Bioinformatics Analysis of RNA Sequencing Data Identifies Biomarkers and Treatment Targets in Preeclampsia

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Research Article

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Abstract

Preeclampsia is widely recognized as a risk factor for pregnancy. This study aimed to identify key targets involved in the progression of preeclampsia. RNA sequencing dataset (GSE303463) for preeclampsia was obtained from the Gene Expression Omnibus (GEO) database. Differentially expressed genes (DEGs) were identified and analyzed between normal control and preeclampsia groups. Functional enrichment analysis was performed using Gene Ontology (GO) and REACTOME. Protein-protein interaction (PPI) network and module analysis were conducted to identify hub genes. Furthermore, we constructed the miRNA-hub gene regulatory network and TF-hub gene regulatory network, as well as drug-hub gene interaction network. Based on the hub genes, drug compounds were speculated using the DrugBank. ROC analysis was then carried out based on the diagnostic value of hub genes. A total of 958 shared DEGs were identified, including 479 up-regulated genes and 479 down-regulated genes in Preeclampsia samples. GO and pathway enrichment analyses indicated that genes were primarily enriched in biological regulation, response to stimulus, ECM proteoglycans and Cell-Cell communication. We identified nine hub genes in the PPI network, including VCAM1, PLEKHA7, SPRED1, PTPN3, EPHA7, GABARAPL2, RPL13, H1-4, GPR17 and PDK1. A miRNA: hsa-miR-6731-5p and hsa-miR-6835-3p were found to be related to the hub genes, TF: BMI1 and HAND2 were identified as TFs of the hub genes and Drugs: Acteoside and Ephedra sinica root were identified as drugs of the hub genes. This discovery-driven investigation might be useful to provide a novel insight into the diagnosis and treatment of preeclampsia. However, more experiments are needed in the future to investigate the functional roles of these genes in preeclampsia.

Keywords: Bioinformatics analysis; Hub genes; Preeclampsia; GEO; Biomarkers

Introduction

Preeclampsia is a leading cause of pregnancy associated with increased risk of fetal and maternal complications [Phipps et al. 2016]. It is characterized by new-onset hypertension with or without proteinuria with maternal end-organ damage after 20 weeks of gestation [Kanasaki and Kalluri, 2009]. Preeclampsia prevalence varies among countries worldwide from 3% to 8% depending on the population studied and criteria used for diagnosis [Vera-Ponce et al. 2025]. Preeclampsia can be potentially affected to both mother and the fetus [Irminger-Finger et al. 2008]. Preeclampsia is heterogeneous and vascular function, and hence it is not common but also shows uncertain progression and outcomes of maternal mortality during pregnancy [Hula et al. 2025]. The course of preeclampsia needs more attention, if left untreated, will experience spontaneous abortion [Mohamedain et al. 2022], hepatic complications [Chandrasekaran and Simon, 2020], kidney complications [Dines et al. 2023], cardiovascular complications [Melchiorre et al. 2014], brain injury [Shi et al. 2026], epilepsy [Boakye et al. 2024] and neuropsychiatric disorders [Mautner et al. 2013]. Risk factors for preeclampsia include gestational diabetes mellitus [Wang et al. 2023], infertility [Hahn et al. 2017], polycystic ovarian syndrome [Deer et al. 2025], obesity [Schiavone et al. 2024], autoimmune disorder [Liu et al. 2023], cancer [Serrand et al. 2021], inflammation [Wang et al. 2022], oxidative stress [Afrose et al. 2025], blood clotting [Han et al. 2014], genetic factors [Tyrmi et al. 2023] and environmental factors [Dasinger et al. 2020]. Although timely treatment with antihypertensive drugs [Odigboegwu et al. 2018] and corticosteroids [Nayeri et al. 2014]. Some patent who do not respond to antihypertensive drugs and corticosteroids are still at considerable risks of developing preeclampsia. In addition, the lack of specific diagnostic tests, biomarkers and signaling pathways for preeclampsia make early diagnosis and treatment challenging. Therefore, preeclampsia remains an important focus of study and it is extremely essential to perform detailed exploration of the molecular pathogenesis of preeclampsia and to further advancement in healthcare for this population.

The etiology of preeclampsia has been studied extensively, but the exact pathogenic factors or triggering agents for preeclampsia are still unidentified, and the underlying molecular mechanisms for initiation and development of preeclampsia remain largely unknown. Recent studies have found that several genes and signaling pathways include FLT1 [Kikas et al. 2020], angiotensinogen (AGT) [Jansaka et al. 2021], AGTR1 [Mo et al. 2023], renin–angiotensin system (REN) [Yu et al. 2019], NOS3 [Zdoukopoulos et al. 2011], Wnt/β-catenin signaling pathway [Wang et al. 2018], MAPK signaling pathway [Guo et al. 2023], HMGB1-RAGE signaling pathway [Zhu et al. 2015], PI3K/AKT signaling pathway [Liu et al. 2023] and TLR4 signaling pathway [Gong et al 2016] are closely associated with the preeclampsia, indicating that genetic alterations and signaling pathways might play a critical role in the progression of preeclampsia. Therefore, researchers consider that individuals who are genetically predisposed to preeclampsia are susceptible to preeclampsia.

Gene expression analysis based on RNA sequencing technology is a widely used, high-throughput and powerful investigation method, which can simultaneously detect expression change of thousands of genes on the mRNA level [Joshi et al. 2021; Prashanth et al. 2021]. By gene expression profiling analysis with RNA sequencing technology, some investigations have found many differently expressed genes (DEGs) which played a essential role in preeclampsia initiation and development and could be assessed as potential molecular targets and diagnostic markers [Rezk et al. 2022].

This investigation aims to identify key genes associated with the pathogenesis of preeclampsia, investigate potential molecular mechanisms, and explore small molecule compounds that could be potential therapeutic agents. In the present investigation, we selected RNA sequencing dataset GSE303463 [Horii et al. 2026] from the Gene Expression Omnibus (GEO) database (available online: https://www.ncbi.nlm.nih.gov/geo) [Clough and Barrett, 2016], and used the DESeq2 package in R software to screen DEGs. Gene ontology (GO) and REACTOME pathway enrichment analysis was also performed for the functional analysis of the DEGs. A protein-protein interaction (PPI) network of the DEGs was constructed by Intact interactome and was visualized by Cytoscape software. Module analysis is performed. Furthermore, a Through miRNA-hub gene regulatory network, TF-hub gene regulatory network and drug-hub gene interaction network analysis of hub genes were constructed to assess the interactions between the miRNAs and hub genes, TFs and hub genes, and drug molecules and hub genes. Furthermore, quantitative receiver operating characteristic (ROC) curve analysis was used to detect diagnostic value of hub genes. The investigation might shed new light on the molecular mechanisms of preeclampsia.

Materials and Methods

RNA-sequencing data source

RNA-sequencing dataset GSE303463 [Horii et al. 2026] was downloaded from the GEO database. The GSE303463 dataset generated on the GPL24676 Illumina NovaSeq 6000 (Homo sapiens) and GPL34281 Illumina NovaSeq X (Homo sapiens) platforms comprises of 60 placental tissue of normal control samples and 22 placental tissue of preeclampsia samples.

Identification of DEGs

The DEGs in RNA-sequencing dataset was determined by using the 'DESeq2' package [Love et al. 2014] according to the criteria log2 foldchange (FC) > 0.206 for up regulated genes, criteria log2 foldchange (FC) < -0.319 for down regulated genes and adjusted $p < 0.05$. The FC and adjusted p -value were determined by the false discovery rate (FDR) procedure and the Benjamini-Hochberg method, respectively [Solari et al. 2017]. The ggplot2 and gplot packages in R software were used to draw the volcano plot and heatmap of DEGs, respectively.

GO and pathway enrichment analyses of DEGs

Gene ontology (GO) term enrichment analysis (http://www.geneontology.org) [Thomas, 2017] and REACTOME (https://reactome.org/) [Fabregat et al. 2018] were performed to analyze the biological processes and signaling pathways of DEGs by using g:Profiler (http://biit.cs.ut.ee/gprofiler/) [Reimand et al. 2007], respectively. Among them, GO annotation of DEGs were classified into three categories: biological process (BP), cellular component (CC), and molecular function (MF). Both GO term and REACTOME pathway enrichment analyses were performed with a threshold of adjusted $p < 0.05$.

Construction of the PPI network and module analysis

The web-based Intact interactome web tool (https://www.ebi.ac.uk/intact/home) [Del Toro et al. 2022] was adopted to obtain PPI relationships for the DEGs followed by visualization using Cytoscape (http://www.cytoscape.org/) [Ono et al.

2025]. Hub gene selection was performed using Network Analyzer, a plug-in application of Cytoscape. Network Analyzer computes 4 methods including node degree [Luo et al. 2017], betweenness [Li et al. 2017], stress [Gilbert et al. 2021] and closeness [Li et al. 2020] to identify important nodes in PPI networks. The Cytoscape plug-in PEWCC [Zaki et al. 2013] of Cytoscape was adopted to detect signicant modules in PPI network. PEWCC is an application designed to explore densely connected regions in a PPI network based on topology.

Construction of the miRNA-hub gene regulatory network

The transcriptional associations between microRNA (miRNA) and hub genes are of great biological significance, and might help in the analysis of various physiological activities [Asli et al. 2008]. The miRNAs and hub genes were analyzed based on the information of miRNA-hub genes stored in the miRNet database (https://www.mirnet.ca/) [Fan et al 2018] Also, the miRNA-hub gene regulatory network was constructed using the Cytoscape softwar [Ono et al. 2025]e.

Construction of the TF-hub gene regulatory network

The transcriptional associations between transcription factors (TFs) and hub genes are of great biological significance, and might help in the analysis of variousphysiological activities [Engelkamp and van Heyningen, 1996]. The TFs and hub genes were analyzed based on the information of TF-hub genes stored in the NetworkAnalyst database (https://www.networkanalyst.ca/) [Zhou et al 2019]. Also, the TF-hub gene regulatory network was constructed using the Cytoscape software [Ono et al. 2025].

Construction of the drug-hub gene interaction network

The selected hub genes that were considered potential therapeutic targets for preeclampsia treatment were imported into DrugBank to explore existing drugs or small molecular compounds. The drugs or small molecular compounds and hub genes were analyzed based on the information of drug-hub genes stored in the NetworkAnalyst database (https://www.networkanalyst.ca/) [Zhou et al 2019]. Also, the drug-hub gene interaction network was constructed using the Cytoscape software [Ono et al. 2025].

Receiver operating characteristic (ROC) curves analysis

ROC curves and the area under the curve (AUC) values were used to evaluate the diagnostic efficacy of hub genes in the RNA-sequencing datasets, which were performed by using the 'pROC' package [Robin et al 2011]. The Y-axis stand for the true positive rate, needed by sensitivity. The X-axis stand for false positive rate, needed by 100%-specificity. Diagnostic value of hub genes were assessed based on the AUC greater than 0.9.

Results

Identification of DEGs

We then utilized the DESeq2 R package to screen and identify the DEGs using the criteria of adjusted $p < 0.05$, and | log2 foldchange (FC) > 0.206 for up regulated genes and criteria log2 foldchange (FC) < -0.319 for down regulated genes. The GSE303463 dataset contained 958 DEGs (479 up-regulated and 479 down-regulated genes) (Table 1). The volcano plot for the DEGs is shown in Fig. 1 and the cluster heat maps of the DEGs is presented in Fig. 2.

GO and pathway enrichment analyses of DEGs

Next, we performed GO term and pathway enrichment analysis of the DEGs in the GEO GSE303463 dataset in endometriosis using the "g:Profiler" web tool. The GO enrichment analysis data could be grouped into three categories, i.e., BP, CC, and MF. Table 2 lists the top GO terms for the DEGs. Using the cutoff criteria of $p < 0.05$, the three categories of GO terms are shown in Fig. 3 and Fig. 4. The GO terms in the BP category were mainly involved in biological regulation, regulation of cellular process, response to stimulus and multicellular organismal process. The GO terms in the CC category were mainly involved in the cell periphery, plasma membrane, plasma membrane and membrane. The MF of the DEGs were mainly enriched in small molecule binding, ion binding, catalytic activity and identical protein binding. The top REACTOME pathways are shown in Fig. 3 and Fig. 4, while the top REACTOME pathways are listed in Table 3. The DEGs were mostly enriched in ECM proteoglycans, extracellular matrix organization, cell-cell communication and metabolism of lipids.

Construction of the PPI network and module analysis

We constructed the PPI network for the DEGs in the GEO GSE303463 dataset using the online Intact interactome database and analyzed the data using the Cytoscape software. The PPI network consisted of 8406 node and 20219 edges (Fig. 5). Thereafter, we further screened the top 10 hub genes (5 up regulated genes and 5 down regulated genes) using the Network Analyzer tool in the Cytoscape software and identified the hub genes as VCAM1, PLEKHA7, SPRED1, PTPN3, EPHA7, GABARAPL2, RPL13, H1-4, GPR17 and PDK1 (Table 4). Fig. 6 and Fig. 7 shows the two most important modules. A significant module 1 including 37 nodes and 96 edges. A significant module 2 including 16 nodes and 34 edges. The genes in Module 1 were mainly enriched in the nervous system development, biological regulation and regulation of cellular process (Fig. 8), while the genes in Module 2 were mainly enriched in response to stimulus, plasma membrane, metabolism and membrane (Fig. 9).

Construction of the miRNA-hub gene regulatory network

Predicting the miRNAs of hub genes was essential for probing the expression regulation mechanism of hub genes. The miRNA-hub gene regulatory network consisted of 2907 (hub gene:440, miRNA: 2467) node and 53894 edges (Fig. 10). In this investigation, we identified the miRNAs associated with hub genes and found SPRED1 was regulated by 365 different miRNAs (ex; hsa-miR-6731-5p), DYRK2 was regulated by 341 different miRNAs (ex; hsa-miR-500b-5p), MYO18A was regulated by 277 different miRNAs (ex; hsa-miR-133a-3p), PRKCA was regulated by 227 different miRNAs (ex; hsa-miR-17-5p), EPHA7 was regulated by 203 different miRNAs (ex; hsa-miR-379-3p), PLEC was regulated by 416 different miRNAs (ex; hsa-miR-6835-3p), ARRDC3 was regulated by 298 different miRNAs (ex; hsa-miR-548n), GAPDH was regulated by 219 different miRNAs (ex; hsa-miR-141-5p), SULF2 was regulated by 142 different miRNAs (ex; hsa-miR-5585-3p) and PDK1 was regulated by 132 different miRNAs (ex; hsa-miR-375) (Table 5).

Construction of the TF-hub gene regulatory network

Predicting the TFs of hub genes was essential for probing the expression regulation mechanism of hub genes. The TF-hub gene regulatory network consisted of 710 (hub gene:276, miRNA: 434) node and 17149 edges (Fig. 11). In this investigation, we identified the TFs linked with hub genes and found MAGI3 was regulated by 77 different TFs (ex; BMI1), SPRED1 was regulated by 71 different TFs (ex; UTX), DYRK2 was regulated by 66 different TFs (ex; CREM), PRKCA was regulated by 61 different TFs (ex; TAL1), PLEKHA7 was regulated by 60 different TFs (ex; GATA4), SULF2 was regulated by 81 different TFs (ex; HAND2), PLEC was regulated by 81 different TFs (ex; MAF), GAPDH was regulated by 64 different TFs (ex; PHF8), PDK1 was regulated by 60 different TFs (ex; EWSR1) and ARRDC3 was regulated by 56 different TFs (ex; HOXB4) (Table 5).

Construction of the drug-hub gene interaction network

Predicting the drug molecules of hub genes was essential for probing the regulation of hub gene expression. In this investigation, we identified the drug molecules linked with hub genes and found up regulated genes such as PRKCA was targeted by 19 different drug molecules (ex; Acteoside), HPGDS was targeted by 18 different drug molecules (ex; S-Hexylglutathione), MAPK8 was targeted by 17 different drug molecules (ex; Encorafenib), RARG was targeted by 17 different drug molecules (ex; Palovarotene) and C3 was targeted by 11 different drug molecules (ex; S-Hydroxycysteine) (Fig. 12 and Table 6), while down regulated genes such as MAOB was targeted by 55 different drug molecules (ex; S- Ephedra sinica root), CA4 was targeted by 34 different drug molecules (ex; Methyclothiazide), FLT1 was targeted by 26 different drug molecules (ex; Selpercatinib), VDR was targeted by 22 different drug molecules (ex; Seocalcitol) and TPI1 was targeted by 17 different drug molecules (ex; 5-fluorotryptophan) (Fig. 13 and Table 6).

Receiver operating characteristic curve (ROC) analysis

The ROC curve analysis showed that hub gene could distinguish preeclampsia from normal control .Based on the RNA-sequencing dataset, the hub genes were verified using the ROC curve, as shown in Fig. 14. The AUC for VCAM1 is 0.918, PLEKHA7 is 0.908, SPRED1 is 0.914, PTPN3 is 0.899, EPHA7 is 0.910, GABARAPL2 is 0.926, RPL13 is 0. 922, H1-4 is 0.920, GPR17 is 0.913 and PDK1 is 0.919, which is above the threshold of 0.8. The diagnosis effect of preeclampsia was better, and the combined diagnosis of hub genes was the best.

Discussion

Preeclampsia is the hypertension with or without proteinuria in pregnancy [Roberts, 2024]. It can have a deleterious impact on other organs in pregnant women and cause kidney and liver damage, brain injury and other serious side effects [Bokslag et al. 2016]. Preeclampsia pathophysiological process remains elusive and complicated. In present investigation, bioinformatics analysis was performed based on the gene expression RNA-sequencing dataset of GSE303463 from the GEO database. A total of 958 DEGs (479 up-regulated and 479 down-regulated genes) were screened out as the preeclampsia related DEGs. SPX (spexin hormone) [Pekal et al. 2022], HSD3B2 [Shimodaira et al. 2012], HK2 [Lv et al. 2018], LTF (lactotransferrin) [Hsu et al. 2023], FSTL3 [Xie et al. 2018], PTX3 [Topcu et al. 2025], LEP (leptin) [Zeng et al. 2023], CYP26A1 [Li et al. 2022] and CP (ceruloplasmin) [Sak et al. 2020] might be important in preeclampsia. HSD3B2 [Jeandron et al. 2012], CNTN6 [Tassano et al. 2018], FSTL3 [Xu et al. 2020], PTX3 [Ibrahim et al. 2012], LEP (leptin) [Müller et al. 2016], CYP26A1 [Liu et al. 2014] and CP (ceruloplasmin) [Ozgüneş et al. 1987] participates in the development of spontaneous abortion. LTF (lactotransferrin) [Lee et al. 2018], FSTL3 [Duan et al. 2023], PTX3 [El-Emshaty et al. 2025], LEP (leptin) [Wang et al. 2025] and CP (ceruloplasmin) [Nobili et al. 2013] were reported to be involved in all processes in the development of hepatic complications. SPX (spexin hormone) [Wang et al. 2026], HK2 [Li et al. 2025], LTF (lactotransferrin) [Videm et al. 2012], FSTL3 [Nizamuddin et al. 2025], PTX3 [Xu et al. 2023], LEP (leptin) [Dessie et al. 2021] and CP (ceruloplasmin) [Arenas de Larriva et al. 2020] plays a key role in the cardiovascular complications. EPHA5 [Overman et al. 2012], HK2 [Mera-Reina et al. 2026], LTF (lactotransferrin) [Xue et al. 2025], PTX3 [Rodriguez-Grande et al. 2014], LEP (leptin) [Garbe et al. 2020] and CP (ceruloplasmin) [Liu et al. 2019] have been found to be alter expressed in brain injury. EPHA5 [Shu et al. 2016], CNTN6 [Juan-Perez et al. 2018], CADM3 [Rebelo et al. 2021], LTF (lactotransferrin) [Youssef et al. 2025], PTX3 [Ravizza et al. 2001], LEP (leptin) [Shan et al. 2023] and CP (ceruloplasmin) [Chen et al. 2023] were found to be associated with epilepsy. SPX (spexin hormone) [Cichoń et al. 2024], EPHA5 [Matoso et al. 2013], HSD3B2 [Johansson et al. 2012], CNTN6 [Hu et al. 2015], LTF (lactotransferrin) [Mahdavi Hezaveh et al. 2025], PTX3 [Xu et al. 2025], LEP (leptin) [de Assis et al. 2021] and CP (ceruloplasmin) [Kuang et al. 2025] are closely involved in progression of neuropsychiatric disorders. SPX (spexin hormone) [Al-Daghri et al. 2019], LTF (lactotransferrin) [Mohandas et al. 2024], FSTL3 [Jiang et al. 2025], PTX3 [Yu et al. 2019], LEP (leptin) [Pérez-Pérez et al. 2020] and ARMS2 [Sun et al. 2017] genes might be related to the high risk of gestational diabetes mellitus. Previous study found that HSD3B2 [Osiński et al. 2005], LTF (lactotransferrin) [Sato et al. 2022], PTX3 [Camaioni et al. 2018], LEP (leptin) [Abdulslam Abdullah et al. 2022] and CP (ceruloplasmin) [Turgut et al. 2013] were associated with prognostic factors in patients with infertility. SPX (spexin hormone) [Özgürlük et al. 2025], HSD3B2 [Yu et al. 2019], PTX3 [Tanılır Çağıran et al. 2024] and LEP (leptin) [Feijing et al. 2025] might be a therapeutic potential biomarkers in polycystic ovarian syndrome. SPX (spexin hormone) [Wojciechowska et al. 2023], HSD3B2 [Lee et al. 2016], HK2 [Cusi et al. 2001], LTF (lactotransferrin) [Jamka et al. 2020], FSTL3 [Li et al. 2023], PTX3 [Xie et al. 2024], LEP (leptin) [Obradovic et al. 2021] and CP (ceruloplasmin) [Arner et al. 2014] might play essential roles in the obesity progression. SPX (spexin hormone) [Yortanli et al. 2025], LTF (lactotransferrin) [Ding et al. 2025], PTX3 [Chiari et al. 2023], LEP (leptin) [Navarini et al. 2018] and CP (ceruloplasmin) [Nagi et al. 2025] played a fundamental role in autoimmune disorders. SPX (spexin hormone) [Turk et al. 2024], OR51B5 [Yang et al. 2025], EPHA5 [Ang et al. 2025], THSD7B [Luo et al. 2024], CADM3 [Ren et al. 2024], HK2 [Palmieri et al. 2009], LTF (lactotransferrin) [Wang et al. 2026], FSTL3 [Chauvin et al. 2025], PTX3 [Wu et al. 2024], CGB3 [Singh et al. 2023], LEP (leptin) [Buonaiuto et al. 2022], CYP26A1 [Osanai and Lee, 2015] and CP (ceruloplasmin) [Chen et al. 2021] were thought to play an important role in cancer progression. A previous study identified SPX (spexin hormone) [Türkel et al. 2022], DGKK (diacylglycerol kinase kappa) [Tu et al. 2023], HK2 [Weber-Stiehl et al. 2024], LTF (lactotransferrin) [Artym et al. 2021], FSTL3 [Li et al. 2023], PTX3 [Ramirez et al. 2019], LEP (leptin) [Pérez-Pérez et al. 2020], CYP26A1 [Snyder et al. 2020] and CP (ceruloplasmin) [Deshmukh et al. 1985] as a potential molecular markers for inflammation. DGKK (diacylglycerol kinase kappa) [Tu et al. 2023], HK2 [Kim et al. 2021], LTF (lactotransferrin) [Ding et al. 2025], PTX3 [Dejanović et al. 2020], LEP (leptin) [Chatterjee et al. 2013], ARMS2 [Chang et al. 2023] and CP (ceruloplasmin) [Colombini et al. 2016] expression was reported to be directly associated with oxidative stress. PTX3 [Napoleone et al. 2004] and LEP (leptin) [Buis et al. 2020] are well known for its critical role in blood clotting. These results suggest that significant DEGs are might be closely related to the occurrence and development of preeclampsia.

In the GO and REACTOME pathways enrichment analysis, a large number of DEGs were found to be enriched in GO terms and signaling pathways, which are consistent with published studies. Signaling pathways such as ECM proteoglycans [Famá and Pinhal, 2025], Extracellular matrix organization [Zhan et al. 2024], nervous system development [Spradley, 2019], O-linked glycosylation [Gómez-Gutiérrez et al. 2019], diseases of metabolism [Li et al. 2025], signaling by receptor tyrosine kinases [Chen et al. 2019], cell-cell communication [Brodowski et al. 2019], metabolism of lipids [Stadler et al. 2023], metabolism [Li et al. 2025] and Metabolism of carbohydrates and carbohydrate derivatives [Nisell et al. 1999] and transport of small molecules [Moura et al. 2024] play a progressive role in preeclampsia. CX3CR1 [Liu et al. 2024], OLFML3 [Chen et al. 2024], VCAM1 [Liu et al. 2021], CTLA4 [Parhizkar et al. 2025], C3 [Lokki et al. 2017], SELE (selectin E) [Palalıoğlu et al. 2023], GH1 [Liao et al. 2017], CLDN1 [Jin et al. 2023], CYP24A1 [Ma et al. 2012], VTN (vitronectin) [Qi et al. 2025], BMP5 [Wang et al. 2024], ADAMTS12 [Namlı Kalem et al. 2018], UNC5C [Wang et al. 2026], FGF10 [Anteby et al. 2005], COL6A1 [Qi et al. 2025], TLR7 [Zhang et al. 2025,] FGF7 [Zhou et al. 2017], SLIT3 [Lim et al. 2014], PDE7B [Li et al. 2025], LUM (lumican) [Liu et al. 2021], WNT2 [Liu et al. 2020], KL (klotho) [Cecati et al. 2025], ALCAM (activated leukocyte cell adhesion molecule) [Wei et al. 2020], POSTN (periostin) [Kobierzycki et al. 2020], CTHRC1 [Li et al. 2022], LGR5 [Wong et al. 2025], GCLM (glutamate-cysteine ligase modifier subunit) [Tan et al. 2026], GJA1 [Cao et al. 2023], DNMT3A [Jia et al. 2025], CASK (calcium/calmodulin dependent serine protein kinase) [Dubbs et al. 2022], PGAP1 [Benabess and Myers, 2025], DOCK1 [Xu et al. 2024], MAPK8 [Liu et al. 2026], MTA1 [Liiberis et al. 2017], COL4A4 [Jehn et al. 2022], MXRA5 [Qian et al. 2019], CUBN (cubilin) [Albejante et al. 2020], TREM1 [Xie et al. 2021], HTRA4 [Kong et al. 2025], FLT1 [Kikas et al. 2020], IL1RL1 [Chen et al. 2014], PPP1R1C [Ebrahimi et al. 2026], HILPDA (hypoxia inducible lipid droplet associated) [Wang et al. 2025], BHLHE40 [Zhang et al. 2025], NDRG1 [Zhang et al. 2025], PTGS2 [Li et al. 2022], ENG (endoglin) [El Hamaoui et al. 2025], GPER1 [Singh et al. 2025], INHA (inhibin subunit alpha) [Mylonas et al. 2006], CRH (corticotropin releasing hormone) [Karteris et al. 2005], SASH1 [Liu et al.

2020], FOSL1 [Chen et al. 2024], TPBG (trophoblast glycoprotein) [Sun et al. 2024], GATA1 [Li et al. 2025], PAPPA2 [Macintire et al. 2014], GBA1 [Dasari et al. 2020], PROCR (protein C receptor) [Andres et al. 2022], INHBA (inhibin subunit beta A) [Jiang et al. 2020], SYDE1 [Lo et al. 2017], BCL6 [Louwen et al. 2022], VEGFA (vascular endothelial growth factor A) [He et al. 2018], NRIP1 [Gu et al. 2024], FLNB (filamin B) [Wei et al. 2019], ERO1A [Fan et al. 2025], ISG15 [Ozmen et al. 2022], NPNT (nephronectin) [Al-Hamed et al. 2022], DUSP1 [Andrieu et al. 2025], HTRA1 [Tossetta et al. 2023], LAMP3 [Tian et al. 2023], ARRDC3 [Cao et al. 2023], CITED2 [Yang and Song, 2025], PLAAT3 [Zou et al. 2025], FOSL2 [Wan et al. 2021], HMOX1 [Rahimi et al. 2024], ANG (angiogenin) [Shaarawy et al. 2005], MCOLN1 [Wu et al. 2025], BCAT2 [Yin et al. 2026], GDF15 [Pereira et al. 2026], CGA (glycoprotein hormones, alpha polypeptide) [Bralewska et al. 2023], VDR (vitamin D receptor) [Rahman et al. 2023], SERPINE1 [Deng et al. 2025], LDLR (low density lipoprotein receptor) [Villalobos-Labra et al. 2023], TIMP3 [Cruz et al. 2022], EBI3 [Darvishzadeh et al. 2026], S100A9 [Mitranovici et al. 2025], CYP2J2 [Ongun et al. 2023], CTSB (cathepsin B) [Kim et al. 2016], SLC2A1 [Park et al. 2026], NCOR2 [Liu et al. 2026], CYP11A1 [Pan et al. 2017], S100A6 [Jurewicz et al. 2014], CLIC3 [Murthi et al. 2012], HEY1 [Qi et al. 2025], KDM3A [Xu et al. 2021], ACER2 [Li et al. 2020], DLX5 [Zadora et al. 2017], BACH1 [Wu et al. 2026], PRDX2 [Wu et al. 2023], MMP15 [Kaitu'u-Lino et al. 2012], ITGA5 [Zhao et al. 2017], ERP44 [Yang et al. 2021], GPX4 [Liao et al. 2025], MMP14 [Ovayolu et al. 2021], CEBPD (CCAAT enhancer binding protein delta) [Zhao et al. 2023], GATA3 [Nie et al. 2025], PADI1 [Ning et al. 2025], ANKRD37 [Tan et al. 2022], PHYHIP [Aisagbonhi et al. 2023], COL17A1 [Knyazev et al. 2026], TET3 [Deng et al. 2025], SIGLEC6 [Kaitu'u-Lino et al. 2025], PPP1R3G [Shi et al. 2024], AFAP1 [Zhang et al. 2021], SH3PXD2A [Chen et al. 2020], KIF17 [Sati et al. 2009], HMGN3 [Bian et al. 2022], GALNT2 [Cui et al. 2017], MLX (MAX dimerization protein MLX) [Li et al. 2025], GLRX (glutaredoxin) [Murdoch et al. 2014], AP2A1 [Manley et al. 2020], ADAMTS4 [Namlı Kalem et al. 2018] and NECTIN4 [Yoshizawa et al. 2023] important role in the development of preeclampsia. CX3CR1 [Parveen et al. 2011], FMO1 [Zhang and Cashman, 2006], SLAMF1 [Degos et al. 2020], VCAM1 [Prados et al. 2011], CTLA4 [Wang et al. 2021], C3 [Shahgald et al. 2022], IL7 [Vilsmaier et al. 2021], ENPP1 [Noor et al. 2024], COLEC10 [Mohammadi et al. 2021], KCNJ5 [Xekouki et al. 2012], FLT1

[Chang et al. 2023], NDRG1 [Meng et al. 2019], GPER1 [Tang et al. 2017], INHA (inhibin subunit alpha) [Ko et al. 2023], CRH (corticotropin releasing hormone) [Madhappan et al. 2003], GATA1 [Xu et al. 2024], PAPPA2 [Wagner and Christians, 2010], PROCR (protein C receptor) [Dendana et al. 2012] and VEGFA (vascular endothelial growth factor A) [Ozden Tokalioglu et al. 2023] have an important role in spontaneous abortion. CXCL14 [Umbaugh et al. 2024], CX3CR1 [Zhang et al. 2020], RSPO2 [Aithabathula et al. 2025], FMO1 [Shi et al. 2022], SLAMF1 [Gomez-Torres et al. 2022], VCAM1 [Fasolato et al. 2024], C3 [Ye et al. 2025], CES1 [Chen et al. 2021], FGF12 [Li et al. 2023], SELE (selectin E) [Zhang et al. 2026], TREM1 [Borjas et al. 2022], FLT1 [Mahasreshti et al. 2003], CRLF1 [Stefanovic et al. 2012], ENG (endoglin) [Alsamman et al. 2018], HCAR2 [Jadeja et al. 2019], ERRFI1 [Luo et al. 2025], MAOB (monoamine oxidase B) [Rao et al. 1993], GAPDH (glyceraldehyde-3-phosphate dehydrogenase) [Shibuya et al. 2002], SMOX (spermine oxidase) [Hu et al. 2024] and GREM2 [Shen et al. 2023] might act as potential biomarkers for the prognosis of hepatic complications. CXCL14 [Zheng et al. 2025], CX3CR1 [Iwahashi et al. 2025], RSPO2 [Singla et al. 2021], DKK2 [Wang et al. 2025], VCAM1 [Singh et al. 2023], CTLA4 [Huang et al. 2025], C3 [Garcia-Arguinzonis et al. 2021], SCN4B [Yang et al. 2019], HAPLN1 [Yan et al. 2024], CES1 [Zhu et al. 2022], TREM1 [Vandestienne et al. 2023], BEX1 [Accornero et al. 2017], FLT1 [Berardi et al. 2022], BHLHE40 [Xu et al. 2023], NDRG1 [Etuze et al. 2025], CRLF1 [Luo et al. 2023], PFKP (phosphofructokinase, platelet) [Su et al. 2026], PTGS2 [An et al. 2025], ENG (endoglin) [Vicen et al. 2021] and MFSD2B [Polzin et al. 2023] contributing to the progression of cardiovascular complications. CXCL14 [Lee et al. 2017], CX3CR1 [Zhu et al. 2026], DKK2 [Shi et al. 2025], EPHA7 [He et al. 2025], VCAM1 [Zhang et al. 2024], C3 [Wei et al. 2020], HAPLN1 [Yang et al. 2024], NCAM1 [Yu et al. 2026], SELE (selectin E) [Wang et al. 2025], IL7 [Szot et al. 2017], TREM1 [Zhang et al. 2025], BEX1 [Khazaei et al. 2010], FLT1 [Krum et al. 2008], BHLHE40 [Sun et al. 2022], PTGS2 [Xiao et al. 2019], ENG (endoglin) [Shen et al. 2014], GPER1 [Xue et al. 2025], CRH (corticotropin releasing hormone) [Roe et al. 1998], SASH1 [Huang et al. 2026] and MAOB (monoamine oxidase B) [Fowler et al. 1999] might be a therapeutic potential biomarkers in brain injury. CXCL14 [Chen et al. 2022], CX3CR1 [Pan et al. 2025], VCAM1 [Şahin et al. 2025], CTLA4 [Quaak et al. 2024], C3 [Wei et al. 2021], SCN4B [Sheilabi et al. 2020], GABRB1 [Monfrini et al. 2023], FGF12

[Pierret et al. 2025], NCAM1 [Kong et al. 2016], CAMK2A [Lintas et al. 2023], NTRK2 [Long et al. 2022], PTGS2 [Yi et al. 2023], GPER1 [Zuo et al. 2020], L1CAM [Li et al. 2025], CRH (corticotropin releasing hormone) [Combi et al. 2005], TENM4 [Suzuki et al. 2025], GAPDH (glyceraldehyde-3-phosphate dehydrogenase) [Zhang et al. 2022], SMOX (spermine oxidase) [Marcoli et al. 2022], SLC38A3 [Alawbathani et al. 2023] and VEGFA (vascular endothelial growth factor A) [Castañeda-Cabral et al. 2019] might play essential roles in the epilepsy. CX3CR1 [Chamera et al. 2024], RSPO2 [Lee et al. 2025], FMO1 [Söderberg et al. 2013], SCN11A [Xu et al. 2024], VCAM1 [Meixensberger et al. 2021], CTLA4 [Fayedeh et al. 2024], C3 [Cao et al. 2024], FAT3 [Okajima et al. 2020], CES1 [Hernandez et al. 2022], FGF12 [Seiffert et al. 2022], TREM1 [Fu et al. 2023], NTRK2 [Camarena et al. 2025], IL1R1 [Luís et al. 2022], ARNT2 [Choi et al. 2024], PTGS2 [Bialek et al. 2020], GNG4 [Bai et al. 2024], GPER1 [Carlson, 2026], L1CAM [Fries et al. 2025], CRH (corticotropin releasing hormone) [Kritas et al. 2014] and TENM4 [Yi et al. 2021] played a fundamental role in neuropsychiatric disorders. CX3CR1 [Szukiewicz et al. 2018], VCAM1 [Oğlak et al. 2025], FRZB (frizzled related protein) [Guan et al. 2021], NCAM1 [Mostafaee et al. 2024], RARRES2 [Huang et al. 2016], SELE (selectin E) [Zhang et al. 2022], IL7 [Keckstein et al. 2020], GH1 [Cui et al. 2025], ENPP1 [Tarquini et al. 2015], CYP24A1 [Milan et al. 2024], FLT1 [Nuzzo et al. 2021], BHLHE40 [Zhao et al. 2021], CRLF1 [Hakan et al. 2012], GPIHBP1 [Watanabe et al. 2025], ENG (endoglin) [Nergiz Avcıoğlu et al. 2022], GPER1 [Guven et al. 2021], SH3BP5 [He and Wu, 2026], VEGFA (vascular endothelial growth factor A) [Zheng et al. 2022], HTRA1 [Tossetta et al. 2022] and GPX3 [Abirami et al. 2025] were thought to play an important role in gestational diabetes mellitus. Altered expression of CX3CR1 [Wang et al. 2021], RSPO2 [Wang et al. 2025], DKK2 [Zhang et al. 2009], ALDH1A [Draskau et al. 2025], VCAM1 [Daniel et al, 1999], CTLA4 [Mikuš et al. 2022], C3 [Bartosik et al. 1987], GABRB1 [Anstee et al. 2013], SELE (selectin E) [Siristatidis et al. 2015], IL7 [Bellelis et al. 2019], TREM1 [Haller-Kikkatalo et al. 2012], NTRK2 [Dorfman et al. 2014], FLT1 [Mrozikiewicz et al. 2024], NDRG1 [Nishigaki et al. 2022], PTGS2 [da Luz et al. 2017], ENG (endoglin) [Chen et al. 2024], INHA (inhibin subunit alpha) [Huhtaniemi, 2022], GATA1 [Bennett-Toomey and Stocco, 2018], GREM2 [Nilsson et al. 2014] and NR5A2 [Morin et al. 2025] were associated with prognosis of patients with infertility. CXCL14 [Wang et al. 2025], RSPO2 [Zhou et al. 2021], EPHA7 [Li et al. 2018], VCAM1 [Candelaria and Richards, 2024], CTLA4 [Khaleel and Alsaffar, 2026], C3 [Abdul-Ameer et al. 2024], GH1 [Gong et al. 2020], ENPP1 [Baba et al. 2007], ENPP2 [Zhang et al. 2024], COL14A1 [Pei et al. 2026], PTGS2 [Liu et al. 2026], ENG (endoglin) [Tal et al. 2013], GPER1 [Zang et al. 2016], CRH (corticotropin releasing hormone) [Zangeneh et al. 2017], GATA1 [Yu et al. 2019], GREM2 [Koroglu et al. 2019], INHBA (inhibin subunit beta A) [Begum and Mohan, 2023], BCL6 [Nikseresht et al. 2024], VEGFA (vascular endothelial growth factor A) [Wei and Zhao, 2020] and ISG15 [Han et al. 2026] are emerging as an important biomarkers in polycystic ovarian syndrome promotion and progression. SSTR1 [Huang et al. 2024], CXCL14 [Cereijo et al. 2021], CX3CR1 [Meyhöfer et al. 2024], RSPO2 [Dong et al. 2022], DKK2 [Deng et al. 2025], ALDH1A1 [Paik et al. 2025], VCAM1 [Yu et al. 2017], CTLA4 [Lindarto et al. 2025], C3 [Al Haj Ahmad et al. 2017], CES1 [Friedrichsen et al. 2013], TREM1 [Subramanian et al. 2017], NTRK2 [Rask-Andersen et al. 2011], FLT1 [Straughen et al. 2013], IL1RL1 [Yu et al. 2020], NDRG1 [Stafeev et al. 2021], ARNT2 [Turer et al. 2018], PFKP (phosphofructokinase, platelet) [Andreasen et al. 2008], GPIHBP1 [Aruga et al. 2017], PTGS2 [Gu et al. 2026] and GPER1 [Son and Im, 2024] have a close relationship with the development and prognosis of obesity. CXCL14 [Chen et al. 2010], CX3CR1 [Li et al. 2024], ALDH1A1 [Yasmeen et al. 2013], SLAMF1 [Vitales-Noyola et al. 2017], VCAM1 [Jublanc et al. 2011], CTLA4 [Hossen et al. 2023], C3 [Szalai et al. 2007], HAPLN1 [Liu et al. 2025], NCAM1 [Jovanova-Nesic et al. 2006], CAMK2A [Sohaei et al. 2023], ADGRG3 [Wang et al. 2018], FLT1 [Yang et al. 2024], IL1RL1 [Ahmadi et al. 2019], BHLHE40 [Tang et al. 2025], ARNT2 [Becquart et al. 2020], GPIHBP1 [Lai et al. 2026], PTGS2 [Martín-Vázquez et al. 2023], ENG (endoglin) [Ma and You, 2025], GPER1 [Zhang et al. 2023] and DERL3 [Geng et al. 2020] plays a critical role in the autoimmune disorders. SSTR1 [Modarai et al. 2016], CXCL14 [Giacobbi et al. 2024], CX3CR1 [Lu et al. 2022], RSPO2 [Srivastava and Srivastava, 2024], FMO1 [Luo et al. 2019], SCN11A [Khan et al. 2025], DKK2 [Shao et al. 2018] CRACD (capping protein inhibiting regulator of actin dynamics) [Kim et al. 2024], EPHA7 [Nikas et al. 2022], ALDH1A1 [Liu et al. 2021], TREM1 [Tang et al. 2025], BEX1 [Wang et al. 2021], NTRK2 [Zhang et al. 2024], FLT1 [Shibuya, 2011], IL1RL1 [Li et al. 2025], KRT14 [Liao et al. 2025], BTNL9 [Mo et al. 2021], ADAM2 [Maheswaran et al. 2015], BHLHE40 [Sethuraman et al. 2018] and NDRG1 [Zhao and Richardson, 2023] were involved in susceptibility to cancer. CXCL14 [McFadyen and Peter, 2021], CX3CR1 [Burgess et al. 2019], RSPO2 [Li et al. 2020], SCN11A [Ebbinghaus et al. 2020], EPHA7 [Dong et al. 2013], ALDH1A1 [Ito et al. 2014], SLAMF1 [Wang et al. 2015], VCAM1 [Yusuf-Makagiansar et al. 2002], CTLA4 [Tan et al. 2014], C3 [Nadar and Lip, 2007], TREM1 [Li et al. 2019], HTRA4 [Wang et al. 2016], NTRK2 [Wei et al. 2025], FLT1 [Xu et al. 2019], IL1RL1 [Yu et al. 2020], BHLHE40 [Zafar et al. 2021], NDRG1 [Etuze et al. 2025], CRLF1 [Yang et al. 2025] and ENG (endoglin) [Meurer and Weiskirchen, 2020] have been reported to play various roles in the pathogenesis or development of inflammation. Previous studies showed CX3CR1 [Yi et al. 2025], ALDH1A1 [Calleja et al. 2021], VCAM1 [Dong et al. 2011], CTLA4 [Jin et al. 2023], C3 [Konopko et al. 2025], CES1 [Luo et al. 2023], FGF12 [Liu et al. 2022], NCAM1 [Zhang et al. 2019], SELE (selectin E) [Zhang et al. 2023], IL7 [Xiao et al. 2023], TREM1 [Zhong et al. 2025], FLT1 [Li et al. 2005], BHLHE40 [Feng et al. 2021], NDRG1 [Malarz et al. 2025], PFKP (phosphofructokinase, platelet) [Wang et al. 2022], GPIHBP1 [Fan et al. 2023], PTGS2 [Yang et al. 2025], ENG (endoglin) [La Sala et al. 2015], GPER1 [Kozieł-Leszczyńska et al. 2025] and SH3BP5 [He and Wu, 2026] plays an important role in the progression of oxidative stress. A previous study showed that CXCL14 [Xue et al. 2026], CTLA4 [Amin et al. 2019], C3 [Hess et al. 2012], SELE (selectin E) [Roldán et al. 2003], GH1 [Cañete et al. 2012], ENPP1 [Lopez et al. 2023], COLEC10 [Bayarri-Olmos et al. 2015], SLC16A10 [Wang et al. 2025], MEGF10 [Richardson et al. 2025], OSR1 [Talati et al. 2010], NDRG1 [Zhang et al. 2023], MFSD2B [Chandrakanthan et al. 2021], GAPDH (glyceraldehyde-3-phosphate dehydrogenase) [Pirovich et al. 2020], PROCR (protein C receptor) [Sung et al. 2014], BIN2 [Volz et al. 2020], DUSP1 [Flores et al. 2023], GPX3 [Jin et al. 1973], HMOX1 [Mustafa et al. 2008], and ANG (angiogenin) [Cucci et al. 2021] are involved in the blood clotting. As a result of these investigations, enriched genes have been implicated as a critical pathogenic factor in preeclampsia and its associated complications. Novel biomarkers for preeclampsia are listed in Table 7.

Through subsequent screening, hub genes are screened out by PPI analysis of DEGs in preeclampsia. VCAM1 [Liu et al. 2021] plays a essential role in endothelial dysfunction and inflammation during preeclampsia pathogenesis. Genome-wide investigation linked PLEKHA7 variants with blood pressure control and hypertension, potentially exacerbating preeclampsia via endothelial dysfunction [Gray et al. 2018]. SPRED1 acts as a negative controller of the RAS/MAPK signaling pathway, and its dysregulation via microRNA-126 leads to impaired angiogenesis in preeclampsia pathogenesis [Hong et al. 2014]. EPHA7 controls cell repulsion, migration, and angiogenesis through Eph/ephrin forward and reverse signaling, potentially disrupting trophoblast invasion and placental vascular remodeling in preeclampsia pathogenesis [Chen and Zheng, 2014]. GABARAPL2 essential for autophagosome formation, lipid droplet degradation, and cellular homeostasis, with emerging links to preeclampsia via placental metabolic and autophagic dysregulation [Pei et al. 2022]. RPL13 emerging evidence suggesting its dysregulation contributes to translational stress and placental dysfunction in preeclampsia pathogenesis [Jacob et al. 2023]. PDK1 serves as a key metabolic regulator that inhibits pyruvate dehydrogenase, promoting glycolysis over oxidative phosphorylation, and its downregulation in preeclampsia leads to decidualization defects and placental metabolic dysfunction [Liu et al. 2026]. EPHA5 promote contact-dependent repulsion between trophoblasts and decidual cells, fine-tuning invasion depth during placentation; dysregulation could lead to shallow spiral artery remodeling and placental ischemia, a preeclampsia hallmark [Buensuceso and Deroo, 2013]. EPHA3 is a tyrosine kinase receptor that mediates repulsive signaling with ephrin-A ligands to control cell positioning, migration, and angiogenesis, with indirect evidence suggesting involvement in preeclampsia via disrupted trophoblast invasion and vascular remodeling [Goldman-Wohl et al. 2004]. PRDX6 is a bifunctional enzyme with glutathione peroxidase and phospholipase A2 activities that scavenges hydrogen peroxide and regulates phospholipid metabolism to combat oxidative stress, with downregulation implicated in preeclampsia pathogenesis through placental ROS accumulation [Li et al. 2010]. GAPDH is a glycolytic enzyme associated in apoptosis, gene regulation, and oxidative stress responses, with altered placental expression contributing to preeclampsia pathogenesis through metabolic and cellular stress pathways [Cale et al. 1997]. RPL12 is essential for protein translation and ribosome assembly, with potential involvement in preeclampsia through disrupted placental protein synthesis and cellular stress responses [Winn et al. 2007]. No evidence directly linking hub genes such as PTPN3, H1-4 and GPR17 to preeclampsia progression. The results suggest that hub genes might affect the disease progression of preeclampsia through the above processes.

The miRNA-hub gene regulatory network, TF-hub gene regulatory network regulatory mechanism also plays a crucial role in the regulation of preeclampsia onset and progression. Hsa-miR-133a-3p [Guo et al. 2021], hsa-miR-17-5p [Ng et al. 2024], hsa-miR-375 [Pillay et al. 2019] and BMI1 [Li et al. 2017] biomarkers were significantly associated with preeclampsia. These findings suggest that hsa-miR-6731-5p, hsa-miR-500b-5p, hsa-miR-379-3p, hsa-miR-6835-3p, hsa-miR-141-5p, UTX, CREM, TAL1, GATA4, MAF, PHF8, EWSR1 and HOXB4 might serve as novel valuable biomarkers for preeclampsia.

The drug-hub gene interaction network analysis identified several potential therapeutic compounds, such as Acteoside, S-Hexylglutathione, Encorafenib, Palovarotene, S-Hydroxycysteine, Ephedra sinica root, Methyclothiazide, Selpercatinib, Seocalcitol and 5-fluorotryptophan, which might target these senescence-related genes, offering promising candidates for future preeclampsia treatment strategies.

ROC curve results showed that when the hub genes were used as independent diagnostic indicators, they were all of diagnostic value for preeclampsia.

In summary, the present study is intended to screen out DEGs that might be associated with preeclampsia and attempts to explore the possible molecular mechanism of the occurrence and progression in preeclampsia. These findings significantly improve the understanding of the cause and underlying molecular events in preeclampsia, and the candidate genes and signaling pathways could be used as therapeutic targets. However, further studies are necessary to clarify the biological function of these biomarkers in the pathogenesis of preeclampsia.

Declarations

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Conflict of interest

The authors declare that they have no conflict of interest.

Ethical approval

Not applicable

Consent to participate

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Written Consent for publication

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Clinical trial number

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Availability of data and materials

The datasets supporting the conclusions of this article are available in the GEO (Gene Expression Omnibus) (https://www.ncbi.nlm.nih.gov/geo/) repository. [(GSE303463) https://www.ncbi.nlm.nih.gov/geo/query/acc.cgi?acc= GSE303463]

Code availability

Not applicable

Author Contributions

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

S.P. - Formal analysis and validation

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Figures

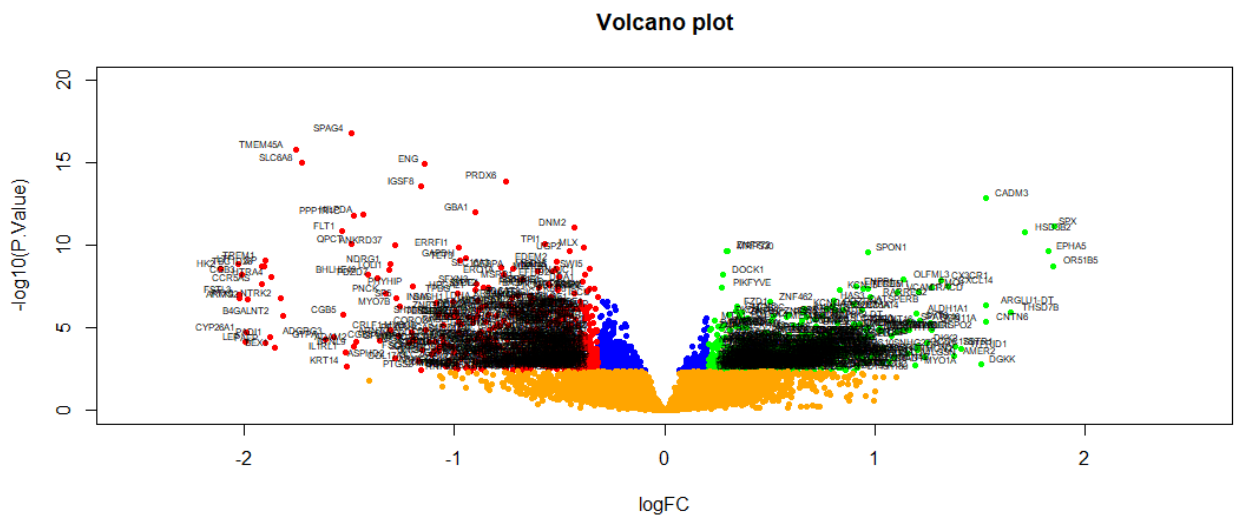


Fig. 1. Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected. Green dot represented up regulated significant genes and red dot represented down regulated significant genes.

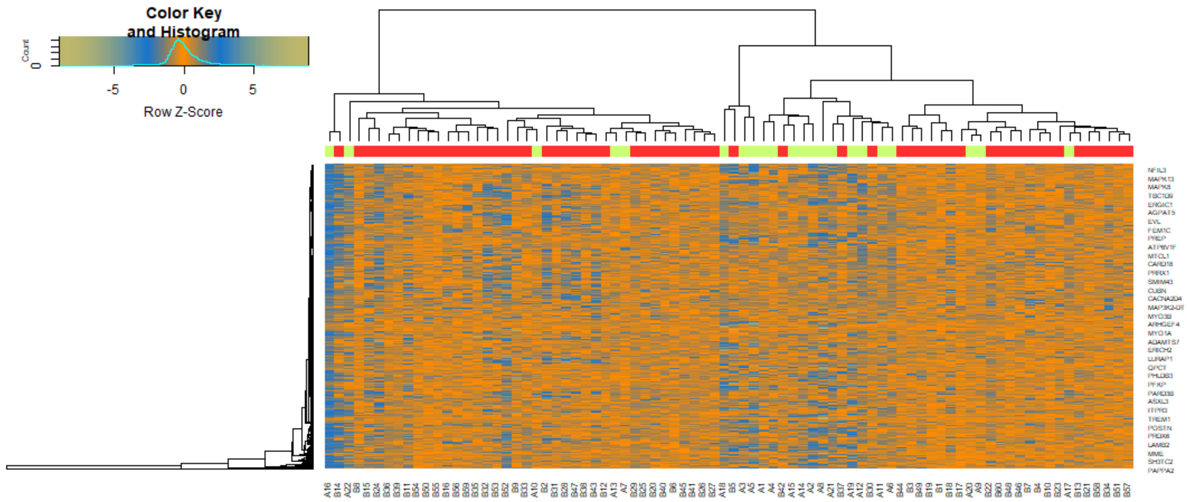
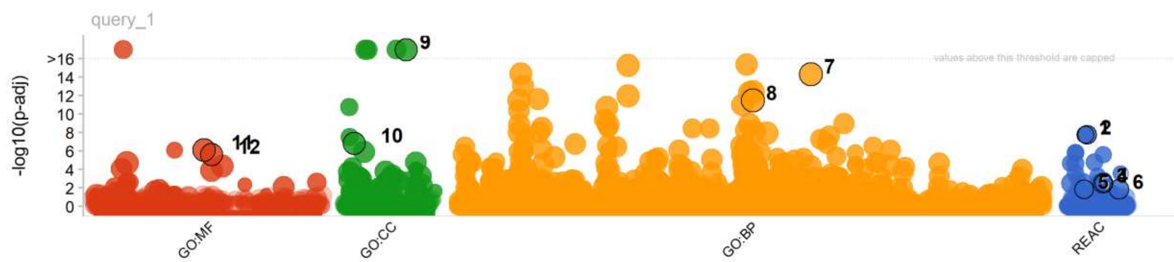


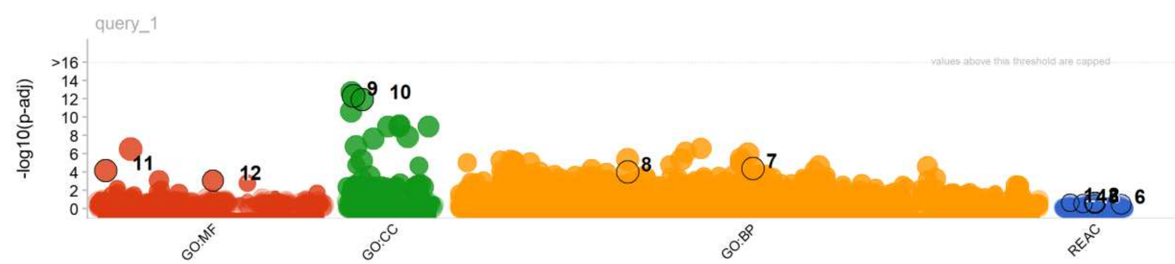
Fig. 2. Heat map of differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1 – A 22 = Preeclampsia; B1 – B 60 = Normal control)



id	source	term_id	term_name	term_size		p_value
1	REAC	REAC:R-HSA-3000178	ECM proteoglycans	76		1.8e-08
2	REAC	REAC:R-HSA-1474244	Extracellular matrix organization	298		1.8e-08
3	REAC	REAC:R-HSA-9675108	Nervous system development	568		2.9e-03
4	REAC	REAC:R-HSA-5173105	O-linked glycosylation	108		2.9e-03
5	REAC	REAC:R-HSA-5668914	Diseases of metabolism	246		1.4e-02
6	REAC	REAC:R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	516		1.4e-02
7	GO:BP	GO:0065007	biological regulation	12743		4.4e-15
8	GO:BP	GO:0050794	regulation of cellular process	11946		3.3e-12
9	GO:CC	GO:0071944	cell periphery	6347		1.6e-18
10	GO:CC	GO:0005886	plasma membrane	5866		1.4e-07
11	GO:MF	GO:0036094	small molecule binding	6577		7.8e-07
12	GO:MF	GO:0043167	ion binding	6377		2.3e-06

g:Profiler (biit.cs.ut.ee/gprofiler)

Fig. 3. GO and REACTOME pathway enrichment analysis for up regulated genes. $p < 0.05$. Abbreviations: BP, biological process; CC, cell component; MF, molecular function. GO, Gene Ontology; REAC, REACTOME. The size of the circle represents the number of genes involved, and the abscissa represents the frequency of the genes involved in the term total genes.



id	source	term_id	term_name	term_size		p_value
1	REAC	REAC:R-HSA-1500931	Cell-Cell communication	150		2.1e-01
2	REAC	REAC:R-HSA-556833	Metabolism of lipids	747		2.1e-01
3	REAC	REAC:R-HSA-1430728	Metabolism	2100		2.1e-01
4	REAC	REAC:R-HSA-1474244	Extracellular matrix organization	298		2.9e-01
5	REAC	REAC:R-HSA-71387	Metabolism of carbohydrates and carbohydrate derivatives	279		2.9e-01
6	REAC	REAC:R-HSA-382551	Transport of small molecules	729		3.4e-01
7	GO:BP	GO:0050896	response to stimulus	8999		4.1e-05
8	GO:BP	GO:0032501	multicellular organismal process	7322		9.7e-05
9	GO:CC	GO:0005737	cytoplasm	12527		4.7e-13
10	GO:CC	GO:0016020	membrane	9953		1.1e-12
11	GO:MF	GO:0003824	catalytic activity	6817		7.0e-05
12	GO:MF	GO:0042802	identical protein binding	2182		8.1e-04

g:Profiler (biit.cs.ut.ee/gprofiler)

Fig. 4. GO and REACTOME pathway enrichment analysis for down regulated genes. $p < 0.05$. Abbreviations: BP, biological process; CC, cell component; MF, molecular function. GO, Gene

Ontology; REAC, REACTOME. The size of the circle represents the number of genes involved, and the abscissa represents the frequency of the genes involved in the term total genes.

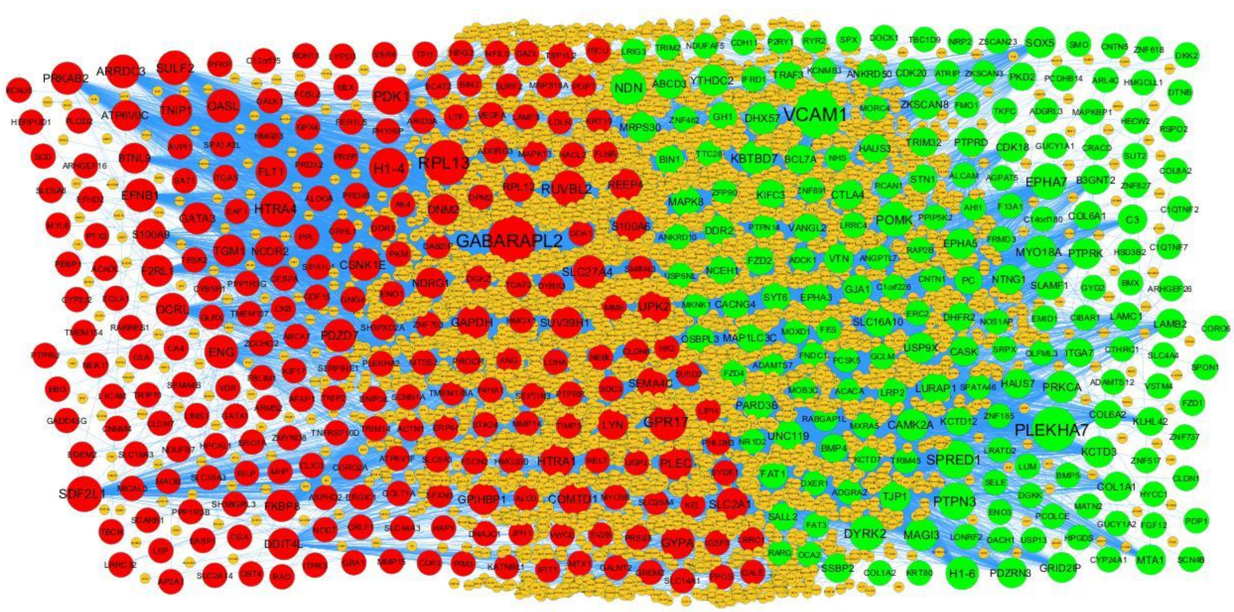


Fig. 5. PPI network of DEGs. Up regulated genes are marked in parrot green; down regulated genes are marked in orange.

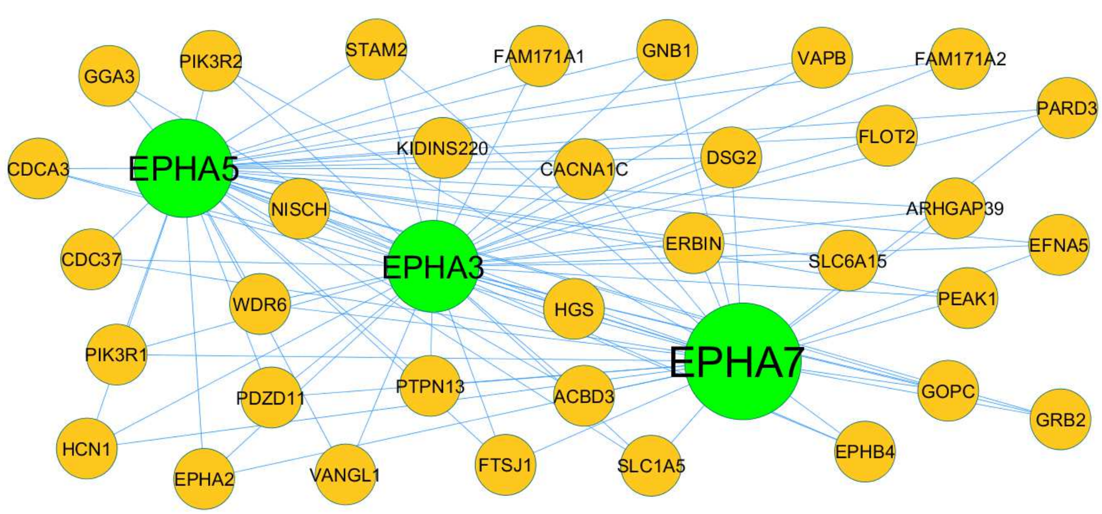
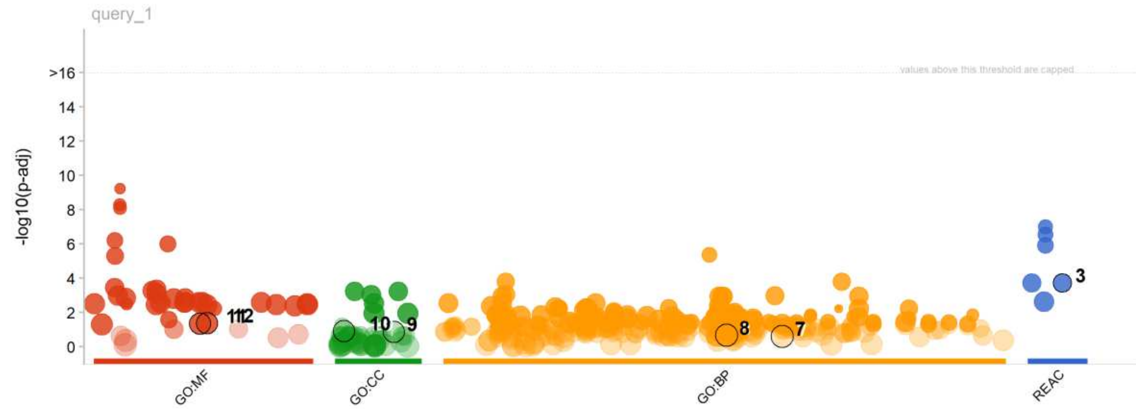


Fig. 6. Modules 1 was isolated form PPI of up regulated genes. Module 1 has 37 nodes and 96edges for up regulated genes. Up regulated genes are marked in green



id	source	term_id	term_name	term_size		p_value
3	REAC	REAC:R-HSA-9675108	Nervous system development	568		1.9e-04
7	GO:BP	GO:0065007	biological regulation	12743		2.5e-01
8	GO:BP	GO:0050794	regulation of cellular process	11946		2.1e-01
9	GO:CC	GO:0071944	cell periphery	6347		1.3e-01
10	GO:CC	GO:0005886	plasma membrane	5866		1.2e-01
11	GO:MF	GO:0036094	small molecule binding	6577		4.5e-02
12	GO:MF	GO:0043167	ion binding	6377		4.2e-02

g:Profiler (biit.cs.ut.ee/gprofiler)

Fig. 7. Enrichment analysis for module 1. The size of the circle represents the number of genes involved, and the abscissa represents the frequency of the genes involved in the term total genes.

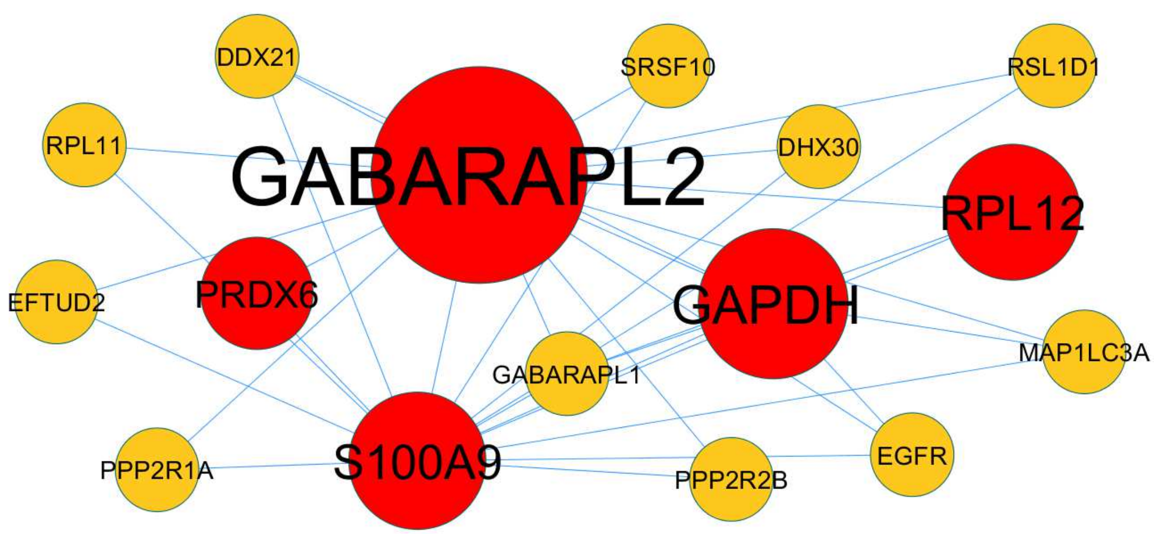
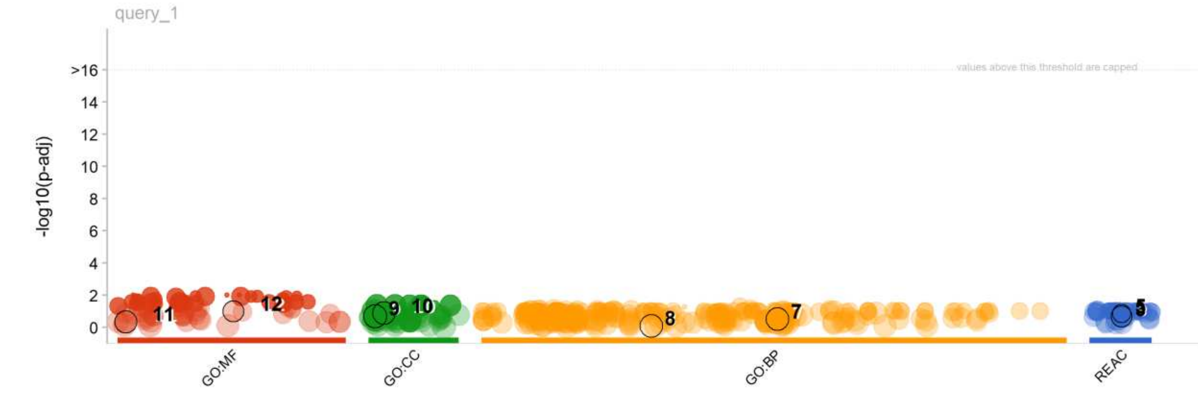


Fig. 8. Module 2 was isolated form PPI of up regulated genes. Module 2 has 16 nodes and 34 edges for down regulated genes. Down regulated genes are marked in red



id	source	term_id	term_name	term_size		p_value
3	REAC	REAC:R-HSA-1430728	Metabolism	2100		2.2e-01
5	REAC	REAC:R-HSA-71387	Metabolism of carbohydrates and carbohydrate derivatives	279		1.4e-01
7	GO:BP	GO:0050896	response to stimulus	8999		3.1e-01
8	GO:BP	GO:0032501	multicellular organismal process	7322		8.3e-01
9	GO:CC	GO:0005737	cytoplasm	12527		2.0e-01
10	GO:CC	GO:0016020	membrane	9953		1.4e-01
11	GO:MF	GO:0003824	catalytic activity	6817		4.5e-01
12	GO:MF	GO:0042802	identical protein binding	2182		1.0e-01

g:Profiler (biit.cs.ut.ee/gprofiler)

Fig. 9. Enrichment analysis for module 2. The size of the circle represents the number of genes involved, and the abscissa represents the frequency of the genes involved in the term total genes.

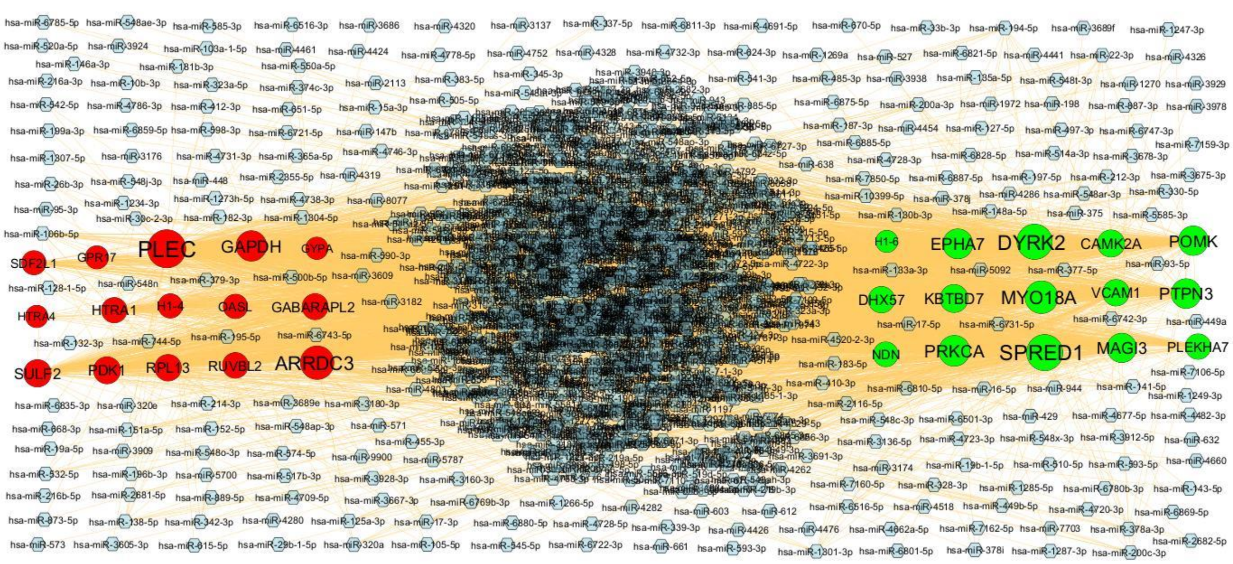
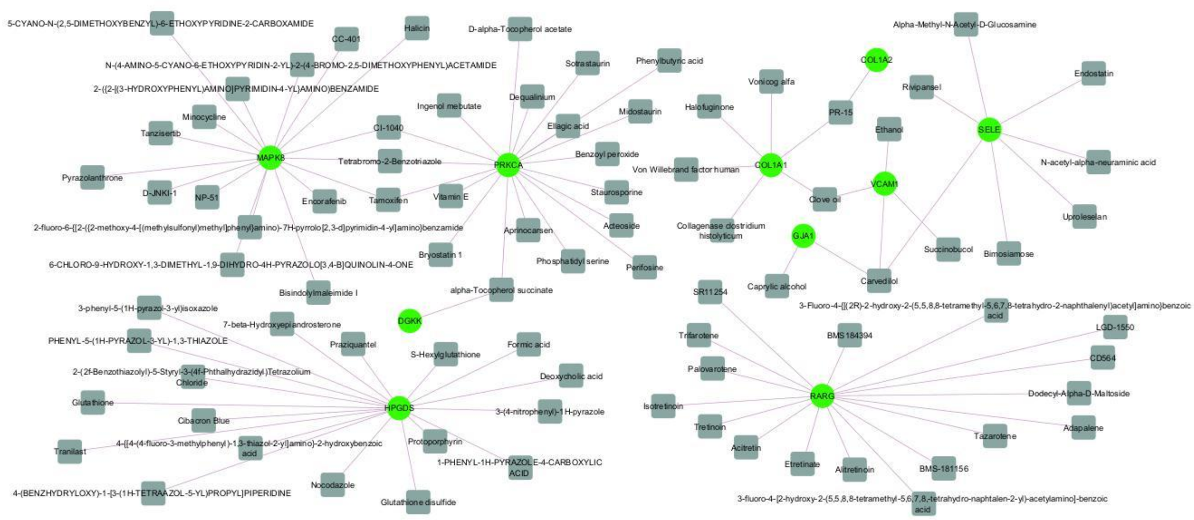


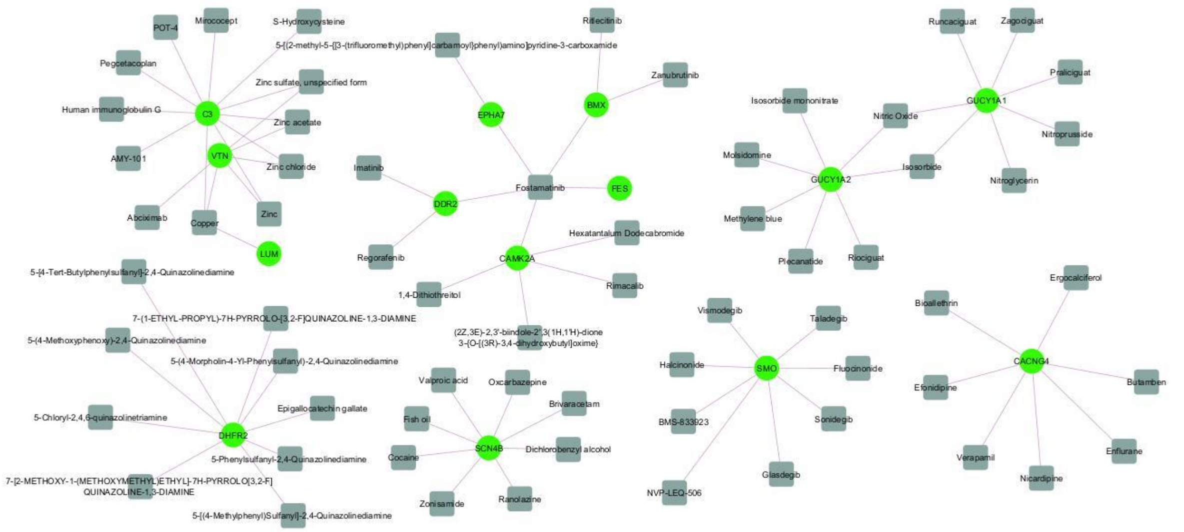
Fig. 10. Hub gene - miRNA regulatory network. The blue color diamond nodes represent the key miRNAs; up regulated genes are marked in green; down regulated genes are marked in red.

Fig. 11. Hub gene - TF regulatory network. The pink color triangle nodes represent the key TFs; up regulated genes are marked in green; down regulated genes are marked in red.

A



B



C

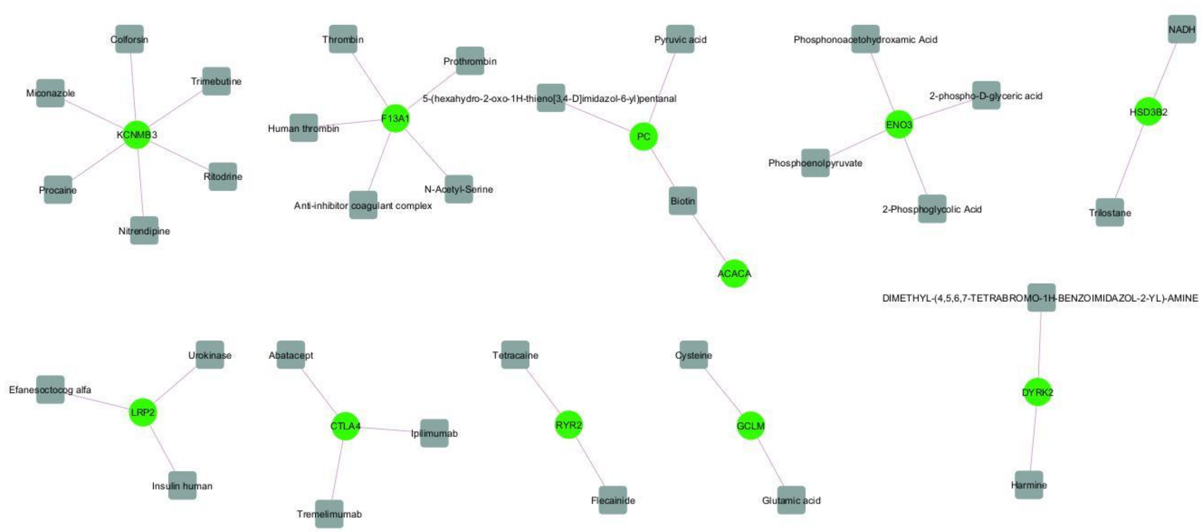
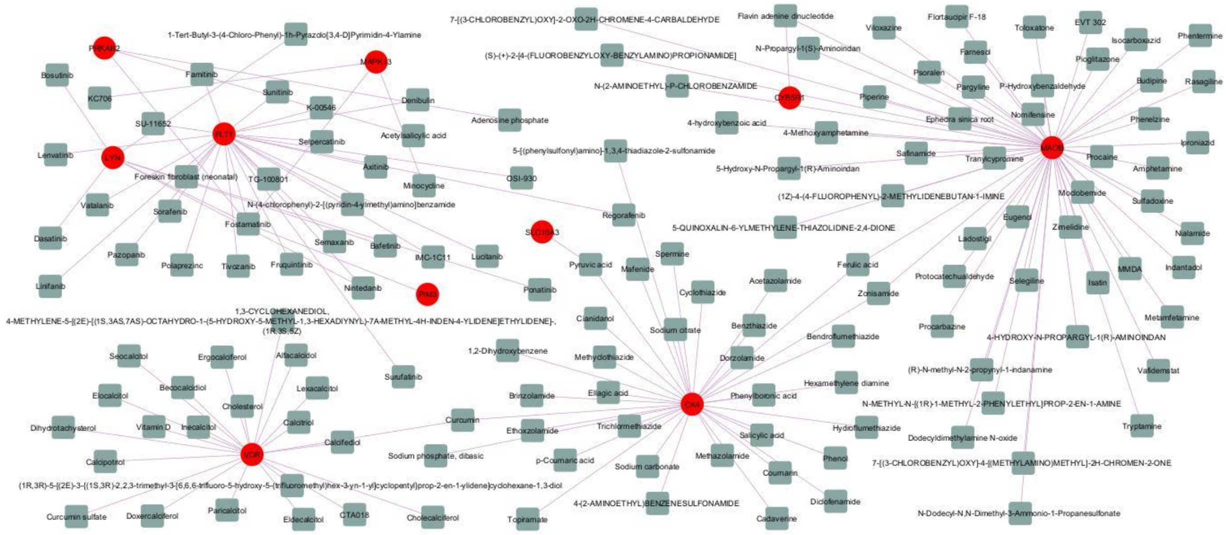


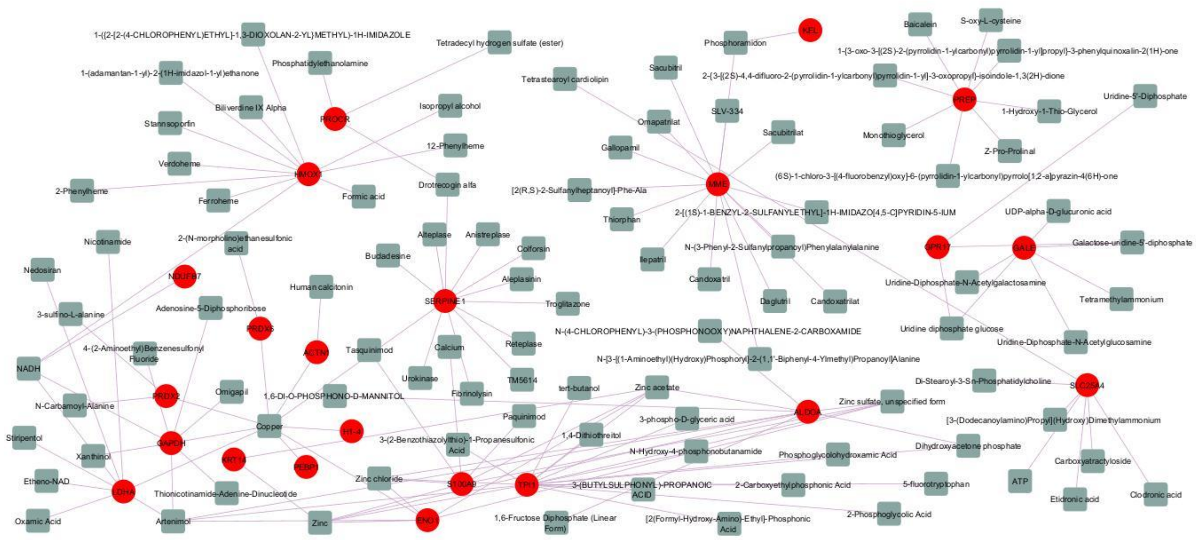
Fig. 12. Three drug-hub gene interaction networks include 1) Network A 2) Network B 3) Network C. The ash color rectangle nodes represent the drug molecule; up regulated genes are marked in green.

A



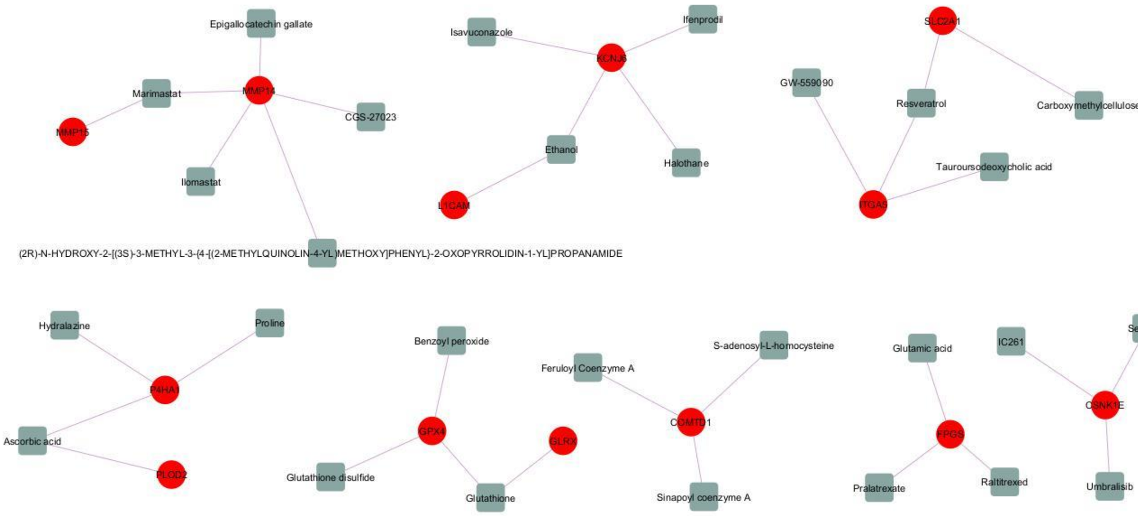
1-Tert-Butyl-3-(4-Chloro-Phenyl)-1h-Pyrazolo[3,4-D]Pyrimidin-4-Ylamine
Bosutinib
KC706
Famitinib
Sunitinib
K-00546
Denibulin
Adenosine phosphate
SU-11652
Lenvatinib
Selpercatinib
Acetylsalicylic acid
Axitinib
OSI-930
Foreskin fibroblast (neonatal)
TG-100801
Minocycline
Vatalanib
Sorafenib
N-(4-chlorophenyl)-2-[(pyridin-4-ylmethyl)amino]benzamide
Dasatinib
Fostamatinib
Semaxanib
Rafetinib
IMC-1C11
Lucitanib
Pazopanib
Polaprezinc
Tivozanib
Fruquintinib
Nintedanib
Ponatinib
Linifanib
Surufatinib
7-[(3-CHLOROBENZYL)OXY]-2-OXO-2H-CHROMENE-4-CARBALDEHYDE
(S)-(+)-2-[4-(FLUOROBENZYLOXY-BENZYLAMINO)PROPIONAMIDE]
N-(2-AMINOETHYL)-P-CHLOROBENZAMIDE
Flavin adenine dinucleotide
N-Propargyl-1(S)-Aminoindan
4-hydroxybenzoic acid
4-Methoxyamphetamine
5-[(phenylsulfonyl)amino]-1,3,4-thiadiazole-2-sulfonamide
5-Hydroxy-N-Propargyl-1(R)-Aminoindan
(1Z)-4-(4-FLUOROPHENYL)-2-METHYLIDENEBUTAN-1-IMINE
5-QUINOXALIN-6-YLMETHYLENE-THIAZOLIDINE-2,4-DIONE
Regorafenib
Viloxazine
Flortaucipir F-18
Toloxatone
EVT 302
Isocarboxazid
Phentermine
Farnesol
Pioglitazone
Psoralen
Pargyline
P-Hydroxybenzaldehyde
Budipine
Rasagiline
Piperine
Ephedra sinica root
Nomifensine
Phenelzine
Iproniazid
Safinamide
Tranylcypromine
Procaine
Amphetamine
Moclobemide
Sulfadoxine
Eugenol
Zimelidine
Nialamide
Ladostigil
Indantadol
Protocatechualdehyde
Selegiline
Isatin
MMDA
Metamfetamine
Procarbazine
4-HYDROXY-N-PROPARGYL-1(R)-AMINOINDAN
(R)-N-methyl-N-2-propynyl-1-indanamine
Vafidemstat
N-METHYL-N-[(1R)-1-METHYL-2-PHENYLETHYL]PROP-2-EN-1-AMINE
Tryptamine
Dodecyldimethylamine N-oxide
7-[(3-CHLOROBENZYL)OXY]-4-[(METHYLAMINO)METHYL]-2H-CHROMEN-2-ONE
N-Dodecyl-N,N-Dimethyl-3-Ammonio-1-Propanesulfonate
Pyruvic acid
Mafenide
Spermine
Ferulic acid
Acetazolamide
Zonisamide
Cyclothiazide
Cianidanol
Benzthiazide
Sodium citrate
Bendroflumethiazide
1,2-Dihydroxybenzene
Dorzolamide
Methyclothiazide
Hexamethylene diamine
Phenylboronic acid
Brinzolamide
Ellagic acid
Hydroflumethiazide
Curcumin
Ethoxzolamide
Trichlormethiazide
Salicylic acid
Sodium phosphate, dibasic
p-Coumaric acid
Methazolamide
Phenol
Sodium carbonate
Coumarin
4-(2-AMINOETHYL)BENZENESULFONAMIDE
Diclofenamide
Topiramate
Cadaverine
1,3-CYCLOHEXANEDIOL,
4-METHYLENE-5-[(2E)-[(1S,3AS,7AS)-OCTAHYDRO-1-(5-HYDROXY-5-METHYL-1,3-HEXADIYNYL)-7A-METHYL-4H-INDEN-4-YLIDENE]ETHYLIDENE]-,
(1R,3S,5Z)
Seocalcitol
Ergocalciferol
Alfacalcidol
Becocalcidiol
Lexacalcitol
Cholesterol
Elocalcitol
Calcitriol
Dihydrotachysterol
Vitamin D
Inecalcitol
Calcifediol
Calcipotriol
(1R,3R)-5-[(2E)-3-[(1S,3R)-2,2,3-trimethyl-3-[6,6,6-trifluoro-5-hydroxy-5-(trifluoromethyl)hex-3-yn-1-yl]cyclopentyl]prop-2-en-1-ylidene]cyclohexane-1,3-diol
Curcumin sulfate
Doxercalciferol
Paricalcitol
Eldecalcitol
CTA018
Cholecalciferol

B



1-({2-[2-(4-CHLOROPHENYL)ETHYL]-1,3-DIOXOLAN-2-YL}METHYL)-1H-IMIDAZOLE
Tetradecyl hydrogen sulfate (ester)
Phosphatidylethanolamine
1-(adamantan-1-yl)-2-(1H-imidazol-1-yl)ethanone
Biliverdine IX Alpha
Isopropyl alcohol
Stannsoporfin
12-Phenylheme
Verdoheme
Drotrecogin alfa
2-Phenylheme
Ferroheme
Formic acid
Nicotinamide
2-(N-morpholino)ethanesulfonic acid
Nedosiran
Alteplase
Anistreplase
Bucladesine
Colforsin
Human calcitonin
Aleplasinin
3-sulfino-L-alanine
Adenosine-5-Diphosphoribose
Troglitazone
4-(2-Aminoethyl)Benzenesulfonyl Fluoride
Tasquinimod
Calcium
Reteplase
NADH
Urokinase
TM5614
Omigapil
Fibrinolysin
N-Carbamoyl-Alanine
1,6-DI-O-PHOSPHONO-D-MANNITOL
Copper
Stiripentol
Xanthinol
3-(2-Benzothiazolylthio)-1-Propanesulfonic Acid
Etheno-NAD
Thionicotinamide-Adenine-Dinucleotide
Zinc chloride
Oxamic Acid
Artenimol
Zinc
Phosphoramidon
Sacubitril
2-{3-[(2S)-4,4-difluoro-2-(pyrrolidin-1-ylcarbonyl)pyrrolidin-1-yl]-3-oxopropyl}-isoindole-1,3(2H)-dione
Tetrastearoyl cardiolipin
SLV-334
Omapatrilat
Sacubitrilat
Gallopamil
[2(R,S)-2-Sulfanylheptanoyl]-Phe-Ala
Thiorphan
2-[(1S)-1-BENZYL-2-SULFANYLETHYL]-1H-IMIDAZO[4,5-C]PYRIDIN-5-IUM
N-(3-Phenyl-2-Sulfanylpropanoyl)Phenylalanylalanine
Ilepatril
Candoxatril
Daglutril
Candoxatrilat
N-(4-CHLOROPHENYL)-3-(PHOSPHONOOXY)NAPHTHALENE-2-CARBOXAMIDE
N-[3-[(1-Aminoethyl)(Hydroxy)Phosphoryl]-2-(1,1'-Biphenyl-4-Ylmethyl)Propanoyl]Alanine
tert-butanol
Zinc acetate
Paquinimod
3-phospho-D-glyceric acid
1,4-Dithiothreitol
N-Hydroxy-4-phosphonobutanamide
3-(BUTYLSULPHONYL)-PROPANOIC ACID
1,6-Fructose Diphosphate (Linear Form)
[2(Formyl-Hydroxy-Amino)-Ethyl]-Phosphonic Acid
Baicalein
S-oxy-L-cysteine
1-{3-oxo-3-[(2S)-2-(pyrrolidin-1-ylcarbonyl)pyrrolidin-1-yl]propyl}-3-phenylquinoxalin-2(1H)-one
Uridine-5'-Diphosphate
1-Hydroxy-1-Thio-Glycerol
Monothioglycerol
Z-Pro-Prolinal
(6S)-1-chloro-3-[(4-fluorobenzyl)oxy]-6-(pyrrolidin-1-ylcarbonyl)pyrrolo[1,2-a]pyrazin-4(6H)-one
UDP-alpha-D-glucuronic acid
Galactose-uridine-5'-diphosphate
Uridine-Diphosphate-N-Acetylgalactosamine
Tetramethylammonium
Uridine diphosphate glucose
Uridine-Diphosphate-N-Acetylglucosamine
Di-Stearoyl-3-Sn-Phosphatidylcholine
Zinc sulfate, unspecified form
[3-(Dodecanoylamino)Propyl](Hydroxy)Dimethylammonium
Dihydroxyacetone phosphate
Phosphoglycolohydroxamic Acid
Carboxyatractyloside
2-Carboxyethylphosphonic Acid
5-fluorotryptophan
ATP
Etidronic acid
Clodronic acid
2-Phosphoglycolic Acid

C



D

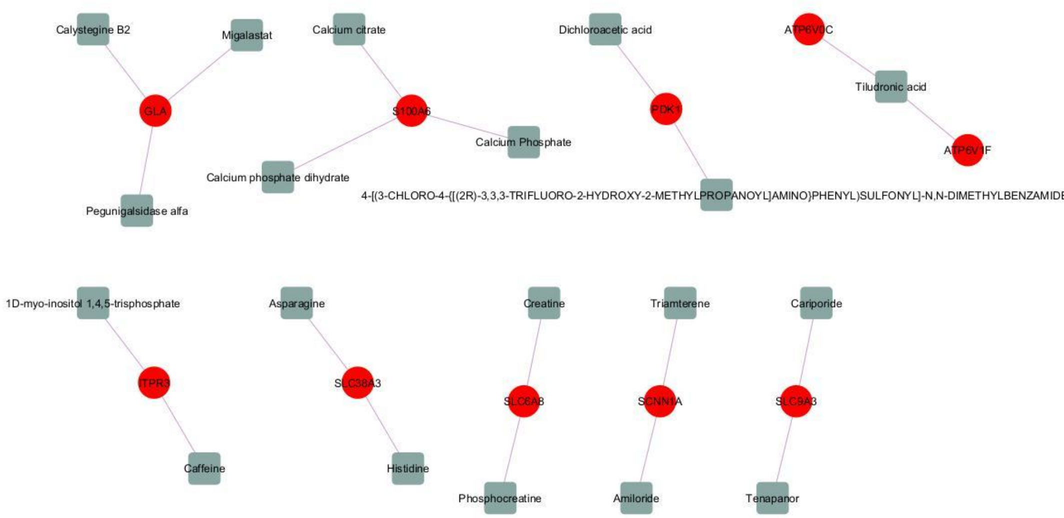


Fig. 13. Four drug-hub gene interaction networks include 1) Network A 2) Network B 3) Network C 4) Network D. The ash rectangle nodes represent the drug molecule; down regulated genes are marked in red

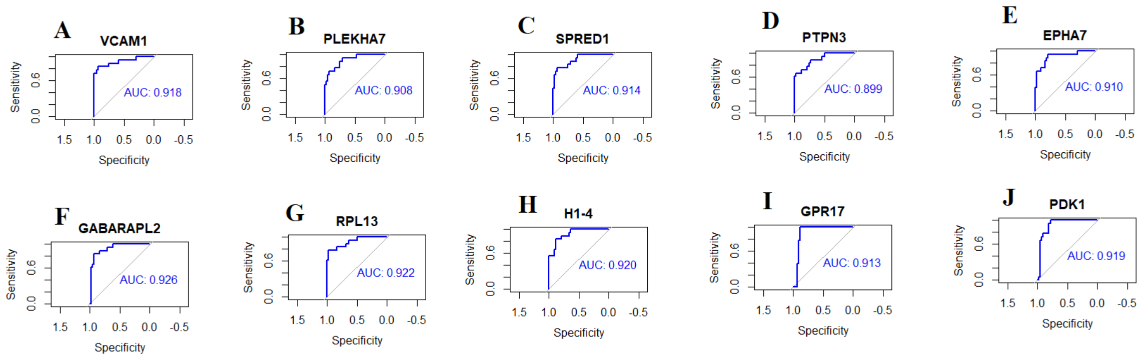


Fig. 14. ROC curve analyses of hub genes. A) VCAM1 B) PLEKHA7 C) SPRED1 D) PTPN3 E) EPHA7 F) GABARAPL2 G) RPL13 H) H1-4 I) GPR17 J) PDK1

Tables

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

Gene Symbol	logFC	pValue	adj.P.Val	tvalue	Regulations	Gene Name
SPX	1.850528	6.78E-12	1.26E-08	6.862236	Up	spexin hormone
OR51B5	1.847356	1.67E-09	9.83E-07	6.026818	Up	olfactory receptor family 51 subfamily B member 5
EPHA5	1.821432	2.21E-10	1.81E-07	6.346175	Up	EPH receptor A5
HSD3B2	1.713664	1.48E-11	2.17E-08	6.74977	Up	hydroxy-delta-5-steroid dehydrogenase, 3 beta- and steroid delta-isomerase 2
THSD7B	1.646815	1.13E-06	0.000133	4.868165	Up	thrombospondin type 1 domain containing 7B
CNTN6	1.529463	4.42E-06	0.000373	4.590515	Up	contactin 6
ARGLU1-DT	1.525697	4.22E-07	6.80E-05	5.058859	Up	ARGLU1 divergent transcript
CADM3	1.52534	1.28E-13	3.74E-10	7.408574	Up	cell adhesion molecule 3
DGKK	1.507192	0.001483	0.024896	3.17799	Up	diacylglycerol kinase kappa
ITPRID1	1.407544	0.000172	0.005517	3.756348	Up	ITPR interacting domain containing 1
SSTR1	1.378842	0.000125	0.004421	3.836995	Up	somatostatin receptor 1
AMER2	1.376611	0.00051	0.012012	3.47562	Up	APC membrane recruitment protein 2
CXCL14	1.349706	2.73E-08	8.74E-06	5.557811	Up	C-X-C motif chemokine ligand 14
CX3CR1	1.313812	1.25E-08	4.48E-06	5.693066	Up	C-X3-C motif chemokine receptor 1
RSPO2	1.270496	1.27E-05	0.000822	4.365228	Up	R-spondin 2
FMO1	1.266541	3.70E-08	1.03E-05	5.504395	Up	flavin containing dimethylaniline monoxygenase 1
SCN11A	1.264133	4.63E-06	0.000382	4.580777	Up	sodium voltage-gated channel alpha subunit 11
DKK2	1.24881	8.38E-05	0.003296	3.933155	Up	dickkopf Wnt signaling pathway inhibitor 2
LGSN	1.233267	0.000576	0.013128	3.442548	Up	lengsin, lens protein with glutamine synthetase domain
SYT6	1.2102	3.72E-06	0.000322	4.626177	Up	synaptotagmin 6
CRACD	1.20889	6.79E-08	1.64E-05	5.396694	Up	capping protein inhibiting regulator of actin dynamics
EPHA7	1.203906	0.000203	0.006272	3.714831	Up	EPH receptor A7
CCDC178	1.202598	0.00014	0.004759	3.808803	Up	coiled-coil domain containing 178

ALDH1A1	1.194659	1.33E-06	0.000151	4.835706	Up	aldehyde dehydrogenase 1 family member A1
MYO1A	1.189788	0.001776	0.028107	3.125374	Up	myosin IA
FNDC1	1.164227	1.33E-05	0.000848	4.355284	Up	fibronectin type III domain containing 1
SPATA46	1.163341	3.89E-06	0.000334	4.617008	Up	spermatogenesis associated 46
HMCN2	1.157754	0.000341	0.009156	3.58181	Up	hemicentin 2
RALYL	1.135192	1.24E-05	0.000811	4.371124	Up	RALY RNA binding protein like
OLFML3	1.13516	1.20E-08	4.38E-06	5.700182	Up	olfactomedin like 3
SLAMF1	1.131309	1.32E-05	0.000846	4.356463	Up	signaling lymphocytic activation molecule family member 1
VCAM1	1.106062	7.19E-08	1.71E-05	5.386383	Up	vascular cell adhesion molecule 1
MYH13	1.098544	1.80E-05	0.001063	4.288969	Up	myosin heavy chain 13
CTLA4	1.089155	0.000603	0.013502	3.430472	Up	cytotoxic T-lymphocyte associated protein 4
C3	1.080235	3.00E-05	0.001583	4.173389	Up	complement C3
SCN4B	1.068566	0.001129	0.020705	3.256187	Up	sodium voltage-gated channel beta subunit 4
SNHG27	1.039656	0.000164	0.005355	3.768814	Up	small nucleolar RNA host gene 27
NRAD1	1.032892	0.001334	0.023327	3.208623	Up	non-coding RNA in the aldehyde dehydrogenase 1A pathway
FAT3	1.026008	1.47E-05	0.000911	4.332761	Up	FAT atypical cadherin 3
HAPLN1	1.020535	1.10E-05	0.000731	4.396652	Up	hyaluronan and proteoglycan link protein 1
CES1	1.018261	1.36E-05	0.000863	4.350046	Up	carboxylesterase 1
GABRB1	1.003588	0.000325	0.008814	3.594279	Up	gamma-aminobutyric acid type A receptor subunit beta1
FGF12	1.003015	0.000398	0.010195	3.541262	Up	fibroblast growth factor 12
FRZB	0.98405	3.57E-05	0.001791	4.133842	Up	frizzled related protein
NCAM1	0.982907	0.000427	0.010623	3.522571	Up	neural cell adhesion molecule 1
RARRES2	0.979269	1.41E-07	2.94E-05	5.264224	Up	retinoic acid receptor responder 2
CHAT	0.974735	0.000737	0.015524	3.375425	Up	choline O-acetyltransferase
FREM1	0.966358	4.46E-08	1.17E-05	5.471759	Up	FRAS1 related extracellular matrix 1
SPON1	0.964507	2.66E-10	2.10E-07	6.317202	Up	spondin 1
CAMK2A	0.963661	9.85E-06	0.000677	4.420503	Up	calcium/calmodulin dependent protein kinase II alpha
CNTN5	0.960648	3.21E-05	0.001663	4.158196	Up	contactin 5
SMKR1	0.956687	0.001322	0.023222	3.211152	Up	small lysine rich protein 1
TMPRSS11F	0.955676	1.25E-05	0.000815	4.368755	Up	transmembrane serine protease 11F
SELE	0.948526	4.40E-05	0.002082	4.085288	Up	selectin E
COL4A4	0.945402	0.000751	0.015683	3.370345	Up	collagen type IV alpha 4 chain
TLCD5	0.9416	4.00E-08	1.09E-05	5.49079	Up	TLC domain containing 5
IL7	0.93623	7.55E-07	9.80E-05	4.946618	Up	interleukin 7
ANO3	0.935033	0.000548	0.012572	3.456344	Up	anoctamin 3
CLDN16	0.933549	0.000355	0.009386	3.571675	Up	claudin 16
GALNT16	0.928849	5.37E-06	0.000426	4.549962	Up	polypeptide N-acetylgalactosaminyltransferase 16
FLRT3	0.928193	3.82E-05	0.001865	4.11837	Up	fibronectin leucine rich transmembrane protein 3
PRRX1	0.916668	0.002683	0.03711	3.001882	Up	paired related homeobox 1
GH1	0.914351	0.001702	0.027186	3.137892	Up	growth hormone 1
MRO	0.911442	0.000468	0.011293	3.498365	Up	maestro
ENPP1	0.908656	2.87E-08	9.01E-06	5.549267	Up	ectonucleotide pyrophosphatase/phosphodiesterase 1
OXER1	0.905365	9.03E-06	0.000638	4.439201	Up	oxoeicosanoid receptor 1

PTPRQ	0.901061	5.57E-06	0.000434	4.54206	Up	protein tyrosine phosphatase receptor type Q
C14orf180	0.900605	0.004225	0.049956	2.860888	Up	chromosome 14 open reading frame 180
CATSPERB	0.89936	3.40E-07	5.76E-05	5.099681	Up	catsper channel auxiliary subunit beta
LCAL1	0.89119	9.95E-06	0.000678	4.418227	Up	lung cancer associated lncRNA 1
IGHG2	0.861689	0.000619	0.013712	3.423029	Up	immunoglobulin heavy constant gamma 2 (G2m marker)
MAP1LC3C	0.86044	0.003232	0.04205	2.9448	Up	microtubule associated protein 1 light chain 3 gamma
CLDN1	0.857047	0.000342	0.009156	3.580867	Up	claudin 1
CNTN1	0.855791	0.002592	0.036155	3.012382	Up	contactin 1
SYPL2	0.849896	0.000414	0.010475	3.531007	Up	synaptophysin like 2
EWSAT1	0.848908	0.000414	0.010475	3.530678	Up	Ewing sarcoma associated transcript 1
SLC16A14	0.848423	8.02E-07	0.000103	4.93489	Up	solute carrier family 16 member 14
EFHB	0.846886	7.10E-05	0.002932	3.972889	Up	EF-hand domain family member B
H1-6	0.846621	0.000167	0.005381	3.764976	Up	H1.6 linker histone, cluster member
MGST1	0.841042	0.002731	0.037568	2.996468	Up	microsomal glutathione S-transferase 1
SLC25A27	0.836188	0.000288	0.008111	3.625944	Up	solute carrier family 25 member 27
COLEC10	0.83189	0.000156	0.00519	3.781157	Up	collectin subfamily member 10
KCNJ5	0.831121	5.01E-08	1.24E-05	5.451001	Up	potassium inwardly rectifying channel subfamily J member 5
SYNPO2L	0.825014	0.002418	0.034487	3.03342	Up	synaptopodin 2 like
SLC16A10	0.821422	4.65E-06	0.000382	4.580029	Up	solute carrier family 16 member 10
LRRC63	0.821392	0.000231	0.006924	3.682179	Up	leucine rich repeat containing 63
TMT1B	0.821086	0.000122	0.004357	3.842703	Up	thiol methyltransferase 1B
VAT1L	0.819771	0.000235	0.006988	3.677974	Up	vesicle amine transport 1 like
SBSPON	0.81901	0.000485	0.01162	3.488848	Up	somatomedin B and thrombospondin type 1 domain containing
IGFLR1	0.809671	0.001108	0.02044	3.261576	Up	IGF like family receptor 1
ZC2HC1A	0.809074	7.53E-07	9.80E-05	4.947295	Up	zinc finger C2HC-type containing 1A
C1QTNF2	0.806585	0.001079	0.020055	3.269055	Up	C1q and TNF related 2
HAS3	0.805416	2.14E-07	4.10E-05	5.186676	Up	hyaluronan synthase 3
CALHM4	0.804403	1.07E-05	0.000715	4.402217	Up	calcium homeostasis modulator family member 4
MEGF10	0.803928	0.000291	0.008176	3.622821	Up	multiple EGF like domains 10
PDZRN3	0.799143	5.24E-07	7.73E-05	5.017158	Up	PDZ domain containing ring finger 3
MXRA5	0.798665	0.00056	0.012804	3.450522	Up	matrix remodeling associated 5
ACOXL	0.798624	0.000133	0.004631	3.820105	Up	acyl-CoA oxidase like
LIX1	0.793298	4.63E-05	0.002172	4.073369	Up	limb and CNS expressed 1
KCNE1	0.793104	0.003823	0.046831	2.892397	Up	potassium voltage-gated channel subfamily E regulatory subunit 1
NAV2-AS4	0.791792	0.001306	0.023027	3.214556	Up	NAV2 antisense RNA 4
CYP24A1	0.791319	0.000334	0.009002	3.587019	Up	cytochrome P450 family 24 subfamily A member 1
COL1A2	0.78912	2.74E-05	0.001484	4.194134	Up	collagen type I alpha 2 chain
EPHA3	0.787872	1.90E-05	0.001106	4.276844	Up	EPH receptor A3
MOXD1	0.782397	0.000114	0.004167	3.85777	Up	monooxygenase DBH like 1
OSR1	0.773432	7.23E-05	0.002963	3.968444	Up	odd-skipped related transcription factor 1
HAAO	0.768352	6.58E-07	9.06E-05	4.973304	Up	3-hydroxyanthranilate 3,4-dioxygenase
ZNF554	0.764575	0.000396	0.01019	3.543036	Up	zinc finger protein 554
LONRF2	0.758669	2.44E-05	0.001371	4.220282	Up	LON peptidase N-terminal domain and ring finger 2

ARTN	0.757898	0.000401	0.010235	3.539244	Up	artemin
COL8A2	0.755105	5.65E-05	0.002522	4.026845	Up	collagen type VIII alpha 2 chain
SMO	0.754257	6.62E-05	0.002825	3.989559	Up	smoothened, frizzled class receptor
SAMD5	0.748499	1.96E-06	0.000196	4.757371	Up	sterile alpha motif domain containing 5
ASXL3	0.740666	0.003019	0.04015	2.965804	Up	ASXL transcriptional regulator 3
GABRA4	0.740552	8.55E-05	0.003331	3.928362	Up	gamma-aminobutyric acid type A receptor subunit alpha4
FAM88B	0.739668	0.000138	0.004719	3.811715	Up	family with sequence similarity 88 member B
VTN	0.738665	0.001434	0.024426	3.187756	Up	vitronectin
CPXM1	0.737414	0.000155	0.005165	3.78316	Up	carboxypeptidase X, M14 family member 1
PCOLCE	0.736118	0.000395	0.010179	3.543661	Up	procollagen C-endopeptidase enhancer
TRIM45	0.734699	3.75E-05	0.00184	4.122339	Up	tripartite motif containing 45
ADGRL3	0.729212	0.000433	0.010702	3.519096	Up	adhesion G protein-coupled receptor L3
SLC4A4	0.729173	8.92E-05	0.003414	3.918228	Up	solute carrier family 4 member 4
TXK	0.72728	0.000397	0.010195	3.54203	Up	TXK tyrosine kinase
COL1A1	0.720246	7.22E-05	0.002963	3.968975	Up	collagen type I alpha 1 chain
BMP5	0.719447	7.62E-06	0.000548	4.475512	Up	bone morphogenetic protein 5
OLFML1	0.719213	0.000593	0.013363	3.434762	Up	olfactomedin like 1
NAV2-AS5	0.718921	0.000109	0.004045	3.868701	Up	NAV2 antisense RNA 5
MAP3K2-DT	0.716605	3.03E-06	0.000276	4.668455	Up	MAP3K2 divergent transcript
ADAMTS7	0.716273	0.000799	0.016348	3.353138	Up	ADAM metallopeptidase with thrombospondin type 1 motif 7
ASPA	0.715299	0.000417	0.0105	3.529317	Up	aspartoacylase
ADAMTS12	0.709431	0.00031	0.008545	3.60646	Up	ADAM metallopeptidase with thrombospondin type 1 motif 12
SRPX	0.709301	8.14E-05	0.003239	3.940109	Up	sushi repeat containing protein X-linked
DLGAP2	0.706131	0.004124	0.049255	2.868551	Up	DLG associated protein 2
MATN2	0.699557	2.72E-05	0.001479	4.195491	Up	matrilin 2
SALL2	0.697999	0.000449	0.01097	3.50957	Up	spalt like transcription factor 2
NDST3	0.690269	0.000128	0.004514	3.830621	Up	N-deacetylase and N-sulfotransferase 3
DYNLT4	0.689913	0.000117	0.004238	3.852106	Up	dynein light chain Tctex-type 4
ADAMTS3	0.688876	3.73E-05	0.001838	4.123437	Up	ADAM metallopeptidase with thrombospondin type 1 motif 3
ERC2	0.683921	3.04E-05	0.001591	4.170086	Up	ELKS/RAB6-interacting/CAST family member 2
UNC5C	0.681171	0.000889	0.017651	3.323626	Up	unc-5 netrin receptor C
CYSLTR1	0.680646	0.000826	0.016845	3.344008	Up	cysteinyl leukotriene receptor 1
LRIG3	0.676476	2.29E-06	0.000223	4.72624	Up	leucine rich repeats and immunoglobulin like domains 3
FGF10	0.674865	0.000628	0.013824	3.419346	Up	fibroblast growth factor 10
OCA2	0.671614	0.004097	0.049079	2.870577	Up	OCA2 melanosomal transmembrane protein
ROBO2	0.667179	0.003043	0.040338	2.963369	Up	roundabout guidance receptor 2
PDE1A	0.666909	0.001026	0.019599	3.283343	Up	phosphodiesterase 1A
ENPP2	0.66683	2.56E-05	0.001415	4.20923	Up	ectonucleotide pyrophosphatase/phosphodiesterase 2
OLFML2A	0.666099	2.49E-05	0.001388	4.216015	Up	olfactomedin like 2A
KCNC4	0.66163	6.29E-07	8.88E-05	4.982241	Up	potassium voltage-gated channel subfamily C member 4
ANKS1B	0.660501	1.10E-06	0.000133	4.872375	Up	ankyrin repeat and sterile alpha motif domain containing 1B
GYG2	0.657627	0.00102	0.019528	3.284986	Up	glycogenin 2
SH3TC2-DT	0.657409	0.000692	0.014871	3.392813	Up	SH3TC2 divergent transcript

COL14A1	0.656547	6.17E-05	0.002692	4.006218	Up	collagen type XIV alpha 1 chain
COL6A1	0.654447	0.000274	0.007796	3.638662	Up	collagen type VI alpha 1 chain
TNFRSF11A	0.65198	7.00E-05	0.002895	3.976401	Up	TNF receptor superfamily member 11a
NOS1AP	0.651823	2.48E-05	0.001388	4.216469	Up	nitric oxide synthase 1 adaptor protein
BHLHE41	0.65136	3.77E-06	0.000325	4.623482	Up	basic helix-loop-helix family member e41
LAMA2	0.650957	0.000325	0.008814	3.594231	Up	laminin subunit alpha 2
TLR7	0.64974	0.000165	0.005355	3.767497	Up	toll like receptor 7
FAM218A	0.649201	0.000113	0.004137	3.860609	Up	family with sequence similarity 218 member A
AGPAT5	0.648498	0.002207	0.032596	3.060805	Up	1-acylglycerol-3-phosphate O-acyltransferase 5
C1orf226	0.648471	5.59E-06	0.000434	4.541281	Up	chromosome 1 open reading frame 226
NALCN	0.648347	5.83E-06	0.000447	4.532618	Up	sodium leak channel, non-selective
PRICKLE1	0.638988	3.47E-05	0.001757	4.140449	Up	prickle planar cell polarity protein 1
PTPRD	0.638012	0.00026	0.007536	3.652437	Up	protein tyrosine phosphatase receptor type D
FGF7	0.631985	0.003384	0.043267	2.930489	Up	fibroblast growth factor 7
RYR2	0.63107	0.000363	0.009591	3.565346	Up	ryanodine receptor 2
KC6	0.630699	0.003216	0.041926	2.946307	Up	keratoconus gene 6
ZNF667	0.626194	0.001021	0.019533	3.284564	Up	zinc finger protein 667
ZNF618	0.62618	0.000209	0.006368	3.708082	Up	zinc finger protein 618
LTBP4	0.625243	0.000313	0.00861	3.604138	Up	latent transforming growth factor beta binding protein 4
CACNA2D4	0.624605	0.002937	0.039445	2.974244	Up	calcium voltage-gated channel auxiliary subunit alpha2delta 4
CACNG4	0.623661	0.001907	0.029476	3.104355	Up	calcium voltage-gated channel auxiliary subunit gamma 4
CSHL1	0.623061	0.002648	0.036821	3.005878	Up	chorionic somatomammotropin hormone like 1
LURAP1	0.617842	0.00195	0.029959	3.097767	Up	leucine rich adaptor protein 1
H2BC4	0.614165	0.000468	0.011293	3.498629	Up	H2B clustered histone 4
SLIT3	0.613719	0.000842	0.017067	3.338718	Up	slit guidance ligand 3
ASTN2	0.61319	0.002089	0.031349	3.077327	Up	astrotactin 2
C1QTNF3	0.612934	6.56E-06	0.000498	4.507416	Up	C1q and TNF related 3
LSS	0.611883	0.000424	0.010551	3.524699	Up	lanosterol synthase
GUCY1A1	0.608054	0.000453	0.011034	3.50739	Up	guanylate cyclase 1 soluble subunit alpha 1
RAPSN	0.606963	0.004207	0.049857	2.862224	Up	receptor associated protein of the synapse
CYBB	0.606699	0.000897	0.017773	3.320905	Up	cytochrome b-245 beta chain
RAB39A	0.60652	8.89E-05	0.003414	3.919033	Up	RAB39A, member RAS oncogene family
SYT15B	0.605557	0.000167	0.005384	3.764041	Up	synaptotagmin 15B
ANK2	0.600588	0.000454	0.01106	3.506234	Up	ankyrin 2
ITGA7	0.599899	0.001141	0.020853	3.253144	Up	integrin subunit alpha 7
PDE7B	0.598097	0.00094	0.018431	3.308036	Up	phosphodiesterase 7B
ANKRD44-IT1	0.594692	0.002013	0.030566	3.088341	Up	ANKRD44 intronic transcript 1
GPR155	0.592749	1.54E-06	0.000169	4.806094	Up	G protein-coupled receptor 155
TBC1D30	0.592019	0.000508	0.012008	3.476329	Up	TBC1 domain family member 30
VANGL2	0.591888	0.000541	0.012497	3.45948	Up	VANGL planar cell polarity protein 2
LRRN3	0.591621	3.87E-05	0.001882	4.115131	Up	leucine rich repeat neuronal 3
SCUBE2	0.591598	0.00253	0.035471	3.019695	Up	signal peptide, CUB domain and EGF like domain containing 2

GUCY1A2	0.590832	0.000897	0.017773	3.320934	Up	guanylate cyclase 1 soluble subunit alpha 2
ANGPTL2	0.590164	0.00021	0.006378	3.706917	Up	angiopoietin like 2
CCND2	0.588713	2.64E-05	0.001452	4.202398	Up	cyclin D2
TFAP2B	0.588575	0.000342	0.009156	3.581305	Up	transcription factor AP-2 beta
PROM1	0.588438	7.83E-05	0.003144	3.949588	Up	prominin 1
LUM	0.586621	0.001055	0.019916	3.275378	Up	lumican
WNT2	0.585255	0.002772	0.037955	2.991916	Up	Wnt family member 2
NPY1R	0.585128	0.002927	0.03936	2.975313	Up	neuropeptide Y receptor Y1
CORO6	0.581626	0.000551	0.01263	3.454504	Up	coronin 6
SLIT2	0.578812	0.001574	0.025941	3.16061	Up	slit guidance ligand 2
PER3	0.577953	2.23E-06	0.000218	4.731697	Up	period circadian regulator 3
ARL4C	0.577104	0.000444	0.010914	3.512465	Up	ARF like GTPase 4C
OGN	0.57448	0.002909	0.039194	2.977215	Up	osteoglycin
KIAA1549	0.569358	0.000119	0.004283	3.848606	Up	KIAA1549
C1QTNF7	0.568964	0.001523	0.025468	3.170244	Up	C1q and TNF related 7
RFX8	0.568666	0.00387	0.04727	2.888529	Up	regulatory factor X8
ABI3BP	0.567873	0.002481	0.035086	3.02561	Up	ABI family member 3 binding protein
FZD2	0.566849	0.001619	0.026292	3.152498	Up	frizzled class receptor 2
EGFL6	0.566017	0.00073	0.015456	3.378159	Up	EGF like domain multiple 6
ACTL10	0.565035	0.000282	0.007971	3.631138	Up	actin like 10
ZSCAN23	0.562712	0.000186	0.00581	3.737589	Up	zinc finger and SCAN domain containing 23
HMGCLL1	0.56271	0.000622	0.013728	3.422016	Up	3-hydroxy-3-methylglutaryl-CoA lyase like 1
COL15A1	0.562576	0.000324	0.008809	3.595691	Up	collagen type XV alpha 1 chain
CD84	0.560769	0.000392	0.010137	3.545419	Up	CD84 molecule
CALHM5	0.560389	0.000691	0.014871	3.392938	Up	calcium homeostasis modulator family member 5
SH3TC2	0.558969	0.001975	0.030193	3.094027	Up	SH3 domain and tetratricopeptide repeats 2
P2RY1	0.558814	0.001468	0.024742	3.181012	Up	purinergic receptor P2Y1
IL12RB2	0.55617	0.000152	0.005082	3.788422	Up	interleukin 12 receptor subunit beta 2
BMX	0.555771	0.000876	0.017483	3.327659	Up	BMX non-receptor tyrosine kinase
HMCN1	0.555303	0.001868	0.02899	3.110388	Up	hemicentin 1
PREX2	0.555218	0.001556	0.025801	3.164075	Up	phosphatidylinositol-3,4,5-trisphosphate dependent Rac exchange factor 2
F13A1	0.552883	0.000235	0.006981	3.67861	Up	coagulation factor XIII A chain
C20orf144	0.546477	0.000439	0.010824	3.515359	Up	chromosome 20 open reading frame 144
BMP4	0.545855	0.000372	0.009723	3.558983	Up	bone morphogenetic protein 4
PCDHB14	0.543535	0.002145	0.032003	3.069331	Up	protocadherin beta 14
EMID1	0.541673	0.001342	0.023392	3.206762	Up	EMI domain containing 1
COL3A1	0.541639	0.001066	0.01997	3.272526	Up	collagen type III alpha 1 chain
PRDM6	0.538361	0.001593	0.026071	3.157189	Up	PR/SET domain 6
B3GLCT	0.53799	2.64E-05	0.001452	4.202146	Up	beta 3-glucosyltransferase
ADGRA2	0.537176	0.001635	0.026514	3.149578	Up	adhesion G protein-coupled receptor A2
CARNS1	0.53332	0.000527	0.012291	3.466395	Up	carnosine synthase 1
ANGPTL7	0.53267	0.002452	0.034701	3.029245	Up	angiopoietin like 7
AFF3	0.532011	0.000168	0.005407	3.762603	Up	ALF transcription elongation factor 3

PEG13	0.531674	0.002304	0.033372	3.047963	Up	paternally expressed 13
CUBN	0.529918	0.001592	0.026071	3.157323	Up	cubilin
FMOD	0.528351	0.002866	0.038742	2.981782	Up	fibromodulin
SCN9A	0.528077	0.000267	0.007677	3.645135	Up	sodium voltage-gated channel alpha subunit 9
GPR68	0.526173	2.51E-05	0.001398	4.213763	Up	G protein-coupled receptor 68
ITGBL1	0.523961	0.000561	0.012833	3.449608	Up	integrin subunit beta like 1
NDN	0.520649	0.003549	0.044456	2.915701	Up	necdin, MAGE family member
ZNF555	0.520202	1.91E-06	0.000194	4.762665	Up	zinc finger protein 555
KL	0.519802	0.003178	0.041562	2.949989	Up	klotho
DACH1	0.519308	0.002142	0.031986	3.069799	Up	dachshund family transcription factor 1
NTNG1	0.518107	0.001971	0.030193	3.094547	Up	netrin G1
DDR2	0.51725	0.000489	0.011665	3.486878	Up	discoidin domain receptor tyrosine kinase 2
DPYSL3	0.516353	0.00297	0.039679	2.970828	Up	dihydropyrimidinase like 3
VSTM4	0.516325	0.003104	0.040898	2.957267	Up	V-set and transmembrane domain containing 4
RAB27B	0.515897	8.35E-05	0.003294	3.934211	Up	RAB27B, member RAS oncogene family
COL21A1	0.511934	0.000146	0.00495	3.797003	Up	collagen type XXI alpha 1 chain
CHKB-DT	0.51151	0.000609	0.013576	3.4275	Up	CHKB divergent transcript
PSEN2	0.510895	0.000739	0.015528	3.374613	Up	presenilin 2
TCF21	0.509061	0.002341	0.033797	3.043149	Up	transcription factor 21
TMEM168	0.506711	3.35E-06	0.000297	4.647935	Up	transmembrane protein 168
NAALADL2	0.504518	0.000111	0.004077	3.865022	Up	N-acetylated alpha-linked acidic dipeptidase like 2
COL6A2	0.504207	0.003308	0.042715	2.937592	Up	collagen type VI alpha 2 chain
HPGDS	0.50356	0.004087	0.049004	2.871396	Up	hematopoietic prostaglandin D synthase
ZNF462	0.500744	2.66E-07	4.83E-05	5.145823	Up	zinc finger protein 462
CDH11	0.500199	0.004006	0.048414	2.877659	Up	cadherin 11
ALCAM	0.499562	0.001535	0.025537	3.168018	Up	activated leukocyte cell adhesion molecule
FRMD3	0.498367	0.002238	0.032771	3.056619	Up	FERM domain containing 3
NCEH1	0.498113	8.90E-05	0.003414	3.9188	Up	neutral cholesterol ester hydrolase 1
POSTN	0.489777	0.001977	0.030193	3.093683	Up	periostin
ANKRD13B	0.488743	0.001936	0.029821	3.099909	Up	ankyrin repeat domain 13B
SCAMP5	0.488456	0.002489	0.035137	3.024633	Up	secretory carrier membrane protein 5
NR1D2	0.488341	2.00E-05	0.001155	4.265206	Up	nuclear receptor subfamily 1 group D member 2
GRID2IP	0.483599	0.001674	0.026871	3.142766	Up	Grid2 interacting protein
HAUS7	0.482686	0.001568	0.025916	3.161732	Up	HAUS augmin like complex subunit 7
AKAP6	0.481368	0.000228	0.006847	3.685405	Up	A-kinase anchoring protein 6
GPR158	0.479167	1.68E-05	0.00102	4.303914	Up	G protein-coupled receptor 158
ARHGAP42	0.47828	0.00028	0.007928	3.633259	Up	Rho GTPase activating protein 42
MTCL1	0.478153	0.001308	0.023035	3.214212	Up	microtubule crosslinking factor 1
ARHGEF10L	0.478135	0.000409	0.010388	3.534333	Up	Rho guanine nucleotide exchange factor 10 like
ADGRB2	0.469499	0.00201	0.030566	3.088684	Up	adhesion G protein-coupled receptor B2
FBN2	0.466036	0.000539	0.012485	3.460647	Up	fibrillin 2
GGTA1	0.465015	0.000834	0.016953	3.341405	Up	glycoprotein alpha-galactosyltransferase 1 (inactive)
CPED1	0.463814	0.001044	0.019794	3.278459	Up	cadherin like and PC-esterase domain containing 1

ZNF658	0.462175	2.52E-05	0.001398	4.213078	Up	zinc finger protein 658
PRKCA	0.461645	0.00019	0.005919	3.732135	Up	protein kinase C alpha
SOX5	0.460669	0.003922	0.047722	2.884408	Up	SRY-box transcription factor 5
FZD4	0.456886	0.002743	0.037649	2.995201	Up	frizzled class receptor 4
ST6GAL1	0.455175	0.001437	0.024426	3.187191	Up	ST6 beta-galactoside alpha-2,6-sialyltransferase 1
CTHRC1	0.452797	0.004056	0.048777	2.87379	Up	collagen triple helix repeat containing 1
LRP2	0.451123	0.001174	0.021327	3.245227	Up	LDL receptor related protein 2
PRKG1	0.45104	0.001051	0.019892	3.276541	Up	protein kinase cGMP-dependent 1
ADCY7	0.450739	0.000738	0.015524	3.375245	Up	adenylate cyclase 7
ITPR1-DT	0.449901	0.001055	0.019916	3.275404	Up	ITPR1 divergent transcript
ZNF197	0.44807	0.001406	0.024153	3.193429	Up	zinc finger protein 197
GIMAP8	0.447712	0.003413	0.043414	2.927889	Up	GTPase, IMAP family member 8
PCSK5	0.44492	0.002709	0.037332	2.999007	Up	proprotein convertase subtilisin/kexin type 5
BIN1	0.444861	0.003407	0.043393	2.928366	Up	bridging integrator 1
DUBR	0.438194	0.000232	0.006948	3.680936	Up	DPPA2 upstream binding RNA
NR3C2	0.438155	8.69E-05	0.00337	3.924566	Up	nuclear receptor subfamily 3 group C member 2
COL5A2	0.435686	0.003723	0.045911	2.900692	Up	collagen type V alpha 2 chain
LGR5	0.433187	0.001199	0.021667	3.239207	Up	leucine rich repeat containing G protein-coupled receptor 5
USP27X-DT	0.43153	0.002608	0.036343	3.010469	Up	USP27X divergent transcript
TC2N	0.429955	0.002936	0.039445	2.974352	Up	tandem C2 domains, nuclear
DTNB	0.428607	0.000204	0.006283	3.713562	Up	dystrobrevin beta
POU2F2	0.428382	0.002413	0.034434	3.03409	Up	POU class 2 homeobox 2
SDSL	0.421378	0.003574	0.044602	2.91353	Up	serine dehydratase like
FAT1	0.421115	0.004152	0.049443	2.866361	Up	FAT atypical cadherin 1
RCAN1	0.418627	8.29E-05	0.003282	3.935802	Up	regulator of calcineurin 1
CDK18	0.412986	0.00128	0.022792	3.22048	Up	cyclin dependent kinase 18
KCTD12	0.409546	0.002265	0.032933	3.053043	Up	potassium channel tetramerization domain containing 12
ANKDD1A	0.409516	0.002063	0.031132	3.081053	Up	ankyrin repeat and death domain containing 1A
ARMH1	0.407867	0.002501	0.035226	3.023249	Up	armadillo like helical domain containing 1
BNC2	0.407164	0.000627	0.013824	3.419577	Up	basonuclin zinc finger protein 2
MAP4K3-DT	0.401372	8.37E-05	0.003296	3.933455	Up	MAP4K3 divergent transcript
ENC1	0.400576	4.95E-05	0.002285	4.057771	Up	ectodermal-neural cortex 1
SYTL5	0.396586	0.002955	0.039546	2.972408	Up	synaptotagmin like 5
TTC28	0.392442	0.001463	0.024701	3.181939	Up	tetratricopeptide repeat domain 28
DYRK2	0.392075	2.41E-06	0.000233	4.715768	Up	dual specificity tyrosine phosphorylation regulated kinase 2
GCLM	0.391874	0.000972	0.018905	3.298512	Up	glutamate-cysteine ligase modifier subunit
CARD18	0.39166	0.000779	0.016042	3.36032	Up	caspase recruitment domain family member 18
SPRED1	0.391137	0.003798	0.046607	2.894468	Up	sprouty related EVH1 domain containing 1
CHKA	0.386732	9.50E-06	0.000658	4.428152	Up	choline kinase alpha
KRT80	0.38381	0.001389	0.023939	3.197014	Up	keratin 80
ARHGEF26	0.381658	0.001833	0.028651	3.116008	Up	Rho guanine nucleotide exchange factor 26
VWA5A	0.379746	0.002666	0.037015	3.003864	Up	von Willebrand factor A domain containing 5A
ZNF404	0.378839	0.002073	0.031194	3.079584	Up	zinc finger protein 404

HECW2	0.377001	0.002435	0.034608	3.031307	Up	HECT, C2 and WW domain containing E3 ubiquitin protein ligase 2
MTSS1	0.376741	0.000404	0.010304	3.537147	Up	MTSS I-BAR domain containing 1
CDKN2B	0.374568	0.000828	0.016853	3.343332	Up	cyclin dependent kinase inhibitor 2B
ZNF844	0.373709	0.000164	0.005355	3.769274	Up	zinc finger protein 844
LRATD2	0.373704	6.92E-05	0.002889	3.979134	Up	LRAT domain containing 2
PC	0.373632	0.000946	0.01851	3.306044	Up	pyruvate carboxylase
BCL7A	0.37243	0.002223	0.03273	3.058664	Up	BAF chromatin remodeling complex subunit BCL7A
PDE5A	0.369133	2.87E-06	0.000267	4.67987	Up	phosphodiesterase 5A
ERICH1	0.368822	0.000151	0.005064	3.789703	Up	glutamate rich 1
MOB3C	0.368198	1.16E-06	0.000135	4.862987	Up	MOB kinase activator 3C
HCG11	0.368131	9.14E-06	0.000643	4.436504	Up	HLA complex group 11
TRIM2	0.366181	0.000111	0.00408	3.864392	Up	tripartite motif containing 2
HYCC1	0.365312	4.41E-05	0.002082	4.084743	Up	hyccin PI4KA lipid kinase complex subunit 1
ZNF697	0.356734	1.73E-06	0.000182	4.782759	Up	zinc finger protein 697
PARD3B	0.35655	0.001066	0.01997	3.27254	Up	par-3 family cell polarity regulator beta
ZNF470	0.354396	5.21E-05	0.002385	4.046189	Up	zinc finger protein 470
GJA1	0.353874	0.004029	0.048565	2.875904	Up	gap junction protein alpha 1
SYT17	0.352943	0.000332	0.008946	3.589337	Up	synaptotagmin 17
CDK20	0.351773	0.00016	0.005285	3.774649	Up	cyclin dependent kinase 20
NFATC2	0.351287	0.00234	0.033797	3.043247	Up	nuclear factor of activated T cells 2
CABLES1	0.350674	0.001758	0.027913	3.128314	Up	Cdk5 and Abl enzyme substrate 1
ZNF564	0.3476	0.002263	0.032933	3.053334	Up	zinc finger protein 564
GSK3B-DT	0.34671	0.000398	0.010195	3.541506	Up	GSK3B divergent transcript
FZD1	0.34577	4.56E-07	7.13E-05	5.043964	Up	frizzled class receptor 1
MFF-DT	0.343542	0.003745	0.046098	2.898854	Up	MFF divergent transcript
FBN1	0.343281	0.001076	0.020055	3.269758	Up	fibrillin 1
KCNMB3	0.343192	0.00356	0.044542	2.914716	Up	potassium calcium-activated channel subfamily M regulatory beta subunit 3
FES	0.343192	0.000373	0.009723	3.55872	Up	FES proto-oncogene, tyrosine kinase
ZXDA	0.340438	7.82E-06	0.00056	4.469935	Up	zinc finger X-linked duplicated A
NRP2	0.340162	0.003375	0.043203	2.931335	Up	neuropilin 2
SLCO2B1	0.338617	0.001707	0.027252	3.136949	Up	solute carrier organic anion transporter family member 2B1
CLCN5	0.338471	1.00E-06	0.000122	4.891648	Up	chloride voltage-gated channel 5
LRRC4	0.338058	0.000948	0.018522	3.305589	Up	leucine rich repeat containing 4
AMER1	0.337196	0.000505	0.011975	3.478001	Up	APC membrane recruitment protein 1
RAP1GAP2	0.335176	0.001118	0.020556	3.258999	Up	RAP1 GTPase activating protein 2
ZNF582	0.334369	0.000188	0.005884	3.73402	Up	zinc finger protein 582
PIP5K1B	0.332918	0.001596	0.026071	3.156693	Up	phosphatidylinositol-4-phosphate 5-kinase type 1 beta
DHFR2	0.331491	0.001536	0.025537	3.167766	Up	dihydrofolate reductase 2
ZNF185	0.330904	0.001592	0.026071	3.157304	Up	zinc finger protein 185 with LIM domain
PTPN3	0.329803	0.001423	0.024295	3.189855	Up	protein tyrosine phosphatase non-receptor type 3
ANKRD50	0.329689	0.00015	0.005041	3.791227	Up	ankyrin repeat domain containing 50
ZNRF3	0.32909	0.004209	0.049857	2.862063	Up	zinc and ring finger 3
ANKRD10	0.324122	0.00277	0.037955	2.992225	Up	ankyrin repeat domain 10

ZFP28	0.322009	0.000631	0.013872	3.417827	Up	ZFP28 zinc finger protein
DHX57	0.321603	0.000764	0.015851	3.365567	Up	DExH-box helicase 57
TLCD2	0.321186	0.002683	0.03711	3.001852	Up	TLC domain containing 2
LAMC1	0.321077	0.000613	0.013602	3.42601	Up	laminin subunit gamma 1
SLC25A32	0.32103	0.002044	0.030917	3.083778	Up	solute carrier family 25 member 32
EVL	0.320775	0.00097	0.018884	3.299088	Up	Enah/Vasp-like
ELMO1	0.316386	0.000757	0.015739	3.368081	Up	engulfment and cell motility 1
TRAF3	0.315581	0.000324	0.008809	3.595063	Up	TNF receptor associated factor 3
ENO3	0.314331	0.000827	0.016853	3.343593	Up	enolase 3
USP9X	0.314221	0.003582	0.044651	2.9128	Up	ubiquitin specific peptidase 9 X-linked
RARG	0.313773	0.003104	0.040898	2.957231	Up	retinoic acid receptor gamma
RABGAP1L	0.312577	0.000796	0.016309	3.354352	Up	RAB GTPase activating protein 1 like
PLEKHM3	0.312342	1.41E-05	0.000884	4.342069	Up	pleckstrin homology domain containing M3
PLEKHA7	0.312244	0.001837	0.028651	3.115441	Up	pleckstrin homology domain containing A7
ZNF441	0.312043	0.000276	0.007841	3.636465	Up	zinc finger protein 441
ADCK1	0.308395	0.000319	0.008724	3.599669	Up	aarF domain containing kinase 1
STN1	0.308342	0.002258	0.032933	3.054069	Up	STN1 subunit of CST complex
NHS	0.307132	0.003445	0.043693	2.924929	Up	NHS actin remodeling regulator
PIP4P2	0.305553	0.001037	0.019698	3.280162	Up	phosphatidylinositol-4,5-bisphosphate 4-phosphatase 2
USP6NL	0.30541	0.001312	0.023084	3.213351	Up	USP6 N-terminal like
DNMT3A	0.305207	0.000154	0.005151	3.784379	Up	DNA methyltransferase 3 alpha
CASK	0.302921	0.000368	0.009664	3.56233	Up	calcium/calmodulin dependent serine protein kinase
PKD2	0.302213	1.64E-06	0.000177	4.793383	Up	polycystin 2, transient receptor potential cation channel
PGAP1	0.301552	0.000267	0.007677	3.645279	Up	post-GPI attachment to proteins inositol deacylase 1
FBXO10	0.301135	0.00327	0.042356	2.941181	Up	F-box protein 10
RALGPS1	0.299541	0.000122	0.004368	3.841241	Up	Ral GEF with PH domain and SH3 binding motif 1
FEM1C	0.298157	0.000196	0.006067	3.724352	Up	fem-1 homolog C
ZNF891	0.297985	0.000567	0.012939	3.447078	Up	zinc finger protein 891
ZNF772	0.297513	1.97E-10	1.74E-07	6.363549	Up	zinc finger protein 772
ERCC6	0.295737	0.001106	0.020423	3.26211	Up	ERCC excision repair 6, chromatin remodeling factor
NCK1-DT	0.294872	0.003388	0.043289	2.930139	Up	NCK1 divergent transcript
B3GNT2	0.291713	0.000854	0.017239	3.33457	Up	UDP-GlcNAc:betaGal beta-1,3-N-acetylglucosaminyltransferase 2
MRPS30	0.291582	2.04E-10	1.74E-07	6.35818	Up	mitochondrial ribosomal protein S30
ABCD3	0.291411	0.000591	0.013327	3.435796	Up	ATP binding cassette subfamily D member 3
MAGI3	0.290339	0.002231	0.032741	3.057616	Up	membrane associated guanylate kinase, WW and PDZ domain containing 3
ZFP90	0.286991	0.001566	0.025913	3.162107	Up	ZFP90 zinc finger protein
AHI1	0.286208	0.00218	0.032307	3.064554	Up	Abelson helper integration site 1
ZKSCAN2	0.285651	3.66E-05	0.001821	4.128253	Up	zinc finger with KRAB and SCAN domains 2
ZNF827	0.285342	0.001729	0.02752	3.133162	Up	zinc finger protein 827
IFRD1	0.284185	0.002698	0.037237	3.000189	Up	interferon related developmental regulator 1
ZNF737	0.281212	6.67E-06	0.0005	4.504068	Up	zinc finger protein 737
TBC1D19	0.281189	0.001065	0.01997	3.272891	Up	TBC1 domain family member 19
ZNF517	0.28028	0.001585	0.026036	3.158647	Up	zinc finger protein 517

TCF12-DT	0.278868	0.000674	0.014582	3.400138	Up	TCF12 divergent transcript
CPLANE1	0.277991	0.002593	0.036155	3.012249	Up	ciliogenesis and planar polarity effector complex subunit 1
KLHL42	0.277975	3.92E-05	0.001905	4.111854	Up	kelch like family member 42
DOCK1	0.274766	5.75E-09	2.31E-06	5.824001	Up	dedicator of cytokinesis 1
MAPK8	0.273324	0.000434	0.010702	3.518685	Up	mitogen-activated protein kinase 8
COPB2-DT	0.2728	0.001603	0.026135	3.155413	Up	COPB2 divergent transcript
TJP1	0.272717	0.00042	0.010538	3.52718	Up	tight junction protein 1
RAP2B	0.272618	0.000716	0.015261	3.383348	Up	RAP2B, member of RAS oncogene family
ARID5B	0.272595	0.001791	0.028288	3.122802	Up	AT-rich interaction domain 5B
ZKSCAN8	0.272102	6.18E-05	0.002692	4.005958	Up	zinc finger with KRAB and SCAN domains 8
PDP1	0.271574	1.03E-05	0.000696	4.410256	Up	pyruvate dehydrogenase phosphatase catalytic subunit 1
PIKFYVE	0.270996	3.54E-08	1.03E-05	5.512149	Up	phosphoinositide kinase, FYVE-type zinc finger containing
MEAK7	0.270286	0.000548	0.012573	3.456028	Up	MTOR associated protein MEAK7
RBAK	0.270026	0.000115	0.004167	3.857536	Up	RB associated KRAB zinc finger
PRAG1	0.269053	0.003332	0.042921	2.935319	Up	PEAK1 related, kinase-activating pseudokinase 1
PPIP5K2	0.265788	8.68E-05	0.00337	3.924691	Up	diphosphoinositol pentakisphosphate kinase 2
RAPH1	0.264852	0.000391	0.010117	3.546274	Up	Ras association (RalGDS/AF-6) and pleckstrin homology domains 1
KCTD7	0.262963	6.82E-05	0.002876	3.982511	Up	potassium channel tetramerization domain containing 7
SLC46A1	0.262151	0.000367	0.009664	3.562823	Up	solute carrier family 46 member 1
MAP2K5	0.260432	8.10E-06	0.000576	4.462583	Up	mitogen-activated protein kinase kinase 5
RAB15	0.258456	0.000987	0.01907	3.29422	Up	RAB15, member RAS oncogene family
KCTD3	0.256738	5.78E-05	0.002568	4.02159	Up	potassium channel tetramerization domain containing 3
MORC4	0.25387	0.001957	0.030044	3.096703	Up	MORC family CW-type zinc finger 4
KBTBD7	0.253783	7.52E-06	0.000543	4.47841	Up	kelch repeat and BTB domain containing 7
PTPRK	0.252369	0.000908	0.017955	3.317518	Up	protein tyrosine phosphatase receptor type K
ZFP3	0.251057	2.67E-05	0.00146	4.200238	Up	ZFP3 zinc finger protein
MTCL2	0.248799	0.001678	0.026892	3.14199	Up	microtubule crosslinking factor 2
ZCCHC14	0.247526	0.002186	0.032369	3.063761	Up	zinc finger CCHC-type containing 14
YTHDC2	0.247332	0.000134	0.00464	3.819201	Up	YTH N6-methyladenosine RNA binding protein C2
BAIAP2-DT	0.2472	0.00149	0.024985	3.176715	Up	BAIAP2 divergent transcript
PARP11	0.246245	0.000183	0.005764	3.740989	Up	poly(ADP-ribose) polymerase family member 11
LAMB2	0.24604	0.000507	0.012	3.476819	Up	laminin subunit beta 2
MKNK1	0.243985	0.003341	0.042987	2.934452	Up	MAPK interacting serine/threonine kinase 1
TKFC	0.243244	0.003866	0.047245	2.888885	Up	triokinase and FMN cyclase
ZKSCAN3	0.242222	7.34E-05	0.002989	3.964983	Up	zinc finger with KRAB and SCAN domains 3
RALGAPA2	0.242033	0.000651	0.014238	3.409562	Up	Ral GTPase activating protein catalytic subunit alpha 2
ACACA	0.23995	0.002072	0.031194	3.079655	Up	acetyl-CoA carboxylase alpha
MTA1	0.23795	3.64E-06	0.000319	4.630839	Up	metastasis associated 1
KIFC3	0.23701	0.001261	0.022564	3.224605	Up	kinesin family member C3
OSBPL3	0.235075	0.004005	0.048414	2.877746	Up	oxysterol binding protein like 3
ATP9B	0.234484	8.94E-05	0.003414	3.917791	Up	ATPase phospholipid transporting 9B (putative)
POMK	0.232871	0.001057	0.019916	3.274876	Up	protein O-mannose kinase
PTAR1	0.232371	0.000128	0.004514	3.829748	Up	protein prenyltransferase alpha subunit repeat containing 1

ZNF362	0.230132	0.001794	0.02829	3.122326	Up	zinc finger protein 362
NRDE2	0.2277	0.002089	0.031349	3.077234	Up	NRDE-2, necessary for RNA interference, domain containing
TBC1D9	0.22767	0.000154	0.005151	3.784253	Up	TBC1 domain family member 9
ZNF490	0.227355	0.000735	0.015524	3.376231	Up	zinc finger protein 490
PTPN14	0.22674	0.001476	0.024832	3.179429	Up	protein tyrosine phosphatase non-receptor type 14
TRIM32	0.226202	0.003428	0.043551	2.926521	Up	tripartite motif containing 32
ZNF181	0.225931	0.000338	0.009072	3.584642	Up	zinc finger protein 181
UNC119	0.224182	0.00136	0.023598	3.203091	Up	unc-119 lipid binding chaperone
RNASEL	0.221416	0.003774	0.046401	2.896426	Up	ribonuclease L
PXK	0.220359	0.002083	0.031323	3.07813	Up	PX domain containing serine/threonine kinase like
MAP4K3	0.220216	0.00324	0.042111	2.943964	Up	mitogen-activated protein kinase kinase kinase kinase 3
ATRIP	0.219879	0.000474	0.011402	3.494856	Up	ATR interacting protein
ZNF571	0.219838	0.002336	0.033797	3.043821	Up	zinc finger protein 571
ZNF527	0.219778	0.004019	0.048534	2.876662	Up	zinc finger protein 527
PABIR1	0.219162	1.02E-05	0.000692	4.412135	Up	PP2A Aalpha (PPP2R1A) and B55A (PPP2R2A) interacting phosphatase regulator 1
MAPKBP1	0.218193	0.000547	0.012572	3.456621	Up	mitogen-activated protein kinase binding protein 1
FPGT	0.214985	0.00384	0.047008	2.891028	Up	fucose-1-phosphate guanylyltransferase
ERCC6L2	0.213868	0.002638	0.036708	3.007013	Up	ERCC excision repair 6 like 2
ZNF136	0.21247	1.29E-05	0.000833	4.361115	Up	zinc finger protein 136
HAUS3	0.212344	0.000929	0.018269	3.311055	Up	HAUS augmin like complex subunit 3
ZNF652	0.208974	0.000752	0.015683	3.36993	Up	zinc finger protein 652
NHLRC2	0.208338	9.86E-05	0.003698	3.894059	Up	NHL repeat containing 2
SSBP2	0.20805	0.00181	0.02848	3.119679	Up	single stranded DNA binding protein 2
MYO18A	0.20803	0.003857	0.047184	2.889661	Up	myosin XVIIIA
USP13	0.207821	0.003929	0.047781	2.883836	Up	ubiquitin specific peptidase 13
NDUFAF5	0.207692	0.003236	0.042075	2.944421	Up	NADH:ubiquinone oxidoreductase complex assembly factor 5
CIBAR1	0.206394	0.001672	0.026871	3.143045	Up	CBY1 interacting BAR domain containing 1
HK2	-2.11468	2.44E-09	0.01162	-5.96551	Down	hexokinase 2
LTF	-2.02731	1.30E-09	0.037568	-6.06732	Down	lactotransferrin
FSTL3	-2.02092	1.01E-07	0.015524	-5.3249	Down	follistatin like 3
PTX3	-2.02069	1.58E-07	0.039445	-5.24333	Down	pentraxin 3
CGB3	-2.00876	5.41E-09	0.037015	-5.8341	Down	chorionic gonadotropin subunit beta 3
LEP	-1.99694	6.58E-05	0.033797	-3.99085	Down	leptin
CYP26A1	-1.98867	1.72E-05	0.042075	-4.29887	Down	cytochrome P450 family 26 subfamily A member 1
ARMS2	-1.9836	1.72E-07	0.005384	-5.22781	Down	age-related maculopathy susceptibility 2
CCR5AS	-1.91887	1.99E-08	0.010195	-5.61253	Down	CCR5 antisense RNA
CP	-1.91883	1.68E-09	0.009002	-6.02612	Down	ceruloplasmin
TBC1D26	-1.90226	1.81E-09	0.043289	-6.01368	Down	TBC1 domain family member 26
TREM1	-1.90178	8.24E-10	0.006378	-6.14029	Down	triggering receptor expressed on myeloid cells 1
PAEP	-1.90115	8.11E-05	0.046401	-3.94108	Down	progestagen associated endometrial protein
PADI1	-1.87806	3.50E-05	2.31E-06	-4.13806	Down	peptidyl arginine deiminase 1
HTRA4	-1.8691	8.37E-09	0.034701	-5.76079	Down	HtrA serine peptidase 4

BEX1	-1.85612	0.000163	0.005407	-3.77028	Down	brain expressed X-linked 1
NTRK2	-1.82599	1.53E-07	0.035086	-5.24834	Down	neurotrophic receptor tyrosine kinase 2
B4GALNT2	-1.81492	1.71E-06	0.007677	-4.78553	Down	beta-1,4-N-acetyl-galactosaminyltransferase 2 (SID blood group)
TMEM45A	-1.75519	1.51E-16	0.001388	-8.25558	Down	transmembrane protein 45A
SLC6A8	-1.72346	9.86E-16	0.04015	-8.02857	Down	solute carrier family 6 member 8
GYPA	-1.61571	5.04E-05	0.010117	-4.05363	Down	glycophorin A (MNS blood group)
ADGRG3	-1.57304	3.24E-05	0.023392	-4.15565	Down	adhesion G protein-coupled receptor G3
FLT1	-1.53686	1.41E-11	0.002963	-6.75736	Down	fms related receptor tyrosine kinase 1
CGB5	-1.53	1.53E-06	0.026036	-4.80668	Down	chorionic gonadotropin subunit beta 5
IL1RL1	-1.51791	0.000275	0.001583	-3.63777	Down	interleukin 1 receptor like 1
KRT14	-1.51338	0.001985	0.000833	-3.09249	Down	keratin 14
QPCT	-1.49185	7.81E-11	0.000233	-6.50415	Down	glutaminyl-peptide cyclotransferase
SPAG4	-1.48829	1.54E-17	0.00464	-8.52409	Down	sperm associated antigen 4
PPP1R1C	-1.48098	1.45E-12	7.13E-05	-7.07947	Down	protein phosphatase 1 regulatory inhibitor subunit 1C
BTNL9	-1.47909	0.000124	4.48E-06	-3.83849	Down	butyrophilin like 9
ADAM2	-1.46571	6.83E-05	0.00408	-3.9823	Down	ADAM metallopeptidase domain 2
HILPDA	-1.43499	1.39E-12	0.002172	-7.08459	Down	hypoxia inducible lipid droplet associated
BHLHE40	-1.40969	5.62E-09	0.000133	-5.82755	Down	basic helix-loop-helix family member e40
PDZD7	-1.36762	8.70E-09	0.005355	-5.75438	Down	PDZ domain containing 7
CGB8	-1.35312	5.32E-05	0.023327	-4.04132	Down	chorionic gonadotropin subunit beta 8
PNCK	-1.32489	8.16E-08	0.002895	-5.36352	Down	pregnancy up-regulated nonubiquitous CaM kinase
LOLI1	-1.30773	3.12E-09	0.047008	-5.92503	Down	lncRNA oncogene in liver cancer 1
NDRG1	-1.30729	1.27E-09	1.64E-05	-6.07101	Down	N-myc downstream regulated 1
CRLF1	-1.30355	1.26E-05	0.009156	-4.3673	Down	cytokine receptor like factor 1
ASPHD2	-1.28133	0.000634	0.000223	-3.41664	Down	aspartate beta-hydroxylase domain containing 2
ANKRD37	-1.28085	9.57E-11	0.04727	-6.47365	Down	ankyrin repeat domain 37
SP5	-1.27647	1.65E-07	0.012939	-5.23452	Down	Sp5 transcription factor
ARNT2	-1.26637	2.80E-05	0.035471	-4.18929	Down	aryl hydrocarbon receptor nuclear translocator 2
MYO7B	-1.26069	4.85E-07	0.013824	-5.03234	Down	myosin VIIB
HBG2	-1.21382	7.89E-05	0.049255	-3.9478	Down	hemoglobin subunit gamma 2
PFKP	-1.20468	1.71E-05	0.010137	-4.29928	Down	phosphofructokinase, platelet
PHYHIP	-1.19849	3.10E-08	0.002285	-5.53595	Down	phytanoyl-CoA 2-hydroxylase interacting protein
SAXO3	-1.19687	4.44E-05	0.000678	-4.0832	Down	stabilizer of axonemal microtubules 3
GPIHBP1	-1.19223	5.50E-05	0.007971	-4.03336	Down	glycosylphosphatidylinositol anchored high density lipoprotein binding protein 1
COL17A1	-1.17166	0.000919	0.026071	-3.31414	Down	collagen type XVII alpha 1 chain
PTGS2	-1.15736	0.003228	0.029476	-2.94513	Down	prostaglandin-endoperoxide synthase 2
IGSF8	-1.15679	2.49E-14	0.040898	-7.62217	Down	immunoglobulin superfamily member 8
FSCN2	-1.15209	0.000221	0.047184	-3.69427	Down	fascin actin-bundling protein 2, retinal
ENG	-1.14262	1.12E-15	0.019599	-8.01262	Down	endoglin
MYO3B	-1.13403	1.40E-05	0.048414	-4.3443	Down	myosin IIIB
MFSD2B	-1.11875	7.18E-05	0.026871	-3.97024	Down	MFSD2 lysolipid transporter B, sphingolipid
GNG4	-1.11087	0.000414	0.044542	-3.5308	Down	G protein subunit gamma 4

GPER1	-1.10017	0.000273	9.83E-07	-3.64005	Down	G protein-coupled estrogen receptor 1
HCAR2	-1.09131	6.75E-05	0.024153	-3.98495	Down	hydroxycarboxylic acid receptor 2
INHA	-1.08636	2.77E-07	0.043393	-5.13878	Down	inhibin subunit alpha
SH3BP5	-1.07583	1.51E-06	0.000135	-4.80936	Down	SH3 domain binding protein 5
SLC14A1	-1.07453	0.000271	0.010623	-3.64139	Down	solute carrier family 14 member 1 (Kidd blood group)
L1CAM	-1.07253	0.000159	0.008809	-3.77605	Down	L1 cell adhesion molecule
PTPRR	-1.07062	0.000132	0.011665	-3.82299	Down	protein tyrosine phosphatase receptor type R
DERL3	-1.05729	3.31E-05	0.049079	-4.15134	Down	derlin 3
CRH	-1.05274	6.81E-05	0.007536	-3.98289	Down	corticotropin releasing hormone
CORO2A	-1.05029	7.21E-06	1.03E-05	-4.48731	Down	coronin 2A
C5orf46	-1.04151	0.002148	0.00519	-3.06893	Down	chromosome 5 open reading frame 46
TENM4	-1.03601	1.82E-06	0.015739	-4.77245	Down	teneurin transmembrane protein 4
DNER	-1.03293	0.000109	0.002385	-3.86998	Down	delta/notch like EGF repeat containing
SLC2A14	-1.0245	0.000867	0.014871	-3.33063	Down	solute carrier family 2 member 14
SASH1	-1.00779	2.72E-07	0.000543	-5.14201	Down	SAM and SH3 domain containing 1
UPK2	-1.00518	0.000125	0.000177	-3.83564	Down	uroplakin 2
JPH2	-1.00278	1.73E-06	0.001838	-4.78289	Down	junctophilin 2
FOSL1	-1.00175	0.000294	0.011293	-3.62083	Down	FOS like 1, AP-1 transcription factor subunit
ZNF114	-0.99576	8.78E-07	0.013363	-4.91728	Down	zinc finger protein 114
TNNI2	-0.99569	0.002427	0.032369	-3.03229	Down	troponin I2, fast skeletal type
ARHGEF4	-0.99316	0.001477	8.74E-06	-3.17921	Down	Rho guanine nucleotide exchange factor 4
SGPP2	-0.98864	1.72E-06	0.007928	-4.78378	Down	sphingosine-1-phosphate phosphatase 2
TPBG	-0.98538	8.55E-08	0.008111	-5.35503	Down	trophoblast glycoprotein
GGT5	-0.98472	0.003128	9.80E-05	-2.95486	Down	gamma-glutamyltransferase 5
ERRFI1	-0.98173	1.41E-10	0.020556	-6.4147	Down	ERBB receptor feedback inhibitor 1
ARHGAP45	-0.9815	1.93E-05	0.000811	-4.2731	Down	Rho GTPase activating protein 45
CKB	-0.97846	3.93E-06	0.002889	-4.61511	Down	creatine kinase B
TET3	-0.97621	8.46E-10	0.003698	-6.13607	Down	tet methylcytosine dioxygenase 3
GATA1	-0.96656	0.000622	0.032933	-3.42182	Down	GATA binding protein 1
RASEF	-0.96566	5.36E-06	0.023939	-4.55005	Down	RAS and EF-hand domain containing
CA4	-0.94825	0.000354	0.004719	-3.57239	Down	carbonic anhydrase 4
MAOB	-0.94705	0.002386	0.013824	-3.0374	Down	monoamine oxidase B
GAPDH	-0.94674	5.47E-10	0.031349	-6.20489	Down	glyceraldehyde-3-phosphate dehydrogenase
VWA5B1	-0.94012	0.0022	0.03936	-3.06181	Down	von Willebrand factor A domain containing 5B1
C12orf75	-0.93578	1.97E-06	0.005355	-4.75648	Down	chromosome 12 open reading frame 75
VWCE	-0.93466	5.57E-05	0.043414	-4.03025	Down	von Willebrand factor C and EGF domains
RNF223	-0.92278	0.004171	0.023027	-2.86496	Down	ring finger protein 223
PRSS22	-0.91071	4.52E-06	0.001063	-4.58613	Down	serine protease 22
TMEM132B	-0.90802	0.002504	0.042356	-3.02283	Down	transmembrane protein 132B
TNR	-0.90603	2.44E-06	0.002825	-4.71335	Down	tenascin R
PAPPA2	-0.90328	4.91E-05	0.008809	-4.05976	Down	pappalysin 2
GBA1	-0.90198	9.38E-13	0.000319	-7.1393	Down	glucosylceramidase beta 1
DIRAS1	-0.90154	0.001078	0.015261	-3.26929	Down	DIRAS family GTPase 1

HPCAL1	-0.89872	4.89E-08	0.001865	-5.4553	Down	hippocalcin like 1
SMOX	-0.89813	0.000303	0.049443	-3.61297	Down	spermine oxidase
OASL	-0.89644	0.001067	0.02848	-3.27231	Down	2'-5'-oligoadenylate synthetase like
SFXN3	-0.8953	2.02E-08	4.38E-06	-5.60995	Down	sideroflexin 3
LDHA	-0.89099	2.07E-07	1.81E-07	-5.19327	Down	lactate dehydrogenase A
GREM2	-0.89028	1.92E-06	0.040338	-4.76213	Down	gremlin 2, DAN family BMP antagonist
GUCA2A	-0.88636	8.56E-07	0.00056	-4.92207	Down	guanylate cyclase activator 2A
SLC44A3	-0.88385	2.06E-05	0.006847	-4.25875	Down	solute carrier family 44 member 3
SLC38A3	-0.88115	0.000271	0.007841	-3.64182	Down	solute carrier family 38 member 3
EHF	-0.8792	0.000178	0.006067	-3.74851	Down	ETS homologous factor
GPR146	-0.87752	4.18E-05	0.004759	-4.09732	Down	G protein-coupled receptor 146
OBSCN	-0.87688	7.03E-07	0.012497	-4.96047	Down	obscurin, cytoskeletal calmodulin and titin-interacting RhoGEF
DDIT4L	-0.87456	1.77E-05	0.017955	-4.2924	Down	DNA damage inducible transcript 4 like
RNU5B-1	-0.87343	0.002804	0.036821	-2.98848	Down	RNA, U5B small nuclear 1
CRYGN	-0.87236	0.000417	0.001757	-3.52898	Down	crystallin gamma N
PROCR	-0.87197	6.21E-07	2.94E-05	-4.98469	Down	protein C receptor
HIF1A-AS3	-0.87018	4.13E-05	0.033372	-4.09991	Down	HIF1A antisense RNA 3
NR5A2	-0.86455	0.00372	0.030193	-2.90101	Down	nuclear receptor subfamily 5 group A member 2
INHBA	-0.86382	9.49E-05	0.013602	-3.90335	Down	inhibin subunit beta A
LIPH	-0.86288	0.000371	0.046607	-3.55973	Down	lipase H
GPT2	-0.86099	3.67E-08	0.023035	-5.50626	Down	glutamic--pyruvic transaminase 2
CHI3L2	-0.85829	0.000978	0.019528	-3.29677	Down	chitinase 3 like 2
SV2B	-0.85672	0.000532	0.048534	-3.46417	Down	synaptic vesicle glycoprotein 2B
SLCO2A1	-0.85332	4.29E-06	0.005517	-4.59685	Down	solute carrier organic anion transporter family member 2A1
MID1	-0.84929	4.38E-07	0.026071	-5.05187	Down	midline 1
CLDN6	-0.8454	4.90E-05	0.00581	-4.06015	Down	claudin 6
JPH1	-0.84299	0.001482	0.003331	-3.17812	Down	junctophilin 1
NECTIN4	-0.84112	1.63E-06	0.008545	-4.79451	Down	nectin cell adhesion molecule 4
SYDE1	-0.84055	3.55E-08	0.03273	-5.51169	Down	synapse defective Rho GTPase activating protein 1
BCL6	-0.83646	3.33E-05	0.004283	-4.14934	Down	BCL6 transcription repressor
VEGFA	-0.83589	0.000103	7.73E-05	-3.88296	Down	vascular endothelial growth factor A
SIGLEC6	-0.83214	6.60E-05	0.000548	-3.99021	Down	sialic acid binding Ig like lectin 6
NRIP1	-0.83203	1.27E-05	0.011975	-4.36494	Down	nuclear receptor interacting protein 1
PPP1R3G	-0.82614	0.000175	0.000434	-3.75208	Down	protein phosphatase 1 regulatory subunit 3G
AK4	-0.81215	0.000107	0.017773	-3.87361	Down	adenylate kinase 4
ERICH2	-0.80956	9.44E-06	0.025916	-4.42952	Down	glutamate rich 2
MX2	-0.80332	4.82E-05	0.001591	-4.06422	Down	MX dynamin like GTPase 2
BIN2	-0.80126	1.82E-06	0.001452	-4.77215	Down	bridging integrator 2
FLNB	-0.79532	5.33E-06	0.013728	-4.55124	Down	filamin B
KCNJ6	-0.7872	0.000122	0.009156	-3.84132	Down	potassium inwardly rectifying channel subfamily J member 6
CHST15	-0.78593	0.001134	0.000194	-3.2551	Down	carbohydrate sulfotransferase 15
SHC3	-0.7849	8.07E-06	0.005919	-4.46324	Down	SHC adaptor protein 3
KEL	-0.78113	0.000165	0.035137	-3.76789	Down	Kell metallo-endopeptidase (Kell blood group)

SLC16A3	-0.77803	2.23E-09	0.047245	-5.98044	Down	solute carrier family 16 member 3
MGAT3	-0.77238	4.03E-07	0.000434	-5.06739	Down	beta-1,4-mannosyl-glycoprotein 4-beta-N-acetylglucosaminyltransferase
DYRK3	-0.76917	0.001802	0.005041	-3.1211	Down	dual specificity tyrosine phosphorylation regulated kinase 3
MMP19	-0.76819	3.47E-06	0.002568	-4.64078	Down	matrix metallopeptidase 19
ERO1A	-0.766	5.40E-09	0.029821	-5.83448	Down	endoplasmic reticulum oxidoreductase 1 alpha
CLDN9	-0.76239	0.000343	0.000276	-3.58035	Down	claudin 9
ISG15	-0.76169	0.000464	0.013872	-3.50067	Down	ISG15 ubiquitin like modifier
AFAP1	-0.75927	0.000393	0.036155	-3.54454	Down	actin filament associated protein 1
VSIG10L	-0.75901	0.000689	0.008814	-3.39386	Down	V-set and immunoglobulin domain containing 10 like
KIF5A	-0.75839	0.002344	0.001791	-3.04275	Down	kinesin family member 5A
NPNT	-0.75518	0.003152	0.000334	-2.95246	Down	nephronectin
PRDX6	-0.7544	1.20E-14	0.011293	-7.71604	Down	peroxiredoxin 6
SNORD15B	-0.75415	0.000371	0.024985	-3.55979	Down	small nucleolar RNA, C/D box 15B
TRIM14	-0.74938	4.59E-05	0.028651	-4.07558	Down	tripartite motif containing 14
SEPTIN3	-0.74592	6.22E-06	0.005064	-4.51879	Down	septin 3
PCP4L1	-0.74461	0.00035	0.041926	-3.57505	Down	Purkinje cell protein 4 like 1
GPR17	-0.74055	0.000423	0.016309	-3.52535	Down	G protein-coupled receptor 17
P4HA1	-0.73971	3.64E-07	0.016348	-5.08673	Down	prolyl 4-hydroxylase subunit alpha 1
ADAMTS4	-0.73354	0.001139	0.000715	-3.25372	Down	ADAM metallopeptidase with thrombospondin type 1 motif 4
DUSP1	-0.73228	5.24E-07	1.26E-08	-5.01729	Down	dual specificity phosphatase 1
KRT19	-0.7299	1.56E-07	0.01851	-5.24516	Down	keratin 19
DAZL	-0.7294	0.000422	0.037332	-3.52583	Down	deleted in azoospermia like
RILP	-0.72502	0.00111	0.001371	-3.26111	Down	Rab interacting lysosomal protein
MXI1	-0.72458	1.59E-06	0.027913	-4.79929	Down	MAX interactor 1, dimerization protein
CEBPA	-0.72247	2.45E-09	2.10E-07	-5.965	Down	CCAAT enhancer binding protein alpha
HTRA1	-0.72213	0.000399	0.000382	-3.54051	Down	HtrA serine peptidase 1
RNU6-9	-0.72139	0.003766	0.000643	-2.89711	Down	RNA, U6 small nuclear 9
TMEM178A	-0.71884	0.000101	0.030193	-3.88701	Down	transmembrane protein 178A
ERICH2-DT	-0.71418	0.000129	0.004137	-3.82856	Down	ERICH2 divergent transcript
MME	-0.71409	8.16E-07	0.04205	-4.93144	Down	membrane metalloendopeptidase
SDC3	-0.70122	1.08E-07	0.012012	-5.31196	Down	syndecan 3
RARRES1	-0.70023	1.20E-06	0.000322	-4.8553	Down	retinoic acid receptor responder 1
LY6K	-0.6982	0.002013	1.17E-05	-3.08827	Down	lymphocyte antigen 6 family member K
USP18	-0.69804	0.000165	0.010914	-3.76662	Down	ubiquitin specific peptidase 18
ABCA12	-0.69574	0.000252	0.024832	-3.65976	Down	ATP binding cassette subfamily A member 12
CBLC	-0.69377	0.001863	0.001663	-3.11121	Down	Cbl proto-oncogene C
SLC9A3	-0.69085	0.003014	0.008724	-2.96629	Down	solute carrier family 9 member A3
NMUR1	-0.687	0.003348	0.006924	-2.93379	Down	neuromedin U receptor 1
ATP13A4	-0.68431	0.004206	0.012485	-2.86231	Down	ATPase 13A4
LAMP3	-0.68393	0.001667	0.004167	-3.144	Down	lysosomal associated membrane protein 3
SLC2A5	-0.68214	0.001328	0.010702	-3.2099	Down	solute carrier family 2 member 5
ARRDC3	-0.68107	8.91E-07	0.030566	-4.91432	Down	arrestin domain containing 3
MSRB1	-0.67727	1.11E-08	0.045911	-5.7132	Down	methionine sulfoxide reductase B1

GPX3	-0.67464	3.01E-05	0.019916	-4.17261	Down	glutathione peroxidase 3
MTSS2	-0.66944	6.06E-05	0.02899	-4.0105	Down	MTSS I-BAR domain containing 2
PHLDB3	-0.66544	3.60E-05	0.036708	-4.13161	Down	pleckstrin homology like domain family B member 3
RDH13	-0.66411	0.000266	0.048777	-3.64624	Down	retinol dehydrogenase 13
SLC28A1	-0.65825	0.002856	0.049004	-2.98279	Down	solute carrier family 28 member 1
LIMD1	-0.65628	4.27E-06	0.048565	-4.59799	Down	LIM domain containing 1
RNU4ATAC	-0.65291	0.002167	0.014582	-3.06636	Down	RNA, U4atac small nuclear
DEGS2	-0.65245	0.000522	0.000122	-3.46932	Down	delta 4-desaturase, sphingolipid 2
RNU4-1	-0.64656	0.003511	0.013576	-2.91909	Down	RNA, U4 small nuclear 1
CITED2	-0.64567	5.80E-05	0.028651	-4.02077	Down	Cbp/p300 interacting transactivator with Glu/Asp rich carboxy-terminal domain 2
NEK11	-0.64349	0.000677	0.006981	-3.39891	Down	NIMA related kinase 11
PLAAT3	-0.64165	1.19E-07	1.09E-05	-5.29541	Down	phospholipase A and acyltransferase 3
ST8SIA6	-0.64164	0.003082	0.032596	-2.95949	Down	ST8 alpha-N-acetyl-neuraminide alpha-2,8-sialyltransferase 6
SDF2L1	-0.63948	3.30E-07	0.021667	-5.10559	Down	stromal cell derived factor 2 like 1
FCRLB	-0.63895	0.002809	0.01097	-2.98789	Down	Fc receptor like B
SEMA4C	-0.63834	1.38E-05	0.006988	-4.34767	Down	semaphorin 4C
ITPR3	-0.63727	0.002432	0.003239	-3.03171	Down	inositol 1,4,5-trisphosphate receptor type 3
PIP5KL1	-0.6325	0.000952	0.024742	-3.3042	Down	phosphatidylinositol-4-phosphate 5-kinase like 1
FAM43A	-0.63125	1.93E-07	0.004238	-5.20635	Down	family with sequence similarity 43 member A
PLOD2	-0.62914	0.000248	3.74E-10	-3.66452	Down	procollagen-lysine,2-oxoglutarate 5-dioxygenase 2
FOSL2	-0.6281	6.87E-05	0.042987	-3.98083	Down	FOS like 2, AP-1 transcription factor subunit
GLIS3	-0.62783	5.39E-05	0.03711	-4.03785	Down	GLIS family zinc finger 3
MICAL3	-0.62717	1.88E-05	0.016042	-4.27903	Down	microtubule associated monooxygenase, calponin and LIM domain containing 3
HMOX1	-0.62649	1.80E-07	0.019794	-5.21938	Down	heme oxygenase 1
PRSS27	-0.62471	0.000261	0.031194	-3.6515	Down	serine protease 27
C8orf58	-0.62404	7.56E-07	0.004045	-4.94636	Down	chromosome 8 open reading frame 58
TMEM91	-0.62219	0.001499	0.026892	-3.1748	Down	transmembrane protein 91
DPP7	-0.62205	2.91E-05	0.009723	-4.18022	Down	dipeptidyl peptidase 7
SCD	-0.62007	7.38E-05	0.017483	-3.9637	Down	stearoyl-CoA desaturase
TNFRSF10D	-0.61785	0.000595	0.025537	-3.43371	Down	TNF receptor superfamily member 10d
FAM222A	-0.61294	0.000303	4.83E-05	-3.61315	Down	family with sequence similarity 222 member A
SCNN1A	-0.61192	0.001627	0.043551	-3.15109	Down	sodium channel epithelial 1 subunit alpha
PRKD3	-0.61016	1.12E-05	0.02044	-4.39341	Down	protein kinase D3
FBLIM1	-0.60852	3.69E-06	0.000911	-4.62809	Down	filamin binding LIM protein 1
IFIT1	-0.60843	0.000797	0.002989	-3.35391	Down	interferon induced protein with tetratricopeptide repeats 1
HEXB	-0.60567	1.43E-06	0.026514	-4.82019	Down	hexosaminidase subunit beta
TCN2	-0.60566	0.001265	0.014238	-3.2238	Down	transcobalamin 2
ANG	-0.6049	3.26E-05	0.0005	-4.15466	Down	angiogenin
MIIP	-0.6046	3.63E-09	0.001479	-5.9001	Down	migration and invasion inhibitory protein
BASP1	-0.59875	3.61E-08	0.017651	-5.50886	Down	brain abundant membrane attached signal protein 1
ZNF175	-0.59414	3.00E-06	0.000382	-4.67074	Down	zinc finger protein 175
ABCA4	-0.59223	0.001114	2.17E-08	-3.25999	Down	ATP binding cassette subfamily A member 4

MCOLN1	-0.58477	8.56E-07	0.037955	-4.92222	Down	mucolipin TRP cation channel 1
AADAT	-0.58318	0.000912	0.033797	-3.31625	Down	aminoadipate aminotransferase
MX1	-0.5806	0.001948	0.002932	-3.09802	Down	MX dynamin like GTPase 1
RASSF7	-0.58015	3.06E-07	0.008946	-5.11977	Down	Ras association domain family member 7
SH3PXD2A	-0.57441	6.70E-05	0.022792	-3.98677	Down	SH3 and PX domains 2A
BCAT2	-0.57149	1.30E-06	1.74E-07	-4.84024	Down	branched chain amino acid transaminase 2
CALM1	-0.56878	3.31E-05	0.000196	-4.15093	Down	calmodulin 1
TPI1	-0.56837	7.69E-11	0.005151	-6.50658	Down	triosephosphate isomerase 1
MFAP5	-0.56834	1.45E-06	0.012833	-4.81803	Down	microfibril associated protein 5
GDF15	-0.56702	0.000204	0.048414	-3.71388	Down	growth differentiation factor 15
LYN	-0.56618	0.000589	0.031986	-3.43652	Down	LYN proto-oncogene, Src family tyrosine kinase
SNORA23	-0.56436	0.001452	0.013712	-3.18403	Down	small nucleolar RNA, H/ACA box 23
ABCC11	-0.56411	0.001904	0.020853	-3.10476	Down	ATP binding cassette subfamily C member 11
CGA	-0.55883	0.000494	0.00337	-3.4841	Down	glycoprotein hormones, alpha polypeptide
CSNK1E	-0.55544	2.02E-08	0.046098	-5.61061	Down	casein kinase 1 epsilon
IPMK	-0.55524	6.80E-06	0.003282	-4.49997	Down	inositol polyphosphate multikinase
F2RL1	-0.55486	0.000487	0.003414	-3.48774	Down	F2R like trypsin receptor 1
WNT9B	-0.55485	0.003586	0.001484	-2.91243	Down	Wnt family member 9B
PFKFB4	-0.55442	1.13E-06	0.000325	-4.86811	Down	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 4
FER1L5	-0.55304	0.002157	0.001398	-3.06775	Down	fer-1 like family member 5
CCDC183	-0.55281	6.94E-05	0.036343	-3.97835	Down	coiled-coil domain containing 183
GRHL3	-0.5522	8.95E-05	0.013502	-3.91741	Down	grainyhead like transcription factor 3
CCSAP	-0.5517	0.00183	0.000638	-3.11652	Down	centriole, cilia and spindle associated protein
VDR	-0.5507	5.55E-05	0.001398	-4.03111	Down	vitamin D receptor
PRRG1	-0.55011	2.32E-08	0.042715	-5.58625	Down	proline rich and Gla domain 1
SERPINE1	-0.54932	0.001554	0.010195	-3.16449	Down	serpin family E member 1
ALDOA	-0.5482	4.48E-06	0.005285	-4.58788	Down	aldolase, fructose-bisphosphate A
ERGIC1	-0.54301	1.22E-07	0.038742	-5.2901	Down	endoplasmic reticulum-golgi intermediate compartment 1
LDLR	-0.54235	3.15E-05	0.01907	-4.16248	Down	low density lipoprotein receptor
TIMP3	-0.54156	0.002431	0.037955	-3.03175	Down	TIMP metallopeptidase inhibitor 3
LYPD3	-0.54068	0.002225	0.004368	-3.05849	Down	LY6/PLAUR domain containing 3
EBI3	-0.53845	0.000515	0.005764	-3.47278	Down	Epstein-Barr virus induced 3
CDO1	-0.53676	4.30E-05	0.044602	-4.09058	Down	cysteine dioxygenase type 1
SNORA74B	-0.53443	0.000541	0.003296	-3.45947	Down	small nucleolar RNA, H/ACA box 74B
NTAN1	-0.53436	2.60E-07	0.008814	-5.15013	Down	N-terminal asparagine amidase
PIK3AP1	-0.53048	6.02E-05	9.06E-05	-4.01185	Down	phosphoinositide-3-kinase adaptor protein 1
PREP	-0.52896	3.64E-09	0.015683	-5.89995	Down	prolyl endopeptidase
EFNB1	-0.52812	3.28E-06	0.005165	-4.65259	Down	ephrin B1
DYNC2I1	-0.5269	5.77E-05	0.012572	-4.02219	Down	dynein 2 intermediate chain 1
HAP1	-0.52322	0.000368	0.003414	-3.56197	Down	huntingtin associated protein 1
SLC26A6	-0.52308	4.38E-05	0.006948	-4.08641	Down	solute carrier family 26 member 6
NANS	-0.52148	2.75E-09	0.033797	-5.94572	Down	N-acetylneuraminate synthase
TGM1	-0.52138	0.000157	0.00861	-3.77976	Down	transglutaminase 1

GDPD3	-0.5198	0.000164	0.024426	-3.76825	Down	glycerophosphodiester phosphodiesterase domain containing 3
MOB3A	-0.51632	2.57E-09	0.001155	-5.95714	Down	MOB kinase activator 3A
IER5L	-0.51582	6.29E-05	0.007677	-4.00169	Down	immediate early response 5 like
EDEM2	-0.5154	9.24E-10	0.000498	-6.12197	Down	ER degradation enhancing alpha-mannosidase like protein 2
ATP6V0C	-0.51491	4.59E-06	0.018884	-4.58271	Down	ATPase H+ transporting V0 subunit c
YPEL4	-0.51447	0.003021	0.030193	-2.96561	Down	yippee like 4
LRRC8A	-0.51423	9.40E-07	0.004167	-4.90371	Down	leucine rich repeat containing 8 VRAC subunit A
SULF2	-0.51365	0.002278	0.009072	-3.05138	Down	sulfatase 2
SUSD2	-0.51339	0.002228	0.010538	-3.05809	Down	sushi domain containing 2
AIF1L	-0.51226	0.003008	0.006283	-2.96696	Down	allograft inflammatory factor 1 like
S100A9	-0.51131	9.09E-05	0.049857	-3.91363	Down	S100 calcium binding protein A9
TECR	-0.51091	5.31E-06	4.10E-05	-4.55198	Down	trans-2,3-enoyl-CoA reductase
PPP1R14B	-0.51033	3.04E-08	0.032933	-5.53899	Down	protein phosphatase 1 regulatory inhibitor subunit 14B
CYP2J2	-0.50765	0.000316	0.01106	-3.60163	Down	cytochrome P450 family 2 subfamily J member 2
DSCR4	-0.50762	0.00193	0.000692	-3.10085	Down	Down syndrome critical region 4
PIK3CB	-0.50687	4.64E-08	0.034434	-5.46463	Down	phosphatidylinositol-4,5-bisphosphate 3-kinase catalytic subunit beta
EFHD2	-0.50549	8.20E-09	0.00102	-5.76432	Down	EF-hand domain family member D2
RHBDD2	-0.50233	3.06E-06	0.002082	-4.66694	Down	rhomboid domain containing 2
FAM184A	-0.50195	0.00156	1.24E-05	-3.16333	Down	family with sequence similarity 184 member A
GPR157	-0.50067	4.89E-06	0.025913	-4.56962	Down	G protein-coupled receptor 157
CTSB	-0.49798	1.45E-06	0.028107	-4.81733	Down	cathepsin B
PPL	-0.49759	0.000383	0.00184	-3.55175	Down	periplakin
CD63	-0.49528	5.29E-07	0.008176	-5.0154	Down	CD63 molecule
IER3	-0.49317	0.000958	0.000822	-3.30266	Down	immediate early response 3
DPM2	-0.49273	9.36E-05	0.009664	-3.90667	Down	dolichyl-phosphate mannosyltransferase subunit 2, regulatory
OCRL	-0.4921	6.10E-07	0.032307	-4.98796	Down	OCRL inositol polyphosphate-5-phosphatase
HSD17B14	-0.48967	0.001036	0.005082	-3.28053	Down	hydroxysteroid 17-beta dehydrogenase 14
NFIL3	-0.4872	2.23E-07	0.01263	-5.17905	Down	nuclear factor, interleukin 3 regulated
ZNF703	-0.48673	0.002065	0.001452	-3.08066	Down	zinc finger protein 703
KIF17	-0.48425	3.45E-05	0.041562	-4.14155	Down	kinesin family member 17
SLC2A1	-0.48158	3.01E-06	5.76E-05	-4.6703	Down	solute carrier family 2 member 1
PKM	-0.47833	1.11E-06	0.024295	-4.87079	Down	pyruvate kinase M1/2
ABCA7	-0.47819	0.001202	0.000218	-3.23837	Down	ATP binding cassette subfamily A member 7
P2RY14	-0.47721	0.000605	0.046831	-3.42955	Down	purinergic receptor P2Y14
ASTE1	-0.47705	0.000193	0.036155	-3.72792	Down	asteroid structure-specific endonuclease 1
NCOR2	-0.47361	0.000681	9.01E-06	-3.39692	Down	nuclear receptor corepressor 2
CYP11A1	-0.47328	0.004007	0.009156	-2.87763	Down	cytochrome P450 family 11 subfamily A member 1
TMEM141	-0.47258	1.50E-05	0.027186	-4.32815	Down	transmembrane protein 141
HMGN3	-0.47157	6.50E-07	0.000373	-4.97562	Down	high mobility group nucleosomal binding domain 3
SH3BGRL3	-0.46971	0.002772	0.039445	-2.99193	Down	SH3 domain binding glutamate rich protein like 3
TMEM154	-0.46854	0.000389	0.001882	-3.54765	Down	transmembrane protein 154
NEURL1	-0.46816	0.000878	0.000846	-3.32688	Down	neuralized E3 ubiquitin protein ligase 1
ZCCHC2	-0.46712	0.000208	0.010824	-3.7088	Down	zinc finger CCHC-type containing 2

LRRC1	-0.46382	0.000514	0.026071	-3.47342	Down	leucine rich repeat containing 1
PP12613	-0.46322	0.000293	0.026135	-3.62113	Down	uncharacterized LOC100192379
EAF1	-0.46163	1.56E-06	0.017773	-4.80331	Down	ELL associated factor 1
UBE2Q2	-0.45923	1.13E-05	0.031349	-4.38987	Down	ubiquitin conjugating enzyme E2 Q2
CNNM4	-0.45771	6.14E-06	0.004514	-4.52147	Down	cyclin and CBS domain divalent metal cation transport mediator 4
CLDN7	-0.45513	1.51E-05	0.019916	-4.32794	Down	claudin 7
FPGS	-0.45452	5.38E-05	0.039546	-4.03832	Down	folylpolyglutamate synthase
UGP2	-0.4544	2.01E-10	0.040898	-6.3604	Down	UDP-glucose pyrophosphorylase 2
PELATON	-0.45182	0.003074	0.002876	-2.96028	Down	plaque enriched lncRNA in atherosclerotic and inflammatory bowel macrophage regulation
HERPUD1	-0.45151	9.65E-06	0.018905	-4.42488	Down	homocysteine inducible ER protein with ubiquitin like domain 1
SLC27A4	-0.45141	7.30E-06	0.025537	-4.48486	Down	solute carrier family 27 member 4
ENO1	-0.44963	0.000107	0.009664	-3.87519	Down	enolase 1
TMEM179B	-0.44911	1.84E-06	0.004514	-4.76974	Down	transmembrane protein 179B
SUV39H1	-0.4489	6.73E-06	0.026071	-4.50208	Down	SUV39H1 histone lysine methyltransferase
S100A6	-0.44507	3.81E-07	0.015683	-5.07834	Down	S100 calcium binding protein A6
GOLT1A	-0.4446	0.002863	0.026292	-2.9821	Down	golgi transport 1A
ZNF614	-0.44326	0.00144	0.028288	-3.18644	Down	zinc finger protein 614
FAM120AOS	-0.44289	6.22E-05	1.74E-07	-4.00415	Down	family with sequence similarity 120 member A opposite strand
CLIC3	-0.44171	9.62E-05	0.012	-3.90001	Down	chloride intracellular channel 3
KATNBL1	-0.43837	0.001341	0.003414	-3.20713	Down	katanin regulatory subunit B1 like 1
RAB25	-0.43824	6.39E-05	0.015528	-3.99779	Down	RAB25, member RAS oncogene family
H1-4	-0.43671	0.000333	0.029959	-3.58784	Down	H1.4 linker histone, cluster member
RFK	-0.43432	0.000272	0.000731	-3.64049	Down	riboflavin kinase
TESK2	-0.4335	0.000175	0.000677	-3.75226	Down	testis associated actin remodelling kinase 2
FRMD4A	-0.43259	5.31E-05	0.02829	-4.04145	Down	FERM domain containing 4A
LAGE3	-0.43098	0.001035	0.000815	-3.28076	Down	L antigen family member 3
REEP4	-0.43055	6.25E-07	0.018431	-4.98347	Down	receptor accessory protein 4
TMEM107	-0.4302	6.82E-07	0.049956	-4.96636	Down	transmembrane protein 107
SAT1	-0.42943	7.97E-05	0.004421	-3.94529	Down	spermidine/spermine N1-acetyltransferase 1
TLCD1	-0.42905	0.001306	0.030917	-3.21471	Down	TLC domain containing 1
DNM2	-0.42881	7.90E-12	0.032741	-6.84028	Down	dynamin 2
FKBP8	-0.42844	7.48E-08	0.039679	-5.37919	Down	FKBP prolyl isomerase 8
ZNF841	-0.42814	0.000478	0.035226	-3.4926	Down	zinc finger protein 841
SCARB1	-0.42736	0.000241	0.010195	-3.67192	Down	scavenger receptor class B member 1
ZNF331	-0.42661	0.000423	0.007796	-3.52534	Down	zinc finger protein 331
PTGES	-0.4248	0.003356	0.019698	-2.93308	Down	prostaglandin E synthase
MAP3K8	-0.42386	2.98E-06	0.010235	-4.67201	Down	mitogen-activated protein kinase kinase kinase 8
PRKAB2	-0.41996	0.001	0.000182	-3.29044	Down	protein kinase AMP-activated non-catalytic subunit beta 2
ARID3A	-0.4197	4.32E-05	0.018522	-4.08962	Down	AT-rich interaction domain 3A
HEY1	-0.41794	0.001412	0.031132	-3.1922	Down	hes related family bHLH transcription factor with YRPW motif 1
NAT2	-0.41659	0.00115	0.000103	-3.25093	Down	N-acetyltransferase 2
GALK1	-0.41477	0.001343	0.013327	-3.2066	Down	galactokinase 1

ARHGEF16	-0.41409	0.000992	0.012573	-3.2929	Down	Rho guanine nucleotide exchange factor 16
PPP1R12C	-0.41347	6.59E-07	0.027252	-4.97302	Down	protein phosphatase 1 regulatory subunit 12C
SIPA1L1	-0.41254	6.59E-06	0.002692	-4.50641	Down	signal induced proliferation associated 1 like 1
PLEKHA2	-0.41241	0.002345	0.01019	-3.04267	Down	pleckstrin homology domain containing A2
ERVH48-1	-0.41005	0.001061	0.014871	-3.27377	Down	endogenous retrovirus group 48 member 1, envelope
KDM3A	-0.40942	5.26E-05	0.009723	-4.04358	Down	lysine demethylase 3A
RAB8B	-0.40926	0.000119	0.01997	-3.84907	Down	RAB8B, member RAS oncogene family
GFUS	-0.40828	0.000164	0.005151	-3.76815	Down	GDP-L-fucose synthase
ACER2	-0.40799	0.001359	0.044456	-3.20329	Down	alkaline ceramidase 2
GALNT2	-0.40685	0.000185	0.02752	-3.73856	Down	polypeptide N-acetylgalactosaminyltransferase 2
GABARAPL2	-0.40572	0.000156	0.005884	-3.78134	Down	GABA type A receptor associated protein like 2
ZNF432	-0.40558	0.000669	0.031194	-3.40183	Down	zinc finger protein 432
FMN1	-0.40458	0.000134	6.80E-05	-3.81857	Down	formin 1
TMEM38B	-0.40447	5.90E-05	0.000426	-4.01664	Down	transmembrane protein 38B
CHCHD10	-0.4035	0.002286	0.024896	-3.05036	Down	coiled-coil-helix-coiled-coil-helix domain containing 10
HMG20B	-0.40317	1.72E-05	0.047781	-4.29888	Down	high mobility group 20B
ATP6V0E1	-0.40296	2.73E-07	0.002082	-5.14125	Down	ATPase H+ transporting V0 subunit e1
NOCT	-0.40272	0.000517	0.006368	-3.47201	Down	nocturnin
BAD	-0.40078	6.86E-07	0.037237	-4.96519	Down	BCL2 associated agonist of cell death
BNIP3L	-0.39882	4.72E-07	0.01997	-5.03749	Down	BCL2 interacting protein 3 like
DLX5	-0.39855	0.000422	0.009386	-3.5262	Down	distal-less homeobox 5
RELT	-0.39615	0.001892	0.001106	-3.10674	Down	RELT TNF receptor
BACH1	-0.39585	2.77E-05	0.025468	-4.19195	Down	BTB domain and CNC homolog 1
MYL6	-0.39487	0.000142	0.024701	-3.8052	Down	myosin light chain 6
TCAF2	-0.3924	0.000882	0.016845	-3.32568	Down	TRPM8 channel associated factor 2
DDA1	-0.39222	1.51E-08	0.022564	-5.66053	Down	DET1 and DDB1 associated 1
LY6E	-0.39106	0.00369	0.000696	-2.9035	Down	lymphocyte antigen 6 family member E
GRHL1	-0.39065	0.002249	0.025941	-3.05526	Down	grainyhead like transcription factor 1
PLEC	-0.38951	0.000144	0.017067	-3.8016	Down	plectin
HACL2	-0.38825	0.000995	0.000658	-3.29205	Down	2-hydroxyacyl-CoA lyase 2
DSCR8	-0.38735	3.66E-05	0.000863	-4.12771	Down	Down syndrome critical region 8
DDR1	-0.38734	4.31E-05	0.018269	-4.08996	Down	discoidin domain receptor tyrosine kinase 1
LRRC32	-0.38683	0.002799	0.016853	-2.989	Down	leucine rich repeat containing 32
TSPYL2	-0.38595	0.002786	0.002692	-2.99042	Down	TSPY like 2
ETNK2	-0.38503	8.52E-05	0.00337	-3.92936	Down	ethanolamine kinase 2
MLX	-0.38494	1.36E-10	0.043203	-6.41991	Down	MAX dimerization protein MLX
ACADL	-0.38454	0.001075	0.00495	-3.27014	Down	acyl-CoA dehydrogenase long chain
SYNGR1	-0.38341	0.001439	0.010179	-3.18669	Down	synaptogyrin 1
AVPI1	-0.38146	0.000177	0.047722	-3.7491	Down	arginine vasopressin induced 1
JPT2	-0.38121	1.14E-06	0.005355	-4.86609	Down	Jupiter microtubule associated homolog 2
DNAJC1	-0.38039	5.38E-09	0.013128	-5.83512	Down	DnaJ heat shock protein family (Hsp40) member C1
FLVCR2	-0.38026	2.68E-05	0.012572	-4.19871	Down	FLVCR choline and putative heme transporter 2
POLR2I	-0.37915	0.000523	0.012008	-3.46877	Down	RNA polymerase II subunit I

ZMYND8	-0.3783	2.50E-06	0.039194	-4.70837	Down	zinc finger MYND-type containing 8
METTL6	-0.37823	5.49E-07	0.020423	-5.00818	Down	methyltransferase 6, tRNA N3-cytidine
SLC10A3	-0.37707	3.14E-06	0.034608	-4.66139	Down	solute carrier family 10 member 3
GADD45G	-0.37685	0.002783	0.043267	-2.99075	Down	growth arrest and DNA damage inducible gamma
ACTN1	-0.37598	0.001212	0.024426	-3.23593	Down	actinin alpha 1
MAFF	-0.37498	0.002263	0.043693	-3.05332	Down	MAF bZIP transcription factor F
GALE	-0.37494	3.54E-05	0.030044	-4.13565	Down	UDP-galactose-4-epimerase
GLRX	-0.37332	0.000845	0.004077	-3.33752	Down	glutaredoxin
SEMA4B	-0.37285	1.24E-06	0.026871	-4.84942	Down	semaphorin 4B
PDLIM2	-0.37274	0.000586	0.006272	-3.438	Down	PDZ and LIM domain 2
PPP1R3B	-0.37079	0.001236	0.000884	-3.2305	Down	protein phosphatase 1 regulatory subunit 3B
RUVBL2	-0.3704	8.30E-05	0.005381	-3.93554	Down	RuvB like AAA ATPase 2
ARLN	-0.36823	5.34E-08	0.020055	-5.43969	Down	allregulin
PRDX2	-0.36746	0.001453	0.010304	-3.18399	Down	peroxiredoxin 2
PDK1	-0.36736	0.000116	1.71E-05	-3.85354	Down	pyruvate dehydrogenase kinase 1
MMP15	-0.36683	6.65E-07	0.023598	-4.97139	Down	matrix metallopeptidase 15
SSR4	-0.36672	0.000721	0.000133	-3.38165	Down	signal sequence receptor subunit 4
OST4	-0.36572	0.000179	0.032933	-3.74644	Down	oligosaccharyltransferase complex subunit 4, non-catalytic
TNIP2	-0.36471	4.81E-08	0.002522	-5.45826	Down	TNFAIP3 interacting protein 2
PIM3	-0.36421	7.56E-05	0.001388	-3.95798	Down	Pim-3 proto-oncogene, serine/threonine kinase
ITGA5	-0.36361	0.001676	0.000151	-3.14243	Down	integrin subunit alpha 5
EDF1	-0.36211	2.37E-06	0.01997	-4.71933	Down	endothelial differentiation related factor 1
ERP44	-0.36155	0.000205	1.03E-05	-3.71268	Down	endoplasmic reticulum protein 44
RPL13	-0.35959	0.002038	0.004357	-3.08471	Down	ribosomal protein L13
SWI5	-0.35958	2.69E-09	0.00146	-5.94924	Down	SWI5 homologous recombination repair protein
ATP6V1F	-0.35919	0.001296	0.019916	-3.21685	Down	ATPase H+ transporting V1 subunit F
DCXR	-0.35903	0.001736	0.032771	-3.132	Down	dicarbonyl and L-xylulose reductase
IMPA2	-0.35899	0.002906	0.023084	-2.97749	Down	inositol monophosphatase 2
EOLA1	-0.35805	0.000354	0.009591	-3.57209	Down	endothelium and lymphocyte associated ASCH domain 1
GPX4	-0.35804	5.42E-06	0.017239	-4.54781	Down	glutathione peroxidase 4
PTPRU	-0.35787	0.000883	0.025801	-3.32541	Down	protein tyrosine phosphatase receptor type U
MRPS18A	-0.35747	4.40E-08	0.012804	-5.47395	Down	mitochondrial ribosomal protein S18A
GBE1	-0.35612	4.63E-07	0.044651	-5.04106	Down	1,4-alpha-glucan branching enzyme 1
MTX1	-0.35601	1.24E-05	0.020705	-4.37107	Down	metaxin 1
OVGP1	-0.35555	0.003652	0.021327	-2.90676	Down	oviductal glycoprotein 1
MMP14	-0.35541	8.94E-05	0.000169	-3.91757	Down	matrix metallopeptidase 14
GLA	-0.35454	4.16E-05	0.0105	-4.09831	Down	galactosidase alpha
POP7	-0.35414	0.000102	0.037649	-3.88616	Down	POP7 ribonuclease P/MRP subunit
STK24	-0.35305	2.97E-05	0.016853	-4.17547	Down	serine/threonine kinase 24
CEBPD	-0.35245	0.000513	0.023222	-3.47383	Down	CCAAT enhancer binding protein delta
SURF2	-0.35234	8.21E-05	0.003296	-3.93815	Down	surfeit 2
RPL12	-0.35227	0.000859	0.015456	-3.333	Down	ribosomal protein L12
HMGB3	-0.35099	0.002561	0.042111	-3.01601	Down	high mobility group box 3

MGAT1	-0.35044	0.001078	0.010475	-3.26927	Down	alpha-1,3-mannosyl-glycoprotein 2-beta-N-acetylglucosaminyltransferase
HIGD1A	-0.34823	1.94E-06	0.019892	-4.75942	Down	HIG1 hypoxia inducible domain family member 1A
PJA1	-0.34778	0.000214	0.03711	-3.70141	Down	praja ring finger ubiquitin ligase 1
CYB5R1	-0.34576	0.002241	0.000848	-3.05632	Down	cytochrome b5 reductase 1
SMIM43	-0.34568	0.000545	0.034487	-3.45745	Down	small integral membrane protein 43
PNPLA2	-0.34419	0.000148	0.049857	-3.79506	Down	patatin like domain 2, triacylglycerol lipase
NEBL	-0.34217	0.001296	0.003414	-3.21693	Down	nebulette
DAB2IP	-0.34209	0.000444	0.000297	-3.51219	Down	DAB2 interacting protein
TRIP10	-0.34204	0.000805	0.000576	-3.35118	Down	thyroid hormone receptor interactor 10
ALG3	-0.34161	2.23E-05	0.030566	-4.24008	Down	ALG3 alpha-1,3- mannosyltransferase
APOO	-0.33865	0.002807	0.015524	-2.98809	Down	apolipoprotein O
PEBP1	-0.33858	5.06E-06	0.001905	-4.56228	Down	phosphatidylethanolamine binding protein 1
NEDD9	-0.33854	0.001383	0.032003	-3.19812	Down	neural precursor cell expressed, developmentally down-regulated 9
SCARNA6	-0.33833	0.004121	0.042921	-2.86876	Down	small Cajal body-specific RNA 6
LIMS1	-0.3375	0.000447	0.012291	-3.5106	Down	LIM zinc finger domain containing 1
GMDS	-0.33573	0.000749	0.015524	-3.37093	Down	GDP-mannose 4,6-dehydratase
AP2A1	-0.33569	0.001406	0.019533	-3.19346	Down	adaptor related protein complex 2 subunit alpha 1
GATA3	-0.33514	0.000752	8.88E-05	-3.36984	Down	GATA binding protein 3
TPRG1L	-0.33427	4.11E-08	0.011402	-5.48596	Down	tumor protein p63 regulated 1 like
DGKZ	-0.33146	1.24E-05	0.001821	-4.37059	Down	diacylglycerol kinase zeta
GLMP	-0.32849	6.82E-07	0.016953	-4.96655	Down	glycosylated lysosomal membrane protein
SMARCA1	-0.32599	0.000177	0.010702	-3.74963	Down	SNF2 related chromatin remodeling ATPase 1
ZNF525	-0.32532	0.002582	0.010475	-3.01351	Down	zinc finger protein 525
KMT2E	-0.32518	0.00081	0.003144	-3.34948	Down	lysine methyltransferase 2E (inactive)
RIOK1	-0.32401	7.20E-05	0.001415	-3.96959	Down	RIO kinase 1
SLC25A4	-0.3239	0.002166	0.010551	-3.06644	Down	solute carrier family 25 member 4
COMTD1	-0.32359	0.000457	0.031323	-3.50471	Down	catechol-O-methyltransferase domain containing 1
SREBF1	-0.32353	0.001689	0.010388	-3.14005	Down	sterol regulatory element binding transcription factor 1
ABHD8	-0.32351	1.40E-05	0.000267	-4.34448	Down	abhydrolase domain containing 8
TNIP1	-0.32304	0.000306	0.004631	-3.60982	Down	TNFAIP3 interacting protein 1
POLR2F	-0.32283	1.54E-05	9.80E-05	-4.32278	Down	RNA polymerase II, I and III subunit F
PEMT	-0.32192	0.001153	0.002963	-3.25035	Down	phosphatidylethanolamine N-methyltransferase
PRSS8	-0.32167	0.000752	0.003294	-3.37	Down	serine protease 8
NDUFB7	-0.32055	0.001288	0.000447	-3.2187	Down	NADH:ubiquinone oxidoreductase subunit B7
SPATA2L	-0.32046	0.001056	0.011034	-3.27526	Down	spermatogenesis associated 2 like
MAPK13	-0.32019	0.003525	0.015851	-2.91784	Down	mitogen-activated protein kinase 13
ISCU	-0.31917	1.26E-07	0.020055	-5.28436	Down	iron-sulfur cluster assembly enzyme

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

GO ID	CATEGORY	GO Name	adjusted_p_value	negative_log10_of_adjusted_p_value	Gene Count	Gene
			Up regulated genes			
GO:0065007	BP	biological regulation	4.36E-15	14.36013404	331	SPX,OR51B5,EPHA5,HSD3B2,CNTN6,DGKK,SSTR1,AMER2,CXCL14,CX3CR1,RSPO2,FMO1,SCN11A,DKK2,SYT6,CRACD,EPHA7,ALDH1A1,OLFML3,SLAMF1,VCAM1,CTLA4,C3,SCN4B,FAT3,HAPLN1,CES1,GABRB1,FGF12,FRZB,NCAM1,RARRES2,CHAT,SPON1,CAMK2A,SELE,IL7,ANO3,FLRT3,PRRX1,GH1,ENPP1,OXER1,IGHG2,CLDN1,CNTN1,EFHB,H1-6,SLC25A27,COLEC10,KCNJ5,SYNPO2L,SLC16A10,LRRC63,C1QTNF2,HAS3,MEGF10,KCNE1,CYP24A1,COL1A2,EPHA3,OSR1,ZNF554,ARTN,SMO,ASXL3,GABRA4,VTN,TRIM45,ADGRL3,SLC4A4,TXK,COL1A1,BMP5,OLFML1,ADAMTS7,ASPA,ADAMTS12,SRPX,DLGAP2,SALL2,ADAMTS3,ERC2,UNC5C,CYSLTR1,FGF10,OCA2,ROBO2,PDE1A,ENPP2,OLFML2A,KCNC4,ANKS1B,COL14A1,COL6A1,TNFRSF11A,NOS1AP,BHLHE41,LAMA2,TLR7,NALCN,PRICKLE1,PTPRD,FGF7,RYR2,ZNF667,ZNF618,LTBP4,CACNG4,LURAP1,SLIT3,ASTN2,C1QTNF3,LSS,GUCY1A1,RAPSN,CYBB,RAB39A,ANK2,ITGA7,PDE7B,GPR155,VANGL2,LRRN3,SCUBE2,GUCY1A2,ANGPTL2,CCND2,TFAP2B,PROM1,LUM,WNT2,NPY1R,SLIT2,PER3,OGN,RFX8,ABI3BP,FZD2,EGFL6,ZSCAN23,COL15A1,CD84,

						SH3TC2,P2RY1,IL12RB2,BMX,PREX2,F13A1,BMP4,PCDHB14,COL3A1,PRDM6,ADGRA2,ANGPTL7,AFF3,FMOD,SCN9A,GPR68,ITGBL1,NDN,ZNF555,KL,DACH1,NTNG1,DDR2,DPYSL3,VSTM4,RAB27B,TCF21,TMEM168,COL6A2,HPGDS,ZNF462,CDH11,ALCAM,NCEH1,POSTN,ANKRD13B,SCAMP5,NR1D2,GRID2IP,HAUS7,AKAP6,GPR158,ARHGAP42,MTCL1,ARHGEF10L,ADGRB2,FBN2,ZNF658,PRKCA,SOX5,FZD4,ST6GAL1,CTHRC1,LRP2,PRKG1,ADCY7,ZNF197,GIMAP8,PCSK5,BIN1,NR3C2,COL5A2,LGR5,DTNB,POU2F2,FAT1,RCAN1,CDK18,KCTD12,ANKDD1A,BNC2,ENC1,TTC28,DYRK2,GCLM,CARD18,SPRED1,ZNF404,HECW2,MTSS1,CDKN2B,ZNF844,PC,BCL7A,PDE5A,MOB3C,TRIM2,ZNF697,ZNF470,GJA1,SYT17,CDK20,NFATC2,CABLES1,ZNF564,FZD1,FBN1,KCNMB3,FES,ZXDA,NRP2,LRRC4,AMER1,RAP1GAP2,ZNF582,PIP5K1B,PTPN3,ZNRF3,ZFP28,TLCD2,LAMC1,EVL,ELMO1,TRAF3,USP9X,RARG,RABGAP1L,PLEKHA7,ZNF441,ADCK1,STN1,PIP4P2,USP6NL,DNMT3A,CASK,PKD2,PGAP1,FBXO10,RALGPS1,ZNF891,ZNF772,ERCC6,MAGI3,ZFP90,AHI1,ZKSCAN2,ZNF827,ZNF737,ZNF517,KLHL42,DOCK1,MAPK8,TJP1,RAP2B,ARID5B,ZKSCAN8,PIKFYVE,MEAK7,RBAK,PRAG1,RAPH1,KCTD7,MAP2K5,RAB15,KBTBD7,PTPRK,ZFP3,MTCL2,YTHDC2,LAMB2,MKNK1,TKFC,ZKSCAN3,RALGAPA2,MTA1,ATP9B,ZNF362,NRDE2,ZNF490,PTPN14,TRIM32,ZNF181,UNC119,RNASEL,PXK,MAP4K3,ATRIP,ZNF571,ZNF527,PABIR1,MAPKBP1,ZNF136,HAUS3,ZNF652,SSBP2,MYO18A,USP13,CIBAR1
GO:0050794	BP	regulation of cellular process	3.28E-12	11.4847394	309	SPX,OR51B5,EPHA5,CNTN6,DGKK,SSTR1,AMER2,CXCL14,CX3CR1,RSPO2,FMO1,SCN11A,DKK2,SYT6,CRACD,EPHA7,ALDH1A1,OLFML3,SLAMF1,VCAM1,CTLA4,C3,SCN4B,FAT3,HAPLN1,CES1,GABRB1,FGF12,FRZB,NCAM1,RARRES2,SPON1,CAMK2A,SELE,IL7,FLRT3,PRRX1,GH1,ENPP1,OXER1,IGHG2,CLDN1,CNTN1,EFHB,H1-6,SLC25A27,COLEC10,KCNJ5,SYNPO2L,LRRC63,C1QTNF2,HAS3,MEGF10,KCNE1,CYP24A1,COL1A2,EPHA3,OSR1,ZNF554,ARTN,SMO,ASXL3,GABRA4,VTN,ADGRL3,

SLC4A4,TXK,COL1A1,BMP5,OLFML1,ADAMTS7,ASPA,ADAMTS12,SRPX,SALL2,ADAMTS3,ERC2,UNC5C,CYSLTR1,FGF10,ROBO2,PDE1A,ENPP2,OLFML2A,ANKS1B,COL14A1,COL6A1,TNFRSF11A,NOS1AP,BHLHE41,LAMA2,TLR7,NALCN,PRICKLE1,PTPRD,FGF7,RYR2,ZNF667,ZNF618,LTBP4,CACNG4,LURAP1,SLIT3,ASTN2,C1QTNF3,GUCY1A1,RAPSN,CYBB,RAB39A,ANK2,ITGA7,PDE7B,GPR155,VANGL2,LRRN3,SCUBE2,GUCY1A2,CCND2,TFAP2B,PROM1,LUM,WNT2,NPY1R,SLIT2,PER3,OGN,RFX8,ABI3BP,FZD2,EGFL6,ZSCAN23,COL15A1,CD84,SH3TC2,P2RY1,IL12RB2,BMX,PREX2,BMP4,COL3A1,PRDM6,ADGRA2,ANGPTL7,AFF3,FMOD,GPR68,ITGBL1,NDN,ZNF555,KL,DACH1,NTNG1,DDR2,DPYSL3,RAB27B,TCF21,TMEM168,COL6A2,HPGDS,ZNF462,CDH11,ALCAM,POSTN,ANKRD13B,SCAMP5,NR1D2,GRID2IP,HAUS7,AKAP6,GPR158,ARHGAP42,MTCL1,ARHGEF10L,ADGRB2,FBN2,ZNF658,PRKCA,SOX5,FZD4,ST6GAL1,CTHRC1,LRP2,PRKG1,ADCY7,ZNF197,GIMAP8,BIN1,NR3C2,COL5A2,LGR5,POU2F2,FAT1,RCAN1,CDK18,KCTD12,ANKDD1A,BNC2,ENC1,TTC28,DYRK2,GCLM,CARD18,SPRED1,ZNF404,HECW2,MTSS1,CDKN2B,ZNF844,PC,BCL7A,PDE5A,MOB3C,TRIM2,ZNF697,ZNF470,GJA1,SYT17,CDK20,NFATC2,CABLES1,ZNF564,FZD1,FBN1,FES,ZXDA,NRP2,LRRC4,AMER1,RAP1GAP2,ZNF582,PIP5K1B,PTPN3,ZNRF3,ZFP28,LAMC1,EVL,ELMO1,TRAF3,USP9X,RARG,RABGAP1L,ZNF441,ADCK1,STN1,PIP4P2,USP6NL,DNMT3A,CASK,PKD2,PGAP1,FBXO10,RALGPS1,ZNF891,ZNF772,ERCC6,MAGI3,ZFP90,AHI1,ZKSCAN2,ZNF827,ZNF737,ZNF517,KLHL42,DOCK1,MAPK8,TJP1,RAP2B,ARID5B,ZKSCAN8,PIKFYVE,MEAK7,RBAK,PRAG1,RAPH1,MAP2K5,RAB15,KBTBD7,PTPRK,ZFP3,MTCL2,YTHDC2,LAMB2,MKNK1,TKFC,ZKSCAN3,RALGAPA2,MTA1,ZNF362,NRDE2,ZNF490,PTPN14,TRIM32,ZNF181,UNC119,RNASEL,PXK,MAP4K3,ATRIP,ZNF571,ZNF527,PABIR1,MAPKBP1,ZNF136,HAUS3,ZNF652,SSBP2,MYO18A,USP13,CIBAR1

GO:0071944	CC	cell periphery	1.62E-18	17.79047008	215	OR51B5,EPHA5,THSD7B,CNTN6,CADM3,DGKK,SSTR1,AMER2,CX3CR1,SCN11A,LGSN,SYT6,EPHA7,MYO1A,HMCN2,SLAMF1,VCAM1,CTLA4,C3,SCN4B,FAT3,HAPLN1,GABRB1,NCAM1,RARRES2,FREM1,SPON1,CNTN5,TMPRSS11F,SELE,COL4A4,IL7,ANO3,CLDN16,FLRT3,GH1,ENPP1,OXER1,PTPRQ,C14ORF180,CATSPERB,IGHG2,CLDN1,CNTN1,SLC16A14,MGST1,COLEC10,KCNJ5,SLC16A10,SBSPON,IGFLR1,HAS3,CALHM4,MEGF10,MXRA5,KCNE1,COL1A2,EPHA3,OSR1,COL8A2,SMO,GABRA4,VTN,PCOLCE,ADGRL3,SLC4A4,TXK,COL1A1,ADAMTS7,ADAMTS12,SRPX,DLGAP2,MATN2,ADAMTS3,ERC2,UNC5C,CYSLTR1,LRIG3,FGF10,ROBO2,ENPP2,OLFML2A,KCNC4,ANKS1B,COL14A1,COL6A1,TNFRSF11A,NOS1AP,LAMA2,TLR7,NALCN,PTPRD,RYR2,LTBP4,CACNA2D4,CACNG4,ASTN2,RAPSN,CYBB,RAB39A,ANK2,ITGA7,VANGL2,LRRN3,ANGPTL2,PROM1,LUM,WNT2,NPY1R,ARL4C,OGN,KIAA1549,ABI3BP,FZD2,EGFL6,COL15A1,CD84,CALHM5,SH3TC2,P2RY1,IL12RB2,BMX,HMCN1,PREX2,F13A1,PCDHB14,EMID1,COL3A1,ADGRA2,ANGPTL7,CUBN,FMOD,SCN9A,GPR68,ITGBL1,KL,NTNG1,DDR2,VSTM4,RAB27B,COL21A1,COL6A2,CDH11,ALCAM,NCEH1,POSTN,ANKRD13B,SCAMP5,GRID2IP,HAUS7,AKAP6,GPR158,MTCL1,ADGRB2,FBN2,PRKCA,FZD4,CTHRC1,LRP2,PRKG1,ADCY7,BIN1,COL5A2,LGR5,DTNB,FAT1,KCTD12,SYTL5,SPRED1,MTSS1,LRATD2,HYCC1,PARD3B,GJA1,SYT17,FZD1,FBN1,KCNMB3,FES,NRP2,SLCO2B1,CLCN5,LRRC4,AMER1,RAP1GAP2,PIP5K1B,PTPN3,ZNRF3,TLCD2,LAMC1,ELMO1,TRAF3,ENO3,PLEKHM3,NHS,PIP4P2,USP6NL,CASK,PKD2,RALGPS1,MAGI3,DOCK1,TJP1,RAP2B,RAPH1,KCTD7,SLC46A1,RAB15,KCTD3,PTPRK,LAMB2,RALGAPA2,OSBPL3,ATP9B,PXK
GO:0005886	CC	plasma membrane	1.39E-07	6.857064666	171	OR51B5,EPHA5,THSD7B,CNTN6,CADM3,DGKK,SSTR1,AMER2,CX3CR1,SCN11A,LGSN,SYT6,EPHA7,MYO1A,HMCN2,SLAMF1,VCAM1,CTLA4,C3,SCN4B,FAT3,GABRB1,NCAM1,CNTN5,TMPRSS11F,SELE,ANO3,CLDN16,FLRT3,ENPP1,OXER1,PTPRQ,C14ORF180,CATS

						PERB,IGHG2,CLDN1,CNTN1,SLC16A14,MGST1,COLEC10,KCNJ5,SLC16A10,IGFLR1,HAS3,CALHM4,MEGF10,KCNE1,EPHA3,SMO,GABRA4,VTN,ADGRL3,SLC4A4,TXK,DLGAP2,ERC2,UNC5C,CYSLTR1,LRIG3,FGF10,ROBO2,ENPP2,KCNC4,ANKS1B,COL6A1,TNFRSF11A,NOS1AP,LAMA2,TLR7,NALCN,PTPRD,RYR2,CACNA2D4,CACNG4,RAPSN,CYBB,RAB39A,ANK2,ITGA7,VANGL2,PROM1,NPY1R,ARL4C,KIAA1549,FZD2,CD84,CALHM5,SH3TC2,P2RY1,IL12RB2,BMX,HMCN1,PREX2,PCDHB14,ADGRA2,CUBN,SCN9A,GPR68,ITGBL1,KL,NTNG1,DDR2,VSTM4,RAB27B,COL6A2,CDH11,ALCAM,NCEH1,ANKRD13B,SCAMP5,GRID2IP,HAUS7,AKAP6,GPR158,MTCL1,ADGRB2,PRKCA,FZD4,LRP2,PRKG1,ADCY7,BIN1,LGR5,DTNB,FAT1,KCTD12,SYTL5,SPRED1,MTSS1,LRATD2,HYCC1,PARD3B,GJA1,SYT17,FZD1,KCNMB3,FES,NRP2,SLCO2B1,CLCN5,LRRC4,AMER1,RAP1GAP2,PIP5K1B,PTPN3,ZNRF3,TLCD2,ELMO1,TRAF3,ENO3,PLEKHM3,NHS,PIP4P2,USP6NL,CASK,PKD2,RALGPS1,MAGI3,DOCK1,TJP1,RAP2B,RAPH1,KCTD7,SLC46A1,RAB15,KCTD3,PTPRK,RALGAPA2,OSBPL3,ATP9B,PXK
GO:0036094	MF	small molecule binding	7.78E-07	6.109125518	199	EPHA5,DGKK,AMER2,FMO1,SYT6,EPHA7,ALDH1A1,MYO1A,HMCN2,MYH13,FAT3,FREM1,SPON1,CAMK2A,SELE,GALNT16,GH1,ENPP1,OXER1,EFHB,COLEC10,VAT1L,ZC2HC1A,PDZRN3,ACOXL,CYP24A1,COL1A2,EPHA3,MOXD1,OSR1,HAAO,ZNF554,LONRF2,ASXL3,CPXM1,TRIM45,ADGRL3,TXK,COL1A1,ADAMTS7,ASPA,ADAMTS12,MATN2,SALL2,ADAMTS3,PDE1A,ENPP2,KCNC4,GYG2,TNFRSF11A,PRICKLE1,RYR2,ZNF667,ZNF618,LTBP4,CACNA2D4,SLIT3,ASTN2,GUCY1A1,RAPSN,CYBB,RAB39A,ITGA7,PDE7B,GPR155,SCUBE2,GUCY1A2,PROM1,SLIT2,ARL4C,EGFL6,ZSCAN23,HMGCLL1,P2RY1,BMX,HMCN1,PREX2,F13A1,PCDHB14,COL3A1,PRDM6,CARNS1,CUBN,ZNF555,KL,DDR2,RAB27B,HPGDS,ZNF462,CDH11,NCEH1,POSTN,NR1D2,ARHGEF10L,FBN2,ZNF658,PRKCA,LRP2,PRKG1,ADCY7,ZNF197,GIMAP8,NR3C2,COL5A2,DTNB,SDSL,FAT1,CDK18,BNC2,SYTL5,DYRK2,CHKA,ARHGEF26,Z

						NF404,ZNF844,PC,PDE5A,MOB3C,TRIM2,ZNF697,ZNF470,SYT17,CDK20,ZNF564,FBN1,FES,ZXDA,NRP2,CLCN5,AMER1,ZNF582,PIP5K1B,DHFR2,ZNF185,ZNRF3,ZFP28,DHX57,ELMO1,TRAF3,ENO3,RARG,PLEKHM3,ZNF441,ADCK1,DNMT3A,CASK,PKD2,RALGPS1,ZNF891,ZNF772,ERCC6,ABCD3,MAGI3,ZFP90,ZKSCAN2,ZNF827,ZNF737,ZNF517,DOCK1,MAPK8,RAP2B,ZKSCAN8,PDP1,PIKFYVE,RBAK,PRAG1,PPIP5K2,SLC46A1,MAP2K5,RAB15,MORC4,ZFP3,ZCCHC14,YTHDC2,MKNK1,TKFC,ZKSCAN3,ACACA,MTA1,KIFC3,OSBPL3,ATP9B,POMK,ZNF362,TBC1D9,ZNF490,TRIM32,ZNF181,RNASEL,PXK,MAP4K3,ZNF571,ZNF527,FPGT,ERCC6L2,ZNF136,ZNF652,MYO18A,USP13
GO:0043167	MF	ion binding	2.33619E-06	5.631492197	192	EPHA5,DGKK,AMER2,FMO1,SYT6,EPHA7,MYO1A,HMCN2,MYH13,FAT3,FREM1,SPON1,CAMK2A,SELE,GALNT16,GH1,ENPP1,OXER1,EFHB,VAT1L,ZC2HC1A,PDZRN3,ACOXL,CYP24A1,COL1A2,EPHA3,MOXD1,OSR1,HAAO,ZNF554,LONRF2,ASXL3,CPXM1,TRIM45,ADGRL3,TXK,COL1A1,ADAMTS7,ASPA,ADAMTS12,MATN2,SALL2,ADAMTS3,PDE1A,ENPP2,KCNC4,GYG2,TNFRSF11A,PRICKLE1,RYR2,ZNF667,ZNF618,LTBP4,CACNA2D4,SLIT3,ASTN2,GUCY1A1,RAPSN,CYBB,RAB39A,ITGA7,PDE7B,SCUBE2,GUCY1A2,SLIT2,ARL4C,EGFL6,ZSCAN23,HMGCLL1,P2RY1,BMX,HMCN1,PREX2,F13A1,PCDHB14,COL3A1,PRDM6,CARNS1,CUBN,ZNF555,DDR2,RAB27B,HPGDS,ZNF462,CDH11,NCEH1,POSTN,NR1D2,ARHGEF10L,FBN2,ZNF658,PRKCA,LRP2,PRKG1,ADCY7,ZNF197,GIMAP8,NR3C2,COL5A2,DTNB,SDSL,FAT1,CDK18,BNC2,SYTL5,DYRK2,CHKA,ARHGEF26,ZNF404,ZNF844,PC,PDE5A,MOB3C,TRIM2,ZNF697,ZNF470,SYT17,CDK20,ZNF564,FBN1,FES,ZXDA,NRP2,CLCN5,AMER1,ZNF582,PIP5K1B,ZNF185,ZNRF3,ZFP28,DHX57,ELMO1,TRAF3,ENO3,RARG,PLEKHM3,ZNF441,ADCK1,DNMT3A,CASK,PKD2,RALGPS1,ZNF891,ZNF772,ERCC6,ABCD3,MAGI3,ZFP90,ZKSCAN2,ZNF827,ZNF737,ZNF517,DOCK1,MAPK8,RAP2B,ZKSCAN8,PDP1,PIKFYVE,RBAK,PRAG1,PPIP5K2,SLC46A1,MAP2K5,RAB15,M

						ORC4,ZFP3,ZCCHC14,YTHDC2,MKNK1,TKFC,ZKSCAN3,ACACA,MTA1,KIFC3,ATP9B,POMK,ZNF362,TBC1D9,ZNF490,TRIM32,ZNF181,RNASEL,PXK,MAP4K3,ZNF571,ZNF527,FPGT,ERCC6L2,ZNF136,ZNF652,MYO18A,USP13
			Down regulated genes			
GO:0050896	BP	response to stimulus	4.08229E-05	4.389096276	239	HK2,LTF,FSTL3,PTX3,LEP,CYP26A1,CP,TREM1,HTRA4,BEX1,NTRK2,ADGRG3,FLT1,IL1RL1,KRT14,PPP1R1C,BTNL9,ADAM2,HILPDA,BHLHE40,PDZD7,NDRG1,CRLF1,ARNT2,HBG2,PFKP,GPIHBP1,PTGS2,ENG,MFSD2B,GNG4,GPER1,HCAR2,INHA,SH3BP5,L1CAM,PTPRR,DERL3,CRH,CORO2A,TENM4,DNER,SASH1,FOSL1,ARHGEF4,TPBG,GGT5,ERRFI1,ARHGAP45,GATA1,MAOB,GAPDH,VWCE,TNR,PAPPA2,GBA1,DIRAS1,SMOX,OASL,GREM2,GUCA2A,SLC38A3,GPR146,OBSCN,DDIT4L,PROCR,NR5A2,INHBA,MID1,SYDE1,BCL6,VEGFA,NRIP1,AK4,MX2,BIN2,FLNB,SHC3,MGAT3,DYRK3,ERO1A,ISG15,NPNT,PRDX6,TRIM14,GPR17,DUSP1,KRT19,CEBPA,HTRA1,MME,USP18,ABCA12,CBLC,NMUR1,LAMP3,SLC2A5,ARRDC3,MSRB1,GPX3,MTSS2,RDH13,LIMD1,CITED2,NEK11,PLAAT3,SDF2L1,FCRLB,SEMA4C,ITPR3,PLOD2,FOSL2,HMOX1,SCD,TNFRSF10D,SCNN1A,PRKD3,IFIT1,ANG,ZNF175,ABCA4,MCOLN1,MX1,RASSF7,BCAT2,GDF15,LYN,CGA,F2RL1,WNT9B,GRHL3,VDR,SERPINE1,LDLR,TIMP3,EBI3,CDO1,PIK3AP1,EFNB1,HAP1,SLC26A6,MOB3A,EDEM2,ATP6V0C,LRRC8A,SULF2,S100A9,PPP1R14B,CYP2J2,PIK3CB,RHBDD2,GPR157,CTSB,PPL,CD63,IER3,OCRL,NFIL3,ZNF703,SLC2A1,PKM,ABCA7,P2RY14,ASTE1,NCOR2,CYP11A1,NEURL1,CLDN7,HERPUD1,SLC27A4,ENO1,SUV39H1,S100A6,CLIC3,TMEM107,DNM2,FKBP8,SCARB1,PTGES,MAP3K8,PRKAB2,HEY1,NAT2,ARHGEF16,PPP1R12C,SIPA1L1,KDM3A,ACER2,GABARAPL2,ZNF432,TMEM38B,CHCHD10,NOCT,BAD,BNIP3L,DLX5,BACH1,LY6E,PLEC,DDR1,LRRC32,TSPYL2,SYNGR1,AVPI1,JPT2,POLR2I,ZMYND8,SLC10A3,GADD45G,SEMA4B,RUVBL2,PRDX2,PDK1,MMP15,TNIP2,PIM3,ITGA5,ERP44,SWI5,IMPA2,GPX4,PTPRU,MMP14,

						GLA,STK24,CEBPD,HMGB3,DAB2IP,TRIP10,PEBP1,NEDD9,LIMS1,GMDS,GATA3,DGKZ,SLC25A4,SREBF1,TNIP1,MAPK13
GO:0032501	BP	multicellular organismal process	9.73976E-05	4.01145167	201	HK2,LTF,FSTL3,PTX3,LEP,CYP26A1,ARMS2,PAEP,BEX1,NTRK2,SLC6A8,ADGRG3,FLT1,IL1RL1,KRT14,BTNL9,ADAM2,HILPDA,BHLHE40,PDZD7,NDRG1,CRLF1,SP5,ARNT2,MYO7B,GPIHBP1,PTGS2,IGSF8,FSCN2,ENG,MYO3B,MFSD2B,GPER1,HCAR2,INHA,L1CAM,PTPRR,CRH,TENM4,DNER,SASH1,JPH2,FOSL1,TNNI2,TPBG,ERRFI1,CKB,GATA1,MAOB,GAPDH,TNR,PAPPA2,GBA1,LDHA,GREM2,SLC38A3,CRYGN,PROCR,NR5A2,INHBA,MID1,SYDE1,BCL6,VEGFA,NRIP1,SHC3,KEL,MGAT3,DYRK3,MMP19,ISG15,KIF5A,NPNT,GPR17,ADAMTS4,DUSP1,KRT19,CEBPA,TMEM178A,MME,ABCA12,NMUR1,SLC2A5,ARRDC3,RDH13,LIMD1,CITED2,PLAAT3,ST8SIA6,SEMA4C,ITPR3,FOSL2,HMOX1,SCD,SCNN1A,HEXB,ANG,BASP1,ABCA4,SH3PXD2A,MFAP5,GDF15,LYN,CGA,F2RL1,WNT9B,GRHL3,CCSAP,VDR,SERPINE1,ALDOA,LDLR,TIMP3,EBI3,NTAN1,EFNB1,DYNC2I1,HAP1,SLC26A6,TGM1,LRRC8A,SULF2,S100A9,CYP2J2,PIK3CB,GPR157,CTSB,PPL,IER3,OCRL,NFIL3,ZNF703,SLC2A1,PKM,ABCA7,NCOR2,NEURL1,CNNM4,FPGS,UGP2,SLC27A4,ENO1,SUV39H1,S100A6,CLIC3,RAB25,TMEM107,SAT1,DNM2,FKBP8,SCARB1,PTGES,MAP3K8,PRKAB2,HEY1,SIPA1L1,KDM3A,RAB8B,FMN1,TMEM38B,HMG20B,NOCT,BAD,DLX5,MYL6,GRHL1,PLEC,DDR1,LRRC32,ETNK2,ACADL,FLVCR2,ZMYND8,GADD45G,MAFF,SEMA4B,PDLIM2,RUVBL2,PRDX2,MMP15,TNIP2,ITGA5,RPL13,EOLA1,OVGP1,MMP14,GLA,STK24,CEBPD,MGAT1,NEBL,DAB2IP,NEDD9,AP2A1,GATA3,DGKZ,SMARCA1,KMT2E,SREBF1,PEMT,MAPK13
GO:0005737	CC	cytoplasm	4.73E-13	12.32506027	333	HK2,LTF,FSTL3,PTX3,LEP,CYP26A1,ARMS2,CP,PADI1,BEX1,NTRK2,B4GALNT2,GYPA,ADGRG3,FLT1,IL1RL1,KRT14,QPCT,SPAG4,PPP1R1C,HILPDA,BHLHE40,PNCK,NDRG1,CRLF1,ANKRD37,ARNT2,MYO7B,HBG2,PFKP,PHYHIP,COL17A1,PTGS2,FSCN2,MYO3B,GPER1,SH3BP5,PTPRR,DERL3,CRH,TEN

M4,DNER,SASH1,JPH2,TNNI2,AR
HGEF4,SGPP2,TPBG,ERRFI1,ARH
GAP45,CKB,TET3,RASEF,CA4,MA
OB,GAPDH,VWCE,GBA1,SMOX,O
ASL,SFXN3,LDHA,EHF,OBSCN,D
DIT4L,PROCR,NR5A2,INHBA,GPT
2,SV2B,SLCO2A1,MID1,JPH1,BCL
6,VEGFA,SIGLEC6,NRIP1,PPP1R3
G,AK4,MX2,BIN2,FLNB,KCNJ6,C
HST15,SHC3,KEL,MGAT3,DYRK3
,ERO1A,ISG15,AFAP1,KIF5A,NPN
T,PRDX6,TRIM14,SEPTIN3,P4HA1
,DUSP1,KRT19,DAZL,RILP,MXI1,
HTRA1,TMEM178A,MME,SDC3,L
Y6K,USP18,ABCA12,SLC9A3,ATP
13A4,LAMP3,SLC2A5,ARRDC3,M
SRB1,MTSS2,RDH13,SLC28A1,LI
MD1,DEGS2,CITED2,PLAAT3,ST8
SIA6,SDF2L1,FCRLB,SEMA4C,ITP
R3,PIP5KL1,PLOD2,MICAL3,HMO
X1,DPP7,SCD,SCNN1A,PRKD3,FB
LIM1,IFIT1,HEXB,TCN2,ANG,BAS
P1,ZNF175,ABCA4,MCOLN1,AAD
AT,MX1,RASSF7,SH3PXD2A,BCA
T2,TPI1,GDF15,LYN,ABCC11,CGA
,IPMK,F2RL1,PFKFB4,FER1L5,CC
SAP,VDR,SERPINE1,ALDOA,ERG
IC1,LDLR,TIMP3,EBI3,CDO1,NTA
N1,PIK3AP1,PREP,EFNB1,DYNC2I
1,HAP1,SLC26A6,NANS,TGM1,GD
PD3,MOB3A,EDEM2,ATP6V0C,LR
RC8A,SULF2,AIF1L,S100A9,TECR
,PPP1R14B,CYP2J2,PIK3CB,RHBD
D2,FAM184A,CTSB,PPL,CD63,IER
3,DPM2,OCRL,HSD17B14,ZNF703,
KIF17,SLC2A1,PKM,ABCA7,CYP1
1A1,TMEM141,HMGN3,SH3BGRL
3,NEURL1,ZCCHC2,LRRC1,UBE2
Q2,FPGS,UGP2,HERPUD1,SLC27A
4,ENO1,TMEM179B,SUV39H1,S10
0A6,GOLT1A,CLIC3,KATNBL1,R
AB25,RFK,TESK2,FRMD4A,LAGE
3,REEP4,SAT1,DNM2,FKBP8,SCA
RB1,PTGES,MAP3K8,PRKAB2,AR
ID3A,HEY1,NAT2,GALK1,ARHGE
F16,PPP1R12C,SIPA1L1,PLEKHA2,
KDM3A,RAB8B,GFUS,ACER2,GA
LNT2,GABARAPL2,FMN1,TMEM3
8B,CHCHD10,ATP6V0E1,NOCT,B
AD,BNIP3L,DLX5,RELT,BACH1,
MYL6,PLEC,TSPYL2,ETNK2,MLX
,ACADL,SYNGR1,JPT2,DNAJC1,F
LVCR2,ZMYND8,METTL6,GADD
45G,ACTN1,MAFF,GALE,GLRX,P
DLIM2,PPP1R3B,RUVBL2,PRDX2,
PDK1,SSR4,OST4,TNIP2,PIM3,ITG
A5,EDF1,ERP44,RPL13,ATP6V1F,
DCXR,IMPA2,EOLA1,GPX4,MRPS
18A,GBE1,MTX1,OVGP1,MMP14,
GLA,POP7,STK24,RPL12,HMGB3,
MGAT1,HIGD1A,PJA1,CYB5R1,P

						NPLA2,NEBL,DAB2IP,TRIP10,ALG3,APOO,PEBP1,NEDD9,LIMS1,GMDS,AP2A1,TPRG1L,DGKZ,GLMP,KMT2E,RIOK1,SLC25A4,COMTD1,SREBF1,TNIP1,POLR2F,PEMT,NDUFB7,SPATA2L,MAPK13,ISCU
GO:0016020	CC	membrane	1.13E-12	11.9451643	282	HK2,LTF,CYP26A1,CP,TREM1,NTRK2,B4GALNT2,TMEM45A,SLC6A8,GYPA,ADGRG3,FLT1,IL1RL1,KRT14,SPAG4,BTNL9,ADAM2,HILPDA,PDZD7,NDRG1,CRLF1,ASPHD2,MYO7B,PFKP,GPIHBP1,COL17A1,PTGS2,IGSF8,ENG,MFSD2B,GNG4,GPER1,HCAR2,INHA,SH3BP5,SLC14A1,L1CAM,PTPRR,DERL3,TENM4,DNER,SLC2A14,UPK2,JPH2,FOSL1,ARHGEF4,SGPP2,TPBG,GGT5,ERRFI1,ARHGAP45,CKB,CA4,MAOB,GAPDH,RNF223,PRSS22,TMEM132B,TNR,PAPPA2,GBA1,DIRAS1,HPCAL1,SMOX,OASL,SFXN3,LDHA,SLC44A3,SLC38A3,GPR146,OBSCN,PROCR,LIPH,SV2B,SLCO2A1,MID1,CLDN6,JPH1,NECTIN4,SYDE1,VEGFA,SIGLEC6,MX2,BIN2,FLNB,KCNJ6,CHST15,SHC3,KEL,SLC16A3,MGAT3,ERO1A,CLDN9,VSIG10L,KIF5A,NPNT,PRDX6,TRIM14,GPR17,P4HA1,ADAMTS4,KRT19,RILP,HTRA1,TMEM178A,MME,SDC3,RARRES1,LY6K,ABCA12,CBLC,SLC9A3,NMUR1,ATP13A4,LAMP3,SLC2A5,ARRDC3,MTSS2,RDH13,SLC28A1,LIMD1,DEGS2,PLAAT3,ST8SIA6,SDF2L1,FCRLB,SEMA4C,ITPR3,PIP5KL1,PLOD2,MICAL3,HMOX1,PRSS27,TMEM91,SCD,TNFRSF10D,SCNN1A,PRKD3,HEXB,TCN2,BASP1,ABCA4,MCOLN1,MX1,LYN,ABCC11,F2RL1,FER1L5,PRRG1,SERPINE1,ALDOA,ERGIC1,LDLR,LYPD3,EBI3,PIK3AP1,PREP,EFNB1,SLC26A6,TGM1,GDPD3,EDEM2,ATP6V0C,LRRC8A,SULF2,SUSD2,AIF1L,S100A9,TECR,CYP2J2,PIK3CB,EFHD2,RHBDD2,GPR157,CTSB,PPL,CD63,IER3,DPM2,OCRL,KIF17,SLC2A1,ABCA7,P2RY14,NCOR2,CYP11A1,TMEM141,SH3BGRL3,TMEM154,NEURL1,LRRC1,CNNM4,CLDN7,FPGS,HERPUD1,SLC27A4,ENO1,TMEM179B,SUV39H1,S100A6,GOLT1A,CLIC3,KATNBL1,RAB25,REEP4,TMEM107,TLCD1,DNM2,FKBP8,SCARB1,PTGES,ARID3A,NAT2,GALK1,SIPA1L1,PLEKHA2,ERVH48-1,KDM3A,RAB8B,ACER2,GALNT2,GABARAPL2,FMN1,TMEM38B,CHCHD10,ATP6V0E1,BAD,BNIP3

						L,RELT,MYL6,TCAF2,LY6E,PLEC,DDR1,LRRC32,MLX,ACADL,SYNGR1,JPT2,DNAJC1,FLVCR2,SLC10A3,ACTN1,SEMA4B,RUVBL2,MMP15,SSR4,OST4,ITGA5,ERP44,RPL13,ATP6V1F,DCXR,PTPRU,MRPS18A,MTX1,MMP14,STK24,SURF2,RPL12,MGAT1,HIGD1A,CYB5R1,SMIM43,PNPLA2,DAB2IP,TRIP10,ALG3,APOO,NEDD9,LIMS1,AP2A1,TPRG1L,DGKZ,GLMP,KMT2E,SLC25A4,COMTD1,SREBF1,PEMT,PRSS8,NDUFB7
GO:0003824	MF	catalytic activity	7.03939E-05	4.152464872	202	HK2,LTF,CYP26A1,CP,TBC1D26,PADI1,HTRA4,NTRK2,B4GALNT2,FLT1,IL1RL1,QPCT,PPP1R1C,ADAM2,PNCK,ASPHD2,MYO7B,HBG2,PFKP,GPIHBP1,PTGS2,ENG,MYO3B,SH3BP5,PTPRR,ARHGEF4,SGPP2,GGT5,ERRFI1,ARHGAP45,CKB,TET3,RASEF,CA4,MAOB,GAPDH,RNF223,PRSS22,PAPPA2,GBA1,DIRAS1,SMOX,OASL,LDHA,GUCA2A,OBSCN,LIPH,GPT2,CHI3L2,MID1,SYDE1,VEGFA,AK4,MX2,CHST15,KEL,MGAT3,DYRK3,MMP19,ERO1A,KIF5A,PRDX6,TRIM14,SEPTIN3,P4HA1,ADAMTS4,DUSP1,HTRA1,MME,RARRES1,USP18,ABCA12,CBLC,ATP13A4,MSRB1,GPX3,MTSS2,RDH13,DEGS2,NEK11,PLAAT3,ST8SIA6,PIP5KL1,PLOD2,MICAL3,HMOX1,PRSS27,DPP7,SCD,PRKD3,HEXB,ANG,ABCA4,AADAT,MX1,SH3PXD2A,BCAT2,TPI1,LYN,ABCC11,IPMK,PFKFB4,SERPINE1,ALDOA,TIMP3,CDO1,NTAN1,PREP,SLC26A6,NANS,TGM1,GDPD3,MOB3A,EDEM2,ATP6V0C,SULF2,TECR,PPP1R14B,CYP2J2,PIK3CB,RHBDD2,CTSB,DPM2,OCRL,HSD17B14,KIF17,PKM,ABCA7,ASTE1,CYP11A1,NEURL1,UBE2Q2,FPGS,UGP2,SLC27A4,ENO1,SUV39H1,CLIC3,RAB25,RFK,TESK2,SAT1,DNM2,FKBP8,PTGES,MAP3K8,PRKAB2,NAT2,GALK1,ARHGEF16,PPP1R12C,SIPA1L1,KDM3A,RAB8B,GFUS,ACER2,GALNT2,NOCT,BAD,MYL6,DDR1,ETNK2,ACADL,POLR2I,METTL6,GALE,GLRX,PPP1R3B,RUVBL2,PRDX2,PDK1,MMP15,PIM3,ERP44,DCXR,IMPA2,GPX4,PTPRU,GBE1,OVGP1,MMP14,GLA,POP7,STK24,MGAT1,PJA1,CYB5R1,PNPLA2,DAB2IP,ALG3,PEBP1,GMDS,DGKZ,SMARCA1,RIOK1,COMTD1,ABHD8,POLR2F,PEMT,PRSS8,NDUFB7,MAPK13

GO:0042802	MF	identical protein binding	0.00080566	3.093848156	80	PTX3,HTRA4,NTRK2,GYPA,BHLHE40,PDZD7,PFKP,PTGS2,ENG,TENM4,ZNF114,RASEF,MAOB,GAPDH,LDHA,GREM2,INHBA,MID1,CLDN6,NECTIN4,BCL6,VEGFA,FLNB,CLDN9,PRDX6,SEPTIN3,P4HA1,DAZL,CEBPA,HTRA1,MME,SDC3,SLC9A3,GPX3,HMOX1,HEXB,ANG,MCOLN1,AADAT,MX1,TPI1,GDF15,ALDOA,LDLR,PIK3AP1,SLC26A6,TGM1,LRRC8A,HSD17B14,NFIL3,SLC2A1,PKM,CLDN7,UGP2,ENO1,S100A6,SAT1,FKBP8,ARID3A,GFUS,TMEM38B,BNIP3L,GRHL1,MLX,ACADL,ACTN1,GALE,RUVBL2,DCXR,IMPA2,GPX4,GLA,CEBPD,DAB2IP,TRIP10,GMDS,GATA3,TPRG1L,TNIP1,ISCU

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-3000178	ECM proteoglycans	1.75E-08	7.755924572	16	HAPLN1,NCAM1,COL4A4,COL1A2,VTN,COL1A1,COL6A1,LAMA2,ITGA7,LUM,COL3A1,FMOD,COL6A2,COL5A2,LAMC1,LAMB2
REAC:R-HSA-1474244	Extracellular matrix organization	1.75E-08	7.755924572	30	VCAM1,HAPLN1,NCAM1,COL4A4,COL1A2,COL8A2,VTN,PCOLCE,COL1A1,ADAMTS3,COL14A1,COL6A1,LAMA2,LTBP4,ITGA7,LUM,COL15A1,BMP4,COL3A1,FMOD,DDR2,COL21A1,COL6A2,FBN2,PRKCA,COL5A2,FBN1,LAMC1,CASK,LAMB2
REAC:R-HSA-9675108	Nervous system development	0.002937334	2.532046669	30	EPHA5,CNTN6,SCN11A,EPHA7,SCN4B,NCAM1,COL4A4,FLRT3,CNTN1,EPHA3,ARTN,UNC5C,ROBO2,COL6A1,LAMA2,SLIT3,ANK2,SLIT2,COL3A1,SCN9A,DPYSL3,COL6A2,ALCAM,PRKCA,COL5A2,FES,NRP2,LAMC1,EVL,DOCK1
REAC:R-HSA-5173105	O-linked glycosylation	0.002937334	2.532046669	11	THSD7B,SPON1,GALNT16,SBSPON,ADAMTS7,ADAMTS12,ADAMTS3,B3GLCT,ST6GAL1,

					B3GNT2,POMK
REAC:R-HSA-5668914	Diseases of metabolism	0.014122013	1.85010339	16	THSD7B,SPON1,SBSPON,CYP24A1,ADAMTS7,ADAMTS12,ADAMTS3,GYG2,LUM,OGN,B3GLCT,CUBN,FMOD,GCLM,PC,ACACA
REAC:R-HSA-9006934	Signaling by Receptor Tyrosine Kinases	0.014389852	1.841943679	26	GABRB1,COL4A4,FLRT3,COL1A2,COL1A1,FGF10,COL6A1,LAMA2,FGF7,CYBB,COL3A1,COL6A2,PRKCA,PCSK5,COL5A2,SPRED1,FES,NRP2,PTPN3,LAMC1,ELMO1,DOCK1,MAP2K5,PTPRK,LAMB2,MKNK1
		Down regulated genes			
REAC:R-HSA-1500931	Cell-Cell communication	0.21406468	0.669454985	12	KRT14,COL17A1,CLDN6,NECTIN4,CLDN9,FBLIM1,ANG,PIK3CB,CLDN7,PLEC,ACTN1,LIMS1
REAC:R-HSA-556833	Metabolism of lipids	0.21406468	0.669454985	36	HILPDA,ARNT2,PTGS2,MFSD2B,SGPP2,GGT5,GBA1,SLC44A3,LIPH,DEGS2,PLAAT3,SCD,PRKD3,HEXB,CGA,VDR,GDPD3,TECR,CYP2J2,PIK3CB,OCRL,HSD17B14,NCOR2,CYP11A1,PTGES,PRKAB2,PLEKHA2,ACER2,GRHL1,ETNK2,ACADL,GPX4,GLA,PNPLA2,SREBF1,PEMT
REAC:R-HSA-1430728	Metabolism	0.21406468	0.669454985	80	HK2,CYP26A1,B4GALNT2,SLC6A8,HILPDA,ARNT2,PFKP,GPIHBP1,PTGS2,MFSD2B,GNG4,SGPP2,GGT5,CKB,CA4,MAOB,GAPDH,GBA1,LDHA,SLC44A3,LIPH,AK4,CHST15,SDC3,DEGS2,PLAAT3,ITPR3,HMOX1,SCD,PRKD3,HEXB,TCN2,AADAT,BCAT2,TPI1,CGA,IPMK,PFKFB4,VDR,ALDOA,LDLR,CDO1,GDPD3,TECR,CYP2J2,PIK3CB,OCRL,HSD17B14,SLC2A1,NCOR2,CYP11A1,UGP2,ENO1,RFK,SAT1,DNM2,PTGES,PRKAB2,NAT2,GALK1,PLEKHA2,ACER2,GRHL1,ETNK2,MLX,ACADL,GALE,GLRX,PDK1,RPL13,DCXR,IMPA2,GPX4,GBE1,GLA,RPL12,PNPLA2,SREBF1,PEMT,NDUFB7
REAC:R-HSA-1474244	Extracellular matrix organization	0.285477707	0.5444278	18	COL17A1,TNR,MMP19,P4HA1,ADAMTS4,HTRA1,SDC3,PLOD2,SH3PXD2A,MFAP5,SERPINE1,CTSB,PLEC,DDR1,ACTN1,MMP15,ITGA5,MMP14

REAC:R-HSA-71387	Metabolism of carbohydrates and carbohydrate derivatives	0.291674284	0.53510186	17	HK2,B4GALNT2,PFKP,GAPDH,CHST15,SDC3,HEXB,TPI1,PFKFB4,ALDOA,SLC2A1,UGP2,ENO1,GALK1,GALE,DCXR,GBE1
REAC:R-HSA-382551	Transport of small molecules	0.343367088	0.464241335	32	CP,GPIHBP1,GNG4,SLC14A1,DERL3,SLC2A14,CA4,SLC44A3,SLC38A3,SLCO2A1,SLC16A3,ABCA12,SLC9A3,ATP13A4,SLC28A1,HMOX1,SCNN1A,ABCA4,MCOLN1,ABCC11,LDLR,SLC26A6,ATP6V0C,LRRC8A,SLC2A1,ABCA7,SLC27A4,ATP6V0E1,ATP6V1F,CYB5R1,AP2A1,SLC25A4

Table 4 Topology table for up and down regulated genes

Regulation	Node	Degree	Betweenness	Stress	Closeness
Up	VCAM1	625	0.075223	2.11E+08	0.376315
Up	PLEKHA7	483	0.055722	1.63E+08	0.357888
Up	SPRED1	330	0.049651	44549972	0.349233
Up	PTPN3	301	0.026722	49953068	0.356824
Up	EPHA7	270	0.031339	47010104	0.35988
Up	NDN	262	0.019329	54538752	0.347501
Up	DYRK2	252	0.023179	50958062	0.350457
Up	POMK	251	0.029285	37471758	0.341528
Up	KBTBD7	227	0.027705	28768730	0.347774
Up	H1-6	196	0.010155	18048328	0.327808
Up	MAGI3	193	0.009098	15998948	0.340159
Up	CAMK2A	181	0.020105	24353716	0.346312
Up	MYO18A	181	0.017111	20625680	0.346241
Up	PRKCA	175	0.019193	23429088	0.340877
Up	DHX57	169	0.009317	19012702	0.340118
Up	ANK2	159	0.013524	22050540	0.344637
Up	YTHDC2	155	0.008172	14651308	0.346569
Up	KCTD3	150	0.013046	13991816	0.343299
Up	TJP1	145	0.012498	16817432	0.358086
Up	UNC119	145	0.016359	15551072	0.33058
Up	SOX5	140	0.01361	14909922	0.322797
Up	PTPRK	140	0.011728	13922588	0.330463
Up	LURAP1	140	0.016053	11173818	0.337144
Up	CTLA4	136	0.015327	12385572	0.33295
Up	USP9X	132	0.013074	15093416	0.342614
Up	ZKSCAN8	132	0.011514	12919336	0.336496
Up	EPHA5	131	0.006915	13008610	0.337185
Up	MRPS30	131	0.007279	9641854	0.33686
Up	PDZRN3	130	0.006029	8373536	0.342684
Up	MTA1	127	0.01032	15266052	0.330424
Up	GRID2IP	127	0.003213	7682312	0.329543
Up	PARD3B	124	0.004636	11995506	0.330437
Up	SLC16A10	124	0.011827	10133042	0.336092
Up	CDK18	122	0.010732	14377134	0.338788
Up	DDR2	121	0.00909	15039242	0.34038
Up	MAPK8	120	0.010665	13213906	0.333956
Up	ABCD3	113	0.009919	11976724	0.340049
Up	MAP1LC3C	111	0.006396	6856136	0.345785
Up	NTNG1	110	0.011539	8614994	0.324542
Up	CASK	108	0.010363	10540100	0.338229

Up	COL1A1	108	0.010854	9810500	0.336039
Up	B3GNT2	107	0.010128	9108864	0.333347
Up	VTN	106	0.010566	9709686	0.330958
Up	BCL7A	105	0.010035	6501654	0.324869
Up	LAMB2	103	0.008765	7864372	0.338802
Up	C3	102	0.008941	9379342	0.334767
Up	HAUS7	102	0.010159	8382116	0.336914
Up	PTPRD	101	0.013243	6437100	0.325359
Up	FAT1	101	0.009892	8671414	0.344241
Up	TRIM32	99	0.009734	9643652	0.332135
Up	SSBP2	99	0.011485	7038146	0.332003
Up	GJA1	97	0.009043	8236076	0.339431
Up	KIFC3	96	0.009861	7320910	0.327936
Up	CDK20	93	0.007734	8022068	0.326801
Up	SLAMF1	91	0.007063	6802776	0.320973
Up	ITGA7	90	0.006282	5157956	0.315396
Up	COL6A1	89	0.007291	5002260	0.318371
Up	FZD2	89	0.007109	6781894	0.314818
Up	TRAF3	88	0.009284	8067184	0.322278
Up	COL6A2	88	0.006475	4520530	0.311562
Up	OSBPL3	88	0.008131	8199664	0.341237
Up	HAUS3	88	0.004434	5867604	0.328538
Up	ANKRD50	88	0.009082	24888736	0.312535
Up	CACNG4	88	0.006735	6417020	0.329079
Up	SYT6	85	0.005982	6505080	0.323331
Up	LRP2	81	0.008565	5686184	0.330411
Up	BMP4	81	0.008405	7844092	0.303265
Up	EPHA3	80	0.005194	5549368	0.332766
Up	GH1	80	0.003667	8139638	0.317349
Up	DHFR2	79	0.005857	9684912	0.308701
Up	VANGL2	78	0.005382	5937904	0.338952
Up	BIN1	77	0.007474	6934030	0.322154
Up	LAMC1	77	0.005668	4461172	0.328487
Up	KLHL42	77	0.007699	4371616	0.31923
Up	STN1	76	0.008877	7959662	0.311527
Up	SALL2	73	0.005339	5791294	0.324154
Up	NCEH1	73	0.007435	5145498	0.319024
Up	PKD2	71	0.007049	7971288	0.309645
Up	KCTD12	70	0.005816	6065668	0.324906
Up	PC	70	0.006538	5192462	0.327565
Up	LRRC4	6	1.60E-04	186736	0.272227
Up	ARHGEF26	5	2.01E-04	338842	0.275872
Up	FZD4	5	2.81E-04	503354	0.279199
Up	GUCY1A2	5	1.54E-06	28430	0.26859
Up	ADGRA2	5	2.88E-06	47968	0.270684
Up	MOXD1	5	3.42E-04	273180	0.284838
Up	EMID1	4	2.91E-04	148072	0.271839
Up	FZD1	4	2.63E-06	45706	0.269382
Up	NOS1AP	4	8.64E-05	203172	0.280232
Up	ADAMTS7	4	1.33E-04	259266	0.280447
Up	PCSK5	4	3.90E-05	115630	0.267122
Up	TKFC	4	9.80E-05	163870	0.265175
Up	DKK2	3	1.25E-04	63570	0.265947
Up	PTPN14	3	4.01E-05	55866	0.273725
Up	GCLM	3	1.35E-04	164660	0.269668
Up	FAT3	3	7.80E-07	16660	0.265318
Up	IFRD1	3	1.38E-05	126336	0.265485
Up	TBC1D9	3	1.77E-05	48592	0.27133
Up	C1QTNF2	2	5.30E-07	2336	0.246474
Up	HSD3B2	2	1.03E-04	55798	0.264708
Up	ANGPTL7	2	3.57E-05	33068	0.264641
Up	ZKSCAN3	2	1.25E-05	18478	0.262541
Up	MKNK1	2	3.64E-05	59036	0.26776
Up	ZSCAN23	2	5.55E-05	44500	0.259254
Up	ADCK1	2	5.44E-05	82704	0.265192
Up	FNDC1	2	2.79E-05	22234	0.256445
Up	FGF12	2	4.85E-05	31738	0.267692
Up	MATN2	2	7.00E-06	15662	0.255541
Up	COL8A2	2	5.30E-07	2336	0.246474
Up	ARL4C	2	4.56E-06	11920	0.260887

Up	DGKK	2	6.00E-08	564	0.258822
Up	SLC4A4	2	5.34E-05	56924	0.264425
Up	KRT80	2	1.21E-05	100400	0.275078
Up	ACACA	2	1.03E-05	48690	0.264641
Up	CRACD	2	1.05E-05	56448	0.270388
Up	COL1A2	2	0	0	0.258075
Up	PCOLCE	2	4.16E-05	20984	0.26391
Up	SMO	2	3.65E-05	114344	0.275474
Up	TTC28	2	3.52E-05	32610	0.268762
Up	PDP1	2	2.46E-04	81418	0.26109
Up	HYCC1	2	1.16E-04	216402	0.272033
Up	ZFP90	2	7.84E-05	123430	0.276072
Up	RABGAP1L	2	6.61E-05	34976	0.258321
Up	LONRF2	2	1.11E-04	80174	0.265443
Up	ALCAM	2	7.06E-05	26014	0.258894
Up	USP6NL	2	1.42E-06	11076	0.265636
Up	PCDHB14	2	1.59E-05	18308	0.260628
Up	ADAMTS12	2	3.28E-05	32738	0.257625
Up	CNTN1	2	5.06E-06	16614	0.269356
Up	USP13	1	0	0	0.255572
Up	GUCY1A1	1	0	0	0.250357
Up	AHI1	1	0	0	0.26139
Up	ZNF827	1	0	0	0.248367
Up	RARG	1	0	0	0.25279
Up	HPGDS	1	0	0	0.253881
Up	MOB3C	1	0	0	0.25764
Up	ZNF462	1	0	0	0.263323
Up	MXRA5	1	0	0	0.260701
Up	ZNF891	1	0	0	0.268865
Up	VSTM4	1	0	0	0.253125
Up	FMO1	1	0	0	0.247665
Up	LRATD2	1	0	0	0.248133
Up	C14orf180	1	0	0	0.247665
Up	FES	1	0	0	0.260701
Up	LUM	1	0	0	0.254227
Up	SELE	1	0	0	0.258846
Up	NR1D2	1	0	0	0.258846
Up	CNTN5	1	0	0	0.242989
Up	FRMD3	1	0	0	0.247665
Up	KCNMB3	1	0	0	0.239445
Up	C1QTNF7	1	0	0	0.261447
Up	SPX	1	0	0	0.241871
Up	P2RY1	1	0	0	0.239445
Up	ZNF517	1	0	0	0.24836
Up	GYG2	1	0	0	0.251556
Up	CORO6	1	0	0	0.25764
Up	KCTD7	1	0	0	0.255572
Up	SPATA46	1	0	0	0.263678
Up	HMGCLL1	1	0	0	0.250813
Up	SPON1	1	0	0	0.261447
Up	RCAN1	1	0	0	0.245495
Up	CLDN1	1	0	0	0.259895
Up	SCN4B	1	0	0	0.261504
Up	OCA2	1	0	0	0.262083
Up	RAP2B	1	0	0	0.273431
Up	TRIM45	1	0	0	0.270292
Up	BMX	1	0	0	0.245495
Up	RSPO2	1	0	0	0.253353
Up	ERC2	1	0	0	0.256814
Up	NHS	1	0	0	0.246959
Up	TRIM2	1	0	0	0.246315
Up	ZNF737	1	0	0	0.258028
Up	HECW2	1	0	0	0.253881
Up	NDUFAF5	1	0	0	0.256829
Up	RYR2	1	0	0	0.243666
Up	ZNF185	1	0	0	0.252365
Up	ZNF618	1	0	0	0.252843
Up	OXER1	1	0	0	0.254635
Up	DTNB	1	0	0	0.252752
Up	ATRIP	1	0	0	0.25779

Up	AGPAT5	1	0	0	0.249792
Up	CIBAR1	1	0	0	0.252145
Up	DOCK1	1	0	0	0.249126
Up	NRP2	1	0	0	0.252175
Up	CYP24A1	1	0	0	0.251986
Up	CTHRC1	1	0	0	0.248875
Up	MORC4	1	0	0	0.25279
Up	DACH1	1	0	0	0.244033
Up	ANKRD10	1	0	0	0.268865
Up	C1orf226	1	0	0	0.252168
Up	SLIT2	1	0	0	0.253881
Up	ENO3	1	0	0	0.261447
Up	BMP5	1	0	0	0.232703
Up	F13A1	1	0	0	0.247606
Up	CDH11	1	0	0	0.246315
Up	MAPKBP1	1	0	0	0.250357
Up	SRPX	1	0	0	0.245029
Up	OLFML3	1	0	0	0.257144
Up	ADGRL3	1	0	0	0.252175
Up	LRIG3	1	0	0	0.252767
Up	PPIP5K2	1	0	0	0.260701
Down	GABARAPL2	581	0.068432	1.93E+08	0.370395
Down	RPL13	496	0.051953	99035364	0.367319
Down	H1-4	361	0.029955	50674462	0.355151
Down	GPR17	328	0.036206	59832338	0.347314
Down	PDK1	320	0.043698	73413778	0.345572
Down	RUVBL2	272	0.030679	51014608	0.357431
Down	HTRA4	272	0.026963	47272036	0.354089
Down	SDF2L1	264	0.032956	30271746	0.346141
Down	SULF2	234	0.024579	41484294	0.353984
Down	HTRA1	224	0.016449	22562572	0.351145
Down	OASL	219	0.010905	21704768	0.342042
Down	PLEC	217	0.024322	34387746	0.352618
Down	GYPA	215	0.017453	29750890	0.331768
Down	GAPDH	213	0.023259	31651092	0.367721
Down	ARRDC3	210	0.020705	34332474	0.340256
Down	ENG	210	0.024011	26297340	0.337537
Down	EFNB1	208	0.020166	32550980	0.355196
Down	UPK2	208	0.024504	22284708	0.337198
Down	PDZD7	202	0.007588	16528586	0.3415
Down	COMTD1	202	0.013052	30909048	0.338802
Down	OCRL	200	0.019425	32517972	0.345544
Down	SLC27A4	196	0.016471	31778082	0.338257
Down	SLC2A1	191	0.020198	25652420	0.356582
Down	CSNK1E	188	0.021546	34049134	0.338393
Down	PRKAB2	188	0.024127	23551654	0.341611
Down	TGM1	182	0.022327	17015074	0.338898
Down	FKBP8	174	0.019342	24016278	0.34132
Down	GATA3	173	0.018338	21880958	0.338297
Down	DDIT4L	172	0.021997	23033640	0.330009
Down	F2RL1	168	0.014549	24405640	0.329608
Down	TNIP1	167	0.019228	16225172	0.347042
Down	SUV39H1	165	0.016556	18604754	0.339308
Down	REEP4	161	0.022987	27856336	0.329182
Down	DNM2	160	0.016666	19986240	0.35388
Down	S100A6	160	0.01856	19093790	0.340352
Down	GPIHBP1	158	0.015402	13863296	0.331323
Down	FLT1	155	0.011484	20809612	0.340863
Down	SEMA4C	147	0.013379	20023316	0.346198
Down	LYN	146	0.015576	19772566	0.343257
Down	NDRG1	144	0.012594	20855776	0.345061
Down	S100A9	142	0.014267	14872710	0.347745
Down	BTNL9	138	0.007663	19153264	0.323394
Down	NCOR2	137	0.014396	14422750	0.335583
Down	ATP6V0C	136	0.015706	14720146	0.335168
Down	RPL12	134	0.006771	11930000	0.358499
Down	PKM	9	0.001349	2792748	0.318939
Down	DGKZ	9	6.72E-04	986708	0.292765
Down	GNG4	8	1.76E-05	198482	0.276126
Down	ALDOA	6	1.37E-04	751826	0.303452

Down	EDEM2	6	2.91E-04	411234	0.281518
Down	SLC16A3	6	2.77E-04	471862	0.27488
Down	ENO1	6	1.41E-04	1043226	0.298388
Down	GLA	5	2.75E-04	353078	0.275709
Down	PTPRU	5	2.28E-04	332962	0.269771
Down	GOLT1A	5	1.67E-04	285754	0.273574
Down	ABCA7	5	3.70E-06	57472	0.270075
Down	SLC9A3	5	1.21E-04	147866	0.276444
Down	PRDX2	5	1.03E-04	906106	0.296264
Down	MRPS18A	4	8.44E-05	419018	0.279626
Down	MYL6	4	2.80E-04	490606	0.284077
Down	ERP44	4	2.16E-04	299678	0.282863
Down	HMG20B	4	5.23E-04	411464	0.273894
Down	TECR	4	2.67E-04	222110	0.274557
Down	HACL2	4	1.99E-04	220486	0.279403
Down	AK4	4	1.94E-04	173752	0.269711
Down	CRLF1	4	8.88E-05	163364	0.274011
Down	PLEKHA2	4	1.23E-06	25604	0.265443
Down	TMEM178A	4	2.63E-06	45706	0.269382
Down	PLOD2	4	2.49E-04	223344	0.283713
Down	PRDX6	4	7.81E-05	461726	0.291962
Down	CKB	4	7.45E-05	552162	0.288099
Down	BASP1	4	1.61E-04	252574	0.283483
Down	PPL	4	4.08E-04	398880	0.273493
Down	SYDE1	4	3.17E-04	331614	0.282274
Down	LRRC1	4	2.39E-04	191544	0.277182
Down	BCL6	3	8.57E-05	88208	0.266512
Down	MME	3	1.28E-04	136382	0.275673
Down	CD63	3	1.05E-04	204638	0.261659
Down	LRRC32	3	8.55E-05	40678	0.268196
Down	LIPH	3	9.17E-05	80846	0.267309
Down	ANG	3	1.20E-04	155592	0.270031
Down	NEBL	3	1.02E-04	138048	0.282028
Down	IGSF8	3	1.49E-04	109558	0.269815
Down	DDR1	3	7.95E-05	92100	0.272615
Down	TIMP3	3	3.20E-05	46572	0.26794
Down	KRT14	3	5.93E-05	227818	0.283226
Down	GRHL1	3	3.46E-05	113442	0.271322
Down	ARHGEF16	3	7.80E-07	16660	0.265318
Down	SLC6A8	3	4.20E-05	54598	0.274422
Down	AP2A1	3	7.63E-05	192130	0.284145
Down	SH3PXD2A	3	1.32E-04	170306	0.274485
Down	PFKP	3	3.39E-05	301720	0.288
Down	LDHA	3	3.15E-05	242650	0.284202
Down	NOCT	3	2.60E-04	171774	0.269832
Down	P4HA1	3	3.05E-05	51002	0.265594
Down	CNNM4	3	1.53E-04	67220	0.268025
Down	GADD45G	2	1.04E-04	70898	0.258496
Down	SAT1	2	3.18E-05	26692	0.254342
Down	MAPK13	2	1.55E-05	51902	0.276471
Down	MMP14	2	4.29E-05	31480	0.255557
Down	ITGA5	2	5.45E-05	167726	0.277704
Down	ACTN1	2	2.80E-05	94850	0.270719
Down	GATA1	2	3.97E-05	37912	0.261244
Down	KRT19	2	4.94E-05	57558	0.280045
Down	LAMP3	2	3.22E-05	79104	0.260636
Down	FOSL2	2	1.30E-05	19526	0.26386
Down	ALG3	2	2.38E-05	52966	0.263232
Down	TNIP2	2	0	0	0.264425
Down	BAD	2	1.62E-05	22940	0.257333
Down	PEBP1	2	5.57E-05	118802	0.27488
Down	SEPTIN3	2	8.54E-05	179260	0.274601
Down	CLIC3	2	8.78E-05	53606	0.254712
Down	HAP1	2	1.83E-05	65294	0.27669
Down	BNIP3L	2	4.97E-05	78198	0.274243
Down	PIM3	2	1.04E-05	17954	0.261415
Down	MYO3B	2	1.47E-05	26520	0.26232
Down	GREM2	2	2.42E-05	23474	0.262993
Down	ARMS2	2	3.64E-05	25204	0.259726
Down	RELT	2	1.15E-04	31916	0.256453

Down	SDC3	2	5.30E-07	6990	0.262026
Down	EAF1	2	7.02E-06	27782	0.275015
Down	SV2B	2	3.69E-05	44076	0.260984
Down	GBA1	2	0	0	0.261724
Down	LDLR	2	1.47E-05	20656	0.263835
Down	FLNB	2	2.50E-05	84298	0.275773
Down	SSR4	2	2.41E-05	66074	0.273138
Down	HK2	2	3.98E-05	80210	0.28101
Down	GALNT2	2	2.13E-05	28660	0.262919
Down	EFHD2	2	5.13E-05	55536	0.263043
Down	PRSS8	2	3.21E-04	147034	0.269919
Down	ZNF703	2	4.97E-05	114378	0.269063
Down	LTF	2	5.13E-06	32384	0.265737
Down	GDF15	2	9.15E-05	73740	0.264574
Down	DNAJC1	2	5.17E-05	54316	0.258178
Down	TPI1	2	7.44E-06	50890	0.266479
Down	DDA1	2	1.24E-05	50074	0.268359
Down	HMOX1	2	1.79E-04	52780	0.264233
Down	DAB2IP	2	7.25E-06	54206	0.270684
Down	SCARB1	2	1.68E-05	13604	0.25382
Down	SLC25A4	2	6.50E-06	16328	0.266504
Down	JPH1	2	3.60E-06	8380	0.258759
Down	L1CAM	2	5.49E-05	47144	0.264733
Down	EBI3	2	1.25E-04	68906	0.26631
Down	SIPA1L1	2	0	0	0.267795
Down	TESK2	2	0		0.267795
Down	BIN2	1	0	0	0.243666
Down	SERPINE1	1	0	0	0.248669
Down	PHYHIP	1	0	0	0.256547
Down	MLX	1	0	0	0.270292
Down	VDR	1	0	0	0.262993
Down	IFIT1	1	0	0	0.246749
Down	SLC38A3	1	0	0	0.237557
Down	PREP	1	0	0	0.268865
Down	PPP1R3B	1	0	0	0.260701
Down	HERPUD1	1	0	0	0.247906
Down	VWCE	1	0	0	0.253071
Down	SURF2	1	0	0	0.258044
Down	FER1L5	1	0	0	0.262083
Down	PTPRR	1	0	0	0.260701
Down	ACADL	1	0	0	0.253125
Down	SFXN3	1	0	0	0.247665
Down	SH3BGRL3	1	0	0	0.248133
Down	CLDN7	1	0	0	0.252175
Down	DYRK3	1	0	0	0.253125
Down	NEK11	1	0	0	0.254473
Down	SPATA2L	1	0	0	0.256547
Down	HPCAL1	1	0	0	0.258846
Down	MAOB	1	0	0	0.258846
Down	MIIP	1	0	0	0.258846
Down	PTX3	1	0	0	0.25764
Down	AVPI1	1	0	0	0.248455
Down	LYPD3	1	0	0	0.241871
Down	RARRES1	1	0	0	0.261447
Down	FBLIM1	1	0	0	0.255572
Down	DPM2	1	0	0	0.239445
Down	CYP2J2	1	0	0	0.236441
Down	CGA	1	0	0	0.247271
Down	LIMS1	1	0	0	0.257199
Down	DAZL	1	0	0	0.243736
Down	VEGFA	1	0	0	0.254219
Down	KEL	1	0	0	0.251556
Down	ERGIC1	1	0	0	0.262107
Down	CA4	1	0	0	0.253064
Down	TMEM107	1	0	0	0.239445
Down	SLC14A1	1	0	0	0.251038
Down	LEP	1	0	0	0.241495
Down	TNFRSF10D	1	0	0	0.251526
Down	OST4	1	0	0	0.254473
Down	SMIM43	1	0	0	0.262862

Down	KCNJ6	1	0	0	0.245495
Down	KIF17	1	0	0	0.262993
Down	PPP1R3G	1	0	0	0.261504
Down	CLDN6	1	0	0	0.250357
Down	EOLA1	1	0	0	0.255572
Down	SLC2A14	1	0	0	0.262862
Down	SLC44A3	1	0	0	0.253422
Down	TRIP10	1	0	0	0.255549
Down	ZMYND8	1	0	0	0.252843
Down	GALK1	1	0	0	0.273431
Down	HBG2	1	0	0	0.273431
Down	AFAP1	1	0	0	0.257199
Down	MICAL3	1	0	0	0.257199
Down	CORO2A	1	0	0	0.257199
Down	ERO1A	1	0	0	0.251526
Down	TCAF2	1	0	0	0.249126
Down	C12orf75	1	0	0	0.248455
Down	POP7	1	0	0	0.258044
Down	PHLDB3	1	0	0	0.258044
Down	CEBPA	1	0	0	0.263571
Down	PROCR	1	0	0	0.263571
Down	ISCU	1	0	0	0.256829
Down	BCAT2	1	0	0	0.243666
Down	GLRX	1	0	0	0.261504
Down	HMGB3	1	0	0	0.261504
Down	KATNBL1	1	0	0	0.254635
Down	ADGRG3	1	0	0	0.252175
Down	TRIM14	1	0	0	0.254635
Down	TMEM154	1	0	0	0.249126
Down	ITPR3	1	0	0	0.257238
Down	SCD	1	0	0	0.254589
Down	FSCN2	1	0	0	0.254227
Down	NDUFB7	1	0	0	0.258846
Down	RILP	1	0	0	0.258846
Down	FPGS	1	0	0	0.25779
Down	UGP2	1	0	0	0.253935
Down	STK24	1	0	0	0.253935
Down	RDH13	1	0	0	0.252767
Down	MTX1	1	0	0	0.247606
Down	MMP15	1	0	0	0.252175
Down	GALE	1	0	0	0.244339
Down	TSPYL2	1	0	0	0.268651
Down	SCNN1A	1	0	0	0.257144
Down	SEMA4B	1	0	0	0.257144
Down	SUSD2	1	0	0	0.257144
Down	ATP6V1F	1	0	0	0.251038
Down	CYB5R1	1	0	0	0.25279
Down	NFIL3	1	0	0	0.243736
Down	ARID3A	1	0	0	0.25279
Down	MTSS2	1	0	0	0.264649
Down	ZCCHC2	1	0	0	0.253881
Down	ASPHD2	1	0	0	0.25779
Down	GPX4	1	0	0	0.249126

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

Regulation	**Hub Genes**	**Degree**	**MicroRNA**	**Regulation**	**Hub Genes**	**Degree**	**TF**
Up	SPRED1	365	hsa-miR-6731-5p	Up	MAGI3	77	BMI1
Up	DYRK2	341	hsa-miR-500b-5p	Up	SPRED1	71	UTX
Up	MYO18A	277	hsa-miR-133a-3p	Up	DYRK2	66	CREM
Up	PRKCA	227	hsa-miR-17-5p	Up	PRKCA	61	TAL1
Up	EPHA7	203	hsa-miR-379-3p	Up	PLEKHA7	60	GATA4
Up	PTPN3	198	hsa-miR-377-5p	Up	MYO18A	60	CTNNB1
Up	POMK	195	hsa-miR-195-5p	Up	KBTBD7	45	HNF4A
Up	MAGI3	189	hsa-miR-6742-3p	Up	ANK2	44	YAP1
Up	KBTBD7	154	hsa-miR-132-3p	Up	EPHA7	43	PHC1

Up	CAMK2A	133	hsa-miR-6743-5p	Up	PTPN3	36	NR1I2
Up	VCAM1	116	hsa-miR-5092	Up	VCAM1	36	ETV1
Up	DHX57	114	hsa-miR-744-5p	Up	CAMK2A	24	RUNX1
Up	PLEKHA7	90	hsa-miR-449a	Up	NDN	17	MTF2
Up	NDN	70	hsa-miR-93-5p	Up	POMK	17	TBX5
Up	H1-6	1	hsa-miR-130b-3p	Up	DHX57	14	BACH1
Down	PLEC	416	hsa-miR-6835-3p	Down	SULF2	81	HAND2
Down	ARRDC3	298	hsa-miR-548n	Down	PLEC	81	MAF
Down	GAPDH	219	hsa-miR-141-5p	Down	GAPDH	64	PHF8
Down	SULF2	142	hsa-miR-5585-3p	Down	PDK1	60	EWSR1
Down	PDK1	132	hsa-miR-375	Down	ARRDC3	56	HOXB4
Down	RPL13	121	hsa-miR-148a-5p	Down	HTRA1	42	TFCP2L1
Down	GABARAPL2	105	hsa-miR-30c-2-3p	Down	OASL	39	TFEB
Down	RUVBL2	97	hsa-miR-128-1-5p	Down	GABARAPL2	36	SOX2
Down	HTRA1	90	hsa-miR-6810-5p	Down	RPL13	34	MEIS1
Down	OASL	63	hsa-miR-182-3p	Down	RUVBL2	33	AP1S2
Down	H1-4	61	hsa-miR-1304-5p	Down	ENG	30	WDR5
Down	SDF2L1	59	hsa-miR-214-3p	Down	SDF2L1	23	EBNA1
Down	GPR17	33	hsa-miR-320e	Down	GYPA	20	PBX1
Down	HTRA4	11	hsa-miR-16-5p	Down	HTRA4	19	RNF2
Down	GYPA	10	hsa-miR-944	Down	GPR17	16	SREBF2

Table 6 Drug- hub gene topology table

Regulations	Gene	Degree	Drug (One Example)
Up	PRKCA	19	Acteoside
Up	HPGDS	18	S-Hexylglutathione
Up	MAPK8	17	Encorafenib
Up	RARG	17	Palovarotene
Up	C3	11	S-Hydroxycysteine
Up	DHFR2	9	Epigallocatechin gallate
Up	SCN4B	8	Oxcarbazepine
Up	SMO	8	Halcinonide
Up	SELE	7	Rivipansel
Up	GUCY1A2	7	Isosorbide mononitrate
Up	GUCY1A1	7	Nitroprusside
Up	CACNG4	7	Bioallethrin
Up	COL1A1	6	Von Willebrand factor human
Up	VTN	6	Abciximab
Up	KCNMB3	6	Nitrendipine
Up	CAMK2A	5	HexatantalumDodecabromide
Up	F13A1	5	Anti-inhibitor coagulant complex
Up	VCAM1	4	Succinobucol
Up	ENO3	4	Phosphoenolpyruvate
Up	DDR2	3	Regorafenib
Up	BMX	3	Zanubrutinib
Up	PC	3	Pyruvic acid
Up	LRP2	3	Efanesoctocog alfa
Up	CTLA4	3	Ipilimumab

Up	GJA1	2	Caprylic alcohol
Up	EPHA7	2	5-[(2-methyl-5-{[3-(trifluoromethyl)phenyl]carbamoyl}phenyl)amino]pyridine-3-carboxamide
Up	HSD3B2	2	Trilostane
Up	RYR2	2	Flecainide
Up	GCLM	2	Glutamic acid
Up	DYRK2	2	Harmine
Up	DGKK	1	alpha-Tocopherol succinate
Up	COL1A2	1	PR-15
Up	LUM	1	Copper
Up	FES	1	Fostamatinib
Up	ACACA	1	Biotin
Down	MAOB	55	Ephedra sinica root
Down	CA4	34	Methyclothiazide
Down	FLT1	26	Selpercatinib
Down	VDR	22	Seocalcitol
Down	TPI1	17	5-fluorotryptophan
Down	MME	15	Sacubitrilat
Down	SERPINE1	12	Troglitazone
Down	HMOX1	11	Isopropyl alcohol
Down	ALDOA	9	Dihydroxyacetone phosphate
Down	GAPDH	8	Omigapil
Down	LDHA	8	Stiripentol
Down	PRE	8	Z-Pro-Prolinal
Down	LYN	7	Dasatinib
Down	S100A9	7	Paquinimod
Down	SLC25A4	7	Carboxyatractyloside
Down	MAPK13	6	Minocycline
Down	ENO1	6	Artenimol
Down	GALE	6	Tetramethylammonium
Down	MMP14	5	Epigallocatechin gallate
Down	KCNJ6	4	Halothane
Down	PRKAB2	3	Acetylsalicylic acid
Down	PROCR	3	Phosphatidylethanolamine
Down	PRDX2	3	3-sulfino-L-alanine
Down	GPR17	3	Uridine-5'-Diphosphate
Down	ITGA5	3	Tauroursodeoxycholic acid
Down	P4HA1	3	Hydralazine
Down	GPX4	3	Benzoyl peroxide
Down	COMTD1	3	Feruloyl Coenzyme A
Down	FPGS	3	Raltitrexed
Down	CSNK1E	3	Umbralisib
Down	GLA	3	Calystegine B2

Down	S100A6	3	Calcium phosphate dihydrate
Down	ITPR3	3	1D-myo-inositol 1,4,5-trisphosphate
Down	PRDX6	2	2-(N-morpholino)ethanesulfonic acid
Down	ACTN1	2	Human calcitonin
Down	KRT14	2	Zinc
Down	SLC2A1	2	Carboxymethylcellulose
Down	PDK1	2	Dichloroacetic acid
Down	SLC38A3	2	Asparagine
Down	SLC6A8	2	Creatine
Down	SCNN1A	2	Triamterene
Down	SLC9A3	2	Cariporide
Down	PIM3	1	Fostamatinib
Down	SLC16A3	1	Pyruvic acid
Down	CYB5R1	1	Flavin adenine dinucleotide
Down	NDUFB7	1	NADH
Down	H1-4	1	Copper
Down	PEBP1	1	Copper
Down	KEL	1	Phosphoramidon
Down	MMP15	1	Marimastat
Down	L1CAM	1	Ethanol
Down	PLOD2	1	Ascorbic acid
Down	GLRX	1	Glutathione
Down	ATP6V1F	1	Tiludronic acid
Down	ATP6V0C	1	Tiludronic acid

Table 7. Novel biomarkers for Preeclampsia

Regulation	Novel biomarkers
Up regulated genes	OR51B5, EPHA5, CNTN6, DGKK, SSTR1, AMER2, CXCL14, RSPO2, FMO1, SCN11A, DKK2, SYT6, CRACD, EPHA7, ALDH1A1, SLAMF1, SCN4B, FAT3, HAPLN1, CES1, GABRB1, FGF12, FRZB, NCAM1, RARRES2, CHAT, SPON1, CAMK2A, IL7, ANO3, FLRT3, PRRX1, ENPP1, OXER1, IGHG2, CNTN1, EFHB, H1-6, SLC25A27, COLEC10, KCNJ5, SYNPO2L, SLC16A10, LRRC63, C1QTNF2, HAS3, MEGF10, KCNE1, COL1A2, EPHA3, OSR1, ZNF554, ARTN, SMO, ASXL3, GABRA4, TRIM45, ADGRL3, SLC4A4, TXK, COL1A1, OLFML1, ADAMTS7, ASPA, SRPX, DLGAP2, SALL2, ADAMTS3, ERC2, CYSLTR1, OCA2, ROBO2, PDE1A, ENPP2, OLFML2A, KCNC4, ANKS1B, COL14A1, TNFRSF11A, NOS1AP, BHLHE41, LAMA2, NALCN, PRICKLE1, PTPRD, RYR2, ZNF667, ZNF618, LTBP4, CACNG4, LURAP1, ASTN2, C1QTNF3, LSS, GUCY1A1, RAPSN, CYBB, RAB39A, ANK2, ITGA7, GPR155, VANGL2, LRRN3, SCUBE2, GUCY1A2, ANGPTL2, CCND2, TFAP2B, PROM1, NPY1R, SLIT2, PER3, OGN, RFX8, ABI3BP, FZD2, EGFL6, ZSCAN23, COL15A1, CD84, SH3TC2, P2RY1, IL12RB2, BMX, PREX2, F13A1, PCDHB14, COL3A1, PRDM6, ADGRA2, ANGPTL7, AFF3, FMOD, SCN9A, GPR68, ITGBL1, NDN, ZNF555, DACH1, NTNG1, DDR2, DPYSL3, VSTM4, RAB27B, TCF21, TMEM168, COL6A2, HPGDS, ZNF462, CDH11, NCEH1, ANKRD13B, SCAMP5, NR1D2, GRID2IP, HAUS7, AKAP6, GPR158, ARHGAP42, MTCL1, ARHGEF10L, ADGRB2, FBN2, ZNF658, PRKCA, SOX5, FZD4, ST6GAL1, LRP2, PRKG1, ADCY7, ZNF197, GIMAP8, PCSK5, BIN1, NR3C2, COL5A2, DTNB, POU2F2, FAT1, RCAN1, CDK18, KCTD12, ANKDD1A, BNC2, ENC1, TTC28, DYRK2, CARD18, SPRED1, ZNF404, HECW2, MTSS1, CDKN2B, ZNF844, PC, BCL7A, PDE5A, MOB3C, TRIM2, ZNF697, ZNF470, SYT17, CDK20, NFATC2, CABLES1, ZNF564, FZD1, FBN1, KCNMB3 FES, ZXDA, NRP2, LRRC4, AMER1, RAP1GAP2, ZNF582, PIP5K1B, PTPN3, ZNRF3, ZFP28, TLCD2, LAMC1, EVL, ELMO1, TRAF3, USP9X, RARG, RABGAP1L, PLEKHA7, ZNF441, ADCK1, STN1, PIP4P2, USP6NL, PKD2, FBXO10, RALGPS1, ZNF891, ZNF772, ERCC6, MAGI3, ZFP90, AHI1, ZKSCAN2, ZNF827, ZNF737, ZNF517, KLHL42, TJP1, RAP2B, ARID5B, ZKSCAN8, PIKFYVE, MEAK7, RBAK, PRAG1, RAPH1, KCTD7, MAP2K5, RAB15, KBTBD7, PTPRK, ZFP3, MTCL2, YTHDC2, LAMB2, MKNK1, TKFC, ZKSCAN3, RALGAPA2, ATP9B, ZNF362, NRDE2, ZNF490, PTPN14, TRIM32, ZNF181, UNC119, RNASEL, PXK, MAP4K3, ATRIP, ZNF571, ZNF527, PABIR1, MAPKBP1, ZNF136,

	HAUS3, ZNF652, SSBP2, MYO18A, USP13, CIBAR1, THSD7B, CNTN6, CADM3, SCN11A, LGSN, MYO1A, HMCN2, FREM1, CNTN5, TMPRSS11F, CLDN16, PTPRQ, C14ORF180, CATSPERB, SLC16A14, MGST1, SBSPON, IGFLR1, CALHM4, COL8A2, PCOLCE, ADGRL3, MATN2, LRIG3, CACNA2D4, ARL4C, KIAA1549, CALHM5, HMCN1, EMID1, COL21A1, SYTL5, LRATD2, HYCC1, PARD3B, SLCO2B1, CLCN5, ENO3, PLEKHM3, NHS, SLC46A1, KCTD3, OSBPL3, MYH13, GALNT16, VAT1L, ZC2HC1A, PDZRN3, ACOXL, HAAO, LONRF2, CPXM1, GYG2, HMGCLL1, CARNS1, SDSL, CHKA, ARHGEF26, DHFR2, ZNF185, DHX57, ABCD3, PDP1, PPIP5K2, MORC4, ZCCHC14, ACACA, KIFC3, POMK, TBC1D9, FPGT and ERCC6L2
Down regulated genes	BEX1, NTRK2, ADGRG3, KRT14, BTNL9, ADAM2, PDZD7, CRLF1, ARNT2, HBG2, PFKP, GPIHBP1, MFSD2B, GNG4, HCAR2, SH3BP5, L1CAM, PTPRR, DERL3, CORO2A, TENM4, DNER, ARHGEF4, GGT5, ERRFI1, ARHGAP45, MAOB, GAPDH, VWCE, TNR, DIRAS1, SMOX, OASL, GREM2, GUCA2A, SLC38A3, GPR146, OBSCN, DDIT4L, NR5A2, MID1, AK4, MX2, BIN2, SHC3, MGAT3, DYRK3, PRDX6, TRIM14, GPR17, KRT19, CEBPA, MME, USP18, ABCA12, CBLC, NMUR1, SLC2A5, MSRB1, GPX3, MTSS2, RDH13, LIMD1, NEK11, SDF2L1, FCRLB, SEMA4C, ITPR3, PLOD2, SCD, TNFRSF10D, SCNN1A, PRKD3, IFIT1, ZNF175, ABCA4, MX1, RASSF7, LYN, F2RL1, WNT9B, GRHL3, CDO1, PIK3AP1, EFNB1, HAP1, SLC26A6, MOB3A, EDEM2, ATP6V0C, LRRC8A, SULF2, PPP1R14B, PIK3CB, RHBDD2, GPR157, PPL, CD63, IER3, OCRL, NFIL3, ZNF703, PKM, ABCA7, P2RY14, ASTE1, NEURL1, CLDN7, HERPUD1, SLC27A4, ENO1, SUV39H1, TMEM107, DNM2, FKBP8, SCARB1, PTGES, MAP3K8, PRKAB2, NAT2, ARHGEF16, PPP1R12C, SIPA1L1, GABARAPL2, ZNF432, TMEM38B, CHCHD10, NOCT, BAD, BNIP3L, LY6E, PLEC, DDR1, LRRC32, TSPYL2, SYNGR1, AVPI1, JPT2, POLR2I, ZMYND8, SLC10A3, GADD45G, SEMA4B, RUVBL2, PDK1, TNIP2, PIM3, SWI5, IMPA2, PTPRU, GLA, STK24, HMGB3, DAB2IP, TRIP10, PEBP1, NEDD9, LIMS1, GMDS, DGKZ, SLC25A4, SREBF1, TNIP1, MAPK13, ARMS2, B4GALNT2, GYPA, QPCT, SPAG4, PNCK, MYO7B, FSCN2, MYO3B, TENM4, JPH2, TNNI2, ARHGEF4, SGPP2, CKB, RASEF, CA4, SFXN3, LDHA, EHF, GPT2, SV2B, SLCO2A1, JPH1, KCNJ6, CHST15, KEL, KIF5A, SEPTIN3, P4HA1, DAZL, RILP, MXI1, TMEM178A, SDC3, LY6K, SLC9A3, ATP13A4, SLC28A1, DEGS2, ST8SIA6, PIP5KL1, MICAL3, DPP7, FBLIM1, HEXB, TCN2, BASP1, AADAT, TPI1, ABCC11, CGA, IPMK, PFKFB4, FER1L5, CCSAP, ALDOA, ERGIC1, NTAN1, PREP, DYNC2I1, NANS, TGM1, GDPD3, AIF1L, TECR, FAM184A, DPM2, HSD17B14, TMEM141, SH3BGRL3, ZCCHC2, LRRC1, UBE2Q2, FPGS, UGP2, TMEM179B, GOLT1A, KATNBL1, RAB25, RFK, TESK2, FRMD4A, LAGE3, REEP4, SAT1, ARID3A, GALK1, PLEKHA2, RAB8B, GFUS, FMN1, ATP6V0E1, RELT, MYL6, ETNK2, ACADL, DNAJC1, FLVCR2, METTL6, ACTN1, MAFF, GALE, PDLIM2, PPP1R3B, SSR4, OST4, EDF1, RPL13, ATP6V1F, DCXR, EOLA1, MRPS18A, GBE1, MTX1, OVGP1, POP7, RPL12, MGAT1, HIGD1A, PJA1, CYB5R1, PNPLA2, NEBL, ALG3, APOO, TPRG1L, GLMP, KMT2E, RIOK1, COMTD1, POLR2F, PEMT, NDUFB7, SPATA2L, ISCU, TBC1D26, ASPHD2, RNF223, PRSS22, LIPH, CHI3L2, MMP19, RARRES1, PRSS27, SMARCA1, ABHD8, PRSS8, CLDN6 and CLDN9