

Supplementary Table 5. GO and KEGG pathways significantly involved in the 743 co-expression DEGs

ID	descriptor	GeneRatio	BgRatio	pValue	FDR	qvalue	geneID	size	DB	enrichmentRatio
hsa04640	Hematopoietic stem cell differentiation	22/335	99/8011	7.15E-11	7.84E-09	7.06E-09	CD2/CD1C	22	pathway_K	0.065672
hsa04061	Viral protein synthesis	22/335	100/8011	8.82E-11	7.84E-09	7.06E-09	IL10/IL24/IL28	22	pathway_K	0.065672
hsa04060	Cytokine-cytokine receptor interaction	39/335	294/8011	8.91E-11	7.84E-09	7.06E-09	LEPR/NGF	39	pathway_K	0.116418
hsa05144	Malaria	15/335	50/8011	9.11E-10	6.01E-08	5.42E-08	ACKR1/SEI	15	pathway_K	0.044776
hsa04062	Chemokine signaling pathway	27/335	189/8011	1.69E-08	8.92E-07	8.04E-07	CXCR2/CC	27	pathway_K	0.080597
hsa04514	Cell adhesion molecules	23/335	147/8011	3.60E-08	1.58E-06	1.43E-06	NEGR1/CC	23	pathway_K	0.068657
hsa05340	Primary immunodeficiency	11/335	38/8011	2.53E-07	9.55E-06	8.61E-06	PTPRC/CD	11	pathway_K	0.032836
hsa04015	Rap1 signaling pathway	26/335	210/8011	5.77E-07	1.90E-05	1.71E-05	EPHA2/NG	26	pathway_K	0.077612
hsa04151	PI3K-Akt signaling pathway	34/335	354/8011	4.26E-06	0.000125	0.000113	EPHA2/NG	34	pathway_K	0.101493
hsa04014	Ras signaling pathway	25/335	232/8011	1.20E-05	0.000316	0.000285	EPHA2/PL	25	pathway_K	0.074627
hsa04360	Axon guidance	20/335	181/8011	6.35E-05	0.001524	0.001374	EPHA2/EFI	20	pathway_K	0.059701
hsa04662	B cell receptor signaling pathway	11/335	82/8011	0.000567	0.011844	0.010673	CR2/PRKC	11	pathway_K	0.032836
hsa04010	MAPK signaling pathway	25/335	295/8011	0.000583	0.011844	0.010673	EPHA2/NG	25	pathway_K	0.074627
hsa04672	Intestinal immune response	8/335	49/8011	0.000864	0.016296	0.014685	IL10/ITGA4	8	pathway_K	0.023881
hsa04080	Neuroactive ligand-receptor interaction	27/335	340/8011	0.000967	0.016629	0.014985	GRIK3/LEP	27	pathway_K	0.080597
hsa04512	ECM-receptor interaction	11/335	88/8011	0.001037	0.016629	0.014985	LAMB3/ITC	11	pathway_K	0.032836
hsa04064	NF-kappa B signaling pathway	12/335	102/8011	0.001071	0.016629	0.014985	ZAP70/IL1	12	pathway_K	0.035821
hsa04660	T cell receptor signaling pathway	12/335	104/8011	0.001271	0.018649	0.016805	PTPRC/IL1	12	pathway_K	0.035821
hsa05150	Staphylococcus aureus infection	10/335	96/8011	0.006612	0.091865	0.082781	SELP/IL10/	10	pathway_K	0.029851
hsa05230	Central carbon metabolism in cancer	8/335	69/8011	0.007776	0.102646	0.092496	SLC2A1/HI	8	pathway_K	0.023881
hsa05310	Asthma	5/335	31/8011	0.008605	0.108175	0.097478	FCER1A/IL	5	pathway_K	0.014925
hsa00982	Drug metabolism-cytochrome P450	8/335	72/8011	0.009995	0.11506	0.103682	GSTM5/FM	8	pathway_K	0.023881
hsa05146	Amoebiasis	10/335	102/8011	0.010024	0.11506	0.103682	CD1C/CD1	10	pathway_K	0.029851
hsa00140	Steroid hormone biosynthesis	7/335	60/8011	0.012076	0.132835	0.1197	HSD11B1/	7	pathway_K	0.020896
hsa00980	Metabolism of drugs and xenobiotics	8/335	76/8011	0.013643	0.143809	0.129589	GSTM5/H9	8	pathway_K	0.023881
hsa00340	Histidine metabolism	4/335	23/8011	0.014163	0.143809	0.129589	AOC1/ALC	4	pathway_K	0.01194
hsa04340	Hedgehog signaling pathway	6/335	50/8011	0.017229	0.162775	0.14668	IHH/BOC/	6	pathway_K	0.01791
hsa04960	Aldosterone synthesis and secretion	5/335	37/8011	0.01801	0.162775	0.14668	SFN/SCNN	5	pathway_K	0.014925
hsa04670	Leukocyte mediated immunity	10/335	112/8011	0.018497	0.162775	0.14668	ITGA4/CLC	10	pathway_K	0.029851
hsa05145	Toxoplasmosis	10/335	112/8011	0.018497	0.162775	0.14668	IL10/LAME	10	pathway_K	0.029851
hsa04510	Focal adhesion	15/335	199/8011	0.019483	0.165917	0.149511	LAMB3/ITC	15	pathway_K	0.044776
hsa05218	Melanoma	7/335	72/8011	0.030199	0.249141	0.224505	PDGFRA/F	7	pathway_K	0.020896
hsa04020	Calcium signaling pathway	14/335	193/8011	0.031374	0.250989	0.22617	PTGER3/P	14	pathway_K	0.041791
hsa00052	Galactose metabolism	4/335	31/8011	0.038798	0.292651	0.263713	GALE/HK2	4	pathway_K	0.01194
hsa00512	Mucin type O glycosylation	4/335	31/8011	0.038798	0.292651	0.263713	GALNT15/	4	pathway_K	0.01194
hsa01521	EGFR tyrosine phosphorylation signaling pathway	7/335	79/8011	0.046544	0.332268	0.299412	PDGFRA/K	7	pathway_K	0.020896
hsa05414	Dilated cardiomyopathy	8/335	96/8011	0.04714	0.332268	0.299412	ITGA4/SGC	8	pathway_K	0.023881
hsa05202	Transcription	13/335	186/8011	0.047826	0.332268	0.299412	SLC45A3/F	13	pathway_K	0.038806
GO:006032	cell chemotaxis	52/673	304/18670	4.38E-21	2.03E-17	1.56E-17	ARHGEF16	52	geneontol	0.077266
GO:003005	lymphocyte chemotaxis	55/673	353/18670	2.85E-20	6.61E-17	5.07E-17	PLA2G2D/	55	geneontol	0.081724
GO:004212	T cell activation	61/673	464/18670	1.40E-18	2.16E-15	1.66E-15	PLA2G2D/	61	geneontol	0.090639
GO:005093	leukocyte chemotaxis	62/673	499/18670	1.21E-17	1.40E-14	1.08E-14	PDE4B/S1F	62	geneontol	0.092125
GO:007005	chemokine signaling pathway	25/673	88/18670	3.83E-16	3.55E-13	2.72E-13	ACKR1/CX	25	geneontol	0.037147
GO:004578	positive regulation of cell chemotaxis	52/673	403/18670	1.20E-15	9.23E-13	7.08E-13	S100A10/T	52	geneontol	0.077266
GO:007061	leukocyte chemotaxis	62/673	298/18670	1.48E-15	9.79E-13	7.51E-13	PLA2G2D/	44	geneontol	0.065379
GO:003022	T cell differentiation	39/673	240/18670	2.47E-15	1.43E-12	1.10E-12	PLA2G2D/	39	geneontol	0.057949
GO:199081	response to hypoxia	25/673	97/18670	4.74E-15	2.19E-12	1.68E-12	ACKR1/CX	25	geneontol	0.037147
GO:199080	cellular response to hypoxia	25/673	97/18670	4.74E-15	2.19E-12	1.68E-12	ACKR1/CX	25	geneontol	0.037147
GO:003211	positive regulation of cell chemotaxis	45/673	323/18670	6.30E-15	2.63E-12	2.02E-12	PTGER3/S	45	geneontol	0.066865
GO:004661	lymphocyte chemotaxis	41/673	272/18670	6.81E-15	2.63E-12	2.02E-12	PLA2G2D/	41	geneontol	0.060921
GO:003292	mononuclear cell chemotaxis	41/673	274/18670	8.81E-15	3.14E-12	2.41E-12	PLA2G2D/	41	geneontol	0.060921
GO:005092	regulation of chemotaxis	36/673	217/18670	1.55E-14	5.11E-12	3.92E-12	S1PR1/S1C	36	geneontol	0.053492
GO:000718	leukocyte chemotaxis	45/673	337/18670	3.04E-14	9.40E-12	7.21E-12	PLA2G2D/	45	geneontol	0.066865
GO:003059	leukocyte chemotaxis	36/673	224/18670	4.23E-14	1.23E-11	9.40E-12	PDE4B/S1F	36	geneontol	0.053492
GO:004303	extracellular matrix organization	50/673	422/18670	1.27E-13	3.47E-11	2.66E-11	DDR2/DPT	50	geneontol	0.074294
GO:005087	regulation of cell chemotaxis	42/673	314/18670	2.12E-13	5.45E-11	4.18E-11	PLA2G2D/	42	geneontol	0.062407
GO:005092	positive regulation of cell chemotaxis	27/673	135/18670	3.09E-13	7.54E-11	5.78E-11	S1PR1/S1C	27	geneontol	0.040119
GO:000721	positive regulation of cell chemotaxis	42/673	319/18670	3.64E-13	8.42E-11	6.46E-11	PTGER3/P	42	geneontol	0.062407
GO:005122	regulation of cell chemotaxis	53/673	485/18670	5.99E-13	1.32E-10	1.01E-10	PLA2G2D/	53	geneontol	0.078752
GO:003019	extracellular matrix organization	45/673	368/18670	7.32E-13	1.54E-10	1.18E-10	DDR2/DPT	45	geneontol	0.066865
GO:004211	B cell proliferation	22/673	95/18670	2.20E-12	4.43E-10	3.40E-10	FCRL3/MN	22	geneontol	0.032689
GO:001972	calcium ion transport	33/673	218/18670	2.73E-12	5.27E-10	4.04E-10	PTGFR/SEL	33	geneontol	0.049034
GO:003158	cell-substrate junction organization	43/673	354/18670	3.02E-12	5.59E-10	4.29E-10	TACSTD2/	43	geneontol	0.063893
GO:000268	regulation of cell chemotaxis	31/673	196/18670	3.90E-12	6.94E-10	5.33E-10	S100A14/S	31	geneontol	0.046062
GO:009752	myeloid leukocyte chemotaxis	32/673	210/18670	4.90E-12	8.40E-10	6.44E-10	PDE4B/S1C	32	geneontol	0.047548
GO:005502	calcium ion transport	50/673	471/18670	8.17E-12	1.35E-09	1.04E-09	PTGER3/P	50	geneontol	0.074294
GO:005148	regulation of cell chemotaxis	42/673	357/18670	1.55E-11	2.47E-09	1.90E-09	PTGER3/P	42	geneontol	0.062407
GO:005062	regulation of cell chemotaxis	31/673	208/18670	1.91E-11	2.94E-09	2.26E-09	PLA2G2D/	31	geneontol	0.046062
GO:003292	regulation of cell chemotaxis	31/673	209/18670	2.16E-11	3.21E-09	2.47E-09	PLA2G2D/	31	geneontol	0.046062
GO:007061	leukocyte chemotaxis	32/673	222/18670	2.22E-11	3.21E-09	2.47E-09	PLA2G2D/	32	geneontol	0.047548
GO:190302	regulation of cell chemotaxis	38/673	304/18670	2.41E-11	3.39E-09	2.60E-09	PLA2G2D/	38	geneontol	0.056464

GO:00508 positive re 44/673	394/18670	2.89E-11	3.94E-09	3.02E-09	CD2/FCRL3	44	geneontol	0.065379
GO:00068 cellular cal 47/673	458/18670	1.13E-10	1.47E-08	1.13E-08	PTGER3/P	47	geneontol	0.069837
GO:00026 positive re 42/673	380/18670	1.14E-10	1.47E-08	1.13E-08	CD2/FCRL3	42	geneontol	0.062407
GO:00026 positive re 23/673	128/18670	1.74E-10	2.18E-08	1.67E-08	S100A14/C	23	geneontol	0.034175
GO:19030 positive re 30/673	218/18670	3.01E-10	3.66E-08	2.81E-08	PTPRC/NL	30	geneontol	0.044577
GO:00181 peptidyl-t 40/673	363/18670	3.51E-10	4.16E-08	3.19E-08	EPHA2/TA	40	geneontol	0.059435
GO:00182 peptidyl-t 40/673	366/18670	4.49E-10	5.19E-08	3.98E-08	EPHA2/TA	40	geneontol	0.059435
GO:00716 granulocyt 22/673	123/18670	4.75E-10	5.37E-08	4.12E-08	PDE4B/S1C	22	geneontol	0.032689
GO:00466 alpha-bet 23/673	138/18670	8.22E-10	9.02E-08	6.92E-08	PLA2G2D/	23	geneontol	0.034175
GO:00224 positive re 32/673	255/18670	8.38E-10	9.02E-08	6.92E-08	PTPRC/IL1	32	geneontol	0.047548
GO:00199 second-m 44/673	439/18670	9.54E-10	1.00E-07	7.70E-08	PTGER3/P	44	geneontol	0.065379
GO:00508 positive re 28/673	202/18670	9.97E-10	1.03E-07	7.87E-08	PTPRC/NL	28	geneontol	0.041605
GO:00024 immune re 46/673	473/18670	1.05E-09	1.05E-07	8.07E-08	PDE4B/ML	46	geneontol	0.068351
GO:00433 negative T 8/673	12/18670	1.19E-09	1.17E-07	9.01E-08	PTPRC/ZA	8	geneontol	0.011887
GO:00975 granulocyt 23/673	141/18670	1.27E-09	1.23E-07	9.41E-08	PDE4B/S1C	23	geneontol	0.034175
GO:00725 cellular div 47/673	493/18670	1.32E-09	1.24E-07	9.53E-08	PTGER3/P	47	geneontol	0.069837
GO:00421 B cell activ 35/673	310/18670	2.38E-09	2.20E-07	1.69E-07	FCRL3/MN	35	geneontol	0.052006
GO:00726 lymphocyt 20/673	111/18670	2.56E-09	2.33E-07	1.79E-07	S1PR1/ZA	20	geneontol	0.029718
GO:00071 cell-matrix 29/673	225/18670	2.80E-09	2.49E-07	1.91E-07	S100A10/L	29	geneontol	0.043091
GO:00329 regulation 37/673	343/18670	2.93E-09	2.56E-07	1.96E-07	TACSTD2/	37	geneontol	0.054978
GO:00026 regulation 20/673	114/18670	4.16E-09	3.50E-07	2.69E-07	S100A14/C	20	geneontol	0.029718
GO:00108 regulation 28/673	215/18670	4.16E-09	3.50E-07	2.69E-07	TACSTD2/	28	geneontol	0.041605
GO:00026 negative re 44/673	463/18670	4.95E-09	4.09E-07	3.14E-07	PLA2G2D/	44	geneontol	0.065379
GO:00305 neutrophil 19/673	104/18670	5.04E-09	4.10E-07	3.14E-07	PDE4B/S1C	19	geneontol	0.028232
GO:00509 leukocyte 110/673	25/18670	6.94E-09	5.51E-07	4.23E-07	SELP/SELL	10	geneontol	0.014859
GO:00450 T cell selec 13/673	47/18670	7.02E-09	5.51E-07	4.23E-07	LY9/PTPRC	13	geneontol	0.019316
GO:00224 regulation 40/673	403/18670	7.41E-09	5.72E-07	4.39E-07	PLA2G2D/	40	geneontol	0.059435
GO:19902 neutrophil 20/673	118/18670	7.71E-09	5.85E-07	4.49E-07	PDE4B/S1C	20	geneontol	0.029718
GO:00329 regulation 39/673	388/18670	8.07E-09	6.03E-07	4.62E-07	TACSTD2/	39	geneontol	0.057949
GO:00301 B cell diffe 21/673	131/18670	9.16E-09	6.73E-07	5.17E-07	FCRL3/PTF	21	geneontol	0.031204
GO:00433 positive T 11/673	34/18670	1.65E-08	1.20E-06	9.17E-07	LY9/PTPRC	11	geneontol	0.016345
GO:00315 actin cytos 18/673	101/18670	1.92E-08	1.34E-06	1.03E-06	S1PR1/PLE	18	geneontol	0.026746
GO:00466 alpha-bet 18/673	101/18670	1.92E-08	1.34E-06	1.03E-06	PLA2G2D/	18	geneontol	0.026746
GO:00450 negative ti 7/673	11/18670	2.23E-08	1.54E-06	1.18E-06	PTPRC/ZA	7	geneontol	0.010401
GO:00308 regulation 14/673	61/18670	2.57E-08	1.75E-06	1.34E-06	FCRL3/MN	14	geneontol	0.020802
GO:00456 regulation 23/673	169/18670	4.42E-08	2.96E-06	2.27E-06	CD2/FCRL3	23	geneontol	0.034175
GO:00512 positive re 34/673	334/18670	5.44E-08	3.60E-06	2.76E-06	FCRL3/PTF	34	geneontol	0.05052
GO:00025 monocyte 14/673	65/18670	6.08E-08	3.97E-06	3.04E-06	S100A12/S	14	geneontol	0.020802
GO:00485 digestive t 20/673	134/18670	7.09E-08	4.56E-06	3.50E-06	IHH/CLDN	20	geneontol	0.029718
GO:00024 dendritic c 9/673	24/18670	7.84E-08	4.97E-06	3.81E-06	CXCR2/CC	9	geneontol	0.013373
GO:00072 Rho protei 25/673	203/18670	8.61E-08	5.38E-06	4.13E-06	ARHGEF16	25	geneontol	0.037147
GO:00072 phospholi 7/673	100/18670	9.77E-08	6.03E-06	4.63E-06	PTGER3/S	17	geneontol	0.02526
GO:00355 G protein- 17/673	13/18670	1.09E-07	6.63E-06	5.09E-06	GPR171/P	7	geneontol	0.010401
GO:00506 regulation 36/673	378/18670	1.20E-07	7.19E-06	5.52E-06	SFN/TACS	36	geneontol	0.053492
GO:00716 mononuck 16/673	90/18670	1.22E-07	7.24E-06	5.55E-06	S100A12/S	16	geneontol	0.023774
GO:00074 axonogen 41/673	468/18670	1.59E-07	9.19E-06	7.05E-06	EPHA2/NE	41	geneontol	0.060921
GO:00022 lymphocyt 23/673	181/18670	1.59E-07	9.19E-06	7.05E-06	CD1C/LY9	23	geneontol	0.034175
GO:00506 epithelial c 39/673	434/18670	1.66E-07	9.46E-06	7.26E-06	EPHA2/SFI	39	geneontol	0.057949
GO:00421 regulation 21/673	156/18670	2.05E-07	1.15E-05	8.81E-06	PLA2G2D/	21	geneontol	0.031204
GO:00451 cellular ext 13/673	61/18670	2.06E-07	1.15E-05	8.81E-06	SELP/SELL	13	geneontol	0.019316
GO:00506 positive re 19/673	130/18670	2.11E-07	1.16E-05	8.91E-06	FCRL3/PTF	19	geneontol	0.028232
GO:00420 T cell proli 23/673	184/18670	2.15E-07	1.17E-05	8.97E-06	PLA2G2D/	23	geneontol	0.034175
GO:00329 positive re 19/673	131/18670	2.38E-07	1.28E-05	9.84E-06	FCRL3/PTF	19	geneontol	0.028232
GO:20001 regulation 15/673	83/18670	2.41E-07	1.28E-05	9.85E-06	EFNA1/IL1	15	geneontol	0.022288
GO:00363 dendritic c 9/673	27/18670	2.55E-07	1.34E-05	1.03E-05	CXCR2/CC	9	geneontol	0.013373
GO:00551 digestive s 20/673	146/18670	2.99E-07	1.55E-05	1.19E-05	IHH/CLDN	20	geneontol	0.029718
GO:00716 regulation 11/673	44/18670	3.19E-07	1.64E-05	1.26E-05	S100A14/C	11	geneontol	0.016345
GO:00108 positive re 18/673	121/18670	3.35E-07	1.70E-05	1.31E-05	S100A10/\	18	geneontol	0.026746
GO:00355 purinergic 8/673	21/18670	3.67E-07	1.83E-05	1.40E-05	GPR171/P	8	geneontol	0.011887
GO:00450 thymic T c 8/673	21/18670	3.67E-07	1.83E-05	1.40E-05	PTPRC/ZA	8	geneontol	0.011887
GO:00482 lymphocyt 13/673	64/18670	3.73E-07	1.84E-05	1.41E-05	CCR2/CXC	13	geneontol	0.019316
GO:00026 positive re 15/673	87/18670	4.57E-07	2.23E-05	1.71E-05	S100A14/C	15	geneontol	0.022288
GO:00312 T cell costi 12/673	56/18670	5.69E-07	2.74E-05	2.10E-05	CD28/ICO	12	geneontol	0.017831
GO:00455 regulation 19/673	139/18670	6.10E-07	2.88E-05	2.21E-05	CD2/PTPR	19	geneontol	0.028232
GO:00706 positive re 19/673	139/18670	6.10E-07	2.88E-05	2.21E-05	FCRL3/PTF	19	geneontol	0.028232
GO:00510 actin filam 20/673	153/18670	6.43E-07	3.01E-05	2.31E-05	TACSTD2/	20	geneontol	0.029718
GO:00350 regulation 19/673	140/18670	6.82E-07	3.16E-05	2.42E-05	ARHGEF16	19	geneontol	0.028232
GO:00312 lymphocyt 12/673	57/18670	6.97E-07	3.20E-05	2.45E-05	CD28/ICO	12	geneontol	0.017831
GO:00074 axon guid 28/673	276/18670	8.70E-07	3.95E-05	3.03E-05	EPHA2/NE	28	geneontol	0.041605
GO:00720 renal syste 29/673	293/18670	9.27E-07	4.16E-05	3.19E-05	TACSTD2/	29	geneontol	0.043091
GO:00974 neuron prc 28/673	277/18670	9.36E-07	4.17E-05	3.20E-05	EPHA2/NE	28	geneontol	0.041605
GO:00514 positive re 9/673	31/18670	9.63E-07	4.25E-05	3.26E-05	S1PR1/GPI	9	geneontol	0.013373
GO:00615 actin filam 20/673	157/18670	9.75E-07	4.26E-05	3.27E-05	TACSTD2/	20	geneontol	0.029718

GO:00024	adaptive ir	33/673	361/18670	1.02E-06	4.39E-05	3.37E-05	CD1C/CD1	33	geneontol	0.049034
GO:00507	regulation	40/673	485/18670	1.07E-06	4.57E-05	3.50E-05	PTGER3/S:	40	geneontol	0.059435
GO:00016	urogenital	31/673	330/18670	1.21E-06	5.10E-05	3.91E-05	TACSTD2/	31	geneontol	0.046062
GO:00324	response t	31/673	330/18670	1.21E-06	5.10E-05	3.91E-05	PDE4B/PT	31	geneontol	0.046062
GO:00435	positive re	9/673	32/18670	1.30E-06	5.41E-05	4.15E-05	P2RY12/PI	9	geneontol	0.013373
GO:00508	antigen re	30/673	316/18670	1.44E-06	5.97E-05	4.58E-05	PDE4B/FCI	30	geneontol	0.044577
GO:00518	positive re	21/673	176/18670	1.55E-06	6.36E-05	4.88E-05	CD28/ICO:	21	geneontol	0.031204
GO:00506	positive re	23/673	206/18670	1.61E-06	6.53E-05	5.01E-05	IL10/OSR1	23	geneontol	0.034175
GO:00434	protein kin	27/673	269/18670	1.67E-06	6.74E-05	5.17E-05	EPHA2/XD	27	geneontol	0.040119
GO:00026	regulation	38/673	458/18670	1.72E-06	6.85E-05	5.26E-05	FCRL3/CD:	38	geneontol	0.056464
GO:00466	positive re	12/673	62/18670	1.81E-06	7.14E-05	5.48E-05	PTPRC/NL	12	geneontol	0.017831
GO:00430	regulation	39/673	479/18670	1.99E-06	7.81E-05	5.99E-05	ARHGEF16	39	geneontol	0.057949
GO:00016	ameboidal	38/673	461/18670	2.01E-06	7.81E-05	5.99E-05	EPHA2/TA	38	geneontol	0.056464
GO:19021	regulation	27/673	272/18670	2.07E-06	7.99E-05	6.13E-05	TAL1/CD2:	27	geneontol	0.040119
GO:19055	macrophag	11/673	53/18670	2.36E-06	9.02E-05	6.92E-05	CX3CR1/C	11	geneontol	0.016345
GO:00716	positive re	8/673	26/18670	2.40E-06	9.11E-05	6.99E-05	S100A14/C	8	geneontol	0.011887
GO:00017	morphoge	22/673	196/18670	2.47E-06	9.30E-05	7.13E-05	EPHA2/TA	22	geneontol	0.032689
GO:00226	regulation	39/673	484/18670	2.56E-06	9.56E-05	7.33E-05	TACSTD2/	39	geneontol	0.057949
GO:00140	positive re	14/673	87/18670	2.59E-06	9.61E-05	7.37E-05	SELP/CD2:	14	geneontol	0.020802
GO:00027	regulation	18/673	139/18670	2.66E-06	9.68E-05	7.43E-05	FCRL3/PTF	18	geneontol	0.026746
GO:00507	positive re	19/673	153/18670	2.67E-06	9.68E-05	7.43E-05	PTGER3/S:	19	geneontol	0.028232
GO:00611	morphoge	21/673	182/18670	2.68E-06	9.68E-05	7.43E-05	EPHA2/TA	21	geneontol	0.031204
GO:00022	response t	31/673	343/18670	2.73E-06	9.80E-05	7.52E-05	PDE4B/PT	31	geneontol	0.046062
GO:00617	leukocyte	10/673	44/18670	2.83E-06	0.000101	7.74E-05	SELP/SELL	10	geneontol	0.014859
GO:00450	positive th	6/673	13/18670	2.96E-06	0.000105	8.04E-05	PTPRC/ZA	6	geneontol	0.008915
GO:01100	regulation	26/673	261/18670	2.99E-06	0.000105	8.04E-05	TACSTD2/	26	geneontol	0.038633
GO:00508	regulation	12/673	65/18670	3.05E-06	0.000106	8.14E-05	FCRL3/PTF	12	geneontol	0.017831
GO:00018	kidney dev	27/673	278/18670	3.14E-06	0.000108	8.32E-05	TACSTD2/	27	geneontol	0.040119
GO:00018	negative r	28/673	296/18670	3.46E-06	0.000119	9.10E-05	EPHA2/CD	28	geneontol	0.041605
GO:00070	actin filam	34/673	400/18670	3.56E-06	0.000121	9.30E-05	TACSTD2/	34	geneontol	0.05052
GO:00313	positive re	33/673	383/18670	3.70E-06	0.000125	9.60E-05	NEGR1/EP	33	geneontol	0.049034
GO:00902	positive re	9/673	36/18670	3.83E-06	0.000127	9.78E-05	P2RY12/PI	9	geneontol	0.013373
GO:19026	regulation	9/673	36/18670	3.83E-06	0.000127	9.78E-05	IL1R1/CXC	9	geneontol	0.013373
GO:00508	B cell rece	17/673	129/18670	3.94E-06	0.00013	9.99E-05	FCRL3/MN	17	geneontol	0.02526
GO:00071	heterophili	10/673	46/18670	4.36E-06	0.000142	0.000109	CADM3/SE	10	geneontol	0.014859
GO:00336	regulation	10/673	46/18670	4.36E-06	0.000142	0.000109	EPHA2/EFI	10	geneontol	0.014859
GO:19013	regulation	35/673	422/18670	4.44E-06	0.000144	0.00011	EPHA2/NP	35	geneontol	0.052006
GO:00718	leukocyte	15/673	104/18670	4.70E-06	0.000151	0.000116	EFNA1/IL1	15	geneontol	0.022288
GO:00336	cell adhesi	12/673	68/18670	5.00E-06	0.000158	0.000122	EPHA2/EFI	12	geneontol	0.017831
GO:00509	positive ch	12/673	68/18670	5.00E-06	0.000158	0.000122	S1PR1/CCI	12	geneontol	0.017831
GO:00326	regulation	19/673	160/18670	5.20E-06	0.000164	0.000126	CD2/SLAM	19	geneontol	0.028232
GO:00019	regulation	16/673	119/18670	5.80E-06	0.000181	0.000139	S100A10/E	16	geneontol	0.023774
GO:00085	epidermis	37/673	464/18670	5.87E-06	0.000182	0.00014	EPHA2/SFI	37	geneontol	0.054978
GO:19026	positive re	8/673	29/18670	5.99E-06	0.000185	0.000142	IL1R1/CXC	8	geneontol	0.011887
GO:00987	cell-cell ac	26/673	273/18670	6.79E-06	0.000205	0.000158	NEXN/CAI	26	geneontol	0.038633
GO:00330	T cell diffe	12/673	70/18670	6.83E-06	0.000205	0.000158	PTPRC/ZA	12	geneontol	0.017831
GO:00326	tumor nec	19/673	163/18670	6.84E-06	0.000205	0.000158	CD2/SLAM	19	geneontol	0.028232
GO:19035	regulation	19/673	163/18670	6.84E-06	0.000205	0.000158	CD2/SLAM	19	geneontol	0.028232
GO:00027	regulation	18/673	149/18670	7.19E-06	0.000215	0.000165	CD1C/CD1	18	geneontol	0.026746
GO:00074	mesoderm	17/673	135/18670	7.34E-06	0.000218	0.000167	EPHA2/TA	17	geneontol	0.02526
GO:00421	positive re	14/673	95/18670	7.52E-06	0.000222	0.00017	PTPRC/ZA	14	geneontol	0.020802
GO:00900	regulation	8/673	30/18670	7.92E-06	0.000232	0.000178	CXCR2/SLI	8	geneontol	0.011887
GO:00518	regulation	24/673	244/18670	8.85E-06	0.000258	0.000198	EPHA2/XD	24	geneontol	0.035661
GO:00070	cell-substr	14/673	97/18670	9.63E-06	0.000278	0.000214	S100A10/L	14	geneontol	0.020802
GO:00457	regulation	32/673	383/18670	9.78E-06	0.000281	0.000216	EPHA2/NP	32	geneontol	0.047548
GO:00512	negative r	32/673	384/18670	1.03E-05	0.000294	0.000225	PODN/TAC	32	geneontol	0.047548
GO:00346	response t	8/673	31/18670	1.03E-05	0.000294	0.000225	PTGFR/TG	8	geneontol	0.011887
GO:00717	tumor nec	19/673	168/18670	1.06E-05	0.0003	0.00023	CD2/SLAM	19	geneontol	0.028232
GO:00023	B cell activ	12/673	73/18670	1.07E-05	0.0003	0.00023	PTPRC/IL1	12	geneontol	0.017831
GO:00703	positive re	22/673	215/18670	1.11E-05	0.000311	0.000238	SLAMF1/P	22	geneontol	0.032689
GO:00327	positive re	7/673	23/18670	1.13E-05	0.000314	0.000241	NLRP3/CD	7	geneontol	0.010401
GO:00017	leukocyte	13/673	86/18670	1.19E-05	0.000328	0.000252	PDE4B/CX	13	geneontol	0.019316
GO:00435	positive re	33/673	405/18670	1.20E-05	0.000328	0.000252	ARHGEF16	33	geneontol	0.049034
GO:00024	lymphocyt	30/673	352/18670	1.26E-05	0.000341	0.000262	CD1C/CD1	30	geneontol	0.044577
GO:00326	negative r	6/673	16/18670	1.26E-05	0.000341	0.000262	SLAMF1/IL	6	geneontol	0.008915
GO:00326	interferon-	15/673	113/18670	1.32E-05	0.000356	0.000273	PDE4B/CD	15	geneontol	0.02288
GO:00355	purinergic	8/673	32/18670	1.33E-05	0.000357	0.000274	GPR171/P:	8	geneontol	0.011887
GO:00315	ruffle orga	10/673	52/18670	1.39E-05	0.000371	0.000284	TACSTD2/	10	geneontol	0.014859
GO:00510	regulation	29/673	338/18670	1.54E-05	0.0004	0.000307	ARHGEF16	29	geneontol	0.043091
GO:00355	G protein-	7/673	24/18670	1.55E-05	0.0004	0.000307	GPR171/P:	7	geneontol	0.010401
GO:00508	positive re	7/673	24/18670	1.55E-05	0.0004	0.000307	PTPRC/TR:	7	geneontol	0.010401
GO:00900	positive re	7/673	24/18670	1.55E-05	0.0004	0.000307	CXCR2/TH	7	geneontol	0.010401
GO:20010	regulation	7/673	24/18670	1.55E-05	0.0004	0.000307	KDR/CXCL	7	geneontol	0.010401

GO:00024	productio	26/673	286/18670	1.55E-05	0.0004	0.000307	FCRL3/PTF	26	geneontol	0.038633
GO:00451	cell fate co	25/673	270/18670	1.65E-05	0.000422	0.000324	TAL1/LY9/	25	geneontol	0.037147
GO:00069	cellular de	10/673	53/18670	1.66E-05	0.000423	0.000324	MNDA/CX	10	geneontol	0.014859
GO:00326	interleukin	8/673	33/18670	1.71E-05	0.000432	0.000331	NLRP3/CD	8	geneontol	0.011887
GO:00726	T cell migr	11/673	65/18670	1.87E-05	0.000471	0.000361	S1PR1/ZAI	11	geneontol	0.016345
GO:00028	regulation	17/673	145/18670	1.91E-05	0.000476	0.000365	CD1C/CD1	17	geneontol	0.02526
GO:00400	negative re	32/673	396/18670	1.91E-05	0.000476	0.000365	PODN/TAC	32	geneontol	0.047548
GO:00028	regulation	18/673	160/18670	1.94E-05	0.000479	0.000368	CD1C/CD1	18	geneontol	0.026746
GO:00326	regulation	10/673	54/18670	1.97E-05	0.000486	0.000373	SLAMF1/IL	10	geneontol	0.014859
GO:00507	positive re	20/673	192/18670	2.13E-05	0.000523	0.000401	TAL1/EFN	20	geneontol	0.029718
GO:19016	response t	20/673	193/18670	2.30E-05	0.00056	0.00043	PTGFR/TG	20	geneontol	0.029718
GO:00026	regulation	5/673	11/18670	2.31E-05	0.00056	0.00043	FGL2/CCL1	5	geneontol	0.007429
GO:00435	regulation	10/673	55/18670	2.34E-05	0.000563	0.000432	P2RY12/PI	10	geneontol	0.014859
GO:00026	negative re	15/673	120/18670	2.74E-05	0.000653	0.000501	FCRL3/CD	15	geneontol	0.022288
GO:00226	gland mor	15/673	120/18670	2.74E-05	0.000653	0.000501	EPHA2/ELF	15	geneontol	0.022288
GO:00326	interleukin	10/673	56/18670	2.75E-05	0.000654	0.000502	SLAMF1/IL	10	geneontol	0.014859
GO:00466	regulation	13/673	93/18670	2.83E-05	0.000667	0.000512	PTPRC/NL	13	geneontol	0.019316
GO:00480	phosphatic	19/673	181/18670	3.06E-05	0.000719	0.000552	NGF/SELP	19	geneontol	0.028232
GO:00456	positive re	13/673	94/18670	3.17E-05	0.000742	0.000569	PTPRC/NL	13	geneontol	0.019316
GO:00018	positive re	35/673	464/18670	3.37E-05	0.000785	0.000602	PDE4B/CD	35	geneontol	0.052006
GO:00326	regulation	7/673	27/18670	3.62E-05	0.000839	0.000644	NLRP3/CD	7	geneontol	0.010401
GO:00026	positive re	21/673	216/18670	3.78E-05	0.00087	0.000668	CD1C/CD1	21	geneontol	0.031204
GO:00458	positive re	17/673	153/18670	3.84E-05	0.000873	0.00067	TSPAN1/S	17	geneontol	0.02526
GO:00480	inositol lip	19/673	184/18670	3.84E-05	0.000873	0.00067	NGF/SELP	19	geneontol	0.028232
GO:00024	dendritic c	5/673	12/18670	3.85E-05	0.000873	0.00067	FGL2/CCL1	5	geneontol	0.007429
GO:20001	negative re	9/673	47/18670	3.89E-05	0.000878	0.000674	EFNA1/CX	9	geneontol	0.013373
GO:00140	regulation	15/673	124/18670	4.04E-05	0.000908	0.000696	SELP/CD2	15	geneontol	0.022288
GO:00455	positive re	12/673	83/18670	4.06E-05	0.000908	0.000696	PTPRC/NL	12	geneontol	0.017831
GO:00027	regulation	20/673	201/18670	4.13E-05	0.00092	0.000706	CD1C/CD1	20	geneontol	0.029718
GO:00467	protein au	22/673	235/18670	4.43E-05	0.00098	0.000752	DDR2/PTP	22	geneontol	0.032689
GO:00322	regulation	13/673	97/18670	4.45E-05	0.00098	0.000752	TACSTD2/	13	geneontol	0.019316
GO:19037	positive re	9/673	48/18670	4.63E-05	0.001017	0.00078	P2RY12/PI	9	geneontol	0.013373
GO:00300	contractile	13/673	98/18670	4.96E-05	0.001078	0.000827	TACSTD2/	13	geneontol	0.019316
GO:00431	stress fiber	13/673	98/18670	4.96E-05	0.001078	0.000827	TACSTD2/	13	geneontol	0.019316
GO:00518	regulation	10/673	60/18670	5.12E-05	0.001103	0.000846	S100A10/F	10	geneontol	0.014859
GO:00901	regulation	10/673	60/18670	5.12E-05	0.001103	0.000846	S100A10/F	10	geneontol	0.014859
GO:00015	ossificatio	31/673	398/18670	5.18E-05	0.00111	0.000852	EPHA2/S1	31	geneontol	0.046062
GO:00465	regulation	22/673	238/18670	5.37E-05	0.001145	0.000878	ARHGEF16	22	geneontol	0.032689
GO:00420	gliogenesis	25/673	290/18670	5.44E-05	0.001155	0.000886	TAL1/LEPR	25	geneontol	0.037147
GO:00026	negative re	9/673	49/18670	5.50E-05	0.001157	0.000887	CD200R1/	9	geneontol	0.013373
GO:00485	digestive t	9/673	49/18670	5.50E-05	0.001157	0.000887	IHH/PDGF	9	geneontol	0.013373
GO:00507	regulation	23/673	256/18670	5.69E-05	0.001193	0.000915	TAL1/EFN	23	geneontol	0.034175
GO:00162	O-glycan	10/673	61/18670	5.93E-05	0.001237	0.000949	MUC1/B3C	10	geneontol	0.014859
GO:00350	positive re	7/673	29/18670	5.98E-05	0.001242	0.000953	GPR35/LP	7	geneontol	0.010401
GO:00024	compleme	5/673	13/18670	6.06E-05	0.001253	0.000962	CR2/CR1/C	5	geneontol	0.007429
GO:00302	bone mine	14/673	114/18670	6.13E-05	0.001261	0.000967	S1PR1/DD	14	geneontol	0.020802
GO:00434	positive re	23/673	258/18670	6.42E-05	0.00131	0.001005	NGF/S100	23	geneontol	0.034175
GO:01200	regulation	18/673	175/18670	6.42E-05	0.00131	0.001005	EPHA2/TA	18	geneontol	0.026746
GO:00326	regulation	13/673	101/18670	6.82E-05	0.001386	0.001063	PDE4B/CD	13	geneontol	0.019316
GO:20001	negative re	28/673	349/18670	7.10E-05	0.001435	0.001101	PODN/TAC	28	geneontol	0.041605
GO:00017	mesoderm	11/673	75/18670	7.39E-05	0.001487	0.001141	EPHA2/TA	11	geneontol	0.016345
GO:00604	regulation	18/673	177/18670	7.45E-05	0.001493	0.001145	EPHA2/TA	18	geneontol	0.026746
GO:00327	positive re	7/673	30/18670	7.56E-05	0.001504	0.001154	PDE4B/PTI	7	geneontol	0.010401
GO:00018	mesoneph	13/673	102/18670	7.57E-05	0.001504	0.001154	TACSTD2/	13	geneontol	0.019316
GO:00303	negative re	27/673	334/18670	8.38E-05	0.001657	0.001271	PODN/TAC	27	geneontol	0.040119
GO:00488	homeosta	22/673	246/18670	8.78E-05	0.001729	0.001326	TAL1/PDE	22	geneontol	0.032689
GO:00072	Ras protei	33/673	448/18670	8.88E-05	0.00173	0.001327	ARHGEF16	33	geneontol	0.049034
GO:00703	ERK1 and	126/673	317/18670	8.90E-05	0.00173	0.001327	EPHA2/SL	26	geneontol	0.038633
GO:00140	phosphatic	16/673	148/18670	8.96E-05	0.00173	0.001327	SELP/CD2	16	geneontol	0.023774
GO:00435	regulation	10/673	64/18670	9.04E-05	0.00173	0.001327	P2RY12/PI	10	geneontol	0.014859
GO:00465	positive re	10/673	64/18670	9.04E-05	0.00173	0.001327	NGF/GPR3	10	geneontol	0.014859
GO:00509	negative re	10/673	64/18670	9.04E-05	0.00173	0.001327	SEMA3G/S	10	geneontol	0.014859
GO:00308	positive re	8/673	41/18670	9.11E-05	0.00173	0.001327	FCRL3/PTF	8	geneontol	0.011887
GO:00468	bone remc	12/673	90/18670	9.12E-05	0.00173	0.001327	EPHA2/LEF	12	geneontol	0.017831
GO:00017	immunolo	5/673	14/18670	9.15E-05	0.00173	0.001327	DOCK2/CC	5	geneontol	0.007429
GO:00433	CD8-posit	5/673	14/18670	9.15E-05	0.00173	0.001327	EOMES/TN	5	geneontol	0.007429
GO:00703	regulation	25/673	300/18670	9.39E-05	0.001767	0.001355	EPHA2/SL	25	geneontol	0.037147
GO:00483	mesoderm	11/673	77/18670	9.44E-05	0.001767	0.001355	EPHA2/TA	11	geneontol	0.016345
GO:00357	endothelia	7/673	31/18670	9.46E-05	0.001767	0.001355	KDR/CXCL	7	geneontol	0.010401
GO:00336	integrin ac	6/673	22/18670	9.76E-05	0.001808	0.001387	SELP/PLEK	6	geneontol	0.008915
GO:00486	reproducti	32/673	431/18670	9.77E-05	0.001808	0.001387	GJB5/GJB3	32	geneontol	0.047548
GO:00083	regulation	16/673	150/18670	0.000105	0.001939	0.001488	PALMD/AF	16	geneontol	0.023774
GO:00614	reproducti	32/673	434/18670	0.000111	0.002033	0.00156	GJB5/GJB3	32	geneontol	0.047548

GO:00310: actomyosin 19/673	199/18670	0.000111	0.002033	0.00156	TACSTD2/	19	geneontol	0.028232
GO:00222: T cell activ 13/673	106/18670	0.000113	0.002057	0.001578	CD1C/LY9,	13	geneontol	0.019316
GO:00507: positive re 34/673	474/18670	0.000117	0.002118	0.001625	NEGR1/NC	34	geneontol	0.05052
GO:00017: formation 14/673	121/18670	0.000118	0.002129	0.001634	EPHA2/TA	14	geneontol	0.020802
GO:00508: regulation 18/673	184/18670	0.000123	0.002211	0.001697	FCRL3/MN	18	geneontol	0.026746
GO:00346: response t 6/673	23/18670	0.000128	0.002289	0.001756	TGFBR3/PI	6	geneontol	0.008915
GO:00604: branching 6/673	23/18670	0.000128	0.002289	0.001756	FGF10/HG	6	geneontol	0.008915
GO:00108: positive re 8/673	43/18670	0.00013	0.002309	0.001771	SELE/P2RY	8	geneontol	0.011887
GO:00073: gastrulatio 18/673	185/18670	0.000132	0.002333	0.00179	EPHA2/TA	18	geneontol	0.026746
GO:00435: skin develc 31/673	419/18670	0.000133	0.002345	0.0018	EPHA2/SFI	31	geneontol	0.046062
GO:20010: positive re 5/673	15/18670	0.000133	0.002345	0.0018	KDR/SMO	5	geneontol	0.007429
GO:00421: positive re 10/673	67/18670	0.000134	0.002346	0.0018	PTPRC/CD	10	geneontol	0.014859
GO:19033: regulation 10/673	67/18670	0.000134	0.002346	0.0018	S100A10/F	10	geneontol	0.014859
GO:00430: regulation 9/673	55/18670	0.00014	0.002436	0.001869	PTPRC/IL1	9	geneontol	0.013373
GO:00420: cytokine b 14/673	123/18670	0.000141	0.002436	0.001869	PTPRC/IL1	14	geneontol	0.020802
GO:20010: negative re 7/673	33/18670	0.000144	0.002486	0.001908	IL10/OSR1	7	geneontol	0.010401
GO:00302: regulation 19/673	203/18670	0.000144	0.002486	0.001908	S1PR1/DD	19	geneontol	0.028232
GO:00070: cell-substr 11/673	81/18670	0.00015	0.002569	0.001971	S100A10/F	11	geneontol	0.016345
GO:00480: focal adhe 11/673	81/18670	0.00015	0.002569	0.001971	S100A10/F	11	geneontol	0.016345
GO:00421: cytokine r 14/673	124/18670	0.000153	0.002604	0.001998	PTPRC/IL1	14	geneontol	0.020802
GO:00380: vascular er 8/673	44/18670	0.000154	0.002604	0.001998	XDH/PDGF	8	geneontol	0.011887
GO:00421: macropha 12/673	95/18670	0.000155	0.002612	0.002004	PTPRC/IL1	12	geneontol	0.017831
GO:00023: immunogl 9/673	56/18670	0.000162	0.002725	0.002091	PTPRC/IL1	9	geneontol	0.013373
GO:00315: membranc 6/673	24/18670	0.000166	0.002777	0.002131	CD2/S100,	6	geneontol	0.008915
GO:00033: epithelial c 7/673	34/18670	0.000176	0.002935	0.002252	RAB25/IHF	7	geneontol	0.010401
GO:00074: salivary gl 7/673	34/18670	0.000176	0.002935	0.002252	FGF10/HG	7	geneontol	0.010401
GO:00488: multicellul 34/673	485/18670	0.00018	0.00299	0.002294	SFN/LEPR/	34	geneontol	0.05052
GO:19002: regulation 8/673	45/18670	0.000181	0.002991	0.002295	SELE/P2RY	8	geneontol	0.011887
GO:00702: cornificatic 13/673	112/18670	0.000198	0.00326	0.002501	LIPM/PKP	13	geneontol	0.019316
GO:19029: regulation 27/673	352/18670	0.000199	0.003268	0.002507	TACSTD2/	27	geneontol	0.040119
GO:00026: negative re 17/673	175/18670	0.000204	0.003341	0.002563	PLA2G2D/	17	geneontol	0.025226
GO:00719: positive re 26/673	334/18670	0.000206	0.003358	0.002577	NGF/S100,	26	geneontol	0.038633
GO:00027: regulation 11/673	84/18670	0.000209	0.003382	0.002595	IL10/NLRP	11	geneontol	0.016345
GO:00514: regulation 11/673	84/18670	0.000209	0.003382	0.002595	TACSTD2/	11	geneontol	0.016345
GO:00310: hair follicle 6/673	25/18670	0.000211	0.003396	0.002605	FGF10/FO,	6	geneontol	0.008915
GO:00509: positive re 6/673	25/18670	0.000211	0.003396	0.002605	S1PR1/CCI	6	geneontol	0.008915
GO:00716: regulation 8/673	46/18670	0.000212	0.003397	0.002606	S100A14/C	8	geneontol	0.011887
GO:00027: negative re 7/673	35/18670	0.000214	0.003397	0.002606	FCRL3/IL1	7	geneontol	0.010401
GO:00483: mesoderm 7/673	35/18670	0.000214	0.003397	0.002606	TAL1/TRIV	7	geneontol	0.010401
GO:00510: positive re 10/673	71/18670	0.00022	0.003484	0.002673	NGF/GPR3	10	geneontol	0.014859
GO:00023: immunogl 18/673	193/18670	0.000224	0.003537	0.002713	FCRL3/PTF	18	geneontol	0.026746
GO:00301: regulation 23/673	281/18670	0.00023	0.003617	0.002775	TSPAN1/S	23	geneontol	0.034175
GO:00420: regulation 13/673	114/18670	0.000236	0.003708	0.002845	PTPRC/IL1	13	geneontol	0.019316
GO:00434: regulation 26/673	337/18670	0.000237	0.003708	0.002845	NGF/S100,	26	geneontol	0.038633
GO:00105: positive re 9/673	59/18670	0.000244	0.003802	0.002917	SELE/AGTF	9	geneontol	0.013373
GO:00601: positive re 10/673	72/18670	0.000247	0.003835	0.002943	SELE/AGTF	10	geneontol	0.014859
GO:00466: positive re 8/673	47/18670	0.000248	0.003835	0.002943	NLRP3/ZA	8	geneontol	0.011887
GO:00107: regulation 24/673	301/18670	0.000251	0.003867	0.002967	TACSTD2/	24	geneontol	0.035661
GO:00028: positive re 12/673	100/18670	0.000252	0.003867	0.002967	CD1C/CD1	12	geneontol	0.017831
GO:00226: digestive s 12/673	100/18670	0.000252	0.003867	0.002967	PTGER3/M	12	geneontol	0.017831
GO:00326: interleukin 13/673	115/18670	0.000258	0.003938	0.003021	MNDA/PY	13	geneontol	0.019316
GO:19039: regulation 5/673	17/18670	0.000259	0.003938	0.003021	CX3CR1/C	5	geneontol	0.007429
GO:19037: regulation 33/673	475/18670	0.000263	0.003992	0.003063	TAL1/CD2,	33	geneontol	0.049034
GO:00509: regulation 6/673	26/18670	0.000266	0.004029	0.003091	S1PR1/CCI	6	geneontol	0.008915
GO:00487: tissue rem 17/673	179/18670	0.000267	0.004033	0.003094	EPHA2/LEI	17	geneontol	0.025226
GO:00326: interleukin 12/673	101/18670	0.000277	0.004165	0.003196	MNDA/PY	12	geneontol	0.017831
GO:00605: epithelial t 25/673	322/18670	0.000282	0.004226	0.003242	EPHA2/TA	25	geneontol	0.037147
GO:00018: embryonic 11/673	87/18670	0.000286	0.004268	0.003275	GJB5/IL10/	11	geneontol	0.016345
GO:00017: establishm 4/673	10/18670	0.000295	0.004341	0.00333	DOCK2/CC	4	geneontol	0.005944
GO:00140: regulation 4/673	10/18670	0.000295	0.004341	0.00333	LRRK2/EDI	4	geneontol	0.005944
GO:00722: cell prolif 4/673	10/18670	0.000295	0.004341	0.00333	OSR1/SH-	4	geneontol	0.005944
GO:00970: dendritic c 4/673	10/18670	0.000295	0.004341	0.00333	CCL19/CCI	4	geneontol	0.005944
GO:20006: regulation 4/673	10/18670	0.000295	0.004341	0.00333	CCL19/CCI	4	geneontol	0.005944
GO:00425: myelinatio 14/673	132/18670	0.000296	0.004341	0.003331	MAL/HGF/	14	geneontol	0.020802
GO:00080: cell recogn 19/673	215/18670	0.000303	0.004402	0.003377	NEXN/IGS	19	geneontol	0.028232
GO:00109: regulation 34/673	499/18670	0.000305	0.004402	0.003377	NEGR1/NC	34	geneontol	0.05052
GO:00074: salivary gl 7/673	37/18670	0.000307	0.004402	0.003377	FGF10/HG	7	geneontol	0.010401
GO:00380: peptidyl-t 7/673	37/18670	0.000307	0.004402	0.003377	KDR/ITK/B	7	geneontol	0.010401
GO:00431: regulation 7/673	37/18670	0.000307	0.004402	0.003377	NPR1/CXC	7	geneontol	0.010401
GO:20002: regulation 7/673	37/18670	0.000307	0.004402	0.003377	PDGFRA/S	7	geneontol	0.010401
GO:20004: positive re 7/673	37/18670	0.000307	0.004402	0.003377	ITGA4/CCF	7	geneontol	0.010401
GO:00011: response t 26/673	343/18670	0.000312	0.004456	0.003419	GJB3/PTGF	26	geneontol	0.038633
GO:19018: regulation 11/673	88/18670	0.000316	0.004504	0.003456	EPHA2/S1	11	geneontol	0.016345

GO:005081 negative re 18/673	199/18670	0.000326	0.004632	0.003554	PLA2G2D/	18	geneontol	0.026746
GO:004301 positive re 6/673	27/18670	0.000332	0.004701	0.003607	IL10/STAP	6	geneontol	0.008915
GO:000711 negative re 23/673	289/18670	0.000344	0.004847	0.003719	PLA2G2D/	23	geneontol	0.034175
GO:000721 ensheathn 14/673	134/18670	0.000346	0.004847	0.003719	MAL/HGF/	14	geneontol	0.020802
GO:000831 axon ensh 14/673	134/18670	0.000346	0.004847	0.003719	MAL/HGF/	14	geneontol	0.020802
GO:004851 embryonic 5/673	18/18670	0.000347	0.004847	0.003719	IHH/PDGF	5	geneontol	0.007429
GO:005071 negative re 15/673	150/18670	0.000348	0.004847	0.003719	CD84/PTPI	15	geneontol	0.022288
GO:000981 embryonic 9/673	62/18670	0.000358	0.004974	0.003816	IHH/FGF1C	9	geneontol	0.013373
GO:004821 macrophag 7/673	38/18670	0.000365	0.005057	0.00388	STAP1/CM	7	geneontol	0.010401
GO:004871 mesenchym 19/673	219/18670	0.000382	0.005278	0.00405	TGFBR3/EF	19	geneontol	0.028232
GO:003431 adherens j 11/673	90/18670	0.000385	0.005307	0.004072	S100A10/F	11	geneontol	0.016345
GO:000271 positive re 12/673	105/18670	0.000398	0.005453	0.004184	CD1C/CD1	12	geneontol	0.017831
GO:000281 positive re 12/673	105/18670	0.000398	0.005453	0.004184	CD1C/CD1	12	geneontol	0.017831
GO:000261 regulation 9/673	63/18670	0.000404	0.005488	0.004211	FCRL3/PTF	9	geneontol	0.013373
GO:004661 regulation 9/673	63/18670	0.000404	0.005488	0.004211	NLRP3/ZA	9	geneontol	0.013373
GO:200041 regulation 9/673	63/18670	0.000404	0.005488	0.004211	ITGA4/CCF	9	geneontol	0.013373
GO:000171 myeloid de 6/673	28/18670	0.00041	0.005516	0.004232	CD2/SLAM	6	geneontol	0.008915
GO:003511 embryonic 6/673	28/18670	0.00041	0.005516	0.004232	OSR1/AFF	6	geneontol	0.008915
GO:004551 regulation 6/673	28/18670	0.00041	0.005516	0.004232	FCRL3/SFR	6	geneontol	0.008915
GO:004851 embryonic 30/673	428/18670	0.000426	0.005713	0.004383	EPHA2/GJI	30	geneontol	0.044577
GO:190551 regulation 7/673	39/18670	0.000431	0.005767	0.004425	CX3CR1/C	7	geneontol	0.010401
GO:003521 organ gro 18/673	204/18670	0.00044	0.005862	0.004498	LEPR/TGFE	18	geneontol	0.026746
GO:000191 positive re 8/673	51/18670	0.000442	0.005862	0.004498	S100A10/k	8	geneontol	0.011887
GO:007251 purine-cor 8/673	51/18670	0.000442	0.005862	0.004498	PDE4B/XD	8	geneontol	0.011887
GO:001061 epithelial c 26/673	351/18670	0.000444	0.005868	0.004503	EPHA2/TA	26	geneontol	0.038633
GO:000171 establishm 4/673	11/18670	0.000451	0.00593	0.00455	DOCK2/CC	4	geneontol	0.005944
GO:003301 positive re 4/673	11/18670	0.000451	0.00593	0.00455	IHH/IL7R/S	4	geneontol	0.005944
GO:000251 chronic inf 5/673	19/18670	0.000458	0.005968	0.004579	IL10/CXCL	5	geneontol	0.007429
GO:000261 negative re 5/673	19/18670	0.000458	0.005968	0.004579	SLIT2/STAI	5	geneontol	0.007429
GO:004661 positive re 5/673	19/18670	0.000458	0.005968	0.004579	PTPRC/ZA	5	geneontol	0.007429
GO:190481 positive re 11/673	92/18670	0.000466	0.006065	0.004653	TNFSF18/I	11	geneontol	0.016345
GO:000191 leukocyte i 12/673	107/18670	0.000474	0.006143	0.004713	CD1C/CD1	12	geneontol	0.017831
GO:000191 regulation 10/673	78/18670	0.000478	0.00618	0.004741	CD1C/CD1	10	geneontol	0.014859
GO:006041 mesenchym 22/673	278/18670	0.000495	0.006384	0.004898	TGFBR3/EF	22	geneontol	0.032689
GO:004871 epidermis 6/673	29/18670	0.000501	0.006409	0.004918	FGF10/FO	6	geneontol	0.008915
GO:005081 regulation 6/673	29/18670	0.000501	0.006409	0.004918	FCRL3/STA	6	geneontol	0.008915
GO:190001 regulation 6/673	29/18670	0.000501	0.006409	0.004918	TACSTD2/	6	geneontol	0.008915
GO:000751 digestion 14/673	139/18670	0.000504	0.006416	0.004923	PTGER3/C	14	geneontol	0.020802
GO:009011 epithelium 26/673	354/18670	0.000505	0.006416	0.004923	EPHA2/TA	26	geneontol	0.038633
GO:000911 cyclic nucl 7/673	40/18670	0.000506	0.006423	0.004928	EPHA2/PD	7	geneontol	0.010401
GO:003271 positive re 9/673	65/18670	0.000512	0.006479	0.004971	PDE4B/CD	9	geneontol	0.013373
GO:000681 calcium ioi 30/673	434/18670	0.000536	0.006738	0.00517	PDE4B/FCI	30	geneontol	0.044577
GO:004871 gland devt 30/673	434/18670	0.000536	0.006738	0.00517	EPHA2/TG	30	geneontol	0.044577
GO:006091 kidney mo 11/673	94/18670	0.000562	0.007044	0.005404	TACSTD2/	11	geneontol	0.016345
GO:005141 positive re 19/673	226/18670	0.000564	0.007058	0.005415	S100A10/F	19	geneontol	0.028232
GO:000191 endothelia 17/673	191/18670	0.000569	0.007101	0.005448	EPHA2/IL1	17	geneontol	0.02526
GO:003001 myeloid ce 29/673	416/18670	0.000576	0.007166	0.005498	EPHA2/TA	29	geneontol	0.043091
GO:007021 regulation 6/673	53/18670	0.000578	0.007167	0.005499	EFNA1/IL1	8	geneontol	0.011887
GO:000681 xenobiotic 13/673	125/18670	0.000582	0.007207	0.005529	GSTM5/S1	13	geneontol	0.019316
GO:015001 regulation 7/673	41/18670	0.000592	0.007253	0.005565	PTPRC/CD	7	geneontol	0.010401
GO:000251 regulation 5/673	20/18670	0.000592	0.007253	0.005565	FGL2/CCL1	5	geneontol	0.007429
GO:003361 positive re 5/673	20/18670	0.000592	0.007253	0.005565	P2RY12/C	5	geneontol	0.007429
GO:004331 CD4-posit 5/673	20/18670	0.000592	0.007253	0.005565	LY9/IRF4/S	5	geneontol	0.007429
GO:000171 B cell hom 6/673	30/18670	0.000608	0.007402	0.005679	DOCK10/C	6	geneontol	0.008915
GO:001071 regulation 6/673	30/18670	0.000608	0.007402	0.005679	PPARG/AC	6	geneontol	0.008915
GO:011001 regulation 11/673	95/18670	0.000615	0.007469	0.005731	TACSTD2/	11	geneontol	0.016345
GO:009011 tissue mig 26/673	360/18670	0.000648	0.007841	0.006016	EPHA2/TA	26	geneontol	0.038633
GO:000191 regulation 16/673	176/18670	0.00065	0.007841	0.006016	IL10/XDH/	16	geneontol	0.023774
GO:003261 regulation 8/673	54/18670	0.000657	0.007841	0.006016	PDE4B/PTI	8	geneontol	0.011887
GO:000281 positive re 4/673	12/18670	0.000657	0.007841	0.006016	CD28/CNF	4	geneontol	0.005944
GO:003601 response t 4/673	12/18670	0.000657	0.007841	0.006016	MST1R/ST	4	geneontol	0.005944
GO:003601 cellular res 4/673	12/18670	0.000657	0.007841	0.006016	MST1R/ST	4	geneontol	0.005944
GO:004261 regulation 4/673	12/18670	0.000657	0.007841	0.006016	FGFR1/SO	4	geneontol	0.005944
GO:190401 epithelial c 12/673	111/18670	0.000662	0.007874	0.006041	IL10/ITGA	12	geneontol	0.017831
GO:190101 regulation 7/673	42/18670	0.000689	0.008173	0.006271	IL10/CD36	7	geneontol	0.010401
GO:004231 molting cy 12/673	112/18670	0.000717	0.008414	0.006456	EPS8L3/FC	12	geneontol	0.017831
GO:004261 hair cycle 12/673	112/18670	0.000717	0.008414	0.006456	EPS8L3/FC	12	geneontol	0.017831
GO:000221 T cell differ 9/673	68/18670	0.000718	0.008414	0.006456	LY9/NLRP	9	geneontol	0.013373
GO:003591 cellular res 9/673	68/18670	0.000718	0.008414	0.006456	XDH/PDGF	9	geneontol	0.013373
GO:190211 positive re 14/673	144/18670	0.000718	0.008414	0.006456	PTPRC/NL	14	geneontol	0.020802
GO:000721 activation 6/673	31/18670	0.000731	0.008542	0.006554	SELE/P2RY	6	geneontol	0.008915
GO:000161 ureteric bu 11/673	97/18670	0.000734	0.008559	0.006567	TACSTD2/	11	geneontol	0.016345
GO:004821 eosinophil 5/673	21/18670	0.000754	0.008753	0.006716	LGALS3/C	5	geneontol	0.007429

GO:00519 regulation	5/673	21/18670	0.000754	0.008753	0.006716	KDR/LRRK	5	geneontol	0.007429
GO:00436 keratinocy	7/673	43/18670	0.000797	0.009172	0.007037	SFN/FGF10	7	geneontol	0.010401
GO:00508 regulation	11/673	98/18670	0.000801	0.009172	0.007037	PLEK/ZAP70	11	geneontol	0.016345
GO:00601 regulation	11/673	98/18670	0.000801	0.009172	0.007037	SELE/AGTF	11	geneontol	0.016345
GO:00721 mesoneph	11/673	98/18670	0.000801	0.009172	0.007037	TACSTD2/	11	geneontol	0.016345
GO:00721 mesoneph	11/673	98/18670	0.000801	0.009172	0.007037	TACSTD2/	11	geneontol	0.016345
GO:00458 positive re	14/673	146/18670	0.000823	0.009408	0.007218	SLC45A3/F	14	geneontol	0.020802
GO:00312 biomineral	15/673	163/18670	0.000836	0.009529	0.007311	S1PR1/DD	15	geneontol	0.022288
GO:00019 positive re	8/673	56/18670	0.000842	0.009553	0.007329	CD1C/CD1	8	geneontol	0.011887
GO:00606 regulation	8/673	56/18670	0.000842	0.009553	0.007329	TACSTD2/	8	geneontol	0.011887
GO:00091 glycoprote	25/673	348/18670	0.000881	0.009976	0.007654	MAN1C1/I	25	geneontol	0.037147
GO:00027 regulation	9/673	70/18670	0.000889	0.009984	0.00766	CD1C/CD1	9	geneontol	0.013373
GO:00105 regulation	9/673	70/18670	0.000889	0.009984	0.00766	SELE/AGTF	9	geneontol	0.013373
GO:00507 positive re	9/673	70/18670	0.000889	0.009984	0.00766	PTPRC/PP	9	geneontol	0.013373
GO:00061 purine nuc	7/673	44/18670	0.000919	0.010142	0.007781	PDE4B/XD	7	geneontol	0.010401
GO:00104 mesenchy	7/673	44/18670	0.000919	0.010142	0.007781	OSR1/IHH	7	geneontol	0.010401
GO:00316 regulation	4/673	13/18670	0.000922	0.010142	0.007781	PTGER3/N	4	geneontol	0.005944
GO:00336 regulation	4/673	13/18670	0.000922	0.010142	0.007781	SELP/PLEK	4	geneontol	0.005944
GO:00431 negative re	4/673	13/18670	0.000922	0.010142	0.007781	SLIT2/ANC	4	geneontol	0.005944
GO:00450 positive re	4/673	13/18670	0.000922	0.010142	0.007781	PTPRC/CD	4	geneontol	0.005944
GO:00601 positive re	4/673	13/18670	0.000922	0.010142	0.007781	PPARG/ST	4	geneontol	0.005944
GO:00603 heart trab	4/673	13/18670	0.000922	0.010142	0.007781	TGFBR3/TI	4	geneontol	0.005944
GO:19051 positive re	4/673	13/18670	0.000922	0.010142	0.007781	PPARG/ST	4	geneontol	0.005944
GO:01200 positive re	11/673	100/18670	0.000948	0.010386	0.007968	EPS8L3/P2	11	geneontol	0.016345
GO:00017 neural cre	8/673	57/18670	0.000949	0.010386	0.007968	ZEB2/SEM	8	geneontol	0.011887
GO:00976 STAT casc	15/673	166/18670	0.001008	0.011002	0.008441	TNFSF18/F	15	geneontol	0.022288
GO:00108 regulation	6/673	33/18670	0.001034	0.01121	0.008601	SFN/FGF10	6	geneontol	0.008915
GO:00199 cGMP-me	6/673	33/18670	0.001034	0.01121	0.008601	NPR1/CD3	6	geneontol	0.008915
GO:00466 alpha-bet	6/673	33/18670	0.001034	0.01121	0.008601	PTPRC/ZA	6	geneontol	0.008915
GO:00327 positive re	10/673	86/18670	0.00104	0.01122	0.008609	CD2/PTPR	10	geneontol	0.014859
GO:00705 response	10/673	86/18670	0.00104	0.01122	0.008609	PTGFR/TG	10	geneontol	0.014859
GO:00025 acute infla	18/673	220/18670	0.001067	0.011483	0.008811	PTGER3/C	18	geneontol	0.026746
GO:00487 branching	14/673	150/18670	0.001073	0.01152	0.008839	EPHA2/TA	14	geneontol	0.020802
GO:00510 regulation	26/673	373/18670	0.001088	0.01166	0.008946	TGFBR3/N	26	geneontol	0.038633
GO:00023 cytokine p	11/673	102/18670	0.001118	0.011956	0.009173	IL10/NLRP	11	geneontol	0.016345
GO:00360 CD8-posit	5/673	23/18670	0.001175	0.012393	0.009509	EOMES/TR	5	geneontol	0.007429
GO:00518 mitochond	5/673	23/18670	0.001175	0.012393	0.009509	KDR/LRRK	5	geneontol	0.007429
GO:00614 establishm	5/673	23/18670	0.001175	0.012393	0.009509	SFN/CLDN	5	geneontol	0.007429
GO:19010 negative re	5/673	23/18670	0.001175	0.012393	0.009509	IL10/HGF/	5	geneontol	0.007429
GO:19032 negative re	5/673	23/18670	0.001175	0.012393	0.009509	IL10/HGF/	5	geneontol	0.007429
GO:20010 negative re	5/673	23/18670	0.001175	0.012393	0.009509	IL10/HGF/	5	geneontol	0.007429
GO:00025 myeloid le	17/673	204/18670	0.001189	0.012448	0.00955	EPHA2/TA	17	geneontol	0.02526
GO:00457 positive re	17/673	204/18670	0.001189	0.012448	0.00955	IL10/CYP1	17	geneontol	0.02526
GO:19029 positive re	17/673	204/18670	0.001189	0.012448	0.00955	S100A10/F	17	geneontol	0.02526
GO:00099 cell-cell re	9/673	73/18670	0.001206	0.012548	0.009627	DOCK2/CC	9	geneontol	0.013373
GO:00024 inflammat	7/673	46/18670	0.001206	0.012548	0.009627	IL10/CD28	7	geneontol	0.010401
GO:00226 ovulation	7/673	46/18670	0.001206	0.012548	0.009627	PTX3/SLIT	7	geneontol	0.010401
GO:00326 regulation	11/673	103/18670	0.001212	0.012582	0.009653	MNDA/PY	11	geneontol	0.016345
GO:00607 cell fate	6/673	34/18670	0.001218	0.012601	0.009668	EOMES/TR	6	geneontol	0.008915
GO:00018 placenta	14/673	152/18670	0.001219	0.012601	0.009668	GJB5/GJB3	14	geneontol	0.020802
GO:00610 regulation	10/673	88/18670	0.001243	0.012759	0.009789	TAL1/EFNA	10	geneontol	0.014859
GO:19035 positive re	10/673	88/18670	0.001243	0.012759	0.009789	CD2/PTPR	10	geneontol	0.014859
GO:19037 regulation	10/673	88/18670	0.001243	0.012759	0.009789	P2RY12/PI	10	geneontol	0.014859
GO:00712 cellular res	17/673	205/18670	0.001254	0.012793	0.009815	PDE4B/IL1	17	geneontol	0.02526
GO:00092 cyclic nucl	4/673	14/18670	0.001255	0.012793	0.009815	PDE4B/PD	4	geneontol	0.005944
GO:00508 positive re	4/673	14/18670	0.001255	0.012793	0.009815	TRAT1/TE	4	geneontol	0.005944
GO:00099 epidermal	25/673	358/18670	0.001312	0.01332	0.01022	EPHA2/SFI	25	geneontol	0.037147
GO:00015 retinoid m	11/673	104/18670	0.001313	0.01332	0.01022	CRABP2/C	11	geneontol	0.016345
GO:00313 negative re	16/673	188/18670	0.001315	0.01332	0.01022	TACSTD2/	16	geneontol	0.023774
GO:00433 CD4-posit	9/673	74/18670	0.00133	0.013438	0.01031	PLA2G2D/	9	geneontol	0.013373
GO:00464 positive re	10/673	89/18670	0.001356	0.013678	0.010494	TNFSF18/I	10	geneontol	0.014859
GO:00109 positive re	21/673	281/18670	0.001361	0.013696	0.010508	NEGR1/NC	21	geneontol	0.031204
GO:00028 regulation	5/673	24/18670	0.001441	0.014376	0.01103	IL10/CD28	5	geneontol	0.007429
GO:00456 positive re	5/673	24/18670	0.001441	0.014376	0.01103	SFN/SFRP	5	geneontol	0.007429
GO:00603 trabecula	5/673	24/18670	0.001441	0.014376	0.01103	TGFBR3/SF	5	geneontol	0.007429
GO:00716 positive re	5/673	24/18670	0.001441	0.014376	0.01103	S100A14/C	5	geneontol	0.007429
GO:01500 neuroinfla	9/673	75/18670	0.001464	0.01457	0.011179	PTPRC/CD	9	geneontol	0.013373
GO:00326 regulation	10/673	90/18670	0.001478	0.014647	0.011237	MNDA/PY	10	geneontol	0.014859
GO:00457 positive re	10/673	90/18670	0.001478	0.014647	0.011237	DDR2/OSF	10	geneontol	0.014859
GO:00322 positive re	8/673	61/18670	0.001491	0.014749	0.011316	S100A10/F	8	geneontol	0.011887
GO:00024 T cell med	11/673	106/18670	0.001534	0.015137	0.011613	CD1C/CD1	11	geneontol	0.016345
GO:00081 actin poly	17/673	209/18670	0.001546	0.015227	0.011683	PLEK/ADD	17	geneontol	0.02526
GO:00017 microglial	7/673	48/18670	0.001559	0.015229	0.011685	PTPRC/ST	7	geneontol	0.010401

GO:000221 leukocyte i 7/673	48/18670	0.001559	0.015229	0.011685	PTPRC/STP	7	geneontol	0.010401
GO:000271 positive re 7/673	48/18670	0.001559	0.015229	0.011685	CD1C/CD1	7	geneontol	0.010401
GO:003521 exocrine s 7/673	48/18670	0.001559	0.015229	0.011685	FGF10/HG	7	geneontol	0.010401
GO:000721 JAK-STAT 14/673	156/18670	0.001564	0.015242	0.011694	TNFSF18/F	14	geneontol	0.020802
GO:003051 regulation 9/673	76/18670	0.001608	0.01564	0.012	S1PR1/DD	9	geneontol	0.013373
GO:001071 negative re 24/673	344/18670	0.001644	0.015834	0.012149	TACSTD2/	24	geneontol	0.035661
GO:000221 lymphocyt 8/673	62/18670	0.001659	0.015834	0.012149	DOCK10/C	8	geneontol	0.011887
GO:003261 interleukin 8/673	62/18670	0.001659	0.015834	0.012149	PDE4B/PTI	8	geneontol	0.011887
GO:001071 macrophag 6/673	36/18670	0.001659	0.015834	0.012149	PPARG/AC	6	geneontol	0.008915
GO:003271 positive re 6/673	36/18670	0.001659	0.015834	0.012149	CD28/TIGI	6	geneontol	0.008915
GO:003511 hindlimb n 6/673	36/18670	0.001659	0.015834	0.012149	OSR1/AFF	6	geneontol	0.008915
GO:009001 foam cell c 6/673	36/18670	0.001659	0.015834	0.012149	PPARG/AC	6	geneontol	0.008915
GO:000171 endoderm 4/673	15/18670	0.001662	0.015834	0.012149	EOMES/PC	4	geneontol	0.005944
GO:006001 regulation 4/673	15/18670	0.001662	0.015834	0.012149	PPARG/ST	4	geneontol	0.005944
GO:190001 positive re 4/673	15/18670	0.001662	0.015834	0.012149	EPS8L3/P2	4	geneontol	0.005944
GO:003211 negative re 25/673	365/18670	0.001711	0.016263	0.012478	PTPRC/IL1	25	geneontol	0.037147
GO:000231 mature B c 5/673	25/18670	0.001749	0.016473	0.012639	DOCK10/L	5	geneontol	0.007429
GO:007201 glomerulu 5/673	25/18670	0.001749	0.016473	0.012639	OSR1/PDC	5	geneontol	0.007429
GO:007261 eosinophil 5/673	25/18670	0.001749	0.016473	0.012639	LGALS3/C	5	geneontol	0.007429
GO:009001 regulation 5/673	25/18670	0.001749	0.016473	0.012639	S100A14/C	5	geneontol	0.007429
GO:001401 regulation 12/673	124/18670	0.001751	0.016473	0.012639	SLC45A3/F	12	geneontol	0.017831
GO:000271 negative re 7/673	49/18670	0.001764	0.016527	0.012681	CD84/PTPI	7	geneontol	0.010401
GO:000831 glial cell m 7/673	49/18670	0.001764	0.016527	0.012681	CX3CR1/C	7	geneontol	0.010401
GO:007121 cellular res 17/673	212/18670	0.001801	0.016843	0.012923	PDE4B/IL1	17	geneontol	0.02526
GO:000261 regulation 14/673	159/18670	0.001873	0.017393	0.013344	PTGER3/C	14	geneontol	0.020802
GO:006051 muscle tiss 27/673	408/18670	0.001874	0.017393	0.013344	TGFBR3/S	27	geneontol	0.040119
GO:003031 embryonic 12/673	125/18670	0.001875	0.017393	0.013344	CRABP2/C	12	geneontol	0.017831
GO:003511 embryonic 12/673	125/18670	0.001875	0.017393	0.013344	CRABP2/C	12	geneontol	0.017831
GO:003431 adherens j 13/673	142/18670	0.001899	0.017577	0.013486	S100A10/C	13	geneontol	0.019316
GO:004881 axon exter 6/673	37/18670	0.001921	0.017648	0.01354	SEMA3G/S	6	geneontol	0.008915
GO:006031 head morp 6/673	37/18670	0.001921	0.017648	0.01354	IHH/PDGF	6	geneontol	0.008915
GO:190221 neuron prc 6/673	37/18670	0.001921	0.017648	0.01354	SEMA3G/S	6	geneontol	0.008915
GO:000641 protein O- 11/673	109/18670	0.001921	0.017648	0.01354	MUC1/B3C	11	geneontol	0.016345
GO:001011 body morp 7/673	50/18670	0.001988	0.018225	0.013983	IHH/PDGF	7	geneontol	0.010401
GO:003431 cell junctio 21/673	290/18670	0.002002	0.018316	0.014053	EPHA2/S1	21	geneontol	0.031204
GO:009731 response t 18/673	233/18670	0.002029	0.018525	0.014213	PTGFR/TG	18	geneontol	0.026746
GO:007011 regulation 10/673	94/18670	0.002054	0.018715	0.014359	S1PR1/DD	10	geneontol	0.014859
GO:004501 regulation 29/673	452/18670	0.002058	0.018715	0.014359	S100A14/M	29	geneontol	0.043091
GO:001611 diterpenoi 11/673	110/18670	0.002067	0.018763	0.014396	CRABP2/C	11	geneontol	0.016345
GO:001061 regulation 21/673	291/18670	0.002087	0.018888	0.014492	EPHA2/TA	21	geneontol	0.031204
GO:000231 T cell linea 5/673	26/18670	0.002101	0.018888	0.014492	LY9/IRF4/S	5	geneontol	0.007429
GO:003351 regulation 5/673	26/18670	0.002101	0.018888	0.014492	SFN/CLDN	5	geneontol	0.007429
GO:005141 negative re 5/673	26/18670	0.002101	0.018888	0.014492	TACSTD2/	5	geneontol	0.007429
GO:006071 cell differe 5/673	26/18670	0.002101	0.018888	0.014492	GJB5/EOM	5	geneontol	0.007429
GO:004561 positive re 25/673	371/18670	0.002132	0.019066	0.014628	NEGR1/NC	25	geneontol	0.037147
GO:000801 regulation 15/673	179/18670	0.002138	0.019066	0.014628	PLEK/ADD	15	geneontol	0.022288
GO:004871 appendag 15/673	179/18670	0.002138	0.019066	0.014628	CRABP2/C	15	geneontol	0.022288
GO:006011 limb devel 15/673	179/18670	0.002138	0.019066	0.014628	CRABP2/C	15	geneontol	0.022288
GO:190511 regulation 4/673	16/18670	0.002154	0.019174	0.014711	PPARG/ST	4	geneontol	0.005944
GO:006051 respiratory 16/673	198/18670	0.002242	0.019918	0.015282	HSD11B1/	16	geneontol	0.023774
GO:007251 endothelia 8/673	65/18670	0.002254	0.019935	0.015295	IL10/ITGA	8	geneontol	0.011887
GO:003081 regulation 15/673	180/18670	0.002257	0.019935	0.015295	PLEK/ADD	15	geneontol	0.022288
GO:007141 cellular res 15/673	180/18670	0.002257	0.019935	0.015295	GSTM5/S1	15	geneontol	0.022288
GO:004331 regulation 17/673	217/18670	0.002305	0.020283	0.015562	TGFBR3/IL	17	geneontol	0.02526
GO:006031 bone deve 17/673	217/18670	0.002305	0.020283	0.015562	TAL1/PTPF	17	geneontol	0.02526
GO:007121 cellular res 18/673	236/18670	0.002333	0.020492	0.015723	PDE4B/IL1	18	geneontol	0.026746
GO:000191 positive re 11/673	112/18670	0.002386	0.020916	0.016048	IL10/ITGA	11	geneontol	0.016345
GO:000851 female gor 10/673	96/18670	0.002404	0.021038	0.016141	PTX3/SLIT	10	geneontol	0.014859
GO:007211 mesoneph 8/673	66/18670	0.002486	0.021661	0.016619	TACSTD2/	8	geneontol	0.011887
GO:003271 positive re 7/673	52/18670	0.002503	0.021661	0.016619	MNDA/PY	7	geneontol	0.010401
GO:005501 sodium ior 7/673	52/18670	0.002503	0.021661	0.016619	NPR1/SCN	7	geneontol	0.010401
GO:006141 renal syste 5/673	27/18670	0.002504	0.021661	0.016619	OSR1/PDC	5	geneontol	0.007429
GO:006141 kidney vas 5/673	27/18670	0.002504	0.021661	0.016619	OSR1/PDC	5	geneontol	0.007429
GO:190161 regulation 5/673	27/18670	0.002504	0.021661	0.016619	CCR2/CXC	5	geneontol	0.007429
GO:003001 actin filam 15/673	182/18670	0.002511	0.021686	0.016639	ADD2/VILL	15	geneontol	0.022288
GO:004561 positive re 6/673	39/18670	0.002537	0.021868	0.016778	SFN/SFRP	6	geneontol	0.008915
GO:004881 stem cell d 19/673	257/18670	0.002546	0.021904	0.016806	TAL1/TAC	19	geneontol	0.028232
GO:001071 negative re 10/673	97/18670	0.002596	0.022255	0.017075	TACSTD2/	10	geneontol	0.014859
GO:003031 osteoclast 10/673	97/18670	0.002596	0.022255	0.017075	EPHA2/EFI	10	geneontol	0.014859
GO:003301 muscle cel 18/673	239/18670	0.002674	0.022883	0.017557	TGFBR3/S	18	geneontol	0.026746
GO:000911 glycoprote 27/673	419/18670	0.002718	0.022918	0.017584	MAN1C1/I	27	geneontol	0.040119
GO:001971 secondary 8/673	67/18670	0.002735	0.022918	0.017584	FMO2/FM	8	geneontol	0.011887
GO:001071 positive re 4/673	17/18670	0.002737	0.022918	0.017584	AGTR1/CD	4	geneontol	0.005944

GO:00312 pseudopod 4/673	17/18670	0.002737	0.022918	0.017584	RAB25/CC	4 geneontol	0.005944
GO:00316 positive re 4/673	17/18670	0.002737	0.022918	0.017584	HGF/ZNF4	4 geneontol	0.005944
GO:00316 heat gener 4/673	17/18670	0.002737	0.022918	0.017584	PTGER3/N	4 geneontol	0.005944
GO:00429 lipoprotein 4/673	17/18670	0.002737	0.022918	0.017584	PPARG/CC	4 geneontol	0.005944
GO:00448 lipoprotein 4/673	17/18670	0.002737	0.022918	0.017584	PPARG/CC	4 geneontol	0.005944
GO:00460 cGMP met 4/673	17/18670	0.002737	0.022918	0.017584	NPR1/PDE	4 geneontol	0.005944
GO:00901 negative re 4/673	17/18670	0.002737	0.022918	0.017584	TACSTD2/	4 geneontol	0.005944
GO:00351 appendage 13/673	148/18670	0.002738	0.022918	0.017584	CRABP2/C	13 geneontol	0.019316
GO:00351 limb morph 13/673	148/18670	0.002738	0.022918	0.017584	CRABP2/C	13 geneontol	0.019316
GO:00603 bone morph 11/673	114/18670	0.002743	0.022918	0.017584	VIT/IHH/TL	11 geneontol	0.016345
GO:00507 interleukin 7/673	53/18670	0.002796	0.02323	0.017823	NLRP3/CD	7 geneontol	0.010401
GO:00506 cytokine sig 18/673	240/18670	0.002797	0.02323	0.017823	CD2/S100,	18 geneontol	0.026746
GO:00313 regulation 10/673	98/18670	0.0028	0.02323	0.017823	CD1C/CD1	10 geneontol	0.014859
GO:00507 regulation 10/673	98/18670	0.0028	0.02323	0.017823	PTPRC/C4I	10 geneontol	0.014859
GO:00708 divalent m 30/673	483/18670	0.002821	0.023358	0.017921	PDE4B/FCI	30 geneontol	0.044577
GO:00022 activation 22/673	319/18670	0.002898	0.023955	0.018379	S100A14/N	22 geneontol	0.032689
GO:00343 cell junction 18/673	241/18670	0.002924	0.024127	0.018511	EPHA2/S1I	18 geneontol	0.026746
GO:00466 female sex 11/673	115/18670	0.002937	0.024127	0.018511	PTX3/SLIT;	11 geneontol	0.016345
GO:19037 positive re 15/673	185/18670	0.002937	0.024127	0.018511	TAL1/PTPF	15 geneontol	0.022288
GO:00026 regulation 5/673	28/18670	0.002959	0.024127	0.018511	IL1R1/ITGA	5 geneontol	0.007429
GO:00108 T cell chem 5/673	28/18670	0.002959	0.024127	0.018511	CCR2/CXC	5 geneontol	0.007429
GO:00605 prostate g 5/673	28/18670	0.002959	0.024127	0.018511	FGF10/SHI	5 geneontol	0.007429
GO:00850 extracellular 5/673	28/18670	0.002959	0.024127	0.018511	IHH/TNXB.	5 geneontol	0.007429
GO:00459 regulation 12/673	132/18670	0.00296	0.024127	0.018511	IL10/OSR1	12 geneontol	0.017831
GO:00313 positive re 8/673	68/18670	0.003004	0.024443	0.018753	CD1C/CD1	8 geneontol	0.011887
GO:00017 cell fate sp 10/673	99/18670	0.003017	0.024501	0.018798	IHH/EOME	10 geneontol	0.014859
GO:00450 positive re 25/673	381/18670	0.003031	0.024574	0.018854	S100A14/N	25 geneontol	0.037147
GO:00071 homophilic 14/673	168/18670	0.003115	0.025209	0.019342	NEXN/CAI	14 geneontol	0.020802
GO:00027 positive re 12/673	133/18670	0.00315	0.025451	0.019527	CD1C/CD1	12 geneontol	0.017831
GO:00971 extrinsic act 17/673	224/18670	0.003203	0.025832	0.019819	NGF/PTPR	17 geneontol	0.02526
GO:19013 negative re 15/673	187/18670	0.003253	0.026185	0.02009	EPHA2/NP	15 geneontol	0.022288
GO:00605 skeletal m 14/673	169/18670	0.003287	0.026197	0.020099	CHRNA1/E	14 geneontol	0.020802
GO:00109 negative re 6/673	41/18670	0.00329	0.026197	0.020099	C4BPB/CR	6 geneontol	0.008915
GO:00351 forelimb m 6/673	41/18670	0.00329	0.026197	0.020099	CRABP2/C	6 geneontol	0.008915
GO:00971 ruffle associ 6/673	41/18670	0.00329	0.026197	0.020099	TACSTD2/	6 geneontol	0.008915
GO:19033 negative re 6/673	41/18670	0.00329	0.026197	0.020099	C4BPB/CR	6 geneontol	0.008915
GO:00426 ovulation 8/673	69/18670	0.003294	0.026197	0.020099	PTX3/SLIT;	8 geneontol	0.011887
GO:00702 lymphocyte 8/673	69/18670	0.003294	0.026197	0.020099	EFNA1/IL1	8 geneontol	0.011887
GO:00725 divalent in 30/673	489/18670	0.003376	0.026806	0.020567	PDE4B/FCI	30 geneontol	0.044577
GO:00900 positive re 4/673	18/18670	0.00342	0.027061	0.020762	S100A14/C	4 geneontol	0.005944
GO:01500 negative re 4/673	18/18670	0.00342	0.027061	0.020762	PTPRC/CD	4 geneontol	0.005944
GO:00001 activation 13/673	152/18670	0.003451	0.027257	0.020913	PTPRC/FGI	13 geneontol	0.019316
GO:00322 negative re 5/673	29/18670	0.003471	0.027322	0.020963	TACSTD2/	5 geneontol	0.007429
GO:19001 negative re 5/673	29/18670	0.003471	0.027322	0.020963	CLDN18/C	5 geneontol	0.007429
GO:00465 developm 10/673	101/18670	0.00349	0.027365	0.020996	PTX3/SLIT;	10 geneontol	0.014859
GO:00140 mesenchyme 9/673	85/18670	0.003494	0.027365	0.020996	ZEB2/SEM	9 geneontol	0.013373
GO:00488 stem cell d 9/673	85/18670	0.003494	0.027365	0.020996	PTPRC/ZEI	9 geneontol	0.013373
GO:00327 negative re 8/673	70/18670	0.003604	0.028133	0.021585	SLAMF1/IL	8 geneontol	0.011887
GO:00720 regulation 8/673	70/18670	0.003604	0.028133	0.021585	PTPRC/CX.	8 geneontol	0.011887
GO:00507 regulation 29/673	472/18670	0.003832	0.029866	0.022915	SLC2A1/CI	29 geneontol	0.043091
GO:00303 lung devel 14/673	172/18670	0.003851	0.029961	0.022987	HSD11B1/	14 geneontol	0.020802
GO:00107 positive re 13/673	154/18670	0.003859	0.029975	0.022998	NGF/S100,	13 geneontol	0.019316
GO:00071 establishm 16/673	210/18670	0.004016	0.031086	0.02385	RHOH/FGF	16 geneontol	0.023774
GO:00507 regulation 16/673	210/18670	0.004016	0.031086	0.02385	CD2/IL10/I	16 geneontol	0.023774
GO:00217 olfactory b 5/673	30/18670	0.004043	0.031141	0.023893	EOMES/SL	5 geneontol	0.007429
GO:00466 regulation 5/673	30/18670	0.004043	0.031141	0.023893	PTPRC/ZA	5 geneontol	0.007429
GO:19032 regulation 5/673	30/18670	0.004043	0.031141	0.023893	IL10/HGF/	5 geneontol	0.007429
GO:00069 phagocyte 24/673	369/18670	0.004056	0.031187	0.023928	LEPR/SLAM	24 geneontol	0.035661
GO:00067 terpenoid 11/673	120/18670	0.004079	0.031315	0.024026	CRABP2/C	11 geneontol	0.016345
GO:00147 striated m 25/673	390/18670	0.004096	0.031394	0.024087	TGFBR3/S;	25 geneontol	0.037147
GO:19040 positive re 17/673	230/18670	0.004188	0.031789	0.02439	IL10/CYP1	17 geneontol	0.02526
GO:00325 regulation 24/673	370/18670	0.004195	0.031789	0.02439	NGF/CRAE	24 geneontol	0.035661
GO:00508 positive re 6/673	43/18670	0.004198	0.031789	0.02439	ZAP70/TR.	6 geneontol	0.008915
GO:00016 gastric acid 4/673	19/18670	0.00421	0.031789	0.02439	PTGER3/N	4 geneontol	0.005944
GO:00017 mesoderm 4/673	19/18670	0.00421	0.031789	0.02439	TRIM15/FC	4 geneontol	0.005944
GO:00023 mature B c 4/673	19/18670	0.00421	0.031789	0.02439	DOCK10/L	4 geneontol	0.005944
GO:00023 alpha-beta 4/673	19/18670	0.00421	0.031789	0.02439	LY9/IRF4/E	4 geneontol	0.005944
GO:00450 regulation 4/673	19/18670	0.00421	0.031789	0.02439	PTPRC/CD	4 geneontol	0.005944
GO:20002 positive re 4/673	19/18670	0.00421	0.031789	0.02439	STAP1/BAI	4 geneontol	0.005944
GO:19035 negative re 8/673	72/18670	0.004292	0.032359	0.024827	SLAMF1/IL	8 geneontol	0.011887
GO:00507 positive re 17/673	139/18670	0.004508	0.033927	0.026031	CD2/IL10/I	12 geneontol	0.017831
GO:00424 hormone r 12/673	232/18670	0.004567	0.034319	0.026331	NGF/CRAE	17 geneontol	0.02526
GO:00016 fever gene 3/673	10/18670	0.004628	0.034326	0.026337	PTGER3/CI	3 geneontol	0.004458

GO:000225	T cell activ	3/673	10/18670	0.004628	0.034326	0.026337	FGL2/LGAI	3	geneontol	0.004458
GO:003262	interleukin	3/673	10/18670	0.004628	0.034326	0.026337	CD84/IL10	3	geneontol	0.004458
GO:004308	penile errec	3/673	10/18670	0.004628	0.034326	0.026337	CNR1/AVF	3	geneontol	0.004458
GO:005190	positive re	3/673	10/18670	0.004628	0.034326	0.026337	KDR/DCN/	3	geneontol	0.004458
GO:006114	lung secre	3/673	10/18670	0.004628	0.034326	0.026337	FGF10/SPI	3	geneontol	0.004458
GO:007262	interleukin	3/673	10/18670	0.004628	0.034326	0.026337	CCL19/CCI	3	geneontol	0.004458
GO:190432	regulation	3/673	10/18670	0.004628	0.034326	0.026337	SHH/SFRP	3	geneontol	0.004458
GO:000170	in utero er	24/673	373/18670	0.004635	0.034326	0.026337	GJB5/GJB3	24	geneontol	0.035661
GO:003110	animal org	8/673	73/18670	0.004672	0.034334	0.026342	TGFBR3/IL	8	geneontol	0.011887
GO:006190	glial cell ac	7/673	58/18670	0.004674	0.034334	0.026342	PTPRC/ST/	7	geneontol	0.010401
GO:000262	positive re	5/673	31/18670	0.00468	0.034334	0.026342	PTGER3/CI	5	geneontol	0.007429
GO:000914	purine ribc	5/673	31/18670	0.00468	0.034334	0.026342	PDE4B/PD	5	geneontol	0.007429
GO:002194	olfactory lk	5/673	31/18670	0.00468	0.034334	0.026342	EOMES/SL	5	geneontol	0.007429
GO:200040	positive re	5/673	31/18670	0.00468	0.034334	0.026342	ITGA4/CCF	5	geneontol	0.007429
GO:003462	response t	21/673	312/18670	0.004714	0.034482	0.026456	SELE/TNFS	21	geneontol	0.031204
GO:200040	regulation	6/673	44/18670	0.004716	0.034482	0.026456	ITGA4/CCF	6	geneontol	0.008915
GO:003030	respiratory	14/673	176/18670	0.004723	0.034482	0.026456	HSD11B1/	14	geneontol	0.020802
GO:009024	regulation	20/673	292/18670	0.004738	0.034541	0.026502	TGFBR3/XI	20	geneontol	0.029718
GO:006104	somite dev	9/673	89/18670	0.004753	0.034593	0.026541	ZEB2/IHH/	9	geneontol	0.013373
GO:004630	positive re	12/673	140/18670	0.004773	0.034634	0.026573	SLAMF1/Z	12	geneontol	0.017831
GO:007202	kidney epi	12/673	140/18670	0.004773	0.034634	0.026573	TACSTD2/	12	geneontol	0.017831
GO:000721	JNK casca	16/673	214/18670	0.004816	0.034887	0.026767	SLAMF1/Z	16	geneontol	0.023774
GO:004352	endothelia	19/673	273/18670	0.004915	0.035551	0.027276	EPHA2/EFI	19	geneontol	0.028232
GO:004212	neurotrans	10/673	106/18670	0.004934	0.03563	0.027337	IL10/CYP1	10	geneontol	0.014859
GO:001402	positive re	8/673	74/18670	0.005077	0.036495	0.028001	PPARG/CC	8	geneontol	0.011887
GO:007202	nephron tl	8/673	74/18670	0.005077	0.036495	0.028001	TACSTD2/	8	geneontol	0.011887
GO:000232	lymphoid p	4/673	20/18670	0.005114	0.036495	0.028001	SHH/FLT3/	4	geneontol	0.005944
GO:000762	copulation	4/673	20/18670	0.005114	0.036495	0.028001	CNR1/AVF	4	geneontol	0.005944
GO:001050	positive re	4/673	20/18670	0.005114	0.036495	0.028001	CCL19/CCI	4	geneontol	0.005944
GO:190392	regulation	4/673	20/18670	0.005114	0.036495	0.028001	PTPRC/ST/	4	geneontol	0.005944
GO:000160	metaneph	9/673	90/18670	0.005117	0.036495	0.028001	OSR1/CXC	9	geneontol	0.013373
GO:001402	neural cre	9/673	90/18670	0.005117	0.036495	0.028001	ZEB2/SEM	9	geneontol	0.013373
GO:000160	branching	7/673	59/18670	0.005142	0.036506	0.028009	TACSTD2/	7	geneontol	0.010401
GO:003272	positive re	7/673	59/18670	0.005142	0.036506	0.028009	MNDA/PY	7	geneontol	0.010401
GO:200003	regulation	7/673	59/18670	0.005142	0.036506	0.028009	ITGA4/KDF	7	geneontol	0.010401
GO:003594	endoderm	6/673	45/18670	0.005279	0.037423	0.028713	LAMB3/ITC	6	geneontol	0.008915
GO:000752	skeletal m	13/673	160/18670	0.005326	0.037699	0.028925	CHRNA1/E	13	geneontol	0.019316
GO:007202	nephron d	12/673	142/18670	0.005343	0.037758	0.02897	TACSTD2/	12	geneontol	0.017831
GO:000924	ribonucleo	5/673	32/18670	0.005385	0.037886	0.029068	PDE4B/PD	5	geneontol	0.007429
GO:006032	face morpl	5/673	32/18670	0.005385	0.037886	0.029068	PDGFRA/C	5	geneontol	0.007429
GO:006134	heart trab	5/673	32/18670	0.005385	0.037886	0.029068	TGFBR3/S:	5	geneontol	0.007429
GO:005104	positive re	14/673	179/18670	0.005476	0.038465	0.029512	NGF/S100,	14	geneontol	0.020802
GO:004552	mast cell	4/673	60/18670	0.005644	0.039546	0.030342	S100A12/C	7	geneontol	0.010401
GO:004432	cellular res	12/673	143/18670	0.005647	0.039546	0.030342	CXCL13/F/	12	geneontol	0.017831
GO:001602	immunogl	16/673	218/18670	0.005741	0.040147	0.030803	PTPRC/IL1	16	geneontol	0.023774
GO:005070	regulation	6/673	46/18670	0.00589	0.040974	0.031437	NLRP3/LPI	6	geneontol	0.008915
GO:005092	negative c	6/673	46/18670	0.00589	0.040974	0.031437	SEMA3G/S	6	geneontol	0.008915
GO:006072	labyrinthin	6/673	46/18670	0.00589	0.040974	0.031437	GJB5/IL10/	6	geneontol	0.008915
GO:003080	regulation	13/673	162/18670	0.005904	0.040974	0.031437	ADD2/VILL	13	geneontol	0.019316
GO:003572	CD4-posit	9/673	92/18670	0.005909	0.040974	0.031437	PLA2G2D/	9	geneontol	0.013373
GO:000270	innate inm	20/673	298/18670	0.005913	0.040974	0.031437	S100A14/M	20	geneontol	0.029718
GO:007202	nephron e	8/673	76/18670	0.005968	0.041291	0.03168	TACSTD2/	8	geneontol	0.011887
GO:000242	acute infla	4/673	21/18670	0.00614	0.04138	0.031748	CXCR2/CN	4	geneontol	0.005944
GO:003022	maintenan	4/673	21/18670	0.00614	0.04138	0.031748	MUC4/TFF	4	geneontol	0.005944
GO:003582	regulation	4/673	21/18670	0.00614	0.04138	0.031748	NPR1/AGT	4	geneontol	0.005944
GO:006072	labyrinthin	4/673	21/18670	0.00614	0.04138	0.031748	GJB5/IL10/	4	geneontol	0.005944
GO:007212	cell prolif	4/673	21/18670	0.00614	0.04138	0.031748	OSR1/SHH	4	geneontol	0.005944
GO:014012	positive re	4/673	21/18670	0.00614	0.04138	0.031748	CCR2/CXC	4	geneontol	0.005944
GO:200030	regulation	4/673	21/18670	0.00614	0.04138	0.031748	SHH/FGFR	4	geneontol	0.005944
GO:000192	regulation	5/673	33/18670	0.006162	0.04138	0.031748	CD1C/CD1	5	geneontol	0.007429
GO:003512	embryonic	5/673	33/18670	0.006162	0.04138	0.031748	CRABP2/C	5	geneontol	0.007429
GO:005072	positive re	5/673	33/18670	0.006162	0.04138	0.031748	NLRP3/LPI	5	geneontol	0.007429
GO:007022	regulation	5/673	33/18670	0.006162	0.04138	0.031748	EFNA1/IL7	5	geneontol	0.007429
GO:190182	positive re	5/673	33/18670	0.006162	0.04138	0.031748	EPHA2/S10	5	geneontol	0.007429
GO:200102	regulation	5/673	33/18670	0.006162	0.04138	0.031748	IL10/HGF/	5	geneontol	0.007429
GO:000302	heart mor	18/673	259/18670	0.006178	0.04138	0.031748	TGFBR3/S:	18	geneontol	0.026746
GO:000224	alpha-bet	7/673	61/18670	0.006183	0.04138	0.031748	LY9/NLRP3	7	geneontol	0.010401
GO:000224	alpha-bet	7/673	61/18670	0.006183	0.04138	0.031748	LY9/NLRP3	7	geneontol	0.010401
GO:005070	interleukin	7/673	61/18670	0.006183	0.04138	0.031748	NLRP3/CD	7	geneontol	0.010401
GO:000262	negative r	3/673	11/18670	0.006195	0.04138	0.031748	FCRL3/IL3:	3	geneontol	0.004458
GO:000292	regulation	3/673	11/18670	0.006195	0.04138	0.031748	PTPRC/CAI	3	geneontol	0.004458
GO:003162	positive re	3/673	11/18670	0.006195	0.04138	0.031748	PTGER3/N	3	geneontol	0.004458
GO:003572	natural kill	3/673	11/18670	0.006195	0.04138	0.031748	PIK3CG/CC	3	geneontol	0.004458

GO:00431: positive re 3/673	11/18670	0.006195	0.04138	0.031748	CXCR2/PD	3 geneontol	0.004458
GO:00453: type I inter 3/673	11/18670	0.006195	0.04138	0.031748	IL10/TLR7/	3 geneontol	0.004458
GO:19059: regulation 3/673	11/18670	0.006195	0.04138	0.031748	FGFR1/SO	3 geneontol	0.004458
GO:00060: glycosamir 10/673	110/18670	0.006396	0.042658	0.03273	B3GNT7/H	10 geneontol	0.014859
GO:00197: B cell med 16/673	221/18670	0.006526	0.043468	0.03335	PTPRC/IL1	16 geneontol	0.023774
GO:00613: trabecula r 6/673	47/18670	0.006551	0.043507	0.033381	TGFBR3/S:	6 geneontol	0.008915
GO:00988: bone grow 6/673	47/18670	0.006551	0.043507	0.033381	LEPR/DDR	6 geneontol	0.008915
GO:00458: negative r 23/673	363/18670	0.00659	0.043679	0.033513	SFN/NGF/	23 geneontol	0.034175
GO:00508: T cell recej 15/673	202/18670	0.006617	0.043679	0.033513	PDE4B/PTI	15 geneontol	0.022288
GO:00507: regulation 14/673	183/18670	0.006627	0.043679	0.033513	NGF/EFNA	14 geneontol	0.020802
GO:00512: negative r 12/673	146/18670	0.006643	0.043679	0.033513	PLA2G2D/	12 geneontol	0.017831
GO:00513: response t 12/673	146/18670	0.006643	0.043679	0.033513	IL10/FAM1	12 geneontol	0.017831
GO:19048: regulation 12/673	146/18670	0.006643	0.043679	0.033513	TNFSF18/F	12 geneontol	0.017831
GO:20002: regulation 12/673	146/18670	0.006643	0.043679	0.033513	CNR1/LFN	12 geneontol	0.017831
GO:00613: renal tubu 8/673	78/18670	0.006972	0.045607	0.034991	TACSTD2/	8 geneontol	0.011887
GO:00706: negative r 8/673	78/18670	0.006972	0.045607	0.034991	PLA2G2D/	8 geneontol	0.011887
GO:00720: nephron n 8/673	78/18670	0.006972	0.045607	0.034991	TACSTD2/	8 geneontol	0.011887
GO:19030: negative r 11/673	129/18670	0.007006	0.045607	0.034991	PLA2G2D/	11 geneontol	0.016345
GO:00364: cell death 5/673	34/18670	0.007015	0.045607	0.034991	IL10/HGF/	5 geneontol	0.007429
GO:00425: tumor nec 5/673	34/18670	0.007015	0.045607	0.034991	IL10/CX3C	5 geneontol	0.007429
GO:00425: regulation 5/673	34/18670	0.007015	0.045607	0.034991	IL10/CX3C	5 geneontol	0.007429
GO:00485: embryonic 5/673	34/18670	0.007015	0.045607	0.034991	IHH/PDGF	5 geneontol	0.007429
GO:00508: synapse oi 25/673	408/18670	0.00718	0.046614	0.035764	EFNA1/IG	25 geneontol	0.037147
GO:00308: prostate g 6/673	48/18670	0.007264	0.046828	0.035928	FGF10/SHI	6 geneontol	0.008915
GO:00468: regulation 6/673	48/18670	0.007264	0.046828	0.035928	LEPR/S1PF	6 geneontol	0.008915
GO:00027: positive re 9/673	95/18670	0.007271	0.046828	0.035928	PTPRC/NL	9 geneontol	0.013373
GO:00355: calcium-m 4/673	22/18670	0.007294	0.046828	0.035928	PTGFR/SEL	4 geneontol	0.005944
GO:00420: interleukin 4/673	22/18670	0.007294	0.046828	0.035928	PTPRC/CD	4 geneontol	0.005944
GO:00434: regulation 4/673	22/18670	0.007294	0.046828	0.035928	ITGA4/LG	4 geneontol	0.005944
GO:00483: immunogly 4/673	22/18670	0.007294	0.046828	0.035928	LAX1/IL33,	4 geneontol	0.005944
GO:00713: cellular res 4/673	22/18670	0.007294	0.046828	0.035928	PTGFR/PP	4 geneontol	0.005944
GO:00217: developm 19/673	284/18670	0.007421	0.047581	0.036507	TAL1/S1PF	19 geneontol	0.028232
GO:00015: vasculoger 8/673	79/18670	0.007519	0.048143	0.036937	EPHA2/TG	8 geneontol	0.011887
GO:00096: response t 21/673	326/18670	0.00767	0.049038	0.037624	PTPRC/NL	21 geneontol	0.031204
GO:00019: cell killing 13/673	168/18670	0.007942	0.05023	0.038539	S100A12/C	13 geneontol	0.019316
GO:00420: type 2 imn 5/673	35/18670	0.007946	0.05023	0.038539	IL10/NLRP	5 geneontol	0.007429
GO:00456: positive re 7/673	64/18670	0.008028	0.05023	0.038539	PPARG/LP	7 geneontol	0.010401
GO:00019: T cell med 6/673	49/18670	0.008032	0.05023	0.038539	CD1C/CD1	6 geneontol	0.008915
GO:00032: regulation 6/673	49/18670	0.008032	0.05023	0.038539	KDR/SCN2	6 geneontol	0.008915
GO:19030: regulation 6/673	49/18670	0.008032	0.05023	0.038539	PTX3/CCL	6 geneontol	0.008915
GO:00082: opsonizati 3/673	12/18670	0.008041	0.05023	0.038539	C4BPB/PT	3 geneontol	0.004458
GO:00315: hemidesm 3/673	12/18670	0.008041	0.05023	0.038539	LAMB3/CC	3 geneontol	0.004458
GO:00455: positive re 3/673	12/18670	0.008041	0.05023	0.038539	CD27/NCK	3 geneontol	0.004458
GO:00465: saliva secr 3/673	12/18670	0.008041	0.05023	0.038539	FGF10/AQ	3 geneontol	0.004458
GO:00604: regulation 3/673	12/18670	0.008041	0.05023	0.038539	PTGER3/N	3 geneontol	0.004458
GO:00606: branching 3/673	12/18670	0.008041	0.05023	0.038539	IL10/ST14/	3 geneontol	0.004458
GO:00704: thrombin- 3/673	12/18670	0.008041	0.05023	0.038539	PLEK/MET,	3 geneontol	0.004458
GO:00725: T-helper 1/3/673	12/18670	0.008041	0.05023	0.038539	LY9/IRF4/E	3 geneontol	0.004458
GO:00972: hepatocyte 3/673	12/18670	0.008041	0.05023	0.038539	PIK3CG/KF	3 geneontol	0.004458
GO:19041: positive re 3/673	12/18670	0.008041	0.05023	0.038539	KDR/DCN/	3 geneontol	0.004458
GO:19055: negative r 3/673	12/18670	0.008041	0.05023	0.038539	CD200R1/	3 geneontol	0.004458
GO:00717: response t 12/673	150/18670	0.008181	0.051037	0.039158	CXCL13/F	12 geneontol	0.017831
GO:00486: regulation 13/673	169/18670	0.00833	0.051897	0.039818	S1PR1/NPI	13 geneontol	0.019316
GO:00027: regulation 29/673	500/18670	0.008364	0.052037	0.039925	SLC2A1/CI	29 geneontol	0.043091
GO:19012: negative r 15/673	208/18670	0.008573	0.052897	0.040585	NGF/IL10/	15 geneontol	0.022288
GO:00305: male genit 4/673	23/18670	0.008582	0.052897	0.040585	PDGFRA/F	4 geneontol	0.005944
GO:00358: renal sodit 4/673	23/18670	0.008582	0.052897	0.040585	NPR1/AGT	4 geneontol	0.005944
GO:00487: positive re 4/673	23/18670	0.008582	0.052897	0.040585	PPARG/SH	4 geneontol	0.005944
GO:19007: regulation 4/673	23/18670	0.008582	0.052897	0.040585	XDH/ADAI	4 geneontol	0.005944
GO:19034: regulation 4/673	23/18670	0.008582	0.052897	0.040585	LRRK2/EDI	4 geneontol	0.005944
GO:20000: regulation 4/673	23/18670	0.008582	0.052897	0.040585	SFRP4/SFR	4 geneontol	0.005944
GO:00507: positive re 18/673	268/18670	0.00867	0.053241	0.040849	CD2/IL10/I	18 geneontol	0.026746
GO:00060: aminoglyc 10/673	115/18670	0.008672	0.053241	0.040849	B3GNT7/H	10 geneontol	0.014859
GO:00329: collagen nr 10/673	115/18670	0.008672	0.053241	0.040849	IHH/PPAR	10 geneontol	0.014859
GO:00140: neural cre: 8/673	81/18670	0.008711	0.053407	0.040976	ZEB2/SEM	8 geneontol	0.011887
GO:00606: ureteric bu 7/673	65/18670	0.008725	0.053423	0.040989	TACSTD2/	7 geneontol	0.010401
GO:00017: endoderm 6/673	50/18670	0.008856	0.05408	0.041493	LAMB3/ITC	6 geneontol	0.008915
GO:00451: intermedia 6/673	50/18670	0.008856	0.05408	0.041493	SHH/KRT1	6 geneontol	0.008915
GO:00712: cellular res 15/673	209/18670	0.008939	0.054433	0.041763	GJB3/PTGF	15 geneontol	0.022288
GO:00027: MyD88-de 5/673	36/18670	0.00896	0.054433	0.041763	TLR10/CD:	5 geneontol	0.007429
GO:00104: regulation 5/673	36/18670	0.00896	0.054433	0.041763	SPDEF/FGI	5 geneontol	0.007429
GO:00604: lung epith: 5/673	36/18670	0.00896	0.054433	0.041763	FGF10/SPC	5 geneontol	0.007429
GO:00105: regulation 16/673	229/18670	0.009048	0.054841	0.042077	EPHA2/EFI	16 geneontol	0.023774

GO:00459: negative re 17/673	249/18670	0.009059	0.054841	0.042077	NPR1/KCN	17 geneontol	0.02526
GO:00015: regulation 25/673	416/18670	0.009063	0.054841	0.042077	SFN/NGF/	25 geneontol	0.037147
GO:00486: smooth m 13/673	171/18670	0.00915	0.055297	0.042427	S1PR1/NPI	13 geneontol	0.019316
GO:00302: entry into 11/673	134/18670	0.009225	0.055455	0.042548	EPHA2/SL	11 geneontol	0.016345
GO:00444: entry into 11/673	134/18670	0.009225	0.055455	0.042548	EPHA2/SL	11 geneontol	0.016345
GO:00518: entry into 11/673	134/18670	0.009225	0.055455	0.042548	EPHA2/SL	11 geneontol	0.016345
GO:00518: entry into 11/673	134/18670	0.009225	0.055455	0.042548	EPHA2/SL	11 geneontol	0.016345
GO:00326: regulation 8/673	82/18670	0.009357	0.056178	0.043102	EPHA2/AC	8 geneontol	0.011887
GO:00713: cellular res 19/673	291/18670	0.009497	0.056943	0.043689	TNFSF18/C	19 geneontol	0.028232
GO:00328: positive re 13/673	172/18670	0.009584	0.057391	0.044033	SLAMF1/X	13 geneontol	0.019316
GO:00027: regulation 6/673	51/18670	0.009739	0.058017	0.044514	PTPRC/IL1	6 geneontol	0.008915
GO:00028: regulation 6/673	51/18670	0.009739	0.058017	0.044514	PTPRC/IL1	6 geneontol	0.008915
GO:00451: intermedia 6/673	51/18670	0.009739	0.058017	0.044514	SHH/KRT1	6 geneontol	0.008915
GO:00514: positive re 6/673	51/18670	0.009739	0.058017	0.044514	S100A10/S	6 geneontol	0.008915
GO:00215: telenceph 17/673	251/18670	0.009763	0.058042	0.044532	SLC2A1/ZI	17 geneontol	0.02526
GO:00160: cell growth 28/673	484/18670	0.009768	0.058042	0.044532	SFN/NGF/	28 geneontol	0.041605
GO:19011: carbohydr 14/673	192/18670	0.009927	0.05859	0.044953	PDE4B/PD	14 geneontol	0.020802
GO:00330: regulation 4/673	24/18670	0.01001	0.05859	0.044953	IHH/IL7R/S	4 geneontol	0.005944
GO:00341: toll-like re 4/673	24/18670	0.01001	0.05859	0.044953	FCRL3/LILF	4 geneontol	0.005944
GO:00440: regulation 4/673	24/18670	0.01001	0.05859	0.044953	NPR1/AGT	4 geneontol	0.005944
GO:19025: regulation 4/673	24/18670	0.01001	0.05859	0.044953	XDH/ADAI	4 geneontol	0.005944
GO:19030: positive re 4/673	24/18670	0.01001	0.05859	0.044953	CCL19/CCI	4 geneontol	0.005944
GO:00016: temperatu 13/673	173/18670	0.010033	0.05859	0.044953	LEPR/PTGF	13 geneontol	0.019316
GO:00703: positive re 13/673	173/18670	0.010033	0.05859	0.044953	SLAMF1/X	13 geneontol	0.019316
GO:00344: substrate 9/673	100/18670	0.010058	0.05859	0.044953	TACSTD2/	9 geneontol	0.013373
GO:00352: segmentat 9/673	100/18670	0.010058	0.05859	0.044953	OSR1/ZEB	9 geneontol	0.013373
GO:20010: regulation 9/673	100/18670	0.010058	0.05859	0.044953	IL10/OSR1	9 geneontol	0.013373
GO:00031: regulation 5/673	37/18670	0.01006	0.05859	0.044953	FGF10/SHI	5 geneontol	0.007429
GO:00511: striated mi 19/673	293/18670	0.010168	0.05859	0.044953	CAPN9/PC	19 geneontol	0.028232
GO:00028: regulation 3/673	13/18670	0.010176	0.05859	0.044953	CNR1/CCR	3 geneontol	0.004458
GO:00104: negative re 3/673	13/18670	0.010176	0.05859	0.044953	SPDEF/SO	3 geneontol	0.004458
GO:00108: positive re 3/673	13/18670	0.010176	0.05859	0.044953	FGF10/FGF	3 geneontol	0.004458
GO:00312: positive re 3/673	13/18670	0.010176	0.05859	0.044953	CCL21/CCI	3 geneontol	0.004458
GO:00325: regulation 3/673	13/18670	0.010176	0.05859	0.044953	CDHR2/CI	3 geneontol	0.004458
GO:00450: positive re 3/673	13/18670	0.010176	0.05859	0.044953	TNFRSF13	3 geneontol	0.004458
GO:00508: white fat c 3/673	13/18670	0.010176	0.05859	0.044953	PPARG/FG	3 geneontol	0.004458
GO:00607: spongiotrc 3/673	13/18670	0.010176	0.05859	0.044953	GJB5/PHLI	3 geneontol	0.004458
GO:00996: protein loc 3/673	13/18670	0.010176	0.05859	0.044953	ADAM22/I	3 geneontol	0.004458
GO:00996: neurotrans 3/673	13/18670	0.010176	0.05859	0.044953	ADAM22/I	3 geneontol	0.004458
GO:19039: negative re 3/673	13/18670	0.010176	0.05859	0.044953	OSR1/ANC	3 geneontol	0.004458
GO:20000: positive re 3/673	13/18670	0.010176	0.05859	0.044953	SFRP1/DKI	3 geneontol	0.004458
GO:00109: negative re 12/673	155/18670	0.01048	0.060262	0.046236	EFNA1/NC	12 geneontol	0.017831
GO:00326: regulation 6/673	52/18670	0.010682	0.06135	0.047071	CD28/TIGI	6 geneontol	0.008915
GO:00105: negative re 8/673	84/18670	0.010755	0.061693	0.047333	LEPR/IL10/	8 geneontol	0.011887
GO:00464: regulation 11/673	137/18670	0.010795	0.061845	0.04745	TNFSF18/F	11 geneontol	0.016345
GO:00513: negative re 27/673	466/18670	0.01083	0.061968	0.047545	SFN/LEPR/	27 geneontol	0.040119
GO:00519: regulation 17/673	254/18670	0.010901	0.062298	0.047798	PDE4B/FCI	17 geneontol	0.02526
GO:20001: negative re 13/673	175/18670	0.01098	0.062674	0.048086	EPHA2/NP	13 geneontol	0.019316
GO:00308: regulation 12/673	156/18670	0.010994	0.062675	0.048087	SFN/OSR1	12 geneontol	0.017831
GO:00027: negative re 5/673	38/18670	0.011249	0.063893	0.049022	PTPRC/CAI	5 geneontol	0.007429
GO:00507: positive re 5/673	38/18670	0.011249	0.063893	0.049022	NLRP3/LPI	5 geneontol	0.007429
GO:19040: positive re 5/673	38/18670	0.011249	0.063893	0.049022	ITGA4/SFR	5 geneontol	0.007429
GO:00309: forebrain c 23/673	381/18670	0.011402	0.064624	0.049582	SLC2A1/ZI	23 geneontol	0.034175
GO:00605: developm 16/673	235/18670	0.011406	0.064624	0.049582	S1PR1/NG	16 geneontol	0.023774
GO:00456: regulation 8/673	85/18670	0.01151	0.064995	0.049867	SFN/SFRP2	8 geneontol	0.011887
GO:00507: positive re 8/673	85/18670	0.01151	0.064995	0.049867	NGF/CRAE	8 geneontol	0.011887
GO:00720: stem cell p 10/673	120/18670	0.011524	0.064995	0.049867	PTPRC/CX	10 geneontol	0.014859
GO:00027: negative re 4/673	25/18670	0.011584	0.064995	0.049867	IL10/CD96	4 geneontol	0.005944
GO:00094: toxin meta 4/673	25/18670	0.011584	0.064995	0.049867	FMO2/FMI	4 geneontol	0.005944
GO:00518: positive re 4/673	25/18670	0.011584	0.064995	0.049867	S100A10/h	4 geneontol	0.005944
GO:19058: negative re 4/673	25/18670	0.011584	0.064995	0.049867	EFNA1/NC	4 geneontol	0.005944
GO:20003: positive re 4/673	25/18670	0.011584	0.064995	0.049867	ITGA4/THE	4 geneontol	0.005944
GO:00507: regulation 6/673	53/18670	0.011689	0.065506	0.05026	NLRP3/LPI	6 geneontol	0.008915
GO:00071: G protein- 17/673	256/18670	0.011716	0.065581	0.050317	GRIK3/PTC	17 geneontol	0.02526
GO:00067: isoprenoid 11/673	139/18670	0.011951	0.066811	0.051261	CRABP2/C	11 geneontol	0.016345
GO:00467: viral entry 16/673	121/18670	0.012171	0.067961	0.052143	EPHA2/SL	10 geneontol	0.014859
GO:00019: hair follicle 8/673	86/18670	0.012302	0.068612	0.052642	FGF10/FO	8 geneontol	0.011887
GO:00305: positive re 5/673	39/18670	0.012531	0.06924	0.053124	OSR1/TFA	5 geneontol	0.007429
GO:00487: regulation 5/673	39/18670	0.012531	0.06924	0.053124	SLC45A3/F	5 geneontol	0.007429
GO:00508: regulation 5/673	39/18670	0.012531	0.06924	0.053124	TRAT1/TE	5 geneontol	0.007429
GO:00075: mesoderm 3/673	14/18670	0.012609	0.06924	0.053124	FGFR1/SO	3 geneontol	0.004458
GO:00107: regulation 3/673	14/18670	0.012609	0.06924	0.053124	NPR1/PDE	3 geneontol	0.004458
GO:00312: regulation 3/673	14/18670	0.012609	0.06924	0.053124	CCL21/CCI	3 geneontol	0.004458

GO:00343: triglycerid c 3/673	14/18670	0.012609	0.06924	0.053124	LPL/GPIIB	3	geneontol	0.004458
GO:00358: positive re 3/673	14/18670	0.012609	0.06924	0.053124	NPR1/AVP	3	geneontol	0.004458
GO:00466: gamma-d 3/673	14/18670	0.012609	0.06924	0.053124	PTPRC/NC	3	geneontol	0.004458
GO:00482: behavioral 3/673	14/18670	0.012609	0.06924	0.053124	THBS4/TH	3	geneontol	0.004458
GO:00509: induction 3/673	14/18670	0.012609	0.06924	0.053124	FGF10/CX	3	geneontol	0.004458
GO:00609: cardiac cel 3/673	14/18670	0.012609	0.06924	0.053124	SOX17/DK	3	geneontol	0.004458
GO:19020: positive re 3/673	14/18670	0.012609	0.06924	0.053124	MAL/SFRP	3	geneontol	0.004458
GO:00510: positive re 25/673	428/18670	0.012627	0.069254	0.053135	CD2/NPR1	25	geneontol	0.037147
GO:00510: negative re 16/673	238/18670	0.012753	0.069822	0.053571	PTGER3/CI	16	geneontol	0.023774
GO:00301: collagen fi 6/673	54/18670	0.012761	0.069822	0.053571	DDR2/DPT	6	geneontol	0.008915
GO:00485: response t 23/673	385/18670	0.012784	0.069866	0.053604	IL10/PPAR	23	geneontol	0.034175
GO:00100: glial cell di 15/673	218/18670	0.012825	0.069924	0.053649	TAL1/SLC4	15	geneontol	0.022288
GO:00322: regulation 15/673	218/18670	0.012825	0.069924	0.053649	ADD2/VILL	15	geneontol	0.022288
GO:00017: somitogen 7/673	70/18670	0.01289	0.070196	0.053858	ZEB2/LFN	7	geneontol	0.010401
GO:00487: skeletal sy 16/673	239/18670	0.013229	0.071546	0.054893	OSR1/VIT	16	geneontol	0.023774
GO:00302: glycosamir 12/673	160/18670	0.013249	0.071546	0.054893	B3GNT7/H	12	geneontol	0.017831
GO:00019: positive re 4/673	26/18670	0.013308	0.071546	0.054893	CD1C/CD1	4	geneontol	0.005944
GO:00107: regulation 4/673	26/18670	0.013308	0.071546	0.054893	STAP1/CM	4	geneontol	0.005944
GO:00301: positive re 4/673	26/18670	0.013308	0.071546	0.054893	SELP/PLEK	4	geneontol	0.005944
GO:00316: negative re 4/673	26/18670	0.013308	0.071546	0.054893	IL10/GPR3	4	geneontol	0.005944
GO:00606: embryonic 4/673	26/18670	0.013308	0.071546	0.054893	GJB5/IL10	4	geneontol	0.005944
GO:00607: prostate g 4/673	26/18670	0.013308	0.071546	0.054893	FGF10/SHI	4	geneontol	0.005944
GO:00725: T-helper 1 4/673	26/18670	0.013308	0.071546	0.054893	LY9/NLRP	4	geneontol	0.005944
GO:00995: synaptic m 4/673	26/18670	0.013308	0.071546	0.054893	SPARCL1/F	4	geneontol	0.005944
GO:19000: positive re 4/673	26/18670	0.013308	0.071546	0.054893	SELP/PLEK	4	geneontol	0.005944
GO:00508: positive re 11/673	142/18670	0.013858	0.074101	0.056854	FCRL3/PTF	11	geneontol	0.016345
GO:00425: positive re 7/673	71/18670	0.013869	0.074101	0.056854	TNFSF18/I	7	geneontol	0.010401
GO:00326: interleukin 6/673	55/18670	0.0139	0.074101	0.056854	CD28/TIGI	6	geneontol	0.008915
GO:00610: positive re 6/673	55/18670	0.0139	0.074101	0.056854	TAL1/EFNA	6	geneontol	0.008915
GO:00019: regulation 5/673	40/18670	0.013907	0.074101	0.056854	AGTR1/AV	5	geneontol	0.007429
GO:00028: negative re 5/673	40/18670	0.013907	0.074101	0.056854	PTPRC/CAI	5	geneontol	0.007429
GO:00715: semaphori 5/673	40/18670	0.013907	0.074101	0.056854	SEMA3G/S	5	geneontol	0.007429
GO:00192: regulation 24/673	410/18670	0.014	0.074101	0.056854	RGL1/SLC	24	geneontol	0.035661
GO:00224: molting cy 8/673	88/18670	0.014007	0.074101	0.056854	FGF10/FO	8	geneontol	0.011887
GO:00224: hair cycle 8/673	88/18670	0.014007	0.074101	0.056854	FGF10/FO	8	geneontol	0.011887
GO:00341: regulation 8/673	88/18670	0.014007	0.074101	0.056854	LEPR/S1PF	8	geneontol	0.011887
GO:00435: regulation 8/673	88/18670	0.014007	0.074101	0.056854	ZEB2/SFRF	8	geneontol	0.011887
GO:00987: skin epider 8/673	88/18670	0.014007	0.074101	0.056854	FGF10/FO	8	geneontol	0.011887
GO:19040: regulation 8/673	88/18670	0.014007	0.074101	0.056854	ITGA4/KDF	8	geneontol	0.011887
GO:00104: negative re 17/673	262/18670	0.014454	0.076377	0.0586	SFN/NGF	17	geneontol	0.02526
GO:00319: response t 12/673	162/18670	0.014501	0.076541	0.058726	IL10/FAM1	12	geneontol	0.017831
GO:00326: chemokine 8/673	89/18670	0.014921	0.078577	0.060288	EPHA2/AC	8	geneontol	0.011887
GO:00600: roof of mc 8/673	89/18670	0.014921	0.078577	0.060288	TGFBR3/O	8	geneontol	0.011887
GO:19030: positive re 6/673	56/18670	0.015107	0.07946	0.060966	ARHGEF16	6	geneontol	0.008915
GO:00028: regulation 4/673	27/18670	0.015187	0.07946	0.060966	IL1R1/CCR	4	geneontol	0.005944
GO:00508: positive re 4/673	27/18670	0.015187	0.07946	0.060966	SELP/PLEK	4	geneontol	0.005944
GO:00602: regulation 4/673	27/18670	0.015187	0.07946	0.060966	LEPR/NML	4	geneontol	0.005944
GO:00722: metanephi 4/673	27/18670	0.015187	0.07946	0.060966	OSR1/CXC	4	geneontol	0.005944
GO:00024: germinal c 3/673	15/18670	0.015346	0.07946	0.060966	KLHL6/CX	3	geneontol	0.004458
GO:00327: positive re 3/673	15/18670	0.015346	0.07946	0.060966	NLRP3/IRF	3	geneontol	0.004458
GO:00343: primary alk 3/673	15/18670	0.015346	0.07946	0.060966	SULT1C4/F	3	geneontol	0.004458
GO:00468: negative re 3/673	15/18670	0.015346	0.07946	0.060966	CLDN18/S	3	geneontol	0.004458
GO:00480: regulation 3/673	15/18670	0.015346	0.07946	0.060966	ZEB2/IHH	3	geneontol	0.004458
GO:00517: positive re 3/673	15/18670	0.015346	0.07946	0.060966	KDR/LRRK	3	geneontol	0.004458
GO:00720: metanephi 3/673	15/18670	0.015346	0.07946	0.060966	OSR1/SHF	3	geneontol	0.004458
GO:00901: epithelial c 3/673	15/18670	0.015346	0.07946	0.060966	CYP1B1/IF	3	geneontol	0.004458
GO:00901: positive re 3/673	15/18670	0.015346	0.07946	0.060966	CSF1R/LPL	3	geneontol	0.004458
GO:20000: regulation 3/673	15/18670	0.015346	0.07946	0.060966	SFRP1/DKI	3	geneontol	0.004458
GO:00902: regulation 5/673	41/18670	0.015382	0.079555	0.061038	FCRL3/PLN	5	geneontol	0.007429
GO:00488: sensory sy 22/673	371/18670	0.015843	0.081851	0.0628	EPHA2/CY	22	geneontol	0.032689
GO:00164: protein pr 20/673	328/18670	0.015865	0.081872	0.062816	NGF/CTSE	20	geneontol	0.029718
GO:00329: negative re 7/673	73/18670	0.015985	0.082126	0.063011	PLA2G2D/	7	geneontol	0.010401
GO:00436: response t 7/673	73/18670	0.015985	0.082126	0.063011	PPARG/ZN	7	geneontol	0.010401
GO:00506: negative re 7/673	73/18670	0.015985	0.082126	0.063011	PLA2G2D/	7	geneontol	0.010401
GO:00603: endochon 7/673	73/18670	0.015985	0.082126	0.063011	VIT/IHH/C	7	geneontol	0.010401
GO:00514: stress-acti 18/673	286/18670	0.01605	0.082367	0.063196	SLAMF1/X	18	geneontol	0.026746
GO:00314: keratinizat 15/673	224/18670	0.016072	0.082387	0.063211	SFN/LIPM	15	geneontol	0.022288
GO:00325: response t 9/673	108/18670	0.016093	0.082405	0.063225	GJB3/OSR	9	geneontol	0.013373
GO:00109: regulation 23/673	394/18670	0.016386	0.083812	0.064305	PDE4B/FCI	23	geneontol	0.034175
GO:00716: anatomica 12/673	165/18670	0.016546	0.084536	0.064486	TAL1/S1PF	12	geneontol	0.017831
GO:00456: negative re 15/673	225/18670	0.016669	0.085074	0.065272	EFNA1/NC	15	geneontol	0.022288
GO:00022: toll-like re 11/673	146/18670	0.016748	0.085382	0.065509	S100A14/F	11	geneontol	0.016345
GO:00463: regulation 13/673	185/18670	0.016801	0.085556	0.065643	SLAMF1/Z	13	geneontol	0.019316

GO:00518	membrane	8/673	91/18670	0.016878	0.085853	0.06587	SCN7A/KC	8	geneontol	0.011887
GO:00026	positive re	5/673	42/18670	0.016957	0.08588	0.065891	PTPRC/CD	5	geneontol	0.007429
GO:00104	regulation	5/673	42/18670	0.016957	0.08588	0.065891	IL10/OSR1	5	geneontol	0.007429
GO:00105	regulation	5/673	42/18670	0.016957	0.08588	0.065891	CCL19/CCI	5	geneontol	0.007429
GO:00970	dendritic c	5/673	42/18670	0.016957	0.08588	0.065891	IRF4/CCL1	5	geneontol	0.007429
GO:00027	positive re	18/673	288/18670	0.017105	0.086198	0.066135	CD2/IL10/I	18	geneontol	0.026746
GO:00435	positive re	7/673	74/18670	0.017125	0.086198	0.066135	ZEB2/CCL1	7	geneontol	0.010401
GO:00031	aortic valv	4/673	28/18670	0.017225	0.086198	0.066135	EFNA1/SLI	4	geneontol	0.005944
GO:00181	keratan su	4/673	28/18670	0.017225	0.086198	0.066135	B3GNT7/C	4	geneontol	0.005944
GO:00326	regulation	4/673	28/18670	0.017225	0.086198	0.066135	IL10/LILRA	4	geneontol	0.005944
GO:00343	protein-lip	4/673	28/18670	0.017225	0.086198	0.066135	AGTR1/LPI	4	geneontol	0.005944
GO:00343	plasma lip	4/673	28/18670	0.017225	0.086198	0.066135	AGTR1/LPI	4	geneontol	0.005944
GO:00426	regulation	4/673	28/18670	0.017225	0.086198	0.066135	EPS8L3/CC	4	geneontol	0.005944
GO:19026	negative r	4/673	28/18670	0.017225	0.086198	0.066135	SEMA3G/S	4	geneontol	0.005944
GO:19037	negative r	4/673	28/18670	0.017225	0.086198	0.066135	OSR1/SFRI	4	geneontol	0.005944
GO:19049	regulation	4/673	28/18670	0.017225	0.086198	0.066135	ITGA4/CCF	4	geneontol	0.005944
GO:00022	hematopo	12/673	166/18670	0.017273	0.086254	0.066178	TAL1/PTPF	12	geneontol	0.017831
GO:00902	negative r	12/673	166/18670	0.017273	0.086254	0.066178	TGFBR3/XI	12	geneontol	0.017831
GO:00025	platelet de	10/673	128/18670	0.017491	0.087155	0.066869	SELP/PLEK	10	geneontol	0.014859
GO:00303	negative r	13/673	186/18670	0.017491	0.087155	0.066869	NPR1/PPA	13	geneontol	0.019316
GO:00420	T-helper c	6/673	58/18670	0.017738	0.088287	0.067738	LY9/NLRP3	6	geneontol	0.008915
GO:00020	epithelial c	14/673	207/18670	0.018147	0.089989	0.069044	EPHA2/SFI	14	geneontol	0.020802
GO:00074	peripheral	7/673	75/18670	0.018321	0.089989	0.069044	NGF/LAM/	7	geneontol	0.010401
GO:00347	cellular ho	10/673	129/18670	0.018372	0.089989	0.069044	CRABP2/C	10	geneontol	0.014859
GO:00017	neutrophil	3/673	16/18670	0.018391	0.089989	0.069044	PDE4B/CX	3	geneontol	0.004458
GO:00022	T-helper c	3/673	16/18670	0.018391	0.089989	0.069044	LY9/IRF4/E	3	geneontol	0.004458
GO:00024	antigen pr	3/673	16/18670	0.018391	0.089989	0.069044	CD1C/CD1	3	geneontol	0.004458
GO:00108	positive re	3/673	16/18670	0.018391	0.089989	0.069044	CCR2/CXC	3	geneontol	0.004458
GO:00108	regulation	3/673	16/18670	0.018391	0.089989	0.069044	PPARG/CC	3	geneontol	0.004458
GO:00308	negative r	3/673	16/18670	0.018391	0.089989	0.069044	MNDA/IL1	3	geneontol	0.004458
GO:00312	pseudopo	3/673	16/18670	0.018391	0.089989	0.069044	CCL21/CCI	3	geneontol	0.004458
GO:00330	negative r	3/673	16/18670	0.018391	0.089989	0.069044	CXCR2/CC	3	geneontol	0.004458
GO:00336	cell-cell ac	3/673	16/18670	0.018391	0.089989	0.069044	ITGA4/CXC	3	geneontol	0.004458
GO:00480	hepatocyt	3/673	16/18670	0.018391	0.089989	0.069044	MST1R/HC	3	geneontol	0.004458
GO:00507	negative r	3/673	16/18670	0.018391	0.089989	0.069044	EFNA1/NC	3	geneontol	0.004458
GO:00705	dendrite s	3/673	16/18670	0.018391	0.089989	0.069044	NEXN/IGS	3	geneontol	0.004458
GO:00722	metaneph	3/673	16/18670	0.018391	0.089989	0.069044	OSR1/PDC	3	geneontol	0.004458
GO:00456	positive re	5/673	43/18670	0.018636	0.091093	0.069891	PPARG/SH	5	geneontol	0.007429
GO:00720	nephron ti	8/673	93/18670	0.019012	0.092836	0.071228	TACSTD2/	8	geneontol	0.011887
GO:00094	response t	18/673	292/18670	0.019378	0.09396	0.07209	GSTM5/S1	18	geneontol	0.026746
GO:00069	substrate-	4/673	29/18670	0.019425	0.09396	0.07209	PTPRC/P2f	4	geneontol	0.005944
GO:00072	nitric oxide	4/673	29/18670	0.019425	0.09396	0.07209	CD36/GUC	4	geneontol	0.005944
GO:00106	epithelial	4/673	29/18670	0.019425	0.09396	0.07209	MUC4/TFF	4	geneontol	0.005944
GO:00343	protein-cc	4/673	29/18670	0.019425	0.09396	0.07209	AGTR1/LPI	4	geneontol	0.005944
GO:00447	modulatio	4/673	29/18670	0.019425	0.09396	0.07209	PTX3/CSF1	4	geneontol	0.005944
GO:00610	negative r	4/673	29/18670	0.019425	0.09396	0.07209	PTPRC/GP	4	geneontol	0.005944
GO:00725	T-helper 1	4/673	29/18670	0.019425	0.09396	0.07209	LY9/NLRP3	4	geneontol	0.005944
GO:01200	negative r	4/673	29/18670	0.019425	0.09396	0.07209	TACSTD2/	4	geneontol	0.005944
GO:00517	interaction	14/673	209/18670	0.019549	0.094458	0.072473	EPHA2/SL	14	geneontol	0.020802
GO:00149	myotube c	9/673	112/18670	0.01995	0.096197	0.073807	SHH/BARX	9	geneontol	0.013373
GO:00508	negative r	9/673	112/18670	0.01995	0.096197	0.073807	PLA2G2D/	9	geneontol	0.013373
GO:00519	negative r	19/673	315/18670	0.020349	0.097878	0.075097	EFNA1/NC	19	geneontol	0.028232
GO:00034	endochonr	5/673	44/18670	0.02042	0.097878	0.075097	DDR2/VIT/	5	geneontol	0.007429
GO:00140	oligodend	5/673	44/18670	0.02042	0.097878	0.075097	SHH/LPAR	5	geneontol	0.007429
GO:00514	regulation	5/673	44/18670	0.02042	0.097878	0.075097	CCL21/TGI	5	geneontol	0.007429
GO:19026	regulation	5/673	44/18670	0.02042	0.097878	0.075097	SEMA3G/S	5	geneontol	0.007429
GO:00060	aminoglyc	12/673	170/18670	0.020426	0.097878	0.075097	B3GNT7/H	12	geneontol	0.017831
GO:00022	CD4-posit	6/673	60/18670	0.020666	0.098926	0.0759	LY9/NLRP3	6	geneontol	0.008915
GO:00068	nitric oxide	7/673	77/18670	0.020886	0.099876	0.076629	IL10/CYP1	7	geneontol	0.010401
GO:00424	odontoger	10/673	132/18670	0.021211	0.101309	0.077729	OSR1/PDC	10	geneontol	0.014859
GO:00507	negative r	18/673	295/18670	0.021229	0.101309	0.077729	EFNA1/NC	18	geneontol	0.026746
GO:00106	positive re	12/673	171/18670	0.021277	0.101431	0.077823	RAB25/KD	12	geneontol	0.017831
GO:00613	renal tubu	8/673	95/18670	0.021333	0.101597	0.07795	TACSTD2/	8	geneontol	0.011887
GO:00026	positive re	3/673	17/18670	0.021745	0.102203	0.078414	IL1R1/ITGA	3	geneontol	0.004458
GO:00073	segment s	3/673	17/18670	0.021745	0.102203	0.078414	OSR1/MEC	3	geneontol	0.004458
GO:00108	regulation	3/673	17/18670	0.021745	0.102203	0.078414	CCR2/CXC	3	geneontol	0.004458
GO:00303	stabilizatio	3/673	17/18670	0.021745	0.102203	0.078414	KCNK2/KC	3	geneontol	0.004458
GO:00359	chondrocy	3/673	17/18670	0.021745	0.102203	0.078414	DDR2/IHH	3	geneontol	0.004458
GO:00433	CD4-posit	3/673	17/18670	0.021745	0.102203	0.078414	LY9/IRF4/E	3	geneontol	0.004458
GO:00450	regulation	3/673	17/18670	0.021745	0.102203	0.078414	TNFRSF13f	3	geneontol	0.004458
GO:00612	retina vasc	3/673	17/18670	0.021745	0.102203	0.078414	CYP1B1/PI	3	geneontol	0.004458
GO:20008	negative r	3/673	17/18670	0.021745	0.102203	0.078414	NTRK2/BC	3	geneontol	0.004458
GO:00034	chondrocy	4/673	30/18670	0.021792	0.102203	0.078414	VIT/IHH/C	4	geneontol	0.005944

GO:003261	interferon-4/673	30/18670	0.021792	0.102203	0.078414	IL10/LILRA	4	geneontol	0.005944
GO:004331	positive re 4/673	30/18670	0.021792	0.102203	0.078414	NLRP3/CC	4	geneontol	0.005944
GO:004821	response t 4/673	30/18670	0.021792	0.102203	0.078414	THBS4/ED	4	geneontol	0.005944
GO:005081	negative re 4/673	30/18670	0.021792	0.102203	0.078414	MNDA/IL1	4	geneontol	0.005944
GO:005141	positive re 4/673	30/18670	0.021792	0.102203	0.078414	CCL21/TGI	4	geneontol	0.005944
GO:003261	regulation 11/673	152/18670	0.021897	0.102591	0.078712	SLAMF1/IL	11	geneontol	0.016345
GO:000851	fibroblast 9/673	114/18670	0.022111	0.103385	0.079321	FAT4/FGF1	9	geneontol	0.013373
GO:004541	endothelia 9/673	114/18670	0.022111	0.103385	0.079321	S1PR1/XDI	9	geneontol	0.013373
GO:000601	glycosamir 6/673	61/18670	0.022246	0.103548	0.079446	OGN/OMI	6	geneontol	0.008915
GO:003411	heterotypic 6/673	61/18670	0.022246	0.103548	0.079446	CD2/PTPR	6	geneontol	0.008915
GO:004561	regulation 6/673	61/18670	0.022246	0.103548	0.079446	SFN/SFRP2	6	geneontol	0.008915
GO:004861	animal org 6/673	61/18670	0.022246	0.103548	0.079446	FGF10/SHH	6	geneontol	0.008915
GO:000851	regulation 7/673	78/18670	0.022257	0.103548	0.079446	IHH/FGF10	7	geneontol	0.010401
GO:000281	negative re 5/673	45/18670	0.022313	0.103598	0.079485	PTPRC/C4I	5	geneontol	0.007429
GO:003251	response t 5/673	45/18670	0.022313	0.103598	0.079485	CLDN4/CA	5	geneontol	0.007429
GO:004211	neurotrans 11/673	153/18670	0.022856	0.106015	0.081339	IL10/CYP1	11	geneontol	0.016345
GO:000751	hemostasis 20/673	341/18670	0.023016	0.106518	0.081725	SELP/C4BF	20	geneontol	0.029718
GO:004261	muscle cel 22/673	385/18670	0.023057	0.106518	0.081725	CAPN9/BC	22	geneontol	0.032689
GO:001041	regulation 12/673	173/18670	0.023057	0.106518	0.081725	TAL1/IL10	12	geneontol	0.017831
GO:001651	negative re 12/673	173/18670	0.023057	0.106518	0.081725	EPHA2/NP	12	geneontol	0.017831
GO:004661	response t 10/673	134/18670	0.023274	0.107411	0.082411	P2RY12/PI	10	geneontol	0.014859
GO:003011	regulation 7/673	79/18670	0.02369	0.109226	0.083803	SELP/PLEK	7	geneontol	0.010401
GO:004871	oligodend 8/673	97/18670	0.023848	0.109843	0.084276	SLC45A3/F	8	geneontol	0.011887
GO:003281	glomerulu 6/673	62/18670	0.023905	0.109996	0.084394	OSR1/PDC	6	geneontol	0.008915
GO:006041	mammary 5/673	46/18670	0.024316	0.111273	0.085374	EPHA2/ELF	5	geneontol	0.007429
GO:000271	regulation 4/673	31/18670	0.024327	0.111273	0.085374	NLRP3/IL1	4	geneontol	0.005944
GO:000661	phosphatic 4/673	31/18670	0.024327	0.111273	0.085374	PLA2G2D/	4	geneontol	0.005944
GO:004581	positive re 4/673	31/18670	0.024327	0.111273	0.085374	IHH/SHH/	4	geneontol	0.005944
GO:190281	positive re 4/673	31/18670	0.024327	0.111273	0.085374	IL10/WT1/	4	geneontol	0.005944
GO:190331	positive re 4/673	31/18670	0.024327	0.111273	0.085374	S100A10/	4	geneontol	0.005944
GO:200031	regulation 13/673	195/18670	0.024708	0.112907	0.086627	IL10/XDH/	13	geneontol	0.019316
GO:200121	regulation 11/673	155/18670	0.024868	0.113523	0.0871	PTPRC/MA	11	geneontol	0.016345
GO:015001	visual syst 21/673	366/18670	0.024977	0.113645	0.087194	EPHA2/CY	21	geneontol	0.031204
GO:000641	protein gly 16/673	258/18670	0.02518	0.113645	0.087194	MAN1C1/I	16	geneontol	0.023774
GO:004341	macromoli 16/673	258/18670	0.02518	0.113645	0.087194	MAN1C1/I	16	geneontol	0.023774
GO:190001	regulation 7/673	80/18670	0.025185	0.113645	0.087194	SELP/PLEK	7	geneontol	0.010401
GO:003281	regulation 15/673	237/18670	0.025243	0.113645	0.087194	SLAMF1/X	15	geneontol	0.022288
GO:000341	chondrocy 3/673	18/18670	0.02541	0.113645	0.087194	VIT/COL21	3	geneontol	0.004458
GO:000341	growth pla 3/673	18/18670	0.02541	0.113645	0.087194	VIT/COL21	3	geneontol	0.004458
GO:000711	negative re 3/673	18/18670	0.02541	0.113645	0.087194	CCR2/P2R	3	geneontol	0.004458
GO:000931	oligosacch 3/673	18/18670	0.02541	0.113645	0.087194	SLC2A1/S1	3	geneontol	0.004458
GO:001081	cholester 3/673	18/18670	0.02541	0.113645	0.087194	PPARG/CC	3	geneontol	0.004458
GO:003101	positive re 3/673	18/18670	0.02541	0.113645	0.087194	SDR16C5/I	3	geneontol	0.004458
GO:003611	phosphatic 3/673	18/18670	0.02541	0.113645	0.087194	PLA2G2D/	3	geneontol	0.004458
GO:004201	interferon- 3/673	18/18670	0.02541	0.113645	0.087194	TNFRSF13I	3	geneontol	0.004458
GO:005101	regulation 3/673	18/18670	0.02541	0.113645	0.087194	IL33/CD22	3	geneontol	0.004458
GO:005181	negative re 3/673	18/18670	0.02541	0.113645	0.087194	FAM107A/	3	geneontol	0.004458
GO:007021	negative re 3/673	18/18670	0.02541	0.113645	0.087194	EFNA1/IL7	3	geneontol	0.004458
GO:009011	chondrocy 3/673	18/18670	0.02541	0.113645	0.087194	VIT/COL21	3	geneontol	0.004458
GO:009011	regulation 3/673	18/18670	0.02541	0.113645	0.087194	CSF1R/LPL	3	geneontol	0.004458
GO:009701	craniofaci 3/673	18/18670	0.02541	0.113645	0.087194	MMP16/FF	3	geneontol	0.004458
GO:015001	positive re 3/673	18/18670	0.02541	0.113645	0.087194	STAP1/IL3	3	geneontol	0.004458
GO:200061	negative re 3/673	18/18670	0.02541	0.113645	0.087194	OVOL1/O	3	geneontol	0.004458
GO:000751	excretion 6/673	63/18670	0.025645	0.114365	0.087746	NPR1/AGT	6	geneontol	0.008915
GO:003431	protein loc 6/673	63/18670	0.025645	0.114365	0.087746	FGF10/AN	6	geneontol	0.008915
GO:190431	positive re 6/673	63/18670	0.025645	0.114365	0.087746	ARHGEF16	6	geneontol	0.008915
GO:000221	somatic re 5/673	47/18670	0.026431	0.116856	0.089657	PTPRC/IL1	5	geneontol	0.007429
GO:000221	somatic di 5/673	47/18670	0.026431	0.116856	0.089657	PTPRC/IL1	5	geneontol	0.007429
GO:000691	acute-pha 5/673	47/18670	0.026431	0.116856	0.089657	PTGER3/CI	5	geneontol	0.007429
GO:001491	positiv re 5/673	47/18670	0.026431	0.116856	0.089657	NR4A3/LP	5	geneontol	0.007429
GO:004331	regulation 5/673	47/18670	0.026431	0.116856	0.089657	NLRP3/IRF	5	geneontol	0.007429
GO:004511	isotype sw 5/673	47/18670	0.026431	0.116856	0.089657	PTPRC/IL1	5	geneontol	0.007429
GO:006161	pri-miRNA 5/673	47/18670	0.026431	0.116856	0.089657	IL10/PPAR	5	geneontol	0.007429
GO:007011	positive re 5/673	47/18670	0.026431	0.116856	0.089657	OSR1/TFA	5	geneontol	0.007429
GO:007021	T cell apo 5/673	47/18670	0.026431	0.116856	0.089657	EFNA1/IL7	5	geneontol	0.007429
GO:004851	negative re 8/673	99/18670	0.026563	0.117263	0.089969	PTX3/TRIM	8	geneontol	0.011887
GO:000221	pattern rec 13/673	197/18670	0.026573	0.117263	0.089969	S100A14/F	13	geneontol	0.019316
GO:003161	regulation 10/673	137/18670	0.026633	0.117414	0.090085	IL10/GPR3	10	geneontol	0.014859
GO:004841	cell matur 12/673	177/18670	0.026943	0.118448	0.090879	TAL1/IHH/	12	geneontol	0.017831
GO:003131	negative re 15/673	239/18670	0.026944	0.118448	0.090879	PTPRC/IL1	15	geneontol	0.022288
GO:007031	regulation 15/673	239/18670	0.026944	0.118448	0.090879	SLAMF1/X	15	geneontol	0.022288
GO:000311	aortic valv 4/673	32/18670	0.027033	0.118498	0.090917	EFNA1/SLI	4	geneontol	0.005944
GO:004251	retinoic ac 4/673	32/18670	0.027033	0.118498	0.090917	CRABP2/A	4	geneontol	0.005944

GO:00488:	regulation	4/673	32/18670	0.027033	0.118498	0.090917	SEMA3G/S	4	geneontol	0.005944
GO:00164:	somatic di	6/673	64/18670	0.027468	0.120177	0.092205	PTPRC/IL1	6	geneontol	0.008915
GO:00300:	lamellipod	6/673	64/18670	0.027468	0.120177	0.092205	EPHA2/S1I	6	geneontol	0.008915
GO:00310:	regenerati	13/673	198/18670	0.027544	0.120398	0.092374	TGFBR3/IL	13	geneontol	0.019316
GO:00512:	protein po	17/673	283/18670	0.028107	0.122744	0.094175	ADD2/VILL	17	geneontol	0.02526
GO:00462:	nitric oxid	7/673	82/18670	0.028367	0.123744	0.094942	IL10/CYP1	7	geneontol	0.010401
GO:00302:	keratinocy	18/673	305/18670	0.02839	0.123744	0.094942	EPHA2/SFI	18	geneontol	0.026746
GO:00080:	neuron rec	5/673	48/18670	0.028659	0.124685	0.095664	NEXN/IGSI	5	geneontol	0.007429
GO:00603:	face devel	5/673	48/18670	0.028659	0.124685	0.095664	PDGFRA/C	5	geneontol	0.007429
GO:00900:	regulation	15/673	241/18670	0.028729	0.12487	0.095806	TGFBR3/N	15	geneontol	0.022288
GO:00725:	reactive ox	17/673	284/18670	0.028939	0.125665	0.096416	IL10/XDH/	17	geneontol	0.02526
GO:00331:	regulation	10/673	139/18670	0.029057	0.126058	0.096717	PLCL1/HG	10	geneontol	0.014859
GO:00190:	viral life cy	19/673	328/18670	0.029293	0.126298	0.096902	EPHA2/SL	19	geneontol	0.028232
GO:00060:	aminoglyc	6/673	65/18670	0.029374	0.126298	0.096902	OGN/OMI	6	geneontol	0.008915
GO:00511:	negative r	6/673	65/18670	0.029374	0.126298	0.096902	PI16/SHH/	6	geneontol	0.008915
GO:00027:	positive re	3/673	19/18670	0.029385	0.126298	0.096902	NLRP3/IL1	3	geneontol	0.004458
GO:00034:	growth pla	3/673	19/18670	0.029385	0.126298	0.096902	VIT/COL2I	3	geneontol	0.004458
GO:00426:	muscle cel	3/673	19/18670	0.029385	0.126298	0.096902	FGF10/DKI	3	geneontol	0.004458
GO:00465:	negative r	3/673	19/18670	0.029385	0.126298	0.096902	PTX3/TRIM	3	geneontol	0.004458
GO:00515:	keratinocy	3/673	19/18670	0.029385	0.126298	0.096902	FGF10/FGF	3	geneontol	0.004458
GO:00604:	negative r	3/673	19/18670	0.029385	0.126298	0.096902	PTGER3/N	3	geneontol	0.004458
GO:00720:	kidney me	3/673	19/18670	0.029385	0.126298	0.096902	OSR1/SHH	3	geneontol	0.004458
GO:00508:	defense re	8/673	101/18670	0.029487	0.126618	0.097147	EPHA2/NL	8	geneontol	0.011887
GO:00423:	keratan su	4/673	33/18670	0.029911	0.128203	0.098363	B3GNT7/C	4	geneontol	0.005944
GO:00606:	mammary 4	/673	33/18670	0.029911	0.128203	0.098363	EPHA2/FG	4	geneontol	0.005944
GO:00425:	regulation	7/673	83/18670	0.030055	0.12858	0.098653	TNFSF18/I	7	geneontol	0.010401
GO:00481:	regulation	7/673	83/18670	0.030055	0.12858	0.098653	S100A6/DI	7	geneontol	0.010401
GO:00713:	cellular res	12/673	180/18670	0.030156	0.128896	0.098895	PPARG/IRF	12	geneontol	0.017831
GO:00447:	multi-mult	14/673	222/18670	0.030733	0.13124	0.100693	SLC2A1/P1	14	geneontol	0.020802
GO:00030:	regulation	5/673	49/18670	0.031004	0.13215	0.101392	AGTR1/AV	5	geneontol	0.007429
GO:20012:	positive re	5/673	49/18670	0.031004	0.13215	0.101392	PTPRC/MA	5	geneontol	0.007429
GO:00326:	interleukin	11/673	161/18670	0.03167	0.134867	0.103476	SLAMF1/IL	11	geneontol	0.016345
GO:00481:	fibroblast	7/673	84/18670	0.031809	0.135212	0.10374	S100A6/DI	7	geneontol	0.010401
GO:00508:	regulation	7/673	84/18670	0.031809	0.135212	0.10374	SELP/PLEK	7	geneontol	0.010401
GO:00190:	viral genor	9/673	122/18670	0.032438	0.137681	0.105635	CD28/CXC	9	geneontol	0.013373
GO:00485:	embryonic	17/673	288/18670	0.03245	0.137681	0.105635	EPHA2/EFI	17	geneontol	0.02526
GO:19035:	positive re	22/673	399/18670	0.032575	0.138084	0.105945	CD2/IL10/I	22	geneontol	0.032689
GO:00072:	integrin-n	8/673	103/18670	0.032624	0.138168	0.106009	PLEK/ITGA	8	geneontol	0.011887
GO:00450:	regulatory	4/673	34/18670	0.032964	0.139099	0.106723	PLA2G2D/	4	geneontol	0.005944
GO:00718:	cellular res	4/673	34/18670	0.032964	0.139099	0.106723	PDE4B/NR	4	geneontol	0.005944
GO:00718:	cellular res	4/673	34/18670	0.032964	0.139099	0.106723	PDE4B/NR	4	geneontol	0.005944
GO:00970:	energy ho	4/673	34/18670	0.032964	0.139099	0.106723	LEPR/NML	4	geneontol	0.005944
GO:00108:	lipid local	22/673	400/18670	0.033353	0.1394	0.106954	PLA2G2D/	22	geneontol	0.032689
GO:00308:	positive re	6/673	67/18670	0.033441	0.1394	0.106954	SFN/ZEB2/	6	geneontol	0.008915
GO:00604:	lung morp	5/673	50/18670	0.033464	0.1394	0.106954	FGF10/SHI	5	geneontol	0.007429
GO:00343:	primary ak	7/673	85/18670	0.033631	0.1394	0.106954	CYP1B1/SI	7	geneontol	0.010401
GO:19039:	negative r	7/673	85/18670	0.033631	0.1394	0.106954	PTX3/TRIM	7	geneontol	0.010401
GO:20010:	reactive nii	7/673	85/18670	0.033631	0.1394	0.106954	IL10/CYP1	7	geneontol	0.010401
GO:00020:	sprouting	12/673	183/18670	0.033637	0.1394	0.106954	EPHA2/IL1	12	geneontol	0.017831
GO:00023:	cytokine s	3/673	20/18670	0.033668	0.1394	0.106954	IL10/NLRP	3	geneontol	0.004458
GO:00028:	positive re	3/673	20/18670	0.033668	0.1394	0.106954	IL1R1/CCR	3	geneontol	0.004458
GO:00100:	response t	3/673	20/18670	0.033668	0.1394	0.106954	FIBIN/LRR	3	geneontol	0.004458
GO:00230:	signal tran	3/673	20/18670	0.033668	0.1394	0.106954	PDGFRA/S	3	geneontol	0.004458
GO:00312:	negative r	3/673	20/18670	0.033668	0.1394	0.106954	CCR2/P2R'	3	geneontol	0.004458
GO:00341:	negative r	3/673	20/18670	0.033668	0.1394	0.106954	CLDN18/S	3	geneontol	0.004458
GO:00360:	fucosylatio	3/673	20/18670	0.033668	0.1394	0.106954	LFNG/FUT	3	geneontol	0.004458
GO:00425:	positive re	3/673	20/18670	0.033668	0.1394	0.106954	CCR2/THB	3	geneontol	0.004458
GO:00487:	smooth m	3/673	20/18670	0.033668	0.1394	0.106954	OSR1/IHH	3	geneontol	0.004458
GO:00517:	nitric-oxid	3/673	20/18670	0.033668	0.1394	0.106954	KDR/LRRK	3	geneontol	0.004458
GO:00517:	regulation	3/673	20/18670	0.033668	0.1394	0.106954	KDR/LRRK	3	geneontol	0.004458
GO:00602:	definitive	7/673	20/18670	0.033668	0.1394	0.106954	TAL1/TGFE	3	geneontol	0.004458
GO:00901:	chemokine	3/673	20/18670	0.033668	0.1394	0.106954	CSF1R/LPL	3	geneontol	0.004458
GO:19055:	positive re	3/673	20/18670	0.033668	0.1394	0.106954	P2RY12/CI	3	geneontol	0.004458
GO:00016:	osteoblast	14/673	225/18670	0.03387	0.140111	0.107499	EPHA2/DC	14	geneontol	0.020802
GO:00356:	multicellul	13/673	204/18670	0.033918	0.140186	0.107557	S1PR1/NPI	13	geneontol	0.019316
GO:00313:	positive re	16/673	268/18670	0.03406	0.140612	0.107884	TAL1/PLEK	16	geneontol	0.023774
GO:00069:	humoral in	20/673	356/18670	0.034082	0.140612	0.107884	S100A12/F	20	geneontol	0.029718
GO:00991:	postsynap	11/673	163/18670	0.034206	0.140997	0.10818	EFNA1/DC	11	geneontol	0.016345
GO:00192:	sensory pe	8/673	104/18670	0.034275	0.141157	0.108302	IL10/CCR2	8	geneontol	0.011887
GO:00488:	dendrite r	10/673	143/18670	0.034366	0.141404	0.108491	EFNA1/DC	10	geneontol	0.014859
GO:00700:	glycosylati	16/673	269/18670	0.03506	0.144132	0.110585	MAN1C1/I	16	geneontol	0.023774
GO:19012:	regulation	18/673	313/18670	0.035314	0.145049	0.111288	NGF/IL10/	18	geneontol	0.026746
GO:00072:	tyrosine pt	7/673	86/18670	0.035521	0.145404	0.11156	TNFSF18/I	7	geneontol	0.010401

GO:00086: extrinsic a	7/673	86/18670	0.035521	0.145404	0.11156	NGF/MAL/	7	geneontol	0.010401
GO:00480: ephrin rec	7/673	86/18670	0.035521	0.145404	0.11156	EPHA2/EFI	7	geneontol	0.010401
GO:00358: modificati	11/673	164/18670	0.035526	0.145404	0.11156	S100A12/F	11	geneontol	0.016345
GO:00508: multicellul	6/673	68/18670	0.035605	0.145597	0.111709	SFN/CLDN	6	geneontol	0.008915
GO:00193: arachidoni	5/673	51/18670	0.036043	0.146843	0.112665	CYP1B1/P	5	geneontol	0.007429
GO:00481: positive re	5/673	51/18670	0.036043	0.146843	0.112665	S100A6/DI	5	geneontol	0.007429
GO:00482: positive re	5/673	51/18670	0.036043	0.146843	0.112665	SELE/SFRP	5	geneontol	0.007429
GO:00486: regulation	5/673	51/18670	0.036043	0.146843	0.112665	SHH/SOX1	5	geneontol	0.007429
GO:00018: tissue hom	14/673	227/18670	0.036086	0.146843	0.112665	S1PR1/IHF	14	geneontol	0.020802
GO:00075: blood coag	19/673	336/18670	0.0361	0.146843	0.112665	SELP/C4BF	19	geneontol	0.028232
GO:00327: positive re	4/673	35/18670	0.036192	0.14696	0.112754	CD36/CCL	4	geneontol	0.005944
GO:00988: regulation	4/673	35/18670	0.036192	0.14696	0.112754	NPR1/AGT	4	geneontol	0.005944
GO:00430: camera-ty	18/673	314/18670	0.03626	0.147106	0.112867	EPHA2/CY	18	geneontol	0.026746
GO:00310: stress-acti	18/673	315/18670	0.037224	0.150886	0.115767	SLAMF1/X	18	geneontol	0.026746
GO:00109: negative re	15/673	250/18670	0.037852	0.152914	0.117322	SFN/NGF/	15	geneontol	0.022288
GO:00159: long-chair	6/673	69/18670	0.037857	0.152914	0.117322	PLA2G2D/	6	geneontol	0.008915
GO:00713: cellular res	6/673	69/18670	0.037857	0.152914	0.117322	GJB3/OSR	6	geneontol	0.008915
GO:20002: positive re	6/673	69/18670	0.037857	0.152914	0.117322	LFNG/SHH	6	geneontol	0.008915
GO:00060: ethanol me	3/673	21/18670	0.038256	0.153989	0.118147	SULT1C4//	3	geneontol	0.004458
GO:00361: phosphatic	3/673	21/18670	0.038256	0.153989	0.118147	PLA2G2D/	3	geneontol	0.004458
GO:00902: positive re	3/673	21/18670	0.038256	0.153989	0.118147	CXCL12/LC	3	geneontol	0.004458
GO:19033: negative re	3/673	21/18670	0.038256	0.153989	0.118147	FAM107A/	3	geneontol	0.004458
GO:00456: regulation	9/673	126/18670	0.038685	0.155536	0.119335	DDR2/TWI	9	geneontol	0.013373
GO:00164: somatic re	5/673	52/18670	0.038741	0.155536	0.119335	PTPRC/IL1	5	geneontol	0.007429
GO:19000: regulation	5/673	52/18670	0.038741	0.155536	0.119335	TACSTD2/	5	geneontol	0.007429
GO:00714: cellular res	19/673	339/18670	0.038932	0.156166	0.119818	SLC2A1/P1	19	geneontol	0.028232
GO:00016: eye develc	20/673	362/18670	0.039471	0.158191	0.121372	EPHA2/CY	20	geneontol	0.029718
GO:19004: regulation	7/673	88/18670	0.039508	0.158204	0.121381	IL10/CD36	7	geneontol	0.010401
GO:20005: positive re	4/673	36/18670	0.039596	0.158419	0.121547	NLRP3/CC	4	geneontol	0.005944
GO:00519: regulation	6/673	70/18670	0.040197	0.160686	0.123285	GRIK3/CCF	6	geneontol	0.008915
GO:00435: negative re	10/673	147/18670	0.040317	0.161025	0.123546	NGF/CHL1	10	geneontol	0.014859
GO:00510: regulation	23/673	432/18670	0.041092	0.163978	0.125811	S100A12/L	23	geneontol	0.034175
GO:00346: cellular res	11/673	168/18670	0.041166	0.164132	0.12593	IL10/CYP1	11	geneontol	0.016345
GO:20000: regulation	15/673	253/18670	0.041312	0.164571	0.126266	TACSTD2/	15	geneontol	0.022288
GO:00060: alcohol me	20/673	364/18670	0.041399	0.164777	0.126424	LEPR/CYP1	20	geneontol	0.029718
GO:00020: blood vess	5/673	53/18670	0.041559	0.16499	0.126588	EPHA2/AG	5	geneontol	0.007429
GO:00327: negative re	5/673	53/18670	0.041559	0.16499	0.126588	SLAMF1/IL	5	geneontol	0.007429
GO:00507: negative re	5/673	53/18670	0.041559	0.16499	0.126588	PTPRC/SFF	5	geneontol	0.007429
GO:00516: localizati	10/673	148/18670	0.041909	0.166006	0.127367	CD2/PTPR	10	geneontol	0.014859
GO:00075: muscle org	22/673	410/18670	0.041919	0.166006	0.127367	TGFB3/S:	22	geneontol	0.032689
GO:00508: coagulatio	19/673	342/18670	0.041923	0.166006	0.127367	SELP/C4BF	19	geneontol	0.028232
GO:00003: response t	14/673	232/18670	0.042078	0.16648	0.127731	IL10/CYP1	14	geneontol	0.020802
GO:00068: lipid trans	20/673	365/18670	0.042388	0.167562	0.128561	PLA2G2D/	20	geneontol	0.029718
GO:19035: negative re	13/673	211/18670	0.04262	0.167671	0.128645	CD84/IL10	13	geneontol	0.019316
GO:00507: negative re	11/673	169/18670	0.042667	0.167671	0.128645	PTPRC/IL1	11	geneontol	0.016345
GO:00017: organ indu	3/673	22/18670	0.043145	0.167671	0.128645	FGF10/FGF	3	geneontol	0.004458
GO:00065: melanin m	3/673	22/18670	0.043145	0.167671	0.128645	ZEB2/CDH	3	geneontol	0.004458
GO:00108: positive re	3/673	22/18670	0.043145	0.167671	0.128645	CD36/LPL	3	geneontol	0.004458
GO:00198: antigen pr	3/673	22/18670	0.043145	0.167671	0.128645	CD1C/CD1	3	geneontol	0.004458
GO:00326: regulation	3/673	22/18670	0.043145	0.167671	0.128645	NLRP3/IRF	3	geneontol	0.004458
GO:00350: negative re	3/673	22/18670	0.043145	0.167671	0.128645	MET/DLC1	3	geneontol	0.004458
GO:00460: cAMP met	3/673	22/18670	0.043145	0.167671	0.128645	EPHA2/PD	3	geneontol	0.004458
GO:00603: regulation	3/673	22/18670	0.043145	0.167671	0.128645	TGFB3/CIL	3	geneontol	0.004458
GO:00604: lung epith	3/673	22/18670	0.043145	0.167671	0.128645	FGF10/SPI	3	geneontol	0.004458
GO:00605: intestinal e	3/673	22/18670	0.043145	0.167671	0.128645	SPDEF/KLF	3	geneontol	0.004458
GO:00714: cellular res	3/673	22/18670	0.043145	0.167671	0.128645	PPARG/CD	3	geneontol	0.004458
GO:00903: positive re	3/673	22/18670	0.043145	0.167671	0.128645	SDR16C5/I	3	geneontol	0.004458
GO:00140: Schwann c	4/673	37/18670	0.043176	0.167671	0.128645	LAMA2/AC	4	geneontol	0.005944
GO:00310: embryonic	4/673	37/18670	0.043176	0.167671	0.128645	IHH/FGF1C	4	geneontol	0.005944
GO:00329: secretion t	4/673	37/18670	0.043176	0.167671	0.128645	FGF10/AGI	4	geneontol	0.005944
GO:00430: T cell hom	4/673	37/18670	0.043176	0.167671	0.128645	SIT1/NCKA	4	geneontol	0.005944
GO:00457: positive re	4/673	37/18670	0.043176	0.167671	0.128645	NMU/CNR	4	geneontol	0.005944
GO:00459: positive re	4/673	37/18670	0.043176	0.167671	0.128645	SLC45A3/F	4	geneontol	0.005944
GO:19053: semi-lunar	4/673	37/18670	0.043176	0.167671	0.128645	EFNA1/SLI	4	geneontol	0.005944
GO:00163: dendrite d	14/673	233/18670	0.043357	0.168175	0.129032	EFNA1/IGS	14	geneontol	0.020802
GO:00720: nephron e	8/673	109/18670	0.043379	0.168175	0.129032	TACSTD2/	8	geneontol	0.011887
GO:00510: positive re	10/673	149/18670	0.043543	0.168529	0.129303	S100A12/T	10	geneontol	0.014859
GO:19039: regulation	10/673	149/18670	0.043543	0.168529	0.129303	CD28/PTX:	10	geneontol	0.014859
GO:00027: positive re	5/673	54/18670	0.044498	0.172081	0.132028	NLRP3/IL1	5	geneontol	0.007429
GO:00192: transmissi	6/673	72/18670	0.045148	0.174305	0.133735	S1PR1/SCI	6	geneontol	0.008915
GO:00518: regulation	6/673	72/18670	0.045148	0.174305	0.133735	KDR/LRRK:	6	geneontol	0.008915
GO:00163: morphoge	10/673	150/18670	0.04522	0.174436	0.133835	OSR1/ZEB:	10	geneontol	0.014859
GO:00032: cardiac ch	11/673	171/18670	0.045783	0.176459	0.135388	TGFB3/KC	11	geneontol	0.016345

GO:00718 response t 4/673	38/18670	0.046933	0.17956	0.137767	PDE4B/NR	4 geneontol	0.005944
GO:00718 response t 4/673	38/18670	0.046933	0.17956	0.137767	PDE4B/NR	4 geneontol	0.005944
GO:00442 sulfur com 5/673	55/18670	0.047558	0.17956	0.137767	OGN/OMI	5 geneontol	0.007429
GO:00302 myofibril a 6/673	73/18670	0.04776	0.17956	0.137767	CAPN9/PC	6 geneontol	0.008915
GO:00456 regulation 6/673	73/18670	0.04776	0.17956	0.137767	SLC45A3/F	6 geneontol	0.008915
GO:00027 negative r 2/673	10/18670	0.048192	0.17956	0.137767	C4BPB/CR	2 geneontol	0.002972
GO:00028 negative r 2/673	10/18670	0.048192	0.17956	0.137767	C4BPB/CR	2 geneontol	0.002972
GO:00069 substrate- 2/673	10/18670	0.048192	0.17956	0.137767	P2RY12/M	2 geneontol	0.002972
GO:00069 hypotonic 2/673	10/18670	0.048192	0.17956	0.137767	AQP5/TSP	2 geneontol	0.002972
GO:00074 foregut m 2/673	10/18670	0.048192	0.17956	0.137767	SHH/SOX1	2 geneontol	0.002972
GO:00107 regulation 2/673	10/18670	0.048192	0.17956	0.137767	GUCY1A2/	2 geneontol	0.002972
GO:00109 negative r 2/673	10/18670	0.048192	0.17956	0.137767	MUC1/TFA	2 geneontol	0.002972
GO:00303 poly-N-ac 2/673	10/18670	0.048192	0.17956	0.137767	B3GNT7/B	2 geneontol	0.002972
GO:00357 endothelia 2/673	10/18670	0.048192	0.17956	0.137767	CXCL13/F	2 geneontol	0.002972
GO:00480 regulation 2/673	10/18670	0.048192	0.17956	0.137767	ZEB2/CDH	2 geneontol	0.002972
GO:00483 positive re 2/673	10/18670	0.048192	0.17956	0.137767	PTPRC/CD	2 geneontol	0.002972
GO:00485 notochord 2/673	10/18670	0.048192	0.17956	0.137767	EPHA2/EFI	2 geneontol	0.002972
GO:00508 positive re 2/673	10/18670	0.048192	0.17956	0.137767	STAP1/PR	2 geneontol	0.002972
GO:00515 response t 2/673	10/18670	0.048192	0.17956	0.137767	BCHE/FOL	2 geneontol	0.002972
GO:00602 regulation 2/673	10/18670	0.048192	0.17956	0.137767	PDE3A/IGF	2 geneontol	0.002972
GO:00605 prostatic b 2/673	10/18670	0.048192	0.17956	0.137767	FGF10/SH	2 geneontol	0.002972
GO:00607 regulation 2/673	10/18670	0.048192	0.17956	0.137767	SHH/SERP	2 geneontol	0.002972
GO:00609 cardiac m 2/673	10/18670	0.048192	0.17956	0.137767	DKK1/WT1	2 geneontol	0.002972
GO:00612 retina vas 2/673	10/18670	0.048192	0.17956	0.137767	CYP1B1/AI	2 geneontol	0.002972
GO:00700 regulation 2/673	10/18670	0.048192	0.17956	0.137767	SLIT2/SLIT	2 geneontol	0.002972
GO:00701 regulation 2/673	10/18670	0.048192	0.17956	0.137767	TFAP2A/A	2 geneontol	0.002972
GO:00703 response t 2/673	10/18670	0.048192	0.17956	0.137767	CD36/LBP	2 geneontol	0.002972
GO:00709 neutrophil 2/673	10/18670	0.048192	0.17956	0.137767	DNASE1L3	2 geneontol	0.002972
GO:00712 cellular res 2/673	10/18670	0.048192	0.17956	0.137767	CD36/LBP	2 geneontol	0.002972
GO:00716 smooth m 2/673	10/18670	0.048192	0.17956	0.137767	SLIT2/LPAI	2 geneontol	0.002972
GO:19017 regulation 2/673	10/18670	0.048192	0.17956	0.137767	LRRK2/PR	2 geneontol	0.002972
GO:19058 regulation 2/673	10/18670	0.048192	0.17956	0.137767	PDE3A/IGF	2 geneontol	0.002972
GO:20005 regulation 2/673	10/18670	0.048192	0.17956	0.137767	CXCL13/F	2 geneontol	0.002972
GO:00074 axonal fas 3/673	23/18670	0.048329	0.17956	0.137767	CNTN4/EP	3 geneontol	0.004458
GO:00075 sex deterr 3/673	23/18670	0.048329	0.17956	0.137767	WT1/DHH	3 geneontol	0.004458
GO:00095 detection 3/673	23/18670	0.048329	0.17956	0.137767	NLRP3/CR	3 geneontol	0.004458
GO:00163 calcium-in 3/673	23/18670	0.048329	0.17956	0.137767	CLDN18/C	3 geneontol	0.004458
GO:00451 intermedia 3/673	23/18670	0.048329	0.17956	0.137767	SHH/KRT1	3 geneontol	0.004458
GO:00513 negative r 3/673	23/18670	0.048329	0.17956	0.137767	CCR2/P2R	3 geneontol	0.004458
GO:00604 lung cell d 3/673	23/18670	0.048329	0.17956	0.137767	FGF10/SPL	3 geneontol	0.004458
GO:00721 metaneph 3/673	23/18670	0.048329	0.17956	0.137767	OSR1/CXC	3 geneontol	0.004458
GO:00901 regulation 3/673	23/18670	0.048329	0.17956	0.137767	KDR/LRRK	3 geneontol	0.004458
GO:01060 neuron pr 3/673	23/18670	0.048329	0.17956	0.137767	CNTN4/EP	3 geneontol	0.004458
GO:19018 negative r 3/673	23/18670	0.048329	0.17956	0.137767	FAM107A/	3 geneontol	0.004458
GO:20001 negative r 7/673	92/18670	0.048333	0.17956	0.137767	SFN/NGF/	7 geneontol	0.010401
GO:00709 neuron de 19/673	348/18670	0.048399	0.17962	0.137845	NGF/IL10/	19 geneontol	0.028232
GO:00162 regulation 10/673	152/18670	0.048704	0.180648	0.138602	TGFBR3/K	10 geneontol	0.014859
GO:00030 vascular pi 11/673	173/18670	0.04905	0.181641	0.139363	NPR1/CXC	11 geneontol	0.016345
GO:00550 striated m 11/673	173/18670	0.04905	0.181641	0.139363	CAPN9/PC	11 geneontol	0.016345
GO:00031 endotheliu 9/673	132/18670	0.049514	0.18273	0.140199	S1PR1/XDI	9 geneontol	0.013373
GO:00086 hexose tra 8/673	112/18670	0.049541	0.18273	0.140199	SLC2A1/SL	8 geneontol	0.011887
GO:00518 modificatic 8/673	112/18670	0.049541	0.18273	0.140199	PTX3/CSF1	8 geneontol	0.011887
GO:19035 mucopolys 8/673	112/18670	0.049541	0.18273	0.140199	B3GNT7/H	8 geneontol	0.011887
GO:19038 negative r 8/673	112/18670	0.049541	0.18273	0.140199	CLDN18/C	8 geneontol	0.011887
GO:00620 collagen-c 57/718	406/19717	1.57E-18	6.10E-16	5.56E-16	TINAGL1/F	57 geneontol	0.079387
GO:00098 external sir 53/718	393/19717	1.53E-16	2.98E-14	2.71E-14	LEPR/TGFE	53 geneontol	0.073816
GO:00312 anchored 23/718	170/19717	6.00E-08	7.79E-06	7.10E-06	NEGR1/CC	23 geneontol	0.032033
GO:00451 membrane 31/718	315/19717	5.61E-07	4.67E-05	4.26E-05	SLC2A1/S1	31 geneontol	0.043175
GO:00988 membrane 31/718	316/19717	6.01E-07	4.67E-05	4.26E-05	SLC2A1/S1	31 geneontol	0.043175
GO:00985 membrane 31/718	328/19717	1.34E-06	8.67E-05	7.91E-05	SLC2A1/S1	31 geneontol	0.043175
GO:00059 cell-cell jui 36/718	459/19717	1.43E-05	0.000794	0.000724	EPHA2/GJI	36 geneontol	0.050139
GO:00056 interstitial 5/718	12/19717	4.04E-05	0.001965	0.001792	VIT/ABI3BI	5 geneontol	0.006964
GO:00466 anchored 10/718	59/19717	4.81E-05	0.002081	0.001897	CD2/EFNA	10 geneontol	0.013928
GO:00056 basement 12/718	95/19717	0.00017	0.006627	0.006043	HMCN1/L	12 geneontol	0.016713
GO:00017 immunolo 7/718	36/19717	0.000274	0.009678	0.008825	ZAP70/CD	7 geneontol	0.009749
GO:00057 Golgi lume 12/718	102/19717	0.000334	0.010831	0.009877	NGF/MUC	12 geneontol	0.016713
GO:00059 microvillus 10/718	83/19717	0.000852	0.025482	0.023238	CD302/S1	10 geneontol	0.013928
GO:00347 sodium ch 5/718	23/19717	0.001231	0.033303	0.03037	GRIK3/SCN	5 geneontol	0.006964
GO:00099 basal plas 6/718	34/19717	0.001284	0.033303	0.03037	TACSTD2/	6 geneontol	0.008357
GO:00444 extracellular 7/718	51/19717	0.002368	0.05757	0.052499	LAMB3/EL	7 geneontol	0.009749
GO:00163 apicolater 4/718	18/19717	0.003548	0.081195	0.074043	CLDN4/MI	4 geneontol	0.005571
GO:00971 tetraspanin 3/718	10/19717	0.004763	0.102941	0.093874	TSPAN15/	3 geneontol	0.004178
GO:00163 basolatera 16/718	217/19717	0.006059	0.124048	0.113122	SLC2A1/T	16 geneontol	0.022284

GO:00701 tight juncti	11/718	128/19717	0.00713	0.133654	0.121882	EPHA2/TA	11	geneontol	0.01532
GO:00986 protein co	5/718	34/19717	0.007319	0.133654	0.121882	ITGA4/CD	5	geneontol	0.006964
GO:00426 mast cell	4/718	22/19717	0.007559	0.133654	0.121882	CXCR2/PIK	4	geneontol	0.005571
GO:00451 basal part	6/718	51/19717	0.010213	0.168043	0.153242	TACSTD2/	6	geneontol	0.008357
GO:00312 intrinsic co	4/718	24/19717	0.010368	0.168043	0.153242	GPIHBP1/F	4	geneontol	0.005571
GO:00163 apical plas	20/718	318/19717	0.012943	0.193942	0.176859	SLC2A1/M	20	geneontol	0.027855
GO:00015 voltage-g	3/718	14/19717	0.012963	0.193942	0.176859	SCN7A/SC	3	geneontol	0.004178
GO:00310 platelet al	8/718	91/19717	0.017843	0.25083	0.228737	SELP/MMF	8	geneontol	0.011142
GO:00448 plasma me	9/718	109/19717	0.018055	0.25083	0.228737	SLC2A1/SE	9	geneontol	0.012535
GO:00325 ruffle mem	8/718	94/19717	0.021281	0.285457	0.260314	EPHA2/EP	8	geneontol	0.011142
GO:00017 ruffle	12/718	172/19717	0.023771	0.296404	0.270297	EPHA2/EP	12	geneontol	0.016713
GO:00347 potassium	8/718	96/19717	0.023818	0.296404	0.270297	GRIK3/KCN	8	geneontol	0.011142
GO:00451 apical part	22/718	384/19717	0.024898	0.296404	0.270297	SLC2A1/M	22	geneontol	0.030641
GO:00083 integrin co	4/718	31/19717	0.025145	0.296404	0.270297	ITGA4/ITG	4	geneontol	0.005571
GO:00312 cell projec	20/718	345/19717	0.02821	0.308812	0.281612	EPHA2/EP	20	geneontol	0.027855
GO:00436 axon termi	9/718	119/19717	0.029891	0.308812	0.281612	GRIK3/KCN	9	geneontol	0.012535
GO:00160 dystrophin	3/718	19/19717	0.030167	0.308812	0.281612	SGCD/KRT	3	geneontol	0.004178
GO:00313 anchored r	3/718	19/19717	0.030167	0.308812	0.281612	GPIHBP1/F	3	geneontol	0.004178
GO:00906 glycoprote	3/718	19/19717	0.030167	0.308812	0.281612	SGCD/KRT	3	geneontol	0.004178
GO:00347 cation cha	14/718	220/19717	0.031009	0.309294	0.282051	GRIK3/PDE	14	geneontol	0.019499
GO:01500 distal axon	17/718	285/19717	0.032411	0.315194	0.287431	GRIK3/KCN	17	geneontol	0.023677
GO:00310 platelet al	6/718	67/19717	0.0349	0.331123	0.301958	MMRN1/F	6	geneontol	0.008357
GO:00059 bicellular	9/718	123/19717	0.035871	0.332235	0.302971	TACSTD2/	9	geneontol	0.012535
GO:00431 terminal br	5/718	51/19717	0.037416	0.338486	0.308672	GRIK3/NM	5	geneontol	0.006964
GO:00059 connexin	3/718	21/19717	0.039253	0.339401	0.309506	GJB5/GJB4	3	geneontol	0.004178
GO:00198 extrinsic	11/718	165/19717	0.039262	0.339401	0.309506	S100A10/S	11	geneontol	0.01532
GO:00198 extrinsic	17/718	295/19717	0.042654	0.356863	0.325431	S100A10/S	17	geneontol	0.023677
GO:00315 brush bor	5/718	53/19717	0.043117	0.356863	0.325431	KCNK1/CC	5	geneontol	0.006964
GO:00165 sarcoplas	6/718	71/19717	0.044434	0.360101	0.328383	XDH/HK2/	6	geneontol	0.008357
GO:00015 microfibr	2/718	10/19717	0.049088	0.372398	0.339598	MFAP4/AC	2	geneontol	0.002786
GO:00442 juxtapan	2/718	10/19717	0.049088	0.372398	0.339598	KCNAB1/C	2	geneontol	0.002786
GO:00315 microvill	3/718	23/19717	0.049562	0.372398	0.339598	S100P/CDI	3	geneontol	0.004178
GO:00347 ion chann	17/718	301/19717	0.049817	0.372398	0.339598	GRIK3/PDE	17	geneontol	0.023677
GO:00055 glycosam	36/672	229/17697	3.86E-13	2.71E-10	2.35E-10	PLA2G2D/	36	geneontol	0.053571
GO:00082 heparin bi	30/672	169/17697	1.48E-12	5.20E-10	4.49E-10	PLA2G2D/	30	geneontol	0.044643
GO:00052 extracellu	29/672	163/17697	3.30E-12	7.74E-10	6.69E-10	TINAGL1/F	29	geneontol	0.043155
GO:00048 cytokine	22/672	96/17697	7.57E-12	1.33E-09	1.15E-09	LEPR/IL1R	22	geneontol	0.032738
GO:00016 G protein-	12/672	26/17697	4.83E-11	5.66E-09	4.89E-09	CXCR2/GP	12	geneontol	0.017857
GO:00049 chemokine	12/672	26/17697	4.83E-11	5.66E-09	4.89E-09	CXCR2/GP	12	geneontol	0.017857
GO:00199 C-C chem	11/672	24/17697	3.47E-10	3.49E-08	3.01E-08	ACKR1/CX	11	geneontol	0.016369
GO:00199 cytokine	23/672	128/17697	4.74E-10	4.17E-08	3.60E-08	LEPR/TGFE	23	geneontol	0.034226
GO:00199 chemokine	12/672	32/17697	9.16E-10	7.16E-08	6.18E-08	ACKR1/ITC	12	geneontol	0.017857
GO:00047 protein tyr	23/672	134/17697	1.21E-09	8.53E-08	7.37E-08	EPHA2/EFI	23	geneontol	0.034226
GO:00164 C-C chem	10/672	23/17697	4.26E-09	2.73E-07	2.35E-07	CXCR2/CC	10	geneontol	0.014881
GO:19016 sulfur com	31/672	250/17697	6.92E-09	4.04E-07	3.49E-07	PLA2G2D/	31	geneontol	0.046131
GO:00047 transmem	15/672	62/17697	7.46E-09	4.04E-07	3.49E-07	EPHA2/EFI	15	geneontol	0.022321
GO:00085 G protein-	22/672	146/17697	3.30E-08	1.66E-06	1.43E-06	NPR1/CAL	22	geneontol	0.032738
GO:00191 transmem	16/672	79/17697	3.63E-08	1.70E-06	1.47E-06	EPHA2/TG	16	geneontol	0.02381
GO:00016 peptide re	22/672	152/17697	6.93E-08	3.05E-06	2.63E-06	NPR1/CAL	22	geneontol	0.032738
GO:00016 G protein-	7/672	13/17697	1.55E-07	6.06E-06	5.23E-06	GPR171/P	7	geneontol	0.010417
GO:00450 G protein-	7/672	13/17697	1.55E-07	6.06E-06	5.23E-06	GPR171/P	7	geneontol	0.010417
GO:00016 purinergic	8/672	20/17697	3.48E-07	1.22E-05	1.06E-05	GPR171/P	8	geneontol	0.011905
GO:00165 nucleotide	8/672	20/17697	3.48E-07	1.22E-05	1.06E-05	GPR171/P	8	geneontol	0.011905
GO:00150 corecepto	11/672	44/17697	5.33E-07	1.78E-05	1.54E-05	TGFBR3/CI	11	geneontol	0.016369
GO:00508 cell adhesi	42/672	499/17697	1.27E-06	4.06E-05	3.51E-05	ARHGEF16	42	geneontol	0.0625
GO:00355 purinergic	8/672	25/17697	2.53E-06	7.72E-05	6.67E-05	GPR171/P	8	geneontol	0.011905
GO:00302 carbohydr	27/672	271/17697	5.02E-06	0.000147	0.000127	TINAGL1/S	27	geneontol	0.040179
GO:00423 chemokine	12/672	66/17697	6.11E-06	0.000172	0.000149	S100A14/C	12	geneontol	0.017857
GO:00051 integrin bi	17/672	132/17697	1.06E-05	0.000287	0.000248	ADAM23/H	17	geneontol	0.025298
GO:00986 cell adhesi	11/672	59/17697	1.16E-05	0.000302	0.000261	TACSTD2/	11	geneontol	0.016369
GO:00986 cell-cell	10/672	50/17697	1.51E-05	0.00038	0.000328	TACSTD2/	10	geneontol	0.014881
GO:00198 growth fac	17/672	137/17697	1.75E-05	0.000423	0.000366	TGFBR3/IL	17	geneontol	0.025298
GO:00306 Rac guany	6/672	17/17697	2.53E-05	0.000594	0.000513	EPS8L3/DC	6	geneontol	0.008929
GO:00480 CCR chem	9/672	43/17697	2.75E-05	0.000625	0.00054	CCR2/CXC	9	geneontol	0.013393
GO:00986 cadherin	6/672	19/17697	5.21E-05	0.001144	0.000988	TACSTD2/	6	geneontol	0.008929
GO:00080 chemokine	9/672	49/17697	8.19E-05	0.001744	0.001507	CXCL13/C	9	geneontol	0.013393
GO:00480 receptor li	36/672	482/17697	9.19E-05	0.0019	0.001641	NGF/TNFS	36	geneontol	0.053571
GO:00049 icosanoid	15/672	15/17697	0.00017	0.003416	0.002951	PTGER3/P	5	geneontol	0.00744
GO:00050 Rho guany	11/672	79/17697	0.000188	0.003672	0.003172	ARHGEF16	11	geneontol	0.016369
GO:00055 collagen	10/672	67/17697	0.000204	0.003885	0.003357	PODN/DD	10	geneontol	0.014881
GO:00508 extracellu	9/672	57/17697	0.000274	0.005062	0.004373	TINAGL1/S	9	geneontol	0.013393
GO:00047 non-mem	8/672	46/17697	0.000301	0.005432	0.004693	ZAP70/ITK	8	geneontol	0.011905
GO:00049 prostaglan	4/672	10/17697	0.00036	0.006178	0.005338	PTGER3/P	4	geneontol	0.005952

GO:00717: lipopeptid 4/672	10/17697	0.00036	0.006178	0.005338	CD1C/CD1	4 geneontol	0.005952
GO:00042: metalloen 12/672	103/17697	0.000529	0.008581	0.007413	MMEL1/AI	12 geneontol	0.017857
GO:00050: guanyl-nu 19/672	214/17697	0.000539	0.008581	0.007413	ARHGEF16	19 geneontol	0.028274
GO:00049: prostanoid 4/672	11/17697	0.000549	0.008581	0.007413	PTGER3/P	4 geneontol	0.005952
GO:00507: RAGE rece 4/672	11/17697	0.000549	0.008581	0.007413	S100A12/S	4 geneontol	0.005952
GO:00050: scavenger 8/672	51/17697	0.000623	0.009514	0.00822	TINAGL1/F	8 geneontol	0.011905
GO:00432: laminin bir 6/672	29/17697	0.000659	0.00986	0.008519	TINAGL1/S	6 geneontol	0.008929
GO:00041: 3',5'-cyclic 4/672	12/17697	0.000799	0.011705	0.010113	PDE4B/PD	4 geneontol	0.005952
GO:00381: pattern rec 5/672	21/17697	0.000954	0.013682	0.011821	CD36/CLE	5 geneontol	0.00744
GO:00170: Rho GTPa 16/672	177/17697	0.00119	0.016168	0.013969	ARHGEF16	16 geneontol	0.02381
GO:00300: extracellul 5/672	22/17697	0.001196	0.016168	0.013969	PODN/PR	5 geneontol	0.00744
GO:00504: transformi 5/672	22/17697	0.001196	0.016168	0.013969	TGFBR3/N	5 geneontol	0.00744
GO:00380: cargo rece 10/672	85/17697	0.001401	0.018582	0.016055	TINAGL1/F	10 geneontol	0.014881
GO:00198: immunogl 5/672	24/17697	0.001813	0.0236	0.020389	FCER1A/M	5 geneontol	0.00744
GO:00051: cytokine ar 18/672	220/17697	0.00189	0.024163	0.020876	TNFSF18/I	18 geneontol	0.026786
GO:00433: proteoglyc 6/672	36/17697	0.002158	0.027087	0.023402	PLA2G2D/	6 geneontol	0.008929
GO:00016: G protein- 21/672	280/17697	0.002427	0.029938	0.025865	S1PR1/S1C	21 geneontol	0.03125
GO:00080: phosphori 10/672	94/17697	0.002987	0.036123	0.031209	PDE4B/PD	10 geneontol	0.014881
GO:00051: cytokine re 21/672	286/17697	0.00312	0.036123	0.031209	TGFBR3/N	21 geneontol	0.03125
GO:00019: fibronectin 5/672	27/17697	0.003134	0.036123	0.031209	ITGA4/CC	5 geneontol	0.00744
GO:00468: ephrin recr 5/672	27/17697	0.003134	0.036123	0.031209	EFNA4/EF	5 geneontol	0.00744
GO:00041: calcium-d 4/672	17/17697	0.003303	0.037453	0.032358	CAPN8/CA	4 geneontol	0.005952
GO:00041: endopepti 28/672	427/17697	0.003684	0.040625	0.035098	MMEL1/C	28 geneontol	0.041667
GO:00041: 3',5'-cyclic 5/672	28/17697	0.003698	0.040625	0.035098	PDE4B/PD	5 geneontol	0.00744
GO:00052: sodium ch 6/672	41/17697	0.004244	0.045898	0.039655	GRIK3/KC	6 geneontol	0.008929
GO:00041: cyclic-nucl 5/672	29/17697	0.004332	0.046138	0.039862	PDE4B/PD	5 geneontol	0.00744
GO:00483: Rac GTPa 8/672	69/17697	0.004502	0.047241	0.040815	EPS8L3/DC	8 geneontol	0.011905
GO:00199: structural 3/672	10/17697	0.005355	0.055364	0.047833	MAL/MAL	3 geneontol	0.004464
GO:00050: Ras guany 12/672	137/17697	0.006015	0.061283	0.052946	ARHGEF16	12 geneontol	0.017857
GO:00083: signaling r 4/672	20/17697	0.006144	0.061699	0.053306	CD36/COL	4 geneontol	0.005952
GO:00452: CXCR cher 3/672	11/17697	0.007158	0.07087	0.061229	CXCL13/C	3 geneontol	0.004464
GO:00018: compleme 4/672	21/17697	0.007365	0.070923	0.061275	CR2/CR1/F	4 geneontol	0.005952
GO:00518: glycolipid 4/672	21/17697	0.007365	0.070923	0.061275	CD1C/SELI	4 geneontol	0.005952
GO:00718: lipoproteir 5/672	33/17697	0.007643	0.071643	0.061897	CD36/LPL/	5 geneontol	0.00744
GO:00718: protein-lip 5/672	33/17697	0.007643	0.071643	0.061897	CD36/LPL/	5 geneontol	0.00744
GO:00483: calcium-d 7/672	61/17697	0.008132	0.075225	0.064992	S100A11/S	7 geneontol	0.010417
GO:00336: sialic acid 13/672	12/17697	0.009277	0.083501	0.072142	SELP/SELE	3 geneontol	0.004464
GO:00082: metallope 14/672	181/17697	0.0093	0.083501	0.072142	MMEL1/AI	14 geneontol	0.020833
GO:00080: growth fac 13/672	163/17697	0.009383	0.083501	0.072142	NGF/IL10/	13 geneontol	0.019345
GO:00012: DNA-bind 27/672	439/17697	0.009791	0.086041	0.074337	ELF3/ZEB2	27 geneontol	0.040179
GO:00170: peptide hc 6/672	49/17697	0.010229	0.086925	0.0751	LEPR/NPR	6 geneontol	0.008929
GO:00171: fibroblast 4/672	23/17697	0.010263	0.086925	0.0751	TGFBR3/C	4 geneontol	0.005952
GO:00466: sphingolip 4/672	23/17697	0.010263	0.086925	0.0751	S1PR1/SEL	4 geneontol	0.005952
GO:00355: signaling a 8/672	80/17697	0.010874	0.091006	0.078626	CD28/TRA	8 geneontol	0.011905
GO:00167: oxidoredu 3/672	13/17697	0.011724	0.095837	0.0828	XDH/AOX	3 geneontol	0.004464
GO:00397: co-recept 3/672	13/17697	0.011724	0.095837	0.0828	DKK2/DKK	3 geneontol	0.004464
GO:00171: Wnt-prote 5/672	37/17697	0.012401	0.100207	0.086576	MST1R/SF	5 geneontol	0.00744
GO:00050: SH3/SH2 e 6/672	52/17697	0.013541	0.108149	0.093437	CD28/STA	6 geneontol	0.008929
GO:00083: steroid hyc 5/672	38/17697	0.013846	0.108149	0.093437	CYP1B1/C	5 geneontol	0.00744
GO:00420: chemoattr 5/672	38/17697	0.013846	0.108149	0.093437	FGF10/GPI	5 geneontol	0.00744
GO:00451: bioactive li 3/672	14/17697	0.014507	0.112068	0.096823	S1PR1/LP	3 geneontol	0.004464
GO:00152: channel ac 27/672	456/17697	0.015472	0.116172	0.100368	GJB4/GJB3	27 geneontol	0.040179
GO:00425: hormone t 9/672	102/17697	0.015506	0.116172	0.100368	LEPR/NPR	9 geneontol	0.013393
GO:00167: transferase 7/672	69/17697	0.015534	0.116172	0.100368	SULT1C2/S	7 geneontol	0.010417
GO:00044: phosphati 4/672	26/17697	0.015843	0.116252	0.100437	PLCL1/CC	4 geneontol	0.005952
GO:00228: passive tra 27/672	457/17697	0.015875	0.116252	0.100437	GJB4/GJB3	27 geneontol	0.040179
GO:00017: phosphoty 5/672	40/17697	0.017064	0.122714	0.10602	SHE/ZAP7	5 geneontol	0.00744
GO:00018: opsonin bi 3/672	15/17697	0.01763	0.122714	0.10602	CR1/PTX3/	3 geneontol	0.004464
GO:00083: mechanos 3/672	15/17697	0.01763	0.122714	0.10602	TMEM150	3 geneontol	0.004464
GO:00445: S100 prote 3/672	15/17697	0.01763	0.122714	0.10602	S100A11/S	3 geneontol	0.004464
GO:00704: oligosacch 3/672	15/17697	0.01763	0.122714	0.10602	SELP/SELL	3 geneontol	0.004464
GO:00454: chemorep 4/672	27/17697	0.018054	0.124428	0.107502	SEMA3G/S	4 geneontol	0.005952
GO:00046: phospholi 4/672	28/17697	0.020446	0.13955	0.120566	PLCL1/CC	4 geneontol	0.005952
GO:00301: low-densit 3/672	16/17697	0.021098	0.141256	0.122041	CD36/THB	3 geneontol	0.004464
GO:00433: heparan s 3/672	16/17697	0.021098	0.141256	0.122041	PLA2G2D/	3 geneontol	0.004464
GO:00016: virus recep 7/672	74/17697	0.022065	0.144969	0.125248	EPHA2/SL	7 geneontol	0.010417
GO:01040: hijacked m 7/672	74/17697	0.022065	0.144969	0.125248	EPHA2/SL	7 geneontol	0.010417
GO:00050: transmem 3/672	17/17697	0.024911	0.16126	0.139323	EPHA2/EF	3 geneontol	0.004464
GO:19907: protein tyr 8/672	93/17697	0.025003	0.16126	0.139323	ARHGEF16	8 geneontol	0.011905
GO:00306: protein bir 12/672	170/17697	0.029004	0.184106	0.159061	CD28/MLP	12 geneontol	0.017857
GO:00381: neuropeptin 3/672	18/17697	0.029069	0.184106	0.159061	SEMA3G/S	3 geneontol	0.004464
GO:00708: growth fac 10/672	134/17697	0.031695	0.198944	0.171881	IL10/EFEM	10 geneontol	0.014881
GO:00050: ephrin recr 3/672	19/17697	0.03357	0.208848	0.180438	EPHA2/EF	3 geneontol	0.004464

GO:000449	monooxygenase activity	8/672	99/17697	0.034606	0.213403	0.184373	FMO2/FMO3	8	geneontology	0.011905
GO:000511	epidermal cell proliferation	4/672	33/17697	0.035247	0.215467	0.186157	EFEMP1/A	4	geneontology	0.005952
GO:000522	voltage-gated ion channel activity	3/672	20/17697	0.03841	0.232779	0.201113	SCN7A/SCN7A-AS1	3	geneontology	0.004464
GO:000462	phospholipase activity	8/672	102/17697	0.040234	0.24004	0.207387	PLA2G2D/PLA2G2B	8	geneontology	0.011905
GO:006111	peptidase activity	14/672	219/17697	0.040291	0.24004	0.207387	NGF/MAL/NGF1A	14	geneontology	0.020833
GO:004311	alcohol binding	7/672	85/17697	0.0426	0.251664	0.217429	RBP7/CRA	7	geneontology	0.010417
GO:004530	protein phosphatase activity	5/672	51/17697	0.043501	0.254846	0.220179	SHE/ZAP70	5	geneontology	0.00744
GO:003041	peptidase activity	12/672	182/17697	0.045193	0.262569	0.22685	NGF/PI16/NGF1A	12	geneontology	0.017857
GO:001701	sodium channel activity	4/672	36/17697	0.046459	0.262934	0.227166	SCN4B/SCN4B-AS1	4	geneontology	0.005952
GO:004211	SH2 domain binding	4/672	36/17697	0.046459	0.262934	0.227166	LAX1/DLC1	4	geneontology	0.005952
GO:000811	sulfotransferase activity	5/672	52/17697	0.046689	0.262934	0.227166	SULT1C2/SULT1C2-AS1	5	geneontology	0.00744
GO:003091	receptor tyrosine kinase activity	6/672	69/17697	0.046752	0.262934	0.227166	ARHGEF16	6	geneontology	0.008929
GO:001621	channel regulator activity	10/672	144/17697	0.047978	0.267689	0.231274	KCNAB1/P	10	geneontology	0.014881
