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Bioinformatics analyses of significant genes, related pathways, and candidate diagnostic biomarkers and molecular targets in SARS-CoV-2/COVID-19

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ABSTRACT

Severe acute respiratory syndrome corona virus 2 (SARS-CoV-2) infection is a leading cause of pneumonia and death. The aim of this investigation is to identify the key genes in SARS-CoV-2 infection and uncover their potential functions. We downloaded the expression profiling by high throughput sequencing of GSE152075 from the Gene Expression Omnibus database. Normalization of the data from primary SARS-CoV-2 infected samples and negative control samples in the database was conducted using R software. Then, joint analysis of the data was performed. Pathway and Gene ontology (GO) enrichment analyses were performed, and the protein-protein interaction (PPI) network, target gene - miRNA regulatory network, target gene - TF regulatory network of the differentially expressed genes (DEGs) were constructed using Cytoscape software. Identification of diagnostic biomarkers was conducted using receiver operating characteristic (ROC) curve analysis. 994 DEGs (496 up regulated and 498 down regulated genes) were identified. Pathway and GO enrichment analysis showed up and down regulated genes mainly enriched in the NOD-like receptor signaling pathway, Ribosome, response to external biotic stimulus and viral transcription in SARS-CoV-2 infection. Down and up regulated genes were selected to establish the PPI network, modules, target gene - miRNA regulatory network, target gene - TF regulatory network revealed that these genes were involved in adaptive immune system, fluid shear stress and atherosclerosis, influenza A and protein processing in endoplasmic reticulum. In total, ten genes (CBL, ISG15, NEDD4, PML, REL, CTNBN1, ERBB2, JUN, RPS8 and STUB1) were identified as good diagnostic biomarkers. In conclusion, the identified DEGs, hub genes and target genes contribute to the understanding of the molecular mechanisms underlying the advancement of SARS-CoV-2 infection and they may be used as diagnostic and molecular targets for the treatment of patients with SARS-CoV-2 infection in the future.

1. Introduction

Pandemic severe acute respiratory syndrome corona virus 2 (SARS-CoV-2)/corona virus disease 2019 (COVID-19) infection has been diagnosed as the cause of a widespread outbreak of respiratory tract infection across worldwide and responsible for 11,230,115 clinical infections and 529,882 death [Rothan and Byrareddy, 2020]. The severity of this infection has ranged from mild to severe. Although there are extensive research on the molecular mechanism in SARS-CoV-2

infection progression, the causes of SARS-CoV-2 infection is still not clear. The occurrence and development of SARS-CoV-2 infection is correlated with genetic [Mohammadpour et al., 2020], host [X. Zhang et al., 2020] and immune factors [Tay et al., 2020]. Therefore, searching for effective biomarkers and investigating their roles in the advancement of SARS-CoV-2 infection is of great importance for illuminate the pathogenesis, diagnosis, prevention, and treatment of SARS-CoV-2 infection.

In present situation, the advancement in molecular biology has

Abbreviations: SARS-CoV-2, Severe acute respiratory syndrome corona virus 2; GO, Gene ontology; PPI, protein-protein interaction; DEGs, differentially expressed genes; ROC, receiver operating characteristic; CBL, Cbl proto-oncogene; ISG15, ISG15 ubiquitin like modifier; NEDD4, NEDD4 E3 ubiquitin protein ligase; PML, promyelocyticleukemia; REL, REL proto-oncogene, NF-kB subunit.

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provided some novel understanding into possible diagnostic and therapeutic biomarkers for SARS-CoV-2 infection. Microarray is a high-throughput technology used for collecting global expression profiling by high throughput sequencing data from recruited samples of various diseases. These high throughput sequencing data are usually installed and accessible in free public websites, such as the NCBI-Gene Expression Omnibus database (NCBI-GEO) (<https://www.ncbi.nlm.nih.gov/geo>) [Clough and Barrett, 2016].

In order to continue the investigation of SARS-CoV-2 infection, expression profiling by high throughput sequencing data was used in the present investigation. The analyzed expression profile microarray data GSE152075 from the Gene Expression Omnibus (GEO) database, which contained SARS-CoV-2 and negative control samples, to perform bioinformatics analyses, including identifying differential expressed genes (DEGs), pathway and gene ontology (GO) enrichment analysis, protein-protein interaction (PPI) network and modules analysis, target gene - miRNA regulatory network, target gene - TF regulatory network analysis and receiver operating characteristic (ROC) curve analysis. The current investigation aimed to identify possible key biomarkers and to gain better understanding into the molecular mechanism of SARS-CoV-2 infection.

2. Materials and methods

2.1. Microarray data

GSE152075 was obtained from NCBI-GEO, a public database of expression profiling by high throughput sequencing, to filter the DEGs between SARS-CoV-2 infection samples and negative control samples. The expression profiling by high throughput sequencing data GSE152075 was based on GPL18573 platform Illumina NextSeq 500 (*Homo sapiens*) and consisted of 430 SARS-CoV-2 infection samples and 54 negative control samples.

2.2. Identification of DEGs

The limma package in R bioconductor [Ritchie et al., 2015] was used to analyze the DEGs between SARS-CoV-2 infection and negative control in the expression profiling by high throughput sequencing data of GSE152075, respectively. The adjusted *P*-value and $|\log_2FC|$ were determined. The Benjamini & Hochberg false discovery rate technique was used as a correction factor for the adjusted *P*-value in limma. The statistically significant DEGs were identified according to $P < 0.05$, and $|\log_2FC| > 1.08$ for up regulated genes and $|\log_2FC| < -1.651$ for down regulated genes.

2.3. Pathway enrichment of DEGs in SARS-CoV-2 infection

ToppGene (ToppFun) (<https://toppgene.cchmc.org/enrichment.jsp>) [Chen et al., 2009] was used to perform pathway enrichment analysis. ToppGene is a systematic and integrative functional annotation tools which allows researchers to resolve biological meaning behind large list of genes. Pathway enrichment analysis including the BIOCYC (<https://biocyc.org/>) [Caspi et al., 2016], Kyoto Encyclopedia of Genes and Genomes (KEGG) (<http://www.genome.jp/kegg/pathway.html>) [Kanehisa et al., 2019], Pathway Interaction Database (PID) (<https://wiki.nci.nih.gov/pages/viewpage.action?pageId=315491760>) [Schaefer et al., 2009], REACTOME (<https://reactome.org/>) [Fabregat et al., 2018], GenMAPP (<http://www.genmapp.org/>) [Dahlquist et al., 2002], MSigDB C2 BIOCARTA (<http://software.broadinstitute.org/gsea/msigdb/collections.jsp>) [Subramanian et al., 2005], PantherDB (<http://www.pantherdb.org/>) [Mi et al., 2017], Pathway Ontology (<http://www.obofoundry.org/ontology/pw.html>) [Petri et al., 2014] and Small Molecule Pathway Database (SMPDB) (<http://smpdb.ca/>) [Jewison et al., 2014] pathway enrichment analysis were carried out for the DEGs. $P < 0.05$ was regarded as statistical significance.

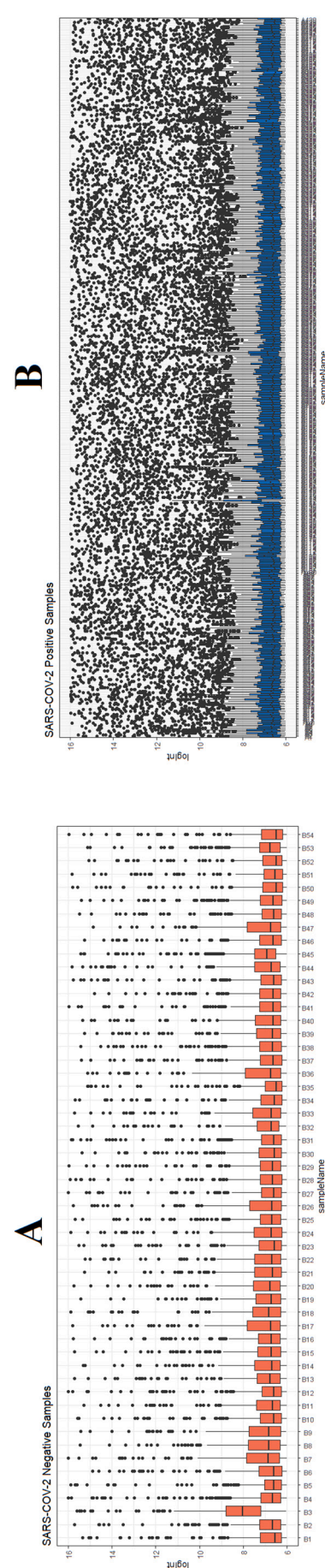


Fig. 1. Box plots of the normalized data. (A) 54 negative control samples (B) 430 SARS-CoV-2 infected samples. Horizontal axis represents the sample symbol and the vertical axis represents the gene expression values. The black line in the box plot represents the median value of gene expression. (A1 - A54 = negative control samples (red color box); B1 - B430 = SARS-CoV-2 infected samples (blue color box)). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

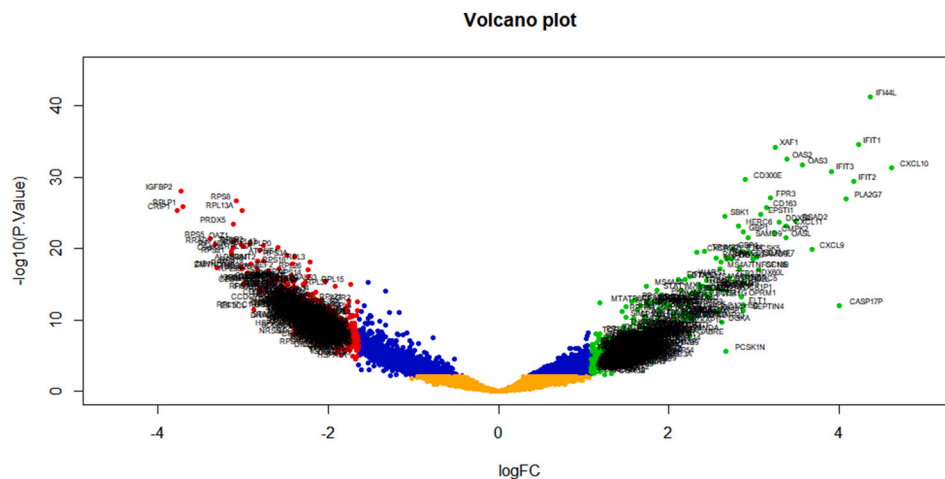


Fig. 2. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

2.4. Gene Ontology (GO) enrichment of DEGs in SARS-CoV-2 infection

In this investigation, we used ToppGene (ToppFun) (<https://toppgene.cchmc.org/enrichment.jsp>) [Chen et al., 2009] program for Gene Ontology (GO) enrichment analysis (<http://www.geneontology.org>) [Thomas, 2017] of the DEGs. The ToppGene analyses of the DEGs mainly contained gene ontology (GO) enrichment analysis. GO enrichment analysis could be further divided into three aspects, namely, biological processes (BP), cellular components (CC), and molecular functions (MF). The cutoff criterion for significant results was a *P* value < 0.05.

2.5. Analysis of protein-protein interaction network and modules

To display the interactions and functions of the DEGs, a protein-protein interaction (PPI) network was constructed based on the database of IID (Integrated Interactions Database) (<http://iid.ophid.utoronto.ca>) [Kotlyar et al., 2019] in this investigation and this PPI database linked with various databases such as Biological General Repository for Interaction Datasets (BioGRID) (<https://thebiogrid.org/>) [Oughtred et al., 2019], IntAct Molecular Interaction Database (<https://www.ebi.ac.uk/intact/>) [Orchard et al., 2014], the Molecular Interaction database (MINT) (<https://mint.bio.uniroma2.it/>) [Licata et al., 2012], InnateDB (<https://www.innatedb.com/>) [Breuer et al., 2013], Database of Interacting Proteins (DIP) (<http://dip.doe-mbi.ucla.edu/dip/Main.cgi>) [Salwinski et al., 2004], Human Protein Reference Database (HPRD) (<http://www.hprd.org/>) [Keshava Prasad et al., 2009] and Biomolecular Interaction Network Database (BIND) (<http://bond.unleashedinformatics.com/>) [Willis and Hogue, 2006]. All the parameters were set as defaults. We enforced Cytoscape 3.8.0 (<http://cytoscape.org/>) [Shannon et al., 2003] software to more intuitively visualize the constructed PPI network. The proteins were expressed as nodes, and the protein interactions are expressed as edges in the PPI network. To screen the potential hub genes that may be associated in the SARS-CoV-2 infection, we implemented the NetworkAnalyzer, a Cytoscape plug-in, and centrality algorithms included node degree [Przulj et al., 2004], betweenness centrality [Nguyen et al., 2011], stress centrality [Shi and Zhang, 2011], closeness centrality [Fadhil et al., 2014] and clustering coefficient [Wang et al., 2012]. The PEWC1 (<http://apps.cytoscape.org/apps/PEWC1>) Cytoscape plug-in was applied to analyze the modules in the PPI networks [Zaki et al., 2013].

2.6. Construction of target genes - miRNA regulatory network

We uploaded the DEGs to the database, miRNet (<https://www.mirnet.ca/>) [Fan and Xia, 2018] to obtain the miRNAs targeting the screened up and down regulated genes. The miRNet database is an online tool with different kinds of information generated from miRNAs investigation and this database is associated with various miRNA databases such as TarBase (<http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=tarbase/index>) [Vlachos et al., 2015], miRTarBase (<http://mirtarbase.mbc.nctu.edu.tw/php/download.php>) [Chou et al., 2018], miRecords (<http://miRecords.umn.edu/miRecords>) [Xiao et al., 2009], miR2Disease (<http://www.mir2disease.org/>) [Jiang et al., 2009], HMDD (<http://www.cuilab.cn/hmdd>) [Huang et al., 2019], PhenomiR (<http://mips.helmholtz-muenchen.de/phenomir/>) [Ruepp et al., 2010], SM2miR (<http://bioinfo.hrbmu.edu.cn/SM2miR/>) [Liu et al., 2013], PharmacomiR (<http://www.pharmaco-mir.org/>) [Rukov et al., 2014], EpimiR (<http://bioinfo.hrbmu.edu.cn/EpimiR/>) [Dai et al., 2014] and starBase (<http://starbase.sysu.edu.cn/>) [Li et al., 2014]. Researchers can build target genes - miRNA interaction networks in the help of this database. The generated list of target genes - miRNA pairs was preserved for further analysis. We then generated the network using Cytoscape software v. 3.8.0 (<http://cytoscape.org/>) [Shannon et al., 2003].

2.7. Construction of target genes - TF regulatory network

We uploaded the DEGs to the database, NetworkAnalyst database (<https://www.networkanalyst.ca/>) [Zhou et al., 2019] to obtain the TFs targeting the screened up and down regulated genes. The TF database is an online tool with different kinds of information generated from TFs investigation and this database is associated with ChEA (<http://amp.pharm.mssm.edu/lib/chea.jsp>) [Wang et al., 2013]. Researchers can build target genes - TF interaction networks in the help of this database. The generated list of target genes - TF pairs was preserved for further analysis. We then generated the network using Cytoscape software v. 3.8.0 (<http://cytoscape.org/>) [Shannon et al., 2003].

2.8. Receiver operating characteristic (ROC) curve analysis of hub genes

The receiver operating characteristic curve (ROC) was generated by predicting the probability of a diagnosis being of high or low integrated score of hub gene expression using the R "pROC" package [Robin et al., 2011]. Area under curve (AUC) analysis was performed to calculate diagnostic value of hub genes.

Table 1

The statistical metrics for key differentially expressed genes (DEGs).

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
IFI44L	4.364742	5.26E-42	1.88E-37	14.94117	Up	Interferon induced protein 44 like
IFIT1	4.225561	2.8E-35	5.02E-31	13.41666	Up	Interferon induced protein with tetratricopeptide repeats 1
XAF1	3.243468	5.64E-35	6.73E-31	13.3461	Up	XIAP associated factor 1
OAS2	3.387757	2.97E-33	2.66E-29	12.9426	Up	2'-5'-oligoadenylate synthetase 2
OAS3	3.571458	1.71E-32	1.23E-28	12.76252	Up	2'-5'-oligoadenylate synthetase 3
CXCL10	4.617597	4.74E-32	2.83E-28	12.65723	Up	C-X-C motif chemokine ligand 10
IFIT3	3.908841	1.41E-31	7.22E-28	12.54377	Up	Interferon induced protein with tetratricopeptide repeats 3
CD300E	2.89973	2.04E-30	9.12E-27	12.26417	Up	CD300e molecule
IFIT2	4.169362	4.24E-30	1.68E-26	12.18699	Up	Interferon induced protein with tetratricopeptide repeats 2
FPR3	3.192924	8.59E-28	2.8E-24	11.61824	Up	formyl peptide receptor 3
PLA2G7	4.083167	1.07E-27	3.18E-24	11.59474	Up	Phospholipase A2 group VII
CD163	3.146477	1.65E-26	3.93E-23	11.29537	Up	CD163 molecule
EPST11	3.07945	1.42E-25	2.82E-22	11.05635	Up	Epithelial stromal interaction 1
SBK1	2.661506	3.43E-25	6.46E-22	10.95752	Up	SH3 domain binding kinase 1
RSAD2	3.482956	1.45E-24	2.6E-21	10.79479	Up	Radical S-adenosyl methionine domain containing 2
DDX58	3.289868	1.85E-24	3.16E-21	10.76734	Up	DExD/H-box helicase 58
CXCL11	3.37324	6.58E-24	1.02E-20	10.62287	Up	C-X-C motif chemokine ligand 11
HERC6	2.817092	7.42E-24	1.11E-20	10.60924	Up	HECT and RLD domain containing E3 ubiquitin protein ligase family member 6
GBP1	2.870574	4.5E-23	6.45E-20	10.40149	Up	Guanylate binding protein 1
CMPK2	3.233123	6.3E-23	8.67E-20	10.36253	Up	Cytidine/uridine monophosphate kinase 2
OASL	3.368659	2.7E-22	3.58E-19	10.19273	Up	2'-5'-oligoadenylate synthetase like
SAMD9	2.92903	3.32E-22	4.24E-19	10.16851	Up	Sterile alpha motif domain containing 9
CXCL9	3.683419	1.14E-20	1.07E-17	9.747066	Up	C-X-C motif chemokine ligand 9
GBP4	2.742686	1.32E-20	1.21E-17	9.729499	Up	Guanylate binding protein 4
TRIM22	2.416207	2.12E-20	1.85E-17	9.67214	Up	Tripartite motif containing 22
IFI44	2.846223	2.17E-20	1.85E-17	9.669085	Up	Interferon induced protein 44
PCSK5	2.939636	3.01E-20	2.45E-17	9.629191	Up	Proproteinconvertasesubtilisin/kexin type 5
CXCR2P1	2.325221	3.55E-20	2.82E-17	9.609234	Up	C-X-C motif chemokine receptor 2 pseudogene 1
SIGLEC1	2.662436	1.59E-19	1.14E-16	9.42497	Up	Sialic acid binding Ig like lectin 1
SLAMF7	3.028959	1.55E-19	1.14E-16	9.428609	Up	SLAM family member 7
PARP9	2.553147	2.05E-19	1.44E-16	9.393624	Up	Poly(ADP-ribose) polymerase family member 9
SAMD9L	2.986266	2.51E-19	1.73E-16	9.36847	Up	Sterile alpha motif domain containing 9 like
DDX60	2.737389	2.75E-19	1.85E-16	9.35739	Up	DExD/H-box helicase 60
IFIT5	2.681662	3.01E-19	2E-16	9.345804	Up	Interferon induced protein with tetratricopeptide repeats 5
MX2	2.60661	6.95E-19	4.29E-16	9.24162	Up	MX dynamin like GTPase 2
TNFSF13B	2.82917	6.01E-18	3.41E-15	8.968649	Up	TNF superfamily member 13b
MS4A7	2.599481	6.66E-18	3.68E-15	8.955436	Up	Membrane spanning 4-domains A7
CCN5	3.054272	7.81E-18	4.17E-15	8.935061	Up	Cellular communication network factor 5
WARS1	2.247774	7.18E-17	3.49E-14	8.647398	Up	Tryptophanyl-tRNA synthetase 1
DDX60L	2.922109	7.22E-17	3.49E-14	8.646556	Up	DExD/H-box 60 like
ZEB2	2.715962	1.19E-16	5.55E-14	8.580364	Up	Zinc finger E-box binding homeobox 2
EIF2AK2	2.105911	1.8E-16	7.96E-14	8.525996	Up	Eukaryotic translation initiation factor 2 alpha kinase 2
DTX3L	2.188977	2.31E-16	9.87E-14	8.493195	Up	Deltex E3 ubiquitin ligase 3L
MS4A6A	2.436612	3E-16	1.21E-13	8.458081	Up	Membrane spanning 4-domains A6A
CYBB	2.77402	3.79E-16	1.51E-13	8.426995	Up	Cytochrome b-245 beta chain
HERC5	2.876745	5.09E-16	1.88E-13	8.387553	Up	HECT and RLD domain containing E3 ubiquitin protein ligase 5
SYNPO2L	2.65971	8.36E-16	2.93E-13	8.320806	Up	Synaptodin 2 like
TRIM5	2.347523	9.31E-16	3.17E-13	8.306202	Up	Tripartite motif containing 5
MSR1	2.396065	2.05E-15	6.68E-13	8.198981	Up	Macrophage scavenger receptor 1
MS4A4A	1.729479	2.14E-15	6.9E-13	8.193277	Up	Membrane spanning 4-domains A4A
SERPING1	2.464626	2.85E-15	8.95E-13	8.153969	Up	Serpin family G member 1
SLC8A1	2.562431	3.5E-15	1.08E-12	8.125779	Up	Solute carrier family 8 member A1
TFEC	2.48422	4.38E-15	1.31E-12	8.094978	Up	Transcription factor EC
MX1	2.148431	5.62E-15	1.65E-12	8.060791	Up	MX dynamin like GTPase 1
MARCHF1	2.491734	5.64E-15	1.65E-12	8.060356	Up	Membrane associated ring-CH-type finger 1
CCR1	2.623864	5.71E-15	1.66E-12	8.058442	Up	C-C motif chemokine receptor 1
STAT1	1.854344	7.31E-15	2.08E-12	8.024277	Up	Signal transducer and activator of transcription 1
ROCK1P1	2.681303	9.42E-15	2.61E-12	7.989222	Up	Rho associated coiled-coil containing protein kinase 1 pseudogene 1
CD84	2.348919	1.1E-14	2.99E-12	7.967208	Up	CD84 molecule
IFI6	2.298351	1.25E-14	3.36E-12	7.950009	Up	Interferon alpha inducible protein 6
CD274	2.497565	1.26E-14	3.38E-12	7.948105	Up	CD274 molecule
OAS1	2.417308	1.42E-14	3.76E-12	7.932102	Up	2'-5'-oligoadenylate synthetase 1
UBE2L6	2.274429	1.45E-14	3.81E-12	7.929222	Up	Ubiquitin conjugating enzyme E2 L6
PKNOX2	1.919941	3.25E-14	8.14E-12	7.815455	Up	PBX/knotted 1 homeobox 2
FCER1G	2.447666	5.51E-14	1.32E-11	7.740594	Up	Fc fragment of IgE receptor Ig
OPRM1	2.846954	6.69E-14	1.6E-11	7.713066	Up	Opioid receptor mu 1
IFITM1	2.470578	8.8E-14	2.06E-11	7.673773	Up	Interferon induced transmembrane protein 1
CD68	2.215624	1.07E-13	2.45E-11	7.645854	Up	CD68 molecule
RAP2C	2.033744	1.27E-13	2.89E-11	7.621172	Up	RAP2C, member of RAS oncogene family
PROX1	1.595242	1.36E-13	3.05E-11	7.610846	Up	Prosperohomeobox 1
CMKLR1	1.929944	1.97E-13	4.28E-11	7.557337	Up	Chemerin chemokine-like receptor 1
LRRK1	1.823013	2.16E-13	4.58E-11	7.544087	Up	Leucine rich repeat kinase 1
CFAP97D1	1.558297	2.51E-13	5.23E-11	7.522299	Up	CFAP97 domain containing 1
PDCD1LG2	1.72885	2.76E-13	5.68E-11	7.508651	Up	Programmed cell death 1 ligand 2

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
SEMA6D	2.115529	3.01E-13	6.09E-11	7.495927	Up	Semaphorin 6D
XRN1	1.886511	3.27E-13	6.54E-11	7.483885	Up	5'-3' exoribonuclease 1
APOL6	1.791201	3.43E-13	6.81E-11	7.477157	Up	Apolipoprotein L6
MTATP6P1	1.192475	3.56E-13	7.04E-11	7.47154	Up	MT-ATP6 pseudogene 1
HMGA2	1.784784	4.92E-13	9.57E-11	7.424121	Up	High mobility group AT-hook 2
TRIM38	1.94382	7.33E-13	1.4E-10	7.36526	Up	Tripartite motif containing 38
FLT1	2.877729	7.33E-13	1.4E-10	7.365317	Up	fms related tyrosine kinase 1
APOA2	1.968915	7.41E-13	1.4E-10	7.36377	Up	Apolipoprotein A2
GRIA4	1.939584	7.87E-13	1.47E-10	7.35477	Up	Glutamate ionotropic receptor AMPA type subunit 4
CCR5	2.122291	9.18E-13	1.69E-10	7.332009	Up	C-C motif chemokine receptor 5 (gene/pseudogene)
IFI16	1.668673	9.51E-13	1.74E-10	7.326709	Up	Interferon gamma inducible protein 16
SRRM4	1.745032	9.23E-13	1.69E-10	7.331201	Up	Serine/arginine repetitive matrix 4
CASP17P	4.004782	9.77E-13	1.77E-10	7.32273	Up	Caspase 17, pseudogene
FRMD3	2.224625	1.11E-12	1.96E-10	7.304438	Up	FERM domain containing 3
SUCNR1	1.490607	1.19E-12	2.08E-10	7.293258	Up	Succinate receptor 1
TLR2	2.005897	1.5E-12	2.55E-10	7.258449	Up	Toll like receptor 2
FAM180B	1.87669	2.35E-12	3.88E-10	7.191158	Up	Family with sequence similarity 180 member B
GBP5	2.376771	2.81E-12	4.54E-10	7.164292	Up	Guanylate binding protein 5
SLFN5	1.626376	3.02E-12	4.79E-10	7.153423	Up	Schlafen family member 5
C12orf50	2.583041	3.07E-12	4.83E-10	7.151364	Up	Chromosome 12 open reading frame 50
SEPTIN4	2.874578	4.27E-12	6.59E-10	7.100909	Up	Septin 4
PROSER1	1.896321	5.12E-12	7.64E-10	7.073317	Up	Proline and serine rich 1
RPH3A	1.45473	5.74E-12	8.46E-10	7.05592	Up	Rabphilin 3A
IDO1	2.549533	7.03E-12	1.02E-09	7.02503	Up	Indoleamine 2,3-dioxygenase 1
ADAP2	2.18801	8.03E-12	1.15E-09	7.004549	Up	ArfGAP with dual PH domains 2
C3AR1	1.894968	1.01E-11	1.4E-09	6.96844	Up	Complement C3a receptor 1
CLEC7A	2.260765	1.09E-11	1.49E-09	6.957423	Up	C-type lectin domain containing 7A
APOL2	2.04707	1.1E-11	1.51E-09	6.955361	Up	Apolipoprotein L2
TAC4	2.208645	1.31E-11	1.77E-09	6.929063	Up	Tachykinin precursor 4
ALOX15P1	2.32282	1.72E-11	2.25E-09	6.88635	Up	Arachidonate 15-lipoxygenase pseudogene 1
OSR1	2.141859	1.71E-11	2.25E-09	6.887078	Up	Odd-skipped related transcription factor 1
KLRD1	2.053116	2.09E-11	2.63E-09	6.856011	Up	Killer cell lectin like receptor D1
GPRIN3	2.169902	2.12E-11	2.65E-09	6.853831	Up	GPRIN family member 3
ACE2	1.727878	2.62E-11	3.15E-09	6.820685	Up	Angiotensin I converting enzyme 2
WNT7A	1.708334	3.55E-11	4.14E-09	6.772873	Up	Wnt family member 7A
HAVCR2	1.869368	4.36E-11	4.93E-09	6.740586	Up	Hepatitis A virus cellular receptor 2
SIM1	1.491927	4.31E-11	4.91E-09	6.742238	Up	SIM bHLH transcription factor 1
TIAM2	2.266147	5.26E-11	5.81E-09	6.710698	Up	TIAM Rac1 associated GEF 2
SP100	1.585579	5.37E-11	5.91E-09	6.707441	Up	SP100 nuclear antigen
FCGR3A	2.229013	5.92E-11	6.45E-09	6.691936	Up	Fc fragment of IgG receptor IIIa
NEDD4	2.064934	6.69E-11	7.14E-09	6.672333	Up	NEDD4 E3 ubiquitin protein ligase
MTND1P23	2.281679	6.89E-11	7.34E-09	6.667634	Up	MT-ND1 pseudogene 23
IKZF3	2.185695	8.19E-11	8.57E-09	6.639906	Up	IKAROS family zinc finger 3
TRIM69	1.911689	1.73E-10	1.69E-08	6.51935	Up	Tripartite motif containing 69
ZNFX1	1.588355	1.82E-10	1.77E-08	6.510661	Up	Zinc finger NFX1-type containing 1
DAB2	1.836422	2.1E-10	1.99E-08	6.487645	Up	DAB adaptor protein 2
CD86	1.721057	2.08E-10	1.98E-08	6.48928	Up	CD86 molecule
DGKA	2.624707	2.25E-10	2.12E-08	6.47636	Up	Diacylglycerol kinase alpha
NCKAP1L	2.114089	4.23E-10	3.79E-08	6.372251	Up	NCK associated protein 1 like
SCGB3A2	1.828089	4.31E-10	3.85E-08	6.369174	Up	Secretoglobulin family 3A member 2
OLR1	1.654019	6.34E-10	5.55E-08	6.304859	Up	Oxidized low density lipoprotein receptor 1
TNIP3	1.470225	8.08E-10	6.9E-08	6.264248	Up	TNFAIP3 interacting protein 3
KMO	1.682789	1.02E-09	8.51E-08	6.225778	Up	Kynurenine 3-monooxygenase
LILRB4	1.664874	1.07E-09	8.93E-08	6.216477	Up	Myeloid cell immunoglobulin like receptor B4
FLI1	1.999217	1.17E-09	9.63E-08	6.201639	Up	Fli-1 proto-oncogene, ETS transcription factor
CD226	1.78962	1.22E-09	9.97E-08	6.194572	Up	CD226 molecule
PLSCR1	1.545703	1.43E-09	1.15E-07	6.167278	Up	Phospholipid scramblase 1
LAIR1	1.802491	1.5E-09	1.2E-07	6.159069	Up	Leukocyte associated immunoglobulin like receptor 1
SYT2	1.958959	1.47E-09	1.18E-07	6.162851	Up	Synaptotagmin 2
SLC7A7	1.738594	1.66E-09	1.3E-07	6.142399	Up	Solute carrier family 7 member 7
GBP1P1	1.74422	1.63E-09	1.28E-07	6.145814	Up	Guanylate binding protein 1 pseudogene 1
LCP2	2.09313	1.81E-09	1.4E-07	6.127384	Up	Lymphocyte cytosolic protein 2
ADAMDEC1	1.823785	2.09E-09	1.58E-07	6.103193	Up	ADAM like decysin 1
MPEG1	1.923011	2.38E-09	1.76E-07	6.080809	Up	Macrophage expressed 1
CCL2	1.559368	2.93E-09	2.15E-07	6.044798	Up	C-C motif chemokine ligand 2
CCL8	1.411341	2.96E-09	2.18E-07	6.042751	Up	C-C motif chemokine ligand 8
GIMAP4	1.951836	4.38E-09	3.07E-07	5.974844	Up	GTPase, IMAP family member 4
MNDA	2.233904	4.53E-09	3.16E-07	5.968886	Up	Myeloid cell nuclear differentiation antigen
CD96	1.841957	4.96E-09	3.43E-07	5.952954	Up	CD96 molecule
MGAT4C	1.665748	5.74E-09	3.93E-07	5.927359	Up	MGAT4 family member C
CDH6	1.447681	5.36E-09	3.69E-07	5.939414	Up	Cadherin 6
PARP14	1.772547	6.14E-09	4.17E-07	5.915551	Up	Poly(ADP-ribose) polymerase family member 14
GREB1	1.54347	6.37E-09	4.3E-07	5.909035	Up	Growth regulating estrogen receptor binding 1
EVI2B	1.999099	8.1E-09	5.31E-07	5.866444	Up	Ecotropic viral integration site 2B
MS4A2	1.79191	6.93E-09	4.65E-07	5.893979	Up	Membrane spanning 4-domains A2
RNF213	1.629395	8.44E-09	5.49E-07	5.859157	Up	Ring finger protein 213

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
APOL3	1.770579	9.07E-09	5.84E-07	5.846397	Up	Apolipoprotein L3
FYB1	1.843964	9.13E-09	5.87E-07	5.84522	Up	FYN binding protein 1
ZEB1	1.758811	8.89E-09	5.74E-07	5.850024	Up	Zinc finger E-box binding homeobox 1
SDS	1.634087	8.23E-09	5.37E-07	5.86362	Up	Serine dehydratase
PRLR	1.189961	7.28E-09	4.85E-07	5.885391	Up	Prolactin receptor
TCF21	1.136084	7.7E-09	5.09E-07	5.875482	Up	Transcription factor 21
MORC4	1.654814	1.03E-08	6.56E-07	5.823594	Up	MORC family CW-type zinc finger 4
FAM241A	1.831224	1.13E-08	7.11E-07	5.806454	Up	Family with sequence similarity 241 member A
SNX20	1.904888	1.14E-08	7.11E-07	5.806298	Up	Sorting nexin 20
BCL2L15	1.601513	1.37E-08	8.34E-07	5.77301	Up	BCL2 like 15
SP110	1.745925	1.44E-08	8.64E-07	5.764226	Up	SP110 nuclear body protein
GABRE	2.25059	1.56E-08	9.33E-07	5.748737	Up	Gamma-aminobutyric acid type A receptor epsilon subunit
REL	1.448019	1.63E-08	9.68E-07	5.741894	Up	REL proto-oncogene, NF-kB subunit
C1QB	1.873759	1.65E-08	9.78E-07	5.738991	Up	Complement C1q B chain
ARL10	1.675692	1.68E-08	9.9E-07	5.735952	Up	ADP ribosylation factor like GTPase 10
BATF2	1.606589	1.64E-08	9.74E-07	5.740513	Up	Basic leucine zipper ATF-like transcription factor 2
EPB41L3	1.678798	1.84E-08	1.07E-06	5.719612	Up	Erythrocyte membrane protein band 4.1 like 3
HELB	1.824415	2.05E-08	1.18E-06	5.699786	Up	DNA helicase B
USP18	1.909051	2.24E-08	1.28E-06	5.683603	Up	Ubiquitin specific peptidase 18
P2RY6	1.25935	2.21E-08	1.27E-06	5.686085	Up	Pyrimidineric receptor P2Y6
SAMD12	1.327908	2.91E-08	1.62E-06	5.636184	Up	Sterile alpha motif domain containing 12
CYSLTR1	1.792811	3.04E-08	1.68E-06	5.627828	Up	Cysteinyl leukotriene receptor 1
TLR7	1.527749	2.96E-08	1.64E-06	5.632999	Up	Toll like receptor 7
KYNU	1.493766	3.44E-08	1.87E-06	5.605486	Up	Kynureninase
PPM1K	1.582102	3.54E-08	1.91E-06	5.600151	Up	Protein phosphatase, Mg ²⁺ /Mn ²⁺ dependent 1K
PLCXD3	1.174956	3E-08	1.66E-06	5.630666	Up	Phosphatidylinositol specific phospholipase C X domain containing 3 cardiomyopathy associated 5
CMYA5	1.535208	3.77E-08	2.01E-06	5.588603	Up	Homeobox B13
HOXB13	1.301191	3.17E-08	1.73E-06	5.620497	Up	Homeobox B13
CLIC2	1.42112	3.56E-08	1.92E-06	5.59884	Up	Chloride intracellular channel 2
IFITM3	1.800881	4.02E-08	2.14E-06	5.576438	Up	Interferon induced transmembrane protein 3
CCL4	1.780438	4.02E-08	2.14E-06	5.576588	Up	C-C motif chemokine ligand 4
EV12A	1.665444	3.99E-08	2.13E-06	5.577824	Up	Ecotropic viral integration site 2A
ADGRE1	1.356324	4.32E-08	2.26E-06	5.56334	Up	Adhesion G protein-coupled receptor E1
BIRC3	1.647514	5.38E-08	2.74E-06	5.522274	Up	Baculoviral IAP repeat containing 3
STAT2	1.76586	5.51E-08	2.78E-06	5.5181	Up	Signal transducer and activator of transcription 2
CASP1	1.708409	5.71E-08	2.86E-06	5.511447	Up	Caspase 1
NAIP1	1.29999	4.75E-08	2.47E-06	5.545542	Up	NAIP pseudogene 1
MUC13	1.832676	5.9E-08	2.94E-06	5.505296	Up	Mucin 13, cell surface associated
MCCR2	1.174515	5.07E-08	2.61E-06	5.533464	Up	Melanocortin 2 receptor
UHRF1BP1	1.323114	7.36E-08	3.58E-06	5.463838	Up	UHRF1 binding protein 1
CD209	1.247667	6.33E-08	3.12E-06	5.49219	Up	CD209 molecule
H4C8	1.480835	8.11E-08	3.89E-06	5.445383	Up	H4 clustered histone 8
ITK	1.608795	8.79E-08	4.15E-06	5.430341	Up	IL2 inducible T cell kinase
KCNJ6	1.418724	9.14E-08	4.28E-06	5.422827	Up	Potassium inwardly rectifying channel subfamily J member 6
FGL2	1.709031	9.46E-08	4.41E-06	5.416461	Up	Fibrinogen like 2
SLAMF8	1.474004	8.35E-08	3.98E-06	5.43999	Up	SLAM family member 8
AIM2	1.455377	8.56E-08	4.07E-06	5.435388	Up	Absent in melanoma 2
TNFSF14	1.871822	9.81E-08	4.53E-06	5.40961	Up	TNF superfamily member 14
SLC30A3	1.280106	8.45E-08	4.02E-06	5.43765	Up	Solute carrier family 30 member 3
TMCO5B	1.352192	8.64E-08	4.09E-06	5.433553	Up	Transmembrane and coiled-coil domains 5B (pseudogene)
INHBA	1.240453	9.12E-08	4.28E-06	5.423251	Up	inhibin subunit beta A
SMCHD1	1.539176	1.28E-07	5.8E-06	5.358335	Up	Structural maintenance of chromosomes flexible hinge domain containing 1
CEACAM1	1.69456	1.39E-07	6.21E-06	5.343195	Up	CEA cell adhesion molecule 1
SPATA5	1.380092	1.51E-07	6.63E-06	5.327484	Up	Spermatogenesis associated 5
AOAH	1.633575	1.54E-07	6.75E-06	5.323212	Up	Acyloxyacyl hydrolase
CXorf21	1.449641	1.46E-07	6.46E-06	5.333105	Up	Chromosome X open reading frame 21
CYSLTR2	1.148797	1.37E-07	6.13E-06	5.345747	Up	Cysteinyl leukotriene receptor 2
PATL1	1.327313	1.73E-07	7.48E-06	5.301107	Up	PAT1 homolog 1, processing body mRNA decay factor
NEXN	1.425681	1.53E-07	6.71E-06	5.324317	Up	Nexilin F-actin binding protein
MILR1	1.254437	1.6E-07	6.99E-06	5.315763	Up	Mast cell immunoglobulin like receptor 1
MUC19	1.226686	1.46E-07	6.45E-06	5.333843	Up	Mucin 19, oligomeric
CD180	1.439893	1.92E-07	8.25E-06	5.281172	Up	CD180 molecule
GAPT	1.654163	2.25E-07	9.43E-06	5.250335	Up	GRB2 binding adaptor protein, transmembrane
HITN3	1.26519	2.22E-07	9.34E-06	5.253085	Up	Histatin 3
GIMAP2	1.419765	2.32E-07	9.7E-06	5.244234	Up	GTPase, IMAP family member 2
SPN	1.467297	2.56E-07	1.06E-05	5.224691	Up	Sialophorin
BCL2L14	1.469832	2.7E-07	1.11E-05	5.214642	Up	BCL2 like 14
ZNF37A	1.467584	2.8E-07	1.15E-05	5.207313	Up	Zinc finger protein 37A
LILRB1	1.307746	2.56E-07	1.06E-05	5.225067	Up	Leukocyte immunoglobulin like receptor B1
CLEC5A	1.103813	2.67E-07	1.1E-05	5.217081	Up	C-type lectin domain containing 5A
REXO1L1P	1.751107	3.66E-07	1.46E-05	5.154936	Up	REXO1 like 1, pseudogene
NUB1	1.389973	4.16E-07	1.63E-05	5.129578	Up	Negative regulator of ubiquitin like proteins 1
BEGAIN	1.096897	3.08E-07	1.25E-05	5.188683	Up	Brain enriched guanylate kinase associated
ACOD1	1.355987	3.06E-07	1.25E-05	5.190265	Up	Aconitate decarboxylase 1
HLA-V	1.190548	4.4E-07	1.7E-05	5.118628	Up	Major histocompatibility complex, class I, V (pseudogene)
RGS18	1.407927	3.87E-07	1.53E-05	5.143797	Up	Regulator of G protein signaling 18

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
NPL	1.473005	4.21E-07	1.64E-05	5.127297	Up	N-acetylneuraminase pyruvate lyase
SERPINB9	1.783502	4.5E-07	1.74E-05	5.113934	Up	Serpin family B member 9
LAMP3	1.532454	4.54E-07	1.75E-05	5.112316	Up	Lysosomal associated membrane protein 3
XIAPP3	1.264898	3.82E-07	1.52E-05	5.146448	Up	X-linked inhibitor of apoptosis pseudogene 3
CXCL13	1.371326	3.59E-07	1.43E-05	5.158934	Up	C-X-C motif chemokine ligand 13
ZBP1	1.459645	4.3E-07	1.67E-05	5.123119	Up	Z-DNA binding protein 1
GVINP1	1.764608	4.75E-07	1.82E-05	5.103137	Up	GTPase, very large interferon inducible pseudogene 1
CDH8	1.270498	4.33E-07	1.68E-05	5.121431	Up	Cadherin 8
SAMD3	1.108386	4.17E-07	1.63E-05	5.129172	Up	Sterile alpha motif domain containing 3
C6orf223	1.189907	4.66E-07	1.79E-05	5.107064	Up	Chromosome 6 open reading frame 223
GOLGA2P11	1.334075	4.99E-07	1.91E-05	5.0935	Up	GOLGA2 pseudogene 11
GIMAP7	1.428916	5.44E-07	2.06E-05	5.076112	Up	GTPase, IMAP family member 7
TLR3	1.415285	6.08E-07	2.27E-05	5.053758	Up	Toll like receptor 3
IL7R	1.634784	6.15E-07	2.29E-05	5.051432	Up	Interleukin 7 receptor
CLEC4E	1.596618	5.92E-07	2.22E-05	5.059079	Up	C-type lectin domain family 4 member E
RTP4	1.446828	6.55E-07	2.42E-05	5.038836	Up	Receptor transporter protein 4
RESF1	1.249528	6.64E-07	2.45E-05	5.036313	Up	Retroelement silencing factor 1
NHSL2	1.611556	6.7E-07	2.47E-05	5.034325	Up	NHS like 2
GZMB	1.326065	6.03E-07	2.26E-05	5.0554	Up	Granzyme B
RPL3L	1.181918	6.05E-07	2.26E-05	5.05487	Up	Ribosomal protein L3 like
PHACTR4	1.097976	7.89E-07	2.87E-05	5.001267	Up	Phosphatase and actin regulator 4
TMEM45A	1.557515	7.93E-07	2.88E-05	5.0003	Up	Transmembrane protein 45A
PSTPIP2	1.43643	7.72E-07	2.82E-05	5.005747	Up	Proline-serine-threonine phosphatase interacting protein 2
RBMS2	1.268104	8.26E-07	2.98E-05	4.992145	Up	RNA binding motif single stranded interacting protein 2
HHLA1	1.477431	8.44E-07	3.04E-05	4.987733	Up	HERV-H LTR-associating 1
DOCK10	1.69722	8.77E-07	3.13E-05	4.979977	Up	dedicator of cytokinesis 10
MICB	1.294464	8.8E-07	3.14E-05	4.979222	Up	MHC class I polypeptide-related sequence B
PTPRC	1.620028	1.1E-06	3.83E-05	4.934075	Up	protein tyrosine phosphatase receptor type C
TRIM21	1.495729	1.14E-06	3.96E-05	4.925887	Up	tripartite motif containing 21
CARD6	1.367466	1.15E-06	3.96E-05	4.925352	Up	caspase recruitment domain family member 6
P2RX7	1.307491	1.02E-06	3.58E-05	4.948849	Up	purinergic receptor P2X 7
KPNA5	1.331122	1.2E-06	4.13E-05	4.91563	Up	karyopherin subunit alpha 5
EPB41L2	1.481556	1.25E-06	4.27E-05	4.907996	Up	erythrocyte membrane protein band 4.1 like 2
NAIP	1.801001	1.25E-06	4.29E-05	4.906724	Up	NLR family apoptosis inhibitory protein
NAV3	1.497703	1.33E-06	4.51E-05	4.895283	Up	neuron navigator 3
TNFSF10	1.326914	1.37E-06	4.62E-05	4.889071	Up	TNF superfamily member 10
ZNF562	1.158943	1.45E-06	4.86E-05	4.876967	Up	zinc finger protein 562
PTPRE	1.655122	1.48E-06	4.94E-05	4.872362	Up	protein tyrosine phosphatase receptor type E
CLEC2B	1.450145	1.6E-06	5.28E-05	4.856081	Up	C-type lectin domain family 2 member B
MUC3A	1.251313	1.34E-06	4.54E-05	4.893436	Up	mucin 3A, cell surface associated
RASGRP3	1.470559	1.61E-06	5.3E-05	4.854873	Up	RAS guanyl releasing protein 3
PTPRO	1.133725	1.4E-06	4.71E-05	4.883694	Up	protein tyrosine phosphatase receptor type O
CD80	1.328242	1.37E-06	4.64E-05	4.887911	Up	CD80 molecule
CX3CR1	1.517085	1.77E-06	5.76E-05	4.835227	Up	C-X3-C motif chemokine receptor 1
ANKRD22	1.370317	1.93E-06	6.19E-05	4.817815	Up	ankyrin repeat domain 22
IGSF6	1.241273	2.12E-06	6.69E-05	4.798272	Up	immunoglobulin superfamily member 6
SHANK1	1.243433	1.78E-06	5.77E-05	4.834796	Up	SH3 and multiple ankyrin repeat domains 1
LST1	1.187335	2.2E-06	6.9E-05	4.790524	Up	leukocyte specific transcript 1
MAS1	1.236547	1.93E-06	6.19E-05	4.817623	Up	MAS1 proto-oncogene, G protein-coupled receptor
BCAT1	1.401393	2.3E-06	7.17E-05	4.781137	Up	branched chain amino acid transaminase 1
GIMAP8	1.162458	1.83E-06	5.93E-05	4.828214	Up	GTPase, IMAP family member 8
IL2RA	1.12475	1.74E-06	5.66E-05	4.839526	Up	interleukin 2 receptor subunit alpha
FLRT2	1.159389	2.6E-06	7.99E-05	4.754781	Up	fibronectinleucine rich transmembrane protein 2
LGMN	1.358023	2.62E-06	8.05E-05	4.752958	Up	legumain
POU2F1	1.267069	2.67E-06	8.15E-05	4.74961	Up	POU class 2 homeobox 1
MMS22L	1.50831	2.76E-06	8.39E-05	4.742025	Up	MMS22 like, DNA repair protein
GIMAP6	1.454484	2.66E-06	8.14E-05	4.750165	Up	GTPase, IMAP family member 6
HLX	1.121891	2.15E-06	6.79E-05	4.795149	Up	H2.0 like homeobox
PCSK1N	2.670381	2.58E-06	7.97E-05	4.756112	Up	proproteinconvertasesubtilisin/kexin type 1 inhibitor
GNB4	1.31276	2.96E-06	8.91E-05	4.727333	Up	G protein subunit beta 4
GPR82	1.186828	2.59E-06	7.99E-05	4.755423	Up	G protein-coupled receptor 82
F13A1	1.092501	2.38E-06	7.41E-05	4.773202	Up	coagulation factor XIII A chain
PLIN2	1.59715	3.03E-06	9.07E-05	4.722811	Up	perilipin 2
IL10RA	1.51063	2.99E-06	8.98E-05	4.725411	Up	interleukin 10 receptor subunit alpha
IRF8	1.375123	2.72E-06	8.27E-05	4.74532	Up	interferon regulatory factor 8
NEGR1	1.578109	3.09E-06	9.22E-05	4.718639	Up	neuronal growth regulator 1
LGALS9	1.367219	3.15E-06	9.38E-05	4.714322	Up	galectin 9
SLC25A28	1.382801	3.16E-06	9.42E-05	4.713303	Up	solute carrier family 25 member 28
LHFPL2	1.342657	3.13E-06	9.33E-05	4.715673	Up	LHFPL tetraspan subfamily member 2
ETV5	1.396365	3.2E-06	9.51E-05	4.71066	Up	ETS variant transcription factor 5
CPA4	1.30789	3.19E-06	9.49E-05	4.7115	Up	carboxypeptidase A4
ADGRE2	1.674494	3.55E-06	0.000104	4.688463	Up	adhesion G protein-coupled receptor E2
C1QC	1.54519	3.52E-06	0.000103	4.690762	Up	complement C1q C chain
PDE4B	1.779679	3.64E-06	0.000106	4.683099	Up	phosphodiesterase 4B
CASP5	1.194079	3.01E-06	9.03E-05	4.724089	Up	caspase 5
TNFAIP6	1.31662	3.12E-06	9.32E-05	4.71604	Up	TNF alpha induced protein 6

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
RAD51D	1.353673	4.01E-06	0.000115	4.662418	Up	RAD51 paralogs D
MLKL	1.498223	4.01E-06	0.000115	4.662418	Up	mixed lineage kinase domain like pseudokinase
TF	1.300212	4.33E-06	0.000123	4.646111	Up	transferrin
DUX4	1.229043	3.34E-06	9.87E-05	4.70198	Up	double homeobox 4
RAB8B	1.420802	4.73E-06	0.000133	4.627161	Up	RAB8B, member RAS oncogene family
PRKCB	1.535003	4.89E-06	0.000136	4.620063	Up	protein kinase C beta
LAP3	1.303203	5.16E-06	0.000142	4.608387	Up	leucineaminopeptidase 3
NT5C3A	1.619246	5.34E-06	0.000147	4.600644	Up	5'-nucleotidase, cytosolic IIIA
LINC00672	1.182716	4.61E-06	0.00013	4.632627	Up	long intergenic non-protein coding RNA 672
GALR1	1.127421	4.84E-06	0.000135	4.622025	Up	galanin receptor 1
HNRNP1P54	1.537465	5.74E-06	0.000156	4.58494	Up	heterogeneous nuclear ribonucleoprotein A1 pseudogene 54
LPAR6	1.280022	5.67E-06	0.000154	4.587715	Up	lysophosphatidic acid receptor 6
ELF1	1.213312	5.84E-06	0.000159	4.581214	Up	E74 like ETS transcription factor 1
C12orf45	1.324257	6.01E-06	0.000162	4.575148	Up	chromosome 12 open reading frame 45
ABCA9	1.352062	5.98E-06	0.000162	4.576191	Up	ATP binding cassette subfamily A member 9
PLEK	1.694314	6.54E-06	0.000175	4.556539	Up	pleckstrin
TLR4	1.595453	6.72E-06	0.000179	4.550496	Up	toll like receptor 4
POU2F3	1.244324	6.16E-06	0.000166	4.569837	Up	POU class 2 homeobox 3
IGF1	1.309296	7.05E-06	0.000186	4.540215	Up	insulin like growth factor 1
SRGAP1	1.1255	7.73E-06	0.000201	4.519761	Up	SLIT-ROBO Rho GTPase activating protein 1
BTN3A1	1.464565	8.25E-06	0.000213	4.505508	Up	butyrophilin subfamily 3 member A1
SFMBT2	1.434304	8.44E-06	0.000217	4.500514	Up	Scm like with four mbt domains 2
PARP15	1.560463	8.77E-06	0.000225	4.49201	Up	poly(ADP-ribose) polymerase family member 15
SHISA9	1.567597	8.79E-06	0.000225	4.491453	Up	shisa family member 9
DOCK2	1.695973	9E-06	0.000229	4.486153	Up	dedicator of cytokinesis 2
CD53	1.568485	9.03E-06	0.00023	4.485447	Up	CD53 molecule
ZSCAN30	1.4585	8.97E-06	0.000229	4.486883	Up	zinc finger and SCAN domain containing 30
ATP6V1B2	1.223216	9.07E-06	0.00023	4.484488	Up	ATPase H+ transporting V1 subunit B2
MICA	1.357472	9.44E-06	0.000239	4.475644	Up	MHC class I polypeptide-related sequence A
CYTIP	1.570089	9.72E-06	0.000245	4.46906	Up	cytohesin 1 interacting protein
POTEC	1.265306	9.13E-06	0.000232	4.483165	Up	POTE ankyrin domain family member C
SAMSN1	1.645995	1.01E-05	0.000253	4.459918	Up	SAM domain, SH3 domain and nuclear localization signals 1
MEFV	1.617695	1.11E-05	0.000274	4.438927	Up	MEFV innate immunity regulator, pyrin
FGF13	1.435322	1.21E-05	0.000294	4.419948	Up	Fibroblast growth factor 13
GBP2	1.472289	1.22E-05	0.000295	4.419003	Up	Guanylate binding protein 2
CLEC12A	1.178271	9.6E-06	0.000242	4.471869	Up	C-type lectin domain family 12 member A
SELL	1.715618	1.24E-05	0.000299	4.415521	Up	Selectin L
IL2RG	1.374905	1.2E-05	0.000291	4.422956	Up	Interleukin 2 receptor subunit gamma
RG51	1.497355	1.24E-05	0.000299	4.415167	Up	Regulator of G protein signaling 1
C2orf91	1.182058	1.11E-05	0.000274	4.438974	Up	Chromosome 2 open reading frame 91
A2M	1.434485	1.32E-05	0.000315	4.400747	Up	Alpha-2-macroglobulin
FNIP2	1.189084	1.33E-05	0.000317	4.399251	Up	Folliculin interacting protein 2
JAK2	1.244303	1.33E-05	0.000317	4.39863	Up	Janus kinase 2
STAR8	1.265528	1.25E-05	0.000302	4.412195	Up	STAR related lipid transfer domain containing 8
UBXN2B	1.244102	1.39E-05	0.000329	4.388232	Up	UBX domain protein 2B
ELMO1	1.450084	1.48E-05	0.000346	4.374172	Up	engulfment and cell motility 1
BRIP1	1.1959	1.48E-05	0.000345	4.37532	Up	BRCA1 interacting protein C-terminal helicase 1
APOBEC3F	1.243196	1.67E-05	0.000382	4.347899	Up	Apolipoprotein B mRNA editing enzyme catalytic subunit 3F
TBC1D8B	1.298686	1.7E-05	0.000389	4.343055	Up	TBC1 domain family member 8B
ACSL4	1.272459	1.81E-05	0.000412	4.328361	Up	Acyl-CoA synthetase long chain family member 4
SF2	1.254429	1.83E-05	0.000416	4.326397	Up	SMC5-SMC6 complex localization factor 2
APOL1	1.214905	1.87E-05	0.000423	4.321889	Up	Apolipoprotein L1
RPAP2	1.205126	1.88E-05	0.000425	4.319893	Up	RNA polymerase II associated protein 2
MPP1	1.340352	1.88E-05	0.000425	4.320496	Up	Membrane palmitoylated protein 1
CDKL5	1.175336	2.04E-05	0.000457	4.302096	Up	Cyclin dependent kinase like 5
LEO1	1.172064	2.09E-05	0.000468	4.295583	Up	LEO1 homolog, Paf1/RNA polymerase II complex component
PIK3CG	1.323604	2.27E-05	0.000502	4.276747	Up	Phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit gamma
TAGAP	1.772345	2.24E-05	0.000495	4.279999	Up	T cell activation RhoGTPase activating protein
APOBEC3A	1.666379	2.36E-05	0.000517	4.267774	Up	Apolipoprotein B mRNA editing enzyme catalytic subunit 3A
PRRG3	1.215028	2.31E-05	0.000507	4.273291	Up	proline rich and Gla domain 3
NMI	1.293142	2.59E-05	0.000561	4.246004	Up	N-myc and STAT interactor
SP140	1.561468	2.58E-05	0.000558	4.247489	Up	SP140 nuclear body protein
SIGLEC14	1.128636	2.07E-05	0.000463	4.298524	Up	Sialic acid binding Ig like lectin 14
BTN3A3	1.319353	2.63E-05	0.000568	4.242993	Up	Butyrophilin subfamily 3 member A3
NSUN3	1.207909	2.66E-05	0.000574	4.240022	Up	NOP2/Sun RNA methyltransferase 3
CLIC4	1.237929	2.69E-05	0.000578	4.237791	Up	Chloride intracellular channel 4
PIK3AP1	1.316146	2.72E-05	0.000583	4.235327	Up	Phosphoinositide-3-kinase adaptor protein 1
FCHSD2	1.188487	2.73E-05	0.000586	4.234227	Up	FCH and double SH3 domains 2
MMP13	1.149568	2.18E-05	0.000486	4.285822	Up	Matrix metalloproteinase 13
BRCA2	1.249275	2.88E-05	0.000614	4.221437	Up	BRCA2 DNA repair associated
SNX10	1.394516	3.03E-05	0.000641	4.210065	Up	Sorting nexin 10
CCND2	1.428378	3.15E-05	0.000664	4.200391	Up	Cyclin D2
SLCO2B1	1.208293	3E-05	0.000635	4.212513	Up	Solute carrier organic anion transporter family member 2B1
RNASE6	1.144929	2.97E-05	0.00063	4.214844	Up	Ribonuclease A family member k6
PARP12	1.310363	3.47E-05	0.000719	4.177798	Up	Poly(ADP-ribose) polymerase family member 12
TRIM34	1.190692	3.39E-05	0.000705	4.183429	Up	Tripartite motif containing 34

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Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
FAM83A	1.166428	3.46E-05	0.000717	4.178643	Up	Family with sequence similarity 83 member A
NXNL2	1.192108	3.18E-05	0.000667	4.198783	Up	Nucleoredoxin like 2
ENTPD1	1.267098	3.68E-05	0.000755	4.164111	Up	Ectonucleoside triphosphate diphosphohydrolase 1
ANKRD20A19P	1.087992	3.2E-05	0.000671	4.197274	Up	Ankyrin repeat domain 20 family member A19, pseudogene
N4BP1	1.113339	3.87E-05	0.000786	4.15221	Up	NEDD4 binding protein 1
ASAH2B	1.162163	3.61E-05	0.000743	4.168543	Up	N-acylsphingosineamidohydrolase 2B
SLC36A1	1.21816	3.87E-05	0.000786	4.152384	Up	Solute carrier family 36 member 1
FAM120C	1.164201	4.2E-05	0.000839	4.13265	Up	Family with sequence similarity 120C
CSGALNACT2	1.275953	4.11E-05	0.000824	4.13797	Up	Chondroitin sulfate N-acetylgalactosaminyltransferase 2
IL18RAP	1.522793	4.08E-05	0.000818	4.139931	Up	Interleukin 18 receptor accessory protein
C4BPB	1.216541	3.96E-05	0.0008	4.146746	Up	Complement component 4 binding protein beta
FSIP2	1.65462	4.47E-05	0.000885	4.117805	Up	Fibrous sheath interacting protein 2
ZNF519	1.26651	4.45E-05	0.000881	4.119177	Up	Zinc finger protein 519
L2HGDH	1.249639	4.72E-05	0.000925	4.104928	Up	L-2-hydroxyglutarate dehydrogenase
HTN1	1.355422	4.67E-05	0.000916	4.107778	Up	Histatin 1
GAB3	1.212632	4.3E-05	0.000855	4.127334	Up	GRB2 associated binding protein 3
ISG15	1.646812	4.53E-05	0.000894	4.114739	Up	ISG15 ubiquitin like modifier
PTPN22	1.319303	4.75E-05	0.000931	4.103367	Up	Protein tyrosine phosphatase non-receptor type 22
FMNL3	1.342896	4.95E-05	0.000964	4.093866	Up	Formin like 3
PDE3B	1.128779	4.31E-05	0.000857	4.126615	Up	Phosphodiesterase 3B
MCM8	1.180785	5.15E-05	0.000996	4.083982	Up	Minichromosome maintenance 8 homologous recombination repair factor
ABCC9	1.45215	5.25E-05	0.001013	4.079654	Up	ATP binding cassette subfamily C member 9
FUT10	1.160291	5.08E-05	0.000986	4.087222	Up	Fucosyltransferase 10
SLFN12L	1.163406	5.28E-05	0.001019	4.077966	Up	Schlafen family member 12 like
ALOX5AP	1.382042	5.39E-05	0.001034	4.073423	Up	Arachidonate 5-lipoxygenase activating protein
RASSF2	1.383003	5.63E-05	0.001075	4.062585	Up	Ras association domain family member 2
CBL	1.145963	5.96E-05	0.001131	4.049127	Up	Cbl proto-oncogene
TRAPP3C	1.245936	5.88E-05	0.001119	4.052097	Up	Trafficking protein particle complex 3 like
HLA-DMA	1.202451	6.32E-05	0.001191	4.034667	Up	Major histocompatibility complex, class II, DM alpha
PBX1	1.502659	6.48E-05	0.001216	4.028741	Up	PBX homeobox 1
STX17	1.108394	6.59E-05	0.001233	4.024773	Up	Syntaxin 17
CCDC13	1.485803	6.69E-05	0.001251	4.020778	Up	Coiled-coil domain containing 13
ATP10B	1.222735	6.85E-05	0.001275	4.015141	Up	ATPase phospholipid transporting 10B (putative)
CASP10	1.177724	7.04E-05	0.001303	4.008517	Up	caspase 10
FKBP5	1.15435	7.22E-05	0.00133	4.002371	Up	FKBP prolyl isomerase 5
ZFYVE26	1.141421	7.26E-05	0.001335	4.001094	Up	Zinc finger FYVE-type containing 26
ZNF429	1.158133	7.47E-05	0.001371	3.993937	Up	Zinc finger protein 429
PML	1.170897	7.47E-05	0.001371	3.99403	Up	Promyelocytic leukemia
MTAP	1.284273	7.65E-05	0.001396	3.988327	Up	Methylthioadenosine phosphorylase
WIPF1	1.298992	7.8E-05	0.001419	3.983514	Up	WAS/WASL interacting protein family member 1
FOXL2NB	1.140412	7.48E-05	0.001371	3.993677	Up	FOXL2 neighbor
ZNF471	1.343063	8.12E-05	0.001464	3.973469	Up	Zinc finger protein 471
AQP9	1.788203	8.1E-05	0.001461	3.974269	Up	Aquaporin 9
LILRA5	1.233838	7.32E-05	0.001346	3.999032	Up	Leukocyte immunoglobulin like receptor A5
RASSF4	1.217162	8.18E-05	0.001473	3.971804	Up	Ras association domain family member 4
ASAP1	1.267081	8.61E-05	0.001537	3.959131	Up	ArfGAP with SH3 domain, ankyrin repeat and PH domain 1
ZCHHC2	1.156022	9.1E-05	0.001611	3.945515	Up	zinc finger CCHC-type containing 2
IKZF1	1.350428	9.18E-05	0.001622	3.943439	Up	IKAROS family zinc finger 1
PECAM1	1.199756	9.29E-05	0.001637	3.940532	Up	Platelet and endothelial cell adhesion molecule 1
ATF7	1.101235	9.48E-05	0.001666	3.935365	Up	Activating transcription factor 7
TRAC	1.145442	8.79E-05	0.00156	3.954078	Up	T cell receptor alpha constant
DDHD1	1.101348	0.000117	0.002003	3.882	Up	DDHD domain containing 1
DOCK8	1.256293	0.000124	0.002092	3.868508	Up	Dedicator of cytokinesis 8
DPYD	1.096511	0.000132	0.002212	3.851793	Up	Dihydropyrimidine dehydrogenase
ZNF670-ZNF695	1.153272	0.00012	0.002032	3.877321	Up	ZNF670-ZNF695 readthrough (NMD candidate)
GADL1	1.290452	0.000131	0.002185	3.855007	Up	Glutamate decarboxylase like 1
MTO1	1.17604	0.000142	0.002343	3.834289	Up	Mitochondrial tRNA translation optimization 1
UNC80	1.249241	0.000143	0.002363	3.831664	Up	unc-80 homolog, NALCN channel complex subunit
ARHGEF3	1.101922	0.000147	0.002415	3.825529	Up	Rho guanine nucleotide exchange factor 3
PNPT1	1.121249	0.000153	0.002482	3.815748	Up	Polyribonucleotide nucleotidyltransferase 1
CARD16	1.275336	0.000147	0.002416	3.825137	Up	Caspase recruitment domain family member 16
PAG1	1.333863	0.000157	0.002534	3.808985	Up	Phosphoprotein membrane anchor with glycosphingolipid microdomains 1
SIGLEC10	1.125839	0.000154	0.002498	3.813569	Up	sialic acid binding Ig like lectin 10
HSD17B2	1.178872	0.000157	0.002534	3.809103	Up	Hydroxysteroid 17-beta dehydrogenase 2
TCAF2	1.171221	0.000163	0.002618	3.798889	Up	TRPM8 channel associated factor 2
SULT1B1	1.143278	0.000169	0.002695	3.789694	Up	Sulfotransferase family 1B member 1
ME2	1.120023	0.000173	0.002737	3.784081	Up	Malic enzyme 2
XRCC2	1.206168	0.000176	0.002771	3.780276	Up	X-ray repair cross complementing 2
ITGA1	1.122798	0.000172	0.002724	3.786023	Up	Integrin subunit alpha 1
SKAP2	1.305645	0.00019	0.002953	3.760276	Up	src kinase associated phosphoprotein 2
SLC2A3	1.54209	0.000193	0.002996	3.755851	Up	Solute carrier family 2 member 3
CREB5	1.292786	0.000187	0.00292	3.764389	Up	cAMP responsive element binding protein 5
LMNB1	1.325282	0.000202	0.003091	3.744801	Up	Lamin B1
CCDC169	1.225647	0.000199	0.003062	3.748292	Up	Coiled-coil domain containing 169
SRGN	1.395781	0.000204	0.003122	3.741582	Up	Serglycin
UTS2B	1.100687	0.000189	0.002945	3.761186	Up	Urotensin 2B

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Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
MGAT4A	1.09469	0.000222	0.003343	3.719791	Up	Alpha-1,3-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase A
SIRPB1	1.257903	0.000207	0.003164	3.737298	Up	Signal regulatory protein beta 1
APOL4	1.091068	0.000224	0.003366	3.717447	Up	Apolipoprotein L4
PRR26	1.094279	0.00019	0.002958	3.759679	Up	Proline rich 26
MCF2L2	1.134066	0.000229	0.003422	3.711936	Up	MCF.2 cell line derived transforming sequence-like 2
FCGR1B	1.118924	0.000216	0.003264	3.72721	Up	Fc fragment of IgG receptor Ib
TMCC3	1.23278	0.000225	0.003375	3.716227	Up	Transmembrane and coiled-coil domain family 3
APBB1IP	1.278172	0.000237	0.003515	3.703005	Up	Amyloid beta precursor protein binding family B member 1 interacting protein
TRANK1	1.505397	0.000246	0.003632	3.692658	Up	Tetratricopeptide repeat and ankyrin repeat containing 1
IRF4	1.139057	0.000263	0.003843	3.675721	Up	Interferon regulatory factor 4
FAM111B	1.126455	0.000307	0.004372	3.634831	Up	Family with sequence similarity 111 member B
STAT4	1.112194	0.000314	0.004444	3.629043	Up	Signal transducer and activator of transcription 4
CLEC2D	1.153323	0.000372	0.005104	3.583403	Up	C-type lectin domain family 2 member D
BEST1	1.476254	0.000374	0.005126	3.581993	Up	Bestrophin 1
ASB3	1.218692	0.000397	0.005372	3.565904	Up	Ankyrin repeat and SOCS box containing 3
ADAM32	1.188404	0.000424	0.005692	3.54831	Up	ADAM metalloproteinase domain 32
NSMAF	1.082937	0.000469	0.00616	3.520958	Up	Neutral sphingomyelinase activation associated factor
DOCK11	1.18681	0.000485	0.006315	3.511925	Up	Dedicator of cytokinesis 11
LRCH4	1.31518	0.000499	0.006462	3.504161	Up	Leucine rich repeats and calponin homology domain containing 4
CCL5	1.086849	0.000513	0.006602	3.496942	Up	C-C motif chemokine ligand 5
TPH2	1.096357	0.000489	0.00635	3.509976	Up	Tryptophan hydroxylase 2
TGFBI	1.129197	0.000565	0.007141	3.470442	Up	Transforming growth factor beta induced
LILRB2	1.158787	0.000535	0.006836	3.485339	Up	Leukocyte immunoglobulin like receptor B2
ARHGAP25	1.209437	0.000569	0.007179	3.468279	Up	Rho GTPase activating protein 25
AIF1	1.090461	0.000563	0.007125	3.471332	Up	Allograft inflammatory factor 1
GPR65	1.200653	0.000695	0.008446	3.412889	Up	G protein-coupled receptor 65
CD69	1.084618	0.00065	0.008035	3.431543	Up	CD69 molecule
SH2B3	1.097413	0.000751	0.009028	3.391242	Up	SH2B adaptor protein 3
CYP46A1	1.111662	0.000825	0.009694	3.364577	Up	Cytochrome P450 family 46 subfamily A member 1
PLXNC1	1.202527	0.000879	0.01022	3.34678	Up	Plexin C1
ANKRD44	1.086383	0.001133	0.012499	3.274151	Up	Ankyrin repeat domain 44
SLA	1.186529	0.001234	0.01345	3.249374	Up	Src like adaptor
FPR2	1.19736	0.001089	0.012101	3.285715	Up	Formyl peptide receptor 2
MKI67	1.118865	0.001219	0.013303	3.252912	Up	Marker of proliferation Ki-67
TLR1	1.086989	0.001273	0.013802	3.240426	Up	Toll like receptor 1
B4GALNT2	1.185321	0.001494	0.015659	3.193436	Up	Beta-1,4-N-acetyl-galactosaminyltransferase 2
PLEKHG2	1.098848	0.001714	0.017482	3.152855	Up	Pleckstrin homology and RhoGEF domain containing G2
DOK3	1.083268	0.00177	0.0179	3.143307	Up	Docking protein 3
FCGR2A	1.130666	0.002304	0.021961	3.063764	Up	Fc fragment of IgG receptor IIa
FCAR	1.102715	0.003361	0.02913	2.946737	Up	Fc fragment of IgA receptor
CXCR2	1.322924	0.003583	0.030517	2.926602	Up	C-X-C motif chemokine receptor 2
FCGR3B	1.24678	0.004846	0.038356	2.829725	Up	Fc fragment of IgG receptor IIIb
IGFBP2	-3.73784	8.51E-29	3.05E-25	-11.8676	Down	Insulin like growth factor binding protein 2
RF58	-3.08153	2.04E-27	5.62E-24	-11.5242	Down	Ribosomal protein S8
RPLP1	-3.70941	1.52E-26	3.88E-23	-11.3042	Down	Ribosomal protein lateral stalk subunit P1
RPL13A	-3.01707	3.96E-26	8.86E-23	-11.1982	Down	Ribosomal protein L13a
CRIP1	-3.7788	4.46E-26	9.38E-23	-11.1852	Down	Cysteine rich protein 1
PRDX5	-3.12136	4.21E-24	6.85E-21	-10.6739	Down	Peroxisomal protein 5
RP55	-3.38962	4.65E-22	5.74E-19	-10.1288	Down	Ribosomal protein S5
OAZ1	-3.1095	6.4E-22	7.64E-19	-10.091	Down	Ornithine decarboxylase antizyme 1
RPLP2	-2.9257	2.06E-21	2.38E-18	-9.9523	Down	Ribosomal protein lateral stalk subunit P2
CKB	-3.02781	2.42E-21	2.7E-18	-9.93321	Down	Creatine kinase B
RRAD	-3.33719	2.69E-21	2.92E-18	-9.92034	Down	RRAD, Ras related glycolysis inhibitor and calcium channel regulator
RRL13	-2.76895	3.23E-21	3.4E-18	-9.89877	Down	Ribosomal protein L13
FAU	-2.9994	5.3E-21	5.42E-18	-9.8393	Down	FAU ubiquitin like and ribosomal protein S30 fusion
RPL18A	-3.11296	6.09E-21	6.06E-18	-9.82253	Down	Ribosomal protein L18a
RPLP0	-2.58894	7.56E-21	7.31E-18	-9.79653	Down	Ribosomal protein lateral stalk subunit P0
RPL10A	-2.80774	1.9E-20	1.7E-17	-9.68532	Down	Ribosomal protein L10a
C9orf24	-3.14279	2.73E-20	2.27E-17	-9.64105	Down	Chromosome 9 open reading frame 24
RPS21	-3.1414	6.74E-20	5.24E-17	-9.53079	Down	Ribosomal protein S21
ATP5IF1	-2.49666	9.56E-20	7.28E-17	-9.48783	Down	ATP synthase inhibitory factor subunit 1
RPS3A	-2.39499	1.56E-19	1.14E-16	-9.42768	Down	Ribosomal protein S3A
ALDH3A1	-2.82934	5.52E-19	3.59E-16	-9.27034	Down	Aldehyde dehydrogenase 3 family member A1
SPINT2	-2.76726	6.05E-19	3.87E-16	-9.25886	Down	Serine peptidase inhibitor, Kunitz type 2
RPL3	-2.21294	6.41E-19	4.03E-16	-9.25163	Down	Ribosomal protein L3
RPS18	-2.42555	1.36E-18	8.23E-16	-9.15751	Down	Ribosomal protein S18
RPS19	-2.91592	1.6E-18	9.54E-16	-9.13679	Down	Ribosomal protein S19
RPS28	-3.02098	4.02E-18	2.36E-15	-9.02004	Down	Ribosomal protein S28
CIB1	-3.31636	4.41E-18	2.54E-15	-9.00824	Down	Calcium and integrin binding 1
ZMYND10	-3.02018	6.69E-18	3.68E-15	-8.95485	Down	Zinc finger MYND-type containing 10
EEF2	-2.58419	7.15E-18	3.88E-15	-8.94632	Down	Eukaryotic translation elongation factor 2
TUBB2A	-2.83331	8.67E-18	4.56E-15	-8.92167	Down	Tubulin beta 2A class IIa
RPL26	-2.24118	8.8E-18	4.57E-15	-8.91971	Down	Ribosomal protein L26
SLC25A6	-2.7047	1.19E-17	6.1E-15	-8.88067	Down	Solute carrier family 25 member 6
RPL35	-2.94803	2.1E-17	1.06E-14	-8.80761	Down	Ribosomal protein L35
GPX4	-2.43601	5.84E-17	2.9E-14	-8.67446	Down	Glutathione peroxidase 4

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
RPS14	-2.24003	8.16E-17	3.9E-14	-8.63049	Down	Ribosomal protein S14
GUK1	-2.60831	8.71E-17	4.1E-14	-8.62204	Down	Guanylate kinase 1
H2AJ	-2.60747	1.32E-16	6.03E-14	-8.56764	Down	H2A.J histone
CAPS	-2.59991	1.68E-16	7.63E-14	-8.53494	Down	Calcyphosine
C11orf88	-2.53534	1.71E-16	7.65E-14	-8.53297	Down	Chromosome 11 open reading frame 88
ROMO1	-2.4989	2.15E-16	9.4E-14	-8.50227	Down	Reactive oxygen species modulator 1
TOMM7	-2.42282	2.33E-16	9.87E-14	-8.49171	Down	Translocase of outer mitochondrial membrane 7
CLDN7	-2.709	2.47E-16	1.03E-13	-8.48433	Down	Claudin 7
ATP5F1E	-2.40484	2.55E-16	1.05E-13	-8.48003	Down	ATP synthase F1 subunit epsilon
CLDN4	-2.6609	2.68E-16	1.09E-13	-8.47352	Down	Claudin 4
LGALS3	-2.04046	3.87E-16	1.52E-13	-8.42436	Down	Galectin 3
PTPRN2	-2.51545	4.31E-16	1.68E-13	-8.40981	Down	Protein tyrosine phosphatase receptor type N2
IGFBP7	-2.86645	4.61E-16	1.77E-13	-8.40095	Down	Insulin like growth factor binding protein 7
ANAPC11	-2.63201	4.65E-16	1.77E-13	-8.39965	Down	Anaphase promoting complex subunit 11
RPL18	-2.62437	4.97E-16	1.85E-13	-8.39073	Down	Ribosomal protein L18
RPS29	-2.27314	5.48E-16	2E-13	-8.37769	Down	Ribosomal protein S29
RPS15	-2.85142	5.9E-16	2.12E-13	-8.36778	Down	Ribosomal protein S15
ARL3	-2.41603	5.92E-16	2.12E-13	-8.36724	Down	ADP ribosylation factor like GTPase 3
CES1	-2.99578	6.94E-16	2.46E-13	-8.34595	Down	Carboxylesterase 1
RPL15	-1.74247	8.64E-16	2.97E-13	-8.31637	Down	Ribosomal protein L15
UQCRCQ	-2.28555	8.58E-16	2.97E-13	-8.31729	Down	Ubiquinol-cytochrome c reductase complex III subunit VII
RPS7	-2.30137	9.69E-16	3.27E-13	-8.30091	Down	Ribosomal protein S7
FAM183A	-2.48465	9.95E-16	3.33E-13	-8.29733	Down	Family with sequence similarity 183 member A
SGSM3	-2.56116	1.5E-15	4.99E-13	-8.2412	Down	Small G protein signaling modulator 3
RPL37	-1.92162	1.9E-15	6.24E-13	-8.20933	Down	Ribosomal protein L37
TUFM	-2.41308	2.31E-15	7.37E-13	-8.18312	Down	Tu translation elongation factor, mitochondrial
NDUFB1	-2.51699	2.56E-15	8.1E-13	-8.16892	Down	NADH:ubiquinoneoxidoreductase core subunit V1
CD9	-2.7876	3.56E-15	1.09E-12	-8.12351	Down	CD9 molecule
ITGB4	-2.54816	3.76E-15	1.14E-12	-8.11592	Down	Integrin subunit beta 4
TCTEX1D2	-2.37609	3.94E-15	1.18E-12	-8.10965	Down	Tctex1 domain containing 2
LMNA	-2.45096	6.71E-15	1.94E-12	-8.03616	Down	Lamin A/C
FAM166B	-2.60751	7.25E-15	2.08E-12	-8.02547	Down	Family with sequence similarity 166 member B
RPS10	-2.81231	7.64E-15	2.15E-12	-8.0182	Down	Ribosomal protein S10
RPS9	-2.46969	8.03E-15	2.25E-12	-8.01126	Down	Ribosomal protein S9
RPL34	-2.15145	1.1E-14	2.99E-12	-7.96816	Down	Ribosomal protein L34
TUBB4B	-2.41131	1.64E-14	4.3E-12	-7.91142	Down	Tubulin beta 4B class IVb
RPL36	-2.5897	1.96E-14	5.09E-12	-7.88659	Down	Ribosomal protein L36
RGL2	-2.454	2.05E-14	5.27E-12	-7.88061	Down	Ral guanine nucleotide dissociation stimulator like 2
RPS17	-2.18352	2.21E-14	5.65E-12	-7.86985	Down	Ribosomal protein S17
S100A6	-2.24289	2.57E-14	6.53E-12	-7.84863	Down	S100 calcium binding protein A6
TMA7	-2.43269	2.99E-14	7.53E-12	-7.82741	Down	Translation machinery associated 7 homolog
TAGLN2	-2.21074	3.7E-14	9.19E-12	-7.79734	Down	Transgelin 2
SSR4	-2.33039	3.91E-14	9.6E-12	-7.78935	Down	Signal sequence receptor subunit 4
CELSR1	-2.55688	3.92E-14	9.6E-12	-7.78913	Down	Cadherin EGF LAG seven-pass G-type receptor 1
C20orf85	-2.43274	4.76E-14	1.16E-11	-7.76151	Down	Chromosome 20 open reading frame 85
CBR1	-2.30231	4.82E-14	1.17E-11	-7.75965	Down	Carbonyl reductase 1
UQCRC11	-2.4152	7.5E-14	1.78E-11	-7.69675	Down	Ubiquinol-cytochrome c reductase, complex III subunit XI
DEGS2	-2.45393	8.11E-14	1.91E-11	-7.68545	Down	Delta 4-desaturase, sphingolipid 2
RPL32	-2.17276	9.14E-14	2.12E-11	-7.66835	Down	Ribosomal protein L32
COMMMD6	-2.2856	9.68E-14	2.23E-11	-7.66018	Down	COMM domain containing 6
C9orf116	-2.29776	1.33E-13	2.99E-11	-7.61483	Down	Chromosome 9 open reading frame 116
KRT19	-2.30104	1.33E-13	2.99E-11	-7.6145	Down	Keratin 19
GCHFR	-2.07815	1.46E-13	3.25E-11	-7.60101	Down	GTP cyclohydrolase I feedback regulator
NDUFA2	-2.13238	1.56E-13	3.44E-11	-7.5918	Down	NADH:ubiquinoneoxidoreductase subunit A2
CLU	-2.31314	1.87E-13	4.11E-11	-7.5649	Down	Clusterin
P4HB	-2.20991	1.89E-13	4.12E-11	-7.56378	Down	Prolyl 4-hydroxylase subunit beta
RPL8	-2.24044	2.03E-13	4.37E-11	-7.55367	Down	Ribosomal protein L8
RPL21	-1.76498	2.07E-13	4.43E-11	-7.55061	Down	Ribosomal protein L21
CCDC78	-2.6623	2.09E-13	4.46E-11	-7.54899	Down	Coiled-coil domain containing 78
ANKRD65	-2.20064	2.27E-13	4.79E-11	-7.5369	Down	Ankyrin repeat domain 65
CTSH	-2.30293	2.39E-13	5E-11	-7.5296	Down	Cathepsin H
BSG	-2.29689	2.55E-13	5.28E-11	-7.52003	Down	Basigin (Ok blood group)
CD82	-2.25739	2.8E-13	5.73E-11	-7.50645	Down	CD82 molecule
NDUFB10	-2.10269	2.89E-13	5.88E-11	-7.50196	Down	NADH:ubiquinoneoxidoreductase subunit B10
AGR2	-1.66274	3.06E-13	6.16E-11	-7.49355	Down	Anterior gradient 2, protein disulphide isomerase family member
MAGED2	-2.23411	4.02E-13	7.89E-11	-7.45392	Down	MAGE family member D2
SMIM22	-2.2976	4.89E-13	9.57E-11	-7.4249	Down	Small integral membrane protein 22
SLC25A25	-2.39116	5.32E-13	1.03E-10	-7.41249	Down	Solute carrier family 25 member 25
CHCHD2	-2.27713	6.81E-13	1.31E-10	-7.37611	Down	Coiled-coil-helix-coiled-coil-helix domain containing 2
CD59	-2.47468	7.61E-13	1.43E-10	-7.35977	Down	CD59 molecule (CD59 blood group)
CYB561	-2.24272	8.47E-13	1.58E-10	-7.34389	Down	Cytochrome b561
RIPK4	-2.21045	9.03E-13	1.67E-10	-7.33447	Down	Receptor interacting serine/threonine kinase 4
CCDC74B	-2.23788	1.02E-12	1.84E-10	-7.31699	Down	Coiled-coil domain containing 74B
TMED9	-2.07164	1.09E-12	1.94E-10	-7.30655	Down	Transmembrane p24 trafficking protein 9
KRT8	-1.9875	1.09E-12	1.94E-10	-7.30677	Down	Keratin 8
RPL36A	-1.77029	1.12E-12	1.98E-10	-7.30189	Down	Ribosomal protein L36a

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Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
STUB1	-2.25135	1.17E-12	2.05E-10	-7.29578	Down	STIP1 homology and U-box containing protein 1
SIVA1	-2.14316	1.22E-12	2.12E-10	-7.28936	Down	SIVA1 apoptosis inducing factor
DGCR6	-2.2715	1.23E-12	2.12E-10	-7.28878	Down	DiGeorge syndrome critical region gene 6
TF3	-2.60239	1.42E-12	2.44E-10	-7.26746	Down	Trefoil factor 3
LAMTOR4	-2.19538	1.46E-12	2.49E-10	-7.26337	Down	Late endosomal/lysosomal adaptor, MAPK and MTOR activator 4
UBXN11	-2.23543	1.51E-12	2.55E-10	-7.25821	Down	UBX domain protein 11
CLSTN1	-2.4655	1.52E-12	2.56E-10	-7.25705	Down	Calsyntenin 1
RTPRF	-2.45237	1.91E-12	3.21E-10	-7.22254	Down	Protein tyrosine phosphatase receptor type F
RPS13	-1.99554	1.99E-12	3.33E-10	-7.21637	Down	Ribosomal protein S13
BLOC1S1	-2.15384	2.21E-12	3.68E-10	-7.20078	Down	Biogenesis of lysosomal organelles complex 1 subunit 1
EEF1G	-2.03648	2.28E-12	3.78E-10	-7.19594	Down	Eukaryotic translation elongation factor 1 gamma
RPL17-C18orf32	-2.47228	2.4E-12	3.94E-10	-7.1883	Down	RPL17-C18orf32 readthrough
S100A13	-2.12811	2.45E-12	4E-10	-7.18524	Down	S100 calcium binding protein A13
ACO2	-2.13458	2.49E-12	4.05E-10	-7.18263	Down	Aconitase 2
ELF3	-1.80801	2.63E-12	4.26E-10	-7.17454	Down	E74 like ETS transcription factor 3
CNN1	-2.54282	2.96E-12	4.73E-10	-7.15647	Down	Cellular communication network factor 1
EIF3CL	-2.88327	3E-12	4.78E-10	-7.15447	Down	Eukaryotic translation initiation factor 3 subunit C like
CITED2	-2.05013	3.28E-12	5.14E-10	-7.14133	Down	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2
KIG	-2.11531	3.68E-12	5.74E-10	-7.12388	Down	cAMP-dependent protein kinase inhibitor gamma
RPL4	-1.66249	3.97E-12	6.18E-10	-7.11206	Down	Ribosomal protein L4
ELOB	-2.24459	4.03E-12	6.25E-10	-7.10981	Down	Elongin B
SELENOH	-2.17241	4.38E-12	6.71E-10	-7.0972	Down	Selenoprotein H
EPHX1	-2.21184	4.39E-12	6.71E-10	-7.09695	Down	Epoxide hydrolase 1
FDXR	-1.95047	4.47E-12	6.8E-10	-7.09428	Down	Ferredoxinreductase
RUVBL2	-2.17919	4.64E-12	7.04E-10	-7.0884	Down	RuvB like AAA ATPase 2
TMEM9	-1.97684	4.68E-12	7.07E-10	-7.08705	Down	Transmembrane protein 9
TADA3	-2.04625	4.77E-12	7.17E-10	-7.08431	Down	Transcriptional adaptor 3
C11orf97	-1.93749	5.07E-12	7.6E-10	-7.0748	Down	Chromosome 11 open reading frame 97
H3-3A	-1.77133	5.68E-12	8.44E-10	-7.05753	Down	H3.3 histone A
STOML3	-2.2801	5.75E-12	8.46E-10	-7.05581	Down	Stomatin like 3
COX6A1	-2.03749	7.2E-12	1.04E-09	-7.02125	Down	Cytochrome c oxidase subunit 6A1
CRBP	-1.92797	7.26E-12	1.05E-09	-7.01992	Down	Cold inducible RNA binding protein
CLDN3	-2.2719	7.48E-12	1.08E-09	-7.01532	Down	Claudin 3
TRAPP2L	-2.06454	8.07E-12	1.15E-09	-7.00374	Down	Trafficking protein particle complex 2 like
MAPK8IP1	-2.16977	8.92E-12	1.26E-09	-6.98834	Down	Mitogen-activated protein kinase 8 interacting protein 1
FBXW9	-2.00762	9.03E-12	1.27E-09	-6.98641	Down	F-box and WD repeat domain containing 9
TMEM205	-2.03788	9.27E-12	1.3E-09	-6.98234	Down	Transmembrane protein 205
RPL27	-1.80071	9.81E-12	1.37E-09	-6.97371	Down	Ribosomal protein L27
IGFBP5	-2.18763	9.94E-12	1.38E-09	-6.97168	Down	Insulin like growth factor binding protein 5
DDR1	-2.21319	1.03E-11	1.41E-09	-6.96655	Down	Discoidin domain receptor tyrosine kinase 1
HSPBP1	-2.12373	1.14E-11	1.54E-09	-6.95109	Down	HSPA (Hsp70) binding protein 1
NDUFAB1	-2.02443	1.31E-11	1.77E-09	-6.92876	Down	NADH:ubiquinoneoxidoreductase subunit AB1
ARL6IP4	-2.00366	1.33E-11	1.79E-09	-6.9263	Down	ADP ribosylation factor like GTPase 6 interacting protein 4
RPL9	-2.11977	1.35E-11	1.81E-09	-6.92447	Down	Ribosomal protein L9
MB	-2.01308	1.42E-11	1.89E-09	-6.91688	Down	Myoglobin
CCDC96	-2.02486	1.45E-11	1.93E-09	-6.9131	Down	Coiled-coil domain containing 96
RPL19	-1.922	1.47E-11	1.95E-09	-6.91098	Down	Ribosomal protein L19
FIS1	-2.0979	1.55E-11	2.04E-09	-6.9032	Down	Fission, mitochondrial 1
NDUFA13	-2.17716	1.69E-11	2.23E-09	-6.88921	Down	NADH:ubiquinoneoxidoreductase subunit A13
LAMB2	-2.13016	1.74E-11	2.26E-09	-6.88503	Down	Laminin subunit beta 2
NOP53	-1.93577	1.75E-11	2.27E-09	-6.88376	Down	NOP53 ribosome biogenesis factor
LRRC10B	-2.193	1.77E-11	2.29E-09	-6.88194	Down	Leucine rich repeat containing 10B
NDUFB7	-1.99539	1.81E-11	2.33E-09	-6.87833	Down	NADH:ubiquinoneoxidoreductase subunit B7
EFNA1	-2.09749	1.84E-11	2.35E-09	-6.87647	Down	Ephrin A1
CD151	-2.16176	1.93E-11	2.46E-09	-6.86841	Down	CD151 molecule (Raph blood group)
EEF1D	-2.07927	1.94E-11	2.46E-09	-6.8682	Down	Eukaryotic translation elongation factor 1 delta
VPS51	-2.1143	1.94E-11	2.46E-09	-6.86763	Down	VPS51 subunit of GARP complex
SEC61B	-2.10649	1.95E-11	2.47E-09	-6.867	Down	SEC61 translocon beta subunit
RPL7A	-1.72213	2.01E-11	2.54E-09	-6.86212	Down	Ribosomal protein L7a
WDR38	-2.26822	2.3E-11	2.86E-09	-6.84142	Down	WD repeat domain 38
SPAG7	-1.94883	2.35E-11	2.92E-09	-6.83761	Down	Sperm associated antigen 7
FAM174A	-2.10937	2.37E-11	2.93E-09	-6.83665	Down	Family with sequence similarity 174 member A
MYL6	-1.66977	2.49E-11	3.07E-09	-6.82893	Down	Myosin light chain 6
CCDC153	-1.96033	2.5E-11	3.07E-09	-6.82813	Down	Coiled-coil domain containing 153
SLPI	-1.73764	2.52E-11	3.09E-09	-6.82689	Down	Secretory leukocyte peptidase inhibitor
VWA7	-2.19447	2.55E-11	3.1E-09	-6.82497	Down	von Willebrand factor A domain containing 7
ENKD1	-2.03365	2.55E-11	3.1E-09	-6.82489	Down	Enkurin domain containing 1
TPPP3	-2.19777	2.57E-11	3.1E-09	-6.82394	Down	Tubulin polymerization promoting protein family member 3
BICD2	-2.11863	2.58E-11	3.11E-09	-6.82296	Down	BICD cargo adaptor 2
ELMO3	-2.00492	2.72E-11	3.25E-09	-6.81491	Down	Engulfment and cell motility 3
ACTR1B	-2.13923	2.81E-11	3.35E-09	-6.81001	Down	Actin related protein 1B
RPS15A	-1.71927	2.95E-11	3.51E-09	-6.80202	Down	Ribosomal protein S15a
TTC29	-2.14236	3.06E-11	3.62E-09	-6.79623	Down	Tetratricopeptide repeat domain 29
STEAP3	-2.19801	3.08E-11	3.63E-09	-6.79521	Down	STEAP3 metalloredutase
POR	-2.25017	3.14E-11	3.68E-09	-6.79232	Down	Cytochrome p450 oxidoreductase
TEF	-2.03069	3.53E-11	4.13E-09	-6.77375	Down	TEF transcription factor, PAR bZIP family member

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Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
TCTEX1D4	-2.00956	3.62E-11	4.2E-09	-6.77001	Down	Tctex1 domain containing 4
CFAP73	-2.26058	3.73E-11	4.32E-09	-6.76518	Down	Cilia and flagella associated protein 73
RPL7	-2.03694	3.91E-11	4.52E-09	-6.7576	Down	Ribosomal protein L7
H1-4	-2.16832	4.02E-11	4.62E-09	-6.75343	Down	H1.4 linker histone, cluster member
NDUFC1	-1.97117	4.08E-11	4.68E-09	-6.75078	Down	NADH:ubiquinoneoxidoreductase subunit C1
GNAI1	-2.01715	4.28E-11	4.89E-09	-6.74353	Down	G protein subunit alpha 11
EDF1	-2.17852	4.33E-11	4.92E-09	-6.74137	Down	Endothelial differentiation related factor 1
ATP6V0B	-2.09527	4.63E-11	5.23E-09	-6.73079	Down	ATPase H+ transporting V0 subunit b
COX4I1	-1.95677	4.66E-11	5.24E-09	-6.72993	Down	Cytochrome c oxidase subunit 4I1
UBL5	-1.88057	4.76E-11	5.31E-09	-6.72642	Down	Ubiquitin like 5
RHPN1	-2.14142	4.76E-11	5.31E-09	-6.72656	Down	Rhopilin Rho GTPase binding protein 1
TACSTD2	-1.75555	4.74E-11	5.31E-09	-6.72733	Down	Tumor associated calcium signal transducer 2
ST6GALNAC2	-2.15379	5.25E-11	5.81E-09	-6.71095	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 2
RPL27A	-1.88393	5.63E-11	6.18E-09	-6.69972	Down	ribosomal protein L27a
SLC44A4	-2.1673	5.67E-11	6.2E-09	-6.69872	Down	Solute carrier family 44 member 4
KRT10	-1.91825	6.32E-11	6.87E-09	-6.68144	Down	Keratin 10
ATP5ME	-1.91934	6.34E-11	6.88E-09	-6.68081	Down	ATP synthase membrane subunit e
RP53	-1.85414	6.46E-11	6.97E-09	-6.67792	Down	Ribosomal protein S3
RP52	-1.91914	6.46E-11	6.97E-09	-6.67784	Down	Ribosomal protein S2
TSTD1	-2.07593	6.51E-11	6.99E-09	-6.67676	Down	Thiosulfate sulfurtransferase like domain containing 1
MIF	-2.26039	6.61E-11	7.08E-09	-6.67434	Down	Macrophage migration inhibitory factor
LRRC45	-1.95779	6.98E-11	7.41E-09	-6.66554	Down	Leucine rich repeat containing 45
POX	-2.11614	7.06E-11	7.47E-09	-6.66638	Down	Protoporphyrinogen oxidase
TSPAN15	-2.01986	7.31E-11	7.71E-09	-6.65816	Down	Tetraspanin 15
DNALI1	-2.50703	7.86E-11	8.25E-09	-6.64649	Down	Dynein axonemal light intermediate chain 1
NDUFB2	-1.9043	8.34E-11	8.7E-09	-6.63705	Down	NADH:ubiquinoneoxidoreductase subunit B2
C22orf15	-1.86954	8.96E-11	9.32E-09	-6.62556	Down	Chromosome 22 open reading frame 15
UQCRC1	-2.09822	9.06E-11	9.37E-09	-6.62365	Down	Ubiquinol-cytochrome c reductase core protein 1
KLF15	-2.05707	9.12E-11	9.4E-09	-6.62271	Down	Kruppel like factor 15
COP9	-1.83599	9E-11	9.34E-09	-6.62469	Down	COP9 signalosome subunit 9
COMT	-2.03395	9.35E-11	9.62E-09	-6.61862	Down	Catechol-O-methyltransferase
CCDC33	-2.2541	9.46E-11	9.68E-09	-6.61677	Down	Coiled-coil domain containing 33
ADIRF	-2.04944	9.47E-11	9.68E-09	-6.61662	Down	Adipogenesis regulatory factor
POLR2L	-1.94897	1.02E-10	1.04E-08	-6.60534	Down	RNA polymerase II subunit L
C12orf75	-2.08732	1.07E-10	1.08E-08	-6.59738	Down	Chromosome 12 open reading frame 75
WFDC21P	-1.96758	1.1E-10	1.12E-08	-6.59199	Down	WAP four-disulfide core domain 21, pseudogene
KRT17	-2.29649	1.14E-10	1.15E-08	-6.58679	Down	Keratin 17
JUN	-2.3899	1.24E-10	1.25E-08	-6.57285	Down	Jun proto-oncogene, AP-1 transcription factor subunit
SELENBP1	-1.8826	1.31E-10	1.32E-08	-6.56412	Down	Selenium binding protein 1
FAM166A	-1.79103	1.33E-10	1.34E-08	-6.5613	Down	Family with sequence similarity 166 member A
FBXW5	-2.05555	1.37E-10	1.37E-08	-6.5566	Down	F-box and WD repeat domain containing 5
ST6GALNAC6	-1.93035	1.47E-10	1.46E-08	-6.54593	Down	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 6
DPY30	-1.87432	1.52E-10	1.51E-08	-6.53998	Down	dpy-30 histone methyltransferase complex regulatory subunit
GSTA2	-2.32644	1.64E-10	1.61E-08	-6.52801	Down	Glutathione S-transferase alpha 2
ALKBH7	-1.81307	1.63E-10	1.61E-08	-6.52861	Down	alkB homolog 7
RHOB	-1.93922	1.67E-10	1.64E-08	-6.52532	Down	Ras homolog family member B
PHB2	-1.91177	1.71E-10	1.67E-08	-6.52137	Down	Prohibitin 2
RHBDD2	-1.95984	1.82E-10	1.77E-08	-6.51046	Down	Rhomboid domain containing 2
NDUFA4	-1.79279	1.87E-10	1.81E-08	-6.50682	Down	NDUFA4 mitochondrial complex associated
LRRC43	-1.95125	1.96E-10	1.89E-08	-6.49844	Down	Leucine rich repeat containing 43
SEC14L3	-2.24879	1.99E-10	1.9E-08	-6.49666	Down	SEC14 like lipid binding 3
PTRHD1	-1.91732	2E-10	1.91E-08	-6.49541	Down	Peptidyl-tRNA hydrolase domain containing 1
COX5B	-1.85593	2.08E-10	1.98E-08	-6.48908	Down	Cytochrome c oxidase subunit 5B
CDC34	-1.87204	2.2E-10	2.08E-08	-6.48018	Down	Cell division cycle 34
POLR2J	-2.01038	2.21E-10	2.08E-08	-6.47939	Down	RNA polymerase II subunit J
SSBP4	-1.92116	2.41E-10	2.26E-08	-6.46491	Down	Single stranded DNA binding protein 4
UNC93B1	-2.12359	2.49E-10	2.33E-08	-6.45959	Down	unc-93 homolog B1, TLR signaling regulator
ARF5	-2.05342	2.64E-10	2.46E-08	-6.44975	Down	ADP ribosylation factor 5
C12orf57	-1.91231	2.64E-10	2.46E-08	-6.44993	Down	Chromosome 12 open reading frame 57
G6orf118	-1.99394	2.68E-10	2.48E-08	-6.44754	Down	Chromosome 6 open reading frame 118
GTF3C5	-1.86664	2.94E-10	2.71E-08	-6.43217	Down	General transcription factor IIIC subunit 5
GDF15	-2.1217	2.95E-10	2.71E-08	-6.43165	Down	Growth differentiation factor 15
TIMM13	-1.72785	2.95E-10	2.71E-08	-6.43202	Down	Translocase of inner mitochondrial membrane 13
TXNL4A	-1.81586	3.06E-10	2.8E-08	-6.42596	Down	Thioredoxin like 4A
JTB	-1.86317	3.1E-10	2.82E-08	-6.42347	Down	Jumping translocation breakpoint
EIF4H	-1.69444	3.1E-10	2.82E-08	-6.4236	Down	Eukaryotic translation initiation factor 4H
KRT15	-1.98286	3.28E-10	2.98E-08	-6.41451	Down	Keratin 15
C5orf49	-1.97644	3.47E-10	3.14E-08	-6.4048	Down	Chromosome 5 open reading frame 49
KLF4	-1.87651	3.48E-10	3.14E-08	-6.40454	Down	Kruppel like factor 4
ASL	-1.96482	3.5E-10	3.15E-08	-6.40364	Down	Argininosuccinatelyase
PSMG3	-1.79635	4.32E-10	3.85E-08	-6.3688	Down	Proteasome assembly chaperone 3
LRP5	-2.01623	4.39E-10	3.91E-08	-6.36595	Down	LDL receptor related protein 5

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
RPL6	-1.69353	4.63E-10	4.11E-08	-6.35735	Down	Ribosomal protein L6
IPT43	-1.95929	4.85E-10	4.3E-08	-6.34947	Down	Intraflagellar transport 43
RPS12	-1.76175	5.07E-10	4.48E-08	-6.342	Down	Ribosomal protein S12
ECRG4	-1.69792	5.93E-10	5.21E-08	-6.31617	Down	ECRG4 augurin precursor
GAS2L2	-2.00846	6.06E-10	5.32E-08	-6.31233	Down	Growth arrest specific 2 like 2
EPCAM	-1.86998	6.45E-10	5.63E-08	-6.30208	Down	Epithelial cell adhesion molecule
COQ4	-1.89504	6.89E-10	6E-08	-6.29095	Down	Coenzyme Q4
ROPN1L	-1.94379	6.94E-10	6.03E-08	-6.28975	Down	Rhopilin associated tail protein 1 like
DUS1L	-1.9312	7.04E-10	6.1E-08	-6.2874	Down	Dihydrouridine synthase 1 like
LRWD1	-1.96416	7.28E-10	6.3E-08	-6.28166	Down	Leucine rich repeats and WD repeat domain containing 1
EPHA2	-2.12037	7.62E-10	6.55E-08	-6.27417	Down	EPH receptor A2
ARHGEF17	-2.10188	7.62E-10	6.55E-08	-6.27408	Down	Rho guanine nucleotide exchange factor 17
ITGA3	-1.95221	7.64E-10	6.55E-08	-6.27368	Down	Integrin subunit alpha 3
MKNK2	-1.87752	7.92E-10	6.78E-08	-6.26758	Down	MAPK interacting serine/threonine kinase 2
ST14	-1.85634	8.18E-10	6.96E-08	-6.26224	Down	Suppression of tumorigenicity 14
SDCI	-1.94685	8.19E-10	6.96E-08	-6.26188	Down	Syndecan 1
FAM3B	-1.79557	8.54E-10	7.24E-08	-6.25498	Down	Family with sequence similarity 3 member B
DENND6B	-1.98885	8.68E-10	7.34E-08	-6.25214	Down	DENN domain containing 6B
HSPA1B	-2.40574	9.36E-10	7.9E-08	-6.23943	Down	Heat shock protein family A (Hsp70) member 1B
NIBAN2	-1.8528	9.55E-10	8.04E-08	-6.23599	Down	Niban apoptosis regulator 2
TBCA	-1.74127	9.99E-10	8.39E-08	-6.22843	Down	Tubulin folding cofactor A
FAM92B	-1.92117	1.05E-09	8.74E-08	-6.22045	Down	Family with sequence similarity 92 member B
ECI1	-1.9122	1.04E-09	8.73E-08	-6.22108	Down	Enoyl-CoA delta isomerase 1
PYCR2	-1.84257	1.09E-09	9.07E-08	-6.21343	Down	Pyrraline-5-carboxylate reductase 2
MMP24OS	-1.8105	1.11E-09	9.22E-08	-6.21018	Down	MMP24 opposite strand
SMDT1	-1.79538	1.14E-09	9.44E-08	-6.20585	Down	Single-pass membrane protein with aspartate rich tail 1
TSPO	-1.97905	1.17E-09	9.63E-08	-6.20134	Down	Translocator protein
AQP5	-2.00579	1.19E-09	9.74E-08	-6.19901	Down	Aquaporin 5
DPCD	-1.75433	1.26E-09	1.02E-07	-6.18959	Down	Deleted in primary ciliary dyskinesia homolog (mouse)
BORCS7	-1.78249	1.31E-09	1.07E-07	-6.18225	Down	BLOC-1 related complex subunit 7
RPL39	-1.76507	1.31E-09	1.07E-07	-6.18206	Down	Ribosomal protein L39
TUBGCP2	-1.76557	1.35E-09	1.09E-07	-6.17805	Down	Tubulin gamma complex associated protein 2
PLTP	-1.96738	1.36E-09	1.1E-07	-6.17642	Down	Phospholipid transfer protein
FAM229B	-1.81567	1.41E-09	1.14E-07	-6.17021	Down	Family with sequence similarity 229 member B
UBXN6	-1.91639	1.43E-09	1.15E-07	-6.16786	Down	UBX domain protein 6
DYNLRB2	-1.92322	1.48E-09	1.18E-07	-6.16145	Down	Dynein light chain roadblock-type 2
RPS16	-1.71746	1.53E-09	1.22E-07	-6.15561	Down	Ribosomal protein S16
UBTD1	-1.86484	1.58E-09	1.25E-07	-6.15075	Down	Ubiquitin domain containing 1
QARS1	-1.78746	1.59E-09	1.26E-07	-6.14997	Down	Glutaminyl-tRNA synthetase 1
PTTG1IP	-1.70207	1.6E-09	1.26E-07	-6.14859	Down	PTTG1 interacting protein
ERP29	-1.67866	1.67E-09	1.31E-07	-6.14154	Down	Endoplasmic reticulum protein 29
BAD	-1.92243	1.69E-09	1.33E-07	-6.13874	Down	BCL2 associated agonist of cell death
DAG1	-1.86819	1.73E-09	1.35E-07	-6.13553	Down	Dystroglycan 1
IMPA2	-1.83886	1.76E-09	1.37E-07	-6.13273	Down	Inositol monophosphatase 2
ZDHC1	-1.93217	1.79E-09	1.39E-07	-6.12939	Down	Zinc finger DHHC-type containing 1
TMEM219	-1.85686	1.81E-09	1.4E-07	-6.12783	Down	Transmembrane protein 219
GADD45GIP1	-1.95262	1.82E-09	1.41E-07	-6.12637	Down	GADD45G interacting protein 1
SCGB1A1	-2.27253	1.83E-09	1.41E-07	-6.12527	Down	Secretoglobin family 1A member 1
CYP4B1	-2.0315	1.84E-09	1.42E-07	-6.12438	Down	Cytochrome P450 family 4 subfamily B member 1
TRAF4	-1.87436	1.88E-09	1.44E-07	-6.1214	Down	TNF receptor associated factor 4
LRRC46	-2.01954	1.88E-09	1.44E-07	-6.12121	Down	Leucine rich repeat containing 46
CXXC5	-1.76708	1.89E-09	1.45E-07	-6.12004	Down	CXXC finger protein 5
AK1	-1.91665	1.94E-09	1.48E-07	-6.11551	Down	Adenylate kinase 1
CRACR2B	-1.90411	2.1E-09	1.59E-07	-6.10201	Down	Calcium release activated channel regulator 2B
RPL31	-1.69576	2.08E-09	1.58E-07	-6.10391	Down	Ribosomal protein L31
GNB2	-1.92728	2.11E-09	1.6E-07	-6.10081	Down	G protein subunit beta 2
IFT140	-1.99792	2.21E-09	1.66E-07	-6.09342	Down	Intraflagellar transport 140
GTPBP6	-1.79662	2.2E-09	1.66E-07	-6.09428	Down	GTP binding protein 6 (putative)
CD81	-1.95946	2.28E-09	1.7E-07	-6.08753	Down	CD81 molecule
YIF1B	-1.73138	2.28E-09	1.7E-07	-6.08774	Down	Yip1 interacting factor homolog B, membrane trafficking protein
B9D1	-1.94385	2.28E-09	1.7E-07	-6.08768	Down	B9 domain containing 1
ATAD3A	-1.81624	2.35E-09	1.75E-07	-6.08241	Down	ATPase family AAA domain containing 3A
HAGH	-1.75223	2.4E-09	1.78E-07	-6.07885	Down	Hydroxyacylglutathione hydrolase
C16orf71	-1.96374	2.7E-09	2E-07	-6.05844	Down	Chromosome 16 open reading frame 71
SNRPD2	-1.70123	2.75E-09	2.03E-07	-6.05528	Down	Small nuclear ribonucleoprotein D2 polypeptide
SPATA20	-1.84884	3.09E-09	2.27E-07	-6.03531	Down	Spermatogenesis associated 20
DNAI2	-1.97169	3.1E-09	2.27E-07	-6.03471	Down	Dynein axonemal intermediate chain 2
PRDX2	-1.87884	3.11E-09	2.27E-07	-6.03451	Down	Peroxiredoxin 2
GSTP1	-2.03222	3.47E-09	2.52E-07	-6.01548	Down	Glutathione S-transferase pi 1
IFT27	-2.06203	3.51E-09	2.54E-07	-6.01319	Down	Intraflagellar transport 27
LRRC23	-1.81779	3.55E-09	2.56E-07	-6.01126	Down	Leucine rich repeat containing 23
COX5A	-1.70885	3.57E-09	2.57E-07	-6.01019	Down	Cytochrome c oxidase subunit 5A

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
ZNF703	-1.79076	3.64E-09	2.62E-07	-6.00685	Down	Zinc finger protein 703
SYTL1	-1.82282	3.69E-09	2.65E-07	-6.0045	Down	Synaptotagmin like 1
GIPC1	-1.81979	3.8E-09	2.71E-07	-5.99964	Down	GIPC PDZ domain containing family member 1
TRIM3	-1.8956	3.79E-09	2.71E-07	-5.99972	Down	Tripartite motif containing 3
DNAJB2	-1.84555	3.86E-09	2.75E-07	-5.99689	Down	DnaJ heat shock protein family (Hsp40) member B2
SNRPB	-1.82123	3.88E-09	2.76E-07	-5.99587	Down	Small nuclear ribonucleoprotein polypeptides B and B1
NTN1	-1.77654	3.97E-09	2.82E-07	-5.9918	Down	Netrin 1
TXNDC17	-1.74537	4.03E-09	2.85E-07	-5.9893	Down	Thioredoxin domain containing 17
CFAP53	-1.8879	4.23E-09	2.99E-07	-5.98078	Down	Cilia and flagella associated protein 53
CYP27A1	-1.73304	4.39E-09	3.07E-07	-5.97444	Down	Cytochrome P450 family 27 subfamily A member 1
PCYT2	-1.95376	4.66E-09	3.24E-07	-5.96388	Down	Phosphate cytidyltransferase 2, ethanolamine
MRPL14	-1.77422	4.91E-09	3.41E-07	-5.95465	Down	Mitochondrial ribosomal protein L14
AAMP	-1.88446	5.18E-09	3.58E-07	-5.94539	Down	Angio associated migratory cell protein
TSPAN7	-1.83513	5.37E-09	3.69E-07	-5.9391	Down	Tetraspanin 7
NDUFS6	-1.75013	5.54E-09	3.8E-07	-5.93353	Down	NADH:ubiquinoneoxidoreductase subunit S6
SERPINF1	-1.77601	5.78E-09	3.94E-07	-5.9262	Down	Serpin family F member 1
RPS27	-1.87492	5.79E-09	3.94E-07	-5.92584	Down	Ribosomal protein S27
NHP2	-1.7269	6.21E-09	4.21E-07	-5.91345	Down	NHP2 ribonucleoprotein
ITPA	-1.72209	6.34E-09	4.29E-07	-5.9098	Down	Inosinetriphosphatase
ATP2C2	-1.98006	6.73E-09	4.52E-07	-5.89916	Down	ATPase secretory pathway Ca ²⁺ transporting 2
DDOST	-1.66934	7.09E-09	4.74E-07	-5.89	Down	Dolichyl–diphosphooligosaccharide–protein glycosyltransferase non–catalytic subunit
CTSD	-1.73829	7.54E-09	5.02E-07	-5.87908	Down	Cathepsin D
DMAC1	-1.71733	7.67E-09	5.08E-07	-5.87619	Down	Distal membrane arm assembly complex 1
CRELD2	-1.8103	7.85E-09	5.19E-07	-5.87193	Down	Cysteine rich with EGF like domains 2
WDR34	-1.87547	8.11E-09	5.31E-07	-5.86622	Down	WD repeat domain 34
ITGB5	-1.76845	8.12E-09	5.31E-07	-5.86599	Down	Integrin subunit beta 5
SLC20A2	-1.77494	8.57E-09	5.56E-07	-5.85654	Down	Solute carrier family 20 member 2
UBXN1	-1.70949	8.74E-09	5.66E-07	-5.85303	Down	UBX domain protein 1
AHNAK2	-1.84514	8.96E-09	5.77E-07	-5.84865	Down	AHNAK nucleoprotein 2
CCDC173	-1.86578	9.67E-09	6.2E-07	-5.83498	Down	Coiled–coil domain containing 173
KRT5	-1.97206	9.96E-09	6.36E-07	-5.82973	Down	Keratin 5
WFD6C6	-1.68198	1.02E-08	6.49E-07	-5.82592	Down	WAP four–disulfide core domain 6
GPR162	-1.83981	1.03E-08	6.57E-07	-5.82304	Down	G protein–coupled receptor 162
PIH1D3	-1.72246	1.04E-08	6.63E-07	-5.82131	Down	PIH1 domain containing 3
PDLIM4	-1.83002	1.06E-08	6.71E-07	-5.8187	Down	PDZ and LIM domain 4
SERTAD1	-1.85245	1.07E-08	6.78E-07	-5.81644	Down	SERTA domain containing 1
SSNA1	-1.78668	1.08E-08	6.85E-07	-5.81449	Down	SS nuclear autoantigen 1
APBB1	-1.77226	1.1E-08	6.92E-07	-5.81197	Down	Amyloid beta precursor protein binding family B member 1
SOC3	-2.21648	1.11E-08	7E-07	-5.80963	Down	Suppressor of cytokine signaling 3
ID1	-1.74246	1.17E-08	7.32E-07	-5.80071	Down	Inhibitor of DNA binding 1, HLH protein
TALDO1	-1.73878	1.18E-08	7.37E-07	-5.79889	Down	Transaldolase 1
DVLI	-1.72485	1.2E-08	7.42E-07	-5.79705	Down	Dishevelled segment polarity protein 1
WDR13	-1.80052	1.21E-08	7.49E-07	-5.79478	Down	WD repeat domain 13
ATG4B	-1.83051	1.25E-08	7.7E-07	-5.78931	Down	Autophagy related 4B cysteine peptidase
S100A2	-1.74848	1.26E-08	7.74E-07	-5.78821	Down	S100 calcium binding protein A2
PRRT3	-1.86062	1.27E-08	7.83E-07	-5.78576	Down	Proline rich transmembrane protein 3
NRSN1	-2.40742	1.3E-08	8E-07	-5.78159	Down	Neurensin 1
RSPH9	-1.77518	1.33E-08	8.17E-07	-5.77748	Down	Radial spoke head component 9
TST	-1.83689	1.35E-08	8.28E-07	-5.77486	Down	Thiosulfate sulfurtransferase
NR2F6	-1.7683	1.39E-08	8.44E-07	-5.77021	Down	Nuclear receptor subfamily 2 group F member 6
NDUFAF3	-1.75745	1.4E-08	8.49E-07	-5.76886	Down	NADH:ubiquinoneoxidoreductase complex assembly factor 3
COA3	-1.66617	1.41E-08	8.51E-07	-5.76798	Down	Cytochrome c oxidase assembly factor 3
CALML4	-1.71073	1.41E-08	8.53E-07	-5.76739	Down	Calmodulin like 4
C9orf135	-1.7951	1.42E-08	8.58E-07	-5.76593	Down	Chromosome 9 open reading frame 135
TMEM190	-1.65688	1.43E-08	8.61E-07	-5.76514	Down	Transmembrane protein 190
PPP4C	-1.78799	1.51E-08	9.04E-07	-5.75519	Down	Protein phosphatase 4 catalytic subunit
DGCR6L	-1.92861	1.51E-08	9.04E-07	-5.75533	Down	DiGeorge syndrome critical region gene 6 like
AGPAT2	-1.7202	1.54E-08	9.22E-07	-5.75124	Down	1–acylglycerol–3–phosphate O–acyltransferase 2
TRPT1	-1.7738	1.66E-08	9.78E-07	-5.73848	Down	tRNAphosphotransferase 1
NME2	-1.66716	1.71E-08	1.01E-06	-5.73229	Down	NME/NM23 nucleoside diphosphate kinase 2
PIN1	-1.69402	1.71E-08	1.01E-06	-5.73229	Down	peptidylprolylcis/trans isomerase, NIMA–interacting 1
CCDC17	-1.9343	1.72E-08	1.01E-06	-5.73136	Down	Coiled–coil domain containing 17
EPPK1	-2.02457	1.78E-08	1.04E-06	-5.72585	Down	Epiplakin 1
SLC2A1	-1.84298	1.79E-08	1.04E-06	-5.72496	Down	Solute carrier family 2 member 1
PROS1	-1.83383	1.8E-08	1.05E-06	-5.72297	Down	Protein S
PRR29	-1.84657	1.89E-08	1.1E-06	-5.71492	Down	Proline rich 29
UBAC1	-1.65795	2.06E-08	1.18E-06	-5.69933	Down	UBA domain containing 1
SPPL2B	-1.81721	2.1E-08	1.21E-06	-5.69541	Down	Signal peptide peptidase like 2B
HSPA2	-1.71269	2.16E-08	1.24E-06	-5.69067	Down	Heat shock protein family A (Hsp70) member 2
ARPC1A	-1.71247	2.25E-08	1.28E-06	-5.68301	Down	Actin related protein 2/3 complex subunit 1A
CMTM4	-1.74281	2.26E-08	1.29E-06	-5.68224	Down	CKLF like MARVEL transmembrane domain containing 4

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
SELENOS	-1.70437	2.31E-08	1.31E-06	-5.67855	Down	Selenoprotein S
SEPTIN5	-1.68975	2.32E-08	1.32E-06	-5.67718	Down	Septin 5
PPP1R16A	-1.87239	2.34E-08	1.32E-06	-5.67597	Down	Protein phosphatase 1 regulatory subunit 16A
SLC27A2	-1.93042	2.42E-08	1.37E-06	-5.6696	Down	Solute carrier family 27 member 2
ERBB2	-1.72934	2.46E-08	1.39E-06	-5.66703	Down	erb-b2 receptor tyrosine kinase 2
IER3	-1.9359	2.59E-08	1.46E-06	-5.65735	Down	Immediate early response 3
TKT	-1.77145	2.62E-08	1.47E-06	-5.65535	Down	Transketolase
COPE	-1.80639	2.81E-08	1.57E-06	-5.64247	Down	Coatomer protein complex subunit epsilon
PTK7	-1.67214	2.83E-08	1.58E-06	-5.64117	Down	Protein tyrosine kinase 7 (inactive)
CFAP157	-2.06081	2.99E-08	1.66E-06	-5.63111	Down	Cilia and flagella associated protein 157
NPEPL1	-1.7489	3.07E-08	1.69E-06	-5.62635	Down	Aminopeptidase like 1
PSMA7	-1.79665	3.1E-08	1.7E-06	-5.62462	Down	Proteasome 20S subunit alpha 7
MORN5	-1.72339	3.09E-08	1.7E-06	-5.62507	Down	MORN repeat containing 5
SURF1	-1.66818	3.07E-08	1.69E-06	-5.62605	Down	SURF1 cytochrome c oxidase assembly factor
WDR54	-1.68738	3.29E-08	1.79E-06	-5.61356	Down	WD repeat domain 54
CYB5R1	-1.81821	3.39E-08	1.84E-06	-5.60801	Down	Cytochrome b5 reductase 1
MLF1	-1.85686	3.49E-08	1.89E-06	-5.60274	Down	Myeloid leukemia factor 1
ALDH3B1	-1.73357	3.64E-08	1.96E-06	-5.59481	Down	Aldehyde dehydrogenase 3 family member B1
GRHPR	-1.68387	3.72E-08	1.99E-06	-5.59096	Down	Glyoxylate and hydroxypruvatereductase
DHX30	-1.68988	4.11E-08	2.17E-06	-5.57235	Down	DExH-box helicase 30
RSPH1	-1.66662	4.09E-08	2.17E-06	-5.57325	Down	Radial spoke head component 1
DNPH1	-1.68015	4.15E-08	2.19E-06	-5.57066	Down	2'-deoxynucleoside 5'-phosphate N-hydrolase 1
BCAM	-1.66855	4.18E-08	2.2E-06	-5.56923	Down	Basal cell adhesion molecule (Lutheran blood group)
CSTB	-1.65596	4.39E-08	2.3E-06	-5.56037	Down	Cystatin B
CBX7	-1.67449	4.46E-08	2.33E-06	-5.55723	Down	Chromobox 7
CCDC89	-1.73873	4.64E-08	2.41E-06	-5.55013	Down	Coiled-coil domain containing 89
PTOV1	-1.7681	4.76E-08	2.47E-06	-5.5453	Down	PTOV1 extended AT-hook containing adaptor protein
REXO2	-1.65952	4.82E-08	2.49E-06	-5.54307	Down	RNA exonuclease 2
GJB3	-1.68607	4.87E-08	2.51E-06	-5.54098	Down	Gap junction protein beta 3
MID1IP1	-1.65858	5.01E-08	2.58E-06	-5.53582	Down	MID1 interacting protein 1
P4HTM	-1.88976	5.27E-08	2.69E-06	-5.52644	Down	Prolyl 4-hydroxylase, transmembrane
COL2A1A	-1.76766	5.3E-08	2.71E-06	-5.52507	Down	Collagen type XXI alpha 1 chain
JUND	-1.67101	5.43E-08	2.76E-06	-5.5206	Down	JunD proto-oncogene, AP-1 transcription factor subunit
NAA38	-1.72707	5.51E-08	2.78E-06	-5.51797	Down	N(alpha)-acetyltransferase 38, NatC auxiliary subunit
METRN	-1.74438	5.56E-08	2.8E-06	-5.51613	Down	Meteorin, glial cell differentiation regulator
GLB1L2	-1.82524	5.72E-08	2.86E-06	-5.51102	Down	Galactosidase beta 1 like 2
CCDC151	-1.70396	5.71E-08	2.86E-06	-5.5112	Down	Coiled-coil domain containing 151
COQ8B	-1.67846	5.78E-08	2.89E-06	-5.50914	Down	Coenzyme Q8B
PGLS	-1.68667	5.99E-08	2.98E-06	-5.50229	Down	6-phosphogluconolactonase
TRIM28	-1.76866	6.21E-08	3.08E-06	-5.49578	Down	Tripartite motif containing 28
POLR2I	-1.68564	6.4E-08	3.16E-06	-5.48986	Down	RNA polymerase II subunit 1
ARHGAP39	-1.7857	6.71E-08	3.29E-06	-5.48124	Down	Rho GTPase activating protein 39
LARP6	-1.65665	6.71E-08	3.29E-06	-5.48114	Down	La ribonucleoprotein 6, translational regulator
SLC2A4RG	-1.66563	6.79E-08	3.32E-06	-5.47885	Down	SLC2A4 regulator
EPS8L2	-1.70851	7.39E-08	3.59E-06	-5.46302	Down	EPS8 like 2
STOML2	-1.65149	7.57E-08	3.67E-06	-5.45837	Down	Stomatin like 2
MAPK15	-2.00822	7.75E-08	3.75E-06	-5.454	Down	Mitogen-activated protein kinase 15
TRAF7	-1.67557	7.86E-08	3.79E-06	-5.45148	Down	TNF receptor associated factor 7
VARS1	-1.6696	8E-08	3.85E-06	-5.44817	Down	Valyl-tRNA synthetase 1
LRRC71	-1.72338	8.01E-08	3.85E-06	-5.44779	Down	Leucine rich repeat containing 71
BALAP3	-1.92147	8.02E-08	3.85E-06	-5.4475	Down	BAL1 associated protein 3
SPEF1	-1.69646	8.14E-08	3.89E-06	-5.44485	Down	Sperm flagellar 1
KEAP1	-1.7721	9.06E-08	4.25E-06	-5.42461	Down	Kelch like ECH associated protein 1
MAZ	-1.67081	9.17E-08	4.28E-06	-5.42228	Down	MYC associated zinc finger protein
ECSIT	-1.65788	9.16E-08	4.28E-06	-5.42247	Down	ECSIT signaling integrator
TXNDC5	-1.6759	9.48E-08	4.42E-06	-5.41602	Down	Thioredoxin domain containing 5
LAMC2	-1.80204	9.6E-08	4.45E-06	-5.41357	Down	Laminin subunit gamma 2
GPX1	-2.0951	1.07E-07	4.92E-06	-5.39316	Down	Glutathione peroxidase 1
MAP9	-1.86892	1.07E-07	4.93E-06	-5.39258	Down	Microtubule associated protein 9
PPP1R32	-1.71146	1.1E-07	5.05E-06	-5.38749	Down	Protein phosphatase 1 regulatory subunit 32
PTPRU	-1.75608	1.22E-07	5.53E-06	-5.36876	Down	Protein tyrosine phosphatase receptor type U
PPEF2	-1.96848	1.25E-07	5.66E-06	-5.36353	Down	Protein phosphatase with EF-hand domain 2
PLXNB1	-1.91303	1.36E-07	6.11E-06	-5.34682	Down	Plexin B1
VILL	-1.68796	1.47E-07	6.49E-06	-5.33183	Down	Villin like
CYC1	-1.65546	1.63E-07	7.09E-06	-5.31278	Down	Cytochrome c1
COX7B	-1.69487	1.7E-07	7.35E-06	-5.30479	Down	Cytochrome c oxidase subunit 7B
FKBP8	-1.65406	1.85E-07	7.97E-06	-5.2886	Down	FKBP prolyl isomerase 8
CCDC74A	-1.71074	1.93E-07	8.26E-06	-5.28032	Down	Coiled-coil domain containing 74A
GADD45B	-1.911	1.93E-07	8.27E-06	-5.27966	Down	Growth arrest and DNA damage inducible beta
LRG1	-1.69928	1.98E-07	8.45E-06	-5.27479	Down	Leucine rich alpha-2-glycoprotein 1
MAN2B1	-1.71474	2.01E-07	8.57E-06	-5.27161	Down	Mannosidase alpha class 2B member 1
FOS	-2.11649	2.06E-07	8.74E-06	-5.26713	Down	Fos proto-oncogene, AP-1 transcription factor subunit

(continued on next page)

Table 1 (continued)

Gene symbol	logFC	p Value	Adj.P.Val	tvalue	Regulation	Gene name
PLXNB2	-1.77759	2.19E-07	9.23E-06	-5.25581	Down	Plexin B2
TRIM8	-1.85833	2.37E-07	9.89E-06	-5.24022	Down	Tripartite motif containing 8
CRIP2	-1.65107	3.17E-07	1.29E-05	-5.18326	Down	Cysteine rich protein 2
SLC25A29	-1.74002	3.79E-07	1.51E-05	-5.14784	Down	Solute carrier family 25 member 29
CTNNB1	-1.7177	3.83E-07	1.52E-05	-5.14585	Down	Catenin beta 1
RPS10-NUDT3	-1.77595	3.86E-07	1.52E-05	-5.14458	Down	RPS10-NUDT3 readthrough
PIGQ	-1.65175	4.32E-07	1.68E-05	-5.12193	Down	Phosphatidylinositol glycan anchor biosynthesis class Q
RPL29	-1.69438	5.39E-07	2.04E-05	-5.07812	Down	Ribosomal protein L29
FCGBP	-1.7369	5.77E-07	2.17E-05	-5.06424	Down	Fc fragment of IgG binding protein
ENPP5	-1.65173	7.24E-07	2.66E-05	-5.01881	Down	Ectonucleotidepyrophosphatase/phosphodiesterase family member 5
CFAP65	-1.73359	7.36E-07	2.7E-05	-5.01556	Down	Cilia and flagella associated protein 65
DHCR24	-1.92576	9.3E-07	3.3E-05	-4.96808	Down	24-dehydrocholesterol reductase
KNDC1	-1.66077	9.69E-07	3.42E-05	-4.95959	Down	Kinase non-catalytic C-lobe domain containing 1
CSRN1	-1.83601	1.02E-06	3.58E-05	-4.94888	Down	Cysteine and serine rich nuclear protein 1
JUNB	-1.87233	1.28E-06	4.36E-05	-4.90251	Down	JunB proto-oncogene, AP-1 transcription factor subunit
CCDC39	-1.77153	1.29E-06	4.38E-05	-4.90117	Down	Coiled-coil domain containing 39
CFAP100	-1.74895	1.6E-06	5.28E-05	-4.85592	Down	Cilia and flagella associated protein 100
CROCC	-1.67639	1.72E-06	5.61E-05	-4.84177	Down	Ciliary rootlet coiled-coil, rootletin
DUSP1	-1.66103	1.83E-06	5.91E-05	-4.82904	Down	Dual specificity phosphatase 1
DLEC1	-1.80414	2.2E-06	6.9E-05	-4.79009	Down	DLEC1 cilia and flagella associated protein
FOSB	-1.90705	4.9E-06	0.000137	-4.61925	Down	FosB proto-oncogene, AP-1 transcription factor subunit
IGHG1	-1.8485	9.31E-06	0.000236	-4.4787	Down	Immunoglobulin heavy constant gamma 1 (G1m marker)
CDHR4	-1.71756	1.3E-05	0.000312	-4.40362	Down	Cadherin related family member 4
IGHG3	-1.66304	1.32E-05	0.000314	-4.40127	Down	Immunoglobulin heavy constant gamma 3 (G3m marker)
HSPA1A	-1.67879	2.88E-05	0.000614	-4.22139	Down	Heat shock protein family A (Hsp70) member 1A

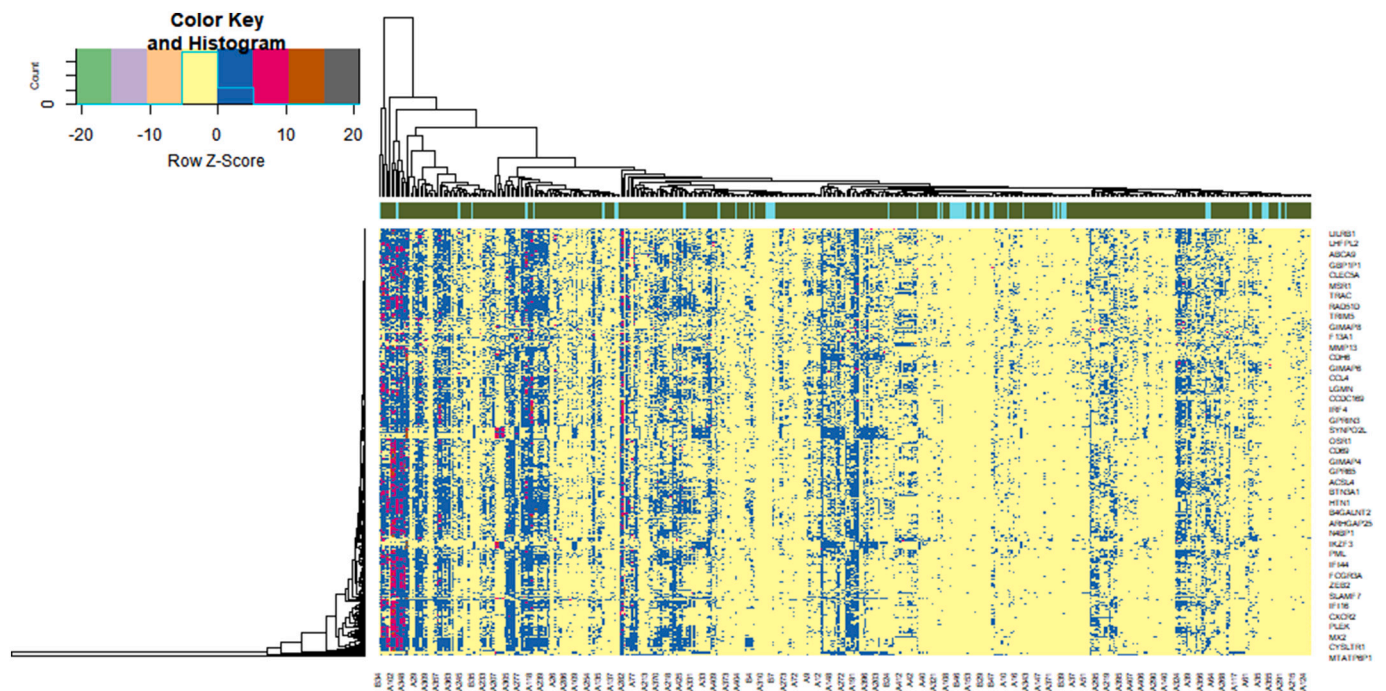


Fig. 3. Heat map of up regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A54 = negative control samples (red color box); B1 – B430 = SARS-CoV-2 infected samples (blue color box)). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

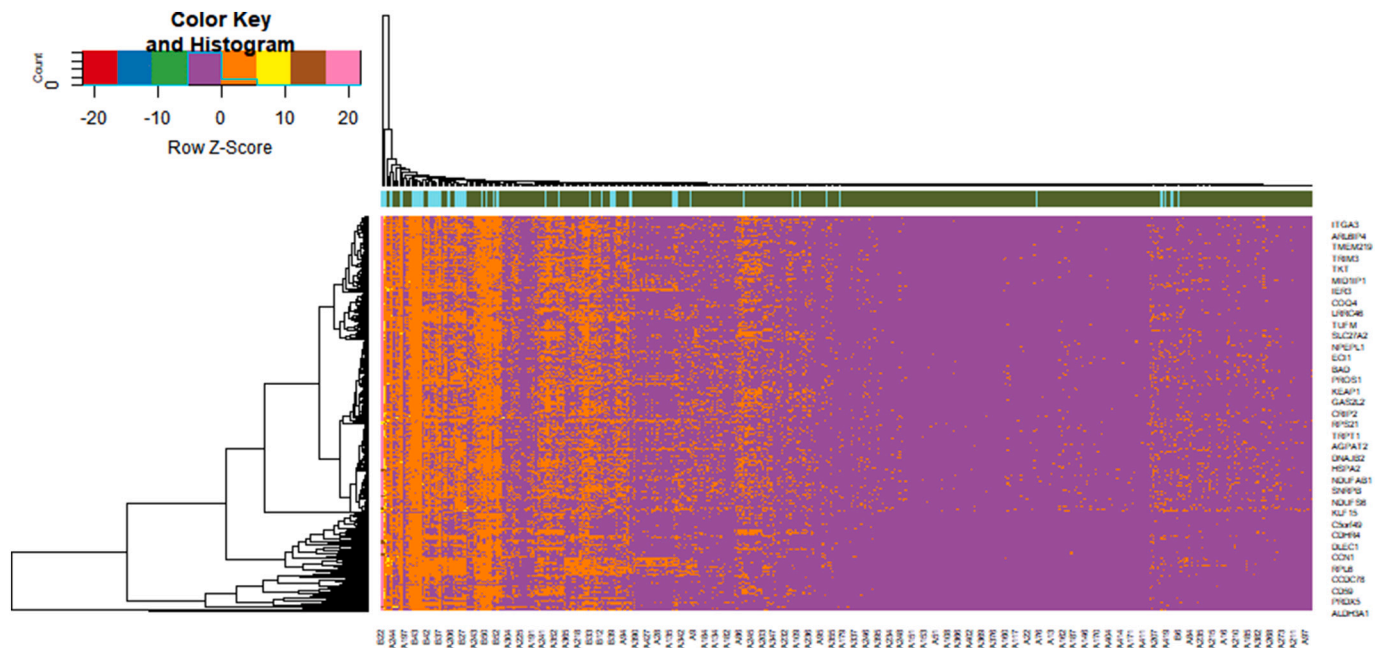


Fig. 4. Heat map of down regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A54 = negative control samples (red color box); B1 – B430 = SARS-CoV-2 infected samples (blue color box)). (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

3. Results

3.1. Data preprocessing and identification of DEGs

Box plots of GSE152075 value were generated and data from each sample were generally normalized (Fig. 1 A and B). Genes screened from the criteria set as $p < 0.05$, and $[\log_2(\text{FC})] > 1.08$ for up regulated genes and $[\log_2(\text{FC})] < -1.651$ for down regulated genes were plotted using limma to visualize the distribution of DEGs between SARS-CoV-2 infection and negative control from this investigation (Fig. 2). Green or red dots represent significantly up regulated or down regulated genes, respectively. A total of 994 genes were designated as DEGs in SARS-CoV-2 infection when compared with the negative controls ($P < 0.05$), including 496 up regulated genes and 498 down regulated genes and are listed in Table 1. Finally, heat maps of gene expression values were constructed with color patterns indicating the variability in gene expression between the SARS-CoV-2 infection and negative control (Figs. 3 and 4).

3.2. Pathway enrichment of DEGs in SARS-CoV-2 infection

Signaling pathway enrichment of up and down regulated genes was conducted using the ToppGene. The up regulated genes were mainly enriched in tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde, S-methyl-5'-thioadenosine degradation, NOD-like receptor signaling pathway, influenza A, IL12-mediated signaling events, TCR signaling in naive CD4+ T cells, interferon signaling, cytokine signaling in immune system, tryptophan metabolism, cysteine metabolism, chemokine signaling pathway, toll-like receptor signaling pathway, inflammation mediated by chemokine and cytokine signaling pathway, apoptosis signaling pathway, innate immune response, angiotensin II signaling and pyrimidine metabolism and are given in Table 2. The down regulated genes were mainly enriched in bile acid

biosynthesis, neutral pathway, 2'-deoxy-alpha-D-ribose 1-phosphate degradation, ribosome, Huntington's disease, ATF-2 transcription factor network, direct p53 effectors, viral mRNA translation, influenza viral RNA transcription and replication, oxidative phosphorylation, RNA polymerase, Parkinson's disease, Alzheimer's disease, vitamin D metabolism and pathway, amyotrophic lateral sclerosis disease, glutathione metabolic, pentose phosphate pathway, and folate and pterine biosynthesis and are given in Table 3.

3.3. Gene ontology (GO) enrichment of DEGs in SARS-CoV-2 infection

The results of GO enrichment analysis of up and down regulated genes in SARS-CoV-2 infection analyzed based on GO BP, CC, and MF using ToppGene are shown in Tables 4 and 5. The up regulated genes were enriched in GO terms such as response to external biotic stimulus, defense response, cell surface, external side of plasma membrane, identical protein binding and hydrolase activity, acting on ester bonds. The down regulated genes were enriched in GO terms such as viral transcription, protein targeting, ribosome, mitochondrial envelope, structural constituent of ribosome and structural molecule activity.

3.4. Analysis of protein-protein interaction network and modules

PPI networks of the identified up regulated genes were constructed using IID, which consisted of 4957 edges and 3395 nodes (Fig. 5). The nodes with the highest node degree, betweenness centrality, stress centrality, closeness centrality and lowest clustering coefficient were screened as hub genes including REL, ISG15, CBL, PML, NEDD4, BTN3A1, BTN3A3, CYSLTR1, STAT1, STX17, INHBA, PDE3B, ZSCAN30 and DUX4 are listed in Table 6. Scatter plot for up regulated genes are shown in Fig. 6. Pathway and GO enrichment analysis for the up regulated genes in this PPI network revealed that these hub genes were significantly enriched in adaptive immune system, interferon signaling,

Table 2
The enriched pathway terms of the up regulated differentially expressed genes.

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
BIOCYC							
142383	Tryptophan degradation to 2-amino-3-carboxymuconate semialdehyde	6.87E-04	1.62E-02	6.45E-02	2.06E-02	3	KMO,IDO1,KYNU
547504	S-methyl-5'-thioadenosine degradation	2.86E-02	1.43E-01	5.72E-01	8.59E-01	1	MTAP
545275	Chondroitin biosynthesis	5.49E-02	2.35E-01	9.40E-01	1.00E+00	1	CSGALNACT2
545364	Thymine degradation	8.12E-02	2.71E-01	1.00E+00	1.00E+00	1	DPYD
782399	UTP and CTP dephosphorylation II	1.07E-01	2.91E-01	1.00E+00	1.00E+00	1	ENTPD1
545297	Serotonin and melatonin biosynthesis	1.07E-01	2.91E-01	1.00E+00	1.00E+00	1	TPH2
1108780	Threonine degradation	1.56E-01	3.59E-01	1.00E+00	1.00E+00	1	SDS
142279	Adenosine nucleotides degradation	2.02E-01	3.75E-01	1.00E+00	1.00E+00	1	NT5C3A
782393	CMP phosphorylation	2.46E-01	3.75E-01	1.00E+00	1.00E+00	1	CMPK2
142359	Leucine degradation	2.87E-01	3.75E-01	1.00E+00	1.00E+00	1	BCAT1
KEGG							
122191	NOD-like receptor signaling pathway	3.16E-10	7.33E-08	4.42E-07	7.33E-08	23	CARD16,MEFV,CCL2,CCL5,AIM2,BIRC3,IFI16,CYBB,NAIP,GBP1,GBP2,STAT1,STAT2,GBP4,GBP5,CARD6,CASP1,CASP5,OAS1,OAS2,OAS3,P2RX7,TLR4
217173	Influenza A	1.38E-08	1.60E-06	9.62E-06	3.19E-06	21	DDX58,HLA-DMA,TLR7,CCL2,CCL5,PML,RSAD2,PRKCB,EIF2AK2,MX1,TNFSF10,CXCL10,STAT1,STAT2,JAK2,CASP1,OAS1,OAS2,OAS3,TLR3,TLR4
99051	Chemokine signaling pathway	1.63E-07	1.03E-05	6.19E-05	3.78E-05	20	CXCL9,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CXCL11,CXCL13,PRKCB,CX3CR1,CXCR2,CXCL10,STAT1,ELMO1,STAT2,ITK,JAK2,DOCK2,GNB4
83051	Cytokine-cytokine receptor interaction	1.90E-06	8.79E-05	5.30E-04	4.40E-04	23	CXCL9,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CXCL11,FLT1,CXCL13,TNFSF13B,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,IL10RA,TNFSF14,TNFSF10,INHBA,CXCL10,IL18RAP
377873	Herpes simplex infection	4.01E-06	1.33E-04	8.01E-04	9.30E-04	18	DDX58,HLA-DMA,CCL2,CCL5,POU2F3,PML,IFIT1,EIF2AK2,SP100,TNFSF14,STAT1,STAT2,JAK2,OAS1,OAS2,OAS3,TLR2,TLR3
83076	Toll-like receptor signaling pathway	5.95E-06	1.73E-04	1.04E-03	1.38E-03	13	TLR7,CXCL9,CCL4,CCL5,CXCL11,CXCL10,STAT1,CD80,CD86,TLR1,TLR2,TLR3,TLR4
213780	Tuberculosis	1.43E-04	3.68E-03	2.22E-02	3.31E-02	15	HLA-DMA,CLEC7A,CD209,FCER1G,FCGR2A,FCGR3A,FCGR3B,IL10RA,STAT1,JAK2,CLEC4E,CASP10,TLR1,TLR2,TLR4
83079	Natural killer cell mediated cytotoxicity	3.99E-03	4.87E-02	2.94E-01	9.25E-01	10	FCER1G,FCGR3A,FCGR3B,MICB,PRKCB,TNFSF10,MICA,KLRD1,LCP2,GZMB
83053	Neuroactive ligand-receptor interaction	1.11E-02	9.54E-02	5.75E-01	1.00E+00	15	MAS1,MC2R,FPR2,FPR3,PRLR,GABRE,GALR1,CYSLTR1,C3AR1,CYSLTR2,GRIA4,OPRM1,P2RX7,P2RY6,LPAR6
83077	Jak-STAT signaling pathway	1.19E-02	9.84E-02	5.93E-01	1.00E+00	10	IL2RA,IL2RG,PRLR,IL7R,IL10RA,STAT1,STAT2,STAT4,JAK2,CCND2
692234	PI3K-Akt signaling pathway	1.52E-02	1.14E-01	6.85E-01	1.00E+00	17	PIK3AP1,PIK3CG,PGF13,FLT1,CREB5,IGF1,IL2RA,IL2RG,PRLR,IL7R,ITGA1,JAK2,CCND2,LPAR6,TLR2,TLR4,GNB4
Pathway interaction database							
137922	IL12-mediated signaling events	6.22E-06	5.91E-04	3.04E-03	5.91E-04	10	HLX,CCL4,CCR5,IL2RA,IL2RG,IL18RAP,STAT1,STAT4,JAK2,GZMB
137998	TCR signaling in naive CD4+ T cells	3.80E-05	1.81E-03	9.27E-03	3.61E-03	9	PRKCB,FYB1,PAG1,ITK,PTPRC,LCP2,CBL,CD80,CD86
138000	IL23-mediated signaling events	4.97E-04	1.18E-02	6.07E-02	4.73E-02	6	CXCL9,CCL2,IL18RAP,STAT1,STAT4,JAK2
138050	Fc-epsilon receptor I signaling in mast cells	1.19E-03	2.27E-02	1.17E-01	1.13E-01	7	MS4A2,FCER1G,WIPF1,PRKCB,ITK,LCP2,CBL
137910	CXCR4-mediated signaling events	5.12E-03	7.36E-02	3.78E-01	4.86E-01	7	PAG1,ITGA1,STAT1,STAT2,JAK2,PTPRC,SGS1
137993	Calcineurin-regulated NFAT-dependent transcription in lymphocytes	1.04E-02	8.06E-02	4.14E-01	9.88E-01	5	IKZF1,POU2F1,IL2RA,DGKA,IRF4
138011	CXCR3-mediated signaling events	1.41E-02	8.06E-02	4.14E-01	1.00E+00	4	CXCL9,CXCL11,CXCL13,CXCL10
138068				4.14E-01	1.00E+00	5	STAT1,JAK2,PTPRO,SH2B3,CBL

(continued on next page)

Table 2 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
137990	Signaling events mediated by Stem cell factor receptor (c-Kit) Regulation of CDC42 activity	1.44E-02 2.03E-01	8.06E-02 5.35E-01	1.00E+00	1.00E+00	2	DOCK10,DOCK11
137939	Direct p53 effectors	5.03E-01	7.75E-01	1.00E+00	1.00E+00	4	PML,BCL2L14,CASP1,CASP10
REACTOME 1269311	Interferon Signaling	3.52E-22	2.44E-19	1.74E-18	2.44E-19	39	USP18,UBE2L6,DDX58,TRIM22,FCGR1B,IFITM3,TRIM38,PML,IRF8,IFITM1,IFIT2,IFIT1,IFIT3,TRIM5,RSAD2,ISG15,OASL,XAF1,IFI6,EIF2AK2,MX1,MX2,SP100,GBP1,GBP2,IRF4,TRIM34,TRIM21,STAT1,STAT2,NEDD4,JAK2,GBP4,GBP5,KPNA5,OAS1,OAS2,OAS3,HERC5
1269310	Cytokine Signaling in Immune system	5.94E-17	2.06E-14	1.47E-13	4.12E-14	66	USP18,UBE2L6,DDX58,TRIM22,F13A1,FCGR1B,IFITM3,RASGRP3,CCL2,CCR1,CCL4,CCL5,CCR5,TRIM38,APBB1IP,PML,IRF8,IFITM1,BIRC3,POU2F1,IFIT2,IFIT1,IFIT3,TRIM5,RSAD2,ISG15,TNFSF13B,OASL,XAF1,IL2RA,IFI6,IL2RG,EIF2AK2,PRLR,MX1,IL7R,MX2,IL10RA,SP100,TNFSF14,CXCL10,GBP1,GBP2,IRF4,TRIM34,TRIM21,IL18RAP,STAT1,STAT2,NEDD4,JAK2,GBP4,GBP5,KPNA5,ZEB1,CASP1,OAS1,OAS2,OAS3,CBL,OPRM1,LGALS9,HAVCR2,CD80,CD86,HERC5
1269312	Interferon alpha/beta signaling	9.40E-17	2.18E-14	1.55E-13	6.52E-14	21	USP18,IFITM3,IRF8,IFITM1,IFIT2,IFIT1,IFIT3,RSAD2,ISG15,OASL,XAF1,IFI6,MX1,MX2,GBP2,IRF4,STAT1,STAT2,OAS1,OAS2,OAS3
1269314	Interferon gamma signaling	9.27E-13	1.61E-10	1.15E-09	6.43E-10	20	TRIM22,FCGR1B,TRIM38,PML,IRF8,TRIM5,OASL,SP100,GBP1,GBP2,IRF4,TRIM34,TRIM21,STAT1,JAK2,GBP4,GBP5,OAS1,OAS2,OAS3
1269203	Innate Immune System	4.34E-11	6.03E-09	4.29E-08	3.01E-08	78	PIK3AP1,UBE2L6,DDX58,LILRB2,CLEC5A,PECAM1,DOK3,CLEC7A,TLR7,SIRPB1,MEFV,CD209,ZBP1,FCAR,MS4A2,FCER1G,FCGR2A,FCGR3A,FCGR3B,RASGRP3,AIM2,MNDA,APBB1IP,SELL,HTN1,HTN3,WIPF1,FPR2,BIRC3,MUC13,IFI16,SLC2A3,ISG15,RAP2C,IL2RA,MUC3A,IL2RG,CD300E,CXCR2,CYBB,LGMN,ATP6V1B2,TRIM21,CLEC12A,ELMO1,ITK,CEACAM1,FGL2,JAK2,CLEC4E,PTPRC,C1QB,C1QC,C3AR1,C4BPB,KLRD1,DOCK2,LAIR1,CASP1,MUC19,SIGLEC14,CASP10,LCP2,OLR1,RNASE6,P2RX7,CD80,CD86,TLR1,TLR2,TLR3,TLR4,CD53,CD68,TNFAIP6,CD180,HERC5,NCKAP1L
1269201	Immunoregulatory interactions between a Lymphoid and a non-Lymphoid cell	1.05E-09	1.21E-07	8.63E-07	7.28E-07	20	LILRB2,TRAC,FCGR3A,MICB,LILRA5,SELL,IFITM1,CD226,CLEC2D,SIGLEC1,SLAMF7,CD300E,LILRB1,SIGLEC10,MICA,KLRD1,CLEC2B,LILRB4,LAIR1,CD96
1269171	Adaptive Immune System	2.91E-09	2.88E-07	2.05E-06	2.02E-06	54	PIK3AP1,UBE2L6,HLA-DMA,LILRB2,TRAC,DTX3L,CD209,BTN3A3,FCGR1B,FCGR3A,RASGRP3,MICB,LILRA5,SELL,IFITM1,RNF213,TRIM69,CD226,CLEC2D,CD274,PRKCB,SIGLEC1,SLAMF7,FYB1,CD300E,PDCC1LG2,CYBB,LGMN,PAG1,PTPN22,TRIM21,LILRB1,ITK,NEDD4,PTPRC,SIGLEC10,MICA,HERC6,KLRD1,CLEC2B,LILRB4,LAIR1,REL,LCP2,CBL,BTN3A1,CD80,CD86,TLR1,TLR2,ASB3,TLR4,CD96,HERC5
1269316	Antiviral mechanism by IFN-stimulated genes	1.28E-06	9.90E-05	7.05E-04	8.91E-04	12	USP18,UBE2L6,DDX58,IFIT1,ISG15,EIF2AK2,MX1,MX2,STAT1,NEDD4,KPNA5,HERC5
1457780	Neutrophil degranulation	4.67E-05	2.70E-03	1.92E-02	3.24E-02	30	LILRB2,CLEC5A,PECAM1,DOK3,SIRPB1,FCAR,FCER1G,FCGR2A,FCGR3B,MNDA,SELL,FPR2,SLC2A3,RAP2C,CXCR2,CYBB,CLEC12A,CEACAM1,FGL2,PTPRC,C3AR1,DOCK2,LAIR1,SIGLEC14,OLR1,TLR2,CD53,CD68,TNFAIP6,NCKAP1L
1269340	Hemostasis	2.20E-04	1.02E-02	7.24E-02	1.53E-01	34	A2M,PDE3B,PECAM1,F13A1,FCER1G,PIK3CG,PLEK,APBB1IP,SELL,DOCK10,SLC8A1,IGF1,SRGN,PRKCB,IL2RA,IL2RG,SPN,DOCK11,DGKA,ITGA1,CEACAM1,CD84,JAK2,SERPING1,DOCK2,SH2B3,DOCK8,SLC7A7,LCP2,TF,OLR1,P2RX7,LHFP2L2,GNB4
1269544	GPCR ligand binding	4.15E-04	1.69E-02	1.21E-01	2.88E-01	26	MC2R,ADGRE2,CXCL9,CCR1,CCL5,CCR5,CXCL11,GPR65,UTS2B,WNT7A,FPR2,FPR3,CXCL13,SUCNR1,CX3CR1,CXCR2,GALR1,CXCL10,CYSLTR1,C3AR1,CYSLTR2,OPRM1,P2RY6,LPAR6,GNB4,ADGRE1

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Table 2 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
Gen MAPP							
MAP00380	Tryptophan metabolism	1.36E-01	7.19E-01	1.00E+00	1.00E+00	3	WARS1,IDO1,KYNU
MAP00272	Cysteine metabolism	2.24E-01	7.19E-01	1.00E+00	1.00E+00	1	SDS
MAP00150	Androgen and estrogen metabolism	3.81E-01	7.19E-01	1.00E+00	1.00E+00	1	HSD17B2
MAP00030	Pentose phosphate	3.81E-01	7.19E-01	1.00E+00	1.00E+00	1	FMNL3
MAP00410	beta Alanine metabolism	3.81E-01	7.19E-01	1.00E+00	1.00E+00	1	DPYD
MAP00970	Aminoacyl-tRNA biosynthesis	3.98E-01	7.19E-01	1.00E+00	1.00E+00	1	WARS1
MAP00193	ATP synthesis	4.15E-01	7.19E-01	1.00E+00	1.00E+00	1	ATP6V1B2
MAP00562	Inositol phosphate metabolism	4.15E-01	7.19E-01	1.00E+00	1.00E+00	1	PIK3CG
MAP00620	Pyruvate metabolism	5.83E-01	7.92E-01	1.00E+00	1.00E+00	1	ME2
MAP00561_	Glycerolipid metabolism	7.35E-01	8.13E-01	1.00E+00	1.00E+00	1	DGKA
MSigDB C2 BIOCARTA (v6.0)							
M4844	Chemokine signaling pathway	1.35E-08	5.37E-06	3.53E-05	5.37E-06	22	PIK3CG,CXCL9,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CXCL11,CXCL13,PRKCB,CX3CR1,CXCR2,CXCL10,STAT1,ELMO1,STAT2,TIAM2,ITK,JAK2,DOCK2,GNB4
M3261	Toll-like receptor signaling pathway	8.30E-07	1.65E-04	1.08E-03	3.30E-04	14	TLR7,PIK3CG,CXCL9,CCL4,CCL5,CXCL11,CXCL10,STAT1,CD80,CD86,TLR1,TLR2,TLR3,TLR4
M9809	Cytokine-cytokine receptor interaction	1.37E-06	1.82E-04	1.20E-03	5.47E-04	23	CXCL9,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CXCL11,FLT1,CXCL13,TNFSF13B,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,IL10RA,TNFSF14,TNFSF10,INHBA,CXCL10,IL18RAP
M5880	Genes encoding proteins affiliated structurally or functionally to extracellular matrix proteins	7.97E-05	4.53E-03	2.98E-02	3.17E-02	15	CLEC5A,CLEC7A,CD209,SEMA6D,MUC13,CLEC2D,MUC3A,CLEC12A,CLEC4E,C1QB,C1QC,CLEC2B,MUC19,LGALS9,PLXNC1
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	2.50E-04	9.41E-03	6.18E-02	9.94E-02	38	A2M,PCSK5,CLEC5A,CLEC7A,F13A1,CD209,SERPINB9,SEMA6D,CXCL9,CCL2,CCL4,CCL5,FGF13,CCL8,MMP13,CXCL11,WNT7A,CXCL13,MUC13,ADAM32,IGF1,TNFSF13B,CLEC2D,MUC3A,TNFSF14,TNFSF10,INHBA,CXCL10,CLEC12A,CLEC4E,ADAMDEC1,SERPING1,C1QB,C1QC,CLEC2B,MUC19,LGALS9,PLXNC1
M16476	Cell adhesion molecules (CAMs)	3.33E-04	9.46E-03	6.21E-02	1.32E-01	12	HLA-DMA,PECAM1,NEGR1,SELL,CD226,CD274,SIGLEC1,PDCD1LG2,SPN,PTPRC,CD80,CD86
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	4.34E-03	6.18E-02	4.05E-01	1.00E+00	43	A2M,PCSK5,CLEC5A,CLEC7A,F13A1,CD209,SERPINB9,SEMA6D,CXCL9,CCL2,CCL4,CCL5,FGF13,CCL8,MMP13,CXCL11,WNT7A,CXCL13,MUC13,ADAM32,IGF1,SRGN,TNFSF13B,CLEC2D,MUC3A,TNFSF14,TNFSF10,INHBA,CXCL10,CLEC12A,FGL2,CCN5,CLEC4E,ADAMDEC1,SERPING1,C1QB,C1QC,CLEC2B,MUC19,LGALS9,TGFB1,PLXNC1,TNFAIP6
M4741	Systemic lupus erythematosus	5.44E-03	6.77E-02	4.45E-01	1.00E+00	10	HLA-DMA,FCGR2A,FCGR3A,FCGR3B,H4C8,TRIM21,C1QB,C1QC,CD80,CD86
M13380	Neuroactive ligand-receptor interaction	9.20E-03	9.39E-02	6.17E-01	1.00E+00	15	MAS1,MC2R,FPR2,FPR3,PRLR,GABRE,GALR1,CYSLTR1,C3AR1,CYSLTR2,GRIA4,OPRM1,P2RX7,P2RY6,LPAR6
M5883	Genes encoding secreted soluble factors	5.65E-02	2.71E-01	1.00E+00	1.00E+00	15	CXCL9,CCL2,CCL4,CCL5,FGF13,CCL8,CXCL11,WNT7A,CXCL13,IGF1,TNFSF13B,TNFSF14,TNFSF10,INHBA,CXCL10
Panther DB							
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	9.11E-04	3.28E-02	1.59E-01	5.91E-02	4	STAT1,STAT4,JAK2,PTPRC
P00006	Apoptosis signaling pathway	2.12E-03	3.28E-02	1.59E-01	6.56E-02	14	PIK3CG,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,ALOX5AP,FPR3,PRKCB,CX3CR1,CXCR2,CXCL10,JAK2
P00047	PDGF signaling pathway	2.54E-02	5.09E-02	2.47E-01	1.53E-01	9	PIK3CG,BIRC3,PRKCB,EIF2AK2,TNFSF10,ATF7,CASP10,REL,GZMB
P00018	EGF receptor signaling pathway	3.52E-02	3.95E-01	1.00E+00	1.00E+00	8	PIK3CG,SRGAP1,FLN1,STAT1,STAT2,STAT4,JAK2,ELF1
P00027				1.00E+00	1.00E+00	7	PIK3CG,GAB3,PRKCB,STAT1,STAT2,STAT4,CBL

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Table 2 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
	Heterotrimeric G-protein signaling pathway-Gqalpha and Go alpha mediated pathway	3.52E-02	3.95E-01				
P00036	Interleukin signaling pathway	4.30E-02	3.95E-01	1.00E+00	1.00E+00	6	IL2RA,CXCR2,IL10RA,STAT1,STAT2,STAT4
P00053	T cell activation	6.03E-02	3.95E-01	1.00E+00	1.00E+00	5	PIK3CG,PTPRC,LCP2,CD80,CD86
P00010	B cell activation	2.18E-01	7.70E-01	1.00E+00	1.00E+00	3	PIK3CG,PRKCB,PTPRC
P00005	Angiogenesis	4.05E-01	7.82E-01	1.00E+00	1.00E+00	5	DOK3,PIK3CG,WNT7A,PRKCB,STAT1
P00026	Heterotrimeric G-protein signaling pathway-Gi alpha and Gs alpha mediated pathway	6.04E-01	7.82E-01	1.00E+00	1.00E+00	4	KCNJ6,RGS1,OPRM1,RGS18
Pathway ontology							
PW:0000234	innate immune response	6.51E-06	3.52E-04	1.61E-03	3.52E-04	5	TLR7,TLR1,TLR2,TLR3,TLR4
PW:0000244	Angiotensin II signaling	2.21E-03	5.98E-02	2.74E-01	1.20E-01	3	CCL2,JAK2,OLR1
PW:0000529	angiotensin (1-7) signaling	7.30E-03	1.09E-01	4.98E-01	3.94E-01	2	MAS1,ACE2
PW:0000209	JAK-STAT signaling	8.07E-03	1.09E-01	4.98E-01	4.36E-01	4	STAT1,STAT2,STAT4,JAK2
PW:0000054	tryptophan metabolic	2.50E-02	1.55E-01	7.07E-01	1.00E+00	3	KMO,IDO1,KYNU
PW:0000243	vascular endothelial growth factor signaling	2.80E-02	1.55E-01	7.07E-01	1.00E+00	3	CCL2,FLT1,PRKCB
PW:0000032	pyrimidine metabolic	4.24E-02	1.85E-01	8.48E-01	1.00E+00	2	DPYD,ENTPD1
PW:0000492	renin-angiotensin system signaling	6.38E-02	2.03E-01	9.28E-01	1.00E+00	2	MAS1,ACE2
PW:0000020	cardiovascular disease	8.12E-02	2.31E-01	1.00E+00	1.00E+00	1	IGF1
PW:0000102	The extracellular signal-regulated RAF/MEK/ERK signaling	5.20E-01	5.73E-01	1.00E+00	1.00E+00	1	FLT1
SMPDB							
SMP00063	Tryptophan metabolism	1.09E-02	5.27E-01	1.00E+00	8.90E-01	3	WARS1,KMO,IDO1
SMP00046	Pyrimidine metabolism	3.12E-02	5.27E-01	1.00E+00	1.00E+00	3	PNPT1,CMPK2,DPYD
SMP00189	Hartnup disorder	5.49E-02	5.27E-01	1.00E+00	1.00E+00	1	SLC7A7
SMP00310	Corticotropin activation of cortisol production	1.32E-01	5.27E-01	1.00E+00	1.00E+00	1	MC2R
SMP00009	Ammonia recycling	2.02E-01	5.27E-01	1.00E+00	1.00E+00	1	SDS
SMP00324	Procainamide (antiarrhythmic) pathway	2.75E-01	5.27E-01	1.00E+00	1.00E+00	2	SLC8A1,ABCC9
SMP00039	Glycerolipid metabolism	2.87E-01	5.27E-01	1.00E+00	1.00E+00	1	DGKA
SMP00045	Amino sugar metabolism	3.26E-01	5.27E-01	1.00E+00	1.00E+00	1	NPL
SMP00033	Methionine metabolism	3.45E-01	5.27E-01	1.00E+00	1.00E+00	1	MTAP
SMP00281	Anistreplase pathway	3.63E-01	5.27E-01	1.00E+00	1.00E+00	1	F13A1

Table 3
The enriched pathway terms of the down regulated differentially expressed genes.

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
BIOCYC 545316	Bile acid biosynthesis, neutral pathway	3.56E-03	1.64E-01	7.81E-01	2.31E-01	3	POR,CYP27A1,SLC27A2
1108781	2'-deoxy-alpha-D-ribose 1-phosphate degradation	6.86E-03	1.64E-01	7.81E-01	4.46E-01	2	ALDH3A1,ALDH3B1
142460	Pentose phosphate pathway	1.01E-02	1.64E-01	7.81E-01	6.57E-01	2	PGLS,TKT
142227	Glutathione redox reactions I	1.01E-02	1.64E-01	7.81E-01	6.57E-01	2	GPX1,GPX4
142277	Purine nucleotides de novo biosynthesis	2.21E-02	2.16E-01	1.00E+00	1.00E+00	4	AK1,ATP5ME,NME2,GUK1
545339	L-dopa degradation	2.77E-02	2.16E-01	1.00E+00	1.00E+00	1	COMT
1108764	Acyl carrier protein metabolism	5.32E-02	2.16E-01	1.00E+00	1.00E+00	1	NDUFAB1
545298	Thyroid hormone biosynthesis	5.32E-02	2.16E-01	1.00E+00	1.00E+00	1	CTSD
142306	Myo-inositol de novo biosynthesis	5.32E-02	2.16E-01	1.00E+00	1.00E+00	1	IMPA2
142424	Fatty acid beta-oxidation (unsaturated, odd number)	5.32E-02	2.16E-01	1.00E+00	1.00E+00	1	ECI1
KEGG 83036	Ribosome	1.38E-47	3.36E-45	2.04E-44	3.36E-45	55	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,RPL36,MRPL14,RPS10-NUDT3,RPL10A,RPL17-C18orf32,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
83100	Huntington's disease	1.81E-12	2.20E-10	1.34E-09	4.40E-10	27	COX5A,UQCRC1,SLC25A6,COX4I1,COX5B,COX6A1,POLR2I,POLR2J,POLR2L,COX7B,UQCRCQ,CYC1,ATP5F1E,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,DNALI1,UQCRC11,GPX1,NDUFA13,DNALI2
82942	Oxidative phosphorylation	7.37E-12	5.97E-10	3.63E-09	1.79E-09	22	COX5A,UQCRC1,COX4I1,COX5B,COX6A1,COX7B,UQCRCQ,CYC1,ATP5F1E,ATP5ME,ATP6V0B,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,UQCRC11,NDUFA13
862188	Non-alcoholic fatty liver disease (NAFLD)	4.94E-10	2.00E-08	1.22E-07	1.20E-07	21	COX5A,UQCRC1,COX4I1,COX5B,COX6A1,COX7B,UQCRCQ,CYC1,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,JUN,UQCRC11,SOCS3,NDUFA13
167325	Protein processing in endoplasmic reticulum	1.59E-04	5.50E-03	3.34E-02	3.85E-02	14	STUB1,HSPBP1,DNAJB2,HSPA1A,HSPA1B,HSPA2,SELENOS,SSR4,DDOST,TXNDC5,SEC61B,ERP29,UBXN6,P4HB
93344	Cardiac muscle contraction	2.38E-04	7.24E-03	4.40E-02	5.79E-02	9	COX5A,UQCRC1,COX4I1,COX5B,COX6A1,COX7B,UQCRCQ,CYC1,UQCRC11
132956	Metabolic pathways	4.74E-04	1.28E-02	7.77E-02	1.15E-01	54	CES1,ACO2,ST6GALNAC6,TST,CKB,COX5A,GRHPR,PGLS,AK1,UQCRC1,ALDH3A1,DEGS2,ALDH3B1,PYCR2,COMT,COX4I1,COX5B,COX6A1,AGPAT2,POLR2I,POLR2J,POLR2L,COX7B,PPOX,ASL,UQCRCQ,CYC1,ATP5F1E,ATP5ME,ATP6V0B,IMPA2,CYP27A1,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,DDOST,NDUFV1,NDUFS6,ITPA,DHCR24,PCYT2,UQCRC11,NME2,QARS1,TALDO1,CBR1,PIGQ,NDUFA13,GUK1,TKTSDC1,FOS,CTNNB1,KEAP1,JUN,CALML4,DUSP1,GSTA2,GSTP1
1474302	Fluid shear stress and atherosclerosis	1.47E-02	2.10E-01	1.00E+00	1.00E+00	9	SDC1,FOS,CTNNB1,KEAP1,JUN,CALML4,DUSP1,GSTA2,GSTP1
83048	MAPK signaling pathway	8.45E-02	6.43E-01	1.00E+00	1.00E+00	11	ECSIT,HSPA1A,HSPA1B,HSPA2,MAPK8IP1,FOS,GADD45B,JUN,JUND,DUSP1,MKNK2
217173	Influenza A	3.23E-01	8.94E-01	1.00E+00	1.00E+00	6	HSPA1A,HSPA1B,HSPA2,SLC25A6,JUN,SOCS3

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Table 3 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
Pathway interaction database							
138006	ATF-2 transcription factor network	6.46E-04	6.91E-02	3.63E-01	6.91E-02	7	FOS,RUVBL2,JUN,JUNB,JUND,DUSP1,SOCS3
137939	Direct p53 effectors	3.01E-03	1.61E-01	8.46E-01	3.22E-01	10	S100A2,FDXR,GDF15,CTSD,JUN,CD82,DUSP1,GPX1,EPHA2,STEAP3
137956	HIF-2-alpha transcription factor network	1.27E-02	3.00E-01	1.00E+00	1.00E+00	4	CITED2,SLC2A1,ELOB,EFNA1
169349	Validated transcriptional targets of AP1 family members Fra1 and Fra2	1.27E-02	3.00E-01	1.00E+00	1.00E+00	4	ITGB4,JUN,JUNB,JUND
137955	ErbB2/ErbB3 signaling events	1.40E-02	3.00E-01	1.00E+00	1.00E+00	4	ERBB2,FOS,BAD,JUN
137918	Stabilization and expansion of the E-cadherin adherens junction	2.21E-02	3.26E-01	1.00E+00	1.00E+00	4	AQP5,CTNNB1,EFNA1,EPHA2
137932	IL6-mediated signaling events	2.80E-02	3.26E-01	1.00E+00	1.00E+00	4	FOS,JUN,JUNB,SOCS3
137954	Arf6 trafficking events	3.01E-02	3.26E-01	1.00E+00	1.00E+00	4	SDC1,CTNNB1,ITGA3,CD59
138045	HIF-1-alpha transcription factor network	3.05E-02	3.26E-01	1.00E+00	1.00E+00	5	CITED2,FOS,SLC2A1,JUN,TFF3
169352	Regulation of Wnt-mediated beta catenin signaling and target gene transcription	6.17E-02	4.20E-01	1.00E+00	1.00E+00	5	KLF4,CCN1,CTNNB1,RUVBL2,JUN
REACTOME							
1269120	Viral mRNA Translation	7.05E-58	1.91E-55	1.39E-54	5.74E-55	52	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,RPL36,RPL10A,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
1269115	Influenza Viral RNA Transcription and Replication	1.05E-50	5.71E-49	4.16E-48	8.56E-48	55	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,RPL36,POLR2I,POLR2J,POLR2L,RPL10A,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
1269109	Influenza Life Cycle	2.60E-50	1.32E-48	9.64E-48	2.12E-47	56	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,HSPA1A,RPL36,POLR2I,POLR2J,POLR2L,RPL10A,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
1269056	Infectious disease	1.05E-50	5.71E-49	4.16E-48	8.56E-48	62	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,HSPA1A,RPL36,SLC25A6,POLR2I,POLR2J,POLR2L,CTNNB1,PSMA7,RPL10A,ELOB,EEF2,CD9,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
1268677	Metabolism of proteins	2.18E-14	5.91E-13	4.30E-12	1.77E-11	96	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,AC02,COPE,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,ST6GALNAC6,KLF4,TUBB2A,TUBB4B,FAU,FBXW5,FKBP8,TADA3,TOMM7,RPL36,EIF4H,FBXW9,SLC25A6,ST6GALNAC2,ARF5,IGFBP2,IGFBP5,TMED9,CTNNB1,CTSD,CTSH,TRAPPC2L,PROS1,CYC1,PSMA7,DAG1,KEAP1,SSR4,DDOST,EIF3CL,RPL10A,SEC61B,GNB2,

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Table 3 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
							TBCA,UBXN1,PIGQ,EEF1D,EEF1G,EEF2, TIMM13,LMNA,CHCHD2,CD59,H3-3A,RPL35, RPL13A,CDC34,RPL3,RPL4,RPL6,RPL7,RPL7A, RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A, RPL19
1270127	Respiratory electron transport, ATP synthesis by chemiosmotic coupling, and heat production by uncoupling proteins.	3.11E-14	7.93E-13	5.77E-12	2.53E-11	24	ECSIT,COX5A,UQCRC1,COX4I1,COX5B, COX6A1,NDUFAF3,COX7B,UQCRCQ,CYC1, ATP5F1E,ATP5ME,NDUFA2,NDUFA4, NDUFAB1,NDUFB2,NDUFB7,NDUFB10, NDUFC1,NDUFV1,NDUFS6,SURF1,UQCR11, NDUFA13
1269649	Gene Expression	3.53E-11	8.46E-10	6.16E-09	2.88E-08	96	RPL21,RPL26,RPL27,RPL27A,NR2F6,RPL29, RPL31,ERBB2,RPL32,RPL34,RPL37,RPL39, RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3, RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12, RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17, RPS18,RPS19,RPS21,RPS27,RPS28,RPS29, GTF3C5,CITED2,FAU,COX5A,PIN1,PRDX5, HSPA1A,VAR1,ZNF703,RPL36,EIF4H, COX4I1,COX5B,FOS,COX6A1,POLR2L,POLR2J, POLR2L,COX7B,NHP2,LAMTOR4,H2AJ, SNRPB,SNRPD2,TMEM219,PSMA7,NDUFA4, SSR4,DDOST,EIF3CL,RPL10A,JUN,JUNB, TXNL4A,SURF1,SEC61B,QARS1,ELOB,PRDX2, EEF1D,EEF1G,EEF2,TRIM28,STEAP3,H3-3A, RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A, RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A, RPL19
1270414	Cellular responses to stress	1.14E-02	1.72E-01	1.00E+00	1.00E+00	21	CITED2,PRDX5,HSPA1A,HSPA1B,HSPA2,FOS, ID1,ANAPC11,LAMTOR4,IGFBP7,H2AJ, PSMA7,JUN,ATG4B,ELOB,GPX1,PRDX2, GSTP1,P4HB,H1-4,H3-3A
1457780	Neutrophil degranulation	1.39E-02	1.96E-01	1.00E+00	1.00E+00	22	MAN2B1,LRG1,TUBB4B,MIF,ALDH3B1, HSPA1A,HSPA1B,AGPAT2,SLPI,CSTB,CTSD, CTSH,DDOST,TXNDC5,PTPRN2,NME2, SLC27A2,LGALS3,GSTP1,ACTR1B,EEF2,CD59
1269203	Innate Immune System	1.75E-01	7.44E-01	1.00E+00	1.00E+00	41	ERBB2,MAN2B1,ECSIT,LRG1,TUBB4B,CLU, PIN1,MIF,ALDH3B1,HSPA1A,HSPA1B,FOS, ARPC1A,AGPAT2,POLR2L,IGHG1,IGHG3,SLPI, CSTB,CTNNB1,CTSD,CTSH,PROS1,ATP6V0B, PSMA7,BAD,DDOST,JUN,TXNDC5,IERS3, PTPRN2,UNC93B1,NME2,SLC27A2,DUSP1, LGALS3,GSTP1,ACTR1B,EEF2,CD59,CDC34
1269193	Antigen processing: Ubiquitination& Proteasome degradation	2.28E-01	8.08E-01	1.00E+00	1.00E+00	11	STUB1,UBAC1,FBXW5,TRAF7,FBXW9, ANAPC11,PSMA7,KEAP1,ELOB,SOCS3,CDC34
Gen MAPP							
MAP00190	Oxidative phosphorylation	1.94E-05	6.01E-04	2.42E-03	6.01E-04	8	COX5A,UQCRC1,COX4I1,COX5B,COX6A1, COX7B,ATP5F1E,ATP6V0B
MAP03020	RNA polymerase	9.32E-04	1.45E-02	5.82E-02	2.89E-02	4	POLR2I,POLR2J,POLR2L,IGFBP7
MAP00480	Glutathione metabolism	2.58E-03	2.66E-02	1.07E-01	7.99E-02	4	GPX1,GPX4,GSTA2,GSTP1
MAP00240	Pyrimidine metabolism	6.32E-03	4.90E-02	1.97E-01	1.96E-01	5	POLR2I,POLR2J,POLR2L,IGFBP7,NME2
MAP00350	Tyrosine metabolism	4.60E-02	1.78E-01	7.18E-01	1.00E+00	3	ALDH3A1,ALDH3B1,COMT
MAP00510	N Glycansbiosynthesis	6.03E-02	2.03E-01	8.17E-01	1.00E+00	2	PPOX,DDOST
MAP00330	Arginine and proline metabolism	8.19E-02	2.03E-01	8.17E-01	1.00E+00	3	CKB,ASL,P4HB
MAP00620	Pyruvate metabolism	2.03E-01	3.50E-01	1.00E+00	1.00E+00	2	GRHPR,HAGH
MAP00030	Pentose phosphate	3.72E-01	5.01E-01	1.00E+00	1.00E+00	1	TALDO1
MAP00020	Citrate cycle TCA cycle	3.89E-01	5.01E-01	1.00E+00	1.00E+00	1	ACO2
MSigDB C2 BIOCARTA (v6.0)							
M7272	Parkinson's disease	2.63E-11	3.18E-09	2.06E-08	9.55E-09	21	COX5A,UQCRC1,SLC25A6,SEPTIN5,COX4I1, COX5B,COX6A1,COX7B,UQCRCQ,CYC1, ATP5F1E,NDUFA2,NDUFA4,NDUFA1,

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Table 3 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
M16024	Alzheimer's disease	3.30E-09	2.40E-07	1.55E-06	1.20E-06	21	NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,UQCR11,COX5A,UQCRC1,COX411,COX5B,COX6A1,APBB1,COX7B,UQCRCQ,CYC1,ATP5F1E,BAD,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,UQCR11
M167	AP-1 transcription factor network	5.62E-04	2.92E-02	1.89E-01	2.04E-01	8	FOS,FOSB,CCN1,CTNNB1,JUN,JUNB,JUND,DUSP1
M166	ATF-2 transcription factor network	9.90E-04	4.49E-02	2.91E-01	3.59E-01	7	FOS,RUVBL2,JUN,JUNB,JUND,DUSP1,SOCS3
M145	Direct p53 effectors	3.93E-03	1.10E-01	7.10E-01	1.00E+00	10	S100A2,FDXR,GDF15,CTSD,JUN,CD82,DUSP1,GPX1,EPHA2,STEAP3
M183	IL6-mediated signaling events	3.72E-02	3.74E-01	1.00E+00	1.00E+00	4	FOS,JUN,JUNB,SOCS3
M3008	Genes encoding structural ECM glycoproteins	3.96E-02	3.74E-01	1.00E+00	1.00E+00	10	LRG1,NTN1,CRELD2,IGFBP2,IGFBP5,IGFBP7,CCN1,LAMB2,LAMC2,VWA7
M12868	Pathways in cancer	1.01E-01	4.94E-01	1.00E+00	1.00E+00	13	ERBB2,FOS,SLC2A1,TRAF4,CTNNB1,BAD,ITGA3,JUN,ELOB,DVL1,LAMB2,LAMC2,GSTP1
M3468	Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix	4.61E-01	7.56E-01	1.00E+00	1.00E+00	7	SERPINF1,P4HTM,SLPI,CSTB,CTSD,CTSH,ST14
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	6.58E-01	8.10E-01	1.00E+00	1.00E+00	26	SERPINF1,PLXNB2,LRG1,S100A2,S100A6,S100A13,NTN1,SDC1,PLXNB1,GDF15,CRELD2,P4HTM,IGFBP2,IGFBP5,IGFBP7,CCN1,SLPI,CSTB,CTSD,CTSH,ST14,COL21A1,LAMB2,LAMC2,VWA7,LGALS3
Panther DB							
P00029	Huntington disease	1.81E-02	6.16E-01	1.00E+00	1.00E+00	8	TUBB2A,TUBB4B,FOS,ARPC1A,ARF5,CYC1,JUN,DNAI2
P04396	Vitamin D metabolism and pathway	2.30E-02	6.16E-01	1.00E+00	1.00E+00	2	FDXR,CYP27A1
P00049	Parkinson disease	2.98E-02	6.16E-01	1.00E+00	1.00E+00	6	STUB1,HSPA1B,HSPA2,SEPTIN5,MAPK15,PSMA7
P00052	TGF-beta signaling pathway	9.89E-02	7.94E-01	1.00E+00	1.00E+00	5	CITED2,GDF15,JUN,JUNB,JUND
P00047	PDGF signaling pathway	1.28E-01	7.94E-01	1.00E+00	1.00E+00	6	FOS,MAPK15,BAD,JUN,MKKN2,ELF3
P00034	Integrin signalling pathway	1.65E-01	7.94E-01	1.00E+00	1.00E+00	7	ARPC1A,RHOB,ITGA3,ITGB4,ITGB5,LAMB2,LAMC2
P00004	Alzheimer disease-presenilin pathway	1.89E-01	7.94E-01	1.00E+00	1.00E+00	5	APBB1,TRIM3,CTNNB1,DVL1,LRP5
P00005	Angiogenesis	2.18E-01	8.21E-01	1.00E+00	1.00E+00	6	FOS,RHOB,CTNNB1,BAD,JUN,DVL1
P00036	Interleukin signaling pathway	2.36E-01	8.21E-01	1.00E+00	1.00E+00	4	FOS,MAPK15,BAD,MKKN2
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	4.10E-01	8.21E-01	1.00E+00	1.00E+00	6	ARPC1A,JUN,JUNB,JUND,COL21A1,GNA11
Pathway ontology							
PW:0000016	Amyotrophic lateral sclerosis disease	5.58E-04	1.67E-02	7.83E-02	3.35E-02	4	BAD,SSR4,GPX1,GPX4
PW:0000134	Glutathione metabolic	2.72E-03	5.44E-02	2.55E-01	1.63E-01	3	GPX1,GPX4,GSTA2
PW:0000574	Pentose phosphate - non-oxidative phase	4.19E-03	6.28E-02	2.94E-01	2.51E-01	2	TALDO1,TKT
PW:0000200	The planar cell polarity Wntsignaling	6.93E-03	6.93E-02	3.24E-01	4.16E-01	3	CELSR1,PTK7,DVL1
PW:0000238	Insulin-like growth factor signaling	4.00E-02	2.59E-01	1.00E+00	1.00E+00	2	IGFBP2,IGFBP5
PW:0000076	Pathway of urea cycle and metabolism of amino groups	4.64E-02	2.59E-01	1.00E+00	1.00E+00	2	CKB,ASL
PW:0000121	Tetrachloroethene degradation	5.32E-02	2.59E-01	1.00E+00	1.00E+00	1	EPHX1
PW:0000201	Canonical Wntsignaling	1.26E-01	2.74E-01	1.00E+00	1.00E+00	3	CTNNB1,DVL1,LRP5
PW:0000143	Insulin signaling	1.64E-01	3.17E-01	1.00E+00	1.00E+00	2	PTPRF,SOCS3
PW:0000540	Obesity disease	1.96E-01	3.63E-01	1.00E+00	1.00E+00	1	SDC1

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Table 3 (continued)

Pathway ID	Pathway name	P-value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
SMPDB							
SMP00031	Pentose Phosphate Pathway	5.65E-03	2.10E-01	9.56E-01	3.00E-01	3	PGLS,TALDO1,TKT
SMP00005	Folate and Pterine Biosynthesis	2.30E-02	2.10E-01	9.56E-01	1.00E+00	2	GCHFR,RUVBL2
SMP00006	Tyrosine Metabolism	2.58E-02	2.10E-01	9.56E-01	1.00E+00	3	MIF,ALDH3A1,COMT
SMP00315	CerebrotendinousXanthomatosis (CTX)	2.77E-02	2.10E-01	9.56E-01	1.00E+00	1	CYP27A1
SMP00003	ArgininosuccinicAciduria	2.77E-02	2.10E-01	9.56E-01	1.00E+00	1	ASL
SMP00386	Desmosterolosis	2.77E-02	2.10E-01	9.56E-01	1.00E+00	1	DHCR24
SMP00346	Porphyria Variegata (PV)	2.77E-02	2.10E-01	9.56E-01	1.00E+00	1	PPOX
SMP00355	Mitochondrial Electron Transport Chain	8.34E-02	5.52E-01	1.00E+00	1.00E+00	2	UQCRC1,ATP5F1E
SMP00050	Purine Metabolism	1.64E-01	6.29E-01	1.00E+00	1.00E+00	2	AK1,GUK1
SMP00320	Intracellular Signalling Through Adenosine Receptor A2a and Adenosine	2.23E-01	6.29E-01	1.00E+00	1.00E+00	2	BAD,JUN

TCR signaling in naive CD4+ T cells, influenza A, cell activation, regulation of immune system process, cell surface, neuroactive ligand-receptor interaction, NOD-like receptor signaling pathway, vesicle membrane, cytokine-cytokine receptor interaction and hemostasis. PPI networks of the identified down regulated genes were constructed using IID, which consisted of 9019 edges and 4233 nodes (Fig. 7). The nodes with the highest node degree, betweenness centrality, stress centrality, closeness centrality and lowest clustering coefficient were screened as hub genes including CTNNB1, JUN, ERBB2, STUB1, RPS8, PIN1, RUVBL2, FOS, PROS1, WDR54, NAA38, GSTA2 and SMDT1 are listed in Table 6. Scatter plot for down regulated genes are shown in Fig. 8. Pathway and GO enrichment analysis for the down regulated genes in this PPI network revealed that these hub genes were significantly enriched in fluid shear stress and atherosclerosis, non-alcoholic fatty liver disease (NAFLD), ErbB2/ErbB3 signaling events, protein processing in endoplasmic reticulum, ribosome, gene expression, ATF-2 transcription factor network, MAPK signaling pathway, metabolism of proteins, cytoskeletal protein binding, regulation of programmed cell death, glutathione metabolism and mitochondrial envelope.

By utilizing module analysis of the PPI network for up regulated genes in PEWCC1, we identified four significant modules based on the degree of importance (Fig. 9). Module 1 contained 154 nodes and 189 edges, Module 2 contained 143 nodes and 200 edges, Module 3 contained 109 nodes and 114 edges and Module 4 contained 19 nodes and 30 edges. Pathway and GO enrichment analyses of the up regulated genes in these modules were mainly enriched in influenza A, interferon signaling, herpes simplex infection, TCR signaling in naive CD4+ T cells, cytokine production, defense response, response to external biotic stimulus and immune effector process. Utilizing module analysis of the PPI network for down regulated genes in PEWCC1, we identified four significant modules based on the degree of importance (Fig. 10). Module 1 contained 140 nodes and 193 edges, Module 2 contained 120 nodes and 142 edges, Module 3 contained 119 nodes and 142 edges and Module 4 contained 76 nodes and 1219 edges. Pathway and GO enrichment analyses of the down regulated genes in these modules were mainly enriched in protein processing in endoplasmic reticulum,

Huntington's disease, oxidative phosphorylation, ribosome, supramolecular fiber, viral process, establishment of protein localization to organelle and viral transcription.

3.5. Construction of target genes - miRNA regulatory network

In order to explore the molecular mechanisms in SARS-CoV-2 infection further, target genes were predicted using the miRNet database. A target genes - miRNA regulatory network for up regulated genes was constructed, which consisted of 2623 nodes and 11,118 edges, including 402 target genes and 2221 miRNAs (Fig. 11). The CCND2 can be targeted by 179 miRNAs (ex; hsa-mir-3916), FAM241A can be targeted by 174 miRNAs (ex; hsa-mir-4306), REL can be targeted by 153 miRNAs (ex; hsa-mir-4261), POU2F1 can be targeted by 150 miRNAs (ex; hsa-mir-3911) and MICA can be targeted by 142 miRNAs (ex; hsa-mir-2392) are listed in Table 7. Pathway and GO enrichment analysis for the up regulated genes in this target genes - miRNA regulatory network revealed that these target genes were significantly enriched in Jak-STAT signaling pathway, adaptive immune system, calcineurin-regulated NFAT-dependent transcription in lymphocytes and natural killer cell mediated cytotoxicity. A target genes - miRNA regulatory network for down regulated genes was constructed, which consisted of 2452 nodes and 7650 edges, including 397 target genes and 2055 miRNAs (Fig. 12). The MKNK2 can be targeted by 195 miRNAs (ex; hsa-mir-1256), TUBB2A can be targeted by 193 miRNAs (ex; hsa-mir-1253), IGFBP5 can be targeted by 144 miRNAs (ex; hsa-mir-1264), PHB2 can be targeted by 132 miRNAs (ex; hsa-mir-1183) and MAZ can be targeted by 122 miRNAs (ex; hsa-mir-1470) are listed in Table 7. Pathway and GO enrichment analysis for the down regulated genes in this target genes - miRNA regulatory network revealed that these target genes were significantly enriched in MAPK signaling pathway, Metabolism of proteins, Genes encoding structural ECM glycoproteins, establishment of protein localization to organelle and regulation of programmed cell death.

Table 4
The enriched GO terms of the up regulated differentially expressed genes.

GO ID	CATEGORY	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0043207	BP	Response to external biotic stimulus	1.24E-55	3.67E-52	3.40E-51	7.34E-52	153	A2M,PIK3AP1,USP18,PDE4B,DDX58,LILRB2,CLEC5A,NT5C3A,TNIP3,CLEC7A,CARD16,TLR7,DTX3L,SIRPB1,TRIM22,MEFV,CD209,ACOD1,ZBP1,SERPINB9,FCER1G,FCGR1B,FCGR3A,IFITM3,PIK3CG,MICB,CXCL9,AIF1,CCL2,CCL4,CCL5,CCR5,CCL8,CXCL11,AIM2,TRIM38,MNDA,PLSCR1,LILRA5,FKBP5,PML,HTN1,HTN3,IKZF3,WIPF1,DDX60,FPR2,IFI44,IRF8,CXCL13,IFITM1,BIRC3,MUC13,APOL1,PARP14,IFI16,BATF2,IFIT2,IFIT1,IFIT3,TRIM5,KMO,RSAD2,ISG15,CD226,OASL,CD274,XAF1,NUB1,SLAMF7,IL2RA,MUC3A,IFI6,NEXN,EIF2AK2,CD300E,PRLR,CX3CR1,MX1,MX2,PDCD1LG2,CYBB,SLAMF8,IL10RA,LGMN,SP100,IDO1,SPN,TAGAP,CXCL10,NAIP,CMPK2,GBP1,IFIT5,GBP2,IRF4,PTPN22,TRIM34,TRIM21,IL18RAP,LILRB1,RTP4,STAT1,STAT2,APOBEC3A,CEACAM1,FGL2,APOBEC3F,CD84,JAK2,CLEC4E,PTPRC,GBP4,GBP5,SIGLEC10,SERPING1,C1QB,C1QC,MICA,PARP9,IFI44L,C4BPB,HERC6,KYNU,KLRD1,CASP1,MUC19,SIGLEC14,MPEG1,OAS1,OAS2,OAS3,ABCC9,RGS1,OPRM1,LGALS9,HAVCR2,NMI,RNASE6,HMGA2,RESF1,P2RX7,CD80,CD86,TLR1,TLR2,TLR3,GZMB,TLR4,CD68,CD180,CD96,HERC5
GO:0006952	BP	Defense response	5.40E-55	1.07E-51	9.88E-51	3.20E-51	163	A2M,PIK3AP1,USP18,DDX58,MAS1,LILRB2,CLEC5A,NT5C3A,TNIP3,CLEC7A,TLR7,DTX3L,TAC4,SIRPB1,ADGRE2,TRIM22,MEFV,CD209,CD163,ACOD1,ZBP1,SERPINB9,MS4A2,FCER1G,FCGR1B,IFITM3,PIK3CG,MICB,CXCL9,AIF1,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CMKLR1,APOL2,CXCL11,AIM2,TRIM38,MNDA,PLSCR1,LILRA5,ALOX5AP,PML,HTN1,HTN3,DDX60,FPR2,FPR3,AOAH,IRF8,CXCL13,IFITM1,BIRC3,APOA2,MUC13,SUCNR1,APOL1,PARP14,IFI16,BATF2,IFIT2,IFIT1,IFIT3,TRIM5,RSAD2,IGF1,ISG15,CD226,OASL,XAF1,NUB1,SIGLEC1,SLAMF7,IL2RA,MUC3A,IFI6,EIF2AK2,CD300E,CX3CR1,MX1,MX2,CXCR2,CYBB,SLAMF8,LGMN,SP100,IDO1,SPN,INHBA,TAGAP,CXCL10,CYSLTR1,NAIP,GBP1,IFIT5,GBP2,IRF4,PTPN22,TRIM34,TRIM21,IL18RAP,LILRB1,RTP4,STAT1,STAT2,ITK,STAT4,APOBEC3A,CEACAM1,FGL2,APOBEC3F,CD84,JAK2,CLEC4E,PTPRC,GBP4,GBP5,SIGLEC10,SERPING1,C1QB,C1QC,C3AR1,MICA,PARP9,IFI44L,C4BPB,HERC6,KYNU,KLRD1,PLA2G7,CASP1,MUC19,SIGLEC14,MPEG1,OAS1,OAS2,OAS3,ABCC9,REL,OLR1,OPRM1,LGALS9,HAVCR2,ACE2,NMI,RNASE6,P2RX7,CD86,TLR1,TLR2,TLR3,GZMB,TLR4,APOL3,CD68,TNFAIP6,CD180,CD96,HERC5,SP140
GO:0098542	BP	Defense response to other organism	6.38E-50	7.56E-47	7.00E-46	3.78E-46	129	A2M,PIK3AP1,USP18,DDX58,CLEC5A,NT5C3A,TNIP3,CLEC7A,TLR7,DTX3L,SIRPB1,TRIM22,MEFV,CD209,ACOD1,ZBP1,SERPINB9,FCER1G,FCGR1B,IFITM3,PIK3CG,MICB,CXCL9,AIF1,CCL2,CCL4,CCL5,CCL8,AIM2,TRIM38,MNDA,PLSCR1,LILRA5,PML,HTN1,HTN3,DDX60,FPR2,IRF8,CXCL13,IFITM1,BIRC3,MUC13,APOL1,PARP14,IFI16,BATF2,IFIT2,IFIT1,IFIT3,TRIM5,RSAD2,ISG15,CD226,OASL,XAF1,NUB1,SLAMF7,IL2RA,MUC3A,IFI6,EIF2AK2,CD300E,CX3CR1,MX1,MX2,CYBB,SLAMF8,LGMN,SP100,SPN,TAGAP,CXCL10,NAIP,GBP1,IFIT5,GBP2,IRF4,PTPN22,TRIM34,TRIM21,IL18RAP,LILRB1,RTP4,STAT1,STAT2,APOBEC3A,CEACAM1,FGL2,APOBEC3F,CD84,JAK2,CLEC4E,PTPRC,GBP4,GBP5,SIGLEC10,SERPING1,C1QB,C1QC,MICA,PARP9,IFI44L,C4BPB,HERC6,KYNU,KLRD1,CASP1,MUC19,SIGLEC14,MPEG1,OAS1,OAS2,OAS3,ABCC9,LGALS9,HAVCR2,NMI,RNASE6,P2RX7,CD86,TLR1,TLR2,TLR3,GZMB,TLR4,APOL3,CD68,TNFAIP6,CD180,CD96,HERC5
GO:0045087	BP	Innate immune response	2.72E-45	2.44E-42	2.26E-41	1.61E-41	113	A2M,PIK3AP1,USP18,DDX58,CLEC5A,TNIP3,CLEC7A,TLR7,DTX3L,SIRPB1,TRIM22,MEFV,CD209,ACOD1,ZBP1,SERPINB9,FCER1G,FCGR1B,

(continued on next page)

Table 4 (continued)

GO ID	CATEGORY	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0002252	BP	Immune effector process	2.88E-45	2.44E-42	2.26E-41	1.71E-41	127	IFITM3,PIK3CG,MICB,AIF1,CCL2,CCL4,CCL5,CCL8,AIM2,TRIM38,MNDA,PLSCR1,LILRA5,PML,DDX60,FPR2,IRF8,IFITM1,BIRC3,MUC13,APOL1,PARP14,IFI16,IFIT2,IFIT1,IFIT3,TRIM5,RSAD2,ISG15,CD226,OASL,XAF1,NUB1,SLAMF7,MUC3A,IFI6,EIF2AK2,CD300E,CX3CR1,MX1,MX2,CYBB,SLAMF8,LGMN,SP100,NAIP,GBP1,IFIT5,GBP2,IRF4,PTPN22,TRIM34,TRIM21,IL18RAP,LILRB1,STAT1,STAT2,APOBEC3A,CEACAM1,APOBEC3F,CD84,JAK2,CLEC4E,GBP4,GBP5,SIGLEC10,SERPING1,C1QB,C1QC,MICA,PARP9,C4BPB,HERC6,KYNU,KLRD1,CASP1,MUC19,SIGLEC14,MPEG1,OAS1,OAS2,OAS3,LGALS9,HAVCR2,NMI,RNASE6,CD86,TLR1,TLR2,TLR3,GZMB,TLR4,CD180,CD96,HERC5
GO:0002682	BP	Regulation of immune system process	2.55E-41	1.89E-38	1.75E-37	1.51E-37	141	A2M,DDX58,HLA-DMA,LILRB2,CLEC5A,NT5C3A,PECAM1,DOK3,HLX,TLR7,DTX3L,TAC4,SIRPB1,ADGRE2,TRIM22,ZBP1,BTN3A3,SERPINB9,FCAR,MS4A2,FCER1G,FCGR2A,FCGR3A,FCGR3B,IFITM3,PIK3CG,MICB,CXCL9,CCL2,CCL5,AIM2,TRIM38,MNDA,PLSCR1,APBB1IP,PML,SELL,WIPF1,DDX60,FPR2,DOCK10,IFITM1,BIRC3,APOA2,SUCNR1,IFI16,IFIT2,IFIT1,IFIT3,MILR1,TRIM5,SLC2A3,RSAD2,ISG15,CD226,OASL,SLAMF7,RAP2C,IL2RA,IFI6,EIF2AK2,CX3CR1,MX1,IL7R,MX2,CXCR2,CYBB,SLAMF8,SPN,TAGAP,DOCK11,CXCL10,GAPT,GBP1,IFIT5,IRF4,PTPN22,TRIM34,IL18RAP,LILRB1,RTP4,CLEC12A,STAT1,ELMO1,STAT2,APOBEC3A,CEACAM1,FGL2,APOBEC3F,CD84,CLEC4E,PTPRC,SERPING1,C1QB,C1QC,C3AR1,MICA,PARP9,IFI44L,C4BPB,KLRD1,DOCK2,LAIR1,SIGLEC14,OAS1,OAS2,OAS3,ABCC9,CBL,OLR1,LGALS9,HAVCR2,RNASE6,P2RX7,CD80,CD86,TLR2,TLR3,GZMB,TLR4,CD53,CD68,TNFAIP6,CD180,CD96,HERC5,NCKAP1L
GO:0034097	BP	Response to cytokine	4.08E-27	1.51E-24	1.40E-23	2.42E-23	99	A2M,PIK3AP1,USP18,PDE4B,DDX58,HLA-DMA,LILRB2,PECAM1,TNIP3,CLEC7A,HLX,EVI2B,IKZF1,TRAC,TLR7,DTX3L,SIRPB1,ADGRE2,CD209,ACOD1,ZBP1,BTN3A3,SERPINB9,MS4A2,FCER1G,FCGR1B,FCGR2A,FCGR3A,H4C8,MICB,AIF1,CCL2,CCR1,CCL4,CCL5,CCL8,CMKLR1,AIM2,TRIM38,MNDA,PLSCR1,PML,SELL,MPP1,FLT1,IKZF3,LEO1,WIPF1,DDX60,FPR2,FPR3,CXCL13,IFITM1,BIRC3,APOA2,MUC13,PARP14,IFI16,IFIT1,MILR1,TRIM5,RSAD2,IGF1,ISG15,CD226,TNFSF13B,CLEC2D,CD274,PRKCB,SLAMF7,FYB1,IL2RA,MUC3A,IL2RG,EIF2AK2,CD300E,CX3CR1,IL7R,CXCR2,PDCD1LG2,SLAMF8,LGMN,PAG1,IDO1,TNFSF14,SPN,INHBA,RASSF2,CXCL10,GBP1,IRF4,PTPN22,SAMSN1,IL18RAP,LILRB1,CLEC12A,STAT1,ELMO1,ITK,CEACAM1,FGL2,APOBEC3F,CD84,JAK2,CLEC4E,PTPRC,PTPRE,GBP5,SERPING1,C1QB,C1QC,C3AR1,MICA,PARP9,C4BPB,KLRD1,CLEC2B,LILRB4,LST1,PLA2G7,ZEB1,DOCK8,LAIR1,MUC19,LCP2,BTN3A1,LGALS9,HAVCR2,NMI,P2RX7,CD80,CD86,TLR1,TLR2,TLR3,TLR4,CD68,ELF1,CD96,HERC5,NCKAP1L
								USP18,DDX58,CARD16,TRIM22,F13A1,MEFV,ACOD1,ACSL4,ZBP1,PNPT1,FCER1G,FCGR1B,IFITM3,CXCL9,SNX10,AIF1,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CMKLR1,CXCL11,AIM2,TRIM38,MNDA,PLSCR1,PML,IRF8,CXCL13,IFITM1,BIRC3,POU2F1,PARP14,IFI16,IFIT2,IFIT1,IFIT3,TRIM5,KMO,RSAD2,MTAP,ISG15,TNFSF13B,OASL,LAMP3,CD274,XAF1,NUB1,IL2RA,IFI6,IL2RG,EIF2AK2,PRLR,CX3CR1,MX1,IL7R,MX2,CXCR2,IL10RA,SP100,TNFSF14,CXCL10,GBP1,GBP2,IRF4,TRIM34,TRIM21,IL18RAP,STAT1,STAT2,STAT4,CEACAM1,JAK2,PTPRC,GBP4,GBP5,PARP9,KYNU,ZEB1,SH2B3,DOCK8,CASP1,OAS1,OAS2,OAS3,

(continued on next page)

Table 4 (continued)

GO ID	CATEGORY	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0001775	BP	Cell activation	4.47E-27	1.56E-24	1.44E-23	2.65E-23	110	REL,CBL,OPRM1,LGALS9,NMI,LMNB1,CD80,CD86,TLR2,TLR3,TLR4,ELF1 HLA-DMA,LILRB2,CLEC5A,PECAM1,DOK3,CLEC7A,HLX,IKZF1,TLR7,TAC4,SIRPB1,ADGRE2,CD209,FCAR,MS4A2,FCER1G,FCGR2A,FCGR3A,FCGR3B,PIK3CG,MICB,AIF1,CCL2,CCL5,PLEK,MNDA,PLSCR1,LILRA5,APBB1IP,SELL,IKZF3,WNT7A,FPR2,DOCK10,SUCNR1,BATF2,MILR1,SLC2A3,RSAD2,IGF1,CD226,TNFSF13B,CD274,PRKCB,SLAMF7,RAP2C,FYB1,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,PDCD1LG2,CYBB,SLAMF8,PAG1,IDO1,TNFSF14,SPN,INHBA,DOCK11,CXCL10,DGKA,GAPT,IRF4,PTPN22,SAMSN1,IL18RAP,LILRB1,CLEC12A,ITK,CEACAM1,FGL2,NEDD4,CD84,JAK2,CLEC4E,PTPRC,PTPRE,C3AR1,MICA,SKAP2,LILRB4,DOCK2,LST1,ZEB1,SH2B3,DOCK8,LAIR1,SIGLEC14,LCP2,CBL,OLR1,BTN3A1,LGALS9,HAVCR2,P2RX7,CD80,CD86,TLR1,TLR2,ENTPD1,TLR3,TLR4,CD53,CD68,TNFAIP6,CD180,NCKAP1L
GO:0045321	BP	Leukocyte activation	4.73E-27	1.56E-24	1.44E-23	2.80E-23	103	HLA-DMA,LILRB2,CLEC5A,PECAM1,DOK3,CLEC7A,HLX,IKZF1,TLR7,TAC4,SIRPB1,ADGRE2,CD209,FCAR,MS4A2,FCER1G,FCGR2A,FCGR3A,FCGR3B,PIK3CG,MICB,AIF1,CCL2,CCL5,MNDA,PLSCR1,APBB1IP,SELL,IKZF3,FPR2,DOCK10,SUCNR1,BATF2,MILR1,SLC2A3,RSAD2,IGF1,CD226,TNFSF13B,CD274,PRKCB,SLAMF7,RAP2C,FYB1,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,PDCD1LG2,CYBB,SLAMF8,PAG1,IDO1,TNFSF14,SPN,INHBA,DOCK11,GAPT,IRF4,PTPN22,SAMSN1,IL18RAP,LILRB1,CLEC12A,ITK,CEACAM1,FGL2,NEDD4,CD84,JAK2,CLEC4E,PTPRC,PTPRE,C3AR1,MICA,SKAP2,LILRB4,DOCK2,LST1,ZEB1,DOCK8,LAIR1,SIGLEC14,LCP2,CBL,OLR1,BTN3A1,LGALS9,HAVCR2,P2RX7,CD80,CD86,TLR1,TLR2,TLR3,TLR4,CD53,CD68,TNFAIP6,CD180,NCKAP1L
GO:0001816	BP	Cytokine production	2.94E-25	8.70E-23	8.06E-22	1.74E-21	78	PCSK5,PDE4B,UBE2L6,DDX58,LILRB2,CLEC5A,CLEC7A,CARD16,TLR7,MEFV,ACOD1,ZBP1,MS4A2,FCER1G,PIK3CG,AIF1,CCL2,CCL5,CMKLR1,AIM2,TRIM38,MNDA,LILRA5,PML,DDX60,IRF8,BIRC3,APOA2,SUCNR1,IFI16,RSAD2,IGF1,ISG15,CD226,SRGN,CD274,EIF2AK2,CX3CR1,PDCD1LG2,CYBB,IDO1,SPN,INHBA,GBP1,IRF4,PTPN22,TRIM21,IL18RAP,LILRB1,STAT1,ITK,CEACAM1,CD84,JAK2,CLEC4E,PTPRC,GBP5,NAV3,C3AR1,CASP1,REL,LCP2,BTN3A1,LGALS9,HAVCR2,ACE2,NMI,P2RX7,CD80,CD86,TLR1,TLR2,TLR3,TLR4,ELF1,CD96,HERC5,NCKAP1L
GO:0019221	BP	Cytokine-mediated signaling pathway	3.58E-25	1.01E-22	9.36E-22	2.12E-21	75	USP18,CARD16,TRIM22,F13A1,ZBP1,FCER1G,FCGR1B,IFITM3,CXCL9,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CMKLR1,CXCL11,AIM2,TRIM38,PML,IRF8,CXCL13,IFITM1,BIRC3,POU2F1,PARP14,IFIT2,IFIT1,IFIT3,TRIM5,RSAD2,MTAP,ISG15,TNFSF13B,OASL,XAF1,IL2RA,IFI6,IL2RG,PRLR,CX3CR1,MX1,IL7R,MX2,CXCR2,IL10RA,SP100,TNFSF14,CXCL10,GBP1,GBP2,IRF4,TRIM34,TRIM21,IL18RAP,STAT1,STAT2,STAT4,CEACAM1,JAK2,PTPRC,PARP9,ZEB1,SH2B3,CASP1,OAS1,OAS2,OAS3,CBL,OPRM1,NMI,LMNB1,CD80,CD86,ELF1
GO:0006954	BP	Inflammatory response	4.75E-24	1.22E-21	1.13E-20	2.81E-20	73	PIK3AP1,USP18,MAS1,TNIP3,CLEC7A,TLR7,TAC4,ADGRE2,MEFV,CD163,ACOD1,MS4A2,FCER1G,PIK3CG,CXCL9,AIF1,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CMKLR1,APOL2,CXCL11,AIM2,PLSCR1,LILRA5,ALOX5AP,FPR2,FPR3,AOAH,CXCL13,BIRC3,APOA2,SUCNR1,IFI16,IGF1,SIGLEC1,IL2RA,CX3CR1,CXCR2,CYBB,SLAMF8,IDO1,SPN,CXCL10,CYSLTR1,NAIP,IL18RAP,JAK2,PTPRC,GBP5,SIGLEC10,C3AR1,PLA2G7,REL,OLR1,OPRM1,LGALS9,HAVCR2,ACE2,NMI,P2RX7,TLR1,TLR2,TLR3,TLR4,APOL3,CD68,TNFAIP6,CD180,CD96

(continued on next page)

Table 4 (continued)

GO ID	CATEGORY	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0031347	BP	Regulation of defense response	1.23E-23	3.04E-21	2.82E-20	7.30E-20	75	A2M,PIK3AP1,USP18,DDX58,MAS1,TNIP3,CLEC7A,TLR7,DTX3L,MEFV,CD209,ACOD1,ZBP1,SERPINB9,FCER1G,PIK3CG,MICB,CCL5,AIM2,TRIM38,MNDA,PLSCR1,LILRA5,ALOX5AP,PML,DDX60,FPR2,AOAH,BIRC3,MUC13,SUCNR1,PARP14,IFI16,IFIT1,TRIM5,RSAD2,IGF1,CD226,IL2RA,MUC3A,CX3CR1,SLAMF8,LGMN,IDO1,SPN,IRF4,PTPN22,IL18RAP,LILRB1,STAT1,CEACAM1,FGL2,APOBEC3F,JAK2,CLEC4E,PTPRC,GBP5,SIGLEC10,SERPING1,MICA,PARP9,PLA2G7,MUC19,LGALS9,HAVCR2,ACE2,NMI,CD86,TLR1,TLR2,TLR3,TLR4,TNFAIP6,CD96,HERC5
GO:0071345	BP	Cellular response to cytokine stimulus	1.72E-23	4.07E-21	3.77E-20	1.02E-19	89	USP18,CARD16,TRIM22,F13A1,ACOD1,ZBP1,PNPT1,FCER1G,FCGR1B,IFITM3,CXCL9,SNX10,AIF1,CCL2,CCR1,CCL4,CCL5,CCR5,CCL8,CMKLR1,CXCL11,AIM2,TRIM38,MNDA,PML,IRF8,CXCL13,IFITM1,BIRC3,POU2F1,PARP14,IFI16,IFIT2,IFIT1,IFIT3,TRIM5,KMO,RSAD2,MTAP,ISG15,TNFSF13B,OASL,XAF1,IL2RA,IFI6,IL2RG,PRLR,CX3CR1,MX1,IL7R,MX2,CXCR2,IL10RA,SP100,TNFSF14,CXCL10,GBP1,GBP2,IRF4,TRIM34,TRIM21,IL18RAP,STAT1,STAT2,STAT4,CEACAM1,JAK2,PTPRC,GBP4,GBP5,PARP9,ZEB1,SH2B3,DOCK8,CASP1,OAS1,OAS2,OAS3,CBL,OPRM1,LGALS9,NMI,LMNB1,CD80,CD86,TLR2,TLR3,TLR4,ELF1
GO:0140352	BP	Export from cell	5.01E-14	4.22E-12	3.91E-11	2.97E-10	91	A2M,PCK5,PDE3B,DDX58,LILRB2,CLEC5A,PECAM1,DOK3,CARD16,TAC4,SIRPB1,ADGRE2,F13A1,FCAR,MS4A2,FCER1G,FCGR2A,FCGR3B,PIK3CG,AIF1,CCR1,CCL5,CCL8,PLEK,MMP13,AIM2,MNDA,LILRA5,PML,SELL,SEPTIN4,WNT7A,FPR2,APOA2,SUCNR1,RPH3A,MILR1,SLC2A3,KMO,SLC8A1,RSAD2,IGF1,ISG15,SRGN,TNFSF13B,CD274,PRKCB,RAP2C,CXCR2,CYBB,GALR1,INHBA,RAB8B,DAB2,GBP1,PTPN22,LILRB1,CLEC12A,CEACAM1,FGL2,CD84,JAK2,CLEC4E,PTPRC,GBP5,SERPING1,C3AR1,DOCK2,LAIR1,CASP1,SIGLEC14,SYT2,LCP2,CBL,TF,OLR1,BTN3A1,OPRM1,LGALS9,HAVCR2,HMGA2,P2RX7,TLR1,TLR2,ENTPD1,TLR4,CD53,CD68,LHFPL2,TNFAIP6,NCKAP1L
GO:0009986	CC	Cell surface	1.56E-12	8.99E-10	6.23E-09	8.99E-10	63	HLA-DMA,MAS1,LILRB2,CLEC5A,PECAM1,CLEC7A,SIRPB1,CD209,CD163,BTN3A3,SEMA6D,MS4A2,FCER1G,FCGR3A,MICB,CXCL9,CCR1,CCR5,LILRA5,SELL,WNT7A,CLIC4,SUCNR1,CD226,CLEC2D,CD274,SLAMF7,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,PDCD1LG2,SLAMF8,SPN,CXCL10,ITGA1,LILRB1,RTP4,CLEC12A,CEACAM1,CCN5,PTPRC,KCNJ6,MICA,KLRD1,TF,BTN3A1,HAVCR2,ACE2,P2RX7,CD80,CD86,TLR2,ENTPD1,TLR3,TLR4,CD53,CD69,ADGRE1,CDH6,CDH8
GO:0009897	CC	External side of plasma membrane	7.07E-12	2.04E-09	1.41E-08	4.08E-09	38	PECAM1,CD209,CD163,BTN3A3,MS4A2,FCER1G,FCGR3A,MICB,CXCL9,CCR1,CCR5,SELL,CD226,CD274,SLAMF7,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,PDCD1LG2,SPN,CXCL10,ITGA1,LILRB1,PTPRC,MICA,KLRD1,TF,BTN3A1,P2RX7,CD80,CD86,TLR2,TLR4,CD69,ADGRE1
GO:0012506	CC	Vesicle membrane	9.50E-09	8.34E-07	5.79E-06	5.48E-06	47	LILRB2,CLEC5A,PECAM1,DOK3,SIRPB1,CD163,FCAR,FCER1G,FCGR1B,FCGR2A,FCGR3B,SELL,WNT7A,FPR2,CLIC4,RPH3A,SLC2A3,MSR1,LAMP3,RAP2C,IL7R,CXCR2,CYBB,RAB8B,DAB2,GBP1,ATP10B,SLC30A3,CLEC12A,CEACAM1,PTPRC,C3AR1,STX17,MARCHF1,LAIR1,SIGLEC14,MPEG1,GRIA4,SYT2,TF,OLR1,TLR1,TLR2,CD53,CD68,LHFPL2,NCKAP1L
GO:0097478	CC	Leaflet of membrane bilayer	1.01E-08	8.34E-07	5.79E-06	5.84E-06	41	PECAM1,CD209,CD163,BTN3A3,MS4A2,FCER1G,FCGR3A,MICB,CXCL9,CCR1,CCR5,SELL,CD226,CD274,SLAMF7,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,PDCD1LG2,SPN,CXCL10,PTPN22,ITGA1,LILRB1,PTPRC,MICA,KLRD1,TF,RGS1,BTN3A1,P2RX7,CD80,CD86,TLR2,TLR4,CD69,GNB4,ADGRE1

(continued on next page)

Table 4 (continued)

GO ID	CATEGORY	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0030659	CC	Cytoplasmic vesicle membrane	1.16E-08	8.39E-07	5.82E-06	6.71E-06	46	LILRB2,CLEC5A,PECAM1,DOK3,SIRPB1,CD163,FCAR,FCER1G,FCGR1B,FCGR2A,FCGR3B,SELL,WNT7A,FPR2,CLIC4,RPH3A,SLC2A3,MSR1,LAMP3,RAP2C,IL7R,CXCR2,CYBB,RAB8B,DAB2,ATP10B,SLC30A3,CLEC12A,CEACAM1,PTPRC,C3AR1,STX17,MARCHF1,LAIR1,SIGLEC14,MPEG1,GRIA4,SYT2,TF,OLR1,TLR1,TLR2,CD53,CD68,LHFPL2,NCKAP1L
GO:0005887	CC	Integral component of plasma membrane	8.34E-08	5.35E-06	3.71E-05	4.81E-05	74	IGSF6,SLCO2B1,MAS1,LILRB2,CLEC5A,MC2R,EVI2B,SIRPB1,ADGRE2,CD163,FCAR,SEMA6D,MS4A2,FCER1G,RASGRP3,CCR1,CCR5,CMKLR1,FLRT2,PLSCR1,SELL,FLT1,GPR65,AQP9,MILR1,SLC2A3,MSR1,SLC8A1,CD226,CLEC2D,IL2RA,IL2RG,CX3CR1,CXCR2,CYBB,GABRE,GALR1,SPN,TNFSF10,CYSLTR1,ITGA1,SLC30A3,IL18RAP,CEACAM1,CD84,PTPRC,PTPRO,KCNJ6,C3AR1,MICA,CLEC2B,SHANK1,CYSLTR2,TMEM45A,ABCC9,GRIA4,SLC7A7,OLR1,OPRM1,SHISA9,P2RX7,P2RY6,PLXNC1,LPAR6,TLR1,TLR2,ENTPD1,TLR3,TLR4,CD53,CD69,ADGRE1,CD96,NCKAP1L
GO:0099503	CC	Secretory vesicle	7.64E-07	2.94E-05	2.04E-04	4.41E-04	51	A2M,PCSK5,PDE4B,LILRB2,CLEC5A,PECAM1,DOK3,SIRPB1,F13A1,FCAR,FCER1G,FCGR2A,FCGR3B,SNX10,MNDA,SELL,SEPTIN4,FPR2,RPH3A,SLC2A3,IGF1,SRGN,LAMP3,RAP2C,CXCR2,CYBB,RAB8B,ITGA1,SLC30A3,CLEC12A,CEACAM1,FGL2,PTPRC,BRCA2,SERPING1,C3AR1,PCSK1N,DOCK2,LAIR1,SIGLEC14,ABCC9,SYT2,TF,OLR1,TLR2,ENTPD1,CD53,CD68,LHFPL2,TNFAIP6,NCKAP1L
GO:0000323	CC	Lytic vacuole	4.55E-04	1.31E-02	9.10E-02	2.63E-01	32	HLA-DMA,TLR7,DTX3L,TAC4,ADGRE2,MS4A2,FCER1G,IFITM3,PIK3CG,MMP13,MNDA,MILR1,SRGN,LAMP3,CXCR2,LGMN,ATP6V1B2,SLC36A1,DAB2,SLC30A3,CD84,C3AR1,STX17,MARCHF1,CBL,LGALS9,RNASE6,TLR3,GZMB,CD68,ZFYVE26,GNB4
GO:0030054	CC	Cell junction	2.90E-02	2.36E-01	1.00E+00	1.00E+00	42	DDX58,PECAM1,SYNPO2L,FGF13,FLRT2,MMP13,APBB1IP,TCAF2,FLT1,CLIC4,RPH3A,SLC8A1,RAP2C,FYB1,NEXN,GABRE,STARD8,DAB2,ITGA1,EPB41L3,SLC30A3,CYP46A1,ITK,CEACAM1,JAK2,FCHSD2,PTPRC,SHANK1,GRIA4,SYT2,LCP2,CBL,LAP3,OPRM1,SHISA9,HAVCR2,P2RX7,CD53,CDH6,CDH8,CD96,EPB41L2
GO:0015629	CC	Actin cytoskeleton	5.70E-02	3.29E-01	1.00E+00	1.00E+00	26	DDX58,SYNPO2L,AIF1,FGF13,MPP1,FLT1,WIPF1,CLIC4,PKNOX2,PRKCB,FYB1,ATP6V1B2,IDO1,SPN,GBP1,IFIT5,GBP2,TIAM2,ASAP1,CEACAM1,NEDD4,CCN5,FCHSD2,PSTPIP2,ACE2,EPB41L2
GO:0042802	MF	Identical protein binding	1.07E-05	1.11E-03	8.32E-03	1.11E-02	78	NPL,PIK3AP1,DDX58,LILRB2,PECAM1,CARD16,MEFV,ZBP1,FCER1G,PIK3CG,CCL4,CCL5,PLEK,AIM2,ALOX5AP,PML,BEST1,FLT1,IKZF3,WARS1,SEPTIN4,APOA2,MUC13,IFIT3,TRIM5,SLAMF7,EIF2AK2,PRLR,MX1,SLAMF8,TNFSF14,TNFSF10,INHBA,GIMAP2,GBP1,BCAT1,GBP2,TRIM21,GIMAP7,CMYA5,UHRF1BP1,LILRB1,STAT1,STAT2,STAT4,CEACAM1,APOBEC3F,CD84,JAK2,MLKL,PTPRC,PTPRE,GBP4,GBP5,BRCA2,PTPRO,C1QB,KYNU,SDS,CLEC2B,SHANK1,DPYD,SMCHD1,CASP1,ABCC9,GRIA4,LRRK1,OLR1,NMI,P2RX7,TLR1,TLR2,ENTPD1,TLR3,TLR4,CD69,CDH6,CDH8
GO:0016788	MF	Hydrolase activity, acting on ester bonds	1.60E-05	1.50E-03	1.13E-02	1.65E-02	54	PCSK5,PDE3B,PDE4B,BRIP1,NT5C3A,PNPT1,MS4A2,XRN1,CCR1,CCL5,CCR5,CCL8,CMKLR1,PLEK,NSMAF,FLT1,GPR65,FPR2,FPR3,AOAH,APOA2,PPM1K,PHACTR4,OASL,PLCXD3,EIF2AK2,CX3CR1,CXCR2,PTPN22,ITGA1,CMYA5,ZEB2,ITK,HELB,APOBEC3F,JAK2,PTPRC,PTPRE,PTPRO,C3AR1,PLA2G7,OAS1,OAS2,OAS3,OPRM1,RNASE6,HMGA2,RESF1,P2RY6,LPAR6,DDHD1,REXO1L1P,RPAP2,NCKAP1L
GO:0004896	MF	Cytokine receptor activity	1.94E-05	1.61E-03	1.21E-02	2.01E-02	11	CCR1,CCR5,CMKLR1,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,IL10RA,IL18RAP

(continued on next page)

Table 4 (continued)

GO ID	CATEGORY	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0038023	MF	Signaling receptor activity	2.14E-05	1.61E-03	1.21E-02	2.21E-02	67	IGSF6,MAS1,LILRB2,MC2R,CLEC7A,EVI2A,TLR7,ADGRE2,MS4A2,FCER1G,FCGR1B,FCGR3A,CCL2,CCR1,CCL5,CCR5,CMKLR1,BEGAIN,FLT1,GPR65,FPR2,FPR3,SUCNR1,RPH3A,TRIM5,CLEC2D,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,SLAMF8,IL10RA,GABRE,GALR1,SPN,CYSLTR1,GPR82,IL18RAP,LILRB1,CLEC4E,PTPRC,PTPRE,PTPRO,C3AR1,KLRD1,LILRB4,SHANK1,CYSLTR2,ABCC9,GRIA4,CBL,OPRM1,SHISA9,P2RX7,P2RY6,PLXNC1,CD80,CD86,LPAR6,TLR1,TLR2,TLR3,TLR4,CD69,ADGRE1
GO:0060089	MF	Molecular transducer activity	2.25E-05	1.61E-03	1.21E-02	2.32E-02	72	IGSF6,MAS1,LILRB2,MC2R,CLEC7A,EVI2A,TLR7,ADGRE2,MS4A2,FCER1G,FCGR1B,FCGR3A,CCL2,CCR1,CCL5,CCR5,CMKLR1,BEGAIN,FLT1,GPR65,FPR2,FPR3,SUCNR1,RPH3A,TRIM5,CLEC2D,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,PROX1,SLAMF8,IL10RA,GABRE,GALR1,SPN,CXCL10,CYSLTR1,GPR82,IL18RAP,LILRB1,CDKL5,CLEC4E,PTPRC,PTPRE,PTPRO,C3AR1,KLRD1,LILRB4,SHANK1,CYSLTR2,ABCC9,GRIA4,CBL,OPRM1,CCND2,SHISA9,P2RX7,P2RY6,PLXNC1,CD80,CD86,LPAR6,TLR1,TLR2,TLR3,TLR4,CD69,ADGRE1,HERC5
GO:0042578	MF	Phosphoric ester hydrolase activity	3.91E-05	2.38E-03	1.79E-02	4.04E-02	35	PDE3B,PDE4B,NT5C3A,MS4A2,CCR1,CCL5,CCR5,CMKLR1,PLEK,NSMAF,FLT1,GPR65,FPR2,FPR3,PPM1K,PHACTR4,PLCXD3,EIF2AK2,CX3CR1,CXCR2,PTPN22,ITGA1,CMYA5,ZEB2,ITK,JAK2,PTPRC,PTPRE,PTPRO,C3AR1,OPRM1,P2RY6,LPAR6,RPAP2,NCKAP1L
GO:0004888	MF	Transmembranesignaling receptor activity	5.06E-05	2.67E-03	2.01E-02	5.23E-02	57	IGSF6,MAS1,LILRB2,MC2R,EVI2A,TLR7,ADGRE2,MS4A2,FCER1G,FCGR1B,FCGR3A,CCL2,CCR1,CCR5,CMKLR1,FLT1,GPR65,FPR2,FPR3,SUCNR1,RPH3A,CLEC2D,IL2RA,IL2RG,PRLR,CX3CR1,IL7R,CXCR2,IL10RA,GABRE,GALR1,SPN,CYSLTR1,GPR82,IL18RAP,LILRB1,PTPRC,PTPRE,PTPRO,C3AR1,KLRD1,SHANK1,CYSLTR2,ABCC9,GRIA4,CBL,OPRM1,SHISA9,P2RX7,P2RY6,PLXNC1,LPAR6,TLR1,TLR3,TLR4,CD69,ADGRE1
GO:0005102	MF	Signaling receptor binding	9.23E-05	3.73E-03	2.80E-02	9.53E-02	69	A2M,PIK3AP1,LILRB2,CLEC7A,TAC4,BTN3A3,SEMA6D,PIK3CG,MICB,CXCL9,CCL2,CCL4,CCL5,FGF13,CCL8,FLT2,MMP13,APOL2,CXCL11,PLSCR1,NSMAF,UTS2B,WNT7A,FPR2,CXCL13,POU2F1,APOA2,IGF1,ISG15,CD226,TNFSF13B,OASL,PRKCB,FYB1,PROX1,TNFSF14,TNFSF10,INHBA,CXCL10,RAB8B,DAB2,ITGA1,LILRB1,RTP4,STAT1,NEDD4,JAK2,CCN5,PTPRC,PCSK1N,MICA,MARCHF1,KLRD1,SHANK1,DOCK2,TCF21,SH2B3,CBL,TF,BTN3A1,LGALS9,TGFBI,ACE2,P2RX7,PLXNC1,CD86,TLR1,TLR2,TLR4
GO:0098772	MF	Molecular function regulator	3.66E-04	1.02E-02	7.69E-02	3.78E-01	69	A2M,MAS1,CARD16,DTX3L,TAC4,SERPIN9,SEMA6D,SRGAP1,RASGRP3,CXCL9,CCL2,CCL4,CCL5,FGF13,CCL8,FLT2,CXCL11,ALOX5AP,NSMAF,FNIP2,WARS1,UTS2B,WNT7A,CXCL13,DOCK10,BIRC3,APOA2,PLEKHG2,IGF1,TNFSF13B,PHACTR4,PRKCB,ARHGFE3,EIF2AK2,PRLR,ADAP2,STARD8,TNFSF14,TNFSF10,INHBA,TAGAP,DOCK11,CXCL10,MCF2L2,NAIP,TBC1D8B,ZEB2,ELMO1,TIAM2,ASAP1,NEDD4,CCN5,SERPING1,PCSK1N,ARHGAP25,PARP9,DOCK2,DOCK8,CASP1,ABCC9,RGS1,LGALS9,CCND2,RGS18,TRAPPC3L,TLR1,TLR3,TLR4,NCKAP1L
GO:0017111	MF	Nucleoside-triphosphatase activity	3.79E-04	1.03E-02	7.76E-02	3.92E-01	55	BRIP1,DDX58,PECAM1,ABCA9,SRGAP1,RASGRP3,CCL2,CCL4,CCL5,CCL8,DDX60,PLSCR1,FNIP2,GPR65,SEPTIN4,DDX60,CXCL13,DOCK10,RNF213,XRCC2,IFIT1,RAP2C,SPATA5,MX1,MX2,ADAP2,ATP6V1B2,STARD8,MCM8,TAGAP,DOCK11,RAB8B,GBP1,GBP2,GIMAP7,SLC30A3,TBC1D8B,TIAM2,ASAP1,HELB,CDKL5,GBP4,GBP5,ARHGAP25,DOCK2,RAD51D,DOCK8,SMCHD1,ABCC9,RGS1,RGS18,PLXNC1,ENTPD1,GNB4,NCKAP1L

Biological process (BP), cellular component (CC) and molecular functions (MF).

Table 5

The enriched GO terms of the down regulated differentially expressed genes.

GO ID	Category	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0019083	BP	Viral transcription	2.08E-45	1.53E-42	1.40E-41	1.07E-41	57	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,RPL36,POLR2I,POLR2J,POLR2L,RPL10A,JUN,TRIM8,TRIM28,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0006605	BP	Protein targeting	3.09E-33	1.23E-30	1.12E-29	1.59E-29	67	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,ERBB2,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,ZDHC1,CLU,TOMM7,RPL36,CIB1,SLC25A6,GIPC1,ROMO1,RPL10A,TSPO,SEC61B,SLC27A2,ATP5F1,FIS1,NDUFA13,TIMM13,UBL5,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0072594	BP	Establishment of protein localization to organelle	1.16E-28	4.29E-26	3.91E-25	6.00E-25	71	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,LRWD1,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,PHB2,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,CLU,TOMM7,RPL36,SLC25A6,ROMO1,BAD,RUVBL2,RPL10A,TSPO,SEC61B,PTTG1IP,SLC27A2,ATP5F1,FIS1,PKIG,NDUFA13,TIMM13,UBL5,LMNA,TRIM28,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0033365	BP	Protein localization to organelle	3.44E-26	1.05E-23	9.54E-23	1.78E-22	105	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,LRWD1,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,PHB2,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,IPT43,TUBB4B,ZMYND10,CLU,PIN1,CCDC151,RSPH9,TOMM7,RPL36,SLC25A6,NOP53,LRRC46,ARL3,MAPK15,LAMTOR4,SSNA1,B9D1,CROCC,CFAP157,IFT140,ROMO1,BAD,DAG1,RUVBL2,DNAL1,RPL10A,CFAP100,RSPH1,TSPO,TRIM8,SEC61B,DYNLRB2,SGSM3,PTTG1IP,SLC27A2,BICD2,IFT27,TCTEX1D2,ATP5F1,DYNC2I2,CFAP73,DVL1,FIS1,CCDC39,PKIG,NDUFA13,TIMM13,UBL5,LMNA,TRIM28,DNAI2,CD81,C11orf97,RPL35,RPL13A,RPL3,CFAP53,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0016032	BP	Viral process	2.59E-25	7.05E-23	6.43E-22	1.34E-21	79	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FKBP8,HSPA1A,HSPA1B,RPL36,EIF4H,SLC25A6,POLR2I,POLR2J,POLR2L,SIVA1,GADD45GIP1,SLC20A2,SLPI,CTNNB1,PSMA7,BAD,DAG1,KEAP1,ITGB5,RPL10A,JUN,TRIM8,KRT8,KRT19,UBXN1,P4HB,TRIM28,EPHA2,TSPAN7,CD81,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0044403	BP	Symbiotic process	3.96E-24	1.01E-21	9.20E-21	2.05E-20	80	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FKBP8,HSPA1A,HSPA1B,RPL36,EIF4H,SLC25A6,POLR2I,POLR2J,POLR2L,SIVA1,GADD45GIP1,SLC20A2,SLPI,CTNNB1,PSMA7,BAD,DAG1,KEAP1,ITGB5,RPL10A,JUN,TRIM8,KRT8,KRT19,GPX1,UBXN1,P4HB,TRIM28,EPHA2,TSPAN7,CD81,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0006886	BP	Intracellular protein transport	4.10E-24	1.01E-21	9.20E-21	2.12E-20	107	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,ERBB2,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,PHB2,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,

(continued on next page)

Table 5 (continued)

GO ID	Category	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0006518	BP	Peptide metabolic process	6.76E-24	1.59E-21	1.45E-20	3.49E-20	81	RPS29,ZDHHHC1,IFT43,TUBB4B,ZMYND10,CLU,CCDC151,RSPH9,TOMM7,RPL36,CIB1,SLC25A6,ARF5,RHOB,LRRC46,ARL3,MAPK15,SSNA1,B9D1,TMED9,CROCC,CFAP157,GIPC1,IFT140,ROMO1,SELENOS,DNALI1,RPL10A,CFAP100,RSPH1,TSPO,SEC61B,DYNLRB2,ERP29,UNC93B1,SGSM3,PTTG1IP,SLC27A2,IFT27,TCTEX1D2,ATP5IF1,DYNC2I2,CFAP73,FIS1,OAZ1,CCDC39,PKIG,NDUFA13,TIMM13,UBL5,LMNA,TRIM28,DNAI2,CD81,C11orf97,RPL35,SYTL1,RPL13A,RPL3,CFAP53,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0009057	BP	Macromolecule catabolic process	6.81E-17	9.77E-15	8.92E-14	3.52E-13	90	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,ERBB2,RPL32,RPL34,RPL37,RPL39,LARP6,RPL36A,RPLP0,RPLP1,RPLP2,CES1,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,TUFM,CIRBP,FAU,CLU,TMA7,PIN1,VARIS1,RPL36,COA3,EIF4H,GADD45GIP1,IGFBP5,MRPL14,CTSH,EIF3CL,RPL10A,SEC61B,QARS1,KRT17,MKNK2,GPX1,GPX4,GSTA2,GSTP1,EEF1D,EEF1G,EEF2,EFNA1,HAGH,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0034622	BP	Cellular protein-containing complex assembly	4.77E-08	3.42E-06	3.12E-05	2.46E-04	63	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,STUB1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,HSPBP1,RPS27,RPS28,RPS29,CIRBP,CLU,PIN1,SCGB1A1,FBXW5,DNAJB2,HSPA1A,HSPA1B,SDC1,RPL36,NOP53,ANAPC11,TRIM3,UBXN11,MAPK15,ECRG4,CTNNB1,CTSD,CTSH,GIPC1,SELENOS,PSMA7,KEAP1,RPL10A,ATG4B,IER3,SEC61B,SGSM3,PTTG1IP,ATP5IF1,GPX1,UBXN6,DVL1,OAZ1,UBXN1,NDUFA13,EFNA1,CD81,RPL35,RPL13A,CDC34,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0007010	BP	Cytoskeleton organization	7.38E-05	2.93E-03	2.68E-02	3.81E-01	65	RPLP0,STUB1,RPS2,RPS3,RPS5,RPS10,RPS14,RPS15,RPS19,RPS27,RPS28,ECSIT,GTF3C5,CIRBP,MID1IP1,ZMYND10,CLU,PIN1,HSPA1A,HSPA1B,CCDC151,TRAF7,COA3,EIF4H,NOP53,ARPC1A,NDUFAF3,NHP2,DHX30,MAPK15,TPPP3,CTNNB1,SNRBP,SNRPD2,NDUFA2,TUBGCP2,NDUFAB1,NDUFB2,RUVBL2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,EIF3CL,DNALI1,CFAP100,TXNL4A,VILL,SURF1,C9orf24,TBCA,DMAC1,CFAP73,GPX4,CCDC39,NDUFA13,DNAI2,H1SMIM22,MAP9,RPS3,TUBB2A,IFT43,TUBB4B,MID1IP1,ZMYND10,PIN1,CCDC78,FBXW5,HSPA1A,HSPA1B,CCDC151,RSPH9,PLXNB1,SPEF1,CIB1,ARPC1A,ID1,PDLIM4,RHOB,LRRC46,ARL3,CELSR1,MAPK15,GAS2L2,SSNA1,B9D1,TPPP3,CTNNB1,CROCC,CFAP157,IFT140,EPPK1,DAG1,TUBGCP2,ARHGEF17,ITGB5,DNALI1,PTK7,CFAP100,RSPH1,VILL,DYNLRB2,SGSM3,BICD2,IFT27,KRT5,TCTEX1D2,KRT8,KRT10,KRT15,KRT17,DYNC2I2,KRT19,CFAP73,DVL1,CCDC39,ACTR1B,LMNA,DNAI2,C11orf97,TACSTD2,CFAP53
GO:0043067	BP	Regulation of programmed cell death	9.44E-05	3.71E-03	3.39E-02	4.88E-01	69	RPL26,ERBB2,RPS3,RPS3A,MAZ,RPS7,PHB2,RPS29,KLF4,CITED2,CLU,PIN1,MIF,FKBP8,PRDX5,HSPA1A,HSPA1B,TRAF7,MAPK8IP1,CIB1,NOP53,GDF15,APBB1,ID1,POR,SIVA1,CLDN7,NIBAN2,NAA38,RHOB,TRAF4,CCN1,CTNNB1,CTSD,CTSH,GADD45B,SELENOS,TMEM219,BAD,ARHGEF17,JUN,TXNDC5,PTPRF,IER3,DHCR24,TSPO,ERP29,NME2,QARS1,RGL2,PTTG1IP,ATP5IF1,DUSP1,GPX1,SOC3,GPX4,FIS1,PRDX2,LGALS3,GSTP1,NDUFA13,EFNA1,LMNA,P4HB,ATAD3A,STEAP3,LRP5,CDC34,EPCAM
GO:0005840	CC	Ribosome	3.69E-35	8.56E-33	6.09E-32	2.57E-32	57	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,RPL36,GADD45GIP1,MRPL14,NDUFAB1,EIF3CL,RPL10A,EEF2,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0005740	CC	Mitochondrial envelope	7.73E-15	3.59E-13	2.55E-12	5.38E-12	59	RPS3,COQ8B,PHB2,TST,ECSIT,SLC25A25,TUFM,COX5A,CLU,FDXR,UQCRC1,SLC25A29,FKBP8,STOML2,MAPK8IP1,TOMM7,COA3,SLC25A6,COX4I1,COX5B,

(continued on next page)

Table 5 (continued)

GO ID	Category	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
GO:0005739	CC	Mitochondrion	1.06E-12	3.36E-11	2.39E-10	7.39E-10	94	COX6A1,NDUF3,COX7B,PPOX,REXO2,MRPL14,ASL, UQCRQ,CYC1,ATP5F1E,ATP5ME,ROMO1,SMDT1, CYP27A1,BAD,NDUFA2,BLOC1S1,NDUFA4,ECI1, NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1, NDUFV1,NDUFS6,SURF1,TSPO,UQCR11,NME2, DMAC1,GPX4,FIS1,LGALS3,NDUFA13,TIMM13, ATAD3A,COQ4,CHCHD2
GO:0031967	CC	Organelle envelope	2.61E-10	7.81E-09	5.57E-08	1.81E-07	68	RPL34,RPS3,ACO2,COQ8B,RPS14,RPS15A,PHB2,TST, ECSIT,SLC25A25,TUFM,CKB,TSTD1,COX5A,CLU,PIN1, FDXR,UQCRC1,SLC25A29,FKBP8,PRDX5,PYCR2, HSPA1A,HSPA1B,HSPA2,VAR1,STOML2,MAPK8IP1, TOMM7,COA3,COMT,SLC25A6,ALKBH7,COX4I1, COX5B,AGR2,COX6A1,NDUFAF3,COX7B,POR,SIVA1, GADD45GIP1,PPOX,DHX30,REXO2,MRPL14,ASL, UQCRQ,CTSD,CYB5R1,CYC1,ATP5F1E,ATP5ME, ROMO1,SMDT1,CYP27A1,BAD,NDUFA2,BLOC1S1, NDUFA4,ECI1,NDUFA1,NDUFB2,NDUFB7,NDUFB10, NDUFC1,NDUFC1,NDUFC1,NDUFC1,NDUFC1,NDUFC1, SURF1,TSPO,UQCR11,NME2,QARS1,DMAC1,SLC27A2, KRT5,ATP5F1,GPX1,GPX4,FIS1,PRDX2,LGALS3, GSTP1,NDUFA13,TIMM13,ATAD3A,COQ4,CHCHD2, LRP5,HAGH
GO:0015630	CC	Microtubule cytoskeleton	1.21E-07	2.56E-06	1.82E-05	8.45E-05	64	RPS3,COQ8B,PHB2,TST,ECSIT,SLC25A25,TUFM, S100A6,COX5A,CLU,FDXR,SCGB1A1,UQCRC1, SLC25A29,FKBP8,DNAJB2,STOML2,MAPK8IP1, TOMM7,COA3,SLC25A6,COX4I1,COX5B,COX6A1, NDUFAF3,COX7B,PPOX,REXO2,MRPL14,ASL,UQCRQ, CTNNB1,CYC1,ATP5F1E,ATP5ME,ROMO1,SMDT1, CYP27A1,BAD,GCHFR,NDUFA2,BLOC1S1,NDUFA4, ECI1,NDUFA1,NDUFB2,NDUFB7,NDUFB10,NDUFC1, NDUFV1,NDUFS6,TXNL4A,SURF1,TSPO,UQCR11, NME2,DMAC1,BICD2,GPX4,FIS1,FAM3B,LGALS3, NDUFA13,TIMM13,LMNA,ATAD3A,COQ4,CHCHD2
GO:0099512	CC	Supramolecular fiber	3.32E-05	5.49E-04	3.91E-03	2.31E-02	61	MAP9,AAMP,LRWD1,RPS3,RPS7,TUBB2A,ENKD1, IFT43,TUBB4B,MID1IP1,ZMYND10,CCDC78,MLF1,AK1, CCDC96,WDR13,HSPA1A,HSPA1B,TADA3,HSPA2, CCDC151,RSPH9,FAM183A,SPEF1,CIB1,SEPTIN5,ID1, ARL3,MAPK15,PPP4C,GAS2L2,SSNA1,B9D1,TPPP3, CTNNB1,CROCC,TCTEX1D4,CTSH,CFAP157,IFT140, SELENOS,LRRC45,KEAP1,TUBGCP2,SPPL2B,RUVBL2, DNALI1,CFAP100,MTB,RSPH1,DYNLRB2,C9orf24,TBCA, BICD2,IFT27,TCTEX1D2,DYNC2I2,CFAP73,UBXN6, DVL1,CCDC39,ACTR1B,DNAI2,C11orf97
GO:0099513	CC	Polymeric cytoskeletal fiber	4.94E-05	7.47E-04	5.32E-03	3.44E-02	54	MAP9,ERBB2,STUB1,TUBB2A,ENKD1,TUBB4B, MID1IP1,AK1,CCDC151,RSPH9,EPS8L2,SPEF1,CIB1, SEPTIN5,APBB1,AQP5,SLC2A1,PDLIM4,ARL3,MAPK15, GAS2L2,TPPP3,CTNNB1,TCTEX1D4,CTSH,AHNAK2, GIP1,IFT140,SELENOS,EPPK1,MYL6,DAG1,KEAP1, ITGA3,TUBGCP2,DNALI1,CFAP100,RSPH1,DYNLRB2, NME2,TBCA,DDR1,IFT27,KRT5,TCTEX1D2,KRT8, KRT10,KRT15,KRT17,DYNC2I2,KRT19,CFAP73,DVL1, CCDC39,LMNA,DNAI2,SYTL1,RPL4,RPL6,RPL7,RPL15
GO:0005929	CC	Cilium	2.00E-04	2.59E-03	1.84E-02	1.39E-01	37	MAP9,ERBB2,TUBB2A,ENKD1,TUBB4B,MID1IP1,AK1, CCDC151,RSPH9,EPS8L2,SPEF1,CIB1,SEPTIN5,APBB1, AQP5,PDLIM4,ARL3,MAPK15,GAS2L2,TPPP3,CTNNB1, TCTEX1D4,CTSH,GIP1,IFT140,SELENOS,EPPK1, MYL6,DAG1,KEAP1,ITGA3,TUBGCP2,DNALI1, CFAP100,RSPH1,DYNLRB2,NME2,TBCA,DDR1,IFT27, KRT5,TCTEX1D2,KRT8,KRT10,KRT15,KRT17,DYNC2I2, KRT19,CFAP73,DVL1,CCDC39,LMNA,DNAI2,SYTL1
GO:0098796	CC	Membrane protein complex	7.06E-04	7.34E-03	5.23E-02	4.91E-01	50	IFT43,CFAP65,TUBB4B,ZMYND10,MLF1,AK1,STOML3, CCDC151,RSPH9,FAM183A,SPEF1,PPEF2,LRRC46, ARL3,MAPK15,SSNA1,B9D1,CROCC,TCTEX1D4,CTSH, CFAP157,IFT140,DNALI1,CFAP100,RSPH1,DYNLRB2, GNA11,SGSM3,IFT27,TCTEX1D2,DYNC2I2,CFAP73, CCDC39,ROPNL1,DNAI2,C11orf97,CFAP53
GO:0030141	CC	Secretory granule			2.14E-01	1.00E+00	34	COPE,COX5A,UQCRC1,HSPA2,STOML2,TOMM7,COA3, SLC25A6,COX4I1,COX6A1,COX7B,CLDN4,LAMTOR4, UQCRQ,CTNNB1,CYC1,ATP5F1E,ATP5ME,ROMO1, ATP6V0B,SELENOS,SMDT1,DAG1,NDUFA2,NDUFA4, ITGA3,SSR4,NDUFA1,NDUFB2,NDUFB7,ITGB4, NDUFB10,NDUFC1,ITGB5,DDOST,NDUFC1,NDUFC1, GJB3,SEC61B,GNA11,GNB2,DMAC1,KRT8,KRT19, SOCS3,DVL1,UBXN1,PIGQ,NDUFA13,LRP5

(continued on next page)

Table 5 (continued)

GO ID	Category	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
			3.76E-03	3.00E-02				MAN2B1,LRG1,TUBB4B,CLU,MIF,SCGB1A1,ALDH3B1,HSPA1A,HSPA1B,TMEM190,AGPAT2,SLPI,ECRG4,CSTB,TCTEX1D4,CTSD,CTSH,CYB5R1,PROS1,DDOST,TXNDC5,MAGED2,PTPRN2,BSG,NME2,BAIAP3,SLC27A2,LGALS3,TFF3,GSTP1,ACTR1B,EEF2,CD9,CD59
GO:1902494	CC	Catalytic complex	5.53E-03	3.74E-02	2.66E-01	1.00E+00	52	STUB1,FBXW5,AK1,UQCRC1,DNAJB2,TADA3,RSPH9,TRAF7,POLR21,POLR2J,POLR2L,ANAPC11,NAAP38,NHP2,PPP4C,UQCRCQ,TCTEX1D4,SNRPB,CTSH,SNRPD2,CYC1,PSMA7,NDUFA2,NDUFA4,KEAP1,NDUFAB1,NDUFB2,RUVBL2,NDUFB7,NDUFB10,NDUFC1,DDOST,NDUFV1,NDUFS6,DNALI1,RSPH1,DPY30,DYNLRB2,GNA11,GNB2,DMAC1,ELOB,IFT27,TCTEX1D2,DYNC2I2,SOCS3,CCDC39,PIGQ,NDUFA13,P4HB,DNAI2,CBX7
GO:0003735	MF	Structural constituent of ribosome	2.35E-38	2.35E-35	1.76E-34	2.35E-35	53	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,FAU,RPL36,MRPL14,RPL10A,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0005198	MF	Structural molecule activity	3.93E-25	1.97E-22	1.47E-21	3.93E-22	77	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,RPL36A,RPLP0,RPLP1,RPLP2,RPS2,RPS3,RPS3A,RPS5,COPE,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,RPS29,TUBB2A,TUBB4B,FAU,NTN1,RPL36,SEPTIN5,CRELD2,CLDN4,CLDN3,CLDN7,MRPL14,IGFBP7,CCN1,CROCC,EPPK1,MYL6,DAG1,RPL10A,VILL,COL21A1,KRT5,KRT10,KRT15,KRT17,KRT19,LAMB2,LAMC2,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0016651	MF	Oxidoreductase activity, acting on NAD(P)H	9.84E-07	9.83E-05	7.36E-04	9.83E-04	15	ECSIT,POR,CYB5R1,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,NDUFS6,TXNDC17,CBR1,NDUFA13
GO:0003723	MF	RNA binding	1.34E-06	1.17E-04	8.76E-04	1.34E-03	84	RPL21,RPL26,RPL27,RPL27A,RPL29,RPL31,RPL32,RPL34,RPL37,RPL39,LARP6,RPL36A,RPLP0,RPS2,RPS3,RPS3A,RPS5,MAZ,SELENOH,RPS7,RPS8,RPS9,RPS10,RPS12,RPS13,RPS14,RPS15,RPS15A,RPS16,RPS17,RPS18,RPS19,RPS21,RPS27,RPS28,TST,TUFM,CFAP65,CIRBP,ARL6IP4,TUBB4B,FAU,HSPA1A,HSPA1B,RPL36,EIF4H,NOP53,NHP2,DHX30,MRPL14,SLPI,CSTB,SNRPB,SNRPD2,EDF1,EPPK1,EIF3CL,RPL10A,JUN,SEC61B,QARS1,TBCA,LGALS3,EEF1D,EEF1G,EEF2,P4HB,TRIM28,H1-4,CBX7,RPL35,RPL13A,RPL3,RPL4,RPL6,RPL7,RPL7A,RPL8,RPL9,RPL13,RPL15,RPL18,RPL18A,RPL19
GO:0016491	MF	Oxidoreductase activity	2.29E-06	1.53E-04	1.14E-03	2.29E-03	50	PHB2,ECSIT,COX5A,GRHPR,FDXR,MIF,UQCRC1,ALDH3A1,DEGS2,ALDH3B1,PRDX5,PCYR2,ALKBH7,COX4I1,COX5B,COX6A1,COX7B,POR,PPOX,P4HTM,UQCRCQ,CYB5R1,CYB561,CYC1,CYP4B1,CYP27A1,NDUFA2,NDUFA4,NDUFAB1,NDUFB2,NDUFB7,NDUFB10,NDUFC1,NDUFV1,DUS1L,NDUFS6,IERS3,SURF1,DHCR24,UQCRC1,SELENBP1,GPX1,GPX4,TXNDC17,PRDX2,CBR1,GSTP1,NDUFA13,P4HB,STEAP3
GO:0050839	MF	Cell adhesion molecule binding	1.28E-05	7.51E-04	5.62E-03	1.28E-02	31	RPL29,RPL34,RPS2,TAGLN2,HSPA1A,EPSS8L2,EIF4H,CLDN7,NIBAN2,CCN1,CTNNB1,GIPC1,ITGA3,ITGB4,ITGB5,PTPRF,BSG,LAMB2,EEF1D,EEF1G,EEF2,CD9,P4HB,EPHA2,CD81,CD151,TACSTD2,EPCAM,RPL6,RPL7A,RPL15
GO:0044877	MF	Protein-containing complex binding	1.19E-04	5.65E-03	4.23E-02	1.19E-01	57	RPLP1,GTPBP6,RPS2,RPS3,CLU,MIF,UQCRC1,DNAJB2,EPSS8L2,EIF4H,ARPC1A,APBB1,ID1,GADD45GIP1,PPP4C,CCN1,GAS2L2,CTNNB1,SNRPB,CTSH,SNRPD2,PROS1,ATP5ME,EDF1,EPPK1,NDUFA4,ITGA3,RUVBL2,ITGB4,ITGB5,CFAP100,PTPRF,VILL,SEC61B,GNA11,GNB2,NME2,BICD2,ELOB,DDR1,KRT8,ATP5IF1,KRT19,CFAP73,LAMB2,FIS1,UBXN1,LGALS3,EEF2,CD9,P4HB,H1-4,H3-3A,CD81,CD151,RPL35,EPCAM
GO:0045296	MF	Cadherin binding	4.26E-04	1.93E-02	1.45E-01	4.25E-01	20	RPL29,RPL34,RPS2,TAGLN2,HSPA1A,EPSS8L2,EIF4H,NIBAN2,CTNNB1,GIPC1,BSG,EEF1D,EEF1G,EEF2,EPHA2,TACSTD2,EPCAM,RPL6,RPL7A,RPL15
GO:0016462	MF	Pyrophosphatase activity			1.00E+00	1.00E+00	44	

(continued on next page)

Table 5 (continued)

GO ID	Category	GO name	P Value	FDR B&H	FDR B&Y	Bonferroni	Gene count	Gene
			1.58E-01	4.43E-01				ERBB2,HSPBP1,RRAD,PLXNB2,TUBB2A,TUFM,TUBB4B,CLU,PIN1,DNAJB2,HSPA1A,HSPA1B,HSPA2,PLXNB1,SEPTIN5,DHX30,ARF5,RHOB,ARL3,ATP5F1E,GIPC1,ATP5ME,ATP6V0B,MYL6,RUVBL2,ITPA,DNALI1,CFAP100,JUN,PTPRN2,ATP2C2,DYNLRB2,ENPP5,GNA11,SGSM3,GNB2,IFT27,ATP5IF1,DYNC2I2,CFAP73,ARHGAP39,EEF2,EPHA2,DNAI2
GO:0030234	MF	Enzyme regulator activity	1.75E-01	4.60E-01	1.00E+00	1.00E+00	33	RPLP1,SERPINF1,RPS7,HSPBP1,KLF4,SCGB1A1,PRDX5,DNAJB2,PLXNB1,MAPK8IP1,CIB1,COX6A1,TRAF4,PPP4C,SPINT2,SLPI,CSTB,CTSH,PROS1,GIPC1,BAD,GCHFR,JUN,SGSM3,QARS1,ATP5IF1,SOC3,OAZ1,ARHGAP39,LGALS3,PKIG,GSTP1,PPP1R16A
GO:0008092	MF	Cytoskeletal protein binding	2.31E-01	5.05E-01	1.00E+00	1.00E+00	31	MAP9,LARP6,STUB1,RPS3,WDR54,S100A6,CLU,PIN1,HSPA2,MAPK8IP1,EPS8L2,SPEF1,ARPC1A,APBB1,CLSTN1,PDLIM4,ARL3,GAS2L2,TPPP3,CROCC,CFAP157,GIPC1,DAG1,TUBGCP2,VILL,C9orf24,TBCA,BICD2,KRT10,ACTR1B,EEF2

Biological process (BP), cellular component (CC) and molecular functions (MF).

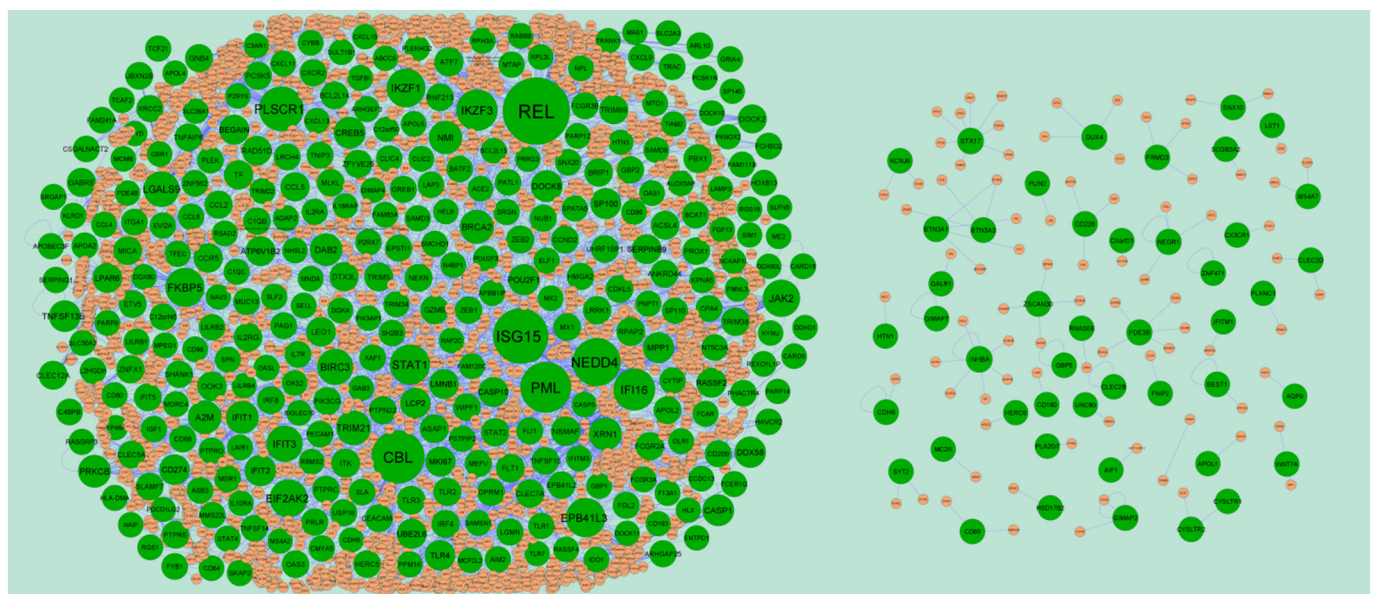


Fig. 5. Protein–protein interaction network of up-regulated genes. Green nodes denotes up-regulated genes. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

3.6. Construction of target genes - TF regulatory network

In order to explore the molecular mechanisms in SARS-CoV-2 infection further, target genes were predicted using the NetworkAnalyst database. A target genes - TF regulatory network for up-regulated genes was constructed, which consisted of 667 nodes and 8759 edges, including 481 target genes and 186 TFs (Fig. 13). The TRIM5 can be targeted by 229 TFs (ex; SPI1), GPRIN3 can be targeted by 208 TFs (ex; SOX2), DDX60L can be targeted by 193 TFs (ex; STAT3), CYSLTR1 can be targeted by 177 TFs (ex; NANOG) and SUCNR1 can be targeted by 177 TFs (ex; RUNX1) are listed in Table 8. Pathway and GO enrichment analysis for the up-regulated genes in this target genes - TF regulatory network revealed that these target genes were significantly enriched in interferon signaling, nucleoside-triphosphatase activity, neuroactive ligand-receptor interaction and GPCR ligand binding. A target genes - TF regulatory network for down-regulated genes was constructed, which

consisted of 681 nodes and 190 edges, including 491 target genes and 186 TFs (Fig. 14). The RPLP0 can be targeted by 304 TFs (ex; MYC), IGFBP7 can be targeted by 255 TFs (ex; SPI1), LMNA can be targeted by 225 TFs (ex; E2F1), CD82 can be targeted by 224 TFs (ex; SOX2) and SERPINF1 can be targeted by 218 TFs (ex; EGR1) are listed in Table 8. Pathway and GO enrichment analysis for the down-regulated genes in this target genes - TF regulatory network revealed that these target genes were significantly enriched in Ribosome, Cellular responses to stress, Metabolism of proteins, Direct p53 effectors and Genes encoding enzymes and their regulators involved in the remodeling of the extracellular matrix.

3.7. Receiver operating characteristic (ROC) curve analysis of hub genes

Based on the data of GSE152075, the patients were divided into the SARS-CoV-2 infection group and the negative control group. The ROC

Table 6
Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Up	REL	201	0.137865	13660696	0.290532	1.02E-04
Up	ISG15	153	0.147569	7318980	0.305511	0.002322
Up	CBL	144	0.109945	16119694	0.293141	0.005494
Up	PML	134	0.130861	10150062	0.303636	0.002313
Up	NEDD4	123	0.084257	7748818	0.284805	1.38E-04
Up	PLSCR1	108	0.079049	4626076	0.283445	8.65E-04
Up	IFI16	92	0.05713	3329890	0.265685	0.001248
Up	IKZF3	89	0.047662	6473464	0.269012	0.003475
Up	STAT1	83	0.08618	6477080	0.308572	0.012654
Up	EPB41L3	78	0.045721	5462282	0.250172	0.001998
Up	FKBP5	77	0.042455	4169942	0.247705	0
Up	IKZF1	75	0.037727	3451372	0.263243	0.005327
Up	EIF2AK2	71	0.041073	3111120	0.279825	0.002558
Up	JAK2	67	0.058008	6696136	0.287843	0.010577
Up	IFIT3	61	0.0308	2085062	0.270662	0.037989
Up	BIRC3	60	0.025398	4304536	0.257634	6.05E-04
Up	LGALS9	58	0.03928	3599082	0.23474	0
Up	TRIM21	53	0.029891	2209668	0.272742	0.003922
Up	BRCA2	49	0.026221	3391544	0.259189	0
Up	A2M	46	0.022839	1402268	0.251541	0.011594
Up	NMI	45	0.020646	2148768	0.252065	0
Up	XRN1	43	0.018956	1781826	0.241458	0
Up	IFIT1	42	0.011327	655198	0.251328	0.053426
Up	PRKCB	42	0.028214	2251900	0.265145	0.001282
Up	DAB2	41	0.019739	2843192	0.252592	0
Up	CREB5	37	0.014872	1521346	0.241423	0.007508
Up	DOCK8	37	0.018961	1287642	0.236731	0
Up	CASP1	36	0.02293	1346102	0.254046	0.010695
Up	TNFSF13B	36	0.026134	2522062	0.209268	0
Up	IFIT2	35	0.00803	457764	0.250364	0.07395
Up	DDX58	34	0.018267	1066706	0.268393	0.012097
Up	POU2F1	33	0.015117	1539214	0.25267	0
Up	SP100	32	0.014873	642820	0.249732	0.013793
Up	MPP1	32	0.0183	1323394	0.240179	0
Up	CD274	30	0.01597	1196802	0.216011	0
Up	TLR4	29	0.010954	1948000	0.235655	0.005698
Up	LCP2	29	0.014433	1897600	0.270461	0.061576
Up	UBE2L6	27	0.01064	521790	0.253691	0
Up	MKI67	27	0.015572	1225298	0.255577	0.008547
Up	BEGAIN	27	0.010807	1028758	0.227748	0
Up	LMNB1	26	0.013549	656640	0.250749	0
Up	SERPINB9	26	0.013806	576582	0.233481	0.003077
Up	CASP10	26	0.008537	762770	0.23405	0.028986
Up	ATP6V1B2	26	0.013048	966760	0.233531	0
Up	LPAR6	26	0.025973	2905084	0.203199	0
Up	RASSF2	26	0.010682	1330660	0.238548	0
Up	NSMAF	25	0.011398	679800	0.24304	0
Up	RAD51D	25	0.014762	970054	0.232682	0.023333
Up	LEO1	25	0.011689	1299496	0.228402	0
Up	CCR5	24	0.014185	700960	0.244167	0.025974
Up	DOK3	24	0.010838	1329198	0.237645	0
Up	TF	23	0.012822	1378352	0.244039	0
Up	CCL5	23	0.010149	870362	0.234673	0
Up	DTX3L	23	0.007854	518468	0.254363	0.004762
Up	ATF7	22	0.009736	514296	0.222836	0.021645
Up	GABRE	22	0.012275	1655310	0.15297	0
Up	TRIM69	22	0.010979	1049468	0.213664	0
Up	DOCK2	21	0.008952	454266	0.243366	0.019048
Up	ASAP1	21	0.004205	566588	0.257208	0.066667
Up	ITK	21	0.006319	800974	0.258798	0.035088
Up	CLEC12A	21	0.01128	1128084	0.167453	0
Up	TRIM5	21	0.004804	670672	0.230791	0.023392
Up	TLR3	20	0.006434	933678	0.244844	0
Up	ACSL4	20	0.009784	577008	0.218132	0
Up	IL2RG	20	0.012929	730352	0.251618	0.036842
Up	CCR1	20	0.007466	451584	0.213748	0.005263
Up	FLT1	20	0.009387	506100	0.260887	0.042105
Up	PBX1	20	0.010237	856804	0.206319	0
Up	MICA	20	0.009274	557130	0.213734	0
Up	RPAP2	20	0.008229	709118	0.209456	0
Up	GZMB	19	0.0077	502452	0.238199	0.023392

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Up	TRIM38	18	0.006837	652828	0.232865	0
Up	CLEC7A	18	0.010071	460878	0.206541	0
Up	FCGR2A	18	0.015917	2214972	0.230351	0
Up	STAT2	18	0.005442	304414	0.255998	0.058333
Up	LRRK1	18	0.006516	835296	0.246956	0
Up	BRIP1	18	0.005883	813844	0.216713	0
Up	ZNFX1	18	0.009085	850748	0.218001	0
Up	TLR2	17	0.011044	990392	0.235129	0.014706
Up	CCL2	17	0.005828	380878	0.227796	0.066667
Up	ZFYVE26	17	0.005923	454010	0.220058	0
Up	ELMO1	17	0.007412	425934	0.21803	0.007353
Up	ZEB2	16	0.004758	674082	0.223187	0
Up	IRF4	16	0.005995	935012	0.206632	0
Up	ANKRD44	16	0.006884	647832	0.220519	0
Up	PCSK5	16	0.004466	469830	0.214323	0
Up	GNB4	16	0.008254	729946	0.197556	0
Up	IFIT5	15	0.005533	258136	0.247386	0.133333
Up	WIPF1	15	0.0058	804922	0.233581	0
Up	PTPN22	15	0.004865	323084	0.261409	0.102564
Up	CDKL5	15	0.005939	736684	0.233481	0
Up	CEACAM1	15	0.003737	381468	0.230254	0
Up	IRF8	15	0.007106	423282	0.234403	0
Up	PTPRE	15	0.008803	1109904	0.236303	0
Up	OPRM1	15	0.005938	435176	0.226202	0
Up	ETV5	15	0.00704	481906	0.22837	0
Up	PIK3CG	15	0.003972	487864	0.225998	0
Up	NEXN	15	0.002702	479126	0.217667	0
Up	APOL2	15	0.012524	816950	0.198855	0
Up	BCL2L14	15	0.006496	502850	0.199572	0
Up	ZBP1	15	0.004372	505018	0.216728	0
Up	TNFAIP6	14	0.007056	342392	0.215469	0
Up	EPB41L2	14	0.00619	513312	0.230807	0.065934
Up	MX1	14	0.005674	356826	0.252748	0
Up	HERC5	14	0.005719	223546	0.238373	0.010989
Up	PTPRC	14	0.005048	781038	0.233148	0
Up	CCND2	14	0.003842	469824	0.218717	0
Up	TNFSF10	14	0.003062	198482	0.210428	0.075758
Up	RNF213	14	0.008838	370994	0.24584	0.010989
Up	UBXN2B	14	0.007949	268840	0.197114	0
Up	UHRF1BP1	14	0.006364	515798	0.211972	0
Up	MLKL	14	0.005612	429344	0.222094	0
Up	SLAMF7	14	0.005187	468840	0.182351	0
Up	CLEC5A	14	0.007404	339152	0.192217	0
Up	PROX1	14	0.006294	456906	0.215298	0
Up	OAS3	14	0.002657	400866	0.211711	0
Up	CIQB	13	0.00591	426604	0.230726	0.038462
Up	ZEB1	13	0.003623	369232	0.234017	0
Up	SHANK1	13	0.00429	154908	0.239668	0.018182
Up	HMG2A	13	0.003891	458618	0.227844	0
Up	MEFV	12	0.002924	195774	0.23496	0.044444
Up	PRLR	12	0.002308	112734	0.242157	0.066667
Up	CXCR2	12	0.004494	235342	0.213762	0
Up	GBP2	12	0.005286	350706	0.216512	0
Up	BCAT1	12	0.005277	291946	0.201767	0
Up	XRCC2	11	0.002369	144266	0.204459	0.090909
Up	FCGR3B	11	0.004371	316674	0.197723	0
Up	USP18	11	0.003914	171776	0.243439	0
Up	LGMN	11	0.005815	250442	0.242877	0
Up	CD68	11	0.005068	386752	0.201382	0
Up	ARHGAP25	11	0.005536	283768	0.178503	0
Up	FGL2	11	0.004362	430858	0.197341	0
Up	GREB1	11	0.00231	203046	0.221311	0
Up	NUB1	11	0.003475	300352	0.215711	0
Up	EPSTI1	11	0.002642	207212	0.227431	0
Up	LRCH4	10	0.004851	491724	0.199414	0
Up	PAG1	10	0.004129	600934	0.223737	0
Up	FLI1	10	0.002249	257778	0.21771	0
Up	TNIP3	10	0.003164	198138	0.221656	0
Up	MUC13	10	0.003494	369682	0.219083	0
Up	CD209	10	0.004284	229124	0.168734	0
Up	FYB1	9	0.003223	327562	0.234268	0.083333
Up	TNFSF14	9	0.001477	190202	0.202833	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Up	FCHSD2	9	0.003345	180210	0.215426	0
Up	TRAC	9	0.004895	685480	0.120276	0
Up	APOA2	9	0.003463	244196	0.21393	0
Up	PECAM1	9	0.001934	273532	0.233615	0
Up	IL7R	9	0.001751	277482	0.234994	0.083333
Up	C4BPB	9	0.004895	318120	0.142496	0
Up	MSR1	9	0.004019	268964	0.21055	0
Up	SLA	9	0.00137	80350	0.246359	0.166667
Up	ITGA1	9	0.004005	234500	0.21156	0
Up	XAF1	9	0.004108	264466	0.242355	0.027778
Up	ZNF562	9	0.003714	157732	0.189111	0
Up	PHACTR4	9	0.00294	333024	0.219688	0
Up	C12orf45	9	0.003392	245266	0.2046	0
Up	ARL10	9	0.004873	312984	0.200074	0
Up	CPA4	9	0.003477	217192	0.194172	0
Up	LAP3	8	0.003719	177004	0.24795	0
Up	INHBA	8	1	30	1	0
Up	PLEK	8	0.00327	205554	0.194114	0
Up	HAVCR2	8	0.00138	211194	0.229752	0
Up	STX17	8	1	56	1	0
Up	CXCL9	8	0.003198	271762	0.201655	0
Up	PTPRO	8	0.003061	266610	0.189429	0
Up	SNX20	8	0.00353	359544	0.18507	0
Up	PATL1	8	0.001907	137140	0.223676	0
Up	BATF2	8	0.00263	330350	0.226484	0
Up	LILRB2	8	0.005018	387814	0.21379	0
Up	CSGALNACT2	8	0.004249	294170	0.156325	0
Up	FAM241A	8	0.003327	266862	0.147085	0
Up	NT5C3A	8	0.003167	311624	0.194195	0
Up	P2RX7	8	0.004658	509032	0.229525	0
Up	SH2B3	8	6.80E-04	214524	0.24333	0
Up	ASB3	8	0.002646	458470	0.198553	0
Up	SMCHD1	7	0.002641	233002	0.22702	0
Up	TLR1	7	0.001598	120514	0.213455	0.190476
Up	TFEC	7	0.002495	179844	0.189859	0
Up	CLIC4	7	0.002592	126676	0.240409	0.047619
Up	CYTIP	7	0.003673	254994	0.182964	0
Up	IGF1	7	0.002575	279198	0.20282	0
Up	SERPING1	7	0.002267	133518	0.170185	0
Up	CCL8	7	2.62E-04	30556	0.203999	0.333333
Up	EVI2A	7	0.003462	232114	0.193195	0
Up	SLF2	7	0.002271	91484	0.19299	0
Up	MTAP	7	0.002614	300022	0.197855	0
Up	MMS22L	7	0.003096	210744	0.177426	0
Up	CMYA5	7	0.002449	141388	0.189495	0
Up	PSTPIP2	7	0.00162	168880	0.234588	0.047619
Up	L2HGDH	7	0.003673	351102	0.144661	0
Up	AIM2	6	2.70E-04	20614	0.221777	0.166667
Up	KPNA5	6	0.002603	219678	0.184682	0
Up	TCF21	6	0.003061	175170	0.181823	0
Up	SKAP2	6	5.06E-04	97282	0.232302	0.066667
Up	IL2RA	6	0.002799	243968	0.210768	0
Up	CIQC	6	8.22E-04	47780	0.204664	0.2
Up	RASGRP3	6	0.002422	91754	0.234858	0.066667
Up	SRGN	6	0.001918	78834	0.203427	0
Up	ELF1	6	0.00145	64438	0.236303	0.066667
Up	STAT4	6	9.08E-04	67378	0.216168	0
Up	ADAP2	6	0.004275	153708	0.228082	0
Up	APOBEC3F	6	0.001837	124698	0.17992	0
Up	SAMD3	6	8.29E-04	97506	0.208893	0
Up	SPATA5	6	0.001466	102106	0.210645	0
Up	HOXB13	6	0.00135	288316	0.173772	0
Up	TRIM34	6	3.38E-04	41452	0.21414	0.266667
Up	PPM1K	6	0.001929	99042	0.196167	0
Up	LILRB1	6	0.002481	315408	0.200676	0
Up	SP110	6	0.002648	189660	0.195427	0
Up	F13A1	5	0.001225	209986	0.173384	0
Up	GBP1	5	7.98E-04	27574	0.234252	0
Up	CCL4	5	0.002943	131188	0.198589	0
Up	SPN	5	0.001197	71028	0.199328	0
Up	FCAR	5	0.001225	175142	0.13726	0
Up	HLA-DMA	5	6.27E-04	37830	0.180128	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Up	FCER1G	5	0.002449	350276	0.189023	0
Up	CD80	5	0.001091	51028	0.190013	0.2
Up	GRIA4	5	0.002449	184500	0.19059	0
Up	PDE3B	5	1	20	1	0
Up	OASL	5	0.002088	142286	0.188837	0
Up	FAM111B	5	0.001932	128164	0.1626	0
Up	NEGR1	5	1	6	1	0
Up	APBB1IP	5	8.23E-04	53636	0.205514	0
Up	SRGAP1	5	8.83E-04	95942	0.18887	0
Up	TRIM22	5	0.001965	150986	0.20391	0
Up	KLRD1	5	0.002449	250340	0.152641	0
Up	PNPT1	5	0.002502	203402	0.182148	0
Up	ARHGEF3	5	0.001328	66582	0.214126	0
Up	RPH3A	5	0.001955	158474	0.164608	0
Up	MTO1	5	0.001856	204862	0.187946	0
Up	TCAF2	4	0.002653	121338	0.18155	0
Up	BTN3A1	4	0.714286	30	0.583333	0
Up	CXCL11	4	6.27E-04	33174	0.189991	0
Up	CLIC2	4	4.92E-04	22978	0.21104	0.166667
Up	SULT1B1	4	0.001478	103752	0.192956	0
Up	N4BP1	4	2.30E-04	33236	0.21386	0
Up	OAS1	4	8.29E-04	47818	0.218059	0
Up	CYBB	4	0.001837	84510	0.194322	0
Up	FAM120C	4	8.91E-04	49716	0.241155	0.166667
Up	FCGR3A	4	0.003671	525390	0.189067	0
Up	SLC2A3	4	6.84E-04	73982	0.153901	0
Up	SELL	4	0.001846	168988	0.223248	0
Up	CARD16	4	0	0	0.206241	1
Up	CD86	4	4.83E-04	36610	0.186731	0.333333
Up	MNDA	4	0.001187	100354	0.218951	0
Up	IFITM3	4	0.001225	65190	0.234252	0.166667
Up	OLR1	4	1.89E-05	2054	0.191709	0
Up	REXO1L1P	4	0.003903	125374	0.235197	0
Up	RGS1	4	0.001837	92544	0.173643	0
Up	TGFBI	4	0.001682	124024	0.198746	0
Up	SAMD9	4	0.00733	1028082	0.158096	0
Up	LAIR1	4	5.36E-05	7340	0.210171	0
Up	ZSCAN30	4	1	12	1	0
Up	CCDC13	4	7.23E-04	100184	0.168264	0
Up	MORC4	4	0.001837	144576	0.21036	0
Up	RSAD2	4	0.001276	57738	0.200442	0
Up	RAB8B	4	0.002036	72736	0.190135	0
Up	SLC30A3	4	0.001837	77898	0.143296	0
Up	GIMAP2	4	1	2	1	0
Up	CD84	4	1.39E-05	1376	0.16407	0
Up	FAM83A	4	2.95E-04	16602	0.221191	0
Up	APOL6	4	8.26E-04	53784	0.192546	0
Up	PLEKHG2	4	0.001343	100370	0.21445	0
Up	SAMSN1	4	7.17E-04	146244	0.197245	0
Up	DUX4	4	1	12	1	0
Up	FRMD3	3	1	6	1	0
Up	BTN3A3	3	0.52381	22	0.5	0
Up	CXCL13	3	7.81E-04	27550	0.194311	0
Up	BEST1	3	0	0	1	0
Up	IDO1	3	6.36E-04	35070	0.195779	0
Up	MX2	3	6.60E-04	44642	0.190601	0
Up	ME2	3	0	0	0.133532	0
Up	DGKA	3	1.87E-04	20280	0.214112	0
Up	OAS2	3	7.16E-04	53360	0.212676	0
Up	CD96	3	9.11E-04	39506	0.194519	0
Up	CDH6	3	0	0	1	0
Up	RBMS2	3	6.50E-04	30974	0.208028	0
Up	CD226	3	1	6	1	0
Up	NHSL2	3	6.26E-04	141200	0.198782	0
Up	PARP9	3	6.10E-04	35572	0.210022	0
Up	DDX60	3	6.61E-04	47406	0.166386	0
Up	RPL3L	3	0.001225	65502	0.206541	0
Up	CARD6	3	2.11E-05	1706	0.178924	0
Up	NPL	3	0	0	0.174945	0
Up	MCM8	3	0.001225	115854	0.165744	0
Up	IL10RA	3	1.80E-04	16370	0.203528	0
Up	BCL2L15	3	3.06E-04	29170	0.198916	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Up	GAB3	3	1.20E-04	49012	0.219747	0
Up	ACE2	3	0.001225	83270	0.18548	0
Up	PARP12	3	0.001256	63342	0.173846	0
Up	RASSF4	3	6.26E-04	46922	0.175114	0
Up	WNT7A	2	1	2	1	0
Up	P2RY6	2	1.57E-04	8618	0.223416	0
Up	ABCC9	2	6.13E-04	21984	0.191529	0
Up	CXCL10	2	1.21E-05	2448	0.163234	0
Up	KCNJ6	2	1	2	1	0
Up	CD69	2	1	2	1	0
Up	DPYD	2	6.13E-04	37850	0.139399	0
Up	MPEG1	2	4.31E-05	5980	0.187267	0
Up	SYT2	2	1	2	1	0
Up	DDHD1	2	1.68E-05	980	0.172852	0
Up	GIMAP7	2	0	0	0	0
Up	OSR1	2	5.54E-05	5484	0.173053	0
Up	CLEC2B	2	0	0	0	0
Up	DOCK10	2	6.13E-04	65400	0.135118	0
Up	GBP5	2	0	0	0	0
Up	ZNF471	2	0	0	0	0
Up	CYSLTR2	2	1	2	1	0
Up	ALOX5AP	2	1.98E-05	1476	0.202055	0
Up	PDE4B	2	8.25E-06	528	0.157615	0
Up	NAIP	2	6.13E-04	36548	0.184536	0
Up	KYNU	2	6.13E-04	59904	0.184881	0
Up	PIK3AP1	2	1.15E-05	5248	0.215768	0
Up	HELB	2	6.64E-06	1140	0.187514	0
Up	FGF13	2	9.56E-05	4934	0.185997	0
Up	SIGLEC10	2	5.36E-05	7340	0.210171	0
Up	PRRG3	2	5.26E-05	3008	0.188478	0
Up	MS4A7	2	1	2	1	0
Up	PCSK1N	2	6.13E-04	66078	0.170773	0
Up	CLEC2D	2	1	2	1	0
Up	POU2F3	2	2.91E-04	30254	0.210754	0
Up	RAP2C	2	2.41E-05	1982	0.176068	0
Up	SNX10	2	1	2	1	0
Up	LST1	1	0	0	1	0
Up	APOL1	1	0	0	1	0
Up	TRANK1	1	0	0	0.16535	0
Up	AQP9	1	0	0	1	0
Up	PLXNC1	1	0	0	1	0
Up	IL18RAP	1	0	0	0.206489	0
Up	MAS1	1	0	0	0.148591	0
Up	HTN1	1	0	0	1	0
Up	HSD17B2	1	0	0	1	0
Up	CX3CR1	1	0	0	1	0
Up	ENTPD1	1	0	0	0.171346	0
Up	CASP5	1	0	0	0.16849	0
Up	AIF1	1	0	0	1	0
Up	MC2R	1	0	0	1	0
Up	PLA2G7	1	0	0	1	0
Up	SP140	1	0	0	0.198891	0
Up	HLX	1	0	0	0.188958	0
Up	MCF2L2	1	0	0	0.189407	0
Up	TIAM2	1	0	0	0.129016	0
Up	UNC80	1	0	0	1	0
Up	SCGB3A2	1	0	0	1	0
Up	CYSLTR1	1	0	0	0.666667	0
Up	IFITM1	1	0	0	1	0
Up	HTN3	1	0	0	0.205256	0
Up	GALR1	1	0	0	1	0
Up	NCKAP1L	1	0	0	0.200504	0
Up	CDH8	1	0	0	0.202657	0
Up	SIM1	1	0	0	0.143782	0
Up	MS4A2	1	0	0	0.194623	0
Up	SLFN5	1	0	0	0.200504	0
Up	C3AR1	1	0	0	0.148591	0
Up	PARP14	1	0	0	0.172196	0
Up	DDX60L	1	0	0	0.140533	0
Up	DOCK11	1	0	0	0.191664	0
Up	SLC36A1	1	0	0	0.148686	0
Up	CD163	1	0	0	0.166777	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Up	FMNL3	1	0	0	0.159191	0
Up	NAV3	1	0	0	0.180846	0
Up	HERC6	1	0	0	1	0
Up	C12orf50	1	0	0	0.192274	0
Up	LILRB4	1	0	0	0.191462	0
Up	RNASE6	1	0	0	1	0
Up	PKNOX2	1	0	0	0.146078	0
Up	CD180	1	0	0	1	0
Up	PLIN2	1	0	0	1	0
Up	APOL4	1	0	0	0.158819	0
Up	PDCD1LG2	1	0	0	0.150871	0
Up	CXorf21	1	0	0	1	0
Up	RGS18	1	0	0	0.14163	0
Up	GIMAP4	1	0	0	0.206489	0
Up	TLR7	1	0	0	0.176792	0
Up	FNIP2	1	0	0	1	0
Up	LAMP3	1	0	0	0.14889	0
Up	CYP46A1	1	0	0	0.161306	0
Down	CTNNB1	252	0.154145	24553626	0.354861	0.004273
Down	JUN	217	0.097293	17282550	0.341002	0.006303
Down	ERBB2	167	0.067682	7958554	0.317551	0.002365
Down	STUB1	141	0.05987	14754274	0.321373	0.005317
Down	RFS8	137	0.019742	4178294	0.302162	0.162301
Down	RPS2	130	0.023432	4016216	0.305755	0.161837
Down	PIN1	127	0.065202	11695326	0.331582	0.004124
Down	RUVBL2	120	0.049748	12251494	0.319304	0.003042
Down	KRT15	119	0.043148	4932624	0.280339	0.003133
Down	FOS	112	0.044908	5880486	0.327051	0.013678
Down	RPL6	112	0.014625	3129654	0.29831	0.200772
Down	RPS3	105	0.014162	3900696	0.311728	0.248535
Down	RPS3A	105	0.012264	3205064	0.307562	0.259707
Down	LGALS3	102	0.044675	5302704	0.299253	0.001212
Down	EEF1G	99	0.040972	6836640	0.307085	0.005369
Down	TRIM28	99	0.040461	10488818	0.308085	0.002148
Down	HSPA1A	98	0.038428	9829298	0.318937	0.007574
Down	KEAP1	90	0.033722	6849240	0.297521	5.22E-04
Down	RPS16	89	0.007126	2084604	0.307131	0.353422
Down	LMNA	88	0.026167	7105776	0.297883	0.002241
Down	RPL8	86	0.009482	2216832	0.296949	0.23803
Down	RPL4	85	0.009974	2644622	0.309114	0.345938
Down	ECSIT	84	0.027843	4603206	0.281628	0.00813
Down	RPL18A	83	0.010393	2126732	0.29921	0.30238
Down	RPL13	83	0.010652	2590136	0.299016	0.204525
Down	BSG	83	0.032837	4624392	0.271548	0.001175
Down	RPL7	80	0.004518	1673154	0.302118	0.383544
Down	RPS13	79	0.002964	986532	0.290507	0.407011
Down	RPL7A	78	0.006539	1622866	0.298459	0.403263
Down	RPS15A	75	0.003857	994406	0.297798	0.411532
Down	RPL3	75	0.004748	1432486	0.295244	0.318919
Down	RPLP0	72	0.004447	1586106	0.303815	0.370892
Down	RPL10A	72	0.005899	1568390	0.291015	0.377543
Down	RPS14	71	0.006224	1539090	0.295768	0.368612
Down	RPL18	71	8.01E-04	512706	0.290791	0.488531
Down	RPL31	70	0.005011	1560714	0.302777	0.361491
Down	SPINT2	67	0.025325	3404170	0.259858	4.52E-04
Down	RPL19	66	0.001755	550456	0.29069	0.5338
Down	RPL21	66	0.001889	861138	0.295181	0.489977
Down	RPL15	66	0.002043	748156	0.295642	0.506294
Down	RPS7	65	0.00247	1146570	0.29964	0.405769
Down	RPS9	65	0.003546	1276298	0.298609	0.375962
Down	RPS19	64	0.002871	954788	0.292692	0.456845
Down	TRAF4	64	0.020717	6148460	0.283083	0
Down	RPS5	61	0.001475	500556	0.287182	0.517486
Down	PHB2	60	0.020813	4081424	0.308245	0.00565
Down	PSMA7	59	0.020553	6163146	0.290345	0.00188
Down	SNRPB	59	0.014643	3189944	0.280679	0.009936
Down	RPLP1	56	0.00868	1636590	0.295936	0.219427
Down	TADA3	55	0.019161	6804262	0.264293	0
Down	RPS12	54	0.001248	504468	0.291871	0.573725
Down	RPS10	53	0.005693	1656148	0.293827	0.332366
Down	EEF1D	51	0.016784	2715650	0.308747	0.019558
Down	ELOB	50	0.015527	2518822	0.270016	0.003265

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Down	SNRPD2	50	0.01382	3266766	0.292692	0.017959
Down	EPHA2	50	0.019089	3828238	0.277057	0
Down	P4HB	49	0.017071	4140348	0.282833	9.25E-04
Down	UBXN1	49	0.014125	4158192	0.260492	0
Down	CLU	47	0.016343	2333422	0.288195	0.00202
Down	RPL36	47	0.002682	977554	0.293	0.385754
Down	RPL27A	47	0.002937	881288	0.291137	0.379278
Down	TUBB2A	43	0.010711	2382874	0.289699	0.016611
Down	NDUFA13	43	0.013825	1482382	0.26897	0.03433
Down	KRT19	42	0.011724	2376878	0.278838	0.021795
Down	JUNB	41	0.005793	960602	0.282239	0.044534
Down	DVL1	40	0.009592	1409636	0.290224	0.018492
Down	TRIM8	40	0.009491	2771384	0.254258	0
Down	TIMM13	40	0.011552	2045510	0.264983	0
Down	FKBP8	39	0.010911	2702796	0.282564	0.001502
Down	RPS15	38	0.003885	840300	0.287897	0.314367
Down	TUBB4B	38	0.00831	3007088	0.29298	0.015647
Down	SOCS3	37	0.012682	1476314	0.287618	0.009009
Down	RPLP2	37	0.003327	879248	0.296652	0.420168
Down	MKMK2	37	0.009633	1236022	0.272151	0.003361
Down	RPL27	37	0.001771	482712	0.280019	0.396396
Down	POLR2L	37	0.006794	2070118	0.256071	0
Down	EEF2	35	0.007394	1918150	0.299727	0.003788
Down	SLC25A6	35	0.010311	2451990	0.284242	0
Down	RPL35	35	0.001539	443808	0.277039	0.357983
Down	GNB2	35	0.011171	3045268	0.267313	0
Down	NME2	34	0.009674	1151836	0.268987	0.006048
Down	RPS18	34	0.001474	737802	0.296146	0.475936
Down	RPL32	34	3.77E-04	158154	0.272561	0.57041
Down	BAD	34	0.0098	1438720	0.277759	0.003565
Down	PPP4C	33	0.011746	1270628	0.265422	0.001894
Down	DPY30	33	0.007431	2190292	0.246961	0
Down	GIPC1	32	0.008754	947838	0.237579	0
Down	PRDX2	32	0.010216	1359500	0.282411	0.028226
Down	MLF1	32	0.009887	2720582	0.232812	0
Down	GADD45GIP1	31	0.007159	1123452	0.279718	0.023656
Down	RPS28	31	0.004343	986682	0.28545	0.260215
Down	ITGB4	31	0.008567	2482952	0.278707	0
Down	RPS27	31	0.002869	653182	0.280982	0.298925
Down	DDOST	31	0.010545	1684644	0.264143	0.006452
Down	ENKD1	31	0.00833	1889922	0.258007	0.002151
Down	CCDC33	31	0.007403	1991110	0.264344	0
Down	NDUFS6	30	0.002996	766474	0.24225	0.066667
Down	JUND	30	0.002872	584444	0.282239	0.073563
Down	KRT8	30	0.012335	2383176	0.292301	0.002299
Down	MYL6	30	0.007064	2580322	0.28032	0
Down	TXNDC5	30	0.007195	2351584	0.240418	0
Down	NDUFV1	29	0.004392	942678	0.248865	0.096059
Down	ARL6IP4	29	0.006682	937970	0.273995	0.002849
Down	UNC93B1	29	0.009991	1145830	0.247578	0.004926
Down	ID1	29	0.007437	2491530	0.244081	0
Down	POLR2J	29	0.00495	1544350	0.244167	0
Down	TUBGCP2	28	0.009528	1230290	0.269981	0.018519
Down	RPS17	28	0.001376	400878	0.274483	0.338624
Down	RPL26	28	0.001839	502830	0.280888	0.272487
Down	CDC34	28	0.003747	1277554	0.252073	0
Down	UBXN11	26	0.007961	1131048	0.242151	0.003077
Down	FBXW5	26	0.005521	1202140	0.251464	0
Down	LRWD1	26	0.006086	1099650	0.24746	0.018462
Down	CBX7	25	0.007406	2514890	0.255804	0
Down	GSTP1	25	0.006496	2001634	0.287519	0
Down	CBR1	25	0.008541	1581450	0.278223	0.01
Down	DAG1	25	0.004076	1073576	0.24985	0
Down	APBB1	24	0.008826	1212628	0.279737	0.008658
Down	UQCRC1	24	0.006002	765246	0.271849	0.018116
Down	ITGB5	24	0.005994	1483232	0.246144	0
Down	TUFM	24	0.003575	1189076	0.279849	0.018116
Down	RPS29	23	0.001922	584746	0.257083	0.324111
Down	RPS21	23	0.001513	252494	0.278987	0.407115
Down	GTF3C5	23	0.004679	1553458	0.255318	0
Down	CCDC151	22	0.005735	957888	0.220721	0
Down	NDUFAF3	22	0.004376	601380	0.262016	0.095238

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Down	MAPK8IP1	22	0.00589	1020306	0.281895	0.010526
Down	CKB	22	0.005847	682536	0.274284	0
Down	POLR2I	22	0.001697	671030	0.22867	0
Down	TRAF7	22	0.005132	903670	0.234661	0
Down	DHX30	22	0.00276	1276710	0.265506	0
Down	ANAPC11	22	0.005247	1127412	0.237484	0
Down	MAGED2	22	0.004168	1380456	0.26266	0
Down	TXNL4A	21	0.005658	611678	0.252042	0
Down	ACTR1B	21	0.006719	1322060	0.243539	0
Down	HSPA2	21	0.004098	516514	0.282929	0.033333
Down	SERTAD1	21	0.00555	628590	0.26072	0.004762
Down	CGDC74B	21	0.002344	830426	0.22954	0
Down	UBAC1	21	0.007669	1047972	0.223937	0
Down	ATAD3A	21	0.00514	1680038	0.279324	0
Down	B9D1	21	0.004407	981018	0.227211	0
Down	NDUFA2	20	0.003404	696876	0.249133	0.168421
Down	AK1	20	0.005788	1033778	0.23834	0
Down	PTPRF	20	0.005558	500712	0.278595	0.019608
Down	DNAJB2	20	0.00507	1293248	0.246217	0
Down	CIRBP	20	0.004752	1801308	0.264932	0
Down	LRRC46	20	0.006477	2017942	0.227496	0
Down	PPP1R16A	20	0.005906	942776	0.227136	0
Down	NOP53	20	0.0035	1602742	0.25538	0
Down	SIVA1	19	0.004933	1560386	0.259243	0
Down	IGHG1	19	0.00669	1979420	0.249058	0
Down	ELF3	19	0.00503	594494	0.272454	0.017544
Down	HSPBP1	19	0.006138	707466	0.277945	0.064327
Down	KRT5	19	0.005695	1232474	0.28066	0.017544
Down	EPPK1	19	0.005577	747020	0.279906	0.005848
Down	PRDX5	19	0.004045	812544	0.270332	0.035088
Down	PTK7	19	0.005459	519038	0.268814	0.011696
Down	OAZ1	19	0.005754	1005134	0.255757	0
Down	PLTP	19	0.005536	1230986	0.211346	0
Down	TRAPPC2L	19	0.006398	1263018	0.246639	0
Down	MIF	18	0.004809	824070	0.276359	0.008333
Down	RPL13A	18	0.001249	720782	0.269859	0.078431
Down	IFT27	18	0.005718	866506	0.221885	0.006536
Down	SLC2A1	17	0.006587	1072186	0.27612	0
Down	SEC61B	17	0.005882	1512838	0.274791	0.022059
Down	TALDO1	17	0.005733	1038514	0.254974	0.007353
Down	SSR4	17	0.003457	813796	0.267399	0.007353
Down	PYCR2	17	0.006306	1426258	0.261456	0
Down	NDUFAB1	16	0.006714	1180470	0.192913	0
Down	COPE	16	0.004619	1041572	0.250346	0
Down	UQCRQ	16	0.002753	548912	0.245563	0.033333
Down	SELENBP1	16	0.003781	732542	0.240557	0
Down	COX5B	16	0.005206	748622	0.252409	0
Down	COX5A	16	0.003701	698376	0.246115	0.016667
Down	COMT	16	0.004377	1308932	0.25615	0
Down	SSBP4	16	0.005835	873628	0.22211	0
Down	S100A6	15	0.002803	721266	0.247489	0
Down	STEAP3	15	0.00426	369524	0.235417	0
Down	VPS51	15	0.004718	381258	0.25021	0.038095
Down	ARL3	15	0.005037	1096782	0.236836	0
Down	TAGLN2	15	0.002738	800172	0.268208	0
Down	BLOC1S1	15	0.006549	1449496	0.265896	0
Down	DNALI1	14	0.003161	593226	0.224989	0
Down	SLC27A2	14	0.003126	376110	0.227347	0
Down	PLXNB1	14	0.002639	494902	0.227994	0
Down	SSNA1	14	0.002663	522754	0.233805	0
Down	LRP5	14	0.005755	1223222	0.213426	0
Down	COX4I1	14	0.002204	361852	0.239754	0.043956
Down	KRT10	14	0.001299	530844	0.274446	0
Down	CD59	14	0.002679	657300	0.255725	0
Down	CD81	14	0.002501	555394	0.235165	0.043956
Down	RPL29	14	0.001112	298754	0.271601	0.098901
Down	RIPK4	14	0.002243	331006	0.231891	0
Down	WDR34	14	0.003181	460974	0.227832	0.076923
Down	CIB1	14	0.002713	806716	0.233752	0
Down	STOML2	14	0.002295	682918	0.257927	0
Down	ATG4B	14	0.004002	629136	0.231466	0
Down	CHCHD2	14	0.002472	686360	0.252961	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Down	UBXN6	13	0.003476	749108	0.24985	0
Down	TKT	13	0.002485	522692	0.266697	0.012821
Down	ALDH3B1	13	0.002164	762136	0.228157	0
Down	AAMP	13	0.00347	959056	0.241533	0
Down	COMMD6	13	0.003946	865962	0.242151	0
Down	BICD2	13	0.002518	564670	0.232176	0
Down	ARPC1A	13	0.004132	1051008	0.215814	0
Down	IFT140	13	0.002008	325234	0.204528	0.076923
Down	NHP2	13	0.002031	787904	0.251085	0
Down	NDUFB7	12	5.85E-04	170496	0.224214	0.106061
Down	AGR2	12	0.00233	494674	0.231982	0
Down	NDUFB10	12	7.99E-04	115894	0.228207	0.075758
Down	CYC1	12	0.002393	432054	0.257703	0.030303
Down	POR	12	0.002125	310980	0.238463	0
Down	CD9	12	0.002225	388858	0.229048	0.075758
Down	DUSP1	12	0.001967	800996	0.23441	0
Down	S100A2	12	0.002334	303968	0.274791	0.022222
Down	RPL34	12	0.001088	533846	0.245346	0
Down	PTOV1	12	0.002509	272616	0.26261	0
Down	RSPH9	12	0.003848	845642	0.213437	0
Down	ST14	12	0.003076	704516	0.238245	0
Down	CLSTN1	11	0.002625	509144	0.254041	0.018182
Down	NDUFA4	11	0.00199	494886	0.264831	0.036364
Down	PLXNB2	11	0.003722	599986	0.224407	0
Down	DGCR6L	11	0.002273	250948	0.252271	0.036364
Down	RRAD	11	0.001826	418124	0.258615	0
Down	ARF5	11	0.005617	795942	0.223913	0
Down	DDR1	11	0.002539	617432	0.23126	0
Down	LAMTOR4	11	0.002559	516732	0.219176	0
Down	MRPL14	11	0.001279	307548	0.22615	0
Down	MAPK15	11	0.003085	708266	0.225953	0
Down	TCTEX1D2	11	0.001301	197546	0.207379	0.127273
Down	TMED9	11	0.003443	1420556	0.199158	0
Down	KLF4	10	5.16E-04	144166	0.248776	0
Down	IFT43	10	0.002694	359698	0.225367	0.133333
Down	GPX1	10	0.00131	211924	0.240571	0
Down	CTSD	10	0.002766	663634	0.253685	0
Down	IER3	10	0.001866	484388	0.25615	0
Down	RHOB	10	0.003222	434242	0.218017	0
Down	KRT17	10	0.001969	423132	0.259162	0
Down	DHCR24	10	0.002291	363014	0.234966	0
Down	SELENOS	10	0.002577	455310	0.222323	0
Down	PSMG3	10	0.001537	490232	0.209813	0
Down	UBTD1	10	0.002405	731090	0.226852	0
Down	KLF15	10	0.001737	298814	0.236648	0
Down	RGL2	9	0.002109	219028	0.250873	0
Down	TRIM3	9	0.001548	323080	0.216184	0
Down	NR2F6	9	0.002452	268586	0.26228	0.027778
Down	COA3	9	0.002181	454840	0.229489	0.083333
Down	SDC1	9	0.001765	407764	0.23332	0
Down	AQP5	9	0.001575	413582	0.225428	0
Down	TTC29	9	0.002561	409630	0.214007	0
Down	ARHGEF17	9	7.18E-04	183410	0.225367	0
Down	S100A13	9	0.002454	226422	0.183966	0
Down	CITED2	9	0.002408	786924	0.231878	0
Down	ZNF703	9	0.002577	529632	0.202351	0
Down	EIF3CL	8	0.002558	557022	0.203349	0
Down	IMPA2	8	0.0024	341720	0.154792	0
Down	EPHX1	8	0.003096	434586	0.24421	0
Down	EDF1	8	5.82E-04	64372	0.260589	0.071429
Down	ZMYND10	8	0.002178	259858	0.216072	0
Down	RHPN1	8	0.001267	185404	0.231827	0
Down	EFNA1	8	0.002672	314678	0.246786	0
Down	IGFBP5	8	0.001838	314004	0.224468	0
Down	GNA11	8	0.001971	462014	0.22505	0
Down	SPPL2B	8	0.002211	316362	0.214669	0
Down	DYNLRB2	8	0.002911	496900	0.235019	0.178571
Down	ELMO3	8	0.001725	282724	0.216094	0
Down	CFAP53	8	9.05E-04	193188	0.228934	0
Down	GDF15	8	0.001528	219270	0.209034	0
Down	ARHGAP39	8	0.001973	336568	0.223756	0
Down	FIS1	8	0.002035	324348	0.203628	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Down	MAZ	7	0.001543	229894	0.275992	0.095238
Down	HSPA1B	7	6.85E-04	89854	0.266219	0.095238
Down	FDXR	7	0.001554	200262	0.213338	0
Down	ERP29	7	0.001062	409508	0.257353	0
Down	RPL37	7	1.38E-04	40630	0.235857	0
Down	RPL36A	7	2.62E-04	96380	0.249506	0
Down	RHBDD2	7	0.001573	263748	0.217131	0.047619
Down	COPS9	7	0.001263	240040	0.232318	0
Down	UBL5	7	7.04E-04	144222	0.231248	0
Down	SPATA20	6	0.001802	424738	0.216162	0
Down	PGLS	6	5.66E-04	142890	0.236863	0
Down	GRHPR	6	0.002133	165784	0.247372	0
Down	SLP1	6	7.44E-04	138430	0.218693	0
Down	ASL	6	5.11E-04	94688	0.196899	0
Down	PTPRU	6	0.001624	181440	0.271371	0.166667
Down	PROS1	6	1	30	1	0
Down	FAU	6	7.30E-07	454	0.242532	0.866667
Down	PTTG1IP	6	0.002027	465732	0.229958	0
Down	LAMB2	6	0.001433	183752	0.212826	0
Down	CCDC153	6	2.01E-04	53400	0.225525	0
Down	TMEM219	6	0.00146	277782	0.15928	0
Down	CSRNP1	6	0.001138	241004	0.22488	0
Down	ATP6V0B	6	7.43E-04	128958	0.223925	0
Down	ITPA	6	0.001092	229808	0.178855	0
Down	PIH1D3	6	0.001897	365260	0.210545	0
Down	DNPH1	5	4.86E-04	161778	0.219522	0
Down	GADD45B	5	6.71E-04	73422	0.231543	0
Down	TSPAN15	5	0.001015	193544	0.194681	0
Down	IGHG3	5	5.03E-04	193512	0.179704	0
Down	ITGA3	5	2.43E-04	38694	0.222513	0.1
Down	ALDH3A1	5	6.36E-04	181618	0.213699	0
Down	GPX4	5	0.00145	337884	0.22099	0
Down	EIF4H	5	9.94E-04	278362	0.239671	0
Down	YIF1B	5	5.73E-04	141588	0.213251	0
Down	CROCC	5	0.001479	179464	0.204618	0
Down	AHNAK2	5	7.63E-04	72192	0.226482	0
Down	PIGQ	5	0.00192	341276	0.195816	0
Down	DPCD	5	2.88E-04	38306	0.243169	0.3
Down	WDR54	5	1	20	1	0
Down	MID1IP1	5	0.001373	301178	0.192006	0
Down	CYB5R1	5	0.001156	212806	0.208292	0
Down	PKIG	5	0.001013	108576	0.217267	0
Down	NAA38	5	1	20	1	0
Down	TMEM9	5	6.02E-04	108484	0.2111	0
Down	CLDN7	4	5.59E-04	54648	0.205984	0
Down	NTN1	4	0.00144	232302	0.200058	0
Down	GSTA2	4	1	12	1	0
Down	CTSH	4	9.85E-04	267376	0.19894	0
Down	CD82	4	0.001102	143252	0.226297	0
Down	PDLIM4	4	6.01E-04	98502	0.22166	0
Down	CRIP2	4	6.32E-04	175956	0.237742	0
Down	GLB1L2	4	2.10E-04	19340	0.192833	0
Down	SURF1	4	5.40E-04	99054	0.200269	0
Down	IGFBP7	4	6.41E-04	89942	0.214691	0
Down	GUK1	4	0.00144	314712	0.203002	0
Down	HAGH	4	9.96E-04	127692	0.194082	0
Down	MAP9	4	4.10E-04	80536	0.235391	0
Down	CMTM4	4	5.01E-04	71496	0.214602	0
Down	ROPN1L	4	0.00144	291918	0.231312	0
Down	TXNDC17	4	6.21E-04	112934	0.200742	0
Down	COQ4	4	1	2	1	0
Down	TFF3	4	0.00144	323244	0.178289	0
Down	SGSM3	4	5.39E-04	86024	0.209475	0
Down	CCDC17	4	5.82E-05	20180	0.224856	0
Down	EPS8L2	4	5.03E-04	136136	0.22384	0
Down	TBCA	3	4.87E-04	69238	0.190871	0
Down	TACSTD2	3	0.001407	248328	0.233976	0
Down	FOSB	3	0	0	0.260036	1
Down	CSTB	3	4.91E-04	102998	0.228432	0
Down	IGFBP2	3	5.19E-04	87110	0.248568	0
Down	SERPINF1	3	9.60E-04	111346	0.188334	0
Down	ECI1	3	5.03E-04	85182	0.225696	0

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Table 6 (continued)

Regulation	Node	Degree	Betweenness	Stress	Closeness	Clustering coefficient
Down	CRIP1	3	9.60E-04	161934	0.200897	0
Down	BCAM	3	4.97E-04	91662	0.219107	0
Down	SLC20A2	3	4.84E-04	83278	0.204487	0
Down	SLC25A25	3	4.87E-04	89270	0.188521	0
Down	PTPRN2	3	4.98E-04	58140	0.211884	0
Down	LRRC45	3	1.28E-04	13376	0.210662	0
Down	SYTL1	3	9.60E-04	139146	0.218417	0
Down	TMEM190	3	4.91E-04	64138	0.182996	0
Down	PCYT2	3	4.85E-04	123268	0.20975	0
Down	ACO2	3	5.42E-04	156434	0.256371	0
Down	SMDT1	3	1	6	1	0
Down	TOMM7	3	5.02E-04	100004	0.196074	0
Down	SPEF1	3	0.001097	180654	0.213163	0
Down	MAN2B1	2	4.80E-04	60454	0.188975	0
Down	AGPAT2	2	1	2	1	0
Down	SPAG7	2	4.80E-04	53634	0.199981	0
Down	SCGB1A1	2	4.80E-04	128656	0.228997	0
Down	CES1	2	0	0	0	0
Down	CD151	2	1	2	1	0
Down	CYB561	2	1	2	1	0
Down	PPOX	2	1.34E-05	3114	0.203877	0
Down	LAMC2	2	2.74E-05	4176	0.203449	0
Down	FBXW9	2	5.46E-06	1248	0.218131	0
Down	CRACR2B	2	4.80E-04	107412	0.162944	0
Down	BORCS7	2	3.79E-06	1022	0.194672	0
Down	CQO8B	2	7.69E-05	17552	0.185871	0
Down	TMEM205	2	4.80E-04	84038	0.193685	0
Down	CRELD2	2	4.80E-04	139720	0.195109	0
Down	PPP1R32	2	1.71E-06	632	0.213426	0
Down	TRPT1	2	5.09E-05	21436	0.236419	0
Down	CELSR1	2	4.80E-04	44172	0.194281	0
Down	RPS10-NUDT3	1	0	0	0.177786	0
Down	CLDN4	1	0	0	0.168324	0
Down	PPEF2	1	0	0	0.182332	0
Down	UQCR11	1	0	0	0.155399	0
Down	CLDN3	1	0	0	0.159414	0
Down	GTPBP6	1	0	0	1	0
Down	ATP2C2	1	0	0	1	0
Down	GJB3	1	0	0	0.212208	0
Down	JTB	1	0	0	0.187115	0
Down	NDUFB2	1	0	0	1	0
Down	LRG1	1	0	0	1	0
Down	GCHFR	1	0	0	1	0
Down	TSPAN7	1	0	0	0.189301	0
Down	TEF	1	0	0	0.199655	0
Down	CAPS	1	0	0	1	0
Down	TST	1	0	0	0.181118	0
Down	PRRT3	1	0	0	0.201793	0
Down	PTRHD1	1	0	0	1	0
Down	DUS1L	1	0	0	0.195302	0
Down	NRSN1	1	0	0	1	0
Down	BAIAP3	1	0	0	1	0
Down	EPCAM	1	0	0	0.212728	0
Down	LRRC23	1	0	0	1	0
Down	C9orf116	1	0	0	1	0
Down	TCTEX1D4	1	0	0	0.20957	0
Down	CFAP65	1	0	0	0.2103	0
Down	KNDC1	1	0	0	0.240487	0
Down	SELENOH	1	0	0	0.180993	0
Down	NPEPL1	1	0	0	0.17941	0
Down	DENND6B	1	0	0	0.231235	0
Down	FAM174A	1	0	0	0.181933	0
Down	RSPH1	1	0	0	0.179658	0
Down	ST6GALNAC6	1	0	0	0.20491	0
Down	CCDC74A	1	0	0	1	0
Down	C12orf57	1	0	0	0.204779	0
Down	LARP6	1	0	0	0.231235	0
Down	DNAI2	1	0	0	0.198541	0
Down	WDR13	1	0	0	1	0
Down	P4HTM	1	0	0	0.188011	0
Down	ST6GALNAC2	1	0	0	0.228032	0
Down	TMA7	1	0	0	0.231235	0
Down	FCGBP	1	0	0	0.182956	0

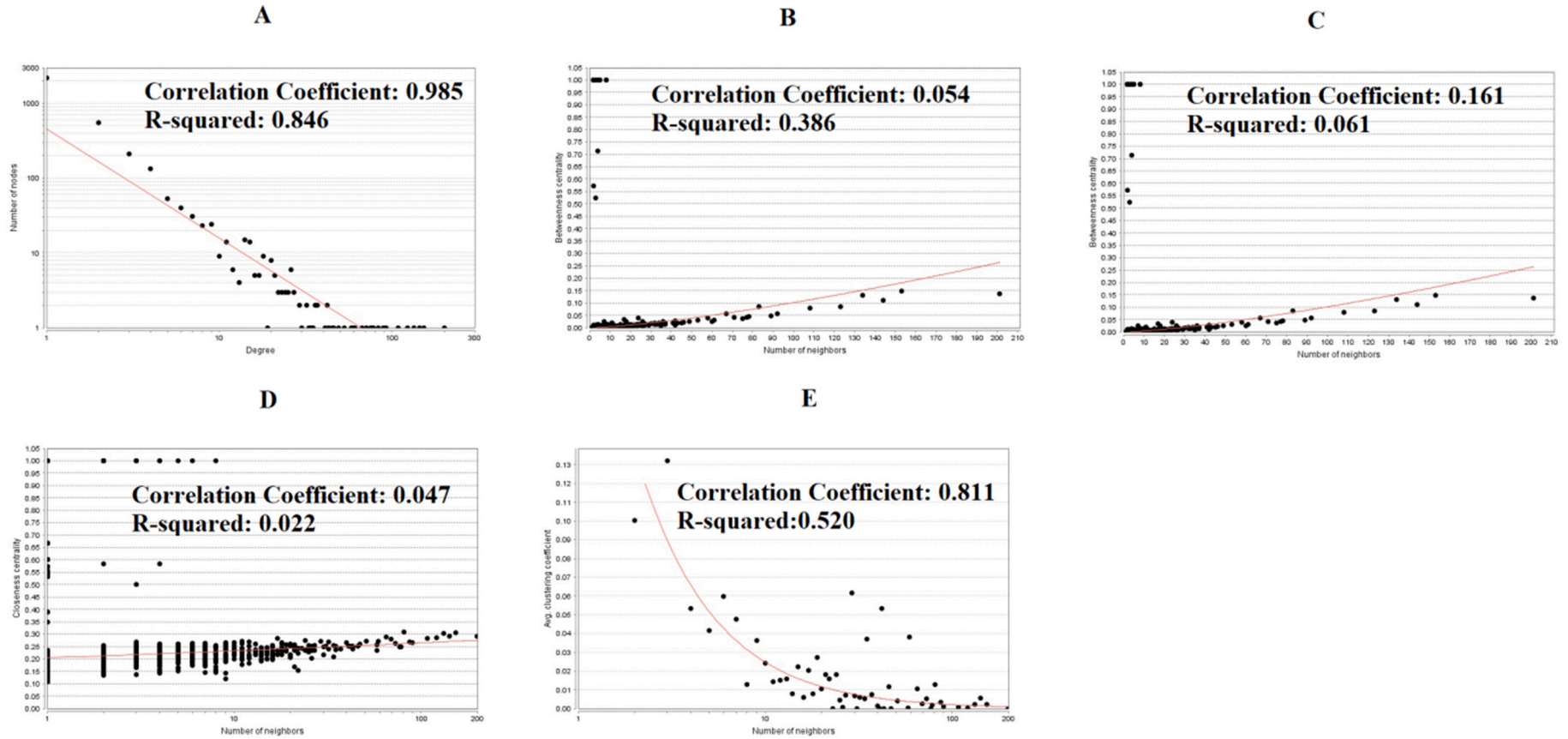


Fig. 6. Scatter plot for up regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality; D-Closeness centrality; E- Clustering coefficient).

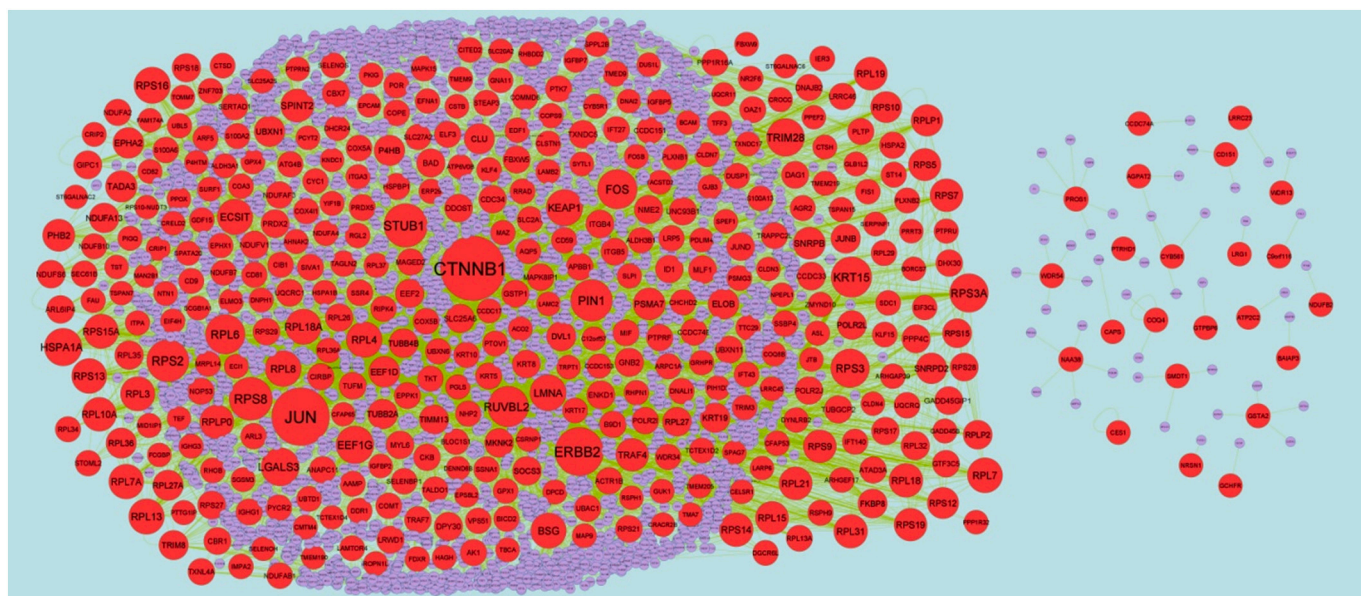


Fig. 7. Protein–protein interaction network of down regulated genes. Red nodes denotes down regulated genes. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

curves were analyzed by R “pROC” package to evaluate the diagnostic accuracy of hub genes for SARS-CoV-2 infection. The area under the curve (AUC) could be mapped to compare different screening genes. Therefore, the ten genes identified, CBL (AUC = 0.852; p value = 8.951754e-04), ISG15 (AUC = 0.900; p value = 2.4385073e-05), NEDD4 (AUC = 0.827; p value = 4.786626e-06), PML (AUC = 0.885; p value = 2.058053e-04), REL (AUC = 0.881; p value = 9.503538e-07), CTNNB1 (AUC = 0.870; p value = 2.837941e-11), ERBB2 (AUC = 0.891; p value = 5.146281e-13), JUN (AUC = 0.850; p value = 8.303965e-11), RPS8 (AUC = 0.858; p value = 1.453081e-11) and STUB1 (AUC = 0.850; p value = 2.400541e-12) might be considered as new biomarkers for SARS-CoV-2 infection and are shown Fig. 15.

4. Discussion

SARS-CoV-2 infection is among the most deadliest infection worldwide. Therefore, uncovering the etiological and molecular pathogenesis underlying SARS-CoV-2 infection is essential for therapy and prevention. In this investigation, we analyzed the expression of genes in microarray dataset based on SARS-CoV-2 infection group and the negative control group. In the current investigation, we extracted the data from GSE152075, which includes 430 SARS-CoV-2 infection samples and 54 negative control samples. We identified 496 up regulated genes and 498 down regulated genes between SARS-CoV-2 infection and negative control samples using bioinformatics analysis. Genes such as IFIT1 [Feng et al., 2018], XAF1 [Long et al., 2013], OAS3 [Gad et al., 2012], CKB (creatine kinase B) [Hara et al., 2009], RPL18A [B. Wang et al., 2018], CIB1 [Godinho-Santos et al., 2016] and EEF2 [Valiente-Echeverría et al., 2014] were linked with advancement of various viral infections, but these genes may be liable for progression of SARS-CoV-2 infection. Genes such as OAS2 [Zhao et al., 2019], CXCL10 [Law et al., 2010] and SPINT2 [Straus et al., 2020] were linked with progression of influenza virus infection, but these genes may be associated with development of SARS-CoV-2 infection.

The pathway enrichment analysis was performed with up and down regulated genes. Enriched genes such as KMO (kynurenine 3-monooxygenase) [Swainson et al., 2019], KYNU (kynureninase) [Finney et al., 2019], BIRC3 [Rouka, 2018], GBP2 [Yu et al., 2020], DDX58 [Zhu et al., 2019], IRF8 [Sun et al., 2016], IFIT2 [Butchi et al., 2014], TRIM5 [van

Manen et al., 2008], RSAD2 [Kurokawa et al., 2019], IFI6 [Richardson et al., 2018], SP100 [Kim et al., 2011], TRIM21 [Fan et al., 2016], CXCL9 [Huang et al., 2012], CCL8 [Rom et al., 2010], CXCL11 [Chalin et al., 2019], ELMO1 [Janardhan et al., 2004], ITK (IL2 inducible T cell kinase) [He et al., 2014], CYP27A1 [Yang et al., 2019], RPS13 [Robichaux et al., 2016], RPS17 [Kenney and Meng, 2015], RPS19 [Ganaie et al., 2014], RPL4 [Chen et al., 2016], RPL13 [Han et al., 2020], RPL18 [R. Wang et al., 2018], RUVBL2 [Morwitzer et al., 2019], JUN (Jun proto-oncogene, AP-1 transcription factor subunit) [Benn et al., 1996] and GPX4 [Brault et al., 2016] were involved in development of different viral infections, but these genes may be responsible for progression of SARS-CoV-2 infection. Enriched genes such as IDO1 [Fox et al., 2015], CCL2 [Lai et al., 2017], AIM2 [Zhang et al., 2017], STAT2 [Warning et al., 2015], GBP5 [Feng et al., 2017], CASP1 [Ren et al., 2017], OAS2 [Zhao et al., 2019], STAT4 [Bot et al., 2003], TRIM22 [Di Pietro et al., 2013], PML (promyelocytic leukemia) [Li et al., 2009], IFITM1 [Yu et al., 2015], ISG15 [Sanyal et al., 2013], MX1 [Verhelst et al., 2012], MX2 [Jin et al., 2001], IRF4 [Ainsua-Enrich et al., 2019], NEDD4 [Lin et al., 2020], HERC5 [Tang et al., 2010], CXCR2 [Washburn et al., 2019], TLR3 [Lim et al., 2019], SOCS3 [Lin et al., 2020] and BAD (BCL2 associated agonist of cell death) [Tran et al., 2013] were key for progression of influenza virus infection, but these genes may be linked with advancement of SARS-CoV-2 infection. Enriched genes such as GBP1 [Niu et al., 2016], USP18 [Xu et al., 2012] and OASL (2'-5'-oligoadenylate synthetase like) [B. Wang et al., 2018] were associated with progression of porcine reproductive and respiratory syndrome viral infection, but these genes may be liable for advancement of SARS-CoV-2 infection. Enriched genes such as STAT1 [Claverie, 2020], P2RX7 [Di Virgilio et al., 2020], TLR4 [Choudhury and Mukherjee, 2020], CCR5 [Patterson et al., 2020], CCL5 [Patterson et al., 2020], JAK2 [Wu and Yang, 2020], IFITM3 [Hachim et al., 2020], TLR7 [Moreno-Eutimio et al., 2020], TLR1 [Choudhury and Mukherjee, 2020], TLR2 [Choudhury and Mukherjee, 2020], RPL9 [Rofeal and El-Malek, 2020] and GPX1 [Seale et al., 2020] were involved in progression of SARS-CoV-2 infection. OAS1 was liable for progression of severe acute respiratory syndrome (SARS) viral infection [Hamano et al., 2005], but this gene may be associated with development of SARS-CoV-2 infection. Enriched genes such as CCL4 [Al-Afif et al., 2015], IFIT3 [Ternette et al., 2011], CCR1 [Miller et al., 2006], CXCL13 [Chalin et al., 2018], CX3CR1 [Anderson et al., 2020] and DUSP1 [Robitaille et al., 2017] were

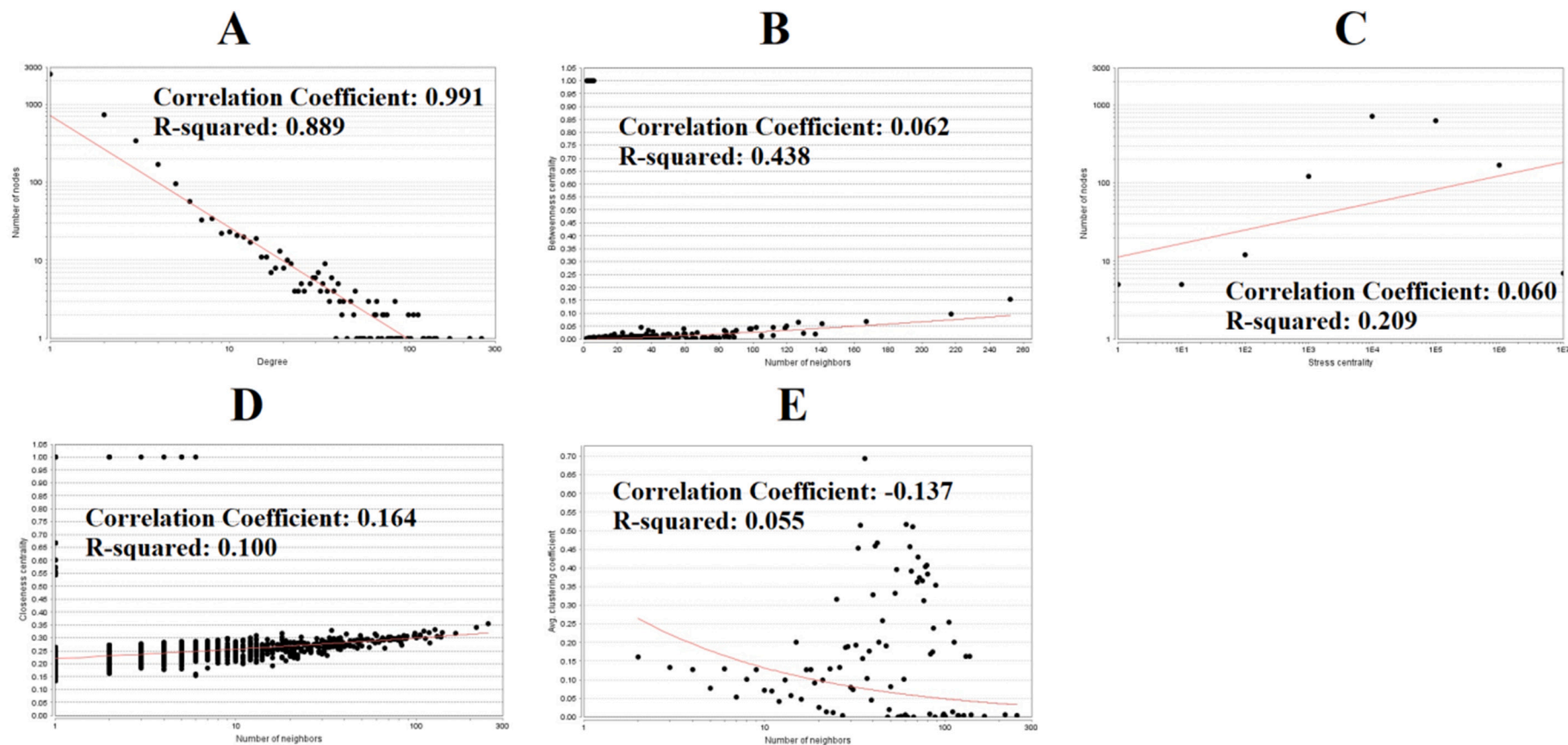
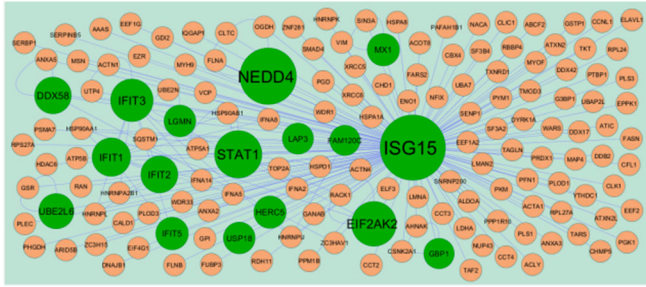
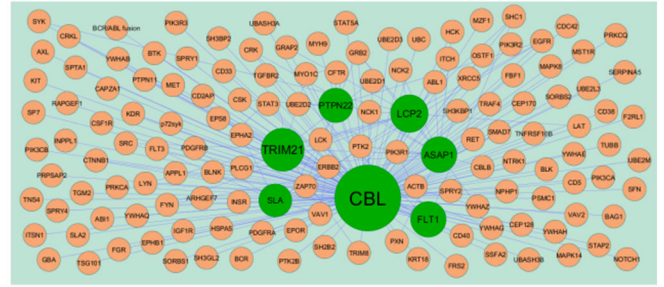


Fig. 8. Scatter plot for down regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality; D-Closeness centrality; E- Clustering coefficient).

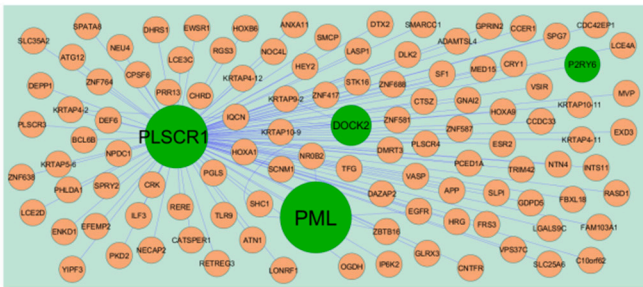
Module 1



Module 2



Module 3



Module 4

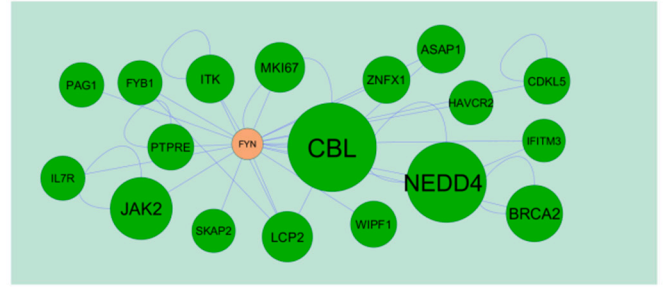
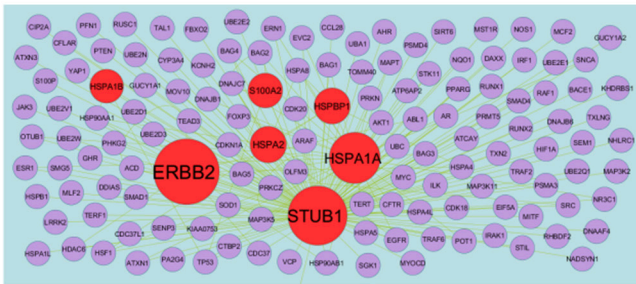
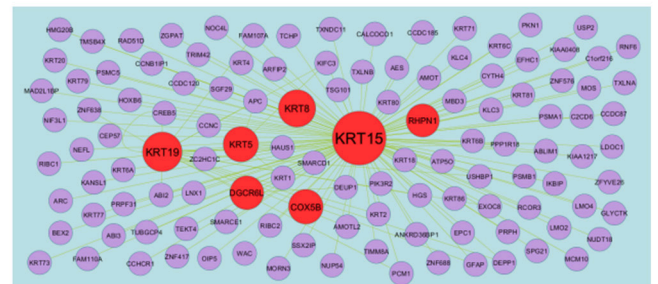


Fig. 9. Modules in PPI network. The green nodes denote the up regulated genes. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

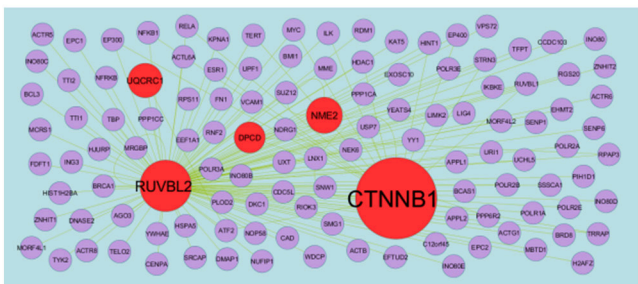
Module 1



Module 2



Module 3



Module 4

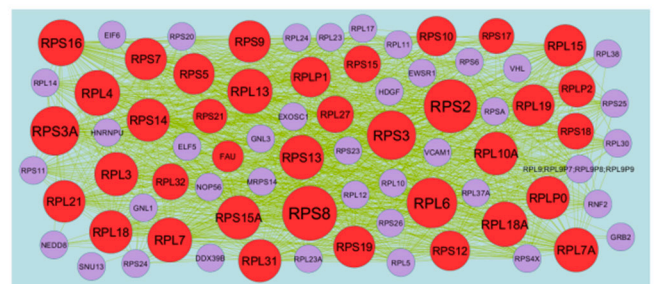


Fig. 10. Modules in PPI network. The red nodes denote the down regulated genes. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

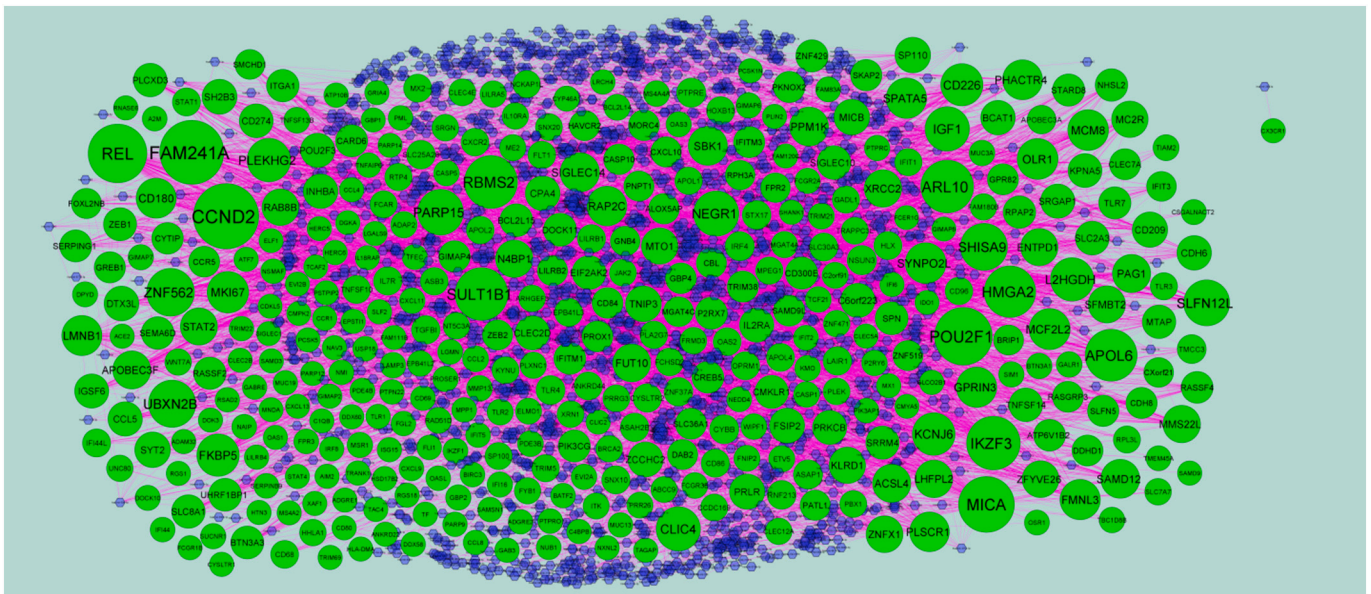


Fig. 11. The network of up regulated genes and their related miRNAs. The green circles nodes are the up regulated genes, and purple diamond nodes are the miRNAs. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

associated with progression of respiratory syncytial virus infection, but these genes may be key for advancement of SARS-CoV-2 infection. The novel biomarkers (CARD16, MEFV (MEFV innate immunity regulator, pyrin), CYBB (cytochrome *b*-245 beta chain), GBP4, CARD6, CASP5, HLX (H2.0 like homeobox), IL2RA, IL2RG, IL18RAP, GZMB (granzyme B), UBE2L6, FCGR1B, TRIM38, EIF2AK2, TRIM34, KPNA5, WARS1, PIK3CG, PRKCB (protein kinase C beta), TIAM2, DOCK2, GNB4, PTPRC (protein tyrosine phosphatase receptor type C), POR (cytochrome *p*450 oxidoreductase), SLC27A2, RPL21, RPL26, RPL27, RPL27A, RPL29, RPL31, RPL32, RPL34, RPL37, RPL39, RPL36A, RPLP0, RPLP1, RPLP2, RPS2, RPS3, RPS3A, RPS5, RPS7, RPS8, RPS9, RPS10, RPS14, RPS15, RPS15A, RPS16, RPS18, RPS21, RPS27, RPS28, RPS29, FAU (FAU ubiquitin like and ribosomal protein S30 fusion), RPL36, MRPL14, RPS10-NUDT3, RPL10A, RPL17-C18orf32, RPL35, RPL13A, RPL3, RPL6, RPL7, RPL7A, RPL8, RPL15, RPL19, FOS (Fos proto-oncogene, AP-1 transcription factor subunit), JUNB (JunB proto-oncogene, AP-1 transcription factor subunit), JUND (JunD proto-oncogene, AP-1 transcription factor subunit), RPS12, COX5A, UQCRC1, COX4I1, COX5B, COX6A1, COX7B, ATP5F1E, ATP6V0B, SLC25A6, SEPTIN5, UQCRCQ (ubiquinol-cytochrome *c* reductase complex III subunit VII), CYC1, NDUFA2, NDUFA4, NDUFAB1, NDUFB2, NDUFB7, NDUFB10, NDUFC1, NDUFV1, NDUFS6, UQCR11, TUBB2A, TUBB4B, ARPC1A, ARF5, DNAI2, SSR4, PGLS (6-phosphogluconolactonase), TALDO1 and TKT (transketolase)) obtained from the pathway enrichment analysis are all may be associated in SARS-CoV-2 infection progression process, which suggesting that these novel biomarkers may serve as diagnostics biomarkers or therapeutic targets for this infection.

The GO enrichment analysis was performed with up and down regulated genes. Enriched genes such as A2M [Chen et al., 2010], CLEC5A [Teng et al., 2016], ZBP1 [T. Zhang et al., 2020], PLSCR1 [Luo et al., 2018], FKBP5 [Hao et al., 2020], FPR2 [Schloer et al., 2019], CD226 [Redlberger-Fritz et al., 2019], PTPN22 [Crabtree et al., 2016], CEACAM1 [Ye et al., 2018], CD80 [Lumsden et al., 2000] CD86 [Lumsden et al., 2000], CD68 [McGuinness et al., 2000], MLKL (mixed lineage kinase domain like pseudokinase) [Gaba et al., 2019] and TRIM28 [Krischuns et al., 2018] were liable for progression of influenza

viral infection, but these genes may be associated with development of SARS-CoV-2 infection. Enriched genes such as LILRB2 [Alaoui et al., 2018], SERPINB9 [Mangan et al., 2017], FCGR3A [Poonia et al., 2010], MICB (MHC class I polypeptide-related sequence B) [Libraty et al., 2014], CD274 [Jeong et al., 2008], SLAMF7 [O'Connell et al., 2019], CMPK2 [El-Diwany et al., 2018], IFIT5 [Rohaim et al., 2018], APOBEC3A [Berger et al., 2011], APOBEC3F [Burdick et al., 2013], HAVCR2 [Sironi et al., 2014], NMI (N-myc and STAT interactor) [Xiong et al., 2019], CD96 [Eriksson et al., 2012], CLEC2D [Varaden et al., 2019], CD53 [Tippett et al., 2013] and CD69 [Yong et al., 2017] were linked with progression of various viral infections, but these genes may be key for progression of SARS-CoV-2 infection. Enriched genes such as CD209 [Amraei et al., 2020], APOL1 [Wu et al., 2020], PARP14 [Webb and Saad, 2020], TF (transferrin) [McLaughlin et al., 2020], ACE2 [Yan et al., 2020], FLT1 [Giardini et al., 2020] and BRCA2 [Singh and Bharara Singh, 2020] were involved in advancement of SARS-CoV-2 infection. Enriched genes such as IFI44 [Busse et al., 2020], IFI44L [Busse et al., 2020], OPRM1 [Dugas, 2013], PECAM1 [Wang et al., 1998], IL7R [Inchley et al., 2013] and TRIM21 [Yahya et al., 2017] were involved in advancement of respiratory syncytial virus infection, but these gene may be associated with development of SARS-CoV-2 infection. Enriched genes such as IFI16 [Chang et al., 2019], SIGLEC10 [Xie et al., 2017] and CD163 [Burkard et al., 2018] were responsible for advancement of porcine reproductive and respiratory syndrome virus infection, but these genes may be linked with development of SARS-CoV-2 infection. The novel biomarkers (PIK3AP1, PDE4B, NT5C3A, TNIP3, CLEC7A, DTX3L, SIRPB1, ACOD1, FCER1G, AIF1, MNDA (myeloid cell nuclear differentiation antigen), LILRA5, HTN1, HTN3, IKZF3, WIPF1, DDX60, MUC13, BATF2, NUB1, MUC3A, NEXN (nexilin F-actin binding protein), CD300E, PRLR (prolactin receptor), PDCD1LG2, SLAMF8, IL10RA, LGMN (legumain), SPN (sialophorin), TAGAP (T cell activation RhoGTPase activating protein), NAIP (NLR family apoptosis inhibitory protein), LILRB1, RTP4, FGL2, CD84, CLEC4E, SERPING1, C1QB, C1QC, MICA (MHC class I polypeptide-related sequence A), PARP9, C4BPB, HERC6, KLRD1, MUC19, SIGLEC14, MPEG1, ABCC9, RGS1, LGALS9, RNASE6, HMG2, RESF1,

Table 7
Target gene - miRNA interaction table.

Regulation	Target genes	Degree	MicroRNA	Regulation	Target genes	Degree	MicroRNA
Up	CCND2	179	hsa-mir-3916	Down	MKNK2	195	hsa-mir-1256
Up	FAM241A	174	hsa-mir-4306	Down	TUBB2A	193	hsa-mir-1253
Up	REL	153	hsa-mir-4261	Down	IGFBP5	144	hsa-mir-1264
Up	POU2F1	150	hsa-mir-3911	Down	PHB2	132	hsa-mir-1183
Up	MICA	142	hsa-mir-2392	Down	MAZ	122	hsa-mir-1470
Up	IKZF3	134	hsa-mir-8082	Down	ZNF703	115	hsa-mir-1293
Up	RBMS2	132	hsa-mir-3975	Down	ENPP5	114	hsa-mir-1205
Up	ARL10	131	hsa-mir-3185	Down	HSPA1B	113	hsa-mir-1276
Up	SULT1B1	131	hsa-mir-4516	Down	NR2F6	105	hsa-mir-1262
Up	APOL6	127	hsa-mir-6088	Down	ITGA3	101	hsa-mir-1255a
Up	HMGA2	126	hsa-mir-4500	Down	EIF4H	97	hsa-mir-3142
Up	ZNF562	111	hsa-mir-8054	Down	RHOB	92	hsa-mir-3163
Up	UBXN2B	109	hsa-mir-6079	Down	PTPRF	90	hsa-mir-1275
Up	SHISA9	109	hsa-mir-7641	Down	RPL18A	85	hsa-mir-1200
Up	SLFN12L	104	hsa-mir-1200	Down	GIPC1	85	hsa-mir-3202
Up	PARP15	104	hsa-mir-1206	Down	BICD2	82	hsa-mir-5690
Up	NEGR1	102	hsa-mir-1179	Down	EEF2	80	hsa-mir-6090
Up	IGF1	98	hsa-mir-1305	Down	TRAF7	80	hsa-mir-1321
Up	CLIC4	97	hsa-mir-1323	Down	FKBP8	77	hsa-mir-4259
Up	PLEKHG2	94	hsa-mir-3167	Down	WDR13	74	hsa-mir-1273f
Up	L2HGDH	93	hsa-mir-1912	Down	RPS15A	73	hsa-mir-3119
Up	KCNJ6	90	hsa-mir-1470	Down	CLDN4	73	hsa-mir-3656
Up	FKBP5	88	hsa-mir-1243	Down	FAM229B	73	hsa-mir-4279
Up	CD226	87	hsa-mir-4257	Down	ERBB2	73	hsa-mir-4441
Up	MKI67	84	hsa-mir-1976	Down	RPL13A	72	hsa-mir-4476
Up	MCF2L2	82	hsa-mir-3923	Down	CLU	69	hsa-mir-8085
Up	OLR1	81	hsa-mir-2054	Down	TRIM28	65	hsa-mir-4450
Up	SYNPO2L	81	hsa-mir-3170	Down	RRAD	62	hsa-mir-4500
Up	MCM8	80	hsa-mir-3652	Down	CLSTN1	62	hsa-mir-8089
Up	SPATA5	79	hsa-mir-3122	Down	EFNA1	62	hsa-mir-2392
Up	GPRIN3	79	hsa-mir-3665	Down	RPL37	61	hsa-mir-5697
Up	FMNL3	78	hsa-mir-2278	Down	FOS	58	hsa-mir-8081
Up	LMNB1	77	hsa-mir-3915	Down	CMTM4	57	hsa-mir-4434
Up	CD180	77	hsa-mir-3926	Down	EPHA2	57	hsa-mir-1182
Up	PHACTR4	76	hsa-mir-3929	Down	TAGLN2	57	hsa-mir-1972
Up	RAP2C	76	hsa-mir-4658	Down	CD59	56	hsa-mir-8067
Up	PLSCR1	75	hsa-mir-4326	Down	PIN1	56	hsa-mir-5090
Up	SIGLEC14	74	hsa-mir-3612	Down	MID1IP1	54	hsa-mir-6860
Up	SBK1	73	hsa-mir-4493	Down	RPS16	53	hsa-mir-8055
Up	PPM1K	72	hsa-mir-3197	Down	ARHGAP39	53	hsa-mir-6130
Up	SAMD12	71	hsa-mir-4287	Down	P4HB	52	hsa-mir-4710
Up	PAG1	68	hsa-mir-4748	Down	SLC2A1	50	hsa-mir-1538
Up	ACSL4	68	hsa-mir-5692b	Down	WFDC6	50	hsa-mir-4259
Up	APOBEC3F	67	hsa-mir-3689c	Down	NDUFAF3	48	hsa-mir-4422
Up	FUT10	67	hsa-mir-4470	Down	CTNNB1	48	hsa-mir-4765
Up	XRCC2	65	hsa-mir-3686	Down	UBL5	45	hsa-mir-5698
Up	N4BP1	65	hsa-mir-3689d	Down	TEF	44	hsa-mir-7703
Up	LHFPL2	65	hsa-mir-4780	Down	RPS19	44	hsa-mir-4770
Up	MMS22L	64	hsa-mir-4252	Down	DHCR24	43	hsa-mir-3911
Up	ENTPD1	64	hsa-mir-4291	Down	RPL27A	42	hsa-mir-4252
Up	SFMBT2	63	hsa-mir-1202	Down	KRT8	42	hsa-mir-7150
Up	STAT2	63	hsa-mir-4266	Down	REXO2	42	hsa-mir-8485
Up	RAB8B	61	hsa-mir-298	Down	DDR1	40	hsa-mir-6133
Up	ZFYVE26	61	hsa-mir-3154	Down	UQCRQ	40	hsa-mir-3122
Up	ZNFX1	61	hsa-mir-5093	Down	SERTAD1	40	hsa-mir-1827
Up	KLRD1	60	hsa-mir-3133	Down	UQCR11	39	hsa-mir-1297
Up	MTO1	60	hsa-mir-4430	Down	JUN	38	hsa-mir-1321
Up	MC2R	59	hsa-mir-4271	Down	ITPA	38	hsa-mir-3135b
Up	TNIP3	57	hsa-mir-3650	Down	PPEF2	38	hsa-mir-6078
Up	MICB	56	hsa-mir-3977	Down	NOP53	36	hsa-mir-8052
Up	SP110	55	hsa-mir-1265	Down	RPLP0	36	hsa-mir-4794
Up	SYT2	55	hsa-mir-3941	Down	SLC25A25	35	hsa-mir-8064
Up	PRLR	54	hsa-mir-1181	Down	IER3	34	hsa-mir-4266
Up	CD209	54	hsa-mir-1273a	Down	CYB561	34	hsa-mir-4303
Up	FSIP2	53	hsa-mir-3125	Down	STEAP3	33	hsa-mir-4488
Up	ZCCHC2	53	hsa-mir-3164	Down	RPS14	33	hsa-mir-4493
Up	CPA4	52	hsa-mir-1827	Down	STOML3	33	hsa-mir-4491
Up	SH2B3	52	hsa-mir-5691	Down	RPL10A	33	hsa-mir-4705
Up	INHBA	51	hsa-mir-3973	Down	BORCS7	33	hsa-mir-5693

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Table 7 (continued)

Regulation	Target genes	Degree	MicroRNA	Regulation	Target genes	Degree	MicroRNA
Up	DTX3L	51	hsa-mir-6086	Down	NTN1	33	hsa-mir-6130
Up	IL2RA	50	hsa-mir-1248	Down	SOCS3	32	hsa-mir-8062
Up	C6orf223	50	hsa-mir-3202	Down	PTK7	32	hsa-mir-2110
Up	BCAT1	50	hsa-mir-3921	Down	DUSP1	30	hsa-mir-4678
Up	CDH6	50	hsa-mir-8085	Down	CITED2	30	hsa-mir-3148
Up	PRKCB	49	hsa-mir-1261	Down	CFAP65	29	hsa-mir-4432
Up	CLEC2D	49	hsa-mir-3714	Down	ARL6IP4	29	hsa-mir-3155b
Up	SRGAP1	49	hsa-mir-4293	Down	RPL17-C18orf32	28	hsa-mir-3609
Up	CCL5	49	hsa-mir-4438	Down	JUNB	28	hsa-mir-4515
Up	POU2F3	49	hsa-mir-4675	Down	RPS9	28	hsa-mir-4642
Up	EIF2AK2	48	hsa-mir-3646	Down	RPL4	27	hsa-mir-3170
Up	IGSF6	48	hsa-mir-4269	Down	RPS3	27	hsa-mir-4477a
Up	SIGLEC10	47	hsa-mir-1302	Down	RGL2	27	hsa-mir-6089
Up	SLC2A3	47	hsa-mir-3907	Down	JUND	27	hsa-mir-3141
Up	KPNA5	47	hsa-mir-3918	Down	RPS21	27	hsa-mir-4748
Up	CD274	47	hsa-mir-3978	Down	TXNL4A	26	hsa-mir-5095
Up	TNFSF14	46	hsa-mir-3149	Down	KLF4	26	hsa-mir-663a
Up	PLCXD3	45	hsa-mir-3182	Down	UNC93B1	26	hsa-mir-151b
Up	SLC8A1	45	hsa-mir-4775	Down	NME2	26	hsa-mir-4792
Up	MTAP	45	hsa-mir-5688	Down	SLPI	26	hsa-mir-9500
Up	CMKLR1	45	hsa-mir-8058	Down	RPL9	25	hsa-mir-5696
Up	SRRM4	45	hsa-mir-8485	Down	GNB2	25	hsa-mir-4472
Up	DOCK11	44	hsa-mir-4463	Down	RPS2	25	hsa-mir-3943
Up	SPN	43	hsa-mir-1913	Down	TMED9	25	hsa-mir-3929
Up	ZEB1	43	hsa-mir-2052	Down	RPS27	24	hsa-mir-6088
Up	BCL2L15	43	hsa-mir-4435	Down	BSG	24	hsa-mir-1299
Up	BTN3A3	42	hsa-mir-3163	Down	RPLP1	24	hsa-mir-4464
Up	UHRF1BP1	42	hsa-mir-4434	Down	DENND6B	24	hsa-mir-3178
Up	RPAP2	41	hsa-mir-3655	Down	RPL34	24	hsa-mir-4284
Up	SEMA6D	41	hsa-mir-3662	Down	ATP6VOB	24	hsa-mir-4316
Up	NHSL2	40	hsa-mir-2113	Down	VPS51	23	hsa-mir-3180
Up	RASSF2	40	hsa-mir-3656	Down	CD81	23	hsa-mir-3937
Up	CD300E	40	hsa-mir-3670	Down	SLC2A4RG	23	hsa-mir-5685
Up	ITGA1	40	hsa-mir-3924	Down	PIGQ	23	hsa-mir-6132
Up	ZNF429	39	hsa-mir-1289	Down	GDF15	23	hsa-mir-4308
Up	STARD8	39	hsa-mir-3649	Down	ANKRD65	23	hsa-mir-4641
Up	P2RX7	39	hsa-mir-4312	Down	SELENOS	23	hsa-mir-1912
Up	CARD6	39	hsa-mir-4537	Down	SLC25A6	22	hsa-mir-5787
Up	PIK3CG	39	hsa-mir-4679	Down	RPS7	22	hsa-mir-1278
Up	TLR7	39	hsa-mir-8087	Down	CCDC39	22	hsa-mir-133b
Up	SERPING1	38	hsa-mir-1262	Down	DGCR6L	22	hsa-mir-661
Up	CREB5	38	hsa-mir-3671	Down	COX6A1	22	hsa-mir-300
Up	IFITM1	38	hsa-mir-4295	Down	TRIM8	21	hsa-mir-6833-3p
Up	RASSF4	37	hsa-mir-4441	Down	TXNDC5	21	hsa-mir-4530
Up	ATP6V1B2	37	hsa-mir-6082	Down	RPL15	21	hsa-mir-218-1-3p
Up	GIMAP4	36	hsa-mir-559	Down	TBCA	21	hsa-mir-3685
Up	CYTIP	36	hsa-mir-6131	Down	ALDH3B1	20	hsa-mir-4271
Up	SKAP2	35	hsa-mir-1273f	Down	SMDT1	20	hsa-mir-5681a
Up	SAMD9L	35	hsa-mir-2110	Down	ARL3	20	hsa-mir-4660
Up	IFITM3	35	hsa-mir-4309	Down	CBX7	20	hsa-mir-6077
Up	PKNOX2	35	hsa-mir-4447	Down	RPS28	20	hsa-mir-4730
Up	SLFN5	35	hsa-mir-4635	Down	TADA3	20	hsa-mir-4274
Up	TRIM38	35	hsa-mir-6077	Down	RPL35	20	hsa-mir-6856-3p
Up	SLC36A1	34	hsa-mir-3147	Down	PTPRN2	20	hsa-mir-4311
Up	CDH8	34	hsa-mir-3183	Down	CAPS	20	hsa-mir-92a-2-5p
Up	GPR82	34	hsa-mir-4267	Down	SPEF1	20	hsa-mir-6129
Up	GREB1	34	hsa-mir-4303	Down	RPL7	19	hsa-mir-4451
Up	MORC4	33	hsa-mir-1321	Down	PSMA7	19	hsa-mir-1197
Up	GBP4	33	hsa-mir-3143	Down	NDUFA2	19	hsa-mir-4751
Up	RASGRP3	33	hsa-mir-4264	Down	RPL32	19	hsa-mir-451b
Up	CLEC7A	33	hsa-mir-4284	Down	PLXNB1	19	hsa-mir-1324
Up	DDHD1	33	hsa-mir-4302	Down	ROMO1	19	hsa-mir-3666
Up	CCR5	33	hsa-mir-4469	Down	ELF3	19	hsa-mir-4428
Up	PROX1	33	hsa-mir-4501	Down	SNRPB	19	hsa-mir-5704
Up	CD84	33	hsa-mir-4736	Down	PCYT2	18	hsa-mir-4285
Up	ALOX5AP	32	hsa-mir-3135b	Down	S100A2	18	hsa-mir-4736
Up	CASP10	32	hsa-mir-4794	Down	HSPA2	18	hsa-mir-4419b
Up	CXCL10	31	hsa-mir-4288	Down	SEC14L3	18	hsa-mir-4323
Up	LILRB2	30	hsa-mir-3920	Down	VWA7	18	hsa-mir-5186
Up	ZEB2	30	hsa-mir-429	Down	RPL3	17	hsa-mir-671-5p
Up	PATL1	30	hsa-mir-4519	Down	RPL36	17	hsa-mir-4270

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Table 7 (continued)

Regulation	Target genes	Degree	MicroRNA	Regulation	Target genes	Degree	MicroRNA
Up	CBL	30	hsa-mir-5192	Down	ELOB	17	hsa-mir-4692
Up	DAB2	30	hsa-mir-604	Down	RPL18	16	hsa-mir-3674
Up	ZNF519	30	hsa-mir-6069	Down	AHNAK2	16	hsa-mir-6165
Up	HAVCR2	30	hsa-mir-6089	Down	RPS17	16	hsa-mir-4433a-5p
Up	PNPT1	30	hsa-mir-7977	Down	AK1	16	hsa-mir-3672
Up	BRIP1	29	hsa-mir-4419b	Down	DVL1	16	hsa-mir-4469
Up	MGAT4C	29	hsa-mir-607	Down	DDOST	16	hsa-mir-4257
Up	FOXL2NB	29	hsa-mir-661	Down	SDC1	16	hsa-mir-4480
Up	CXorf21	27	hsa-mir-3666	Down	BCAM	16	hsa-mir-6087
Up	SMCHD1	27	hsa-mir-421	Down	CDC34	15	hsa-mir-631
Up	RPH3A	27	hsa-mir-4739	Down	TUBB4B	15	hsa-mir-301a-3p
Up	IFIT3	27	hsa-mir-5095	Down	KRT10	15	hsa-mir-548ah-5p
Up	FPR2	27	hsa-mir-558	Down	TMEM9	15	hsa-mir-4487
Up	GNB4	27	hsa-mir-633	Down	SIVA1	15	hsa-mir-581
Up	NSUN3	26	hsa-mir-935	Down	CBR1	15	hsa-mir-3174
Up	CYBB	25	hsa-mir-1282	Down	RUVBL2	15	hsa-mir-5047
Up	PTPRE	25	hsa-mir-1298-3p	Down	CD82	15	hsa-mir-4294
Up	IRF4	25	hsa-mir-4313	Down	CXXC5	15	hsa-mir-4679
Up	ASAP1	25	hsa-mir-4432	Down	LRG1	15	hsa-mir-1976
Up	TLR4	24	hsa-mir-4694-3p	Down	GPX1	15	hsa-mir-1587
Up	SLC25A28	23	hsa-mir-4644	Down	LRRC45	15	hsa-mir-4484
Up	RNF213	23	hsa-mir-4738-3p	Down	RPS5	14	hsa-mir-3166
Up	STX17	23	hsa-mir-5589-5p	Down	LRWD1	14	hsa-mir-4468
Up	TMCC3	23	hsa-mir-6126	Down	GUK1	14	hsa-mir-4505
Up	ZNF37A	23	hsa-mir-764	Down	CALML4	14	hsa-mir-190b
Up	TGFB1	22	hsa-mir-1322	Down	TRAPPC2L	14	hsa-mir-4533
Up	LAIR1	22	hsa-mir-4454	Down	RPL7A	13	hsa-mir-744-5p
Up	APOBEC3A	22	hsa-mir-640	Down	UBXN11	13	hsa-mir-217
Up	ASAH2B	22	hsa-mir-6800-3p	Down	IMPA2	13	hsa-mir-4421
Up	IL7R	22	hsa-mir-8052	Down	SELENOH	13	hsa-mir-4459
Up	CYSLTR2	22	hsa-mir-9500	Down	CD9	13	hsa-mir-4460
Up	OPRM1	21	hsa-mir-564	Down	TSPAN15	13	hsa-mir-4307
Up	HLX	20	hsa-mir-1260b	Down	ADIRF	13	hsa-mir-3689d
Up	SLC30A3	20	hsa-mir-4270	Down	COMT	12	hsa-mir-3919
Up	ANKRD44	20	hsa-mir-4502	Down	OAZ1	12	hsa-mir-6070
Up	LILRB1	20	hsa-mir-5096	Down	PRRT3	12	hsa-mir-3655
Up	APOL4	20	hsa-mir-5481	Down	CLDN7	12	hsa-mir-4478
Up	EPB41L3	20	hsa-mir-548u	Down	PRDX5	12	hsa-mir-1286
Up	TNFSF10	20	hsa-mir-5697	Down	CKB	11	hsa-mir-551a
Up	HOXB13	20	hsa-mir-6133	Down	SLC27A2	11	hsa-mir-6832-3p
Up	SNX10	20	hsa-mir-6806-3p	Down	HSPA1A	11	hsa-mir-4424
Up	CD86	20	hsa-mir-8055	Down	RPL21	11	hsa-mir-652-3p
Up	MX2	19	hsa-mir-2117	Down	RPL36A	11	hsa-mir-760
Up	IFI44L	19	hsa-mir-4256	Down	METRN	11	hsa-mir-6864-3p
Up	STAT1	19	hsa-mir-605-5p	Down	ARHGEF17	11	hsa-mir-4320
Up	FCHSD2	19	hsa-mir-6074	Down	SSBP4	11	sa-mir-5007-5p
Up	OAS2	19	hsa-mir-620	Down	ECSIT	11	hsa-mir-8071
Up	APOL2	18	hsa-mir-1273e	Down	RPS10	10	hsa-mir-421
Up	CD96	18	hsa-mir-1273g-3p	Down	GADD45GIP1	10	hsa-mir-6881-3p
Up	CXCR2	18	hsa-mir-6832-5p	Down	DHX30	10	hsa-mir-1260b
Up	FLT1	18	hsa-mir-6844	Down	RIPK4	10	hsa-mir-548an
Up	CD68	18	hsa-mir-6867-3p	Down	RPL19	10	hsa-mir-5197-5p
Up	PLA2G7	18	hsa-mir-7702	Down	RPS8	10	hsa-mir-1303
Up	ASB3	18	hsa-mir-7849-3p	Down	RPS15	10	hsa-mir-505-3p
Up	MPEG1	17	hsa-mir-450a-1-3p	Down	EDF1	10	hsa-mir-6783-5p
Up	APOL1	17	hsa-mir-6764-5p	Down	RPS3A	9	hsa-mir-342-3p
Up	TRIM5	16	hsa-mir-3689f	Down	COX7B	9	hsa-mir-4310
Up	RTP4	16	hsa-mir-4676-3p	Down	FDXR	9	hsa-mir-4777-3p
Up	IFIT1	16	hsa-mir-578	Down	YIF1B	9	hsa-mir-3190-3p
Up	GADL1	16	hsa-mir-6504-3p	Down	IFT140	9	hsa-mir-558
Up	NCKAP1L	16	hsa-mir-6739-3p	Down	TKT	9	hsa-mir-206
Up	TRAPPC3L	15	hsa-mir-1293	Down	DAG1	9	hsa-mir-3676-3p
Up	TLR3	15	hsa-mir-137	Down	RPL8	9	hsa-mir-296-3p
Up	KYNU	15	hsa-mir-4494	Down	DNALI1	9	hsa-mir-4768-3p
Up	FCAR	15	hsa-mir-5685	Down	CCDC74B	9	hsa-mir-3140-3p
Up	SP100	15	hsa-mir-6073	Down	PGLS	9	hsa-mir-664b-3p
Up	CCDC169	15	hsa-mir-8067	Down	SPINT2	9	hsa-mir-3182
Up	PRRG3	15	hsa-mir-8070	Down	CFAP73	9	hsa-mir-6715b-5p
Up	SNX20	14	hsa-mir-3116	Down	LMNA	8	hsa-mir-340-5p
Up	XRN1	14	hsa-mir-5011-5p	Down	CD151	8	hsa-mir-506-3p
Up	RPL3L	14	hsa-mir-548ac	Down	PLXNB2	8	hsa-mir-493-3p

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Table 7 (continued)

Regulation	Target genes	Degree	MicroRNA	Regulation	Target genes	Degree	MicroRNA
Up	JAK2	14	hsa-mir-5692a	Down	ID1	8	hsa-mir-520h
Up	PLEK	14	hsa-mir-5696	Down	TIMM13	8	hsa-mir-15a-5p
Up	PBX1	14	hsa-mir-617	Down	NDUFA4	8	hsa-mir-147a
Up	CLEC4E	14	hsa-mir-6742-3p	Down	RPS12	8	hsa-mir-331-3p
Up	ARHGEF3	13	hsa-mir-557	Down	TRAF4	8	hsa-mir-221-3p
Up	ZNF471	13	hsa-mir-6760-5p	Down	RPL26	8	hsa-mir-935
Up	FRMD3	13	hsa-mir-6873-3p	Down	LAMC2	8	hsa-mir-622
Up	SRGN	13	hsa-mir-7978	Down	RPL27	8	hsa-mir-107
Up	MGAT4A	12	hsa-mir-3132	Down	CCDC74A	8	hsa-mir-636
Up	ADAP2	12	hsa-mir-3199	Down	RPL29	8	hsa-mir-1914-5p
Up	BRCA2	12	hsa-mir-4691-3p	Down	FAM166B	8	hsa-mir-6715a-3p
Up	NT5C3A	12	hsa-mir-499b-3p	Down	RPL31	7	hsa-mir-100-5p
Up	SLC7A7	12	hsa-mir-5701	Down	UQCRC1	7	hsa-mir-183-5p
Up	WNT7A	12	hsa-mir-572	Down	KEAP1	7	hsa-mir-141-3p
Up	CLEC12A	12	hsa-mir-603	Down	STOML2	7	hsa-mir-31-5p
Up	LILRA5	12	hsa-mir-658	Down	TUFM	7	hsa-mir-339-5p
Up	PLXNC1	12	hsa-mir-7853-5p	Down	PPP4C	7	hsa-mir-1229-3p
Up	IL10RA	12	hsa-mir-8064	Down	PRDX2	7	hsa-mir-10a-5p
Up	HHLA1	12	hsa-mir-8075	Down	TXNDC17	7	hsa-mir-137
Up	FAM180B	12	hsa-mir-938	Down	COMMD6	7	hsa-mir-4423-5p
Up	ETV5	11	hsa-mir-1539	Down	SPAG7	7	hsa-mir-216b-3p
Up	FYB1	11	hsa-mir-206	Down	SLC44A4	7	hsa-mir-764
Up	C2orf91	11	hsa-mir-508-5p	Down	GTF3C5	6	hsa-mir-222-3p
Up	ME2	11	hsa-mir-6512-3p	Down	POLR2L	6	hsa-mir-744-5p
Up	UNC80	11	hsa-mir-7974	Down	CTSD	6	hsa-mir-503-5p
Up	TLR2	10	hsa-mir-101-5p	Down	ITGB4	6	hsa-mir-16-5p
Up	PRR26	10	hsa-mir-218-1-3p	Down	COX5A	6	hsa-mir-20a-5p
Up	BCL2L14	10	hsa-mir-4527	Down	AAMP	6	hsa-mir-130b-5p
Up	FNIP2	10	hsa-mir-507	Down	CHCHD2	6	hsa-mir-320b
Up	CCL2	10	hsa-mir-518a-5p	Down	UBXN1	6	hsa-mir-373-3p
Up	ITK	10	hsa-mir-6083	Down	MIF	6	hsa-mir-451a
Up	TRIM21	10	hsa-mir-6124	Down	TUBGCP2	5	hsa-mir-92a-3p
Up	ELMO1	10	hsa-mir-6736-3p	Down	HSPBP1	5	hsa-mir-7-5p
Up	ABCC9	10	hsa-mir-890	Down	EIF3CL	5	hsa-mir-7155-3p
Up	MMP13	9	hsa-mir-100-5p	Down	GSTP1	5	hsa-mir-133a-3p
Up	PDE3B	9	hsa-mir-130b-3p	Down	RPS18	5	hsa-mir-218-5p
Up	TNFSF13B	9	hsa-mir-202-3p	Down	POLR2I	5	hsa-mir-1268a
Up	TIAM2	9	hsa-mir-3692-3p	Down	ROPN1L	5	hsa-mir-128-3p
Up	WIPF1	9	hsa-mir-3917	Down	DNAJB2	5	hsa-mir-1238-3p
Up	MS4A4A	9	hsa-mir-4700-3p	Down	MAP9	5	hsa-mir-548m
Up	TCF21	9	hsa-mir-5088-5p	Down	RPLP2	4	hsa-mir-766-3p
Up	RAD51D	9	hsa-mir-550b-2-5p	Down	SLC25A29	4	hsa-mir-15b-5p
Up	FCGR3B	9	hsa-mir-6740-3p	Down	RPL13	4	hsa-mir-744-5p
Up	CASP1	9	hsa-mir-6837-3p	Down	LAMTOR4	4	hsa-mir-424-5p
Up	P2RY6	8	hsa-mir-1269a	Down	SELENBP1	4	hsa-mir-20a-5p
Up	EPB41L2	8	hsa-mir-222-3p	Down	STUB1	4	hsa-mir-1178-3p
Up	KMO	8	hsa-mir-302f	Down	FAU	4	hsa-mir-140-3p
Up	BTN3A1	8	hsa-mir-324-5p	Down	ATAD3A	4	hsa-mir-149-5p
Up	GALR1	8	hsa-mir-411-5p	Down	NHP2	4	hsa-mir-330-5p
Up	CASP5	8	hsa-mir-4480	Down	CRIP2	4	hsa-mir-449a
Up	CXCL11	8	hsa-mir-4511	Down	RPL39	4	hsa-mir-30c-5p
Up	LAMP3	8	hsa-mir-548b-3p	Down	POR	4	hsa-mir-214-3p
Up	MUC3A	8	hsa-mir-6785-5p	Down	RPS29	4	hsa-mir-484
Up	GIMAP6	7	hsa-mir-5003-5p	Down	MAPK8IP1	4	hsa-mir-346
Up	PTPRC	7	hsa-mir-4464	Down	IGFBP2	4	hsa-mir-491-3p
Up	FCGR2A	7	hsa-mir-29b-2-5p	Down	EEF1D	4	hsa-mir-149-5p
Up	SIM1	7	hsa-mir-4455	Down	SNRPD2	4	hsa-mir-296-3p
Up	TBC1D8B	7	hsa-mir-7158-3p	Down	KNDC1	4	hsa-mir-550b-2-5p
Up	MSR1	7	hsa-mir-7108-3p	Down	COX5B	4	hsa-mir-3120-3p
Up	EVI2A	7	hsa-mir-329-3p	Down	BAIAP3	4	hsa-mir-4462
Up	PROSER1	7	hsa-mir-21-5p	Down	RPS13	3	hsa-let-7a-5p
Up	SUCNR1	6	hsa-mir-1277-5p	Down	ITGB5	3	hsa-mir-155-5p
Up	GIMAP7	6	hsa-mir-513b-5p	Down	TST	3	hsa-mir-548b-3p
Up	CYP46A1	6	hsa-mir-6828-5p	Down	SGSM3	3	hsa-mir-19b-3p
Up	TFEC	6	hsa-mir-769-5p	Down	TPPP3	3	hsa-mir-99a-5p
Up	OAS3	6	hsa-mir-502-5p	Down	NPEPL1	3	hsa-mir-19a-3p
Up	IFI16	6	hsa-mir-136-5p	Down	LRP5	3	hsa-mir-23a-3p
Up	GBP2	6	hsa-mir-4709-5p	Down	DUS1L	3	hsa-mir-193b-3p
Up	FAM83A	5	hsa-mir-5090	Down	HAGH	3	hsa-mir-30d-5p
Up	IFTT2	5	hsa-mir-645	Down	MYL6	3	hsa-mir-106b-5p
Up	DPYD	5	hsa-mir-302b-3p	Down	NDUFB10	3	hsa-mir-132-3p

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Table 7 (continued)

Regulation	Target genes	Degree	MicroRNA	Regulation	Target genes	Degree	MicroRNA
Up	CSGALNACT2	5	hsa-mir-377-3p	Down	TALDO1	3	hsa-mir-378a-5p
Up	LGMN	5	hsa-mir-642a-5p	Down	C12orf57	3	hsa-mir-615-3p
Up	PDE4B	5	hsa-mir-330-5p	Down	ACTR1B	3	hsa-mir-99b-5p
Up	DOCK10	5	hsa-mir-218-5p	Down	GNA11	3	hsa-mir-3922-5p
Up	TNFAIP6	4	hsa-mir-19b-2-5p	Down	ARPC1A	3	hsa-let-7i-5p
Up	FPR3	4	hsa-mir-718	Down	SSNA1	3	hsa-mir-1-3p
Up	NAIP	4	hsa-mir-221-3p	Down	ST14	3	hsa-mir-27b-3p
Up	PIK3AP1	4	hsa-mir-32-5p	Down	LGALS3	3	hsa-mir-128-3p
Up	MPP1	4	hsa-mir-15b-5p	Down	TACSTD2	3	hsa-mir-125b-1-3p
Up	CD69	4	hsa-mir-92a-3p	Down	APBB1	3	hsa-mir-148b-3p
Up	NMI	4	hsa-mir-29a-3p	Down	PTPRU	3	hsa-mir-574-5p
Up	SERPINB9	4	hsa-mir-127-3p	Down	COPE	3	hsa-mir-1301-3p
Up	USP18	4	hsa-mir-215-5p	Down	CCDC33	3	hsa-mir-6822-3p
Up	NSMAF	4	hsa-mir-25-3p	Down	CSTB	3	hsa-mir-125b-2-3p
Up	OSR1	4	hsa-mir-451a	Down	ATG4B	2	hsa-let-7b-5p
Up	TMEM45A	4	hsa-mir-181a-5p	Down	EEF1G	2	hsa-mir-218-5p
Up	IKZF1	4	hsa-mir-19a-3p	Down	RPL6	2	hsa-mir-16-5p
Up	IFT5	4	hsa-mir-146a-5p	Down	CIB1	2	hsa-mir-26b-5p
Up	NEDD4	4	hsa-mir-590-3p	Down	NDUFB2	2	hsa-mir-205-5p
Up	SLCO2B1	3	hsa-mir-4673	Down	ECI1	2	hsa-mir-155-5p
Up	LRCH4	3	hsa-mir-484	Down	CIRBP	2	hsa-mir-30a-5p
Up	PML	3	hsa-mir-378a-3p	Down	AGPAT2	2	hsa-mir-744-5p
Up	MUC13	3	hsa-mir-148b-3p	Down	EPHX1	2	hsa-mir-193b-3p
Up	FLI1	3	hsa-mir-145-5p	Down	GPX4	2	hsa-mir-124-3p
Up	BATF2	3	hsa-mir-375	Down	PYCR2	2	hsa-mir-92b-3p
Up	OASL	3	hsa-mir-1-3p	Down	CELSR1	2	hsa-mir-615-3p
Up	PTPN22	3	hsa-mir-624-3p	Down	CRELD2	2	hsa-mir-93-5p
Up	NUB1	3	hsa-mir-183-5p	Down	PTTG1IP	2	hsa-mir-98-5p
Up	SAMSN1	3	hsa-mir-7-5p	Down	KRT5	2	hsa-mir-196a-5p
Up	BIRC3	3	hsa-mir-98-5p	Down	AGR2	2	hsa-mir-197-3p
Up	A2M	3	hsa-mir-128-3p	Down	JTB	2	hsa-mir-222-3p
Up	FGL2	3	hsa-mir-155-5p	Down	SLC20A2	2	hsa-mir-877-3p
Up	IFI44	3	hsa-mir-146a-5p	Down	FOSB	2	hsa-mir-224-5p
Up	TRIM22	3	hsa-mir-26b-5p	Down	IGFBP7	2	hsa-mir-1-3p
Up	CXCL9	3	hsa-mir-34a-5p	Down	NDUFS6	2	hsa-mir-27b-3p
Up	PTPRO	3	hsa-mir-20a-5p	Down	ERP29	2	hsa-mir-122-5p
Up	HERC6	3	hsa-mir-591	Down	PTOV1	2	hsa-mir-378a-5p
Up	SLF2	3	hsa-mir-192-5p	Down	SEC61B	2	hsa-mir-324-5p
Up	IL18RAP	2	hsa-mir-4677-3p	Down	UBXN6	2	hsa-mir-186-5p
Up	IRF8	2	hsa-mir-646	Down	COL21A1	2	hsa-mir-29c-3p
Up	GIMAP2	2	hsa-mir-193b-3p	Down	MLF1	2	hsa-mir-422a
Up	ATP10B	2	hsa-mir-148b-3p	Down	PIH1D3	2	hsa-mir-591
Up	IFI6	2	hsa-mir-1225-3p	Down	PKIG	2	hsa-mir-331-3p
Up	EPSTI1	2	hsa-mir-654-5p	Down	KRT19	2	hsa-mir-193b-3p
Up	CLEC5A	2	hsa-mir-125a-5p	Down	PROS1	2	hsa-mir-494-3p
Up	MUC19	2	hsa-mir-5195-3p	Down	MAGED2	2	hsa-mir-877-3p
Up	GAB3	2	hsa-mir-124-3p	Down	GPR162	2	hsa-mir-93-3p
Up	DGKA	2	hsa-mir-484	Down	LAMB2	2	hsa-mir-196b-5p
Up	C4BPB	2	hsa-mir-142-3p	Down	FIS1	2	hsa-mir-505-3p
Up	HERC5	2	hsa-mir-3529-3p	Down	ENKD1	2	hsa-mir-193b-3p
Up	ISG15	2	hsa-mir-1-3p	Down	ARF5	2	hsa-mir-18a-3p
Up	MX1	2	hsa-mir-204-5p	Down	GRHPR	2	hsa-mir-1180-3p
Up	DDX58	2	hsa-mir-10b-5p	Down	CYC1	2	hsa-mir-661
Up	PLIN2	2	hsa-mir-30a-5p	Down	CCDC153	2	hsa-mir-3677-5p
Up	RSAD2	2	hsa-mir-146a-5p	Down	RHBDD2	1	hsa-let-7e-5p
Up	DDX60	2	hsa-mir-1-3p	Down	CYB5R1	1	hsa-mir-16-5p
Up	TRANK1	2	hsa-mir-26b-5p	Down	CCDC96	1	hsa-mir-25-3p
Up	TLR1	2	hsa-mir-335-5p	Down	MB	1	hsa-mir-26b-5p
Up	HSD17B2	2	hsa-mir-124-3p	Down	MAN2B1	1	hsa-mir-30a-5p
Up	GABRE	2	hsa-mir-98-5p	Down	PPOX	1	hsa-mir-30a-5p
Up	CLIC2	2	hsa-mir-26b-5p	Down	COX4I1	1	hsa-mir-92a-3p
Up	PSTPIP2	2	hsa-mir-24-3p	Down	GCHFR	1	hsa-mir-92a-3p
Up	CCL4	2	hsa-mir-195-5p	Down	DNPH1	1	hsa-mir-92a-3p
Up	CCL8	2	hsa-mir-23a-3p	Down	PSMG3	1	hsa-mir-92a-3p
Up	LGALS9	2	hsa-mir-22-3p	Down	ANAPC11	1	hsa-mir-100-5p
Up	NAV3	2	hsa-mir-21-5p	Down	CES1	1	hsa-mir-197-3p
Up	PARP9	2	hsa-mir-124-3p	Down	CCDC151	1	hsa-mir-10a-5p
Up	CCR1	2	hsa-mir-181d-3p	Down	EPS8L2	1	hsa-mir-34a-5p
Up	ADGRE2	2	hsa-mir-20a-5p	Down	WDR34	1	hsa-mir-221-3p
Up	TF	2	hsa-mir-19a-3p	Down	GJB3	1	hsa-mir-1-3p
Up	FAM120C	2	hsa-mir-18a-5p	Down	DPY30	1	hsa-mir-1-3p

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Table 7 (continued)

Regulation	Target genes	Degree	MicroRNA	Regulation	Target genes	Degree	MicroRNA
Up	ATF7	2	hsa-mir-16-5p	Down	PPP1R16A	1	hsa-mir-1-3p
Up	SHANK1	2	hsa-let-7e-5p	Down	C6orf118	1	hsa-mir-1-3p
Up	LILRB4	2	hsa-let-7a-5p	Down	WDR54	1	hsa-mir-23b-3p
Up	GIMAP8	1	hsa-mir-1226-3p	Down	CTSH	1	hsa-mir-124-3p
Up	FCER1G	1	hsa-mir-1225-3p	Down	POLR2J	1	hsa-mir-124-3p
Up	CMYA5	1	hsa-mir-877-3p	Down	CFAP53	1	hsa-mir-124-3p
Up	GRIA4	1	hsa-mir-484	Down	TCTEX1D2	1	hsa-mir-133a-3p
Up	TAC4	1	hsa-mir-335-5p	Down	S100A6	1	hsa-mir-141-3p
Up	ADAM32	1	hsa-mir-335-5p	Down	ALDH3A1	1	hsa-mir-145-5p
Up	NXNL2	1	hsa-mir-335-5p	Down	KLF15	1	hsa-mir-376a-3p
Up	TRIM69	1	hsa-mir-335-5p	Down	KRT15	1	hsa-mir-340-3p
Up	ANKRD22	1	hsa-mir-335-5p	Down	SSR4	1	hsa-mir-331-3p
Up	RGS18	1	hsa-mir-335-5p	Down	LRRC10B	1	hsa-mir-331-3p
Up	XAF1	1	hsa-mir-335-5p	Down	MRPL14	1	hsa-mir-324-5p
Up	CYSLTR1	1	hsa-mir-335-5p	Down	AQP5	1	hsa-mir-335-5p
Up	OAS1	1	hsa-mir-335-5p	Down	SERPINF1	1	hsa-mir-335-5p
Up	HTN3	1	hsa-mir-335-5p	Down	PLTP	1	hsa-mir-335-5p
Up	HLA-DMA	1	hsa-mir-335-5p	Down	PDLIM4	1	hsa-mir-335-5p
Up	MS4A2	1	hsa-mir-335-5p	Down	TRIM3	1	hsa-mir-335-5p
Up	ADGRE1	1	hsa-mir-335-5p	Down	VILL	1	hsa-mir-335-5p
Up	TAGAP	1	hsa-mir-374a-5p	Down	FAM3B	1	hsa-mir-335-5p
Up	RGS1	1	hsa-mir-374a-5p	Down	SPATA20	1	hsa-mir-335-5p
Up	DOK3	1	hsa-mir-320a	Down	DYNLRB2	1	hsa-mir-335-5p
Up	ELF1	1	hsa-mir-194-5p	Down	TTC29	1	hsa-mir-335-5p
Up	CD80	1	hsa-mir-146a-5p	Down	C9orf24	1	hsa-mir-335-5p
Up	IDO1	1	hsa-mir-153-3p	Down	SYTL1	1	hsa-mir-335-5p
Up	EVI2B	1	hsa-mir-142-3p	Down	C20orf85	1	hsa-mir-335-5p
Up	STAT4	1	hsa-mir-141-3p	Down	C16orf71	1	hsa-mir-335-5p
Up	PARP14	1	hsa-mir-124-3p	Down	TMEM190	1	hsa-mir-335-5p
Up	GBP1	1	hsa-mir-124-3p	Down	RSPH9	1	hsa-mir-335-5p
Up	TCAF2	1	hsa-mir-15b-5p	Down	GAS2L2	1	hsa-mir-335-5p
Up	AIM2	1	hsa-mir-1-3p	Down	TSTD1	1	hsa-mir-335-5p
Up	CDKL5	1	hsa-mir-222-3p	Down	NDUFV1	1	hsa-mir-484
Up	FAM111B	1	hsa-mir-192-5p	Down	NDUFA13	1	hsa-mir-484
Up	SAMD3	1	hsa-mir-192-5p	Down	EPPK1	1	hsa-mir-193b-3p
Up	CMPK2	1	hsa-mir-192-5p	Down	RHPN1	1	hsa-mir-18a-3p
Up	PCSK5	1	hsa-mir-107	Down	COQ8B	1	hsa-mir-92b-3p
Up	PARP12	1	hsa-mir-98-5p	Down	NDUFAB1	1	hsa-mir-615-3p
Up	PCSK1N	1	hsa-mir-31-5p	Down	TOMM7	1	hsa-mir-615-3p
Up	SAMD9	1	hsa-mir-30a-5p	Down	BAD	1	hsa-mir-330-5p
Up	SIGLEC1	1	hsa-mir-27a-3p	Down	TSPAN7	1	hsa-mir-744-5p
Up	ACE2	1	hsa-mir-26b-5p	Down	LARP6	1	hsa-mir-744-5p
Up	CXCL13	1	hsa-mir-26b-5p	Down	TMEM205	1	hsa-mir-935
Up	CLEC2B	1	hsa-mir-26b-5p	Down	COQ4	1	hsa-mir-1908-5p
Up	RNASE6	1	hsa-mir-26b-5p				
Up	MNDA	1	hsa-mir-26b-5p				
Up	FCGR1B	1	hsa-mir-26b-5p				
Up	C1QB	1	hsa-mir-26b-5p				
Up	CX3CR1	1	hsa-mir-296-3p				

Degree – No of miRNA interact with target gene. We taken any one miRNA in table.

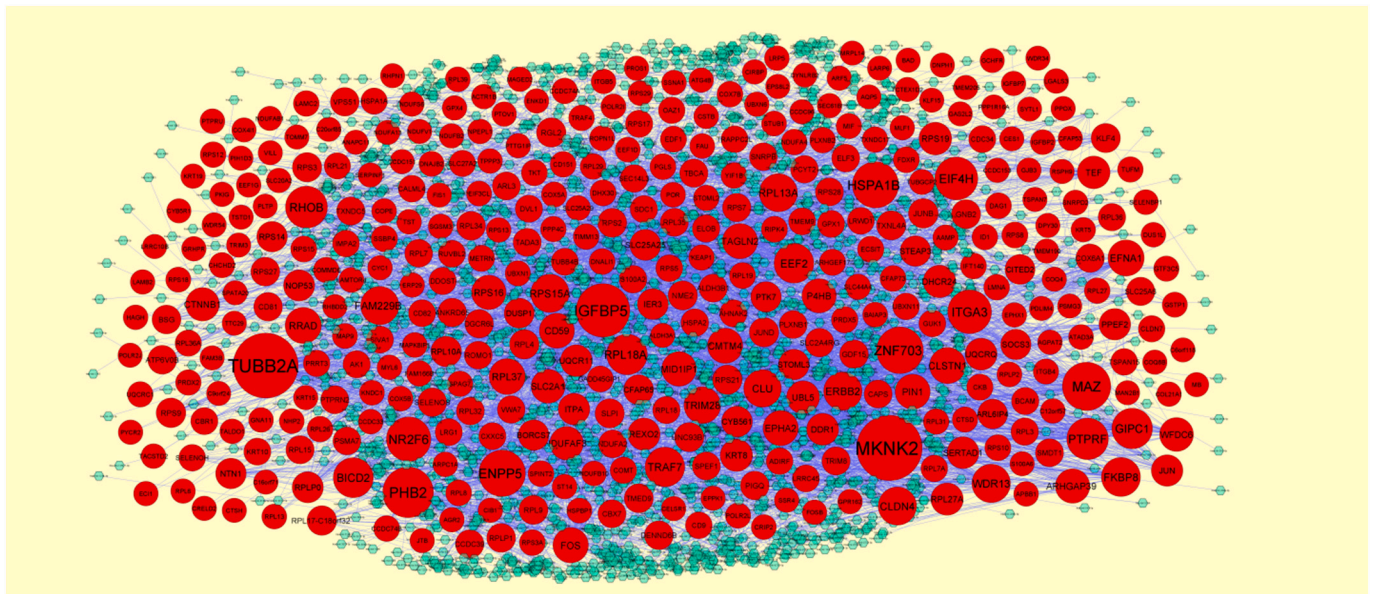


Fig. 12. The network of down regulated genes and their related miRNAs. The red circles nodes are the down regulated genes, and blue diamond nodes are the miRNAs. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

CD180, HLA-DMA, MAS1, BTN3A3, SEMA6D, MS4A2, SELL (selectin L), WNT7A, CLIC4, SUCNR1, ITGA1, CLEC12A, CCN5, KCNJ6, BTN3A1, ENTPD1, ADGRE1, CDH6, CDH8, NPL (*N*-acetylneuraminatase pyruvate lyase), PLEK (pleckstrin), ALOX5AP, BEST1, SEPTIN4, APOA2, TNFSF14, TNFSF10, INHBA (inhibin subunit beta A), GIMAP2, BCAT1, GIMAP7, CMYA5, UHRF1BP1, PTPRE (protein tyrosine phosphatase receptor type E), PTPRO (protein tyrosine phosphatase receptor type O), SDS (serine dehydratase), CLEC2B, SHANK1, DPYD (dihydropyrimidine dehydrogenase), SMCHD1, GRIA4, LRRK1, OLR1, POLR2I, POLR2J, POLR2L, TRIM8 and EIF3CL) obtained from the GO enrichment analysis are all may be associated in SARS-CoV-2 infection progression process, which suggesting that these novel biomarkers may serve as diagnostics biomarkers or therapeutic targets for this infection.

Using the app NetworkAnalyzer in Cytoscape, we filtered up and down regulated hub genes in the PPI network and its modules. Hub

genes such as CBL (Cbl proto-oncogene) [Yang and Henderson, 2005], CTNBN1 [Tornesello et al., 2013], ERBB2 [Sasso et al., 2020], PIN1 [Lim et al., 2011] and HSPBP1 [Ceccin et al., 2019] were linked with progression of viral infections, but these genes may be liable for development of SARS-CoV-2 infection. The novel biomarkers (REL (REL proto-oncogene, NF- κ B subunit), CYSLTR1, STX17, PDE3B, ZSCAN30, DUX4, LAP3, FAM120C, SLA (Src like adaptor), LCP2, ASAP1, P2RY6, PAG1, FYB1, MKI67, SKAP2, ZNF1, CDKL5, STUB1, PROS1, WDR54, NAA38, GSTA2, SMDT1, HSPA1B, S100A2, HSPA2, HSPA1A, KRT19, KRT5, DGCR6L, KRT8, KRT15, RHPN1, DPCD (deleted in primary ciliary dyskinesia homolog (mouse)) and NME2) obtained from the PPI network and modules are all may be associated in SARS-CoV-2 infection progression process, which suggesting that these novel biomarkers may serve as diagnostics biomarkers or therapeutic targets for this infection.

The target gene - miRNA regulatory network and target gene - TF

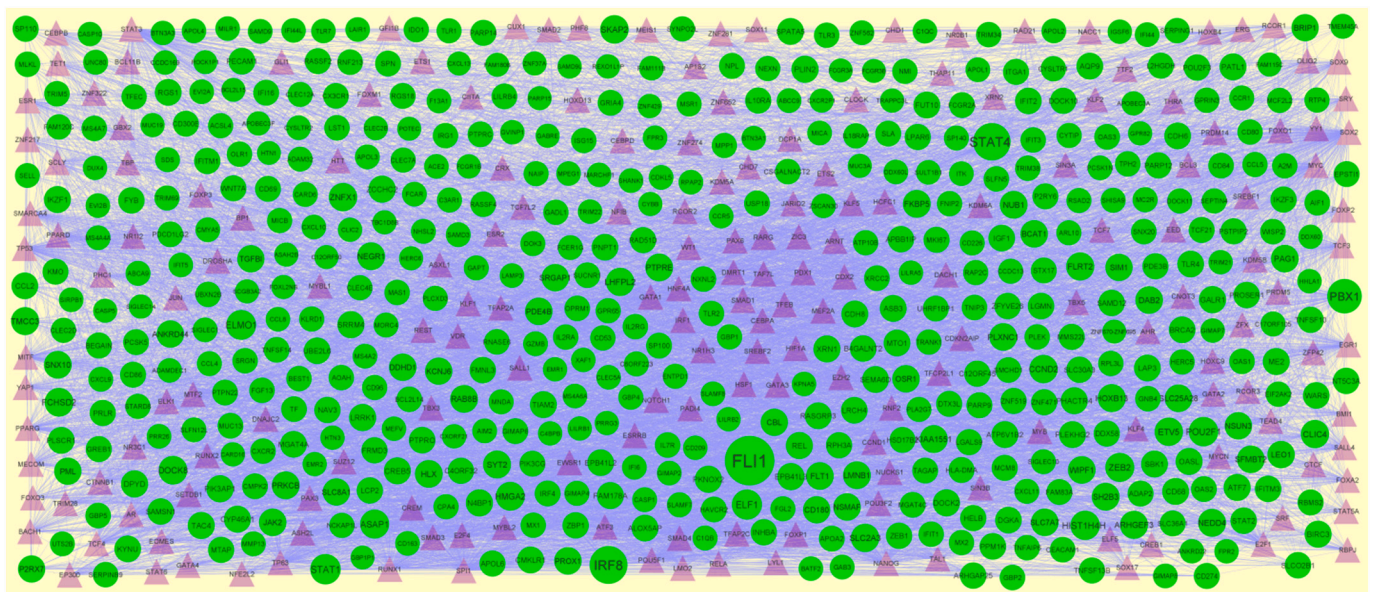


Fig. 13. The network of up regulated genes and their related TFs. The green circles nodes are the up regulated genes, and purple triangle nodes are the TFs. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

Table 8

Target gene - TF interaction table.

Regulation	TF	Degree	Target gene	Regulation	TF	Degree	Target gene
Up	SPI1	229	TRIM5	Down	MYC	304	RPLP0
Up	SOX2	208	GPRIN3	Down	SPI1	255	IGFBP7
Up	STAT3	193	DDX60L	Down	E2F1	225	LMNA
Up	NANOG	177	CYSLTR1	Down	SOX2	224	CD82
Up	RUNX1	177	SUCNR1	Down	EGR1	218	SERPINF1
Up	AR	171	APOBEC3F	Down	RUNX1	207	ARHGAP39
Up	MYC	148	MS4A2	Down	FLI1	205	FIS1
Up	TP63	147	CCR5	Down	POU5F1	203	CES1
Up	SMAD4	142	MILR1	Down	CREM	197	MLF1
Up	POU5F1	137	PLIN2	Down	NANOG	192	SLC2A1
Up	EGR1	136	SAMD9L	Down	TP63	186	POR
Up	TP53	135	CXCL11	Down	FOXP1	167	EIF4H
Up	HNF4A	132	FCER1G	Down	HNF4A	167	NTN1
Up	GATA1	125	SLCO2B1	Down	SIN3B	166	ID1
Up	MITF	119	UTS2B	Down	TP53	165	PLTP
Up	GATA2	117	TNFSF14	Down	CREB1	163	QARS
Up	PPARG	112	ZNF519	Down	MITF	157	CSORF49
Up	REST	110	SHISA9	Down	ZFX	146	APBB1
Up	TCF4	108	KCNJ6	Down	TAL1	137	TOMM7
Up	SUZ12	107	NHSL2	Down	STAT3	128	NDUFA13
Up	E2F1	94	LAP3	Down	TFAP2C	125	CDC34
Up	RUNX2	91	LILRB1	Down	GATA1	124	CCDC151
Up	SMARCA4	91	UBE2L6	Down	GATA2	123	VWA7
Up	SALL4	88	MGAT4C	Down	SETDB1	121	CBX7
Up	TCF3	88	SBK1	Down	SRY	119	KRT17
Up	PPARD	85	PPM1K	Down	PPARG	117	FBXW9
Up	MECOM	85	SIGLEC10	Down	REST	115	C12ORF57
Up	SMAD3	82	IL7R	Down	AR	113	SOCS3
Up	TAL1	77	MTAP	Down	SOX9	112	ENKD1
Up	CUX1	74	IFIT5	Down	TET1	108	RPS10
Up	SETDB1	72	CLEC2D	Down	ASH2L	102	SELENBP1
Up	MTF2	72	LRRK1	Down	XRN2	101	RPL35
Up	CREM	71	FMNL3	Down	KLF1	101	SNRPB
Up	ESR1	71	PTPN22	Down	ERG	99	CYB5R1
Up	BACH1	69	NCKAP1L	Down	PPARD	99	DLEC1
Up	NR3C1	67	PTPRO	Down	KDM5A	96	MAZ
Up	YAP1	66	SLC30A3	Down	E2F4	94	JUN
Up	TFAP2C	65	CD96	Down	SMAD4	90	RPL21
Up	FOXA2	65	CMPK2	Down	SUZ12	87	GPR162
Up	SCLY	65	SH2B3	Down	TTF2	85	BAIAP3
Up	SOX9	64	CMKLR1	Down	SMARCA4	85	NDUFS6
Up	SRY	63	IRF4	Down	MYCN	85	PRDX2
Up	ASH2L	60	SFMBT2	Down	CCND1	85	UBXN6
Up	EOMES	59	B4GALNT2	Down	FOXO3	84	CCDC37
Up	KLF4	59	POU2F1	Down	TFCP2L1	84	VARS
Up	ERG	58	ALOX5AP	Down	VDR	83	PLXNB2
Up	TRIM28	58	ARL10	Down	HOXC9	82	ATP5E
Up	VDR	57	DUX4	Down	YY1	82	VPS51
Up	CEBPB	57	IKZF1	Down	SMAD3	79	CSRNP1
Up	RELA	56	C17ORF105	Down	TCF3	79	ITGB5
Up	POU3F2	56	GAPT	Down	ZNF281	77	CRIP1
Up	KDM5B	56	OSR1	Down	CUX1	75	POLR2L
Up	TEAD4	56	PAG1	Down	FOXA2	72	ITGA3
Up	OLIG2	56	ZEB1	Down	MYBL2	72	KRT15
Up	LMO2	55	BTN3A3	Down	NR0B1	71	CKB
Up	CREB1	54	PRLR	Down	ETS1	71	NDUFV1
Up	RCOR3	54	TAC4	Down	TBX5	69	AK1
Up	EP300	53	CCDC13	Down	ATF3	69	LARP6
Up	SIN3B	53	CDH8	Down	DACH1	69	PSMA7
Up	E2F4	53	FAM178A	Down	EOMES	68	RPLP1
Up	ATF3	50	GBP5	Down	ESR1	67	GLB1L2
Up	HOXB4	49	CD53	Down	SMAD2	66	TRAF7
Up	FOXP3	49	MTO1	Down	YAP1	64	TTC29
Up	TFAP2A	48	MPP1	Down	SALL4	63	ACO2
Up	MYB	47	RAB8B	Down	CTCF	63	NDUFAB1
Up	SMAD2	46	NSUN3	Down	MTF2	62	ERBB2
Up	YY1	46	SPATA5	Down	RBPJ	62	TMA7
Up	EZH2	45	PARP12	Down	RAD21	62	TSPAN15
Up	RCOR1	45	SMCHD1	Down	PHF8	61	BICD2
Up	FOXP1	44	CX3CR1	Down	RCOR3	60	ARL3
Up	IRF1	44	EPSTI1	Down	DMRT1	60	PPP4C
Up	BMI1	44	IKZF3	Down	EP300	59	CCDC33
Up	JARID2	44	LRCH4	Down	TCF4	59	DGCR6
Up	GATA4	44	MKI67	Down	TCF7	59	RPS3

(continued on next page)

Table 8 (continued)

Regulation	TF	Degree	Target gene	Regulation	TF	Degree	Target gene
Up	MYCN	44	OAS3	Down	GFI1B	55	TXNL4A
Up	TET1	44	SDS	Down	CNOT3	54	RPS19
Up	FOXO3	43	C12ORF45	Down	HOXB4	53	CITED2
Up	RNF2	43	PCSK5	Down	ESRRB	53	FAM129B
Up	FOXP2	43	STAT4	Down	WT1	53	NR2F6
Up	STAT5A	42	CMYA5	Down	TFAP2A	53	SLC25A6
Up	NFE2L2	42	PLEK	Down	RUNX2	52	COL21A1
Up	RBPJ	41	CSGALNACT2	Down	ZFP42	52	RPS14
Up	DMRT1	41	DOCK2	Down	FOXP3	51	RPL29
Up	JUN	40	CCL2	Down	SOX17	51	SLC25A25
Up	EWSR1	39	RPL3L	Down	SCLY	49	ROPN1L
Up	KLF1	38	BCAT1	Down	RELA	49	TFF3
Up	SOX17	38	SNX10	Down	GATA4	48	FAM174A
Up	PAX3	37	BTN3A1	Down	PRDM14	48	PTPRF
Up	ZNF281	37	IL2RG	Down	ELF1	48	SSBP4
Up	MEIS1	37	SLAMF7	Down	SRF	48	TRIM28
Up	ZNF217	36	C4ORF32	Down	CEBPB	47	B9D1
Up	CTNNB1	36	MSR1	Down	MEIS1	46	ALKBH7
Up	PRDM14	36	TLR1	Down	ELK1	46	BLOC1S1
Up	GFI1B	35	CLEC5A	Down	SIN3A	46	MAPK8IP1
Up	RAD21	31	LGALS9	Down	NFE2L2	44	ALDH3A1
Up	NR0B1	31	RTP4	Down	FOXP2	44	C10ORF32
Up	MYBL2	31	SKAP2	Down	BCL3	42	ATPIF1
Up	HOXC9	31	SLC36A1	Down	DCP1A	41	AAMP
Up	TFPC2L1	29	DOCK8	Down	LMO2	41	ALDH3B1
Up	STAT6	28	APOL6	Down	KDM5B	40	ANAPC11
Up	DNAJC2	28	CCL5	Down	CHD1	40	C11ORF31
Up	TBX3	28	CCND2	Down	MECOM	40	WDR13
Up	CTCF	28	GIMAP8	Down	NR3C1	39	ZNF703
Up	SOX11	28	RASSF2	Down	TBP	37	TSPO
Up	CCND1	28	TAGAP	Down	STAT4	37	UQCRCQ
Up	NR1H3	27	EMR2	Down	HSF1	36	UNC93B1
Up	ZFX	27	STX17	Down	SOX11	34	UQCRC11
Up	ELK1	26	BATF2	Down	EZH2	33	ST6GALNAC6
Up	TBX5	26	ME2	Down	BMI1	33	UBAC1
Up	PHC1	25	TIAM2	Down	THAP11	32	JTB
Up	SRF	24	CD274	Down	EWSR1	32	RPS9
Up	WT1	23	ATP6V1B2	Down	STAT5A	32	SYTL1
Up	CDX2	23	TPH2	Down	PAX6	32	VIMP
Up	ZFP42	22	DTX3L	Down	TEAD4	32	YIF1B
Up	ARNT	22	GRIA4	Down	DNAJC2	31	GADD45GIP1
Up	EED	22	PLXNC1	Down	BACH1	31	IER3
Up	TCF7	22	PTPRE	Down	ELF5	31	RPS7
Up	GATA3	22	TMCC3	Down	TFEB	31	S100A6
Up	LYL1	20	GIMAP6	Down	TAF7L	30	EDF1
Up	PAX6	20	PHACTR4	Down	PBX1	30	ROMO1
Up	ASXL1	19	FLI1	Down	MEF2A	28	COX4I1
Up	CNOT3	19	SLC7A7	Down	CDX2	28	CXXC5
Up	TTF2	18	ATF7	Down	RCOR1	28	CYC1
Up	PHF8	18	MLKL	Down	ZNF217	28	FOS
Up	ELF5	18	SELL	Down	NUCKS1	28	FOSB
Up	HTT	18	TMEM45A	Down	SREBF1	27	FAU
Up	NR1I2	17	GADL1	Down	OLIG2	27	GRHPR
Up	DACH1	17	RPAP2	Down	ASXL1	27	PRDX5
Up	AHR	17	SRGAP1	Down	GATA3	27	SPINT2
Up	NFIB	16	APBB1IP	Down	RNF2	25	HSPA2
Up	NUCKS1	16	IRF8	Down	ESR2	25	MB
Up	ESRRB	16	KYNU	Down	SREBF2	24	COX6A1
Up	TCF7L2	16	MUC13	Down	ARNT	24	ELF3
Up	MEF2A	16	RASGRP3	Down	STAT1	24	JUND
Up	NACCI	16	RBMS2	Down	PRDM5	24	RHBDD2
Up	DROSHA	15	ATP10B	Down	NACCI	23	PPP1R16A
Up	PRDM5	15	RAP2C	Down	MYB	23	SLPI
Up	CEBPD	14	LHFPL2	Down	PADI4	22	RPS16
Up	SREBF1	14	TGFB1	Down	CLOCK	22	RRAD
Up	SMAD1	14	TRIM38	Down	AP1S2	21	COQ4
Up	TBP	13	DGKA	Down	NR1H3	21	SLC2A4RG
Up	HSF1	13	FYB	Down	RARG	21	STUB1
Up	NOTCH1	12	BRIP1	Down	AHR	20	RPL3
Up	XRN2	12	CD68	Down	IRF8	19	RPL36A
Up	RCOR2	11	BEGAIN	Down	NR1I2	18	HSPA1A
Up	PADI4	11	CXCL9	Down	JARID2	18	MAPK15
Up	SREBF2	11	REL	Down	CEBPA	18	S100A13
Up	KDM5A	11	ZFYVE26	Down	PDX1	17	HAGH
Up	BCL3	10	DAB2	Down	PAX3	16	RPS12
Up	SIN3A	10	PIK3AP1	Down	SMAD1	16	TXNDC17

(continued on next page)

Table 8 (continued)

Regulation	TF	Degree	Target gene	Regulation	TF	Degree	Target gene
Up	CHD1	10	STAT1	Down	TBX3	15	NAA38
Up	CEBPA	10	TF	Down	TCF7L2	15	TST
Up	ESR2	10	WISP2	Down	PHC1	14	HSPA1B
Up	TAF7L	9	HLA-DMA	Down	KDM6A	14	POLR2J
Up	THAP11	9	NPL	Down	HIF1A	13	GLTSCR2
Up	TFEB	8	OASL	Down	CRX	12	DHX30
Up	CRX	7	PBX1	Down	NFIB	12	FDXR
Up	GBX2	6	ABCA9	Down	LYL1	12	PTTG1IP
Up	ZIC3	6	HOXB13	Down	RCOR2	11	IFT27
Up	PDX1	6	NT5C3A	Down	POU3F2	10	KRT10
Up	FOXM1	5	ELMO1	Down	HCFC1	10	RPL10A
Up	CLOCK	5	FKBP5	Down	HTT	10	TACSTD2
Up	THRA	5	IFITM1	Down	EED	10	TRAF4
Up	HIF1A	5	INHBA	Down	DROSHA	9	BCAM
Up	RARG	5	KIAA1551	Down	ZIC3	9	DENND6B
Up	ETS1	5	LEO1	Down	ETS2	9	TUFM
Up	CHD7	4	DDHD1	Down	ZNF263	8	CYB561
Up	GLI1	4	GZMB	Down	NR4A2	8	RPL26
Up	SALL1	4	PARP14	Down	IRF1	8	TUBB2A
Up	ZNF274	4	CEACAM1	Down	FOXO1	7	ITPA
Up	BP1	3	CCL4	Down	CEBPD	7	MRPL14
Up	FOXO1	3	FUT10	Down	NOTCH1	7	RPL18A
Up	KLF2	3	NXNL2	Down	ZNF652	7	RPS5
Up	DCP1A	3	PROSER1	Down	TCF21	7	RUVBL2
Up	KLF5	3	SLC2A3	Down	THRA	7	SIVA1
Up	ETS2	2	GALR1	Down	STAT6	6	CMTM4
Up	ZNF322	2	GREB1	Down	FOXM1	5	GTF3C5
Up	HCFC1	2	HIST1H4H	Down	KLF5	5	KLF4
Up	CDKN2AIP	2	NUB1	Down	KLF2	5	PYCR2
Up	BCL11B	2	SP110	Down	HOXD13	3	COX5A
Up	CIITA	2	TLR4	Down	CIITA	3	ECSIT
Up	MYBL1	1	ADAM32	Down	CHD7	2	RPS9
Up	HOXD13	1	LGMN	Down	SALL1	2	TPPP3
Up	KDM6A	1	MCM8	Down	IKZF1	1	ATP6V0B
Up	ZNF652	1	WNT7A	Down	BP1	1	CBR1
Up	AP1S2	1	XRN1	Down	MYBL1	1	COA3
				Down	CDKN2AIP	1	CROCC
				Down	ZNF274	1	RPS29
				Down	HOXA2	1	TUBB4B
				Down	BCL11B	1	UBTD1

Degree – No of TF interact with target gene. We taken any one TF in table.

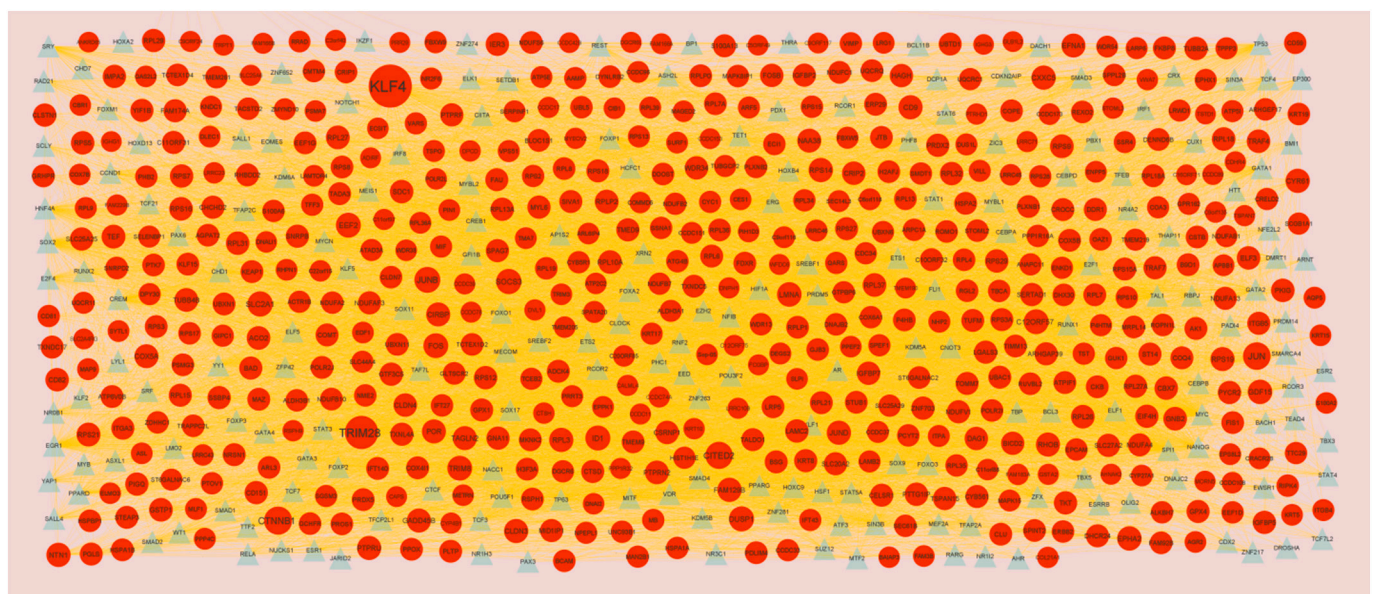


Fig. 14. The network of down regulated genes and their related TFs. The green circles nodes are the down regulated genes, and blue triangle nodes are the TFs. (For interpretation of the references to color in this figure legend, the reader is referred to the web version of this article.)

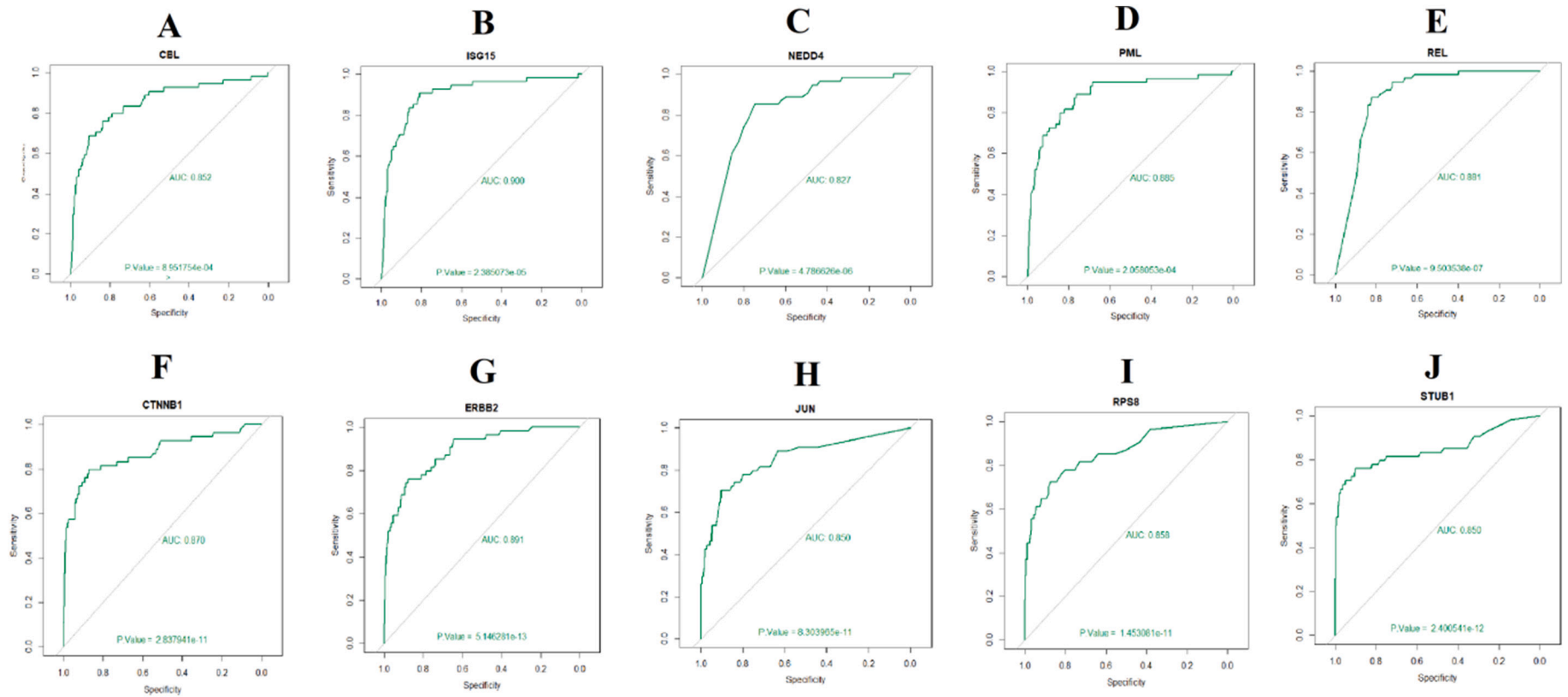


Fig. 15. ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for SARS-CoV-2 infection. A) CBL B) ISG15 C) NEDD4 D) PML E) REL F) CTNNB1 G) ERBB2 H) JUN I) RPS8 J) STUB1.

regulatory network were constructed with up and down regulated genes and the top target genes were obtained. CCND2 was associated with development of hepatitis B virus infection [Park et al., 2010], but this gene may be liable for progression of SARS-CoV-2 infection. The novel biomarkers (FAM241A, POU2F1, GPRIN3, DDX60L, MKNK2, IGFBP5, PHB2, MAZ (MYC associated zinc finger protein), IGFBP7, LMNA (lamin A/C), CD82 and SERPINF1) obtained from the target gene - miRNA regulatory network and target gene - TF regulatory network are all may be associated in SARS-CoV-2 infection progression process, which suggesting that these novel biomarkers may serve as diagnostics biomarkers or therapeutic targets for this infection.

In conclusion, we identified several abnormally expressed genes in PE that may participate in the pathogenesis of SARS-CoV-2 infection. Our study provides a comprehensive bioinformatics analysis of DEGs in SARS-CoV-2 infection, helps to understand the underlying molecular mechanisms of SARS-CoV-2 infection, and may provide potential biomarkers and therapeutic targets for SARS-CoV-2 infection. Further experiments are required to confirm the expression and potential functions of the identified genes in SARS-CoV-2 infection.

CRedit authorship contribution statement

Basavaraj Vastrad was associated with methodology and review and editing. Dr Chanabasayya Vastrad was performed software, supervision, formal analysis and validation. Anandkumar Tengli performed editing and reviewing the manuscript.

Declaration of competing interest

The authors declare that they have no competing interests.

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Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent

No informed consent because this study does not contain human or animals participants.

Availability of data and materials

The datasets supporting the conclusions of this article are available in the GEO (Gene Expression Omnibus) (<https://www.ncbi.nlm.nih.gov/geo/>) repository. [(GSE152075) (<https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE152075>)].

Consent for publication

Not applicable.

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