7	0.63%	0.024981
GO:0002573~myeloid leukocyte differentiatio	6	0.54%	0.063669
GO:0045638~negative regulation of myeloid c	4	0.36%	0.069637
GO:0045670~regulation of osteoclast differer	4	0.36%	0.069637
GO:0030316~osteoclast differentiation	4	0.36%	0.091299
GO:0048534~hemopoietic or lymphoid organ	17	1.52%	0.093025
GO:0030097~hemopoiesis	16	1.43%	0.098623
GO:0002520~immune system development	17	1.52%	0.116874
GO:0051093~negative regulation of developr	9	0.81%	0.136133
GO:0030099~myeloid cell differentiation	9	0.81%	0.155467
GO:0045639~positive regulation of myeloid c	3	0.27%	0.253662
GO:0050793~regulation of developmental pro	20	1.79%	0.270145
GO:0051094~positive regulation of developm	8	0.72%	0.319107
GO:0045596~negative regulation of cell differ	6	0.54%	0.33732
GO:0002521~leukocyte differentiation	8	0.72%	0.385125
GO:0045595~regulation of cell differentiation	12	1.07%	0.477352
GO:0045597~positive regulation of cell differe	4	0.36%	0.754627
GO:0045165~cell fate commitment	3	0.27%	0.955029
GO:0002376~immune system process	33	2.95%	0.956468

Median: 0.3508793236375377 Geo: 0.14658367233857106

Term	Count	%	PValue
GO:0048489~synaptic vesicle transport	9	0.81%	0.004764
GO:0001505~regulation of neurotransmitter l	13	1.16%	0.089241
GO:0016079~synaptic vesicle exocytosis	4	0.36%	0.16939
GO:0003001~generation of a signal involved	10	0.89%	0.350879
GO:0045055~regulated secretory pathway	8	0.72%	0.356681
GO:0007269~neurotransmitter secretion	7	0.63%	0.390062
GO:0006887~exocytosis	8	0.72%	0.413622

Median: 0.43415643114745134 Geo: 0.14675904481537738

Term	Count	%	PValue
GO:0048583~regulation of response to stimul	9	0.81%	0.01677
GO:0031347~regulation of defense response	4	0.36%	0.434156
GO:0050727~regulation of inflammatory resp	4	0.36%	0.434156

Median: 0.24998858310372712 Geo: 0.15290988756460436

Term	Count	%	PValue
wd repeat	13	1.16%	0.025128
IPR001680:WD40 repeat	13	1.16%	0.035564
SM00320:WD40	13	1.16%	0.053411
repeat:WD 6	5	0.45%	0.170135

repeat:WD 5	5	0.45%	0.242372
repeat:WD 4	5	0.45%	0.257606
repeat:WD 3	5	0.45%	0.288595
repeat:WD 2	5	0.45%	0.304286
repeat:WD 1	5	0.45%	0.304286
repeat:WD 7	3	0.27%	0.5158

Median: 0.15565765283845925 Geo: 0.1529854602605251

Term	Count	%	PValue
GO:0051186~cofactor metabolic process	20	1.79%	0.055485
GO:0006732~coenzyme metabolic process	17	1.52%	0.067256
GO:0051188~cofactor biosynthetic process	9	0.81%	0.244059
GO:0009108~coenzyme biosynthetic process	6	0.54%	0.601449

Median: 0.15899314901573366 Geo: 0.15637827340600607

Term	Count	%	PValue
GO:0000302~response to reactive oxygen sp	6	0.54%	0.069757
GO:0009725~response to hormone stimulus	15	1.34%	0.083759
GO:0043627~response to estrogen stimulus	6	0.54%	0.146779
GO:0006979~response to oxidative stress	10	0.89%	0.171207
GO:0042542~response to hydrogen peroxide	4	0.36%	0.183882
GO:0048545~response to steroid hormone sti	7	0.63%	0.541646

Median: 0.3508793236375377 Geo: 0.1679204348599385

Term	Count	%	PValue
GO:0065009~regulation of a molecular functi	40	3.58%	0.01017
GO:0050790~regulation of catalytic activity	36	3.22%	0.012368
GO:0043085~positive regulation of catalytic a	22	1.97%	0.029565
GO:0043549~regulation of kinase activity	17	1.52%	0.156675
GO:0051338~regulation of transferase activit	17	1.52%	0.188353
GO:0045859~regulation of protein kinase acti	16	1.43%	0.201339
GO:0033674~positive regulation of kinase act	10	0.89%	0.350879
GO:0051347~positive regulation of transferas	10	0.89%	0.392012
GO:0007200~G-protein signaling, coupled to	7	0.63%	0.400431
GO:0032147~activation of protein kinase acti	5	0.45%	0.438703
GO:0045860~positive regulation of protein ki	9	0.81%	0.459439
GO:0007205~protein kinase C activation	3	0.27%	0.553633
GO:0000165~MAPKKK cascade	10	0.89%	0.621474

Median: 0.200554335921077 Geo: 0.16822064139055293

Term	Count	%	PValue
PIRSF001741:membrane-associated guanylat	3	0.27%	0.023567
SM00072:GuKc	5	0.45%	0.026247
GO:0008022~protein C-terminus binding	8	0.72%	0.029859
domain:Guanylate kinase-like	3	0.27%	0.057758
domain:SH3	7	0.63%	0.075448
IPR008145:Guanylate kinase/L-type calcium c	4	0.36%	0.07839
domain:PDZ 3	3	0.27%	0.121188

GO:0030165~PDZ domain binding	6	0.54%	0.17311
IPR008144:Guanylate kinase	3	0.27%	0.200554
domain:PDZ 1	3	0.27%	0.29823
domain:PDZ 2	3	0.27%	0.29823
IPR000108:Neutrophil cytosol factor 2	3	0.27%	0.345817
IPR001452:Src homology-3	9	0.81%	0.397693
SM00326:SH3	9	0.81%	0.46892
SH3 domain	8	0.72%	0.47937
IPR001478:PDZ/DHR/GLGF	3	0.27%	0.971386
SM00228:PDZ	3	0.27%	0.975655

Median: 0.10305094387637022 Geo: 0.1746413970914796

Term	Count	%	PValue
GO:0010003~gastrulation (sensu Mammalia)	4	0.36%	0.042285
GO:0001702~gastrulation with mouth forming	4	0.36%	0.103051
GO:0048276~gastrulation (sensu Vertebrata)	4	0.36%	0.103051
GO:0007369~gastrulation	4	0.36%	0.479537
GO:0003002~regionalization	6	0.54%	0.754437

Median: 0.146778845974888 Geo: 0.175730085063464

Term	Count	%	PValue
GO:0014070~response to organic cyclic subst	6	0.54%	0.076153
GO:0043627~response to estrogen stimulus	6	0.54%	0.146779
GO:0042493~response to drug	9	0.81%	0.485498

Median: 0.2310913261201935 Geo: 0.17766634724831248

Term	Count	%	PValue
GO:0008270~zinc ion binding	90	8.05%	0.027333
zinc-finger	34	3.04%	0.155905
zinc	45	4.03%	0.306277
metal-binding	60	5.37%	0.763395

Median: 0.21535379537979749 Geo: 0.17768583122794948

Term	Count	%	PValue
GO:0016323~basolateral plasma membrane	13	1.16%	0.010827
GO:0005912~adherens junction	9	0.81%	0.055736
GO:0005925~focal adhesion	5	0.45%	0.158264
GO:0005924~cell-substrate adherens junction	5	0.45%	0.191629
GO:0030055~cell-matrix junction	5	0.45%	0.239078
GO:0005913~cell-cell adherens junction	3	0.27%	0.447158
GO:0030054~cell junction	11	0.98%	0.58202
GO:0005911~intercellular junction	6	0.54%	0.872536

Median: 0.15546695149387 Geo: 0.17829203345072625

Term	Count	%	PValue
GO:0005184~neuropeptide hormone activity	5	0.45%	0.057794
GO:0007218~neuropeptide signaling pathway	9	0.81%	0.155467
GO:0005179~hormone activity	8	0.72%	0.630778

Median: 0.1719070097875019 Geo: 0.17861075696769138

Term	Count	%	PValue
serine/threonine-specific protein kinase	6	0.54%	0.054413
PIRSF000564:kinase-related transforming prot	4	0.36%	0.171907
rno04340:Hedgehog signaling pathway	4	0.36%	0.609158

Median: 0.48112562038876727 Geo: 0.1787057436525346

Term	Count	%	PValue
GO:0044456~synapse part	19	1.70%	2.22E-04
GO:0045202~synapse	27	2.42%	3.62E-04
GO:0045211~postsynaptic membrane	12	1.07%	0.018502
GO:0008144~drug binding	4	0.36%	0.240467
synapse	13	1.16%	0.283011
Postsynaptic cell membrane	8	0.72%	0.384888
GO:0030534~adult behavior	4	0.36%	0.403104
neurotransmitter receptor	5	0.45%	0.462802
GO:0005230~extracellular ligand-gated ion ch	5	0.45%	0.481126
GO:0030594~neurotransmitter receptor activ	7	0.63%	0.565097
cell junction	14	1.25%	0.609355
GO:0042165~neurotransmitter binding	7	0.63%	0.642168
IPR006202:Neurotransmitter-gated ion-chann	3	0.27%	0.748186
IPR006029:Neurotransmitter-gated ion-chann	3	0.27%	0.748186
IPR006201:Neurotransmitter-gated ion-chann	3	0.27%	0.748186
GO:0015276~ligand-gated ion channel activit	5	0.45%	0.772342
GO:0022834~ligand-gated channel activity	5	0.45%	0.772342

Median: 0.1803019793844538 Geo: 0.18582633481789906

Term	Count	%	PValue
GO:0007270~nerve-nerve synaptic transmiss	6	0.54%	0.097158
GO:0007612~learning	5	0.45%	0.107637
GO:0048169~regulation of long-term neurona	3	0.27%	0.147649
GO:0007611~learning and/or memory	8	0.72%	0.180302
GO:0048167~regulation of synaptic plasticity	6	0.54%	0.194764
GO:0050803~regulation of synapse structure	6	0.54%	0.247342
GO:0048168~regulation of neuronal synaptic	3	0.27%	0.57052

Median: 0.21008051367698122 Geo: 0.18658182674770896

Term	Count	%	PValue
GO:0006605~protein targeting	20	1.79%	0.046078
GO:0017038~protein import	9	0.81%	0.142436
GO:0006913~nucleocytoplasmic transport	11	0.98%	0.184392
GO:0051169~nuclear transport	11	0.98%	0.210081
GO:0006606~protein import into nucleus	7	0.63%	0.267542
GO:0051170~nuclear import	7	0.63%	0.287429
GO:0000060~protein import into nucleus, tra	3	0.27%	0.402649

Median: 0.19868478281630433 Geo: 0.1885086380593916

Term	Count	%	PValue
GO:0006665~sphingolipid metabolic process	6	0.54%	0.137856
GO:0006672~ceramide metabolic process	4	0.36%	0.198685
GO:0046519~sphingoid metabolic process	4	0.36%	0.244569

Median: 0.22585340278900806 Geo: 0.18852812202274055

Term	Count	%	PValue
GO:0015833~peptide transport	8	0.72%	0.039498
GO:0046883~regulation of hormone secretio	5	0.45%	0.089544
GO:0002790~peptide secretion	5	0.45%	0.107637
GO:0046888~negative regulation of hormone	3	0.27%	0.189177
GO:0030073~insulin secretion	4	0.36%	0.198685
GO:0046879~hormone secretion	6	0.54%	0.225853
GO:0050796~regulation of insulin secretion	3	0.27%	0.232012
GO:0030072~peptide hormone secretion	4	0.36%	0.260231
GO:0003001~generation of a signal involved	10	0.89%	0.350879
GO:0051046~regulation of secretion	7	0.63%	0.369321
GO:0051048~negative regulation of secretio	3	0.27%	0.422933

Median: 0.20076639204212415 Geo: 0.19510207483180358

Term	Count	%	PValue
IPR001841:Zinc finger, RING-type	11	0.98%	0.152621
SM00184:RING	11	0.98%	0.200766
zinc finger region:RING-type	5	0.45%	0.242372

Median: 0.17259375798038148 Geo: 0.19665995517085125

Term	Count	%	PValue
GO:0040011~locomotion	9	0.81%	0.096192
GO:0030334~regulation of cell migration	7	0.63%	0.1582
GO:0040013~negative regulation of locomoti	4	0.36%	0.16939
GO:0040012~regulation of locomotion	8	0.72%	0.172594
GO:0051270~regulation of cell motility	7	0.63%	0.238419
GO:0030336~negative regulation of cell migr	3	0.27%	0.297004
GO:0051271~negative regulation of cell motil	3	0.27%	0.361117

Median: 0.1927075177175326 Geo: 0.19770529455139862

Term	Count	%	PValue
GO:0009056~catabolic process	46	4.11%	0.060783
GO:0044248~cellular catabolic process	39	3.49%	0.068095
GO:0030163~protein catabolic process	16	1.43%	0.12049
GO:0006511~ubiquitin-dependent protein cat	12	1.07%	0.134647
GO:0043632~modification-dependent macro	12	1.07%	0.144872
GO:0019941~modification-dependent protein	12	1.07%	0.144872
GO:0051603~proteolysis involved in cellular	12	1.07%	0.166495
GO:0044257~cellular protein catabolic proces	12	1.07%	0.183691
GO:0004843~ubiquitin-specific protease activ	6	0.54%	0.201724
GO:0019783~small conjugating protein-speci	6	0.54%	0.211598
GO:0016790~thiolester hydrolase activity	7	0.63%	0.228439

GO:0004221~ubiquitin thiolesterase activity	5	0.45%	0.318674
GO:0043285~biopolymer catabolic process	16	1.43%	0.421516
GO:0044265~cellular macromolecule cataboli	19	1.70%	0.425693
GO:0009057~macromolecule catabolic proces	23	2.06%	0.437564
GO:0008234~cysteine-type peptidase activity	10	0.89%	0.518148

Median: 0.3402131629373112 Geo: 0.20091348973280643

Term	Count	%	PValue
GO:0009058~biosynthetic process	98	8.77%	0.01976
GO:0044249~cellular biosynthetic process	67	5.99%	0.249013
GO:0009059~macromolecule biosynthetic pro	50	4.47%	0.431413
GO:0006412~translation	31	2.77%	0.767586

Median: 0.15219034199850132 Geo: 0.20388043471441814

Term	Count	%	PValue
GO:0009892~negative regulation of metaboli	28	2.50%	0.082998
GO:0000122~negative regulation of transcrip	12	1.07%	0.106427
GO:0016481~negative regulation of transcrip	20	1.79%	0.108749
GO:0045892~negative regulation of transcrip	15	1.34%	0.145618
GO:0031324~negative regulation of cellular r	24	2.15%	0.15219
GO:0045934~negative regulation of nucleoba	20	1.79%	0.171513
GO:0016564~transcription repressor activity	14	1.25%	0.250078
GO:0006357~regulation of transcription from	23	2.06%	0.714292
GO:0006366~transcription from RNA polymer	25	2.24%	0.933218

Median: 0.20425774245182154 Geo: 0.2051856545880777

Term	Count	%	PValue
GO:0043549~regulation of kinase activity	17	1.52%	0.156675
GO:0051338~regulation of transferase activit	17	1.52%	0.188353
GO:0045859~regulation of protein kinase acti	16	1.43%	0.201339
GO:0043086~negative regulation of catalytic	8	0.72%	0.204258
GO:0006469~negative regulation of protein k	6	0.54%	0.225853
GO:0033673~negative regulation of kinase ac	6	0.54%	0.225853
GO:0051348~negative regulation of transfera	6	0.54%	0.247342

Median: 0.24894442110152143 Geo: 0.21358808151445924

Term	Count	%	PValue
IPR013753:Ras	9	0.81%	0.152954
IPR003578:Ras small GTPase, Rho type	3	0.27%	0.248944
SM00174:RHO	3	0.27%	0.255899

Median: 0.23201158734523689 Geo: 0.21679040728369364

Term	Count	%	PValue
GO:0006665~sphingolipid metabolic process	6	0.54%	0.137856
GO:0006687~glycosphingolipid metabolic pro	3	0.27%	0.232012
GO:0006664~glycolipid metabolic process	3	0.27%	0.318554

Median: 0.2103440663828989 Geo: 0.21685062964976048

Term	Count	%	PValue
GO:0050804~regulation of synaptic transmiss	6	0.54%	0.204959
GO:0031644~regulation of neurological proce	7	0.63%	0.210344
GO:0051969~regulation of transmission of ne	6	0.54%	0.236529

Median: 0.23477854425515898 Geo: 0.22626350310823068

Term	Count	%	PValue
GO:0016477~cell migration	21	1.88%	0.210149
GO:0051674~localization of cell	27	2.42%	0.234779
GO:0006928~cell motility	27	2.42%	0.234779

Median: 0.213759410366611 Geo: 0.22973313871178894

Term	Count	%	PValue
GO:0006099~tricarboxylic acid cycle	4	0.36%	0.155251
GO:0046356~acetyl-CoA catabolic process	4	0.36%	0.16939
GO:0006084~acetyl-CoA metabolic process	5	0.45%	0.193598
GO:0009109~coenzyme catabolic process	4	0.36%	0.213759
GO:0009060~aerobic respiration	4	0.36%	0.260231
GO:0051187~cofactor catabolic process	4	0.36%	0.307828
GO:0045333~cellular respiration	4	0.36%	0.387391

Median: 0.44053360278966125 Geo: 0.22979315384796073

Term	Count	%	PValue
GO:0060090~molecular adaptor activity	6	0.54%	0.04997
GO:0005070~SH3/SH2 adaptor activity	3	0.27%	0.440534
GO:0030674~protein binding, bridging	5	0.45%	0.551213

Median: 0.3185542039557815 Geo: 0.2348694799133672

Term	Count	%	PValue
GO:0045428~regulation of nitric oxide biosyn	3	0.27%	0.127677
GO:0006809~nitric oxide biosynthetic process	3	0.27%	0.318554
GO:0046209~nitric oxide metabolic process	3	0.27%	0.318554

Median: 0.2640537134097305 Geo: 0.24588531886167345

Term	Count	%	PValue
GO:0016868~intramolecular transferase activ	3	0.27%	0.100971
GO:0016866~intramolecular transferase activ	4	0.36%	0.182498
GO:0016853~isomerase activity	9	0.81%	0.345609
Carbohydrate transport and metabolism	7	0.63%	0.573973

Median: 0.21316646918908094 Geo: 0.24597617148673978

Term	Count	%	PValue
GO:0004468~lysine N-acetyltransferase activ	3	0.27%	0.137908
GO:0004402~histone acetyltransferase activi	3	0.27%	0.137908
GO:0016746~transferase activity, transferrin	12	1.07%	0.162026
GO:0008415~acyltransferase activity	11	0.98%	0.206846
GO:0016747~transferase activity, transferrin	11	0.98%	0.213166
GO:0016410~N-acyltransferase activity	5	0.45%	0.244245

GO:0008080~N-acetyltransferase activity	4	0.36%	0.362031
acyltransferase	6	0.54%	0.457428
GO:0016407~acetyltransferase activity	4	0.36%	0.599807

Median: 0.3846404082940681 Geo: 0.24846768359367194

Term	Count	%	PValue
GO:0006643~membrane lipid metabolic proc	14	1.25%	0.099218
GO:0044255~cellular lipid metabolic process	33	2.95%	0.38464
GO:0006629~lipid metabolic process	39	3.49%	0.401942

Median: 0.34773517538872534 Geo: 0.24956754803083364

Term	Count	%	PValue
rno04662:B cell receptor signaling pathway	9	0.81%	0.050096
rno04360:Axon guidance	11	0.98%	0.220624
rno04650:Natural killer cell mediated cytotoxi	9	0.81%	0.288715
rno04210:Apoptosis	7	0.63%	0.406755
rno04660:T cell receptor signaling pathway	8	0.72%	0.42779
rno04370:VEGF signaling pathway	6	0.54%	0.435149

Median: 0.32482771592771276 Geo: 0.24979656724149604

Term	Count	%	PValue
GO:0035258~steroid hormone receptor bindi	5	0.45%	0.025487
GO:0003713~transcription coactivator activit	14	1.25%	0.060449
GO:0048518~positive regulation of biological	70	6.26%	0.121497
activator	14	1.25%	0.123257
GO:0008134~transcription factor binding	26	2.33%	0.124756
GO:0003712~transcription cofactor activity	19	1.70%	0.14302
GO:0009893~positive regulation of metabolic	28	2.50%	0.201809
GO:0016563~transcription activator activity	19	1.70%	0.273589
GO:0031325~positive regulation of cellular m	24	2.15%	0.376066
GO:0048522~positive regulation of cellular pr	58	5.19%	0.380492
GO:0045935~positive regulation of nucleobas	19	1.70%	0.487533
GO:0045893~positive regulation of transcript	15	1.34%	0.509516
GO:0045941~positive regulation of transcript	17	1.52%	0.607714
GO:0045944~positive regulation of transcript	10	0.89%	0.702208
GO:0006357~regulation of transcription from	23	2.06%	0.714292
GO:0006366~transcription from RNA polymer	25	2.24%	0.933218

Median: 0.261572969683048 Geo: 0.2505067926553862

Term	Count	%	PValue
GO:0005778~peroxisomal membrane	4	0.36%	0.187301
GO:0031903~microbody membrane	4	0.36%	0.187301
GO:0044439~peroxisomal part	4	0.36%	0.261573
GO:0044438~microbody part	4	0.36%	0.261573
GO:0005777~peroxisome	7	0.63%	0.28454
GO:0042579~microbody	7	0.63%	0.28454
GO:0007031~peroxisome organization and bi	3	0.27%	0.318554

Median: 0.18151085579993848 Geo: 0.25534676871162876

Term	Count	%	PValue
GO:0015630~microtubule cytoskeleton	22	1.97%	0.125925
GO:0007017~microtubule-based process	16	1.43%	0.181511
GO:0005874~microtubule	8	0.72%	0.728409

Median: 0.36267773691844213 Geo: 0.25565972459880804

Term	Count	%	PValue
GO:0006643~membrane lipid metabolic proc	14	1.25%	0.099218
GO:0006644~phospholipid metabolic process	9	0.81%	0.362678
GO:0006650~glycerophospholipid metabolic	5	0.45%	0.464381

Median: 0.25291158153882726 Geo: 0.2570069622144935

Term	Count	%	PValue
GO:0001565~phorbol ester receptor activity	3	0.27%	0.137908
IPR002219:Protein kinase C, phorbol ester/dia	5	0.45%	0.237707
zinc finger region:Phorbol-ester/DAG-type	3	0.27%	0.246277
Phorbol-ester binding	4	0.36%	0.259546
SM00109:C1	5	0.45%	0.277455
GO:0019992~diacylglycerol binding	3	0.27%	0.495685

Median: 0.2646648643314025 Geo: 0.257178985179388

Term	Count	%	PValue
GO:0031981~nuclear lumen	31	2.77%	0.137206
GO:0043233~organelle lumen	38	3.40%	0.201213
GO:0031974~membrane-enclosed lumen	38	3.40%	0.201213
GO:0044428~nuclear part	45	4.03%	0.264665
GO:0005667~transcription factor complex	13	1.16%	0.312198
GO:0005654~nucleoplasm	22	1.97%	0.320442
GO:0044451~nucleoplasm part	17	1.52%	0.505927

Median: 0.23201158734523689 Geo: 0.2583443959260503

Term	Count	%	PValue
GO:0006903~vesicle targeting	3	0.27%	0.147649
GO:0051650~establishment of vesicle localiz	3	0.27%	0.210485
GO:0051648~vesicle localization	3	0.27%	0.232012
GO:0051640~organelle localization	4	0.36%	0.307828
GO:0051656~establishment of organelle loca	3	0.27%	0.518472

Median: 0.25368116831589566 Geo: 0.25999331869230846

Term	Count	%	PValue
GO:0042745~circadian sleep/wake cycle	3	0.27%	0.189177
GO:0048512~circadian behavior	3	0.27%	0.210485
GO:0030431~sleep	3	0.27%	0.232012
GO:0007622~rhythmic behavior	3	0.27%	0.275351
GO:0048511~rhythmic process	9	0.81%	0.276768
GO:0007623~circadian rhythm	5	0.45%	0.438703

Median: 0.43323106073215817 Geo: 0.26210156016547564

Term	Count	%	PValue
GO:0030031~cell projection biogenesis	8	0.72%	0.018509
GO:0048699~generation of neurons	27	2.42%	0.093349
GO:0022008~neurogenesis	29	2.59%	0.105274
GO:0048858~cell projection morphogenesis	20	1.79%	0.129073
GO:0030030~cell projection organization and	20	1.79%	0.129073
GO:0032990~cell part morphogenesis	20	1.79%	0.129073
GO:0030182~neuron differentiation	20	1.79%	0.370018
GO:0048666~neuron development	15	1.34%	0.405516
GO:0031175~neurite development	13	1.16%	0.460946
GO:0000902~cell morphogenesis	28	2.50%	0.512472
GO:0032989~cellular structure morphogenes	28	2.50%	0.512472
GO:0000904~cellular morphogenesis during c	12	1.07%	0.520972
GO:0048812~neurite morphogenesis	11	0.98%	0.525559
GO:0048667~neuron morphogenesis during c	11	0.98%	0.525559
GO:0009653~anatomical structure morphoge	59	5.28%	0.618174
GO:0007409~axonogenesis	8	0.72%	0.784897

Median: 0.2920008222498741 Geo: 0.27413750077368854

Term	Count	%	PValue
GO:0033014~tetrapyrrole biosynthetic proces	3	0.27%	0.168192
GO:0006779~porphyrin biosynthetic process	3	0.27%	0.168192
GO:0051188~cofactor biosynthetic process	9	0.81%	0.244059
GO:0033013~tetrapyrrole metabolic process	3	0.27%	0.339943
GO:0006778~porphyrin metabolic process	3	0.27%	0.339943
GO:0046483~heterocycle metabolic process	7	0.63%	0.531976

Median: 0.2589829024123425 Geo: 0.2748545576081132

Term	Count	%	PValue
GO:0009310~amine catabolic process	7	0.63%	0.174917
GO:0044270~nitrogen compound catabolic pr	7	0.63%	0.192318
binding site:Pyridoxal phosphate (covalent)	4	0.36%	0.258983
GO:0009063~amino acid catabolic process	5	0.45%	0.38641
rno00252:Alanine and aspartate metabolism	3	0.27%	0.465956

Median: 0.315135754469714 Geo: 0.27852397661412764

Term	Count	%	PValue
GO:0005773~vacuole	13	1.16%	0.212609
GO:0005764~lysosome	11	0.98%	0.315136
GO:0000323~lytic vacuole	11	0.98%	0.322484

Median: 0.3837679797429484 Geo: 0.28680725809930663

Term	Count	%	PValue
GO:0001701~in utero embryonic developmer	8	0.72%	0.09846
GO:0009790~embryonic development	21	1.88%	0.308097
GO:0043009~chordate embryonic developme	9	0.81%	0.459439

GO:0009792~embryonic development ending	9	0.81%	0.485498

Median: 0.43870341527122014 Geo: 0.29161371042556156

Term	Count	%	PValue
GO:0051241~negative regulation of multicellu	9	0.81%	7.98E-04
GO:0008016~regulation of heart contraction	5	0.45%	0.281088
GO:0003015~heart process	5	0.45%	0.373214
GO:0060047~heart contraction	5	0.45%	0.373214
GO:0035150~regulation of tube size	5	0.45%	0.412681
GO:0050880~regulation of blood vessel size	5	0.45%	0.412681
GO:0003018~vascular process in circulatory	5	0.45%	0.438703
GO:0008217~regulation of blood pressure	6	0.54%	0.452147
GO:0042311~vasodilation	3	0.27%	0.553633
GO:0035295~tube development	11	0.98%	0.584276
GO:0035239~tube morphogenesis	8	0.72%	0.611771
GO:0008015~blood circulation	10	0.89%	0.726533
GO:0003013~circulatory system process	10	0.89%	0.726533

Median: 0.2779018162955732 Geo: 0.29279001064309174

Term	Count	%	PValue
GO:0043284~biopolymer biosynthetic proces	7	0.63%	0.134529
GO:0033692~cellular polysaccharide biosynth	4	0.36%	0.213759
GO:0000271~polysaccharide biosynthetic pro	4	0.36%	0.229067
GO:0009250~glucan biosynthetic process	3	0.27%	0.232012
GO:0005978~glycogen biosynthetic process	3	0.27%	0.232012
GO:0005977~glycogen metabolic process	4	0.36%	0.323792
GO:0006073~glucan metabolic process	4	0.36%	0.339757
GO:0044264~cellular polysaccharide metabol	5	0.45%	0.412681
GO:0005976~polysaccharide metabolic proce	5	0.45%	0.42573
GO:0016051~carbohydrate biosynthetic proc	6	0.54%	0.675549

Median: 0.2934854081935494 Geo: 0.2955976854979881

Term	Count	%	PValue
GO:0051093~negative regulation of develop	9	0.81%	0.136133
GO:0050771~negative regulation of axonoge	3	0.27%	0.147649
GO:0050767~regulation of neurogenesis	6	0.54%	0.225853
GO:0050768~negative regulation of neuroge	3	0.27%	0.361117
GO:0050770~regulation of axonogenesis	3	0.27%	0.518472
GO:0007409~axonogenesis	8	0.72%	0.784897

Median: 0.3419389271765082 Geo: 0.3125283750727572

Term	Count	%	PValue
isomerase	7	0.63%	0.237841
Rotamase	3	0.27%	0.29287
GO:0003755~peptidyl-prolyl cis-trans isomer	3	0.27%	0.341939
GO:0016853~isomerase activity	9	0.81%	0.345609
GO:0016859~cis-trans isomerase activity	3	0.27%	0.362203

Median: 0.3185542039557815 Geo: 0.3141499002215701

Term	Count	%	PValue
GO:0007043~intercellular junction assembly	3	0.27%	0.210485
GO:0045216~intercellular junction assembly	3	0.27%	0.318554
GO:0007028~cytoplasm organization and bio	3	0.27%	0.462387

Median: 0.4768385859093126 Geo: 0.31852749595736973

Term	Count	%	PValue
GO:0006767~water-soluble vitamin metabolic	9	0.81%	0.007896
GO:0006769~nicotinamide metabolic process	5	0.45%	0.089544
GO:0006766~vitamin metabolic process	9	0.81%	0.106836
GO:0019362~pyridine nucleotide metabolic p	5	0.45%	0.107637
GO:0044262~cellular carbohydrate metabolic	26	2.33%	0.11154
GO:0006098~pentose-phosphate shunt	3	0.27%	0.168192
GO:0006066~alcohol metabolic process	23	2.06%	0.243199
GO:0006739~NADP metabolic process	3	0.27%	0.253662
rno00010:Glycolysis / Gluconeogenesis	5	0.45%	0.360616
GO:0005975~carbohydrate metabolic process	30	2.68%	0.364572
glycolysis	4	0.36%	0.400613
GO:0016616~oxidoreductase activity, acting	7	0.63%	0.471222
GO:0006007~glucose catabolic process	7	0.63%	0.482455
GO:0006006~glucose metabolic process	10	0.89%	0.514797
GO:0046365~monosaccharide catabolic proce	7	0.63%	0.531976
GO:0019320~hexose catabolic process	7	0.63%	0.531976
GO:0046164~alcohol catabolic process	7	0.63%	0.56072
GO:0019318~hexose metabolic process	11	0.98%	0.659195
GO:0005996~monosaccharide metabolic proc	11	0.98%	0.67824
binding site:Substrate	6	0.54%	0.716583
GO:0050662~coenzyme binding	9	0.81%	0.750593
GO:0044275~cellular carbohydrate catabolic	7	0.63%	0.767266
GO:0016052~carbohydrate catabolic process	7	0.63%	0.813781
GO:0006096~glycolysis	4	0.36%	0.861085

Median: 0.32733578102708194 Geo: 0.32861072017313064

Term	Count	%	PValue
GO:0006821~chloride transport	6	0.54%	0.16533
GO:0031404~chloride ion binding	5	0.45%	0.185787
GO:0043168~anion binding	5	0.45%	0.197106
GO:0008509~anion transmembrane transpor	10	0.89%	0.276798
GO:0015698~inorganic anion transport	11	0.98%	0.294678
GO:0006820~anion transport	13	1.16%	0.327336
GO:0005253~anion channel activity	5	0.45%	0.331305
chloride channel	4	0.36%	0.400613
GO:0005254~chloride channel activity	4	0.36%	0.480429
chloride	4	0.36%	0.501672
GO:0022836~gated channel activity	11	0.98%	0.933086

Median: 0.38303656691347576 Geo: 0.3286281289729965

Term	Count	%	PValue
GO:0019198~transmembrane receptor protei	3	0.27%	0.177206
GO:0004725~protein tyrosine phosphatase ac	6	0.54%	0.383037
SM00194:PTPc	4	0.36%	0.522872

Median: 0.3137784044701102 Geo: 0.35567081697826736

Term	Count	%	PValue
GO:0016575~histone deacetylation	3	0.27%	0.210485
GO:0004407~histone deacetylase activity	3	0.27%	0.259361
GO:0033558~protein deacetylase activity	3	0.27%	0.259361
GO:0006476~protein amino acid deacetylatio	3	0.27%	0.275351
GO:0016811~hydrolase activity, acting on car	5	0.45%	0.306082
GO:0019213~deacetylase activity	3	0.27%	0.321475
GO:0016570~histone modification	4	0.36%	0.464591
GO:0016569~covalent chromatin modificatior	4	0.36%	0.479537
GO:0016568~chromatin modification	7	0.63%	0.570116
GO:0016810~hydrolase activity, acting on car	6	0.54%	0.664852

Median: 0.37687762029993876 Geo: 0.35655060468790495

Term	Count	%	PValue
GO:0031300~intrinsic to organelle membrane	9	0.81%	0.177475
GO:0031301~integral to organelle membrane	8	0.72%	0.216569
GO:0030173~integral to Golgi membrane	4	0.36%	0.323272
GO:0031228~intrinsic to Golgi membrane	4	0.36%	0.430483
GO:0030176~integral to endoplasmic reticulu	3	0.27%	0.570731
GO:0031227~intrinsic to endoplasmic reticulu	3	0.27%	0.673033

Median: 0.4075141240870743 Geo: 0.35866557898917073

Term	Count	%	PValue
IPR000162:GPCR, family 3, metabotropic gluta	3	0.27%	0.08858
IPR001828:Extracellular ligand-binding recept	5	0.45%	0.310163
IPR000337:GPCR, family 3	4	0.36%	0.354689
IPR011500:GPCR, family 3, nine cysteines reg	3	0.27%	0.46034
GO:0008066~glutamate receptor activity	7	0.63%	0.608926
GO:0008067~metabotropic glutamate, GABA-	5	0.45%	0.779334

Median: 0.3606164229489288 Geo: 0.36505968111636955

Term	Count	%	PValue
rno05210:Colorectal cancer	9	0.81%	0.144588
rno05215:Prostate cancer	9	0.81%	0.20278
rno05212:Pancreatic cancer	8	0.72%	0.209256
rno05219:Bladder cancer	5	0.45%	0.22194
rno05213:Endometrial cancer	6	0.54%	0.258366
rno04664:Fc epsilon RI signaling pathway	7	0.63%	0.308233
rno05214:Glioma	6	0.54%	0.35282
rno04930:Type II diabetes mellitus	5	0.45%	0.360616
rno04910:Insulin signaling pathway	10	0.89%	0.420725
rno04012:ErbB signaling pathway	7	0.63%	0.480269

rno05221:Acute myeloid leukemia	5	0.45%	0.499266
rno05220:Chronic myeloid leukemia	6	0.54%	0.601857
rno05223:Non-small cell lung cancer	4	0.36%	0.679289
rno04620:Toll-like receptor signaling pathway	6	0.54%	0.689423
rno05218:Melanoma	5	0.45%	0.694744

Median: 0.6107688362713029 Geo: 0.36786362508084713

Term	Count	%	PValue
GO:0043412~biopolymer modification	104	9.30%	0.010652
GO:0006464~protein modification process	101	9.03%	0.011152
GO:0043687~post-translational protein modif	81	7.25%	0.052405
serine/threonine-specific protein kinase	6	0.54%	0.054413
GO:0006796~phosphate metabolic process	58	5.19%	0.203992
GO:0006793~phosphorus metabolic process	58	5.19%	0.203992
phosphotransferase	9	0.81%	0.270275
IPR008271:Serine/threonine protein kinase, ac	14	1.25%	0.389865
atp-binding	39	3.49%	0.418874
ATP	11	0.98%	0.436506
binding site:ATP	15	1.34%	0.467178
GO:0016740~transferase activity	91	8.14%	0.503766
Serine/threonine-protein kinase	13	1.16%	0.523432
domain:Protein kinase	13	1.16%	0.606836
IPR000719:Protein kinase, core	18	1.61%	0.614701
IPR002290:Serine/threonine protein kinase	9	0.81%	0.665432
GO:0016310~phosphorylation	41	3.67%	0.697755
GO:0004713~protein-tyrosine kinase activity	15	1.34%	0.727277
GO:0004674~protein serine/threonine kinase	26	2.33%	0.739647
GO:0006468~protein amino acid phosphoryla	34	3.04%	0.74446
GO:0016301~kinase activity	43	3.85%	0.775186
GO:0016772~transferase activity, transferring	50	4.47%	0.806929
active site:Proton acceptor	16	1.43%	0.829169
kinase	22	1.97%	0.878988
GO:0016773~phosphotransferase activity, alc	35	3.13%	0.882313
SM00220:S_TKc	16	1.43%	0.886968
nucleotide phosphate-binding region:ATP	15	1.34%	0.911234
GO:0004672~protein kinase activity	29	2.59%	0.915438

Median: 0.36474197152379556 Geo: 0.3745507585387694

Term	Count	%	PValue
domain:Helix-loop-helix motif	6	0.54%	0.103468
SM00353:HLH	7	0.63%	0.226373
DNA-binding region:Basic motif	6	0.54%	0.346947
IPR001092:Basic helix-loop-helix dimerisation	6	0.54%	0.364742
GO:0003705~RNA polymerase II transcription	3	0.27%	0.440534
IPR011598:Helix-loop-helix DNA-binding	3	0.27%	0.803061
GO:0003702~RNA polymerase II transcription	5	0.45%	0.986203

Median: 0.40335407232030307 Geo: 0.3871980889214496

Term	Count	%	PValue
GO:0009719~response to endogenous stimul	28	2.50%	0.170654
GO:0006974~response to DNA damage stimu	15	1.34%	0.366557
GO:0006281~DNA repair	12	1.07%	0.403354
GO:0006260~DNA replication	11	0.98%	0.533056
GO:0006259~DNA metabolic process	32	2.86%	0.647067

Median: 0.3945131660035479 Geo: 0.39080685877127763

Term	Count	%	PValue
IPR013766:Thioredoxin domain	3	0.27%	0.297638
GO:0045454~cell redox homeostasis	5	0.45%	0.373214
IPR006662:Thioredoxin-related	3	0.27%	0.415812
IPR012335:Thioredoxin fold	6	0.54%	0.505016

Median: 0.577788008160159 Geo: 0.40749427993885956

Term	Count	%	PValue
IPR001881:EGF-like calcium-binding	9	0.81%	0.027665
SM00179:EGF_CA	9	0.81%	0.039536
domain:EGF-like 1	6	0.54%	0.132888
IPR000152:Aspartic acid and asparagine hydr	7	0.63%	0.164861
IPR006209:EGF-like	8	0.72%	0.193811
egf-like domain	11	0.98%	0.205223
IPR000742:EGF-like, type 3	10	0.89%	0.212821
domain:EGF-like 3; calcium-binding	3	0.27%	0.220383
IPR013091:EGF calcium-binding	5	0.45%	0.251909
IPR006210:EGF	10	0.89%	0.254032
SM00181:EGF	10	0.89%	0.280013
domain:EGF-like 2	4	0.36%	0.316111
domain:EGF-like 2; calcium-binding	3	0.27%	0.423992
IPR013032:EGF-like region	11	0.98%	0.511755
rno04610:Complement and coagulation casca	5	0.45%	0.528473
serine proteinase	3	0.27%	0.627103
GO:0007596~blood coagulation	5	0.45%	0.688275
GO:0050817~coagulation	5	0.45%	0.697531
GO:0007599~hemostasis	5	0.45%	0.724107
active site:Charge relay system	5	0.45%	0.853922
serine protease	5	0.45%	0.860029
domain:Peptidase S1	3	0.27%	0.864596
IPR001314:Peptidase S1A, chymotrypsin	5	0.45%	0.871184
GO:0050878~regulation of body fluid levels	5	0.45%	0.897558
IPR001254:Peptidase S1 and S6, chymotrypsi	5	0.45%	0.903363
GO:0008236~serine-type peptidase activity	9	0.81%	0.911622
GO:0017171~serine hydrolase activity	9	0.81%	0.911622
SM00020:Tryp_SPc	5	0.45%	0.912062
GO:0004252~serine-type endopeptidase acti	7	0.63%	0.957408
protease	12	1.07%	0.976645

Median: 0.40647718696843593 Geo: 0.41412682105793264

Term	Count	%	PValue
GO:0006323~DNA packaging	16	1.43%	0.206447
IPR002164:Nucleosome assembly protein (NA	3	0.27%	0.273309
GO:0006334~nucleosome assembly	6	0.54%	0.31441
GO:0006325~establishment and/or maintena	14	1.25%	0.371224
GO:0031497~chromatin assembly	6	0.54%	0.406477
GO:0000786~nucleosome	4	0.36%	0.489057
GO:0065004~protein-DNA complex assembly	7	0.63%	0.570116
GO:0051276~chromosome organization and	15	1.34%	0.64874
GO:0006333~chromatin assembly or disasse	6	0.54%	0.739903

Median: 0.532431042883997 Geo: 0.4177511484099943

Term	Count	%	PValue
GO:0046851~negative regulation of bone re	4	0.36%	0.059801
GO:0030279~negative regulation of ossificati	3	0.27%	0.127677
GO:0046850~regulation of bone remodeling	5	0.45%	0.242656
GO:0030278~regulation of ossification	4	0.36%	0.323792
GO:0048771~tissue remodeling	11	0.98%	0.51045
GO:0030282~bone mineralization	3	0.27%	0.518472
GO:0046849~bone remodeling	10	0.89%	0.54639
GO:0001503~ossification	8	0.72%	0.65935
GO:0031214~biomineral formation	8	0.72%	0.65935
GO:0001649~osteoblast differentiation	3	0.27%	0.84536
GO:0001501~skeletal development	11	0.98%	0.892239
GO:0009888~tissue development	12	1.07%	0.993113

Median: 0.4126814261238582 Geo: 0.42114604607328787

Term	Count	%	PValue
GO:0000245~spliceosome assembly	3	0.27%	0.402649
GO:0000377~RNA splicing, via transesterifica	5	0.45%	0.412681
GO:0000398~nuclear mRNA splicing, via splic	5	0.45%	0.412681
GO:0000375~RNA splicing, via transesterifica	5	0.45%	0.412681
GO:0008380~RNA splicing	9	0.81%	0.468157

Median: 0.46654621200982815 Geo: 0.42269776100474143

Term	Count	%	PValue
GO:0046058~cAMP metabolic process	4	0.36%	0.229067
GO:0006171~cAMP biosynthetic process	3	0.27%	0.382033
GO:0009187~cyclic nucleotide metabolic proc	4	0.36%	0.55106
GO:0009190~cyclic nucleotide biosynthetic p	3	0.27%	0.662001

Median: 0.9529865236334002 Geo: 0.42284236028087474

Term	Count	%	PValue
GO:0007187~G-protein signaling, coupled to	14	1.25%	0.031366
GO:0019932~second-messenger-mediated si	24	2.15%	0.049374
GO:0019935~cyclic-nucleotide-mediated sign	14	1.25%	0.065869
GO:0007188~G-protein signaling, coupled to	11	0.98%	0.066354
G protein-coupled receptor	11	0.98%	0.068436

GO:0019933~cAMP-mediated signaling	11	0.98%	0.127194
GO:0008227~amine receptor activity	4	0.36%	0.46613
rno04080:Neuroactive ligand-receptor interac	17	1.52%	0.673005
PIRSF002406:vertebrate rhodopsin	4	0.36%	0.841308
transducer	20	1.79%	0.952739
g-protein coupled receptor	18	1.61%	0.952987
IPR000276:Rhodopsin-like GPCR superfamily	12	1.07%	0.999899
receptor	36	3.22%	0.999976
GO:0007166~cell surface receptor linked sigr	76	6.80%	1
GO:0060089~molecular transducer activity	86	7.69%	1
GO:0004871~signal transducer activity	86	7.69%	1
GO:0007186~G-protein coupled receptor prot	44	3.94%	1
GO:0004872~receptor activity	60	5.37%	1
GO:0004888~transmembrane receptor activit	38	3.40%	1
GO:0004930~G-protein coupled receptor acti	27	2.42%	1
GO:0001584~rhodopsin-like receptor activity	16	1.43%	1

Median: 0.7093029113193254 Geo: 0.4274336816670745

Term	Count	%	PValue
IPR013753:Ras	9	0.81%	0.152954
IPR003579:Ras small GTPase, Rab type	3	0.27%	0.709303
SM00175:RAB	3	0.27%	0.719805

Median: 0.3316371203131925 Geo: 0.43087329622529147

Term	Count	%	PValue
GO:0031226~intrinsic to plasma membrane	57	5.10%	0.258809
GO:0044459~plasma membrane part	87	7.78%	0.295558
GO:0005887~integral to plasma membrane	55	4.92%	0.325735
GO:0005886~plasma membrane	106	9.48%	0.337539
topological domain:Cytoplasmic	69	6.17%	0.764369
topological domain:Extracellular	43	3.85%	0.99537

Median: 0.44945922077534506 Geo: 0.43464513235413105

Term	Count	%	PValue
GO:0051094~positive regulation of developm	8	0.72%	0.319107
GO:0048871~multicellular organismal homeo	4	0.36%	0.449459
GO:0001894~tissue homeostasis	4	0.36%	0.449459
GO:0045453~bone resorption	3	0.27%	0.553633

Median: 0.685960066589173 Geo: 0.4362470704578489

Term	Count	%	PValue
GO:0018193~peptidyl-amino acid modificatio	10	0.89%	0.171207
GO:0018108~peptidyl-tyrosine phosphorylati	4	0.36%	0.68596
GO:0018212~peptidyl-tyrosine modification	4	0.36%	0.706929

Median: 0.40963610445819626 Geo: 0.44729887337555274

Term	Count	%	PValue
repeat:2	6	0.54%	0.388537

repeat:1	6	0.54%	0.388537
repeat:3	5	0.45%	0.430735
repeat:4	4	0.36%	0.615625

Median: 0.4774561483027405 Geo: 0.4484195189382892

Term	Count	%	PValue
GO:0005739~mitochondrion	48	4.29%	0.270112
GO:0031966~mitochondrial membrane	17	1.52%	0.338256
GO:0019866~organelle inner membrane	15	1.34%	0.439673
GO:0005743~mitochondrial inner membrane	14	1.25%	0.470146
GO:0005740~mitochondrial envelope	17	1.52%	0.484766
GO:0031967~organelle envelope	23	2.06%	0.556712
GO:0031975~envelope	23	2.06%	0.556712
GO:0044429~mitochondrial part	20	1.79%	0.576142

Median: 0.4293023416983348 Geo: 0.4612341902779416

Term	Count	%	PValue
GO:0015629~actin cytoskeleton	15	1.34%	0.308413
GO:0016459~myosin complex	5	0.45%	0.429302
GO:0003774~motor activity	8	0.72%	0.741087

Median: 0.48151244734237886 Geo: 0.47505105782779394

Term	Count	%	PValue
GO:0007368~determination of left/right symr	3	0.27%	0.462387
GO:0009855~determination of bilateral symn	3	0.27%	0.481512
GO:0009799~determination of symmetry	3	0.27%	0.481512

Median: 0.4460592396549603 Geo: 0.4885246371145563

Term	Count	%	PValue
GO:0015291~secondary active transmembrai	13	1.16%	0.32978
GO:0015293~symporter activity	9	0.81%	0.421411
GO:0022804~active transmembrane transpor	22	1.97%	0.446059
GO:0015294~solute:cation symporter activity	5	0.45%	0.584325
GO:0015370~solute:sodium symporter activit	3	0.27%	0.768165

Median: 0.5088209052108131 Geo: 0.4962598576338997

Term	Count	%	PValue
GO:0042733~embryonic digit morphogenesis	3	0.27%	0.127677
GO:0030326~embryonic limb morphogenesis	4	0.36%	0.494285
GO:0035113~embryonic appendage morphog	4	0.36%	0.494285
GO:0035108~limb morphogenesis	4	0.36%	0.508821
GO:0035107~appendage morphogenesis	4	0.36%	0.508821
GO:0048736~appendage development	4	0.36%	0.508821
GO:0060173~limb development	4	0.36%	0.508821
GO:0007389~pattern specification process	10	0.89%	0.54639
GO:0009952~anterior/posterior pattern forma	5	0.45%	0.58499
GO:0003002~regionalization	6	0.54%	0.754437
GO:0048598~embryonic morphogenesis	6	0.54%	0.89166

Median: 0.6014490269812658 Geo: 0.4973764616269408

Term	Count	%	PValue
GO:0046466~membrane lipid catabolic proce	3	0.27%	0.297004
GO:0016042~lipid catabolic process	6	0.54%	0.601449
GO:0044242~cellular lipid catabolic process	3	0.27%	0.688803

Median: 0.8277224214823803 Geo: 0.5022243656471842

Term	Count	%	PValue
propeptide:Removed in mature form	9	0.81%	0.175615
GO:0048503~GPI anchor binding	3	0.27%	0.827722
gpi-anchor	3	0.27%	0.87146

Median: 0.7482201941461548 Geo: 0.5043113219971841

Term	Count	%	PValue
IPR013089:Kelch related	3	0.27%	0.176793
IPR013069:BTB/POZ	4	0.36%	0.390294
IPR011333:BTB/POZ fold	4	0.36%	0.74822
IPR000210:BTB/POZ-like	4	0.36%	0.767953
SM00225:BTB	4	0.36%	0.82276

Median: 0.6629167877214965 Geo: 0.5180844925108304

Term	Count	%	PValue
GO:0016891~endoribonuclease activity, prod	3	0.27%	0.280132
GO:0016893~endonuclease activity, active w	3	0.27%	0.300856
GO:0004519~endonuclease activity	5	0.45%	0.636226
GO:0004540~ribonuclease activity	4	0.36%	0.689608
GO:0004521~endoribonuclease activity	3	0.27%	0.715294
GO:0004518~nuclease activity	7	0.63%	0.731114

Median: 0.5088209052108131 Geo: 0.5218217098726277

Term	Count	%	PValue
GO:0042552~myelination	4	0.36%	0.464591
GO:0007272~ensheathment of neurons	4	0.36%	0.508821
GO:0008366~axon ensheathment	4	0.36%	0.508821
GO:0001508~regulation of action potential	4	0.36%	0.616436

Median: 0.5849051118463864 Geo: 0.5232757559198661

Term	Count	%	PValue
IPR013087:Zinc finger, C2H2-type/integrase,	8	0.72%	0.332645
IPR015880:Zinc finger, C2H2-like	9	0.81%	0.543597
SM00355:ZnF_C2H2	9	0.81%	0.584905
IPR007087:Zinc finger, C2H2-type	12	1.07%	0.585557
IPR001909:KRAB box	3	0.27%	0.633491

Median: 0.6445007927650344 Geo: 0.5232873981612741

Term	Count	%	PValue
GO:0009401~phosphoenolpyruvate-depende	3	0.27%	0.189177

GO:0015293~symporter activity	9	0.81%	0.421411
GO:0005351~sugar:hydrogen ion symporter a	3	0.27%	0.610061
GO:0051119~sugar transmembrane transport	3	0.27%	0.67894
GO:0015144~carbohydrate transmembrane t	3	0.27%	0.748128
GO:0008643~carbohydrate transport	4	0.36%	0.831163

Median: 0.5536331420138444 Geo: 0.5271280856259419

Term	Count	%	PValue
GO:0000096~sulfur amino acid metabolic pro	3	0.27%	0.297004
GO:0044272~sulfur compound biosynthetic p	3	0.27%	0.553633
GO:0006790~sulfur metabolic process	4	0.36%	0.890767

Median: 0.601409864525576 Geo: 0.5314855310753033

Term	Count	%	PValue
GO:0051174~regulation of phosphorus metab	6	0.54%	0.383436
GO:0019220~regulation of phosphate metabo	6	0.54%	0.383436
GO:0042325~regulation of phosphorylation	5	0.45%	0.562107
GO:0001932~regulation of protein amino acid	4	0.36%	0.640713
GO:0033238~regulation of amine metabolic p	4	0.36%	0.652439
GO:0006521~regulation of amino acid metabo	4	0.36%	0.652439

Median: 0.6966402340618993 Geo: 0.5381382996526384

Term	Count	%	PValue
GO:0050869~negative regulation of B cell act	3	0.27%	0.072716
GO:0051250~negative regulation of lymphocy	3	0.27%	0.382033
GO:0002521~leukocyte differentiation	8	0.72%	0.385125
GO:0050864~regulation of B cell activation	3	0.27%	0.442854
GO:0030183~B cell differentiation	3	0.27%	0.536282
GO:0051249~regulation of lymphocyte activa	5	0.45%	0.538554
GO:0050865~regulation of cell activation	5	0.45%	0.562107
GO:0042113~B cell activation	4	0.36%	0.628711
GO:0045321~leukocyte activation	11	0.98%	0.69664
GO:0050670~regulation of lymphocyte prolife	3	0.27%	0.701535
GO:0032944~regulation of mononuclear cell p	3	0.27%	0.701535
GO:0032943~mononuclear cell proliferation	4	0.36%	0.706929
GO:0046651~lymphocyte proliferation	4	0.36%	0.706929
GO:0051251~positive regulation of lymphocy	3	0.27%	0.713831
GO:0001775~cell activation	12	1.07%	0.731025
GO:0046649~lymphocyte activation	8	0.72%	0.773536
GO:0030098~lymphocyte differentiation	4	0.36%	0.795871

Median: 0.5464358420691726 Geo: 0.5464881667450793

Term	Count	%	PValue
repeat:LRR 4	4	0.36%	0.296977
repeat:LRR 3	4	0.36%	0.37346
repeat:LRR 2	4	0.36%	0.411215
repeat:LRR 1	4	0.36%	0.411215
leucine-rich repeat	6	0.54%	0.681657

IPR001611:Leucine-rich repeat	6	0.54%	0.823577
IPR003591:Leucine-rich repeat, typical subtyp	3	0.27%	0.862004
SM00369:LRR_TYP	3	0.27%	0.876519

Median: 0.5819051364898118 Geo: 0.5596950020270177

Term	Count	%	PValue
GO:0048646~anatomical structure formation	12	1.07%	0.301312
GO:0048514~blood vessel morphogenesis	10	0.89%	0.54639
GO:0001568~blood vessel development	11	0.98%	0.577108
GO:0001525~angiogenesis	8	0.72%	0.586703
GO:0001944~vasculature development	11	0.98%	0.605447
GO:0009887~organ morphogenesis	19	1.70%	0.910833

Median: 0.7146631166959486 Geo: 0.5600330435588263

Term	Count	%	PValue
GO:0007626~locomotory behavior	13	1.16%	0.260627
rno04620:Toll-like receptor signaling pathway	6	0.54%	0.689423
GO:0042330~taxis	6	0.54%	0.739903
GO:0006935~chemotaxis	6	0.54%	0.739903

Median: 0.595986061875998 Geo: 0.5617526454231732

Term	Count	%	PValue
rno01040:Polyunsaturated fatty acid biosynth	3	0.27%	0.319739
lipid synthesis	5	0.45%	0.462802
fatty acid biosynthesis	3	0.27%	0.516909
GO:0006633~fatty acid biosynthetic process	4	0.36%	0.675063
GO:0046394~carboxylic acid biosynthetic pro	4	0.36%	0.780118
GO:0016053~organic acid biosynthetic proce	4	0.36%	0.780118

Median: 0.6014490269812658 Geo: 0.5625121080973473

Term	Count	%	PValue
GO:0004623~phospholipase A2 activity	3	0.27%	0.42142
GO:0004091~carboxylesterase activity	7	0.63%	0.42217
GO:0016042~lipid catabolic process	6	0.54%	0.601449
GO:0004620~phospholipase activity	4	0.36%	0.668674
GO:0016298~lipase activity	4	0.36%	0.787124

Median: 0.5787287488791943 Geo: 0.5668905827307934

Term	Count	%	PValue
GO:0051128~regulation of cellular componen	6	0.54%	0.33732
GO:0008064~regulation of actin polymerizati	3	0.27%	0.536282
GO:0030832~regulation of actin filament leng	3	0.27%	0.553633
GO:0032535~regulation of cellular componen	3	0.27%	0.57052
GO:0032956~regulation of actin cytoskeleton	3	0.27%	0.586938
GO:0051493~regulation of cytoskeleton orga	3	0.27%	0.662001
GO:0033043~regulation of organelle organiza	3	0.27%	0.662001
GO:0008154~actin polymerization and/or dep	3	0.27%	0.7257

Median: 0.5999486537353009 Geo: 0.5669168044626316

Term	Count	%	PValue
GO:0043123~positive regulation of I-kappaB	6	0.54%	0.394966
GO:0043122~regulation of I-kappaB kinase/N	6	0.54%	0.452147
GO:0007249~I-kappaB kinase/NF-kappaB cas	7	0.63%	0.74775
GO:0009967~positive regulation of signal tra	8	0.72%	0.773536

Median: 1.0 Geo: 0.5670533146296532

Term	Count	%	PValue
GO:0009582~detection of abiotic stimulus	5	0.45%	0.170357
GO:0009581~detection of external stimulus	5	0.45%	0.26816
GO:0050954~sensory perception of mechanic	5	0.45%	0.412681
GO:0007608~sensory perception of smell	5	0.45%	1
GO:0007606~sensory perception of chemical	6	0.54%	1
GO:0050906~detection of stimulus during se	5	0.45%	1
GO:0051606~detection of stimulus	7	0.63%	1

Median: 0.609218857807939 Geo: 0.5802975779525337

Term	Count	%	PValue
GO:0009890~negative regulation of biosynth	4	0.36%	0.434156
GO:0017148~negative regulation of translati	3	0.27%	0.57052
GO:0031327~negative regulation of cellular	3	0.27%	0.647918
GO:0051248~negative regulation of protein	5	0.45%	0.706588

Median: 0.6213308430829785 Geo: 0.6021493472760941

Term	Count	%	PValue
IPR001440:Tetratricopeptide TPR-1	4	0.36%	0.509556
IPR011990:Tetratricopeptide-like helical	5	0.45%	0.592901
TPR repeat	4	0.36%	0.621331
IPR013026:Tetratricopeptide region	4	0.36%	0.642694
SM00028:TPR	4	0.36%	0.656174

Median: 0.6928277524443143 Geo: 0.6074386132124397

Term	Count	%	PValue
GO:0055086~nucleobase, nucleoside and nuc	21	1.88%	0.079074
GO:0009117~nucleotide metabolic process	19	1.70%	0.109776
GO:0015992~proton transport	7	0.63%	0.358964
GO:0006163~purine nucleotide metabolic pro	8	0.72%	0.394626
GO:0006818~hydrogen transport	7	0.63%	0.421131
hydrogen ion transport	4	0.36%	0.435119
GO:0009144~purine nucleoside triphosphate	6	0.54%	0.46343
GO:0009165~nucleotide biosynthetic process	10	0.89%	0.498742
GO:0009141~nucleoside triphosphate metabo	6	0.54%	0.507789
GO:0006164~purine nucleotide biosynthetic	6	0.54%	0.540067
GO:0015077~monovalent inorganic cation tra	8	0.72%	0.566816
GO:0009108~coenzyme biosynthetic process	6	0.54%	0.601449
GO:0009199~ribonucleoside triphosphate me	5	0.45%	0.6286
GO:0009205~purine ribonucleoside triphosph	5	0.45%	0.6286

GO:0016469~proton-transporting two-sector	4	0.36%	0.632594
GO:0009150~purine ribonucleotide metabolic	6	0.54%	0.639677
GO:0022890~inorganic cation transmembran	10	0.89%	0.64058
GO:0009152~purine ribonucleotide biosynthe	5	0.45%	0.669169
GO:0009201~ribonucleoside triphosphate bio	4	0.36%	0.68596
GO:0009206~purine ribonucleoside triphosph	4	0.36%	0.68596
GO:0009145~purine nucleoside triphosphate	4	0.36%	0.68596
GO:0015662~ATPase activity, coupled to tran	4	0.36%	0.699695
GO:0009259~ribonucleotide metabolic proces	6	0.54%	0.700848
GO:0009142~nucleoside triphosphate biosyn	4	0.36%	0.706929
GO:0009260~ribonucleotide biosynthetic proc	5	0.45%	0.715446
GO:0046034~ATP metabolic process	4	0.36%	0.717004
GO:0015405~P-P-bond-hydrolysis-driven tran	9	0.81%	0.733388
GO:0015399~primary active transmembrane	9	0.81%	0.733388
GO:0046961~hydrogen ion transporting ATPa	3	0.27%	0.737562
GO:0015986~ATP synthesis coupled proton tr	3	0.27%	0.748188
GO:0043492~ATPase activity, coupled to mov	8	0.72%	0.775888
GO:0006753~nucleoside phosphate metaboli	3	0.27%	0.788436
GO:0006754~ATP biosynthetic process	3	0.27%	0.788436
GO:0015078~hydrogen ion transmembrane t	6	0.54%	0.788459
GO:0042625~ATPase activity, coupled to tran	5	0.45%	0.805609
GO:0019829~cation-transporting ATPase acti	3	0.27%	0.848745
GO:0042626~ATPase activity, coupled to tran	7	0.63%	0.871155
GO:0006119~oxidative phosphorylation	4	0.36%	0.876716
GO:0016820~hydrolase activity, acting on aci	7	0.63%	0.888939
GO:0042623~ATPase activity, coupled	12	1.07%	0.897126
rno00190:Oxidative phosphorylation	5	0.45%	0.94111
GO:0016887~ATPase activity	13	1.16%	0.952816

Median: 0.7013168766235801 Geo: 0.6297977628010818

Term	Count	%	PValue
GO:0048511~rhythmic process	9	0.81%	0.276768
GO:0001541~ovarian follicle development	3	0.27%	0.402649
GO:0048608~reproductive structure develop	5	0.45%	0.502071
GO:0008406~gonad development	5	0.45%	0.502071
GO:0045137~development of primary sexual	5	0.45%	0.596168
GO:0022601~menstrual cycle phase	3	0.27%	0.662001
GO:0022602~menstrual cycle process	3	0.27%	0.675627
GO:0008585~female gonad development	3	0.27%	0.688803
GO:0046660~female sex differentiation	3	0.27%	0.713831
GO:0046545~development of primary female	3	0.27%	0.713831
GO:0042698~menstrual cycle	3	0.27%	0.7257
GO:0007548~sex differentiation	5	0.45%	0.756788
GO:0003006~reproductive developmental pr	5	0.45%	0.786396
GO:0032504~multicellular organism reprodu	4	0.36%	0.803388
GO:0048609~reproductive process in a multi	4	0.36%	0.803388
GO:0022414~reproductive process	13	1.16%	0.835992

Median: 0.5984469718441101	Geo: 0.6323830465290332		
Term	Count	%	PValue
GO:0007276~gamete generation	15	1.34%	0.566156
GO:0048232~male gamete generation	11	0.98%	0.598447
GO:0007283~spermatogenesis	11	0.98%	0.598447
GO:0019953~sexual reproduction	17	1.52%	0.624193
GO:0000003~reproduction	25	2.24%	0.799089

Median: 0.6418794153582141	Geo: 0.6434810458513377		
Term	Count	%	PValue
domain:C2 2	3	0.27%	0.557944
domain:C2 1	3	0.27%	0.557944
IPR000008:C2 calcium-dependent membrane	5	0.45%	0.725815
SM00239:C2	5	0.45%	0.758815

Median: 0.5705196311967391	Geo: 0.6563294464415198		
Term	Count	%	PValue
GO:0040014~regulation of multicellular orga	3	0.27%	0.536282
GO:0035264~multicellular organism growth	3	0.27%	0.57052
GO:0040008~regulation of growth	7	0.63%	0.924063

Median: 0.7446078402660412	Geo: 0.6575850095074384		
Term	Count	%	PValue
GO:0000785~chromatin	10	0.89%	0.502927
GO:0005694~chromosome	15	1.34%	0.744608
GO:0044427~chromosomal part	13	1.16%	0.759317

Median: 0.5620393231910041	Geo: 0.6810252212277741		
Term	Count	%	PValue
GO:0001608~nucleotide receptor activity, G-	4	0.36%	0.562039
GO:0016502~nucleotide receptor activity	4	0.36%	0.562039
IPR000276:Rhodopsin-like GPCR superfamily	12	1.07%	0.999899

Median: 0.6427726332095793	Geo: 0.7001764684951715		
Term	Count	%	PValue
IPR002126:Cadherin	4	0.36%	0.61543
SM00112:CA	4	0.36%	0.642773
GO:0007156~homophilic cell adhesion	6	0.54%	0.867733

Median: 0.793690309997469	Geo: 0.7071541215403462		
Term	Count	%	PValue
GO:0045860~positive regulation of protein ki	9	0.81%	0.459439
GO:0043405~regulation of MAP kinase activit	5	0.45%	0.764474
GO:0000187~activation of MAPK activity	3	0.27%	0.822907
GO:0043406~positive regulation of MAP kinas	3	0.27%	0.865197

Median: 0.779359351302318	Geo: 0.708304923911514		
Term	Count	%	PValue

GO:0009605~response to external stimulus	42	3.76%	0.465649
GO:0006954~inflammatory response	17	1.52%	0.676617
GO:0009611~response to wounding	23	2.06%	0.882102
GO:0006952~defense response	22	1.97%	0.905651

Median: 0.8552131779570957 Geo: 0.7091622268294516

Term	Count	%	PValue
GO:0022892~substrate-specific transporter a	65	5.81%	0.10346
GO:0005215~transporter activity	81	7.25%	0.112579
GO:0022891~substrate-specific transmembra	48	4.29%	0.401987
GO:0022857~transmembrane transporter act	52	4.65%	0.446023
transport	57	5.10%	0.500143
GO:0022890~inorganic cation transmembran	10	0.89%	0.64058
GO:0015075~ion transmembrane transporter	37	3.31%	0.666394
GO:0006811~ion transport	40	3.58%	0.704556
GO:0006813~potassium ion transport	8	0.72%	0.743226
potassium	6	0.54%	0.751663
GO:0030955~potassium ion binding	5	0.45%	0.779334
GO:0008324~cation transmembrane transpor	26	2.33%	0.820017
potassium transport	5	0.45%	0.823461
ion transport	22	1.97%	0.854332
GO:0022803~passive transmembrane transpo	17	1.52%	0.855213
GO:0015267~channel activity	17	1.52%	0.855213
Ionic channel	13	1.16%	0.888466
voltage-gated channel	6	0.54%	0.896856
GO:0015672~monovalent inorganic cation tra	14	1.25%	0.89821
GO:0006812~cation transport	23	2.06%	0.925976
GO:0030001~metal ion transport	18	1.61%	0.928702
GO:0022836~gated channel activity	11	0.98%	0.933086
GO:0005216~ion channel activity	14	1.25%	0.940465
GO:0031420~alkali metal ion binding	6	0.54%	0.950483
GO:0046873~metal ion transmembrane trans	12	1.07%	0.950868
GO:0022838~substrate specific channel activ	14	1.25%	0.954803
GO:0022832~voltage-gated channel activity	6	0.54%	0.957042
GO:0005244~voltage-gated ion channel activ	6	0.54%	0.957042
GO:0005267~potassium channel activity	4	0.36%	0.973171
GO:0005261~cation channel activity	8	0.72%	0.988112
GO:0022843~voltage-gated cation channel ac	3	0.27%	0.996715

Median: 0.6691685395032168 Geo: 0.7168766539023791

Term	Count	%	PValue
GO:0007179~transforming growth factor beta	4	0.36%	0.616436
GO:0007178~transmembrane receptor protei	5	0.45%	0.669169
GO:0007167~enzyme linked receptor protein	12	1.07%	0.89312

Median: 0.6660073746312482 Geo: 0.7181513531178823

Term	Count	%	PValue
GO:0004601~peroxidase activity	3	0.27%	0.666007

GO:0016684~oxidoreductase activity, acting	3	0.27%	0.666007
GO:0016209~antioxidant activity	3	0.27%	0.835007

Median: 0.7350892210174229 Geo: 0.7192759782543552

Term	Count	%	PValue
GO:0042692~muscle cell differentiation	4	0.36%	0.591074
GO:0014706~striated muscle development	6	0.54%	0.648871
GO:0007517~muscle development	8	0.72%	0.821308
GO:0007519~skeletal muscle development	4	0.36%	0.849722

Median: 0.9984766275751946 Geo: 0.7250339984678495

Term	Count	%	PValue
GO:0048029~monosaccharide binding	3	0.27%	0.382226
GO:0030246~carbohydrate binding	8	0.72%	0.998477
GO:0005529~sugar binding	5	0.45%	0.998658

Median: 0.7884358417100072 Geo: 0.7321529665083604

Term	Count	%	PValue
GO:0006730~one-carbon compound metaboli	6	0.54%	0.571327
GO:0043414~biopolymer methylation	3	0.27%	0.788436
GO:0032259~methylation	3	0.27%	0.871273

Median: 0.6691685395032168 Geo: 0.7523899992015123

Term	Count	%	PValue
GO:0051789~response to protein stimulus	5	0.45%	0.669169
GO:0006986~response to unfolded protein	5	0.45%	0.669169
GO:0009607~response to biotic stimulus	8	0.72%	0.95117

Median: 0.7994349606199997 Geo: 0.7551374387493411

Term	Count	%	PValue
Mitochondrion	23	2.06%	0.658318
transit peptide	12	1.07%	0.799435
transit peptide:Mitochondrion	9	0.81%	0.8182

Median: 0.8350065324763454 Geo: 0.7573085527457687

Term	Count	%	PValue
GO:0030594~neurotransmitter receptor activ	7	0.63%	0.565097
GO:0042165~neurotransmitter binding	7	0.63%	0.642168
GO:0004983~neuropeptide Y receptor activit	3	0.27%	0.652657
GO:0008188~neuropeptide receptor activity	3	0.27%	0.835007
GO:0042923~neuropeptide binding	3	0.27%	0.835007
GO:0042277~peptide binding	9	0.81%	0.886941
GO:0001653~peptide receptor activity	4	0.36%	0.975391

Median: 0.7481884961189249 Geo: 0.7666946662279888

Term	Count	%	PValue
GO:0002009~morphogenesis of an epitheliu	6	0.54%	0.675549
GO:0016331~morphogenesis of embryonic e	3	0.27%	0.748188

GO:0048598~embryonic morphogenesis	6	0.54%	0.89166

Median: 0.8437420023447036 Geo: 0.7823281244291606

Term	Count	%	PValue
GO:0016064~immunoglobulin mediated immu	4	0.36%	0.523135
GO:0019724~B cell mediated immunity	4	0.36%	0.55106
GO:0002449~lymphocyte mediated immunity	4	0.36%	0.663889
GO:0002460~adaptive immune response bas	4	0.36%	0.706929
GO:0002250~adaptive immune response	4	0.36%	0.706929
GO:0002443~leukocyte mediated immunity	4	0.36%	0.754627
GO:0006959~humoral immune response	4	0.36%	0.843742
GO:0050776~regulation of immune response	5	0.45%	0.847884
GO:0002682~regulation of immune system pı	5	0.45%	0.872566
immune response	3	0.27%	0.955648
GO:0002252~immune effector process	4	0.36%	0.971089
GO:0002526~acute inflammatory response	3	0.27%	0.98349
GO:0006955~immune response	12	1.07%	0.999982

Median: 0.8311187328631705 Geo: 0.7899641669263333

Term	Count	%	PValue
GO:0031965~nuclear membrane	5	0.45%	0.656212
GO:0044453~nuclear membrane part	4	0.36%	0.771129
GO:0005635~nuclear envelope	6	0.54%	0.831119
GO:0005643~nuclear pore	3	0.27%	0.833261
GO:0046930~pore complex	3	0.27%	0.877853

Median: 0.8000862740701508 Geo: 0.7916258582136574

Term	Count	%	PValue
GO:0042107~cytokine metabolic process	4	0.36%	0.706929
GO:0001816~cytokine production	5	0.45%	0.800086
GO:0042089~cytokine biosynthetic process	3	0.27%	0.877096

Median: 0.758827055718108 Geo: 0.7991755408655077

Term	Count	%	PValue
GO:0006497~protein amino acid lipidation	3	0.27%	0.7257
GO:0042158~lipoprotein biosynthetic process	3	0.27%	0.758827
GO:0042157~lipoprotein metabolic process	3	0.27%	0.926887

Median: 0.8160828494606095 Geo: 0.8081255298438712

Term	Count	%	PValue
GO:0016337~cell-cell adhesion	13	1.16%	0.792443
GO:0022610~biological adhesion	30	2.68%	0.816083
GO:0007155~cell adhesion	30	2.68%	0.816083

Median: 0.9232974364126381 Geo: 0.8238423678796846

Term	Count	%	PValue
GO:0016126~sterol biosynthetic process	3	0.27%	0.536282
GO:0016125~sterol metabolic process	4	0.36%	0.831163

GO:0008203~cholesterol metabolic process	3	0.27%	0.923297
GO:0006694~steroid biosynthetic process	3	0.27%	0.936727
GO:0008202~steroid metabolic process	5	0.45%	0.984434

Median: 0.9362941363435059 Geo: 0.8360218956586637

Term	Count	%	PValue
GO:0005843~cytosolic small ribosomal subun	3	0.27%	0.408313
GO:0015935~small ribosomal subunit	3	0.27%	0.733306
ribonucleoprotein	8	0.72%	0.797397
GO:0005830~cytosolic ribosome (sensu Euka	3	0.27%	0.818051
rno03010:Ribosome	4	0.36%	0.848076
GO:0033279~ribosomal subunit	4	0.36%	0.936294
ribosomal protein	5	0.45%	0.941543
ribosome	3	0.27%	0.958014
GO:0030529~ribonucleoprotein complex	17	1.52%	0.996945
GO:0003735~structural constituent of ribosor	7	0.63%	0.99988
GO:0005840~ribosome	7	0.63%	0.999957

Median: 0.8700920567964969 Geo: 0.8419358538470354

Term	Count	%	PValue
GO:0003777~microtubule motor activity	4	0.36%	0.728459
GO:0007018~microtubule-based movement	5	0.45%	0.847884
GO:0005875~microtubule associated complex	5	0.45%	0.8923
GO:0030705~cytoskeleton-dependent intrace	5	0.45%	0.911724

Median: 0.8453599387629621 Geo: 0.8498359253984246

Term	Count	%	PValue
GO:0007126~meiosis	3	0.27%	0.84536
GO:0051327~M phase of meiotic cell cycle	3	0.27%	0.84536
GO:0051321~meiotic cell cycle	3	0.27%	0.858859

Median: 0.8437813998480348 Geo: 0.861373682922828

Term	Count	%	PValue
GO:0005615~extracellular space	88	7.87%	0.774662
GO:0044421~extracellular region part	91	8.14%	0.843781
GO:0005576~extracellular region	94	8.41%	0.97776

Median: 0.8877030784420337 Geo: 0.866705571947067

Term	Count	%	PValue
GO:0015179~L-amino acid transmembrane tr	3	0.27%	0.666007
GO:0006865~amino acid transport	4	0.36%	0.837557
GO:0015171~amino acid transmembrane trar	3	0.27%	0.848745
GO:0046942~carboxylic acid transport	5	0.45%	0.885656
GO:0015849~organic acid transport	5	0.45%	0.889751
GO:0015837~amine transport	4	0.36%	0.924703
GO:0046943~carboxylic acid transmembrane	3	0.27%	0.95976
GO:0005342~organic acid transmembrane tra	3	0.27%	0.961621

Median: 0.9354118585438735 Geo: 0.8733251539872539

Term	Count	%	PValue
IPR000047:Helix-turn-helix motif, lambda-like	3	0.27%	0.633491
IPR001356:Homeobox	5	0.45%	0.921786
SM00389:HOX	5	0.45%	0.935412
IPR012287:Homeodomain-related	4	0.36%	0.95928
Homeobox	4	0.36%	0.969529

Median: 0.9013406927694274 Geo: 0.8824357299623315

Term	Count	%	PValue
GO:0045792~negative regulation of cell size	3	0.27%	0.748188
GO:0016049~cell growth	7	0.63%	0.869474
GO:0008361~regulation of cell size	7	0.63%	0.891665
GO:0040007~growth	13	1.16%	0.911017
GO:0040008~regulation of growth	7	0.63%	0.924063
GO:0001558~regulation of cell growth	4	0.36%	0.966943

Median: 0.8924802767520075 Geo: 0.8834873488794694

Term	Count	%	PValue
GO:0006816~calcium ion transport	6	0.54%	0.823628
calcium transport	3	0.27%	0.889928
GO:0015674~di-, tri-valent inorganic cation tr	7	0.63%	0.895033
GO:0030001~metal ion transport	18	1.61%	0.928702

Median: 0.981699345405155 Geo: 0.8890739249359461

Term	Count	%	PValue
GO:0009897~external side of plasma membra	6	0.54%	0.404713
IPR003598:Immunoglobulin subtype 2	4	0.36%	0.945364
SM00408:IGc2	4	0.36%	0.963565
IPR013151:Immunoglobulin	4	0.36%	0.971303
SM00409:IG	7	0.63%	0.981699
IPR003599:Immunoglobulin subtype	5	0.45%	0.99162
immunoglobulin domain	6	0.54%	0.996245
IPR007110:Immunoglobulin-like	8	0.72%	0.999529
IPR013783:Immunoglobulin-like fold	7	0.63%	0.999939

Median: 0.8515833251974014 Geo: 0.8906688475145337

Term	Count	%	PValue
GO:0046906~tetrapyrrole binding	8	0.72%	0.851583
GO:0020037~heme binding	8	0.72%	0.851583
GO:0004497~monooxygenase activity	4	0.36%	0.974304

Median: 0.9962434132282394 Geo: 0.8976463845659044

Term	Count	%	PValue
membrane	163	14.58%	0.3784
topological domain:Cytoplasmic	69	6.17%	0.764369
transmembrane region	83	7.42%	0.872932
transmembrane	117	10.47%	0.910233

GO:0044425~membrane part	261	23.35%	0.977345
GO:0016020~membrane	313	28.00%	0.991044
topological domain:Extracellular	43	3.85%	0.99537
glycoprotein	85	7.60%	0.997117
glycosylation site:N-linked (GlcNAc...)	68	6.08%	0.998767
signal	60	5.37%	0.999805
GO:0031224~intrinsic to membrane	216	19.32%	0.999831
GO:0016021~integral to membrane	214	19.14%	0.999877
disulfide bond	43	3.85%	0.999931
signal peptide	51	4.56%	0.999983

Median: 0.9770492762883788 Geo: 0.898924811484142

Term	Count	%	PValue
Serine protease inhibitor	3	0.27%	0.659227
protease inhibitor	3	0.27%	0.850183
GO:0004867~serine-type endopeptidase inhi	3	0.27%	0.963399
GO:0004866~endopeptidase inhibitor activity	4	0.36%	0.9907
GO:0030414~protease inhibitor activity	4	0.36%	0.991503
GO:0004857~enzyme inhibitor activity	7	0.63%	0.994834

Median: 0.9024340852042524 Geo: 0.8997282058107576

Term	Count	%	PValue
GO:0042060~wound healing	8	0.72%	0.839849
GO:0042246~tissue regeneration	3	0.27%	0.871273
GO:0031099~regeneration	3	0.27%	0.933595
GO:0048589~developmental growth	3	0.27%	0.959249

Median: 0.9522219354712798 Geo: 0.9072825421771014

Term	Count	%	PValue
GO:0005201~extracellular matrix structural c	4	0.36%	0.771531
GO:0044420~extracellular matrix part	4	0.36%	0.89221
GO:0005578~proteinaceous extracellular ma	9	0.81%	0.952222
GO:0031012~extracellular matrix	9	0.81%	0.963879
extracellular matrix	3	0.27%	0.973042

Median: 0.9356066609929128 Geo: 0.9188051673289847

Term	Count	%	PValue
GO:0050776~regulation of immune response	5	0.45%	0.847884
GO:0002682~regulation of immune system p	5	0.45%	0.872566
GO:0002253~activation of immune response	3	0.27%	0.926887
GO:0051240~positive regulation of multicellu	5	0.45%	0.944326
GO:0050778~positive regulation of immune r	3	0.27%	0.961214
GO:0002684~positive regulation of immune s	3	0.27%	0.966578

Median: 0.9414350302664871 Geo: 0.9229533304598382

Term	Count	%	PValue
GO:0008201~heparin binding	3	0.27%	0.795615
GO:0005539~glycosaminoglycan binding	3	0.27%	0.929526

GO:0030247~polysaccharide binding	3	0.27%	0.941435
GO:0001871~pattern binding	3	0.27%	0.963399
GO:0030246~carbohydrate binding	8	0.72%	0.998477

Median: 0.9456647511946196 Geo: 0.9352281958909899

Term	Count	%	PValue
GO:0006508~proteolysis	36	3.22%	0.876179
GO:0008233~peptidase activity	28	2.50%	0.945665
GO:0004175~endopeptidase activity	16	1.43%	0.98724

Median: 0.9504320986748979 Geo: 0.9412154711720149

Term	Count	%	PValue
ank repeat	4	0.36%	0.916184
IPR002110:Ankyrin	4	0.36%	0.950432
SM00248:ANK	4	0.36%	0.957554

Median: 0.9658152263361006 Geo: 0.9730433063544447

Term	Count	%	PValue
growth factor	4	0.36%	0.962854
GO:0005125~cytokine activity	8	0.72%	0.965815
GO:0008083~growth factor activity	4	0.36%	0.9907