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Identification of key genes and signaling pathway in the pathogenesis of Huntington's disease via bioinformatics and next generation sequencing data analysis

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Abstract

Huntington's disease (HD) is the primary cause of progressive motor deficits, psychiatric symptoms, and cognitive impairment. The exact molecular mechanisms of HD pathogenesis are largely unknown. This investigation aims to identify the hub genes, miRNA and TFs in HD and explore their potential molecular regulatory network. Next generation sequencing (NGS) dataset (GSE105041) was extracted from the Gene Expression Omnibus (GEO) database. An integrated bioinformatics pipeline including identification of differentially expressed genes (DEGs), Gene ontology and REACTOME pathway enrichment analysis, protein-protein interaction (PPI) network and module analysis, miRNA-hub gene regulatory network analysis and TF-hub gene regulatory network analysis, and receiver operating characteristic curve (ROC) analysis were applied to identify hub genes, miRNA and TFs, and key drivers of HD pathogenesis. We identified 958 DEGs in the discovery phase, consisting of 479 up regulated genes and 479 down regulated genes. GO and REACTOME enrichment analyses of the 479 up regulated genes and 479 down regulated genes showed that they were mainly involved in multicellular organismal process, developmental process, signaling by GPCR and MHC class II antigen presentation. Further analysis of the PPI network using Cytoscape and PEWCC plugins identified 10 hub genes, including LRRK2, MTUS2, HOXA1, IL7R, ERBB3, EGFR, TEX101, WDR76, NEDD4L and COMT. Possible target miRNAs and TFs, including hsa-mir-1292-5p, hsa-mir-4521, ESRRB and SREBF1, were predicted by constructing a miRNA-hub gene regulatory network analysis and TF-hub gene regulatory network. This investigation used bioinformatics methods to explore the molecular pathogenesis of HD, and identified potential molecular markers. These molecular markers might provide novel ideas and methods for the early diagnosis, treatment, and monitoring of HD.

Keywords: Huntington's disease; bioinformatics; biomarkers; next generation sequencing; differentially expressed genes

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Introduction

Huntington's disease (HD) is a rare, inherited, neurodegenerative disorder that manifests as progressive motor deficits, psychiatric symptoms, and cognitive impairment [1]. It is estimated to affect 2.7 per 100,000 individuals of the global population [2]. HD prevalence observed in childhood, adolescence, and adulthood, but in most cases, this occurs in middle aged adulthood [3]. HD is characterized by involuntary movements, slight difficulty with executive functions, and depressed mood [4]. Several risk factors have been proposed to cause HD, including genetic inheritance [5], environmental variables [6], inflammation [7], hypertension [8], cardiovascular diseases [9] and diabetes mellitus [10]. Despite emerging proof providing considerable mechanistic insight into this condition, the exact molecular mechanism of HD is still being debated. As HD has not clear picture of pathogenesis and a not satisfactory response to drug treatment, it is necessary to explore the molecular mechanism of HD to develop effective diagnosis, prognosis and target treatments.

Several investigations has described that significant molecular biomarkers and signaling pathways in HD were identified as prognostic or therapeutic factors, such as Huntingtin (HTT) protein [11], arachidonate 5-lipoxygenase (ALOX5) [12], type II CRISPR RNA-guided endonuclease Cas9 (CRISPR/Cas9) [13], interleukin-6 (IL6) [14], RE1 silencing transcription Factor (REST) [15], insulin/IGF1 (IIS) signaling pathway [16], hippo signaling pathway [17], PI3K/AKT/FoxO1 signaling pathway [18], cAMP/CREB/BDNF signaling pathway [19] and GLP-1 Receptor/PI3K/Akt/BDNF signaling pathway [20]. The identification of novel biomarkers and signaling pathway might be helpful to improve the clinical outcome of HD patients.

Bioinformatics and next generation sequencing (NGS) data analysis are a well-orchestrated tool for screening prognosis and diagnosis relevant biomarkers, which can contribute to the advancement of HD treatment [21]. At current, NGS data downloaded from Gene Expression Omnibus (GEO) database [https://www.ncbi.nlm.nih.gov/geo/] [22] can be used to detect genes expression levels and to provide the technical support for monitoring mRNA expression and cell function prediction in various diseases [23-24].

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During the last decades, NGS technology and bioinformatics analysis have been widely used to screen genetic alterations at the genome level, which have helped us identify the differentially expressed genes (DEGs) and functional pathways involved in the progression of HD. Thus, in the current investigation, NGS dataset (GSE105041) [25] from GEO was downloaded and analyzed to obtain DEGs between HD and normal control samples. Subsequently, Gene Ontology (GO), REACTOME pathway enrichment analysis protein-protein interaction (PPI) network analyses, miRNA-hub gene regulatory network analyses and TF-hub gene regulatory network analyses were performed to help us understand the molecular mechanisms underlying progression of HD. Finally, candidate hub genes were verified by receiver operating characteristic curve (ROC) analysis. In short, these results indicated that the biomarkers might have potential value in prognosis, diagnosis and therapeutic targets of HD.

Materials and Methods

Next generation sequencing (NGS) data source

GSE105041 [25] NGS dataset was downloaded from the GEO database. The GSE105041 dataset was generated utilizing the GPL16791 Illumina HiSeq 2500 (Homo sapiens) platform and contained 28 HD samples and 20 normal control samples.

Identification of DEGs

The DEGs between HD and normal control samples were screened using DESeq2 [26] . DESeq2 is an R Bioconductor tool that allows users to identify DEGs across experimental conditions. The adjusted P-values (adj. P) and Benjamini and Hochberg false discovery rate were applied to provide a balance between discovery of statistically significant genes and limitations of false-positives [27]. logFC (fold change) > 1.966 for up regulated genes, logFC (fold change) < -0.7343 for down regulated genes and adj. P-value <0.05 were considered statistically significant. Significant DEGs were visualized using volcano plot and heatmaps. Both visualizations were completed by“ggplot2” and “gplot” an R Bioconductor packages for data analysis and visualization.

GO and pathway enrichment analyses of DEGs

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Gene Ontology (GO) annotation (http://www.geneontology.org) [28] and REACTOME (https://reactome.org/) [29] pathway enrichment analysis were performed for DEGs. GO Annotation such as analysis of biological processes (BP), cell components (CC), and molecular functions (MF). REACTOME is an online database for pathway enrichment analysis of a large amount of genetic information. GO functional annotation analysis and REACTOME pathway enrichment analysis were performed in the website g:Profiler (http://biit.cs.ut.ee/gprofiler/) [30] import our gene name into the website for enrichment analysis. The significant enrichment threshold was set as p-value < 0.05, GO functions and pathways with the lowest p-values were selected as the top.

Construction of the PPI network and module analysis

The protein-protein interaction (PPI) network was created from the "Integrated Interactions Database (IID)" (http://iid.ophid.utoronto.ca/search_by_proteins/) [31] database for DEGs and is designed to discover the interaction of DEGs and their interactions with other genes, and Cytoscape (v 3.10.2) (http://www.cytoscape.org/) [32] was used to edit the graphics. The node degree [33], betweenness [34], stress [35] and closeness [36] algorithms of Network Analyzer in Cytoscape was used to explore hub genes. The plug-in PEWCC Cytoscape software is an APP for clustering a given network based on topology to find densely connected regions in PPI network [37]. The most significant module in the PPI networks was identified using PEWCC. Subsequently, the GO and REACTOME pathway enrichment analyses and for genes in this module were performed using g:Profiler.

Construction of the miRNA-hub gene regulatory network

miRNAs constitute major control modes of gene expression, negatively regulate target genes by combining with the 3′ untranslated region of mRNA. To choose the miRNAs, miRNA-hub gene regulatory network has been visualized by the miRNet (https://www.mirnet.ca/) [38] online platform, which has been widely used as a bioinformatics tool. Constructed a miRNA-hub gene regulatory network graph using Cytoscape (v. 3.10.2) http://www.cytoscape.org/) [32] to show the interactions intuitively.

Construction of the TF-hub gene regulatory network

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TFs constitute major control modes of gene expression, such as transcription and post transcription. To choose the TFs, TF-hub gene regulatory network has been visualized by the NetworkAnalyst database (https://www.networkanalyst.ca/) [39] online platform, which has been widely used as a bioinformatics tool. Constructed a TF-hub gene regulatory network graph using Cytoscape (v. 3.10.2) http://www.cytoscape.org/) [32] to show the interactions intuitively.

Receiver operating characteristic curve (ROC) analysis

The multivariate modeling with combined selected hub genes were used to identify molecular biomarkers with high sensitivity and specificity for HD diagnosis. One data used as training dataset and other data used as validation dataset iteratively. The receiver operator characteristic curves were plotted and area under curve (AUC) was determined separately to check the performance of each model using the R packages "pROC" [40]. A AUC > 0.8 designated that the model had a excellent fitting effect.

Results

Identification of DEGs

GSE105041 was selected and underwent DEGs analysis using "DESeq2" package in R software. 958 DEGs were identified either up or down regulated in all, including 479 up and 479 down regulated genes (|logFC (fold change) > 1.966 for up regulated genes, logFC (fold change) < -0.7343 for down regulated genes and adj. P-value <0.05) (Table 1). As shown in Fig 1, all 958 DEGs were plotted that green ones represented up regulation, red ones indicated down regulation. What's more, the expression levels of all the DEGs were presented in the heatmap (Fig. 2), and these genes were well clustered between HD and normal control samples.

GO and pathway enrichment analyses of DEGs

To obtain a deeper insight into the biological functions of DEGs, GO annotation and REACTOME pathway enrichment analyses were performed. The top enriched GO terms were shown in Table 2. The GO terms were comprised of 3 parts: BP, CC and MF. DEGs of BP were involved in multicellular organismal process, biological regulation and developmental process. CC analysis revealed that DEGs were markedly enriched neuron projection, membrane, cell periphery and cellular

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anatomical entity. For MF analysis, the top significantly enriched terms were DNA-binding transcription factor activity, molecular transducer activity, ion binding and protein binding. Besides, the enriched REACTOME pathways as presented in Table 3, including signaling by GPCR, Class A/1 (Rhodopsin-like receptors, MHC class II antigen presentation and impaired BRCA2 binding to PALB2.

Construction of the PPI network and module analysis

The IID database was used to identify the PPI pairs. As revealed in Fig 3 , 7583 nodes (genes) and 15228 edges (interactions) were established in the constructed PPI network. According to the node degree, betweenness, stress and closeness value, the hub genes were determined. The results shown that LRRK2, MTUS2, HOXA1, IL7R, ERBB3, EGFR, TEX101, WDR76, NEDD4L and COMT were the hub gene with the highest node degree, betweenness, stress and closeness (Table 4). Furthermore, the 2 significant modules were extracted from the PPI network. Module 1 contained 13 gene nodes and 24 edges (Fig. 4A). Module 2 contained 19 genes nodes and 38 edges (Fig. 4B). The functional and pathway analyses of genes involved in two significant modules were analyzed using g:Profiler. Results showed that genes in module 1 was mainly enriched in multicellular organismal process. Module 2 was mainly enriched in cellular anatomical entity, multicellular organismal process and protein binding.

Construction of the miRNA-hub gene regulatory network

MiRNA-hub gene regulatory network was generated using the miRNet web tool. The network contained 2208 nodes (miRNA: 1938; Hub Gene: 270) and 9807 edges (Fig. 5). EPAS1 was regulated by 89 miRNAs (ex: hsa-mir-1292-5p); KRT8 was regulated by 65 miRNAs (ex: hsa-mir-432-3p); ERBB3 was regulated by 53 miRNAs (ex: hsa-mir-6801-3p); HOXA1 was regulated by 45 miRNAs (ex: hsa-mir-10a); HSPA2 was regulated by 45 miRNAs (ex: hsa-mir-7977); CCND2 was regulated by 365 miRNAs (ex: hsa-mir-4521); MAP1B was regulated by 249 miRNAs (ex: hsa-mir-363-3p); TOP2A was regulated by 104 miRNAs (ex: hsa-mir-4487); EGFR was regulated by 83 miRNAs (ex: hsa-mir-21-5p); NEDD4L was regulated by 76 miRNAs (ex: hsa-mir-6807-5p) (Table 5).

Construction of the TF-hub gene regulatory network

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TF-hub gene regulatory network was generated using the NetworkAnalyst web tool. The network contained 465 nodes (TF: 187; Hub Gene: 278) and 5830 edges (Fig. 6). EPAS1 was regulated by 49 TFs (ex: ESRRB); TGM2 was regulated by 43 TFs (ex: SMAD4); HOXA1 was regulated by 37 TFs (ex: EED); KRT8 was regulated by 31 TFs (ex: ATF3); MTUS2 was regulated by 30 TFs (ex: TBX5); NEDD4L was regulated by 50 TFs (ex: SREBF1); CCND2 was regulated by 42 TFs (ex: SMARCA4); EGFR was regulated by 39 TFs (ex: ARNT); MAP1B was regulated by 35 TFs (ex: EP300); DCLK1 was regulated by 31 TFs (ex: CREB1) (Table 5).

Receiver operating characteristic curve (ROC) analysis

To validate the diagnostic effectiveness of LRRK2, MTUS2, HOXA1, IL7R, ERBB3, EGFR, TEX101, WDR76, NEDD4L and COMT for HD by ROC analysis. The larger the AUC, the more the capability of the molecular biomarker to diagnose HD with excellent specificity and sensitivity. As shown in Fig 7, the AUC value of LRRK2 was 0.910; AUC value of MTUS2 was 0.912; AUC value of HOXA1 was 0.891; AUC value of IL7R was 0.894; AUC value of ERBB3 was 0.896; AUC value of EGFR was 0.916; AUC value of TEX101 was 0.900; AUC value of WDR76 was 0.882; AUC value of NEDD4L was 0.887; AUC value of NEDD4L was 0.907.

Discussion

HD is the main cause of neurodegenerative disease globally [41]. Due to the extremely complex CNS disorders that occur in patients with HD, once HD has reached the terminal stage, it is often more difficult to treat than other CNS diseases. Although many investigations have studied the molecular pathogenesis of HD, it has not been clarified completely [42]. Therefore, it is necessary to identify potential biomarkers for early diagnosis and targeted therapy of HD. This investigation used NGS data to conduct bioinformatics analysis for identifying target genes and pathways involved in the occurrence and advancement of HD. The results of this investigation suggest that novel biomarkers and signaling pathways may play a key role in the pathogenesis of HD.

We first downloaded HD related NGS dataset, GSE105041 from the GEO database, which were used for analysis to obtain DEGs. A total of 958 DEGs were

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identified in HD patients compared with the normal control samples, including 479 up regulated and 479 down regulated genes. HSPA2 [43] might be a potential target for Alzheimer's disease treatment. BCAS1 [44] and MAG (myelin associated glycoprotein) [45] engages in the development of multiple sclerosis. Previous studies have demonstrated that BCAS1 [46] and MAG (myelin associated glycoprotein) [47] are linked with the development mechanisms of schizophrenia. Levels of BCAS1 [48], MAG (myelin associated glycoprotein) [49], ZNF208 [50] and PEG3 [51] are increased in patients with stroke. MAG (myelin associated glycoprotein) [52] participate in pathogenic processes of Parkinson's disease. Recent evidence indicates that BCAS1 [46], MAG (myelin associated glycoprotein) [49] and CES1P1 [53] are key to progression of inflammation. Previous research suggested some cardiac biomarkers, such as ZNF208 [54] and PEG3 [55] could be valuable in the diagnosis and prognosis of cardiovascular diseases. The above results suggest that significant DEGs might be involved in the progression of HD.

To obtain a deeper understanding into the biological functions of DEGs, GO annotation and REACTOME pathway enrichment analyses were performed. These enrichment analyses were used to explore the molecular mechanisms of enriched genes involved in the occurrence and advancement of HD. Signaling pathways include signaling by GPCR [56] and extracellular matrix organization [57] were responsible for advancement of HD. Research has shown that CBLN2 [58], MOG (myelin oligodendrocyte glycoprotein) [59], ROS1 [60], LGR6 [61], GJA5 [62], SUCNR1 [63], REN (renin) [64], VEGFC (vascular endothelial growth factor C) [65], TLR2 [66], FGF12 [67], WT1 [68], SLC22A3 [69], CSRP3 [70], PAPPA2 [71], ACAN (aggrecan) [72], SHH (sonic hedgehog signaling molecule) [73], PDC (phosducin) [74], AGTR1 [75], XDH (xanthine dehydrogenase) [76], P2RX7 [77], NTSR1 [78], SIRT2 [79], RBP4 [80], BMP2 [81], ERBB3 [82], HAS2 [83], CDH13 [84], CSMD1 [85], NR3C2 [86], EPAS1 [87], TRPC6 [88], MMP3 [89], ERAP2 [90], HLA-DRB1 [91], CD74 [92], VWF (von Willebrand factor) [93], MTTP (microsomal triglyceride transfer protein) [94], NEDD4L [95], CASP1 [96], BRCA2 [97], EFNB2 [98], PLCE1 [99], EGFR (epidermal growth factor receptor) [100], ABCA1 [101], CRHR2 [102], RND3 [103], COMT (catechol-O-methyltransferase) [104] and SMAD9 [105] plays an important role in the pathogenesis of hypertension. Studies have revealed that NEUROD4 [106],

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SOX10 [107], MOG (myelin oligodendrocyte glycoprotein) [108], NR5A2 [109], GLRA3 [110], FA2H [111], SERPINA [112], HOXB9 [113], TGM2 [114], LRRK2 [115], ROS1 [116], CD22 [117], LGR6 [118], GDF3 [119], GPR17 [120], TF (transferrin) [121], NEUROD1 [122], RELN (reelin) [123], LCP1 [124], DYSF (dysferlin) [125], LGR5 [126], SUCNR1 [127], ASCL2 [128], HOXA5 [129], MSR1 [130], REN (renin) [131], NEU4 [132], VEGFC (vascular endothelial growth factor C) [133], OLIG2 [134], SLC1A1 [135], TLR2 [136], WT1 [137], SYK (spleen associated tyrosine kinase) [138], BMP8B [139], GDF6 [140], NKX6- 1 [141], SLC22A3 [142], CADM2 [143], FREM1 [144], TWIST2 [145], WNT16 [146], KISS1 [147], TMEM176B [148], MYL9 [149], IL7R [150], MBP (myelin basic protein) [151], GPR37 [152], ACAN (aggrecan) [153], SHH (sonic hedgehog signaling molecule) [154], HOXD9 [155], PROK1 [156], AGTR1 [157], TIE1 [158], P2RX7 [159], NTSR1 [160], VTN (vitronectin) [161], SIRT2 [162], RBP4 [163], LPAR5 [164], IL2RG [165], BMP2 [166], EPAS1 [167], HAS2 [168], ERMN (ermin) [169], CSMD1 [170], NKX6-1 [171], POU2F3 [172], NR3C2 [173], TRPC6 [174], CCL25 [175], MMP3 [176], ERAP2 [177], FGF19 [178], HLA-DRB1 [179], NKX2-3 [180], CD74 [92], HLA-DRA [181], VWF (von Willebrand factor) [182], BCL6B [183], ANGPT2 [184], LRRC19 [185], TTPA (alpha tocopherol transfer protein) [186], NEDD4L [187], CASP1 [188], NR2E1 [189], PDE2A [190], CCND2 [191], TET1 [192], AFF2 [193], ZBTB20 [194], EFNB2 [195], DCLK1 [196], PLCE1 [197], EGFR (epidermal growth factor receptor) [198], ABCA1 [199], NFIB (nuclear factor I B) [200], PDPN (podoplanin) [201], PLXNA4 [202], FOXG1 [203], MAP1B [204], SLCO1B1 [205], RND3 [206], COMT (catechol-O-methyltransferase) [207], GPR39 [208], RHCG (Rh family C glycoprotein) [209], FBLN7 [210], LIFR (LIF receptor subunit alpha) [211], TRAF5 [212], HDC (histidine decarboxylase) [213], SLFN11 [214], CIITA (class II major histocompatibility complex transactivator) [215], DAPK2 [216] and CDO1 [217] plays a key role in inflammation. NEUROD4 [218], NR5A2 [219], GLRA3 [220], DMRT2 [221], NKX2-2 [222], TGM2 [223], LRRK2 [224], CD22 [225], GDF3 [226], TF (transferrin) [227], KLRC3 [228], NEUROD1 [229], KCNH6 [230], LGR5 [231], SUCNR1 [63], TFAP2B [232], MSR1 [233], REN (renin) [234], TLR2 [235], PCSK2 [236], SLC24A2 [237], HOXA3 [238], MNX1 [239], SLC22A3 [240], CADM2 [241], TSPAN8 [242], KISS1 [243], IL7R [244], MBP (myelin basic protein) [245], XAF1 [246], SHH (sonic hedgehog signaling molecule) [247], AGTR1 [248],

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VTN (vitronectin) [249], SIRT2 [250], RBP4 [251], ISM1 [252], BMP2 [253], SPINK1 [254], ERBB3 [255], CDH13 [256], NPY4R [257], NR3C2 [258], TRPC6 [259], CCL25 [260], MMP3 [261], FGF19 [262], HLA-DMB [263], HLA-DRB1 [264], PLEK (pleckstrin) [265], CD74 [266], VWF (von Willebrand factor) [267], MTTP (microsomal triglyceride transfer protein) [268], HLA-DMA [269], CASQ1 [270], ANGPT2 [271], CASP1 [272], NR2E1 [273], CCND2 [274], OAS1 [275], EGFR (epidermal growth factor receptor) [276], LAMA1 [277], ABCA1 [278], SLCO1B1 [205], CRHR2 [279], ANK1 [280], GPR39 [281], GRB14 [282] and TXNRD2 [283] have been known to be involved in diabetes mellitus progression. SOX10 [284], MOG (myelin oligodendrocyte glycoprotein) [285], TGM2 [286], LRRK2 [287], CD22 [288], GPR17 [120], TF (transferrin) [289], RELN (reelin) [290], DYSF (dysferlin) [291], HOXA5 [292], REN (renin) [293], CNTN1 [294], SLC1A1 [295], TLR2 [296], WT1 [297], MOBP (myelin associated oligodendrocyte basic protein) [298], MYRF (myelin regulatory factor) [299], IL7R [300], MBP (myelin basic protein) [151], SHH (sonic hedgehog signaling molecule) [301], NTSR1 [302], BMP2 [303], ERMN (ermin) [304], MMP3 [305], HLA-DRB5 [306], HLA-DMB [307], HLA-DRB1 [308], HLA-DRA [309], CASP1 [310], OAS1 [311], DCLK1 [312], EGFR (epidermal growth factor receptor) [313], COMT (catechol-O-methyltransferase) [314] and CIITA (class II major histocompatibility complex transactivator) [315] have a significant prognostic potential in multiple sclerosis. SOX10 [316], MOG (myelin oligodendrocyte glycoprotein) [317], CNGB1 [318], TGM2 [319], LRRK2 [320], CHRNA4 [321], RELN (reelin) [322], HTR2C [323], RIT2 [324], ACSL6 [325], C6 [326], REN (renin) [327], OLIG2 [328], TLR2 [329], SEMA3D [330], PCDH15 [331], FGF14 [332], TSPAN8 [333], ACAN (aggrecan) [334], SHH (sonic hedgehog signaling molecule) [335], P2RX7 [336], NTSR1 [337], RBP4 [338], TACR3 [339], ERBB3 [340], ERMN (ermin) [341], CDH13 [342], CSMD1 [343], NTF3 [344], FRMPD4 [345], GRIA4 [346], GRIA2 [347], SNCB (synuclein beta) [348], NR3C2 [349], MMP3 [350], GABRB2 [351], HLA-DRB1 [352], VWF (von Willebrand factor) [353], MTTP (microsomal triglyceride transfer protein) [354], MDGA1 [355], CASP1 [356], POU3F2 [357], LDB2 [358], NR2E1 [359], CHRNA5 [360], GAS7 [361], BRCA2 [362], ST8SIA2 [363], ZBTB20 [364], EFNB2 [365], DCLK1 [366], EGFR (epidermal growth factor receptor) [367], ABCA1 [368], GRM3 [369], COMT (catechol-O-methyltransferase) [370], LDB2 [371], EFNB2 [372] and DCLK1 [373] are

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molecular markers for the diagnosis and prognosis of schizophrenia. MOG (myelin oligodendrocyte glycoprotein) [374], SERPINA1 [375], LRRK2 [376], CHRNA4 [377], TF (transferrin) [121], RELN (reelin) [378], HTR2C [379], OPRK1 [380], DSCAM (DS cell adhesion molecule) [381], REN (renin) [382], OLIG2 [383], CNTN1 [384], TLR2 [385], WT1 [386], SHH (sonic hedgehog signaling molecule) [387], AGTR1 [388], SIRT2 [389], RBP4 [390], ERBB3 [391], CDH13 [392], NTF3 [344], GRIA4 [393], GRIA2 [394], NR3C2 [395], TRPC6 [396], FGF19 [397], EMX1 [398], VWF (von Willebrand factor) [399], MDGA1 [400], NEDD4L [401], CASP1 [402], TET1 [403], ZBTB20 [404], VAX1 [405], EGFR (epidermal growth factor receptor) [406], ABCA1 [407], PDPN (podoplanin) [408], SCN4B [409], MAP1B [410], CRHR2 [279], GRM3 [411], COMT (catechol-O-methyltransferase) [412], GPR39 [413], CIITA (class II major histocompatibility complex transactivator) [215], ZNF354C [414], KIF15 [415] and SLC1A1 [416] were found to be a key biomarkers to promote its occurrence and progression of depression. FA2H [417], TGM2 [418], LRRK2 [419], GPR17 [420], RELN (reelin) [421], RIT2 [324], REN (renin) [422], TLR2 [423], SYK (spleen associated tyrosine kinase) [138], GRID2 [424], SHH (sonic hedgehog signaling molecule) [425], XDH (xanthine dehydrogenase) [426], VTN (vitronectin) [427], SIRT2 [428], OAS3 [429], TTPA (alpha tocopherol transfer protein) [430], EGFR (epidermal growth factor receptor) [431], ABCA1 [432], WEE1 [433], MAP1B [434], ANK1 [435], GRM3 [436], COMT (catechol-O-methyltransferase) [437], GPR39 [438], HDC (histidine decarboxylase) [439] and TXNRD2 [440] have been proved to participate in neurodegenerative diseases. Altered expression of FA2H [441], DSCAM (DS cell adhesion molecule) [442], OLIG2 [328], PCDH15 [443], GRID2 [424], CTTNBP2 [444], AFF2 [445], SYNE2 [446] and EGFR (epidermal growth factor receptor) [447] are associated with autism spectrum disorder. FA2H [111], SERPINA1 [448], HOXB9 [113], TGM2 [449], LRRK2 [450], ROS1 [451], CFC1 [452], GDF3 [453], TF (transferrin) [121], RXFP1 [454], RELN (reelin) [455], HTR2C [456], MYL7 [457], DYSF (dysferlin) [458], GJA5 [459], IRX1 [460], TLL1 [461], SUCNR1 [462], KERA (keratocan) [463], TFAP2B [464], HOXA5 [465], ACSL6 [466], DSCAM (DS cell adhesion molecule) [467], MSR1 [468], REN (renin) [64], VEGFC (vascular endothelial growth factor C) [469], TLR2 [470], PCSK2 [471], FGF12 [472], SLC22A3 [142], HSPB7 [473], CSRP3 [474], KLRD1 [475], PTPRO (protein tyrosine phosphatase receptor type O) [476], IL7R [477], CUX2

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[478], ACAN (aggrecan) [479], SHH (sonic hedgehog signaling molecule) [480], MEOX1 [481], AGTR1 [482], VTN (vitronectin) [483], SIRT2 [79], RBP4 [484], IL2RG [485], EPAS1 [486], CDH13 [487], TRPC6 [488], MMP3 [261], PCDHGA3 [489], FGF19 [490], TBX18 [491], HLA-DRB1 [492]. CD74 [493], VWF (von Willebrand factor) [267], MTTP (microsomal triglyceride transfer protein) [494], ANGPT2 [184], AKR1C3 [495], NEDD4L [496], CASP1 [497], LDB2 [498], CHRNA5 [499], CCND2 [500], BRCA2 [97], ZBTB20 [501], EFNB2 [502], CYP7B1 [503], DCLK1 [504], RBM20 [505], PLCE1 [197], EGFR (epidermal growth factor receptor) [276], ABCA1 [506], PDPN (podoplanin) [507], SCN4B [508], SLCO1B1 [509], CRHR2 [510], RND3 [511], COMT (catechol-O-methyltransferase) [512], GPR39 [513], GRB14 [514], HDC (histidine decarboxylase) [515], DAPK2 [516], SMAD9 [517], TXNRD2 [518] and KIF15 [519] are altered expressed in cardiovascular diseases. Previous studies have proven that the FGF8 [520], SERPINA1 [521], LRRK2 [522], CHRNA4 [523], TF (transferrin) [524], TRDN (triadin) [525], NR0B1 [526], RELN (reelin) [527], HTR2C [528], RIT2 [529], REN (renin) [530], TLR2 [531], MOBP (myelin associated oligodendrocyte basic protein) [532], TNR (tenascin R) [533], ADGRB1 [534], GPR37 [535], SHH (sonic hedgehog signaling molecule) [536], XDH (xanthine dehydrogenase) [537], SIRT2 [538], BMP2 [539], HAS2 [540], CSMD1 [541], NTF3 [542], SNCB (synuclein beta) [543], MMP3 [544], HLA-DRB5 [545], HLA-DRB1 [546], HLA-DRA [547], VWF (von Willebrand factor) [548], AKR1C3 [549], CASP1 [550], CHRNA5 [551], TET1 [552], LRRN3 [553], EGFR (epidermal growth factor receptor) [554], PLXNA4 [555], FOXG1 [556], MAP1B [557], ANK1 [558], ATP10B [559], RND3 [560], COMT (catechol-O-methyltransferase) [561], LIFR (LIF receptor subunit alpha) [562] and TRAF5 [212] are involved in Parkinson's disease. Recent studies have shown that SERPINA1 [563], LRRK2 [522], CHRNA4 [564], CD22 [565], TF (transferrin) [566], PCDH11Y [567], RXFP1 [568], RELN (reelin) [569], DYSF (dysferlin) [570], RIT2 [324], OPRK1 [571], SHISA7 [572], MSR1 [573], REN (renin) [574], OLIG2 [575], CNTN1 [576], TLR2 [577], WT1 [578], SYK (spleen associated tyrosine kinase) [579], FGF14 [580], INSC (INSC spindle orientation adaptor protein) [581], BARHL1 [582], PRKCH (protein kinase C eta) [583], SLC24A4 [584], TMEM176B [585], MBP (myelin basic protein) [586], ACAN (aggrecan) [587], SHH (sonic hedgehog signaling molecule) [588], SIRT2 [589], RBP4 [590], ISM1 [591], HOXB6 [592], CDH13 [593], NTF3 [594], TRPC6

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[595], MMP3 [596], HLA-DRB5 [597], HLA-DRB1 [546], CD74 [598], VWF (von Willebrand factor) [599], MDGA1 [600], ANGPT2 [601], NEDD4L [602], CASP1 [603], CHRNA5 [604], CCND2 [605], BRCA2 [606], TET1 [607], ZBTB20 [608], OAS1 [609], EGFR (epidermal growth factor receptor) [610], ABCA1 [611], PLXNA4 [612], FOXG1 [613], WEE1 [433], MAP1B [614], ANK1 [615], GRM3 [436], COMT (catechol-O-methyltransferase) [616], SLC10A4 [617], GPR39 [618] and LIFR (LIF receptor subunit alpha) [562] could promote Alzheimer's disease progression. SERPINA1 [619], LRRK2 [620], CHRNA4 [621], TLR2 [622], MOBP (myelin associated oligodendrocyte basic protein) [623], AATK (apoptosis associated tyrosine kinase) [624], MBP (myelin basic protein) [625], SHH (sonic hedgehog signaling molecule) [626], XDH (xanthine dehydrogenase) [627], RBP4 [628], GRIA2 [629], NR3C2 [630], HLA-DRB5 [631], HLA-DRA [631], NEDD4L [632], CASP1 [633], EFNB2 [634], CYP7B1 [635], EGFR (epidermal growth factor receptor) [636], MAP1B [637], GRM3 [638] and AFF2 [639] plays a central role in amyotrophic lateral sclerosis. Aberrant expression of TGM2 [640], NEUROD1 [641], PRKG2 [642], RIT2 [324], TLR2 [643], MYRF (myelin regulatory factor) [642], SIRT2 [644], MMP3 [645], CASP1 [646], POU3F2 [647] and COMT (catechol-O-methyltransferase) [648] have been observed in HD. SERPINA1 [521], LRRK2 [649], TF (transferrin) [650], REN (renin) [651], TLR2 [652], MOBP (myelin associated oligodendrocyte basic protein) [653], SYK (spleen associated tyrosine kinase) [654], MBP (myelin basic protein) [625], SHH (sonic hedgehog signaling molecule) [655], RBP4 [590], SNCB (synuclein beta) [543], MMP3 [656], VWF (von Willebrand factor) [657], EGFR (epidermal growth factor receptor) [658], ABCA1 [659] and GPR39 [618] are associated with the clinical stages of dementia. Altered expression of LRRK2 [660], GPR17 [661], TF (transferrin) [662], NEUROD1 [663], RELN (reelin) [664], LCP1 [665], TFAP2B [666], HOXA5 [667], MSR1 [668], REN (renin) [669], OLIG2 [670], TLR2 [671], WT1 [672], SLC22A3 [673], CADM2 [674], PRKCH (protein kinase C eta) [675], MBP (myelin basic protein) [676], XAF1 [677], GPR37 [678], SHH (sonic hedgehog signaling molecule) [679], VTN (vitronectin) [680], SIRT2 [681], RBP4 [682], BMP2 [683], CDH13 [684], NR3C2 [685], TRPC6 [686], MMP3 [687], FGF19 [688], HLA-DRB1 [689], CD74 [690], VWF (von Willebrand factor) [691], ANGPT2 [692], CHRDL1 [693], AKR1C3 [694], NEDD4L [695], CASP1 [696], PDE2A [697], GAS7 [698], TET1 [699], EFNB2 [700], EGFR (epidermal growth

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factor receptor) [701], ABCA1 [702], PDPN (podoplanin) [703], SLCO1B1 [704], COMT (catechol-O-methyltransferase) [705] and GPR39 [706] have been reported to be associated with stroke. CHRNA4 [707], RELN (reelin) [708], VEGFC (vascular endothelial growth factor C) [709], FRMPD4 [710], SCN4B [711], SLCO5A1 [712] and GPR39 [713] are involved in the development of epilepsy. RELN (reelin) [714], HTR2C [379], GABRR1 [715], RIT2 [324], DSCAM (DS cell adhesion molecule) [381], TLR2 [716], PCDH15 [331], TSPAN8 [333], LHX5 [717], MBP (myelin basic protein) [718], CUX2 [719], ACAN (aggrecan) [334], SHH (sonic hedgehog signaling molecule) [720], P2RX7 [721], CACNA2D4 [722], CDH13 [392], CSMD1 [723], NTF3 [724], GRIA4 [725], GRIA2 [725], MMP3 [726], GABRB2 [727], HLA-DRB1 [728], VWF (von Willebrand factor) [353], MDGA1 [355], LDB2 [729], NR2E1 [730], BRCA2 [362], ST8SIA2 [731], KITLG (KIT ligand) [732], GRM3 [733] and COMT (catechol-O-methyltransferase) [412] could act as diagnosis and prognosis biomarkers for bipolar disorder. However, further investigations are needed to explore and confirm the potentially significant GO terms and signaling pathways for HD and to achieve a comprehensive understanding of this process.

Based on the PPI network constructed and modules analysed by the online database IID, we identified hub genes. LRRK2 [115], HOXA1 [734], IL7R [150], EGFR (epidermal growth factor receptor) [198], NEDD4L [187] and COMT (catechol-O-methyltransferase) [207] have been identified in inflammation. LRRK2 [224], IL7R [244], ERBB3 [255] and EGFR (epidermal growth factor receptor) [276] altered expression has been closely associated with diabetes mellitus. LRRK2 [287], IL7R [300], EGFR (epidermal growth factor receptor) [313] and COMT (catechol-O-methyltransferase) [314] have been revealed to be altered expressed in multiple sclerosis. LRRK2 [320], ERBB3 [340], EGFR (epidermal growth factor receptor) [367] and COMT (catechol-O-methyltransferase) [370] have been identified to be involved in the development of schizophrenia. Previous studies have shown that LRRK2 [376], ERBB3 [391], EGFR (epidermal growth factor receptor) [406], NEDD4L [401] and COMT (catechol-O-methyltransferase) [412] might influence the prognosis in depression. LRRK2 [419], EGFR (epidermal growth factor receptor) [431] and COMT (catechol-O-methyltransferase) [437] have been demonstrated to be regulated in neurodegenerative diseases. LRRK2 [450], HOXA1 [735], IL7R [477], EGFR

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(epidermal growth factor receptor) [276], NEDD4L [496] and COMT (catechol-O-methyltransferase) [512] are associated with cardiovascular diseases development. Altered expression of LRRK2 [522], EGFR (epidermal growth factor receptor) [554] and COMT (catechol-O-methyltransferase) [561] promotes Parkinson's disease. A previous study reported that the LRRK2 [522], MTUS2 [736], EGFR (epidermal growth factor receptor) [610], NEDD4L [602] and COMT (catechol-O-methyltransferase) [616] genes were associated with Alzheimer's disease. LRRK2 [620], EGFR (epidermal growth factor receptor) [636] and NEDD4L [632] are critical in amyotrophic lateral sclerosis development. In many clinical studies, LRRK2 [649] and EGFR (epidermal growth factor receptor) [658] have been linked to the start of dementia. LRRK2 [660], EGFR (epidermal growth factor receptor) [701], NEDD4L [695], COMT (catechol-O-methyltransferase) [705] and CDK18 [737] are involved in the regulation of stroke. ERBB3 [82], EGFR (epidermal growth factor receptor) [100], NEDD4L [95] and COMT (catechol-O-methyltransferase) [104] expression levels were significantly altered in hypertension. A previous study found that EGFR (epidermal growth factor receptor) [447] is positively correlated with the severity of autism spectrum disorder, suggesting its potential as a biomarker for autism spectrum disorder. COMT (catechol-O-methyltransferase) [648] is known to be involved in the development of HD. COMT (catechol-O-methyltransferase) [412] protein levels might together be helpful for diagnosing bipolar disorder. Our findings suggest that novel biomarkers include TEX101, WDR76, KRT86, ZNF835, ZNF572 and BEGAIN (brain enriched guanylate kinase associated) might influence the progression of HD. However, the exact pathogenic mechanism remains unknown. This investigation might provide reference for research the connection between HD and its associated complication.

MiRNA-hub gene regulatory network analyses and TF-hub gene regulatory network are formed from the interactions of hub genes, miRNAs and TFs, and participate in all steps of the life process, including biosignal transfer, gene expression control, energy and substance metabolism, and cell cycle control. Previous studies have been reported that EPAS1 [167], HOXA1 [734], TGM2 [114], CCND2 [191], MAP1B [204], EGFR (epidermal growth factor receptor) [198], NEDD4L [187], DCLK1 [196], hsa-mir-363-3p [738], SMAD4 [739], ATF3 [740], TBX5 [741] and CREB1 [742] increased the risk of inflammation

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development. Previous studies have reported that EPAS1 [486], HOXA1 [735], TGM2 [449], CCND2 [500], EGFR (epidermal growth factor receptor) [276], NEDD4L [496], DCLK1 [504], hsa-mir-363-3p [738], hsa-mir-21-5p [743], SMAD4 [744], ATF3 [745], TBX5 [746], SREBF1 [747], SMARCA4 [748] and CREB1 [749] were regulated in cardiovascular diseases. Studies reported that ERBB3 [255], TGM2 [223], CCND2 [274], EGFR (epidermal growth factor receptor) [276], hsa-mir-21-5p [750], ATF3 [751], SREBF1 [752], ARNT (aryl hydrocarbon receptor nuclear translocator) [753] and CREB1 [754] play important roles in diabetes mellitus. ERBB3 [340], TGM2 [319], EGFR (epidermal growth factor receptor) [367], DCLK1 [366], SMAD4 [755], SREBF1 [756] and CREB1 [757] participated in the regulation of schizophrenia. ERBB3 [391], MAP1B [410], EGFR (epidermal growth factor receptor) [406], NEDD4L [401], hsa-mir-21-5p [758] and CREB1 [759] were involved in depression. ERBB3 [82], EGFR (epidermal growth factor receptor) [100], NEDD4L [95] and SREBF1 [760] regulated the pathogenesis of hypertension. HSPA2 [43], MTUS2 [736], CCND2 [605], MAP1B [614], EGFR (epidermal growth factor receptor) [610], NEDD4L [602], hsa-mir-4487 [761], hsa-mir-21-5p [762] and CREB1 [763] were involved in regulating the occurrence of Alzheimer's disease. TGM2 [286], EGFR (epidermal growth factor receptor) [313] and DCLK1 [312] have been shown to be associated with multiple sclerosis. Altered levels of TGM2 [418], MAP1B [434], EGFR (epidermal growth factor receptor) [431], hsa-mir-21-5p [764] and CREB1 [765] have been observed in neurodegenerative diseases patients. Some studies have shown that TGM2 [640], hsa-mir-10a [766], ATF3 [767] and CREB1 [768] plays a certain role in HD. Altered expression of MAP1B [557], EGFR (epidermal growth factor receptor) [554], SREBF1 [769] and CREB1 [770] promotes Parkinson's disease. MAP1B [637], EGFR (epidermal growth factor receptor) [636], NEDD4L [632], hsa-mir-21-5p [771], ATF3 [772] and SREBF1 [773] were significantly altered in patients with amyotrophic lateral sclerosis. A previous study reported that the EGFR (epidermal growth factor receptor) [658], hsa-mir-21-5p [762] and SREBF1 [774] biomarkers were associated with the dementia. Previous studies have shown that EGFR (epidermal growth factor receptor) [701], NEDD4L [695], hsa-mir-21-5p [775] and ATF3 [776] are closely associated with stroke. EGFR (epidermal growth factor receptor) [447] have recently been found in autism spectrum disorder. Altered expression of hsa-mir-4521 [777] was found to promote the epilepsy. Hence, the results of miRNA-hub gene regulatory

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network analyses and TF-hub gene regulatory network were in accordance with experimental results on HD. The roles of novel biomarkers in the network were determined, such as KRT8, TOP2A, hsa-mir-1292-5p, hsa-mir-432-3p, hsa-mir-6801-3p, hsa-mir-7977, hsa-mir-6807-5p, ESRRB (estrogen related receptor beta), EED (embryonic ectoderm development) and EP300, which expanded our knowledge on development of HD. Hence, our findings might be a novel clue for the diagnosis and treatment of HD.

Conclusion

Based on the current investigation, it is feasible to use bioinformatics methods to screen and identify essential molecular markers and signaling pathways related to HD. Bioinformatics methods can be used to analyze NGS data to discover disease-related molecular features such as gene expression, protein structure, and metabolite levels. In this study, the hub genes, miRNA and TFs related to HD were identified. Our findings will help to encourage further studies on the biological functions of hub genes, miRNA and TFs.

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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

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The datasets supporting the conclusions of this article are available in the GEO (Gene Expression Omnibus) (https://www.ncbi.nlm.nih.gov/geo/) repository. [(GSE105041) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc=GSE105041]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Author Contributions

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

C. V. - Software and investigation

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Tables

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

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulation	Gene Name
DEFB115	7.110542	4.32E-08	7.20E-06	5.477247	Up	defensin beta 115
HSPA2	5.997933	8.18E-79	2.45E-74	18.79576	Up	heat shock protein family A (Hsp70) member 2
BCAS1	5.94002	1.09E-14	2.34E-11	7.727801	Up	brain enriched myelin associated protein 1
MAG	5.797827	1.74E-06	0.000119	4.781914	Up	myelin associated glycoprotein
VSX2	5.568724	5.48E-10	2.38E-07	6.204621	Up	visual system homeobox 2
GNGT2	5.356246	1.85E-06	0.000126	4.769157	Up	G protein subunit gamma transducin 2
CABP5	5.23748	1.67E-05	0.000682	4.305326	Up	calcium binding protein 5
PDE6H	5.080812	2.65E-06	0.000168	4.695935	Up	phosphodiesterase 6H
RAX	5.062758	9.82E-10	3.98E-07	6.112371	Up	retina and anterior neural fold homeobox
CBLN2	5.054733	2.07E-08	4.11E-06	5.606277	Up	cerebellin 2 precursor
CPLX4	5.038099	0.000573	0.009575	3.444098	Up	complexin 4
DAZ4	4.967106	0.00533	0.044273	2.786367	Up	deleted in azoospermia 4
NEUROD4	4.850219	3.18E-05	0.001105	4.160329	Up	neuronal differentiation 4
SOX10	4.743981	1.37E-06	9.86E-05	4.82927	Up	SRY-box transcription factor 10
AIPL1	4.565972	1.22E-06	8.98E-05	4.85273	Up	aryl hydrocarbon receptor interacting protein like 1
CACNA1F	4.548864	2.44E-06	0.000157	4.713244	Up	calcium voltage-gated channel subunit alpha1 F
RBP3	4.538884	4.01E-09	1.24E-06	5.883825	Up	retinol binding protein 3
XIST	4.528396	3.24E-05	0.00112	4.156202	Up	X inactive specific transcript
FAM138A	4.491981	0.000442	0.008024	3.513733	Up	family with sequence similarity 138 member A
MOG	4.447683	4.33E-07	4.04E-05	5.054059	Up	myelin oligodendrocyte glycoprotein
CCL3L3	4.444327	5.50E-05	0.001664	4.033107	Up	C-C motif chemokine ligand 3 like 3
RD3	4.411706	4.70E-09	1.41E-06	5.857506	Up	RD3 regulator of GUCY2D
MEG3	4.352411	6.45E-14	9.21E-11	7.498658	Up	maternally expressed 3
LACTBL1	4.325642	0.002389	0.025943	3.037095	Up	lactamase beta like 1
ENPP6	4.321214	2.04E-07	2.41E-05	5.195501	Up	ectonucleotidepyrophosphatase/phosphodiesterase 6
NR5A2	4.320597	7.75E-09	1.92E-06	5.773789	Up	nuclear receptor subfamily 5 group A member 2
KRT86	4.296997	6.92E-09	1.83E-06	5.792837	Up	keratin 86

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PPP1R16B	4.294209	3.84E-08	6.62E-06	5.498112	Up	protein phosphatase 1 regulatory subunit 16B
NPY4R	4.291743	2.89E-09	9.64E-07	5.937649	Up	neuropeptide Y receptor Y4
KRT81	4.278477	1.03E-06	7.81E-05	4.885166	Up	keratin 81
GLRA3	4.275975	0.000737	0.011477	3.375463	Up	glycine receptor alpha 3
GABRR3	4.274913	0.001523	0.019098	3.170348	Up	gamma-aminobutyric acid type A receptor subunit rho3
CALCB	4.262059	1.80E-11	1.28E-08	6.721793	Up	calcitonin related polypeptide beta
RCVRN	4.258188	1.46E-10	7.55E-08	6.409617	Up	recoverin
RP1	4.188043	9.94E-06	0.000464	4.418429	Up	RP1 axonemal microtubule associated
FAM138E	4.180768	0.000713	0.011185	3.384703	Up	family with sequence similarity 138 member E
CNGB1	4.178366	6.52E-08	9.88E-06	5.403902	Up	cyclic nucleotide gated channel subunit beta 1
UGT8	4.084139	3.13E-08	5.68E-06	5.534126	Up	UDP glycosyltransferase 8
NXNL1	4.07912	8.81E-05	0.002361	3.921335	Up	nucleoredoxin like 1
PCDH11X	4.052922	3.73E-09	1.17E-06	5.895696	Up	protocadherin 11 X-linked
FA2H	4.025201	1.69E-07	2.08E-05	5.23093	Up	fatty acid 2-hydroxylase
HMGA1P7	4.024596	6.98E-05	0.001985	3.976974	Up	high mobility group AT-hook 1 pseudogene 7
CRX	4.013635	2.90E-05	0.001032	4.18121	Up	cone-rod homeobox
EDN3	3.945415	4.63E-07	4.30E-05	5.041041	Up	endothelin 3
FAM138F	3.900855	0.005162	0.043362	2.796743	Up	family with sequence similarity 138 member F
KCTD8	3.894739	2.77E-06	0.000174	4.68729	Up	potassium channel tetramerization domain containing 8
ANO3	3.889539	3.80E-08	6.60E-06	5.499828	Up	anoctamin 3
KLRC4	3.886156	9.29E-05	0.002466	3.908542	Up	killer cell lectin like receptor C4
TMEM235	3.853094	0.000651	0.010463	3.409518	Up	transmembrane protein 235
VSTM2B	3.812474	6.96E-06	0.000349	4.494982	Up	V-set and transmembrane domain containing 2B
RAX2	3.730411	5.03E-05	0.001551	4.05426	Up	retina and anterior neural fold homeobox 2
DMRT2	3.725977	1.56E-05	0.00065	4.320408	Up	doublesex and mab-3 related transcription factor 2
SPANXC	3.720563	0.001006	0.014224	3.288827	Up	SPANX family member C
LRIT1	3.715804	0.000574	0.009588	3.443447	Up	leucine rich repeat, Ig-like and transmembrane domains 1
CFC1B	3.714674	1.13E-05	0.000508	4.390883	Up	cripto, FRL-1, cryptic family 1B
SPATA8	3.686688	6.67E-05	0.001923	3.987896	Up	spermatogenesis associated 8
SAMD7	3.667534	0.000119	0.002984	3.849013	Up	sterile alpha motif domain containing 7

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PRDM13	3.665392	9.10E-07	7.18E-05	4.910244	Up	PR/SET domain 13
KIAA0087	3.663094	2.10E-06	0.000139	4.743564	Up	KIAA0087 lncRNA
NKX2-2	3.643561	2.79E-06	0.000175	4.685757	Up	NK2 homeobox 2
FAM163A	3.63944	1.34E-05	0.000574	4.353407	Up	family with sequence similarity 163 member A
FREM3	3.626608	0.000293	0.00589	3.621119	Up	FRAS1 related extracellular matrix 3
WFDC8	3.624957	0.000379	0.007157	3.554522	Up	WAP four-disulfide core domain 8
KRT83	3.615358	0.000159	0.003737	3.776072	Up	keratin 83
COL6A4P2	3.594132	2.31E-07	2.63E-05	5.172196	Up	collagen type VI alpha 4 pseudogene 2
KCNV2	3.589787	1.30E-10	6.98E-08	6.426724	Up	potassium voltage-gated channel modifier subfamily V member 2
FGF8	3.582839	3.11E-08	5.68E-06	5.535157	Up	fibroblast growth factor 8
SERPINA1	3.574188	6.24E-07	5.37E-05	4.983527	Up	serpin family A member 1
ACCS	3.56611	7.28E-09	1.87E-06	5.784378	Up	1-aminocyclopropane-1-carboxylate synthase homolog (inactive)
IGFL3	3.562357	3.60E-07	3.55E-05	5.08906	Up	IGF like family member 3
GALNT9	3.552211	5.02E-08	8.06E-06	5.450517	Up	polypeptide N-acetylgalactosaminyltransferase 9
EPYC	3.545442	5.04E-07	4.60E-05	5.02464	Up	epiphycan
PLPPR1	3.544781	1.84E-05	0.000735	4.283865	Up	phospholipid phosphatase related 1
HMX1	3.541933	2.28E-07	2.62E-05	5.174958	Up	H6 family homeobox 1
TTC24	3.52829	6.52E-06	0.000331	4.508915	Up	tetratricopeptide repeat domain 24
HOXB9	3.526125	1.60E-06	0.000111	4.798704	Up	homeobox B9
DCAF4L2	3.517397	4.11E-05	0.001339	4.101083	Up	DDB1 and CUL4 associated factor 4 like 2
TGM2	3.516942	2.10E-07	2.46E-05	5.190613	Up	transglutaminase 2
CDC20B	3.513494	0.000192	0.004302	3.729679	Up	cell division cycle 20B
LRRK2	3.498847	1.67E-07	2.08E-05	5.233007	Up	leucine rich repeat kinase 2
WIF1	3.494687	0.00122	0.016221	3.234054	Up	WNT inhibitory factor 1
ROS1	3.486059	1.55E-05	0.000646	4.322112	Up	ROS proto-oncogene 1, receptor tyrosine kinase
CHRNA4	3.482283	1.81E-05	0.000725	4.287454	Up	cholinergic receptor nicotinic alpha 4 subunit
TMEM125	3.47329	0.000592	0.009775	3.435353	Up	transmembrane protein 125
CFC1	3.471491	4.56E-05	0.001451	4.076993	Up	cripto, FRL-1, cryptic family 1
SAMSN1	3.463566	0.000156	0.003669	3.781396	Up	SAM domain, SH3 domain and nuclear localization signals 1

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CD22	3.459175	3.23E-06	0.000192	4.655871	Up	CD22 molecule
EVI2A	3.391541	2.64E-14	4.40E-11	7.614851	Up	ecotropic viral integration site 2A
LGR6	3.37667	1.46E-10	7.55E-08	6.40975	Up	leucine rich repeat containing G protein-coupled receptor 6
KLRK1	3.368531	0.000913	0.013371	3.315945	Up	killer cell lectin like receptor K1
HAGLROS	3.358623	3.81E-08	6.60E-06	5.499613	Up	HAGLR opposite strand lncRNA
GALNT13	3.344539	2.55E-07	2.79E-05	5.153837	Up	polypeptide N-acetylgalactosaminyltransferase 13
CA10	3.342556	0.001836	0.021707	3.115578	Up	carbonic anhydrase 10
GDF3	3.341778	2.12E-05	0.000807	4.251436	Up	growth differentiation factor 3
GNAT1	3.332394	2.37E-05	0.00088	4.226835	Up	G protein subunit alpha transducin 1
SV2B	3.324983	8.60E-05	0.002316	3.926995	Up	synaptic vesicle glycoprotein 2B
CXorf65	3.323107	0.000857	0.01283	3.333663	Up	chromosome X open reading frame 65
GPR17	3.320271	1.45E-05	0.000616	4.3361	Up	G protein-coupled receptor 17
TF	3.320142	4.62E-09	1.40E-06	5.860239	Up	transferrin
SIX6	3.314319	9.51E-08	1.31E-05	5.33594	Up	SIX homeobox 6
GUCA1C	3.30227	1.66E-05	0.00068	4.306755	Up	guanylatecyclase activator 1C
KLRC3	3.298067	0.004259	0.038146	2.858327	Up	killer cell lectin like receptor C3
GAL3ST1	3.297754	2.63E-09	8.98E-07	5.953424	Up	galactose-3-O-sulfotransferase 1
DGKK	3.297687	1.88E-08	3.80E-06	5.62255	Up	diacylglycerol kinase kappa
SULT1B1	3.291224	0.004112	0.037395	2.86946	Up	sulfotransferase family 1B member 1
GABRG1	3.288523	0.000459	0.008227	3.503548	Up	gamma-aminobutyric acid type A receptor subunit gamma1
HOXD3	3.274237	1.65E-07	2.06E-05	5.234918	Up	homeobox D3
TRDN	3.272585	1.10E-06	8.17E-05	4.873739	Up	triadin
FAM135B	3.264816	1.46E-07	1.88E-05	5.258047	Up	family with sequence similarity 135 member B
SAG	3.263111	0.003579	0.034112	2.913026	Up	S-antigen visual arrestin
LAMC2	3.256234	4.88E-07	4.48E-05	5.030888	Up	laminin subunit gamma 2
NEUROD1	3.252675	0.003048	0.030525	2.962882	Up	neuronal differentiation 1
DSC1	3.249103	9.19E-08	1.28E-05	5.341965	Up	desmocollin 1
NWD2	3.239384	0.000459	0.008227	3.503551	Up	NACHT and WD repeat domain containing 2
CLRN1	3.236691	5.41E-05	0.00164	4.03735	Up	clarin 1
ADAMTS19	3.226713	6.26E-06	0.000322	4.517573	Up	ADAM metallopeptidase with thrombospondin type 1

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						motif 19
NR0B1	3.22315	1.45E-06	0.000103	4.817868	Up	nuclear receptor subfamily 0 group B member 1
TRPC6	3.221762	2.10E-06	0.000139	4.743299	Up	transient receptor potential cation channel subfamily C member 6
PCDH11Y	3.213475	0.00032	0.006312	3.598413	Up	protocadherin 11 Y-linked
SLC38A4	3.211641	7.51E-06	0.000372	4.478752	Up	solute carrier family 38 member 4
SCML4	3.198848	0.000151	0.003578	3.789422	Up	Scmpolycomb group protein like 4
RXFP1	3.180298	3.27E-05	0.001126	4.154054	Up	relaxin family peptide receptor 1
PRKG2	3.176973	2.09E-05	0.000798	4.255397	Up	protein kinase cGMP-dependent 2
NAA11	3.176044	3.85E-05	0.00127	4.116079	Up	N-alpha-acetyltransferase 11, NatA catalytic subunit
GUCY2D	3.171508	1.49E-05	0.00063	4.329904	Up	guanylatecyclase 2D, retinal
UGT2B26P	3.17111	0.001302	0.016992	3.215474	Up	UDP glucuronosyltransferase family 2 member B26, pseudogene
KCNH6	3.170129	3.11E-07	3.15E-05	5.116859	Up	potassium voltage-gated channel subfamily H member 6
RELN	3.167201	5.22E-08	8.24E-06	5.443712	Up	reelin
LCP1	3.165393	1.24E-05	0.000539	4.370377	Up	lymphocyte cytosolic protein 1
HTR2C	3.139805	0.000199	0.004419	3.72027	Up	5-hydroxytryptamine receptor 2C
ZNF648	3.124971	8.31E-07	6.67E-05	4.927922	Up	zinc finger protein 648
VIT	3.123611	0.000177	0.004067	3.749654	Up	vitrin
MYL7	3.11473	5.52E-07	4.92E-05	5.007441	Up	myosin light chain 7
DYSF	3.112839	2.85E-07	2.97E-05	5.133203	Up	dysferlin
CMTM5	3.111941	1.15E-05	0.000513	4.387318	Up	CKLF like MARVEL transmembrane domain containing 5
MYCT1	3.104293	0.000925	0.013461	3.312376	Up	MYC target 1
GABRR1	3.096436	3.03E-05	0.001067	4.17108	Up	gamma-aminobutyric acid type A receptor subunit rho1
OMG	3.096404	2.18E-05	0.000824	4.245762	Up	oligodendrocyte myelin glycoprotein
ADAMTS20	3.089632	1.86E-08	3.79E-06	5.624619	Up	ADAM metallopeptidase with thrombospondin type 1 motif 20
HOXA4	3.08822	1.13E-08	2.66E-06	5.710483	Up	homeobox A4
CCDC26	3.087223	0.000109	0.002785	3.868991	Up	CCDC26 long non-coding RNA
GJA5	3.081772	2.16E-06	0.000142	4.737444	Up	gap junction protein alpha 5
APELA	3.07933	0.000544	0.009239	3.458292	Up	apelin receptor early endogenous ligand

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CFAP47	3.06795	3.44E-06	0.000204	4.642403	Up	cilia and flagella associated protein 47
GPR45	3.067407	2.89E-06	0.000179	4.678491	Up	G protein-coupled receptor 45
TTTY14	3.063412	0.001517	0.019054	3.171438	Up	testis-specific transcript, Y-linked 14
HOXA7	3.057898	1.05E-05	0.000485	4.406796	Up	homeobox A7
MTUS2	3.057819	3.22E-07	3.23E-05	5.110316	Up	microtubule associated scaffold protein 2
ETNPPL	3.046337	1.90E-07	2.32E-05	5.208413	Up	ethanolamine-phosphate phospho-lyase
C2orf27A	3.042341	1.84E-11	1.28E-08	6.718312	Up	chromosome 2 open reading frame 27A
LGI3	3.031069	2.79E-10	1.35E-07	6.310158	Up	leucine rich repeat LGI family member 3
CTTNBP2	3.009021	5.00E-06	0.000274	4.564813	Up	cortactin binding protein 2
CRTAC1	3.005197	2.32E-14	4.10E-11	7.631317	Up	cartilage acidic protein 1
SLC17A8	2.993846	6.77E-07	5.66E-05	4.967837	Up	solute carrier family 17 member 8
RIPPLY2	2.990377	0.000101	0.002635	3.887299	Up	ripply transcriptional repressor 2
IRX1	2.989597	5.13E-11	3.14E-08	6.56703	Up	iroquoishomeobox 1
SLPI	2.985161	4.99E-06	0.000274	4.565074	Up	secretory leukocyte peptidase inhibitor
LGR5	2.9848	5.84E-07	5.12E-05	4.996587	Up	leucine rich repeat containing G protein-coupled receptor 5
MYO1G	2.970949	8.11E-05	0.002219	3.941159	Up	myosin IG
CSMD3	2.969081	8.36E-08	1.21E-05	5.359267	Up	CUB and Sushi multiple domains 3
IMPG2	2.966592	1.70E-09	6.44E-07	6.024548	Up	interphotoreceptor matrix proteoglycan 2
CATSPERB	2.966392	0.000299	0.005976	3.616333	Up	cation channel sperm associated auxiliary subunit beta
TLL1	2.965591	1.47E-08	3.21E-06	5.66557	Up	tolloid like 1
FEV	2.964321	0.004266	0.038199	2.857792	Up	FEV transcription factor, ETS family member
ADAM29	2.95636	0.006168	0.049002	2.738696	Up	ADAM metallopeptidase domain 29
TULP1	2.954801	2.85E-06	0.000178	4.681518	Up	TUB like protein 1
RIT2	2.94934	0.005799	0.046898	2.758953	Up	Ras like without CAAX 2
FRMPD4	2.941354	1.16E-07	1.55E-05	5.299362	Up	FERM and PDZ domain containing 4
OPRK1	2.939487	0.000659	0.010564	3.405978	Up	opioid receptor kappa 1
FAM138B	2.937612	0.005141	0.043285	2.79804	Up	family with sequence similarity 138 member B
MATK	2.934718	6.67E-07	5.59E-05	4.970632	Up	megakaryocyte-associated tyrosine kinase
EYA1	2.933485	0.000374	0.0071	3.557645	Up	EYA transcriptional coactivator and phosphatase 1
NETO1	2.930609	2.40E-06	0.000155	4.716303	Up	neuropilin and tolloid like 1

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DBX2	2.917661	0.000204	0.004506	3.714581	Up	developing brain homeobox 2
ELFN2	2.909247	5.47E-09	1.52E-06	5.832145	Up	extracellular leucine rich repeat and fibronectin type III domain containing 2
SGCZ	2.909033	0.000644	0.010382	3.412338	Up	sarcoglycan zeta
SYT6	2.905935	2.21E-06	0.000144	4.733148	Up	synaptotagmin 6
CLIC5	2.90523	5.16E-07	4.65E-05	5.020226	Up	chloride intracellular channel 5
GRIA4	2.903823	0.000201	0.004455	3.717836	Up	glutamate ionotropic receptor AMPA type subunit 4
RASSF6	2.89797	0.000219	0.00477	3.695682	Up	Ras association domain family member 6
SUCNR1	2.886124	7.42E-05	0.002076	3.962398	Up	succinate receptor 1
GPR20	2.884667	9.27E-07	7.28E-05	4.906491	Up	G protein-coupled receptor 20
KERA	2.874707	7.84E-05	0.002161	3.949269	Up	keratocan
VSX1	2.867751	0.000236	0.005027	3.67742	Up	visual system homeobox 1
PRPH2	2.866275	4.88E-05	0.001519	4.061228	Up	peripherin 2
CCDC162P	2.849859	0.002173	0.024362	3.065461	Up	coiled-coil domain containing 162, pseudogene
HAGLR	2.847014	1.27E-06	9.34E-05	4.84389	Up	HOXD antisense growth-associated long non-coding RNA
CYP2S1	2.844484	3.18E-06	0.00019	4.658997	Up	cytochrome P450 family 2 subfamily S member 1
CPLX3	2.841511	0.00132	0.017179	3.211578	Up	complexin 3
TFAP2B	2.839099	7.70E-05	0.002133	3.953554	Up	transcription factor AP-2 beta
ARFGEF3	2.83901	1.05E-10	5.94E-08	6.459522	Up	ARFGEF family member 3
HMX3	2.834837	5.92E-06	0.00031	4.529102	Up	H6 family homeobox 3
ASCL2	2.83021	0.000228	0.004925	3.685739	Up	achaete-scute family bHLH transcription factor 2
CYP2C8	2.829247	0.00415	0.037584	2.866556	Up	cytochrome P450 family 2 subfamily C member 8
HOXA6	2.823354	3.57E-05	0.001197	4.133632	Up	homeobox A6
SHISA7	2.821712	1.14E-05	0.000511	4.388632	Up	shisa family member 7
HOXA5	2.821638	2.32E-07	2.63E-05	5.171799	Up	homeobox A5
RNF125	2.818563	2.01E-11	1.35E-08	6.705198	Up	ring finger protein 125
ACSL6	2.814389	1.82E-06	0.000124	4.772893	Up	acyl-CoA synthetase long chain family member 6
IGF2-AS	2.808065	0.001164	0.015727	3.247571	Up	IGF2 antisense RNA
COL25A1	2.799477	7.87E-13	6.74E-10	7.163424	Up	collagen type XXV alpha 1 chain
IRX6	2.793352	0.001212	0.016131	3.236149	Up	iroquoishomeobox 6
KCTD14	2.776363	0.000399	0.007439	3.540738	Up	potassium channel tetramerization domain containing

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ADAMTS17	2.774187	2.52E-07	2.78E-05	5.15629	Up	ADAM metallopeptidase with thrombospondin type 1 motif 17
COL20A1	2.770818	0.003266	0.031906	2.941484	Up	collagen type XX alpha 1 chain
RHOH	2.769619	1.26E-08	2.84E-06	5.691588	Up	ras homolog family member H
DSCAM	2.767774	4.73E-05	0.001484	4.068793	Up	DS cell adhesion molecule
C6	2.766533	1.89E-05	0.000748	4.277041	Up	complement C6
MSR1	2.756258	0.000925	0.013461	3.312489	Up	macrophage scavenger receptor 1
REN	2.753343	0.001411	0.018125	3.192301	Up	renin
CCL25	2.748831	5.80E-06	0.000305	4.533635	Up	C-C motif chemokine ligand 25
TDRD9	2.747644	0.0005	0.008765	3.480506	Up	tudor domain containing 9
SLCO4A1	2.747393	9.60E-06	0.000453	4.426096	Up	solute carrier organic anion transporter family member 4A1
NEU4	2.747307	1.33E-06	9.58E-05	4.835332	Up	neuraminidase 4
CAPSL	2.745426	3.34E-07	3.34E-05	5.103299	Up	calcyphosine like
VEGFC	2.736853	1.60E-06	0.000111	4.798056	Up	vascular endothelial growth factor C
OLIG2	2.735913	8.27E-06	0.000403	4.458131	Up	oligodendrocyte transcription factor 2
SLC16A3	2.732449	6.37E-08	9.71E-06	5.407981	Up	solute carrier family 16 member 3
KRT7	2.728914	7.12E-05	0.002015	3.972187	Up	keratin 7
ODAM	2.721912	5.62E-05	0.001694	4.028075	Up	odontogenic, ameloblast associated
AANAT	2.715768	2.53E-09	8.82E-07	5.959673	Up	aralkylamine N-acetyltransferase
C14orf39	2.698805	2.93E-08	5.50E-06	5.54533	Up	chromosome 14 open reading frame 39
CNTN1	2.697987	1.36E-05	0.000581	4.350598	Up	contactin 1
DACH2	2.695478	0.001176	0.015834	3.244527	Up	dachshund family transcription factor 2
SLC1A1	2.694725	3.93E-07	3.80E-05	5.072513	Up	solute carrier family 1 member 1
TLR2	2.691894	4.69E-07	4.34E-05	5.038506	Up	toll like receptor 2
ADGRG2	2.688763	1.91E-13	2.20E-10	7.354876	Up	adhesion G protein-coupled receptor G2
C7	2.685575	0.00018	0.004121	3.745122	Up	complement C7
PCSK2	2.681608	0.000507	0.008849	3.476984	Up	proproteinconvertasesubtilisin/kexin type 2
FGF12	2.680626	8.69E-08	1.23E-05	5.352279	Up	fibroblast growth factor 12
PRSS56	2.678452	7.40E-06	0.000368	4.481844	Up	serine protease 56
DMGDH	2.675672	1.58E-14	3.17E-11	7.680554	Up	dimethylglycine dehydrogenase

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SEMA3D	2.675406	5.94E-06	0.00031	4.528456	Up	semaphorin 3D
CDH22	2.675071	0.000183	0.004146	3.741595	Up	cadherin 22
GPRIN3	2.668888	2.62E-07	2.83E-05	5.148604	Up	GPRIN family member 3
WT1	2.66394	2.94E-07	3.03E-05	5.126945	Up	WT1 transcription factor
FENDRR	2.662305	3.89E-05	0.001276	4.114117	Up	FOXF1 adjacent non-coding developmental regulatory RNA
MOBP	2.660656	0.000975	0.013962	3.297606	Up	myelin associated oligodendrocyte basic protein
SYK	2.656205	0.002028	0.023243	3.086139	Up	spleen associated tyrosine kinase
RAPGEF4	2.645148	3.04E-06	0.000185	4.668159	Up	Rap guanine nucleotide exchange factor 4
PLEKHH2	2.64312	3.05E-08	5.62E-06	5.538426	Up	pleckstrin homology, MyTH4 and FERM domain containing H2
RAC2	2.641885	0.000593	0.00978	3.434931	Up	Rac family small GTPase 2
HOTAIRM1	2.641142	1.59E-07	2.00E-05	5.241801	Up	HOXA transcript antisense RNA, myeloid-specific 1
ITGA11	2.637586	1.50E-05	0.00063	4.32922	Up	integrin subunit alpha 11
SLC8A3	2.634238	5.79E-06	0.000305	4.533878	Up	solute carrier family 8 member A3
SULF1	2.633925	6.87E-11	4.06E-08	6.523527	Up	sulfatase 1
KCNG4	2.62879	0.002739	0.028595	2.99564	Up	potassium voltage-gated channel modifier subfamily G member 4
BMP8B	2.627512	1.79E-08	3.73E-06	5.630905	Up	bone morphogenetic protein 8b
OLFM3	2.625413	0.000492	0.008652	3.485048	Up	olfactomedin 3
HOXA1	2.622552	1.84E-08	3.78E-06	5.62658	Up	homeobox A1
GDF6	2.616498	1.92E-06	0.000129	4.761679	Up	growth differentiation factor 6
ACSM5	2.612395	0.001153	0.015668	3.250181	Up	acyl-CoA synthetase medium chain family member 5
EPHA8	2.604878	0.000282	0.005719	3.63151	Up	EPH receptor A8
MYRF	2.60265	6.41E-13	5.66E-10	7.191422	Up	myelin regulatory factor
LRRC26	2.585029	0.000783	0.012025	3.35891	Up	leucine rich repeat containing 26
NR1H4	2.581649	0.000548	0.009293	3.456266	Up	nuclear receptor subfamily 1 group H member 4
CNTN6	2.577722	1.68E-07	2.08E-05	5.23201	Up	contactin 6
SLC24A2	2.572543	6.46E-05	0.001883	3.99517	Up	solute carrier family 24 member 2
KCND2	2.57179	0.002462	0.02655	3.027933	Up	potassium voltage-gated channel subfamily D member 2
SLC30A2	2.570835	0.00115	0.015635	3.251048	Up	solute carrier family 30 member 2
PCDH15	2.565971	0.003496	0.033496	2.920368	Up	protocadherin related 15

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KRT8P32	2.563823	0.00168	0.020386	3.141619	Up	keratin 8 pseudogene 32
ECSCR	2.561451	0.001226	0.016267	3.232728	Up	endothelial cell surface expressed chemotaxis and apoptosis regulator
NKX6-1	2.55669	1.89E-08	3.80E-06	5.62212	Up	NK6 homeobox 1
CERKL	2.555141	5.03E-06	0.000276	4.563384	Up	ceramide kinase like
GPRIN2	2.552812	3.33E-05	0.001138	4.149664	Up	G protein regulated inducer of neurite outgrowth 2
GFI1B	2.538791	0.000214	0.004684	3.7018	Up	growth factor independent 1B transcriptional repressor
HOXA3	2.538536	1.16E-06	8.54E-05	4.863096	Up	homeobox A3
DCAF12L2	2.53759	3.06E-06	0.000185	4.66681	Up	DDB1 and CUL4 associated factor 12 like 2
MNX1	2.525019	0.000386	0.00727	3.549245	Up	motor neuron and pancreas homeobox 1
SKOR2	2.52402	0.002559	0.027269	3.016227	Up	SKI family transcriptional corepressor 2
HPGD	2.519015	0.001157	0.015692	3.249364	Up	15-hydroxyprostaglandin dehydrogenase
ASIC4	2.51304	9.99E-05	0.002618	3.890819	Up	acid sensing ion channel subunit family member 4
HOXA13	2.511447	0.003181	0.031428	2.949667	Up	homeobox A13
PDE6A	2.511221	0.00097	0.013905	3.299224	Up	phosphodiesterase 6A
PHF24	2.498496	7.19E-05	0.002025	3.969914	Up	PHD finger protein 24
ARHGEF5	2.498446	0.000678	0.010807	3.398164	Up	Rho guanine nucleotide exchange factor 5
GRIA2	2.487359	0.000367	0.006984	3.562702	Up	glutamate ionotropic receptor AMPA type subunit 2
LIMS2	2.482373	5.46E-09	1.52E-06	5.832384	Up	LIM zinc finger domain containing 2
KCNS3	2.476562	1.05E-06	7.88E-05	4.882874	Up	potassium voltage-gated channel modifier subfamily S member 3
FGF14	2.476395	0.000163	0.003804	3.770051	Up	fibroblast growth factor 14
C8G	2.463893	2.37E-06	0.000153	4.719343	Up	complement C8 gamma chain
HOXA2	2.463068	5.40E-05	0.00164	4.037458	Up	homeobox A2
VWA2	2.461759	1.61E-08	3.50E-06	5.649492	Up	von Willebrand factor A domain containing 2
SLC22A3	2.457886	4.74E-08	7.69E-06	5.46071	Up	solute carrier family 22 member 3
ESRP1	2.457022	1.22E-05	0.000534	4.373664	Up	epithelial splicing regulatory protein 1
EGFLAM	2.456938	2.03E-05	0.000785	4.262057	Up	EGF like, fibronectin type III and laminin G domains
INSC	2.45412	0.000183	0.004146	3.741786	Up	INSC spindle orientation adaptor protein
SPTBN5	2.453905	6.37E-07	5.41E-05	4.979575	Up	spectrin beta, non-erythrocytic 5
BARHL1	2.45327	0.000239	0.00508	3.673532	Up	BarH like homeobox 1
SIGLEC1	2.44737	0.001063	0.014812	3.273409	Up	sialic acid binding Ig like lectin 1

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DAPL1	2.443657	1.37E-09	5.40E-07	6.059324	Up	death associated protein like 1
HSPB7	2.442008	4.33E-06	0.000246	4.594896	Up	heat shock protein family B (small) member 7
LHX9	2.435548	2.06E-06	0.000137	4.747391	Up	LIM homeobox 9
AGMO	2.435159	5.30E-09	1.52E-06	5.837311	Up	alkylglycerolmonooxygenase
CADM2	2.432617	0.000883	0.01302	3.325422	Up	cell adhesion molecule 2
SNX22	2.430004	1.75E-08	3.69E-06	5.635137	Up	sorting nexin 22
MMP3	2.429809	0.000843	0.012674	3.338314	Up	matrix metallopeptidase 3
PRKCH	2.404825	4.47E-05	0.001428	4.081708	Up	protein kinase C eta
FREM1	2.403718	8.31E-06	0.000404	4.45702	Up	FRAS1 related extracellular matrix 1
TNR	2.4017	0.00395	0.03638	2.88212	Up	tenascin R
TRIM43B	2.398931	0.001191	0.015949	3.241037	Up	tripartite motif containing 43B
SYT15	2.397053	1.60E-12	1.33E-09	7.065696	Up	synaptotagmin 15
TSPAN19	2.395733	1.97E-06	0.000132	4.756406	Up	tetraspanin 19
CSRP3	2.395219	5.87E-05	0.001748	4.017788	Up	cysteine and glycine rich protein 3
HMX2	2.394124	0.00374	0.035105	2.899278	Up	H6 family homeobox 2
LHFPL3	2.387614	0.002427	0.026276	3.032264	Up	LHFPL tetraspan subfamily member 3
TLX1	2.387007	0.003302	0.032094	2.938127	Up	T cell leukemiahomeobox 1
TWIST2	2.38555	4.02E-05	0.00131	4.106426	Up	twist family bHLH transcription factor 2
KLRD1	2.374049	1.69E-05	0.000686	4.302718	Up	killer cell lectin like receptor D1
TMEM151A	2.369544	5.42E-09	1.52E-06	5.83378	Up	transmembrane protein 151A
MYRFL	2.366182	0.001417	0.018176	3.191106	Up	myelin regulatory factor like
WNT16	2.366157	0.000102	0.002648	3.885716	Up	Wnt family member 16
HOXD4	2.363336	6.00E-07	5.22E-05	4.991277	Up	homeobox D4
NBEAP2	2.362785	2.42E-10	1.21E-07	6.332059	Up	neurobeachinpseudogene 2
DPP6	2.358455	9.79E-07	7.47E-05	4.895841	Up	dipeptidyl peptidase like 6
GRID2	2.357256	0.003225	0.031721	2.945408	Up	glutamate ionotropic receptor delta type subunit 2
TBX3	2.354682	1.06E-05	0.00049	4.40377	Up	T-box transcription factor 3
TSPAN8	2.35172	0.002135	0.02414	3.070808	Up	tetraspanin 8
SNCB	2.348215	2.01E-07	2.39E-05	5.198732	Up	synuclein beta
REPS2	2.345969	1.38E-07	1.80E-05	5.268317	Up	RALBP1 associated Eps domain containing 2
PRIMA1	2.344237	0.00017	0.003922	3.760498	Up	proline rich membrane anchor 1

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KISS1	2.340898	0.000309	0.006147	3.607441	Up	KiSS-1 metastasis suppressor
C6orf132	2.340463	0.001934	0.022566	3.100169	Up	chromosome 6 open reading frame 132
MCTP2	2.339513	1.22E-07	1.62E-05	5.289742	Up	multiple C2 and transmembrane domain containing 2
SLC24A4	2.339503	0.000704	0.011099	3.387966	Up	solute carrier family 24 member 4
DIRAS3	2.337985	5.68E-05	0.001707	4.025583	Up	DIRAS family GTPase 3
ADGRB1	2.337007	8.19E-05	0.002234	3.938884	Up	adhesion G protein-coupled receptor B1
PEX5L	2.330311	7.82E-06	0.000384	4.470098	Up	peroxisomal biogenesis factor 5 like
UGT3A2	2.327039	0.002338	0.025568	3.043567	Up	UDP glycosyltransferase family 3 member A2
KRT8	2.320967	7.38E-05	0.002071	3.963717	Up	keratin 8
CNTN3	2.317492	0.001269	0.0167	3.222957	Up	contactin 3
NGB	2.316738	0.000109	0.002786	3.868687	Up	neuroglobin
SOX14	2.297077	0.001012	0.014272	3.287216	Up	SRY-box transcription factor 14
SYT9	2.29552	9.40E-07	7.32E-05	4.903858	Up	synaptotagmin 9
TRIM29	2.291201	8.13E-05	0.002223	3.940537	Up	tripartite motif containing 29
OLIG1	2.290536	0.001017	0.01431	3.285899	Up	oligodendrocyte transcription factor 1
FAM216B	2.290337	0.001972	0.02282	3.094389	Up	family with sequence similarity 216 member B
SERPINI1	2.288529	1.98E-07	2.37E-05	5.201594	Up	serpin family I member 1
CREG2	2.284752	1.23E-06	9.03E-05	4.851018	Up	cellular repressor of E1A stimulated genes 2
TMEM176B	2.280119	5.31E-06	0.000289	4.552052	Up	transmembrane protein 176B
MYL9	2.27808	0.000118	0.002967	3.850852	Up	myosin light chain 9
GABRA3	2.271727	1.92E-09	7.10E-07	6.004536	Up	gamma-aminobutyric acid type A receptor subunit alpha3
CSF2RA	2.26671	0.000187	0.00421	3.736227	Up	colony stimulating factor 2 receptor subunit alpha
ST8SIA6	2.26561	0.000537	0.009192	3.461525	Up	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6
PTPRB	2.263941	5.58E-07	4.96E-05	5.005315	Up	protein tyrosine phosphatase receptor type B
PTPRO	2.262052	0.000654	0.010503	3.407997	Up	protein tyrosine phosphatase receptor type O
ATP13A5	2.258508	1.67E-05	0.000682	4.305111	Up	ATPase 13A5
EVI2B	2.254225	2.76E-06	0.000174	4.687749	Up	ecotropic viral integration site 2B
LHX5	2.254225	0.000136	0.003287	3.815783	Up	LIM homeobox 5
CLDN11	2.254155	6.06E-06	0.000314	4.524305	Up	claudin 11
KRT8P10	2.251815	0.000943	0.013627	3.307044	Up	keratin 8 pseudogene 10

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CASP4	2.250589	0.000572	0.009565	3.444685	Up	caspase 4
CNTNAP5	2.248545	0.000763	0.01177	3.365963	Up	contactin associated protein family member 5
CTSW	2.246494	6.54E-05	0.001894	3.992574	Up	cathepsin W
ZNF385B	2.246346	0.000601	0.009869	3.431163	Up	zinc finger protein 385B
SMLR1	2.243262	0.001069	0.014877	3.271764	Up	small leucine rich protein 1
AATK	2.237433	2.84E-07	2.97E-05	5.133504	Up	apoptosis associated tyrosine kinase
SLC1A7	2.228737	0.000104	0.002682	3.881691	Up	solute carrier family 1 member 7
MAB21L1	2.228104	0.000267	0.005533	3.644934	Up	mab-21 like 1
QRFPR	2.228084	0.003888	0.035992	2.887137	Up	pyroglutamylatedRFamide peptide receptor
PTGER3	2.222667	8.55E-05	0.002309	3.928429	Up	prostaglandin E receptor 3
TTC29	2.217872	0.004585	0.040104	2.834797	Up	tetratricopeptide repeat domain 29
PRDM12	2.217854	8.60E-05	0.002316	3.927031	Up	PR/SET domain 12
KRT87P	2.214135	0.002375	0.02586	3.038821	Up	keratin 87, pseudogene
XKR4	2.211907	0.001097	0.015151	3.264372	Up	XK related 4
IL7R	2.209089	7.16E-05	0.00202	3.970763	Up	interleukin 7 receptor
MBP	2.207562	3.27E-06	0.000194	4.65328	Up	myelin basic protein
OPCML	2.205932	4.64E-08	7.56E-06	5.464768	Up	opioid binding protein/cell adhesion molecule like
XAF1	2.202625	1.95E-05	0.000763	4.270758	Up	XIAP associated factor 1
MYO7B	2.202431	4.38E-06	0.000248	4.592301	Up	myosin VIIB
UBE2E2	2.201351	4.73E-07	4.36E-05	5.037092	Up	ubiquitin conjugating enzyme E2 E2
PACRG-AS3	2.198737	0.000556	0.009393	3.452004	Up	PACRG antisense RNA 3
SLCO2A1	2.198369	0.000231	0.004974	3.682495	Up	solute carrier organic anion transporter family member 2A1
MATN4	2.191109	1.87E-06	0.000126	4.767031	Up	matrilin 4
CUX2	2.188378	0.000458	0.008211	3.504379	Up	cut like homeobox 2
PLLP	2.187719	2.24E-05	0.000844	4.239343	Up	plasmolipin
PTPRT	2.184041	0.001885	0.022105	3.107825	Up	protein tyrosine phosphatase receptor type T
SUSD3	2.182676	0.001487	0.018776	3.17729	Up	sushi domain containing 3
UNC5A	2.182186	2.84E-06	0.000178	4.682026	Up	unc-5 netrin receptor A
WFDC1	2.181192	0.000421	0.00772	3.526518	Up	WAP four-disulfide core domain 1
SLC7A14	2.180944	0.000938	0.013596	3.308457	Up	solute carrier family 7 member 14

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EXTL1	2.180468	3.36E-07	3.35E-05	5.102155	Up	exostosin like glycosyltransferase 1
GPR37	2.177362	5.11E-07	4.65E-05	5.021971	Up	G protein-coupled receptor 37
PAPPA2	2.173378	5.39E-05	0.001638	4.038076	Up	pappalysin 2
ACAN	2.170105	0.003644	0.034522	2.907398	Up	aggrecan
SHH	2.169207	2.12E-05	0.000807	4.251458	Up	sonic hedgehog signaling molecule
MEOX1	2.166825	0.005667	0.046172	2.766429	Up	mesenchyme homeobox 1
HOXD1	2.15819	0.000516	0.008979	3.472297	Up	homeobox D1
PDC	2.15811	0.000533	0.009173	3.463657	Up	phosducin
HOXD9	2.154342	0.000371	0.007054	3.559663	Up	homeobox D9
SPOCK3	2.153545	0.001823	0.021584	3.117721	Up	SPARC (osteonectin), cwcv and kazal like domains proteoglycan 3
P2RX5	2.153066	1.07E-06	8.02E-05	4.878978	Up	purinergic receptor P2X 5
RNF43	2.152324	6.23E-06	0.000322	4.51848	Up	ring finger protein 43
PROK1	2.15016	0.000663	0.010609	3.404325	Up	prokineticin 1
WT1-AS	2.149217	3.16E-05	0.001102	4.161932	Up	WT1 antisense RNA
AGTR1	2.146112	0.000194	0.004329	3.726962	Up	angiotensin II receptor type 1
TIE1	2.144	0.00097	0.013905	3.299168	Up	tyrosine kinase with immunoglobulin like and EGF like domains 1
CMAHP	2.142085	0.000139	0.003351	3.80974	Up	cytidinemonophospho-N-acetylneuraminic acid hydroxylase, pseudogene
FZD10	2.139724	0.0057	0.046363	2.764549	Up	frizzled class receptor 10
RCAN2	2.139447	5.16E-07	4.65E-05	5.020209	Up	regulator of calcineurin 2
LGI4	2.139318	0.002107	0.023908	3.074678	Up	leucine rich repeat LGI family member 4
CCDC80	2.138313	5.79E-06	0.000305	4.533792	Up	coiled-coil domain containing 80
KIZ	2.133687	1.01E-08	2.43E-06	5.728822	Up	kizunacentrosomal protein
EN1	2.129293	5.87E-05	0.001748	4.018094	Up	engrailed homeobox 1
RASGEF1B	2.129235	0.000275	0.005636	3.637874	Up	RasGEF domain family member 1B
XDH	2.125904	0.004074	0.037205	2.872396	Up	xanthine dehydrogenase
RERG	2.125852	0.000594	0.009783	3.434553	Up	RAS like estrogen regulated growth inhibitor
SUSD4	2.119268	2.58E-08	4.96E-06	5.567877	Up	sushi domain containing 4
P2RX7	2.116849	4.69E-05	0.001475	4.070714	Up	purinergic receptor P2X 7
PDE6G	2.116327	2.93E-05	0.001038	4.178541	Up	phosphodiesterase 6G

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H19	2.112086	0.002554	0.027269	3.016883	Up	H19 imprinted maternally expressed transcript
PRRG4	2.108829	0.001329	0.017244	3.209747	Up	proline rich and Gla domain 4
HOXA-AS3	2.10731	0.000375	0.007105	3.557278	Up	HOXA cluster antisense RNA 3
MDGA2	2.103677	0.000732	0.011407	3.37744	Up	MAM domain containing glycosylphosphatidylinositol anchor 2
LAMP3	2.097799	1.46E-06	0.000103	4.816886	Up	lysosomal associated membrane protein 3
PSCA	2.094469	0.001842	0.021732	3.114623	Up	prostate stem cell antigen
NTSR1	2.094365	0.000247	0.0052	3.664969	Up	neurotensin receptor 1
EWSAT1	2.092756	0.002912	0.029702	2.976869	Up	Ewing sarcoma associated transcript 1
ZPLD1	2.092415	2.85E-07	2.97E-05	5.133019	Up	zonapellucida like domain containing 1
VTN	2.092212	3.45E-05	0.001167	4.141402	Up	vitronectin
DYNLRB2	2.089414	1.66E-05	0.000681	4.306223	Up	dynein light chain roadblock-type 2
SIRT2	2.084193	4.33E-12	3.42E-09	6.926029	Up	sirtuin 2
ATP6V0D2	2.082939	7.89E-05	0.002172	3.947658	Up	ATPase H+ transporting V0 subunit d2
ITGB6	2.075512	0.002922	0.029777	2.975835	Up	integrin subunit beta 6
RBP4	2.07256	0.000416	0.007658	3.529648	Up	retinol binding protein 4
LPAR5	2.071622	8.93E-05	0.002386	3.917951	Up	lysophosphatidic acid receptor 5
SPON1	2.069551	4.95E-05	0.001532	4.057814	Up	spondin 1
BARX1	2.061839	0.000304	0.006067	3.611889	Up	BARX homeobox 1
NRK	2.056965	0.000417	0.007665	3.529219	Up	Nik related kinase
MMP10	2.053457	0.000246	0.005187	3.666393	Up	matrix metallopeptidase 10
STK32B	2.046941	6.53E-06	0.000331	4.50851	Up	serine/threonine kinase 32B
ISM1	2.045614	0.000265	0.005489	3.647361	Up	isthmin 1
NEFM	2.044972	1.75E-09	6.57E-07	6.01936	Up	neurofilament medium chain
COLCA1	2.043849	0.00311	0.030934	2.956629	Up	colorectal cancer associated 1
CLDN16	2.041339	0.004418	0.039153	2.846651	Up	claudin 16
STMND1	2.03859	0.003375	0.032594	2.931352	Up	stathmin domain containing 1
CHMP1B2P	2.037521	0.003963	0.036439	2.881127	Up	charged multivesicular body protein 1B2, pseudogene
POU2F3	2.035739	5.84E-05	0.001743	4.019225	Up	POU class 2 homeobox 3
FNDC1	2.033783	5.00E-05	0.001542	4.055746	Up	fibronectin type III domain containing 1
SLC1A6	2.033753	0.003001	0.030271	2.967622	Up	solute carrier family 1 member 6

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IL2RG	2.031451	0.002519	0.027036	3.021011	Up	interleukin 2 receptor subunit gamma
HOXB6	2.029184	0.001759	0.021063	3.128183	Up	homeobox B6
OTOS	2.02856	9.89E-06	0.000462	4.41966	Up	otospiralin
BMP2	2.025881	2.70E-08	5.13E-06	5.559778	Up	bone morphogenetic protein 2
CPB1	2.025296	0.004628	0.040245	2.831873	Up	carboxypeptidase B1
NR3C2	2.024886	2.53E-07	2.78E-05	5.155436	Up	nuclear receptor subfamily 3 group C member 2
AFAP1L2	2.024224	6.28E-09	1.68E-06	5.809179	Up	actin filament associated protein 1 like 2
SEC14L6	2.023407	3.58E-05	0.001198	4.132743	Up	SEC14 like lipid binding 6
C3orf36	2.021444	0.000234	0.00501	3.67917	Up	chromosome 3 putative open reading frame 36
TACR3	2.019654	0.003031	0.030407	2.964593	Up	tachykinin receptor 3
HTR1F	2.019439	0.001983	0.022907	3.092739	Up	5-hydroxytryptamine receptor 1F
KRT5	2.018892	0.000919	0.013423	3.314178	Up	keratin 5
COL10A1	2.018588	0.000121	0.00303	3.843854	Up	collagen type X alpha 1 chain
EPAS1	2.015091	1.61E-09	6.18E-07	6.033288	Up	endothelial PAS domain protein 1
CDK18	2.011465	3.79E-08	6.60E-06	5.500448	Up	cyclin dependent kinase 18
TYRP1	2.011407	0.000375	0.007114	3.556768	Up	tyrosinase related protein 1
CACNA2D4	2.01057	0.000447	0.008078	3.510788	Up	calcium voltage-gated channel auxiliary subunit alpha2delta 4
SPINK1	2.006323	0.000933	0.01354	3.309988	Up	serine peptidase inhibitor Kazal type 1
SLITRK2	2.00536	0.002615	0.027667	3.009732	Up	SLIT and NTRK like family member 2
HSPB8	2.000149	9.71E-11	5.60E-08	6.471401	Up	heat shock protein family B (small) member 8
ERBB3	2.000107	0.001979	0.022871	3.093324	Up	erb-b2 receptor tyrosine kinase 3
PNPLA4	1.998572	2.83E-13	3.03E-10	7.302267	Up	patatin like phospholipase domain containing 4
INHBE	1.996495	0.000985	0.014018	3.294882	Up	inhibin subunit beta E
AOAH	1.994582	5.39E-07	4.84E-05	5.01189	Up	acyloxyacyl hydrolase
KIF12	1.991606	0.001306	0.017024	3.214684	Up	kinesin family member 12
HAS2	1.990877	0.000122	0.003042	3.841869	Up	hyaluronan synthase 2
ERMN	1.986065	4.59E-05	0.001455	4.075396	Up	ermin
TMEM215	1.985992	0.00303	0.030407	2.964662	Up	transmembrane protein 215
SLCO6A1	1.985968	0.004528	0.039737	2.838838	Up	solute carrier organic anion transporter family member 6A1
SYT13	1.980375	0.001239	0.016394	3.229748	Up	synaptotagmin 13

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PPP4R4	1.980214	1.38E-11	1.03E-08	6.760295	Up	protein phosphatase 4 regulatory subunit 4
CDH13	1.978525	7.62E-06	0.000376	4.475586	Up	cadherin 13
ITIH3	1.977811	4.76E-05	0.001494	4.067044	Up	inter-alpha-trypsin inhibitor heavy chain 3
SFTA3	1.976536	1.61E-05	0.000665	4.313689	Up	surfactant associated 3
CSMD1	1.974488	0.002168	0.024359	3.066235	Up	CUB and Sushi multiple domains 1
DOCK10	1.973422	0.000992	0.014083	3.292923	Up	dedicator of cytokinesis 10
NTF3	1.972112	8.43E-05	0.002285	3.931783	Up	neurotrophin 3
GRHL2	1.968668	0.000642	0.010354	3.413214	Up	grainyhead like transcription factor 2
ZNF208	-6.5181	2.63E-09	8.98E-07	-5.95291	Down	zinc finger protein 208
ZNF728	-5.30593	7.56E-09	1.91E-06	-5.77806	Down	zinc finger protein 728
ZNF257	-4.94232	2.35E-06	0.000153	-4.72058	Down	zinc finger protein 257
CES1P1	-4.75441	0.000404	0.0075	-3.53774	Down	carboxylesterase 1 pseudogene 1
PEG3	-4.30367	0.000792	0.012152	-3.35545	Down	paternally expressed 3
RPSAP53	-4.13334	1.28E-13	1.68E-10	-7.40776	Down	ribosomal protein SA pseudogene 53
ZNF492	-4.09495	7.67E-09	1.92E-06	-5.77545	Down	zinc finger protein 492
ZIM2	-4.05336	0.005514	0.045292	-2.77536	Down	zinc finger imprinted 2
ZNF560	-3.74107	3.68E-07	3.60E-05	-5.08504	Down	zinc finger protein 560
ZNF676	-3.48744	5.88E-06	0.000309	-4.5305	Down	zinc finger protein 676
ERAP2	-3.37294	1.82E-16	5.47E-13	-8.23315	Down	endoplasmic reticulum aminopeptidase 2
RBM22P13	-3.27934	0.000343	0.006605	-3.58025	Down	RNA binding motif protein 22 pseudogene 13
OR2L13	-3.25253	2.67E-07	2.85E-05	-5.14553	Down	olfactory receptor family 2 subfamily L member 13
RN7SKP180	-3.06514	0.004326	0.038572	-2.85339	Down	RN7SK pseudogene 180
BEND4	-2.90887	6.38E-06	0.000326	-4.51331	Down	BEN domain containing 4
EEF1GP1	-2.89069	8.36E-09	2.04E-06	-5.76107	Down	eukaryotic translation elongation factor 1 gamma pseudogene 1
HLA-DQB2	-2.6706	0.000455	0.008176	-3.50582	Down	major histocompatibility complex, class II, DQ beta 2
RPS10P31	-2.66117	0.002555	0.027269	-3.01675	Down	ribosomal protein S10 pseudogene 31
RPS26P32	-2.59725	2.20E-07	2.55E-05	-5.18138	Down	ribosomal protein S26 pseudogene 32
RPL17P25	-2.54118	0.00071	0.011154	-3.38578	Down	ribosomal protein L17 pseudogene 25
PCDHGA3	-2.50991	0.000315	0.006227	-3.60304	Down	protocadherin gamma subfamily A, 3
SLCO1B1	-2.49752	0.000818	0.012393	-3.34648	Down	solute carrier organic anion transporter family member 1B1

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RPL6P4	-2.46467	1.06E-05	0.00049	-4.40408	Down	ribosomal protein L6 pseudogene 4
ARL14EPL	-2.43519	0.002807	0.029018	-2.98809	Down	ADP ribosylation factor like GTPase 14 effector protein like
PCDHB8	-2.43016	3.82E-14	6.04E-11	-7.56687	Down	protocadherin beta 8
ACTG1P20	-2.42568	2.56E-11	1.67E-08	-6.66996	Down	actin gamma 1 pseudogene 20
KNOP1P1	-2.39034	0.000416	0.007658	-3.52974	Down	lysine rich nucleolar protein 1 pseudogene 1
HLA-DRB5	-2.37191	0.000141	0.003394	-3.80556	Down	major histocompatibility complex, class II, DR beta 5
ZNF98	-2.34342	3.67E-05	0.00122	-4.12723	Down	zinc finger protein 98
SALL1P1	-2.33513	7.94E-05	0.00218	-3.94631	Down	spalt like transcription factor 1 pseudogene 1
FGF19	-2.33214	0.000439	0.007989	-3.51519	Down	fibroblast growth factor 19
ELK2BP	-2.30421	0.001775	0.021191	-3.12545	Down	ETS transcription factor ELK2B, pseudogene
BTBD6P1	-2.30297	0.000179	0.004107	-3.74645	Down	BTB domain containing 6 pseudogene 1
UBE2CP3	-2.29732	4.72E-05	0.001484	-4.06898	Down	ubiquitin conjugating enzyme E2 C pseudogene 3
RN7SKP230	-2.27899	0.000814	0.012357	-3.34799	Down	RN7SK pseudogene 230
HNRNPA1P65	-2.26849	0.003638	0.0345	-2.90796	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 65
CHCHD3P1	-2.24294	0.000618	0.010035	-3.42378	Down	coiled-coil-helix-coiled-coil-helix domain containing 3 pseudogene 1
CTB-3M24.3	-2.23645	0.004147	0.037569	-2.86678	Down	uncharacterized CTB-3M24.3
OAS3	-2.2294	3.28E-13	3.39E-10	-7.2823	Down	2'-5'-oligoadenylate synthetase 3
RPS26P39	-2.21798	9.14E-05	0.002436	-3.9123	Down	ribosomal protein S26 pseudogene 39
SUCLA2P2	-2.21532	0.005002	0.042458	-2.80691	Down	SUCLA2 pseudogene 2
HS3ST4	-2.19502	1.10E-05	0.000501	-4.39637	Down	heparansulfate-glucosamine 3-sulfotransferase 4
RNU6-181P	-2.18885	0.001513	0.019023	-3.17216	Down	RNA, U6 small nuclear 181, pseudogene
DMRTA2	-2.18405	3.12E-07	3.15E-05	-5.11623	Down	DMRT like family A2
BEX5	-2.17331	3.08E-07	3.13E-05	-5.11865	Down	brain expressed X-linked 5
SNORA54	-2.15751	0.000575	0.009591	-3.44319	Down	small nucleolar RNA, H/ACA box 54
ARL2BPP4	-2.14887	0.001975	0.022834	-3.09402	Down	ADP ribosylation factor like GTPase 2 binding protein pseudogene 4
DHFRP2	-2.11862	0.000341	0.006565	-3.58218	Down	dihydrofolatereductasepseudogene 2
TBX18	-2.10778	0.001436	0.018319	-3.18724	Down	T-box transcription factor 18
THEGL	-2.08882	3.38E-05	0.001152	-4.14598	Down	theg spermatid protein like
HLA-DMB	-2.05803	6.98E-05	0.001985	-3.97689	Down	major histocompatibility complex, class II, DM beta

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ZAR1	-2.05692	1.32E-05	0.000568	-4.35672	Down	zygote arrest 1
RPL9P27	-2.04764	0.003348	0.03243	-2.93387	Down	ribosomal protein L9 pseudogene 27
RPS13P3	-2.04216	0.003469	0.033293	-2.92277	Down	ribosomal protein S13 pseudogene 3
HNRNPA1P63	-2.03235	0.000868	0.012901	-3.33013	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 63
CD24P2	-2.02942	0.000142	0.003394	-3.80545	Down	CD24 molecule pseudogene 2
TRG-GCC1-5	-2.02489	0.000104	0.00268	-3.88213	Down	tRNA-Gly (anticodon GCC) 1-5
CYP4F11	-1.9933	0.000998	0.014148	-3.29121	Down	cytochrome P450 family 4 subfamily F member 11
SUMO1P2	-1.99196	0.004081	0.037235	-2.8718	Down	SUMO1 pseudogene 2
GAPDHP48	-1.98215	0.00558	0.045645	-2.7715	Down	glyceraldehyde 3 phosphate dehydrogenase pseudogene 48
TAS2R46	-1.9808	0.004652	0.040376	-2.83021	Down	taste 2 receptor member 46
CTBP2P3	-1.98015	0.001462	0.018562	-3.18215	Down	CTBP2 pseudogene 3
RPL7P10	-1.97956	0.005141	0.043285	-2.79808	Down	ribosomal protein L7 pseudogene 10
ANKRD20A7P	-1.96855	0.000569	0.009541	-3.44583	Down	ankyrin repeat domain 20 family member A7, pseudogene
FABP7P1	-1.96702	0.001339	0.017363	-3.2074	Down	fatty acid binding protein 7 pseudogene 1
RPS26P31	-1.95557	0.000215	0.004692	-3.70102	Down	ribosomal protein S26 pseudogene 31
RPS7P15	-1.93523	0.002366	0.025794	-3.04003	Down	ribosomal protein S7 pseudogene 15
EMX1	-1.92323	0.000183	0.00415	-3.74104	Down	empty spiracles homeobox 1
RPS26P11	-1.91816	2.42E-07	2.72E-05	-5.16402	Down	ribosomal protein S26 pseudogene 11
MKRN4P	-1.91454	4.94E-06	0.000272	-4.56733	Down	makorin ring finger protein 4, pseudogene
GABRB2	-1.90578	6.58E-06	0.000333	-4.50686	Down	gamma-aminobutyric acid type A receptor subunit beta2
ANKRD29	-1.90397	2.42E-05	0.000898	-4.22178	Down	ankyrin repeat domain 29
RN7SKP80	-1.90343	0.000269	0.005557	-3.64329	Down	RN7SK pseudogene 80
SFPQP1	-1.89933	0.003142	0.031209	-2.95349	Down	splicing factor proline and glutamine rich pseudogene 1
HMGB1P27	-1.88379	3.51E-05	0.001182	-4.13751	Down	high mobility group box 1 pseudogene 27
HLA-DRB1	-1.88314	0.001139	0.015537	-3.25378	Down	major histocompatibility complex, class II, DR beta 1
CRHR2	-1.88235	0.000775	0.011938	-3.36148	Down	corticotropin releasing hormone receptor 2
HNRNPA1P37	-1.88083	0.003247	0.031826	-2.94338	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 37
RPL18AP16	-1.86017	0.003025	0.030382	-2.96516	Down	ribosomal protein L18a pseudogene 16

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CFL1P6	-1.84229	0.004001	0.036726	-2.87808	Down	cofilin 1 pseudogene 6
GAPDHP35	-1.83922	3.05E-06	0.000185	-4.66727	Down	glyceraldehyde 3 phosphate dehydrogenase pseudogene 35
RPL7P44	-1.83349	0.006282	0.049575	-2.7327	Down	ribosomal protein L7 pseudogene 44
RPL21P1	-1.82383	0.00231	0.025376	-3.04715	Down	ribosomal protein L21 pseudogene 1
PHF2P2	-1.81937	0.00319	0.031471	-2.94877	Down	PHD finger protein 2 pseudogene 2
YWHAZP7	-1.81721	0.00125	0.016499	-3.2273	Down	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta pseudogene 7
TUBBP2	-1.80621	2.94E-07	3.03E-05	-5.12696	Down	tubulin beta pseudogene 2
RPS26P47	-1.806	5.61E-06	0.000298	-4.54067	Down	ribosomal protein S26 pseudogene 47
RPL26P13	-1.80591	0.001866	0.021974	-3.11081	Down	ribosomal protein L26 pseudogene 13
HLA-DOA	-1.80287	0.002065	0.023541	-3.08076	Down	major histocompatibility complex, class II, DO alpha
HMGN1P26	-1.79963	0.002649	0.027929	-3.00574	Down	high mobility group nucleosome binding domain 1 pseudogene 26
NKX2-3	-1.77761	0.004799	0.041262	-2.82024	Down	NK2 homeobox 3
RPL6P2	-1.7681	0.004827	0.041478	-2.81835	Down	ribosomal protein L6 pseudogene 2
RPL31P28	-1.76701	0.002381	0.025896	-3.03807	Down	ribosomal protein L31 pseudogene 28
ROPN1	-1.76663	0.002338	0.025568	-3.04351	Down	rhophilin associated tail protein 1
HNRNPA1P57	-1.75587	0.005324	0.044241	-2.78674	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 57
RPS2P28	-1.75519	0.003864	0.035826	-2.88909	Down	ribosomal protein S2 pseudogene 28
PLEK	-1.75398	0.000235	0.005014	-3.67859	Down	pleckstrin
TEX101	-1.75365	0.002279	0.025151	-3.05125	Down	testis expressed 101
RPS3AP12	-1.74702	0.003243	0.031806	-2.94368	Down	RPS3A pseudogene 12
FTLP17	-1.74701	0.00587	0.047287	-2.75495	Down	ferritin light chain pseudogene 17
CARD16	-1.74301	5.36E-06	0.00029	-4.55017	Down	caspase recruitment domain family member 16
HSPA8P14	-1.72681	0.001129	0.015453	-3.25618	Down	heat shock protein family A (Hsp70) member 8 pseudogene 14
HDC	-1.72669	0.002689	0.028207	-3.00122	Down	histidine decarboxylase
KCNMB3P1	-1.72371	0.005202	0.043598	-2.79427	Down	KCNMB3 pseudogene 1
RPS26P53	-1.72215	7.37E-05	0.00207	-3.96399	Down	ribosomal protein S26 pseudogene 53
DHRS3	-1.72144	3.15E-06	0.00019	-4.66063	Down	dehydrogenase/reductase 3
HNRNPA1P43	-1.71834	0.005299	0.04413	-2.78828	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 43

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CTBP2P6	-1.71596	0.000444	0.008046	-3.51218	Down	CTBP2 pseudogene 6
ACTG1P10	-1.71103	2.82E-05	0.001011	-4.18767	Down	actin gamma 1 pseudogene 10
ZNF835	-1.69626	4.28E-05	0.001383	-4.0919	Down	zinc finger protein 835
SP3P	-1.65988	1.02E-05	0.000474	-4.41287	Down	Sp3 transcription factor pseudogene
NFU1P1	-1.6597	0.00231	0.025376	-3.04719	Down	NFU1 iron-sulfur cluster scaffold pseudogene 1
CROCCP4	-1.65935	0.001276	0.016764	-3.22122	Down	CROCC pseudogene 4
CD74	-1.65426	0.003948	0.036376	-2.88225	Down	CD74 molecule
FGF3	-1.65387	0.006118	0.048754	-2.74137	Down	fibroblast growth factor 3
HLA-DRA	-1.64614	0.004545	0.039857	-2.8376	Down	major histocompatibility complex, class II, DR alpha
DYNLL1P4	-1.64466	0.004296	0.038388	-2.85557	Down	dynein light chain LC8-type 1 pseudogene 4
ACTG1P23	-1.64233	0.000601	0.009869	-3.43125	Down	actin gamma 1 pseudogene 23
NEK2P2	-1.64075	0.00095	0.013701	-3.30505	Down	NEK2 pseudogene 2
TCEAL2	-1.63593	2.85E-05	0.001017	-4.18477	Down	transcription elongation factor A like 2
HNRNPA1P21	-1.63513	0.003914	0.036156	-2.88503	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 21
RPS26P8	-1.62857	3.92E-07	3.80E-05	-5.07271	Down	ribosomal protein S26 pseudogene 8
RPS11P2	-1.6179	0.006034	0.048308	-2.74591	Down	ribosomal protein S11 pseudogene 2
CFL1P3	-1.61783	0.002129	0.024121	-3.07158	Down	cofilin 1 pseudogene 3
SCARNA7	-1.61205	0.002804	0.028995	-2.98844	Down	small Cajal body-specific RNA 7
RPL26P27	-1.60566	0.001191	0.015949	-3.24091	Down	ribosomal protein L26 pseudogene 27
CALB2	-1.59844	2.50E-05	0.000921	-4.21489	Down	calbindin 2
ZNF718	-1.59345	4.41E-17	1.65E-13	-8.40148	Down	zinc finger protein 718
PRPS1L1	-1.59297	0.001575	0.019543	-3.16055	Down	phosphoribosyl pyrophosphate synthetase 1 like 1
RN7SKP71	-1.5882	0.003128	0.03108	-2.95487	Down	RN7SK pseudogene 71
NEK2P3	-1.58668	0.00028	0.005703	-3.63293	Down	NEK2 pseudogene 3
RPL6P22	-1.58454	0.002883	0.029478	-2.97992	Down	ribosomal protein L6 pseudogene 22
SLFN11	-1.57905	2.85E-05	0.001017	-4.18511	Down	schlafen family member 11
RPS26P10	-1.57842	0.000468	0.008338	-3.49871	Down	ribosomal protein S26 pseudogene 10
PRSS33	-1.55413	0.000228	0.004929	-3.68534	Down	serine protease 33
TUBB3P1	-1.54989	0.000577	0.009609	-3.44238	Down	tubulin beta 3 class III pseudogene 1
ANK1	-1.54506	0.003039	0.030461	-2.96381	Down	ankyrin 1

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RPL23P2	-1.53136	0.004965	0.042338	-2.80928	Down	ribosomal protein L23 pseudogene 2
VWF	-1.53118	0.000274	0.005627	-3.63867	Down	von Willebrand factor
SLFN13	-1.52944	0.000156	0.003665	-3.78209	Down	schlafen family member 13
PSMC1P11	-1.52904	0.004969	0.042356	-2.80905	Down	proteasome 26S subunit, ATPase 1 pseudogene 11
CIITA	-1.52888	7.61E-05	0.002118	-3.95628	Down	class II major histocompatibility complex transactivator
SLCO5A1	-1.52227	0.000155	0.003665	-3.78221	Down	solute carrier organic anion transporter family member 5A1
RPS24P4	-1.51994	0.004516	0.039678	-2.83969	Down	ribosomal protein S24 pseudogene 4
MTTP	-1.51558	0.000119	0.002999	-3.84718	Down	microsomal triglyceride transfer protein
GCM1	-1.51127	0.004488	0.039495	-2.84163	Down	glial cells missing transcription factor 1
GAPDHP63	-1.50616	0.002098	0.023842	-3.07594	Down	glyceraldehyde 3 phosphate dehydrogenase pseudogene 63
SLC26A7	-1.50442	0.000377	0.007135	-3.55585	Down	solute carrier family 26 member 7
RBMXP3	-1.49698	0.001785	0.021257	-3.12384	Down	RBMX pseudogene 3
SRP14P1	-1.49337	0.00032	0.006312	-3.59835	Down	signal recognition particle 14 pseudogene 1
ATP10B	-1.48972	0.000982	0.014006	-3.29553	Down	ATPase phospholipid transporting 10B (putative)
RPS18P14	-1.48562	0.001583	0.019596	-3.15896	Down	ribosomal protein S18 pseudogene 14
RPS12P8	-1.48441	0.002754	0.028673	-2.99391	Down	ribosomal protein S12 pseudogene 8
GLULP1	-1.47204	0.000588	0.009732	-3.43711	Down	glutamate-ammonia ligase pseudogene 1
ZNF454	-1.47178	5.53E-06	0.000296	-4.54378	Down	zinc finger protein 454
RPL39P32	-1.46907	0.004084	0.037244	-2.8716	Down	ribosomal protein L39 pseudogene 32
HNRNPA1P38	-1.4668	0.001168	0.015767	-3.24659	Down	heterogeneous nuclear ribonucleoprotein A1pseudogene 38
ZNF572	-1.4642	4.86E-06	0.000269	-4.57058	Down	zinc finger protein 572
CNN2P2	-1.46374	0.001904	0.022275	-3.10482	Down	calponin 2 pseudogene 2
RDXP2	-1.45663	0.003661	0.034634	-2.90597	Down	radixinpseudogene 2
HMGN2P17	-1.45283	0.003262	0.031906	-2.9419	Down	high mobility group nucleosomal binding domain 2 pseudogene 17
PCDHA11	-1.44799	2.17E-06	0.000142	-4.73733	Down	protocadherin alpha 11
EPHA5	-1.44441	1.98E-06	0.000133	-4.75502	Down	EPH receptor A5
COPS5P1	-1.44436	0.004106	0.037374	-2.8699	Down	COP9 signalosome subunit 5 pseudogene 1
HNRNPA1P28	-1.43926	0.00447	0.039436	-2.84295	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 28

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HLA-DMA	-1.4341	1.27E-05	0.000549	-4.36557	Down	major histocompatibility complex, class II, DM alpha
PPIAL4A	-1.43037	0.002662	0.027996	-3.00432	Down	peptidylprolylisomerase A like 4A
MDGA1	-1.42959	4.51E-05	0.00144	-4.07952	Down	MAM domain containing glycosylphosphatidylinositol anchor 1
RPS26P7	-1.42571	0.000193	0.004319	-3.72808	Down	ribosomal protein S26 pseudogene 7
FRG1DP	-1.42516	0.001589	0.019624	-3.15792	Down	FSHD region gene 1 family member D, pseudogene
RPL5P28	-1.41257	0.000984	0.014018	-3.29507	Down	ribosomal protein L5 pseudogene 28
CCT6P4	-1.41243	0.005813	0.046991	-2.75812	Down	chaperonin containing TCP1 subunit 6 pseudogene 4
RPL7AP34	-1.41025	0.002534	0.027112	-3.01921	Down	ribosomal protein L7a pseudogene 34
ROPN1B	-1.40762	0.006154	0.048953	-2.73946	Down	rhophilin associated tail protein 1B
RPS26P13	-1.39247	0.002595	0.02757	-3.01208	Down	ribosomal protein S26 pseudogene 13
RPS6P26	-1.38561	0.004385	0.038942	-2.84903	Down	ribosomal protein S6 pseudogene 26
RBMXP1	-1.38361	0.002774	0.028777	-2.99169	Down	RBMX pseudogene 1
CASQ1	-1.3819	0.002648	0.027929	-3.00588	Down	calsequestrin 1
CASC8	-1.37588	0.002488	0.026795	-3.02483	Down	cancer susceptibility 8
BCL6B	-1.37317	0.00448	0.039459	-2.8422	Down	BCL6B transcription repressor
TUBBP6	-1.36852	0.000861	0.012856	-3.3324	Down	tubulin beta class I pseudogene 6
C1QBPP2	-1.36084	1.79E-05	0.000722	-4.28903	Down	complement C1q binding protein pseudogene 2
HSP90AB4P	-1.36066	0.005694	0.046339	-2.7649	Down	heat shock protein 90 alpha family class B member 4, pseudogene
ANGPT2	-1.36042	0.000275	0.005634	-3.63817	Down	angiopoietin 2
HNRNPA1P33	-1.35524	0.004127	0.037469	-2.86829	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 33
HMGB1P40	-1.35495	0.001268	0.016691	-3.22323	Down	high mobility group box 1 pseudogene 40
CFL1P5	-1.34169	0.0001	0.002624	-3.88984	Down	cofilin 1 pseudogene 5
PPIAP13	-1.33704	0.001678	0.020386	-3.14195	Down	peptidylprolylisomerase A pseudogene 13
GRM3	-1.33682	0.005736	0.046568	-2.76249	Down	glutamate metabotropic receptor 3
CHRDL1	-1.32563	2.12E-05	0.000806	-4.25206	Down	chordin like 1
FDPSP9	-1.31262	0.003182	0.031428	-2.94961	Down	farnesyldiphosphate synthase pseudogene 9
EMX2OS	-1.30573	0.002641	0.027874	-3.00672	Down	EMX2 opposite strand/antisense RNA
ZNF441	-1.30004	5.17E-05	0.001584	-4.04764	Down	zinc finger protein 441
GJA1P1	-1.29857	3.41E-05	0.001158	-4.14411	Down	gap junction protein alpha 1 pseudogene 1

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KCNJ2	-1.29843	0.001293	0.016914	-3.21743	Down	potassium inwardly rectifying channel subfamily J member 2
NEK2P4	-1.29095	0.000181	0.004132	-3.74391	Down	NEK2 pseudogene 4
EMX2	-1.28809	0.005571	0.045597	-2.77201	Down	empty spiracles homeobox 2
RPS5P5	-1.28068	0.004628	0.040245	-2.83186	Down	RPS5 pseudogene 5
BCAR1P1	-1.27904	0.000286	0.005766	-3.62747	Down	BCAR1 pseudogene 1
ZNF439	-1.27824	0.004881	0.041803	-2.8148	Down	zinc finger protein 439
TCP1P2	-1.27592	0.004798	0.041262	-2.82032	Down	t-complex 1 pseudogene 2
YPEL5P2	-1.27498	0.005312	0.044188	-2.78748	Down	YPEL5 pseudogene 2
RPS14P10	-1.27394	0.002458	0.026531	-3.02848	Down	ribosomal protein S14 pseudogene 10
RPL7AP8	-1.27352	0.006342	0.049972	-2.72955	Down	ribosomal protein L7a pseudogene 8
FOXD2	-1.27066	7.84E-05	0.002161	-3.9491	Down	forkhead box D2
HSPD1P2	-1.26986	0.004793	0.041261	-2.82064	Down	heat shock protein family D (Hsp60) member 1 pseudogene 2
RPL7AP5	-1.26974	0.004989	0.042407	-2.80775	Down	ribosomal protein L7a pseudogene 5
HSPD1P3	-1.26847	0.004447	0.0393	-2.84461	Down	heat shock protein family D (Hsp60) member 1 pseudogene 3
GLB1L3	-1.25746	0.000527	0.009104	-3.46656	Down	galactosidase beta 1 like 3
FEN1P1	-1.25677	0.002266	0.025077	-3.05291	Down	flap structure-specific endonuclease 1 pseudogene 1
OAS2	-1.25627	0.003453	0.033195	-2.92426	Down	2'-5'-oligoadenylate synthetase 2
HNRNPKP3	-1.2486	0.003281	0.03201	-2.94008	Down	heterogeneous nuclear ribonucleoprotein K pseudogene 3
NPM1P31	-1.24845	0.001712	0.020672	-3.13604	Down	nucleophosmin 1 pseudogene 31
MICB	-1.24236	1.11E-05	0.000502	-4.39516	Down	MHC class I polypeptide-related sequence B
EEF1GP5	-1.24159	0.002209	0.024635	-3.06058	Down	eukaryotic translation elongation factor 1 gamma pseudogene 5
RPS27AP2	-1.24132	0.001547	0.019312	-3.16573	Down	RPS27A pseudogene 2
RPL10P3	-1.24052	0.004426	0.039195	-2.8461	Down	ribosomal protein L10 pseudogene 3
LEMD1	-1.23435	0.005189	0.043526	-2.79507	Down	LEM domain containing 1
RPSAP11	-1.23358	0.000969	0.013905	-3.29935	Down	ribosomal protein SA pseudogene 11
HMGN2P46	-1.23341	0.000995	0.014119	-3.29206	Down	high mobility group nucleosomal binding domain 2 pseudogene 46
HNRNPCL2	-1.23199	0.00045	0.008115	-3.50912	Down	heterogeneous nuclear ribonucleoprotein C like 2
PPIGP1	-1.22891	0.000603	0.009869	-3.43031	Down	peptidylprolylisomerase G pseudogene 1

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TECRP2	-1.22333	0.000134	0.00326	-3.81828	Down	trans-2,3-enoyl-CoA reductasepseudogene 2
ACTG1P9	-1.22114	0.000416	0.007658	-3.52976	Down	actin gamma 1 pseudogene 9
FCGBP	-1.22019	0.000528	0.009112	-3.4661	Down	Fc gamma binding protein
RPS15AP5	-1.2099	0.001664	0.020269	-3.1444	Down	ribosomal protein S15a pseudogene 5
RPL19P4	-1.20963	0.002841	0.029219	-2.9844	Down	ribosomal protein L19 pseudogene 4
DUSP5P1	-1.20845	0.001903	0.022273	-3.10496	Down	dual specificity phosphatase 5 pseudogene 1
GLULP4	-1.20828	0.001625	0.019934	-3.15142	Down	glutamate-ammonia ligase pseudogene 4
CDC42P3	-1.20442	0.005333	0.044273	-2.78621	Down	cell division cycle 42 pseudogene 3
LRRC19	-1.20365	0.005563	0.045554	-2.77251	Down	leucine rich repeat containing 19
RND3	-1.20135	0.000586	0.009706	-3.43803	Down	Rho family GTPase 3
MGAT4C	-1.19789	0.00168	0.020386	-3.14157	Down	MGAT4 family member C
SDHCP3	-1.19731	0.000337	0.006535	-3.58494	Down	succinate dehydrogenase complex subunit C pseudogene 3
RPS4XP22	-1.19684	0.001181	0.015853	-3.24353	Down	ribosomal protein S4X pseudogene 22
RPL19P21	-1.19594	0.000773	0.011902	-3.36245	Down	ribosomal protein L19 pseudogene 21
VPS35P1	-1.19337	0.001018	0.014324	-3.28548	Down	VPS35 pseudogene 1
SCARNA10	-1.19248	0.001118	0.015371	-3.25899	Down	small Cajal body-specific RNA 10
XRCC6P3	-1.19242	0.003803	0.035479	-2.89409	Down	X-ray repair cross complementing 6 pseudogene 3
FTH1P1	-1.18656	0.005239	0.043852	-2.79194	Down	ferritin heavy chain 1 pseudogene 1
COMT	-1.18454	2.26E-05	0.000848	-4.23729	Down	catechol-O-methyltransferase
REREP3	-1.18335	0.006156	0.048953	-2.73937	Down	arginine-glutamic acid dipeptide repeats pseudogene 3
TTPA	-1.18313	4.35E-05	0.001397	-4.08807	Down	alpha tocopherol transfer protein
FDPSP8	-1.17991	0.000554	0.009365	-3.45312	Down	farnesyldiphosphate synthase pseudogene 8
GDI2P1	-1.17983	0.003733	0.035046	-2.8999	Down	GDP dissociation inhibitor 2 pseudogene 1
GSTT2B	-1.17609	8.80E-05	0.00236	-3.92159	Down	glutathione S-transferase theta 2B
PCNPP3	-1.17603	0.000181	0.004132	-3.74388	Down	PEST containing nuclear protein pseudogene 3
AKR1C3	-1.17428	0.000323	0.006343	-3.59593	Down	aldo-ketoreductase family 1 member C3
PRKXP1	-1.17232	0.000121	0.00303	-3.8442	Down	PRKX pseudogene 1
FANCD2P1	-1.1713	0.003847	0.035703	-2.89046	Down	FANCD2 pseudogene 1
RPS10P5	-1.1705	0.00628	0.049575	-2.73279	Down	ribosomal protein S10 pseudogene 5
RPL29P17	-1.16925	0.001179	0.015844	-3.24397	Down	ribosomal protein L29 pseudogene 17

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LARP4P	-1.16751	0.000814	0.012357	-3.34808	Down	LARP4 pseudogene
SLC10A4	-1.16702	0.000102	0.002648	-3.8857	Down	solute carrier family 10 member 4
NEDD4L	-1.16243	0.000852	0.012782	-3.33539	Down	NEDD4 like E3 ubiquitin protein ligase
SPANXA2-OT1	-1.16028	0.002853	0.029276	-2.98317	Down	SPANXA2 overlapping transcript 1
THAP12P3	-1.15874	0.003039	0.030461	-2.96373	Down	THAP domain containing 12 pseudogene 3
RPL6P3	-1.15825	0.002622	0.027733	-3.0089	Down	ribosomal protein L6 pseudogene 3
CASP1	-1.1574	0.001537	0.019231	-3.16754	Down	caspase 1
RPL31P51	-1.15422	0.000422	0.007736	-3.52567	Down	ribosomal protein L31 pseudogene 51
CKS1BP6	-1.15327	0.001717	0.0207	-3.13529	Down	CDC28 protein kinase regulatory subunit 1B pseudogene 6
RPL21P20	-1.14925	0.00234	0.025568	-3.04333	Down	ribosomal protein L21 pseudogene 20
BLACAT1	-1.14708	0.000784	0.012043	-3.35836	Down	BLACAT1 overlapping LEMD1 locus
C15orf32	-1.14473	7.41E-05	0.002076	-3.96263	Down	chromosome 15 putative open reading frame 32
SLC4A11	-1.14386	0.004531	0.039754	-2.83861	Down	solute carrier family 4 member 11
FAM86FP	-1.14293	6.90E-11	4.06E-08	-6.52277	Down	family with sequence similarity 86, member A pseudogene
HES2	-1.14145	0.003274	0.031956	-2.9408	Down	hes family bHLH transcription factor 2
HSPD1P12	-1.13776	0.001977	0.022856	-3.09363	Down	heat shock protein family D (Hsp60) member 1 pseudogene 12
HNRNPA1P52	-1.13497	0.001853	0.021841	-3.11282	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 52
SETP3	-1.13368	0.000391	0.007333	-3.54599	Down	SET pseudogene 3
RPS10P6	-1.13267	0.001959	0.022737	-3.09643	Down	ribosomal protein S10 pseudogene 6
RPL10P8	-1.12907	0.00084	0.012645	-3.33923	Down	ribosomal protein L10 pseudogene 8
RPL13AP3	-1.12745	0.001808	0.021458	-3.12014	Down	ribosomal protein L13a pseudogene 3
SNHG5	-1.12449	6.98E-06	0.000349	-4.49433	Down	small nucleolar RNA host gene 5
SETP22	-1.12404	0.003809	0.035503	-2.89359	Down	SET pseudogene 22
RPS15AP12	-1.12087	0.002759	0.028696	-2.99342	Down	ribosomal protein S15a pseudogene 12
RPS7P3	-1.12077	0.004861	0.041683	-2.81612	Down	ribosomal protein S7 pseudogene 3
RPS14P2	-1.11945	0.003594	0.034195	-2.91174	Down	ribosomal protein S14 pseudogene 2
SDHCP2	-1.11327	0.002445	0.026438	-3.03003	Down	succinate dehydrogenase complex subunit C pseudogene 2
GSTT2	-1.11139	0.000398	0.00743	-3.54146	Down	glutathione S-transferase theta 2 (gene/pseudogene)

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RPL9P18	-1.10792	0.002032	0.023269	-3.08558	Down	ribosomal protein L9 pseudogene 18
ACTG1P1	-1.10489	2.17E-05	0.000823	-4.24634	Down	actin gamma 1 pseudogene 1
RPL31P12	-1.10449	0.004113	0.037395	-2.86939	Down	ribosomal protein L31 pseudogene 12
RPS15P7	-1.1033	0.000742	0.011526	-3.37359	Down	ribosomal protein S15 pseudogene 7
ACTG1P12	-1.1024	0.000337	0.006535	-3.58469	Down	actin gamma 1 pseudogene 12
FDPSP5	-1.10019	0.001157	0.015692	-3.24925	Down	farnesyldiphosphate synthase pseudogene 5
GAS1	-1.09707	0.000748	0.011614	-3.37119	Down	growth arrest specific 1
POU3F2	-1.09236	6.64E-05	0.00192	-3.98865	Down	POU class 3 homeobox 2
BEGAIN	-1.09147	0.006329	0.049881	-2.73024	Down	brain enriched guanylate kinase associated
LDB2	-1.08575	2.53E-05	0.000925	-4.21211	Down	LIM domain binding 2
RN7SL585P	-1.08221	0.002694	0.028228	-3.00064	Down	RNA, 7SL, cytoplasmic 585, pseudogene
PCDHGB3	-1.08018	0.00246	0.026536	-3.0282	Down	protocadherin gamma subfamily B, 3
GPR39	-1.07871	0.000335	0.006499	-3.58695	Down	G protein-coupled receptor 39
KIAA0408	-1.07585	0.003182	0.031428	-2.94957	Down	KIAA0408
NUP50P3	-1.07535	0.001469	0.018622	-3.18066	Down	nucleoporin 50 pseudogene 3
PCDHA7	-1.07491	0.002208	0.024635	-3.06069	Down	protocadherin alpha 7
FAM107A	-1.07269	0.005598	0.045768	-2.77043	Down	family with sequence similarity 107 member A
FRG1EP	-1.07104	0.001072	0.014905	-3.27085	Down	FSHD region gene 1 family member E, pseudogene
ZBTB8OSP1	-1.07083	0.005774	0.046797	-2.76033	Down	zinc finger and BTB domain containing 8 opposite strand pseudogene 1
HSP90AA3P	-1.06798	0.000401	0.007463	-3.53939	Down	heat shock protein 90 alpha family class A member 3, pseudogene
NR2E1	-1.0628	0.00276	0.028696	-2.99329	Down	nuclear receptor subfamily 2 group E member 1
PCDHB17P	-1.06232	0.000421	0.007723	-3.52628	Down	protocadherin beta 17 pseudogene
SLC25A18	-1.06028	0.006261	0.049474	-2.73381	Down	solute carrier family 25 member 18
YWHAEP7	-1.05809	0.001601	0.01976	-3.15566	Down	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein epsilon pseudogene 7
HMGB1P9	-1.05371	0.005093	0.04299	-2.80106	Down	high mobility group box 1 pseudogene 9
NCAPD2P1	-1.05114	0.000364	0.006951	-3.56456	Down	non-SMC condensin I complex subunit D2 pseudogene 1
PTMAP7	-1.05022	0.002048	0.023381	-3.08324	Down	prothymosin alpha pseudogene 7
IPCEF1	-1.05018	0.002085	0.023722	-3.07786	Down	interaction protein for cytohesin exchange factors 1

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CHRNA5	-1.04453	2.02E-07	2.39E-05	-5.19753	Down	cholinergic receptor nicotinic alpha 5 subunit
DRAXIN	-1.03529	1.99E-07	2.38E-05	-5.19996	Down	dorsal inhibitory axon guidance protein
TVP23A	-1.03515	0.000265	0.005487	-3.6476	Down	trans-golgi network vesicle protein 23 homolog A
PDE2A	-1.03427	0.003691	0.034814	-2.90346	Down	phosphodiesterase 2A
RPS27P21	-1.03101	0.003808	0.035503	-2.89361	Down	ribosomal protein S27 pseudogene 21
TRIM36	-1.02626	0.000217	0.004737	-3.69782	Down	tripartite motif containing 36
RHCG	-1.02326	0.005582	0.045648	-2.77138	Down	Rh family C glycoprotein
RPL31P10	-1.02316	0.003257	0.031896	-2.94238	Down	ribosomal protein L31 pseudogene 10
CCNE2	-1.02188	2.52E-05	0.000925	-4.2126	Down	cyclin E2
DAPK2	-1.01814	0.000496	0.0087	-3.48309	Down	death associated protein kinase 2
GAS7	-1.01557	0.00162	0.019905	-3.15232	Down	growth arrest specific 7
RPL19P6	-1.0153	0.003486	0.033419	-2.92128	Down	ribosomal protein L19 pseudogene 6
HNRNPKP1	-1.01469	0.000339	0.006548	-3.5835	Down	heterogeneous nuclear ribonucleoprotein K pseudogene 1
UBA52P4	-1.01146	0.002318	0.025439	-3.04617	Down	ubiquitin A-52 residue ribosomal protein fusion product 1 pseudogene 4
BCAP31P2	-1.01109	0.00586	0.047259	-2.7555	Down	B cell receptor associated protein 31 pseudogene 2
RPS26P3	-1.00727	3.90E-05	0.001276	-4.11357	Down	ribosomal protein S26 pseudogene 3
RPS5P3	-1.00688	0.004576	0.040076	-2.83547	Down	RPS5 pseudogene 3
SKIDA1	-1.00591	0.00042	0.007711	-3.527	Down	SKI/DACH domain containing 1
CYYR1	-1.00278	9.81E-05	0.002588	-3.89521	Down	cysteine and tyrosine rich 1
PPP1R14BP2	-1.00076	4.35E-05	0.001397	-4.08814	Down	protein phosphatase 1 regulatory inhibitor subunit 14B pseudogene 2
BTF3P7	-1.00033	0.001046	0.014637	-3.27794	Down	basic transcription factor 3 pseudogene 7
CCND2	-0.99889	0.000442	0.008024	-3.51355	Down	cyclin D2
ISLR2	-0.99378	0.004124	0.037466	-2.86851	Down	immunoglobulin superfamily containing leucine rich repeat 2
BRCA2	-0.99233	7.41E-10	3.17E-07	-6.15718	Down	BRCA2 DNA repair associated
RNF112	-0.99201	0.001279	0.016791	-3.22063	Down	ring finger protein 112
GRB14	-0.98798	0.000716	0.011234	-3.38323	Down	growth factor receptor bound protein 14
RPL4P2	-0.98591	0.004445	0.039294	-2.84475	Down	ribosomal protein L4 pseudogene 2
TET1	-0.98381	0.001299	0.016968	-3.21614	Down	tetmethylcytosinedioxygenase 1
ST8SIA2	-0.98371	6.38E-07	5.41E-05	-4.97922	Down	ST8 alpha-N-acetyl-neuraminide alpha-2,8-

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						sialyltransferase 2
RPS26P28	-0.98287	0.001421	0.018197	-3.19026	Down	ribosomal protein S26 pseudogene 28
FEZF1	-0.97698	0.001459	0.018532	-3.1828	Down	FEZ family zinc finger 1
LHX2	-0.97655	0.002856	0.029294	-2.98278	Down	LIM homeobox 2
VDAC1P7	-0.97453	0.000234	0.00501	-3.67929	Down	voltage dependent anion channel 1 pseudogene 7
HMGB1P24	-0.97184	0.001884	0.022105	-3.10788	Down	high mobility group box 1 pseudogene 24
C11orf91	-0.96958	0.00498	0.042377	-2.8083	Down	chromosome 11 open reading frame 91
MAML3	-0.96673	2.45E-06	0.000157	-4.71244	Down	mastermind like transcriptional coactivator 3
FAM86MP	-0.96508	0.005149	0.043329	-2.79753	Down	family with sequence similarity 86, member A pseudogene
FBLN7	-0.96299	5.97E-06	0.000311	-4.52739	Down	fibulin 7
GRAMD1C	-0.96173	0.000222	0.00482	-3.69208	Down	GRAM domain containing 1C
RPS26P50	-0.9614	8.62E-06	0.000416	-4.44921	Down	ribosomal protein S26 pseudogene 50
DDX18P1	-0.95567	0.004906	0.041937	-2.81316	Down	DEAD-box helicase 18 pseudogene 1
RPSAP17	-0.95259	0.001623	0.019922	-3.15171	Down	ribosomal protein SA pseudogene 17
EEF1B2P1	-0.9523	0.003454	0.033195	-2.92418	Down	eukaryotic translation elongation factor 1 beta 2 pseudogene 1
ALMS1-IT1	-0.95019	0.000586	0.009706	-3.43815	Down	ALMS1 intronic transcript 1
PCDHB16	-0.94843	4.08E-06	0.000234	-4.60708	Down	protocadherin beta 16
ACTG1P14	-0.94615	9.30E-05	0.002468	-3.90806	Down	actin gamma 1 pseudogene 14
AFF2	-0.94536	0.000359	0.006875	-3.56842	Down	ALF transcription elongation factor 2
PPIAP9	-0.94513	0.00274	0.0286	-2.99548	Down	peptidylprolylisomerase A pseudogene 9
CCT5P2	-0.94505	0.000956	0.01377	-3.30306	Down	chaperonin containing TCP1 subunit 5 pseudogene 2
RPL39P36	-0.94412	0.004044	0.037009	-2.87469	Down	ribosomal protein L39 pseudogene 36
CASC15	-0.94335	0.004233	0.037951	-2.86024	Down	cancer susceptibility 15
ZBTB20	-0.9413	4.21E-05	0.001368	-4.09539	Down	zinc finger and BTB domain containing 20
TMSB10P1	-0.94023	0.003665	0.03464	-2.90562	Down	thymosin beta 10 pseudogene 1
SETBP1	-0.93865	0.001011	0.014272	-3.28744	Down	SET binding protein 1
SMAD9	-0.93459	8.46E-07	6.75E-05	-4.92445	Down	SMAD family member 9
PSMD10P2	-0.93445	0.003543	0.033831	-2.9162	Down	proteasome 26S subunit, non-ATPase, 10 pseudogene 2
OAS1	-0.93009	0.00339	0.032723	-2.92993	Down	2'-5'-oligoadenylate synthetase 1
FAM111B	-0.92941	9.48E-06	0.000448	-4.42873	Down	FAM111 trypsin like peptidase B

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TIAM2	-0.92808	0.000238	0.005054	-3.67533	Down	TIAM Rac1 associated GEF 2
RPS3AP49	-0.92744	0.002962	0.03003	-2.97166	Down	RPS3A pseudogene 49
CFL1P2	-0.9246	0.003313	0.032172	-2.93709	Down	cofilin 1 pseudogene 2
FLRT2	-0.92346	0.001645	0.020086	-3.14788	Down	fibronectinleucine rich transmembrane protein 2
HMGN3P1	-0.9219	0.00069	0.010931	-3.3936	Down	high mobility group nucleosomal binding domain 3 pseudogene 1
RPL3P12	-0.91902	0.003164	0.031356	-2.95133	Down	ribosomal protein L3 pseudogene 12
RDXP1	-0.91849	1.12E-05	0.000503	-4.39311	Down	RDX pseudogene 1
FAM86GP	-0.91827	0.00145	0.018435	-3.18444	Down	family with sequence similarity 86, member A pseudogene
PCDHGA5	-0.91764	0.001606	0.019773	-3.15474	Down	protocadherin gamma subfamily A, 5
VAX1	-0.91441	0.000822	0.012432	-3.34519	Down	ventral anterior homeobox 1
PCDHB11	-0.90952	0.002029	0.023248	-3.08595	Down	protocadherin beta 11
FZD8	-0.90949	0.000366	0.006973	-3.56356	Down	frizzled class receptor 8
NPM1P19	-0.90833	0.004608	0.040207	-2.83326	Down	nucleophosmin 1 pseudogene 19
ZNF354C	-0.90703	5.20E-08	8.24E-06	-5.44433	Down	zinc finger protein 354C
RPL3P1	-0.90682	0.006242	0.049387	-2.73482	Down	ribosomal protein L3 pseudogene 1
EFNB2	-0.90594	0.001114	0.015318	-3.2601	Down	ephrin B2
SLC22A23	-0.90346	0.000803	0.012246	-3.35166	Down	solute carrier family 22 member 23
LZTS1	-0.90267	0.000205	0.004536	-3.71254	Down	leucine zipper tumor suppressor 1
SYNE2	-0.90168	0.003264	0.031906	-2.94176	Down	spectrin repeat containing nuclear envelope protein 2
TUBB2BP1	-0.90163	0.002532	0.02711	-3.01944	Down	tubulin beta 2B class IIbpseudogene 1
ACRV1	-0.9015	0.002922	0.029777	-2.97578	Down	acrosomal vesicle protein 1
CYP7B1	-0.89773	0.000521	0.009024	-3.46965	Down	cytochrome P450 family 7 subfamily B member 1
SACS	-0.89689	4.83E-13	4.67E-10	-7.23006	Down	sacsin molecular chaperone
SHTN1	-0.89662	0.002953	0.029983	-2.97263	Down	shootin 1
DCLK1	-0.8961	6.35E-05	0.001856	-3.9993	Down	doublecortin like kinase 1
TRR-TCT1-1	-0.89042	0.001841	0.021732	-3.11472	Down	tRNA-Arg (anticodon TCT) 1-1
CD24P4	-0.88954	0.004984	0.042379	-2.80805	Down	CD24 molecule pseudogene 4
RPS20P3	-0.8878	0.004303	0.038412	-2.85509	Down	ribosomal protein S20 pseudogene 3
RBM20	-0.88217	0.003357	0.032456	-2.93297	Down	RNA binding motif protein 20
CDCA7	-0.87919	0.002447	0.026438	-3.02986	Down	cell division cycle associated 7

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RPSAP41	-0.87888	3.13E-06	0.000189	-4.66236	Down	ribosomal protein SA pseudogene 41
XKRX	-0.87871	0.001962	0.022761	-3.0959	Down	XK related X-linked
HMGB1P10	-0.87867	0.002058	0.023489	-3.08175	Down	high mobility group box 1 pseudogene 10
VDAC1P5	-0.86725	0.003938	0.036301	-2.8831	Down	voltage dependent anion channel 1 pseudogene 5
KITLG	-0.86607	0.000565	0.009495	-3.44803	Down	KIT ligand
FTLP2	-0.8651	0.000919	0.013423	-3.31423	Down	ferritin light chain pseudogene 2
LRRN3	-0.86439	0.004067	0.037172	-2.87292	Down	leucine rich repeat neuronal 3
DAZAP2P1	-0.86397	0.001969	0.022806	-3.09491	Down	DAZ associated protein 2 pseudogene 1
BRI3P1	-0.86035	0.003013	0.030324	-2.96639	Down	brain protein I3 pseudogene 1
SRGAP2B	-0.85992	2.74E-05	0.000995	-4.19383	Down	SLIT-ROBO Rho GTPase activating protein 2B
RNU6-3P	-0.85948	0.004169	0.037672	-2.86506	Down	RNA, U6 small nuclear 3, pseudogene
ZDHHC23	-0.85611	0.004755	0.04101	-2.82318	Down	zinc finger DHHC-type palmitoyltransferase 23
DYNLL1P2	-0.85562	0.002974	0.030111	-2.9704	Down	dynein light chain LC8-type 1 pseudogene 2
RPS2P35	-0.85533	0.006127	0.048801	-2.74092	Down	ribosomal protein S2 pseudogene 35
PLCE1	-0.85337	7.02E-06	0.000351	-4.4931	Down	phospholipase C epsilon 1
GLI3	-0.85198	5.70E-05	0.00171	-4.02483	Down	GLI family zinc finger 3
PWARSN	-0.85063	7.10E-05	0.002014	-3.97298	Down	PraderWilli/Angelman region RNA, SNRPN neighbor
PCDHGA8	-0.84814	7.65E-05	0.002123	-3.95501	Down	protocadherin gamma subfamily A, 8
EGFR	-0.84806	1.59E-05	0.00066	-4.31629	Down	epidermal growth factor receptor
TXNRD2	-0.84752	0.000466	0.008323	-3.49936	Down	thioredoxinreductase 2
TUFMP1	-0.84427	0.001158	0.015693	-3.24909	Down	Tu translation elongation factor, mitochondrial pseudogene 1
LIFR	-0.8442	4.29E-05	0.001385	-4.09109	Down	LIF receptor subunit alpha
SYT14	-0.84331	0.000101	0.002625	-3.88889	Down	synaptotagmin 14
ILF2P1	-0.84166	0.00275	0.028659	-2.99442	Down	interleukin enhancer binding factor 2 pseudogene 1
HAT1	-0.84068	1.47E-05	0.000624	-4.33264	Down	histone acetyltransferase 1
CEP295NL	-0.84065	0.002572	0.02739	-3.01472	Down	CEP295 N-terminal like
TRAF5	-0.84057	0.004178	0.0377	-2.8644	Down	TNF receptor associated factor 5
ME2P1	-0.8379	0.000307	0.00612	-3.60911	Down	malic enzyme 2 pseudogene 1
ITPRIPL1	-0.83313	0.001722	0.020729	-3.1344	Down	ITPRIP like 1
EFS	-0.8328	0.000516	0.008979	-3.47234	Down	embryonal Fyn-associated substrate

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LAMA1	-0.83099	0.000295	0.005919	-3.6193	Down	laminin subunit alpha 1
POM121L8P	-0.8308	0.00202	0.023175	-3.08723	Down	POM121 transmembranenucleoporin like 8, pseudogene
TSSC2	-0.82634	0.001009	0.014254	-3.28806	Down	tumor suppressing subtransferable candidate 2 (pseudogene)
RPS27AP12	-0.82517	0.001606	0.019773	-3.15477	Down	RPS27A pseudogene 12
LYPD6	-0.8245	3.40E-05	0.001156	-4.14467	Down	LY6/PLAUR domain containing 6
YWHAZP6	-0.82354	0.00287	0.02939	-2.98136	Down	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein zeta pseudogene 6
GSE1	-0.82334	0.000134	0.00326	-3.81856	Down	Gse1 coiled-coil protein
ABCA1	-0.82273	1.57E-06	0.00011	-4.80246	Down	ATP binding cassette subfamily A member 1
KIF15	-0.82141	0.00215	0.024239	-3.06868	Down	kinesin family member 15
IMMTP1	-0.82109	0.002558	0.027269	-3.01642	Down	inner membrane mitochondrial protein pseudogene 1
CDCA7L	-0.82025	0.003409	0.032836	-2.92826	Down	cell division cycle associated 7 like
RMI2	-0.819	2.52E-07	2.78E-05	-5.15601	Down	RecQ mediated genome instability 2
ZNF702P	-0.81742	0.005996	0.048081	-2.74798	Down	zinc finger protein 702, pseudogene
CDO1	-0.81226	0.002486	0.026785	-3.02506	Down	cysteine dioxygenase type 1
EIF4EP5	-0.81122	0.003188	0.031457	-2.94901	Down	eukaryotic translation initiation factor 4E pseudogene 5
ESCO2	-0.80875	1.01E-05	0.000468	-4.41608	Down	establishment of sister chromatid cohesion N-acetyltransferase 2
ICE2P1	-0.80707	0.002613	0.027667	-3.00993	Down	interactor of little elongation complex ELL subunit 2 pseudogene 1
B3GNT5	-0.80567	1.84E-08	3.78E-06	-5.62667	Down	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 5
ENC1	-0.79898	0.00018	0.004121	-3.74504	Down	ectodermal-neural cortex 1
RAB37	-0.79586	0.005542	0.045444	-2.77373	Down	RAB37, member RAS oncogene family
NFIB	-0.7958	0.000327	0.006392	-3.59284	Down	nuclear factor I B
PTBP1P	-0.793	0.000789	0.012111	-3.35665	Down	polypyrimidine tract binding protein 1 pseudogene
TOP2A	-0.79186	0.000613	0.009971	-3.42596	Down	DNA topoisomerase II alpha
ACTBP2	-0.79131	0.003054	0.030565	-2.96227	Down	ACTB pseudogene 2
ZNF367	-0.79008	0.000562	0.009462	-3.44943	Down	zinc finger protein 367
TLE1P1	-0.78986	2.10E-05	0.000802	-4.25346	Down	TLE family member 1 pseudogene 1
KIF5C	-0.78799	0.005504	0.045248	-2.77593	Down	kinesin family member 5C
PDPN	-0.78749	0.003317	0.032204	-2.93669	Down	podoplanin

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CD37	-0.78057	0.000517	0.008989	-3.47168	Down	CD37 molecule
PLXNA4	-0.77672	0.002238	0.024866	-3.05672	Down	plexin A4
RPL9P25	-0.77421	0.003218	0.031667	-2.94613	Down	ribosomal protein L9 pseudogene 25
MAPRE1P2	-0.77044	0.004077	0.037219	-2.87214	Down	MAPRE1 pseudogene 2
SCN4B	-0.76995	0.001825	0.021599	-3.11739	Down	sodium voltage-gated channel beta subunit 4
SRSF9P1	-0.76844	0.005531	0.045384	-2.77434	Down	serine and arginine rich splicing factor 9 pseudogene 1
FOXG1	-0.76504	0.00311	0.030934	-2.95665	Down	forkhead box G1
TTC9	-0.76313	0.000641	0.01035	-3.41347	Down	tetratricopeptide repeat domain 9
RPL23AP21	-0.76308	0.000977	0.013966	-3.29713	Down	ribosomal protein L23a pseudogene 21
WEE1	-0.75861	1.12E-06	8.33E-05	-4.86949	Down	WEE1 G2 checkpoint kinase
MAGOH3P	-0.75382	0.000982	0.014005	-3.29568	Down	mago homolog 3, pseudogene
FRG1JP	-0.75334	0.003588	0.034161	-2.91225	Down	FSHD region gene 1 family member J, pseudogene
WDR76	-0.7525	2.04E-05	0.000788	-4.26076	Down	WD repeat domain 76
CERS6	-0.75233	0.005797	0.046898	-2.75906	Down	ceramide synthase 6
PWAR5	-0.74954	5.07E-05	0.001559	-4.05224	Down	PraderWilli/Angelman region RNA 5
RMI1	-0.74939	0.000535	0.00918	-3.46248	Down	RecQ mediated genome instability 1
KIRREL3	-0.74659	0.002813	0.029045	-2.98748	Down	kirre like nephrin family adhesion molecule 3
ATP11A	-0.74402	8.87E-07	7.04E-05	-4.91523	Down	ATPase phospholipid transporting 11A
MAP1B	-0.73915	4.01E-06	0.000231	-4.61112	Down	microtubule associated protein 1B
EXO1	-0.73771	1.17E-08	2.72E-06	-5.70361	Down	exonuclease 1
ZNF600	-0.7369	0.000535	0.00918	-3.46247	Down	zinc finger protein 600
CBX1P1	-0.73562	0.002117	0.023989	-3.07333	Down	chromobox 1 pseudogene 1
MORF4	-0.73511	0.005899	0.047477	-2.75335	Down	mortality factor 4 (pseudogene)
FAM133CP	-0.73439	0.003152	0.031277	-2.95252	Down	family with sequence similarity 133, member A pseudogene
ATAD2	-0.73433	1.32E-05	0.000568	-4.35638	Down	ATPase family AAA domain containing 2

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						

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GO:0032501	BP	multicellular organismal process	1.73E-28	27.76302663	272	HSPA2,BCAS1,MAG,VSX2,PDE6H,RAX,CBLN2,CPLX4,DAZ4,NEUROD4,SOX10,AIPL1,CACNA1F,RBP3,MOG,RD3,NR5A2,KRT86,PPP1R16B,KRT81,GLRA3,GABRR3,RCVRN,RP1,CNGB1,UGT8,NXNL1,FA2H,CRX,EDN3,RAX2,DMRT2,CFC1B,PRDM13,NKX2-2,KRT83,FGF8,SERPINA1,EPYC,PLPPR1,HOXB9,TGM2,LRRK2,ROS1,CHRNA4,CFC1,SAMSN1,CD22,LGR6,KLRK1,CA10,GDF3,GNAT1,GPR17,TF,SIX6,GUCA1C,KLRC3,GAL3ST1,DGKK,GABRG1,HOXD3,TRDN,NEUROD1,CLRN1,NR0B1,PCDH11Y,RXFP1,PRKG2,GUCY2D,KCNH6,RELN,LCP1,HTR2C,VIT,MYL7,DYSF,MYCT1,GABRR1,OMG,HOXA4,GJA5,APELA,CFAP47,HOXA7,CRTAC1,SLC17A8,RIPPLY2,IRX1,LGR5,CSMD3,IMPG2,CATSPERB,TLL1,FEV,ADAM29,TULP1,RIT2,OPRK1,EYA1,NETO1,SGCZ,CLIC5,SUCNR1,KERA,VSX1,PRPH2,CPLX3,TFAP2B,HMX3,ASCL2,HOXA6,SHISA7,HOXA5,RNF125,ACSL6,IRX6,RHOH,DSCAM,C6,MSR1,REN,TDRD9,NEU4,VEGFC,OLIG2,KRT7,C14ORF39,CNTN1,DACH2,SLC1A1,TLR2,ADGRG2,PCSK2,FGF12,PRSS56,SEMA3D,GPRIN3,WT1,MOBP,SYK,RAC2,ITGA11,SLC8A3,SULF1,BMP8B,OLFM3,GDF6,EPHA8,MYRF,NR1H4,CNTN6,SLC24A2,KCND2,PCDH15,ECSCR,NKX6-1,GPRIN2,GFI1B,HOXA3,MNX1,SKOR2,HPGD,ASIC4,HOXA13,PDE6A,PHF24,ARHGEF5,LIMS2,FGF14,HOXA2,SLC22A3,ESRP1,INSC,BARHL1,DAPL1,HSPB7,LHX9,CADM2,PRKCH,FREM1,TNR,CSRP3,HMX2,LHFPL3,TWIST2,KLRD1,WNT16,HOXD4,GRID2,TBX3,TSPAN8,KISS1,SLC24A4,ADGRB1,KRT8,SOX14,OLIG1,SERPINI1,TMEM176B,MYL9,GABRA3,ST8SIA6,PTPRB,PTPRO,EVI2B,LHX5,CLDN11,AATK,SLC1A7,MAB21L1,PTGER3,PRDM12,IL7R,MBP,OPCML,XAF1,MYO7B,CUX2,PLLP,UNC5A,EXTL1,GPR37,PAPPA2,ACAN,SHH,MEOX1,HOXD1,PDC,HOXD9,P2RX5,PROK1,AGTR1,TIE1,FZD10,LGI4,EN1,XDH,P2RX7,PDE6G,MDGA2,NTSR1,VTN,SIRT2,ITGB6,RBP4,LPAR5,BARX1,ISM1,STMND1,IL2RG,HOXB6,OTOS,BMP2,AFAP1L2,TACR3,KRT5,COL10A1,EPAS1,CACNA2D4,SPINK1,SLITRK2,ERBB3,HAS2,ERMN,TMEM215,PPP4R4,C

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						DH13,CSMD1,DOCK10,NTF3,GRHL2
GO:0065007	BP	biological regulation	2.90E-11	10.53701183	327	HSPA2,MAG,VSX2,GNGT2,CABP5,PDE6H,RAX,CBLN2,CPLX4,DAZ4,NEUROD4,SOX10,AIPL1,CACNA1F,XIST,MOG,CCL3L3,RD3,MEG3,NR5A2,PPP1R16B,NPY4R,GLRA3,GABRR3,CALCB,RCVRN,RP1,CNGB1,FA2H,CRX,EDN3,KCTD8,ANO3,KLRC4,RAX2,DMRT2,SAMD7,PRDM13,NKX2-2,WFDC8,KCNV2,FGF8,SERPINA1,PLPPR1,HMX1,HOXB9,TGM2,CDC20B,LRRK2,WIF1,ROS1,CHRNA4,CFC1,SAMSN1,CD22,LGR6,KLRK1,GDF3,GNAT1,SV2B,GPR17,TF,SIX6,GUCA1C,KLRC3,DGKK,SULT1B1,GABRG1,HOXD3,TRDN,SAG,LAMC2,NEUROD1,CLRN1,NR0B1,TRPC6,PCDH11Y,RXFP1,PRKG2,GUCY2D,KCNH6,RELN,LCP1,HTR2C,ZNF648,VIT,DYSF,CMTM5,GABRR1,ADAMTS20,HOXA4,GJA5,APELA,GPR45,HOXA7,LGI3,CTTNBP2,SLC17A8,RIPPLY2,IRX1,SLPI,LGR5,MYO1G,CSMD3,FEV,TULP1,RIT2,FRMPD4,OPRK1,MATK,EYA1,NETO1,DBX2,SYT6,CLIC5,GRIA4,RASSF6,SUCNR1,GPR20,VSX1,CYP2S1,CPLX3,TFAP2B,ARFGEF3,HMX3,ASCL2,CYP2C8,HOXA6,SHISA7,HOXA5,RNF125,IRX6,RHOH,DSCAM,C6,MSR1,REN,CCL25,TDRD9,SLCO4A1,NEU4,VEGFC,OLIG2,ODAM,AANAT,C14ORF39,CNTN1,SLC1A1,TLR2,ADGRG2,C7,PCSK2,FGF12,PRSS56,SEMA3D,WT1,SYK,RAPGEF4,PLEKHH2,RAC2,ITGA11,SLC8A3,SULF1,KCNG4,BMP8B,OLFM3,HOXA1,GDF6,EPHA8,MYRF,LRRC26,NR1H4,CNTN6,SLC24A2,KCND2,ECSCR,NKX6-1,CERKL,GFI1B,HOXA3,MNX1,SKOR2,HPGD,HOXA13,PDE6A,PHF24,ARHGEF5,GRIA2,LIMS2,KCNS3,FGF14,C8G,HOXA2,VWA2,SLC22A3,ESRP1,EGFLAM,INSC,SPTBN5,BARHL1,DAPL1,HSPB7,LHX9,MMP3,PRKCH,TNR,TRIM43B,SYT15,CSRP3,HMX2,TLX1,TWIST2,KLRD1,MYRFL,WNT16,HOXD4,DPP6,GRID2,TBX3,TSPAN8,SNCB,REPS2,KISS1,MCTP2,SLC24A4,DIRAS3,ADGRB1,PEX5L,KRT8,SOX14,SYT9,TRIM29,OLIG1,SERPINI1,TMEM176B,MYL9,GABRA3,PTPRB,PTPRO,EVI2B,LHX5,CASP4,ZNF385B,SLC1A7,MAB21L1,QRFPR,PTGER3,PRDM12,XKR4,IL7R,MBP,XAF1,UBE2E2,CUX2,PTPRT,UNC5

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						A,WFDC1,GPR37,PAPPA2,ACAN,SHH,MEOX1,HOXD1,PDC,HOXD9,SPOCK3,P2RX5,RNF43,PROK1,AGTR1,TIE1,FZD10,RCAN2,LGI4,CCDC80,EN1,RASGEF1B,XDH,RERG,SUSD4,P2RX7,PDE6G,LAMP3,PSCA,NTSR1,VTN,SIRT2,ATP6V0D2,ITGB6,RBP4,LPAR5,SPON1,BARX1,STK32B,ISM1,STMND1,POU2F3,SLC1A6,IL2RG,HOXB6,BMP2,NR3C2,AFAP1L2,TACR3,HTR1F,KRT5,EPAS1,CDK18,TYRP1,CACNA2D4,SPINK1,SLITRK2,HSPB8,ERBB3,PNPLA4,INHBE,AOAH,HAS2,ERMN,TMEM215,SYT13,PPP4R4,CDH13,ITIH3,DOCK10,NTF3,GRHL2
GO:0043005	CC	neuron projection	6.03E-13	12.2194139	71	MAG,PDE6H,CPLX4,CACNA1F,RD3,NPY4R,GLRA3,RCVRN,RP1,CNGB1,NXNL1,PLPPR1,LRRK2,CHRNA4,GNAT1,GUCA1C,GABRG1,SAG,CLRN1,GUCY2D,RELN,HTR2C,MYL7,LGI3,CTTNBP2,SLC17A8,TULP1,RIT2,FRMPD4,OPRK1,NETO1,GRIA4,PRPH2,CPLX3,SHISA7,DSCAM,NEU4,CNTN1,SLC1A1,PCSK2,SLC8A3,EPHA8,CNTN6,KCND2,PCDH15,CERKL,PDE6A,GRIA2,SPTBN5,CADM2,GRID2,SNCB,KISS1,SLC24A4,ADGRB1,GABRA3,PTPRO,CLDN11,MBP,UNC5A,PDC,PDE6G,NTSR1,SIRT2,NEFM,STMND1,TACR3,HTR1F,ERMN,CDH13,DOCK10
GO:0016020	CC	membrane	4.89E-09	8.310495669	261	HSPA2,MAG,GNGT2,PDE6H,CPLX4,SOX10,CACNA1F,MOG,LACTBL1,ENPP6,PPP1R16B,NPY4R,GLRA3,GABRR3,RCVRN,CNGB1,UGT8,PCDH11X,FA2H,KCTD8,ANO3,KLRC4,TMEM235,VSTM2B,DMRT2,LRIT1,FAM163A,FREM3,KCNV2,FGF8,SERPINA1,GALNT9,PLPPR1,TGM2,LRRK2,ROS1,CHRNA4,TMEM125,CFC1,CD22,EVI2A,LGR6,KLRK1,GALNT13,GNAT1,SV2B,GPR17,TF,GUCA1C,KLRC3,GAL3ST1,DGKK,GABRG1,TRDN,SAG,DSC1,CLRN1,NR0B1,TRPC6,PCDH11Y,SLC38A4,RXFP1,PRKG2,GUCY2D,KCNH6,RELN,LCP1,HTR2C,DYSF,CMTM5,MYCT1,GABRR1,OMG,GJA5,APELA,CFAP47,GPR45,HOXA7,SLC17A8,LGR5,MYO1G,CSMD3,IMPG2,CATSPERB,TLL1,ADAM29,TULP1,RIT2,OPRK1,MATK,NETO1,SGCZ,SYT6,CLIC5,GRIA4,SUCNR1,GPR20,PRPH2,CYP2S1,CPLX3,ARFGEF3,CYP2C8,SHISA7,RNF125,ACSL6,COL25A1,RHOH,DSCAM,C6,MSR1,REN,SLCO4A

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						1,NEU4,VEGFC,SLC16A3,CNTN1,SLC1A1,TLR2,ADGRG2,C7,PCSK2,SEMA3D,CDH22,GPRIN3,SYK,RAPGEF4,PLEKHH2,RAC2,ITGA11,SLC8A3,SULF1,KCNG4,OLFM3,EPHA8,MYRF,LRRC26,CNTN6,SLC24A2,KCND2,SLC30A2,PCDH15,ECSCR,GPRIN2,GFI1B,HPGD,ASIC4,PDE6A,ARHGEF5,GRIA2,LIMS2,KCNS3,C8G,SLC22A3,INSC,SPTBN5,SIGLEC1,DAPL1,AGMO,CADM2,SNX22,PRKCH,FREM1,TNR,SYT15,TSPAN19,LHFPL3,KLRD1,TMEM151A,MYRFL,DPP6,GRID2,TSPAN8,REPS2,PRIMA1,KISS1,MCTP2,SLC24A4,DIRAS3,ADGRB1,PEX5L,UGT3A2,KRT8,CNTN3,SYT9,TMEM176B,GABRA3,ST8SIA6,PTPRB,PTPRO,ATP13A5,EVI2B,CLDN11,CASP4,CNTNAP5,CTSW,SMLR1,AATK,SLC1A7,QRFPR,PTGER3,XKR4,IL7R,MBP,OPCML,SLCO2A1,PLLP,PTPRT,SUSD3,UNC5A,SLC7A14,EXTL1,GPR37,PAPPA2,SHH,P2RX5,RNF43,AGTR1,TIE1,FZD10,CCDC80,KIZ,RASGEF1B,RERG,SUSD4,P2RX7,PDE6G,PRRG4,MDGA2,LAMP3,PSCA,NTSR1,ZPLD1,VTN,SIRT2,ATP6V0D2,ITGB6,LPAR5,NRK,CLDN16,POU2F3,SLC1A6,IL2RG,BMP2,NR3C2,AFAP1L2,TACR3,HTR1F,KRT5,TYRP1,CACNA2D4,SLITRK2,ERBB3,PNPLA4,HAS2,TMEM215,SLCO6A1,SYT13,CDH13,CSMD1,DOCK10,GRHL2
GO:0003700	MF	DNA-binding transcription factor activity	1.50E-07	6.823757099	61	VSX2,RAX,NEUROD4,SOX10,NR5A2,CRX,RAX2,DMRT2,NKX2-2,HMX1,HOXB9,SIX6,HOXD3,NEUROD1,ZNF648,HOXA4,HOXA7,IRX1,FEV,DBX2,VSX1,TFAP2B,HMX3,ASCL2,HOXA6,HOXA5,IRX6,OLIG2,WT1,HOXA1,MYRF,NR1H4,NKX6-1,GFI1B,HOXA3,MNX1,SKOR2,HOXA13,HOXA2,BARHL1,LHX9,HMX2,TLX1,TWIST2,MYRFL,HOXD4,TBX3,SOX14,OLIG1,LHX5,CUX2,MEOX1,HOXD1,HOXD9,EN1,BARX1,POU2F3,HOXB6,NR3C2,EPAS1,GRHL2
GO:0060089	MF	molecular transducer activity	0.001264797	2.897979073	54	NR5A2,NPY4R,GLRA3,GABRR3,ROS1,CHRNA4,EVI2A,LGR6,KLRK1,GPR17,KLRC3,GABRG1,RXFP1,GUCY2D,HTR2C,GABRR1,GPR45,LGR5,OPRK1,GRIA4,SUCNR1,GPR20,TLR2,ADGRG2,ITGA11,EPHA8,NR1H4,HPGD,GRIA2,DAPL1,KLRD1,GRID2,ADGRB1,GABRA3,PTPRB,PTPRO,QRFPR,PTGER3,IL7R,

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						PTPRT,UNC5A,GPR37,P2RX5,AGTR1,TIE1,FZD10,P2RX7,NTSR1,LPAR5,IL2RG,NR3C2,TACR3,HTR1F,ERBB3
Down regulated genes						
GO:0032501	BP	multicellular organismal process	6.70E-07	6.173808043	113	ERAP2,OR2L13,HLA-DQB2,PCDHGA3,PCDHB8,HLA-DRB5,FGF19,OAS3,DMRTA2,TBX18,HLA-DMB,ZAR1,CYP4F11,TAS2R46,EMX1,GABRB2,HLA-DRB1,HLA-DOA,NKX2-3,ROPN1,PLEK,CARD16,DHRS3,CD74,FGF3,HLA-DRA,PRPS1L1,VWF,MTTP,GCM1,SLC26A7,ZNF572,PCDHA11,EPHA5,HLA-DMA,MDGA1,ROPN1B,CASQ1,BCL6B,ANGPT2,CHRDL1,KCNJ2,EMX2,OAS2,MICB,LRRC19,TTPA,AKR1C3,NEDD4L,CASP1,HES2,POU3F2,BEGAIN,LDB2,PCDHGB3,PCDHA7,FAM107A,NR2E1,CHRNA5,DRAXIN,PDE2A,GAS7,CCND2,ISLR2,BRCA2,RNF112,TET1,ST8SIA2,FEZF1,LHX2,PCDHB16,AFF2,ZBTB20,OAS1,TIAM2,FLRT2,PCDHGA5,VAX1,PCDHB11,FZD8,EFNB2,LZTS1,SYNE2,ACRV1,CYP7B1,SHTN1,DCLK1,RBM20,KITLG,LRRN3,SRGAP2B,PLCE1,GLI3,PCDHGA8,EGFR,LAMA1,ABCA1,B3GNT5,ENC1,NFIB,TOP2A,KIF5C,PDPN,PLXNA4,SCN4B,FOXG1,TTC9,WEE1,RMI1,KIRREL3,ATP11A,MAP1B,EXO1
GO:0032502	BP	developmental process	1.39113E-05	4.856631963	96	HLA-DQB2,PCDHGA3,PCDHB8,FGF19,DMRTA2,TBX18,ZAR1,EMX1,GABRB2,HLA-DRB1,HLA-DOA,NKX2-3,ROPN1,PLEK,DHRS3,CD74,FGF3,HLA-DRA,PRPS1L1,GCM1,PCDHA11,EPHA5,MDGA1,ROPN1B,CASQ1,ANGPT2,CHRDL1,EMX2,FOXD2,OAS2,COMT,TTPA,AKR1C3,NEDD4L,SLC4A11,HES2,GAS1,POU3F2,LDB2,PCDHGB3,PCDHA7,NR2E1,DRAXIN,PDE2A,RHCG,GAS7,ISLR2,BRCA2,RNF112,TET1,ST8SIA2,FEZF1,LHX2,PCDHB16,AFF2,SMAD9,TIAM2,FLRT2,PCDHGA5,VAX1,PCDHB11,FZD8,EFNB2,LZTS1,SYNE2,ACRV1,CYP7B1,SHTN1,DCLK1,RBM20,KITLG,LRRN3,SRGAP2B,PLCE1,GLI3,PCDHGA8,EGFR,LAMA1,ABCA1,CDO1,ESCO2,B3GNT

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						5,ENC1,NFIB,TOP2A,KIF5C,PDPN,PLXNA4,FOXG1,TTC9,WEE1,RMI1,KIRREL3,ATP11A,MAP1B,EXO1
GO:0071944	CC	cell periphery	0.000228619	3.640886922	88	OR2L13,HLA-DQB2,PCDHGA3,SLCO1B1,PCDHB8,HLA-DRB5,OAS3,HLA-DMB,TAS2R46,GABRB2,HLA-DRB1,CRHR2,HLA-DOA,PLEK,TEX101,DHRS3,CD74,HLA-DRA,ANK1,VWF,SLCO5A1,MTTP,SLC26A7,ATP10B,PCDHA11,EPHA5,HLA-DMA,MDGA1,CASQ1,ANGPT2,GRM3,CHRDL1,KCNJ2,MICB,LRRC19,RND3,COMT,SLC10A4,NEDD4L,CASP1,SLC4A11,GAS1,LDB2,PCDHGB3,GPR39,PCDHA7,FAM107A,IPCEF1,CHRNA5,PDE2A,TRIM36,RHCG,GAS7,ISLR2,GRB14,FBLN7,GRAMD1C,PCDHB16,FLRT2,PCDHGA5,PCDHB11,FZD8,EFNB2,SLC22A23,LZTS1,SYNE2,DCLK1,XKRX,KITLG,LRRN3,PLCE1,PCDHGA8,EGFR,LIFR,TRAF5,EFS,LAMA1,LYPD6,ABCA1,RAB37,PDPN,CD37,PLXNA4,SCN4B,KIRREL3,ATP11A,MAP1B,EXO1
GO:0110165	CC	cellular anatomical entity	0.052838233	1.277051714	204	ZNF208,ZNF257,PEG3,ZNF492,ZIM2,ZNF560,ZNF676,ERAP2,OR2L13,HLA-DQB2,PCDHGA3,SLCO1B1,PCDHB8,HLA-DRB5,ZNF98,FGF19,OAS3,HS3ST4,RNU6-181P,DMRTA2,BEX5,SNORA54,TBX18,HLA-DMB,ZAR1,CYP4F11,TAS2R46,EMX1,GABRB2,ANKRD29,HLA-DRB1,CRHR2,HLA-DOA,NKX2-3,ROPN1,PLEK,TEX101,CARD16,HDC,DHRS3,ZNF835,CD74,FGF3,HLA-DRA,TCEAL2,SCARNA7,CALB2,ZNF718,PRPS1L1,SLFN11,PRSS33,ANK1,VWF,SLFN13,CIITA,SLCO5A1,MTTP,GCM1,SLC26A7,ATP10B,ZNF454,ZNF572,PCDHA11,EPHA5,HLA-DMA,PPIAL4A,MDGA1,ROPN1B,CASQ1,BCL6B,ANGPT2,GRM3,CHRDL1,ZNF441,KCNJ2,EMX2,ZNF439,FOXD2,GLB1L3,OAS2,MICB,LEMD1,HNRNPCL2,LRRC19,RND3,MGAT4C,SCARNA10,COMT,TTPA,GSTT2B,AKR1C3,SLC10A4,NEDD4L,CASP1,SLC4A11,HES2,SNHG5,GAS1,POU3F2,BEGAIN,LDB2,PCDHGB3,GPR39,PCDHA7,FAM107

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						A,NR2E1,SLC25A18,PTMAP7,IPCEF1,CHRNA5,DRAXIN,TVP23A,PDE2A,TRIM36,RHCG,CCNE2,DAPK2,GAS7,CYYR1,CCND2,ISLR2,BRCA2,RNF112,GRB14,TET1,ST8SIA2,FEZF1,LHX2,MAML3,FBLN7,GRAMD1C,PCDHB16,AFF2,ZBTB20,SETBP1,SMAD9,OAS1,FAM111B,TIAM2,FLRT2,PCDHGA5,VAX1,PCDHB11,FZD8,ZNF354C,EFNB2,SLC22A23,LZTS1,SYNE2,ACRV1,CYP7B1,SACS,SHTN1,DCLK1,RBM20,CDCA7,XKRX,KITLG,LRRN3,RNU6-3P,ZDHHC23,PLCE1,GLI3,PCDHGA8,EGFR,TXNRD2,LIFR,SYT14,HAT1,CEP295NL,TRAF5,ITPRIPL1,EFS,LAMA1,LYPD6,ABCA1,KIF15,CDCA7L,RMI2,CDO1,ESCO2,B3GNT5,ENC1,RAB37,NFIB,TOP2A,ZNF367,KIF5C,PDPN,CD37,PLXNA4,SCN4B,FOXG1,WEE1,WDR76,CERS6,PWAR5,RMI1,KIRREL3,ATP11A,MAP1B,EXO1,ZNF600,ATAD2
GO:0043167	MF	ion binding	0.007259471	2.139095026	86	ZNF208,ZNF728,ZNF257,PEG3,ZNF492,ZIM2,ZNF560,ZNF676,ERAP2,PCDHGA3,PCDHB8,ZNF98,OAS3,DMRTA2,ZAR1,CYP4F11,PLEK,HDC,ZNF835,CALB2,ZNF718,PRPS1L1,SLFN11,SLFN13,CIITA,GCM1,ATP10B,ZNF454,ZNF572,PCDHA11,EPHA5,CASQ1,BCL6B,ANGPT2,ZNF441,KCNJ2,ZNF439,OAS2,RND3,MGAT4C,COMT,TTPA,AKR1C3,PCDHGB3,GPR39,PCDHA7,NR2E1,PTMAP7,PDE2A,TRIM36,DAPK2,RNF112,TET1,ST8SIA2,FEZF1,LHX2,FBLN7,PCDHB16,ZBTB20,SMAD9,OAS1,PCDHGA5,PCDHB11,ZNF354C,CYP7B1,DCLK1,RBM20,PLCE1,GLI3,PCDHGA8,EGFR,TXNRD2,TRAF5,ABCA1,KIF15,CDO1,ESCO2,RAB37,TOP2A,ZNF367,KIF5C,WEE1,ATP11A,EXO1,ZNF600,ATAD2
GO:0005515	MF	protein binding	0.197688552	0.704018481	162	ZIM2,OR2L13,HLA-DQB2,SLCO1B1,PCDHB8,FGF19,OAS3,DMRTA2,BEX5,TBX18,HLA-DMB,ZAR1,CYP4F11,EMX1,ANKRD29,HLA-DRB1,CRHR2,HLA-DOA,ROPN1,PLEK,TEX101,CARD16,HDC,ZNF835,CD74,FGF3,HLA-DRA,PRPS1L1,SLFN11,ANK1,VWF,CIITA,SLCO5A1,MTTP,GCM1,ATP10B,ZNF572,EPHA5,HLA-DMA,MDGA1,ROPN1B,CASQ1,BCL6B,ANGPT2,GRM3,CHRDL1,ZNF441,KCNJ2,EMX2,ZNF439,FOXD2,OAS2,MICB,LEMD1,HNRNPCL2,F

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					CGBP,LRRC19,RND3,COMT,TTPA,SLC10A4,NEDD4L,CASP1,SLC4A11,HES2,GAS1,POU3F2,BEGAIN,LDB2,GPR39,KIAA0408,PCDHA7,FAM107A,NR2E1,SLC25A18,PTMAP7,IPCEF1,CHRNA5,DRAXIN,TVP23A,PDE2A,TRIM36,RHCG,CCNE2,DAPK2,GAS7,CCND2,ISLR2,BRCA2,RNF112,GRB14,TET1,FEZF1,LHX2,MAML3,FBLN7,GRAMD1C,AFF2,ZBTB20,SETBP1,SMAD9,OAS1,FAM111B,TIAM2,FLRT2,VAX1,FZD8,EFNB2,SLC22A23,LZTS1,SYNE2,ACRV1,SACS,SHTN1,DCLK1,RBM20,CDCA7,KITLG,LRRN3,SRGAP2B,ZDHHC23,PLCE1,GLI3,EGFR,TXNRD2,LIFR,SYT14,HAT1,CEP295NL,TRAF5,ITPRIPL1,EFS,LAMA1,LYPD6,GSE1,ABCA1,KIF15,CDCA7L,RMI2,ESCO2,B3GNT5,ENC1,RAB37,NFIB,TOP2A,KIF5C,PDPN,CD37,PLXNA4,SCN4B,FOXG1,TTC9,WEE1,WDR76,CERS6,RMI1,KIRREL3,ATP11A,MAP1B,EXO1,ZNF600,ATAD2

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-372790	Signaling by GPCR	0.001831322	2.737235241	33	GNGT2,CCL3L3,NPY4R,CALCB,EDN3,PLPPR1,GNAT1,GPR17,DGKK,TRPC6,RXFP1,HTR2C,GPR45,OPRK1,SUCNR1,GPR20,CCL25,ARHGEF5,MMP3,PRKCH,WNT16,KISS1,QRFPR,PTGER3,GPR37,SHH,PROK1,AGTR1,FZD10,NTSR1,LPAR5,TACR3,HTR1F
REAC:R-HSA-373076	Class A/1 (Rhodopsin-like receptors)	0.002350507	2.628838538	20	CCL3L3,NPY4R,EDN3,PLPPR1,GPR17,RXFP1,HTR2C,OPRK1,SUCNR1,CCL25,KISS1,QRFPR,PTGER3,GPR37,PROK1,AGTR1,NTSR1,LPAR5,TACR3,HTR1F
REAC:R-HSA-2187338	Visual phototransduction	0.003426961	2.465090857	10	RBP3,RCVRN,CNGB1,GNAT1,GUCA1C,SAG,GUCY2D,PDE6A,PDE6G,RBP4

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REAC:R-HSA-416476	G alpha (q) signalling events	0.003789587	2.421408108	15	GNGT2,EDN3,GPR17,DGKK,TRPC6,HTR2C,MMP3,PRKCH,KISS1,QRFPR,PROK1,AGTR1,NTSR1,LPAR5,TACR3
REAC:R-HSA-1474244	Extracellular matrix organization	0.077160068	1.112607397	19	LAMC2,TLL1,COL25A1,COL20A1,ITGA11,MMP3,TNR,MATN4,ACAN,SPOCK3,VTN,ITGB6,MMP10,BMP2,COL10A1
REAC:R-HSA-112316	Neuronal System	0.081031341	1.091346975	17	GNGT2,GLRA3,GABRR3,KCNV2,CHRNA4,KCNH6,GABRR1,GRIA4,SLC1A1,KCNG4,KCND2,GRIA2,KCNS3,SYT9,GABRA3,SLC1A7,SLC1A6,SLITRK2
		Down regulated genes			
REAC:R-HSA-2132295	MHC class II antigen presentation	0.001728425	2.762349402	9	HLA-DQB2,HLA-DRB5,HLA-DMB,HLA-DRB1,HLA-DOA,CD74,HLA-DRA,HLA-DMA,KIF15
REAC:R-HSA-9709603	Impaired BRCA2 binding to PALB2	0.006498292	2.187200791	4	BRCA2,RMI2,RMI1,EXO1
REAC:R-HSA-212436	Generic Transcription Pathway	0.008691777	2.060891443	27	ZNF208,ZNF257,ZNF492,ZIM2,ZNF560,ZNF676,ZNF718,ZNF454,ZNF441,ZNF439,NEDD4L,CASP1,NR2E1,CCNE2,CCND2,MAML3,ZNF354C,GLI3,EGFR,LIFR,RMI2,PLXNA4,FOXG1,RMI1,EXO1,ZNF600,ATAD2
REAC:R-HSA-373760	L1CAM interactions	0.166427153	0.778775816	5	ANK1,SHTN1,EGFR,LAMA1,SCN4B
REAC:R-HSA-9675108	Nervous system development	0.319870221	0.49502619	11	ANK1,EPHA5,POU3F2,ST8SIA2,LHX2,EFNB2,SHTN1,EGFR,LAMA1,PLXNA4,SCN4B
REAC:R-HSA-422475	Axon guidance	0.388986872	0.410065056	10	ANK1,EPHA5,ST8SIA2,LHX2,EFNB2,SHTN1,EGFR,LAMA1,PLXNA4,SCN4B

Table 4 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	LRRK2	2065	0.426799	1.66E+09	0.422513
Up	MTUS2	365	0.06286	1.09E+08	0.340427
Up	HOXA1	343	0.06019	90465692	0.334569
Up	IL7R	213	0.020119	75029162	0.332777
Up	ERBB3	183	0.023007	54478670	0.328182
Up	HSPA2	169	0.025264	26982364	0.347894
Up	VTN	156	0.019301	39349834	0.325925
Up	NGB	153	0.012904	43209872	0.322022
Up	PTPRO	145	0.016135	58789496	0.320145

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Up	TRIM29	142	0.021423	24787840	0.353688
Up	KRT8	133	0.018241	11960092	0.358707
Up	EPAS1	133	0.016997	46030946	0.318491
Up	CMTM5	132	0.022505	39425454	0.312776
Up	TGM2	128	0.013739	35874980	0.327163
Up	HTR2C	119	0.01463	29801140	0.309318
Up	PTGER3	114	0.011755	57432426	0.307661
Up	CRX	110	0.01555	18754254	0.312428
Up	MEOX1	108	0.012928	37326000	0.312338
Up	CDK18	105	0.010248	16129628	0.321981
Up	KRT5	105	0.011726	9195808	0.364677
Up	TF	103	0.013902	14371596	0.32831
Up	CPLX4	103	0.014304	14250944	0.304804
Up	FGF8	97	0.011874	97100750	0.28144
Up	HOXB9	93	0.011465	10148944	0.321598
Up	WT1	91	0.011359	19156616	0.316325
Up	AGTR1	85	0.012534	15145724	0.309331
Up	GPR37	84	0.014145	10021384	0.322556
Up	MBP	79	0.01132	16084668	0.311875
Up	ASIC4	76	0.008961	9938418	0.314619
Up	SLC30A2	74	0.009651	10382838	0.293069
Up	SIRT2	72	0.009054	20736428	0.297824
Up	GFI1B	72	0.007502	11487200	0.306393
Up	LAMP3	68	0.008781	35460672	0.290699
Up	UBE2E2	66	0.007302	13886568	0.311811
Up	SERPINA1	65	0.006167	9468458	0.316167
Up	ESRP1	65	0.005712	14800834	0.303997
Up	ZNF648	63	0.004614	4651986	0.3086
Up	FZD10	59	0.003954	15834278	0.300909
Up	PPP1R16B	57	0.005241	5398454	0.310636
Up	SYK	57	0.007225	16655064	0.304951
Up	TBX3	56	0.00413	14613826	0.305874
Up	TLR2	55	0.005254	16860320	0.302192
Up	NEFM	55	0.006068	3423344	0.347958
Up	PLLP	55	0.007718	5344234	0.309608
Up	AATK	53	0.003429	15757914	0.2843
Up	DSC1	52	0.004746	2873620	0.343715
Up	DYSF	50	0.005008	14657052	0.290309
Up	KRT86	49	0.003429	2609968	0.326824
Up	SUSD3	48	0.006422	4316214	0.303341
Up	SUSD4	48	0.008078	10969566	0.284706
Up	SLC7A14	48	0.005637	6810888	0.284407
Up	PSCA	47	0.006493	3552014	0.296079
Up	KRT83	47	0.002095	3314108	0.302421
Up	SLC1A1	46	0.005841	13038218	0.295698
Up	HSPB8	46	0.005079	5379610	0.302506
Up	CASP4	45	0.002466	11353644	0.295618
Up	ARHGEF5	45	0.004101	8318728	0.303584
Up	VSX2	43	0.00244	6654422	0.295433
Up	ENPP6	43	0.004374	5113176	0.286373
Up	LCP1	42	0.00289	2854402	0.313993
Up	MYL9	42	0.004022	2855656	0.340015
Up	SOX14	41	0.004124	2656140	0.29979
Up	TFAP2B	41	0.004867	4451476	0.277994
Up	NR1H4	41	0.003648	8425316	0.286925
Up	TRDN	40	0.006069	11065016	0.277597
Up	CYP2S1	38	0.004398	3731738	0.295215
Up	GJA5	37	0.004125	7560344	0.282995
Up	C3orf36	37	0.002128	4720970	0.302276
Up	SLC16A3	36	0.001685	3915838	0.303389
Up	SYT6	36	0.002686	3331366	0.313721
Up	CABP5	36	0.003956	5242638	0.278514
Up	EYA1	35	0.002166	2112516	0.302977
Up	PTPRB	35	0.002625	7010946	0.288311
Up	SPATA8	35	0.00241	3332832	0.309154
Up	DCAF4L2	35	8.52E-04	4279592	0.288037
Up	FA2H	34	0.003026	3355016	0.291056
Up	KRT81	34	0.001747	1923380	0.302252
Up	NR5A2	33	0.003652	6166520	0.275779
Up	KRT7	33	0.001665	1197220	0.32363

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Up	KCNS3	33	0.003481	9504920	0.265932
Up	ARFGEF3	32	0.004171	2050248	0.325589
Up	HOXA5	32	0.00247	4046166	0.293591
Up	UGT8	32	0.003862	3533390	0.296461
Up	SOX10	31	0.004156	1656926	0.292234
Up	IRX6	31	0.003345	1464890	0.293501
Up	EVI2B	31	0.002524	3460890	0.276423
Up	CDH13	31	0.002	4957748	0.281597
Up	CDC20B	31	0.001979	2166354	0.30224
Up	ATP6V0D2	30	0.004071	3208344	0.293364
Up	CNTN1	29	0.003654	2112402	0.29667
Up	FGF12	29	0.00386	1926182	0.296786
Up	RHOH	29	0.00238	6242168	0.277973
Up	CLRN1	28	0.002396	3413464	0.255432
Up	CA10	28	0.00436	17264728	0.256904
Up	GPRIN2	27	9.68E-04	2184966	0.279665
Up	MMP3	27	0.002532	3822392	0.283715
Up	PLPPR1	27	0.002285	4395962	0.284364
Up	SLPI	26	0.00258	1283190	0.300313
Up	NR3C2	26	0.001498	4998810	0.281618
Up	CCDC26	26	0.001625	3763782	0.283492
Up	FAM163A	26	0.001089	2370890	0.292753
Up	LHX5	26	7.34E-04	2060336	0.292515
Up	RNF125	25	0.002267	1110168	0.309419
Up	OLIG1	25	0.002501	3508262	0.264596
Up	P2RX7	25	0.001931	4053530	0.283864
Up	RAC2	24	0.001489	4373470	0.286059
Up	XAF1	24	0.002099	4502046	0.288618
Up	NEU4	24	0.001351	2793438	0.2883
Up	P2RX5	24	0.003567	10115080	0.262226
Up	KIZ	23	0.001933	3342692	0.290977
Up	RNF43	23	6.44E-04	1129246	0.28166
Up	HSPB7	23	0.001154	2641912	0.288574
Up	AIPL1	23	0.002407	8383106	0.276604
Up	HOXD4	22	0.002892	5829962	0.268779
Up	HOXB6	22	0.001197	2012182	0.289445
Up	IL2RG	22	0.001368	923550	0.278004
Up	RIPPLY2	22	0.001543	1814730	0.287807
Up	REPS2	22	0.001234	3623584	0.280836
Up	DIRAS3	21	0.002698	2225682	0.290643
Up	PRKCH	21	0.001176	2293112	0.281211
Up	LIMS2	3	8.93E-04	2890752	0.316101
Up	CHRNA4	2	9.30E-05	57660	0.232541
Up	GPR17	1	0	0	0.243896
Up	PDC	1	0	0	0.238061
Up	GABRA3	1	0	0	0.274432
Up	RASGEF1B	1	0	0	0.274432
Up	DOCK10	1	0	0	0.274432
Up	KCTD8	1	0	0	0.274432
Up	TYRP1	1	0	0	0.247172
Up	ITGB6	1	0	0	0.245818
Up	PEX5L	1	0	0	0.264016
Up	SPOCK3	1	0	0	0.221017
Up	ACAN	1	0	0	0.221017
Up	CSF2RA	1	0	0	0.238969
Up	PRRG4	1	0	0	0.247099
Up	PDE6H	1	0	0	0.236258
Up	FGF14	1	0	0	0.228608
Up	VWA2	1	0	0	0.258111
Up	NEUROD1	1	0	0	0.258111
Up	TTC29	1	0	0	0.243567
Up	CPLX3	1	0	0	0.261286
Up	RAPGEF4	1	0	0	0.29703
Up	ADGRB1	1	0	0	0.243896
Up	RBP3	1	0	0	0.250703
Up	MMP10	1	0	0	0.263273
Up	HOXA3	1	0	0	0.226153
Up	CTSW	1	0	0	0.206055
Up	KLRC4	1	0	0	0.231625
Up	MATK	1	0	0	0.29703

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Up	WT1-AS	1	0	0	0.29703
Up	MSR1	1	0	0	0.225447
Up	PDE6A	1	0	0	0.250322
Up	ITIH3	1	0	0	0.243591
Up	SPANXC	1	0	0	0.226721
Down	EGFR	1027	0.179164	9.72E+08	0.378211
Down	TEX101	282	0.037067	1.19E+08	0.333891
Down	WDR76	193	0.017748	65310882	0.332763
Down	NEDD4L	179	0.031075	37251130	0.332238
Down	COMT	153	0.023755	31355344	0.333876
Down	CD74	147	0.012548	50462234	0.319256
Down	BRCA2	127	0.023128	9342512	0.357338
Down	SMAD9	121	0.016778	24375000	0.317119
Down	TOP2A	121	0.011712	36616638	0.31398
Down	CCND2	115	0.009736	31781164	0.309381
Down	MAP1B	108	0.01559	11537464	0.362134
Down	LZTS1	103	0.010135	16974036	0.312828
Down	CDCA7L	91	0.010282	16352494	0.319014
Down	HAT1	84	0.011082	6811070	0.35675
Down	DCLK1	82	0.012086	26828188	0.301459
Down	FOXG1	81	0.00738	28549024	0.303316
Down	SYNE2	75	0.006597	17756958	0.315706
Down	ZNF572	73	0.00582	8202720	0.318197
Down	GSE1	69	0.006668	10817930	0.312055
Down	ZNF835	69	0.006698	8437944	0.298328
Down	FAM107A	67	0.008997	6204376	0.349707
Down	EFNB2	67	0.007659	21152468	0.305025
Down	TRAF5	63	0.006152	17094862	0.305837
Down	BEGAIN	58	0.005087	5999830	0.311837
Down	KIAA0408	57	0.003057	6740132	0.308412
Down	ROPN1	57	0.006343	4739842	0.306529
Down	CASP1	55	0.006179	4267142	0.333275
Down	FGF3	54	0.005401	22888110	0.2783
Down	SHTN1	52	0.003616	7420600	0.307499
Down	RPS10P5	50	0.002712	10656682	0.291537
Down	PCDHGA5	50	0.006464	19095174	0.27012
Down	TTPA	49	0.006194	6988386	0.296346
Down	OAS3	48	0.003116	11577468	0.297368
Down	HNRNPCL2	46	0.005545	14614544	0.290509
Down	HLA-DRA	46	0.00631	6048244	0.294916
Down	PCDHB11	44	0.006778	3747934	0.315746
Down	HSP90AB4P	44	0.004901	12561226	0.288245
Down	ABCA1	43	0.005241	2758902	0.331178
Down	ZIM2	42	0.00258	2033710	0.301867
Down	WEE1	41	0.003834	13034552	0.290665
Down	ESCO2	41	0.002026	6691168	0.303001
Down	HLA-DRB1	40	0.00443	4227118	0.297754
Down	TXNRD2	39	0.002858	3365734	0.294469
Down	ZDHHC23	39	0.004334	15303220	0.286773
Down	LYPD6	38	0.006147	16132610	0.264025
Down	MGAT4C	37	0.005376	14503496	0.260398
Down	KIF5C	36	0.002997	5157046	0.299128
Down	RPS26P11	35	0.0022	1760410	0.316404
Down	PCDHB16	33	0.003061	9302856	0.271066
Down	KIF15	33	0.002702	8508874	0.290531
Down	GAS7	32	0.002565	9122468	0.280752
Down	NR2E1	32	0.002878	3963786	0.294207
Down	EXO1	31	0.002316	2146796	0.309179
Down	LAMA1	30	0.003133	5541138	0.291167
Down	SLC22A23	29	0.003831	3743208	0.295652
Down	ANK1	29	0.003023	3966852	0.297578
Down	KCNJ2	29	0.001467	5712206	0.288015
Down	BCL6B	29	8.11E-04	2278108	0.276847
Down	GLI3	28	0.002985	4686512	0.290899
Down	EFS	27	0.00207	4138476	0.285467
Down	SLFN11	27	0.001794	1342702	0.321394
Down	BEX5	27	0.002154	3604602	0.275359
Down	ATAD2	27	0.001956	5254618	0.295595
Down	LHX2	26	0.002711	3310902	0.268522
Down	SACS	26	0.002124	1743268	0.309406

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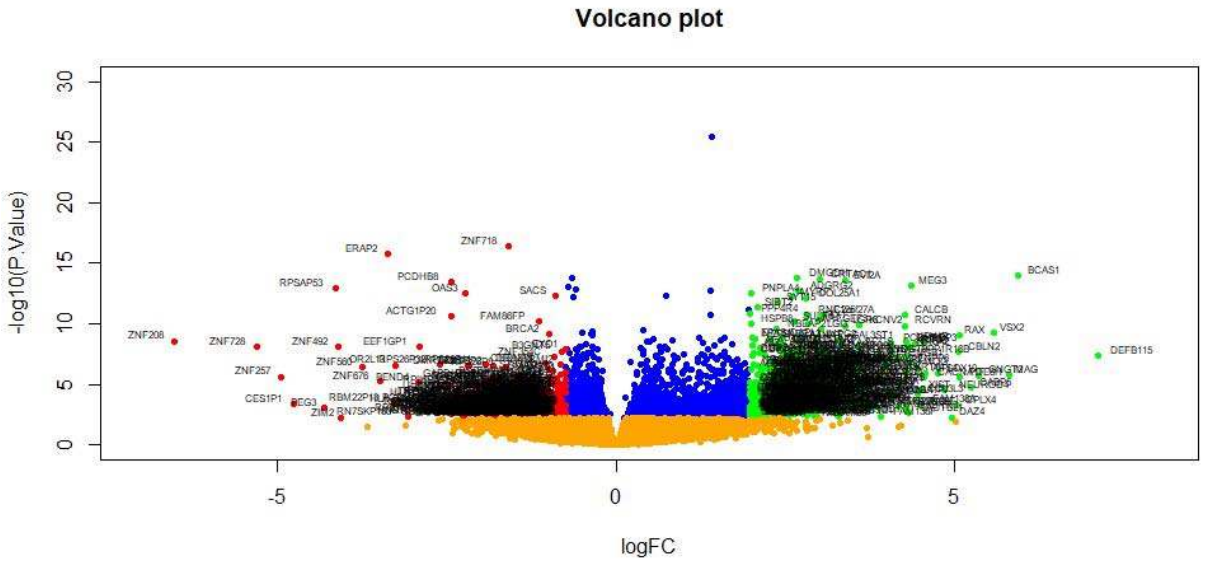
Down	ZNF439	26	7.86E-04	1222072	0.301891
Down	RMI1	26	0.002335	3560864	0.285038
Down	VWF	25	0.002648	2435596	0.302687
Down	RNF112	24	9.54E-04	2296682	0.293251
Down	CERS6	23	0.003131	1837854	0.294355
Down	NFIB	22	0.001669	3115050	0.298222
Down	ENC1	22	0.001312	2857622	0.284727
Down	FOXD2	22	0.002027	3738352	0.255915
Down	TRIM36	22	0.001438	3567752	0.274213
Down	LDB2	21	0.001899	4933676	0.277953
Down	RBM20	20	0.001168	2282714	0.290777
Down	ZNF354C	20	0.001634	3603082	0.268779
Down	RMI2	20	0.001287	2492542	0.285284
Down	KITLG	19	0.002445	2658876	0.265281
Down	LIFR	19	0.001445	3001834	0.280773
Down	RPL13AP3	19	4.64E-04	1184062	0.284642
Down	TCEAL2	19	0.001201	925024	0.299234
Down	RHCG	19	0.00107	1764812	0.256634
Down	SETBP1	19	0.002166	3725070	0.293183
Down	CCNE2	17	0.001258	2102308	0.291358
Down	CIITA	17	9.18E-04	2247336	0.274879
Down	ANKRD29	17	0.002444	3819246	0.257847
Down	OAS1	16	6.71E-04	2325408	0.283206
Down	RND3	16	0.001312	1907720	0.285102
Down	GRB14	16	5.55E-04	1294256	0.28271
Down	HLA-DRB5	16	0.00104	2489364	0.281367
Down	FAM111B	16	6.09E-04	1137354	0.292042
Down	ZBTB20	16	7.85E-04	1913934	0.295687
Down	DAPK2	16	0.001445	2123014	0.271115
Down	ANGPT2	15	7.72E-04	1997922	0.264264
Down	MICB	15	0.001236	694588	0.301435
Down	VAX1	14	9.30E-04	6625528	0.261061
Down	LEMD1	14	7.68E-04	1119390	0.276403
Down	SLC25A18	14	2.89E-04	683874	0.275599
Down	MAML3	13	0.001196	2089024	0.277994
Down	CD37	12	0.001366	827848	0.277597
Down	ITPRIPL1	12	0.001084	854844	0.273778
Down	CDO1	12	0.001663	1622684	0.243364
Down	GRAMD1C	12	0.001663	2837530	0.273797
Down	GCM1	12	0.001614	5340150	0.214775
Down	HLA-DMB	11	7.69E-04	1427290	0.25948
Down	AKR1C3	11	4.04E-04	914096	0.256556
Down	TIAM2	11	3.25E-04	1227328	0.262771
Down	PEG3	11	4.41E-04	755256	0.278771
Down	PLXNA4	10	7.07E-04	388922	0.285134
Down	PLCE1	10	4.55E-04	797494	0.282215
Down	HLA-DQB2	9	0.001351	1657934	0.255372
Down	FZD8	9	3.33E-04	206364	0.286708
Down	ATP11A	9	3.82E-04	666602	0.289058
Down	EMX2	9	0.001186	1940426	0.259524
Down	XKRX	9	6.85E-04	810808	0.24794
Down	ZNF441	9	5.65E-04	2703346	0.228877
Down	TET1	9	2.05E-04	172412	0.273906
Down	CHRDL1	9	5.27E-04	1286290	0.249556
Down	CDCA7	9	9.20E-05	265188	0.281284
Down	FBLN7	1	0	0	0.274432
Down	HLA-DMA	1	0	0	0.23774
Down	EMX1	1	0	0	0.225353
Down	KIRREL3	1	0	0	0.265867
Down	CHRNA5	1	0	0	0.208882
Down	GSTT2B	1	0	0	0.229486
Down	FGF19	1	0	0	0.222961
Down	PCDHGA8	1	0	0	0.212679

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

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Regulation	Hub Genes	Degree	MicroRNA	Regulation	Hub Genes	Degree	TF
Up	EPAS1	89	hsa-mir-1292-5p	Up	EPAS1	49	ESRRB
Up	KRT8	65	hsa-mir-432-3p	Up	TGM2	43	SMAD4
Up	ERBB3	53	hsa-mir-6801-3p	Up	HOXA1	37	EED
Up	HOXA1	45	hsa-mir-10a	Up	KRT8	31	ATF3
Up	HSPA2	45	hsa-mir-7977	Up	MTUS2	30	TBX5
Up	IL7R	40	hsa-mir-21-3p	Up	HSPA2	27	JARID2
Up	TGM2	27	hsa-mir-452-5p	Up	ERBB3	25	CLOCK
Up	TRIM29	27	hsa-mir-761	Up	PTPRO	25	SOX11
Up	PTPRO	18	hsa-mir-429	Up	VTN	20	PBX1
Up	MTUS2	18	hsa-mir-133a-3p	Up	IL7R	16	TCF4
Up	LRRK2	14	hsa-mir-149-5p	Up	LRRK2	16	PPARD
Up	HTR2C	12	hsa-mir-22-5p	Up	HTR2C	15	TFCP2L1
Up	VTN	7	hsa-mir-16-5p	Up	TRIM29	15	YAP1
Up	CMTM5	2	hsa-mir-520f-3p	Up	CMTM5	15	SCLY
Up	NGB	1	hsa-mir-146a-5p	Up	NGB	5	PAX6
Down	CCND2	365	hsa-mir-4521	Down	NEDD4L	50	SREBF1
Down	MAP1B	249	hsa-mir-363-3p	Down	CCND2	42	SMARCA4
Down	TOP2A	104	hsa-mir-4487	Down	EGFR	39	ARNT
Down	EGFR	83	hsa-mir-21-5p	Down	MAP1B	35	EP300
Down	NEDD4L	76	hsa-mir-6807-5p	Down	DCLK1	31	CREB1
Down	HAT1	73	hsa-mir-1185-2-3p	Down	COMT	29	SETDB1
Down	SMAD9	58	hsa-mir-1273h-5p	Down	CDCA7L	27	DCP1A
Down	WDR76	52	hsa-mir-6858-3p	Down	BRCA2	26	MYCN
Down	CDCA7L	45	hsa-mir-124-3p	Down	HAT1	25	CUX1
Down	COMT	40	hsa-mir-1908-3p	Down	TOP2A	25	FOXM1
Down	BRCA2	37	hsa-mir-1245a	Down	LZTS1	20	NR3C1
Down	DCLK1	28	hsa-mir-125b-5p	Down	WDR76	14	BACH1
Down	CD74	15	hsa-mir-92a-1-5p	Down	CD74	12	IRF8
Down	LZTS1	9	hsa-mir-204-5p	Down	TEX101	9	RCOR3
Down	TEX101	7	hsa-mir-27a-5p	Down	SMAD9	9	TET1

Figures



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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.

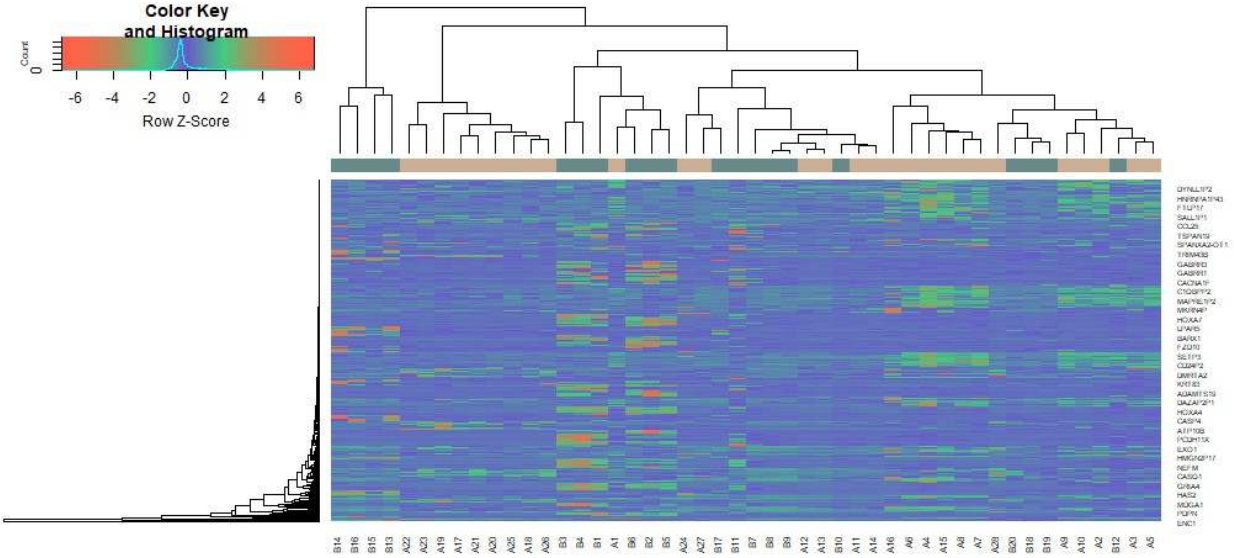


Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A28 = HD samples; B1 – B20 = Normal control samples)

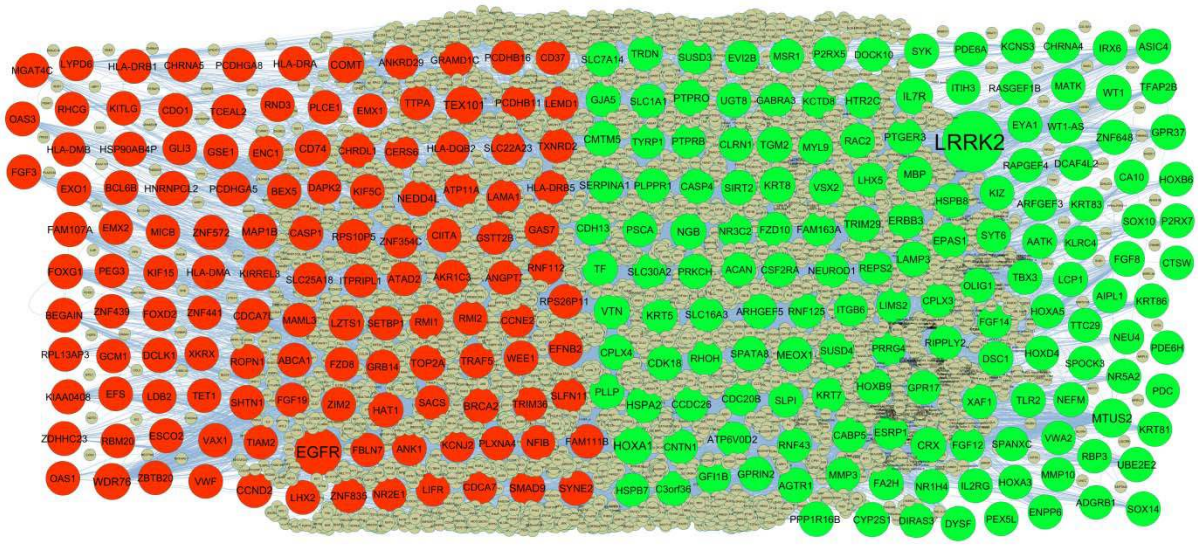


Fig. 3. PPI network of DEGs. Up regulated genes are marked in parrot green; down regulated genes are marked in red.

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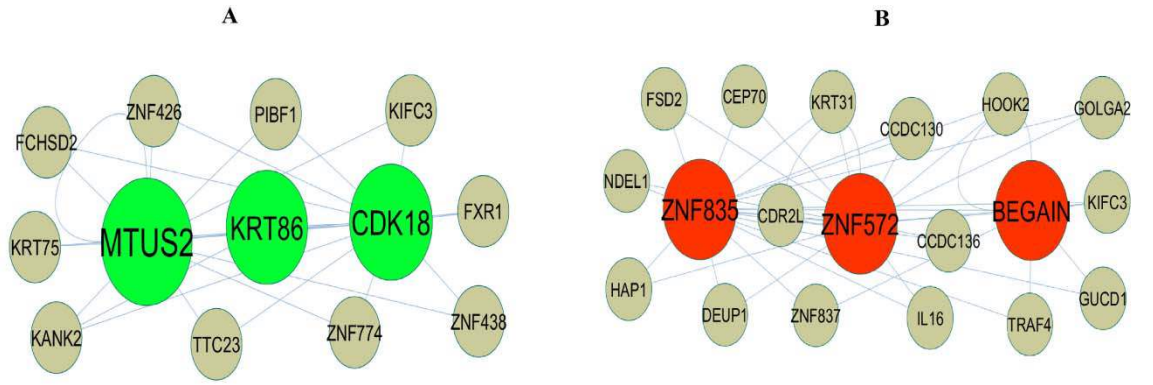


Fig. 4. Modules selected from the PPI network. (A) The most significant module was obtained from PPI network with 13 nodes and 24 edges for up regulated genes (B) The most significant module was obtained from PPI network with 19 nodes and 38 edges for down regulated genes. Up regulated genes are marked in parrot green; down regulated genes are marked in red.

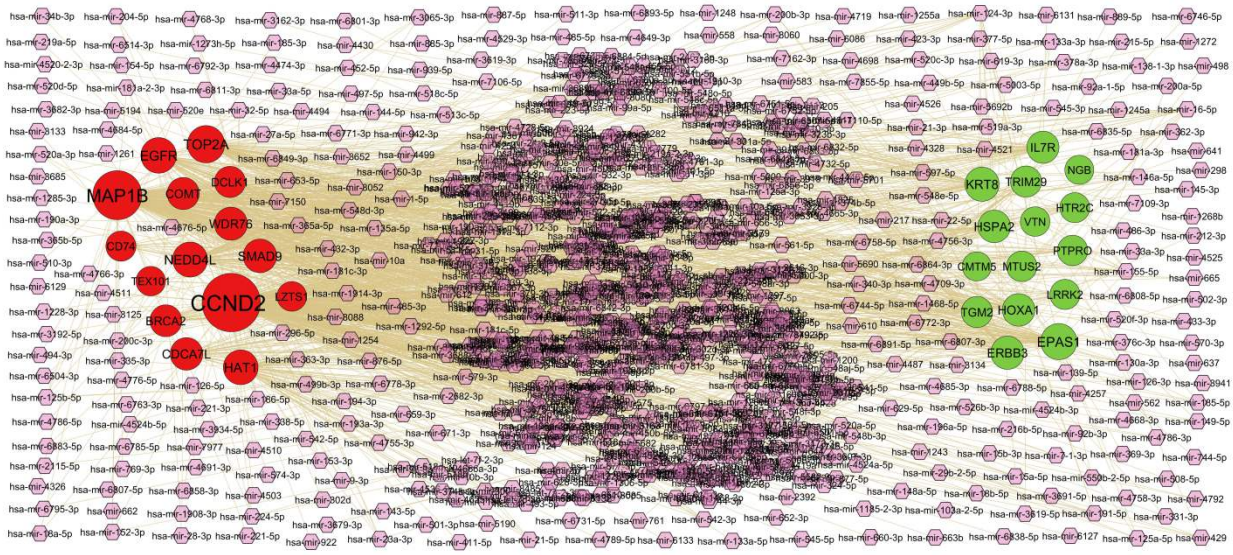


Fig. 5. Hub gene - miRNA regulatory network. The purple color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

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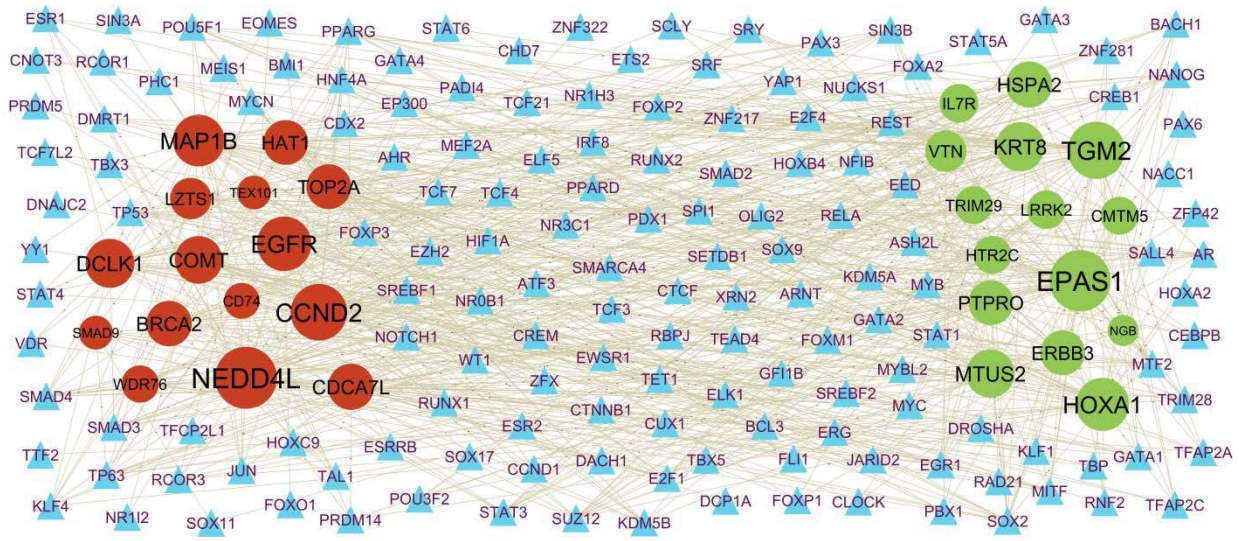


Fig. 6. Hub gene - TF regulatory network. The blue color triangle nodes represent the key TFs; up regulated genes are marked in dark green; down regulated genes are marked in dark red.

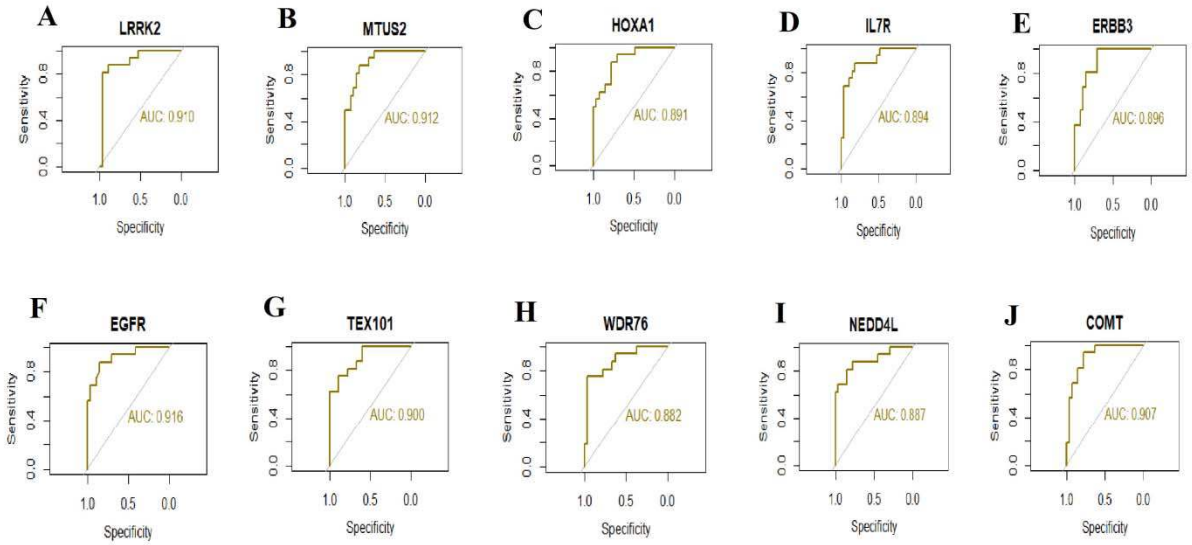


Fig. 7. ROC curve analyses of hub genes. A) LRRK2 B) MTUS2 C) HOXA1 D) IL7R

E) ERBB3 F) EGFR G) TEX101 H) WDR76 I) NEDD4L J) COMT