

Supplementary information for

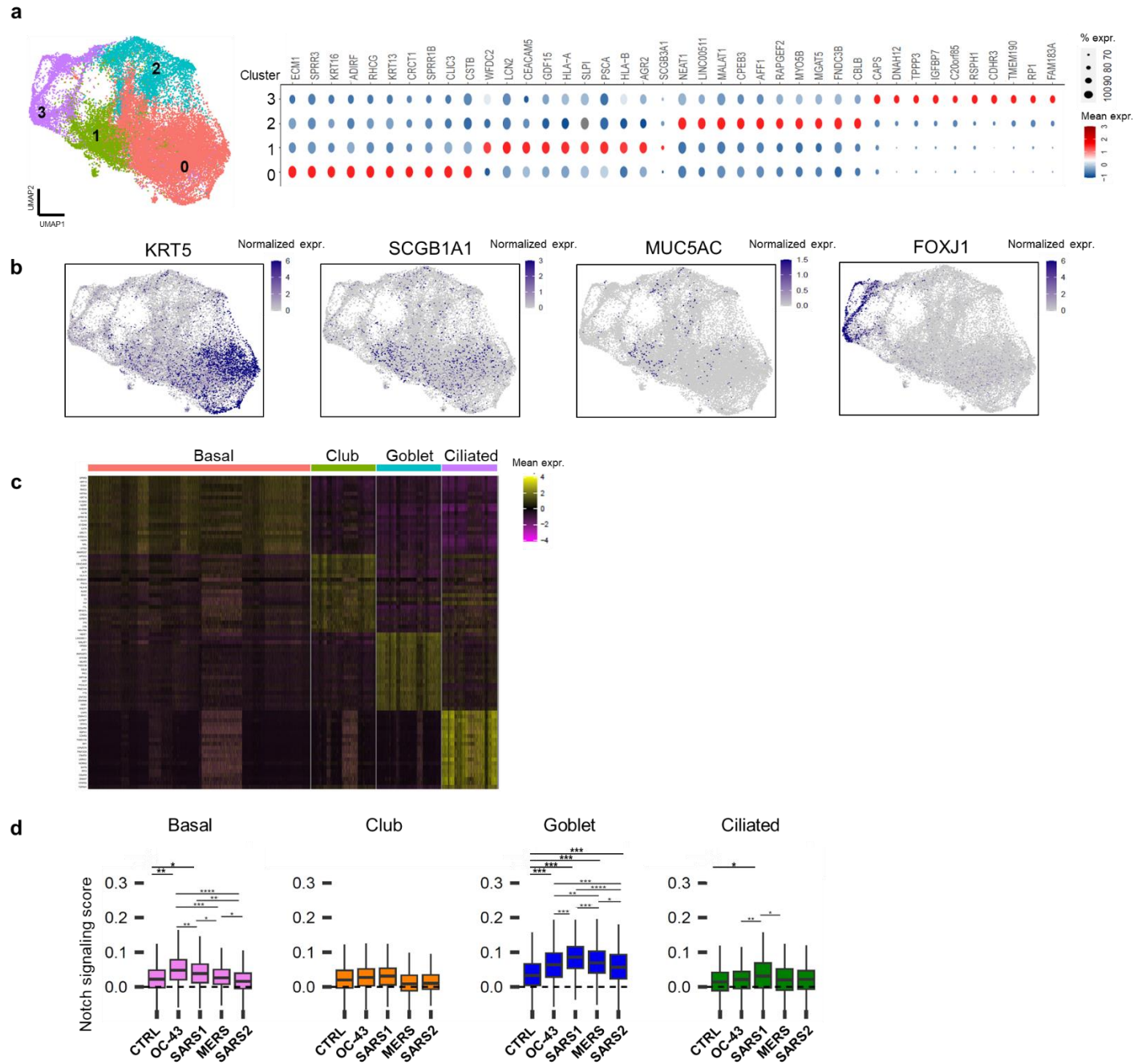
Diverse Cellular Tropisms and Immune Responses
in Beta-Coronavirus Infections in Human Bronchial Epithelial Organoids

Park et al.

Supplementary Fig. S1 –S5

Supplementary Table S1 – S3

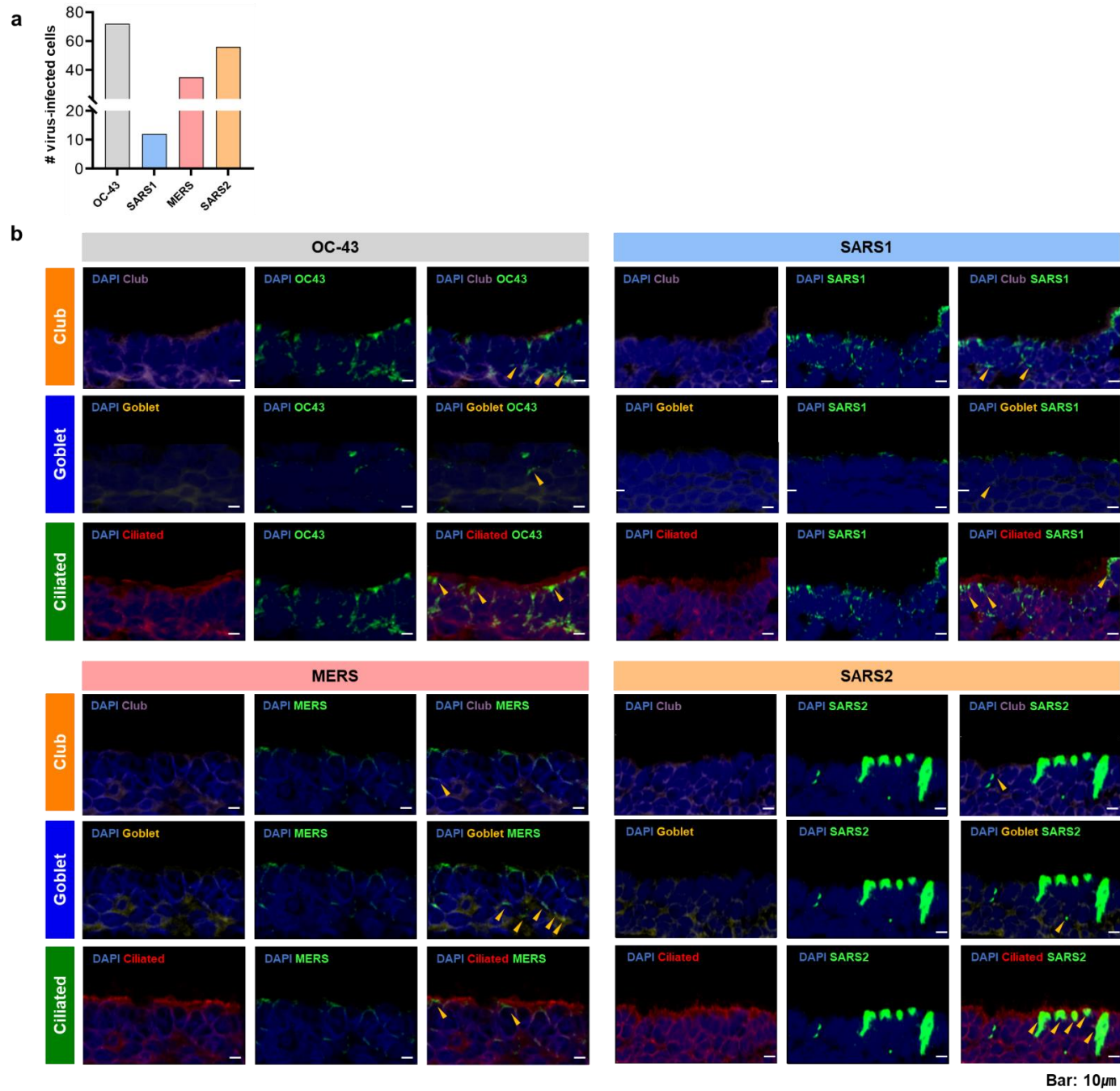
Fig. S1



Supplementary Fig. S1

a UMAP embedding colored on the basis of major four gene clusters with a dot plot showing the top 10 enriched DEGs in each cluster. **b** UMAP plots colored by normalized expression of representative marker genes in each cluster (basal cell, *KRT5*; club cell, *SCGB3A2*; goblet cell, *MUC5AC*; and ciliated cell, *FOXJ1*). **c** Heat map of cluster-specific DEGs in four major cell types in HBE organoids. The color indicates the normalized gene expression and the representative genes are shown on the left. **d** Expression scores of 32 Notch signaling–related genes for four major cell types infected by four Beta-CoVs, with mock-infected controls.

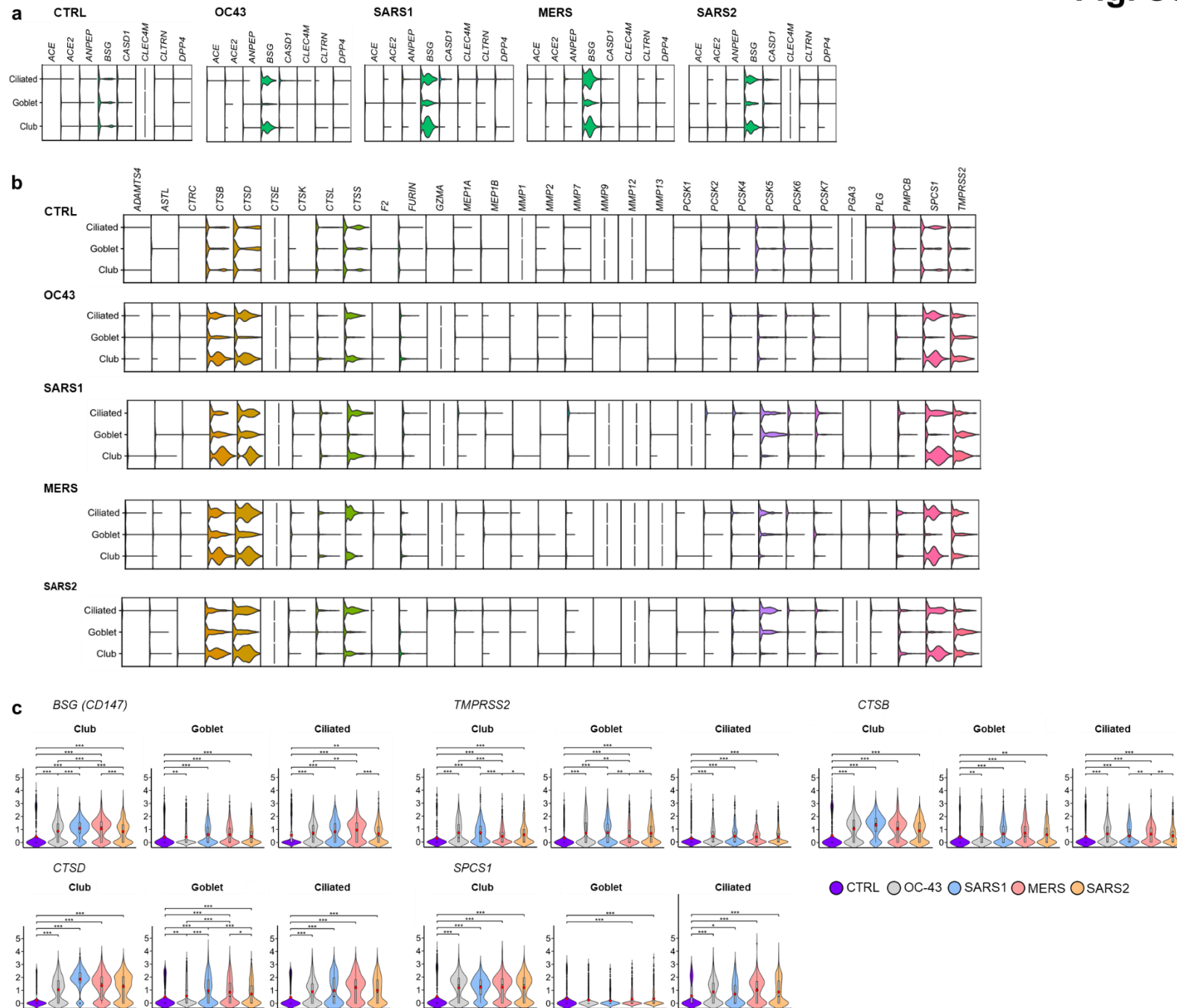
Fig. S2



Supplementary Fig. S2

a The number of virus-infected cells in HBE organoids infected by one of four beta-CoVs. The number of virus-infected cells of triplicates ($n = 3$) was summed and expressed as bar height. **b** Representative immunofluorescence (IF) with RNAscope (ISH) images of HBE organoids infected by the four distinct beta-CoVs OC-43, SARS-CoV, MERS-CoV, and SARS-CoV-2 across three different cell types: club cells (SCGB3A2, purple), ciliated cells (acetylated α -tubulin, red), and goblet cells (MUC5AC, orange). The color bars above and to the left of the images indicate the cell types and virus strains. The orange arrows indicate detected viral genomes in each cell type. The scale bar indicates 10 μ m.

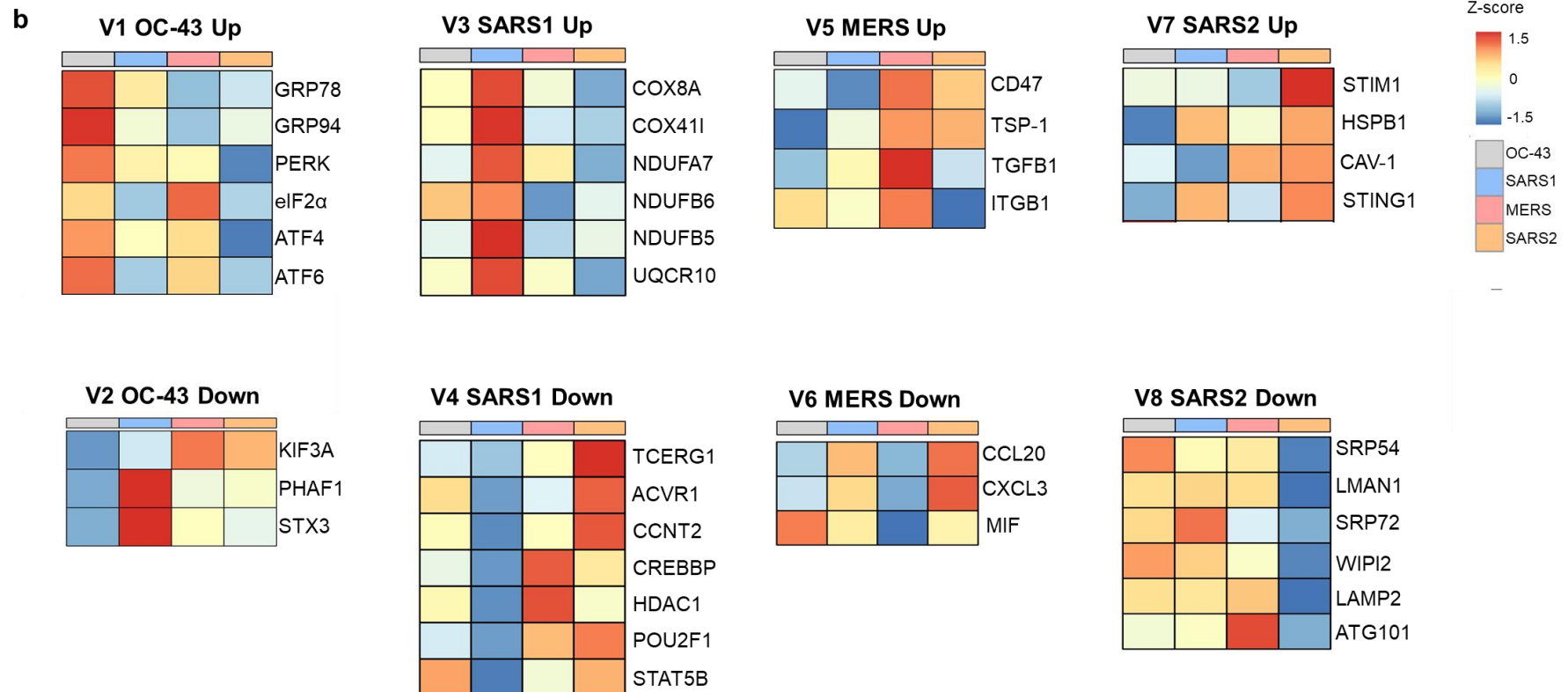
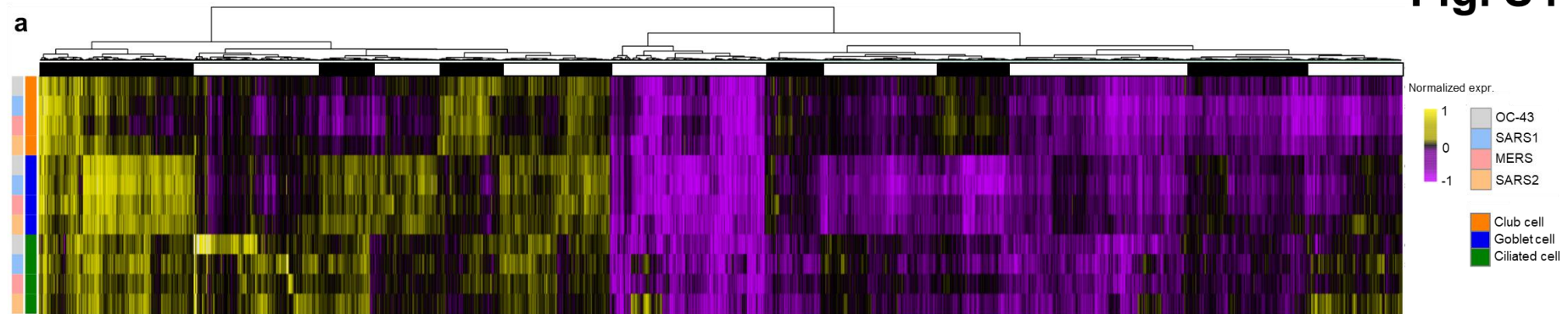
Fig. S3



Supplementary Fig. S3

a & b Stacked violin plots displaying expression levels of genes encoding eight known receptors (**a**) and 31 known proteases for beta-CoVs (**b**) in three different cell types infected with different virus strains, with mock-infected controls. **c** Violin plots showing expression levels of *BSG* (*CD147*), *TMPRSS2*, *CTSB*, *CTSD*, and *SPCS1* in three cell types infected with different virus strains, with mock-infected controls. The average expression value for each gene is marked with a red dot. Wilcoxon rank-sum test was performed. $*p < 0.05$, $**p < 0.01$, and $***p < 0.001$.

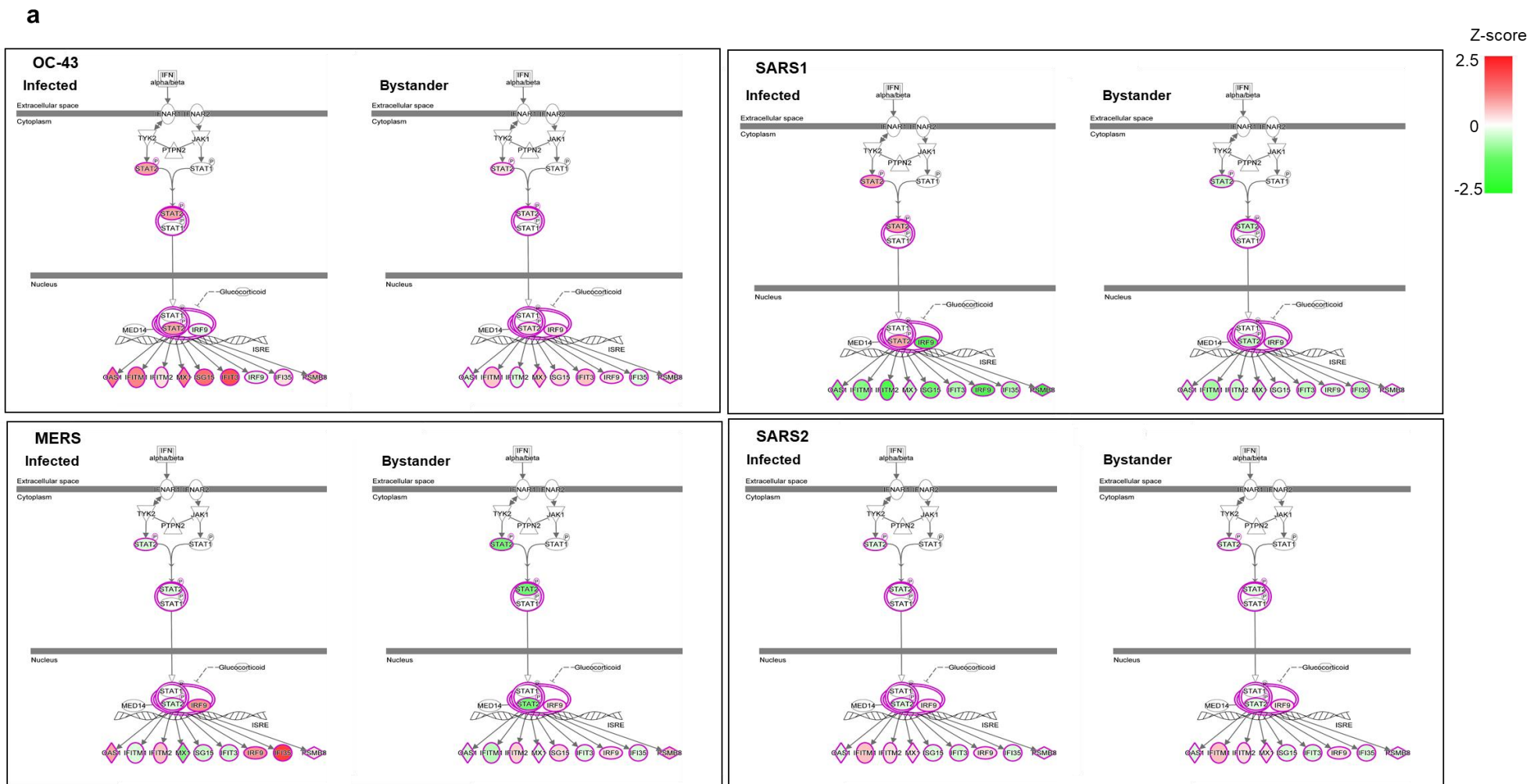
Fig. S4



Supplementary Fig. S4

a K-means clustering of commonly expressed, but highly variable genes ($n = 7,128$). The color intensity of the heat map represents the normalized gene expression compared with control, identifying 14 distinct clusters that reflect shared and specific expression patterns for cell types. The color bar (left) indicates different virus strains and cell types. **b** Heat maps of relative expression compared with the control for each module-related gene set: OC-43–, SARS-CoV–, MERS-CoV–, and SARS-CoV-2–specific upregulation and downregulation modules. Each gene expression value is represented as a Z-score. The color bar above the heat map indicates different virus strains

Fig. S5



Supplementary Fig. S5

a The IFN signaling pathway predicted in the IPA dataset overlaid on IFN α response-related genes that were differentially expressed between infected and bystander cells in four different beta-CoV-infected samples. The gene expression of infected and bystander cells was normalized by comparison with corresponding control. Of the 96 IFN α -associated ISGs, only genes statistically matched with the pathway are shown. The relative expression values were represented as a Z-score. All upregulated genes are shown in red, while the downregulated genes are shown in green.

Supplementary Table S1. A list of DEG for clustering

[cluster 0]

Gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	Cluster
SPRR3	0	2.5029191	0.998	0.979	0	0
KRT13	0	2.179721966	0.985	0.94	0	0
ECM1	0	2.114570471	0.993	0.934	0	0
RHCG	0	2.067605692	0.988	0.938	0	0
KRT6A	0	2.061022883	0.953	0.859	0	0
KRT16	0	2.038325095	0.972	0.902	0	0
S100A2	0	1.997182213	0.942	0.886	0	0
ADIRF	0	1.917155577	0.997	0.942	0	0
S100A9	0	1.891096658	1	0.995	0	0
CSTB	0	1.819855806	1	0.995	0	0
SPRR1B	0	1.781777527	0.974	0.921	0	0
CLIC3	0	1.757579934	0.99	0.935	0	0
S100A8	0	1.698813681	0.978	0.949	0	0
CSTA	0	1.689437352	0.984	0.895	0	0
CRCT1	0	1.643862768	0.963	0.869	0	0
S100A14	0	1.596224584	0.997	0.963	0	0
HOPX	0	1.52885338	0.998	0.966	0	0
MAL	0	1.465237347	0.99	0.961	0	0
LYPD2	0	1.447038173	0.971	0.932	0	0
ANKRD37	0	1.428210805	0.98	0.933	0	0
JUNB	0	1.398880128	0.996	0.957	0	0
SPINK5	0	1.373856255	0.934	0.822	0	0
KRT17	0	1.326444222	0.991	0.96	0	0
TGFB1	0	1.282084422	0.972	0.907	0	0
EIF4EBP1	0	1.175920012	0.975	0.907	0	0
MT1X	0	1.174907792	0.96	0.875	0	0
LDHA	0	1.123580387	0.986	0.923	0	0
KRT14	0	1.097306807	0.761	0.72	0	0
FTH1	0	1.095479227	1	0.998	0	0
BHLHE40	0	1.095170183	0.991	0.941	0	0
CRABP2	0	1.063944484	0.955	0.86	0	0

ETHE1	0	1.042757353	0.988	0.929	0	0
SPINK7	0	1.040622849	0.869	0.826	0	0
SERPINB1	0	1.037221027	0.984	0.959	0	0
KRT15	0	1.028742969	0.98	0.91	0	0
C15orf48	0	1.003391015	0.999	0.989	0	0
PITX1	0	0.994748929	0.985	0.92	0	0
NCCRP1	0	0.988626735	0.997	0.97	0	0
LGALS1	0	0.96706652	0.87	0.773	0	0
PRSS3	0	0.923284083	0.9	0.751	0	0
CLCA4	0	0.923233077	0.923	0.811	0	0
PRSS22	0	0.906682366	0.996	0.973	0	0
TM4SF1	0	0.902520696	0.956	0.907	0	0
EMP1	0	0.881301902	0.988	0.93	0	0
H1-2	0	0.876916756	0.991	0.93	0	0
TMPRSS11E	0	0.87676983	0.967	0.916	0	0
IER5	0	0.855314431	0.991	0.924	0	0
CYSRT1	0	0.843741054	0.969	0.891	0	0
GADD45A	0	0.843094024	0.98	0.927	0	0
SNHG12	0	0.81818751	0.971	0.886	0	0
KRT7	0	0.773767617	0.998	0.987	0	0
SERPINB2	0	0.773451786	0.972	0.919	0	0
ACTG1	0	0.753576657	0.996	0.978	0	0
H2AW	0	0.753538735	0.977	0.913	0	0
KLK11	0	0.75348345	0.936	0.854	0	0
SNCG	0	0.750810976	0.953	0.889	0	0
KRT5	0	0.746110134	0.83	0.739	0	0
GADD45B	0	0.742271842	0.981	0.919	0	0
ADM	0	0.738614925	0.978	0.935	0	0
PRSS27	0	0.733463192	0.973	0.914	0	0
HPGD	0	0.733443919	0.968	0.893	0	0
UPP1	0	0.732746463	0.977	0.904	0	0
HES1	0	0.721696333	0.98	0.925	0	0
PHLDA1	0	0.714366287	0.976	0.928	0	0
ZFP36	0	0.694679525	0.982	0.945	0	0
CNFN	0	0.692019124	0.948	0.88	0	0
SERPINB5	0	0.68516825	0.853	0.8	0	0
METRNL	0	0.681542179	0.974	0.9	0	0

KLK10	0	0.66493064	0.938	0.868	0	0
UPK1B	0	0.664026599	0.976	0.927	0	0
KRT4	0	0.663849328	0.914	0.869	0	0
MARCKSL1	0	0.653323478	0.967	0.919	0	0
KRT6B	0	0.63087216	0.833	0.739	0	0
MXD1	0	0.628374483	0.994	0.951	0	0
IFI27	0	0.617196273	0.945	0.861	0	0
CCNDBP1	0	0.612189172	0.982	0.951	0	0
NFKBIA	0	0.595600444	0.979	0.916	0	0
EEF1A2	0	0.592914361	0.942	0.876	0	0
APOBEC3A	0	0.584881221	0.913	0.832	0	0
SULT2B1	0	0.577044332	0.924	0.865	0	0
KRT18	0	0.576141858	0.978	0.924	0	0
SPRR1A	0	0.566619704	0.81	0.757	0	0
PI3	3.24E-287	0.561226641	0.83	0.744	6.48E-284	0
FABP5	0	0.558599687	0.94	0.871	0	0
PLAU	0	0.557825237	0.971	0.914	0	0
AREG	0	0.556270281	0.959	0.904	0	0
RTKN2	0	0.553347658	0.961	0.873	0	0
DNAJB1	0	0.55099886	0.992	0.964	0	0
TCN1	0	0.547877738	0.884	0.758	0	0
SPRR2A	0	0.533911678	0.833	0.743	0	0
IL36G	0	0.5300703	0.906	0.86	0	0
ANGPTL4	0	0.525419975	0.951	0.845	0	0
NRARP	0	0.522338825	0.928	0.855	0	0
TMPRSS11B	0	0.508749941	0.923	0.884	0	0
MSMO1	0	0.505810111	0.965	0.919	0	0
LY6D	0	0.498264273	0.853	0.69	0	0
SCNN1B	0	0.495858592	0.955	0.887	0	0
S100A4	5.53E-256	0.492395189	0.952	0.917	1.11E-252	0
S100A12	0	0.490772232	0.889	0.818	0	0
ISG15	1.97E-238	0.490617732	0.975	0.927	3.94E-235	0
CXCL17	0	0.488356772	0.974	0.928	0	0
S100A7	1.78E-41	0.487246369	0.754	0.737	3.55E-38	0
SLC6A8	0	0.479844743	0.924	0.865	0	0
IVL	0	0.461861706	0.929	0.864	0	0
CDC42EP1	0	0.46174313	0.958	0.897	0	0

HILPDA	5.19E-288	0.452820289	0.959	0.93	1.04E-284	0
IL1B	0	0.452728652	0.864	0.746	0	0
PLAAT4	2.55E-95	0.450349861	0.957	0.947	5.11E-92	0
PGAM1	2.13592098625937e-310	0.446473403	0.972	0.941	4.27E-307	0
MAB21L4	0	0.445349839	0.967	0.924	0	0
DDIT4	1.11E-285	0.440654198	0.99	0.97	2.23E-282	0
CCDC68	0	0.439560043	0.934	0.845	0	0
CEACAM1	0	0.435063956	0.96	0.895	0	0
MAP3K9-DT	0	0.433777817	0.91	0.843	0	0
HS3ST1	0	0.432106496	0.972	0.94	0	0
CA2	0	0.431670355	0.89	0.801	0	0
ANXA3	0	0.418374136	0.964	0.9	0	0
ID1	1.49E-178	0.401676987	0.897	0.818	2.97E-175	0
SBSN	1.35E-293	0.401646078	0.855	0.809	2.69E-290	0
C10orf99	0	0.401567142	0.859	0.796	0	0
BTG1	4.29E-221	0.394938204	0.909	0.84	8.58E-218	0
CCL20	1.13E-105	0.391953332	0.876	0.857	2.26E-102	0
CLDN4	1.78620294039455e-317	0.381740671	0.988	0.97	3.57240588078909e-314	0
HSPB8	0	0.376771	0.962	0.897	0	0
IER3	1.04E-253	0.371153587	0.959	0.909	2.09E-250	0
DSG3	5.85E-243	0.367029815	0.853	0.77	1.17E-239	0
CEBPD	2.43E-185	0.365920698	0.97	0.923	4.87E-182	0
RNF39	0	0.362789064	0.935	0.854	0	0
ELOVL4	0	0.362304663	0.903	0.819	0	0
DEPP1	7.44364589211113e-312	0.361491186	0.907	0.833	0.00E+00	0
SPRR2D	0	0.361467532	0.863	0.805	0	0
CDA	0	0.356930394	0.871	0.8	0	0
SCD	2.53E-178	0.351206447	0.908	0.844	5.06E-175	0
ACTB	2.56E-307	0.346560678	0.993	0.98	5.12E-304	0
SNHG29	2.07E-238	0.325301035	0.958	0.901	4.14E-235	0
TNFSF9	0	0.316106692	0.895	0.815	0	0
AVPI1	0	0.314676247	0.938	0.886	0	0
MAP3K8	4.61E-224	0.314480088	0.963	0.927	9.21E-221	0
DUSP1	2.25E-205	0.309239617	0.971	0.933	4.50E-202	0
GRPEL2	0	0.307087652	0.944	0.848	0	0
TPTEP2-CSNK1E	4.74E-231	0.304345758	0.945	0.892	9.49E-228	0
SOX9	3.87E-268	0.303957234	0.882	0.845	7.74E-265	0

IL1A	0	0.300034208	0.887	0.782	0	0
RSAD2	1.23E-118	0.299182349	0.922	0.874	2.46E-115	0
PPP1R15A	1.52E-223	0.284595538	0.982	0.953	3.03E-220	0
CRNN	0	0.281400539	0.891	0.887	0	0
CITED2	3.88E-199	0.280370576	0.894	0.852	7.77E-196	0
ANXA9	0	0.280201265	0.936	0.888	0	0
RESF1	1.98E-233	0.278786644	0.969	0.912	3.97E-230	0
PKP1	0	0.277400366	0.874	0.755	0	0
A2ML1	0	0.270449185	0.89	0.819	0	0
CAPN14	0	0.268376577	0.909	0.835	0	0
KRT23	5.57E-166	0.261361189	0.962	0.918	1.11E-162	0
FMO2	0	0.257537394	0.89	0.818	0	0
GPX3	1.82E-201	0.257232722	0.922	0.888	3.63E-198	0
PTHLH	5.28E-182	0.256860333	0.797	0.758	1.06E-178	0
LAYN	0	0.255923222	0.874	0.802	0	0
KRT78	7.22E-273	0.255124957	0.926	0.889	1.44E-269	0
ARRDC2	4.47E-273	0.254694374	0.93	0.872	8.95E-270	0
SERPINB13	1.52E-239	0.254022447	0.831	0.731	3.04E-236	0
PLAUR	1.96E-170	0.253940045	0.863	0.807	3.92E-167	0
CEACAM6	8.11E-273	0.252302944	0.991	0.941	1.62E-269	0
IER2	1.01E-116	0.252093759	0.939	0.906	2.02E-113	0
SPINK1	7.88E-264	0.24983998	0.805	0.729	1.58E-260	0
DSC2	1.13E-172	0.245414134	0.868	0.832	2.27E-169	0
ST3GAL4	5.31E-204	0.24327521	0.956	0.917	1.06E-200	0
KLK8	0	0.242746753	0.89	0.847	0	0
ACKR3	3.00E-254	0.23184077	0.872	0.811	6.00E-251	0
MEX3D	2.00E-239	0.231331004	0.88	0.803	4.01E-236	0
S100A6	2.27E-267	0.231097804	0.999	0.999	4.54E-264	0
LINC00520	0	0.229518183	0.846	0.79	0	0
SERPINB3	4.33E-87	0.227632135	0.749	0.677	8.65E-84	0
ID4	2.59E-308	0.227580807	0.9	0.811	5.19E-305	0
MUC21	0	0.22707092	0.861	0.885	0	0
RAB32	1.45161168084381e-313	0.223336027	0.892	0.814	2.90322336168762e-310	0
LAMA4	6.66E-216	0.217812459	0.889	0.815	1.33E-212	0
KLF4	2.35E-219	0.212472142	0.869	0.812	4.70E-216	0
FAT2	4.34E-181	0.211865341	0.857	0.804	8.68E-178	0
SAMD9	2.88E-145	0.209143752	0.938	0.889	5.76E-142	0

TXNIP	2.17E-175	0.208012196	0.987	0.942	4.34E-172	0
H2BC4	4.65E-164	0.204131085	0.922	0.877	9.30E-161	0
GLRX	1.28E-92	0.202025707	0.918	0.873	2.57E-89	0
KLK7	8.36E-137	0.201971744	0.802	0.799	1.67E-133	0
TMPRSS11A	0	0.201659633	0.879	0.767	0	0
GJB2	2.31E-98	0.197358066	0.829	0.776	4.63E-95	0
BST2	1.84E-223	0.194885575	0.943	0.866	3.69E-220	0
FLG	2.47032822920623e-323	0.194149144	0.832	0.79	4.94065645841247e-320	0
CEACAM7	1.14E-121	0.193852566	0.883	0.866	2.29E-118	0
ARRDC4	1.24E-238	0.189648993	0.884	0.794	2.48E-235	0
PLP2	2.47E-178	0.188719594	0.9	0.834	4.93E-175	0
GCHFR	9.73E-137	0.188487078	0.955	0.923	1.95E-133	0
CLEC2B	4.53E-248	0.185008605	0.813	0.725	9.07E-245	0
VAMP5	2.71E-179	0.178417531	0.938	0.889	5.42E-176	0
GABRP	1.30E-172	0.177343918	0.94	0.893	2.59E-169	0
TMCC3	1.08E-258	0.176320594	0.963	0.905	2.17E-255	0
CTSV	6.42E-206	0.176182787	0.866	0.811	1.28E-202	0
RAB40B	9.01E-151	0.174762895	0.825	0.783	1.80E-147	0
FGFBP1	1.45E-50	0.173372589	0.84	0.83	2.90E-47	0
GJB6	0	0.170354087	0.864	0.806	0	0
ARL4A	8.62E-54	0.168605365	0.877	0.861	1.72E-50	0
PDLIM4	1.80E-133	0.165080052	0.912	0.865	3.60E-130	0
ZNF600	2.80E-236	0.164614477	0.837	0.778	5.60E-233	0
CXCL8	3.12E-25	0.15572483	0.836	0.833	6.25E-22	0
TSC22D3	4.09E-64	0.153272482	0.962	0.933	8.18E-61	0
AIF1L	1.82E-255	0.150451218	0.901	0.862	3.65E-252	0
SCNN1G	2.07942136573436e-316	0.147799068	0.924	0.847	4.15884273146872e-313	0
LINC01559	2.98E-180	0.147534553	0.893	0.83	5.96E-177	0
SFN	1.12E-53	0.144016377	0.908	0.868	2.24E-50	0
SERPINB7	7.24E-242	0.14221763	0.871	0.809	1.45E-238	0
SMC4	9.03E-103	0.141290386	0.913	0.858	1.81E-99	0
DDIT3	2.13E-127	0.138483601	0.918	0.854	4.26E-124	0
ZNF365	0	0.137448939	0.881	0.827	0	0
ALOX15B	0	0.136306934	0.893	0.839	0	0
PNLIPRP3	3.87E-151	0.134766953	0.915	0.86	7.73E-148	0
EPHB3	8.68E-238	0.134133705	0.876	0.823	1.74E-234	0
LINC00551	2.98E-143	0.133660988	0.857	0.795	5.97E-140	0

TNFRSF12A	1.70E-107	0.129875221	0.972	0.941	3.40E-104	0
HK2	2.93E-79	0.128245867	0.927	0.872	5.86E-76	0
HERPUD1	1.36E-146	0.128181278	0.897	0.796	2.72E-143	0
PHLDA2	4.51E-58	0.124668719	0.967	0.943	9.02E-55	0
SDR16C5	3.65E-201	0.124259751	0.854	0.756	7.31E-198	0
SLC39A2	9.31352724190207e-317	0.124076132	0.841	0.814	1.86270544838041e-313	0
DKK1	1.44E-75	0.121206597	0.833	0.815	2.88E-72	0
FAM3D	2.01E-53	0.120083199	0.955	0.922	4.02E-50	0
AOC1	2.74E-32	0.118118873	0.922	0.924	5.48E-29	0
LEMD1	6.13E-154	0.117532723	0.822	0.814	1.23E-150	0
KRTDAP	1.24E-176	0.115665983	0.757	0.687	2.48E-173	0
LY6K	5.39E-113	0.111647964	0.832	0.814	1.08E-109	0
IGFBP6	6.57E-137	0.110796851	0.733	0.659	1.31E-133	0
ASS1	2.70E-42	0.109224852	0.882	0.849	5.39E-39	0
KLK12	1.03E-228	0.106574153	0.856	0.84	2.05E-225	0
TGM1	8.68E-263	0.106449719	0.877	0.793	1.74E-259	0
SOX4	7.69E-40	0.102903303	0.974	0.947	1.54E-36	0
ASPG	0	0.10225872	0.91	0.891	0	0
CXCL2	4.97E-21	0.101736932	0.84	0.801	9.94E-18	0
NMU	3.07E-101	0.101369198	0.814	0.763	6.13E-98	0
UCA1	2.24E-85	0.100375319	0.769	0.75	4.49E-82	0
CITED4	1.85E-55	0.100300629	0.886	0.843	3.71E-52	0
CLCA2	8.09E-138	0.099743771	0.69	0.562	1.62E-134	0
RBP7	0	0.098641714	0.829	0.743	0	0
MAF	1.09E-78	0.098337081	0.884	0.814	2.19E-75	0
ID2	6.25E-27	0.097716448	0.752	0.727	1.25E-23	0
CYP4F3	1.75E-95	0.096912802	0.897	0.832	3.51E-92	0
SLURP2	2.87E-190	0.09621882	0.707	0.667	5.74E-187	0
LGALS7	1.03E-211	0.095282899	0.839	0.801	2.05E-208	0
P2RY1	1.06E-193	0.094799031	0.871	0.767	2.13E-190	0
CKS2	1.48E-61	0.093573195	0.85	0.801	2.97E-58	0
BMP2	1.87E-131	0.093445597	0.852	0.767	3.73E-128	0
SMIM5	2.84E-79	0.089385584	0.896	0.858	5.68E-76	0
FAM83D	1.77E-99	0.089259817	0.811	0.786	3.54E-96	0
SLURP1	2.09E-214	0.088622775	0.832	0.806	4.18E-211	0
C11orf96	8.99E-71	0.087117986	0.809	0.816	1.80E-67	0
TUBA1C	2.29E-44	0.085064535	0.912	0.865	4.59E-41	0

NDUFA4L2	1.25E-95	0.084979402	0.459	0.406	2.50E-92	0
HES5	1.00E-66	0.084960305	0.861	0.836	2.00E-63	0
HCAR3	0	0.084408246	0.906	0.768	0	0
PLK2	3.44E-35	0.081972023	0.826	0.815	6.89E-32	0
KLK6	9.00E-121	0.081896268	0.79	0.771	1.80E-117	0
SLC6A14	4.02E-49	0.081531994	0.964	0.935	8.04E-46	0
KLK13	8.95E-157	0.081382603	0.845	0.808	1.79E-153	0
SLAMF9	6.71E-237	0.080987956	0.736	0.74	1.34E-233	0
TNS1-AS1	1.26E-99	0.080317131	0.745	0.705	2.53E-96	0
SMIM12	2.26E-67	0.079719322	0.894	0.845	4.51E-64	0
TPRG1	4.60E-210	0.078879233	0.826	0.766	9.20E-207	0
HS3ST6	1.54E-58	0.078844204	0.92	0.903	3.07E-55	0
ID3	6.25E-07	0.07869451	0.732	0.723	0.001250651	0
MME	4.16E-197	0.075671611	0.916	0.841	8.32E-194	0
LINC01405	4.35E-242	0.073727618	0.823	0.825	8.70E-239	0
SDC1	1.08E-46	0.071188616	0.958	0.925	2.16E-43	0
KLK5	5.00E-91	0.070471122	0.817	0.796	1.00E-87	0
FBLN1	1.03E-57	0.06710109	0.864	0.798	2.07E-54	0
MT1E	2.94E-24	0.065906484	0.634	0.579	5.89E-21	0
KRTAP19-1	2.71E-122	0.065659693	0.756	0.694	5.41E-119	0
GJA1	4.60E-71	0.06411362	0.757	0.741	9.21E-68	0
KLF10	6.00E-24	0.063812829	0.897	0.865	1.20E-20	0
CXCL3	0.02733204	0.063801978	0.832	0.836	1	0
EREG	5.62E-17	0.063529949	0.923	0.899	1.12E-13	0
HSPA6	0.886171091	0.062938278	0.9	0.899	1	0
HSPA5	1.02E-79	0.062436959	0.942	0.884	2.04E-76	0
DEFB1	3.71E-57	0.06123163	0.811	0.81	7.43E-54	0
MT1G	1.21E-82	0.061000139	0.788	0.709	2.42E-79	0
GPNMB	4.39E-113	0.060803042	0.877	0.802	8.79E-110	0
LINC01589	1.43E-96	0.060379279	0.793	0.769	2.85E-93	0
ICAM1	2.03E-05	0.060335286	0.893	0.881	0.040611565	0
PDZK1IP1	1.45E-38	0.057820139	0.889	0.853	2.91E-35	0
CORO1A	1.21E-100	0.056060538	0.878	0.819	2.42E-97	0
CYP3A5	8.45E-98	0.055377289	0.867	0.802	1.69E-94	0
SLAMF7	5.21E-101	0.055225549	0.845	0.802	1.04E-97	0
LINC01705	6.94E-111	0.053390361	0.903	0.854	1.39E-107	0
FTL	1.79E-150	0.052191603	0.996	0.977	3.58E-147	0

IRF1	1.27E-24	0.051493072	0.932	0.898	2.54E-21	0
GALNT5	1.23E-10	0.051323984	0.915	0.892	2.46E-07	0
ARSI	3.92E-191	0.049532869	0.855	0.734	7.84E-188	0
SPRR2E	7.38E-66	0.049530912	0.75	0.752	1.48E-62	0
KRT6C	1.86E-119	0.049116251	0.727	0.655	3.72E-116	0
H2BC5	2.70E-23	0.048502755	0.919	0.893	5.40E-20	0
GPX2	3.85E-31	0.047957579	0.754	0.749	7.70E-28	0
SPINK8	6.33E-181	0.047847441	0.833	0.789	1.27E-177	0
PRR5-ARHGAP8	1.67E-15	0.046479377	0.797	0.798	3.34E-12	0
MACC1-DT	1.10E-21	0.046463017	0.828	0.79	2.20E-18	0
ITGA5	6.77E-30	0.046341187	0.851	0.833	1.35E-26	0
EDN2	3.13E-29	0.046269395	0.827	0.837	6.27E-26	0
LAMB3	9.15E-24	0.045656536	0.86	0.815	1.83E-20	0
CALML5	2.88E-38	0.045467031	0.725	0.719	5.77E-35	0
CHAC1	1.38E-131	0.043613164	0.835	0.723	2.75E-128	0
DMKN	9.92E-87	0.042846612	0.962	0.925	1.98E-83	0
RNASE7	2.32E-135	0.042656075	0.818	0.723	4.64E-132	0
SLC5A1	1.78E-63	0.042635643	0.863	0.816	3.57E-60	0
MCPH1-DT	6.41E-41	0.042136402	0.765	0.803	1.28E-37	0
SH2D1B	2.36E-89	0.041409263	0.864	0.88	4.71E-86	0
ANG	1.06E-61	0.040476501	0.819	0.738	2.11E-58	0
KLK4	1.18E-58	0.040216081	0.736	0.694	2.36E-55	0
TMPRSS11F	5.79E-96	0.039235567	0.904	0.843	1.16E-92	0
ZNF57	1.22E-19	0.038515754	0.81	0.801	2.43E-16	0
RGS20	3.52E-31	0.037288859	0.849	0.817	7.05E-28	0
EGR1	1.47E-10	0.034858038	0.884	0.862	2.95E-07	0
IL23A	6.54E-24	0.034152753	0.738	0.732	1.31E-20	0
CENPW	6.12E-36	0.033690695	0.805	0.758	1.22E-32	0
LINC01269	6.73E-66	0.030612486	0.883	0.812	1.35E-62	0
SERPING1	9.00E-60	0.029489932	0.782	0.724	1.80E-56	0
SERPINB4	1.94E-68	0.028871251	0.609	0.514	3.88E-65	0
SLC2A3	2.59E-18	0.028789132	0.62	0.615	5.17E-15	0
TP63	0.003530063	0.028286955	0.559	0.559	1	0
TPM2	1.49E-12	0.027723887	0.751	0.722	2.98E-09	0
TENT5B	4.30E-19	0.026879117	0.799	0.779	8.59E-16	0
CPA4	3.80E-18	0.025992194	0.772	0.751	7.60E-15	0
CIART	0.001953115	0.025811666	0.881	0.876	1	0

PLAT	6.55E-151	0.025717143	0.704	0.553	1.31E-147	0
AQP5	1.66E-15	0.025565353	0.645	0.683	3.33E-12	0
FABP3	0.080151909	0.024153313	0.813	0.822	1	0
VGLL3	1.70E-44	0.023463545	0.793	0.724	3.40E-41	0
BARD1	8.37E-50	0.022972055	0.878	0.815	1.67E-46	0
TUBB2A	1.30E-12	0.022235115	0.825	0.794	2.60E-09	0
PCLAF	1.61E-47	0.021713303	0.849	0.787	3.21E-44	0
COL17A1	0.001392562	0.020811323	0.549	0.561	1	0
FBLN2	6.63E-05	0.020757375	0.86	0.841	0.132530166	0
ZNF556	3.20E-14	0.020555372	0.776	0.806	6.40E-11	0
BRINP2	2.91E-12	0.020495916	0.731	0.712	5.82E-09	0
H3C10	3.82E-19	0.01956788	0.871	0.838	7.64E-16	0
SMOC2	9.10E-48	0.019082323	0.717	0.658	1.82E-44	0
FAM43A	2.83E-38	0.018756866	0.8	0.735	5.66E-35	0
RASD1	6.98E-82	0.018489958	0.738	0.634	1.40E-78	0
H3C12	8.75E-10	0.018000027	0.816	0.785	1.75E-06	0
CAVIN1	3.43E-06	0.016807157	0.628	0.601	0.006868834	0
AQP3	1.23E-05	0.016135343	0.931	0.937	0.024693971	0
PLAAT3	1.66E-17	0.015961736	0.93	0.902	3.33E-14	0
C2CD4A	1.16E-47	0.015817699	0.778	0.707	2.32E-44	0
KPRP	4.96E-48	0.015796006	0.724	0.73	9.91E-45	0
HAS2	3.36E-68	0.01510732	0.612	0.509	6.72E-65	0
APOD	7.77E-23	0.014618845	0.885	0.854	1.55E-19	0
LINC02154	8.01E-42	0.014378471	0.802	0.742	1.60E-38	0
NR4A1	0.442920798	0.013960266	0.809	0.811	1	0
TNFAIP2	7.25E-45	0.013498786	0.906	0.851	1.45E-41	0
ATP11B-DT	1.00E-07	0.013300267	0.669	0.669	0.000200771	0
POU2F3	8.92E-13	0.013106945	0.743	0.703	1.78E-09	0
CALB1	6.52E-18	0.01267462	0.775	0.768	1.30E-14	0
SNAI2	9.60E-14	0.012637393	0.828	0.809	1.92E-10	0
HMOX1	1.46E-05	0.012498454	0.859	0.85	0.029203761	0
HAMP	5.68E-34	0.011779109	0.771	0.769	1.14E-30	0
CCDC13-AS1	3.34E-31	0.010654701	0.62	0.555	6.68E-28	0
CCND1	1.37E-21	0.010489389	0.971	0.952	2.74E-18	0
GNE	2.59E-39	0.010476392	0.923	0.878	5.18E-36	0
ASB2	2.58E-62	0.009859928	0.782	0.846	5.15E-59	0
FOSL1	3.43E-15	0.009842068	0.855	0.819	6.87E-12	0

EDIL3-DT	1.40E-64	0.009151344	0.633	0.729	2.79E-61	0
TIMP3	2.98E-65	0.008493767	0.562	0.661	5.97E-62	0
HSD11B1	4.18E-45	0.008339865	0.549	0.473	8.37E-42	0
EBI3	2.71E-82	0.007911182	0.832	0.744	5.43E-79	0
MYC	3.38E-24	0.007507436	0.671	0.728	6.75E-21	0
SLC30A1	1.46E-10	0.007349122	0.836	0.805	2.91E-07	0
CALD1	1.78E-11	0.007058402	0.697	0.661	3.56E-08	0
HSD17B2	7.13E-09	0.007035661	0.737	0.768	1.43E-05	0
CXCL14	4.75E-11	0.006983921	0.617	0.65	9.51E-08	0
UBE2S	2.00E-11	0.006931926	0.847	0.817	3.99E-08	0
SOD2	0.000236727	0.00688709	0.925	0.913	0.473454252	0
MSN	2.08E-05	0.00664073	0.734	0.756	0.041512935	0
ADGRF2	2.34E-17	0.005997081	0.815	0.782	4.67E-14	0
TICRR	8.42E-35	0.005923466	0.869	0.817	1.68E-31	0
CLDN14	1.49E-16	0.005730125	0.764	0.723	2.97E-13	0
G0S2	0.006068698	0.005681325	0.812	0.804	1	0
IGFL2-AS1	5.87E-44	0.005518084	0.747	0.673	1.17E-40	0
WFDC5	1.29E-81	0.005067328	0.631	0.52	2.57E-78	0
GAST	8.06E-26	0.005054401	0.718	0.666	1.61E-22	0
TLL2	3.40E-39	0.004745149	0.767	0.831	6.80E-36	0
OASL	6.82E-44	0.004385321	0.736	0.659	1.36E-40	0
TMPO	9.45E-57	0.004172686	0.847	0.778	1.89E-53	0
TWIST1	4.51E-06	0.003848286	0.733	0.741	0.00902967	0
PHF19	0.055050943	0.00349944	0.784	0.773	1	0
APOL1	1.13E-06	0.003271768	0.831	0.813	0.002259732	0
HEG1	2.60E-51	0.002688895	0.893	0.839	5.21E-48	0
KRT80	3.43E-14	0.002014659	0.881	0.849	6.87E-11	0
INA	0.000362846	0.001906776	0.587	0.592	0.725692844	0
TRAF1	2.43E-27	0.001852924	0.685	0.745	4.85E-24	0
C12orf42	2.29E-128	0.000446382	0.845	0.727	4.59E-125	0
BIRC5	1.43E-09	0.00041673	0.567	0.603	2.87E-06	0
MUCL1	0.009442989	0.000396961	0.709	0.72	1	0
FRMD6	0.633776538	0.000292864	0.692	0.691	1	0
IL1RL1	4.28E-18	0.000237241	0.621	0.671	8.56E-15	0
PRSS41	4.33E-102	0.000139279	0.682	0.795	8.66E-99	0
HIF1A-AS1	0.379238803	7.02E-05	0.754	0.747	1	0
KCTD12	0.005207218	4.70E-06	0.721	0.737	1	0

[cluster 1]

Gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	Cluster
WFDC2	0	1.903861499	0.975	0.875	0	1
LCN2	0	1.339272532	0.998	0.997	0	1
CEACAM5	0	1.191650273	0.988	0.929	0	1
GDF15	0	1.130097767	0.987	0.952	0	1
SLPI	0	1.097787857	1	0.997	0	1
HLA-A	0	1.067230855	0.993	0.979	0	1
SCGB3A1	5.07E-192	1.020613176	0.738	0.697	1.01E-188	1
PSCA	0	1.014988816	1	0.996	0	1
HLA-B	0	0.936611955	0.975	0.957	0	1
AGR2	0	0.936078438	0.97	0.934	0	1
SAA1	0	0.889042757	0.938	0.873	0	1
C3	0	0.826496663	0.958	0.914	0	1
PIP	0	0.81941712	0.819	0.657	0	1
FTL	0	0.813952567	0.995	0.986	0	1
RPS27L	0	0.773787136	0.981	0.955	0	1
CYB5A	0	0.752992446	0.964	0.921	0	1
IGFBP3	1.57E-304	0.701926322	0.913	0.816	3.15E-301	1
IFI6	1.03071314253281e-311	0.632456239	0.96	0.934	0.00E+00	1
CFB	0	0.620874175	0.909	0.82	0	1
NDUFB2	4.31E-282	0.61882947	0.958	0.915	8.62E-279	1
TUBA1B	0	0.615993872	0.921	0.839	0	1
CEACAM6	3.93E-206	0.604280955	0.994	0.964	7.85E-203	1
S100A6	7.84E-262	0.58347548	1	0.999	1.57E-258	1
CEBPB	4.29E-262	0.582712402	0.973	0.938	8.57E-259	1
PFN1	1.42E-225	0.568206969	0.985	0.962	2.83E-222	1
PRSS23	0	0.564697083	0.929	0.87	0	1
PHLDA2	4.73E-187	0.558532149	0.983	0.952	9.47E-184	1
STOM	1.17E-242	0.544958855	0.875	0.781	2.34E-239	1
GSN	2.68E-151	0.534365856	0.981	0.97	5.36E-148	1
PIGR	9.75E-189	0.533370773	0.777	0.68	1.95E-185	1
ZG16B	0	0.531771265	0.874	0.829	0	1
MUC1	1.67E-150	0.525783724	0.952	0.937	3.34E-147	1
VSTM2L	3.79E-200	0.524727816	0.925	0.843	7.58E-197	1

PARK7	4.05E-248	0.518579036	0.94	0.872	8.10E-245	1
SAA2	1.57E-117	0.51689989	0.9	0.865	3.13E-114	1
CDKN1A	7.92E-158	0.510544169	0.955	0.919	1.58E-154	1
HSP90AB1	1.90E-199	0.508276076	0.974	0.946	3.79E-196	1
AKR1C2	4.89E-235	0.50690978	0.857	0.782	9.78E-232	1
SELENOM	0	0.506291035	0.841	0.76	0	1
LGALS3BP	2.62E-272	0.498832587	0.967	0.93	5.25E-269	1
PSME2	2.27E-263	0.481525277	0.938	0.892	4.54E-260	1
PSMB8	4.9554784277877e-321	0.474287834	0.925	0.874	9.91095685557541e-318	1
HSPE1	4.24E-181	0.468558845	0.928	0.877	8.48E-178	1
MESP1	0	0.4555766	0.869	0.785	0	1
CD74	8.80E-156	0.447142482	0.828	0.725	1.76E-152	1
CLDN10	0	0.446622254	0.905	0.862	0	1
RDH10	5.99E-100	0.442169412	0.952	0.936	1.20E-96	1
CYCS	1.34E-232	0.432978101	0.939	0.871	2.67E-229	1
FAM3D	8.08E-245	0.430146961	0.981	0.932	1.62E-241	1
PRDX1	6.06E-113	0.406159943	0.933	0.906	1.21E-109	1
ARRB2	0	0.40046294	0.927	0.85	0	1
NDUFA4	6.04E-118	0.397856765	0.96	0.947	1.21E-114	1
NDUFAB1	1.10E-170	0.392357444	0.932	0.888	2.20E-167	1
SOD1	2.69E-158	0.389101213	0.906	0.884	5.38E-155	1
CXCL17	2.48E-109	0.387848409	0.984	0.947	4.97E-106	1
EPCAM	2.24E-143	0.384465765	0.833	0.777	4.48E-140	1
HSP90B1	1.05E-107	0.380516164	0.897	0.874	2.09E-104	1
DDIT3	1.88E-137	0.378483159	0.935	0.881	3.75E-134	1
DYNLT1	8.70E-142	0.375830035	0.977	0.966	1.74E-138	1
SDC1	2.87E-110	0.37408809	0.974	0.937	5.74E-107	1
DHCR24	4.83E-113	0.371383644	0.874	0.824	9.65E-110	1
CALM1	5.17E-88	0.360269887	0.963	0.96	1.03E-84	1
CP	1.03E-146	0.357755733	0.747	0.63	2.05E-143	1
CYBA	2.51E-100	0.357292699	0.953	0.92	5.02E-97	1
IFITM2	4.51E-65	0.35056065	0.94	0.917	9.03E-62	1
DUOXA2	1.12E-138	0.343324533	0.825	0.751	2.23E-135	1
ACTB	3.94E-57	0.341528632	0.99	0.987	7.88E-54	1
STEAP4	3.08E-143	0.340537621	0.912	0.873	6.15E-140	1
NMB	1.55E-127	0.337626058	0.85	0.81	3.11E-124	1
CTSC	5.27E-167	0.337317846	0.897	0.817	1.05E-163	1

TFPI2	1.33E-204	0.337003656	0.872	0.812	2.66E-201	1
PDZK1IP1	3.51E-127	0.335243199	0.909	0.866	7.01E-124	1
TIMP1	6.94E-176	0.333691389	0.825	0.801	1.39E-172	1
DDIT4	5.79E-82	0.326281481	0.994	0.979	1.16E-78	1
TMEM45B	1.12E-123	0.323713224	0.934	0.898	2.23E-120	1
HSPA5	2.33E-58	0.320927408	0.937	0.912	4.67E-55	1
YIF1A	2.77E-200	0.316249783	0.874	0.854	5.54E-197	1
TXN	4.17E-108	0.313429261	0.962	0.962	8.35E-105	1
MPC2	8.93E-122	0.31073665	0.928	0.892	1.79E-118	1
TNFSF10	2.28E-66	0.309054028	0.872	0.845	4.55E-63	1
RBP1	1.93E-83	0.305335779	0.926	0.878	3.86E-80	1
METTL5	5.77E-144	0.303097388	0.902	0.855	1.15E-140	1
DUOX2	3.38E-143	0.300858745	0.891	0.806	6.75E-140	1
MICOS13	1.81E-74	0.293253786	0.918	0.888	3.63E-71	1
EID1	2.69E-83	0.291817606	0.844	0.838	5.39E-80	1
CEACAM7	1.53E-149	0.291175469	0.927	0.866	3.07E-146	1
CHCHD10	9.02E-106	0.287179643	0.936	0.923	1.80E-102	1
NCL	1.70E-86	0.287128172	0.816	0.723	3.40E-83	1
AQP3	1.64E-57	0.286427703	0.955	0.93	3.28E-54	1
DHRS9	5.30E-48	0.28577475	0.985	0.973	1.06E-44	1
CBR1	3.63E-167	0.284059413	0.89	0.849	7.26E-164	1
TXNIP	4.79E-54	0.28371333	0.982	0.964	9.58E-51	1
RRM2B	1.71E-162	0.283564269	0.825	0.791	3.43E-159	1
PLIN2	2.61E-158	0.282460958	0.911	0.851	5.23E-155	1
MRPL17	9.20E-228	0.278433025	0.865	0.834	1.84E-224	1
PSMB9	2.13E-180	0.277943921	0.909	0.855	4.26E-177	1
TGM2	5.32E-243	0.276116238	0.771	0.707	1.06E-239	1
SOX4	2.52E-60	0.27576715	0.979	0.959	5.03E-57	1
MANF	7.64E-84	0.275476609	0.849	0.828	1.53E-80	1
GCHFR	1.32E-149	0.274966095	0.974	0.934	2.65E-146	1
SLC6A14	5.09E-65	0.272336667	0.978	0.945	1.02E-61	1
ARPC1B	1.45E-90	0.270492801	0.84	0.843	2.90E-87	1
TTC3	9.41E-69	0.270472136	0.907	0.859	1.88E-65	1
HLA-DQB1	6.49E-184	0.269801377	0.84	0.767	1.30E-180	1
HSPA8	3.36E-73	0.268057599	0.938	0.888	6.71E-70	1
TUBA1C	1.07E-88	0.267653178	0.925	0.884	2.14E-85	1
MSMB	4.82E-268	0.267203799	0.871	0.81	9.64E-265	1

SLC25A4	1.32E-86	0.26398774	0.869	0.85	2.64E-83	1
PLAAT4	2.17E-128	0.26153163	0.985	0.947	4.33E-125	1
CCND1	1.23E-37	0.261469342	0.966	0.962	2.47E-34	1
BANF1	3.48E-99	0.260462109	0.911	0.88	6.95E-96	1
HTATIP2	3.13E-177	0.258943095	0.898	0.86	6.27E-174	1
TMEM70	1.72E-93	0.25824351	0.855	0.826	3.43E-90	1
TNFRSF12A	1.48E-57	0.257195732	0.974	0.955	2.96E-54	1
C4orf48	2.17E-79	0.256076496	0.903	0.876	4.34E-76	1
PRDX4	4.72E-195	0.255494378	0.844	0.796	9.44E-192	1
H2BC5	1.57E-52	0.253531999	0.925	0.904	3.14E-49	1
IFITM1	1.35E-165	0.253275986	0.786	0.712	2.70E-162	1
TCIM	4.09E-211	0.252436287	0.834	0.728	8.18E-208	1
CYP4B1	6.78E-42	0.24255086	0.836	0.803	1.36E-38	1
HSP90AA1	3.98E-116	0.242194964	0.976	0.971	7.96E-113	1
EPHX1	5.20E-90	0.236258205	0.904	0.881	1.04E-86	1
HMGB3	1.57E-67	0.234202108	0.852	0.81	3.13E-64	1
MGST3	3.05E-44	0.233936157	0.885	0.878	6.09E-41	1
TMEM176A	0	0.233929887	0.909	0.843	0	1
SNHG29	2.60E-72	0.232141443	0.964	0.926	5.20E-69	1
ZFP36L1	7.72E-40	0.229512863	0.976	0.966	1.54E-36	1
CXCL8	6.24E-20	0.228650052	0.86	0.83	1.25E-16	1
AKR1C1	1.96E-96	0.226415927	0.741	0.726	3.91E-93	1
SEZ6L2	1.80E-263	0.225549725	0.852	0.779	3.61E-260	1
BIRC3	1.04E-79	0.224468966	0.901	0.849	2.08E-76	1
FABP5	1.40E-43	0.223076367	0.94	0.903	2.81E-40	1
CDKN2A	8.29E-31	0.222957928	0.842	0.815	1.66E-27	1
WNT7B	1.10E-91	0.22294259	0.929	0.881	2.20E-88	1
CCNO	2.30E-75	0.221469431	0.788	0.721	4.61E-72	1
TUBB2A	7.52E-124	0.220787163	0.833	0.807	1.50E-120	1
SOD2	1.38E-49	0.220637603	0.944	0.915	2.76E-46	1
CYP1B1	5.27E-164	0.219225322	0.808	0.804	1.05E-160	1
BPIFB1	3.06E-48	0.218958861	0.533	0.566	6.12E-45	1
DUSP23	1.97E-107	0.217946971	0.861	0.826	3.95E-104	1
CYP1A1	3.68E-303	0.217844062	0.923	0.911	7.36E-300	1
SERPINA1	1.59E-106	0.215689654	0.831	0.777	3.17E-103	1
KRT23	1.21E-36	0.214103401	0.945	0.942	2.42E-33	1
NME1	1.51E-128	0.21375418	0.875	0.844	3.02E-125	1

CCDC85B	2.85E-80	0.212668628	0.94	0.907	5.70E-77	1
PTGR1	1.26E-55	0.212271558	0.9	0.863	2.52E-52	1
TMEM176B	0	0.212269337	0.911	0.831	0	1
BPIFA1	8.39E-36	0.206173104	0.583	0.561	1.68E-32	1
TSC22D3	2.12E-47	0.205614613	0.968	0.945	4.25E-44	1
APRT	2.22E-57	0.205537614	0.926	0.903	4.44E-54	1
PRDX5	4.68E-66	0.203457994	0.972	0.969	9.36E-63	1
CYP2B7P.1	3.59E-67	0.194612426	0.746	0.695	7.18E-64	1
CALM2	8.81E-68	0.194497163	0.95	0.942	1.76E-64	1
ANXA5	2.36E-38	0.194389734	0.862	0.862	4.72E-35	1
HLA-DRB1	8.30E-66	0.187033445	0.794	0.774	1.66E-62	1
SCGB1A1	1.76E-41	0.184048187	0.589	0.68	3.52E-38	1
HSPD1	2.83E-47	0.18349551	0.875	0.805	5.66E-44	1
ADSS1	2.08E-105	0.181695729	0.864	0.837	4.16E-102	1
ID1	2.72E-22	0.180780154	0.852	0.863	5.44E-19	1
CD14	1.15E-146	0.179179708	0.812	0.755	2.31E-143	1
SERPINB11	2.21E-100	0.177422798	0.886	0.833	4.42E-97	1
IER3	2.68E-47	0.176549231	0.965	0.931	5.36E-44	1
RAMP1	2.03E-42	0.176496827	0.706	0.676	4.05E-39	1
EPRS1	1.03E-76	0.174786661	0.774	0.723	2.05E-73	1
CLDN3	5.95E-55	0.171025464	0.804	0.732	1.19E-51	1
ZFP36L2	7.12E-23	0.170613076	0.885	0.846	1.42E-19	1
VMO1	2.17E-115	0.168444443	0.739	0.695	4.34E-112	1
NR2F2	6.47E-31	0.167836381	0.874	0.821	1.29E-27	1
LRRC26	5.56E-91	0.166977416	0.867	0.804	1.11E-87	1
TFF3	5.93E-104	0.1659959	0.746	0.652	1.19E-100	1
SLC1A5	1.64E-49	0.165511822	0.681	0.665	3.28E-46	1
LDHB	5.24E-29	0.165366554	0.818	0.836	1.05E-25	1
BST2	6.82E-39	0.162508482	0.925	0.905	1.36E-35	1
CKLF	2.39E-83	0.160794772	0.806	0.792	4.79E-80	1
APOD	9.60E-80	0.160095182	0.886	0.868	1.92E-76	1
ZMAT3	1.71E-60	0.159598374	0.841	0.766	3.41E-57	1
UCP2	8.57E-22	0.159516067	0.786	0.784	1.71E-18	1
CYSTM1	1.76E-50	0.159263471	0.94	0.914	3.52E-47	1
TF	7.64E-79	0.159051614	0.796	0.708	1.53E-75	1
NFIC	1.35E-54	0.15823204	0.805	0.764	2.70E-51	1
PEG10	5.15E-43	0.157655137	0.707	0.719	1.03E-39	1

HACD3	5.50E-47	0.151561141	0.777	0.711	1.10E-43	1
TFF1	0	0.148512938	0.845	0.751	0	1
TBC1D22A-DT	1.87E-80	0.146959549	0.841	0.746	3.74E-77	1
TUBB4B	3.19E-34	0.146059168	0.89	0.882	6.38E-31	1
CCDC80	2.59E-18	0.145480667	0.746	0.701	5.18E-15	1
CX3CL1	4.45E-198	0.144650034	0.839	0.734	8.91E-195	1
RENO1	3.16E-106	0.142096776	0.898	0.809	6.31E-103	1
TAGLN2	1.63E-20	0.141678714	0.904	0.899	3.26E-17	1
CXCL6	1.07E-43	0.140411285	0.825	0.817	2.14E-40	1
STS	1.73E-32	0.136833157	0.918	0.892	3.45E-29	1
DUT	3.16E-68	0.135671227	0.906	0.863	6.32E-65	1
PRKAR2B	6.87E-70	0.134928354	0.83	0.768	1.37E-66	1
VAMP5	8.02E-38	0.133796901	0.933	0.912	1.60E-34	1
SLC34A2	1.80E-19	0.130907687	0.706	0.657	3.60E-16	1
ISG15	2.10E-54	0.130899777	0.985	0.948	4.20E-51	1
LINC01559	6.39E-26	0.13085705	0.895	0.858	1.28E-22	1
AQP5	1.39E-24	0.130436343	0.677	0.659	2.78E-21	1
MYH9	7.84E-40	0.130361536	0.913	0.853	1.57E-36	1
GLRX	6.95E-28	0.127336856	0.928	0.892	1.39E-24	1
SLC27A5	2.76E-85	0.125478051	0.851	0.816	5.52E-82	1
FOLR1	1.95E-200	0.125298777	0.81	0.728	3.91E-197	1
HLA-DRA	1.83E-46	0.124641828	0.751	0.652	3.65E-43	1
RPP38	1.32E-25	0.123702056	0.805	0.765	2.64E-22	1
CEBPD	1.75E-53	0.12335416	0.977	0.943	3.51E-50	1
KLF10	2.17E-44	0.12295976	0.924	0.875	4.33E-41	1
TEF	0.042169609	0.121854089	0.828	0.812	1	1
MUC4	4.64E-28	0.121075723	0.888	0.842	9.28E-25	1
SSB	7.35E-43	0.12097834	0.849	0.792	1.47E-39	1
ITM2C	1.33E-80	0.120651322	0.783	0.763	2.66E-77	1
CDC42EP3	1.18E-15	0.120636763	0.845	0.809	2.37E-12	1
TXNRD1	5.84E-17	0.118795161	0.927	0.921	1.17E-13	1
LEPROTL1	1.45E-32	0.118485916	0.881	0.849	2.90E-29	1
EGLN3	1.22E-05	0.116457319	0.855	0.84	0.024309212	1
GSTO1	8.17E-22	0.115598533	0.874	0.85	1.63E-18	1
NTN4	3.77E-35	0.111098997	0.942	0.912	7.53E-32	1
SAA4	2.19E-31	0.111083845	0.833	0.813	4.39E-28	1

CKS2	1.33E-19	0.110883372	0.85	0.824	2.66E-16	1
PLAAT3	4.91E-21	0.110796597	0.933	0.915	9.82E-18	1
ICAM1	3.97E-27	0.109559266	0.913	0.883	7.95E-24	1
NXN	1.19E-50	0.108323369	0.961	0.912	2.38E-47	1
GPX8	4.06E-73	0.108230456	0.699	0.588	8.12E-70	1
NQO1	5.53E-25	0.106772869	0.758	0.707	1.11E-21	1
APOL6	3.27E-18	0.106391917	0.869	0.871	6.55E-15	1
CXCL1	4.75E-19	0.10301857	0.851	0.818	9.51E-16	1
SEMA3B	4.35E-69	0.102485192	0.768	0.686	8.70E-66	1
PGAM1	1.47E-25	0.102057767	0.971	0.956	2.94E-22	1
H3C10	2.06E-31	0.1009018	0.849	0.858	4.13E-28	1
KRT81	4.74E-15	0.100731751	0.737	0.765	9.48E-12	1
ELF3-AS1	2.37E-05	0.095660134	0.852	0.847	0.047458546	1
ANG	1.31E-28	0.094993589	0.777	0.783	2.62E-25	1
ABHD2	2.91E-15	0.093710808	0.88	0.855	5.82E-12	1
JDP2	2.79E-42	0.093643104	0.844	0.779	5.57E-39	1
MIA	3.34E-35	0.093070516	0.785	0.737	6.68E-32	1
INHBB	1.04E-41	0.091626808	0.772	0.767	2.09E-38	1
STMN1	3.36E-22	0.091048776	0.754	0.77	6.71E-19	1
MTHFD2	1.89E-28	0.089330162	0.723	0.744	3.78E-25	1
EDN2	1.84E-25	0.089224674	0.862	0.826	3.67E-22	1
AARS1	4.14E-23	0.088949642	0.727	0.69	8.29E-20	1
G0S2	3.49E-41	0.086764202	0.835	0.804	6.98E-38	1
H2BC4	1.72E-10	0.086220641	0.919	0.899	3.45E-07	1
MYL9	3.31E-44	0.086191263	0.734	0.737	6.62E-41	1
LYZ	9.25E-93	0.08571384	0.767	0.692	1.85E-89	1
AZGP1	1.36E-106	0.083814261	0.702	0.771	2.72E-103	1
SPAG4	2.51E-68	0.083380633	0.831	0.794	5.01E-65	1
ADRB2	8.12E-21	0.083337934	0.825	0.812	1.62E-17	1
MB	6.58E-53	0.082207514	0.744	0.705	1.32E-49	1
CCK	1.65E-82	0.081739928	0.657	0.647	3.30E-79	1
DPCD	1.54E-18	0.080638717	0.837	0.831	3.08E-15	1
WFDC21P	9.32E-07	0.079976781	0.891	0.865	0.001864658	1
MT2A	0.000921231	0.079863758	0.669	0.658	1	1
ALDH3B1	1.33E-17	0.079509469	0.868	0.843	2.65E-14	1
RARRES2	2.09E-19	0.079432571	0.749	0.691	4.19E-16	1
ARTN	6.88E-31	0.077156951	0.781	0.788	1.38E-27	1

DEGS2	1.63E-12	0.077151139	0.807	0.813	3.25E-09	1
BHLHE41	1.51E-39	0.077057662	0.812	0.769	3.03E-36	1
TSPAN1	1.94E-58	0.075928428	0.927	0.915	3.87E-55	1
SLFN5	1.25E-09	0.075777936	0.765	0.763	2.50E-06	1
SNHG16	3.80E-08	0.075339139	0.85	0.865	7.59E-05	1
TYMP	9.03E-09	0.07514767	0.928	0.921	1.81E-05	1
AREG	7.60E-34	0.070739212	0.967	0.928	1.52E-30	1
MIR205HG	0.000101026	0.070700855	0.879	0.877	0.202051853	1
ANPEP	7.84E-69	0.069450842	0.783	0.737	1.57E-65	1
CKB	1.96E-07	0.069121405	0.915	0.9	0.000391303	1
SLC1A1	3.44E-34	0.068052923	0.819	0.769	6.88E-31	1
SMIM5	1.11E-09	0.068032086	0.901	0.874	2.23E-06	1
BABAM2	1.48E-18	0.067736431	0.889	0.846	2.97E-15	1
KYNU	3.53E-29	0.066790826	0.869	0.815	7.05E-26	1
NUCB2	7.40E-15	0.065676682	0.825	0.821	1.48E-11	1
HILPDA	9.20E-19	0.065178863	0.969	0.942	1.84E-15	1
MYH14	5.02E-31	0.064865591	0.857	0.809	1.00E-27	1
IL1R1	4.82E-14	0.064425365	0.802	0.78	9.64E-11	1
KDELR3	1.04E-68	0.064251493	0.744	0.762	2.08E-65	1
AKR1C3	4.41E-31	0.064200419	0.706	0.729	8.82E-28	1
ID3	7.68E-30	0.064002663	0.788	0.717	1.54E-26	1
SERPINB3	1.56E-23	0.063585806	0.658	0.728	3.12E-20	1
HLA-DRB5	3.06E-21	0.06205874	0.775	0.721	6.12E-18	1
RHOB	1.56E-22	0.061925221	0.808	0.756	3.11E-19	1
FCGBP	2.13E-32	0.061876782	0.651	0.567	4.26E-29	1
IQSEC1	1.99E-07	0.061608881	0.805	0.801	0.00039765	1
RPL39L	6.21E-59	0.061263281	0.724	0.614	1.24E-55	1
FBXO2	6.07E-35	0.061029016	0.709	0.704	1.21E-31	1
H4C3	3.10E-26	0.060525887	0.694	0.679	6.21E-23	1
STATH	2.26E-33	0.059271376	0.793	0.729	4.53E-30	1
IRAK3	1.98E-29	0.059084633	0.843	0.778	3.96E-26	1
DNPH1	5.09E-16	0.058895701	0.828	0.819	1.02E-12	1
VIM	1.41E-05	0.058764478	0.568	0.58	0.028262791	1
ALCAM	1.81E-23	0.058689437	0.911	0.869	3.63E-20	1
RHOF	1.06E-15	0.058364454	0.847	0.838	2.11E-12	1
NUPR1	2.84E-11	0.057889873	0.603	0.557	5.67E-08	1
PDK4	5.47E-40	0.057487782	0.807	0.721	1.09E-36	1

UGDH	1.22E-07	0.05742952	0.767	0.733	0.000244827	1
FSTL1	7.75E-10	0.056794313	0.724	0.754	1.55E-06	1
SFN	0.418071605	0.056006512	0.885	0.891	1	1
MYADM	2.10E-13	0.055337965	0.738	0.687	4.21E-10	1
CFAP298	5.25E-16	0.055245094	0.808	0.764	1.05E-12	1
KNOP1	2.54E-14	0.055233071	0.776	0.731	5.09E-11	1
KRT18	6.20E-11	0.054208189	0.969	0.95	1.24E-07	1
ELOVL6	4.55E-07	0.054196105	0.84	0.822	0.000909217	1
IL32	8.38E-49	0.054002233	0.798	0.85	1.68E-45	1
CASC8	0.08824084	0.053509841	0.843	0.837	1	1
ST3GAL4	2.34E-19	0.053475795	0.962	0.934	4.68E-16	1
AIMP2	1.18E-16	0.052950838	0.776	0.773	2.37E-13	1
HLA-DPA1	1.48E-38	0.052774968	0.759	0.663	2.95E-35	1
HERPUD1	0.002696596	0.05271454	0.861	0.85	1	1
EDIL3-DT	1.93E-66	0.052622471	0.782	0.656	3.86E-63	1
FABP3	4.73E-48	0.050832372	0.854	0.81	9.47E-45	1
C11orf96	2.54E-26	0.050434628	0.858	0.804	5.08E-23	1
TAGLN	1.86E-15	0.05042215	0.797	0.761	3.72E-12	1
PTAFR	1.94E-10	0.048378327	0.836	0.83	3.88E-07	1
COTL1	2.04E-11	0.047537225	0.725	0.744	4.08E-08	1
UPK1B	0.002706233	0.047292702	0.961	0.953	1	1
ANAPC5	7.11E-11	0.047151799	0.848	0.821	1.42E-07	1
FSTL3	4.51E-16	0.046872228	0.838	0.817	9.02E-13	1
IQCD	3.21E-12	0.046683735	0.818	0.78	6.41E-09	1
ATP12A	0.007760153	0.046618855	0.722	0.706	1	1
TRIB3	4.57E-46	0.046519169	0.826	0.748	9.15E-43	1
ARG2	8.91E-16	0.046440679	0.718	0.707	1.78E-12	1
PARM1	1.96E-31	0.046074975	0.661	0.607	3.92E-28	1
APOL1	4.34E-05	0.045741641	0.839	0.82	0.086784014	1
PPM1L	3.03E-16	0.045399901	0.869	0.819	6.06E-13	1
IFT22	5.64E-15	0.044630808	0.73	0.675	1.13E-11	1
HDGFL3	2.07E-10	0.044378308	0.706	0.737	4.15E-07	1
TMEM120B	0.002310705	0.043424563	0.764	0.772	1	1
GCLM	8.65E-13	0.042824413	0.776	0.748	1.73E-09	1
HES6	4.41E-20	0.041864816	0.732	0.681	8.83E-17	1
DDX60	4.50E-08	0.041457475	0.817	0.787	9.00E-05	1
CRYAB	1.07E-05	0.041033868	0.833	0.834	0.021471627	1

LINC01269	0.017694458	0.041003361	0.852	0.85	1	1
FLOT2	0.068517707	0.040625924	0.827	0.819	1	1
MT1F	1.73E-17	0.040026588	0.682	0.673	3.47E-14	1
HNMT	2.38E-48	0.039875105	0.732	0.754	4.76E-45	1
TMEM45A	8.71E-65	0.037912361	0.77	0.657	1.74E-61	1
RNASE1	5.15E-29	0.037262829	0.581	0.561	1.03E-25	1
LINC01429	5.61E-58	0.037259249	0.777	0.659	1.12E-54	1
UBE2S	5.82E-06	0.035664547	0.852	0.83	0.011630307	1
BCL2A1	2.79E-30	0.035434084	0.792	0.712	5.57E-27	1
MUC16	4.32E-51	0.034603335	0.726	0.608	8.64E-48	1
CXCL5	1.45E-37	0.033846839	0.729	0.652	2.91E-34	1
EMP3	2.30E-13	0.033721402	0.76	0.749	4.60E-10	1
COMETT	7.20E-35	0.033270162	0.782	0.715	1.44E-31	1
SAA2-SAA4	0.000275282	0.033227895	0.787	0.773	0.550563034	1
DUSP6	8.75E-10	0.033173478	0.693	0.716	1.75E-06	1
SPTSSB	7.82E-09	0.032846144	0.824	0.839	1.56E-05	1
S100A4	1.74E-06	0.031845035	0.941	0.935	0.003478327	1
CXCL14	7.08E-134	0.0316992	0.787	0.603	1.42E-130	1
AOC1	1.61E-43	0.031449912	0.955	0.917	3.21E-40	1
PPP1R3C	2.86E-17	0.031349244	0.902	0.876	5.72E-14	1
CLIC5	1.68E-15	0.030948774	0.685	0.624	3.35E-12	1
TBC1D10A	6.56E-06	0.030517579	0.887	0.862	0.013112689	1
GPNMB	1.85E-06	0.030346169	0.826	0.846	0.003702295	1
ATF3	2.97E-08	0.030345462	0.852	0.818	5.94E-05	1
ITGB4	6.98E-06	0.030041681	0.824	0.85	0.013960507	1
FBLN2	6.99E-18	0.029778686	0.874	0.847	1.40E-14	1
THBD	5.80E-26	0.02906848	0.835	0.774	1.16E-22	1
BPIFA2	2.16E-116	0.028968603	0.723	0.554	4.31E-113	1
PTCHD4	4.70E-06	0.028309647	0.674	0.668	0.009404766	1
FCHO1	1.11E-19	0.028210546	0.866	0.841	2.23E-16	1
H3C12	4.97E-17	0.028154525	0.824	0.798	9.94E-14	1
NR4A1	2.14E-27	0.02799079	0.864	0.799	4.27E-24	1
UGGT2	1.02E-08	0.027794061	0.769	0.725	2.04E-05	1
SMIM12	8.83E-05	0.027573092	0.888	0.869	0.176679214	1
ASB2	1.11E-51	0.0263429	0.878	0.799	2.21E-48	1
SLC26A2	0.342509382	0.025542247	0.69	0.7	1	1
RDH10-AS1	5.14E-06	0.025226168	0.805	0.798	0.010281636	1

RHOBTB3	0.201224893	0.024566158	0.851	0.852	1	1
MT-TF	3.68E-15	0.02401484	0.76	0.759	7.35E-12	1
GJB2	0.006819867	0.023250539	0.82	0.802	1	1
GADD45G	2.02E-25	0.022290845	0.803	0.734	4.04E-22	1
IL1RL1	1.60E-09	0.021930999	0.659	0.641	3.20E-06	1
NCOA7	0.010158825	0.021692903	0.757	0.774	1	1
PPBP	6.10E-110	0.02163151	0.638	0.472	1.22E-106	1
PSIP1	0.000491754	0.021188879	0.683	0.682	0.983508922	1
SULT1E1	8.68E-10	0.020945047	0.844	0.806	1.74E-06	1
TMEM61	2.89E-14	0.020473522	0.747	0.725	5.78E-11	1
IFIT1	1.59E-19	0.020438046	0.683	0.749	3.17E-16	1
FAM171B	8.31E-08	0.020410732	0.802	0.794	0.000166111	1
PTGS2	4.19E-33	0.018319332	0.762	0.7	8.38E-30	1
GFOD1	2.58E-07	0.018302374	0.771	0.732	0.000516438	1
MT-ND6	4.24E-17	0.018182698	0.773	0.711	8.47E-14	1
IRF1	4.43E-13	0.018166571	0.924	0.915	8.86E-10	1
ABCC11	1.85E-39	0.018048898	0.878	0.804	3.69E-36	1
PSAT1	4.01E-12	0.016906227	0.6	0.65	8.01E-09	1
GSTA1	3.96E-13	0.016888908	0.65	0.705	7.93E-10	1
ALDH3A1	0.000570769	0.016847229	0.716	0.743	1	1
CIART	4.32E-22	0.016684918	0.92	0.871	8.64E-19	1
SGK1	6.00E-05	0.01638992	0.77	0.743	0.120082179	1
BANK1	7.48E-05	0.016184288	0.765	0.734	0.149591866	1
HMGN3	6.66E-28	0.016037613	0.926	0.906	1.33E-24	1
KRT80	0.000363472	0.015942621	0.848	0.87	0.726944353	1
TMEM105	6.22E-35	0.015430059	0.829	0.744	1.24E-31	1
AKR1B10	3.36E-12	0.015166027	0.641	0.585	6.73E-09	1
MTX2	1.40E-09	0.015059513	0.93	0.901	2.81E-06	1
MAP9	0.003119601	0.01486311	0.721	0.703	1	1
HLA-DQA1	9.09E-30	0.014794174	0.727	0.639	1.82E-26	1
CYP2A7	0.001576764	0.014389767	0.639	0.631	1	1
LSS	9.04E-06	0.01417723	0.878	0.854	0.018072685	1
CYP27A1	7.09E-21	0.014138092	0.641	0.709	1.42E-17	1
TREM1	7.63E-21	0.014092794	0.754	0.682	1.53E-17	1
TPM2	0.116246168	0.014009093	0.74	0.737	1	1
C16orf74	0.472719049	0.014003094	0.723	0.73	1	1
SCIN	1.60E-07	0.013955579	0.806	0.768	0.000320212	1

DEFB1	0.000530513	0.013534329	0.82	0.809	1	1
STC1	8.63E-10	0.013390788	0.56	0.52	1.73E-06	1
C4orf19	9.91E-20	0.013320082	0.909	0.859	1.98E-16	1
CLGN	4.66E-13	0.012927859	0.635	0.574	9.32E-10	1
PRKAR2A	4.26E-10	0.012837039	0.822	0.786	8.52E-07	1
HMOX1	6.40E-08	0.012467734	0.88	0.85	0.000127974	1
HLA-G	0.372174368	0.011870277	0.621	0.613	1	1
TFCP2L1	1.18E-11	0.011821777	0.771	0.725	2.35E-08	1
ALPK3	5.14E-16	0.01123772	0.798	0.74	1.03E-12	1
PEBP4	1.41E-05	0.011214978	0.728	0.694	0.028270021	1
SNAP25-AS1	2.89E-39	0.011188767	0.792	0.697	5.78E-36	1
IFIT2	0.154209348	0.01109466	0.499	0.505	1	1
MAFB	2.03E-35	0.010982929	0.742	0.645	4.06E-32	1
GGNBP1	5.43E-67	0.010554883	0.841	0.722	1.09E-63	1
COL17A1	4.52E-36	0.009839007	0.467	0.571	9.03E-33	1
LAMB3	0.119314036	0.009742365	0.831	0.841	1	1
HAS3	0.004201248	0.009702837	0.558	0.58	1	1
PLAT	3.20E-32	0.008987503	0.555	0.651	6.41E-29	1
MUC5AC	1.07E-26	0.008987124	0.762	0.697	2.14E-23	1
MTR	4.08E-48	0.008801303	0.828	0.727	8.17E-45	1
DNAJB4	2.16E-05	0.008603468	0.87	0.844	0.04327214	1
MYC	0.000525237	0.008368149	0.701	0.695	1	1
IFIT3	0.000359205	0.00759522	0.668	0.693	0.718409238	1
H2BC11	0.002985332	0.007572716	0.904	0.887	1	1
ADAMTS1	0.01397222	0.007346457	0.572	0.583	1	1
PCLAF	7.45E-09	0.007189292	0.788	0.827	1.49E-05	1
PXDN	0.349637967	0.007185684	0.673	0.677	1	1
WNK2	9.25E-10	0.006995029	0.854	0.821	1.85E-06	1
MX2	0.000787583	0.006784106	0.857	0.836	1	1
TP63	0.302163703	0.006626175	0.549	0.561	1	1
THBS1	2.66E-30	0.006516446	0.85	0.775	5.32E-27	1
EPPK1	2.13E-12	0.006481829	0.675	0.62	4.27E-09	1
IGSF11	1.15E-18	0.006438062	0.809	0.747	2.30E-15	1
TIMP3	6.36E-133	0.006369886	0.768	0.576	1.27E-129	1
ALKAL1	9.71E-18	0.006127895	0.626	0.567	1.94E-14	1
INA	0.088392927	0.006078781	0.604	0.587	1	1
CENPW	1.32E-07	0.00594388	0.815	0.778	0.000263219	1

GOLGA7B-DT	1.31E-29	0.005544985	0.842	0.767	2.62E-26	1
TMEM132B	8.54E-28	0.005462328	0.749	0.672	1.71E-24	1
TMEM47	3.78E-37	0.005331781	0.763	0.666	7.56E-34	1
AGBL1	5.92E-13	0.005202958	0.767	0.713	1.18E-09	1
RGS16	9.56E-24	0.00504652	0.649	0.724	1.91E-20	1
JUN	1.54E-10	0.004796338	0.833	0.79	3.09E-07	1
MARCHF1	0.057973645	0.004687982	0.657	0.648	1	1
LINC01482	2.61E-36	0.004674719	0.698	0.599	5.23E-33	1
NTNG2	2.56E-11	0.004524574	0.695	0.651	5.12E-08	1
POLR2B	5.06E-25	0.003747678	0.883	0.82	1.01E-21	1
POLD3	3.65E-05	0.003633192	0.875	0.85	0.073045877	1
SLC7A5	0.104794655	0.003595059	0.824	0.816	1	1
RARRES1	6.12E-14	0.003490189	0.692	0.716	1.22E-10	1
KDR	5.46E-18	0.003467022	0.48	0.541	1.09E-14	1
NALF1	1.72E-11	0.003154794	0.701	0.647	3.45E-08	1
LINC02343	6.70E-13	0.003045497	0.657	0.598	1.34E-09	1
AGPAT5	0.000129126	0.002809724	0.705	0.68	0.25825209	1
EVI5L	1.26E-14	0.002572862	0.826	0.773	2.52E-11	1
PCLO	8.94E-05	0.002470462	0.813	0.785	0.178868822	1
DUSP14	0.808504395	0.002355626	0.79	0.788	1	1
ZBTB10	3.76E-22	0.002226465	0.799	0.729	7.53E-19	1
NKAIN3	4.70E-72	0.002050264	0.761	0.625	9.41E-69	1
SLC41A2	0.37439618	0.001639165	0.794	0.785	1	1
NTN1	7.70E-46	0.001489209	0.85	0.755	1.54E-42	1
SHISA8	2.03E-21	0.001447054	0.776	0.706	4.06E-18	1
TMEM178B	0.023726696	0.001282676	0.635	0.646	1	1
FIGN	0.029519755	0.001137963	0.64	0.625	1	1
KRT7	1.64E-05	0.000978985	0.997	0.992	0.032836818	1
PKIB	0.131217763	0.000911614	0.693	0.685	1	1
ZNF57	5.14E-06	0.000632248	0.831	0.801	0.010282374	1
FOS	8.76E-12	0.000615081	0.897	0.869	1.75E-08	1
KRT86	2.34E-08	0.000564998	0.782	0.748	4.68E-05	1
HIF1A-AS1	2.25E-22	0.000481985	0.807	0.741	4.49E-19	1
LIF	4.10E-12	0.000117967	0.81	0.761	8.20E-09	1
GJC1	0.001485478	0.000103604	0.805	0.787	1	1

[cluster 2]

Gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	Cluster
NEAT1	0	2.188422151	0.999	0.994	0	2
LINC00511	0	1.91583351	0.979	0.916	0	2
MALAT1	0	1.808228876	0.999	0.996	0	2
CPEB3	0	1.742394345	0.966	0.95	0	2
AFF1	0	1.635794408	0.975	0.957	0	2
RAPGEF2	0	1.59402561	0.948	0.92	0	2
MYO5B	0	1.538782112	0.967	0.938	0	2
MGAT5	0	1.523114981	0.948	0.916	0	2
FNDC3B	0	1.51874427	0.981	0.951	0	2
CBLB	0	1.518737017	0.945	0.867	0	2
PATJ	0	1.475088214	0.97	0.931	0	2
INPP4B	0	1.460542768	0.981	0.951	0	2
XIST	0	1.438713179	0.963	0.888	0	2
PICALM	0	1.403536442	0.966	0.95	0	2
FAM214A	0	1.337703603	0.959	0.929	0	2
FTX	0	1.31002613	0.957	0.856	0	2
ZNF292	0	1.302255175	0.971	0.938	0	2
ZSWIM6	0	1.291634287	0.934	0.876	0	2
WSB1	0	1.28086546	0.951	0.916	0	2
MACF1	0	1.266640241	0.97	0.926	0	2
EXOC6B	0	1.266603005	0.961	0.924	0	2
TMTC2	0	1.264847128	0.951	0.891	0	2
GPCPD1	0	1.255376111	0.979	0.964	0	2
RBM47	0	1.239557358	0.971	0.946	0	2
SPIRE1	0	1.227854416	0.954	0.921	0	2
RALGPS2	0	1.223610759	0.946	0.935	0	2
B4GALT5	0	1.219369829	0.984	0.968	0	2
PHLPP1	0	1.213528462	0.94	0.918	0	2
DOCK9	0	1.198710352	0.972	0.923	0	2
ETV6	0	1.194764894	0.963	0.941	0	2
RASAL2	0	1.191173643	0.971	0.928	0	2
SMAD3	0	1.189462294	0.964	0.942	0	2
GTF2IRD1	0	1.18488014	0.944	0.922	0	2

KDM6A	0	1.180424557	0.952	0.897	0	2
FHIP1A	0	1.161838026	0.947	0.896	0	2
SOS1	0	1.142554874	0.938	0.908	0	2
LPP	0	1.137558178	0.97	0.893	0	2
RICTOR	0	1.132378193	0.951	0.928	0	2
QKI	0	1.123910029	0.964	0.936	0	2
ABHD3	0	1.113618094	0.942	0.933	0	2
ABTB2	0	1.112151868	0.94	0.921	0	2
EFNA5	0	1.097363134	0.935	0.768	0	2
LINC-PINT	0	1.083348209	0.941	0.877	0	2
HIVEP2	0	1.082583815	0.934	0.895	0	2
NEBL	0	1.081518472	0.966	0.933	0	2
TSC22D2	0	1.079245774	0.966	0.938	0	2
HIF1A-AS3	0	1.073026403	0.886	0.886	0	2
SAMD12	0	1.060784603	0.941	0.857	0	2
THRB	0	1.060347846	0.901	0.794	0	2
MT-CO3	0	1.055582707	0.999	0.996	0	2
MAML2	0	1.035967662	0.966	0.866	0	2
MAML3	0	1.034979345	0.919	0.84	0	2
ZBTB20	0	1.021852225	0.937	0.831	0	2
STAG1	0	1.018134411	0.886	0.814	0	2
CDYL	0	1.009459597	0.97	0.964	0	2
SH3PXD2B	0	0.994010891	0.93	0.874	0	2
TANC2	0	0.99289945	0.943	0.875	0	2
CLIP1	0	0.987044806	0.965	0.946	0	2
CDKAL1	0	0.966427532	0.934	0.829	0	2
KIAA1217	0	0.964380235	0.957	0.905	0	2
MT-ATP8	0	0.960238531	0.947	0.917	0	2
TPCN1	0	0.950282241	0.921	0.844	0	2
NDRG1	0	0.946839608	0.931	0.926	0	2
MT-CO2	0	0.94007361	0.999	0.997	0	2
INSR	0	0.936227564	0.933	0.921	0	2
SRGAP1	0	0.932658313	0.935	0.854	0	2
MAP3K9	0	0.924829404	0.924	0.899	0	2
SREBF2	0	0.912807157	0.933	0.891	0	2
ATG9B	0	0.911920874	0.953	0.931	0	2
PSD3	0	0.910786804	0.95	0.862	0	2

MAP3K5	0	0.901418902	0.943	0.872	0	2
MACC1	0	0.900109545	0.977	0.951	0	2
SVIL	0	0.895956842	0.935	0.878	0	2
SSBP2	0	0.883548671	0.937	0.893	0	2
MT-ND5	0	0.883308337	0.992	0.993	0	2
MT-ND1	0	0.882604441	0.993	0.99	0	2
MBD5	0	0.882151198	0.931	0.876	0	2
SIPA1L1	0	0.873014011	0.9	0.832	0	2
SPIDR	0	0.869768491	0.919	0.832	0	2
MRTFA	0	0.855037355	0.907	0.819	0	2
CHKA	0	0.852914227	0.925	0.901	0	2
ARHGEF3	0	0.849126952	0.942	0.862	0	2
DPYD	0	0.846709851	0.903	0.857	0	2
SLC20A1	2.76E-218	0.844806695	0.906	0.921	5.51E-215	2
MT-CYB	0	0.841764415	0.998	0.997	0	2
DENND2C	0	0.837567187	0.927	0.945	0	2
HDAC9	0	0.8340189	0.959	0.918	0	2
PTPN3	0	0.828699181	0.933	0.88	0	2
SAMD4A	0	0.828690433	0.86	0.832	0	2
MT-RNR1	0	0.827018328	1	0.999	0	2
NR6A1	0	0.818676891	0.905	0.871	0	2
PLD1	0	0.814732029	0.915	0.896	0	2
RUNX1	0	0.81432389	0.921	0.846	0	2
MEIS1	0	0.814007237	0.887	0.834	0	2
RAI14	0	0.811270307	0.921	0.868	0	2
CLIP4	0	0.808412952	0.931	0.884	0	2
IKZF2	0	0.808188227	0.94	0.891	0	2
PAFAH1B1	0	0.807985468	0.95	0.929	0	2
MT-ATP6	0	0.805969123	0.997	0.995	0	2
PRKCH	0	0.801786934	0.936	0.907	0	2
TPST1	0	0.797116111	0.95	0.913	0	2
MT-ND3	0	0.79539357	0.997	0.996	0	2
MT-ND4	0	0.794208277	0.998	0.998	0	2
MAGI1	0	0.791549374	0.948	0.859	0	2
SNX25	0	0.790826776	0.841	0.862	0	2
MECOM	0	0.788164945	0.929	0.827	0	2
MT-ND2	0	0.785534889	0.995	0.996	0	2

MTUS1-DT	0	0.784596444	0.915	0.89	0	2
TSHZ2	0	0.778679459	0.884	0.773	0	2
MT-CO1	8.93282545256474e-318	0.778053556	1	0.998	1.78656509051295e-314	2
ARHGEF10L	0	0.777708593	0.949	0.893	0	2
CAMK1D	0	0.776528494	0.902	0.77	0	2
ITGB8	1.62E-297	0.773984367	0.976	0.967	3.23E-294	2
TMEM117	0	0.772413282	0.888	0.826	0	2
ZHX2	0	0.771114972	0.891	0.84	0	2
PTPN12	0	0.767476506	0.905	0.905	0	2
ATXN1	0	0.766646377	0.92	0.875	0	2
GRHL1	0	0.761180597	0.942	0.919	0	2
TBC1D5	0	0.75580829	0.896	0.798	0	2
PALM2AKAP2	0	0.752823561	0.91	0.862	0	2
PCSK5	0	0.75225083	0.912	0.857	0	2
AEBP2	0	0.751972145	0.918	0.865	0	2
ARHGAP10	0	0.748272188	0.895	0.867	0	2
TALAM1	1.02E-298	0.743275742	0.906	0.83	2.03E-295	2
CERS6	0	0.743148068	0.948	0.859	0	2
ZCCHC7	0	0.738327667	0.851	0.766	0	2
BMPR1B	0	0.736933822	0.924	0.831	0	2
DOCK5	0	0.719331307	0.874	0.867	0	2
RASA1	0	0.717681598	0.928	0.865	0	2
KYNU	0	0.715956339	0.879	0.813	0	2
MAST4	0	0.710003548	0.927	0.85	0	2
DENND4A	0	0.703993465	0.884	0.789	0	2
AGAP1	0	0.700372903	0.853	0.705	0	2
GULP1	0	0.69187805	0.912	0.84	0	2
IGF2BP3	0	0.690237314	0.905	0.816	0	2
SORBS2	7.4961264512029e-314	0.689100443	0.938	0.9	1.49922529024058e-310	2
SESTD1	0	0.688372519	0.884	0.869	0	2
SRGAP3	0	0.687241295	0.902	0.797	0	2
INTS6	0	0.683457757	0.884	0.794	0	2
RAD51B	0	0.677154163	0.895	0.766	0	2
FBXL17	0	0.676556364	0.903	0.826	0	2
DENND1B	0	0.676523778	0.937	0.89	0	2
NR3C2	0	0.671674441	0.838	0.718	0	2
TNRC6B	0	0.669407528	0.891	0.806	0	2

KDM3A	0	0.661126786	0.93	0.921	0	2
KLRD1	0	0.658366931	0.792	0.808	0	2
MYOF	1.89E-300	0.655049214	0.92	0.888	3.78E-297	2
PDK1	0	0.654399425	0.876	0.804	0	2
STS	6.90E-272	0.651087954	0.937	0.888	1.38E-268	2
MEIS2	0	0.647420892	0.866	0.815	0	2
ALCAM	1.68E-252	0.647036345	0.942	0.863	3.35E-249	2
EPS8	0	0.643640233	0.884	0.801	0	2
TMC1	0	0.641106776	0.782	0.814	0	2
NRIP1	0	0.640696779	0.937	0.898	0	2
EXOC4	0	0.638935707	0.935	0.856	0	2
ZMYND8	0	0.631838906	0.917	0.88	0	2
FMNL2	0	0.626792918	0.842	0.802	0	2
PTPRM	0	0.626792147	0.85	0.788	0	2
CGNL1	0	0.624540565	0.89	0.876	0	2
FER1L6	0	0.622432145	0.826	0.742	0	2
GAB1	0	0.6168525	0.854	0.818	0	2
WWC1	0	0.61678831	0.927	0.895	0	2
LINC01705	5.16E-208	0.6165398	0.897	0.877	1.03E-204	2
UNC13B	0	0.604635601	0.838	0.805	0	2
MYO1E	0	0.602739164	0.953	0.905	0	2
LINC02649	0	0.597204301	0.843	0.833	0	2
NTN4	4.96197045037406e-318	0.596950616	0.933	0.914	9.92394090074811e-315	2
KAT2B	0	0.593911528	0.906	0.893	0	2
VPS13B	0	0.59277251	0.891	0.808	0	2
LINC01004	0	0.591910587	0.911	0.793	0	2
DNAAF9	0	0.590765977	0.916	0.836	0	2
SEMA5A	0	0.59024748	0.923	0.86	0	2
NABP1	0	0.588052607	0.929	0.904	0	2
PYGB	0	0.588001135	0.904	0.829	0	2
TACC2	0	0.584702497	0.906	0.844	0	2
FNIP2	0	0.580655142	0.922	0.86	0	2
FHIT	0	0.577378343	0.859	0.772	0	2
ATG7	0	0.575306132	0.863	0.802	0	2
ARHGAP30	0	0.57508653	0.867	0.83	0	2
TMCC3	4.72E-199	0.573410832	0.94	0.936	9.44E-196	2
XDH	0	0.57330514	0.909	0.897	0	2

DLEU2	0	0.571439137	0.853	0.754	0	2
PITX1-AS1	0	0.566738413	0.861	0.793	0	2
SMYD3	0	0.564169393	0.864	0.708	0	2
FAM13A	4.47E-243	0.563756238	0.897	0.876	8.94E-240	2
FGD6	0	0.55845519	0.873	0.819	0	2
MLLT3	0	0.550865212	0.826	0.742	0	2
PDZD2	0	0.544579598	0.884	0.851	0	2
C11orf80	0	0.544446243	0.895	0.853	0	2
GPHN	0	0.542836592	0.795	0.765	0	2
BCAS3	2.40E-297	0.538659768	0.898	0.837	4.80E-294	2
DOCK4	0	0.536601374	0.842	0.74	0	2
FBXL2	0	0.535103018	0.906	0.839	0	2
GRHL2	2.85E-251	0.534478082	0.846	0.782	5.70E-248	2
TRIO	1.99143039869231e-319	0.529086031	0.895	0.764	3.98286079738462e-316	2
RNF152	0	0.524779493	0.833	0.803	0	2
TIAM1	0	0.524742144	0.877	0.832	0	2
RHOBTB3	0	0.524362861	0.913	0.84	0	2
OSBPL10	0	0.520283182	0.881	0.842	0	2
STXBP1	0	0.5172065	0.858	0.855	0	2
NBEA	4.11E-302	0.516666544	0.898	0.727	8.22E-299	2
GBE1	0	0.515393846	0.895	0.82	0	2
LINC02257	0	0.513382512	0.904	0.822	0	2
NSMCE2	1.48219693752374e-323	0.509818841	0.9	0.844	2.96439387504748e-320	2
ABL2	0	0.508171165	0.887	0.799	0	2
NFIA	5.22E-261	0.500752474	0.933	0.808	1.04E-257	2
ACER2	0	0.500429431	0.882	0.835	0	2
EXT1	9.14E-246	0.499809306	0.812	0.649	1.83E-242	2
SCARB1	0	0.498041935	0.875	0.824	0	2
ADARB2	0	0.497383163	0.768	0.612	0	2
C4orf19	5.73E-257	0.494014788	0.896	0.861	1.15E-253	2
GABRE	0	0.490707493	0.866	0.813	0	2
BTBD9	1.73E-272	0.489731158	0.884	0.804	3.45E-269	2
SETX	0	0.485546561	0.88	0.817	0	2
LPIN1	0	0.484455277	0.944	0.928	0	2
RIN2	1.61E-221	0.482254326	0.911	0.879	3.22E-218	2
CDC42BPA	0	0.482217063	0.905	0.78	0	2
PACS1	0	0.481744195	0.884	0.821	0	2

PRKN	0	0.478193375	0.831	0.776	0	2
ARID5B	5.29048375896378e-314	0.478081056	0.894	0.877	1.05809675179276e-310	2
PBX1	5.06E-267	0.477951082	0.89	0.79	1.01E-263	2
BACH2	0	0.474226124	0.849	0.783	0	2
BCAT1	6.47E-207	0.471680938	0.904	0.861	1.29E-203	2
AHDC1	0	0.46990956	0.928	0.895	0	2
PLEKHG1	0	0.468386815	0.907	0.818	0	2
GPRC5D-AS1	0	0.467081961	0.857	0.826	0	2
TRPS1	0	0.464952442	0.858	0.765	0	2
PFKFB4	0	0.464742328	0.841	0.796	0	2
LIMCH1	9.38E-230	0.463844925	0.672	0.609	1.88E-226	2
RANBP17	0	0.458995277	0.89	0.803	0	2
MTATP6P1	1.67E-196	0.458860724	0.896	0.877	3.35E-193	2
SLC20A2	1.33E-191	0.452816796	0.937	0.921	2.65E-188	2
PPM1L	3.5804354356653e-316	0.448839597	0.896	0.813	7.16087087133061e-313	2
SNHG14	0	0.447805851	0.844	0.77	0	2
KCNQ1OT1	0	0.440078741	0.789	0.75	0	2
RAB31	2.19673295496825e-317	0.439358234	0.902	0.85	4.39346590993649e-314	2
ARL15	0	0.435667965	0.814	0.714	0	2
PNLIPRP3	7.30E-84	0.434678896	0.912	0.886	1.46E-80	2
PRKCA	1.09E-306	0.432234052	0.835	0.8	2.18E-303	2
IL6R	0	0.431989796	0.837	0.821	0	2
AMN1	6.55E-164	0.431309137	0.903	0.889	1.31E-160	2
FER	5.88E-270	0.421968473	0.831	0.768	1.18E-266	2
KLF12	5.88E-170	0.419293508	0.831	0.797	1.18E-166	2
CPNE8	6.21E-273	0.418938592	0.886	0.826	1.24E-269	2
HS6ST2	0	0.41743767	0.819	0.76	0	2
FGF13	0	0.413007255	0.824	0.692	0	2
SEMA3C	9.11E-240	0.412790549	0.849	0.833	1.82E-236	2
LGR4	5.13E-272	0.407279467	0.831	0.788	1.03E-268	2
TTLL5	1.85E-275	0.405615992	0.883	0.81	3.70E-272	2
TFCP2L1	0	0.404973055	0.811	0.718	0	2
APBB2	1.07795242609643e-319	0.402946405	0.832	0.73	2.15590485219286e-316	2
C3	5.55E-81	0.398910991	0.95	0.916	1.11E-77	2
SPNS2	7.14E-164	0.390481448	0.947	0.954	1.43E-160	2
OGDH	2.40E-242	0.389805172	0.872	0.841	4.81E-239	2
WNT2B	0	0.388005736	0.838	0.818	0	2

PDE4D	3.47E-123	0.387591519	0.793	0.688	6.94E-120	2
BABAM2	3.49E-213	0.385539369	0.877	0.848	6.99E-210	2
CPEB2	2.28E-285	0.382137257	0.869	0.872	4.55E-282	2
CFAP20DC	7.50E-106	0.38203786	0.838	0.846	1.50E-102	2
ELOVL7	0	0.381106288	0.88	0.867	0	2
SPDYA	0	0.379736365	0.861	0.779	0	2
KLF7	1.02E-254	0.378287353	0.867	0.793	2.04E-251	2
DAPK2	0	0.376504887	0.798	0.829	0	2
C12orf56	1.13E-221	0.376192729	0.838	0.787	2.26E-218	2
EEPD1	0	0.373777541	0.82	0.833	0	2
GMDS-DT	8.70E-251	0.372058233	0.882	0.761	1.74E-247	2
MTSS1	1.51E-164	0.368495756	0.906	0.894	3.02E-161	2
EHBP1	4.93E-245	0.365471713	0.812	0.667	9.86E-242	2
ASAP2	3.07E-250	0.360267815	0.87	0.835	6.15E-247	2
IMMP2L	1.15E-188	0.359586829	0.824	0.716	2.31E-185	2
CCDC18-AS1	1.68E-284	0.352730061	0.832	0.783	3.36E-281	2
PLOD2	8.21E-105	0.352640525	0.775	0.747	1.64E-101	2
SMOC1	0	0.350253017	0.696	0.707	0	2
LINC01473	8.11866196521562e-314	0.346026546	0.876	0.744	1.62373239304312e-310	2
ELOVL6	1.72E-228	0.34224442	0.847	0.821	3.45E-225	2
USP32	8.47E-251	0.339517782	0.846	0.808	1.69E-247	2
CNNM2	6.52E-211	0.337350361	0.81	0.758	1.30E-207	2
ASAP1	1.17E-231	0.337127365	0.886	0.805	2.35E-228	2
ADCY9	1.44E-280	0.334683699	0.866	0.829	2.89E-277	2
MXD1	1.54E-39	0.331038093	0.971	0.975	3.08E-36	2
BICRAL	5.33E-219	0.331007819	0.856	0.831	1.07E-215	2
ARHGAP24	2.26E-187	0.330467176	0.781	0.727	4.52E-184	2
PLXDC2	8.42E-270	0.329155395	0.842	0.795	1.68E-266	2
PCBP1-AS1	1.70E-247	0.326900807	0.865	0.833	3.41E-244	2
PAPSS1	9.20E-134	0.326244312	0.907	0.889	1.84E-130	2
PLSCR2	0	0.321215084	0.844	0.732	0	2
DAPK1	9.88131291682493e-324	0.320006838	0.781	0.709	1.97626258336499e-320	2
MYH9	1.25E-158	0.316981721	0.896	0.856	2.50E-155	2
GRIP1	2.13E-215	0.316642243	0.798	0.667	4.27E-212	2
ITPR1	9.93E-230	0.312027228	0.752	0.75	1.99E-226	2
DMGDH	2.15E-192	0.311555455	0.839	0.769	4.29E-189	2
TENT5A	5.76E-154	0.310894785	0.828	0.845	1.15E-150	2

CDK14	8.64E-306	0.309341425	0.815	0.754	1.73E-302	2
GNE	7.61E-134	0.308989568	0.885	0.906	1.52E-130	2
MUC16	1.50E-49	0.305219397	0.681	0.617	3.00E-46	2
ST3GAL6	1.66E-209	0.303403321	0.784	0.781	3.32E-206	2
EOLA2-DT	0	0.29961345	0.851	0.73	0	2
NINL	0	0.298192504	0.846	0.835	0	2
PTPRN2	1.11E-231	0.297009058	0.796	0.737	2.21E-228	2
RDH10	2.16E-46	0.29637198	0.954	0.936	4.33E-43	2
CNST	1.33E-174	0.292485903	0.867	0.872	2.67E-171	2
CPNE4	0	0.291270914	0.799	0.711	0	2
RDH10-AS1	3.61E-168	0.291189147	0.791	0.8	7.22E-165	2
ERO1B	5.61E-234	0.290369373	0.788	0.768	1.12E-230	2
HK2	1.51E-65	0.290253508	0.886	0.905	3.02E-62	2
PRIM2	5.01E-199	0.289018795	0.821	0.786	1.00E-195	2
FRMD5	3.26E-249	0.287297983	0.786	0.722	6.52E-246	2
TMPRSS11F	7.07E-236	0.286765857	0.936	0.865	1.41E-232	2
PAG1	0	0.286514067	0.827	0.756	0	2
CAMKMT	1.73E-125	0.284549086	0.824	0.726	3.46E-122	2
SHROOM3	1.31E-96	0.283069619	0.905	0.894	2.62E-93	2
IRS2	1.85E-143	0.280501576	0.809	0.846	3.69E-140	2
MUC4	1.04E-89	0.280148697	0.853	0.848	2.07E-86	2
RAP1GAP2	2.34E-297	0.279313248	0.832	0.791	4.67E-294	2
WNK2	2.61E-294	0.278632245	0.836	0.825	5.23E-291	2
STEAP4	8.37E-90	0.277534261	0.908	0.874	1.67E-86	2
KAZN	1.51E-139	0.277524835	0.868	0.827	3.01E-136	2
FUT11	1.41E-160	0.276126241	0.864	0.851	2.82E-157	2
THSD4	3.28E-213	0.274181232	0.826	0.664	6.56E-210	2
DGKH	1.77E-139	0.271178517	0.843	0.759	3.54E-136	2
SLC44A3-AS1	4.48E-149	0.2701415	0.856	0.824	8.97E-146	2
RESF1	5.51E-47	0.269918831	0.933	0.945	1.10E-43	2
CRY1	5.22E-152	0.269390558	0.807	0.844	1.04E-148	2
NFIB	1.72E-138	0.268469885	0.788	0.655	3.43E-135	2
TIAM2	2.89E-304	0.267736133	0.846	0.772	5.77E-301	2
MFSD4B	3.23E-222	0.267225108	0.827	0.777	6.47E-219	2
TXNRD1	2.39E-80	0.265631645	0.944	0.918	4.79E-77	2
ANKRD36C	7.89E-83	0.264232314	0.808	0.764	1.58E-79	2
MATN1	0.000104688	0.263595257	0.469	0.489	0.209376304	2

PRELID2	8.02E-299	0.263143081	0.833	0.714	1.60E-295	2
TBCK	1.13E-178	0.262476329	0.826	0.765	2.25E-175	2
RIPK1	3.01E-185	0.261399632	0.847	0.803	6.01E-182	2
TENM4	1.21E-129	0.260715524	0.734	0.74	2.42E-126	2
LINC01344	1.43E-202	0.260645088	0.858	0.719	2.86E-199	2
A2ML1	8.16E-20	0.259321411	0.877	0.854	1.63E-16	2
ZFPM2-AS1	1.91E-204	0.257571453	0.895	0.822	3.83E-201	2
TGFB2	1.97E-290	0.257121833	0.883	0.743	3.94E-287	2
CCSER1	4.16E-163	0.256390524	0.751	0.669	8.33E-160	2
IQSEC1	7.05E-199	0.255554215	0.852	0.792	1.41E-195	2
DUOX2	1.42E-100	0.255049437	0.84	0.815	2.84E-97	2
NXN	1.37E-84	0.254512704	0.902	0.923	2.74E-81	2
GLCCI1	6.15E-135	0.254373316	0.796	0.75	1.23E-131	2
LRMDA	3.70E-136	0.25431814	0.837	0.731	7.41E-133	2
HMGCS1	5.12E-83	0.253062599	0.881	0.88	1.02E-79	2
MSI2	4.53E-130	0.252571369	0.86	0.775	9.06E-127	2
HEG1	3.00E-121	0.252362114	0.882	0.866	6.00E-118	2
WDR43	4.42E-136	0.251257456	0.804	0.758	8.84E-133	2
ATP2C2	6.56E-99	0.250287509	0.781	0.727	1.31E-95	2
TTC3	3.46E-97	0.248589501	0.853	0.869	6.93E-94	2
KANK1	5.54E-221	0.248503079	0.845	0.707	1.11E-217	2
MOB3B	4.45E-294	0.248355735	0.809	0.735	8.89E-291	2
SH3TC2	0	0.248346737	0.889	0.812	0	2
PIK3IP1-DT	0	0.247706241	0.795	0.77	0	2
DHRS9	4.17E-30	0.246638771	0.969	0.976	8.35E-27	2
ATP6V0D2	0	0.245426382	0.844	0.846	0	2
NTN1	2.44E-201	0.245039428	0.823	0.76	4.89E-198	2
ZMAT3	7.77E-132	0.24425436	0.851	0.764	1.55E-128	2
MICAL3	5.01E-238	0.244198777	0.842	0.789	1.00E-234	2
DLG2	2.85E-241	0.241839433	0.805	0.743	5.70E-238	2
LINC01876	5.14E-132	0.241011049	0.829	0.701	1.03E-128	2
PIGN	7.48E-188	0.238579804	0.798	0.781	1.50E-184	2
LUCAT1	3.24E-213	0.237820488	0.828	0.643	6.48E-210	2
ROBO1	7.43E-307	0.235950595	0.818	0.646	1.49E-303	2
NR2F2-AS1	8.98E-241	0.235264465	0.774	0.764	1.80E-237	2
LURAP1L-AS1	3.97E-123	0.234039601	0.743	0.747	7.94E-120	2
LINC00862	0	0.233897863	0.785	0.738	0	2

NEDD4	7.82E-243	0.225468176	0.868	0.796	1.56E-239	2
RIMS2	7.65E-258	0.224934141	0.864	0.745	1.53E-254	2
ITGA2	8.21E-77	0.224259628	0.895	0.873	1.64E-73	2
ARHGAP26	2.21E-160	0.223109516	0.806	0.73	4.41E-157	2
NAV2	7.89E-109	0.222772702	0.863	0.816	1.58E-105	2
GCLC	7.32E-101	0.222455698	0.818	0.767	1.46E-97	2
LINC00342	1.96E-81	0.221227249	0.731	0.699	3.91E-78	2
FUT10	4.83E-146	0.21883643	0.861	0.819	9.66E-143	2
SYTL3	3.40E-118	0.217019815	0.789	0.72	6.80E-115	2
VRK2	2.65E-105	0.216286185	0.878	0.862	5.30E-102	2
MICAL2	5.01E-120	0.216219861	0.828	0.777	1.00E-116	2
ITGA5	8.00E-96	0.211917467	0.849	0.841	1.60E-92	2
FKBP5	2.68E-97	0.211499773	0.777	0.746	5.36E-94	2
NAALADL2	1.37E-99	0.211239774	0.847	0.74	2.73E-96	2
BIRC3	6.93E-54	0.209204153	0.88	0.852	1.39E-50	2
MX2	2.53E-90	0.205937584	0.809	0.845	5.06E-87	2
BARD1	1.80E-146	0.20313085	0.823	0.854	3.61E-143	2
MTR	5.87E-175	0.201355336	0.782	0.735	1.17E-171	2
ZNF337-AS1	1.41E-145	0.199748022	0.779	0.786	2.82E-142	2
FRMD3	1.14E-194	0.198395336	0.828	0.751	2.29E-191	2
PVT1	2.53E-118	0.197760682	0.787	0.743	5.05E-115	2
SLC24A3	0	0.196391883	0.869	0.808	0	2
ADAMTS17	0	0.196248415	0.833	0.821	0	2
PCDH7	3.53E-97	0.195625863	0.81	0.701	7.05E-94	2
DUSP5-DT	6.00E-197	0.194754076	0.836	0.805	1.20E-193	2
PPP1R9A	4.83E-106	0.194726854	0.825	0.719	9.65E-103	2
SLC30A4	9.11E-231	0.194111586	0.841	0.789	1.82E-227	2
PACS2	6.51E-155	0.19289123	0.861	0.805	1.30E-151	2
MMADHC-DT	5.95E-120	0.192875699	0.778	0.76	1.19E-116	2
NDRG4	1.44E-256	0.191247973	0.905	0.849	2.89E-253	2
ELAVL2	1.64E-244	0.190686245	0.779	0.668	3.27E-241	2
APOLD1	7.64E-114	0.190115496	0.741	0.792	1.53E-110	2
MAF	1.90E-48	0.187990145	0.828	0.857	3.81E-45	2
TRIM14	3.09E-143	0.18773989	0.822	0.818	6.17E-140	2
FAT1	4.66E-79	0.186846364	0.794	0.783	9.32E-76	2
ZSCAN31	1.91E-131	0.185966173	0.853	0.783	3.82E-128	2
SHANK2	3.92E-103	0.185899156	0.85	0.786	7.84E-100	2

DCAKD	2.06E-107	0.18572083	0.813	0.816	4.12E-104	2
IARS1	9.64E-78	0.185263458	0.786	0.765	1.93E-74	2
SLCO3A1	1.16E-85	0.184652719	0.856	0.82	2.32E-82	2
SAMD12-AS1	6.27E-147	0.184627871	0.727	0.711	1.25E-143	2
STOX2	3.15E-138	0.183108003	0.797	0.782	6.30E-135	2
RPS6KC1	3.33E-122	0.181772534	0.803	0.785	6.66E-119	2
APBA1	0	0.180524828	0.826	0.745	0	2
PHLDB2	1.82E-111	0.179369624	0.775	0.708	3.65E-108	2
LARGE1	4.87E-173	0.1793287	0.701	0.615	9.74E-170	2
LTBP1	1.15E-101	0.178351158	0.783	0.679	2.31E-98	2
CRIM1	9.60E-56	0.178170735	0.783	0.761	1.92E-52	2
MYOM1	2.77E-206	0.178027733	0.814	0.783	5.54E-203	2
LINC01619	4.18E-215	0.177668891	0.811	0.69	8.35E-212	2
IGSF11	1.93E-179	0.177059069	0.754	0.757	3.86E-176	2
EGFR	2.15E-42	0.176443092	0.85	0.845	4.30E-39	2
ZNHIT6	4.51E-182	0.176355547	0.826	0.695	9.02E-179	2
EVC	5.52E-151	0.175247668	0.881	0.816	1.10E-147	2
PARD3B	4.44E-70	0.174974966	0.807	0.725	8.87E-67	2
B4GALNT3	5.19E-102	0.173833778	0.825	0.808	1.04E-98	2
PCLO	8.50E-123	0.173475191	0.813	0.785	1.70E-119	2
SEMA6A	7.59E-192	0.172220654	0.781	0.703	1.52E-188	2
STYK1	3.31E-189	0.170673373	0.886	0.839	6.61E-186	2
CYP2B7P.1	3.96E-117	0.170314851	0.825	0.68	7.92E-114	2
OSBP2	1.03E-150	0.168002021	0.822	0.784	2.07E-147	2
PTAFR	3.28E-99	0.16780346	0.831	0.831	6.56E-96	2
SLC1A1	1.22E-134	0.165974816	0.788	0.775	2.44E-131	2
CD109	1.11E-111	0.165468547	0.871	0.748	2.21E-108	2
THSD7A	2.66E-192	0.164602112	0.816	0.679	5.33E-189	2
PALS2	2.14E-213	0.163071664	0.765	0.759	4.29E-210	2
GRK3	7.52E-176	0.161822486	0.818	0.725	1.50E-172	2
LINC02615	4.58E-161	0.159734362	0.853	0.811	9.16E-158	2
MT-ND6	1.85E-109	0.157743123	0.702	0.725	3.70E-106	2
TANGO6	3.67E-101	0.152612302	0.753	0.665	7.35E-98	2
IRAK3	5.73E-55	0.149973123	0.826	0.781	1.15E-51	2
CNTN3	5.11E-86	0.149283824	0.754	0.696	1.02E-82	2
ABTB3	5.24E-166	0.146318086	0.761	0.674	1.05E-162	2
SCNN1G	5.38E-57	0.145314502	0.865	0.893	1.08E-53	2

PRKAR2A	2.16E-57	0.144864833	0.802	0.79	4.32E-54	2
TNFAIP2	3.34E-76	0.144321721	0.879	0.882	6.68E-73	2
RNF150	2.19E-231	0.143969487	0.862	0.742	4.39E-228	2
FRMD6	3.16E-66	0.143397564	0.772	0.677	6.32E-63	2
RRP12	1.35E-104	0.14325674	0.85	0.815	2.70E-101	2
RCC1L	6.10E-62	0.143152143	0.834	0.827	1.22E-58	2
ZBTB16	6.15E-161	0.142778954	0.811	0.675	1.23E-157	2
GALNT5	2.57E-57	0.140864998	0.936	0.898	5.13E-54	2
NOCT	4.69E-99	0.139823665	0.786	0.779	9.37E-96	2
MANCR	1.32E-167	0.138524077	0.883	0.777	2.65E-164	2
WVOX	5.59E-62	0.137962649	0.779	0.678	1.12E-58	2
DENND1A	2.99E-86	0.136874865	0.819	0.756	5.99E-83	2
SEMA3B	2.80E-97	0.136564348	0.75	0.689	5.59E-94	2
HRH1	1.02E-83	0.13578875	0.804	0.769	2.04E-80	2
ITGA3	1.23E-64	0.135779773	0.843	0.763	2.46E-61	2
RPS6KA5	3.98E-90	0.134682415	0.778	0.795	7.96E-87	2
EPB41L2	1.04E-109	0.134088844	0.813	0.778	2.08E-106	2
MTHFD1L	1.68E-101	0.133572353	0.801	0.739	3.37E-98	2
SNX31	1.02E-142	0.133429367	0.797	0.802	2.03E-139	2
SNAPC1	6.93E-50	0.132791895	0.745	0.793	1.39E-46	2
CTC1	2.98E-123	0.132260856	0.832	0.788	5.97E-120	2
DOCK8	3.58E-64	0.132045643	0.816	0.792	7.16E-61	2
H2BC11	3.77E-52	0.131463276	0.828	0.901	7.55E-49	2
CDC14A	1.10E-97	0.131350295	0.823	0.7	2.21E-94	2
TBXAS1	4.26E-251	0.131273039	0.835	0.742	8.51E-248	2
MAGI2	5.80E-78	0.131214026	0.776	0.728	1.16E-74	2
DUOXA2	3.11E-38	0.13049491	0.738	0.768	6.22E-35	2
NIBAN1	6.37E-88	0.129784396	0.782	0.705	1.27E-84	2
POLR2B	6.67E-80	0.129643353	0.797	0.836	1.33E-76	2
CELF2	6.14E-153	0.129152733	0.791	0.703	1.23E-149	2
PIK3AP1	1.15E-98	0.128565051	0.883	0.855	2.31E-95	2
HLCS	2.59E-81	0.128423501	0.804	0.743	5.18E-78	2
UBA6-DT	1.57E-98	0.128273649	0.872	0.829	3.13E-95	2
IGFN1	0	0.126755153	0.933	0.886	0	2
MID1	6.97E-85	0.125403125	0.866	0.758	1.39E-81	2
EREG	8.25E-19	0.124733215	0.912	0.912	1.65E-15	2
MYH14	2.36E-35	0.122828917	0.828	0.815	4.72E-32	2

ANKRD33B	5.72E-84	0.121339998	0.864	0.861	1.14E-80	2
SH3GL3	2.89E-121	0.121269133	0.82	0.759	5.78E-118	2
HIP1	3.67E-96	0.120296823	0.717	0.75	7.34E-93	2
MAPKBP1	1.27E-79	0.11915621	0.786	0.779	2.55E-76	2
WNT7B	9.76E-50	0.118453119	0.864	0.893	1.95E-46	2
CYP4F3	3.35E-23	0.116950089	0.864	0.868	6.70E-20	2
CADPS2	2.48E-172	0.115670302	0.756	0.564	4.95E-169	2
ZDHC14	1.06E-124	0.114659149	0.835	0.767	2.13E-121	2
DIRC3	1.24E-219	0.114264617	0.79	0.734	2.49E-216	2
PLCXD1	4.70E-163	0.112838619	0.833	0.819	9.40E-160	2
SLFN5	1.22E-51	0.112796027	0.835	0.75	2.45E-48	2
SGO1-AS1	1.87E-117	0.112785294	0.786	0.759	3.74E-114	2
TBC1D10A	1.70E-29	0.112302792	0.858	0.868	3.39E-26	2
ERRFI1-DT	1.02E-131	0.111293963	0.842	0.783	2.04E-128	2
TBC1D4	4.30E-115	0.108359847	0.716	0.673	8.60E-112	2
URB1	1.64E-37	0.106269683	0.731	0.74	3.29E-34	2
ST8SIA6	1.83E-114	0.106249935	0.797	0.788	3.66E-111	2
SLC5A1	1.00E-63	0.10617614	0.872	0.836	2.00E-60	2
DDX60	4.53E-45	0.106052012	0.781	0.794	9.05E-42	2
PTCHD4	5.40E-153	0.105719305	0.81	0.643	1.08E-149	2
DTNB	9.54E-62	0.105320428	0.715	0.701	1.91E-58	2
ALOX12P2.1	2.47E-98	0.104602194	0.848	0.742	4.95E-95	2
UST	2.57E-51	0.104402664	0.779	0.755	5.14E-48	2
KC6	9.30E-277	0.104362842	0.767	0.524	1.86E-273	2
RNF103-CHMP3	1.02E-45	0.103180757	0.848	0.797	2.04E-42	2
NALF1	5.15E-130	0.101839769	0.77	0.634	1.03E-126	2
PTH2R	1.29E-121	0.101090189	0.846	0.797	2.59E-118	2
CARD11	2.87E-142	0.101040865	0.68	0.735	5.74E-139	2
LDLR	2.54E-16	0.09913367	0.902	0.903	5.08E-13	2
GRB10	9.08E-115	0.098572269	0.814	0.723	1.82E-111	2
ADAMTS14	4.17E-293	0.098503748	0.721	0.751	8.33E-290	2
SCFD2	3.11E-62	0.098393568	0.756	0.686	6.23E-59	2
TRPV4	5.75E-61	0.098085573	0.836	0.795	1.15E-57	2
RBM46	6.67E-186	0.097481116	0.739	0.725	1.33E-182	2
CCDC62	2.09E-137	0.097064443	0.724	0.669	4.18E-134	2
IQCJ-SCHIP1	1.14E-102	0.094407526	0.769	0.663	2.29E-99	2

RAPGEF4	1.50E-132	0.094054656	0.799	0.665	3.01E-129	2
EVI5L	9.17E-66	0.093657736	0.794	0.778	1.83E-62	2
ENC1	1.16E-35	0.093386826	0.823	0.767	2.31E-32	2
SH3TC2-DT	1.13E-122	0.092897206	0.784	0.8	2.27E-119	2
TTC28	9.71E-127	0.092800764	0.781	0.656	1.94E-123	2
PPM1H	3.93E-66	0.092717204	0.859	0.761	7.86E-63	2
LINC01950	0	0.092577901	0.853	0.743	0	2
ANAPC5	3.14E-55	0.092301662	0.789	0.832	6.28E-52	2
MIR181A1HG	1.96E-168	0.091922694	0.79	0.641	3.92E-165	2
SEMA3A	1.79E-82	0.091432403	0.77	0.649	3.57E-79	2
NPR3	4.57E-230	0.090315551	0.885	0.756	9.14E-227	2
MAP2	1.46E-86	0.088756894	0.823	0.733	2.93E-83	2
MIPOL1	4.45E-54	0.088710336	0.798	0.742	8.91E-51	2
MYO16-AS1	1.95E-61	0.086892715	0.807	0.787	3.90E-58	2
DNM3	6.23E-74	0.086562438	0.732	0.72	1.25E-70	2
VTRNA1-3	2.01E-05	0.08616316	0.792	0.76	0.040257528	2
LINC01090	3.92E-64	0.084930956	0.798	0.754	7.85E-61	2
HIVEP3	6.56E-74	0.083453804	0.778	0.733	1.31E-70	2
ZPLD1	1.41E-85	0.082967286	0.702	0.681	2.81E-82	2
CLMP	6.57E-37	0.082856575	0.745	0.73	1.31E-33	2
TNS1	1.53E-51	0.08270774	0.788	0.738	3.05E-48	2
TICRR	3.21E-173	0.082312967	0.76	0.861	6.42E-170	2
RENO1	1.60E-49	0.082136989	0.872	0.813	3.20E-46	2
SLC7A11	6.39E-106	0.081556623	0.741	0.583	1.28E-102	2
PPARGC1A	3.71E-75	0.081554402	0.766	0.75	7.41E-72	2
GUCY2C-AS1	1.24E-44	0.081497053	0.818	0.805	2.48E-41	2
UGGT2	6.79E-30	0.080428303	0.724	0.734	1.36E-26	2
BICD1	1.63E-48	0.079774312	0.701	0.651	3.27E-45	2
LINC02899	2.86E-98	0.079553984	0.7	0.642	5.71E-95	2
SPTBN4	5.60E-69	0.079221092	0.731	0.773	1.12E-65	2
FRMPD4	1.11E-106	0.078992068	0.81	0.719	2.23E-103	2
NAALADL2-AS2	1.47E-152	0.078901053	0.852	0.755	2.95E-149	2
ANK3	2.97E-140	0.078633578	0.874	0.715	5.94E-137	2
CACNB4	2.50E-156	0.078622082	0.699	0.694	4.99E-153	2
EDARADD	1.31E-58	0.078574664	0.806	0.78	2.62E-55	2
GFOD1	1.06E-56	0.078242521	0.797	0.727	2.12E-53	2
USP45	5.66E-28	0.077998007	0.785	0.798	1.13E-24	2

DLGAP1	1.92E-46	0.077296129	0.75	0.753	3.85E-43	2
CHST11	1.01E-91	0.077082959	0.796	0.67	2.03E-88	2
FUT8	7.63E-47	0.076685163	0.751	0.668	1.53E-43	2
DRAM1	7.59E-46	0.076511604	0.755	0.815	1.52E-42	2
FAT2	9.75E-17	0.076433005	0.85	0.83	1.95E-13	2
CALCRL-AS1	6.60E-42	0.075400565	0.671	0.613	1.32E-38	2
ADAM7-AS1	5.97E-77	0.075234567	0.723	0.717	1.19E-73	2
NCKAP5	1.60E-60	0.074717855	0.768	0.689	3.19E-57	2
LHFPL6	1.13E-58	0.074242922	0.792	0.76	2.26E-55	2
SCD5	9.38E-30	0.073798142	0.785	0.816	1.88E-26	2
CYP3A5	1.59E-37	0.073662354	0.828	0.839	3.17E-34	2
UTRN	3.08E-44	0.0735445	0.804	0.729	6.16E-41	2
LINC02889	2.74E-97	0.071841249	0.813	0.677	5.47E-94	2
KCNMB2-AS1	1.10E-194	0.07123715	0.863	0.673	2.20E-191	2
IRAG2	6.10E-42	0.070899684	0.844	0.864	1.22E-38	2
LINC00578	3.56E-27	0.068802143	0.756	0.693	7.11E-24	2
SPRY4-AS1	4.56E-67	0.068116893	0.704	0.752	9.13E-64	2
FOSL1	5.84E-17	0.068040991	0.853	0.836	1.17E-13	2
GPC6	9.04E-46	0.068023942	0.662	0.658	1.81E-42	2
ZEB1	4.68E-113	0.067668312	0.681	0.535	9.36E-110	2
FSTL3	2.15E-17	0.067243813	0.846	0.815	4.29E-14	2
KIF26B	1.90E-64	0.067031552	0.83	0.759	3.80E-61	2
DNAJC16	1.22E-29	0.066334817	0.833	0.792	2.44E-26	2
DST	3.35E-49	0.064761284	0.814	0.729	6.69E-46	2
KRT86	5.88E-72	0.064705447	0.799	0.745	1.18E-68	2
SLC41A2	1.47E-73	0.063936966	0.84	0.776	2.94E-70	2
ALK	2.93E-51	0.062763036	0.775	0.726	5.86E-48	2
SMC4	1.17E-26	0.062222558	0.859	0.894	2.33E-23	2
MME	7.07E-32	0.060766412	0.868	0.884	1.41E-28	2
HCCS-DT	5.92E-87	0.060003177	0.767	0.684	1.18E-83	2
INHBB	9.61E-45	0.059946662	0.837	0.755	1.92E-41	2
LINC02925	1.87E-121	0.058987767	0.866	0.764	3.73E-118	2
CDH3	1.16E-34	0.057992742	0.826	0.771	2.33E-31	2
SCNN1B	0.010957169	0.05794854	0.916	0.926	1	2
ABCC3	1.91E-101	0.057797262	0.752	0.609	3.82E-98	2
AARS1	4.07E-11	0.057305717	0.694	0.696	8.15E-08	2
CRADD	1.38E-27	0.057000279	0.756	0.731	2.77E-24	2

EYA4	1.74E-53	0.056926342	0.711	0.615	3.49E-50	2
TMEM11-DT	2.67E-103	0.055621163	0.842	0.79	5.35E-100	2
TDP1	1.74E-18	0.05550948	0.81	0.775	3.49E-15	2
SERPINB9	6.95E-21	0.055308433	0.814	0.807	1.39E-17	2
LINC01482	4.74E-83	0.055145537	0.641	0.609	9.48E-80	2
NETO2	9.57E-22	0.055144069	0.745	0.702	1.91E-18	2
GPAT3	2.11E-37	0.05449991	0.749	0.727	4.22E-34	2
PLD5	1.29E-72	0.054346131	0.698	0.627	2.58E-69	2
FAM126A	5.55E-48	0.05422808	0.763	0.775	1.11E-44	2
SAMD4A-AS1	4.09E-55	0.054206931	0.838	0.791	8.18E-52	2
DGKI	3.24E-110	0.053801924	0.8	0.708	6.48E-107	2
ATP13A2	1.55E-27	0.053622263	0.834	0.808	3.11E-24	2
RTKN2	9.22E-09	0.053158795	0.899	0.926	1.84E-05	2
CD83	3.34E-40	0.053017112	0.809	0.84	6.68E-37	2
TMEM132B	8.06E-97	0.052947637	0.773	0.668	1.61E-93	2
MUC5AC	6.98E-256	0.052705762	0.887	0.674	1.40E-252	2
CCDC68	0.00048272	0.051809308	0.879	0.896	0.965440488	2
CX3CL1	4.63E-23	0.051768791	0.731	0.754	9.26E-20	2
LINC02154	7.82E-46	0.050845877	0.793	0.771	1.56E-42	2
DPP6	1.19E-42	0.050375862	0.722	0.674	2.38E-39	2
LSS	2.63E-24	0.050074564	0.884	0.853	5.25E-21	2
RGS20	4.41E-25	0.049985182	0.86	0.83	8.82E-22	2
TMPRSS9	1.25E-24	0.049925687	0.762	0.721	2.51E-21	2
NEDD9	1.84E-20	0.049547609	0.763	0.74	3.69E-17	2
ALPK3	1.71E-30	0.049450652	0.749	0.749	3.42E-27	2
CP	1.21E-40	0.049258959	0.733	0.632	2.42E-37	2
GPC5	2.34E-41	0.049053045	0.636	0.62	4.68E-38	2
IL1R1	2.18E-17	0.048770802	0.789	0.782	4.36E-14	2
GNG7	3.15E-11	0.047539357	0.731	0.757	6.29E-08	2
GABRP	1.52E-13	0.04695059	0.93	0.916	3.05E-10	2
BMP6	1.13E-82	0.046207414	0.63	0.664	2.27E-79	2
FRAS1	3.31E-68	0.045423244	0.828	0.727	6.61E-65	2
EIF3C	5.81E-07	0.045382077	0.735	0.745	0.001161431	2
TMEM178B	3.65E-40	0.04468354	0.676	0.638	7.31E-37	2
DENND2B	9.23E-18	0.044328055	0.823	0.784	1.85E-14	2
MMP16	4.50E-28	0.044265749	0.756	0.689	9.01E-25	2
LINC02542	3.78E-91	0.04324641	0.749	0.648	7.55E-88	2

MARCHF1	1.83E-36	0.042912816	0.7	0.64	3.66E-33	2
MT-TF	1.45E-40	0.042694511	0.704	0.77	2.90E-37	2
BCL10-AS1	1.82E-28	0.042488521	0.71	0.664	3.64E-25	2
LINC02057	2.49E-29	0.042400921	0.776	0.716	4.99E-26	2
CAMK2A	4.00E-96	0.041853428	0.772	0.824	8.00E-93	2
PEBP4	4.56E-06	0.04150775	0.727	0.694	0.009126311	2
MIR3681HG	2.96E-81	0.041484538	0.767	0.651	5.91E-78	2
P3H2	3.65E-33	0.041438114	0.69	0.726	7.30E-30	2
AKAP12	1.56E-64	0.041139009	0.721	0.741	3.11E-61	2
POLE2	2.63E-112	0.041018076	0.804	0.645	5.27E-109	2
SYT16	8.24E-60	0.039701354	0.746	0.76	1.65E-56	2
SLIT2	7.22E-74	0.039186551	0.78	0.671	1.44E-70	2
ABHD2	2.26E-12	0.038956422	0.869	0.857	4.52E-09	2
PDZRN3	2.19E-36	0.038210998	0.719	0.751	4.38E-33	2
AGBL1	2.14E-18	0.038033882	0.77	0.712	4.28E-15	2
LIF	1.52E-122	0.038006097	0.888	0.747	3.05E-119	2
SLC7A5	4.15E-24	0.037977098	0.777	0.825	8.29E-21	2
LINC02006	6.36E-149	0.037954093	0.764	0.563	1.27E-145	2
IRS1	3.89E-07	0.03788292	0.676	0.682	0.000777859	2
LINC00393	5.47E-30	0.037034972	0.712	0.647	1.09E-26	2
GJC1	2.12E-56	0.036686809	0.744	0.798	4.24E-53	2
LINC00886	9.84E-45	0.036161918	0.813	0.73	1.97E-41	2
ARRDC2	5.86E-06	0.036057362	0.887	0.907	0.01171048	2
CIART	0.001333263	0.035551277	0.886	0.877	1	2
SGMS2	1.19E-13	0.035000457	0.858	0.83	2.37E-10	2
TMEM105	1.01E-129	0.03472051	0.885	0.734	2.01E-126	2
PGAM1P5	6.71E-34	0.03448017	0.791	0.776	1.34E-30	2
FAIM2	0.008170091	0.033614003	0.581	0.604	1	2
CD70	1.21E-82	0.033524039	0.811	0.682	2.42E-79	2
CAPN14	9.39E-12	0.033382721	0.846	0.881	1.88E-08	2
COL4A5	1.74E-42	0.033079993	0.719	0.621	3.48E-39	2
MUC1	2.17E-12	0.032952195	0.962	0.935	4.33E-09	2
HEATR4	1.41E-33	0.032788647	0.811	0.817	2.82E-30	2
CCDC146	1.75E-88	0.03275167	0.833	0.702	3.50E-85	2
FAM222A	4.17E-40	0.032378714	0.681	0.694	8.34E-37	2
HS3ST2	6.61E-58	0.031935259	0.722	0.773	1.32E-54	2
CNIH3	1.54E-15	0.03164323	0.793	0.751	3.08E-12	2

LINC01269	0.035217192	0.03148473	0.844	0.852	1	2
TGM2	9.69E-10	0.030260556	0.732	0.715	1.94E-06	2
SLIT3	1.98E-80	0.029577406	0.765	0.638	3.96E-77	2
MYO1H	6.02E-26	0.029282193	0.864	0.814	1.20E-22	2
FBXL7	8.20E-69	0.028794235	0.63	0.498	1.64E-65	2
LINC01588	4.72E-15	0.028517435	0.777	0.779	9.43E-12	2
FAM153B	6.91E-55	0.028317365	0.793	0.683	1.38E-51	2
WDPCP	5.40E-31	0.028243865	0.799	0.731	1.08E-27	2
LAMA3	1.36E-21	0.027631664	0.692	0.68	2.72E-18	2
ZNF608	1.95E-41	0.027030464	0.808	0.717	3.90E-38	2
GPR176	4.20E-70	0.026499118	0.815	0.696	8.41E-67	2
BANK1	2.99E-17	0.025934558	0.722	0.743	5.98E-14	2
LDLRAD3	2.87E-109	0.025193252	0.761	0.596	5.74E-106	2
SNTB1	2.50E-22	0.025111611	0.782	0.729	5.00E-19	2
FOSB	1.92E-10	0.025094536	0.775	0.743	3.84E-07	2
TULP2	1.06E-19	0.024853492	0.695	0.726	2.12E-16	2
PDK4	1.08E-13	0.024357594	0.696	0.741	2.17E-10	2
CKAP2L	3.86E-153	0.024348139	0.856	0.68	7.72E-150	2
LINC02306	3.47E-57	0.024271694	0.646	0.668	6.95E-54	2
PEMT	1.80E-10	0.02418679	0.756	0.795	3.60E-07	2
C12orf42	3.07E-45	0.023525614	0.747	0.8	6.14E-42	2
FIGN	3.03E-13	0.023317856	0.656	0.622	6.06E-10	2
PXDN	1.51E-140	0.023230342	0.831	0.647	3.01E-137	2
IRF1	3.08E-11	0.022917245	0.889	0.922	6.17E-08	2
SCAMP5	1.39E-11	0.02217986	0.692	0.709	2.77E-08	2
ST6GAL1	9.81E-62	0.022023261	0.842	0.728	1.96E-58	2
HEXD-IT1	2.47E-06	0.021953695	0.752	0.721	0.004946787	2
NUMBL	5.05E-11	0.021952074	0.755	0.728	1.01E-07	2
MAP3K8	8.97E-15	0.021220545	0.921	0.952	1.79E-11	2
RRM2B	2.89E-11	0.02086377	0.827	0.791	5.79E-08	2
PPP1R3C	2.65E-09	0.020694535	0.856	0.885	5.30E-06	2
PTPRD	6.25E-16	0.020335045	0.552	0.529	1.25E-12	2
DPH6-DT	2.22E-88	0.020325735	0.813	0.671	4.44E-85	2
BMP2	5.54E-10	0.020271305	0.782	0.819	1.11E-06	2
CSGALNACT1	6.90E-06	0.020142875	0.691	0.715	0.013800089	2
CXCL5	2.83E-122	0.019460083	0.811	0.636	5.66E-119	2
GOLGA7B-DT	8.45E-20	0.019427362	0.824	0.77	1.69E-16	2

CLIC5	2.36E-21	0.019021526	0.583	0.643	4.72E-18	2
AJAP1	1.17E-34	0.018815667	0.687	0.726	2.35E-31	2
ZNF114	1.90E-51	0.01868269	0.513	0.613	3.79E-48	2
TCHH	8.63E-10	0.018199441	0.703	0.654	1.73E-06	2
FYN	4.39E-22	0.018176608	0.726	0.655	8.78E-19	2
LINC02343	1.00E-29	0.017921362	0.581	0.612	2.00E-26	2
FAM153A	0.006753066	0.017241083	0.766	0.776	1	2
SHOC1	3.84E-15	0.016914542	0.742	0.779	7.69E-12	2
VGLL3	5.93E-06	0.016702568	0.775	0.759	0.011862727	2
GNA14	1.49E-21	0.016603876	0.813	0.761	2.99E-18	2
POU2F3	1.49E-14	0.016295537	0.756	0.719	2.98E-11	2
KDR	5.52E-27	0.016149258	0.49	0.539	1.10E-23	2
RIPPLY3	1.44E-48	0.015525841	0.721	0.607	2.88E-45	2
CPA4	7.70E-11	0.015401306	0.8	0.756	1.54E-07	2
BBOX1-AS1	1.92E-75	0.015311185	0.791	0.661	3.83E-72	2
SULT1E1	6.89E-09	0.014719933	0.798	0.815	1.38E-05	2
LINC01564	2.08E-141	0.014608664	0.775	0.579	4.16E-138	2
SLC1A2	3.28E-18	0.014166837	0.84	0.784	6.56E-15	2
TMEM120B	8.04E-16	0.014138214	0.733	0.778	1.61E-12	2
THBS1	1.23E-27	0.014012689	0.845	0.776	2.46E-24	2
FAM171B	1.05E-10	0.01365982	0.819	0.791	2.10E-07	2
DTNA	6.42E-72	0.013337844	0.846	0.723	1.28E-68	2
TLL2	5.93E-31	0.012814	0.859	0.784	1.19E-27	2
LAMB3	8.73E-13	0.012686943	0.876	0.833	1.75E-09	2
NEFM	1.99E-10	0.012664238	0.7	0.669	3.98E-07	2
FAM43A	3.05E-30	0.012503707	0.835	0.759	6.09E-27	2
PRSS41	2.17E-47	0.012304903	0.814	0.718	4.35E-44	2
SLAMF7	1.28E-05	0.011284652	0.844	0.822	0.025613106	2
SLC9B1	2.13E-34	0.011025556	0.584	0.662	4.26E-31	2
GGNBP1	5.84E-50	0.010958522	0.828	0.724	1.17E-46	2
KCNMA1	1.15E-11	0.010622516	0.688	0.643	2.29E-08	2
TDRP	0.009085945	0.010502809	0.767	0.748	1	2
KLKP1.1	0.024404697	0.010394957	0.667	0.655	1	2
ZNF556	0.000968789	0.010360697	0.793	0.789	1	2
MAFB	3.96E-17	0.010101428	0.716	0.65	7.91E-14	2
P2RY1	2.26E-11	0.009394766	0.791	0.83	4.52E-08	2
NR4A1	2.20E-34	0.009334447	0.741	0.823	4.40E-31	2

PICART1	3.75E-79	0.00925812	0.796	0.657	7.49E-76	2
NFIC	8.70E-07	0.008791615	0.784	0.768	0.001740851	2
LBH	1.47E-13	0.008651838	0.858	0.812	2.94E-10	2
RASSF8	4.67E-35	0.008246798	0.747	0.653	9.35E-32	2
KLK4	0.012057141	0.008231026	0.724	0.716	1	2
NID1	5.36E-42	0.007866531	0.638	0.732	1.07E-38	2
ARMH1	8.39E-41	0.007378196	0.816	0.726	1.68E-37	2
TMEM176A	3.69E-26	0.007263275	0.904	0.844	7.38E-23	2
HNMT	5.08E-06	0.006904908	0.778	0.746	0.01015676	2
RN7SL1	3.41E-12	0.006847547	0.721	0.763	6.82E-09	2
LINC00551	0.520888381	0.006827715	0.833	0.828	1	2
PRKAR2B	0.000146863	0.00678211	0.759	0.781	0.293725137	2
MAN1A1	0.077403876	0.006308611	0.662	0.665	1	2
UHRF1	7.43E-06	0.006003738	0.57	0.532	0.014861713	2
HSD11B1	1.68E-05	0.005714563	0.546	0.509	0.033661448	2
BAMBI	0.001158981	0.00564845	0.721	0.694	1	2
RXFP1	2.29E-16	0.004892317	0.612	0.663	4.59E-13	2
ARHGEF38	1.50E-18	0.004798091	0.814	0.764	3.01E-15	2
WNT9A	2.41E-18	0.004719232	0.768	0.814	4.83E-15	2
SMOC2	0.712816427	0.004601215	0.695	0.689	1	2
PARM1	1.42E-36	0.004382989	0.7	0.599	2.85E-33	2
P2RX4	0.011280638	0.003825037	0.836	0.823	1	2
EML2-AS1	1.07E-06	0.003682556	0.719	0.756	0.002145427	2
CCK	4.70E-13	0.003675039	0.599	0.658	9.40E-10	2
CPN1	0.000870065	0.003592483	0.749	0.726	1	2
CYP1B1	3.16E-11	0.003412254	0.841	0.798	6.32E-08	2
WFDC5	3.25E-09	0.002959219	0.622	0.573	6.50E-06	2
SERPINB11	0.041048405	0.002717439	0.845	0.84	1	2
SHLD1	1.15E-34	0.002327532	0.691	0.771	2.31E-31	2
MSTO1	2.71E-10	0.002176854	0.761	0.746	5.43E-07	2
CYP2A6	0.101970835	0.002141313	0.585	0.568	1	2
FLOT2	2.08E-17	0.002116042	0.862	0.812	4.16E-14	2
HLA-G	1.08E-80	0.002103921	0.738	0.591	2.16E-77	2
IGFL2-AS1	6.18E-06	0.00176776	0.743	0.708	0.012354376	2
KLK5	1.07E-07	0.001734176	0.837	0.802	0.000214513	2
SLC6A14	0.016319009	0.001703679	0.959	0.949	1	2
ALKAL1	3.26E-47	0.001276786	0.674	0.558	6.51E-44	2

ARMC7	1.40E-26	0.000788658	0.778	0.699	2.80E-23	2
DTL	3.24E-124	0.000626748	0.777	0.595	6.49E-121	2
LEMD1	0.000314659	0.000578768	0.825	0.818	0.629318066	2
CALD1	9.33E-13	0.00053939	0.725	0.673	1.87E-09	2

[cluster 3]

Gene	p_val	avg_log2FC	pct.1	pct.2	p_val_adj	Cluster
CAPS	0	3.343273268	0.904	0.777	0	3
DNAH12	0	3.182045944	0.867	0.663	0	3
IGFBP7	0	2.887347202	0.882	0.672	0	3
TPPP3	0	2.863753412	0.871	0.703	0	3
C20orf85	0	2.704793195	0.843	0.714	0	3
RSPH1	0	2.636854305	0.885	0.688	0	3
CDHR3	0	2.592955092	0.888	0.645	0	3
TMEM190	0	2.527381378	0.871	0.689	0	3
RP1	0	2.399826804	0.858	0.69	0	3
CFAP276	0	2.367620084	0.835	0.692	0	3
FAM183A	0	2.358047553	0.854	0.675	0	3
C9orf24	0	2.252935489	0.843	0.661	0	3
LRRIQ1	0	2.222381288	0.863	0.66	0	3
MORN2	0	2.186569526	0.869	0.777	0	3
SNTN	0	2.182814454	0.848	0.668	0	3
PIFO	0	2.137641378	0.851	0.656	0	3
C5orf49	0	2.135788542	0.849	0.695	0	3
DNAH7	0	2.125685445	0.893	0.675	0	3
CFAP54	0	2.085372475	0.859	0.609	0	3
TSPAN1	0	2.074384357	0.945	0.912	0	3
DNAH5	0	2.068329338	0.886	0.685	0	3
NEK10	0	2.054196492	0.877	0.638	0	3
DNAH6	0	2.050064626	0.86	0.601	0	3
RFX3	0	2.040037781	0.847	0.68	0	3
CETN2	0	2.032242133	0.882	0.757	0	3
DYNLRB2	0	2.021160158	0.837	0.697	0	3
MAPK10	0	1.99980062	0.915	0.752	0	3

CFAP47	0	1.984125275	0.875	0.648	0	3
HOATZ	0	1.973978792	0.817	0.666	0	3
DNAAF1	0	1.910928879	0.931	0.702	0	3
EFHC1	0	1.909187562	0.943	0.721	0	3
PPIL6	0	1.88143371	0.86	0.588	0	3
CFAP43	0	1.87701624	0.86	0.651	0	3
ZMYND10	0	1.859847985	0.865	0.686	0	3
ROPN1L	0	1.826235907	0.821	0.662	0	3
CCN2	0	1.819572622	0.914	0.81	0	3
DTHD1	0	1.812819921	0.812	0.645	0	3
PIERCE1	0	1.810907157	0.832	0.683	0	3
KIF9	0	1.800978172	0.891	0.716	0	3
CLXN	0	1.798133228	0.869	0.647	0	3
SAA1	0	1.797286394	0.925	0.877	0	3
TMC5	0	1.795422115	0.892	0.71	0	3
DNAH3	0	1.790254517	0.897	0.662	0	3
ARMC3	0	1.756686254	0.846	0.671	0	3
ODF3B	0	1.755962496	0.895	0.777	0	3
CFAP300	0	1.746215731	0.868	0.669	0	3
DNAH11	0	1.740334515	0.935	0.767	0	3
ZBBX	0	1.737141587	0.892	0.658	0	3
CALM2	0	1.715959158	0.956	0.941	0	3
TMEM232	0	1.711363753	0.829	0.673	0	3
FAM229B	0	1.711223655	0.869	0.634	0	3
AGBL4	0	1.710652435	0.88	0.69	0	3
DNAH9	0	1.708723953	0.874	0.636	0	3
HYDIN	0	1.704304494	0.907	0.715	0	3
CAPSL	0	1.698933327	0.825	0.687	0	3
SPAG17	0	1.691157163	0.868	0.711	0	3
PACRG	0	1.674615291	0.863	0.648	0	3
STK33	0	1.671647015	0.868	0.627	0	3
AGR3	0	1.670689425	0.812	0.653	0	3
CROCC2	0	1.667006301	0.905	0.71	0	3
CCDC170	0	1.663461865	0.841	0.614	0	3
ANK3	0	1.663404709	0.862	0.721	0	3
CFAP95	0	1.661937059	0.85	0.653	0	3
FOXJ1	0	1.66133332	0.831	0.684	0	3

ULK4	0	1.657969216	0.88	0.641	0	3
WDR49	0	1.651498791	0.847	0.659	0	3
CFAP157	0	1.644392393	0.953	0.762	0	3
DYNLT2B	0	1.642165584	0.878	0.777	0	3
IGFBP2	0	1.634449929	0.86	0.658	0	3
LRRC23	0	1.631391478	0.908	0.71	0	3
CFAP299	0	1.627575869	0.837	0.589	0	3
RFX2	0	1.619832923	0.878	0.681	0	3
DCDC1	0	1.616910119	0.841	0.66	0	3
SPATA17	0	1.607660568	0.83	0.625	0	3
7SK.4	0	1.60621734	0.974	0.814	0	3
HMG3	0	1.59327976	0.946	0.904	0	3
CFAP73	0	1.580436828	0.886	0.694	0	3
NME5	0	1.572060207	0.867	0.639	0	3
SPAG6	0	1.553098042	0.853	0.645	0	3
EFCAB2	0	1.548884766	0.906	0.676	0	3
SPA17	0	1.540899631	0.812	0.666	0	3
IFT57	0	1.536027752	0.852	0.673	0	3
CCDC78	0	1.525072791	0.903	0.66	0	3
SPEF2	0	1.520197631	0.849	0.621	0	3
BCYRN1	0	1.516098496	0.862	0.829	0	3
SAA2	0	1.507732377	0.931	0.861	0	3
DYNC2H1	0	1.507598583	0.862	0.675	0	3
MORN5	0	1.505224819	0.837	0.697	0	3
DIAPH2	0	1.500676952	0.892	0.676	0	3
RSPH9	0	1.500318904	0.878	0.619	0	3
RRAD	0	1.499049275	0.876	0.769	0	3
SAXO2	0	1.490929373	0.841	0.627	0	3
CFAP251	0	1.486652683	0.865	0.633	0	3
CFAP70	0	1.480042842	0.877	0.649	0	3
CTXN1	0	1.471010655	0.884	0.632	0	3
LDLRAD1	0	1.462735111	0.839	0.688	0	3
CKB	0	1.461361943	0.934	0.897	0	3
DNALI1	0	1.457171717	0.814	0.628	0	3
CCDC146	0	1.450593752	0.857	0.701	0	3
CLMN	0	1.44616702	0.897	0.679	0	3
C4orf47	0	1.444997988	0.924	0.694	0	3

MLF1	0	1.438675454	0.882	0.662	0	3
AKAP14	0	1.433950416	0.831	0.623	0	3
FAM81B	0	1.431878423	0.845	0.604	0	3
SPATA18	0	1.4315882	0.871	0.622	0	3
CDC20B	0	1.424370956	0.681	0.664	0	3
DNAI4	0	1.414836577	0.831	0.659	0	3
CSPP1	0	1.413157409	0.904	0.691	0	3
CLU	0	1.412178635	0.833	0.615	0	3
CLDN3	0	1.410656762	0.846	0.727	0	3
C4orf48	0	1.409902259	0.94	0.871	0	3
ENKUR	0	1.401555139	0.81	0.619	0	3
RARRES1	0	1.399843831	0.864	0.688	0	3
ERICH3	0	1.39709164	0.847	0.681	0	3
PSENN	0	1.395061162	0.907	0.895	0	3
NEK11	0	1.389212486	0.863	0.672	0	3
SYNE1	0	1.386573945	0.856	0.539	0	3
TEKT1	0	1.368229644	0.827	0.633	0	3
TSGA10	0	1.367493872	0.891	0.689	0	3
CFAP210	0	1.366222131	0.857	0.565	0	3
PCSK1N	0	1.355476374	0.918	0.773	0	3
DYNLT5	0	1.352789444	0.896	0.687	0	3
NPHP1	0	1.349482654	0.879	0.67	0	3
DYDC2	0	1.347660894	0.811	0.473	0	3
AK9	0	1.347047212	0.891	0.706	0	3
DNAI7	0	1.335561484	0.874	0.64	0	3
ARHGAP18	0	1.331944573	0.853	0.678	0	3
HSP90AA1	0	1.326376666	0.98	0.97	0	3
DNAI1	0	1.316215052	0.897	0.678	0	3
WDR86-AS1	0	1.310865846	0.814	0.65	0	3
PROM1	0	1.310563776	0.886	0.672	0	3
CD74	0	1.30911426	0.855	0.724	0	3
TEX9	0	1.307230175	0.902	0.649	0	3
CFAP53	0	1.303087577	0.817	0.645	0	3
NFIA	0	1.295683038	0.902	0.816	0	3
CEP126	0	1.295502923	0.858	0.618	0	3
KIAA0825	0	1.288821483	0.817	0.67	0	3
CST6	0	1.280676858	0.947	0.898	0	3

CHST9	0	1.277892728	0.847	0.564	0	3
TTC29	0	1.272823447	0.843	0.68	0	3
ANKRD44-AS1	0	1.269471679	0.841	0.602	0	3
ANKRD36C	0	1.262140691	0.907	0.749	0	3
TCTN1	0	1.257791877	0.904	0.73	0	3
CCDC30	0	1.24993955	0.881	0.648	0	3
WDR54	0	1.243427282	0.825	0.669	0	3
CFAP298	0	1.238819699	0.868	0.756	0	3
MIA	0	1.233842681	0.904	0.72	0	3
CABCOCO1	0	1.2303569	0.877	0.661	0	3
DZIP3	0	1.220939195	0.855	0.64	0	3
MRPS31	0	1.220648386	0.868	0.736	0	3
LMNTD1	0	1.211183875	0.862	0.674	0	3
TSPAN19	0	1.210421849	0.909	0.728	0	3
FAM216B	0	1.208492235	0.786	0.663	0	3
LRRC46	0	1.200338721	0.842	0.698	0	3
CIBAR2	0	1.199080829	0.855	0.682	0	3
FHAD1	0	1.19872109	0.823	0.586	0	3
SSB	0	1.198074699	0.897	0.786	0	3
ADGB	0	1.194428299	0.829	0.655	0	3
C11orf97	0	1.192927484	0.828	0.62	0	3
PLEKHS1	0	1.19192566	0.853	0.723	0	3
CYSTM1	0	1.191126109	0.953	0.913	0	3
MAP3K19	0	1.185341562	0.834	0.66	0	3
CFAP46	0	1.182854212	0.9	0.696	0	3
CCDC113	0	1.182467809	0.828	0.639	0	3
MSI2	0	1.177349768	0.914	0.768	0	3
CFAP221	0	1.157567796	0.883	0.681	0	3
GON7	0	1.150858886	0.834	0.678	0	3
CC2D2A	0	1.145261478	0.804	0.599	0	3
PIP	0	1.14243965	0.836	0.659	0	3
DNAAF11	0	1.141198889	0.862	0.666	0	3
BTBD9	0	1.130023553	0.931	0.799	0	3
LRRC10B	0	1.126991705	0.884	0.692	0	3
IFT88	0	1.124201799	0.878	0.688	0	3
IFT22	0	1.113783559	0.825	0.661	0	3
CDKN2A	0	1.107258813	0.912	0.805	0	3

ODAD2	0	1.105658583	0.841	0.616	0	3
WDR38	0	1.101758361	0.81	0.659	0	3
MNS1	0	1.101243245	0.792	0.594	0	3
CFAP52	0	1.100493217	0.843	0.607	0	3
CCDC74A	0	1.09980122	0.834	0.602	0	3
PRDX1	0	1.098581422	0.922	0.908	0	3
LXN	0	1.097956063	0.813	0.665	0	3
HSP90AB1	0	1.094976852	0.961	0.949	0	3
IFTAP	0	1.089156026	0.844	0.7	0	3
CFAP45	0	1.088110233	0.815	0.639	0	3
BBS9	0	1.087975325	0.856	0.66	0	3
EPCAM	0	1.087781893	0.901	0.767	0	3
SERPINI2	0	1.081682253	0.854	0.688	0	3
PDE4D	0	1.081095816	0.851	0.681	0	3
LRGUK	0	1.080603766	0.892	0.663	0	3
DYNLT1	0	1.07880438	0.963	0.968	0	3
CDHR4	0	1.076328192	0.892	0.677	0	3
ENAH	0	1.075924124	0.901	0.693	0	3
MS4A8	0	1.074070699	0.861	0.659	0	3
TUBA4B	0	1.071374311	0.812	0.563	0	3
DRC1	0	1.070955977	0.851	0.641	0	3
CRIP1	0	1.069043806	0.767	0.672	0	3
DGKH	0	1.068447405	0.88	0.755	0	3
METTL7A	0	1.065255356	0.845	0.664	0	3
MOK	0	1.064671177	0.905	0.722	0	3
HSPE1	0	1.06160677	0.896	0.884	0	3
FAM227A	0	1.058199	0.886	0.757	0	3
TOGARAM2	0	1.05599128	0.896	0.691	0	3
VSTM2L	0	1.055424431	0.914	0.846	0	3
RUVBL1	0	1.049690398	0.796	0.634	0	3
CCDC17	0	1.049391417	0.908	0.667	0	3
HSPD1	0	1.048179092	0.919	0.8	0	3
C12orf75	0	1.043303393	0.876	0.678	0	3
SPATA6L	0	1.041593665	0.876	0.703	0	3
PRDX5	9.90E-253	1.035184604	0.963	0.97	1.98E-249	3
HSPBP1	0	1.033337194	0.839	0.682	0	3
HSPH1	0	1.032869181	0.954	0.878	0	3

LINC00342	0	1.024764395	0.843	0.683	0	3
TMEM231	0	1.023132624	0.813	0.623	0	3
DMD	0	1.02300435	0.84	0.651	0	3
CFAP100	0	1.021697867	0.896	0.676	0	3
TMEM67	0	1.017983501	0.869	0.699	0	3
ALDH1A1	0	1.016533936	0.822	0.67	0	3
OMG	0	1.015090122	0.763	0.658	0	3
SPACA9	0	1.0147954	0.823	0.706	0	3
EFCAB6	0	1.014484368	0.876	0.714	0	3
SOD1	0	1.012132857	0.88	0.888	0	3
EXOC4	0	1.00983205	0.941	0.857	0	3
UTRN	0	1.006539607	0.84	0.725	0	3
CCDC80	0	1.00166377	0.84	0.688	0	3
CFAP69	0	1.000723935	0.85	0.671	0	3
TTLL5	0	0.994150184	0.909	0.808	0	3
CNTNAP3	0	0.988290219	0.853	0.667	0	3
NUCB2	0	0.988088624	0.864	0.815	0	3
BCAS3	0	0.984500582	0.906	0.837	0	3
NAALADL2	0	0.984051537	0.871	0.739	0	3
CFAP141	0	0.98297328	0.789	0.662	0	3
MT-ND3	7.74E-187	0.982628993	0.992	0.996	1.55E-183	3
PPP1R42	0	0.981984579	0.82	0.561	0	3
HLA-DRA	0	0.981470154	0.882	0.634	0	3
DRC3	0	0.980926584	0.864	0.686	0	3
ENDOG	0	0.980708589	0.827	0.736	0	3
NEK5	0	0.979801272	0.872	0.65	0	3
PLAC8	0	0.977265144	0.926	0.897	0	3
UCP2	0	0.9769023	0.854	0.774	0	3
DNAI2	0	0.975777888	0.837	0.618	0	3
CYP4B1	0	0.973972138	0.881	0.797	0	3
TEX26	0	0.971742866	0.822	0.702	0	3
DNAI3	0	0.9703545	0.799	0.623	0	3
AGAP1	0	0.96920308	0.864	0.707	0	3
IQUB	0	0.968610899	0.864	0.608	0	3
MT-ND2	1.77E-278	0.967732044	0.997	0.996	3.54E-275	3
CFAP77	0	0.966087018	0.872	0.584	0	3
DNAJA4	0	0.964559052	0.901	0.754	0	3

EFCAB10	0	0.964095036	0.808	0.486	0	3
C7orf57	0	0.963274868	0.883	0.59	0	3
PLCH1	0	0.962873114	0.828	0.593	0	3
LINC02166	0	0.961073061	0.841	0.723	0	3
ALCAM	0	0.954465422	0.904	0.871	0	3
MAG1	0	0.952840572	0.911	0.867	0	3
WVOX	0	0.947431027	0.845	0.67	0	3
MAP9	0	0.946874176	0.822	0.688	0	3
KIAA2012	0	0.939738639	0.851	0.636	0	3
WDPCP	0	0.938005396	0.852	0.724	0	3
RIPOR2	0	0.928870473	0.871	0.671	0	3
CFAP44	0	0.926613034	0.806	0.602	0	3
TUBA1A	0	0.921347631	0.802	0.681	0	3
SHANK2	0	0.92028308	0.89	0.781	0	3
MAML2	0	0.919210567	0.903	0.878	0	3
FOCAD	0	0.917720678	0.852	0.633	0	3
EFHC2	0	0.915455246	0.85	0.61	0	3
RGS22	0	0.913260612	0.846	0.642	0	3
DLEC1	0	0.912900088	0.908	0.701	0	3
GLIS3	0	0.911863288	0.852	0.683	0	3
CERS6	0	0.911411534	0.938	0.863	0	3
ANKFN1	0	0.91100445	0.828	0.639	0	3
KCND2	0	0.906720252	0.879	0.767	0	3
DNPH1	0	0.905729631	0.889	0.81	0	3
DNAL1	0	0.903520176	0.878	0.735	0	3
TRIO	0	0.902998805	0.897	0.767	0	3
CEP83	0	0.901886978	0.853	0.701	0	3
LEKR1	0	0.900489563	0.879	0.755	0	3
ODAD1	0	0.900021765	0.897	0.73	0	3
CALM1	0	0.899247723	0.949	0.962	0	3
FBXL13	0	0.89879699	0.854	0.669	0	3
CRACDL	0	0.89855429	0.865	0.689	0	3
IQCH	0	0.897883598	0.857	0.683	0	3
TUBB4B	0	0.896530755	0.917	0.878	0	3
NBEA	0	0.895872625	0.86	0.738	0	3
DZIP1L	0	0.894310039	0.885	0.742	0	3
DNAH10	0	0.893379353	0.879	0.612	0	3

SORBS2	0	0.892654734	0.909	0.905	0	3
LINC01765	0	0.891395385	0.8	0.726	0	3
DPCD	0	0.888248174	0.858	0.828	0	3
LINC01091	0	0.885511766	0.893	0.64	0	3
ABHD2	0	0.885409442	0.915	0.85	0	3
DOC2A	0	0.885024727	0.88	0.748	0	3
ESRRG	0	0.884160008	0.845	0.648	0	3
WFDC21P	0	0.883522318	0.94	0.858	0	3
CFAP61	0	0.878891853	0.881	0.681	0	3
MID1	0	0.875226686	0.913	0.754	0	3
TTLL9	0	0.872322317	0.848	0.627	0	3
FRMPD2	0	0.871105768	0.873	0.649	0	3
HSPA8	0	0.86951441	0.926	0.891	0	3
EXT1	0	0.868347439	0.825	0.652	0	3
TNRC6B	0	0.865728229	0.897	0.807	0	3
NEK1	0	0.864488629	0.84	0.635	0	3
ZC3H3	3.23E-221	0.863617678	0.855	0.829	6.46E-218	3
TAGLN2	0	0.859723791	0.896	0.9	0	3
VWA3B	0	0.851635325	0.797	0.68	0	3
CCDC153	0	0.843192162	0.825	0.626	0	3
RSPH4A	0	0.842508323	0.812	0.621	0	3
CNTNAP3B	0	0.835659685	0.888	0.711	0	3
ANKRD18A	0	0.831675615	0.911	0.719	0	3
SHROOM3	0	0.831028937	0.938	0.889	0	3
PLEKHG7	0	0.830507845	0.908	0.725	0	3
LINC01876	0	0.829843626	0.833	0.704	0	3
PARK7	0	0.829738254	0.901	0.88	0	3
GIHCG	0	0.827495441	0.768	0.648	0	3
TTLL10	0	0.826770286	0.893	0.659	0	3
C6orf118	0	0.82651966	0.863	0.717	0	3
ARMH1	0	0.812684842	0.867	0.72	0	3
SERPINB9	4.58E-131	0.805728856	0.855	0.801	9.16E-128	3
BICC1	0	0.802337728	0.793	0.589	0	3
DAW1	0	0.801111983	0.815	0.656	0	3
CFAP126	0	0.799076027	0.712	0.656	0	3
CCDC162P	0	0.792866017	0.923	0.818	0	3
SLC34A2	0	0.792224908	0.823	0.64	0	3

MT-ATP6	8.33E-123	0.791751119	0.992	0.996	1.67E-119	3
ATP2C2	0	0.79162582	0.931	0.705	0	3
MUC16	0	0.791035791	0.794	0.6	0	3
FAM27C	0	0.789107922	0.818	0.645	0	3
CAMKMT	0	0.78815788	0.859	0.723	0	3
PGM2L1	0	0.786632803	0.858	0.678	0	3
ALDH3B1	0	0.779922611	0.881	0.841	0	3
TEKT2	0	0.778140272	0.802	0.684	0	3
LDLRAD4	0	0.777391179	0.86	0.64	0	3
STOML3	0	0.777075673	0.841	0.632	0	3
CCDC148	0	0.77641277	0.856	0.662	0	3
NAV2	0	0.775635255	0.918	0.809	0	3
ZBED5-AS1	0	0.772785066	0.835	0.729	0	3
PARD3B	0	0.771918762	0.855	0.72	0	3
RN7SL1	0	0.768647919	0.917	0.731	0	3
STMND1	0	0.768352888	0.787	0.611	0	3
MUC12	0	0.767905921	0.858	0.624	0	3
BAIAP3	0	0.767040692	0.886	0.696	0	3
NQO1	0	0.763835808	0.841	0.696	0	3
ANXA5	0	0.761251953	0.896	0.857	0	3
ACBD3-AS1	0	0.759497884	0.84	0.676	0	3
RNF103- CHMP3	0	0.758268235	0.892	0.791	0	3
MPC2	0	0.757822212	0.893	0.898	0	3
RUNX1	0	0.756394544	0.925	0.848	0	3
DENND2B	0	0.752028212	0.887	0.775	0	3
PIH1D2	0	0.751500285	0.805	0.674	0	3
CNTRL	0	0.742400949	0.816	0.63	0	3
GPR162	0	0.741530898	0.878	0.452	0	3
PPM1H	0	0.740538004	0.879	0.76	0	3
CCNO	4.85E-274	0.740356079	0.784	0.723	9.70E-271	3
CDC14A	0	0.739231953	0.872	0.695	0	3
NWD1	0	0.73803336	0.815	0.697	0	3
PALLD	0	0.734689895	0.852	0.693	0	3
TXN	1.40E-154	0.733939298	0.953	0.963	2.79E-151	3
AK8	0	0.731933977	0.835	0.598	0	3
DIXDC1	0	0.730522323	0.881	0.713	0	3

SLC38A4-AS1	0	0.726267362	0.831	0.647	0	3
SGMS2	0	0.725939671	0.923	0.82	0	3
FAM13A	7.78652691411057e-312	0.72425078	0.944	0.869	0.00E+00	3
CFAP97D2	0	0.723181646	0.812	0.687	0	3
GCLM	0	0.720678987	0.864	0.734	0	3
ECRG4	0	0.720632705	0.865	0.722	0	3
CHST6	0	0.718747123	0.857	0.768	0	3
SRGAP3	0	0.711700307	0.905	0.799	0	3
DST	0	0.711617592	0.877	0.721	0	3
LINC02934	0	0.710375924	0.865	0.709	0	3
CAMK1D	5.71945741347726e-311	0.70841047	0.877	0.778	1.14E-307	3
LRRC51	0	0.707842402	0.813	0.691	0	3
CDC42EP3	0	0.707699421	0.904	0.801	0	3
SPEF1	0	0.705407142	0.845	0.675	0	3
TAGLN3	0	0.702072794	0.872	0.599	0	3
CEP128	0	0.700984537	0.817	0.636	0	3
WFDC2	7.92E-257	0.696548913	0.942	0.883	1.58E-253	3
DMKN	1.74E-231	0.696523885	0.947	0.945	3.48E-228	3
TSHZ2	1.79E-261	0.696203787	0.859	0.78	3.58E-258	3
RIN2	2.07E-222	0.694526201	0.921	0.879	4.15E-219	3
RIIAD1	0	0.69337618	0.83	0.58	0	3
PIGR	9.36821329316452e-316	0.693335541	0.786	0.681	1.8736426586329e-312	3
ARPC1B	0	0.692236824	0.85	0.841	0	3
CCDC190	0	0.691692286	0.818	0.398	0	3
C1orf87	0	0.689903471	0.846	0.639	0	3
STOX1	0	0.688863058	0.821	0.654	0	3
IQCD	0	0.684471535	0.84	0.777	0	3
LRRC34	0	0.683233538	0.853	0.596	0	3
NCOA7	0	0.681306328	0.88	0.754	0	3
KAZN	0	0.678951646	0.893	0.824	0	3
LRRC49	0	0.675072872	0.843	0.703	0	3
ATXN1	1.13E-234	0.674051854	0.929	0.875	2.26E-231	3
NDUFAB1	1.25E-246	0.673729279	0.909	0.893	2.50E-243	3
SRGAP3-AS2	0	0.672866551	0.803	0.657	0	3
VNN3P	0	0.67097661	0.908	0.732	0	3
CASC2	0	0.670377118	0.797	0.623	0	3
DENND1A	0	0.664991937	0.88	0.748	0	3

DHCR24	0	0.660898391	0.879	0.825	0	3
ERBB4	0	0.660746168	0.787	0.627	0	3
ABCA13	0	0.658625089	0.871	0.771	0	3
BANF1	4.77203679414331e-318	0.655750253	0.893	0.883	9.54407358828661e-315	3
TMEM212	0	0.655011439	0.793	0.575	0	3
MGST3	0	0.653334809	0.889	0.877	0	3
STOM	0	0.652906744	0.861	0.785	0	3
PLCE1	0	0.651738475	0.732	0.618	0	3
SLCO3A1	0	0.65096822	0.898	0.814	0	3
HMGB3	0	0.648939727	0.895	0.804	0	3
PRICKLE2	0	0.64639473	0.833	0.601	0	3
SNHG16	0	0.645233822	0.909	0.856	0	3
RIBC1	0	0.638785507	0.839	0.569	0	3
RIBC2	0	0.638597246	0.76	0.648	0	3
PLCB4	0	0.637452595	0.854	0.626	0	3
MROH9	0	0.635583245	0.817	0.573	0	3
KIAA1217	1.12E-200	0.634026786	0.946	0.908	2.24E-197	3
PSD3	1.89E-217	0.631488427	0.905	0.871	3.78E-214	3
CEP112	0	0.631368557	0.767	0.649	0	3
MT-ATP8	9.09E-264	0.629824615	0.957	0.916	1.82E-260	3
ARHGEF38	0	0.629589418	0.897	0.753	0	3
KATNAL2	0	0.625328097	0.812	0.618	0	3
HLA-DRB1	0	0.619524809	0.863	0.763	0	3
SYTL3	0	0.618328154	0.845	0.713	0	3
DNAAF6	0	0.616140019	0.766	0.611	0	3
FAM166B	0	0.615834256	0.791	0.633	0	3
MYB	0	0.614365925	0.824	0.687	0	3
RBP1	2.78E-190	0.613956513	0.912	0.881	5.56E-187	3
CYBA	7.80E-187	0.613335378	0.942	0.923	1.56E-183	3
COL21A1	0	0.612657891	0.842	0.392	0	3
COBL	0	0.611115438	0.865	0.682	0	3
FBXL2	0	0.610892378	0.906	0.841	0	3
MIR99AHG	0	0.606861458	0.847	0.701	0	3
MPDZ	0	0.606254241	0.827	0.615	0	3
ZMYND8	2.77E-247	0.60420226	0.894	0.884	5.55E-244	3
FGF14	0	0.602589868	0.753	0.616	0	3
GULP1	3.12E-227	0.600992705	0.895	0.844	6.24E-224	3

AKAP6	0	0.600413906	0.833	0.707	0	3
HLA-DPA1	0	0.598736977	0.835	0.654	0	3
DRAIC	0	0.59801379	0.8	0.677	0	3
SIPA1L1	1.14E-200	0.59429594	0.898	0.834	2.28E-197	3
KCNE1	0	0.592523194	0.891	0.686	0	3
DDAH1	0	0.592228314	0.843	0.701	0	3
CRLF1	0	0.592066565	0.891	0.682	0	3
ATP6AP1-DT	0	0.591048073	0.816	0.691	0	3
EFNA5	9.30E-175	0.590626916	0.824	0.79	1.86E-171	3
ZBTB20	1.09E-231	0.588605281	0.917	0.837	2.19E-228	3
GMDS-DT	0	0.588523039	0.861	0.768	0	3
PLPPR3	0	0.587309016	0.835	0.651	0	3
EPS8	2.82E-233	0.584416002	0.877	0.804	5.64E-230	3
C8orf34	0	0.583286679	0.824	0.624	0	3
MYOF	1.10E-182	0.582522752	0.931	0.887	2.20E-179	3
PCDH7	0	0.580637936	0.801	0.705	0	3
ERICH2	0	0.580617888	0.808	0.627	0	3
LDHB	1.13E-235	0.580150241	0.851	0.83	2.27E-232	3
CDKL1	0	0.579901198	0.842	0.685	0	3
MICOS13	3.08E-285	0.576267894	0.906	0.891	6.15E-282	3
NCALD	0	0.575619929	0.815	0.576	0	3
C17orf97	0	0.575158034	0.756	0.696	0	3
CCDC74B	0	0.569840754	0.833	0.656	0	3
C11orf16	0	0.5679349	0.821	0.707	0	3
IL5RA	0	0.567632301	0.753	0.614	0	3
CSRP3-AS1	0	0.563155574	0.864	0.544	0	3
URB1	0	0.561210433	0.876	0.717	0	3
LINC-PINT	1.03E-154	0.560481323	0.94	0.879	2.06E-151	3
CATSPERD	0	0.559545992	0.8	0.541	0	3
RIC3	0	0.558982998	0.895	0.778	0	3
PCSK5	5.11E-239	0.555300688	0.925	0.856	1.02E-235	3
CCDC171	0	0.554530632	0.765	0.659	0	3
ACTN1	0	0.553758004	0.819	0.721	0	3
SMYD3	2.00E-278	0.553208805	0.834	0.717	4.01E-275	3
CENPK	0	0.552648673	0.764	0.605	0	3
MYEF2	0	0.552278459	0.861	0.704	0	3
RAMP1	0	0.550391472	0.81	0.66	0	3

RFX3-DT	0	0.549010004	0.865	0.738	0	3
FOXP2	0	0.548327393	0.844	0.652	0	3
TTC3	7.16E-200	0.54772983	0.877	0.865	1.43E-196	3
LINC02345	0	0.547426077	0.843	0.621	0	3
HACD3	0	0.546075009	0.806	0.709	0	3
NFIB	0	0.543186698	0.81	0.655	0	3
C22orf15	0	0.542109497	0.766	0.673	0	3
DYNLT4	0	0.541859091	0.806	0.6	0	3
JUN	2.43E-243	0.538372864	0.882	0.784	4.86E-240	3
WWC1	6.33E-262	0.538333889	0.928	0.896	1.27E-258	3
GRHL2	3.17E-224	0.534519501	0.854	0.782	6.34E-221	3
MEIG1	0	0.532361707	0.83	0.678	0	3
SYT8	0	0.530325224	0.84	0.746	0	3
TXNRD1	1.85E-148	0.529591575	0.902	0.925	3.69E-145	3
MRLN	0	0.528521233	0.845	0.706	0	3
MYO1E	1.10E-196	0.528237726	0.935	0.909	2.19E-193	3
NR3C2	1.14E-203	0.527017973	0.833	0.722	2.28E-200	3
FER	2.31E-268	0.524236822	0.855	0.766	4.62E-265	3
JAZF1	0	0.521059729	0.883	0.812	0	3
RCAN3	4.77892684224758e-311	0.51726268	0.896	0.851	9.56E-308	3
GNA14	0	0.50958214	0.874	0.753	0	3
MTATP6P1	4.99E-258	0.504290659	0.931	0.872	9.99E-255	3
ELN-AS1	0	0.503461558	0.781	0.652	0	3
LRRC37A5P.1	0	0.501819182	0.748	0.684	0	3
UGDH	0	0.501445574	0.811	0.727	0	3
GSTA1	2.07E-303	0.500191145	0.726	0.691	4.14E-300	3
B4GALNT3	0	0.499277933	0.904	0.796	0	3
PSIP1	0	0.495894805	0.722	0.676	0	3
SLC25A4	7.30E-262	0.494141923	0.9	0.846	1.46E-258	3
ALOX12P2.1	0	0.491990998	0.866	0.742	0	3
POLD3	2.15E-290	0.491325421	0.882	0.85	4.29E-287	3
EID1	3.85E-241	0.491232361	0.852	0.837	7.70E-238	3
VPS13B	4.52E-241	0.490485707	0.888	0.81	9.04E-238	3
HLA-DRB5	0	0.490151195	0.858	0.709	0	3
RRP12	0	0.48851257	0.876	0.812	0	3
RAD51B	3.38E-167	0.486818517	0.799	0.785	6.76E-164	3
TRPV4	0	0.486762666	0.857	0.793	0	3

SAA4	0	0.486435229	0.869	0.808	0	3
MACC1	9.00E-108	0.485107621	0.95	0.955	1.80E-104	3
CASC15	0	0.484908753	0.833	0.631	0	3
MT-ND5	1.29E-111	0.484241144	0.994	0.993	2.58E-108	3
CNTNAP3P2	0	0.483757731	0.838	0.709	0	3
NFIC	0	0.483285505	0.838	0.76	0	3
GALNT18	0	0.482580868	0.771	0.562	0	3
ITGA3	0	0.481160819	0.835	0.766	0	3
MT2A	2.77E-71	0.481085966	0.693	0.655	5.55E-68	3
MT-ND4	2.14E-35	0.480246845	0.999	0.998	4.28E-32	3
MACF1	3.47E-110	0.476199568	0.949	0.931	6.94E-107	3
KIAA0319	0	0.468548718	0.835	0.622	0	3
TMEM45B	1.51E-162	0.465302626	0.925	0.901	3.02E-159	3
TANC2	3.59E-119	0.465269197	0.903	0.883	7.18E-116	3
PPP1R9A	0	0.459682566	0.81	0.724	0	3
LINC00240	0	0.458959155	0.741	0.636	0	3
HDAC9	5.63E-88	0.457931358	0.899	0.928	1.13E-84	3
CRIM1	3.50384787196959e-310	0.457180576	0.832	0.754	7.01E-307	3
SCGB2A1	0	0.454896356	0.813	0.61	0	3
GCLC	2.02468101665743e-320	0.454391186	0.862	0.761	4.04936203331486e-317	3
FLOT2	0	0.451278801	0.855	0.814	0	3
DOCK4	1.35E-211	0.449906935	0.861	0.739	2.71E-208	3
ATG7	4.29E-185	0.445776443	0.859	0.804	8.57E-182	3
HSPA1A	2.46E-130	0.44564981	0.967	0.921	4.93E-127	3
ACAT1	0	0.44511789	0.801	0.683	0	3
NDUFA4	3.45E-110	0.443644395	0.904	0.956	6.91E-107	3
SEMA3C	7.27E-199	0.443231545	0.903	0.825	1.45E-195	3
EYA1	0	0.442201327	0.836	0.628	0	3
PDLIM4	2.34E-147	0.441998992	0.9	0.889	4.69E-144	3
FAT1	5.71E-257	0.441123982	0.882	0.769	1.14E-253	3
LRMDA	1.42E-259	0.440769598	0.826	0.735	2.84E-256	3
NDUFB2	1.42E-99	0.438593526	0.911	0.923	2.83E-96	3
IRAK3	0	0.434374961	0.847	0.779	0	3
SLFN5	2.07E-235	0.434111869	0.783	0.76	4.13E-232	3
TYMP	5.13E-209	0.433620489	0.943	0.919	1.03E-205	3
POLR2B	2.29E-169	0.433161828	0.893	0.82	4.58E-166	3
DEUP1	0	0.433035947	0.743	0.56	0	3

MRTFA	3.45E-145	0.43022364	0.897	0.823	6.90E-142	3
GDA	0	0.427259621	0.846	0.739	0	3
LINC00589	0	0.427243346	0.745	0.629	0	3
TEKT4	0	0.427109046	0.83	0.737	0	3
SAA2-SAA4	0	0.425192931	0.851	0.763	0	3
DEGS2	0	0.423444706	0.873	0.802	0	3
CDC42BPA	2.29E-162	0.421271911	0.849	0.792	4.57E-159	3
EML6	0	0.41955219	0.83	0.745	0	3
MEIS2	2.72E-169	0.416884641	0.882	0.814	5.45E-166	3
DMGDH	2.45E-283	0.416784741	0.837	0.771	4.90E-280	3
PSPH	1.32656625908375e-320	0.412277563	0.723	0.651	2.65313251816749e-317	3
GPR39	0	0.411341125	0.767	0.631	0	3
TBC1D5	1.12E-120	0.410308019	0.836	0.81	2.23E-117	3
ARHGAP24	3.78E-156	0.41029648	0.817	0.723	7.55E-153	3
IARS1	1.28E-244	0.40872313	0.829	0.759	2.57E-241	3
HHLA2	0	0.407358718	0.851	0.558	0	3
ST6GAL1	0	0.406449408	0.836	0.732	0	3
SERPINA1	0	0.406443388	0.872	0.772	0	3
GLCCI1	8.81E-255	0.403919723	0.849	0.742	1.76E-251	3
MUC1	6.69E-80	0.403240289	0.912	0.944	1.34E-76	3
LAMC2	1.47E-211	0.403191992	0.888	0.847	2.94E-208	3
PACS1	2.41E-165	0.402639699	0.858	0.826	4.81E-162	3
ZNF462	0	0.402005601	0.825	0.718	0	3
LINC02889	0	0.401735703	0.784	0.685	0	3
NCL	2.07E-118	0.400864345	0.812	0.727	4.14E-115	3
PPM1E	0	0.396318231	0.799	0.673	0	3
ZFPM2-AS1	1.34E-241	0.395197494	0.836	0.833	2.68E-238	3
GSN	1.75E-78	0.393840196	0.966	0.973	3.50E-75	3
KLF12	9.95E-190	0.393701225	0.867	0.793	1.99E-186	3
CCNA1	1.52E-291	0.392392214	0.776	0.659	3.03E-288	3
ANAPC5	4.83E-236	0.391377177	0.882	0.816	9.67E-233	3
MAP1B	0	0.391265532	0.772	0.625	0	3
CLIP4	3.04E-137	0.391186787	0.907	0.889	6.08E-134	3
TACC2	2.79E-137	0.38952803	0.904	0.846	5.58E-134	3
LINC01572	0	0.388821188	0.75	0.671	0	3
RGCC	5.98922324327807e-314	0.388671989	0.797	0.763	1.19784464865561e-310	3
NSMCE2	3.98E-148	0.388264729	0.892	0.847	7.95E-145	3

TDRP	0	0.385249923	0.845	0.736	0	3
DTNA	0	0.384033491	0.807	0.733	0	3
MT-RNR1	5.61E-11	0.38351001	0.999	0.999	1.12E-07	3
SNHG14	6.57E-197	0.382704024	0.853	0.77	1.31E-193	3
IGFBP5	0	0.382469092	0.706	0.515	0	3
CD109	1.66E-187	0.378656179	0.779	0.765	3.33E-184	3
CCDC181	0	0.376727561	0.737	0.594	0	3
HLA-DQB1	0	0.375235986	0.847	0.768	0	3
IFITM2	1.03E-70	0.37480014	0.889	0.925	2.06E-67	3
MYH14	0	0.374399687	0.884	0.806	0	3
CNTN3	0.00E+00	0.37377577	0.792	0.692	2.09E-305	3
TNFAIP3	9.96E-181	0.369521479	0.906	0.875	1.99E-177	3
STIL	1.63E-284	0.36786065	0.732	0.683	3.26E-281	3
SPIDR	9.67E-107	0.367736554	0.901	0.837	1.93E-103	3
FABP6	0.00E+00	0.365206834	0.732	0.672	4.94E-306	3
SMIM6	1.07E-299	0.364154791	0.715	0.559	2.15E-296	3
TENM4	3.80E-304	0.36414598	0.871	0.718	7.61E-301	3
FUT8	0	0.364098526	0.79	0.664	0	3
PSMB8	6.14E-103	0.362901764	0.867	0.884	1.23E-99	3
MICAL2	1.31E-252	0.362550261	0.873	0.771	2.61E-249	3
FAM153B	0	0.362534043	0.864	0.675	0	3
DOCK8	1.85E-261	0.362077484	0.83	0.79	3.70E-258	3
CNNM2	1.17E-170	0.361990205	0.827	0.757	2.34E-167	3
CRYAB	1.25E-202	0.361843624	0.775	0.843	2.51E-199	3
MTX2	8.19E-202	0.360302151	0.944	0.9	1.64E-198	3
CCDC60	0	0.358398055	0.694	0.547	0	3
ATP12A	3.47E-175	0.357445342	0.817	0.692	6.93E-172	3
BMPR1B	4.41E-98	0.356243848	0.881	0.84	8.82E-95	3
MIR4713HG	0	0.356206582	0.836	0.748	0	3
PLAAT2	7.88E-247	0.356144324	0.831	0.818	1.58E-243	3
FSTL1	0	0.351059637	0.838	0.735	0	3
DNER	0	0.350420328	0.86	0.602	0	3
ANLN	5.94E-91	0.350287135	0.671	0.643	1.19E-87	3
CHCHD10	1.52E-86	0.348471239	0.888	0.931	3.03E-83	3
RPP38	3.00E-152	0.346651853	0.792	0.768	6.01E-149	3
INPP4B	2.14E-52	0.345811771	0.956	0.956	4.29E-49	3
CDKN1A	1.62E-52	0.345226413	0.912	0.927	3.24E-49	3

HES6	2.26E-232	0.344510847	0.795	0.672	4.52E-229	3
FUT10	1.89E-63	0.343556024	0.832	0.825	3.79E-60	3
P2RX4	6.17E-166	0.34310498	0.868	0.818	1.23E-162	3
LKAAEAR1	0	0.339897155	0.797	0.641	0	3
SLC7A2	0	0.339312886	0.779	0.485	0	3
ASAP1	3.17E-177	0.338886348	0.873	0.81	6.34E-174	3
LINC02057	0	0.336937076	0.766	0.72	0	3
PARD6G-AS1	0	0.336541196	0.858	0.788	0	3
MAP3K2-DT	0	0.335901735	0.806	0.743	0	3
MIR205HG	3.85E-134	0.335758665	0.919	0.87	7.70E-131	3
MSTO1	2.23E-285	0.335677286	0.809	0.738	4.47E-282	3
DUSP14	5.54E-255	0.334764622	0.798	0.787	1.11E-251	3
CDKAL1	6.41E-87	0.333258308	0.899	0.837	1.28E-83	3
LINC01473	1.49E-176	0.332724679	0.821	0.756	2.99E-173	3
PTPRM	3.99E-153	0.331991001	0.87	0.787	7.97E-150	3
MTHFD2	8.01E-205	0.32995614	0.77	0.736	1.60E-201	3
VIM	2.85E-284	0.329302926	0.656	0.566	5.71E-281	3
PKP4-AS1	2.45E-68	0.329265447	0.713	0.755	4.91E-65	3
AQP4-AS1	0	0.328362071	0.773	0.682	0	3
PTPRN2	6.35E-270	0.32801989	0.854	0.73	1.27E-266	3
MIR100HG	0	0.327157541	0.756	0.672	0	3
FYB2	0	0.326510325	0.804	0.72	0	3
E2F7	6.39E-272	0.326048327	0.761	0.735	1.28E-268	3
GPX8	0	0.324599213	0.777	0.578	0	3
PBX1	4.39E-91	0.324051542	0.831	0.802	8.79E-88	3
SQLE	3.91E-118	0.321604168	0.847	0.821	7.82E-115	3
LEPROTL1	9.01E-186	0.321425463	0.866	0.852	1.80E-182	3
MIPOL1	4.29E-290	0.320949299	0.806	0.742	8.58E-287	3
VRK2	1.74E-113	0.320599601	0.897	0.86	3.48E-110	3
MAST4	5.31E-85	0.319839328	0.886	0.858	1.06E-81	3
IKZF2	5.14E-46	0.319471622	0.889	0.9	1.03E-42	3
SETX	2.48E-107	0.319400594	0.863	0.822	4.97E-104	3
MYH9	1.65E-93	0.319383993	0.888	0.858	3.30E-90	3
TRIM2	3.40E-77	0.318971643	0.908	0.902	6.80E-74	3
PVT1	4.67E-176	0.318194885	0.81	0.741	9.35E-173	3
TBCK	3.78E-196	0.317761817	0.827	0.767	7.56E-193	3
AEBP2	2.48E-83	0.317674408	0.895	0.87	4.95E-80	3

MFSD4B	2.80E-197	0.317311659	0.816	0.78	5.61E-194	3
HSP90B1	9.44E-62	0.316945578	0.852	0.882	1.89E-58	3
IL18	1.30E-222	0.316539328	0.857	0.865	2.59E-219	3
PKIB	0	0.316000552	0.834	0.663	0	3
LTBP1	7.38E-187	0.315909444	0.76	0.685	1.48E-183	3
NEBL	5.05E-58	0.314286952	0.923	0.94	1.01E-54	3
C4orf19	1.31E-92	0.3137996	0.904	0.861	2.63E-89	3
FKBP5	2.52E-156	0.312909783	0.809	0.741	5.03E-153	3
NTN4	1.61E-78	0.311925108	0.929	0.915	3.22E-75	3
RBM47	1.32E-54	0.310389593	0.951	0.95	2.64E-51	3
CRADD	2.67E-252	0.308772586	0.802	0.724	5.33E-249	3
LRRC36	0	0.308596534	0.874	0.68	0	3
DNAJB4	2.33E-210	0.308109502	0.879	0.843	4.66E-207	3
FAM153A	0	0.308014331	0.875	0.758	0	3
HSPA1B	5.21E-128	0.307985615	0.983	0.941	1.04E-124	3
EGFR	2.21E-90	0.306860485	0.879	0.841	4.41E-87	3
LGR4	8.58E-112	0.306300135	0.832	0.788	1.72E-108	3
ZMAT3	8.65E-134	0.305073312	0.786	0.776	1.73E-130	3
BABAM2	3.63E-111	0.304325703	0.872	0.849	7.27E-108	3
RPS6KA5	6.81E-176	0.303599087	0.836	0.786	1.36E-172	3
STOX2	2.04E-305	0.302682159	0.86	0.773	4.07E-302	3
MICAL3	1.18E-234	0.302419824	0.857	0.788	2.36E-231	3
MAGI2	2.46E-271	0.301354779	0.79	0.727	4.92E-268	3
DNAAF9	7.17E-139	0.300959205	0.876	0.845	1.43E-135	3
ATF3	1.91E-98	0.300515915	0.864	0.817	3.83E-95	3
FOS	5.11E-133	0.299721004	0.906	0.868	1.02E-129	3
MAPKBP1	2.78E-270	0.297696341	0.844	0.77	5.56E-267	3
LUCAT1	1.90E-238	0.297450961	0.763	0.658	3.79E-235	3
HDGFL3	3.06E-266	0.295851209	0.796	0.722	6.13E-263	3
ARHGAP26	1.17E-230	0.294284505	0.832	0.728	2.35E-227	3
CFAP20DC	5.56E-104	0.293683081	0.836	0.846	1.11E-100	3
SERPINE1	2.00E-266	0.293345391	0.778	0.741	3.99E-263	3
AKR1C1	1.39E-162	0.292719833	0.737	0.727	2.78E-159	3
SCIN	0	0.292464639	0.843	0.763	0	3
IMMP2L	3.33E-86	0.290826636	0.757	0.729	6.67E-83	3
MUC4	2.17E-102	0.290673142	0.884	0.844	4.33E-99	3
UST	1.02E-208	0.289887538	0.806	0.751	2.04E-205	3

GIPC2	0	0.289253329	0.773	0.734	0	3
CCDC18-AS1	5.24E-173	0.288434274	0.854	0.781	1.05E-169	3
PRKCA	6.18E-85	0.287856717	0.83	0.801	1.24E-81	3
SMIM35	0	0.286887149	0.757	0.721	0	3
CCSER1	1.56E-166	0.283200312	0.759	0.67	3.12E-163	3
CKLF	9.70E-252	0.2831879	0.837	0.787	1.94E-248	3
EHBP1	1.15E-87	0.283170444	0.725	0.684	2.29E-84	3
MT-ND1	8.78E-19	0.282706518	0.983	0.991	1.76E-15	3
LPP	9.68E-44	0.282404564	0.908	0.904	1.94E-40	3
APBB2	2.26E-107	0.282165674	0.799	0.738	4.51E-104	3
SNORD3A	0	0.281615913	0.873	0.802	0	3
EPRS1	1.67E-133	0.278075422	0.771	0.725	3.34E-130	3
RHOB	9.09E-119	0.277391547	0.805	0.758	1.82E-115	3
CEP85L	5.29E-303	0.276908805	0.773	0.613	1.06E-299	3
KIF26B	3.21E-135	0.275881694	0.819	0.763	6.41E-132	3
SPTSSB	0	0.274481565	0.857	0.834	0	3
PLK4	4.23E-163	0.274247215	0.665	0.562	8.45E-160	3
FHIT	3.73E-80	0.273996054	0.821	0.78	7.46E-77	3
TIMP1	2.58E-100	0.269689933	0.814	0.803	5.15E-97	3
HLA-B	5.59E-42	0.26882126	0.943	0.963	1.12E-38	3
UNC13B	1.12E-63	0.268076258	0.839	0.806	2.25E-60	3
HSD17B6	5.33E-142	0.268054288	0.802	0.645	1.07E-138	3
BIRC3	8.21E-103	0.264848695	0.812	0.864	1.64E-99	3
THSD4	4.90E-110	0.264669431	0.704	0.687	9.80E-107	3
IRS2	7.20E-78	0.264559246	0.89	0.833	1.44E-74	3
ETV6	4.37E-48	0.26454733	0.951	0.944	8.75E-45	3
NRP2	6.54119812584211e-316	0.261562821	0.769	0.73	1.30823962516842e-312	3
SLC20A2	4.56E-57	0.261506363	0.927	0.923	9.12E-54	3
JDP2	2.92E-207	0.260216858	0.812	0.785	5.83E-204	3
DPH6-DT	0	0.259937053	0.771	0.681	0	3
CYCS	2.72E-58	0.259642697	0.898	0.879	5.44E-55	3
PTGR1	3.47E-92	0.259297522	0.842	0.873	6.93E-89	3
CCDC18	6.11E-188	0.258628364	0.706	0.677	1.22E-184	3
ARHGEF3	1.77E-61	0.258558412	0.89	0.872	3.54E-58	3
HLA-DQA1	0	0.258529551	0.784	0.633	0	3
APRT	1.55E-75	0.257833073	0.869	0.913	3.11E-72	3
OGDH	9.47E-99	0.257404741	0.901	0.837	1.89E-95	3

VTRNA1-3	1.46E-152	0.256935161	0.799	0.76	2.92E-149	3
CASC8	2.54E-232	0.254096907	0.843	0.837	5.08E-229	3
CLIC5	1.14420576755326e-313	0.253839309	0.76	0.613	2.28841153510651e-310	3
CREB5	2.61E-292	0.252866735	0.782	0.707	5.22E-289	3
SH3RF3	0	0.251912721	0.802	0.661	0	3
WAKMAR2	0	0.251884357	0.861	0.696	0	3
TRPS1	6.70E-81	0.249579827	0.8	0.776	1.34E-77	3
GBP1	0	0.247741384	0.756	0.773	0	3
IGF2BP3	1.02E-77	0.246628997	0.837	0.829	2.04E-74	3
PRKAR2A	8.89E-131	0.245701581	0.786	0.792	1.78E-127	3
PSME2	1.11E-55	0.245251878	0.858	0.906	2.21E-52	3
MYADM	3.50E-268	0.243948289	0.809	0.677	6.99E-265	3
ALOX15	7.32E-268	0.243930262	0.685	0.602	1.46E-264	3
SSBP2	4.41E-47	0.24389127	0.908	0.898	8.82E-44	3
LINC00886	0	0.243764331	0.779	0.737	0	3
METTL5	3.20E-94	0.24369483	0.831	0.868	6.40E-91	3
TMTCC2	4.72E-30	0.243179684	0.918	0.898	9.44E-27	3
CDK1	3.22E-127	0.24291291	0.665	0.571	6.44E-124	3
SHISA8	4.64E-193	0.241340192	0.704	0.719	9.28E-190	3
BPIFB1	3.19E-91	0.241071379	0.615	0.552	6.39E-88	3
PDE7B	6.46E-305	0.239448989	0.825	0.78	1.29E-301	3
NEDD9	0	0.23936521	0.835	0.729	0	3
UGGT2	2.63E-184	0.23907911	0.756	0.729	5.25E-181	3
DNAJC16	1.11E-134	0.238285551	0.838	0.793	2.22E-131	3
CNST	1.55E-33	0.23767199	0.876	0.87	3.10E-30	3
LINC00578	1.22E-224	0.235404964	0.769	0.692	2.44E-221	3
PRDX4	8.37E-144	0.235206641	0.842	0.798	1.67E-140	3
CYP27A1	0	0.233797972	0.764	0.688	0	3
CP	2.66E-64	0.233264478	0.694	0.641	5.31E-61	3
GRIK2	5.72E-191	0.232993461	0.706	0.615	1.14E-187	3
FRMD5	1.55E-124	0.232732949	0.807	0.72	3.11E-121	3
STMN1	4.52E-104	0.232365664	0.795	0.763	9.04E-101	3
LINC01931	0	0.232240344	0.72	0.705	0	3
ITGB8	4.09E-14	0.232089117	0.961	0.97	8.17E-11	3
SHLD1	4.44E-73	0.230750044	0.776	0.756	8.88E-70	3
CCDC85B	1.35E-88	0.230199165	0.877	0.917	2.71E-85	3
PAFAH1B1	9.02E-24	0.229712446	0.916	0.935	1.80E-20	3

TIMM8A	2.02E-238	0.228919356	0.798	0.739	4.04E-235	3
ALDH3A1	1.48E-159	0.22863977	0.715	0.742	2.97E-156	3
EPPK1	0	0.228452727	0.771	0.607	0	3
CRY1	6.76E-69	0.227293406	0.878	0.832	1.35E-65	3
LINC01392	0	0.226968154	0.771	0.677	0	3
HLCS	4.63E-183	0.226613657	0.777	0.749	9.26E-180	3
NMB	2.97E-94	0.224403727	0.786	0.821	5.94E-91	3
ZBTB10	2.90E-279	0.224303069	0.826	0.727	5.79E-276	3
DUT	1.76E-74	0.224109569	0.855	0.873	3.51E-71	3
SDK2	2.24E-52	0.223384694	0.778	0.682	4.48E-49	3
SCD5	1.17E-155	0.222858124	0.866	0.802	2.35E-152	3
TDP1	1.92E-198	0.222699859	0.847	0.77	3.84E-195	3
ZNF608	0	0.222464673	0.819	0.717	0	3
SGK1	6.39E-118	0.221917974	0.798	0.739	1.28E-114	3
WNT9A	6.04044658605508e-320	0.22127648	0.883	0.795	1.20808931721102e-316	3
TEF	1.11E-59	0.219476792	0.823	0.813	2.22E-56	3
DDX60	1.21E-152	0.219394495	0.843	0.783	2.43E-149	3
AKR1C3	3.90E-203	0.217724544	0.713	0.727	7.80E-200	3
AGPAT5	1.44E-130	0.216336015	0.75	0.674	2.88E-127	3
REL-DT	1.85E-262	0.21629826	0.848	0.826	3.69E-259	3
SCAMP5	2.68E-302	0.216172841	0.795	0.692	5.36E-299	3
XIST	8.48E-38	0.214471675	0.923	0.896	1.70E-34	3
TPCN1	2.75E-46	0.214146426	0.882	0.853	5.50E-43	3
CNIH3	1.58E-176	0.213232722	0.781	0.755	3.16E-173	3
CHST11	2.54E-223	0.212709949	0.702	0.688	5.09E-220	3
AARS1	1.32E-123	0.212048607	0.684	0.698	2.65E-120	3
LDLR	1.62E-53	0.211826537	0.931	0.898	3.24E-50	3
SNTB1	0	0.211644954	0.848	0.72	0	3
DNM3	9.02E-190	0.21070399	0.83	0.705	1.80E-186	3
PAPSS1	4.87E-39	0.210375955	0.893	0.891	9.74E-36	3
LINC01344	1.05E-90	0.20935651	0.749	0.74	2.09E-87	3
ASAP2	1.61E-50	0.208868022	0.85	0.839	3.21E-47	3
PDK4	1.38E-143	0.208531252	0.788	0.726	2.76E-140	3
CEBPB	1.27E-28	0.207612862	0.934	0.945	2.54E-25	3
VNN1	1.07E-129	0.206151307	0.771	0.661	2.15E-126	3
SDCBP2-AS1	2.10E-286	0.205825963	0.729	0.695	4.19E-283	3
CDC20	1.34E-126	0.205434261	0.586	0.606	2.68E-123	3

MT-CYB	3.11E-07	0.20438065	0.992	0.998	0.000621026	3
IQSEC1	4.28E-89	0.202370549	0.828	0.797	8.55E-86	3
PRKAR2B	3.18E-157	0.202122083	0.799	0.774	6.37E-154	3
RASAL2	2.11E-27	0.201929058	0.941	0.934	4.22E-24	3
PHLDB2	6.23E-59	0.201703827	0.772	0.711	1.25E-55	3
PRSS23	3.39E-61	0.200979222	0.89	0.878	6.78E-58	3
GSTO1	1.90E-60	0.200892036	0.829	0.858	3.80E-57	3
NXN	1.08E-27	0.200735828	0.908	0.921	2.16E-24	3
ARL15	3.01E-43	0.200619763	0.774	0.723	6.01E-40	3
FYB1	1.01E-05	0.199083741	0.579	0.571	0.020150707	3
KANK1	6.84E-95	0.198897189	0.811	0.716	1.37E-91	3
NMNAT2	0	0.198190826	0.803	0.712	0	3
USP45	4.42E-33	0.19798289	0.778	0.798	8.83E-30	3
AGBL1	1.41E-79	0.196366382	0.802	0.709	2.81E-76	3
UBE2S	3.27E-88	0.196323807	0.826	0.835	6.54E-85	3
MECOM	1.35E-41	0.196191732	0.843	0.843	2.70E-38	3
RAB31	1.55E-44	0.195852653	0.856	0.858	3.11E-41	3
DUSP23	1.23E-93	0.193997753	0.878	0.824	2.47E-90	3
TOP2A	1.28E-93	0.193716704	0.584	0.513	2.56E-90	3
CPNE8	6.80E-47	0.193647434	0.863	0.831	1.36E-43	3
CNNM1	5.26E-181	0.193322347	0.683	0.813	1.05E-177	3
CBR1	1.62E-58	0.192152644	0.854	0.855	3.25E-55	3
ITGB4	6.33E-63	0.191924104	0.844	0.846	1.27E-59	3
TNNT3	0	0.191859419	0.79	0.723	0	3
PSAT1	3.39E-184	0.189848357	0.644	0.641	6.78E-181	3
AKR1C2	1.37E-25	0.18945281	0.774	0.797	2.75E-22	3
TRNP1	2.27E-269	0.189093817	0.808	0.752	4.54E-266	3
NHS	0	0.188949309	0.861	0.687	0	3
PLAAT3	4.05E-33	0.1884076	0.894	0.921	8.09E-30	3
FYN	8.87E-267	0.188064107	0.716	0.658	1.77E-263	3
LIMCH1	3.46E-47	0.187720951	0.712	0.604	6.93E-44	3
ADCY9	5.25E-87	0.18754624	0.803	0.84	1.05E-83	3
TNNC2	4.76E-242	0.18600453	0.755	0.736	9.52E-239	3
APOL6	2.50E-47	0.185578642	0.841	0.875	4.99E-44	3
PATJ	3.99E-10	0.184557242	0.926	0.939	7.97E-07	3
ITM2C	2.29E-257	0.183799205	0.8	0.761	4.58E-254	3
PALMD	1.18E-186	0.183662954	0.734	0.735	2.36E-183	3

VWC2L	0	0.182268637	0.769	0.627	0	3
MTHFD1L	1.17E-135	0.181546316	0.771	0.745	2.34E-132	3
RRM2B	4.64E-100	0.181154531	0.774	0.8	9.29E-97	3
PHGDH	9.46E-224	0.181028467	0.702	0.627	1.89E-220	3
CYB5A	1.91E-14	0.180707295	0.914	0.93	3.82E-11	3
FTX	8.24E-29	0.18023448	0.888	0.87	1.65E-25	3
LINC01088	1.23E-114	0.178556558	0.632	0.716	2.45E-111	3
HDAC11	2.40E-12	0.177887086	0.836	0.861	4.79E-09	3
LINC01588	8.27E-87	0.17577801	0.791	0.776	1.65E-83	3
LINC02539	1.79E-279	0.175514208	0.494	0.722	3.58E-276	3
MBD5	1.44E-35	0.175298675	0.887	0.884	2.88E-32	3
COL4A5	1.76E-117	0.175142092	0.721	0.623	3.52E-114	3
RANBP17	7.73E-48	0.174398187	0.839	0.813	1.55E-44	3
ZSWIM6	1.43E-23	0.174223606	0.908	0.882	2.85E-20	3
LRRC26	4.06E-36	0.173981683	0.824	0.813	8.12E-33	3
GBE1	1.82E-28	0.173801229	0.844	0.83	3.64E-25	3
BICRAL	2.80E-60	0.173406265	0.85	0.832	5.60E-57	3
PTTG1	9.00E-126	0.172783413	0.78	0.703	1.80E-122	3
TP53AIP1	9.26E-299	0.172210494	0.743	0.702	1.85E-295	3
WDR43	6.46E-49	0.172018808	0.811	0.758	1.29E-45	3
TUBA1B	6.50E-49	0.171565334	0.787	0.862	1.30E-45	3
AQP3	8.77E-13	0.170970549	0.918	0.936	1.75E-09	3
MGLL	5.56E-63	0.170223806	0.884	0.903	1.11E-59	3
ZCCHC7	1.03E-25	0.169169868	0.788	0.778	2.05E-22	3
MAD2L1	5.04E-199	0.168491848	0.718	0.611	1.01E-195	3
ZFP36L2	2.01E-34	0.168092028	0.878	0.848	4.02E-31	3
PACS2	2.88E-68	0.167279233	0.836	0.811	5.75E-65	3
PIGN	8.32E-38	0.166219339	0.801	0.781	1.66E-34	3
DCAKD	6.57E-52	0.165567949	0.834	0.813	1.31E-48	3
LINC01429	1.78E-69	0.165399106	0.725	0.67	3.57E-66	3
SAMD12	5.57E-47	0.164075908	0.837	0.875	1.11E-43	3
TIAM2	1.84E-64	0.16354313	0.786	0.784	3.68E-61	3
STYK1	1.66E-80	0.163256074	0.845	0.846	3.32E-77	3
SLC26A2	5.50E-295	0.16315105	0.775	0.687	1.10E-291	3
EOLA2-DT	1.97E-68	0.162997249	0.791	0.742	3.94E-65	3
DIAPH2-AS1	0	0.162729	0.751	0.675	0	3
BHLHE41	1.43E-101	0.162121905	0.786	0.774	2.86E-98	3

TEX49	9.23E-228	0.161841496	0.759	0.694	1.85E-224	3
NR2F2	3.53E-25	0.161817364	0.857	0.825	7.07E-22	3
HSPA5	5.46E-20	0.161587028	0.875	0.922	1.09E-16	3
ABCC11	2.96E-81	0.161176613	0.752	0.826	5.93E-78	3
LINC01004	5.01E-39	0.161097472	0.848	0.806	1.00E-35	3
ERRFI1-DT	4.17E-26	0.159277595	0.782	0.794	8.33E-23	3
TANGO6	1.90E-122	0.156913914	0.784	0.662	3.80E-119	3
RPL39L	3.61E-157	0.15654327	0.707	0.619	7.23E-154	3
SLC7A11	2.54E-126	0.155868967	0.711	0.592	5.08E-123	3
DTNB	1.40E-126	0.155340414	0.703	0.703	2.80E-123	3
TMEM120B	2.85E-85	0.155193473	0.743	0.775	5.70E-82	3
SLC1A5	5.16E-94	0.154645266	0.699	0.663	1.03E-90	3
CLGN	9.05E-226	0.154366665	0.683	0.568	1.81E-222	3
LINC02615	1.07E-121	0.153841823	0.811	0.819	2.15E-118	3
ZNHIT6	9.02E-73	0.152347675	0.702	0.718	1.80E-69	3
GRK3	5.52E-104	0.152145052	0.718	0.743	1.10E-100	3
FBXL17	1.58E-31	0.151417615	0.845	0.837	3.16E-28	3
NUMBL	2.82E-281	0.150095724	0.813	0.719	5.64E-278	3
IGFBP3	2.02E-23	0.150065939	0.815	0.834	4.03E-20	3
PEMT	3.21E-99	0.148328433	0.847	0.78	6.42E-96	3
GPHN	1.19E-24	0.148158144	0.793	0.766	2.38E-21	3
MYO16-AS1	1.79E-94	0.147689522	0.779	0.792	3.57E-91	3
ITGA2	3.39E-32	0.14734975	0.859	0.88	6.78E-29	3
PLOD2	1.09E-27	0.147095526	0.795	0.745	2.18E-24	3
PLEKHG1	4.81E-36	0.146900963	0.854	0.828	9.61E-33	3
PEBP4	1.78E-106	0.146457993	0.801	0.683	3.57E-103	3
TGFB2	1.16E-115	0.144662874	0.865	0.749	2.33E-112	3
MACC1-DT	2.60E-86	0.144188954	0.804	0.812	5.19E-83	3
EPHX1	1.22E-38	0.143475795	0.852	0.89	2.44E-35	3
SESTD1	1.41E-10	0.142845648	0.873	0.871	2.81E-07	3
OSBPL10	2.11E-17	0.142379328	0.859	0.847	4.23E-14	3
RARRES2	1.05E-118	0.141558677	0.631	0.711	2.10E-115	3
GADD45G	3.15E-155	0.14155253	0.848	0.728	6.31E-152	3
TRIM14	6.76E-40	0.141294988	0.805	0.821	1.35E-36	3
ALPK3	6.03E-164	0.140394761	0.781	0.744	1.21E-160	3
CTC1	3.70E-12	0.140176667	0.799	0.795	7.40E-09	3
PSMB9	4.27E-62	0.138875961	0.813	0.872	8.53E-59	3

MYL9	5.21E-215	0.138432806	0.674	0.746	1.04E-211	3
CXCL6	4.99E-44	0.138334588	0.836	0.815	9.98E-41	3
PTCHD4	2.73E-94	0.137365648	0.623	0.676	5.47E-91	3
KCNMB2-AS1	1.22E-172	0.136959057	0.756	0.694	2.45E-169	3
FNDC3B	2.70E-13	0.135990923	0.947	0.958	5.39E-10	3
EGLN3	8.99E-17	0.135614167	0.849	0.841	1.80E-13	3
DENND4A	9.18E-41	0.135593761	0.872	0.793	1.84E-37	3
SLC32A1	0	0.135459892	0.753	0.546	0	3
RPS6KC1	1.77E-99	0.135174272	0.756	0.793	3.54E-96	3
MRPL17	2.54E-51	0.135010613	0.805	0.844	5.09E-48	3
TMEM61	2.75E-299	0.134198712	0.759	0.724	5.50E-296	3
INHBB	8.11E-108	0.133702988	0.779	0.766	1.62E-104	3
DOCK5	1.71E-23	0.133223905	0.862	0.869	3.42E-20	3
PTAFR	7.19E-51	0.132101141	0.816	0.834	1.44E-47	3
SLC41A2	1.11E-153	0.131825904	0.78	0.787	2.22E-150	3
PRKN	8.02E-43	0.131079999	0.821	0.779	1.60E-39	3
CCN1	1.54E-64	0.130554229	0.853	0.801	3.08E-61	3
NR6A1	2.12E-19	0.13043418	0.874	0.876	4.24E-16	3
DLEU2	5.52E-23	0.129754356	0.8	0.765	1.10E-19	3
ITGA6	9.27E-47	0.129196723	0.696	0.677	1.85E-43	3
VMO1	3.72E-114	0.128585642	0.768	0.692	7.43E-111	3
NUPR1	6.26E-129	0.127231706	0.57	0.563	1.25E-125	3
HRH1	1.32E-76	0.127193185	0.724	0.783	2.63E-73	3
LAMA3	1.63E-11	0.127150497	0.692	0.68	3.27E-08	3
HMGCS1	9.01E-23	0.126399428	0.915	0.875	1.80E-19	3
CADPS2	6.74E-131	0.125476725	0.695	0.578	1.35E-127	3
LAT2	2.35E-147	0.124758703	0.764	0.641	4.71E-144	3
HSPA6	3.82E-20	0.124323747	0.912	0.898	7.64E-17	3
BACH2	3.53E-26	0.124240693	0.843	0.786	7.06E-23	3
EYA4	3.89E-125	0.123797319	0.711	0.617	7.79E-122	3
KCNE4	0	0.123373175	0.904	0.661	0	3
ITGB1BP1	9.46E-66	0.123231433	0.802	0.83	1.89E-62	3
CAV1	1.15E-52	0.12322539	0.73	0.648	2.30E-49	3
IFIT1	1.70E-58	0.123176858	0.694	0.745	3.41E-55	3
FGFBP1	2.50E-22	0.122317229	0.813	0.839	5.01E-19	3
FBN2	1.45E-187	0.12220676	0.741	0.693	2.89E-184	3
FAIM2	2.27E-192	0.122139064	0.765	0.574	4.55E-189	3

SH3GL3	9.43E-105	0.121717941	0.823	0.76	1.89E-101	3
SCGB3A1	1.38E-88	0.121436844	0.702	0.704	2.77E-85	3
MTSS1	4.74E-16	0.119486654	0.89	0.897	9.47E-13	3
HEATR4	6.22E-91	0.118918072	0.817	0.816	1.24E-87	3
PXDN	5.87E-209	0.118847302	0.74	0.666	1.17E-205	3
GFOD1	4.82E-72	0.118671311	0.75	0.736	9.64E-69	3
MAP2	6.15E-76	0.118425712	0.793	0.74	1.23E-72	3
NEDD4	6.57E-79	0.118361397	0.756	0.816	1.31E-75	3
CENPF	7.24E-169	0.117304519	0.671	0.483	1.45E-165	3
SNAPC1	5.91E-11	0.116932642	0.802	0.783	1.18E-07	3
SLC16A13	3.46E-21	0.116092697	0.784	0.77	6.92E-18	3
GUCY2C-AS1	4.25E-59	0.114871772	0.855	0.799	8.50E-56	3
BANK1	7.17E-81	0.114628516	0.821	0.727	1.43E-77	3
SCFD2	1.14E-77	0.114509736	0.762	0.686	2.28E-74	3
IL6R	6.53E-38	0.113908833	0.84	0.821	1.31E-34	3
SEMA3A	1.11E-40	0.113149796	0.704	0.663	2.21E-37	3
PLP2	1.86E-28	0.112642751	0.844	0.874	3.72E-25	3
RASSF8	6.74E-206	0.111660726	0.721	0.66	1.35E-202	3
FRAS1	6.06E-170	0.110584309	0.666	0.755	1.21E-166	3
SGO1-AS1	3.81E-76	0.110521035	0.787	0.76	7.63E-73	3
TAGLN	6.37E-158	0.109987944	0.789	0.763	1.27E-154	3
MAP3K5	7.11E-13	0.109368138	0.884	0.883	1.42E-09	3
TMEM47	1.82E-196	0.109267663	0.742	0.672	3.63E-193	3
RAPGEF4	1.25E-91	0.108775211	0.655	0.691	2.49E-88	3
ZBTB16	6.53E-58	0.108658798	0.737	0.69	1.31E-54	3
SHOC1	5.20E-149	0.108321539	0.75	0.776	1.04E-145	3
MSN	4.19E-77	0.108311255	0.797	0.736	8.38E-74	3
FBXO2	2.97E-109	0.107566638	0.742	0.699	5.93E-106	3
LBH	6.48E-79	0.107088561	0.786	0.825	1.30E-75	3
KLKP1.1	3.75E-45	0.106940109	0.68	0.654	7.50E-42	3
HTATIP2	1.71E-83	0.106164084	0.794	0.877	3.41E-80	3
CYP2B7P.1	7.35E-38	0.10546399	0.752	0.695	1.47E-34	3
MYO5B	1.10E-17	0.105171249	0.931	0.945	2.19E-14	3
TCIM	4.83E-77	0.105005981	0.814	0.734	9.66E-74	3
CCND2	8.11E-59	0.104720409	0.738	0.701	1.62E-55	3
USP32	1.80E-38	0.103811781	0.855	0.808	3.59E-35	3
ENC1	9.69E-22	0.103240739	0.805	0.771	1.94E-18	3

FRMD3	2.64E-38	0.101820781	0.792	0.758	5.28E-35	3
SLC7A5	3.03E-18	0.101812467	0.808	0.819	6.07E-15	3
MT1E	1.48E-32	0.101210492	0.557	0.618	2.96E-29	3
SREBF2	2.80E-15	0.100006363	0.922	0.894	5.60E-12	3
STARD9	1.16E-127	0.099162692	0.739	0.766	2.31E-124	3
RASA1	4.95E-23	0.098454625	0.841	0.881	9.90E-20	3
BPIFA1	1.27E-20	0.098441702	0.532	0.569	2.53E-17	3
DUSP6	4.05E-18	0.098316781	0.684	0.717	8.09E-15	3
AZGP1	1.25E-54	0.098164343	0.759	0.76	2.49E-51	3
ABL2	6.55E-20	0.097998429	0.835	0.809	1.31E-16	3
THBS1	1.55E-74	0.097782767	0.807	0.784	3.10E-71	3
GNG7	4.80E-54	0.09748538	0.819	0.743	9.60E-51	3
SPTBN4	1.92E-89	0.096966316	0.819	0.758	3.84E-86	3
NR2F2-AS1	1.19E-33	0.09663548	0.799	0.76	2.37E-30	3
CDH3	3.31E-24	0.096236139	0.8	0.777	6.63E-21	3
HEXD-IT1	9.49E-175	0.095687946	0.808	0.713	1.90E-171	3
PCLO	1.12E-18	0.095558314	0.813	0.786	2.24E-15	3
MYOM1	9.05E-62	0.095417953	0.81	0.784	1.81E-58	3
NTN1	5.58E-40	0.094307482	0.81	0.764	1.12E-36	3
TFF3	2.11E-56	0.094019716	0.725	0.658	4.22E-53	3
DLGAP1	3.04E-49	0.093466759	0.794	0.746	6.09E-46	3
DPP6	8.15E-50	0.092617405	0.684	0.681	1.63E-46	3
RXFP1	1.91E-87	0.091864685	0.736	0.643	3.81E-84	3
DUSP2	6.83E-72	0.089842707	0.9	0.833	1.37E-68	3
KLF2	2.99E-93	0.089604338	0.741	0.696	5.98E-90	3
LINC02899	3.22E-82	0.089528272	0.736	0.637	6.44E-79	3
MTR	6.75E-29	0.089471907	0.778	0.737	1.35E-25	3
RNF150	7.04E-32	0.089386105	0.768	0.76	1.41E-28	3
EDN1	4.55E-48	0.088765347	0.807	0.796	9.11E-45	3
MT-ND6	4.40E-35	0.087977812	0.712	0.723	8.80E-32	3
SLC1A1	4.67E-48	0.087856566	0.808	0.772	9.34E-45	3
GPAT3	1.16E-125	0.087761035	0.841	0.713	2.32E-122	3
H4C3	6.96E-53	0.087492561	0.649	0.686	1.39E-49	3
LINC02457	1.56E-216	0.087261395	0.741	0.622	3.13E-213	3
LINC02006	8.09E-41	0.086614773	0.587	0.596	1.62E-37	3
MT-TF	3.76E-79	0.086183365	0.753	0.76	7.53E-76	3
CDK14	2.47E-20	0.086001066	0.786	0.761	4.94E-17	3

IFIT3	7.74E-172	0.085957723	0.526	0.714	1.55E-168	3
PRIM2	1.63E-35	0.085838232	0.783	0.793	3.25E-32	3
RHOF	6.09E-20	0.084592608	0.813	0.844	1.22E-16	3
ADRB2	1.65E-42	0.084584701	0.841	0.81	3.30E-39	3
PAPPA2	9.26E-241	0.08446623	0.804	0.751	1.85E-237	3
RIPK1	2.06E-07	0.084454595	0.805	0.811	0.00041252	3
IL1R1	9.84E-25	0.082901791	0.777	0.784	1.97E-21	3
C11orf80	1.72E-08	0.082880768	0.871	0.858	3.44E-05	3
KRT81	2.14E-44	0.082647456	0.702	0.77	4.29E-41	3
CSGALNACT1	5.68E-130	0.082038698	0.808	0.696	1.14E-126	3
NME1	3.25E-20	0.081646986	0.829	0.852	6.50E-17	3
BICD1	1.43E-36	0.08103949	0.73	0.648	2.86E-33	3
KCTD12	1.24E-65	0.08099302	0.689	0.735	2.47E-62	3
YIF1A	3.41E-22	0.080941621	0.827	0.862	6.82E-19	3
EEPD1	4.05E-09	0.080871822	0.822	0.832	8.09E-06	3
THSD7A	5.93E-51	0.080109538	0.745	0.694	1.19E-47	3
IL32	1.99E-64	0.080013044	0.794	0.85	3.99E-61	3
PGAM1P5	8.75E-19	0.079626574	0.785	0.778	1.75E-15	3
SPATA21	7.98E-36	0.079531152	0.744	0.739	1.60E-32	3
FGD6	4.13E-10	0.079219515	0.847	0.825	8.26E-07	3
MLLT3	4.63E-11	0.078911457	0.775	0.752	9.26E-08	3
MEIS1	1.62E-15	0.078907457	0.881	0.837	3.24E-12	3
CALCRL-AS1	3.67E-75	0.078193598	0.662	0.616	7.35E-72	3
CCDC62	2.31E-47	0.077282187	0.719	0.671	4.62E-44	3
TCHH	3.53E-38	0.076802046	0.715	0.654	7.06E-35	3
KC6	4.94E-77	0.076548765	0.681	0.544	9.88E-74	3
PIPOX	4.74E-115	0.076221905	0.823	0.701	9.47E-112	3
BCL10-AS1	7.79E-68	0.075589022	0.671	0.672	1.56E-64	3
PPARGC1A	1.19E-75	0.073572432	0.769	0.75	2.38E-72	3
TNFRSF12A	1.08E-15	0.073541654	0.931	0.962	2.16E-12	3
HIP1	2.31E-22	0.073303513	0.768	0.741	4.62E-19	3
CYP1B1	3.06E-21	0.073123806	0.783	0.808	6.12E-18	3
SAMD12-AS1	3.74E-12	0.072154812	0.725	0.712	7.47E-09	3
LINC01564	7.04E-145	0.071932807	0.715	0.594	1.41E-141	3
H19	4.11E-68	0.07115112	0.622	0.487	8.22E-65	3
TENT5A	0.000109875	0.070509221	0.856	0.84	0.219749363	3
MANF	4.81E-81	0.070416554	0.721	0.848	9.63E-78	3

KCNQ1OT1	3.98E-24	0.069976745	0.797	0.75	7.97E-21	3
ZNF337-AS1	9.94E-27	0.069298118	0.803	0.782	1.99E-23	3
CIB3	1.11E-105	0.06928653	0.856	0.721	2.22E-102	3
ARMC7	4.17E-57	0.066588902	0.674	0.717	8.34E-54	3
CD6	9.07E-49	0.066520121	0.684	0.706	1.81E-45	3
CHKA	1.54E-10	0.066126133	0.912	0.904	3.07E-07	3
LINC01090	1.58E-20	0.065596662	0.754	0.762	3.16E-17	3
EVI5L	1.34E-32	0.065434141	0.796	0.779	2.68E-29	3
SFN	2.56E-38	0.065424039	0.83	0.9	5.12E-35	3
SEZ6L2	8.45E-25	0.065346009	0.787	0.791	1.69E-21	3
TREM1	2.49E-64	0.065201172	0.662	0.698	4.98E-61	3
ATP13A2	1.73E-09	0.06446904	0.786	0.817	3.45E-06	3
IQCJ-SCHIP1	4.13E-28	0.064230507	0.655	0.684	8.25E-25	3
DTL	9.76E-126	0.064054838	0.75	0.604	1.95E-122	3
COTL1	9.25E-35	0.063744443	0.764	0.737	1.85E-31	3
RIPOR3-AS1	2.25E-127	0.063684714	0.854	0.733	4.50E-124	3
PALM2AKAP2	6.35E-13	0.062816788	0.857	0.871	1.27E-09	3
PXN-AS1	3.60E-19	0.062005095	0.812	0.812	7.20E-16	3
HS6ST2	1.31E-18	0.0618047	0.787	0.767	2.62E-15	3
GAS2L3	2.25E-208	0.061798753	0.756	0.543	4.50E-205	3
ERO1B	3.07E-09	0.0616921	0.788	0.769	6.15E-06	3
HCCS-DT	1.38E-42	0.061478115	0.717	0.694	2.76E-39	3
NETO2	0.001188319	0.060904411	0.692	0.711	1	3
EMP3	1.17E-65	0.060572887	0.726	0.754	2.34E-62	3
STAG1	2.86E-12	0.059601184	0.861	0.82	5.71E-09	3
FLNA	2.32E-46	0.059409048	0.655	0.684	4.64E-43	3
ZG16B	3.48E-13	0.059226561	0.811	0.84	6.95E-10	3
CPN1	4.28E-70	0.058664153	0.616	0.747	8.57E-67	3
RIPPLY3	9.94E-197	0.058536752	0.802	0.598	1.99E-193	3
SRGAP1	1.16E-14	0.058388326	0.836	0.872	2.31E-11	3
SNAP25-AS1	5.24E-63	0.058237709	0.608	0.729	1.05E-59	3
HJV	2.96E-35	0.058149483	0.803	0.762	5.92E-32	3
IRS1	2.47E-18	0.057876826	0.723	0.675	4.93E-15	3
UBE2C	1.67E-107	0.057552379	0.59	0.722	3.35E-104	3
C16orf74	3.11E-23	0.057287787	0.738	0.727	6.23E-20	3
CRTAC1	1.92E-50	0.057240428	0.584	0.608	3.84E-47	3
TTC28	8.65E-13	0.057035073	0.685	0.674	1.73E-09	3

CXCL5	6.58E-43	0.056724076	0.657	0.665	1.32E-39	3
CD14	5.73E-139	0.056120056	0.626	0.786	1.15E-135	3
SVIL	3.60E-07	0.056113357	0.892	0.886	0.000719257	3
SH3TC2	2.48E-44	0.056094127	0.76	0.835	4.95E-41	3
RIMS2	2.33E-55	0.055604123	0.674	0.778	4.66E-52	3
ANPEP	9.47E-64	0.054809985	0.722	0.748	1.89E-60	3
LYZ	2.15E-39	0.054253795	0.645	0.713	4.30E-36	3
MAN1A1	7.05E-63	0.053813394	0.699	0.659	1.41E-59	3
DUOXA2	2.11E-12	0.053223378	0.786	0.759	4.23E-09	3
STS	1.19E-36	0.053140592	0.84	0.905	2.38E-33	3
CACNB4	3.41E-109	0.053090907	0.812	0.676	6.81E-106	3
EIF3C	3.17E-19	0.052223946	0.788	0.737	6.33E-16	3
SLC30A1	2.34E-50	0.052139623	0.749	0.834	4.68E-47	3
GEM	1.02E-19	0.051524071	0.829	0.77	2.05E-16	3
LINC00862	4.91E-25	0.050560063	0.711	0.751	9.82E-22	3
MMADHC-DT	6.58E-35	0.05053365	0.83	0.753	1.32E-31	3
STC2	6.96E-56	0.050341521	0.545	0.536	1.39E-52	3
AHDC1	4.73E-13	0.050253522	0.867	0.905	9.47E-10	3
PRELID2	0.002076171	0.049987202	0.742	0.731	1	3
HIVEP3	4.08E-10	0.04929125	0.727	0.742	8.15E-07	3
MOB3B	1.37E-14	0.049278847	0.749	0.746	2.74E-11	3
IFIT2	6.78E-38	0.048925434	0.502	0.504	1.36E-34	3
GPC6	1.09E-18	0.048722244	0.654	0.659	2.18E-15	3
EDARADD	8.59E-29	0.048264245	0.743	0.791	1.72E-25	3
TMPRSS9	2.81E-111	0.047992049	0.84	0.71	5.62E-108	3
MMP20	5.18E-48	0.047646679	0.859	0.771	1.04E-44	3
ADSS1	1.45E-28	0.047558711	0.793	0.849	2.89E-25	3
CPNE4	2.16E-10	0.047395726	0.758	0.719	4.32E-07	3
GPR156	1.67E-74	0.046732238	0.677	0.64	3.34E-71	3
UHRF1	3.17E-67	0.046362919	0.651	0.52	6.34E-64	3
PPM1L	1.78E-07	0.046278385	0.832	0.826	0.000356233	3
SPNS3	3.03E-51	0.046148028	0.744	0.785	6.06E-48	3
RRM2	1.17E-83	0.046009186	0.569	0.681	2.35E-80	3
P3H2	1.54E-20	0.045819913	0.776	0.712	3.08E-17	3
PARM1	3.12E-47	0.045567716	0.619	0.615	6.25E-44	3
SPRY4-AS1	3.37E-41	0.045524722	0.805	0.735	6.75E-38	3
NIBAN1	1.17E-23	0.044330219	0.677	0.724	2.33E-20	3

SEMA3B	6.26E-21	0.044197469	0.737	0.693	1.25E-17	3
PEG10	3.03E-19	0.043736266	0.668	0.725	6.06E-16	3
ROBO1	1.01E-07	0.043347323	0.708	0.667	0.00020186	3
TGM2	4.27E-15	0.042870879	0.689	0.722	8.54E-12	3
ELF3-AS1	2.14E-30	0.042821012	0.791	0.856	4.28E-27	3
GRB10	5.51E-26	0.042764722	0.719	0.74	1.10E-22	3
AIMP2	2.30E-36	0.04269974	0.734	0.779	4.61E-33	3
NID1	1.72E-27	0.042331196	0.778	0.708	3.45E-24	3
PLAT	1.31E-74	0.041980105	0.502	0.657	2.61E-71	3
SPDYA	1.79E-10	0.041713432	0.808	0.789	3.57E-07	3
BBOX1-AS1	2.11E-32	0.041434538	0.709	0.678	4.23E-29	3
FAM171B	2.02E-68	0.041307739	0.776	0.798	4.04E-65	3
LINC02925	2.29E-73	0.041196342	0.696	0.793	4.58E-70	3
KNOP1	4.57E-10	0.04068145	0.728	0.739	9.15E-07	3
IRAG2	1.12E-06	0.040207001	0.84	0.864	0.00223992	3
LIF	4.27E-72	0.038560265	0.751	0.772	8.53E-69	3
KDEL3	3.02E-32	0.038381832	0.731	0.764	6.05E-29	3
KRT86	5.89E-45	0.038185235	0.835	0.74	1.18E-41	3
NMU	2.25E-16	0.037599467	0.742	0.798	4.50E-13	3
NEAT1	0.000313645	0.037451071	0.995	0.995	0.627290726	3
EML2-AS1	3.88E-13	0.037173172	0.71	0.756	7.76E-10	3
LDLRAD3	1.73E-43	0.03700423	0.692	0.611	3.46E-40	3
MCTP1	6.92E-15	0.03687292	0.685	0.734	1.38E-11	3
OSBP2	4.46E-47	0.036779174	0.723	0.8	8.93E-44	3
GGNBP1	5.42E-26	0.036603239	0.785	0.734	1.08E-22	3
LINC00393	2.01E-21	0.036511572	0.623	0.663	4.02E-18	3
POLE2	5.50E-26	0.035765262	0.733	0.66	1.10E-22	3
MUCL1	3.96E-16	0.03558214	0.685	0.719	7.92E-13	3
IFI30	1.03E-27	0.034870667	0.596	0.635	2.06E-24	3
LRP3	1.63E-77	0.034582728	0.616	0.747	3.25E-74	3
MMP16	1.31E-70	0.034353742	0.812	0.682	2.62E-67	3
BCAT1	4.58E-19	0.034179814	0.827	0.875	9.17E-16	3
CD70	1.39E-30	0.033553198	0.695	0.703	2.77E-27	3
NOCT	0.000232336	0.033194197	0.793	0.778	0.464672488	3
PFN1	7.94E-26	0.033180995	0.934	0.971	1.59E-22	3
CARD11	4.50E-21	0.033067125	0.737	0.725	9.01E-18	3
THBD	1.96E-06	0.03249536	0.752	0.789	0.003925007	3

ALKAL1	2.46E-73	0.032433577	0.624	0.569	4.92E-70	3
LINC02343	4.40E-157	0.032258699	0.792	0.578	8.79E-154	3
MT1F	2.36E-29	0.032063167	0.626	0.682	4.72E-26	3
FIGN	1.47E-12	0.031648596	0.617	0.629	2.95E-09	3
SELENOM	7.76E-55	0.031485307	0.69	0.786	1.55E-51	3
TMEM178B	4.15E-36	0.031342426	0.712	0.634	8.29E-33	3
CXCL1	5.69E-08	0.030850604	0.823	0.823	0.000113813	3
TP63	2.46E-21	0.030847398	0.489	0.57	4.92E-18	3
CITED4	2.31E-07	0.030684627	0.837	0.871	0.000461374	3
MX2	1.15E-18	0.030346097	0.802	0.845	2.29E-15	3
SLC44A3-AS1	1.83E-08	0.030137227	0.796	0.834	3.65E-05	3
RCC1L	0.000415891	0.030067705	0.814	0.83	0.831781179	3
FAM126A	0.001882571	0.030029971	0.783	0.772	1	3
WNK2	9.92E-14	0.029635703	0.819	0.828	1.98E-10	3
ADARB2	1.75E-14	0.029604979	0.691	0.628	3.49E-11	3
SMIM5	0.454814918	0.029462905	0.885	0.877	1	3
MAMSTR	3.14E-50	0.028851362	0.797	0.716	6.27E-47	3
GPR176	4.45E-77	0.028397549	0.617	0.73	8.89E-74	3
ADGRF2	5.29E-21	0.028343898	0.828	0.796	1.06E-17	3
MGAT5	9.40E-15	0.028300472	0.931	0.919	1.88E-11	3
MB	1.10E-13	0.028233087	0.684	0.715	2.20E-10	3
SYT16	1.01E-19	0.028218445	0.8	0.751	2.03E-16	3
TRIB3	1.13E-22	0.027742836	0.731	0.765	2.26E-19	3
IL23A	0.000240455	0.027600248	0.758	0.732	0.480909612	3
PRKCH	0.422858639	0.027323604	0.917	0.911	1	3
STATH	2.05E-08	0.026979718	0.767	0.734	4.11E-05	3
ST3GAL6	3.19E-08	0.026503356	0.817	0.776	6.38E-05	3
TENT5B	2.07E-10	0.026167897	0.777	0.792	4.14E-07	3
AKAP12	4.69E-17	0.025555657	0.724	0.74	9.37E-14	3
FER1L6	0.000623714	0.0255536	0.772	0.753	1	3
NKAIN3	6.15E-54	0.024726811	0.749	0.631	1.23E-50	3
TMPO	8.47E-17	0.02453061	0.766	0.824	1.69E-13	3
ID2	0.00010774	0.024506559	0.761	0.737	0.215480801	3
DUOX2	0.021943933	0.023828695	0.818	0.819	1	3
LINC00964	1.32E-21	0.023669822	0.585	0.613	2.64E-18	3
FCGBP	8.30E-34	0.023476524	0.671	0.566	1.66E-30	3
INHBA	1.80E-107	0.023398141	0.764	0.581	3.60E-104	3

PTPRD	3.46E-09	0.023104957	0.576	0.526	6.91E-06	3
KRT80	0.00784449	0.022996229	0.866	0.867	1	3
UBA6-DT	3.98E-19	0.02284191	0.789	0.843	7.97E-16	3
MT-CO3	2.21E-33	0.022533819	0.989	0.998	4.41E-30	3
MAFB	4.03E-05	0.022433242	0.692	0.656	0.080503494	3
LARGE1	5.34E-08	0.022346102	0.623	0.63	0.000106872	3
FOLR1	2.88E-06	0.021889338	0.765	0.737	0.005759699	3
HS3ST6	2.19E-23	0.021644123	0.867	0.919	4.38E-20	3
GRIP1	0.340526391	0.021411416	0.698	0.686	1	3
ARG2	0.03742445	0.021399074	0.713	0.709	1	3
EGR1	4.08E-16	0.020766238	0.831	0.881	8.16E-13	3
NAALADL2-AS2	0.0021753	0.019720446	0.769	0.77	1	3
SLIT2	1.35E-14	0.019712815	0.71	0.685	2.69E-11	3
INTS6	0.026797905	0.019614997	0.817	0.807	1	3
CD83	1.34E-16	0.019259348	0.804	0.84	2.68E-13	3
IFITM1	0.621675328	0.018693404	0.719	0.725	1	3
PHF19	6.69E-23	0.018514891	0.769	0.78	1.34E-19	3
MCPH1-DT	8.89E-15	0.018206182	0.828	0.775	1.78E-11	3
COMETT	5.07E-25	0.018030054	0.768	0.719	1.01E-21	3
ARTN	8.86E-85	0.01721983	0.667	0.806	1.77E-81	3
FBLN1	2.84E-20	0.01713128	0.781	0.842	5.68E-17	3
LINC02306	1.06E-78	0.017091064	0.793	0.644	2.12E-75	3
MYC	1.52E-07	0.016907629	0.718	0.693	0.000303685	3
CFB	2.81E-11	0.01674128	0.809	0.838	5.63E-08	3
MARCHF1	4.19E-09	0.016602258	0.682	0.644	8.37E-06	3
BCL2A1	0.014305272	0.015939887	0.719	0.726	1	3
ELOVL6	0.193834682	0.015927558	0.816	0.827	1	3
SLIT3	2.79E-49	0.015767774	0.555	0.674	5.58E-46	3
RGS16	7.49E-28	0.015665284	0.759	0.705	1.50E-24	3
MESP1	1.89E-56	0.015105979	0.713	0.812	3.78E-53	3
BPIFA2	4.09E-74	0.015029306	0.714	0.56	8.18E-71	3
TPM2	9.09E-19	0.015021018	0.677	0.747	1.82E-15	3
CLDN14	9.33E-41	0.014569297	0.664	0.758	1.87E-37	3
ZPLD1	8.60E-17	0.014503145	0.63	0.693	1.72E-13	3
MIR3681HG	7.60E-14	0.014423536	0.711	0.662	1.52E-10	3
FRMPD4	3.27E-07	0.013931752	0.73	0.734	0.00065372	3
ADAMTS1	2.38E-25	0.013691332	0.657	0.569	4.76E-22	3

LINC02542	1.41E-11	0.013547749	0.701	0.658	2.82E-08	3
MXRA5	5.25E-27	0.013343187	0.679	0.585	1.05E-23	3
RNASE1	2.17E-43	0.013213771	0.496	0.574	4.34E-40	3
TBC1D4	2.37E-06	0.013052197	0.716	0.675	0.004736385	3
IGSF11	9.97E-23	0.013033715	0.817	0.747	1.99E-19	3
FOSB	1.15E-61	0.012933335	0.852	0.731	2.29E-58	3
GJC1	1.53E-09	0.012874513	0.759	0.795	3.06E-06	3
FCHO1	4.91E-05	0.01267667	0.839	0.846	0.098173586	3
CYP2A6	6.27E-63	0.012662278	0.692	0.551	1.25E-59	3
PLXDC2	0.000202257	0.01220226	0.782	0.806	0.404513519	3
CCDC13-AS1	7.87E-162	0.011396427	0.403	0.62	1.57E-158	3
ADAMTS14	1.63E-10	0.0104402	0.77	0.742	3.26E-07	3
CENPW	2.47E-10	0.010404236	0.744	0.79	4.95E-07	3
CALD1	0.000215064	0.01029168	0.663	0.684	0.430128173	3
DGKI	0.028189422	0.010078165	0.723	0.722	1	3
LSS	0.000490453	0.010000166	0.877	0.855	0.98090611	3
NALF1	1.79E-26	0.009802915	0.732	0.643	3.58E-23	3
ABCC3	1.42E-19	0.009445841	0.571	0.641	2.83E-16	3
PPBP	2.27E-43	0.008927315	0.601	0.482	4.53E-40	3
BIRC5	5.66E-10	0.008738742	0.612	0.579	1.13E-06	3
ZNF114	0.021925042	0.008516333	0.581	0.6	1	3
BAMBI	3.16E-22	0.008188755	0.65	0.706	6.31E-19	3
HNMT	2.42E-11	0.008173392	0.771	0.748	4.84E-08	3
ZEB1	0.000389594	0.008008549	0.551	0.56	0.77918843	3
PICART1	1.56E-53	0.007912613	0.579	0.695	3.11E-50	3
TRAF1	4.89E-16	0.007655641	0.762	0.704	9.78E-13	3
GPC5	1.86E-25	0.00745654	0.698	0.611	3.73E-22	3
DLG2	1.53E-14	0.00734868	0.708	0.76	3.06E-11	3
ANG	1.33E-33	0.007240018	0.708	0.794	2.67E-30	3
AKR1B10	1.56E-22	0.007223154	0.531	0.604	3.12E-19	3
HSD17B2	0.014646628	0.00712215	0.738	0.753	1	3
OASL	9.06E-10	0.006894383	0.657	0.708	1.81E-06	3
LINC01619	5.68E-16	0.006729437	0.765	0.7	1.14E-12	3
TWIST1	0.116627227	0.006443664	0.726	0.738	1	3
SOS1	4.84E-05	0.006363772	0.895	0.916	0.096788475	3
RHOBTB3	2.63E-26	0.006048022	0.792	0.861	5.25E-23	3
DKK1	0.442255499	0.006047449	0.819	0.826	1	3

BMP6	0.179393478	0.005254786	0.67	0.657	1	3
FBXL7	0.024292904	0.005114497	0.521	0.519	1	3
TMEM105	3.69E-08	0.005098144	0.723	0.763	7.39E-05	3
NTNG2	0.381237198	0.004104333	0.666	0.657	1	3
C12orf42	2.32E-193	0.003217776	0.597	0.823	4.63E-190	3
TIMP3	1.09E-08	0.002858017	0.65	0.6	2.17E-05	3
MYO1H	1.83E-131	0.002549555	0.674	0.845	3.66E-128	3
CKAP2L	0.012878452	0.002250838	0.71	0.707	1	3
LINC02649	9.73E-06	0.000915159	0.857	0.831	0.019461663	3
GOLGA7B-DT	2.30E-67	0.000631299	0.666	0.797	4.60E-64	3
LINC01950	0.104529231	0.000501249	0.771	0.758	1	3
FTL	4.71E-37	0.000497938	0.975	0.989	9.42E-34	3
EBI3	5.05E-61	0.000203411	0.686	0.809	1.01E-57	3
ALK	1.38E-126	9.27E-05	0.578	0.758	2.76E-123	3
FGF13	5.50E-10	2.05E-05	0.669	0.72	1.10E-06	3

Supplementary Table S2. A list of functions associated with cell type specific gene modules

[G1 common Up]

	Term	Matched	Total	P.value
1	TNF-alpha Signaling via NF-kB	46	200	1.76E-23
2	Hypoxia	45	200	1.41E-22
3	p53 Pathway	28	200	2.25E-09
4	UV Response Up	21	158	5.49E-07
5	Ubiquitin-Dependent Protein Catabolic Process (GO:0006511)	33	367	4.02E-06
6	Autophagosome Assembly (GO:0000045)	12	65	4.92E-06
7	Cellular Response To Nutrient Levels (GO:0031669)	13	78	6.52E-06
8	IL-2/STAT5 Signaling	22	199	6.70E-06
9	Apoptosis	19	161	1.10E-05
10	Regulation Of p38MAPK Cascade (GO:1900744)	8	37	5.80E-05
11	Cellular Response To Starvation (GO:0009267)	15	126	8.24E-05
12	Autophagosome Organization (GO:1905037)	10	61	8.73E-05
13	Unfolded Protein Response	14	113	9.13E-05
14	Phosphorylation (GO:0016310)	33	429	9.45E-05
15	Macroautophagy (GO:0016236)	13	104	0.000147221
16	Estrogen Response Early	19	200	0.00021575
17	Protein Ubiquitination (GO:0016567)	32	434	0.000258182
18	Protein Modification Process (GO:0036211)	46	711	0.000280252
19	Negative Regulation Of Cell Cycle (GO:0045786)	11	85	0.0003456
20	Cellular Response To Hypoxia (GO:0071456)	10	72	0.000357617
21	Cellular Response To Decreased Oxygen Levels (GO:0036294)	10	73	0.000400602
22	Negative Regulation Of Intracellular Signal Transduction (GO:1902532)	20	231	0.000504628
23	Regulation Of Glucose Metabolic Process (GO:0010906)	6	28	0.000524369
24	Regulation Of DNA-templated Transcription (GO:0006355)	100	1922	0.000576176
25	Proteasomal Protein Catabolic Process (GO:0010498)	19	220	0.000710984
26	Retrograde Transport, Endosome To Golgi (GO:0042147)	11	94	0.000823469
27	Negative Regulation Of I-kappaB kinase/NF-kappaB Signaling (GO:0043124)	7	42	0.000904625
28	Positive Regulation Of Protein Modification Process (GO:0031401)	19	225	0.000931685
29	Modification-Dependent Protein Catabolic Process (GO:0019941)	17	192	0.00100948
30	Regulation Of Phosphorylation (GO:0042325)	10	82	0.001017935
31	Regulation Of Transcription By RNA Polymerase II (GO:0006357)	103	2028	0.001075929

32	Proteasome-Mediated Ubiquitin-Dependent Protein Catabolic Process (GO:0043161)	24	319	0.001108598
33	Endoplasmic Reticulum To Golgi Vesicle-Mediated Transport (GO:0006888)	12	115	0.00135176
34	Epidermal Growth Factor Receptor Signaling Pathway (GO:0007173)	7	45	0.001379839
35	COPII-coated Vesicle Cargo Loading (GO:0090110)	4	14	0.001489524
36	Cholesterol Homeostasis (GO:0042632)	9	72	0.001505878
37	Regulation Of Phosphatidylinositol 3-Kinase Activity (GO:0043551)	6	34	0.001544303
38	Regulation Of Epidermal Growth Factor Receptor Signaling Pathway (GO:0042058)	7	46	0.001575353
39	mTORC1 Signaling	17	200	0.001576613
40	Glycolysis	17	200	0.001576613
41	Sterol Homeostasis (GO:0055092)	9	73	0.001661308
42	Cellular Response To Leptin Stimulus (GO:0044320)	3	7	0.001673368
43	Positive Regulation Of Fibroblast Migration (GO:0010763)	3	7	0.001673368
44	Positive Regulation Of p38MAPK Cascade (GO:1900745)	5	24	0.001768503
45	Positive Regulation Of Peptidyl-Threonine Phosphorylation (GO:0010800)	5	24	0.001768503
46	Protein Transport (GO:0015031)	23	313	0.001891591
47	Positive Regulation Of Sprouting Angiogenesis (GO:1903672)	4	15	0.001970931
48	Regulation Of Carbohydrate Metabolic Process (GO:0006109)	4	15	0.001970931
49	Negative Regulation Of Phosphorylation (GO:0042326)	9	75	0.002010671
50	Negative Regulation Of Transcription By RNA Polymerase II (GO:0000122)	45	763	0.002143288
51	Negative Regulation Of DNA-templated Transcription (GO:0045892)	57	1025	0.002245205
52	Protein Polyubiquitination (GO:0000209)	18	226	0.002401305
53	Positive Regulation Of Protein Phosphorylation (GO:0001934)	26	377	0.002415739
54	Negative Regulation Of Natural Killer Cell Mediated Cytotoxicity (GO:0045953)	4	16	0.002550077
55	Response To Leptin (GO:0044321)	3	8	0.00260246
56	Leptin-Mediated Signaling Pathway (GO:0033210)	3	8	0.00260246
57	Regulation Of JNK Cascade (GO:0046328)	11	110	0.002957688
58	Cytosolic Transport (GO:0016482)	12	127	0.003133124
59	Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0017015)	11	111	0.003174036
60	Golgi Vesicle Transport (GO:0048193)	16	197	0.00336716
61	Protein Autophosphorylation (GO:0046777)	14	162	0.003389845
62	Positive Regulation Of Transcription By RNA Polymerase II (GO:0045944)	52	938	0.003666793
63	Negative Regulation Of Protein Exit From Endoplasmic Reticulum (GO:0070862)	3	9	0.003794654
64	Protein K11-linked Deubiquitination (GO:0035871)	3	9	0.003794654
65	Protein Localization (GO:0008104)	24	351	0.003872663
66	Inflammatory Response	16	200	0.003903834
67	Vesicle-Mediated Transport (GO:0016192)	27	411	0.003931058
68	Skin Development (GO:0043588)	8	68	0.00398009

69	ERBB Signaling Pathway (GO:0038127)	7	54	0.004020054
70	Regulation Of Lipid Metabolic Process (GO:0019216)	7	54	0.004020054
71	Regulation Of Blood Vessel Endothelial Cell Migration (GO:0043535)	7	54	0.004020054
72	TGF-beta Signaling	7	54	0.004020054
73	Regulation Of Epithelial Cell Differentiation (GO:0030856)	4	18	0.004037792
74	Negative Regulation Of ERBB Signaling Pathway (GO:1901185)	4	18	0.004037792
75	Cellular Response To Glucose Starvation (GO:0042149)	6	42	0.004667373
76	Keratinocyte Differentiation (GO:0030216)	6	42	0.004667373
77	Protein K48-linked Ubiquitination (GO:0070936)	8	70	0.004760166
78	Regulation Of Tissue Remodeling (GO:0034103)	4	19	0.004963682
79	Response To Sterol (GO:0036314)	3	10	0.005269817
80	Negative Regulation Of Natural Killer Cell Mediated Immunity (GO:0002716)	3	10	0.005269817
81	Regulation Of B Cell Apoptotic Process (GO:0002902)	3	10	0.005269817
82	Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0007179)	8	72	0.005652358
83	Triglyceride Homeostasis (GO:0070328)	5	31	0.005687208
84	Negative Regulation Of Developmental Growth (GO:0048640)	5	31	0.005687208
85	Selective Autophagy (GO:0061912)	7	58	0.005996992
86	Negative Regulation Of Phosphate Metabolic Process (GO:0045936)	4	20	0.006021852
87	Receptor Metabolic Process (GO:0043112)	4	20	0.006021852
88	Protein Modification By Small Protein Conjugation (GO:0032446)	24	364	0.006048839
89	Apoptotic Process (GO:0006915)	17	228	0.006054062
90	Positive Regulation Of Stress-Activated MAPK Cascade (GO:0032874)	10	105	0.006346859
91	Positive Regulation Of Phosphorylation (GO:0042327)	17	231	0.006872269
92	Regulation Of Homotypic Cell-Cell Adhesion (GO:0034110)	3	11	0.007044405
93	Lysosomal Microautophagy (GO:0016237)	3	11	0.007044405
94	Positive Regulation Of DNA-templated Transcription (GO:0045893)	64	1243	0.007154701
95	Regulation Of I-kappaB kinase/NF-kappaB Signaling (GO:0043122)	17	232	0.007164053
96	Regulation Of Fat Cell Differentiation (GO:0045598)	8	75	0.007222424
97	Regulation Of Sprouting Angiogenesis (GO:1903670)	5	33	0.007467433
98	Regulation Of Cell Adhesion Mediated By Integrin (GO:0033628)	5	33	0.007467433
99	Positive Regulation Of JNK Cascade (GO:0046330)	8	77	0.008438248
100	Cellular Response To Vascular Endothelial Growth Factor Stimulus (GO:0035924)	5	34	0.008488665
101	Endosomal Transport (GO:0016197)	14	180	0.008496538
102	Protein Phosphorylation (GO:0006468)	30	500	0.008759596
103	KRAS Signaling Up	15	200	0.009088273
104	Early Endosome To Golgi Transport (GO:0034498)	3	12	0.009131751
105	Intrinsic Apoptotic Signaling Pathway By P53 Class Mediator (GO:0072332)	5	35	0.009602585

106	Regulation Of Cell Cycle (GO:0051726)	20	298	0.00962395
107	Negative Regulation Of Cellular Component Organization (GO:0051129)	8	79	0.009801117
108	Autophagy Of Mitochondrion (GO:0000422)	6	49	0.00996715
109	Negative Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process (GO:0043154)	6	49	0.00996715
110	Regulation Of Secretion By Cell (GO:1903530)	7	64	0.010212199
111	Positive Regulation Of Peptidyl-Tyrosine Phosphorylation (GO:0050731)	11	130	0.010287993
112	Cellular Response To Transforming Growth Factor Beta Stimulus (GO:0071560)	9	96	0.010350333
113	Regulation Of Peptidyl-Threonine Phosphorylation (GO:0010799)	5	36	0.010812993
114	Regulation Of Macrophage Cytokine Production (GO:0010935)	3	13	0.011542331
115	Negative Regulation Of Myoblast Differentiation (GO:0045662)	3	13	0.011542331
116	Positive Regulation Of Histone Deacetylation (GO:0031065)	3	13	0.011542331
117	Acylglycerol Homeostasis (GO:0055090)	4	24	0.011723507
118	Positive Regulation Of Vascular Endothelial Growth Factor Production (GO:0010575)	4	24	0.011723507
119	Positive Regulation Of Programmed Cell Death (GO:0043068)	17	245	0.011947801
120	Regulation Of Protein Phosphorylation (GO:0001932)	18	265	0.012119836
121	Mitochondrion Disassembly (GO:0061726)	5	37	0.012123547
122	Negative Regulation Of Stress-Activated MAPK Cascade (GO:0032873)	5	37	0.012123547
123	COPI Coating Of Golgi Vesicle (GO:0048205)	2	5	0.013190447
124	COPI-coated Vesicle Budding (GO:0035964)	2	5	0.013190447
125	Golgi Transport Vesicle Coating (GO:0048200)	2	5	0.013190447
126	PERK-mediated Unfolded Protein Response (GO:0036499)	2	5	0.013190447
127	Regulation Of Macrophage Apoptotic Process (GO:2000109)	2	5	0.013190447
128	Regulation Of Nitric Oxide Mediated Signal Transduction (GO:0010749)	2	5	0.013190447
129	Regulation Of pro-B Cell Differentiation (GO:2000973)	2	5	0.013190447
130	Cellular Heat Acclimation (GO:0070370)	2	5	0.013190447
131	Cellular Response To Cold (GO:0070417)	2	5	0.013190447
132	Cerebral Cortex Cell Migration (GO:0021795)	2	5	0.013190447
133	Chondrocyte Development (GO:0002063)	2	5	0.013190447
134	Telencephalon Cell Migration (GO:0022029)	2	5	0.013190447
135	Heat Acclimation (GO:0010286)	2	5	0.013190447
136	Lipid Droplet Disassembly (GO:1905691)	2	5	0.013190447
137	mRNA 5'-Splice Site Recognition (GO:0000395)	2	5	0.013190447
138	Protein Targeting To Vacuole Involved In Autophagy (GO:0071211)	2	5	0.013190447
139	Radial Glial Cell Differentiation (GO:0060019)	2	5	0.013190447
140	Rho Protein Signal Transduction (GO:0007266)	6	52	0.013200661
141	Sprouting Angiogenesis (GO:0002040)	6	52	0.013200661
142	Sterol Transport (GO:0015918)	4	25	0.013548416

143	Vesicle Cargo Loading (GO:0035459)	4	25	0.013548416
144	Endoderm Development (GO:0007492)	3	14	0.014284013
145	Lipoprotein Biosynthetic Process (GO:0042158)	3	14	0.014284013
146	Negative Regulation Of Leukocyte Mediated Cytotoxicity (GO:0001911)	3	14	0.014284013
147	Positive Regulation Of Angiogenesis (GO:0045766)	10	119	0.014692985
148	Regulation Of Osteoblast Differentiation (GO:0045667)	8	85	0.014872251
149	Macromolecule Catabolic Process (GO:0009057)	8	85	0.014872251
150	Positive Regulation Of Canonical Wnt Signaling Pathway (GO:0090263)	8	85	0.014872251
151	Nuclear-Transcribed mRNA Catabolic Process, Deadenylation-Dependent Decay (GO:0000288)	5	39	0.015058947
152	Regulation Of Epidermal Growth Factor-Activated Receptor Activity (GO:0007176)	4	26	0.015544209
153	Regulation Of Vascular Endothelial Growth Factor Production (GO:0010574)	4	26	0.015544209
154	Positive Regulation Of Phosphatidylinositol 3-Kinase Activity (GO:0043552)	4	26	0.015544209
155	Epidermal Cell Differentiation (GO:0009913)	6	54	0.01572503
156	Organelle Disassembly (GO:1903008)	6	54	0.01572503
157	Positive Regulation Of Intracellular Signal Transduction (GO:1902533)	30	525	0.01638001
158	Regulation Of Protein Dephosphorylation (GO:0035304)	5	40	0.016690307
159	Regulation Of Small Molecule Metabolic Process (GO:0062012)	5	40	0.016690307
160	Cellular Response To Heat (GO:0034605)	5	40	0.016690307
161	Positive Regulation Of Insulin Secretion (GO:0032024)	5	40	0.016690307
162	Peptidyl-Serine Phosphorylation (GO:0018105)	12	158	0.016838325
163	Endomembrane System Organization (GO:0010256)	14	196	0.016960854
164	Positive Regulation Of Protein Metabolic Process (GO:0051247)	14	196	0.016960854
165	Regulation Of Cellular Response To Heat (GO:1900034)	3	15	0.017362292
166	DNA Alkylation (GO:0006305)	3	15	0.017362292
167	Glycosaminoglycan Catabolic Process (GO:0006027)	3	15	0.017362292
168	Positive Regulation Of Glucose Metabolic Process (GO:0010907)	3	15	0.017362292
169	Receptor Catabolic Process (GO:0032801)	3	15	0.017362292
170	Chaperone Cofactor-Dependent Protein Refolding (GO:0051085)	4	27	0.017715496
171	Intrinsic Apoptotic Signaling Pathway (GO:0097193)	9	105	0.017845565
172	Second-Messenger-Mediated Signaling (GO:0019932)	7	72	0.018738997
173	Mitotic Spindle	14	199	0.019089865
174	SMAD Protein Complex Assembly (GO:0007183)	2	6	0.019293793
175	Actin Filament Reorganization (GO:0090527)	2	6	0.019293793
176	Aggrephagy (GO:0035973)	2	6	0.019293793
177	Aldehyde Biosynthetic Process (GO:0046184)	2	6	0.019293793
178	Vascular Associated Smooth Muscle Cell Development (GO:0097084)	2	6	0.019293793
179	Glycosylceramide Biosynthetic Process (GO:0046476)	2	6	0.019293793

180	Vascular Associated Smooth Muscle Contraction (GO:0014829)	2	6	0.019293793
181	Negative Regulation Of p38MAPK Cascade (GO:1903753)	2	6	0.019293793
182	Nucleotide-Binding Oligomerization Domain Containing 2 Signaling Pathway (GO:0070431)	2	6	0.019293793
183	Positive Regulation Of Aspartic-Type Endopeptidase Activity Involved In Amyloid Precursor Protein Catabolic Process (GO:1902961)	2	6	0.019293793
184	Regulation Of Rab Protein Signal Transduction (GO:0032483)	2	6	0.019293793
185	Regulation Of Bile Acid Metabolic Process (GO:1904251)	2	6	0.019293793
186	Estrogen Response Late	14	200	0.019842673
187	Cellular Response To Reactive Oxygen Species (GO:0034614)	7	73	0.020074879
188	Positive Regulation Of Secretion By Cell (GO:1903532)	7	73	0.020074879
189	Endosome To Lysosome Transport (GO:0008333)	6	57	0.02010824
190	Wnt-beta Catenin Signaling	5	42	0.020295289
191	Ras Protein Signal Transduction (GO:0007265)	11	144	0.020734222
192	Regulation Of Natural Killer Cell Activation (GO:0032814)	3	16	0.020780503
193	Mitophagy (GO:0000423)	3	16	0.020780503
194	Cellular Response To Oxygen-Containing Compound (GO:1901701)	24	406	0.020781246
195	Regulation Of Autophagy (GO:0010506)	16	241	0.021009481
196	Response To Tumor Necrosis Factor (GO:0034612)	9	108	0.021053638
197	Cholesterol Homeostasis	7	74	0.021475756
198	Regulation Of Epithelial Cell Proliferation (GO:0050678)	8	91	0.021621319
199	Response To Organic Cyclic Compound (GO:0014070)	6	58	0.021736463
200	Positive Regulation Of Wnt Signaling Pathway (GO:0030177)	9	109	0.022209687
201	Regulation Of Primary Metabolic Process (GO:0080090)	5	43	0.022274323
202	Intracellular Glucose Homeostasis (GO:0001678)	5	43	0.022274323
203	Chondrocyte Differentiation (GO:0002062)	4	29	0.022600298
204	Integrated Stress Response Signaling (GO:0140467)	4	29	0.022600298
205	Lipid Droplet Organization (GO:0034389)	4	29	0.022600298
206	mRNA Splice Site Recognition (GO:0006376)	4	29	0.022600298
207	Peptidyl-Tyrosine Dephosphorylation (GO:0035335)	4	29	0.022600298
208	Positive Regulation Of Cellular Catabolic Process (GO:0031331)	11	146	0.022701852
209	Response To Unfolded Protein (GO:0006986)	5	44	0.024374335
210	Positive Regulation Of Chemotaxis (GO:0050921)	5	44	0.024374335
211	Positive Regulation Of Protein Secretion (GO:0050714)	7	76	0.024477985
212	Regulation Of Ras Protein Signal Transduction (GO:0046578)	7	76	0.024477985
213	Regulation Of Leukocyte Chemotaxis (GO:0002688)	3	17	0.024540029
214	Regulation Of Receptor Signaling Pathway Via STAT (GO:1904892)	3	17	0.024540029
215	Positive Regulation Of Glial Cell Differentiation (GO:0045687)	3	17	0.024540029
216	Positive Regulation Of Regulatory T Cell Differentiation (GO:0045591)	3	17	0.024540029

217	Negative Regulation Of Nucleic Acid-Templated Transcription (GO:1903507)	26	456	0.024793232
218	Intrinsic Apoptotic Signaling Pathway In Response To Endoplasmic Reticulum Stress (GO:0070059)	4	30	0.025320344
219	Positive Regulation Of Lipid Kinase Activity (GO:0090218)	4	30	0.025320344
220	Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway (GO:0007178)	10	130	0.025573164
221	Regulation Of Canonical Wnt Signaling Pathway (GO:0060828)	14	207	0.025754983
222	Regulation Of Collateral Sprouting (GO:0048670)	2	7	0.026341981
223	Mitral Valve Development (GO:0003174)	2	7	0.026341981
224	Myeloid Leukocyte Mediated Immunity (GO:0002444)	2	7	0.026341981
225	Negative Regulation Of T Cell Mediated Cytotoxicity (GO:0001915)	2	7	0.026341981
226	Negative Regulation Of Lipid Kinase Activity (GO:0090219)	2	7	0.026341981
227	Peptidyl-Proline Hydroxylation To 4-hydroxy-L-proline (GO:0018401)	2	7	0.026341981
228	Peptidyl-Serine Autophosphorylation (GO:0036289)	2	7	0.026341981
229	Positive Regulation Of Adipose Tissue Development (GO:1904179)	2	7	0.026341981
230	Positive Regulation Of Aspartic-Type Peptidase Activity (GO:1905247)	2	7	0.026341981
231	Positive Regulation Of Astrocyte Differentiation (GO:0048711)	2	7	0.026341981
232	Regulation Of Protein Modification Process (GO:0031399)	5	45	0.026597531
233	Positive Regulation Of Innate Immune Response (GO:0045089)	5	45	0.026597531
234	Regulation Of Apoptotic Process (GO:0042981)	37	705	0.027615172
235	Negative Regulation Of Protein Modification Process (GO:0031400)	7	78	0.027756175
236	Positive Regulation Of Apoptotic Process (GO:0043065)	17	270	0.027898434
237	Regulation Of Epidermal Cell Differentiation (GO:0045604)	3	18	0.028640484
238	Regulation Of Lymphocyte Activation (GO:0051249)	3	18	0.028640484
239	Autophagy Of Nucleus (GO:0044804)	3	18	0.028640484
240	Maintenance Of Gastrointestinal Epithelium (GO:0030277)	3	18	0.028640484
241	Positive Regulation Of Response To Endoplasmic Reticulum Stress (GO:1905898)	3	18	0.028640484
242	Positive Regulation Of Stress-Activated Protein Kinase Signaling Cascade (GO:0070304)	3	18	0.028640484
243	Positive Regulation Of Blood Vessel Endothelial Cell Migration (GO:0043536)	5	46	0.028945915
244	Glycerophospholipid Metabolic Process (GO:0006650)	6	62	0.029132982
245	Cellular Response To Organic Cyclic Compound (GO:0071407)	11	152	0.029422121
246	Positive Regulation Of Catabolic Process (GO:0009896)	7	79	0.029501807
247	Monocarboxylic Acid Metabolic Process (GO:0032787)	8	97	0.030291592
248	'De Novo' Post-Translational Protein Folding (GO:0051084)	4	32	0.031328109
249	Heterochromatin Formation (GO:0031507)	4	32	0.031328109
250	Supramolecular Fiber Organization (GO:0097435)	19	316	0.031674444
251	N-glycan Processing (GO:0006491)	3	19	0.033079892
252	Establishment Of Skin Barrier (GO:0061436)	3	19	0.033079892
253	Positive Regulation Of Axon Extension (GO:0045773)	3	19	0.033079892

254	Positive Regulation Of Histone Methylation (GO:0031062)	3	19	0.033079892
255	Positive Regulation Of Macroautophagy (GO:0016239)	6	64	0.033383213
256	Cellular Response To Insulin Stimulus (GO:0032869)	8	99	0.033645917
257	Regulation Of Intrinsic Apoptotic Signaling Pathway (GO:2001242)	5	48	0.034025216
258	Regulation Of Tumor Necrosis Factor-Mediated Signaling Pathway (GO:0010803)	5	48	0.034025216
259	Regulation Of DNA Binding (GO:0051101)	5	48	0.034025216
260	Regulation Of Epidermis Development (GO:0045682)	2	8	0.034255173
261	Cellular Response To Muramyl Dipeptide (GO:0071225)	2	8	0.034255173
262	Regulation Of Vesicle Fusion (GO:0031338)	2	8	0.034255173
263	Skin Morphogenesis (GO:0043589)	2	8	0.034255173
264	Endothelial Cell Chemotaxis (GO:0035767)	2	8	0.034255173
265	Ubiquitin-Dependent Protein Catabolic Process Via The C-end Degron Rule Pathway (GO:0140627)	2	8	0.034255173
266	Hyaluronan Catabolic Process (GO:0030214)	2	8	0.034255173
267	Immune Response-Inhibiting Cell Surface Receptor Signaling Pathway (GO:0002767)	2	8	0.034255173
268	Negative Regulation Of Retrograde Protein Transport, ER To Cytosol (GO:1904153)	2	8	0.034255173
269	Positive Regulation Of Macrophage Cytokine Production (GO:0060907)	2	8	0.034255173
270	Protein Localization To Perinuclear Region Of Cytoplasm (GO:1905719)	2	8	0.034255173
271	Regulation Of Aspartic-Type Endopeptidase Activity Involved In Amyloid Precursor Protein Catabolic Process (GO:1902959)	2	8	0.034255173
272	Signal Transduction By P53 Class Mediator (GO:0072331)	4	33	0.034619241
273	Negative Regulation Of Blood Vessel Endothelial Cell Migration (GO:0043537)	4	33	0.034619241
274	Positive Regulation Of Epidermal Growth Factor Receptor Signaling Pathway (GO:0045742)	4	33	0.034619241
275	Positive Regulation Of Protein Dephosphorylation (GO:0035307)	4	33	0.034619241
276	Protein K63-linked Deubiquitination (GO:0070536)	4	33	0.034619241
277	Regulation Of Small GTPase Mediated Signal Transduction (GO:0051056)	9	118	0.034725203
278	Inflammatory Response (GO:0006954)	15	236	0.034737525
279	Regulation Of Organelle Organization (GO:0033043)	8	100	0.035414082
280	Regulation Of Cell Population Proliferation (GO:0042127)	39	766	0.03628515
281	Regulation Of Protein-Containing Complex Assembly (GO:0043254)	9	119	0.036364204
282	DNA Methylation (GO:0006306)	3	20	0.037854848
283	Fc-gamma Receptor Signaling Pathway Involved In Phagocytosis (GO:0038096)	3	20	0.037854848
284	Regulation Of Fibroblast Migration (GO:0010762)	3	20	0.037854848
285	Negative Regulation Of Cyclin-Dependent Protein Kinase Activity (GO:1904030)	3	20	0.037854848
286	Negative Regulation Of miRNA Transcription (GO:1902894)	3	20	0.037854848
287	Nuclear-Transcribed mRNA poly(A) Tail Shortening (GO:0000289)	3	20	0.037854848
288	Positive Regulation Of Lipid Storage (GO:0010884)	3	20	0.037854848
289	Protein Deacylation (GO:0035601)	3	20	0.037854848
290	Regulation Of Endocytosis (GO:0030100)	6	66	0.038015587

291	Negative Regulation Of JNK Cascade (GO:0046329)	4	34	0.038103323
292	Protein Targeting To Vacuole (GO:0006623)	4	34	0.038103323
293	Protein Catabolic Process (GO:0030163)	8	102	0.039136308
294	Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process (GO:0043281)	7	84	0.03933858
295	Regulation Of Interferon-Beta Production (GO:0032648)	5	50	0.039624069
296	Positive Regulation Of Fat Cell Differentiation (GO:0045600)	5	50	0.039624069
297	Intracellular Protein Transport (GO:0006886)	19	325	0.040279326
298	Epithelial Mesenchymal Transition	13	200	0.0405236
299	Regulation Of Kinase Activity (GO:0043549)	7	85	0.041534279
300	Positive Regulation Of Endothelial Cell Migration (GO:0010595)	7	85	0.041534279
301	Positive Regulation Of Macromolecule Biosynthetic Process (GO:0010557)	9	122	0.041596785
302	Endoderm Formation (GO:0001706)	4	35	0.041780842
303	Regulation Of Stress-Activated MAPK Cascade (GO:0032872)	5	51	0.042621105
304	Cholesterol Transport (GO:0030301)	5	51	0.042621105
305	Regulation Of Ceramide Biosynthetic Process (GO:2000303)	2	9	0.042958195
306	Camera-Type Eye Morphogenesis (GO:0048593)	2	9	0.042958195
307	Response To Histamine (GO:0034776)	2	9	0.042958195
308	Glucan Biosynthetic Process (GO:0009250)	2	9	0.042958195
309	Transferrin Transport (GO:0033572)	2	9	0.042958195
310	Glycogen Biosynthetic Process (GO:0005978)	2	9	0.042958195
311	Vasoconstriction (GO:0042310)	2	9	0.042958195
312	Wound Healing, Spreading Of Epidermal Cells (GO:0035313)	2	9	0.042958195
313	Kinetochore Assembly (GO:0051382)	2	9	0.042958195
314	Mitral Valve Morphogenesis (GO:0003183)	2	9	0.042958195
315	Negative Regulation Of Toll-Like Receptor 4 Signaling Pathway (GO:0034144)	2	9	0.042958195
316	Piecemeal Microautophagy Of The Nucleus (GO:0034727)	2	9	0.042958195
317	Positive Regulation Of Leukocyte Apoptotic Process (GO:2000108)	2	9	0.042958195
318	Regulation Of Bile Acid Biosynthetic Process (GO:0070857)	2	9	0.042958195
319	Regulation Of Histone Deacetylation (GO:0031063)	3	21	0.042960669
320	Regulation Of Lipid Storage (GO:0010883)	3	21	0.042960669
321	Skin Epidermis Development (GO:0098773)	3	21	0.042960669
322	Focal Adhesion Assembly (GO:0048041)	3	21	0.042960669
323	Negative Regulation Of Biomineral Tissue Development (GO:0070168)	3	21	0.042960669
324	Negative Regulation Of miRNA Metabolic Process (GO:2000629)	3	21	0.042960669
325	Positive Regulation Of Epithelial Cell Proliferation (GO:0050679)	9	123	0.043448117
326	Positive Regulation Of Cell Population Proliferation (GO:0008284)	26	483	0.045002943
327	Protein Dephosphorylation (GO:0006470)	9	124	0.045353923

328	COPII-coated Vesicle Budding (GO:0090114)	4	36	0.045651828
329	Histone Deacetylation (GO:0016575)	4	36	0.045651828
330	Positive Regulation Of Interferon-Beta Production (GO:0032728)	4	36	0.045651828
331	Regulation Of Protein Localization To Nucleus (GO:1900180)	5	52	0.045750943
332	Negative Regulation Of Response To Stimulus (GO:0048585)	5	52	0.045750943
333	Glucose Homeostasis (GO:0042593)	7	87	0.046160454
334	Regulation Of Mitotic Cell Cycle (GO:0007346)	9	125	0.0473147
335	Fc Receptor Mediated Stimulatory Signaling Pathway (GO:0002431)	3	22	0.048391536
336	Regulation Of Regulatory T Cell Differentiation (GO:0045589)	3	22	0.048391536
337	Natural Killer Cell Mediated Immunity (GO:0002228)	3	22	0.048391536
338	Negative Regulation Of Protein Localization To Nucleus (GO:1900181)	3	22	0.048391536
339	Glycoprotein Metabolic Process (GO:0009100)	5	53	0.04901412
340	Negative Regulation Of Cysteine-Type Endopeptidase Activity (GO:2000117)	5	53	0.04901412
341	Negative Regulation Of Transferase Activity (GO:0051348)	4	37	0.049715866

[G2 common Down]

	Term	Matched	Total	P.value
1	Oxidative Phosphorylation	68	200	2.80E-18
2	Cilium Assembly (GO:0060271)	73	243	3.56E-16
3	Cilium Organization (GO:0044782)	68	228	5.46E-15
4	Myc Targets V1	59	200	5.77E-13
5	Mitochondrial Translation (GO:0032543)	37	98	3.82E-12
6	Mitochondrial Gene Expression (GO:0140053)	36	103	9.85E-11
7	Organelle Assembly (GO:0070925)	74	322	4.53E-10
8	Plasma Membrane Bounded Cell Projection Assembly (GO:0120031)	66	275	5.88E-10
9	Cilium Movement (GO:0003341)	24	59	3.96E-09
10	Fatty Acid Catabolic Process (GO:0009062)	24	61	8.74E-09
11	Fatty Acid Metabolism	43	158	1.16E-08
12	Translation (GO:0006412)	55	234	3.36E-08
13	Fatty Acid Oxidation (GO:0019395)	21	52	4.30E-08
14	Fatty Acid Beta-Oxidation (GO:0006635)	20	49	7.28E-08
15	Axoneme Assembly (GO:0035082)	18	41	8.52E-08
16	Axonemal Dynein Complex Assembly (GO:0070286)	17	37	8.56E-08
17	Proton Motive Force-Driven Mitochondrial ATP Synthesis (GO:0042776)	20	53	3.37E-07
18	Oxidative Phosphorylation (GO:0006119)	22	63	4.29E-07
19	Proton Motive Force-Driven ATP Synthesis (GO:0015986)	21	60	7.49E-07
20	Positive Regulation Of Protein Localization To Cajal Body (GO:1904871)	8	10	7.71E-07

21	Regulation Of Protein Localization To Cajal Body (GO:1904869)	8	10	7.71E-07
22	mTORC1 Signaling	46	200	8.35E-07
23	E2F Targets	45	200	2.07E-06
24	Positive Regulation Of Establishment Of Protein Localization To Telomere (GO:1904851)	7	9	5.65E-06
25	NADH Dehydrogenase Complex Assembly (GO:0010257)	18	53	7.45E-06
26	Mitochondrial Respiratory Chain Complex I Assembly (GO:0032981)	18	53	7.45E-06
27	Mitochondrial Respiratory Chain Complex Assembly (GO:0033108)	25	90	8.61E-06
28	Cellular Respiration (GO:0045333)	24	85	9.55E-06
29	Mitochondrion Organization (GO:0007005)	37	162	1.13E-05
30	Interferon Alpha Response	26	97	1.16E-05
31	Interferon Gamma Response	43	200	1.17E-05
32	DNA Repair	35	150	1.18E-05
33	Intraciliary Anterograde Transport (GO:0035720)	9	16	1.28E-05
34	Purine Deoxyribonucleotide Catabolic Process (GO:0009155)	5	5	1.60E-05
35	Regulation Of Establishment Of Protein Localization To Telomere (GO:0070203)	7	10	1.70E-05
36	Outer Dynein Arm Assembly (GO:0036158)	10	21	2.83E-05
37	Positive Regulation Of Peptidase Activity (GO:0010952)	11	25	2.83E-05
38	Mitochondrial Electron Transport, NADH To Ubiquinone (GO:0006120)	13	34	3.28E-05
39	Positive Regulation Of Telomerase RNA Localization To Cajal Body (GO:1904874)	8	14	3.42E-05
40	Positive Regulation Of Protein Localization To Chromosome, Telomeric Region (GO:1904816)	7	11	4.24E-05
41	Epithelial Cilium Movement Involved In Extracellular Fluid Movement (GO:0003351)	9	20	0.00012448
42	Aerobic Respiration (GO:0009060)	17	59	0.000140527
43	Purine Nucleotide Metabolic Process (GO:0006163)	12	34	0.000162316
44	Protein-Containing Complex Assembly (GO:0065003)	58	328	0.000173909
45	Motile Cilium Assembly (GO:0044458)	8	17	0.000204498
46	Regulation Of Telomerase RNA Localization To Cajal Body (GO:1904872)	8	17	0.000204498
47	Determination Of Left/Right Symmetry (GO:0007368)	14	45	0.000220864
48	Adipogenesis	39	200	0.000263259
49	Aerobic Electron Transport Chain (GO:0019646)	18	68	0.000293541
50	Protein Stabilization (GO:0050821)	40	208	0.000298789
51	Peroxisome	24	104	0.000314334
52	Mitochondrial ATP Synthesis Coupled Electron Transport (GO:0042775)	18	70	0.000431718
53	Ribosomal Large Subunit Biogenesis (GO:0042273)	15	54	0.000526402
54	Coenzyme A Metabolic Process (GO:0015936)	7	15	0.000554354
55	Medium-Chain fatty-acyl-CoA Metabolic Process (GO:0036112)	4	5	0.000663734
56	succinyl-CoA Catabolic Process (GO:1901289)	4	5	0.000663734
57	Cilium Movement Involved In Cell Motility (GO:0060294)	5	8	0.000671273
58	Purine Nucleoside Bisphosphate Catabolic Process (GO:0034034)	5	8	0.000671273
59	Regulation Of Mitotic Centrosome Separation (GO:0046602)	5	8	0.000671273
60	Ribonucleoside Bisphosphate Catabolic Process (GO:0034031)	5	8	0.000671273
61	succinyl-CoA Metabolic Process (GO:0006104)	5	8	0.000671273
62	Regulation Of Mitochondrial Membrane Potential (GO:0051881)	12	39	0.000686799
63	Negative Regulation Of Intrinsic Apoptotic Signaling Pathway (GO:2001243)	16	61	0.000697765
64	Cilium-Dependent Cell Motility (GO:0060285)	8	20	0.000782866

65	Sulfur Compound Catabolic Process (GO:0044273)	8	20	0.000782866
66	Regulation Of Cell Cycle Process (GO:0010564)	27	130	0.00081477
67	protein-RNA Complex Assembly (GO:0022618)	30	150	0.000832399
68	acetyl-CoA Metabolic Process (GO:0006084)	7	16	0.000892343
69	Regulation Of Cell Communication By Electrical Coupling (GO:0010649)	6	12	0.000898104
70	Purine Ribonucleotide Catabolic Process (GO:0009154)	9	25	0.000908862
71	Regulation Of Endopeptidase Activity (GO:0052548)	17	69	0.001040846
72	Estrogen Response Late	37	200	0.001045173
73	RNA Splicing, Via Transesterification Reactions With Bulged Adenosine As Nucleophile (GO:0000377)	34	180	0.001127943
74	Cellular Response To Chemical Stress (GO:0062197)	20	89	0.001361563
75	Peptidyl-Cysteine Modification (GO:0018198)	5	9	0.001373524
76	Negative Regulation Of Oxidative Stress-Induced Intrinsic Apoptotic Signaling Pathway (GO:1902176)	7	17	0.001373836
77	Substantia Nigra Development (GO:0021762)	12	42	0.001421466
78	Peptidyl-Proline Modification (GO:0018208)	9	27	0.001701746
79	Nucleotide Catabolic Process (GO:0009166)	4	6	0.001817124
80	Positive Regulation Of Cyclin-Dependent Protein Kinase Activity (GO:1904031)	7	18	0.002036375
81	Positive Regulation Of Establishment Of Protein Localization (GO:1904951)	7	18	0.002036375
82	Regulation Of Oxidative Stress-Induced Intrinsic Apoptotic Signaling Pathway (GO:1902175)	7	18	0.002036375
83	Transcription By RNA Polymerase III (GO:0006383)	9	28	0.002266154
84	Regulation Of G1/S Transition Of Mitotic Cell Cycle (GO:2000045)	22	106	0.002391871
85	Regulation Of Stem Cell Population Maintenance (GO:2000036)	14	56	0.002416897
86	Inner Mitochondrial Membrane Organization (GO:0007007)	10	34	0.002756717
87	mRNA Splicing, Via Spliceosome (GO:0000398)	37	211	0.002773955
88	RNA Modification (GO:0009451)	13	51	0.002835011
89	Microtubule Bundle Formation (GO:0001578)	13	51	0.002835011
90	Macromolecule Biosynthetic Process (GO:0009059)	33	183	0.002894995
91	COPII Vesicle Coating (GO:0048208)	7	19	0.002921215
92	NADP Metabolic Process (GO:0006739)	7	19	0.002921215
93	Vesicle Targeting, Rough ER To cis-Golgi (GO:0048207)	7	19	0.002921215
94	Establishment Of Mitotic Spindle Orientation (GO:0000132)	9	29	0.002969721
95	Positive Regulation Of Peptidyl-Threonine Phosphorylation (GO:0010800)	8	24	0.003059953
96	Cellular Response To Heat (GO:0034605)	11	40	0.003096189
97	Regulation Of Protein Dephosphorylation (GO:0035304)	11	40	0.003096189
98	Amyloid-Beta Metabolic Process (GO:0050435)	6	15	0.003635898
99	Negative Regulation Of Cell-Substrate Junction Organization (GO:0150118)	6	15	0.003635898
100	Negative Regulation Of Focal Adhesion Assembly (GO:0051895)	6	15	0.003635898
101	G2-M Checkpoint	35	200	0.00366723
102	Glycolysis	35	200	0.00366723
103	7-Methylguanosine Cap Hypermethylation (GO:0036261)	4	7	0.003870783
104	NADH Metabolic Process (GO:0006734)	4	7	0.003870783
105	Notch Receptor Processing (GO:0007220)	4	7	0.003870783
106	RNA Capping (GO:0036260)	4	7	0.003870783
107	siRNA Processing (GO:0030422)	4	7	0.003870783
108	Positive Regulation Of DNA Biosynthetic Process (GO:2000573)	15	65	0.0039612

109	Protein Targeting To Mitochondrion (GO:0006626)	14	59	0.004046851
110	ATP Biosynthetic Process (GO:0006754)	8	25	0.004072235
111	protein-DNA Complex Disassembly (GO:0032986)	7	20	0.004072637
112	Regulation Of Cell Communication By Electrical Coupling Involved In Cardiac Conduction (GO:1901844)	5	11	0.004168796
113	Regulation Of Peptidyl-Threonine Phosphorylation (GO:0010799)	10	36	0.004358299
114	Positive Regulation Of Protein Localization To Nucleus (GO:1900182)	16	72	0.00443272
115	Epithelial Cell Differentiation (GO:0030855)	25	132	0.004601404
116	Bile Acid Metabolism	22	112	0.004836207
117	Negative Regulation Of Cell-Matrix Adhesion (GO:0001953)	9	31	0.00488519
118	Non-Motile Cilium Assembly (GO:1905515)	9	31	0.00488519
119	Positive Regulation Of G1/S Transition Of Mitotic Cell Cycle (GO:1900087)	9	31	0.00488519
120	Activation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process (GO:0006919)	15	67	0.005356748
121	Spliceosomal snRNP Assembly (GO:0000387)	10	37	0.005394891
122	Regulation Of Protein Ubiquitination (GO:0031396)	22	113	0.005397019
123	Chaperone-Mediated Protein Complex Assembly (GO:0051131)	7	21	0.00553715
124	Gene Expression (GO:0010467)	47	296	0.006204242
125	NADPH Regeneration (GO:0006740)	5	12	0.006505013
126	acetyl-CoA Biosynthetic Process (GO:0006085)	5	12	0.006505013
127	Cristae Formation (GO:0042407)	5	12	0.006505013
128	Positive Regulation Of ERAD Pathway (GO:1904294)	5	12	0.006505013
129	heme Metabolism	34	200	0.006551736
130	Fatty Acid Metabolic Process (GO:0006631)	23	122	0.006761258
131	Regulation Of Microtubule Polymerization Or Depolymerization (GO:0031110)	8	27	0.006849219
132	Amyloid-Beta Formation (GO:0034205)	4	8	0.007070305
133	Box C/D snoRNP Assembly (GO:0000492)	4	8	0.007070305
134	Membrane Lipid Catabolic Process (GO:0046466)	4	8	0.007070305
135	Positive Regulation Of Ligase Activity (GO:0051351)	4	8	0.007070305
136	Negative Regulation Of Apoptotic Signaling Pathway (GO:2001234)	17	82	0.007152916
137	Positive Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process (GO:0043280)	21	109	0.007302094
138	Blood Vessel Endothelial Cell Migration (GO:0043534)	7	22	0.007362622
139	Protein Peptidyl-Prolyl Isomerization (GO:0000413)	7	22	0.007362622
140	Nicotinamide Nucleotide Metabolic Process (GO:0046496)	6	17	0.007413789
141	ERAD Pathway (GO:0036503)	18	89	0.007500868
142	Regulation Of Apoptotic Signaling Pathway (GO:2001233)	11	45	0.008145113
143	Determination Of Bilateral Symmetry (GO:0009855)	8	28	0.008682448
144	Monocarboxylic Acid Metabolic Process (GO:0032787)	19	97	0.008694397
145	Positive Regulation Of Double-Strand Break Repair (GO:2000781)	17	84	0.009138938
146	Positive Regulation Of Protein Ubiquitination (GO:0031398)	17	84	0.009138938
147	ATP Metabolic Process (GO:0046034)	9	34	0.009400941
148	Establishment Of Mitotic Spindle Localization (GO:0040001)	9	34	0.009400941
149	Negative Regulation Of Oxidative Stress-Induced Cell Death (GO:1903202)	7	23	0.009597372
150	Extracellular Transport (GO:0006858)	5	13	0.009624863
151	Intraciliary Retrograde Transport (GO:0035721)	5	13	0.009624863
152	Membrane Protein Intracellular Domain Proteolysis (GO:0031293)	5	13	0.009624863

153	Microtubule-Based Transport (GO:0099111)	5	13	0.009624863
154	Ubiquinone Biosynthetic Process (GO:0006744)	5	13	0.009624863
155	Positive Regulation Of Stem Cell Population Maintenance (GO:1902459)	10	40	0.009684652
156	Regulation Of Microtubule Cytoskeleton Organization (GO:0070507)	10	40	0.009684652
157	Nucleosome Disassembly (GO:0006337)	6	18	0.010102503
158	mRNA Processing (GO:0006397)	35	214	0.010655709
159	Positive Regulation Of Dephosphorylation (GO:0035306)	8	29	0.01085873
160	Positive Regulation Of Endopeptidase Activity (GO:0010950)	8	29	0.01085873
161	Autocrine Signaling (GO:0035425)	3	5	0.01117043
162	fatty-acyl-CoA Catabolic Process (GO:0036115)	3	5	0.01117043
163	Negative Regulation Of Trophoblast Cell Migration (GO:1901164)	3	5	0.01117043
164	Plus-End-Directed Organelle Transport Along Microtubule (GO:0072386)	3	5	0.01117043
165	Positive Regulation Of Mitochondrial Membrane Potential (GO:0010918)	3	5	0.01117043
166	Regulation Of Long-Chain Fatty Acid Import Across Plasma Membrane (GO:0010746)	3	5	0.01117043
167	Cellular Response To Amino Acid Stimulus (GO:0071230)	9	35	0.011448715
168	Establishment Of Spindle Orientation (GO:0051294)	9	35	0.011448715
169	Positive Regulation Of Telomere Maintenance Via Telomere Lengthening (GO:1904358)	9	35	0.011448715
170	Regulation Of Apoptotic Process (GO:0042981)	97	705	0.011512053
171	Epithelial Cilium Movement Involved In Determination Of Left/Right Asymmetry (GO:0060287)	4	9	0.011627745
172	Ether Lipid Biosynthetic Process (GO:0008611)	4	9	0.011627745
173	Regulation Of Attachment Of Spindle Microtubules To Kinetochore (GO:0051988)	4	9	0.011627745
174	Regulation Of High Voltage-Gated Calcium Channel Activity (GO:1901841)	4	9	0.011627745
175	Ubiquitin-Dependent ERAD Pathway (GO:0030433)	15	73	0.0120453
176	Negative Regulation Of Peptidase Activity (GO:0010466)	13	60	0.012108423
177	Regulation Of Proteolysis Involved In Protein Catabolic Process (GO:1903050)	7	24	0.012289256
178	Organelle Disassembly (GO:1903008)	12	54	0.012786334
179	Regulation Of Viral Genome Replication (GO:0045069)	14	67	0.01296408
180	Peptide Biosynthetic Process (GO:0043043)	27	158	0.013320975
181	UV Response Up	27	158	0.013320975
182	Cytoplasmic Translational Initiation (GO:0002183)	8	30	0.013412884
183	Negative Regulation Of Protein Dephosphorylation (GO:0035308)	6	19	0.01341695
184	Inner Dynein Arm Assembly (GO:0036159)	5	14	0.013636865
185	Negative Regulation Of Peptidyl-Threonine Phosphorylation (GO:0010801)	5	14	0.013636865
186	Ubiquinone Metabolic Process (GO:0006743)	5	14	0.013636865
187	tRNA Methylation (GO:0030488)	9	36	0.01381219
188	Positive Regulation Of DNA Repair (GO:0045739)	17	89	0.016050759
189	Cellular Response To Oxidative Stress (GO:0034599)	21	117	0.01606858
190	Regulation Of Protein Autophosphorylation (GO:0031952)	8	31	0.016379043
191	Negative Regulation Of Stem Cell Population Maintenance (GO:1902455)	6	20	0.017421663
192	Regulation Of Necroptotic Process (GO:0060544)	6	20	0.017421663
193	Acidic Amino Acid Transport (GO:0015800)	4	10	0.017713649
194	Negative Regulation Of Mitochondrial Outer Membrane Permeabilization Involved In Apoptotic Signaling Pathway (GO:1901029)	4	10	0.017713649
195	Positive Regulation Of DNA-templated DNA Replication (GO:2000105)	4	10	0.017713649
196	Purine Ribonucleoside Triphosphate Biosynthetic Process (GO:0009206)	4	10	0.017713649

197	Removal Of Superoxide Radicals (GO:0019430)	4	10	0.017713649
198	Small Nucleolar Ribonucleoprotein Complex Assembly (GO:0000491)	4	10	0.017713649
199	tRNA Threonylcarbamoyladenine Metabolic Process (GO:0070525)	4	10	0.017713649
200	Transcription By RNA Polymerase II (GO:0006366)	31	192	0.018393582
201	Defense Response To Protozoan (GO:0042832)	5	15	0.018637358
202	Dolichol-Linked Oligosaccharide Biosynthetic Process (GO:0006488)	5	15	0.018637358
203	Positive Regulation Of Cyclin-Dependent Protein Serine/Threonine Kinase Activity (GO:0045737)	5	15	0.018637358
204	Mitotic Spindle Assembly Checkpoint Signaling (GO:0007094)	7	26	0.019228204
205	Mitotic Spindle Checkpoint Signaling (GO:0071174)	7	26	0.019228204
206	Spindle Assembly Checkpoint Signaling (GO:0071173)	7	26	0.019228204
207	Left/Right Pattern Formation (GO:0060972)	8	32	0.019790157
208	Mitochondrial Membrane Organization (GO:0007006)	8	32	0.019790157
209	Positive Regulation Of Telomere Maintenance Via Telomerase (GO:0032212)	8	32	0.019790157
210	Very Long-Chain Fatty Acid Metabolic Process (GO:0000038)	8	32	0.019790157
211	DNA Strand Resection Involved In Replication Fork Processing (GO:0110025)	3	6	0.020523764
212	Hyaluronan Biosynthetic Process (GO:0030213)	3	6	0.020523764
213	Intraciliary Transport Involved In Cilium Assembly (GO:0035735)	3	6	0.020523764
214	Negative Regulation Of Double-Strand Break Repair Via Nonhomologous End Joining (GO:2001033)	3	6	0.020523764
215	Negative Regulation Of Response To Reactive Oxygen Species (GO:1901032)	3	6	0.020523764
216	Negative Regulation Of Stress-Activated Protein Kinase Signaling Cascade (GO:0070303)	3	6	0.020523764
217	Peptidyl-Arginine Modification (GO:0018195)	3	6	0.020523764
218	Positive Regulation Of ER-associated Ubiquitin-Dependent Protein Catabolic Process (GO:1903071)	3	6	0.020523764
219	Positive Regulation Of mRNA Binding (GO:1902416)	3	6	0.020523764
220	Positive Regulation Of Unsaturated Fatty Acid Biosynthetic Process (GO:2001280)	3	6	0.020523764
221	Protein Localization To Ciliary Membrane (GO:1903441)	3	6	0.020523764
222	Proteolysis Involved In Protein Catabolic Process (GO:0051603)	15	78	0.021529438
223	Regulation Of Innate Immune Response (GO:0045088)	15	78	0.021529438
224	Porphyrin-Containing Compound Biosynthetic Process (GO:0006779)	6	21	0.022175476
225	Negative Regulation Of Cell-Substrate Adhesion (GO:0010812)	9	39	0.023057266
226	Negative Regulation Of Mitochondrion Organization (GO:0010823)	9	39	0.023057266
227	Positive Regulation Of Intrinsic Apoptotic Signaling Pathway (GO:2001244)	9	39	0.023057266
228	DNA Metabolic Process (GO:0006259)	43	288	0.023157964
229	ncRNA Catabolic Process (GO:0034661)	8	33	0.023677517
230	Positive Regulation Of Protein Dephosphorylation (GO:0035307)	8	33	0.023677517
231	Positive Regulation Of Telomerase Activity (GO:0051973)	8	33	0.023677517
232	Negative Regulation Of Innate Immune Response (GO:0045824)	11	52	0.023797562
233	Positive Regulation Of Protein Modification By Small Protein Conjugation Or Removal (GO:1903322)	15	79	0.023962697
234	Regulation Of Mitotic Cell Cycle Phase Transition (GO:1901990)	16	86	0.024092731
235	Maturation Of 5.8S rRNA (GO:0000460)	5	16	0.02470797
236	Regulation Of DNA Strand Elongation (GO:0060382)	5	16	0.02470797
237	Regulation Of Response To Cytokine Stimulus (GO:0060759)	5	16	0.02470797
238	Regulation Of Protein Catabolic Process (GO:0042176)	21	122	0.024794963
239	Defense Response To Virus (GO:0051607)	30	189	0.024891305
240	Antiviral Innate Immune Response (GO:0140374)	10	46	0.025451639

241	Cellular Response To Superoxide (GO:0071451)	4	11	0.02545358
242	Negative Regulation Of Release Of Sequestered Calcium Ion Into Cytosol (GO:0051280)	4	11	0.02545358
243	Negative Regulation Of Ryanodine-Sensitive Calcium-Release Channel Activity (GO:0060315)	4	11	0.02545358
244	Pentose-Phosphate Shunt (GO:0006098)	4	11	0.02545358
245	Regulation Of Cilium Movement (GO:0003352)	4	11	0.02545358
246	Regulation Of Microtubule-Based Movement (GO:0060632)	4	11	0.02545358
247	Regulation Of Response To Oxidative Stress (GO:1902882)	4	11	0.02545358
248	Tetrahydrofolate Metabolic Process (GO:0046653)	4	11	0.02545358
249	Negative Regulation Of Protein Localization (GO:1903828)	9	40	0.026939642
250	Positive Regulation Of Catalytic Activity (GO:0043085)	9	40	0.026939642
251	Positive Regulation Of Cell Cycle G1/S Phase Transition (GO:1902808)	9	40	0.026939642
252	Mitochondrial Transport (GO:0006839)	11	53	0.027144531
253	Negative Regulation Of Viral Genome Replication (GO:0045071)	11	53	0.027144531
254	Regulation Of Proteasomal Protein Catabolic Process (GO:0061136)	11	53	0.027144531
255	RNA Processing (GO:0006396)	29	183	0.027593266
256	NAD Metabolic Process (GO:0019674)	6	22	0.027730305
257	Membrane Protein Ectodomain Proteolysis (GO:0006509)	6	22	0.027730305
258	Positive Regulation Of Protein Autophosphorylation (GO:0031954)	6	22	0.027730305
259	Regulation Of Intracellular Steroid Hormone Receptor Signaling Pathway (GO:0033143)	6	22	0.027730305
260	Membrane Protein Proteolysis (GO:0033619)	8	34	0.028070316
261	Smoothed Signaling Pathway (GO:0007224)	8	34	0.028070316
262	Transcription Initiation-Coupled Chromatin Remodeling (GO:0045815)	8	34	0.028070316
263	Negative Regulation Of Mitotic Metaphase/Anaphase Transition (GO:0045841)	7	28	0.02852033
264	Positive Regulation Of mRNA Processing (GO:0050685)	7	28	0.02852033
265	Protein Insertion Into Mitochondrial Membrane (GO:0051204)	7	28	0.02852033
266	Regulation Of DNA Damage Response, Signal Transduction By P53 Class Mediator (GO:0043516)	7	28	0.02852033
267	Vesicle Coating (GO:0006901)	7	28	0.02852033
268	Protein Monoubiquitination (GO:0006513)	10	47	0.029250105
269	Regulation Of Signal Transduction By P53 Class Mediator (GO:1901796)	10	47	0.029250105
270	Regulation Of Double-Strand Break Repair (GO:2000779)	16	88	0.029320872
271	Regulation Of Cell Cycle G1/S Phase Transition (GO:1902806)	14	74	0.029345526
272	Protein Maturation (GO:0051604)	20	117	0.029911503
273	Estrogen Response Early	31	200	0.030774695
274	Negative Regulation Of Protein Catabolic Process (GO:0042177)	11	54	0.030817561
275	Negative Regulation Of Viral Process (GO:0048525)	12	61	0.031809606
276	Amyloid Precursor Protein Metabolic Process (GO:0042982)	5	17	0.031913889
277	Branched-Chain Amino Acid Catabolic Process (GO:0009083)	5	17	0.031913889
278	Carbohydrate Derivative Transport (GO:1901264)	5	17	0.031913889
279	Cell Migration Involved In Sprouting Angiogenesis (GO:0002042)	5	17	0.031913889
280	Purine-Containing Compound Biosynthetic Process (GO:0072522)	5	17	0.031913889
281	Ribosome Biogenesis (GO:0042254)	25	155	0.032025521
282	Aldehyde Catabolic Process (GO:0046185)	3	7	0.033013526
283	Establishment Of Centrosome Localization (GO:0051660)	3	7	0.033013526
284	Leukocyte Aggregation (GO:0070486)	3	7	0.033013526

285	Malate Metabolic Process (GO:0006108)	3	7	0.033013526
286	Mammary Gland Epithelial Cell Differentiation (GO:0060644)	3	7	0.033013526
287	Positive Regulation Of Membrane Potential (GO:0045838)	3	7	0.033013526
288	Positive Regulation Of Ryanodine-Sensitive Calcium-Release Channel Activity (GO:0060316)	3	7	0.033013526
289	Purine Ribonucleoside Monophosphate Catabolic Process (GO:0009169)	3	7	0.033013526
290	Regulation Of Cyclic-Nucleotide Phosphodiesterase Activity (GO:0051342)	3	7	0.033013526
291	Regulation Of Hydrogen Peroxide-Induced Cell Death (GO:1903205)	3	7	0.033013526
292	Regulation Of Protein Glycosylation (GO:0060049)	3	7	0.033013526
293	snRNA Transcription By RNA Polymerase III (GO:0042796)	3	7	0.033013526
294	tRNA Transcription By RNA Polymerase III (GO:0042797)	3	7	0.033013526
295	Regulation Of Intrinsic Apoptotic Signaling Pathway (GO:2001242)	10	48	0.033433026
296	U2-type Prespliceosome Assembly (GO:1903241)	6	23	0.034130171
297	Morphogenesis Of An Epithelium (GO:0002009)	7	29	0.034139937
298	Axonal Transport Of Mitochondrion (GO:0019896)	4	12	0.034927879
299	Microtubule Anchoring At Microtubule Organizing Center (GO:0072393)	4	12	0.034927879
300	Negative Regulation Of JUN Kinase Activity (GO:0043508)	4	12	0.034927879
301	Negative Regulation Of Cell Cycle Phase Transition (GO:1901988)	4	12	0.034927879
302	Negative Regulation Of Mitochondrial Membrane Permeability (GO:0035795)	4	12	0.034927879
303	Negative Regulation Of Substrate Adhesion-Dependent Cell Spreading (GO:1900025)	4	12	0.034927879
304	Oligosaccharide-Lipid Intermediate Biosynthetic Process (GO:0006490)	4	12	0.034927879
305	Quinone Biosynthetic Process (GO:1901663)	4	12	0.034927879
306	Regulation Of Platelet-Derived Growth Factor Receptor Signaling Pathway (GO:0010640)	4	12	0.034927879
307	RNA Methylation (GO:0001510)	12	62	0.035640606
308	Regulation Of Cell Division (GO:0051302)	15	83	0.035782288
309	DNA Integrity Checkpoint Signaling (GO:0031570)	9	42	0.036039843
310	Proton Transmembrane Transport (GO:1902600)	10	49	0.03801667
311	Reactive Oxygen Species Pathway	10	49	0.03801667
312	Positive Regulation Of Protein Metabolic Process (GO:0051247)	30	196	0.038399518
313	COPII-coated Vesicle Budding (GO:0090114)	8	36	0.038476117
314	Positive Regulation Of Double-Strand Break Repair Via Homologous Recombination (GO:1905168)	8	36	0.038476117
315	Unfolded Protein Response	19	113	0.039082718
316	Positive Regulation Of Mitotic Cell Cycle Phase Transition (GO:1901992)	12	63	0.039787276
317	Negative Regulation Of Epithelial Cell Proliferation (GO:0050680)	13	70	0.039931256
318	fatty-acyl-CoA Metabolic Process (GO:0035337)	5	18	0.040302895
319	Glucose 6-Phosphate Metabolic Process (GO:0051156)	5	18	0.040302895
320	Mitochondrial Fusion (GO:0008053)	5	18	0.040302895
321	Regulation Of Defense Response To Virus (GO:0050688)	5	18	0.040302895
322	GPI Anchor Biosynthetic Process (GO:0006506)	7	30	0.040448177
323	Response To Amino Acid (GO:0043200)	7	30	0.040448177
324	mRNA Catabolic Process (GO:0006402)	9	43	0.041296316
325	Negative Regulation Of Cell Junction Assembly (GO:1901889)	6	24	0.041410485
326	Peroxisome Organization (GO:0007031)	6	24	0.041410485
327	Regulation Of Ryanodine-Sensitive Calcium-Release Channel Activity (GO:0060314)	6	24	0.041410485
328	Secondary Alcohol Biosynthetic Process (GO:1902653)	6	24	0.041410485

329	Chromatin Organization (GO:0006325)	39	268	0.041580725
330	Regulation Of DNA Repair (GO:0006282)	21	129	0.042562183
331	Negative Regulation Of Programmed Cell Death (GO:0043069)	53	381	0.042740889
332	Dicarboxylic Acid Metabolic Process (GO:0043648)	10	50	0.043015848
333	Ribosome Assembly (GO:0042255)	10	50	0.043015848
334	Regulation Of Cellular Response To Stress (GO:0080135)	18	107	0.043556053
335	RNA Catabolic Process (GO:0006401)	11	57	0.04393265
336	Protein Localization To Organelle (GO:0033365)	22	137	0.044027833
337	Negative Regulation Of Cell Death (GO:0060548)	12	64	0.044260286
338	Negative Regulation Of Endothelial Cell Proliferation (GO:0001937)	8	37	0.044533602
339	Regulation Of Phosphoprotein Phosphatase Activity (GO:0043666)	8	37	0.044533602
340	ncRNA Processing (GO:0034470)	17	100	0.044812998
341	DNA-templated Transcription (GO:0006351)	30	199	0.045635945
342	Regulation Of Peptidyl-Serine Phosphorylation (GO:0033135)	16	93	0.045995097
343	ERBB2 Signaling Pathway (GO:0038128)	4	13	0.04617368
344	T Cell Differentiation In Thymus (GO:0033077)	4	13	0.04617368
345	acyl-CoA Biosynthetic Process (GO:0071616)	4	13	0.04617368
346	Amyloid Precursor Protein Catabolic Process (GO:0042987)	4	13	0.04617368
347	Endonucleolytic Cleavage Of Tricistronic rRNA Transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000479)	4	13	0.04617368
348	Ether Lipid Metabolic Process (GO:0046485)	4	13	0.04617368
349	Mitochondrial Fission (GO:0000266)	4	13	0.04617368
350	Negative Regulation Of DNA Damage Response, Signal Transduction By P53 Class Mediator (GO:0043518)	4	13	0.04617368
351	Negative Regulation Of Receptor Internalization (GO:0002091)	4	13	0.04617368
352	Peptidyl-Methionine Modification (GO:0018206)	4	13	0.04617368
353	Regulation Of Fatty Acid Beta-Oxidation (GO:0031998)	4	13	0.04617368
354	Regulation Of Response To Stress (GO:0080134)	4	13	0.04617368
355	Regulation Of Trophoblast Cell Migration (GO:1901163)	4	13	0.04617368
356	Spliceosomal tri-snRNP Complex Assembly (GO:0000244)	4	13	0.04617368
357	Establishment Of Protein Localization To Mitochondrion (GO:0072655)	9	44	0.047045924
358	Protein Localization (GO:0008104)	49	351	0.047208
359	AMP Biosynthetic Process (GO:0006167)	3	8	0.048579484
360	Establishment Of Protein Localization To Chromatin (GO:0071169)	3	8	0.048579484
361	Positive Regulation Of Early Endosome To Late Endosome Transport (GO:2000643)	3	8	0.048579484
362	Positive Regulation Of Fatty Acid Beta-Oxidation (GO:0032000)	3	8	0.048579484
363	Positive Regulation Of Protein Localization To Early Endosome (GO:1902966)	3	8	0.048579484
364	Positive Regulation Of Protein Localization To Endosome (GO:1905668)	3	8	0.048579484
365	Regulation Of ER-associated Ubiquitin-Dependent Protein Catabolic Process (GO:1903069)	3	8	0.048579484
366	Regulation Of Protein Localization To Early Endosome (GO:1902965)	3	8	0.048579484
367	Response To Misfolded Protein (GO:0051788)	3	8	0.048579484
368	Semaphorin-Plexin Signaling Pathway Involved In Axon Guidance (GO:1902287)	3	8	0.048579484
369	tRNA Transcription (GO:0009304)	3	8	0.048579484
370	Tetrahydrofolate Interconversion (GO:0035999)	3	8	0.048579484
371	Translational Termination (GO:0006415)	3	8	0.048579484
372	rRNA Processing (GO:0006364)	17	101	0.048584762

373	Myc Targets V2	11	58	0.049044266
374	Cholesterol Biosynthetic Process (GO:0006695)	6	25	0.049597561
375	Regulation Of Double-Strand Break Repair Via Nonhomologous End Joining (GO:2001032)	6	25	0.049597561
376	RNA-templated DNA Biosynthetic Process (GO:0006278)	5	19	0.049905029
377	Cellular Response To Misfolded Protein (GO:0071218)	5	19	0.049905029
378	Heme Biosynthetic Process (GO:0006783)	5	19	0.049905029
379	Intrinsic Apoptotic Signaling Pathway In Response To DNA Damage By P53 Class Mediator (GO:0042771)	5	19	0.049905029
380	Nucleotide Biosynthetic Process (GO:0009165)	5	19	0.049905029
381	Protein Insertion Into Membrane (GO:0051205)	5	19	0.049905029
382	tRNA Metabolic Process (GO:0006399)	5	19	0.049905029
383	Telomere Maintenance Via Telomerase (GO:0007004)	5	19	0.049905029

[G3 club Up]

	Term	Matched	Total	P.value
1	Adiponectin-Activated Signaling Pathway (GO:0033211)	3	5	2.85E-06
2	Cytoplasmic Translation (GO:0002181)	7	93	2.89E-06
3	Peptide Biosynthetic Process (GO:0043043)	8	158	1.08E-05
4	Translation (GO:0006412)	9	234	2.73E-05
5	Macromolecule Biosynthetic Process (GO:0009059)	8	183	3.12E-05
6	Signal Peptide Processing (GO:0006465)	3	13	7.83E-05
7	Ribonucleoprotein Complex Biogenesis (GO:0022613)	6	118	0.00013836
8	Negative Regulation Of Release Of Cytochrome C From Mitochondria (GO:0090201)	3	16	0.000151111
9	Oxidative Phosphorylation	7	200	0.000387176
10	U2-type Prespliceosome Assembly (GO:1903241)	3	23	0.000461893
11	Protein Targeting To ER (GO:0045047)	3	23	0.000461893
12	Ribosome Biogenesis (GO:0042254)	6	155	0.000600413
13	Regulation Of Phospholipid Transport (GO:2001138)	2	6	0.000646949
14	Gene Expression (GO:0010467)	8	296	0.000830889
15	Endosome To Melanosome Transport (GO:0035646)	2	8	0.001197142
16	Endosome To Pigment Granule Transport (GO:0043485)	2	8	0.001197142
17	Positive Regulation Of Phospholipid Transport (GO:2001140)	2	10	0.001907272
18	Negative Regulation Of Mitochondrion Organization (GO:0010823)	3	39	0.002205649
19	RNA Transport (GO:0050658)	3	39	0.002205649
20	Myc Targets V1	6	200	0.002223963
21	Positive Regulation Of Lipid Transport (GO:0032370)	2	11	0.002320974
22	tRNA Splicing, Via Endonucleolytic Cleavage And Ligation (GO:0006388)	2	11	0.002320974
23	Ribosomal Small Subunit Biogenesis (GO:0042274)	4	84	0.002391145
24	Regulation Of Release Of Cytochrome C From Mitochondria (GO:0090199)	3	41	0.002547977
25	Positive Regulation Of Heterotypic Cell-Cell Adhesion (GO:0034116)	2	14	0.003790332
26	Regulation Of DNA Binding (GO:0051101)	3	48	0.003996746

27	Fatty Acid Metabolism	5	158	0.004125605
28	Establishment Of Protein Localization To Endoplasmic Reticulum (GO:0072599)	2	16	0.004954965
29	Ribosomal Small Subunit Assembly (GO:0000028)	2	17	0.005591283
30	Intracellular Protein Transport (GO:0006886)	7	325	0.006109633
31	Peptide Metabolic Process (GO:0006518)	3	56	0.006163373
32	Ganglioside Metabolic Process (GO:0001573)	2	19	0.006969442
33	Heme Biosynthetic Process (GO:0006783)	2	19	0.006969442
34	RNA Splicing, Via Transesterification Reactions With Bulged Adenosine As Nucleophile (GO:0000377)	5	180	0.007111253
35	Regulation Of Meiotic Cell Cycle (GO:0051445)	2	20	0.007710306
36	Protein Processing (GO:0016485)	4	117	0.007769373
37	RNA Methylation (GO:0001510)	3	62	0.008170007
38	Spliceosomal Complex Assembly (GO:0000245)	3	62	0.008170007
39	Anaphase-Promoting Complex-Dependent Catabolic Process (GO:0031145)	2	21	0.00848505
40	Porphyrin-Containing Compound Biosynthetic Process (GO:0006779)	2	21	0.00848505
41	Positive Regulation Of Signal Transduction By P53 Class Mediator (GO:1901798)	2	21	0.00848505
42	Regulation Of Toll-Like Receptor 4 Signaling Pathway (GO:0034143)	2	23	0.010134277
43	Protein Targeting (GO:0006605)	4	129	0.010858296
44	Adipogenesis	5	200	0.010910361
45	Regulation Of Heterotypic Cell-Cell Adhesion (GO:0034114)	2	24	0.011007822
46	Negative Regulation Of Protein Transport (GO:0051224)	2	25	0.011913369
47	Organophosphate Ester Transport (GO:0015748)	2	25	0.011913369
48	Regulation Of Cell Size (GO:0008361)	2	25	0.011913369
49	mRNA Splicing, Via Spliceosome (GO:0000398)	5	211	0.013501127
50	mRNA Processing (GO:0006397)	5	214	0.014273856
51	Protein K11-linked Ubiquitination (GO:0070979)	2	29	0.015846502
52	Regulation Of Potassium Ion Transport (GO:0043266)	2	30	0.01690529
53	Negative Regulation Of Apoptotic Signaling Pathway (GO:2001234)	3	82	0.017384554
54	protein-RNA Complex Assembly (GO:0022618)	4	150	0.017976057
55	Cellular Respiration (GO:0045333)	3	85	0.019113402
56	Proteasome-Mediated Ubiquitin-Dependent Protein Catabolic Process (GO:0043161)	6	319	0.01996768
57	Regulation Of Potassium Ion Transmembrane Transport (GO:1901379)	2	33	0.020255887
58	Positive Regulation Of Binding (GO:0051099)	3	91	0.022846937
59	Regulation Of Receptor Internalization (GO:0002090)	2	36	0.023858926
60	Spliceosomal snRNP Assembly (GO:0000387)	2	37	0.025114097
61	Regulation Of Macroautophagy (GO:0016241)	3	96	0.026239527
62	Maturation Of SSU-rRNA (GO:0030490)	2	38	0.026395669
63	RNA Splicing (GO:0008380)	3	98	0.027668071
64	Negative Regulation Of Protein Secretion (GO:0050709)	2	39	0.02770324
65	Regulation Of Monoatomic Cation Transmembrane Transport (GO:1904062)	2	39	0.02770324
66	Negative Regulation Of Secretion By Cell (GO:1903531)	2	40	0.029036414
67	ncRNA Processing (GO:0034470)	3	100	0.029137374
68	Positive Regulation Of Viral Process (GO:0048524)	2	41	0.030394799
69	Negative Regulation Of Lens Fiber Cell Differentiation (GO:1902747)	1	5	0.03281375
70	Regulation Of Mast Cell Chemotaxis (GO:0060753)	1	5	0.03281375

71	Pentose-Phosphate Shunt, Non-Oxidative Branch (GO:0009052)	1	5	0.03281375
72	Regulation Of Protein Targeting (GO:1903533)	1	5	0.03281375
73	Peptidyl-Diphthamide Biosynthetic Process From Peptidyl-Histidine (GO:0017183)	1	5	0.03281375
74	Peptidyl-Diphthamide Metabolic Process (GO:0017182)	1	5	0.03281375
75	Plasma Membrane Raft Assembly (GO:0044854)	1	5	0.03281375
76	Plasma Membrane Raft Organization (GO:0044857)	1	5	0.03281375
77	Positive Regulation Of Activin Receptor Signaling Pathway (GO:0032927)	1	5	0.03281375
78	Positive Regulation Of Mitotic Cytokinesis (GO:1903490)	1	5	0.03281375
79	Insulin Processing (GO:0030070)	1	5	0.03281375
80	Ketone Body Biosynthetic Process (GO:0046951)	1	5	0.03281375
81	mRNA 3'-End Processing By Stem-Loop Binding And Cleavage (GO:0006398)	1	5	0.03281375
82	Morphogenesis Of An Endothelium (GO:0003159)	1	5	0.03281375
83	Regulation Of DNA Damage Response, Signal Transduction By P53 Class Mediator Resulting In Transcription Of P21 Class Mediator (GO:1902162)	1	5	0.03281375
84	Energy Derivation By Oxidation Of Organic Compounds (GO:0015980)	2	43	0.033185646
85	Regulation Of Cellular Component Size (GO:0032535)	2	43	0.033185646
86	Regulation Of G1/S Transition Of Mitotic Cell Cycle (GO:2000045)	3	106	0.03378876
87	RNA Processing (GO:0006396)	4	183	0.034005108
88	Regulation Of Viral Entry Into Host Cell (GO:0046596)	2	44	0.034617343
89	Establishment Of Protein Localization To Mitochondrion (GO:0072655)	2	44	0.034617343
90	Protein Modification By Small Protein Conjugation (GO:0032446)	6	364	0.034955598
91	Ubiquitin-Dependent Protein Catabolic Process (GO:0006511)	6	367	0.036157025
92	Regulation Of Epidermal Growth Factor Receptor Signaling Pathway (GO:0042058)	2	46	0.0375514
93	Positive Regulation Of Cell-Cell Adhesion (GO:0022409)	2	46	0.0375514
94	Regulation Of Signal Transduction By P53 Class Mediator (GO:1901796)	2	47	0.039053018
95	Regulation Of T Cell Differentiation (GO:0045580)	2	47	0.039053018
96	Regulation Of Lens Fiber Cell Differentiation (GO:1902746)	1	6	0.039247128
97	Response To Increased Oxygen Levels (GO:0036296)	1	6	0.039247128
98	Ribosomal Small Subunit Export From Nucleus (GO:0000056)	1	6	0.039247128
99	Positive Regulation Of Lymphocyte Apoptotic Process (GO:0070230)	1	6	0.039247128
100	Ganglioside Catabolic Process (GO:0006689)	1	6	0.039247128
101	Positive Regulation Of Pinocytosis (GO:0048549)	1	6	0.039247128
102	Positive Regulation Of Protein K63-linked Ubiquitination (GO:1902523)	1	6	0.039247128
103	Positive Regulation Of Protein Localization To Centrosome (GO:1904781)	1	6	0.039247128
104	Positive Regulation Of Toll-Like Receptor 3 Signaling Pathway (GO:0034141)	1	6	0.039247128
105	Ketone Body Metabolic Process (GO:1902224)	1	6	0.039247128
106	Leucine Metabolic Process (GO:0006551)	1	6	0.039247128
107	Oligosaccharide Metabolic Process (GO:0009311)	2	48	0.040577206
108	Regulation Of Mitotic Metaphase/Anaphase Transition (GO:0030071)	2	49	0.042123604
109	Negative Regulation Of Cysteine-Type Endopeptidase Activity Involved In Apoptotic Process (GO:0043154)	2	49	0.042123604
110	Ribosome Assembly (GO:0042255)	2	50	0.043691853
111	tRNA Processing (GO:0008033)	2	50	0.043691853
112	Intracellular Iron Ion Homeostasis (GO:0006879)	2	50	0.043691853
113	7-Methylguanosine Cap Hypermethylation (GO:0036261)	1	7	0.045638035
114	Negative Regulation Of Fatty Acid Oxidation (GO:0046322)	1	7	0.045638035

115	Regulation Of Cytoplasmic Translational Elongation (GO:1900247)	1	7	0.045638035
116	Regulation Of Establishment Of Protein Localization To Mitochondrion (GO:1903747)	1	7	0.045638035
117	Negative Regulation Of Mitochondrial Membrane Potential (GO:0010917)	1	7	0.045638035
118	RNA Capping (GO:0036260)	1	7	0.045638035
119	Regulation Of Oxidative Stress-Induced Cell Death (GO:1903201)	1	7	0.045638035
120	Blood Coagulation, Intrinsic Pathway (GO:0007597)	1	7	0.045638035
121	Peptidyl-Proline Hydroxylation To 4-hydroxy-L-proline (GO:0018401)	1	7	0.045638035
122	rRNA Pseudouridine Synthesis (GO:0031118)	1	7	0.045638035
123	Regulation Of Alpha-Beta T Cell Proliferation (GO:0046640)	1	7	0.045638035
124	Regulation Of Protein Localization To Nucleus (GO:1900180)	2	52	0.046892493
125	Negative Regulation Of Cysteine-Type Endopeptidase Activity (GO:2000117)	2	53	0.048524186

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	Term	Matched	Total	P.value
1	Regulation Of DNA-templated Transcription (GO:0006355)	47	1922	2.80E-08
2	Positive Regulation Of DNA-templated Transcription (GO:0045893)	35	1243	8.51E-08
3	Regulation Of Transcription By RNA Polymerase II (GO:0006357)	45	2028	9.46E-07
4	Positive Regulation Of Transcription By RNA Polymerase II (GO:0045944)	26	938	6.22E-06
5	Negative Regulation Of Nucleic Acid-Templated Transcription (GO:1903507)	17	456	6.95E-06
6	Regulation Of Gene Expression (GO:0010468)	29	1127	7.31E-06
7	Regulation Of Developmental Growth (GO:0048638)	5	29	1.18E-05
8	Inositol Lipid-Mediated Signaling (GO:0048017)	5	33	2.27E-05
9	Positive Regulation Of Developmental Process (GO:0051094)	11	233	3.74E-05
10	Phosphatidylinositol-Mediated Signaling (GO:0048015)	6	62	4.70E-05
11	Positive Regulation Of Cell Differentiation (GO:0045597)	12	283	4.74E-05
12	Negative Regulation Of DNA-templated Transcription (GO:0045892)	25	1025	7.83E-05
13	Mitral Valve Morphogenesis (GO:0003183)	3	9	9.15E-05
14	Regulation Of Cilium Assembly (GO:1902017)	6	71	0.000101242
15	Positive Regulation Of Autophagy (GO:0010508)	7	107	0.000136648
16	Positive Regulation Of Gene Expression (GO:0010628)	15	480	0.00017646
17	Positive Regulation Of Nucleic Acid-Templated Transcription (GO:1903508)	16	557	0.000278373
18	Toll-Like Receptor Signaling Pathway (GO:0002224)	4	31	0.00029756
19	Atrioventricular Valve Development (GO:0003171)	3	13	0.000301982
20	Selective Autophagy (GO:0061912)	5	58	0.000354792
21	Cellular Response To Starvation (GO:0009267)	7	126	0.000374227
22	Organelle Organization (GO:0006996)	13	418	0.000498619
23	Pharyngeal System Development (GO:0060037)	3	16	0.000577704
24	Regulation Of Phosphoprotein Phosphatase Activity (GO:0043666)	4	37	0.0005946
25	Ventricular Septum Development (GO:0003281)	4	37	0.0005946
26	Chromatin Remodeling (GO:0006338)	9	228	0.000706553

27	Negative Regulation Of Multicellular Organismal Process (GO:0051241)	9	231	0.000775315
28	UV Response Dn	7	144	0.000831182
29	Protein Phosphorylation (GO:0006468)	14	500	0.000856449
30	Regulation Of Microtubule-Based Process (GO:0032886)	4	41	0.000882364
31	Positive Regulation Of Cell Growth (GO:0030307)	6	106	0.000890233
32	Atrioventricular Valve Morphogenesis (GO:0003181)	3	19	0.000976692
33	Cardiac Ventricle Development (GO:0003231)	3	19	0.000976692
34	Regulation Of Autophagy Of Mitochondrion (GO:1903146)	3	19	0.000976692
35	Regulation Of Autophagy (GO:0010506)	9	241	0.001044988
36	Ear Development (GO:0043583)	2	5	0.001074631
37	Negative Regulation Of Microtubule Depolymerization (GO:0007026)	3	20	0.0011402
38	Positive Regulation Of NF-kappaB Transcription Factor Activity (GO:0051092)	7	152	0.001140262
39	Insulin Receptor Signaling Pathway (GO:0008286)	4	47	0.00147974
40	Positive Regulation Of Cellular Process (GO:0048522)	15	594	0.001581919
41	Aggrephagy (GO:0035973)	2	6	0.001600801
42	Establishment Of Mitotic Sister Chromatid Cohesion (GO:0034087)	2	6	0.001600801
43	Transcription-Dependent Tethering Of RNA Polymerase II Gene DNA At Nuclear Periphery (GO:0000972)	2	6	0.001600801
44	Pharyngeal Arch Artery Morphogenesis (GO:0061626)	2	6	0.001600801
45	Positive Regulation Of Growth (GO:0045927)	5	81	0.001633115
46	Endocardial Cushion Development (GO:0003197)	3	23	0.001730737
47	Negative Regulation Of Protein Depolymerization (GO:1901880)	3	23	0.001730737
48	Regulation Of Mitochondrion Organization (GO:0010821)	4	50	0.001864405
49	Regulation Of Microtubule Depolymerization (GO:0031114)	3	24	0.001962781
50	Regulation Of Protein Localization To Nucleus (GO:1900180)	4	52	0.002156226
51	Protein-Containing Complex Organization (GO:0043933)	6	126	0.002162795
52	Regulation Of Extent Of Cell Growth (GO:0061387)	2	7	0.002225638
53	Establishment Of Centrosome Localization (GO:0051660)	2	7	0.002225638
54	Mitral Valve Development (GO:0003174)	2	7	0.002225638
55	Positive Regulation Of Plasma Membrane Bounded Cell Projection Assembly (GO:0120034)	5	88	0.00235399
56	Positive Regulation Of Cell Migration (GO:0030335)	9	272	0.002394997
57	Ventricular Septum Morphogenesis (GO:0060412)	3	27	0.002771685
58	Regulation Of Androgen Receptor Signaling Pathway (GO:0060765)	3	27	0.002771685
59	Regulation Of Cell Growth (GO:0001558)	8	227	0.002816852
60	Pattern Recognition Receptor Signaling Pathway (GO:0002221)	4	56	0.002831581
61	Negative Regulation Of Transcription By RNA Polymerase II (GO:0000122)	17	763	0.002943076
62	Regulation Of Glial Cell Proliferation (GO:0060251)	2	8	0.002947031
63	Manganese Ion Transport (GO:0006828)	2	8	0.002947031
64	Positive Regulation Of Mitochondrial Calcium Ion Concentration (GO:0051561)	2	8	0.002947031
65	Negative Regulation Of Gene Expression (GO:0010629)	10	336	0.003013657
66	Regulation Of Protein Transport (GO:0051223)	3	28	0.003080473
67	JNK Cascade (GO:0007254)	3	29	0.003409568
68	Protein Acetylation (GO:0006473)	3	29	0.003409568
69	Negative Regulation Of Macromolecule Metabolic Process (GO:0010605)	7	186	0.003570636
70	Histone Acetylation (GO:0016573)	4	60	0.003639053

71	Artery Morphogenesis (GO:0048844)	3	30	0.003759377
72	Negative Regulation Of Carbohydrate Metabolic Process (GO:0045912)	3	30	0.003759377
73	Positive Regulation Of JUN Kinase Activity (GO:0043507)	3	30	0.003759377
74	I-kappaB Phosphorylation (GO:0007252)	2	9	0.003762903
75	Calcium Import Into The Mitochondrion (GO:0036444)	2	9	0.003762903
76	Iron Ion Transmembrane Transport (GO:0034755)	2	9	0.003762903
77	Microtubule Anchoring (GO:0034453)	2	9	0.003762903
78	Cellular Response To Insulin Stimulus (GO:0032869)	5	99	0.003917954
79	Regulation Of Gluconeogenesis (GO:0006111)	3	31	0.004130287
80	Negative Regulation Of Microtubule Polymerization Or Depolymerization (GO:0031111)	3	31	0.004130287
81	Regulation Of Cell Morphogenesis (GO:0022604)	3	31	0.004130287
82	Regulation Of Intracellular Signal Transduction (GO:1902531)	9	297	0.004277075
83	NIK/NF-kappaB Signaling (GO:0038061)	3	32	0.004522668
84	Phosphate Ion Transmembrane Transport (GO:0035435)	2	10	0.004671211
85	Mitotic Spindle	7	199	0.005154385
86	heme Metabolism	7	200	0.005295012
87	Exit From Mitosis (GO:0010458)	2	11	0.005669941
88	Regulation Of Axon Extension (GO:0030516)	3	35	0.005832038
89	Regulation Of Proteasomal Ubiquitin-Dependent Protein Catabolic Process (GO:0032434)	5	109	0.005884867
90	Regulation Of JNK Cascade (GO:0046328)	5	110	0.006113683
91	Negative Regulation Of Extrinsic Apoptotic Signaling Pathway (GO:2001237)	4	70	0.006309338
92	Regulation Of Notch Signaling Pathway (GO:0008593)	4	70	0.006309338
93	Myeloid Leukocyte Differentiation (GO:0002573)	4	71	0.006632104
94	Proteasome-Mediated Ubiquitin-Dependent Protein Catabolic Process (GO:0043161)	9	319	0.006748226
95	Cardiac Right Ventricle Morphogenesis (GO:0003215)	2	12	0.006757113
96	Negative Regulation Of Cardiac Muscle Hypertrophy (GO:0010614)	2	12	0.006757113
97	Negative Regulation Of Stem Cell Differentiation (GO:2000737)	2	12	0.006757113
98	Regulation Of Ossification (GO:0030278)	3	37	0.006818239
99	Negative Regulation Of Stress-Activated MAPK Cascade (GO:0032873)	3	37	0.006818239
100	Protein Acylation (GO:0043543)	3	37	0.006818239
101	Positive Regulation Of Signal Transduction (GO:0009967)	8	266	0.007231966
102	Negative Regulation Of Epithelial Cell Apoptotic Process (GO:1904036)	3	38	0.007346164
103	Chromatin Organization (GO:0006325)	8	268	0.007550738
104	Organelle Transport Along Microtubule (GO:0072384)	3	39	0.00789764
105	Positive Regulation Of Lymphocyte Differentiation (GO:0045621)	3	39	0.00789764
106	Cellular Response To Interleukin-4 (GO:0071353)	2	13	0.007930777
107	Mitochondrial Fission (GO:0000266)	2	13	0.007930777
108	Negative Regulation Of Viral Transcription (GO:0032897)	2	13	0.007930777
109	Positive Regulation Of Cardiac Muscle Cell Proliferation (GO:0060045)	2	13	0.007930777
110	Protein Import Into Peroxisome Matrix (GO:0016558)	2	13	0.007930777
111	Protein-Containing Complex Assembly (GO:0065003)	9	328	0.008027988
112	Regulation Of Fat Cell Differentiation (GO:0045598)	4	75	0.008032189
113	Regulation Of Plasma Membrane Bounded Cell Projection Assembly (GO:0120032)	4	75	0.008032189
114	Nucleosome Organization (GO:0034728)	4	75	0.008032189

115	Regulation Of Ras Protein Signal Transduction (GO:0046578)	4	76	0.008410181
116	Regulation Of Protein-Containing Complex Assembly (GO:0043254)	5	119	0.008461551
117	Regulation Of Glycolytic Process (GO:0006110)	3	40	0.008472897
118	Regulation Of Microtubule Cytoskeleton Organization (GO:0070507)	3	40	0.008472897
119	Aortic Valve Development (GO:0003176)	3	40	0.008472897
120	Establishment Or Maintenance Of Epithelial Cell Apical/Basal Polarity (GO:0045197)	3	40	0.008472897
121	Positive Regulation Of Stem Cell Population Maintenance (GO:1902459)	3	40	0.008472897
122	Lipoprotein Biosynthetic Process (GO:0042158)	2	14	0.009189016
123	Mitochondrial Calcium Ion Transmembrane Transport (GO:0006851)	2	14	0.009189016
124	Nuclear Pore Organization (GO:0006999)	2	14	0.009189016
125	Polarized Epithelial Cell Differentiation (GO:0030859)	2	14	0.009189016
126	Positive Regulation Of Protein-Containing Complex Disassembly (GO:0043243)	2	14	0.009189016
127	Regulation Of Carbohydrate Catabolic Process (GO:0043470)	2	14	0.009189016
128	Response To Insulin (GO:0032868)	4	79	0.00961348
129	Positive Regulation Of Catabolic Process (GO:0009896)	4	79	0.00961348
130	Cardiac Ventricle Morphogenesis (GO:0003208)	3	42	0.009695603
131	Stress-Activated MAPK Cascade (GO:0051403)	3	42	0.009695603
132	Protein Polyubiquitination (GO:0000209)	7	226	0.010061002
133	Intracellular Glucose Homeostasis (GO:0001678)	3	43	0.010343438
134	Regulation Of JUN Kinase Activity (GO:0043506)	3	43	0.010343438
135	Regulation Of Cellular Response To Heat (GO:1900034)	2	15	0.010529941
136	Activation Of NF-kappaB-inducing Kinase Activity (GO:0007250)	2	15	0.010529941
137	Regulation Of Multicellular Organism Growth (GO:0040014)	2	15	0.010529941
138	Positive Regulation Of Osteoblast Differentiation (GO:0045669)	3	44	0.011015827
139	Positive Regulation Of Ubiquitin-Dependent Protein Catabolic Process (GO:2000060)	4	83	0.011384429
140	Chromosome Organization (GO:0051276)	3	45	0.011712929
141	Mitotic Nuclear Division (GO:0140014)	3	45	0.011712929
142	Positive Regulation Of Double-Strand Break Repair (GO:2000781)	4	84	0.011857721
143	Cell Surface Receptor Signaling Pathway Involved In Heart Development (GO:0061311)	2	16	0.011951694
144	Vasculature Development (GO:0001944)	2	16	0.011951694
145	Mitophagy (GO:0000423)	2	16	0.011951694
146	Negative Regulation Of Anoikis (GO:2000811)	2	16	0.011951694
147	Positive Regulation Of Cardiac Muscle Tissue Growth (GO:0055023)	2	16	0.011951694
148	Regulation Of Cell Cycle Process (GO:0010564)	5	130	0.012098982
149	Protein Localization (GO:0008104)	9	351	0.012138455
150	Regulation Of Osteoblast Differentiation (GO:0045667)	4	85	0.012343465
151	Response To Glucose (GO:0009749)	3	46	0.012434886
152	Negative Regulation Of Cold-Induced Thermogenesis (GO:0120163)	3	46	0.012434886
153	Positive Regulation Of Peptide Hormone Secretion (GO:0090277)	3	46	0.012434886
154	Positive Regulation Of TOR Signaling (GO:0032008)	3	47	0.01318183
155	Regulation Of T Cell Differentiation (GO:0045580)	3	47	0.01318183
156	Negative Regulation Of Apoptotic Process (GO:0043066)	11	482	0.013227271
157	Glucose Homeostasis (GO:0042593)	4	87	0.013352749
158	Rac Protein Signal Transduction (GO:0016601)	2	17	0.013452446

159	Regulation Of Viral Transcription (GO:0046782)	2	17	0.013452446
160	Hippo Signaling (GO:0035329)	2	17	0.013452446
161	Positive Regulation Of SMAD Protein Signal Transduction (GO:0060391)	2	17	0.013452446
162	Regulation Of Double-Strand Break Repair (GO:2000779)	4	88	0.013876501
163	Retrograde Vesicle-Mediated Transport, Golgi To Endoplasmic Reticulum (GO:0006890)	3	48	0.013953877
164	Autophagy Of Mitochondrion (GO:0000422)	3	49	0.014751134
165	Positive Regulation Of Proteasomal Protein Catabolic Process (GO:1901800)	4	90	0.014962729
166	Endocytosis (GO:0006897)	6	189	0.014963465
167	Regulation Of Defense Response To Virus (GO:0050688)	2	18	0.015030399
168	Cardiac Atrium Morphogenesis (GO:0003209)	2	18	0.015030399
169	Cellular Response To Inorganic Substance (GO:0071241)	2	18	0.015030399
170	Endothelial Cell Proliferation (GO:0001935)	2	18	0.015030399
171	Heart Trabecula Morphogenesis (GO:0061384)	2	18	0.015030399
172	Mesenchyme Morphogenesis (GO:0072132)	2	18	0.015030399
173	Mitochondrial Fusion (GO:0008053)	2	18	0.015030399
174	Negative Regulation Of Nervous System Development (GO:0051961)	2	18	0.015030399
175	Regulation Of T Cell Cytokine Production (GO:0002724)	2	18	0.015030399
176	Positive Regulation Of DNA-binding Transcription Factor Activity (GO:0051091)	7	246	0.015437503
177	Positive Regulation Of Binding (GO:0051099)	4	91	0.0155254
178	Phosphorylation (GO:0016310)	10	429	0.015557043
179	Regulation Of Epithelial Cell Migration (GO:0010632)	3	50	0.015573694
180	Regulation Of TORC1 Signaling (GO:1903432)	3	50	0.015573694
181	Intracellular Calcium Ion Homeostasis (GO:0006874)	5	139	0.015769069
182	Regulation Of Cell Differentiation (GO:0045595)	6	193	0.016427384
183	Regulation Of Protein-Containing Complex Disassembly (GO:0043244)	2	19	0.016683781
184	Cellular Response To Lectin (GO:1990858)	2	19	0.016683781
185	Establishment Of Epithelial Cell Polarity (GO:0090162)	2	19	0.016683781
186	Stimulatory C-type Lectin Receptor Signaling Pathway (GO:0002223)	2	19	0.016683781
187	Mitotic Sister Chromatid Cohesion (GO:0007064)	2	19	0.016683781
188	Phosphate Ion Transport (GO:0006817)	2	19	0.016683781
189	Pore Complex Assembly (GO:0046931)	2	19	0.016683781
190	Rho Protein Signal Transduction (GO:0007266)	3	52	0.01729503
191	Cardiac Muscle Tissue Development (GO:0048738)	3	52	0.01729503
192	Regulation Of Proteolysis (GO:0030162)	3	52	0.01729503
193	Positive Regulation Of Protein Metabolic Process (GO:0051247)	6	196	0.017588236
194	Positive Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway (GO:0090100)	4	95	0.017908575
195	Actin Filament Organization (GO:0007015)	5	144	0.018097811
196	Actin Cytoskeleton Reorganization (GO:0031532)	3	53	0.018193935
197	Negative Regulation Of Metabolic Process (GO:0009892)	3	53	0.018193935
198	Protein Modification Process (GO:0036211)	14	711	0.018276502
199	Actin Filament-Based Transport (GO:0099515)	2	20	0.01841085
200	Regulation Of Necroptotic Process (GO:0060544)	2	20	0.01841085
201	Regulation Of Phosphatase Activity (GO:0010921)	2	20	0.01841085
202	Regulation Of Toll-Like Receptor Signaling Pathway (GO:0034121)	2	20	0.01841085

203	Stress-Activated Protein Kinase Signaling Cascade (GO:0031098)	2	20	0.01841085
204	Myoblast Differentiation (GO:0045445)	2	20	0.01841085
205	Negative Regulation Of Stem Cell Population Maintenance (GO:1902455)	2	20	0.01841085
206	Pulmonary Valve Development (GO:0003177)	2	20	0.01841085
207	Regulation Of Cardiac Muscle Cell Proliferation (GO:0060043)	2	20	0.01841085
208	Regulation Of Macroautophagy (GO:0016241)	4	96	0.018537916
209	Regulation Of Cold-Induced Thermogenesis (GO:0120161)	5	146	0.019089573
210	Regulation Of Myoblast Differentiation (GO:0045661)	3	54	0.019118396
211	Protein K63-linked Ubiquitination (GO:0070534)	3	54	0.019118396
212	TGF-beta Signaling	3	54	0.019118396
213	MAPK Cascade (GO:0000165)	4	98	0.019837405
214	Phosphatidylinositol Biosynthetic Process (GO:0006661)	4	98	0.019837405
215	Regulation Of Histone Deacetylation (GO:0031063)	2	21	0.020209892
216	Endocardial Cushion Morphogenesis (GO:0003203)	2	21	0.020209892
217	Macrophage Differentiation (GO:0030225)	2	21	0.020209892
218	Mitochondrial Calcium Ion Homeostasis (GO:0051560)	2	21	0.020209892
219	Negative Regulation Of miRNA Metabolic Process (GO:2000629)	2	21	0.020209892
220	Positive Regulation Of T Cell Cytokine Production (GO:0002726)	2	21	0.020209892
221	Positive Regulation Of Transcription Regulatory Region DNA Binding (GO:2000679)	2	21	0.020209892
222	Regulation Of Anoikis (GO:2000209)	2	21	0.020209892
223	Regulation Of Cardiac Conduction (GO:1903779)	2	21	0.020209892
224	Cellular Component Assembly (GO:0022607)	7	260	0.020248752
225	Negative Regulation Of DNA-binding Transcription Factor Activity (GO:0043433)	5	149	0.020643205
226	Regulation Of Stem Cell Population Maintenance (GO:2000036)	3	56	0.021044125
227	Cellular Response To Peptide (GO:1901653)	3	56	0.021044125
228	Fc-epsilon Receptor Signaling Pathway (GO:0038095)	2	22	0.022079221
229	Regulation Of Intracellular Steroid Hormone Receptor Signaling Pathway (GO:0033143)	2	22	0.022079221
230	Negative Regulation Of Cell Development (GO:0010721)	2	22	0.022079221
231	Negative Regulation Of Protein Localization To Nucleus (GO:1900181)	2	22	0.022079221
232	Organelle Fission (GO:0048285)	2	22	0.022079221
233	Positive Regulation Of Cilium Assembly (GO:0045724)	2	22	0.022079221
234	Regulation Of Canonical Wnt Signaling Pathway (GO:0060828)	6	207	0.022325341
235	mRNA Transport (GO:0051028)	3	58	0.023072382
236	Positive Regulation Of Mitochondrion Organization (GO:0010822)	3	58	0.023072382
237	Cellular Response To Growth Factor Stimulus (GO:0071363)	5	155	0.02399322
238	Response To BMP (GO:0071772)	2	23	0.024017177
239	Regulation Of Cardiac Muscle Hypertrophy (GO:0010611)	2	23	0.024017177
240	Regulation Of miRNA Transcription (GO:1902893)	3	59	0.024124967
241	Regulation Of Multicellular Organismal Development (GO:2000026)	3	59	0.024124967
242	Regulation Of Type I Interferon Production (GO:0032479)	3	59	0.024124967
243	Heart Morphogenesis (GO:0003007)	3	59	0.024124967
244	Negative Regulation Of Protein-Containing Complex Assembly (GO:0031333)	3	59	0.024124967
245	Positive Regulation Of Protein Binding (GO:0032092)	3	59	0.024124967
246	Negative Regulation Of MAPK Cascade (GO:0043409)	4	105	0.024821267

247	PI3K/AKT/mTOR Signaling	4	105	0.024821267
248	Regulation Of Extrinsic Apoptotic Signaling Pathway (GO:2001236)	3	60	0.025203176
249	Iron Ion Transport (GO:0006826)	2	24	0.026022126
250	Negative Regulation Of Cell Junction Assembly (GO:1901889)	2	24	0.026022126
251	Outflow Tract Septum Morphogenesis (GO:0003148)	2	24	0.026022126
252	Positive Regulation Of BMP Signaling Pathway (GO:0030513)	2	24	0.026022126
253	BMP Signaling Pathway (GO:0030509)	3	61	0.026306984
254	Response To Tumor Necrosis Factor (GO:0034612)	4	108	0.027168179
255	Fat Cell Differentiation (GO:0045444)	3	62	0.027436363
256	mRNA Export From Nucleus (GO:0006406)	3	62	0.027436363
257	Protein Lipidation (GO:0006497)	3	62	0.027436363
258	Protein-Containing Complex Disassembly (GO:0032984)	3	62	0.027436363
259	Positive Regulation Of Wnt Signaling Pathway (GO:0030177)	4	109	0.027978973
260	Regulation Of Wnt Signaling Pathway (GO:0030111)	4	109	0.027978973
261	Cellular Response To Hexose Stimulus (GO:0071331)	2	25	0.028092464
262	Osteoclast Differentiation (GO:0030316)	2	25	0.028092464
263	Positive Regulation Of Interleukin-2 Production (GO:0032743)	2	25	0.028092464
264	Protein Autophosphorylation (GO:0046777)	5	162	0.02832214
265	Proteasomal Protein Catabolic Process (GO:0010498)	6	220	0.028950898
266	Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0017015)	4	111	0.029643535
267	Negative Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway (GO:0090101)	4	111	0.029643535
268	Response To Metal Ion (GO:0010038)	3	64	0.029771661
269	Positive Regulation Of T Cell Differentiation (GO:0045582)	3	64	0.029771661
270	Positive Regulation Of Macroautophagy (GO:0016239)	3	64	0.029771661
271	Fc Receptor Signaling Pathway (GO:0038093)	2	26	0.030226609
272	Regulation Of Nucleotide-Excision Repair (GO:2000819)	2	26	0.030226609
273	Regulation Of Potassium Ion Transmembrane Transporter Activity (GO:1901016)	2	26	0.030226609
274	Dendritic Spine Organization (GO:0097061)	2	26	0.030226609
275	Establishment Or Maintenance Of Apical/Basal Cell Polarity (GO:0035088)	2	26	0.030226609
276	Organelle Fusion (GO:0048284)	2	26	0.030226609
277	Regulation Of Cardiac Muscle Cell Contraction (GO:0086004)	2	26	0.030226609
278	RNA Export From Nucleus (GO:0006405)	3	65	0.030977476
279	Autophagosome Assembly (GO:0000045)	3	65	0.030977476
280	Canonical Wnt Signaling Pathway (GO:0060070)	3	65	0.030977476
281	Regulation Of Cell-Matrix Adhesion (GO:0001952)	3	65	0.030977476
282	Regulation Of Cytokine Production (GO:0001817)	5	167	0.031698966
283	Regulation Of Cell Population Proliferation (GO:0042127)	14	766	0.031818956
284	Cellular Response To BMP Stimulus (GO:0071773)	3	66	0.032208653
285	Response To Endoplasmic Reticulum Stress (GO:0034976)	4	114	0.032248313
286	Regulation Of Microtubule Polymerization Or Depolymerization (GO:0031110)	2	27	0.032423008
287	Regulation Of Transcription Regulatory Region DNA Binding (GO:2000677)	2	27	0.032423008
288	Negative Regulation Of Notch Signaling Pathway (GO:0045746)	2	27	0.032423008
289	Positive Regulation Of TORC1 Signaling (GO:1904263)	2	27	0.032423008
290	Positive Regulation Of Filopodium Assembly (GO:0051491)	2	27	0.032423008

291	Positive Regulation Of Ubiquitin-Protein Transferase Activity (GO:0051443)	2	27	0.032423008
292	Regulation Of SMAD Protein Signal Transduction (GO:0060390)	2	27	0.032423008
293	Regulation Of Sodium Ion Transmembrane Transport (GO:1902305)	2	28	0.03468013
294	Regulation Of Cardiac Muscle Cell Action Potential (GO:0098901)	2	28	0.03468013
295	Cellular Response To Oxidative Stress (GO:0034599)	4	117	0.034983265
296	Regulation Of Protein Binding (GO:0043393)	4	118	0.035923941
297	Regulation Of Heart Contraction (GO:0008016)	3	69	0.036053601
298	Positive Regulation Of Cellular Biosynthetic Process (GO:0031328)	5	174	0.036834209
299	Cellular Response To Tumor Necrosis Factor (GO:0071356)	4	119	0.036879156
300	Regulation Of Neuron Migration (GO:2001222)	2	29	0.036996473
301	Chondrocyte Differentiation (GO:0002062)	2	29	0.036996473
302	mRNA Splice Site Recognition (GO:0006376)	2	29	0.036996473
303	Negative Regulation Of Epithelial Cell Proliferation (GO:0050680)	3	70	0.037385436
304	Negative Regulation Of Supramolecular Fiber Organization (GO:1902904)	3	71	0.038742203
305	Innate Immune Response Activating Cell Surface Receptor Signaling Pathway (GO:0002220)	2	30	0.039370555
306	Positive Regulation Of Protein Targeting To Mitochondrion (GO:1903955)	2	30	0.039370555
307	Positive Regulation Of Macromolecule Biosynthetic Process (GO:0010557)	4	122	0.039832135
308	Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0007179)	3	72	0.040123795
309	Positive Regulation Of Protein Localization To Nucleus (GO:1900182)	3	72	0.040123795
310	Regulation Of Cell Migration (GO:0030334)	9	434	0.040279723
311	Ubiquitin-Dependent Protein Catabolic Process (GO:0006511)	8	367	0.04048071
312	Positive Regulation Of Epithelial Cell Proliferation (GO:0050679)	4	123	0.040845595
313	Import Into Nucleus (GO:0051170)	3	74	0.042961
314	Regulation Of Cell Cycle G1/S Phase Transition (GO:1902806)	3	74	0.042961
315	Cholesterol Homeostasis	3	74	0.042961
316	Positive Regulation Of Intracellular Protein Transport (GO:0090316)	4	126	0.04397339
317	Regulation Of Metaphase/Anaphase Transition Of Cell Cycle (GO:1902099)	2	32	0.044286144
318	Gluconeogenesis (GO:0006094)	2	32	0.044286144
319	Negative Regulation Of Fat Cell Differentiation (GO:0045599)	2	32	0.044286144
320	Negative Regulation Of Proteasomal Ubiquitin-Dependent Protein Catabolic Process (GO:0032435)	2	32	0.044286144
321	Phosphatidylinositol 3-Kinase Signaling (GO:0014065)	2	32	0.044286144
322	Positive Regulation Of Telomere Maintenance Via Telomerase (GO:0032212)	2	32	0.044286144
323	Protein Transmembrane Import Into Intracellular Organelle (GO:0044743)	2	32	0.044286144
324	Notch Signaling	2	32	0.044286144
325	Regulation Of BMP Signaling Pathway (GO:0030510)	3	75	0.044416369
326	Regulation Of Anatomical Structure Morphogenesis (GO:0022603)	4	127	0.045045115
327	Positive Regulation Of Protein Secretion (GO:0050714)	3	76	0.045896077
328	Regulation Of Potassium Ion Transmembrane Transport (GO:1901379)	2	33	0.046824811
329	Ventricular Cardiac Muscle Tissue Morphogenesis (GO:0055010)	2	33	0.046824811
330	Monoubiquitinated Protein Deubiquitination (GO:0035520)	2	33	0.046824811
331	Negative Regulation Of Small Molecule Metabolic Process (GO:0062014)	2	33	0.046824811
332	Positive Regulation Of RNA Metabolic Process (GO:0051254)	2	33	0.046824811
333	Positive Regulation Of Cytokine Production Involved In Immune Response (GO:0002720)	2	33	0.046824811
334	Positive Regulation Of Establishment Of Protein Localization To Mitochondrion (GO:1903749)	2	33	0.046824811

335	Positive Regulation Of Release Of Sequestered Calcium Ion Into Cytosol (GO:0051281)	2	33	0.046824811
336	Positive Regulation Of Telomerase Activity (GO:0051973)	2	33	0.046824811
337	Regulation Of G0 To G1 Transition (GO:0070316)	2	33	0.046824811
338	Regulation Of DNA Repair (GO:0006282)	4	129	0.047232207
339	Embryonic Organ Development (GO:0048568)	3	77	0.047399989
340	Negative Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0030512)	3	77	0.047399989
341	Positive Regulation Of JNK Cascade (GO:0046330)	3	77	0.047399989
342	Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway (GO:0007178)	4	130	0.048347548
343	Negative Regulation Of Programmed Cell Death (GO:0043069)	8	381	0.048521402
344	Cellular Response To Nutrient Levels (GO:0031669)	3	78	0.048927963
345	Negative Regulation Of Protein Modification Process (GO:0031400)	3	78	0.048927963
346	Cellular Response To Amyloid-Beta (GO:1904646)	2	34	0.04941554
347	Cellular Response To Glucose Stimulus (GO:0071333)	2	34	0.04941554
348	Response To Estrogen (GO:0043627)	2	34	0.04941554
349	Establishment Of Mitotic Spindle Localization (GO:0040001)	2	34	0.04941554
350	Transcription Initiation-Coupled Chromatin Remodeling (GO:0045815)	2	34	0.04941554
351	Positive Regulation Of Organelle Organization (GO:0010638)	2	34	0.04941554
352	Regulation Of DNA Biosynthetic Process (GO:2000278)	2	34	0.04941554
353	Defense Response To Virus (GO:0051607)	5	189	0.049475576
354	Regulation Of Nucleic Acid-Templated Transcription (GO:1903506)	9	452	0.049776102

[G5 goblet Up]

	Term	Matched	Total	P.value
1	Negative Regulation Of Organelle Assembly (GO:1902116)	4	36	0.000104691
2	Regulation Of Stress Granule Assembly (GO:0062028)	2	5	0.000459552
3	Cellular Response To Interleukin-6 (GO:0071354)	3	23	0.000503658
4	Phosphatidylethanolamine Metabolic Process (GO:0046337)	3	25	0.000647585
5	Negative Regulation Of Centriole Replication (GO:0046600)	2	6	0.000686233
6	Endocytic Recycling (GO:0032456)	4	64	0.000973807
7	Endosomal Transport (GO:0016197)	6	180	0.001518704
8	Peptidyl-Serine Dephosphorylation (GO:0070262)	2	9	0.001624891
9	CRD-mediated mRNA Stabilization (GO:0070934)	2	10	0.002022009
10	Negative Regulation Of Centrosome Duplication (GO:0010826)	2	10	0.002022009
11	Wound Healing (GO:0042060)	4	80	0.002228141
12	Negative Regulation Of Nuclear-Transcribed mRNA Catabolic Process, Deadenylation-Dependent Decay (GO:1900152)	2	11	0.002460272
13	G2-M Checkpoint	6	200	0.002579813
14	Response To Interleukin-6 (GO:0070741)	2	12	0.002939106

15	Positive Regulation Of Cell Adhesion (GO:0045785)	4	88	0.003149992
16	Negative Regulation Of Endoplasmic Reticulum Unfolded Protein Response (GO:1900102)	2	13	0.003457942
17	Protein Modification Process (GO:0036211)	12	711	0.003600411
18	Positive Regulation Of Cytoplasmic Translation (GO:2000767)	2	14	0.004016219
19	Cellular Response To Growth Factor Stimulus (GO:0071363)	5	155	0.004313196
20	Negative Regulation Of ERK1 And ERK2 Cascade (GO:0070373)	3	48	0.004342085
21	Receptor Recycling (GO:0001881)	2	17	0.005922153
22	Positive Regulation Of Translation (GO:0045727)	4	108	0.006519322
23	Regulation Of Centriole Replication (GO:0046599)	2	19	0.007379922
24	Regulation Of Multicellular Organismal Development (GO:2000026)	3	59	0.007727854
25	Phosphatidylserine Metabolic Process (GO:0006658)	2	20	0.008163347
26	Cellular Response To Estradiol Stimulus (GO:0071392)	2	20	0.008163347
27	Negative Regulation Of Kinase Activity (GO:0033673)	3	62	0.008857856
28	Positive Regulation Of Viral Life Cycle (GO:1903902)	2	22	0.009836664
29	Protein Dephosphorylation (GO:0006470)	4	124	0.010498363
30	Regulation Of Nuclear-Transcribed mRNA Catabolic Process, Deadenylation-Dependent Decay (GO:1900151)	2	23	0.010725525
31	Diacylglycerol Metabolic Process (GO:0046339)	2	23	0.010725525
32	Positive Regulation Of DNA-templated Transcription (GO:0045893)	16	1243	0.011072402
33	Regulation Of Cytoplasmic Translation (GO:2000765)	2	24	0.011648509
34	Stress Granule Assembly (GO:0034063)	2	24	0.011648509
35	Proteoglycan Metabolic Process (GO:0006029)	2	25	0.012605114
36	Cellular Response To Epidermal Growth Factor Stimulus (GO:0071364)	2	27	0.014617205
37	Negative Regulation Of Cellular Biosynthetic Process (GO:0031327)	4	137	0.014688921
38	Alpha-Amino Acid Metabolic Process (GO:1901605)	2	29	0.016757884
39	Positive Regulation Of Viral Genome Replication (GO:0045070)	2	29	0.016757884
40	Regulation Of Cell Cycle (GO:0051726)	6	298	0.016879519
41	Response To Epidermal Growth Factor (GO:0070849)	2	30	0.017875243
42	Lamellipodium Organization (GO:0097581)	2	30	0.017875243
43	Dephosphorylation (GO:0016311)	4	147	0.018542533
44	Response To Estradiol (GO:0032355)	2	31	0.019023318
45	Vesicle-Mediated Transport To The Plasma Membrane (GO:0098876)	3	83	0.019403252
46	Notch Signaling	2	32	0.020201642
47	Positive Regulation Of Amide Metabolic Process (GO:0034250)	3	85	0.020654216
48	Cellular Response To Organic Cyclic Compound (GO:0071407)	4	152	0.020683516
49	Protein Targeting To Vacuole (GO:0006623)	2	34	0.022647195
50	Intracellular Protein Transport (GO:0006886)	6	325	0.024613039
51	Protein Autophosphorylation (GO:0046777)	4	162	0.025406214

52	Regulation Of ERK1 And ERK2 Cascade (GO:0070372)	5	244	0.026481055
53	Retrograde Transport, Endosome To Golgi (GO:0042147)	3	94	0.026820942
54	Vesicle Organization (GO:0016050)	3	94	0.026820942
55	Positive Regulation Of Transcription By RNA Polymerase II (GO:0045944)	12	938	0.027659798
56	Response To Transforming Growth Factor Beta (GO:0071559)	2	38	0.027881288
57	Positive Regulation Of Protein Tyrosine Kinase Activity (GO:0061098)	2	38	0.027881288
58	Nuclear-Transcribed mRNA Catabolic Process, Deadenylation-Dependent Decay (GO:0000288)	2	39	0.029258691
59	Regulation Of Protein Tyrosine Kinase Activity (GO:0061097)	2	39	0.029258691
60	Positive Regulation Of Monoatomic Ion Transport (GO:0043270)	2	40	0.03066278
61	Negative Regulation Of mRNA Catabolic Process (GO:1902373)	2	41	0.032093132
62	Regulation Of Microtubule-Based Process (GO:0032886)	2	41	0.032093132
63	Positive Regulation Of Viral Process (GO:0048524)	2	41	0.032093132
64	Positive Regulation Of Calcium Ion Transmembrane Transport (GO:1904427)	2	42	0.033549325
65	DNA Replication-Dependent Chromatin Assembly (GO:0006335)	1	5	0.033787114
66	ERBB2-EGFR Signaling Pathway (GO:0038134)	1	5	0.033787114
67	Regulation Of Hyaluronan Biosynthetic Process (GO:1900125)	1	5	0.033787114
68	Regulation Of Interleukin-1-Mediated Signaling Pathway (GO:2000659)	1	5	0.033787114
69	Negative Regulation Of Protein Kinase Activity By Regulation Of Protein Phosphorylation (GO:0044387)	1	5	0.033787114
70	Negative Regulation Of Vitamin Metabolic Process (GO:0046137)	1	5	0.033787114
71	Bundle Of His cell-Purkinje Myocyte Adhesion Involved In Cell Communication (GO:0086073)	1	5	0.033787114
72	Regulation Of Protein Deubiquitination (GO:0090085)	1	5	0.033787114
73	Peptidyl-Diphthamide Biosynthetic Process From Peptidyl-Histidine (GO:0017183)	1	5	0.033787114
74	Peptidyl-Diphthamide Metabolic Process (GO:0017182)	1	5	0.033787114
75	Pexophagy (GO:0000425)	1	5	0.033787114
76	Phagosome Acidification (GO:0090383)	1	5	0.033787114
77	Regulation Of Vitamin D Biosynthetic Process (GO:0060556)	1	5	0.033787114
78	Dermatan Sulfate Metabolic Process (GO:0030205)	1	5	0.033787114
79	Dermatan Sulfate Proteoglycan Metabolic Process (GO:0050655)	1	5	0.033787114
80	Detection Of Virus (GO:0009597)	1	5	0.033787114
81	Positive Regulation Of Osteoblast Proliferation (GO:0033690)	1	5	0.033787114
82	Heparan Sulfate Proteoglycan Catabolic Process (GO:0030200)	1	5	0.033787114
83	Kidney Morphogenesis (GO:0060993)	1	5	0.033787114
84	Negative Regulation Of Axon Regeneration (GO:0048681)	1	5	0.033787114
85	Negative Regulation Of Cardiac Muscle Cell Differentiation (GO:2000726)	1	5	0.033787114
86	Regulation Of Calcdiol 1-Monooxygenase Activity (GO:0060558)	1	5	0.033787114
87	Negative Regulation Of Cellular Response To Hypoxia (GO:1900038)	1	5	0.033787114
88	Regulation Of Chromosome Organization (GO:0033044)	2	43	0.035030946

89	Regulation Of Endothelial Cell Apoptotic Process (GO:2000351)	2	43	0.035030946
90	Positive Regulation Of Cell-Matrix Adhesion (GO:0001954)	2	43	0.035030946
91	Regulation Of Cellular Component Size (GO:0032535)	2	43	0.035030946
92	RNA Splicing, Via Transesterification Reactions With Bulged Adenosine As Nucleophile (GO:0000377)	4	180	0.035427196
93	Negative Regulation Of MAPK Cascade (GO:0043409)	3	105	0.035546956
94	Regulation Of Nucleic Acid-Templated Transcription (GO:1903506)	7	452	0.036228892
95	Mitotic Spindle Assembly (GO:0090307)	2	44	0.036537583
96	Positive Regulation Of Nucleic Acid-Templated Transcription (GO:1903508)	8	557	0.038053176
97	Epidermal Growth Factor Receptor Signaling Pathway (GO:0007173)	2	45	0.038068828
98	Glycerophospholipid Biosynthetic Process (GO:0046474)	3	108	0.038151193
99	Regulation Of Cellular Response To Hypoxia (GO:1900037)	1	6	0.040407308
100	ATF6-mediated Unfolded Protein Response (GO:0036500)	1	6	0.040407308
101	Regulation Of Collagen Fibril Organization (GO:1904026)	1	6	0.040407308
102	Regulation Of Glial Cell Differentiation (GO:0045685)	1	6	0.040407308
103	Negative Regulation Of Neuron Projection Regeneration (GO:0070571)	1	6	0.040407308
104	Regulation Of Histamine Secretion By Mast Cell (GO:1903593)	1	6	0.040407308
105	SMAD Protein Complex Assembly (GO:0007183)	1	6	0.040407308
106	Adenosine To Inosine Editing (GO:0006382)	1	6	0.040407308
107	Regulation Of Microtubule Binding (GO:1904526)	1	6	0.040407308
108	Atrioventricular Valve Formation (GO:0003190)	1	6	0.040407308
109	Cardiac Muscle Cell-Cardiac Muscle Cell Adhesion (GO:0086042)	1	6	0.040407308
110	Regulation Of Saliva Secretion (GO:0046877)	1	6	0.040407308
111	Regulation Of Transforming Growth Factor Beta2 Production (GO:0032909)	1	6	0.040407308
112	Positive Regulation Of Aspartic-Type Endopeptidase Activity Involved In Amyloid Precursor Protein Catabolic Process (GO:1902961)	1	6	0.040407308
113	Response To Lead Ion (GO:0010288)	1	6	0.040407308
114	Desmosome Organization (GO:0002934)	1	6	0.040407308
115	Positive Regulation Of Kidney Development (GO:0090184)	1	6	0.040407308
116	Histidine Catabolic Process (GO:0006548)	1	6	0.040407308
117	Histidine Metabolic Process (GO:0006547)	1	6	0.040407308
118	Protein Import Into Peroxisome Matrix, Receptor Recycling (GO:0016562)	1	6	0.040407308
119	Proteoglycan Catabolic Process (GO:0030167)	1	6	0.040407308
120	RNA Metabolic Process (GO:0016070)	3	111	0.040850355
121	Mitotic Sister Chromatid Segregation (GO:0000070)	3	111	0.040850355
122	Epithelial To Mesenchymal Transition (GO:0001837)	2	47	0.04120354
123	Cytoplasmic Microtubule Organization (GO:0031122)	2	48	0.042806215
124	Modification-Dependent Protein Catabolic Process (GO:0019941)	4	192	0.04321398
125	Positive Regulation Of miRNA Metabolic Process (GO:2000630)	2	49	0.044431915

126	Mitotic Metaphase Plate Congression (GO:0007080)	2	50	0.046080253
127	Regulation Of Cytoplasmic Translational Elongation (GO:1900247)	1	7	0.046982473
128	Negative Regulation Of Lipid Kinase Activity (GO:0090219)	1	7	0.046982473
129	Negative Regulation Of Monooxygenase Activity (GO:0032769)	1	7	0.046982473
130	Negative Regulation Of Muscle Hypertrophy (GO:0014741)	1	7	0.046982473
131	Cellular Response To Angiotensin (GO:1904385)	1	7	0.046982473
132	Cellular Response To Interferon-Alpha (GO:0035457)	1	7	0.046982473
133	Plasma Membrane To Endosome Transport (GO:0048227)	1	7	0.046982473
134	Positive Regulation Of DNA Demethylation (GO:1901537)	1	7	0.046982473
135	Positive Regulation Of Aspartic-Type Peptidase Activity (GO:1905247)	1	7	0.046982473
136	Positive Regulation Of Attachment Of Mitotic Spindle Microtubules To Kinetochore (GO:1902425)	1	7	0.046982473
137	Dermatan Sulfate Proteoglycan Biosynthetic Process (GO:0050651)	1	7	0.046982473
138	Diacylglycerol Biosynthetic Process (GO:0006651)	1	7	0.046982473
139	Positive Regulation Of Isomerase Activity (GO:0010912)	1	7	0.046982473
140	Monosaccharide Biosynthetic Process (GO:0046364)	1	7	0.046982473
141	Regulation Of Attachment Of Mitotic Spindle Microtubules To Kinetochore (GO:1902423)	1	7	0.046982473
142	SMAD Protein Signal Transduction (GO:0060395)	2	51	0.04775085
143	Metaphase Plate Congression (GO:0051310)	2	51	0.04775085
144	Positive Regulation Of Telomere Maintenance (GO:0032206)	2	52	0.049443327

[G6 goblet Down]

	Term	Matched	Total	P.value
1	Monoatomic Cation Transmembrane Transport (GO:0098655)	7	281	0.000496398
2	Galactosylceramide Metabolic Process (GO:0006681)	2	7	0.00050119
3	Protein Retention In ER Lumen (GO:0006621)	2	7	0.00050119
4	Cellular Response To Cholesterol (GO:0071397)	2	10	0.001063621
5	Maintenance Of Protein Localization In Endoplasmic Reticulum (GO:0035437)	2	11	0.001295792
6	Cotranslational Protein Targeting To Membrane (GO:0006613)	2	13	0.001825848
7	Intracellular Sterol Transport (GO:0032366)	2	15	0.002442074
8	Cellular Response To Sterol (GO:0036315)	2	15	0.002442074
9	Inorganic Cation Transmembrane Transport (GO:0098662)	6	284	0.002892204
10	Intracellular Lipid Transport (GO:0032365)	2	18	0.003524226
11	Response To Cholesterol (GO:0070723)	2	18	0.003524226
12	Regulation Of Cardiac Conduction (GO:1903779)	2	21	0.004790701
13	Protein Targeting To ER (GO:0045047)	2	23	0.005734661
14	Chloride Transport (GO:0006821)	3	77	0.006603442

15	Sterol Transport (GO:0015918)	2	25	0.006756442
16	Calcium Ion Transmembrane Transport (GO:0070588)	3	80	0.007338228
17	Calcium Ion Homeostasis (GO:0055074)	3	102	0.014186572
18	Calcium Ion Transport (GO:0006816)	3	112	0.018179053
19	Branching Morphogenesis Of An Epithelial Tube (GO:0048754)	2	42	0.018363945
20	Chloride Transmembrane Transport (GO:1902476)	2	48	0.023602999
21	Retrograde Vesicle-Mediated Transport, Golgi To Endoplasmic Reticulum (GO:0006890)	2	48	0.023602999
22	Galactolipid Biosynthetic Process (GO:0019375)	1	5	0.024508444
23	Galactosylceramide Biosynthetic Process (GO:0006682)	1	5	0.024508444
24	Glycoside Metabolic Process (GO:0016137)	1	5	0.024508444
25	Glycosyl Compound Catabolic Process (GO:1901658)	1	5	0.024508444
26	Regulation Of Hydrogen Peroxide Metabolic Process (GO:0010310)	1	5	0.024508444
27	Glycosylceramide Catabolic Process (GO:0046477)	1	5	0.024508444
28	Glycosylceramide Metabolic Process (GO:0006677)	1	5	0.024508444
29	Venous Blood Vessel Morphogenesis (GO:0048845)	1	5	0.024508444
30	Hexose Catabolic Process (GO:0019320)	1	5	0.024508444
31	Histamine Metabolic Process (GO:0001692)	1	5	0.024508444
32	Regulation Of Mitotic Spindle Checkpoint (GO:1903504)	1	5	0.024508444
33	Positive Regulation Of Vascular Associated Smooth Muscle Cell Differentiation (GO:1905065)	1	5	0.024508444
34	Nucleoside Transport (GO:0015858)	1	5	0.024508444
35	Pentose-Phosphate Shunt, Non-Oxidative Branch (GO:0009052)	1	5	0.024508444
36	Positive Regulation Of T Cell Differentiation In Thymus (GO:0033089)	1	5	0.024508444
37	Glycoprotein Metabolic Process (GO:0009100)	2	53	0.028379286
38	Cellular Response To Alcohol (GO:0097306)	2	53	0.028379286
39	Spinal Cord Dorsal/Ventral Patterning (GO:0021513)	1	6	0.029338317
40	Galactose Metabolic Process (GO:0006012)	1	6	0.029338317
41	Vascular Associated Smooth Muscle Cell Development (GO:0097084)	1	6	0.029338317
42	Glycosylceramide Biosynthetic Process (GO:0046476)	1	6	0.029338317
43	Positive Regulation Of Striated Muscle Contraction (GO:0045989)	1	6	0.029338317
44	Norepinephrine Transport (GO:0015874)	1	6	0.029338317
45	Catecholamine Uptake (GO:0090493)	1	6	0.029338317
46	Regulation Of Smooth Muscle Cell Differentiation (GO:0051150)	1	6	0.029338317
47	Response To Increased Oxygen Levels (GO:0036296)	1	6	0.029338317
48	Dendrite Arborization (GO:0140059)	1	6	0.029338317
49	Dorsal Aorta Development (GO:0035907)	1	6	0.029338317
50	Dorsal Aorta Morphogenesis (GO:0035912)	1	6	0.029338317
51	Monoatomic Anion Transmembrane Transport (GO:0098656)	2	54	0.02937733
52	Regulation Of Epithelial To Mesenchymal Transition Involved In Endocardial Cushion Formation (GO:1905005)	1	7	0.034144519
53	Glycoside Catabolic Process (GO:0016139)	1	7	0.034144519
54	Venous Blood Vessel Development (GO:0060841)	1	7	0.034144519
55	Ventricular Trabecula Myocardium Morphogenesis (GO:0003222)	1	7	0.034144519
56	Neuron Projection Arborization (GO:0140058)	1	7	0.034144519
57	Regulation Of Positive Chemotaxis (GO:0050926)	1	7	0.034144519
58	Cardiac Atrium Development (GO:0003230)	1	7	0.034144519

59	Protein Deglycosylation (GO:0006517)	1	7	0.034144519
60	Osteoblast Development (GO:0002076)	1	7	0.034144519
61	Catecholamine Transport (GO:0051937)	1	7	0.034144519
62	Proximal/Distal Pattern Formation (GO:0009954)	1	7	0.034144519
63	Positive Regulation Of Cardiac Epithelial To Mesenchymal Transition (GO:0062043)	1	7	0.034144519
64	Negative Regulation Of Appetite (GO:0032099)	1	7	0.034144519
65	Dopamine Uptake (GO:0090494)	1	7	0.034144519
66	Epithelial To Mesenchymal Transition Involved In Endocardial Cushion Formation (GO:0003198)	1	8	0.038927164
67	Negative Regulation Of Mitotic Nuclear Division (GO:0045839)	1	8	0.038927164
68	Vascular Associated Smooth Muscle Cell Differentiation (GO:0035886)	1	8	0.038927164
69	Negative Regulation Of Ubiquitin Protein Ligase Activity (GO:1904667)	1	8	0.038927164
70	Regulation Of Mitotic Sister Chromatid Segregation (GO:0033047)	1	8	0.038927164
71	Neurotransmitter Reuptake (GO:0098810)	1	8	0.038927164
72	Nicotinamide Nucleotide Biosynthetic Process (GO:0019359)	1	8	0.038927164
73	Cobalamin Transport (GO:0015889)	1	8	0.038927164
74	Serotonin Uptake (GO:0051610)	1	8	0.038927164
75	Inorganic Anion Transmembrane Transport (GO:0098661)	2	63	0.038965778
76	Golgi Lumen Acidification (GO:0061795)	1	9	0.043686365
77	Toxin Transport (GO:1901998)	1	9	0.043686365
78	Negative Regulation Of Protein Autophosphorylation (GO:0031953)	1	9	0.043686365
79	Aminoglycan Metabolic Process (GO:0006022)	1	9	0.043686365
80	Calcium Ion Transport Into Cytosol (GO:0060402)	1	9	0.043686365
81	Oligosaccharide Catabolic Process (GO:0009313)	1	9	0.043686365
82	Cellular Response To Oxygen Levels (GO:0071453)	1	9	0.043686365
83	Monoatomic Anion Homeostasis (GO:0055081)	1	9	0.043686365
84	Chloride Ion Homeostasis (GO:0055064)	1	9	0.043686365
85	Chondroitin Sulfate Proteoglycan Metabolic Process (GO:0050654)	1	9	0.043686365
86	Dopamine Transport (GO:0015872)	1	9	0.043686365
87	Serotonin Transport (GO:0006837)	1	9	0.043686365
88	Smooth Muscle Tissue Development (GO:0048745)	1	9	0.043686365
89	Regulation Of Heart Contraction (GO:0008016)	2	69	0.045927474
90	Neutrophil Chemotaxis (GO:0030593)	2	70	0.047129284
91	Nitrogen Compound Transport (GO:0071705)	3	163	0.047272011
92	SRP-dependent Cotranslational Protein Targeting To Membrane (GO:0006614)	1	10	0.048422237
93	Regulation Of Mitotic Sister Chromatid Separation (GO:0010965)	1	10	0.048422237
94	Regulation Of Respiratory Burst (GO:0060263)	1	10	0.048422237
95	Cellular Response To Increased Oxygen Levels (GO:0036295)	1	10	0.048422237
96	Monoamine Transport (GO:0015844)	1	10	0.048422237
97	Sarcoplasmic Reticulum Calcium Ion Transport (GO:0070296)	1	10	0.048422237
98	Regulation Of Cardiac Muscle Cell Apoptotic Process (GO:0010665)	1	10	0.048422237

[G7 ciliated Up]

	Term	Matched	Total	P.value
1	Regulation Of Neurotransmitter Receptor Activity (GO:0099601)	4	42	0.001974685
2	Maintenance Of Protein Location In Extracellular Region (GO:0071694)	2	6	0.002348162
3	Regulation Of AMPA Receptor Activity (GO:2000311)	3	24	0.003400877
4	Negative Regulation Of Cell Projection Organization (GO:0031345)	4	50	0.003752914
5	Positive Regulation Of ATP Biosynthetic Process (GO:2001171)	2	8	0.004309962
6	Positive Regulation Of Calcium Ion-Dependent Exocytosis (GO:0045956)	2	8	0.004309962
7	Tetrahydrofolate Interconversion (GO:0035999)	2	8	0.004309962
8	Positive Regulation Of Filopodium Assembly (GO:0051491)	3	27	0.004778611
9	Synaptic Transmission, Glutamatergic (GO:0035249)	3	27	0.004778611
10	Negative Regulation Of Neuron Projection Development (GO:0010977)	4	54	0.004953511
11	Enzyme-Linked Receptor Protein Signaling Pathway (GO:0007167)	6	124	0.005176692
12	Positive Regulation Of ATP Metabolic Process (GO:1903580)	2	9	0.005494938
13	Sequestering Of Extracellular Ligand From Receptor (GO:0035581)	2	9	0.005494938
14	Error-Prone Translesion Synthesis (GO:0042276)	2	9	0.005494938
15	Cellular Response To Cytokine Stimulus (GO:0071345)	10	308	0.00637662
16	Negative Regulation Of Adenylate Cyclase Activity (GO:0007194)	2	10	0.006811166
17	Tetrahydrofolate Metabolic Process (GO:0046653)	2	11	0.008255134
18	Negative Regulation Of Cyclase Activity (GO:0031280)	2	11	0.008255134
19	Positive Regulation Of Purine Nucleotide Biosynthetic Process (GO:1900373)	2	12	0.009823395
20	Positive Regulation Of Regulated Secretory Pathway (GO:1903307)	2	12	0.009823395
21	Action Potential (GO:0001508)	3	35	0.009923264
22	Glutamate Receptor Signaling Pathway (GO:0007215)	3	35	0.009923264
23	Nervous System Development (GO:0007399)	12	433	0.009955076
24	Monoatomic Cation Transmembrane Transport (GO:0098655)	9	281	0.010263108
25	Actin Filament Organization (GO:0007015)	6	144	0.010484797
26	Inorganic Cation Transmembrane Transport (GO:0098662)	9	284	0.010946787
27	Negative Regulation Of Lyase Activity (GO:0051350)	2	13	0.011512571
28	Response To Chemokine (GO:1990868)	2	13	0.011512571
29	Protein Glycosylation (GO:0006486)	6	147	0.011526075
30	Respiratory Electron Transport Chain (GO:0022904)	2	14	0.013319348
31	Regulation Of ATP Biosynthetic Process (GO:2001169)	2	14	0.013319348
32	Negative Regulation Of Cilium Assembly (GO:1902018)	2	14	0.013319348
33	Regulation Of Monoatomic Cation Transmembrane Transport (GO:1904062)	3	39	0.013350317
34	Anterograde Trans-Synaptic Signaling (GO:0098916)	7	199	0.014117102

35	Calcium Ion Transport (GO:0006816)	5	112	0.014416824
36	DNA Double-Strand Break Processing (GO:0000729)	2	15	0.015240479
37	Folic Acid-Containing Compound Metabolic Process (GO:0006760)	2	15	0.015240479
38	Regulation Of MAP Kinase Activity (GO:0043405)	5	114	0.015459583
39	Apoptotic Nuclear Changes (GO:0030262)	2	16	0.017272775
40	Sulfation (GO:0051923)	2	16	0.017272775
41	Protein Alpha-1,2-Demannosylation (GO:0036508)	2	16	0.017272775
42	DNA-templated DNA Replication Maintenance Of Fidelity (GO:0045005)	3	43	0.01737137
43	Regulation Of Filopodium Assembly (GO:0051489)	3	43	0.01737137
44	Calcium Ion Transmembrane Transport (GO:0070588)	4	80	0.019185331
45	Positive Regulation Of Fatty Acid Metabolic Process (GO:0045923)	2	17	0.019413115
46	Regulation Of Adenylate Cyclase Activity (GO:0045761)	2	17	0.019413115
47	Cellular Response To Organic Substance (GO:0071310)	4	82	0.020806534
48	Positive Regulation Of Glycolytic Process (GO:0045821)	2	18	0.021658435
49	Response To Cytokine (GO:0034097)	5	125	0.022097763
50	Negative Regulation Of Peptidyl-Serine Phosphorylation (GO:0033137)	2	19	0.024005731
51	Cellular Response To Lectin (GO:1990858)	2	19	0.024005731
52	Stimulatory C-type Lectin Receptor Signaling Pathway (GO:0002223)	2	19	0.024005731
53	Chemical Synaptic Transmission (GO:0007268)	8	273	0.024264424
54	Peripheral Nervous System Development (GO:0007422)	2	20	0.026452061
55	Porphyrin-Containing Compound Biosynthetic Process (GO:0006779)	2	21	0.028994538
56	Protein O-linked Glycosylation (GO:0006493)	4	93	0.031205271
57	Positive Regulation Of Synaptic Transmission, Glutamatergic (GO:0051968)	2	22	0.031630334
58	Regulation Of Synaptic Transmission, Glutamatergic (GO:0051966)	3	55	0.033059665
59	Actin Nucleation (GO:0045010)	2	23	0.034356675
60	Translesion Synthesis (GO:0019985)	2	23	0.034356675
61	Positive Regulation Of Protein Targeting To Membrane (GO:0090314)	2	23	0.034356675
62	Neuromuscular Junction Development (GO:0007528)	2	24	0.037170844
63	Response To Purine-Containing Compound (GO:0014074)	2	24	0.037170844
64	Ribonucleoside Bisphosphate Metabolic Process (GO:0033875)	2	25	0.040070177
65	Purine Nucleoside Bisphosphate Metabolic Process (GO:0034032)	2	25	0.040070177
66	Regulation Of Nucleotide-Excision Repair (GO:2000819)	2	26	0.043052063
67	Positive Regulation Of Kinase Activity (GO:0033674)	4	104	0.044178155
68	Cortical Cytoskeleton Organization (GO:0030865)	2	27	0.046113944
69	Microtubule Polymerization Or Depolymerization (GO:0031109)	2	27	0.046113944

70	Cytokine-Mediated Signaling Pathway (GO:0019221)	7	257	0.047179318
71	Protein N-linked Glycosylation (GO:0006487)	3	64	0.048349347
72	Regulation Of Protein Targeting To Membrane (GO:0090313)	2	28	0.049253313
73	Limb Development (GO:0060173)	2	28	0.049253313
74	Regulation Of Calcium Ion-Dependent Exocytosis (GO:0017158)	2	28	0.049253313

[G8 ciliated Down]

	Term	Matched	Total	P.value
1	Positive Regulation Of Plasma Membrane Bounded Cell Projection Assembly (GO:0120034)	3	88	0.000777494
2	Positive Regulation Of Lamellipodium Assembly (GO:0010592)	2	23	0.001009406
3	Positive Regulation Of Filopodium Assembly (GO:0051491)	2	27	0.001393156
4	Positive Regulation Of Lamellipodium Organization (GO:1902745)	2	31	0.001836089
5	Regulation Of Lamellipodium Assembly (GO:0010591)	2	33	0.002079453
6	Inner Mitochondrial Membrane Organization (GO:0007007)	2	34	0.002206559
7	Regulation Of Filopodium Assembly (GO:0051489)	2	43	0.003510585
8	Positive Regulation Of Transcription Initiation By RNA Polymerase II (GO:0060261)	2	52	0.005095421
9	Regulation Of Multicellular Organismal Development (GO:2000026)	2	59	0.006515664
10	Regulation Of Embryonic Development (GO:0045995)	2	62	0.007173281
11	Mitotic Spindle	3	199	0.007834243
12	Apical Junction	3	200	0.007942344
13	Positive Regulation Of Podosome Assembly (GO:0071803)	1	5	0.010208974
14	Regulation Of Blood Vessel Remodeling (GO:0060312)	1	5	0.010208974
15	Regulation Of Protein Localization To Plasma Membrane (GO:1903076)	2	80	0.011712056
16	Parallel Actin Filament Bundle Assembly (GO:0030046)	1	6	0.012238541
17	L-methionine Salvage (GO:0071267)	1	6	0.012238541
18	Termination Of RNA Polymerase II Transcription (GO:0006369)	1	7	0.014264049
19	Purine-Containing Compound Metabolic Process (GO:0072521)	1	7	0.014264049
20	Regulation Of Lipoprotein Metabolic Process (GO:0050746)	1	7	0.014264049
21	Regulation Of Microvillus Organization (GO:0032530)	1	7	0.014264049
22	Positive Regulation Of Extracellular Matrix Disassembly (GO:0090091)	1	7	0.014264049
23	Regulation Of Podosome Assembly (GO:0071801)	1	8	0.016285505
24	Positive Regulation Of Protein-Containing Complex Assembly (GO:0031334)	2	98	0.017213026
25	Chromatin Organization (GO:0006325)	3	268	0.017434063
26	Regulation Of Protein Lipidation (GO:1903059)	1	9	0.018302918
27	Positive Regulation Of Tissue Remodeling (GO:0034105)	1	9	0.018302918
28	Nucleoside Metabolic Process (GO:0009116)	1	9	0.018302918
29	Regulation Of Cellular Response To Stress (GO:0080135)	2	107	0.020301574
30	Negative Regulation Of Lymphocyte Migration (GO:2000402)	1	10	0.020316294
31	Negative Regulation Of Myotube Differentiation (GO:0010832)	1	11	0.022325642

32	Aspartate Family Amino Acid Catabolic Process (GO:0009068)	1	11	0.022325642
33	Protein Insertion Into Mitochondrial Inner Membrane (GO:0045039)	1	12	0.02433097
34	Negative Regulation Of Mononuclear Cell Migration (GO:0071676)	1	12	0.02433097
35	Regulation Of Lymphocyte Migration (GO:2000401)	1	12	0.02433097
36	Protein Localization To Phagophore Assembly Site (GO:0034497)	1	13	0.026332285
37	Antigen Processing And Presentation Of Endogenous Peptide Antigen Via MHC Class I Via ER Pathway (GO:0002484)	1	13	0.026332285
38	Antigen Processing And Presentation Of Endogenous Peptide Antigen Via MHC Class I Via ER Pathway, TAP-independent (GO:0002486)	1	13	0.026332285
39	Antigen Processing And Presentation Of Endogenous Peptide Antigen Via MHC Class Ib (GO:0002476)	1	13	0.026332285
40	Antigen Processing And Presentation Of Peptide Antigen Via MHC Class Ib (GO:0002428)	1	13	0.026332285
41	Regulation Of DNA Metabolic Process (GO:0051052)	2	124	0.02671175
42	Establishment Of Apical/Basal Cell Polarity (GO:0035089)	1	14	0.028329595
43	Phagolysosome Assembly (GO:0001845)	1	14	0.028329595
44	Regulation Of Extracellular Matrix Disassembly (GO:0010715)	1	14	0.028329595
45	Positive Regulation Of Telomere Maintenance In Response To DNA Damage (GO:1904507)	1	14	0.028329595
46	Primary Alcohol Metabolic Process (GO:0034308)	1	14	0.028329595
47	Regulation Of DNA Repair (GO:0006282)	2	129	0.028733972
48	Regulation Of Clathrin-Dependent Endocytosis (GO:2000369)	1	15	0.030322908
49	Phagosome Maturation (GO:0090382)	1	15	0.030322908
50	Golgi To Endosome Transport (GO:0006895)	1	15	0.030322908
51	Regulation Of Telomere Maintenance In Response To DNA Damage (GO:1904505)	1	15	0.030322908
52	Dendritic Spine Morphogenesis (GO:0060997)	1	15	0.030322908
53	DNA-templated Transcription Termination (GO:0006353)	1	16	0.032312232
54	Protein Localization To Mitochondrion (GO:0070585)	1	16	0.032312232
55	Mitophagy (GO:0000423)	1	16	0.032312232
56	Regulation Of DNA Strand Elongation (GO:0060382)	1	16	0.032312232
57	Negative Regulation Of Anoikis (GO:2000811)	1	16	0.032312232
58	Negative Regulation Of Striated Muscle Cell Differentiation (GO:0051154)	1	17	0.034297574
59	Maintenance Of Protein Localization In Organelle (GO:0072595)	1	18	0.036278942
60	Maintenance Of Protein Location In Nucleus (GO:0051457)	1	18	0.036278942
61	Glycerolipid Catabolic Process (GO:0046503)	1	18	0.036278942
62	Vesicle Transport Along Actin Filament (GO:0030050)	1	18	0.036278942
63	Positive Regulation Of Stress-Activated Protein Kinase Signaling Cascade (GO:0070304)	1	18	0.036278942
64	Autophagy Of Nucleus (GO:0044804)	1	18	0.036278942
65	Positive Regulation Of Extracellular Matrix Organization (GO:1903055)	1	18	0.036278942
66	Arp2/3 Complex-Mediated Actin Nucleation (GO:0034314)	1	19	0.038256344
67	Negative Regulation Of Axon Extension Involved In Axon Guidance (GO:0048843)	1	19	0.038256344
68	Regulation Of Autophagy Of Mitochondrion (GO:1903146)	1	19	0.038256344
69	Negative Regulation Of Protein Localization To Cell Periphery (GO:1904376)	1	20	0.040229788
70	Negative Regulation Of Protein Localization To Plasma Membrane (GO:1903077)	1	20	0.040229788
71	Actin Filament-Based Transport (GO:0099515)	1	20	0.040229788
72	Innate Immune Response In Mucosa (GO:0002227)	1	21	0.042199281
73	Antigen Processing And Presentation Of Endogenous Peptide Antigen (GO:0002483)	1	21	0.042199281
74	Regulation Of Anoikis (GO:2000209)	1	21	0.042199281
75	Natural Killer Cell Mediated Immunity (GO:0002228)	1	22	0.044164831

76	Negative Regulation Of Extrinsic Apoptotic Signaling Pathway Via Death Domain Receptors (GO:1902042)	1	23	0.046126446
77	Actin Nucleation (GO:0045010)	1	23	0.046126446
78	Regulation Of Myotube Differentiation (GO:0010830)	1	23	0.046126446
79	Regulation Of Axon Extension Involved In Axon Guidance (GO:0048841)	1	23	0.046126446
80	Double-Strand Break Repair (GO:0006302)	2	168	0.046452202
81	mRNA Polyadenylation (GO:0006378)	1	24	0.048084133
82	Natural Killer Cell Mediated Cytotoxicity (GO:0042267)	1	24	0.048084133

Supplementary Table S3. A list of functions associated with virus specific gene modules

[V1 OC-43 Up]

	Term	Matched	Total	P.value
1	Ribonucleoprotein Complex Biogenesis (GO:0022613)	8	118	4.74E-05
2	Negative Regulation Of Wound Healing (GO:0061045)	4	28	0.000232985
3	Translation (GO:0006412)	10	234	0.000267796
4	Ribosome Biogenesis (GO:0042254)	8	155	0.000315548
5	Ribosomal Small Subunit Biogenesis (GO:0042274)	6	84	0.00032136
6	Maturation Of LSU-rRNA From Tricistronic rRNA Transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463)	3	14	0.000431185
7	Membrane Assembly (GO:0071709)	4	38	0.00077106
8	rRNA Processing (GO:0006364)	6	101	0.000859184
9	Positive Regulation Of Animal Organ Morphogenesis (GO:0110110)	2	5	0.001167889
10	Maturation Of LSU-rRNA (GO:0000470)	3	20	0.001286535
11	Response To Endoplasmic Reticulum Stress (GO:0034976)	6	114	0.001608041
12	tRNA Processing (GO:0008033)	4	50	0.00217178
13	Endosome Transport Via Multivesicular Body Sorting Pathway (GO:0032509)	3	24	0.002211735
14	Multivesicular Body Sorting Pathway (GO:0071985)	3	24	0.002211735
15	Regulation Of Wound Healing, Spreading Of Epidermal Cells (GO:1903689)	2	7	0.00241733
16	Positive Regulation Of Epithelial Tube Formation (GO:1905278)	2	7	0.00241733
17	Kidney Mesenchyme Development (GO:0072074)	2	7	0.00241733
18	mRNA Metabolic Process (GO:0016071)	5	85	0.002425261
19	Ribosomal Large Subunit Biogenesis (GO:0042273)	4	54	0.002882629
20	Golgi Ribbon Formation (GO:0090161)	2	8	0.003199897
21	Positive Regulation Of Ubiquitin Protein Ligase Activity (GO:1904668)	2	8	0.003199897
22	ncRNA Export From Nucleus (GO:0097064)	2	8	0.003199897
23	Cytoplasmic Translation (GO:0002181)	5	93	0.003581955
24	Regulation Of Developmental Growth (GO:0048638)	3	29	0.003835659
25	Negative Regulation Of Gene Expression (GO:0010629)	10	336	0.004057721
26	Presynaptic Membrane Organization (GO:0097090)	2	9	0.004084553
27	Macromolecule Biosynthetic Process (GO:0009059)	7	183	0.004108352
28	RNA Methylation (GO:0001510)	4	62	0.004751218
29	Positive Regulation Of Transcription From RNA Polymerase II Promoter In Response To Endoplasmic Reticulum Stress (GO:1990440)	2	10	0.005068989
30	Metanephric Mesenchyme Development (GO:0072075)	2	10	0.005068989

31	Negative Regulation Of Proteasomal Ubiquitin-Dependent Protein Catabolic Process (GO:0032435)	3	32	0.005082821
32	Regulation Of Cell Differentiation (GO:0045595)	7	193	0.005476925
33	Gene Expression (GO:0010467)	9	296	0.005486012
34	Regulation Of Keratinocyte Migration (GO:0051547)	2	11	0.006150933
35	Central Nervous System Neuron Axonogenesis (GO:0021955)	2	11	0.006150933
36	Positive Regulation Of Branching Involved In Ureteric Bud Morphogenesis (GO:0090190)	2	11	0.006150933
37	Positive Regulation Of Endoplasmic Reticulum Unfolded Protein Response (GO:1900103)	2	11	0.006150933
38	Lysosomal Membrane Organization (GO:0097212)	2	11	0.006150933
39	DNA Repair	6	150	0.006240878
40	DNA-templated Transcription (GO:0006351)	7	199	0.006447412
41	Negative Regulation Of Stem Cell Differentiation (GO:2000737)	2	12	0.007328152
42	Cellular Response To Leucine Starvation (GO:1990253)	2	12	0.007328152
43	Negative Regulation Of Cell Cycle Phase Transition (GO:1901988)	2	12	0.007328152
44	RNA 3'-End Processing (GO:0031123)	3	38	0.008239755
45	mRNA Transcription By RNA Polymerase II (GO:0042789)	3	38	0.008239755
46	Regulation Of IRE1-mediated Unfolded Protein Response (GO:1903894)	2	13	0.00859845
47	Negative Regulation Of Ubiquitin-Dependent Protein Catabolic Process (GO:2000059)	3	39	0.008855413
48	Negative Regulation Of Mitotic Cell Cycle Phase Transition (GO:1901991)	3	40	0.009497328
49	Chromatin Organization (GO:0006325)	8	268	0.009595627
50	Positive Regulation Of Transcription From RNA Polymerase II Promoter Involved In Cellular Response To Chemical Stimulus (GO:1901522)	2	14	0.009959666
51	Regulation Of Branching Involved In Ureteric Bud Morphogenesis (GO:0090189)	2	14	0.009959666
52	Negative Regulation Of Cilium Assembly (GO:1902018)	2	14	0.009959666
53	Cellular Response To Amino Acid Starvation (GO:0034198)	3	42	0.010860777
54	Regulation Of Ubiquitin-Dependent Protein Catabolic Process (GO:2000058)	3	42	0.010860777
55	Negative Regulation Of Endoplasmic Reticulum Stress-Induced Intrinsic Apoptotic Signaling Pathway (GO:1902236)	2	15	0.011409675
56	Negative Regulation Of Focal Adhesion Assembly (GO:0051895)	2	15	0.011409675
57	Negative Regulation Of Platelet Activation (GO:0010544)	2	15	0.011409675
58	Cellular Response To Corticosteroid Stimulus (GO:0071384)	2	15	0.011409675
59	Coenzyme A Metabolic Process (GO:0015936)	2	15	0.011409675
60	Retrograde Axonal Transport (GO:0008090)	2	15	0.011409675
61	Presynapse Assembly (GO:0099054)	2	15	0.011409675
62	Protein Localization To Microtubule Organizing Center (GO:1905508)	2	15	0.011409675
63	Negative Regulation Of Cell-Substrate Junction Organization (GO:0150118)	2	15	0.011409675
64	Regulation Of Chromosome Organization (GO:0033044)	3	43	0.011582692
65	mRNA Transcription (GO:0009299)	3	43	0.011582692

66	Regulation Of Stem Cell Proliferation (GO:0072091)	2	16	0.012946387
67	Endoplasmic Reticulum Tubular Network Organization (GO:0071786)	2	16	0.012946387
68	Late Endosome To Lysosome Transport (GO:1902774)	2	16	0.012946387
69	Maturation Of 5.8S rRNA (GO:0000460)	2	16	0.012946387
70	Chromatin Remodeling (GO:0006338)	7	228	0.013025946
71	Endosomal Transport (GO:0016197)	6	180	0.014509528
72	Negative Regulation Of Vascular Associated Smooth Muscle Cell Proliferation (GO:1904706)	2	17	0.014567749
73	Peptidyl-Threonine Dephosphorylation (GO:0035970)	2	17	0.014567749
74	Cellular Response To Glucocorticoid Stimulus (GO:0071385)	2	17	0.014567749
75	Regulation Of Ubiquitin Protein Ligase Activity (GO:1904666)	2	17	0.014567749
76	Regulation Of Vacuole Organization (GO:0044088)	2	17	0.014567749
77	Response To Interferon-Alpha (GO:0035455)	2	17	0.014567749
78	Positive Regulation Of Transcription From RNA Polymerase II Promoter In Response To Stress (GO:0036003)	2	17	0.014567749
79	Protein Localization To Centrosome (GO:0071539)	2	17	0.014567749
80	Negative Regulation Of Cellular Senescence (GO:2000773)	2	17	0.014567749
81	Negative Regulation Of Neuron Death (GO:1901215)	4	88	0.015953264
82	Regulation Of Cell-Cell Adhesion Mediated By Cadherin (GO:2000047)	2	18	0.016271739
83	ERAD Pathway (GO:0036503)	4	89	0.016564572
84	Negative Regulation Of Macromolecule Metabolic Process (GO:0010605)	6	186	0.016794412
85	Mitotic Sister Chromatid Cohesion (GO:0007064)	2	19	0.01805637
86	RNA Modification (GO:0009451)	3	51	0.018341523
87	Myoblast Differentiation (GO:0045445)	2	20	0.01991969
88	Regulation Of Proteasomal Protein Catabolic Process (GO:0061136)	3	53	0.020307943
89	Organelle Disassembly (GO:1903008)	3	54	0.021332964
90	Endoplasmic Reticulum Organization (GO:0007029)	3	54	0.021332964
91	Protein K63-linked Ubiquitination (GO:0070534)	3	54	0.021332964
92	Golgi Vesicle Transport (GO:0048193)	6	197	0.021605871
93	Glycolysis	6	200	0.023064332
94	Peptide Metabolic Process (GO:0006518)	3	56	0.023466699
95	tRNA Aminoacylation (GO:0043039)	2	22	0.023874744
96	Regulation Of Organelle Organization (GO:0033043)	4	100	0.024264693
97	protein-RNA Complex Assembly (GO:0022618)	5	150	0.024830498
98	Visual Perception (GO:0007601)	4	101	0.025055417
99	Positive Regulation Of Morphogenesis Of An Epithelium (GO:1905332)	2	23	0.025962734
100	Heparan Sulfate Proteoglycan Biosynthetic Process (GO:0015012)	2	23	0.025962734

101	Negative Regulation Of Cell Differentiation (GO:0045596)	6	207	0.026721444
102	Homophilic Cell Adhesion Via Plasma Membrane Adhesion Molecules (GO:0007156)	3	60	0.028068633
103	PI3K/AKT/mTOR Signaling	4	105	0.028372839
104	Unfolded Protein Response	4	113	0.035758118

[V2 OC-43 Down]

	Term	Matched	Total	P.value
1	Positive Regulation Of Cellular Extravasation (GO:0002693)	2	12	0.001283478
2	Cytoskeleton Organization (GO:0007010)	4	111	0.001591244
3	TNF-alpha Signaling via NF-kB	5	200	0.002101995
4	Apical Junction	5	200	0.002101995
5	T Cell Migration (GO:0072678)	2	17	0.00260634
6	Organelle Organization (GO:0006996)	7	418	0.002793087
7	Regulation Of Histone Modification (GO:0031056)	2	18	0.002923575
8	Regulation Of Protein Export From Nucleus (GO:0046825)	2	22	0.004362764
9	Cholesterol Homeostasis	3	74	0.004536146
10	Positive Regulation Of Oxidoreductase Activity (GO:0051353)	2	23	0.004764343
11	Positive Regulation Of Cellular Process (GO:0048522)	8	594	0.005298791
12	Protein Modification By Small Protein Conjugation (GO:0032446)	6	364	0.006026596
13	Positive Regulation Of Endothelial Cell Migration (GO:0010595)	3	85	0.006670898
14	Golgi To Plasma Membrane Protein Transport (GO:0043001)	2	28	0.007015271
15	Regulation Of Cell Population Proliferation (GO:0042127)	9	766	0.007526066
16	Positive Regulation Of Leukocyte Migration (GO:0002687)	2	31	0.008554857
17	Regulation Of Protein Localization To Cell Surface (GO:2000008)	2	31	0.008554857
18	Regulation Of Cell Morphogenesis (GO:0022604)	2	31	0.008554857
19	Inositol Lipid-Mediated Signaling (GO:0048017)	2	33	0.009657557
20	Positive Regulation Of Vasculature Development (GO:1904018)	3	104	0.011571013
21	Establishment Of Protein Localization To Plasma Membrane (GO:0061951)	2	38	0.012673019
22	Positive Regulation Of Nucleic Acid-Templated Transcription (GO:1903508)	7	557	0.012806591
23	mRNA 3'-End Processing (GO:0031124)	2	40	0.013979735
24	Stress-Activated MAPK Cascade (GO:0051403)	2	42	0.01534224
25	Regulation Of Endothelial Cell Apoptotic Process (GO:2000351)	2	43	0.016044075
26	Positive Regulation Of Angiogenesis (GO:0045766)	3	119	0.016582892

27	Positive Regulation Of Nucleocytoplasmic Transport (GO:0046824)	2	44	0.016759451
28	Positive Regulation Of Chemotaxis (GO:0050921)	2	44	0.016759451
29	Positive Regulation Of Blood Vessel Endothelial Cell Migration (GO:0043536)	2	46	0.018230299
30	Negative Regulation Of Hydrolase Activity (GO:0051346)	2	47	0.018985506
31	Golgi To Plasma Membrane Transport (GO:0006893)	2	47	0.018985506
32	Myelination (GO:0042552)	2	48	0.019753727
33	Positive Regulation Of Cell Population Proliferation (GO:0008284)	6	483	0.021816994
34	DNA Methylation Involved In Embryo Development (GO:0043045)	1	5	0.022300459
35	Regulation Of Endothelial Cell-Matrix Adhesion Via Fibronectin (GO:1904904)	1	5	0.022300459
36	Regulation Of Establishment Of T Cell Polarity (GO:1903903)	1	5	0.022300459
37	His-Purkinje System Development (GO:0003164)	1	5	0.022300459
38	ISG15-protein Conjugation (GO:0032020)	1	5	0.022300459
39	Negative Regulation Of Transcription From RNA Polymerase II Promoter In Response To Stress (GO:0097201)	1	5	0.022300459
40	Regulation Of Neutrophil Extravasation (GO:2000389)	1	5	0.022300459
41	Presynaptic Active Zone Organization (GO:1990709)	1	5	0.022300459
42	Plasma Membrane Raft Assembly (GO:0044854)	1	5	0.022300459
43	Plus-End-Directed Organelle Transport Along Microtubule (GO:0072386)	1	5	0.022300459
44	Regulation Of 3'-UTR-mediated mRNA Stabilization (GO:1905868)	1	5	0.022300459
45	Protein K63-linked Ubiquitination (GO:0070534)	2	54	0.02462916
46	Regulation Of Blood Vessel Endothelial Cell Migration (GO:0043535)	2	54	0.02462916
47	Regulation Of Cellular Response To Hypoxia (GO:1900037)	1	6	0.026701191
48	Vascular Associated Smooth Muscle Contraction (GO:0014829)	1	6	0.026701191
49	Aggrephagy (GO:0035973)	1	6	0.026701191
50	Insulin Secretion Involved In Cellular Response To Glucose Stimulus (GO:0035773)	1	6	0.026701191
51	Protein Catabolic Process In The Vacuole (GO:0007039)	1	6	0.026701191
52	Mitochondrial tRNA Processing (GO:0090646)	1	6	0.026701191
53	Receptor-Mediated Virion Attachment To Host Cell (GO:0046813)	1	6	0.026701191
54	Selective Autophagy (GO:0061912)	2	58	0.028123643
55	Protein Glycosylation (GO:0006486)	3	147	0.02872942
56	Histone Acetylation (GO:0016573)	2	60	0.029941187
57	Positive Regulation Of Insulin-Like Growth Factor Receptor Signaling Pathway (GO:0043568)	1	7	0.031082335
58	Mitochondrial tRNA Modification (GO:0070900)	1	7	0.031082335
59	Regulation Of Transcription From RNA Polymerase II Promoter In Response To Hypoxia (GO:0061418)	1	7	0.031082335
60	Negative Regulation Of RNA Catabolic Process (GO:1902369)	1	7	0.031082335
61	Regulation Of Embryonic Development (GO:0045995)	2	62	0.031804317

62	Phosphatidylinositol-Mediated Signaling (GO:0048015)	2	62	0.031804317
63	Cellular Response To Growth Factor Stimulus (GO:0071363)	3	155	0.032870117
64	Positive Regulation Of Mast Cell Degranulation (GO:0043306)	1	8	0.035443978
65	Androgen Biosynthetic Process (GO:0006702)	1	8	0.035443978
66	Isoprenoid Biosynthetic Process (GO:0008299)	1	8	0.035443978
67	Isoprenoid Metabolic Process (GO:0006720)	1	8	0.035443978
68	p38MAPK Cascade (GO:0038066)	1	8	0.035443978
69	Manganese Ion Transport (GO:0006828)	1	8	0.035443978
70	Regulation Of Cell Killing (GO:0031341)	1	8	0.035443978
71	Regulation Of Endocytosis (GO:0030100)	2	66	0.035663562
72	Regulation Of Macromolecule Metabolic Process (GO:0060255)	3	162	0.036735122
73	Negative Regulation Of Extrinsic Apoptotic Signaling Pathway (GO:2001237)	2	70	0.039693969
74	Protein K48-linked Ubiquitination (GO:0070936)	2	70	0.039693969
75	Synaptic Vesicle Fusion To Presynaptic Active Zone Membrane (GO:0031629)	1	9	0.039786204
76	I-kappaB Phosphorylation (GO:0007252)	1	9	0.039786204
77	Vasoconstriction (GO:0042310)	1	9	0.039786204
78	High-Density Lipoprotein Particle Assembly (GO:0034380)	1	9	0.039786204
79	Regulation Of Leukocyte Mediated Cytotoxicity (GO:0001910)	1	9	0.039786204
80	Apical Protein Localization (GO:0045176)	1	9	0.039786204
81	Neurotransmitter Receptor Transport To Postsynaptic Membrane (GO:0098969)	1	9	0.039786204
82	Positive Regulation Of Vasculogenesis (GO:2001214)	1	9	0.039786204
83	Organic Hydroxy Compound Catabolic Process (GO:1901616)	1	9	0.039786204
84	Regulation Of ER To Golgi Vesicle-Mediated Transport (GO:0060628)	1	9	0.039786204
85	Regulation Of Cellular Extravasation (GO:0002691)	1	9	0.039786204
86	Negative Regulation Of Supramolecular Fiber Organization (GO:1902904)	2	71	0.040727465
87	Plasma Membrane Organization (GO:0007009)	2	72	0.041771097
88	Second-Messenger-Mediated Signaling (GO:0019932)	2	72	0.041771097
89	tRNA Threonylcarbamoyladenosine Metabolic Process (GO:0070525)	1	10	0.0441091
90	T Cell Chemotaxis (GO:0010818)	1	10	0.0441091
91	Positive Regulation Of Phospholipid Transport (GO:2001140)	1	10	0.0441091
92	Histone H3-K14 Acetylation (GO:0044154)	1	10	0.0441091
93	Regulation Of mRNA Polyadenylation (GO:1900363)	1	10	0.0441091
94	Inositol Phosphate Biosynthetic Process (GO:0032958)	1	10	0.0441091
95	Regulation Of Peptidyl-Lysine Acetylation (GO:2000756)	1	10	0.0441091
96	Maintenance Of Synapse Structure (GO:0099558)	1	10	0.0441091

97	Protein Localization To Endosome (GO:0036010)	1	10	0.0441091
98	Purine Nucleoside Bisphosphate Biosynthetic Process (GO:0034033)	1	10	0.0441091
99	Mitotic G1/S Transition Checkpoint Signaling (GO:0044819)	1	10	0.0441091
100	Coenzyme A Biosynthetic Process (GO:0015937)	1	10	0.0441091
101	Regulation Of Amyloid Precursor Protein Biosynthetic Process (GO:0042984)	1	10	0.0441091
102	Ribonucleoside Bisphosphate Biosynthetic Process (GO:0034030)	1	10	0.0441091
103	Regulation Of Plasma Membrane Bounded Cell Projection Assembly (GO:0120032)	2	75	0.044961712

[V3 SARS1 Up]

	Term	Matched	Total	P.value
1	Oxidative Phosphorylation (GO:0006119)	15	85	1.29E-20
2	Oxidative Phosphorylation	24	200	3.16E-20
3	Aerobic Electron Transport Chain (GO:0019646)	13	68	3.59E-14
4	Mitochondrial ATP Synthesis Coupled Electron Transport (GO:0042775)	13	70	5.35E-14
5	Proton Motive Force-Driven ATP Synthesis (GO:0015986)	11	60	5.73E-12
6	Macromolecule Biosynthetic Process (GO:0009059)	16	183	1.07E-11
7	Peptide Biosynthetic Process (GO:0043043)	15	158	1.49E-11
8	Translation (GO:0006412)	17	234	4.58E-11
9	Aerobic Respiration (GO:0009060)	10	59	1.23E-10
10	Myc Targets V1	14	200	4.07E-09
11	Cellular Respiration (GO:0045333)	9	63	5.19E-09
12	Cytoplasmic Translation (GO:0002181)	10	93	1.21E-08
13	Mitochondrial Electron Transport, NADH To Ubiquinone (GO:0006120)	7	34	1.94E-08
14	Proton Motive Force-Driven Mitochondrial ATP Synthesis (GO:0042776)	8	53	2.41E-08
15	Gene Expression (GO:0010467)	15	296	8.58E-08
16	Energy Derivation By Oxidation Of Organic Compounds (GO:0015980)	6	43	2.33E-06
17	Mitochondrial Electron Transport, Cytochrome C To Oxygen (GO:0006123)	4	16	1.08E-05
18	Mitochondrial Respiratory Chain Complex Assembly (GO:0033108)	7	90	1.76E-05
19	Intracellular Protein Transmembrane Transport (GO:0065002)	5	46	5.83E-05
20	Reactive Oxygen Species Pathway	5	49	7.93E-05
21	Adipogenesis	9	200	8.93E-05
22	NADH Dehydrogenase Complex Assembly (GO:0010257)	5	53	0.000115941
23	Mitochondrial Respiratory Chain Complex I Assembly (GO:0032981)	5	53	0.000115941
24	Protein Secretion	6	96	0.000238889
25	Establishment Of Vesicle Localization (GO:0051650)	3	18	0.000538204
26	Substantia Nigra Development (GO:0021762)	4	42	0.000555209
27	Positive Regulation Of Signal Transduction By P53 Class Mediator (GO:1901798)	3	21	0.000859886
28	Protein Neddylation (GO:0045116)	3	22	0.000989061
29	Autophagy Of Mitochondrion (GO:0000422)	4	49	0.001000519

30	ATP Biosynthetic Process (GO:0006754)	3	25	0.001448027
31	Regulation Of Cell Size (GO:0008361)	3	25	0.001448027
32	Negative Regulation Of Lipid Metabolic Process (GO:0045833)	3	26	0.001626073
33	ATP Synthesis Coupled Electron Transport (GO:0042773)	2	7	0.001660143
34	Post-Translational Protein Targeting To Membrane, Translocation (GO:0031204)	2	7	0.001660143
35	RNA Splicing (GO:0008380)	5	98	0.00197835
36	Mitochondrial Translation (GO:0032543)	5	98	0.00197835
37	Nucleic Acid Transport (GO:0050657)	2	8	0.002200366
38	Positive Regulation Of Membrane Invagination (GO:1905155)	2	8	0.002200366
39	Negative Regulation Of Protein Metabolic Process (GO:0051248)	6	147	0.002230951
40	Regulation Of Phospholipid Metabolic Process (GO:1903725)	2	9	0.002812236
41	Positive Regulation Of Phagocytosis, Engulfment (GO:0060100)	2	9	0.002812236
42	Protein Transmembrane Import Into Intracellular Organelle (GO:0044743)	3	32	0.002981136
43	mRNA Processing (GO:0006397)	7	214	0.003409232
44	TORC1 Signaling (GO:0038202)	2	10	0.003494428
45	Regulation Of Phagocytosis, Engulfment (GO:0060099)	2	10	0.003494428
46	Protein Deneddylation (GO:0000338)	2	10	0.003494428
47	Mitochondrial Respirasome Assembly (GO:0097250)	2	10	0.003494428
48	Negative Regulation Of Catabolic Process (GO:0009895)	4	72	0.004135857
49	Negative Regulation Of Amyloid Fibril Formation (GO:1905907)	2	11	0.004245631
50	Mitochondrion Disassembly (GO:0061726)	3	37	0.004518211
51	Mitochondrial Electron Transport, Ubiquinol To Cytochrome C (GO:0006122)	2	12	0.005064556
52	Negative Regulation Of Cytokine Production (GO:0001818)	6	178	0.005698578
53	RNA Splicing, Via Transesterification Reactions With Bulged Adenosine As Nucleophile (GO:0000377)	6	180	0.006010513
54	Post-Translational Protein Targeting To Endoplasmic Reticulum Membrane (GO:0006620)	2	14	0.006900494
55	Protein Localization To Vacuole (GO:0072665)	2	14	0.006900494
56	Protein Maturation By Iron-Sulfur Cluster Transfer (GO:0097428)	2	14	0.006900494
57	Ribosomal Small Subunit Biogenesis (GO:0042274)	4	84	0.007135083
58	Regulation Of Amyloid Fibril Formation (GO:1905906)	2	15	0.007915011
59	Activin Receptor Signaling Pathway (GO:0032924)	2	16	0.008992258
60	Golgi Vesicle Transport (GO:0048193)	6	197	0.00918487
61	rRNA Modification (GO:0000154)	2	17	0.01013103
62	Regulation Of Protein Neddylation (GO:2000434)	2	18	0.011330137
63	Protein Import Into Mitochondrial Matrix (GO:0030150)	2	18	0.011330137
64	Mitotic Cytokinetic Process (GO:1902410)	2	18	0.011330137
65	Regulation Of Proteolysis (GO:0030162)	3	52	0.011642966
66	Protein Stabilization (GO:0050821)	6	208	0.011788548
67	protein-RNA Complex Assembly (GO:0022618)	5	150	0.011855099
68	mRNA Splicing, Via Spliceosome (GO:0000398)	6	211	0.012580593
69	Negative Regulation Of Protein Catabolic Process (GO:0042177)	3	54	0.012897287
70	Negative Regulation Of Phosphate Metabolic Process (GO:0045936)	2	20	0.013904682
71	Regulation Of Meiotic Cell Cycle (GO:0051445)	2	20	0.013904682
72	Negative Regulation Of Cytokine Production Involved In Inflammatory Response (GO:1900016)	2	20	0.013904682
73	Peptide Metabolic Process (GO:0006518)	3	56	0.014225919

74	Mitochondrial Gene Expression (GO:0140053)	4	103	0.014332534
75	Fatty Acid Metabolism	5	158	0.014567989
76	Macroautophagy (GO:0016236)	4	104	0.014803225
77	Pperoxisome	4	104	0.014803225
78	Anaphase-Promoting Complex-Dependent Catabolic Process (GO:0031145)	2	21	0.015277822
79	Regulation Of Anoikis (GO:2000209)	2	21	0.015277822
80	Mitochondrial Cytochrome C Oxidase Assembly (GO:0033617)	2	22	0.016706703
81	U2-type Prespliceosome Assembly (GO:1903241)	2	23	0.018190213
82	Protein Targeting To ER (GO:0045047)	2	23	0.018190213
83	Regulation Of T Cell Migration (GO:2000404)	2	23	0.018190213
84	Spliceosomal Complex Assembly (GO:0000245)	3	62	0.018662567
85	Positive Regulation Of Mitotic Cell Cycle Phase Transition (GO:1901992)	3	63	0.019468197
86	RNA Splicing, Via Transesterification Reactions (GO:0000375)	2	24	0.019727259
87	Negative Regulation Of Protein Transport (GO:0051224)	2	25	0.021316761
88	Negative Regulation Of Proteolysis Involved In Protein Catabolic Process (GO:1903051)	2	25	0.021316761
89	Organophosphate Ester Transport (GO:0015748)	2	25	0.021316761
90	Ribonucleoprotein Complex Biogenesis (GO:0022613)	4	118	0.022433118
91	Respiratory Chain Complex IV Assembly (GO:0008535)	2	26	0.022957656
92	Cellular Response To Acid Chemical (GO:0071229)	2	27	0.024648894
93	Iron-Sulfur Cluster Assembly (GO:0016226)	2	27	0.024648894
94	Metallo-Sulfur Cluster Assembly (GO:0031163)	2	27	0.024648894
95	RNA Processing (GO:0006396)	5	183	0.02563917
96	TOR Signaling (GO:0031929)	2	29	0.028178272
97	Regulation Of Protein Modification By Small Protein Conjugation Or Removal (GO:1903320)	2	29	0.028178272
98	Protein K11-linked Ubiquitination (GO:0070979)	2	29	0.028178272
99	Multivesicular Body Assembly (GO:0036258)	2	29	0.028178272
100	Response To Amino Acid (GO:0043200)	2	30	0.030014386
101	Multivesicular Body Organization (GO:0036257)	2	30	0.030014386
102	Vesicle Budding From Membrane (GO:0006900)	2	32	0.033824503
103	Regulation Of TOR Signaling (GO:0032006)	3	78	0.033829699
104	KRAS Signaling Up	5	200	0.035609354
105	Positive Regulation Of Reproductive Process (GO:2000243)	2	33	0.035796563
106	intra-Golgi Vesicle-Mediated Transport (GO:0006891)	2	33	0.035796563
107	Protein Localization To Organelle (GO:0033365)	4	137	0.036042125
108	Regulation Of Cytokinesis (GO:0032465)	3	80	0.036064935
109	Coagulation	4	138	0.036865337
110	DNA Repair	4	150	0.047586599

[V4 SARS1 Down]

	Term	Matched	Total	P.value
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1	Regulation Of Transcription By RNA Polymerase II (GO:0006357)	39	2028	2.39E-06
2	Negative Regulation Of DNA-templated Transcription (GO:0045892)	24	1025	1.28E-05
3	Positive Regulation Of DNA-templated Transcription (GO:0045893)	26	1243	3.79E-05
4	Negative Regulation Of Transcription By RNA Polymerase II (GO:0000122)	19	763	4.86E-05
5	Positive Regulation Of Transcription By RNA Polymerase II (GO:0045944)	21	938	8.82E-05
6	Regulation Of Vasculature Development (GO:1901342)	4	30	0.000135744
7	Positive Regulation Of Neurogenesis (GO:0050769)	5	75	0.000536768
8	RNA Processing (GO:0006396)	7	183	0.00124349
9	Negative Regulation Of Protein Modification By Small Protein Conjugation Or Removal (GO:1903321)	4	54	0.001328125
10	Regulation Of Stem Cell Population Maintenance (GO:2000036)	4	56	0.001521471
11	Positive Regulation Of Erythrocyte Differentiation (GO:0045648)	3	26	0.001525295
12	Regulation Of DNA-templated Transcription (GO:0006355)	30	1922	0.001528026
13	Regulation Of Mitophagy (GO:1901524)	2	7	0.001588439
14	Positive Regulation Of Gluconeogenesis (GO:0045722)	2	7	0.001588439
15	Phosphatidylinositol Biosynthetic Process (GO:0006661)	5	98	0.001794236
16	Tra	4	59	0.001846985
17	Protein Localization To Golgi Apparatus (GO:0034067)	3	28	0.00189711
18	Activation Of GTPase Activity (GO:0090630)	5	102	0.002139233
19	Phosphatidylinositol-Mediated Signaling (GO:0048015)	4	62	0.00221784
20	Phosphatidylinositol Metabolic Process (GO:0046488)	4	63	0.002352062
21	Negative Regulation Of Intracellular Steroid Hormone Receptor Signaling Pathway (GO:0033144)	3	31	0.002552931
22	Regulation Of Gluconeogenesis (GO:0006111)	3	31	0.002552931
23	Regulation Of Transcription By RNA Polymerase I (GO:0006356)	3	32	0.002798855
24	Inositol Lipid-Mediated Signaling (GO:0048017)	3	33	0.003058888
25	Embryonic Limb Morphogenesis (GO:0030326)	3	34	0.003333285
26	Regulation Of Protein Ubiquitination (GO:0031396)	5	113	0.003335683
27	Regulation Of Erythrocyte Differentiation (GO:0045646)	3	36	0.003926142
28	Positive Regulation Of Myeloid Cell Differentiation (GO:0045639)	3	36	0.003926142
29	Negative Regulation Of Platelet-Derived Growth Factor Receptor Signaling Pathway (GO:0010642)	2	11	0.004064417
30	Exit From Mitosis (GO:0010458)	2	11	0.004064417
31	Positive Regulation Of Axonogenesis (GO:0050772)	3	38	0.004579268
32	Positive Regulation Of Cellular Biosynthetic Process (GO:0031328)	6	174	0.004588519
33	Positive Regulation Of Developmental Process (GO:0051094)	7	233	0.00479535
34	Axonal Transport Of Mitochondrion (GO:0019896)	2	12	0.00484903
35	Regulation Of Retinoic Acid Receptor Signaling Pathway (GO:0048385)	2	12	0.00484903
36	Positive Regulation Of Histone H3-K4 Methylation (GO:0051571)	2	12	0.00484903
37	Positive Regulation Of GTPase Activity (GO:0043547)	7	234	0.004907253
38	Positive Regulation Of Stem Cell Population Maintenance (GO:1902459)	3	40	0.005294353
39	Regulation Of Cell Migration (GO:0030334)	10	434	0.005409879
40	Ephrin Receptor Signaling Pathway (GO:0048013)	3	43	0.006486494
41	Regulation Of Histone H3-K4 Methylation (GO:0051569)	2	14	0.006608583
42	Negative Regulation Of Receptor Signaling Pathway Via STAT (GO:1904893)	2	14	0.006608583
43	Regulation Of Non-Canonical Wnt Signaling Pathway (GO:2000050)	2	14	0.006608583
44	Mitochondrion Transport Along Microtubule (GO:0047497)	2	14	0.006608583

45	mRNA Metabolic Process (GO:0016071)	4	85	0.006881764
46	Regulation Of Insulin Receptor Signaling Pathway (GO:0046626)	3	44	0.006916439
47	Regulation Of Cell Differentiation (GO:0045595)	6	193	0.007519851
48	Positive Regulation Of Glucose Metabolic Process (GO:0010907)	2	15	0.007581182
49	Sympathetic Nervous System Development (GO:0048485)	2	15	0.007581182
50	Positive Regulation Of Multicellular Organismal Process (GO:0051240)	9	387	0.007709211
51	Negative Regulation Of Wnt Signaling Pathway (GO:0030178)	5	140	0.008195327
52	Regulation Of Cell Population Proliferation (GO:0042127)	14	766	0.008316531
53	Negative Regulation Of Receptor Signaling Pathway Via JAK-STAT (GO:0046426)	2	16	0.008614128
54	Embryo Development Ending In Birth Or Egg Hatching (GO:0009792)	2	17	0.009706289
55	Negative Regulation Of Rho Protein Signal Transduction (GO:0035024)	2	17	0.009706289
56	Negative Regulation Of Signal Transduction (GO:0009968)	7	267	0.009825751
57	Regulation Of Interferon-Beta Production (GO:0032648)	3	50	0.00984843
58	Regulation Of Angiogenesis (GO:0045765)	6	205	0.009955476
59	Regulation Of Defense Response To Virus (GO:0050688)	2	18	0.010856548
60	ncRNA-mediated Post-Transcriptional Gene Silencing (GO:0035194)	2	18	0.010856548
61	Positive Regulation Of Nucleic Acid-Templated Transcription (GO:1903508)	11	557	0.010931045
62	Regulation Of Proteolysis (GO:0030162)	3	52	0.010962986
63	Cellular Response To Alcohol (GO:0097306)	3	53	0.011546474
64	Regulation Of Organelle Organization (GO:0033043)	4	100	0.012038722
65	Positive Regulation Of Histone Methylation (GO:0031062)	2	19	0.012063803
66	Negative Regulation Of Protein Ubiquitination (GO:0031397)	3	54	0.012147555
67	Epidermal Cell Differentiation (GO:0009913)	3	54	0.012147555
68	Regulation Of Blood Vessel Endothelial Cell Migration (GO:0043535)	3	54	0.012147555
69	TGF-beta Signaling	3	54	0.012147555
70	Response To Peptide Hormone (GO:0043434)	3	55	0.01276631
71	Actin Filament-Based Transport (GO:0099515)	2	20	0.013326967
72	Negative Regulation Of Stem Cell Population Maintenance (GO:1902455)	2	20	0.013326967
73	Protein Deacylation (GO:0035601)	2	20	0.013326967
74	Positive Regulation Of Cell Motility (GO:2000147)	6	221	0.01401415
75	Regulation Of miRNA Transcription (GO:1902893)	3	59	0.01541945
76	Glycerophospholipid Biosynthetic Process (GO:0046474)	4	108	0.015587604
77	Negative Regulation Of Developmental Process (GO:0051093)	4	109	0.016072625
78	protein-DNA Complex Organization (GO:0071824)	3	60	0.016127559
79	Membrane Organization (GO:0061024)	5	167	0.016582525
80	Positive Regulation Of Neuron Apoptotic Process (GO:0043525)	2	23	0.017441262
81	Small GTPase Mediated Signal Transduction (GO:0007264)	4	112	0.01758423
82	Spliceosomal Complex Assembly (GO:0000245)	3	62	0.017597891
83	Regulation Of Neuroblast Proliferation (GO:1902692)	2	24	0.018917481
84	Protein Kinase B Signaling (GO:0043491)	2	24	0.018917481
85	Negative Regulation Of Cell Population Proliferation (GO:0008285)	8	379	0.019859504
86	Negative Regulation Of Stress Fiber Assembly (GO:0051497)	2	25	0.02044439
87	Lamellipodium Assembly (GO:0030032)	2	25	0.02044439
88	Positive Regulation Of Cell Projection Organization (GO:0031346)	4	118	0.020866243

89	Negative Regulation Of Insulin Receptor Signaling Pathway (GO:0046627)	2	26	0.022020985
90	Regulation Of Chromatin Organization (GO:1902275)	2	27	0.023646278
91	Regulation Of Peptidase Activity (GO:0052547)	2	27	0.023646278
92	Establishment Of Protein Localization To Vacuole (GO:0072666)	2	27	0.023646278
93	Positive Regulation Of Mitotic Cell Cycle (GO:0045931)	2	27	0.023646278
94	Negative Regulation Of Cellular Response To Insulin Stimulus (GO:1900077)	2	27	0.023646278
95	Protein Autoubiquitination (GO:0051865)	3	71	0.025112081
96	Regulation Of Protein Transport (GO:0051223)	2	28	0.025319295
97	Negative Regulation Of Actin Filament Bundle Assembly (GO:0032232)	2	28	0.025319295
98	Regulation Of Anatomical Structure Morphogenesis (GO:0022603)	4	127	0.026453035
99	Regulation Of Rho Protein Signal Transduction (GO:0035023)	3	73	0.026981692
100	Regulation Of DNA Repair (GO:0006282)	4	129	0.027804832
101	Golgi Organization (GO:0007030)	4	130	0.028495934
102	G2-M Checkpoint	5	200	0.032816267
103	Interferon Gamma Response	5	200	0.032816267
104	p53 Pathway	5	200	0.032816267
105	Hedgehog Signaling	2	36	0.040308767

[V5 MERS Up]

	Term	Matched	Total	P.value
1	Regulation Of Cholesterol Biosynthetic Process (GO:0045540)	3	15	1.81E-05
2	Regulation Of Cell Migration (GO:0030334)	8	434	0.000134139
3	Phosphatidylcholine Acyl-Chain Remodeling (GO:0036151)	2	7	0.000250719
4	Regulation Of Sterol Biosynthetic Process (GO:0106118)	2	8	0.000333537
5	Positive Regulation Of Wound Healing (GO:0090303)	3	40	0.000369691
6	Extracellular Matrix Organization (GO:0030198)	5	176	0.000380029
7	Positive Regulation Of Skeletal Muscle Tissue Development (GO:0048643)	2	9	0.000427863
8	Extracellular Matrix Disassembly (GO:0022617)	3	44	0.000490629
9	Cellular Component Disassembly (GO:0022411)	3	46	0.000559542
10	Extracellular Structure Organization (GO:0043062)	4	109	0.000580412
11	External Encapsulating Structure Organization (GO:0045229)	4	110	0.000600737
12	Regulation Of Alcohol Biosynthetic Process (GO:1902930)	2	11	0.000650726
13	Regulation Of Vascular Wound Healing (GO:0061043)	2	12	0.000779106
14	Phosphatidylcholine Metabolic Process (GO:0046470)	3	55	0.000945518
15	Regulation Of Endothelial Cell Chemotaxis (GO:2001026)	2	14	0.001069372
16	Positive Regulation Of Endothelial Cell Chemotaxis (GO:2001028)	2	14	0.001069372
17	Coagulation	4	138	0.001398504
18	Phosphatidylcholine Biosynthetic Process (GO:0006656)	2	19	0.001986892
19	Negative Regulation Of Cell Adhesion (GO:0007162)	3	72	0.002060153
20	Cholesterol Homeostasis	3	74	0.002228089

21	Histone H2A Acetylation (GO:0043968)	2	21	0.002429044
22	Positive Regulation Of Endocytosis (GO:0045807)	3	79	0.002684403
23	Negative Regulation Of Cellular Process (GO:0048523)	7	537	0.002691697
24	Regulation Of Cholesterol Metabolic Process (GO:0090181)	2	23	0.002913234
25	Protein N-linked Glycosylation Via Asparagine (GO:0018279)	2	23	0.002913234
26	Positive Regulation Of Nucleic Acid-Templated Transcription (GO:1903508)	7	557	0.003295554
27	Positive Regulation Of Striated Muscle Cell Differentiation (GO:0051155)	2	25	0.00343887
28	Negative Regulation Of Endothelial Cell Apoptotic Process (GO:2000352)	2	26	0.003717047
29	Positive Regulation Of Mitotic Cell Cycle (GO:0045931)	2	27	0.004005366
30	Negative Regulation Of Notch Signaling Pathway (GO:0045746)	2	27	0.004005366
31	Negative Regulation Of Macromolecule Biosynthetic Process (GO:0010558)	3	98	0.0049247
32	Endodermal Cell Differentiation (GO:0035987)	2	31	0.005258625
33	Positive Regulation Of Mononuclear Cell Migration (GO:0071677)	2	31	0.005258625
34	Negative Regulation Of Chemotaxis (GO:0050922)	2	31	0.005258625
35	Complement	4	200	0.0053199
36	Regulation Of Angiogenesis (GO:0045765)	4	205	0.005800521
37	Positive Regulation Of Vasculature Development (GO:1904018)	3	104	0.005809134
38	Peroxisome	3	104	0.005809134
39	Semaphorin-Plexin Signaling Pathway (GO:0071526)	2	34	0.006301555
40	Regulation Of DNA Biosynthetic Process (GO:2000278)	2	34	0.006301555
41	Glycerophospholipid Biosynthetic Process (GO:0046474)	3	108	0.006448277
42	Endoderm Formation (GO:0001706)	2	35	0.00666844
43	Response To Endoplasmic Reticulum Stress (GO:0034976)	3	114	0.007482913
44	Positive Regulation Of Cell Motility (GO:2000147)	4	221	0.007531417
45	Negative Regulation Of Epithelial Cell Apoptotic Process (GO:1904036)	2	38	0.007825843
46	Protein Processing (GO:0016485)	3	117	0.008034942
47	Regulation Of Receptor-Mediated Endocytosis (GO:0048259)	2	39	0.008230333
48	Histone H4 Acetylation (GO:0043967)	2	39	0.008230333
49	Positive Regulation Of Angiogenesis (GO:0045766)	3	119	0.008415974
50	Regulation Of Mitotic Cell Cycle (GO:0007346)	3	125	0.009622229
51	Regulation Of Endothelial Cell Apoptotic Process (GO:2000351)	2	43	0.009939917
52	Positive Regulation Of Chemotaxis (GO:0050921)	2	44	0.010389885
53	Establishment Of Protein Localization To Mitochondrion (GO:0072655)	2	44	0.010389885
54	Regulation Of DNA Repair (GO:0006282)	3	129	0.010479606
55	Organic Hydroxy Compound Transport (GO:0015850)	2	45	0.010848748
56	Regulation Of Protein Modification Process (GO:0031399)	2	45	0.010848748
57	Zymogen Activation (GO:0031638)	2	45	0.010848748
58	Positive Regulation Of DNA-templated Transcription (GO:0045893)	10	1243	0.010943071
59	Regulation Of Interleukin-10 Production (GO:0032653)	2	46	0.011316441
60	Positive Regulation Of Cell-Cell Adhesion (GO:0022409)	2	46	0.011316441
61	Negative Regulation Of Cell Motility (GO:2000146)	3	133	0.011380036
62	Regulation Of Wound Healing (GO:0061041)	2	47	0.011792897
63	Negative Regulation Of T Cell Activation (GO:0050868)	2	49	0.012771842
64	Regulation Of Protein Phosphorylation (GO:0001932)	4	265	0.013953955

65	Regulation Of Cell Adhesion (GO:0030155)	3	144	0.014081078
66	Negative Regulation Of Response To External Stimulus (GO:0032102)	3	146	0.014607954
67	Mitochondrial Transport (GO:0006839)	2	53	0.014832051
68	Positive Regulation Of Cell Migration (GO:0030335)	4	272	0.015218682
69	TGF-beta Signaling	2	54	0.015368048
70	Axon Guidance (GO:0007411)	3	149	0.015419067
71	Negative Regulation Of Gene Expression Via CpG Island Methylation (GO:0044027)	1	5	0.017379514
72	Regulation Of Focal Adhesion Disassembly (GO:0120182)	1	5	0.017379514
73	Neuroblast Proliferation (GO:0007405)	1	5	0.017379514
74	Blood Vessel Endothelial Cell Proliferation Involved In Sprouting Angiogenesis (GO:0002043)	1	5	0.017379514
75	Regulation Of Protein Targeting (GO:1903533)	1	5	0.017379514
76	Regulation Of Superoxide Metabolic Process (GO:0090322)	1	5	0.017379514
77	Plasma Membrane Raft Assembly (GO:0044854)	1	5	0.017379514
78	Plasma Membrane Raft Organization (GO:0044857)	1	5	0.017379514
79	Positive Regulation Of Cholesterol Biosynthetic Process (GO:0045542)	1	5	0.017379514
80	Positive Regulation Of Focal Adhesion Disassembly (GO:0120183)	1	5	0.017379514
81	Equilibrioception (GO:0050957)	1	5	0.017379514
82	tRNA Transport (GO:0051031)	1	5	0.017379514
83	Xenobiotic Transport Across Blood-Brain Barrier (GO:1990962)	1	5	0.017379514
84	Insulin Processing (GO:0030070)	1	5	0.017379514
85	Positive Regulation Of Skeletal Muscle Fiber Development (GO:0048743)	1	5	0.017379514
86	Positive Regulation Of Sterol Biosynthetic Process (GO:0106120)	1	5	0.017379514
87	Regulation Of Cell Population Proliferation (GO:0042127)	7	766	0.017462343
88	Protein Targeting To Mitochondrion (GO:0006626)	2	59	0.018170554
89	Mitotic Cytokinesis (GO:0000281)	2	59	0.018170554
90	Histone Acetylation (GO:0016573)	2	60	0.018755127
91	Positive Regulation Of Cell Junction Assembly (GO:1901890)	2	61	0.01934758
92	Negative Regulation Of Cell Migration (GO:0030336)	3	163	0.019536423
93	Regulation Of T Cell Activation (GO:0050863)	2	62	0.019947854
94	Regulation Of Cell Cycle (GO:0051726)	4	298	0.020541503
95	ATF6-mediated Unfolded Protein Response (GO:0036500)	1	6	0.02081953
96	Regulation Of Entry Of Bacterium Into Host Cell (GO:2000535)	1	6	0.02081953
97	Negative Regulation Of Plasminogen Activation (GO:0010757)	1	6	0.02081953
98	Regulation Of Intestinal Cholesterol Absorption (GO:0030300)	1	6	0.02081953
99	Regulation Of Phospholipid Transport (GO:2001138)	1	6	0.02081953
100	Phospholipase C-activating Dopamine Receptor Signaling Pathway (GO:0060158)	1	6	0.02081953
101	Choline Transport (GO:0015871)	1	6	0.02081953
102	Positive Regulation Of Toll-Like Receptor 3 Signaling Pathway (GO:0034141)	1	6	0.02081953
103	Leukotriene Transport (GO:0071716)	1	6	0.02081953
104	Negative Regulation Of CD4-positive, Alpha-Beta T Cell Proliferation (GO:2000562)	1	6	0.02081953
105	Protein N-linked Glycosylation (GO:0006487)	2	64	0.02117162
106	Myogenesis	3	200	0.033070333
107	Myc Targets V1	3	200	0.033070333
108	Inflammatory Response	3	200	0.033070333

[V6 MERS Down]

	Term	Matched	Total	P.value
1	Regulation Of G0 To G1 Transition (GO:0070316)	2	33	0.0011157
2	Connective Tissue Development (GO:0061448)	2	38	0.001478588
3	Cell Chemotaxis (GO:0060326)	2	50	0.002547877
4	Rho Protein Signal Transduction (GO:0007266)	2	52	0.002752822
5	Regulation Of Cyclin-Dependent Protein Kinase Activity (GO:1904029)	2	53	0.002858117
6	TNF-alpha Signaling via NF-kB	3	200	0.003277995
7	Inflammatory Response	3	200	0.003277995
8	Chemokine-Mediated Signaling Pathway (GO:0070098)	2	57	0.003297984
9	Cellular Response To Chemokine (GO:1990869)	2	59	0.003529054
10	Regulation Of Nucleic Acid-Templated Transcription (GO:1903506)	4	452	0.004428953
11	Neutrophil Chemotaxis (GO:0030593)	2	70	0.004930456
12	Granulocyte Chemotaxis (GO:0071621)	2	73	0.005350392
13	Neutrophil Migration (GO:1990266)	2	77	0.005935017
14	Regulation Of Cyclin-Dependent Protein Serine/Threonine Kinase Activity (GO:0000079)	2	79	0.006237826
15	Calcium-Mediated Signaling (GO:0019722)	2	85	0.007187738
16	Regulation Of Striated Muscle Tissue Development (GO:0016202)	1	6	0.008967338
17	Placenta Blood Vessel Development (GO:0060674)	1	6	0.008967338
18	Mitotic Nuclear Membrane Disassembly (GO:0007077)	1	6	0.008967338
19	Positive Regulation Of DNA-templated Transcription (GO:0045893)	6	1243	0.009323432
20	Positive Regulation Of Cold-Induced Thermogenesis (GO:0120162)	2	98	0.009454923
21	Regulation Of Transforming Growth Factor Beta Activation (GO:1901388)	1	7	0.010454324
22	Negative Regulation Of Appetite (GO:0032099)	1	7	0.010454324
23	Positive Regulation Of Metabolic Process (GO:0009893)	2	108	0.011387949
24	Fucose Catabolic Process (GO:0019317)	1	8	0.011939153
25	L-fucose Catabolic Process (GO:0042355)	1	8	0.011939153
26	L-fucose Metabolic Process (GO:0042354)	1	8	0.011939153
27	Positive Regulation Of Calcium Ion Import Across Plasma Membrane (GO:1905665)	1	8	0.011939153
28	Nuclear Membrane Disassembly (GO:0051081)	1	8	0.011939153
29	Brown Fat Cell Differentiation (GO:0050873)	1	8	0.011939153
30	Positive Regulation Of Transcription By RNA Polymerase II (GO:0045944)	5	938	0.012048238
31	Regulation Of Protein Serine/Threonine Kinase Activity (GO:0071900)	2	112	0.012205934
32	Regulation Of DNA Metabolic Process (GO:0051052)	2	124	0.014809355
33	Regulation Of Calcium Ion Import Across Plasma Membrane (GO:1905664)	1	10	0.014902355
34	snRNA Transcription By RNA Polymerase II (GO:0042795)	1	10	0.014902355
35	calcineurin-NFAT Signaling Cascade (GO:0033173)	1	10	0.014902355
36	Calcineurin-Mediated Signaling (GO:0097720)	1	11	0.016380734

37	Adipose Tissue Development (GO:0060612)	1	12	0.017856968
38	Negative Regulation Of Voltage-Gated Calcium Channel Activity (GO:1901386)	1	12	0.017856968
39	Positive Regulation Of Voltage-Gated Calcium Channel Activity (GO:1901387)	1	12	0.017856968
40	snRNA Transcription (GO:0009301)	1	12	0.017856968
41	Ras Protein Signal Transduction (GO:0007265)	2	144	0.019628373
42	Regulation Of Cold-Induced Thermogenesis (GO:0120161)	2	146	0.020142113
43	Establishment Of Chromosome Localization (GO:0051303)	1	14	0.020803015
44	Formation Of Cytoplasmic Translation Initiation Complex (GO:0001732)	1	14	0.020803015
45	Protein Modification Process (GO:0036211)	4	711	0.020831409
46	Positive Regulation Of Cell Activation (GO:0050867)	1	15	0.022272833
47	UV Response Up	2	158	0.02334179
48	Positive Regulation Of Lymphocyte Migration (GO:2000403)	1	16	0.023740519
49	Regulation Of Transforming Growth Factor Beta Production (GO:0071634)	1	16	0.023740519
50	Nuclear Chromosome Segregation (GO:0098813)	1	16	0.023740519
51	Regulation Of Gene Expression (GO:0010468)	5	1127	0.024779057
52	Triglyceride Biosynthetic Process (GO:0019432)	1	17	0.025206075
53	Rac Protein Signal Transduction (GO:0016601)	1	17	0.025206075
54	Positive Regulation Of calcineurin-NFAT Signaling Cascade (GO:0070886)	1	19	0.02813081
55	Positive Regulation Of Calcineurin-Mediated Signaling (GO:0106058)	1	19	0.02813081
56	Inositol Phosphate-Mediated Signaling (GO:0048016)	1	19	0.02813081
57	Negative Regulation Of Calcium Ion Transmembrane Transport (GO:1903170)	1	19	0.02813081
58	Calcium-Mediated Signaling Using Intracellular Calcium Source (GO:0035584)	1	20	0.029589996
59	Negative Regulation Of Phosphate Metabolic Process (GO:0045936)	1	20	0.029589996
60	Monocarboxylic Acid Catabolic Process (GO:0072329)	1	20	0.029589996
61	Myoblast Differentiation (GO:0045445)	1	20	0.029589996
62	Placenta Development (GO:0001890)	1	22	0.032502015
63	Acylglycerol Biosynthetic Process (GO:0046463)	1	22	0.032502015
64	Transcription By RNA Polymerase II (GO:0006366)	2	192	0.033444134
65	Cellular Lipid Catabolic Process (GO:0044242)	1	23	0.033954856
66	Regulation Of T Cell Migration (GO:2000404)	1	23	0.033954856
67	Positive Regulation Of Cell Population Proliferation (GO:0008284)	3	483	0.03507837
68	Positive Regulation Of Cellular Response To Transforming Growth Factor Beta Stimulus (GO:1903846)	1	24	0.035405588
69	Positive Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0030511)	1	24	0.035405588
70	heme Metabolism	2	200	0.036030988
71	Positive Regulation Of T Cell Migration (GO:2000406)	1	25	0.036854213
72	Regulation Of Cell Size (GO:0008361)	1	25	0.036854213
73	Plasma Membrane Invagination (GO:0099024)	1	26	0.038300736
74	Monoubiquitinated Histone H2A Deubiquitination (GO:0035522)	1	27	0.039745158
75	Monoubiquitinated Histone Deubiquitination (GO:0035521)	1	27	0.039745158
76	Clathrin-Dependent Endocytosis (GO:0072583)	1	27	0.039745158
77	Cortical Cytoskeleton Organization (GO:0030865)	1	27	0.039745158
78	Positive Regulation Of Calcium Ion Transmembrane Transporter Activity (GO:1901021)	1	27	0.039745158
79	Negative Regulation Of Cation Channel Activity (GO:2001258)	1	28	0.041187484
80	RNA Biosynthetic Process (GO:0032774)	1	29	0.042627715

81	Regulation Of Voltage-Gated Calcium Channel Activity (GO:1901385)	1	29	0.042627715
82	Phagocytosis, Engulfment (GO:0006911)	1	30	0.044065855
83	Cytoplasmic Translational Initiation (GO:0002183)	1	30	0.044065855
84	Negative Regulation Of Calcium Ion Transmembrane Transporter Activity (GO:1901020)	1	30	0.044065855
85	Positive Regulation Of GTPase Activity (GO:0043547)	2	234	0.047843515
86	Vasculogenesis (GO:0001570)	1	33	0.048367756
87	Monoubiquitinated Protein Deubiquitination (GO:0035520)	1	33	0.048367756
88	Inflammatory Response (GO:0006954)	2	236	0.04857758
89	Histone Deubiquitination (GO:0016578)	1	34	0.04979756
90	Regulation Of calcineurin-NFAT Signaling Cascade (GO:0070884)	1	34	0.04979756
91	Positive Regulation Of Nucleic Acid-Templated Transcription (GO:1903508)	3	557	0.050019875
92	Histone H3 Acetylation (GO:0043966)	1	36	0.052650941
93	mRNA Transcription By RNA Polymerase II (GO:0042789)	1	38	0.055496039
94	Positive Regulation Of Cation Channel Activity (GO:2001259)	1	38	0.055496039
95	Cytokine-Mediated Signaling Pathway (GO:0019221)	2	257	0.056531071
96	Internal Peptidyl-Lysine Acetylation (GO:0018393)	1	39	0.056915489
97	Lymphocyte Migration (GO:0072676)	1	41	0.059748204
98	Monocyte Chemotaxis (GO:0002548)	1	42	0.061161476
99	Positive Regulation Of Calcium Ion Transmembrane Transport (GO:1904427)	1	42	0.061161476
100	mRNA Transcription (GO:0009299)	1	43	0.062572694
101	Positive Regulation Of Transcription Elongation By RNA Polymerase II (GO:0032968)	1	43	0.062572694
102	Regulation Of Cellular Component Size (GO:0032535)	1	43	0.062572694
103	Lymphocyte Chemotaxis (GO:0048247)	1	44	0.063981862
104	Regulation Of Insulin Receptor Signaling Pathway (GO:0046626)	1	44	0.063981862
105	Triglyceride Metabolic Process (GO:0006641)	1	45	0.065388982
106	Chromosome Organization (GO:0051276)	1	45	0.065388982
107	Male Gonad Development (GO:0008584)	1	46	0.066794057
108	Development Of Primary Male Sexual Characteristics (GO:0046546)	1	46	0.066794057
109	Regulation Of Cell Communication (GO:0010646)	1	49	0.070997042
110	Metaphase Plate Congression (GO:0051310)	1	51	0.073788859
111	Positive Regulation Of Protein Localization To Cell Periphery (GO:1904377)	1	51	0.073788859
112	Positive Regulation Of Protein Localization To Plasma Membrane (GO:1903078)	1	51	0.073788859
113	Cartilage Development (GO:0051216)	1	52	0.075181725
114	Positive Regulation Of Transcription Initiation By RNA Polymerase II (GO:0060261)	1	52	0.075181725
115	Gonad Development (GO:0008406)	1	53	0.076572566
116	Blood Vessel Morphogenesis (GO:0048514)	1	53	0.076572566
117	RNA Polymerase II Preinitiation Complex Assembly (GO:0051123)	1	56	0.080732968
118	Positive Regulation Of DNA-templated Transcription Initiation (GO:2000144)	1	56	0.080732968
119	Positive Regulation Of DNA-templated Transcription, Elongation (GO:0032786)	1	56	0.080732968
120	Regulation Of Transcription Initiation By RNA Polymerase II (GO:0060260)	1	57	0.082115738
121	Myeloid Cell Differentiation (GO:0030099)	1	57	0.082115738
122	DNA-templated Transcription Initiation (GO:0006352)	1	59	0.084875248
123	Transcription Preinitiation Complex Assembly (GO:0070897)	1	59	0.084875248
124	protein-DNA Complex Organization (GO:0071824)	1	60	0.086251994

125	Histone Acetylation (GO:0016573)	1	60	0.086251994
126	Fatty Acid Catabolic Process (GO:0009062)	1	61	0.087626738
127	Fat Cell Differentiation (GO:0045444)	1	62	0.088999482
128	Antimicrobial Humoral Immune Response Mediated By Antimicrobial Peptide (GO:0061844)	1	65	0.093105746
129	Cellular Response To Type II Interferon (GO:0071346)	1	66	0.094470521
130	Phagocytosis (GO:0006909)	1	69	0.098552943
131	Negative Regulation Of Epithelial Cell Proliferation (GO:0050680)	1	70	0.099909792
132	Regulation Of Actin Filament-Based Process (GO:0032970)	1	70	0.099909792
133	Regulation Of Cell Cycle G1/S Phase Transition (GO:1902806)	1	74	0.105317475
134	Regulation Of Cell Population Proliferation (GO:0042127)	3	766	0.105962602
135	Negative Regulation Of Phosphorylation (GO:0042326)	1	75	0.10666448
136	Regulation Of DNA Replication (GO:0006275)	1	75	0.10666448
137	Transcription Initiation At RNA Polymerase II Promoter (GO:0006367)	1	76	0.108009525
138	Regulation Of Transcription Elongation By RNA Polymerase II (GO:0034243)	1	77	0.109352612
139	Cellular Response To Nutrient Levels (GO:0031669)	1	78	0.110693745
140	Positive Regulation Of Protein Localization To Membrane (GO:1905477)	1	79	0.112032925
141	Response To Insulin (GO:0032868)	1	79	0.112032925
142	Regulation Of Protein Localization To Plasma Membrane (GO:1903076)	1	80	0.113370155
143	Glycoprotein Biosynthetic Process (GO:0009101)	1	80	0.113370155
144	Wound Healing (GO:0042060)	1	80	0.113370155
145	Response To Type II Interferon (GO:0034341)	1	80	0.113370155
146	Positive Regulation Of Multicellular Organismal Process (GO:0051240)	2	387	0.11406004
147	Cellular Response To Interleukin-1 (GO:0071347)	1	81	0.114705439
148	Histone Modification (GO:0016570)	1	81	0.114705439
149	Regulation Of Phosphorylation (GO:0042325)	1	82	0.116038779
150	Positive Regulation Of Amide Metabolic Process (GO:0034250)	1	85	0.120027161
151	Response To Interleukin-1 (GO:0070555)	1	85	0.120027161
152	Integrin-Mediated Signaling Pathway (GO:0007229)	1	85	0.120027161
153	Regulation Of Mitotic Cell Cycle Phase Transition (GO:1901990)	1	86	0.121352752
154	IL-6/JAK/STAT3 Signaling	1	87	0.122676413
155	Cellular Response To Peptide Hormone Stimulus (GO:0071375)	1	89	0.125317954
156	Regulation Of Epithelial Cell Proliferation (GO:0050678)	1	91	0.127951805
157	Regulation Of RNA Metabolic Process (GO:0051252)	1	91	0.127951805
158	Regulation Of Actin Cytoskeleton Organization (GO:0032956)	1	91	0.127951805
159	Cytoplasmic Translation (GO:0002181)	1	93	0.13057799
160	Positive Regulation Of Transmembrane Receptor Protein Serine/Threonine Kinase Signaling Pathway (GO:0090100)	1	95	0.133196528
161	Phosphorylation (GO:0016310)	2	429	0.134991381
162	Cellular Response To Insulin Stimulus (GO:0032869)	1	99	0.138410753
163	Antimicrobial Humoral Response (GO:0019730)	1	100	0.139709564
164	Androgen Response	1	100	0.139709564
165	Hemopoiesis (GO:0030097)	1	101	0.141006482
166	Activation Of GTPase Activity (GO:0090630)	1	102	0.14230151
167	Regulation Of RNA Splicing (GO:0043484)	1	102	0.14230151
168	Positive Regulation Of Vasculature Development (GO:1904018)	1	104	0.144885907

169	Regulation Of G1/S Transition Of Mitotic Cell Cycle (GO:2000045)	1	106	0.147462776
170	Regulation Of Cellular Response To Stress (GO:0080135)	1	107	0.148748394
171	Response To Tumor Necrosis Factor (GO:0034612)	1	108	0.150032137
172	Positive Regulation Of Translation (GO:0045727)	1	108	0.150032137
173	Cell-Matrix Adhesion (GO:0007160)	1	109	0.151314009
174	Regulation Of Transforming Growth Factor Beta Receptor Signaling Pathway (GO:0017015)	1	111	0.153872149
175	Cytoskeleton Organization (GO:0007010)	1	111	0.153872149
176	Regulation Of DNA-templated Transcription (GO:0006355)	5	1922	0.155886568
177	Regulation Of Cytoskeleton Organization (GO:0051493)	1	114	0.157695389
178	Positive Regulation Of Gene Expression (GO:0010628)	2	480	0.161481688
179	Cellular Response To Molecule Of Bacterial Origin (GO:0071219)	1	117	0.161501926
180	Regulation Of Small GTPase Mediated Signal Transduction (GO:0051056)	1	118	0.162767072
181	Positive Regulation Of Cell Cycle Process (GO:0090068)	1	118	0.162767072
182	Cellular Response To Tumor Necrosis Factor (GO:0071356)	1	119	0.164030373
183	Positive Regulation Of Angiogenesis (GO:0045766)	1	119	0.164030373
184	Fatty Acid Metabolic Process (GO:0006631)	1	122	0.16780923
185	Positive Regulation Of Macromolecule Biosynthetic Process (GO:0010557)	1	122	0.16780923
186	Receptor-Mediated Endocytosis (GO:0006898)	1	122	0.16780923
187	Protein Dephosphorylation (GO:0006470)	1	124	0.170319289
188	Cellular Response To Lipopolysaccharide (GO:0071222)	1	124	0.170319289
189	Protein Phosphorylation (GO:0006468)	2	500	0.172130407
190	Protein Targeting (GO:0006605)	1	129	0.17656246
191	Regulation Of DNA Repair (GO:0006282)	1	129	0.17656246
192	Regulation Of Cell Cycle Process (GO:0010564)	1	130	0.177805633
193	Spermatogenesis	1	135	0.183994333
194	Actin Filament Organization (GO:0007015)	1	144	0.195020703
195	Protein Glycosylation (GO:0006486)	1	147	0.198664048
196	Dephosphorylation (GO:0016311)	1	147	0.198664048
197	Skeletal System Development (GO:0001501)	1	149	0.201084084
198	protein-RNA Complex Assembly (GO:0022618)	1	150	0.202291451
199	DNA Repair	1	150	0.202291451
200	Fatty Acid Metabolism	1	158	0.211887095
201	Response To Lipopolysaccharide (GO:0032496)	1	159	0.213078677
202	Protein Autophosphorylation (GO:0046777)	1	162	0.21664298
203	Positive Regulation Of Cellular Process (GO:0048522)	2	594	0.223550464
204	Positive Regulation Of Cellular Biosynthetic Process (GO:0031328)	1	174	0.230744768
205	Positive Regulation Of Hydrolase Activity (GO:0051345)	1	176	0.233071081
206	Positive Regulation Of ERK1 And ERK2 Cascade (GO:0070374)	1	179	0.236547805
207	Negative Regulation Of Macromolecule Metabolic Process (GO:0010605)	1	186	0.244601013
208	Regulation Of Signal Transduction (GO:0009966)	1	193	0.252572076
209	Positive Regulation Of Protein Metabolic Process (GO:0051247)	1	196	0.255963299
210	DNA-templated Transcription (GO:0006351)	1	199	0.259339647
211	Mitotic Spindle	1	199	0.259339647
212	Xenobiotic Metabolism	1	200	0.260461801

213	Hypoxia	1	200	0.260461801
214	Glycolysis	1	200	0.260461801
215	p53 Pathway	1	200	0.260461801
216	Myogenesis	1	200	0.260461801
217	KRAS Signaling Up	1	200	0.260461801
218	Complement	1	200	0.260461801
219	Epithelial Mesenchymal Transition	1	200	0.260461801
220	Regulation Of Translation (GO:0006417)	1	202	0.262701182
221	Regulation Of Angiogenesis (GO:0045765)	1	205	0.266047966
222	Regulation Of GTPase Activity (GO:0043087)	1	214	0.276000442
223	Cellular Response To Lipid (GO:0071396)	1	228	0.291223256
224	Translation (GO:0006412)	1	234	0.297652179
225	Regulation Of ERK1 And ERK2 Cascade (GO:0070372)	1	244	0.308241984
226	Chromatin Organization (GO:0006325)	1	268	0.333031594
227	Regulation Of Intracellular Signal Transduction (GO:1902531)	1	297	0.361841285
228	Regulation Of Transcription By RNA Polymerase II (GO:0006357)	4	2028	0.362471601
229	Cellular Response To Cytokine Stimulus (GO:0071345)	1	308	0.37245128
230	Positive Regulation Of MAPK Cascade (GO:0043410)	1	310	0.374361961
231	Supramolecular Fiber Organization (GO:0097435)	1	316	0.380060324
232	Intracellular Protein Transport (GO:0006886)	1	325	0.388513901
233	Negative Regulation Of Gene Expression (GO:0010629)	1	336	0.398694799
234	Positive Regulation Of Macromolecule Metabolic Process (GO:0010604)	1	364	0.423875933
235	Negative Regulation Of Cell Population Proliferation (GO:0008285)	1	379	0.436943333
236	DNA Damage Response (GO:0006974)	1	384	0.441235113
237	Negative Regulation Of DNA-templated Transcription (GO:0045892)	2	1025	0.459435518
238	Cellular Response To Oxygen-Containing Compound (GO:1901701)	1	406	0.459746189
239	Organelle Organization (GO:0006996)	1	418	0.469591816
240	Nervous System Development (GO:0007399)	1	433	0.481655138
241	Negative Regulation Of Nucleic Acid-Templated Transcription (GO:1903507)	1	456	0.499638682
242	Negative Regulation Of Cellular Process (GO:0048523)	1	537	0.558293842
243	Negative Regulation Of Transcription By RNA Polymerase II (GO:0000122)	1	763	0.688938189

[V7 SARS2 Up]

	Term	Matched	Total	P.value
1	Endoplasmic Reticulum Calcium Ion Homeostasis (GO:0032469)	2	20	0.000406374
2	Vesicle-Mediated Transport (GO:0016192)	4	411	0.003155194
3	Negative Regulation Of Endoplasmic Reticulum Calcium Ion Concentration (GO:0032471)	1	5	0.007478193
4	Response To Peptidoglycan (GO:0032494)	1	5	0.007478193
5	Short-Chain Fatty Acid Catabolic Process (GO:0019626)	1	5	0.007478193
6	Presynaptic Active Zone Organization (GO:1990709)	1	5	0.007478193

7	Adenosine To Inosine Editing (GO:0006382)	1	6	0.008967338
8	Maintenance Of Lens Transparency (GO:0036438)	1	6	0.008967338
9	Mitochondrion-Endoplasmic Reticulum Membrane Tethering (GO:1990456)	1	6	0.008967338
10	Short-Chain Fatty Acid Metabolic Process (GO:0046459)	1	6	0.008967338
11	Regulation Of ATPase-coupled Calcium Transmembrane Transporter Activity (GO:1901894)	1	7	0.010454324
12	Negative Regulation Of Protein-Containing Complex Disassembly (GO:0043242)	1	8	0.011939153
13	RNA Metabolic Process (GO:0016070)	2	111	0.011999071
14	Apical Protein Localization (GO:0045176)	1	9	0.013421829
15	Negative Regulation Of Response To Cytokine Stimulus (GO:0060761)	1	10	0.014902355
16	Response To Cytokine (GO:0034097)	2	125	0.015036251
17	Mitochondrion Distribution (GO:0048311)	1	11	0.016380734
18	Adipose Tissue Development (GO:0060612)	1	12	0.017856968
19	MyD88-dependent Toll-Like Receptor Signaling Pathway (GO:0002755)	1	12	0.017856968
20	Axonal Transport Of Mitochondrion (GO:0019896)	1	12	0.017856968
21	Regulation Of Macrophage Cytokine Production (GO:0010935)	1	13	0.019331061
22	Negative Regulation Of Toll-Like Receptor Signaling Pathway (GO:0034122)	1	13	0.019331061
23	Negative Regulation Of Interleukin-12 Production (GO:0032695)	1	13	0.019331061
24	Protein Localization To Phagophore Assembly Site (GO:0034497)	1	13	0.019331061
25	Protein Localization To Synapse (GO:0035418)	1	13	0.019331061
26	Maturation Of LSU-rRNA From Tricistronic rRNA Transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000463)	1	14	0.020803015
27	Branched-Chain Amino Acid Metabolic Process (GO:0009081)	1	15	0.022272833
28	Presynapse Assembly (GO:0099054)	1	15	0.022272833
29	Negative Regulation Of ATP-dependent Activity (GO:0032780)	1	16	0.023740519
30	Maturation Of 5.8S rRNA (GO:0000460)	1	16	0.023740519
31	Negative Regulation Of Cytokine Production Involved In Immune Response (GO:0002719)	1	16	0.023740519
32	Base Conversion Or Substitution Editing (GO:0016553)	1	17	0.025206075
33	Nervous System Development (GO:0007399)	3	433	0.026546858
34	Vesicle-Mediated Transport In Synapse (GO:0099003)	1	18	0.026669505
35	Regulation Of Protein-Containing Complex Disassembly (GO:0043244)	1	19	0.02813081
36	Interleukin-1-Mediated Signaling Pathway (GO:0070498)	1	19	0.02813081
37	Negative Regulation Of Cytokine Production (GO:0001818)	2	178	0.029105193
38	Maturation Of LSU-rRNA (GO:0000470)	1	20	0.029589996
39	Glutamate Metabolic Process (GO:0006536)	1	20	0.029589996
40	Regulation Of Toll-Like Receptor Signaling Pathway (GO:0034121)	1	20	0.029589996
41	RNA Processing (GO:0006396)	2	183	0.030626813
42	Maturation Of 5.8S rRNA From Tricistronic rRNA Transcript (SSU-rRNA, 5.8S rRNA, LSU-rRNA) (GO:0000466)	1	21	0.031047063
43	Vesicle Transport Along Microtubule (GO:0047496)	1	22	0.032502015
44	Protein Localization To Cell Junction (GO:1902414)	1	23	0.033954856
45	Response To dsRNA (GO:0043331)	1	25	0.036854213
46	Response To Interferon-Beta (GO:0035456)	1	29	0.042627715
47	Negative Regulation Of Calcium Ion Transmembrane Transporter Activity (GO:1901020)	1	30	0.044065855
48	Toll-Like Receptor Signaling Pathway (GO:0002224)	1	31	0.045501907
49	Glutamine Family Amino Acid Metabolic Process (GO:0009064)	1	31	0.045501907
50	Negative Regulation Of Interleukin-6 Production (GO:0032715)	1	34	0.04979756

51	Response To Exogenous dsRNA (GO:0043330)	1	35	0.051225288
52	Dendrite Morphogenesis (GO:0048813)	1	35	0.051225288
53	tRNA Methylation (GO:0030488)	1	36	0.052650941
54	Synaptic Vesicle Cycle (GO:0099504)	1	37	0.054074524
55	Connective Tissue Development (GO:0061448)	1	38	0.055496039
56	Negative Regulation Of Type I Interferon Production (GO:0032480)	1	38	0.055496039
57	Signal Release From Synapse (GO:0099643)	1	38	0.055496039
58	Organelle Transport Along Microtubule (GO:0072384)	1	39	0.056915489
59	Anterograde Axonal Transport (GO:0008089)	1	39	0.056915489
60	Vesicle Cytoskeletal Trafficking (GO:0099518)	1	39	0.056915489
61	Regulation Of Cytokine-Mediated Signaling Pathway (GO:0001959)	1	40	0.058332876
62	Notch Signaling Pathway (GO:0007219)	1	40	0.058332876
63	Synaptic Vesicle Exocytosis (GO:0016079)	1	41	0.059748204
64	Ceramide Biosynthetic Process (GO:0046513)	1	42	0.061161476
65	Neurotransmitter Secretion (GO:0007269)	1	43	0.062572694
66	Negative Regulation Of Immune System Process (GO:0002683)	1	44	0.063981862
67	Negative Regulation Of Response To Biotic Stimulus (GO:0002832)	1	45	0.065388982
68	Negative Regulation Of Tumor Necrosis Factor Production (GO:0032720)	1	47	0.06819709
69	Response To Organonitrogen Compound (GO:0010243)	1	47	0.06819709
70	Negative Regulation Of Tumor Necrosis Factor Superfamily Cytokine Production (GO:1903556)	1	49	0.070997042
71	Neurogenesis (GO:0022008)	1	49	0.070997042
72	Dicarboxylic Acid Metabolic Process (GO:0043648)	1	50	0.072393966
73	Regulation Of Interleukin-12 Production (GO:0032655)	1	50	0.072393966
74	Gene Expression (GO:0010467)	2	296	0.07240662
75	Amide Biosynthetic Process (GO:0043604)	1	51	0.073788859
76	Negative Regulation Of MAP Kinase Activity (GO:0043407)	1	51	0.073788859
77	Regulated Exocytosis (GO:0045055)	1	51	0.073788859
78	Negative Regulation Of Innate Immune Response (GO:0045824)	1	52	0.075181725
79	Negative Regulation Of Protein Catabolic Process (GO:0042177)	1	54	0.077961385
80	Ceramide Metabolic Process (GO:0006672)	1	55	0.079348185
81	Membrane Lipid Biosynthetic Process (GO:0046467)	1	57	0.082115738
82	Endosome To Lysosome Transport (GO:0008333)	1	57	0.082115738
83	Regulation Of Type I Interferon Production (GO:0032479)	1	59	0.084875248
84	Negative Regulation Of Cytokine-Mediated Signaling Pathway (GO:0001960)	1	59	0.084875248
85	Negative Regulation Of Peptidase Activity (GO:0010466)	1	60	0.086251994
86	Fatty Acid Catabolic Process (GO:0009062)	1	61	0.087626738
87	Autophagosome Organization (GO:1905037)	1	61	0.087626738
88	RNA Methylation (GO:0001510)	1	62	0.088999482
89	Endocytic Recycling (GO:0032456)	1	64	0.091738984
90	Autophagosome Assembly (GO:0000045)	1	65	0.093105746
91	Negative Regulation Of Endopeptidase Activity (GO:0010951)	1	66	0.094470521
92	Negative Regulation Of Immune Response (GO:0050777)	1	66	0.094470521
93	tRNA Modification (GO:0006400)	1	67	0.09583331
94	Protein Localization (GO:0008104)	2	351	0.096905262

95	Regulation Of Endopeptidase Activity (GO:0052548)	1	69	0.098552943
96	Response To Molecule Of Bacterial Origin (GO:0002237)	1	69	0.098552943
97	Synapse Assembly (GO:0007416)	1	71	0.101264667
98	Regulation Of Cellular Localization (GO:0060341)	1	72	0.102617571
99	Negative Regulation Of Catabolic Process (GO:0009895)	1	72	0.102617571
100	DNA Replication (GO:0006260)	1	73	0.103968506
101	Sphingolipid Biosynthetic Process (GO:0030148)	1	77	0.109352612
102	Actomyosin Structure Organization (GO:0031032)	1	77	0.109352612
103	Cell Morphogenesis Involved In Neuron Differentiation (GO:0048667)	1	77	0.109352612
104	Regulation Of Innate Immune Response (GO:0045088)	1	78	0.110693745
105	Negative Regulation Of Cellular Component Organization (GO:0051129)	1	79	0.112032925
106	Negative Regulation Of Protein Serine/Threonine Kinase Activity (GO:0071901)	1	80	0.113370155
107	Negative Regulation Of NF-kappaB Transcription Factor Activity (GO:0032088)	1	81	0.114705439
108	Cellular Response To Interleukin-1 (GO:0071347)	1	81	0.114705439
109	Response To Interleukin-1 (GO:0070555)	1	85	0.120027161
110	Exocytosis (GO:0006887)	1	86	0.121352752
111	Organelle Organization (GO:0006996)	2	418	0.12942372
112	Protein O-linked Glycosylation (GO:0006493)	1	93	0.13057799
113	Sphingolipid Metabolic Process (GO:0006665)	1	94	0.131888213
114	Cell Junction Assembly (GO:0034329)	1	95	0.133196528
115	Regulation Of Protein Localization (GO:0032880)	1	97	0.135807442
116	Monocarboxylic Acid Metabolic Process (GO:0032787)	1	97	0.135807442
117	Lysosomal Transport (GO:0007041)	1	105	0.146175281
118	Negative Regulation Of MAPK Cascade (GO:0043409)	1	105	0.146175281
119	Response To Lipid (GO:0033993)	1	110	0.152594012
120	Cytoskeleton Organization (GO:0007010)	1	111	0.153872149
121	Negative Regulation Of Defense Response (GO:0031348)	1	112	0.155148423
122	Regulation Of MAP Kinase Activity (GO:0043405)	1	114	0.157695389
123	Regulation Of Interleukin-6 Production (GO:0032675)	1	114	0.157695389
124	Regulation Of Protein Catabolic Process (GO:0042176)	1	122	0.16780923
125	Fatty Acid Metabolic Process (GO:0006631)	1	122	0.16780923
126	Organonitrogen Compound Biosynthetic Process (GO:1901566)	1	123	0.169065176
127	Regulation Of Tumor Necrosis Factor Production (GO:0032680)	1	127	0.174070661
128	Protein Targeting (GO:0006605)	1	129	0.17656246
129	Golgi Organization (GO:0007030)	1	130	0.177805633
130	Synapse Organization (GO:0050808)	1	131	0.179046992
131	Plasma Membrane Bounded Cell Projection Organization (GO:0120036)	1	132	0.180286538
132	Protein Localization To Plasma Membrane (GO:0072659)	1	137	0.186457184
133	Intracellular Calcium Ion Homeostasis (GO:0006874)	1	139	0.188912849
134	Protein Localization To Cell Periphery (GO:1990778)	1	142	0.192582915
135	Actin Filament Organization (GO:0007015)	1	144	0.195020703
136	Negative Regulation Of Response To External Stimulus (GO:0032102)	1	146	0.197451374
137	Neuron Projection Morphogenesis (GO:0048812)	1	146	0.197451374
138	Negative Regulation Of Protein Metabolic Process (GO:0051248)	1	147	0.198664048

139	Protein Glycosylation (GO:0006486)	1	147	0.198664048
140	Negative Regulation Of DNA-binding Transcription Factor Activity (GO:0043433)	1	149	0.201084084
141	Neuron Development (GO:0048666)	1	150	0.202291451
142	Positive Regulation Of NF-kappaB Transcription Factor Activity (GO:0051092)	1	152	0.204700896
143	Regulation Of Cellular Component Organization (GO:0051128)	1	153	0.205902979
144	Response To Lipopolysaccharide (GO:0032496)	1	159	0.213078677
145	Mitochondrion Organization (GO:0007005)	1	162	0.21664298
146	Positive Regulation Of ERK1 And ERK2 Cascade (GO:0070374)	1	179	0.236547805
147	Endocytosis (GO:0006897)	1	189	0.248027194
148	Protein Localization To Membrane (GO:0072657)	1	192	0.251438351
149	Neuron Projection Development (GO:0031175)	1	192	0.251438351
150	Modification-Dependent Protein Catabolic Process (GO:0019941)	1	192	0.251438351
151	Regulation Of Programmed Cell Death (GO:0043067)	1	195	0.254834547
152	Endomembrane System Organization (GO:0010256)	1	196	0.255963299
153	Regulation Of ERK1 And ERK2 Cascade (GO:0070372)	1	244	0.308241984
154	Positive Regulation Of DNA-binding Transcription Factor Activity (GO:0051091)	1	246	0.310341344
155	Cytokine-Mediated Signaling Pathway (GO:0019221)	1	257	0.321778189
156	Cellular Component Assembly (GO:0022607)	1	260	0.324865372
157	Negative Regulation Of Signal Transduction (GO:0009968)	1	267	0.332016062
158	Central Nervous System Development (GO:0007417)	1	283	0.348086647
159	DNA Metabolic Process (GO:0006259)	1	288	0.353031597
160	Cellular Response To Cytokine Stimulus (GO:0071345)	1	308	0.37245128
161	Positive Regulation Of MAPK Cascade (GO:0043410)	1	310	0.374361961
162	Supramolecular Fiber Organization (GO:0097435)	1	316	0.380060324
163	Organelle Assembly (GO:0070925)	1	322	0.3857085
164	Intracellular Protein Transport (GO:0006886)	1	325	0.388513901
165	Protein Modification By Small Protein Conjugation (GO:0032446)	1	364	0.423875933
166	Ubiquitin-Dependent Protein Catabolic Process (GO:0006511)	1	367	0.426512647
167	Phosphorylation (GO:0016310)	1	429	0.47846444
168	Protein Ubiquitination (GO:0016567)	1	434	0.482449859
169	Regulation Of Nucleic Acid-Templated Transcription (GO:1903506)	1	452	0.496555045
170	Protein Phosphorylation (GO:0006468)	1	500	0.532376114
171	Regulation Of Apoptotic Process (GO:0042981)	1	705	0.659514027
172	Protein Modification Process (GO:0036211)	1	711	0.662678442
173	Positive Regulation Of Transcription By RNA Polymerase II (GO:0045944)	1	938	0.763576488
174	Regulation Of DNA-templated Transcription (GO:0006355)	2	1922	0.798022186
175	Regulation Of Transcription By RNA Polymerase II (GO:0006357)	2	2028	0.82279888
176	Regulation Of Gene Expression (GO:0010468)	1	1127	0.824706214
177	Positive Regulation Of DNA-templated Transcription (GO:0045893)	1	1243	0.854327184
178	IL-2/STAT5 Signaling	2	199	0.035703458
179	Estrogen Response Early	2	200	0.036030988
180	Spermatogenesis	1	135	0.183994333
181	Mitotic Spindle	1	199	0.259339647
182	Myogenesis	1	200	0.260461801

183	KRAS Signaling Up	1	200	0.260461801
184	Interferon Gamma Response	1	200	0.260461801
185	p53 Pathway	1	200	0.260461801
186	Complement	1	200	0.260461801
187	mTORC1 Signaling	1	200	0.260461801
188	Estrogen Response Late	1	200	0.260461801

[V8 SARS2 Down]

	Term	Matched	Total	P.value
1	Cotranslational Protein Targeting To Membrane (GO:0006613)	4	13	2.73E-06
2	Androgen Response	7	100	1.64E-05
3	Endoplasmic Reticulum To Golgi Vesicle-Mediated Transport (GO:0006888)	7	115	4.07E-05
4	SRP-dependent Cotranslational Protein Targeting To Membrane (GO:0006614)	3	10	5.89E-05
5	Cellular Response To Starvation (GO:0009267)	7	126	7.28E-05
6	Chromosome Condensation (GO:0030261)	4	32	0.000122018
7	Negative Regulation Of DNA Metabolic Process (GO:0051053)	4	49	0.000646481
8	Protein Targeting To ER (GO:0045047)	3	23	0.000805524
9	Protein Transport (GO:0015031)	9	313	0.0010043
10	Golgi Vesicle Transport (GO:0048193)	7	197	0.001100153
11	mTORC1 Signaling	7	200	0.001200692
12	Glycolysis	7	200	0.001200692
13	Regulation Of Immunoglobulin Production (GO:0002637)	3	27	0.001299401
14	Response To UV-C (GO:0010225)	2	7	0.001317017
15	Protein Retention In ER Lumen (GO:0006621)	2	7	0.001317017
16	Glycolytic Process (GO:0006096)	3	29	0.001604243
17	Gluconeogenesis (GO:0006094)	3	32	0.002139523
18	Positive Regulation Of DNA Binding (GO:0043388)	3	33	0.002339678
19	Positive Regulation Of Immunoglobulin Production (GO:0002639)	3	34	0.00255106
20	Hexose Biosynthetic Process (GO:0019319)	3	35	0.002773876
21	Maintenance Of Protein Localization In Endoplasmic Reticulum (GO:0035437)	2	11	0.003377091
22	Positive Regulation Of Production Of Molecular Mediator Of Immune Response (GO:0002702)	3	38	0.003512893
23	Cellular Response To Nutrient Levels (GO:0031669)	4	78	0.003634693
24	Regulation Of Hematopoietic Stem Cell Differentiation (GO:1902036)	2	12	0.004031154
25	Early Endosome To Golgi Transport (GO:0034498)	2	12	0.004031154
26	Carbohydrate Catabolic Process (GO:0016052)	3	41	0.004361594
27	Negative Regulation Of DNA Recombination (GO:0045910)	3	41	0.004361594
28	Cranial Nerve Development (GO:0021545)	2	13	0.004739003
29	Autophagosome Maturation (GO:0097352)	3	44	0.005324462
30	Regulation Of DNA Recombination (GO:0000018)	3	44	0.005324462
31	Chromosome Organization (GO:0051276)	3	45	0.005671488
32	Intracellular Protein Transmembrane Transport (GO:0065002)	3	46	0.00603178
33	Regulation Of Clathrin-Dependent Endocytosis (GO:2000369)	2	15	0.006312476
34	Positive Regulation Of Sprouting Angiogenesis (GO:1903672)	2	15	0.006312476
35	Intracellular Sterol Transport (GO:0032366)	2	15	0.006312476
36	Retrograde Vesicle-Mediated Transport, Golgi To Endoplasmic Reticulum (GO:0006890)	3	48	0.006792671

37	Glycoprotein Catabolic Process (GO:0006516)	2	16	0.007176338
38	Intracellular Cholesterol Transport (GO:0032367)	2	16	0.007176338
39	Negative Regulation Of Anoikis (GO:2000811)	2	16	0.007176338
40	Pyruvate Metabolic Process (GO:0006090)	3	50	0.007608098
41	Regulation Of Hematopoietic Progenitor Cell Differentiation (GO:1901532)	2	17	0.008090459
42	Carbohydrate Derivative Catabolic Process (GO:1901136)	2	17	0.008090459
43	Regulation Of Macromolecule Biosynthetic Process (GO:0010556)	3	53	0.008935387
44	Apoptosis	5	161	0.009845411
45	Positive Regulation Of Kinase Activity (GO:0033674)	4	104	0.009980061
46	Macroautophagy (GO:0016236)	4	104	0.009980061
47	Double-Strand Break Repair (GO:0006302)	5	168	0.011681476
48	Glucose Metabolic Process (GO:0006006)	3	59	0.011973914
49	Positive Regulation Of Transcription Regulatory Region DNA Binding (GO:2000679)	2	21	0.012232602
50	Regulation Of Anoikis (GO:2000209)	2	21	0.012232602
51	Double-Strand Break Repair Via Homologous Recombination (GO:0000724)	4	111	0.012451835
52	Autophagosome Organization (GO:1905037)	3	61	0.013102723
53	Unfolded Protein Response	4	113	0.013223634
54	Protein-Containing Complex Disassembly (GO:0032984)	3	62	0.013689145
55	Telomere Organization (GO:0032200)	3	63	0.014290313
56	Autophagosome Assembly (GO:0000045)	3	65	0.01553706
57	Protein Exit From Endoplasmic Reticulum (GO:0032527)	2	24	0.01582607
58	Intracellular Protein Transport (GO:0006886)	7	325	0.016372583
59	Telomere Maintenance (GO:0000723)	3	68	0.017518753
60	L-amino Acid Transport (GO:0015807)	2	26	0.018441565
61	Regulation Of Vascular Endothelial Growth Factor Production (GO:0010574)	2	26	0.018441565
62	Regulation Of Cellular Biosynthetic Process (GO:0031326)	3	70	0.018914596
63	Phospholipid Biosynthetic Process (GO:0008654)	2	27	0.019812941
64	Transcription By RNA Polymerase III (GO:0006383)	2	28	0.021225726
65	Regulation Of DNA Replication (GO:0006275)	3	75	0.022666717
66	Vacuolar Acidification (GO:0007035)	2	29	0.022679173
67	E2F Targets	5	200	0.023037596
68	Oxidative Phosphorylation	5	200	0.023037596
69	DNA Geometric Change (GO:0032392)	2	30	0.024172544
70	Negative Regulation Of Blood Vessel Morphogenesis (GO:2000181)	3	77	0.024272712
71	Positive Regulation Of Extrinsic Apoptotic Signaling Pathway (GO:2001238)	2	31	0.025705111
72	Regulation Of Cyclin-Dependent Protein Serine/Threonine Kinase Activity (GO:0000079)	3	79	0.025938762
73	Very Long-Chain Fatty Acid Metabolic Process (GO:0000038)	2	32	0.027276153
74	Heterochromatin Formation (GO:0031507)	2	32	0.027276153
75	Intracellular pH Reduction (GO:0051452)	2	32	0.027276153
76	Macromolecule Modification (GO:0043412)	3	81	0.027664778
77	Negative Regulation Of NF-kappaB Transcription Factor Activity (GO:0032088)	3	81	0.027664778
78	Regulation Of Sprouting Angiogenesis (GO:1903670)	2	33	0.028884962
79	Protein Modification Process (GO:0036211)	11	711	0.029081618
80	Positive Regulation Of Protein Kinase Activity (GO:0045860)	4	145	0.029842861
81	Negative Regulation Of Mitotic Cell Cycle (GO:0045930)	2	34	0.030530834
82	Positive Regulation Of Organelle Organization (GO:0010638)	2	34	0.030530834
83	Defense Response To Gram-positive Bacterium (GO:0050830)	3	85	0.031296118
84	mRNA Metabolic Process (GO:0016071)	3	85	0.031296118
85	Negative Regulation Of Angiogenesis (GO:0016525)	3	86	0.032241165
86	Base-Excision Repair (GO:0006284)	2	36	0.033931007
87	Mitochondrion Disassembly (GO:0061726)	2	37	0.035683948

88	Negative Regulation Of Type I Interferon Production (GO:0032480)	2	38	0.037471232
89	Positive Regulation Of Protein Tyrosine Kinase Activity (GO:0061098)	2	38	0.037471232
90	Fatty Acid Metabolism	4	158	0.039016793
91	Regulation Of Protein Tyrosine Kinase Activity (GO:0061097)	2	39	0.039292201
92	Heterochromatin Organization (GO:0070828)	2	39	0.039292201
93	COPI Coating Of Golgi Vesicle (GO:0048205)	1	5	0.039610856
94	COPI-coated Vesicle Budding (GO:0035964)	1	5	0.039610856
95	Golgi Transport Vesicle Coating (GO:0048200)	1	5	0.039610856
96	Aminophospholipid Transport (GO:0015917)	1	5	0.039610856
97	Nucleotide-Binding Domain, Leucine Rich Repeat Containing Receptor Signaling Pathway (GO:0035872)	1	5	0.039610856
98	Regulation Of Protein Depolymerization (GO:1901879)	1	5	0.039610856
99	Cellular Response To Iron Ion (GO:0071281)	1	5	0.039610856
100	Regulation Of Tooth Mineralization (GO:0070170)	1	5	0.039610856
101	Sphingomyelin Biosynthetic Process (GO:0006686)	1	5	0.039610856
102	Positive Regulation Of Hemoglobin Biosynthetic Process (GO:0046985)	1	5	0.039610856
103	Trigeminal Nerve Development (GO:0021559)	1	5	0.039610856
104	Glycosyl Compound Biosynthetic Process (GO:1901659)	1	5	0.039610856
105	Wybutosine Biosynthetic Process (GO:0031591)	1	5	0.039610856
106	Wybutosine Metabolic Process (GO:0031590)	1	5	0.039610856
107	Lipid Droplet Disassembly (GO:1905691)	1	5	0.039610856
108	Protection From Natural Killer Cell Mediated Cytotoxicity (GO:0042270)	1	5	0.039610856