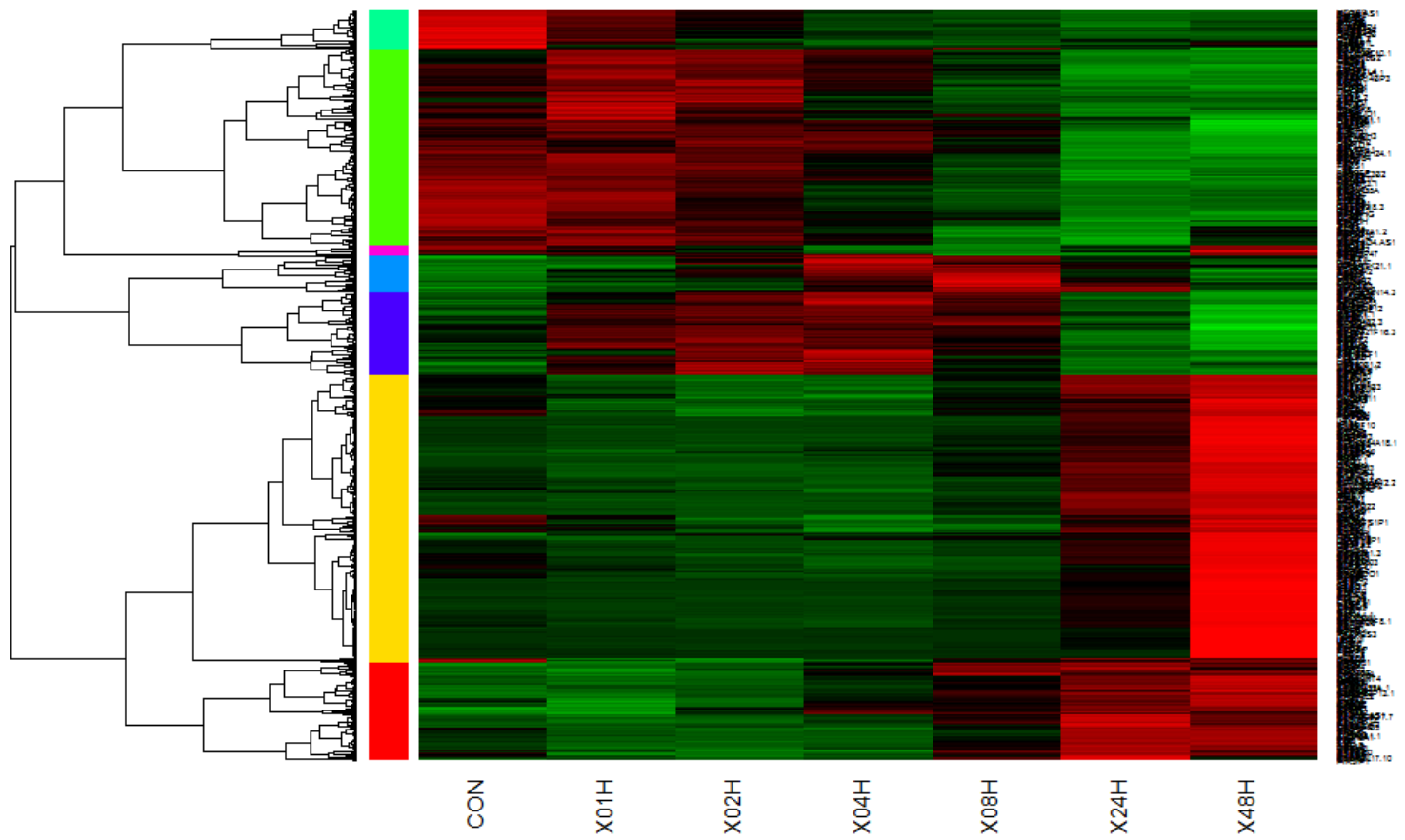
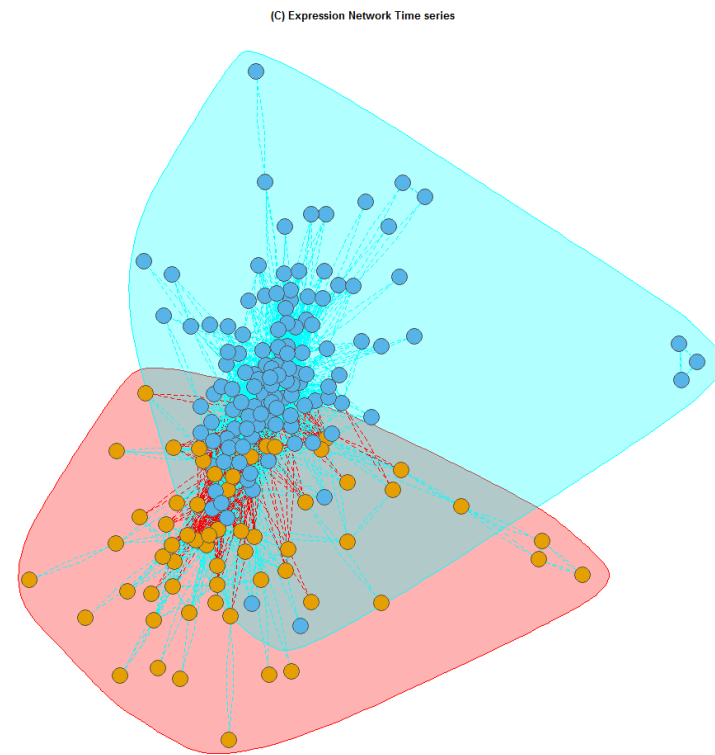
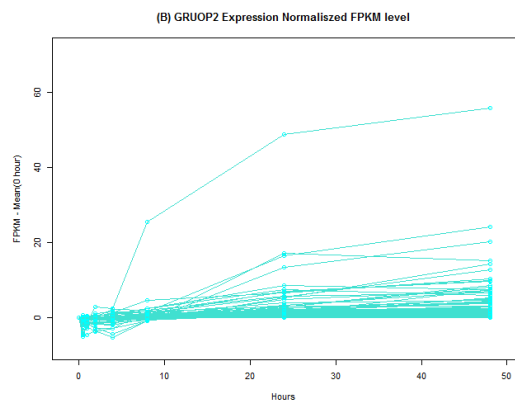
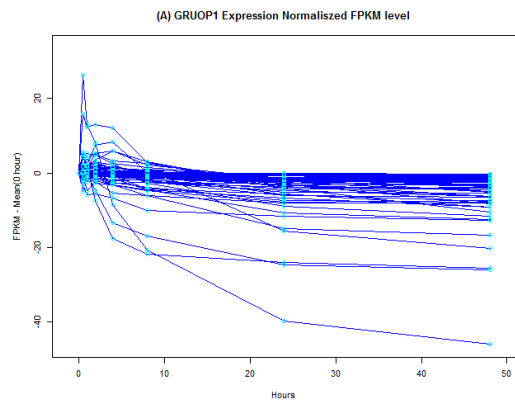


**Construction of a transcriptome-driven network at the early stage of
infection with influenza A H1N1 in human lung alveolar epithelial cells**

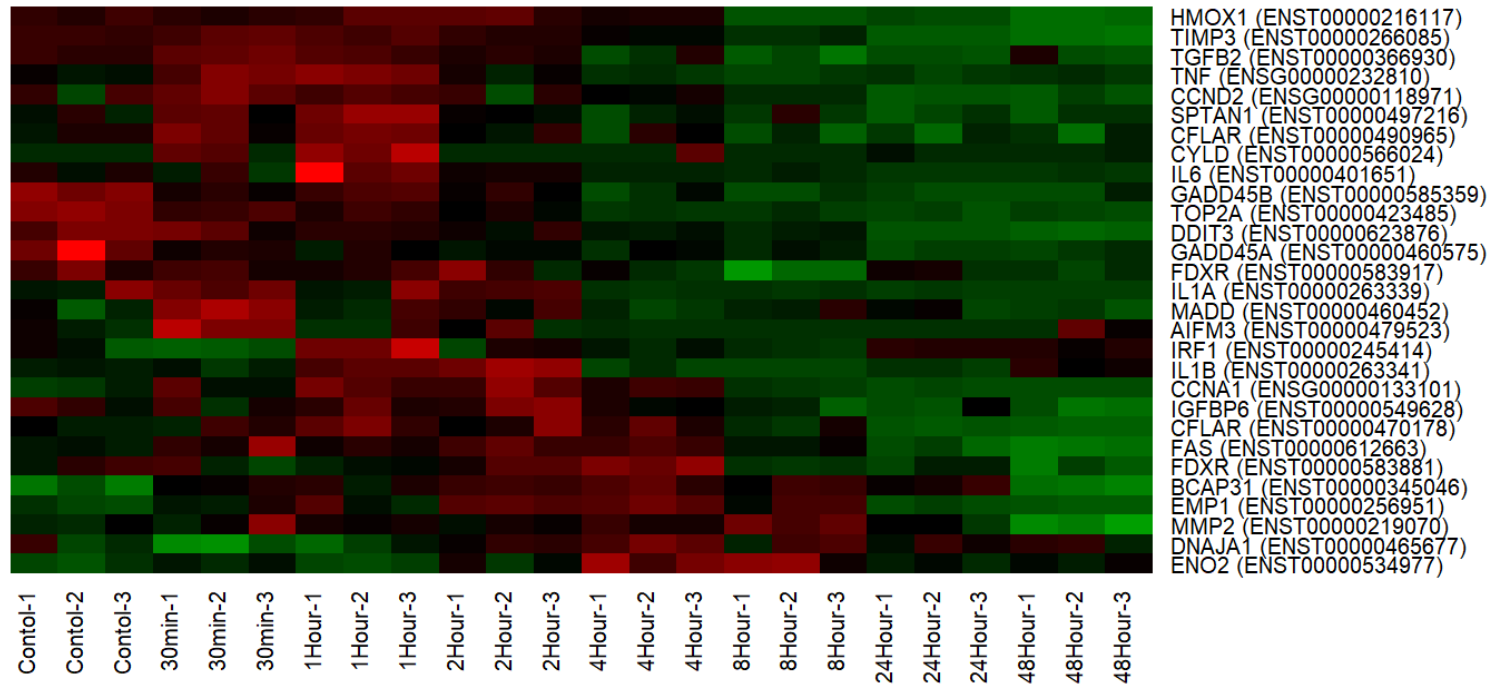
Supplementary Figure



Supplemental Figure 1. Time-series Gene Expression hierarchical clustering. Clearly two groups are divided.

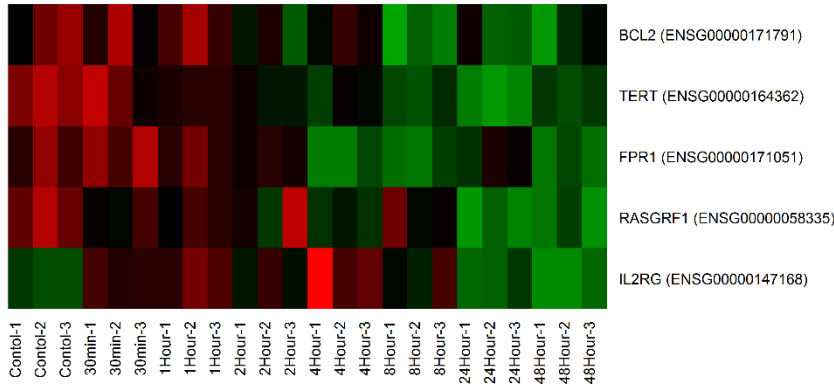


Supplemental Figure 2. Visualization of differential expression gene sets (DEGs) of non-coding RNA in the two groups.

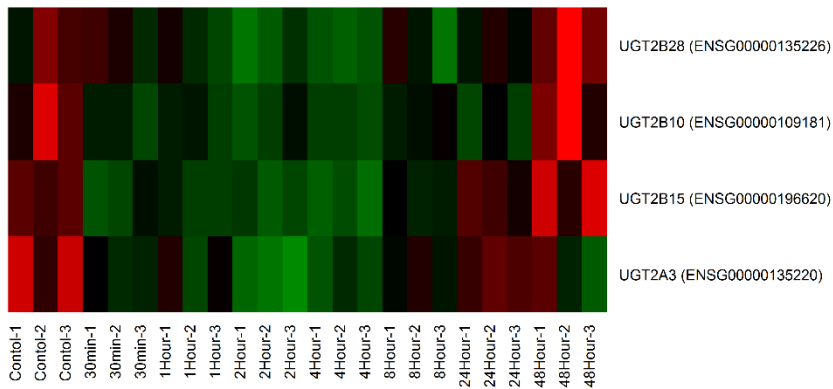


Supplemental Figure 3. Genes mediating programmed cell death (apoptosis).

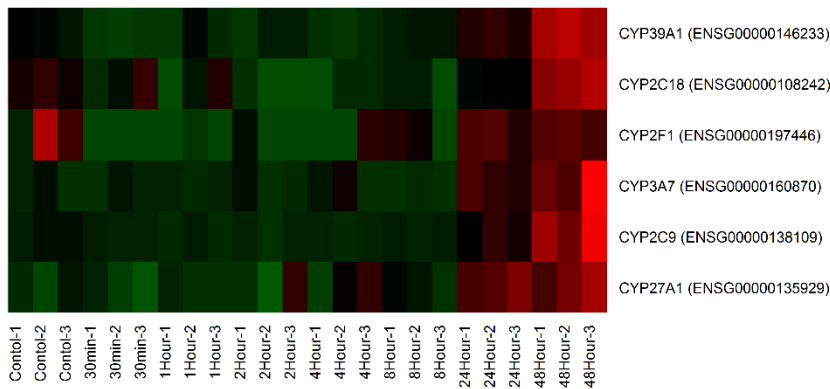
(A) Glycoprotein Gp120 downregulates



(B) UDP related genes

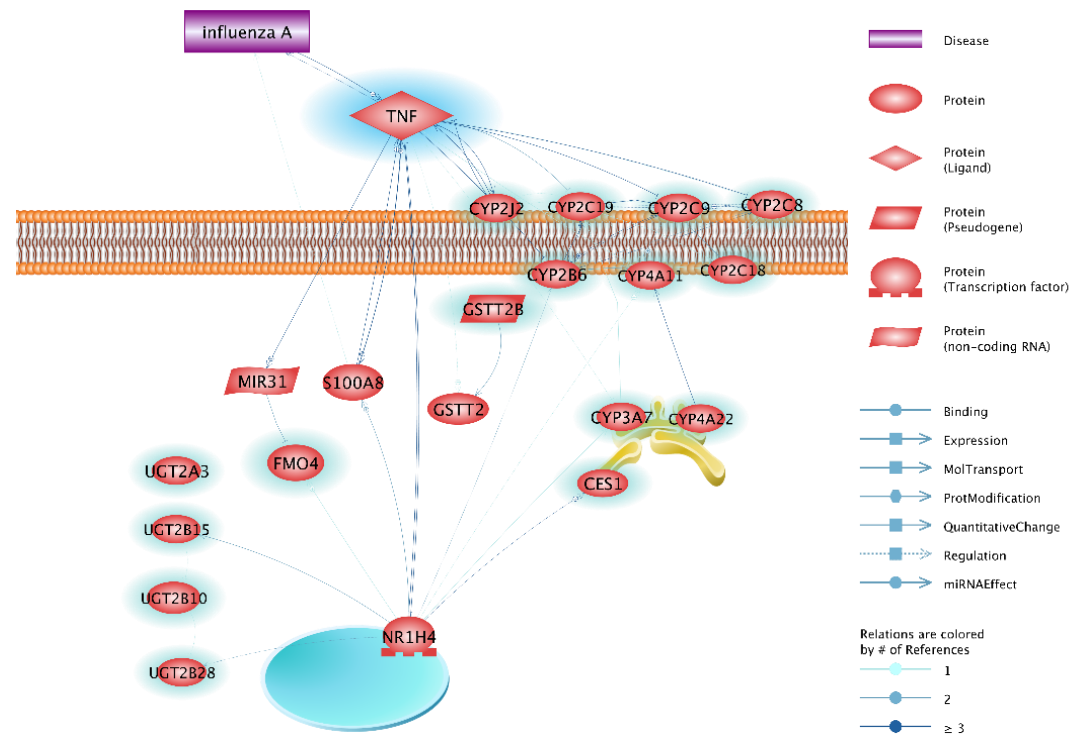


(C) CYP related genes



Supplemental Figure 4. Expression patterns of gp120 and two categories DMEs; (A) Identification of related gene sets in the Gp120-regulated category on the RNA-seq; green, decrease in gene expression; red, increase

in gene expression. The vertical axis corresponds to the sample increase time, and the horizontal axis to the gene list of 'env:Envelope surface glycoprotein Gp120 downregulates' by DAVID enrichments analysis. (B) Identification of related gene sets in UDP glycosyltransferases on the RNA-seq. (C) Identification of related gene sets in cytochrome P450 on the RNA-seq. The expression of CYP39A1 (P-value = 3.55E-11) decreased rapidly over the entire research period. Cytochrome P450 family 39 catalyzes many reactions involved in drug metabolism and synthesis of cholesterol, steroids, and other lipids. This endoplasmic reticulum protein is involved in the conversion of cholesterol to bile acids. Its substrates include the oxysterols 25-hydroxycholesterol, 27-hydroxycholesterol, and 24-hydroxycholesterol (Lorbek et al., 2012; Nicholson et al., 1998). CYP26A1 (P-value=6.14E-08) is a heme-containing enzyme responsible for metabolizing all-trans retinoic acid (at-RA) hydroxylase (Foti et al., 2016). CYP27A1 (P-value=0.0005) oxidizes cholesterol intermediates as part of the bile synthesis pathway. Since the conversion of cholesterol to bile acids is the major route for removing cholesterol from the body, this protein is important for overall cholesterol homeostasis.



Supplemental Figure 5. The reconstruction signaling and regulatory network of DMEs pathway at an early stage.

(A) Schema of drug metabolizing enzyme (DME)–regulated pathways in influenza–infected cells. The genes highlighted in cyan are those related to the “UGT family” and “cytochrome p450” according to the enrichment gene analysis. The remaining genes were identified through network analysis (PATHWAY studio). All genes in Figure.

Reference

Foti, R. S., Isoherranen, N., Zelter, A., Dickmann, L. J., Buttrick, B. R., Diaz, P. and Douguet, D. (2016). Identification of Tazarotenic Acid as the First Xenobiotic Substrate of Human Retinoic Acid Hydroxylase CYP26A1 and CYP26B1. *The Journal of pharmacology and experimental therapeutics* **357**, 281-292.

Lorbek, G., Lewinska, M. and Rozman, D. (2012). Cytochrome P450s in the synthesis of cholesterol and bile acids--from mouse models to human diseases. *The FEBS journal* **279**, 1516-1533.

Nicholson, K. G., Webster, R. G. and Hay, A. J. (1998). Textbook of Influenza. Blackwell Science.

Supplemental Table 1. Result list of Ballgown (Genes)

ensembl ID	pval	qval	SD	GENE_SYMBOL	GENE_DESC
ENSG00000128262	7.11E-15	4.99E-12	0.207962017	POM121L9P	POM121 transmembrane nucleoporin-like 9, pseudogene
ENSG00000099998	3.59E-14	1.78E-11	0.312566934	GGT5	gamma-glutamyltransferase 5
ENSG00000115112	1.19E-13	4.56E-11	0.145640619	TFCP2L1	transcription factor CP2-like 1
ENSG00000197561	1.25E-13	4.70E-11	0.440952604	ELANE	elastase, neutrophil expressed
ENSG00000006611	5.66E-13	1.40E-10	0.208272942	USH1C	Usher syndrome 1C
ENSG00000110436	9.59E-13	2.12E-10	0.065089946	SLC1A2	solute carrier family 1 (glial high affinity glutamate transporter), member 2
ENSG00000280953	4.67E-12	7.32E-10	0.002656927	LINC01163	long intergenic non-protein coding RNA 1163
ENSG00000054179	1.25E-11	1.62E-09	0.195440891	ENTPD2	ectonucleoside triphosphate diphosphohydrolase 2
ENSG00000171303	1.34E-11	1.73E-09	0.24596992	KCNK3	potassium channel, two pore domain subfamily K, member 3
ENSG00000076641	1.84E-11	2.24E-09	0.132919468	PAG1	phosphoprotein membrane anchor with glycosphingolipid microdomains 1
ENSG00000147689	2.42E-11	2.79E-09	0.064864781	FAM83A	family with sequence similarity 83, member A
ENSG00000012504	3.00E-11	3.31E-09	0.20953971	NR1H4	nuclear receptor subfamily 1, group H, member 4
ENSG00000111816	3.16E-11	3.45E-09	0.226073148	FRK	fyn-related Src family tyrosine kinase
ENSG00000009709	3.44E-11	3.69E-09	0.063653179	PAX7	paired box 7
ENSG00000146233	3.55E-11	3.79E-09	0.107643774	CYP39A1	cytochrome P450, family 39, subfamily A, polypeptide 1
ENSG00000159166	3.96E-11	4.12E-09	0.05350551	LAD1	ladinin 1
ENSG00000268104	5.20E-11	5.15E-09	0.098147022	SLC6A14	solute carrier family 6 (amino acid transporter), member 14
ENSG00000173376	8.66E-11	7.94E-09	0.097806228	NDNF	neuron-derived neurotrophic factor
ENSG00000132688	9.11E-11	8.26E-09	0.186738648	NES	nestin
ENSG00000101349	1.08E-10	9.47E-09	0.015844128	PAK7	p21 protein (Cdc42/Rac)-activated kinase 7
ENSG00000144730	1.37E-10	1.16E-08	0.127603252	IL17RD	interleukin 17 receptor D
ENSG00000093134	1.53E-10	1.28E-08	0.073972981	VNN3	vanin 3
ENSG00000115165	1.78E-10	1.45E-08	0.028982316	CYTIP	cytohesin 1 interacting protein
ENSG00000081138	2.00E-10	1.59E-08	0.026287198	CDH7	cadherin 7, type 2
ENSG00000150540	2.54E-10	1.93E-08	0.035629874	HNMT	histamine N-methyltransferase
ENSG00000197872	2.78E-10	2.09E-08	0.133795466	FAM49A	family with sequence similarity 49, member A
ENSG00000173930	3.08E-10	2.28E-08	0.092682326	SLCO4C1	solute carrier organic anion transporter family, member 4C1
ENSG00000120675	3.78E-10	2.72E-08	0.029198016	DNAJC15	DnaJ (Hsp40) homolog, subfamily C, member 15
ENSG00000183023	4.21E-10	2.94E-08	0.041800944	SLC8A1	solute carrier family 8 (sodium/calcium exchanger), member 1
ENSG00000176723	6.63E-10	4.34E-08	0.093998112	ZNF843	zinc finger protein 843
ENSG00000128849	7.86E-10	4.99E-08	0.08825828	CGNL1	cingulin-like 1
ENSG00000183186	8.53E-10	5.32E-08	0.167963444	C2CD4C	C2 calcium-dependent domain containing 4C
ENSG00000229921	8.76E-10	5.41E-08	0.22976696	KIF25-AS1	KIF25 antisense RNA 1
ENSG00000120262	1.55E-09	8.64E-08	0.095003429	CCDC170	coiled-coil domain containing 170
ENSG00000231419	1.64E-09	9.07E-08	0.009646384	LINC00689	long intergenic non-protein coding RNA 689
ENSG00000197558	1.90E-09	1.02E-07	0.046766482	SSPO	SCO-spondin
ENSG00000126882	2.03E-09	1.08E-07	0.105131785	FAM78A	family with sequence similarity 78, member A
ENSG00000158865	2.13E-09	1.12E-07	0.114308565	SLC5A11	solute carrier family 5 (sodium/inositol cotransporter), member 11
ENSG00000154188	2.21E-09	1.15E-07	0.067619717	ANGPT1	angiopoietin 1
ENSG00000170298	2.22E-09	1.15E-07	0.186611131	LGALS9B	lectin, galactoside-binding, soluble, 9B
ENSG00000130829	2.22E-09	1.15E-07	0.228952342	DUSP9	dual specificity phosphatase 9
ENSG00000138639	2.39E-09	1.23E-07	0.111565741	ARHGAP24	Rho GTPase activating protein 24
ENSG00000103449	2.39E-09	1.23E-07	0.052708066	SALL1	spalt-like transcription factor 1
ENSG00000052850	2.66E-09	1.34E-07	0.161446364	ALX4	ALX homeobox 4
ENSG00000101445	3.05E-09	1.49E-07	0.040036826	PPP1R16B	protein phosphatase 1, regulatory subunit 16B
ENSG00000221866	3.18E-09	1.53E-07	0.093542416	PLXNA4	plexin A4
ENSG00000154133	3.49E-09	1.66E-07	0.050290187	ROBO4	roundabout guidance receptor 4
ENSG00000166446	3.51E-09	1.67E-07	0.165073796	CDYL2	chromodomain protein, Y-like 2
ENSG00000235142	3.61E-09	1.71E-07	0.023224838	LOC100422737	uncharacterized LOC100422737
ENSG00000151090	3.82E-09	1.80E-07	0.11069643	THRB	thyroid hormone receptor, beta
ENSG00000169860	4.12E-09	1.91E-07	0.211869667	P2RY1	purinergic receptor P2Y, G-protein coupled, 1
ENSG00000102271	4.23E-09	1.96E-07	0.179099895	KLHL4	kelch-like family member 4
ENSG00000110002	4.89E-09	2.21E-07	0.110708369	VWASA	von Willebrand factor A domain containing 5A
ENSG00000205978	5.34E-09	2.39E-07	0.04622568	NYNRIN	NYN domain and retroviral integrase containing
ENSG00000232810	5.40E-09	2.41E-07	0.134369501	TNF	tumor necrosis factor
ENSG00000176928	5.53E-09	2.46E-07	0.212111259	GCNT4	glucosaminyl (N-acetyl) transferase 4, core 2
ENSG00000164330	5.72E-09	2.52E-07	0.167068951	EBF1	early B-cell factor 1
ENSG00000142700	5.89E-09	2.58E-07	0.104519265	DMRTA2	DMRT-like family A2
ENSG00000169562	7.16E-09	3.05E-07	0.047306033	GJB1	gap junction protein, beta 1, 32kDa
ENSG00000162415	7.34E-09	3.11E-07	0.150024022	ZSWIM5	zinc finger, SWIM-type containing 5
ENSG00000165244	7.42E-09	3.13E-07	0.153338092	ZNF367	zinc finger protein 367
ENSG00000196542	8.59E-09	3.53E-07	0.035944483	SPTSSB	serine palmitoyltransferase, small subunit B

ENSG00000246877	9.19E-09	3.74E-07	0.078532631	DNM1P35	dynamin 1 pseudogene 35
ENSG00000109819	1.07E-08	4.26E-07	0.015622717	PPARGC1A	peroxisome proliferator-activated receptor gamma, coactivator 1 alpha
ENSG00000135333	1.09E-08	4.35E-07	0.055178244	EPHA7	EPH receptor A7
ENSG00000162552	1.15E-08	4.54E-07	0.226192254	WNT4	wingless-type MMTV integration site family, member 4
ENSG00000011465	1.21E-08	4.71E-07	0.020085886	DCN	decorin
ENSG00000100167	1.24E-08	4.82E-07	0.118787323	4Z616	septin 3
ENSG00000189057	1.34E-08	5.13E-07	0.125332331	FAM111B	family with sequence similarity 111, member B
ENSG00000089250	1.47E-08	5.51E-07	0.019301233	NOS1	nitric oxide synthase 1 (neuronal)
ENSG00000178977	1.91E-08	6.79E-07	0.132797173	LINC00324	long intergenic non-protein coding RNA 324
ENSG00000167723	2.01E-08	7.10E-07	0.066635471	TRPV3	transient receptor potential cation channel, subfamily V, member 3
ENSG00000175984	2.02E-08	7.11E-07	0.051013899	DENN2C	DENN/MADD domain containing 2C
ENSG0000079482	2.06E-08	7.22E-07	0.138656556	OPHN1	oligophrenin 1
ENSG00000137507	2.29E-08	7.88E-07	0.07929953	LRRC32	leucine rich repeat containing 32
ENSG00000125780	2.30E-08	7.90E-07	0.053277257	TGM3	transglutaminase 3
ENSG00000237289	2.47E-08	8.40E-07	0.115654904	CKMT1B	creatine kinase, mitochondrial 1B
ENSG00000115461	2.83E-08	9.42E-07	0.08888194	IGFBP5	insulin-like growth factor binding protein 5
ENSG00000168065	3.11E-08	1.02E-06	0.117072418	SLC22A11	solute carrier family 22 (organic anion/urate transporter), member 11
ENSG00000180875	3.42E-08	1.10E-06	0.165832764	GREM2	gremlin 2, DAN family BMP antagonist
ENSG00000182179	3.96E-08	1.25E-06	0.232419832	UBA7	ubiquitin-like modifier activating enzyme 7
ENSG00000172771	4.50E-08	1.39E-06	0.073068742	EFCAB12	EF-hand calcium binding domain 12
ENSG00000108852	4.75E-08	1.46E-06	0.076146079	MPP2	membrane protein, palmitoylated 2 (MAGUK p55 subfamily member 2)
ENSG00000186998	5.10E-08	1.56E-06	0.122825872	EMID1	EMI domain containing 1
ENSG00000135643	5.17E-08	1.57E-06	0.143806596	KCNMB4	potassium channel subfamily M regulatory beta subunit 4
ENSG00000169245	5.21E-08	1.58E-06	0.084800595	CXCL10	chemokine (C-X-C motif) ligand 10
ENSG00000131738	5.74E-08	1.71E-06	0.321625365	KRT33B	keratin 33B, type I
ENSG00000065413	5.76E-08	1.71E-06	0.040579153	ANKRD44	ankyrin repeat domain 44
ENSG00000095596	6.14E-08	1.80E-06	0.18550694	CYP26A1	cytochrome P450, family 26, subfamily A, polypeptide 1
ENSG00000184005	6.20E-08	1.81E-06	0.101332368	ST6GALNAC3	ST6 (alpha-N-acetylneuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 3
ENSG00000160588	6.76E-08	1.95E-06	0.149051734	MPZL3	myelin protein zero-like 3
ENSG00000172995	6.82E-08	1.96E-06	0.022730106	ARPP21	cAMP-regulated phosphoprotein, 21kDa
ENSG00000100346	6.96E-08	2.00E-06	0.042180705	CACNA11	calcium channel, voltage-dependent, T type, alpha 11 subunit
ENSG00000165929	7.03E-08	2.02E-06	0.129943424	TC2N	tandem C2 domains, nuclear
ENSG00000138615	7.28E-08	2.08E-06	0.036953783	CILP	cartilage intermediate layer protein, nucleotide pyrophosphohydrolase
ENSG00000138109	7.46E-08	2.12E-06	0.097664271	CYP2C9	cytochrome P450, family 2, subfamily C, polypeptide 9
ENSG00000066032	7.50E-08	2.13E-06	0.059129411	CTNNA2	catenin (cadherin-associated protein), alpha 2
ENSG00000149256	7.52E-08	2.14E-06	0.011279457	TENM4	teneurin transmembrane protein 4
ENSG00000071991	7.91E-08	2.23E-06	0.036498115	CDH19	cadherin 19, type 2
ENSG00000115590	9.31E-08	2.57E-06	0.068493847	IL1R2	interleukin 1 receptor, type II
ENSG00000128917	1.03E-07	2.81E-06	0.081029982	DLL4	delta-like 4 (Drosophila)
ENSG00000180509	1.15E-07	3.09E-06	0.014806034	KCNE1	potassium channel, voltage gated subfamily E regulatory beta subunit 1
ENSG00000130052	1.17E-07	3.13E-06	0.035852442	STARD8	StAR-related lipid transfer (START) domain containing 8
ENSG00000095303	1.17E-07	3.14E-06	0.050730557	PTGS1	prostaglandin-endoperoxide synthase 1 (prostaglandin G/H synthase and cyclooxygenase)
ENSG00000165887	1.18E-07	3.15E-06	0.22145593	ANKRD2	ankyrin repeat domain 2 (stretch responsive muscle)
ENSG00000269502	1.18E-07	3.16E-06	0.02821564	DMRTC1	DMRT-like family C1
ENSG00000154493	1.20E-07	3.19E-06	0.043789534	C10orf90	chromosome 10 open reading frame 90
ENSG00000152217	1.22E-07	3.24E-06	0.055822129	SETBP1	SET binding protein 1
ENSG00000151150	1.23E-07	3.26E-06	0.019328283	ANK3	ankyrin 3, node of Ranvier (ankyrin G)
ENSG00000245105	1.27E-07	3.34E-06	0.196904486	A2M-AS1	A2M antisense RNA 1 (head to head)
ENSG00000101463	1.37E-07	3.55E-06	0.156371044	SYNDIG1	synapse differentiation inducing 1
ENSG00000124256	1.41E-07	3.66E-06	0.040849488	ZBP1	Z-DNA binding protein 1
ENSG00000171916	1.43E-07	3.70E-06	0.044956043	LGALS9B	lectin, galactoside-binding, soluble, 9B
ENSG00000153822	1.43E-07	3.70E-06	0.073804953	KCNJ16	potassium channel, inwardly rectifying subfamily J, member 16
ENSG00000150471	1.50E-07	3.83E-06	0.027046805	ADGRL3	adhesion G protein-coupled receptor L3
ENSG00000138316	1.51E-07	3.85E-06	0.071280932	ADAMTS14	ADAM metalloproteinase with thrombospondin type 1 motif, 14
ENSG00000064886	1.79E-07	4.46E-06	0.031741628	CHI3L2	chitinase 3-like 2
ENSG00000128268	2.00E-07	4.92E-06	0.042225373	MGAT3	mannosyl (beta-1,4)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase
ENSG00000171872	2.08E-07	5.06E-06	0.045183362	KLF17	Kruppel-like factor 17
ENSG00000047365	2.17E-07	5.25E-06	0.050147639	ARAP2	ArfGAP with RhoGAP domain, ankyrin repeat and PH domain 2
ENSG00000164989	2.50E-07	5.92E-06	0.036084698	CCDC171	coiled-coil domain containing 171
ENSG00000115602	2.68E-07	6.29E-06	0.023788417	IL1RL1	interleukin 1 receptor-like 1
ENSG00000102387	3.00E-07	6.93E-06	0.149503142	TAF7L	TAF7-like RNA polymerase II, TATA box binding protein (TBP)-associated factor, 50kDa
ENSG00000183508	3.13E-07	7.16E-06	0.084237226	FAM46C	family with sequence similarity 46, member C
ENSG00000008277	3.14E-07	7.17E-06	0.05399062	ADAM22	ADAM metalloproteinase domain 22
ENSG00000164418	3.50E-07	7.89E-06	0.076518642	GRIK2	glutamate receptor, ionotropic, kainate 2
ENSG00000196605	3.68E-07	8.20E-06	0.120632891	ZNF846	

ENSG00000147614	3.74E-07	8.31E-06	0.094383174	ATP6V0D2	ATPase, H+ transporting, lysosomal 38kDa, V0 subunit d2
ENSG00000117148	3.80E-07	8.44E-06	0.238090834	ACTL8	actin-like 8
ENSG00000253882	3.83E-07	8.50E-06	0.10106545	LOC154761	family with sequence similarity 115, member C pseudogene
ENSG00000121743	3.91E-07	8.64E-06	0.071218613	GJA3	gap junction protein, alpha 3, 46kDa
ENSG00000127152	3.93E-07	8.69E-06	0.113923721	BCL11B	B-cell CLL/lymphoma 11B (zinc finger protein)
ENSG00000206585	3.98E-07	8.76E-06	0.276472029	RNVU1-7	RNA, variant U1 small nuclear 7
ENSG00000152128	4.17E-07	9.12E-06	0.030906507	TMEM163	transmembrane protein 163
ENSG00000133135	4.48E-07	9.68E-06	0.06726596	RNF128	ring finger protein 128, E3 ubiquitin protein ligase
ENSG00000163207	4.74E-07	1.02E-05	0.089845948	IVL	involucrin
ENSG00000197110	5.33E-07	1.12E-05	0.112718262	IFNL3	interferon, lambda 3
ENSG00000144481	5.62E-07	1.17E-05	0.02056143	TRPM8	transient receptor potential cation channel, subfamily M, member 8
ENSG00000160716	5.66E-07	1.18E-05	0.098538754	CHRNB2	cholinergic receptor, nicotinic, beta 2 (neuronal)
ENSG00000073737	5.66E-07	1.18E-05	0.079247094	DHRS9	dehydrogenase/reductase (SDR family) member 9
ENSG00000100968	5.80E-07	1.20E-05	0.020828291	NFATC4	nuclear factor of activated T-cells, cytoplasmic, calcineurin-dependent 4
ENSG00000187688	5.94E-07	1.23E-05	0.132031024	TRPV2	transient receptor potential cation channel, subfamily V, member 2
ENSG00000168918	5.99E-07	1.24E-05	0.067498765	INPP5D	inositol polyphosphate-5-phosphatase D
ENSG00000159588	6.07E-07	1.25E-05	0.201176655	CCDC17	coiled-coil domain containing 17
ENSG00000143355	6.14E-07	1.26E-05	0.044999735	LHX9	LIM homeobox 9
ENSG00000170153	6.28E-07	1.29E-05	0.071777776	RNF150	ring finger protein 150
ENSG00000140451	6.49E-07	1.32E-05	0.166137096	PIF1	PIF1 5'-to-3' DNA helicase
ENSG00000091428	6.57E-07	1.33E-05	0.023914083	RAPGEF4	Rap guanine nucleotide exchange factor (GEF) 4
ENSG00000165923	6.65E-07	1.35E-05	0.138496451	AGBL2	ATP/GTP binding protein-like 2
ENSG00000106560	6.68E-07	1.35E-05	0.0858168	GIMAP2	GTPase, IMAP family member 2
ENSG00000106789	6.82E-07	1.38E-05	0.167731389	CORO2A	coronin, actin binding protein, 2A
ENSG00000184911	7.01E-07	1.41E-05	0.033215985	DMRTC1B	DMRT-like family C1B
ENSG00000186226	7.77E-07	1.54E-05	0.089851216	LCE1E	late cornified envelope 1E
ENSG00000164488	7.78E-07	1.54E-05	0.068147986	DACT2	dishevelled-binding antagonist of beta-catenin 2
ENSG00000080573	7.91E-07	1.57E-05	0.171341853	COL5A3	collagen, type V, alpha 3
ENSG00000236366	8.21E-07	1.61E-05	0.032584373	LOC153910	uncharacterized LOC153910
ENSG00000173077	8.23E-07	1.62E-05	0.06695456	42705	deleted in esophageal cancer 1
ENSG00000197748	8.28E-07	1.62E-05	0.040599622	CFAP43	cilia and flagella associated protein 43
ENSG00000236714	8.76E-07	1.70E-05	0.039804612	LOC101926975	uncharacterized LOC101926975
ENSG00000180730	8.79E-07	1.70E-05	0.062563456	SHISA2	shisa family member 2
ENSG00000269313	8.94E-07	1.73E-05	0.048513232	MAGIX	MAGI family member, X-linked
ENSG00000106689	9.19E-07	1.76E-05	0.123843133	LHX2	LIM homeobox 2
ENSG00000006747	9.29E-07	1.78E-05	0.018209122	SCIN	scinderin
ENSG00000159625	9.44E-07	1.80E-05	0.027282401	DRC7	dynein regulatory complex subunit 7
ENSG00000184675	1.00E-06	1.89E-05	0.105095581	AMER1	APC membrane recruitment protein 1
ENSG00000148735	1.11E-06	2.06E-05	0.014632719	PLEKHS1	pleckstrin homology domain containing, family S member 1
ENSG00000227640	1.15E-06	2.11E-05	0.063614951	SOX21-AS1	SOX21 antisense RNA 1 (head to head)
ENSG00000213417	1.18E-06	2.17E-05	0.102830885	KRTAP2-4	keratin associated protein 2-4
ENSG00000134317	1.29E-06	2.35E-05	0.039266323	GRHL1	grainyhead-like transcription factor 1
ENSG00000138606	1.32E-06	2.39E-05	0.145639577	SHF	Src homology 2 domain containing F
ENSG00000114251	1.33E-06	2.40E-05	0.090846815	WNT5A	wingless-type MMTV integration site family, member 5A
ENSG00000189275	1.37E-06	2.47E-05	0.05965797	LINC01164	long intergenic non-protein coding RNA 1164
ENSG00000153012	1.38E-06	2.48E-05	0.021615986	LG12	leucine-rich repeat LGI family, member 2
ENSG00000064300	1.44E-06	2.58E-05	0.143348169	NGFR	nerve growth factor receptor
ENSG00000006210	1.44E-06	2.58E-05	0.058222973	CX3CL1	chemokine (C-X3-C motif) ligand 1
ENSG00000227258	1.45E-06	2.59E-05	0.199902224	SMIM2-AS1	SMIM2 antisense RNA 1
ENSG00000256340	1.48E-06	2.64E-05	0.056400924	ABCC6P1	ATP-binding cassette, sub-family C, member 6 pseudogene 1 (functional)
ENSG00000183908	1.55E-06	2.74E-05	0.015440176	LRRC55	leucine rich repeat containing 55
ENSG00000133106	1.55E-06	2.75E-05	0.095805356	EPST11	epithelial stromal interaction 1 (breast)
ENSG00000099985	1.56E-06	2.76E-05	0.065183663	OSM	oncostatin M
ENSG00000068831	1.59E-06	2.81E-05	0.073148324	RASGRP2	RAS guanyl releasing protein 2 (calcium and DAG-regulated)
ENSG00000204291	1.63E-06	2.86E-05	0.098030201	COL15A1	collagen, type XV, alpha 1
ENSG00000112379	1.71E-06	2.98E-05	0.070888309	ARFGEF3	ARFGEF family member 3
ENSG00000235750	1.72E-06	2.99E-05	0.030906426	KIAA0040	KIAA0040
ENSG00000179914	1.83E-06	3.15E-05	0.047613294	ITLN1	intelectin 1 (galactofuranose binding)
ENSG00000137812	1.83E-06	3.16E-05	0.071181925	CASC5	cancer susceptibility candidate 5
ENSG00000224805	1.89E-06	3.25E-05	0.246738241	LINC00853	long intergenic non-protein coding RNA 853
ENSG00000050438	1.90E-06	3.26E-05	0.020141897	SLC4A8	solute carrier family 4, sodium bicarbonate cotransporter, member 8
ENSG00000148702	1.93E-06	3.30E-05	0.182440554	HABP2	hyaluronan binding protein 2
ENSG00000085552	1.94E-06	3.32E-05	0.04143977	IGSF9	immunoglobulin superfamily, member 9
ENSG00000056487	2.02E-06	3.43E-05	0.070205525	PHF21B	PHD finger protein 21B
ENSG00000117016	2.13E-06	3.58E-05	0.103263899	RIMS3	regulating synaptic membrane exocytosis 3

ENSG00000131477	2.17E-06	3.64E-05	0.102531231	RAMP2	receptor (G protein-coupled) activity modifying protein 2
ENSG00000164684	2.22E-06	3.71E-05	0.020009506	ZNF704	zinc finger protein 704
ENSG00000141854	2.25E-06	3.75E-05	0.408513544	LOC113230	uncharacterized protein LOC113230
ENSG00000273706	2.29E-06	3.81E-05	0.106194794	LHX1	LIM homeobox 1
ENSG00000137752	2.40E-06	3.97E-05	0.068219387	CASP1	caspase 1, apoptosis-related cysteine peptidase
ENSG00000185304	2.48E-06	4.08E-05	0.032587647	RGPD2	RANBP2-like and GRIP domain containing 2
ENSG00000176533	2.50E-06	4.11E-05	0.048193713	GNG7	guanine nucleotide binding protein (G protein), gamma 7
ENSG00000140937	2.52E-06	4.13E-05	0.042013239	CDH11	cadherin 11, type 2, OB-cadherin (osteoblast)
ENSG00000007968	2.53E-06	4.15E-05	0.050208149	E2F2	E2F transcription factor 2
ENSG00000078725	2.60E-06	4.26E-05	0.074582965	BRINP1	bone morphogenetic protein/retinoic acid inducible neural-specific 1
ENSG00000149212	2.61E-06	4.27E-05	0.050217149	SESN3	sestrin 3
ENSG00000184731	2.85E-06	4.61E-05	0.053872996	FAM110C	family with sequence similarity 110, member C
ENSG00000135378	2.87E-06	4.63E-05	0.056928072	PRRG4	proline rich Gla (G-carboxyglutamic acid) 4 (transmembrane)
ENSG00000112303	3.10E-06	4.94E-05	0.150875828	VNN2	vanin 2
ENSG00000144410	3.15E-06	5.00E-05	0.057032428	CPO	carboxypeptidase O
ENSG00000188994	3.39E-06	5.35E-05	0.092890696	ZNF292	zinc finger protein 292
ENSG00000182459	3.50E-06	5.48E-05	0.058783305	TEX19	testis expressed 19
ENSG00000135472	3.61E-06	5.63E-05	0.017195783	FAIM2	Fas apoptotic inhibitory molecule 2
ENSG00000160013	3.64E-06	5.67E-05	0.03716578	PTGIR	prostaglandin I2 (prostacyclin) receptor (IP)
ENSG00000054938	3.71E-06	5.76E-05	0.112365187	CHRD2	chordin-like 2
ENSG00000108771	3.86E-06	5.96E-05	0.066027249	DHX58	DEXH (Asp-Glu-X-His) box polypeptide 58
ENSG00000224259	3.89E-06	6.00E-05	0.061270141	LINC01133	long intergenic non-protein coding RNA 1133
ENSG00000136869	3.90E-06	6.01E-05	0.035327488	TLR4	toll-like receptor 4
ENSG00000154330	4.05E-06	6.19E-05	0.021622744	PGM5	phosphoglucomutase 5
ENSG00000127129	4.06E-06	6.20E-05	0.201719539	EDN2	endothelin 2
ENSG00000137460	4.23E-06	6.43E-05	0.137146543	FHDC1	FH2 domain containing 1
ENSG00000155307	4.33E-06	6.56E-05	0.014797565	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1
ENSG00000176204	4.47E-06	6.72E-05	0.010347376	LRRTM4	leucine rich repeat transmembrane neuronal 4
ENSG00000121903	4.48E-06	6.73E-05	0.108815649	ZSCAN20	zinc finger and SCAN domain containing 20
ENSG00000120156	4.73E-06	7.06E-05	0.038824669	TEK	TEK tyrosine kinase, endothelial
ENSG00000137265	4.78E-06	7.12E-05	0.016725978	IRF4	interferon regulatory factor 4
ENSG00000133101	5.01E-06	7.40E-05	0.085139483	CCNA1	cyclin A1
ENSG00000120693	5.24E-06	7.69E-05	0.085292362	SMAD9	SMAD family member 9
ENSG00000042980	5.29E-06	7.75E-05	0.030215273	ADAM28	ADAM metallopeptidase domain 28
ENSG00000165730	5.31E-06	7.78E-05	0.087499878	STOX1	storkhead box 1
ENSG00000117707	5.32E-06	7.78E-05	0.042723013	PROX1	prospero homeobox 1
ENSG00000139200	5.53E-06	8.07E-05	0.091352784	PIANP	PILR alpha associated neural protein
ENSG00000172296	5.91E-06	8.56E-05	0.030635142	SPTLC3	serine palmitoyltransferase, long chain base subunit 3
ENSG00000185742	6.10E-06	8.81E-05	0.049902017	C11orf87	chromosome 11 open reading frame 87
ENSG00000106018	6.12E-06	8.83E-05	0.004859246	VIPR2	vasoactive intestinal peptide receptor 2
ENSG00000275713	6.34E-06	9.08E-05	0.062735822	HIST1H2BH	histone cluster 1, H2bh
ENSG00000237803	6.38E-06	9.13E-05	0.007023858	LINC00211	long intergenic non-protein coding RNA 211
ENSG00000230747	6.53E-06	9.30E-05	0.037069116	LOC105373495	uncharacterized LOC105373495
ENSG00000214691	6.82E-06	9.65E-05	0.021088538	LOC388942	uncharacterized LOC388942
ENSG00000116141	6.87E-06	9.72E-05	0.066332004	MARK1	MAP/microtubule affinity-regulating kinase 1
ENSG00000186517	6.93E-06	9.78E-05	0.10680614	ARHGAP30	Rho GTPase activating protein 30
ENSG00000135925	6.98E-06	9.85E-05	0.024297081	WNT10A	wingless-type MMTV integration site family, member 10A
ENSG00000117115	7.07E-06	9.96E-05	0.064414991	PADI2	peptidyl arginine deiminase, type II
ENSG00000198483	7.49E-06	0.000104616	0.024850883	ANKRD35	ankyrin repeat domain 35
ENSG00000109758	7.65E-06	0.00010629	0.138494928	HGFAC	HGF activator
ENSG00000130700	7.76E-06	0.000107634	0.072248613	GATA5	GATA binding protein 5
ENSG00000146267	7.91E-06	0.000109394	0.058043677	FAXC	failed axon connections homolog
ENSG00000178033	8.61E-06	0.000118174	0.028323922	FAM26E	family with sequence similarity 26, member E
ENSG00000277363	8.65E-06	0.00011858	0.084881979	SRCIN1	SRC kinase signaling inhibitor 1
ENSG00000276600	8.70E-06	0.000119193	0.08507578	RAB7B	RAB7B, member RAS oncogene family
ENSG00000111249	8.73E-06	0.000119399	0.03864879	CUX2	cut-like homeobox 2
ENSG00000137941	8.97E-06	0.000122194	0.100119372	TTL7	tubulin tyrosine ligase-like family member 7
ENSG00000048740	9.00E-06	0.000122625	0.020137218	CELF2	CUGBP, Elav-like family member 2
ENSG00000070526	9.16E-06	0.000124392	0.025783482	ST6GALNAC1	ST6 (alpha-N-acetyl-neuraminyl-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 1
ENSG00000188825	9.25E-06	0.000125517	0.087160521	LINC00910	long intergenic non-protein coding RNA 910
ENSG00000108242	9.41E-06	0.000127449	0.021116908	CYP2C18	cytochrome P450, family 2, subfamily C, polypeptide 18
ENSG00000009950	9.49E-06	0.000128432	0.165685626	MLXIPL	MLX interacting protein-like
ENSG00000096006	9.51E-06	0.000128551	0.12383872	CRISP3	cysteine-rich secretory protein 3
ENSG00000139445	9.83E-06	0.00013211	0.03075152	FOXN4	forkhead box N4
ENSG00000275869	1.01E-05	0.000135328	0.086367451	LOC102723655	TP53-target gene 3 protein

ENSG00000203867	1.03E-05	0.000137792	0.097740451	RBM20	RNA binding motif protein 20
ENSG00000257588	1.03E-05	0.000138306	0.067439057	LOC101927318	uncharacterized LOC101927318
ENSG00000168702	1.05E-05	0.000139465	0.015727346	LRP1B	low density lipoprotein receptor-related protein 1B
ENSG00000178235	1.05E-05	0.000140201	0.018307279	SLITRK1	SLIT and NTRK-like family, member 1
ENSG00000179363	1.06E-05	0.000140549	0.089507813	TMEM31	transmembrane protein 31
ENSG00000144821	1.08E-05	0.000143575	0.071684922	MYH15	myosin, heavy chain 15
ENSG00000142619	1.10E-05	0.000146292	0.088870644	PADI3	peptidyl arginine deiminase, type III
ENSG00000139547	1.10E-05	0.000146318	0.101289901	RDH16	retinol dehydrogenase 16 (all-trans)
ENSG00000132465	1.10E-05	0.000146318	0.051480846	JCHAIN	joining chain of multimeric IgA and IgM
ENSG00000231574	1.14E-05	0.000150688	0.030943323	KCCAT211	renal clear cell carcinoma-associated transcript 211
ENSG00000196353	1.17E-05	0.000154163	0.125699703	CPNE4	copine IV
ENSG00000150628	1.19E-05	0.000155803	0.14676851	SPATA4	spermatogenesis associated 4
ENSG00000099725	1.20E-05	0.000156307	0.033017004	PRKY	protein kinase, Y-linked, pseudogene
ENSG00000147697	1.21E-05	0.000157932	0.05710624	GSDMC	gasdermin C
ENSG00000142149	1.22E-05	0.000158402	0.047214969	HUNK	hormonally up-regulated Neu-associated kinase
ENSG00000187492	1.28E-05	0.000165757	0.072962486	CDHR4	cadherin-related family member 4
ENSG00000162733	1.39E-05	0.00017755	0.047605098	DDR2	discoidin domain receptor tyrosine kinase 2
ENSG00000246922	1.39E-05	0.00017755	0.107744418	UBAP1L	ubiquitin associated protein 1-like
ENSG00000135338	1.43E-05	0.000182095	0.114420133	LCA5	Leber congenital amaurosis 5
ENSG00000104413	1.47E-05	0.000186483	0.055115393	ESRP1	epithelial splicing regulatory protein 1
ENSG00000106178	1.50E-05	0.000189519	0.122219405	CCL24	chemokine (C-C motif) ligand 24
ENSG000002028137	1.51E-05	0.000191009	0.034667648	TNFRSF1B	tumor necrosis factor receptor superfamily, member 1B
ENSG00000189420	1.57E-05	0.000197536	0.068571509	ZFP92	ZFP92 zinc finger protein
ENSG00000261115	1.59E-05	0.000199727	0.066382112	TMEM178B	transmembrane protein 178B
ENSG00000102174	1.60E-05	0.000200934	0.087113732	PHEX	phosphate regulating endopeptidase homolog, X-linked
ENSG00000185015	1.61E-05	0.000201438	0.057028747	CA13	carbonic anhydrase XIII
ENSG00000136928	1.61E-05	0.000202058	0.026479436	GABBR2	gamma-aminobutyric acid (GABA) B receptor, 2
ENSG00000174951	1.66E-05	0.000207807	0.112983581	FUT1	fucosyltransferase 1 (galactoside 2-alpha-L-fucosyltransferase, H blood group)
ENSG00000251381	1.68E-05	0.000209864	0.022677882	LINC00958	long intergenic non-protein coding RNA 958
ENSG00000272636	1.72E-05	0.000213288	0.047542843	DOC2B	double C2-like domains, beta
ENSG00000123977	1.78E-05	0.000220693	0.059578165	DAW1	dynein assembly factor with WDR repeat domains 1
ENSG00000188921	1.79E-05	0.000220844	0.07168551	HACD4	3-hydroxyacyl-CoA dehydratase 4
ENSG00000125337	1.82E-05	0.000223973	0.169443497	KIF25	kinesin family member 25
ENSG00000182836	1.82E-05	0.000224866	0.021235718	PLCXD3	phosphatidylinositol-specific phospholipase C, X domain containing 3
ENSG00000007062	1.85E-05	0.000227979	0.017688345	PROM1	prominin 1
ENSG00000121005	1.92E-05	0.000234658	0.067641024	CRISPLD1	cysteine-rich secretory protein LCCL domain containing 1
ENSG00000071073	1.93E-05	0.000236077	0.078933929	MGAT4A	mannosyl (alpha-1,3-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase, isozyme A
ENSG00000123843	1.95E-05	0.000238101	0.088966899	C4BPB	complement component 4 binding protein, beta
ENSG00000196620	1.95E-05	0.000238332	0.103252581	UGT2B15	UDP glucuronosyltransferase 2 family, polypeptide B15
ENSG00000198734	1.95E-05	0.000238456	0.044920881	F5	coagulation factor V (proaccelerin, labile factor)
ENSG00000158220	1.97E-05	0.000240483	0.028531048	ESY3	extended synaptotagmin-like protein 3
ENSG00000163501	2.00E-05	0.00024337	0.053170608	IIHH	indian hedgehog
ENSG00000117069	2.05E-05	0.00024812	0.019107819	ST6GALNAC5	ST6 (alpha-N-acetyl-neuraminy-2,3-beta-galactosyl-1,3)-N-acetylgalactosaminide alpha-2,6-sialyltransferase 5
ENSG00000142583	2.07E-05	0.000250105	0.021302075	SLC2A5	solute carrier family 2 (facilitated glucose/fructose transporter), member 5
ENSG00000111199	2.13E-05	0.000255902	0.03595225	TRPV4	transient receptor potential cation channel, subfamily V, member 4
ENSG00000166341	2.13E-05	0.000255992	0.019894068	DCHS1	dachsous cadherin-related 1
ENSG00000086696	2.22E-05	0.000264855	0.008350724	HSD17B2	hydroxysteroid (17-beta) dehydrogenase 2
ENSG00000062038	2.22E-05	0.000265558	0.036809525	CDH3	cadherin 3, type 1, P-cadherin (placental)
ENSG00000069188	2.28E-05	0.000271126	0.044982042	SDK2	sidekick cell adhesion molecule 2
ENSG00000186648	2.33E-05	0.000276677	0.049766156	LRRC16B	leucine rich repeat containing 16B
ENSG00000171051	2.37E-05	0.000280431	0.174814036	FPR1	formyl peptide receptor 1
ENSG00000243137	2.39E-05	0.00028265	0.067327797	PSG4	pregnancy specific beta-1-glycoprotein 4
ENSG00000122420	2.47E-05	0.000290264	0.033507523	PTGFR	prostaglandin F receptor (FP)
ENSG00000258867	2.50E-05	0.000292281	0.013281141	LINC01146	long intergenic non-protein coding RNA 1146
ENSG00000015520	2.55E-05	0.000297022	0.021128833	NPC1L1	NPC1-like 1
ENSG00000129244	2.56E-05	0.000297467	0.03504848	ATP1B2	ATPase, Na ⁺ /K ⁺ transporting, beta 2 polypeptide
ENSG00000172985	2.62E-05	0.000304113	0.057428523	SH3RF3	SH3 domain containing ring finger 3
ENSG00000175048	2.64E-05	0.000305229	0.204086181	ZDHHC14	zinc finger, DHHC-type containing 14
ENSG00000182308	2.71E-05	0.000312645	0.125037881	DCAF4L1	DDb1 and CUL4 associated factor 4-like 1
ENSG00000188897	2.80E-05	0.000321651	0.015345622	LOC400499	uncharacterized LOC400499
ENSG00000163884	2.81E-05	0.000322639	0.052258569	KLF15	Kruppel-like factor 15
ENSG00000168135	2.89E-05	0.000330344	0.076019599	KCNJ4	potassium channel, inwardly rectifying subfamily J, member 4
ENSG00000143603	2.93E-05	0.000333911	0.009850026	KCNN3	potassium channel, calcium activated intermediate/small conductance subfamily N alpha, member 3
ENSG00000231528	3.03E-05	0.000343995	0.013544861	FAM225A	family with sequence similarity 225, member A (non-protein coding)
ENSG00000215246	3.06E-05	0.000347435	0.020402201	LOC100506688	uncharacterized LOC100506688

ENSG00000183709	3.11E-05	0.000351985	0.12402046	IFNL2	interferon, lambda 2
ENSG00000107954	3.11E-05	0.000352542	0.088354258	NEURL1	neutralized E3 ubiquitin protein ligase 1
ENSG00000169247	3.15E-05	0.000356079	0.016308375	SH3TC2	SH3 domain and tetratricopeptide repeats 2
ENSG00000131203	3.20E-05	0.000361571	0.052982136	IDO1	indoleamine 2,3-dioxygenase 1
ENSG00000115232	3.24E-05	0.000364649	0.034673104	ITGA4	integrin, alpha 4 (antigen CD49D; alpha 4 subunit of VLA-4 receptor)
ENSG00000255571	3.31E-05	0.000371728	0.032556138	LINC00925	long intergenic non-protein coding RNA 925
ENSG00000165807	3.32E-05	0.000373126	0.053876792	PPP1R36	protein phosphatase 1, regulatory subunit 36
ENSG00000234928	3.32E-05	0.000373395	0.046132633	LOC101929374	uncharacterized LOC101929374
ENSG00000088726	3.33E-05	0.000373893	0.061593644	TMEM40	transmembrane protein 40
ENSG00000133317	3.33E-05	0.000373893	0.024704307	LGALS12	lectin, galactoside-binding, soluble, 12
ENSG00000106772	3.35E-05	0.00037564	0.016507005	PRUNE2	prune homolog 2 (Drosophila)
ENSG00000197943	3.37E-05	0.000377133	0.077108706	PLCG2	phospholipase C, gamma 2 (phosphatidylinositol-specific)
ENSG00000171033	3.44E-05	0.000383545	0.033279477	PKIA	protein kinase (cAMP-dependent, catalytic) inhibitor alpha
ENSG00000134917	3.57E-05	0.000396649	0.05134043	ADAMTS8	ADAM metalloproteinase with thrombospondin type 1 motif, 8
ENSG00000198336	3.66E-05	0.000406072	0.020082892	MYL4	myosin, light chain 4, alkali; atrial, embryonic
ENSG00000050555	3.83E-05	0.000422474	0.122660765	LAMC3	laminin, gamma 3
ENSG00000080224	3.84E-05	0.000423641	0.035475628	EPHA6	EPH receptor A6
ENSG00000138771	3.91E-05	0.000430053	0.043326026	SHROOM3	shroom family member 3
ENSG00000127324	3.92E-05	0.000431085	0.086158304	TSPAN8	tetraspanin 8
ENSG00000251158	4.00E-05	0.000438642	0.031497895	LOC101929573	putative POM121-like protein 1-like
ENSG00000135144	4.27E-05	0.000463634	0.067447162	DTX1	deltex 1, E3 ubiquitin ligase
ENSG00000116785	4.43E-05	0.000478298	0.085862383	CFHR3	complement factor H-related 3
ENSG00000198848	4.45E-05	0.000479695	0.044701211	CES1	carboxylesterase 1
ENSG00000149527	4.48E-05	0.000481999	0.019453367	PLCH2	phospholipase C, eta 2
ENSG00000109943	4.51E-05	0.000484474	0.045317144	CRTAM	cytotoxic and regulatory T cell molecule
ENSG00000184838	4.54E-05	0.000487713	0.056997455	PRR16	proline rich 16
ENSG00000144218	4.57E-05	0.000490243	0.02082777	AFF3	AF4/FMR2 family, member 3
ENSG00000125804	4.62E-05	0.000494911	0.02378819	FAM182A	family with sequence similarity 182, member A
ENSG00000129159	4.63E-05	0.000495585	0.007350271	KCNK1	potassium channel, voltage gated Shaw related subfamily C, member 1
ENSG00000171786	4.75E-05	0.000505723	0.133024093	NHLH1	nescent helix loop helix 1
ENSG00000171388	4.75E-05	0.000505975	0.046970049	APLN	apelin
ENSG00000182256	4.79E-05	0.000509386	0.01141726	GABRG3	gamma-aminobutyric acid (GABA) A receptor, gamma 3
ENSG00000163121	5.00E-05	0.00052847	0.081936195	NEURL3	neutralized E3 ubiquitin protein ligase 3
ENSG00000143278	5.18E-05	0.000545355	0.047969089	F13B	coagulation factor XIII, B polypeptide
ENSG00000101331	5.20E-05	0.000546536	0.082498648	CCM2L	cerebral cavernous malformation 2-like
ENSG00000276203	5.40E-05	0.000565904	0.0120131	ANKRD20A3	ankyrin repeat domain 20 family, member A3
ENSG00000127311	5.52E-05	0.000576855	0.083810861	HELB	helicase (DNA) B
ENSG00000114378	5.55E-05	0.000579661	0.051204642	HYAL1	hyaluronoglucosaminidase 1
ENSG00000134817	5.58E-05	0.000582124	0.244918594	APLNR	apelin receptor
ENSG00000135447	5.61E-05	0.000585205	0.022714994	PPP1R1A	protein phosphatase 1, regulatory (inhibitor) subunit 1A
ENSG00000215644	5.66E-05	0.000588966	0.039193465	GCGR	glucagon receptor
ENSG00000164362	5.72E-05	0.000594645	0.047033169	TERT	telomerase reverse transcriptase
ENSG00000166473	5.73E-05	0.000594832	0.044710401	PKD1L2	polycystic kidney disease 1-like 2 (gene/pseudogene)
ENSG00000060566	5.77E-05	0.000598783	0.027031749	CREB3L3	cAMP responsive element binding protein 3-like 3
ENSG00000138271	5.86E-05	0.000606938	0.138503045	GPR87	G protein-coupled receptor 87
ENSG00000066405	5.92E-05	0.000612028	0.011624731	CLDN18	claudin 18
ENSG00000100298	5.96E-05	0.000615612	0.203690321	APOBEC3H	apolipoprotein B mRNA editing enzyme, catalytic polypeptide-like 3H
ENSG00000159618	6.00E-05	0.000619794	0.01456013	ADGRG5	adhesion G protein-coupled receptor G5
ENSG00000147168	6.01E-05	0.000620986	0.056143963	IL2RG	interleukin 2 receptor, gamma
ENSG00000115616	6.19E-05	0.000636334	0.089112895	SLC9A2	solute carrier family 9, subfamily A (NHE2, cation proton antiporter 2), member 2
ENSG00000127252	6.22E-05	0.000638788	0.160729858	HRASL5	HRAS-like suppressor
ENSG00000167037	6.29E-05	0.000645663	0.037874639	SGSM1	small G protein signaling modulator 1
ENSG00000132554	6.39E-05	0.000654431	0.03378146	RGS22	regulator of G-protein signaling 22
ENSG00000182557	6.42E-05	0.000657101	0.047152231	SPNS3	spinster homolog 3 (Drosophila)
ENSG00000169435	6.43E-05	0.000658379	0.143164869	RASSF6	Ras association (RalGDS/AF-6) domain family member 6
ENSG00000092470	6.44E-05	0.000659134	0.160327749	WDR76	WD repeat domain 76
ENSG00000184828	6.60E-05	0.000673701	0.013742592	ZBTB7C	zinc finger and BTB domain containing 7C
ENSG00000178226	6.82E-05	0.000692576	0.063960689	PRSS36	protease, serine, 36
ENSG00000151490	6.85E-05	0.000695447	0.049830863	PTPRO	protein tyrosine phosphatase, receptor type, O
ENSG00000154451	6.90E-05	0.000698794	0.008693324	GBP5	guanylate binding protein 5
ENSG00000175697	7.24E-05	0.000727303	0.034459241	GPR156	G protein-coupled receptor 156
ENSG00000124935	7.72E-05	0.000768186	0.100160496	SCGB1D2	secretoglobin, family 1D, member 2
ENSG00000277893	7.73E-05	0.000768969	0.038327934	SRDSA2	steroid-5-alpha-reductase, alpha polypeptide 2 (3-oxo-5 alpha-steroid delta 4-dehydrogenase alpha 2)
ENSG00000160145	7.74E-05	0.000769165	0.020264981	KALRN	kalirin, RhoGEF kinase
ENSG00000250075	7.75E-05	0.000769561	0.03995397	LOC101927237	uncharacterized LOC101927237

ENSG00000126759	7.88E-05	0.000781453	0.102089799	CFP	complement factor properdin
ENSG00000064835	7.89E-05	0.000782554	0.043361136	POU1F1	POU class 1 homeobox 1
ENSG00000237330	7.99E-05	0.000790496	0.03235186	RNF223	ring finger protein 223
ENSG00000182040	8.01E-05	0.000791854	0.015712369	USH1G	Usher syndrome 1G (autosomal recessive)
ENSG00000257838	8.09E-05	0.000799581	0.053265169	LOC653786	otoancorin pseudogene
ENSG00000130940	8.15E-05	0.000804549	0.035168149	CASZ1	castor zinc finger 1
ENSG00000134830	8.22E-05	0.000810641	0.027860472	CSAR2	complement component 5a receptor 2
ENSG00000102524	8.37E-05	0.000823778	0.179843278	TNFSF13B	tumor necrosis factor (ligand) superfamily, member 13b
ENSG00000160161	8.37E-05	0.000824187	0.116653851	CILP2	cartilage intermediate layer protein 2
ENSG00000153002	8.48E-05	0.00083331	0.005131472	CPB1	carboxypeptidase B1 (tissue)
ENSG00000105549	8.59E-05	0.000841937	0.031113177	THEG	theg spermatid protein
ENSG00000205403	8.72E-05	0.000854393	0.095518865	CFI	complement factor I
ENSG00000149548	8.91E-05	0.000870002	0.064235816	CCDC15	coiled-coil domain containing 15
ENSG00000274600	8.95E-05	0.00087331	0.086110751	RIMBP3B	RIMS binding protein 3B
ENSG00000102970	9.15E-05	0.000891163	0.075153791	CCL17	chemokine (C-C motif) ligand 17
ENSG00000171236	9.23E-05	0.00089698	0.031404021	LRG1	leucine-rich alpha-2-glycoprotein 1
ENSG00000185432	9.39E-05	0.000909501	0.0205311	METTL7A	methyltransferase like 7A
ENSG00000119547	9.47E-05	0.000915791	0.049562537	ONECUT2	one cut homeobox 2
ENSG00000186510	9.50E-05	0.000918238	0.026102078	CLCNKA	chloride channel, voltage-sensitive Ka
ENSG00000254703	9.69E-05	0.000934939	0.067757277	SENCR	smooth muscle and endothelial cell enriched migration/differentiation-associated long non-coding RNA
ENSG00000180229	9.89E-05	0.000951702	0.106749211	HERC2P3	hct domain and RLD 2 pseudogene 3
ENSG00000160870	9.95E-05	0.000955818	0.041281854	CYP3A7	cytochrome P450, family 3, subfamily A, polypeptide 7
ENSG00000183128	0.000100383	0.000963554	0.081441009	CALHM3	calcium homeostasis modulator 3
ENSG00000143546	0.00010272	0.000982511	0.019393078	S100A8	S100 calcium binding protein A8
ENSG00000135116	0.000103548	0.00098997	0.255372846	HRK	harakiri, BCL2 interacting protein
ENSG00000255398	0.000105023	0.001001955	0.05658719	HCAR3	hydroxycarboxylic acid receptor 3
ENSG00000156886	0.000105954	0.001009414	0.01481011	ITGAD	integrin, alpha D
ENSG00000133083	0.000107365	0.001019513	0.038425871	DCLK1	doublecortin-like kinase 1
ENSG00000233705	0.000107778	0.00102201	0.014248075	SLC26A4-AS1	SLC26A4 antisense RNA 1
ENSG00000076258	0.000109541	0.001035589	0.098770391	FMO4	flavin containing monooxygenase 4
ENSG00000165071	0.000110369	0.001042449	0.059614177	TMEM71	transmembrane protein 71
ENSG00000149922	0.000112273	0.001057001	0.11419932	TBX6	T-box 6
ENSG00000138083	0.00011347	0.001066097	0.051685301	SIX3	SIX homeobox 3
ENSG00000069431	0.000114133	0.001070797	0.014546693	ABCC9	ATP-binding cassette, sub-family C (CFTR/MRP), member 9
ENSG00000113494	0.000115154	0.001078636	0.007233556	PRLR	prolactin receptor
ENSG00000118620	0.000116008	0.001085673	0.070938269	ZNF430	zinc finger protein 430
ENSG00000166143	0.000116475	0.001088761	0.252755202	PPP1R14D	protein phosphatase 1, regulatory (inhibitor) subunit 14D
ENSG00000141574	0.000118292	0.001103209	0.041335294	SECTM1	secreted and transmembrane 1
ENSG00000140600	0.000122783	0.001139095	0.038809721	SH3GL3	SH3-domain GRB2-like 3
ENSG00000167157	0.000123225	0.001142385	0.237800298	PRRX2	paired related homeobox 2
ENSG00000271133	0.00012325	0.001142385	0.084711838	LOC101927811	uncharacterized LOC101927811
ENSG00000127325	0.000124281	0.001150315	0.03484952	BEST3	bestrophin 3
ENSG00000158473	0.000126666	0.001169254	0.097148932	CD1D	CD1d molecule
ENSG00000111860	0.000129133	0.001189332	0.077959625	CEP85L	centrosomal protein 85kDa-like
ENSG00000110076	0.000129894	0.001195257	0.048968451	NRXN2	neurexin 2
ENSG00000257842	0.00013	0.001195939	0.023637431	LOC102725045	uncharacterized LOC102725045
ENSG00000227507	0.000131604	0.001208262	0.249323703	LTB	lymphotoxin beta (TNF superfamily, member 3)
ENSG00000249306	0.000133864	0.001224599	0.038818439	LINC01411	long intergenic non-protein coding RNA 1411
ENSG00000184584	0.000135573	0.00123828	0.083813583	TMEM173	transmembrane protein 173
ENSG00000108924	0.000139202	0.001264336	0.025127953	HLF	hepatic leukemia factor
ENSG00000173868	0.000139499	0.001266472	0.115969105	PHOSPHO1	phosphatase, orphan 1
ENSG00000179674	0.000140741	0.00127632	0.115102137	ARL14	ADP-ribosylation factor-like 14
ENSG00000126016	0.000141151	0.001279471	0.015077207	AMOT	angiomin
ENSG00000109705	0.000141245	0.001280041	0.074573901	NKX3-2	NK3 homeobox 2
ENSG00000250138	0.000142667	0.001292638	0.011079861	LOC728093	putative POM121-like protein 1-like
ENSG00000174015	0.000144449	0.001303849	0.071061445	SPERT	spermatid associated
ENSG00000167332	0.000145025	0.001308182	0.022025856	OR51E2	olfactory receptor, family 51, subfamily E, member 2
ENSG00000146453	0.000145381	0.001310816	0.058730859	PNLDC1	poly(A)-specific ribonuclease (PARN)-like domain containing 1
ENSG00000260057	0.000147391	0.001325996	0.019078723	LINC01571	long intergenic non-protein coding RNA 1571
ENSG00000166924	0.000148535	0.001334296	0.077588371	NYAP1	neuronal tyrosine-phosphorylated phosphoinositide-3-kinase adaptor 1
ENSG00000060140	0.000149153	0.001338594	0.041867091	STYK1	serine/threonine/tyrosine kinase 1
ENSG00000204021	0.000150743	0.00134989	0.018191123	LIPK	lipase, family member K
ENSG00000151388	0.000152556	0.001362232	0.044762264	ADAMTS12	ADAM metalloproteinase with thrombospondin type 1 motif, 12
ENSG00000107295	0.000152607	0.001362386	0.033213242	SH3GL2	SH3-domain GRB2-like 2
ENSG00000147234	0.000153353	0.001368449	0.012023945	FRMPD3	FERM and PDZ domain containing 3

ENSG00000165556	0.000154582	0.001378507	0.039258089	CDX2	caudal type homeobox 2
ENSG00000091656	0.000154697	0.001378926	0.048139022	ZFHX4	zinc finger homeobox 4
ENSG00000171195	0.000155665	0.001384829	0.00843556	MUC7	mucin 7, secreted
ENSG00000103485	0.00015804	0.001404115	0.052884393	QPRT	quinolinate phosphoribosyltransferase
ENSG00000028277	0.000163738	0.001446224	0.087556489	POU2F2	POU class 2 homeobox 2
ENSG00000139364	0.000164155	0.001449592	0.008848006	TMEM132B	transmembrane protein 132B
ENSG00000205693	0.000165691	0.001446094	0.037540257	MANSC4	MANSC domain containing 4
ENSG00000147676	0.00017262	0.001513834	0.038643576	MAL2	mal, T-cell differentiation protein 2 (gene/pseudogene)
ENSG00000236333	0.000173495	0.001520203	0.013977601	TRHDE-AS1	TRHDE antisense RNA 1
ENSG00000157445	0.000176117	0.00154152	0.03469272	CACNA2D3	calcium channel, voltage-dependent, alpha 2/delta subunit 3
ENSG00000165023	0.000177355	0.001551015	0.040907292	DIRAS2	DIRAS family, GTP-binding RAS-like 2
ENSG00000038295	0.000180917	0.001577084	0.142859589	TLL1	tollid-like 1
ENSG00000268738	0.000182231	0.001586484	0.083507798	HSFX2	heat shock transcription factor family, X linked 2
ENSG00000123570	0.00018539	0.001609531	0.026850776	RAB9B	RAB9B, member RAS oncogene family
ENSG00000118971	0.000185903	0.001613645	0.205226279	CCND2	cyclin D2
ENSG00000103546	0.000191375	0.001655432	0.004097347	SLC6A2	solute carrier family 6 (neurotransmitter transporter), member 2
ENSG00000248309	0.000193291	0.001667106	0.002515414	MEF2C-AS1	MEF2C antisense RNA 1
ENSG00000126217	0.000197702	0.001701912	0.01964929	MCF2L	MCF2 cell line derived transforming sequence-like
ENSG00000189045	0.00019843	0.001707453	0.048950499	ANKDD1B	ankyrin repeat and death domain containing 1B
ENSG00000164588	0.000199075	0.001711196	0.006167881	HCN1	hyperpolarization activated cyclic nucleotide gated potassium channel 1
ENSG00000133433	0.000200945	0.00172399	0.101997862	GSTT2B	glutathione S-transferase theta 2B (gene/pseudogene)
ENSG00000005001	0.000203919	0.001745833	0.203319681	PRSS22	protease, serine, 22
ENSG00000265763	0.000206887	0.001766785	0.105816155	ZNF488	zinc finger protein 488
ENSG00000114757	0.00020811	0.00177574	0.008587537	PEX5L	peroxisomal biogenesis factor 5-like
ENSG00000181690	0.000208539	0.001778605	0.070249372	PLAG1	pleiomorphic adenoma gene 1
ENSG00000138622	0.000210464	0.001791323	0.035766665	HCN4	hyperpolarization activated cyclic nucleotide gated potassium channel 4
ENSG00000120279	0.000210795	0.001793762	0.052441724	MYCT1	myc target 1
ENSG00000116014	0.000211678	0.001799754	0.227287564	KISS1R	KISS1 receptor
ENSG00000135744	0.000215494	0.001828644	0.098476884	AGT	angiotensinogen (serpin peptidase inhibitor, clade A, member 8)
ENSG00000123243	0.000216007	0.001831224	0.023329711	ITIH5	inter-alpha-trypsin inhibitor heavy chain family, member 5
ENSG00000089558	0.000217176	0.001839255	0.050998858	KCNH4	potassium channel, voltage gated eag related subfamily H, member 4
ENSG00000133107	0.000219363	0.001855424	0.0170285	TRPC4	transient receptor potential cation channel, subfamily C, member 4
ENSG00000184599	0.000219572	0.00185642	0.066688948	FAM19A3	family with sequence similarity 19 (chemokine (C-C motif)-like), member A3
ENSG00000130038	0.000220946	0.001866623	0.027211402	CRACR2A	calcium release activated channel regulator 2A
ENSG00000086205	0.000221635	0.001871922	0.020856126	FOLH1	folate hydrolase (prostate-specific membrane antigen) 1
ENSG00000141668	0.000222434	0.001876472	0.073252926	CBLN2	cerebellin 2 precursor
ENSG00000160838	0.000225752	0.001900386	0.057479295	LRRC71	leucine rich repeat containing 71
ENSG00000003096	0.000229064	0.001924689	0.021057824	KLHL13	kelch-like family member 13
ENSG00000105855	0.0002329	0.001952087	0.118680837	ITGB8	integrin, beta 8
ENSG00000248538	0.000233691	0.001957502	0.063205858	LOC101929128	uncharacterized LOC101929128
ENSG00000015413	0.000242276	0.002019447	0.033171697	DPEP1	dipeptidase 1 (renal)
ENSG00000053918	0.000244013	0.002029766	0.04638128	KCNQ1	potassium channel, voltage gated KQT-like subfamily Q, member 1
ENSG00000213967	0.00024811	0.002059222	0.019869802	ZNF726	zinc finger protein 726
ENSG00000182393	0.000248995	0.002064466	0.08084156	IFNL1	interferon, lambda 1
ENSG00000143365	0.000258372	0.002130737	0.008582183	RORC	RAR-related orphan receptor C
ENSG00000133019	0.000258453	0.002130737	0.018533868	CHRM3	cholinergic receptor, muscarinic 3
ENSG00000082126	0.000258896	0.00213352	0.037704444	MPP4	membrane protein, palmitoylated 4 (MAGUK p55 subfamily member 4)
ENSG00000159784	0.000260193	0.002141173	0.044963894	FAM131B	family with sequence similarity 131, member B
ENSG00000141449	0.000268623	0.002201207	0.032856611	GREB1L	growth regulation by estrogen in breast cancer-like
ENSG00000197599	0.000276455	0.002257663	0.191184724	CCDC154	coiled-coil domain containing 154
ENSG00000185518	0.0002769	0.002260838	0.005425109	SV2B	synaptic vesicle glycoprotein 2B
ENSG00000170290	0.000278683	0.002273579	0.153566865	SLN	sarcolipin
ENSG00000107859	0.000283261	0.002305379	0.076674289	PITX3	paired-like homeodomain 3
ENSG00000256594	0.000283784	0.002309175	0.213573501	LOC374443	C-type lectin domain family 2, member D pseudogene
ENSG00000135605	0.000289518	0.002348789	0.094706873	TEC	tec protein tyrosine kinase
ENSG00000079689	0.000290607	0.002356635	0.0263625	SCGN	secretagogin, EF-hand calcium binding protein
ENSG00000214711	0.000298334	0.002406891	0.019856119	CAPN14	calpain 14
ENSG00000136531	0.000301042	0.002425854	0.032284842	SCN2A	sodium channel, voltage gated, type II alpha subunit
ENSG00000242258	0.000308445	0.002476682	0.046293008	LINC00996	long intergenic non-protein coding RNA 996
ENSG00000259974	0.000314373	0.002517331	0.206163247	LINC00261	long intergenic non-protein coding RNA 261
ENSG00000157613	0.000317923	0.00253977	0.134460114	CREB3L1	cAMP responsive element binding protein 3-like 1
ENSG00000221955	0.000322429	0.002572229	0.109674942	SLC12A8	solute carrier family 12, member 8
ENSG00000007264	0.000323561	0.002580755	0.064122832	MATK	megakaryocyte-associated tyrosine kinase
ENSG00000187772	0.000331013	0.002630914	0.054328284	LIN28B	lin-28 homolog B (C. elegans)
ENSG00000151623	0.000333353	0.002646419	0.05589458	NR3C2	nuclear receptor subfamily 3, group C, member 2

ENSG00000130176	0.000337695	0.002675145	0.079732338	CNN1	calponin 1, basic, smooth muscle
ENSG00000204421	0.000340772	0.002696378	0.116101124	LY6G6C	lymphocyte antigen 6 complex, locus G6C
ENSG00000256164	0.000345128	0.002727134	0.157596711	CCND2-AS1	CCND2 antisense RNA 1
ENSG00000185467	0.000348951	0.002755737	0.207432651	KPNA7	karyopherin alpha 7 (importin alpha 8)
ENSG00000011201	0.000357733	0.002815805	0.015912743	ANOS1	anosmin 1
ENSG00000189090	0.000362581	0.002848459	0.065948349	FAM25G	family with sequence similarity 25, member G
ENSG00000276476	0.000366197	0.002874096	0.072725664	LINC00540	long intergenic non-protein coding RNA 540
ENSG00000177181	0.000373925	0.002927976	0.067737499	RIMKLA	ribosomal modification protein rimK-like family member A
ENSG000000087301	0.00037914	0.002960269	0.068572386	TXNDC16	thioredoxin domain containing 16
ENSG00000163673	0.000383001	0.002988129	0.019762826	DCLK3	doublecortin-like kinase 3
ENSG00000197880	0.000386763	0.003012282	0.034503449	MDS2	myelodysplastic syndrome 2 translocation associated
ENSG00000228358	0.000390606	0.003038143	0.057303633	LOC105377390	uncharacterized LOC105377390
ENSG00000168939	0.000393455	0.00305914	0.047120565	SPRY3	sprouty RTK signaling antagonist 3
ENSG00000111732	0.00040113	0.003108716	0.032973285	AICDA	activation-induced cytidine deaminase
ENSG00000104967	0.000403181	0.003122238	0.151281357	NOVA2	neuro-oncological ventral antigen 2
ENSG00000116819	0.000407106	0.00314665	0.142436756	TFAP2E	transcription factor AP-2 epsilon (activating enhancer binding protein 2 epsilon)
ENSG00000164047	0.000410695	0.003170774	0.05060759	CAMP	cathelicidin antimicrobial peptide
ENSG00000163689	0.000413682	0.003192023	0.033798099	C3orf67	chromosome 3 open reading frame 67
ENSG00000115604	0.00042187	0.003250271	0.157633406	IL18R1	interleukin 18 receptor 1
ENSG00000160097	0.000428166	0.003293178	0.050232281	FNDC5	fibronectin type III domain containing 5
ENSG00000163590	0.000428552	0.003294898	0.087045636	PPM1L	protein phosphatase, Mg2+/Mn2+ dependent, 1L
ENSG00000255819	0.00043277	0.003323561	0.065021853	KLRC4-KLRK1	KLRC4-KLRK1 readthrough
ENSG00000248905	0.000440982	0.003378346	0.042710942	FMN1	formin 1
ENSG00000139970	0.000447256	0.003416129	0.024834536	RTN1	reticulin 1
ENSG00000234155	0.000447848	0.003418721	0.226046454	LOC101928820	uncharacterized LOC101928820
ENSG00000113430	0.000450484	0.003435036	0.142585388	IRX4	iroquois homeobox 4
ENSG00000119915	0.000453033	0.003449897	0.179696861	ELOVL3	ELOVL fatty acid elongase 3
ENSG00000186446	0.000453325	0.003450186	0.020635726	ZNF501	zinc finger protein 501
ENSG00000160801	0.000458518	0.003485151	0.034535315	PTH1R	parathyroid hormone 1 receptor
ENSG00000162711	0.000466423	0.003538629	0.021724821	NLRP3	NLR family, pyrin domain containing 3
ENSG00000197587	0.00046657	0.00353908	0.0431936	DMBX1	diencephalon/mesencephalon homeobox 1
ENSG00000109667	0.00049066	0.003692238	0.029936755	SLC2A9	solute carrier family 2 (facilitated glucose transporter), member 9
ENSG00000137462	0.000497106	0.003732464	0.132808883	TLR2	toll-like receptor 2
ENSG00000196433	0.000498158	0.003738299	0.132718333	ASMT	acetylserotonin O-methyltransferase
ENSG00000230006	0.000500173	0.003751345	0.002422476	ANKRD36BP2	ankyrin repeat domain 36B pseudogene 2
ENSG00000129451	0.000500559	0.003752856	0.016923471	KLK10	kallikrein-related peptidase 10
ENSG00000196569	0.000502151	0.003762018	0.026456327	LAMA2	laminin, alpha 2
ENSG00000227028	0.000511955	0.003822112	0.006460544	SLC8A1-AS1	SLC8A1 antisense RNA 1
ENSG00000132938	0.000514241	0.003836364	0.011276431	MTUS2	microtubule associated tumor suppressor candidate 2
ENSG00000144810	0.000516524	0.003851979	0.007280765	COL8A1	collagen, type VIII, alpha 1
ENSG00000149294	0.000516794	0.00385329	0.008599602	NCAM1	neural cell adhesion molecule 1
ENSG00000153684	0.000520736	0.003879837	0.027644488	GOLGA8F	golgin A8 family, member F
ENSG00000006128	0.000530194	0.003940218	0.042472351	TAC1	tachykinin, precursor 1
ENSG00000112218	0.00053089	0.003944665	0.020873086	GPR63	G protein-coupled receptor 63
ENSG00000131773	0.000533566	0.003962379	0.044186786	KHDRBS3	KH domain containing, RNA binding, signal transduction associated 3
ENSG00000105866	0.000536008	0.003976168	0.074693152	SP4	Sp4 transcription factor
ENSG00000164626	0.000536748	0.003980204	0.053672296	KCNK5	potassium channel, two pore domain subfamily K, member 5
ENSG00000115607	0.00054754	0.004051378	0.015191709	IL18RAP	interleukin 18 receptor accessory protein
ENSG00000135929	0.000547696	0.004051793	0.045979491	CYP27A1	cytochrome P450, family 27, subfamily A, polypeptide 1
ENSG00000167077	0.000550298	0.004066158	0.015067618	MEI1	meiotic double-stranded break formation protein 1
ENSG00000185274	0.000551341	0.004071362	0.036154326	WBSCR17	Williams-Beuren syndrome chromosome region 17
ENSG00000179826	0.000572668	0.004211285	0.016574642	MRGPRX3	MAS-related GPR, member X3
ENSG00000225684	0.000573424	0.004214561	0.004797899	FAM225B	family with sequence similarity 225, member B (non-protein coding)
ENSG00000261341	0.000577382	0.004241353	0.02465378	LOC105372440	uncharacterized LOC105372440
ENSG00000183629	0.000581819	0.00426933	0.03844199	GOLGA8G	golgin A8 family, member G
ENSG00000169436	0.000582245	0.004270917	0.030443606	COL22A1	collagen, type XXII, alpha 1
ENSG00000182230	0.00058733	0.004302018	0.014708848	FAM153B	family with sequence similarity 153, member B
ENSG00000197444	0.000588839	0.004311605	0.0341173	OGDHL	oxoglutarate dehydrogenase-like
ENSG00000039600	0.000591816	0.004331755	0.030450222	SOX30	SRY (sex determining region Y)-box 30
ENSG00000150722	0.000593455	0.004341409	0.032677055	PPP1R1C	protein phosphatase 1, regulatory (inhibitor) subunit 1C
ENSG00000169862	0.000594084	0.004344993	0.024313627	CTNND2	catenin (cadherin-associated protein), delta 2
ENSG00000180785	0.000600197	0.004382862	0.012467307	ORS1E1	olfactory receptor, family 51, subfamily E, member 1
ENSG00000061918	0.000610751	0.004445576	0.099385811	GUCY1B3	guanylate cyclase 1, soluble, beta 3
ENSG00000142347	0.000611583	0.00445013	0.06143343	MYO1F	myosin IF
ENSG00000182162	0.000617737	0.004486802	0.022984882	P2RY8	purinergic receptor P2Y, G-protein coupled, 8

ENSG00000214381	0.000638154	0.0046137	0.095364276	LINC00488	long intergenic non-protein coding RNA 488
ENSG00000091128	0.000659739	0.004756244	0.022188099	LAMB4	laminin, beta 4
ENSG00000233539	0.000665696	0.004794002	0.042486406	LOC730338	uncharacterized LOC730338
ENSG00000162654	0.000673049	0.004837637	0.010354246	GBP4	guanylate binding protein 4
ENSG00000179766	0.000675684	0.004850582	0.023215754	ATP8B5P	ATPase, class I, type 8B, member 5, pseudogene
ENSG00000102935	0.000679395	0.004872924	0.026206716	ZNF423	zinc finger protein 423
ENSG00000135443	0.000680211	0.004876404	0.034374146	KRT85	keratin 85, type II
ENSG00000260691	0.000687165	0.004917399	0.020899507	ANKRD20A1	ankyrin repeat domain 20 family, member A1
ENSG00000198681	0.000696221	0.004975207	0.070256398	MAGEA1	melanoma antigen family A1
ENSG00000197980	0.000709278	0.005054319	0.031557196	LEKR1	leucine, glutamate and lysine rich 1
ENSG00000205015	0.000710652	0.005060567	0.087037722	LOC400558	uncharacterized LOC400558
ENSG00000188959	0.000719384	0.005116485	0.031111635	C9orf152	chromosome 9 open reading frame 152
ENSG00000088756	0.00072503	0.005150343	0.006949886	ARHGAP28	Rho GTPase activating protein 28
ENSG00000231453	0.000734993	0.005213839	0.102426451	LINC01305	long intergenic non-protein coding RNA 1305
ENSG00000125910	0.00073556	0.005215238	0.341473001	S1PR4	sphingosine-1-phosphate receptor 4
ENSG00000158813	0.000735574	0.005215238	0.056119293	EDA	ectodysplasin A
ENSG00000107562	0.000755286	0.005331786	0.056702595	CXCL12	chemokine (C-X-C motif) ligand 12
ENSG00000189068	0.000761432	0.0053668	0.039634924	VSTM1	V-set and transmembrane domain containing 1
ENSG00000146530	0.000764397	0.005382108	0.068423787	VWDE	von Willebrand factor D and EGF domains
ENSG00000164266	0.000794558	0.005577107	0.057634541	SPINK1	serine peptidase inhibitor, Kazal type 1
ENSG00000136573	0.000800144	0.005610518	0.008216753	BLK	BLK proto-oncogene, Src family tyrosine kinase
ENSG00000143110	0.000803037	0.00562789	0.044401193	C1orf162	chromosome 1 open reading frame 162
ENSG00000080293	0.000811463	0.005676197	0.005650925	SCTR	secretin receptor
ENSG00000164694	0.000814427	0.005692042	0.024477755	FNDC1	fibronectin type III domain containing 1
ENSG00000106031	0.000818618	0.005711533	0.187604975	HOXA13	homeobox A13
ENSG00000175676	0.000826881	0.005763258	0.036595869	GOLGA8DP	golgin A8 family, member D, pseudogene
ENSG00000157766	0.000827391	0.005765495	0.007999916	ACAN	aggregran
ENSG00000152977	0.000827485	0.005765495	0.012446717	ZIC1	Zic family member 1
ENSG00000225492	0.000833291	0.005799	0.017237182	GBP1P1	guanylate binding protein 1, interferon-inducible pseudogene 1
ENSG00000111727	0.000850985	0.005912033	0.111215799	HCFC2	host cell factor C2
ENSG00000216775	0.000854091	0.005928547	0.067325907	LOC730101	uncharacterized LOC730101
ENSG00000269821	0.00086757	0.006005733	0.007547643	KCNQ1OT1	KCNQ1 opposite strand/antisense transcript 1 (non-protein coding)
ENSG00000157103	0.000887777	0.006120643	0.007243418	SLC6A1	solute carrier family 6 (neurotransmitter transporter), member 1
ENSG00000162944	0.000889661	0.00612948	0.027330985	RFTN2	raftlin family member 2
ENSG00000234602	0.000890323	0.006131962	0.06832797	MCIDAS	multiciliate differentiation and DNA synthesis associated cell cycle protein
ENSG00000224417	0.000893479	0.006150579	0.032394131	LOC105378138	uncharacterized LOC105378138
ENSG00000215483	0.000913626	0.00627336	0.021422431	LINC00598	long intergenic non-protein coding RNA 598
ENSG00000165309	0.000914393	0.006274774	0.03261973	ARMC3	armadillo repeat containing 3
ENSG00000122733	0.000930759	0.006377705	0.021388078	PHF24	PHD finger protein 24
ENSG00000106565	0.000931765	0.006380693	0.019346581	TMEM176B	transmembrane protein 176B
ENSG00000178776	0.000936411	0.006406043	0.070704746	C5orf46	chromosome 5 open reading frame 46
ENSG00000169629	0.000937376	0.00641157	0.09444461	RGPD8	RANBP2-like and GRIP domain containing 8
ENSG00000258479	0.000946464	0.006467213	0.080386288	LINC00640	long intergenic non-protein coding RNA 640
ENSG00000132185	0.000966667	0.006588676	0.047768062	FCRLA	Fc receptor-like A
ENSG00000153902	0.000973265	0.006628371	0.110034518	LGI4	leucine-rich repeat LGI family, member 4
ENSG00000128655	0.000973305	0.006628371	0.05105011	PDE11A	phosphodiesterase 11A
ENSG00000149050	0.000976692	0.006649213	0.058467663	ZNF214	zinc finger protein 214
ENSG00000157423	0.00098025	0.00666786	0.021508175	HYDIN	HYDIN, axonemal central pair apparatus protein
ENSG00000197594	0.000993247	0.006745004	0.053411856	ENPP1	ectonucleotide pyrophosphatase/phosphodiesterase 1
ENSG00000233816	0.000998645	0.006778268	0.093699979	IFNA13	interferon, alpha 13
ENSG00000163803	0.001021884	0.006919852	0.022311754	PLB1	phospholipase B1
ENSG00000123453	0.001022499	0.006921712	0.018156768	SARDH	sarcosine dehydrogenase
ENSG00000182263	0.001023442	0.00692695	0.051813043	FIGN	figetin
ENSG00000078295	0.001027358	0.006950541	0.004551709	ADCY2	adenylate cyclase 2 (brain)
ENSG00000172410	0.00104092	0.007031215	0.079177179	INSL5	insulin-like 5
ENSG00000261231	0.00104442	0.007051353	0.007403586	LOC101927132	uncharacterized LOC101927132
ENSG00000168280	0.001062966	0.007157577	0.027090439	KIF5C	kinesin family member 5C
ENSG00000249231	0.001071853	0.007211455	0.01636026	CASC16	cancer susceptibility candidate 16 (non-protein coding)
ENSG00000175874	0.001076234	0.007234949	0.079067233	CREG2	cellular repressor of E1A-stimulated genes 2
ENSG00000145287	0.001079961	0.007252819	0.033838288	PLAC8	placenta-specific 8
ENSG00000125872	0.00108507	0.007281126	0.018623492	LRRN4	leucine rich repeat neuronal 4
ENSG00000141497	0.001085993	0.007286118	0.061946004	ZMYND15	zinc finger, MYND-type containing 15
ENSG00000100055	0.001094534	0.007338397	0.050769301	CYTH4	cytohesin 4
ENSG00000119913	0.001113407	0.007439401	0.035412136	TECTB	tectorin beta
ENSG00000057593	0.001126683	0.007515772	0.009273754	F7	coagulation factor VII (serum prothrombin conversion accelerator)

ENSG00000281706	0.001128286	0.00752277	0.029259899	LINC01012	long intergenic non-protein coding RNA 1012
ENSG00000039987	0.001143077	0.007602714	0.016394444	BEST2	bestrophin 2
ENSG00000139737	0.001150323	0.007643414	0.06124153	SLAIN1	SLAIN motif family, member 1
ENSG00000165197	0.001159508	0.007695657	0.129099375	FIGF	c-fos induced growth factor (vascular endothelial growth factor D)
ENSG00000159904	0.001169314	0.007745591	0.026255508	ZNF890P	zinc finger protein 890, pseudogene
ENSG00000156711	0.001175583	0.007780787	0.076097856	MAPK13	mitogen-activated protein kinase 13
ENSG00000144550	0.001197415	0.007898928	0.072628224	CPNE9	copine family member IX
ENSG00000017483	0.001207595	0.007956452	0.065581284	SLC38A5	solute carrier family 38, member 5
ENSG00000134258	0.001209684	0.007966345	0.04204786	VTCN1	V-set domain containing T cell activation inhibitor 1
ENSG00000197446	0.001219271	0.008019103	0.008020571	CYP2F1	cytochrome P450, family 2, subfamily F, polypeptide 1
ENSG00000277632	0.001233719	0.008104963	0.058798312	CCL3	chemokine (C-C motif) ligand 3
ENSG00000267551	0.001253444	0.008213348	0.120948555	LOC100996351	uncharacterized LOC100996351
ENSG00000162706	0.001276011	0.008341264	0.052552175	CADM3	cell adhesion molecule 3
ENSG00000132518	0.001276818	0.008345023	0.009453319	GUCY2D	guanylate cyclase 2D, membrane (retina-specific)
ENSG00000237292	0.001294093	0.008433556	0.105053073	LOC101928973	uncharacterized LOC101928973
ENSG00000186417	0.001317193	0.008564911	0.007951825	GLDN	gliomedin
ENSG00000113763	0.001320922	0.008585041	0.0312833	UNC5A	unc-5 netrin receptor A
ENSG00000139287	0.001322293	0.008592586	0.003939375	TPH2	tryptophan hydroxylase 2
ENSG00000111344	0.001323478	0.00859754	0.014689487	RASAL1	RAS protein activator like 1 (GAP1 like)
ENSG00000158560	0.001325004	0.008606081	0.018441282	DYNC111	dynein, cytoplasmic 1, intermediate chain 1
ENSG00000182795	0.001336576	0.008667413	0.058062439	C1orf116	chromosome 1 open reading frame 116
ENSG00000012817	0.001352668	0.008756426	0.014797914	KDM5D	lysine (K)-specific demethylase 5D
ENSG00000162723	0.001361913	0.008807875	0.300623788	SLAMF9	SLAM family member 9
ENSG00000162040	0.001390963	0.008965842	0.154391212	HS3ST6	heparan sulfate (glucosamine) 3-O-sulfotransferase 6
ENSG00000204334	0.001395965	0.008993813	0.109964535	ERICH2	glutamate-rich 2
ENSG00000168634	0.001417476	0.009113657	0.011375577	WFDC13	WAP four-disulfide core domain 13
ENSG00000107187	0.001434482	0.009209909	0.041904162	LHX3	LIM homeobox 3
ENSG00000242715	0.001488333	0.009506186	0.031851379	CCDC169	coiled-coil domain containing 169
ENSG00000169896	0.001501382	0.009574513	0.081119993	ITGAM	integrin, alpha M (complement component 3 receptor 3 subunit)
ENSG00000165269	0.001535027	0.009758504	0.090458127	AQP7	aquaporin 7
ENSG00000087250	0.001542805	0.009804888	0.054236823	MT3	metallothionein 3
ENSG00000251085	0.001564973	0.009921001	0.091788134	LOC101927230	uncharacterized LOC101927230
ENSG00000205420	0.00156709	0.009929783	0.014534096	KRT6A	keratin 6A, type II
ENSG00000128422	0.001590345	0.010047426	0.070841975	KRT17	keratin 17, type I
ENSG00000188508	0.001602696	0.010112906	0.059311499	KRTDAP	keratinocyte differentiation-associated protein
ENSG00000205057	0.001632226	0.010272177	0.140723167	CLUU1OS	chronic lymphocytic leukemia up-regulated 1 opposite strand
ENSG00000183690	0.001644248	0.010336654	0.042830371	EFHC2	EF-hand domain (C-terminal) containing 2
ENSG00000000938	0.001648732	0.010356846	0.007382865	FGR	FGR proto-oncogene, Src family tyrosine kinase
ENSG00000237515	0.001663123	0.010427941	0.009897437	SHISA9	shisa family member 9
ENSG00000232645	0.001671914	0.010475555	0.101294969	LINC01431	long intergenic non-protein coding RNA 1431
ENSG00000196263	0.001691516	0.010584778	0.036811818	ZNF471	zinc finger protein 471
ENSG00000254415	0.00169923	0.010621622	0.028866763	SIGLEC14	sialic acid binding Ig-like lectin 14
ENSG00000197085	0.001702653	0.010634853	0.010873859	NPSR1-AS1	NPSR1 antisense RNA 1
ENSG00000149972	0.001717197	0.010705991	0.008113085	CNTN5	contactin 5
ENSG00000188112	0.001725682	0.010750662	0.027200363	C6orf132	chromosome 6 open reading frame 132
ENSG00000203926	0.001728102	0.010764091	0.035401665	SPANXA2	SPANX family, member A2
ENSG00000276289	0.001728915	0.010766212	0.029289124	LOC102723475	putative uncharacterized protein LOC388820
ENSG00000223393	0.001733189	0.010784228	0.065190577	LOC101927604	uncharacterized LOC101927604
ENSG00000149418	0.001739855	0.010819094	0.029164939	ST14	suppression of tumorigenicity 14 (colon carcinoma)
ENSG00000138376	0.001760989	0.010928817	0.053993671	BARD1	BRCA1 associated RING domain 1
ENSG00000170477	0.001766488	0.010951258	0.014423023	KRT4	keratin 4, type II
ENSG00000162999	0.001779569	0.011004954	0.084783532	DUSP19	dual specificity phosphatase 19
ENSG00000115041	0.001785613	0.011037893	0.062051359	KCNIP3	Kv channel interacting protein 3, calsenilin
ENSG00000095637	0.001785924	0.01103814	0.015803987	SORBS1	sorbin and SH3 domain containing 1
ENSG00000105383	0.001816904	0.011193935	0.013924102	CD33	CD33 molecule
ENSG00000167011	0.001820237	0.011212771	0.030163479	NAT16	N-acetyltransferase 16 (GCN5-related, putative)
ENSG00000166603	0.001844275	0.011336207	0.033351888	MC4R	melanocortin 4 receptor
ENSG00000177301	0.001851715	0.0113757	0.00317796	KCNA2	potassium channel, voltage gated shaker related subfamily A, member 2
ENSG00000153563	0.001862061	0.011428909	0.050140725	CD8A	CD8a molecule
ENSG00000141469	0.001893738	0.011600604	0.004220655	SLC14A1	solute carrier family 14 (urea transporter), member 1 (Kidd blood group)
ENSG00000135226	0.001913563	0.011702682	0.032073917	UGT2B28	UDP glucuronosyltransferase 2 family, polypeptide B28
ENSG00000183160	0.001918167	0.011729078	0.016540877	TMEM119	transmembrane protein 119
ENSG00000183150	0.00194667	0.011889084	0.044976686	GPR19	G protein-coupled receptor 19
ENSG00000231674	0.001987636	0.012113838	0.019486417	LINC00410	long intergenic non-protein coding RNA 410
ENSG00000152315	0.001994129	0.012144321	0.061805446	KCNK13	potassium channel, two pore domain subfamily K, member 13

ENSG00000204624	0.002039038	0.01237894	0.022436988	PTCHD2	patched domain containing 2
ENSG00000163285	0.002056454	0.012467943	0.015992549	GABRG1	gamma-aminobutyric acid (GABA) A receptor, gamma 1
ENSG00000168348	0.002059971	0.012483967	0.014786645	INSM2	insulinoma-associated 2
ENSG00000109181	0.002065262	0.012510167	0.040142058	UGT2B10	UDP glucuronosyltransferase 2 family, polypeptide B10
ENSG00000163006	0.002075814	0.012564736	0.098414104	CCDC138	coiled-coil domain containing 138
ENSG00000176092	0.002087394	0.01262732	0.026129955	AIM1L	absent in melanoma 1-like
ENSG00000074317	0.002098743	0.012679024	0.02146475	SNCB	synuclein, beta
ENSG00000136383	0.002103829	0.012705981	0.039449424	ALPK3	alpha-kinase 3
ENSG00000213214	0.002111348	0.012740435	0.024321275	ARHGEF35	Rho guanine nucleotide exchange factor (GEF) 35
ENSG00000133962	0.002124858	0.012812076	0.009103988	CATSPERB	catsper channel auxiliary subunit beta
ENSG00000064787	0.002128276	0.01283079	0.010095816	BCAS1	breast carcinoma amplified sequence 1
ENSG00000018625	0.002158412	0.012987472	0.021780299	ATP1A2	ATPase, Na+/K+ transporting, alpha 2 polypeptide
ENSG00000071909	0.002216453	0.013281759	0.007154868	MYO3B	myosin IIIB
ENSG00000167207	0.002250507	0.013456118	0.008270972	NOD2	nucleotide-binding oligomerization domain containing 2
ENSG00000171435	0.002252538	0.01346628	0.029137741	KSR2	kinase suppressor of ras 2
ENSG00000164045	0.002269643	0.013560574	0.083140599	CDC25A	cell division cycle 25A
ENSG00000250312	0.002309473	0.013766565	0.043833011	ZNF718	zinc finger protein 718
ENSG00000255587	0.002373333	0.014099411	0.06230469	RAB44	RAB44, member RAS oncogene family
ENSG00000214146	0.002383484	0.014149397	0.028840252	LOC647323	uncharacterized LOC647323
ENSG00000271550	0.002439595	0.014450891	0.120181946	BNIP3P11	BCL2/adenovirus E1B 19kDa interacting protein 3 pseudogene 11
ENSG00000261279	0.002457378	0.014547057	0.054130402	ULK4P1	ULK4 pseudogene 1
ENSG00000187955	0.002494926	0.014737907	0.0096505	COL14A1	collagen, type XIV, alpha 1
ENSG00000139714	0.002498594	0.014755293	0.045480841	MORN3	MORN repeat containing 3
ENSG00000136828	0.002514869	0.014829897	0.052791367	RALGPS1	Ral GEF with PH domain and SH3 binding motif 1
ENSG00000128285	0.0026379	0.01542361	0.004979103	MCHR1	melanin-concentrating hormone receptor 1
ENSG00000171551	0.002650028	0.015483404	0.044929121	ECEL1	endothelin converting enzyme-like 1
ENSG00000181984	0.002661606	0.015539901	0.027664929	GOLGA8EP	golgin A8 family, member E, pseudogene
ENSG00000169918	0.002667062	0.015569525	0.012090552	OTUD7A	OTU deubiquitinase 7A
ENSG00000136514	0.002699131	0.015724941	0.027448922	RTP4	receptor (chemosensory) transporter protein 4
ENSG00000224383	0.002699478	0.015724941	0.127541319	PRR29	proline rich 29
ENSG00000115361	0.002706392	0.015760708	0.031357548	ACADL	acyl-CoA dehydrogenase, long chain
ENSG00000215458	0.002717472	0.015809406	0.006830302	AATBC	apoptosis associated transcript in bladder cancer
ENSG00000169181	0.00274328	0.015928622	0.004846652	GSG1L	GSG1-like
ENSG00000184845	0.002755831	0.01599144	0.075940395	DRD1	dopamine receptor D1
ENSG00000109182	0.002758113	0.015998943	0.00802594	CWH43	cell wall biogenesis 43 C-terminal homolog
ENSG00000104848	0.002779092	0.016098885	0.022084616	KCNA7	potassium channel, voltage gated shaker related subfamily A, member 7
ENSG00000176040	0.002780202	0.016103024	0.054384097	TMPRSS7	transmembrane protease, serine 7
ENSG00000013725	0.002835941	0.016374625	0.007955242	CD6	CD6 molecule
ENSG00000147606	0.002844238	0.016415545	0.029399627	SLC26A7	solute carrier family 26 (anion exchanger), member 7
ENSG00000070729	0.002846682	0.016425532	0.010574435	CNGB1	cyclic nucleotide gated channel beta 1
ENSG00000215808	0.002864773	0.016505991	0.162449763	LINC01139	long intergenic non-protein coding RNA 1139
ENSG00000171446	0.002866707	0.01651246	0.029919846	KRT27	keratin 27, type I
ENSG00000165379	0.002883025	0.016587682	0.006313106	LRFV5	leucine rich repeat and fibronectin type III domain containing 5
ENSG00000166682	0.002885899	0.016599527	0.058137616	TMPRSS5	transmembrane protease, serine 5
ENSG00000176438	0.002908162	0.016715776	0.005089679	SYNE3	spectrin repeat containing, nuclear envelope family member 3
ENSG00000234199	0.002929453	0.016821532	0.091338214	LINC01191	long intergenic non-protein coding RNA 1191
ENSG00000169064	0.002947477	0.016905952	0.035323401	ZBBX	zinc finger, B-box domain containing
ENSG00000198939	0.002971022	0.017014636	0.046709585	ZFP2	ZFP2 zinc finger protein
ENSG00000110675	0.003017651	0.017233198	0.021551817	ELMOD1	ELMO/CED-12 domain containing 1
ENSG00000204103	0.003027494	0.01727972	0.042496289	MAFB	v-maf avian musculoaponeurotic fibrosarcoma oncogene homolog B
ENSG00000249911	0.003047065	0.017350077	0.044671461	LINC01265	long intergenic non-protein coding RNA 1265
ENSG00000163216	0.003051046	0.017367884	0.089149972	SPRR2D	small proline-rich protein 2D
ENSG00000179873	0.003069597	0.017461281	0.016082669	NLRP11	NLR family, pyrin domain containing 11
ENSG00000116396	0.003075364	0.017489202	0.068466267	KCNK4	potassium channel, voltage gated Shaw related subfamily C, member 4
ENSG00000160883	0.003084983	0.017536556	0.040846105	HK3	hexokinase 3 (white cell)
ENSG00000180861	0.003113748	0.017664418	0.007822232	LINC01559	long intergenic non-protein coding RNA 1559
ENSG00000229563	0.003121093	0.017687495	0.01529469	LINC01204	long intergenic non-protein coding RNA 1204
ENSG00000227630	0.003148215	0.017823832	0.003003614	LINC01132	long intergenic non-protein coding RNA 1132
ENSG00000237594	0.003153643	0.017847383	0.045145219	LOC150051	homeobox protein cut-like 1
ENSG00000250979	0.003167184	0.017908818	0.017655905	LOC392232	transient receptor potential cation channel, subfamily A, member 1 pseudogene
ENSG00000237877	0.003242008	0.018250804	0.099636783	LINC01473	long intergenic non-protein coding RNA 1473
ENSG00000133661	0.003245028	0.018260235	0.116280124	SFTPD	surfactant protein D
ENSG00000197410	0.003274942	0.018416795	0.007543053	DCHS2	dachsous cadherin-related 2
ENSG00000127084	0.003307382	0.018555277	0.014374788	FGD3	FYVE, RhoGEF and PH domain containing 3
ENSG00000007314	0.003360027	0.018821516	0.020769911	SCN4A	sodium channel, voltage gated, type IV alpha subunit

ENSG00000188883	0.003402022	0.01902273	0.064818264	KLRG2	killer cell lectin-like receptor subfamily G, member 2
ENSG00000076716	0.003410084	0.019065192	0.022818967	GPC4	glypican 4
ENSG00000021645	0.003429402	0.019151866	0.013922501	NRXN3	neurexin 3
ENSG00000127377	0.003438494	0.019189775	0.009202918	CRYGN	crystallin, gamma N
ENSG00000267254	0.003442185	0.019199846	0.191766594	ZNF790-AS1	ZNF790 antisense RNA 1
ENSG00000148483	0.003447267	0.019222929	0.021939227	TMEM236	transmembrane protein 236
ENSG00000072133	0.003459858	0.019281574	0.091880762	RPS6KA6	ribosomal protein S6 kinase, 90kDa, polypeptide 6
ENSG00000171772	0.003486633	0.019416821	0.008846877	SYCE1	synaptonemal complex central element protein 1
ENSG00000175691	0.003527755	0.01959281	0.144241363	ZNF77	zinc finger protein 77
ENSG00000205269	0.003538102	0.019645292	0.079110827	TMEM170B	transmembrane protein 170B
ENSG00000163817	0.003547547	0.019682385	0.010486735	SLC6A20	solute carrier family 6 (proline IMINO transporter), member 20
ENSG00000182218	0.003588931	0.019871374	0.018891649	HHIPL1	HHIP-like 1
ENSG00000152454	0.003643046	0.02013541	0.153719939	ZNF256	zinc finger protein 256
ENSG00000196132	0.003653282	0.02017776	0.013343227	MYT1	myelin transcription factor 1
ENSG00000166394	0.003662348	0.020209665	0.019012088	CYB5R2	cytochrome b5 reductase 2
ENSG00000083782	0.003663443	0.020212476	0.009695339	EPYC	epiphycan
ENSG00000250634	0.003703411	0.02040258	0.004896071	LINC01182	long intergenic non-protein coding RNA 1182
ENSG00000065328	0.003764367	0.020671272	0.105374356	MCM10	minichromosome maintenance 10 replication initiation factor
ENSG00000206596	0.003780677	0.020746849	0.152973828	RNU1-27P	RNA, U1 small nuclear 27, pseudogene
ENSG00000182771	0.003846148	0.021052219	0.120421049	GRID1	glutamate receptor, ionotropic, delta 1
ENSG00000100170	0.00384973	0.02106899	0.012877533	SLC5A1	solute carrier family 5 (sodium/glucose cotransporter), member 1
ENSG00000164761	0.003859646	0.021111909	0.02975882	TNFRSF11B	tumor necrosis factor receptor superfamily, member 11b
ENSG00000234965	0.003900378	0.021300376	0.06017324	SHISA8	shisa family member 8
ENSG00000065609	0.003905202	0.02131814	0.051065173	SNAP91	synaptosomal-associated protein, 91kDa
ENSG00000269834	0.003979981	0.021650886	0.045566427	ZNF528-AS1	ZNF528 antisense RNA 1
ENSG00000242600	0.003982715	0.021662862	0.066029809	MBL1P	mannose-binding lectin (protein A) 1, pseudogene
ENSG00000232139	0.003985606	0.021672798	0.030273689	LINC00867	long intergenic non-protein coding RNA 867
ENSG00000117595	0.003992018	0.021704765	0.013933229	IRF6	interferon regulatory factor 6
ENSG00000109424	0.004012109	0.021805269	0.055642826	UCP1	uncoupling protein 1 (mitochondrial, proton carrier)
ENSG00000150510	0.004066692	0.022060693	0.086165984	FAM124A	family with sequence similarity 124A
ENSG00000224189	0.004113537	0.022279198	0.034769071	HAGLR	HOXD antisense growth-associated long non-coding RNA
ENSG00000178462	0.004137491	0.022394039	0.045567561	TUBAL3	tubulin, alpha-like 3
ENSG00000134769	0.00415365	0.022469551	0.013111345	DTNA	dystrobrevin, alpha
ENSG00000167851	0.004225297	0.022802605	0.014018565	CD300A	CD300a molecule
ENSG00000182950	0.004269939	0.022997802	0.283750857	ODF3L1	outer dense fiber of sperm tails 3-like 1
ENSG00000141540	0.004283513	0.023055059	0.083004467	TTYH2	tweety family member 2
ENSG00000104722	0.004300345	0.023129766	0.017305822	NEFM	neurofilament, medium polypeptide
ENSG00000188487	0.004344151	0.023323461	0.035832186	INSC	inscuteable homolog (Drosophila)
ENSG00000129682	0.004378421	0.023488871	0.00926258	FGF13	fibroblast growth factor 13
ENSG00000156299	0.00443863	0.023761783	0.037341968	TIAM1	T-cell lymphoma invasion and metastasis 1
ENSG00000125492	0.004553632	0.024313502	0.03604648	BARHL1	BarH-like homeobox 1
ENSG00000168546	0.004557366	0.024330254	0.050545522	GFRA2	GDNF family receptor alpha 2
ENSG00000173083	0.004588726	0.024472003	0.041611633	HPSE	heparanase
ENSG00000198108	0.004593258	0.024486552	0.105901351	CHSY3	chondroitin sulfate synthase 3
ENSG00000140470	0.004603496	0.024516254	0.011900217	ADAMTS17	ADAM metalloproteinase with thrombospondin type 1 motif, 17
ENSG00000204381	0.004633082	0.024650444	0.044265866	LAYN	layilin
ENSG00000221878	0.00466488	0.024777535	0.003607409	PSG7	pregnancy specific beta-1-glycoprotein 7 (gene/pseudogene)
ENSG00000169403	0.004725507	0.025060329	0.025343873	PTAFR	platelet-activating factor receptor
ENSG00000129810	0.004761425	0.025224527	0.119956106	SGOL1	shugoshin-like 1 (S. pombe)
ENSG00000174576	0.004789189	0.025348525	0.035412144	NPAS4	neuronal PAS domain protein 4
ENSG00000121797	0.004812608	0.025446018	0.053428951	CCRL2	chemokine (C-C motif) receptor-like 2
ENSG00000188032	0.004891747	0.02581752	0.015898507	C19orf67	chromosome 19 open reading frame 67
ENSG00000122574	0.00492429	0.025972438	0.051638763	WIPF3	WAS/WASL interacting protein family, member 3
ENSG00000178217	0.004926055	0.025978382	0.00859399	SH2D4B	SH2 domain containing 4B
ENSG00000115339	0.004926759	0.02597873	0.031342852	GALNT3	polypeptide N-acetylgalactosaminyltransferase 3
ENSG00000198963	0.004947741	0.026075861	0.002087298	RORB	RAR-related orphan receptor B
ENSG00000106013	0.004956314	0.026110805	0.065059625	ANKRD7	ankyrin repeat domain 7
ENSG00000170743	0.004957916	0.026112591	0.014068687	SYT9	synaptotagmin IX
ENSG00000229015	0.004972187	0.026168721	0.041079895	LOC100506790	uncharacterized LOC100506790
ENSG00000161180	0.005020227	0.026392975	0.013792018	CCDC116	coiled-coil domain containing 116
ENSG00000140968	0.00503332	0.026441327	0.017285484	IRF8	interferon regulatory factor 8
ENSG00000152969	0.005035277	0.026448193	0.009175561	JAKMIP1	janus kinase and microtubule interacting protein 1
ENSG00000116329	0.005040601	0.026465919	0.012100254	OPRD1	opioid receptor, delta 1
ENSG00000070808	0.005051271	0.026515104	0.042773982	CAMK2A	calcium/calmodulin-dependent protein kinase II alpha
ENSG00000185904	0.005053534	0.02652356	0.087991001	LINC00839	long intergenic non-protein coding RNA 839

ENSG00000206026	0.005079951	0.026621034	0.002741715	SMIM21	small integral membrane protein 21
ENSG00000134533	0.005115584	0.026770794	0.022783854	RERG	RAS-like, estrogen-regulated, growth inhibitor
ENSG00000172201	0.005118243	0.026780341	0.03488459	ID4	inhibitor of DNA binding 4, dominant negative helix-loop-helix protein
ENSG00000152785	0.005139288	0.026869739	0.007183323	BMP3	bone morphogenetic protein 3
ENSG00000141505	0.005163044	0.026980087	0.175158429	ASGR1	asialoglycoprotein receptor 1
ENSG00000251247	0.005276061	0.027467057	0.031126698	ZNF345	zinc finger protein 345
ENSG00000120471	0.005400324	0.028036517	0.02061314	TP53AI1	tumor protein p53 regulated apoptosis inducing protein 1
ENSG00000248771	0.005409162	0.028057355	0.071919185	LINC01207	long intergenic non-protein coding RNA 1207
ENSG00000137251	0.005451764	0.02824236	0.027048539	TINAG	tubulointerstitial nephritis antigen
ENSG00000185668	0.005460159	0.028275521	0.020959374	POU3F1	POU class 3 homeobox 1
ENSG00000151883	0.005506774	0.028465765	0.021871376	PARP8	poly (ADP-ribose) polymerase family, member 8
ENSG00000116106	0.005519123	0.028515119	0.118115933	EPHA4	EPH receptor A4
ENSG00000116703	0.005536152	0.028588588	0.031997655	PDC	phosducin
ENSG00000113946	0.005546426	0.028634384	0.038239964	CLDN16	claudin 16
ENSG00000140623	0.005590525	0.028821853	0.033225776	42625	septin 12
ENSG00000235480	0.005605373	0.028880121	0.016260382	LOC105373496	uncharacterized LOC105373496
ENSG00000214407	0.00560862	0.028885883	0.155547474	LOC152225	uncharacterized LOC152225
ENSG00000170681	0.005613173	0.028902851	0.119619989	MURC	muscle-related coiled-coil protein
ENSG00000164796	0.005620194	0.028930188	0.014027548	CSMD3	CUB and Sushi multiple domains 3
ENSG00000162951	0.005647933	0.029047938	0.003146493	LRRTM1	leucine rich repeat transmembrane neuronal 1
ENSG00000149131	0.005722079	0.029388633	0.017199864	SERPING1	serpin peptidase inhibitor, clade G (C1 inhibitor), member 1
ENSG00000233776	0.005732102	0.029432499	0.165564289	LINC01251	long intergenic non-protein coding RNA 1251
ENSG00000106526	0.005742888	0.029476733	0.017862941	ACTR3C	ARP3 actin-related protein 3 homolog C (yeast)
ENSG00000118513	0.005799915	0.029717247	0.033627981	MYB	v-myb avian myeloblastosis viral oncogene homolog
ENSG00000146950	0.0058431	0.029930727	0.033445587	SHROOM2	shroom family member 2
ENSG00000102384	0.00585122	0.029953033	0.062842032	CENPI	centromere protein 1
ENSG00000168004	0.005931523	0.030292206	0.019010981	HRASL5	HRAS-like suppressor family, member 5
ENSG00000186086	0.005946054	0.030347386	0.029549305	NBPF6	neuroblastoma breakpoint family, member 6
ENSG00000164512	0.006056545	0.03083401	0.031985937	ANKRD55	ankyrin repeat domain 55
ENSG00000173295	0.006078097	0.030926157	0.152643324	FAM86B3P	family with sequence similarity 86, member A pseudogene
ENSG00000090382	0.006150263	0.031252514	0.028805504	LYZ	lysozyme
ENSG00000181450	0.006197644	0.03146187	0.123947304	ZNF678	zinc finger protein 678
ENSG00000183148	0.006255802	0.031701774	0.01508871	ANKRD20A2	ankyrin repeat domain 20 family, member A2
ENSG00000165259	0.006292668	0.031854728	0.072992864	HDX	highly divergent homeobox
ENSG00000259954	0.006295845	0.031857117	0.099610446	IL21R-AS1	IL21R antisense RNA 1
ENSG00000101883	0.006319423	0.031940699	0.083729898	RHOXF1	Rhox homeobox family, member 1
ENSG00000182168	0.006331331	0.031988975	0.02542122	UNC5C	unc-5 netrin receptor C
ENSG00000134571	0.006338987	0.032019711	0.051894937	MYBPC3	myosin binding protein C, cardiac
ENSG00000233382	0.006364794	0.032126097	0.104708305	NKAPP1	NFKB activating protein pseudogene 1
ENSG00000187527	0.006376902	0.032168821	0.007154221	ATP13A5	ATPase type 13A5
ENSG00000095587	0.006377987	0.032168821	0.032002932	TLL2	tollid-like 2
ENSG00000278848	0.006388239	0.032212548	0.102420703	LOC102723655	TP53-target gene 3 protein
ENSG00000133863	0.006458444	0.032482081	0.012123935	TEX15	testis expressed 15
ENSG00000086991	0.006498237	0.032637871	0.009024291	NOX4	NADPH oxidase 4
ENSG00000182901	0.006529685	0.032791777	0.067828842	RG57	regulator of G-protein signaling 7
ENSG00000170099	0.006551215	0.032883717	0.060913831	SERPINA6	serpin peptidase inhibitor, clade A (alpha-1 antiproteinase, antitrypsin), member 6
ENSG00000133808	0.006599333	0.033100719	0.038878268	MICALCL	MICAL C-terminal like
ENSG00000203783	0.006614926	0.033158507	0.043765094	PRR9	proline rich 9
ENSG00000112320	0.006660998	0.033352498	0.034924253	SOBP	sine oculis binding protein homolog
ENSG00000228836	0.006753404	0.033728087	0.015115412	CT45A5	cancer/testis antigen family 45, member A5
ENSG00000132677	0.006775552	0.033826256	0.006692405	RHBG	Rh family, B glycoprotein (gene/pseudogene)
ENSG00000172061	0.006803628	0.033949768	0.021153632	LRRC15	leucine rich repeat containing 15
ENSG00000156395	0.006818424	0.034015264	0.007892134	SORCS3	sortilin-related VPS10 domain containing receptor 3
ENSG00000113805	0.006886495	0.034304414	0.007768123	CNTN3	contactin 3 (plasmacytoma associated)
ENSG00000055118	0.006919206	0.034442083	0.035254901	KCNH2	potassium channel, voltage gated eag related subfamily H, member 2
ENSG00000119125	0.006929078	0.034482792	0.023972999	GDA	guanine deaminase
ENSG00000135218	0.006969967	0.034652396	0.016923146	CD36	CD36 molecule (thrombospondin receptor)
ENSG00000100629	0.007008335	0.034830391	0.048211712	CEP128	centrosomal protein 128kDa
ENSG00000251533	0.007038597	0.03495945	0.096597075	LINC00605	long intergenic non-protein coding RNA 605
ENSG00000089169	0.007055463	0.035038947	0.006426881	RPH3A	rabphilin 3A
ENSG00000155011	0.007061157	0.035054401	0.058372377	DKK2	dickkopf WNT signaling pathway inhibitor 2
ENSG00000157856	0.007085922	0.035155913	0.030582127	DRC1	dynein regulatory complex subunit 1
ENSG00000176402	0.007110255	0.035272339	0.095603485	GJC3	gap junction protein, gamma 3, 30.2kDa
ENSG00000182896	0.00712673	0.035330717	0.016205821	TMEM95	transmembrane protein 95
ENSG00000233154	0.007135573	0.035363469	0.024051241	LOC101929023	uncharacterized LOC101929023

ENSG00000112175	0.007172097	0.035497994	0.004869148	BMP5	bone morphogenetic protein 5
ENSG00000143297	0.007220346	0.035667859	0.003095647	FCRL5	Fc receptor-like 5
ENSG00000128340	0.007223204	0.03567618	0.035185344	RAC2	ras-related C3 botulinum toxin substrate 2 (rho family, small GTP binding protein Rac2)
ENSG00000177932	0.007226816	0.035689692	0.114565969	ZNF354C	zinc finger protein 354C
ENSG00000164342	0.007255336	0.035808821	0.027486465	TLR3	toll-like receptor 3
ENSG00000249241	0.007265738	0.035851468	0.047678998	LOC101060498	uncharacterized LOC101060498
ENSG00000177363	0.007294405	0.035971125	0.080584391	LRRN4CL	LRRN4 C-terminal like
ENSG00000165443	0.007322276	0.036082349	0.037196008	PHYHIPL	phytanoyl-CoA 2-hydroxylase interacting protein-like
ENSG00000172967	0.007368945	0.036255282	0.01525377	XKR3	XK, Kell blood group complex subunit-related family, member 3
ENSG00000203989	0.007436626	0.036544113	0.004481367	RHOXF2B	Rhox homeobox family, member 2B
ENSG00000158764	0.007446798	0.036585269	0.031142781	ITLN2	intelectin 2
ENSG00000258689	0.007456167	0.036622461	0.082857713	LINC01269	long intergenic non-protein coding RNA 1269
ENSG00000114646	0.007510007	0.036846907	0.097059566	CSPG5	chondroitin sulfate proteoglycan 5 (neuroglycan C)
ENSG00000109458	0.007511872	0.036851613	0.117656171	GAB1	GRB2-associated binding protein 1
ENSG00000118017	0.007513738	0.036851891	0.014920886	A4GNT	alpha-1,4-N-acetylglucosaminyltransferase
ENSG00000147231	0.007526587	0.036888249	0.022428303	Cxorf57	chromosome X open reading frame 57
ENSG00000080166	0.00753166	0.036908671	0.005096757	DCT	dopachrome tautomerase
ENSG00000107831	0.007635227	0.037326352	0.060661302	FGF8	fibroblast growth factor 8 (androgen-induced)
ENSG00000112246	0.007656444	0.03740313	0.002834353	SIM1	single-minded family bHLH transcription factor 1
ENSG00000131831	0.007699998	0.037567969	0.06020866	RAI2	retinoic acid induced 2
ENSG00000253203	0.007707419	0.037589017	0.034125162	GUSBP3	glucuronidase, beta pseudogene 3
ENSG00000250722	0.007709188	0.03759314	0.023617617	SEPP1	selenoprotein P, plasma, 1
ENSG00000223382	0.007750557	0.037765771	0.02355955	LOC105378622	uncharacterized LOC105378622
ENSG00000169885	0.007770314	0.037839406	0.153793497	CALML6	calmodulin-like 6
ENSG00000158869	0.007784887	0.037894204	0.135580852	FCER1G	Fc fragment of IgE, high affinity I, receptor for; gamma polypeptide
ENSG00000128284	0.007823161	0.038052716	0.010823762	APOL3	apolipoprotein L, 3
ENSG00000135374	0.007823993	0.038052716	0.005109342	ELF5	E74-like factor 5 (ets domain transcription factor)
ENSG00000135363	0.007883244	0.038276881	0.074377977	LMO2	LIM domain only 2 (rhombotin-like 1)
ENSG00000058335	0.007966371	0.038593063	0.011689197	RASGRF1	Ras protein-specific guanine nucleotide-releasing factor 1
ENSG00000128253	0.007972957	0.038620376	0.125814131	RFPL2	ret finger protein-like 2
ENSG00000150051	0.00810252	0.039173404	0.02436659	MKX	mohawk homeobox
ENSG00000187730	0.008105026	0.039180867	0.12386551	GABRD	gamma-aminobutyric acid (GABA) A receptor, delta
ENSG00000178171	0.008131333	0.039280061	0.00519638	AMER3	APC membrane recruitment protein 3
ENSG00000157368	0.008156443	0.039373332	0.038878239	IL34	interleukin 34
ENSG00000261186	0.008187014	0.039478784	0.122156028	LOC102723927	uncharacterized LOC102723927
ENSG00000234380	0.008227032	0.039664858	0.042496407	LINC01426	long intergenic non-protein coding RNA 1426
ENSG00000177692	0.00822883	0.03966633	0.097778778	DNAJC28	DnaJ (Hsp40) homolog, subfamily C, member 28
ENSG00000204882	0.008239695	0.039709304	0.037879875	GPR20	G protein-coupled receptor 20
ENSG00000124134	0.008245436	0.039722865	0.009645374	KCNS1	potassium voltage-gated channel, modifier subfamily S, member 1
ENSG00000132693	0.008254216	0.039751055	0.006016411	CRP	C-reactive protein, pentraxin-related
ENSG00000242759	0.008287079	0.039885729	0.012443042	LINC00882	long intergenic non-protein coding RNA 882
ENSG00000124568	0.00840979	0.04038564	0.036710986	SLC17A1	solute carrier family 17 (organic anion transporter), member 1
ENSG00000143847	0.008418541	0.040413362	0.01539055	PPFIA4	protein tyrosine phosphatase, receptor type, f polypeptide (PTPRF), interacting protein (liprin), alpha 4
ENSG00000122025	0.008440888	0.040501541	0.01479604	FLT3	fms-related tyrosine kinase 3
ENSG00000163239	0.008442244	0.040501676	0.013445578	TDRD10	tudor domain containing 10
ENSG00000144847	0.00850298	0.040741861	0.034618998	IGSF11	immunoglobulin superfamily, member 11
ENSG00000198010	0.008516307	0.040796116	0.005393561	DLGAP2	discs, large (Drosophila) homolog-associated protein 2
ENSG00000256576	0.00851957	0.040806948	0.150127298	LOC100996246	uncharacterized LOC100996246
ENSG00000142611	0.008642919	0.041310292	0.036593874	PRDM16	PR domain containing 16
ENSG00000171517	0.008726041	0.041639158	0.019914075	LPAR3	lysophosphatidic acid receptor 3
ENSG00000188779	0.008739783	0.04169017	0.034896994	SKOR1	SKI family transcriptional corepressor 1
ENSG00000181896	0.008742235	0.041692005	0.147110229	ZNF101	zinc finger protein 101
ENSG00000170516	0.008829634	0.042046993	0.035692519	COX7B2	cytochrome c oxidase subunit VIIb2
ENSG00000087589	0.008833027	0.042051117	0.014690078	CASS4	Cas scaffolding protein family member 4
ENSG00000151025	0.008866802	0.042187245	0.00722389	GPR158	G protein-coupled receptor 158
ENSG00000187242	0.008953449	0.042539852	0.023591647	KRT12	keratin 12, type I
ENSG00000181995	0.008985587	0.042657703	0.005666298	LINC00301	long intergenic non-protein coding RNA 301
ENSG00000185052	0.009064183	0.042990728	0.023730625	SLC24A3	solute carrier family 24 (sodium/potassium/calcium exchanger), member 3
ENSG00000135298	0.00906989	0.043012785	0.012658308	ADGRB3	adhesion G protein-coupled receptor B3
ENSG00000225556	0.009089392	0.04309376	0.00897163	C2CD4D	C2 calcium-dependent domain containing 4D
ENSG00000123700	0.009148843	0.043306509	0.056046965	KCNJ2	potassium channel, inwardly rectifying subfamily J, member 2
ENSG00000248587	0.009154979	0.043330517	0.026579461	GDNF-AS1	GDNF antisense RNA 1 (head to head)
ENSG00000160505	0.009159056	0.043344776	0.011426904	NLRP4	NLR family, pyrin domain containing 4
ENSG00000132010	0.00920876	0.04354457	0.022034252	ZNF20	zinc finger protein 20
ENSG00000203697	0.009271848	0.043792033	0.011864738	CAPN8	calpain 8

ENSG00000260220	0.009273978	0.043792852	0.01120183	CCDC187	coiled-coil domain containing 187
ENSG00000145241	0.009334918	0.044028634	0.125123455	CENPC	centromere protein C
ENSG00000115423	0.00946382	0.044496883	0.018517602	DNAH6	dynein, axonemal, heavy chain 6
ENSG00000023892	0.009504217	0.044630687	0.115278297	DEF6	DEF6 guanine nucleotide exchange factor
ENSG00000148680	0.009524861	0.044717317	0.061531339	HTR7	5-hydroxytryptamine (serotonin) receptor 7, adenylate cyclase-coupled
ENSG00000169605	0.009529205	0.044727396	0.095615747	GKN1	gastrokine 1
ENSG00000145700	0.00953601	0.044749022	0.022621331	ANKRD31	ankyrin repeat domain 31
ENSG00000158517	0.009588786	0.044960406	0.019893168	NCF1	neutrophil cytosolic factor 1
ENSG00000234284	0.009599063	0.045003413	0.129857644	ZNF879	zinc finger protein 879
ENSG00000182885	0.009632071	0.045137378	0.030795241	ADGRG3	adhesion G protein-coupled receptor G3
ENSG00000117643	0.009709764	0.045412606	0.032759734	MAN1C1	mannosidase, alpha, class 1C, member 1
ENSG00000148704	0.00989569	0.046165523	0.045622537	VAX1	ventral anterior homeobox 1
ENSG00000123388	0.009904631	0.046196653	0.058461064	HOXC11	homeobox C11
ENSG00000226629	0.00993594	0.046326761	0.003228956	LINC00974	long intergenic non-protein coding RNA 974
ENSG00000271236	0.01001669	0.046623883	0.025530662	SUMO2P15	SUMO2 pseudogene 15
ENSG00000171049	0.010058788	0.04677635	0.008517486	FPR2	formyl peptide receptor 2
ENSG00000196391	0.010100385	0.046932269	0.039987608	ZNF774	zinc finger protein 774
ENSG00000196972	0.010121507	0.047014319	0.04149644	SMIM10L2B	small integral membrane protein 10 like 2B
ENSG00000110203	0.010140387	0.04707779	0.079673557	FOLR3	folate receptor 3 (gamma)
ENSG00000228630	0.010281694	0.047655098	0.055996265	HOTAIR	HOX transcript antisense RNA
ENSG00000198021	0.010324927	0.047833697	0.037986874	SPANXA1	sperm protein associated with the nucleus, X-linked, family member A1
ENSG00000160111	0.010332896	0.047854282	0.007768186	CPAMD8	C3 and PZP-like, alpha-2-macroglobulin domain containing 8
ENSG00000171791	0.010339166	0.047877875	0.018406794	BCL2	B-cell CLL/lymphoma 2
ENSG00000215018	0.01034923	0.047913583	0.017601472	COL28A1	collagen, type XXVIII, alpha 1
ENSG00000233396	0.010351363	0.047918008	0.135394354	LOC101928979	uncharacterized LOC101928979
ENSG00000135220	0.010359537	0.047944947	0.090089068	UGT2A3	UDP glucuronosyltransferase 2 family, polypeptide A3
ENSG00000165025	0.010390949	0.048057548	0.023035368	SYK	spleen tyrosine kinase
ENSG00000156475	0.010401053	0.048087894	0.002725004	PPP2R2B	protein phosphatase 2, regulatory subunit B, beta
ENSG00000251620	0.010405917	0.048094	0.019091329	STPG2-AS1	STPG2 antisense RNA 1
ENSG00000163359	0.010445522	0.048259629	0.009367705	COL6A3	collagen, type VI, alpha 3
ENSG00000186051	0.010459255	0.04829666	0.034956733	TAL2	T-cell acute lymphocytic leukemia 2
ENSG00000118514	0.01052738	0.048556171	0.122173896	ALDH8A1	aldehyde dehydrogenase 8 family, member A1
ENSG00000138653	0.010576571	0.048749924	0.005314489	NDST4	N-deacetylase/N-sulfotransferase (heparan glucosaminyl) 4
ENSG00000160963	0.010597	0.048821977	0.087587664	COL26A1	collagen, type XXVI, alpha 1
ENSG00000226995	0.010607789	0.048855102	0.006788336	LINC00658	long intergenic non-protein coding RNA 658
ENSG00000168594	0.010645069	0.048995258	0.007906971	ADAM29	ADAM metalloproteinase domain 29
ENSG00000164556	0.010652584	0.049017055	0.045579065	FAM183BP	acyloxyacyl hydrolase (neutrophil)
ENSG00000189325	0.010693185	0.049137244	0.009067982	C6orf222	chromosome 6 open reading frame 222
ENSG00000174473	0.010771549	0.04941926	0.022430632	GALNTL6	polypeptide N-acetylgalactosaminyltransferase-like 6
ENSG00000180767	0.010774026	0.049425054	0.148831329	CHST13	carbohydrate (chondroitin 4) sulfotransferase 13
ENSG00000188981	0.010871776	0.049822958	0.024588402	MSANTD1	Myb/SANT-like DNA-binding domain containing 1

Supplement Table 2. The number of genes in WGCNA sub-modules.

Gene Lv.	BLUE				grey	TURQUOISE				total
Module	black	blue	brown	green		pink	red	turquoise	yellow	
# of Genes ($\beta = 0.9$)	417				8	588				1013
# of Genes ($\beta = 0.25$)	69	142	123	83		44	75	361	108	

Supplement Table 3. DAVIDS results in WGCNA sub-modules.

Group	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	d Enrichm	Bonferroni	Benjamini	FDR
blue	BBID	109.Chemokine_families	7	0.904393	3.14E-04	ENSG00000006210,	17	25	358	5.896471	0.005638	0.005638	0.231253
blue	BIOCARTA	h_eicosanoidPathway:Eicosanoid Metabolism	4	0.516796	0.013038	ENSG00000160013,	36	21	1437	7.603175	0.645399	0.645399	12.99209
blue	BIOCARTA	h_nuclearRsPathway:Nuclear Receptors in Lipid Metabolis	4	0.516796	0.054569	ENSG00000186951,	36	36	1437	4.435185	0.988122	0.891014	44.84806
blue	COG_ONTOLOGY	Secondary metabolites biosynthesis, transport, and catab	11	1.421189	1.24E-05	ENSG00000108242,	59	65	1950	5.59322	1.98E-04	1.98E-04	0.008786
blue	GOTERM_BP_FAT	GO:0007610~behavior	36	4.651163	2.13E-05	ENSG00000204640,	475	469	13528	2.186098	0.050452	0.050452	0.037509
blue	GOTERM_BP_FAT	GO:0007626~locomotory behavior	25	3.229974	3.65E-05	ENSG00000204640,	475	274	13528	2.59854	0.08471	0.043292	0.064124
blue	GOTERM_BP_FAT	GO:0048598~embryonic morphogenesis	26	3.359173	8.23E-05	ENSG00000149256,	475	307	13528	2.411987	0.180929	0.064363	0.14453
blue	GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	16	2.067183	9.06E-05	ENSG00000143556,	475	137	13528	3.326131	0.197408	0.053493	0.159237
blue	GOTERM_BP_FAT	GO:0006935~chemotaxis	17	2.196382	1.57E-04	ENSG00000156234,	475	160	13528	3.026	0.316987	0.073414	0.275897
blue	GOTERM_BP_FAT	GO:0042330~taxis	17	2.196382	1.57E-04	ENSG00000156234,	475	160	13528	3.026	0.316987	0.073414	0.275897
blue	GOTERM_BP_FAT	GO:0007218~neuropeptide signaling pathway	12	1.550388	3.97E-04	ENSG00000197487,	475	93	13528	3.674839	0.618378	0.148328	0.695671
blue	GOTERM_BP_FAT	GO:0007267~cell-cell signaling	38	4.909561	6.10E-04	ENSG00000156234,	475	600	13528	1.803733	0.772642	0.190715	1.067677
blue	GOTERM_BP_FAT	GO:0001501~skeletal system development	24	3.100775	8.86E-04	ENSG00000009709,	475	319	13528	2.142696	0.883493	0.235647	1.545848
blue	GOTERM_BP_FAT	GO:0006952~defense response	38	4.909561	9.43E-04	ENSG00000164047,	475	615	13528	1.75974	0.898674	0.224602	1.645403
blue	GOTERM_BP_FAT	GO:0009611~response to wounding	34	4.392765	9.73E-04	ENSG00000135218,	475	530	13528	1.827019	0.905643	0.210272	1.696182
blue	GOTERM_BP_FAT	GO:0043583~ear development	11	1.421189	0.001785	ENSG00000152977,	475	95	13528	3.297684	0.986895	0.325691	3.092474
blue	GOTERM_BP_FAT	GO:0042471~ear morphogenesis	9	1.162791	0.002067	ENSG00000152977,	475	66	13528	3.883636	0.993388	0.341799	3.571773
blue	GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	13	1.679587	0.002464	ENSG00000152977,	475	133	13528	2.783759	0.997485	0.36898	4.244805
blue	GOTERM_BP_FAT	GO:0060429~epithelium development	18	2.325581	0.002715	ENSG00000143556,	475	227	13528	2.258326	0.998634	0.375712	4.667558
blue	GOTERM_BP_FAT	GO:0007423~sensory organ development	18	2.325581	0.002976	ENSG00000152977,	475	229	13528	2.238603	0.999276	0.382502	5.105359
blue	GOTERM_BP_FAT	GO:0030182~neuron differentiation	28	3.617571	0.003241	ENSG00000135333,	475	438	13528	1.820639	0.99962	0.388725	5.547296
blue	GOTERM_BP_FAT	GO:0030326~embryonic limb morphogenesis	10	1.29199	0.003359	ENSG00000106031,	475	87	13528	3.273563	0.999715	0.381356	5.744566
blue	GOTERM_BP_FAT	GO:0035113~embryonic appendage morphogenesis	10	1.29199	0.003359	ENSG00000106031,	475	87	13528	3.273563	0.999715	0.381356	5.744566
blue	GOTERM_BP_FAT	GO:0045165~cell fate commitment	13	1.679587	0.003548	ENSG00000009709,	475	139	13528	2.663597	0.99982	0.38059	6.056846
blue	GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduct	87	11.24031	0.00357	ENSG00000135333,	475	1856	13528	1.335	0.999829	0.366603	6.094102
blue	GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	14	1.808786	0.003931	ENSG00000006210,	475	159	13528	2.507673	0.999929	0.379872	6.691097
blue	GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signalir	57	7.364341	0.004437	ENSG000000054179,	475	1123	13528	1.445557	0.999979	0.40176	7.52075
blue	GOTERM_BP_FAT	GO:0007586~digestion	10	1.29199	0.004542	ENSG00000015520,	475	91	13528	3.12967	0.999984	0.394678	7.691403
blue	GOTERM_BP_FAT	GO:0006805~xenobiotic metabolic process	5	0.645995	0.004613	ENSG00000135226,	475	20	13528	7.12	0.999987	0.385948	7.806831
blue	GOTERM_BP_FAT	GO:0048608~reproductive structure development	12	1.550388	0.004724	ENSG00000106031,	475	126	13528	2.712381	0.99999	0.380404	7.988358
blue	GOTERM_BP_FAT	GO:0006954~inflammatory response	22	2.842377	0.005383	ENSG00000143546,	475	325	13528	1.927877	0.999998	0.407706	9.052545
blue	GOTERM_BP_FAT	GO:0002064~epithelial cell development	5	0.645995	0.005543	ENSG00000119547,	475	21	13528	6.780952	0.999999	0.404659	9.309438
blue	GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	18	2.325581	0.005877	ENSG00000182636,	475	245	13528	2.092408	0.999999	0.411165	9.843692
blue	GOTERM_BP_FAT	GO:0007389~pattern specification process	19	2.45478	0.006261	ENSG00000009709,	475	267	13528	2.026667	1	0.419671	10.45384
blue	GOTERM_BP_FAT	GO:0006955~immune response	38	4.909561	0.006454	ENSG00000143556,	475	690	13528	1.568464	1	0.418197	10.7587
blue	GOTERM_BP_FAT	GO:0008585~female gonad development	8	1.033592	0.006874	ENSG00000204837,	475	64	13528	3.56	1	0.427526	11.42012
blue	GOTERM_BP_FAT	GO:0000902~cell morphogenesis	23	2.971576	0.007389	ENSG00000182636,	475	356	13528	1.84	1	0.44032	12.22428
blue	GOTERM_BP_FAT	GO:0048568~embryonic organ development	14	1.808786	0.007554	ENSG00000152977,	475	172	13528	2.31814	1	0.437235	12.48118
blue	GOTERM_BP_FAT	GO:0009410~response to xenobiotic stimulus	5	0.645995	0.00776	ENSG00000135226,	475	23	13528	6.191304	1	0.436013	12.79984
blue	GOTERM_BP_FAT	GO:0002088~lens development in camera-type eye	5	0.645995	0.00776	ENSG00000146950,	475	23	13528	6.191304	1	0.436013	12.79984
blue	GOTERM_BP_FAT	GO:0035107~appendage morphogenesis	10	1.29199	0.007858	ENSG00000106031,	475	99	13528	2.876768	1	0.430442	12.95042
blue	GOTERM_BP_FAT	GO:0035108~limb morphogenesis	10	1.29199	0.007858	ENSG00000106031,	475	99	13528	2.876768	1	0.430442	12.95042
blue	GOTERM_BP_FAT	GO:0007409~axonogenesis	15	1.937984	0.008081	ENSG00000182636,	475	193	13528	2.213472	1	0.430163	13.29404
blue	GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	16	2.067183	0.00822	ENSG00000182636,	475	213	13528	2.139343	1	0.42663	13.50733
blue	GOTERM_BP_FAT	GO:0048666~neuron development	22	2.842377	0.008394	ENSG00000182636,	475	339	13528	1.84826	1	0.424619	13.77436
blue	GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	17	2.196382	0.008822	ENSG00000135218,	475	235	13528	2.060255	1	0.432034	14.42527

blue	GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	18	2.325581	0.00897	ENSG00000182636,	475	256	13528	2.0025	1	0.429062	14.64954
blue	GOTERM_BP_FAT	GO:0031175~neuron projection development	18	2.325581	0.00897	ENSG00000182636,	475	256	13528	2.0025	1	0.429062	14.64954
blue	GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	15	1.937984	0.009196	ENSG00000185052,	475	196	13528	2.179592	1	0.428979	14.99194
blue	GOTERM_BP_FAT	GO:0050953~sensory perception of light stimulus	16	2.067183	0.009292	ENSG00000101850,	475	216	13528	2.10963	1	0.424425	15.13635
blue	GOTERM_BP_FAT	GO:0007601~visual perception	16	2.067183	0.009292	ENSG00000101850,	475	216	13528	2.10963	1	0.424425	15.13635
blue	GOTERM_BP_FAT	GO:0042474~middle ear morphogenesis	4	0.516796	0.009404	ENSG00000183691,	475	13	13528	8.763077	1	0.420611	15.30529
blue	GOTERM_BP_FAT	GO:0031328~positive regulation of cellular biosynthetic p	37	4.780362	0.009953	ENSG00000012504,	475	685	13528	1.538336	1	0.431256	16.12568
blue	GOTERM_BP_FAT	GO:0060173~limb development	10	1.29199	0.010086	ENSG00000106031,	475	103	13528	2.765049	1	0.428194	16.32485
blue	GOTERM_BP_FAT	GO:0048736~appendage development	10	1.29199	0.010086	ENSG00000106031,	475	103	13528	2.765049	1	0.428194	16.32485
blue	GOTERM_BP_FAT	GO:0046660~female sex differentiation	8	1.033592	0.010289	ENSG00000204837,	475	69	13528	3.302029	1	0.427401	16.62546
blue	GOTERM_BP_FAT	GO:0046545~development of primary female sexual char	8	1.033592	0.010289	ENSG00000204837,	475	69	13528	3.302029	1	0.427401	16.62546
blue	GOTERM_BP_FAT	GO:0030030~cell projection organization	23	2.971576	0.010706	ENSG00000182636,	475	368	13528	1.78	1	0.433159	17.24094
blue	GOTERM_BP_FAT	GO:0007369~gastrulation	8	1.033592	0.011098	ENSG00000149256,	475	70	13528	3.254857	1	0.437887	17.81549
blue	GOTERM_BP_FAT	GO:0045088~regulation of innate immune response	7	0.904393	0.011162	ENSG00000171855,	475	54	13528	3.691852	1	0.432963	17.9092
blue	GOTERM_BP_FAT	GO:0009891~positive regulation of biosynthetic process	37	4.780362	0.012224	ENSG00000012504,	475	695	13528	1.516201	1	0.456081	19.44545
blue	GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiati	17	2.196382	0.012364	ENSG00000182636,	475	244	13528	1.984262	1	0.453187	19.6458
blue	GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	15	1.937984	0.013278	ENSG00000185052,	475	205	13528	2.083902	1	0.470525	20.94365
blue	GOTERM_BP_FAT	GO:0045137~development of primary sexual characterist	11	1.421189	0.013789	ENSG00000106031,	475	127	13528	2.466772	1	0.476801	21.65987
blue	GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	17	2.196382	0.014251	ENSG00000168918,	475	248	13528	1.952258	1	0.481613	22.30301
blue	GOTERM_BP_FAT	GO:0050900~leukocyte migration	7	0.904393	0.014372	ENSG00000006210,	475	57	13528	3.497544	1	0.478141	22.46983
blue	GOTERM_BP_FAT	GO:0048511~rhythmic process	11	1.421189	0.014507	ENSG00000204640,	475	128	13528	2.4475	1	0.475116	22.65639
blue	GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron diff	15	1.937984	0.015702	ENSG00000182636,	475	209	13528	2.044019	1	0.496217	24.28808
blue	GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	11	1.421189	0.016026	ENSG00000135218,	475	130	13528	2.409846	1	0.497227	24.72575
blue	GOTERM_BP_FAT	GO:0007168~receptor guanylyl cyclase signaling pathway	3	0.387597	0.016733	ENSG00000172367,	475	6	13528	14.24	1	0.506308	25.67157
blue	GOTERM_BP_FAT	GO:0008406~gonad development	10	1.29199	0.016805	ENSG00000204837,	475	112	13528	2.542857	1	0.501856	25.76638
blue	GOTERM_BP_FAT	GO:0050727~regulation of inflammatory response	8	1.033592	0.016946	ENSG00000006210,	475	76	13528	2.997895	1	0.498945	25.95298
blue	GOTERM_BP_FAT	GO:0007548~sex differentiation	12	1.550388	0.017239	ENSG00000106031,	475	151	13528	2.263311	1	0.499211	26.34012
blue	GOTERM_BP_FAT	GO:0015758~glucose transport	5	0.645995	0.017654	ENSG00000100170,	475	29	13528	4.910345	1	0.501896	26.88517
blue	GOTERM_BP_FAT	GO:0040012~regulation of locomotion	14	1.808786	0.017769	ENSG00000168539,	475	192	13528	2.076667	1	0.498628	27.03602
blue	GOTERM_BP_FAT	GO:0009953~dorsal/ventral pattern formation	7	0.904393	0.018174	ENSG00000009709,	475	60	13528	3.322667	1	0.501042	27.5625
blue	GOTERM_BP_FAT	GO:0016042~lipid catabolic process	13	1.679587	0.018776	ENSG00000204140,	475	173	13528	2.140116	1	0.507101	28.34017
blue	GOTERM_BP_FAT	GO:0008643~carbohydrate transport	7	0.904393	0.01958	ENSG00000100170,	475	61	13528	3.268197	1	0.516579	29.36558
blue	GOTERM_BP_FAT	GO:0008645~hexose transport	5	0.645995	0.019821	ENSG00000100170,	475	30	13528	4.746667	1	0.515625	29.66941
blue	GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	15	1.937984	0.020314	ENSG00000135144,	475	216	13528	1.977778	1	0.519153	30.28948
blue	GOTERM_BP_FAT	GO:0048732~gland development	11	1.421189	0.020337	ENSG00000101144,	475	135	13528	2.320593	1	0.514422	30.31804
blue	GOTERM_BP_FAT	GO:0015749~monosaccharide transport	5	0.645995	0.022145	ENSG00000100170,	475	31	13528	4.593548	1	0.539801	32.54403
blue	GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	23	2.971576	0.023292	ENSG00000182636,	475	397	13528	1.649975	1	0.553033	33.92173
blue	GOTERM_BP_FAT	GO:0048585~negative regulation of response to stimulus	9	1.162791	0.02404	ENSG00000168918,	475	100	13528	2.5632	1	0.559536	34.80666
blue	GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	15	1.937984	0.024187	ENSG00000168918,	475	221	13528	1.933032	1	0.556783	34.97889
blue	GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	22	2.842377	0.027282	ENSG00000185052,	475	380	13528	1.648842	1	0.596201	38.51054
blue	GOTERM_BP_FAT	GO:0010907~positive regulation of glucose metabolic pr	4	0.516796	0.027283	ENSG00000109819,	475	19	13528	5.995789	1	0.591298	38.51126
blue	GOTERM_BP_FAT	GO:0032102~negative regulation of response to external	6	0.775194	0.030052	ENSG00000136250,	475	50	13528	3.4176	1	0.622435	41.51764
blue	GOTERM_BP_FAT	GO:0003013~circulatory system process	13	1.679587	0.030836	ENSG00000135744,	475	186	13528	1.990538	1	0.627245	42.34292
blue	GOTERM_BP_FAT	GO:0008015~blood circulation	13	1.679587	0.030836	ENSG00000135744,	475	186	13528	1.990538	1	0.627245	42.34292
blue	GOTERM_BP_FAT	GO:0045913~positive regulation of carbohydrate metabo	4	0.516796	0.031283	ENSG00000109819,	475	20	13528	5.696	1	0.627879	42.80886
blue	GOTERM_BP_FAT	GO:0010676~positive regulation of cellular carbohydrate	4	0.516796	0.031283	ENSG00000109819,	475	20	13528	5.696	1	0.627879	42.80886
blue	GOTERM_BP_FAT	GO:0042036~negative regulation of cytokine biosynthetic	4	0.516796	0.031283	ENSG00000168918,	475	20	13528	5.696	1	0.627879	42.80886
blue	GOTERM_BP_FAT	GO:0042417~dopamine metabolic process	4	0.516796	0.031283	ENSG00000169418,	475	20	13528	5.696	1	0.627879	42.80886

blue	GOTERM_BP_FAT	GO:0050778~positive regulation of immune response	11	1.421189	0.031403	ENSG00000171855,	475	145	13528	2.160552	1	0.624617	42.93267
blue	GOTERM_BP_FAT	GO:0001708~cell fate specification	6	0.775194	0.032396	ENSG00000103449,	475	51	13528	3.350588	1	0.631627	43.95228
blue	GOTERM_BP_FAT	GO:0048592~eye morphogenesis	7	0.904393	0.033554	ENSG00000101144,	475	69	13528	2.889275	1	0.640203	45.12052
blue	GOTERM_BP_FAT	GO:0043010~camera-type eye development	9	1.162791	0.034187	ENSG00000101144,	475	107	13528	2.395514	1	0.642685	45.74919
blue	GOTERM_BP_FAT	GO:0010557~positive regulation of macromolecule biosynthesis	33	4.263566	0.035418	ENSG00000012504,	475	654	13528	1.437064	1	0.651463	46.95193
blue	GOTERM_BP_FAT	GO:0045923~positive regulation of fatty acid metabolic process	4	0.516796	0.035573	ENSG00000186951,	475	21	13528	5.424762	1	0.6487	47.10191
blue	GOTERM_BP_FAT	GO:0021532~neural tube patterning	4	0.516796	0.035573	ENSG00000009709,	475	21	13528	5.424762	1	0.6487	47.10191
blue	GOTERM_BP_FAT	GO:0007223~Wnt receptor signaling pathway, calcium mobilization	4	0.516796	0.035573	ENSG00000169071,	475	21	13528	5.424762	1	0.6487	47.10191
blue	GOTERM_BP_FAT	GO:0046903~secretion	18	2.325581	0.036092	ENSG00000165269,	475	300	13528	1.7088	1	0.649767	47.59966
blue	GOTERM_BP_FAT	GO:0032956~regulation of actin cytoskeleton organization	8	1.033592	0.036441	ENSG00000146950,	475	89	13528	2.56	1	0.649067	47.93181
blue	GOTERM_BP_FAT	GO:0030335~positive regulation of cell migration	8	1.033592	0.036441	ENSG00000119547,	475	89	13528	2.56	1	0.649067	47.93181
blue	GOTERM_BP_FAT	GO:0048878~chemical homeostasis	27	3.488372	0.037335	ENSG00000156234,	475	512	13528	1.501875	1	0.653896	48.77495
blue	GOTERM_BP_FAT	GO:0019934~cGMP-mediated signaling	3	0.387597	0.037462	ENSG00000135218,	475	9	13528	9.493333	1	0.650968	48.8935
blue	GOTERM_BP_FAT	GO:0045671~negative regulation of osteoclast differentiation	3	0.387597	0.037462	ENSG00000168918,	475	9	13528	9.493333	1	0.650968	48.8935
blue	GOTERM_BP_FAT	GO:0044003~modification by symbiont of host morphology	3	0.387597	0.037462	ENSG00000164342,	475	9	13528	9.493333	1	0.650968	48.8935
blue	GOTERM_BP_FAT	GO:0009617~response to bacterium	13	1.679587	0.039259	ENSG00000171855,	475	193	13528	1.918342	1	0.664361	50.54569
blue	GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	9	1.162791	0.039311	ENSG00000100312,	475	110	13528	2.330182	1	0.660761	50.59285
blue	GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	9	1.162791	0.039311	ENSG00000100312,	475	110	13528	2.330182	1	0.660761	50.59285
blue	GOTERM_BP_FAT	GO:0030595~leukocyte chemotaxis	5	0.645995	0.039495	ENSG00000006210,	475	37	13528	3.848649	1	0.658449	50.75829
blue	GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	38	4.909561	0.041095	ENSG00000128340,	475	787	13528	1.375146	1	0.669301	52.18076
blue	GOTERM_BP_FAT	GO:0032970~regulation of actin filament-based process	8	1.033592	0.042442	ENSG00000146950,	475	92	13528	2.476522	1	0.677393	53.34806
blue	GOTERM_BP_FAT	GO:0031349~positive regulation of defense response	7	0.904393	0.042477	ENSG00000171855,	475	73	13528	2.730959	1	0.673795	53.37813
blue	GOTERM_BP_FAT	GO:0001654~eye development	10	1.29199	0.042483	ENSG00000101144,	475	132	13528	2.157576	1	0.669978	53.38319
blue	GOTERM_BP_FAT	GO:0003006~reproductive developmental process	16	2.067183	0.043603	ENSG00000169071,	475	262	13528	1.739237	1	0.67588	54.33309
blue	GOTERM_BP_FAT	GO:0003002~regionalization	13	1.679587	0.044739	ENSG00000009709,	475	197	13528	1.879391	1	0.681695	55.27722
blue	GOTERM_BP_FAT	GO:0042035~regulation of cytokine biosynthetic process	7	0.904393	0.044919	ENSG00000197272,	475	74	13528	2.694054	1	0.679453	55.42506
blue	GOTERM_BP_FAT	GO:0007498~mesoderm development	7	0.904393	0.044919	ENSG00000101144,	475	74	13528	2.694054	1	0.679453	55.42506
blue	GOTERM_BP_FAT	GO:0051216~cartilage development	7	0.904393	0.044919	ENSG00000054938,	475	74	13528	2.694054	1	0.679453	55.42506
blue	GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	9	1.162791	0.044925	ENSG00000100312,	475	113	13528	2.268319	1	0.675795	55.4297
blue	GOTERM_BP_FAT	GO:0017156~calcium ion-dependent exocytosis	4	0.516796	0.045008	ENSG00000100312,	475	23	13528	4.953043	1	0.672817	55.49809
blue	GOTERM_BP_FAT	GO:0014821~phasic smooth muscle contraction	3	0.387597	0.04576	ENSG00000135744,	475	10	13528	8.544	1	0.67538	56.11031
blue	GOTERM_BP_FAT	GO:0060134~prepulse inhibition	3	0.387597	0.04576	ENSG00000198785,	475	10	13528	8.544	1	0.67538	56.11031
blue	GOTERM_BP_FAT	GO:0050829~defense response to Gram-negative bacterium	3	0.387597	0.04576	ENSG00000143556,	475	10	13528	8.544	1	0.67538	56.11031
blue	GOTERM_BP_FAT	GO:0045123~cellular extravasation	3	0.387597	0.04576	ENSG00000006210,	475	10	13528	8.544	1	0.67538	56.11031
blue	GOTERM_BP_FAT	GO:0042472~inner ear morphogenesis	6	0.775194	0.045794	ENSG00000152977,	475	56	13528	3.051429	1	0.672052	56.13728
blue	GOTERM_BP_FAT	GO:0001775~cell activation	17	2.196382	0.046452	ENSG00000054179,	475	287	13528	1.686969	1	0.673829	56.66634
blue	GOTERM_BP_FAT	GO:0060326~cell chemotaxis	5	0.645995	0.046601	ENSG00000006210,	475	39	13528	3.651282	1	0.671495	56.78508
blue	GOTERM_BP_FAT	GO:0033555~multicellular organismal response to stress	5	0.645995	0.046601	ENSG00000164418,	475	39	13528	3.651282	1	0.671495	56.78508
blue	GOTERM_BP_FAT	GO:0006109~regulation of carbohydrate metabolic process	5	0.645995	0.046601	ENSG00000012504,	475	39	13528	3.651282	1	0.671495	56.78508
blue	GOTERM_BP_FAT	GO:0045321~leukocyte activation	15	1.937984	0.046654	ENSG00000164342,	475	242	13528	1.765289	1	0.668417	56.8271
blue	GOTERM_BP_FAT	GO:0010565~regulation of cellular ketone metabolic process	6	0.775194	0.048815	ENSG00000186951,	475	57	13528	2.997895	1	0.681907	58.51591
blue	GOTERM_BP_FAT	GO:0001503~ossification	9	1.162791	0.048946	ENSG00000152580,	475	115	13528	2.22887	1	0.679482	58.61588
blue	GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organismal growth	15	1.937984	0.049381	ENSG00000137752,	475	244	13528	1.75082	1	0.6794	58.94748
blue	GOTERM_BP_FAT	GO:0001704~formation of primary germ layer	5	0.645995	0.050403	ENSG00000101144,	475	40	13528	3.56	1	0.683703	59.71673
blue	GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	9	1.162791	0.051041	ENSG00000100312,	475	116	13528	2.209655	1	0.685077	60.18984
blue	GOTERM_BP_FAT	GO:0008285~negative regulation of cell proliferation	20	2.583979	0.052024	ENSG00000182636,	475	361	13528	1.577839	1	0.68891	60.90877
blue	GOTERM_BP_FAT	GO:0048729~tissue morphogenesis	12	1.550388	0.052144	ENSG00000101144,	475	180	13528	1.898667	1	0.68651	60.99559
blue	GOTERM_BP_FAT	GO:0048706~embryonic skeletal system development	7	0.904393	0.052763	ENSG00000009709,	475	77	13528	2.589091	1	0.687685	61.44088

blue	GOTERM_BP_FAT	GO:0008016~regulation of heart contraction	7	0.904393	0.052763	ENSG00000178342,	475	77	13528	2.589091	1	0.687685	61.44088
blue	GOTERM_BP_FAT	GO:0006182~cGMP biosynthetic process	3	0.387597	0.054659	ENSG00000169418,	475	11	13528	7.767273	1	0.697654	62.77574
blue	GOTERM_BP_FAT	GO:0002089~lens morphogenesis in camera-type eye	3	0.387597	0.054659	ENSG00000146950,	475	11	13528	7.767273	1	0.697654	62.77574
blue	GOTERM_BP_FAT	GO:0051272~positive regulation of cell motion	8	1.033592	0.056275	ENSG00000119547,	475	98	13528	2.324898	1	0.705323	63.87875
blue	GOTERM_BP_FAT	GO:0040017~positive regulation of locomotion	8	1.033592	0.056275	ENSG00000119547,	475	98	13528	2.324898	1	0.705323	63.87875
blue	GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	12	1.550388	0.057394	ENSG00000143184,	475	183	13528	1.867541	1	0.709499	64.62418
blue	GOTERM_BP_FAT	GO:0030003~cellular cation homeostasis	15	1.937984	0.063867	ENSG00000185052,	475	254	13528	1.68189	1	0.745503	68.66046
blue	GOTERM_BP_FAT	GO:0010259~multicellular organismal aging	3	0.387597	0.064106	ENSG00000168918,	475	12	13528	7.12	1	0.743882	68.80084
blue	GOTERM_BP_FAT	GO:0050905~neuromuscular process	6	0.775194	0.065646	ENSG00000174498,	475	62	13528	2.756129	1	0.749485	69.69093
blue	GOTERM_BP_FAT	GO:0022602~ovulation cycle process	6	0.775194	0.065646	ENSG00000204837,	475	62	13528	2.756129	1	0.749485	69.69093
blue	GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	12	1.550388	0.066901	ENSG00000143184,	475	188	13528	1.817872	1	0.753372	70.39878
blue	GOTERM_BP_FAT	GO:0006575~cellular amino acid derivative metabolic pro	11	1.421189	0.06711	ENSG00000169418,	475	166	13528	1.887229	1	0.751624	70.51553
blue	GOTERM_BP_FAT	GO:0048593~camera-type eye morphogenesis	5	0.645995	0.06725	ENSG00000101144,	475	44	13528	3.236364	1	0.749519	70.59298
blue	GOTERM_BP_FAT	GO:0001656~metanephros development	5	0.645995	0.06725	ENSG00000100170,	475	44	13528	3.236364	1	0.749519	70.59298
blue	GOTERM_BP_FAT	GO:0060348~bone development	9	1.162791	0.067323	ENSG00000152580,	475	123	13528	2.083902	1	0.747073	70.63327
blue	GOTERM_BP_FAT	GO:0043482~cellular pigment accumulation	2	0.258398	0.068852	ENSG00000146950,	475	2	13528	28.48	1	0.752332	71.46826
blue	GOTERM_BP_FAT	GO:0001869~negative regulation of complement activati	2	0.258398	0.068852	ENSG00000175899,	475	2	13528	28.48	1	0.752332	71.46826
blue	GOTERM_BP_FAT	GO:0001868~regulation of complement activation, lectin	2	0.258398	0.068852	ENSG00000175899,	475	2	13528	28.48	1	0.752332	71.46826
blue	GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	20	2.583979	0.068897	ENSG00000185052,	475	374	13528	1.522995	1	0.749788	71.49267
blue	GOTERM_BP_FAT	GO:0046890~regulation of lipid biosynthetic process	5	0.645995	0.071864	ENSG00000136931,	475	45	13528	3.164444	1	0.762101	73.04831
blue	GOTERM_BP_FAT	GO:0050768~negative regulation of neurogenesis	5	0.645995	0.071864	ENSG00000101144,	475	45	13528	3.164444	1	0.762101	73.04831
blue	GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	14	1.808786	0.073187	ENSG00000164342,	475	236	13528	1.689492	1	0.765862	73.71565
blue	GOTERM_BP_FAT	GO:0015908~fatty acid transport	4	0.516796	0.073335	ENSG00000135218,	475	28	13528	4.068571	1	0.763907	73.78937
blue	GOTERM_BP_FAT	GO:0030334~regulation of cell migration	11	1.421189	0.073732	ENSG00000119547,	475	169	13528	1.853728	1	0.763169	73.98633
blue	GOTERM_BP_FAT	GO:0045834~positive regulation of lipid metabolic proce	5	0.645995	0.076636	ENSG00000186951,	475	46	13528	3.095652	1	0.774157	75.38318
blue	GOTERM_BP_FAT	GO:0021537~telencephalon development	6	0.775194	0.077115	ENSG00000106689,	475	65	13528	2.628923	1	0.773761	75.60672
blue	GOTERM_BP_FAT	GO:0006022~aminoglycan metabolic process	6	0.775194	0.077115	ENSG00000173376,	475	65	13528	2.628923	1	0.773761	75.60672
blue	GOTERM_BP_FAT	GO:0002684~positive regulation of immune system proc	14	1.808786	0.077143	ENSG00000168918,	475	238	13528	1.675294	1	0.77133	75.61997
blue	GOTERM_BP_FAT	GO:0044057~regulation of system process	17	2.196382	0.078919	ENSG00000114646,	475	309	13528	1.566861	1	0.776762	76.4318
blue	GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	6	0.775194	0.081163	ENSG00000187173,	475	66	13528	2.589091	1	0.784001	77.42095
blue	GOTERM_BP_FAT	GO:0006690~icosanoid metabolic process	5	0.645995	0.081562	ENSG00000134716,	475	47	13528	3.029787	1	0.783235	77.59288
blue	GOTERM_BP_FAT	GO:0021904~dorsal/ventral neural tube patterning	3	0.387597	0.08445	ENSG00000009709,	475	14	13528	6.102857	1	0.792759	78.79973
blue	GOTERM_BP_FAT	GO:0007263~nitric oxide mediated signal transduction	3	0.387597	0.08445	ENSG00000135218,	475	14	13528	6.102857	1	0.792759	78.79973
blue	GOTERM_BP_FAT	GO:0048512~circadian behavior	3	0.387597	0.08445	ENSG00000204640,	475	14	13528	6.102857	1	0.792759	78.79973
blue	GOTERM_BP_FAT	GO:0046068~cGMP metabolic process	3	0.387597	0.08445	ENSG00000169418,	475	14	13528	6.102857	1	0.792759	78.79973
blue	GOTERM_BP_FAT	GO:0030204~chondroitin sulfate metabolic process	3	0.387597	0.08445	ENSG00000173376,	475	14	13528	6.102857	1	0.792759	78.79973
blue	GOTERM_BP_FAT	GO:0048589~developmental growth	7	0.904393	0.084576	ENSG00000152580,	475	87	13528	2.291494	1	0.790876	78.85106
blue	GOTERM_BP_FAT	GO:0042698~ovulation cycle	6	0.775194	0.085322	ENSG00000204837,	475	67	13528	2.550448	1	0.7915	79.15193
blue	GOTERM_BP_FAT	GO:0050801~ion homeostasis	21	2.713178	0.085378	ENSG00000185052,	475	409	13528	1.462298	1	0.78936	79.17435
blue	GOTERM_BP_FAT	GO:0045638~negative regulation of myeloid cell differen	4	0.516796	0.08642	ENSG00000168918,	475	30	13528	3.797333	1	0.791168	79.58739
blue	GOTERM_BP_FAT	GO:0046620~regulation of organ growth	4	0.516796	0.08642	ENSG00000183691,	475	30	13528	3.797333	1	0.791168	79.58739
blue	GOTERM_BP_FAT	GO:0050729~positive regulation of inflammatory respons	4	0.516796	0.08642	ENSG00000006210,	475	30	13528	3.797333	1	0.791168	79.58739
blue	GOTERM_BP_FAT	GO:0010721~negative regulation of cell development	5	0.645995	0.086641	ENSG00000101144,	475	48	13528	2.966667	1	0.789715	79.67427
blue	GOTERM_BP_FAT	GO:0021915~neural tube development	6	0.775194	0.089591	ENSG00000009709,	475	68	13528	2.512941	1	0.798825	80.79801
blue	GOTERM_BP_FAT	GO:0007398~ectoderm development	12	1.550388	0.09123	ENSG00000187173,	475	199	13528	1.717387	1	0.802679	81.39655
blue	GOTERM_BP_FAT	GO:0001655~urogenital system development	8	1.033592	0.091491	ENSG00000100170,	475	110	13528	2.071273	1	0.801407	81.49035
blue	GOTERM_BP_FAT	GO:0055114~oxidation reduction	30	3.875969	0.092358	ENSG00000138109,	475	639	13528	1.337089	1	0.802364	81.79856
blue	GOTERM_BP_FAT	GO:0046456~icosanoid biosynthetic process	4	0.516796	0.093306	ENSG00000107317,	475	31	13528	3.674839	1	0.803597	82.12994

blue	GOTERM_BP_FAT	GO:0006811~ion transport	35	4.521964	0.093639	ENSG00000100170,	475	768	13528	1.297917	1	0.80261	82.24484
blue	GOTERM_BP_FAT	GO:0007631~feeding behavior	6	0.775194	0.093969	ENSG00000197587,	475	69	13528	2.476522	1	0.801622	82.35824
blue	GOTERM_BP_FAT	GO:0005976~polysaccharide metabolic process	8	1.033592	0.094881	ENSG00000136250,	475	111	13528	2.052613	1	0.802717	82.6677
blue	GOTERM_BP_FAT	GO:0042116~macrophage activation	3	0.387597	0.095257	ENSG00000164342,	475	15	13528	5.696	1	0.801908	82.794
blue	GOTERM_BP_FAT	GO:0045124~regulation of bone resorption	3	0.387597	0.095257	ENSG00000168918,	475	15	13528	5.696	1	0.801908	82.794
blue	GOTERM_BP_FAT	GO:0046850~regulation of bone remodeling	3	0.387597	0.095257	ENSG00000168918,	475	15	13528	5.696	1	0.801908	82.794
blue	GOTERM_BP_FAT	GO:0050773~regulation of dendrite development	3	0.387597	0.095257	ENSG00000115297,	475	15	13528	5.696	1	0.801908	82.794
blue	GOTERM_BP_FAT	GO:0001662~behavioral fear response	3	0.387597	0.095257	ENSG00000164418,	475	15	13528	5.696	1	0.801908	82.794
blue	GOTERM_BP_FAT	GO:0002209~behavioral defense response	3	0.387597	0.095257	ENSG00000164418,	475	15	13528	5.696	1	0.801908	82.794
blue	GOTERM_BP_FAT	GO:0019725~cellular homeostasis	23	2.971576	0.098105	ENSG00000185052,	475	466	13528	1.405665	1	0.809663	83.72186
blue	GOTERM_BP_FAT	GO:0048705~skeletal system morphogenesis	8	1.033592	0.098339	ENSG00000133937,	475	112	13528	2.034286	1	0.80837	83.79597
blue	GOTERM_BP_FAT	GO:0042742~defense response to bacterium	8	1.033592	0.098339	ENSG00000171855,	475	112	13528	2.034286	1	0.80837	83.79597
blue	GOTERM_BP_FAT	GO:0019216~regulation of lipid metabolic process	8	1.033592	0.098339	ENSG00000186951,	475	112	13528	2.034286	1	0.80837	83.79597
blue	GOTERM_BP_FAT	GO:0007229~integrin-mediated signaling pathway	6	0.775194	0.098454	ENSG00000008277,	475	70	13528	2.441143	1	0.806681	83.83225
blue	GOTERM_BP_FAT	GO:0051173~positive regulation of nitrogen compound m	30	3.875969	0.098668	ENSG00000012504,	475	644	13528	1.326708	1	0.805335	83.89952
blue	GOTERM_CC_FAT	GO:0005576~extracellular region	116	14.98708	9.36E-09	ENSG00000143556,	442	2010	12782	1.668931	2.83E-06	2.83E-06	1.25E-05
blue	GOTERM_CC_FAT	GO:0044421~extracellular region part	66	8.527132	9.72E-08	ENSG00000054179,	442	960	12782	1.98815	2.94E-05	1.47E-05	1.30E-04
blue	GOTERM_CC_FAT	GO:0005615~extracellular space	50	6.459948	9.26E-07	ENSG00000137745,	442	685	12782	2.110843	2.80E-04	9.33E-05	0.001239
blue	GOTERM_CC_FAT	GO:0030054~cell junction	37	4.780362	5.07E-05	ENSG00000100170,	442	518	12782	2.065611	0.015201	0.003822	0.067824
blue	GOTERM_CC_FAT	GO:0044459~plasma membrane part	107	13.82429	1.38E-04	ENSG00000114646,	442	2203	12782	1.404578	0.040855	0.008308	0.18459
blue	GOTERM_CC_FAT	GO:0005886~plasma membrane	165	21.31783	2.71E-04	ENSG00000114646,	442	3777	12782	1.26332	0.078676	0.013564	0.362296
blue	GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	61	7.881137	0.002807	ENSG00000114646,	442	1215	12782	1.451878	0.572173	0.114224	3.690819
blue	GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	59	7.622739	0.004153	ENSG00000114646,	442	1188	12782	1.436191	0.715442	0.145383	5.414739
blue	GOTERM_CC_FAT	GO:0045202~synapse	23	2.971576	0.00581	ENSG00000068831,	442	355	12782	1.873596	0.827886	0.177585	7.497843
blue	GOTERM_CC_FAT	GO:0042995~cell projection	38	4.909561	0.006027	ENSG00000100170,	442	697	12782	1.576621	0.83889	0.166871	7.768159
blue	GOTERM_CC_FAT	GO:0043235~receptor complex	11	1.421189	0.006776	ENSG00000164418,	442	116	12782	2.742276	0.871698	0.170282	8.69368
blue	GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	12	1.550388	0.00703	ENSG00000164418,	442	135	12782	2.570538	0.881238	0.162683	9.005649
blue	GOTERM_CC_FAT	GO:0031012~extracellular matrix	22	2.842377	0.008405	ENSG00000154485,	442	345	12782	1.844082	0.921849	0.178058	10.67677
blue	GOTERM_CC_FAT	GO:0044456~synapse part	17	2.196382	0.01126	ENSG00000135333,	442	246	12782	1.998437	0.967283	0.216729	14.05623
blue	GOTERM_CC_FAT	GO:0031091~platelet alpha granule	7	0.904393	0.01233	ENSG00000135218,	442	56	12782	3.614819	0.976404	0.221027	15.29134
blue	GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	20	2.583979	0.015096	ENSG00000154485,	442	320	12782	1.80741	0.989884	0.249564	18.4102
blue	GOTERM_CC_FAT	GO:0015629~actin cytoskeleton	17	2.196382	0.024084	ENSG00000133055,	442	269	12782	1.827566	0.999365	0.351488	27.82662
blue	GOTERM_CC_FAT	GO:0030425~dendrite	12	1.550388	0.02575	ENSG00000164418,	442	163	12782	2.128973	0.999621	0.354471	29.45761
blue	GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	209	27.00258	0.037231	ENSG00000114646,	442	5485	12782	1.10191	0.999899	0.452877	39.80231
blue	GOTERM_CC_FAT	GO:0033267~axon part	6	0.775194	0.037892	ENSG00000164418,	442	54	12782	3.213172	0.999991	0.441943	40.35259
blue	GOTERM_CC_FAT	GO:0005912~adherens junction	11	1.421189	0.042268	ENSG00000143556,	442	155	12782	2.052284	0.999998	0.462635	43.88126
blue	GOTERM_CC_FAT	GO:0030141~secretory granule	12	1.550388	0.047575	ENSG00000100312,	442	180	12782	1.927903	1	0.487838	47.90077
blue	GOTERM_CC_FAT	GO:0005624~membrane fraction	38	4.909561	0.048039	ENSG00000135218,	442	809	12782	1.35835	1	0.476086	48.23961
blue	GOTERM_CC_FAT	GO:0043005~neuron projection	19	2.45478	0.049313	ENSG00000135333,	442	342	12782	1.606586	1	0.470776	49.15853
blue	GOTERM_CC_FAT	GO:0016021~integral to membrane	201	25.96899	0.050153	ENSG00000114646,	442	5297	12782	1.097344	1	0.462899	49.75617
blue	GOTERM_CC_FAT	GO:0005626~insoluble fraction	39	5.03876	0.051023	ENSG00000135218,	442	839	12782	1.344247	1	0.455726	50.36804
blue	GOTERM_CC_FAT	GO:0034702~ion channel complex	13	1.679587	0.051332	ENSG00000108818,	442	205	12782	1.833859	1	0.445352	50.58417
blue	GOTERM_CC_FAT	GO:0005884~actin filament	5	0.645995	0.05189	ENSG00000007237,	442	41	12782	3.526653	1	0.437133	50.97127
blue	GOTERM_CC_FAT	GO:0031093~platelet alpha granule lumen	5	0.645995	0.05189	ENSG00000175899,	442	41	12782	3.526653	1	0.437133	50.97127
blue	GOTERM_CC_FAT	GO:0000267~cell fraction	48	6.20155	0.058869	ENSG00000135218,	442	1083	12782	1.281709	1	0.468382	55.58485
blue	GOTERM_CC_FAT	GO:0060205~cytoplasmic membrane-bounded vesicle lum	5	0.645995	0.06426	ENSG00000175899,	442	44	12782	3.286199	1	0.487576	58.8702
blue	GOTERM_CC_FAT	GO:0005911~cell-cell junction	12	1.550388	0.06505	ENSG00000176402,	442	190	12782	1.826435	1	0.480694	59.33223
blue	GOTERM_CC_FAT	GO:0043025~cell soma	11	1.421189	0.065853	ENSG00000164418,	442	168	12782	1.893477	1	0.474232	59.79703

blue	GOTERM_CC_FAT	GO:0030864~cortical actin cytoskeleton	4	0.516796	0.070691	ENSG00000146950,	442	28	12782	4.131222	1	0.488771	62.49494
blue	GOTERM_CC_FAT	GO:0005903~brush border	5	0.645995	0.073287	ENSG00000100170,	442	46	12782	3.143321	1	0.491377	63.87221
blue	GOTERM_CC_FAT	GO:0031983~vesicle lumen	5	0.645995	0.073287	ENSG00000175899,	442	46	12782	3.143321	1	0.491377	63.87221
blue	GOTERM_CC_FAT	GO:0070161~anchoring junction	11	1.421189	0.074526	ENSG00000143556,	442	172	12782	1.849442	1	0.487407	64.5128
blue	GOTERM_CC_FAT	GO:0008305~integrin complex	4	0.516796	0.076914	ENSG00000156886,	442	29	12782	3.988766	1	0.488999	65.71835
blue	GOTERM_CC_FAT	GO:0031941~filamentous actin	3	0.387597	0.092777	ENSG00000146950,	442	15	12782	5.78371	1	0.548296	72.81321
blue	GOTERM_CC_FAT	GO:0009986~cell surface	18	2.325581	0.09471	ENSG00000135218,	442	348	12782	1.495787	1	0.546501	73.57786
blue	GOTERM_CC_FAT	GO:0030424~axon	10	1.29199	0.099374	ENSG00000164418,	442	159	12782	1.818777	1	0.555357	75.34179
blue	GOTERM_MF_FAT	GO:0005125~cytokine activity	19	2.45478	2.85E-04	ENSG00000156234,	475	195	12983	2.663179	0.173457	0.173457	0.426469
blue	GOTERM_MF_FAT	GO:0016712~oxidoreductase activity, acting on paired do	7	0.904393	6.45E-04	ENSG00000108242,	475	30	12983	6.377614	0.35034	0.193985	0.962941
blue	GOTERM_MF_FAT	GO:0003700~transcription factor activity	56	7.235142	7.83E-04	ENSG00000028277,	475	975	12983	1.569874	0.407293	0.159999	1.166582
blue	GOTERM_MF_FAT	GO:0030246~carbohydrate binding	26	3.359173	0.001276	ENSG00000164764,	475	354	12983	2.007481	0.573717	0.191976	1.89469
blue	GOTERM_MF_FAT	GO:0008009~chemokine activity	8	1.033592	0.001288	ENSG00000143184,	475	46	12983	4.753501	0.577219	0.158173	1.912843
blue	GOTERM_MF_FAT	GO:0020037~heme binding	13	1.679587	0.001551	ENSG00000108242,	475	121	12983	2.936564	0.645358	0.158673	2.298816
blue	GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	38	4.909561	0.001578	ENSG00000028277,	475	607	12983	1.711104	0.651755	0.139888	2.338703
blue	GOTERM_MF_FAT	GO:0005509~calcium ion binding	52	6.718346	0.00173	ENSG00000143556,	475	919	12983	1.546569	0.685461	0.134615	2.561482
blue	GOTERM_MF_FAT	GO:0008395~steroid hydroxylase activity	5	0.645995	0.001737	ENSG00000108242,	475	15	12983	9.110877	0.686974	0.121072	2.572023
blue	GOTERM_MF_FAT	GO:0042379~chemokine receptor binding	8	1.033592	0.001882	ENSG00000143184,	475	49	12983	4.46247	0.715796	0.118215	2.782928
blue	GOTERM_MF_FAT	GO:0046906~tetrapyrrole binding	13	1.679587	0.002668	ENSG00000108242,	475	129	12983	2.754451	0.832184	0.149782	3.925163
blue	GOTERM_MF_FAT	GO:0016298~lipase activity	11	1.421189	0.00351	ENSG00000136250,	475	100	12983	3.006589	0.904513	0.177766	5.132881
blue	GOTERM_MF_FAT	GO:0019825~oxygen binding	7	0.904393	0.004442	ENSG00000108242,	475	43	12983	4.449498	0.94891	0.204498	6.454609
blue	GOTERM_MF_FAT	GO:0015267~channel activity	27	3.488372	0.0048	ENSG00000165269,	475	412	12983	1.791216	0.95981	0.205133	6.956852
blue	GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	27	3.488372	0.004995	ENSG00000165269,	475	413	12983	1.786879	0.964732	0.199873	7.229157
blue	GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	26	3.359173	0.005928	ENSG00000165269,	475	398	12983	1.785549	0.981164	0.219835	8.525433
blue	GOTERM_MF_FAT	GO:0005216~ion channel activity	25	3.229974	0.007869	ENSG00000108878,	475	386	12983	1.770248	0.994892	0.266854	11.16465
blue	GOTERM_MF_FAT	GO:0070330~aromatase activity	5	0.645995	0.012068	ENSG00000108242,	475	25	12983	5.466526	0.9997	0.362741	16.63586
blue	GOTERM_MF_FAT	GO:0008227~amine receptor activity	6	0.775194	0.01612	ENSG00000133019,	475	41	12983	3.999897	0.999981	0.435238	21.61515
blue	GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	11	1.421189	0.01786	ENSG00000164418,	475	127	12983	2.367393	0.999994	0.452235	23.66727
blue	GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	11	1.421189	0.01786	ENSG00000164418,	475	127	12983	2.367393	0.999994	0.452235	23.66727
blue	GOTERM_MF_FAT	GO:0005261~cation channel activity	18	2.325581	0.024344	ENSG00000108878,	475	275	12983	1.789045	1	0.543404	30.88086
blue	GOTERM_MF_FAT	GO:0004629~phospholipase C activity	5	0.645995	0.025299	ENSG00000133019,	475	31	12983	4.408489	1	0.540694	31.88725
blue	GOTERM_MF_FAT	GO:0030247~polysaccharide binding	12	1.550388	0.025633	ENSG00000101144,	475	154	12983	2.129815	1	0.529598	32.23625
blue	GOTERM_MF_FAT	GO:0001871~pattern binding	12	1.550388	0.025633	ENSG00000101144,	475	154	12983	2.129815	1	0.529598	32.23625
blue	GOTERM_MF_FAT	GO:0005529~sugar binding	14	1.808786	0.026729	ENSG00000115339,	475	195	12983	1.962343	1	0.529557	33.36998
blue	GOTERM_MF_FAT	GO:0004620~phospholipase activity	8	1.033592	0.031748	ENSG00000133019,	475	83	12983	2.634471	1	0.577715	38.33799
blue	GOTERM_MF_FAT	GO:0004383~guanylate cyclase activity	3	0.387597	0.032184	ENSG00000169418,	475	8	12983	10.24974	1	0.568492	38.75201
blue	GOTERM_MF_FAT	GO:0009055~electron carrier activity	15	1.937984	0.032341	ENSG00000108242,	475	221	12983	1.855156	1	0.556633	38.9009
blue	GOTERM_MF_FAT	GO:0042165~neurotransmitter binding	9	1.162791	0.0346	ENSG00000133019,	475	103	12983	2.388288	1	0.568317	41.00371
blue	GOTERM_MF_FAT	GO:0022836~gated channel activity	19	2.45478	0.035809	ENSG00000108878,	475	310	12983	1.675226	1	0.568279	42.10187
blue	GOTERM_MF_FAT	GO:0008237~metallopeptidase activity	13	1.679587	0.036191	ENSG00000154485,	475	183	12983	1.941662	1	0.559924	42.44494
blue	GOTERM_MF_FAT	GO:0005179~hormone activity	9	1.162791	0.043889	ENSG00000197487,	475	108	12983	2.277719	1	0.619826	48.96214
blue	GOTERM_MF_FAT	GO:0030955~potassium ion binding	10	1.29199	0.044752	ENSG00000185052,	475	128	12983	2.135362	1	0.615479	49.64822
blue	GOTERM_MF_FAT	GO:0004180~carboxypeptidase activity	5	0.645995	0.044822	ENSG00000109625,	475	37	12983	3.693599	1	0.604759	49.70282
blue	GOTERM_MF_FAT	GO:0008235~metalloexopeptidase activity	5	0.645995	0.048706	ENSG00000109625,	475	38	12983	3.596399	1	0.625075	52.68286
blue	GOTERM_MF_FAT	GO:0004745~retinol dehydrogenase activity	3	0.387597	0.049296	ENSG00000080511,	475	10	12983	8.199789	1	0.618949	53.12004
blue	GOTERM_MF_FAT	GO:0008144~drug binding	6	0.775194	0.056368	ENSG00000100312,	475	57	12983	2.877119	1	0.65924	58.08314
blue	GOTERM_MF_FAT	GO:0046873~metal ion transmembrane transporter activ	19	2.45478	0.056562	ENSG00000108878,	475	328	12983	1.583293	1	0.650477	58.21187
blue	GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	8	1.033592	0.058647	ENSG00000133019,	475	95	12983	2.301695	1	0.654385	59.57519

blue	GOTERM_MF_FAT	GO:0005506~iron ion binding	18	2.325581	0.059959	ENSG00000108242,	475	308	12983	1.597362	1	0.653218	60.41077
blue	GOTERM_MF_FAT	GO:0004435~phosphoinositide phospholipase C activity	4	0.516796	0.061368	ENSG00000133019,	475	25	12983	4.373221	1	0.652726	61.29101
blue	GOTERM_MF_FAT	GO:0004181~metallocarboxypeptidase activity	4	0.516796	0.061368	ENSG00000109625,	475	25	12983	4.373221	1	0.652726	61.29101
blue	GOTERM_MF_FAT	GO:0008238~exopeptidase activity	7	0.904393	0.061944	ENSG00000102174,	475	77	12983	2.484785	1	0.647196	61.64538
blue	GOTERM_MF_FAT	GO:0005251~delayed rectifier potassium channel activity	3	0.387597	0.068928	ENSG00000178342,	475	12	12983	6.833158	1	0.678865	65.70897
blue	GOTERM_MF_FAT	GO:0030528~transcription regulator activity	67	8.656331	0.069595	ENSG00000028277,	475	1512	12983	1.211168	1	0.673392	66.07536
blue	GOTERM_MF_FAT	GO:0005539~glycosaminoglycan binding	10	1.29199	0.070786	ENSG00000101144,	475	140	12983	1.952331	1	0.671952	66.72055
blue	GOTERM_MF_FAT	GO:0050840~extracellular matrix binding	4	0.516796	0.074034	ENSG00000124466,	475	27	12983	4.049279	1	0.680755	68.42157
blue	GOTERM_MF_FAT	GO:0008201~heparin binding	8	1.033592	0.082604	ENSG00000101144,	475	103	12983	2.122923	1	0.714068	72.52907
blue	GOTERM_MF_FAT	GO:0003714~transcription corepressor activity	10	1.29199	0.083938	ENSG00000171855,	475	145	12983	1.885009	1	0.712362	73.12185
blue	HIV_INTERACTION	env:Envelope surface glycoprotein gp120	25	3.229974	0.002098	ENSG00000162551,	40	529	1394	1.646975	0.020784	0.020784	1.253279
blue	INTERPRO	IPR017970:Homeobox, conserved site	26	3.359173	5.91E-07	ENSG00000028277,	582	232	16659	3.20783	5.68E-04	5.68E-04	9.29E-04
blue	INTERPRO	IPR001356:Homeobox	26	3.359173	7.52E-07	ENSG00000028277,	582	235	16659	3.166879	7.23E-04	3.62E-04	0.001182
blue	INTERPRO	IPR012287:Homeodomain-related	25	3.229974	3.23E-06	ENSG00000009709,	582	238	16659	3.006692	0.0031	0.001035	0.005074
blue	INTERPRO	IPR001128:Cytochrome P450	10	1.29199	2.47E-04	ENSG00000108242,	582	61	16659	4.692412	0.211177	0.057579	0.38692
blue	INTERPRO	IPR017972:Cytochrome P450, conserved site	10	1.29199	2.80E-04	ENSG00000108242,	582	62	16659	4.616728	0.235902	0.05239	0.43875
blue	INTERPRO	IPR001811:Small chemokine, interleukin-8-like	8	1.033592	4.85E-04	ENSG00000143184,	582	41	16659	5.585114	0.37287	0.07482	0.759652
blue	INTERPRO	IPR017973:Cytochrome P450, C-terminal region	9	1.162791	6.77E-04	ENSG00000108242,	582	56	16659	4.600239	0.478699	0.088862	1.058962
blue	INTERPRO	IPR002401:Cytochrome P450, E-class, group I	8	1.033592	0.001457	ENSG00000108242,	582	49	16659	4.673259	0.754031	0.16081	2.266074
blue	INTERPRO	IPR013098:Immunoglobulin I-set	13	1.679587	0.003254	ENSG00000152580,	582	138	16659	2.696437	0.956525	0.294182	4.995296
blue	INTERPRO	IPR011511:Variant SH3	8	1.033592	0.007326	ENSG00000126217,	582	65	16659	3.522918	0.999153	0.50704	10.91654
blue	INTERPRO	IPR018249:EF-HAND 2	16	2.067183	0.008575	ENSG00000143546,	582	215	16659	2.130137	0.999748	0.529142	12.66357
blue	INTERPRO	IPR018247:EF-HAND 1	16	2.067183	0.009282	ENSG00000143546,	582	217	16659	2.110504	0.999873	0.526489	13.63691
blue	INTERPRO	IPR001089:Small chemokine, C-X-C	4	0.516796	0.009293	ENSG00000156234,	582	13	16659	8.807296	0.999874	0.498886	13.65247
blue	INTERPRO	IPR002402:Cytochrome P450, E-class, group II	3	0.387597	0.011321	ENSG00000160868,	582	5	16659	17.17423	0.999982	0.542663	16.38911
blue	INTERPRO	IPR018039:Intermediate filament protein, conserved site	8	1.033592	0.012599	ENSG00000132688,	582	72	16659	3.180412	0.999995	0.556532	18.07215
blue	INTERPRO	IPR016044:Filament	8	1.033592	0.012599	ENSG00000132688,	582	72	16659	3.180412	0.999995	0.556532	18.07215
blue	INTERPRO	IPR003598:Immunoglobulin subtype 2	15	1.937984	0.01292	ENSG00000169071,	582	205	16659	2.094418	0.999996	0.542466	18.49084
blue	INTERPRO	IPR001079:Galectin, carbohydrate recognition domain	4	0.516796	0.014039	ENSG00000170298,	582	15	16659	7.63299	0.999999	0.550711	19.93134
blue	INTERPRO	IPR001452:Src homology-3 domain	15	1.937984	0.017447	ENSG00000111816,	582	213	16659	2.015754	1	0.609634	24.17298
blue	INTERPRO	IPR013320:Concanavalin A-like lectin/glucanase, subgroup	8	1.033592	0.017747	ENSG00000165323,	582	77	16659	2.973892	1	0.596117	24.53633
blue	INTERPRO	IPR011992:EF-Hand type	16	2.067183	0.018697	ENSG00000143546,	582	236	16659	1.940591	1	0.596595	25.67503
blue	INTERPRO	IPR018048:Small chemokine, C-X-C, conserved site	4	0.516796	0.019928	ENSG00000156234,	582	17	16659	6.734991	1	0.602317	27.12772
blue	INTERPRO	IPR006210:EGF-like	14	1.808786	0.024203	ENSG00000114646,	582	201	16659	1.993691	1	0.657457	31.96821
blue	INTERPRO	IPR013088:Zinc finger, NHR/GATA-type	6	0.775194	0.031897	ENSG00000186951,	582	51	16659	3.367495	1	0.742272	39.92881
blue	INTERPRO	IPR002017:Spectrin repeat	4	0.516796	0.03518	ENSG00000126217,	582	21	16659	5.452135	1	0.76201	43.053
blue	INTERPRO	IPR018248:EF hand	10	1.29199	0.038329	ENSG00000143546,	582	130	16659	2.201824	1	0.777736	45.90566
blue	INTERPRO	IPR001664:Intermediate filament protein	7	0.904393	0.041767	ENSG00000132688,	582	73	16659	2.744739	1	0.793731	48.8676
blue	INTERPRO	IPR000203:GPS	5	0.645995	0.0424	ENSG00000144820,	582	38	16659	3.766278	1	0.786398	49.39585
blue	INTERPRO	IPR000834:Peptidase M14, carboxypeptidase A	4	0.516796	0.044518	ENSG00000109625,	582	23	16659	4.978037	1	0.790832	51.12783
blue	INTERPRO	IPR000906:ZU5	3	0.387597	0.045387	ENSG00000151150,	582	10	16659	8.587113	1	0.7858	51.82196
blue	INTERPRO	IPR013032:EGF-like region, conserved site	17	2.196382	0.051984	ENSG00000114646,	582	293	16659	1.660761	1	0.819465	56.79775
blue	INTERPRO	IPR013787:S100/CaBP-9k-type, calcium binding, subdoma	4	0.516796	0.066447	ENSG00000196420,	582	27	16659	4.24055	1	0.881602	66.0739
blue	INTERPRO	IPR019391:Storkhead-box protein, winged-helix domain	2	0.258398	0.068538	ENSG00000173320,	582	2	16659	28.62371	1	0.881688	67.24891
blue	INTERPRO	IPR001751:S100/CaBP-9k-type, calcium binding	4	0.516796	0.07257	ENSG00000196420,	582	28	16659	4.089102	1	0.888777	69.40835
blue	INTERPRO	IPR013513:Integrin alpha chain, C-terminal, cytoplasmic r	3	0.387597	0.073468	ENSG00000156886,	582	13	16659	6.605472	1	0.884563	69.87058
blue	INTERPRO	IPR001628:Zinc finger, nuclear hormone receptor-type	5	0.645995	0.075683	ENSG00000186951,	582	46	16659	3.111273	1	0.885034	70.98315
blue	INTERPRO	IPR000832:GPCR, family 2, secretin-like	5	0.645995	0.075683	ENSG00000215644,	582	46	16659	3.111273	1	0.885034	70.98315

blue	INTERPRO	IPR000884:Thrombospondin, type 1 repeat	6	0.775194	0.076021	ENSG00000143341,	582	65	16659	2.642189	1	0.879104	71.14989
blue	INTERPRO	IPR000742:EGF-like, type 3	12	1.550388	0.077883	ENSG00000149256,	582	194	16659	1.770539	1	0.878538	72.05022
blue	INTERPRO	IPR001723:Steroid hormone receptor	5	0.645995	0.080555	ENSG00000186951,	582	47	16659	3.045076	1	0.880705	73.29686
blue	INTERPRO	IPR003585:Neurexin/syndecan/glycophorin C	3	0.387597	0.083792	ENSG00000175161,	582	14	16659	6.133652	1	0.884515	74.73696
blue	INTERPRO	IPR003654:Paired-like homeodomain protein, OAR	3	0.387597	0.083792	ENSG00000197587,	582	14	16659	6.133652	1	0.884515	74.73696
blue	INTERPRO	IPR000536:Nuclear hormone receptor, ligand-binding, co	5	0.645995	0.085579	ENSG00000186951,	582	48	16659	2.981637	1	0.883704	75.50081
blue	INTERPRO	IPR008946:Nuclear hormone receptor, ligand-binding	5	0.645995	0.085579	ENSG00000186951,	582	48	16659	2.981637	1	0.883704	75.50081
blue	INTERPRO	IPR017983:GPCR, family 2, secretin-like, conserved site	5	0.645995	0.085579	ENSG00000215644,	582	48	16659	2.981637	1	0.883704	75.50081
blue	INTERPRO	IPR018159:Spectrin/alpha-actinin	4	0.516796	0.092358	ENSG00000126217,	582	31	16659	3.693382	1	0.897073	78.20567
blue	INTERPRO	IPR008085:Thrombospondin, type 1 repeat, subgroup	3	0.387597	0.094523	ENSG00000143341,	582	15	16659	5.724742	1	0.89713	79.00856
blue	INTERPRO	IPR001064:Beta and gamma crystallin	3	0.387597	0.094523	ENSG00000168582,	582	15	16659	5.724742	1	0.89713	79.00856
blue	INTERPRO	IPR013151:Immunoglobulin	12	1.550388	0.096638	ENSG00000152580,	582	202	16659	1.700418	1	0.897071	79.76633
blue	KEGG_PATHWAY	hsa00830:Retinol metabolism	10	1.29199	8.80E-05	ENSG00000108242,	179	54	5085	5.260708	0.011891	0.011891	0.103204
blue	KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	22	2.842377	2.02E-04	ENSG00000160013,	179	256	5085	2.441297	0.027042	0.013614	0.236353
blue	KEGG_PATHWAY	hsa00982:Drug metabolism	10	1.29199	2.64E-04	ENSG00000108242,	179	62	5085	4.581907	0.03522	0.011881	0.309012
blue	KEGG_PATHWAY	hsa00591:Linoleic acid metabolism	7	0.904393	3.35E-04	ENSG00000108242,	179	28	5085	7.101955	0.044551	0.011329	0.392607
blue	KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	19	2.45478	0.004346	ENSG00000156234,	179	262	5085	2.060109	0.447006	0.111732	4.984907
blue	KEGG_PATHWAY	hsa00980:Metabolism of xenobiotics by cytochrome P450	8	1.033592	0.004611	ENSG00000108242,	179	60	5085	3.787709	0.466627	0.099455	5.280718
blue	KEGG_PATHWAY	hsa00590:Arachidonic acid metabolism	7	0.904393	0.012857	ENSG00000108242,	179	56	5085	3.550978	0.827942	0.222302	14.09341
blue	KEGG_PATHWAY	hsa04062:Chemokine signaling pathway	13	1.679587	0.030081	ENSG00000143184,	179	187	5085	1.974875	0.984295	0.405018	30.13035
blue	KEGG_PATHWAY	hsa00983:Drug metabolism	5	0.645995	0.062119	ENSG00000135226,	179	43	5085	3.303235	0.999837	0.620581	52.89782
blue	KEGG_PATHWAY	hsa04020:Calcium signaling pathway	11	1.421189	0.088024	ENSG00000133019,	179	176	5085	1.775489	0.999996	0.714391	66.09662
blue	PIR_SUPERFAMILY	PIRSF038749:interferon lambda	3	0.387597	0.004148	ENSG00000183709,	280	3	7396	26.41429	0.6916	0.6916	5.356435
blue	PIR_SUPERFAMILY	PIRSF000045:cytochrome P450 CYP2D6	5	0.645995	0.013408	ENSG00000108242,	280	25	7396	5.282857	0.978075	0.851929	16.37081
blue	PIR_SUPERFAMILY	PIRSF002522:CXC chemokine	4	0.516796	0.014191	ENSG00000156234,	280	14	7396	7.546939	0.982489	0.740319	17.24594
blue	PIR_SUPERFAMILY	PIRSF002353:S-100 protein	4	0.516796	0.032894	ENSG00000196420,	280	19	7396	5.560902	0.999923	0.90618	35.78775
blue	PIR_SUPERFAMILY	PIRSF002281:beta/gamma crystallins	3	0.387597	0.062298	ENSG00000168582,	280	11	7396	7.203896	1	0.973766	57.3398
blue	PIR_SUPERFAMILY	PIRSF800007:secretin receptor-like G protein-coupled rec	5	0.645995	0.072392	ENSG00000215644,	280	42	7396	3.144558	1	0.971114	63.03665
blue	PIR_SUPERFAMILY	PIRSF000601:tyrosine-protein kinase, proto-oncogene SR	3	0.387597	0.072944	ENSG00000111816,	280	12	7396	6.603571	1	0.953211	63.32685
blue	PIR_SUPERFAMILY	PIRSF002352:parvalbumin	2	0.258398	0.074028	ENSG00000122543,	280	2	7396	26.41429	1	0.934174	63.89075
blue	PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	6	0.775194	0.07921	ENSG00000187242,	280	61	7396	2.598126	1	0.925346	66.47709
blue	SMART	SM00389:HOX	26	3.359173	3.96E-06	ENSG00000028277,	352	235	9079	2.853651	8.24E-04	8.24E-04	0.004998
blue	SMART	SM00199:SCY	8	1.033592	8.78E-04	ENSG00000143184,	352	41	9079	5.032705	0.166955	0.087287	1.101695
blue	SMART	SM00276:GLECT	4	0.516796	0.018442	ENSG00000170298,	352	15	9079	6.87803	0.979179	0.724895	20.92796
blue	SMART	SM00408:IGc2	15	1.937984	0.02752	ENSG00000169071,	352	205	9079	1.887264	0.996986	0.765693	29.67345
blue	SMART	SM00326:SH3	15	1.937984	0.036399	ENSG00000111816,	352	213	9079	1.816381	0.999553	0.786144	37.35709
blue	SMART	SM00181:EGF	14	1.808786	0.047911	ENSG00000114646,	352	201	9079	1.7965	0.999963	0.817687	46.16953
blue	SMART	SM00218:ZUS	3	0.387597	0.054623	ENSG00000151150,	352	10	9079	7.737784	0.999992	0.811585	50.76554
blue	SMART	SM00631:Zn_pept	4	0.516796	0.057255	ENSG00000109625,	352	23	9079	4.485672	0.999995	0.784101	52.46665
blue	SMART	SM00303:GPS	5	0.645995	0.057746	ENSG00000144820,	352	38	9079	3.393765	0.999996	0.747071	52.77775
blue	SMART	SM00294:4.1m	3	0.387597	0.09989	ENSG00000175161,	352	14	9079	5.526989	1	0.887967	73.48673
blue	SP_PIR_KEYWORDS	signal	179	23.12661	2.36E-12	ENSG00000114646,	644	3250	19235	1.645038	1.05E-09	1.05E-09	3.34E-09
blue	SP_PIR_KEYWORDS	glycoprotein	209	27.00258	2.83E-09	ENSG00000114646,	644	4318	19235	1.445673	1.26E-06	6.32E-07	4.01E-06
blue	SP_PIR_KEYWORDS	Secreted	102	13.17829	5.32E-09	ENSG00000143556,	644	1689	19235	1.803752	2.38E-06	7.92E-07	7.54E-06
blue	SP_PIR_KEYWORDS	disulfide bond	152	19.63824	1.28E-08	ENSG00000114646,	644	2924	19235	1.552646	5.74E-06	1.44E-06	1.82E-05
blue	SP_PIR_KEYWORDS	Homeobox	27	3.488372	1.71E-07	ENSG00000028277,	644	242	19235	3.332382	7.65E-05	1.53E-05	2.43E-04
blue	SP_PIR_KEYWORDS	developmental protein	52	6.718346	3.83E-06	ENSG00000114646,	644	779	19235	1.993757	0.001708	2.85E-04	0.005421
blue	SP_PIR_KEYWORDS	cell junction	32	4.134367	1.29E-05	ENSG00000095637,	644	399	19235	2.39543	0.005741	8.22E-04	0.018256

blue	SP_PIR_KEYWORDS	cytokine	19	2.45478	3.81E-05	ENSG00000143546,	644	181	19235	3.135316	0.016868	0.002124	0.053927
blue	SP_PIR_KEYWORDS	Monooxygenase	12	1.550388	5.44E-05	ENSG00000108242,	644	78	19235	4.595079	0.024015	0.002697	0.077047
blue	SP_PIR_KEYWORDS	calcium	49	6.330749	7.40E-05	ENSG00000143556,	644	803	19235	1.822581	0.032519	0.0033	0.104769
blue	SP_PIR_KEYWORDS	microsome	13	1.679587	2.20E-04	ENSG00000108242,	644	106	19235	3.663058	0.093638	0.008898	0.311254
blue	SP_PIR_KEYWORDS	transmembrane protein	39	5.03876	4.94E-04	ENSG00000135218,	644	642	19235	1.814412	0.198288	0.018249	0.698314
blue	SP_PIR_KEYWORDS	chemotaxis	10	1.29199	6.41E-04	ENSG00000143184,	644	72	19235	4.148335	0.24916	0.021802	0.904515
blue	SP_PIR_KEYWORDS	heme	13	1.679587	7.44E-04	ENSG00000108242,	644	121	19235	3.20896	0.282872	0.02347	1.048749
blue	SP_PIR_KEYWORDS	synapse	18	2.325581	8.44E-04	ENSG00000068831,	644	213	19235	2.524057	0.314327	0.024843	1.18938
blue	SP_PIR_KEYWORDS	ionic channel	23	2.971576	0.001094	ENSG00000108878,	644	318	19235	2.160265	0.386887	0.030113	1.539196
blue	SP_PIR_KEYWORDS	cleavage on pair of basic residues	20	2.583979	0.001999	ENSG00000197487,	644	271	19235	2.204281	0.591175	0.051256	2.796327
blue	SP_PIR_KEYWORDS	pancreas	5	0.645995	0.002604	ENSG00000129538,	644	18	19235	8.29667	0.688263	0.062703	3.628388
blue	SP_PIR_KEYWORDS	polymorphism	421	54.39276	0.00294	ENSG00000198521,	644	11550	19235	1.088696	0.731816	0.066923	4.087145
blue	SP_PIR_KEYWORDS	postsynaptic cell membrane	11	1.421189	0.0038	ENSG00000164418,	644	110	19235	2.986801	0.817639	0.081569	5.252941
blue	SP_PIR_KEYWORDS	membrane	242	31.26615	0.003894	ENSG00000114646,	644	6256	19235	1.15538	0.82516	0.079687	5.379377
blue	SP_PIR_KEYWORDS	inflammatory response	9	1.162791	0.004135	ENSG00000197272,	644	77	19235	3.491066	0.843083	0.080738	5.703321
blue	SP_PIR_KEYWORDS	metalloprotease	13	1.679587	0.004836	ENSG00000154485,	644	151	19235	2.571418	0.885476	0.089914	6.640265
blue	SP_PIR_KEYWORDS	electron transfer	7	0.904393	0.006208	ENSG00000108242,	644	50	19235	4.181522	0.93819	0.109513	8.44816
blue	SP_PIR_KEYWORDS	ion transport	32	4.134367	0.006759	ENSG00000100170,	644	578	19235	1.653592	0.951757	0.114196	9.164714
blue	SP_PIR_KEYWORDS	cell membrane	95	12.2739	0.006979	ENSG00000114646,	644	2194	19235	1.293282	0.956308	0.113441	9.449685
blue	SP_PIR_KEYWORDS	lipid degradation	9	1.162791	0.008039	ENSG00000203837,	644	86	19235	3.125722	0.972891	0.125083	10.80978
blue	SP_PIR_KEYWORDS	lipoprotein	34	4.392765	0.009676	ENSG00000135218,	644	642	19235	1.581795	0.987042	0.14377	12.87305
blue	SP_PIR_KEYWORDS	Intermediate filament	8	1.033592	0.015388	ENSG00000132688,	644	78	19235	3.063386	0.999024	0.212605	19.73126
blue	SP_PIR_KEYWORDS	iron	18	2.325581	0.01567	ENSG00000108242,	644	285	19235	1.886401	0.999141	0.209696	20.05742
blue	SP_PIR_KEYWORDS	extracellular matrix	16	2.067183	0.015854	ENSG00000137745,	644	241	19235	1.982939	0.99921	0.205817	20.26898
blue	SP_PIR_KEYWORDS	chondroitin sulfate proteoglycan	4	0.516796	0.017822	ENSG00000049089,	644	17	19235	7.027768	0.999677	0.222128	22.4986
blue	SP_PIR_KEYWORDS	Lectin	12	1.550388	0.018026	ENSG00000115339,	644	159	19235	2.25419	0.999706	0.218384	22.72612
blue	SP_PIR_KEYWORDS	carboxypeptidase	5	0.645995	0.02118	ENSG00000109625,	644	32	19235	4.666877	0.99993	0.24531	26.17111
blue	SP_PIR_KEYWORDS	differentiation	25	3.229974	0.021227	ENSG00000114646,	644	460	19235	1.623262	0.999932	0.239686	26.22165
blue	SP_PIR_KEYWORDS	zymogen	14	1.808786	0.021431	ENSG00000136250,	644	206	19235	2.029865	0.999938	0.235852	26.43869
blue	SP_PIR_KEYWORDS	egf-like domain	15	1.937984	0.022917	ENSG00000114646,	644	230	19235	1.947914	0.999968	0.244281	28.00641
blue	SP_PIR_KEYWORDS	sh3 domain	14	1.808786	0.025056	ENSG00000111816,	644	210	19235	1.991201	0.999988	0.258064	30.20812
blue	SP_PIR_KEYWORDS	potassium	10	1.29199	0.025629	ENSG00000185052,	644	126	19235	2.370477	0.999991	0.257386	30.78744
blue	SP_PIR_KEYWORDS	gpi-anchor	10	1.29199	0.025629	ENSG00000124466,	644	126	19235	2.370477	0.999991	0.257386	30.78744
blue	SP_PIR_KEYWORDS	transmembrane	189	24.4186	0.026146	ENSG00000114646,	644	4973	19235	1.135141	0.999993	0.256262	31.3058
blue	SP_PIR_KEYWORDS	cgrp biosynthesis	3	0.387597	0.027328	ENSG00000169418,	644	8	19235	11.2005	0.999996	0.260728	32.47846
blue	SP_PIR_KEYWORDS	voltage-gated channel	11	1.421189	0.029353	ENSG00000168135,	644	150	19235	2.190321	0.999998	0.271725	34.44363
blue	SP_PIR_KEYWORDS	proteoglycan	6	0.775194	0.033864	ENSG00000114646,	644	54	19235	3.318668	1	0.301012	38.63171
blue	SP_PIR_KEYWORDS	nadp	11	1.421189	0.036952	ENSG00000080511,	644	156	19235	2.106078	1	0.317854	41.3545
blue	SP_PIR_KEYWORDS	potassium transport	9	1.162791	0.039114	ENSG00000185052,	644	115	19235	2.337497	1	0.327216	43.19278
blue	SP_PIR_KEYWORDS	neurotransmitter receptor	6	0.775194	0.041375	ENSG00000164418,	644	57	19235	3.144001	1	0.336757	45.05868
blue	SP_PIR_KEYWORDS	dna-binding	77	9.94832	0.041421	ENSG00000198521,	644	1868	19235	1.231176	1	0.331238	45.09549
blue	SP_PIR_KEYWORDS	phosphorus-oxygen lyase	3	0.387597	0.042025	ENSG00000169418,	644	10	19235	8.960404	1	0.329561	45.58449
blue	SP_PIR_KEYWORDS	Immunoglobulin domain	24	3.100775	0.043682	ENSG00000133055,	644	470	19235	1.525175	1	0.33466	46.9035
blue	SP_PIR_KEYWORDS	cell adhesion	22	2.842377	0.045538	ENSG00000135218,	644	422	19235	1.5571	1	0.340765	48.34552
blue	SP_PIR_KEYWORDS	liver	6	0.775194	0.046899	ENSG00000160868,	644	59	19235	3.037425	1	0.343615	49.37945
blue	SP_PIR_KEYWORDS	integrin	5	0.645995	0.04725	ENSG00000008277,	644	41	19235	3.642441	1	0.340369	49.64271
blue	SP_PIR_KEYWORDS	deafness	8	1.033592	0.050305	ENSG00000166866,	644	100	19235	2.389441	1	0.352939	51.88396
blue	SP_PIR_KEYWORDS	palmitate	13	1.679587	0.054674	ENSG00000163746,	644	213	19235	1.82293	1	0.372128	54.92767

blue	SP_PIR_KEYWORDS	chromoprotein	6	0.775194	0.055967	ENSG00000108242,	644	62	19235	2.890453	1	0.373797	55.79366
blue	SP_PIR_KEYWORDS	metalloprotein	9	1.162791	0.056454	ENSG00000108242,	644	124	19235	2.16784	1	0.371136	56.11567
blue	SP_PIR_KEYWORDS	oxidoreductase	27	3.488372	0.059371	ENSG00000138109,	644	562	19235	1.43494	1	0.381208	58.00003
blue	SP_PIR_KEYWORDS	hormone	7	0.904393	0.071138	ENSG00000197487,	644	87	19235	2.403173	1	0.433758	64.8636
blue	SP_PIR_KEYWORDS	Chondrogenesis	3	0.387597	0.077871	ENSG00000054938,	644	14	19235	6.400288	1	0.458934	68.30615
blue	SP_PIR_KEYWORDS	receptor	64	8.268734	0.084226	ENSG00000135333,	644	1583	19235	1.207551	1	0.480815	71.26517
blue	SP_PIR_KEYWORDS	plasma	7	0.904393	0.0913	ENSG00000175899,	644	93	19235	2.24813	1	0.504194	74.25588
blue	SP_PIR_KEYWORDS	Short QT syndrome	2	0.258398	0.096976	ENSG00000053918,	644	3	19235	19.91201	1	0.5207	76.44356
blue	SP_PIR_KEYWORDS	carboxylic ester hydrolase	3	0.387597	0.098336	ENSG00000136250,	644	16	19235	5.600252	1	0.52023	76.94136
blue	UP_SEQ_FEATURE	signal peptide	179	23.12661	4.12E-12	ENSG00000114646,	644	3250	19113	1.634604	7.72E-09	7.72E-09	7.04E-09
blue	UP_SEQ_FEATURE	disulfide bond	149	19.25065	9.86E-09	ENSG00000114646,	644	2819	19113	1.568679	1.85E-05	9.23E-06	1.68E-05
blue	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	200	25.83979	1.22E-08	ENSG00000114646,	644	4129	19113	1.437567	2.28E-05	7.60E-06	2.08E-05
blue	UP_SEQ_FEATURE	DNA-binding region:Homeobox	24	3.100775	1.14E-07	ENSG00000009709,	644	190	19113	3.748872	2.13E-04	5.34E-05	1.95E-04
blue	UP_SEQ_FEATURE	topological domain:Extracellular	129	16.66667	3.72E-05	ENSG00000114646,	644	2719	19113	1.408068	0.067343	0.013847	0.063517
blue	UP_SEQ_FEATURE	topological domain:Cytoplasmic	151	19.50904	1.27E-04	ENSG00000114646,	644	3374	19113	1.328235	0.211661	0.038862	0.216508
blue	UP_SEQ_FEATURE	metal ion-binding site:Iron (heme axial ligand)	11	1.421189	0.001696	ENSG00000108242,	644	98	19113	3.331268	0.958332	0.364918	2.854731
blue	UP_SEQ_FEATURE	region of interest:Head	9	1.162791	0.003083	ENSG00000132688,	644	73	19113	3.659002	0.996913	0.514489	5.13162
blue	UP_SEQ_FEATURE	region of interest:Linker 12	8	1.033592	0.005571	ENSG00000132688,	644	64	19113	3.709821	0.999971	0.687121	9.090307
blue	UP_SEQ_FEATURE	sequence variant	434	56.07235	0.007564	ENSG00000198521,	644	11992	19113	1.074091	0.999999	0.758613	12.14957
blue	UP_SEQ_FEATURE	compositionally biased region:Poly-Ala	24	3.100775	0.007573	ENSG00000009709,	644	393	19113	1.812432	0.999999	0.725731	12.16284
blue	UP_SEQ_FEATURE	region of interest:Coil 1B	8	1.033592	0.009052	ENSG00000132688,	644	70	19113	3.391837	1	0.757947	14.37048
blue	UP_SEQ_FEATURE	region of interest:Linker 1	8	1.033592	0.009052	ENSG00000132688,	644	70	19113	3.391837	1	0.757947	14.37048
blue	UP_SEQ_FEATURE	region of interest:Coil 1A	8	1.033592	0.009052	ENSG00000132688,	644	70	19113	3.391837	1	0.757947	14.37048
blue	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	7	0.904393	0.009293	ENSG00000007306,	644	54	19113	3.847222	1	0.73932	14.7247
blue	UP_SEQ_FEATURE	region of interest:Rod	8	1.033592	0.009759	ENSG00000132688,	644	71	19113	3.344064	1	0.730556	15.40702
blue	UP_SEQ_FEATURE	region of interest:Tail	8	1.033592	0.012995	ENSG00000132688,	644	75	19113	3.165714	1	0.804534	20.00039
blue	UP_SEQ_FEATURE	domain:Galectin 1	3	0.387597	0.015491	ENSG00000170298,	644	6	19113	14.83929	1	0.839049	23.3833
blue	UP_SEQ_FEATURE	domain:Galectin 2	3	0.387597	0.015491	ENSG00000170298,	644	6	19113	14.83929	1	0.839049	23.3833
blue	UP_SEQ_FEATURE	domain:SH3	13	1.679587	0.016789	ENSG00000074966,	644	177	19113	2.179782	1	0.845012	25.08762
blue	UP_SEQ_FEATURE	domain:Ig-like C2-type	9	1.162791	0.022869	ENSG00000138615,	644	103	19113	2.593273	1	0.909822	32.61056
blue	UP_SEQ_FEATURE	compositionally biased region:Poly-Pro	23	2.971576	0.023269	ENSG00000149256,	644	413	19113	1.652802	1	0.901701	33.08029
blue	UP_SEQ_FEATURE	propeptide:Removed in mature form	15	1.937984	0.023304	ENSG00000124466,	644	229	19113	1.944011	1	0.889977	33.12069
blue	UP_SEQ_FEATURE	transmembrane region	188	24.28941	0.026291	ENSG00000114646,	644	4911	19113	1.136138	1	0.906984	36.52542
blue	UP_SEQ_FEATURE	domain:Guanylate cyclase	3	0.387597	0.027654	ENSG00000169418,	644	8	19113	11.12946	1	0.908029	38.02515
blue	UP_SEQ_FEATURE	domain:GPS	5	0.645995	0.031905	ENSG00000144820,	644	36	19113	4.122024	1	0.928574	42.48824
blue	UP_SEQ_FEATURE	calcium-binding region:2; high affinity	4	0.516796	0.03211	ENSG00000196420,	644	21	19113	5.653061	1	0.921578	42.69563
blue	UP_SEQ_FEATURE	domain:ZU5	3	0.387597	0.034774	ENSG00000151150,	644	9	19113	9.892857	1	0.929366	45.32824
blue	UP_SEQ_FEATURE	domain:Ig-like C2-type 6	5	0.645995	0.034852	ENSG00000152580,	644	37	19113	4.010618	1	0.92224	45.40355
blue	UP_SEQ_FEATURE	domain:Ig-like C2-type 7	4	0.516796	0.036275	ENSG00000152580,	644	22	19113	5.396104	1	0.922838	46.76095
blue	UP_SEQ_FEATURE	lipid moiety-binding region:S-palmitoyl cysteine	12	1.550388	0.042724	ENSG00000163746,	644	181	19113	1.96764	1	0.946023	52.52231
blue	UP_SEQ_FEATURE	domain:EF-hand 2	12	1.550388	0.044158	ENSG00000196420,	644	182	19113	1.956829	1	0.945814	53.72157
blue	UP_SEQ_FEATURE	domain:EF-hand 1	12	1.550388	0.044158	ENSG00000196420,	644	182	19113	1.956829	1	0.945814	53.72157
blue	UP_SEQ_FEATURE	domain:Kringle	3	0.387597	0.050828	ENSG00000169071,	644	11	19113	8.094156	1	0.961423	58.93265
blue	UP_SEQ_FEATURE	domain:VWFA	6	0.775194	0.057212	ENSG00000143341,	644	62	19113	2.87212	1	0.971495	63.39925
blue	UP_SEQ_FEATURE	repeat:LRR 18	4	0.516796	0.060963	ENSG00000179542,	644	27	19113	4.396825	1	0.974769	65.80549
blue	UP_SEQ_FEATURE	region of interest:Coil 2	6	0.775194	0.063905	ENSG00000187242,	644	64	19113	2.782366	1	0.976392	67.5881
blue	UP_SEQ_FEATURE	DNA-binding region:Nuclear receptor	5	0.645995	0.06392	ENSG00000186951,	644	45	19113	3.297619	1	0.973665	67.59675
blue	UP_SEQ_FEATURE	zinc finger region:NR C4-type	5	0.645995	0.06392	ENSG00000186951,	644	45	19113	3.297619	1	0.973665	67.59675

blue	UP_SEQ_FEATURE	chain:Oncomodulin	2	0.258398	0.066154	ENSG00000122543,	644	2	19113	29.67857	1	0.974287	68.89114
blue	UP_SEQ_FEATURE	binding site:Substrate	16	2.067183	0.077905	ENSG00000103485,	644	297	19113	1.598846	1	0.985265	74.93552
blue	UP_SEQ_FEATURE	region of interest:Ligand-binding	4	0.516796	0.078674	ENSG00000186951,	644	30	19113	3.957143	1	0.984169	75.28961
blue	UP_SEQ_FEATURE	glycosylation site:O-linked (Xyl...) (glycosaminoglycan)	3	0.387597	0.078736	ENSG00000179399,	644	14	19113	6.359694	1	0.982403	75.31814
blue	UP_SEQ_FEATURE	domain:Beta/gamma crystallin 'Greek key' 4	3	0.387597	0.078736	ENSG00000168582,	644	14	19113	6.359694	1	0.982403	75.31814
blue	UP_SEQ_FEATURE	short sequence motif:OAR	3	0.387597	0.078736	ENSG00000197587,	644	14	19113	6.359694	1	0.982403	75.31814
blue	UP_SEQ_FEATURE	domain:Beta/gamma crystallin 'Greek key' 2	3	0.387597	0.088888	ENSG00000168582,	644	15	19113	5.935714	1	0.988533	79.56967
blue	UP_SEQ_FEATURE	domain:Beta/gamma crystallin 'Greek key' 1	3	0.387597	0.088888	ENSG00000168582,	644	15	19113	5.935714	1	0.988533	79.56967
blue	UP_SEQ_FEATURE	short sequence motif:GFFKR motif	3	0.387597	0.088888	ENSG00000156886,	644	15	19113	5.935714	1	0.988533	79.56967
blue	UP_SEQ_FEATURE	domain:Beta/gamma crystallin 'Greek key' 3	3	0.387597	0.088888	ENSG00000168582,	644	15	19113	5.935714	1	0.988533	79.56967
blue	UP_SEQ_FEATURE	region of interest:Beta-galactoside binding 1	2	0.258398	0.097574	ENSG00000170298,	644	3	19113	19.78571	1	0.99181	82.64975
blue	UP_SEQ_FEATURE	repeat:DUF1309_1	2	0.258398	0.097574	ENSG00000181781,	644	3	19113	19.78571	1	0.99181	82.64975
blue	UP_SEQ_FEATURE	domain:ASD1	2	0.258398	0.097574	ENSG00000146950,	644	3	19113	19.78571	1	0.99181	82.64975
blue	UP_SEQ_FEATURE	region of interest:Beta-galactoside binding 2	2	0.258398	0.097574	ENSG00000170298,	644	3	19113	19.78571	1	0.99181	82.64975
blue	UP_SEQ_FEATURE	DNA-binding region:CUT	2	0.258398	0.097574	ENSG00000119547,	644	3	19113	19.78571	1	0.99181	82.64975
blue	UP_SEQ_FEATURE	repeat:DUF1309_2	2	0.258398	0.097574	ENSG00000181781,	644	3	19113	19.78571	1	0.99181	82.64975
blue	UP_SEQ_FEATURE	DNA-binding region:T-box	3	0.387597	0.099401	ENSG00000121075,	644	16	19113	5.564732	1	0.991606	83.23934
brown	BIOCARTA	h_mhcPathway:Antigen Processing and Presentation	3	0.332226	0.013947	ENSG00000204287,	28	10	1437	15.39643	0.587228	0.587228	13.25671
brown	BIOCARTA	h_tcrPathway:Lck and Fyn tyrosine kinases in initiation o	3	0.332226	0.01685	ENSG00000204287,	28	11	1437	13.99675	0.657199	0.414508	15.80803
brown	BIOCARTA	h_ctlPathway:CTL mediated immune response against tar	3	0.332226	0.030715	ENSG00000180644,	28	15	1437	10.26429	0.859895	0.480621	27.08524
brown	BIOCARTA	h_CSKPathway:Activation of Csk by cAMP-dependent Pro	3	0.332226	0.038876	ENSG00000204287,	28	17	1437	9.056723	0.917758	0.464482	33.06843
brown	BIOCARTA	h_ctla4Pathway:The Co-Stimulatory Signal During T-cell A	3	0.332226	0.04777	ENSG00000204287,	28	19	1437	8.103383	0.954213	0.460304	39.08121
brown	BIOCARTA	h_th1th2Pathway:Th1/Th2 Differentiation	3	0.332226	0.052471	ENSG00000204287,	28	20	1437	7.698214	0.966479	0.432169	42.05922
brown	BIOCARTA	h_inflamPathway:Cytokines and Inflammatory Response	3	0.332226	0.083801	ENSG00000204287,	28	26	1437	5.921703	0.995969	0.545106	58.7781
brown	Category	Term	Count	%	Pvalue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
brown	GOTERM_BP_FAT	GO:0007608~sensory perception of smell	136	15.06091	1.54E-87	ENSG00000221931,	530	431	13528	8.054144	2.65E-84	2.65E-84	2.61E-84
brown	GOTERM_BP_FAT	GO:0007606~sensory perception of chemical stimulus	141	15.61462	1.50E-86	ENSG00000221931,	530	478	13528	7.529202	2.58E-83	1.29E-83	2.54E-83
brown	GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signalin	196	21.70543	1.73E-79	ENSG00000178394,	530	1123	13528	4.45486	2.97E-76	9.90E-77	2.92E-76
brown	GOTERM_BP_FAT	GO:0007600~sensory perception	157	17.38649	2.35E-68	ENSG00000221931,	530	810	13528	4.947347	4.02E-65	1.01E-65	3.96E-65
brown	GOTERM_BP_FAT	GO:0050890~cognition	157	17.38649	5.05E-61	ENSG00000221931,	530	909	13528	4.408527	8.65E-58	1.73E-58	8.52E-58
brown	GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduct	212	23.4773	8.31E-53	ENSG00000178394,	530	1856	13528	2.915517	1.42E-49	2.37E-50	1.40E-49
brown	GOTERM_BP_FAT	GO:0050877~neurological system process	166	18.38317	2.80E-50	ENSG00000221931,	530	1210	13528	3.501712	4.80E-47	6.85E-48	4.72E-47
brown	GOTERM_BP_FAT	GO:0042742~defense response to bacterium	20	2.214839	6.17E-08	ENSG00000203970,	530	112	13528	4.557951	1.06E-04	1.32E-05	1.04E-04
brown	GOTERM_BP_FAT	GO:0009617~response to bacterium	20	2.214839	2.04E-04	ENSG00000203970,	530	193	13528	2.645029	0.295107	0.038111	0.343879
brown	GOTERM_BP_FAT	GO:0006952~defense response	43	4.761905	3.03E-04	ENSG00000088827,	530	615	13528	1.784642	0.404631	0.050536	0.509505
brown	GOTERM_BP_FAT	GO:0007586~digestion	12	1.328904	8.22E-04	ENSG00000137392,	530	91	13528	3.365872	0.755523	0.120197	1.377955
brown	GOTERM_BP_FAT	GO:0009566~fertilization	11	1.218162	9.78E-04	ENSG00000118245,	530	79	13528	3.554048	0.813239	0.130491	1.639213
brown	GOTERM_BP_FAT	GO:0007218~neuropeptide signaling pathway	12	1.328904	9.87E-04	ENSG00000105954,	530	93	13528	3.293488	0.815829	0.122032	1.652745
brown	GOTERM_BP_FAT	GO:0006955~immune response	43	4.761905	0.00292	ENSG00000173369,	530	690	13528	1.590659	0.993342	0.300924	4.817
brown	GOTERM_BP_FAT	GO:0042953~lipoprotein transport	4	0.442968	0.005808	ENSG00000081479,	530	10	13528	10.20981	0.999954	0.486031	9.366255
brown	GOTERM_BP_FAT	GO:0007338~single fertilization	7	0.775194	0.029245	ENSG00000118245,	530	60	13528	2.977862	1	0.958399	39.41492
brown	GOTERM_BP_FAT	GO:0019953~sexual reproduction	27	2.990033	0.03666	ENSG00000118245,	530	458	13528	1.504721	1	0.976848	46.77163
brown	GOTERM_BP_FAT	GO:0007602~phototransduction	5	0.55371	0.038587	ENSG00000122375,	530	33	13528	3.867353	1	0.976413	48.54029
brown	GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	16	1.771872	0.043043	ENSG00000178394,	530	235	13528	1.73784	1	0.981107	52.42249
brown	GOTERM_BP_FAT	GO:0007603~phototransduction, visible light	3	0.332226	0.045788	ENSG00000198691,	530	9	13528	8.508176	1	0.981988	54.67513
brown	GOTERM_BP_FAT	GO:0007200~activation of phospholipase C activity by G	6	0.664452	0.051713	ENSG00000110148,	530	52	13528	2.945138	1	0.986883	59.19935
brown	GOTERM_BP_FAT	GO:0044241~lipid digestion	3	0.332226	0.055783	ENSG00000143921,	530	10	13528	7.657358	1	0.988575	62.05734
brown	GOTERM_BP_FAT	GO:0009583~detection of light stimulus	5	0.55371	0.064741	ENSG00000122375,	530	39	13528	3.272375	1	0.99318	67.69765

brown	GOTERM_BP_FAT	GO:0055006~cardiac cell development	3	0.332226	0.066456	ENSG00000163217,	530	11	13528	6.961235	1	0.992636	68.68322
brown	GOTERM_BP_FAT	GO:0055013~cardiac muscle cell development	3	0.332226	0.066456	ENSG00000163217,	530	11	13528	6.961235	1	0.992636	68.68322
brown	GOTERM_BP_FAT	GO:0060193~positive regulation of lipase activity	7	0.775194	0.072764	ENSG00000110148,	530	75	13528	2.382289	1	0.994369	72.07064
brown	GOTERM_BP_FAT	GO:0070170~regulation of tooth mineralization	2	0.221484	0.076682	ENSG00000137674,	530	2	13528	25.52453	1	0.994802	73.99742
brown	GOTERM_BP_FAT	GO:0048663~neuron fate commitment	5	0.55371	0.080548	ENSG00000115844,	530	42	13528	3.038634	1	0.995161	75.77577
brown	GOTERM_BP_FAT	GO:0050909~sensory perception of taste	5	0.55371	0.092047	ENSG00000169777,	530	44	13528	2.900515	1	0.997291	80.41305
brown	GOTERM_CC_FAT	GO:0005886~plasma membrane	269	29.78959	5.16E-23	ENSG00000178394,	547	3777	12782	1.664243	1.27E-20	1.27E-20	6.69E-20
brown	GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	321	35.54817	3.65E-14	ENSG00000088827,	547	5485	12782	1.36754	8.99E-12	4.49E-12	4.73E-11
brown	GOTERM_CC_FAT	GO:0016021~integral to membrane	312	34.5515	6.29E-14	ENSG00000088827,	547	5297	12782	1.376373	1.55E-11	5.15E-12	8.14E-11
brown	GOTERM_CC_FAT	GO:0005576~extracellular region	146	16.16833	2.42E-11	ENSG00000173369,	547	2010	12782	1.697338	5.96E-09	1.49E-09	3.14E-08
brown	GOTERM_CC_FAT	GO:0005882~intermediate filament	27	2.990033	6.60E-08	ENSG00000204889,	547	183	12782	3.447658	1.62E-05	3.25E-06	8.55E-05
brown	GOTERM_CC_FAT	GO:0045111~intermediate filament cytoskeleton	27	2.990033	1.03E-07	ENSG00000204889,	547	187	12782	3.373911	2.53E-05	4.22E-06	1.33E-04
brown	GOTERM_CC_FAT	GO:0045095~keratin filament	16	1.771872	4.20E-06	ENSG00000139648,	547	88	12782	4.248629	0.001034	1.48E-04	0.005447
brown	GOTERM_CC_FAT	GO:0044447~axoneme part	4	0.442968	0.033724	ENSG00000168454,	547	17	12782	5.498226	0.999784	0.651775	35.88783
brown	GOTERM_CC_FAT	GO:0045179~apical cortex	3	0.332226	0.042979	ENSG00000163586,	547	8	12782	8.762797	0.99998	0.699033	43.40475
brown	GOTERM_CC_FAT	GO:0045177~apical part of cell	14	1.550388	0.043337	ENSG00000091138,	547	179	12782	1.827622	0.999982	0.663743	43.67831
brown	GOTERM_CC_FAT	GO:0005903~brush border	6	0.664452	0.045375	ENSG00000091138,	547	46	12782	3.047929	0.999989	0.64601	45.21325
brown	GOTERM_CC_FAT	GO:0016324~apical plasma membrane	11	1.218162	0.05857	ENSG00000169344,	547	133	12782	1.932647	1	0.709826	54.25451
brown	GOTERM_CC_FAT	GO:0005615~extracellular space	39	4.318937	0.059396	ENSG00000173369,	547	685	12782	1.33041	1	0.686114	54.77242
brown	GOTERM_CC_FAT	GO:0009434~microtubule-based flagellum	4	0.442968	0.072854	ENSG00000168454,	547	23	12782	4.063906	1	0.735306	62.47641
brown	GOTERM_CC_FAT	GO:0005930~axoneme	5	0.55371	0.096413	ENSG00000138892,	547	41	12782	2.84969	1	0.810369	73.118
brown	GOTERM_MF_FAT	GO:0004984~olfactory receptor activity	137	15.17165	5.47E-89	ENSG00000221931,	509	431	12983	8.107754	2.94E-86	2.94E-86	7.95E-86
brown	GOTERM_MF_FAT	GO:0003823~antigen binding	13	1.439646	1.31E-06	ENSG00000211899,	509	56	12983	5.921239	7.04E-04	3.52E-04	0.001908
brown	GOTERM_MF_FAT	GO:0001653~peptide receptor activity	13	1.439646	0.001663	ENSG00000110148,	509	114	12983	2.908679	0.590841	0.257612	2.391438
brown	GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein coupled	13	1.439646	0.001663	ENSG00000110148,	509	114	12983	2.908679	0.590841	0.257612	2.391438
brown	GOTERM_MF_FAT	GO:0001584~rhodopsin-like receptor activity	4	0.442968	0.01006	ENSG00000157219,	509	12	12983	8.502292	0.995615	0.74267	13.67603
brown	GOTERM_MF_FAT	GO:0008188~neuropeptide receptor activity	6	0.664452	0.019129	ENSG00000110148,	509	40	12983	3.826031	0.999969	0.874368	24.49196
brown	GOTERM_MF_FAT	GO:0042923~neuropeptide binding	6	0.664452	0.021107	ENSG00000110148,	509	41	12983	3.732714	0.999989	0.851821	26.6767
brown	GOTERM_MF_FAT	GO:0005212~structural constituent of eye lens	4	0.442968	0.026904	ENSG00000105370,	509	17	12983	6.001618	1	0.876588	32.74529
brown	GOTERM_MF_FAT	GO:0004982~N-formyl peptide receptor activity	3	0.332226	0.028157	ENSG00000187474,	509	7	12983	10.93152	1	0.852972	33.99315
brown	GOTERM_MF_FAT	GO:0042277~peptide binding	15	1.66113	0.028619	ENSG00000204287,	509	203	12983	1.884745	1	0.823162	34.4486
brown	GOTERM_MF_FAT	GO:0005529~sugar binding	14	1.550388	0.042948	ENSG00000156575,	509	195	12983	1.831263	1	0.905323	47.19061
brown	GOTERM_MF_FAT	GO:0005179~hormone activity	9	0.996678	0.061083	ENSG00000134200,	509	108	12983	2.125573	1	0.953898	60.0177
brown	GOTERM_MF_FAT	GO:0030246~carbohydrate binding	21	2.325581	0.062354	ENSG00000088827,	509	354	12983	1.51312	1	0.943929	60.798
brown	GOTERM_MF_FAT	GO:0048029~monosaccharide binding	5	0.55371	0.069926	ENSG00000118004,	509	40	12983	3.18836	1	0.949935	65.15908
brown	GOTERM_MF_FAT	GO:0008227~amine receptor activity	5	0.55371	0.075204	ENSG00000157219,	509	41	12983	3.110595	1	0.950155	67.92674
brown	GOTERM_MF_FAT	GO:0004951~cholecystokinin receptor activity	2	0.221484	0.076728	ENSG00000110148,	509	2	12983	25.50688	1	0.942615	68.68715
brown	GOTERM_MF_FAT	GO:0018685~alkane 1-monooxygenase activity	2	0.221484	0.076728	ENSG00000162365,	509	2	12983	25.50688	1	0.942615	68.68715
brown	GOTERM_MF_FAT	GO:0017127~cholesterol transporter activity	3	0.332226	0.077818	ENSG00000084674,	509	12	12983	6.376719	1	0.934059	69.22063
brown	GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	8	0.885936	0.07852	ENSG00000110148,	509	95	12983	2.147947	1	0.924461	69.55959
brown	GOTERM_MF_FAT	GO:0004993~serotonin receptor activity	3	0.332226	0.089657	ENSG00000157219,	509	13	12983	5.886202	1	0.939334	74.49419
brown	HIV_INTERACTION	gag:capsid	7	0.775194	2.98E-05	ENSG00000204287,	31	31	1394	10.15401	4.17E-04	4.17E-04	0.020249
brown	HIV_INTERACTION	env:Envelope transmembrane glycoprotein gp41	10	1.10742	0.003277	ENSG00000173369,	31	152	1394	2.958404	0.044917	0.022717	2.205197
brown	HIV_INTERACTION	env:Envelope surface glycoprotein gp120	20	2.214839	0.003892	ENSG00000196126,	31	529	1394	1.700104	0.053128	0.018033	2.614061
brown	HIV_INTERACTION_CATEGORY	gag:Pr55(Gag) relocalizes	3	0.332226	0.002617	ENSG00000204287,	31	4	1394	33.72581	0.158797	0.158797	2.643257
brown	HIV_INTERACTION_CATEGORY	env:Envelope surface glycoprotein gp120 interacts with	10	1.10742	0.002716	ENSG00000173369,	31	148	1394	3.038361	0.164328	0.085849	2.742703
brown	HIV_INTERACTION_CATEGORY	gag:Pr55(Gag) relocalized by	3	0.332226	0.004303	ENSG00000204287,	31	5	1394	26.98065	0.247676	0.090502	4.312922
brown	HIV_INTERACTION_CATEGORY	gag:capsid downregulates	3	0.332226	0.004303	ENSG00000204287,	31	5	1394	26.98065	0.247676	0.090502	4.312922

brown	HIV_INTERACTION_CATEGORY	env:Envelope transmembrane glycoprotein gp41 upregul	5	0.55371	0.007738	ENSG00000204287,	31	38	1394	5.916808	0.40113	0.120303	7.635423
brown	HIV_INTERACTION_CATEGORY	gag:Pr55(Gag) co-localizes with	3	0.332226	0.021835	ENSG00000204287,	31	11	1394	12.26393	0.767081	0.252793	20.20596
brown	HIV_INTERACTION_CATEGORY	env:Envelope surface glycoprotein gp160, precursor asso	3	0.332226	0.03471	ENSG00000204287,	31	14	1394	9.635945	0.902855	0.321988	30.31545
brown	HIV_INTERACTION_CATEGORY	env:Envelope transmembrane glycoprotein gp41 incorpo	3	0.332226	0.03471	ENSG00000204287,	31	14	1394	9.635945	0.902855	0.321988	30.31545
brown	HIV_INTERACTION_CATEGORY	env:Envelope surface glycoprotein gp120 inhibits	5	0.55371	0.034819	ENSG00000204287,	31	59	1394	3.810826	0.903578	0.28405	30.39606
brown	HIV_INTERACTION_CATEGORY	env:Envelope surface glycoprotein gp120 inhibited by	5	0.55371	0.034819	ENSG00000108700,	31	59	1394	3.810826	0.903578	0.28405	30.39606
brown	HIV_INTERACTION_CATEGORY	nef:Nef downregulates	4	0.442968	0.062206	ENSG00000204287,	31	43	1394	4.183046	0.985576	0.411313	48.14228
brown	HIV_INTERACTION_CATEGORY	env:Envelope surface glycoprotein gp120 upregulates	7	0.775194	0.08514	ENSG00000204287,	31	146	1394	2.155988	0.997185	0.479285	59.73997
brown	HIV_INTERACTION_CATEGORY	tat:Tat downregulates	6	0.664452	0.086396	ENSG00000204287,	31	112	1394	2.408986	0.997429	0.449188	60.30139
brown	INTERPRO	IPR017452:GPCR, rhodopsin-like superfamily	174	19.2691	2.53E-92	ENSG00000178394,	636	726	16659	6.277756	1.94E-89	1.94E-89	3.87E-89
brown	INTERPRO	IPR000276:7TM GPCR, rhodopsin-like	172	19.04762	3.47E-90	ENSG00000178394,	636	727	16659	6.197062	2.66E-87	1.33E-87	5.29E-87
brown	INTERPRO	IPR000725:Olfactory receptor	136	15.06091	3.59E-88	ENSG00000221931,	636	428	16659	8.323135	2.76E-85	9.19E-86	5.48E-85
brown	INTERPRO	IPR003596:Immunoglobulin V-set, subgroup	22	2.436323	8.22E-13	ENSG00000124557,	636	78	16659	7.387881	6.31E-10	1.58E-10	1.25E-09
brown	INTERPRO	IPR013106:Immunoglobulin V-set	31	3.433001	2.52E-08	ENSG00000088827,	636	249	16659	3.261025	1.93E-05	3.87E-06	3.84E-05
brown	INTERPRO	IPR013783:Immunoglobulin-like fold	46	5.094131	1.44E-06	ENSG00000124557,	636	553	16659	2.178836	0.001104	1.84E-04	0.002196
brown	INTERPRO	IPR003597:Immunoglobulin C1-set	13	1.439646	8.74E-06	ENSG00000204287,	636	68	16659	5.007561	0.006686	9.58E-04	0.013336
brown	INTERPRO	IPR016044:Filament	12	1.328904	8.25E-05	ENSG00000173908,	636	72	16659	4.365566	0.061376	0.007886	0.12584
brown	INTERPRO	IPR001664:Intermediate filament protein	12	1.328904	9.38E-05	ENSG00000173908,	636	73	16659	4.305764	0.069518	0.007974	0.143137
brown	INTERPRO	IPR007110:Immunoglobulin-like	38	4.208195	9.77E-05	ENSG00000088827,	636	501	16659	1.986725	0.072261	0.007472	0.148996
brown	INTERPRO	IPR015544:Olfactory receptor MOR256	7	0.775194	1.32E-04	ENSG00000203664,	636	22	16659	8.334262	0.096744	0.009207	0.20207
brown	INTERPRO	IPR018039:Intermediate filament protein, conserved site	11	1.218162	3.84E-04	ENSG00000173908,	636	72	16659	4.001769	0.255168	0.024251	0.58394
brown	INTERPRO	IPR003006:Immunoglobulin/major histocompatibility com	12	1.328904	4.56E-04	ENSG00000204287,	636	87	16659	3.612882	0.295666	0.026602	0.694371
brown	INTERPRO	IPR015539:Olfactory receptor MOR103	4	0.442968	0.001011	ENSG00000186440,	636	6	16659	17.46226	0.540254	0.053993	1.532952
brown	INTERPRO	IPR004020:Pyrim	6	0.664452	0.001216	ENSG00000142405,	636	22	16659	7.143654	0.607094	0.060379	1.840004
brown	INTERPRO	IPR002957:Keratin, type I	7	0.775194	0.001377	ENSG00000173908,	636	33	16659	5.556175	0.652826	0.063982	2.081184
brown	INTERPRO	IPR003267:Small proline-rich	6	0.664452	0.002232	ENSG00000198854,	636	25	16659	6.286415	0.820173	0.096001	3.35338
brown	INTERPRO	IPR007659:Keratin, high-sulphur matrix protein	3	0.332226	0.00827	ENSG00000212900,	636	4	16659	19.64505	0.998301	0.298341	11.90763
brown	INTERPRO	IPR002494:Keratin, high sulphur B2 protein	7	0.775194	0.008515	ENSG00000196224,	636	47	16659	3.901144	0.998594	0.292233	12.23907
brown	INTERPRO	IPR007111:NACHT nucleoside triphosphatase	5	0.55371	0.010394	ENSG00000142405,	636	23	16659	5.694217	0.999673	0.330502	14.74525
brown	INTERPRO	IPR014853:Conserved-cysteine-rich domain	4	0.442968	0.011844	ENSG00000205592,	636	13	16659	8.059507	0.999894	0.353207	16.63205
brown	INTERPRO	IPR001855:Beta defensin	4	0.442968	0.011844	ENSG00000203970,	636	13	16659	8.059507	0.999894	0.353207	16.63205
brown	INTERPRO	IPR006207:Cystine knot, C-terminal	5	0.55371	0.013985	ENSG00000104415,	636	25	16659	5.238679	0.99998	0.388387	19.34817
brown	INTERPRO	IPR001314:Peptidase S1A, chymotrypsin	10	1.10742	0.017784	ENSG00000154646,	636	104	16659	2.518596	0.999999	0.450741	23.96442
brown	INTERPRO	IPR008197:Whey acidic protein, 4-disulphide core	4	0.442968	0.017807	ENSG00000101443,	636	15	16659	6.984906	0.999999	0.437266	23.99087
brown	INTERPRO	IPR018114:Peptidase S1/S6, chymotrypsin/Hap, active site	10	1.10742	0.018819	ENSG00000154646,	636	105	16659	2.494609	1	0.44213	25.17819
brown	INTERPRO	IPR003054:Type II keratin	5	0.55371	0.020697	ENSG00000139648,	636	28	16659	4.677392	1	0.460858	27.3352
brown	INTERPRO	IPR001846:von Willebrand factor, type D	4	0.442968	0.025155	ENSG00000205592,	636	17	16659	6.163152	1	0.515524	32.2252
brown	INTERPRO	IPR000826:Formyl/methionyl peptide receptor	3	0.332226	0.02682	ENSG00000187474,	636	7	16659	11.22574	1	0.525582	33.97021
brown	INTERPRO	IPR001254:Peptidase S1 and S6, chymotrypsin/Hap	10	1.10742	0.033229	ENSG00000154646,	636	116	16659	2.258051	1	0.591374	40.30693
brown	INTERPRO	IPR018378:C-type lectin, conserved site	8	0.885936	0.03671	ENSG00000118004,	636	82	16659	2.555453	1	0.616138	43.50575
brown	INTERPRO	IPR011029:DEATH-like	7	0.775194	0.042051	ENSG00000142405,	636	67	16659	2.736623	1	0.655041	48.10349
brown	INTERPRO	IPR002231:5-Hydroxytryptamine receptor	3	0.332226	0.043717	ENSG00000157219,	636	9	16659	8.731132	1	0.65796	49.464
brown	INTERPRO	IPR013091:EGF calcium-binding	7	0.775194	0.056319	ENSG00000169344,	636	72	16659	2.54658	1	0.740516	58.7298
brown	INTERPRO	IPR004000:Actin/actin-like	5	0.55371	0.060087	ENSG00000163017,	636	39	16659	3.358128	1	0.753341	61.17518
brown	INTERPRO	IPR018453:Protease inhibitor I8, cysteine-rich trypsin inh	3	0.332226	0.063529	ENSG00000205592,	636	11	16659	7.143654	1	0.763133	63.28998
brown	INTERPRO	IPR007951:PMG	3	0.332226	0.063529	ENSG00000206107,	636	11	16659	7.143654	1	0.763133	63.28998
brown	INTERPRO	IPR016186:C-type lectin-like	8	0.885936	0.070594	ENSG00000118004,	636	95	16659	2.20576	1	0.790242	67.29816
brown	INTERPRO	IPR008836:Semenogelin	2	0.221484	0.074784	ENSG00000124157,	636	2	16659	26.1934	1	0.800789	69.47835

brown	INTERPRO	IPR012510:Actin-binding, Xin repeat	2	0.221484	0.074784	ENSG00000163092,	636	2	16659	26.1934	1	0.800789	69.47835
brown	INTERPRO	IPR009126:Cholecystokinin receptor	2	0.221484	0.074784	ENSG00000110148,	636	2	16659	26.1934	1	0.800789	69.47835
brown	INTERPRO	IPR007960:Mammalian taste receptor	4	0.442968	0.074887	ENSG00000169777,	636	26	16659	4.029753	1	0.792614	69.53004
brown	INTERPRO	IPR018069:Whey acidic protein, 4-disulphide core, conserved	3	0.332226	0.085727	ENSG00000101443,	636	13	16659	6.04463	1	0.828803	74.54812
brown	INTERPRO	IPR017942:Lipid-binding serum glycoprotein, N-terminal	3	0.332226	0.085727	ENSG00000186190,	636	13	16659	6.04463	1	0.828803	74.54812
brown	INTERPRO	IPR001304:C-type lectin	7	0.775194	0.092603	ENSG00000118004,	636	82	16659	2.236022	1	0.845223	77.3191
brown	INTERPRO	IPR012351:Four-helical cytokine, core	5	0.55371	0.097252	ENSG00000162891,	636	46	16659	2.847108	1	0.852874	79.02965
brown	KEGG_PATHWAY	hsa04740:Olfactory transduction	128	14.17497	2.09E-81	ENSG00000221931,	255	379	5085	6.734751	2.59E-79	2.59E-79	2.41E-78
brown	KEGG_PATHWAY	hsa05332:Graft-versus-host disease	8	0.885936	0.002777	ENSG00000204287,	255	39	5085	4.090498	0.291677	0.158381	3.16043
brown	KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	24	2.657807	0.004085	ENSG00000178394,	255	256	5085	1.869485	0.398026	0.155644	4.616497
brown	KEGG_PATHWAY	hsa05330:Allograft rejection	6	0.664452	0.031713	ENSG00000204287,	255	36	5085	3.323529	0.981614	0.631766	31.07414
brown	KEGG_PATHWAY	hsa05320:Autoimmune thyroid disease	7	0.775194	0.040077	ENSG00000204287,	255	51	5085	2.737024	0.993729	0.637369	37.64421
brown	KEGG_PATHWAY	hsa04940:Type 1 diabetes mellitus	6	0.664452	0.056316	ENSG00000204287,	255	42	5085	2.848739	0.999244	0.698178	48.79502
brown	OMIM_DISEASE	Genome-wide association and linkage analyses of hemophilia A	4	0.442968	0.00723	ENSG00000172464,	102	15	3671	9.597386	0.715042	0.715042	8.496445
brown	PIR_SUPERFAMILY	PIRSF000006:rhodopsin-like G protein-coupled receptors	168	18.60465	7.28E-76	ENSG00000178394,	387	686	7396	4.680272	1.65E-73	1.65E-73	9.31E-73
brown	PIR_SUPERFAMILY	PIRSF003152:G protein-coupled olfactory receptor, class 1	121	13.39978	3.98E-70	ENSG00000221931,	387	353	7396	6.550834	9.00E-68	4.50E-68	5.09E-67
brown	PIR_SUPERFAMILY	PIRSF001974:immunoglobulin V region	13	1.439646	3.73E-07	ENSG00000211642,	387	39	7396	6.37037	8.44E-05	2.81E-05	4.77E-04
brown	PIR_SUPERFAMILY	PIRSF038651:G protein-coupled olfactory receptor, class 2	13	1.439646	3.45E-05	ENSG00000205497,	387	58	7396	4.283525	0.00777	0.001948	0.044117
brown	PIR_SUPERFAMILY	PIRSF001712:mas-related G protein-coupled receptor	5	0.55371	0.001193	ENSG00000172938,	387	10	7396	9.555556	0.236444	0.052524	1.51446
brown	PIR_SUPERFAMILY	PIRSF037494:NALP protein	5	0.55371	0.002587	ENSG00000142405,	387	12	7396	7.962963	0.4431	0.092954	3.25713
brown	PIR_SUPERFAMILY	PIRSF002282:cytoskeletal keratin	10	1.10742	0.004063	ENSG00000173908,	387	61	7396	3.132969	0.601535	0.123175	5.071929
brown	PIR_SUPERFAMILY	PIRSF005569:ultra-high-sulfur keratin	4	0.442968	0.00936	ENSG00000212721,	387	9	7396	8.493827	0.880602	0.233301	11.32789
brown	PIR_SUPERFAMILY	PIRSF001135:trypsin	7	0.775194	0.009996	ENSG00000007038,	387	36	7396	3.716049	0.896728	0.222962	12.05274
brown	SMART	SM00406:IGv	22	2.436323	2.04E-15	ENSG00000124557,	260	78	9079	9.849014	3.02E-13	3.02E-13	2.39E-12
brown	SMART	SM00407:IGc1	13	1.439646	3.96E-07	ENSG00000204287,	260	68	9079	6.675735	5.98E-05	2.99E-05	4.74E-04
brown	SMART	SM00041:CT	5	0.55371	0.005103	ENSG00000104415,	260	25	9079	6.983846	0.538175	0.227036	5.933475
brown	SMART	SM00020:Tryp_SPc	10	1.10742	0.005827	ENSG00000154646,	260	116	9079	3.010279	0.586228	0.197971	6.748213
brown	SMART	SM00217:WAP	4	0.442968	0.008097	ENSG00000101443,	260	15	9079	9.311795	0.707005	0.217702	9.262088
brown	SMART	SM00216:VWD	4	0.442968	0.011603	ENSG00000205592,	260	17	9079	8.21629	0.828349	0.254511	13.02322
brown	SMART	SM00268:ACTIN	5	0.55371	0.024337	ENSG00000163017,	260	39	9079	4.476824	0.975775	0.412266	25.51402
brown	SMART	SM00034:CLECT	7	0.775194	0.029334	ENSG00000118004,	260	82	9079	2.98091	0.988843	0.429908	29.9487
brown	SMART	SM00328:BPI1	3	0.332226	0.051408	ENSG00000186190,	260	13	9079	8.058284	0.999654	0.587482	46.7922
brown	SMART	SM00303:GPS	4	0.442968	0.093331	ENSG00000130943,	260	38	9079	3.675709	1	0.77224	69.00548
brown	SP_PIR_KEYWORDS	g-protein coupled receptor	183	20.26578	6.52E-94	ENSG00000178394,	707	816	19235	6.101459	2.74E-91	2.74E-91	9.15E-91
brown	SP_PIR_KEYWORDS	olfaction	135	14.95017	2.09E-91	ENSG00000221931,	707	409	19235	8.980143	8.79E-89	4.40E-89	2.94E-88
brown	SP_PIR_KEYWORDS	transducer	185	20.48726	1.92E-90	ENSG00000178394,	707	874	19235	5.758814	8.04E-88	2.68E-88	2.69E-87
brown	SP_PIR_KEYWORDS	sensory transduction	148	16.38981	2.18E-81	ENSG00000221931,	707	595	19235	6.767333	9.16E-79	2.29E-79	3.06E-78
brown	SP_PIR_KEYWORDS	disulfide bond	298	33.00111	3.58E-69	ENSG00000173369,	707	2924	19235	2.772756	1.50E-66	3.01E-67	5.03E-66
brown	SP_PIR_KEYWORDS	receptor	208	23.03433	2.35E-63	ENSG00000178394,	707	1583	19235	3.574828	9.86E-61	1.64E-61	3.30E-60
brown	SP_PIR_KEYWORDS	cell membrane	220	24.36323	1.09E-46	ENSG00000178394,	707	2194	19235	2.728091	4.57E-44	6.53E-45	1.53E-43
brown	SP_PIR_KEYWORDS	glycoprotein	327	36.21262	5.59E-46	ENSG00000173369,	707	4318	19235	2.060335	2.35E-43	2.93E-44	7.85E-43
brown	SP_PIR_KEYWORDS	transmembrane	297	32.89037	1.15E-21	ENSG00000178394,	707	4973	19235	1.624841	4.82E-19	5.35E-20	1.61E-18
brown	SP_PIR_KEYWORDS	membrane	324	35.8804	6.24E-14	ENSG00000088827,	707	6256	19235	1.409033	2.62E-11	2.62E-12	8.76E-11
brown	SP_PIR_KEYWORDS	Secreted	121	13.39978	9.38E-13	ENSG00000088827,	707	1689	19235	1.949075	3.94E-10	3.58E-11	1.32E-09
brown	SP_PIR_KEYWORDS	polymorphism	506	56.03544	6.12E-11	ENSG00000173369,	707	11550	19235	1.191904	2.57E-08	2.14E-09	8.59E-08
brown	SP_PIR_KEYWORDS	signal	184	20.37652	4.53E-10	ENSG00000173369,	707	3250	19235	1.540307	1.90E-07	1.46E-08	6.37E-07
brown	SP_PIR_KEYWORDS	keratin	25	2.768549	5.11E-10	ENSG00000173908,	707	144	19235	4.723352	2.15E-07	1.53E-08	7.17E-07
brown	SP_PIR_KEYWORDS	defensin	14	1.550388	9.48E-10	ENSG00000203970,	707	40	19235	9.522277	3.98E-07	2.65E-08	1.33E-06

brown	SP_PIR_KEYWORDS	antibiotic	17	1.882614	2.27E-09	ENSG00000203970,	707	68	19235	6.801627	9.54E-07	5.96E-08	3.19E-06
brown	SP_PIR_KEYWORDS	immunoglobulin c region	8	0.885936	2.94E-09	ENSG00000211669,	707	9	19235	24.18356	1.24E-06	7.27E-08	4.13E-06
brown	SP_PIR_KEYWORDS	Antimicrobial	17	1.882614	4.47E-09	ENSG00000203970,	707	71	19235	6.514234	1.88E-06	1.04E-07	6.27E-06
brown	SP_PIR_KEYWORDS	immunoglobulin	11	1.218162	9.18E-08	ENSG00000211899,	707	31	19235	9.653922	3.86E-05	2.03E-06	1.29E-04
brown	SP_PIR_KEYWORDS	heterotetramer	13	1.439646	7.04E-06	ENSG00000211899,	707	69	19235	5.125864	0.002953	1.48E-04	0.009889
brown	SP_PIR_KEYWORDS	Intermediate filament	12	1.328904	1.25E-04	ENSG00000173908,	707	78	19235	4.185616	0.051106	0.002495	0.175294
brown	SP_PIR_KEYWORDS	G protein-coupled receptor	14	1.550388	3.35E-04	ENSG00000178394,	707	116	19235	3.283544	0.131162	0.00637	0.469134
brown	SP_PIR_KEYWORDS	neuropeptide	7	0.775194	0.001564	ENSG00000105954,	707	35	19235	5.441301	0.481809	0.028179	2.174744
brown	SP_PIR_KEYWORDS	transmembrane protein	38	4.208195	0.004688	ENSG00000178394,	707	642	19235	1.610354	0.86103	0.078939	6.387332
brown	SP_PIR_KEYWORDS	Pyrrrolidone carboxylic acid	8	0.885936	0.011249	ENSG00000173369,	707	67	19235	3.248538	0.991362	0.173093	14.69336
brown	SP_PIR_KEYWORDS	hormone	9	0.996678	0.014514	ENSG00000134200,	707	87	19235	2.814466	0.997846	0.210356	18.56556
brown	SP_PIR_KEYWORDS	Immunoglobulin domain	28	3.100775	0.014947	ENSG00000124557,	707	470	19235	1.620813	0.998209	0.208844	19.06656
brown	SP_PIR_KEYWORDS	zymogen	15	1.66113	0.020089	ENSG00000137757,	707	206	19235	1.981056	0.999801	0.262432	24.80303
brown	SP_PIR_KEYWORDS	eye lens protein	4	0.442968	0.022801	ENSG00000105370,	707	17	19235	6.401531	0.999938	0.283977	27.67448
brown	SP_PIR_KEYWORDS	pyroglutamic acid	6	0.664452	0.026041	ENSG00000173369,	707	46	19235	3.548675	0.999985	0.308852	30.97095
brown	SP_PIR_KEYWORDS	Lectin	12	1.328904	0.03277	ENSG00000118004,	707	159	19235	2.053321	0.999999	0.363275	37.37667
brown	SP_PIR_KEYWORDS	digestion	3	0.332226	0.040807	ENSG00000137392,	707	9	19235	9.068835	1	0.42122	44.30329
brown	SP_PIR_KEYWORDS	protease inhibitor	9	0.996678	0.043245	ENSG00000126838,	707	107	19235	2.288398	1	0.430301	46.2589
brown	SP_PIR_KEYWORDS	Serine protease	10	1.10742	0.06323	ENSG00000154646,	707	136	19235	2.000478	1	0.553743	60.04897
brown	SP_PIR_KEYWORDS	seminal vesicle	2	0.221484	0.072063	ENSG00000124157,	707	2	19235	27.20651	1	0.592409	65.02696
brown	SP_PIR_KEYWORDS	Serine protease inhibitor	7	0.775194	0.073486	ENSG00000126838,	707	80	19235	2.380569	1	0.589538	65.77313
brown	SP_PIR_KEYWORDS	cleavage on pair of basic residues	16	1.771872	0.075392	ENSG00000105954,	707	271	19235	1.606288	1	0.589254	66.74901
brown	SP_PIR_KEYWORDS	duplication	14	1.550388	0.078155	ENSG00000211899,	707	228	19235	1.670575	1	0.593203	68.11782
brown	SP_PIR_KEYWORDS	egf-like domain	14	1.550388	0.082216	ENSG00000086570,	707	230	19235	1.656048	1	0.603042	70.03499
brown	SP_PIR_KEYWORDS	carbon-carbon lyase	3	0.332226	0.09149	ENSG00000134240,	707	14	19235	5.829966	1	0.634856	74.01889
brown	SP_PIR_KEYWORDS	gpi-anchor	9	0.996678	0.0926	ENSG00000163295,	707	126	19235	1.943322	1	0.630433	74.46157
brown	UP_SEQ_FEATURE	disulfide bond	290	32.11517	5.56E-68	ENSG00000173369,	702	2819	19113	2.800881	1.07E-64	1.07E-64	9.51E-65
brown	UP_SEQ_FEATURE	topological domain:Extracellular	250	27.68549	2.48E-47	ENSG00000178394,	702	2719	19113	2.503356	4.78E-44	2.39E-44	4.24E-44
brown	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	319	35.32669	1.41E-46	ENSG00000088827,	702	4129	19113	2.103476	2.71E-43	9.04E-44	2.41E-43
brown	UP_SEQ_FEATURE	topological domain:Cytoplasmic	264	29.23588	2.08E-37	ENSG00000178394,	702	3374	19113	2.130348	4.01E-34	1.00E-34	3.56E-34
brown	UP_SEQ_FEATURE	transmembrane region	290	32.11517	2.38E-20	ENSG00000178394,	702	4911	19113	1.607755	4.60E-17	9.19E-18	4.08E-17
brown	UP_SEQ_FEATURE	signal peptide	184	20.37652	4.18E-10	ENSG00000173369,	702	3250	19113	1.541439	8.07E-07	1.35E-07	7.16E-07
brown	UP_SEQ_FEATURE	sequence variant	515	57.03212	9.93E-10	ENSG00000173369,	702	11992	19113	1.16925	1.92E-06	2.74E-07	1.70E-06
brown	UP_SEQ_FEATURE	region of interest:Rod	11	1.218162	2.53E-04	ENSG00000173908,	702	71	19113	4.218189	0.386054	0.059159	0.431852
brown	UP_SEQ_FEATURE	region of interest:Head	11	1.218162	3.18E-04	ENSG00000173908,	702	73	19113	4.102623	0.459221	0.066024	0.543875
brown	UP_SEQ_FEATURE	region of interest:Tail	11	1.218162	3.98E-04	ENSG00000173908,	702	75	19113	3.993219	0.536094	0.073932	0.679067
brown	UP_SEQ_FEATURE	region of interest:Coil 2	10	1.10742	5.17E-04	ENSG00000173908,	702	64	19113	4.25414	0.63127	0.086708	0.88118
brown	UP_SEQ_FEATURE	region of interest:Linker 12	10	1.10742	5.17E-04	ENSG00000173908,	702	64	19113	4.25414	0.63127	0.086708	0.88118
brown	UP_SEQ_FEATURE	region of interest:Coil 1B	10	1.10742	0.001004	ENSG00000173908,	702	70	19113	3.889499	0.856208	0.149232	1.705778
brown	UP_SEQ_FEATURE	region of interest:Linker 1	10	1.10742	0.001004	ENSG00000173908,	702	70	19113	3.889499	0.856208	0.149232	1.705778
brown	UP_SEQ_FEATURE	region of interest:Coil 1A	10	1.10742	0.001004	ENSG00000173908,	702	70	19113	3.889499	0.856208	0.149232	1.705778
brown	UP_SEQ_FEATURE	domain:DAPIIN	6	0.664452	0.001025	ENSG00000142405,	702	22	19113	7.425408	0.861709	0.14117	1.739787
brown	UP_SEQ_FEATURE	repeat:3	18	1.993355	0.002385	ENSG00000134249,	702	214	19113	2.290079	0.990029	0.280463	4.005538
brown	UP_SEQ_FEATURE	repeat:4	16	1.771872	0.00296	ENSG00000134249,	702	182	19113	2.393538	0.996724	0.3171	4.948741
brown	UP_SEQ_FEATURE	repeat:1	19	2.104097	0.003835	ENSG00000134249,	702	243	19113	2.128821	0.999399	0.370949	6.367815
brown	UP_SEQ_FEATURE	region of interest:CH3	3	0.332226	0.003932	ENSG00000211899,	702	3	19113	27.2265	0.999501	0.360612	6.522567
brown	UP_SEQ_FEATURE	repeat:2	19	2.104097	0.004354	ENSG00000134249,	702	246	19113	2.102859	0.99978	0.373646	7.198424
brown	UP_SEQ_FEATURE	repeat:8	12	1.328904	0.004644	ENSG00000168454,	702	120	19113	2.72265	0.999874	0.376735	7.659756

brown	UP_SEQ_FEATURE	repeat:5	14	1.550388	0.005247	ENSG00000168454,	702	157	19113	2.42784	0.999961	0.39813	8.614374
brown	UP_SEQ_FEATURE	region of interest:CH2	3	0.332226	0.007672	ENSG00000211899,	702	4	19113	20.41987	1	0.507291	12.35439
brown	UP_SEQ_FEATURE	repeat:7	12	1.328904	0.007935	ENSG00000168454,	702	129	19113	2.532697	1	0.502846	12.75022
brown	UP_SEQ_FEATURE	domain:NACHT	5	0.55371	0.010623	ENSG00000142405,	702	24	19113	5.672187	1	0.591864	16.71087
brown	UP_SEQ_FEATURE	domain:CTCK	5	0.55371	0.012287	ENSG00000104415,	702	25	19113	5.445299	1	0.629969	19.07689
brown	UP_SEQ_FEATURE	repeat:9	10	1.10742	0.013404	ENSG00000168454,	702	103	19113	2.643349	1	0.647181	20.63034
brown	UP_SEQ_FEATURE	active site:Charge relay system	15	1.66113	0.013509	ENSG00000154646,	702	196	19113	2.08366	1	0.635645	20.77473
brown	UP_SEQ_FEATURE	domain:Peptidase S1	10	1.10742	0.015939	ENSG00000154646,	702	106	19113	2.568537	1	0.682895	24.05045
brown	UP_SEQ_FEATURE	repeat:6	12	1.328904	0.016344	ENSG00000168454,	702	143	19113	2.284741	1	0.678867	24.58427
brown	UP_SEQ_FEATURE	repeat:10	9	0.996678	0.02209	ENSG00000168454,	702	94	19113	2.606792	1	0.773868	31.7822
brown	UP_SEQ_FEATURE	domain:Ig-like	6	0.664452	0.02384	ENSG00000158477,	702	45	19113	3.630199	1	0.788232	33.84172
brown	UP_SEQ_FEATURE	repeat:13	8	0.885936	0.024192	ENSG00000168454,	702	78	19113	2.792461	1	0.782312	34.24984
brown	UP_SEQ_FEATURE	region of interest:CH1	3	0.332226	0.024954	ENSG00000211899,	702	7	19113	11.6685	1	0.782184	35.12236
brown	UP_SEQ_FEATURE	domain:C-type lectin	8	0.885936	0.025737	ENSG00000118004,	702	79	19113	2.757113	1	0.782359	36.0087
brown	UP_SEQ_FEATURE	repeat:12	8	0.885936	0.027347	ENSG00000168454,	702	80	19113	2.72265	1	0.792774	37.79548
brown	UP_SEQ_FEATURE	site:Stutter	5	0.55371	0.031604	ENSG00000139648,	702	33	19113	4.125227	1	0.829811	42.2959
brown	UP_SEQ_FEATURE	repeat:15	7	0.775194	0.035941	ENSG00000168454,	702	67	19113	2.844559	1	0.859466	46.56472
brown	UP_SEQ_FEATURE	repeat:11	8	0.885936	0.036424	ENSG00000168454,	702	85	19113	2.562494	1	0.855633	47.02096
brown	UP_SEQ_FEATURE	propeptide:Removed in mature form	15	1.66113	0.043324	ENSG00000163017,	702	229	19113	1.783395	1	0.894545	53.15481
brown	UP_SEQ_FEATURE	lipid moiety-binding region:GPI-anchor amidated serine	6	0.664452	0.047332	ENSG00000169344,	702	54	19113	3.025166	1	0.909244	56.40431
brown	UP_SEQ_FEATURE	domain:VWFD 2	3	0.332226	0.049725	ENSG00000205592,	702	10	19113	8.167949	1	0.914644	58.24148
brown	UP_SEQ_FEATURE	domain:VWFD 1	3	0.332226	0.049725	ENSG00000205592,	702	10	19113	8.167949	1	0.914644	58.24148
brown	UP_SEQ_FEATURE	domain:VWFD 3	3	0.332226	0.049725	ENSG00000205592,	702	10	19113	8.167949	1	0.914644	58.24148
brown	UP_SEQ_FEATURE	repeat:14	7	0.775194	0.054047	ENSG00000168454,	702	74	19113	2.575479	1	0.926868	61.37678
brown	UP_SEQ_FEATURE	repeat:Xin 3	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 7	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 4	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 1	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 13	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 8	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 6	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 11	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	short sequence motif:Engrailed homology 1 repressor	2	0.221484	0.07201	ENSG00000128610,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 16	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 15	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 5	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 9	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	region of interest:3 X 5 AA repeats of C-C-X(3)	2	0.221484	0.07201	ENSG00000212900,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 2	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 17	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 12	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 10	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	repeat:Xin 14	2	0.221484	0.07201	ENSG00000163092,	702	2	19113	27.2265	1	0.967749	72.18445
brown	UP_SEQ_FEATURE	region of interest:Pore-forming 2	3	0.332226	0.080207	ENSG00000095981,	702	13	19113	6.283037	1	0.976543	76.10474
brown	UP_SEQ_FEATURE	region of interest:Pore-forming 1	3	0.332226	0.080207	ENSG00000095981,	702	13	19113	6.283037	1	0.976543	76.10474
brown	UP_SEQ_FEATURE	domain:Ig-like 2	4	0.442968	0.088752	ENSG00000211890,	702	29	19113	3.755379	1	0.983037	79.63389
brown	UP_SEQ_FEATURE	domain:Ig-like 1	4	0.442968	0.088752	ENSG00000211890,	702	29	19113	3.755379	1	0.983037	79.63389
grey	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR

grey	GOTERM_BP_FAT	GO:0006811~ion transport	22	5.729167	0.002027	ENSG00000101204,	187	768	13528	2.072304	0.906317	0.906317	3.215978
grey	GOTERM_BP_FAT	GO:0008015~blood circulation	9	2.34375	0.004201	ENSG00000101306,	187	186	13528	3.500431	0.992653	0.914284	6.558129
grey	GOTERM_BP_FAT	GO:0003013~circulatory system process	9	2.34375	0.004201	ENSG00000101306,	187	186	13528	3.500431	0.992653	0.914284	6.558129
grey	GOTERM_BP_FAT	GO:0019229~regulation of vasoconstriction	4	1.041667	0.011192	ENSG00000006638,	187	34	13528	8.510852	0.999998	0.987451	16.58332
grey	GOTERM_BP_FAT	GO:0008217~regulation of blood pressure	6	1.5625	0.012257	ENSG000000044012,	187	100	13528	4.340535	0.999999	0.972623	18.01935
grey	GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	11	2.864583	0.012613	ENSG00000105641,	187	318	13528	2.502405	1	0.948313	18.49381
grey	GOTERM_BP_FAT	GO:0007155~cell adhesion	18	4.6875	0.016307	ENSG00000148600,	187	700	13528	1.860229	1	0.959147	23.26976
grey	GOTERM_BP_FAT	GO:0022610~biological adhesion	18	4.6875	0.016514	ENSG00000148600,	187	701	13528	1.857576	1	0.937716	23.52955
grey	GOTERM_BP_FAT	GO:0051240~positive regulation of multicellular organism	9	2.34375	0.019417	ENSG00000006638,	187	244	13528	2.668362	1	0.942747	27.08621
grey	GOTERM_BP_FAT	GO:0006941~striated muscle contraction	4	1.041667	0.025194	ENSG00000101306,	187	46	13528	6.29063	1	0.963436	33.70751
grey	GOTERM_BP_FAT	GO:0010840~regulation of circadian sleep/wake cycle, wake	2	0.520833	0.02731	ENSG00000181408,	187	2	13528	72.34225	1	0.9605	35.9885
grey	GOTERM_BP_FAT	GO:0010841~positive regulation of circadian sleep/wake	2	0.520833	0.02731	ENSG00000181408,	187	2	13528	72.34225	1	0.9605	35.9885
grey	GOTERM_BP_FAT	GO:0060048~cardiac muscle contraction	3	0.78125	0.027579	ENSG00000101306,	187	19	13528	11.42246	1	0.948542	36.27263
grey	GOTERM_BP_FAT	GO:0042752~regulation of circadian rhythm	3	0.78125	0.033269	ENSG00000181408,	187	21	13528	10.33461	1	0.962764	42.02195
grey	GOTERM_BP_FAT	GO:0006814~sodium ion transport	6	1.5625	0.033667	ENSG00000105641,	187	130	13528	3.338873	1	0.953779	42.40525
grey	GOTERM_BP_FAT	GO:0007156~homophilic cell adhesion	6	1.5625	0.034628	ENSG00000148600,	187	131	13528	3.313385	1	0.947011	43.32105
grey	GOTERM_BP_FAT	GO:0016337~cell-cell adhesion	9	2.34375	0.03708	ENSG00000148600,	187	276	13528	2.358986	1	0.947119	45.59669
grey	GOTERM_BP_FAT	GO:0015698~inorganic anion transport	5	1.302083	0.039272	ENSG00000105641,	187	93	13528	3.889368	1	0.946183	47.55756
grey	GOTERM_BP_FAT	GO:0045776~negative regulation of blood pressure	3	0.78125	0.039373	ENSG000000044012,	187	23	13528	9.435945	1	0.936551	47.64666
grey	GOTERM_BP_FAT	GO:0060047~heart contraction	3	0.78125	0.039373	ENSG00000101306,	187	23	13528	9.435945	1	0.936551	47.64666
grey	GOTERM_BP_FAT	GO:0003015~heart process	3	0.78125	0.039373	ENSG00000101306,	187	23	13528	9.435945	1	0.936551	47.64666
grey	GOTERM_BP_FAT	GO:0051048~negative regulation of secretion	4	1.041667	0.039838	ENSG00000138798,	187	55	13528	5.261254	1	0.928329	48.05285
grey	GOTERM_BP_FAT	GO:0032971~regulation of muscle filament sliding	2	0.520833	0.040686	ENSG00000101306,	187	3	13528	48.22816	1	0.922016	48.78748
grey	GOTERM_BP_FAT	GO:0050873~brown fat cell differentiation	3	0.78125	0.042572	ENSG00000181856,	187	24	13528	9.042781	1	0.921017	50.38582
grey	GOTERM_BP_FAT	GO:0006493~protein amino acid O-linked glycosylation	3	0.78125	0.045865	ENSG00000118017,	187	25	13528	8.68107	1	0.926398	53.06436
grey	GOTERM_BP_FAT	GO:0043954~cellular component maintenance	3	0.78125	0.045865	ENSG00000148600,	187	25	13528	8.68107	1	0.926398	53.06436
grey	GOTERM_BP_FAT	GO:0060415~muscle tissue morphogenesis	3	0.78125	0.052718	ENSG00000101306,	187	27	13528	8.038027	1	0.943464	58.21072
grey	GOTERM_BP_FAT	GO:0055008~cardiac muscle tissue morphogenesis	3	0.78125	0.052718	ENSG00000101306,	187	27	13528	8.038027	1	0.943464	58.21072
grey	GOTERM_BP_FAT	GO:0007268~synaptic transmission	9	2.34375	0.053804	ENSG00000101204,	187	298	13528	2.184833	1	0.939563	58.97553
grey	GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	8	2.083333	0.055554	ENSG00000138798,	187	248	13528	2.333621	1	0.937913	60.18082
grey	GOTERM_BP_FAT	GO:0006936~muscle contraction	6	1.5625	0.060098	ENSG00000101306,	187	153	13528	2.836951	1	0.944602	63.1578
grey	GOTERM_BP_FAT	GO:0051046~regulation of secretion	7	1.822917	0.060401	ENSG00000138798,	187	202	13528	2.50691	1	0.938971	63.34867
grey	GOTERM_BP_FAT	GO:0009611~response to wounding	13	3.385417	0.062177	ENSG00000168542,	187	530	13528	1.774432	1	0.937625	64.44888
grey	GOTERM_BP_FAT	GO:0044057~regulation of system process	9	2.34375	0.063687	ENSG00000006638,	187	309	13528	2.107056	1	0.935601	65.35988
grey	GOTERM_BP_FAT	GO:0042753~positive regulation of circadian rhythm	2	0.520833	0.066891	ENSG00000181408,	187	5	13528	28.9369	1	0.938336	67.22136
grey	GOTERM_BP_FAT	GO:0007267~cell-cell signaling	14	3.645833	0.070586	ENSG00000101204,	187	600	13528	1.687986	1	0.942013	69.25112
grey	GOTERM_BP_FAT	GO:0006812~cation transport	13	3.385417	0.079664	ENSG00000101204,	187	553	13528	1.700631	1	0.95607	73.74819
grey	GOTERM_BP_FAT	GO:0042320~regulation of circadian sleep/wake cycle, RE	2	0.520833	0.079726	ENSG00000181408,	187	6	13528	24.11408	1	0.951682	73.7767
grey	GOTERM_BP_FAT	GO:0042989~sequestering of actin monomers	2	0.520833	0.079726	ENSG00000158427,	187	6	13528	24.11408	1	0.951682	73.7767
grey	GOTERM_BP_FAT	GO:0006954~inflammatory response	9	2.34375	0.079838	ENSG00000147571,	187	325	13528	2.003324	1	0.947263	73.82806
grey	GOTERM_BP_FAT	GO:0003012~muscle system process	6	1.5625	0.082269	ENSG00000101306,	187	168	13528	2.583652	1	0.947488	74.92021
grey	GOTERM_BP_FAT	GO:0030036~actin cytoskeleton organization	7	1.822917	0.091164	ENSG00000139132,	187	226	13528	2.240689	1	0.958715	78.56227
grey	GOTERM_BP_FAT	GO:0060537~muscle tissue development	5	1.302083	0.093739	ENSG00000101306,	187	125	13528	2.89369	1	0.958858	79.52028
grey	GOTERM_CC_FAT	GO:0005576~extracellular region	56	14.58333	4.29E-06	ENSG00000138798,	194	2010	12782	1.835647	8.19E-04	8.19E-04	0.005338
grey	GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	33	8.59375	8.81E-04	ENSG00000113721,	194	1188	12782	1.830183	0.154976	0.080748	1.090698
grey	GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	33	8.59375	0.00128	ENSG00000113721,	194	1215	12782	1.789513	0.217	0.078305	1.580553
grey	GOTERM_CC_FAT	GO:0034702~ion channel complex	10	2.604167	0.00396	ENSG00000101204,	194	205	12782	3.21398	0.531374	0.172617	4.816502
grey	GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	102	26.5625	0.004968	ENSG00000221932,	194	5485	12782	1.225238	0.613722	0.173239	6.006962

grey	GOTERM_CC_FAT	GO:0044459~plasma membrane part	48	12.5	0.007164	ENSG00000167434,	194	2203	12782	1.435568	0.746717	0.204572	8.555382
grey	GOTERM_CC_FAT	GO:0016021~integral to membrane	98	25.52083	0.007816	ENSG00000221932,	194	5297	12782	1.21897	0.776579	0.192732	9.29946
grey	GOTERM_CC_FAT	GO:0044456~synapse part	10	2.604167	0.012316	ENSG00000101204,	194	246	12782	2.678317	0.90624	0.256121	14.28642
grey	GOTERM_CC_FAT	GO:0045202~synapse	12	3.125	0.019027	ENSG00000101204,	194	355	12782	2.227153	0.974504	0.334816	21.25606
grey	GOTERM_CC_FAT	GO:0034706~sodium channel complex	3	0.78125	0.02093	ENSG00000007314,	194	15	12782	13.17732	0.982402	0.332355	23.13474
grey	GOTERM_CC_FAT	GO:0034703~cation channel complex	6	1.5625	0.049741	ENSG00000007314,	194	132	12782	2.994845	0.999941	0.587658	46.98877
grey	GOTERM_CC_FAT	GO:0030054~cell junction	14	3.645833	0.050475	ENSG00000101204,	194	518	12782	1.780719	0.999949	0.561494	47.49609
grey	GOTERM_CC_FAT	GO:0045211~postsynaptic membrane	6	1.5625	0.053818	ENSG00000101204,	194	135	12782	2.928293	0.999974	0.556377	49.74949
grey	GOTERM_CC_FAT	GO:0044421~extracellular region part	22	5.729167	0.054855	ENSG00000138798,	194	960	12782	1.509901	0.999979	0.536842	50.43042
grey	GOTERM_CC_FAT	GO:0030141~secretory granule	7	1.822917	0.055152	ENSG00000138798,	194	180	12782	2.562257	0.99998	0.514406	50.62408
grey	GOTERM_CC_FAT	GO:0030017~sarcomere	5	1.302083	0.060981	ENSG00000101306,	194	98	12782	3.361561	0.999994	0.528155	54.28231
grey	GOTERM_CC_FAT	GO:0005886~plasma membrane	68	17.70833	0.067648	ENSG00000138798,	194	3777	12782	1.186203	0.999998	0.54478	58.15995
grey	GOTERM_CC_FAT	GO:0030016~myofibril	5	1.302083	0.087298	ENSG00000101306,	194	111	12782	2.967865	1	0.620644	67.89915
grey	GOTERM_CC_FAT	GO:0044449~contractile fiber part	5	1.302083	0.091767	ENSG00000101306,	194	113	12782	2.915336	1	0.620009	69.80055
grey	GOTERM_CC_FAT	GO:0005615~extracellular space	16	4.166667	0.094943	ENSG00000138798,	194	685	12782	1.538957	1	0.614296	71.08843
grey	GOTERM_MF_FAT	GO:0005216~ion channel activity	15	3.90625	0.002296	ENSG00000101204,	198	386	12983	2.548084	0.60309	0.60309	3.157535
grey	GOTERM_MF_FAT	GO:0022836~gated channel activity	13	3.385417	0.002762	ENSG00000101204,	198	310	12983	2.749739	0.671037	0.426447	3.786847
grey	GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	15	3.90625	0.00303	ENSG00000101204,	198	398	12983	2.471258	0.704769	0.334133	4.147585
grey	GOTERM_MF_FAT	GO:0015276~ligand-gated ion channel activity	8	2.083333	0.003214	ENSG00000101204,	198	127	12983	4.130438	0.725876	0.27642	4.394146
grey	GOTERM_MF_FAT	GO:0022834~ligand-gated channel activity	8	2.083333	0.003214	ENSG00000101204,	198	127	12983	4.130438	0.725876	0.27642	4.394146
grey	GOTERM_MF_FAT	GO:0015267~channel activity	15	3.90625	0.004118	ENSG00000101204,	198	412	12983	2.387283	0.80961	0.282323	5.596533
grey	GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	15	3.90625	0.004206	ENSG00000101204,	198	413	12983	2.381503	0.81631	0.246041	5.713902
grey	GOTERM_MF_FAT	GO:0030414~peptidase inhibitor activity	8	2.083333	0.008784	ENSG00000164530,	198	153	12983	3.428534	0.971185	0.397515	11.58719
grey	GOTERM_MF_FAT	GO:0005261~cation channel activity	11	2.864583	0.009289	ENSG00000101204,	198	275	12983	2.622828	0.976517	0.374332	12.21314
grey	GOTERM_MF_FAT	GO:0005272~sodium channel activity	4	1.041667	0.01235	ENSG00000007314,	198	32	12983	8.196338	0.993232	0.425964	15.92454
grey	GOTERM_MF_FAT	GO:0004867~serine-type endopeptidase inhibitor activity	6	1.5625	0.012976	ENSG00000215018,	198	92	12983	4.27635	0.994754	0.408464	16.66494
grey	GOTERM_MF_FAT	GO:0005248~voltage-gated sodium channel activity	3	0.78125	0.021124	ENSG00000007314,	198	15	12983	13.11414	0.999813	0.54172	25.77123
grey	GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	9	2.34375	0.023089	ENSG00000105641,	198	228	12983	2.588317	0.999917	0.542767	27.82409
grey	GOTERM_MF_FAT	GO:0004866~endopeptidase inhibitor activity	7	1.822917	0.023179	ENSG00000215018,	198	145	12983	3.165482	0.99992	0.51578	27.9169
grey	GOTERM_MF_FAT	GO:0046873~metal ion transmembrane transporter activ	11	2.864583	0.028136	ENSG00000101204,	198	328	12983	2.199018	0.99999	0.559348	32.85825
grey	GOTERM_MF_FAT	GO:0031404~chloride ion binding	5	1.302083	0.029494	ENSG00000141540,	198	77	12983	4.257838	0.999994	0.551716	34.15551
grey	GOTERM_MF_FAT	GO:0015111~iodide transmembrane transporter activity	2	0.520833	0.030118	ENSG00000105641,	198	2	12983	65.57071	0.999995	0.536223	34.74434
grey	GOTERM_MF_FAT	GO:0031402~sodium ion binding	6	1.5625	0.032767	ENSG00000105641,	198	117	12983	3.3626	0.999998	0.545164	37.18814
grey	GOTERM_MF_FAT	GO:0005328~neurotransmitter:sodium symporter activity	3	0.78125	0.036383	ENSG00000111181,	198	20	12983	9.835606	1	0.562948	40.38777
grey	GOTERM_MF_FAT	GO:0015370~solute:sodium symporter activity	4	1.041667	0.044202	ENSG00000111181,	198	52	12983	5.043901	1	0.615776	46.79604
grey	GOTERM_MF_FAT	GO:0005326~neurotransmitter transporter activity	3	0.78125	0.050815	ENSG00000111181,	198	24	12983	8.196338	1	0.649448	51.70975
grey	GOTERM_MF_FAT	GO:0043168~anion binding	5	1.302083	0.051257	ENSG00000141540,	198	92	12983	3.563625	1	0.634779	52.02298
grey	GOTERM_MF_FAT	GO:0004857~enzyme inhibitor activity	9	2.34375	0.054218	ENSG00000164530,	198	270	12983	2.18569	1	0.638891	54.0708
grey	GOTERM_MF_FAT	GO:0008144~drug binding	4	1.041667	0.055435	ENSG00000068976,	198	57	12983	4.601453	1	0.630944	54.88942
grey	GOTERM_MF_FAT	GO:0030594~neurotransmitter receptor activity	5	1.302083	0.056432	ENSG00000101204,	198	95	12983	3.45109	1	0.622038	55.54947
grey	GOTERM_MF_FAT	GO:0042165~neurotransmitter binding	5	1.302083	0.071548	ENSG00000101204,	198	103	12983	3.183044	1	0.696909	64.52018
grey	GOTERM_MF_FAT	GO:0022843~voltage-gated cation channel activity	6	1.5625	0.07322	ENSG00000007314,	198	147	12983	2.676355	1	0.691391	65.40171
grey	GOTERM_MF_FAT	GO:0005230~extracellular ligand-gated ion channel activ	4	1.041667	0.096168	ENSG00000101204,	198	72	12983	3.642817	1	0.778082	75.61838
grey	INTERPRO	IPR003599:Immunoglobulin subtype	14	3.645833	0.002263	ENSG00000132185,	263	330	16659	2.687245	0.653698	0.653698	3.180957
grey	INTERPRO	IPR007110:Immunoglobulin-like	17	4.427083	0.005863	ENSG00000132185,	263	501	16659	2.149336	0.936202	0.747417	8.046988
grey	INTERPRO	IPR008160:Collagen triple helix repeat	6	1.5625	0.010434	ENSG00000168542,	263	84	16659	4.524443	0.992617	0.80528	13.89756
grey	INTERPRO	IPR001073:Complement C1q protein	4	1.041667	0.013626	ENSG00000102924,	263	32	16659	7.917776	0.998372	0.799146	17.7764
grey	INTERPRO	IPR013783:Immunoglobulin-like fold	17	4.427083	0.014322	ENSG00000132185,	263	553	16659	1.947229	0.998831	0.740825	18.60076

grey	INTERPRO	IPR013098:Immunoglobulin I-set	7	1.822917	0.021983	ENSG00000080854	263	138	16659	3.21301	0.99997	0.823384	27.17517
grey	INTERPRO	IPR001909:Krueppel-associated box	12	3.125	0.025413	ENSG00000186300	263	355	16659	2.141145	0.999994	0.821111	30.73537
grey	INTERPRO	IPR008983:Tumour necrosis factor-like	4	1.041667	0.033608	ENSG00000102924	263	45	16659	5.630418	1	0.864646	38.59685
grey	INTERPRO	IPR002350:Proteinase inhibitor I1, Kazal	4	1.041667	0.035547	ENSG00000152583	263	46	16659	5.508018	1	0.847732	40.33153
grey	INTERPRO	IPR000175:Sodium:neurotransmitter symporter	3	0.78125	0.038864	ENSG00000111181	263	20	16659	9.501331	1	0.843567	43.19321
grey	INTERPRO	IPR013151:Immunoglobulin	8	2.083333	0.041295	ENSG00000132185	263	202	16659	2.508602	1	0.833742	45.20881
grey	INTERPRO	IPR003598:Immunoglobulin subtype 2	8	2.083333	0.043687	ENSG00000221932	263	205	16659	2.471891	1	0.824855	47.12753
grey	INTERPRO	IPR002172:Low density lipoprotein-receptor, class A, cyst	4	1.041667	0.043866	ENSG00000203985	263	50	16659	5.067376	1	0.801083	47.26844
grey	INTERPRO	IPR006643:ZASP	2	0.520833	0.046446	ENSG00000154553	263	3	16659	42.22814	1	0.796043	49.26255
grey	INTERPRO	IPR002345:Lipocalin	3	0.78125	0.058317	ENSG00000122133	263	25	16659	7.601065	1	0.846598	57.56597
grey	INTERPRO	IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding	16	4.166667	0.066528	ENSG00000197013	263	621	16659	1.632005	1	0.866504	62.54981
grey	INTERPRO	IPR016323:Thymosin beta-4, chordata	2	0.520833	0.07621	ENSG00000158427	263	5	16659	25.33688	1	0.887215	67.72611
grey	INTERPRO	IPR001152:Thymosin beta-4	2	0.520833	0.07621	ENSG00000158427	263	5	16659	25.33688	1	0.887215	67.72611
grey	INTERPRO	IPR000566:Lipocalin-related protein and Bos/Can/Equ alle	3	0.78125	0.089834	ENSG00000122133	263	32	16659	5.938332	1	0.913475	73.89051
grey	INTERPRO	IPR002126:Cadherin	5	1.302083	0.090786	ENSG00000148600	263	108	16659	2.99251	1	0.904086	74.27748
grey	INTERPRO	IPR012674:Calycin	3	0.78125	0.094673	ENSG00000122133	263	33	16659	5.758382	1	0.902446	75.80283
grey	INTERPRO	IPR013106:Immunoglobulin V-set	8	2.083333	0.098878	ENSG00000158887	263	249	16659	2.035091	1	0.901754	77.35776
grey	KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	9	2.34375	0.009089	ENSG00000138798	59	262	5085	2.960603	0.535597	0.535597	9.336065
grey	KEGG_PATHWAY	hsa04020:Calcium signaling pathway	7	1.822917	0.014379	ENSG00000006638	59	176	5085	3.42787	0.703776	0.455736	14.39847
grey	KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	7	1.822917	0.069794	ENSG00000006638	59	256	5085	2.35666	0.997706	0.868107	54.00242
grey	KEGG_PATHWAY	hsa00500:Starch and sucrose metabolism	3	0.78125	0.082368	ENSG00000068976	59	42	5085	6.156174	0.999269	0.835548	60.25433
grey	PIR_SUPERFAMILY	PIRSF005559:zinc finger protein ZFP-36	8	2.083333	0.006143	ENSG00000186300	119	137	7396	3.629271	0.539946	0.539946	6.887331
grey	PIR_SUPERFAMILY	PIRSF002444:gamma-aminobutyric acid transporter	3	0.78125	0.029361	ENSG00000111181	119	17	7396	10.96787	0.976597	0.847021	29.18602
grey	PIR_SUPERFAMILY	PIRSF500452:beta crystallin B	2	0.520833	0.04711	ENSG00000100053	119	3	7396	41.43417	0.997712	0.868238	42.81271
grey	PIR_SUPERFAMILY	PIRSF001828:Thymosin_beta	2	0.520833	0.077288	ENSG00000158427	119	5	7396	24.8605	0.99996	0.920643	60.60474
grey	PIR_SUPERFAMILY	PIRSF001630:serpin	3	0.78125	0.096803	ENSG00000197249	119	33	7396	5.650115	0.999997	0.923136	69.24373
grey	SMART	SM00409:IG	14	3.645833	0.005195	ENSG00000132185	160	330	9079	2.407311	0.450622	0.450622	5.760248
grey	SMART	SM00110:C1Q	4	1.041667	0.018027	ENSG00000102924	160	32	9079	7.092969	0.876557	0.648655	18.71519
grey	SMART	SM00280:KAZAL	4	1.041667	0.046256	ENSG00000152583	160	46	9079	4.934239	0.995688	0.837235	41.69388
grey	SMART	SM00349:KRAB	12	3.125	0.047168	ENSG00000186300	160	355	9079	1.918099	0.996137	0.750699	42.32592
grey	SMART	SM00735:ZM	2	0.520833	0.05163	ENSG00000154553	160	3	9079	37.82917	0.997749	0.704544	45.3286
grey	SMART	SM00192:LDLa	4	1.041667	0.056815	ENSG00000203985	160	50	9079	4.5395	0.998801	0.674082	48.6384
grey	SMART	SM00408:IGc2	8	2.083333	0.068467	ENSG00000221932	160	205	9079	2.21439	0.999713	0.688133	55.41983
grey	SMART	SM00152:THY	2	0.520833	0.084569	ENSG00000158427	160	5	9079	22.6975	0.999961	0.719218	63.4502
grey	SP_PIR_KEYWORDS	signal	89	23.17708	4.39E-08	ENSG00000122133	300	3250	19235	1.75581	1.34E-05	1.34E-05	5.88E-05
grey	SP_PIR_KEYWORDS	disulfide bond	76	19.79167	5.08E-06	ENSG00000122133	300	2924	19235	1.666507	0.001554	7.77E-04	0.006812
grey	SP_PIR_KEYWORDS	glycoprotein	100	26.04167	1.33E-05	ENSG00000122133	300	4318	19235	1.48487	0.004066	0.001357	0.017844
grey	SP_PIR_KEYWORDS	Secreted	47	12.23958	1.28E-04	ENSG00000173467	300	1689	19235	1.784182	0.038496	0.009766	0.171805
grey	SP_PIR_KEYWORDS	Immunoglobulin domain	17	4.427083	0.002924	ENSG00000132185	300	470	19235	2.319113	0.591848	0.164081	3.849117
grey	SP_PIR_KEYWORDS	ionic channel	13	3.385417	0.004289	ENSG00000101204	300	318	19235	2.621122	0.731595	0.196847	5.598268
grey	SP_PIR_KEYWORDS	cell adhesion	15	3.90625	0.006591	ENSG00000148600	300	422	19235	2.279028	0.867806	0.251039	8.481791
grey	SP_PIR_KEYWORDS	ion transport	18	4.6875	0.009278	ENSG00000101204	300	578	19235	1.996713	0.942288	0.299903	11.74462
grey	SP_PIR_KEYWORDS	sodium channel	4	1.041667	0.010077	ENSG00000007314	300	29	19235	8.843678	0.95492	0.291332	12.69441
grey	SP_PIR_KEYWORDS	collagen	6	1.5625	0.016342	ENSG00000168542	300	95	19235	4.049474	0.99354	0.396015	19.81645
grey	SP_PIR_KEYWORDS	transmembrane	95	24.73958	0.016898	ENSG00000138798	300	4973	19235	1.224831	0.994566	0.37755	20.42161
grey	SP_PIR_KEYWORDS	neurotransmitter transport	4	1.041667	0.019569	ENSG00000111181	300	37	19235	6.931532	0.997637	0.395872	23.27155
grey	SP_PIR_KEYWORDS	cell junction	13	3.385417	0.02292	ENSG00000101204	300	399	19235	2.089014	0.999171	0.42061	26.71251
grey	SP_PIR_KEYWORDS	protease inhibitor	6	1.5625	0.025852	ENSG00000164530	300	107	19235	3.595327	0.999669	0.435877	29.60593

grey	SP_PIR_KEYWORDS	chloride	5	1.302083	0.029412	ENSG00000141540,	300	75	19235	4.274444	0.999892	0.456112	32.97723
grey	SP_PIR_KEYWORDS	Sodium	6	1.5625	0.034916	ENSG00000105641,	300	116	19235	3.316379	0.999981	0.493237	37.89618
grey	SP_PIR_KEYWORDS	Sodium transport	6	1.5625	0.034916	ENSG00000105641,	300	116	19235	3.316379	0.999981	0.493237	37.89618
grey	SP_PIR_KEYWORDS	Serine protease inhibitor	5	1.302083	0.036067	ENSG00000215018,	300	80	19235	4.007292	0.999987	0.483773	38.88158
grey	SP_PIR_KEYWORDS	Cardiomyopathy	4	1.041667	0.038489	ENSG00000101306,	300	48	19235	5.343056	0.999994	0.486873	40.90758
grey	SP_PIR_KEYWORDS	synapse	8	2.083333	0.049308	ENSG00000101204,	300	213	19235	2.408138	1	0.557078	49.22366
grey	SP_PIR_KEYWORDS	glycosyltransferase	8	2.083333	0.050598	ENSG00000068976,	300	214	19235	2.396885	1	0.548161	50.1399
grey	SP_PIR_KEYWORDS	Signal-anchor	12	3.125	0.065267	ENSG00000153976,	300	421	19235	1.827553	1	0.625996	59.53173
grey	SP_PIR_KEYWORDS	transmembrane protein	16	4.166667	0.077346	ENSG00000138798,	300	642	19235	1.597923	1	0.673621	66.00596
grey	SP_PIR_KEYWORDS	disease mutation	33	8.59375	0.080286	ENSG00000138798,	300	1591	19235	1.329887	1	0.671586	67.42965
grey	SP_PIR_KEYWORDS	transport	34	8.854167	0.092125	ENSG00000187848,	300	1670	19235	1.305369	1	0.708371	72.62173
grey	SP_PIR_KEYWORDS	postsynaptic cell membrane	5	1.302083	0.092585	ENSG00000101204,	300	110	19235	2.914394	1	0.695528	72.80678
grey	SP_PIR_KEYWORDS	Symport	5	1.302083	0.094937	ENSG00000111181,	300	111	19235	2.888138	1	0.690867	73.73646
grey	UP_SEQ_FEATURE	signal peptide	89	23.17708	5.90E-08	ENSG00000122133,	300	3250	19113	1.744674	5.38E-05	5.38E-05	9.22E-05
grey	UP_SEQ_FEATURE	disulfide bond	75	19.53125	3.25E-06	ENSG00000122133,	300	2819	19113	1.695016	0.002962	0.001482	0.005078
grey	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	95	24.73958	4.30E-05	ENSG00000122133,	300	4129	19113	1.465839	0.038451	0.012985	0.067108
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1; degenerate	10	2.604167	1.29E-04	ENSG00000186300,	300	122	19113	5.222131	0.111399	0.029095	0.202005
grey	UP_SEQ_FEATURE	topological domain:Extracellular	67	17.44792	1.48E-04	ENSG00000138798,	300	2719	19113	1.569904	0.125978	0.02657	0.230265
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	13	3.385417	6.46E-04	ENSG00000186300,	300	252	19113	3.286627	0.445436	0.093589	1.004318
grey	UP_SEQ_FEATURE	topological domain:Cytoplasmic	74	19.27083	0.001836	ENSG00000138798,	300	3374	19113	1.397315	0.812922	0.212948	2.82905
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	13	3.385417	0.002323	ENSG00000186300,	300	293	19113	2.826724	0.880079	0.232883	3.566052
grey	UP_SEQ_FEATURE	domain:Kazal-like	5	1.302083	0.003444	ENSG00000152583,	300	40	19113	7.96375	0.956989	0.295022	5.244189
grey	UP_SEQ_FEATURE	domain:KRAB	13	3.385417	0.006312	ENSG00000152454,	300	332	19113	2.494669	0.996894	0.438667	9.413268
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	14	3.645833	0.006616	ENSG00000186300,	300	376	19113	2.372181	0.997651	0.42324	9.845276
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 14	8	2.083333	0.011916	ENSG00000152454,	300	157	19113	3.246369	0.999982	0.5979	17.07021
grey	UP_SEQ_FEATURE	domain:C1q	4	1.041667	0.012326	ENSG00000102924,	300	31	19113	8.220645	0.999988	0.581094	17.60622
grey	UP_SEQ_FEATURE	transmembrane region	95	24.73958	0.014351	ENSG00000138798,	300	4911	19113	1.232427	0.999998	0.610004	20.20406
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	12	3.125	0.016465	ENSG00000152454,	300	334	19113	2.288982	1	0.635567	22.83536
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 15	7	1.822917	0.018943	ENSG00000152454,	300	134	19113	3.328134	1	0.663821	25.81567
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	14	3.645833	0.025931	ENSG00000197013,	300	451	19113	1.977694	1	0.755726	33.6502
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	13	3.385417	0.031869	ENSG00000197013,	300	417	19113	1.986163	1	0.806211	39.69223
grey	UP_SEQ_FEATURE	site:Reactive bond	4	1.041667	0.033186	ENSG00000178172,	300	45	19113	5.663111	1	0.802096	40.96086
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	8	2.083333	0.039169	ENSG00000152454,	300	201	19113	2.535721	1	0.838306	46.41489
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	14	3.645833	0.044254	ENSG00000197013,	300	488	19113	1.827746	1	0.859941	50.67489
grey	UP_SEQ_FEATURE	region of interest:C-terminal arm	2	0.520833	0.046203	ENSG00000100053,	300	3	19113	42.47333	1	0.859283	52.223
grey	UP_SEQ_FEATURE	domain:Fibronectin type-III	4	1.041667	0.064966	ENSG00000177363,	300	59	19113	4.319322	1	0.930299	64.96572
grey	UP_SEQ_FEATURE	domain:LDL-receptor class A 1	3	0.78125	0.066259	ENSG00000203985,	300	27	19113	7.078889	1	0.926108	65.71462
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8; degenerate	2	0.520833	0.075817	ENSG00000198039,	300	5	19113	25.484	1	0.943656	70.80311
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 16	5	1.302083	0.078326	ENSG00000105750,	300	103	19113	3.092718	1	0.942789	72.01647
grey	UP_SEQ_FEATURE	domain:Ig-like C2-type	5	1.302083	0.078326	ENSG00000221932,	300	103	19113	3.092718	1	0.942789	72.01647
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	14	3.645833	0.080231	ENSG00000197013,	300	538	19113	1.657881	1	0.940687	72.9058
grey	UP_SEQ_FEATURE	domain:Cadherin 1	5	1.302083	0.082721	ENSG00000148600,	300	105	19113	3.03381	1	0.939935	74.02875
grey	UP_SEQ_FEATURE	domain:Cadherin 2	5	1.302083	0.082721	ENSG00000148600,	300	105	19113	3.03381	1	0.939935	74.02875
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 18	4	1.041667	0.084595	ENSG00000197013,	300	66	19113	3.861212	1	0.937941	74.84505
grey	UP_SEQ_FEATURE	domain:MAGE	3	0.78125	0.089045	ENSG00000221867,	300	32	19113	5.972813	1	0.94129	76.68793
grey	UP_SEQ_FEATURE	domain:Collagen-like 6	2	0.520833	0.090279	ENSG00000171502,	300	6	19113	21.23667	1	0.938183	77.17625
grey	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	15	3.90625	0.097902	ENSG00000197013,	300	608	19113	1.571793	1	0.946944	79.98643
tur	BIOCARTA	h_stemPathway:Regulation of hematopoiesis by cytokines	3	0.415512	0.07475	ENSG00000153563,	45	15	1437	6.386667	0.999713	0.999713	58.11504

tur	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
tur	COG_ONTOLOGY	DNA replication, recombination, and repair	5	0.692521	0.092437	ENSG000000091128,	48	72	1950	2.821181	0.7166	0.7166	47.38388
tur	GOTERM_BP_FAT	GO:0051047~positive regulation of secretion	12	1.66205	2.11E-04	ENSG00000118702,	375	109	13528	3.971523	0.368345	0.368345	0.366492
tur	GOTERM_BP_FAT	GO:0006936~muscle contraction	14	1.939058	3.26E-04	ENSG00000165887,	375	153	13528	3.30095	0.507424	0.298163	0.564327
tur	GOTERM_BP_FAT	GO:0003012~muscle system process	14	1.939058	7.96E-04	ENSG00000165887,	375	168	13528	3.006222	0.822616	0.438127	1.372673
tur	GOTERM_BP_FAT	GO:0044057~regulation of system process	20	2.770083	9.91E-04	ENSG00000111245,	375	309	13528	2.33493	0.883891	0.416263	1.706152
tur	GOTERM_BP_FAT	GO:0048609~reproductive process in a multicellular orga	27	3.739612	0.001057	ENSG00000198021,	375	487	13528	2.000033	0.899396	0.368282	1.81869
tur	GOTERM_BP_FAT	GO:0032504~multicellular organism reproduction	27	3.739612	0.001057	ENSG00000198021,	375	487	13528	2.000033	0.899396	0.368282	1.81869
tur	GOTERM_BP_FAT	GO:0008016~regulation of heart contraction	9	1.246537	0.001263	ENSG00000105866,	375	77	13528	4.216519	0.935718	0.367081	2.16953
tur	GOTERM_BP_FAT	GO:0051050~positive regulation of transport	16	2.216066	0.001376	ENSG00000160716,	375	223	13528	2.588317	0.949723	0.347648	2.361465
tur	GOTERM_BP_FAT	GO:0030855~epithelial cell differentiation	12	1.66205	0.001469	ENSG00000163216,	375	137	13528	3.159825	0.958981	0.329153	2.520147
tur	GOTERM_BP_FAT	GO:0050871~positive regulation of B cell activation	6	0.831025	0.001972	ENSG00000159958,	375	33	13528	6.55903	0.986261	0.378982	3.368604
tur	GOTERM_BP_FAT	GO:0001820~serotonin secretion	3	0.415512	0.002245	ENSG00000108405,	375	3	13528	36.07467	0.992416	0.386256	3.826426
tur	GOTERM_BP_FAT	GO:0008284~positive regulation of cell proliferation	23	3.185596	0.002655	ENSG00000105894,	375	414	13528	2.004148	0.996897	0.408465	4.510832
tur	GOTERM_BP_FAT	GO:0050864~regulation of B cell activation	7	0.969529	0.002703	ENSG00000159958,	375	51	13528	4.951425	0.997201	0.387303	4.58959
tur	GOTERM_BP_FAT	GO:0006928~cell motion	25	3.462604	0.00331	ENSG00000146013,	375	475	13528	1.898667	0.999255	0.425367	5.993618
tur	GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	16	2.216066	0.003835	ENSG00000112559,	375	248	13528	2.327398	0.999763	0.449042	6.452118
tur	GOTERM_BP_FAT	GO:0051046~regulation of secretion	14	1.939058	0.0041	ENSG00000118702,	375	202	13528	2.500224	0.999867	0.448421	6.88415
tur	GOTERM_BP_FAT	GO:0060429~epithelium development	15	2.077562	0.00431	ENSG00000182175,	375	227	13528	2.383789	0.999916	0.443678	7.224349
tur	GOTERM_BP_FAT	GO:0045423~regulation of granulocyte macrophage colo	3	0.415512	0.004408	ENSG00000112116,	375	4	13528	27.056	0.999932	0.431317	7.382012
tur	GOTERM_BP_FAT	GO:0006837~serotonin transport	3	0.415512	0.004408	ENSG00000108405,	375	4	13528	27.056	0.999932	0.431317	7.382012
tur	GOTERM_BP_FAT	GO:0032645~regulation of granulocyte macrophage colo	3	0.415512	0.004408	ENSG00000112116,	375	4	13528	27.056	0.999932	0.431317	7.382012
tur	GOTERM_BP_FAT	GO:0008015~blood circulation	13	1.800554	0.005606	ENSG00000111245,	375	186	13528	2.521348	0.999995	0.492523	9.29694
tur	GOTERM_BP_FAT	GO:0003013~circulatory system process	13	1.800554	0.005606	ENSG00000111245,	375	186	13528	2.521348	0.999995	0.492523	9.29694
tur	GOTERM_BP_FAT	GO:0007610~behavior	24	3.3241	0.005778	ENSG00000105894,	375	469	13528	1.846038	0.999997	0.484416	9.569961
tur	GOTERM_BP_FAT	GO:0002694~regulation of leukocyte activation	12	1.66205	0.006452	ENSG00000159958,	375	166	13528	2.607807	0.999999	0.504862	10.62738
tur	GOTERM_BP_FAT	GO:0007276~gamete generation	21	2.908587	0.006806	ENSG00000198021,	375	395	13528	1.917894	1	0.506533	11.17844
tur	GOTERM_BP_FAT	GO:0007409~axonogenesis	13	1.800554	0.007466	ENSG00000146013,	375	193	13528	2.4299	1	0.522839	12.19871
tur	GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiati	15	2.077562	0.00804	ENSG00000146013,	375	244	13528	2.217705	1	0.533406	13.07494
tur	GOTERM_BP_FAT	GO:0051249~regulation of lymphocyte activation	11	1.523546	0.008064	ENSG00000159958,	375	148	13528	2.681225	1	0.519423	13.11217
tur	GOTERM_BP_FAT	GO:0032103~positive regulation of response to external	7	0.969529	0.008344	ENSG00000170989,	375	64	13528	3.945667	1	0.517128	13.53727
tur	GOTERM_BP_FAT	GO:0003001~generation of a signal involved in cell-cell s	8	1.108033	0.009087	ENSG00000164082,	375	85	13528	3.395263	1	0.533543	14.65444
tur	GOTERM_BP_FAT	GO:0050865~regulation of cell activation	12	1.66205	0.009438	ENSG00000159958,	375	175	13528	2.473691	1	0.533671	15.17803
tur	GOTERM_BP_FAT	GO:0021954~central nervous system neuron developmer	5	0.692521	0.011216	ENSG00000149295,	375	32	13528	5.636667	1	0.583105	17.78139
tur	GOTERM_BP_FAT	GO:0001934~positive regulation of protein amino acid p	8	1.108033	0.011558	ENSG00000118971,	375	89	13528	3.242667	1	0.581335	18.27406
tur	GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	13	1.800554	0.011741	ENSG00000018625,	375	205	13528	2.287662	1	0.574744	18.53626
tur	GOTERM_BP_FAT	GO:0048232~male gamete generation	17	2.354571	0.011872	ENSG00000198021,	375	308	13528	1.991134	1	0.566904	18.72404
tur	GOTERM_BP_FAT	GO:0007283~spermatogenesis	17	2.354571	0.011872	ENSG00000198021,	375	308	13528	1.991134	1	0.566904	18.72404
tur	GOTERM_BP_FAT	GO:0031175~neuron projection development	15	2.077562	0.011939	ENSG00000146013,	375	256	13528	2.11375	1	0.557463	18.8193
tur	GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron diff	13	1.800554	0.013508	ENSG00000146013,	375	209	13528	2.243879	1	0.591442	21.0281
tur	GOTERM_BP_FAT	GO:0048584~positive regulation of response to stimulus	14	1.939058	0.014222	ENSG00000159958,	375	236	13528	2.140023	1	0.599514	22.01507
tur	GOTERM_BP_FAT	GO:0015858~nucleoside transport	3	0.415512	0.0146	ENSG00000197506,	375	7	13528	15.46057	1	0.598578	22.53277
tur	GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	13	1.800554	0.015497	ENSG00000146013,	375	213	13528	2.20174	1	0.610265	23.74678
tur	GOTERM_BP_FAT	GO:0015672~monovalent inorganic cation transport	17	2.354571	0.015684	ENSG00000136531,	375	318	13528	1.92852	1	0.604641	23.99757
tur	GOTERM_BP_FAT	GO:0046887~positive regulation of hormone secretion	5	0.692521	0.016857	ENSG00000118702,	375	36	13528	5.01037	1	0.621576	25.55551
tur	GOTERM_BP_FAT	GO:0045761~regulation of adenylate cyclase activity	8	1.108033	0.016996	ENSG00000150594,	375	96	13528	3.006222	1	0.615068	25.7378
tur	GOTERM_BP_FAT	GO:0007194~negative regulation of adenylate cyclase ac	6	0.831025	0.017658	ENSG00000150594,	375	55	13528	3.935418	1	0.619922	26.60062
tur	GOTERM_BP_FAT	GO:0051350~negative regulation of lyase activity	6	0.831025	0.017658	ENSG00000150594,	375	55	13528	3.935418	1	0.619922	26.60062

tur	GOTERM_BP_FAT	GO:0031280~negative regulation of cyclase activity	6	0.831025	0.017658	ENSG00000150594,	375	55	13528	3.935418	1	0.619922	26.60062
tur	GOTERM_BP_FAT	GO:0042327~positive regulation of phosphorylation	8	1.108033	0.017899	ENSG00000118971,	375	97	13528	2.97523	1	0.615874	26.91268
tur	GOTERM_BP_FAT	GO:0031279~regulation of cyclase activity	8	1.108033	0.019804	ENSG00000150594,	375	99	13528	2.915125	1	0.644576	29.33565
tur	GOTERM_BP_FAT	GO:0009968~negative regulation of signal transduction	13	1.800554	0.020102	ENSG00000150681,	375	221	13528	2.122039	1	0.641472	29.70774
tur	GOTERM_BP_FAT	GO:0044093~positive regulation of molecular function	26	3.601108	0.020741	ENSG00000112559,	375	586	13528	1.600582	1	0.644643	30.49908
tur	GOTERM_BP_FAT	GO:0010562~positive regulation of phosphorus metabolism	8	1.108033	0.020808	ENSG00000118971,	375	100	13528	2.885973	1	0.637578	30.58165
tur	GOTERM_BP_FAT	GO:0045937~positive regulation of phosphate metabolism	8	1.108033	0.020808	ENSG00000118971,	375	100	13528	2.885973	1	0.637578	30.58165
tur	GOTERM_BP_FAT	GO:0007281~germ cell development	8	1.108033	0.021847	ENSG00000143768,	375	101	13528	2.857399	1	0.647606	31.84913
tur	GOTERM_BP_FAT	GO:0030817~regulation of cAMP biosynthetic process	8	1.108033	0.021847	ENSG00000150594,	375	101	13528	2.857399	1	0.647606	31.84913
tur	GOTERM_BP_FAT	GO:0051339~regulation of lyase activity	8	1.108033	0.021847	ENSG00000150594,	375	101	13528	2.857399	1	0.647606	31.84913
tur	GOTERM_BP_FAT	GO:0006811~ion transport	32	4.432133	0.021962	ENSG00000113946,	375	768	13528	1.503111	1	0.641654	31.98835
tur	GOTERM_BP_FAT	GO:0001932~regulation of protein amino acid phosphorylation	11	1.523546	0.022081	ENSG00000112559,	375	173	13528	2.293765	1	0.635916	32.13151
tur	GOTERM_BP_FAT	GO:0021953~central nervous system neuron differentiation	5	0.692521	0.024006	ENSG00000149295,	375	40	13528	4.509333	1	0.659418	34.41386
tur	GOTERM_BP_FAT	GO:0030814~regulation of cAMP metabolic process	8	1.108033	0.024032	ENSG00000150594,	375	103	13528	2.801916	1	0.652397	34.44359
tur	GOTERM_BP_FAT	GO:0048666~neuron development	17	2.354571	0.026652	ENSG00000146013,	375	339	13528	1.809054	1	0.683509	37.43245
tur	GOTERM_BP_FAT	GO:0007267~cell-cell signaling	26	3.601108	0.027283	ENSG00000164082,	375	600	13528	1.563236	1	0.685077	38.13298
tur	GOTERM_BP_FAT	GO:0009628~response to abiotic stimulus	18	2.493075	0.027353	ENSG00000064300,	375	368	13528	1.764522	1	0.679076	38.20956
tur	GOTERM_BP_FAT	GO:0002696~positive regulation of leukocyte activation	8	1.108033	0.027583	ENSG00000159958,	375	106	13528	2.722616	1	0.675365	38.46365
tur	GOTERM_BP_FAT	GO:0032989~cellular component morphogenesis	19	2.631579	0.027777	ENSG00000146013,	375	397	13528	1.726495	1	0.671116	38.66851
tur	GOTERM_BP_FAT	GO:0007411~axon guidance	8	1.108033	0.028842	ENSG00000064300,	375	107	13528	2.697171	1	0.678616	39.83206
tur	GOTERM_BP_FAT	GO:0019953~sexual reproduction	21	2.908587	0.029557	ENSG00000198021,	375	458	13528	1.654079	1	0.681219	40.59587
tur	GOTERM_BP_FAT	GO:0032225~regulation of synaptic transmission, dopamine	3	0.415512	0.029622	ENSG00000149295,	375	10	13528	10.8224	1	0.675665	40.66304
tur	GOTERM_BP_FAT	GO:0007188~G-protein signaling, coupled to cAMP nucleotide	7	0.969529	0.030183	ENSG00000124089,	375	85	13528	2.970855	1	0.676401	41.25752
tur	GOTERM_BP_FAT	GO:0031424~keratinization	5	0.692521	0.030407	ENSG00000163216,	375	43	13528	4.194729	1	0.673012	41.49325
tur	GOTERM_BP_FAT	GO:0003006~reproductive developmental process	14	1.939058	0.030531	ENSG00000118971,	375	262	13528	1.927654	1	0.668469	41.62223
tur	GOTERM_BP_FAT	GO:0030534~adult behavior	7	0.969529	0.031722	ENSG00000164082,	375	86	13528	2.93631	1	0.676737	42.85471
tur	GOTERM_BP_FAT	GO:0043085~positive regulation of catalytic activity	23	3.185596	0.031755	ENSG00000112559,	375	520	13528	1.59561	1	0.671223	42.8838
tur	GOTERM_BP_FAT	GO:0030802~regulation of cyclic nucleotide biosynthetic process	8	1.108033	0.032851	ENSG00000150594,	375	110	13528	2.623612	1	0.678127	44.00052
tur	GOTERM_BP_FAT	GO:0030808~regulation of nucleotide biosynthetic process	8	1.108033	0.032851	ENSG00000150594,	375	110	13528	2.623612	1	0.678127	44.00052
tur	GOTERM_BP_FAT	GO:0006813~potassium ion transport	10	1.385042	0.033753	ENSG00000162687,	375	160	13528	2.254667	1	0.682526	44.9009
tur	GOTERM_BP_FAT	GO:0030001~metal ion transport	21	2.908587	0.034071	ENSG00000136531,	375	465	13528	1.629178	1	0.680431	45.21407
tur	GOTERM_BP_FAT	GO:0050867~positive regulation of cell activation	8	1.108033	0.034266	ENSG00000159958,	375	111	13528	2.599976	1	0.677062	45.40559
tur	GOTERM_BP_FAT	GO:0014059~regulation of dopamine secretion	3	0.415512	0.035551	ENSG00000149295,	375	11	13528	9.838545	1	0.685324	46.65321
tur	GOTERM_BP_FAT	GO:0030216~keratinocyte differentiation	6	0.831025	0.035569	ENSG00000163216,	375	66	13528	3.279515	1	0.680198	46.67084
tur	GOTERM_BP_FAT	GO:0042471~ear morphogenesis	6	0.831025	0.035569	ENSG00000121742,	375	66	13528	3.279515	1	0.680198	46.67084
tur	GOTERM_BP_FAT	GO:0046883~regulation of hormone secretion	6	0.831025	0.035569	ENSG00000118702,	375	66	13528	3.279515	1	0.680198	46.67084
tur	GOTERM_BP_FAT	GO:0030182~neuron differentiation	20	2.770083	0.035621	ENSG00000137707,	375	438	13528	1.647245	1	0.675493	46.72097
tur	GOTERM_BP_FAT	GO:0048610~reproductive cellular process	10	1.385042	0.036114	ENSG00000143768,	375	162	13528	2.226831	1	0.675421	47.19145
tur	GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	11	1.523546	0.036256	ENSG00000170989,	375	188	13528	2.110752	1	0.671772	47.32641
tur	GOTERM_BP_FAT	GO:0030799~regulation of cyclic nucleotide metabolic process	8	1.108033	0.037215	ENSG00000150594,	375	113	13528	2.553959	1	0.676452	48.22893
tur	GOTERM_BP_FAT	GO:0050795~regulation of behavior	5	0.692521	0.037723	ENSG00000170989,	375	46	13528	3.921159	1	0.676526	48.70066
tur	GOTERM_BP_FAT	GO:0009416~response to light stimulus	9	1.246537	0.037799	ENSG00000163207,	375	138	13528	2.352696	1	0.672283	48.76266
tur	GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	13	1.800554	0.040069	ENSG00000146013,	375	245	13528	1.914166	1	0.689227	50.82881
tur	GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucleotide	8	1.108033	0.040327	ENSG00000124089,	375	115	13528	2.509542	1	0.686864	51.05835
tur	GOTERM_BP_FAT	GO:0050731~positive regulation of peptidyl-tyrosine phosphorylation	5	0.692521	0.040366	ENSG00000099985,	375	47	13528	3.83773	1	0.682526	51.09274
tur	GOTERM_BP_FAT	GO:0007626~locomotory behavior	14	1.939058	0.041477	ENSG00000164082,	375	274	13528	1.843231	1	0.687979	52.06635
tur	GOTERM_BP_FAT	GO:0010720~positive regulation of cell development	6	0.831025	0.041875	ENSG00000064300,	375	69	13528	3.136928	1	0.686956	52.41094
tur	GOTERM_BP_FAT	GO:0002675~positive regulation of acute inflammatory response	3	0.415512	0.041895	ENSG00000099985,	375	12	13528	9.018667	1	0.682609	52.42783

tur	GOTERM_BP_FAT	GO:0006140~regulation of nucleotide metabolic process	8	1.108033	0.041945	ENSG00000150594,	375	116	13528	2.487908	1	0.678581	52.47099
tur	GOTERM_BP_FAT	GO:0010648~negative regulation of cell communication	13	1.800554	0.043311	ENSG00000150681,	375	248	13528	1.891011	1	0.686092	53.6332
tur	GOTERM_BP_FAT	GO:0006955~immune response	28	3.878116	0.043598	ENSG00000161031,	375	690	13528	1.4639	1	0.684193	53.87418
tur	GOTERM_BP_FAT	GO:0030334~regulation of cell migration	10	1.385042	0.045262	ENSG00000126218,	375	169	13528	2.134596	1	0.693814	55.24761
tur	GOTERM_BP_FAT	GO:0051606~detection of stimulus	8	1.108033	0.045306	ENSG00000161031,	375	118	13528	2.44574	1	0.689933	55.2835
tur	GOTERM_BP_FAT	GO:0015837~amine transport	8	1.108033	0.045306	ENSG00000110195,	375	118	13528	2.44574	1	0.689933	55.2835
tur	GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	11	1.523546	0.045979	ENSG00000170989,	375	196	13528	2.024599	1	0.691219	55.82793
tur	GOTERM_BP_FAT	GO:0048870~cell motility	15	2.077562	0.046316	ENSG00000146013,	375	307	13528	1.762606	1	0.689785	56.09802
tur	GOTERM_BP_FAT	GO:0051674~localization of cell	15	2.077562	0.046316	ENSG00000146013,	375	307	13528	1.762606	1	0.689785	56.09802
tur	GOTERM_BP_FAT	GO:0006468~protein amino acid phosphorylation	27	3.739612	0.047735	ENSG00000171094,	375	667	13528	1.460294	1	0.696892	57.21791
tur	GOTERM_BP_FAT	GO:0043583~ear development	7	0.969529	0.047884	ENSG00000121742,	375	95	13528	2.658133	1	0.694003	57.33392
tur	GOTERM_BP_FAT	GO:0019933~cAMP-mediated signaling	7	0.969529	0.047884	ENSG00000124089,	375	95	13528	2.658133	1	0.694003	57.33392
tur	GOTERM_BP_FAT	GO:0045995~regulation of embryonic development	3	0.415512	0.048626	ENSG00000156574,	375	13	13528	8.324923	1	0.695709	57.90728
tur	GOTERM_BP_FAT	GO:0009913~epidermal cell differentiation	6	0.831025	0.048816	ENSG00000163216,	375	72	13528	3.006222	1	0.693197	58.05291
tur	GOTERM_BP_FAT	GO:0006937~regulation of muscle contraction	6	0.831025	0.048816	ENSG00000111245,	375	72	13528	3.006222	1	0.693197	58.05291
tur	GOTERM_BP_FAT	GO:0030030~cell projection organization	17	2.354571	0.050259	ENSG00000146013,	375	368	13528	1.666493	1	0.700106	59.14462
tur	GOTERM_BP_FAT	GO:0008277~regulation of G-protein coupled receptor p	5	0.692521	0.051966	ENSG00000150681,	375	51	13528	3.536732	1	0.708605	60.4006
tur	GOTERM_BP_FAT	GO:0007605~sensory perception of sound	7	0.969529	0.052056	ENSG00000155719,	375	97	13528	2.603326	1	0.705435	60.46548
tur	GOTERM_BP_FAT	GO:0051251~positive regulation of lymphocyte activation	7	0.969529	0.052056	ENSG00000159958,	375	97	13528	2.603326	1	0.705435	60.46548
tur	GOTERM_BP_FAT	GO:0032990~cell part morphogenesis	13	1.800554	0.052657	ENSG00000146013,	375	256	13528	1.831917	1	0.705914	60.89859
tur	GOTERM_BP_FAT	GO:0001763~morphogenesis of a branching structure	6	0.831025	0.053797	ENSG00000171791,	375	74	13528	2.924973	1	0.710101	61.70728
tur	GOTERM_BP_FAT	GO:0045401~positive regulation of interleukin-3 biosynt	2	0.277008	0.05453	ENSG00000179639,	375	2	13528	36.07467	1	0.711417	62.21924
tur	GOTERM_BP_FAT	GO:0045399~regulation of interleukin-3 biosynthetic pro	2	0.277008	0.05453	ENSG00000179639,	375	2	13528	36.07467	1	0.711417	62.21924
tur	GOTERM_BP_FAT	GO:0032672~regulation of interleukin-3 production	2	0.277008	0.05453	ENSG00000179639,	375	2	13528	36.07467	1	0.711417	62.21924
tur	GOTERM_BP_FAT	GO:0006812~cation transport	23	3.185596	0.0552	ENSG00000136531,	375	553	13528	1.500393	1	0.712275	62.68069
tur	GOTERM_BP_FAT	GO:0051954~positive regulation of amine transport	3	0.415512	0.055716	ENSG00000149295,	375	14	13528	7.730286	1	0.71211	63.03348
tur	GOTERM_BP_FAT	GO:0007186~G-protein coupled receptor protein signalir	41	5.67867	0.057513	ENSG00000164082,	375	1123	13528	1.317063	1	0.720237	64.23581
tur	GOTERM_BP_FAT	GO:0051345~positive regulation of hydrolase activity	10	1.385042	0.060829	ENSG00000124089,	375	179	13528	2.015345	1	0.737202	66.35809
tur	GOTERM_BP_FAT	GO:0043279~response to alkaloid	5	0.692521	0.061735	ENSG00000164082,	375	54	13528	3.340247	1	0.739136	66.91734
tur	GOTERM_BP_FAT	GO:0008344~adult locomotory behavior	5	0.692521	0.061735	ENSG00000164082,	375	54	13528	3.340247	1	0.739136	66.91734
tur	GOTERM_BP_FAT	GO:0006939~smooth muscle contraction	4	0.554017	0.062106	ENSG00000149295,	375	33	13528	4.372687	1	0.737914	67.14331
tur	GOTERM_BP_FAT	GO:0046324~regulation of glucose import	4	0.554017	0.062106	ENSG00000105550,	375	33	13528	4.372687	1	0.737914	67.14331
tur	GOTERM_BP_FAT	GO:0050801~ion homeostasis	18	2.493075	0.062987	ENSG00000160716,	375	409	13528	1.587638	1	0.739664	67.67536
tur	GOTERM_BP_FAT	GO:0048511~rhythmic process	8	1.108033	0.064665	ENSG00000118702,	375	128	13528	2.254667	1	0.745843	68.66533
tur	GOTERM_BP_FAT	GO:0050671~positive regulation of lymphocyte proliferat	5	0.692521	0.065192	ENSG00000159958,	375	55	13528	3.279515	1	0.7455	68.9707
tur	GOTERM_BP_FAT	GO:0050954~sensory perception of mechanical stimulus	7	0.969529	0.065866	ENSG00000155719,	375	103	13528	2.451676	1	0.745963	69.3564
tur	GOTERM_BP_FAT	GO:0048520~positive regulation of behavior	4	0.554017	0.066775	ENSG00000170989,	375	34	13528	4.244078	1	0.747694	69.87018
tur	GOTERM_BP_FAT	GO:0010827~regulation of glucose transport	4	0.554017	0.066775	ENSG00000105550,	375	34	13528	4.244078	1	0.747694	69.87018
tur	GOTERM_BP_FAT	GO:0050806~positive regulation of synaptic transmission	4	0.554017	0.066775	ENSG00000160716,	375	34	13528	4.244078	1	0.747694	69.87018
tur	GOTERM_BP_FAT	GO:0002684~positive regulation of immune system proc	12	1.66205	0.066925	ENSG00000159958,	375	238	13528	1.818891	1	0.745324	69.95402
tur	GOTERM_BP_FAT	GO:0048839~inner ear development	6	0.831025	0.067494	ENSG00000121742,	375	79	13528	2.739848	1	0.745223	70.2702
tur	GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	10	1.385042	0.067909	ENSG00000170989,	375	183	13528	1.971293	1	0.744314	70.49948
tur	GOTERM_BP_FAT	GO:0042472~inner ear morphogenesis	5	0.692521	0.068749	ENSG00000162676,	375	56	13528	3.220952	1	0.745652	70.95718
tur	GOTERM_BP_FAT	GO:0032946~positive regulation of mononuclear cell pro	5	0.692521	0.068749	ENSG00000159958,	375	56	13528	3.220952	1	0.745652	70.95718
tur	GOTERM_BP_FAT	GO:0070665~positive regulation of leukocyte proliferatio	5	0.692521	0.068749	ENSG00000159958,	375	56	13528	3.220952	1	0.745652	70.95718
tur	GOTERM_BP_FAT	GO:0009408~response to heat	5	0.692521	0.068749	ENSG00000171791,	375	56	13528	3.220952	1	0.745652	70.95718
tur	GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	8	1.108033	0.069056	ENSG00000124089,	375	130	13528	2.219979	1	0.744194	71.12327
tur	GOTERM_BP_FAT	GO:0042127~regulation of cell proliferation	30	4.155125	0.070114	ENSG00000105894,	375	787	13528	1.375146	1	0.746642	71.68748

tur	GOTERM_BP_FAT	GO:0045577~regulation of B cell differentiation	3	0.415512	0.07088	ENSG00000147168,	375	16	13528	6.764	1	0.74755	72.08951
tur	GOTERM_BP_FAT	GO:0002026~regulation of the force of heart contraction	3	0.415512	0.07088	ENSG00000018625,	375	16	13528	6.764	1	0.74755	72.08951
tur	GOTERM_BP_FAT	GO:0010647~positive regulation of cell communication	15	2.077562	0.073422	ENSG00000160716,	375	329	13528	1.644742	1	0.757231	73.38605
tur	GOTERM_BP_FAT	GO:0045786~negative regulation of cell cycle	6	0.831025	0.073466	ENSG00000137707,	375	81	13528	2.672198	1	0.754517	73.40805
tur	GOTERM_BP_FAT	GO:0046903~secretion	14	1.939058	0.073844	ENSG00000164082,	375	300	13528	1.683484	1	0.753445	73.59575
tur	GOTERM_BP_FAT	GO:0032101~regulation of response to external stimulus	9	1.246537	0.074231	ENSG00000170989,	375	159	13528	2.041962	1	0.75243	73.78646
tur	GOTERM_BP_FAT	GO:0048562~embryonic organ morphogenesis	8	1.108033	0.07597	ENSG00000121742,	375	133	13528	2.169905	1	0.75787	74.62832
tur	GOTERM_BP_FAT	GO:0000187~activation of MAPK activity	6	0.831025	0.076557	ENSG00000150594,	375	82	13528	2.63961	1	0.757795	74.90676
tur	GOTERM_BP_FAT	GO:0007422~peripheral nervous system development	4	0.554017	0.076577	ENSG00000146013,	375	36	13528	4.008296	1	0.755078	74.91592
tur	GOTERM_BP_FAT	GO:0010927~cellular component assembly involved in m	4	0.554017	0.076577	ENSG00000111245,	375	36	13528	4.008296	1	0.755078	74.91592
tur	GOTERM_BP_FAT	GO:0045596~negative regulation of cell differentiation	11	1.523546	0.077614	ENSG00000064300,	375	216	13528	1.837136	1	0.757114	75.40068
tur	GOTERM_BP_FAT	GO:0002252~immune effector process	8	1.108033	0.078362	ENSG00000069431,	375	134	13528	2.153711	1	0.757785	75.74452
tur	GOTERM_BP_FAT	GO:0015844~monoamine transport	3	0.415512	0.078906	ENSG00000108405,	375	17	13528	6.366118	1	0.757522	75.99165
tur	GOTERM_BP_FAT	GO:0050850~positive regulation of calcium-mediated sig	3	0.415512	0.078906	ENSG00000153563,	375	17	13528	6.366118	1	0.757522	75.99165
tur	GOTERM_BP_FAT	GO:0008306~associative learning	3	0.415512	0.078906	ENSG00000149295,	375	17	13528	6.366118	1	0.757522	75.99165
tur	GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	6	0.831025	0.079718	ENSG00000159958,	375	83	13528	2.607807	1	0.758474	76.35656
tur	GOTERM_BP_FAT	GO:0009266~response to temperature stimulus	6	0.831025	0.079718	ENSG00000064300,	375	83	13528	2.607807	1	0.758474	76.35656
tur	GOTERM_BP_FAT	GO:0050769~positive regulation of neurogenesis	5	0.692521	0.080001	ENSG00000064300,	375	59	13528	3.057175	1	0.757051	76.48261
tur	GOTERM_BP_FAT	GO:0032224~positive regulation of synaptic transmission	2	0.277008	0.080673	ENSG00000006128,	375	3	13528	24.04978	1	0.757374	76.77893
tur	GOTERM_BP_FAT	GO:0045425~positive regulation of granulocyte macroph	2	0.277008	0.080673	ENSG00000179639,	375	3	13528	24.04978	1	0.757374	76.77893
tur	GOTERM_BP_FAT	GO:0015860~purine nucleoside transport	2	0.277008	0.080673	ENSG00000197506,	375	3	13528	24.04978	1	0.757374	76.77893
tur	GOTERM_BP_FAT	GO:0032656~regulation of interleukin-13 production	2	0.277008	0.080673	ENSG00000149021,	375	3	13528	24.04978	1	0.757374	76.77893
tur	GOTERM_BP_FAT	GO:0033603~positive regulation of dopamine secretion	2	0.277008	0.080673	ENSG00000160716,	375	3	13528	24.04978	1	0.757374	76.77893
tur	GOTERM_BP_FAT	GO:0051051~negative regulation of transport	8	1.108033	0.080797	ENSG00000112559,	375	135	13528	2.137758	1	0.75527	76.83337
tur	GOTERM_BP_FAT	GO:0051971~positive regulation of transmission of nerve	4	0.554017	0.081701	ENSG00000160716,	375	37	13528	3.899964	1	0.756629	77.22568
tur	GOTERM_BP_FAT	GO:0001667~ameboidal cell migration	4	0.554017	0.081701	ENSG00000107562,	375	37	13528	3.899964	1	0.756629	77.22568
tur	GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	6	0.831025	0.082947	ENSG00000159958,	375	84	13528	2.576762	1	0.759445	77.75618
tur	GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	6	0.831025	0.082947	ENSG00000159958,	375	84	13528	2.576762	1	0.759445	77.75618
tur	GOTERM_BP_FAT	GO:0050804~regulation of synaptic transmission	8	1.108033	0.083276	ENSG00000149295,	375	136	13528	2.122039	1	0.758274	77.89423
tur	GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduct	62	8.587258	0.083786	ENSG00000164082,	375	1856	13528	1.20508	1	0.757892	78.10675
tur	GOTERM_BP_FAT	GO:0007612~learning	5	0.692521	0.083943	ENSG00000105894,	375	60	13528	3.006222	1	0.756009	78.17182
tur	GOTERM_BP_FAT	GO:0007565~female pregnancy	7	0.969529	0.084435	ENSG00000204941,	375	110	13528	2.295661	1	0.75557	78.37427
tur	GOTERM_BP_FAT	GO:0051336~regulation of hydrolase activity	15	2.077562	0.085709	ENSG00000134571,	375	337	13528	1.605697	1	0.758437	78.89092
tur	GOTERM_BP_FAT	GO:0040012~regulation of locomotion	10	1.385042	0.085716	ENSG00000126218,	375	192	13528	1.878889	1	0.755965	78.89348
tur	GOTERM_BP_FAT	GO:0048477~oogenesis	4	0.554017	0.08697	ENSG00000143768,	375	38	13528	3.797333	1	0.758706	79.39037
tur	GOTERM_BP_FAT	GO:0006940~regulation of smooth muscle contraction	4	0.554017	0.08697	ENSG00000018625,	375	38	13528	3.797333	1	0.758706	79.39037
tur	GOTERM_BP_FAT	GO:0009595~detection of biotic stimulus	3	0.415512	0.087198	ENSG00000161031,	375	18	13528	6.012444	1	0.757189	79.47981
tur	GOTERM_BP_FAT	GO:0046823~negative regulation of nucleocytoplasmic tr	3	0.415512	0.087198	ENSG00000112559,	375	18	13528	6.012444	1	0.757189	79.47981
tur	GOTERM_BP_FAT	GO:0051270~regulation of cell motion	10	1.385042	0.087873	ENSG00000126218,	375	193	13528	1.869154	1	0.757518	79.74164
tur	GOTERM_BP_FAT	GO:0002703~regulation of leukocyte mediated immunity	5	0.692521	0.087979	ENSG00000113520,	375	61	13528	2.95694	1	0.755519	79.78221
tur	GOTERM_BP_FAT	GO:0016049~cell growth	5	0.692521	0.087979	ENSG00000143768,	375	61	13528	2.95694	1	0.755519	79.78221
tur	GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	9	1.246537	0.089909	ENSG00000064300,	375	166	13528	1.955855	1	0.760918	80.51227
tur	GOTERM_BP_FAT	GO:0045165~cell fate commitment	8	1.108033	0.090972	ENSG00000171791,	375	139	13528	2.07624	1	0.76275	80.90366
tur	GOTERM_BP_FAT	GO:0022602~ovulation cycle process	5	0.692521	0.092106	ENSG00000118971,	375	62	13528	2.909247	1	0.764824	81.31309
tur	GOTERM_BP_FAT	GO:0031646~positive regulation of neurological system p	4	0.554017	0.092378	ENSG00000160716,	375	39	13528	3.699966	1	0.763535	81.40984
tur	GOTERM_BP_FAT	GO:0033555~multicellular organismal response to stress	4	0.554017	0.092378	ENSG00000150594,	375	39	13528	3.699966	1	0.763535	81.40984
tur	GOTERM_BP_FAT	GO:0050927~positive regulation of positive chemotaxis	3	0.415512	0.095737	ENSG00000170989,	375	19	13528	5.696	1	0.773936	82.5688
tur	GOTERM_BP_FAT	GO:0014073~response to tropane	3	0.415512	0.095737	ENSG00000164082,	375	19	13528	5.696	1	0.773936	82.5688

tur	GOTERM_BP_FAT	GO:0050926~regulation of positive chemotaxis	3	0.415512	0.095737	ENSG00000170989,	375	19	13528	5.696	1	0.773936	82.5688
tur	GOTERM_BP_FAT	GO:0042220~response to cocaine	3	0.415512	0.095737	ENSG00000164082,	375	19	13528	5.696	1	0.773936	82.5688
tur	GOTERM_BP_FAT	GO:0050433~regulation of catecholamine secretion	3	0.415512	0.095737	ENSG00000149295,	375	19	13528	5.696	1	0.773936	82.5688
tur	GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	16	2.216066	0.097065	ENSG00000160716,	375	374	13528	1.543301	1	0.776526	83.00793
tur	GOTERM_BP_FAT	GO:0051224~negative regulation of protein transport	4	0.554017	0.097921	ENSG00000112559,	375	40	13528	3.607467	1	0.777367	83.2854
tur	GOTERM_CC_FAT	GO:0005576~extracellular region	92	12.74238	5.50E-06	ENSG000000066468,	372	2010	12782	1.572706	0.001748	0.001748	0.007415
tur	GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	59	8.171745	9.89E-05	ENSG00000164082,	372	1215	12782	1.668521	0.030955	0.015599	0.133219
tur	GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	58	8.033241	9.89E-05	ENSG00000164082,	372	1188	12782	1.677519	0.030961	0.010429	0.133248
tur	GOTERM_CC_FAT	GO:0034702~ion channel complex	16	2.216066	9.51E-04	ENSG00000136531,	372	205	12782	2.681773	0.261123	0.072865	1.274786
tur	GOTERM_CC_FAT	GO:0044421~extracellular region part	44	6.094183	0.002909	ENSG00000105894,	372	960	12782	1.574843	0.604044	0.169137	3.851592
tur	GOTERM_CC_FAT	GO:0009986~cell surface	21	2.908587	0.00291	ENSG00000146013,	372	348	12782	2.073461	0.604113	0.143103	3.852295
tur	GOTERM_CC_FAT	GO:0044459~plasma membrane part	85	11.77285	0.004051	ENSG00000146013,	372	2203	12782	1.325746	0.724945	0.168395	5.325285
tur	GOTERM_CC_FAT	GO:0005886~plasma membrane	134	18.55956	0.004632	ENSG00000146013,	372	3777	12782	1.219028	0.771574	0.168537	6.06795
tur	GOTERM_CC_FAT	GO:0009897~external side of plasma membrane	12	1.66205	0.010783	ENSG00000155719,	372	170	12782	2.425427	0.968176	0.318227	13.59794
tur	GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	18	2.493075	0.012282	ENSG00000167346,	372	320	12782	1.932762	0.980354	0.324965	15.34699
tur	GOTERM_CC_FAT	GO:0034707~chloride channel complex	6	0.831025	0.021294	ENSG00000151572,	372	55	12782	3.748387	0.998935	0.463261	25.18727
tur	GOTERM_CC_FAT	GO:0031012~extracellular matrix	18	2.493075	0.023718	ENSG00000167346,	372	345	12782	1.792707	0.999516	0.470654	27.64739
tur	GOTERM_CC_FAT	GO:0030017~sarcomere	8	1.108033	0.023809	ENSG00000165887,	372	98	12782	2.804916	0.99953	0.445369	27.73787
tur	GOTERM_CC_FAT	GO:0005615~extracellular space	30	4.155125	0.026848	ENSG00000105894,	372	685	12782	1.504827	0.999826	0.461074	30.71277
tur	GOTERM_CC_FAT	GO:0030016~myofibril	8	1.108033	0.042704	ENSG00000165887,	372	111	12782	2.476412	0.999999	0.603553	44.4769
tur	GOTERM_CC_FAT	GO:0042383~sarcolemma	6	0.831025	0.044773	ENSG00000136531,	372	67	12782	3.077034	1	0.597637	46.0735
tur	GOTERM_CC_FAT	GO:0044449~contractile fiber part	8	1.108033	0.046279	ENSG00000165887,	372	113	12782	2.432582	1	0.58785	47.20867
tur	GOTERM_CC_FAT	GO:0043292~contractile fiber	8	1.108033	0.062464	ENSG00000165887,	372	121	12782	2.27175	1	0.680022	58.08694
tur	GOTERM_CC_FAT	GO:0031672~A band	3	0.415512	0.077145	ENSG00000134571,	372	16	12782	6.44254	1	0.739116	66.12005
tur	GOTERM_CC_FAT	GO:0034703~cation channel complex	8	1.108033	0.089724	ENSG00000136531,	372	132	12782	2.082437	1	0.775688	71.84313
tur	GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	23	3.185596	0.001942	ENSG00000136531,	365	398	12983	2.055545	0.675491	0.675491	2.816381
tur	GOTERM_MF_FAT	GO:0015267~channel activity	23	3.185596	0.002921	ENSG00000136531,	365	412	12983	1.985696	0.816172	0.571248	4.208275
tur	GOTERM_MF_FAT	GO:0005216~ion channel activity	22	3.047091	0.002937	ENSG00000136531,	365	386	12983	2.027298	0.817877	0.433167	4.230935
tur	GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	23	3.185596	0.003038	ENSG00000136531,	365	413	12983	1.980888	0.828246	0.356236	4.373334
tur	GOTERM_MF_FAT	GO:0005179~hormone activity	10	1.385042	0.003308	ENSG00000118702,	365	108	12983	3.293506	0.853179	0.31867	4.753302
tur	GOTERM_MF_FAT	GO:0008083~growth factor activity	12	1.66205	0.005693	ENSG00000105894,	365	161	12983	2.65117	0.963321	0.423584	8.048376
tur	GOTERM_MF_FAT	GO:0016247~channel regulator activity	7	0.969529	0.006009	ENSG00000150594,	365	59	12983	4.220153	0.969488	0.39257	8.477003
tur	GOTERM_MF_FAT	GO:0032036~myosin heavy chain binding	3	0.415512	0.007411	ENSG00000111245,	365	5	12983	21.34192	0.986528	0.416316	10.35674
tur	GOTERM_MF_FAT	GO:0005261~cation channel activity	16	2.216066	0.010853	ENSG00000136531,	365	275	12983	2.069519	0.998197	0.504423	14.8182
tur	GOTERM_MF_FAT	GO:0046873~metal ion transmembrane transporter activ	18	2.493075	0.011192	ENSG00000136531,	365	328	12983	1.952005	0.998522	0.478833	15.24645
tur	GOTERM_MF_FAT	GO:0005337~nucleoside transmembrane transporter activ	3	0.415512	0.019626	ENSG00000197506,	365	8	12983	13.3387	0.99999	0.647718	25.27222
tur	GOTERM_MF_FAT	GO:0017022~myosin binding	4	0.554017	0.022672	ENSG00000111245,	365	22	12983	6.467248	0.999998	0.669287	28.61248
tur	GOTERM_MF_FAT	GO:0016917~GABA receptor activity	4	0.554017	0.028601	ENSG00000187730,	365	24	12983	5.928311	1	0.725392	34.71982
tur	GOTERM_MF_FAT	GO:0022836~gated channel activity	16	2.216066	0.028634	ENSG00000136531,	365	310	12983	1.835864	1	0.699257	34.75237
tur	GOTERM_MF_FAT	GO:0005267~potassium channel activity	9	1.246537	0.033624	ENSG00000162687,	365	133	12983	2.406983	1	0.732917	39.50887
tur	GOTERM_MF_FAT	GO:0004714~transmembrane receptor protein tyrosine k	6	0.831025	0.039543	ENSG00000171094,	365	67	12983	3.185361	1	0.767769	44.73195
tur	GOTERM_MF_FAT	GO:0015459~potassium channel regulator activity	4	0.554017	0.042667	ENSG00000150594,	365	28	12983	5.081409	1	0.773517	47.31565
tur	GOTERM_MF_FAT	GO:0005254~chloride channel activity	6	0.831025	0.051262	ENSG00000151572,	365	72	12983	2.964155	1	0.815976	53.85607
tur	GOTERM_MF_FAT	GO:0017116~single-stranded DNA-dependent ATP-depe	2	0.277008	0.055289	ENSG00000140451,	365	2	12983	35.56986	1	0.823289	56.6528
tur	GOTERM_MF_FAT	GO:0031420~alkali metal ion binding	12	1.66205	0.056623	ENSG00000162687,	365	228	12983	1.872098	1	0.815015	57.54369
tur	GOTERM_MF_FAT	GO:0015932~nucleobase, nucleoside, nucleotide and nuc	3	0.415512	0.057122	ENSG00000197506,	365	14	12983	7.622114	1	0.802438	57.87234
tur	GOTERM_MF_FAT	GO:0031404~chloride ion binding	6	0.831025	0.064807	ENSG00000151572,	365	77	12983	2.771678	1	0.828534	62.64644
tur	GOTERM_MF_FAT	GO:0005253~anion channel activity	6	0.831025	0.067734	ENSG00000151572,	365	78	12983	2.736143	1	0.828921	64.3287

tur	GOTERM_MF_FAT	GO:0030247~polysaccharide binding	9	1.246537	0.068337	ENSG00000105894,	365	154	12983	2.078758	1	0.81871	64.66596
tur	GOTERM_MF_FAT	GO:0001871~pattern binding	9	1.246537	0.068337	ENSG00000105894,	365	154	12983	2.078758	1	0.81871	64.66596
tur	GOTERM_MF_FAT	GO:0005246~calcium channel regulator activity	3	0.415512	0.080837	ENSG00000164082,	365	17	12983	6.277035	1	0.858038	71.02834
tur	GOTERM_MF_FAT	GO:0043141~ATP-dependent 5'-3' DNA helicase activity	2	0.277008	0.08178	ENSG00000140451,	365	3	12983	23.71324	1	0.850427	71.46222
tur	GOTERM_MF_FAT	GO:0005415~nucleoside:sodium symporter activity	2	0.277008	0.08178	ENSG00000197506,	365	3	12983	23.71324	1	0.850427	71.46222
tur	GOTERM_MF_FAT	GO:0043142~single-stranded DNA-dependent ATPase ac	2	0.277008	0.08178	ENSG00000140451,	365	3	12983	23.71324	1	0.850427	71.46222
tur	GOTERM_MF_FAT	GO:0005198~structural molecule activity	25	3.462604	0.083588	ENSG00000165887,	365	634	12983	1.402597	1	0.846163	72.27694
tur	GOTERM_MF_FAT	GO:0001882~nucleoside binding	55	7.617729	0.093368	ENSG00000077935,	365	1612	12983	1.213612	1	0.868256	76.32161
tur	GOTERM_MF_FAT	GO:0005201~extracellular matrix structural constituent	6	0.831025	0.093728	ENSG00000112769,	365	86	12983	2.481618	1	0.859835	76.45947
tur	GOTERM_MF_FAT	GO:0004713~protein tyrosine kinase activity	9	1.246537	0.095477	ENSG00000171094,	365	166	12983	1.928487	1	0.855821	77.11813
tur	GOTERM_MF_FAT	GO:0005244~voltage-gated ion channel activity	10	1.385042	0.096605	ENSG00000136531,	365	195	12983	1.824096	1	0.850062	77.53394
tur	GOTERM_MF_FAT	GO:0005125~cytokine activity	10	1.385042	0.096605	ENSG00000143768,	365	195	12983	1.824096	1	0.850062	77.53394
tur	GOTERM_MF_FAT	GO:0022832~voltage-gated channel activity	10	1.385042	0.096605	ENSG00000136531,	365	195	12983	1.824096	1	0.850062	77.53394
tur	HIV_INTERACTION	env:Envelope surface glycoprotein gp120	22	3.047091	0.040845	ENSG00000138308,	41	529	1394	1.413989	0.340998	0.340998	22.15213
tur	HIV_INTERACTION_CATEGORY	env:Envelope surface glycoprotein gp120 downregulates	7	0.969529	0.002132	ENSG00000007312,	41	49	1394	4.857143	0.08962	0.08962	1.976657
tur	INTERPRO	IPR003599:Immunoglobulin subtype	22	3.047091	4.97E-04	ENSG00000069122,	473	330	16659	2.347992	0.325358	0.325358	0.759725
tur	INTERPRO	IPR010007:Sperm associated with nucleus, X chromosom	4	0.554017	0.001671	ENSG00000203923,	473	9	16659	15.65328	0.733688	0.483946	2.531164
tur	INTERPRO	IPR003267:Small proline-rich	5	0.692521	0.005018	ENSG00000163216,	473	25	16659	7.043975	0.981294	0.734545	7.420243
tur	INTERPRO	IPR002049:EGF-like, laminin	6	0.831025	0.00578	ENSG00000009128,	473	41	16659	5.154128	0.989799	0.682194	8.501582
tur	INTERPRO	IPR008266:Tyrosine protein kinase, active site	9	1.246537	0.006265	ENSG00000171094,	473	97	16659	3.267823	0.993065	0.629989	9.183143
tur	INTERPRO	IPR000233:Cadherin cytoplasmic region	4	0.554017	0.015624	ENSG00000140937,	473	19	16659	7.41471	0.999996	0.874576	21.44463
tur	INTERPRO	IPR007110:Immunoglobulin-like	24	3.3241	0.016242	ENSG00000069122,	473	501	16659	1.68718	0.999998	0.842836	22.19743
tur	INTERPRO	IPR002190:MAGE protein	5	0.692521	0.016639	ENSG00000176746,	473	35	16659	5.03141	0.999998	0.809682	22.67715
tur	INTERPRO	IPR013106:Immunoglobulin V-set	14	1.939058	0.025647	ENSG00000160588,	473	249	16659	1.980234	1	0.898068	32.84848
tur	INTERPRO	IPR010294:ADAM-TS Spacer 1	4	0.554017	0.026276	ENSG00000138316,	473	23	16659	6.125195	1	0.878307	33.51067
tur	INTERPRO	IPR013273:Peptidase M12B, ADAM-TS	4	0.554017	0.029414	ENSG00000138316,	473	24	16659	5.869979	1	0.883153	36.72022
tur	INTERPRO	IPR001818:Peptidase M10A and M12B, matrixin and adar	5	0.692521	0.032903	ENSG00000167346,	473	43	16659	4.095334	1	0.889785	40.11778
tur	INTERPRO	IPR011992:EF-Hand type	13	1.800554	0.037129	ENSG00000111245,	473	236	16659	1.940078	1	0.89996	44.0059
tur	INTERPRO	IPR001245:Tyrosine protein kinase	8	1.108033	0.050638	ENSG00000171094,	473	118	16659	2.387788	1	0.946925	54.90903
tur	INTERPRO	IPR006025:Peptidase M, neutral zinc metallopeptidases, z	7	0.969529	0.055144	ENSG00000072657,	473	96	16659	2.568116	1	0.949771	58.07959
tur	INTERPRO	IPR017338:Fibroblast growth factor, 15/19/21	2	0.277008	0.055865	ENSG00000105550,	473	2	16659	35.21987	1	0.941689	58.56738
tur	INTERPRO	IPR013151:Immunoglobulin	11	1.523546	0.062394	ENSG00000162706,	473	202	16659	1.917914	1	0.950097	62.74799
tur	INTERPRO	IPR008085:Thrombospondin, type 1 repeat, subgroup	3	0.415512	0.06595	ENSG00000126759,	473	15	16659	7.043975	1	0.950119	64.85559
tur	INTERPRO	IPR008211:Laminin, N-terminal	3	0.415512	0.073998	ENSG00000009128,	473	16	16659	6.603726	1	0.959262	69.22106
tur	INTERPRO	IPR000342:Regulator of G protein signalling	4	0.554017	0.075903	ENSG00000150681,	473	35	16659	4.025128	1	0.955931	70.17734
tur	INTERPRO	IPR002110:Ankyrin	12	1.66205	0.077117	ENSG00000165887,	473	238	16659	1.775792	1	0.951338	70.77229
tur	INTERPRO	IPR000169:Peptidase, cysteine peptidase active site	4	0.554017	0.081138	ENSG00000136943,	473	36	16659	3.913319	1	0.952283	72.66459
tur	INTERPRO	IPR001699:Transcription factor, T-box	3	0.415512	0.08234	ENSG00000092607,	473	17	16659	6.215272	1	0.947931	73.20739
tur	INTERPRO	IPR018186:Transcription factor, T-box, conserved site	3	0.415512	0.08234	ENSG00000092607,	473	17	16659	6.215272	1	0.947931	73.20739
tur	INTERPRO	IPR011657:Na dependent nucleoside transporter, C-termi	2	0.277008	0.082618	ENSG00000197506,	473	3	16659	23.47992	1	0.941694	73.33165
tur	INTERPRO	IPR011642:Nucleoside recognition	2	0.277008	0.082618	ENSG00000197506,	473	3	16659	23.47992	1	0.941694	73.33165
tur	INTERPRO	IPR002455:GPCR, family 3, gamma-aminobutyric acid rec	2	0.277008	0.082618	ENSG00000175697,	473	3	16659	23.47992	1	0.941694	73.33165
tur	INTERPRO	IPR018270:Concentrative nucleoside transporter, metazo	2	0.277008	0.082618	ENSG00000197506,	473	3	16659	23.47992	1	0.941694	73.33165
tur	INTERPRO	IPR002668:Na dependent nucleoside transporter	2	0.277008	0.082618	ENSG00000197506,	473	3	16659	23.47992	1	0.941694	73.33165
tur	INTERPRO	IPR008276:Concentrative nucleoside transporter	2	0.277008	0.082618	ENSG00000197506,	473	3	16659	23.47992	1	0.941694	73.33165
tur	INTERPRO	IPR017948:Transforming growth factor beta, conserved s	4	0.554017	0.086526	ENSG00000143768,	473	37	16659	3.807554	1	0.942927	75.02046
tur	INTERPRO	IPR001839:Transforming growth factor beta	4	0.554017	0.086526	ENSG00000143768,	473	37	16659	3.807554	1	0.942927	75.02046
tur	INTERPRO	IPR005821:Ion transport	7	0.969529	0.092499	ENSG00000136531,	473	110	16659	2.241265	1	0.94781	77.41003

tur	INTERPRO	IPR001590:Peptidase M12B, ADAM/reprolysin	4	0.554017	0.097737	ENSG00000138316,	473	39	16659	3.612295	1	0.950861	79.32803
tur	INTERPRO	IPR002870:Peptidase M12B, propeptide	4	0.554017	0.097737	ENSG00000138316,	473	39	16659	3.612295	1	0.950861	79.32803
tur	INTERPRO	IPR010909:PLAC	3	0.415512	0.099816	ENSG00000138316,	473	19	16659	5.561033	1	0.94873	80.04603
tur	KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	13	1.800554	0.021411	ENSG00000124089,	125	256	5085	2.065781	0.909503	0.909503	21.72504
tur	KEGG_PATHWAY	hsa04510:Focal adhesion	11	1.523546	0.024107	ENSG00000111245,	125	201	5085	2.226269	0.933376	0.741884	24.1314
tur	KEGG_PATHWAY	hsa05414:Dilated cardiomyopathy	7	0.969529	0.024133	ENSG00000111245,	125	92	5085	3.095217	0.933567	0.594995	24.15361
tur	KEGG_PATHWAY	hsa05340:Primary immunodeficiency	4	0.554017	0.052593	ENSG00000159958,	125	35	5085	4.649143	0.997514	0.7767	45.74233
tur	KEGG_PATHWAY	hsa05410:Hypertrophic cardiomyopathy (HCM)	6	0.831025	0.055595	ENSG00000111245,	125	85	5085	2.871529	0.998252	0.719121	47.6561
tur	KEGG_PATHWAY	hsa04640:Hematopoietic cell lineage	6	0.831025	0.057922	ENSG00000105383,	125	86	5085	2.83814	0.998671	0.668405	49.09752
tur	KEGG_PATHWAY	hsa04912:GnRH signaling pathway	6	0.831025	0.090134	ENSG00000138308,	125	98	5085	2.490612	0.999972	0.776386	65.6645
tur	KEGG_PATHWAY	hsa04916:Melanogenesis	6	0.831025	0.093168	ENSG00000070808,	125	99	5085	2.465455	0.999981	0.742556	66.93835
tur	OMIM_DISEASE	Genome-wide association analysis of susceptibility and c	5	0.692521	0.022811	ENSG00000162779,	107	38	3671	4.514265	0.990544	0.990544	25.15042
tur	OMIM_DISEASE	Genome-wide association to body mass index and waist	3	0.415512	0.045141	ENSG00000162706,	107	12	3671	8.577103	0.999911	0.990585	44.0053
tur	PIR_SUPERFAMILY	PIRSF005491:tumor associated protein MAGE	5	0.692521	0.003112	ENSG00000176746,	222	21	7396	7.932218	0.505561	0.505561	3.905975
tur	PIR_SUPERFAMILY	PIRSF002504:cadherin	4	0.554017	0.020614	ENSG00000140937,	222	20	7396	6.663063	0.990972	0.904986	23.37867
tur	PIR_SUPERFAMILY	PIRSF005770:regulator of G protein signaling, RGS4 type	3	0.415512	0.055832	ENSG00000150681,	222	13	7396	7.68815	0.999998	0.986805	52.02441
tur	PIR_SUPERFAMILY	PIRSF037961:FGF-19_FGF-21	2	0.277008	0.058873	ENSG00000105550,	222	2	7396	33.31532	0.999999	0.967557	53.96318
tur	PIR_SUPERFAMILY	PIRSF037059:relaxin	2	0.277008	0.058873	ENSG00000107014,	222	2	7396	33.31532	0.999999	0.967557	53.96318
tur	PIR_SUPERFAMILY	PIRSF500319:relaxin precursor	2	0.277008	0.058873	ENSG00000107014,	222	2	7396	33.31532	0.999999	0.967557	53.96318
tur	PIR_SUPERFAMILY	PIRSF037961:fibroblast growth factor, 15/19/21 types	2	0.277008	0.058873	ENSG00000105550,	222	2	7396	33.31532	0.999999	0.967557	53.96318
tur	PIR_SUPERFAMILY	PIRSF002413:folate-binding protein	2	0.277008	0.087003	ENSG00000110195,	222	3	7396	22.21021	1	0.983661	68.76631
tur	PIR_SUPERFAMILY	PIRSF002337:Actin	3	0.415512	0.090108	ENSG00000117148,	222	17	7396	5.879173	1	0.971471	70.09761
tur	SMART	SM00409:IG	22	3.047091	0.001043	ENSG00000069122,	276	330	9079	2.192995	0.168632	0.168632	1.273431
tur	SMART	SM00180:EGF_Lam	6	0.831025	0.00755	ENSG00000091128,	276	41	9079	4.813892	0.738527	0.488655	8.888666
tur	SMART	SM00219:TyrKc	8	1.108033	0.066853	ENSG00000171094,	276	118	9079	2.230165	0.999995	0.983133	57.25387
tur	SMART	SM00136:LamNT	3	0.415512	0.083009	ENSG00000091128,	276	16	9079	6.167799	1	0.97839	65.50667
tur	SMART	SM00315:RGS	4	0.554017	0.088476	ENSG00000150681,	276	35	9079	3.75942	1	0.962347	67.9493
tur	SMART	SM00425:TBOX	3	0.415512	0.092258	ENSG00000092607,	276	17	9079	5.804987	1	0.94247	69.54496
tur	SP_PIR_KEYWORDS	signal	151	20.91413	9.70E-09	ENSG00000183396,	575	3250	19235	1.554239	4.07E-06	4.07E-06	1.36E-05
tur	SP_PIR_KEYWORDS	Secreted	88	12.18837	3.11E-07	ENSG00000066468,	575	1689	19235	1.74292	1.30E-04	6.52E-05	4.37E-04
tur	SP_PIR_KEYWORDS	glycoprotein	171	23.68421	3.15E-05	ENSG00000146013,	575	4318	19235	1.324762	0.013111	0.004389	0.044219
tur	SP_PIR_KEYWORDS	cleavage on pair of basic residues	22	3.047091	6.88E-05	ENSG00000140937,	575	271	19235	2.715675	0.0284	0.007177	0.096511
tur	SP_PIR_KEYWORDS	polymorphism	382	52.90859	8.80E-04	ENSG00000183396,	575	11550	19235	1.106384	0.308543	0.071134	1.228886
tur	SP_PIR_KEYWORDS	amidation	7	0.969529	0.001852	ENSG00000118702,	575	44	19235	5.321937	0.540045	0.121411	2.569182
tur	SP_PIR_KEYWORDS	hormone	9	1.246537	0.004434	ENSG00000118702,	575	87	19235	3.46057	0.844626	0.233552	6.049276
tur	SP_PIR_KEYWORDS	disulfide bond	111	15.37396	0.005157	ENSG00000123843,	575	2924	19235	1.269901	0.885426	0.237243	7.003506
tur	SP_PIR_KEYWORDS	extracellular matrix	16	2.216066	0.006021	ENSG00000167346,	575	241	19235	2.220891	0.920382	0.245098	8.131016
tur	SP_PIR_KEYWORDS	ionic channel	19	2.631579	0.007366	ENSG00000136531,	575	318	19235	1.998715	0.954846	0.266383	9.860777
tur	SP_PIR_KEYWORDS	Immunoglobulin domain	25	3.462604	0.007771	ENSG00000069122,	575	470	19235	1.779371	0.961953	0.257087	10.37662
tur	SP_PIR_KEYWORDS	laminin egf-like domain	5	0.692521	0.01162	ENSG00000091128,	575	30	19235	5.575362	0.992533	0.335087	15.13624
tur	SP_PIR_KEYWORDS	growth factor	10	1.385042	0.016779	ENSG00000105894,	575	131	19235	2.553601	0.999167	0.420385	21.14934
tur	SP_PIR_KEYWORDS	tyrosine-protein kinase	9	1.246537	0.018115	ENSG00000171094,	575	111	19235	2.712338	0.999529	0.421387	22.64033
tur	SP_PIR_KEYWORDS	chloride channel	6	0.831025	0.02548	ENSG00000151572,	575	56	19235	3.584161	0.99998	0.513711	30.40143
tur	SP_PIR_KEYWORDS	tumor antigen	5	0.692521	0.025987	ENSG00000176746,	575	38	19235	4.401602	0.999984	0.498183	30.90817
tur	SP_PIR_KEYWORDS	lipoprotein	29	4.01662	0.029885	ENSG00000146013,	575	642	19235	1.51108	0.999997	0.526595	34.69151
tur	SP_PIR_KEYWORDS	keratinization	5	0.692521	0.030721	ENSG00000163216,	575	40	19235	4.181522	0.999998	0.516317	35.47727
tur	SP_PIR_KEYWORDS	muscle protein	6	0.831025	0.033105	ENSG00000111245,	575	60	19235	3.345217	0.999999	0.524034	37.67058
tur	SP_PIR_KEYWORDS	cardiac muscle	4	0.554017	0.033594	ENSG00000165887,	575	24	19235	5.575362	0.999999	0.511237	38.11137

tur	SP_PIR_KEYWORDS	heart	4	0.554017	0.033594	ENSG00000165887,	575	24	19235	5.575362	0.999999	0.511237	38.11137
tur	SP_PIR_KEYWORDS	duplication	13	1.800554	0.041139	ENSG000000064300,	575	228	19235	1.907361	1	0.569754	44.76495
tur	SP_PIR_KEYWORDS	developmental protein	33	4.570637	0.042185	ENSG000000064300,	575	779	19235	1.417101	1	0.559955	45.40537
tur	SP_PIR_KEYWORDS	cytokine	11	1.523546	0.045379	ENSG00000105894,	575	181	19235	2.033005	1	0.570886	47.90672
tur	SP_PIR_KEYWORDS	transmembrane protein	28	3.878116	0.047421	ENSG000000064300,	575	642	19235	1.458973	1	0.571797	49.44948
tur	SP_PIR_KEYWORDS	muscle contraction	3	0.415512	0.048136	ENSG000000111245,	575	12	19235	8.363043	1	0.562564	49.98005
tur	SP_PIR_KEYWORDS	tyrosine-specific protein kinase	5	0.692521	0.054431	ENSG000000066468,	575	48	19235	3.484601	1	0.594224	54.43004
tur	SP_PIR_KEYWORDS	Cardiomyopathy	5	0.692521	0.054431	ENSG000000069431,	575	48	19235	3.484601	1	0.594224	54.43004
tur	SP_PIR_KEYWORDS	differentiation	21	2.908587	0.06036	ENSG000000112559,	575	460	19235	1.527164	1	0.619458	58.2824
tur	SP_PIR_KEYWORDS	chloride	6	0.831025	0.073311	ENSG000000151572,	575	75	19235	2.676174	1	0.679967	65.66927
tur	SP_PIR_KEYWORDS	potassium channel	6	0.831025	0.083569	ENSG000000162687,	575	78	19235	2.573244	1	0.716596	70.63739
tur	SP_PIR_KEYWORDS	ovary	2	0.277008	0.086884	ENSG000000107014,	575	3	19235	22.30145	1	0.719016	72.09396
tur	SP_PIR_KEYWORDS	zymogen	11	1.523546	0.089787	ENSG000000197253,	575	206	19235	1.786281	1	0.719605	73.31446
tur	SP_PIR_KEYWORDS	collagen degradation	3	0.415512	0.090016	ENSG000000167346,	575	17	19235	5.903325	1	0.709199	73.40865
tur	SP_PIR_KEYWORDS	Signal transduction inhibitor	4	0.554017	0.091485	ENSG000000150681,	575	36	19235	3.716908	1	0.704236	74.00493
tur	SP_PIR_KEYWORDS	ion transport	24	3.3241	0.098913	ENSG000000136531,	575	578	19235	1.389018	1	0.722943	76.83531
tur	UP_SEQ_FEATURE	signal peptide	151	20.91413	1.17E-08	ENSG000000183396,	573	3250	19113	1.549772	1.76E-05	1.76E-05	1.95E-05
tur	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	164	22.71468	4.86E-05	ENSG000000146013,	573	4129	19113	1.32487	0.070378	0.035831	0.080757
tur	UP_SEQ_FEATURE	sequence variant	398	55.12465	4.14E-04	ENSG000000183396,	573	11992	19113	1.107046	0.462887	0.187129	0.685717
tur	UP_SEQ_FEATURE	domain:Ig-like V-type	11	1.523546	0.004119	ENSG000000160588,	573	124	19113	2.959002	0.997961	0.787514	6.628767
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 1	5	0.692521	0.007031	ENSG000000091128,	573	26	19113	6.414619	0.999975	0.879738	11.06287
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 2	5	0.692521	0.008062	ENSG000000091128,	573	27	19113	6.177041	0.999995	0.867997	12.58482
tur	UP_SEQ_FEATURE	topological domain:Extracellular	103	14.26593	0.008463	ENSG000000183396,	573	2719	19113	1.263579	0.999997	0.838365	13.17053
tur	UP_SEQ_FEATURE	disulfide bond	105	14.54294	0.012515	ENSG000000123843,	573	2819	19113	1.24242	1	0.90585	18.88185
tur	UP_SEQ_FEATURE	domain:MAGE	5	0.692521	0.014692	ENSG000000176746,	573	32	19113	5.211878	1	0.915286	21.80338
tur	UP_SEQ_FEATURE	region of interest:Domain II and I	3	0.415512	0.02221	ENSG000000050555,	573	8	19113	12.50851	1	0.965656	31.14865
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 3	4	0.554017	0.026899	ENSG000000091128,	573	22	19113	6.064731	1	0.975785	36.43449
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 11	3	0.415512	0.027997	ENSG000000091128,	573	9	19113	11.11867	1	0.971329	37.6153
tur	UP_SEQ_FEATURE	domain:Laminin G-like 5	3	0.415512	0.027997	ENSG000000021645,	573	9	19113	11.11867	1	0.971329	37.6153
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 9	3	0.415512	0.034312	ENSG000000091128,	573	10	19113	10.00681	1	0.982249	44.01971
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 10	3	0.415512	0.04112	ENSG000000091128,	573	11	19113	9.097097	1	0.988912	50.22869
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 8	3	0.415512	0.04112	ENSG000000091128,	573	11	19113	9.097097	1	0.988912	50.22869
tur	UP_SEQ_FEATURE	domain:TSP type-1 1	5	0.692521	0.041986	ENSG000000126759,	573	44	19113	3.790457	1	0.986325	50.97004
tur	UP_SEQ_FEATURE	domain:TSP type-1 2	5	0.692521	0.041986	ENSG000000126759,	573	44	19113	3.790457	1	0.986325	50.97004
tur	UP_SEQ_FEATURE	topological domain:Cytoplasmic	118	16.34349	0.045013	ENSG000000183396,	573	3374	19113	1.166571	1	0.986671	53.48142
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 7	3	0.415512	0.048386	ENSG000000091128,	573	12	19113	8.339005	1	0.987462	56.13766
tur	UP_SEQ_FEATURE	domain:EGF-like 2	7	0.969529	0.048421	ENSG000000126218,	573	88	19113	2.65332	1	0.984059	56.16495
tur	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 2	4	0.554017	0.050201	ENSG000000132915,	573	28	19113	4.765146	1	0.982904	57.5076
tur	UP_SEQ_FEATURE	metal ion-binding site:Divalent metal cation 1	4	0.554017	0.050201	ENSG000000132915,	573	28	19113	4.765146	1	0.982904	57.5076
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 6	3	0.415512	0.056075	ENSG000000091128,	573	13	19113	7.697543	1	0.986846	61.6696
tur	UP_SEQ_FEATURE	domain:Laminin EGF-like 4	3	0.415512	0.056075	ENSG000000091128,	573	13	19113	7.697543	1	0.986846	61.6696
tur	UP_SEQ_FEATURE	peptide:Relaxin B chain	2	0.277008	0.05896	ENSG000000107014,	573	2	19113	33.35602	1	0.987011	63.57076
tur	UP_SEQ_FEATURE	peptide:Relaxin A chain	2	0.277008	0.05896	ENSG000000107014,	573	2	19113	33.35602	1	0.987011	63.57076
tur	UP_SEQ_FEATURE	domain:EF-hand 3	7	0.969529	0.062865	ENSG000000111245,	573	94	19113	2.483959	1	0.988084	66.00259
tur	UP_SEQ_FEATURE	domain:TSP type-1 4	4	0.554017	0.06455	ENSG000000126759,	573	31	19113	4.304003	1	0.987154	67.00439
tur	UP_SEQ_FEATURE	domain:Laminin G-like 4	3	0.415512	0.0726	ENSG000000021645,	573	15	19113	6.671204	1	0.991029	71.41834
tur	UP_SEQ_FEATURE	site:Stutter	4	0.554017	0.075045	ENSG000000006059,	573	33	19113	4.043154	1	0.990756	72.64526
tur	UP_SEQ_FEATURE	domain:RGS	4	0.554017	0.075045	ENSG000000150681,	573	33	19113	4.043154	1	0.990756	72.64526

tur	UP_SEQ_FEATURE	DNA-binding region:T-box	3	0.415512	0.081376	ENSG00000092607,	573	16	19113	6.254254	1	0.992554	75.5956
tur	UP_SEQ_FEATURE	domain:Laminin N-terminal	3	0.415512	0.081376	ENSG00000009128,	573	16	19113	6.254254	1	0.992554	75.5956
tur	UP_SEQ_FEATURE	repeat:ANK 1	12	1.66205	0.087836	ENSG00000165887,	573	231	19113	1.73278	1	0.99397	78.2958
tur	UP_SEQ_FEATURE	repeat:ANK 2	12	1.66205	0.089227	ENSG00000165887,	573	232	19113	1.725311	1	0.99333	78.83925
tur	UP_SEQ_FEATURE	domain:TSP type-1 3	4	0.554017	0.092087	ENSG00000126759,	573	36	19113	3.706225	1	0.993264	79.91682
tur	UP_SEQ_FEATURE	domain:EF-hand 1	10	1.385042	0.096947	ENSG00000111245,	573	182	19113	1.832748	1	0.993916	81.63028
tur	UP_SEQ_FEATURE	domain:PH 2	4	0.554017	0.098093	ENSG00000178385,	573	37	19113	3.606056	1	0.993255	82.01405
tur	UP_SEQ_FEATURE	repeat:ANK 5	8	1.108033	0.098662	ENSG00000165887,	573	131	19113	2.037009	1	0.992345	82.20151
yellow	Category	Term	Count	%	PValue	Genes	List Total	Pop Hits	Pop Total	Fold Enric	Bonferron	Benjamini	FDR
yellow	GOTERM_BP_FAT	GO:0003013~circulatory system process	13	2.857143	2.28E-04	ENSG00000128917,	258	186	13528	3.66475	0.317386	0.317386	0.383075
yellow	GOTERM_BP_FAT	GO:0008015~blood circulation	13	2.857143	2.28E-04	ENSG00000128917,	258	186	13528	3.66475	0.317386	0.317386	0.383075
yellow	GOTERM_BP_FAT	GO:0006355~regulation of transcription, DNA-dependent	51	11.20879	0.002465	ENSG00000175322,	258	1773	13528	1.508257	0.983972	0.873397	4.069755
yellow	GOTERM_BP_FAT	GO:0045449~regulation of transcription	69	15.16484	0.002616	ENSG00000175322,	258	2601	13528	1.390986	0.987578	0.768407	4.315258
yellow	GOTERM_BP_FAT	GO:0060341~regulation of cellular localization	13	2.857143	0.002825	ENSG00000123612,	258	248	13528	2.748562	0.991247	0.694125	4.6513
yellow	GOTERM_BP_FAT	GO:0030901~midbrain development	4	0.879121	0.00316	ENSG00000186051,	258	16	13528	13.10853	0.995013	0.992345	5.188989
yellow	GOTERM_BP_FAT	GO:0051252~regulation of RNA metabolic process	51	11.20879	0.003886	ENSG00000175322,	258	1813	13528	1.47498	0.998528	0.662735	6.344982
yellow	GOTERM_BP_FAT	GO:0051705~behavioral interaction between organisms	5	1.098901	0.004194	ENSG00000126010,	258	35	13528	7.490587	0.999123	0.63419	6.83154
yellow	GOTERM_BP_FAT	GO:0002285~lymphocyte activation during immune resp	4	0.879121	0.004477	ENSG00000197943,	258	18	13528	11.65202	0.999456	0.609163	7.27648
yellow	GOTERM_BP_FAT	GO:0002263~cell activation during immune response	5	1.098901	0.004649	ENSG00000137462,	258	36	13528	7.282515	0.999592	0.579879	7.54563
yellow	GOTERM_BP_FAT	GO:0002366~leukocyte activation during immune respon	5	1.098901	0.004649	ENSG00000137462,	258	36	13528	7.282515	0.999592	0.579879	7.54563
yellow	GOTERM_BP_FAT	GO:0050801~ion homeostasis	17	3.736264	0.00516	ENSG00000172005,	258	409	13528	2.179413	0.999828	0.579588	8.341681
yellow	GOTERM_BP_FAT	GO:0035176~social behavior	4	0.879121	0.005243	ENSG00000126010,	258	19	13528	11.03876	0.99985	0.550848	8.469784
yellow	GOTERM_BP_FAT	GO:0007586~digestion	7	1.538462	0.007702	ENSG00000198788,	258	91	13528	4.033393	0.999998	0.660121	12.20565
yellow	GOTERM_BP_FAT	GO:0007610~behavior	18	3.956044	0.008349	ENSG00000126010,	258	469	13528	2.012396	0.999999	0.660485	13.16504
yellow	GOTERM_BP_FAT	GO:0008544~epidermis development	10	2.197802	0.008616	ENSG00000158813,	258	184	13528	2.84968	0.999999	0.644872	13.55762
yellow	GOTERM_BP_FAT	GO:0042438~melanin biosynthetic process	3	0.659341	0.009334	ENSG00000123447,	258	8	13528	19.66279	1	0.649077	14.60604
yellow	GOTERM_BP_FAT	GO:0042756~drinking behavior	3	0.659341	0.009334	ENSG00000143839,	258	8	13528	19.66279	1	0.649077	14.60604
yellow	GOTERM_BP_FAT	GO:0006582~melanin metabolic process	3	0.659341	0.011851	ENSG00000123447,	258	9	13528	17.47804	1	0.712951	18.18704
yellow	GOTERM_BP_FAT	GO:0008217~regulation of blood pressure	7	1.538462	0.011972	ENSG00000143839,	258	100	13528	3.670388	1	0.694783	18.3553
yellow	GOTERM_BP_FAT	GO:0006873~cellular ion homeostasis	15	3.296703	0.012322	ENSG00000172005,	258	374	13528	2.102972	1	0.684548	18.84056
yellow	GOTERM_BP_FAT	GO:0021700~developmental maturation	7	1.538462	0.012532	ENSG00000143839,	258	101	13528	3.634047	1	0.671028	19.1308
yellow	GOTERM_BP_FAT	GO:0007398~ectoderm development	10	2.197802	0.013882	ENSG00000158813,	258	199	13528	2.63488	1	0.689869	20.97212
yellow	GOTERM_BP_FAT	GO:0048469~cell maturation	6	1.318681	0.013966	ENSG00000143839,	258	75	13528	4.194729	1	0.674308	21.08536
yellow	GOTERM_BP_FAT	GO:0055082~cellular chemical homeostasis	15	3.296703	0.013979	ENSG00000172005,	258	380	13528	2.069767	1	0.657622	21.10331
yellow	GOTERM_BP_FAT	GO:0044057~regulation of system process	13	2.857143	0.015196	ENSG00000117013,	258	309	13528	2.205966	1	0.672146	22.72709
yellow	GOTERM_BP_FAT	GO:0045087~innate immune response	8	1.758242	0.01628	ENSG00000115607,	258	138	13528	3.039658	1	0.681947	24.14589
yellow	GOTERM_BP_FAT	GO:0007411~axon guidance	7	1.538462	0.016282	ENSG00000162068,	258	107	13528	3.430269	1	0.667094	24.14933
yellow	GOTERM_BP_FAT	GO:0042592~homeostatic process	24	5.274725	0.016321	ENSG00000172005,	258	751	13528	1.675657	1	0.65358	24.1991
yellow	GOTERM_BP_FAT	GO:0007625~grooming behavior	3	0.659341	0.017659	ENSG00000101200,	258	11	13528	14.30021	1	0.668893	25.91718
yellow	GOTERM_BP_FAT	GO:0000904~cell morphogenesis involved in differentiati	11	2.417582	0.018352	ENSG00000162068,	258	244	13528	2.363833	1	0.66979	26.79163
yellow	GOTERM_BP_FAT	GO:0048878~chemical homeostasis	18	3.956044	0.018371	ENSG00000172005,	258	512	13528	1.843387	1	0.657326	26.81635
yellow	GOTERM_BP_FAT	GO:0019228~regulation of action potential in neuron	5	1.098901	0.019156	ENSG00000172005,	258	54	13528	4.85501	1	0.660387	27.79558
yellow	GOTERM_BP_FAT	GO:0051048~negative regulation of secretion	5	1.098901	0.02036	ENSG00000123612,	258	55	13528	4.766737	1	0.67091	29.27226
yellow	GOTERM_BP_FAT	GO:0030182~neuron differentiation	16	3.516484	0.02052	ENSG00000162068,	258	438	13528	1.915401	1	0.662194	29.46751
yellow	GOTERM_BP_FAT	GO:0007187~G-protein signaling, coupled to cyclic nucle	7	1.538462	0.022399	ENSG00000143199,	258	115	13528	3.191641	1	0.683318	31.71126
yellow	GOTERM_BP_FAT	GO:0007166~cell surface receptor linked signal transduct	48	10.54945	0.022845	ENSG00000126010,	258	1856	13528	1.356055	1	0.6797	32.23343
yellow	GOTERM_BP_FAT	GO:0006350~transcription	53	11.64835	0.024796	ENSG00000175322,	258	2101	13528	1.322707	1	0.699296	34.4762
yellow	GOTERM_BP_FAT	GO:0019229~regulation of vasoconstriction	4	0.879121	0.02629	ENSG00000135643,	258	34	13528	6.168719	1	0.710497	36.14607

yellow	GOTERM_BP_FAT	GO:0055074~calcium ion homeostasis	9	1.978022	0.027291	ENSG00000108702,	258	188	13528	2.510143	1	0.714255	37.24255
yellow	GOTERM_BP_FAT	GO:0046632~alpha-beta T cell differentiation	3	0.659341	0.028147	ENSG00000113302,	258	14	13528	11.23588	1	0.715914	38.16544
yellow	GOTERM_BP_FAT	GO:0007617~mating behavior	3	0.659341	0.028147	ENSG00000101200,	258	14	13528	11.23588	1	0.715914	38.16544
yellow	GOTERM_BP_FAT	GO:0031016~pancreas development	4	0.879121	0.028362	ENSG0000016082,	258	35	13528	5.99247	1	0.70937	38.3952
yellow	GOTERM_BP_FAT	GO:0048666~neuron development	13	2.857143	0.028835	ENSG00000162068,	258	339	13528	2.010748	1	0.706306	38.89856
yellow	GOTERM_BP_FAT	GO:0051960~regulation of nervous system development	9	1.978022	0.030355	ENSG00000148704,	258	192	13528	2.457849	1	0.716151	40.48863
yellow	GOTERM_BP_FAT	GO:0007409~axonogenesis	9	1.978022	0.031229	ENSG00000162068,	258	193	13528	2.445114	1	0.717843	41.38535
yellow	GOTERM_BP_FAT	GO:0021517~ventral spinal cord development	3	0.659341	0.032077	ENSG0000016082,	258	15	13528	10.48682	1	0.719161	42.2431
yellow	GOTERM_BP_FAT	GO:0030001~metal ion transport	16	3.516484	0.032301	ENSG00000117013,	258	465	13528	1.804184	1	0.713474	42.46784
yellow	GOTERM_BP_FAT	GO:0050877~neurological system process	33	7.252747	0.034612	ENSG00000126010,	258	1210	13528	1.430021	1	0.730491	44.73809
yellow	GOTERM_BP_FAT	GO:0042063~gliogenesis	5	1.098901	0.034946	ENSG00000184486,	258	65	13528	4.033393	1	0.72617	45.05911
yellow	GOTERM_BP_FAT	GO:0006940~regulation of smooth muscle contraction	4	0.879121	0.03508	ENSG00000101405,	258	38	13528	5.51938	1	0.719909	45.18748
yellow	GOTERM_BP_FAT	GO:0042552~myelination	4	0.879121	0.03508	ENSG00000172005,	258	38	13528	5.51938	1	0.719909	45.18748
yellow	GOTERM_BP_FAT	GO:0030908~protein splicing	2	0.43956	0.037636	ENSG00000163501,	258	2	13528	52.43411	1	0.737809	47.58139
yellow	GOTERM_BP_FAT	GO:0016539~intein-mediated protein splicing	2	0.43956	0.037636	ENSG00000163501,	258	2	13528	52.43411	1	0.737809	47.58139
yellow	GOTERM_BP_FAT	GO:0019935~cyclic-nucleotide-mediated signaling	7	1.538462	0.037685	ENSG00000143199,	258	130	13528	2.823375	1	0.73102	47.62668
yellow	GOTERM_BP_FAT	GO:0016477~cell migration	11	2.417582	0.038353	ENSG00000148704,	258	276	13528	2.089765	1	0.730211	48.23539
yellow	GOTERM_BP_FAT	GO:0051046~regulation of secretion	9	1.978022	0.03924	ENSG00000123612,	258	202	13528	2.336173	1	0.731454	49.03345
yellow	GOTERM_BP_FAT	GO:0050767~regulation of neurogenesis	8	1.758242	0.039266	ENSG00000148704,	258	166	13528	2.526945	1	0.724817	49.05653
yellow	GOTERM_BP_FAT	GO:0006955~immune response	21	4.615385	0.039808	ENSG00000186827,	258	690	13528	1.595821	1	0.723016	49.53802
yellow	GOTERM_BP_FAT	GO:0001508~regulation of action potential	5	1.098901	0.040249	ENSG00000172005,	258	68	13528	3.855449	1	0.720367	49.92698
yellow	GOTERM_BP_FAT	GO:0045664~regulation of neuron differentiation	7	1.538462	0.041382	ENSG0000016082,	258	133	13528	2.75969	1	0.723925	50.91298
yellow	GOTERM_BP_FAT	GO:0055065~metal ion homeostasis	9	1.978022	0.042158	ENSG00000108702,	258	205	13528	2.301985	1	0.724269	51.57802
yellow	GOTERM_BP_FAT	GO:0042391~regulation of membrane potential	7	1.538462	0.042663	ENSG00000172005,	258	134	13528	2.739095	1	0.722303	52.00606
yellow	GOTERM_BP_FAT	GO:0051051~negative regulation of transport	7	1.538462	0.043969	ENSG00000123612,	258	135	13528	2.718806	1	0.727076	53.09665
yellow	GOTERM_BP_FAT	GO:0046631~alpha-beta T cell activation	3	0.659341	0.045037	ENSG00000113302,	258	18	13528	8.739018	1	0.729719	53.97136
yellow	GOTERM_BP_FAT	GO:0019098~reproductive behavior	3	0.659341	0.045037	ENSG00000101200,	258	18	13528	8.739018	1	0.729719	53.97136
yellow	GOTERM_BP_FAT	GO:0007272~ensheathment of neurons	4	0.879121	0.045194	ENSG00000172005,	258	42	13528	4.993725	1	0.725024	54.09844
yellow	GOTERM_BP_FAT	GO:0008366~axon ensheathment	4	0.879121	0.045194	ENSG00000172005,	258	42	13528	4.993725	1	0.725024	54.09844
yellow	GOTERM_BP_FAT	GO:0048663~neuron fate commitment	4	0.879121	0.045194	ENSG0000016082,	258	42	13528	4.993725	1	0.725024	54.09844
yellow	GOTERM_BP_FAT	GO:0048667~cell morphogenesis involved in neuron diffe	9	1.978022	0.046363	ENSG00000162068,	258	209	13528	2.257928	1	0.728432	55.03546
yellow	GOTERM_BP_FAT	GO:0009725~response to hormone stimulus	13	2.857143	0.04782	ENSG00000155846,	258	367	13528	1.857339	1	0.733885	56.17824
yellow	GOTERM_BP_FAT	GO:0048812~neuron projection morphogenesis	9	1.978022	0.050783	ENSG00000162068,	258	213	13528	2.215526	1	0.749848	58.41874
yellow	GOTERM_BP_FAT	GO:0007498~mesoderm development	5	1.098901	0.052152	ENSG00000113196,	258	74	13528	3.542845	1	0.753846	59.41673
yellow	GOTERM_BP_FAT	GO:0043010~camera-type eye development	6	1.318681	0.053176	ENSG00000148704,	258	107	13528	2.94023	1	0.755389	60.14869
yellow	GOTERM_BP_FAT	GO:0006816~calcium ion transport	7	1.538462	0.053811	ENSG00000119411,	258	142	13528	2.58478	1	0.754329	60.5959
yellow	GOTERM_BP_FAT	GO:0002125~maternal aggressive behavior	2	0.43956	0.055921	ENSG00000101200,	258	3	13528	34.95607	1	0.762749	62.04993
yellow	GOTERM_BP_FAT	GO:0060406~positive regulation of penile erection	2	0.43956	0.055921	ENSG00000101405,	258	3	13528	34.95607	1	0.762749	62.04993
yellow	GOTERM_BP_FAT	GO:0031175~neuron projection development	10	2.197802	0.056055	ENSG00000162068,	258	256	13528	2.048207	1	0.758523	62.14064
yellow	GOTERM_BP_FAT	GO:0010033~response to organic substance	21	4.615385	0.057883	ENSG00000155846,	258	721	13528	1.527207	1	0.764827	63.35609
yellow	GOTERM_BP_FAT	GO:0007204~elevation of cytosolic calcium ion concentra	6	1.318681	0.058548	ENSG00000101200,	258	110	13528	2.860042	1	0.763937	63.78926
yellow	GOTERM_BP_FAT	GO:0006811~ion transport	22	4.835165	0.059073	ENSG00000117013,	258	768	13528	1.502019	1	0.762236	64.12756
yellow	GOTERM_BP_FAT	GO:0006874~cellular calcium ion homeostasis	8	1.758242	0.060379	ENSG00000108702,	258	183	13528	2.292201	1	0.76516	64.95703
yellow	GOTERM_BP_FAT	GO:0006812~cation transport	17	3.736264	0.060849	ENSG00000117013,	258	553	13528	1.611898	1	0.763188	65.25114
yellow	GOTERM_BP_FAT	GO:0019725~cellular homeostasis	15	3.296703	0.061302	ENSG00000172005,	258	466	13528	1.687793	1	0.761153	65.53195
yellow	GOTERM_BP_FAT	GO:0006357~regulation of transcription from RNA polym	21	4.615385	0.061604	ENSG00000155846,	258	727	13528	1.514603	1	0.758293	65.71828
yellow	GOTERM_BP_FAT	GO:0051050~positive regulation of transport	9	1.978022	0.062973	ENSG00000186827,	258	223	13528	2.116175	1	0.761533	66.55084
yellow	GOTERM_BP_FAT	GO:0001525~angiogenesis	7	1.538462	0.06323	ENSG00000128917,	258	148	13528	2.479992	1	0.758496	66.70487

yellow	GOTERM_BP_FAT	GO:0001947~heart looping	3	0.659341	0.064734	ENSG00000113196,	258	22	13528	7.150106	1	0.762396	67.59332
yellow	GOTERM_BP_FAT	GO:0007267~cell-cell signaling	18	3.956044	0.066565	ENSG00000101200,	258	600	13528	1.573023	1	0.767883	68.64526
yellow	GOTERM_BP_FAT	GO:0051674~localization of cell	11	2.417582	0.0689	ENSG00000148704,	258	307	13528	1.878747	1	0.775683	69.93992
yellow	GOTERM_BP_FAT	GO:0048870~cell motility	11	2.417582	0.0689	ENSG00000148704,	258	307	13528	1.878747	1	0.775683	69.93992
yellow	GOTERM_BP_FAT	GO:0019226~transmission of nerve impulse	12	2.637363	0.070952	ENSG00000172005,	258	350	13528	1.797741	1	0.781695	71.03606
yellow	GOTERM_BP_FAT	GO:0014031~mesenchymal cell development	4	0.879121	0.072543	ENSG00000016082,	258	51	13528	4.112479	1	0.785257	71.85987
yellow	GOTERM_BP_FAT	GO:0048762~mesenchymal cell differentiation	4	0.879121	0.072543	ENSG00000016082,	258	51	13528	4.112479	1	0.785257	71.85987
yellow	GOTERM_BP_FAT	GO:0050670~regulation of lymphocyte proliferation	5	1.098901	0.073205	ENSG00000186827,	258	83	13528	3.158681	1	0.784373	72.19655
yellow	GOTERM_BP_FAT	GO:0042441~eye pigment metabolic process	2	0.43956	0.07386	ENSG00000123447,	258	4	13528	26.21705	1	0.783472	72.52554
yellow	GOTERM_BP_FAT	GO:0048069~eye pigmentation	2	0.43956	0.07386	ENSG00000123447,	258	4	13528	26.21705	1	0.783472	72.52554
yellow	GOTERM_BP_FAT	GO:0006726~eye pigment biosynthetic process	2	0.43956	0.07386	ENSG00000123447,	258	4	13528	26.21705	1	0.783472	72.52554
yellow	GOTERM_BP_FAT	GO:0060405~regulation of penile erection	2	0.43956	0.07386	ENSG00000101405,	258	4	13528	26.21705	1	0.783472	72.52554
yellow	GOTERM_BP_FAT	GO:0002118~aggressive behavior	2	0.43956	0.07386	ENSG00000101200,	258	4	13528	26.21705	1	0.783472	72.52554
yellow	GOTERM_BP_FAT	GO:0051480~cytosolic calcium ion homeostasis	6	1.318681	0.074333	ENSG00000101200,	258	118	13528	2.666141	1	0.781747	72.76077
yellow	GOTERM_BP_FAT	GO:0032944~regulation of mononuclear cell proliferation	5	1.098901	0.075776	ENSG00000186827,	258	84	13528	3.121078	1	0.784496	73.46665
yellow	GOTERM_BP_FAT	GO:0070663~regulation of leukocyte proliferation	5	1.098901	0.075776	ENSG00000186827,	258	84	13528	3.121078	1	0.784496	73.46665
yellow	GOTERM_BP_FAT	GO:0060485~mesenchyme development	4	0.879121	0.07595	ENSG00000016082,	258	52	13528	4.033393	1	0.781456	73.55092
yellow	GOTERM_BP_FAT	GO:0007200~activation of phospholipase C activity by G	4	0.879121	0.07595	ENSG00000132911,	258	52	13528	4.033393	1	0.781456	73.55092
yellow	GOTERM_BP_FAT	GO:0000902~cell morphogenesis	12	2.637363	0.078228	ENSG00000162068,	258	356	13528	1.767442	1	0.787852	74.62764
yellow	GOTERM_BP_FAT	GO:0019932~second-messenger-mediated signaling	9	1.978022	0.07994	ENSG00000143199,	258	235	13528	2.008115	1	0.791544	75.40927
yellow	GOTERM_BP_FAT	GO:0006875~cellular metal ion homeostasis	8	1.758242	0.080453	ENSG00000108702,	258	196	13528	2.140168	1	0.790073	75.63929
yellow	GOTERM_BP_FAT	GO:0021515~cell differentiation in spinal cord	3	0.659341	0.081042	ENSG00000016082,	258	25	13528	6.292093	1	0.788944	75.90067
yellow	GOTERM_BP_FAT	GO:0006813~potassium ion transport	7	1.538462	0.084806	ENSG00000117013,	258	160	13528	2.293992	1	0.800801	77.50986
yellow	GOTERM_BP_FAT	GO:0009719~response to endogenous stimulus	13	2.857143	0.084899	ENSG00000155846,	258	405	13528	1.68307	1	0.797683	77.54803
yellow	GOTERM_BP_FAT	GO:0055066~di-, tri-valent inorganic cation homeostasis	9	1.978022	0.086174	ENSG00000108702,	258	239	13528	1.974506	1	0.799268	78.06932
yellow	GOTERM_BP_FAT	GO:0044243~multicellular organismal catabolic process	3	0.659341	0.086732	ENSG00000156140,	258	26	13528	6.050089	1	0.798032	78.29367
yellow	GOTERM_BP_FAT	GO:0048066~pigmentation during development	3	0.659341	0.086732	ENSG00000123447,	258	26	13528	6.050089	1	0.798032	78.29367
yellow	GOTERM_BP_FAT	GO:0060180~female mating behavior	2	0.43956	0.09146	ENSG000000101200,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0002002~regulation of angiotensin levels in blood	2	0.43956	0.09146	ENSG00000143839,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0002293~alpha-beta T cell differentiation during imm	2	0.43956	0.09146	ENSG00000113302,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0060177~regulation of angiotensin metabolic proces	2	0.43956	0.09146	ENSG00000143839,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0002312~B cell activation during immune response	2	0.43956	0.09146	ENSG00000197943,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0002287~alpha-beta T cell activation during immune	2	0.43956	0.09146	ENSG00000113302,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0002292~T cell differentiation during immune respon	2	0.43956	0.09146	ENSG00000113302,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0045924~regulation of female receptivity	2	0.43956	0.09146	ENSG00000101200,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0002313~mature B cell differentiation during immune	2	0.43956	0.09146	ENSG00000197943,	258	5	13528	20.97364	1	0.812418	80.10998
yellow	GOTERM_BP_FAT	GO:0007618~mating	3	0.659341	0.092538	ENSG00000101200,	258	27	13528	5.826012	1	0.813028	80.50377
yellow	GOTERM_BP_FAT	GO:0030030~cell projection organization	12	2.637363	0.092748	ENSG00000162068,	258	368	13528	1.709808	1	0.810552	80.57954
yellow	GOTERM_BP_FAT	GO:0055080~cation homeostasis	10	2.197802	0.095689	ENSG00000115616,	258	286	13528	1.83336	1	0.817638	81.61256
yellow	GOTERM_BP_FAT	GO:0048858~cell projection morphogenesis	9	1.978022	0.095923	ENSG00000162068,	258	245	13528	1.926151	1	0.81531	81.69246
yellow	GOTERM_BP_FAT	GO:0060284~regulation of cell development	8	1.758242	0.096289	ENSG00000148704,	258	205	13528	2.046209	1	0.813452	81.81681
yellow	GOTERM_CC_FAT	GO:0005576~extracellular region	63	13.84615	2.18E-05	ENSG00000148386,	238	2010	12782	1.683319	0.004701	0.004701	0.027681
yellow	GOTERM_CC_FAT	GO:0031224~intrinsic to membrane	127	27.91209	8.58E-04	ENSG00000171124,	238	5485	12782	1.243509	0.169179	0.088506	1.083122
yellow	GOTERM_CC_FAT	GO:0016021~integral to membrane	121	26.59341	0.002444	ENSG00000171124,	238	5297	12782	1.22681	0.410489	0.161511	3.057444
yellow	GOTERM_CC_FAT	GO:0044421~extracellular region part	31	6.813187	0.003327	ENSG00000162068,	238	960	12782	1.734252	0.51315	0.164688	4.141225
yellow	GOTERM_CC_FAT	GO:0005887~integral to plasma membrane	36	7.912088	0.003986	ENSG00000126010,	238	1188	12782	1.627451	0.578022	0.158493	4.94332
yellow	GOTERM_CC_FAT	GO:0031226~intrinsic to plasma membrane	36	7.912088	0.005671	ENSG00000126010,	238	1215	12782	1.591285	0.707233	0.185133	6.963428
yellow	GOTERM_CC_FAT	GO:0001533~cornified envelope	4	0.879121	0.007471	ENSG00000203782,	238	22	12782	9.764706	0.802047	0.206569	9.07837

yellow	GOTERM_CC_FAT	GO:0005886~plasma membrane	88	19.34066	0.009931	ENSG00000126010,	238	3777	12782	1.251289	0.884181	0.236213	11.89729
yellow	GOTERM_CC_FAT	GO:0044459~plasma membrane part	54	11.86813	0.024201	ENSG00000126010,	238	2203	12782	1.31644	0.994967	0.444544	26.72358
yellow	GOTERM_CC_FAT	GO:0045121~membrane raft	7	1.538462	0.050215	ENSG00000121743,	238	143	12782	2.628959	0.999985	0.671371	47.99746
yellow	GOTERM_CC_FAT	GO:0005615~extracellular space	20	4.395604	0.051887	ENSG00000108702,	238	685	12782	1.568055	0.99999	0.648753	49.14773
yellow	GOTERM_CC_FAT	GO:0005578~proteinaceous extracellular matrix	11	2.417582	0.074807	ENSG00000169436,	238	320	12782	1.84614	1	0.753294	62.72434
yellow	GOTERM_CC_FAT	GO:0034702~ion channel complex	8	1.758242	0.087837	ENSG00000117013,	238	205	12782	2.095839	1	0.782937	68.86519
yellow	GOTERM_MF_FAT	GO:0015267~channel activity	18	3.956044	0.002653	ENSG00000117013,	251	412	12983	2.259834	0.686835	0.686835	3.683847
yellow	GOTERM_MF_FAT	GO:0022803~passive transmembrane transporter activity	18	3.956044	0.002705	ENSG00000117013,	251	413	12983	2.254363	0.693867	0.446707	3.754541
yellow	GOTERM_MF_FAT	GO:0022838~substrate specific channel activity	16	3.516484	0.010284	ENSG00000117013,	251	398	12983	2.079401	0.989084	0.778166	13.58797
yellow	GOTERM_MF_FAT	GO:0003700~transcription factor activity	30	6.593407	0.012692	ENSG00000091656,	251	975	12983	1.591542	0.996235	0.752289	16.5111
yellow	GOTERM_MF_FAT	GO:0022836~gated channel activity	13	2.857143	0.017052	ENSG00000117013,	251	310	12983	2.169117	0.999456	0.777587	21.57159
yellow	GOTERM_MF_FAT	GO:0005216~ion channel activity	15	3.296703	0.017538	ENSG00000117013,	251	386	12983	2.010043	0.999561	0.724362	22.11708
yellow	GOTERM_MF_FAT	GO:0003677~DNA binding	59	12.96703	0.02027	ENSG00000175322,	251	2331	12983	1.309215	0.99987	0.721528	25.12194
yellow	GOTERM_MF_FAT	GO:0005509~calcium ion binding	27	5.934066	0.03106	ENSG00000128917,	251	919	12983	1.519671	0.999999	0.821566	35.96593
yellow	GOTERM_MF_FAT	GO:0005229~intracellular calcium activated chloride chan	2	0.43956	0.038143	ENSG00000132911,	251	2	12983	51.7251	1	0.848668	42.27076
yellow	GOTERM_MF_FAT	GO:0031895~V1B vasopressin receptor binding	2	0.43956	0.038143	ENSG00000101200,	251	2	12983	51.7251	1	0.848668	42.27076
yellow	GOTERM_MF_FAT	GO:0031855~oxytocin receptor binding	2	0.43956	0.038143	ENSG00000101200,	251	2	12983	51.7251	1	0.848668	42.27076
yellow	GOTERM_MF_FAT	GO:0008188~neuropeptide receptor activity	4	0.879121	0.041332	ENSG00000126010,	251	40	12983	51.7251	1	0.841911	44.91703
yellow	GOTERM_MF_FAT	GO:0022839~ion gated channel activity	3	0.659341	0.041532	ENSG00000135643,	251	17	12983	9.127959	1	0.814592	45.07923
yellow	GOTERM_MF_FAT	GO:0005267~potassium channel activity	7	1.538462	0.043671	ENSG00000117013,	251	133	12983	2.722374	1	0.803307	46.78529
yellow	GOTERM_MF_FAT	GO:0042923~neuropeptide binding	4	0.879121	0.043981	ENSG00000126010,	251	41	12983	5.046351	1	0.77952	47.029
yellow	GOTERM_MF_FAT	GO:0043565~sequence-specific DNA binding	19	4.175824	0.047282	ENSG00000214513,	251	607	12983	1.619072	1	0.779513	49.55524
yellow	GOTERM_MF_FAT	GO:0031894~V1A vasopressin receptor binding	2	0.43956	0.056667	ENSG00000101200,	251	3	12983	34.4834	1	0.817228	56.13886
yellow	GOTERM_MF_FAT	GO:0031893~vasopressin receptor binding	2	0.43956	0.056667	ENSG00000101200,	251	3	12983	34.4834	1	0.817228	56.13886
yellow	GOTERM_MF_FAT	GO:0005113~patched binding	2	0.43956	0.056667	ENSG00000163501,	251	3	12983	34.4834	1	0.817228	56.13886
yellow	GOTERM_MF_FAT	GO:0031404~chloride ion binding	5	1.098901	0.061111	ENSG00000039987,	251	77	12983	3.358773	1	0.821338	58.96922
yellow	GOTERM_MF_FAT	GO:0001653~peptide receptor activity	6	1.318681	0.069226	ENSG00000126010,	251	114	12983	2.722374	1	0.841832	63.7049
yellow	GOTERM_MF_FAT	GO:0008528~peptide receptor activity, G-protein couple	6	1.318681	0.069226	ENSG00000126010,	251	114	12983	2.722374	1	0.841832	63.7049
yellow	GOTERM_MF_FAT	GO:0005244~voltage-gated ion channel activity	8	1.758242	0.084186	ENSG00000117013,	251	195	12983	2.122055	1	0.881759	71.1309
yellow	GOTERM_MF_FAT	GO:0022832~voltage-gated channel activity	8	1.758242	0.084186	ENSG00000117013,	251	195	12983	2.122055	1	0.881759	71.1309
yellow	GOTERM_MF_FAT	GO:0005125~cytokine activity	8	1.758242	0.084186	ENSG00000108702,	251	195	12983	2.122055	1	0.881759	71.1309
yellow	GOTERM_MF_FAT	GO:0005261~cation channel activity	10	2.197802	0.084763	ENSG00000117013,	251	275	12983	1.880913	1	0.869603	71.38711
yellow	HIV_INTERACTION	env:Envelope surface glycoprotein gp120	12	2.637363	0.089951	ENSG00000204007,	21	529	1394	1.505806	0.571861	0.571861	41.86757
yellow	INTERPRO	IPR013087:Zinc finger, C2H2-type/integrase, DNA-binding	25	5.494505	8.76E-04	ENSG00000175322,	319	621	16659	2.102358	0.403618	0.403618	1.282596
yellow	INTERPRO	IPR007087:Zinc finger, C2H2-type	28	6.153846	0.002299	ENSG00000175322,	319	784	16659	1.865092	0.742768	0.49282	3.334204
yellow	INTERPRO	IPR015880:Zinc finger, C2H2-like	28	6.153846	0.002894	ENSG00000175322,	319	797	16659	1.83467	0.81915	0.434491	4.181028
yellow	INTERPRO	IPR017970:Homeobox, conserved site	12	2.637363	0.005114	ENSG00000148704,	319	232	16659	2.701167	0.951449	0.530594	7.276953
yellow	INTERPRO	IPR001356:Homeobox	12	2.637363	0.005622	ENSG00000148704,	319	235	16659	2.666684	0.964071	0.485851	7.971526
yellow	INTERPRO	IPR012287:Homeodomain-related	12	2.637363	0.006172	ENSG00000148704,	319	238	16659	2.633071	0.974087	0.456015	8.719575
yellow	INTERPRO	IPR013032:EGF-like region, conserved site	13	2.857143	0.010865	ENSG00000156076,	319	293	16659	2.317042	0.998412	0.601787	14.86854
yellow	INTERPRO	IPR001909:Krueppel-associated box	14	3.076923	0.019209	ENSG00000175322,	319	355	16659	2.059482	0.999989	0.760801	24.85919
yellow	INTERPRO	IPR011598:Helix-loop-helix DNA-binding	6	1.318681	0.022278	ENSG00000113196,	319	84	16659	3.730184	0.999998	0.771669	28.25014
yellow	INTERPRO	IPR004075:Interleukin-1 receptor, type I/Toll precursor	3	0.659341	0.02466	ENSG00000115607,	319	13	16659	12.05136	1	0.770798	30.78274
yellow	INTERPRO	IPR016321:Nonapeptide hormone precursor	2	0.43956	0.037814	ENSG00000101200,	319	2	16659	52.22257	1	0.873507	43.33494
yellow	INTERPRO	IPR000981:Neurohypophysial hormone	2	0.43956	0.037814	ENSG00000101200,	319	2	16659	52.22257	1	0.873507	43.33494
yellow	INTERPRO	IPR006141:Intein splicing site	2	0.43956	0.037814	ENSG00000163501,	319	2	16659	52.22257	1	0.873507	43.33494
yellow	INTERPRO	IPR003587:Hedgehog/intein hint, N-terminal	2	0.43956	0.056183	ENSG00000163501,	319	3	16659	34.81505	1	0.941749	57.3458
yellow	INTERPRO	IPR001767:Peptidase C46, hedgehog protein, hint region	2	0.43956	0.056183	ENSG00000163501,	319	3	16659	34.81505	1	0.941749	57.3458

yellow	INTERPRO	IPR001657:Peptidase C46, hedgehog protein	2	0.43956	0.056183	ENSG00000163501,	319	3	16659	34.81505	1	0.941749	57.3458
yellow	INTERPRO	IPR003586:Hedgehog/intein hint domain, C-terminal	2	0.43956	0.056183	ENSG00000163501,	319	3	16659	34.81505	1	0.941749	57.3458
yellow	INTERPRO	IPR000320:Hedgehog amino-terminal signaling region	2	0.43956	0.056183	ENSG00000163501,	319	3	16659	34.81505	1	0.941749	57.3458
yellow	INTERPRO	IPR005821:Ion transport	6	1.318681	0.059663	ENSG00000117013,	319	110	16659	2.848504	1	0.938698	59.60539
yellow	INTERPRO	IPR008957:Fibronectin, type III-like fold	8	1.758242	0.062628	ENSG00000080224,	319	184	16659	2.270547	1	0.934493	61.44207
yellow	INTERPRO	IPR003129:Laminin G, thrombospondin-type, N-terminal	3	0.659341	0.065305	ENSG00000169436,	319	22	16659	7.12126	1	0.929797	63.03292
yellow	INTERPRO	IPR001092:Basic helix-loop-helix dimerisation region bHL	6	1.318681	0.067409	ENSG00000113196,	319	114	16659	2.748556	1	0.92373	64.24072
yellow	INTERPRO	IPR000157:Toll-Interleukin receptor	3	0.659341	0.070649	ENSG00000115607,	319	23	16659	6.81164	1	0.921357	66.02781
yellow	INTERPRO	IPR003961:Fibronectin, type III	8	1.758242	0.072469	ENSG00000080224,	319	190	16659	2.198845	1	0.915062	66.99516
yellow	INTERPRO	IPR003302:Cornein (SPRR)	2	0.43956	0.074203	ENSG00000169474,	319	4	16659	26.11129	1	0.908751	67.89293
yellow	INTERPRO	IPR000742:EGF-like, type 3	8	1.758242	0.078932	ENSG00000128917,	319	194	16659	2.153508	1	0.911569	70.22664
yellow	INTERPRO	IPR006207:Cystine knot, C-terminal	3	0.659341	0.081739	ENSG00000198788,	319	25	16659	6.266708	1	0.9089	71.53615
yellow	INTERPRO	IPR006210:EGF-like	8	1.758242	0.091029	ENSG00000128917,	319	201	16659	2.07851	1	0.922663	75.49681
yellow	INTERPRO	IPR006209:EGF	6	1.318681	0.096221	ENSG00000128917,	319	127	16659	2.467208	1	0.925372	77.48005
yellow	INTERPRO	IPR016160:Aldehyde dehydrogenase, conserved site	3	0.659341	0.09928	ENSG00000137462,	319	28	16659	5.595275	1	0.923499	78.57755
yellow	KEGG_PATHWAY	hsa04080:Neuroactive ligand-receptor interaction	12	2.637363	0.006586	ENSG00000126010,	94	256	5085	2.535738	0.444591	0.444591	6.921253
yellow	KEGG_PATHWAY	hsa04060:Cytokine-cytokine receptor interaction	11	2.417582	0.020525	ENSG00000175189,	94	262	5085	2.271195	0.842092	0.602623	20.15831
yellow	OMIM_DISEASE	A genomewide association study of skin pigmentation in	2	0.43956	0.047458	ENSG00000123447,	60	3	3671	40.78889	0.998946	0.998946	43.69533
yellow	OMIM_DISEASE	Sequence variants in the autophagy gene IRGM and mul	2	0.43956	0.077859	ENSG00000113302,	60	5	3671	24.47333	0.999989	0.996702	61.61811
yellow	PIR_SUPERFAMILY	PIRSF001815:Nonapeptide_hormone_precursor	2	0.43956	0.036441	ENSG00000101200,	137	2	7396	53.9854	0.996829	0.996829	35.96919
yellow	PIR_SUPERFAMILY	PIRSF001815:nonapeptide hormone precursor	2	0.43956	0.036441	ENSG00000101200,	137	2	7396	53.9854	0.996829	0.996829	35.96919
yellow	PIR_SUPERFAMILY	PIRSF005559:zinc finger protein ZFP-36	7	1.538462	0.040204	ENSG00000175322,	137	137	7396	2.758378	0.998271	0.958421	38.90834
yellow	PIR_SUPERFAMILY	PIRSF009400:Peptidase_C46	2	0.43956	0.054164	ENSG00000163501,	137	3	7396	35.99027	0.999822	0.943703	48.76537
yellow	PIR_SUPERFAMILY	PIRSF009400:hedgehog protein	2	0.43956	0.054164	ENSG00000163501,	137	3	7396	35.99027	0.999822	0.943703	48.76537
yellow	PIR_SUPERFAMILY	PIRSF002642:transcription factor isl-1	2	0.43956	0.071563	ENSG0000016082,	137	4	7396	26.9927	0.99999	0.943714	59.00555
yellow	SMART	SM00389:HOX	12	2.637363	0.015296	ENSG00000148704,	202	235	9079	2.295092	0.893016	0.893016	16.72254
yellow	SMART	SM00355:ZnF_C2H2	28	6.153846	0.016768	ENSG00000175322,	202	797	9079	1.579015	0.913872	0.706524	18.188
yellow	SMART	SM00003:NH	2	0.43956	0.04379	ENSG00000101200,	202	2	9079	44.94554	0.998486	0.885166	41.23279
yellow	SMART	SM00349:KRAB	14	3.076923	0.051586	ENSG00000175322,	202	355	9079	1.7725	0.999538	0.853383	46.67494
yellow	SMART	SM00306:HintN	2	0.43956	0.064964	ENSG00000163501,	202	3	9079	29.9637	0.999941	0.857434	54.95119
yellow	SMART	SM00305:HintC	2	0.43956	0.064964	ENSG00000163501,	202	3	9079	29.9637	0.999941	0.857434	54.95119
yellow	SMART	SM00210:TSPN	3	0.659341	0.08436	ENSG00000169436,	202	22	9079	6.128938	0.999997	0.881145	64.87523
yellow	SMART	SM00255:TIR	3	0.659341	0.091093	ENSG00000115607,	202	23	9079	5.862462	0.999999	0.86172	67.82193
yellow	SP_PIR_KEYWORDS	glycoprotein	127	27.91209	2.97E-08	ENSG00000171124,	361	4318	19235	1.567134	9.40E-06	9.40E-06	4.00E-05
yellow	SP_PIR_KEYWORDS	Secreted	59	12.96703	4.42E-06	ENSG00000148386,	361	1689	19235	1.861261	0.001399	7.00E-04	0.005949
yellow	SP_PIR_KEYWORDS	signal	95	20.87912	5.65E-06	ENSG00000148386,	361	3250	19235	1.55749	0.00179	5.97E-04	0.007617
yellow	SP_PIR_KEYWORDS	cleavage on pair of basic residues	16	3.516484	1.94E-04	ENSG00000175189,	361	271	19235	3.145833	0.059596	0.015244	0.260859
yellow	SP_PIR_KEYWORDS	disulfide bond	80	17.58242	3.82E-04	ENSG00000126010,	361	2924	19235	1.457799	0.114041	0.023926	0.513394
yellow	SP_PIR_KEYWORDS	dna-binding	54	11.86813	0.001435	ENSG00000175322,	361	1868	19235	1.540288	0.365612	0.073044	1.915962
yellow	SP_PIR_KEYWORDS	developmental protein	28	6.153846	0.00162	ENSG00000163501,	361	779	19235	1.915162	0.401878	0.070792	2.161092
yellow	SP_PIR_KEYWORDS	transcription regulation	55	12.08791	0.004804	ENSG00000175322,	361	2026	19235	1.446466	0.782728	0.173724	6.283345
yellow	SP_PIR_KEYWORDS	Homeobox	12	2.637363	0.006089	ENSG00000148704,	361	242	19235	2.64211	0.855729	0.193554	7.900412
yellow	SP_PIR_KEYWORDS	autocatalytic cleavage	4	0.879121	0.006733	ENSG00000198788,	361	21	19235	10.14906	0.882517	0.192769	8.701051
yellow	SP_PIR_KEYWORDS	ionic channel	14	3.076923	0.007161	ENSG00000117013,	361	318	19235	2.345773	0.897538	0.187074	9.230436
yellow	SP_PIR_KEYWORDS	transmembrane	114	25.05495	0.01011	ENSG00000171124,	361	4973	19235	1.221438	0.960094	0.235426	12.79696
yellow	SP_PIR_KEYWORDS	Transcription	54	11.86813	0.011419	ENSG00000175322,	361	2071	19235	1.389308	0.973763	0.244251	14.33773
yellow	SP_PIR_KEYWORDS	Signal-anchor	16	3.516484	0.013501	ENSG00000198108,	361	421	19235	2.02499	0.986551	0.264921	16.73695
yellow	SP_PIR_KEYWORDS	cell membrane	55	12.08791	0.022182	ENSG00000126010,	361	2194	19235	1.335707	0.999184	0.377531	26.08664

yellow	SP_PIR_KEYWORDS	voltage-gated channel	8	1.758242	0.02299	ENSG00000117013,	361	150	19235	2.841736	0.999372	0.369221	26.90488
yellow	SP_PIR_KEYWORDS	Albinism	3	0.659341	0.0274	ENSG00000123447,	361	14	19235	11.41769	0.99985	0.40433	31.22857
yellow	SP_PIR_KEYWORDS	tumor antigen	4	0.879121	0.033846	ENSG00000123447,	361	38	19235	5.608689	0.999982	0.454683	37.12258
yellow	SP_PIR_KEYWORDS	amidated carboxyl end	3	0.659341	0.039475	ENSG00000101200,	361	17	19235	9.402803	0.999997	0.48929	41.88317
yellow	SP_PIR_KEYWORDS	receptor	40	8.791209	0.047109	ENSG00000126010,	361	1583	19235	1.346369	1	0.534587	47.80798
yellow	SP_PIR_KEYWORDS	palmitate	9	1.978022	0.047601	ENSG00000126010,	361	213	19235	2.251375	1	0.521074	48.17006
yellow	SP_PIR_KEYWORDS	tandem repeat	5	1.098901	0.05208	ENSG00000198788,	361	75	19235	3.55217	1	0.537301	51.36048
yellow	SP_PIR_KEYWORDS	chloride	5	1.098901	0.05208	ENSG00000039987,	361	75	19235	3.55217	1	0.537301	51.36048
yellow	SP_PIR_KEYWORDS	potassium channel	5	1.098901	0.058571	ENSG00000117013,	361	78	19235	3.415548	1	0.564763	55.66146
yellow	SP_PIR_KEYWORDS	membrane	132	29.01099	0.064797	ENSG00000171124,	361	6256	19235	1.124248	1	0.587223	59.45399
yellow	SP_PIR_KEYWORDS	potassium transport	6	1.318681	0.065051	ENSG00000117013,	361	115	19235	2.779959	1	0.573821	59.60198
yellow	SP_PIR_KEYWORDS	cataract	4	0.879121	0.0669	ENSG00000121743,	361	50	19235	4.262604	1	0.570115	60.66576
yellow	SP_PIR_KEYWORDS	egf-like domain	9	1.978022	0.068272	ENSG00000128917,	361	230	19235	2.084969	1	0.564054	61.4377
yellow	SP_PIR_KEYWORDS	calcium	22	4.835165	0.077293	ENSG00000151005,	361	803	19235	1.459796	1	0.597774	66.17621
yellow	SP_PIR_KEYWORDS	peroxidase	3	0.659341	0.079028	ENSG00000095303,	361	25	19235	6.393906	1	0.593392	67.02317
yellow	SP_PIR_KEYWORDS	potassium	6	1.318681	0.088142	ENSG00000117013,	361	126	19235	2.537264	1	0.622808	71.15938
yellow	UP_SEQ_FEATURE	glycosylation site:N-linked (GlcNAc...)	122	26.81319	4.47E-08	ENSG00000171124,	358	4129	19113	1.577469	4.74E-05	4.74E-05	7.11E-05
yellow	UP_SEQ_FEATURE	signal peptide	95	20.87912	5.09E-06	ENSG00000148386,	358	3250	19113	1.56058	0.005389	0.002698	0.0081
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 8	22	4.835165	4.13E-05	ENSG00000175322,	358	417	19113	2.816647	0.042941	0.014523	0.065775
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 7	23	5.054945	4.40E-05	ENSG00000175322,	358	451	19113	2.722683	0.045648	0.011613	0.070018
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 6	24	5.274725	5.01E-05	ENSG00000175322,	358	488	19113	2.625653	0.051859	0.010594	0.079801
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 5	25	5.494505	8.13E-05	ENSG00000175322,	358	538	19113	2.480867	0.082701	0.014284	0.129324
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 2	26	5.714286	2.07E-04	ENSG00000175322,	358	608	19113	2.283051	0.1977	0.030978	0.329675
yellow	UP_SEQ_FEATURE	topological domain:Cytoplasmic	90	19.78022	3.05E-04	ENSG00000126010,	358	3374	19113	1.424109	0.276956	0.039725	0.484969
yellow	UP_SEQ_FEATURE	topological domain:Extracellular	75	16.48352	4.63E-04	ENSG00000126010,	358	2719	19113	1.472644	0.388223	0.053135	0.73395
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 4	24	5.274725	5.40E-04	ENSG00000175322,	358	575	19113	2.22838	0.436534	0.05575	0.856289
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 10	17	3.736264	5.85E-04	ENSG00000175322,	358	334	19113	2.717367	0.462668	0.054903	0.926851
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 9	18	3.956044	7.58E-04	ENSG00000175322,	358	376	19113	2.555821	0.552971	0.064893	1.199747
yellow	UP_SEQ_FEATURE	disulfide bond	75	16.48352	0.001293	ENSG00000126010,	358	2819	19113	1.420404	0.746947	0.10031	2.038976
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 3	24	5.274725	0.001539	ENSG00000175322,	358	622	19113	2.059997	0.805266	0.110295	2.422928
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 12	13	2.857143	0.002894	ENSG00000175691,	358	252	19113	2.754157	0.953954	0.185522	4.509673
yellow	UP_SEQ_FEATURE	DNA-binding region:Homeobox	11	2.417582	0.003134	ENSG00000148704,	358	190	19113	3.0909	0.964334	0.188074	4.87462
yellow	UP_SEQ_FEATURE	transmembrane region	113	24.83516	0.008743	ENSG00000171124,	358	4911	19113	1.228441	0.999911	0.422246	13.04801
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 11	12	2.637363	0.022364	ENSG00000175691,	358	293	19113	2.18655	1	0.736696	30.23888
yellow	UP_SEQ_FEATURE	domain:KRAB	13	2.857143	0.022756	ENSG00000175322,	358	332	19113	2.090504	1	0.723808	30.68349
yellow	UP_SEQ_FEATURE	domain:EGF-like 4	5	1.098901	0.023037	ENSG00000128917,	358	58	19113	4.602437	1	0.709908	30.99929
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1	18	3.956044	0.026647	ENSG00000189420,	358	542	19113	1.773042	1	0.744835	34.94869
yellow	UP_SEQ_FEATURE	site:Cleavage; by autolysis	3	0.659341	0.035129	ENSG00000163501,	358	16	19113	10.0103	1	0.822053	43.41019
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 13	9	1.978022	0.035291	ENSG00000167766,	358	201	19113	2.390519	1	0.809668	43.5616
yellow	UP_SEQ_FEATURE	compositionally biased region:Gly-rich	10	2.197802	0.03533	ENSG00000169436,	358	238	19113	2.243205	1	0.796405	43.59737
yellow	UP_SEQ_FEATURE	lipid moiety-binding region:Cholesterol glycine ester	2	0.43956	0.054998	ENSG00000163501,	358	3	19113	35.59218	1	0.909555	59.36785
yellow	UP_SEQ_FEATURE	site:Involved in cholesterol transfer	2	0.43956	0.054998	ENSG00000163501,	358	3	19113	35.59218	1	0.909555	59.36785
yellow	UP_SEQ_FEATURE	lipid moiety-binding region:N-palmitoyl cysteine	2	0.43956	0.054998	ENSG00000163501,	358	3	19113	35.59218	1	0.909555	59.36785
yellow	UP_SEQ_FEATURE	site:Essential for auto-cleavage	2	0.43956	0.054998	ENSG00000163501,	358	3	19113	35.59218	1	0.909555	59.36785
yellow	UP_SEQ_FEATURE	site:Involved in auto-cleavage	2	0.43956	0.054998	ENSG00000163501,	358	3	19113	35.59218	1	0.909555	59.36785
yellow	UP_SEQ_FEATURE	domain:Helix-loop-helix motif	6	1.318681	0.062709	ENSG00000113196,	358	114	19113	2.809909	1	0.929014	64.33724
yellow	UP_SEQ_FEATURE	propeptide:Removed in mature form	9	1.978022	0.066007	ENSG00000116996,	358	229	19113	2.098229	1	0.931842	66.28324
yellow	UP_SEQ_FEATURE	compositionally biased region:Poly-Ala	13	2.857143	0.066458	ENSG00000169436,	358	393	19113	1.766024	1	0.926342	66.54148

yellow	UP_SEQ_FEATURE	domain:TSP N-terminal	3	0.659341	0.068035	ENSG00000169436,	358	23	19113	6.963687	1	0.924249	67.43018
yellow	UP_SEQ_FEATURE	domain:TIR	3	0.659341	0.073331	ENSG00000115607,	358	24	19113	6.673534	1	0.932527	70.25523
yellow	UP_SEQ_FEATURE	repeat:TNFR-Cys 2	3	0.659341	0.078755	ENSG00000186827,	358	25	19113	6.406592	1	0.939805	72.90912
yellow	UP_SEQ_FEATURE	repeat:TNFR-Cys 1	3	0.659341	0.078755	ENSG00000186827,	358	25	19113	6.406592	1	0.939805	72.90912
yellow	UP_SEQ_FEATURE	domain:CTCK	3	0.659341	0.078755	ENSG00000198788,	358	25	19113	6.406592	1	0.939805	72.90912
yellow	UP_SEQ_FEATURE	zinc finger region:C2H2-type 1; degenerate	6	1.318681	0.07878	ENSG00000175322,	358	122	19113	2.625653	1	0.934339	72.92087
yellow	UP_SEQ_FEATURE	DNA-binding region:Basic motif	7	1.538462	0.081886	ENSG00000113196,	358	161	19113	2.321229	1	0.936035	74.33848

Supplemental Table 4. Cytochrome P450 gene symbols and major functions.

gene_name	id	GENE_DESC	P-val	Functions
CYP39A1	ENSG00000146233	cytochrome P450, family 39, subfamily A, polypeptide 1	3.55E-11	7-alpha hydroxylation of 24-hydroxycholesterol
CYP26A1	ENSG00000095596	cytochrome P450, family 26, subfamily A, polypeptide 1	6.14E-08	retinoic acid hydroxylase
CYP2C9	ENSG00000138109	cytochrome P450, family 2, subfamily C, polypeptide 9	7.46E-08	drug and steroid metabolism
CYP2C18	ENSG00000108242	cytochrome P450, family 2, subfamily C, polypeptide 18	9.41E-06	drug and steroid metabolism
CYP3A7	ENSG00000160870	cytochrome P450, family 3, subfamily A, polypeptide 7	9.95E-05	drug and steroid metabolism
CYP27A1	ENSG00000135929	cytochrome P450, family 27, subfamily A, polypeptide 1	0.000547696	bile acid biosynthesis
CYP2F1	ENSG00000197446	cytochrome P450, family 2, subfamily F, polypeptide 1	0.001219271	drug and steroid metabolism