Comprehensive analysis of next-generation sequencing data in COVID-19 and its secondary complications

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Abstract

The ongoing pandemic of coronavirus disease 2019 (COVID-19) has made a serious public health threat globally. To discover key molecular changes in COVID-19 and its secondary complications, we analyzed next-generation sequencing (NGS) data of COVID-19. NGS data (GSE163151) was screened and downloaded from the Gene Expression Omnibus database (GEO). Differentially expressed genes (DEGs) were identified in the present study, using DESeq2 package in R programming software. Gene ontology (GO) and pathway enrichment analysis were performed, and the protein-protein interaction (PPI) network, module analysis, miRNA-hub gene regulatory network and TF-hub gene regulatory network were established. Subsequently, receiver operating characteristic curve (ROC) analysis was used to validate the diagonostics valuesof the hub genes. Firstly, 954 DEGs (477 up regulated and 477 down regulated) were identified from the four NGS dataset. GO enrichment analysis revealed enrichment of DEGs in genes related to the immune system process and multicellular organismal process, and REACTOME pathway enrichment analysis showed enrichment of DEGs in the immune system and formation of the cornified envelope. Hub genes were identified from the PPI network, module analysis, miRNA-hub gene regulatory network and TF-hub gene regulatory network. Furthermore, the ROC analysis indicate that COVID-19 and its secondary complications with following hub genes, namely, RPL10, FYN, FLNA, EEF1A1, UBA52, BMI1, ACTN2, CRMP1, TRIM42 and PTCH1, had good diagnostics values. This study identified several genes associated with COVID-19 and its secondary complications, which improves our knowledge of the disease mechanism.

Keywords: COVID-19; differentially expressed genes; next-generation sequencing data analysis; hub genes; protein-protein interaction network

Introduction

Coronavirus Disease 2019 (COVID-19) also known as severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) and was first reported in Wuhan city, Hubei province, China in December 2019 [1]. Within a short period of time, COVID-19 has raced around the world and World Health Organization (WHO) officially declared the COVID-19 epidemic as a health emergency [2]. The number of infected cases and deaths due to COVID-19 is rising severely and on 17th December 2021, there are more than 273,327,260 confirmed cases with over 5,355,724 deaths across 200 countries (Worldometer 2020).

COVID-19 can kill the tissue of lungs [3], heart [4], central nervous system [5], liver [6] and kidneys [7]. COVID-19 infection is characterized by an increased risk of acute respiratory failure [8], pneumonia [9], acute respiratory distress syndrome [10], acute liver injury [11], acute cardiac injury [12], secondary infection [13], central nervous system (CNS) disorders [14], acute kidney injury [15], septic shock [16], diabetes mellitus [17], hypertension [18], disseminated intravascular coagulation [19], blood clots [20], multisystem inflammatory syndrome in children [21], chronic fatigue [22] and rhabdomyolysis [23]. The higher prevalence and limited treatments of COVID-19 infection lead to substantial public health and global burdens [24]. Therefore, it is necessary to improve our understanding of COVID-19 molecular pathogenesis and to develop better screening methods for COVID-19 infection and its secondary complications.

The COVID-19 infection and its secondary complications are an extremely complicated pathophysiological process and regulated by various genetic factors and pathways [25]. Five novel genetic factor for COVID-19 infection and its secondary complications including APOL1 [26], ACE2 [27], CXCL10 [28], IFNAR2 [29] and MBL2 [30] as potential biomarkers of COVID-19 infection and its secondary complications. Signaling pathway includes JAK-STAT signaling pathway [31], ACE-2\Mas\BDNF signaling pathway [32], IFN-AhR signaling pathway [33] and toll-like receptor 4-mediated inflammatory signaling pathway [34] were responsible for progression of COVID-19 infection and its secondary complications. Recently, next generation sequencing (NGS) technology is widely used in COVID-19 investigation, with the pronounced advantages relying on its ability to together determine the expression data of huge genes one time [35]. Based on the massive NGS datasets information stored in a large number of public databases such as Gene Expression Omnibus (GEO) database and ArrayExpress,

the target data could be mined, integrated, and reanalyzed by bioinformatics method, which provide useful clues for the investigation of numerous diseases [36-37].

We downloaded NGS dataset GSE163151 [38], from GEO (http://www.ncbi.nlm.nih.gov/geo/) [39], which contain gene expression data from COVID-19 samples and non COVID-19 samples. We then performed bioinformatics analysis, including identifying DEGs, gene ontology (GO) enrichment analysis, pathway enrichment analysis and protein-protein interaction (PPI) network and module analysis. The functions of the hub genes were further assessed by miRNA-hub gene regulatory network and TF-hub gene regulatory network construction and analysis. The findings were further validated by receiver operating characteristic curve (ROC) analysis. The aim of this investigation was to identify DEGs and important signaling pathways, and to explore potential candidate biomarkers for the diagnosis and therapeutic targets in COVID-19 infection and its secondary complications.

Materials and methods

Data resources

We used "COVID-19" as a keyword on the Gene Expression Omnibus (GEO) database, and NGS dataset (GSE163151) [38] was collected. GSE163151 was in GPL24676 platform Illumina NovaSeq 6000 (Homo sapiens), which included 148 COVID-19 samples and 31 non COVID-19 samples.

Identification of DEGs

The DESeq2 package of R software [40] was used to analyze the DEGs between COVID-19 and non COVID-19 in the NGS data of GSE163151. The adjusted P-value and [logFC] were calculated. The Benjamini & Hochberg false discovery rate method was used as a correction factor for the adjusted P-value in DESeq2 [41]. The statistically significant DEGs were identified according to adjusted $P < .05$, and [logFC] > 2.576 for up regulated genes and [logFC] < -2.813 for down regulated genes. ggplot2 and gplot in R software was subsequently performed to plot the volcano plot and heat map.

GO and pathway enrichment analyses of DEGs

The g:Profiler (http://biit.cs.ut.ee/gprofiler/) [42] is an online functional annotation tool was used to perform Gene Ontology (GO) and REACTOME pathway enrichment analyses. GO enrichment analysis (http://www.geneontology.org) [43] has three independent branches: biological process (BP), cellular component (CC). and molecular function (MF). The REACTOME (https://reactome.org/) [44] pathway database facilitates the systematic analysis of the intracellular metabolic pathways and functions of gene products. P value <0.05 as the cutoff criterion was considered statistically significant.

Construction of the PPI network and module analysis

IID (Integrated Interactions Database) interactome (http://iid.ophid.utoronto.ca/search_by_proteins/) [45] is a database that provides a function for predicted protein interactions and providing systematic data regarding cellular processes. Subsequently, PPI networks was constructed using the Cytoscape software version 3.8.2 (http://www.cytoscape.org/) [46]. In addition, the node degree [47], betweenness centrality [48], stress centrality [49] and closeness centrality [50] of each protein node in the PPI network was calculated using Network Analyzer. In order to screen the clusters of original PPI network, module analysis by PEWCC1 plug-in [51] was carried out in Cytoscape software. The criteria for the network module screening were set beyond the number of nodes and PEWCC1 scores. Moreover, the GO and pathway enrichment analysis for DEGs were performed by g:Profiler software in the modules with a threshold of p<0.05.

MiRNA-hub gene regulatory network construction

The miRNet database (https://www.mirnet.ca/) [52] is an open-source platform mainly focusing on miRNA-hub gene interactions. miRNet utilizes fourteen established miRNA- hub gene prediction databases, including TarBase, miRTarBase, miRecords, miRanda (S mansoni only), miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR, EpimiR, starBase, TransmiR, ADmiRE, and TAM 2.0. Subsequently, the network of the hub genes and their targeted miRNAs was visualized by Cytoscape software version 3.8.2 [46].

TF-hub gene regulatory network construction

The NetworkAnalyst database (https://www.networkanalyst.ca/) [53] is an open-source platform mainly focusing on TF-hub gene interactions. NetworkAnalyst database utilizes fourteen established TF- hub gene prediction database Jasper. . Subsequently, the network of the hub genes and their targeted TFs was visualized by Cytoscape software version 3.8.2 [46].

Receiver operating characteristic curve (ROC) analysis

ROC curve analyses to resolve the specificity, sensitivity, likelihood ratios, positive predictive values, and negative predictive values for all potential thresholds of the ROC curve were accomplished using the pROC package in R statistical software [54]. ROC analysis was performed to discriminate COVID-19 from non COVID-19. The area under the curve (AUC) was calculated and used to compare the diagnostic value of hub genes.

Results

Identification of DEGs

To identify DEGs in the omental white adipocytes between ISO and IRO subjects, we retrieved relevant Expression profiling by high throughput sequencing of GSE163151 from GEO database. A total of 954 DEGs were identified from the NGS dataset, including 477 up regulated genes and 477 down regulated genes COVID-19 compared to non COVID-19. The expression levels of the up regulated and down regulated genes are displayed in Table 1. The expression levels of these DEGs are visualized in the form of a heatmap (Fig. 1). Volcano plots were generated to visualize fold changes of the DEGs had [logFC] > 2.576 for up regulated genes and [logFC] < -2.813 for down regulated genes, and adjusted $P<0.05$ (Fig. 2).

GO and pathway enrichment analyses of DEGs

To identify key genes related to sepsis, gene functions were annotated using the g:Profiler online software database. DEGs were classified into the three functional groups of GO analysis: BP, CC and MF (Table 2). GO enrichment analysis showed that DEGs were primarily enriched in immune system process, regulation of immune system process, multicellular organismal process and anatomical structure development were significantly enriched in BP; membrane, cell periphery, cell

periphery and extracellular region were significantly enriched in CC; and in the MF, DEGs were mainly enriched in molecular transducer activity, protein binding, transporter activity and receptor ligand activity. DEGs were found to be significantly enriched in nine classical pathways, including the immune system, peptide chain elongation, formation of the cornified envelope and GPCR ligand binding and are listed in Table 3.

Construction of the PPI network and module analysis

The PPI network of the DEGs in COVID-19 was constructed based on the information obtained from the IID interactome database**.** The PPI network included 4020 nodes and 7417 edges, representative of proteins and protein-protein interactions, respectively (Fig. 3). Moreover, RPL10, FYN, FLNA, EEF1A1, UBA52, BMI1, ACTN2, CRMP1, TRIM42 and PTCH1 were identified as hub genes. Table 4 shows the hub genes with the highest node degree, betweenness centrality, stress centrality and closeness centrality, whereas the hub selected using the Network Analyzer plugin. PEWCC1 was used to identify the significant modules in the PPI network and the two significant modules were selected (Fig. 4A and Fig. 4B). Following GO annotation and pathway screening, the module 1 (19 nodes and 41 edges) was revealed to be associated with immune system, adaptive immune system, immune system process, cytokine signaling in immune system and regulation of immune system process, and module 2 (7 nodes and 7 edges) was revealed to be associated with developmental biology, neuronal system, cell periphery and multicellular organismal process.

MiRNA-hub gene regulatory network construction

miRNet was applied to screen the targeted miRNAs of the hub genes. As illustrated in Fig. 5, the interaction network consists of nodes 2287 (293 hub genes and 1994 miRNAs) and 10353 edges. The top targeted hub genes for miRNAs were MAPK1 that was modulated by 286 miRNAs (ex; hsa-mir-320a), ATM that was modulated by 134 miRNAs (ex; hsa-mir-1910-3p), VIM that was modulated by 117 miRNAs (ex; hsa-mir-766-3p), FLNA that was modulated by 106 miRNAs (ex; hsa-mir-124-3p), EEF1A1 that was modulated by 96 miRNAs (ex; hsa-mir-4736), BMI1 that was modulated by 115 miRNAs (ex; hsa-mir-559), GDI1 that was modulated by 104 miRNAs (ex; hsa-mir-186-3p), SOCS1 that was modulated by 62 miRNAs

(ex; hsa-mir-4495), PTCH1 that was modulated by 52 miRNAs (ex; hsa-mir-3689a-5p) and DCX that was modulated by 39 miRNAs (ex; hsa-mir-6842-5p), and are listed in Table 5.

TF-hub gene regulatory network construction

NetworkAnalyst was applied to screen the targeted TFs of the hub genes. As illustrated in Fig. 6, the interaction network consists of nodes 379 (294 hub genes and 85 TFs) and 2385 edges. The top targeted hub genes for TFs were UBA52 that was modulated by 12 TFs (ex; SREBF1), SNCA that was modulated by 11 TFs (ex; ELK1), FYN that was modulated by 10 TFs (ex; NFYA), ATM that was modulated by 10 TFs (ex; ELF5), FLNA that was modulated by 10 TFs (ex; TP53), RBFOX1 that was modulated by 19 TFs (ex; EGR1), PTCH1 that was modulated by 18 TFs (ex; E2F6), DCX that was modulated by 15 TFs (ex; FOXL1), KRT13 that was modulated by 12 TFs (ex; STAT3) and HSF2 that was modulated by 12 TFs (ex; NFIC), and are listed in Table 5.

Receiver operating characteristic curve (ROC) analysis

To identify novel biomarkers for COVID-19, ROC curves of data derived from COVID-19 and non COVID-19 from dataset GSE163151 was analyzed using the pROC package in R statistical software (Fig.7). ROC curves were generated, and the AUC was used to compare the different hub genes. RPL10 (AUC = 0.938), FYN (AUC = 0.960), FLNA (AUC = 0.944), EEF1A1 (AUC = 0.910), UBA52 (AUC = 0.941), BMI1 (AUC = 0.951), ACTN2 (AUC = 0.926), CRMP1 (AUC = 0.954), TRIM42 (AUC = 0.895) and PTCH1 (AUC = 0.923) have the largest AUC area. These findings suggest that RPL10, FYN, FLNA, EEF1A1, UBA52, BMI1, ACTN2, CRMP1, TRIM42 and PTCH1 are the most relevant biomarker for COVID-19.

Discussion

COVID-19 infection and its secondary complications are the one of the leading causes of death worldwide and thus place heavy burdens on the healthcare systems and global economy [55]. However, the molecular mechanisms of COVID-19 infection and its secondary complications remain poorly understood. Most cases of COVID-19 infection and its secondary complications without an early discovery

are not candidates for curative therapies, which might be one of the reasons for the poor patient prognosis. Thus, molecular markers for diagnosis and treatment with high performance are urgently demanded. NGS technology enables us to search the genetic modifications in COVID-19 infection and its secondary complications, and has been proved to be a useful approach to identify novel molecular markers in other diseases.

In the current investigation, NGS dataset was analyzed to obtain DEGs between COVID-19 and non COVID-19. A total of 954 DEGs were identified, including 477 up regulated genes and 477 down regulated genes. A recent study found that the altered expression of BNIP3L [56], NOX4 [57] and SOCS1 [58] are crucial for the progression of diseases related to lungs, but these genes might be novel targets for COVID-19. BNIP3L [59], NOX4 [60] and SOCS1 [61] plays an important role in the renal diseases, but these genes might be involved in the progression of COVID-19. BNIP3L [62], HBA2 [63], SNCA (synuclein alpha) [64], NAT2 [65] and DAO (D-amino acid oxidase) [66] have been reported to have a crucial role in CNS disorders, but these genes might be involved in the progression of COVID-19. Ouyang et al. [67], Vendrov et al. [68], Alikhah et al. [69], Khelil et al. [70] and Xia et al. [71] found that BNIP3L, NOX4, SOCS1, NAT2, MYOCD (myocardin) and expression were altered in cardiovascular diseases, but these genes might be involved in the progression of COVID-19. HBA2 [72], NOX4 [73], NAT2 [74] and MYOCD (myocardin) [75] are important in the development of hypertension, but these genes might be involved in the progression of COVID-19. NOX4 [76], SOCS1 [69] and NAT2 [77] expressions were shown to play an important role in diabetes mellitus, but these genes might be involved in the progression of COVID-19. NOX4 [78] and SOCS1 [79] were reported to be associated with liver injury, but these genes might be novel targets for COVID-19. NOX4 [80] and SOCS1 [81] were shown to participate in facilitating the secondary infections. A previous study revealed that SOCS1 [82] are involved in progression COVID-19 infection.

GO and REACTOME pathway enrichment analyses were performed to explore interactions among the DEGs. Pathways include immune system [83], adaptive immune system [84], neutrophil degranulation [85], cytokine signaling in immune system [86] and GPCR ligand binding [87] were responsible for progression of COVID-19 infection. A previous study demonstrated that the

expression levels of AHSP (alpha hemoglobin stabilizing protein) [88], IL7R [89], FBXO7 [90], KLRB1 [91], PIP4K2A [92], NFE2 [93], CCR2 [94], CLEC12A [95], NLRP12 [96], PECAM1 [97], TRIM10 [98], ICAM3 [99], EEF1A1 [100], CCR4 [101], PTPRC (protein tyrosine phosphatase receptor type C) [102], CX3CR1 [103], TSPAN32 [104], EOMES (eomesodermin) [105], ATM (ATM serine/threonine kinase) [106], CD28 [107], LRRK2 [108], CCL5 [109], CD33 [110], FCRL3 [111], CCR3 [112], FGL2 [113], GZMA (granzyme A) [114], PICALM (phosphatidylinositol binding clathrin assembly protein) [115], ALOX5 [116], MME (membrane metalloendopeptidase) [117], VIM (vimentin) [118], CD93 [119], GCA (grancalcin) [120], CD226 [121], CD1D [122], TNFSF4 [123], LEF1 [124], TLR4 [125], CCR7 [126], DPP4 [127], NLRC4 [128], ITGB3 [129], RASGRP1 [130], TLR2 [131], DOCK2 [132], CSF1R [133], PRKCB (protein kinase C beta) [134], CAMK4 [135], CXCL5 [136], CD36 [137], P2RY12 [138], LILRB2 [139], CD5 [140], SLC25A37 [141], ADIPOR1 [142], PECAM1 [143], RGS10 [144], RGS18 [145], ANK1 [146], RNF182 [147], NPRL3 [148], NINJ2 [149], KCNA3 [150], ABCG2 [151], MS4A6A [152], WDR45 [153], RAB39B [154], SORL1 [155], LRRN3 [156], DPM2 [157], SLC4A10 [158], PINK1 [159], RPL6 [160], STAT4 [161], DUSP6 [162], MYOCD (myocardin) [163], OPRD1 [164], CLCN1 [165], CXCL10 [166], KLF15 [167], RBFOX1 [168], DDC (dopa decarboxylase) [169], APOA4 [170], BMI1 [171], GRIA1 [172], SLC24A2 [173], NPAS4 [174], GAP43 [175], GABRB2 [176], TSLP (thymic stromal lymphopoietin) [177], PADI6 [178], CCL2 [179], STC1 [180], SLC6A4 [181], IL17A [182], CNTN6 [183], GRM8 [184], CRMP1 [185], HAPLN2 [186], PCK1 [187], GABRG2 [188], EPHA5 [189], ST8SIA2 [190], FAIM2 [191], SLC6A3 [192], PDYN (prodynorphin) [193], HAMP (hepcidin antimicrobial peptide) [194], CXCL9 [195], CSMD2 [196], SLC6A15 [197], SLC10A2 [198], ATP1B4 [199], SIGLECL1 [200] and SLC18A1 [201] were altered in patients with CNS disorders, but these genes might be involved in the progression of COVID-19. IL7R [202], S1PR1 [203], NFE2 [204], CCR2 [205], NLRP12 [206], PECAM1 [207], PIM1 [208], AP1S2 [209], ITK (IL2 inducible T cell kinase) [210], CCR4 [211], CX3CR1 [212], FOXO3 [213], CD28 [214], GPX1 [215], PRDX6 [216], LRRK2 [217], CCL5 [218], ETS1 [219], CCR3 [220], SELPLG (selectin P ligand) [221], VIM (vimentin) [222], CD1D [223], SIGLEC9 [224], TLR4 [225], FLNA (filamin A) [226], CCR7 [227], DPP4 [228], NLRC4 [229], TLR2 [230], DOCK2 [231], CD40LG [232], CD36 [233], MAPK1 [234], TGFBR2 [235], LTA4H

[236], PECAM1 [237], VCAN (versican) [238], NPRL3 [239], CDC27 [240], PINK1 [241], TGFBI (transforming growth factor beta induced) [242], CR1 [243], AKT3 [244], STAT4 [245], CXCL10 [246], CRP (C-reactive protein) [247], IL17F [248], CD34 [249], BCL3 [250], TSLP (thymic stromal lymphopoietin) [251], CCL2 [252], F10 [253], STC1 [254], POSTN (periostin) [255], IL17A [256], SMOC2 [257], SFTPA2 [258], FAIM2 [259], LHX9 [260], HRG (histidine rich glycoprotein) [261] and CA9 [262] have been reported to be related to lung diseases, but these genes might be involved in the progression of COVID-19. SLC4A1 [263], CCR2 [264], FGL2 [265], CD84 [266], TLR4 [267], ITGB3 [268], TLR2 [267], CD36 [269], MFSD2B [270], PLXDC2 [271], KLF15 [272], C6 [273] and HRG (histidine rich glycoprotein) [274] plays important roles in blood clotting processes. Altered expression of SLC4A1 [275], S1PR1 [276], NFE2 [277], CCR2 [278], NLRP12 [279], PECAM1 [280], ICAM3 [281], CX3CR1 [282], CD247 [283], FOXO3 [284], CD28 [285], GPX1 [286], TLR1 [287], PRDX6 [288], CCL5 [289], FCRL3 [290], ETS1 [291], FGL2 [292], CD93 [293], CD1D [294], TNFSF4 [295], TAL1 [296], TLR4 [297], CCR7 [298], DPP4 [299], NLRC4 [300], RASGRP1 [301], FYN (FYN proto-oncogene, Src family tyrosine kinase) [302], TLR2 [303], CAMK4 [304], FCGR3B [305], CXCL5 [306], CD27 [307], CD36 [308], MGAM (maltase-glucoamylase) [309], CA2 [310], TGFBR2 [311], PADI4 [312], CD5 [313], ADIPOR1 [314], VCAN (versican) [315], SPTB (spectrin beta, erythrocytic) [316], ABCG2 [317], PINK1 [318], OGT (O-linked N-acetylglucosamine (GlcNAc) transferase) [319], AKT3 [320], STAT4 [321], FSTL3 [322], CXCL10 [323], KLF15 [324], FABP1 [325], ACTA2 [326], CRP (C-reactive protein) [327], BMI1 [328], WNT7A [329], IL17F [330], UBD (ubiquitin D) [331], CD34 [332], BCL3 [333], SERPINA5 [334], ADGRF5 [335], CCL2 [336], SCT (secretin) [337], CHAC1 [338], STC1 [339], POSTN (periostin) [340], SAA1 [341], ABCG8 [342], IL17A [343], PTCH1 [344], SMOC2 [345], AHSG (alpha 2-HS glycoprotein) [346], CXCL9 [347], GPR176 [348] and CLCA1 [349] contributes to the progression of renal diseases, but these genes might be involved in the progression of COVID-19. S1PR1 [350], CCR2 [351], CLEC12A [352], KLRG1 [353], NLRP12 [354], PECAM1 [355], ICAM3 [356], PIM1 [357], EEF1A1 [358], MPEG1 [359], CCR4 [360], CX3CR1 [361], EOMES (eomesodermin) [362], LYZ (lysozyme) [363], CD244 [364], GNLY (granulysin) [365], ZAP70 [366], FOXO3 [367], CD28 [368], GPX1 [369], TLR1 [370], PRDX6 [371], TLR6 [370], C5AR2 [372], LRRK2 [373], CCL5 [374], ETS1

[375], SH2D1A [376], CCR3 [377], GZMA (granzyme A) [378], CD48 [379], LTB (lymphotoxin beta) [380], THEMIS (thymocyte selection associated) [381], PICALM (phosphatidylinositol binding clathrin assembly protein) [382], PTAFR (platelet activating factor receptor) [383], BSG (basigin (Ok blood group)) [384], ALOX5 [385], VIM (vimentin) [386], CD1D [387], TNFSF4 [388], CORO1A [389], TAL1 [390], ICAM2 [391], TLR4 [392], FLNA (filamin A) [393], CCR7 [394], DPP4 [395], NLRC4 [396], TLR2 [397], CSF1R [398], LGALS1 [399], CXCL5 [400], CD27 [401], CD36 [402], LYST (lysosomal trafficking regulator) [403], RNF125 [404], GPR183 [405], FCGR2A [406], CD5 [407], RGS10 [408], VCAN (versican) [409], ANXA6 [410], FKBP8 [411], PPM1A [412], MAF1 [413], GPR183 [414], OGT (O-linked N-acetylglucosamine (GlcNAc) transferase) [415], MKRN1 [416], STAT4 [417], DUSP6 [418], COL5A1 [419], CXCL10 [420], SPRR2A [421], KLF15 [422], DDC (dopa decarboxylase) [423], CRP (C-reactive protein) [424], CD34 [425], BCL3 [426], GAP43 [427], TSLP (thymic stromal lymphopoietin) [428], CCL2 [429], IL17A [430], AHSG (alpha 2-HS glycoprotein) [431], DLL4 [432], HRG (histidine rich glycoprotein) [433], FGF4 [434], CXCL9 [435], ANKS4B [436], C8B [437], SLC39A2 [438] and LAMP3 [439] were shown to participate in facilitating the secondary infections. S1PR1 [440], PPBP (pro-platelet basic protein) [441], CCR2 [442], NLRP12 [443], PECAM1 [444], TRIM10 [445], DEFA3 [446], FCN1 [447], PIM1 [448], KAT2B [449], S1PR4 [447], CCR4 [450], PTPRC (protein tyrosine phosphatase receptor type C) [451], CX3CR1 [452], FOXO3 [453], KLRD1 [454], CD28 [455], GPX1 [456], TLR6 [457], CCL5 [458], ETS1 [459], CCR3 [460], FGL2 [461], ALOX5 [462], SELPLG (selectin P ligand) [463], VIM (vimentin) [464], CD93 [465], CD1D [466], TNFSF4 [467], LEF1 [468], ICAM2 [469], TLR4 [470], FLNA (filamin A) [471], CCR7 [472], DPP4 [473], NLRC4 [474], PLCL2 [475], ITGB3 [476], TLR2 [477], CSF1R [478], CXCL5 [479], CD27 [480], CD36 [481], MAPK1 [482], P2RY12 [483], TGFBR2 [484], FCGR2A [485], CD53 [486], LTA4H [487], LILRB2 [488], ADIPOR1 [489], GPR146 [490], RGS10 [491], VCAN (versican) [492], NINJ2 [493], PDE3B [494], LRRC25 [495], AIDA (axininteractor, dorsalization associated) [496], ABCC4 [497], RPL7 [498], MAF1 [499], HACD1 [500], PINK1 [501], CR1 [502], OGT (O-linked N-acetylglucosamine (GlcNAc) transferase) [503], AKT3 [504], TUBB1 [505], F13A1 [506], DUSP6 [507], MYOCD (myocardin) [508], PEAR1 [509], FSTL3 [510], NTRK3 [511], ECM1 [512], CXCL10 [513], KLF15 [514], RBFOX1 [515],

TFAP2B [516], NFKBIL1 [517], ACTN2 [518], APOA4 [519], ACTA2 [520], CRP (C-reactive protein) [521], BMI1 [522], IL17F [523], BCL3 [524], HSF2 [525], TSLP (thymic stromal lymphopoietin) [526], KCNJ11 [527], CCL2 [528], APLNR (apelin receptor) [529], STC1 [530], DAND5 [531], POSTN (periostin) [532], S100A7 [533], SPRR2B [534], SLC6A4 [535], MYOZ1 [536], ABCG8 [537], IL17A [538], PTCH1 [539], NDRG4 [540], FAIM2 [541], TNFRSF11B [542], TDGF1 [543], CXCL9 [544], SLCO1B1 [545], EMP1 [546] and SLC39A2 [547] have been reported to be expressed in cardiovascular diseases, but these genes might be involved in the progression of COVID-19. Hu et al. [548], Zhang et al. [549], Abid et al. [550], Zhang et al. [551], Satoh et al. [552], Ahadzadeh et al. [553], Rudemiller et al. [283], Perros et al. [554], Morris et al. [555], Vinh et al. [556], Ardanaz et al. [557], Nie et al. [558], Song et al. [559], Fan et al. [560], Almodovar et al. [561], Grylls et al. [562], Liu et al. [563], Cai et al. [564], Li et al. [565], Liu et al. [566], Kurahara et al. [567], Holmes et al. [568], Santulli et al. [569], Beitelshees et al. [570], Pravenec et al. [571], Chen et al. [572], Chang et al. [573], Pei et al. [574], Park et al. [575], Claude et al. [576], Saraji et al. [577], Acuña et al. [578], Barnes et al. [579], Sahoo et al. [580], Olivi et al. [581], Antonelli et al. [582], Jiang et al. [583], Kominami et al. [584], Marks et al. [585], Hage, [586], Li et al. [587], Diana et al. [588], Liu et al. [589], Singh et al. [590], Shimizu et al. [591], Huang et al. [525], Zhancheng et al. [592], Alsheikh et al. [593], Zaw et al. [594], Nowzari et al. [529], Zhang et al. [595], Davis et al. [596], Le et al. [597] and Kim et al. [598] found that S1PR1, KRT1, CCR2, NLRP12, PECAM1, PIM1, CX3CR1, CD247, GNLY (granulysin), FOXO3, CD28, GPX1, CCL5, ETS1, FGL2, ALOX5, TLR4, FLNA (filamin A), CCR7, ITGB3, FYN (FYN proto-oncogene, Src family tyrosine kinase), TLR2, CAMK4, CXCL5, CD36, TGFBR2, VCAN (versican), ABCG2, IL10RA, ABCC4, PINK1, SLC12A1, OGT (O-linked N-acetylglucosamine (GlcNAc) transferase), MYOCD (myocardin), PEAR1, CXCL10, KLF15, NFKBIL1, ACTA2, CRP (C-reactive protein), BMI1, GRIA1, WNT7A, IL17F, CD34, HSF2, KCNJ11, CCL2, SCT (secretin), APLNR (apelin receptor), SLC6A4, IL17A, SLC2A2 and SLC6A3 were related to the progression of hypertension, but these genes might be involved in the progression of COVID-19. Mahallawi and Suliman [599], Vanderheiden et al [600], Moustaqil et al [601], Li et al [602], McGee et al [603], Spoerl et al [604], Seale et al [605], Jeong et al [606], Pérez-García et al [607], Murch, [608], Virant-Klun and Strle [609], Bonyek-Silva et al [610], Neri et al [611], Delaveris et al

[612], Brandão et al [613], Solerte et al [614], Duncan-Lowey et al [615], Zheng et al [616], Jamaly et al [617], Nassir et al [618], Liang et al [619], Vietzen et al [620], Kisserli et al [621], Ercan et al [622], Oliviero Ercan et al [623], Mpekoulis et al [624], Acar et al [625], Maione et al [626], Ehsani, [627] and Callahan et al [628] showed that TLR8, CCR2, NLRP12, PECAM1, ITK (IL2 inducible T cell kinase), CCR4, GPX1, TLR1, CCL5, CD33, BSG (basigin (Ok blood group)), ALOX5, SELPLG (selectin P ligand), SIGLEC9, TLR4, DPP4, NLRC4, TLR2, CAMK4, FCGR3B, CXCL5, KLRC2, CR1, F13A1, CXCL10, DDC (dopa decarboxylase), CRP (C-reactive protein), IL17A, HAMP (hepcidin antimicrobial peptide) and CXCL9 were associated with progression of COVID 19. Ahmad et al [629], Sireesh et al [630], Di Prospero et al [631], Anjosa et al [632], Aparicio et al [633], Rau et al [634], Kim et al [635], Thude et al [636], Njerve et al. [452], Eldor et al [637], Ferjeni et al [638], Zurawek et al [639], Yang et al. [106], Li et al. [285], Liu et al [640], Pacifici et al [641], Huang et al [642], Zhang et al [643], Pawłowicz et al [644], Ramos-Lopez et al [645], Bonyek-Silva et al [610], Abu El-Ella et al [646], Mi et al [647], Swafford et al [648], Doody et al [649], Barchetta et al [650], Xu et al [651], Li et al [652], Demirci et al [653], Hasani Ranjbar et al [654], Puchałowicz and Rać [655], Fejes et al [656], Kawabata et al [657], Haseda et al [658], Fernández-Real et al [659], Peters et al [660], Sun et al [661], Mao et al [662], Sano et al [663], Szabó et al [664], Shalaby et al [665], Yu et al [666], Xiang et al [667], Abdelmajed et al [668], Antonelli et al [669], Maeda et al [670], Wong et al. [519], Lee et al [671], Kochetova et al [672], Wang et al [673], Tripaldi et al [674], Izumi et al [675], Pehlić et al [676], Bursova et al [677], Haghvirdizadeh et al [678], Igoillo-Esteve et al [679], Xiu et al [680], Lorenzo et al [681], Abed et al [682], Qiu et al [683], Tabassum et al [684], Rees et al [685], Mancuso et al [686], Laukkanen et al [687], Kang et al [688], Wu et al [689], Licito et al [690], Salek Maghsoudi et al [691] and Porta et al [692] were reported that TLR8, NFE2, CCR2, PECAM1, FCN1, CD3D, LST1, CCR4, PTPRC (protein tyrosine phosphatase receptor type C), CX3CR1, CD247, ZAP70, FOXO3, ATM (ATM serine/threonine kinase), CD28, GPX1, PRDX6, LRRK2, CCL5, FCRL3, ETS1, CD48, ALOX5, CD226, CD1D, IKZF1, TLR4, DPP4, NLRC4, RASGRP1, TLR2, CXCL5, CD36, P2RY12, ITGB7, CD300E, TFRC (transferrin receptor), ADIPOR1, ANK1, CD52, PDE3B, ABCG2, KLRC3, SORL1, PINK1, STAT4, CXCL10, TFAP2B, APOA4, CRP (C-reactive protein), GRIA1, WNT7A, CD34, STATH (statherin), IL12RB2, GAP43, KCNJ11, CCL2,

SLC6A4, PAX4, ABCG8, IL17A, DOK5, PCK1, AHSG (alpha 2-HS glycoprotein), SLC2A2, FAIM2, HAMP (hepcidin antimicrobial peptide), SLCO1B1, SERPINA12 and SLC19A3 an important target gene of diabetes mellitus, but these genes might be involved in the progression of COVID-19. She et al. [693], Malik et al. [694], Ma et al. [695], Sutti et al. [696], Piccolo et al. [697], Yan et al. [698], Xiao et al. [699], Selzner et al. [700], Ito et al. [701], Zhang and Niu [702], Wang et al. [703], DeSantis et al. [704], Roh et al. [705], Wang et al. [232], Tacke et al. [706], Fernández-Real et al. [707], Fu et al. [708], Dibra et al. [709], Goodwin et al. [710], Malik et al. [711], Bukong et al. [712], Sachar and Ma [713], Shi et al. [714], Zhang et al. [715], Chalin et al. [716], Kawakami et al. [717], Zhang et al. [718], Li et al. [719], Mak and Uetrecht [720], Wu et al. [721], Huang et al. [722], Tan et al. [723], Sun et al. [724], Zhang et al. [725], Bartneck et al. [726], Shams et al. [727], Mustafa and Clarke [728] and Song et al. [729] suggested that activity of CCR2, PECAM1, PIM1, CX3CR1, FOXO3, GPX1, CCL5, SIGLEC9, TLR4, DPP4, NLRC4, TLR2, CD40LG, CXCL5, CD36, TGFBR2, IL27RA, FECH (ferrochelatase), PECAM1, VCAN (versican), ABCG2, PINK1, OGT (O-linked N-acetylglucosamine (GlcNAc) transferase), CXCL10, FABP1, CRP (C-reactive protein), TSLP (thymic stromal lymphopoietin), CCL2, SCT (secretin), POSTN (periostin), IL17A, DLL4, EMCN (endomucin), HRG (histidine rich glycoprotein), FGF4, OTC (ornithine carbamoyltransferase) and CXCL9 were involved in liver injury, but these genes might be involved in the progression of COVID-19.

The PPI network of the DEGs was constructed, and modules were extracted and analyzed. The hub genes were identified by using topological parameters includes node degree, betweenness centrality, stress centrality and closeness centrality. Thus, RPL10, UBA52, TRIM42, THEMIS, TRAT1, LCK, GRIA2, CALB2, CAMKV, DCLK1 and SNAP91 can be a novel molecular markers of COVID-19 and provide new insight to improve therapeutic strategies for COVID-19 complications.

As a prediction tool, the miRNA-hub gene regulatory network (miRNet) and TF-hub gene regulatory network (NetworkAnalyst) databases were utilized to confirm the potential genes, miRNA and TF. hsa-mir-1910-3p [730] and STAT3 [731] are associated with COVID-19. Cao et al. [732], Krause et al. [733], Haghnazari et al. [734], Ao et al. [735] and Zhang et al. [736] showed that the hsa-

mir-766-3p, SREBF1, TP53, EGR1 and STAT3 biomarkers might be related to the pathophysiology of diabetes mellitus, but these genes might be involved in the progression of COVID-19. hsa-mir-124-3p [737], SREBF1 [738], ELK1 [739], NFYA (Nuclear transcription factor Y subunit alpha) [740], TP53 [741], EGR1 [742] and STAT3 [743] have been shown as a promising biomarkers in hypertension, but these genes might be involved in the progression of COVID-19. SREBF1 [744], TP53 [745] and EGR1 [746] have been revealed to be highly expressed in CNS disorders, but these genes might be involved in the progression of COVID-19. SREBF1 [747], ELF5 [748], TP53 [749], EGR1 [750], E2F6 [751] and STAT3 [752] have been demonstrated to function in cardiovascular diseases, but these genes might be involved in the progression of COVID-19. ELK1 [753], EGR1 [754] and STAT3 [755] plays a key role in the development of the lung diseases, but these genes might be involved in the progression of COVID-19. Previous studies have reported that EGR1 [756], FOXL1 [757] and STAT3 [758] exhibit significant associations with liver injury, but these genes might be involved in the progression of COVID-19. EGR1 [759] and STAT3 [760] plays important roles in blood clotting processes. Studies have shown that EGR1 [761] and STAT3 [762] altered expressed in secondary infections. Altered expression of EGR1 [763] and STAT3 [764] were observed to be associated with the progression of renal diseases, but these genes might be involved in the progression of COVID-19. Thus, GDI1, DCX, KRT13, hsa-mir-320a, hsa-mir-4736, hsa-mir-559, hsa-mir-186-3p, hsa-mir-4495, hsa-mir-3689a-5p and hsa-mir-6842-5p can be a novel molecular markers of COVID-19 and provide new insight to improve therapeutic strategies for COVID-19 complications.

In conclusion, a comprehensive bioinformatics analysis of DEGs and pathways involved in the occurrence and development of COVID-19 and its secondary complications was performed, and we explored and obtained key regulatory genes and pathways contributing to the progression of COVID-19 and its secondary complications to improve prognosis. Moreover, these results may promote the understanding of molecular mechanisms and clinically related molecular targets for prognosis in COVID-19 and its secondary complications, and provide new insight into the occurrence and development of COVID-19 and its secondary complications.

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Conflict of interest

The authors declare that they have no conflict of interest.

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. [(GSE163151) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE163151)]

Consent for publication

Not applicable.

Competing interests

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Muttanagouda Giriyappagoudar - Acquisition of resources and investigation

Basavaraj Vastrad - Writing original draft, and review and editing

Rajeshwari Horakeri - Formal analysis and validation

Chanabasayya Vastrad - Software and investigation

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Figures

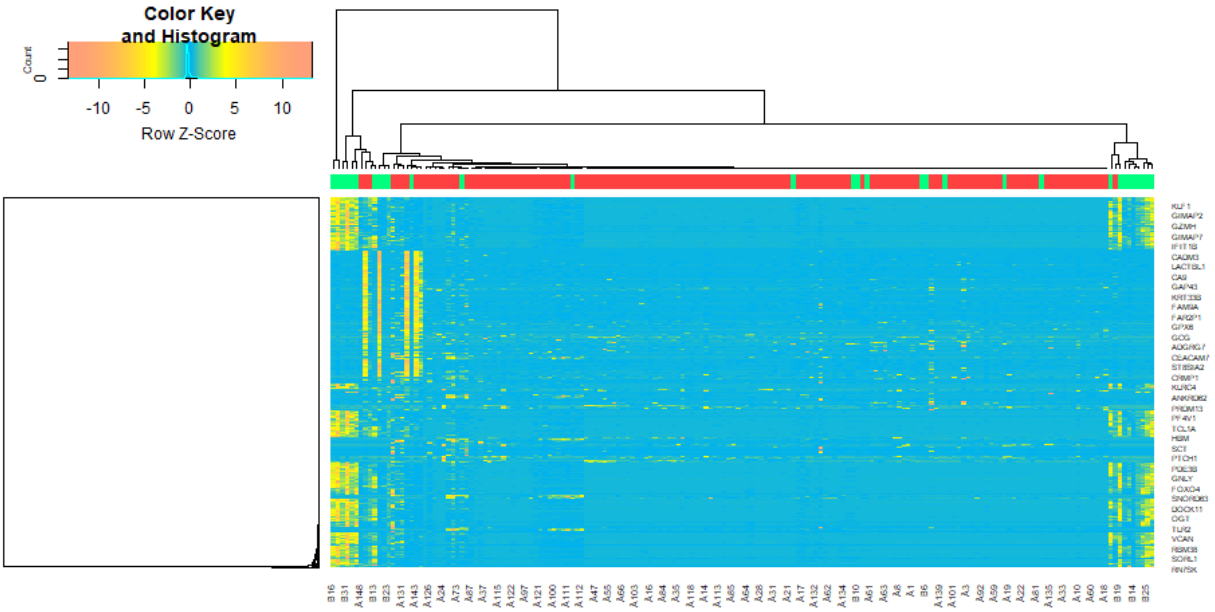

Fig. 1. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

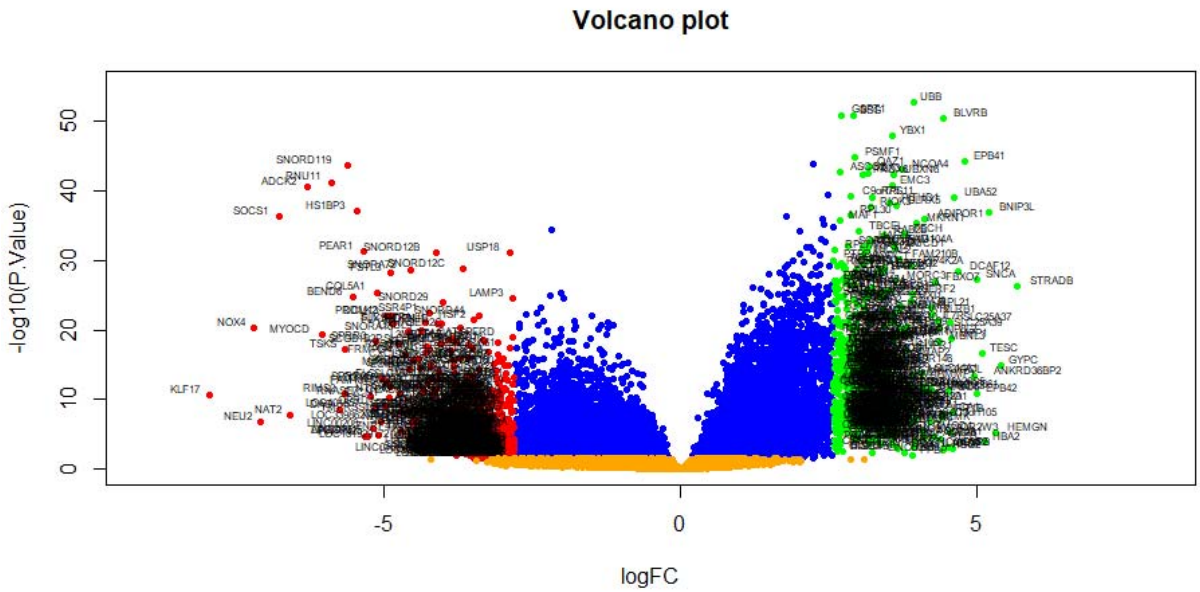

Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A37 = normal control samples; B1 – B47 = HF samples)

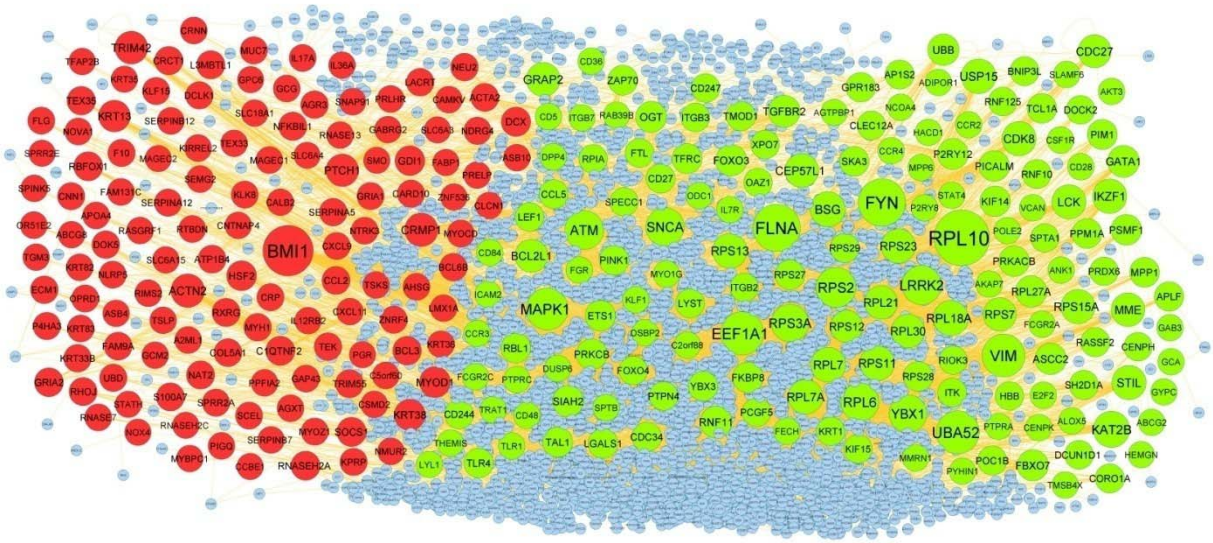

Fig. 3. PPI network of DEGs. Up regulated genes are marked in green; down regulated genes are marked in red

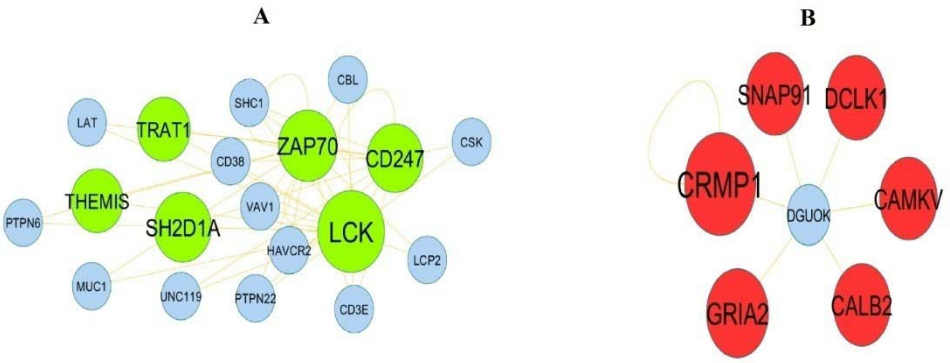

Fig. 4. Modules of isolated form PPI of DEGs. (A) The most significant module was obtained from PPI network with 19 nodes and 41 edges for up regulated genes (B) The most significant module was obtained from PPI network with 7 nodes and 7 edges for down regulated genes. Up regulated genes are marked in green; down regulated genes are marked in red

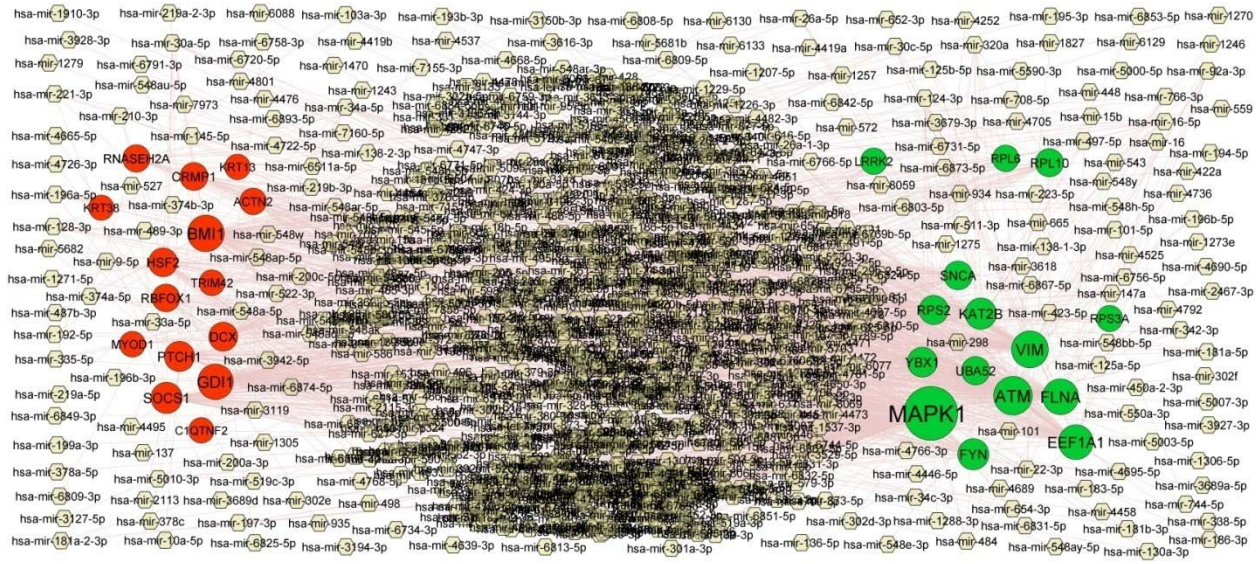

Fig. 5. Target gene - miRNA regulatory network between target genes. The white color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

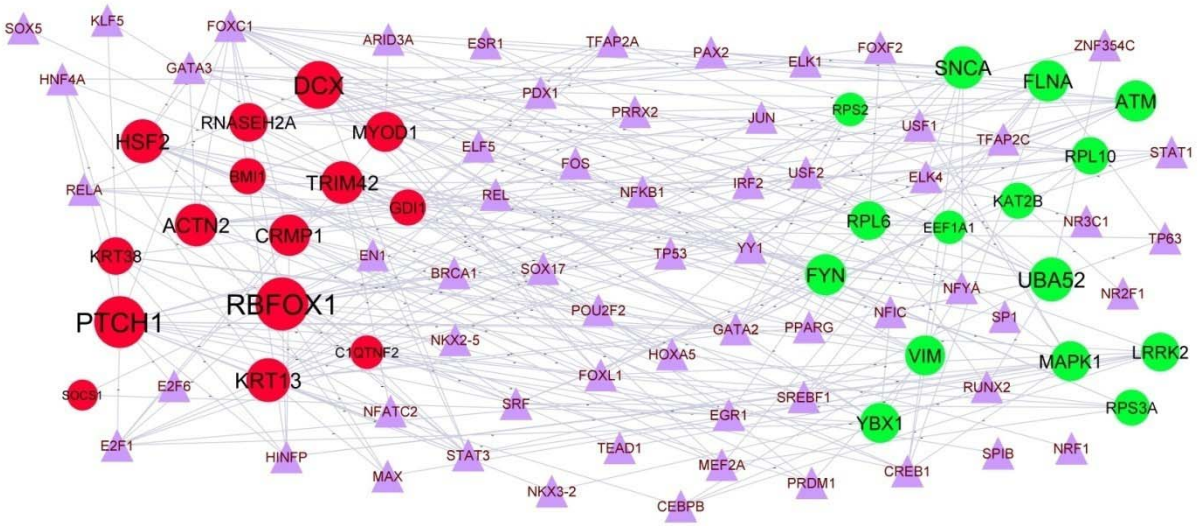

Fig. 6. Target gene - TF regulatory network between target genes. The purple color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

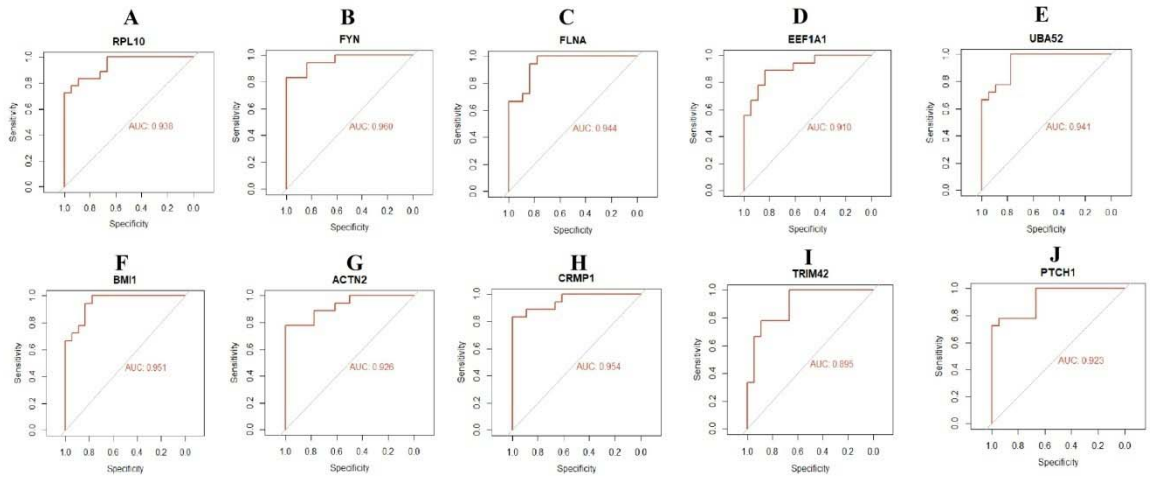

Fig. 7. ROC curve analyses of hub genes. A) RPL10 B) FYN C) FLNA D) EEF1A1 E) UBA52 F) BMI1 G) ACTN2 H) CRMP1 I) TRIM42 J) PTCH1

Tables

Table 1 The statistical metrics for key differentially expressed genes (DEGs)

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	GeneName
STRADB	5.6692	5.86E-27	1.08E-24	10.75108	Up	STE20 related adaptor beta
GYPC	5.389359	1.32E-15	3.12E-14	7.992686	Up	glycophorin C (Gerbich blood group)
HEMGN	5.298035	6.92E-06	2.74E-05	4.496254	Up	hemogen
BNIP3L	5.188255	1.34E-37	1.15E-34	12.81541	Up	BCL2 interacting protein 3 like
HBA2	5.119211	0.000121	0.000375	3.84466	Up	hemoglobin subunit alpha 2
TESC	5.076576	2.51E-17	8.28E-16	8.467447	Up	tescalcin

EPB42	4.988492	1.48E-11	1.72E-10	6.75032	Up	erythrocyte membrane protein band 4.2
SNCA	4.988469	6.31E-28	1.37E-25	10.95473	Up	synuclein alpha
ANKRD36BP2	4.941332	4.15E-14	7.49E-13	7.556295	Up	ankyrin repeat domain 36B pseudogene 2
EPB41	4.790249	4.64E-45	1.54E-41	14.08581	Up	erythrocyte membrane protein band 4.1
DCAF12	4.684627	3.29E-29	8.67E-27	11.21904	Up	DDB1 and CUL4 associated factor 12
UBA52	4.613918	7.05E-40	7.44E-37	13.21642	Up	ubiquitin A-52 residue ribosomal protein fusion product 1
CA1	4.590298	7.31E-09	5.14E-08	5.783543	Up	carbonic anhydrase 1
GYPB	4.588309	0.000962	0.002468	3.301334	Up	glycophorin B (MNS blood group)
MPP1	4.563224	1.42E-19	6.99E-18	9.050837	Up	membrane palmitoylated protein 1
OR2W3	4.539012	5.59E-06	2.26E-05	4.541349	Up	olfactory receptor family 2 subfamily W member 3
SLC25A37	4.530599	6.92E-22	5.35E-20	9.614928	Up	solute carrier family 25 member 37
NEIL3	4.519543	5.56E-12	7.00E-11	6.890468	Up	nei like DNA glycosylase 3
ALAS2	4.496061	0.000864	0.002241	3.331414	Up	5'-aminolevulinate synthase 2
AHSP	4.446545	0.001186	0.002977	3.24221	Up	alpha hemoglobin stabilizing protein
IFIT1B	4.43437	1.26E-08	8.48E-08	5.691309	Up	interferon induced protein with tetratricopeptide repeats 1B
HBG2	4.432305	0.002002	0.004769	3.089957	Up	hemoglobin subunit gamma 2
BLVRB	4.426594	3.48E-51	2.02E-47	15.04953	Up	biliverdinreductase B
C1orf105	4.412989	3.89E-08	2.39E-07	5.495838	Up	chromosome 1 open reading frame 105
GYPA	4.374622	4.42E-05	0.00015	4.084504	Up	glycophorin A (MNS blood group)
MBNL3	4.359314	3.69E-19	1.67E-17	8.945828	Up	muscleblind like splicing regulator 3
SLC25A39	4.358353	4.90E-21	3.22E-19	9.411251	Up	solute carrier family 25 member 39
IL7R	4.325144	6.04E-22	4.72E-20	9.628772	Up	interleukin 7 receptor
FBXO7	4.299306	1.06E-27	2.20E-25	10.90761	Up	F-box protein 7
SLC4A1	4.261381	2.34E-05	8.38E-05	4.229508	Up	solute carrier family 4 member 1 (Diego blood group)
KLRB1	4.251568	5.45E-23	4.98E-21	9.872941	Up	killer cell lectin like receptor B1
RPL21	4.211341	5.00E-24	5.50E-22	10.10974	Up	ribosomal protein L21
GZMK	4.198108	1.92E-07	1.03E-06	5.206478	Up	granzyme K
S1PR1	4.192497	6.66E-12	8.26E-11	6.864784	Up	sphingosine-1-phosphate receptor 1
DNAJC6	4.127316	8.73E-12	1.06E-10	6.826011	Up	DnaJ heat shock protein family (Hsp40) member C6
RNA28S5	4.11918	1.36E-12	1.88E-11	7.087965	Up	RNA, 28S ribosomal 5
PAGE2B	4.113734	3.63E-05	0.000125	4.130006	Up	PAGE family member 2B
ADIPOR1	4.10098	1.12E-36	8.14E-34	12.6497	Up	adiponectin receptor 1
TMOD1	4.095793	3.74E-06	1.57E-05	4.625295	Up	tropomodulin 1
SLC14A1	4.072584	1.71E-14	3.30E-13	7.671094	Up	solute carrier family 14 member 1 (Kidd blood group)
SOX6	4.066733	1.43E-12	1.96E-11	7.081318	Up	SRY-box transcription factor 6
MKRN1	3.971963	4.03E-36	2.75E-33	12.54888	Up	makorin ring finger protein 1
ABCC13	3.966921	5.04E-08	3.03E-07	5.449723	Up	ATP binding cassette subfamily C member 13 (pseudogene)
KLF1	3.964868	8.02E-11	8.23E-10	6.500154	Up	Kruppel like factor 1
CLC	3.956993	7.69E-05	0.000248	3.953914	Up	Charcot-Leyden crystal galectin
KRT1	3.950445	1.26E-07	6.99E-07	5.284537	Up	keratin 1
GATA1	3.935595	2.73E-09	2.07E-08	5.947243	Up	GATA binding protein 1
UBB	3.934318	1.37E-53	3.17E-49	15.41165	Up	ubiquitin B
PPBP	3.912112	0.009778	0.019439	2.58357	Up	pro-platelet basic protein

MAP3K7CL	3.905122	2.40E-14	4.53E-13	7.627226	Up	MAP3K7 C-terminal like
SERF2	3.902194	7.55E-26	1.11E-23	10.5127	Up	small EDRK-rich factor 2
TLR8	3.880248	2.06E-12	2.75E-11	7.030279	Up	toll like receptor 8
MXI1	3.877346	7.51E-25	9.46E-23	10.29393	Up	MAX interactor 1, dimerization protein
PIP4K2A	3.875012	5.88E-30	1.87E-27	11.37021	Up	phosphatidylinositol-5-phosphate 4-kinase type 2 alpha
POLE2	3.862719	3.08E-09	2.31E-08	5.927269	Up	DNA polymerase epsilon 2, accessory subunit
FOLR3	3.854242	3.03E-07	1.56E-06	5.121693	Up	folate receptor gamma
RPL39	3.823737	2.61E-21	1.80E-19	9.477138	Up	ribosomal protein L39
TNFAIP8L2	3.822019	4.34E-20	2.39E-18	9.179234	Up	TNF alpha induced protein 8 like 2
NFE2	3.807887	2.40E-11	2.69E-10	6.679075	Up	nuclear factor, erythroid 2
GLIPR1	3.796955	1.02E-17	3.67E-16	8.571281	Up	GLI pathogenesis related 1
TRAT1	3.795535	1.84E-09	1.45E-08	6.011622	Up	T cell receptor associated transmembrane adaptor 1
FECH	3.767999	1.70E-34	9.85E-32	12.24913	Up	ferrochelatase
HBM	3.760768	0.00477	0.010323	2.822168	Up	hemoglobin subunit mu
CCR2	3.758019	6.79E-21	4.31E-19	9.376967	Up	C-C motif chemokine receptor 2
CLEC12A	3.750834	1.78E-10	1.71E-09	6.378787	Up	C-type lectin domain family 12 member A
CPVL	3.750572	1.66E-20	9.80E-19	9.282426	Up	carboxypeptidasevitellogenic like
TARP	3.744019	3.74E-10	3.34E-09	6.264629	Up	TCR gamma alternate reading frame protein
NCAPG	3.734243	9.26E-10	7.68E-09	6.121727	Up	non-SMC condensin I complex subunit G
KLRG1	3.7262	2.39E-09	1.84E-08	5.968936	Up	killer cell lectin like receptor G1
GPR146	3.722762	7.21E-16	1.80E-14	8.066841	Up	G protein-coupled receptor 146
WHAMMP1	3.722244	9.03E-14	1.54E-12	7.454369	Up	WAS protein homolog associated with actin, golgi membranes and microtubules pseudogene 1
NCOA4	3.712736	8.35E-44	1.76E-40	13.88018	Up	nuclear receptor coactivator 4
RBM38	3.710614	3.82E-24	4.22E-22	10.13612	Up	RNA binding motif protein 38
TRIM58	3.693841	1.13E-07	6.33E-07	5.304896	Up	tripartite motif containing 58
GIMAP2	3.682527	6.99E-17	2.11E-15	8.347169	Up	GTPase, IMAP family member 2
FAM210B	3.680115	5.51E-31	2.00E-28	11.57505	Up	family with sequence similarity 210 member B
SIRPB2	3.677038	1.57E-10	1.52E-09	6.398673	Up	signal regulatory protein beta 2
E2F2	3.675692	3.93E-10	3.51E-09	6.256693	Up	E2F transcription factor 2
NSUN3	3.672535	1.64E-23	1.61E-21	9.992992	Up	NOP2/Sun RNA methyltransferase 3
LYL1	3.672322	5.95E-21	3.85E-19	9.390921	Up	LYL1 basic helix-loop-helix family member
MYL4	3.666213	0.00063	0.001687	3.418418	Up	myosin light chain 4
DDX11L10	3.659579	0.000971	0.002488	3.298846	Up	DEAD/H-box helicase 11 like 10 (pseudogene)
GLRX5	3.635999	1.11E-38	1.07E-35	13.0075	Up	glutaredoxin 5
SKA3	3.635185	5.42E-09	3.89E-08	5.833718	Up	spindle and kinetochore associated complex subunit 3
MORC3	3.617837	8.30E-28	1.77E-25	10.92983	Up	MORC family CW-type zinc finger 3
GUCD1	3.616566	1.85E-32	7.93E-30	11.86289	Up	guanylylcyclase domain containing 1
NUSAP1	3.612423	6.39E-20	3.41E-18	9.137457	Up	nucleolar and spindle associated protein 1
NLRP12	3.605707	9.56E-10	7.91E-09	6.116514	Up	NLR family pyrin domain containing 12
UBXN6	3.599532	4.85E-43	7.49E-40	13.7536	Up	UBX domain protein 6
PECAM1	3.593671	1.15E-19	5.80E-18	9.073701	Up	platelet and endothelial cell adhesion molecule 1
RGS10	3.592196	7.97E-22	6.04E-20	9.600371	Up	regulator of G protein signaling 10

SWT1	3.591791	3.17E-19	1.45E-17	8.962537	Up	SWT1 RNA endoribonuclease homolog
MBOAT2	3.586764	6.21E-23	5.61E-21	9.859887	Up	membrane bound O-acyltransferase domain containing 2
FAM104A	3.586158	5.29E-33	2.61E-30	11.96695	Up	family with sequence similarity 104 member A
TRIM10	3.582281	4.90E-07	2.41E-06	5.030379	Up	tripartite motif containing 10
SLFN14	3.579883	3.19E-06	1.36E-05	4.658212	Up	schlafen family member 14
PHOSPHO1	3.567976	2.02E-10	1.91E-09	6.359487	Up	phosphoethanolamine/phosphocholine phosphatase 1
ISCA1	3.56776	5.33E-22	4.19E-20	9.641672	Up	iron-sulfur cluster assembly 1
DEFA3	3.565264	3.21E-05	0.000112	4.158329	Up	defensin alpha 3
YBX1	3.563586	1.06E-48	4.91E-45	14.66637	Up	Y-box binding protein 1
ICAM3	3.557797	1.48E-19	7.28E-18	9.046192	Up	intercellular adhesion molecule 3
BEND2	3.556012	0.000283	0.000819	3.630395	Up	BEN domain containing 2
EMC3	3.555132	1.72E-41	2.35E-38	13.493	Up	ER membrane protein complex subunit 3
YOD1	3.554974	2.00E-17	6.74E-16	8.493589	Up	YOD1 deubiquitinase
FCER1A	3.549443	1.87E-12	2.52E-11	7.043709	Up	Fc fragment of IgE receptor Ia
FCN1	3.526943	1.92E-10	1.83E-09	6.367547	Up	ficolin 1
PITHD1	3.524477	5.99E-39	6.04E-36	13.05449	Up	PITH domain containing 1
RPS15A	3.516288	1.52E-26	2.57E-24	10.66299	Up	ribosomal protein S15a
CFP	3.506043	1.43E-14	2.81E-13	7.693477	Up	complement factor properdin
RGS18	3.484481	4.51E-08	2.74E-07	5.469602	Up	regulator of G protein signaling 18
HBQ1	3.479164	9.88E-06	3.79E-05	4.419885	Up	hemoglobin subunit theta 1
LILRA1	3.478823	2.08E-08	1.34E-07	5.6048	Up	leukocyte immunoglobulin like receptor A1
C11orf21	3.468276	6.24E-14	1.10E-12	7.502844	Up	chromosome 11 open reading frame 21
FGFBP2	3.465362	2.29E-12	3.04E-11	7.015395	Up	fibroblast growth factor binding protein 2
VCAN	3.458726	2.59E-13	4.09E-12	7.314079	Up	versican
PIM1	3.458446	1.01E-22	8.72E-21	9.810871	Up	Pim-1 proto-oncogene, serine/threonine kinase
EEF1A1	3.435629	1.75E-29	4.84E-27	11.27462	Up	eukaryotic translation elongation factor 1 alpha 1
CYBB	3.434998	1.77E-21	1.25E-19	9.517993	Up	cytochrome b-245 beta chain
ANK1	3.433899	2.23E-13	3.57E-12	7.333943	Up	ankyrin 1
NHSL2	3.430393	1.23E-15	2.93E-14	8.001247	Up	NHS like 2
RAB2B	3.427487	2.38E-34	1.35E-31	12.22162	Up	RAB2B, member RAS oncogene family
AP1S2	3.419506	4.29E-15	9.27E-14	7.846011	Up	adaptor related protein complex 1 subunit sigma 2
TUBB1	3.418087	1.24E-05	4.69E-05	4.370407	Up	tubulin beta 1 class VI
FAXDC2	3.416985	1.53E-29	4.37E-27	11.2863	Up	fatty acid hydroxylase domain containing 2
MPEG1	3.412707	2.79E-26	4.56E-24	10.60615	Up	macrophage expressed 1
ITK	3.411104	2.91E-13	4.56E-12	7.298284	Up	IL2 inducible T cell kinase
SESN3	3.407964	1.77E-23	1.74E-21	9.985325	Up	sestrin 3
GPR174	3.40592	2.87E-09	2.17E-08	5.938901	Up	G protein-coupled receptor 174
CD3D	3.403249	2.04E-16	5.60E-15	8.219953	Up	CD3d molecule
KAT2B	3.39691	3.08E-29	8.21E-27	11.22483	Up	lysine acetyltransferase 2B
CD8B	3.394188	1.96E-10	1.85E-09	6.364741	Up	CD8b molecule
LST1	3.392948	2.83E-14	5.25E-13	7.605987	Up	leukocyte specific transcript 1
S1PR4	3.386888	6.03E-11	6.30E-10	6.543046	Up	sphingosine-1-phosphate receptor 4
VN1R1	3.380027	3.98E-08	2.44E-07	5.491661	Up	vomeronasal 1 receptor 1

BCL2L1	3.379882	2.18E-25	2.93E-23	10.41204	Up	BCL2 like 1
MEF2B	3.374835	4.82E-07	2.37E-06	5.033429	Up	myocyte enhancer factor 2B
GZMH	3.372974	8.49E-09	5.90E-08	5.758463	Up	granzyme H
CD52	3.363921	2.19E-15	4.98E-14	7.930223	Up	CD52 molecule
MMRN1	3.357269	0.000188	0.000565	3.734219	Up	multimerin 1
GIMAP1	3.356536	6.25E-16	1.57E-14	8.084304	Up	GTPase, IMAP family member 1
VRK1	3.343837	2.83E-19	1.32E-17	8.974986	Up	VRK serine/threonine kinase 1
NCF1B	3.33496	6.16E-08	3.64E-07	5.41406	Up	neutrophil cytosolic factor 1B pseudogene
USP12	3.334764	6.17E-26	9.29E-24	10.53176	Up	ubiquitin specific peptidase 12
SPECC1	3.333839	3.48E-29	9.08E-27	11.21396	Up	sperm antigen with calponin homology and coiled-coil domains 1
F13A1	3.320919	4.06E-06	1.69E-05	4.608479	Up	coagulation factor XIII A chain
SPTA1	3.318384	1.70E-05	6.25E-05	4.301326	Up	spectrin alpha, erythrocytic 1
SPTB	3.31192	2.18E-11	2.45E-10	6.693328	Up	spectrin beta, erythrocytic
BTLA	3.301833	7.80E-08	4.50E-07	5.37165	Up	B and T lymphocyte associated
GRAP	3.291113	7.32E-09	5.14E-08	5.783312	Up	GRB2 related adaptor protein
SAMD3	3.290401	8.04E-14	1.38E-12	7.46962	Up	sterile alpha motif domain containing 3
CCR4	3.284953	9.22E-05	0.000293	3.910128	Up	C-C motif chemokine receptor 4
GNG11	3.28215	5.91E-05	0.000195	4.016202	Up	G protein subunit gamma 11
PARPBP	3.282073	2.54E-11	2.83E-10	6.67104	Up	PARP1 binding protein
VNN2	3.277435	1.87E-16	5.19E-15	8.230086	Up	vanin 2
PTPRC	3.274516	3.61E-16	9.42E-15	8.151125	Up	protein tyrosine phosphatase receptor type C
CX3CR1	3.270638	6.86E-09	4.84E-08	5.794334	Up	C-X3-C motif chemokine receptor 1
TSPAN32	3.270145	2.46E-08	1.56E-07	5.576359	Up	tetraspanin 32
ANKRD44	3.267203	1.00E-19	5.15E-18	9.088418	Up	ankyrin repeat domain 44
KIF14	3.252132	4.85E-10	4.25E-09	6.224015	Up	kinesin family member 14
CD247	3.251185	1.98E-11	2.25E-10	6.707229	Up	CD247 molecule
FCRL1	3.236705	7.74E-08	4.47E-07	5.373062	Up	Fc receptor like 1
KIAA1586	3.235396	4.80E-15	1.02E-13	7.832092	Up	KIAA1586
RPL9	3.234618	6.68E-27	1.21E-24	10.73896	Up	ribosomal protein L9
SIAH2	3.233805	4.83E-19	2.13E-17	8.916208	Up	siah E3 ubiquitin protein ligase 2
EOMES	3.232839	9.79E-11	9.82E-10	6.470232	Up	eomesodermin
P2RY10	3.228379	2.53E-09	1.93E-08	5.959515	Up	P2Y receptor family member 10
TBC1D10C	3.227403	3.39E-18	1.30E-16	8.69761	Up	TBC1 domain family member 10C
LCK	3.225268	3.37E-19	1.54E-17	8.955928	Up	LCK proto-oncogene, Src family tyrosine kinase
RPS11	3.222672	7.00E-40	7.44E-37	13.21699	Up	ribosomal protein S11
S1PR5	3.2217	1.01E-10	1.01E-09	6.466152	Up	sphingosine-1-phosphate receptor 5
LYZ	3.214331	3.20E-26	5.19E-24	10.59338	Up	lysozyme
HBB	3.213553	1.69E-07	9.18E-07	5.230561	Up	hemoglobin subunit beta
GIMAP6	3.212923	6.76E-22	5.26E-20	9.617231	Up	GTPase, IMAP family member 6
PTGDR	3.206378	9.19E-13	1.31E-11	7.14215	Up	prostaglandin D2 receptor
RNF182	3.205488	5.29E-12	6.67E-11	6.89754	Up	ring finger protein 182
RIOK3	3.20499	2.12E-38	1.97E-35	12.95786	Up	RIO kinase 3
CD244	3.204459	5.54E-12	6.98E-11	6.890993	Up	CD244 molecule

ODC1	3.200705	9.84E-31	3.46E-28	11.52526	Up	ornithine decarboxylase 1
GZMM	3.195721	2.98E-07	1.54E-06	5.124528	Up	granzyme M
GNLY	3.195716	7.13E-09	5.02E-08	5.787835	Up	granulysin
P2RY8	3.195259	2.59E-11	2.89E-10	6.668057	Up	P2Y receptor family member 8
HAGH	3.194697	1.37E-33	7.24E-31	12.07845	Up	hydroxyacylglutathione hydrolase
KLRF1	3.194343	3.81E-09	2.81E-08	5.892159	Up	killer cell lectin like receptor F1
CR1L	3.193816	6.85E-12	8.47E-11	6.860739	Up	complement C3b/C4b receptor 1 like
RN7SK	3.1918	8.42E-23	7.37E-21	9.829273	Up	RNA component of 7SK nuclear ribonucleoprotein
GYPE	3.191069	7.39E-05	0.000239	3.963348	Up	glycophorin E (MNS blood group)
RN7SL1	3.188144	1.98E-09	1.55E-08	5.999331	Up	RNA component of signal recognition particle 7SL1
TXK	3.181514	3.35E-10	3.03E-09	6.281751	Up	TXK tyrosine kinase
OAZ1	3.180204	2.72E-44	6.31E-41	13.96033	Up	ornithine decarboxylase antizyme 1
PF4V1	3.174615	0.000231	0.000681	3.682469	Up	platelet factor 4 variant 1
FCRL6	3.174093	6.91E-08	4.05E-07	5.393552	Up	Fc receptor like 6
DCUN1D1	3.166555	4.22E-33	2.13E-30	11.98574	Up	defective in cullinneddylation 1 domain containing 1
KIF15	3.163953	4.26E-10	3.77E-09	6.244181	Up	kinesin family member 15
LILRA2	3.163637	1.04E-06	4.84E-06	4.883207	Up	leukocyte immunoglobulin like receptor A2
ZAP70	3.159649	3.47E-12	4.50E-11	6.957191	Up	zeta chain of T cell receptor associated protein kinase 70
TANGO2	3.156083	1.50E-25	2.10E-23	10.44765	Up	transport and golgi organization 2 homolog
RPL35A	3.154177	1.17E-32	5.35E-30	11.90071	Up	ribosomal protein L35a
YBX3	3.153547	3.35E-43	5.98E-40	13.78024	Up	Y-box binding protein 3
RPS12	3.141628	3.79E-32	1.57E-29	11.8025	Up	ribosomal protein S12
NPRL3	3.133192	2.72E-17	8.92E-16	8.458095	Up	NPR3 like, GATOR1 complex subunit
FOXO3	3.132895	1.92E-26	3.18E-24	10.64099	Up	forkhead box O3
RHAG	3.129782	1.11E-05	4.22E-05	4.394618	Up	Rh associated glycoprotein
DOCK11	3.129264	7.48E-16	1.86E-14	8.062468	Up	dedicator of cytokinesis 11
ATM	3.128499	8.59E-33	4.07E-30	11.92667	Up	ATM serine/threonine kinase
KLRD1	3.118647	4.53E-15	9.73E-14	7.839295	Up	killer cell lectin like receptor D1
CDKN3	3.116314	7.11E-11	7.33E-10	6.518268	Up	cyclin dependent kinase inhibitor 3
MFNG	3.112593	1.90E-08	1.24E-07	5.620842	Up	MFNG O-fucosylpeptide 3-beta-N-acetylglucosaminyltransferase
C2orf88	3.106306	4.30E-07	2.14E-06	5.055089	Up	chromosome 2 open reading frame 88
ARHGAP15	3.10047	1.78E-12	2.40E-11	7.050758	Up	Rho GTPase activating protein 15
CD28	3.092069	4.49E-07	2.23E-06	5.046748	Up	CD28 molecule
AKAP7	3.091832	4.75E-19	2.10E-17	8.917938	Up	A-kinase anchoring protein 7
GPX1	3.086934	7.23E-24	7.80E-22	10.07356	Up	glutathione peroxidase 1
TLR1	3.086774	1.21E-15	2.89E-14	8.003282	Up	toll like receptor 1
NINJ2	3.086642	1.81E-20	1.06E-18	9.27297	Up	ninjurin 2
RPIA	3.086172	5.06E-25	6.45E-23	10.33185	Up	ribose 5-phosphate isomerase A
PRDX6	3.074591	4.17E-43	6.91E-40	13.76441	Up	peroxiredoxin 6
PCMTD1	3.072725	1.18E-32	5.35E-30	11.90053	Up	protein-L-isoaspartate (D-aspartate) O-methyltransferase domain containing 1
FCGR2C	3.072582	4.90E-09	3.54E-08	5.850368	Up	Fc fragment of IgG receptor IIc (gene/pseudogene)
TLR6	3.066185	8.73E-16	2.14E-14	8.04354	Up	toll like receptor 6
MICAL2	3.063794	1.87E-31	6.99E-29	11.66751	Up	microtubule associated monooxygenase, calponin and LIM domain containing 2

ADGRE3	3.063041	7.67E-07	3.65E-06	4.9435	Up	adhesion G protein-coupled receptor E3
TNS1	3.05964	4.23E-30	1.38E-27	11.39895	Up	tensin 1
PRF1	3.052224	1.08E-10	1.08E-09	6.455226	Up	perforin 1
C5AR2	3.041309	3.76E-11	4.07E-10	6.613043	Up	complement component 5a receptor 2
BPGM	3.040329	1.56E-15	3.63E-14	7.972246	Up	bisphosphoglyceratemutase
LRRK2	3.039186	7.74E-15	1.59E-13	7.771708	Up	leucine rich repeat kinase 2
HCG27	3.034802	4.48E-16	1.15E-14	8.124937	Up	HLA complex group 27
TMEM71	3.034193	5.27E-15	1.12E-13	7.820215	Up	transmembrane protein 71
CCL5	3.032489	2.10E-16	5.76E-15	8.216289	Up	C-C motif chemokine ligand 5
AOAH	3.029779	7.22E-17	2.17E-15	8.343382	Up	acyloxyacyl hydrolase
CD33	3.029021	7.07E-07	3.39E-06	4.959427	Up	CD33 molecule
FCRL3	3.027538	1.46E-06	6.58E-06	4.816973	Up	Fc receptor like 3
ETS1	3.021079	6.01E-23	5.44E-21	9.863282	Up	ETS proto-oncogene 1, transcription factor
SH2D1A	3.020195	1.20E-07	6.71E-07	5.292963	Up	SH2 domain containing 1A
SLC7A7	3.019232	6.53E-14	1.15E-12	7.497042	Up	solute carrier family 7 member 7
PYHIN1	3.019127	4.51E-13	6.81E-12	7.239176	Up	pyrin and HIN domain family member 1
SLAMF6	3.019035	1.05E-09	8.63E-09	6.101758	Up	SLAM family member 6
ITGB2	3.01723	2.92E-14	5.39E-13	7.601918	Up	integrin subunit beta 2
CMTM2	3.017059	5.69E-12	7.15E-11	6.887269	Up	CKLF like MARVEL transmembrane domain containing 2
DPEP2	3.010991	3.84E-12	4.93E-11	6.942984	Up	dipeptidase 2
TBCEL	3.009596	6.39E-35	3.80E-32	12.32816	Up	tubulin folding cofactor E like
TMSB4X	2.993542	3.67E-19	1.66E-17	8.946572	Up	thymosin beta 4 X-linked
ANXA6	2.991511	2.84E-15	6.34E-14	7.897767	Up	annexin A6
PDE3B	2.990006	3.11E-14	5.72E-13	7.593461	Up	phosphodiesterase 3B
CCR3	2.987791	4.98E-06	2.03E-05	4.565723	Up	C-C motif chemokine receptor 3
GIMAP8	2.986445	6.26E-17	1.91E-15	8.360276	Up	GTPase, IMAP family member 8
OSBP2	2.980819	2.37E-24	2.72E-22	10.18265	Up	oxysterol binding protein 2
FGL2	2.979692	6.36E-23	5.72E-21	9.857485	Up	fibrinogen like 2
GZMA	2.977734	3.76E-11	4.07E-10	6.613093	Up	granzyme A
THRA1/BTR	2.970734	5.31E-05	0.000177	4.041327	Up	uncharacterized LOC105371807
R3HDM4	2.969846	4.17E-19	1.86E-17	8.932454	Up	R3H domain containing 4
LRRC25	2.967274	4.86E-10	4.26E-09	6.223704	Up	leucine rich repeat containing 25
TCL1A	2.963311	4.85E-05	0.000163	4.062682	Up	TCL1 family AKT coactivator A
XK	2.957738	7.07E-07	3.39E-06	4.959403	Up	X-linked Kx blood group
RPS27	2.957597	1.67E-21	1.20E-19	9.523668	Up	ribosomal protein S27
RPL18A	2.954809	6.62E-21	4.25E-19	9.37961	Up	ribosomal protein L18a
FGR	2.954468	1.08E-09	8.83E-09	6.097722	Up	FGR proto-oncogene, Src family tyrosine kinase
GPR141	2.949077	9.53E-06	3.67E-05	4.427612	Up	G protein-coupled receptor 141
AGTPBP1	2.946564	1.01E-21	7.55E-20	9.576291	Up	ATP/GTP binding protein 1
TCP11L2	2.945901	2.83E-29	7.65E-27	11.23216	Up	t-complex 11 like 2
CD48	2.943822	1.65E-12	2.24E-11	7.061661	Up	CD48 molecule
LTB	2.942649	2.18E-10	2.04E-09	6.348233	Up	lymphotoxin beta
PSMF1	2.941026	1.15E-45	4.46E-42	14.18377	Up	proteasome inhibitor subunit 1

THEMIS	2.940271	1.46E-17	5.07E-16	8.52993	Up	thymocyte selection associated
KCNA3	2.936566	3.48E-10	3.14E-09	6.275811	Up	potassium voltage-gated channel subfamily A member 3
PICALM	2.935008	3.69E-27	7.07E-25	10.79364	Up	phosphatidylinositol binding clathrin assembly protein
TXNDC16	2.934936	6.96E-11	7.21E-10	6.52143	Up	thioredoxin domain containing 16
OST4	2.929687	7.27E-15	1.50E-13	7.779685	Up	oligosaccharyltransferase complex subunit 4, non-catalytic
TIGIT	2.928102	9.35E-13	1.33E-11	7.139743	Up	T cell immunoreceptor with Ig and ITIM domains
PTAFR	2.924695	5.19E-21	3.38E-19	9.4052	Up	platelet activating factor receptor
MYO1G	2.923691	4.88E-12	6.18E-11	6.90905	Up	myosin IG
MPP6	2.923654	3.37E-18	1.30E-16	8.698278	Up	membrane palmitoylated protein 6
ACSL6	2.923548	1.45E-08	9.61E-08	5.667896	Up	acyl-CoA synthetase long chain family member 6
JAZF1	2.922907	2.36E-16	6.39E-15	8.202464	Up	JAZF zinc finger 1
C1orf162	2.919377	1.35E-14	2.67E-13	7.700929	Up	chromosome 1 open reading frame 162
ABCG2	2.9172	3.76E-05	0.00013	4.121565	Up	ATP binding cassette subfamily G member 2 (Junior blood group)
ADCY7	2.914856	2.12E-15	4.83E-14	7.934248	Up	adenylatecyclase 7
LRRC8C	2.913384	1.06E-12	1.49E-11	7.12288	Up	leucine rich repeat containing 8 VRAC subunit C
CXCR2P1	2.912523	2.97E-07	1.54E-06	5.125132	Up	C-X-C motif chemokine receptor 2 pseudogene 1
FAM117A	2.912304	7.72E-20	4.03E-18	9.117006	Up	family with sequence similarity 117 member A
FOXO4	2.911731	1.54E-19	7.54E-18	9.041859	Up	forkhead box O4
BSG	2.911151	1.15E-51	8.91E-48	15.12244	Up	basigin (Ok blood group)
RPS2	2.907776	3.90E-25	5.12E-23	10.3568	Up	ribosomal protein S2
RBL1	2.90312	3.73E-17	1.18E-15	8.421108	Up	RB transcriptional corepressor like 1
RPS28	2.902884	7.40E-18	2.72E-16	8.60856	Up	ribosomal protein S28
CCDC7	2.901658	1.63E-17	5.58E-16	8.517843	Up	coiled-coil domain containing 7
ALOX5	2.899678	9.84E-13	1.39E-11	7.132698	Up	arachidonate 5-lipoxygenase
MFSD2B	2.898011	6.41E-07	3.09E-06	4.978392	Up	major facilitator superfamily domain containing 2B
P2RY13	2.896262	2.91E-09	2.19E-08	5.93678	Up	purinergic receptor P2Y13
AIDA	2.894022	1.54E-16	4.37E-15	8.253315	Up	axininteractor, dorsalization associated
LY86	2.893811	1.77E-09	1.40E-08	6.017528	Up	lymphocyte antigen 86
CHPT1	2.892286	1.62E-16	4.55E-15	8.24713	Up	choline phosphotransferase 1
SMG1P1	2.890959	1.09E-09	8.93E-09	6.095497	Up	SMG1 pseudogene 1
MME	2.88451	6.24E-12	7.79E-11	6.874104	Up	membrane metalloendopeptidase
PTPN4	2.881189	2.37E-28	5.41E-26	11.04301	Up	protein tyrosine phosphatase non-receptor type 4
SELPLG	2.875341	1.42E-14	2.80E-13	7.694119	Up	selectin P ligand
RPL30	2.875066	2.46E-37	2.04E-34	12.76831	Up	ribosomal protein L30
C9orf78	2.874814	6.13E-40	7.11E-37	13.22694	Up	chromosome 9 open reading frame 78
RPS3A	2.874666	1.39E-22	1.18E-20	9.77842	Up	ribosomal protein S3A
VIM	2.87178	5.29E-17	1.63E-15	8.380141	Up	vimentin
CD93	2.870199	4.48E-13	6.76E-12	7.2403	Up	CD93 molecule
IL10RA	2.866432	9.78E-15	1.97E-13	7.742024	Up	interleukin 10 receptor subunit alpha
GCA	2.865947	2.06E-13	3.31E-12	7.344811	Up	grancalcin
KLRC3	2.865929	3.70E-07	1.87E-06	5.083824	Up	killer cell lectin like receptor C3
STAT4	2.865161	1.33E-11	1.56E-10	6.765006	Up	signal transducer and activator of transcription 4
DUSP6	2.861854	1.13E-19	5.74E-18	9.075413	Up	dual specificity phosphatase 6

IPCEF1	2.861567	2.07E-16	5.69E-15	8.217737	Up	interaction protein for cytohesin exchange factors 1
MS4A6A	2.85983	5.01E-19	2.19E-17	8.912001	Up	membrane spanning 4-domains A6A
WDR45	2.858844	3.54E-27	6.84E-25	10.79746	Up	WD repeat domain 45
RHBDD1	2.857453	5.18E-21	3.38E-19	9.405502	Up	rhomboid domain containing 1
GPR171	2.855969	1.16E-07	6.49E-07	5.29992	Up	G protein-coupled receptor 171
RAB39B	2.852638	5.64E-06	2.28E-05	4.539575	Up	RAB39B, member RAS oncogene family
SIGLEC10	2.8488	6.76E-13	9.85E-12	7.184252	Up	sialic acid binding Ig like lectin 10
TMEM170B	2.846406	4.83E-14	8.65E-13	7.536322	Up	transmembrane protein 170B
FTL	2.843167	8.28E-19	3.54E-17	8.856189	Up	ferritin light chain
DPY19L1P1	2.834863	1.90E-12	2.55E-11	7.041829	Up	DPY19L1 pseudogene 1
SULT1B1	2.831202	9.74E-09	6.68E-08	5.735277	Up	sulfotransferase family 1B member 1
CD96	2.830752	9.38E-16	2.29E-14	8.034741	Up	CD96 molecule
CD226	2.829186	2.79E-11	3.09E-10	6.657384	Up	CD226 molecule
CD1D	2.828952	1.30E-11	1.53E-10	6.768857	Up	CD1d molecule
TNFSF4	2.828613	8.38E-08	4.81E-07	5.358685	Up	TNF superfamily member 4
ANTXRLP1	2.8274	1.03E-06	4.77E-06	4.88672	Up	ANTXR like pseudogene 1
RNF11	2.826399	4.51E-22	3.59E-20	9.658881	Up	ring finger protein 11
SORL1	2.825569	7.78E-33	3.76E-30	11.93497	Up	sortilin related receptor 1
LRRN3	2.819534	1.83E-10	1.75E-09	6.374986	Up	leucine rich repeat neuronal 3
FKBP8	2.819091	1.13E-21	8.25E-20	9.564463	Up	FKBP prolylisomerase 8
SLC38A5	2.811217	6.57E-07	3.16E-06	4.973724	Up	solute carrier family 38 member 5
CCDC18	2.808533	1.17E-18	4.86E-17	8.81722	Up	coiled-coil domain containing 18
LEF1	2.807881	2.76E-14	5.13E-13	7.609047	Up	lymphoid enhancer binding factor 1
FCMR	2.807228	2.60E-09	1.98E-08	5.955204	Up	Fc fragment of IgM receptor
WASH7P	2.805737	1.48E-06	6.65E-06	4.814502	Up	WASP family homolog 7, pseudogene
CORO1A	2.803864	5.34E-15	1.13E-13	7.818645	Up	coronin 1A
RPS29	2.802143	9.99E-24	1.03E-21	10.04171	Up	ribosomal protein S29
TAL1	2.801551	7.29E-07	3.49E-06	4.953577	Up	TAL bHLH transcription factor 1, erythroid differentiation factor
SMIM24	2.796414	1.13E-06	5.22E-06	4.867166	Up	small integral membrane protein 24
CEP57L1	2.795249	1.06E-17	3.81E-16	8.566892	Up	centrosomal protein 57 like 1
CDC34	2.795231	8.75E-25	1.09E-22	10.27917	Up	cell division cycle 34, ubiqiutin conjugating enzyme
CENPI	2.795095	3.14E-06	1.34E-05	4.661392	Up	centromere protein I
CENPH	2.794635	2.50E-12	3.29E-11	7.003499	Up	centromere protein H
IKZF1	2.793474	1.57E-16	4.43E-15	8.251153	Up	IKAROS family zinc finger 1
ABCC4	2.788953	5.20E-16	1.32E-14	8.106739	Up	ATP binding cassette subfamily C member 4
XPO7	2.780822	2.16E-27	4.28E-25	10.84281	Up	exportin 7
DPM2	2.779758	9.89E-28	2.07E-25	10.91393	Up	dolichyl-phosphate mannosyltransferase subunit 2, regulatory
ICAM2	2.77572	1.86E-07	1.00E-06	5.213064	Up	intercellular adhesion molecule 2
ATP8A1	2.77569	9.10E-14	1.55E-12	7.453316	Up	ATPase phospholipid transporting 8A1
CD84	2.772569	1.49E-12	2.05E-11	7.074964	Up	CD84 molecule
CD8A	2.768405	2.33E-16	6.32E-15	8.203855	Up	CD8a molecule
GAB3	2.768294	1.39E-13	2.28E-12	7.397746	Up	GRB2 associated binding protein 3
STIL	2.767477	2.06E-19	9.92E-18	9.010185	Up	STIL centriolar assembly protein

RPS13	2.767296	2.59E-28	5.83E-26	11.0351	Up	ribosomal protein S13
CDYL	2.76653	1.38E-29	4.04E-27	11.29574	Up	chromodomain Y like
SIGLEC9	2.76621	6.55E-08	3.85E-07	5.403057	Up	sialic acid binding Ig like lectin 9
TLR4	2.763446	1.27E-10	1.25E-09	6.43028	Up	toll like receptor 4
RBP7	2.762295	4.31E-08	2.63E-07	5.477509	Up	retinol binding protein 7
FLNA	2.761021	1.46E-13	2.39E-12	7.3911	Up	filamin A
HK3	2.759887	1.26E-06	5.76E-06	4.845885	Up	hexokinase 3
RPL13AP5	2.75838	2.31E-10	2.15E-09	6.339504	Up	ribosomal protein L13a pseudogene 5
CPPED1	2.756265	6.92E-30	2.14E-27	11.35605	Up	calcineurin like phosphoesterase domain containing 1
RPL27A	2.755545	1.74E-29	4.84E-27	11.27538	Up	ribosomal protein L27a
CDC27	2.753253	8.55E-22	6.44E-20	9.593043	Up	cell division cycle 27
AGAP7P	2.750859	4.21E-07	2.10E-06	5.059367	Up	ArfGAP with GTPase domain, ankyrin repeat and PH domain 7, pseudogene
RPL7	2.74922	1.29E-25	1.83E-23	10.46241	Up	ribosomal protein L7
RASSF2	2.747666	5.30E-15	1.12E-13	7.819644	Up	Ras association domain family member 2
CCR7	2.747317	1.54E-13	2.52E-12	7.383463	Up	C-C motif chemokine receptor 7
DPP4	2.746658	2.57E-10	2.38E-09	6.322465	Up	dipeptidyl peptidase 4
NLRC4	2.74589	1.35E-08	9.04E-08	5.679757	Up	NLR family CARD domain containing 4
NCF1C	2.741582	1.64E-07	8.95E-07	5.235685	Up	neutrophil cytosolic factor 1C pseudogene
ITM2A	2.740206	3.52E-08	2.19E-07	5.513264	Up	integral membrane protein 2A
NPAT	2.732249	1.23E-17	4.31E-16	8.550131	Up	nuclear protein, coactivator of histone transcription
KLRC4	2.730902	1.06E-07	5.97E-07	5.316508	Up	killer cell lectin like receptor C4
PLCL2	2.726941	1.60E-25	2.20E-23	10.44193	Up	phospholipase C like 2
RPL37	2.726498	4.87E-28	1.07E-25	10.97809	Up	ribosomal protein L37
ITGB3	2.726131	0.002392	0.005596	3.036655	Up	integrin subunit beta 3
RASGRP1	2.722267	1.76E-16	4.91E-15	8.23744	Up	RAS guanyl releasing protein 1
GVINP1	2.7192	6.78E-18	2.50E-16	8.618637	Up	GTPase, very large interferon inducible pseudogene 1
MBNL1	2.718762	7.10E-22	5.45E-20	9.612266	Up	muscleblind like splicing regulator 1
FYN	2.715432	3.66E-17	1.16E-15	8.423282	Up	FYN proto-oncogene, Src family tyrosine kinase
CENPK	2.715178	9.54E-16	2.32E-14	8.032622	Up	centromere protein K
DLEU2	2.710239	5.99E-13	8.83E-12	7.200685	Up	deleted in lymphocytic leukemia 2
CELF2	2.709487	3.81E-16	9.93E-15	8.144377	Up	CUGBP Elav-like family member 2
TLR2	2.707008	1.61E-10	1.56E-09	6.394283	Up	toll like receptor 2
GSPT1	2.706656	1.10E-51	8.91E-48	15.12564	Up	G1 to S phase transition 1
TBXAS1	2.704726	3.78E-11	4.08E-10	6.612536	Up	thromboxane A synthase 1
SRRD	2.703952	3.54E-21	2.40E-19	9.445292	Up	SRR1 domain containing
DOCK2	2.700629	7.18E-14	1.25E-12	7.484528	Up	dedicator of cytokinesis 2
CSF1R	2.69993	1.00E-19	5.15E-18	9.088601	Up	colony stimulating factor 1 receptor
PRKCB	2.699272	2.04E-10	1.93E-09	6.357925	Up	protein kinase C beta
CAMK4	2.699039	4.76E-09	3.44E-08	5.855418	Up	calcium/calmodulin dependent protein kinase IV
LGALS1	2.697736	6.97E-10	5.92E-09	6.166681	Up	galectin 1
PLXDC2	2.696823	8.51E-15	1.73E-13	7.759759	Up	plexin domain containing 2
DLGAP5	2.696585	1.66E-08	1.09E-07	5.644568	Up	DLG associated protein 5
PPM1A	2.695131	2.75E-30	9.25E-28	11.43637	Up	protein phosphatase, Mg2+/Mn2+ dependent 1A

CLEC2D	2.694217	4.51E-18	1.71E-16	8.665036	Up	C-type lectin domain family 2 member D
MAF1	2.692708	1.38E-36	9.67E-34	12.63372	Up	MAF1 homolog, negative regulator of RNA polymerase III
TESPA1	2.691873	2.95E-08	1.85E-07	5.544467	Up	thymocyte expressed, positive selection associated 1
CD40LG	2.689503	3.34E-07	1.71E-06	5.103361	Up	CD40 ligand
SCML4	2.684635	7.04E-09	4.96E-08	5.789935	Up	Scmpolycomb group protein like 4
FCGR3B	2.683821	3.11E-06	1.32E-05	4.663733	Up	Fc fragment of IgG receptor IIIb
ASCC2	2.681714	1.64E-43	3.16E-40	13.83186	Up	activating signal cointegrator 1 complex subunit 2
CXCL5	2.679517	7.36E-06	2.90E-05	4.483111	Up	C-X-C motif chemokine ligand 5
PATE3	2.678911	0.000318	0.000909	3.60045	Up	prostate and testis expressed 3
HACD1	2.678777	8.30E-05	0.000266	3.935525	Up	3-hydroxyacyl-CoA dehydratase 1
MS4A7	2.677885	2.33E-13	3.72E-12	7.328093	Up	membrane spanning 4-domains A7
USP15	2.677548	3.85E-20	2.14E-18	9.192112	Up	ubiquitin specific peptidase 15
DMTN	2.672292	7.40E-16	1.84E-14	8.063757	Up	dematin actin binding protein
CD27	2.671643	1.67E-08	1.10E-07	5.643465	Up	CD27 molecule
RPS23	2.667919	1.96E-21	1.37E-19	9.507375	Up	ribosomal protein S23
C19orf38	2.667335	2.03E-08	1.31E-07	5.60952	Up	chromosome 19 open reading frame 38
CD36	2.665492	4.67E-16	1.20E-14	8.119843	Up	CD36 molecule
NKG7	2.665268	1.39E-08	9.30E-08	5.674334	Up	natural killer cell granule protein 7
LYST	2.660604	1.25E-26	2.17E-24	10.68058	Up	lysosomal trafficking regulator
FAM78A	2.660507	1.22E-13	2.03E-12	7.414193	Up	family with sequence similarity 78 member A
NRROS	2.660497	3.90E-08	2.40E-07	5.49537	Up	negative regulator of reactive oxygen species
SMG1P2	2.659878	1.85E-06	8.23E-06	4.76876	Up	SMG1 pseudogene 2
SLC4A10	2.657494	3.31E-06	1.40E-05	4.650402	Up	solute carrier family 4 member 10
PINK1	2.654989	1.69E-25	2.32E-23	10.43653	Up	PTEN induced kinase 1
DSC3	2.654439	7.76E-09	5.41E-08	5.773603	Up	desmocollin 3
MGAM	2.653734	4.55E-15	9.77E-14	7.838705	Up	maltase-glucoamylase
RNF125	2.653442	4.60E-19	2.03E-17	8.921586	Up	ring finger protein 125
CA2	2.653401	7.72E-08	4.46E-07	5.373628	Up	carbonic anhydrase 2
CDK8	2.653028	6.77E-18	2.50E-16	8.618743	Up	cyclin dependent kinase 8
TRABD2A	2.65128	4.39E-12	5.59E-11	6.923919	Up	TraB domain containing 2A
MEGF9	2.648444	1.72E-18	6.88E-17	8.774469	Up	multiple EGF like domains 9
MAPK1	2.64738	1.45E-27	2.96E-25	10.87885	Up	mitogen-activated protein kinase 1
SLC12A1	2.646388	0.001731	0.004186	3.13291	Up	solute carrier family 12 member 1
EVI2A	2.64473	3.33E-10	3.01E-09	6.282503	Up	ecotropic viral integration site 2A
TGFBI	2.643588	8.63E-19	3.66E-17	8.851591	Up	transforming growth factor beta induced
GIMAP7	2.643411	2.86E-16	7.58E-15	8.179057	Up	GTPase, IMAP family member 7
EFCAB13	2.642395	1.24E-11	1.47E-10	6.775257	Up	EF-hand calcium binding domain 13
GPR183	2.640334	8.32E-13	1.19E-11	7.15574	Up	G protein-coupled receptor 183
KLRC2	2.639756	3.76E-08	2.32E-07	5.501707	Up	killer cell lectin like receptor C2
CLEC1B	2.639431	0.002794	0.006414	2.989505	Up	C-type lectin domain family 1 member B
POC1B	2.63862	1.41E-26	2.40E-24	10.67002	Up	POC1 centriolar protein B
RNF10	2.637756	6.67E-30	2.09E-27	11.35929	Up	ring finger protein 10
RPL6	2.636813	1.42E-23	1.43E-21	10.00696	Up	ribosomal protein L6

CD300C	2.633535	9.53E-07	4.45E-06	4.901198	Up	CD300c molecule
APLF	2.633043	8.90E-15	1.80E-13	7.754093	Up	aprataxin and PNKP like factor
DENND4A	2.631157	2.25E-22	1.86E-20	9.729632	Up	DENN domain containing 4A
GRAP2	2.629285	3.24E-09	2.42E-08	5.919161	Up	GRB2 related adaptor protein 2
P2RY12	2.626852	6.40E-07	3.09E-06	4.978769	Up	purinergic receptor P2Y12
CR1	2.622316	2.58E-06	1.12E-05	4.70149	Up	complement C3b/C4b receptor 1 (Knops blood group)
PPT1	2.621929	9.31E-28	1.96E-25	10.91945	Up	palmitoyl-protein thioesterase 1
ITGB7	2.619199	7.24E-14	1.26E-12	7.483362	Up	integrin subunit beta 7
TERC	2.617629	6.61E-16	1.66E-14	8.077585	Up	telomerase RNA component
TGFBR2	2.615355	8.00E-25	9.98E-23	10.28773	Up	transforming growth factor beta receptor 2
PDE5A	2.615066	2.31E-09	1.78E-08	5.974622	Up	phosphodiesterase 5A
IL27RA	2.613057	3.69E-10	3.31E-09	6.266617	Up	interleukin 27 receptor subunit alpha
CD300E	2.612867	4.46E-06	1.84E-05	4.588578	Up	CD300e molecule
FCGR2A	2.612431	5.20E-08	3.11E-07	5.444436	Up	Fc fragment of IgG receptor IIa
RASGRP2	2.610196	5.61E-10	4.86E-09	6.200983	Up	RAS guanyl releasing protein 2
SLFN12L	2.608766	5.64E-10	4.88E-09	6.20021	Up	schlafen family member 12 like
OGT	2.604898	4.73E-26	7.34E-24	10.55676	Up	O-linked N-acetylglucosamine (GlcNAc) transferase
TFRC	2.604478	5.08E-20	2.77E-18	9.162301	Up	transferrin receptor
DNA2	2.603276	1.35E-12	1.87E-11	7.088859	Up	DNA replication helicase/nuclease 2
GMPR	2.602796	5.49E-22	4.30E-20	9.638657	Up	guanosine monophosphate reductase
CD53	2.602608	2.24E-10	2.10E-09	6.343748	Up	CD53 molecule
RPL7A	2.60211	2.83E-32	1.20E-29	11.82691	Up	ribosomal protein L7a
PRKACB	2.599788	2.56E-16	6.85E-15	8.192252	Up	protein kinase cAMP-activated catalytic subunit beta
PADI4	2.599037	8.20E-05	0.000263	3.938414	Up	peptidyl arginine deiminase 4
RPS7	2.597321	2.38E-20	1.36E-18	9.243913	Up	ribosomal protein S7
TNFRSF10C	2.595388	1.76E-06	7.84E-06	4.779311	Up	TNF receptor superfamily member 10c
ST6GALNAC4	2.594638	2.73E-17	8.95E-16	8.457487	Up	ST6 N-acetylgalactosaminide alpha-2,6-sialyltransferase 4
C16orf54	2.594344	2.82E-15	6.30E-14	7.898832	Up	chromosome 16 open reading frame 54
CTSE	2.593317	0.000409	0.001142	3.534398	Up	cathepsin E
WHAMMP3	2.589619	4.60E-08	2.79E-07	5.466112	Up	WAS protein homolog associated with actin, golgi membranes and microtubules pseudogene 3
RPL10	2.588914	7.79E-27	1.40E-24	10.72476	Up	ribosomal protein L10
C15orf54	2.585655	2.61E-07	1.36E-06	5.149622	Up	chromosome 15 putative open reading frame 54
LTA4H	2.584093	7.33E-28	1.57E-25	10.9411	Up	leukotriene A4 hydrolase
LILRB2	2.583654	8.58E-08	4.91E-07	5.354527	Up	leukocyte immunoglobulin like receptor B2
PCGF5	2.583604	5.20E-25	6.59E-23	10.32917	Up	polycomb group ring finger 5
PLXNC1	2.581426	4.97E-12	6.28E-11	6.906555	Up	plexin C1
PTPRA	2.581152	8.30E-31	2.96E-28	11.53991	Up	protein tyrosine phosphatase receptor type A
MEMO1	2.581022	2.50E-17	8.24E-16	8.468062	Up	Methylation modifier for class I HLA
CD5	2.578351	1.12E-12	1.57E-11	7.114287	Up	CD5 molecule
GBGT1	2.576886	4.55E-09	3.30E-08	5.862939	Up	globoside alpha-1,3-N-acetylgalactosaminyltransferase 1 (FORS blood group)
AKR1E2	2.576271	1.61E-09	1.28E-08	6.032788	Up	aldo-ketoreductase family 1 member E2
AKT3	2.576022	4.12E-13	6.27E-12	7.25152	Up	AKT serine/threonine kinase 3

KLF17	-7.94835	2.16E-11	2.43E-10	-6.69471	Down	Kruppel like factor 17
NOX4	-7.20056	4.88E-21	3.21E-19	-9.41179	Down	NADPH oxidase 4
NEU2	-7.08061	1.48E-07	8.12E-07	-5.25489	Down	neuraminidase 2
SOCS1	-6.76766	4.85E-37	3.75E-34	-12.7156	Down	suppressor of cytokine signaling 1
NAT2	-6.59058	1.84E-08	1.20E-07	-5.62598	Down	N-acetyltransferase 2
ADCK2	-6.28931	2.95E-41	3.81E-38	-13.4531	Down	aarF domain containing kinase 2
MYOCD	-6.0489	4.16E-20	2.30E-18	-9.18374	Down	myocardin
RNU11	-5.89045	5.22E-42	7.57E-39	-13.5805	Down	RNA, U11 small nuclear
DAO	-5.75321	3.08E-09	2.31E-08	-5.92744	Down	D-amino acid oxidase
TSKS	-5.66687	6.72E-18	2.49E-16	-8.61951	Down	testis specific serine kinase substrate
RIMS2	-5.66574	1.28E-11	1.51E-10	-6.77062	Down	regulating synaptic membrane exocytosis 2
SNORD119	-5.60492	1.94E-44	5.00E-41	-13.9845	Down	small nucleolar RNA, C/D box 119
BEND6	-5.51819	1.86E-25	2.52E-23	-10.4275	Down	BEN domain containing 6
HS1BP3	-5.45957	8.17E-38	7.29E-35	-12.8539	Down	HCLS1 binding protein 3
PEAR1	-5.35075	4.86E-32	1.94E-29	-11.7815	Down	platelet endothelial aggregation receptor 1
APOOP5	-5.31722	1.73E-05	6.36E-05	-4.29687	Down	apolipoprotein O pseudogene 5
PWRN2	-5.26575	2.28E-05	8.17E-05	-4.23547	Down	Prader-Willi region non-protein coding RNA 2
RNASE7	-5.22234	4.12E-11	4.43E-10	-6.59956	Down	ribonuclease A family member 7
SPRR3	-5.13217	4.98E-19	2.18E-17	-8.91273	Down	small proline rich protein 3
COL5A1	-5.11578	3.58E-26	5.76E-24	-10.5829	Down	collagen type V alpha 1 chain
FLG	-5.03783	9.01E-14	1.53E-12	-7.45467	Down	filaggrin
OPRD1	-4.98517	8.13E-10	6.80E-09	-6.14237	Down	opioid receptor delta 1
DCLK2	-4.954	8.00E-23	7.05E-21	-9.8345	Down	doublecortin like kinase 2
SPRR2D	-4.94857	3.13E-13	4.87E-12	-7.28884	Down	small proline rich protein 2D
CLCN1	-4.92296	5.97E-11	6.24E-10	-6.54447	Down	chloride voltage-gated channel 1
FAM131C	-4.88822	1.22E-12	1.70E-11	-7.10274	Down	family with sequence similarity 131 member C
FSTL3	-4.88328	6.50E-29	1.66E-26	-11.1586	Down	follistatin like 3
PRDM13	-4.87435	7.96E-23	7.05E-21	-9.83495	Down	PR/SET domain 13
FJX1	-4.85137	1.04E-21	7.75E-20	-9.57264	Down	four-jointed box kinase 1
SCGB1B2P	-4.76252	9.03E-19	3.82E-17	-8.84645	Down	secretoglobin family 1B member 2, pseudogene
NTRK3	-4.72218	1.40E-11	1.64E-10	-6.75783	Down	neurotrophic receptor tyrosine kinase 3
ZNRF4	-4.71672	3.13E-06	1.34E-05	-4.66178	Down	zinc and ring finger 4
TMPRSS11B	-4.7125	6.70E-09	4.74E-08	-5.79815	Down	transmembrane serine protease 11B
FRMPD4	-4.65263	4.25E-17	1.32E-15	-8.40591	Down	FERM and PDZ domain containing 4
SNORA15	-4.6018	1.54E-20	9.27E-19	-9.29007	Down	small nucleolar RNA, H/ACA box 15
TEK	-4.59023	3.66E-09	2.71E-08	-5.89889	Down	TEK receptor tyrosine kinase
ECM1	-4.58485	5.49E-15	1.15E-13	-7.81518	Down	extracellular matrix protein 1
SNORA72	-4.55701	2.22E-29	6.05E-27	-11.2538	Down	small nucleolar RNA, H/ACA box 72
GCG	-4.53938	2.49E-07	1.31E-06	-5.1588	Down	glucagon
ISX	-4.50807	2.15E-16	5.89E-15	-8.21341	Down	intestine specific homeobox
RHCG	-4.45583	2.63E-09	2.00E-08	-5.95323	Down	Rh family C glycoprotein
NANOS3	-4.42884	1.87E-07	1.01E-06	-5.21149	Down	nanos C2HC-type zinc finger 3
TMEM229A	-4.42081	7.68E-13	1.11E-11	-7.16669	Down	transmembrane protein 229A

CXCL10	-4.41151	1.61E-16	4.53E-15	-8.24796	Down	C-X-C motif chemokine ligand 10
SPRR2A	-4.38496	3.27E-15	7.22E-14	-7.88008	Down	small proline rich protein 2A
CXCL9	-4.3651	1.28E-20	7.81E-19	-9.31018	Down	C-X-C motif chemokine ligand 9
SPRR2E	-4.34904	1.54E-09	1.23E-08	-6.03976	Down	small proline rich protein 2E
CXCL11	-4.34557	7.38E-12	9.07E-11	-6.85002	Down	C-X-C motif chemokine ligand 11
KRT78	-4.31471	5.40E-12	6.81E-11	-6.89457	Down	keratin 78
SLC9A7P1	-4.31	6.81E-22	5.28E-20	-9.61657	Down	solute carrier family 9 member 7 pseudogene 1
VSTM2L	-4.2897	1.52E-17	5.26E-16	-8.52532	Down	V-set and transmembrane domain containing 2 like
KLF15	-4.27517	2.28E-18	8.98E-17	-8.74271	Down	Kruppel like factor 15
CRNN	-4.24585	2.87E-08	1.80E-07	-5.54935	Down	cornulin
SSR4P1	-4.23567	3.02E-23	2.85E-21	-9.93211	Down	signal sequence receptor subunit 4 pseudogene 1
RASGRF1	-4.23553	5.13E-18	1.93E-16	-8.65034	Down	Ras protein specific guanine nucleotide releasing factor 1
SLCO1B1	-4.23037	6.20E-07	3.00E-06	-4.98484	Down	solute carrier organic anion transporter family member 1B1
RBFOX1	-4.22319	1.40E-15	3.29E-14	-7.98505	Down	RNA binding fox-1 homolog 1
SLC18A1	-4.22073	8.73E-14	1.49E-12	-7.45883	Down	solute carrier family 18 member A1
KRT82	-4.19258	2.53E-05	8.99E-05	-4.21238	Down	keratin 82
CEACAM7	-4.18863	1.93E-11	2.20E-10	-6.71116	Down	CEA cell adhesion molecule 7
MUC22	-4.17039	6.55E-07	3.16E-06	-4.9742	Down	mucin 22
HCG22	-4.16729	4.84E-06	1.98E-05	-4.57172	Down	HLA complex group 22
FAM71A	-4.15584	9.96E-12	1.20E-10	-6.80711	Down	family with sequence similarity 71 member A
GABRG3	-4.15495	3.71E-12	4.78E-11	-6.94776	Down	gamma-aminobutyric acid type A receptor subunit gamma3
DDC	-4.13465	2.66E-09	2.02E-08	-5.95141	Down	dopa decarboxylase
FRZB	-4.12982	3.70E-12	4.77E-11	-6.94807	Down	frizzled related protein
SNORD12B	-4.1124	6.22E-32	2.45E-29	-11.7607	Down	small nucleolar RNA, C/D box 12B
TFAP2B	-4.10231	2.60E-06	1.13E-05	-4.69978	Down	transcription factor AP-2 beta
HAGLR	-4.10105	8.33E-14	1.43E-12	-7.46504	Down	HOXD antisense growth-associated long non-coding RNA
NFKBIL1	-4.09146	1.45E-21	1.05E-19	-9.53829	Down	NFKB inhibitor like 1
PRSS35	-4.08354	1.34E-14	2.65E-13	-7.70171	Down	serine protease 35
SLC39A5	-4.06356	1.10E-18	4.60E-17	-8.82445	Down	solute carrier family 39 member 5
GPC6	-4.06006	1.30E-07	7.22E-07	-5.27833	Down	glypican 6
ACTN2	-4.04771	1.63E-10	1.57E-09	-6.39244	Down	actinin alpha 2
FAM170B	-4.04731	1.58E-09	1.26E-08	-6.03575	Down	family with sequence similarity 170 member B
PIGQ	-4.03966	1.19E-18	4.93E-17	-8.81522	Down	phosphatidylinositol glycan anchor biosynthesis class Q
ROPN1B	-4.03732	1.18E-21	8.57E-20	-9.55993	Down	rhophilin associated tail protein 1B
SERPINB12	-4.02967	6.90E-08	4.04E-07	-5.3937	Down	serpin family B member 12
SNORD29	-4.01462	1.22E-24	1.50E-22	-10.2471	Down	small nucleolar RNA, C/D box 29
NLRP5	-3.99985	4.73E-08	2.86E-07	-5.46117	Down	NLR family pyrin domain containing 5
TBX22	-3.97147	0.00069	0.001834	-3.39346	Down	T-box transcription factor 22
SPATA31D1	-3.97049	1.45E-08	9.64E-08	-5.66733	Down	SPATA31 subfamily D member 1
PAX1	-3.95073	7.14E-08	4.17E-07	-5.38753	Down	paired box 1
C6	-3.9434	1.68E-08	1.11E-07	-5.64186	Down	complement C6
IL36A	-3.93463	0.000363	0.001027	-3.56555	Down	interleukin 36 alpha
APOA4	-3.93434	2.29E-05	8.19E-05	-4.23494	Down	apolipoprotein A4

L3MBTL1	-3.92617	2.59E-19	1.22E-17	-8.98481	Down	L3MBTL histone methyl-lysine binding protein 1
SLC17A4	-3.91173	0.001679	0.004074	-3.1419	Down	solute carrier family 17 member 4
TMPRSS11F	-3.91153	1.31E-07	7.25E-07	-5.2776	Down	transmembrane serine protease 11F
FABP1	-3.88136	0.00028	0.00081	-3.63327	Down	fatty acid binding protein 1
MTMR9LP	-3.87514	7.68E-18	2.81E-16	-8.60421	Down	myotubularin related protein 9 like, pseudogene
ACTA2	-3.85152	1.55E-19	7.56E-18	-9.04131	Down	actin alpha 2, smooth muscle
CRP	-3.82792	0.001434	0.00353	-3.18775	Down	C-reactive protein
DCX	-3.81921	3.92E-09	2.89E-08	-5.88733	Down	doublecortin
IQCF3	-3.81786	0.000236	0.000695	-3.67683	Down	IQ motif containing F3
BMI1	-3.81627	1.52E-14	2.96E-13	-7.68617	Down	BMI1 proto-oncogene, polycomb ring finger
BLACAT1	-3.81491	1.09E-09	8.90E-09	-6.09615	Down	bladder cancer associated transcript 1
GRIA1	-3.81462	1.39E-05	5.19E-05	-4.34602	Down	glutamate ionotropic receptor AMPA type subunit 1
SLC22A11	-3.80383	2.63E-09	2.00E-08	-5.95341	Down	solute carrier family 22 member 11
RHOJ	-3.78775	0.000953	0.002447	-3.304	Down	ras homolog family member J
WNT7A	-3.78765	6.68E-19	2.89E-17	-8.88018	Down	Wnt family member 7A
IL17F	-3.78554	0.011509	0.02238	-2.52685	Down	interleukin 17F
KPRP	-3.77729	7.68E-07	3.66E-06	-4.94322	Down	keratinocyte proline rich protein
LILRP2	-3.774	4.55E-06	1.87E-05	-4.58462	Down	leukocyte immunoglobulin-like receptor pseudogene 2
LAMB2P1	-3.77304	1.19E-11	1.41E-10	-6.78134	Down	laminin subunit beta 2 pseudogene 1
SPATA31A1	-3.76564	0.003063	0.006966	-2.96132	Down	SPATA31 subfamily A member 1
FAM162B	-3.73213	3.54E-08	2.20E-07	-5.51241	Down	family with sequence similarity 162 member B
CAMKV	-3.72991	1.41E-08	9.41E-08	-5.67209	Down	CaM kinase like vesicle associated
UBD	-3.72309	1.12E-16	3.25E-15	-8.2918	Down	ubiquitin D
RNASEH2C	-3.72194	4.68E-21	3.09E-19	-9.41607	Down	ribonuclease H2 subunit C
UGT2B10	-3.71752	0.003246	0.007326	-2.9434	Down	UDP glucuronosyltransferase family 2 member B10
TMEM130	-3.71475	6.83E-10	5.82E-09	-6.17003	Down	transmembrane protein 130
CNTNAP4	-3.71219	0.000268	0.000779	-3.64442	Down	contactin associated protein family member 4
CD34	-3.69604	6.87E-06	2.73E-05	-4.49754	Down	CD34 molecule
TAL2	-3.6844	2.51E-08	1.59E-07	-5.57285	Down	TAL bHLH transcription factor 2
FAR2P1	-3.68408	0.000565	0.001531	-3.44783	Down	fatty acyl-CoA reductase 2 pseudogene 1
SNORD12C	-3.67205	1.54E-29	4.37E-27	-11.2857	Down	small nucleolar RNA, C/D box 12C
TRIM55	-3.67032	6.43E-13	9.42E-12	-7.19113	Down	tripartite motif containing 55
PRNT	-3.66925	4.56E-06	1.88E-05	-4.58404	Down	prion locus lncRNA, testis expressed
TPPP2	-3.6546	2.81E-09	2.13E-08	-5.94224	Down	tubulin polymerization promoting protein family member 2
MUC7	-3.65182	4.27E-06	1.77E-05	-4.5977	Down	mucin 7, secreted
STATH	-3.64233	6.24E-12	7.79E-11	-6.87417	Down	statherin
PRR23C	-3.6384	1.42E-08	9.45E-08	-5.67127	Down	proline rich 23C
C16orf82	-3.63371	0.005889	0.012424	-2.75387	Down	chromosome 16 open reading frame 82
CSMD2	-3.63163	2.99E-11	3.29E-10	-6.64716	Down	CUB and Sushi multiple domains 2
SLC6A15	-3.63152	9.94E-08	5.64E-07	-5.32774	Down	solute carrier family 6 member 15
KRT13	-3.62474	3.57E-11	3.88E-10	-6.62081	Down	keratin 13
ILDR2	-3.61108	6.07E-09	4.32E-08	-5.81471	Down	immunoglobulin like domain containing receptor 2
ARHGAP28	-3.60877	4.55E-06	1.87E-05	-4.58444	Down	Rho GTPase activating protein 28

AADACL3	-3.59998	0.000147	0.000449	-3.79688	Down	arylacetamidedeacetylase like 3
SLC24A2	-3.5983	2.67E-07	1.39E-06	-5.14534	Down	solute carrier family 24 member 2
SNORD79	-3.58757	8.12E-17	2.41E-15	-8.32945	Down	small nucleolar RNA, C/D box 79
NPAS4	-3.58487	7.28E-07	3.49E-06	-4.95367	Down	neuronal PAS domain protein 4
IL12RB2	-3.57933	6.19E-14	1.09E-12	-7.50399	Down	interleukin 12 receptor subunit beta 2
BCL3	-3.57839	1.78E-18	7.10E-17	-8.77071	Down	BCL3 transcription coactivator
CALB2	-3.56676	1.47E-07	8.06E-07	-5.25657	Down	calbindin 2
SPRED3	-3.56454	5.66E-10	4.90E-09	-6.1996	Down	sprouty related EVH1 domain containing 3
TSPAN10	-3.55779	5.76E-13	8.51E-12	-7.20597	Down	tetraspanin 10
LRIT1	-3.55489	0.000333	0.000949	-3.58836	Down	leucine rich repeat, Ig-like and transmembrane domains 1
CATSPER4	-3.5524	8.32E-05	0.000266	-3.93509	Down	cation channel sperm associated 4
GABRQ	-3.5344	5.88E-06	2.36E-05	-4.53083	Down	gamma-aminobutyric acid type A receptor subunit theta
C18orf63	-3.51739	0.009623	0.01917	-2.58908	Down	chromosome 18 open reading frame 63
SERPINA5	-3.51654	0.000604	0.001626	-3.42964	Down	serpin family A member 5
SDK2	-3.50944	4.10E-18	1.56E-16	-8.67586	Down	sidekick cell adhesion molecule 2
FETUB	-3.50855	0.000168	0.00051	-3.76245	Down	fetuin B
SLC2A7	-3.50327	0.001191	0.002987	-3.24114	Down	solute carrier family 2 member 7
ASTN1	-3.50108	4.73E-07	2.33E-06	-5.03699	Down	astrotactin 1
ANKRD30BL	-3.50006	3.34E-10	3.02E-09	-6.2823	Down	ankyrin repeat domain 30B like
SNTG1	-3.49895	0.000709	0.001879	-3.38616	Down	syntrophin gamma 1
CARD10	-3.49551	4.44E-14	7.97E-13	-7.54749	Down	caspase recruitment domain family member 10
HSF2	-3.4942	2.80E-22	2.26E-20	-9.70767	Down	heat shock transcription factor 2
KLK8	-3.49286	1.64E-07	8.91E-07	-5.23655	Down	kallikrein related peptidase 8
OR2H1	-3.48863	0.005001	0.010754	-2.80696	Down	olfactory receptor family 2 subfamily H member 1
C8A	-3.48432	0.023709	0.042098	-2.2618	Down	complement C8 alpha chain
RBP3	-3.46834	2.14E-07	1.14E-06	-5.18659	Down	retinol binding protein 3
GAP43	-3.46767	0.000471	0.0013	-3.49655	Down	growth associated protein 43
SLC10A2	-3.46575	0.002949	0.006734	-2.97297	Down	solute carrier family 10 member 2
GABRB2	-3.46462	5.74E-08	3.40E-07	-5.42682	Down	gamma-aminobutyric acid type A receptor subunit beta2
HTR1D	-3.46033	0.005672	0.012018	-2.76618	Down	5-hydroxytryptamine receptor 1D
SMCO2	-3.43542	9.66E-06	3.72E-05	-4.42454	Down	single-pass membrane protein with coiled-coil domains 2
TSLP	-3.43208	2.28E-06	9.95E-06	-4.7271	Down	thymic stromal lymphopoietin
POM121L2	-3.43169	0.000455	0.001259	-3.50586	Down	POM121 transmembranenucleoporin like 2
SERPINB7	-3.42669	4.10E-08	2.51E-07	-5.48661	Down	serpin family B member 7
SPRR1B	-3.42164	2.12E-09	1.64E-08	-5.98828	Down	small proline rich protein 1B
COL6A5	-3.41224	5.36E-05	0.000179	-4.03939	Down	collagen type VI alpha 5 chain
SNORD102	-3.40875	4.59E-15	9.84E-14	-7.83766	Down	small nucleolar RNA, C/D box 102
RNASE13	-3.40865	2.46E-06	1.07E-05	-4.71116	Down	ribonuclease A family member 13 (inactive)
FXYD4	-3.40226	0.001353	0.003348	-3.20458	Down	FXYD domain containing ion transport regulator 4
ANKS4B	-3.39886	1.41E-06	6.39E-06	-4.82345	Down	ankyrin repeat and sterile alpha motif domain containing 4B
KCNJ11	-3.39379	5.60E-07	2.73E-06	-5.00443	Down	potassium inwardly rectifying channel subfamily J member 11
C1QTNF2	-3.39289	3.90E-08	2.40E-07	-5.49543	Down	C1q and TNF related 2
MYOD1	-3.39111	4.44E-11	4.76E-10	-6.58846	Down	myogenic differentiation 1

SNORD44	-3.38822	9.28E-23	8.03E-21	-9.81953	Down	small nucleolar RNA, C/D box 44
ZNF99	-3.38588	2.34E-09	1.80E-08	-5.97252	Down	zinc finger protein 99
PADI6	-3.38369	4.27E-07	2.13E-06	-5.05657	Down	peptidyl arginine deiminase 6
GPX6	-3.38024	0.004884	0.010534	-2.81461	Down	glutathione peroxidase 6
BTBD16	-3.38007	2.03E-08	1.31E-07	-5.60939	Down	BTB domain containing 16
KLHL1	-3.37252	0.002288	0.005379	-3.0501	Down	kelch like family member 1
MAGEC3	-3.36978	0.000355	0.001006	-3.57171	Down	MAGE family member C3
SNORD111B	-3.36709	1.01E-11	1.21E-10	-6.8053	Down	small nucleolar RNA, C/D box 111B
ADGRF5	-3.36615	5.39E-13	8.02E-12	-7.21501	Down	adhesion G protein-coupled receptor F5
CCL2	-3.3624	3.30E-08	2.06E-07	-5.5245	Down	C-C motif chemokine ligand 2
PAH	-3.36109	0.004114	0.009055	-2.86929	Down	phenylalanine hydroxylase
CIDEC	-3.35066	0.008587	0.017341	-2.62809	Down	cell death inducing DFFA like effector c
TMPRSS11E	-3.34375	5.94E-10	5.13E-09	-6.19191	Down	transmembrane serine protease 11E
MS4A10	-3.34359	0.001027	0.002617	-3.28304	Down	membrane spanning 4-domains A10
ERICH6B	-3.33613	0.001124	0.002835	-3.25755	Down	glutamate rich 6B
PLEKHA2	-3.33608	2.80E-19	1.31E-17	-8.97613	Down	pleckstrin homology domain containing A2
C8B	-3.33192	0.002526	0.005858	-3.02026	Down	complement C8 beta chain
KIRREL2	-3.32576	8.09E-07	3.83E-06	-4.93319	Down	kirre like nephrin family adhesion molecule 2
FAM9A	-3.32368	0.001029	0.002621	-3.28254	Down	family with sequence similarity 9 member A
KRT35	-3.32094	0.000174	0.000526	-3.75379	Down	keratin 35
SCT	-3.32054	5.23E-11	5.52E-10	-6.56417	Down	secretin
PRLHR	-3.31948	0.000436	0.001213	-3.51711	Down	prolactin releasing hormone receptor
ACTG2	-3.31704	2.86E-06	1.23E-05	-4.68083	Down	actin gamma 2, smooth muscle
A2ML1	-3.31703	7.26E-11	7.47E-10	-6.51525	Down	alpha-2-macroglobulin like 1
KCNJ6	-3.31042	1.28E-05	4.81E-05	-4.36434	Down	potassium inwardly rectifying channel subfamily J member 6
GRIA2	-3.3081	0.001103	0.002789	-3.26291	Down	glutamate ionotropic receptor AMPA type subunit 2
PPFIA2	-3.30721	1.57E-07	8.58E-07	-5.24416	Down	PTPRF interacting protein alpha 2
TPSAB1	-3.30498	4.92E-06	2.01E-05	-4.56803	Down	tryptase alpha/beta 1
GDI1	-3.3029	4.94E-19	2.17E-17	-8.91359	Down	GDP dissociation inhibitor 1
DEFB121	-3.30278	0.011412	0.022213	-2.52982	Down	defensin beta 121
F10	-3.2978	7.53E-07	3.59E-06	-4.94725	Down	coagulation factor X
TGM3	-3.29132	1.03E-08	7.07E-08	-5.72505	Down	transglutaminase 3
SMR3B	-3.28995	0.006115	0.012844	-2.74154	Down	submaxillary gland androgen regulated protein 3B
C7orf33	-3.28962	0.001936	0.004629	-3.0999	Down	chromosome 7 open reading frame 33
ZP4	-3.28768	9.53E-05	0.000302	-3.90236	Down	zonapellucida glycoprotein 4
SLC38A3	-3.28086	3.54E-05	0.000123	-4.13541	Down	solute carrier family 38 member 3
SHOX	-3.27361	1.02E-07	5.77E-07	-5.323	Down	short stature homeobox
FBXW12	-3.26997	0.000134	0.000412	-3.81943	Down	F-box and WD repeat domain containing 12
TRIM60	-3.26521	0.003074	0.00699	-2.96022	Down	tripartite motif containing 60
PSG5	-3.26386	0.005588	0.011875	-2.77101	Down	pregnancy specific beta-1-glycoprotein 5
CPNE9	-3.2589	4.13E-09	3.03E-08	-5.87891	Down	copine family member 9
FAM47C	-3.25697	0.002412	0.005635	-3.03421	Down	family with sequence similarity 47 member C
DCDC2C	-3.24891	1.59E-06	7.12E-06	-4.79971	Down	doublecortin domain containing 2C

GDA	-3.24884	1.13E-17	3.99E-16	-8.56006	Down	guanine deaminase
TMEM100	-3.2455	0.00405	0.008937	-2.87426	Down	transmembrane protein 100
GFRAL	-3.24337	0.001506	0.003688	-3.17354	Down	GDNF family receptor alpha like
KRT38	-3.24142	0.006674	0.013864	-2.71268	Down	keratin 38
CHAC1	-3.23967	9.39E-10	7.78E-09	-6.11952	Down	ChaC glutathione specific gamma-glutamylcyclotransferase 1
APLNR	-3.23657	2.28E-05	8.16E-05	-4.23597	Down	apelin receptor
STC1	-3.23437	1.95E-06	8.62E-06	-4.7587	Down	stanniocalcin 1
ONECUT3	-3.23033	0.000411	0.001148	-3.53281	Down	one cut homeobox 3
P4HA3	-3.22889	1.12E-06	5.15E-06	-4.86985	Down	prolyl 4-hydroxylase subunit alpha 3
ASB4	-3.22868	7.75E-05	0.00025	-3.95206	Down	ankyrin repeat and SOCS box containing 4
SCEL	-3.21964	1.80E-11	2.05E-10	-6.72167	Down	sciellin
OCSTAMP	-3.21818	0.000178	0.000537	-3.74792	Down	osteoclast stimulatory transmembrane protein
FAM27E2	-3.21763	1.14E-08	7.73E-08	-5.70846	Down	family with sequence similarity 27 member E2
DAND5	-3.21563	0.000585	0.001579	-3.43843	Down	DAN domain BMP antagonist family member 5
CSMD3	-3.21265	6.55E-06	2.61E-05	-4.50771	Down	CUB and Sushi multiple domains 3
SERPINA12	-3.20522	0.005426	0.011567	-2.78058	Down	serpin family A member 12
BPESC1	-3.20461	0.016472	0.030654	-2.39829	Down	blepharophimosis, epicanthus inversus and ptosis candidate 1
NOVA1	-3.20337	1.22E-07	6.79E-07	-5.29059	Down	NOVA alternative splicing regulator 1
LHFPL5	-3.20085	0.000137	0.000423	-3.81263	Down	LHFPL tetraspan subfamily member 5
POSTN	-3.19648	3.06E-10	2.79E-09	-6.29551	Down	periostin
MAGEC1	-3.19382	0.004052	0.008941	-2.87405	Down	MAGE family member C1
TRIM42	-3.19262	0.000164	0.000497	-3.76945	Down	tripartite motif containing 42
HOTAIR	-3.18731	0.006375	0.013306	-2.72785	Down	HOX transcript antisense RNA
CDR1	-3.18696	7.07E-12	8.72E-11	-6.85619	Down	cerebellar degeneration related protein 1
C11orf91	-3.18647	4.05E-12	5.19E-11	-6.93532	Down	chromosome 11 open reading frame 91
MUC21	-3.17732	1.80E-10	1.72E-09	-6.37786	Down	mucin 21, cell surface associated
OC90	-3.16712	0.009532	0.019009	-2.59235	Down	otoconin 90
RNASEH2A	-3.16128	8.94E-16	2.18E-14	-8.04064	Down	ribonuclease H2 subunit A
C8orf49	-3.16021	0.010709	0.020999	-2.55204	Down	chromosome 8 putative open reading frame 49
S100A7	-3.15727	0.00012	0.000373	-3.84659	Down	S100 calcium binding protein A7
EMP1	-3.15709	1.98E-10	1.88E-09	-6.36253	Down	epithelial membrane protein 1
SPRR2B	-3.1556	0.000388	0.001091	-3.54813	Down	small proline rich protein 2B
OR51E2	-3.1531	0.001199	0.003009	-3.23901	Down	olfactory receptor family 51 subfamily E member 2
SNORD82	-3.14527	4.18E-11	4.48E-10	-6.59767	Down	small nucleolar RNA, C/D box 82
FAM25A	-3.14451	3.67E-06	1.54E-05	-4.62938	Down	family with sequence similarity 25 member A
TEX35	-3.1405	0.001386	0.003421	-3.19757	Down	testis expressed 35
KRT36	-3.13838	8.87E-05	0.000283	-3.91948	Down	keratin 36
POTEC	-3.13522	0.007953	0.01621	-2.65404	Down	POTE ankyrin domain family member C
TEX33	-3.13288	0.00929	0.018587	-2.60118	Down	testis expressed 33
SLC6A4	-3.13096	1.13E-10	1.12E-09	-6.44815	Down	solute carrier family 6 member 4
TMEFF2	-3.12943	0.000118	0.000367	-3.85028	Down	transmembrane protein with EGF like and two follistatin like domains 2
GALP	-3.12767	0.02539	0.044638	-2.23542	Down	galanin like peptide
PAX4	-3.12742	0.003174	0.007189	-2.95036	Down	paired box 4

CRYBA2	-3.12584	0.019745	0.03589	-2.33116	Down	crystallin beta A2
TUBA3C	-3.12409	0.000587	0.001584	-3.43748	Down	tubulin alpha 3c
MC2R	-3.12166	0.017862	0.0329	-2.36846	Down	melanocortin 2 receptor
SYT14	-3.11957	0.009895	0.01964	-2.57947	Down	synaptotagmin 14
NAT16	-3.11895	0.000394	0.001105	-3.54411	Down	N-acetyltransferase 16 (putative)
IZUMO2	-3.11644	0.006291	0.013161	-2.7322	Down	IZUMO family member 2
MYOZ1	-3.11505	0.000212	0.000631	-3.70384	Down	myozenin 1
ATP1B4	-3.11457	1.25E-05	4.72E-05	-4.36877	Down	ATPase Na+/K+ transporting family member beta 4
PGLYRP4	-3.11388	1.38E-05	5.18E-05	-4.34631	Down	peptidoglycan recognition protein 4
KRT42P	-3.11246	7.19E-11	7.40E-10	-6.51674	Down	keratin 42 pseudogene
DEFB132	-3.11179	0.016178	0.030175	-2.40488	Down	defensin beta 132
LMX1A	-3.11176	5.35E-06	2.17E-05	-4.55074	Down	LIM homeobox transcription factor 1 alpha
SAA1	-3.10837	5.97E-14	1.05E-12	-7.50882	Down	serum amyloid A1
ASB11	-3.10718	1.06E-05	4.06E-05	-4.40367	Down	ankyrin repeat and SOCS box containing 11
CNPY1	-3.10654	0.025122	0.044223	-2.23952	Down	canopy FGF signaling regulator 1
MGAT5B	-3.10541	2.53E-07	1.33E-06	-5.15513	Down	alpha-1,6-mannosylglycoprotein 6-beta-N-acetylglucosaminyltransferase B
OTUD6A	-3.1043	0.000208	0.000618	-3.70953	Down	OTU deubiquitinase 6A
BCL6B	-3.10254	1.84E-08	1.20E-07	-5.626	Down	BCL6B transcription repressor
ABCG8	-3.10116	0.001069	0.002713	-3.27174	Down	ATP binding cassette subfamily G member 8
SLC17A7	-3.09869	0.000109	0.000343	-3.86874	Down	solute carrier family 17 member 7
SAA2	-3.09548	8.46E-15	1.72E-13	-7.76043	Down	serum amyloid A2
UNC93A	-3.09233	0.019462	0.035432	-2.33657	Down	unc-93 homolog A
IL17A	-3.08938	0.021206	0.038215	-2.30429	Down	interleukin 17A
SPINK5	-3.08923	7.89E-12	9.66E-11	-6.84045	Down	serine peptidase inhibitor Kazal type 5
SNORD127	-3.08634	1.72E-09	1.36E-08	-6.02271	Down	small nucleolar RNA, C/D box 127
AGR3	-3.08479	2.91E-16	7.69E-15	-8.17693	Down	anterior gradient 3, protein disulphide isomerase family member
ANKRD26P3	-3.08399	9.99E-06	3.83E-05	-4.41732	Down	ankyrin repeat domain 26 pseudogene 3
FAM47A	-3.08324	0.001193	0.002993	-3.24062	Down	family with sequence similarity 47 member A
DOK5	-3.08307	0.007347	0.015105	-2.6807	Down	docking protein 5
GLYCAM1	-3.08251	0.005978	0.012588	-2.74901	Down	glycosylation dependent cell adhesion molecule 1 (pseudogene)
SLC6A17	-3.0815	4.08E-06	1.70E-05	-4.60704	Down	solute carrier family 6 member 17
SNORD56	-3.08116	3.94E-17	1.24E-15	-8.41472	Down	small nucleolar RNA, C/D box 56
SLC17A2	-3.07765	0.028414	0.049193	-2.19152	Down	solute carrier family 17 member 2
MTRNR2L2	-3.07658	4.38E-13	6.63E-12	-7.24322	Down	MT-RNR2 like 2
PAMR1	-3.07598	3.83E-11	4.14E-10	-6.61044	Down	peptidase domain containing associated with muscle regeneration 1
FCRL4	-3.07554	5.34E-05	0.000178	-4.04027	Down	Fc receptor like 4
CNN1	-3.07536	1.95E-06	8.62E-06	-4.75865	Down	calponin 1
SNORD76	-3.07108	5.90E-19	2.56E-17	-8.89381	Down	small nucleolar RNA, C/D box 76
HABP2	-3.07082	2.01E-05	7.29E-05	-4.26368	Down	hyaluronan binding protein 2
DCLK1	-3.06807	4.21E-13	6.39E-12	-7.2486	Down	doublecortin like kinase 1
GDPD4	-3.06697	0.002337	0.00548	-3.04364	Down	glycerophosphodiesterphosphodiesterase domain containing 4
IGFL1	-3.06039	0.024237	0.042906	-2.25336	Down	IGF like family member 1
KIAA0087	-3.05975	0.000147	0.00045	-3.79581	Down	KIAA0087 lncRNA

C5orf60	-3.05184	0.021275	0.03832	-2.30308	Down	chromosome 5 open reading frame 60
SLC15A5	-3.05166	0.012843	0.024653	-2.48809	Down	solute carrier family 15 member 5
HMGB3P1	-3.05146	0.000963	0.002469	-3.30124	Down	high mobility group box 3 pseudogene 1
CAND1.11	-3.04999	4.46E-07	2.21E-06	-5.04834	Down	uncharacterized LOC100130460
ACOXL	-3.04835	1.02E-09	8.43E-09	-6.10572	Down	acyl-CoA oxidase like
CNTN6	-3.04832	0.008037	0.016359	-2.65053	Down	contactin 6
PRAMEF20	-3.04639	0.013521	0.025791	-2.46973	Down	PRAME family member 20
SPATA31E1	-3.04281	0.000208	0.00062	-3.70859	Down	SPATA31 subfamily E member 1
PRAMEF19	-3.04123	0.02708	0.047197	-2.21036	Down	PRAME family member 19
SKIDA1	-3.04109	5.53E-10	4.80E-09	-6.2032	Down	SKI/DACH domain containing 1
PTCH1	-3.03738	1.15E-10	1.14E-09	-6.44621	Down	patched 1
GRM8	-3.03561	7.76E-05	0.00025	-3.95167	Down	glutamate metabotropic receptor 8
RPE65	-3.03463	7.45E-06	2.93E-05	-4.48039	Down	retinoid isomerohydrolase RPE65
IL1RAPL1	-3.0343	0.009762	0.019414	-2.58415	Down	interleukin 1 receptor accessory protein like 1
CRCT1	-3.03399	3.46E-05	0.00012	-4.14099	Down	cysteine rich C-terminal 1
CYP4F24P	-3.03277	0.002019	0.004806	-3.08748	Down	cytochrome P450 family 4 subfamily F member 24, pseudogene
CRMP1	-3.02996	2.93E-11	3.24E-10	-6.64983	Down	collapsin response mediator protein 1
SLC22A10	-3.02962	0.015749	0.029479	-2.41469	Down	solute carrier family 22 member 10
P2RX6	-3.02876	3.54E-11	3.85E-10	-6.62231	Down	purinergic receptor P2X 6
CES5A	-3.02202	6.93E-06	2.75E-05	-4.49593	Down	carboxylesterase 5A
SNORD47	-3.02178	2.59E-16	6.90E-15	-8.19102	Down	small nucleolar RNA, C/D box 47
TRIML2	-3.02162	0.009531	0.019007	-2.59241	Down	tripartite motif family like 2
ADGRG7	-3.01934	0.006931	0.01434	-2.70016	Down	adhesion G protein-coupled receptor G7
PRR27	-3.01891	0.011252	0.021933	-2.53478	Down	proline rich 27
C2orf78	-3.01761	0.003827	0.008493	-2.89207	Down	chromosome 2 open reading frame 78
NMUR2	-3.01573	0.020222	0.036667	-2.3222	Down	neuromedin U receptor 2
SNORD61	-3.01437	1.87E-12	2.51E-11	-7.04418	Down	small nucleolar RNA, C/D box 61
SNORD14D	-3.0138	4.18E-12	5.34E-11	-6.9309	Down	small nucleolar RNA, C/D box 14D
RTP3	-3.01324	0.006262	0.013112	-2.73373	Down	receptor transporter protein 3
FZD9	-3.01279	1.13E-08	7.69E-08	-5.70939	Down	frizzled class receptor 9
HAPLN2	-3.01045	0.000299	0.000861	-3.61607	Down	hyaluronan and proteoglycan link protein 2
SOHLH1	-3.00624	0.000523	0.001428	-3.46858	Down	spermatogenesis and oogenesis specific basic helix-loop-helix 1
PRELP	-3.00498	7.81E-12	9.56E-11	-6.84202	Down	proline and arginine rich end leucine rich repeat protein
PRR30	-3.00471	0.009684	0.019276	-2.58692	Down	proline rich 30
KRT39	-3.00407	5.03E-06	2.05E-05	-4.56342	Down	keratin 39
SMOC2	-3.00303	9.00E-06	3.49E-05	-4.4398	Down	SPARC related modular calcium binding 2
SEMG2	-3.00291	0.000347	0.000987	-3.57726	Down	semenogelin 2
PCK1	-3.00161	0.000574	0.001553	-3.44353	Down	phosphoenolpyruvatecarboxykinase 1
TECTB	-3.00058	0.023306	0.041517	-2.26839	Down	tectorin beta
SNORD87	-2.99888	1.53E-16	4.35E-15	-8.25408	Down	small nucleolar RNA, C/D box 87
OR56B4	-2.9981	1.32E-05	4.97E-05	-4.35595	Down	olfactory receptor family 56 subfamily B member 4
ZFP42	-2.99642	0.001125	0.002838	-3.25713	Down	ZFP42 zinc finger protein
OR51E1	-2.99589	0.028654	0.049568	-2.18822	Down	olfactory receptor family 51 subfamily E member 1

HTR1F	-2.99376	7.36E-08	4.28E-07	-5.38216	Down	5-hydroxytryptamine receptor 1F
POM121L4P	-2.99375	0.008886	0.017888	-2.6164	Down	POM121 transmembranenucleoporin like 4, pseudogene
SALRNA3	-2.99294	0.005578	0.011857	-2.77164	Down	senescence associated long non-coding RNA 3
RTBDN	-2.99275	2.45E-07	1.29E-06	-5.16174	Down	retbindin
PANDAR	-2.99054	4.21E-07	2.11E-06	-5.05905	Down	promoter of CDKN1A antisense DNA damage activated RNA
CALCR	-2.98712	0.007337	0.015085	-2.68117	Down	calcitonin receptor
LACRT	-2.98708	0.001166	0.002931	-3.24707	Down	lacritin
MYBPC1	-2.98683	0.00029	0.000838	-3.62399	Down	myosin binding protein C1
ASB10	-2.98648	0.003355	0.007547	-2.93317	Down	ankyrin repeat and SOCS box containing 10
GABRG2	-2.98577	0.005414	0.011543	-2.78133	Down	gamma-aminobutyric acid type A receptor subunit gamma2
MYL10	-2.98523	0.007423	0.015243	-2.67724	Down	myosin light chain 10
PCDHA9	-2.98085	4.95E-06	2.02E-05	-4.56695	Down	protocadherin alpha 9
KRT33B	-2.98065	0.00098	0.002509	-3.29629	Down	keratin 33B
MMP27	-2.98026	0.015612	0.029263	-2.41787	Down	matrix metallopeptidase 27
ADAM21P1	-2.97795	0.005943	0.012525	-2.75092	Down	ADAM metallopeptidase domain 21 pseudogene 1
SNORD63	-2.97751	2.45E-12	3.23E-11	-7.0063	Down	small nucleolar RNA, C/D box 63
CABP2	-2.97651	0.007238	0.014899	-2.68571	Down	calcium binding protein 2
NAA11	-2.97466	0.026456	0.046221	-2.21945	Down	N-alpha-acetyltransferase 11, NatA catalytic subunit
CDH16	-2.97388	8.23E-07	3.89E-06	-4.92988	Down	cadherin 16
FAM205BP	-2.97159	0.005107	0.01096	-2.80023	Down	transmembrane protein C9orf144B pseudogene
MSMB	-2.96904	9.98E-14	1.68E-12	-7.44123	Down	microseminoprotein beta
HOXC8	-2.96864	0.000634	0.001697	-3.41672	Down	homeobox C8
LGALS17A	-2.96487	1.53E-06	6.87E-06	-4.80782	Down	galectin 14 pseudogene
SLC7A14	-2.96445	0.000191	0.000572	-3.7308	Down	solute carrier family 7 member 14
AHSG	-2.96373	0.017019	0.031564	-2.3863	Down	alpha 2-HS glycoprotein
SIGLECL1	-2.96332	0.014793	0.027908	-2.43741	Down	SIGLEC family like 1
SCARNA16	-2.96284	1.06E-15	2.57E-14	-8.01935	Down	small Cajal body-specific RNA 16
EPHA5	-2.95764	4.20E-10	3.72E-09	-6.24642	Down	EPH receptor A5
NDRG4	-2.95536	1.85E-14	3.56E-13	-7.66078	Down	NDRG family member 4
BLACE	-2.95315	0.000363	0.001027	-3.56554	Down	B cell acute lymphoblastic leukemia expressed
SNORD1C	-2.95278	3.62E-12	4.68E-11	-6.9511	Down	small nucleolar RNA, C/D box 1C
GCM2	-2.9507	1.37E-05	5.11E-05	-4.34935	Down	glial cells missing transcription factor 2
ANHX	-2.95069	0.014005	0.026576	-2.45713	Down	anomalous homeobox
SMPX	-2.94954	0.003427	0.007694	-2.92662	Down	small muscle protein X-linked
GABRG1	-2.94766	0.012291	0.023725	-2.50367	Down	gamma-aminobutyric acid type A receptor subunit gamma1
GPR176	-2.94651	3.87E-07	1.95E-06	-5.07539	Down	G protein-coupled receptor 176
KRT83	-2.94464	0.018764	0.034287	-2.35019	Down	keratin 83
PNLIP	-2.9434	0.015644	0.029314	-2.41711	Down	pancreatic lipase
WNT8A	-2.94186	0.000807	0.002108	-3.35042	Down	Wnt family member 8A
RXRG	-2.94142	0.000266	0.000773	-3.64663	Down	retinoid X receptor gamma
CLCA1	-2.94124	0.003369	0.007576	-2.93188	Down	chloride channel accessory 1
ZNF536	-2.9406	1.80E-06	8.00E-06	-4.77495	Down	zinc finger protein 536
AGXT	-2.93657	0.00039	0.001097	-3.54644	Down	alanine--glyoxylate and serine--pyruvate aminotransferase

SNAP91	-2.93441	0.000394	0.001106	-3.54392	Down	synaptosome associated protein 91
PRDM7	-2.9334	2.72E-05	9.62E-05	-4.1955	Down	PR/SET domain 7
PSG4	-2.93208	0.023164	0.041294	-2.27071	Down	pregnancy specific beta-1-glycoprotein 4
PCDHB3	-2.93135	5.67E-08	3.37E-07	-5.42891	Down	protocadherin beta 3
TMEM247	-2.93088	0.008385	0.016973	-2.63618	Down	transmembrane protein 247
MYH1	-2.93009	0.000224	0.000664	-3.68981	Down	myosin heavy chain 1
CPLX4	-2.93007	0.018977	0.03462	-2.34598	Down	complexin 4
HNRNPKP3	-2.92865	5.26E-05	0.000176	-4.04367	Down	heterogeneous nuclear ribonucleoprotein K pseudogene 3
ST8SIA2	-2.91896	0.000121	0.000376	-3.84404	Down	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 2
CETN1	-2.91403	4.10E-05	0.00014	-4.1017	Down	centrin 1
SNORD22	-2.91349	1.43E-13	2.35E-12	-7.39353	Down	small nucleolar RNA, C/D box 22
SFTPA2	-2.91089	0.02099	0.037867	-2.30816	Down	surfactant protein A2
SNORD80	-2.90835	1.25E-15	2.96E-14	-7.99985	Down	small nucleolar RNA, C/D box 80
LACTBL1	-2.90814	0.001322	0.003281	-3.21119	Down	lactamase beta like 1
DLL4	-2.90715	2.75E-06	1.18E-05	-4.6889	Down	delta like canonical Notch ligand 4
MAGEC2	-2.90422	0.023749	0.042155	-2.26116	Down	MAGE family member C2
FAM71C	-2.90302	0.002345	0.005494	-3.04271	Down	family with sequence similarity 71 member C
PLA2G2D	-2.90101	0.014685	0.027727	-2.44006	Down	phospholipase A2 group IID
HCAR1	-2.89933	4.68E-06	1.92E-05	-4.57865	Down	hydroxycarboxylic acid receptor 1
ANKRD62	-2.89844	5.69E-08	3.37E-07	-5.42838	Down	ankyrin repeat domain 62
CXCL2	-2.89749	8.25E-11	8.42E-10	-6.49603	Down	C-X-C motif chemokine ligand 2
EMCN	-2.89745	0.016851	0.031293	-2.38994	Down	endomucin
ABCA8	-2.89712	0.000712	0.001885	-3.385	Down	ATP binding cassette subfamily A member 8
IGFN1	-2.89677	1.46E-06	6.58E-06	-4.817	Down	immunoglobulin like and fibronectin type III domain containing 1
SERPINA13P	-2.89568	0.010375	0.020449	-2.56306	Down	serpin family A member 13, pseudogene
SLC2A2	-2.89438	0.00805	0.016381	-2.64997	Down	solute carrier family 2 member 2
RASL12	-2.89333	0.000106	0.000334	-3.87565	Down	RAS like family 12
GLYAT	-2.89319	0.005484	0.011678	-2.77715	Down	glycine-N-acyltransferase
OR7E5P	-2.89287	0.005622	0.011936	-2.76907	Down	olfactory receptor family 7 subfamily E member 5 pseudogene
FAM182A	-2.89164	4.49E-07	2.23E-06	-5.04683	Down	family with sequence similarity 182 member A
PDZRN3	-2.89019	3.86E-07	1.95E-06	-5.07565	Down	PDZ domain containing ring finger 3
SMIM21	-2.88979	0.005251	0.01123	-2.79124	Down	small integral membrane protein 21
FAIM2	-2.88956	3.73E-10	3.34E-09	-6.26504	Down	Fas apoptotic inhibitory molecule 2
SLC39A2	-2.88936	0.002929	0.006691	-2.97513	Down	solute carrier family 39 member 2
CADM3	-2.88848	0.007747	0.015832	-2.66292	Down	cell adhesion molecule 3
SLCO1C1	-2.88734	0.000717	0.001898	-3.38281	Down	solute carrier organic anion transporter family member 1C1
IL36RN	-2.88704	0.000112	0.000351	-3.86262	Down	interleukin 36 receptor antagonist
USP18	-2.88653	7.15E-32	2.76E-29	-11.749	Down	ubiquitin specific peptidase 18
PASD1	-2.88447	0.003487	0.007813	-2.92116	Down	PAS domain containing repressor 1
ALLC	-2.88398	0.01492	0.028119	-2.43431	Down	allantoicase
MIP	-2.88208	0.00056	0.00152	-3.45015	Down	major intrinsic protein of lens fiber
SNORA61	-2.87634	3.23E-18	1.25E-16	-8.70318	Down	small nucleolar RNA, H/ACA box 61
CACNG2	-2.87618	0.000952	0.002446	-3.30421	Down	calcium voltage-gated channel auxiliary subunit gamma 2

SYNGR4	-2.87375	0.013113	0.025108	-2.48069	Down	synaptogyrin 4
TFAP2D	-2.87375	0.017934	0.033014	-2.36697	Down	transcription factor AP-2 delta
LHX9	-2.87226	0.005438	0.011589	-2.77989	Down	LIM homeobox 9
SLCO1B7	-2.87205	0.000608	0.001634	-3.42793	Down	solute carrier organic anion transporter family member 1B7 (putative)
AKAP4	-2.8684	0.003332	0.007499	-2.93535	Down	A-kinase anchoring protein 4
CST5	-2.86824	0.002671	0.006163	-3.00321	Down	cystatin D
SLC6A3	-2.8676	0.000301	0.000865	-3.61478	Down	solute carrier family 6 member 3
GADL1	-2.86643	0.001824	0.004385	-3.11751	Down	glutamate decarboxylase like 1
IL20RA	-2.86506	1.28E-11	1.51E-10	-6.77092	Down	interleukin 20 receptor subunit alpha
TNFRSF11B	-2.86494	5.43E-06	2.20E-05	-4.54732	Down	TNF receptor superfamily member 11b
DSG1	-2.86321	0.003366	0.00757	-2.93217	Down	desmoglein 1
FBP2	-2.86165	0.015673	0.029357	-2.41644	Down	fructose-bisphosphatase 2
RIMS4	-2.85931	0.000441	0.001225	-3.51399	Down	regulating synaptic membrane exocytosis 4
CNTN5	-2.85904	7.66E-09	5.36E-08	-5.77583	Down	contactin 5
OR1J1	-2.85362	0.001453	0.003571	-3.18386	Down	olfactory receptor family 1 subfamily J member 1
HRG	-2.85096	0.021097	0.038048	-2.30624	Down	histidine rich glycoprotein
FANCD2OS	-2.85054	0.001054	0.002679	-3.27569	Down	FANCD2 opposite strand
CRTAC1	-2.84601	0.000222	0.000658	-3.69203	Down	cartilage acidic protein 1
ETV3L	-2.84515	0.01483	0.027963	-2.4365	Down	ETS variant transcription factor 3 like
SERPINA9	-2.84423	0.000578	0.001563	-3.44159	Down	serpin family A member 9
GALNTL5	-2.84316	0.002061	0.004896	-3.08136	Down	polypeptide N-acetylgalactosaminyltransferase like 5
SLC19A3	-2.84171	0.002949	0.006734	-2.97297	Down	solute carrier family 19 member 3
AGBL4	-2.83997	6.68E-13	9.76E-12	-7.18575	Down	ATP/GTP binding protein like 4
CA9	-2.83995	0.000106	0.000333	-3.87678	Down	carbonic anhydrase 9
SLITRK3	-2.83954	0.018683	0.034164	-2.3518	Down	SLIT and NTRK like family member 3
PDYN	-2.83446	0.009974	0.019772	-2.57674	Down	prodynorphin
CFHR5	-2.83134	0.012485	0.024055	-2.49813	Down	complement factor H related 5
DCAF8L2	-2.83123	0.001652	0.004015	-3.14657	Down	DDB1 and CUL4 associated factor 8 like 2
LAMP3	-2.83094	2.56E-25	3.40E-23	-10.3968	Down	lysosomal associated membrane protein 3
NANOG	-2.83059	0.00283	0.006485	-2.9856	Down	Nanoghomeobox
PGR	-2.83034	0.000122	0.000377	-3.84298	Down	progesterone receptor
FBXL7	-2.82992	4.16E-09	3.05E-08	-5.87754	Down	F-box and leucine rich repeat protein 7
MFAP5	-2.8297	0.02228	0.039911	-2.28556	Down	microfibril associated protein 5
SMO	-2.82828	2.13E-07	1.13E-06	-5.18801	Down	smoothened, frizzled class receptor
CATSPERD	-2.82511	1.17E-19	5.87E-18	-9.07215	Down	cation channel sperm associated auxiliary subunit delta
PCDHA6	-2.82469	0.000163	0.000497	-3.76963	Down	protocadherin alpha 6
CHIA	-2.82131	0.01624	0.030276	-2.40348	Down	chitinase acidic
FGF4	-2.8208	0.003486	0.007812	-2.92123	Down	fibroblast growth factor 4
THCAT155	-2.81881	0.000121	0.000375	-3.84464	Down	thyroid cancer-associated transcript 155
IL1A	-2.8187	7.99E-07	3.79E-06	-4.93557	Down	interleukin 1 alpha
UPK2	-2.81717	0.001717	0.004156	-3.13527	Down	uroplakin 2
TDGF1	-2.81688	0.002199	0.005192	-3.06191	Down	teratocarcinoma-derived growth factor 1
OTC	-2.81572	0.027302	0.047541	-2.20718	Down	ornithine carbamoyltransferase

LY6G6C	-2.81508	6.12E-05	0.000201	-4.00799	Down	lymphocyte antigen 6 family member G6C
HAMP	-2.8142	0.000455	0.001259	-3.50597	Down	hepcidin antimicrobial peptide
CCBE1	-2.81307	7.43E-14	1.29E-12	-7.48003	Down	collagen and calcium binding EGF domains 1
ITGBL1	-2.81304	1.36E-10	1.33E-09	-6.41988	Down	integrin subunit beta like 1

Table 2 The enriched GO terms of the up and down regulated differentially expressed genes

GO ID	CATEGORY	GO Name	Adjusted p value	negative log10 of adjusted p value	Gene Count	Gene
Up regulated genes						
GO:0002376	BP	immune system process	1.33E-41	40.87672363	204	GYPC,BNIP3L,TESC,EPB42,SNCA,GYPB,MPP1,ALAS2,AHSP,IFIT1B,GYPA,IL7R,FBXO7,SLC4A1,KLRB1,S1PR1,KLF1,CLC,KRT1,GATA1,PPBP,TLR8,PIP4K2A,FOLR3,RPL39,TNFAIP8L2,NFE2,GLIPR1,TRAT1,CCR2,CLEC12A,KLRG1,TRIM58,FAM210B,LYL1,GLRX5,NLRP12,PECAM1,TRIM10,DEFA3,ICAM3,FCER1A,FCN1,PITHD1,CFP,LILRA1,PIM1,EEF1A1,CYBB,AP1S2,FAXDC2,MPEG1,ITK,GPR174,CD3D,KAT2B,CD8B,LST1,S1PR4,BCL2L1,SPTA1,BTLA,CCR4,PTPRC,CX3CR1,TSPAN32,CD247,FCRL1,EOMES,TBC1D10C,LCK,LYZ,HBB,PTGDR,RIOK3,CD244,GZMM,GNLY,KLRF1,CR1L,TXK,PF4V1,KIF15,LILRA2,ZAP70,FOXO3,RHAG,DOCK11,ATM,KLRD1,MFNG,CD28,GPX1,TLR1,PRDX6,TLR6,ADGRE3,PRF1,C5AR2,BPGM,LRRK2,CCL5,CD33,FCRL3,ETS1,SH2D1A,SLC7A7,PYHIN1,SLAMF6,ITGB2,CCR3,FGL2,GZMA,FGR,CD48,LTB,PSMF1,THEMIS,PICALM,TIGIT,PTAFR,MYO1G,ADCY7,BSG,ALOX5,LY86,MME,SELPLG,RPL30,VIM,CD93,GCA,GPR171,SIGLEC10,FTL,CD96,CD226,CD1D,TNFSF4,LEF1,FCMR,CORO1A,TAL1,IKZF1,ICAM2,ATP8A1,CD84,CD8A,GAB3,SIGLEC9,TLR4,FLNA,HK3,CPPED1,RASSF2,CCR7,DPP4,NLRC4,ITM2A,PLCL2,ITGB3,RASGRP1,FYN,TLR2,DOCK2,CSF1R,PRKCB,CAMK4,LGALS1,CLEC2D,TESPA1,CD40LG,FCGR3B,CXCL5,USP15,DMTN,CD27,CD36,LYST,NRROS,MGAM,RNF125,CA2,MAPK1,GPR183,KLRC2,CD300C,GRAP2,P2RY12,CR1,ITGB7,TGFBR2,IL27RA,CD300E,FCGR2A,RASGRP2,TFRC,CD53,PRKACB,PADI4,CTSE,LTA4H,LILRB2,CD5
GO:0002682	BP	regulation of immune system process	4.82E-25	24.31700356	117	TESC,SNCA,MPP1,IFIT1B,IL7R,FBXO7,KLRB1,CLC,KRT1,GATA1,TLR8,TNFAIP8L2,NFE2,TRAT1,CCR2,FAM210B,ICAM3,FCER1A,FCN1,PITHD1,CFP,LILRA1,FAXDC2,ITK,CD3D,KAT2B,CD8

GO:0016020	CC	membrane	7.97E-09	8.098726789	290	B,LST1,SPTA1,BTLA,PTPRC,CX3CR1,TSPAN32,CD247,TBC1D10C,LCK,PTGDR,RIOK3,CD244,KLRF1,CR1L,TXK,LILRA2,ZAP70,FOXO3,ATM,KLRD1,CD28,GPX1,TLR6,C5AR2,LRRK2,CCL5,CD33,FCRL3,ETS1,SH2D1A,PYHIN1,SLAMF6,ITGB2,FGL2,FGR,CD48,PSMF1,THEMIS,TIGIT,PTAFR,MYO1G,ADCY7,GPR171,CD96,CD226,CD1D,TNFSF4,LEF1,CORO1A,TAL1,ICAM2,CD84,CD8A,SIGLEC9,TLR4,RASSF2,CCR7,DPP4,NLRC4,PLCL2,RASGRP1,FYN,CSF1R,PRKCB,CAMK4,LGALS1,CLEC2D,TESPA1,CD40LG,FCGR3B,CD27,CD36,RNF125,CA2,MAPK1,GPR183,KLRC2,CD300C,GRAP2,P2RY12,CR1,ITGB7,TGFBR2,IL27RA,CD300E,FCGR2A,TFRC,PRKACB,LILRB2,CD5STRADB,GYPC,BNIP3L,TESC,EPB42,SNCA,EPB41,UBA52,GYPB,MPP1,OR2W3,SLC25A37,ALAS2,BLVRB,GYPA,SLC25A39,IL7R,SLC4A1,KLRB1,RPL21,S1PR1,ADIPOR1,TMOD1,SLC14A1,KRT1,UBB,TLR8,PIP4K2A,FOLR3,GLIPR1,TRAT1,FECH,CCR2,CLEC12A,TARP,NCAPG,KLRG1,GPR146,GIMAP2,FAM210B,SIRPB2,UBXN6,PECAM1,RGS10,MBOAT2,YBX1,ICAM3,EMC3,FCER1A,FCN1,RPS15A,RGS18,LILRA1,VCAN,PIM1,EEF1A1,CYBB,ANK1,RAB2B,AP1S2,FAXDC2,MPEG1,ITK,GPR174,CD3D,CD8B,LST1,S1PR4,VN1R1,BCL2L1,GZMH,CD52,GIMAP1,VRK1,SPECC1,SPTA1,SPTB,BTLA,GRAP,CCR4,GNG11,VNN2,PTPRC,CX3CR1,TSPAN32,KIF14,CD247,FCRL1,RPL9,P2RY10,TBC1D10C,LCK,RPS11,S1PR5,PTGDR,RNF182,CD244,GZMM,P2RY8,KLRF1,CR1L,GYPE,TXK,FCRL6,KIF15,LILRA2,ZAP70,RPL35A,RPS12,NPRL3,FOXO3,RHAG,KLRD1,MFNG,C2ORF88,ARHGAP15,CD28,AKAP7,TLR1,NINJ2,PRDX6,PCMTD1,FCGR2C,TLR6,ADGRE3,PRF1,C5AR2,LRRK2,TMEM71,CD33,FCRL3,SLC7A7,SLAMF6,ITGB2,CMTM2,DPEP2,ANXA6,PDE3B,CCR3,OSBP2,GZMA,LRRC25,XK,RPL18A,FGR,GPR141,CD48,LTB,PSMF1,KCNA3,PICALM,OST4,TIGIT,PTAFR,MYO1G,MPP6,ACSL6,C1ORF162,ABCG2,ADCY7,LRRC8C,BSG,RPS2,RPS28,ALOX5,MFSD2B,P2RY13,AIDA,CHPT1,MME,PTPN4,SELPLG,RPL30,VIM,CD93,IL10RA,GCA,KLRC3,IPCEF1,MS4A6A,WDR45,RHBDD1,GPR171,RAB39B,SIGLEC10,TMEM170B,FTL,CD96,CD226,CD1D,TNFSF4,SORL1,LRRN3,FKBP8,SLC38A5,FCMR,CORO1A,RPS29,SMIM24,ABCC4,DPM2,ICAM2,ATP8A1,CD84,CD8A,RPS13,CDYL,SIGLEC9,TLR4,F

						LNA,CPPED1,RPL27A,CDC27,RPL7,RASSF2,CCR7,DPP4,ITM2A,KLRC4,ITGB3,RASGRP1,FYN,TLR2,TBXAS1,DOCK2,CSF1R,PRKCB,PLXDC2,PPM1A,CLEC2D,MAF1,TESPA1,CD40LG,FCGR3B,HACD1,MS4A7,USP15,DMTN,CD27,RPS23,C19ORF38,CD36,NKG7,LYST,NRROS,SLC4A10,PINK1,DSC3,MGAM,RNF125,CA2,TRABD2A,MEGF9,MAPK1,SLC12A1,EVI2A,TGFBI,GPR183,KLRC2,CLEC1B,RPL6,CD300C,APLF,GRAP2,P2RY12,CR1,PPT1,ITGB7,TGFBR2,IL27RA,CD300E,FCGR2A,RASGRP2,OGT,TFRC,CD53,RPL7A,PRKACB,RPS7,TNFRSF10C,ST6GALNAC4,C16ORF54,RPL10,LILRB2,PLXNC1,PTPRA,MEMO1,CD5,GBGT1,AKT3
GO:0071944	CC	cell periphery	1.07E-08	7.972281868	204	GYPC,TESC,EPB42,SNCA,EPB41,UBA52,GYPB,MPP1,OR2W3,BLVRB,GYPA,IL7R,SLC4A1,KLRB1,S1PR1,ADIPOR1,TMOD1,SLC14A1,CLC,KRT1,UBB,TLR8,PIP4K2A,FOLR3,GLIPR1,TRAT1,CCR2,CLEC12A,KLRG1,GPR146,SIRPB2,PECAM1,RGS10,PHOSPHO1,ICAM3,FCER1A,FCN1,CFP,RGS18,LILRA1,VCAN,PIM1,EEF1A1,CYBB,ANK1,RAB2B,AP1S2,ITK,GPR174,CD3D,CD8B,S1PR4,VN1R1,CD52,MMRN1,F13A1,SPTA1,SPTB,BTLA,CCR4,GNG11,VNN2,PTPRC,CX3CR1,TSPAN32,KIF14,CD247,FCRL1,P2RY10,TBC1D10C,LCK,S1PR5,PTGDR,CD244,P2RY8,KLRF1,GYPE,TXK,FCRL6,LILRA2,ZAP70,RHAG,KLRD1,C2ORF88,CD28,AKAP7,TLR1,NINJ2,TLR6,ADGRE3,PRF1,C5AR2,LRRK2,CD33,FCRL3,SLC7A7,SLAMF6,ITGB2,ANXA6,CCR3,OSBP2,FGL2,GZMA,XK,FGR,GPR141,CD48,LTB,KCNA3,PICALM,TIGIT,PTAFR,MYO1G,MPP6,ACSL6,ABCG2,ADCY7,LRRC8C,BSG,MFSD2B,P2RY13,MME,PTPN4,SELPLG,VIM,CD93,IL10RA,GCA,IPCEF1,GPR171,RAB39B,SIGLEC10,TMEM170B,CD96,CD226,CD1D,TNFSF4,SORL1,LRRN3,SLC38A5,FCMR,CORO1A,ABCC4,ICAM2,ATP8A1,CD84,CD8A,SIGLEC9,TLR4,FLNA,CPPED1,RASSF2,CCR7,DPP4,ITM2A,ITGB3,RASGRP1,FYN,TLR2,CSF1R,PRKCB,LGALS1,PPM1A,CLEC2D,MAF1,CD40LG,FCGR3B,USP15,DMTN,CD27,CD36,NKG7,NRROS,SLC4A10,DSC3,MGAM,CA2,TRABD2A,MEGF9,MAPK1,SLC12A1,TGFBI,GPR183,KLRC2,CLEC1B,CD300C,GRAP2,P2RY12,CR1,ITGB7,TGFBR2,IL27RA,CD300E,FCGR2A,RASGRP2,OGT,TFRC,CD53,PRKACB,TNFRSF10C,LILRB2,PLXNC1,PTPRA,CD5
GO:0060089	MF	molecular transducer	3.94E-14	13.40438399	90	OR2W3,IL7R,KLRB1,S1PR1,ADIPOR1,KRT1,TLR8,FOLR3,CCR2,

		activity				KLRG1,GPR146,
GO:0005515	MF	protein binding	6.26448E-05	4.203115121	377	PECAM1,FCER1A,FCN1,LILRA1,ITK,GPR174,CD3D,CD8B,S1PR4,VN1R1,BTLA,CCR4,PTPRC,CX3CR1,CD247,FCRL1,P2RY10,LCK,S1PR5,PTGDR,CD244,P2RY8,KLRF1,TXK,FCRL6,LILRA2,ZAP70,KLRD1,CD28,TLR1,TLR6,ADGRE3,C5AR2,CD33,FCRL3,ITGB2,CCR3,FGR,GPR141,CD48,PTAFR,BSG,P2RY13,CD93,IL10RA,KLRC3,GPR171,SORL1,LEF1,FCMR,CD8A,TLR4,CCR7,ITGB3,FYN,TLR2,CSF1R,CLEC2D,FCGR3B,CD27,CD36,EVI2A,GPR183,KLRC2,CLEC1B,CD300C,APLF,P2RY12,CR1,ITGB7,TGFBR2,IL27RA,CD300E,FCGR2A,TNFRSF10C,LILRB2,PLXNC1,PTPRA,CD5 STRADB,GYPC,HEMGN,BNIP3L,TESC,EPB42,SNCA,EPB41,DCAF12,UBA52,CA1,GYPB,MPP1,SLC25A37,ALAS2,AHSP,IFIT1B,BLVRB,C1ORF105,GYPA,MBNL3,IL7R,FBXO7,SLC4A1,KLRB1,RPL21,GZMK,S1PR1,DNAJC6,ADIPOR1,TMOD1,SLC14A1,SOX6,MKRN1,KLF1,CLC,KRT1,GATA1,UBB,PPBP,MAP3K7CL,TLR8,MXI1,PIP4K2A,POLE2,FOLR3,TNFAIP8L2,NFE2,GLIPR1,TRAT1,FECH,HBM,CCR2,CLEC12A,NCAPG,KLRG1,NCOA4,RBM38,TRIM58,GIMAP2,FAM210B,E2F2,LYL1,MYL4,GLRX5,SKA3,MORC3,GUCD1,NUSAP1,NLRP12,UBXN6,PECAM1,RGS10,FAM104A,TRIM10,PHOSPHO1,DEFA3,YBX1,ICAM3,BEND2,EMC3,YOD1,FCER1A,FCN1,RPS15A,CFP,RGS18,HBQ1,FGFBP2,VCAN,PIM1,EEF1A1,CYBB,ANK1,NHSL2,RAB2B,AP1S2,FAXDC2,ITK,SESN3,CD3D,KAT2B,CD8B,S1PR4,BCL2L1,MEF2B,MMRN1,GIMAP1,VRK1,USP12,SPECC1,F13A1,SPTA1,SPTB,BTLA,GRAP,SAMD3,CCR4,GNG11,PARPBP,VNN2,PTPRC,CX3CR1,ANKRD44,KIF14,CD247,RPL9,SIAH2,EOMES,TBC1D10C,LCK,RPS11,S1PR5,LYZ,HBB,PTGDR,RNF182,RIOK3,CD244,ODC1,GZMM,GNLY,HAGH,KLRF1,CR1L,TXK,OAZ1,PF4V1,FCRL6,DCUN1D1,KIF15,ZAP70,RPL35A,YBX3,RPS12,NPRL3,FOXO3,RHAG,DOCK11,ATM,KLRD1,CDKN3,C2ORF88,CD28,AKAP7,GPX1,TLR1,NINJ2,RPIA,PRDX6,PCMTD1,TLR6,MICAL2,TNS1,PRF1,C5AR2,BPGM,LRRK2,TMEM71,CCL5,AOAH,CD33,FCRL3,ETS1,SH2D1A,PYHIN1,SLAMF6,ITGB2,CMTM2,TBCEL,TMSB4X,ANXA6,PDE3B,CCR3,OSBP2,FGL2,GZMA,LRRC25,TCL1A,XK,RPS27,RPL18A,FGR,GPR141,AGTPBP1,TCP11L2,CD48,LTB,PSMF1,THEMIS,KCNA3,PICALM,TXNDC16,OST4,TIGIT,PTAFR,MYO1G,MPP6,AC

						SL6,JAZF1,ABCG2,LRRC8C,FOXO4,BSG,RPS2,RBL1,RPS28,CCDC7,ALOX5,P2RY13,AIDA,LY86,CHPT1,MME,PTPN4,SELPLG,RPL30,C9ORF78,RPS3A,VIM,CD93,IL10RA,GCA,STAT4,DUSP6,IPCEF1,MS4A6A,WDR45,RHBDD1,RAB39B,SIGLEC10,TMEM170B,FTL,SULT1B1,CD226,CD1D,TNFSF4,RNF11,SORL1,LRRN3,FKBP8,LEF1,CORO1A,TAL1,CEP57L1,CDC34,CENPI,CENPH,IKZF1,ABCC4,XPO7,DPM2,ICAM2,ATP8A1,CD84,CD8A,STIL,RPS13,CDYL,SIGLEC9,TLR4,RBP7,FLNA,HK3,RPL27A,CDC27,RPL7,RASSF2,CCR7,DPP4,NLRC4,ITM2A,NPAT,PLCL2,RPL37,ITGB3,RASGRP1,MBNL1,FYN,CENPK,TLR2,GSPT1,DOCK2,CSF1R,PRKCB,CAMK4,LGALS1,PLXDC2,DLGAP5,PPM1A,CLEC2D,MAF1,TESPA1,CD40LG,SCML4,ASCC2,CXCL5,HACD1,MS4A7,USP15,DMTN,CD27,RPS23,C19ORF38,CD36,NKG7,LYST,FAM78A,NRROS,PINK1,DSC3,MGAM,RNF125,CA2,CDK8,TRABD2A,MAPK1,EVI2A,TGFBI,GIMAP7,KLRC2,CLEC1B,POC1B,RNF10,RPL6,CD300C,APLF,DENND4A,GRAP2,CR1,PPT1,ITGB7,TGFBR2,PDE5A,IL27RA,CD300E,FCGR2A,OGT,TFRC,DNA2,CD53,RPL7A,PRKACB,PADI4,RPS7,TNFRSF10C,C16ORF54,CTSE,RPL10,LTA4H,LILRB2,PCGF5,PLXNC1,PTPRA,MEMO1,CD5,AKT3
			Down regulated genes			
GO:0032501	BP	multicellular organismal process	3.09E-10	9.510489754	228	NOX4,SOCS1,MYOCD,RIMS2,BEND6,PEAR1,SPRR3,COL5A1,FLG,OPRD1,DCLK2,SPRR2D,CLCN1,FSTL3,FJX1,NTRK3,TEK,ECM1,ISX,NANOS3,CXCL10,SPRR2A,SPRR2E,KRT78,VSTM2L,KLF15,RASGRF1,RBFOX1,KRT82,GABRG3,DDC,FRZB,TFAP2B,NFKBIL1,SLC39A5,GPC6,ACTN2,ROPN1B,SERPINB12,NLRP5,TBX22,SPATA31D1,PAX1,C6,APOA4,L3MBTL1,FABP1,ACTA2,CRP,DCX,BMI1,GRIA1,RHOJ,WNT7A,IL17F,SPATA31A1,UBD,CD34,TAL2,TPPP2,STATH,KRT13,ILDR2,SLC24A2,NPAS4,IL12RB2,BCL3,SPRED3,CATSPER4,GABRQ,SERPINA5,SDK2,ASTN1,CARD10,HSF2,KLK8,OR2H1,RBP3,GAP43,GABRB2,HTR1D,TSLP,SERPINB7,SPRR1B,FXYD4,KCNJ11,MYOD1,PADI6,KLHL1,ADGRF5,CCL2,TMPRSS11E,FAM9A,KRT35,SCT,PRLHR,ACTG2,PPFIA2,GDI1,F10,TGM3,SMR3B,SLC38A3,SHOX,PSG5,CPNE9,GDA,TMEM100,GFRAL,KRT38,CHAC1,APLNR,STC1,ASB4,SCEL,OCSTAMP,DAND5,CSMD3,NOVA1,LHFPL5,POSTN,OC90,S100A7,SPRR2B,OR51E2,KRT36,SLC6A4,TMEFF2,PAX4,C

						RYBA2,MC2R,MYOZ1,LMX1A,SAA1,BCL6B,ABCG8,SLC17A7,IL17A,SPINK5,DOK5,SLC6A17,CNN1,HABP2,DCLK1,CNTN6,SPATA31E1,PTCH1,GRM8,RPE65,IL1RAPL1,CRMP1,P2RX6,NMUR2,RTP3,FZD9,HAPLN2,SOHLH1,PRELP,KRT39,SMOC2,SEMG2,PCK1,OR56B4,ZFP42,OR51E1,CALCR,LACRT,MYBPC1,GABRG2,MYL10,KRT33B,CABP2,HOXC8,AHSG,EPHA5,NDRG4,GCM2,ANHX,SMPX,GABRG1,KRT83,PNLIP,WNT8A,ZNF536,PSG4,PCDHB3,MYH1,CPLX4,ST8SIA2,SFTPA2,DLL4,PLA2G2D,EMCN,IGFN1,SLC2A2,FAIM2,SLCO1C1,IL36RN,PASD1,MIP,CACNG2,TFAP2D,LHX9,SLC6A3,IL20RA,TNFRSF11B,DSG1,CNTN5,OR1J1,HRG,GALNTL5,AGBL4,SLITRK3,PDYN,NANOG,PGR,MFAP5,SMO,CATSPERD,PCDHA6,CHIA,FGF4,IL1A,UPK2,TDGF1,OTC,HAMP,CCBE1
GO:0048856	BP	anatomical structure development	1.49378E-05	4.825714082	172	NOX4,SOCS1,MYOCD,RIMS2,BEND6,SPRR3,COL5A1,FLG,DCLK2,SPRR2D,FSTL3,FJX1,NTRK3,TEK,ECM1,ISX,RHCG,NANOS3,CXCL10,SPRR2A,CXCL9,SPRR2E,KRT78,VSTM2L,KLF15,RASGRF1,RBFOX1,KRT82,DDC,FRZB,TFAP2B,SLC39A5,GPC6,ACTN2,ROPN1B,SERPINB12,NLRP5,TBX22,PAX1,C6,L3MBTL1,ACTA2,DCX,BMI1,RHOJ,WNT7A,IL17F,UBD,CD34,TAL2,STATH,KRT13,ILDR2,NPAS4,BCL3,SPRED3,CATSPER4,SERPINA5,SDK2,ASTN1,CARD10,KLK8,GAP43,GABRB2,SERPINB7,SPRR1B,MYOD1,PADI6,KLHL1,ADGRF5,CCL2,FAM9A,KRT35,SCT,ACTG2,PPFIA2,GDI1,TGM3,SLC38A3,SHOX,CPNE9,GDA,TMEM100,GFRAL,KRT38,CHAC1,APLNR,STC1,ASB4,SCEL,OCSTAMP,DAND5,CSMD3,LHFPL5,POSTN,OC90,S100A7,EMP1,SPRR2B,KRT36,SLC6A4,TMEFF2,PAX4,CRYBA2,MC2R,MYOZ1,LMX1A,SLC17A7,IL17A,SPINK5,DOK5,SLC6A17,DCLK1,CNTN6,PTCH1,RPE65,IL1RAPL1,CRMP1,NMUR2,FZD9,HAPLN2,SOHLH1,PRELP,KRT39,SMOC2,SEMG2,PCK1,ZFP42,CALCR,GABRG2,KRT33B,HOXC8,AHSG,EPHA5,NDRG4,GCM2,ANHX,KRT83,WNT8A,RXRG,ZNF536,PCDHB3,ST8SIA2,DLL4,PLA2G2D,EMCN,IGFN1,FAIM2,TFAP2D,LHX9,SLC6A3,TNFRSF11B,DSG1,CNTN5,HRG,GALNTL5,AGBL4,CA9,SLITRK3,NANOG,PGR,MFAP5,SMO,CATSPERD,PCDHA6,FGF4,IL1A,UPK2,TDGF1,OTC,HAMP,CCBE1
GO:0071944	CC	cell periphery	1.20E-07	6.919036824	183	NOX4,RIMS2,PEAR1,SPRR3,COL5A1,FLG,OPRD1,SPRR2D,CLCN1,NTRK3,TMPRSS11B,TEK,EC

						M1,RHCG,CXCL10,SPRR2A,CXCL9,SPRR2E,VSTM2L,RASGRF1,SLCO1B1,CEACAM7,GABRG3,SLC39A5,GPC6,ACTN2,SERPINB12,NLRP5,C6,APOA4,L3MBTL1,SLC17A4,TMPRSS11F,FABP1,GRIA1,SLC22A11,RHOJ,WNT7A,CAMKV,TMEM130,CNTNAP4,CD34,MUC7,CSMD2,SLC6A15,SLC24A2,IL12RB2,BCL3,CALB2,SPRED3,CATSPER4,GABRQ,SERPINA5,SDK2,SLC2A7,ASTN1,SNTG1,OR2H1,C8A,RBP3,GAP43,SLC10A2,GABRB2,HTR1D,SPRR1B,COL6A5,FXYD4,ANKS4B,KCNJ11,ADGRF5,TMPRSS11E,C8B,KIRREL2,PRLHR,ACTG2,KCNJ6,GRIA2,TPSAB1,F10,TGM3,ZP4,SLC38A3,CPNE9,DCDC2C,TMEM100,GFRAL,APLNR,STC1,SCEL,CSMD3,SERPINA12,LHFPL5,POSTN,MUC21,OC90,S100A7,EMP1,SPRR2B,OR51E2,SLC6A4,TMEFF2,MC2R,ATP1B4,ABCG8,SLC17A7,UNC93A,IL17A,SPINK5,SLC6A17,SLC17A2,FCRL4,DCLK1,CNTN6,PTCH1,GRM8,RPE65,IL1RAPL1,P2RX6,ADGRG7,NMUR2,FZD9,HAPLN2,PRELP,SMOC2,TECTB,OR56B4,OR51E1,HTR1F,RTBDN,CALCR,GABRG2,PCDHA9,MMP27,CABP2,CDH16,SLC7A14,AHSG,SIGLECL1,EPHA5,NDRG4,GABRG1,GPR176,WNT8A,CLCA1,SNAP91,PCDHB3,CPLX4,DLL4,HCAR1,EMCN,ABCA8,SLC2A2,RASL12,FAIM2,SLC39A2,CADM3,SLCO1C1,MIP,CACNG2,SLC6A3,IL20RA,TNFRSF11B,DSG1,FBP2,RIMS4,CNTN5,OR1J1,HRG,SLC19A3,CA9,SLITRK3,PDYN,LAMP3,MFAP5,SMO,CATSPERD,PCDHA6,UPK2,TDGF1,LY6G6C,HAMP,CCBE1,ITGBL1
GO:0005576	CC	extracellular region	2.73857E-05	4.562476942	135	RIMS2,RNASE7,SPRR3,COL5A1,FSTL3,FJX1,TMPRSS11B,TEK,ECM1,GCG,RHCG,CXCL10,CXCL9,CXCL11,KRT78,VSTM2L,CRNN,CEACAM7,DDC,FRZB,PRSS35,SLC39A5,GPC6,ACTN2,SERPINB12,C6,IL36A,APOA4,TMPRSS11F,FABP1,ACTA2,CRP,GRIA1,SLC22A11,RHOJ,WNT7A,IL17F,KPRP,CD34,MUC7,STATH,KRT13,SERPINA5,FETUB,KLK8,C8A,RBP3,GABRB2,TSLP,SERPINB7,COL6A5,RNASE13,C1QTNF2,GPX6,CCL2,TMPRSS11E,C8B,KRT35,SCT,ACTG2,A2ML1,PPFIA2,TPSAB1,DEFB121,F10,TGM3,SMR3B,ZP4,PSG5,CPNE9,KRT38,STC1,SCEL,DAND5,SERPINA12,POSTN,OC90,S100A7,KRT36,TMEFF2,GALP,PGLYRP4,DEFB132,SAA1,SAA2,IL17A,SPINK5,PAMR1,HABP2,IGFL1,CES5A,PRR27,HAPLN2,PRELP,SMOC2,SEMG2,PCK1,TECTB,RTBDN,LACRT,KRT33B,CDH16,MSMB,AHSG,KRT83,PNLIP,WNT8A,CLCA1,PSG4,SFTPA

						2,PLA2G2D,CXCL2,EMCN,IL36RN,CST5,TNFRSF11B,FBP2,CNTN5,HRG,CRTAC1,SERPINA9,PDYN,CFHR5,MFAP5,SMO,PCDHA6,CHIA,FGF4,IL1A,UPK2,TDGF1,LY6G6C,HAMP,CCBE1,ITGBL1
GO:0005215	MF	transporter activity	0.00243328	2.613807854	46	CLCN1,RHCG,SLCO1B1,SLC18A1,GABRG3,SLC39A5,APOA4,SLC17A4,FABP1,GRIA1,SLC22A11,SLC6A15,SLC24A2,CATSPER4,GABRQ,SLC2A7,SLC10A2,GABRB2,FXYD4,KCNJ11,KCNJ6,GRIA2,SLC38A3,SLC6A4,ATP1B4,ABCG8,SLC17A7,SLC6A17,SLC17A2,SLC15A5,SLC22A10,P2RX6,NMUR2,RTBDN,GABRG2,SLC7A14,GABRG1,CLCA1,ABCA8,SLC2A2,SLC39A2,SLCO1C1,MIP,CACNG2,SLC6A3,SLC19A3
GO:0048018	MF	receptor ligand activity	0.003433187	2.464302482	24	GCG,CXCL10,CXCL9,CXCL11,IL36A,WNT7A,IL17F,TSLP,CCL2,SCT,STC1,DAND5,GALP,IL17A,LACRT,WNT8A,CXCL2,IL36RN,TNFRSF11B,PDYN,FGF4,IL1A,TDGF1,HAMP

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

Pathway ID	Pathway Name	Adjusted p value	Negative log10 of adjusted p value	Gene Count	Gene
		Up regulated genes			
REAC:R-HSA-168256	Immune System	2.64E-16	15.57769494	124	UBA52,CA1,IL7R,FBXO7,KLRB1,S1PR1,MKRN1,KRT1,UBB,PPBP,TLR8,FOLR3,GLIPR1,TRAT1,CCR2,CLEC12A,KLRG1,PECAM1,TRIM10,DEFA3,ICAM3,FCER1A,FCN1,CFP,LILRA1,PIM1,EEF1A1,CYBB,AP1S2,TUBB1,ITK,CD3D,CD8B,BCL2L1,F13A1,BTLA,PTPRC,SIAH2,TBC1D10C,LCK,LYZ,HBB,RNF182,GZMM,GNLY,KLRF1,TXK,KIF15,LILRA2,ZAP70,FOXO3,KLRD1,CD28,TLR1,PRDX6,TLR6,ADGRE3,C5AR2,CCL5,CD33,SH2D1A,SLAMF6,ITGB2,FGL2,FGR,LTB,PSMF1,PTAFR,ALOX5,LY86,MME,PTPN4,VIM,CD93,IL10RA,GCA,STAT4,DUSP6,SIGLEC10,FTL,CD96,CD226,CD1D,TNFSF4,CDC34,ICAM2,ATP8A1,CD8A,SIGLEC9,TLR4,FLNA,HK3,CPPED1,CDC27,NLRC4,RASGRP1,FYN,TLR2,DOCK2,CSF1R,PRKCB,CLEC2D,CD40LG,FCGR3B,CD27,CD36,MGAM,RNF125,MAPK1,KLRC2,CD300C,GRAP2,CR1,ITGB7,IL27RA,CD300E,FCGR2A,RASGRP2,CD53,PRKACB,CTSE,LTA4H,LILRB2,AKT3
REAC:R-HSA-156902	Peptide chain elongation	8.24E-16	15.0843032	25	UBA52,RPL21,RPL39,RPS15A,EEF1A1,RPL9,RPS11,RPL35A,RPS12,RPS27,RPL18A,RPS2,RPS28,RPL30,RPS3A,RPS29,RPS13,RPL27A,RPL7,RPL37,RPS23,RPL6,RPL7A,RPS7,RPL10

REAC:R-HSA-1280218	Adaptive Immune System	2.11E-10	9.675166881	59	UBA52,FBXO7,KLRB1,MKRN1,UBB,TRAT1,KLRG1,ICAM3,LILRA1,CYBB,AP1S2,TUBB1,ITK,CD3D,CD8B,BTLA,PTPRC,SIAH2,LCK,RNF182,KLRF1,KIF15,LILRA2,ZAP70,KLRD1,CD28,TLR1,TLR6,CD33,SH2D1A,SLAMF6,ITGB2,PSMF1,SIGLEC10,CD96,CD226,CD1D,CDC34,ICAM2,CD8A,SIGLEC9,TLR4,CDC27,RASGRP1,FYN,TLR2,PRKCB,CLEC2D,CD40LG,CD36,CD300C,GRAP2,ITGB7,CD300E,RASGRP2,PRKACB,CTSE,LILRB2,AKT3
REAC:R-HSA-6798695	Neutrophil degranulation	5.18E-09	8.285894675	41	KRT1,PPBP,FOLR3,GLIPR1,CLEC12A,PECAM1,FCN1,CFP,EEF1A1,CYBB,PTPRC,TBC1D10C,LYZ,HBB,PRDX6,ADGRE3,CD33,ITGB2,FGL2,FGR,PTAFR,ALOX5,MME,CD93,GCA,FTL,ATP8A1,SIGLEC9,HK3,CPPED1,TLR2,DOCK2,FCGR3B,CD36,MGAM,MAPK1,CR1,FCGR2A,CD53,LTA4H,LILRB2
REAC:R-HSA-1266738	Developmental Biology	0.017303809	1.761858284	49	UBA52,RPL21,KRT1,UBB,RPL39,RPS15A,ANK1,TUBB1,KAT2B,MEF2B,SPTA1,SPTB,PTPRC,RPL9,SIAH2,RPS11,RPL35A,RPS12,FOXO3,RPS27,RPL18A,PSMF1,RPS2,RPS28,RPL30,RPS3A,LEF1,RPS29,TAL1,RPS13,RPL27A,RPL7,RPL37,ITGB3,FYN,GSPT1,RPS23,CD36,DSC3,CDK8,MAPK1,RPL6,RPL7A,PRKACB,RPS7,RPL10,PLXNC1,PTPRA,AKT3
REAC:R-HSA-1280215	Cytokine Signaling in Immune system	0.018629985	1.729787493	34	UBA52,CA1,IL7R,S1PR1,UBB,CCR2,TRIM10,PIM1,BCL2L1,F13A1,LCK,FOXO3,CCL5,ITGB2,LTB,PSMF1,PTAFR,ALOX5,PTPN4,VIM,IL10RA,STAT4,DUSP6,TNFSF4,FLNA,FYN,CSF1R,CD40LG,CD27,CD36,MAPK1,GRAP2,IL27RA,AKT3
Down regulated genes					
REAC:R-HSA-6809371	Formation of the cornified envelope	6.56E-09	8.182861425	19	SPRR3,FLG,SPRR2D,SPRR2A,SPRR2E,KRT78,KRT82,KRT13,KLK8,SPRR1B,KRT35,KRT38,SPRR2B,KRT36,SPINK5,KRT39,KRT33B,KRT83,DSG1
REAC:R-HSA-500792	GPCR ligand binding	0.004336498	2.362860876	24	OPRD1,GCG,CXCL10,CXCL9,CXCL11,WNT7A,HTR1D,CCL2,SCT,PRLHR,APLNR,MC2R,SAA1,PTCH1,GRM8,NMUR2,FZD9,HTR1F,CALCR,WNT8A,HCAR1,CXCL2,PDYN,SMO
REAC:R-HSA-1266738	Developmental Biology	0.036992565	1.431885558	39	SPRR3,COL5A1,FLG,SPRR2D,SPRR2A,SPRR2E,KRT78,KRT82,DCX,KRT13,KLK8,GAP43,SPRR1B,COL6A5,MYOD1,KRT35,KRT38,ONECUT3,DAND5,SPRR2B,KRT36,PAX4,TUBA3C,SPINK5,DOK5,CNTN6,CRMP1,KRT39,PCK1,KRT33B,EPHA5,KRT83,ST8SIA2,SLC2A2,CACNG2,LHX9,DSG1,NANOG,TDGF1
REAC:R-HSA-112316	Neuronal System	0.036992565	1.431885558	19	NTRK3,RASGRF1,GABRG3,ACTN2,GRIA1,GABRQ,GABRB2,KCNJ11,KCNJ6,GRIA2,PPFIA2,SLC6A4,TUBA3C,SLC17A7,IL1RAPL1,GABRG2,CACNG2,SLC6A3,SL

					ITRK3
REAC:R-HSA-425407	SLC-mediated transmembrane transport	0.036992565	1.431885558	14	RHCG,SLCO1B1,SLC18A1,SLC39A5,SLC22A11,SLC6A15,SLC24A2,SLC2A7,SLC38A3,SLC17A7,SLC2A2,SLC39A2,SLCO1C1,SLC6A3
REAC:R-HSA-112315	Transmission across Chemical Synapses	0.036992565	1.431885558	15	RASGRF1,GABRG3,ACTN2,GRIA1,GABRQ,GABRB2,KCNJ6,GRIA2,PPFIA2,SLC6A4,TUBA3C,SLC17A7,GABRG2,CACNG2,SLC6A3

Table 4 Topology table for up and down regulated genes.

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	RPL10	279	0.096784	19125450	0.318023
Up	FYN	200	0.092588	10630456	0.325961
Up	FLNA	200	0.095159	17487266	0.328553
Up	EEF1A1	160	0.075128	12371266	0.329877
Up	UBA52	159	0.074301	13364056	0.331926
Up	VIM	157	0.078983	13722248	0.322656
Up	MAPK1	147	0.066504	10687126	0.322086
Up	RPS2	130	0.024864	3664136	0.310438
Up	LRRK2	122	0.043741	8281608	0.318503
Up	ATM	119	0.062868	6983920	0.320438
Up	SNCA	113	0.053554	6954282	0.325247
Up	RPL6	112	0.019704	3467368	0.301814
Up	YBX1	107	0.037384	5706018	0.324012
Up	RPS3A	105	0.015436	2956094	0.311524
Up	KAT2B	94	0.032211	6306600	0.296897
Up	RPL18A	83	0.010227	1715822	0.305378
Up	BSG	83	0.036303	3040074	0.28726
Up	RPL7	80	0.005872	1577768	0.298555
Up	RPS13	79	0.004273	1017884	0.295453
Up	USP15	79	0.030614	3729172	0.29985
Up	RPS11	78	0.010604	1650764	0.304867
Up	RPL7A	78	0.005853	1517638	0.303988
Up	IKZF1	75	0.026481	3588864	0.291648
Up	RPS15A	75	0.005231	1021176	0.287384
Up	CDK8	75	0.026126	4405286	0.269531
Up	STIL	75	0.023928	4661980	0.277305
Up	LCK	74	0.018809	2455766	0.302795
Up	RPS23	74	0.006443	1292032	0.304242
Up	GRAP2	71	0.026428	3749000	0.300345
Up	CEP57L1	70	0.022709	2905352	0.27947
Up	MME	68	0.024081	2324348	0.288334
Up	RPL30	68	0.006923	1111494	0.298111
Up	RPL21	66	0.00284	650016	0.294131
Up	RPS7	65	0.00645	1330956	0.307651
Up	CDC27	62	0.021352	1976848	0.285095
Up	BCL2L1	62	0.021338	3397156	0.287034
Up	RPS12	54	0.001812	438388	0.293485
Up	TGFBR2	53	0.020172	3559042	0.275173
Up	GATA1	51	0.016923	2109708	0.285704
Up	RNF11	51	0.014931	1589406	0.291967
Up	FOXO3	47	0.018032	2813620	0.301361
Up	UBB	47	0.013355	2671330	0.282364
Up	RPL27A	47	0.003912	689062	0.286787
Up	ASCC2	47	0.01708	2386158	0.274213
Up	FBXO7	45	0.013386	1808908	0.270769
Up	SIAH2	44	0.011729	1068008	0.281511
Up	OGT	43	0.015274	1629520	0.260646
Up	PRKCB	42	0.009629	1847798	0.276788
Up	P2RY12	41	0.016474	2515352	0.219419
Up	PSMF1	40	0.010448	1189298	0.269712
Up	FKBP8	39	0.011985	1434236	0.277478
Up	PICALM	39	0.007744	1262108	0.286091
Up	KIF14	39	0.011628	2432982	0.250343

Up	PRKACB	38	0.012579	1851874	0.271447
Up	ETS1	37	0.009517	1200910	0.289375
Up	TFRC	34	0.011083	2862212	0.28031
Up	TAL1	34	0.008906	1158012	0.278345
Up	PIM1	33	0.008699	1321210	0.277133
Up	PPM1A	33	0.011297	1552082	0.291606
Up	ZAP70	32	0.005533	789428	0.272036
Up	LGALS1	32	0.009468	2150804	0.273409
Up	MPP1	32	0.009984	1552246	0.262885
Up	RBL1	31	0.008082	1028460	0.258829
Up	RPS28	31	0.003095	901410	0.264115
Up	YBX3	31	0.008078	854008	0.295301
Up	RPS27	31	0.003899	761430	0.282185
Up	PINK1	30	0.007808	914072	0.275381
Up	TLR4	29	0.009118	998880	0.260477
Up	GPR183	29	0.012007	3097810	0.224732
Up	TCL1A	29	0.007419	1074920	0.278519
Up	SKA3	29	0.009573	1355572	0.238149
Up	CDC34	28	0.006821	743818	0.280801
Up	APLF	28	0.009394	1609564	0.253975
Up	TMOD1	27	0.00461	570902	0.267463
Up	SH2D1A	26	0.0074	650010	0.271741
Up	CD27	26	0.012454	1603950	0.249875
Up	RASSF2	26	0.00651	1235238	0.25992
Up	CORO1A	25	0.008358	1070480	0.262747
Up	POC1B	25	0.007528	940030	0.249393
Up	AP1S2	25	0.007735	1649726	0.240175
Up	BNIP3L	24	0.009238	768204	0.25522
Up	CD244	24	0.007225	617130	0.262318
Up	RNF10	24	0.005112	623918	0.272647
Up	LYST	24	0.006723	1170054	0.255872
Up	CCL5	23	0.004869	863688	0.235768
Up	RPS29	23	0.002796	530852	0.261462
Up	DCUN1D1	23	0.005491	677134	0.260884
Up	FTL	22	0.004661	605380	0.252456
Up	ITGB3	22	0.005653	585272	0.266822
Up	PCGF5	22	0.005033	1200316	0.26311
Up	CD247	21	0.003508	379662	0.272851
Up	ITK	21	0.002652	447304	0.28161
Up	PTPN4	21	0.00507	683112	0.287013
Up	DOCK2	21	0.002931	536892	0.257631
Up	XPO7	21	0.007831	669850	0.261975
Up	CLEC12A	21	0.008995	1301280	0.20401
Up	RNF125	21	0.002956	855292	0.247622
Up	LEF1	21	0.005011	1325288	0.251632
Up	KRT1	20	0.00459	1037136	0.283081
Up	PRDX6	20	0.004595	891646	0.269531
Up	HBB	20	0.006745	1415624	0.219707
Up	CENPH	20	0.00535	829176	0.222487
Up	FOXO4	19	0.004428	649012	0.272499
Up	SPTA1	19	0.005092	1612130	0.238901
Up	ITGB2	19	0.005364	904352	0.269803
Up	KIF15	19	0.005836	485776	0.263889
Up	SPECC1	19	0.001081	211202	0.273652
Up	RPIA	19	0.004939	731008	0.239272
Up	OAZ1	19	0.005448	729430	0.255643
Up	RIOK3	18	0.003593	607166	0.250484
Up	DPP4	3	1.81E-04	30002	0.195924
Up	CSF1R	3	2.78E-04	90550	0.259886
Up	TRAT1	3	1.40E-05	9952	0.254782
Up	MMRN1	3	9.42E-05	16258	0.201772
Up	CD36	2	2.42E-04	40714	0.247378
Up	CD28	2	1.69E-05	5896	0.239486
Up	THEMIS	2	0	0	0.236869
Up	PTPRC	2	5.62E-05	20510	0.240839
Up	CD48	2	5.52E-05	12432	0.238276
Up	FECH	2	3.03E-04	35800	0.250735
Up	CCR3	2	1.81E-05	5664	0.193177
Up	VCAN	2	1.81E-05	5664	0.193177
Up	TMSB4X	2	1.10E-04	8416	0.227152

Up	C2orf88	2	3.92E-04	57348	0.222376
Up	MYO1G	2	2.01E-04	86162	0.247898
Up	CD5	2	1.40E-05	9952	0.253911
Up	TLR1	1	0	0	0.20666
Up	RAB39B	1	0	0	0.183638
Up	SLAMF6	1	0	0	0.213688
Up	CD84	1	0	0	0.213688
Up	GAB3	1	0	0	0.230986
Up	OSBP2	1	0	0	0.183908
Up	ANK1	1	0	0	0.192842
Up	SPTB	1	0	0	0.192842
Up	FCGR2A	1	0	0	0.148498
Up	MPP6	1	0	0	0.201579
Up	PTPRA	1	0	0	0.245845
Up	FCGR2C	1	0	0	0.245845
Up	IL7R	1	0	0	0.245845
Up	ICAM2	1	0	0	0.214718
Up	ABCG2	1	0	0	0.217008
Up	CCR2	1	0	0	0.176756
Up	CCR4	1	0	0	0.190796
Up	HEMGN	1	0	0	0.222228
Up	ITGB7	1	0	0	0.247316
Up	AGTPBP1	1	0	0	0.211033
Up	DUSP6	1	0	0	0.243634
Up	E2F2	1	0	0	0.205621
Up	NCOA4	1	0	0	0.191151
Up	AKT3	1	0	0	0.217857
Up	KLF1	1	0	0	0.249223
Up	P2RY8	1	0	0	0.24269
Up	LYL1	1	0	0	0.21775
Up	AKAP7	1	0	0	0.213506
Up	FGR	1	0	0	0.245439
Up	ODC1	1	0	0	0.203606
Up	POLE2	1	0	0	0.248066
Up	GYPC	1	0	0	0.208173
Up	HACD1	1	0	0	0.171091
Up	ALOX5	1	0	0	0.218438
Up	STAT4	1	0	0	0.167537
Up	CENPK	1	0	0	0.182004
Up	GCA	1	0	0	0.206384
Up	ADIPOR1	1	0	0	0.187547
Up	PYHIN1	1	0	0	0.183386
Down	BMI1	230	0.102406	17070736	0.330721
Down	ACTN2	69	0.027262	3272210	0.283121
Down	CRMP1	67	0.021828	2532308	0.27819
Down	TRIM42	62	0.016514	2831788	0.270148
Down	PTCH1	59	0.02905	5713468	0.256576
Down	KRT13	51	0.015993	1567378	0.279062
Down	KRT38	46	0.00957	1443654	0.253959
Down	MYOD1	44	0.012184	1507906	0.279802
Down	HSF2	34	0.008921	1026102	0.264341
Down	GDI1	33	0.010623	3149808	0.242177
Down	DCX	29	0.008783	1120900	0.275136
Down	SOCS1	28	0.009666	1232274	0.281314
Down	C1QTNF2	27	0.014256	1573062	0.247042
Down	RNASEH2A	26	0.010097	1308858	0.225339
Down	RBFOX1	26	0.006411	694610	0.260038
Down	GRIA2	24	0.009704	1856074	0.23631
Down	BCL3	22	0.004709	633890	0.283442
Down	TEX35	21	0.006515	1671680	0.217999
Down	CRCT1	20	0.005407	589416	0.277343
Down	NFKBIL1	19	0.00564	715326	0.230827
Down	L3MBTL1	19	0.004845	974986	0.252456
Down	NAT2	18	0.004878	477380	0.26469
Down	RXRG	18	0.004253	912032	0.226959
Down	CCL2	17	0.00367	514314	0.214695
Down	S100A7	17	0.005738	1063496	0.258445
Down	TRIM55	17	0.001944	622240	0.242148
Down	RHOJ	17	0.004742	1048516	0.227978
Down	ATP1B4	17	0.009467	2094472	0.191598

Down	ACTA2	16	0.004866	595656	0.24402
Down	FAM9A	16	0.003775	904348	0.238107
Down	COL5A1	15	0.005552	497794	0.243161
Down	DOK5	14	0.004191	450170	0.24896
Down	ECM1	13	0.003757	491098	0.2314
Down	KRT33B	13	0.002769	292912	0.251049
Down	SERPINA5	13	0.003643	727366	0.23088
Down	MYH1	13	0.003148	420694	0.253831
Down	TEK	13	0.002631	464848	0.246344
Down	BCL6B	13	9.70E-04	284416	0.232892
Down	AGR3	13	0.002131	305446	0.258612
Down	LACRT	13	0.005474	769496	0.235657
Down	NEU2	13	0.004543	791368	0.224556
Down	DCLK1	11	0.001151	199324	0.232662
Down	UBD	11	0.005561	557354	0.267284
Down	P4HA3	11	0.002476	334132	0.228498
Down	F10	10	0.003404	370848	0.197167
Down	SPRR2A	10	0.001186	230212	0.253638
Down	CNN1	10	0.001421	306466	0.225897
Down	KPRP	10	0.002336	354414	0.236771
Down	SERPINA12	10	0.002755	460954	0.207034
Down	MUC7	10	0.00381	775800	0.202618
Down	KLF15	10	0.002379	215104	0.25014
Down	CARD10	10	0.001148	259962	0.240492
Down	NDRG4	10	0.002543	535888	0.212928
Down	CRP	9	0.002991	300966	0.174388
Down	MYOZ1	9	8.57E-04	91180	0.251932
Down	OPRD1	9	0.002017	295140	0.239687
Down	GRIA1	9	0.002485	381938	0.234307
Down	MYOCD	9	3.24E-04	101768	0.255042
Down	ZNRF4	9	1.20E-04	24676	0.222118
Down	KLK8	8	0.002575	466234	0.224934
Down	SCEL	8	0.001297	228834	0.240218
Down	FLG	8	0.003624	681266	0.221823
Down	NLRP5	8	8.61E-04	97632	0.22019
Down	CXCL9	8	0.00235	391790	0.200751
Down	MAGEC1	7	0.002991	338754	0.165538
Down	AHSG	7	0.001492	265244	0.243871
Down	GAP43	7	4.07E-04	37796	0.234431
Down	NTRK3	7	0.001344	114306	0.259231
Down	NOVA1	7	0.002034	232030	0.210325
Down	IL17A	7	0.002991	676242	0.138653
Down	KIRREL2	7	0.001442	238494	0.228355
Down	FAM131C	7	0.002031	227590	0.217644
Down	RTBDN	7	0.002644	221836	0.198741
Down	RNASE7	7	7.63E-04	122422	0.205822
Down	OR51E2	7	5.15E-04	171360	0.205337
Down	C5orf60	6	4.98E-04	80870	0.214213
Down	A2ML1	6	0.002007	287508	0.183983
Down	KRT36	6	8.01E-04	152482	0.239988
Down	KRT83	6	1.95E-04	23122	0.219107
Down	GCG	6	1	12	1
Down	RIMS2	6	6.87E-04	86836	0.261684
Down	APOA4	6	0.001069	193416	0.207828
Down	AGXT	6	2.00E-04	17112	0.257582
Down	SEMG2	6	0.001772	171076	0.206394
Down	SERPINB12	6	8.72E-04	87756	0.256314
Down	PRLHR	6	9.98E-04	332596	0.160559
Down	KRT82	6	0.001594	348096	0.202813
Down	CRNN	6	0.001508	380388	0.156302
Down	SNAP91	5	1.22E-05	3072	0.206118
Down	PPFIA2	5	0.001497	222084	0.209314
Down	SERPINB7	5	2.49E-04	65308	0.214891
Down	CSMD2	5	9.14E-05	19920	0.254491
Down	CLCN1	5	0.001039	72430	0.224518
Down	RNASE13	5	0.001386	106482	0.230032
Down	PRELP	5	8.56E-04	86816	0.198181
Down	RASGRF1	5	0.00102	205892	0.213836
Down	CAMKV	5	5.04E-04	92154	0.206118
Down	LMX1A	5	5.18E-04	79796	0.23023

Down	PIGQ	5	0.001995	319740	0.204291
Down	SPINK5	5	0.001521	114058	0.189381
Down	NMUR2	5	6.62E-04	153344	0.230654
Down	CXCL11	4	4.37E-04	76278	0.20042
Down	TEX33	4	0.001496	220272	0.14507
Down	GCM2	4	6.09E-05	10256	0.21312
Down	TSKS	4	5.77E-04	65574	0.258179
Down	GABRG2	4	4.99E-04	112032	0.179679
Down	CALB2	4	5.41E-06	1700	0.206097
Down	SLC18A1	4	1	12	1
Down	MYBPC1	4	5.73E-04	90388	0.210756
Down	TGM3	4	6.30E-04	100846	0.178782
Down	ASB10	4	5.65E-04	58652	0.232865
Down	TFAP2B	4	0.001007	153402	0.203039
Down	TSLP	4	6.29E-05	17446	0.237881
Down	ABCG8	4	0.001015	145492	0.20167
Down	SLC6A15	4	5.18E-04	142272	0.191846
Down	IL12RB2	4	0.001496	135186	0.201245
Down	CNTNAP4	4	0.001496	120594	0.169085
Down	IL36A	4	0.002993	440686	0.204197
Down	ASB4	4	0.001005	105922	0.185559
Down	ZNF536	3	9.98E-04	76070	0.181666
Down	NOX4	1	0	0	0.20666
Down	CCBE1	1	0	0	0.219683
Down	RNASEH2C	1	0	0	0.183908
Down	GPC6	1	0	0	0.183503
Down	SLC6A3	1	0	0	0.245439
Down	SMO	1	0	0	0.204197
Down	MAGEC2	1	0	0	0.186007
Down	FABP1	1	0	0	0.247316
Down	SLC6A4	1	0	0	0.245439
Down	SPRR2E	1	0	0	0.206309
Down	STATH	1	0	0	0.168488
Down	PGR	1	0	0	0.228942
Down	KRT35	1	0	0	0.230694

Table 5 miRNA - target gene and TF - target gene interaction

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	MAPK1	286	hsa-mir-320a	Up	UBA52	12	SREBF1
Up	ATM	134	hsa-mir-1910-3p	Up	SNCA	11	ELK1
Up	VIM	117	hsa-mir-766-3p	Up	FYN	10	NFYA
Up	FLNA	106	hsa-mir-124-3p	Up	ATM	10	ELF5
Up	EEF1A1	96	hsa-mir-4736	Up	FLNA	10	TP53
Up	KAT2B	62	hsa-mir-1246	Up	VIM	9	POU2F2
Up	FYN	61	hsa-mir-147a	Up	YBX1	9	CEBPB
Up	YBX1	48	hsa-mir-16-5p	Up	MAPK1	9	USF2
Up	RPS2	40	hsa-mir-34a-5p	Up	RPL6	8	NR3C1
Up	SNCA	37	hsa-mir-221-3p	Up	LRRK2	8	FOXC1
Up	UBA52	32	hsa-mir-484	Up	RPL10	7	TFAP2A
Up	RPL10	31	hsa-mir-22-3p	Up	KAT2B	6	STAT1
Up	RPL6	14	hsa-mir-193b-3p	Up	RPS3A	6	HOXA5
Up	LRRK2	14	hsa-mir-3127-5p	Up	EEF1A1	4	GATA2
Up	RPS3A	11	hsa-mir-342-3p	Up	RPS2	4	IRF2
Down	BMI1	115	hsa-mir-559	Down	RBFOX1	19	EGR1
Down	GDI1	104	hsa-mir-186-3p	Down	PTCH1	18	E2F6
Down	SOCS1	62	hsa-mir-4495	Down	DCX	15	FOXL1
Down	PTCH1	52	hsa-mir-3689a-5p	Down	KRT13	12	STAT3
Down	DCX	39	hsa-mir-6842-5p	Down	HSF2	12	NFIC
Down	HSF2	38	hsa-mir-26a-5p	Down	TRIM42	11	GATA2
Down	CRMP1	29	hsa-mir-30a-5p	Down	ACTN2	11	USF1
Down	RBFOX1	27	hsa-mir-219a-5p	Down	CRMP1	10	ZNF354C
Down	RNASEH2A	24	hsa-mir-548h-5p	Down	MYOD1	9	GATA3
Down	ACTN2	16	hsa-mir-3119	Down	RNASEH2A	8	PAX2
Down	MYOD1	8	hsa-mir-101-3p	Down	KRT38	7	HINFP
Down	TRIM42	8	hsa-mir-6867-5p	Down	GDI1	6	SOX5
Down	C1QTNF2	5	hsa-mir-520c-3p	Down	BMI1	6	SP1
Down	KRT13	5	hsa-mir-1343-3p	Down	C1QTNF2	4	PRDM1

Down	KRT38	2	hsa-mir-335-5p	Down	SOCS1	2	EN1