

PVRIG Expression is an Independent Prognostic Factor and a New Target for Immunotherapy in Hepatocellular Carcinoma

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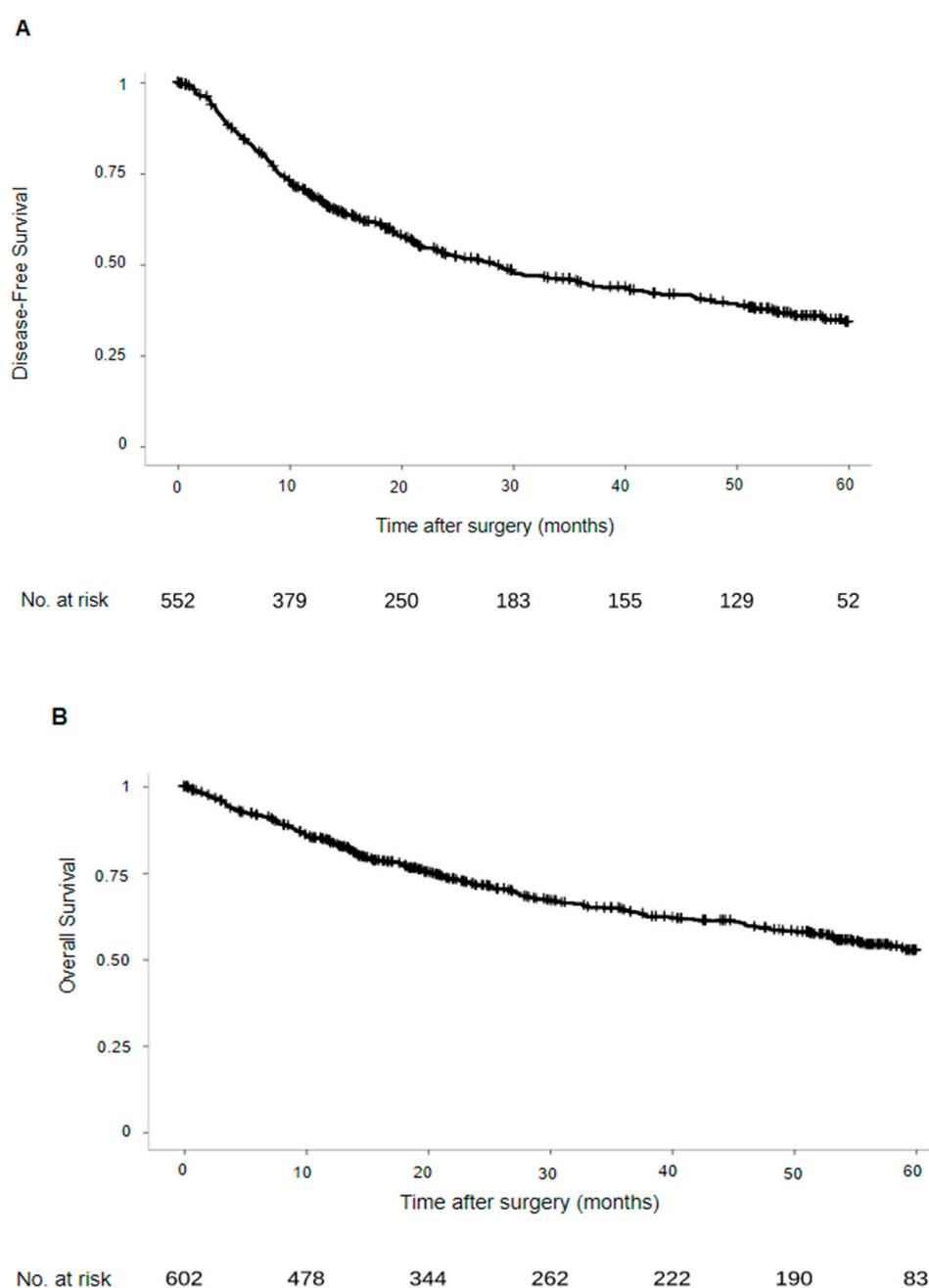


Figure S1. Survival in patient with HCC. (A) Kaplan-Meier DFS curve in the whole cohort of HCC patients (n=552). (B) Kaplan-Meier OS curve in the whole cohort of HCC patients (n=602). The p-value is for log rank test.

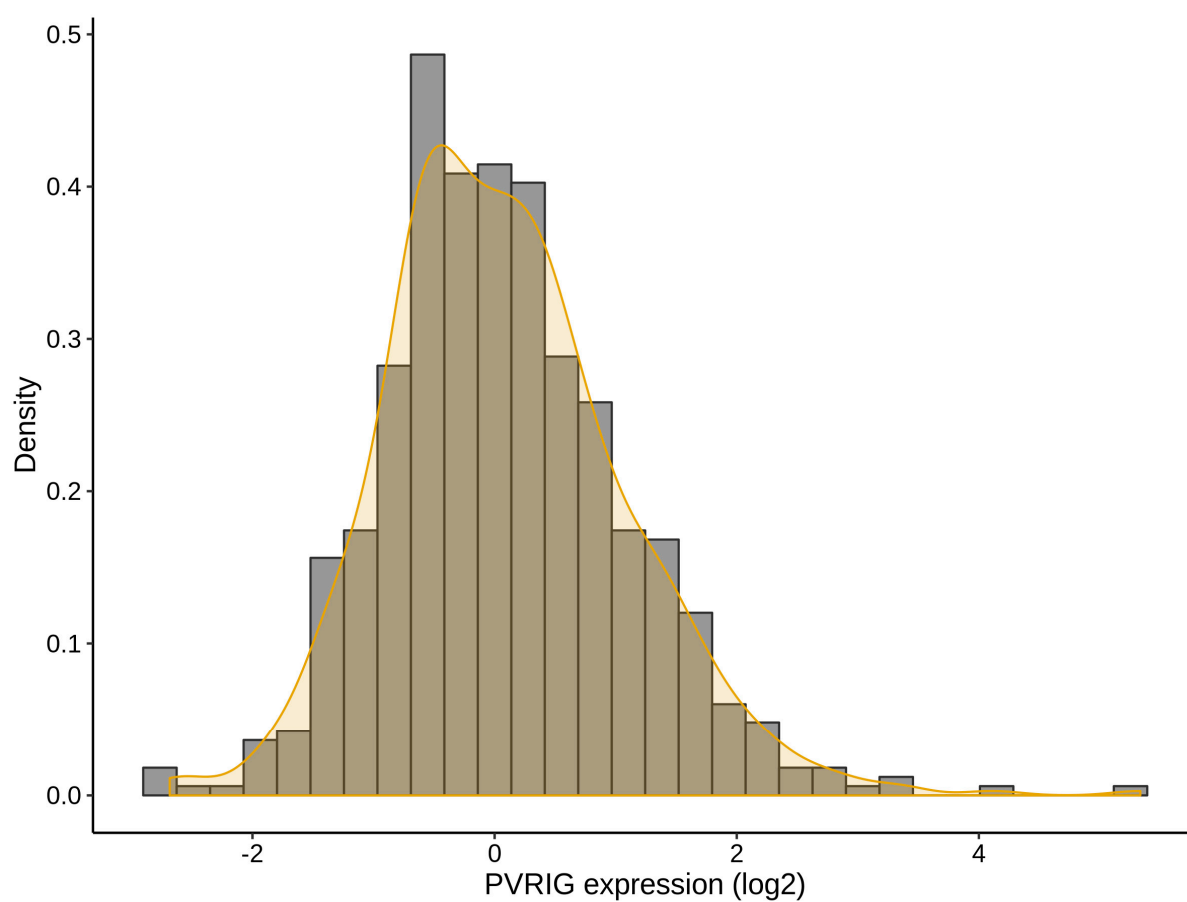


Figure S2: Distribution of *PVRIG* expression in HCC samples. Histogram of distribution of *PVRIG* mRNA expression levels (log2) across the 602 clinical samples. The orange line represents the density curve of distribution.

Table S1. Data sets included in the study

Reference	Source of data	Samples (N)	HCC samples (n)	healthy liver samples (n)	Technological platform
The Cancer Genome Atlas Research Network. <i>Cell</i> 2017	https://www.cbioportal.org/	360	360	0	Illumina HiSeq RNA-seq
Roessler et al., <i>Cancer Res</i> 2010	GEO: GSE14520	481	242	239	Affymetrix Human Genome U133A 2.0 Array; Affymetrix HT Human Genome U133A Array
Villa et al., <i>Gut</i> 206	GEO: GSE54236	161	81	80	Agilent-014850 Whole Human Genome Microarray 4x44K G4112F
Total		1002	683	319	

Table S2. Association between expression of members of TIGIT/DNAM-1 axis and PD-1/PD-L1 axis related RNA expression and survival in HCC and survival in HCC

Gene symbol	Overall Survival		Disease-Free Survival	
	Univariate	Multivariate	Univariate	Multivariate
DNAM-1	2.85×10^{-2}	0.52	1.03×10^{-3}	0.14
PD-L1	0.51	-	0.67	-
TACTILE	1.56×10^{-2}	0.57	7.17×10^{-4}	0.77
CTLA-4	4.87×10^{-2}	0.79	5.08×10^{-3}	0.49
KIR2DL5A	0.18	-	0.19	-
NECTIN-1	1.84×10^{-2}	5.48×10^{-3}	6.38×10^{-2}	-
NECTIN-2	0.98	-	0.41	-
NECTIN-3	0.40	-	2.16×10^{-2}	0.61
PD-1	3.48×10^{-2}	0.20	1.21×10^{-3}	0.36
PVR	7.28×10^{-2}	-	0.66	-
PVRIG	3.16×10^{-6}	4.57×10^{-4}	1.43×10^{-4}	0.37
TIGIT	0.22	-	2.98×10^{-2}	0.85

Table S3. List of the 181 genes differentially expressed between PVRIG High and Low groups in the learning set (GSE14520, n=242)

Entrez ID	Symbol	Full name	Genomic loc	NCBI link	Fold change	p-value	Adjusted p-value	Upregulated (Red/Green)
79037	PVRIG	PVR related immunoglobulin domain containing	7q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=79037+AND+homo+sapiens	1.52	1.0E-38	1.2E-34	PVRIG_High
914	CD2	CD2 molecule	1p13.1	https://www.ncbi.nlm.nih.gov/gene/?term=914+AND+homo+sapiens	2.48	1.3E-19	7.1E-16	PVRIG_High
1043	CD52	CD52 molecule	1p36.11	https://www.ncbi.nlm.nih.gov/gene/?term=1043+AND+homo+sapiens	2.45	1.3E-18	3.9E-15	PVRIG_High
962	CD48	CD48 molecule	1q23.3	https://www.ncbi.nlm.nih.gov/gene/?term=962+AND+homo+sapiens	2.14	1.7E-18	3.9E-15	PVRIG_High
5880	RAC2	Rac family small GTPase 2	22q13.1	https://www.ncbi.nlm.nih.gov/gene/?term=5880+AND+homo+sapiens	2.21	6.9E-18	1.3E-14	PVRIG_High
80342	TRAF3IP3	TRAF3 interacting protein 3	1q32.2	https://www.ncbi.nlm.nih.gov/gene/?term=80342+AND+homo+sapiens	1.67	2.5E-17	4.1E-14	PVRIG_High
11151	CORO1A	coronin 1A	16p11.2	https://www.ncbi.nlm.nih.gov/gene/?term=11151+AND+homo+sapiens	2.36	3.8E-17	4.9E-14	PVRIG_High
6352	CCL5	C-C motif chemokine ligand 5	17q12	https://www.ncbi.nlm.nih.gov/gene/?term=6352+AND+homo+sapiens	2.95	3.9E-17	4.9E-14	PVRIG_High
10125	RASGRP1	RAS guanyl releasing protein 1	15q14	https://www.ncbi.nlm.nih.gov/gene/?term=10125+AND+homo+sapiens	1.94	8.9E-17	8.4E-14	PVRIG_High
10659	CELF2	CUGBP Elav-like family member 2	10p14	https://www.ncbi.nlm.nih.gov/gene/?term=10659+AND+homo+sapiens	2.25	2.2E-16	1.9E-13	PVRIG_High
6404	SELPLG	selectin P ligand	12q24.11	https://www.ncbi.nlm.nih.gov/gene/?term=6404+AND+homo+sapiens	1.64	3.3E-16	2.5E-13	PVRIG_High
3001	GZMA	granzyme A	5q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=3001+AND+homo+sapiens	2.00	4.5E-16	3.2E-13	PVRIG_High
3003	GZMK	granzyme K	5q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=3003+AND+homo+sapiens	1.85	5.5E-16	3.6E-13	PVRIG_High

5790	PTPRC AP	protein tyrosine phosphatase, re- ceptor type C as- sociated protein	11q13.2	https://www.ncbi.nlm.nih.gov/gene/?term=5790+AND+homo+sapiens	1.56	6.0E-16	3.6E-13	PVRIG_High
3059	HCLS1	hematopoietic cell-specific Lyn substrate 1	3q13.33	https://www.ncbi.nlm.nih.gov/gene/?term=3059+AND+homo+sapiens	1.94	7.7E-15	3.8E-12	PVRIG_High
925	CD8A	CD8a molecule	2p11.2	https://www.ncbi.nlm.nih.gov/gene/?term=925+AND+homo+sapiens	2.60	8.6E-15	4.0E-12	PVRIG_High
9806	SPOCK2	SPARC (oste- onectin), cwcw and kazal like do- mains proteogly- can 2	10q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=9806+AND+homo+sapiens	1.64	9.2E-15	4.0E-12	PVRIG_High
8530	CST7	cystatin F	20p11.21	https://www.ncbi.nlm.nih.gov/gene/?term=8530+AND+homo+sapiens	1.61	9.3E-15	4.0E-12	PVRIG_High
2533	FYB1	FYN binding pro- tein 1	5p13.1	https://www.ncbi.nlm.nih.gov/gene/?term=2533+AND+homo+sapiens	1.65	1.2E-14	5.1E-12	PVRIG_High
3937	LCP2	lymphocyte cyto- solic protein 2	5q35.1	https://www.ncbi.nlm.nih.gov/gene/?term=3937+AND+homo+sapiens	1.67	1.4E-14	5.7E-12	PVRIG_High
3561	IL2RG	interleukin 2 re- ceptor subunit gamma	Xq13.1	https://www.ncbi.nlm.nih.gov/gene/?term=3561+AND+homo+sapiens	2.17	2.0E-14	7.7E-12	PVRIG_High
5579	PRKCB	protein kinase C beta	16p12.2- p12.1	https://www.ncbi.nlm.nih.gov/gene/?term=5579+AND+homo+sapiens	1.55	2.7E-14	1.0E-11	PVRIG_High
22914	KLRK1	killer cell lectin like receptor K1	12p13.2	https://www.ncbi.nlm.nih.gov/gene/?term=22914+AND+homo+sapiens	1.80	3.6E-14	1.3E-11	PVRIG_High
445347	TARP	TCR gamma al- ternate reading frame protein	7p14.1	https://www.ncbi.nlm.nih.gov/gene/?term=445347+AND+homo+sapiens	1.64	4.1E-14	1.4E-11	PVRIG_High
5788	PTPRC	protein tyrosine phosphatase, re- ceptor type C	1q31.3- q32.1	https://www.ncbi.nlm.nih.gov/gene/?term=5788+AND+homo+sapiens	2.50	4.2E-14	1.4E-11	PVRIG_High

5293	PIK3CD	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit delta	1p36.22	https://www.ncbi.nlm.nih.gov/gene/?term=5293+AND+homo+sapiens	1.78	5.2E-14	1.7E-11	PVRIG_High
4046	LSP1	lymphocyte-specific protein 1	11p15.5	https://www.ncbi.nlm.nih.gov/gene/?term=4046+AND+homo+sapiens	1.51	7.4E-14	2.3E-11	PVRIG_High
3560	IL2RB	interleukin 2 receptor subunit beta	22q12.3	https://www.ncbi.nlm.nih.gov/gene/?term=3560+AND+homo+sapiens	1.61	7.8E-14	2.3E-11	PVRIG_High
3932	LCK	LCK proto-oncogene, Src family tyrosine kinase	1p35.2	https://www.ncbi.nlm.nih.gov/gene/?term=3932+AND+homo+sapiens	1.56	7.9E-14	2.3E-11	PVRIG_High
9595	CYTIP	cytohesin 1 interacting protein	2q24.1	https://www.ncbi.nlm.nih.gov/gene/?term=9595+AND+homo+sapiens	1.87	9.7E-14	2.7E-11	PVRIG_High
969	CD69	CD69 molecule	12p13.31	https://www.ncbi.nlm.nih.gov/gene/?term=969+AND+homo+sapiens	1.67	9.9E-14	2.7E-11	PVRIG_High
963	CD53	CD53 molecule	1p13.3	https://www.ncbi.nlm.nih.gov/gene/?term=963+AND+homo+sapiens	2.22	1.1E-13	3.0E-11	PVRIG_High
5450	POU2A F1	POU class 2 associating factor 1	11q23.1	https://www.ncbi.nlm.nih.gov/gene/?term=5450+AND+homo+sapiens	3.28	1.6E-13	3.9E-11	PVRIG_High
3689	ITGB2	integrin subunit beta 2	21q22.3	https://www.ncbi.nlm.nih.gov/gene/?term=3689+AND+homo+sapiens	2.07	2.4E-13	6.0E-11	PVRIG_High
4050	LTB	lymphotoxin beta	6p21.33	https://www.ncbi.nlm.nih.gov/gene/?term=4050+AND+homo+sapiens	1.68	2.7E-13	6.6E-11	PVRIG_High
55303	GIMAP 4	GTPase, IMAP family member 4	7q36.1	https://www.ncbi.nlm.nih.gov/gene/?term=55303+AND+homo+sapiens	1.61	7.2E-13	1.6E-10	PVRIG_High
6351	CCL4	C-C motif chemokine ligand 4	17q12	https://www.ncbi.nlm.nih.gov/gene/?term=6351+AND+homo+sapiens	2.00	9.2E-13	2.0E-10	PVRIG_High
4818	NKG7	natural killer cell granule protein 7	19q13.41	https://www.ncbi.nlm.nih.gov/gene/?term=4818+AND+homo+sapiens	1.86	9.3E-13	2.0E-10	PVRIG_High
6503	SLA	Src like adaptor	8q24.22	https://www.ncbi.nlm.nih.gov/gene/?term=6503+AND+homo+sapiens	1.72	1.2E-12	2.6E-10	PVRIG_High

54440	SASH3	SAM and SH3 domain containing 3	Xq26.1	https://www.ncbi.nlm.nih.gov/gene/?term=54440+AND+homo+sapiens	1.58	1.8E-12	3.8E-10	PVRIG_High
3512	JCHAIN	joining chain of multimeric IgA and IgM	4q13.3	https://www.ncbi.nlm.nih.gov/gene/?term=3512+AND+homo+sapiens	4.06	2.3E-12	4.6E-10	PVRIG_High
199	AIF1	allograft inflammatory factor 1	6p21.33	https://www.ncbi.nlm.nih.gov/gene/?term=199+AND+homo+sapiens	1.64	3.9E-12	7.7E-10	PVRIG_High
4283	CXCL9	C-X-C motif chemokine ligand 9	4q21.1	https://www.ncbi.nlm.nih.gov/gene/?term=4283+AND+homo+sapiens	4.04	8.7E-12	1.6E-09	PVRIG_High
9535	GMFG	glia maturation factor gamma	19q13.2	https://www.ncbi.nlm.nih.gov/gene/?term=9535+AND+homo+sapiens	1.69	9.2E-12	1.7E-09	PVRIG_High
6402	SELL	selectin L	1q24.2	https://www.ncbi.nlm.nih.gov/gene/?term=6402+AND+homo+sapiens	1.60	1.0E-11	1.8E-09	PVRIG_High
2123	EVI2A	ecotropic viral integration site 2A	17q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=2123+AND+homo+sapiens	1.66	1.2E-11	2.0E-09	PVRIG_High
7351	UCP2	uncoupling protein 2	11q13.4	https://www.ncbi.nlm.nih.gov/gene/?term=7351+AND+homo+sapiens	2.06	1.4E-11	2.4E-09	PVRIG_High
712	C1QA	complement C1q A chain	1p36.12	https://www.ncbi.nlm.nih.gov/gene/?term=712+AND+homo+sapiens	2.18	1.5E-11	2.6E-09	PVRIG_High
113	ADCY7	adenylate cyclase 7	16q12.1	https://www.ncbi.nlm.nih.gov/gene/?term=113+AND+homo+sapiens	1.51	1.7E-11	2.9E-09	PVRIG_High
5341	PLEK	pleckstrin	2p14	https://www.ncbi.nlm.nih.gov/gene/?term=5341+AND+homo+sapiens	2.11	1.8E-11	3.0E-09	PVRIG_High
2124	EVI2B	ecotropic viral integration site 2B	17q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=2124+AND+homo+sapiens	2.03	2.6E-11	4.0E-09	PVRIG_High
7456	WIPF1	WAS/WASL interacting protein family member 1	2q31.1	https://www.ncbi.nlm.nih.gov/gene/?term=7456+AND+homo+sapiens	1.83	3.9E-11	5.9E-09	PVRIG_High
4065	LY75	lymphocyte antigen 75	2q24.2	https://www.ncbi.nlm.nih.gov/gene/?term=4065+AND+homo+sapiens	1.97	4.3E-11	6.4E-09	PVRIG_High

6772	STAT1	signal transducer and activator of transcription 1	2q32.2	https://www.ncbi.nlm.nih.gov/gene/?term=6772+AND+homo+sapiens	1.94	4.6E-11	6.6E-09	PVRIG_High
6614	SIG-LEC1	sialic acid binding Ig like lectin 1	20p13	https://www.ncbi.nlm.nih.gov/gene/?term=6614+AND+homo+sapiens	1.50	5.3E-11	7.5E-09	PVRIG_High
5551	PRF1	perforin 1	10q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=5551+AND+homo+sapiens	1.71	7.2E-11	9.6E-09	PVRIG_High
3587	IL10RA	interleukin 10 receptor subunit alpha	11q23.3	https://www.ncbi.nlm.nih.gov/gene/?term=3587+AND+homo+sapiens	1.82	9.4E-11	1.2E-08	PVRIG_High
397	ARHG-DIB	Rho GDP dissociation inhibitor beta	12p12.3	https://www.ncbi.nlm.nih.gov/gene/?term=397+AND+homo+sapiens	1.70	1.1E-10	1.4E-08	PVRIG_High
51237	MZB1	marginal zone B and B1 cell specific protein	5q31.2	https://www.ncbi.nlm.nih.gov/gene/?term=51237+AND+homo+sapiens	1.70	1.1E-10	1.4E-08	PVRIG_High
56833	SLAMF8	SLAM family member 8	1q23.2	https://www.ncbi.nlm.nih.gov/gene/?term=56833+AND+homo+sapiens	1.75	1.5E-10	1.8E-08	PVRIG_High
64092	SAMSN1	SAM domain, SH3 domain and nuclear localization signals 1	21q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=64092+AND+homo+sapiens	1.97	1.5E-10	1.9E-08	PVRIG_High
713	C1QB	complement C1q B chain	1p36.12	https://www.ncbi.nlm.nih.gov/gene/?term=713+AND+homo+sapiens	2.17	1.6E-10	1.9E-08	PVRIG_High
7805	LAPTM5	lysosomal protein transmembrane 5	1p35.2	https://www.ncbi.nlm.nih.gov/gene/?term=7805+AND+homo+sapiens	1.91	1.6E-10	1.9E-08	PVRIG_High
9672	SDC3	syndecan 3	1p35.2	https://www.ncbi.nlm.nih.gov/gene/?term=9672+AND+homo+sapiens	1.55	1.7E-10	2.0E-08	PVRIG_High
915	CD3D	CD3d molecule coactosin like F-actin binding	11q23.3	https://www.ncbi.nlm.nih.gov/gene/?term=915+AND+homo+sapiens	1.67	2.4E-10	2.8E-08	PVRIG_High
23406	COTL1	protein 1	16q24.1	https://www.ncbi.nlm.nih.gov/gene/?term=23406+AND+homo+sapiens	1.69	3.6E-10	4.1E-08	PVRIG_High

55340	GIMAP5	GTPase, IMAP family member 5	7q36.1	https://www.ncbi.nlm.nih.gov/gene/?term=55340+AND+homo+sapiens	1.64	7.5E-10	8.0E-08	PVRIG_High
60489	APO-BEC3G	apolipoprotein B mRNA editing enzyme catalytic subunit 3G	22q13.1	https://www.ncbi.nlm.nih.gov/gene/?term=60489+AND+homo+sapiens	1.87	9.1E-10	9.5E-08	PVRIG_High
7453	WARS	tryptophanyl-tRNA synthetase	14q32.2	https://www.ncbi.nlm.nih.gov/gene/?term=7453+AND+homo+sapiens	1.99	1.2E-09	1.2E-07	PVRIG_High
10875	FGL2	fibrinogen like 2	7q11.23	https://www.ncbi.nlm.nih.gov/gene/?term=10875+AND+homo+sapiens	1.58	1.3E-09	1.2E-07	PVRIG_High
3115	HLA-DPB1	major histocompatibility complex, class II, DP beta 1	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3115+AND+homo+sapiens	1.77	1.8E-09	1.7E-07	PVRIG_High
7305	TYROBP	TYRO protein tyrosine kinase binding protein	19q13.12	https://www.ncbi.nlm.nih.gov/gene/?term=7305+AND+homo+sapiens	1.82	2.2E-09	2.1E-07	PVRIG_High
1230	CCR1	C-C motif chemokine receptor 1	3p21.31	https://www.ncbi.nlm.nih.gov/gene/?term=1230+AND+homo+sapiens	1.67	4.9E-09	4.3E-07	PVRIG_High
3002	GZMB	granzyme B	14q12	https://www.ncbi.nlm.nih.gov/gene/?term=3002+AND+homo+sapiens	1.66	5.5E-09	4.8E-07	PVRIG_High
51816	ADA2	adenosine deaminase 2	22q11.1	https://www.ncbi.nlm.nih.gov/gene/?term=51816+AND+homo+sapiens	1.80	6.8E-09	5.9E-07	PVRIG_High
6001	RGS10	regulator of G protein signaling 10	10q26.11	https://www.ncbi.nlm.nih.gov/gene/?term=6001+AND+homo+sapiens	1.72	7.6E-09	6.5E-07	PVRIG_High
9447	AIM2	absent in melanoma 2	1q23.1-q23.2	https://www.ncbi.nlm.nih.gov/gene/?term=9447+AND+homo+sapiens	1.54	8.1E-09	6.9E-07	PVRIG_High
6890	TAP1	transporter 1, ATP binding cassette subfamily B member	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=6890+AND+homo+sapiens	1.76	1.1E-08	8.7E-07	PVRIG_High
55843	ARHGA P15	Rho GTPase activating protein 15	2q22.2-q22.3	https://www.ncbi.nlm.nih.gov/gene/?term=55843+AND+homo+sapiens	1.51	1.1E-08	9.0E-07	PVRIG_High

100132417	FCGR1CP	Fc fragment of IgG receptor Ic, pseudogene	1q21.1	https://www.ncbi.nlm.nih.gov/gene/?term=100132417+AND+homo+sapiens	1.67	1.2E-08	9.2E-07	PVRIG_High
64581	CLEC7A	C-type lectin domain containing 7A	12p13.2	https://www.ncbi.nlm.nih.gov/gene/?term=64581+AND+homo+sapiens	1.53	1.2E-08	9.6E-07	PVRIG_High
3659	IRF1	interferon regulatory factor 1	5q31.1	https://www.ncbi.nlm.nih.gov/gene/?term=3659+AND+homo+sapiens	1.59	1.3E-08	1.0E-06	PVRIG_High
3957	LGALS2	galectin 2	22q13.1	https://www.ncbi.nlm.nih.gov/gene/?term=3957+AND+homo+sapiens	1.51	1.5E-08	1.2E-06	PVRIG_High
3575	IL7R	interleukin 7 receptor	5p13.2	https://www.ncbi.nlm.nih.gov/gene/?term=3575+AND+homo+sapiens	1.78	2.0E-08	1.5E-06	PVRIG_High
27299	ADAMDEC1	ADAM like decysin 1	8p21.2	https://www.ncbi.nlm.nih.gov/gene/?term=27299+AND+homo+sapiens	2.00	2.5E-08	1.8E-06	PVRIG_High
4318	MMP9	matrix metallo-peptidase 9	20q13.12	https://www.ncbi.nlm.nih.gov/gene/?term=4318+AND+homo+sapiens	2.13	2.7E-08	1.9E-06	PVRIG_High
6363	CCL19	C-C motif chemokine ligand 19	9p13.3	https://www.ncbi.nlm.nih.gov/gene/?term=6363+AND+homo+sapiens	3.83	4.4E-08	3.0E-06	PVRIG_High
6373	CXCL11	C-X-C motif chemokine ligand 11	4q21.1	https://www.ncbi.nlm.nih.gov/gene/?term=6373+AND+homo+sapiens	2.99	5.2E-08	3.5E-06	PVRIG_High
1536	CYBB	cytochrome b-245 beta chain	Xp21.1-p11.4	https://www.ncbi.nlm.nih.gov/gene/?term=1536+AND+homo+sapiens	1.68	5.3E-08	3.6E-06	PVRIG_High
51316	PLAC8	placenta specific 8	4q21.22	https://www.ncbi.nlm.nih.gov/gene/?term=51316+AND+homo+sapiens	1.97	5.5E-08	3.7E-06	PVRIG_High
25816	TNFAIP8	TNF alpha induced protein 8	5q23.1	https://www.ncbi.nlm.nih.gov/gene/?term=25816+AND+homo+sapiens	1.67	6.4E-08	4.2E-06	PVRIG_High
1439	CSF2RB	colony stimulating factor 2 receptor beta common subunit	22q12.3	https://www.ncbi.nlm.nih.gov/gene/?term=1439+AND+homo+sapiens	1.93	8.2E-08	5.3E-06	PVRIG_High
3620	IDO1	indoleamine 2,3-dioxygenase 1	8p11.21	https://www.ncbi.nlm.nih.gov/gene/?term=3620+AND+homo+sapiens	1.99	8.4E-08	5.4E-06	PVRIG_High

5552	SRGN	serglycin	10q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=5552+AND+homo+sapiens	2.15	8.5E-08	5.4E-06	PVRIG_High
6039	RNASE6	ribonuclease A family member k6	14q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=6039+AND+homo+sapiens	1.53	1.0E-07	6.5E-06	PVRIG_High
474344	GIMAP6	GTPase, IMA family member 6	7q36.1	https://www.ncbi.nlm.nih.gov/gene/?term=474344+AND+homo+sapiens	1.52	1.1E-07	6.8E-06	PVRIG_High
6355	CCL8	C-C motif chemokine ligand 8	17q12	https://www.ncbi.nlm.nih.gov/gene/?term=6355+AND+homo+sapiens	1.81	1.3E-07	7.8E-06	PVRIG_High
3113	HLA-DPA1	major histocompatibility complex, class II, DP alpha 1	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3113+AND+homo+sapiens	1.86	1.4E-07	8.6E-06	PVRIG_High
3109	HLA-DMB	major histocompatibility complex, class II, DM beta	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3109+AND+homo+sapiens	1.54	1.5E-07	8.9E-06	PVRIG_High
10346	TRIM22	tripartite motif containing 22	11p15.4	https://www.ncbi.nlm.nih.gov/gene/?term=10346+AND+homo+sapiens	1.78	2.0E-07	1.2E-05	PVRIG_High
10563	CXCL13	C-X-C motif chemokine ligand 13	4q21.1	https://www.ncbi.nlm.nih.gov/gene/?term=10563+AND+homo+sapiens	1.59	2.2E-07	1.3E-05	PVRIG_High
5996	RGS1	regulator of G protein signaling 1	1q31.2	https://www.ncbi.nlm.nih.gov/gene/?term=5996+AND+homo+sapiens	1.73	2.2E-07	1.3E-05	PVRIG_High
10261	IGSF6	immunoglobulin superfamily member 6	16p12.2	https://www.ncbi.nlm.nih.gov/gene/?term=10261+AND+homo+sapiens	1.56	3.6E-07	2.0E-05	PVRIG_High
7852	CXCR4	C-X-C motif chemokine receptor 4	2q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=7852+AND+homo+sapiens	1.73	3.8E-07	2.1E-05	PVRIG_High
972	CD74	CD74 molecule	5q33.1	https://www.ncbi.nlm.nih.gov/gene/?term=972+AND+homo+sapiens	1.54	5.8E-07	3.1E-05	PVRIG_High

894	CCND2	cyclin D2	12p13.32	https://www.ncbi.nlm.nih.gov/gene/?term=894+AND+homo+sapiens	1.88	5.9E-07	3.1E-05	PVRIG_High
3600	IL15	interleukin 15	4q31.21	https://www.ncbi.nlm.nih.gov/gene/?term=3600+AND+homo+sapiens	1.51	6.7E-07	3.4E-05	PVRIG_High
9770	RASSF2	Ras association domain family member 2	20p13	https://www.ncbi.nlm.nih.gov/gene/?term=9770+AND+homo+sapiens	1.58	8.5E-07	4.3E-05	PVRIG_High
3627	CXCL10	C-X-C motif chemokine ligand 10	4q21.1	https://www.ncbi.nlm.nih.gov/gene/?term=3627+AND+homo+sapiens	2.38	8.8E-07	4.4E-05	PVRIG_High
6275	S100A4	S100 calcium binding protein A4	1q21.3	https://www.ncbi.nlm.nih.gov/gene/?term=6275+AND+homo+sapiens	2.03	1.4E-06	6.8E-05	PVRIG_High
64231	MS4A6A	membrane spanning 4-domains A6A	11q12.2	https://www.ncbi.nlm.nih.gov/gene/?term=64231+AND+homo+sapiens	1.60	1.5E-06	7.2E-05	PVRIG_High
10797	MTHFD2	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase	2p13.1	https://www.ncbi.nlm.nih.gov/gene/?term=10797+AND+homo+sapiens	2.10	1.5E-06	7.2E-05	PVRIG_High
5698	PSMB9	proteasome subunit beta 9	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=5698+AND+homo+sapiens	1.73	1.8E-06	8.5E-05	PVRIG_High
5699	PSMB10	proteasome subunit beta 10	16q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=5699+AND+homo+sapiens	1.64	2.0E-06	9.3E-05	PVRIG_High
2633	GBP1	guanylate binding protein 1	1p22.2	https://www.ncbi.nlm.nih.gov/gene/?term=2633+AND+homo+sapiens	1.87	2.7E-06	1.2E-04	PVRIG_High
9332	CD163	CD163 molecule	12p13.31	https://www.ncbi.nlm.nih.gov/gene/?term=9332+AND+homo+sapiens	1.62	3.0E-06	1.3E-04	PVRIG_High

3123	HLA-DRB1	major histocompatibility complex, class II, DR beta 1	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3123+AND+homo+sapiens	1.79	3.8E-06	1.6E-04	PVRIG_High
6362	CCL18	C-C motif chemokine ligand 18	17q12	https://www.ncbi.nlm.nih.gov/gene/?term=6362+AND+homo+sapiens	1.67	4.7E-06	2.0E-04	PVRIG_High
5272	SERPINE1	serpin family B member 9	6p25.2	https://www.ncbi.nlm.nih.gov/gene/?term=5272+AND+homo+sapiens	1.55	9.3E-06	3.6E-04	PVRIG_High
6347	CCL2	C-C motif chemokine ligand 2	17q12	https://www.ncbi.nlm.nih.gov/gene/?term=6347+AND+homo+sapiens	2.04	1.4E-05	5.1E-04	PVRIG_High
91316	GUSBP11	glucuronidase, beta pseudogene 11	22q11.23	https://www.ncbi.nlm.nih.gov/gene/?term=91316+AND+homo+sapiens	1.94	1.6E-05	5.5E-04	PVRIG_High
5920	RARRES3	retinoic acid receptor responder 3	11q12.3	https://www.ncbi.nlm.nih.gov/gene/?term=5920+AND+homo+sapiens	1.54	1.9E-05	6.5E-04	PVRIG_High
3965	LGALS9	galectin 9	17q11.2	https://www.ncbi.nlm.nih.gov/gene/?term=3965+AND+homo+sapiens	1.50	2.4E-05	7.9E-04	PVRIG_High
4332	MNDA	myeloid cell nuclear differentiation antigen	1q23.1	https://www.ncbi.nlm.nih.gov/gene/?term=4332+AND+homo+sapiens	1.53	3.0E-05	9.6E-04	PVRIG_High
8877	SPHK1	sphingosine kinase 1	17q25.1	https://www.ncbi.nlm.nih.gov/gene/?term=8877+AND+homo+sapiens	1.77	3.6E-05	1.1E-03	PVRIG_High
2207	FCER1G	Fc fragment of IgE receptor Ig	1q23.3	https://www.ncbi.nlm.nih.gov/gene/?term=2207+AND+homo+sapiens	1.51	4.4E-05	1.3E-03	PVRIG_High
8519	IFITM1	induced transmembrane protein 1	11p15.5	https://www.ncbi.nlm.nih.gov/gene/?term=8519+AND+homo+sapiens	1.51	4.9E-05	1.4E-03	PVRIG_High
51338	MS4A4A	membrane spanning 4-domains A4A	11q12.2	https://www.ncbi.nlm.nih.gov/gene/?term=51338+AND+homo+sapiens	1.54	5.3E-05	1.6E-03	PVRIG_High

3117	HLA-DQA1	major histocompatibility complex, class II, DQ alpha 1	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3117+AND+homo+sapiens	2.81	5.8E-05	1.7E-03	PVRIG_High
10123	ARL4C	ADP ribosylation factor like GTPase 4C	2q37.1	https://www.ncbi.nlm.nih.gov/gene/?term=10123+AND+homo+sapiens	1.54	5.9E-05	1.7E-03	PVRIG_High
5360	PLTP	phospholipid transfer protein	20q13.12	https://www.ncbi.nlm.nih.gov/gene/?term=5360+AND+homo+sapiens	1.69	7.4E-05	2.1E-03	PVRIG_High
922	CD5L	CD5 molecule like	1q23.1	https://www.ncbi.nlm.nih.gov/gene/?term=922+AND+homo+sapiens	1.62	7.5E-05	2.1E-03	PVRIG_High
8826	IQGAP1	IQ motif containing GTPase activating protein 1	15q26.1	https://www.ncbi.nlm.nih.gov/gene/?term=8826+AND+homo+sapiens	1.52	7.8E-05	2.1E-03	PVRIG_High
11031	RAB31	RAB31, member RAS oncogene family	18p11.22	https://www.ncbi.nlm.nih.gov/gene/?term=11031+AND+homo+sapiens	1.55	9.2E-05	2.4E-03	PVRIG_High
597	BCL2A1	BCL2 related protein A1	15q25.1	https://www.ncbi.nlm.nih.gov/gene/?term=597+AND+homo+sapiens	1.55	1.7E-04	3.9E-03	PVRIG_High
8531	YBX3	Y-box binding protein 3	12p13.2	https://www.ncbi.nlm.nih.gov/gene/?term=8531+AND+homo+sapiens	1.79	1.7E-04	3.9E-03	PVRIG_High
10964	IFI44L	interferon induced protein 44 like	1p31.1	https://www.ncbi.nlm.nih.gov/gene/?term=10964+AND+homo+sapiens	2.04	1.8E-04	4.0E-03	PVRIG_High
6366	CCL21	C-C motif chemokine ligand 21	9p13.3	https://www.ncbi.nlm.nih.gov/gene/?term=6366+AND+homo+sapiens	1.54	2.4E-04	5.0E-03	PVRIG_High
5734	PTGER4	prostaglandin E receptor 4	5p13.1	https://www.ncbi.nlm.nih.gov/gene/?term=5734+AND+homo+sapiens	1.53	2.6E-04	5.2E-03	PVRIG_High
3371	TNC	tenascin C	9q33.1	https://www.ncbi.nlm.nih.gov/gene/?term=3371+AND+homo+sapiens	2.06	2.7E-04	5.4E-03	PVRIG_High
4599	MX1	MX dynamin like GTPase 1	21q22.3	https://www.ncbi.nlm.nih.gov/gene/?term=4599+AND+homo+sapiens	1.50	2.8E-04	5.5E-03	PVRIG_High
10457	GPNMB	glycoprotein nmb	7p15.3	https://www.ncbi.nlm.nih.gov/gene/?term=10457+AND+homo+sapiens	1.67	3.8E-04	6.8E-03	PVRIG_High

3122	HLA-DRA	major histocompatibility complex, class II, DR alpha	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3122+AND+homo+sapiens	1.79	3.9E-04	6.9E-03	PVRIG_High
29940	DSE	dermatan sulfate epimerase	6q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=29940+AND+homo+sapiens	1.55	4.7E-04	7.9E-03	PVRIG_High
1520	CTSS	cathepsin S	1q21.3	https://www.ncbi.nlm.nih.gov/gene/?term=1520+AND+homo+sapiens	1.57	5.9E-04	9.3E-03	PVRIG_High
4321	MMP12	matrix metallo-peptidase 12	11q22.2	https://www.ncbi.nlm.nih.gov/gene/?term=4321+AND+homo+sapiens	1.70	6.9E-04	1.0E-02	PVRIG_High
822	CAPG	capping actin protein, gelsolin like	2p11.2	https://www.ncbi.nlm.nih.gov/gene/?term=822+AND+homo+sapiens	1.64	7.2E-04	1.1E-02	PVRIG_High
26509	MYOF	myoferlin	10q23.33	https://www.ncbi.nlm.nih.gov/gene/?term=26509+AND+homo+sapiens	2.10	9.2E-04	1.3E-02	PVRIG_High
56925	LXN	latexin	3q25.32	https://www.ncbi.nlm.nih.gov/gene/?term=56925+AND+homo+sapiens	1.57	1.4E-03	1.7E-02	PVRIG_High
240	ALOX5	arachidonate 5-lipoxygenase	10q11.21	https://www.ncbi.nlm.nih.gov/gene/?term=240+AND+homo+sapiens	1.58	1.5E-03	1.7E-02	PVRIG_High
3428	IFI16	interferon gamma inducible protein 16	1q23.1	https://www.ncbi.nlm.nih.gov/gene/?term=3428+AND+homo+sapiens	1.57	1.7E-03	1.9E-02	PVRIG_High
8821	INPP4B	inositol polyphosphate-4-phosphatase type II B	4q31.21	https://www.ncbi.nlm.nih.gov/gene/?term=8821+AND+homo+sapiens	1.99	2.1E-03	2.2E-02	PVRIG_High
4053	LTBP2	latent transforming growth factor beta binding protein 2	14q24.3	https://www.ncbi.nlm.nih.gov/gene/?term=4053+AND+homo+sapiens	1.51	2.6E-03	2.5E-02	PVRIG_High
57823	SLAMF7	SLAM family member 7	1q23.3	https://www.ncbi.nlm.nih.gov/gene/?term=57823+AND+homo+sapiens	1.54	2.6E-03	2.5E-02	PVRIG_High
3223	HOXC6	homeobox C6	12q13.13	https://www.ncbi.nlm.nih.gov/gene/?term=3223+AND+homo+sapiens	1.70	3.1E-03	2.8E-02	PVRIG_High

9547	CXCL14	C-X-C motif chemokine ligand 14	5q31.1	https://www.ncbi.nlm.nih.gov/gene/?term=9547+AND+homo+sapiens	1.64	3.6E-03	3.1E-02	PVRIG_High
2950	GSTP1	glutathione S-transferase pi 1	11q13.2	https://www.ncbi.nlm.nih.gov/gene/?term=2950+AND+homo+sapiens	1.67	3.6E-03	3.1E-02	PVRIG_High
2171	FABP5	fatty acid binding protein 5	8q21.13	https://www.ncbi.nlm.nih.gov/gene/?term=2171+AND+homo+sapiens	1.59	4.2E-03	3.4E-02	PVRIG_High
10512	SEMA3C	semaphorin 3C	7q21.11	https://www.ncbi.nlm.nih.gov/gene/?term=10512+AND+homo+sapiens	1.86	4.4E-03	3.5E-02	PVRIG_High
6387	CXCL12	C-X-C motif chemokine ligand 12	10q11.21	https://www.ncbi.nlm.nih.gov/gene/?term=6387+AND+homo+sapiens	1.59	4.8E-03	3.7E-02	PVRIG_High
165	AEBP1	AE binding protein 1	7p13	https://www.ncbi.nlm.nih.gov/gene/?term=165+AND+homo+sapiens	1.71	5.2E-03	3.9E-02	PVRIG_High
10631	POSTN	periostin	13q13.3	https://www.ncbi.nlm.nih.gov/gene/?term=10631+AND+homo+sapiens	1.79	5.9E-03	4.3E-02	PVRIG_High
8740	TNFSF14	TNF superfamily member 14	19p13.3	https://www.ncbi.nlm.nih.gov/gene/?term=8740+AND+homo+sapiens	1.59	6.3E-03	4.5E-02	PVRIG_High
9023	CH25H	cholesterol 25-hydroxylase	10q23.31	https://www.ncbi.nlm.nih.gov/gene/?term=9023+AND+homo+sapiens	1.65	6.5E-03	4.5E-02	PVRIG_High
2669	GEM	GTP binding protein overexpressed in skeletal muscle	8q22.1	https://www.ncbi.nlm.nih.gov/gene/?term=2669+AND+homo+sapiens	2.25	6.8E-03	4.6E-02	PVRIG_High
3119	HLA-DQB1	major histocompatibility complex, class II, DQ beta 1	6p21.32	https://www.ncbi.nlm.nih.gov/gene/?term=3119+AND+homo+sapiens	1.67	7.6E-03	5.0E-02	PVRIG_High
1466	CSRP2	cysteine and glycine rich protein 2	12q21.2	https://www.ncbi.nlm.nih.gov/gene/?term=1466+AND+homo+sapiens	-1.58	2.3E-05	7.8E-04	PVRIG_Low
3303	HSPA1A	heat shock protein family A	6p21.33	https://www.ncbi.nlm.nih.gov/gene/?term=3303+AND+homo+sapiens	-1.55	1.5E-04	3.5E-03	PVRIG_Low

		(Hsp70) member 1A						
3290	HSD11B1	hydroxysteroid 11-beta dehydrogenase 1	1q32.2	https://www.ncbi.nlm.nih.gov/gene/?term=3290+AND+homo+sapiens	-1.73	5.2E-04	8.5E-03	PVRIG_Low
1803	DPP4	dipeptidyl peptidase 4	2q24.2	https://www.ncbi.nlm.nih.gov/gene/?term=1803+AND+homo+sapiens	-1.56	5.3E-04	8.7E-03	PVRIG_Low
10681	GNB5	G protein subunit beta 5	15q21.2	https://www.ncbi.nlm.nih.gov/gene/?term=10681+AND+homo+sapiens	-1.69	1.1E-03	1.4E-02	PVRIG_Low
23460	ABCA6	ATP binding cassette subfamily A member 6	17q24.2-q24.3	https://www.ncbi.nlm.nih.gov/gene/?term=23460+AND+homo+sapiens	-1.50	1.8E-03	2.0E-02	PVRIG_Low
10050	SLC17A4	solute carrier family 17 member 4	6p22.2	https://www.ncbi.nlm.nih.gov/gene/?term=10050+AND+homo+sapiens	-1.50	2.0E-03	2.1E-02	PVRIG_Low
23600	AMACR	alpha-methylacyl-CoA racemase	5p13.2	https://www.ncbi.nlm.nih.gov/gene/?term=23600+AND+homo+sapiens	-1.59	2.1E-03	2.2E-02	PVRIG_Low
10882	C1QL1	complement C1q like 1	17q21.31	https://www.ncbi.nlm.nih.gov/gene/?term=10882+AND+homo+sapiens	-1.81	2.6E-03	2.5E-02	PVRIG_Low
5313	PKLR	pyruvate kinase L/R	1q22	https://www.ncbi.nlm.nih.gov/gene/?term=5313+AND+homo+sapiens	-1.52	3.5E-03	3.0E-02	PVRIG_Low
53841	CDHR5	cadherin related family member 5	11p15.5	https://www.ncbi.nlm.nih.gov/gene/?term=53841+AND+homo+sapiens	-1.51	3.8E-03	3.2E-02	PVRIG_Low
4311	MME	membrane metalloendopeptidase	3q25.2	https://www.ncbi.nlm.nih.gov/gene/?term=4311+AND+homo+sapiens	-2.37	5.8E-03	4.2E-02	PVRIG_Low
5756	TWF1	twinfilin actin binding protein 1	12q12	https://www.ncbi.nlm.nih.gov/gene/?term=5756+AND+homo+sapiens	-1.51	6.1E-03	4.4E-02	PVRIG_Low
1491	CTH	cystathionine gamma-lyase	1p31.1	https://www.ncbi.nlm.nih.gov/gene/?term=1491+AND+homo+sapiens	-1.56	6.4E-03	4.5E-02	PVRIG_Low
64388	GREM2	gremlin 2, DAN family BMP antagonist	1q43	https://www.ncbi.nlm.nih.gov/gene/?term=64388+AND+homo+sapiens	-3.01	6.4E-03	4.5E-02	PVRIG_Low

Table S4. Ontology analysis of the 181 genes differentially expressed between *PVRIG* High and Low groups in the learning set (GSE14520, n=242)

GO ID	Description	p-value	Adjusted p-value	Fold enrichment	GeneRatio	BgRatio
GO:0050900	leukocyte migration	1.99E-23	4.83E-20	8.85	35/153	478/18493
GO:0030595	leukocyte chemotaxis	6.31E-23	7.65E-20	14.48	26/153	217/18493
GO:0060326	cell chemotaxis	1.17E-20	9.46E-18	11.06	27/153	295/18493
GO:0042110	T cell activation	5.82E-20	3.52E-17	8.31	31/153	451/18493
GO:0007159	leukocyte cell-cell adhesion	1.73E-19	8.36E-17	9.98	27/153	327/18493
GO:0048247	lymphocyte chemotaxis	2.51E-18	1.01E-15	28.78	15/153	63/18493
GO:0072676	lymphocyte migration	1.42E-17	4.90E-15	19.57	17/153	105/18493
GO:0050863	regulation of T cell activation	6.39E-17	1.93E-14	9.51	24/153	305/18493
GO:0009615	response to virus	1.33E-16	3.57E-14	9.21	24/153	315/18493
GO:0070661	leukocyte proliferation	1.47E-16	3.57E-14	9.82	23/153	283/18493
GO:0030593	neutrophil chemotaxis	1.90E-16	4.18E-14	19.15	16/153	101/18493
GO:0034341	response to interferon-gamma	2.38E-16	4.81E-14	12.21	20/153	198/18493
GO:0097529	myeloid leukocyte migration	2.63E-16	4.90E-14	12.15	20/153	199/18493
GO:1903037	regulation of leukocyte cell-cell adhesion	3.16E-16	5.46E-14	9.49	23/153	293/18493
GO:0071346	cellular response to interferon-gamma	4.96E-16	8.01E-14	12.90	19/153	178/18493
GO:0002688	regulation of leukocyte chemotaxis	6.69E-16	1.01E-13	17.74	16/153	109/18493

GO:0097530	granulocyte migration	9.95E-16	1.41E-13	15.33	17/153	134/18493
GO:1990266	neutrophil migration	1.05E-15	1.41E-13	17.27	16/153	112/18493
GO:0070663	regulation of leukocyte proliferation	1.30E-15	1.66E-13	11.19	20/153	216/18493
GO:0051249	regulation of lymphocyte activation	1.86E-15	2.25E-13	6.91	27/153	472/18493
GO:0071621	granulocyte chemotaxis	3.22E-15	3.72E-13	16.12	16/153	120/18493
GO:0046651	lymphocyte proliferation	5.21E-15	5.52E-13	9.61	21/153	264/18493
GO:0050870	positive regulation of T cell activation	5.24E-15	5.52E-13	11.37	19/153	202/18493
GO:0032943	mononuclear cell proliferation	6.06E-15	6.11E-13	9.54	21/153	266/18493
GO:0002690	positive regulation of leukocyte chemotaxis	7.43E-15	7.19E-13	20.14	14/153	84/18493
GO:0002685	regulation of leukocyte migration	9.70E-15	9.04E-13	12.09	18/153	180/18493
GO:0050920	regulation of chemotaxis	1.07E-14	9.63E-13	10.94	19/153	210/18493
GO:0070098	chemokine-mediated signaling pathway	1.24E-14	1.07E-12	19.45	14/153	87/18493
GO:0022407	regulation of cell-cell adhesion	1.43E-14	1.20E-12	7.48	24/153	388/18493
GO:1903039	positive regulation of leukocyte cell-cell adhesion	1.52E-14	1.23E-12	10.73	19/153	214/18493
GO:0022409	positive regulation of cell-cell adhesion	2.35E-14	1.84E-12	9.63	20/153	251/18493
GO:1990868	response to chemokine	4.43E-14	3.25E-12	17.81	14/153	95/18493
GO:1990869	cellular response to chemokine	4.43E-14	3.25E-12	17.81	14/153	95/18493
GO:0002687	positive regulation of leukocyte migration	7.38E-14	5.26E-12	14.98	15/153	121/18493
GO:0050670	regulation of lymphocyte proliferation	9.46E-14	6.54E-12	10.61	18/153	205/18493
GO:0032944	regulation of mononuclear cell proliferation	1.03E-13	6.90E-12	10.56	18/153	206/18493
GO:0050867	positive regulation of cell activation	1.05E-13	6.90E-12	7.24	23/153	384/18493
GO:0042098	T cell proliferation	1.20E-13	7.62E-12	11.54	17/153	178/18493
GO:0045785	positive regulation of cell adhesion	2.12E-13	1.32E-11	7.00	23/153	397/18493
GO:1901623	regulation of lymphocyte chemotaxis	3.97E-13	2.40E-11	41.84	9/153	26/18493
GO:0002696	positive regulation of leukocyte activation	4.90E-13	2.89E-11	7.15	22/153	372/18493
GO:0032103	positive regulation of response to external stimulus	5.59E-13	3.22E-11	8.14	20/153	297/18493
GO:2000401	regulation of lymphocyte migration	1.72E-12	9.69E-11	22.53	11/153	59/18493
GO:0042129	regulation of T cell proliferation	2.42E-12	1.33E-10	11.85	15/153	153/18493
GO:0050921	positive regulation of chemotaxis	3.70E-12	1.99E-10	13.02	14/153	130/18493
GO:0002548	monocyte chemotaxis	4.41E-12	2.32E-10	20.77	11/153	64/18493

GO:0001819	positive regulation of cytokine production	6.00E-12	3.09E-10	6.30	22/153	422/18493
GO:0051607	defense response to virus	6.76E-12	3.41E-10	9.01	17/153	228/18493
GO:2000403	positive regulation of lymphocyte migration	1.11E-11	5.51E-10	30.22	9/153	36/18493
GO:0050852	T cell receptor signaling pathway	2.63E-11	1.27E-09	11.28	14/153	150/18493
GO:0051251	positive regulation of lymphocyte activation	3.98E-11	1.89E-09	6.90	19/153	333/18493
GO:0072678	T cell migration	4.96E-11	2.31E-09	20.49	10/153	59/18493
GO:0002697	regulation of immune effector process	9.38E-11	4.28E-09	5.78	21/153	439/18493
GO:0030217	T cell differentiation	1.06E-10	4.78E-09	8.26	16/153	234/18493
GO:0071674	mononuclear cell migration	1.09E-10	4.81E-09	15.64	11/153	85/18493
GO:0071356	cellular response to tumor necrosis factor	1.13E-10	4.91E-09	8.23	16/153	235/18493
GO:0035747	natural killer cell chemotaxis	1.30E-10	5.51E-09	65.93	6/153	11/18493
GO:2000106	regulation of leukocyte apoptotic process	1.41E-10	5.90E-09	15.28	11/153	87/18493
GO:0019882	antigen processing and presentation	2.09E-10	8.58E-09	9.67	14/153	175/18493
GO:2000107	negative regulation of leukocyte apoptotic process	3.24E-10	1.31E-08	21.33	9/153	51/18493
GO:0034612	response to tumor necrosis factor	4.26E-10	1.69E-08	7.52	16/153	257/18493
GO:0042102	positive regulation of T cell proliferation	4.67E-10	1.83E-08	13.71	11/153	97/18493
GO:0050851	antigen receptor-mediated signaling pathway	4.77E-10	1.83E-08	7.47	16/153	259/18493
GO:0002683	negative regulation of immune system process	5.90E-10	2.23E-08	5.53	20/153	437/18493
GO:0042119	neutrophil activation	9.32E-10	3.47E-08	5.10	21/153	498/18493
GO:0050671	positive regulation of lymphocyte proliferation	9.91E-10	3.64E-08	10.99	12/153	132/18493
GO:0032946	positive regulation of mononuclear cell proliferation	1.08E-09	3.91E-08	10.91	12/153	133/18493
GO:0071887	leukocyte apoptotic process	1.36E-09	4.83E-08	12.43	11/153	107/18493
GO:0002429	immune response-activating cell surface receptor signaling pathway	1.57E-09	5.51E-08	5.55	19/153	414/18493
GO:0010818	T cell chemotaxis	1.79E-09	6.14E-08	31.34	7/153	27/18493
GO:0070665	positive regulation of leukocyte proliferation	1.80E-09	6.14E-08	10.43	12/153	139/18493
GO:0043312	neutrophil degranulation	3.55E-09	1.19E-07	4.98	20/153	485/18493
GO:0060333	interferon-gamma-mediated signaling pathway	3.63E-09	1.20E-07	13.43	10/153	90/18493
GO:0002283	neutrophil activation involved in immune response	3.94E-09	1.28E-07	4.95	20/153	488/18493
GO:2000406	positive regulation of T cell migration	4.01E-09	1.28E-07	28.20	7/153	30/18493

GO:0002449	lymphocyte mediated immunity	4.02E-09	1.28E-07	5.97	17/153	344/18493
GO:0002768	immune response-regulating cell surface receptor signaling pathway	5.13E-09	1.61E-07	5.16	19/153	445/18493
GO:1902105	regulation of leukocyte differentiation	5.65E-09	1.75E-07	6.84	15/153	265/18493
GO:0002446	neutrophil mediated immunity	5.75E-09	1.76E-07	4.84	20/153	499/18493
GO:0002478	antigen processing and presentation of exogenous peptide antigen	7.78E-09	2.35E-07	10.55	11/153	126/18493
GO:0019886	antigen processing and presentation of exogenous peptide antigen via MHC class II	8.40E-09	2.51E-07	12.33	10/153	98/18493
GO:0140131	positive regulation of lymphocyte chemotaxis	1.02E-08	3.02E-07	36.26	6/153	20/18493
GO:0002495	antigen processing and presentation of peptide antigen via MHC class II	1.13E-08	3.29E-07	11.97	10/153	101/18493
GO:0002504	antigen processing and presentation of peptide or polysaccharide antigen via MHC class II	1.24E-08	3.58E-07	11.85	10/153	102/18493
GO:0045123	cellular extravasation	1.38E-08	3.92E-07	17.91	8/153	54/18493
GO:0019884	antigen processing and presentation of exogenous antigen	1.49E-08	4.19E-07	9.92	11/153	134/18493
GO:0001909	leukocyte mediated cytotoxicity	1.65E-08	4.58E-07	11.51	10/153	105/18493
GO:0048002	antigen processing and presentation of peptide antigen	2.18E-08	6.00E-07	9.57	11/153	139/18493
GO:0070371	ERK1 and ERK2 cascade	2.45E-08	6.66E-07	5.67	16/153	341/18493
GO:0002407	dendritic cell chemotaxis	2.61E-08	7.03E-07	31.53	6/153	23/18493
GO:1902107	positive regulation of leukocyte differentiation	2.73E-08	7.25E-07	9.36	11/153	142/18493
GO:0030098	lymphocyte differentiation	2.77E-08	7.28E-07	5.62	16/153	344/18493
GO:2000404	regulation of T cell migration	3.43E-08	8.90E-07	21.15	7/153	40/18493
GO:0030101	natural killer cell activation	3.46E-08	8.90E-07	12.80	9/153	85/18493
GO:1903708	positive regulation of hemopoiesis	4.03E-08	1.03E-06	7.93	12/153	183/18493
GO:0036336	dendritic cell migration	5.84E-08	1.47E-06	27.89	6/153	26/18493
GO:1903706	regulation of hemopoiesis	7.04E-08	1.76E-06	4.92	17/153	418/18493
GO:0007162	negative regulation of cell adhesion	7.36E-08	1.82E-06	6.13	14/153	276/18493
GO:0070372	regulation of ERK1 and ERK2 cascade	8.18E-08	2.00E-06	5.60	15/153	324/18493
GO:0032680	regulation of tumor necrosis factor production	1.02E-07	2.48E-06	9.52	10/153	127/18493
GO:0032640	tumor necrosis factor production	1.18E-07	2.84E-06	9.37	10/153	129/18493

GO:0070374	positive regulation of ERK1 and ERK2 cascade	1.31E-07	3.10E-06	6.41	13/153	245/18493
GO:1903555	regulation of tumor necrosis factor superfamily cytokine production	1.37E-07	3.22E-06	9.23	10/153	131/18493
GO:0010819	regulation of T cell chemotaxis	1.47E-07	3.43E-06	37.77	5/153	16/18493
GO:0032760	positive regulation of tumor necrosis factor production	1.56E-07	3.59E-06	13.25	8/153	73/18493
GO:0002699	positive regulation of immune effector process	1.73E-07	3.95E-06	6.94	12/153	209/18493
GO:0071706	tumor necrosis factor superfamily cytokine production	1.82E-07	4.12E-06	8.95	10/153	135/18493
GO:0006874	cellular calcium ion homeostasis	1.89E-07	4.24E-06	4.59	17/153	448/18493
GO:0045580	regulation of T cell differentiation	2.09E-07	4.64E-06	8.82	10/153	137/18493
GO:1903557	positive regulation of tumor necrosis factor superfamily cytokine production	2.14E-07	4.71E-06	12.72	8/153	76/18493
GO:0055074	calcium ion homeostasis	2.83E-07	6.17E-06	4.46	17/153	461/18493
GO:0090026	positive regulation of monocyte chemotaxis	2.85E-07	6.17E-06	33.57	5/153	18/18493
GO:0006816	calcium ion transport	3.36E-07	7.21E-06	4.68	16/153	413/18493
GO:0042267	natural killer cell mediated cytotoxicity	4.88E-07	1.04E-05	14.59	7/153	58/18493
GO:0072503	cellular divalent inorganic cation homeostasis	5.43E-07	1.14E-05	4.25	17/153	483/18493
GO:0033622	integrin activation	6.64E-07	1.39E-05	28.78	5/153	21/18493
GO:0002573	myeloid leukocyte differentiation	7.58E-07	1.57E-05	6.75	11/153	197/18493
GO:0002228	natural killer cell mediated immunity	7.77E-07	1.59E-05	13.65	7/153	62/18493
GO:0001906	cell killing	7.85E-07	1.60E-05	7.65	10/153	158/18493
GO:0071677	positive regulation of mononuclear cell migration	8.53E-07	1.72E-05	27.47	5/153	22/18493
GO:0032729	positive regulation of interferon-gamma production	8.68E-07	1.74E-05	13.43	7/153	63/18493
GO:0097048	dendritic cell apoptotic process	9.10E-07	1.79E-05	48.35	4/153	10/18493
GO:2000668	regulation of dendritic cell apoptotic process	9.10E-07	1.79E-05	48.35	4/153	10/18493
GO:0045621	positive regulation of lymphocyte differentiation	1.11E-06	2.18E-05	10.29	8/153	94/18493
GO:0045619	regulation of lymphocyte differentiation	1.23E-06	2.39E-05	7.28	10/153	166/18493
GO:0070838	divalent metal ion transport	1.36E-06	2.59E-05	4.21	16/153	459/18493
GO:0090025	regulation of monocyte chemotaxis	1.36E-06	2.59E-05	25.18	5/153	24/18493
GO:0050663	cytokine secretion	1.42E-06	2.69E-05	6.33	11/153	210/18493
GO:0072511	divalent inorganic cation transport	1.48E-06	2.77E-05	4.19	16/153	462/18493

GO:0072677	eosinophil migration	1.69E-06	3.14E-05	24.17	5/153	25/18493
GO:0007204	positive regulation of cytosolic calcium ion concentration	1.82E-06	3.36E-05	5.09	13/153	309/18493
GO:0002448	mast cell mediated immunity	2.07E-06	3.80E-05	15.77	6/153	46/18493
GO:0045088	regulation of innate immune response	2.13E-06	3.88E-05	4.64	14/153	365/18493
GO:0043900	regulation of multi-organism process	2.58E-06	4.66E-05	4.56	14/153	371/18493
GO:0031349	positive regulation of defense response	2.69E-06	4.82E-05	4.25	15/153	427/18493
GO:0032496	response to lipopolysaccharide	3.06E-06	5.45E-05	4.85	13/153	324/18493
GO:0050707	regulation of cytokine secretion	3.13E-06	5.53E-05	6.57	10/153	184/18493
GO:0002237	response to molecule of bacterial origin	4.70E-06	8.25E-05	4.66	13/153	337/18493
GO:0070555	response to interleukin-1	4.92E-06	8.57E-05	7.16	9/153	152/18493
GO:0051209	release of sequestered calcium ion into cytosol	5.46E-06	9.36E-05	8.34	8/153	116/18493
GO:0051928	positive regulation of calcium ion transport	5.46E-06	9.36E-05	8.34	8/153	116/18493
GO:0002703	regulation of leukocyte mediated immunity	5.49E-06	9.36E-05	6.17	10/153	196/18493
GO:0045582	positive regulation of T cell differentiation	5.67E-06	9.57E-05	10.19	7/153	83/18493
GO:0001911	negative regulation of leukocyte mediated cytotoxicity	5.73E-06	9.57E-05	32.23	4/153	15/18493
GO:0010820	positive regulation of T cell chemotaxis	5.73E-06	9.57E-05	32.23	4/153	15/18493
GO:0032735	positive regulation of interleukin-12 production	6.10E-06	1.01E-04	18.89	5/153	32/18493
GO:0051283	negative regulation of sequestering of calcium ion	6.20E-06	1.02E-04	8.19	8/153	118/18493
GO:0002819	regulation of adaptive immune response	6.40E-06	1.05E-04	6.93	9/153	157/18493
GO:0006959	humoral immune response	6.86E-06	1.12E-04	4.50	13/153	349/18493
GO:0051282	regulation of sequestering of calcium ion	7.02E-06	1.12E-04	8.06	8/153	120/18493
GO:0043547	positive regulation of GTPase activity	7.06E-06	1.12E-04	4.18	14/153	405/18493
GO:0048872	homeostasis of number of cells	7.06E-06	1.12E-04	5.36	11/153	248/18493
GO:0051480	regulation of cytosolic calcium ion concentration	7.08E-06	1.12E-04	4.49	13/153	350/18493
GO:0045730	respiratory burst	7.15E-06	1.12E-04	18.31	5/153	33/18493
GO:0045576	mast cell activation	7.45E-06	1.16E-04	12.72	6/153	57/18493
GO:0031341	regulation of cell killing	8.38E-06	1.29E-04	9.61	7/153	88/18493
GO:0050715	positive regulation of cytokine secretion	8.42E-06	1.29E-04	7.86	8/153	123/18493
GO:0051208	sequestering of calcium ion	8.42E-06	1.29E-04	7.86	8/153	123/18493
GO:0048525	negative regulation of viral process	1.05E-05	1.59E-04	9.30	7/153	91/18493

GO:0006968	cellular defense response	1.11E-05	1.67E-04	11.89	6/153	61/18493
GO:0050691	regulation of defense response to virus by host	1.11E-05	1.67E-04	16.79	5/153	36/18493
GO:0043087	regulation of GTPase activity	1.13E-05	1.68E-04	3.77	15/153	481/18493
GO:0050922	negative regulation of chemotaxis	1.22E-05	1.81E-04	11.70	6/153	62/18493
GO:0031342	negative regulation of cell killing	1.26E-05	1.86E-04	26.86	4/153	18/18493
GO:0071347	cellular response to interleukin-1	1.27E-05	1.86E-04	7.44	8/153	130/18493
GO:0032649	regulation of interferon-gamma production	1.39E-05	2.03E-04	8.91	7/153	95/18493
GO:0097553	calcium ion transmembrane import into cytosol	1.41E-05	2.05E-04	7.33	8/153	132/18493
GO:0032651	regulation of interleukin-1 beta production	1.47E-05	2.12E-04	11.33	6/153	64/18493
GO:0050792	regulation of viral process	1.68E-05	2.41E-04	6.15	9/153	177/18493
GO:0071496	cellular response to external stimulus	1.87E-05	2.67E-04	4.42	12/153	328/18493
GO:0007520	myoblast fusion	1.89E-05	2.68E-04	15.11	5/153	40/18493
GO:1901739	regulation of myoblast fusion	1.97E-05	2.77E-04	24.17	4/153	20/18493
GO:0071622	regulation of granulocyte chemotaxis	2.41E-05	3.34E-04	14.39	5/153	42/18493
GO:0071675	regulation of mononuclear cell migration	2.41E-05	3.34E-04	14.39	5/153	42/18493
GO:0048245	eosinophil chemotaxis	2.42E-05	3.34E-04	23.02	4/153	21/18493
GO:0032609	interferon-gamma production	2.84E-05	3.91E-04	7.98	7/153	106/18493
GO:0001779	natural killer cell differentiation	2.93E-05	4.00E-04	21.98	4/153	22/18493
GO:0002706	regulation of lymphocyte mediated immunity	2.94E-05	4.00E-04	6.62	8/153	146/18493
GO:0043303	mast cell degranulation	3.04E-05	4.11E-04	13.74	5/153	44/18493
GO:0051924	regulation of calcium ion transport	3.08E-05	4.14E-04	5.06	10/153	239/18493
GO:0032611	interleukin-1 beta production	3.13E-05	4.19E-04	9.93	6/153	73/18493
GO:0030099	myeloid cell differentiation	3.30E-05	4.39E-04	3.88	13/153	405/18493
GO:0002279	mast cell activation involved in immune response	3.40E-05	4.45E-04	13.43	5/153	45/18493
GO:0002686	negative regulation of leukocyte migration	3.40E-05	4.45E-04	13.43	5/153	45/18493
GO:0060402	calcium ion transport into cytosol	3.40E-05	4.45E-04	6.49	8/153	149/18493
GO:0090023	positive regulation of neutrophil chemotaxis	3.53E-05	4.60E-04	21.02	4/153	23/18493
GO:0070664	negative regulation of leukocyte proliferation	3.66E-05	4.74E-04	9.67	6/153	75/18493
GO:0001910	regulation of leukocyte mediated cytotoxicity	3.94E-05	5.07E-04	9.54	6/153	76/18493

GO:0002460	adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3.96E-05	5.07E-04	4.10	12/153	354/18493
GO:0032652	regulation of interleukin-1 production	4.25E-05	5.41E-04	9.42	6/153	77/18493
GO:0043903	regulation of symbiosis, encompassing mutualism through parasitism	4.95E-05	6.25E-04	5.36	9/153	203/18493
GO:0050901	leukocyte tethering or rolling	4.98E-05	6.25E-04	19.34	4/153	25/18493
GO:0071624	positive regulation of granulocyte chemotaxis	4.98E-05	6.25E-04	19.34	4/153	25/18493
GO:0045089	positive regulation of innate immune response	5.40E-05	6.72E-04	4.30	11/153	309/18493
GO:0050727	regulation of inflammatory response	5.41E-05	6.72E-04	3.70	13/153	425/18493
GO:0008154	actin polymerization or depolymerization	5.54E-05	6.85E-04	5.28	9/153	206/18493
GO:0032655	regulation of interleukin-12 production	5.70E-05	7.00E-04	12.09	5/153	50/18493
GO:0060142	regulation of syncytium formation by plasma membrane fusion	5.84E-05	7.11E-04	18.60	4/153	26/18493
GO:1902624	positive regulation of neutrophil migration	5.84E-05	7.11E-04	18.60	4/153	26/18493
GO:0060401	cytosolic calcium ion transport	5.89E-05	7.14E-04	6.01	8/153	161/18493
GO:0002468	dendritic cell antigen processing and presentation	6.39E-05	7.66E-04	36.26	3/153	10/18493
GO:1902713	regulation of interferon-gamma secretion	6.39E-05	7.66E-04	36.26	3/153	10/18493
GO:0002695	negative regulation of leukocyte activation	6.71E-05	8.01E-04	5.90	8/153	164/18493
GO:0032615	interleukin-12 production	6.90E-05	8.19E-04	11.62	5/153	52/18493
GO:1903038	negative regulation of leukocyte cell-cell adhesion	7.00E-05	8.26E-04	6.94	7/153	122/18493
GO:0000768	syncytium formation by plasma membrane fusion	7.56E-05	8.81E-04	11.40	5/153	53/18493
GO:0045071	negative regulation of viral genome replication	7.56E-05	8.81E-04	11.40	5/153	53/18493
GO:0140253	cell-cell fusion	7.56E-05	8.81E-04	11.40	5/153	53/18493
GO:0035456	response to interferon-beta	7.90E-05	9.07E-04	17.27	4/153	28/18493
GO:0090022	regulation of neutrophil chemotaxis	7.90E-05	9.07E-04	17.27	4/153	28/18493
GO:2000108	positive regulation of leukocyte apoptotic process	7.90E-05	9.07E-04	17.27	4/153	28/18493
GO:0031295	T cell costimulation	8.28E-05	9.42E-04	11.19	5/153	54/18493
GO:0043901	negative regulation of multi-organism process	8.29E-05	9.42E-04	5.72	8/153	169/18493
GO:0032612	interleukin-1 production	8.45E-05	9.57E-04	8.34	6/153	87/18493

GO:0001776	leukocyte homeostasis	9.01E-05	1.01E-03	8.24	6/153	88/18493
GO:0006949	syncytium formation	9.05E-05	1.01E-03	10.99	5/153	55/18493
GO:0031294	lymphocyte costimulation	9.05E-05	1.01E-03	10.99	5/153	55/18493
GO:0050854	regulation of antigen receptor-mediated signaling pathway	1.07E-04	1.19E-03	10.60	5/153	57/18493
GO:0070228	regulation of lymphocyte apoptotic process	1.07E-04	1.19E-03	10.60	5/153	57/18493
GO:0042100	B cell proliferation	1.09E-04	1.20E-03	7.97	6/153	91/18493
GO:0050777	negative regulation of immune response	1.10E-04	1.20E-03	6.46	7/153	131/18493
GO:0043122	regulation of I-kappaB kinase/NF-kappaB signaling	1.13E-04	1.23E-03	4.81	9/153	226/18493
GO:0033623	regulation of integrin activation	1.16E-04	1.26E-03	30.22	3/153	12/18493
GO:0008064	regulation of actin polymerization or depolymerization	1.19E-04	1.28E-03	5.43	8/153	178/18493
GO:0034694	response to prostaglandin	1.19E-04	1.28E-03	15.60	4/153	31/18493
GO:1902622	regulation of neutrophil migration	1.19E-04	1.28E-03	15.60	4/153	31/18493
GO:0030832	regulation of actin filament length	1.24E-04	1.32E-03	5.40	8/153	179/18493
GO:0046631	alpha-beta T cell activation	1.26E-04	1.34E-03	6.31	7/153	134/18493
GO:0030888	regulation of B cell proliferation	1.27E-04	1.34E-03	10.24	5/153	59/18493
GO:0002791	regulation of peptide secretion	1.33E-04	1.40E-03	3.38	13/153	465/18493
GO:0046633	alpha-beta T cell proliferation	1.35E-04	1.42E-03	15.11	4/153	32/18493
GO:2000116	regulation of cysteine-type endopeptidase activity	1.37E-04	1.43E-03	4.69	9/153	232/18493
GO:0051250	negative regulation of lymphocyte activation	1.45E-04	1.51E-03	6.18	7/153	137/18493
GO:0001771	immunological synapse formation	1.49E-04	1.52E-03	27.89	3/153	13/18493
GO:0035723	interleukin-15-mediated signaling pathway	1.49E-04	1.52E-03	27.89	3/153	13/18493
GO:0045059	positive thymic T cell selection	1.49E-04	1.52E-03	27.89	3/153	13/18493
GO:0071350	cellular response to interleukin-15	1.49E-04	1.52E-03	27.89	3/153	13/18493
GO:0050866	negative regulation of cell activation	1.50E-04	1.52E-03	5.26	8/153	184/18493
GO:0019058	viral life cycle	1.50E-04	1.52E-03	4.18	10/153	289/18493
GO:0070229	negative regulation of lymphocyte apoptotic process	1.53E-04	1.54E-03	14.65	4/153	33/18493
GO:1903900	regulation of viral life cycle	1.66E-04	1.67E-03	6.04	7/153	140/18493
GO:0052548	regulation of endopeptidase activity	1.86E-04	1.86E-03	3.48	12/153	417/18493
GO:0070234	positive regulation of T cell apoptotic process	1.89E-04	1.88E-03	25.90	3/153	14/18493

GO:0070672	response to interleukin-15	1.89E-04	1.88E-03	25.90	3/153	14/18493
GO:0002707	negative regulation of lymphocyte mediated immunity	1.93E-04	1.91E-03	13.81	4/153	35/18493
GO:0032418	lysosome localization	2.01E-04	1.98E-03	9.30	5/153	65/18493
GO:0070232	regulation of T cell apoptotic process	2.16E-04	2.12E-03	13.43	4/153	36/18493
GO:0061756	leukocyte adhesion to vascular endothelial cell	2.41E-04	2.35E-03	13.07	4/153	37/18493
GO:0050688	regulation of defense response to virus	2.49E-04	2.42E-03	8.89	5/153	68/18493
GO:0031348	negative regulation of defense response	2.55E-04	2.46E-03	4.86	8/153	199/18493
GO:0071222	cellular response to lipopolysaccharide	2.55E-04	2.46E-03	4.86	8/153	199/18493
GO:0097696	STAT cascade	2.64E-04	2.54E-03	5.60	7/153	151/18493
GO:0033077	T cell differentiation in thymus	2.66E-04	2.55E-03	8.76	5/153	69/18493
GO:0032731	positive regulation of interleukin-1 beta production	2.67E-04	2.55E-03	12.72	4/153	38/18493
GO:1903532	positive regulation of secretion by cell	2.81E-04	2.67E-03	3.56	11/153	373/18493
GO:1904951	positive regulation of establishment of protein localization	2.86E-04	2.70E-03	3.32	12/153	437/18493
GO:0001818	negative regulation of cytokine production	2.86E-04	2.70E-03	4.25	9/153	256/18493
GO:0051271	negative regulation of cellular component movement	2.88E-04	2.70E-03	3.55	11/153	374/18493
GO:0050708	regulation of protein secretion	2.92E-04	2.73E-03	3.31	12/153	438/18493
GO:0019932	second-messenger-mediated signaling	2.98E-04	2.77E-03	3.30	12/153	439/18493
GO:0009612	response to mechanical stimulus	3.02E-04	2.79E-03	4.74	8/153	204/18493
GO:0007249	I-kappaB kinase/NF-kappaB signaling	3.03E-04	2.79E-03	4.22	9/153	258/18493
GO:0031668	cellular response to extracellular stimulus	3.03E-04	2.79E-03	4.22	9/153	258/18493
GO:0061844	antimicrobial humoral immune response mediated by antimicrobial peptide	3.05E-04	2.79E-03	8.51	5/153	71/18493
GO:0001959	regulation of cytokine-mediated signaling pathway	3.09E-04	2.83E-03	5.46	7/153	155/18493
GO:0031334	positive regulation of protein complex assembly	3.12E-04	2.84E-03	4.20	9/153	259/18493
GO:0052547	regulation of peptidase activity	3.17E-04	2.87E-03	3.28	12/153	442/18493
GO:0043270	positive regulation of ion transport	3.21E-04	2.89E-03	4.18	9/153	260/18493
GO:0110053	regulation of actin filament organization	3.21E-04	2.89E-03	4.18	9/153	260/18493
GO:0071219	cellular response to molecule of bacterial origin	3.22E-04	2.89E-03	4.69	8/153	206/18493
GO:0070227	lymphocyte apoptotic process	3.25E-04	2.91E-03	8.39	5/153	72/18493

GO:0002577	regulation of antigen processing and presentation	3.47E-04	3.07E-03	21.33	3/153	17/18493
GO:0048535	lymph node development	3.47E-04	3.07E-03	21.33	3/153	17/18493
GO:0072643	interferon-gamma secretion	3.47E-04	3.07E-03	21.33	3/153	17/18493
GO:0002761	regulation of myeloid leukocyte differentiation	3.72E-04	3.28E-03	6.36	6/153	114/18493
GO:0030336	negative regulation of cell migration	3.74E-04	3.28E-03	3.73	10/153	324/18493
GO:0040013	negative regulation of locomotion	3.76E-04	3.29E-03	3.44	11/153	386/18493
GO:0043254	regulation of protein complex assembly	3.80E-04	3.31E-03	3.22	12/153	451/18493
GO:0018108	peptidyl-tyrosine phosphorylation	3.84E-04	3.34E-03	3.44	11/153	387/18493
GO:0042269	regulation of natural killer cell mediated cytotoxicity	3.95E-04	3.40E-03	11.51	4/153	42/18493
GO:0043300	regulation of leukocyte degranulation	3.95E-04	3.40E-03	11.51	4/153	42/18493
GO:0018212	peptidyl-tyrosine modification	4.10E-04	3.49E-03	3.41	11/153	390/18493
GO:0002544	chronic inflammatory response	4.14E-04	3.49E-03	20.14	3/153	18/18493
GO:0051767	nitric-oxide synthase biosynthetic process	4.14E-04	3.49E-03	20.14	3/153	18/18493
GO:0051769	regulation of nitric-oxide synthase biosynthetic process	4.14E-04	3.49E-03	20.14	3/153	18/18493
GO:0070230	positive regulation of lymphocyte apoptotic process	4.14E-04	3.49E-03	20.14	3/153	18/18493
GO:1901741	positive regulation of myoblast fusion	4.14E-04	3.49E-03	20.14	3/153	18/18493
GO:0019079	viral genome replication	4.27E-04	3.59E-03	6.20	6/153	117/18493
GO:0032956	regulation of actin cytoskeleton organization	4.42E-04	3.69E-03	3.65	10/153	331/18493
GO:0007584	response to nutrient	4.42E-04	3.69E-03	4.48	8/153	216/18493
GO:1903901	negative regulation of viral life cycle	4.44E-04	3.70E-03	7.85	5/153	77/18493
GO:0019730	antimicrobial humoral response	4.47E-04	3.71E-03	6.15	6/153	118/18493
GO:0060759	regulation of response to cytokine stimulus	4.51E-04	3.73E-03	5.13	7/153	165/18493
GO:0033209	tumor necrosis factor-mediated signaling pathway	4.68E-04	3.85E-03	6.09	6/153	119/18493
GO:0002715	regulation of natural killer cell mediated immunity	4.73E-04	3.88E-03	10.99	4/153	44/18493
GO:0007015	actin filament organization	4.76E-04	3.90E-03	3.35	11/153	397/18493
GO:0010560	positive regulation of glycoprotein biosynthetic process	4.88E-04	3.98E-03	19.08	3/153	19/18493
GO:0002704	negative regulation of leukocyte mediated immunity	5.16E-04	4.15E-03	10.74	4/153	45/18493
GO:0014911	positive regulation of smooth muscle cell migration	5.16E-04	4.15E-03	10.74	4/153	45/18493
GO:0032653	regulation of interleukin-10 production	5.16E-04	4.15E-03	10.74	4/153	45/18493
GO:0032732	positive regulation of interleukin-1 production	5.16E-04	4.15E-03	10.74	4/153	45/18493

GO:0031589	cell-substrate adhesion	5.20E-04	4.17E-03	3.58	10/153	338/18493
GO:0051222	positive regulation of protein transport	5.29E-04	4.22E-03	3.31	11/153	402/18493
GO:0042116	macrophage activation	5.30E-04	4.22E-03	7.55	5/153	80/18493
GO:2000146	negative regulation of cell motility	5.32E-04	4.22E-03	3.57	10/153	339/18493
GO:0022408	negative regulation of cell-cell adhesion	5.40E-04	4.27E-03	4.98	7/153	170/18493
GO:0051047	positive regulation of secretion	5.51E-04	4.34E-03	3.29	11/153	404/18493
GO:0031952	regulation of protein autophosphorylation	5.61E-04	4.40E-03	10.51	4/153	46/18493
GO:0045824	negative regulation of innate immune response	5.61E-04	4.40E-03	10.51	4/153	46/18493
GO:0033630	positive regulation of cell adhesion mediated by integrin	5.71E-04	4.45E-03	18.13	3/153	20/18493
GO:0035458	cellular response to interferon-beta	5.71E-04	4.45E-03	18.13	3/153	20/18493
GO:1902903	regulation of supramolecular fiber organization	5.83E-04	4.52E-03	3.52	10/153	343/18493
GO:0032613	interleukin-10 production	6.09E-04	4.70E-03	10.29	4/153	47/18493
GO:0150076	neuroinflammatory response	6.09E-04	4.70E-03	10.29	4/153	47/18493
GO:0002285	lymphocyte activation involved in immune response	6.20E-04	4.76E-03	4.86	7/153	174/18493
GO:0014910	regulation of smooth muscle cell migration	6.27E-04	4.81E-03	7.28	5/153	83/18493
GO:0071216	cellular response to biotic stimulus	6.50E-04	4.97E-03	4.22	8/153	229/18493
GO:0009409	response to cold	6.60E-04	4.97E-03	10.07	4/153	48/18493
GO:0045058	T cell selection	6.60E-04	4.97E-03	10.07	4/153	48/18493
GO:0045061	thymic T cell selection	6.62E-04	4.97E-03	17.27	3/153	21/18493
GO:0050857	positive regulation of antigen receptor-mediated signaling pathway	6.62E-04	4.97E-03	17.27	3/153	21/18493
GO:0070233	negative regulation of T cell apoptotic process	6.62E-04	4.97E-03	17.27	3/153	21/18493
GO:0070542	response to fatty acid	6.63E-04	4.97E-03	7.19	5/153	84/18493
GO:0030041	actin filament polymerization	7.09E-04	5.30E-03	4.75	7/153	178/18493
GO:0002831	regulation of response to biotic stimulus	7.46E-04	5.56E-03	5.58	6/153	130/18493
GO:0070231	T cell apoptotic process	7.72E-04	5.73E-03	9.67	4/153	50/18493
GO:0002705	positive regulation of leukocyte mediated immunity	7.77E-04	5.75E-03	5.54	6/153	131/18493
GO:0043123	positive regulation of I-kappaB kinase/NF-kappaB signaling	7.82E-04	5.78E-03	4.67	7/153	181/18493
GO:0002886	regulation of myeloid leukocyte mediated immunity	8.32E-04	6.13E-03	9.48	4/153	51/18493

GO:0050729	positive regulation of inflammatory response	8.41E-04	6.17E-03	5.45	6/153	133/18493
GO:0033273	response to vitamin	8.62E-04	6.26E-03	6.79	5/153	89/18493
GO:0060337	type I interferon signaling pathway	8.62E-04	6.26E-03	6.79	5/153	89/18493
GO:0071357	cellular response to type I interferon	8.62E-04	6.26E-03	6.79	5/153	89/18493
GO:0002691	regulation of cellular extravasation	8.71E-04	6.26E-03	15.77	3/153	23/18493
GO:0032753	positive regulation of interleukin-4 production	8.71E-04	6.26E-03	15.77	3/153	23/18493
GO:0034695	response to prostaglandin E	8.71E-04	6.26E-03	15.77	3/153	23/18493
GO:1903020	positive regulation of glycoprotein metabolic process	8.71E-04	6.26E-03	15.77	3/153	23/18493
GO:0002763	positive regulation of myeloid leukocyte differentiation	8.96E-04	6.42E-03	9.30	4/153	52/18493
GO:0014909	smooth muscle cell migration	9.07E-04	6.46E-03	6.71	5/153	90/18493
GO:0045069	regulation of viral genome replication	9.07E-04	6.46E-03	6.71	5/153	90/18493
GO:0070588	calcium ion transmembrane transport	9.39E-04	6.67E-03	3.60	9/153	302/18493
GO:0002702	positive regulation of production of molecular mediator of immune response	9.53E-04	6.69E-03	6.64	5/153	91/18493
GO:0045639	positive regulation of myeloid cell differentiation	9.53E-04	6.69E-03	6.64	5/153	91/18493
GO:0046634	regulation of alpha-beta T cell activation	9.53E-04	6.69E-03	6.64	5/153	91/18493
GO:2000117	negative regulation of cysteine-type endopeptidase activity	9.53E-04	6.69E-03	6.64	5/153	91/18493
GO:0042113	B cell activation	9.61E-04	6.72E-03	3.59	9/153	303/18493
GO:0045661	regulation of myoblast differentiation	9.63E-04	6.72E-03	9.12	4/153	53/18493
GO:0032535	regulation of cellular component size	9.77E-04	6.80E-03	3.29	10/153	367/18493
GO:0060143	positive regulation of syncytium formation by plasma membrane fusion	9.89E-04	6.87E-03	15.11	3/153	24/18493
GO:0050730	regulation of peptidyl-tyrosine phosphorylation	1.01E-03	6.97E-03	3.95	8/153	245/18493
GO:0050714	positive regulation of protein secretion	1.03E-03	7.13E-03	3.93	8/153	246/18493
GO:0045637	regulation of myeloid cell differentiation	1.09E-03	7.49E-03	3.90	8/153	248/18493
GO:0034340	response to type I interferon	1.10E-03	7.57E-03	6.43	5/153	94/18493
GO:0002230	positive regulation of defense response to virus by host	1.12E-03	7.62E-03	14.50	3/153	25/18493
GO:0150077	regulation of neuroinflammatory response	1.12E-03	7.62E-03	14.50	3/153	25/18493
GO:0010951	negative regulation of endopeptidase activity	1.15E-03	7.80E-03	3.87	8/153	250/18493

GO:0010959	regulation of metal ion transport	1.17E-03	7.93E-03	3.21	10/153	376/18493
GO:0032970	regulation of actin filament-based process	1.17E-03	7.93E-03	3.21	10/153	376/18493
GO:0001960	negative regulation of cytokine-mediated signaling pathway	1.18E-03	7.99E-03	8.63	4/153	56/18493
GO:0002218	activation of innate immune response	1.21E-03	8.11E-03	3.84	8/153	252/18493
GO:2001243	negative regulation of intrinsic apoptotic signaling pathway	1.21E-03	8.13E-03	6.30	5/153	96/18493
GO:0031954	positive regulation of protein autophosphorylation	1.26E-03	8.35E-03	13.95	3/153	26/18493
GO:0043950	positive regulation of cAMP-mediated signaling	1.26E-03	8.35E-03	13.95	3/153	26/18493
GO:0051125	regulation of actin nucleation	1.26E-03	8.35E-03	13.95	3/153	26/18493
GO:0042108	positive regulation of cytokine biosynthetic process	1.27E-03	8.40E-03	8.48	4/153	57/18493
GO:0007187	G protein-coupled receptor signaling pathway, coupled to cyclic nucleotide second messenger	1.33E-03	8.82E-03	3.78	8/153	256/18493
GO:0051235	maintenance of location	1.35E-03	8.88E-03	3.42	9/153	318/18493
GO:0051092	positive regulation of NF-kappaB transcription factor activity	1.36E-03	8.96E-03	4.97	6/153	146/18493
GO:0007229	integrin-mediated signaling pathway	1.39E-03	9.13E-03	6.10	5/153	99/18493
GO:0032673	regulation of interleukin-4 production	1.40E-03	9.19E-03	13.43	3/153	27/18493
GO:0007259	JAK-STAT cascade	1.41E-03	9.21E-03	4.93	6/153	147/18493
GO:0034113	heterotypic cell-cell adhesion	1.44E-03	9.37E-03	8.19	4/153	59/18493
GO:0071774	response to fibroblast growth factor	1.46E-03	9.48E-03	4.90	6/153	148/18493
GO:0010466	negative regulation of peptidase activity	1.51E-03	9.75E-03	3.70	8/153	261/18493
GO:0002286	T cell activation involved in immune response	1.52E-03	9.78E-03	5.98	5/153	101/18493
GO:0046632	alpha-beta T cell differentiation	1.52E-03	9.78E-03	5.98	5/153	101/18493
GO:0051346	negative regulation of hydrolase activity	1.52E-03	9.78E-03	2.90	11/153	458/18493
GO:0010830	regulation of myotube differentiation	1.53E-03	9.80E-03	8.06	4/153	60/18493
GO:0060761	negative regulation of response to cytokine stimulus	1.53E-03	9.80E-03	8.06	4/153	60/18493
GO:0043304	regulation of mast cell degranulation	1.56E-03	9.96E-03	12.95	3/153	28/18493
GO:2001233	regulation of apoptotic signaling pathway	1.57E-03	9.97E-03	3.09	10/153	391/18493
GO:0002456	T cell mediated immunity	1.59E-03	1.00E-02	5.92	5/153	102/18493

GO:1901222	regulation of NIK/NF-kappaB signaling	1.59E-03	1.00E-02	5.92	5/153	102/18493
GO:0046635	positive regulation of alpha-beta T cell activation	1.63E-03	1.03E-02	7.93	4/153	61/18493
GO:0014812	muscle cell migration	1.66E-03	1.04E-02	5.87	5/153	103/18493
GO:0002793	positive regulation of peptide secretion	1.66E-03	1.04E-02	3.65	8/153	265/18493
GO:0030168	platelet activation	1.67E-03	1.05E-02	4.77	6/153	152/18493
GO:0032102	negative regulation of response to external stimulus	1.70E-03	1.06E-02	3.31	9/153	329/18493
GO:0032623	interleukin-2 production	1.73E-03	1.07E-02	7.80	4/153	62/18493
GO:0033006	regulation of mast cell activation involved in immune response	1.73E-03	1.07E-02	12.50	3/153	29/18493
GO:0033032	regulation of myeloid cell apoptotic process	1.73E-03	1.07E-02	12.50	3/153	29/18493
GO:0046640	regulation of alpha-beta T cell proliferation	1.73E-03	1.07E-02	12.50	3/153	29/18493
GO:0050718	positive regulation of interleukin-1 beta secretion	1.73E-03	1.07E-02	12.50	3/153	29/18493
GO:0071295	cellular response to vitamin	1.73E-03	1.07E-02	12.50	3/153	29/18493
GO:0009266	response to temperature stimulus	1.75E-03	1.07E-02	4.07	7/153	208/18493
GO:0010810	regulation of cell-substrate adhesion	1.80E-03	1.10E-02	4.05	7/153	209/18493
GO:0002708	positive regulation of lymphocyte mediated immunity	1.80E-03	1.10E-02	5.76	5/153	105/18493
GO:0002532	production of molecular mediator involved in inflammatory response	1.84E-03	1.12E-02	7.67	4/153	63/18493
GO:0050868	negative regulation of T cell activation	1.88E-03	1.14E-02	5.70	5/153	106/18493
GO:0032733	positive regulation of interleukin-10 production	1.91E-03	1.15E-02	12.09	3/153	30/18493
GO:0043372	positive regulation of CD4-positive, alpha-beta T cell differentiation	1.91E-03	1.15E-02	12.09	3/153	30/18493
GO:0046596	regulation of viral entry into host cell	1.91E-03	1.15E-02	12.09	3/153	30/18493
GO:0002260	lymphocyte homeostasis	1.95E-03	1.17E-02	7.55	4/153	64/18493
GO:0031343	positive regulation of cell killing	1.95E-03	1.17E-02	7.55	4/153	64/18493
GO:0030833	regulation of actin filament polymerization	2.03E-03	1.22E-02	4.59	6/153	158/18493
GO:0014902	myotube differentiation	2.04E-03	1.22E-02	5.60	5/153	108/18493
GO:0032481	positive regulation of type I interferon production	2.06E-03	1.22E-02	7.44	4/153	65/18493
GO:0033627	cell adhesion mediated by integrin	2.06E-03	1.22E-02	7.44	4/153	65/18493
GO:0051258	protein polymerization	2.09E-03	1.24E-02	3.52	8/153	275/18493

GO:0042554	superoxide anion generation	2.11E-03	1.24E-02	11.70	3/153	31/18493
GO:0002292	T cell differentiation involved in immune response	2.18E-03	1.28E-02	7.33	4/153	66/18493
GO:0050918	positive chemotaxis	2.18E-03	1.28E-02	7.33	4/153	66/18493
GO:2001242	regulation of intrinsic apoptotic signaling pathway	2.24E-03	1.31E-02	4.50	6/153	161/18493
GO:0019722	calcium-mediated signaling	2.40E-03	1.40E-02	3.85	7/153	220/18493
GO:0031670	cellular response to nutrient	2.43E-03	1.42E-02	7.11	4/153	68/18493
GO:0001774	microglial cell activation	2.53E-03	1.46E-02	10.99	3/153	33/18493
GO:0002269	leukocyte activation involved in inflammatory response	2.53E-03	1.46E-02	10.99	3/153	33/18493
GO:0032633	interleukin-4 production	2.53E-03	1.46E-02	10.99	3/153	33/18493
GO:0033028	myeloid cell apoptotic process	2.53E-03	1.46E-02	10.99	3/153	33/18493
GO:0032945	negative regulation of mononuclear cell proliferation	2.70E-03	1.55E-02	6.91	4/153	70/18493
GO:0050672	negative regulation of lymphocyte proliferation	2.70E-03	1.55E-02	6.91	4/153	70/18493
GO:1901224	positive regulation of NIK/NF-kappaB signaling	2.70E-03	1.55E-02	6.91	4/153	70/18493
GO:0050716	positive regulation of interleukin-1 secretion	2.75E-03	1.57E-02	10.66	3/153	34/18493
GO:2000249	regulation of actin cytoskeleton reorganization	2.75E-03	1.57E-02	10.66	3/153	34/18493
GO:2000516	positive regulation of CD4-positive, alpha-beta T cell activation	2.75E-03	1.57E-02	10.66	3/153	34/18493
GO:0048660	regulation of smooth muscle cell proliferation	2.77E-03	1.57E-02	4.32	6/153	168/18493
GO:0051051	negative regulation of transport	2.79E-03	1.58E-02	2.69	11/153	495/18493
GO:0001768	establishment of T cell polarity	2.93E-03	1.65E-02	24.17	2/153	10/18493
GO:0071104	response to interleukin-9	2.93E-03	1.65E-02	24.17	2/153	10/18493
GO:0048659	smooth muscle cell proliferation	2.93E-03	1.65E-02	4.27	6/153	170/18493
GO:0033280	response to vitamin D	2.99E-03	1.68E-02	10.36	3/153	35/18493
GO:0043368	positive T cell selection	2.99E-03	1.68E-02	10.36	3/153	35/18493
GO:0097305	response to alcohol	3.15E-03	1.76E-02	3.66	7/153	231/18493
GO:0038061	NIK/NF-kappaB signaling	3.23E-03	1.80E-02	5.04	5/153	120/18493
GO:0043367	CD4-positive, alpha-beta T cell differentiation	3.31E-03	1.84E-02	6.53	4/153	74/18493
GO:0046718	viral entry into host cell	3.34E-03	1.86E-02	4.99	5/153	121/18493
GO:0050853	B cell receptor signaling pathway	3.46E-03	1.92E-02	4.95	5/153	122/18493
GO:0032642	regulation of chemokine production	3.47E-03	1.92E-02	6.45	4/153	75/18493

GO:0010831	positive regulation of myotube differentiation	3.51E-03	1.93E-02	9.80	3/153	37/18493
GO:0038083	peptidyl-tyrosine autophosphorylation	3.51E-03	1.93E-02	9.80	3/153	37/18493
GO:0050856	regulation of T cell receptor signaling pathway	3.51E-03	1.93E-02	9.80	3/153	37/18493
GO:0001767	establishment of lymphocyte polarity	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:0033089	positive regulation of T cell differentiation in thymus	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:0033632	regulation of cell-cell adhesion mediated by integrin	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:0045060	negative thymic T cell selection	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:0045953	negative regulation of natural killer cell mediated cytotoxicity	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:0072567	chemokine (C-X-C motif) ligand 2 production	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:1904995	negative regulation of leukocyte adhesion to vascular endothelial cell	3.56E-03	1.93E-02	21.98	2/153	11/18493
GO:0010559	regulation of glycoprotein biosynthetic process	3.79E-03	2.04E-02	9.54	3/153	38/18493
GO:0019835	cytolysis	4.08E-03	2.19E-02	9.30	3/153	39/18493
GO:0033003	regulation of mast cell activation	4.08E-03	2.19E-02	9.30	3/153	39/18493
GO:0043029	T cell homeostasis	4.08E-03	2.19E-02	9.30	3/153	39/18493
GO:0050864	regulation of B cell activation	4.21E-03	2.25E-02	3.96	6/153	183/18493
GO:0002551	mast cell chemotaxis	4.25E-03	2.25E-02	20.14	2/153	12/18493
GO:0002716	negative regulation of natural killer cell mediated immunity	4.25E-03	2.25E-02	20.14	2/153	12/18493
GO:0038110	interleukin-2-mediated signaling pathway	4.25E-03	2.25E-02	20.14	2/153	12/18493
GO:0043383	negative T cell selection	4.25E-03	2.25E-02	20.14	2/153	12/18493
GO:0043922	negative regulation by host of viral transcription	4.25E-03	2.25E-02	20.14	2/153	12/18493
GO:0051279	regulation of release of sequestered calcium ion into cytosol	4.38E-03	2.29E-02	6.04	4/153	80/18493
GO:0002820	negative regulation of adaptive immune response	4.38E-03	2.29E-02	9.07	3/153	40/18493
GO:0030890	positive regulation of B cell proliferation	4.38E-03	2.29E-02	9.07	3/153	40/18493
GO:0051281	positive regulation of release of sequestered calcium ion into cytosol	4.38E-03	2.29E-02	9.07	3/153	40/18493
GO:0061900	glial cell activation	4.38E-03	2.29E-02	9.07	3/153	40/18493
GO:0045765	regulation of angiogenesis	4.51E-03	2.35E-02	2.86	9/153	381/18493

GO:0050731	positive regulation of peptidyl-tyrosine phosphorylation	4.55E-03	2.37E-02	3.90	6/153	186/18493
GO:0030574	collagen catabolic process	4.70E-03	2.44E-02	8.84	3/153	41/18493
GO:0032602	chemokine production	4.78E-03	2.48E-02	5.90	4/153	82/18493
GO:0071352	cellular response to interleukin-2	5.00E-03	2.54E-02	18.60	2/153	13/18493
GO:0097531	mast cell migration	5.00E-03	2.54E-02	18.60	2/153	13/18493
GO:1900025	negative regulation of substrate adhesion-dependent cell spreading	5.00E-03	2.54E-02	18.60	2/153	13/18493
GO:0002700	regulation of production of molecular mediator of immune response	5.00E-03	2.54E-02	4.54	5/153	133/18493
GO:0030260	entry into host cell	5.00E-03	2.54E-02	4.54	5/153	133/18493
GO:0044409	entry into host	5.00E-03	2.54E-02	4.54	5/153	133/18493
GO:0051806	entry into cell of other organism involved in symbiotic interaction	5.00E-03	2.54E-02	4.54	5/153	133/18493
GO:0051828	entry into other organism involved in symbiotic interaction	5.00E-03	2.54E-02	4.54	5/153	133/18493
GO:1904892	regulation of STAT cascade	5.00E-03	2.54E-02	4.54	5/153	133/18493
GO:0045429	positive regulation of nitric oxide biosynthetic process	5.03E-03	2.55E-02	8.63	3/153	42/18493
GO:0050706	regulation of interleukin-1 beta secretion	5.03E-03	2.55E-02	8.63	3/153	42/18493
GO:1904407	positive regulation of nitric oxide metabolic process	5.03E-03	2.55E-02	8.63	3/153	42/18493
GO:0043491	protein kinase B signaling	5.16E-03	2.61E-02	3.34	7/153	253/18493
GO:0007565	female pregnancy	5.17E-03	2.61E-02	3.80	6/153	191/18493
GO:0043154	negative regulation of cysteine-type endopeptidase activity involved in apoptotic process	5.21E-03	2.61E-02	5.76	4/153	84/18493
GO:0097306	cellular response to alcohol	5.21E-03	2.61E-02	5.76	4/153	84/18493
GO:0002792	negative regulation of peptide secretion	5.32E-03	2.66E-02	4.48	5/153	135/18493
GO:0051091	positive regulation of DNA-binding transcription factor activity	5.39E-03	2.69E-02	3.32	7/153	255/18493
GO:0045445	myoblast differentiation	5.43E-03	2.71E-02	5.69	4/153	85/18493
GO:0002639	positive regulation of immunoglobulin production	5.74E-03	2.84E-02	8.24	3/153	44/18493
GO:0033628	regulation of cell adhesion mediated by integrin	5.74E-03	2.84E-02	8.24	3/153	44/18493
GO:0032823	regulation of natural killer cell differentiation	5.80E-03	2.84E-02	17.27	2/153	14/18493

GO:0051770	positive regulation of nitric-oxide synthase biosynthetic process	5.80E-03	2.84E-02	17.27	2/153	14/18493
GO:0060263	regulation of respiratory burst	5.80E-03	2.84E-02	17.27	2/153	14/18493
GO:0070669	response to interleukin-2	5.80E-03	2.84E-02	17.27	2/153	14/18493
GO:0071361	cellular response to ethanol	5.80E-03	2.84E-02	17.27	2/153	14/18493
GO:2000402	negative regulation of lymphocyte migration	5.80E-03	2.84E-02	17.27	2/153	14/18493
GO:0048871	multicellular organismal homeostasis	5.89E-03	2.88E-02	2.57	10/153	471/18493
GO:0035710	CD4-positive, alpha-beta T cell activation	5.89E-03	2.88E-02	5.56	4/153	87/18493
GO:0007189	adenylate cyclase-activating G protein-coupled receptor signaling pathway	6.01E-03	2.93E-02	4.35	5/153	139/18493
GO:1903018	regulation of glycoprotein metabolic process	6.11E-03	2.97E-02	8.06	3/153	45/18493
GO:1904894	positive regulation of STAT cascade	6.13E-03	2.98E-02	5.49	4/153	88/18493
GO:0043062	extracellular structure organization	6.35E-03	3.07E-02	2.71	9/153	402/18493
GO:0045807	positive regulation of endocytosis	6.38E-03	3.08E-02	4.29	5/153	141/18493
GO:0044344	cellular response to fibroblast growth factor stimulus	6.57E-03	3.16E-02	4.26	5/153	142/18493
GO:0106106	cold-induced thermogenesis	6.57E-03	3.16E-02	4.26	5/153	142/18493
GO:0120161	regulation of cold-induced thermogenesis	6.57E-03	3.16E-02	4.26	5/153	142/18493
GO:0002830	positive regulation of type 2 immune response	6.65E-03	3.16E-02	16.12	2/153	15/18493
GO:0030852	regulation of granulocyte differentiation	6.65E-03	3.16E-02	16.12	2/153	15/18493
GO:0033631	cell-cell adhesion mediated by integrin	6.65E-03	3.16E-02	16.12	2/153	15/18493
GO:0050961	detection of temperature stimulus involved in sensory perception	6.65E-03	3.16E-02	16.12	2/153	15/18493
GO:0050965	detection of temperature stimulus involved in sensory perception of pain	6.65E-03	3.16E-02	16.12	2/153	15/18493
GO:2000484	positive regulation of interleukin-8 secretion	6.65E-03	3.16E-02	16.12	2/153	15/18493
GO:0031667	response to nutrient levels	6.79E-03	3.22E-02	2.51	10/153	481/18493
GO:0002720	positive regulation of cytokine production involved in immune response	6.90E-03	3.25E-02	7.72	3/153	47/18493
GO:0043370	regulation of CD4-positive, alpha-beta T cell differentiation	6.90E-03	3.25E-02	7.72	3/153	47/18493
GO:0046638	positive regulation of alpha-beta T cell differentiation	6.90E-03	3.25E-02	7.72	3/153	47/18493

GO:0002822	regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	6.96E-03	3.27E-02	4.20	5/153	144/18493
GO:0002440	production of molecular mediator of immune response	7.01E-03	3.29E-02	3.16	7/153	268/18493
GO:1903169	regulation of calcium ion transmembrane transport	7.16E-03	3.35E-02	4.17	5/153	145/18493
GO:0050702	interleukin-1 beta secretion	7.32E-03	3.41E-02	7.55	3/153	48/18493
GO:0098586	cellular response to virus	7.32E-03	3.41E-02	7.55	3/153	48/18493
GO:0032930	positive regulation of superoxide anion generation	7.56E-03	3.51E-02	15.11	2/153	16/18493
GO:0033033	negative regulation of myeloid cell apoptotic process	7.56E-03	3.51E-02	15.11	2/153	16/18493
GO:2001267	regulation of cysteine-type endopeptidase activity involved in apoptotic signaling pathway	7.56E-03	3.51E-02	15.11	2/153	16/18493
GO:0006909	phagocytosis	7.70E-03	3.56E-02	2.83	8/153	342/18493
GO:0042035	regulation of cytokine biosynthetic process	7.72E-03	3.56E-02	5.14	4/153	94/18493
GO:0046456	icosanoid biosynthetic process	7.75E-03	3.56E-02	7.40	3/153	49/18493
GO:0050704	regulation of interleukin-1 secretion	7.75E-03	3.56E-02	7.40	3/153	49/18493
GO:0032271	regulation of protein polymerization	7.75E-03	3.56E-02	3.49	6/153	208/18493
GO:1903305	regulation of regulated secretory pathway	7.79E-03	3.57E-02	4.08	5/153	148/18493
GO:0043281	regulation of cysteine-type endopeptidase activity involved in apoptotic process	7.93E-03	3.62E-02	3.47	6/153	209/18493
GO:0051701	interaction with host	7.93E-03	3.62E-02	3.47	6/153	209/18493
GO:0043434	response to peptide hormone	7.98E-03	3.64E-02	2.61	9/153	417/18493
GO:0030316	osteoclast differentiation	8.01E-03	3.65E-02	5.09	4/153	95/18493
GO:0001913	T cell mediated cytotoxicity	8.19E-03	3.71E-02	7.25	3/153	50/18493
GO:0045010	actin nucleation	8.19E-03	3.71E-02	7.25	3/153	50/18493
GO:0006898	receptor-mediated endocytosis	8.23E-03	3.72E-02	2.79	8/153	346/18493
GO:1990845	adaptive thermogenesis	8.23E-03	3.72E-02	4.03	5/153	150/18493
GO:0031532	actin cytoskeleton reorganization	8.31E-03	3.74E-02	5.04	4/153	96/18493
GO:0120162	positive regulation of cold-induced thermogenesis	8.31E-03	3.74E-02	5.04	4/153	96/18493
GO:0090066	regulation of anatomical structure size	8.46E-03	3.75E-02	2.43	10/153	497/18493
GO:1901342	regulation of vasculature development	8.47E-03	3.75E-02	2.58	9/153	421/18493

GO:0016064	immunoglobulin mediated immune response	8.48E-03	3.75E-02	3.42	6/153	212/18493
GO:0030198	extracellular matrix organization	8.50E-03	3.75E-02	2.78	8/153	348/18493
GO:0002418	immune response to tumor cell	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0002689	negative regulation of leukocyte chemotaxis	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0002710	negative regulation of T cell mediated immunity	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0061081	positive regulation of myeloid leukocyte cytokine production involved in immune response	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0071605	monocyte chemotactic protein-1 production	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0071637	regulation of monocyte chemotactic protein-1 production	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0090280	positive regulation of calcium ion import	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:1903978	regulation of microglial cell activation	8.52E-03	3.75E-02	14.22	2/153	17/18493
GO:0060627	regulation of vesicle-mediated transport	8.57E-03	3.77E-02	2.427093997	10/153	498/18493
GO:0007254	JNK cascade	8.66E-03	3.79E-02	3.40476848	6/153	213/18493
GO:0019724	B cell mediated immunity	8.66E-03	3.79E-02	3.40	6/153	213/18493
GO:0030838	positive regulation of actin filament polymerization	8.92E-03	3.89E-02	4.93	4/153	98/18493
GO:0048661	positive regulation of smooth muscle cell proliferation	8.92E-03	3.89E-02	4.93	4/153	98/18493
GO:2000379	positive regulation of reactive oxygen species metabolic process	8.92E-03	3.89E-02	4.93	4/153	98/18493
GO:0032720	negative regulation of tumor necrosis factor production	9.13E-03	3.96E-02	6.97	3/153	52/18493
GO:0043030	regulation of macrophage activation	9.13E-03	3.96E-02	6.97	3/153	52/18493
GO:0051403	stress-activated MAPK cascade	9.49E-03	4.11E-02	2.98	7/153	284/18493
GO:0032816	positive regulation of natural killer cell activation	9.54E-03	4.12E-02	13.43	2/153	18/18493
GO:0002824	positive regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	9.56E-03	4.12E-02	4.83	4/153	100/18493
GO:0010522	regulation of calcium ion transport into cytosol	9.56E-03	4.12E-02	4.83	4/153	100/18493
GO:0031529	ruffle organization	9.62E-03	4.12E-02	6.84	3/153	53/18493
GO:0032663	regulation of interleukin-2 production	9.62E-03	4.12E-02	6.84	3/153	53/18493
GO:0032722	positive regulation of chemokine production	9.62E-03	4.12E-02	6.84	3/153	53/18493
GO:0097193	intrinsic apoptotic signaling pathway	1.00E-02	4.28E-02	2.95	7/153	287/18493

GO:0051495	positive regulation of cytoskeleton organization	1.01E-02	4.30E-02	3.30	6/153	220/18493
GO:0010524	positive regulation of calcium ion transport into cytosol	1.01E-02	4.30E-02	6.71	3/153	54/18493
GO:0043949	regulation of cAMP-mediated signaling	1.01E-02	4.30E-02	6.71	3/153	54/18493
GO:1903556	negative regulation of tumor necrosis factor superfamily cytokine production	1.01E-02	4.30E-02	6.71	3/153	54/18493
GO:0045861	negative regulation of proteolysis	1.01E-02	4.30E-02	2.69	8/153	359/18493
GO:0008630	intrinsic apoptotic signaling pathway in response to DNA damage	1.02E-02	4.33E-02	4.74	4/153	102/18493
GO:0007188	adenylate cyclase-modulating G protein-coupled receptor signaling pathway	1.03E-02	4.34E-02	3.28	6/153	221/18493
GO:0044706	multi-multicellular organism process	1.03E-02	4.34E-02	3.28	6/153	221/18493
GO:0007160	cell-matrix adhesion	1.05E-02	4.40E-02	3.27	6/153	222/18493
GO:0051048	negative regulation of secretion	1.05E-02	4.40E-02	3.27	6/153	222/18493
GO:2001234	negative regulation of apoptotic signaling pathway	1.05E-02	4.40E-02	3.27	6/153	222/18493
GO:0010829	negative regulation of glucose transmembrane transport	1.06E-02	4.41E-02	12.72	2/153	19/18493
GO:0016048	detection of temperature stimulus	1.06E-02	4.41E-02	12.72	2/153	19/18493
GO:0030502	negative regulation of bone mineralization	1.06E-02	4.41E-02	12.72	2/153	19/18493
GO:0046641	positive regulation of alpha-beta T cell proliferation	1.06E-02	4.41E-02	12.72	2/153	19/18493
GO:0050860	negative regulation of T cell receptor signaling pathway	1.06E-02	4.41E-02	12.72	2/153	19/18493
GO:0090382	phagosome maturation	1.06E-02	4.41E-02	12.72	2/153	19/18493
GO:0001912	positive regulation of leukocyte mediated cytotoxicity	1.06E-02	4.41E-02	6.59	3/153	55/18493
GO:1903428	positive regulation of reactive oxygen species biosynthetic process	1.06E-02	4.41E-02	6.59	3/153	55/18493
GO:0042130	negative regulation of T cell proliferation	1.12E-02	4.61E-02	6.48	3/153	56/18493
GO:0050701	interleukin-1 secretion	1.12E-02	4.61E-02	6.48	3/153	56/18493
GO:0002821	positive regulation of adaptive immune response	1.13E-02	4.64E-02	4.60	4/153	105/18493
GO:0042089	cytokine biosynthetic process	1.13E-02	4.64E-02	4.60	4/153	105/18493
GO:0046777	protein autophosphorylation	1.16E-02	4.76E-02	3.19	6/153	227/18493
GO:0042107	cytokine metabolic process	1.17E-02	4.76E-02	4.56	4/153	106/18493
GO:0031579	membrane raft organization	1.17E-02	4.76E-02	12.09	2/153	20/18493

GO:0032682	negative regulation of chemokine production	1.17E-02	4.76E-02	12.09	2/153	20/18493
GO:0032928	regulation of superoxide anion generation	1.17E-02	4.76E-02	12.09	2/153	20/18493
GO:0071305	cellular response to vitamin D	1.17E-02	4.76E-02	12.09	2/153	20/18493
GO:0050766	positive regulation of phagocytosis	1.17E-02	4.76E-02	6.36	3/153	57/18493
GO:2000514	regulation of CD4-positive, alpha-beta T cell activation	1.17E-02	4.76E-02	6.36	3/153	57/18493
GO:0031669	cellular response to nutrient levels	1.18E-02	4.80E-02	3.18	6/153	228/18493
GO:0002294	CD4-positive, alpha-beta T cell differentiation involved in immune response	1.29E-02	5.17E-02	6.15	3/153	59/18493
GO:0019883	antigen processing and presentation of endogenous antigen	1.29E-02	5.17E-02	11.51	2/153	21/18493
GO:0043302	positive regulation of leukocyte degranulation	1.29E-02	5.17E-02	11.51	2/153	21/18493
GO:0050951	sensory perception of temperature stimulus	1.29E-02	5.17E-02	11.51	2/153	21/18493
GO:1904994	regulation of leukocyte adhesion to vascular endothelial cell	1.29E-02	5.17E-02	11.51	2/153	21/18493
GO:0051897	positive regulation of protein kinase B signaling	1.30E-02	5.21E-02	3.60	5/153	168/18493
GO:0002758	innate immune response-activating signal transduction	1.31E-02	5.23E-02	3.11	6/153	233/18493
GO:0002287	alpha-beta T cell activation involved in immune response	1.35E-02	5.37E-02	6.04	3/153	60/18493
GO:0002293	alpha-beta T cell differentiation involved in immune response	1.35E-02	5.37E-02	6.04	3/153	60/18493
GO:1903902	positive regulation of viral life cycle	1.35E-02	5.37E-02	6.04	3/153	60/18493
GO:0048771	tissue remodeling	1.36E-02	5.40E-02	3.55	5/153	170/18493
GO:2001235	positive regulation of apoptotic signaling pathway	1.36E-02	5.40E-02	3.55	5/153	170/18493
GO:0002698	negative regulation of immune effector process	1.36E-02	5.40E-02	4.36	4/153	111/18493
GO:0033002	muscle cell proliferation	1.38E-02	5.48E-02	3.07	6/153	236/18493
GO:0001503	ossification	1.39E-02	5.49E-02	2.54	8/153	380/18493
GO:0001659	temperature homeostasis	1.39E-02	5.50E-02	3.53	5/153	171/18493
GO:0002347	response to tumor cell	1.41E-02	5.50E-02	10.99	2/153	22/18493
GO:0006925	inflammatory cell apoptotic process	1.41E-02	5.50E-02	10.99	2/153	22/18493
GO:0032703	negative regulation of interleukin-2 production	1.41E-02	5.50E-02	10.99	2/153	22/18493
GO:0032727	positive regulation of interferon-alpha production	1.41E-02	5.50E-02	10.99	2/153	22/18493

GO:0042454	ribonucleoside catabolic process	1.41E-02	5.50E-02	10.99	2/153	22/18493
GO:0045663	positive regulation of myoblast differentiation	1.41E-02	5.50E-02	10.99	2/153	22/18493
GO:0071379	cellular response to prostaglandin stimulus	1.41E-02	5.50E-02	10.99	2/153	22/18493
GO:0032479	regulation of type I interferon production	1.45E-02	5.62E-02	4.28	4/153	113/18493
GO:0051153	regulation of striated muscle cell differentiation	1.45E-02	5.62E-02	4.28	4/153	113/18493
GO:0045428	regulation of nitric oxide biosynthetic process	1.47E-02	5.71E-02	5.85	3/153	62/18493
GO:0032606	type I interferon production	1.49E-02	5.77E-02	4.24	4/153	114/18493
GO:1903409	reactive oxygen species biosynthetic process	1.53E-02	5.90E-02	4.20	4/153	115/18493
GO:0010499	proteasomal ubiquitin-independent protein catabolic process	1.54E-02	5.90E-02	10.51	2/153	23/18493
GO:0071404	cellular response to low-density lipoprotein particle stimulus	1.54E-02	5.90E-02	10.51	2/153	23/18493
GO:0002637	regulation of immunoglobulin production	1.54E-02	5.90E-02	5.76	3/153	63/18493
GO:0046637	regulation of alpha-beta T cell differentiation	1.54E-02	5.90E-02	5.76	3/153	63/18493
GO:0031098	stress-activated protein kinase signaling cascade	1.55E-02	5.95E-02	2.70	7/153	313/18493
GO:1904062	regulation of cation transmembrane transport	1.58E-02	6.04E-02	2.69	7/153	314/18493
GO:0045670	regulation of osteoclast differentiation	1.60E-02	6.12E-02	5.67	3/153	64/18493
GO:0050710	negative regulation of cytokine secretion	1.60E-02	6.12E-02	5.67	3/153	64/18493
GO:0001952	regulation of cell-matrix adhesion	1.62E-02	6.20E-02	4.13	4/153	117/18493
GO:0001516	prostaglandin biosynthetic process	1.67E-02	6.29E-02	10.07	2/153	24/18493
GO:0032897	negative regulation of viral transcription	1.67E-02	6.29E-02	10.07	2/153	24/18493
GO:0033081	regulation of T cell differentiation in thymus	1.67E-02	6.29E-02	10.07	2/153	24/18493
GO:0046457	prostanoid biosynthetic process	1.67E-02	6.29E-02	10.07	2/153	24/18493
GO:0050855	regulation of B cell receptor signaling pathway	1.67E-02	6.29E-02	10.07	2/153	24/18493
GO:2000482	regulation of interleukin-8 secretion	1.67E-02	6.29E-02	10.07	2/153	24/18493
GO:0002377	immunoglobulin production	1.70E-02	6.43E-02	3.36	5/153	180/18493
GO:0002709	regulation of T cell mediated immunity	1.74E-02	6.53E-02	5.49	3/153	66/18493
GO:0010812	negative regulation of cell-substrate adhesion	1.74E-02	6.53E-02	5.49	3/153	66/18493
GO:0032677	regulation of interleukin-8 production	1.74E-02	6.53E-02	5.49	3/153	66/18493
GO:0019751	polyol metabolic process	1.77E-02	6.62E-02	4.03	4/153	120/18493

GO:0002507	tolerance induction	1.80E-02	6.71E-02	9.67	2/153	25/18493
GO:0032461	positive regulation of protein oligomerization	1.80E-02	6.71E-02	9.67	2/153	25/18493
GO:0045662	negative regulation of myoblast differentiation	1.80E-02	6.71E-02	9.67	2/153	25/18493
GO:0050858	negative regulation of antigen receptor-mediated signaling pathway	1.80E-02	6.71E-02	9.67	2/153	25/18493
GO:0071902	positive regulation of protein serine/threonine kinase activity	1.81E-02	6.74E-02	2.62	7/153	323/18493
GO:0046328	regulation of JNK cascade	1.86E-02	6.89E-02	3.28	5/153	184/18493
GO:1901652	response to peptide	1.88E-02	6.96E-02	2.26	9/153	481/18493
GO:2000377	regulation of reactive oxygen species metabolic process	1.89E-02	7.02E-02	3.27	5/153	185/18493
GO:0019933	cAMP-mediated signaling	1.93E-02	7.15E-02	3.25	5/153	186/18493
GO:0070168	negative regulation of biomineral tissue development	1.94E-02	7.17E-02	9.30	2/153	26/18493
GO:0006801	superoxide metabolic process	1.95E-02	7.21E-02	5.26	3/153	69/18493
GO:0034763	negative regulation of transmembrane transport	1.97E-02	7.24E-02	3.90	4/153	124/18493
GO:0031099	regeneration	2.02E-02	7.41E-02	3.21	5/153	188/18493
GO:0042531	positive regulation of tyrosine phosphorylation of STAT protein	2.03E-02	7.43E-02	5.18	3/153	70/18493
GO:0048662	negative regulation of smooth muscle cell proliferation	2.03E-02	7.43E-02	5.18	3/153	70/18493
GO:1904427	positive regulation of calcium ion transmembrane transport	2.03E-02	7.43E-02	5.18	3/153	70/18493
GO:0043406	positive regulation of MAP kinase activity	2.05E-02	7.51E-02	2.81	6/153	258/18493
GO:0001101	response to acid chemical	2.07E-02	7.55E-02	2.55	7/153	332/18493
GO:0002920	regulation of humoral immune response	2.07E-02	7.55E-02	3.84	4/153	126/18493
GO:0043921	modulation by host of viral transcription	2.08E-02	7.56E-02	8.95	2/153	27/18493
GO:0052472	modulation by host of symbiont transcription	2.08E-02	7.56E-02	8.95	2/153	27/18493
GO:1990776	response to angiotensin	2.08E-02	7.56E-02	8.95	2/153	27/18493
GO:1901654	response to ketone	2.10E-02	7.60E-02	3.18	5/153	190/18493
GO:0051155	positive regulation of striated muscle cell differentiation	2.11E-02	7.62E-02	5.11	3/153	71/18493
GO:0045471	response to ethanol	2.13E-02	7.68E-02	3.81	4/153	127/18493
GO:0007596	blood coagulation	2.13E-02	7.68E-02	2.53	7/153	334/18493

GO:0043405	regulation of MAP kinase activity	2.16E-02	7.78E-02	2.53	7/153	335/18493
GO:0050709	negative regulation of protein secretion	2.18E-02	7.84E-02	3.78	4/153	128/18493
GO:0009988	cell-cell recognition	2.19E-02	7.84E-02	5.04	3/153	72/18493
GO:0030278	regulation of ossification	2.23E-02	7.93E-02	3.13	5/153	193/18493
GO:0002888	positive regulation of myeloid leukocyte mediated immunity	2.23E-02	7.93E-02	8.63	2/153	28/18493
GO:0032647	regulation of interferon-alpha production	2.23E-02	7.93E-02	8.63	2/153	28/18493
GO:0052312	modulation of transcription in other organism involved in symbiotic interaction	2.23E-02	7.93E-02	8.63	2/153	28/18493
GO:0061082	myeloid leukocyte cytokine production	2.23E-02	7.93E-02	8.63	2/153	28/18493
GO:0072606	interleukin-8 secretion	2.23E-02	7.93E-02	8.63	2/153	28/18493
GO:0032273	positive regulation of protein polymerization	2.24E-02	7.93E-02	3.75	4/153	129/18493
GO:0046425	regulation of JAK-STAT cascade	2.24E-02	7.93E-02	3.75	4/153	129/18493
GO:0006809	nitric oxide biosynthetic process	2.27E-02	8.01E-02	4.97	3/153	73/18493
GO:0032637	interleukin-8 production	2.27E-02	8.01E-02	4.97	3/153	73/18493
GO:0007599	hemostasis	2.29E-02	8.08E-02	2.50	7/153	339/18493
GO:0050817	coagulation	2.32E-02	8.18E-02	2.49	7/153	340/18493
GO:0022617	extracellular matrix disassembly	2.35E-02	8.26E-02	4.90	3/153	74/18493
GO:1903531	negative regulation of secretion by cell	2.36E-02	8.30E-02	3.08	5/153	196/18493
GO:0032607	interferon-alpha production	2.39E-02	8.35E-02	8.34	2/153	29/18493
GO:0045954	positive regulation of natural killer cell mediated cytotoxicity	2.39E-02	8.35E-02	8.34	2/153	29/18493
GO:0050869	negative regulation of B cell activation	2.39E-02	8.35E-02	8.34	2/153	29/18493
GO:0070373	negative regulation of ERK1 and ERK2 cascade	2.43E-02	8.50E-02	4.83	3/153	75/18493
GO:0001773	myeloid dendritic cell activation	2.54E-02	8.80E-02	8.06	2/153	30/18493
GO:0002828	regulation of type 2 immune response	2.54E-02	8.80E-02	8.06	2/153	30/18493
GO:0010543	regulation of platelet activation	2.54E-02	8.80E-02	8.06	2/153	30/18493
GO:0032743	positive regulation of interleukin-2 production	2.54E-02	8.80E-02	8.06	2/153	30/18493
GO:0032814	regulation of natural killer cell activation	2.54E-02	8.80E-02	8.06	2/153	30/18493
GO:0038111	interleukin-7-mediated signaling pathway	2.54E-02	8.80E-02	8.06	2/153	30/18493

GO:0042590	antigen processing and presentation of exogenous peptide antigen via MHC class I	2.54E-02	8.80E-02	8.06	2/153	30/18493
GO:1902905	positive regulation of supramolecular fiber organization	2.55E-02	8.81E-02	3.02	5/153	200/18493
GO:0002718	regulation of cytokine production involved in immune response	2.60E-02	8.97E-02	4.71	3/153	77/18493
GO:0046209	nitric oxide metabolic process	2.60E-02	8.97E-02	4.71	3/153	77/18493
GO:0014065	phosphatidylinositol 3-kinase signaling	2.65E-02	9.11E-02	3.55	4/153	136/18493
GO:1904064	positive regulation of cation transmembrane transport	2.65E-02	9.11E-02	3.55	4/153	136/18493
GO:0031100	animal organ regeneration	2.69E-02	9.16E-02	4.65	3/153	78/18493
GO:0071260	cellular response to mechanical stimulus	2.69E-02	9.16E-02	4.65	3/153	78/18493
GO:0002717	positive regulation of natural killer cell mediated immunity	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0043552	positive regulation of phosphatidylinositol 3-kinase activity	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0045589	regulation of regulatory T cell differentiation	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0048873	homeostasis of number of cells within a tissue	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0055094	response to lipoprotein particle	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0098760	response to interleukin-7	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0098761	cellular response to interleukin-7	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:1902230	negative regulation of intrinsic apoptotic signaling pathway in response to DNA damage	2.70E-02	9.16E-02	7.80	2/153	31/18493
GO:0072593	reactive oxygen species metabolic process	2.74E-02	9.26E-02	2.63	6/153	276/18493
GO:0017157	regulation of exocytosis	2.75E-02	9.26E-02	2.96	5/153	204/18493
GO:0032869	cellular response to insulin stimulus	2.75E-02	9.26E-02	2.96	5/153	204/18493
GO:0050728	negative regulation of inflammatory response	2.84E-02	9.58E-02	3.48	4/153	139/18493
GO:0030851	granulocyte differentiation	2.87E-02	9.59E-02	7.55	2/153	32/18493
GO:0048841	regulation of axon extension involved in axon guidance	2.87E-02	9.59E-02	7.55	2/153	32/18493
GO:0071353	cellular response to interleukin-4	2.87E-02	9.59E-02	7.55	2/153	32/18493
GO:0042509	regulation of tyrosine phosphorylation of STAT protein	2.87E-02	9.59E-02	4.53	3/153	80/18493
GO:0050764	regulation of phagocytosis	2.87E-02	9.59E-02	4.53	3/153	80/18493
GO:2001057	reactive nitrogen species metabolic process	2.87E-02	9.59E-02	4.53	3/153	80/18493

GO:0046330	positive regulation of JNK cascade	2.91E-02	9.70E-02	3.45	4/153	140/18493
GO:0001914	regulation of T cell mediated cytotoxicity	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:0009164	nucleoside catabolic process	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:0016601	Rac protein signal transduction	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:0030947	regulation of vascular endothelial growth factor receptor signaling pathway	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:0045066	regulatory T cell differentiation	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:0071354	cellular response to interleukin-6	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:0071402	cellular response to lipoprotein particle stimulus	3.04E-02	1.00E-01	7.33	2/153	33/18493
GO:2001056	positive regulation of cysteine-type endopeptidase activity	3.11E-02	1.03E-01	3.38	4/153	143/18493
GO:0002526	acute inflammatory response	3.11E-02	1.03E-01	2.86	5/153	211/18493
GO:0007009	plasma membrane organization	3.15E-02	1.04E-01	4.37	3/153	83/18493
GO:0007260	tyrosine phosphorylation of STAT protein	3.15E-02	1.04E-01	4.37	3/153	83/18493
GO:0010922	positive regulation of phosphatase activity	3.21E-02	1.05E-01	7.11	2/153	34/18493
GO:0030224	monocyte differentiation	3.21E-02	1.05E-01	7.11	2/153	34/18493
GO:0090322	regulation of superoxide metabolic process	3.21E-02	1.05E-01	7.11	2/153	34/18493
GO:1903131	mononuclear cell differentiation	3.21E-02	1.05E-01	7.11	2/153	34/18493
GO:0008277	regulation of G protein-coupled receptor signaling pathway	3.25E-02	1.06E-01	3.33	4/153	145/18493
GO:0019935	cyclic-nucleotide-mediated signaling	3.28E-02	1.07E-01	2.82	5/153	214/18493
GO:0002262	myeloid cell homeostasis	3.32E-02	1.08E-01	3.31	4/153	146/18493
GO:0046427	positive regulation of JAK-STAT cascade	3.35E-02	1.09E-01	4.27	3/153	85/18493
GO:0048246	macrophage chemotaxis	3.39E-02	1.10E-01	6.91	2/153	35/18493
GO:0070670	response to interleukin-4	3.39E-02	1.10E-01	6.91	2/153	35/18493
GO:0090218	positive regulation of lipid kinase activity	3.39E-02	1.10E-01	6.91	2/153	35/18493
GO:0048524	positive regulation of viral process	3.45E-02	1.12E-01	4.22	3/153	86/18493
GO:0034767	positive regulation of ion transmembrane transport	3.46E-02	1.12E-01	3.27	4/153	148/18493
GO:0072330	monocarboxylic acid biosynthetic process	3.52E-02	1.13E-01	2.48	6/153	293/18493
GO:0034765	regulation of ion transmembrane transport	3.53E-02	1.13E-01	2.13	8/153	454/18493

GO:0002455	humoral immune response mediated by circulating immunoglobulin	3.54E-02	1.13E-01	3.24	4/153	149/18493
GO:0002673	regulation of acute inflammatory response	3.54E-02	1.13E-01	3.24	4/153	149/18493
GO:0061025	membrane fusion	3.54E-02	1.13E-01	3.24	4/153	149/18493
GO:0006692	prostanoid metabolic process	3.57E-02	1.14E-01	6.71	2/153	36/18493
GO:0006693	prostaglandin metabolic process	3.57E-02	1.14E-01	6.71	2/153	36/18493
GO:0042092	type 2 immune response	3.57E-02	1.14E-01	6.71	2/153	36/18493
GO:0090279	regulation of calcium ion import	3.57E-02	1.14E-01	6.71	2/153	36/18493
GO:0000187	activation of MAPK activity	3.61E-02	1.15E-01	3.22	4/153	150/18493
GO:0008360	regulation of cell shape	3.69E-02	1.17E-01	3.20	4/153	151/18493
GO:0002823	negative regulation of adaptive immune response based on somatic recombination of immune receptors built from immunoglobulin superfamily domains	3.75E-02	1.18E-01	6.53	2/153	37/18493
GO:0014912	negative regulation of smooth muscle cell migration	3.75E-02	1.18E-01	6.53	2/153	37/18493
GO:0048846	axon extension involved in axon guidance	3.75E-02	1.18E-01	6.53	2/153	37/18493
GO:0070741	response to interleukin-6	3.75E-02	1.18E-01	6.53	2/153	37/18493
GO:0071276	cellular response to cadmium ion	3.75E-02	1.18E-01	6.53	2/153	37/18493
GO:1902284	neuron projection extension involved in neuron projection guidance	3.75E-02	1.18E-01	6.53	2/153	37/18493
GO:0000302	response to reactive oxygen species	3.87E-02	1.22E-01	2.70	5/153	224/18493
GO:0048145	regulation of fibroblast proliferation	3.87E-02	1.22E-01	4.03	3/153	90/18493
GO:0002714	positive regulation of B cell mediated immunity	3.94E-02	1.24E-01	6.36	2/153	38/18493
GO:0002891	positive regulation of immunoglobulin mediated immune response	3.94E-02	1.24E-01	6.36	2/153	38/18493
GO:0030204	chondroitin sulfate metabolic process	3.94E-02	1.24E-01	6.36	2/153	38/18493
GO:0048010	vascular endothelial growth factor receptor signaling pathway	3.98E-02	1.24E-01	3.98	3/153	91/18493
GO:0048144	fibroblast proliferation	3.98E-02	1.24E-01	3.98	3/153	91/18493
GO:0090630	activation of GTPase activity	3.98E-02	1.24E-01	3.98	3/153	91/18493
GO:1901570	fatty acid derivative biosynthetic process	3.98E-02	1.24E-01	3.98	3/153	91/18493
GO:0060560	developmental growth involved in morphogenesis	4.06E-02	1.27E-01	2.66	5/153	227/18493

GO:0051896	regulation of protein kinase B signaling	4.12E-02	1.28E-01	2.65	5/153	228/18493
GO:1902229	regulation of intrinsic apoptotic signaling pathway in response to DNA damage	4.13E-02	1.28E-01	6.20	2/153	39/18493
GO:0030203	glycosaminoglycan metabolic process	4.16E-02	1.29E-01	3.08	4/153	157/18493
GO:0071375	cellular response to peptide hormone stimulus	4.26E-02	1.32E-01	2.36	6/153	307/18493
GO:1903426	regulation of reactive oxygen species biosynthetic process	4.31E-02	1.33E-01	3.86	3/153	94/18493
GO:0030225	macrophage differentiation	4.32E-02	1.33E-01	6.04	2/153	40/18493
GO:0097028	dendritic cell differentiation	4.32E-02	1.33E-01	6.04	2/153	40/18493
GO:0006644	phospholipid metabolic process	4.32E-02	1.33E-01	2.04	8/153	473/18493
GO:0022604	regulation of cell morphogenesis	4.37E-02	1.35E-01	2.04	8/153	474/18493
GO:0002367	cytokine production involved in immune response	4.43E-02	1.36E-01	3.82	3/153	95/18493
GO:0016485	protein processing	4.43E-02	1.36E-01	2.34	6/153	310/18493
GO:0035821	modification of morphology or physiology of other organism	4.49E-02	1.38E-01	3.00	4/153	161/18493
GO:1990138	neuron projection extension	4.49E-02	1.38E-01	3.00	4/153	161/18493
GO:0030866	cortical actin cytoskeleton organization	4.52E-02	1.38E-01	5.90	2/153	41/18493
GO:0010771	negative regulation of cell morphogenesis involved in differentiation	4.54E-02	1.39E-01	3.78	3/153	96/18493
GO:0043902	positive regulation of multi-organism process	4.57E-02	1.40E-01	2.98	4/153	162/18493
GO:0032872	regulation of stress-activated MAPK cascade	4.59E-02	1.40E-01	2.57	5/153	235/18493
GO:0001666	response to hypoxia	4.66E-02	1.42E-01	2.31	6/153	314/18493
GO:0001953	negative regulation of cell-matrix adhesion	4.72E-02	1.43E-01	5.76	2/153	42/18493
GO:0002437	inflammatory response to antigenic stimulus	4.72E-02	1.43E-01	5.76	2/153	42/18493
GO:0032459	regulation of protein oligomerization	4.72E-02	1.43E-01	5.76	2/153	42/18493
GO:0043124	negative regulation of I-kappaB kinase/NF-kappaB signaling	4.72E-02	1.43E-01	5.76	2/153	42/18493
GO:0045581	negative regulation of T cell differentiation	4.72E-02	1.43E-01	5.76	2/153	42/18493
GO:0070302	regulation of stress-activated protein kinase signaling cascade	4.73E-02	1.43E-01	2.55	5/153	237/18493
GO:0048015	phosphatidylinositol-mediated signaling	4.75E-02	1.43E-01	2.95	4/153	164/18493
GO:1903829	positive regulation of cellular protein localization	4.91E-02	1.47E-01	2.28	6/153	318/18493

GO:2000045	regulation of G1/S transition of mitotic cell cycle	4.92E-02	1.47E-01	2.91	4/153	166/18493
GO:0002534	cytokine production involved in inflammatory response	4.92E-02	1.47E-01	5.62	2/153	43/18493
GO:0042771	intrinsic apoptotic signaling pathway in response to DNA damage by p53 class mediator	4.92E-02	1.47E-01	5.62	2/153	43/18493
GO:0050654	chondroitin sulfate proteoglycan metabolic process	4.92E-02	1.47E-01	5.62	2/153	43/18493
GO:1900087	positive regulation of G1/S transition of mitotic cell cycle	4.92E-02	1.47E-01	5.62	2/153	43/18493
GO:1901658	glycosyl compound catabolic process	4.92E-02	1.47E-01	5.62	2/153	43/18493
GO:1902667	regulation of axon guidance	4.92E-02	1.47E-01	5.62	2/153	43/18493
GO:0042742	defense response to bacterium	4.97E-02	1.48E-01	2.27	6/153	319/18493
GO:0006022	aminoglycan metabolic process	5.01E-02	1.49E-01	2.90	4/153	167/18493
GO:0048017	inositol lipid-mediated signaling	5.01E-02	1.49E-01	2.90	4/153	167/18493
GO:0050848	regulation of calcium-mediated signaling	5.02E-02	1.49E-01	3.63	3/153	100/18493
GO:0120034	positive regulation of plasma membrane bounded cell projection assembly	5.02E-02	1.49E-01	3.63	3/153	100/18493
GO:0046394	carboxylic acid biosynthetic process	4.09E-03	1.25E-01	8.98	3/15	412/18493
GO:0016053	organic acid biosynthetic process	4.12E-03	1.25E-01	8.96	3/15	413/18493
GO:0046718	viral entry into host cell	4.22E-03	1.25E-01	20.38	2/15	121/18493
GO:0090101	negative regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	4.35E-03	1.25E-01	20.05	2/15	123/18493
GO:0044282	small molecule catabolic process	4.64E-03	1.25E-01	8.58	3/15	431/18493
GO:0030260	entry into host cell	5.07E-03	1.25E-01	18.54	2/15	133/18493
GO:0034620	cellular response to unfolded protein	5.07E-03	1.25E-01	18.54	2/15	133/18493
GO:0044409	entry into host	5.07E-03	1.25E-01	18.54	2/15	133/18493
GO:0051806	entry into cell of other organism involved in symbiotic interaction	5.07E-03	1.25E-01	18.54	2/15	133/18493
GO:0051828	entry into other organism involved in symbiotic interaction	5.07E-03	1.25E-01	18.54	2/15	133/18493
GO:0009408	response to heat	6.00E-03	1.25E-01	17.01	2/15	145/18493
GO:0051092	positive regulation of NF-kappaB transcription factor activity	6.08E-03	1.25E-01	16.89	2/15	146/18493
GO:0035967	cellular response to topologically incorrect protein	6.49E-03	1.25E-01	16.33	2/15	151/18493

GO:0090288	negative regulation of cellular response to growth factor stimulus	7.25E-03	1.25E-01	15.41	2/15	160/18493
GO:0006986	response to unfolded protein	8.06E-03	1.25E-01	14.59	2/15	169/18493
GO:0042989	sequestering of actin monomers	8.08E-03	1.25E-01	123.29	1/15	10/18493
GO:0002003	angiotensin maturation	8.89E-03	1.25E-01	112.08	1/15	11/18493
GO:0010172	embryonic body morphogenesis	8.89E-03	1.25E-01	112.08	1/15	11/18493
GO:0016322	neuron remodeling	8.89E-03	1.25E-01	112.08	1/15	11/18493
GO:0018065	protein-cofactor linkage	8.89E-03	1.25E-01	112.08	1/15	11/18493
GO:0033632	regulation of cell-cell adhesion mediated by integrin	8.89E-03	1.25E-01	112.08	1/15	11/18493
GO:0090084	negative regulation of inclusion body assembly	8.89E-03	1.25E-01	112.08	1/15	11/18493
GO:0002002	regulation of angiotensin levels in blood	9.69E-03	1.25E-01	102.74	1/15	12/18493
GO:0035641	locomotory exploration behavior	9.69E-03	1.25E-01	102.74	1/15	12/18493
GO:0097201	negative regulation of transcription from RNA polymerase II promoter in response to stress	9.69E-03	1.25E-01	102.74	1/15	12/18493
GO:0035966	response to topologically incorrect protein	1.00E-02	1.25E-01	13.05	2/15	189/18493
GO:0006694	steroid biosynthetic process	1.04E-02	1.25E-01	12.78	2/15	193/18493
GO:0009086	methionine biosynthetic process	1.05E-02	1.25E-01	94.84	1/15	13/18493
GO:0032530	regulation of microvillus organization	1.05E-02	1.25E-01	94.84	1/15	13/18493
GO:0032536	regulation of cell projection size	1.05E-02	1.25E-01	94.84	1/15	13/18493
GO:0070431	nucleotide-binding oligomerization domain containing 2 signaling pathway	1.05E-02	1.25E-01	94.84	1/15	13/18493
GO:0071872	cellular response to epinephrine stimulus	1.05E-02	1.25E-01	94.84	1/15	13/18493
GO:1903054	negative regulation of extracellular matrix organization	1.05E-02	1.25E-01	94.84	1/15	13/18493
GO:0007626	locomotory behavior	1.05E-02	1.25E-01	12.71	2/15	194/18493
GO:0000098	sulfur amino acid catabolic process	1.13E-02	1.25E-01	88.06	1/15	14/18493
GO:0050667	homocysteine metabolic process	1.13E-02	1.25E-01	88.06	1/15	14/18493
GO:0090399	replicative senescence	1.13E-02	1.25E-01	88.06	1/15	14/18493
GO:0099558	maintenance of synapse structure	1.13E-02	1.25E-01	88.06	1/15	14/18493
GO:1901386	negative regulation of voltage-gated calcium channel activity	1.13E-02	1.25E-01	88.06	1/15	14/18493

GO:0009266	response to temperature stimulus	1.20E-02	1.25E-01	11.85	2/15	208/18493
GO:0032271	regulation of protein polymerization	1.20E-02	1.25E-01	11.85	2/15	208/18493
GO:0010715	regulation of extracellular matrix disassembly	1.21E-02	1.25E-01	82.19	1/15	15/18493
GO:0033540	fatty acid beta-oxidation using acyl-CoA oxidase	1.21E-02	1.25E-01	82.19	1/15	15/18493
GO:0033631	cell-cell adhesion mediated by integrin	1.21E-02	1.25E-01	82.19	1/15	15/18493
GO:0051701	interaction with host	1.21E-02	1.25E-01	11.80	2/15	209/18493
GO:0071871	response to epinephrine	1.29E-02	1.25E-01	77.05	1/15	16/18493
GO:0090083	regulation of inclusion body assembly	1.29E-02	1.25E-01	77.05	1/15	16/18493
GO:0006457	protein folding	1.31E-02	1.25E-01	11.31	2/15	218/18493
GO:0042445	hormone metabolic process	1.31E-02	1.25E-01	11.31	2/15	218/18493
GO:2001234	negative regulation of apoptotic signaling pathway	1.36E-02	1.25E-01	11.11	2/15	222/18493
GO:0006555	methionine metabolic process	1.37E-02	1.25E-01	72.52	1/15	17/18493
GO:0006704	glucocorticoid biosynthetic process	1.45E-02	1.25E-01	68.49	1/15	18/18493
GO:0010224	response to UV-B	1.45E-02	1.25E-01	68.49	1/15	18/18493
GO:1905065	positive regulation of vascular smooth muscle cell differentiation	1.45E-02	1.25E-01	68.49	1/15	18/18493
GO:0090092	regulation of transmembrane receptor protein serine/threonine kinase signaling pathway	1.51E-02	1.25E-01	10.49	2/15	235/18493
GO:0001991	regulation of systemic arterial blood pressure by circulatory renin-angiotensin	1.53E-02	1.25E-01	64.89	1/15	19/18493
GO:0006534	cysteine metabolic process	1.53E-02	1.25E-01	64.89	1/15	19/18493
GO:0051016	barbed-end actin filament capping	1.53E-02	1.25E-01	64.89	1/15	19/18493
GO:1901673	regulation of mitotic spindle assembly	1.53E-02	1.25E-01	64.89	1/15	19/18493
GO:1902236	negative regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	1.53E-02	1.25E-01	64.89	1/15	19/18493
GO:0051131	chaperone-mediated protein complex assembly	1.61E-02	1.25E-01	61.64	1/15	20/18493
GO:0097242	amyloid-beta clearance	1.61E-02	1.25E-01	61.64	1/15	20/18493
GO:0000097	sulfur amino acid biosynthetic process	1.69E-02	1.25E-01	58.71	1/15	21/18493
GO:0009070	serine family amino acid biosynthetic process	1.69E-02	1.25E-01	58.71	1/15	21/18493
GO:0046034	ATP metabolic process	1.70E-02	1.25E-01	9.86	2/15	250/18493

GO:0051091	positive regulation of DNA-binding transcription factor activity	1.77E-02	1.25E-01	9.67	2/15	255/18493
GO:0032069	regulation of nuclease activity	1.77E-02	1.25E-01	56.04	1/15	22/18493
GO:0070841	inclusion body assembly	1.77E-02	1.25E-01	56.04	1/15	22/18493
GO:0009067	aspartate family amino acid biosynthetic process	1.85E-02	1.25E-01	53.60	1/15	23/18493
GO:0010226	response to lithium ion	1.85E-02	1.25E-01	53.60	1/15	23/18493
GO:0034976	response to endoplasmic reticulum stress	1.89E-02	1.25E-01	9.34	2/15	264/18493
GO:0016054	organic acid catabolic process	1.90E-02	1.25E-01	9.30	2/15	265/18493
GO:0046395	carboxylic acid catabolic process	1.90E-02	1.25E-01	9.30	2/15	265/18493
GO:0032528	microvillus organization	1.93E-02	1.25E-01	51.37	1/15	24/18493
GO:0035640	exploration behavior	1.93E-02	1.25E-01	51.37	1/15	24/18493
GO:1900120	regulation of receptor binding	1.93E-02	1.25E-01	51.37	1/15	24/18493
GO:0006735	NADH regeneration	2.01E-02	1.25E-01	49.31	1/15	25/18493
GO:0008211	glucocorticoid metabolic process	2.01E-02	1.25E-01	49.31	1/15	25/18493
GO:0009404	toxin metabolic process	2.01E-02	1.25E-01	49.31	1/15	25/18493
GO:0031116	positive regulation of microtubule polymerization	2.01E-02	1.25E-01	49.31	1/15	25/18493
GO:0061621	canonical glycolysis	2.01E-02	1.25E-01	49.31	1/15	25/18493
GO:0061718	glucose catabolic process to pyruvate	2.01E-02	1.25E-01	49.31	1/15	25/18493
GO:0051258	protein polymerization	2.04E-02	1.25E-01	8.97	2/15	275/18493
GO:0003081	regulation of systemic arterial blood pressure by renin-angiotensin	2.09E-02	1.25E-01	47.42	1/15	26/18493
GO:0042026	protein refolding	2.09E-02	1.25E-01	47.42	1/15	26/18493
GO:0051152	positive regulation of smooth muscle cell differentiation	2.09E-02	1.25E-01	47.42	1/15	26/18493
GO:0061615	glycolytic process through fructose-6-phosphate	2.09E-02	1.25E-01	47.42	1/15	26/18493
GO:0061620	glycolytic process through glucose-6-phosphate	2.09E-02	1.25E-01	47.42	1/15	26/18493
GO:0090169	regulation of spindle assembly	2.09E-02	1.25E-01	47.42	1/15	26/18493
GO:0009205	purine ribonucleoside triphosphate metabolic process	2.11E-02	1.25E-01	8.81	2/15	280/18493
GO:0090287	regulation of cellular response to growth factor stimulus	2.13E-02	1.25E-01	8.74	2/15	282/18493
GO:0044550	secondary metabolite biosynthetic process	2.17E-02	1.25E-01	45.66	1/15	27/18493
GO:0009167	purine ribonucleoside monophosphate metabolic process	2.19E-02	1.25E-01	8.62	2/15	286/18493

GO:0009199	ribonucleoside triphosphate metabolic process	2.19E-02	1.25E-01	8.62	2/15	286/18493
GO:0009126	purine nucleoside monophosphate metabolic process	2.21E-02	1.25E-01	8.59	2/15	287/18493
GO:0009144	purine nucleoside triphosphate metabolic process	2.21E-02	1.25E-01	8.59	2/15	287/18493
GO:0019058	viral life cycle	2.23E-02	1.25E-01	8.53	2/15	289/18493
GO:0007020	microtubule nucleation	2.25E-02	1.25E-01	44.03	1/15	28/18493
GO:0072330	monocarboxylic acid biosynthetic process	2.29E-02	1.25E-01	8.42	2/15	293/18493
GO:0031112	positive regulation of microtubule polymerization or depolymerization	2.33E-02	1.25E-01	42.51	1/15	29/18493
GO:0009161	ribonucleoside monophosphate metabolic process	2.40E-02	1.25E-01	8.22	2/15	300/18493
GO:1902235	regulation of endoplasmic reticulum stress-induced intrinsic apoptotic signaling pathway	2.41E-02	1.25E-01	41.10	1/15	30/18493
GO:0045648	positive regulation of erythrocyte differentiation	2.49E-02	1.25E-01	39.77	1/15	31/18493
GO:0051085	chaperone cofactor-dependent protein refolding	2.49E-02	1.25E-01	39.77	1/15	31/18493
GO:1905063	regulation of vascular smooth muscle cell differentiation	2.49E-02	1.25E-01	39.77	1/15	31/18493
GO:0009141	nucleoside triphosphate metabolic process	2.50E-02	1.25E-01	8.03	2/15	307/18493
GO:0006007	glucose catabolic process	2.57E-02	1.25E-01	38.53	1/15	32/18493
GO:0016486	peptide hormone processing	2.57E-02	1.25E-01	38.53	1/15	32/18493
GO:0001666	response to hypoxia	2.61E-02	1.25E-01	7.85	2/15	314/18493
GO:0033198	response to ATP	2.64E-02	1.25E-01	37.36	1/15	33/18493
GO:0008202	steroid metabolic process	2.67E-02	1.25E-01	7.75	2/15	318/18493
GO:0071868	cellular response to monoamine stimulus	2.72E-02	1.25E-01	36.26	1/15	34/18493
GO:0071870	cellular response to catecholamine stimulus	2.72E-02	1.25E-01	36.26	1/15	34/18493
GO:0009123	nucleoside monophosphate metabolic process	2.73E-02	1.25E-01	7.66	2/15	322/18493
GO:0036293	response to decreased oxygen levels	2.78E-02	1.25E-01	7.59	2/15	325/18493
GO:0070423	nucleotide-binding oligomerization domain containing signaling pathway	2.80E-02	1.25E-01	35.22	1/15	35/18493
GO:1901020	negative regulation of calcium ion transmembrane transporter activity	2.80E-02	1.25E-01	35.22	1/15	35/18493
GO:1901099	negative regulation of signal transduction in absence of ligand	2.80E-02	1.25E-01	35.22	1/15	35/18493

GO:2001240	negative regulation of extrinsic apoptotic signaling pathway in absence of ligand	2.80E-02	1.25E-01	35.22	1/15	35/18493
GO:0001662	behavioral fear response	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0002209	behavioral defense response	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0006699	bile acid biosynthetic process	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0010591	regulation of lamellipodium assembly	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0033120	positive regulation of RNA splicing	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0035872	nucleotide-binding domain, leucine rich repeat containing receptor signaling pathway	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0051084	'de novo' posttranslational protein folding	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0060236	regulation of mitotic spindle organization	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:1900115	extracellular regulation of signal transduction	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:1900116	extracellular negative regulation of signal transduction	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:1901385	regulation of voltage-gated calcium channel activity	2.88E-02	1.25E-01	34.25	1/15	36/18493
GO:0050435	amyloid-beta metabolic process	2.96E-02	1.25E-01	33.32	1/15	37/18493
GO:0051693	actin filament capping	2.96E-02	1.25E-01	33.32	1/15	37/18493
GO:0007178	transmembrane receptor protein serine/threonine kinase signaling pathway	3.02E-02	1.25E-01	7.25	2/15	340/18493
GO:0006734	NADH metabolic process	3.04E-02	1.25E-01	32.44	1/15	38/18493
GO:0042596	fear response	3.04E-02	1.25E-01	32.44	1/15	38/18493
GO:0071867	response to monoamine	3.04E-02	1.25E-01	32.44	1/15	38/18493
GO:0071869	response to catecholamine	3.04E-02	1.25E-01	32.44	1/15	38/18493
GO:1902903	regulation of supramolecular fiber organization	3.07E-02	1.25E-01	7.19	2/15	343/18493
GO:1903053	regulation of extracellular matrix organization	3.12E-02	1.25E-01	31.61	1/15	39/18493
GO:0070482	response to oxygen levels	3.17E-02	1.25E-01	7.07	2/15	349/18493
GO:0001990	regulation of systemic arterial blood pressure by hormone	3.20E-02	1.25E-01	30.82	1/15	40/18493
GO:0006458	'de novo' protein folding	3.20E-02	1.25E-01	30.82	1/15	40/18493
GO:0030835	negative regulation of actin filament depolymerization	3.20E-02	1.25E-01	30.82	1/15	40/18493
GO:0090224	regulation of spindle organization	3.20E-02	1.25E-01	30.82	1/15	40/18493

GO:1903170	negative regulation of calcium ion transmembrane transport	3.20E-02	1.25E-01	30.82	1/15	40/18493
GO:0035886	vascular smooth muscle cell differentiation	3.28E-02	1.26E-01	30.07	1/15	41/18493
GO:1901028	regulation of mitochondrial outer membrane permeabilization involved in apoptotic signaling pathway	3.28E-02	1.26E-01	30.07	1/15	41/18493
GO:0042551	neuron maturation	3.35E-02	1.27E-01	29.35	1/15	42/18493
GO:0007212	dopamine receptor signaling pathway	3.43E-02	1.27E-01	28.67	1/15	43/18493
GO:0010613	positive regulation of cardiac muscle hypertrophy	3.43E-02	1.27E-01	28.67	1/15	43/18493
GO:0014742	positive regulation of muscle hypertrophy	3.43E-02	1.27E-01	28.67	1/15	43/18493
GO:0031113	regulation of microtubule polymerization	3.43E-02	1.27E-01	28.67	1/15	43/18493
GO:1903573	negative regulation of response to endoplasmic reticulum stress	3.43E-02	1.27E-01	28.67	1/15	43/18493
GO:0032535	regulation of cellular component size	3.48E-02	1.27E-01	6.72	2/15	367/18493
GO:0000096	sulfur amino acid metabolic process	3.51E-02	1.27E-01	28.02	1/15	44/18493
GO:0033628	regulation of cell adhesion mediated by integrin	3.51E-02	1.27E-01	28.02	1/15	44/18493
GO:0009069	serine family amino acid metabolic process	3.59E-02	1.28E-01	27.40	1/15	45/18493
GO:1900034	regulation of cellular response to heat	3.59E-02	1.28E-01	27.40	1/15	45/18493
GO:0001961	positive regulation of cytokine-mediated signaling pathway	3.67E-02	1.28E-01	26.80	1/15	46/18493
GO:0008206	bile acid metabolic process	3.67E-02	1.28E-01	26.80	1/15	46/18493
GO:0032757	positive regulation of interleukin-8 production	3.67E-02	1.28E-01	26.80	1/15	46/18493
GO:2001239	regulation of extrinsic apoptotic signaling pathway in absence of ligand	3.67E-02	1.28E-01	26.80	1/15	46/18493
GO:0045646	regulation of erythrocyte differentiation	3.75E-02	1.30E-01	26.23	1/15	47/18493
GO:0010639	negative regulation of organelle organization	3.78E-02	1.30E-01	6.42	2/15	384/18493
GO:1902743	regulation of lamellipodium organization	3.82E-02	1.31E-01	25.68	1/15	48/18493
GO:0003044	regulation of systemic arterial blood pressure mediated by a chemical signal	3.90E-02	1.32E-01	25.16	1/15	49/18493
GO:2001233	regulation of apoptotic signaling pathway	3.90E-02	1.32E-01	6.31	2/15	391/18493
GO:0010171	body morphogenesis	3.98E-02	1.33E-01	24.66	1/15	50/18493
GO:0030834	regulation of actin filament depolymerization	3.98E-02	1.33E-01	24.66	1/15	50/18493

GO:0009066	aspartate family amino acid metabolic process	4.06E-02	1.33E-01	24.17	1/15	51/18493
GO:0030514	negative regulation of BMP signaling pathway	4.06E-02	1.33E-01	24.17	1/15	51/18493
GO:0097345	mitochondrial outer membrane permeabilization	4.06E-02	1.33E-01	24.17	1/15	51/18493
GO:2001258	negative regulation of cation channel activity	4.06E-02	1.33E-01	24.17	1/15	51/18493
GO:0051150	regulation of smooth muscle cell differentiation	4.14E-02	1.33E-01	23.71	1/15	52/18493
GO:0060760	positive regulation of response to cytokine stimulus	4.14E-02	1.33E-01	23.71	1/15	52/18493
GO:0009435	NAD biosynthetic process	4.22E-02	1.33E-01	23.26	1/15	53/18493
GO:0010823	negative regulation of mitochondrion organization	4.22E-02	1.33E-01	23.26	1/15	53/18493
GO:0030042	actin filament depolymerization	4.22E-02	1.33E-01	23.26	1/15	53/18493
GO:0043954	cellular component maintenance	4.22E-02	1.33E-01	23.26	1/15	53/18493
GO:0019320	hexose catabolic process	4.29E-02	1.33E-01	22.83	1/15	54/18493
GO:0031295	T cell costimulation	4.29E-02	1.33E-01	22.83	1/15	54/18493
GO:0051090	regulation of DNA-binding transcription factor activity	4.29E-02	1.33E-01	5.98	2/15	412/18493
GO:0031294	lymphocyte costimulation	4.37E-02	1.35E-01	22.42	1/15	55/18493
GO:0044273	sulfur compound catabolic process	4.45E-02	1.37E-01	22.02	1/15	56/18493
GO:0030837	negative regulation of actin filament polymerization	4.53E-02	1.38E-01	21.63	1/15	57/18493
GO:1902110	positive regulation of mitochondrial membrane permeability involved in apoptotic process	4.53E-02	1.38E-01	21.63	1/15	57/18493
GO:0010803	regulation of tumor necrosis factor-mediated signaling pathway	4.68E-02	1.40E-01	20.90	1/15	59/18493
GO:0070059	intrinsic apoptotic signaling pathway in response to endoplasmic reticulum stress	4.68E-02	1.40E-01	20.90	1/15	59/18493
GO:1902686	mitochondrial outer membrane permeabilization involved in programmed cell death	4.68E-02	1.40E-01	20.90	1/15	59/18493
GO:0002753	cytoplasmic pattern recognition receptor signaling pathway	4.76E-02	1.40E-01	20.55	1/15	60/18493
GO:0061077	chaperone-mediated protein folding	4.76E-02	1.40E-01	20.55	1/15	60/18493
GO:0090307	mitotic spindle assembly	4.76E-02	1.40E-01	20.55	1/15	60/18493
GO:0035794	positive regulation of mitochondrial membrane permeability	4.84E-02	1.42E-01	20.21	1/15	61/18493
GO:0019748	secondary metabolic process	4.91E-02	1.43E-01	19.88	1/15	62/18493

GO:1902108	regulation of mitochondrial membrane permeability involved in apoptotic process	4.99E-02	1.44E-01	19.57	1/15	63/18493
GO:1905710	positive regulation of membrane permeability	4.99E-02	1.44E-01	19.57	1/15	63/18493
GO:0043254	regulation of protein complex assembly	5.05E-02	1.44E-01	5.47	2/15	451/18493
GO:0046365	monosaccharide catabolic process	5.07E-02	1.44E-01	19.26	1/15	64/18493
GO:1901880	negative regulation of protein depolymerization	5.07E-02	1.44E-01	19.26	1/15	64/18493
GO:0033627	cell adhesion mediated by integrin	5.15E-02	1.44E-01	18.97	1/15	65/18493
GO:0051926	negative regulation of calcium ion transport	5.15E-02	1.44E-01	18.97	1/15	65/18493
GO:0032677	regulation of interleukin-8 production	5.22E-02	1.44E-01	18.68	1/15	66/18493
GO:0030032	lamellipodium assembly	5.30E-02	1.44E-01	18.40	1/15	67/18493
GO:0006625	protein targeting to peroxisome	5.38E-02	1.44E-01	18.13	1/15	68/18493
GO:0072662	protein localization to peroxisome	5.38E-02	1.44E-01	18.13	1/15	68/18493
GO:0072663	establishment of protein localization to peroxisome	5.38E-02	1.44E-01	18.13	1/15	68/18493
GO:1901607	alpha-amino acid biosynthetic process	5.38E-02	1.44E-01	18.13	1/15	68/18493
GO:0043574	peroxisomal transport	5.45E-02	1.44E-01	17.87	1/15	69/18493
GO:0032272	negative regulation of protein polymerization	5.53E-02	1.44E-01	17.61	1/15	70/18493
GO:1901264	carbohydrate derivative transport	5.53E-02	1.44E-01	17.61	1/15	70/18493
GO:0019674	NAD metabolic process	5.61E-02	1.44E-01	17.36	1/15	71/18493
GO:0031110	regulation of microtubule polymerization or depolymerization	5.61E-02	1.44E-01	17.36	1/15	71/18493
GO:0038034	signal transduction in absence of ligand	5.61E-02	1.44E-01	17.36	1/15	71/18493
GO:0043242	negative regulation of protein complex disassembly	5.61E-02	1.44E-01	17.36	1/15	71/18493
GO:0046785	microtubule polymerization	5.61E-02	1.44E-01	17.36	1/15	71/18493
GO:0097192	extrinsic apoptotic signaling pathway in absence of ligand	5.61E-02	1.44E-01	17.36	1/15	71/18493
GO:0006635	fatty acid beta-oxidation	5.69E-02	1.44E-01	17.12	1/15	72/18493
GO:0033555	multicellular organismal response to stress	5.69E-02	1.44E-01	17.12	1/15	72/18493
GO:0043312	neutrophil degranulation	5.75E-02	1.44E-01	5.08	2/15	485/18493
GO:0031397	negative regulation of protein ubiquitination	5.76E-02	1.44E-01	16.89	1/15	73/18493
GO:0032637	interleukin-8 production	5.76E-02	1.44E-01	16.89	1/15	73/18493
GO:0046902	regulation of mitochondrial membrane permeability	5.76E-02	1.44E-01	16.89	1/15	73/18493

GO:0002283	neutrophil activation involved in immune response	5.82E-02	1.44E-01	5.05	2/15	488/18493
GO:0009150	purine ribonucleotide metabolic process	5.82E-02	1.44E-01	5.05	2/15	488/18493
GO:0006096	glycolytic process	5.84E-02	1.44E-01	16.66	1/15	74/18493
GO:0010611	regulation of cardiac muscle hypertrophy	5.84E-02	1.44E-01	16.66	1/15	74/18493
GO:0022617	extracellular matrix disassembly	5.84E-02	1.44E-01	16.66	1/15	74/18493
GO:0032507	maintenance of protein location in cell	5.84E-02	1.44E-01	16.66	1/15	74/18493
GO:0006757	ATP generation from ADP	5.92E-02	1.44E-01	16.44	1/15	75/18493
GO:0043618	regulation of transcription from RNA polymerase II promoter in response to stress	5.92E-02	1.44E-01	16.44	1/15	75/18493
GO:0051051	negative regulation of transport	5.97E-02	1.44E-01	4.98	2/15	495/18493
GO:0014743	regulation of muscle hypertrophy	5.99E-02	1.44E-01	16.22	1/15	76/18493
GO:0051145	smooth muscle cell differentiation	5.99E-02	1.44E-01	16.22	1/15	76/18493
GO:0090066	regulation of anatomical structure size	6.01E-02	1.44E-01	4.96	2/15	497/18493
GO:0042119	neutrophil activation	6.03E-02	1.44E-01	4.95	2/15	498/18493
GO:0002446	neutrophil mediated immunity	6.05E-02	1.44E-01	4.94	2/15	499/18493
GO:0032413	negative regulation of ion transmembrane transporter activity	6.07E-02	1.44E-01	16.01	1/15	77/18493
GO:0034644	cellular response to UV	6.15E-02	1.44E-01	15.81	1/15	78/18493
GO:0042866	pyruvate biosynthetic process	6.15E-02	1.44E-01	15.81	1/15	78/18493
GO:0051289	protein homotetramerization	6.15E-02	1.44E-01	15.81	1/15	78/18493
GO:1905897	regulation of response to endoplasmic reticulum stress	6.15E-02	1.44E-01	15.81	1/15	78/18493
GO:0030512	negative regulation of transforming growth factor beta receptor signaling pathway	6.22E-02	1.45E-01	15.61	1/15	79/18493
GO:1901879	regulation of protein depolymerization	6.22E-02	1.45E-01	15.61	1/15	79/18493
GO:0007031	peroxisome organization	6.37E-02	1.45E-01	15.22	1/15	81/18493
GO:0032436	positive regulation of proteasomal ubiquitin-dependent protein catabolic process	6.37E-02	1.45E-01	15.22	1/15	81/18493
GO:0043620	regulation of DNA-templated transcription in response to stress	6.37E-02	1.45E-01	15.22	1/15	81/18493
GO:0090559	regulation of membrane permeability	6.37E-02	1.45E-01	15.22	1/15	81/18493

GO:1903845	negative regulation of cellular response to transforming growth factor beta stimulus	6.37E-02	1.45E-01	15.22	1/15	81/18493
GO:1903321	negative regulation of protein modification by small protein conjugation or removal	6.53E-02	1.47E-01	14.85	1/15	83/18493
GO:0042446	hormone biosynthetic process	6.60E-02	1.47E-01	14.68	1/15	84/18493
GO:0046031	ADP metabolic process	6.60E-02	1.47E-01	14.68	1/15	84/18493
GO:0050886	endocrine process	6.60E-02	1.47E-01	14.68	1/15	84/18493
GO:0097581	lamellipodium organization	6.60E-02	1.47E-01	14.68	1/15	84/18493
GO:0008652	cellular amino acid biosynthetic process	6.68E-02	1.49E-01	14.50	1/15	85/18493
GO:1901019	regulation of calcium ion transmembrane transporter activity	6.76E-02	1.50E-01	14.34	1/15	86/18493

Table S5. Logistic regression results measuring association between *PVRIG* groups and functional gene sets

Variables			Total (N)	PVRIG-High (n)	Statistic	p-value	log(OR) (CI)	OR
Bindea-T_cells			602	301	11.56	6.73E-31	1.68 (1.4-1.97)	5.35
Bindea-B_cells			602	301	11.01	3.39E-28	1.48 (1.23-1.76)	4.41
Bindea-Cytotoxic_cells			602	301	10.92	8.86E-28	1.5 (1.24-1.78)	4.48
Bindea-Th1_cells			602	301	9.66	4.27E-22	1.14 (0.92-1.38)	3.13
Bindea-Tgd			602	301	9.58	9.56E-22	1.07 (0.86-1.29)	2.91
Bindea-aDC			602	301	8.98	2.79E-19	1.01 (0.79-1.23)	2.74
Bindea-Tem			602	301	8.29	1.18E-16	0.85 (0.66-1.06)	2.34
Bindea-TFH			602	301	8.2	2.43E-16	0.86 (0.66-1.07)	2.37
Bindea-NK_CD56dim_cells			602	301	7.79	6.82E-15	0.8 (0.6-1.0)	2.22
Bindea-NK_cells			602	301	7.51	5.72E-14	0.73 (0.54-0.92)	2.07
Bindea-CD8_T_cells			602	301	7.45	9.13E-14	0.73 (0.54-0.92)	2.07
Bindea-iDC			602	301	7.36	1.86E-13	0.7 (0.52-0.89)	2.01
Bindea-Macrophages			602	301	6.92	4.48E-12	0.66 (0.48-0.85)	1.93
Bindea-NK_CD56bright_cells			602	301	6.59	4.44E-11	0.62 (0.44-0.8)	1.85
Bindea-Tcm			602	301	6.54	6.34E-11	0.61 (0.43-0.79)	1.83
Bindea-DC			602	301	6.44	1.23E-10	0.59 (0.41-0.77)	1.8
Bindea-Neutrophils			602	301	6.23	4.75E-10	0.57 (0.4-0.76)	1.77
Bindea-T_helper_cells			602	301	6.2	5.56E-10	0.57 (0.39-0.75)	1.76
Bindea-Th2_cells			602	301	5.51	3.63E-08	0.49 (0.32-0.66)	1.62
Bindea-Eosinophils			602	301	4.75	2.01E-06	0.41 (0.25-0.59)	1.51
Bindea-Mast_cells			602	301	4.58	4.72E-06	0.4 (0.23-0.57)	1.49
Bindea-Treg			602	301	4.19	2.76E-05	0.37 (0.2-0.54)	1.44
Bindea-pDC			602	301	4.11	4.03E-05	0.35 (0.19-0.53)	1.42
Bindea-Th17_cells			602	301	0.51	6.13E-01	0.04 (-0.12-0.2)	1.04
TILs-Lymphoids			602	301	11.71	1.09E-31	2.19 (1.84-2.58)	8.97
TILs-TIL_score			602	301	11.52	1.01E-30	1.81 (1.52-2.14)	6.13
TILs-Myeloids			602	301	9.09	1.02E-19	1.01 (0.8-1.24)	2.75
TILs-Stroma			602	301	4.81	1.50E-06	0.44 (0.26-0.62)	1.55
TILs-Cancer			602	301	0.15	8.82E-01	0.01 (-0.15-0.17)	1.01
ICR			602	301	10.7	9.80E-27	1.62 (1.34-1.93)	5.05
Ayers-TIS			602	301	10.64	1.92E-26	1.5 (1.23-1.79)	4.47
Coppola-TLS			602	301	10.47	1.15E-25	1.27 (1.04-1.52)	3.57
Rooney-Cyto_act			602	301	10.29	7.66E-25	1.44 (1.18-1.72)	4.22
APMS_score			602	301	4.7	2.56E-06	0.41 (0.24-0.58)	1.51
Kieffer - CAF-S1			602	301	7.07	1.54E-12	0.67 (0.49-0.86)	1.96
Givel - CAF-S4			602	301	6.09	1.16E-09	0.6 (0.41-0.8)	1.82
Biffi - iCAF			602	301	5.34	9.11E-08	0.48 (0.31-0.66)	1.61
Biffi - myCAF			602	301	5.25	1.48E-07	0.46 (0.29-0.64)	1.59
CAF-S1	iCAF myCAF	Kieffer - wound-myCAF	602	301	6.05	1.42E-09	0.55 (0.38-0.73)	1.74
		Kieffer - ecm-myCAF	602	301	5.64	1.71E-08	0.51 (0.34-0.69)	1.66
		Kieffer - TGFβ-myCAF	602	301	5.54	3.00E-08	0.5 (0.33-0.68)	1.65
		Kieffer - IFNγ-iCAF	602	301	9.39	6.26E-21	1.01 (0.81-1.23)	2.75
		Kieffer - IL-iCAF	602	301	7.8	6.27E-15	0.78 (0.59-0.98)	2.18

	Kieffer - detox-iCAF	602	301	6.55	5.84E-11	0.64 (0.45-0.83)	1.89
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