**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`s 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 GSE73374 from the Gene Expression Omnibus (GEO) database. The NGS dataset GSE73374 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`s 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 $\geq 2$, node score cutoff = 0.2, K − core $\geq 2$, 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| | | | | | | 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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 |

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|---|---|---|---|---|---|---|
| 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, |

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| | | | | | | PTGS2,IRAK3,TLR2,ALOX15B,<br>MEFV,PI3,PIGR,OASL,F2RL2,IG<br>FBP5,FFAR4,CCR2,JUNB,RND1,<br>CHRNA5,KCNJ2,BHLHA15,VWF<br>,SLC7A11,NOD2,DMBT1,IL20RA<br>,TYMP,HSPA6,ADGRF1,NAMPT,<br>GNA15,S100P,PDPN,THEMIS2,C<br>LEC6A,P2RY6,ADAMTS1,ADCY<br>AP1,PGC,ATF3,TIMP1,UCN2,FC<br>AR,SLAMF8,FAP,CTSL,SIGLEC9<br>,SELE,SLC1A3,ICAM1,EDNRA,F<br>OSL1,CD300C,RASGRP4,AREG,<br>LYZ,PIM2,SLC7A5,PF4V1,IL13R<br>A2,COL4A1,CH25H,LY6D,COL5<br>A2,SNAI1,FFAR2,MARCO,MXR<br>A5,CCL4L2,EGR1,TNFRSF17,M<br>DFI,ST3GAL4,SRGN,IFITM2,CE<br>ACAM6,CCL11,IFNG,PTAFR,TR<br>EM2,INHBA,SERPING1,CLC,AP<br>OE,FGR,CRISP3,CTSK,SAA4,AL<br>PL,CCR1,NR4A3,IL6,CTHRC1,P<br>DCD1LG2,SFRP1,CCL4,SNX10,N<br>FAM1,KRT6A,SPP1,CLDN1,CA2,<br>IL11,PHLDA2,CLDN18,NNMT,C<br>OL15A1,KYNU,FGFBP1,RAB31,<br>TNFRSF18,TNFRSF4,COL1A1,F<br>AM20A,RNF186,MMP12,COL3A<br>1,MMP2,C2CD4B,PLEK,IFI44L,L<br>ILRB4,IL1A,ITGA5,CCL1,MLN,G<br>PR4,WNT2,SIRPB1,HAPLN3,HB<br>EGF,ADGRE3,GPX2,CD24,CCL3<br>L3,PDE4B,AQP5,SCNN1B,GLDC,<br>REG1A,UBD,SPHK1,AOX1,CYP7<br>B1,GPR141,STC2,BPIFB1,LAMP3<br>,TFF2,ITGAX,POSTN,REG1B,G0<br>S2,GZMB,OLR1,SELP,THY1,MU<br>C5AC,BCL2A1,FGF7,SERPINA3,<br>TWIST1,CCL8,CSF2,PLAU,CD17<br>7,CA9,GFPT2,TDO2,TFF1,STC1,I<br>TLN1,CTLA4,C4BPA,TNIP3,PAD<br>I4,ORM1,MMP13,WFDC2,HBD,H<br>RH2,FOSB,LBP,CST1,PGLYRP1,<br>GAS1,MASP1,KLK6,VSNL1,FFA<br>R3,RETN,ODAM,GIP,MPO,HAS1<br>,LEFTY1,HP,SCGB2A1,CYP24A1 |
| GO:0042221 | BP | response to chemical | 1.59E-45 | 44.79866426 | 230 | AQP9,CXCL8,CXCL2,DUOX2,C<br>XCL5,S100A12,CXCL3,PROK2,S<br>100A8,CXCR1,PYCR1,OSM,IL15<br>RA,LRG1,TNFAIP6,CXCL1,S100<br>A9,IFITM1,C2,XBP1,MMP3,FPR2<br>,CXCL6,IFITM3,HK2,APOBEC3A<br>,IL1B,SLC6A14,CHAC1,FPR1,NO<br>S2,GBP5,ZBP1,LILRA6,CHI3L1,T<br>GM2,TREM1,CSF3R,WNT5A,HG<br>F,CXCL9,GBP1,ADM,ALDH1A2,<br>CXCL11,LILRB3,PLAUR,CXCL1<br>0,LIPG,FIBIN,LILRB2,SLC11A1,<br>GDF15,IL1RN,ADGRE2,PRDX4,S<br>TAT1,LILRA5,CYP27B1,LILRA1,<br>ZC3H12A,SLPI,CMTM2,CSF3,FB |

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| | | | | | | 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 |

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| | | | | | | ,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 |

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| | | | | | | 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 |

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| | | | | | | 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 |

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| | | | | | | 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, |

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| | | | | | | 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 |

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| | | | | | | 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

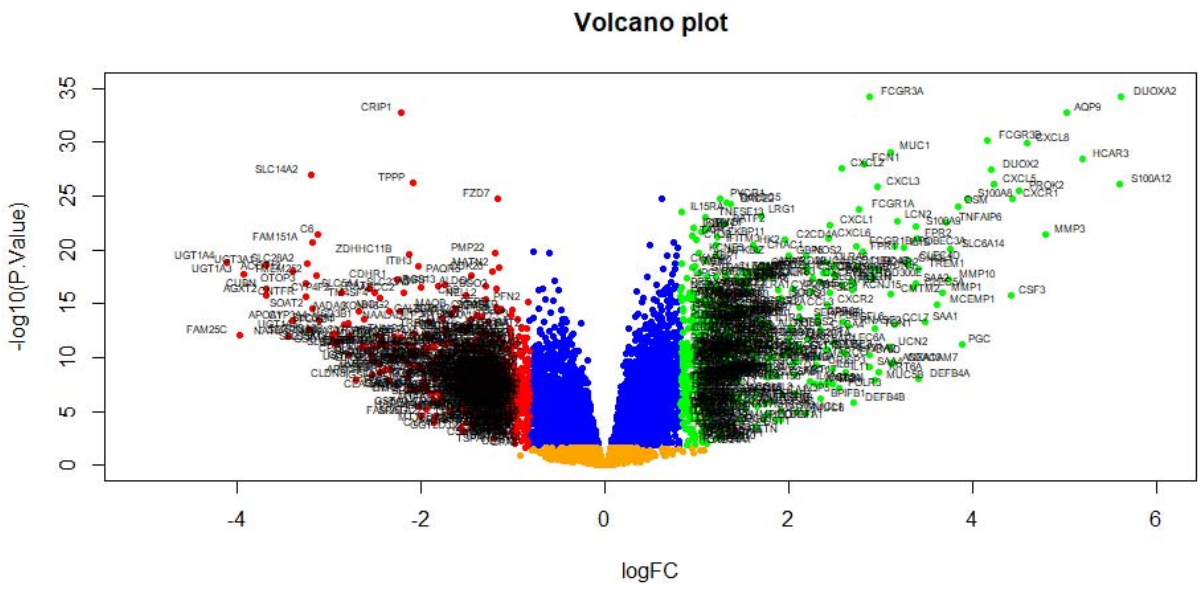


**Fig. 1**. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

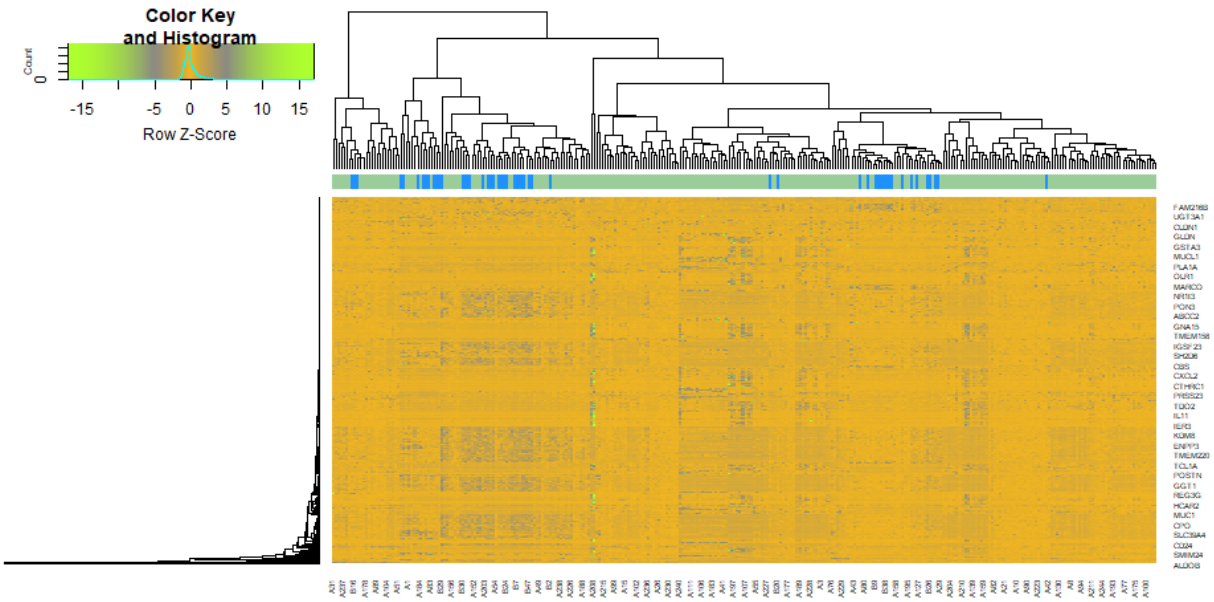

**Fig. 2.** Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A254 = CD samples; B1 – B50 = normal control samples)

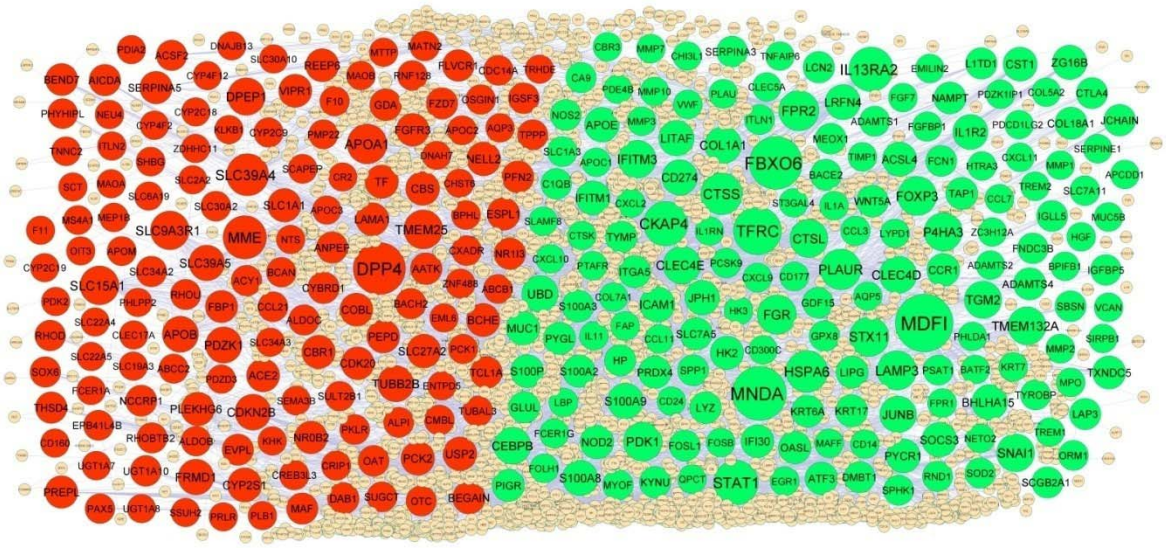


**Fig. 3.** PPI network of DEGs. Up regulated genes are marked in green; down regulated genes are marked in red

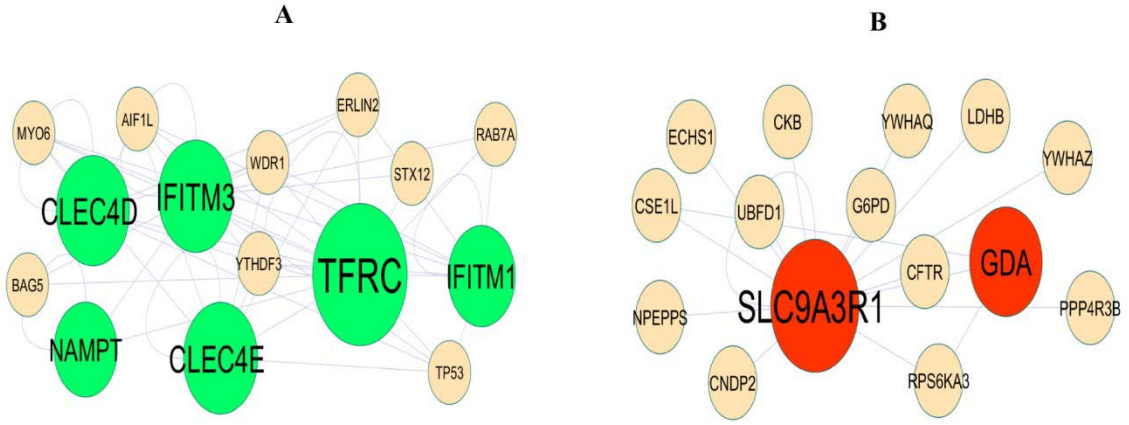


**Fig. 4.** Modules selected from the DEG PPI between patients with FSGS and normal controls. (A) The most significant module was obtained from PPI network with 15 nodes and 49 edges for up regulated genes (B) The most significant module was obtained from PPI network with 15 nodes and 17 edges for down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

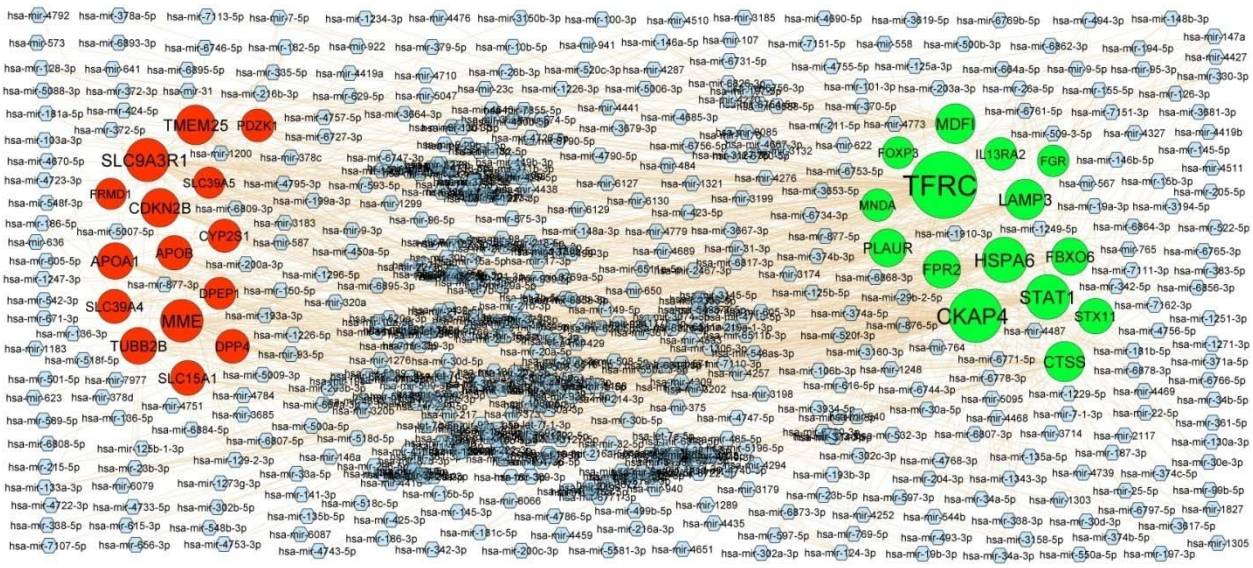


**Fig. 5.** Target gene - miRNA regulatory network between target genes. The blue color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

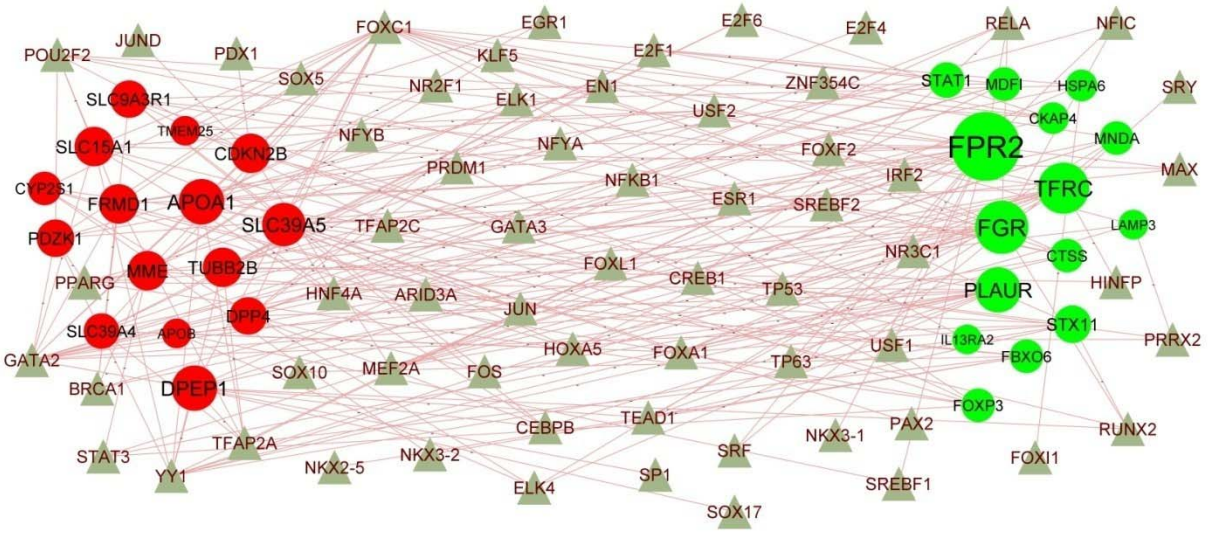


**Fig. 6.** Target gene - TF regulatory network between target genes. The olive color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

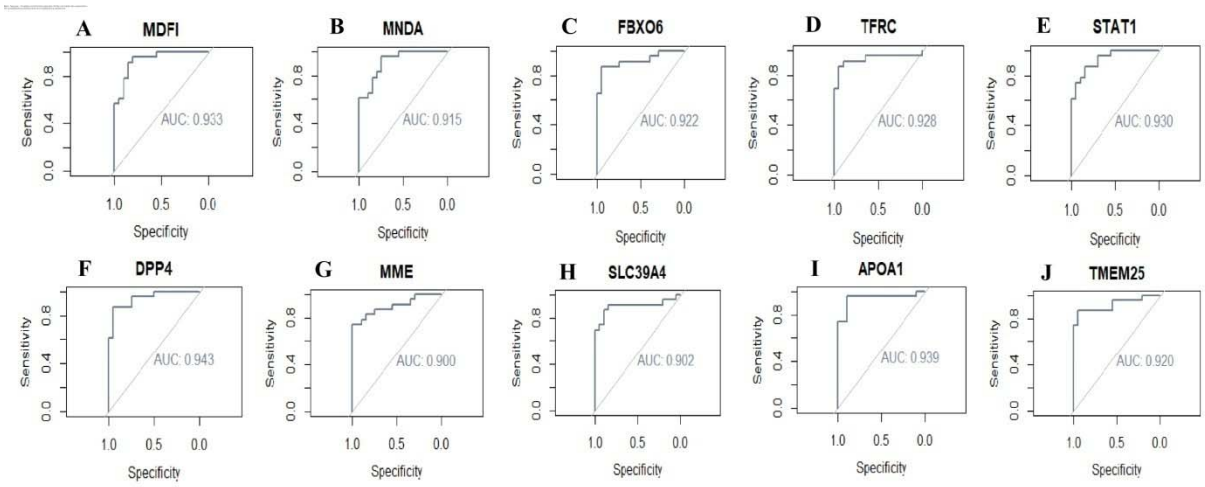


**Fig. 7.** ROC curve analyses of hub genes. A) MDFI B) MNDA C) FBXO6 D) TFRC E) STAT1 F) DPP4 G) MME H) SLC39A4 I) APOA1 J) TMEM25