Identification of candidate biomarkers and pathways associated with multiple sclerosis using bioinformatics and next generation sequencing data analysis

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Abstract

Multiple sclerosis (MS) is the main reason for disability caused by autoimmunity. However, effective biomarkers for MS have not been identified. This study explored the molecular mechanisms and potential therapeutic targets for MS occurrence and progression using bioinformatics and next generation sequencing (NGS) data analysis. NGS data GSE138614, including patients with MS and 25 normal control samples, were obtained from Gene Expression Omnibus (GEO) database Differentially expressed genes (DEGs) were filtered and subjected to gene ontology (GO) and pathway enrichment analyses. Protein–protein interaction (PPI) network and module analyses were performed based on the DEGs. MiRNA-hub gene regulatory network and TF-hub gene regulatory network analysis were built by Cytoscape to predict the underlying microRNAs (miRNAs) and transcription factors (TFs) associated with hub genes. We also validated the identified hub genes via receiver operating characteristic (ROC) curve analysis. A total of 959 DEGs (479 up regulated genes and 480 down regulated genes) were detected. The GO terms and pathways of DEGs involve immune system process, developmental process, immune system and regulation of cholesterol biosynthesis by SREBP (SREBF). The network analysis revealed that hub genes include LCK, PYHIN1, SLAMF1, DOK2, TAB2, CFTR, RHOB, LMNA, EGLN3 and ERBB3 might be involved in the development of MS. The present investigation illustrates a characteristic gene profile in MS, which might contribute to the interpretation of the progression of MS and provide novel biomarkers and therapeutic targets for MS.

Keywords: multiple sclerosis; differentially expressed genes; protein–protein interaction; bioinformatics; hub genes

Introduction

Multiple sclerosis (MS) is the commonest autoimmune inflammatory disorder of CNS white matter [1]. MS is one of leading causes of disability in children's, young aged adults and middle aged adults in many developed countries [2-4] and it affects 2.3 million people worldwide with an expected increase in the number of cases in future [5]. Main features of MS include selective primary demyelination with partial preservation of axons and reactive astrocytic gliosis [6]. It might affect many other organs and cause other diseases include spasticity [7], paralysis [8], bladder, bowel and sexual dysfunction [9], psychiatric disorders [10], cardiovascular diseases [11], neurodegenerative diseases [12], spinal cord injury [13], obesity [14], diabetes mellitus [15] and hypertension [16]. Autoimmune inflammation is triggered by both genetic susceptibility [17] and environmental factors [18]. However, the etiology and symptoms of MS are complex in clinical practice, making its diagnosis challenging.

Correct early diagnosis assessment of MS is very difficult, even though much disease related genes and cellular pathways related to MS have appeared [19]. The common treatments of MS are interferons, glatiramer acetate, teriflunomide, sphingosine 1-phosphate receptor modulators, fumarates, cladribine and monoclonal antibodies [20], but there are no valid treatment tactics available to treat MS. Therefore, it is vitally important to explore potential diagnostic and prognostic biomarkers and therapeutic targets of MS.

The fast development of next generation sequencing (NGS) technology and bioinformatics analysis based on high-throughput data, provide new tactics to identify differentially expressed genes (DEGs) and discover therapeutic targets for the initiation and evolution of MS [21]. Aberrant expression of genes plays an essential role in the initiation and progression of MS, so mastering the alteration in the characteristics of critical genes promotes to comprehensively understanding of MS progression and screen related molecular markers [22]. Recently, studies identified altered expression of genes includes CLEC16A [23], KIAA0350, IL2RA, RPL5 and CD58 [24], SLC9A9 [25], IL22RA2 [26] and ANKRD55 [27] in MS. Indeed, some researchers found signaling pathways include mTOR signaling pathway [28], Keap1/Nrf2/ARE signaling pathway [29], NF-κB

signaling pathways [30], wnt signaling pathway [31] and Nogo-A/NgR signaling pathway [32] in MS.

However, the use of bioinformatics analysis method to find the relevant genes and pathways of MS has not yet been confirmed. In the current study, we downloaded NGS dataset, namely, GSE138614 [33], from the NCBI Gene Expression Omnibus (GEO) [https://www.ncbi.nlm.nih.gov/geo/] [34] database, including NGS data from 73 patients with MS and 25 normal control samples. We identified DEGs using the DESeq2 in R software. The GO term and pathway enrichment analyses were performed via g:Profiler. Subsequently, protein-protein interaction network, module, miRNA-hub gene regulatory network and TF-hub gene regulatory network analysis were conducted, and the findings were further validated by receiver operating characteristic (ROC) curve analysis. Therefore, our investigation provides a deep understanding of susceptibility genes and pathways in MS and might provide appropriate drug targets for MS therapies.

Materials and Methods

Next generation sequencing data source

GEO is a public functional genomics data repository of high throughput NGS data. The GSE138614 [33] NGS dataset generated using the GPL21697 NextSeq 550 (Homo sapiens). The GSE138614 dataset contained 73 MS samples and 25 normal control samples.

Identification of DEGs

Determining DEGs between MS and normal control samples was performed using DESeq2 package [35] in R software. The adjusted P-values (adj. P) and Benjamini and Hochberg false discovery rate were applied to strike a balance between finding statistically important genes and limiting false positives [36]. |log FC (fold change)| > 2.2 for up regulated genes, |log FC (fold change)| < -0.866 for down regulated genes and adj. P-value < 0.05 were considered statistically significant. DEGs were visualized by the “volcano” and “heatmap” by using ggplot2 and gplot packages in R software.

GO and pathway enrichment analyses of DEGs

Online tool g:Profiler (http://biit.cs.ut.ee/gprofiler/) [37] was used to perform the GO functional annotation (http://www.geneontology.org) [38] and REACTOME (https://reactome.org/) [39] pathway enrichment analyses. GO enrichment analysis is a premier bioinformatics analysis for identifying high-quality functional gene annotation based on biological process (BP), cellular component (CC) and molecular function (MF). The REACTOME is a resource of databases for the clarification of high-level features and effects of biological systems. p-value <0.05 was considered as the threshold.

Construction of the PPI network and module analysis

Information of DEGs' protein experimental interactions and prediction was obtained by Human Integrated Protein-Protein Interaction rEference (HiPPIE, http://cbdm-01.zdv.uni-mainz.de/~mschaefer/hippie/index.php) [40]. Subsequently, a specific PPI network of DEGs was constructed by cytoscape (version 3.10.1, http://www.cytoscape.org/) [41] based on the interactions retrieved from HiPPIE. To screen the hub genes that might be involved in MS, we applied the Network Analyzer plug-in, using various parameters such as node degree [42], betweenness [43], stress [44] and closeness [45]. In addition, PEWCC analysis [46] in cytoscape was used to identify the significant modules of the PPI network

Construction of the miRNA-hub gene regulatory network

miRNet database (https://www.mirnet.ca/) [47] is used to explore miRNA- hub gene interactions for the input hub genes from PPI network and assess the effect of the miRNA on the expression of the hub gene. In this investigation, the miRNAs of the hub genes were predicted from TarBase, miRTarBase, miRecords, miRanda (S mansoni only), miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR, EpimiR, starBase, TransmiR, ADmiRE and TAM 2 databases and a miRNA-hub gene regulatory network was constructed and visualized by the cytoscape software [41].

Construction of the TF-hub gene regulatory network

NetworkAnalyst (https://www.networkanalyst.ca/) [48] is used to explore TF- hub gene interactions for the input hub genes from PPI network and assess the effect of the TF on the expression of the hub gene. In this investigation, the TFs of the hub

genes were predicted from JASPER database and TF-hub gene regulatory network was constructed and visualized by the cytoscape software [41].

Receiver operating characteristic curve (ROC) analysis

ROC curve analysis, which shows indicators of accuracy such as the area under the curve (AUC), provides the fundamental principle and rationale for distinguishing between the specificity and sensitivity of diagnostic performance of hub genes. We used the pROC package in R software [49] to conduct our ROC curve analysis. Expressions of hub genes within the training and validating datasets were illustrated for assessment. When the area under the curve (AUC) exceeds 0.8, the hub gene will be regarded as good diagnostic value for MS.

Results

Identification of DEGs

NGS dataset GSE138614 was analyzed by "DESeq2" package in R with adj. P-value < 0.05, |log FC (fold change)| > 2.2 for up regulated genes and |log FC (fold change)| < -0.866 for down regulated genes as the threshold. In NGS dataset GSE138614, we isolated 959 DEGs, which contains 479 up regulated genes and 480 down regulated genes (Table 1). A volcano plot and DEG heatmap are illustrated in Fig. 1 and Fig. 2.

GO and pathway enrichment analyses of DEGs

In the GO analyses, the most enriched BP terms were associated with immune system process, response to stimulus, developmental process and multicellular organismal process (Table 2). The most enriched terms for CC were mainly associated with membrane, protein-containing complex, cellular anatomical entity and cytoplasm (Table 2). The most enriched MF terms were associated with antigen binding, signaling receptor binding, molecular function regulator activity and molecular function activator activity (Table 2). In the REACTOME pathway enrichment analysis, the DEGs were enriched in immune system, TCR signaling, regulation of cholesterol biosynthesis by SREBP (SREBF) and degradation of the extracellular matrix (Table 3).

Construction of the PPI network and module analysis

The interactions of 959 DEGs were analyzed using the HiPPIE online database to investigate the PPI network underlying MS. The network model was visualized using Cytoscape (version 3.10.1). The network contains 4247 genes and 6403 interaction pairs. The top hub genes were calculated by 4 algorithms of the Cytoscape plugin Network Analyzer (Table 4). Subsequently, the top intersecting genes analyzed according to these 4 algorithms were selected as hub genes, which included LCK, PYHIN1, SLAMF1, DOK2, TAB2, CFTR, RHOB, LMNA, EGLN3 and ERBB3. The PEWCC plug-in identified a total of two gene modules, among which module 1 having 47 nodes and 54 edges (Fig.4A) and module 2 having 28 nodes and 32 edges (Fig.4B). Genes in these modules were thought to be central to the development of MS, so we uploaded them to g:Profiler database for enrichment analysis to further clarify their biological effects. The results suggested that hub genes were primarily involved in immune system process, immune system, signaling by interleukins, Class A/1 (Rhodopsin-like receptors), developmental process, cellular anatomical entity and cytoplasm.

Construction of the miRNA-hub gene regulatory network

For the hub genes we identified from PPI network, a miRNA - hub gene regulatory network was constructed including 230 interaction pairs among the selected hub genes and 1973 miRNAs, and 8791 interactions (Fig.5). While IKZF3 was found to be regulated by 147 miRNAs (ex: hsa-mir-6794-3p); TAB2 was found to be regulated by 118 miRNAs (ex: hsa-mir-3689a-3p); C6orf141 was found to be regulated by 59 miRNAs (ex: hsa-mir-4449); SDC1 was found to be regulated by 47 miRNAs (ex: hsa-mir-146a-5p); CCR4 was found to be regulated by 45 miRNAs (ex: hsa-mir-4695-5p); RHOB was found to be regulated by 216 miRNAs (ex: hsa-mir-4651); LGALS3BP was found to be regulated by 99 miRNAs (ex: hsa-mir-548q); SFN was found to be regulated by 91 miRNAs (ex: hsa-mir-8485); CDH1 was found to be regulated by 75 miRNAs (ex: hsa-mir-195-5p); POLR2F was found to be regulated by 68 miRNAs (ex: hsa-mir-4739) (Table 5).

Construction of the TF-hub gene regulatory network

For the hub genes we identified from PPI network, a TF - hub gene regulatory network was constructed including 232 interaction pairs among the selected hub

genes and 80 TFs, and 1809 interactions (Fig.6). While LTF was found to be regulated by 15 TFs (ex: BRCA1); CD79A was found to be regulated by 10 TFs (ex: HNF4A); LCK was found to be regulated by 10 TFs (ex: NFKB1); IKZF3 was found to be regulated by 9 TFs (ex: TEAD1); TAB2 was found to be regulated by 8 TFs (ex: ELK4); MAP1LC3A was found to be regulated by 14 TFs (ex: TFAP2C); CFTR was found to be regulated by 10 TFs (ex: NR2F1); LLGL2 was found to be regulated by 8 TFs (ex: FOXO3); POLR2F was found to be regulated by 8 TFs (ex: NRF1); FOXE1 was found to be regulated by 8 TFs (ex: NFYA) (Table 5).

Receiver operating characteristic curve (ROC) analysis

Validated by ROC curves, we found 10 hub genes had high sensitivity and specificity, including LCK (AUC□=□0.931), PYHIN1 (AUC□=□0.902), SLAMF1 (AUC□=□0.912), DOK2 (AUC□=□0.933), TAB2 (AUC□=□0.916), CFTR (AUC□=□0.920), RHOB (AUC□=□0.935), LMNA (AUC□=□0.921), EGLN3 (AUC□=□0.927) and ERBB3 (AUC□=□0.925) (Fig. 7). These hub genes might be biomarkers of MS and have positive implications for early medical intervention of the disease.

Discussion

MS is a high-incidence autoimmune inflammatory and non-traumatic disabling disease, often resulting in heterogeneous array of symptoms and signs because of differential involvement of motor, sensory, visual and autonomic systems [50]. However, in most cases, the clinical results are suboptimal. Therefore, understanding the pathological changes and molecular mechanisms of MS is essential for clinical diagnosis and treatment. Efficient NGS and bioinformatics analyses help us understand the molecular mechanisms of the disease onset and advancement, which is invaluable for biomarkers and therapeutic target identification [51-52]. In our study, 959 DEGs were identified between MS patients and normal controls based on NGS dataset. IGHV4-39 [53] was closely associated with MS. PLAC8 [54] was involved in obesity. PLAC8 [54] was linked to diabetes mellitus. Known biological roles of the DEGs strengthen the reliability of our results.

GO and REACTOME pathway enrichment analyses were used to explore the molecular mechanisms of the genes involved in the occurrence and development of MS. It is well known that the pathways include immune system [55], TCR signaling [56], cytokine signaling in immune system [57], degradation of the extracellular matrix [58], extracellular matrix organization [58], metabolism of lipids [59] and metabolism [60] plays an important role only in MS. CCL18 [61], FCRL3 [62], EOMES (eomesodermin) [63], CCR2 [64], IL2RB [65], CCL4 [66], FASLG (Fas ligand) [67], CD24 [68], IKZF3 [69], CD2 [70], CD28 [71], IL7R [72], HLA-DRB5 [73], ICOS (inducible T cell costimulator) [74], CCL5 [75], CTLA4 [76], IRF4 [77], C6 [78], NCR1 [79], CHIT1 [80], CD52 [81], CD163 [82], HGF (hepatocyte growth factor) [83], DIO3 [84], SIGLEC1 [85], TTR (transthyretin) [86], IL9 [87], VEGFA (vascular endothelial growth factor A) [88], CR2 [89], ANGPTL4 [90], CHI3L1 [91], MAG (myelin associated glycoprotein) [92], CNP (2',3'-cyclic nucleotide 3' phosphodiesterase) [93], CMTM5 [94], SEMA4D [95], NGFR (nerve growth factor receptor) [96], TF (transferrin) [97], MYRF (myelin regulatory factor) [98], MOG (myelin oligodendrocyte glycoprotein) [99], ADAMTS4 [100], BMP2 [101], HTRA1 [102], PNPLA3 [103], DYSF (dysferlin) [104], NINJ2 [105], LRP2 [106], ADAMTS14 [107] and DHCR7 [108] might play an important role in regulating the occurrence and development of MS. The expression of CCL18 [109], SLAMF7 [110], GPR174 [111], CCR4 [112], POU4F2 [113]. CCR2 [114], IL2RB [115], CCL4 [116], CCL24 [117], FASLG (Fas ligand) [118], CD24 [119], TDGF1 [120], CD28 [121], IL7R [122], CYP11B1 [123], CCL5 [124], CCL3 [125], LTF (lactotransferrin) [126], GPNMB (glycoprotein nmb) [127], CD209 [128], IL2RG [129], CHIT1 [130], TAB2 [131], CD163 [132], ALOX15B [133], NMRK2 [134], HGF (hepatocyte growth factor) [135], TRPM8 [136], DIO3 [137], SIGLEC1 [138], TTR (transthyretin) [139], IL24 [140], F13A1 [141], IL9 [142], VEGFA (vascular endothelial growth factor A) [143], RASAL1 [144], ADM (adrenomedullin) [145], ANGPTL4 [146], CHI3L1 [147], LDB3 [148], CNP (2',3'-cyclic nucleotide 3' phosphodiesterase) [149], HES6 [150], CMTM5 [151], PLXNB3 [152], KLK8 [153], CDKN1C [154], INSIG1 [155], GREM1 [156], ATF3 [157], HK2 [158], MCAM (melanoma cell adhesion molecule) [159], SEMA4D [160], GLUL (glutamate-ammonia ligase) [161], S1PR5 [162], FN3K [163], MEIS1 [164], ADAMTS4 [165], BIN1 [166], BMP2 [167], LMNA (lamin A/C) [168], ERBB3 [169], DLL1 [170], THBS2 [171], GADD45B [172], MYH6

[173]. PNPLA3 [174], ACTN2 [175], MMP15 [176], SVEP1 [177], CPB2 [178], DYSF (dysferlin) [179], ADAMTSL2 [180], NINJ2 [181], LRP2 [106], PHLDA3 [182], LIPC (lipase C, hepatic type) [183], CARNS1 [184], PRODH (proline dehydrogenase 1) [185], TRPV6 [186], CNDP1 [187], DHCR7 [188], KCNE5 [189] SAA1 [190], ADSS1 [191], ACADS (acyl-CoA dehydrogenase short chain) [192], ADAP1 [193], KLK10 [194], HCN2 [195], F11 [196], RNASE1 [197], GNLY (granulysin) [198], EVA1A [199], CIRBP (cold inducible RNA binding protein) [200], EDIL3 [201], NOXA1 [202], ANGPTL2 [203], CYP2A6 [204] and CTNNA3 [205] might be associated with cardiovascular diseases progression. The abnormal expression of CCL18 [206], EOMES (eomesodermin) [207], GZMA (granzyme A) [208], HLA-DRB5 [209], GPNMB (glycoprotein nmb) [210], PRPH (peripherin) [211], HGF (hepatocyte growth factor) [212], TTR (transthyretin) [213], VEGFA (vascular endothelial growth factor A) [214], CHI3L1 [215], AATK (apoptosis associated tyrosine kinase) [216], SREBF1 [217], OLIG2 [218], ATF3 [219], NGFR (nerve growth factor receptor) [220], ADAMTS4 [221], LMNA (lamin A/C) [222], MT3 [223], DAO (D-amino acid oxidase) [224], AATK (apoptosis associated tyrosine kinase) [216] and LGALS3BP [225] might be related to the progression of amyotrophic lateral sclerosis. SLAMF7 [226], GPR174 [227], FCRL3 [228], SLAMF6 [229], EOMES (eomesodermin) [230], CCR4 [231], CCR2 [232], CD48 [233], CD3E [234], CCL26 [235], CCL4 [236], SLAMF1 [237], CD24 [238], IKZF3 [239], CD2 [240], CD28 [241], IL7R [242], FCGR2B [243], UBASH3A [244], CD1C [245], ICOS (inducible T cell costimulator) [246], CD3G [247], CCL3 [248], LTF (lactotransferrin) [249], GPNMB (glycoprotein nmb) [250], CTLA4 [251], IRF4 [252], TNFRSF9 [253], FCRL5 [254], LAIR2 [255], TAB2 [256], CD52 [257], CD163 [258], MSR1 [259], HGF (hepatocyte growth factor) [260], SIGLEC1 [261], TTR (transthyretin) [262], IL24 [263], IL9 [264], CHI3L1 [265], CDH1 [266], OLIG2 [267], NKX6-2 [268]. HK2 [269], PNPLA3 [270], CPB2 [271], SEMA4C [272], LRP2 [273], SLC5A11 [274], F11 [275], ANGPTL2 [276] and CYP2A6 [277] genes might be related to the pathophysiology of autoimmune disease. A recent study revealed that SLAMF7 [278], FCRL3 [279], CCR4 [280], GZMA (granzyme A) [281], CCR2 [282], CD48 [283], CD3E [284], CCL4 [285], FASLG (Fas ligand) [286], SLAMF1 [287], CD28 [288], IL7R [289], UBASH3A [290], CD3D [291], ICOS (inducible T cell costimulator) [292], CCL5 [293], CCL3 [294], LTF (lactotransferrin) [295], CTLA4 [296], TNFRSF9 [253], C6 [297], IL5RA [298],

IL2RG [299], NPY2R [300], DRD3 [301], CD52 [302], CD163 [303], IQGAP2 [304], PRPH (peripherin) [305], MSR1 [306], HGF (hepatocyte growth factor) [307], TTR (transthyretin) [308], IL9 [309], ADM (adrenomedullin) [310], ANGPTL4 [311], CHI3L1 [312], CDH1 [313], SREBF1 [314], CDKN1C [315], TSC22D4 [316], CFTR (CF transmembrane conductance regulator) [317], INSIG1 [318], HSD17B3 [319], GREM1 [320], ATF3 [321], HK2 [322], TF (transferrin) [323], GLUL (glutamate-ammonia ligase) [324], DMRT2 [325], FN3K [326], TREH (trehalase) [327], ADAMTS4 [328], BMP2 [329], LMNA (lamin A/C) [330], ERBB3 [331], HSD11B1 [332], DLL1 [333], NKX2-2 [334], FGF11 [335], ASPA (aspartoacylase) [336], FASN (fatty acid synthase) [337], PNPLA3 [338], ADORA1 [339], WNT7A [340], LIPC (lipase C, hepatic type) [341], GPR142 [342], GPD1 [343], LIPE (lipase E, hormone sensitive type) [344], CNDP1 [187], DHCR7 [345], SAA1 [346], TKTL1 [347], ACADS (acyl-CoA dehydrogenase short chain) [348], SCD (stearoyl-CoA desaturase) [349], FFAR1 [350], HCN2 [195], F11 [351], GPIHBP1 [352], ANGPTL2 [203], MAPK8IP1 [353], CYP2A6 [354] and CTNNA3 [355] expression was altered in diabetes mellitus. Alerted expression of MS4A2 [356], CD48 [357], HLA-DRB5 [358], FCGR2B [359], CCL5 [360], CCL3 [361], LTF (lactotransferrin) [362], GPNMB (glycoprotein nmb) [363], CTLA4 [364], TRIML2 [365], PTGDR (prostaglandin D2 receptor) [366], DRD3 [367], LHCGR (luteinizing hormone/choriogonadotropin receptor) [368], CD163 [369], PRPH (peripherin) [211], MSR1 [370], HGF (hepatocyte growth factor) [371], TTR (transthyretin) [372], IL9 [373], ADM (adrenomedullin) [374], CHI3L1 [375], CNP (2',3'-cyclic nucleotide 3' phosphodiesterase) [376], CDH1 [377], OLIG2 [378], KLK8 [379]. CFTR (CF transmembrane conductance regulator) [380], ABCA2 [381], HK2 [382], NGFR (nerve growth factor receptor) [383], TF (transferrin) [384], GLUL (glutamate-ammonia ligase) [324], ADAMTS4 [385], BIN1 [386], HSPA2 [387], LMNA (lamin A/C) [388], HSD11B1 [389], HTRA1 [390], APLP1 [391], MT3 [392], ADORA1 [393], DYSF (dysferlin) [394], SLC24A4 [395], RHOB (ras homolog family member B) [396], NINJ2 [397], LRP2 [398], LIPC (lipase C, hepatic type) [399], DHCR7 [400], SCD (stearoyl-CoA desaturase) [401], F11 [402], PFKL (phosphofructokinase, liver type) [403], ALDH1A1 [404], SPON1 [405] and CTNNA3 [406] are significantly associated with the Alzheimer's Disease. CCR4 [407], CCR2 [408], CD48 [409], CD28 [410], CCL3 [411], CTLA4 [412], C6 [413], MICB (MHC class I polypeptide-related sequence B) [414], DRD3 [415],

HGF (hepatocyte growth factor) [416], DIO3 [417], TTR (transthyretin) [418], GRHL3 [419], VEGFA (vascular endothelial growth factor A) [420], ADM (adrenomedullin) [421], CHI3L1 [422], SOX3 [423], MAG (myelin associated glycoprotein) [424], CNP (2',3'-cyclic nucleotide 3' phosphodiesterase) [425], SREBF1 [426], OLIG2 [427], ATF3 [428], NGFR (nerve growth factor receptor) [429], TF (transferrin) [430], GLUL (glutamate-ammonia ligase) [324]. MOG (myelin oligodendrocyte glycoprotein) [431], ERBB3 [432], NHLH2 [433], GADD45B [434], PADI2 [435], ADORA1 [436], NINJ2 [437], WNT7A [438], DAO (D-amino acid oxidase) [439], PRODH (proline dehydrogenase 1) [440] and HCRTR1 [441] could regulate the development of psychiatric disorders. CCR2 [442], FASLG (Fas ligand) [443], GPNMB (glycoprotein nmb) [444], NPY2R [445], TRPM8 [446], TTR (transthyretin) [447], ADM (adrenomedullin) [448], CHI3L1 [375], CDH1 [377], HIP1R [449], SEMA4D [450], HAPLN2 [451], MYRF (myelin regulatory factor) [452], BIN1 [453], BMP2 [454], APLP1 [391], SEPTIN4 [455], DAO (D-amino acid oxidase) [456], TKTL1 [347], ADAP1 [457], HPDL (4-hydroxyphenylpyruvate dioxygenase like) [458], NME3 [459], SPON1 [460] and LGALS3BP [225] were revealed to be altered expressed in neurodegenerative diseases. CCR2 [461], FASLG (Fas ligand) [462], CD28 [463], LYZ (lysozyme) [464], CCL5 [465], CCL3 [466], C6 [467], MSR1 [468], HGF (hepatocyte growth factor) [469], VEGFA (vascular endothelial growth factor A) [470], ADM (adrenomedullin) [471], CR2 [472], MAG (myelin associated glycoprotein) [473], CDH1 [474], OLIG2 [475], SEMA4D [476], ADAMTS4 [477], BMP2 [478], ERBB3 [479] and NKX2-2 [480] have been identified as a hub gene in spinal cord injury in several studies. CCR2 [481], FASLG (Fas ligand) [286], CD24 [482], CD28 [483], LYZ (lysozyme) [484], IL7R [485], CCL5 [486], LTF (lactotransferrin) [487], GPNMB (glycoprotein nmb) [488], CTLA4 [489], IRF4 [490], CHIT1 [491], NPY2R [492], TAB2 [131], CD52 [302], CD163 [493], MSR1 [306], HGF (hepatocyte growth factor) [494], TRPM8 [495], TTR (transthyretin) [496], F13A1 [497], ADM (adrenomedullin) [498], COL9A3 [499], ANGPTL4 [500], CHI3L1 [501], BMP8A [502], SREBF1 [503], CDKN1C [504], INSIG1 [505], ATF3 [506], HK2 [507], TF (transferrin) [508], MOG (myelin oligodendrocyte glycoprotein) [509], ADAMTS4 [510], BMP2 [511], HSPA2 [512], LMNA (lamin A/C) [330], HSD11B1 [513], NKX2-2 [514], NHLH2 [433], FGF11 [515], ASPA (aspartoacylase) [336], FASN (fatty acid

synthase) [516], PNPLA3 [517], MMP15 [518], CBR1 [519], LRP2 [520], WNT7A [340], GPR142 [521], GPD1 [343], LIPE (lipase E, hormone sensitive type) [522], CNDP1 [523], SAA1 [524], ACADS (acyl-CoA dehydrogenase short chain) [348], SCD (stearoyl-CoA desaturase) [525], GPIHBP [526], LMF1 [527], IGSF1 [528], LSS (lanosterol synthase) [529], ALDH1A1 [530], ANGPTL2 [531], NENF (neudesin neurotrophic factor) [532] and CYP2A6 [533] are potential prognostic biomarkers for obesity. CCR2 [534], CCL4 [535], TNFRSF13B [536], FASLG (Fas ligand) [537], CD28 [538], CYP11B1 [539], CCL5 [540], LTF (lactotransferrin) [541], CTLA4 [542], DRD3 [543], HGF (hepatocyte growth factor) [494], TRPM8 [544], IL9 [545], NPPC (natriuretic peptide C) [546], ANGPTL4 [547], CHI3L1 [548], SREBF1 [549], GDF2 [550], CFTR (CF transmembrane conductance regulator) [551], ATF3 [552], HK2 [553], NGFR (nerve growth factor receptor) [554], MEIS1 [555], MOG (myelin oligodendrocyte glycoprotein) [556], BMP2 [557], LMNA (lamin A/C) [558], ERBB3 [331], HSD11B1 [559], THBS2 [560], FASN (fatty acid synthase) [561], PNPLA3 [562], SLC45A3 [563], WNT7A [564], SCNN1G [565], TRPV5 [566], ACADS (acyl-CoA dehydrogenase short chain) [567], GNLY (granulysin) [568], NOXA1 [569], ANGPTL2 [570], SPON1 [571], CYP2A6 [572] and RASA3 [573] altered expression have been closely associated with the hypertension. FASLG (Fas ligand) [574], GJC2 [575] and GJB1 [576] have been identified to be involved in the development of spasticity. CD24 [577], CD28 [578], HLA-DRB5 [579], LTF (lactotransferrin) [580], GPNMB (glycoprotein nmb) [581], TNFRSF9 [582], LRRC37A2 [583], DRD3 [584], CD163 [369], HGF (hepatocyte growth factor) [585], TRPM8 [446], TTR (transthyretin) [586], VEGFA (vascular endothelial growth factor A) [587], CHI3L1 [588], MAG (myelin associated glycoprotein) [589], SREBF1 [217], HIP1R [590], HK2 [591], GPR37 [592], NGFR (nerve growth factor receptor) [593], TF (transferrin) [594], HAPLN2 [451], MOG (myelin oligodendrocyte glycoprotein) [595], BIN1 [596], BMP2 [597], GADD45B [598], UNC5B [599], ADORA1 [600], SEPTIN4 [601], DHCR7 [602], SCD (stearoyl-CoA desaturase) [603], GIPC1 [604], ALDH1A1 [605] and CTNNA3 [606] participate in pathogenic processes of Parkinson's disease. At present, investigation on these key regulatory genes and related molecular pathways is lacking. The interactions of these genes and pathways in the progression of MS still need attention, research and verification.

In this investigation, we identified hub genes from PPI network and modules that may be utilized as diagnostic and/or therapeutic targets in MS. HiPPIE analyses revealed evidence of potent protein-protein interaction between DEGs. SLAMF1 [237], TAB2 [256] and HGF (hepatocyte growth factor) [260] might play an important role in the onset, development, and treatment of autoimmune disease. SLAMF1 [287], CFTR (CF transmembrane conductance regulator) [317], LMNA (lamin A/C) [330], ERBB3 [331], HGF (hepatocyte growth factor) [307] and CCL5 [293] might play an important role in the pathophysiology of diabetes mellitus. TAB2 [131], LMNA (lamin A/C) [168], ERBB3 [169], HGF (hepatocyte growth factor) [135] and CCL5 [124] were abnormally expressed in cardiovascular diseases. TAB2 [131], LMNA (lamin A/C) [330], HGF (hepatocyte growth factor) [494] and CCL5 [486] migt play an important role in the occurrence and development of obesity. CFTR (CF transmembrane conductance regulator) [380], RHOB (ras homolog family member B) [396], LMNA (lamin A/C) [388], HGF (hepatocyte growth factor) [371], CCL5 [360] and NGFR (nerve growth factor receptor) [383] were altered expression in the Alzheimer's Disease. CFTR (CF transmembrane conductance regulator) [551], LMNA (lamin A/C) [558], ERBB3 [331], HGF (hepatocyte growth factor) [494], CCL5 [540] and NGFR (nerve growth factor receptor) [554] have been demonstrated to accelerate hypertension progression. LMNA (lamin A/C) [222], HGF (hepatocyte growth factor) [212] and NGFR (nerve growth factor receptor) [220] expression migh be regarded as an indicator of susceptibility of amyotrophic lateral sclerosis. Altered expression of ERBB3 [432], HGF (hepatocyte growth factor) [416] and NGFR (nerve growth factor receptor) [429] are associated with poor prognosis in patients with psychiatric disorders. ERBB3 [479], HGF (hepatocyte growth factor) [469] and CCL5 [465] genes are a potential biomarkers for the detection and prognosis of spinal cord injury. A previous study reported that HGF (hepatocyte growth factor) [83], CCL5 [75] and NGFR (nerve growth factor receptor) [96] are altered expressed in MS. HGF (hepatocyte growth factor) [585] and NGFR (nerve growth factor receptor) [593] are a key initiators of Parkinson's disease. This investigation suggests that LCK (LCK proto-oncogene, Src family tyrosine kinase), PYHIN1, DOK2, EGLN3, SDC1 and FSCN1 might be a novel therapeutic targets for MS, and the related molecular mechanism is worthy of further exploration. The results clearly indicate that the hub genes discovered by PPI network and modules analysis might be essential for conditions beyond than underlying MS.

In addition, miRNA-hub gene regulatory network and TF-hub gene regulatory network were constructed. The roles of hub genes, miRNAs and TFs in the pathogenesis of MS are discussed. IKZF3 [69], hsa-mir-146a-5p [607], BRCA1 [608] and NFKB1 [609] can participate in the occurrence and development of MS. IKZF3 [239], TAB2 [256], CCR4 [231], LTF (lactotransferrin) [249], CDH1 [266], BRCA1 [610], NFKB1 [611] and FOXO3 [612] might play an important role in the occurrence and development of autoimmune disease. TAB2 [131], CCR4 [112], LTF (lactotransferrin) [126], hsa-mir-146a-5p [613], hsa-mir-8485 [614], BRCA1 [615], NFKB1 [616], TEAD1 [617], TFAP2C [618], FOXO3 [619] and NRF1 [620] risk factors have been shown to increase susceptibility to cardiovascular diseases. Several studies have shown that TAB2 [131], LTF (lactotransferrin) [487], BRCA1 [621], NFKB1 [622], TEAD1 [623], FOXO3 [624] and NRF1 [625] can be involved in the disease progression of **obesity**., Altered expression of CCR4 [280], LTF (lactotransferrin) [295], CDH1 [313], CFTR (CF transmembrane conductance regulator) [317], hsa-mir-146a-5p [626], hsa-mir-195-5p [627], hsa-mir-4739 [628], HNF4A [629], NFKB1 [630], NR2F1 [631], FOXO3 [632] and NRF1 [633] are observed in diabetes mellitus. CCR4 [407], hsa-mir-146a-5p [634] and NFKB1 [635] were associated with psychiatric disorders. LTF (lactotransferrin) [362], RHOB (ras homolog family member B) [396], CDH1 [377], CFTR (CF transmembrane conductance regulator) [380], hsa-mir-146a-5p [636], hsa-mir-195-5p [637], BRCA1 [638], ELK4 [639] and FOXO3 [640] might offer useful information for treating Alzheimer's Disease. LTF (lactotransferrin) [541], CFTR (CF transmembrane conductance regulator) [551], hsa-mir-195-5p [627], BRCA1 [641], NFKB1 [642], TFAP2C [643], FOXO3 [644] and NRF1 [645] are associated with poor prognosis in patients with hypertension. Increasing evidence has convincingly demonstrated that altered expression of LTF (lactotransferrin) [580], hsa-mir-146a-5p [646], hsa-mir-195-5p [637], HNF4A [647], NFKB1 [648], NR2F1 [649], FOXO3 [650] and NRF1 [651] are a prognosis factors in Parkinson's disease. LGALS3BP [225] and BRCA1 [652] has been reported involved in the amyotrophic lateral sclerosis. Recent studies have shown that elevated expression of LGALS3BP [225], CDH1 [377], hsa-mir-146a-5p [653], BRCA1 [654], HNF4A [655], FOXO3 [656] and NRF1 [657] might be associated with the progression of neurodegenerative diseases. Studies have found that low CDH1 [474] and FOXO3 [658] expression was associated with spinal cord injury. However, the roles of novel biomarkers include

C6orf141, SDC1, CD79A, LCK (LCK proto-oncogene, Src family tyrosine kinase), SFN (stratifin), POLR2F, MAP1LC3A, LLGL2, FOXE1, hsa-mir-6794-3p, hsa-mir-3689a-3p, hsa-mir-4449, hsa-mir-4695-5p, hsa-mir-4651, hsa-mir-548q and NFYA (nuclear transcription factor Y subunit alpha) in MS have not been reported until now. These results could help elucidate the molecular mechanism underlying MS pathogenesis and provide potential targets for MS therapy. Further investigations are needed to confirm our putative finding.

In conclusion, the current investigation exhibits the global profile of DEGs and relative signaling pathways that might participate in the initiation and development of MS. In the molecular pathogenesis of acne, the possible crucial genes are LCK, PYHIN1, SLAMF1, DOK2, TAB2, CFTR, RHOB, LMNA, EGLN3 and ERBB3, and the possible important signaling pathways are immune system, TCR signaling, regulation of cholesterol biosynthesis by SREBP (SREBF) and degradation of the extracellular matrix. These results could help elucidate the molecular mechanism underlying acne pathogenesis and provide potential targets for MS therapy. Further investigations are needed to confirm our putative finding.

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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. [(GSE138614) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE138614]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

B. V. - Writing original draft, and review and editing

C. V. - Software and investigation

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Tables

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

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
IGLC3	10.06961	2.36E-36	9.29E-33	12.59107	Up	immunoglobulin lambda constant 3 (Kern-Oz+ marker)
IGLC2	9.980379	9.51E-42	5.14E-38	13.53658	Up	immunoglobulin lambda constant 2
IGKV4-1	9.853402	2.85E-43	2.02E-39	13.79185	Up	immunoglobulin kappa variable 4-1
RNA5SP202	9.73263	1.60E-07	5.17E-06	5.241145	Up	RNA, 5S ribosomal pseudogene 202
IGHG3	9.579062	3.62E-46	3.92E-42	14.26483	Up	immunoglobulin heavy constant gamma 3 (G3m marker)
IGHG1	9.086903	5.08E-82	2.19E-77	19.18358	Up	immunoglobulin heavy constant gamma 1 (G1m marker)
RNA5S9	9.009309	4.37E-10	3.59E-08	6.24025	Up	RNA, 5S ribosomal 9
IGHG2	8.987913	1.88E-44	1.63E-40	13.98661	Up	immunoglobulin heavy constant gamma 2 (G2m marker)
IGHV4-39	8.87895	9.53E-36	3.43E-32	12.48055	Up	immunoglobulin heavy variable 4-39
IGKV3-11	8.857399	2.23E-35	7.42E-32	12.41262	Up	immunoglobulin kappa variable 3-11
IGHV1-2	8.751044	6.38E-25	1.02E-21	10.30954	Up	immunoglobulin heavy variable 1-2
IGHV3-7	8.714308	1.78E-46	2.56E-42	14.31435	Up	immunoglobulin heavy variable 3-7

IGKV1-5	8.525895	2.19E-38	1.05E-34	12.9555	Up	immunoglobulin kappa variable 1-5
IGHV3-30	8.375043	3.33E-24	4.80E-21	10.14941	Up	immunoglobulin heavy variable 3-30
IGLV2-11	8.37053	1.55E-18	1.05E-15	8.786014	Up	immunoglobulin lambda variable 2-11
IGKC	8.317001	5.20E-70	1.12E-65	17.68786	Up	immunoglobulin kappa constant
IGHV4-34	8.216539	2.34E-21	2.57E-18	9.4887	Up	immunoglobulin heavy variable 4-34
IGLV3-21	8.215488	3.50E-19	2.70E-16	8.951673	Up	immunoglobulin lambda variable 3-21
IGKV3-15	8.163341	2.32E-22	2.87E-19	9.726642	Up	immunoglobulin kappa variable 3-15
IGLV1-44	8.146692	5.45E-21	5.61E-18	9.400075	Up	immunoglobulin lambda variable 1-44
IGHV3-23	8.105742	8.78E-32	2.23E-28	11.73159	Up	immunoglobulin heavy variable 3-23
IGHV4-59	8.097631	1.55E-32	4.48E-29	11.87728	Up	immunoglobulin heavy variable 4-59
IGHV2-5	8.052062	2.82E-26	5.53E-23	10.60531	Up	immunoglobulin heavy variable 2-5
IGKV3-20	7.830961	7.84E-27	1.61E-23	10.72411	Up	immunoglobulin kappa variable 3-20
IGHV3-21	7.705562	4.67E-14	1.14E-11	7.540844	Up	immunoglobulin heavy variable 3-21
IGKV1-9	7.499405	2.42E-17	1.36E-14	8.471443	Up	immunoglobulin kappa variable 1-9
JCHAIN	7.360576	4.95E-38	2.14E-34	12.89263	Up	joining chain of multimeric IgA and IgM
RNA5SP74	7.321259	5.89E-06	0.000107	4.530446	Up	RNA, 5S ribosomal pseudogene 74
MTND1P23	7.310865	2.46E-22	2.95E-19	9.720756	Up	MT-ND1 pseudogene 23
IGHM	7.2494	3.26E-43	2.02E-39	13.78214	Up	immunoglobulin heavy constant mu
RNA5-8SP6	7.226277	4.22E-07	1.17E-05	5.058973	Up	RNA, 5.8S ribosomal pseudogene 6
IGLV2-14	7.133414	2.58E-20	2.38E-17	9.234999	Up	immunoglobulin lambda variable 2-14
IGHA1	7.111494	4.58E-32	1.24E-28	11.78644	Up	immunoglobulin heavy constant alpha 1
IGHV1-18	7.103404	3.30E-16	1.44E-13	8.16198	Up	immunoglobulin heavy variable 1-18
IGHV1-3	6.909408	3.20E-13	6.34E-11	7.285773	Up	immunoglobulin heavy variable 1-3
IGLV3-19	6.895603	8.38E-16	3.20E-13	8.048572	Up	immunoglobulin lambda variable 3-19
RNA5-8SN4	6.885809	2.32E-08	1.03E-06	5.585954	Up	RNA, 5.8S ribosomal N4
IGHV4-4	6.749457	2.62E-16	1.17E-13	8.189652	Up	immunoglobulin heavy variable 4-4
IGHV1-69D	6.642154	1.14E-10	1.16E-08	6.446557	Up	immunoglobulin heavy variable 1-69D
IGHV4-30-2	6.631824	1.23E-22	1.56E-19	9.791384	Up	immunoglobulin heavy variable 4-30-2
IGHV1-46	6.62993	3.19E-17	1.75E-14	8.439262	Up	immunoglobulin heavy variable 1-46
IGKV1-12	6.564886	3.43E-17	1.83E-14	8.430757	Up	immunoglobulin kappa variable 1-12
FCRL5	6.47703	1.12E-31	2.68E-28	11.7112	Up	Fc receptor like 5
IGLV2-23	6.405091	3.33E-11	3.93E-09	6.631369	Up	immunoglobulin lambda variable 2-23
IGHV3-33	6.248309	3.50E-21	3.69E-18	9.446561	Up	immunoglobulin heavy variable 3-33
IGHV5-51	6.23901	2.51E-13	5.17E-11	7.318333	Up	immunoglobulin heavy variable 5-51
IGHV2-26	6.210374	6.52E-11	7.03E-09	6.531189	Up	immunoglobulin heavy variable 2-26
IGKV1-27	6.129594	3.83E-13	7.43E-11	7.261278	Up	immunoglobulin kappa variable 1-27
IGLV1-40	6.059396	2.40E-13	4.97E-11	7.324256	Up	immunoglobulin lambda variable 1-40
IGHV2-70	6.057597	1.97E-12	3.23E-10	7.036262	Up	immunoglobulin heavy variable 2-70
IGLV2-8	6.057078	6.45E-09	3.51E-07	5.804549	Up	immunoglobulin lambda variable 2-8
IGKV1-17	5.943759	9.14E-13	1.62E-10	7.142943	Up	immunoglobulin kappa variable 1-17
IGHV3-48	5.943452	5.17E-13	9.67E-11	7.220735	Up	immunoglobulin heavy variable 3-48
FAM30A	5.919962	1.33E-25	2.40E-22	10.45899	Up	family with sequence similarity 30 member A
IGHV3-53	5.875865	8.59E-10	6.43E-08	6.133671	Up	immunoglobulin heavy variable 3-53

IGKV1-16	5.84343	5.28E-11	5.81E-09	6.562845	Up	immunoglobulin kappa variable 1-16
IGLV2-18	5.815317	1.79E-06	3.95E-05	4.775712	Up	immunoglobulin lambda variable 2-18
IGHV4-61	5.766141	4.69E-13	8.97E-11	7.23396	Up	immunoglobulin heavy variable 4-61
IGHG4	5.744639	5.31E-19	3.96E-16	8.905529	Up	immunoglobulin heavy constant gamma 4 (G4m marker)
IGHV3-74	5.742772	6.28E-14	1.47E-11	7.5021	Up	immunoglobulin heavy variable 3-74
CCL18	5.700544	2.41E-06	5.07E-05	4.715676	Up	C-C motif chemokine ligand 18
IGKV2-24	5.557589	4.46E-08	1.79E-06	5.471597	Up	immunoglobulin kappa variable 2-24
IGKV5-2	5.547014	1.68E-06	3.74E-05	4.788956	Up	immunoglobulin kappa variable 5-2
IGKV1-6	5.49746	8.93E-07	2.20E-05	4.913766	Up	immunoglobulin kappa variable 1-6
IGHV3-15	5.492425	5.62E-17	2.89E-14	8.372986	Up	immunoglobulin heavy variable 3-15
IGHV3-49	5.480636	1.74E-08	8.11E-07	5.635571	Up	immunoglobulin heavy variable 3-49
IGHJ5	5.451962	8.30E-12	1.12E-09	6.833241	Up	immunoglobulin heavy joining 5
IGKV6-21	5.376049	8.08E-05	0.000954	3.941974	Up	immunoglobulin kappa variable 6-21 (non-functional)
IGHV3-11	5.364442	3.27E-08	1.37E-06	5.526245	Up	immunoglobulin heavy variable 3-11
IGHV3-20	5.350349	2.53E-05	0.000367	4.211688	Up	immunoglobulin heavy variable 3-20
IGLV6-57	5.334184	8.27E-07	2.05E-05	4.928818	Up	immunoglobulin lambda variable 6-57
IGLV3-10	5.332133	3.20E-05	0.000446	4.158513	Up	immunoglobulin lambda variable 3-10
IGKV3D-11	5.308549	3.99E-09	2.36E-07	5.88469	Up	immunoglobulin kappa variable 3D-11
IGKV2-30	5.270766	1.87E-08	8.60E-07	5.623272	Up	immunoglobulin kappa variable 2-30
IGHV4-55	5.181429	6.06E-08	2.29E-06	5.41712	Up	immunoglobulin heavy variable 4-55 (pseudogene)
IGLV1-47	5.13828	2.24E-09	1.43E-07	5.97945	Up	immunoglobulin lambda variable 1-47
IGHV4-28	5.13505	7.08E-11	7.58E-09	6.518881	Up	immunoglobulin heavy variable 4-28
LRRC37A2	5.113237	9.02E-11	9.37E-09	6.482541	Up	leucine rich repeat containing 37 member A2
IGHV7-4-1	5.089007	0.000321	0.002932	3.597749	Up	immunoglobulin heavy variable 7-4-1
RNA5SP336	5.078075	0.000197	0.001967	3.723358	Up	RNA, 5S ribosomal pseudogene 336
IGLV3-25	5.067368	8.14E-08	2.94E-06	5.363939	Up	immunoglobulin lambda variable 3-25
IGHV3-64D	5.059654	6.20E-06	0.000112	4.519591	Up	immunoglobulin heavy variable 3-64D
IGHJ3P	5.006431	2.65E-10	2.36E-08	6.318075	Up	immunoglobulin heavy joining 3P (pseudogene)
IGHA2	4.954369	1.33E-13	2.91E-11	7.402731	Up	immunoglobulin heavy constant alpha 2 (A2m marker)
IGLL5	4.908842	5.73E-09	3.18E-07	5.824311	Up	immunoglobulin lambda like polypeptide 5
IGLV10-54	4.847455	3.35E-07	9.65E-06	5.102469	Up	immunoglobulin lambda variable 10-54
IGHV2-70D	4.839897	9.56E-08	3.35E-06	5.334951	Up	immunoglobulin heavy variable 2-70D
IGHV1-69	4.839832	1.44E-06	3.31E-05	4.818946	Up	immunoglobulin heavy variable 1-69
STOML3	4.838278	3.22E-09	1.97E-07	5.920014	Up	stomatin like 3
MTCO1P53	4.789025	4.92E-08	1.93E-06	5.454246	Up	MT-CO1 pseudogene 53
IGKV1-8	4.778191	1.37E-06	3.17E-05	4.829013	Up	immunoglobulin kappa variable 1-8
IGHV3-43	4.751148	1.10E-05	0.000182	4.39621	Up	immunoglobulin heavy variable 3-43
IGLV4-69	4.749838	2.92E-06	5.97E-05	4.676391	Up	immunoglobulin lambda variable 4-69
IGLV7-46	4.656717	8.24E-06	0.000142	4.458826	Up	immunoglobulin lambda variable 7-46
IGLV7-43	4.647697	1.16E-05	0.000191	4.384866	Up	immunoglobulin lambda variable 7-43
SLAMF7	4.622828	1.03E-27	2.23E-24	10.91002	Up	SLAM family member 7
IGHJ6	4.543851	3.64E-08	1.50E-06	5.507313	Up	immunoglobulin heavy joining 6

RASSF6	4.517662	2.37E-17	1.35E-14	8.47416	Up	Ras association domain family member 6
IGLV8-61	4.460752	1.17E-05	0.000193	4.382357	Up	immunoglobulin lambda variable 8-61
IGKJ5	4.442739	6.83E-07	1.74E-05	4.966237	Up	immunoglobulin kappa joining 5
SHOX2	4.415867	1.04E-18	7.24E-16	8.830798	Up	short stature homeobox 2
FCRL2	4.355734	8.48E-11	8.85E-09	6.491869	Up	Fc receptor like 2
OR2U1P	4.351839	0.000349	0.003127	3.576222	Up	olfactory receptor family 2 subfamily U member 1 pseudogene
IGHV6-1	4.346739	9.49E-07	2.32E-05	4.901993	Up	immunoglobulin heavy variable 6-1
IGKV1D-13	4.331848	0.000309	0.002844	3.60765	Up	immunoglobulin kappa variable 1D-13
FAM216B	4.296144	1.10E-11	1.44E-09	6.793259	Up	family with sequence similarity 216 member B
IGLC7	4.273698	0.007229	0.034225	2.686091	Up	immunoglobulin lambda constant 7
IGHV3-72	4.267119	1.47E-06	3.34E-05	4.815936	Up	immunoglobulin heavy variable 3-72
OR2U2P	4.263762	8.85E-05	0.001029	3.920133	Up	olfactory receptor family 2 subfamily U member 2 pseudogene
IGKV2D-29	4.242053	0.000106	0.001192	3.877329	Up	immunoglobulin kappa variable 2D-29
IGKV3D-20	4.216622	6.63E-06	0.000118	4.505145	Up	immunoglobulin kappa variable 3D-20
NUGGC	4.21585	8.93E-18	5.51E-15	8.586927	Up	nuclear GTPase, germinal center associated
IGKV6D-21	4.187105	0.000299	0.002773	3.615749	Up	immunoglobulin kappa variable 6D-21 (non-functional)
IGHV3-13	4.126908	0.000308	0.002837	3.608343	Up	immunoglobulin heavy variable 3-13
PYHIN1	4.122934	2.38E-21	2.57E-18	9.487043	Up	pyrin and HIN domain family member 1
IGHJ4	4.114152	7.38E-06	0.000129	4.482513	Up	immunoglobulin heavy joining 4
MS4A1	4.099287	9.04E-20	8.14E-17	9.099923	Up	membrane spanning 4-domains A1
IGHV1-24	4.096599	9.49E-05	0.001091	3.903344	Up	immunoglobulin heavy variable 1-24
IGHV3-73	4.04934	0.000121	0.00132	3.844329	Up	immunoglobulin heavy variable 3-73
MS4A2	4.047018	1.86E-07	5.87E-06	5.212516	Up	membrane spanning 4-domains A2
P2RY10	4.044454	5.16E-13	9.67E-11	7.220951	Up	P2Y receptor family member 10
GPR174	4.03373	2.64E-12	4.22E-10	6.995816	Up	G protein-coupled receptor 174
PPIAP45	4.009258	3.28E-05	0.000454	4.153074	Up	peptidylprolyl isomerase A pseudogene 45
IGKJ4	3.963444	2.63E-07	7.90E-06	5.148218	Up	immunoglobulin kappa joining 4
OR2G1P	3.956149	9.61E-06	0.000162	4.425788	Up	olfactory receptor family 2 subfamily G member 1 pseudogene
FCRL3	3.954047	4.93E-11	5.49E-09	6.57309	Up	Fc receptor like 3
RN7SL472P	3.924574	1.01E-10	1.04E-08	6.465662	Up	RNA, 7SL, cytoplasmic 472, pseudogene
LY9	3.894804	5.19E-15	1.59E-12	7.822278	Up	lymphocyte antigen 9
IGKV1D-39	3.844402	5.11E-05	0.000657	4.050325	Up	immunoglobulin kappa variable 1D-39
IGHV3-66	3.82856	0.000175	0.001794	3.752313	Up	immunoglobulin heavy variable 3-66
ADGB	3.804221	8.77E-14	1.96E-11	7.458206	Up	androglobin
CLEC10A	3.791609	3.28E-13	6.47E-11	7.282393	Up	C-type lectin domain containing 10A
IGKJ3	3.790449	3.30E-07	9.53E-06	5.105588	Up	immunoglobulin kappa joining 3
DNAJC5B	3.787386	4.41E-14	1.08E-11	7.548378	Up	DnaJ heat shock protein family (Hsp40) member C5 beta
RPL13P12	3.769631	8.34E-16	3.20E-13	8.049139	Up	ribosomal protein L13 pseudogene 12
TRAV4	3.700919	1.15E-06	2.73E-05	4.864692	Up	T cell receptor alpha variable 4
AADACL2	3.693007	3.65E-13	7.13E-11	7.268053	Up	arylacetamide deacetylase like 2
FNDC1	3.666067	3.11E-15	1.02E-12	7.88639	Up	fibronectin type III domain containing 1
PALM3	3.647856	9.16E-25	1.41E-21	10.27472	Up	paralemmin 3

HOXB7	3.646834	1.40E-10	1.37E-08	6.415967	Up	homeobox B7
SLAMF6	3.620622	1.38E-21	1.61E-18	9.543929	Up	SLAM family member 6
OR2J2	3.603544	0.001357	0.009357	3.203636	Up	olfactory receptor family 2 subfamily J member 2
IGKV1D-16	3.587261	0.000242	0.002332	3.670803	Up	immunoglobulin kappa variable 1D-16
TRAT1	3.584333	5.06E-11	5.59E-09	6.569169	Up	T cell receptor associated transmembrane adaptor 1
IGLV3-9	3.578656	0.000674	0.005332	3.399775	Up	immunoglobulin lambda variable 3-9
TRAJ19	3.569176	4.70E-08	1.86E-06	5.462481	Up	T cell receptor alpha joining 19 (non-functional)
IGKV1-39	3.558538	0.000115	0.001267	3.856816	Up	immunoglobulin kappa variable 1-39
SBK3	3.557441	1.60E-05	0.000251	4.313795	Up	SH3 domain binding kinase family member 3
ISL1-DT	3.543877	3.38E-05	0.000466	4.145965	Up	ISL1 divergent transcript
STRIT1	3.540798	0.001724	0.011251	3.134135	Up	small transmembrane regulator of ion transport 1
OR2J4P	3.53933	0.002307	0.014191	3.047602	Up	olfactory receptor family 2 subfamily J member 4 pseudogene
ZBED2	3.536452	3.54E-08	1.46E-06	5.512586	Up	zinc finger BED-type containing 2
EOMES	3.53325	2.50E-14	6.48E-12	7.621738	Up	eomesodermin
ISL1	3.528071	0.009222	0.041161	2.60371	Up	ISL LIM homeobox 1
IGLV5-45	3.525068	0.000449	0.003839	3.509379	Up	immunoglobulin lambda variable 5-45
TTR	3.495699	2.57E-08	1.13E-06	5.568266	Up	transthyretin
OTX2	3.492617	7.18E-06	0.000126	4.488303	Up	orthodenticle homeobox 2
RAET1K	3.472459	2.17E-06	4.64E-05	4.73698	Up	retinoic acid early transcript 1K pseudogene
IGKV1D-12	3.456014	0.002777	0.016517	2.991368	Up	immunoglobulin kappa variable 1D-12
CCR4	3.454034	1.82E-08	8.38E-07	5.628614	Up	C-C motif chemokine receptor 4
GZMA	3.424963	4.71E-11	5.28E-09	6.579703	Up	granzyme A
NMRAL2P	3.40656	8.86E-09	4.57E-07	5.751261	Up	NmrA like redox sensor 2, pseudogene
C20orf85	3.401077	0.002022	0.012781	3.086996	Up	chromosome 20 open reading frame 85
SPAG17	3.397014	1.28E-15	4.59E-13	7.996966	Up	sperm associated antigen 17
POU4F2	3.37904	3.50E-06	6.95E-05	4.638842	Up	POU class 4 homeobox 2
IGKV3D-15	3.369577	0.00643	0.031388	2.724986	Up	immunoglobulin kappa variable 3D-15
CD79A	3.362021	3.47E-12	5.26E-10	6.957247	Up	CD79a molecule
CCR2	3.337673	9.44E-21	9.49E-18	9.342108	Up	C-C motif chemokine receptor 2
CD48	3.334282	1.10E-15	3.98E-13	8.015633	Up	CD48 molecule
GZMK	3.334223	3.07E-08	1.30E-06	5.537183	Up	granzyme K
IGKV1D-33	3.325079	0.00458	0.024266	2.835182	Up	immunoglobulin kappa variable 1D-33
MYLK3	3.314138	6.10E-16	2.53E-13	8.087355	Up	myosin light chain kinase 3
IGKV1-33	3.311733	0.001478	0.009994	3.17897	Up	immunoglobulin kappa variable 1-33
RGS21	3.310956	1.18E-06	2.78E-05	4.85949	Up	regulator of G protein signaling 21
CFAP107	3.290338	1.21E-09	8.55E-08	6.07912	Up	cilia and flagella associated protein 107
NEK2-DT	3.286039	1.07E-05	0.000177	4.403138	Up	NEK2 divergent transcript
PLEKHG4B	3.275951	2.07E-12	3.37E-10	7.029904	Up	pleckstrin homology and RhoGEF domain containing G4B
RPL36P11	3.261967	3.66E-14	9.30E-12	7.572599	Up	ribosomal protein L36 pseudogene 11
TRAV17	3.261329	0.00108	0.007797	3.268735	Up	T cell receptor alpha variable 17
CD3E	3.253453	9.68E-20	8.54E-17	9.092489	Up	CD3 epsilon subunit of T-cell receptor complex
CCL26	3.236983	3.18E-05	0.000443	4.160164	Up	C-C motif chemokine ligand 26

IGKV1D-8	3.235089	8.48E-05	0.000994	3.930382	Up	immunoglobulin kappa variable 1D-8
ITGAD	3.234555	4.78E-13	9.10E-11	7.231428	Up	integrin subunit alpha D
DOK2	3.227083	1.72E-12	2.86E-10	7.05538	Up	docking protein 2
OR5V1	3.226278	0.002043	0.012881	3.083934	Up	olfactory receptor family 5 subfamily V member 1
TDRD15	3.225782	5.50E-08	2.13E-06	5.43421	Up	tudor domain containing 15
IL2RB	3.2222	6.36E-13	1.16E-10	7.192572	Up	interleukin 2 receptor subunit beta
CCL4	3.204984	3.56E-18	2.33E-15	8.691929	Up	C-C motif chemokine ligand 4
MOGAT2	3.186868	2.52E-06	5.25E-05	4.706782	Up	monoacylglycerol O-acyltransferase 2
GZMH	3.172865	3.60E-11	4.19E-09	6.619505	Up	granzyme H
CCDC194	3.163823	1.49E-10	1.45E-08	6.406147	Up	coiled-coil domain containing 194
RNU6-968P	3.160787	2.02E-05	0.000304	4.262574	Up	RNA, U6 small nuclear 968, pseudogene
DYDC2	3.144851	1.31E-09	9.07E-08	6.066751	Up	DPY30 domain containing 2
CCL24	3.143753	0.00933	0.041495	2.599736	Up	C-C motif chemokine ligand 24
CFAP45	3.135547	1.94E-13	4.07E-11	7.352974	Up	cilia and flagella associated protein 45
TPSAB1	3.12225	0.000181	0.001841	3.74393	Up	tryptase alpha/beta 1
TRAJ18	3.117743	2.11E-07	6.53E-06	5.189219	Up	T cell receptor alpha joining 18
NRK	3.112536	1.99E-07	6.22E-06	5.200297	Up	Nik related kinase
IGHV3-69-1	3.106028	0.004192	0.022669	2.863372	Up	immunoglobulin heavy variable 3-69-1 (pseudogene)
PURPL	3.105211	5.41E-07	1.44E-05	5.011114	Up	p53 upregulated regulator of p53 levels
PELATON	3.096723	1.98E-11	2.45E-09	6.707322	Up	plaque enriched lncRNA in atherosclerotic and inflammatory bowel macrophage regulation
SIX3	3.086613	5.13E-06	9.54E-05	4.559224	Up	SIX homeobox 3
CIBAR2	3.086592	5.15E-06	9.56E-05	4.55856	Up	CBY1 interacting BAR domain containing 2
VWA5B1	3.081662	1.21E-10	1.21E-08	6.437767	Up	von Willebrand factor A domain containing 5B1
EPS8L3	3.07738	6.03E-15	1.78E-12	7.803265	Up	EPS8 like 3
TNFRSF13B	3.071467	3.72E-09	2.24E-07	5.895979	Up	TNF receptor superfamily member 13B
IGHD	3.042595	0.00049	0.004121	3.486128	Up	immunoglobulin heavy constant delta
TRAJ26	3.041591	6.00E-05	0.000747	4.012995	Up	T cell receptor alpha joining 26
FASLG	3.035234	9.82E-09	4.94E-07	5.733761	Up	Fas ligand
SLAMF1	3.032021	2.19E-10	2.00E-08	6.347082	Up	signaling lymphocytic activation molecule family member 1
OR9Q1	3.030789	0.000775	0.005971	3.361476	Up	olfactory receptor family 9 subfamily Q member 1
MZB1	3.023392	2.24E-11	2.75E-09	6.689692	Up	marginal zone B and B1 cell specific protein
RN7SKP24	3.0214	3.79E-05	0.000512	4.120084	Up	RN7SK pseudogene 24
SLC35D3	3.00786	0.000902	0.006744	3.319313	Up	solute carrier family 35 member D3
TRBV29-1	2.999279	6.67E-05	0.000814	3.987802	Up	T cell receptor beta variable 29-1
TRBV27	2.999151	1.90E-05	0.000289	4.276293	Up	T cell receptor beta variable 27
CD24	2.993973	1.27E-13	2.78E-11	7.409756	Up	CD24 molecule
IKZF3	2.986933	3.70E-26	6.95E-23	10.57983	Up	IKAROS family zinc finger 3
HMGB1P46	2.97631	2.71E-05	0.000388	4.196647	Up	high mobility group box 1 pseudogene 46
RPL31P11	2.953352	0.000173	0.001778	3.75499	Up	ribosomal protein L31 pseudogene 11
LAX1	2.951106	3.55E-15	1.15E-12	7.86994	Up	lymphocyte transmembrane adaptor 1
DAW1	2.949018	8.62E-14	1.94E-11	7.460532	Up	dynein assembly factor with WD repeats 1
TDGF1	2.948046	1.16E-13	2.57E-11	7.420777	Up	teratocarcinoma-derived growth factor 1

C6orf118	2.947575	1.67E-17	9.87E-15	8.514895	Up	chromosome 6 open reading frame 118
CD2	2.946345	3.31E-12	5.07E-10	6.963863	Up	CD2 molecule
CD28	2.934272	9.71E-12	1.28E-09	6.810744	Up	CD28 molecule
CDCA4P3	2.916556	0.000275	0.002601	3.637315	Up	cell division cycle associated 4 pseudogene 3
IGLV1-36	2.91503	0.000262	0.002501	3.64978	Up	immunoglobulin lambda variable 1-36
MTCO1P20	2.906685	1.71E-05	0.000264	4.299813	Up	MT-CO1 pseudogene 20
FCMR	2.905066	5.48E-16	2.32E-13	8.100306	Up	Fc mu receptor
CLIC6	2.90361	4.06E-10	3.40E-08	6.251579	Up	chloride intracellular channel 6
LYZ	2.894631	2.53E-17	1.40E-14	8.466434	Up	lysozyme
IL7R	2.891134	5.79E-18	3.68E-15	8.63658	Up	interleukin 7 receptor
DNAAF6	2.888379	8.83E-06	0.000151	4.444065	Up	dynein axonemal assembly factor 6
RPL19P18	2.868322	0.00018	0.001831	3.745787	Up	ribosomal protein L19 pseudogene 18
FTH1P22	2.867966	1.57E-06	3.54E-05	4.802458	Up	ferritin heavy chain 1 pseudogene 22
HSH2D	2.859222	1.23E-10	1.22E-08	6.435854	Up	hematopoietic SH2 domain containing
HLA-DRB5	2.858566	5.14E-19	3.90E-16	8.909132	Up	major histocompatibility complex, class II, DR beta 5
NPY2R	2.850473	1.48E-07	4.85E-06	5.254884	Up	neuropeptide Y receptor Y2
FCGR2B	2.846979	8.43E-15	2.40E-12	7.760976	Up	Fc gamma receptor IIb
TUBA4B	2.845888	8.14E-07	2.03E-05	4.93197	Up	tubulin alpha 4b
UBASH3A	2.843522	2.54E-10	2.27E-08	6.32425	Up	ubiquitin associated and SH3 domain containing A
RTP1	2.843383	6.43E-17	3.27E-14	8.357137	Up	receptor transporter protein 1
PLA2G2D	2.842058	1.24E-06	2.92E-05	4.848548	Up	phospholipase A2 group IID
RNU1-28P	2.837998	0.000198	0.001979	3.721723	Up	RNA, U1 small nuclear 28, pseudogene
SNORA20	2.837636	5.99E-08	2.28E-06	5.418984	Up	small nucleolar RNA, H/ACA box 20
VTRNA1-1	2.834068	6.85E-05	0.000832	3.98147	Up	vault RNA 1-1
TRAV13-1	2.826954	0.000183	0.001855	3.741495	Up	T cell receptor alpha variable 13-1
TPSB2	2.813938	1.35E-05	0.000218	4.351269	Up	tryptase beta 2
CYP11B1	2.809674	0.000243	0.00234	3.669596	Up	cytochrome P450 family 11 subfamily B member 1
RNU1-27P	2.799543	0.000306	0.002819	3.610416	Up	RNA, U1 small nuclear 27, pseudogene
TRAV19	2.793145	0.00054	0.004449	3.46011	Up	T cell receptor alpha variable 19
TRAJ24	2.792995	4.51E-05	0.000591	4.079457	Up	T cell receptor alpha joining 24
DRD3	2.779148	0.011431	0.048376	2.529247	Up	dopamine receptor D3
GLYATL1P1	2.772553	7.56E-08	2.77E-06	5.377354	Up	glycine-N-acyltransferase like 1 pseudogene 1
MTHFD2P1	2.770835	0.000606	0.004892	3.428857	Up	methylenetetrahydrofolate dehydrogenase (NADP+ dependent) 2, methenyltetrahydrofolate cyclohydrolase pseudogene 1
TRAJ40	2.767175	0.000847	0.006412	3.336948	Up	T cell receptor alpha joining 40
CD1C	2.764589	0.004532	0.024076	2.838512	Up	CD1c molecule
P2RY8	2.764298	5.82E-14	1.38E-11	7.51206	Up	P2Y receptor family member 8
FOXJ1	2.74989	3.20E-13	6.34E-11	7.285762	Up	forkhead box J1
CLECL1P	2.749365	5.06E-10	4.07E-08	6.21722	Up	C-type lectin like 1, pseudogene
MTATP8P1	2.747186	2.46E-06	5.16E-05	4.711101	Up	MT-ATP8 pseudogene 1
CEACAM16	2.742541	0.00066	0.005235	3.405872	Up	CEA cell adhesion molecule 16, tectorial membrane component
TRAJ48	2.740958	0.002142	0.013374	3.069795	Up	T cell receptor alpha joining 48

NLRP7	2.737118	0.000504	0.004212	3.478366	Up	NLR family pyrin domain containing 7
RNA5SP70	2.727898	0.001619	0.010722	3.152497	Up	RNA, 5S ribosomal pseudogene 70
LAIR2	2.714968	9.59E-08	3.36E-06	5.334241	Up	leukocyte associated immunoglobulin like receptor 2
TRAV12-3	2.712699	0.01031	0.044765	2.565246	Up	T cell receptor alpha variable 12-3
TRAJ7	2.711564	0.000206	0.002043	3.711376	Up	T cell receptor alpha joining 7
PRR32	2.70912	0.005376	0.027369	2.783599	Up	proline rich 32
TRAJ16	2.702491	7.77E-05	0.000924	3.951339	Up	T cell receptor alpha joining 16
TRAJ22	2.701987	4.44E-06	8.47E-05	4.589868	Up	T cell receptor alpha joining 22
RN7SL402P	2.699484	0.000205	0.002033	3.712903	Up	RNA, 7SL, cytoplasmic 402, pseudogene
PGBD3P4	2.69755	0.000265	0.00252	3.647307	Up	piggyBac transposable element derived 3 pseudogene 4
STMND1	2.696951	1.40E-13	3.02E-11	7.396773	Up	stathmin domain containing 1
TRBV20-1	2.691503	0.002456	0.014935	3.028758	Up	T cell receptor beta variable 20-1
XIRP2	2.688695	0.000442	0.003793	3.513666	Up	xin actin binding repeat containing 2
CD3D	2.683004	2.17E-08	9.75E-07	5.597557	Up	CD3 delta subunit of T-cell receptor complex
RNU6-511P	2.682155	0.002676	0.016024	3.002662	Up	RNA, U6 small nuclear 511, pseudogene
TRBC1	2.67945	4.39E-09	2.56E-07	5.868623	Up	T cell receptor beta constant 1
DNAI3	2.677946	6.71E-12	9.33E-10	6.86369	Up	dynein axonemal intermediate chain 3
TRBV28	2.676431	7.63E-05	0.000912	3.955707	Up	T cell receptor beta variable 28
C6orf141	2.671448	4.08E-07	1.14E-05	5.06539	Up	chromosome 6 open reading frame 141
TAB2	2.67141	1.32E-19	1.12E-16	9.058631	Up	TGF-beta activated kinase 1 (MAP3K7) binding protein 2
ICOS	2.667114	1.43E-07	4.71E-06	5.261213	Up	inducible T cell costimulator
CLEC12A	2.659187	3.08E-07	8.97E-06	5.11862	Up	C-type lectin domain family 12 member A
MGC4859	2.65776	2.92E-05	0.000412	4.179632	Up	uncharacterized LOC79150
PCP4	2.655991	8.68E-11	9.04E-09	6.488321	Up	Purkinje cell protein 4
LHCGR	2.655985	2.33E-15	7.79E-13	7.922579	Up	luteinizing hormone/choriogonadotropin receptor
IL24	2.647003	1.13E-08	5.55E-07	5.710622	Up	interleukin 24
PCAT19	2.633966	1.32E-15	4.70E-13	7.99318	Up	prostate cancer associated transcript 19
TRAJ11	2.625397	0.00062	0.004982	3.422847	Up	T cell receptor alpha joining 11
CD3G	2.62514	3.53E-10	3.04E-08	6.273298	Up	CD3 gamma subunit of T-cell receptor complex
SYNDIG1L	2.624628	1.93E-08	8.82E-07	5.617938	Up	synapse differentiation inducing 1 like
CCL5	2.624212	2.07E-19	1.69E-16	9.009623	Up	C-C motif chemokine ligand 5
CCL3	2.623699	0.000512	0.004264	3.474447	Up	C-C motif chemokine ligand 3
RNU7-156P	2.623599	0.000359	0.003202	3.568366	Up	RNA, U7 small nuclear 156 pseudogene
TNNI3	2.6183	9.47E-06	0.00016	4.428842	Up	troponin I3, cardiac type
TRAV12-2	2.61039	0.005577	0.028165	2.77165	Up	T cell receptor alpha variable 12-2
TRAJ13	2.60595	0.000403	0.003519	3.538071	Up	T cell receptor alpha joining 13
SIGLEC6	2.603157	0.007482	0.035107	2.674612	Up	sialic acid binding Ig like lectin 6
TRAJ6	2.601095	0.000117	0.001282	3.853341	Up	T cell receptor alpha joining 6
RNU6-35P	2.59925	0.004154	0.022517	2.866189	Up	RNA, U6 small nuclear 35, pseudogene
GPR101	2.592832	0.001003	0.007342	3.289802	Up	G protein-coupled receptor 101
EIF4BP8	2.591835	0.002684	0.01606	3.001769	Up	eukaryotic translation initiation factor 4B pseudogene 8
TRBV6-7	2.590423	0.0027	0.016141	3.000024	Up	T cell receptor beta variable 6-7 (non-functional)

LTF	2.588857	6.12E-09	3.35E-07	5.813371	Up	lactotransferrin
HISLA	2.588239	5.33E-15	1.62E-12	7.818945	Up	HIF1A stabilizing long noncoding RNA
ITK	2.587415	3.19E-12	4.90E-10	6.969221	Up	IL2 inducible T cell kinase
H4C13	2.586782	1.24E-10	1.23E-08	6.434549	Up	H4 clustered histone 13
AKR1C4	2.584239	0.004611	0.0244	2.832995	Up	aldo-keto reductase family 1 member C4
C1orf87	2.583897	1.29E-10	1.28E-08	6.42812	Up	chromosome 1 open reading frame 87
TRAJ10	2.582	5.61E-06	0.000103	4.54065	Up	T cell receptor alpha joining 10
SAGE1	2.581355	3.06E-06	6.19E-05	4.666984	Up	sarcoma antigen 1
CD52	2.577628	4.68E-10	3.82E-08	6.229474	Up	CD52 molecule
FAM183A	2.572989	6.72E-06	0.00012	4.502302	Up	family with sequence similarity 183 member A
TRAV8-2	2.570789	0.003151	0.018189	2.952654	Up	T cell receptor alpha variable 8-2
HOXB3	2.569759	1.23E-09	8.63E-08	6.076834	Up	homeobox B3
RN7SL193P	2.561035	3.74E-06	7.34E-05	4.625084	Up	RNA, 7SL, cytoplasmic 193, pseudogene
KRT17P6	2.560245	3.39E-05	0.000468	4.145302	Up	keratin 17 pseudogene 6
POTEF	2.556908	0.001515	0.010186	3.171751	Up	POTE ankyrin domain family member F
CATSPERD	2.554109	1.27E-06	2.97E-05	4.844565	Up	cation channel sperm associated auxiliary subunit delta
TRBV18	2.551622	0.001041	0.007568	3.279325	Up	T cell receptor beta variable 18
TRARG1	2.550504	6.54E-05	0.000801	3.992425	Up	trafficking regulator of GLUT4 (SLC2A4) 1
CD163	2.548294	2.86E-19	2.29E-16	8.97382	Up	CD163 molecule
HS3ST3A1	2.545491	4.47E-07	1.23E-05	5.047973	Up	heparan sulfate-glucosamine 3-sulfotransferase 3A1
GPNMB	2.538488	9.75E-16	3.63E-13	8.030017	Up	glycoprotein nmb
CTLA4	2.532196	9.04E-09	4.62E-07	5.747878	Up	cytotoxic T-lymphocyte associated protein 4
MTND4P24	2.531531	0.000135	0.001441	3.81732	Up	MT-ND4 pseudogene 24
SLC25A52	2.520769	3.79E-07	1.07E-05	5.079159	Up	solute carrier family 25 member 52
GZMAP1	2.509274	0.007505	0.035193	2.673572	Up	granzyme A pseudogene 1
MYO3A	2.506414	6.19E-08	2.33E-06	5.413334	Up	myosin IIIA
TFAP2D	2.506182	0.009684	0.042651	2.586905	Up	transcription factor AP-2 delta
IRF4	2.506033	4.39E-15	1.36E-12	7.843299	Up	interferon regulatory factor 4
GSDMA	2.505793	1.31E-05	0.000212	4.35768	Up	gasdermin A
MTATP6P13	2.495667	0.004151	0.022504	2.866451	Up	MT-ATP6 pseudogene 13
TRAV14DV4	2.490731	0.002978	0.017422	2.97	Up	T cell receptor alpha variable 14/delta variable 4
SDC1	2.489358	3.56E-09	2.15E-07	5.903655	Up	syndecan 1
FAM187B2P	2.484456	2.36E-06	4.99E-05	4.719493	Up	family with sequence similarity 187, member B pseudogene
FCGBP	2.483683	1.02E-14	2.83E-12	7.736488	Up	Fc gamma binding protein
TNFRSF9	2.483264	2.03E-07	6.34E-06	5.196241	Up	TNF receptor superfamily member 9
GOLGA2P1	2.481862	0.006786	0.032701	2.707148	Up	GOLGA2 pseudogene 1
LCK	2.478524	9.73E-12	1.28E-09	6.810462	Up	LCK proto-oncogene, Src family tyrosine kinase
TEKT4	2.475929	0.001821	0.011748	3.117976	Up	tektin 4
CD209	2.473703	1.45E-17	8.70E-15	8.531105	Up	CD209 molecule
TRBV5-6	2.473344	0.001131	0.008078	3.255731	Up	T cell receptor beta variable 5-6
IGLV1-51	2.471567	5.64E-09	3.15E-07	5.827198	Up	immunoglobulin lambda variable 1-51
ANKRD66	2.469538	1.96E-07	6.15E-06	5.202745	Up	ankyrin repeat domain 66

LIPM	2.465883	0.000101	0.001144	3.88933	Up	lipase family member M
MTCYBP34	2.465014	0.000516	0.004292	3.472334	Up	MT-CYB pseudogene 34
FNDC1-IT1	2.464882	0.003157	0.018214	2.952018	Up	FNDC1 intronic transcript 1
KRT18P38	2.462628	0.007763	0.03611	2.662228	Up	keratin 18 pseudogene 38
TRAJ3	2.459336	0.000135	0.001441	3.817419	Up	T cell receptor alpha joining 3
MAT1A	2.455929	7.26E-06	0.000127	4.486051	Up	methionine adenosyltransferase 1A
C6	2.455485	1.38E-09	9.56E-08	6.057323	Up	complement C6
IQGAP2	2.455181	5.84E-23	7.65E-20	9.866097	Up	IQ motif containing GTPase activating protein 2
NCR1	2.455156	4.27E-05	0.000564	4.092151	Up	natural cytotoxicity triggering receptor 1
TRBV5-5	2.45292	0.002186	0.013602	3.063716	Up	T cell receptor beta variable 5-5
TUBAL3	2.452748	1.63E-06	3.66E-05	4.794631	Up	tubulin alpha like 3
RNA5SP131	2.451042	0.000411	0.00357	3.533179	Up	RNA, 5S ribosomal pseudogene 131
RPS2P4	2.448819	1.68E-06	3.75E-05	4.78838	Up	ribosomal protein S2 pseudogene 4
GOLGA2P2Y	2.442343	0.011923	0.049989	2.514429	Up	GOLGA2 pseudogene 2 Y-linked
NUTM2E	2.431876	0.000339	0.003057	3.583589	Up	NUT family member 2E
MUC3A	2.430954	5.74E-08	2.20E-06	5.426803	Up	mucin 3A, cell surface associated
TRBV7-5	2.430215	0.000905	0.00676	3.31837	Up	T cell receptor beta variable 7-5 (pseudogene)
CDC20B	2.426913	1.07E-05	0.000177	4.402978	Up	cell division cycle 20B
HMGB3P25	2.416022	0.000209	0.002064	3.707642	Up	high mobility group box 3 pseudogene 25
CAPSL	2.414583	8.22E-08	2.96E-06	5.362138	Up	calcyphosine like
RNU6-1300P	2.41242	4.15E-06	8.00E-05	4.603615	Up	RNA, U6 small nuclear 1300, pseudogene
MTDHP3	2.408667	0.000129	0.001389	3.828466	Up	metadherin pseudogene 3
TRAC	2.399511	6.67E-13	1.21E-10	7.18597	Up	T cell receptor alpha constant
DNAH3	2.398772	1.42E-10	1.39E-08	6.413737	Up	dynein axonemal heavy chain 3
CDA	2.393538	8.51E-09	4.43E-07	5.758063	Up	cytidine deaminase
PRSS21	2.393048	1.54E-05	0.000242	4.3232	Up	serine protease 21
XCL2	2.391791	0.000731	0.005688	3.377769	Up	X-C motif chemokine ligand 2
TEKT1	2.390847	3.49E-10	3.00E-08	6.275413	Up	tektin 1
FOXL2	2.386873	1.15E-07	3.91E-06	5.301612	Up	forkhead box L2
MS4A14	2.385237	1.33E-20	1.31E-17	9.305517	Up	membrane spanning 4-domains A14
KRTDAP	2.374026	0.000643	0.005129	3.412752	Up	keratinocyte differentiation associated protein
B4GALNT2	2.370002	0.00018	0.001836	3.744989	Up	beta-1,4-N-acetyl-galactosaminyltransferase 2
GTF2A1L	2.368646	8.96E-05	0.001039	3.917096	Up	general transcription factor IIA subunit 1 like
TRAJ31	2.365751	0.00431	0.023139	2.854569	Up	T cell receptor alpha joining 31
MTCO1P22	2.365348	5.75E-06	0.000105	4.535255	Up	MT-CO1 pseudogene 22
C19orf84	2.364238	2.31E-07	7.06E-06	5.172245	Up	chromosome 19 open reading frame 84
ART5	2.364133	0.000751	0.005813	3.370403	Up	ADP-ribosyltransferase 5
CRABP1	2.358903	1.30E-06	3.04E-05	4.839467	Up	cellular retinoic acid binding protein 1
TRAJ20	2.357867	0.001601	0.010619	3.155711	Up	T cell receptor alpha joining 20
TTLL10	2.355612	0.000288	0.002691	3.625933	Up	tubulin tyrosine ligase like 10
RNU6-1061P	2.352412	0.011441	0.0484	2.528932	Up	RNA, U6 small nuclear 1061, pseudogene
TRIML2	2.351192	0.00055	0.004519	3.455087	Up	tripartite motif family like 2
MCIDAS	2.348837	0.010757	0.046234	2.550493	Up	multiciliate differentiation and DNA synthesis

						associated cell cycle protein
GSTO3P	2.348156	0.008548	0.03889	2.629632	Up	glutathione S-transferase omega 3, pseudogene
PRPH	2.347791	6.58E-09	3.56E-07	5.801376	Up	peripherin
AOC1	2.347765	1.55E-10	1.49E-08	6.400321	Up	amine oxidase copper containing 1
IL5RA	2.34749	1.90E-10	1.78E-08	6.3695	Up	interleukin 5 receptor subunit alpha
RN7SL219P	2.34365	2.37E-06	5.00E-05	4.719207	Up	RNA, 7SL, cytoplasmic 219, pseudogene
MYH2	2.34313	0.000574	0.004681	3.443796	Up	myosin heavy chain 2
NDUFB4P12	2.342175	0.000186	0.001877	3.737979	Up	NADH:ubiquinone oxidoreductase subunit B4 pseudogene 12
RNU6-1148P	2.338507	0.006894	0.033122	2.701939	Up	RNA, U6 small nuclear 1148, pseudogene
KRT42P	2.338178	0.000638	0.005097	3.414928	Up	keratin 42, pseudogene
TRGV5P	2.336804	0.000153	0.0016	3.786682	Up	T cell receptor gamma variable 5P (pseudogene)
SIK1	2.33675	1.63E-05	0.000253	4.310826	Up	salt inducible kinase 1
TUBB6P1	2.335907	0.000688	0.005416	3.394155	Up	tubulin beta 6 class V pseudogene 1
F13A1	2.335434	4.04E-15	1.29E-12	7.853544	Up	coagulation factor XIII A chain
RN7SKP13	2.335324	0.007426	0.034922	2.677113	Up	RN7SK pseudogene 13
WT1	2.335307	0.007073	0.033715	2.693375	Up	WT1 transcription factor
TRAJ27	2.331792	0.010904	0.046741	2.545769	Up	T cell receptor alpha joining 27
RNU1-136P	2.330118	0.000521	0.004328	3.469568	Up	RNA, U1 small nuclear 136, pseudogene
MAPK15	2.328436	4.35E-06	8.32E-05	4.593858	Up	mitogen-activated protein kinase 15
CD8B	2.325886	1.22E-06	2.88E-05	4.851934	Up	CD8b molecule
TRAJ9	2.325496	0.00099	0.007271	3.293281	Up	T cell receptor alpha joining 9
MS4A7	2.323466	6.42E-16	2.64E-13	8.080988	Up	membrane spanning 4-domains A7
TRBJ1-3	2.322928	0.001232	0.008648	3.231414	Up	T cell receptor beta joining 1-3
PPIAP75	2.322255	0.008801	0.039728	2.61969	Up	peptidylprolyl isomerase A pseudogene 75
OR2T6	2.32019	0.000615	0.004953	3.424955	Up	olfactory receptor family 2 subfamily T member 6
RPL29P2	2.315552	0.00056	0.004582	3.450492	Up	ribosomal protein L29 pseudogene 2
MSR1	2.314735	4.26E-15	1.34E-12	7.847069	Up	macrophage scavenger receptor 1
ALOX15B	2.312127	2.87E-08	1.23E-06	5.549073	Up	arachidonate 15-lipoxygenase type B
PTGDR	2.310319	3.59E-11	4.18E-09	6.620262	Up	prostaglandin D2 receptor
LPAR3	2.308994	4.29E-14	1.07E-11	7.551827	Up	lysophosphatidic acid receptor 3
CFAP157	2.306183	3.27E-09	1.99E-07	5.917616	Up	cilia and flagella associated protein 157
RNU6-959P	2.305238	0.005255	0.026928	2.79099	Up	RNA, U6 small nuclear 959, pseudogene
GML	2.304102	0.004183	0.022632	2.864052	Up	glycosylphosphatidylinositol anchored molecule like
CDHR4	2.302566	7.92E-05	0.000939	3.946747	Up	cadherin related family member 4
CRNN	2.301304	0.000364	0.003238	3.56489	Up	cornulin
JSRP1	2.295409	6.15E-06	0.000111	4.521046	Up	junctional sarcoplasmic reticulum protein 1
RNU6-657P	2.290608	0.010939	0.046853	2.544651	Up	RNA, U6 small nuclear 657, pseudogene
JAML	2.289737	3.55E-17	1.87E-14	8.426856	Up	junction adhesion molecule like
MTCYBP41	2.287487	0.000642	0.005125	3.413158	Up	MT-CYB pseudogene 41
HMGB3P18	2.286238	0.001475	0.009982	3.179617	Up	high mobility group box 3 pseudogene 18
TMIE	2.284492	1.04E-17	6.32E-15	8.569709	Up	transmembrane inner ear
H2BL1P	2.280991	5.65E-05	0.000713	4.027136	Up	H2B.L histone variant 1, pseudogene

PIWIL3	2.279502	0.001176	0.00834	3.244689	Up	piwi like RNA-mediated gene silencing 3
DNAH11	2.278761	1.70E-14	4.55E-12	7.671124	Up	dynein axonemal heavy chain 11
GBP5	2.278653	1.06E-19	9.18E-17	9.082386	Up	guanylate binding protein 5
CORO1CP1	2.277287	0.006374	0.031172	2.727898	Up	CORO1C pseudogene 1
NTS	2.275531	1.40E-05	0.000223	4.344611	Up	neurotensin
NMRK2	2.270988	3.93E-05	0.000526	4.111797	Up	nicotinamide riboside kinase 2
HGF	2.268418	1.66E-24	2.47E-21	10.21721	Up	hepatocyte growth factor
RNASE10	2.267054	0.001389	0.009522	3.196931	Up	ribonuclease A family member 10 (inactive)
HPAT5	2.266209	0.009324	0.041482	2.599926	Up	human pluripotency-associated transcript 5
TRAJ45	2.265859	0.001591	0.010573	3.157624	Up	T cell receptor alpha joining 45
LCN8	2.265686	0.003233	0.018567	2.944636	Up	lipocalin 8
RIBC2	2.26544	1.86E-11	2.32E-09	6.716557	Up	RIB43A domain with coiled-coils 2
RNA5SP488	2.264995	0.000493	0.00414	3.48428	Up	RNA, 5S ribosomal pseudogene 488
TRBV7-7	2.263429	0.002496	0.015135	3.023849	Up	T cell receptor beta variable 7-7
C11orf86	2.262763	0.008643	0.039199	2.625867	Up	chromosome 11 open reading frame 86
CDRT15P3	2.262597	0.000493	0.004136	3.484634	Up	CDRT15 pseudogene 3
SLC22A31	2.261314	0.008327	0.038137	2.63853	Up	solute carrier family 22 member 31
ZBBX	2.259523	9.53E-13	1.68E-10	7.137187	Up	zinc finger B-box domain containing
DPRXP6	2.258929	0.010238	0.044526	2.567697	Up	divergent-paired related homeobox pseudogene 6
SNORA70F	2.258601	0.000905	0.006757	3.318612	Up	small nucleolar RNA, H/ACA box 70F
RNA5SP435	2.258059	0.000386	0.003394	3.549721	Up	RNA, 5S ribosomal pseudogene 435
POM121L2	2.257763	0.000632	0.005062	3.417396	Up	POM121 transmembrane nucleoporin like 2
MICB	2.255347	1.56E-15	5.43E-13	7.972207	Up	MHC class I polypeptide-related sequence B
TRPM8	2.245189	3.57E-09	2.15E-07	5.903173	Up	transient receptor potential cation channel subfamily M member 8
MYB	2.244675	9.27E-08	3.27E-06	5.340392	Up	MYB proto-oncogene, transcription factor
FOXF2	2.243871	1.56E-10	1.50E-08	6.399118	Up	forkhead box F2
OR1J1	2.243868	0.000766	0.005912	3.364943	Up	olfactory receptor family 1 subfamily J member 1
RNU6-908P	2.240717	0.002102	0.013177	3.075371	Up	RNA, U6 small nuclear 908, pseudogene
ADGRG6	2.240372	8.19E-18	5.13E-15	8.596877	Up	adhesion G protein-coupled receptor G6
C1orf141	2.239853	1.49E-07	4.87E-06	5.254042	Up	chromosome 1 open reading frame 141
RNU1-18P	2.234506	0.000102	0.00116	3.885486	Up	RNA, U1 small nuclear 18, pseudogene
TRBC2	2.231132	1.32E-12	2.23E-10	7.091838	Up	T cell receptor beta constant 2
IL2RG	2.230515	1.94E-20	1.82E-17	9.265833	Up	interleukin 2 receptor subunit gamma
MTND2P28	2.227591	2.20E-08	9.81E-07	5.595516	Up	MT-ND2 pseudogene 28
MRC1	2.221527	7.32E-17	3.64E-14	8.341755	Up	mannose receptor C-type 1
TRBV5-4	2.218166	0.001092	0.007855	3.26561	Up	T cell receptor beta variable 5-4
FOLR2	2.217489	3.12E-12	4.85E-10	6.972088	Up	folate receptor beta
RNU6-194P	2.217308	4.30E-06	8.24E-05	4.596379	Up	RNA, U6 small nuclear 194, pseudogene
DIO3	2.216404	3.82E-06	7.46E-05	4.620962	Up	iodothyronine deiodinase 3
LRRC77P	2.214253	5.16E-06	9.58E-05	4.55817	Up	leucine rich repeat containing 77, pseudogene
CD96	2.214213	3.69E-14	9.33E-12	7.571419	Up	CD96 molecule
SIGLEC1	2.212265	5.50E-13	1.02E-10	7.212406	Up	sialic acid binding Ig like lectin 1

UCN3	2.207121	0.001763	0.01145	3.127513	Up	urocortin 3
TRBV7-9	2.205271	0.000171	0.001762	3.757925	Up	T cell receptor beta variable 7-9
CHIT1	2.204519	1.96E-08	8.93E-07	5.615236	Up	chitinase 1
POTEI	2.203428	0.004518	0.02403	2.839531	Up	POTE ankyrin domain family member I
MROH2B	2.202867	0.009771	0.042954	2.583835	Up	maestro heat like repeat family member 2B
OR4G6P	-25.5969	2.95E-15	9.72E-13	-7.89321	Down	olfactory receptor family 4 subfamily G member 6 pseudogene
ADGRG7	-8.58446	1.25E-09	8.77E-08	-6.07346	Down	adhesion G protein-coupled receptor G7
OR4F4	-5.85182	4.62E-05	0.000603	-4.07412	Down	olfactory receptor family 4 subfamily F member 4
FAM138E	-5.09552	0.004962	0.025791	-2.80949	Down	family with sequence similarity 138 member E
NKX2-4	-2.4967	7.16E-06	0.000126	-4.48897	Down	NK2 homeobox 4
PLAC8	-2.43595	1.09E-12	1.86E-10	-7.11872	Down	placenta associated 8
RXFP4	-2.31739	4.79E-09	2.74E-07	-5.85445	Down	relaxin family peptide/INSL5 receptor 4
ICOSLG	-2.26241	6.48E-08	2.42E-06	-5.40495	Down	inducible T cell costimulator ligand
SFN	-2.18937	2.38E-06	5.03E-05	-4.71783	Down	stratifin
PLAC9P1	-2.17385	5.14E-10	4.11E-08	-6.21474	Down	placenta associated 9 pseudogene 1
CIROP	-2.15476	4.28E-15	1.34E-12	-7.84642	Down	ciliated left-right organizer metallopeptidase
GRHL3	-2.15109	8.85E-10	6.59E-08	-6.12882	Down	grainyhead like transcription factor 3
UGT2B17	-2.0886	0.003996	0.021856	-2.8785	Down	UDP glucuronosyltransferase family 2 member B17
IL9	-2.0504	2.48E-11	3.02E-09	-6.67429	Down	interleukin 9
TMEM88B	-2.02877	1.63E-10	1.56E-08	-6.39237	Down	transmembrane protein 88B
ADAMTS14	-1.98454	2.04E-10	1.89E-08	-6.35815	Down	ADAM metallopeptidase with thrombospondin type 1 motif 14
TMEFF1	-1.96678	0.000496	0.004154	-3.48293	Down	transmembrane protein with EGF like and two follistatin like domains 1
STC2	-1.95851	1.40E-09	9.58E-08	-6.05591	Down	stanniocalcin 2
GJC2	-1.94723	4.47E-09	2.60E-07	-5.86577	Down	gap junction protein gamma 2
C11orf96	-1.89951	5.87E-07	1.54E-05	-4.9953	Down	chromosome 11 open reading frame 96
PPP1R12BP1	-1.87007	4.35E-06	8.32E-05	-4.5938	Down	protein phosphatase 1 regulatory subunit 12B pseudogene 1
TEX44	-1.86075	0.000975	0.007184	-3.29758	Down	testis expressed 44
NPPC	-1.85514	2.39E-05	0.00035	-4.22482	Down	natriuretic peptide C
DAO	-1.85111	2.48E-09	1.58E-07	-5.96267	Down	D-amino acid oxidase
CPAMD8	-1.81242	2.23E-10	2.03E-08	-6.34426	Down	C3 and PZP like alpha-2-macroglobulin domain containing 8
CIR1P2	-1.78812	4.72E-10	3.85E-08	-6.22817	Down	CIR1 pseudogene 2
VEGFA	-1.77755	9.36E-09	4.76E-07	-5.74197	Down	vascular endothelial growth factor A
RASAL1	-1.75144	2.18E-10	1.99E-08	-6.34826	Down	RAS protein activator like 1
SYS1-DBNDD2	-1.74965	2.18E-08	9.76E-07	-5.5967	Down	SYS1-DBNDD2 readthrough (NMD candidate)
ADM	-1.74493	1.85E-10	1.75E-08	-6.37338	Down	adrenomedullin
SMIM32	-1.72996	0.000227	0.002209	-3.68712	Down	small integral membrane protein 32
IL31RA	-1.71948	3.16E-05	0.000441	-4.16133	Down	interleukin 31 receptor A
CHRM5	-1.70513	0.000132	0.001419	-3.82215	Down	cholinergic receptor muscarinic 5
CA9	-1.6961	0.00052	0.00432	-3.47013	Down	carbonic anhydrase 9
CTSV	-1.67945	4.15E-09	2.45E-07	-5.8779	Down	cathepsin V
SLC25A48	-1.67882	2.73E-12	4.32E-10	-6.99105	Down	solute carrier family 25 member 48

KCNG4	-1.67471	1.46E-07	4.80E-06	-5.25699	Down	potassium voltage-gated channel modifier subfamily G member 4
SAA2	-1.67305	6.51E-05	0.000798	-3.99357	Down	serum amyloid A2
HILPDA	-1.66926	1.50E-07	4.90E-06	-5.25282	Down	hypoxia inducible lipid droplet associated
ZNF705G	-1.66674	0.002099	0.013167	-3.07583	Down	zinc finger protein 705G
LIPC	-1.65244	1.92E-14	5.09E-12	-7.65593	Down	lipase C, hepatic type
C8orf74	-1.63296	0.004414	0.023601	-2.84698	Down	chromosome 8 open reading frame 74
MAP6D1	-1.62728	8.99E-08	3.18E-06	-5.34601	Down	MAP6 domain containing 1
COL9A3	-1.61567	6.37E-10	4.92E-08	-6.18102	Down	collagen type IX alpha 3 chain
CARNS1	-1.60946	2.28E-08	1.01E-06	-5.5892	Down	carnosine synthase 1
CR2	-1.59638	3.99E-09	2.36E-07	-5.88464	Down	complement C3d receptor 2
GACAT3	-1.58916	1.62E-05	0.000253	-4.31132	Down	gastric cancer associated transcript 3
COL9A2	-1.5776	8.27E-10	6.24E-08	-6.13958	Down	collagen type IX alpha 2 chain
HOXD1	-1.57645	0.000192	0.001932	-3.72954	Down	homeobox D1
RPS2P1	-1.57446	2.27E-05	0.000335	-4.23686	Down	ribosomal protein S2 pseudogene 1
EXD1	-1.57368	9.89E-08	3.45E-06	-5.32869	Down	exonuclease 3'-5' domain containing 1
RNU6-1160P	-1.56615	4.63E-07	1.27E-05	-5.0409	Down	RNA, U6 small nuclear 1160, pseudogene
SEMA3B	-1.56577	3.81E-11	4.38E-09	-6.61132	Down	semaphorin 3B
SAPCD2	-1.55972	4.14E-09	2.44E-07	-5.87865	Down	suppressor APC domain containing 2
INSM1	-1.55295	8.21E-07	2.04E-05	-4.9304	Down	INSM transcriptional repressor 1
USP17L1	-1.54908	1.02E-05	0.000171	-4.41202	Down	ubiquitin specific peptidase 17 like family member 1
ANGPTL4	-1.54676	3.85E-10	3.26E-08	-6.25993	Down	angiopoietin like 4
CHI3L1	-1.52703	2.86E-05	0.000406	-4.18397	Down	chitinase 3 like 1
DBNDD2	-1.51549	2.63E-08	1.15E-06	-5.56424	Down	dysbindin domain containing 2
C1orf116	-1.50814	1.31E-06	3.05E-05	-4.83869	Down	chromosome 1 open reading frame 116
TUBB4A	-1.50726	6.02E-13	1.11E-10	-7.19997	Down	tubulin beta 4A class IVa
SOX3	-1.50447	1.06E-05	0.000176	-4.40462	Down	SRY-box transcription factor 3
MAG	-1.49487	9.59E-09	4.87E-07	-5.73789	Down	myelin associated glycoprotein
TACSTD2	-1.49391	6.27E-06	0.000113	-4.51714	Down	tumor associated calcium signal transducer 2
SCNN1G	-1.4925	0.000323	0.002946	-3.59583	Down	sodium channel epithelial 1 subunit gamma
AATK	-1.48396	4.36E-07	1.20E-05	-5.05236	Down	apoptosis associated tyrosine kinase
GCM1	-1.47853	0.000469	0.003975	-3.49777	Down	glial cells missing transcription factor 1
PRODH	-1.47777	0.000856	0.006465	-3.33407	Down	proline dehydrogenase 1
SCART1	-1.46813	3.45E-12	5.26E-10	-6.95791	Down	scavenger receptor family member expressed on T cells 1
RPS2P30	-1.46804	2.80E-06	5.76E-05	-4.68509	Down	ribosomal protein S2 pseudogene 30
CHP2	-1.46103	6.24E-05	0.000772	-4.00345	Down	calcineurin like EF-hand protein 2
CYP1D1P	-1.45656	9.56E-06	0.000162	-4.42679	Down	cytochrome P450 family 1 subfamily D member 1, pseudogene
CHADL	-1.45485	4.76E-06	8.95E-05	-4.57529	Down	chondroadherin like
GPR142	-1.44715	0.002327	0.014298	-3.04493	Down	G protein-coupled receptor 142
LDB3	-1.44172	5.69E-09	3.17E-07	-5.82568	Down	LIM domain binding 3
CNP	-1.43958	4.57E-09	2.64E-07	-5.86196	Down	2',3'-cyclic nucleotide 3' phosphodiesterase
GPD1	-1.43924	1.66E-06	3.71E-05	-4.79136	Down	glycerol-3-phosphate dehydrogenase 1
FAM53A	-1.43394	7.66E-08	2.79E-06	-5.37493	Down	family with sequence similarity 53 member A

SCHIP1	-1.4323	5.93E-10	4.67E-08	-6.19224	Down	schwannomin interacting protein 1
PRR18	-1.43204	1.47E-11	1.87E-09	-6.75125	Down	proline rich 18
PKD1L2	-1.43021	2.05E-10	1.89E-08	-6.35734	Down	polycystin 1 like 2 (gene/pseudogene)
BMP8A	-1.42783	6.42E-06	0.000115	-4.51205	Down	bone morphogenetic protein 8a
TBATA	-1.42227	0.005126	0.026449	-2.79899	Down	thymus, brain and testes associated
ACP7	-1.42143	6.42E-06	0.000115	-4.51206	Down	acid phosphatase 7, tartrate resistant (putative)
CPB1	-1.41151	1.18E-10	1.18E-08	-6.44218	Down	carboxypeptidase B1
DMBT1	-1.40963	4.05E-07	1.13E-05	-5.06664	Down	deleted in malignant brain tumors 1
KBTBD11-OT1	-1.40851	5.83E-14	1.38E-11	-7.5119	Down	KBTBD11 overlapping transcript 1
BTG4	-1.39705	1.19E-05	0.000196	-4.37852	Down	BTG anti-proliferation factor 4
ZP3P1	-1.39348	0.000496	0.004154	-3.48297	Down	ZP3 pseudogene 1
FOXE1	-1.39161	5.34E-05	0.000682	-4.04025	Down	forkhead box E1
HMGB1P43	-1.39063	0.011328	0.048074	-2.53241	Down	high mobility group box 1 pseudogene 43
MAP1LC3B2	-1.39043	9.11E-10	6.71E-08	-6.12423	Down	microtubule associated protein 1 light chain 3 beta 2
PDIA2	-1.39039	4.72E-05	0.000614	-4.06884	Down	protein disulfide isomerase family A member 2
OR2K2	-1.38589	0.000106	0.001192	-3.87698	Down	olfactory receptor family 2 subfamily K member 2
WASH8P	-1.38517	3.11E-10	2.72E-08	-6.29321	Down	WAS protein family homolog 8, pseudogene
OPLAH	-1.37796	3.15E-07	9.16E-06	-5.1142	Down	5-oxoprolinase, ATP-hydrolysing
HES6	-1.37734	2.85E-06	5.85E-05	-4.68151	Down	hes family bHLH transcription factor 6
COL11A2	-1.37719	3.97E-09	2.36E-07	-5.8855	Down	collagen type XI alpha 2 chain
RPL26P18	-1.37191	0.003986	0.021822	-2.87923	Down	ribosomal protein L26 pseudogene 18
TRPV6	-1.37042	1.53E-15	5.38E-13	-7.97437	Down	transient receptor potential cation channel subfamily V member 6
RNU6-913P	-1.36459	0.000116	0.001273	-3.85534	Down	RNA, U6 small nuclear 913, pseudogene
CDH1	-1.35955	2.46E-06	5.15E-05	-4.71141	Down	cadherin 1
RABGEF1	-1.35858	6.90E-14	1.60E-11	-7.48975	Down	RAB guanine nucleotide exchange factor 1
FTCD	-1.35811	5.92E-06	0.000107	-4.52907	Down	formimidoyltransferase cyclodeaminase
ARC	-1.35638	0.000132	0.001418	-3.82262	Down	activity regulated cytoskeleton associated protein
RN7SL520P	-1.35291	2.78E-05	0.000395	-4.19115	Down	RNA, 7SL, cytoplasmic 520, pseudogene
SREBF1	-1.35236	3.84E-10	3.26E-08	-6.26023	Down	sterol regulatory element binding transcription factor 1
TMTC4	-1.35104	2.82E-12	4.45E-10	-6.98634	Down	transmembrane O-mannosyltransferase targeting cadherins 4
GDF2	-1.35047	0.00945	0.041907	-2.59532	Down	growth differentiation factor 2
RN7SKP145	-1.34966	0.007267	0.034367	-2.68438	Down	RN7SK pseudogene 145
CPHXL	-1.34658	9.52E-10	6.94E-08	-6.11722	Down	cytoplasmic polyadenylated homeobox like
ABCF2P1	-1.34609	6.24E-05	0.000772	-4.00338	Down	ATP binding cassette subfamily F member 2 pseudogene 1
RNU6-871P	-1.3446	5.86E-05	0.000733	-4.01851	Down	RNA, U6 small nuclear 871, pseudogene
PYY2	-1.34242	0.001853	0.011924	-3.11276	Down	peptide YY 2 (pseudogene)
LIPE	-1.33945	6.74E-08	2.49E-06	-5.39807	Down	lipase E, hormone sensitive type
RN7SL808P	-1.33791	0.005177	0.026632	-2.79578	Down	RNA, 7SL, cytoplasmic 808, pseudogene
FAM178B	-1.33665	1.47E-07	4.80E-06	-5.25679	Down	family with sequence similarity 178 member B
COL16A1	-1.33577	2.73E-08	1.18E-06	-5.5578	Down	collagen type XVI alpha 1 chain
TXNDC8	-1.3356	0.008816	0.039772	-2.6191	Down	thioredoxin domain containing 8
CNDP1	-1.32376	3.30E-09	2.01E-07	-5.91585	Down	carnosine dipeptidase 1

DHCR7	-1.31902	1.10E-09	7.89E-08	-6.0937	Down	7-dehydrocholesterol reductase
GLOD5	-1.31444	0.008251	0.037863	-2.64162	Down	glyoxalase domain containing 5
FXYD4	-1.3054	1.96E-05	0.000296	-4.26995	Down	FXYD domain containing ion transport regulator 4
RNU6-448P	-1.29755	0.000886	0.006645	-3.32442	Down	RNA, U6 small nuclear 448, pseudogene
KIF19	-1.29668	9.09E-06	0.000155	-4.4378	Down	kinesin family member 19
SSPOP	-1.28665	1.82E-06	4.00E-05	-4.77245	Down	SCO-spondin, pseudogene
KCNE5	-1.28331	0.000132	0.001419	-3.82237	Down	potassium voltage-gated channel subfamily E regulatory subunit 5
GALNT6	-1.28089	7.63E-08	2.78E-06	-5.37557	Down	polypeptide N-acetylgalactosaminyltransferase 6
MARCKSL1	-1.27718	2.96E-13	5.96E-11	-7.29603	Down	MARCKS like 1
PTPRVP	-1.27707	0.000509	0.004249	-3.47574	Down	protein tyrosine phosphatase receptor type V, pseudogene
LLCFC1	-1.27694	2.58E-07	7.78E-06	-5.15203	Down	LLLL and CFNLAS motif containing 1
SEC14L5	-1.27009	2.77E-08	1.20E-06	-5.55509	Down	SEC14 like lipid binding 5
ZNF536	-1.26683	9.24E-10	6.78E-08	-6.12198	Down	zinc finger protein 536
HAGHL	-1.26683	2.35E-06	4.97E-05	-4.72094	Down	hydroxyacylglutathione hydrolase like
CMTM5	-1.26256	8.45E-06	0.000145	-4.45353	Down	CKLF like MARVEL transmembrane domain containing 5
MAP1LC3A	-1.26085	2.02E-08	9.14E-07	-5.61058	Down	microtubule associated protein 1 light chain 3 alpha
KCNH8	-1.25847	8.45E-10	6.34E-08	-6.13626	Down	potassium voltage-gated channel subfamily H member 8
KRT8P7	-1.25462	0.001897	0.012139	-3.10594	Down	keratin 8 pseudogene 7
GJB1	-1.25104	1.61E-06	3.62E-05	-4.79718	Down	gap junction protein beta 1
PLXNB3	-1.25085	1.30E-05	0.000211	-4.35928	Down	plexin B3
HSF4	-1.24951	7.66E-08	2.79E-06	-5.375	Down	heat shock transcription factor 4
AGPAT4	-1.2483	2.57E-14	6.60E-12	-7.61852	Down	1-acylglycerol-3-phosphate O-acyltransferase 4
OLIG2	-1.2468	6.55E-09	3.55E-07	-5.80216	Down	oligodendrocyte transcription factor 2
FAM66B	-1.2459	1.27E-09	8.83E-08	-6.07177	Down	family with sequence similarity 66 member B
MT1X	-1.24513	4.34E-09	2.54E-07	-5.87081	Down	metallothionein 1X
MAL	-1.24447	3.18E-09	1.95E-07	-5.92201	Down	mal, T cell differentiation protein
HIP1R	-1.24233	3.09E-09	1.91E-07	-5.92669	Down	huntingtin interacting protein 1 related
RAB7B	-1.23808	5.56E-09	3.13E-07	-5.82942	Down	RAB7B, member RAS oncogene family
SLC16A8	-1.23674	2.52E-05	0.000365	-4.213	Down	solute carrier family 16 member 8
KLK8	-1.23402	0.009277	0.041343	-2.60167	Down	kallikrein related peptidase 8
C5orf64	-1.2318	3.15E-12	4.89E-10	-6.9707	Down	chromosome 5 putative open reading frame 64
PLCH2	-1.23176	4.91E-07	1.33E-05	-5.02999	Down	phospholipase C eta 2
PLLP	-1.23035	3.30E-09	2.01E-07	-5.91604	Down	plasmolipin
RPL21P87	-1.22842	7.77E-05	0.000924	-3.95131	Down	ribosomal protein L21 pseudogene 87
CUEDC1	-1.22447	4.17E-08	1.69E-06	-5.48359	Down	CUE domain containing 1
SLC36A3	-1.20856	0.003125	0.018073	-2.95512	Down	solute carrier family 36 member 3
GTSCR1	-1.20661	1.31E-06	3.05E-05	-4.83825	Down	Gilles de la Tourette syndrome chromosome region, candidate 1
SLC5A11	-1.20504	2.04E-06	4.40E-05	-4.74955	Down	solute carrier family 5 member 11
USH1C	-1.20258	4.00E-07	1.12E-05	-5.06895	Down	USH1 protein network component harmonin
IGSF8	-1.2002	1.63E-06	3.66E-05	-4.79464	Down	immunoglobulin superfamily member 8
AQP6	-1.19959	4.38E-05	0.000576	-4.0865	Down	aquaporin 6
TRPV5	-1.19788	9.50E-08	3.34E-06	-5.336	Down	transient receptor potential cation channel

						subfamily V member 5
SAA1	-1.19714	0.011799	0.049583	-2.51809	Down	serum amyloid A1
PACSIN3	-1.19589	7.99E-09	4.18E-07	-5.76869	Down	protein kinase C and casein kinase substrate in neurons 3
CDKN1C	-1.18913	8.26E-08	2.97E-06	-5.36142	Down	cyclin dependent kinase inhibitor 1C
RPS17P2	-1.18857	0.00053	0.004384	-3.46497	Down	ribosomal protein S17 pseudogene 2
TMEM125	-1.18801	7.43E-06	0.00013	-4.48097	Down	transmembrane protein 125
CDC42EP1	-1.18648	3.05E-05	0.000427	-4.16995	Down	CDC42 effector protein 1
SH3BP5	-1.18398	1.02E-10	1.05E-08	-6.46359	Down	SH3 domain binding protein 5
NKX6-2	-1.18193	5.91E-06	0.000107	-4.52958	Down	NK6 homeobox 2
GREB1L	-1.18126	1.52E-13	3.24E-11	-7.38512	Down	GREB1 like retinoic acid receptor coactivator
ADSS1	-1.18068	5.13E-09	2.92E-07	-5.84296	Down	adenylosuccinate synthase 1
SNHG18	-1.18066	4.72E-12	6.84E-10	-6.91373	Down	small nucleolar RNA host gene 18
TKTL1	-1.18012	0.002703	0.016157	-2.99969	Down	transketolase like 1
ACSBG1	-1.17794	3.08E-11	3.68E-09	-6.64263	Down	acyl-CoA synthetase bubblegum family member 1
TSC22D4	-1.17652	1.37E-06	3.16E-05	-4.8299	Down	TSC22 domain family member 4
CFTR	-1.17646	8.77E-10	6.54E-08	-6.13031	Down	CF transmembrane conductance regulator
INSIG1	-1.17271	2.88E-12	4.52E-10	-6.98354	Down	insulin induced gene 1
NDUFB4P10	-1.17243	4.01E-06	7.76E-05	-4.61107	Down	NADH:ubiquinone oxidoreductase subunit B4 pseudogene 10
ZNF775	-1.16714	2.67E-05	0.000383	-4.19988	Down	zinc finger protein 775
OXCT2P1	-1.16652	6.87E-05	0.000833	-3.9809	Down	3-oxoacid CoA-transferase 2 pseudogene 1
OR13A1	-1.16053	0.00028	0.002632	-3.63357	Down	olfactory receptor family 13 subfamily A member 1
SRCIN1	-1.15582	1.39E-06	3.21E-05	-4.82642	Down	SRC kinase signaling inhibitor 1
MTCO2P16	-1.15506	0.001228	0.00863	-3.23224	Down	MT-CO2 pseudogene 16
HSD17B3	-1.15395	1.27E-08	6.17E-07	-5.69005	Down	hydroxysteroid 17-beta dehydrogenase 3
TNFAIP6	-1.15327	2.08E-09	1.36E-07	-5.99131	Down	TNF alpha induced protein 6
TMEM151A	-1.15207	0.000192	0.001933	-3.72916	Down	transmembrane protein 151A
SMG1P5	-1.15115	2.88E-10	2.54E-08	-6.30498	Down	SMG1 pseudogene 5
ACADS	-1.15036	6.18E-05	0.000765	-4.00585	Down	acyl-CoA dehydrogenase short chain
TMCO5A	-1.14873	0.000199	0.001989	-3.72015	Down	transmembrane and coiled-coil domains 5A
RPL21P98	-1.14841	0.001034	0.007526	-3.28099	Down	ribosomal protein L21 pseudogene 98
CALB2	-1.1453	0.000608	0.004905	-3.42785	Down	calbindin 2
ALDOC	-1.14393	9.75E-09	4.92E-07	-5.73495	Down	aldolase, fructose-bisphosphate C
PTPRH	-1.14327	1.61E-06	3.63E-05	-4.79659	Down	protein tyrosine phosphatase receptor type H
GREM1	-1.14058	2.91E-07	8.57E-06	-5.12917	Down	gremlin 1, DAN family BMP antagonist
VWA1	-1.13959	1.87E-05	0.000284	-4.2803	Down	von Willebrand factor A domain containing 1
SEPHS1P6	-1.13752	8.58E-08	3.06E-06	-5.35454	Down	selenophosphate synthetase 1 pseudogene 6
CES4A	-1.13652	5.61E-08	2.17E-06	-5.43093	Down	carboxylesterase 4A
CT69	-1.13517	1.61E-08	7.58E-07	-5.64948	Down	cancer/testis associated transcript 69
DUXB	-1.13504	2.91E-08	1.24E-06	-5.54674	Down	double homeobox B
CERCAM	-1.13131	6.41E-05	0.000789	-3.9971	Down	cerebral endothelial cell adhesion molecule
RBP7	-1.13025	2.93E-09	1.83E-07	-5.93556	Down	retinol binding protein 7
ADAP1	-1.13024	0.000467	0.003964	-3.4988	Down	ArfGAP with dual PH domains 1

ATF3	-1.1283	5.77E-05	0.000725	-4.02211	Down	activating transcription factor 3
ABCA2	-1.12624	6.76E-07	1.73E-05	-4.96812	Down	ATP binding cassette subfamily A member 2
USP17L8	-1.12353	0.001162	0.008267	-3.24797	Down	ubiquitin specific peptidase 17 like family member 8
SGK2	-1.12215	4.14E-11	4.71E-09	-6.59897	Down	serum/glucocorticoid regulated kinase 2
PLEKHG3	-1.12182	8.96E-08	3.17E-06	-5.34667	Down	pleckstrin homology and RhoGEF domain containing G3
HK2	-1.11819	5.19E-07	1.39E-05	-5.01908	Down	hexokinase 2
MCAM	-1.11676	1.87E-08	8.57E-07	-5.6239	Down	melanoma cell adhesion molecule
CLUHP6	-1.1163	0.000212	0.002092	-3.70383	Down	clustered mitochondria homolog pseudogene 6
GLDN	-1.116	2.24E-06	4.78E-05	-4.73018	Down	gliomedin
GPR37	-1.11385	3.94E-09	2.35E-07	-5.88683	Down	G protein-coupled receptor 37
RAB33A	-1.11375	8.65E-08	3.08E-06	-5.35304	Down	RAB33A, member RAS oncogene family
EFS	-1.11365	7.10E-06	0.000125	-4.49068	Down	embryonal Fyn-associated substrate
IFNA2	-1.11336	0.001008	0.007372	-3.28835	Down	interferon alpha 2
OR1L4	-1.11121	0.000382	0.003368	-3.55215	Down	olfactory receptor family 1 subfamily L member 4
KLK10	-1.11115	0.001556	0.010385	-3.16409	Down	kallikrein related peptidase 10
SPINK14	-1.10969	0.001417	0.009666	-3.19123	Down	serine peptidase inhibitor Kazal type 14 (putative)
ADAT3	-1.10248	0.00613	0.030286	-2.74077	Down	adenosine deaminase tRNA specific 3
HPDL	-1.09775	0.000373	0.003301	-3.55838	Down	4-hydroxyphenylpyruvate dioxygenase like
SEMA4D	-1.09761	9.11E-12	1.22E-09	-6.81991	Down	semaphorin 4D
TAS2R40	-1.09749	3.29E-08	1.37E-06	-5.5254	Down	taste 2 receptor member 40
SCD	-1.09633	1.55E-09	1.05E-07	-6.03958	Down	stearoyl-CoA desaturase
NGFR	-1.09596	0.000633	0.005065	-3.41718	Down	nerve growth factor receptor
FFAR1	-1.09551	0.000539	0.004445	-3.46048	Down	free fatty acid receptor 1
NTNG2	-1.09364	1.86E-07	5.87E-06	-5.21246	Down	netrin G2
ATP8B5P	-1.09325	6.11E-07	1.59E-05	-4.98778	Down	ATPase phospholipid transporting 8B5, pseudogene
HAS1	-1.08963	0.001462	0.00991	-3.18214	Down	hyaluronan synthase 1
BOLA3P4	-1.0893	0.000269	0.002552	-3.64336	Down	bolA family member 3 pseudogene 4
SCAND1	-1.08879	0.000102	0.001155	-3.88687	Down	SCAN domain containing 1
KEL	-1.08795	9.34E-07	2.29E-05	-4.90498	Down	Kell metallo-endopeptidase (Kell blood group)
TF	-1.08614	4.45E-06	8.49E-05	-4.58907	Down	transferrin
GLUL	-1.08529	3.35E-13	6.59E-11	-7.27937	Down	glutamate-ammonia ligase
DMRTA2	-1.08454	0.00027	0.002555	-3.64292	Down	DMRT like family A2
HCN2	-1.08452	1.22E-05	0.000199	-4.37429	Down	hyperpolarization activated cyclic nucleotide gated potassium and sodium channel 2
KREMEN2	-1.08396	0.008639	0.039188	-2.62603	Down	kringle containing transmembrane protein 2
PCBP4	-1.08211	8.02E-07	2.00E-05	-4.93481	Down	poly(rC) binding protein 4
GNG8	-1.07967	0.001042	0.007573	-3.279	Down	G protein subunit gamma 8
PET117	-1.07921	0.005362	0.027322	-2.78442	Down	PET117 cytochrome c oxidase chaperone
ARSI	-1.0763	0.000273	0.002582	-3.63973	Down	arylsulfatase family member I
VN1R83P	-1.07587	9.23E-12	1.23E-09	-6.81808	Down	vomeronasal 1 receptor 83 pseudogene
DMRT2	-1.07541	1.45E-06	3.33E-05	-4.81741	Down	doublesex and mab-3 related transcription factor 2
AOX1	-1.07437	3.88E-13	7.49E-11	-7.25956	Down	aldehyde oxidase 1
VN1R12P	-1.07392	0.000468	0.003966	-3.49847	Down	vomeronasal 1 receptor 12, pseudogene

PALM2AKAP2	-1.07266	0.004208	0.022746	-2.86215	Down	PALM2 and AKAP2 fusion
TM7SF2	-1.07245	8.68E-08	3.09E-06	-5.35232	Down	transmembrane 7 superfamily member 2
OR2AE1	-1.07197	0.000663	0.005256	-3.40454	Down	olfactory receptor family 2 subfamily AE member 1
S1PR5	-1.07064	1.03E-06	2.49E-05	-4.88548	Down	sphingosine-1-phosphate receptor 5
SKOR1	-1.07037	5.11E-07	1.37E-05	-5.02203	Down	SKI family transcriptional corepressor 1
ROGDI	-1.06973	4.00E-06	7.76E-05	-4.61115	Down	rogdi atypical leucine zipper
C1orf122	-1.06792	0.000133	0.001425	-3.82084	Down	chromosome 1 open reading frame 122
ELF3	-1.06694	0.006759	0.032606	-2.70851	Down	E74 like ETS transcription factor 3
GLULP1	-1.06518	0.00391	0.021524	-2.88533	Down	glutamate-ammonia ligase pseudogene 1
RNU5D-1	-1.06486	0.000254	0.002435	-3.65774	Down	RNA, U5D small nuclear 1
PLEKHG4	-1.06471	7.68E-05	0.000916	-3.95429	Down	pleckstrin homology and RhoGEF domain containing G4
TPRN	-1.06362	0.000202	0.002014	-3.71595	Down	taperin
ZNF367	-1.06358	2.10E-08	9.47E-07	-5.60353	Down	zinc finger protein 367
NACAD	-1.06132	1.53E-05	0.00024	-4.32504	Down	NAC alpha domain containing
HMSD	-1.06044	5.81E-09	3.20E-07	-5.82213	Down	histocompatibility minor serpin domain containing
HAPLN2	-1.05998	0.000179	0.001822	-3.74747	Down	hyaluronan and proteoglycan link protein 2
LLGL2	-1.05978	5.41E-05	0.000689	-4.03729	Down	LLGL scribble cell polarity complex component 2
SYNJ2	-1.0597	2.16E-09	1.39E-07	-5.98562	Down	synaptojanin 2
GOLGA6A	-1.05921	0.00096	0.007093	-3.30197	Down	golgin A6 family member A
MYCN	-1.05745	1.41E-09	9.61E-08	-6.05467	Down	MYCN proto-oncogene, bHLH transcription factor
HPN	-1.05702	7.64E-05	0.000913	-3.95536	Down	hepsin
SHC2	-1.05563	0.000168	0.001731	-3.76322	Down	SHC adaptor protein 2
FN3K	-1.05529	2.10E-09	1.37E-07	-5.99005	Down	fructosamine 3 kinase
IFNA13	-1.05056	0.002515	0.015217	-3.02148	Down	interferon alpha 13
SERPINE3	-1.04996	8.55E-07	2.12E-05	-4.92236	Down	serpin family E member 3
TLE2	-1.04971	1.42E-05	0.000227	-4.34026	Down	TLE family member 2, transcriptional corepressor
MYRF	-1.04962	2.41E-06	5.07E-05	-4.71565	Down	myelin regulatory factor
GAMT	-1.04568	5.35E-06	9.88E-05	-4.55057	Down	guanidinoacetate N-methyltransferase
TREH	-1.04504	7.17E-05	0.000865	-3.97041	Down	trehalase
MEIS1	-1.04497	1.45E-13	3.11E-11	-7.39188	Down	Meis homeobox 1
COL6A4P1	-1.04494	0.002048	0.012905	-3.08321	Down	collagen type VI alpha 4 pseudogene 1
OR5C1	-1.04369	0.000393	0.003449	-3.54464	Down	olfactory receptor family 5 subfamily C member 1
DUXAP9	-1.04104	0.001512	0.010169	-3.17238	Down	double homeobox A pseudogene 9
SPANXA2-OT1	-1.0401	2.18E-05	0.000324	-4.24578	Down	SPANXA2 overlapping transcript 1
BNC1	-1.03976	0.001374	0.009453	-3.19997	Down	basonuclin 1
HCRTR1	-1.03799	0.00132	0.009159	-3.21168	Down	hypocretin receptor 1
MOG	-1.03632	4.45E-06	8.48E-05	-4.5894	Down	myelin oligodendrocyte glycoprotein
SBF1	-1.03609	1.35E-05	0.000217	-4.35224	Down	SET binding factor 1
ADAMTS4	-1.03468	1.91E-05	0.00029	-4.27468	Down	ADAM metallopeptidase with thrombospondin type 1 motif 4
CA14	-1.03434	1.20E-05	0.000196	-4.37831	Down	carbonic anhydrase 14
INF2	-1.03405	4.82E-05	0.000625	-4.06405	Down	inverted formin 2
RPS7P6	-1.02978	0.007576	0.035453	-2.67041	Down	ribosomal protein S7 pseudogene 6

TMEM171	-1.02953	0.000624	0.005007	-3.42099	Down	transmembrane protein 171
OSBPL5	-1.02719	1.63E-06	3.66E-05	-4.79442	Down	oxysterol binding protein like 5
BIN1	-1.02589	8.26E-06	0.000142	-4.45834	Down	bridging integrator 1
NME3	-1.02561	0.000868	0.006538	-3.33023	Down	NME/NM23 nucleoside diphosphate kinase 3
CDK18	-1.02418	6.65E-07	1.71E-05	-4.97123	Down	cyclin dependent kinase 18
RAB6C	-1.02323	6.07E-07	1.59E-05	-4.98886	Down	RAB6C, member RAS oncogene family
PTPDC1	-1.02128	4.67E-16	2.02E-13	-8.11983	Down	protein tyrosine phosphatase domain containing 1
ARL2BP	-1.02123	0.009939	0.043518	-2.57796	Down	ADP ribosylation factor like GTPase 2 binding protein
FSCN1	-1.02095	4.83E-06	9.07E-05	-4.57224	Down	fascin actin-bundling protein 1
TEX45	-1.01757	0.000455	0.00388	-3.50599	Down	testis expressed 45
F11	-1.01421	0.006907	0.033157	-2.70129	Down	coagulation factor XI
RNU6-539P	-1.01311	0.008659	0.039248	-2.62523	Down	RNA, U6 small nuclear 539, pseudogene
TP53TG5	-1.01256	7.85E-11	8.30E-09	-6.50339	Down	TP53 target 5
BNIP3P30	-1.01107	0.00119	0.008419	-3.24138	Down	BCL2 interacting protein 3 pseudogene 30
MTFR2	-1.01087	0.001029	0.007494	-3.28244	Down	mitochondrial fission regulator 2
RHOU	-1.01083	1.94E-10	1.81E-08	-6.36576	Down	ras homolog family member U
STMN4	-1.01036	5.09E-06	9.49E-05	-4.561	Down	stathmin 4
GOLGA6B	-1.01012	0.003058	0.017791	-2.96182	Down	golgin A6 family member B
ACAA2P1	-1.00787	0.000293	0.002727	-3.62156	Down	ACAA2 pseudogene 1
DIPK1C	-1.00776	6.63E-08	2.47E-06	-5.40089	Down	divergent protein kinase domain 1C
PAQR4	-1.00722	0.000513	0.00427	-3.47391	Down	progestin and adipoQ receptor family member 4
RNASE1	-1.00569	5.03E-06	9.41E-05	-4.56333	Down	ribonuclease A family member 1, pancreatic
RN7SKP112	-1.00383	0.011031	0.04716	-2.54171	Down	RN7SK pseudogene 112
GNLY	-1.00246	0.00111	0.007953	-3.26115	Down	granulysin
MVK	-1.00215	2.64E-07	7.92E-06	-5.14755	Down	mevalonate kinase
SH3PXD2B	-1.00066	4.24E-08	1.71E-06	-5.48036	Down	SH3 and PX domains 2B
MKRN3	-0.99835	6.32E-11	6.83E-09	-6.53594	Down	makorin ring finger protein 3
BMP2	-0.99813	1.39E-06	3.21E-05	-4.8262	Down	bone morphogenetic protein 2
HSPA2	-0.99499	2.36E-05	0.000347	-4.2275	Down	heat shock protein family A (Hsp70) member 2
GPIHBP1	-0.99465	0.000366	0.003255	-3.56314	Down	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1
CUTALP	-0.99364	4.70E-11	5.28E-09	-6.5801	Down	cutA divalent cation tolerance like, pseudogene
LMNA	-0.99073	4.46E-06	8.49E-05	-4.58883	Down	lamin A/C
FAM21FP	-0.99019	0.000411	0.003574	-3.53276	Down	family with sequence similarity 21 member F, pseudogene
PLA2G4C	-0.98917	1.28E-08	6.21E-07	-5.68874	Down	phospholipase A2 group IVC
ERBB3	-0.98788	7.80E-08	2.83E-06	-5.37173	Down	erb-b2 receptor tyrosine kinase 3
KIRREL2	-0.9864	0.001412	0.009651	-3.1921	Down	kirre like nephrin family adhesion molecule 2
EQTN	-0.98575	3.23E-05	0.000449	-4.15668	Down	equatorin
HSD11B1	-0.98561	1.31E-05	0.000212	-4.35873	Down	hydroxysteroid 11-beta dehydrogenase 1
GCAWKR	-0.98395	2.96E-07	8.68E-06	-5.12591	Down	gastric cancer associated WDR5 and KAT2A binding lncRNA
HTRA1	-0.98379	6.06E-08	2.29E-06	-5.41709	Down	HtrA serine peptidase 1
DLL1	-0.98191	1.74E-06	3.85E-05	-4.78204	Down	delta like canonical Notch ligand 1
C22orf23	-0.98123	0.000159	0.001654	-3.77704	Down	chromosome 22 open reading frame 23

EEPD1	-0.98041	5.70E-08	2.19E-06	-5.42782	Down	endonuclease/exonuclease/phosphatase family domain containing 1
RHBG	-0.97935	0.000155	0.001625	-3.78216	Down	Rh family B glycoprotein
NKX2-2	-0.97848	2.50E-05	0.000363	-4.21466	Down	NK2 homeobox 2
BNIP3P22	-0.97812	0.002088	0.013104	-3.07747	Down	BCL2 interacting protein 3 pseudogene 22
PTGDS	-0.97717	8.64E-05	0.001009	-3.92579	Down	prostaglandin D2 synthase
PFKL	-0.9767	3.38E-08	1.40E-06	-5.52059	Down	phosphofructokinase, liver type
CPHXL2	-0.97544	2.43E-05	0.000354	-4.22153	Down	cytoplasmic polyadenylated homeobox like 2
RNU6-883P	-0.9742	0.001176	0.00834	-3.24469	Down	RNA, U6 small nuclear 883, pseudogene
EVA1A	-0.97408	0.000787	0.006044	-3.35718	Down	eva-1 homolog A, regulator of programmed cell death
LMF1	-0.97228	7.95E-06	0.000138	-4.46645	Down	lipase maturation factor 1
THBS2	-0.96985	4.42E-07	1.22E-05	-5.04971	Down	thrombospondin 2
SH3TC2	-0.96976	1.00E-06	2.44E-05	-4.89076	Down	SH3 domain and tetratricopeptide repeats 2
NHLH2	-0.96855	4.32E-10	3.56E-08	-6.24193	Down	nescient helix-loop-helix 2
IGSF1	-0.96849	3.90E-06	7.59E-05	-4.6165	Down	immunoglobulin superfamily member 1
SH3TC2-DT	-0.96743	8.97E-08	3.17E-06	-5.34653	Down	SH3TC2 divergent transcript
SDCBPP1	-0.96429	0.000598	0.004835	-3.43258	Down	syndecan binding protein pseudogene 1
PEBP4	-0.96338	0.005803	0.029036	-2.75872	Down	phosphatidylethanolamine binding protein 4
PIWIL2	-0.96277	2.52E-12	4.07E-10	-7.00245	Down	piwi like RNA-mediated gene silencing 2
PLEKHH1	-0.96265	2.32E-07	7.07E-06	-5.17191	Down	pleckstrin homology, MyTH4 and FERM domain containing H1
CDR2L	-0.96189	2.61E-05	0.000376	-4.20535	Down	cerebellar degeneration related protein 2 like
MT1G	-0.96078	0.006926	0.033214	-2.70038	Down	metallothionein 1G
GADD45B	-0.96044	0.00068	0.005367	-3.39734	Down	growth arrest and DNA damage inducible beta
APLP1	-0.95975	1.23E-06	2.90E-05	-4.85033	Down	amyloid beta precursor like protein 1
ST3GAL4	-0.95865	2.32E-06	4.92E-05	-4.72321	Down	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
PHLDB1	-0.95847	1.10E-05	0.000183	-4.39583	Down	pleckstrin homology like domain family B member 1
GASK1A	-0.95807	2.90E-08	1.23E-06	-5.54764	Down	golgi associated kinase 1A
IFNA11P	-0.9562	0.006539	0.031756	-2.71946	Down	interferon alpha 11, pseudogene
FGF11	-0.95394	3.13E-05	0.000437	-4.16414	Down	fibroblast growth factor 11
CELP	-0.9536	0.006239	0.030684	-2.73497	Down	carboxyl ester lipase pseudogene
OR7M1P	-0.95184	0.000328	0.002978	-3.59229	Down	olfactory receptor family 7 subfamily M member 1 pseudogene
SHB	-0.95102	5.54E-07	1.47E-05	-5.00661	Down	SH2 domain containing adaptor protein B
UNC5B	-0.95086	7.25E-06	0.000127	-4.48629	Down	unc-5 netrin receptor B
ENOSF1	-0.95059	2.07E-07	6.44E-06	-5.19266	Down	enolase superfamily member 1
RPL18AP11	-0.95045	0.000115	0.001267	-3.85682	Down	ribosomal protein L18a pseudogene 11
MYH6	-0.94772	0.000502	0.004193	-3.47992	Down	myosin heavy chain 6
CPA2	-0.94756	0.001466	0.009934	-3.18136	Down	carboxypeptidase A2
KIAA0087	-0.94673	0.000496	0.004154	-3.48286	Down	KIAA0087 lncRNA
CNPY1	-0.94622	0.008357	0.03822	-2.63728	Down	canopy FGF signaling regulator 1
SNX22	-0.94612	1.54E-05	0.000242	-4.32328	Down	sorting nexin 22
NKAIN4	-0.94576	9.87E-05	0.001126	-3.89383	Down	sodium/potassium transporting ATPase interacting 4
TRAPPC13P1	-0.94569	0.004002	0.021882	-2.87797	Down	trafficking protein particle complex 13 pseudogene 1

ASPA	-0.94357	7.00E-09	3.73E-07	-5.79102	Down	aspartoacylase
CIRBP	-0.94321	5.90E-08	2.26E-06	-5.4218	Down	cold inducible RNA binding protein
CYP26C1	-0.94295	0.001299	0.009041	-3.21617	Down	cytochrome P450 family 26 subfamily C member 1
FASN	-0.94282	9.91E-06	0.000166	-4.41909	Down	fatty acid synthase
MRI1	-0.94276	7.70E-07	1.93E-05	-4.94285	Down	methylthioribose-1-phosphate isomerase 1
RASSF2	-0.94155	7.28E-10	5.53E-08	-6.15981	Down	Ras association domain family member 2
PPP2R2B-IT1	-0.94033	5.79E-09	3.20E-07	-5.82274	Down	PPP2R2B intronic transcript 1
CRB2	-0.93983	0.000441	0.003791	-3.51407	Down	crumbs cell polarity complex component 2
MAN1B1-DT	-0.93874	4.92E-05	0.000635	-4.05954	Down	MAN1B1 divergent transcript
GIPC1	-0.93779	1.39E-07	4.60E-06	-5.26592	Down	GIPC PDZ domain containing family member 1
PNPLA3	-0.93702	0.000457	0.003893	-3.5046	Down	patatin like phospholipase domain containing 3
LSS	-0.93642	1.41E-07	4.64E-06	-5.26417	Down	lanosterol synthase
BTBD16	-0.9358	9.04E-06	0.000154	-4.43891	Down	BTB domain containing 16
DHRS13	-0.93563	0.000134	0.001436	-3.81845	Down	dehydrogenase/reductase 13
GPR62	-0.93533	0.000184	0.001868	-3.7394	Down	G protein-coupled receptor 62
FAM170A	-0.93455	0.011451	0.048423	-2.52861	Down	family with sequence similarity 170 member A
LGI3	-0.93188	4.12E-06	7.95E-05	-4.60543	Down	leucine rich repeat LGI family member 3
ACTN2	-0.93164	1.81E-08	8.36E-07	-5.62918	Down	actinin alpha 2
PRKCQ	-0.93126	3.06E-08	1.30E-06	-5.53787	Down	protein kinase C theta
MMP15	-0.93064	7.82E-05	0.000928	-3.94991	Down	matrix metallopeptidase 15
CLUL1	-0.92888	0.000432	0.003727	-3.51962	Down	clusterin like 1
LLGL1	-0.92882	3.44E-05	0.000474	-4.14203	Down	LLGL scribble cell polarity complex component 1
CBR1	-0.92716	6.69E-10	5.12E-08	-6.17335	Down	carbonyl reductase 1
PRODH	-0.92655	0.000754	0.005832	-3.36927	Down	proline dehydrogenase 1
MT1M	-0.92632	3.89E-05	0.000523	-4.11397	Down	metallothionein 1M
ARHGAP23	-0.92549	4.34E-06	8.30E-05	-4.59464	Down	Rho GTPase activating protein 23
SAMMSON	-0.92401	0.003759	0.020876	-2.8977	Down	survival associated mitochondrial melanoma specific oncogenic non-coding RNA
PADI2	-0.924	8.93E-06	0.000152	-4.44152	Down	peptidyl arginine deiminase 2
PCDHA7	-0.92362	3.29E-06	6.58E-05	-4.65161	Down	protocadherin alpha 7
EDIL3	-0.9236	3.62E-07	1.03E-05	-5.0879	Down	EGF like repeats and discoidin domains 3
MPP2	-0.92176	5.07E-06	9.47E-05	-4.56169	Down	MAGUK p55 scaffold protein 2
SVEP1	-0.92159	1.68E-05	0.00026	-4.30418	Down	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
PPEF1	-0.91856	0.000379	0.003347	-3.55414	Down	protein phosphatase with EF-hand domain 1
SLC45A3	-0.91757	0.000551	0.004521	-3.45481	Down	solute carrier family 45 member 3
NOXA1	-0.91728	0.008565	0.038948	-2.62895	Down	NADPH oxidase activator 1
EEF1B2P8	-0.91725	0.007005	0.033474	-2.69663	Down	eukaryotic translation elongation factor 1 beta 2 pseudogene 8
MT3	-0.91628	4.13E-06	7.98E-05	-4.6045	Down	metallothionein 3
ADORA1	-0.91619	1.17E-05	0.000192	-4.38366	Down	adenosine A1 receptor
ALDH1A1	-0.91544	8.65E-08	3.08E-06	-5.353	Down	aldehyde dehydrogenase 1 family member A1
ANGPTL2	-0.91525	3.50E-07	1.00E-05	-5.09406	Down	angiopoietin like 2
GLIDR	-0.91428	2.50E-10	2.24E-08	-6.32676	Down	glioblastoma down-regulated RNA
DISP3	-0.91261	0.000376	0.003326	-3.55619	Down	dispatched RND transporter family member 3

TAS2R39	-0.91223	1.82E-06	4.00E-05	-4.77277	Down	taste 2 receptor member 39
PSG6	-0.90903	0.00306	0.017796	-2.96167	Down	pregnancy specific beta-1-glycoprotein 6
IRF5P1	-0.90851	0.008743	0.039546	-2.62193	Down	interferon regulatory factor 5 pseudogene 1
NENF	-0.90814	2.30E-06	4.87E-05	-4.72554	Down	neudesin neurotrophic factor
EVI5L	-0.90753	4.71E-06	8.87E-05	-4.57728	Down	ecotropic viral integration site 5 like
TNFSF9	-0.90646	3.81E-05	0.000514	-4.11868	Down	TNF superfamily member 9
PAQR6	-0.9052	2.09E-05	0.000314	-4.2547	Down	progestin and adipoQ receptor family member 6
ITPRID1	-0.90499	0.000288	0.002691	-3.62598	Down	ITPR interacting domain containing 1
PDE8A	-0.90395	6.96E-16	2.79E-13	-8.07119	Down	phosphodiesterase 8A
TTYH1	-0.90289	7.17E-06	0.000126	-4.4887	Down	tweety family member 1
GPC2	-0.90266	0.000203	0.002017	-3.71541	Down	glypican 2
CPB2	-0.90204	3.49E-08	1.44E-06	-5.51504	Down	carboxypeptidase B2
KAZN	-0.90149	1.47E-09	1.00E-07	-6.04722	Down	kazrin, periplakin interacting protein
DYSF	-0.89981	3.49E-05	0.000479	-4.13874	Down	dysferlin
TRIM61	-0.89943	8.58E-06	0.000147	-4.45025	Down	tripartite motif containing 61
PCCB	-0.89936	8.92E-09	4.59E-07	-5.75013	Down	propionyl-CoA carboxylase subunit beta
CAPN13	-0.89908	0.000436	0.003752	-3.51734	Down	calpain 13
SEMA4C	-0.89797	4.27E-05	0.000563	-4.09261	Down	semaphorin 4C
MATN1	-0.89776	0.000536	0.004426	-3.46184	Down	matrilin 1
NEU4	-0.89766	0.006026	0.029899	-2.74634	Down	neuraminidase 4
IPO13	-0.89766	4.63E-06	8.76E-05	-4.58092	Down	importin 13
SLC25A13	-0.89677	4.58E-11	5.17E-09	-6.58403	Down	solute carrier family 25 member 13
ERF	-0.89652	0.001857	0.011941	-3.11216	Down	ETS2 repressor factor
RTKN	-0.8965	7.00E-06	0.000124	-4.4937	Down	rhotekin
KCNIP1-OT1	-0.89637	0.006228	0.030643	-2.73552	Down	KCNIP1 overlapping transcript 1
MTCO1P47	-0.89621	0.000818	0.00624	-3.34668	Down	MT-CO1 pseudogene 47
ZNF146	-0.89503	6.54E-16	2.66E-13	-8.07883	Down	zinc finger protein 146
TSPAN15	-0.89296	5.27E-07	1.41E-05	-5.01621	Down	tetraspanin 15
MEIOB	-0.89275	0.000114	0.001257	-3.85887	Down	meiosis specific with OB-fold
ZNF784	-0.89191	3.11E-05	0.000436	-4.16497	Down	zinc finger protein 784
TMEM229A	-0.89108	1.41E-06	3.25E-05	-4.82326	Down	transmembrane protein 229A
MAPK8IP1	-0.88969	7.77E-06	0.000135	-4.47147	Down	mitogen-activated protein kinase 8 interacting protein 1
CYCSP23	-0.88942	0.000119	0.001307	-3.8474	Down	CYCS pseudogene 23
CAPN8	-0.88907	0.00809	0.037301	-2.6483	Down	calpain 8
TRAPPC6A	-0.88601	0.000414	0.00359	-3.53122	Down	trafficking protein particle complex subunit 6A
SPON1	-0.88559	1.87E-07	5.88E-06	-5.21197	Down	spondin 1
SLC24A4	-0.88531	6.23E-08	2.34E-06	-5.41205	Down	solute carrier family 24 member 4
RPS2P32	-0.88508	0.000264	0.002512	-3.64846	Down	ribosomal protein S2 pseudogene 32
EGLN3	-0.88502	4.15E-14	1.04E-11	-7.55626	Down	egl-9 family hypoxia inducible factor 3
FAM86B2	-0.88456	0.000477	0.00403	-3.4933	Down	family with sequence similarity 86 member B2
MRPS26	-0.88435	6.59E-05	0.000806	-3.99071	Down	mitochondrial ribosomal protein S26
ADAMTSL2	-0.88353	9.87E-05	0.001126	-3.8937	Down	ADAMTS like 2

LCTL	-0.88352	6.74E-05	0.000821	-3.98516	Down	lactase like
MARCOL	-0.88232	3.85E-05	0.000519	-4.11641	Down	MARCO like
TST	-0.88163	0.000585	0.004755	-3.43833	Down	thiosulfate sulfurtransferase
CHPF	-0.88086	0.000174	0.001788	-3.75338	Down	chondroitin polymerizing factor
SEPTIN4	-0.8808	4.09E-07	1.14E-05	-5.06469	Down	septin 4
CYP2A6	-0.88079	7.68E-07	1.93E-05	-4.94339	Down	cytochrome P450 family 2 subfamily A member 6
ZNF837	-0.88038	0.001954	0.01243	-3.09717	Down	zinc finger protein 837
C20orf202	-0.87967	2.13E-05	0.000318	-4.25048	Down	chromosome 20 open reading frame 202
RHOB	-0.87907	1.15E-07	3.91E-06	-5.30158	Down	ras homolog family member B
ROM1	-0.87831	6.53E-06	0.000117	-4.50848	Down	retinal outer segment membrane protein 1
CTNNA3	-0.87727	8.85E-08	3.14E-06	-5.34884	Down	catenin alpha 3
F3	-0.87671	0.000162	0.001684	-3.77164	Down	coagulation factor III, tissue factor
NINJ2	-0.876	0.000193	0.001941	-3.72783	Down	ninjurin 2
LRP2	-0.87593	4.22E-07	1.17E-05	-5.05873	Down	LDL receptor related protein 2
POLR2F	-0.87591	3.10E-05	0.000434	-4.16576	Down	RNA polymerase II, I and III subunit F
CADM4	-0.87402	5.99E-08	2.28E-06	-5.41924	Down	cell adhesion molecule 4
MEX3D	-0.87287	0.000207	0.00205	-3.71028	Down	mex-3 RNA binding family member D
OR1L6	-0.87124	0.002826	0.016744	-2.98606	Down	olfactory receptor family 1 subfamily L member 6
BEST1	-0.87099	4.50E-09	2.61E-07	-5.86453	Down	bestrophin 1
WNT7A	-0.87051	0.00124	0.008697	-3.22948	Down	Wnt family member 7A
ASPHD1	-0.87041	0.000103	0.001172	-3.88266	Down	aspartate beta-hydroxylase domain containing 1
ABHD17A	-0.8695	0.001751	0.01139	-3.12956	Down	abhydrolase domain containing 17A, depalmitoylase
JAKMIP3	-0.86832	7.19E-07	1.82E-05	-4.95616	Down	Janus kinase and microtubule interacting protein 3
PHLDA3	-0.86654	0.000843	0.006387	-3.33833	Down	pleckstrin homology like domain family A member 3
LGALS3BP	-0.86636	1.17E-05	0.000192	-4.38371	Down	galectin 3 binding protein
RASA3	-0.86609	1.35E-11	1.74E-09	-6.76331	Down	RAS p21 protein activator 3

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	1.48E-86	85.8309114	199	IGLC3,IGLC2,IGKV4-1,IGHG1,IGHG2,IGHV4-39,IGKV3-11,IGHV1-2,IGHV3-7,IGKV1-5,IGHV3-30,IGLV2-11,IGHV4-34,IGLV3-21,IGKV3-15,IGLV1-44,IGHV3-23,IGHV4-59,IGHV2-5,IGKV3-20,IGHV3-21,IGKV1-9,JCHAIN,IGHM,IGLV2-14,IGHA1,IGHV1-18,IGHV1-3,IGLV3-19,IGHV4-4,IGHV1-69D,IGHV4-30-2,IGHV1-46,IGKV1-12,IGLV2-23,IGHV3-33,IGHV5-51,IGHV2-26,IGKV1-

						27,IGLV1-40,IGHV2-70,IGLV2-8,IGKV1-17,IGHV3-48,IGHV3-53,IGKV1-16,IGLV2-18,IGHV4-61,IGHG4,IGHV3-74,CCL18,IGKV2-24,IGKV5-2,IGKV1-6,IGHV3-15,IGHV3-49,IGKV6-21,IGHV3-11,IGHV3-20,IGLV6-57,IGLV3-10,IGKV3D-11,IGKV2-30,IGLV1-47,IGHV4-28,IGHV7-4-1,IGLV3-25,IGHV3-64D,IGHA2,IGLL5,IGLV10-54,IGHV2-70D,IGHV1-69,IGKV1-8,IGHV3-43,IGLV4-69,IGLV7-46,IGLV7-43,SLAMF7,IGLV8-61,IGHV6-1,IGKV1D-13,IGHV3-72,IGKV2D-29,IGKV3D-20,IGKV6D-21,IGHV3-13,PYHIN1,MS4A1,IGHV1-24,IGHV3-73,MS4A2,GPR174,FCRL3,LY9,IGKV1D-39,IGHV3-66,CLEC10A,TRAV4,SLAMF6,IGKV1D-16,TRAT1,IGLV3-9,IGKV1-39,EOMES,IGLV5-45,IGKV1D-12,CCR4,GZMA,POU4F2,IGKV3D-15,CD79A,CCR2,CD48,IGKV1D-33,IGKV1-33,TRAV17,CD3E,CCL26,IGKV1D-8,ITGAD,IL2RB,CCL4,CCL24,TNFRSF13B,FASLG,SLAMF1,MZB1,TRBV29-1,TRBV27,CD24,IKZF3,LAX1,TDGF1,CD2,CD28,IGLV1-36,FCMR,LYZ,IL7R,HSH2D,HLA-DRB5,FCGR2B,UBASH3A,PLA2G2D,TRAV13-1,CYP11B1,TRAV19,CD1C,FOXJ1,TRAV12-3,TRBV20-1,CD3D,TRBC1,TRBV28,ICOS,CD3G,CCL5,CCL3,TRAV12-2,TRBV6-7,LTF,ITK,H4C13,TRAV8-2,TRBV18,GPNMB,CTLA4,IRF4,TRAV14DV4,TNFRSF9,LCK,CD209,TRBV5-6,IGLV1-51,TRAJ3,C6,NCR1,TRBV5-5,TRAC,XCL2,TRAJ31,TRIML2,IL5RA,CD8B,TRBJ1-3,PTGDR,JAML,GBP5,TRBV7-7,MICB,MYB,TRBC2,IL2RG,MRC1,TRBV5-4,CD96,TRBV7-9,CHIT1
GO:0050896	BP	response to stimulus	5.48E-37	36.26088329	264	IGLC3,IGLC2,IGKV4-1,IGHG1,IGHG2,IGHV4-39,IGKV3-11,IGHV1-2,IGHV3-7,IGKV1-5,IGHV3-30,IGLV2-11,IGHV4-34,IGLV3-21,IGKV3-15,IGLV1-44,IGHV3-23,IGHV4-59,IGHV2-5,IGKV3-20,IGHV3-21,IGKV1-9,JCHAIN,IGHM,IGLV2-14,IGHA1,IGHV1-18,IGHV1-3,IGLV3-19,IGHV4-4,IGHV1-

69D,IGHV4-30-2,IGHV1-
46,IGKV1-12,FCRL5,IGLV2-
23,IGHV3-33,IGHV5-51,IGHV2-
26,IGKV1-27,IGLV1-40,IGHV2-
70,IGLV2-8,IGKV1-17,IGHV3-
48,IGHV3-53,IGKV1-16,IGLV2-
18,IGHV4-61,IGHG4,IGHV3-
74,CCL18,IGKV2-24,IGKV5-
2,IGKV1-6,IGHV3-15,IGHV3-
49,IGKV6-21,IGHV3-11,IGHV3-
20,IGLV6-57,IGLV3-10,IGKV3D-
11,IGKV2-30,IGLV1-47,IGHV4-
28,IGHV7-4-1,IGLV3-25,IGHV3-
64D,IGHA2,IGLL5,IGLV10-
54,IGHV2-70D,IGHV1-
69,STOML3,IGKV1-8,IGHV3-
43,IGLV4-69,IGLV7-46,IGLV7-
43,SLAMF7,RASSF6,IGLV8-
61,SHOX2,FCRL2,IGHV6-
1,IGKV1D-13,IGHV3-72,IGKV2D-
29,IGKV3D-20,NUGGC,IGKV6D-
21,IGHV3-
13,PYHIN1,MS4A1,IGHV1-
24,IGHV3-
73,MS4A2,P2RY10,GPR174,FCRL3
,LY9,IGKV1D-39,IGHV3-
66,CLEC10A,TRAV4,PALM3,SLA
MF6,OR2J2,IGKV1D-
16,TRAT1,IGLV3-9,IGKV1-
39,EOMES,ISL1,IGLV5-
45,TTR,OTX2,IGKV1D-
12,CCR4,GZMA,POU4F2,IGKV3D-
15,CD79A,CCR2,CD48,IGKV1D-
33,MYLK3,IGKV1-
33,RGS21,PLEKHG4B,TRAV17,CD
3E,CCL26,IGKV1D-
8,ITGAD,DOK2,OR5V1,IL2RB,CC
L4,CCL24,TPSAB1,NRK,EPS8L3,T
NFRSF13B,FASLG,SLAMF1,OR9Q
1,MZB1,TRBV29-
1,TRBV27,CD24,IKZF3,LAX1,TDG
F1,CD2,CD28,IGLV1-
36,FCMR,LYZ,IL7R,HSH2D,HLA-
DRB5,NPY2R,FCGR2B,UBASH3A,
RTP1,PLA2G2D,TRAV13-
1,CYP11B1,TRAV19,DRD3,CD1C,
P2RY8,FOXJ1,NLRP7,TRAV12-
3,TRBV20-
1,CD3D,TRBC1,TRBV28,TAB2,IC
OS,CLEC12A,PCP4,LHCGR,IL24,C
D3G,CCL5,CCL3,TNNI3,TRAV12-
2,GPR101,TRBV6-
7,LTF,ITK,AKR1C4,TRAV8-
2,TRBV18,TRARG1,CD163,GPNM
B,CTLA4,MYO3A,IRF4,GSDMA,T
RAV14DV4,SDC1,LCK,CD209,TR
BV5-6,IGLV1-
51,TRAJ3,C6,IQGAP2,NCR1,TRBV
5-
5,TRAC,CDA,XCL2,MS4A14,TRAJ
31,CRABP1,TRIML2,AOC1,IL5RA,

						SIK1,F13A1,WT1,MAPK15,CD8B,MS4A7,TRBJ1-3,OR2T6,MSR1,ALOX15B,PTGDR,LPAR3,GML,CRNN,JAML,GBP5,NTS,HGF,RNASE10,LCN8,TRBV7-7,MICB,TRPM8,MYB,OR1J1,ADGRG6,TRBC2,IL2RG,MRC1,TRBV5-4,FOLR2,DIO3,CD96,SIGLEC1,UCN3,TRBV7-9,CHIT1,MROH2B
GO:0016020	CC	membrane	5.40E-18	17.26794982	246	IGLC3,IGLC2,IGKV4-1,IGHG3,IGHG1,IGHG2,IGHV4-39,IGKV3-11,IGHV1-2,IGHV3-7,IGKV1-5,IGHV3-30,IGLV2-11,IGHV4-34,IGLV3-21,IGKV3-15,IGLV1-44,IGHV3-23,IGHV4-59,IGHV2-5,IGKV3-20,IGHV3-21,IGKV1-9,IGHM,IGLV2-14,IGHA1,IGHV1-18,IGHV1-3,IGLV3-19,IGHV4-4,IGHV1-69D,IGHV4-30-2,IGHV1-46,IGKV1-12,FCRL5,IGLV2-23,IGHV3-33,IGHV5-51,IGHV2-26,IGKV1-27,IGLV1-40,IGHV2-70,IGLV2-8,IGKV1-17,IGHV3-48,IGHV3-53,IGKV1-16,IGLV2-18,IGHV4-61,IGHG4,IGHV3-74,IGKV2-24,IGKV5-2,IGKV1-6,IGHV3-15,IGHV3-49,IGKV6-21,IGHV3-11,IGHV3-20,IGLV6-57,IGLV3-10,IGKV3D-11,IGKV2-30,IGLV1-47,IGHV4-28,LRRC37A2,IGHV7-4-1,IGLV3-25,IGHV3-64D,IGHA2,IGLL5,IGLV10-54,IGHV2-70D,IGHV1-69,STOML3,IGKV1-8,IGHV3-43,IGLV4-69,IGLV7-46,IGLV7-43,SLAMF7,IGLV8-61,FCRL2,IGHV6-1,IGKV1D-13,IGHV3-72,IGKV2D-29,IGKV3D-20,IGKV6D-21,IGHV3-13,MS4A1,IGHV1-24,IGHV3-73,MS4A2,P2RY10,GPR174,FCRL3,LY9,IGKV1D-39,IGHV3-66,CLEC10A,DNAJC5B,TRAV4,AADACL2,PALM3,SLAMF6,OR2J2,IGKV1D-16,TRAT1,IGLV3-9,IGKV1-39,STRIT1,IGLV5-45,IGKV1D-12,CCR4,GZMA,IGKV3D-15,CD79A,CCR2,CD48,IGKV1D-33,IGKV1-33,RGS21,TRAV17,CD3E,IGKV1D-8,ITGAD,OR5V1,IL2RB,MOGAT2,GZMH,NRK,EPS8L3,TNFRSF13B,IGHD,FASLG,SLAMF1,OR9Q1,SLC35D3,TRBV29-1,TRBV27,CD24,LAX1,TDGF1,CD2,CD28,IGLV1-36,FCMR,CLIC6,IL7R,HLA-

						DRB5,NPY2R,FCGR2B,RTP1,TRAV13-1,CYP11B1,TRAV19,DRD3,CD1C,P2RY8,LAIR2,TRAV12-3,TRBV20-1,CD3D,TRBC1,TRBV28,TAB2,ICOS,CLEC12A,LHCGR,CD3G,SYNDIG1L,TRAV12-2,SIGLEC6,GPR101,TRBV6-7,LTF,ITK,H4C13,CD52,TRAV8-2,CATSPERD,TRBV18,TRARG1,CD163,HS3ST3A1,GPNMB,CTLA4,SLC25A52,IRF4,GSDMA,TRAV14DV4,SDC1,TNFRSF9,LCK,CD209,TRBV5-6,IGLV1-51,TRAJ3,C6,IQGAP2,NCR1,TRBV5-5,MUC3A,TRAC,PRSS21,MS4A14,B4GALNT2,TRAJ31,PRPH,AOC1,IL5RA,CD8B,MS4A7,TRBJ1-3,OR2T6,MSR1,ALOX15B,PTGDR,LPAR3,CFAP157,GML,CDHR4,CRNN,JSRP1,JAML,TMIE,GBP5,NMRK2,HGF,TRBV7-7,SLC22A31,MICB,TRPM8,MYB,OR1J1,ADGRG6,TRBC2,IL2RG,MRC1,TRBV5-4,FOLR2,DIO3,CD96,SIGLEC1,TRBV7-9
GO:0032991	CC	protein-containing complex	8.21E-09	8.085775725	188	IGLC3,IGLC2,IGKV4-1,IGHG1,IGHG2,IGHV4-39,IGKV3-11,IGHV1-2,IGHV3-7,IGKV1-5,IGHV3-30,IGLV2-11,IGHV4-34,IGLV3-21,IGKV3-15,IGLV1-44,IGHV3-23,IGHV4-59,IGHV2-5,IGKV3-20,IGHV3-21,IGKV1-9,JCHAIN,IGHM,IGLV2-14,IGHA1,IGHV1-18,IGHV1-3,IGLV3-19,IGHV4-4,IGHV1-69D,IGHV4-30-2,IGHV1-46,IGKV1-12,FCRL5,IGLV2-23,IGHV3-33,IGHV5-51,IGHV2-26,IGKV1-27,IGLV1-40,IGHV2-70,IGLV2-8,IGKV1-17,IGHV3-48,IGHV3-53,IGKV1-16,IGLV2-18,IGHV4-61,IGHG4,IGHV3-74,IGKV2-24,IGKV5-2,IGKV1-6,IGHV3-15,IGHV3-49,IGKV6-21,IGHV3-11,IGHV3-20,IGLV6-57,IGLV3-10,IGKV3D-11,IGKV2-30,IGLV1-47,IGHV4-28,IGHV7-4-1,IGLV3-25,IGHV3-64D,IGHA2,IGLL5,IGLV10-54,IGHV2-70D,IGHV1-69,IGKV1-8,IGHV3-43,IGLV4-69,IGLV7-46,IGLV7-43,IGLV8-61,IGHV6-1,IGKV1D-13,IGHV3-72,IGKV2D-29,IGKV3D-20,IGKV6D-21,IGHV3-13,PYHIN1,IGHV1-24,IGHV3-73,MS4A2,IGKV1D-39,IGHV3-66,TRAV4,IGKV1D-

						16,TRAT1,IGLV3-9,IGKV1-39,ISL1,IGLV5-45,TTR,OTX2,IGKV1D-12,POU4F2,IGKV3D-15,CD79A,IGKV1D-33,IGKV1-33,TRAV17,CD3E,IGKV1D-8,ITGAD,IL2RB,RNU6-968P,DYDC2,SIX3,MZB1,TRBV29-1,TRBV27,DAW1,CD2,CD28,IGLV1-36,CLIC6,HLA-DRB5,RNU1-28P,TRAV13-1,RNU1-27P,TRAV19,TRAV12-3,TRBV20-1,CD3D,RNU6-511P,TRBC1,DNAI3,TRBV28,PCP4,LHCGR,CD3G,TNNI3,TRAV12-2,RNU6-35P,GPR101,TRBV6-7,LTF,H4C13,SAGE1,TRAV8-2,CATSPERD,TRBV18,CTLA4,MYO3A,TFAP2D,IRF4,TRAV14DV4,SDC1,TRBV5-6,IGLV1-51,TRAJ3,MAT1A,C6,NCR1,TRBV5-5,CDC20B,RNU6-1300P,TRAC,DNAH3,GTF2A1L,RNU6-1061P,IL5RA,MYH2,F13A1,RNU1-136P,CD8B,TRBJ1-3,MSR1,RNU6-959P,RNU6-657P,DNAH11,TRBV7-7,POM121L2,MYB,FOXF2,RNU1-18P,TRBC2,IL2RG,TRBV5-4,RNU6-194P,TRBV7-9
GO:0003823	MF	antigen binding	3.83E-117	116.4163807	90	IGLC3,IGLC2,IGKV4-1,IGHG1,IGHG2,IGHV4-39,IGKV3-11,IGHV1-2,IGHV3-7,IGKV1-5,IGHV3-30,IGLV2-11,IGHV4-34,IGLV3-21,IGKV3-15,IGLV1-44,IGHV3-23,IGHV4-59,IGHV2-5,IGKV3-20,IGHV3-21,JCHAIN,IGHM,IGLV2-14,IGHA1,IGHV1-18,IGHV1-3,IGLV3-19,IGHV4-4,IGHV1-69D,IGHV4-30-2,IGHV1-46,IGLV2-23,IGHV3-33,IGHV5-51,IGHV2-26,IGLV1-40,IGHV2-70,IGLV2-8,IGKV1-17,IGHV3-48,IGHV3-53,IGKV1-16,IGHV4-61,IGHG4,IGHV3-74,IGKV5-2,IGHV3-15,IGHV3-49,IGHV3-11,IGHV3-20,IGLV6-57,IGKV2-30,IGLV1-47,IGHV4-28,IGHV7-4-1,IGLV3-25,IGHV3-64D,IGHA2,IGLL5,IGHV2-70D,IGHV1-69,IGHV3-43,IGLV7-43,IGHV6-1,IGHV3-72,IGHV3-13,IGHV1-24,IGHV3-73,IGKV1D-39,IGHV3-66,IGKV1D-16,IGKV1-39,IGKV1D-12,CD48,IGKV1D-33,IGKV1-33,SLAMF1,IL7R,HLA-DRB5,TRAV19,CD1C,TRAV12-3,TRBC1,TRBV28,TRAV12-2,CD209,IGLV1-51,TRBC2,TRBV7-

GO:0005102	MF	signaling receptor binding	5.32E-22	21.27396289	83	IGLC3,IGLC2,IGHG1,IGHG2,IGHV4-39,IGHV1-2,IGHV3-7,IGHV3-30,IGHV4-34,IGHV3-23,IGHV4-59,IGHV2-5,IGHV3-21,JCHAIN,IGHM,IGHA1,IGHV1-18,IGHV1-3,IGHV4-4,IGHV1-69D,IGHV4-30-2,IGHV1-46,IGHV3-33,IGHV5-51,IGHV2-26,IGHV2-70,IGHV3-48,IGHV3-53,IGHV4-61,IGHG4,IGHV3-74,CCL18,IGHV3-15,IGHV3-49,IGHV3-11,IGHV3-20,IGHV4-28,IGHV7-4-1,IGHV3-64D,IGHA2,IGLL5,IGHV2-70D,IGHV1-69,IGHV3-43,IGHV6-1,IGHV3-72,IGHV3-13,MS4A1,IGHV1-24,IGHV3-73,IGHV3-66,TRAT1,TTR,CCR2,CD3E,CCL26,ITGAD,DOK2,CCL4,CCL24,FASLG,TDGF1,CD2,CLIC6,RTP1,TRAV19,DRD3,TRBC1,IL24,CD3G,CCL5,CCL3,GPNMB,LCK,XCL2,CD8B,JAML,NTS,HGF,MICB,TRBC2,UCN3,TRBV7-9
				Down regulated genes		
GO:0032502	BP	developmental process	7.18E-09	8.144080437	176	NKX2-4,PLAC8,SFN,CIROP,GRHL3,IL9,TMEFF1,STC2,GJC2,NPPC,CPAMD8,VEGFA,RASAL1,ADM,IL31RA,CA9,COL9A3,CR2,COL9A2,HOXD1,SEMA3B,SAPCD2,INSM1,ANGPTL4,CHI3L1,SOX3,MAG,TACSTD2,AATK,GCM1,CHADL,LDB3,CNP,BMP8A,TBATA,DMBT1,BTG4,FOXE1,HES6,COL11A2,CDH1,ARC,SREBF1,GDF2,TXNDC8,MARCKSL1,ZNF536,CMTM5,GJB1,PLXNB3,HSF4,OLIG2,MT1X,MAL,HIP1R,RAB7B,KLK8,PLLP,USH1C,IGSF8,AQP6,CDKN1C,CDC42EP1,NKX6-2,GREB1L,ACSBG1,TSC22D4,CFTR,INSIG1,SRCIN1,HSD17B3,TNFAIP6,ALDOC,GREM1,ATF3,ABCA2,HK2,MCAM,GLDN,GPR37,IFNA2,SEMA4D,NGFR,NTNG2,KEL,TF,GLUL,DMRTA2,KREMEN2,GNG8,DMRT2,PALM2AKAP2,S1PR5,ROGDI,ELF3,TPRN,HAPLN2,SYNJ2,MYCN,HPN,FN3K,IFNA13,TLE2,MYRF,GAMT,TREH,MEIS1,BNC1,MOG,SBF1,ADAMTS4,INF2,BIN1,RHOU,STMN4,SH3PXD2B,BMP2,HSPA2,LMNA,ERBB3,HSD11B1,HTRA1,DLL1,NKX2-2,THBS2,SH3TC2,NHLH2,PIWIL2,MT1G,GADD45B,APLP1,PHLDB1,

						FGF11,SHB,UNC5B,MYH6,ASPA,CYP26C1,FASN,RASSF2,CRB2,PNPLA3,ACTN2,PRKCQ,MMP15,LLGL1,CBR1,PADI2,PCDHA7,SVEP1,SLC45A3,MT3,ADORA1,DISP3,TNFSF9,GPC2,CPB2,KAZN,DYSF,SEMA4C,MATN1,NEU4,ERF,ZNF784,SLC24A4,ADAMTSL2,LCTL,TST,SEPTIN4,RHOB,ROM1,F3,NINJ2,LRP2,WNT7A,PHLDA3
GO:0032501	BP	multicellular organismal process	2.67E-08	7.573717421	197	OR4F4,PLAC8,RXFP4,ICOSLG,SFN,CIROP,GRHL3,IL9,TMEFF1,STC2,GJC2,NPPC,CPAMD8,VEGFA,RASAL1,ADM,IL31RA,CHRM5,HILPDA,LIPC,COL9A3,CR2,COL9A2,HOXD1,SEMA3B,INSM1,ANGPTL4,CHI3L1,SOX3,MAG,TACSTD2,SCNN1G,AATK,GCM1,CHADL,LDB3,CNP,BMP8A,TBATA,BTG4,FOXE1,OR2K2,HES6,COL11A2,TRPV6,CDH1,RABGEF1,ARC,SREBF1,TMTC4,GDF2,COL16A1,TXNDC8,KCNE5,MARCKSL1,LLCFC1,ZNF536,GJB1,PLXNB3,HSF4,OLIG2,MT1X,MAL,HIP1R,RAB7B,KLK8,PLLP,USH1C,IGSF8,AQP6,TRPV5,SAA1,CDKN1C,NKX6-2,GREB1L,ACSBG1,TSC22D4,CFTR,INSIG1,OR13A1,SRCIN1,HSD17B3,TNFAIP6,GREM1,VWA1,ABCA2,HK2,MCAM,GLDN,GPR37,IFNA2,OR1L4,SEMA4D,TAS2R40,SCD,NGFR,FFAR1,NTNG2,KEL,TF,GLUL,DMRTA2,HCN2,KREMEN2,GNG8,DMRT2,OR2AE1,S1PR5,ROGDI,ELF3,TPRN,HMSD,HAPLN2,SYNJ2,MYCN,HPN,IFNA13,MYRF,GAMT,MEIS1,OR5C1,BNC1,HCRTR1,MOG,SBF1,ADAMTS4,BIN1,F11,STMN4,SH3PXD2B,BMP2,HSPA2,GPIHBP1,LMNA,PLA2G4C,ERBB3,EQTN,HSD11B1,DLL1,NKX2-2,THBS2,SH3TC2,NHLH2,PIWIL2,MT1G,APLP1,ST3GAL4,PHLDB1,FGF11,SHB,UNC5B,MYH6,ASPA,CYP26C1,FASN,RASSF2,CRB2,GIPC1,ACTN2,PRKCQ,MMP15,LLGL1,PADI2,PCDHA7,MPP2,SVEP1,PPEF1,SLC45A3,MT3,ADORA1,ALDH1A1,DISP3,TAS2R39,PSG6,TNFSF9,GPC2,CPB2,KAZN,DYSF,SEMA4C,MATN1,NEU4,MAPK8IP1,CAPN8,SLC24A4,ADAMTSL2,LCTL,SEPTIN4,RHOB,ROM1,CTNNA3,F3,NINJ2,LRP2,OR1L6,BEST1,WNT7A
GO:0110165	CC	cellular anatomical entity	0.067162031	1.17287618	386	ADGRG7,OR4F4,NKX2-4,PLAC8,RXFP4,ICOSLG,SFN,CIROP,GRHL3,UGT2B17,IL9,TMEM88B,ADAMTS14,TMEFF1,STC2,GJC2

,TEX44,NPPC,DAO,CPAMD8,VEGFA,RASAL1,SYS1-DBNDD2,ADM,SMIM32,IL31RA,CHRM5,CA9,CTSV,SLC25A48,KCNG4,SAA2,HILPDA,ZNF705G,LIPC,MAP6D1,COL9A3,CARNS1,CR2,COL9A2,HOXD1,EXD1,RNU6-1160P,SEMA3B,SAPCD2,INSM1,ANGPTL4,CHI3L1,DBNDD2,C1ORF116,TUBB4A,SOX3,MAG,TACSTD2,SCNN1G,AATK,GCM1,PRODH,SCART1,CHP2,CHADL,GPR142,LDB3,CNP,GPD1,FAM53A,PKD1L2,BMP8A,TBATA,ACP7,CPB1,DMBT1,BTG4,FOXE1,MAP1LC3B2,PDIA2,OR2K2,OPLAH,HES6,COL11A2,TRPV6,RNU6-913P,CDH1,RABGEF1,FTCD,ARC,SREBF1,TMTC4,GDF2,CPHXL,RNU6-871P,LIPE,COL16A1,TXNDC8,CNDP1,DHCR7,FXYD4,RNU6-448P,KIF19,KCNE5,GALNT6,MARCKSL1,LLCFC1,SEC14L5,ZNF536,CMTM5,MAP1LC3A,KCNH8,GJB1,PLXNB3,HSF4,AGPAT4,OLIG2,MT1X,MAL,HIP1R,RAB7B,SLC16A8,KLK8,PLCH2,PLLP,SLC36A3,SLC5A11,USH1C,IGSF8,AQP6,TRPV5,SAA1,PACSIN3,CDKN1C,TMEM125,CDC42EP1,SH3BP5,NKX6-2,GREB1L,ADSS1,TKTL1,ACSBG1,TSC22D4,CFTR,INSIG1,ZNF775,OR13A1,SRCIN1,HSD17B3,TNFAIP6,TMEM151A,ACADS,TMCO5A,CALB2,ALDOC,PTPRH,GREM1,VWA1,CES4A,DUXB,CERCAM,RBP7,ADAP1,ATF3,ABCA2,SGK2,PLEKHG3,HK2,MCAM,GLDN,GPR37,RAB33A,EFS,IFNA2,OR1L4,KLK10,SPINK14,HPDL,SEMA4D,TAS2R40,SCD,NGFR,FFAR1,NTNG2,HAS1,SCAND1,KEL,TF,GLUL,DMRTA2,HCN2,KREMEN2,PCBP4,GNG8,PET117,ARSI,DMRT2,AOX1,PALM2AKAP2,TM7SF2,OR2AE1,S1PR5,SKOR1,ROGDI,ELF3,RNU5D-1,PLEKHG4,TPRN,ZNF367,NACAD,HMSD,HAPLN2,LLGL2,SYNJ2,GOLGA6A,MYCN,HPN,SHC2,FN3K,IFNA13,SERPINE3,TLE2,MYRF,GAMT,TREH,MEIS1,OR5C1,BNC1,HCRTR1,MOG,SBF1,ADAMTS4,CA14,INF2,TMEM171,OSBPL5,BIN1,NME3,CDK18,RAB6C,PTPDC1,ARL2BP,FSCN1,F11,RNU6-539P,TP53TG5,MTFR2,RHOU,STMN4,GOLGA6B,DIPK1C,PAQR4,RNASE1,GNLY,MVK,SH3PXD2B,BMP2,HSPA2,GPIHBP1,LMNA,PLA2G4C,ERBB3,KIRREL2,EQTN,HSD11

						B1,HTRA1,DLL1,EEPD1,RHBG,NKX2-2,PFKL,CPHXL2,RNU6-883P,EVA1A,LMF1,THBS2,SH3TC2,NHLH2,IGSF1,PEBP4,PIWIL2,PLEKHH1,MT1G,GADD45B,APLP1,ST3GAL4,PHLDB1,GASK1A,FGF11,SHB,UNC5B,ENOSF1,MYH6,CPA2,SNX22,NKAIN4,ASPA,CIRBP,CYP26C1,FASN,MRI1,RASSF2,CRB2,GIPC1,PNPLA3,LSS,DHRS13,GPR62,FAM170A,LGI3,ACTN2,PRKCQ,MMP15,CLUL1,LLGL1,CBR1,MT1M,ARHGAP23,PADI2,PCDHA7,EDIL3,MPP2,SVEP1,PPEF1,SLC45A3,NOXA1,MT3,ADORA1,ALDH1A1,ANGPTL2,DISP3,TAS2R39,PSG6,NENF,EVI5L,TNFSF9,PAQR6,PDE8A,TTYH1,GPC2,CPB2,KAZN,DYSF,TRIM61,PCCB,CAPN13,SEMA4C,MATN1,NEU4,IPO13,SLC25A13,ERF,RTKN,ZNF146,TSPAN15,ZNF784,TMEM229A,MAPK8IP1,CAPN8,TRAPPC6A,SPON1,SLC24A4,EGLN3,MRPS26,ADAMTSL2,LCTL,MARCOL,TST,CHPF,SEPTIN4,CYP2A6,ZNF837,RHOB,ROM1,CTNNA3,F3,NINJ2,LRP2,POLR2F,CADM4,MEX3D,OR1L6,BEST1,WNT7A,ASPHD1,ABHD17A,JAKMIP3,PHLDA3,LGALS3BP,RASA3
GO:0005737	CC	cytoplasm	0.067885536	1.168222749	243	PLAC8,ICOSLG,SFN,CIROP,UGT2B17,STC2,TEX44,NPPC,DAO,VEGFA,RASAL1,ADM,CTSV,SLC25A48,HILPDA,LIPC,MAP6D1,COL9A3,CARNS1,COL9A2,EXD1,SEMA3B,SAPCD2,CHI3L1,DBNDD2,C1ORF116,TUBB4A,MAG,TACSTD2,AATK,PRODH,SCART1,CHP2,GPR142,LDB3,CNP,GPD1,TBATA,CPB1,DMBT1,BTG4,MAP1LC3B2,PDIA2,OPLAH,COL11A2,CDH1,RABGEF1,FTCD,ARC,SREBF1,TMTC4,LIPE,COL16A1,TXNDC8,CNDP1,DHCR7,KIF19,GALNT6,MARCKSL1,SEC14L5,MAP1LC3A,GJB1,AGPAT4,OLIG2,MT1X,MAL,HIP1R,RAB7B,KLK8,PLCH2,USH1C,AQP6,SAA1,PACSIN3,CDKN1C,CDC42EP1,SH3BP5,ADSS1,TKTL1,ACSBG1,TSC22D4,CFTR,INSIG1,SRCIN1,HSD17B3,TNFAIP6,ACADS,CALB2,ALDOC,PTPRH,VWA1,CERCAM,RBP7,ADAP1,ABCA2,SGK2,PLEKHG3,HK2,GPR37,RAB33A,EFS,KLK10,HPDL,SCD,NGFR,HAS1,KEL,TF,GLUL,KREMEN2,PCBP4,PET117,ARSI,AOX1,TM7SF2,S1PR5,ROGDI,ELF3,PLEKHG4,NACAD,LLGL2,SYNJ2,GOLGA6A,HPN,SHC2,FN3K,MYRF,GAMT,BNC1,SBF1,INF2,OSBP

						L5,BIN1,NME3,CDK18,RAB6C,PTPDC1,ARL2BP,FSCN1,TP53TG5,MTFR2,RHOU,STMN4,GOLGA6B,DIPK1C,GNLY,MVK,SH3PXD2B,HSPA2,LMNA,PLA2G4C,EQTN,HSD11B1,HTRA1,DLL1,RHBG,PFKL,EVA1A,LMF1,THBS2,SH3TC2,PIWIL2,MT1G,GADD45B,APLP1,ST3GAL4,PHLDB1,GASK1A,FGF11,SHB,ENOSF1,MYH6,CPA2,SNX22,ASPA,CIRBP,CYP26C1,FASN,MRI1,RASSF2,CRB2,GIPC1,PNPLA3,LSS,DHRS13,GPR62,LGI3,ACTN2,PRKCQ,LLGL1,CBR1,MT1M,ARHGAP23,PADI2,MPP2,SVEP1,PPEF1,NOXA1,MT3,ADORA1,ALDH1A1,DISP3,NENF,PDE8A,TTYH1,GPC2,KAZN,DYSF,TRIM61,PCCB,CAPN13,SEMA4C,NEU4,IPO13,SLC25A13,ERF,RTKN,ZNF146,TSPAN15,MAPK8IP1,CAPN8,TRAPPC6A,SPON1,SLC24A4,EGLN3,MRPS26,LCTL,TST,CHPF,SEPTIN4,CYP2A6,RHOB,CTNNA3,LRP2,POLR2F,MEX3D,BEST1,WNT7A,ABHD17A,JAKMIP3,PHLDA3,LGALS3BP,RASA3
GO:0098772	MF	molecular function regulator activity	0.047007711	1.327830892	63	SFN,IL9,STC2,NPPC,CPAMD8,VEGFA,RASAL1,ADM,CA9,SEMA3B,ANGPTL4,BMP8A,RABGEF1,GDF2,FXYD4,KCNE5,CMTM5,MAL,PACSIN3,CDKN1C,SH3BP5,CFTR,GREM1,ADAP1,ABCA2,SGK2,PLEKHG3,IFNA2,SPINK14,SEMA4D,FFAR1,PLEKHG4,HMSD,LLGL2,IFNA13,SERPINE3,SBF1,BIN1,ARL2BP,RHOU,SH3PXD2B,BMP2,GPIHBP1,ERBB3,HTRA1,DLL1,IGSF1,FGF11,CRB2,MMP15,LLGL1,ARHGAP23,NOXA1,MT3,ALDH1A1,NENF,EVI5L,TNFSF9,SEMA4C,RTKN,MAPK8IP1,WNT7A,RASA3
GO:0140677	MF	molecular function activator activity	0.047007711	1.327830892	44	IL9,STC2,NPPC,VEGFA,RASAL1,ADM,CA9,SEMA3B,BMP8A,RABGEF1,GDF2,CMTM5,MAL,SH3BP5,GREM1,ADAP1,PLEKHG3,IFNA2,SEMA4D,FFAR1,PLEKHG4,LLGL2,IFNA13,SBF1,RHOU,SH3PXD2B,BMP2,GPIHBP1,ERBB3,HTRA1,DLL1,FGF11,MMP15,LLGL1,ARHGAP23,NOXA1,MT3,ALDH1A1,NENF,EVI5L,TNFSF9,SEMA4C,WNT7A,RASA3

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	7.08E-38	37.15022242	113	IGLC3,IGLC2,IGKV4-1,IGHG1,IGHG2,IGHV4-39,IGKV3-11,IGHV1-2,IGHV3-7,IGKV1-5,IGHV3-30,IGLV2-11,IGHV4-34,IGLV3-21,IGKV3-15,IGLV1-44,IGHV3-23,IGHV4-59,IGHV2-5,IGKV3-20,IGHM,IGLV2-14,IGLV3-19,IGHV1-46,IGKV1-12,IGLV2-23,IGHV3-33,IGLV1-40,IGHV2-70,IGLV2-8,IGKV1-17,IGHV3-48,IGHV3-53,IGKV1-16,IGHG4,IGKV5-2,IGHV3-11,IGLV6-57,IGKV2-30,IGLV1-47,IGLV3-25,IGHV1-69,IGLV7-43,SLAMF7,IGKV3D-20,IGHV3-13,MS4A2,IGKV1D-39,CLEC10A,SLAMF6,IGKV1D-16,TRAT1,IGKV1-39,TTR,IGKV1D-12,CD79A,CCR2,IGKV1D-33,IGKV1-33,CD3E,IL2RB,CCL4,TNFRSF13B,FASLG,CD28,LYZ,IL7R,HLA-DRB5,FCGR2B,TUBA4B,TRAV19,CD1C,LAIR2,CD3D,TRBC1,TAB2,CLEC12A,IL24,CD3G,CCL5,CCL3,SIGLEC6,LTF,ITK,CTLA4,IRF4,SDC1,TNFRSF9,LCK,CD209,IGLV1-51,C6,IQGAP2,NCR1,TUBAL3,MUC3A,TRAC,CDA,AOC1,IL5RA,MYH2,F13A1,CD8B,JAML,GBP5,HGF,MICB,IL2RG,MRC1,CD96,SIGLEC1,TRBV7-9,CHIT1
REAC:R-HSA-202403	TCR signaling	9.31E-06	5.031017738	12	TRAT1,CD3E,HLA-DRB5,TRAV19,CD3D,TRBC1,TAB2,CD3G,ITK,LCK,TRAC,TRBV7-9
REAC:R-HSA-449147	Signaling by Interleukins	0.009177632	2.037269376	18	IGHG1,IGHG4,CCR2,IL2RB,CCL4,FASLG,IL7R,TAB2,IL24,CCL5,CCL3,IRF4,SDC1,LCK,IL5RA,F13A1,HGF,IL2RG
REAC:R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	0.033564699	1.474117249	13	P2RY10,CCR4,CCR2,CCL4,NPY2R,DRD3,LHCGR,CCL5,CCL3,XCL2,PTGDR,LPAR3,NTS

REAC:R-HSA-1280215	Cytokine Signaling in Immune system	0.036661634	1.435788182	22	IGHG1,IGHG4,CCR2,IL2RB,CCL4,TNFRSF13B,FASLG,IL7R,HLA-DRB5,TAB2,IL24,CCL5,CCL3,IRF4,SDC1,TNFRSF9,LCK,IL5RA,F13A1,GBP5,HGF,IL2RG
REAC:R-HSA-500792	GPCR ligand binding	0.164500063	0.783833932	14	P2RY10,CCR4,CCR2,CCL4,NPY2R,DRD3,LHCGR,CCL5,CCL3,XCL2,PTGDR,LPAR3,NTS,UCN3
Down regulated genes					
REAC:R-HSA-1655829	Regulation of cholesterol biosynthesis by SREBP (SREBF)	0.020632763	1.68544262	7	DHCR7,INSIG1,SCD,TM7SF2,MVK,FASN,LSS
REAC:R-HSA-1474228	Degradation of the extracellular matrix	0.020632763	1.68544262	11	CTSV,COL9A3,COL9A2,COL11A2,CDH1,COL16A1,ADAMTS4,HTRA1,MMP15,CAPN13,CAPN8
REAC:R-HSA-8957322	Metabolism of steroids	0.032317344	1.490564341	11	SREBF1,DHCR7,INSIG1,HSD17B3,SCD,TM7SF2,MVK,HSD11B1,FASN,LSS,LRP2
REAC:R-HSA-1474244	Extracellular matrix organization	0.230258584	0.63778417	14	ADAMTS14,CTSV,COL9A3,COL9A2,COL11A2,CDH1,COL16A1,ADAMTS4,BMP2,HTRA1,MMP15,CAPN13,MATN1,CAPN8
REAC:R-HSA-556833	Metabolism of lipids	0.240535296	0.618821186	26	HILPDA,ANGPTL4,GPD1,SREBF1,LIPE,DHCR7,AGPAT4,ACSBG1,INSIG1,HSD17B3,ACADS,SCD,ARSI,TM7SF2,SYNJ2,SBF1,OSBPL5,MVK,PLA2G4C,HSD11B1,FASN,PNPLA3,LSS,CBR1,PCCB,LRP2
REAC:R-HSA-1430728	Metabolism	0.324955932	0.488175531	58	UGT2B17,DAO,CA9,HILPDA,CARNS1,ANGPTL4,PRODH,GPD1,OPLAH,FTCD,SREBF1,LIPE,DHCR7,AGPAT4,SLC16A8,PLCH2,ADSS1,ACSBG1,INSIG1,HSD17B3,ACADS,ALDOC,HK2,SCD,FFAR1,HAS1,GLUL,GNG8,ARSI,AOX1,TM7SF2,SYNJ2,GAMT,SBF1,CA14,OSBPL5,NME3,MVK,GPIHBP1,PLA2G4C,HSD11B1,PFKL,ST3GAL4,ASPA,CYP26C1,FASN,MRI1,PNPLA3,LSS,CBR1,ALDH1A1,GPC2,PCCB,SLC25A13,TST,CHPF,CYP2A6,LRP2

Table 4 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	LCK	140	0.058833	16807950	0.307962
Up	PYHIN1	126	0.052288	14469590	0.28918
Up	SLAMF1	93	0.043579	6854232	0.274257
Up	DOK2	92	0.028643	6940372	0.287996
Up	TAB2	83	0.038875	9755578	0.310568
Up	C6orf141	72	0.024145	6150196	0.26301
Up	IKZF3	61	0.027978	4317696	0.263618
Up	POTEF	56	0.021911	5211510	0.250074
Up	NPY2R	56	0.022163	4152490	0.252513
Up	FOXL2	48	0.015502	2987768	0.259676
Up	SDC1	47	0.021521	2719126	0.274329
Up	CCR2	42	0.013268	4601914	0.250282
Up	FASLG	41	0.012687	1582940	0.275241
Up	CD79A	41	0.015733	4708198	0.245121
Up	IGHG1	40	0.00989	3641634	0.262781
Up	IGHA1	39	0.012825	2142462	0.268995
Up	CCR4	35	0.012921	3385226	0.248806
Up	IGHG2	33	0.006747	2674868	0.248616
Up	LTF	32	0.007394	1952246	0.24638
Up	TNFRSF13B	31	0.009736	2745188	0.234327
Up	ITK	30	0.004789	847972	0.279322
Up	IGKC	30	0.007807	2266182	0.253317
Up	HGF	29	0.00803	1507282	0.26043
Up	POTEI	29	0.010191	2696488	0.237292
Up	IGHA2	27	0.005708	3642692	0.220584
Up	P2RY8	25	0.00726	1510550	0.225971
Up	ZBBX	25	0.00844	825726	0.254877
Up	MYB	24	0.006732	1591432	0.252106
Up	CLEC12A	24	0.007916	2190268	0.221546
Up	GML	24	0.007403	1542574	0.244538
Up	TTR	21	0.005401	1289472	0.265576
Up	CD3E	21	0.005	822592	0.256707
Up	CCL5	21	0.006503	628572	0.23117
Up	ISL1	20	0.006034	1101492	0.241668
Up	IL2RB	20	0.004493	463700	0.267851
Up	TDGF1	20	0.008132	1032370	0.224947
Up	LYZ	19	0.004719	1308102	0.254416
Up	CRNN	19	0.004615	1699386	0.214018
Up	JCHAIN	19	0.002072	1086114	0.224971
Up	IQGAP2	18	0.00411	1091974	0.249793
Up	WT1	18	0.004077	1563748	0.238918
Up	CDA	18	0.005444	1258070	0.215724
Up	TEKT4	18	0.006382	836454	0.233136
Up	IL2RG	16	0.002901	291022	0.248279
Up	CTLA4	16	0.00267	370240	0.252695
Up	MAPK15	16	0.003406	820796	0.24729
Up	FOXJ1	15	0.004646	699482	0.238297
Up	IGLL5	15	0.003041	1619426	0.216866
Up	IRF4	14	0.004554	911852	0.223813
Up	TRIML2	14	0.003726	745092	0.229898
Up	SLAMF7	14	0.003102	658976	0.244638
Up	FOXF2	14	0.003977	970700	0.217874
Up	PRPH	14	0.00387	667282	0.240264
Up	CD2	13	0.002636	285328	0.255959
Up	TNNI3	11	1	110	1
Up	TUBAL3	11	0.001148	432370	0.250119
Up	RIBC2	11	0.003753	482112	0.22895
Up	DRD3	10	0.002836	245256	0.249188
Up	CDC20B	10	0.001734	432434	0.218732
Up	IGHM	10	0.001962	771212	0.259421
Up	TUBA4B	10	3.81E-04	146958	0.244439
Up	PLEKHG4B	10	0.002575	439176	0.228677
Up	TNFRSF9	9	0.001472	194238	0.217818
Up	FCGR2B	9	0.001661	223634	0.239732
Up	CD3D	9	0.001659	395762	0.238068
Up	UBASH3A	9	0.001652	322436	0.246856

Up	ICOS	8	0.00148	240124	0.2304
Up	CD28	8	9.20E-04	300772	0.227432
Up	CD209	8	0.001913	624752	0.174561
Up	HOXB7	8	0.001334	573180	0.2304
Up	TRARG1	8	0.002105	371424	0.193223
Up	IGHG3	8	8.36E-04	230950	0.21568
Up	SIK1	7	0.001327	404776	0.237867
Up	TRAT1	7	4.69E-04	65264	0.254003
Up	XIRP2	7	0.001263	101636	0.235926
Up	IL7R	6	2.94E-04	36312	0.233008
Up	IL5RA	6	0.001036	224104	0.204815
Up	CCL3	6	0.00102	264856	0.199301
Up	SLAMF6	6	2.94E-05	9606	0.204368
Up	F13A1	6	9.51E-04	178910	0.222644
Up	HSH2D	6	9.54E-04	223244	0.220504
Up	OTX2	6	0.001421	140220	0.183128
Up	MYH2	6	4.43E-04	116614	0.22614
Up	NCR1	5	9.67E-04	237432	0.221116
Up	GSDMA	5	3.69E-04	127942	0.213844
Up	PRSS21	5	0.001421	119730	0.239215
Up	TEKT1	5	9.78E-04	219492	0.196069
Up	MS4A1	4	9.51E-04	195172	0.241253
Up	IGHG4	4	2.00E-04	21808	0.212274
Up	IL24	4	9.98E-04	136230	0.210474
Up	PCP4	4	5.07E-04	62300	0.201567
Up	CD48	3	1.54E-04	17404	0.237586
Up	ITGAD	3	9.48E-04	106298	0.212906
Up	CLEC10A	3	1	6	1
Up	NLRP7	3	0	0	0.191609
Up	CD3G	2	0	0	0.212798
Up	GTF2A1L	2	4.74E-04	113092	0.185552
Up	CCL18	2	4.74E-04	97832	0.224432
Up	TFAP2D	2	8.04E-05	19550	0.230425
Up	LAIR2	2	8.88E-06	4128	0.193003
Up	GPR101	2	4.74E-04	84402	0.214355
Up	DNAJC5B	2	4.74E-04	63948	0.208066
Up	UCN3	1	0	0	1
Up	CLIC6	1	0	0	0.199489
Up	POU4F2	1	0	0	0.227297
Up	FCGBP	1	0	0	0.191748
Up	ART5	1	0	0	0.19167
Up	LHCGR	1	0	0	0.212584
Up	CD8B	1	0	0	0.161303
Up	IGLC7	1	0	0	0.178225
Up	IGLC2	1	0	0	0.209025
Up	LPAR3	1	0	0	1
Down	CFTR	448	0.23294	51911534	0.355249
Down	RHOB	310	0.15555	38047904	0.326878
Down	LMNA	234	0.131093	28009940	0.33655
Down	EGLN3	218	0.089938	27288494	0.300527
Down	ERBB3	164	0.07109	20481052	0.305288
Down	SFN	151	0.063891	14207304	0.312361
Down	CDH1	99	0.045914	9295142	0.323496
Down	LGALS3BP	96	0.041894	6685572	0.314245
Down	LLGL2	85	0.029632	6429240	0.269322
Down	MAP1LC3A	80	0.027842	8446748	0.288804
Down	MRPS26	80	0.02894	2657506	0.278585
Down	FOXE1	74	0.024085	8242508	0.261495
Down	POLR2F	69	0.024818	5551166	0.235767
Down	LRP2	62	0.025207	2775392	0.265426
Down	GPR37	62	0.021578	8569080	0.250386
Down	FASN	62	0.018313	4007430	0.303248
Down	TSC22D4	60	0.022958	4955946	0.269545
Down	HSPA2	51	0.017989	2628066	0.303248
Down	RABGEF1	48	0.016655	4511302	0.270495
Down	ACTN2	47	0.015872	1936132	0.261122
Down	DYSF	46	0.016541	2367264	0.266095
Down	CDK18	44	0.015072	4414490	0.268039
Down	TMEM171	44	0.016979	2402824	0.260671
Down	HIP1R	43	0.01693	2178882	0.287192

Down	BIN1	43	0.013341	2910812	0.262814
Down	GIPC1	41	0.015352	2965838	0.269959
Down	PFKL	41	0.017113	2200404	0.297016
Down	SLC25A13	41	0.012474	2982996	0.285154
Down	CA14	38	0.012126	3428272	0.22986
Down	PACSIN3	36	0.008301	1977144	0.264411
Down	NGFR	35	0.010558	2189410	0.266061
Down	SREBF1	35	0.012699	1366254	0.265559
Down	CMTM5	35	0.012218	2566464	0.225922
Down	CIRBP	32	0.010017	1802488	0.2613
Down	MAPK8IP1	30	0.012444	1435146	0.263635
Down	TF	30	0.009455	2568540	0.260542
Down	SBF1	30	0.012372	1266794	0.27754
Down	CBR1	30	0.013504	1693874	0.296974
Down	HK2	29	0.008798	1761438	0.253728
Down	IPO13	28	0.010874	1797866	0.256441
Down	TNFSF9	28	0.008188	1801388	0.230475
Down	INF2	28	0.003516	1545810	0.249247
Down	LLGL1	27	0.009508	1070324	0.282823
Down	FSCN1	27	0.010468	1439798	0.286724
Down	ATF3	26	0.005532	1667062	0.248835
Down	MARCKSL1	26	0.007311	1435148	0.24605
Down	SCAND1	26	0.010071	2109302	0.212359
Down	SHB	26	0.007591	964476	0.277449
Down	CTNNA3	25	0.00672	834614	0.263816
Down	PLEKHG3	25	0.006247	1054996	0.280473
Down	TSPAN15	24	0.008179	1096016	0.229722
Down	ERF	24	0.006312	1775804	0.248177
Down	MKRN3	24	0.007051	890546	0.252362
Down	ARHGAP23	24	0.007333	1371270	0.258025
Down	ADAMTS4	23	0.007022	1763788	0.237105
Down	IGSF8	22	0.006733	1435756	0.223695
Down	CUEDC1	22	0.007581	2106760	0.246107
Down	MYH6	22	0.006908	1582100	0.238418
Down	PHLDA3	22	0.004658	1584334	0.240785
Down	MEIS1	21	0.006568	1318744	0.218347
Down	CERCAM	21	0.00931	747112	0.230538
Down	APLP1	20	0.004911	829966	0.230715
Down	PRKCQ	20	0.006504	735740	0.278382
Down	AATK	20	0.003035	692730	0.264876
Down	PTPDC1	20	0.003353	1160564	0.253256
Down	ABCA2	20	0.008648	1517904	0.260349
Down	GALNT6	20	0.006483	3415268	0.206934
Down	VEGFA	19	0.004622	1026228	0.232507
Down	NME3	19	0.005723	1121392	0.23615
Down	ELF3	19	0.002774	768426	0.243832
Down	CTSV	19	0.005403	1153110	0.217101
Down	TLE2	18	0.003774	2368808	0.22454
Down	HTRA1	18	0.005805	918226	0.209232
Down	GLUL	17	0.003346	592544	0.243762
Down	DMBT1	16	0.001848	609084	0.239039
Down	EVI5L	16	0.005983	869332	0.233008
Down	CNP	16	0.004968	644810	0.27189
Down	CDC42EP1	15	0.004362	481862	0.271295
Down	INSIG1	15	0.002963	1520474	0.224623
Down	ST3GAL4	15	0.004884	545722	0.184006
Down	MCAM	15	0.00422	477230	0.268807
Down	MYCN	14	0.003305	769538	0.227776
Down	KLK10	14	0.001971	1124350	0.204666
Down	ALDOC	13	0.003062	1091856	0.242976
Down	TRAPPC6A	13	0.004934	312962	0.22769
Down	SEMA4C	12	0.00317	479158	0.247667
Down	RHOU	12	0.001547	375864	0.239868
Down	ZNF146	12	0.004459	843410	0.235137
Down	HSF4	11	0.002579	251034	0.20733
Down	CA9	11	9.11E-04	113280	0.258959
Down	DHCR7	10	0.002641	362558	0.258246
Down	CDR2L	9	0.002382	406166	0.216444
Down	MAL	9	0.00305	533156	0.219084
Down	PLLP	9	0.002396	255530	0.22801

Down	PLEKHG4	8	0.001024	145762	0.212466
Down	PCCB	7	0.001531	206160	0.221348
Down	GJB1	7	6.42E-04	160668	0.240579
Down	AGPAT4	7	0.001284	240210	0.202534
Down	RTKN	6	0.001641	132644	0.263224
Down	UNC5B	6	0.001445	200958	0.223849
Down	NOXA1	6	0.002369	378880	0.214115
Down	SCD	6	6.70E-04	111220	0.23965
Down	SCHIP1	5	9.48E-04	170190	0.199991
Down	GCM1	5	0.001021	282572	0.216355
Down	TACSTD2	5	0.001036	180184	0.236547
Down	TTYH1	5	0.001011	145006	0.212306
Down	PTPRH	5	5.11E-04	42036	0.263388
Down	GNG8	4	9.55E-04	132524	0.214148
Down	NENF	4	0.001421	188832	0.207851
Down	FGF11	4	5.52E-04	129372	0.215691
Down	SEMA3B	3	1	6	1
Down	PPEF1	2	3.02E-06	3356	0.226845
Down	GOLGA6A	2	4.74E-04	73866	0.206751
Down	SYNJ2	2	2.56E-04	79302	0.242808
Down	ICOSLG	1	0	0	0.187264
Down	LDB3	1	0	0	0.207066
Down	GPIHBP1	1	0	0	0.173413
Down	CNDP1	1	0	0	0.200057
Down	THBS2	1	0	0	0.178905
Down	TNFAIP6	1	0	0	0.187773
Down	EDIL3	1	0	0	0.206701
Down	EEPD1	1	0	0	0.215284
Down	MT3	1	0	0	0.209856
Down	EFS	1	0	0	0.18547
Down	HSD17B3	1	0	0	0.191792
Down	MPP2	1	0	0	0.177453
Down	PRODH	1	0	0	0.232699
Down	NTNG2	1	0	0	0.20019
Down	NINJ2	1	0	0	1
Down	MTFR2	1	0	0	0.201615
Down	LSS	1	0	0	0.196498
Down	S1PR5	1	0	0	0.20019
Down	TUBB4A	1	0	0	0.236985
Down	KREMEN2	1	0	0	0.25182
Down	HPN	1	0	0	0.169716
Down	PHLDB1	1	0	0	0.231094

Table 5 MiRNA - hub gene and TF – hub gene topology table

Regulation	Hub Genes	Degree	MicroRNA	Regulation	Hub Genes	Degree	TF
Up	IKZF3	147	hsa-mir-6794-3p	Up	LTF	15	BRCA1
Up	TAB2	118	hsa-mir-3689a-3p	Up	CD79A	10	HNF4A
Up	C6orf141	59	hsa-mir-4449	Up	LCK	10	NFKB1
Up	SDC1	47	hsa-mir-146a-5p	Up	IKZF3	9	TEAD1
Up	CCR4	45	hsa-mir-4695-5p	Up	TAB2	8	ELK4
Up	SLAMF1	30	hsa-mir-4778-3p	Up	PYHIN1	8	JUND
Up	FASLG	25	hsa-mir-362-3p	Up	DOK2	8	USF2
Up	FOXL2	19	hsa-mir-3915	Up	POTEF	7	STAT3
Up	CCR2	11	hsa-mir-6514-3p	Up	CCR4	6	MEF2A
Up	CD79A	7	hsa-mir-520f-3p	Up	SLAMF1	6	YY1
Up	PYHIN1	7	hsa-mir-1277-5p	Up	SDC1	6	PPARG
Up	LCK	6	hsa-mir-520c-3p	Up	FASLG	5	ARID3A
Up	DOK2	5	hsa-mir-365b-3p	Up	NPY2R	5	ELF5
Up	NPY2R	4	hsa-mir-302f	Up	FOXL2	4	CEBPB
Up	POTEF	2	hsa-mir-16-5p	Up	CCR2	4	TP53
Down	RHOB	216	hsa-mir-4651	Down	MAP1LC3A	14	TFAP2C
Down	LGALS3BP	99	hsa-mir-548q	Down	CFTR	10	NR2F1
Down	SFN	91	hsa-mir-8485	Down	LLGL2	8	FOXO3
Down	CDH1	75	hsa-mir-195-5p	Down	POLR2F	8	NRF1
Down	POLR2F	68	hsa-mir-4739	Down	FOXE1	8	NFYA
Down	EGLN3	58	hsa-mir-122-5p	Down	LGALS3BP	8	HOXA5

Down	ERBB3	53	hsa-mir-6842-5p	Down	MRPS26	8	SOX17
Down	LMNA	50	hsa-mir-744-5p	Down	LRP2	8	E2F6
Down	LLGL2	40	hsa-mir-200c-3p	Down	CDH1	7	ESR1
Down	FOXE1	29	hsa-mir-4723-3p	Down	SFN	6	FOS
Down	GPR37	22	hsa-mir-186-5p	Down	RHOB	5	RELA
Down	CFTR	16	hsa-mir-154-5p	Down	EGLN3	4	POU2F2
Down	LRP2	15	hsa-mir-196a-5p	Down	ERBB3	4	GATA2
Down	MRPS26	14	hsa-mir-3065-5p	Down	LMNA	4	JUN
Down	MAP1LC3A	6	hsa-mir-22-3p	Down	GPR37	4	FOXL1

Figures

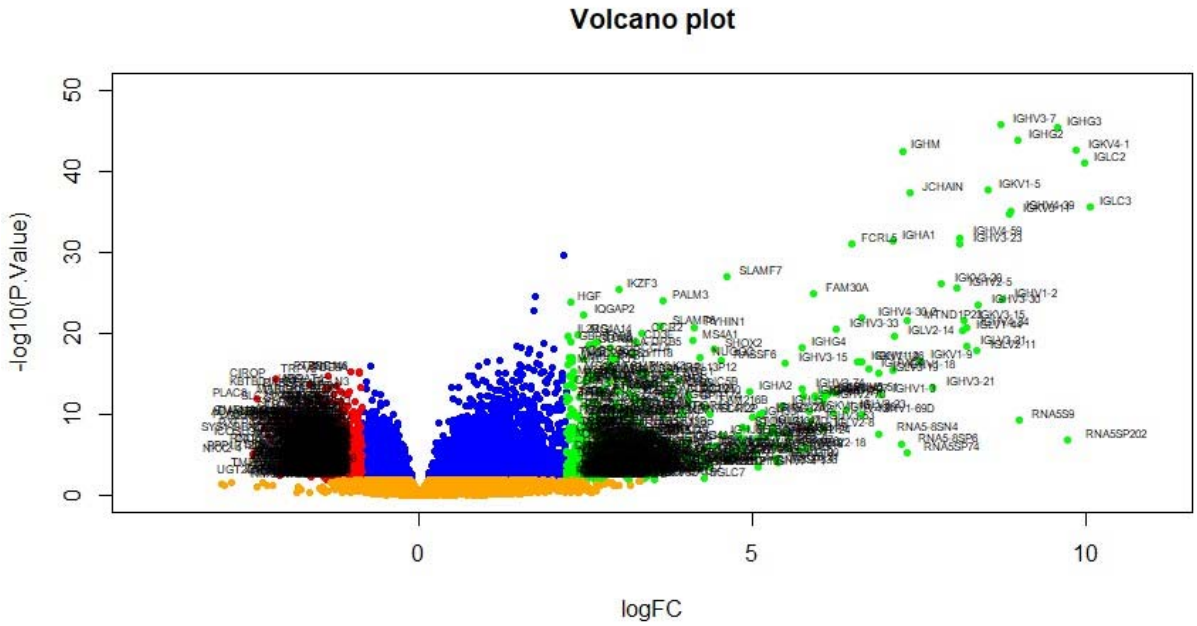

Fig. 1. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

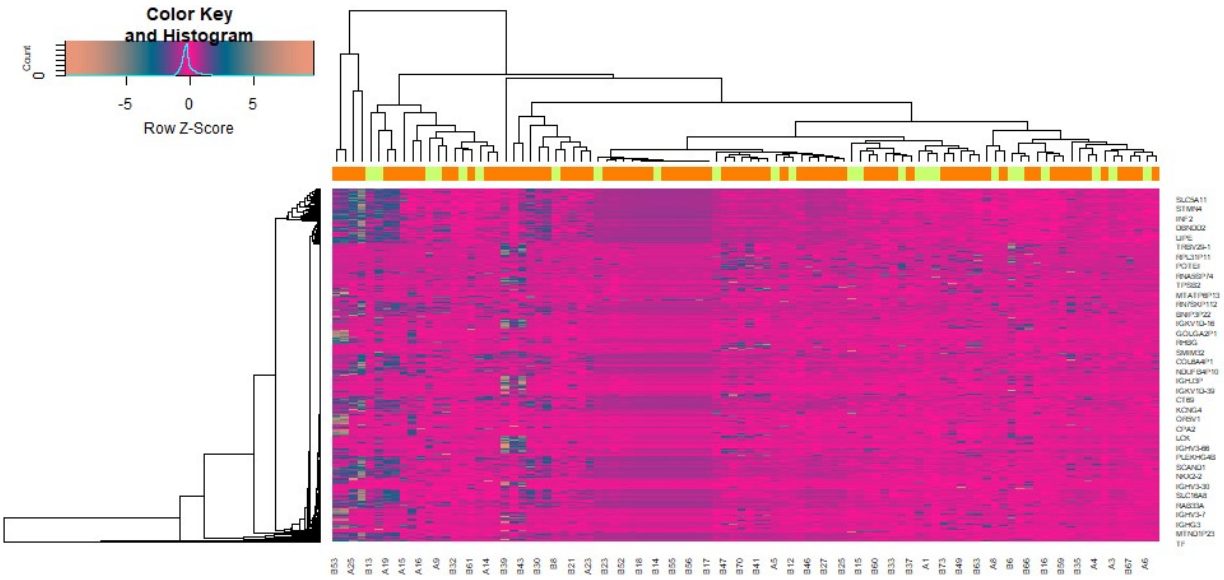

Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A25 = Normal control samples; B1 – B 73 = MS samples)

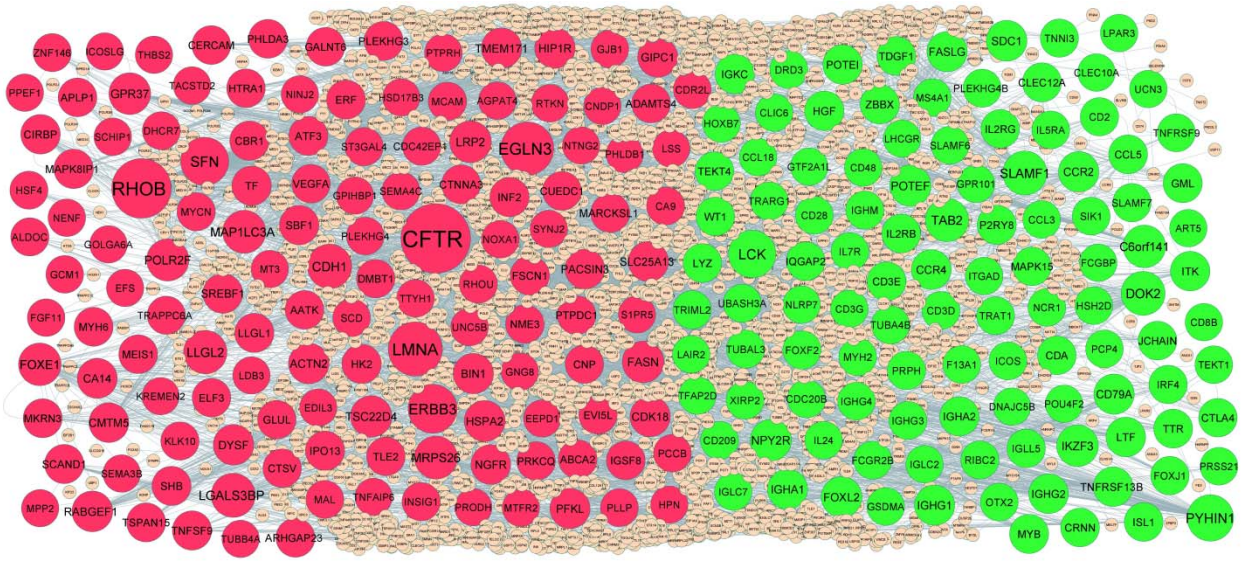

Fig. 3. PPI network of DEGs. Up regulated genes are marked in parrot green; down regulated genes are marked in red.

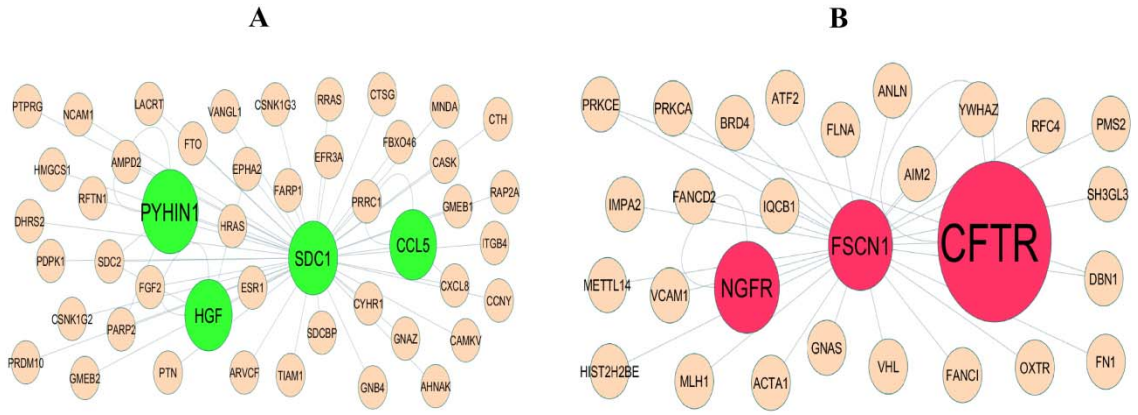

Fig. 4. Modules selected from the PPI network. (A) The most significant module was obtained from PPI network with 47 nodes and 54 edges for up regulated genes (B) The most significant module was obtained from PPI network with 28 nodes and 32 edges for down regulated genes. Up regulated genes are marked in parrot green; down regulated genes are marked in red

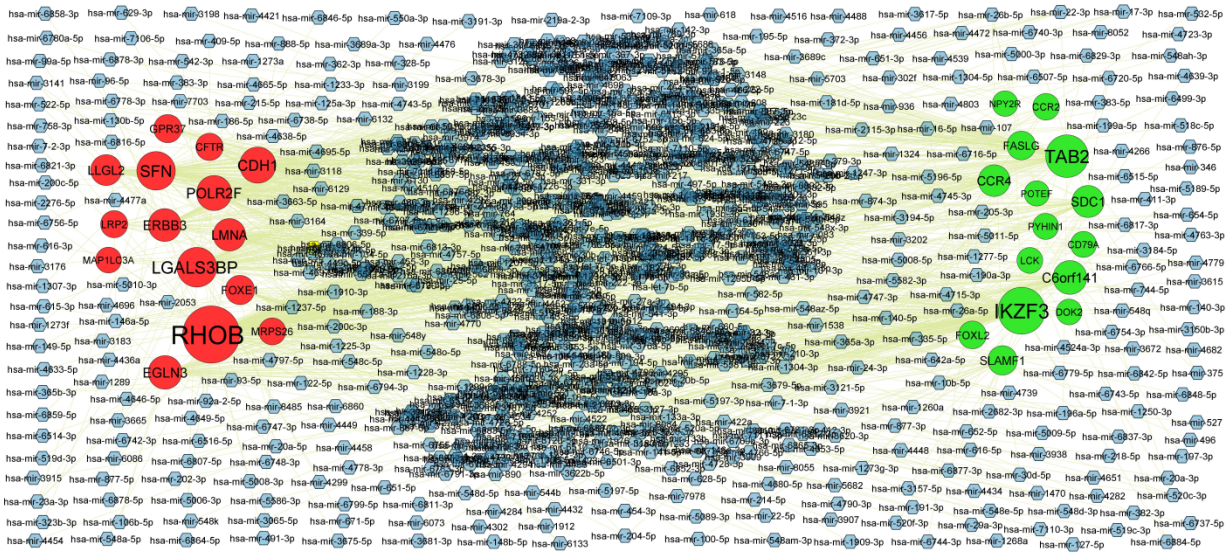

Fig. 5. Hub gene - miRNA regulatory network. The blue color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

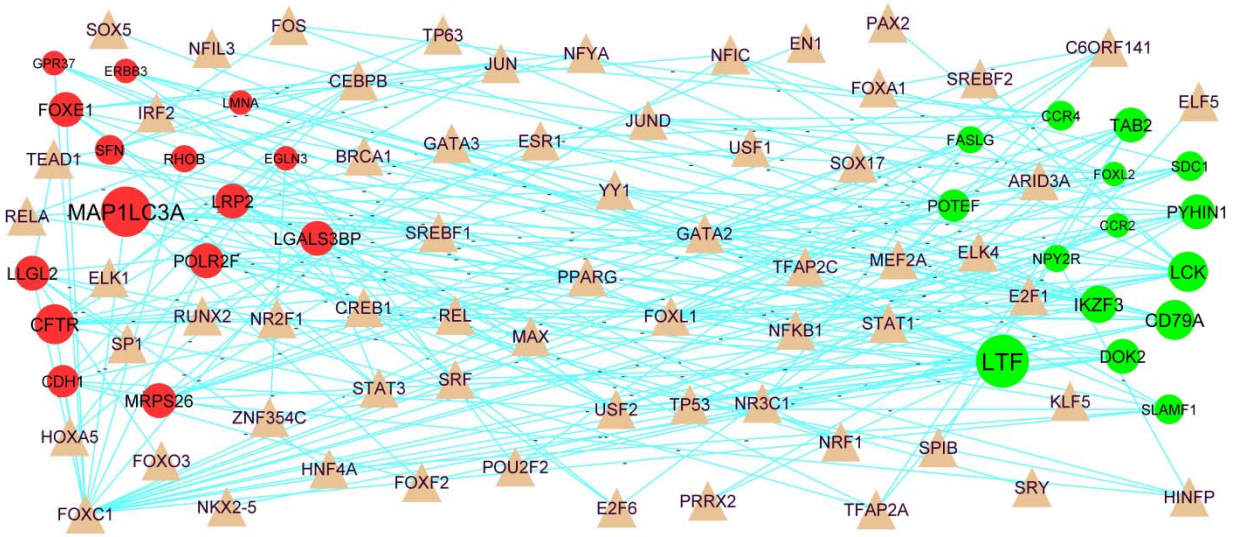

Fig. 6. Hub gene - TF regulatory network. The brown color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

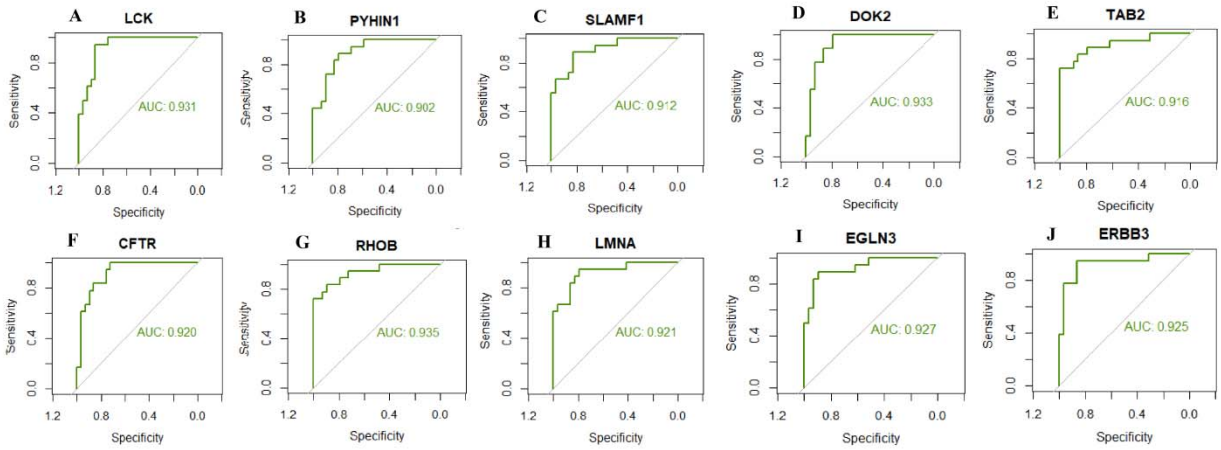

Fig. 7. ROC curve analyses of hub genes. A) LCK B) PYHIN1 C) SLAMF1 D) DOK2 E) TAB2 F) CFTR G) RHOB H) LMNA I) EGLN3 J) ERBB3