Identification of hub genes and key pathways in pediatric Crohn`s disease using next generation sequencing and bioinformatics analysis

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Abstract

Pediatric Crohn Disease (CD) also known as inflammatory bowel diseases, affects millions of people all over the world. The aim of this investigation is to identify the key genes in CD and uncover their potential functions. We downloaded the next generation sequencing (NGS) dataset GSE101794 from the Gene Expression Omnibus (GEO) database. The NGS dataset GSE101794 was used to screen differentially expressed genes (DEGs) between samples from patients with CD and healthy controls. Gene ontology (GO) and REACTOME pathway enrichment analyses were applied for the DEGs. Subsequently, a protein - protein interaction (PPI) network, modules, miRNA- hub gene regulatory network and TF - hub gene regulatory network were constructed to identify hub genes, miRNAs and TFs. Receiver operating characteristic curve (ROC) analysis was applied to validate the hub genes. A total of 957 DEGs were identified, including 478 up regulated genes and 479 down regulated genes. GO and REACTOME results suggested that several Go terms and pathways are involved in response to stimulus, extracellular region, signaling receptor binding, small molecule metabolic process, membrane, transporter activity, immune system and biological oxidations. The top centrality hub genes MDFI, MNDA, FBXO6, TFRC, STAT1, DPP4, MME, SLC39A4, APOA1 and TMEM25 were screened out as the critical genes among the DEGs from the PPI network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network. This investigation identified key genes and signal pathways, which might help us improve our understanding of the molecular mechanisms of CD and identify some novel therapeutic targets for CD.

Keywords: Pediatric Crohn`s Disease; bioinformatics; differentially expressed genes; pathway enrichment analysis; protein-protein interaction network

Introduction

Pediatric Crohn Disease (CD) is an group of inflammatory bowel diseases and characterized by transmural inflammation in gastrointestinal tract [1]. CD predominately affects before the age of 18, however 25% of cases are diagnosed [2]. The prevalence of CD has been growing steadily in both developed and developing nations [3]. The pathogenesis of CD remains incompletely understood, but genetics factors, epigenetic factors, microbial exposure, immune response and environment factors are believed to contribute [4]. Moreover, CD is commonly associated with other complications such as anemia [5], autoimmune liver disease [6], type 1 diabetes mellitus [7], coagulation and fibrinolysis [8] and colorectal cancer [9]. The etiology of CD has been investigated extensively, but the exact pathogenic factors or triggering agents for CD are still unknown, and the underlying molecular mechanisms for induction and advancement of CD remain largely unidentified. Therefore, the discovery of effective biomarkers for the treatment of CD is very essential.

Accumulating evidence had shows that genes [10] and signaling pathways [11] mainly contribute to the occurrence and advancement of CD. Genes include MDR1 [12], ACE2 [13], NUDT15 [14], HNF4A [15] and IL23R [16] are responsible for progression of CD. Signaling pathways include JAK/STAT signaling pathway [17], STING signaling pathway [18], TLRs and dectin-1 signaling pathways [19], NF□κB and MAPK signaling pathways [20] and P2X7R-Pannexin-1 signaling pathway [21] are involved in advancement of CD. However, the prevalence and factors responsible for CD etiology are still not fully known.

Next generation sequencing (NGS) is the latest technology, which can detect multiple genes at the same time and minimize system errors and has extremely high sensitivity [22]. At present situation, this technology has been widely used in the investigation of various diseases, which has opened up a milestone in the field of genomics research on CD [23]. In the process of this investigation on CD, based on this technology, we can find and analyze the gene expression of CD at the molecular level.

In this investigation, we downloaded NGS dataset GSE101794 [24] based on the Gene Expression Omnibus database (GEO, https://www.ncbi.nlm.nih.gov/geo/)

[25]. First, differentially expressed genes (DEGs) were analyzed from the samples by limma. These underwent gene ontology (GO) and REACTOME pathway enrichment analyses, followed by the construction of a protein-protein interaction (PPI) network, modules, miRNA-hub gene regulatory network and TF-hub gene regulatory network to identify hub genes. Receiver operating characteristic curve (ROC) analysis was conducted to validate the hub genes, which could be used as molecular biomarkers or diagnostic targets for CD therapy. Collectively, our investigation will help the advancement of a genetic diagnosis for CD and more effective measures of prevention and treatment.

Materials and Methods

Next generation sequencing data source

NGS data was downloaded from the GEO database. GSE101794 [24] includes 254 CD samples and 50 healthy control samples. This dataset was obtained from the NGS platform of GPL11154 Illumina HiSeq 2000 (Homo sapiens).

Identification of DEGs

As a fully functional package, the limma package [26] in R software includes the original data input of NGS, as well as a liner model for analyzing differentially expressed genes. We screened DEGs between CD samples and healthy control samples by utilizing limma package with a adjust $p < 0.05$, and a log (Fold Change) > 0.822 for up regulated genes and log (Fold Change) < -0.825 for down regulated genes. And the volcano plot and heat map were drawn by ggplot2 package and gplot package in R software.

GO and pathway enrichment analyses of DEGs

One online tool, g:Profiler (http://biit.cs.ut.ee/gprofiler/) [27], was applied to carried out the functional annotation for DEGs. GO (http://www.geneontology.org) [28] generally perform enrichment analysis of genomes. GO include biological processes (BP) ,cellular components (CC) and molecular functions (MF) in the GO enrichment analysis. REACTOME (https://reactome.org/) [29] is a comprehensive database of genomic, chemical, and systemic functional information. Therefore, g:Profiler was used to make analysis of GO and

REACTOME. P□<□0.05 value was set as the cutoff criterion for significant GO and pathway enrichment.

Construction of the PPI network and module analysis

Human Integrated Protein-Protein Interaction rEference (HiPPIE) interactome database [30] was used to construct a PPI network for the DEGs, which was visualized in Cytoscape (version 3.9.1) [31]. The Network Analyzer plug-in can be used to screen hub genes with the node degree [32] , betweenness [33], stress [34] and closeness [35]. PEWCC1 [36] Plug-in was used to filter key modules in the PPI network with a degree□cutoff ≥ 2, node□score□cutoff = 0.2, K − core ≥ 2, and max.depth = 100 as the cutoff criteria .

miRNA-hub gene regulatory network construction

The hub genes and miRNA network was generated by miRNet database (https://www.mirnet.ca/) [37]. miRNA-hub gene interaction database: TarBase, miRTarBase, miRecords, miRanda (S mansoni only), miR2Disease, HMDD, PhenomiR, SM2miR, PharmacomiR, EpimiR, starBase, TransmiR, ADmiRE, and TAM 2.0 databases. The analysis results of miRNet was then imported into Cytoscape software (version 3.9.1) [31] for further visualization.

TF-hub gene regulatory network construction

The hub genes and TF network was generated by NetworkAnalyst database (https://www.networkanalyst.ca/) [38]. TF-hub gene interaction database: JASPAR database. The analysis results of NetworkAnalyst was then imported into Cytoscape software (version 3.9.1) [31] for further visualization.

Receiver operating characteristic curve (ROC) analysis

ROC curve analysis was performed to evaluate the sensitivity (true positive rate) and specificity (true negative rate) of the hub genes for CD diagnosis and we investigated how large the area under the curve (AUC) was by using the statistical R software package pROC package [39].

Results

Identification of DEGs

NGS dataset was obtained from the NCBI GEO database. Using the limma R software tool, DEGs were extracted from the GSE101794 NGS dataset (|logFC | > 0.822 for up regulated genes, |logFC | < -0.825 for down regulated genes and adj. p value < 0.05). As the volcano plots illustrated, NGS data from GSE101794 identified 957 differentially expressed genes with 478 genes up regulated genes and 479 genes down regulated genes in CD samples compared with the expression in healthy control samples (Fig. 1) and are listed in Table 1. The heatmap exhibited the expression difference genes between CD samples and healthy control samples (Fig. 2).

GO and pathway enrichment analyses of DEGs

A total of 957 DEGs were uploaded to g:Profiler for GO and REACTOME pathway enrichment analyses. The terms of each GO category are provided in Table 2. Most DEGs were enriched in the BP: response to stimulus, response to chemical, small molecule metabolic process and regulation of biological quality; CC: extracellular region, intrinsic component of membrane, membrane and cytoplasm; and MF: signaling receptor binding, molecular transducer activity, transporter activity and catalytic activity. The results of REACTOME pathway enrichment are shown in Table 3. The REACTOME pathway enrichment analysis confirmed that the DEGs were mainly associated with immune system, neutrophil degranulation, biological oxidations and metabolism.

Construction of the PPI network and module analysis

957 DEGs were imported into the HiPPIE database to explore the interrelationships between the various genes. 957 DEGs were used to establish the PPI network using the Cytoscape software. The PPI network consisted of 4030 nodes and 6196 edges (Fig. 3). The Network Analyzer in Cytoscape was used to screen the top genes with high node degree, betweenness, stress and closeness indicating the hub genes from the PPI network, including MDFI, MNDA, FBXO6, TFRC, STAT1, DPP4, MME, SLC39A4, APOA1 and TMEM25 and are listed in Table 4. Based on the degree of importance, two key modules were then screened from the PPI network using the PEWCC1 plug-in, and GO and pathway enrichment analysis was performed. Module 1 contained a total of 15 nodes and 49 edges (Fig. 4A), and module 2 contained a total of 15 nodes and 17 edges (Fig.

4B). The results showed that Module 1 was mainly related to immune system, response to stimulus, cytokine signaling in immune system, intrinsic component of membrane and response to chemical. Module 2 was primarily involved in the regulation of biological quality.

miRNA-hub gene regulatory network construction

To explore the key genes and miRNA involved in CD, miRNA-hub gene regulatory network of the hub genes was constructed. miRNA-hub gene regulatory network with 2377 nodes (miRNA: 2058; hub gene: 319) and 11302 edges (Fig. 5) and are listed in Table 5, which showed that 162 miRNAs (ex; hsa-mir-629-5p) could regulate TFRC expression; 102 miRNAs (ex; hsa-mir-25-5p) could regulate CKAP4 expression; 65 miRNAs (ex; hsa-mir-3714) could regulate HSPA6 expression; 63 miRNAs (ex; hsa-mir-146a) could regulate STAT1 expression; 43 miRNAs (ex; hsa-mir-4651) could regulate LAMP3 expression; 56 miRNAs (ex; hsa-mir-6130) could regulate SLC9A3R1 expression; 54 miRNAs (ex; hsa-mir-518f-5p) could regulate MME expression; 41 miRNAs (ex; hsa-mir-522-5p) could regulate TMEM25 expression; 35 miRNAs (ex; hsa-mir-641) could regulate CDKN2B expression; 27 miRNAs (ex; hsa-mir-148a-3p) could regulate TUBB2B expression.

TF-hub gene regulatory network construction

To explore the key genes and TF involved in CD, TF-hub gene regulatory network of the hub genes was constructed. TF-hub gene regulatory network with 405 nodes (TF: 82; hub gene: 323) and 2514 edges (Fig. 6) and are listed in Table 5, which showed that 24 TFs (ex; NFYA) could regulate FPR2 expression; 16 TFs (ex; FOXA1) could regulate FGR expression; 15 TFs (ex; ESR1) could regulate TFRC expression; 12 TFs (ex; FOS) could regulate PLAUR expression; 8 TFs (ex; ARID3A) could regulate STX11 expression; 12 TFs (ex; PRDM1) could regulate APOA1 expression; 12 TFs (ex; GATA2) could regulate DPEP1 expression; 11 TFs (ex; HOXA5) could regulate SLC39A5 expression; 9 TFs (ex; BRCA1) could regulate MME expression; 9 TFs (ex; JUND) could regulate CDKN2B expression.

Receiver operating characteristic curve (ROC) analysis

The ROC curves (Fig. 7) of these three genes showed that their AUC are as follows: MDFI (AUC = 0.933), MNDA (AUC = 0.915), FBXO6 (AUC = 0.922), TFRC (AUC = 0.922), STAT1 (AUC = 0.930), DPP4 (AUC = 0.943), MME (AUC = 0.900), SLC39A4 (AUC = 0.902), APOA1 (AUC = 0.939) and TMEM25 (AUC = 0.920). Since ROC curves had good specificity and sensitivity, MDFI, MNDA, FBXO6, TFRC, STAT1, DPP4, MME, SLC39A4, APOA1 and TMEM25 had excellent diagnostic efficiency for distinguishing CD and healthy control.

Discussion

A NGS study is an ideal way to comprehensively investigate CD. In this investigation, NGS data was analyzed for identification potential biomarkers and explore molecular mechanisms of CD. Although CD is an inflammatory disease, it has recently been established that both inflammatory responses occur early during CD [40]. In the present investigation, NGS dataset (GSE101794) was downloaded from the GEO database. A total of 957 DEGs were screened: 478 up regulated genes and 479 down regulated genes. Lee et al [41], Gijsbers et al [42], Hashash et al [43], Wnorowski et al [44] and Kyodo et al [45] found that FCGR3A, CXCL8, MUC1, HCAR3 and DUOX2 might play an important role in the pathophysiology of CD. Nourse et al [46] and Nakashima et al [47] found that FCGR3A and MUC1 was altered expressed in coagulation and fibrinolysis. These coagulation and fibrinolysis responsible genes might positively linked with CD. Ying et al. [48], Huang et al. [49], Liu et al. [50], Yang et al [51], Bao et al [52], Zhang et al [53], Zhang et al [54], Ye et al [55] and Xi et al [56] showed that FCGR3A, AQP9, MUC1, HCAR3, CXCL2, DUOX2, CRIP1, TPPP (tubulin polymerization promoting protein) and FZD7 play an important role in the occurrence and development of colorectal cancer. These colorectal cancer responsible genes might be associated with CD. The altered expression of FCGR3A [57], FCGR3B [58], MUC1 [59] and CXCL2 [60] might be associated with autoimmune disease progression. These autoimmune disease responsible genes might found to be substantially related to CD. MacFie et al. [61], Walana et al. [62], Asano et al. [63] and Kvorjak et al. [64] studied the clinical and prognostic value of DUOXA2, CXCL8, FCGR3A, FCGR3B, MUC1 and DUOX2 in patients with ulcerative colitis. The altered expression of CXCL8 [65] and FCN1 [66] contributes to the type 1 diabetes mellitus progression. These type 1 diabetes mellitus responsible genes might play an important role in CD. Kerr et al. [67] and Ampuero et al [68] demonstrated that altered expression of C6 and SLC28A2 were found to be substantially related to anemia. These anemia responsible genes might be key genes in CD.

GO and REACTOME pathway enrichment analysis found that genes in patients with CD were enriched. Many pathways are associated with the pathogenesis of CD. Signaling pathway include immune system [69], neutrophil degranulation [70], cytokine signaling in immune system [71], extracellular matrix organization [72], post-translational protein phosphorylation [73], biological oxidations [74], metabolism [75] and metabolism of lipids [76] were responsible for progression of CD. CXCL5 [77], CXCL3 [78], PROK2 [79], CXCR1 [80], PYCR1 [81], OSM (oncostatin M) [82], IL15RA [83], LRG1 [84], LCN2 [85], BATF2 [86], CXCL1 [87], S100A9 [88], IFITM1 [89], MYOF (myoferlin) [90], XBP1 [91], MMP3 [92], TAP1 [93], FPR2 [94], CXCL6 [95], C2CD4A [96], IFITM3 [97], IL1B [98], SLC6A14 [99], FPR1 [100], NOS2 [101], CHI3L1 [102], TGM2 [103], MUC4 [104], TREM1 [105], WNT5A [106], HGF (hepatocyte growth factor) [107], CXCL9 [108], GBP1 [109], S100A11 [110], ADM (adrenomedullin) [111], CXCL11 [112], CXCL10 [113], LILRB2 [114], GDF15 [115], IL1RN [116] STAT1 [117], SLAMF7 [105], CYP27B1 [118], NETO2 [119], TFPI2 [120], ZC3H12A [121], MMP1 [122], CSF3 [123], SOCS3 [124], TLR8 [125], HTRA3 [126], CEBPB (CCAAT enhancer binding protein beta) [127], CD55 [128], CXCR2 [129], CCL28 [130], CBR3 [131], CCL3 [132], FCGR2A [48], ACSL1 [133], CCL2 [134], SOD2 [135], CD14 [136], IGFBP2 [137], CD274 [138], DERL3 [139], SERPINE1 [140], IDO1 [141], PDK1 [142], FOXP3 [143], CD163 [144], APCDD1 [145], CCL7 [146], PTGS2 [147], TLR2 [148], PIGR (polymeric immunoglobulin receptor) [149], IGFBP5 [150], CCR2 [151], VWF (von Willebrand factor) [152], SLC7A11 [153], NOD2 [154], DMBT1 [155], IL20RA [156], TYMP (thymidine phosphorylase) [144], S100P [157], PDPN (podoplanin) [158], ADAMTS1 [159], ATF3 [160], TIMP1 [161], UCN2 [162], SELE (selectin E) [163], ICAM1 [164], FOSL1 [165], AREG (amphiregulin) [166], PIM2 [167], SLC7A5 [168], CH25H [169], COL5A2 [170], SNAI1 [171], MXRA5 [172], EGR1 [173], TNFRSF17 [174], MDFI (MyoD family inhibitor) [175], SRGN (serglycin) [176], CEACAM6 [177], CCL11 [178], IFNG (interferon gamma) [179], TREM2 [180], INHBA (inhibin subunit beta A) [181], APOE (apolipoprotein E) [182], FGR (FGR proto-oncogene, Src family tyrosine kinase)

[183], CTSK (cathepsin K) [184], CCR1 [185], IL6 [186], CTHRC1 [187], PDCD1LG2 [188], SFRP1 [189], CCL4 [190], SNX10 [191], SPP1 [192], CLDN1 [193], CA2 [194], IL11 [195], PHLDA2 [196], NNMT (nicotinamide N-methyltransferase) [197], FGFBP1 [198], RAB31 [199], COL1A1 [200], RNF186 [201], MMP12 [202], MMP2 [203], IL1A [204], ITGA5 [205], CCL1 [206], GPR4 [207], WNT2 [208], GPX2 [209], CD24 [210], PDE4B [211], AQP5 [212], REG1A [213], UBD (ubiquitin D) [214], SPHK1 [215], AOX1 [216], CYP7B1 [217], STC2 [218], TFF2 [219], POSTN (periostin) [220], GZMB (granzyme B) [221], MUC5AC [222], SERPINA3 [223], TWIST1 [224], CCL8 [225], CSF2 [226], PLAU (plasminogen activator, urokinase) [227], CD177 [228], CA9 [229], GFPT2 [230], TDO2 [231], TFF1 [232], STC1 [233], ITLN1 [234], CTLA4 [235], MMP13 [236], LBP (lipopolysaccharide binding protein) [237], CST1 [238], GAS1 [239], KLK6 [240], VSNL1 [241], RETN (resistin) [242], ODAM (odontogenic, ameloblast associated) [243], MPO (myeloperoxidase) [244], HP (haptoglobin) [245], SCGB2A1 [246], CYP24A1 [247], TXNDC5 [248], PDZK1IP1 [249], CEACAM5 [250], MMP10 [251], FOLH1 [252], LAP3 [253], PSAT1 [254], EMILIN2 [255], SRPX2 [256], EGFL6 [257], VCAN (versican) [258], TCN1 [259], CLCA4 [260], ZG16B [261], STEAP4 [262], ACSL4 [263], ADAMTS4 [264], RARRES1 [265], APOC1 [266], SLC5A8 [267], MUC5B [268], CA1 [194], SPINK4 [269], CEMIP (cell migration inducing hyaluronidase 1) [270], MMP7 [271], ANGPTL2 [114], FJX1 [272], MUCL1 [273], MUC6 [274], THBS2 [275], KRT7 [276], CEACAM3 [277], ALDOC (aldolase, fructose-bisphosphate C) [278], CUBN (cubilin) [279], LRAT (lecithin retinol acyltransferase) [280], CBS (cystathionine beta-synthase) [281], CYP2S1 [282], ABCG2 [283], CYP3A4 [284], APOA1 [285], FMO5 [286], GUCA2B [287], FBP1 [288], SULT2B1 [289], AKR1B10 [290], GSTA1 [291], CYP2J2 [292], PDK2 [293], DPEP1 [294], APOB (apolipoprotein B) [295], CES2 [296], SLC23A1 [297], UGT1A1 [298], UGT1A6 [299], GUCA2A [300], KHK (ketohexokinase) [301], CYP2D6 [302], CYP3A5 [303], SLC16A9 [304], CYP2C8 [305], NPC1L1 [306], ACY1 [307], DDC (dopa decarboxylase) [308], B4GALNT2 [309], UGT2B7 [310], CRABP1 [159], HMGCS2 [311], PCK1 [312], CYP2C19 [313], FABP2 [314], DEGS2 [315], EDN2 [316], CYP2C9 [313], NR0B2 [317], ALDOB (aldolase, fructose-bisphosphate B) [318], CNR1 [319], UGT1A7 [320], ABCC2 [321], TM4SF4 [322], PFN2 [323], MAOB (monoamine oxidase B) [324], ZDHHC11 [325], FLVCR1 [326], ANXA13 [327], HTR1D

[328], ABCB1 [329], PLA2R1 [330], ACE2 [331], F10 [332], SLC6A4 [333], FABP6 [334], SLC22A5 [335], DPP4 [336], GNG4 [337], TMIGD1 [338], ACE (angiotensin I converting enzyme) [339], PHLPP2 [340], USP2 [341], GRIA4 [342], OTOP2 [343], SLC2A5 [344], SLC1A1 [304], HSD17B2 [345], AOC1 [346], ABCG5 [347], ENPEP (glutamyl aminopeptidase) [348], SCIN (scinderin) [349], GFRA1 [350], PLEKHG6 [351], TM4SF5 [352], CHRNA7 [353], CLDN8 [354], SI (sucrase-isomaltase) [355], TM6SF2 [356], TF (transferrin) [357], RNF128 [358], MEP1A [359], LCT (lactase) [360], SLC34A2 [361], AQP3 [362], ALPI (alkaline phosphatase, intestinal) [363], SHISA3 [364], SSTR1 [365], B3GALT5 [366], SCTR (secretin receptor) [367], FGFR3 [368], TMEM236 [369], NEU4 [370], KISS1 [371], BEST4 [372], MUC17 [373], SLC30A10 [374], ZG16 [375], MS4A1 [376], APOM (apolipoprotein M) [377] and GSTA2 [378] were previously reported to be critical for the development of colorectal cancer. These colorectal cancer responsible genes might be candidate genes for CD. Recently, increasing evidence demonstrated that CXCL5 [379], S100A8 [380], LCN2 [381], CXCL1 [382], S100A9 [383], CXCL9 [384], CXCL11 [385], CXCL10 [386], NCF2 [387], SLC11A1 [388], GDF15 [389], IL1RN [390], STAT1 [391], CYP27B1 [392], SOCS3 [393], TLR8 [394], CD55 [395], ADGRG3 [396], CCL3 [397], FCGR2A [398], CCL2 [399], CD14 [400], IGFBP2 [401], PCSK9 [402], IDO1 [403], FOXP3 [404], CD163 [405], CCL7 [406], TLR2 [407], CCR2 [408], IL20RA [409], S100P [410], ADAMTS1 [411], TIMP1 [412], ICAM1 [413], IFNG (interferon gamma) [414], TREM2 [415], APOE (apolipoprotein E) [416], CCR1 [417], IL6 [418], CTHRC1 [419], PDCD1LG2 [420], CCL4 [421], IL11 [422], COL1A1 [423], MMP2 [424], IL1A [425], CD24 [426], POSTN (periostin) [427], GZMB (granzyme B) [428], BCL2A1 [429], CSF2 [430], TDO2 [431], CTLA4 [432], PADI4 [433], MPO (myeloperoxidase) [434], HP (haptoglobin) [435], MUC5B [436], MMP7 [437], PON3 [438], ABHD6 [439], AICDA (activation induced cytidine deaminase) [440], UGT1A6 [441], CYP2D6 [442], CYP3A5 [443], DGAT1 [444], FCRL4 [445], SLC22A4 [446], DPP4 [447], ACE (angiotensin I converting enzyme) [448], SLC5A11 [449], VIPR1 [450], FCRL3 [451], CD160 [452] and IL22RA2 [453] were altered expression in autoimmune diseases. These autoimmune diseases responsible genes might be critical for the development of CD. Recently, study found that CXCL5 [454], S100A12 [455], OSM (oncostatin M) [456], LRG1 [457], LCN2 [458], CXCL1 [459], S100A9 [460], IFITM1 [461], XBP1 [462], MMP3 [457], IFITM3 [463], IL1B [464],

GBP5 [465], HGF (hepatocyte growth factor) [466], CXCL9 [467], SLC11A1 [468], IL1RN [469], STAT1 [470], CYP27B1 [471], MMP1 [472], SOCS3 [473], TLR8 [474], CD55 [475], CCL28 [476], FCGR2A [477], CCL2 [478], CFB (complement factor B) [479], CD14 [480], GPR84 [481], PCSK9 [482], FOXP3 [483], LPL (lipoprotein lipase) [484], IL1R2 [485], TLR2 [486], MEFV (MEFV innate immuity regulator, pyrin) [487], VWF (von Willebrand factor) [488], NOD2 [489], DMBT1 [490], HSPA6 [491], TIMP1 [492], ICAM1 [493], EGR1 [494], CCL11 [495], IFNG (interferon gamma) [496], APOE (apolipoprotein E) [497] FGR (FGR proto-oncogene, Src family tyrosine kinase) [498], IL6 [499], SPP1 [192], IL11 [500], RNF186 [501], MMP2 [502], CD24 [503], SPHK1 [504], GZMB (granzyme B) [505], MUC5AC [506], SERPINA3 [507], TWIST1 [508], PLAU (plasminogen activator, urokinase) [509], CA2 [510], CA9 [510], CTLA4 [511], PADI4 [512], MMP13 [513], MPO (myeloperoxidase) [244], LEFTY1 [514], CA1 [515], MMP7 [513], ABCG2 [516], CYP2J2 [517], AICDA (activation induced cytidine deaminase) [518], CYP2D6 [519], CYP3A5 [520], CNR1 [521], TRPV3 [522], ABCB1 [523], SLC22A4 [524], SLC22A5[524], ACE (angiotensin I converting enzyme) [525], PHLPP2 [526], CCR9 [527], AOC1 [528], SI (sucrase-isomaltase) [529], BTNL2 [530] and SLC26A3 [531] are associated with the risk of ulcerative colitis. Many studies have indicated that S100A12 [532], S100A8 [533], OSM (oncostatin M) [534], LCN2 [535], TNFAIP6 [536], S100A9 [533], XBP1 [537], CXCL6 [42], IL1B [464], GBP5 [465], CHI3L1 [538], TREM1 [539], HGF (hepatocyte growth factor) [540], CXCL9 [541], GBP1 [542], ADM (adrenomedullin) [543], CXCL10 [544], SLC11A1 [468], IL1RN [545], STAT1 [546], CLEC5A [547], CYP27B1 [548], MMP1 [549], SOCS3 [550], TLR8 [474], CD55 [551], CXCR2 [552], FCGR2A [41], TFRC (transferrin receptor) [553], CFB (complement factor B) [554], CD14 [555], IGFBP2 [556], CLEC7A [557], IDO1 [558], FOXP3 [559], CD163 [560], ADORA2B [561], TLR2 [562], MEFV (MEFV innate immuity regulator, pyrin) [487], IGFBP5 [563], CCR2 [564], CHRNA5 [565], VWF (von Willebrand factor) [566], NOD2 [567], DMBT1 [568], IL20RA [569], ATF3 [570], TIMP1 [571], FAP (fibroblast activation protein alpha) [572], ICAM1 [493], IL13RA2 [573], EGR1 [494], TNFRSF17 [574], CEACAM6 [575], CCL11 [576], IFNG (interferon gamma) [577], APOE (apolipoprotein E) [578], IL6 [499], CCL4 [579], SPP1 [580], NNMT (nicotinamide N-methyltransferase) [44], COL1A1 [581], MMP2 [582], GPX2 [583], CD24 [584], REG1A [585], UBD (ubiquitin D) [586], AOX1 [587], POSTN (periostin) [588], GZMB (granzyme B) [589], SELP (selectin P) [590], MUC5AC [591], CCL8 [592], PLAU (plasminogen activator, urokinase) [593], CD177 [594], TFF1 [595], CTLA4 [596], MMP13 [597], LBP (lipopolysaccharide binding protein) [598], MPO (myeloperoxidase) [599], LEFTY1 [514], HP (haptoglobin) [600], CEACAM5 [601], FOLH1 [602], TNFAIP2 [603], MMP7 [597], CLEC12A [604], CBS (cystathionine beta-synthase) [605], PEPD (peptidase D) [606], ABCG2 [607], CYP3A4 [608], CYP2J2 [609], SLC23A1 [610], UGT1A1 [611], GUCA2A [612], CYP2D6 [613], APOC3 [614], CYP2C18 [615], DGAT1 [616], SULT1A2 [617], CYP2C19 [618], CNR1 [521], ABCB1 [619], ACE2 [620], SLC6A4 [621], SLC22A4 [622], MGAT3 [623], SLC22A5 [624], DPP4 [625], TMIGD1 [626], ACE (angiotensin I converting enzyme) [525], SLC15A1 [627], CCR9 [628], GP2 [629], CLDN8 [630], SI (sucrase-isomaltase) [631], TF (transferrin) [632], MEP1A [633], LCT (lactase) [634], BTNL2 [635], VIPR1 [636], F11 [637], ALPI (alkaline phosphatase, intestinal) [638], FCRL3 [639], BCHE (butyrylcholinesterase) [640] and SLC26A3 [641] plays a substantial role in CD. S100A8 [642], OSM (oncostatin M) [643], LCN2 [644], S100A9 [642], HGF (hepatocyte growth factor) [645], GDF15 [646], STAT1 [647], MMP1 [648], TLR8 [649], CD55 [650], SOD2 [651], DYSF (dysferlin) [652], FOXP3 [653], TLR2 [654], VWF (von Willebrand factor) [655], COL4A1 [656], IFNG (interferon gamma) [657], APOE (apolipoprotein E) [658], IL6 [659], CCL4 [421], IL11 [660], MMP2 [661], CSF2 [662], PLAU (plasminogen activator, urokinase) [663], CTLA4 [664], MPO (myeloperoxidase) [665], LEFTY1 [666], HP (haptoglobin) [667], CUBN (cubilin) [668], ABCG2 [669], CYP3A4 [670], APOA1 [671], UGT1A1 [672], CYP2D6 [673], CYP2C8 [674], PCK1 [675], ABCC2 [676], FLVCR1 [677] and ACE (angiotensin I converting enzyme) [678] were identified to be closely associated with anemia. These anemia responsible genes might be candidate biomarkers or therapeutic targets for CD. CXCR1 [679], CXCL1 [680], C2 [681], MMP3 [682], TAP1 [683], NOS2 [684], CXCL10 [685], SLC11A1 [686], GDF15 [687], IL1RN [688], PYGL (glycogen phosphorylase L) [689], CYP27B1 [690], SOCS3 [691], CD55 [692], CXCR2 [693], CCL3 [694], CCL2 [695], SOD2 [696], CD14 [697], IGFBP2 [698], PCSK9 [699], CD274 [700], IDO1 [701], FOXP3 [702], CD163 [703], LPL (lipoprotein lipase) [704], TLR2 [705], CCR2 [706], VWF (von Willebrand factor) [707], NOD2 [708], ATF3 [709], TIMP1 [682], ICAM1 [710], FFAR2 [711], IFNG (interferon gamma) [712], APOE (apolipoprotein E) [713], IL6 [714], CCL4 [715], CA2

[716], MMP12 [717], MMP2 [718], CCL1 [719], CD24 [720], PLAU (plasminogen activator, urokinase) [721], CTLA4 [722], MASP1 [723], MPO (myeloperoxidase) [724], HP (haptoglobin) [725], MMP10 [726], CD300E [727], CUBN (cubilin) [728], SLC19A3 [729], APOB (apolipoprotein B) [730], APOC3 [731], HMGCS2 [732], OTC (ornithine transcarbamylase) [733], ACE2 [734], SLC22A4 [735], SLC22A5 [735], DPP4 [736], ACE (angiotensin I converting enzyme) [737], SLC6A19 [738], BTNL2 [739], FCRL3 [451], BCHE (butyrylcholinesterase) [740] and APOM (apolipoprotein M) [741] might be involved in type 1 diabetes mellitus. These type 1 diabetes mellitus responsible genes might be important participant in CD. IL1B [742], C4BPB [743], ADM (adrenomedullin) [744], GDF15 [745], IL1RN [746], SOD2 [747], TLR2 [748], VWF (von Willebrand factor) [749], APOE (apolipoprotein E) [750], IL6 [751], CCL4 [752], AQP5 [753], SELP (selectin P) [754], PLAU (plasminogen activator, urokinase) [755], MASP1 [756], MPO (myeloperoxidase) [757], MMP10 [758], EMILIN2 [759], ACE2 [760], F10 [761], ACE (angiotensin I converting enzyme) [762], F11 [763] and APOM (apolipoprotein M) [764] participates in the occurrence and development of coagulation and fibrinolysis. These coagulation and fibrinolysis responsible genes might be relevant to the pathological basis of CD susceptibility. Collectively, results of enriched GO and REACTOME pathway analysis were positively correlated with experimental findings. However, further studies are needed to explore and confirm the potentially significant GO terms and pathways for CD and to achieve a comprehensive understanding of this process.

Construction of PPI network a nd modules of DEGs might be helpful for understanding the relationship of developmental CD. TMEM25 is confirmed to be altered expressed in colorectal cancer [765]. This colorectal cancer gene might be linked with progression of CD. To the date, there are still no reports on the correlation between the hub genes of MNDA (myeloid cell nuclear differentiation antigen), FBXO6, CLEC4D, NAMPT (nicotinamide phosphoribosyltransferase), CLEC4E, MME (membrane metalloendopeptidase), SLC39A4, SLC9A3R1 and GDA (guanine deaminase) with CD and its associated complications. These hub genes might serve as potential biomarkers for CD.

We built a miRNA-hub gene regulatory network and TF-hub gene regulatory network of hub genes in CD based on the Cytoscape software. Finally, we got hub genes, miRNAs and TFs of CD. CDKN2B [766], hsa-mir-629-5p [767], hsa-mir-

146a [768], ESR1 [769], PRDM1 [770] and GATA2 [771] have been discovered to be involved in the CD. CDKN2B [772], hsa-mir-146a [768] and ESR1 [773] have been thought of as a specific and exclusive biomarkers for ulcerative colitis. CDKN2B [774], hsa-mir-25-5p [775], hsa-mir-146a [768], hsa-mir-148a-3p [776], NFYA (Nuclear Transcription Factor Y Subunit Alpha) [777], FOXA1 [778], ESR1 [779], ARID3A [780], PRDM1 [781], GATA2 [782], HOXA5 [783] and BRCA1 [784] were significantly associated in colorectal cancer. Theses colorectal cancer biomarkers might plays important regulatory roles in CD. hsa-mir-146a [785], GATA2 [786] and BRCA1 [787] have been identified as a key biomarkers in anemia. These anemia biomarkers might closely related to the occurrence of CD. Recently, increasing evidence demonstrated that hsa-mir-146a [788] and hsa-mir-148a-3p [789] were altered expressed in type 1 diabetes mellitus. These type 1 diabetes mellitus responsible biomarkers might constitute a potential therapeutic target of CD. hsa-mir-4651 [790] levels are correlated with disease severity in patients with coagulation and fibrinolysis. This coagulation and fibrinolysis responsible biomarker might associated with CD. PRDM1 [791] and GATA2 [792] are associated with progression to autoimmune disease. These autoimmune disease related biomarkers might be associated with the development and progression of CD. CKAP4, LAMP3, PLAUR (plasminogen activator, urokinase receptor), STX11, TUBB2B, SLC39A5, hsa-mir-3714, hsa-mir-518f-5p, hsa-mir-522-5p, hsa-mir-641, hsa-mir-3179, FOS (Fos Proto-Oncogene, AP-1 Transcription Factor Subunit) and JUND (JunD Proto-Oncogene, AP-1 Transcription Factor Subunit) were defined as novel biomarkers that might provide new ideas for further studies on CD.

In conclusion, we identified several key genes that are potentially associated with the development of CD using bioinformatics analyses of DEGs between patients with CD and healthy controls. These genes and their pathways will further our understanding of CD etiology, and help improve diagnosis, prevention, and treatment. Our findings suggest that the MDFI, MNDA, FBXO6, TFRC, STAT1, DPP4, MME, SLC39A4, APOA1 and TMEM25 can be considered candidate biomarkers or therapeutic targets for CD.

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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. [(GSE101794) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE101794]

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)

GeneSymbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
FCGR3A	2.874443	6.15E-35	4.19E-31	14.05761	Up	Fc fragment of IgG receptor IIIa
DUOXA2	5.621747	6.37E-35	4.19E-31	14.05353	Up	dual oxidase maturation factor 2
AQP9	5.024869	1.79E-33	5.88E-30	13.6632	Up	aquaporin 9
FCGR3B	4.1596	7.60E-31	2.00E-27	12.94766	Up	Fc fragment of IgG receptor IIIb
CXCL8	4.589577	1.12E-30	2.45E-27	12.9015	Up	C-X-C motif chemokine ligand 8
MUC1	3.108919	7.86E-30	1.48E-26	12.66866	Up	mucin 1, cell surface associated
HCAR3	5.204407	3.98E-29	6.54E-26	12.47396	Up	hydroxycarboxylic acid receptor 3
FCN1	2.818167	1.00E-28	1.32E-25	12.36261	Up	ficolin 1
CXCL2	2.576388	2.85E-28	3.40E-25	12.23633	Up	C-X-C motif chemokine ligand 2
DUOX2	4.211098	3.68E-28	4.03E-25	12.20528	Up	dual oxidase 2
CXCL5	4.22827	8.76E-27	7.30E-24	11.81884	Up	C-X-C motif chemokine ligand 5
S100A12	5.609086	8.88E-27	7.30E-24	11.81726	Up	S100 calcium binding protein A12
CXCL3	2.966092	1.55E-26	1.20E-23	11.74905	Up	C-X-C motif chemokine ligand 3
PROK2	4.50603	3.11E-26	2.27E-23	11.66323	Up	prokineticin 2
S100A8	3.9467	1.99E-25	1.14E-22	11.434	Up	S100 calcium binding protein A8
CXCR1	4.431181	1.99E-25	1.14E-22	11.43359	Up	C-X-C motif chemokine receptor 1
PYCR1	1.25011	2.00E-25	1.14E-22	11.43334	Up	pyrroline-5-carboxylate reductase 1
TXNDC5	1.318771	4.08E-25	2.23E-22	11.34471	Up	thioredoxin domain containing 5
BACE2	1.370183	6.06E-25	3.19E-22	11.2953	Up	beta-secretase 2
OSM	3.845022	8.62E-25	4.36E-22	11.25138	Up	oncostatin M
FCGR1A	2.770666	1.87E-24	9.13E-22	11.15414	Up	Fc fragment of IgG receptor Ia
IL15RA	0.833676	3.43E-24	1.61E-21	11.07846	Up	interleukin 15 receptor subunit alpha
LRG1	1.706527	6.23E-24	2.83E-21	11.00325	Up	leucine rich alpha-2-glycoprotein 1
TNFSF13	1.093218	8.94E-24	3.92E-21	10.95768	Up	TNF superfamily member 13
LCN2	3.180833	1.94E-23	8.22E-21	10.85993	Up	lipocalin 2
TNFAIP6	3.722352	2.98E-23	1.22E-20	10.80547	Up	TNF alpha induced protein 6
BATF2	1.298582	3.93E-23	1.57E-20	10.77012	Up	basic leucine zipper ATF-like transcription factor 2
CXCL1	2.452749	5.96E-23	2.31E-20	10.71704	Up	C-X-C motif chemokine ligand 1
S100A9	3.383101	7.61E-23	2.86E-20	10.68604	Up	S100 calcium binding protein A9
IFITM1	0.959416	9.24E-23	3.38E-20	10.66112	Up	interferon induced transmembrane protein 1
MYOF	1.096054	1.04E-22	3.69E-20	10.64614	Up	myoferlin

C2	1.086022	1.42E-22	4.91E-20	10.60644	Up	complement C2
XBP1	1.051606	2.10E-22	7.07E-20	10.5564	Up	X-box binding protein 1
MMP3	4.801131	3.94E-22	1.26E-19	10.47536	Up	matrix metallopeptidase 3
TAP1	0.950819	4.88E-22	1.53E-19	10.44764	Up	transporter 1, ATP binding cassette subfamily B member
FKBP11	1.224185	6.92E-22	2.12E-19	10.40272	Up	FKBP prolyl isomerase 11
FPR2	3.39368	8.87E-22	2.65E-19	10.37062	Up	formyl peptide receptor 2
CXCL6	2.432049	9.80E-22	2.86E-19	10.35766	Up	C-X-C motif chemokine ligand 6
C2CD4A	1.960308	1.09E-21	3.12E-19	10.34355	Up	C2 calcium dependent domain containing 4A
C1QB	0.991551	1.33E-21	3.73E-19	10.31773	Up	complement C1q B chain
IFITM3	1.216148	3.17E-21	8.34E-19	10.20525	Up	interferon induced transmembrane protein 3
HK2	1.619239	3.80E-21	9.80E-19	10.18156	Up	hexokinase 2
FCGR1B	2.738991	4.83E-21	1.20E-18	10.15018	Up	Fc fragment of IgG receptor Ib
APOBEC3A	3.160507	5.29E-21	1.29E-18	10.13843	Up	apolipoprotein B mRNA editing enzyme catalytic subunit 3A
IL1B	3.260058	7.02E-21	1.67E-18	10.10135	Up	interleukin 1 beta
SLC6A14	3.756565	8.56E-21	1.97E-18	10.07548	Up	solute carrier family 6 member 14
CHAC1	1.650312	1.18E-20	2.62E-18	10.03377	Up	ChaC glutathione specific gamma-glutamylcyclotransferase 1
FPR1	2.812962	1.57E-20	3.39E-18	9.995431	Up	formyl peptide receptor 1
KCNE3	1.022175	2.25E-20	4.63E-18	9.948103	Up	potassium voltage-gated channel subfamily E regulatory subunit 3
NOS2	2.18239	3.19E-20	6.35E-18	9.902444	Up	nitric oxide synthase 2
NFKBIZ	1.212531	3.68E-20	7.11E-18	9.883481	Up	NFKB inhibitor zeta
GBP5	2.004261	3.94E-20	7.40E-18	9.874461	Up	guanylate binding protein 5
ZBP1	1.096772	1.10E-19	2.05E-17	9.737352	Up	Z-DNA binding protein 1
CLEC4D	3.296142	1.15E-19	2.10E-17	9.73207	Up	C-type lectin domain family 4 member D
LILRA6	2.40512	1.49E-19	2.65E-17	9.697149	Up	leukocyte immunoglobulin like receptor A6
CKAP4	0.830255	2.06E-19	3.52E-17	9.653887	Up	cytoskeleton associated protein 4
CHI3L1	3.298167	2.22E-19	3.74E-17	9.644283	Up	chitinase 3 like 1
TGM2	0.97404	3.12E-19	5.13E-17	9.598358	Up	transglutaminase 2
ANKRD22	1.73289	3.49E-19	5.60E-17	9.583237	Up	ankyrin repeat domain 22
CLEC4E	2.746676	3.55E-19	5.62E-17	9.581157	Up	C-type lectin domain family 4 member E
HSD11B1	2.494625	3.64E-19	5.64E-17	9.577702	Up	hydroxysteroid 11-beta dehydrogenase 1
MUC4	2.183898	3.64E-19	5.64E-17	9.577592	Up	mucin 4, cell surface associated
VWA1	0.947404	4.32E-19	6.60E-17	9.554756	Up	von Willebrand factor A domain containing 1
C4BPB	1.70239	5.04E-19	7.54E-17	9.533897	Up	complement component 4 binding protein beta
HCAR2	2.913055	5.27E-19	7.78E-17	9.528035	Up	hydroxycarboxylic acid receptor 2
TREM1	3.409486	5.35E-19	7.82E-17	9.525926	Up	triggering receptor expressed on myeloid cells 1
IER3	1.764968	7.24E-19	1.02E-16	9.485053	Up	immediate early response 3
FCN3	2.983635	8.64E-19	1.21E-16	9.461122	Up	ficolin 3
PDZK1IP1	1.787127	9.10E-19	1.26E-16	9.454101	Up	PDZK1 interacting protein 1
CSF3R	2.205124	9.71E-19	1.32E-16	9.445436	Up	colony stimulating factor 3 receptor
WNT5A	1.518413	1.07E-18	1.44E-16	9.432169	Up	Wnt family member 5A
HGF	1.642413	1.13E-18	1.50E-16	9.425262	Up	hepatocyte growth factor
CXCL9	2.416097	1.17E-18	1.54E-16	9.420263	Up	C-X-C motif chemokine ligand 9

CLEC12A	1.312481	1.22E-18	1.57E-16	9.41463	Up	C-type lectin domain family 12 member A
CEACAM5	2.372293	1.39E-18	1.77E-16	9.396751	Up	CEA cell adhesion molecule 5
GBP1	1.569599	1.47E-18	1.86E-16	9.388719	Up	guanylate binding protein 1
S100A11	1.018691	1.49E-18	1.87E-16	9.38716	Up	S100 calcium binding protein A11
ADM	1.518372	1.53E-18	1.90E-16	9.383893	Up	adrenomedullin
ALDH1A2	2.494864	2.11E-18	2.56E-16	9.340013	Up	aldehyde dehydrogenase 1 family member A2
CXCL11	2.499506	2.27E-18	2.67E-16	9.329981	Up	C-X-C motif chemokine ligand 11
MAFF	1.116261	2.92E-18	3.40E-16	9.295743	Up	MAF bZIP transcription factor F
CFI	1.215373	3.38E-18	3.86E-16	9.275703	Up	complement factor I
LILRB3	1.825429	3.51E-18	3.98E-16	9.270572	Up	leukocyte immunoglobulin like receptor B3
TMPRSS3	1.319994	3.92E-18	4.41E-16	9.25525	Up	transmembrane serine protease 3
CD300E	2.911025	4.31E-18	4.80E-16	9.242482	Up	CD300e molecule
PLAUR	1.724453	4.37E-18	4.83E-16	9.240457	Up	plasminogen activator, urokinase receptor
CXCL10	2.255539	4.70E-18	5.15E-16	9.230665	Up	C-X-C motif chemokine ligand 10
LIPG	0.88763	4.82E-18	5.24E-16	9.226986	Up	lipase G, endothelial type
NCF2	1.433177	4.91E-18	5.30E-16	9.224397	Up	neutrophil cytosolic factor 2
HK3	1.564083	5.41E-18	5.78E-16	9.211197	Up	hexokinase 3
MMP10	3.746319	6.07E-18	6.38E-16	9.195523	Up	matrix metallopeptidase 10
FIBIN	1.552086	6.23E-18	6.50E-16	9.19194	Up	fin bud initiation factor homolog
LILRB2	1.466461	7.10E-18	7.36E-16	9.173799	Up	leukocyte immunoglobulin like receptor B2
FOLH1	2.672621	9.22E-18	9.40E-16	9.137882	Up	folate hydrolase 1
SLC11A1	2.342049	9.32E-18	9.43E-16	9.136449	Up	solute carrier family 11 member 1
GDF15	1.498939	1.11E-17	1.10E-15	9.112422	Up	growth differentiation factor 15
IL1RN	2.710793	1.19E-17	1.17E-15	9.103112	Up	interleukin 1 receptor antagonist
SLC39A8	1.125491	1.28E-17	1.26E-15	9.092606	Up	solute carrier family 39 member 8
SAA2	3.385445	1.39E-17	1.36E-15	9.080754	Up	serum amyloid A2
PRR16	1.536857	1.52E-17	1.46E-15	9.068799	Up	proline rich 16
NFE2	2.582068	1.83E-17	1.73E-15	9.043368	Up	nuclear factor, erythroid 2
ADGRE2	1.162262	3.03E-17	2.73E-15	8.972895	Up	adhesion G protein-coupled receptor E2
PRDX4	0.830543	3.40E-17	2.99E-15	8.956974	Up	peroxiredoxin 4
STAT1	1.221407	3.42E-17	2.99E-15	8.956404	Up	signal transducer and activator of transcription 1
CLEC5A	3.348941	3.49E-17	3.04E-15	8.953418	Up	C-type lectin domain containing 5A
SLAMF7	1.106839	4.08E-17	3.51E-15	8.93167	Up	SLAM family member 7
LILRA5	2.051658	4.47E-17	3.77E-15	8.918844	Up	leukocyte immunoglobulin like receptor A5
PYGL	1.216674	4.85E-17	3.96E-15	8.907415	Up	glycogen phosphorylase L
KCNJ15	2.687279	5.13E-17	4.16E-15	8.899667	Up	potassium inwardly rectifying channel subfamily J member 15
CYP27B1	1.884038	5.41E-17	4.37E-15	8.892143	Up	cytochrome P450 family 27 subfamily B member 1
LILRA1	1.555378	6.30E-17	4.96E-15	8.870736	Up	leukocyte immunoglobulin like receptor A1
NETO2	0.827415	6.36E-17	4.98E-15	8.869464	Up	neuropilin and tolloid like 2
TFPI2	2.253869	7.18E-17	5.58E-15	8.852581	Up	tissue factor pathway inhibitor 2
ZC3H12A	0.970997	8.56E-17	6.54E-15	8.827803	Up	zinc finger CCCH-type containing 12A
MMP1	3.679204	8.69E-17	6.57E-15	8.825704	Up	matrix metallopeptidase 1

SLPI	2.454275	9.16E-17	6.84E-15	8.818343	Up	secretory leukocyte peptidase inhibitor
LAP3	0.919821	1.12E-16	8.19E-15	8.789925	Up	leucine aminopeptidase 3
CMTM2	3.104589	1.46E-16	1.05E-14	8.752906	Up	CKLF like MARVEL transmembrane domain containing 2
PILRA	1.327943	1.51E-16	1.07E-14	8.747736	Up	paired immunoglobin like type 2 receptor alpha
CSF3	4.421519	1.88E-16	1.32E-14	8.716744	Up	colony stimulating factor 3
TYROBP	0.946812	2.26E-16	1.56E-14	8.690859	Up	transmembrane immune signaling adaptor TYROBP
FBXO6	0.826638	2.31E-16	1.59E-14	8.687779	Up	F-box protein 6
PSAT1	0.89902	2.70E-16	1.85E-14	8.665348	Up	phosphoserine aminotransferase 1
SOCS3	1.911655	2.88E-16	1.96E-14	8.65645	Up	suppressor of cytokine signaling 3
COL18A1	1.076767	3.39E-16	2.26E-14	8.633316	Up	collagen type XVIII alpha 1 chain
TLR8	1.305339	3.53E-16	2.33E-14	8.62745	Up	toll like receptor 8
HTRA3	1.294446	3.74E-16	2.44E-14	8.619309	Up	HtrA serine peptidase 3
CLIC6	1.127444	4.05E-16	2.62E-14	8.607814	Up	chloride intracellular channel 6
LILRA2	1.896919	4.06E-16	2.62E-14	8.607554	Up	leukocyte immunoglobulin like receptor A2
GPX8	1.148096	4.45E-16	2.84E-14	8.594247	Up	glutathione peroxidase 8 (putative)
C19orf38	1.155296	4.48E-16	2.84E-14	8.593538	Up	chromosome 19 open reading frame 38
SAMD9L	0.935307	4.55E-16	2.88E-14	8.591245	Up	sterile alpha motif domain containing 9 like
LITAF	1.010416	4.72E-16	2.96E-14	8.585888	Up	lipopolysaccharide induced TNF factor
FNDC3B	0.835649	5.21E-16	3.22E-14	8.571922	Up	fibronectin type III domain containing 3B
CEBPB	1.120221	7.82E-16	4.69E-14	8.513811	Up	CCAAT enhancer binding protein beta
IGSF6	1.184155	7.87E-16	4.70E-14	8.51282	Up	immunoglobulin superfamily member 6
CD55	1.303765	8.96E-16	5.31E-14	8.494195	Up	CD55 molecule (Cromer blood group)
MCEMP1	3.618149	1.13E-15	6.67E-14	8.460719	Up	mast cell expressed membrane protein 1
CXCR2	2.414397	1.16E-15	6.82E-14	8.456893	Up	C-X-C motif chemokine receptor 2
CCL28	1.263327	1.27E-15	7.43E-14	8.44388	Up	C-C motif chemokine ligand 28
IFI30	1.084391	1.41E-15	8.23E-14	8.428448	Up	IFI30 lysosomal thiol reductase
ADGRG3	1.473201	1.62E-15	9.32E-14	8.409247	Up	adhesion G protein-coupled receptor G3
CBR3	1.127031	1.99E-15	1.14E-13	8.378723	Up	carbonyl reductase 3
CCL3	2.11812	2.34E-15	1.32E-13	8.355786	Up	C-C motif chemokine ligand 3
CTSS	0.965265	2.35E-15	1.32E-13	8.354916	Up	cathepsin S
FCGR2A	1.59213	2.40E-15	1.34E-13	8.351787	Up	Fc fragment of IgG receptor IIa
EMILIN2	0.855845	3.15E-15	1.74E-13	8.312447	Up	elastin microfibril interfacer 2
JCHAIN	1.25521	3.17E-15	1.74E-13	8.311478	Up	joining chain of multimeric IgA and IgM
ACSL1	1.594451	3.67E-15	1.98E-13	8.290169	Up	acyl-CoA synthetase long chain family member 1
CCL2	1.401123	3.77E-15	2.02E-13	8.286188	Up	C-C motif chemokine ligand 2
SLC38A5	0.851469	4.08E-15	2.15E-13	8.274709	Up	solute carrier family 38 member 5
SOD2	1.511524	4.14E-15	2.17E-13	8.272469	Up	superoxide dismutase 2
TFRC	0.848187	5.07E-15	2.62E-13	8.242884	Up	transferrin receptor
CFB	1.082022	6.01E-15	3.08E-13	8.217991	Up	complement factor B
IGLL5	1.528254	6.27E-15	3.19E-13	8.211852	Up	immunoglobulin lambda like polypeptide 5
OSCAR	1.473262	6.59E-15	3.34E-13	8.204563	Up	osteoclast associated Ig-like receptor
CD14	1.095278	7.44E-15	3.76E-13	8.18669	Up	CD14 molecule

PSTPIP2	0.992808	8.93E-15	4.42E-13	8.159782	Up	proline-serine-threonine phosphatase interacting protein 2
SGIP1	1.314786	1.11E-14	5.43E-13	8.127123	Up	SH3GL interacting endocytic adaptor 1
CASP5	1.341148	1.18E-14	5.70E-13	8.118891	Up	caspase 5
MNDA	1.478483	1.34E-14	6.44E-13	8.099782	Up	myeloid cell nuclear differentiation antigen
IGFBP2	1.060726	1.42E-14	6.76E-13	8.091466	Up	insulin like growth factor binding protein 2
GPR84	2.317344	1.44E-14	6.84E-13	8.089268	Up	G protein-coupled receptor 84
DYSF	1.170904	1.51E-14	7.10E-13	8.08273	Up	dysferlin
PCSK9	1.473897	1.64E-14	7.71E-13	8.069979	Up	proprotein convertase subtilisin/kexin type 9
CD274	1.294519	1.65E-14	7.71E-13	8.069373	Up	CD274 molecule
CLEC7A	0.970417	1.74E-14	8.01E-13	8.061623	Up	C-type lectin domain containing 7A
DERL3	1.419108	2.21E-14	1.00E-12	8.025921	Up	derlin 3
SERPINE1	2.114809	2.34E-14	1.05E-12	8.017549	Up	serpin family E member 1
IDO1	1.699676	2.44E-14	1.10E-12	8.01096	Up	indoleamine 2,3-dioxygenase 1
PDK1	0.845911	2.57E-14	1.15E-12	8.003091	Up	pyruvate dehydrogenase kinase 1
GLUL	1.071422	2.59E-14	1.15E-12	8.002098	Up	glutamate-ammonia ligase
SRPX2	1.298505	2.69E-14	1.19E-12	7.996559	Up	sushi repeat containing protein X-linked 2
MZB1	1.389104	2.73E-14	1.20E-12	7.994432	Up	marginal zone B and B1 cell specific protein
PLA2G7	1.310422	3.35E-14	1.45E-12	7.963918	Up	phospholipase A2 group VII
SRD5A3	0.928125	3.57E-14	1.54E-12	7.954087	Up	steroid 5 alpha-reductase 3
FOXP3	1.137182	3.67E-14	1.56E-12	7.950066	Up	forkhead box P3
SCN1B	0.966572	3.69E-14	1.57E-12	7.9492	Up	sodium voltage-gated channel beta subunit 1
CD163	0.859795	3.98E-14	1.68E-12	7.938005	Up	CD163 molecule
LYPD1	2.312055	4.35E-14	1.80E-12	7.924619	Up	LY6/PLAUR domain containing 1
EGFL6	2.585554	4.56E-14	1.87E-12	7.917571	Up	EGF like domain multiple 6
VCAN	1.141309	4.58E-14	1.87E-12	7.916996	Up	versican
SAA1	3.491647	4.60E-14	1.87E-12	7.916339	Up	serum amyloid A1
FCER1G	1.088497	6.36E-14	2.56E-12	7.867574	Up	Fc fragment of IgE receptor Ig
LPL	1.198285	6.80E-14	2.71E-12	7.857456	Up	lipoprotein lipase
IL1R2	1.776325	7.04E-14	2.80E-12	7.852161	Up	interleukin 1 receptor type 2
APCDD1	1.016298	7.63E-14	3.00E-12	7.840162	Up	APC down-regulated 1
CCL7	3.147925	7.73E-14	3.03E-12	7.838246	Up	C-C motif chemokine ligand 7
GBP4	1.072828	7.94E-14	3.11E-12	7.834047	Up	guanylate binding protein 4
COL5A3	0.958334	1.08E-13	4.11E-12	7.78814	Up	collagen type V alpha 3 chain
RNASE2	2.65289	1.12E-13	4.27E-12	7.782002	Up	ribonuclease A family member 2
ADORA2B	1.125733	1.29E-13	4.86E-12	7.76097	Up	adenosine A2b receptor
PTGS2	2.01817	1.50E-13	5.61E-12	7.737162	Up	prostaglandin-endoperoxide synthase 2
IRAK3	0.90654	1.80E-13	6.60E-12	7.710276	Up	interleukin 1 receptor associated kinase 3
TLR2	1.114946	1.99E-13	7.26E-12	7.694313	Up	toll like receptor 2
TCN1	2.941416	2.15E-13	7.76E-12	7.682701	Up	transcobalamin 1
ALOX15B	1.748302	2.15E-13	7.76E-12	7.682567	Up	arachidonate 15-lipoxygenase type B
MEFV	1.339803	2.18E-13	7.84E-12	7.680573	Up	MEFV innate immuity regulator, pyrin
PI3	2.014865	2.38E-13	8.50E-12	7.666945	Up	peptidase inhibitor 3

CLCA4	2.354097	2.50E-13	8.84E-12	7.65996	Up	chloride channel accessory 4
PIGR	1.48943	2.55E-13	9.00E-12	7.656572	Up	polymeric immunoglobulin receptor
OASL	1.167584	2.89E-13	1.00E-11	7.637503	Up	2'-5'-oligoadenylate synthetase like
F2RL2	1.210797	3.02E-13	1.04E-11	7.630478	Up	coagulation factor II thrombin receptor like 2
IGFBP5	1.325087	4.21E-13	1.42E-11	7.579641	Up	insulin like growth factor binding protein 5
FFAR4	1.389724	4.33E-13	1.45E-11	7.575382	Up	free fatty acid receptor 4
QPCT	0.985443	4.70E-13	1.56E-11	7.562548	Up	glutaminyl-peptide cyclotransferase
CCR2	0.850477	4.77E-13	1.58E-11	7.560337	Up	C-C motif chemokine receptor 2
ZG16B	1.340262	5.06E-13	1.67E-11	7.551157	Up	zymogen granule protein 16B
JUNB	0.845055	5.14E-13	1.70E-11	7.548616	Up	JunB proto-oncogene, AP-1 transcription factor subunit
RND1	1.074192	5.38E-13	1.77E-11	7.541713	Up	Rho family GTPase 1
CHRNA5	1.013297	6.49E-13	2.07E-11	7.512615	Up	cholinergic receptor nicotinic alpha 5 subunit
KCNJ2	1.240292	7.36E-13	2.32E-11	7.493103	Up	potassium inwardly rectifying channel subfamily J member 2
BHLHA15	1.636385	7.64E-13	2.40E-11	7.48721	Up	basic helix-loop-helix family member a15
VWF	1.331264	7.83E-13	2.46E-11	7.483499	Up	von Willebrand factor
SLC7A11	1.284759	8.39E-13	2.59E-11	7.472612	Up	solute carrier family 7 member 11
NOD2	1.053995	1.14E-12	3.41E-11	7.425012	Up	nucleotide binding oligomerization domain containing 2
LYPD6B	1.562121	1.60E-12	4.64E-11	7.371307	Up	LY6/PLAUR domain containing 6B
DMBT1	1.798811	1.63E-12	4.68E-11	7.368707	Up	deleted in malignant brain tumors 1
IL20RA	2.206886	1.71E-12	4.87E-11	7.361561	Up	interleukin 20 receptor subunit alpha
TYMP	0.992778	1.85E-12	5.26E-11	7.348798	Up	thymidine phosphorylase
HSPA6	1.323078	1.88E-12	5.32E-11	7.346761	Up	heat shock protein family A (Hsp70) member 6
ADGRF1	2.000393	1.95E-12	5.49E-11	7.340771	Up	adhesion G protein-coupled receptor F1
NAMPT	1.340688	2.22E-12	6.19E-11	7.320295	Up	nicotinamide phosphoribosyltransferase
GNA15	1.033482	3.07E-12	8.41E-11	7.268653	Up	G protein subunit alpha 15
STEAP1	1.3461	3.16E-12	8.60E-11	7.264476	Up	STEAP family member 1
S100P	1.459599	3.50E-12	9.42E-11	7.248047	Up	S100 calcium binding protein P
CEACAM3	1.690449	3.59E-12	9.63E-11	7.2439	Up	CEA cell adhesion molecule 3
PDPN	1.424551	3.71E-12	9.89E-11	7.238934	Up	podoplanin
THEMIS2	0.894362	4.08E-12	1.08E-10	7.223752	Up	thymocyte selection associated family member 2
CLEC6A	2.489049	4.18E-12	1.10E-10	7.219716	Up	C-type lectin domain containing 6A
P2RY6	0.834246	4.53E-12	1.18E-10	7.207107	Up	pyrimidinergic receptor P2Y6
ADAMTS1	0.864317	5.74E-12	1.47E-10	7.169206	Up	ADAM metallopeptidase with thrombospondin type 1 motif 1
ADCYAP1	2.065148	5.81E-12	1.48E-10	7.167398	Up	adenylate cyclase activating polypeptide 1
PGC	3.884311	5.98E-12	1.52E-10	7.162639	Up	progastricsin
ATF3	0.99383	8.24E-12	2.02E-10	7.111193	Up	activating transcription factor 3
STEAP4	1.361612	8.71E-12	2.11E-10	7.102171	Up	STEAP4 metalloreductase
TIMP1	1.24969	9.08E-12	2.20E-10	7.095622	Up	TIMP metallopeptidase inhibitor 1
UCN2	3.096502	1.05E-11	2.50E-10	7.071615	Up	urocortin 2
TTC39A	0.854449	1.06E-11	2.51E-10	7.071017	Up	tetratricopeptide repeat domain 39A
FCAR	2.138055	1.07E-11	2.54E-10	7.068504	Up	Fc fragment of IgA receptor
SLAMF8	0.93677	1.19E-11	2.78E-10	7.051517	Up	SLAM family member 8

PRSS23	0.853919	1.25E-11	2.90E-10	7.043876	Up	serine protease 23
PHLDA1	0.90708	1.31E-11	3.02E-10	7.036279	Up	pleckstrin homology like domain family A member 1
STX11	1.078346	1.40E-11	3.21E-10	7.025543	Up	syntaxin 11
SPAG4	1.317261	1.53E-11	3.44E-10	7.011401	Up	sperm associated antigen 4
FAP	1.798038	1.56E-11	3.50E-10	7.007883	Up	fibroblast activation protein alpha
CTSL	0.857925	1.69E-11	3.78E-10	6.99462	Up	cathepsin L
SIGLEC9	1.062336	1.73E-11	3.86E-10	6.991092	Up	sialic acid binding Ig like lectin 9
ADAMTS2	1.162469	1.75E-11	3.89E-10	6.989267	Up	ADAM metallopeptidase with thrombospondin type 1 motif 2
SELE	2.400806	1.85E-11	4.09E-10	6.980092	Up	selectin E
LAMC3	2.420987	2.00E-11	4.40E-10	6.967105	Up	laminin subunit gamma 3
SLC1A3	1.501118	2.08E-11	4.56E-10	6.960761	Up	solute carrier family 1 member 3
ICAM1	1.087271	2.28E-11	4.94E-10	6.945912	Up	intercellular adhesion molecule 1
EDNRA	1.017151	2.31E-11	4.97E-10	6.943703	Up	endothelin receptor type A
GLT1D1	2.112095	2.50E-11	5.30E-10	6.931256	Up	glycosyltransferase 1 domain containing 1
FOSL1	1.980963	2.63E-11	5.55E-10	6.922983	Up	FOS like 1, AP-1 transcription factor subunit
CD300C	0.860847	2.64E-11	5.57E-10	6.922314	Up	CD300c molecule
RASGRP4	0.876725	2.81E-11	5.89E-10	6.9117	Up	RAS guanyl releasing protein 4
ALDH1L1	1.499599	2.82E-11	5.91E-10	6.91101	Up	aldehyde dehydrogenase 1 family member L1
PRSS22	1.564696	2.88E-11	5.99E-10	6.907865	Up	serine protease 22
AREG	1.359747	2.94E-11	6.11E-10	6.904211	Up	amphiregulin
LYZ	1.073137	3.12E-11	6.43E-10	6.894502	Up	lysozyme
APOL4	0.831339	3.13E-11	6.43E-10	6.894221	Up	apolipoprotein L4
PIM2	1.081642	3.28E-11	6.73E-10	6.886279	Up	Pim-2 proto-oncogene, serine/threonine kinase
SLC7A5	0.940495	3.44E-11	7.02E-10	6.878815	Up	solute carrier family 7 member 5
MYEOV	1.621732	3.60E-11	7.31E-10	6.870917	Up	myeloma overexpressed
PF4V1	2.587262	3.65E-11	7.41E-10	6.868616	Up	platelet factor 4 variant 1
IL13RA2	2.624209	4.15E-11	8.33E-10	6.847764	Up	interleukin 13 receptor subunit alpha 2
ACSL4	1.017261	4.40E-11	8.79E-10	6.838099	Up	acyl-CoA synthetase long chain family member 4
COL4A1	1.084643	4.91E-11	9.68E-10	6.819881	Up	collagen type IV alpha 1 chain
CH25H	0.948713	5.00E-11	9.84E-10	6.816982	Up	cholesterol 25-hydroxylase
LY6D	2.874509	5.87E-11	1.13E-09	6.790137	Up	lymphocyte antigen 6 family member D
COL5A2	0.946657	5.89E-11	1.13E-09	6.789786	Up	collagen type V alpha 2 chain
JPH1	0.921535	6.08E-11	1.16E-09	6.784312	Up	junctophilin 1
SNAI1	1.418288	6.14E-11	1.17E-09	6.782783	Up	snail family transcriptional repressor 1
L1TD1	1.947341	6.73E-11	1.27E-09	6.767526	Up	LINE1 type transposase domain containing 1
FFAR2	1.305954	6.78E-11	1.27E-09	6.766253	Up	free fatty acid receptor 2
LRFN4	0.85521	6.96E-11	1.30E-09	6.761775	Up	leucine rich repeat and fibronectin type III domain containing 4
ADAMTS4	1.630569	7.12E-11	1.33E-09	6.758001	Up	ADAM metallopeptidase with thrombospondin type 1 motif 4
PLA1A	1.343608	8.03E-11	1.50E-09	6.737962	Up	phospholipase A1 member A
MARCO	2.30106	1.14E-10	2.05E-09	6.679197	Up	macrophage receptor with collagenous structure
RARRES1	1.254143	1.15E-10	2.07E-09	6.677623	Up	retinoic acid receptor responder 1
MXRA5	0.848658	1.16E-10	2.08E-09	6.676176	Up	matrix remodeling associated 5

PSG4	1.833699	1.18E-10	2.10E-09	6.674081	Up	pregnancy specific beta-1-glycoprotein 4
CCL4L2	1.769671	1.24E-10	2.20E-09	6.664941	Up	C-C motif chemokine ligand 4 like 2
EGR1	1.176686	1.35E-10	2.37E-09	6.651223	Up	early growth response 1
TNFRSF17	0.848825	1.35E-10	2.37E-09	6.651018	Up	TNF receptor superfamily member 17
MDFI	0.92631	1.36E-10	2.38E-09	6.650185	Up	MyoD family inhibitor
ST3GAL4	1.080362	1.41E-10	2.46E-09	6.643827	Up	ST3 beta-galactoside alpha-2,3-sialyltransferase 4
SRGN	0.96492	1.52E-10	2.64E-09	6.630568	Up	serglycin
IFITM2	0.902514	1.64E-10	2.82E-09	6.61773	Up	interferon induced transmembrane protein 2
CEACAM6	1.41048	1.69E-10	2.90E-09	6.612785	Up	CEA cell adhesion molecule 6
CCL11	0.967948	1.77E-10	3.02E-09	6.604665	Up	C-C motif chemokine ligand 11
IFNG	2.094963	2.35E-10	3.89E-09	6.556704	Up	interferon gamma
PTAFR	0.87103	2.58E-10	4.23E-09	6.540719	Up	platelet activating factor receptor
TREM2	1.324259	2.68E-10	4.36E-09	6.534523	Up	triggering receptor expressed on myeloid cells 2
ANXA10	3.114036	3.00E-10	4.82E-09	6.515455	Up	annexin A10
INHBA	2.051365	3.01E-10	4.83E-09	6.514679	Up	inhibin subunit beta A
CEACAM7	3.134053	3.39E-10	5.36E-09	6.494545	Up	CEA cell adhesion molecule 7
CEACAM4	1.643827	3.46E-10	5.46E-09	6.491039	Up	CEA cell adhesion molecule 4
SERPING1	0.846139	3.50E-10	5.53E-09	6.488766	Up	serpin family G member 1
CLC	1.047139	3.52E-10	5.54E-09	6.488117	Up	Charcot-Leyden crystal galectin
APOE	0.870166	4.08E-10	6.34E-09	6.462616	Up	apolipoprotein E
FGR	0.956661	5.61E-10	8.48E-09	6.407546	Up	FGR proto-oncogene, Src family tyrosine kinase
EVA1A	0.857866	5.67E-10	8.57E-09	6.405606	Up	eva-1 homolog A, regulator of programmed cell death
CRISP3	2.310204	5.73E-10	8.64E-09	6.404043	Up	cysteine rich secretory protein 3
CTSK	1.062566	5.91E-10	8.88E-09	6.39847	Up	cathepsin K
TNS4	1.279248	6.77E-10	1.00E-08	6.375071	Up	tensin 4
COL7A1	1.756607	6.98E-10	1.03E-08	6.369662	Up	collagen type VII alpha 1 chain
SAA4	2.878274	7.09E-10	1.04E-08	6.366856	Up	serum amyloid A4, constitutive
ALPL	1.340696	8.16E-10	1.18E-08	6.342572	Up	alkaline phosphatase, biomineralization associated
CCR1	0.848728	8.38E-10	1.21E-08	6.337905	Up	C-C motif chemokine receptor 1
UBTD1	0.879112	8.45E-10	1.22E-08	6.336314	Up	ubiquitin domain containing 1
NR4A3	1.310486	1.01E-09	1.44E-08	6.30478	Up	nuclear receptor subfamily 4 group A member 3
IL6	2.473034	1.25E-09	1.74E-08	6.267713	Up	interleukin 6
CTHRC1	1.35846	1.31E-09	1.81E-08	6.259994	Up	collagen triple helix repeat containing 1
PDCD1LG2	0.865996	1.44E-09	1.97E-08	6.242396	Up	programmed cell death 1 ligand 2
JSRP1	1.26645	1.69E-09	2.26E-08	6.214655	Up	junctional sarcoplasmic reticulum protein 1
SFRP1	1.084986	1.86E-09	2.47E-08	6.197456	Up	secreted frizzled related protein 1
CCL4	1.337402	2.02E-09	2.66E-08	6.182875	Up	C-C motif chemokine ligand 4
SNX10	0.988835	2.03E-09	2.67E-08	6.182405	Up	sorting nexin 10
NFAM1	0.996744	2.15E-09	2.82E-08	6.172106	Up	NFAT activating protein with ITAM motif 1
B3GNT6	1.198121	2.16E-09	2.82E-08	6.171326	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 6
TMEM132A	1.192256	2.20E-09	2.88E-08	6.167464	Up	transmembrane protein 132A
CPXM1	1.111511	2.31E-09	3.00E-08	6.158974	Up	carboxypeptidase X, M14 family member 1

KRT6A	2.987806	2.38E-09	3.08E-08	6.153789	Up	keratin 6A
SPP1	1.475232	2.50E-09	3.21E-08	6.144708	Up	secreted phosphoprotein 1
CLDN1	1.302536	2.51E-09	3.22E-08	6.14411	Up	claudin 1
CA2	1.813954	2.53E-09	3.24E-08	6.142684	Up	carbonic anhydrase 2
IL11	2.614168	2.66E-09	3.39E-08	6.133689	Up	interleukin 11
PHLDA2	0.985161	3.09E-09	3.89E-08	6.107356	Up	pleckstrin homology like domain family A member 2
CLDN18	1.253572	3.10E-09	3.90E-08	6.106719	Up	claudin 18
NNMT	1.27587	3.33E-09	4.17E-08	6.093585	Up	nicotinamide N-methyltransferase
APOC1	1.081595	3.57E-09	4.43E-08	6.081305	Up	apolipoprotein C1
COL15A1	0.85256	3.77E-09	4.64E-08	6.071476	Up	collagen type XV alpha 1 chain
KRT17	2.066623	4.43E-09	5.38E-08	6.042477	Up	keratin 17
KYNU	1.162912	4.56E-09	5.52E-08	6.037179	Up	kynureninase
LYPD5	0.927052	4.96E-09	5.97E-08	6.021761	Up	LY6/PLAUR domain containing 5
MEOX1	0.902901	5.03E-09	6.04E-08	6.019229	Up	mesenchyme homeobox 1
FGFBP1	1.868015	5.09E-09	6.10E-08	6.017003	Up	fibroblast growth factor binding protein 1
RAB31	0.859544	5.76E-09	6.80E-08	5.994852	Up	RAB31, member RAS oncogene family
COL6A3	0.926291	5.84E-09	6.88E-08	5.992241	Up	collagen type VI alpha 3 chain
B4GALNT3	0.93002	6.01E-09	7.06E-08	5.987087	Up	beta-1,4-N-acetyl-galactosaminyltransferase 3
TNFRSF18	0.835407	7.57E-09	8.71E-08	5.944928	Up	TNF receptor superfamily member 18
SLC5A8	1.771435	7.62E-09	8.75E-08	5.943601	Up	solute carrier family 5 member 8
TNFRSF4	0.9292	7.80E-09	8.89E-08	5.939538	Up	TNF receptor superfamily member 4
COL1A1	1.069939	1.01E-08	1.12E-07	5.891838	Up	collagen type I alpha 1 chain
FAM20A	1.23275	1.01E-08	1.12E-07	5.891167	Up	FAM20A golgi associated secretory pathway pseudokinase
RNF186	1.089567	1.03E-08	1.13E-07	5.888989	Up	ring finger protein 186
MMP12	1.381414	1.05E-08	1.15E-07	5.884708	Up	matrix metallopeptidase 12
DEFB4A	3.410488	1.06E-08	1.16E-07	5.882977	Up	defensin beta 4A
COL3A1	1.014439	1.10E-08	1.20E-07	5.876219	Up	collagen type III alpha 1 chain
KRT23	1.447713	1.21E-08	1.30E-07	5.858314	Up	keratin 23
MMP2	0.952538	1.26E-08	1.34E-07	5.851889	Up	matrix metallopeptidase 2
MUC5B	2.941403	1.26E-08	1.35E-07	5.851265	Up	mucin 5B, oligomeric mucus/gel-forming
C2CD4B	0.906295	1.38E-08	1.46E-07	5.834352	Up	C2 calcium dependent domain containing 4B
TSHZ2	0.831876	1.52E-08	1.59E-07	5.816235	Up	teashirt zinc finger homeobox 2
PLEK	1.135102	1.53E-08	1.61E-07	5.814585	Up	pleckstrin
IFI44L	0.837938	1.57E-08	1.63E-07	5.810547	Up	interferon induced protein 44 like
TNFAIP2	0.862706	1.75E-08	1.81E-07	5.789744	Up	TNF alpha induced protein 2
LILRB4	1.005113	1.83E-08	1.88E-07	5.781966	Up	leukocyte immunoglobulin like receptor B4
IL1A	2.234711	1.90E-08	1.94E-07	5.775021	Up	interleukin 1 alpha
TMEM158	1.453932	1.91E-08	1.95E-07	5.774217	Up	transmembrane protein 158
SLC17A9	0.894481	2.06E-08	2.09E-07	5.759528	Up	solute carrier family 17 member 9
ITGA5	0.856581	2.25E-08	2.25E-07	5.743368	Up	integrin subunit alpha 5
SBSN	2.423611	2.54E-08	2.52E-07	5.720488	Up	suprabasin
CCL1	2.350388	2.60E-08	2.58E-07	5.715744	Up	C-C motif chemokine ligand 1

MLN	2.482379	2.73E-08	2.69E-07	5.706932	Up	motilin
GPR4	1.033672	2.93E-08	2.86E-07	5.693726	Up	G protein-coupled receptor 4
WNT2	2.285788	3.34E-08	3.24E-07	5.668811	Up	Wnt family member 2
SIRPB1	0.981149	5.05E-08	4.73E-07	5.589771	Up	signal regulatory protein beta 1
HAPLN3	1.079058	5.74E-08	5.33E-07	5.565371	Up	hyaluronan and proteoglycan link protein 3
FAM167B	0.843095	5.86E-08	5.43E-07	5.5614	Up	family with sequence similarity 167 member B
PFKFB3	0.919481	6.44E-08	5.91E-07	5.543093	Up	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
FOLR3	2.545579	7.19E-08	6.55E-07	5.521935	Up	folate receptor gamma
HBEGF	0.964975	7.28E-08	6.62E-07	5.519586	Up	heparin binding EGF like growth factor
ADGRE3	0.870741	7.85E-08	7.10E-07	5.504986	Up	adhesion G protein-coupled receptor E3
GPX2	0.868794	8.48E-08	7.60E-07	5.489972	Up	glutathione peroxidase 2
CD24	0.996198	1.49E-07	1.26E-06	5.380312	Up	CD24 molecule
CCL3L3	1.514133	1.57E-07	1.32E-06	5.369243	Up	C-C motif chemokine ligand 3 like 3
PDE4B	0.843066	1.93E-07	1.58E-06	5.328805	Up	phosphodiesterase 4B
AQP5	2.081121	2.08E-07	1.69E-06	5.313563	Up	aquaporin 5
SCNN1B	1.292425	2.21E-07	1.78E-06	5.301771	Up	sodium channel epithelial 1 subunit beta
GLDC	0.920458	2.47E-07	1.97E-06	5.279481	Up	glycine decarboxylase
PI15	1.655681	2.51E-07	2.00E-06	5.275764	Up	peptidase inhibitor 15
REG1A	1.442024	2.72E-07	2.14E-06	5.260285	Up	regenerating family member 1 alpha
CA1	1.928578	2.99E-07	2.34E-06	5.240919	Up	carbonic anhydrase 1
UBD	1.078489	3.01E-07	2.35E-06	5.239404	Up	ubiquitin D
SPHK1	0.903454	3.01E-07	2.35E-06	5.239367	Up	sphingosine kinase 1
AOX1	1.300457	3.28E-07	2.54E-06	5.222541	Up	aldehyde oxidase 1
CYP7B1	1.109294	5.24E-07	3.88E-06	5.127231	Up	cytochrome P450 family 7 subfamily B member 1
GPR141	0.878571	5.36E-07	3.96E-06	5.122544	Up	G protein-coupled receptor 141
STC2	1.378255	5.40E-07	3.98E-06	5.121019	Up	stanniocalcin 2
DHRS9	0.897578	5.98E-07	4.35E-06	5.100025	Up	dehydrogenase/reductase 9
SPINK4	1.136607	6.46E-07	4.66E-06	5.084278	Up	serine peptidase inhibitor Kazal type 4
CEMIP	1.456309	6.61E-07	4.75E-06	5.079573	Up	cell migration inducing hyaluronidase 1
BPIFB1	2.350464	7.17E-07	5.11E-06	5.062781	Up	BPI fold containing family B member 1
LAMP3	0.887861	7.23E-07	5.15E-06	5.060893	Up	lysosomal associated membrane protein 3
TFF2	1.597553	8.50E-07	5.98E-06	5.027399	Up	trefoil factor 2
MMP7	1.814309	1.03E-06	7.15E-06	4.986588	Up	matrix metallopeptidase 7
ITGAX	0.828478	1.06E-06	7.31E-06	4.981626	Up	integrin subunit alpha X
POSTN	0.911217	1.19E-06	8.08E-06	4.956983	Up	periostin
CAPN8	0.894431	1.41E-06	9.40E-06	4.921948	Up	calpain 8
KCNN3	0.918088	1.54E-06	1.01E-05	4.902542	Up	potassium calcium-activated channel subfamily N member 3
TNFRSF6B	1.493799	1.55E-06	1.02E-05	4.901288	Up	TNF receptor superfamily member 6b
DEFB4B	2.702989	1.68E-06	1.09E-05	4.884867	Up	defensin beta 4B
REG1B	1.745649	1.73E-06	1.12E-05	4.878249	Up	regenerating family member 1 beta
G0S2	1.068455	1.96E-06	1.26E-05	4.851875	Up	G0/G1 switch 2
SLC6A12	0.872742	2.14E-06	1.37E-05	4.832302	Up	solute carrier family 6 member 12

ANGPTL2	0.825843	2.28E-06	1.44E-05	4.819058	Up	angiopoietin like 2
S100A3	1.399455	2.67E-06	1.66E-05	4.785015	Up	S100 calcium binding protein A3
GZMB	0.995908	2.73E-06	1.70E-05	4.78052	Up	granzyme B
OLR1	0.951851	2.93E-06	1.81E-05	4.76509	Up	oxidized low density lipoprotein receptor 1
SELP	0.850794	3.56E-06	2.15E-05	4.722795	Up	selectin P
THY1	0.838668	3.70E-06	2.23E-05	4.713864	Up	Thy-1 cell surface antigen
MUC5AC	1.656517	4.18E-06	2.48E-05	4.687234	Up	mucin 5AC, oligomeric mucus/gel-forming
TFCP2L1	1.141815	4.28E-06	2.53E-05	4.682095	Up	transcription factor CP2 like 1
CA12	0.854919	4.57E-06	2.68E-05	4.667701	Up	carbonic anhydrase 12
BCL2A1	0.870153	5.21E-06	3.02E-05	4.638815	Up	BCL2 related protein A1
FGF7	0.921756	5.39E-06	3.11E-05	4.631387	Up	fibroblast growth factor 7
SERPINA3	1.067197	6.15E-06	3.50E-05	4.602051	Up	serpin family A member 3
TWIST1	1.525118	6.59E-06	3.72E-05	4.586671	Up	twist family bHLH transcription factor 1
FJX1	0.862822	7.01E-06	3.94E-05	4.572753	Up	four-jointed box kinase 1
CCL8	0.956639	7.84E-06	4.36E-05	4.547734	Up	C-C motif chemokine ligand 8
CSF2	1.919612	8.24E-06	4.57E-05	4.53649	Up	colony stimulating factor 2
CA4	1.277709	8.55E-06	4.72E-05	4.528015	Up	carbonic anhydrase 4
MUCL1	2.093183	1.15E-05	6.14E-05	4.460884	Up	mucin like 1
ART3	0.978362	1.24E-05	6.57E-05	4.444012	Up	ADP-ribosyltransferase 3 (inactive)
PLAU	1.172812	1.27E-05	6.73E-05	4.437891	Up	plasminogen activator, urokinase
CD177	1.777379	1.32E-05	6.98E-05	4.42887	Up	CD177 molecule
CA9	1.309415	1.35E-05	7.11E-05	4.424281	Up	carbonic anhydrase 9
GFPT2	0.942613	1.39E-05	7.31E-05	4.417281	Up	glutamine-fructose-6-phosphate transaminase 2
TDO2	0.877816	1.49E-05	7.77E-05	4.401811	Up	tryptophan 2,3-dioxygenase
TFF1	1.002843	1.58E-05	8.18E-05	4.388179	Up	trefoil factor 1
MUC6	2.182507	1.62E-05	8.37E-05	4.382471	Up	mucin 6, oligomeric mucus/gel-forming
STC1	1.112886	2.52E-05	0.000124	4.279113	Up	stanniocalcin 1
ITLN1	0.830345	2.62E-05	0.000129	4.269482	Up	intelectin 1
CTLA4	0.83377	3.00E-05	0.000145	4.237138	Up	cytotoxic T-lymphocyte associated protein 4
C4BPA	1.132468	4.45E-05	0.000207	4.143021	Up	complement component 4 binding protein alpha
TNIP3	0.943226	4.54E-05	0.000212	4.137839	Up	TNFAIP3 interacting protein 3
PADI4	1.005183	5.07E-05	0.000233	4.111296	Up	peptidyl arginine deiminase 4
GALNT15	0.926009	5.13E-05	0.000236	4.108152	Up	polypeptide N-acetylgalactosaminyltransferase 15
ORM1	1.85636	5.63E-05	0.000256	4.085532	Up	orosomucoid 1
MMP13	1.472771	5.81E-05	0.000263	4.077892	Up	matrix metallopeptidase 13
WFDC2	1.005696	5.84E-05	0.000265	4.076559	Up	WAP four-disulfide core domain 2
DEFA1	1.909918	6.41E-05	0.000288	4.053721	Up	defensin alpha 1
HBD	1.727907	6.70E-05	0.000299	4.04269	Up	hemoglobin subunit delta
HRH2	0.909991	8.84E-05	0.000381	3.973665	Up	histamine receptor H2
FOSB	1.035925	0.000113	0.000476	3.91086	Up	FosB proto-oncogene, AP-1 transcription factor subunit
TWIST2	0.858154	0.000119	0.000496	3.898297	Up	twist family bHLH transcription factor 2
LBP	1.348738	0.000151	0.000614	3.836926	Up	lipopolysaccharide binding protein

LDHD	0.847132	0.000157	0.000634	3.827736	Up	lactate dehydrogenase D
CCDC60	1.211324	0.000159	0.000641	3.8242	Up	coiled-coil domain containing 60
CST1	1.638315	0.000275	0.001044	3.680571	Up	cystatin SN
S100A2	1.061546	0.000286	0.001079	3.67018	Up	S100 calcium binding protein A2
PGLYRP1	1.122262	0.00036	0.001323	3.608379	Up	peptidoglycan recognition protein 1
P4HA3	0.879979	0.000447	0.0016	3.549376	Up	prolyl 4-hydroxylase subunit alpha 3
THBS2	0.955889	0.000494	0.001749	3.522004	Up	thrombospondin 2
GLDN	0.91532	0.000503	0.001775	3.516956	Up	gliomedin
GAS1	1.055316	0.000698	0.002366	3.425357	Up	growth arrest specific 1
MASP1	0.9575	0.000824	0.002722	3.37832	Up	MBL associated serine protease 1
KLK6	1.251653	0.001089	0.003475	3.297966	Up	kallikrein related peptidase 6
VSNL1	0.9372	0.00119	0.00376	3.272114	Up	visinin like 1
FFAR3	0.977914	0.001245	0.00392	3.258968	Up	free fatty acid receptor 3
KRT7	1.064893	0.001284	0.004027	3.249898	Up	keratin 7
RETN	1.479056	0.00156	0.004785	3.192099	Up	resistin
ODAM	1.267788	0.001877	0.005631	3.136454	Up	odontogenic, ameloblast associated
GIP	1.281853	0.002243	0.006566	3.08218	Up	gastric inhibitory polypeptide
SPTSSB	0.965911	0.00251	0.007205	3.0475	Up	serine palmitoyltransferase small subunit B
MPO	0.975982	0.003295	0.009125	2.962183	Up	myeloperoxidase
HAS1	1.069758	0.00332	0.00917	2.959842	Up	hyaluronan synthase 1
LEFTY1	1.2042	0.003538	0.009677	2.939586	Up	left-right determination factor 1
HP	0.981181	0.004573	0.012084	2.85686	Up	haptoglobin
SCGB2A1	0.912595	0.005908	0.01507	2.772345	Up	secretoglobin family 2A member 1
HOXD10	1.058949	0.00681	0.017056	2.724587	Up	homeobox D10
MSMB	1.114911	0.010826	0.025288	2.564032	Up	microseminoprotein beta
HOXD11	0.893881	0.012209	0.028085	2.521107	Up	homeobox D11
CYP24A1	0.983436	0.014553	0.032593	2.457378	Up	cytochrome P450 family 24 subfamily A member 1
CRIP1	-2.21326	1.64E-33	5.88E-30	-13.6736	Down	cysteine rich protein 1
SLC14A2	-3.19781	1.18E-27	1.19E-24	-12.0639	Down	solute carrier family 14 member 2
TPPP	-2.09047	5.93E-27	5.57E-24	-11.8667	Down	tubulin polymerization promoting protein
FZD7	-1.16118	1.62E-25	1.12E-22	-11.4593	Down	frizzled class receptor 7
C6	-3.12355	3.56E-22	1.17E-19	-10.4885	Down	complement C6
FAM151A	-3.18879	1.88E-21	5.14E-19	-10.2734	Down	family with sequence similarity 151 member A
PMP22	-1.19984	2.15E-20	4.49E-18	-9.95445	Down	peripheral myelin protein 22
ZDHHC11B	-2.13041	2.78E-20	5.62E-18	-9.92051	Down	zinc finger DHHC-type containing 11B
UGT1A4	-4.1168	1.27E-19	2.28E-17	-9.71921	Down	UDP glucuronosyltransferase family 1 member A4
SLC28A2	-3.23899	2.05E-19	3.52E-17	-9.65468	Down	solute carrier family 28 member 2
UGT3A1	-3.67923	2.92E-19	4.86E-17	-9.60734	Down	UDP glycosyltransferase family 3 member A1
ITIH3	-2.02559	3.21E-19	5.22E-17	-9.59446	Down	inter-alpha-trypsin inhibitor heavy chain 3
MATN2	-1.15557	4.64E-19	7.02E-17	-9.54497	Down	matrilin 2
CDK20	-1.21979	9.37E-19	1.28E-16	-9.45025	Down	cyclin dependent kinase 20
ACOT12	-3.39435	1.21E-18	1.57E-16	-9.41609	Down	acyl-CoA thioesterase 12

UGT1A3	-3.92715	2.12E-18	2.56E-16	-9.33926	Down	UDP glucuronosyltransferase family 1 member A3
TMEM252	-3.13515	2.15E-18	2.56E-16	-9.33766	Down	transmembrane protein 252
PAQR5	-1.46024	2.16E-18	2.56E-16	-9.33679	Down	progestin and adipoQ receptor family member 5
CDHR1	-2.25431	5.45E-18	5.78E-16	-9.21022	Down	cadherin related family member 1
OTOP3	-3.25374	1.41E-17	1.36E-15	-9.07929	Down	otopetrin 3
RGS13	-1.73582	1.84E-17	1.73E-15	-9.04214	Down	regulator of G protein signaling 13
ALDOC	-1.2969	2.26E-17	2.09E-15	-9.01374	Down	aldolase, fructose-bisphosphate C
ADIRF	-1.80928	2.28E-17	2.10E-15	-9.0124	Down	adipogenesis regulatory factor
SLC23A3	-1.99851	3.29E-17	2.92E-15	-8.9618	Down	solute carrier family 23 member 3
BCO2	-1.18586	4.39E-17	3.72E-15	-8.92141	Down	beta-carotene oxygenase 2
SLC5A4	-2.55701	4.53E-17	3.80E-15	-8.91689	Down	solute carrier family 5 member 4
CUBN	-3.6901	4.74E-17	3.89E-15	-8.91073	Down	cubilin
LRAT	-2.4987	8.61E-17	6.54E-15	-8.82703	Down	lecithin retinol acyltransferase
CYP4F2	-2.87167	9.08E-17	6.82E-15	-8.81951	Down	cytochrome P450 family 4 subfamily F member 2
ABCC2	-2.18275	9.23E-17	6.85E-15	-8.81729	Down	ATP binding cassette subfamily C member 2
AGXT2	-3.68568	1.52E-16	1.07E-14	-8.74699	Down	alanine--glyoxylate aminotransferase 2
CBS	-1.51748	1.66E-16	1.16E-14	-8.73484	Down	cystathionine beta-synthase
CNTFR	-3.25539	2.22E-16	1.55E-14	-8.69306	Down	ciliary neurotrophic factor receptor
TM4SF4	-2.44288	3.14E-16	2.12E-14	-8.64399	Down	transmembrane 4 L six family member 4
NELL2	-1.3007	3.48E-16	2.31E-14	-8.62934	Down	neural EGFL like 2
PFN2	-0.83983	6.41E-16	3.90E-14	-8.54233	Down	profilin 2
PEPD	-1.17964	2.26E-15	1.28E-13	-8.36063	Down	peptidase D
SOAT2	-3.17835	2.95E-15	1.64E-13	-8.3219	Down	sterol O-acyltransferase 2
MAOB	-1.63372	3.04E-15	1.68E-13	-8.31775	Down	monoamine oxidase B
CYP2S1	-1.12586	3.50E-15	1.90E-13	-8.29704	Down	cytochrome P450 family 2 subfamily S member 1
SCAPER	-1.01369	3.96E-15	2.11E-13	-8.27891	Down	S-phase cyclin A associated protein in the ER
ABCG2	-2.22885	4.53E-15	2.37E-13	-8.25928	Down	ATP binding cassette subfamily G member 2 (Junior blood group)
EML6	-1.17263	4.71E-15	2.45E-13	-8.25382	Down	EMAP like 6
KCNH6	-2.35211	4.85E-15	2.51E-13	-8.24938	Down	potassium voltage-gated channel subfamily H member 6
AADAC	-2.67676	5.65E-15	2.90E-13	-8.22705	Down	arylacetamide deacetylase
GAL3ST1	-1.67372	1.00E-14	4.93E-13	-8.14304	Down	galactose-3-O-sulfotransferase 1
ZDHHC11	-1.39477	1.06E-14	5.20E-13	-8.13414	Down	zinc finger DHHC-type containing 11
ELL3	-1.02261	1.31E-14	6.29E-13	-8.10372	Down	elongation factor for RNA polymerase II 3
FLVCR1	-1.3377	1.68E-14	7.80E-13	-8.06665	Down	FLVCR heme transporter 1
TRPV3	-1.77064	2.14E-14	9.80E-13	-8.03065	Down	transient receptor potential cation channel subfamily V member 3
HSD3B1	-2.62228	2.54E-14	1.13E-12	-8.00527	Down	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 1
TPPP3	-0.94721	2.61E-14	1.16E-12	-8.00098	Down	tubulin polymerization promoting protein family member 3
MYOM3	-1.45464	2.95E-14	1.29E-12	-7.98297	Down	myomesin 3
CYP3A4	-3.1114	3.68E-14	1.56E-12	-7.94983	Down	cytochrome P450 family 3 subfamily A member 4
APOA1	-3.40113	4.20E-14	1.75E-12	-7.92984	Down	apolipoprotein A1
NAALADL1	-1.91193	4.38E-14	1.81E-12	-7.92345	Down	N-acetylated alpha-linked acidic dipeptidase like

						1
ANXA13	-1.2634	4.39E-14	1.81E-12	-7.92319	Down	annexin A13
SLC34A3	-2.79268	6.68E-14	2.68E-12	-7.86023	Down	solute carrier family 34 member 3
FOXD1	-2.83812	8.13E-14	3.17E-12	-7.83055	Down	forkhead box D1
FAM47E	-1.46799	1.30E-13	4.89E-12	-7.75971	Down	family with sequence similarity 47 member E
SLC46A3	-0.91329	1.73E-13	6.41E-12	-7.71553	Down	solute carrier family 46 member 3
MYBL1	-1.04112	1.97E-13	7.22E-12	-7.69601	Down	MYB proto-oncogene like 1
SAT2	-0.84324	1.98E-13	7.24E-12	-7.69511	Down	spermidine/spermine N1-acetyltransferase family member 2
TRPM6	-1.72394	2.03E-13	7.35E-12	-7.69187	Down	transient receptor potential cation channel subfamily M member 6
CDC14A	-0.90705	2.03E-13	7.35E-12	-7.69159	Down	cell division cycle 14A
UGT1A5	-3.21401	2.62E-13	9.21E-12	-7.6525	Down	UDP glucuronosyltransferase family 1 member A5
HTR1D	-1.56585	2.73E-13	9.56E-12	-7.64637	Down	5-hydroxytryptamine receptor 1D
PLB1	-1.74078	3.54E-13	1.21E-11	-7.60622	Down	phospholipase B1
ABCB1	-1.53026	3.72E-13	1.27E-11	-7.5985	Down	ATP binding cassette subfamily B member 1
COL17A1	-1.02976	3.80E-13	1.29E-11	-7.59542	Down	collagen type XVII alpha 1 chain
PTGR1	-1.32147	5.43E-13	1.78E-11	-7.54037	Down	prostaglandin reductase 1
ASPA	-1.36715	5.75E-13	1.88E-11	-7.53125	Down	aspartoacylase
TNNC2	-2.07104	6.16E-13	1.99E-11	-7.52068	Down	troponin C2, fast skeletal type
FMO5	-1.22637	6.41E-13	2.06E-11	-7.51451	Down	flavin containing dimethylaniline monoxygenase 5
GUCA2B	-2.92841	7.10E-13	2.25E-11	-7.49858	Down	guanylate cyclase activator 2B
FBP1	-1.21929	7.22E-13	2.28E-11	-7.49598	Down	fructose-bisphosphatase 1
SULT2B1	-1.27523	7.95E-13	2.48E-11	-7.48104	Down	sulfotransferase family 2B member 1
ZSWIM5	-1.02198	8.13E-13	2.53E-11	-7.47756	Down	zinc finger SWIM-type containing 5
SERPINA9	-2.96523	8.28E-13	2.57E-11	-7.47476	Down	serpin family A member 9
CYP3A7	-2.47734	8.58E-13	2.63E-11	-7.46912	Down	cytochrome P450 family 3 subfamily A member 7
GDPD2	-1.94584	8.59E-13	2.63E-11	-7.46896	Down	glycerophosphodiester phosphodiesterase domain containing 2
FAM25C	-3.97397	9.00E-13	2.75E-11	-7.4617	Down	family with sequence similarity 25 member C
SLC36A1	-0.94089	1.02E-12	3.10E-11	-7.44175	Down	solute carrier family 36 member 1
MEP1B	-2.43255	1.06E-12	3.20E-11	-7.43605	Down	meprin A subunit beta
NAT8	-3.44665	1.10E-12	3.29E-11	-7.43085	Down	N-acetyltransferase 8 (putative)
MS4A10	-2.77504	1.20E-12	3.59E-11	-7.41637	Down	membrane spanning 4-domains A10
FMO1	-2.29273	1.26E-12	3.72E-11	-7.40958	Down	flavin containing dimethylaniline monoxygenase 1
SSUH2	-1.37876	1.35E-12	3.97E-11	-7.39896	Down	ssu-2 homolog
AKR1B10	-1.37891	1.45E-12	4.26E-11	-7.38699	Down	aldo-keto reductase family 1 member B10
FADS6	-2.21842	1.50E-12	4.37E-11	-7.38237	Down	fatty acid desaturase 6
RHOBTB2	-0.88794	1.50E-12	4.38E-11	-7.38151	Down	Rho related BTB domain containing 2
SLC19A3	-1.15111	1.56E-12	4.52E-11	-7.3761	Down	solute carrier family 19 member 3
UGT1A10	-1.88552	1.64E-12	4.71E-11	-7.36762	Down	UDP glucuronosyltransferase family 1 member A10
PLA2R1	-0.8442	1.69E-12	4.84E-11	-7.36278	Down	phospholipase A2 receptor 1
DHDH	-2.43704	2.24E-12	6.25E-11	-7.31855	Down	dihydrodiol dehydrogenase
MAF	-1.02611	3.06E-12	8.39E-11	-7.26944	Down	MAF bZIP transcription factor

RUNDC3B	-1.23978	3.06E-12	8.39E-11	-7.26929	Down	RUN domain containing 3B
SLC5A12	-2.88443	3.30E-12	8.94E-11	-7.25732	Down	solute carrier family 5 member 12
TRHDE	-1.67892	3.38E-12	9.13E-11	-7.25355	Down	thyrotropin releasing hormone degrading enzyme
BPHL	-0.87438	3.64E-12	9.74E-11	-7.24172	Down	biphenyl hydrolase like
SLC13A1	-2.95032	3.92E-12	1.04E-10	-7.23013	Down	solute carrier family 13 member 1
ACE2	-1.77853	4.40E-12	1.15E-10	-7.21176	Down	angiotensin converting enzyme 2
CD207	-1.49904	4.44E-12	1.16E-10	-7.21022	Down	CD207 molecule
PLCH2	-0.95494	4.76E-12	1.24E-10	-7.19905	Down	phospholipase C eta 2
C9orf24	-2.27676	5.08E-12	1.31E-10	-7.18886	Down	chromosome 9 open reading frame 24
F10	-1.09091	5.33E-12	1.37E-10	-7.18116	Down	coagulation factor X
GSTA2	-2.91791	5.78E-12	1.47E-10	-7.16796	Down	glutathione S-transferase alpha 2
MME	-1.72511	6.07E-12	1.53E-10	-7.16031	Down	membrane metalloendopeptidase
SUSD2	-2.16035	6.33E-12	1.59E-10	-7.15351	Down	sushi domain containing 2
LAMA1	-1.4208	6.58E-12	1.65E-10	-7.14721	Down	laminin subunit alpha 1
SLC6A4	-2.52069	7.51E-12	1.86E-10	-7.12609	Down	solute carrier family 6 member 4
FABP6	-2.62289	8.00E-12	1.97E-10	-7.11604	Down	fatty acid binding protein 6
GSTA1	-2.45544	8.03E-12	1.98E-10	-7.11533	Down	glutathione S-transferase alpha 1
GCNT4	-1.47494	8.22E-12	2.02E-10	-7.11149	Down	glucosaminyl (N-acetyl) transferase 4
TFEC	-0.98089	8.34E-12	2.04E-10	-7.10921	Down	transcription factor EC
NR1I3	-1.61669	8.37E-12	2.04E-10	-7.10875	Down	nuclear receptor subfamily 1 group I member 3
FRMD1	-2.39398	8.49E-12	2.07E-10	-7.10638	Down	FERM domain containing 1
MGAM	-2.08963	9.15E-12	2.21E-10	-7.09431	Down	maltase-glucoamylase
ACSF2	-1.08441	9.67E-12	2.33E-10	-7.08536	Down	acyl-CoA synthetase family member 2
SLC28A1	-2.64247	9.95E-12	2.38E-10	-7.08076	Down	solute carrier family 28 member 1
EMB	-0.86395	1.02E-11	2.43E-10	-7.07721	Down	embigin
C2orf88	-1.33818	1.14E-11	2.68E-10	-7.05839	Down	chromosome 2 open reading frame 88
MRO	-1.95637	1.16E-11	2.71E-10	-7.05654	Down	maestro
SMIM24	-1.90059	1.17E-11	2.74E-10	-7.05448	Down	small integral membrane protein 24
FCRL4	-1.85169	1.22E-11	2.84E-10	-7.04782	Down	Fc receptor like 4
CYP2J2	-1.5037	1.39E-11	3.19E-10	-7.02658	Down	cytochrome P450 family 2 subfamily J member 2
CYP4F3	-1.11608	1.40E-11	3.21E-10	-7.02513	Down	cytochrome P450 family 4 subfamily F member 3
CD8B	-1.02494	1.45E-11	3.30E-10	-7.02009	Down	CD8b molecule
SFRP5	-2.62926	1.47E-11	3.34E-10	-7.01795	Down	secreted frizzled related protein 5
SLC22A4	-1.07989	1.50E-11	3.39E-10	-7.01459	Down	solute carrier family 22 member 4
OAT	-1.39181	1.50E-11	3.39E-10	-7.01427	Down	ornithine aminotransferase
CHN2	-1.05728	2.10E-11	4.60E-10	-6.95916	Down	chimerin 2
PKLR	-2.28927	2.12E-11	4.63E-10	-6.95779	Down	pyruvate kinase L/R
MGAT3	-0.88505	2.18E-11	4.74E-10	-6.95311	Down	beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase
PREPL	-0.91789	2.30E-11	4.96E-10	-6.94468	Down	prolyl endopeptidase like
PDK2	-0.82657	2.31E-11	4.97E-10	-6.94383	Down	pyruvate dehydrogenase kinase 2
TREH	-2.04241	2.47E-11	5.28E-10	-6.93272	Down	trehalase
DPEP1	-2.10782	2.48E-11	5.28E-10	-6.93243	Down	dipeptidase 1

REEP6	-1.78055	3.09E-11	6.39E-10	-6.89615	Down	receptor accessory protein 6
APOB	-2.54565	3.13E-11	6.43E-10	-6.89425	Down	apolipoprotein B
PRODH	-1.9383	3.15E-11	6.46E-10	-6.89306	Down	proline dehydrogenase 1
CES2	-1.27663	3.52E-11	7.17E-10	-6.87467	Down	carboxylesterase 2
SLC22A5	-1.03939	4.30E-11	8.62E-10	-6.84185	Down	solute carrier family 22 member 5
SLC35G1	-0.98131	5.10E-11	1.00E-09	-6.81364	Down	solute carrier family 35 member G1
CPO	-2.79382	5.23E-11	1.02E-09	-6.80936	Down	carboxypeptidase O
CNGA1	-1.32981	6.08E-11	1.16E-09	-6.7843	Down	cyclic nucleotide gated channel subunit alpha 1
DPP4	-1.3168	6.14E-11	1.17E-09	-6.78267	Down	dipeptidyl peptidase 4
GNG4	-1.22678	6.45E-11	1.22E-09	-6.77443	Down	G protein subunit gamma 4
PON3	-1.20007	6.87E-11	1.29E-09	-6.76408	Down	paraoxonase 3
MYZAP	-0.91344	6.97E-11	1.30E-09	-6.76174	Down	myocardial zonula adherens protein
SLC1A7	-2.07887	8.45E-11	1.56E-09	-6.72951	Down	solute carrier family 1 member 7
SLC39A4	-1.19322	8.50E-11	1.57E-09	-6.72849	Down	solute carrier family 39 member 4
SLC10A2	-2.33718	8.51E-11	1.57E-09	-6.72827	Down	solute carrier family 10 member 2
ABHD6	-0.91209	8.73E-11	1.61E-09	-6.7241	Down	abhydrolase domain containing 6, acylglycerol lipase
ACOX2	-0.99032	9.17E-11	1.68E-09	-6.71591	Down	acyl-CoA oxidase 2
XPNPEP2	-2.20521	9.35E-11	1.71E-09	-6.71253	Down	X-prolyl aminopeptidase 2
SOX8	-1.42903	9.36E-11	1.71E-09	-6.71239	Down	SRY-box transcription factor 8
DNASE1	-1.81195	9.40E-11	1.71E-09	-6.71174	Down	deoxyribonuclease 1
TMIGD1	-1.82521	9.62E-11	1.75E-09	-6.70774	Down	transmembrane and immunoglobulin domain containing 1
CYP2B6	-1.70524	1.01E-10	1.83E-09	-6.69939	Down	cytochrome P450 family 2 subfamily B member 6
ACE	-1.55454	1.24E-10	2.20E-09	-6.665	Down	angiotensin I converting enzyme
PHLPP2	-1.10875	1.26E-10	2.23E-09	-6.66286	Down	PH domain and leucine rich repeat protein phosphatase 2
SLC23A1	-1.83352	1.35E-10	2.38E-09	-6.65053	Down	solute carrier family 23 member 1
SLC6A20	-1.23448	1.43E-10	2.50E-09	-6.64136	Down	solute carrier family 6 member 20
NPY	-2.32012	1.52E-10	2.63E-09	-6.63102	Down	neuropeptide Y
SLC9A3R1	-0.83951	1.58E-10	2.72E-09	-6.62478	Down	SLC9A3 regulator 1
USP2	-1.44203	1.61E-10	2.77E-09	-6.62081	Down	ubiquitin specific peptidase 2
SLC15A1	-1.83073	1.94E-10	3.27E-09	-6.58979	Down	solute carrier family 15 member 1
GSTA5	-2.53797	1.98E-10	3.34E-09	-6.58647	Down	glutathione S-transferase alpha 5
AICDA	-1.8617	2.04E-10	3.42E-09	-6.5813	Down	activation induced cytidine deaminase
HEBP1	-0.86362	2.11E-10	3.53E-09	-6.57555	Down	heme binding protein 1
CHAD	-1.55517	2.22E-10	3.71E-09	-6.56646	Down	chondroadherin
MS4A8	-1.57781	2.34E-10	3.88E-09	-6.55754	Down	membrane spanning 4-domains A8
GRIA4	-1.07611	2.40E-10	3.97E-09	-6.55303	Down	glutamate ionotropic receptor AMPA type subunit 4
UGT1A1	-2.50883	2.50E-10	4.10E-09	-6.54628	Down	UDP glucuronosyltransferase family 1 member A1
SEC14L2	-1.0591	2.55E-10	4.17E-09	-6.54327	Down	SEC14 like lipid binding 2
KLKB1	-1.35701	2.61E-10	4.27E-09	-6.53881	Down	kallikrein B1
IGSF9	-1.82372	2.77E-10	4.50E-09	-6.52874	Down	immunoglobulin superfamily member 9
UGT1A6	-2.15218	2.93E-10	4.73E-09	-6.51939	Down	UDP glucuronosyltransferase family 1 member A6

TMEM229A	-1.80774	3.27E-10	5.19E-09	-6.50028	Down	transmembrane protein 229A
OTOP2	-2.44849	3.71E-10	5.82E-09	-6.47875	Down	otopetrin 2
CMBL	-1.11509	3.79E-10	5.93E-09	-6.47507	Down	carboxymethylenebutenolidase homolog
CCR9	-1.36986	4.09E-10	6.35E-09	-6.46209	Down	C-C motif chemokine receptor 9
CREB3L3	-1.90211	4.34E-10	6.70E-09	-6.45208	Down	cAMP responsive element binding protein 3 like 3
SLC25A34	-0.99999	4.59E-10	7.08E-09	-6.44215	Down	solute carrier family 25 member 34
RHOU	-0.83838	4.85E-10	7.45E-09	-6.43286	Down	ras homolog family member U
AQP7	-1.57299	5.05E-10	7.74E-09	-6.42582	Down	aquaporin 7
PDXP	-0.8554	5.15E-10	7.88E-09	-6.42237	Down	pyridoxal phosphatase
SLC2A5	-1.05554	5.42E-10	8.24E-09	-6.41355	Down	solute carrier family 2 member 5
SLC1A1	-1.26045	5.51E-10	8.36E-09	-6.41061	Down	solute carrier family 1 member 1
SLC7A9	-2.04599	5.53E-10	8.38E-09	-6.4101	Down	solute carrier family 7 member 9
ZNF488	-1.45706	5.82E-10	8.77E-09	-6.40122	Down	zinc finger protein 488
SLC13A2	-1.76107	5.86E-10	8.81E-09	-6.40005	Down	solute carrier family 13 member 2
SLC5A11	-2.08823	5.93E-10	8.90E-09	-6.39791	Down	solute carrier family 5 member 11
GDA	-1.28752	6.25E-10	9.34E-09	-6.38878	Down	guanine deaminase
GUCA2A	-1.91011	6.40E-10	9.54E-09	-6.38465	Down	guanylate cyclase activator 2A
KCNG1	-1.01451	6.67E-10	9.90E-09	-6.37763	Down	potassium voltage-gated channel modifier subfamily G member 1
CDHR2	-1.28806	6.76E-10	1.00E-08	-6.3753	Down	cadherin related family member 2
CYBRD1	-1.01838	7.08E-10	1.04E-08	-6.36709	Down	cytochrome b reductase 1
APOM	-1.12151	7.13E-10	1.05E-08	-6.3661	Down	apolipoprotein M
HSD17B2	-1.21716	7.16E-10	1.05E-08	-6.36535	Down	hydroxysteroid 17-beta dehydrogenase 2
ENTPD5	-0.98865	7.46E-10	1.09E-08	-6.35809	Down	ectonucleoside triphosphate diphosphohydrolase 5 (inactive)
SH2D6	-1.13503	8.34E-10	1.21E-08	-6.33865	Down	SH2 domain containing 6
ASAH2	-1.42529	8.96E-10	1.29E-08	-6.32615	Down	N-acylsphingosine amidohydrolase 2
SLC27A2	-0.85582	9.10E-10	1.30E-08	-6.32353	Down	solute carrier family 27 member 2
CYP4F12	-1.12487	1.05E-09	1.49E-08	-6.2983	Down	cytochrome P450 family 4 subfamily F member 12
SLC6A19	-1.98535	1.06E-09	1.50E-08	-6.29597	Down	solute carrier family 6 member 19
CBR1	-0.91008	1.10E-09	1.55E-08	-6.29043	Down	carbonyl reductase 1
SMLR1	-2.39032	1.26E-09	1.75E-08	-6.26669	Down	small leucine rich protein 1
KHK	-1.62288	1.27E-09	1.76E-08	-6.26531	Down	ketohexokinase
AOC1	-1.11933	1.47E-09	2.00E-08	-6.23913	Down	amine oxidase copper containing 1
SHBG	-2.33864	1.48E-09	2.01E-08	-6.23782	Down	sex hormone binding globulin
CYP2D6	-1.5921	1.60E-09	2.15E-08	-6.22451	Down	cytochrome P450 family 2 subfamily D member 6
LGALS2	-0.93835	1.61E-09	2.16E-08	-6.22332	Down	galectin 2
DEPDC7	-1.06058	1.63E-09	2.19E-08	-6.22086	Down	DEP domain containing 7
GRAMD1C	-0.93424	1.74E-09	2.33E-08	-6.20939	Down	GRAM domain containing 1C
ABCG5	-1.43248	2.02E-09	2.66E-08	-6.1828	Down	ATP binding cassette subfamily G member 5
PANK1	-0.82879	2.11E-09	2.77E-08	-6.17523	Down	pantothenate kinase 1
APOA4	-2.4464	2.16E-09	2.83E-08	-6.17079	Down	apolipoprotein A4
GATM	-1.14873	2.17E-09	2.84E-08	-6.17025	Down	glycine amidinotransferase
SEMA6C	-0.90344	2.17E-09	2.84E-08	-6.16999	Down	semaphorin 6C

RHOD	-0.90768	2.30E-09	2.99E-08	-6.15979	Down	ras homolog family member D
PRKG2	-1.7059	2.38E-09	3.08E-08	-6.15369	Down	protein kinase cGMP-dependent 2
OSGIN1	-0.97868	2.41E-09	3.11E-08	-6.15145	Down	oxidative stress induced growth inhibitor 1
SLC17A8	-2.13543	2.47E-09	3.18E-08	-6.14711	Down	solute carrier family 17 member 8
CYP3A5	-1.15695	2.50E-09	3.21E-08	-6.14495	Down	cytochrome P450 family 3 subfamily A member 5
ENPEP	-1.85312	2.58E-09	3.30E-08	-6.13904	Down	glutamyl aminopeptidase
SCIN	-1.23591	2.65E-09	3.37E-08	-6.13474	Down	scinderin
AGMO	-1.31486	3.07E-09	3.89E-08	-6.10807	Down	alkylglycerol monooxygenase
CDHR5	-1.41432	3.09E-09	3.90E-08	-6.10699	Down	cadherin related family member 5
EDN3	-1.16923	3.38E-09	4.22E-08	-6.09079	Down	endothelin 3
FCER1A	-0.96786	3.41E-09	4.25E-08	-6.08937	Down	Fc fragment of IgE receptor Ia
SLC16A9	-1.45271	3.48E-09	4.33E-08	-6.08574	Down	solute carrier family 16 member 9
CYP2C8	-1.46689	3.49E-09	4.34E-08	-6.08541	Down	cytochrome P450 family 2 subfamily C member 8
TMEM25	-0.95952	3.60E-09	4.47E-08	-6.07956	Down	transmembrane protein 25
APOC3	-2.53337	3.74E-09	4.62E-08	-6.07287	Down	apolipoprotein C3
BCAN	-1.21451	3.88E-09	4.78E-08	-6.06603	Down	brevican
SLC5A9	-1.61954	4.09E-09	5.02E-08	-6.05656	Down	solute carrier family 5 member 9
MMP28	-0.98946	4.39E-09	5.35E-08	-6.0438	Down	matrix metallopeptidase 28
GFRA1	-0.90126	4.42E-09	5.38E-08	-6.04274	Down	GDNF family receptor alpha 1
GP2	-1.43768	4.86E-09	5.86E-08	-6.02543	Down	glycoprotein 2
ARHGDIG	-1.23072	5.13E-09	6.13E-08	-6.01575	Down	Rho GDP dissociation inhibitor gamma
MT1F	-1.23495	5.54E-09	6.57E-08	-6.00194	Down	metallothionein 1F
BEND7	-0.94152	5.84E-09	6.88E-08	-5.99219	Down	BEN domain containing 7
CTSE	-1.15768	5.84E-09	6.88E-08	-5.99212	Down	cathepsin E
PLEKHG6	-1.01281	6.39E-09	7.44E-08	-5.97595	Down	pleckstrin homology and RhoGEF domain containing G6
LCN15	-2.14998	6.77E-09	7.86E-08	-5.96531	Down	lipocalin 15
NAGS	-0.95765	7.16E-09	8.29E-08	-5.95516	Down	N-acetylglutamate synthase
PRAP1	-1.51495	7.47E-09	8.62E-08	-5.94737	Down	proline rich acidic protein 1
CYP2C18	-1.3031	7.65E-09	8.75E-08	-5.94295	Down	cytochrome P450 family 2 subfamily C member 18
TM4SF5	-1.71219	7.69E-09	8.79E-08	-5.94204	Down	transmembrane 4 L six family member 5
SUGCT	-0.93957	8.06E-09	9.16E-08	-5.93344	Down	succinyl-CoA:glutarate-CoA transferase
PFKFB4	-0.83586	8.14E-09	9.24E-08	-5.93167	Down	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
FCAMR	-1.32453	8.98E-09	1.01E-07	-5.91365	Down	Fc fragment of IgA and IgM receptor
PDZK1	-1.84999	9.16E-09	1.03E-07	-5.91003	Down	PDZ domain containing 1
NPC1L1	-1.62971	9.34E-09	1.05E-07	-5.90638	Down	NPC1 like intracellular cholesterol transporter 1
DHRS11	-1.06591	9.73E-09	1.08E-07	-5.89885	Down	dehydrogenase/reductase 11
RAB17	-1.24238	1.02E-08	1.12E-07	-5.89064	Down	RAB17, member RAS oncogene family
ACY1	-0.87198	1.08E-08	1.18E-07	-5.87912	Down	aminoacylase 1
CHRNA7	-1.24456	1.09E-08	1.19E-07	-5.87784	Down	cholinergic receptor nicotinic alpha 7 subunit
CXADR	-1.02836	1.12E-08	1.22E-07	-5.87312	Down	CXADR Ig-like cell adhesion molecule
CLDN8	-2.70297	1.13E-08	1.23E-07	-5.87109	Down	claudin 8
KDM8	-1.09656	1.13E-08	1.23E-07	-5.87085	Down	lysine demethylase 8

AMN	-1.27415	1.14E-08	1.24E-07	-5.86903	Down	amnion associated transmembrane protein
SYT8	-1.5447	1.15E-08	1.24E-07	-5.86844	Down	synaptotagmin 8
GGT1	-0.91761	1.16E-08	1.25E-07	-5.86606	Down	gamma-glutamyltransferase 1
SI	-1.54949	1.24E-08	1.33E-07	-5.85365	Down	sucrase-isomaltase
DDC	-1.16774	1.32E-08	1.40E-07	-5.84303	Down	dopa decarboxylase
IGSF23	-2.33986	1.39E-08	1.47E-07	-5.83324	Down	immunoglobulin superfamily member 23
THSD4	-1.00421	1.40E-08	1.48E-07	-5.83164	Down	thrombospondin type 1 domain containing 4
B4GALNT2	-1.40965	1.49E-08	1.57E-07	-5.81983	Down	beta-1,4-N-acetyl-galactosaminyltransferase 2
C1orf115	-0.89347	1.53E-08	1.60E-07	-5.81488	Down	chromosome 1 open reading frame 115
BACH2	-1.14297	1.66E-08	1.72E-07	-5.80037	Down	BTB domain and CNC homolog 2
INPP5J	-1.10762	1.71E-08	1.77E-07	-5.79462	Down	inositol polyphosphate-5-phosphatase J
UGT1A8	-1.97633	1.79E-08	1.84E-07	-5.78625	Down	UDP glucuronosyltransferase family 1 member A8
PRLR	-0.95366	1.89E-08	1.93E-07	-5.77596	Down	prolactin receptor
SLC3A1	-1.48191	2.02E-08	2.05E-07	-5.76372	Down	solute carrier family 3 member 1
TM6SF2	-1.43253	2.09E-08	2.11E-07	-5.75706	Down	transmembrane 6 superfamily member 2
DAB1	-1.59473	2.10E-08	2.12E-07	-5.75608	Down	DAB adaptor protein 1
SLC17A4	-1.18253	2.20E-08	2.21E-07	-5.74777	Down	solute carrier family 17 member 4
RGS11	-0.95369	2.33E-08	2.33E-07	-5.73637	Down	regulator of G protein signaling 11
TMEM220	-0.90811	2.35E-08	2.34E-07	-5.73502	Down	transmembrane protein 220
UGT2B7	-1.39693	2.44E-08	2.43E-07	-5.72779	Down	UDP glucuronosyltransferase family 2 member B7
TUBAL3	-1.15718	2.64E-08	2.62E-07	-5.71276	Down	tubulin alpha like 3
IGSF3	-0.82829	2.90E-08	2.84E-07	-5.69525	Down	immunoglobulin superfamily member 3
TF	-1.09342	3.17E-08	3.09E-07	-5.67842	Down	transferrin
MAOA	-1.01987	3.40E-08	3.29E-07	-5.6653	Down	monoamine oxidase A
RNF128	-0.91581	3.42E-08	3.31E-07	-5.66397	Down	ring finger protein 128
MEP1A	-1.40203	3.49E-08	3.37E-07	-5.66025	Down	meprin A subunit alpha
LEAP2	-1.37703	3.53E-08	3.41E-07	-5.65804	Down	liver enriched antimicrobial peptide 2
EPB41L4B	-0.93804	3.73E-08	3.58E-07	-5.64748	Down	erythrocyte membrane protein band 4.1 like 4B
OIT3	-1.11141	3.92E-08	3.74E-07	-5.6381	Down	oncoprotein induced transcript 3
IYD	-0.99919	4.10E-08	3.91E-07	-5.62969	Down	iodotyrosine deiodinase
ARL14	-0.87251	4.13E-08	3.94E-07	-5.62816	Down	ADP ribosylation factor like GTPase 14
PCOLCE2	-1.94355	4.29E-08	4.08E-07	-5.62092	Down	procollagen C-endopeptidase enhancer 2
GGN	-1.38702	4.71E-08	4.43E-07	-5.60321	Down	gametogenetin
ENPP3	-1.30749	4.85E-08	4.55E-07	-5.59761	Down	ectonucleotide pyrophosphatase/phosphodiesterase 3
CLDN15	-0.96287	5.17E-08	4.83E-07	-5.58541	Down	claudin 15
CD1C	-1.01938	5.45E-08	5.07E-07	-5.57547	Down	CD1c molecule
LCT	-2.00487	5.73E-08	5.33E-07	-5.56556	Down	lactase
SEMA3B	-0.85542	5.81E-08	5.39E-07	-5.56299	Down	semaphorin 3B
CHP2	-1.16747	6.06E-08	5.59E-07	-5.55489	Down	calcineurin like EF-hand protein 2
DTX1	-0.86266	6.30E-08	5.78E-07	-5.54761	Down	deltex E3 ubiquitin ligase 1
SULT2A1	-2.00364	6.65E-08	6.08E-07	-5.5369	Down	sulfotransferase family 2A member 1
SLC30A2	-1.14913	7.89E-08	7.12E-07	-5.504	Down	solute carrier family 30 member 2

UGT2A3	-1.55446	8.31E-08	7.47E-07	-5.49388	Down	UDP glucuronosyltransferase family 2 member A3
KCNJ13	-1.94285	8.65E-08	7.73E-07	-5.4861	Down	potassium inwardly rectifying channel subfamily J member 13
DGAT1	-0.90409	8.71E-08	7.78E-07	-5.48481	Down	diacylglycerol O-acyltransferase 1
PCK2	-0.83498	9.01E-08	8.02E-07	-5.47827	Down	phosphoenolpyruvate carboxykinase 2, mitochondrial
BTNL2	-2.11909	9.03E-08	8.03E-07	-5.4777	Down	butyrophilin like 2
SLC34A2	-1.33318	9.33E-08	8.27E-07	-5.47137	Down	solute carrier family 34 member 2
C10orf99	-1.47863	9.55E-08	8.44E-07	-5.46682	Down	chromosome 10 open reading frame 99
CRABP1	-1.69536	9.64E-08	8.51E-07	-5.46498	Down	cellular retinoic acid binding protein 1
CEACAM18	-2.05585	9.78E-08	8.62E-07	-5.46217	Down	CEA cell adhesion molecule 18
B4GALNT4	-0.84004	1.03E-07	9.03E-07	-5.45262	Down	beta-1,4-N-acetyl-galactosaminyltransferase 4
A1CF	-0.95687	1.04E-07	9.13E-07	-5.45008	Down	APOBEC1 complementation factor
GLP2R	-0.93091	1.07E-07	9.31E-07	-5.44549	Down	glucagon like peptide 2 receptor
SLC51B	-1.06236	1.10E-07	9.58E-07	-5.43936	Down	solute carrier family 51 subunit beta
ESPL1	-0.86331	1.15E-07	9.92E-07	-5.43117	Down	extra spindle pole bodies like 1, separase
SPIB	-0.97912	1.16E-07	1.00E-06	-5.42848	Down	Spi-B transcription factor
CHST6	-0.87059	1.18E-07	1.01E-06	-5.4261	Down	carbohydrate sulfotransferase 6
APOC2	-0.91731	1.46E-07	1.24E-06	-5.38341	Down	apolipoprotein C2
BEGAIN	-0.95788	1.53E-07	1.29E-06	-5.3747	Down	brain enriched guanylate kinase associated
MYO1A	-1.13185	1.53E-07	1.29E-06	-5.37464	Down	myosin IA
NTS	-1.82111	1.72E-07	1.43E-06	-5.35094	Down	neurotensin
MT1H	-1.38668	1.74E-07	1.44E-06	-5.34938	Down	metallothionein 1H
BMP3	-1.09531	1.77E-07	1.47E-06	-5.34555	Down	bone morphogenetic protein 3
SLC5A1	-1.25865	1.77E-07	1.47E-06	-5.3454	Down	solute carrier family 5 member 1
SULT1A2	-1.231	1.96E-07	1.60E-06	-5.32588	Down	sulfotransferase family 1A member 2
SEMA3G	-0.82641	2.02E-07	1.64E-06	-5.31959	Down	semaphorin 3G
SLC51A	-0.92287	2.02E-07	1.65E-06	-5.31901	Down	solute carrier family 51 subunit alpha
KCNJ3	-1.01778	2.14E-07	1.73E-06	-5.30815	Down	potassium inwardly rectifying channel subfamily J member 3
HMGCS2	-1.87833	2.21E-07	1.79E-06	-5.30122	Down	3-hydroxy-3-methylglutaryl-CoA synthase 2
SOWAHA	-1.02692	2.27E-07	1.83E-06	-5.29636	Down	sosondowah ankyrin repeat domain family member A
PBLD	-0.92684	2.29E-07	1.84E-06	-5.2944	Down	phenazine biosynthesis like protein domain containing
AATK	-0.9337	2.30E-07	1.84E-06	-5.29367	Down	apoptosis associated tyrosine kinase
PCK1	-1.81398	2.30E-07	1.84E-06	-5.29354	Down	phosphoenolpyruvate carboxykinase 1
CYP2C19	-1.90115	2.40E-07	1.92E-06	-5.2848	Down	cytochrome P450 family 2 subfamily C member 19
OSR2	-0.93518	2.50E-07	1.99E-06	-5.27705	Down	odd-skipped related transciption factor 2
DNAJB13	-1.51818	2.57E-07	2.04E-06	-5.27172	Down	DnaJ heat shock protein family (Hsp40) member B13
AQP3	-0.89529	2.57E-07	2.04E-06	-5.27161	Down	aquaporin 3 (Gill blood group)
TINAG	-1.01898	2.63E-07	2.08E-06	-5.26647	Down	tubulointerstitial nephritis antigen
MLXIPL	-1.18179	2.79E-07	2.20E-06	-5.25475	Down	MLX interacting protein like
PHGR1	-1.08838	2.80E-07	2.20E-06	-5.25432	Down	proline, histidine and glycine rich 1
FABP2	-1.29429	2.84E-07	2.23E-06	-5.25122	Down	fatty acid binding protein 2
VIPR1	-0.82569	3.26E-07	2.53E-06	-5.22356	Down	vasoactive intestinal peptide receptor 1

SLC2A2	-1.78781	3.48E-07	2.69E-06	-5.21048	Down	solute carrier family 2 member 2
TTC36	-1.50467	3.58E-07	2.76E-06	-5.20474	Down	tetratricopeptide repeat domain 36
HSD17B3	-1.43818	3.58E-07	2.76E-06	-5.20464	Down	hydroxysteroid 17-beta dehydrogenase 3
SERPINA5	-0.97668	3.66E-07	2.82E-06	-5.20034	Down	serpin family A member 5
F11	-1.3448	4.10E-07	3.12E-06	-5.17704	Down	coagulation factor XI
EVPL	-0.85841	4.29E-07	3.24E-06	-5.16792	Down	envoplakin
NCKAP5	-0.97004	4.58E-07	3.44E-06	-5.15459	Down	NCK associated protein 5
SLC9A2	-1.14633	4.85E-07	3.63E-06	-5.1428	Down	solute carrier family 9 member A2
ALPI	-1.46942	5.16E-07	3.82E-06	-5.13026	Down	alkaline phosphatase, intestinal
TUBB2B	-1.0163	5.56E-07	4.09E-06	-5.11503	Down	tubulin beta 2B class IIb
SOX6	-0.90407	5.90E-07	4.31E-06	-5.1027	Down	SRY-box transcription factor 6
NCCRP1	-1.08312	6.19E-07	4.49E-06	-5.09286	Down	NCCRP1, F-box associated domain containing
CALB1	-1.08596	6.21E-07	4.50E-06	-5.09232	Down	calbindin 1
SLC39A5	-1.02954	6.31E-07	4.57E-06	-5.089	Down	solute carrier family 39 member 5
GOLT1A	-1.22333	6.37E-07	4.61E-06	-5.08711	Down	golgi transport 1A
DEGS2	-0.91103	7.45E-07	5.29E-06	-5.05466	Down	delta 4-desaturase, sphingolipid 2
COBL	-0.82663	7.97E-07	5.63E-06	-5.04079	Down	cordon-bleu WH2 repeat protein
SHISA3	-1.28894	8.63E-07	6.06E-06	-5.02421	Down	shisa family member 3
VIL1	-1.04567	9.29E-07	6.48E-06	-5.00883	Down	villin 1
NPPC	-1.76393	1.04E-06	7.15E-06	-4.98631	Down	natriuretic peptide C
MT1A	-1.85094	1.07E-06	7.36E-06	-4.98019	Down	metallothionein 1A
SSTR1	-1.00082	1.09E-06	7.48E-06	-4.97566	Down	somatostatin receptor 1
B3GALT5	-0.88643	1.13E-06	7.70E-06	-4.96888	Down	beta-1,3-galactosyltransferase 5
SCTR	-1.3885	1.34E-06	8.98E-06	-4.93266	Down	secretin receptor
FGFR3	-0.8719	1.36E-06	9.11E-06	-4.92942	Down	fibroblast growth factor receptor 3
CDKN2B	-0.9211	1.39E-06	9.31E-06	-4.92435	Down	cyclin dependent kinase inhibitor 2B
EDN2	-1.35653	1.74E-06	1.13E-05	-4.87626	Down	endothelin 2
CR2	-1.27934	1.80E-06	1.17E-05	-4.86938	Down	complement C3d receptor 2
CAPN13	-1.2259	1.85E-06	1.20E-05	-4.86374	Down	calpain 13
ESPN	-0.95143	1.91E-06	1.23E-05	-4.85727	Down	espin
CYP2C9	-1.18688	2.02E-06	1.29E-05	-4.84482	Down	cytochrome P450 family 2 subfamily C member 9
MROH7	-0.9837	2.10E-06	1.34E-05	-4.83621	Down	maestro heat like repeat family member 7
AKR1B15	-0.87445	2.27E-06	1.44E-05	-4.82007	Down	aldo-keto reductase family 1 member B15
PHYHIPL	-1.09081	2.60E-06	1.63E-05	-4.79049	Down	phytanoyl-CoA 2-hydroxylase interacting protein like
TMEM236	-0.87545	2.62E-06	1.64E-05	-4.78928	Down	transmembrane protein 236
NR0B2	-1.16962	2.69E-06	1.67E-05	-4.78352	Down	nuclear receptor subfamily 0 group B member 2
CRYM	-1.05964	2.81E-06	1.74E-05	-4.7743	Down	crystallin mu
MAMDC2	-0.87796	2.81E-06	1.75E-05	-4.77401	Down	MAM domain containing 2
ABCG8	-1.10211	2.83E-06	1.76E-05	-4.77267	Down	ATP binding cassette subfamily G member 8
MOGAT2	-0.99828	2.86E-06	1.77E-05	-4.77038	Down	monoacylglycerol O-acyltransferase 2
PLA2G12B	-1.20738	3.41E-06	2.07E-05	-4.7317	Down	phospholipase A2 group XIIB
CA3	-1.05183	3.45E-06	2.10E-05	-4.72914	Down	carbonic anhydrase 3

GSTA3	-2.03323	3.58E-06	2.16E-05	-4.72141	Down	glutathione S-transferase alpha 3
MEF2B	-0.93771	3.68E-06	2.21E-05	-4.71546	Down	myocyte enhancer factor 2B
METTL7B	-0.82838	3.73E-06	2.24E-05	-4.71235	Down	methyltransferase like 7B
FCRL3	-0.98572	4.18E-06	2.48E-05	-4.68743	Down	Fc receptor like 3
MT1G	-1.00802	4.22E-06	2.50E-05	-4.68507	Down	metallothionein 1G
ARG2	-0.97106	4.23E-06	2.51E-05	-4.68479	Down	arginase 2
ERICH4	-1.53783	4.33E-06	2.55E-05	-4.67979	Down	glutamate rich 4
PDZD7	-0.87704	4.48E-06	2.63E-05	-4.67223	Down	PDZ domain containing 7
ANPEP	-1.02838	4.51E-06	2.65E-05	-4.67055	Down	alanyl aminopeptidase, membrane
GPD1	-1.14017	4.62E-06	2.70E-05	-4.66551	Down	glycerol-3-phosphate dehydrogenase 1
PDIA2	-1.10723	4.91E-06	2.86E-05	-4.65208	Down	protein disulfide isomerase family A member 2
NEU4	-1.05556	5.00E-06	2.91E-05	-4.648	Down	neuraminidase 4
IGSF10	-1.05489	5.01E-06	2.92E-05	-4.6473	Down	immunoglobulin superfamily member 10
CEACAM20	-1.56527	5.55E-06	3.20E-05	-4.62462	Down	CEA cell adhesion molecule 20
HNF4G	-0.97687	5.70E-06	3.27E-05	-4.61898	Down	hepatocyte nuclear factor 4 gamma
APOBEC1	-0.92689	6.00E-06	3.43E-05	-4.60758	Down	apolipoprotein B mRNA editing enzyme catalytic subunit 1
MALRD1	-1.22989	6.18E-06	3.51E-05	-4.60108	Down	MAM and LDL receptor class A domain containing 1
HAPLN4	-1.94109	6.27E-06	3.55E-05	-4.59775	Down	hyaluronan and proteoglycan link protein 4
MTTP	-1.46442	6.47E-06	3.66E-05	-4.59054	Down	microsomal triglyceride transfer protein
ALDOB	-1.39874	6.69E-06	3.77E-05	-4.58335	Down	aldolase, fructose-bisphosphate B
CD160	-1.02734	7.46E-06	4.17E-05	-4.55874	Down	CD160 molecule
KISS1	-1.68302	7.67E-06	4.28E-05	-4.55255	Down	KiSS-1 metastasis suppressor
CIDEC	-1.06877	8.81E-06	4.85E-05	-4.52143	Down	cell death inducing DFFA like effector c
OTC	-1.02707	9.48E-06	5.18E-05	-4.50475	Down	ornithine transcarbamylase
CA7	-1.47128	9.77E-06	5.32E-05	-4.49803	Down	carbonic anhydrase 7
ENPP7	-1.67765	1.00E-05	5.46E-05	-4.49158	Down	ectonucleotide pyrophosphatase/phosphodiesterase 7
OXT	-1.4911	1.06E-05	5.75E-05	-4.47839	Down	oxytocin/neurophysin I prepropeptide
C17orf78	-1.43396	1.22E-05	6.49E-05	-4.44714	Down	chromosome 17 open reading frame 78
CRIP3	-0.85908	1.23E-05	6.55E-05	-4.44479	Down	cysteine rich protein 3
PRDM7	-0.8967	1.57E-05	8.13E-05	-4.39003	Down	PR/SET domain 7
TTLL6	-0.88331	1.63E-05	8.43E-05	-4.3804	Down	tubulin tyrosine ligase like 6
CNR1	-1.04386	1.64E-05	8.46E-05	-4.37962	Down	cannabinoid receptor 1
DNAH7	-0.93477	1.69E-05	8.73E-05	-4.37162	Down	dynein axonemal heavy chain 7
BCHE	-0.94573	1.75E-05	8.97E-05	-4.36449	Down	butyrylcholinesterase
SDR16C5	-1.02036	1.81E-05	9.25E-05	-4.35641	Down	short chain dehydrogenase/reductase family 16C member 5
BEST4	-1.22695	2.22E-05	0.000111	-4.30836	Down	bestrophin 4
SPATA22	-1.84038	2.45E-05	0.000121	-4.28531	Down	spermatogenesis associated 22
FAM25G	-2.0054	2.71E-05	0.000133	-4.26126	Down	family with sequence similarity 25 member G
ABCA8	-0.83395	2.82E-05	0.000138	-4.25225	Down	ATP binding cassette subfamily A member 8
CHST5	-0.8251	2.94E-05	0.000143	-4.24188	Down	carbohydrate sulfotransferase 5
MT1M	-1.17444	3.29E-05	0.000158	-4.21526	Down	metallothionein 1M
TMEM72	-1.25999	3.75E-05	0.000178	-4.184	Down	transmembrane protein 72

MUC17	-0.98963	4.15E-05	0.000195	-4.15954	Down	mucin 17, cell surface associated
SLC26A3	-1.05936	5.84E-05	0.000265	-4.07633	Down	solute carrier family 26 member 3
SLC30A10	-0.84831	6.52E-05	0.000293	-4.04922	Down	solute carrier family 30 member 10
VPREB3	-1.13091	6.69E-05	0.000299	-4.04317	Down	V-set pre-B cell surrogate light chain 3
NPW	-1.14783	7.12E-05	0.000315	-4.02781	Down	neuropeptide W
C8G	-0.93968	8.86E-05	0.000382	-3.97306	Down	complement C8 gamma chain
CLCN1	-1.29277	8.91E-05	0.000384	-3.97168	Down	chloride voltage-gated channel 1
ASPDH	-1.04951	9.31E-05	0.000399	-3.96078	Down	aspartate dehydrogenase domain containing
UCN3	-0.91864	9.57E-05	0.000408	-3.95382	Down	urocortin 3
TMEM82	-0.86814	9.75E-05	0.000415	-3.94907	Down	transmembrane protein 82
PDZD3	-0.83788	9.75E-05	0.000415	-3.94907	Down	PDZ domain containing 3
TMEM253	-0.86977	0.000107	0.000452	-3.92532	Down	transmembrane protein 253
MT1B	-1.85582	0.000109	0.000458	-3.92154	Down	metallothionein 1B
FDCSP	-1.50884	0.000111	0.000464	-3.91745	Down	follicular dendritic cell secreted protein
ENHO	-0.95157	0.000115	0.000482	-3.90652	Down	energy homeostasis associated
MYRFL	-0.91168	0.000134	0.000549	-3.86932	Down	myelin regulatory factor like
RIMS2	-0.85699	0.000136	0.000557	-3.86519	Down	regulating synaptic membrane exocytosis 2
CCL21	-1.06686	0.000155	0.000627	-3.83114	Down	C-C motif chemokine ligand 21
ABHD12B	-1.20419	0.000155	0.000628	-3.83048	Down	abhydrolase domain containing 12B
RBP2	-1.44584	0.000159	0.00064	-3.82485	Down	retinol binding protein 2
FCER2	-0.88675	0.000191	0.000754	-3.77688	Down	Fc fragment of IgE receptor II
REG3G	-1.43675	0.000206	0.000808	-3.75671	Down	regenerating family member 3 gamma
FAM216B	-0.97954	0.000267	0.001016	-3.68863	Down	family with sequence similarity 216 member B
IL22RA2	-0.86199	0.000308	0.001155	-3.65031	Down	interleukin 22 receptor subunit alpha 2
CCDC152	-0.89588	0.000323	0.001202	-3.63784	Down	coiled-coil domain containing 152
SCT	-0.95737	0.000336	0.001243	-3.62741	Down	secretin
SLC52A1	-0.83723	0.000348	0.001283	-3.61777	Down	solute carrier family 52 member 1
CYP4F11	-1.56631	0.000361	0.001325	-3.60766	Down	cytochrome P450 family 4 subfamily F member 11
ZG16	-1.15903	0.000364	0.001334	-3.60562	Down	zymogen granule protein 16
ITLN2	-1.22884	0.000384	0.001398	-3.59098	Down	intelectin 2
GGTLC3	-1.54261	0.000569	0.001973	-3.48296	Down	gamma-glutamyltransferase light chain family member 3
GATA5	-0.87368	0.000689	0.002338	-3.42919	Down	GATA binding protein 5
TCL1A	-1.0076	0.000832	0.002744	-3.37572	Down	TCL1 family AKT coactivator A
UPK3A	-0.98477	0.000845	0.002782	-3.37129	Down	uroplakin 3A
CLEC17A	-0.86143	0.000877	0.002871	-3.36061	Down	C-type lectin domain containing 17A
MLIP	-0.94967	0.001068	0.003417	-3.3036	Down	muscular LMNA interacting protein
KCTD19	-1.08705	0.001152	0.003648	-3.28167	Down	potassium channel tetramerization domain containing 19
FRMPD1	-0.87135	0.001839	0.005532	-3.14273	Down	FERM and PDZ domain containing 1
CAMP	-0.99071	0.002152	0.006329	-3.09485	Down	cathelicidin antimicrobial peptide
NPY4R	-0.95866	0.002431	0.007029	-3.05739	Down	neuropeptide Y receptor Y4
UGT1A7	-0.98619	0.002739	0.007782	-3.0203	Down	UDP glucuronosyltransferase family 1 member A7
MS4A1	-0.87672	0.002778	0.007874	-3.01595	Down	membrane spanning 4-domains A1

C5orf67	-1.2023	0.002881	0.008129	-3.00455	Down	chromosome 5 putative open reading frame 67
TMEM130	-0.85245	0.003942	0.010648	-2.90493	Down	transmembrane protein 130
UGT2B4	-0.91324	0.006405	0.016169	-2.74532	Down	UDP glucuronosyltransferase family 2 member B4
PAX5	-0.83378	0.007897	0.019344	-2.67411	Down	paired box 5
TSPAN19	-0.97361	0.009871	0.023406	-2.59665	Down	tetraspanin 19
CDH18	-0.8559	0.018962	0.040841	-2.35886	Down	cadherin 18
CPA5	-0.86764	0.021418	0.045342	-2.31249	Down	carboxypeptidase A5

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:0050896	BP	response to stimulus	9.29E-53	52.03195621	350	FCGR3A,DUOXA2,AQP9,FCGR3B,CXCL8,MUC1,HCAR3,FCN1,CXCL2,DUOX2,CXCL5,S100A12,CXCL3,PROK2,S100A8,CXCR1,PYCR1,OSM,FCGR1A,IL15RA,LRG1,TNFSF13,LCN2,TNFAIP6,BATF2,CXCL1,S100A9,IFITM1,MYOF,C2,XBP1,MMP3,TAP1,FPR2,CXCL6,C2CD4A,C1QB,IFITM3,HK2,FCGR1B,APOBEC3A,IL1B,SLC6A14,CHAC1,FPR1,NOS2,NFKBIZ,GBP5,ZBP1,CLEC4D,LILRA6,CHI3L1,TGM2,CLEC4E,MUC4,VWA1,C4BPB,HCAR2,TREM1,IER3,FCN3,CSF3R,WNT5A,HGF,CXCL9,GBP1,S100A11,ADM,ALDH1A2,CXCL11,CFI,LILRB3,PLAUR,CXCL10,LIPG,NCF2,FIBIN,LILRB2,SLC11A1,GDF15,IL1RN,SAA2,ADGRE2,PRDX4,STAT1,CLEC5A,SLAMF7,LILRA5,PYGL,CYP27B1,LILRA1,NETO2,TFPI2,ZC3H12A,MMP1,SLPI,CMTM2,PILRA,CSF3,TYROBP,FBXO6,SOCS3,TLR8,HTRA3,LILRA2,GPX8,LITAF,CEBPB,IGSF6,CD55,CXCR2,CCL28,ADGRG3,CBR3,CCL3,CTSS,FCGR2A,JCHAIN,ACSL1,CCL2,SOD2,TFRC,CFB,IGLL5,OSCAR,CD14,SGIP1,CASP5,MNDA,IGFBP2,GPR84,DYSF,PCSK9,CD274,CLEC7A,DERL3,SERPINE1,IDO1,PDK1,GLUL,MZB1,PLA2G7,FOXP3,SCN1B,CD163,LYPD1,SAA1,FCER1G,LPL,IL1R2,APCDD1,CCL7,GBP4,RNASE2,ADORA2B,

						PTGS2,IRAK3,TLR2,ALOX15B,MEFV,PI3,PIGR,OASL,F2RL2,IGFBP5,FFAR4,CCR2,JUNB,RND1,CHRNA5,KCNJ2,BHLHA15,VWF,SLC7A11,NOD2,DMBT1,IL20RA,TYMP,HSPA6,ADGRF1,NAMPT,GNA15,S100P,PDPN,THEMIS2,CLEC6A,P2RY6,ADAMTS1,ADCYAP1,PGC,ATF3,TIMP1,UCN2,FCAR,SLAMF8,FAP,CTSL,SIGLEC9,SELE,SLC1A3,ICAM1,EDNRA,FOSL1,CD300C,RASGRP4,AREG,LYZ,PIM2,SLC7A5,PF4V1,IL13RA2,COL4A1,CH25H,LY6D,COL5A2,SNAI1,FFAR2,MARCO,MXRA5,CCL4L2,EGR1,TNFRSF17,MDFI,ST3GAL4,SRGN,IFITM2,CEACAM6,CCL11,IFNG,PTAFR,TREM2,INHBA,SERPING1,CLC,APOE,FGR,CRISP3,CTSK,SAA4,ALPL,CCR1,NR4A3,IL6,CTHRC1,PDCD1LG2,SFRP1,CCL4,SNX10,NFAM1,KRT6A,SPP1,CLDN1,CA2,IL11,PHLDA2,CLDN18,NNMT,COL15A1,KYNU,FGFBP1,RAB31,TNFRSF18,TNFRSF4,COL1A1,FAM20A,RNF186,MMP12,COL3A1,MMP2,C2CD4B,PLEK,IFI44L,LILRB4,IL1A,ITGA5,CCL1,MLN,GPR4,WNT2,SIRPB1,HAPLN3,HBEGF,ADGRE3,GPX2,CD24,CCL3L3,PDE4B,AQP5,SCNN1B,GLDC,REG1A,UBD,SPHK1,AOX1,CYP7B1,GPR141,STC2,BPIFB1,LAMP3,TFF2,ITGAX,POSTN,REG1B,G0S2,GZMB,OLR1,SELP,THY1,MUC5AC,BCL2A1,FGF7,SERPINA3,TWIST1,CCL8,CSF2,PLAU,CD177,CA9,GFPT2,TDO2,TFF1,STC1,ITLN1,CTLA4,C4BPA,TNIP3,PADI4,ORM1,MMP13,WFDC2,HBD,HRH2,FOSB,LBP,CST1,PGLYRP1,GAS1,MASP1,KLK6,VSNL1,FFAR3,RETN,ODAM,GIP,MPO,HAS1,LEFTY1,HP,SCGB2A1,CYP24A1
GO:0042221	BP	response to chemical	1.59E-45	44.79866426	230	AQP9,CXCL8,CXCL2,DUOX2,CXCL5,S100A12,CXCL3,PROK2,S100A8,CXCR1,PYCR1,OSM,IL15RA,LRG1,TNFAIP6,CXCL1,S100A9,IFITM1,C2,XBP1,MMP3,FPR2,CXCL6,IFITM3,HK2,APOBEC3A,IL1B,SLC6A14,CHAC1,FPR1,NOS2,GBP5,ZBP1,LILRA6,CHI3L1,TGM2,TREM1,CSF3R,WNT5A,HGF,CXCL9,GBP1,ADM,ALDH1A2,CXCL11,LILRB3,PLAUR,CXCL10,LIPG,FIBIN,LILRB2,SLC11A1,GDF15,IL1RN,ADGRE2,PRDX4,STAT1,LILRA5,CYP27B1,LILRA1,ZC3H12A,SLPI,CMTM2,CSF3,FB

						XO6,SOCS3,HTRA3,LILRA2,GPX8,LITAF,CEBPB,CD55,CXCR2,CCL28,CBR3,CCL3,CTSS,ACSL1,CCL2,SOD2,TFRC,CD14,MNDA,IGFBP2,PCSK9,CD274,CLEC7A,DERL3,SERPINE1,IDO1,PDK1,GLUL,MZB1,PLA2G7,FOXP3,SCN1B,LYPD1,SAA1,FCER1G,LPL,IL1R2,CCL7,GBP4,RNASE2,PTGS2,IRAK3,TLR2,MEFV,PIGR,OASL,IGFBP5,FFAR4,CCR2,JUNB,CHRNA5,BHLHA15,SLC7A11,NOD2,DMBT1,IL20RA,TYMP,HSPA6,GNA15,S100P,P2RY6,ATF3,TIMP1,UCN2,FCAR,SLAMF8,CTSL,SELE,SLC1A3,ICAM1,EDNRA,FOSL1,AREG,PF4V1,IL13RA2,COL4A1,CH25H,LY6D,COL5A2,FFAR2,MXRA5,CCL4L2,EGR1,TNFRSF17,IFITM2,CCL11,IFNG,PTAFR,TREM2,INHBA,APOE,ALPL,CCR1,NR4A3,IL6,PDCD1LG2,SFRP1,CCL4,SNX10,SPP1,CLDN1,CA2,CLDN18,NNMT,KYNU,FGFBP1,RAB31,TNFRSF18,TNFRSF4,COL1A1,MMP12,COL3A1,MMP2,LILRB4,IL1A,ITGA5,CCL1,WNT2,HAPLN3,HBEGF,GPX2,CD24,CCL3L3,PDE4B,AQP5,SCNN1B,GLDC,REG1A,UBD,SPHK1,AOX1,CYP7B1,STC2,LAMP3,TFF2,POSTN,REG1B,SELP,FGF7,TWIST1,CCL8,CSF2,PLAU,CA9,GFPT2,TDO2,TFF1,STC1,TNIP3,MMP13,HBD,HRH2,FOSB,LBP,CST1,GAS1,VSNL1,FFAR3,RETN,GIP,MPO,HAS1,LEFTY1,HP,SCGB2A1,CYP24A1
GO:0005576	CC	extracellular region	2.96E-69	68.52811	267	FCGR3A,FCGR3B,CXCL8,MUC1,FCN1,CXCL2,DUOX2,CXCL5,S100A12,CXCL3,PROK2,S100A8,TXNDC5,OSM,IL15RA,LRG1,TNFSF13,LCN2,TNFAIP6,CXCL1,S100A9,MYOF,C2,MMP3,CXCL6,C1QB,IL1B,SLC6A14,CKAP4,CHI3L1,TGM2,MUC4,VWA1,C4BPB,TREM1,FCN3,PDZK1IP1,CSF3R,WNT5A,HGF,CXCL9,CEACAM5,GBP1,S100A11,ADM,CXCL11,CFI,PLAUR,CXCL10,LIPG,HK3,MMP10,FIBIN,LILRB2,FOLH1,GDF15,IL1RN,SAA2,PRDX4,LILRA5,PYGL,TFPI2,MMP1,SLPI,LAP3,CMTM2,PILRA,CSF3,PSAT1,COL18A1,HTRA3,CLIC6,LILRA2,CD55,CCL28,IFI30,CBR3,CCL3,CTSS,EMILIN2,JCHAIN,CCL2,SOD2,TFRC,CFB,IGLL5,OSCAR,CD14,MNDA,IGFBP2,DYSF,PCSK9,CD274,SERPINE1,GLUL,SRPX2,MZB1

						,PLA2G7,SCN1B,CD163,LYPD1,EGFL6,VCAN,SAA1,LPL,IL1R2,CCL7,COL5A3,RNASE2,TCN1,ALOX15B,PI3,CLCA4,PIGR,F2RL2,IGFBP5,QPCT,ZG16B,VWF,LYPD6B,DMBT1,HSPA6,ADGRF1,NAMPT,S100P,ADAMTS1,ADCYAP1,PGC,STEAP4,TIMP1,UCN2,FCAR,PRSS23,FAP,CTSL,ADAMTS2,SELE,LAMC3,ICAM1,GLT1D1,ALDH1L1,PRSS22,AREG,LYZ,APOL4,SLC7A5,PF4V1,IL13RA2,ACSL4,COL4A1,LY6D,COL5A2,ADAMTS4,PLA1A,RARRES1,MXRA5,PSG4,CCL4L2,ST3GAL4,SRGN,CEACAM6,CCL11,IFNG,TREM2,INHBA,CEACAM7,SERPING1,APOE,FGR,CRISP3,CTSK,COL7A1,SAA4,ALPL,IL6,CTHRC1,PDCD1LG2,SFRP1,CCL4,TMEM132A,CPXM1,KRT6A,SPP1,CA2,IL11,APOC1,COL15A1,LYPD5,FGFBP1,COL6A3,TNFRSF18,SLC5A8,COL1A1,FAM20A,MMP12,COL3A1,MMP2,MUC5B,PLEK,TNFAIP2,LILRB4,IL1A,SBSN,CCL1,MLN,WNT2,HAPLN3,FOLR3,HBEGF,ADGRE3,CCL3L3,AQP5,SCNN1B,PI15,REG1A,CA1,AOX1,STC2,SPINK4,CEMIP,BPIFB1,TFF2,MMP7,POSTN,TNFRSF6B,REG1B,ANGPTL2,GZMB,OLR1,SELP,THY1,MUC5AC,FGF7,SERPINA3,FJX1,CCL8,CSF2,CA4,MUCL1,ART3,PLAU,CD177,TFF1,MUC6,STC1,ITLN1,C4BPA,ORM1,MMP13,WFDC2,HBD,LBP,CST1,PGLYRP1,THBS2,GLDN,MASP1,KLK6,KRT7,RETN,ODAM,GIP,MPO,LEFTY1,HP,SCGB2A1,MSMB
GO:0031224	CC	intrinsic component of membrane	3.83E-10	9.416830792	193	FCGR3A,DUOXA2,AQP9,FCGR3B,MUC1,HCAR3,DUOX2,CXCR1,BACE2,FCGR1A,IL15RA,TNFSF13,IFITM1,MYOF,XBP1,TAP1,FKBP11,FPR2,IFITM3,FCGR1B,SLC6A14,FPR1,KCNE3,CLEC4D,LILRA6,CKAP4,TGM2,CLEC4E,HSD11B1,MUC4,HCAR2,TREM1,IER3,PDZK1IP1,CSF3R,CLEC12A,CEACAM5,LILRB3,TMPRSS3,CD300E,PLAUR,NCF2,LILRB2,FOLH1,SLC11A1,SLC39A8,ADGRE2,CLEC5A,SLAMF7,LILRA5,KCNJ15,LILRA1,NETO2,CMTM2,PILRA,TYROBP,TLR8,CLIC6,LILRA2,GPX8,C19ORF38,LITAF,FNDC3B,IGSF6,CD55,MCEMP1,CXCR2,ADGRG3,FCGR2A,ACSL1,SLC38A5,TFRC,OSCAR,CD14,GPR84,DYSF,CD274,CLEC7A,DERL3,SRD5A

						3,SCN1B,CD163,LYPD1,FCER1G,IL1R2,APCDD1,ADORA2B,TLR2,CLCA4,PIGR,F2RL2,FFAR4,CCR2,CHRNA5,KCNJ2,SLC7A11,NOD2,LYPD6B,IL20RA,ADGRF1,STEAP1,CEACAM3,PDPN,CLEC6A,P2RY6,STEAP4,FCAR,SLAMF8,STX11,SPAG4,FAP,SIGLEC9,SELE,SLC1A3,ICAM1,EDNRA,CD300C,AREG,SLC7A5,IL13RA2,ACSL4,CH25H,LY6D,JPH1,FFAR2,LRFN4,ADAMTS4,MARCO,RARRES1,TNFRSF17,ST3GAL4,IFITM2,CEACAM6,PTAFR,TREM2,CEACAM7,CEACAM4,EVA1A,CRISP3,CTSK,ALPL,CCR1,IL6,PDCD1LG2,NFAM1,TMEM132A,CLDN1,CLDN18,COL15A1,LYPD5,B4GALNT3,TNFRSF18,SLC5A8,TNFRSF4,RNF186,LILRB4,TMEM158,SLC17A9,ITGA5,GPR4,SIRPB1,FOLR3,HBEGF,ADGRE3,CD24,PDE4B,AQP5,SCNN1B,CYP7B1,GPR141,DHRS9,LAMP3,ITGAX,KCNN3,SLC6A12,OLR1,SELP,THY1,CA12,CA4,ART3,CD177,CA9,ITLN1,CTLA4,GALNT15,HBD,HRH2,GLDN,GAS1,FFAR3,SPTSSB,HAS1
GO:0005102	MF	signaling receptor binding	2.10E-21	20.67857475	105	CXCL8,FCN1,CXCL2,CXCL5,S100A12,CXCL3,PROK2,S100A8,OSM,LRG1,TNFSF13,CXCL1,S100A9,TAP1,FPR2,CXCL6,IL1B,CHAC1,FPR1,CLEC4D,MUC4,WNT5A,HGF,CXCL9,ADM,CXCL11,PLAUR,CXCL10,LILRB2,GDF15,IL1RN,STAT1,NETO2,CMTM2,PILRA,CSF3,TYROBP,CLIC6,CCL28,CCL3,JCHAIN,CCL2,IGLL5,IGFBP2,PCSK9,CLEC7A,SERPINE1,SRPX2,LYPD1,EGFL6,SAA1,LPL,CCL7,TLR2,CCR2,RND1,VWF,TYMP,NAMPT,GNA15,PDPN,ADCYAP1,TIMP1,UCN2,FAP,ICAM1,AREG,PF4V1,MARCO,CCL4L2,CCL11,IFNG,INHBA,APOE,FGR,IL6,CTHRC1,SFRP1,CCL4,SPP1,IL11,COL3A1,IL1A,ITGA5,CCL1,MLN,WNT2,HBEGF,CCL3L3,REG1A,STC2,TFF2,ITGAX,ANGPTL2,THY1,FGF7,CCL8,CSF2,CD177,TFF1,STC1,LBP,RETN,GIP,LEFTY1
GO:0060089	MF	molecular transducer activity	2.22E-09	8.652916956	78	FCGR3A,FCGR3B,HCAR3,FCN1,CXCR1,FCGR1A,IL15RA,FPR2,FCGR1B,FPR1,CLEC4D,LILRA6,CLEC4E,HCAR2,TREM1,CSF3R,LILRB3,CD300E,PLAUR,LILRB2,ADGRE2,LILRA5,LILRA1,TLR8,LI

						LRA2,IGSF6,CXCR2,ADGRG3,FCGR2A,OSCAR,CD14,GPR84,CLEC7A,FCER1G,IL1R2,ADORA2B,TLR2,PIGR,F2RL2,FFAR4,CCR2,CHRNA5,NOD2,DMBT1,IL20RA,ADGRF1,CLEC6A,P2RY6,FCAR,SLAMF8,SELE,ICAM1,EDNRA,CD300C,IL13RA2,FFAR2,MARCO,TNFRSF17,PTAFR,TREM2,FGR,CCR1,NR4A3,NFAM1,TNFRSF18,TNFRSF4,GPR4,FOLR3,ADGRE3,REG1A,SPHK1,GPR141,ITGAX,TNFRSF6B,REG1B,HRH2,PGLYRP1,FFAR3
			Down regulated genes			
GO:0044281	BP	small molecule metabolic process	3.66E-32	31.43686714	125	UGT1A4,ACOT12,UGT1A3,ALDOC,BCO2,CUBN,LRAT,CYP4F2,AGXT2,CBS,PEPD,SOAT2,CYP2S1,ABCG2,CYP3A4,APOA1,UGT1A5,PLB1,PTGR1,ASPA,FMO5,GUCA2B,FBP1,SULT2B1,CYP3A7,FMO1,AKR1B10,SLC19A3,UGT1A10,DHDH,BPHL,PLCH2,MME,GSTA1,ACSF2,CYP2J2,CYP4F3,OAT,PKLR,PDK2,DPEP1,APOB,PRODH,CES2,PON3,ABHD6,ACOX2,CYP2B6,SLC23A1,AICDA,UGT1A1,SEC14L2,UGT1A6,PDXP,GDA,GUCA2A,ENTPD5,ASAH2,SLC27A2,CYP4F12,CBR1,KHK,CYP2D6,PANK1,APOA4,GATM,PRKG2,CYP3A5,AGMO,SLC16A9,CYP2C8,APOC3,NAGS,CYP2C18,PFKFB4,NPC1L1,ACY1,GGT1,DDC,B4GALNT2,INPP5J,UGT1A8,UGT2B7,IYD,ENPP3,SULT2A1,UGT2A3,DGAT1,PCK2,CRABP1,APOC2,SULT1A2,HMGCS2,PCK1,CYP2C19,MLXIPL,FABP2,TTC36,HSD17B3,DEGS2,NPPC,EDN2,CYP2C9,AKR1B15,NR0B2,CRYM,MOGAT2,CA3,ARG2,GPD1,APOBEC1,MALRD1,ALDOB,OTC,CA7,CNR1,SDR16C5,ASPDH,PDZD3,RBP2,SLC52A1,CYP4F11,GGTLC3,UGT1A7,UGT2B4
GO:0065008	BP	regulation of biological quality	2.51E-17	16.6006119	156	SLC28A2,UGT1A3,CDHR1,BCO2,CUBN,LRAT,CYP4F2,NELL2,PFN2,SOAT2,MAOB,CYP2S1,KCNH6,FLVCR1,TRPV3,HSD3B1,CYP3A4,APOA1,SLC34A3,FOXD1,HTR1D,PLB1,ABCB1,CYP3A7,AKR1B10,RHOBTB2,TRHDE,ACE2,F10,MME,SLC6A4,GCNT4,SLC22A4,PREPL,PDK2,APOB,SLC22A5,SLC35G1,DPP4,SLC1A7,SLC39A4,ABHD6,ACOX2,SOX8,TMIGD1,ACE,NPY,SLC9A3R1,USP2,U

						GT1A1,KLKB1,IGSF9,CCR9,RHOU,PDXP,SLC2A5,SLC1A1,CDHR2,CYBRD1,APOM,HSD17B2,CYP4F12,CYP2D6,ABCG5,APOA4,GATM,SEMA6C,RHOD,SLC17A8,CYP3A5,ENPEP,SCIN,CDHR5,EDN3,CYP2C8,TMEM25,APOC3,MT1F,CYP2C18,DHRS11,RAB17,CHRNA7,CXADR,KDM8,SYT8,UGT1A8,PRLR,TM6SF2,UGT2B7,TF,MAOA,RNF128,OIT3,IYD,SEMA3B,SULT2A1,SLC30A2,DGAT1,PCK2,SLC34A2,CRABP1,A1CF,SLC51B,APOC2,MT1H,SEMA3G,KCNJ3,PBLD,PCK1,AQP3,MLXIPL,HSD17B3,F11,SLC9A2,CALB1,SLC39A5,VIL1,MT1A,SCTR,EDN2,CYP2C9,AKR1B15,NR0B2,CRYM,ABCG8,PLA2G12B,MT1G,ANPEP,APOBEC1,MALRD1,MTTP,KISS1,OTC,CA7,ENPP7,OXT,TTLL6,CNR1,BCHE,SDR16C5,MT1M,MUC17,SLC26A3,SLC30A10,CLCN1,UCN3,MT1B,RIMS2,CCL21,SCT,CYP4F11,TCL1A,UPK3A,UGT1A7,MS4A1,UGT2B4
GO:0016020	CC	membrane	3.52E-15	14.45289565	297	SLC14A2,FZD7,C6,FAM151A,PMP22,ZDHHC11B,UGT1A4,SLC28A2,UGT3A1,UGT1A3,TMEM252,PAQR5,CDHR1,OTOP3,RGS13,SLC23A3,SLC5A4,CUBN,LRAT,CYP4F2,ABCC2,CNTFR,TM4SF4,PFN2,SOAT2,MAOB,CYP2S1,ABCG2,KCNH6,AADAC,GAL3ST1,ZDHHC11,FLVCR1,TRPV3,HSD3B1,CYP3A4,APOA1,NAALADL1,ANXA13,SLC34A3,SLC46A3,TRPM6,UGT1A5,HTR1D,PLB1,ABCB1,COL17A1,FMO5,SERPINA9,CYP3A7,GDPD2,SLC36A1,MEP1B,NAT8,MS4A10,FMO1,FADS6,RHOBTB2,SLC19A3,UGT1A10,PLA2R1,SLC5A12,TRHDE,BPHL,SLC13A1,ACE2,CD207,PLCH2,F10,MME,SUSD2,LAMA1,SLC6A4,FABP6,GCNT4,FRMD1,MGAM,SLC28A1,EMB,C2ORF88,SMIM24,FCRL4,CYP2J2,CYP4F3,CD8B,SLC22A4,MGAT3,TREH,DPEP1,REEP6,APOB,PRODH,SLC22A5,SLC35G1,CPO,CNGA1,DPP4,GNG4,MYZAP,SLC1A7,SLC39A4,SLC10A2,ABHD6,XPNPEP2,TMIGD1,CYP2B6,ACE,PHLPP2,SLC23A1,SLC6A20,SLC9A3R1,USP2,SLC15A1,MS4A8,GRIA4,UGT1A1,KLKB1,IGSF9,UGT1A6,TMEM229A,OTOP2,CCR9,CREB3L3,SLC25A34,RHOU,AQP7,PDXP,SLC2A5,SLC1A1,SLC7A9,SLC13A2,SLC5A11,

						KCNG1,CDHR2,CYBRD1,HSD17B2,ENTPD5,ASAH2,SLC27A2,CYP4F12,SLC6A19,SMLR1,AOC1,CYP2D6,GRAMD1C,ABCG5,GATM,SEMA6C,RHOD,PRKG2,SLC17A8,CYP3A5,ENPEP,SCIN,AGMO,CDHR5,FCER1A,SLC16A9,CYP2C8,TMEM25,BCAN,SLC5A9,GFRA1,GP2,ARHGDIG,PLEKHG6,CYP2C18,TM4SF5,FCAMR,PDZK1,NPC1L1,RAB17,CHRNA7,CXADR,CLDN8,AMN,SYT8,GGT1,SI,IGSF23,B4GALNT2,C1ORF115,INPP5J,UGT1A8,PRLR,SLC3A1,TM6SF2,SLC17A4,RGS11,TMEM220,UGT2B7,IGSF3,TF,MAOA,RNF128,MEP1A,EPB41L4B,IYD,ARL14,ENPP3,CLDN15,CD1C,LCT,SEMA3B,CHP2,SLC30A2,UGT2A3,KCNJ13,DGAT1,BTNL2,SLC34A2,B4GALNT4,GLP2R,SLC51B,CHST6,BEGAIN,MYO1A,SLC5A1,SEMA3G,SLC51A,KCNJ3,AATK,CYP2C19,AQP3,FABP2,VIPR1,SLC2A2,HSD17B3,SERPINA5,F11,EVPL,SLC9A2,ALPI,SLC39A5,GOLT1A,DEGS2,COBL,SHISA3,VIL1,SSTR1,B3GALT5,SCTR,FGFR3,CR2,CYP2C9,MROH7,TMEM236,MAMDC2,ABCG8,MOGAT2,FCRL3,PDZD7,ANPEP,NEU4,CEACAM20,MALRD1,MTTP,CD160,KISS1,OTC,ENPP7,C17ORF78,CNR1,BCHE,SDR16C5,BEST4,ABCA8,CHST5,TMEM72,MUC17,SLC26A3,SLC30A10,C8G,CLCN1,TMEM82,PDZD3,TMEM253,ENHO,MYRFL,RIMS2,ABHD12B,FCER2,IL22RA2,SLC52A1,CYP4F11,ZG16,UPK3A,CLEC17A,MLIP,FRMPD1,NPY4R,UGT1A7,MS4A1,TMEM130,UGT2B4,TSPAN19,CDH18
GO:0005737	CC	cytoplasm	0.000130754	3.883545569	305	CRIP1,TPPP,FZD7,ZDHHC11B,UGT1A4,SLC28A2,UGT3A1,ITIH3,CDK20,ACOT12,UGT1A3,RGS13,ALDOC,ADIRF,BCO2,CUBN,LRAT,CYP4F2,AGXT2,CBS,NELL2,PFN2,SOAT2,MAOB,CYP2S1,SCAPER,ABCG2,EML6,AADAC,GAL3ST1,ZDHHC11,ELL3,FLVCR1,HSD3B1,TPPP3,MYOM3,CYP3A4,APOA1,ANXA13,FAM47E,SLC46A3,SAT2,CDC14A,UGT1A5,COL17A1,PTGR1,ASPA,TNNC2,FMO5,FBP1,SULT2B1,SERPINA9,CYP3A7,GDPD2,SLC36A1,NAT8,FMO1,SSUH2,AKR1B10,RHOBTB2,UGT1A10,MAF,TRHDE,BPHL,ACE2,CD207,PLCH2,C9ORF24,F

						10,GSTA2,MME,SLC6A4,FABP6,GSTA1,GCNT4,NR1I3,MGAM,ACSF2,SLC28A1,CYP2J2,CYP4F3,CD8B,SLC22A4,OAT,PKLR,MGAT3,PREPL,PDK2,REEP6,APOB,PRODH,CES2,SLC22A5,SLC35G1,DPP4,MYZAP,SLC39A4,ABHD6,ACOX2,SOX8,DNASE1,TMIGD1,CYP2B6,ACE,PHLPP2,SLC23A1,NPY,SLC9A3R1,USP2,GSTA5,AICDA,HEBP1,GRIA4,UGT1A1,SEC14L2,UGT1A6,CMBL,CREB3L3,SLC25A34,RHOU,AQP7,PDXP,SLC2A5,SLC1A1,GDA,CYBRD1,HSD17B2,ENTPD5,SH2D6,ASAH2,SLC27A2,CYP4F12,CBR1,KHK,AOC1,CYP2D6,LGALS2,GRAMD1C,PANK1,APOA4,GATM,SEMA6C,RHOD,PRKG2,SLC17A8,CYP3A5,ENPEP,SCIN,AGMO,CYP2C8,TMEM25,APOC3,BCAN,MMP28,GFRA1,GP2,ARHGDIG,MT1F,CTSE,PLEKHG6,NAGS,PRAP1,CYP2C18,TM4SF5,SUGCT,PFKFB4,NPC1L1,RAB17,ACY1,CXADR,CLDN8,KDM8,AMN,SYT8,SI,DDC,B4GALNT2,BACH2,INPP5J,UGT1A8,PRLR,SLC3A1,TM6SF2,DAB1,SLC17A4,UGT2B7,TUBAL3,TF,MAOA,RNF128,EPB41L4B,IYD,ARL14,ENPP3,CD1C,LCT,SEMA3B,CHP2,DTX1,SULT2A1,SLC30A2,DGAT1,PCK2,CRABP1,B4GALNT4,A1CF,ESPL1,SPIB,CHST6,APOC2,BEGAIN,MYO1A,NTS,MT1H,SLC5A1,SULT1A2,SLC51A,HMGCS2,PBLD,AATK,PCK1,CYP2C19,DNAJB13,AQP3,TINAG,MLXIPL,FABP2,SLC2A2,HSD17B3,SERPINA5,EVPL,TUBB2B,NCCRP1,CALB1,GOLT1A,DEGS2,COBL,SHISA3,VIL1,NPPC,MT1A,SSTR1,B3GALT5,SCTR,FGFR3,CDKN2B,CAPN13,ESPN,CYP2C9,AKR1B15,PHYHIPL,NR0B2,CRYM,MAMDC2,MOGAT2,CA3,GSTA3,MEF2B,MT1G,ARG2,ANPEP,GPD1,PDIA2,NEU4,HNF4G,APOBEC1,MALRD1,MTTP,ALDOB,KISS1,CIDEC,OTC,CA7,ENPP7,OXT,CRIP3,TTLL6,CNR1,DNAH7,BCHE,SDR16C5,ABCA8,CHST5,MT1M,MUC17,SLC30A10,VPREB3,PDZD3,MT1B,MYRFL,RIMS2,ABHD12B,RBP2,REG3G,IL22RA2,CYP4F11,ZG16,TCL1A,UPK3A,FRMPD1,CAMP,UGT1A7,TMEM130,UGT2B4,PAX5
GO:0005215	MF	transporter	7.05E-13	12.15198762	76	SLC14A2,SLC28A2,OTOP3,SLC23A3,SLC5A4,ABCC2,ABCG2,KC

		activity				NH6,FLVCR1,TRPV3,APOA1,SLC34A3,SLC46A3,TRPM6,ABCB1,SLC36A1,SLC19A3,SLC5A12,SLC13A1,SLC6A4,SLC28A1,SLC22A4,APOB,SLC22A5,CNGA1,SLC1A7,SLC39A4,SLC10A2,SLC23A1,SLC6A20,SLC9A3R1,SLC15A1,GRIA4,OTOP2,AQP7,SLC2A5,SLC1A1,SLC7A9,SLC13A2,SLC5A11,KCNG1,CYBRD1,APOM,SLC27A2,SLC6A19,GRAMD1C,ABCG5,APOA4,SLC17A8,SLC16A9,SLC5A9,NPC1L1,CHRNA7,SLC3A1,SLC17A4,SLC30A2,KCNJ13,SLC34A2,SLC51B,SLC5A1,SLC51A,KCNJ3,AQP3,FABP2,SLC2A2,SLC9A2,SLC39A5,ABCG8,MTTP,CNR1,BEST4,ABCA8,SLC26A3,SLC30A10,CLCN1,SLC52A1
GO:0003824	MF	catalytic activity	1.63E-08	7.788820119	190	TPPP,ZDHHC11B,UGT1A4,UGT3A1,CDK20,ACOT12,UGT1A3,RGS13,ALDOC,BCO2,LRAT,CYP4F2,AGXT2,CBS,PFN2,PEPD,SOAT2,MAOB,CYP2S1,AADAC,GAL3ST1,ZDHHC11,HSD3B1,CYP3A4,NAALADL1,SAT2,TRPM6,CDC14A,UGT1A5,PLB1,PTGR1,ASPA,FMO5,FBP1,SULT2B1,CYP3A7,GDPD2,MEP1B,NAT8,FMO1,AKR1B10,RHOBTB2,UGT1A10,DHDH,TRHDE,BPHL,ACE2,PLCH2,F10,GSTA2,MME,GSTA1,GCNT4,MGAM,ACSF2,CYP2J2,CYP4F3,OAT,PKLR,MGAT3,PREPL,PDK2,TREH,DPEP1,PRODH,CES2,CPO,DPP4,PON3,ABHD6,ACOX2,XPNPEP2,DNASE1,CYP2B6,ACE,PHLPP2,USP2,GSTA5,AICDA,UGT1A1,KLKB1,UGT1A6,CMBL,RHOU,PDXP,GDA,CYBRD1,HSD17B2,ENTPD5,ASAH2,SLC27A2,CYP4F12,CBR1,KHK,AOC1,CYP2D6,ABCG5,PANK1,GATM,RHOD,PRKG2,CYP3A5,ENPEP,AGMO,CYP2C8,MMP28,CTSE,NAGS,CYP2C18,SUGCT,PFKFB4,DHRS11,RAB17,ACY1,KDM8,GGT1,SI,DDC,THSD4,B4GALNT2,INPP5J,UGT1A8,SLC3A1,RGS11,UGT2B7,TUBAL3,MAOA,RNF128,MEP1A,IYD,ARL14,ENPP3,LCT,DTX1,SULT2A1,UGT2A3,DGAT1,PCK2,B4GALNT4,ESPL1,CHST6,BEGAIN,SULT1A2,HMGCS2,PBLD,AATK,PCK1,CYP2C19,TINAG,HSD17B3,F11,ALPI,TUBB2B,NCCRP1,DEGS2,B3GALT5,FGFR3,CDKN2B,CAPN13,CYP2C9,AKR1B15,CRYM,ABCG8,MOGAT2,PLA2G12B,CA3,GSTA3,METTL7B,ARG2

,ANPEP,GPD1,PDIA2,NEU4,APOBEC1,ALDOB,OTC,CA7,ENPP7,PRDM7,TTLL6,BCHE,SDR16C5,CHST5,ASPDH,ABHD12B,CYP4F11,GGTLC3,UGT1A7,UGT2B4,CPA5

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	1.36E-32	31.86676367	173	FCGR3A,FCGR3B,CXCL8,MUC1,FCN1,CXCL2,S100A12,S100A8,CXCR1,TXNDC5,OSM,FCGR1A,IL15RA,LRG1,TNFSF13,LCN2,TNFAIP6,CXCL1,S100A9,IFITM1,C2,MMP3,TAP1,FPR2,IFITM3,FCGR1B,IL1B,FPR1,NOS2,GBP5,ZBP1,CLEC4D,LILRA6,CKAP4,CHI3L1,CLEC4E,MUC4,C4BPB,TREM1,FCN3,CSF3R,HGF,CLEC12A,GBP1,S100A11,CFI,LILRB3,CD300E,PLAUR,CXCL10,NCF2,HK3,LILRB2,SLC11A1,IL1RN,PRDX4,STAT1,CLEC5A,SLAMF7,LILRA5,PYGL,LILRA1,MMP1,SLPI,PILRA,CSF3,TYROBP,FBXO6,SOCS3,TLR8,LILRA2,CD55,MCEMP1,CXCR2,IFI30,ADGRG3,CCL3,CTSS,FCGR2A,CCL2,SOD2,CFB,OSCAR,CD14,MNDA,GPR84,CD274,CLEC7A,SAA1,FCER1G,IL1R2,GBP4,RNASE2,PTGS2,IRAK3,TLR2,TCN1,MEFV,PI3,PIGR,OASL,QPCT,CCR2,JUNB,NOD2,IL20RA,HSPA6,S100P,CEACAM3,CLEC6A,TIMP1,FCAR,CTSL,SIGLEC9,ICAM1,CD300C,RASGRP4,LYZ,IL13RA2,EGR1,TNFRSF17,IFITM2,CEACAM6,CCL11,IFNG,PTAFR,TREM2,SERPING1,FGR,CRISP3,CTSK,CCR1,IL6,PDCD1LG2,CCL4,NFAM1,IL11,RAB31,TNFRSF18,TNFRSF4,COL1A1,COL3A1,MMP2,MUC5B,LILRB4,IL1A,SIRPB1,FOLR3,ADGRE3,CCL3L3,CA1,BPIFB1,ITGAX,TNFRSF6B,OLR1,MUC5AC,SERPINA3,TWIST1,CSF2,MUCL1,PLAU,CD177,MUC6,ITLN1,CTLA4,C4BPA,ORM1,LBP,PGLYRP1,MASP1,RETN,MPO,HP
REAC:R-HSA-6798695	Neutrophil degranulation	4.94E-23	22.30602471	69	FCGR3B,FCN1,S100A12,S100A8,CXCR1,TXNDC5,LRG1,LCN2,TNFAIP6,CXCL1,S100A9,FPR2,FPR1,CLEC4D,CKAP4,CHI3L1,CLEC12A,S100A11,LILRB3,PLAUR,HK3,LILRB2,SLC11A1,PRDX4,CL

					EC5A,PYGL,SLPI,TYROBP,CD55,MCEMP1,CXCR2,ADGRG3,CTSS,FCGR2A,OSCAR,CD14,MNDA,GPR84,FCER1G,RNASE2,TLR2,TCN1,PIGR,QPCT,HSPA6,S100P,CEACAM3,FCAR,SIGLEC9,LYZ,CEACAM6,PTAFR,FGR,CRISP3,NFAM1,RAB31,SIRPB1,FOLR3,ADGRE3,ITGAX,OLR1,SERPINA3,PLAU,CD177,ORM1,PGLYRP1,RETN,MPO,HP
REAC:R-HSA-1280215	Cytokine Signaling in Immune system	1.19E-11	10.92316521	65	CXCL8,MUC1,CXCL2,S100A12,OSM,FCGR1A,IL15RA,TNFSF13,LCN2,CXCL1,IFITM1,MMP3,IFITM3,FCGR1B,IL1B,FPR1,NOS2,GBP5,CSF3R,HGF,GBP1,CXCL10,IL1RN,STAT1,MMP1,CSF3,SOCS3,IFI30,CCL3,CCL2,SOD2,SAA1,IL1R2,GBP4,PTGS2,IRAK3,OASL,CCR2,JUNB,NOD2,IL20RA,TIMP1,ICAM1,IL13RA2,EGR1,TNFRSF17,IFITM2,CCL11,IFNG,PTAFR,CCR1,IL6,CCL4,IL11,TNFRSF18,TNFRSF4,MMP2,IL1A,CCL3L3,CA1,ITGAX,TNFRSF6B,TWIST1,CSF2,LBP
REAC:R-HSA-449147	Signaling by Interleukins	8.77E-11	10.05675882	49	CXCL8,MUC1,CXCL2,S100A12,OSM,IL15RA,LCN2,CXCL1,MMP3,IL1B,FPR1,NOS2,CSF3R,HGF,CXCL10,IL1RN,STAT1,MMP1,CSF3,SOCS3,CCL3,CCL2,SOD2,SAA1,IL1R2,PTGS2,IRAK3,CCR2,JUNB,NOD2,IL20RA,TIMP1,ICAM1,IL13RA2,CCL11,IFNG,PTAFR,CCR1,IL6,CCL4,IL11,MMP2,IL1A,CCL3L3,CA1,ITGAX,TWIST1,CSF2,LBP
REAC:R-HSA-1474244	Extracellular matrix organization	7.95E-09	8.099726468	35	MMP3,MMP10,MMP1,COL18A1,CTSS,EMILIN2,SERPINE1,VCAN,COL5A3,VWF,ADAMTS1,TIMP1,CTSL,ADAMTS2,LAMC3,ICAM1,COL4A1,COL5A2,ADAMTS4,CEACAM6,CTSK,COL7A1,SPP1,COL15A1,COL6A3,COL1A1,MMP12,COL3A1,MMP2,ITGA5,MMP7,ITGAX,CAPN8,MMP13,P4HA3
REAC:R-HSA-8957275	Post-translational protein phosphorylation	0.000420336	3.376403719	14	CKAP4,VWA1,PCSK9,VCAN,IGFBP5,TIMP1,PRSS23,APOE,EVA1A,IL6,TMEM132A,SPP1,FAM20A,STC2
		Down regulated genes			
REAC:R-HSA-211859	Biological oxidations	5.76E-23	22.23922047	44	UGT1A4,UGT3A1,UGT1A3,CYP4F2,MAOB,CYP2S1,AADAC,CYP3A4,UGT1A5,CYP3A7,FMO1,UGT1A10,BPHL,GSTA2,GSTA1,CYP2J2,CYP4F3,DPEP1,CES2,CYP2B6,GSTA5,UGT1A1,UGT1A6,CMBL,CYP4F12,AOC1,CYP2D6,CYP3A5,CYP2C8,CYP2C18,ACY1,GGT1,UGT1A8,UGT2B7,MAOA,SULT2A1,UGT2A3,SULT1A2,CYP2C19,CYP2C9,GSTA3,CYP4F11,UGT1A7,UGT2B4
REAC:R-HSA-1430728	Metabolism	3.14E-17	16.50354928	127	UGT1A4,UGT3A1,ACOT12,UGT1A3,ALDOC,BCO2,CUBN,LRAT,CYP4F2,ABCC2,AGXT2,CBS,MAOB,CYP2S1,ABCG2,AADAC,HSD3B1,CYP3A4,APOA1,UGT1A5,PLB1,ABCB1,PTGR1,ASPA,FBP1,CYP3A7,FMO1,AKR1B10,SLC19

					A3,UGT1A10,PLA2R1,BPHL,PLCH2,GSTA2,FABP6,GSTA1,ACSF2,CYP2J2,CYP4F3,OAT,PDK2,DPEP1,APOB,PRODH,CES2,SLC22A5,GNG4,PON3,SLC10A2,ACOX2,CYP2B6,SLC23A1,GSTA5,UGT1A1,UGT1A6,CMBL,GDA,APOM,HSD17B2,ENTPD5,ASAH2,SLC27A2,CYP4F12,CBR1,KHK,AOC1,CYP2D6,PANK1,APOA4,GATM,PRKG2,CYP3A5,AGMO,CYP2C8,APOC3,BCAN,NAGS,CYP2C18,PFKFB4,ACY1,AMN,GGT1,DDC,B4GALNT2,INPP5J,UGT1A8,UGT2B7,MAOA,IYD,ENPP3,SULT2A1,UGT2A3,DGAT1,PCK2,CHST6,APOC2,SULT1A2,HMGCS2,PCK1,CYP2C19,MLXIPL,FABP2,SLC2A2,HSD17B3,ALPI,DEGS2,B3GALT5,CYP2C9,AKR1B15,CRYM,MOGAT2,CA3,GSTA3,ARG2,GPD1,ALDOB,CIDEC,OTC,CA7,ENPP7,BCHE,CHST5,RBP2,SLC52A1,CYP4F11,UGT1A7,UGT2B4
REAC:R-HSA-382551	Transport of small molecules	9.61E-11	10.01740696	57	SLC14A2,SLC28A2,SLC5A4,CUBN,ABCC2,SOAT2,ABCG2,TRPV3,APOA1,SLC34A3,TRPM6,ABCB1,SLC36A1,SLC5A12,SLC13A1,SLC28A1,EMB,SLC22A4,APOB,SLC22A5,GNG4,SLC1A7,SLC39A4,SLC6A20,SLC15A1,CREB3L3,AQP7,SLC1A1,SLC7A9,SLC13A2,SLC5A11,CYBRD1,SLC6A19,ABCG5,APOA4,SLC17A8,APOC3,SLC5A9,LCN15,AMN,SLC3A1,TF,SLC30A2,SLC34A2,APOC2,SLC5A1,AQP3,SLC2A2,SLC9A2,SLC39A5,ABCG8,MTTP,BEST4,ABCA8,SLC26A3,SLC30A10,CLCN1
REAC:R-HSA-196854	Metabolism of vitamins and cofactors	4.58018E-05	4.339117741	19	BCO2,CUBN,LRAT,APOA1,PLB1,AKR1B10,SLC19A3,APOB,SLC23A1,APOM,PANK1,APOA4,PRKG2,APOC3,AMN,ENPP3,APOC2,RBP2,SLC52A1
REAC:R-HSA-8978868	Fatty acid metabolism	6.07836E-05	4.216213497	18	ACOT12,CYP4F2,PTGR1,ACSF2,CYP2J2,CYP4F3,DPEP1,SLC22A5,PON3,ACOX2,SLC27A2,CBR1,CYP2C8,GGT1,CYP2C19,HSD17B3,CYP2C9,CYP4F11
REAC:R-HSA-556833	Metabolism of lipids	9.20398E-05	4.036024109	43	ACOT12,CUBN,CYP4F2,HSD3B1,CYP3A4,APOA1,PLB1,PTGR1,PLA2R1,FABP6,ACSF2,CYP2J2,CYP4F3,DPEP1,SLC22A5,PON3,SLC10A2,ACOX2,HSD17B2,ASAH2,SLC27A2,CBR1,CYP2D6,AGMO,CYP2C8,GGT1,INPP5J,SULT2A1,DGAT1,HMGCS2,CYP2C19,FABP2,HSD17B3,ALPI,DEGS2,CYP2C9,AKR1B15,MOGAT2,GPD1,CIDEC,ENPP7,BCHE,CYP4F11

Table 4 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	MDFI	179	0.084998	10956728	0.255074
Up	MNDA	156	0.073077	11522720	0.247112
Up	FBXO6	149	0.080585	14249060	0.297002
Up	TFRC	119	0.076431	8552912	0.311036

Up	STAT1	98	0.062496	12148376	0.291259
Up	IL13RA2	97	0.046536	9015258	0.27117
Up	CKAP4	97	0.062869	6763152	0.294911
Up	HSPA6	80	0.040976	9201716	0.271116
Up	CTSS	80	0.017125	4248576	0.269607
Up	PLAUR	74	0.02663	7748590	0.254847
Up	FPR2	71	0.026099	5889462	0.235095
Up	STX11	67	0.029718	4945568	0.248655
Up	LAMP3	66	0.03509	4736486	0.271372
Up	FGR	65	0.030528	7392644	0.261067
Up	FOXP3	64	0.028674	5676114	0.242948
Up	PDK1	63	0.029687	3257746	0.257837
Up	P4HA3	59	0.026343	5195112	0.238454
Up	CTSL	58	0.018736	3765964	0.273438
Up	TMEM132A	58	0.026332	2920712	0.251061
Up	SNAI1	57	0.025149	6123030	0.249969
Up	IFITM3	57	0.022261	4497802	0.276769
Up	CLEC4E	56	0.010819	3112666	0.272659
Up	TGM2	54	0.0264	2950720	0.270042
Up	CLEC4D	53	0.006962	2219580	0.265216
Up	CEBPB	52	0.019554	4633596	0.256227
Up	COL1A1	50	0.019796	4856846	0.252416
Up	JUNB	49	0.018339	3569156	0.256064
Up	UBD	48	0.018227	3794204	0.254107
Up	S100A9	43	0.016613	3554202	0.255641
Up	BHLHA15	43	0.017822	2276476	0.217582
Up	LITAF	42	0.017431	1613028	0.249984
Up	S100A8	42	0.01507	2914992	0.254977
Up	CD274	42	0.017	2303206	0.229396
Up	ICAM1	40	0.015753	2566826	0.249473
Up	IL1R2	40	0.016679	3323990	0.232123
Up	LRFN4	40	0.015696	2361120	0.227592
Up	SOCS3	38	0.014311	2913308	0.252511
Up	APOE	37	0.013402	2556904	0.237258
Up	JPH1	37	0.016235	3164258	0.254283
Up	ZG16B	36	0.013691	1760002	0.242669
Up	ACSL4	34	0.020915	1675904	0.260408
Up	IFITM1	34	0.005772	1537272	0.262242
Up	PYCR1	33	0.01102	1741382	0.229724
Up	CST1	33	0.011117	1570568	0.240048
Up	MUC1	32	0.012018	2627260	0.262071
Up	NOD2	31	0.010769	1692850	0.217464
Up	HK2	29	0.011282	1316402	0.235095
Up	TXNDC5	28	0.010871	908766	0.25582
Up	S100P	27	0.007016	1585650	0.235867
Up	IFI30	27	0.010907	1495782	0.216983
Up	ATF3	26	0.006017	976130	0.250124
Up	CCR1	26	0.012527	2073064	0.2229
Up	OASL	25	0.004802	1284438	0.218646
Up	S100A2	24	0.005398	1391344	0.237468
Up	SLC7A5	24	0.010412	2084270	0.267189
Up	PRDX4	24	0.011959	1499402	0.268402
Up	ITGA5	23	0.011398	1324946	0.260526
Up	PYGL	23	0.009341	950672	0.233701
Up	KRT17	23	0.007821	1798646	0.239547
Up	ADAMTS4	23	0.008032	1882446	0.221916
Up	S100A3	22	0.006256	865610	0.230013
Up	COL18A1	22	0.00682	1228158	0.237595
Up	KRT6A	22	0.006508	1335012	0.237876
Up	PIGR	22	0.007596	1257552	0.240335
Up	LIPG	22	0.008405	1694944	0.236839
Up	TAP1	21	0.015452	1335246	0.248226
Up	NAMPT	21	0.012477	1456638	0.268151
Up	WNT5A	20	0.00708	1176172	0.21421
Up	TYMP	20	0.0055	1161492	0.227656
Up	LYZ	19	0.009736	1536452	0.246175
Up	JCHAIN	19	0.004167	681364	0.219553
Up	LCN2	18	0.004458	877488	0.220239
Up	L1TD1	18	0.006208	867480	0.211551
Up	KYNU	18	0.00257	326982	0.219063

Up	GLUL	17	0.004709	598366	0.214438
Up	HP	17	0.006065	773042	0.24308
Up	LAP3	17	0.006365	574366	0.218172
Up	SCGB2A1	17	0.006224	950856	0.218777
Up	FOSL1	16	0.003839	582604	0.234615
Up	CTLA4	16	0.005302	517954	0.225752
Up	DMBT1	16	0.00462	763208	0.233973
Up	NOS2	15	0.005061	454982	0.248011
Up	FCN1	15	0.004688	755632	0.177941
Up	SERPINA3	15	0.00353	876334	0.218599
Up	SPP1	15	0.004467	399884	0.231669
Up	SBSN	15	0.00419	698920	0.209982
Up	BACE2	15	0.004691	561540	0.206936
Up	IGLL5	15	0.004707	853268	0.220904
Up	MEOX1	14	0.006081	971858	0.211262
Up	GDF15	13	0.005085	379080	0.219278
Up	C1QB	13	0.004139	711346	0.231896
Up	IGFBP5	13	0.003234	353514	0.226426
Up	FNDC3B	13	0.004388	775238	0.225588
Up	GPX8	12	0.003567	316812	0.217971
Up	MYOF	12	0.002085	511704	0.236937
Up	RND1	11	0.004001	441798	0.205414
Up	CA9	11	0.001316	261604	0.221757
Up	SOD2	11	0.003236	226272	0.197457
Up	SPHK1	10	0.002786	324700	0.204838
Up	TYROBP	10	0.002626	401066	0.186264
Up	ITLN1	10	0.003097	360374	0.211118
Up	ADAMTS1	10	0.003542	389798	0.180012
Up	ORM1	9	0.001475	343028	0.211918
Up	SLC1A3	9	0.00174	168060	0.225335
Up	PSAT1	9	0.003551	357996	0.20973
Up	SLC7A11	8	8.27E-04	210062	0.224705
Up	PCSK9	6	6.65E-04	62018	0.193953
Up	FGFBP1	6	6.22E-04	95582	0.191679
Up	CCL3	6	0.00179	261772	0.184843
Up	FCER1G	4	0.001491	335442	0.172248
Up	MMP2	4	0.002021	313902	0.221354
Up	EGR1	3	3.96E-04	152864	0.223283
Up	CXCL9	3	8.95E-04	97446	0.23493
Up	FPR1	3	9.94E-04	125054	0.158091
Up	CD177	3	8.03E-04	117200	0.222357
Up	SERPINE1	2	9.39E-05	13094	0.193347
Up	PLAU	2	5.95E-04	109428	0.207834
Up	TREM2	2	5.42E-04	92426	0.192855
Up	VCAN	2	7.93E-05	10682	0.176311
Up	MUC5B	2	2.14E-04	53410	0.206204
Up	VWF	2	2.52E-04	77324	0.235273
Up	FAP	2	9.88E-04	249868	0.243065
Up	LBP	2	2.64E-04	31958	0.231043
Up	FOSB	1	0	0	0.203873
Up	CHI3L1	1	0	0	0.213335
Up	PDZK1IP1	1	0	0	0.195385
Up	MAFF	1	0	0	0.180205
Up	SIRPB1	1	0	0	0.157024
Up	CCL7	1	0	0	0.18228
Up	BATF2	1	0	0	0.203873
Up	TREM1	1	0	0	0.157024
Up	PDCD1LG2	1	0	0	0.186601
Up	APOC1	1	0	0	0.215011
Up	CBR3	1	0	0	0.199534
Up	ST3GAL4	1	0	0	0.203101
Up	HTRA3	1	0	0	0.206744
Up	MMP3	1	0	0	0.19177
Up	CXCL10	1	0	0	0.234396
Up	ADAMTS2	1	0	0	0.181621
Up	CLEC5A	1	0	0	0.193729
Up	CCL11	1	0	0	0.234396
Up	MMP10	1	0	0	0.19177
Up	BPIFB1	1	0	0	0.1953
Up	CXCL11	1	0	0	0.234396

Up	LYPD1	1	0	0	0.176427
Up	APCDD1	1	0	0	0.180036
Up	MPO	1	0	0	0.187681
Up	CTSK	1	0	0	0.214736
Up	EMILIN2	1	0	0	0.180343
Up	HK3	1	0	0	0.190354
Up	CXCL2	1	0	0	0.234396
Up	IL1A	1	0	0	0.188402
Up	MMP7	1	0	0	0.163092
Up	MMP1	1	0	0	0.163092
Up	IL11	1	0	0	0.19086
Up	KRT7	1	0	0	0.193263
Up	HGF	1	0	0	0.19805
Up	FGF7	1	0	0	0.178994
Up	COL7A1	1	0	0	0.201554
Up	PHLDA1	1	0	0	0.203244
Up	AQP5	1	0	0	0.203244
Up	TIMP1	1	0	0	0.229004
Up	IL1RN	1	0	0	0.188402
Up	CD300C	1	0	0	0.146944
Up	ZC3H12A	1	0	0	0.192551
Up	CD24	1	0	0	0.207031
Up	PDE4B	1	0	0	0.215011
Up	CD14	1	0	0	0.179425
Up	SLAMF8	1	0	0	0.189762
Up	NETO2	1	0	0	0.193263
Up	TNFAIP6	1	0	0	0.173534
Up	FOLH1	1	0	0	0.216563
Up	COL5A2	1	0	0	0.212635
Up	PTAFR	1	0	0	0.216784
Up	QPCT	1	0	0	0.207031
Down	DPP4	146	0.088346	18433168	0.306135
Down	MME	92	0.045711	5732044	0.276407
Down	SLC39A4	84	0.041292	5141718	0.261866
Down	APOA1	70	0.04121	4975600	0.273885
Down	TMEM25	65	0.030086	6170260	0.26061
Down	SLC15A1	64	0.023948	4841378	0.249938
Down	SLC9A3R1	63	0.036981	3056048	0.272493
Down	DPEP1	56	0.02022	4240888	0.232378
Down	PDZK1	48	0.019465	1313806	0.242816
Down	TUBB2B	48	0.021876	4355476	0.262207
Down	APOB	47	0.026727	3337078	0.275366
Down	CDKN2B	46	0.016386	3553010	0.246945
Down	FRMD1	44	0.017303	2299844	0.23103
Down	SLC39A5	44	0.013709	2783492	0.232137
Down	CYP2S1	35	0.013734	1542642	0.229789
Down	NELL2	34	0.012894	2324222	0.22001
Down	CBS	33	0.011313	2156234	0.228224
Down	USP2	33	0.014587	1941420	0.245859
Down	SLC27A2	33	0.013207	1632562	0.231389
Down	PCK2	32	0.016901	1787444	0.242684
Down	SLC1A1	31	0.012739	1832650	0.235839
Down	PLEKHG6	31	0.012211	1825192	0.236937
Down	BCHE	30	0.010959	1974510	0.220396
Down	TF	30	0.011997	1409792	0.264483
Down	CBR1	30	0.010265	2295726	0.249256
Down	ACE2	29	0.014781	2220904	0.258999
Down	REEP6	29	0.013786	1455822	0.240263
Down	VIPR1	29	0.007956	1100074	0.219721
Down	COBL	28	0.007781	1891418	0.23979
Down	LAMA1	28	0.013127	2529168	0.244246
Down	PEPD	28	0.006207	937018	0.232392
Down	FGFR3	27	0.008229	1984138	0.218006
Down	CDK20	27	0.010407	1349032	0.21303
Down	NR0B2	26	0.010528	2248952	0.23851
Down	ESPL1	26	0.008325	1490364	0.221573
Down	BEGAIN	26	0.009838	840182	0.232768
Down	PREPL	26	0.009712	1188132	0.217794
Down	SERPINA5	25	0.009599	1284528	0.223917
Down	FBP1	24	0.009723	1885054	0.234191

Down	BEND7	23	0.010026	1521240	0.215622
Down	PFN2	22	0.007166	2000886	0.222308
Down	DAB1	21	0.006844	1460020	0.235811
Down	TCL1A	21	0.006074	778630	0.233796
Down	GDA	21	0.005269	457558	0.23362
Down	FLVCR1	21	0.00483	1031152	0.218777
Down	AATK	20	0.005801	1367900	0.227721
Down	CYBRD1	20	0.005385	1135650	0.231602
Down	MAF	19	0.004658	1109032	0.214633
Down	AICDA	19	0.004526	661380	0.211729
Down	NR1I3	19	0.006645	869248	0.23203
Down	FZD7	19	0.007489	702890	0.231936
Down	THSD4	19	0.007395	1007792	0.211595
Down	ANPEP	18	0.002212	808348	0.237637
Down	EVPL	18	0.004327	991330	0.222087
Down	NCCRP1	17	0.003274	949286	0.200749
Down	UGT1A10	15	0.004831	499104	0.217229
Down	OAT	15	0.004719	665404	0.219362
Down	IGSF3	15	0.006106	529990	0.246054
Down	ACY1	14	0.004105	487284	0.195072
Down	RHOD	14	0.004775	630170	0.223184
Down	SLC34A2	14	0.003403	756570	0.198304
Down	ALDOC	13	0.006657	994674	0.251108
Down	BACH2	13	0.003206	433820	0.219805
Down	SOX6	13	0.004619	403446	0.210279
Down	RHOBTB2	13	0.002685	483394	0.218908
Down	ACSF2	13	0.00545	413602	0.204474
Down	RHOU	12	0.003132	609256	0.209479
Down	TPPP	12	0.003397	576782	0.210235
Down	OTC	12	0.003559	724486	0.194921
Down	TUBAL3	11	0.001709	434420	0.222604
Down	EPB41L4B	11	0.003205	367618	0.217617
Down	SUGCT	11	0.003584	490942	0.210081
Down	ALPI	11	0.002106	371580	0.211228
Down	SLC30A2	10	0.00406	610250	0.158309
Down	CCL21	10	0.002326	315492	0.20996
Down	PHYHIPL	10	0.00303	454298	0.197709
Down	PKLR	10	0.003101	503436	0.20112
Down	CXADR	10	0.003363	319176	0.228796
Down	CMBL	10	0.002661	303178	0.216178
Down	CDC14A	9	0.004604	597600	0.226489
Down	MATN2	9	0.003003	564792	0.213109
Down	RNF128	9	0.002148	315406	0.224367
Down	ALDOB	8	0.00168	130786	0.211974
Down	PAX5	8	0.002086	490288	0.204692
Down	BCAN	8	0.002227	288800	0.194864
Down	CREB3L3	8	0.002332	333690	0.194845
Down	SULT2B1	8	0.001595	324306	0.201604
Down	OSGIN1	8	0.00305	432592	0.191005
Down	F10	7	0.002494	602030	0.179762
Down	CYP2C9	7	0.002505	533328	0.177267
Down	ABCC2	6	0.001803	112214	0.223258
Down	CRIP1	6	0.001677	175498	0.177807
Down	PCK1	6	0.002367	228116	0.226107
Down	ZNF488	6	0.001178	127616	0.215046
Down	PMP22	5	0.001743	186820	0.209022
Down	SCAPER	5	0.001046	107342	0.196521
Down	APOM	5	0.001988	384908	0.17328
Down	APOC2	5	3.30E-05	2806	0.213165
Down	MS4A1	4	0.001013	114048	0.198421
Down	ABCB1	4	5.89E-04	44562	0.203029
Down	TNNC2	4	0.001491	176298	0.155976
Down	BPHL	4	0.001032	104248	0.187839
Down	SHBG	4	4.97E-04	36714	0.145167
Down	MEP1B	3	0	0	1
Down	UGT1A7	3	4.97E-04	52424	0.178494
Down	SEMA3B	3	2.71E-04	32110	0.200709
Down	MAOB	2	4.97E-04	125334	0.173797
Down	ITLN2	2	0	0	0.174331
Down	ENTPD5	2	0.001607	289624	0.234574

Down	CHST6	2	2.07E-04	15004	0.184648
Down	NEU4	2	0.001438	166974	0.210907
Down	CYP4F2	2	1	2	1
Down	AQP3	2	4.97E-04	25334	0.195319
Down	FCER1A	2	4.97E-04	88340	0.147922
Down	PDK2	1	0	0	0.204995
Down	PHLPP2	1	0	0	0.214153
Down	MAOA	1	0	0	0.148069
Down	MTTP	1	0	0	0.215923
Down	SLC6A19	1	0	0	0.205729
Down	SLC22A4	1	0	0	0.195385
Down	KLKB1	1	0	0	0.18296
Down	SLC22A5	1	0	0	0.195385
Down	CYP2C18	1	0	0	0.15058
Down	EML6	1	0	0	0.207748
Down	DNAJB13	1	0	0	1
Down	UGT1A8	1	0	0	0.151465
Down	ZDHHC11	1	0	0	0.215923
Down	CYP2C19	1	0	0	0.15058
Down	PLB1	1	0	0	0.178304
Down	CYP4F12	1	0	0	0.666667
Down	NTS	1	0	0	0.205729
Down	SLC30A10	1	0	0	0.136677
Down	SLC34A3	1	0	0	0.195385
Down	KHK	1	0	0	0.197554
Down	PDZD3	1	0	0	0.18252
Down	F11	1	0	0	0.18296
Down	SCT	1	0	0	0.180149
Down	CR2	1	0	0	0.207769
Down	OIT3	1	0	0	0.148534
Down	CD160	1	0	0	0.178756
Down	PRLR	1	0	0	0.201614
Down	SLC19A3	1	0	0	0.195385
Down	TRHDE	1	0	0	0.227759
Down	APOC3	1	0	0	0.215011
Down	SLC2A2	1	0	0	0.215923
Down	SSUH2	1	0	0	0.175825
Down	PDIA2	1	0	0	0.192551
Down	DNAH7	1	0	0	0.227759
Down	CLEC17A	1	0	0	0.184631

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

Regulation	Target Genes	Degree	MicroRNA	Regulation	Target Genes	Degree	TF
Up	TFRC	162	hsa-mir-629-5p	Up	FPR2	24	NFYA
Up	CKAP4	102	hsa-mir-25-5p	Up	FGR	16	FOXA1
Up	HSPA6	65	hsa-mir-3714	Up	TFRC	15	ESR1
Up	STAT1	63	hsa-mir-146a	Up	PLAUR	12	FOS
Up	LAMP3	43	hsa-mir-4651	Up	STX11	8	ARID3A
Up	CTSS	42	hsa-mir-147a	Up	STAT1	7	RELA
Up	MDFI	41	hsa-mir-4685-3p	Up	FBXO6	6	SOX10
Up	PLAUR	31	hsa-mir-129-2-3p	Up	MNDA	6	SRF
Up	FPR2	31	hsa-mir-4757-5p	Up	CTSS	6	SREBF2
Up	FBXO6	30	hsa-mir-3681-3p	Up	MDFI	6	GATA3
Up	STX11	21	hsa-mir-136-3p	Up	FOXP3	6	STAT3
Up	IL13RA2	9	hsa-mir-148b-3p	Up	HSPA6	5	TFAP2C
Up	MNDA	7	hsa-mir-181a-5p	Up	CKAP4	5	POU2F2
Up	FOXP3	5	hsa-mir-372-3p	Up	IL13RA2	4	PRRX2
Up	FGR	3	hsa-mir-155-5p	Up	LAMP3	4	NR3C1
Down	SLC9A3R1	56	hsa-mir-6130	Down	APOA1	12	PRDM1
Down	MME	54	hsa-mir-518f-5p	Down	DPEP1	12	GATA2
Down	TMEM25	41	hsa-mir-522-5p	Down	SLC39A5	11	HOXA5
Down	CDKN2B	35	hsa-mir-641	Down	MME	9	BRCA1
Down	TUBB2B	27	hsa-mir-148a-3p	Down	CDKN2B	9	JUND
Down	APOA1	26	hsa-mir-3179	Down	FRMD1	9	JUN
Down	SLC15A1	19	hsa-mir-1827	Down	SLC15A1	9	MAX
Down	APOB	17	hsa-mir-30a-5p	Down	TUBB2B	9	HINFP
Down	SLC39A4	15	hsa-mir-484	Down	SLC9A3R1	8	CEBPB

Down	DPP4	14	hsa-mir-124-3p	Down	DPP4	8	FOXC1
Down	CYP2S1	11	hsa-mir-1343-3p	Down	PDZK1	8	IRF2
Down	PDZK1	10	hsa-mir-374a-5p	Down	SLC39A4	7	ZNF354C
Down	DPEP1	6	hsa-mir-941	Down	CYP2S1	6	FOXL1
Down	FRMD1	2	hsa-mir-146a-5p	Down	APOB	4	ELK4
Down	SLC39A5	2	hsa-mir-26b-3p	Down	TMEM25	4	USF2

Figures

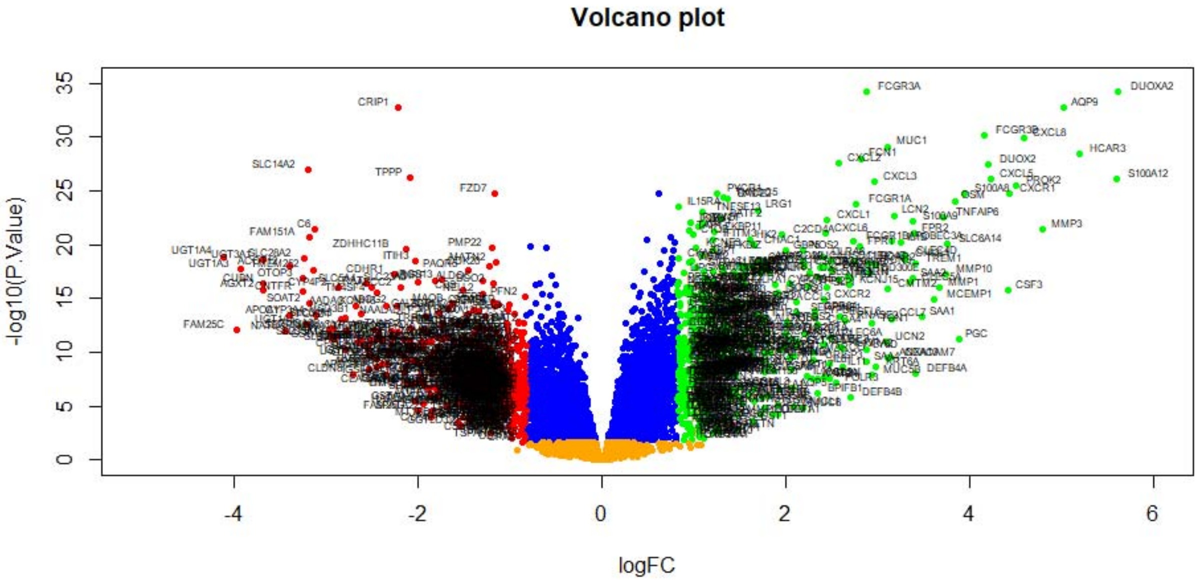

Fig. 1. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

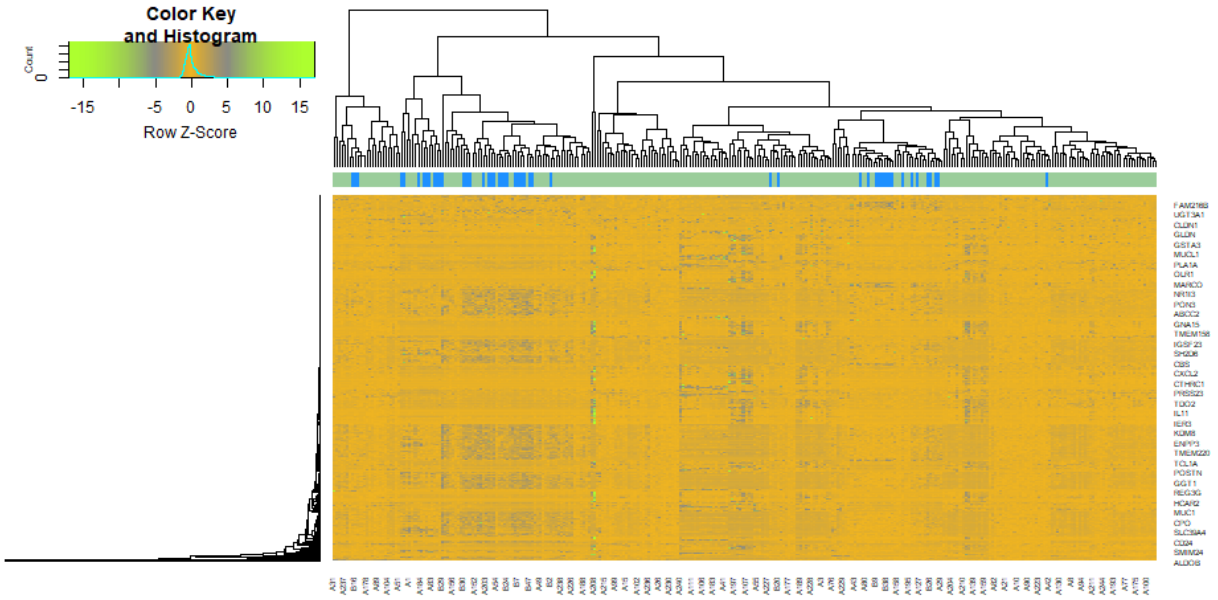

Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A254 = CD samples; B1 – B50 = normal control samples)

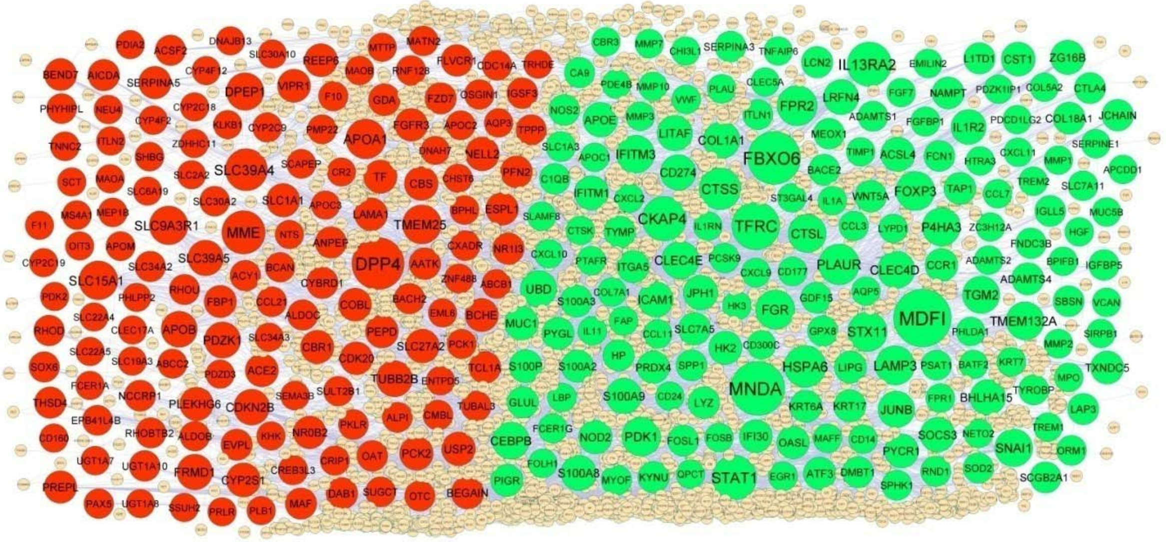

Fig. 3. PPI network of DEGs. Up regulated genes are marked in green; down regulated genes are marked in red

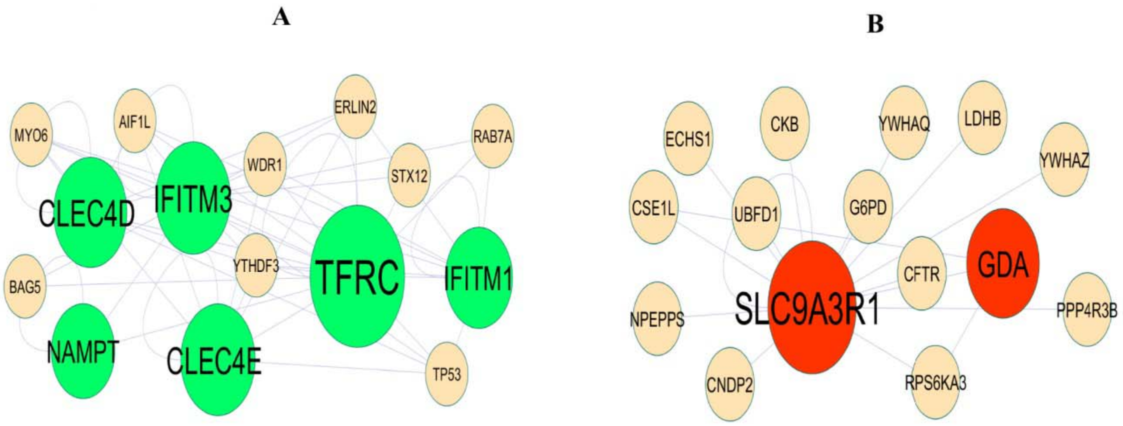

Fig. 4. Modules selected from the DEG PPI between patients with FSGS and normal controls. (A) The most significant module was obtained from PPI network with 15 nodes and 49 edges for up regulated genes (B) The most significant module was obtained from PPI network with 15 nodes and 17 edges for down regulated genes. Up regulated genes are marked in green; down regulated genes are marked in red

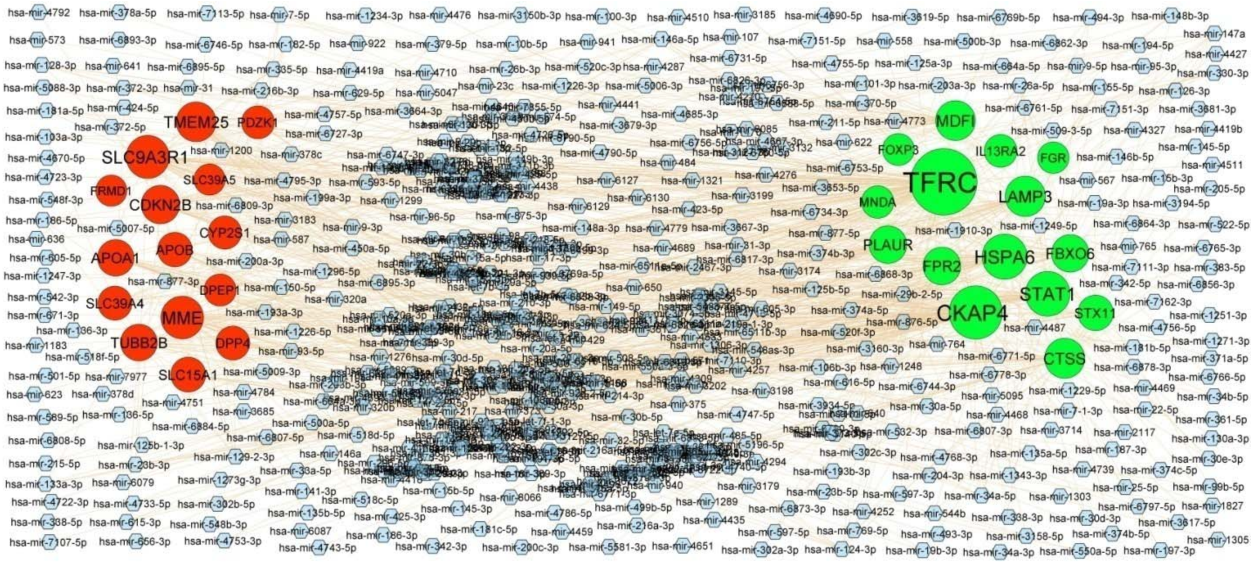

Fig. 5. Target gene - miRNA regulatory network between target genes. The blue color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

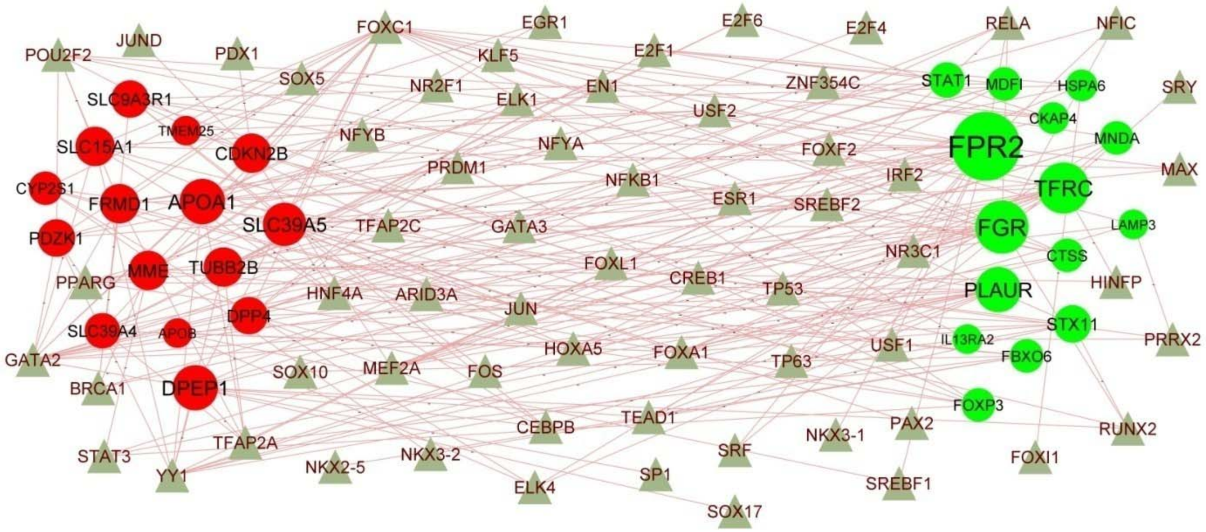

Fig. 6. Target gene - TF regulatory network between target genes. The olive color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

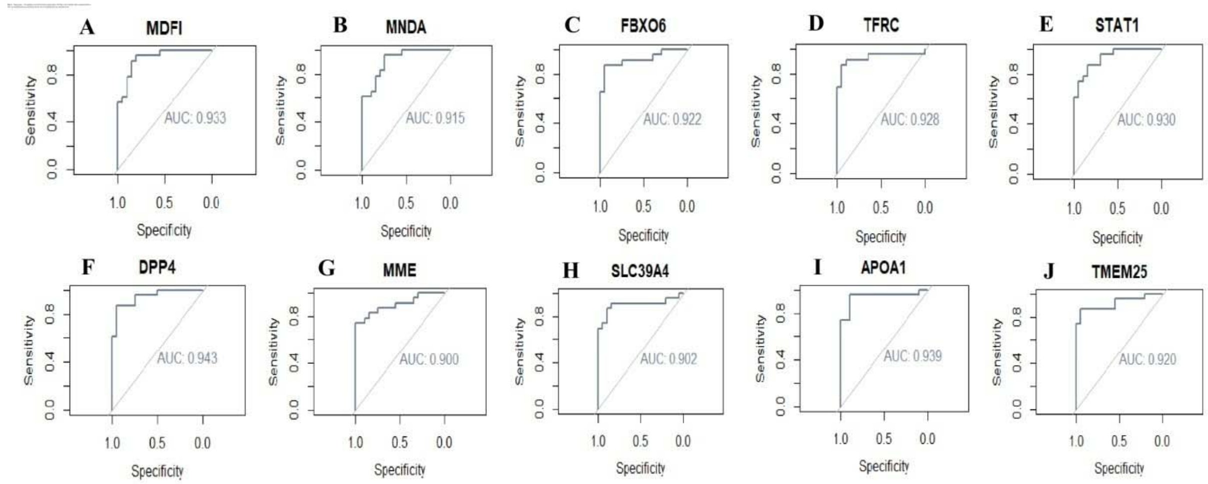

Fig. 7. ROC curve analyses of hub genes. A) MDFI B) MNDA C) FBXO6 D) TFRC E) STAT1 F) DPP4 G) MME H) SLC39A4 I) APOA1 J) TMEM25