Distinct Molecular Mechanisms Analysis of Obesity Based on Gene Expression Profiles

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Research

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Abstract

Background

Obesity is the most common metabolic disorder worldwide. Its progression rate has remained high in recent years.

Objectives

Therefore, the aim of this study was to diagnose important differentially expressed genes (DEGs) associated in its development, which may be used as novel biomarkers or potential therapeutic targets for obesity.

Methods

The gene expression profile of E-MTAB-6728 was downloaded from the database. After screening DEGs in each ArrayExpress dataset, we further used the robust rank aggregation method to diagnose 876 significant DEGs including 438 up regulated and 438 down regulated genes. Pathway enrichment analyses and Gene Ontology (GO) were performed by online tool ToppCluster. These DEGs were shown to be significantly enriched in different obesity related pathways and GO functions. Then, the mentha, miRNet and NetworkAnalyst databases were used to construct the protein–protein interaction network, target genes - miRNA regulatory network and target genes - TF regulatory network. The module analysis was performed by the PEWCC1 plug-in of Cytoscape based on the whole PPI network.

Results

We finally filtered out HSPA8, ESR1, YWHAH, RPL14, SOD2, BTG2, LYZ and EFNA1 hub genes. Hub genes were validated by ICH analysis, Receiver operating curve (ROC) analysis and RT-PCR. The robust DEGs linked with the development of obesity were screened through the ArrayExpress database, and integrated bioinformatics analysis was conducted.

Conclusions

Our study provides reliable molecular biomarkers for screening and diagnosis, prognosis as well as novel therapeutic targets for obesity.

Introduction

Obesity comes under metabolic disorder and is now so common in global population [1]. Obesity occurs in children age between 5 to 19 years as well as more common in women than in men [2]. It is linked with pathogenesis of many disorders such as heart disease [3], hyperlipidaemia [4], hyperinsulinaemia [5], hypertension [6], atherosclerosis [7], insulin resistance [8] and cancer [9]. Important candidate genes and relevant signaling pathways linked with obesity remains largely unknown. As a result, seek of an earlier diagnosis and better prognosis, deeper understanding of genetic and molecular mechanisms about obesity is necessary.

Accumulative evidence suggested that many genes and signaling pathways participate in obesity progression. Polymorphisms in UCP2 and UCP3 were responsible for development of obesity [10]. TNF α and lipoprotein lipase were important for advancement of obesity [11]. SLC6A14 [12] and JHDM2A [13] were lined with pathogenesis of obesity. Human salivary (AMY1) and pancreatic (AMY2) amylase genes were diagnosed with growth of obesity [14]. Signaling pathways such as inflammatory signaling pathway [15], TLR4 signaling pathway [16], calcineurin-dependent signaling pathways [17], mTOR Complex1–S6K1 signaling pathway [18] and leptin-signaling pathway [19] were important for development of obesity. Therefore, it is key to understand the molecular mechanisms associated in development of obesity, which facilitates effective diagnosis, prognosis and treatment. However, the essential genes of development of obesity remain largely unknown.

In present trends, the application of high-throughput analysis in gene expression is becoming more valuable in clinical and medical research [20], molecular classification [21], prognosis prediction [22], diagnoses [23] and new targeted drug discovery [24]. In this study, the original microarray data (E-MTAB-6728) was downloaded from ArrayExpress. The gene expression profiles of adipocytes from obese patients were extracted and compared with those in adipocytes from lean persons (controls) to identify the differently expressed genes (DEGs). Subsequently, the DEGs were screened with the application of limma (<http://www.bioconductor.org/packages/release/bioc/html/limma.html>) followed by gene ontology (GO), pathway enrichment analysis using different pathway databases, Protein–protein interaction network construction and analysis, module analysis, target gene - miRNA interaction network construction and analysis, and target gene - TF interaction network construction and analysis. The results provide information about the key pathways and genes that will contribute to further research on the diagnosis, prognosis and treatment for obesity.

Materials And Methods

Microarray Data

The microarray expression profile of E-MTAB-6728 was downloaded from ArrayExpress (<https://www.ebi.ac.uk/>). E-MTAB-6728 was based on A-MEXP-1171 - Illumina HumanHT-12 v3.0 Expression BeadChip and was submitted by Bjune et al [25]. The E-MTAB-6728 dataset about expression of genes from adipocytes from obese patients compared to adipocytes from lean persons (controls). There are twenty-four samples including twelve adipocytes from obese patients and twelve adipocytes from lean persons (controls). The overall design of the experiment was microarray analysis of adiposities from obese patients versus adipocytes from lean persons (controls).

Identification of DEGs between obese patients and lean persons

The raw data files were acquired for the analysis as IDAT files (Illumina platform) forms and were converted into gene symbols and then processed to background correction and quartile data normalization using the effective multiarray average algorithm in the beadarray package. The analysis was carried out via R software (version 3.5.2). Hierarchical clustering analysis was applied to categorize the samples into two groups with similar expression patterns in twelve adiposities from obese patients and twelve adipocytes from lean persons (controls). The paired Student's t-test based on the Limma package in R was used to diagnose DEGs between two experimental conditions. Multiple testing correction was performed by the Benjamini–Hochberg method to obtain the FDR (false discovery rate) value. Then, the Log2 Fold change ($\log_2FC$) was determined. DEGs with an $FDR < 0.05$ and $|\log_2FC| \geq 0.5$ were considered to be statistically significant.

Pathway enrichment analysis of DEGs

To further analyses the potential pathway of the overlapping DEGs, the online software ToppCluster (<https://toppcluster.cchmc.org/>) [26] which integrates different pathway data bases such as BIOCYC (<https://biocyc.org/>) [27], Kyoto Encyclopedia of Genes and Genomes (KEGG) (<http://www.genome.jp/kegg/pathway.html>) [28], Pathway Interaction Database (PID) (<https://wiki.nci.nih.gov/pages/viewpage.action?pageId=315491760>) [29], REACTOME (<https://reactome.org/>) [30], GenMAPP (<http://www.genmapp.org/>) [31], MSigDB C2 BIOCARTEA (v6.0) (<http://software.broadinstitute.org/gsea/msigdb/collections.jsp>) [32], PantherDB (<http://www.pantherdb.org/>) [33], Pathway Ontology (<http://www.obofoundry.org/ontology/pw.html>) [34] and Small Molecule Pathway Database (SMPDB) (<http://smpdb.ca/>) [35] were used to perform pathway enrichment analysis. $P < 0.05$ and counts > 2 were set as the threshold values.

Gene ontology (GO) enrichment analysis of DEGs

The DEGs (up and down regulated) were subjected to GO (<http://www.geneontology.org/>) [36] enrichment analysis. The GO analysis having terms under the three categories such as cellular component (CC), molecular function (MF) and biological process (BP). GO enrichment analyses were performed using ToppCluster (<https://toppcluster.cchmc.org/>) [26] online tool. The cut-off value for a significant GO term and pathway was set to $p\text{-value} < 0.05$ and count ≥ 2 .

Integration of PPI network and module analysis

Online tool mentha (<https://mentha.uniroma2.it/>) [37] is the popular online tool which integrates different PPI databases such as The Molecular INTERaction Database (MINT, <https://mint.bio.uniroma2.it/>) [38], IntAc (<https://www.ebi.ac.uk/intact/>) [39], Database of Interacting Proteins (DIP, <https://dip.doe-mbi.ucla.edu/dip/Main.cgi>) [40], MatrixDB (<http://matrixdb.univ-lyon1.fr/>) [41] and Biological General Repository for Interaction Datasets (BioGRID, <https://thebiogrid.org/>) [42] for evaluating protein–protein interaction (PPI) network. Therefore, the interactions of genes (up and down regulated) were analyzed by online tool mentha. To prevent uncertain PPI, a high confidence with interaction score more than 0.7 was set as significance. After that, PPI network was constructed by cytoscape software (version 3.5.1) (<http://www.cytoscape.org/>) [43]. The plug-in CytoNCA [44] showed hub genes based on 5 centrality mathematical calculation methods such as node degree [45], betweenness [46], stress [47], closeness [48] and clustering coefficient [49], the number of genes within 5 centrality mathematical calculation methods were represented the significance of the disorder. Module analysis was done by the plug-in PEWCC1 [50]. Representative modules were listed by the criteria of both PEWCC1 scores and the number of nodes more than 3.

Construction of target genes - miRNA regulatory network

Generation of target genes - miRNA regulatory network by online tool miRNet (<https://www.mirnet.ca/>) [51] which integrates 10 miRNA databases such as TarBase (<http://diana.imis.athena-innovation.gr/DianaTools/index.php?r=tarbase/index>) [52], miRTarBase (<http://mirtarbase.mbc.nctu.edu.tw/php/download.php>) [53], miRecords (<http://miRecords.umn.edu/miRecords>) [54], miR2Disease (<http://www.mir2disease.org/>) [55], HMDD (<http://www.cuilab.cn/hmdd>) [56], PhenomiR (<http://mips.helmholtz-muenchen.de/phenomir/>) [57], SM2miR (<http://bioinfo.hrbmu.edu.cn/SM2miR/>) [58], PharmacomiR (<http://www.pharmaco-mir.org/>) [59], EpimiR (<http://bioinfo.hrbmu.edu.cn/EpimiR/>) [60] and starBase (<http://starbase.sysu.edu.cn/>) [61]. Target genes (up and down regulated) - miRNA were predicted using the overrepresentation enrichment analysis method, and interactions between the target genes (up and down regulated) - miRNA interaction was obtained. Then, the target gene - miRNA regulatory network was visualized by using the Cytoscape software (<http://www.cytoscape.org/>) [43].

Construction of target genes - TF regulatory network

TFs controls the expression of genes by interacting with their target genes at the during transcription stage. Generation of target genes - TF regulatory network by online tool NetworkAnalyst (<https://www.networkanalyst.ca/>) [62] online tool which integrates one TFs database ENCODE (<https://www.encodeproject.org/pipelines/ENCPL138KID/>) [63] and target genes - TF regulatory network was visualized by Cytoscape software (<http://www.cytoscape.org/>) [43].

Validation of hub genes

Immunohistochemical analysis of adipose tissues was performed utilizing human protein atlas (www.proteinatlas.org) [64]. Statistical analysis was performed using pROC package [65] in R. Receiver operating curve (ROC) and area under the curve (AUC) analyses were estimated for diagnostic value of hub genes. When the AUC value was > 0.6 , the DEGs were considered to be capable of distinguishing patients with obesity patients from normal lean with excellent specificity and sensitivity. RT-PCR was used to verify and compare the expression levels of five up regulated and down regulated hub genes Total cellular RNA was extracted from cell culture of adipocytes of normal and obesity with 1 ml TRI Reagent® (Sigma, USA). Reverse transcription cDNA kit (Thermo Fisher Scientific, Waltham, MA, USA) and random primers were used to synthesize cDNA. RT-PCR was performed using QuantStudio 7 Flex real-time PCR system

(Thermo Fisher Scientific, Waltham, MA, USA). The conditions for RT-PCR amplification were as follows: 95°C for 120 seconds followed by 40 cycles of 95°C for 15 seconds, annealing temperature for 45 seconds. Each sample was run in triplicate. Relative expression level for each target gene was normalized by the Ct value of β -actin (internal control) using a $2^{-\Delta\Delta CT}$ relative quantification method [66]. The primer pairs used in the experiments are listed in Table 1.

Results

Data Normalization

Each array was normalized (centered) by quartile data normalization using the beadarray package in R bioconductor. Fig. 1A and Fig. 1B shows a boxplot of (before and after normalization) gene expression in each of the two groups in the E-MTAB-6728 dataset.

Identification of DEGs between obese patients and lean persons

To preliminarily understand the mechanism contributing to the obesity, 24 patients (adipocytes from 12 obese patients and 12 lean persons) were selected for subsequent analysis. A total of 876 DEGs (Log FC > 0.524 for up regulated genes, Log FC < -0.394 for down regulated genes, P < 0.05) were diagnosed (Table 2). Among them, 438 genes were up regulated and 438 genes were down regulated. Up regulated and down regulated gene expression heat map are shown in Fig. 2 and Fig.3. Volcano map for DEGs is shown in Fig. 4.

Pathway enrichment analysis of DEGs

To preliminarily comprehend the function of DEGs, we submitted up regulated genes and down regulated genes, respectively, to the online software ToppCluster diagnose related pathways from different pathway databases (BIOCYC, KEGG, PID, REACTOME, GenMAPP, MSigDB C2 BIOCARTA, PantherDB and SMPDB). Pathway enrichment analysis results showed that up regulated genes were significantly enriched in thyroid hormone metabolism II (via conjugation and/or degradation), serotonin degradation, ECM-receptor interaction, focal adhesion, IL6-mediated signaling events, glypican 1 network, collagen formation, binding and uptake of ligands by scavenger receptors, steroid hormone metabolism, glycosaminoglycan degradation, genes encoding collagen proteins, genes encoding structural ECM glycoproteins, integrin signalling pathway, axon guidance mediated by Slit/Robo, hypertension, integrin signaling, suprofen pathway and mefenamic acid pathway (Table 3). Down regulated genes were mainly significantly enriched in the super pathway of methionine degradation, fatty acid beta-oxidation, ribosome, propanoate metabolism, FoxO family signaling, HIF-2-alpha transcription factor network, eukaryotic translation elongation, metabolism of amino acids and derivatives, selenoamino acid metabolism, nitrogen metabolism, CDK regulation of DNA replication, PTEN dependent cell cycle arrest and apoptosis, p38 MAPK pathway, serine glycine biosynthesis, glycine, serine and threonine metabolic, transulfuration of homocysteine metabolism, methionine metabolism and ketone body metabolism (Table 4).

Gene ontology (GO) enrichment analysis of DEGs

The results of GO enrichment analysis of up and down regulated genes in obese patients analyzed based on GO terms such as Biological Process (BP), Cellular Component (CC) and Molecular Function (MF) using ToppCluster are shown in Table 5 and Table 6. Up regulated genes were significantly enriched in BP, CC and MF related to blood vessel morphogenesis, cardiovascular system development, extracellular matrix, extracellular matrix component, growth factor binding and integrin binding. Down regulated genes were significantly enriched in BP, CC and MF related to organic acid biosynthetic process, cellular amide metabolic process, cytosolic small ribosomal subunit, ribosome, structural constituent of ribosome and transcription factor binding.

Integration of PPI network and module analysis

The mentha database and Cytoscape were used to construct a PPI network of up and down regulated genes. A total of 7271 nodes 16270 edges are included in the PPI networks of up regulated genes (Fig. 5). The up regulated hub genes such as HSPA8, HSPA5, ERBB2, STAT3, YWHAH, SPTAN1, STEAP2, COL11A1, NEK6, CPG2 and NOTCH3 with highest node degree distribution, betweenness centrality, stress centrality, closeness centrality and low clustering coefficient are listed in Table 7, and statistical results and scatter plot for node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustering coefficient are shown in Fig. 6A - 6E. These up regulated hub genes were mainly enriched in toxoplasmosis, Parkinson disease, focal adhesion, proteoglycans in cancer, PI3K-Akt signaling pathway, cytokine signaling in immune system, protein digestion and absorption and blood vessel morphogenesis. A total of 7276 nodes 19862 edges are included in the PPI networks of down regulated genes (Fig. 7). The down regulated hub genes such as ESR1, FBL, CSNK2B, ARRB1, PCM1, RPS2, RPS3, PTEN, SIRT1, ZNF581, CKB, FBXO11, UBR2 and INTS6 with highest node degree distribution, betweenness centrality, stress centrality, closeness centrality and low clustering coefficient are listed in Table 7, and statistical results and scatter plot for node degree distribution, betweenness centrality, stress centrality, closeness centrality and clustering coefficient are shown in Fig. 8A - 8E. These down regulated hub genes were mainly enriched in regulation of nuclear SMAD2/3 signaling, the SARS-coronavirus life cycle, herpes simplex infection, macromolecule catabolic process, ribosome, cellular amide metabolic process, FoxO signaling pathway, AMPK signaling pathway, metabolic pathways, nucleolus, negative regulation of nucleic acid-templated transcription and nucleoplasm part.

Subsequently, we performed module analysis of the whole network by the PEWCC1 plug-in. 1798 modules were extracted from the PPI network (up regulated). The four most significant modules were selected (module 12 (49 nodes and 99 edges), module 17 (46 nodes and 110 edges), module 26 (41 nodes and 91 edges) and module 68 (68 had 14 nodes and 25 edges)) in this PPI network (Fig. 9). Pathway and GO enrichment analysis showed that HSPA8, ERBB2, HSPA5, SPP1, YWHAH, STAT3, MSN and ITGB5 were included in module 12, module 17, module 26 and module 68, and participated in toxoplasmosis, focal adhesion, Parkinson disease, ECM-receptor interaction, negative regulation of multicellular organismal process, regulation of locomotion, cell migration and extracellular structure organization. Meanwhile, 2079 modules were extracted from the PPI network (down regulated). The four most significant modules were selected (module 15 (66 nodes and 754 edges), module 28 (46 nodes and 146 edges), module 60 (31 nodes and 146 edges) and module 86 (23 nodes and 67 edges)) in this PPI network (Fig. 10). Pathway and GO enrichment analysis showed that ESR1, SRSF3, SIN3A, CSNK2A2, RPL14, KHDRBS1, SIRT1 and

CSNK2B were included in module 15, module 28, module 60 and module 86, and participated in regulation of nuclear SMAD2/3 signaling, herpes simplex infection, signaling events mediated by HDAC Class I, metabolism of lipids and lipoproteins, cellular amide metabolic process, translation, organic acid biosynthetic process and transcription factor binding.

Construction of target genes - miRNA regulatory network

Up and down regulated target genes interacts with miRNA are shown Fig. 11 and Fig. 12. The up regulated targeted genes (SOD2 (degree = 257, ex; hsa-mir-3144-3p), CCND1 (degree = 251, ex; hsa-mir-7706), TUBB2A (degree = 193, ex; hsa-mir-7162-3p), CCND2 (degree = 179, ex; hsa-mir-5692c) and TMEM189 (degree = 146, ex; hsa-mir-548z)) are listed in Table 8. These up regulated target genes were mainly enriched in hypertension, focal adhesion and phagosome. Similarly, down regulated targeted genes (BTG2 (degree = 247, ex; hsa-mir-6075), TXNIP (degree = 228, ex; hsa-mir-3194-3p), MED28 (degree = 203, ex; hsa-mir-6861-5p), CNBP (degree = 197, ex; hsa-mir-4651) and MKNK2 (degree = 195, ex; hsa-mir-3650)) are listed in Table 8. These down regulated target genes were mainly enriched in cellular amide metabolic process, negative regulation of nucleic acid-templated transcription, nucleoplasm part, DNA-binding transcription factor activity and p38 MAPK pathway.

Construction of target genes - TF regulatory network

Up and down regulated target genes interacts with TFs are shown Fig. 13 and Fig. 14. Up regulated targeted genes (YWHAH (degree = 70, ex; MAZ), LYZ (degree = 62, ex; TFDPI), HP (degree = 60, ex; KLF9), TRAM2 (degree = 54, ex; KLF16) and CCND1 (degree = 51, ex; EZH2) are listed in Table 9. These up regulated target genes were mainly enriched in PI3K-Akt signaling pathway, neutrophil degranulation, amb2 Integrin signaling and focal adhesion. Similarly, top five down regulated targeted genes (EFNA1 (degree = 91, ex; TFDPI), MED16 (degree = 85, ex; MAZ), RWDD2A (degree = 82, ex; KDM5B), ADD3 (degree = 82, ex; SAP30) and AIP (degree = 82, ex; PHF8) are listed in Table 9. These down regulated target genes were mainly enriched in HIF-2-alpha transcription factor network, fatty acid, triacylglycerol, and ketone body metabolism, chromosome and transcription factor binding.

Validation of hub genes

Immunohistochemical analysis demonstrated that the expression of STAT3, CORO1C, SERPINH1, MVP and ITGB5 were highly expressed in adipose tissues, whereas PCM1, SIRT1, EEF1G, PTEN and RPS2 were low expressed in adipose tissue (Fig. 15). ROC curve analyses and the AUC were used to assess the discriminatory ability of ten DEGs (STAT3, CORO1C, SERPINH1, MVP, ITGB5, PCM1, SIRT1, EEF1G, PTEN and RPS2). The AUCs of all these four DEGs, including STAT3 (0.951), CORO1C (0.799), SERPINH1 (0.924), MVP (0.938), ITGB5 (0.938), PCM1 (0.826), SIRT1 (0.799), EEF1G (0.913), PTEN (0.833) and RPS2 (0.840), were more than 0.6 (Fig. 16), which had great diagnostic value for obesity. Then, we also performed RT-PCR to detect obesity patients and lean controls, finding that STAT3, CORO1C, SERPINH1, MVP and ITGB5 levels were elevated in adipose tissues of obesity patients compared with normal lean tissues, whereas PCM1, SIRT1, EEF1G, PTEN and RPS2 levels were decreased in adipose tissues of obesity patients compared with normal lean tissues (Fig. 17).

Discussion

Obesity remains a leading cause of heart disease, hyperlipidaemia, hyperinsulinaemia, hypertension, atherosclerosis, insulin resistance and cancer in worldwide, despite continuously improved detection and treatment strategies. Due to microarray technology, it is easier to analyze the genetic modifications underlying obesity development and progression. In addition, through bioinformatics tools it is possible to diagnose new biomarkers, new pathways and to construct networks that could be valuable for the management of obesity patients.

In our study, a total of 876 DEGs were diagnosed from gene expression dataset, consisting of 438 up regulated genes and 438 down regulated genes in obese patients compared to lean persons. Genes such as PTGDS (prostaglandin D2 synthase) [67], LBP (lipopolysaccharide binding protein) [68], EGFL6 [69], STAT3 [70] and HDAC9 [71] were responsible for development of obesity. Genes such as CYP11A1 [72] and WNT11 [73] were diagnosed with growth of prostate cancer, but these genes may be responsible for improvement of obesity associated cancer. GPR146 was responsible for development of insulin resistance [74], but this gene may be associated with development of obesity. RFX1 was responsible for progression of heart disease [75], but this gene may be diagnosed with growth of obesity. ZHX2 was liable for development of atherosclerosis [76], but this gene may be associated with progression of obesity. CLDN1 was responsible for progression of hypertension [77], but this gene may be diagnosed with progression of obesity.

Pathway enrichment analysis for up regulated genes was implemented. Enriched genes such as SULT1A1 [78], SULT1A2 [78], COL6A1 [79], COL6A2 [80], SOS1 [81], STAT1 [82], COL5A2 [83] and RND3 [84] were responsible for progression of heart disease, but these genes may be responsible for advancement of obesity. Enriched genes such as COL1A2 [85] and COL3A1 [86] were involved in development of hypertension, but these genes may be diagnosed with growth of obesity. Enriched genes such as DAG1 [87], ITGAV (integrin subunit alpha V) [88], LAMA5 [89], SPP1 [90], COL11A1 [91], COL12A1 [92], SERPINH1 [93] and RHOC [94] were responsible for advancement of various cancer types such as bladder cancer, colorectal cancer, gastric cancer, pancreatic cancer, lung cancer and endometrial cancer, but these genes may be involved in development of obesity associated cancer. Enriched genes such as LAMB3 [95], THBS1 [96], TIMP1 [97], LOX (lysyl oxidase) [98], MMP9 [99], HSD11B1 [100], ITGB2 [101], HMOX1 [102], SOD2 [103] and AKR1C3 [104] were responsible for progression of obesity. COL15A1 was important for development of atherosclerosis [105], but this gene may be associated with development of obesity. Our study found that ITGB5, LAMB2, COL16A1, CRTAP (cartilage associated protein) and ACTN1 are up regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target. Pathway enrichment analysis for down regulated genes was implemented. CBS (cystathionine-beta-synthase) was responsible for progression of atherosclerosis [106], but this gene may be identified with development of obesity. Enriched genes such as MAT2B [107], FOXO1 [108], FOXO3 [109], SIRT1 [110], ACACB (acetyl-CoA carboxylase beta) [111], ELK1 [112], MAP3K5 [113] and CTH (cystathionine gamma-lyase) [114] were important for development for obesity. Genes such as RPL14 [115], RPL29 [116], RPS12 [117], RPS15A [118], RPS2 [119], RPS27 [120], RPS3 [121], RBL2 [122], EEF1D [123], ACACA (acetyl-CoA carboxylase alpha) [124], ORC2 [125], PHGDH (phosphoglycerate dehydrogenase) [126] and SHMT1 [127] were involved in

progression of various cancer types, but these genes may be liable for progression of obesity associated cancer. CDKN1B was liable for development of hyperinsulinemia [128], but this gene may be involved in progression of obesity. MCM6 was identified with progression of heart disease [129], but this gene may be responsible for advancement of obesity. EEF2K was diagnosed with progression of hypertension [130], but this gene may be involved in development of obesity. Our study found that BCKDHA (branched chain keto acid dehydrogenase E1, alpha polypeptide), PCCA (propionyl-CoA carboxylase subunit alpha), RPL17, RPL18, RPL18A, RPL21, RPL35, RPL9, RPS17, RPS18, RPS29, RPS9, RSL24D1, MAPK10, ZFAND5, EEF1G, ALDH6A1, LDHC, MKNK2, RPS6KA5 and GATM (glycine amidinotransferase) are down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target.

GO enrichment analysis for up regulated genes was implemented. Enriched genes such as AMOT (angiomin) [131], CCDC80 [132], CXCL10 [133], ERBB2 [134], KLF4 [135], LEP (leptin) [136], MFG8 [137], SLIT2 [138], TNMD (tenomodulin) [139], ADAMTS5 [140], ELN (elastin) [141], HTRA1 [142], LUM (lumican) [143], MFAP5 [144] and IL1RN [145] were responsible for progression of obesity. Enriched genes such as ANGPT1 [146], NOTCH3 [147] and TGFBR2 [148] were associated with development of hypertension, but these genes may be responsible for progression of obesity. Enriched genes such as CXCL12 [149] and IGFBP6 [150] were involved in progression of insulin resistance, but these genes may be associated with development of obesity. Enriched genes such as NRCAM (neuronal cell adhesion molecule) [151], NRP2 [152], RSP3 [153], SRPX2 [154], THY1 [155], CD248 [156], CLEC3B [157], CST3 [158], CTHRC1 [159] and GPC1 [160] were liable for development of various cancer types, but these genes may be responsible for development of obesity associated cancer. Enriched genes such as NFRSF12A [161] and FMOD (fibromodulin) [162] were liable for development of atherosclerosis, but these genes may be identified with development of obesity. Enriched genes such as TYMP (thymidine phosphorylase) [163], ALPL (alkaline phosphatase, biomineralization associated) [164], EFEMP1 [165], MFAP4 [166] and IGFBP5 [167] were diagnosed with development of heart disease, but these genes may be responsible for progression of obesity. Our study found that PTGER4, SPARC (secreted protein acidic and cysteine rich), ADAMTSL4, FBLN2, FCGBP (Fc fragment of IgG binding protein) and VASN (vasorin) are down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target. GO enrichment analysis for down regulated genes was implemented. Enriched genes such as ACADL (acyl-CoA dehydrogenase long chain) [168], AGT (angiotensinogen) [169], FADS1 [170], PDK4 [171], PER2 [172] and SLC27A2 [173] were liable for progression of obesity. Enriched genes such as ACS2 [174] and HSD17B12 [175] were diagnosed with growth of various cancer types such as gastric cancer and ovarian cancer, but these genes may be involved in development of obesity associated cancer. ELOVL6 was associated with development of insulin resistance [176], but this gene may be identified with obesity. Enriched genes such as GLUL (glutamate-ammonia ligase) [177] and HADC1 [178] were important for development of heart disease, but these genes may be linked with development of obesity. SCP2 was important for advancement of atherosclerosis [179], but this gene may be responsible for development of obesity. Our study found BCAT2, NAALAD2, SC5D, TMLHE (trimethyllysine hydroxylase, epsilon), MRPL55 and SLC25A23 are down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target.

We further diagnosed hub genes (up and down regulated) specifically expressed in obesity by constructing PPI network. HSPA8 was responsible for development of hypertension [180], but this gene may be linked with progression of obesity. Up regulated hub genes such as HSPA5 [181] and YWHAH [182] were identified with progression of obesity. Up regulated hub genes such as SPTAN1 [183], STEAP2 [184] and NEK6 [185] were liable for progression of various cancer types, but these genes may be diagnosed with growth of obesity associated cancer. Our study found COG2 is up regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target. Down regulated hub genes such as ARRB1 [186], FBXO11 [187], UBR2 [188] and INTS6 [189] were identified with growth of various cancer types, but these genes may be liable for advancement of cancer associated obesity. Genes such as ESR1 [190] and PTEN [191] were diagnosed with progression of obesity. CKB was involved in progression of hypertension [192], but this gene may be associated with development of obesity. Our study found FBL, CSNK2B, PCM1 and ZNF581 are down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target.

Module analysis for up regulated genes was implemented. Up regulated hub genes in modules such as CDK14 [193], LMO2 [194], MSN [195] and TAGLN2 [196] were responsible for pathogenesis of various cancers, but these genes may be identified with development of cancer associated obesity. Up regulated hub genes such as IRAK1 [197] and CYR61 [198] were associated with development of obesity. Module analysis for down regulated genes was implemented. Down regulated hub genes such as SRSF3 [199], SAFB [200], SIN3A [201], TRIM24 [202] and AUTS2 [203] were lined with development of various cancer types, but these genes may responsible for advancement of cancer associated obesity. ZBTB16 was liable for development of obesity [204]. CSNK2A2 was involved in development of heart disease [205]. Our study found KHDRBS1, RBMX, RBBP4 and DCAF7 are down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target.

Target genes - miRNA regulatory network up regulated genes was constructed and analyzed. CCND1 was responsible for progression of obesity [206]. CCND2 was associated with development of insulin resistance [207]. Our study found TUBB2A and TMEM189 are up regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target. Target genes - miRNA regulatory network down regulated genes was constructed and analyzed. BTG2 was important for development of obesity [208]. TXNIP was linked with progression of insulin resistance [209]. MED28 was liable for advancement of breast cancer [210], but this gene may be links with progression of cancer associated obesity. Our study found CNBP is down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target.

Target genes - TF regulatory network up regulated genes was constructed and analyzed. HP was responsible for development of obesity [211]. Our study found LYZ and TRAM2 are up regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target. Target genes - TF regulatory network down regulated genes was constructed and analyzed. EFNA1 was responsible for pathogenesis of gastric cancer [212], but this gene may involved in development of cancer associated obesity. Our study found MED16, RWDD2A, ADD3 and AIP are down regulated in obesity and has potential as a novel diagnostic and prognostic biomarker, and therapeutic target. All hub genes were validated by ICH analysis and were verified on the human protein atlas. Finally, all hub genes were validated by ROC analysis using pROC package in R software and RT-PCR.

In conclusion, robust DEGs linked with the progression of obesity were screened through the ArrayExpress database, and integrated bioinformatics analysis was conducted. The findings of this study are important for providing reliable molecular biomarkers for screening and diagnosis, prognosis, as well as novel

therapeutic targets for obesity.

Declarations

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Author Contributions

Basavaraj Vastrad was associated with methodology, manuscript preparation, review and editing. Chanabasayya Vastrad was performed software, supervision, formal analysis and validation.

Availability of data and materials

The datasets supporting the conclusions of this article are available in the ArrayExpress (<https://www.ebi.ac.uk/arrayexpress/>) repository. [E-MTAB-6728] (<https://www.ebi.ac.uk/arrayexpress/experiments/E-MTAB-6728/>)]

Consent for publication

Not applicable.

Competing interests

The authors declare that they have no competing interests.

Conflict of interest

The authors declare that they have no conflict of interest.

Ethical approval

This article does not contain any studies with human participants or animals performed by any of the authors.

Informed consent

No informed consent because this study does not contain human or animals participants.

References

1. Cole TJ, Bellizzi MC, Flegal KM, Dietz WH (2000) Establishing a standard definition for child overweight and obesity worldwide: international survey. *BMJ* 320(7244):1240-1243
2. Krotkiewski M, Björntorp P, Sjöström L, Smith U (1983) Impact of obesity on metabolism in men and women. Importance of regional adipose tissue distribution. *J Clin Invest* 72(3):1150-1162. doi:1172/JCI111040
3. Freedman DS, Khan LK, Dietz WH, Srinivasan SR, Berenson GS (2001) Relationship of childhood obesity to coronary heart disease risk factors in adulthood: the Bogalusa Heart Study. *Pediatrics* 108(3):712-718.
4. Locsey L, Asztalos L, Kincses Z, Berczi C, Paragh G (1998) The importance of obesity and hyperlipidaemia in patients with renal transplants. *Int Urol Nephrol* 30(6):767-775.
5. Becker S, Dossus L, Kaaks R (2009) Obesity related hyperinsulinaemia and hyperglycaemia and cancer development. *Arch Physiol Biochem* 115(2):86-96. doi:1080/13813450902878054
6. Rahmouni K, Correia ML, Haynes WG, Mark AL (2005) Obesity-associated hypertension: new insights into mechanisms. *Hypertension* 45(1):9-14. doi:1161/01.HYP.0000151325.83008.b4
7. Lovren F, Teoh H, Verma S (2015) Obesity and atherosclerosis: mechanistic insights. *Can J Cardiol* 31(2):177-183. doi:1016/j.cjca.2014.11.031
8. Stepan CM, Bailey ST, Bhat S, Brown EJ, Banerjee RR, Wright CM, Patel HR, Ahima RS, Lazar MA (2001) The hormone resistin links obesity to diabetes. *Nature* 409(6818):307-312. doi:1038/35053000
9. Calle EE, Kaaks R (2004) Overweight, obesity and cancer: epidemiological evidence and proposed mechanisms. *Nat Rev Cancer* 4(8):579-591. doi:1038/nrc1408
10. Jia JJ, Zhang X, Ge CR, Jois M (2009) The polymorphisms of UCP2 and UCP3 genes associated with fat metabolism, obesity and diabetes. *Obes Rev* 10(5):519-526. doi:1111/j.1467-789X.2009.00569.x
11. Kern PA (1997) Potential role of TNFalpha and lipoprotein lipase as candidate genes for obesity. *J Nutr* 127(9):1917S-1922S. doi:1093/jn/127.9.1917S
12. Suviolahti E, Oksanen LJ, Ohman M, Cantor RM, Ridderstrale M, Tuomi T, Kaprio J, Rissanen A, Mustajoki P, Jousilahti P et al (2003) The SLC6A14 gene shows evidence of association with obesity. *J Clin Invest*. 112(11):1762-1772. doi:1172/JCI17491

13. Okada Y, Tateishi K, Zhang Y (2010) Histone demethylase JHDM2A is involved in male infertility and obesity. *J Androl* 31(1):75-8. doi:2164/jandrol.109.008052
14. Carpenter D, Dhar S, Mitchell LM, Fu B, Tyson J, Shwan NA, Yang F, Thomas MG, Armour JA (2015) Obesity, starch digestion and amylase: association between copy number variants at human salivary (AMY1) and pancreatic (AMY2) amylase genes. *Hum Mol Genet* 24(12):3472-3480. doi:1093/hmg/ddv098
15. Tanti JF, Ceppo F, Jager J, Berthou F (2013) Implication of inflammatory signaling pathways in obesity-induced insulin resistance. *Front Endocrinol (Lausanne)* 3:181. doi:3389/fendo.2012.00181
16. Kim KA, Gu W, Lee IA, Joh EH, Kim DH (2012) High fat diet-induced gut microbiota exacerbates inflammation and obesity in mice via the TLR4 signaling pathway. *PLoS One* 7(10):e47713. doi:1371/journal.pone.0047713
17. Briones AM, Nguyen Dinh Cat A, Callera GE, Yogi A, Burger D, He Y, Corrêa JW, Gagnon AM, Gomez-Sanchez CE, Gomez-Sanchez EP et al (2012) Adipocytes produce aldosterone through calcineurin-dependent signaling pathways: implications in diabetes mellitus-associated obesity and vascular dysfunction. *Hypertension* 59(5):1069-1078. doi:1161/HYPERTENSIONAHA.111.190223
18. Dann SG, Selvaraj A, Thomas G (2007) mTOR Complex1-S6K1 signaling: at the crossroads of obesity, diabetes and cancer. *Trends Mol Med* 13(6):252-259. doi:1016/j.molmed.2007.04.002
19. Mattevi VS, Zembruski VM, Hutz MH (2002) Association analysis of genes involved in the leptin-signaling pathway with obesity in Brazil. *Int J Obes Relat Metab Disord* 26(9):1179-1185. doi:1038/sj.ijo.0802067
20. Li H, Li X, Guo J, Wu G, Dong C, Pang Y, Gao S, Wang Y (2018) Identification of biomarkers and mechanisms of diabetic cardiomyopathy using microarray data. *Cardiol J*. doi:5603/CJ.a2018.0113
21. Wei L, Wang J, Lampert E, Schlanger S, DePriest AD, Hu Q, Gomez EC, Murakam M, Glenn ST, Conroy J. et al (2017) Intratumoral and Intertumoral Genomic Heterogeneity of Multifocal Localized Prostate Cancer Impacts Molecular Classifications and Genomic Prognosticators. *Eur Urol* 71(2):183-192. doi:1016/j.eururo.2016.07.008
22. Yan Y, Xu Z, Qian L, Zeng S, Zhou Y, Chen X, Wei J, Gong Z (2019) Identification of CAV1 and DCN as potential predictive biomarkers for lung adenocarcinoma. *Am J Physiol Lung Cell Mol Physiol*. doi:1152/ajplung.00364.2018
23. Fan G, Tu Y, Chen C, Sun H, Wan C, Cai X (2018) DNA methylation biomarkers for hepatocellular carcinoma. *Cancer Cell Int* 18:140. doi:10.1186/s12935-018-0629-5
24. Jia L, Jia R, Li Y, Li X, Jia Q, Zhang H (2018) LCK as a Potential Therapeutic Target for Acute Rejection after Kidney Transplantation: A Bioinformatics Clue. *J Immunol Res* 2018:6451298. doi:1155/2018/6451298
25. Bjune JI, Haugen C, Gudbrandsen O, Nordbø OP, Nielsen HJ, Våge V, Njølstad PR, Sagen JV, Dankel SN, Mellgren G (2018) IRX5 regulates adipocyte amyloid precursor protein and mitochondrial respiration in obesity. *Int J Obes (Lond)*. doi:1038/s41366-018-0275-y
26. Kaimal V, Bardes EE, Tabar SC, Jegga AG, Aronow BJ (2010) ToppCluster: a multiple gene list feature analyzer for comparative enrichment clustering and network-based dissection of biological systems. *Nucleic Acids Res* 38(Web Server issue):W96-W102. doi:1093/nar/gkq418
27. Caspi R, Billington R, Ferrer L, Foerster H, Fulcher CA, Keseler IM, Kothari A, Krummenacker M, Latendresse M et al (2016) The MetaCyc database of metabolic pathways and enzymes and the BioCyc collection of pathway/genome databases. *Nucleic. Acids. Res* 44 (D1):D471-D480. doi:1093/nar/gkv1164
28. Tanabe M, Kanehisa M (2012) Using the KEGG database resource. *Curr. Bioinformatics*. Chapter 1:Unit1.12. doi:10.1002/0471250953.bi0112s38
29. Schaefer CF, Anthony K, Krupa S, Buchoff J, Day M, Hannay T, Buetow KH (2009) PID: the Pathway Interaction Database. *Nucleic. Acids. Res* 37(Database issue):D674-D679. doi:1093/nar/gkn653
30. Sidiropoulos K, Viteri G, Sevilla C, Jupe S, Webber M, Orlic-Milacic M, Jassal B, May B, Shamovsky V, Duenas C et al (2017) Reactome enhanced pathway visualization. *Bioinformatics* 33 (21):3461-3467. doi:1093/bioinformatics/btx441
31. Dahlquist KD, Salomonis N, Vranizan K, Lawlor SC, Conklin BR (2002) GenMAPP, a new tool for viewing and analyzing microarray data on biological pathways. *Nat. Genet* 31 (1):19-20. doi:1038/ng0502-19
32. Subramanian A, Tamayo P, Mootha VK, Mukherjee S, Ebert BL, Gillette MA, Paulovich A, Pomeroy SL, Golub TR, Lander ES et al (2005) Gene set enrichment analysis: a knowledge-based approach for interpreting genome-wide expression profiles. *Proc. Natl. Acad. Sci. U. A* 102 (43):15545-15550. doi:10.1073/pnas.0506580102
33. Mi H, Huang X, Muruganujan A, Tang H, Mills C, Kang D, Thomas PD (2017) PANTHER version 11: expanded annotation data from Gene Ontology and Reactome pathways, and data analysis tool enhancements. *Nucleic. Acids. Res* 45 (D1):D183-D189. doi:1093/nar/gkw1138
34. Petri V, Jayaraman P, Tutaj M, Hayman GT, Smith JR, De Pons J, Laulederkind SJ, Lowry TF, Nigam R et al (2014) The pathway ontology - updates and applications. *J. Biomed. Semantics* 5(1):7. doi:1186/2041-1480-5-7
35. Jewison T, Su Y, Disfany FM, Liang Y, Knox C, Maciejewski A, Poelzer J, Huynh J, Zhou Y, Arndt D et al (2014) SMPDB 2.0: big improvements to the Small Molecule Pathway Database. *Nucleic Acids Res* 42(Database issue):D478-D484. doi:1093/nar/gkt1067
36. Ashburner M, Ball CA, Blake JA, Botstein D, Butler H, Cherry JM, Davis AP, Dolinski K, Dwight SS et al (2000) Gene ontology: tool for the unification of biology. The Gene Ontology Consortium. *Nat Genet*. 25(1):25-29. doi:1038/75556
37. Calderone A, Castagnoli L, Cesareni G (2013) mentha: a resource for browsing integrated protein-interaction networks. *Nat Methods* 10(8):690-691. doi:1038/nmeth.2561
38. Licata L, Briganti L, Peluso D, Perfetto L, Iannuccelli M, Galeota E, Sacco F, Palma A, Nardozza AP, Santonico E et al (2012) MINT, the molecular interaction database: 2012 update. *Nucleic Acids Res* 40(Database issue):D857-D861. doi:1093/nar/gkr930

39. Orchard S, Ammari M, Aranda B, Breuza L, Briganti L, Broackes-Carter F, Campbell NH, Chavali G, Chen C, del-Toro N et al (2014) The MIntAct project—IntAct as a common curation platform for 11 molecular interaction databases. *Nucleic Acids Res* 42(Database issue):D358-D363. doi:1093/nar/gkt1115
40. Salwinski L, Miller CS, Smith AJ, Pettit FK, Bowie JU, Eisenberg D (2004) The Database of Interacting Proteins: 2004 update. *Nucleic Acids Res* 32(Database issue):D449-D451. doi:1093/nar/gkh086
41. Clerc O, Deniaud M, Vallet SD, Naba A, Rivet A, Perez S, Thierry-Mieg N, Ricard-Blum S (2019) MatrixDB: integration of new data with a focus on glycosaminoglycan interactions. *Nucleic Acids Res* 47(D1):D376-D381. doi:1093/nar/gky1035
42. Oughtred R, Stark C, Breitkreutz BJ, Rust J, Boucher L, Chang C, Kolas N, O'Donnell L, Leung G, McAdam R et al (2019) The BioGRID interaction database: 2019 update. *Nucleic Acids Res* 47(D1):D529-D541. doi:1093/nar/gky1079
43. Shannon P, Markiel A, Ozier O, Baliga NS, Wang JT, Ramage D, Amin N, Schwikowski B, Ideker T. (2003) Cytoscape: a software environment for integrated models of biomolecular interaction networks. *Genome. Res* 3 (11):2498-2504. doi:1101/gr.1239303
44. Tang Y, Li M, Wang J, Pan Y, Wu FX. (2015) CytoNCA: a cytoscape plugin for centrality analysis and evaluation of protein interaction networks. *Biosystems* 127:67-72. doi:1016/j.biosystems.2014.11.005
45. Aittokallio T, Schwikowski B (2006) Graph-based methods for analysing networks in cell biology. *Brief Bioinform* 7(3):243-255. doi:1093/bib/bbl022
46. Ashtiani M, Salehzadeh-Yazdi A, Razaghi-Moghadam Z, Hennig H, Wolkenhauer O, Mirzaie M, Jafari M (2018) A systematic survey of centrality measures for protein-protein interaction networks. *BMC Syst Biol* 12(1):80. doi:1186/s12918-018-0598-2
47. Shi Z, Zhang B (2011) Fast network centrality analysis using GPUs. *BMC Bioinformatics* 12:149. doi:1186/1471-2105-12-149
48. Dopazo J, Erten C (2017) Graph-theoretical comparison of normal and tumor networks in identifying BRCA genes. *BMC Syst Biol* 11(1):110. doi:1186/s12918-017-0495-0
49. Li M, Lu Y, Niu Z, Wu FX (2017) United Complex Centrality for Identification of Essential Proteins from PPI Networks. *IEEE/ACM Trans Comput Biol Bioinform* 14(2):370-380. doi:1109/TCBB.2015.2394487
50. Zaki N., Efimov D. and Berenguères J (2013) Protein complex detection using interaction reliability assessment and weighted clustering coefficient. *BMC Bioinformatics* 14:163. doi:1186/1471-2105-14-163
51. Fan Y, Xia J (2018) miRNet-Functional Analysis and Visual Exploration of miRNA-Target Interactions in a Network Context. *Methods Mol Biol* 1819:215-233. doi:1007/978-1-4939-8618-7_10
52. Vlachos IS, Paraskevopoulou MD, Karagkouni D, Georgakilas G, Vergoulis T, Kanellos I, Anastasopoulos IL, Maniou S, Karathanou K, Kalfakakou D et al (2015) DIANA-TarBase v7.0: indexing more than half a million experimentally supported miRNA:mRNA interactions. *Nucleic Acids Res* 43(Database issue):D153-D159. doi:1093/nar/gku1215
53. Chou CH, Shrestha S, Yang CD, Chang NW, Lin YL, Liao KW, Huang WC, Sun TH, Tu SJ, Lee WH et al (2018) miRTarBase update 2018: a resource for experimentally validated microRNA-target interactions. *Nucleic Acids Res* 46(D1):D296-D302. doi:1093/nar/gkx1067
54. Xiao F, Zuo Z, Cai G, Kang S, Gao X, Li T (2009) miRecords: an integrated resource for microRNA-target interactions. *Nucleic Acids Res* 37(Database issue):D105-D110. doi:1093/nar/gkn851
55. Jiang Q, Wang Y, Hao Y, Juan L, Teng M, Zhang X, Li M, Wang G, Liu Y (2009) miR2Disease: a manually curated database for microRNA deregulation in human disease. *Nucleic Acids Res* 37(Database issue):D98-104. doi:1093/nar/gkn714
56. Huang Z, Shi J, Gao Y, Cui C, Zhang S, Li J, Zhou Y, Cui Q (2019) HMDD v3.0: a database for experimentally supported human microRNA-disease associations. *Nucleic Acids Res* 47(D1):D1013-D1017. doi:1093/nar/gky1010Z
57. Ruepp A, Kowarsch A, Schmidl D, Buggenthin F, Brauner B, Dunger I, Fobo G, Frishman G, Montrone C, Theis FJ (2010) PhenomiR: a knowledgebase for microRNA expression in diseases and biological processes. *Genome Biol* 11(1):R6. doi:1186/gb-2010-11-1-r6
58. Liu X, Wang S, Meng F, Wang J, Zhang Y, Dai E, Yu X, Li X, Jiang W (2013) SM2miR: a database of the experimentally validated small molecules' effects on microRNA expression. *Bioinformatics* 29(3):409-411. doi:1093/bioinformatics/bts698
59. Rukov JL, Wilentzik R, Jaffe I, Vinther J, Shomron N (2014) Pharmaco-miR: linking microRNAs and drug effects. *Brief Bioinform* 15(4):648-659. doi:1093/bib/bbs082
60. Dai E, Yu X, Zhang Y, Meng F, Wang S, Liu X, Liu D, Wang J, Li X, Jiang W (2014) EpimiR: a database of curated mutual regulation between miRNAs and epigenetic modifications. *Database (Oxford)* 2014:bau023. doi:1093/database/bau023
61. Li JH, Liu S, Zhou H, Qu LH, Yang JH (2014) starBase v2.0: decoding miRNA-ceRNA, miRNA-ncRNA and protein-RNA interaction networks from large-scale CLIP-Seq data. *Nucleic Acids Res* 42(Database issue):D92-D97. doi:1093/nar/gkt1248
62. Zhou G, Soufan O, Ewald J, Hancock REW, Basu N, Xia J (2019) NetworkAnalyst 3.0: a visual analytics platform for comprehensive gene expression profiling and meta-analysis. *Nucleic Acids Res.* doi:1093/nar/gkz240
63. Davis CA, Hitz BC, Sloan CA, Chan ET, Davidson JM, Gabdank I, Hilton JA, Jain K, Baymuradov UK, Narayanan AK et al (2018) The Encyclopedia of DNA elements (ENCODE): data portal update. *Nucleic Acids Res* 46(D1):D794-D801. doi:1093/nar/gkx1081
64. Uhlen M, Oksvold P, Fagerberg L, Lundberg E, Jonasson K, Forsberg M, Zwahlen M, Kampf C, Wester K, Hober S et al. (2010) Towards a knowledge-based Human Protein Atlas. *Nat Biotechnol* 28(12):1248-1250. doi:1038/nbt1210-1248
65. Robin X, Turck N, Hainard A, Tiberti N, Lisacek F, Sanchez JC, Müller M (2011) pROC: an open-source package for R and S+ to analyze and compare ROC curves. *BMC Bioinformatics* 12:77. doi:1186/1471-2105-12-77
66. Livak KJ, Schmittgen TD. Analysis of relative gene expression data using real-time quantitative PCR and the 2⁻(Delta Delta C(T)) Method. *Methods.* 2001;25(4):402–408. doi:1006/meth.2001.1262

67. Urbanet R, Nguyen Dinh Cat A, Feraco A, Venteclef N, El Moghrabi S, Sierra-Ramos C, Alvarez de la Rosa D, Adler GK, Quilliot D et al (2015) Adipocyte Mineralocorticoid Receptor Activation Leads to Metabolic Syndrome and Induction of Prostaglandin D2 Synthase. *Hypertension* 66(1):149-157. doi:1161/HYPERTENSIONAHA
68. Moreno-Navarrete JM, Ortega F, Serino M, Luche E, Waget A, Pardo G, Salvador J, Ricart W, Frühbeck G, Burcelin R et al (2012) Circulating lipopolysaccharide-binding protein (LBP) as a marker of obesity-related insulin resistance. *Int J Obes (Lond)* 36(11):1442-1449. doi:1038/ijo.2011.256
69. Oberauer R, Rist W, Lenter MC, Hamilton BS, Neubauer H (2010) EGFL6 is increasingly expressed in human obesity and promotes proliferation of adipose tissue-derived stromal vascular cells. *Mol Cell Biochem* 343(1-2):257-269. doi:1007/s11010-010-0521-7
70. Ernst MB, Wunderlich CM, Hess S, Paehler M, Mesaros A, Koralov SB, Kleinridders A, Husch A, Münzberg H, Hampel B et al (2009) Enhanced Stat3 activation in POMC neurons provokes negative feedback inhibition of leptin and insulin signaling in obesity. *J Neurosci* 29(37):11582-11593. doi:1523/JNEUROSCI.5712-08.2009
71. Chatterjee TK, Basford JE, Knoll E, Tong WS, Blanco V, Blomkalns AL, Rudich S, Lentsch AB, Hui DY, Weintraub NL (2014) HDAC9 knockout mice are protected from adipose tissue dysfunction and systemic metabolic disease during high-fat feeding. *Diabetes* 63(1):176-187. doi:2337/db13-1148
72. Kumazawa T, Tsuchiya N, Wang L, Sato K, Kamoto T, Ogawa O, Nakamura A, Kato T, Habuchi T (2004) Microsatellite polymorphism of steroid hormone synthesis gene CYP11A1 is associated with advanced prostate cancer. *Int J Cancer* 110(1):140-144. doi:1002/ijc.20070
73. Uysal-Onganer P, Kawano Y, Caro M, Walker MM, Diez S, Darrington RS, Waxman J, Kypta RM (2010) Wnt-11 promotes neuroendocrine-like differentiation, survival and migration of prostate cancer cells. *Mol Cancer* 9:55. doi:1186/1476-4598-9-55
74. Kolar GR, Grote SM, Yosten GL (2017) Targeting orphan G protein-coupled receptors for the treatment of diabetes and its complications: C-peptide and GPR146. *J Intern Med* 281(1):25-40. doi:1111/joim.12528
75. Du P, Gao K, Cao Y, Yang S, Wang Y, Guo R, Zhao M, Jia S (2019) RFX1 downregulation contributes to TLR4 overexpression in CD14+ monocytes via epigenetic mechanisms in coronary artery disease. *Clin Epigenetics* 11(1):44. doi:1186/s13148-019-0646-9
76. Erbilgin A, Seldin MM, Wu X, Mehrabian M, Zhou Z, Qi H, Dabirian KS, Sevag Packard RR, Hsieh W, Bensinger SJ et al (2018) Transcription Factor Zfx2 Deficiency Reduces Atherosclerosis and Promotes Macrophage Apoptosis in Mice. *Arterioscler Thromb Vasc Biol* 38(9):2016-2027. doi:1161/ATVBAHA.118.311266
77. Matsuoka H, Tamura A, Kinehara M, Shima A, Uda A, Tahara H, Michihara A (2018) Levels of tight junction protein CLDN1 are regulated by microRNA-124 in the cerebellum of stroke-prone spontaneously hypertensive rats. *Biochem Biophys Res Commun* 498(4):817-823. doi:1016/j.bbrc.2018.03.063
78. O'Halloran AM, Patterson CC, Horan P, Maree A, Curtin R, Stanton A, McKeown PP, Shields DC (2009) Genetic polymorphisms in platelet-related proteins and coronary artery disease: investigation of candidate genes, including N-acetylgalactosaminyltransferase 4 (GALNT4) and sulphotransferase 1A1/2 (SULT1A1/2). *J Thromb Thrombolysis* 27(2):175-184. doi:1007/s11239-008-0196-z
79. Davies GE, Howard CM, Farrer MJ, Coleman MM, Bennett LB, Cullen LM, Wyse RK, Burn J, Williamson R, Kessling AM (1995) Genetic variation in the COL6A1 region is associated with congenital heart defects in trisomy 21 (Down's syndrome). *Ann Hum Genet* 59(3):253-269.
80. Grossman TR, Gamliel A, Wessells RJ, Taghli-Lamalle O, Jepsen K, Ocorr K, Korenberg JR, Peterson KL, Rosenfeld MG, Bodmer R et al (2011) Overexpression of DSCAM and COL6A2 cooperatively generates congenital heart defects. *PLoS Genet* 7(11):e1002344. doi:1371/journal.pgen.1002344
81. Roberts AE, Araki T, Swanson KD, Montgomery KT, Schiripo TA, Joshi VA, Li L, Yassin Y, Tamburino AM, Neel BG et al (2007) Germline gain-of-function mutations in SOS1 cause Noonan syndrome. *Nat Genet* 39(1):70-74. doi:1038/ng1926
82. Chmielewski S, Piaszyk-Borychowska A, Wesoly J, Bluyssen HA (2016) STAT1 and IRF8 in Vascular Inflammation and Cardiovascular Disease: Diagnostic and Therapeutic Potential. *Int Rev Immunol* 35(5):434-454. doi:3109/08830185.2015.1087519
83. Azuaje F, Zhang L, Jeanty C, Puhl SL, Rodius S, Wagner DR (2013) Analysis of a gene co-expression network establishes robust association between Col5a2 and ischemic heart disease. *BMC Med Genomics* 6:13. doi:1186/1755-8794-6-13
84. Yue X, Yang X, Lin X, Yang T, Yi X, Dai Y, Guo J, Li T, Shi J, Wei L et al (2014) Rnd3 haploinsufficient mice are predisposed to hemodynamic stress and develop apoptotic cardiomyopathy with heart failure. *Cell Death Dis* 5:e1284. doi:1038/cddis.2014.235
85. Tian DZ, Wei W, Dong YJ (2016) Influence of COL1A2 gene variants on the incidence of hypertensive intracerebral hemorrhage in a Chinese population. *Genet Mol Res* 15(1). doi:4238/gmr.15017369
86. Samokhin AO, Stephens T, Wertheim BM, Wang RS, Vargas SO, Yung LM, Cao M, Brown M, Arons E, Dieffenbach PB et al (2018) NEDD9 targets COL3A1 to promote endothelial fibrosis and pulmonary arterial hypertension. *Sci Transl Med* 10(445). doi:1126/scitranslmed.aap7294
87. Champelovier P, Besse A, Boucard N, Simon A, Leroux D, Pinel N, Praloran V, Seigneurin D (2001) Dag-1 carcinoma cell in studying the mechanisms of progression and therapeutic resistance in bladder cancer. *Eur Urol* 39(3):343-348. doi:1159/000052465
88. Flum M, Kleemann M, Schneider H, Weis B, Fischer S, Handrick R, Otte K (2018) miR-217-5p induces apoptosis by directly targeting PRKCI, BAG3, ITGAV and MAPK1 in colorectal cancer cells. *J Cell Commun Signal* 12(2):451-466. doi:1007/s12079-017-0410-x
89. Bartolini A, Cardaci S, Lamba S, Oddo D, Marchiò C, Cassoni P, Amoreo CA, Corti G, Testori A, Bussolino F et al (2016) BCAM and LAMA5 Mediate the Recognition between Tumor Cells and the Endothelium in the Metastatic Spreading of KRAS-Mutant Colorectal Cancer. *Clin Cancer Res* 22(19):4923-4933. doi:1158/1078-0432.CCR-15-2664
90. Junnila S, Kakkola A, Mizuguchi T, Hirata K, Karjalainen-Lindsberg ML, Puolakkainen P, Monni O (2010) Gene expression analysis identifies overexpression of CXCL1, SPARC, SPP1, and SULF1 in gastric cancer. *Genes Chromosomes Cancer* 49(1):28-39. doi:1002/gcc.20715
91. García-Pravia C, Galván JA, Gutiérrez-Corral N, Solar-García L, García-Pérez E, García-Ocaña M, Del Amo-Iribarren J, Menéndez-Rodríguez P, García-García J, de Los Toyos JR et al (2013) Overexpression of COL11A1 by cancer-associated fibroblasts: clinical relevance of a stromal marker in pancreatic cancer. *PLoS One* 8(10):e78327. doi:1371/journal.pone.0078327

92. Duan S, Gong B, Wang P, Huang H, Luo L, Liu F (2018) Novel prognostic biomarkers of gastric cancer based on gene expression microarray: COL12A1, GSTA3, FGA and FGG. *Mol Med Rep* 18(4):3727-3736. doi:3892/mmr.2018.9368
93. Kamikawaji K, Seki N, Watanabe M, Mataka H, Kumamoto T, Takagi K, Mizuno K, Inoue H (2016) Regulation of LOXL2 and SERPINH1 by antitumor microRNA-29a in lung cancer with idiopathic pulmonary fibrosis. *J Hum Genet* 61(12):985-993. doi:1038/jhg.2016.99
94. Liu BL, Sun KX, Zong ZH, Chen S, Zhao Y (2016) MicroRNA-372 inhibits endometrial carcinoma development by targeting the expression of the Ras homolog gene family member C (RhoC). *Oncotarget* 7(6):6649-6664. doi:18632/oncotarget.6544
95. Jiao H, Kulyté A, Näslund E, Thorell A, Gerdhem P, Kere J, Arner P, Dahlman I (2016) Whole-Exome Sequencing Suggests LAMB3 as a Susceptibility Gene for Morbid Obesity. *Diabetes* 65(10):2980-2989. doi:2337/db16-0522
96. Matsuo Y, Tanaka M, Yamakage H, Sasaki Y, Muranaka K, Hata H, Ikai I, Shimatsu A, Inoue M, Chun TH et al (2015) Thrombospondin 1 as a novel biological marker of obesity and metabolic syndrome. *Metabolism* 64(11):1490-1499. doi:1016/j.metabol.2015.07.016
97. Meissburger B, Stachorski L, Röder E, Rudofsky G, Wolfrum C (2011) Tissue inhibitor of matrix metalloproteinase 1 (TIMP1) controls adipogenesis in obesity in mice and in humans. *Diabetologia* 54(6):1468-1479. doi:1007/s00125-011-2093-9
98. Chen JY, Tsai PJ, Tai HC, Tsai RL, Chang YT, Wang MC, Chiou YW, Yeh ML, Tang MJ et al (2013) Increased aortic stiffness and attenuated lysyl oxidase activity in obesity. *Arterioscler Thromb Vasc Biol* 33(4):839-846. doi:1161/ATVBAHA.112.300036
99. Derosa G, Ferrari I, D'Angelo A, Tinelli C, Salvadeo SA, Ciccarelli L, Piccinni MN, Gravina A, Ramondetti F, Maffioli P et al (2008) Matrix metalloproteinase-2 and -9 levels in obese patients. *Endothelium* 15(4):219-224. doi:1080/10623320802228815
100. Nascimento FV, Piccoli V, Beer MA, Frankenberg AD, Crispim D, Gerchman F (2015) Association of HSD11B1 polymorphic variants and adipose tissue gene expression with metabolic syndrome, obesity and type 2 diabetes mellitus: a systematic review. *Diabetol Metab Syndr* 7:38. doi:1186/s13098-015-0036-1
101. Awaya T, Yokosaki Y, Yamane K, Usui H, Kohno N, Eboshida A (2008) Gene-environment association of an ITGB2 sequence variant with obesity in ethnic Japanese. *Obesity (Silver Spring)* 16(6):1463-1466. doi:1038/oby.2008.68
102. Moreno-Navarrete JM, Ortega F, Rodríguez A, Latorre J, Becerril S, Sabater-Masdeu M, Ricart W, Frühbeck G, Fernández-Real JM (2017) HMOX1 as a marker of iron excess-induced adipose tissue dysfunction, affecting glucose uptake and respiratory capacity in human adipocytes. *Diabetologia* 60(5):915-926. doi:1007/s00125-017-4228-0
103. Aguer C, Pasqua M, Thrush AB, Moffat C, McBurney M, Jardine K, Zhang R, Beauchamp B, Dent R, McPherson R et al (2013) Increased proton leak and SOD2 expression in myotubes from obese non-diabetic subjects with a family history of type 2 diabetes. *Biochim Biophys Acta* 1832(10):1624-1633. doi:1016/j.bbadis.2013.05.008
104. Svensson PA, Gabrielsson BG, Jernås M, Gummesson A, Sjöholm K (2008) Regulation of human aldoketoreductase 1C3 (AKR1C3) gene expression in the adipose tissue. *Cell Mol Biol Lett* 13(4):599-613. doi:2478/s11658-008-0025-6
105. Connelly JJ, Cherepanova OA, Doss JF, Karaoli T, Lillard TS, Markunas CA, Nelson S, Wang T, Ellis PD, Langford CF et al (2013) Epigenetic regulation of COL15A1 in smooth muscle cell replicative aging and atherosclerosis. *Hum Mol Genet* 22(25):5107-5120. doi:1093/hmg/ddt365
106. Nordström M, Kjellström T (1992) Age dependency of cystathionine beta-synthase activity in human fibroblasts in homocyst(e)inemia and atherosclerotic vascular disease. *Atherosclerosis* 94(2-3):213-221.
107. Zhao C, Chen X, Wu W, Wang W, Pang W, Yang G (2016) MAT2B promotes adipogenesis by modulating SAME levels and activating AKT/ERK pathway during porcine intramuscular preadipocyte differentiation. *Exp Cell Res* 344(1):11-21. doi:1016/j.yexcr.2016.02.019
108. Farmer SR (2003) The forkhead transcription factor Foxo1: a possible link between obesity and insulin resistance. *Mol Cell* 11(1):6-8.
109. Boal F, Roumegoux J, Alfarano C, Timotin A, Calise D, Anesia R, Drougard A, Knauf C, Lagente C, Roncalli J et al (2015) Apelin regulates FoxO3 translocation to mediate cardioprotective responses to myocardial injury and obesity. *Sci Rep* 5:16104. doi:1038/srep16104
110. Zillikens MC, Meurs JB, Rivadeneira F, Amin N, Hofman A, Oostra BA, Sijbrands EJ, Witteman JC, Pols HA, Duijn CM et al (2009) SIRT1 genetic variation is related to BMI and risk of obesity. *Diabetes* 58(12):2828-2834. doi:2337/db09-0536
111. Riancho JA, Vázquez L, García-Pérez MA, Sainz J, Olmos JM, Hernández JL, Pérez-López J, Amado JA, Zarrabeitia MT, Cano A et al (2011) Association of ACACB polymorphisms with obesity and diabetes. *Mol Genet Metab* 104(4):670-676. doi:1016/j.ymgme.2011.08.013
112. Pang L, You L, Ji C, Shi C, Chen L, Yang L, Huang F, Zhou Y, Zhang J, Chen X et al (2016) miR-1275 inhibits adipogenesis via ELK1 and its expression decreases in obese subjects. *J Mol Endocrinol* 57(1):33-43. doi:1530/JME-16-0007
113. Haim Y, Blüher M, Konrad D, Goldstein N, Klötting N, Harman-Boehm I, Kirshtein B, Ginsberg D, Tarnovscki T, Gepner Y et al (2017) ASK1 (MAP3K5) is transcriptionally upregulated by E2F1 in adipose tissue in obesity, molecularly defining a human dys-metabolic obese phenotype. *Mol Metab* 6(7):725-736. doi:1016/j.molmet.2017.05.003
114. Cai J, Shi X, Wang H, Fan J, Feng Y, Lin X, Yang J, Cui Q, Tang C, Xu G et al (2016) Cystathionine γ lyase-hydrogen sulfide increases peroxisome proliferator-activated receptor γ activity by sulfhydration at C139 site thereby promoting glucose uptake and lipid storage in adipocytes. *Biochim Biophys Acta* 1861(5):419-429. doi:1016/j.bbailp.2016.03.001
115. Shriver SP, Shriver MD, Tirpak DL, Bloch LM, Hunt JD, Ferrell RE, Siegfried JM (1998) Trinucleotide repeat length variation in the human ribosomal protein L14 gene (RPL14): localization to 3p21.3 and loss of heterozygosity in lung and oral cancers. *Mutat Res* 406(1):9-23.
116. Liu JJ, Huang BH, Zhang J, Carson DD, Hooi SC (2006) Repression of HIP/RPL29 expression induces differentiation in colon cancer cells. *J Cell Physiol* 207(2):287-292. doi:1002/jcp.20589
117. Chen D, Zhang R, Shen W, Fu H, Liu S, Sun K, Sun X (2013) RPS12-specific shRNA inhibits the proliferation, migration of BGC823 gastric cancer cells with S100A4 as a downstream effector. *Int J Oncol* 42(5):1763-1769. doi:3892/ijo.2013.1872

118. Zhao X, Shen L, Feng Y, Yu H, Wu X, Chang J, Shen X, Qiao J, Wang J (2015) Decreased expression of RPS15A suppresses proliferation of lung cancer cells. *Tumour Biol* 36(9):6733-6740. doi:1007/s13277-015-3371-9
119. Wang M, Hu Y, Stearns ME (2009) RPS2: a novel therapeutic target in prostate cancer. *J Exp Clin Cancer Res* 28:6. doi:1186/1756-9966-28-6
120. Dutton-Regester K, Gartner JJ, Emmanuel R, Qutob N, Davies MA, Gershenwald JE, Robinson W, Robinson S, Rosenberg SA, Scolyer RA et al (2014) A highly recurrent RPS27 5'UTR mutation in melanoma. *Oncotarget* 5(10):2912-2917. doi:18632/oncotarget.2048
121. Youn H, Son B, Kim W, Jun SY, Lee JS, Lee JM, Kang C, Kim J, Youn B (2015) Dissociation of MIF-rpS3 complex and sequential NF- κ B activation is involved in IR-induced metastatic conversion of NSCLC. *J Cell Biochem* 116(11):2504-2516. doi:1002/jcb.25195
122. Zhu Y, Gu J, Li Y, Peng C, Shi M, Wang X, Wei G, Ge O, Wang D, Zhang B et al (2018) MiR-17-5p enhances pancreatic cancer proliferation by altering cell cycle profiles via disruption of RBL2/E2F4-repressing complexes. *Cancer Lett* 412:59-68. doi:1016/j.canlet.2017.09.044
123. Flores IL, Kawahara R, Miguel MC, Granato DC, Domingues RR, Macedo CC, Carnielli CM, Yokoo S, Rodrigues PC, Monteiro BV et al (2016) EEF1D modulates proliferation and epithelial-mesenchymal transition in oral squamous cell carcinoma. *Clin Sci (Lond)* 130(10):785-99. doi:1042/CS20150646
124. Svensson RU, Parker SJ, Eichner LJ, Kolar MJ, Wallace M, Brun SN, Lombardo PS, Nostrand JL, Hutchins A, Vera L et al (2016) Inhibition of acetyl-CoA carboxylase suppresses fatty acid synthesis and tumor growth of non-small-cell lung cancer in preclinical models. *Nat Med* 22(10):1108-1119. doi:1038/nm.4181
125. Song B, Liu XS, Rice SJ, Kuang S, Elzey BD, Konieczny SF, Ratliff TL, Hazbun T, Chiorean EG, Liu X (2013) Plk1 phosphorylation of orc2 and hbo1 contributes to gemcitabine resistance in pancreatic cancer. *Mol Cancer Ther* 12(1):58-68. doi:1158/1535-7163.MCT-12-0632
126. Mullarky E, Mattaini KR, Vander Heiden MG, Cantley LC, Locasale JW (2011) PHGDH amplification and altered glucose metabolism in human melanoma. *Pigment Cell Melanoma Res* 24(6):1112-1115. doi:1111/j.1755-148X.2011.00919.x
127. Komlósi V, Hitre E, Pap E, Adleff V, Réti A, Székely E, Bíró A, Rudnai P, Schoket B, Müller J et al (2010) SHMT1 1420 and MTHFR 677 variants are associated with rectal but not colon cancer. *BMC Cancer* 10:525. doi:1186/1471-2407-10-525.
128. Uchida T, Nakamura T, Hashimoto N, Matsuda T, Kotani K, Sakaue H, Kido Y, Hayashi Y, Nakayama KI, White MF et al (2005) Deletion of Cdkn1b ameliorates hyperglycemia by maintaining compensatory hyperinsulinemia in diabetic mice. *Nat Med* 11(2):175-182. doi:1038/nm1187
129. Smith CE, Coltell O, Sorlí JV, Estruch R, Martínez-González MÁ, Salas-Salvadó J, Fitó M, Arós F, Dashti HS, Lai CQ et al (2016) Associations of the MCM6-rs3754686 proxy for milk intake in Mediterranean and American populations with cardiovascular biomarkers, disease and mortality: Mendelian randomization. *Sci Rep* 6:33188. doi:1038/srep33188
130. Usui T, Okada M, Hara Y, Yamawaki H (2013) Eukaryotic elongation factor 2 kinase regulates the development of hypertension through oxidative stress-dependent vascular inflammation. *Am J Physiol Heart Circ Physiol* 305(5):H756-H768. doi:1152/ajpheart.00373.2013
131. Roudier E, Chapados N, Decary S, Gineste C, Le Bel C, Lavoie JM, Bergeron R, Birot O (2009) Angiotensin p80/p130 ratio: a new indicator of exercise-induced angiogenic activity in skeletal muscles from obese and non-obese rats? *J Physiol* 587(Pt 16):4105-4119. doi:1113/jphysiol.2009.175554
132. Grill JI, Neumann J, Herbst A, Ofner A, Hiltwein F, Marschall MK, Zierahn H, Wolf E, Schneider MR, Kolligs FT (2017) Loss of DRO1/CCDC80 results in obesity and promotes adipocyte differentiation. *Mol Cell Endocrinol* 439:286-296. doi:1016/j.mce.2016.09.014
133. Herder C, Hauner H, Kempf K, Kolb H, Skurk T (2007) Constitutive and regulated expression and secretion of interferon-gamma-inducible protein 10 (IP-10/CXCL10) in human adipocytes. *Int J Obes (Lond)* 31(3):403-410. doi:1038/sj.ijo.0803432
134. Mousa U, Onur H, Utkan G (2012) Is obesity always a risk factor for all breast cancer patients? c-erbB2 expression is significantly lower in obese patients with early stage breast cancer. *Clin Transl Oncol.* 14(12):923-30. doi:1007/s12094-012-0878-z
135. Wang C, Ha X, Li W, Xu P, Gu Y, Wang T, Wang Y, Xie J, Zhang J (2016) Correlation of A2bAR and KLF4/KLF15 with Obesity-Dyslipidemia Induced Inflammation in Uyghur Population. *Mediators Inflamm* 2016:7015620. doi:1155/2016/7015620
136. Mammès O, Betoulle D, Aubert R, Giraud V, Tuzet S, Petiet A, Colas-Linhart N, Fumeron F (1998) Novel polymorphisms in the 5' region of the LEP gene: association with leptin levels and response to low-calorie diet in human obesity. *Diabetes* 47(3):487-489.
137. Khalifeh-Soltani A, McKleroy W, Sakuma S, Cheung YY, Tharp K, Qiu Y, Turner SM, Chawla A, Stahl A, Atabai K (2014) Mfge8 promotes obesity by mediating the uptake of dietary fats and serum fatty acids. *Nat Med* 20(2):175-183. doi:1038/nm.3450
138. Lim R, Lappas M. Slit2 exerts anti-inflammatory actions in human placenta and is decreased with maternal obesity. *Am J Reprod Immunol.* 2015;73(1):66-78. doi:1111/aji.12334
139. Saiki A, Olsson M, Jernås M, Gummeson A, McTernan PG, Andersson J, Jacobson P, Sjöholm K, Olsson B, Yamamura S et al (2009) Tenomodulin is highly expressed in adipose tissue, increased in obesity, and down-regulated during diet-induced weight loss. *J Clin Endocrinol Metab* 94(10):3987-3994. doi:1210/jc.2009-0292
140. Bauters D, Spincemaille P, Geys L, Cassiman D, Vermeersch P, Bedossa P, Scroyen I, Lijnen HR (2016) ADAMTS5 deficiency protects against non-alcoholic steatohepatitis in obesity. *Liver Int* 36(12):1848-1859. doi:1111/liv.13181
141. Martinez-Santibanez G, Singer K, Cho KW, DelProposto JL, Mergian T, Lumeng CN (2015) Obesity-induced remodeling of the adipose tissue elastin network is independent of the metalloelastase MMP-12. *Adipocyte* 4(4):264-72. doi:1080/21623945.2015.1027848
142. Tiaden AN, Bahrenberg G, Mirsaidi A, Glanz S, Blüher M, Richards PJ (2016) Novel Function of Serine Protease HTRA1 in Inhibiting Adipogenic Differentiation of Human Mesenchymal Stem Cells via MAP Kinase-Mediated MMP Upregulation. *Stem Cells* 34(6):1601-1614. doi:1002/stem.2297
143. Wolff G, Taranko AE, Meln I, Weinmann J, Sijmonsma T, Lerch S, Heide D4, Billeter AT, Tews D, Kronic D et al (2019) Diet-dependent function of the extracellular matrix proteoglycan Lumican in obesity and glucose homeostasis. *Mol Meta* 19:97-106. doi:1016/j.molmet.2018.10.007
144. Vaittinen M, Kolehmainen M, Rydén M, Eskelinen M, Wabitsch M, Pihlajamäki J, Uusitupa M, Pulkkinen L (2015) MFAP5 is related to obesity-associated adipose tissue and extracellular matrix remodeling and inflammation. *Obesity (Silver Spring)* 23(7):1371-1378. doi:1002/oby.21103

145. Somm E, Cettour-Rose P, Asensio C, Charollais A, Klein M, Theander-Carrillo C, Juge-Aubry CE, Dayer JM, Nicklin MJ, Meda P et al (2006) Interleukin-1 receptor antagonist is upregulated during diet-induced obesity and regulates insulin sensitivity in rodents. *Diabetologia* 49(2):387-393. doi:1007/s00125-005-0046-x
146. Andraweera PH, Dekker GA, Thompson SD, North RA, McCowan LM, Roberts CT (2012) A functional variant in ANGPT1 and the risk of pregnancies with hypertensive disorders and small-for-gestational-age infants. *Mol Hum Reprod* 18(6):325-332. doi:1093/molehr/gar081
147. Li X, Zhang X, Leathers R, Makino A, Huang C, Parsa P, Macias J, Yuan JX, Jamieson SW, Thistlethwaite PA (2009) Notch3 signaling promotes the development of pulmonary arterial hypertension. *Nat Med* 15(11):1289-1297. doi:1038/nm.2021
148. Chen J, Zhao X, Wang H, Chen Y, Wang W, Zhou W, Wang X, Tang J, Zhao Y, Lu X et al (2014) Common variants in TGFB2 and miR-518 genes are associated with hypertension in the Chinese population. *Am J Hypertens* 27(10):1268-1276. doi:1093/ajh/hpu047
149. Kim D, Kim J, Yoon JH, Ghim J, Yea K, Song P, Park S, Lee A, Hong CP, Jang MS et al (2014) CXCL12 secreted from adipose tissue recruits macrophages and induces insulin resistance in mice. *Diabetologia* 57(7):1456-1465. doi:1007/s00125-014-3237-5
150. Lu S, Purohit S, Sharma A, Zhi W, He M, Wang Y, Li CJ, She JX (2012) Serum insulin-like growth factor binding protein 6 (IGFBP6) is increased in patients with type 1 diabetes and its complications. *Int J Clin Exp Med* 5(3):229-237.
151. Górka B, Skubis-Zegadło J, Mikula M, Bardadin K, Paliczka E, Czarnocka B (2007) NrCAM, a neuronal system cell-adhesion molecule, is induced in papillary thyroid carcinomas. *Br J Cancer* 97(4):531-538. doi:1038/sj.bjc.6603915
152. Yasuoka H, Kodama R, Tsujimoto M, Yoshidome K, Akamatsu H, Nakahara M, Inagaki M, Sanke T, Nakamura Y (2009) Neuropilin-2 expression in breast cancer: correlation with lymph node metastasis, poor prognosis, and regulation of CXCR4 expression. *BMC Cancer* 9:220. doi:1186/1471-2407-9-220
153. Gong X, Yi J, Carmon KS, Crumbley CA, Xiong W, Thomas A, Fan X, Guo S, An Z, Chang JT et al (2015) Aberrant RSP03-LGR4 signaling in Keap1-deficient lung adenocarcinomas promotes tumor aggressiveness. *Oncogene* 34(36):4692-4701. doi:1038/ncr.2014.417
154. Tanaka K, Arai T, Maegawa M, Matsumoto K, Kaneda H, Kudo K, Fujita Y, Yokote H, Yanagihara K, Yamada Y et al (2009) SRPX2 is overexpressed in gastric cancer and promotes cellular migration and adhesion. *Int J Cancer* 124(5):1072-1080. doi:1002/ijc.24065
155. Abeysinghe HR, Cao Q, Xu J, Pollock S, Veyberman Y, Guckert NL, Keng P, Wang N (2003) THY1 expression is associated with tumor suppression of human ovarian cancer. *Cancer Genet Cytogenet* 143(2):125-132.
156. Aquea G, Bresky G, Lancellotti D, Madariaga JA, Zaffiri V, Urzua U, Haberle S, Bernal G (2014) Increased expression of P2RY2, CD248 and EphB1 in gastric cancers from Chilean patients. *Asian Pac J Cancer Prev* 15(5):1931-1936.
157. Liu J, Liu Z, Liu Q, Li L, Fan X, Wen T, An G (2018) CLEC3B is downregulated and inhibits proliferation in clear cell renal cell carcinoma. *Oncol Rep* 40(4):2023-2035. doi:3892/or.2018.6590
158. Yan Y, Fan Q, Wang L, Zhou Y, Li J, Zhou K (2017) LncRNA Snhg1, a non-degradable sponge for miR-338, promotes expression of proto-oncogene CST3 in primary esophageal cancer cells. *Oncotarget* 8(22):35750-35760. doi:18632/oncotarget.16189
159. Kim HC, Kim YS, Oh HW, Kim K, Oh SS, Kim JT, Kim BY, Lee SJ, Choe YK, Kim DH et al (2014) Collagen triple helix repeat containing 1 (CTHRC1) acts via ERK-dependent induction of MMP9 to promote invasion of colorectal cancer cells. *Oncotarget* 5(2):519-529. doi:18632/oncotarget.1714
160. Duan L, Hu XQ, Feng DY, Lei SY, Hu GH (2013) GPC-1 may serve as a predictor of perineural invasion and a prognosticator of survival in pancreatic cancer. *Asian J Surg* 36(1):7-12. doi:1016/j.asjsur.2012.08.001
161. Lyu M, Cui Y, Zhao T, Ning Z, Ren J, Jin X, Fan G, Zhu Y (2018) Tnfrsf12a-Mediated Atherosclerosis Signaling and Inflammatory Response as a Common Protection Mechanism of Shuxueing Injection Against Both Myocardial and Cerebral Ischemia-Reperfusion Injuries. *Front Pharmacol* 9:312. doi:3389/fphar.2018.00312
162. Shami A, Tengryd C, Asciutto G, Bengtsson E, Nilsson J, Hultgårdh-Nilsson A, Gonçalves I (2015) Expression of fibromodulin in carotid atherosclerotic plaques is associated with diabetes and cerebrovascular events. *Atherosclerosis* 241(2):701-708. doi:1016/j.atherosclerosis.2015.06.023
163. Li W, Yue H (2018) Thymidine phosphorylase: A potential new target for treating cardiovascular disease. *Trends Cardiovasc Med* 28(3):157-171. doi:1016/j.tcm.2017.10.003
164. Haarhaus M, Brandenburg V, Kalantar-Zadeh K, Stenvinkel P, Magnusson P (2017) Alkaline phosphatase: a novel treatment target for cardiovascular disease in CKD. *Nat Rev Nephrol* 13(7):429-442. doi:1038/nrneph.2017.60
165. Ellinghaus E, Ellinghaus D, Krusche P, Greiner A, Schreiber C, Nikolaus S, Gieger C, Strauch K, Lieb W, Rosenstiel P et al (2017) Genome-wide association analysis for chronic venous disease identifies EFEMP1 and KCNH8 as susceptibility loci. *Sci Rep* 7:45652. doi:1038/srep45652
166. Wulf-Johansson H, Lock Johansson S, Schlosser A, Trommelholt Holm A, Rasmussen LM, Mickley H, Diederichsen AC, Munkholm H, Poulsen TS, Tornøe I et al (2013) Localization of microfibrillar-associated protein 4 (MFAP4) in human tissues: clinical evaluation of serum MFAP4 and its association with various cardiovascular conditions. *PLoS One* 8(12):e82243. doi:1371/journal.pone.0082243
167. Song SE, Kim YW, Kim JY, Lee DH, Kim JR, Park SY (2013) IGFBP5 mediates high glucose-induced cardiac fibroblast activation. *J Mol Endocrinol* 50(3):291-303. doi:1530/JME-12-0194
168. Zhang D, Christianson J, Liu ZX, Tian L, Choi CS, Neschen S, Dong J, Wood PA, Shulman GI (2010) Resistance to high-fat diet-induced obesity and insulin resistance in mice with very long-chain acyl-CoA dehydrogenase deficiency. *Cell Metab* 11(5):402-411. doi:1016/j.cmet.2010.03.012
169. Giacchetti G, Faloia E, Sardu C, Camilloni MA, Mariniello B, Gatti C, Garrapa GG, Guerrieri M, Mantero F (2000) Gene expression of angiotensinogen in adipose tissue of obese patients. *Int J Obes Relat Metab Disord* 24 Suppl 2:S142-S143.
170. Dumont J, Goumidi L, Grenier-Boley B, Cottel D, Marécaux N, Montaye M, Wagner A, Arveiler D, Simon C, Ferrières J et al (2018) Dietary linoleic acid interacts with FADS1 genetic variability to modulate HDL-cholesterol and obesity-related traits. *Clin Nutr* 37(5):1683-1689. doi:1016/j.clnu.2017.07.012

171. Wan Z, Frier BC, Williams DB, Wright DC (2012) Epinephrine induces PDK4 mRNA expression in adipose tissue from obese, insulin resistant rats. *Obesity* (Silver Spring) 20(2):453-456. doi:1038/oby.2011.252
172. Milagro FI, Gómez-Abellán P, Campión J, Martínez JA, Ordovás JM, Garaulet M (2012) CLOCK, PER2 and BMAL1 DNA methylation: association with obesity and metabolic syndrome characteristics and monounsaturated fat intake. *Chronobiol Int* 29(9):1180-1194. doi:10.1016/j.cbi.2012.07.007
173. Caimari A, Oliver P, Rodenburg W, Keijzer J, Palou A (2010) Slc27a2 expression in peripheral blood mononuclear cells as a molecular marker for overweight development. *Int J Obes (Lond)* 34(5):831-839. doi:1038/ijo.2010.17
174. Hur H, Kim YB, Ham IH, Lee D (2015) Loss of ACSS2 expression predicts poor prognosis in patients with gastric cancer. *J Surg Oncol* 112(6):585-591. doi:1002/jso.24043
175. Szajnik M, Szczepanski MJ, Elishaev E, Visus C, Lenzner D, Zabel M, Glura M, DeLeo AB, Whiteside TL (2012) 17 β Hydroxysteroid dehydrogenase type 12 (HSD17B12) is a marker of poor prognosis in ovarian carcinoma. *Gynecol Oncol* 127(3):587-594. doi:1016/j.ygyno.2012.08.010
176. Matsuzaka T, Shimano H, Yahagi N, Kato T, Atsumi A, Yamamoto T, Inoue N, Ishikawa M, Okada S, Ishigaki N et al (2007) Crucial role of a long-chain fatty acid elongase, Elovl6, in obesity-induced insulin resistance. *Nat Med* 13(10):1193-1202. doi:1038/nm1662
177. Huggins GS, Berkowitz RI, Blackburn GL, Bray GA, Cheskin L, Clark JM, Coday M, Espeland MA, Evans M, Foreyt JP et al (2016) Prospective Association of GLUL rs10911021 With Cardiovascular Morbidity and Mortality Among Individuals With Type 2 Diabetes: The Look AHEAD Study. *Diabetes* 65(1):297-302. doi:10.2337/db15-0890
178. Konishi H, Okuda A, Ohno Y, Kihara A (2010) Characterization of HACD1 K64Q mutant found in arrhythmogenic right ventricular dysplasia patients. *J Biochem* 148(5):617-622. doi:1093/jb/mvq092
179. He H, Wang J, Yannie PJ, Kakiyama G, Korzun WJ, Ghosh S (2018) Sterol carrier protein-2 deficiency attenuates diet-induced dyslipidemia and atherosclerosis in mice. *J Biol Chem* 293(24):9223-9231. doi:1074/jbc.RA118.002290
180. Oguri M, Kato K, Yokoi K, Watanabe S, Metoki N, Yoshida H, Satoh K, Aoyagi Y, Nishigaki Y, Yoshida H et al (2009) Association of polymorphisms of THBS2 and HSPA8 with hypertension in Japanese individuals with chronic kidney disease. *Mol Med Rep* 2(2):205-211. doi:10.3892/mmr.00000085
181. Xiang R, Fan LL, Huang H, Chen YQ, He W, Guo S, Li JJ, Jin JY, Du R, Yan R et al (2018) Increased Reticulon 3 (RTN3) Leads to Obesity and Hypertriglyceridemia by Interacting With Heat Shock Protein Family A (Hsp70) Member 5 (HSPA5). *Circulation* 138(17):1828-1838. doi:10.1161/CIRCULATIONAHA.117.030718
182. Capobianco V, Nardelli C, Ferrigno M, Iaffaldano L, Pilone V, Forestieri P, Zambrano N, Sacchetti L (2012) miRNA and protein expression profiles of visceral adipose tissue reveal miR-141/YWHAG and miR-520e/RAB11A as two potential miRNA/protein target pairs associated with severe obesity. *J Proteome Res* 11(6):3358-3369. doi:1021/pr300152z
183. Hinrichsen I, Ernst BP, Nuber F, Passmann S, Schäfer D, Steinke V, Friedrichs N, Plotz G, Zeuzem S, Brieger A (2014) Reduced migration of MLH1 deficient colon cancer cells depends on SPTAN1. *Mol Cancer* 13:11. doi:1186/1476-4598-13-11
184. Whiteland H, Spencer-Harty S, Morgan C, Kynaston H, Thomas DH, Bose P, Fenn N, Lewis P, Jenkins S, Doak SH (2014) A role for STEAP2 in prostate cancer progression. *Clin Exp Metastasis* 31(8):909-920. doi:1007/s10585-014-9679-9
185. Cao X, Xia Y, Yang J, Jiang J, Chen L, Ni R, Li L, Gu Z (2012) Clinical and biological significance of never in mitosis gene A-related kinase 6 (NEK6) expression in hepatic cell cancer. *Pathol Oncol Res* 18(2):201-207. doi:1007/s12253-011-9429-0
186. Zecchini V, Madhu B, Russell R, Pértiga-Gomes N, Warren A, Gaude E, Borlido J, Stark R, Ireland-Zecchini H, Rao R et al Nuclear ARRB1 induces pseudohypoxia and cellular metabolism reprogramming in prostate cancer. *EMBO J*. 2014 Jun 17;33(12):1365-1382. doi:10.1093/emboj/ekd387
187. Xue J, Chi Y, Chen Y, Huang S, Ye X, Niu J, Wang W, Pfeffer LM, Shao ZM, Wu ZH et al (2016) MiRNA-621 sensitizes breast cancer to chemotherapy by suppressing FBXO11 and enhancing p53 activity. *Oncogene* 35(4):448-458. doi:1038/onc.2015.96
188. Mao J, Liang Z, Zhang B, Yang H, Li X, Fu H, Zhang X, Yan Y, Xu W, Qian H (2017) UBR2 Enriched in p53 Deficient Mouse Bone Marrow Mesenchymal Stem Cell-Exosome Promoted Gastric Cancer Progression via Wnt/ β -Catenin Pathway. *Stem Cells* 35(11):2267-2279. doi:1002/stem.2702
189. Peng H, Ishida M, Li L, Saito A, Kamiya A, Hamilton JP, Fu R, Olaru AV, An F, Popescu I et al (2015) Pseudogene INTS6P1 regulates its cognate gene INTS6 through competitive binding of miR-17-5p in hepatocellular carcinoma. *Oncotarget* 6(8):5666-5677. doi:10.18632/oncotarget.3290
190. Liou TH, Chen HH, Wang W, Wu SF, Lee YC, Yang WS, Lee WJ (2011) ESR1, FTO, and UCP2 genes interact with bariatric surgery affecting weight loss and glycemic control in severely obese patients. *Obes Surg*;21(11):1758-1765. doi:1007/s11695-011-0457-3
191. Pal A, Barber TM, Bunt M, Rudge SA, Zhang Q, Lachlan KL, Cooper NS, Linden H, Levy JC, Wakelam MJ et al (2012) PTEN mutations as a cause of constitutive insulin sensitivity and obesity. *N Engl J Med* 367(11):1002-1011. doi:1056/NEJMoa1113966
192. Karamat FA, Oudman I, Ris-Stalpers C, Afink GB, Keijser R, Clark JF, Montfrans GA, Brewster LM (2014) Resistance artery creatine kinase mRNA and blood pressure in humans. *Hypertension* 63(1):68-73. doi:10.1161/HYPERTENSIONAHA.113.01352
193. Wang B, Zou A, Ma L, Chen X, Wang L, Zeng X, Tan T (2017) miR-455 inhibits breast cancer cell proliferation through targeting CDK14. *Eur J Pharmacol* 807:138-143. doi:1016/j.ejphar.2017.03.016
194. Ma S, Guan XY, Beh PS, Wong KY, Chan YP, Yuen HF, Vielkind J, Chan KW (2007) The significance of LMO2 expression in the progression of prostate cancer. *J Pathol* 211(3):278-285. doi:1002/path.2109
195. Wang CC, Liao JY, Lu YS, Chen JW, Yao YT, Lien HC (2012) Differential expression of moesin in breast cancers and its implication in epithelial-mesenchymal transition. *Histopathology* 61(1):78-87. doi:10.1111/j.1365-2559.2012.04204.x
196. Yoshino H, Chiyomaru T, Enokida H, Kawakami K, Tatarano S, Nishiyama K, Nohata N, Seki N, Nakagawa M (2011) The tumour-suppressive function of miR-1 and miR-133a targeting TAGLN2 in bladder cancer. *Br J Cancer* 104(5):808-818. doi:1038/bjc.2011.23

197. Ahmad R, Shihab PK, Thomas R, Alghanim M, Hasan A, Sindhu S, Behbehani K (2015) Increased expression of the interleukin-1 receptor-associated kinase (IRAK)-1 is associated with adipose tissue inflammatory state in obesity. *Diabetol Metab Syndr* 7:71. doi:1186/s13098-015-0067-7
198. Bouchard L, Tchernof A, Deshaies Y, Lebel S, Hould FS, Marceau P, Vohl MC (2007) CYR61 polymorphisms are associated with plasma HDL-cholesterol levels in obese individuals. *Clin Genet* 72(3):224-229. doi:1111/j.1399-0004.2007.00855.x
199. Gautrey H, Jackson C, Dittrich AL, Browell D, Lennard T, Tyson-Capper A (2015) SRSF3 and hnRNP H1 regulate a splicing hotspot of HER2 in breast cancer cells. *RNA Biol* 12(10):1139-1151. doi:1080/15476286.2015.1076610
200. Hammerich-Hille S, Bardout VJ, Hilsenbeck SG, Osborne CK, Oesterreich S (2010) Low SAFB levels are associated with worse outcome in breast cancer patients. *Breast Cancer Res Treat* 121(2):503-509. doi:1007/s10549-008-0297-6
201. Ellison-Zelski SJ, Alarid ET (2010) Maximum growth and survival of estrogen receptor-alpha positive breast cancer cells requires the Sin3A transcriptional repressor. *Mol Cancer* 9:263. doi:1186/1476-4598-9-263
202. Tsai WW, Wang Z, Yiu TT, Akdemir KC, Xia W, Winter S, Tsai CY, Shi X, Schwarzer D, Plunkett W et al (2010) TRIM24 links a non-canonical histone signature to breast cancer. *Nature* 468(7326):927-932. doi:1038/nature09542
203. Han Y, Ru GQ, Mou X, Wang HJ, Ma Y, He XL, Yan Z, Huang D (2015) AUTS2 is a potential therapeutic target for pancreatic cancer patients with liver metastases. *Med Hypotheses* 85(2):203-206. doi:1016/j.mehy.2015.04.029
204. Bendlová B, Vaňková M, Hill M, Vacínová G, Lukášová P, Vejražková D, Šedová L, Šeda O, Včelák J (2017) ZBTB16 gene variability influences obesity-related parameters and serum lipid levels in Czech adults. *Physiol Res* 66(Supplementum 3):S425-S431.
205. Saxena R, Bjonnes A, Prescott J, Dib P, Natt P, Lane J, Lerner M, Cooper JA, Ye Y, Li KW et al (2014) Genome-wide association study identifies variants in casein kinase II (CSNK2A2) to be associated with leukocyte telomere length in a Punjabi Sikh diabetic cohort. *Circ Cardiovasc Genet* 7(3):287-295. doi:1161/CIRCGENETICS.113.000412
206. Thun GA, Imboden M, Berger W, Rochat T, Probst-Hensch NM (2013) The association of a variant in the cell cycle control gene CCND1 and obesity on the development of asthma in the Swiss SAPALDIA study. *J Asthma*. 50(2):147-154. doi:3109/02770903.2012.757776
207. Yaghootkar H, Stancáková A, Freathy RM, Vangipurapu J, Weedon MN, Xie W, Wood AR, Ferrannini E, Mari A, Ring SM et al (2015) Association analysis of 29,956 individuals confirms that a low-frequency variant at CCND2 halves the risk of type 2 diabetes by enhancing insulin secretion. *Diabetes* 64(6):2279-2285. doi:2337/db14-1456
208. Kim S, Hong JW, Park KW (2016) B cell translocation gene 2 (Btg2) is regulated by Stat3 signaling and inhibits adipocyte differentiation. *Mol Cell Biochem* 413(1-2):145-153. doi:1007/s11010-015-2648-z
209. Chutkow WA, Birkenfeld AL, Brown JD, Lee HY, Frederick DW, Yoshioka J, Patwari P, Kursawe R, Cushman SW, Plutzky J et al (2010) Deletion of the alpha-arrestin protein Txnip in mice promotes adiposity and adipogenesis while preserving insulin sensitivity. *Diabetes* 59(6):1424-1434. doi:2337/db09-1212
210. Lee MF, Pan MH, Chiou YS, Cheng AC, Huang H (2011) Resveratrol modulates MED28 (Magacin/EG-1) expression and inhibits epidermal growth factor (EGF)-induced migration in MDA-MB-231 human breast cancer cells. *J Agric Food Chem* 59(21):11853-11861. doi:1021/jf202426k
211. Chiellini C, Bertacca A, Novelli SE, Görgün CZ, Ciccarone A, Giordano A, Xu H, Soukas A, Costa M, Gandini D et al (2002) Obesity modulates the expression of haptoglobin in the white adipose tissue via TNFalpha. *J Cell Physiol* 190(2):251-258. doi:1002/jcp.10061
212. Nakamura R, Kataoka H, Sato N, Kanamori M, Ihara M, Igarashi H, Ravshanov S, Wang YJ, Li ZY, Shimamura T et al (2005) EPHA2/EFNA1 expression in human gastric cancer. *Cancer Sci* 96(1):42-47. doi:1111/j.1349-7006.2005.00007.x

Tables

Table 1. Primers used for quantitative PCR

Primer sequence (5'→3')		
Gene	Forward	Reverse
STAT3	CAGCAGCTTGACACACGGTA	AAACACCAAAGTGGCATGTGA
CORO1C	ATGAGGCGAGTGGTACGACA	ATCCCAGGTCACACGAGAAAC
SERPINH1	TCAGTGAGCTTCGCTGATGAC	CATGGCGTTGACTAGCAGGG
MVP	TACATCCGGCAGGACAATGAG	CTGTGCAGTAGTGACGTGGG
ITGB5	TCTCGGTGTGATCTGAGGG	TGGCGAACCTGTAGCTGGA
PCM1	CGGAGTCGTCACCAGGAGT	GCTGTTGCTCTACCTTGGGAAT
SIRT1	TAGCCTTGTCAGATAAGGAAGGA	ACAGCTTCACAGTCAACTTTGT
EEF1G	AACCGCACCCCTGAATTTCTC	GGCGTTGCTCTCAAACACAC
PTEN	TGGATTCGACTTAGACTTGACCT	GGTGGGTTATGGTCTTCAAAGG
RPS2	GGCCTCTCTCAAGGATGAGGT	GTCCCGATAGCAACAAATGC

Table 2 The statistical metrics for key differentially expressed genes (DEGs)

Illumina Id	Gene Symbol	logFC	p Value	Adj P value	t value	Regulation	Gene Name
ILMN_1664464	PTGDS	1.820427	5.99E-10	5.99E-10	9.552145	Up	prostaglandin D2 synthase
ILMN_1732538	LBP	2.225478	6.05E-10	6.05E-10	9.547636	Up	lipopolysaccharide binding protein
ILMN_1768820	CYP11A1	0.714722	8.98E-10	8.98E-10	9.362374	Up	cytochrome P450 family 11 subfamily A member 1
ILMN_1716309	EGFL6	3.153351	2.55E-09	2.55E-09	8.884119	Up	EGF like domain multiple 6
ILMN_2401978	STAT3	0.708174	8.88E-09	8.88E-09	8.328804	Up	signal transducer and activator of transcription 3
ILMN_1785852	NABP1	1.234646	9.01E-09	9.01E-09	8.322415	Up	nucleic acid binding protein 1
ILMN_1709750	SUSD1	0.818338	1.47E-08	1.47E-08	8.108538	Up	sushi domain containing 1
ILMN_1800512	HMOX1	1.385702	3.42E-08	3.42E-08	7.747992	Up	hemeoxygenase 1
ILMN_2057479	EGFL6	3.924423	3.64E-08	3.64E-08	7.721939	Up	EGF like domain multiple 6
ILMN_2141118	INSYN1	0.859189	5.67E-08	5.67E-08	7.535199	Up	inhibitory synaptic factor 1
ILMN_1715662	CCDC80	0.999509	8.82E-08	8.82E-08	7.351189	Up	coiled-coil domain containing 80
ILMN_2109708	TYMP	1.207265	1.12E-07	1.12E-07	7.250807	Up	thymidine phosphorylase
ILMN_2400372	SULT1A2	1.110385	1.61E-07	1.61E-07	7.102387	Up	sulfotransferase family 1A member 2
ILMN_1755792	STK38L	0.554845	1.67E-07	1.67E-07	7.089178	Up	serine/threonine kinase 38 like
ILMN_1663618	STAT3	0.567385	1.71E-07	1.71E-07	7.07883	Up	signal transducer and activator of transcription 3
ILMN_1798528	SULT1A2	1.001497	2.89E-07	2.89E-07	6.86514	Up	sulfotransferase family 1A member 2
ILMN_1660021	PLIN3	0.659133	8.1E-07	8.1E-07	6.452309	Up	perilipin 3
ILMN_1910180	NRP2	1.230106	8.62E-07	8.62E-07	6.427843	Up	neuropilin 2
ILMN_1741404	MSC	1.576437	9.09E-07	9.09E-07	6.406619	Up	musculin
ILMN_1676067	SEMA3G	1.155506	9.21E-07	9.21E-07	6.401565	Up	semaphorin 3G
ILMN_1722809	NRCAM	1.386089	1.03E-06	1.03E-06	6.356808	Up	neuronal cell adhesion molecule
ILMN_1652631	GLIPR2	1.728391	1.1E-06	1.1E-06	6.332413	Up	GLI pathogenesis related 2
ILMN_1690939	TYMP	0.635845	1.11E-06	1.11E-06	6.327574	Up	thymidine phosphorylase
ILMN_1750674	SDSL	0.768954	1.11E-06	1.11E-06	6.325979	Up	serine dehydratase like
ILMN_1687216	PCBP3	0.721533	1.56E-06	1.56E-06	6.192409	Up	poly(rC) binding protein 3
ILMN_2104295	TMEM178A	0.848363	1.6E-06	1.6E-06	6.184294	Up	transmembrane protein 178A
ILMN_1726589	CD248	1.778343	1.77E-06	1.77E-06	6.143392	Up	CD248 molecule
ILMN_2169439	ITGAV	0.911775	2.01E-06	2.01E-06	6.094822	Up	integrin subunit alpha V
ILMN_1658926	NOTCH3	1.789129	2.13E-06	2.13E-06	6.07107	Up	notch 3
ILMN_1698732	PALLD	1.949881	2.4E-06	2.4E-06	6.025117	Up	palladin, cytoskeletal associated protein
ILMN_1715684	LAMB3	1.217439	2.54E-06	2.54E-06	6.002744	Up	laminin subunit beta 3
ILMN_1675656	PPFIBP2	0.586918	2.79E-06	2.79E-06	5.966758	Up	PPFIA binding protein 2
ILMN_1751028	SERPINH1	0.710927	2.9E-06	2.9E-06	5.951672	Up	serpin family H member 1
ILMN_1701603	ALPL	1.630113	2.95E-06	2.95E-06	5.943838	Up	alkaline phosphatase, biomineralization associated
ILMN_1775542	FCMR	0.672225	3.36E-06	3.36E-06	5.893893	Up	Fc fragment of IgM receptor
ILMN_1720484	CRTAP	1.04261	3.58E-06	3.58E-06	5.86966	Up	cartilage associated protein
ILMN_1793695	ITIH5	1.374714	4.1E-06	4.1E-06	5.816395	Up	inter-alpha-trypsin inhibitor heavy chain family member 5
ILMN_1714586	VGLL3	1.26809	4.16E-06	4.16E-06	5.810654	Up	vestigial like family member 3
ILMN_1732197	MN1	0.948733	4.26E-06	4.26E-06	5.802156	Up	MN1 proto-oncogene, transcriptional regulator
ILMN_1680874	TUBB2B	1.715743	4.64E-06	4.64E-06	5.768826	Up	tubulin beta 2B class IIb
ILMN_1656900	SULT1A3	1.129801	6.1E-06	6.1E-06	5.662817	Up	sulfotransferase family 1A member 3
ILMN_2344373	MVP	0.650428	6.34E-06	6.34E-06	5.647981	Up	major vault protein

ILMN_1676449	SLIT2	1.051292	7.26E-06	7.26E-06	5.595914	Up	slit guidance ligand 2
ILMN_1715416	NUP188	0.674676	7.47E-06	7.47E-06	5.584899	Up	nucleoporin 188
ILMN_1789507	COL11A1	1.258588	7.99E-06	7.99E-06	5.558827	Up	collagen type XI alpha 1 chain
ILMN_1658425	DAG1	0.528968	8.18E-06	8.18E-06	5.549832	Up	dystroglycan 1
ILMN_1678403	TMEM178A	0.540004	8.25E-06	8.25E-06	5.546888	Up	transmembrane protein 178A
ILMN_1801516	GPC1	0.702812	8.47E-06	8.47E-06	5.536387	Up	glypican 1
ILMN_1718285	HOXC8	0.916774	8.51E-06	8.51E-06	5.534712	Up	homeobox C8
ILMN_1734184	PLBD2	0.814142	8.63E-06	8.63E-06	5.52926	Up	phospholipase B domain containing 2
ILMN_1809928	COL6A2	1.55151	8.7E-06	8.7E-06	5.526418	Up	collagen type VI alpha 2 chain
ILMN_2139970	ALDH1A3	2.346733	9.12E-06	9.12E-06	5.508259	Up	aldehyde dehydrogenase 1 family member A3
ILMN_1658619	WWC1	0.614241	9.14E-06	9.14E-06	5.507185	Up	WW and C2 domain containing 1
ILMN_2111237	MN1	0.93355	9.31E-06	9.31E-06	5.5002	Up	MN1 proto-oncogene, transcriptional regulator
ILMN_1853824	MGAT3	0.828545	1.13E-05	1.13E-05	5.424362	Up	mannosyl (beta-1,4-)-glycoprotein beta-1,4-N-acetylglucosaminyltransferase
ILMN_1750101	S100A11	0.735352	1.19E-05	1.19E-05	5.404472	Up	S100 calcium binding protein A11
ILMN_1803338	CCDC80	0.979808	1.2E-05	1.2E-05	5.403253	Up	coiled-coil domain containing 80
ILMN_1701613	RARRES3	1.103884	1.25E-05	1.25E-05	5.387103	Up	retinoic acid receptor responder 3
ILMN_1803236	CLCA2	0.574002	1.26E-05	1.26E-05	5.384393	Up	chloride channel accessory 2
ILMN_1807439	ALDH1A3	1.954717	1.31E-05	1.31E-05	5.369138	Up	aldehyde dehydrogenase 1 family member A3
ILMN_1759374	LINC00545	1.309512	1.39E-05	1.39E-05	5.345927	Up	long intergenic non-protein coding RNA 545
ILMN_1803277	MVP	0.916886	1.4E-05	1.4E-05	5.344141	Up	major vault protein
ILMN_1771179	CYB561	0.539323	1.46E-05	1.46E-05	5.327812	Up	cytochrome b561
ILMN_1887987	LINC00968	0.855428	1.54E-05	1.54E-05	5.307616	Up	long intergenic non-protein coding RNA 968
ILMN_1689968	PLEKHO2	0.895733	1.58E-05	1.58E-05	5.29842	Up	pleckstrin homology domain containing O2
ILMN_1763587	TNMD	2.019209	1.69E-05	1.69E-05	5.272155	Up	tenomodulin
ILMN_1814282	AEN	0.629178	1.81E-05	1.81E-05	5.245312	Up	apoptosis enhancing nuclease
ILMN_2336133	SULT1A4	0.781945	1.82E-05	1.82E-05	5.24246	Up	sulfotransferase family 1A member 4
ILMN_1783909	COL6A2	1.730795	1.94E-05	1.94E-05	5.218859	Up	collagen type VI alpha 2 chain
ILMN_1691884	STC2	1.156543	2.19E-05	2.19E-05	5.171969	Up	stanniocalcin 2
ILMN_1732151	COL6A1	1.298231	2.36E-05	2.36E-05	5.143952	Up	collagen type VI alpha 1 chain
ILMN_1752299	RAB6B	0.714693	2.59E-05	2.59E-05	5.109432	Up	RAB6B, member RAS oncogene family
ILMN_1677814	ABCC3	1.564486	2.67E-05	2.67E-05	5.097746	Up	ATP binding cassette subfamily C member 3
ILMN_1779147	ENC1	0.85892	2.74E-05	2.74E-05	5.087435	Up	ectodermal-neural cortex 1
ILMN_1750409	RAB9A	0.555529	2.78E-05	2.78E-05	5.081386	Up	RAB9A, member RAS oncogene family
ILMN_1666594	IRF8	1.300268	2.88E-05	2.88E-05	5.068737	Up	interferon regulatory factor 8
ILMN_1796316	MMP9	1.65811	3.26E-05	3.26E-05	5.020792	Up	matrix metalloproteinase 9
ILMN_1813139	ANKDD1A	1.12868	3.44E-05	3.44E-05	5.000054	Up	ankyrin repeat and death domain containing 1A
ILMN_2306661	UNC13C	0.623986	3.56E-05	3.56E-05	4.987296	Up	unc-13 homolog C
ILMN_2188722	GLS	0.666142	3.56E-05	3.56E-05	4.987083	Up	glutaminase
ILMN_2062620	NMT2	0.699357	3.57E-05	3.57E-05	4.986309	Up	N-myristoyltransferase 2
ILMN_1771688	RAB7B	0.985922	3.77E-05	3.77E-05	4.966148	Up	RAB7B, member RAS oncogene family
ILMN_1749868	FAM171A1	0.805476	3.84E-05	3.84E-05	4.95859	Up	family with sequence similarity 171 member A1
ILMN_1801226	DOCK6	0.88875	3.94E-05	3.94E-05	4.949344	Up	dedicator of cytokinesis 6
ILMN_1657129	SKAP2	0.56751	3.95E-05	3.95E-05	4.947644	Up	src kinase associated phosphoprotein 2

ILMN_1678757	BCYRN1	1.528559	4.21E-05	4.21E-05	4.923778	Up	brain cytoplasmic RNA 1
ILMN_1773079	COL3A1	1.465245	4.58E-05	4.58E-05	4.891919	Up	collagen type III alpha 1 chain
ILMN_1729596	INF2	0.717482	4.84E-05	4.84E-05	4.870531	Up	inverted formin, FH2 and WH2 domain containing
ILMN_1779416	SCUBE2	0.812412	4.93E-05	4.93E-05	4.86363	Up	signal peptide, CUB domain and EGF like domain containing 2
ILMN_2397721	GLB1	0.668144	5.28E-05	5.28E-05	4.837888	Up	galactosidase beta 1
ILMN_1691364	STAT1	0.649399	5.38E-05	5.38E-05	4.830063	Up	signal transducer and activator of transcription 1
ILMN_1735155	GLB1	0.738614	5.47E-05	5.47E-05	4.824387	Up	galactosidase beta 1
ILMN_1800354	CST3	0.562598	5.91E-05	5.91E-05	4.794968	Up	cystatin C
ILMN_1804007	NANOS3	0.541781	6.12E-05	6.12E-05	4.781403	Up	nanos C2HC-type zinc finger 3
ILMN_2335557	ITIH5	0.80499	6.15E-05	6.15E-05	4.779724	Up	inter-alpha-trypsin inhibitor heavy chain family member 5
ILMN_1686367	HSPA8	0.557034	6.18E-05	6.18E-05	4.777626	Up	heat shock protein family A (Hsp70) member 8
ILMN_2313730	RHOC	0.613535	6.46E-05	6.46E-05	4.760619	Up	ras homolog family member C
ILMN_2379130	IRAK1	0.562669	6.98E-05	6.98E-05	4.731406	Up	interleukin 1 receptor associated kinase 1
ILMN_1660871	NEK6	0.613802	7.12E-05	7.12E-05	4.723617	Up	NIMA related kinase 6
ILMN_1690105	STAT1	0.563232	7.21E-05	7.21E-05	4.718878	Up	signal transducer and activator of transcription 1
ILMN_1667295	VASN	0.99406	7.24E-05	7.24E-05	4.717494	Up	vasorin
ILMN_1754842	DLGAP4	0.561107	7.94E-05	7.94E-05	4.682126	Up	DLG associated protein 4
ILMN_1789733	CLIP3	0.953388	7.98E-05	7.98E-05	4.680665	Up	CAP-Gly domain containing linker protein 3
ILMN_1720430	PPDPF	0.580876	8.33E-05	8.33E-05	4.664348	Up	pancreatic progenitor cell differentiation and proliferation factor
ILMN_2378376	CYB561	0.526267	8.52E-05	8.52E-05	4.655456	Up	cytochrome b561
ILMN_2411236	NRCAM	1.443196	8.72E-05	8.72E-05	4.646872	Up	neuronal cell adhesion molecule
ILMN_1805992	SHTN1	0.731593	9.13E-05	9.13E-05	4.629195	Up	shootin 1
ILMN_1735124	OXT	0.578334	9.16E-05	9.16E-05	4.627921	Up	oxytocin/neurophysin I prepropeptide
ILMN_1693826	HAVCR2	0.722164	9.19E-05	9.19E-05	4.626647	Up	hepatitis A virus cellular receptor 2
ILMN_1791569	PLXNA1	0.62569	9.48E-05	9.48E-05	4.615066	Up	plexin A1
ILMN_2224486	C3orf14	0.788002	0.000102	0.000102	4.588076	Up	chromosome 3 open reading frame 14
ILMN_2038775	TUBB2A	1.288125	0.00011	0.00011	4.55718	Up	tubulin beta 2A class IIa
ILMN_1763640	NCKAP5L	0.532109	0.000113	0.000113	4.548191	Up	NCK associated protein 5 like
ILMN_1731862	ITIH5	0.857364	0.000119	0.000119	4.527192	Up	inter-alpha-trypsin inhibitor heavy chain family member 5
ILMN_1796734	SPARC	0.8005	0.000127	0.000127	4.504283	Up	secreted protein acidic and cysteine rich
ILMN_1707804	SLX1A-SULT1A3	0.634745	0.000127	0.000127	4.503092	Up	SLX1A-SULT1A3 readthrough (NMD candidate)
ILMN_2374352	DBNDD1	0.617377	0.000129	0.000129	4.498243	Up	dysbindin domain containing 1
ILMN_2121816	GPR137B	0.679236	0.00013	0.00013	4.495797	Up	G protein-coupled receptor 137B
ILMN_1908923	GRIN2B	1.478932	0.000132	0.000132	4.488805	Up	glutamate ionotropic receptor NMDA type subunit 2B
ILMN_1745806	PEMT	1.18577	0.000136	0.000136	4.478651	Up	phosphatidylethanolamine N-methyltransferase
ILMN_1782412	IRX2	0.640361	0.000138	0.000138	4.471406	Up	iroquoishomeobox 2
ILMN_2171295	CDK14	0.526289	0.000139	0.000139	4.47008	Up	cyclin dependent kinase 14
ILMN_1794190	CCPG1	0.595489	0.000142	0.000142	4.461295	Up	cell cycle progression 1
ILMN_1757387	UCHL1	1.625354	0.000147	0.000147	4.44834	Up	ubiquitin C-terminal hydrolase L1
ILMN_1744487	MFRP	1.085469	0.000153	0.000153	4.432535	Up	membrane frizzled-related protein
ILMN_1683146	FTH1	0.709387	0.000153	0.000153	4.431824	Up	ferritin heavy chain 1

ILMN_1728512	YWHAH	0.734671	0.000154	0.000154	4.429773	Up	tyrosine 3-monooxygenase/tryptophan 5-monooxygenase activation protein eta
ILMN_2352131	ERBB2	0.825698	0.000161	0.000161	4.412124	Up	erb-b2 receptor tyrosine kinase 2
ILMN_1656378	NMT2	0.637872	0.000163	0.000163	4.409175	Up	N-myristoyltransferase 2
ILMN_1788783	TRAM2	0.731691	0.000169	0.000169	4.395858	Up	translocation associated membrane protein 2
ILMN_1812461	WISP2	1.648741	0.000172	0.000172	4.389102	Up	WNT1 inducible signaling pathway protein 2
ILMN_1796755	ITGB5	0.824151	0.000178	0.000178	4.37583	Up	integrin subunit beta 5
ILMN_1675062	MYL9	0.704484	0.000184	0.000184	4.361427	Up	myosin light chain 9
ILMN_1705984	HNMT	0.55377	0.000195	0.000195	4.34004	Up	histamine N-methyltransferase
ILMN_1733415	MFAP5	1.982064	0.000204	0.000204	4.323196	Up	microfibril associated protein 5
ILMN_1721605	SMYD2	0.535837	0.00021	0.00021	4.311879	Up	SET and MYND domain containing 2
ILMN_2179717	FAM189A2	0.524393	0.000212	0.000212	4.308716	Up	family with sequence similarity 189 member A2
ILMN_1787127	SLC43A2	0.574814	0.000217	0.000217	4.300207	Up	solute carrier family 43 member 2
ILMN_1744517	GNS	0.548078	0.00022	0.00022	4.293593	Up	glucosamine (N-acetyl)-6-sulfatase
ILMN_1754660	ZCCHC24	0.577849	0.000221	0.000221	4.292656	Up	zinc finger CCHC-type containing 24
ILMN_1685824	B4GALT5	0.642948	0.000222	0.000222	4.291033	Up	beta-1,4-galactosyltransferase 5
ILMN_1685714	INHBB	0.880027	0.000232	0.000232	4.27473	Up	inhibin subunit beta B
ILMN_1713124	AKR1C3	0.814393	0.000233	0.000233	4.272982	Up	aldo-ketoreductase family 1 member C3
ILMN_2404795	SULT1A1	0.54791	0.000243	0.000243	4.25676	Up	sulfotransferase family 1A member 1
ILMN_1668374	ITGB5	0.846685	0.000254	0.000254	4.239363	Up	integrin subunit beta 5
ILMN_1774229	SLC7A4	0.588643	0.000254	0.000254	4.238984	Up	solute carrier family 7 member 4
ILMN_1798496	HOXB8	0.831195	0.000268	0.000268	4.218942	Up	homeobox B8
ILMN_1654262	ZMAT3	0.568561	0.000269	0.000269	4.216909	Up	zinc finger matrin-type 3
ILMN_1736730	CARMIL1	0.532451	0.000283	0.000283	4.198429	Up	capping protein regulator and myosin 1 linker 1
ILMN_1658639	SLC46A3	0.534039	0.000287	0.000287	4.192647	Up	solute carrier family 46 member 3
ILMN_1695880	LOX	1.159643	0.00029	0.00029	4.189243	Up	lysyl oxidase
ILMN_2343278	PLPP1	0.762711	0.000294	0.000294	4.182978	Up	phospholipid phosphatase 1
ILMN_2162989	TMEM189	0.5836	0.000297	0.000297	4.179119	Up	transmembrane protein 189
ILMN_1812433	HP	1.60106	0.000303	0.000303	4.172329	Up	haptoglobin
ILMN_2044813	TUBB2A	1.233632	0.000309	0.000309	4.164915	Up	tubulin beta 2A class IIa
ILMN_1692077	MXRA7	0.862596	0.000312	0.000312	4.160596	Up	matrix remodeling associated 7
ILMN_1759513	RND3	0.776115	0.000319	0.000319	4.151717	Up	Rho family GTPase 3
ILMN_1701195	PLA2G7	0.874848	0.000321	0.000321	4.150019	Up	phospholipase A2 group VII
ILMN_1809496	COPG2	0.790334	0.000324	0.000324	4.145622	Up	coatomer protein complex subunit gamma 2
ILMN_2336781	SOD2	0.621923	0.000333	0.000333	4.135996	Up	superoxide dismutase 2
ILMN_2095133	SPTAN1	0.557462	0.000359	0.000359	4.106471	Up	spectrin alpha, non-erythrocytic 1
ILMN_1674620	SGCE	0.622138	0.000374	0.000374	4.090801	Up	sarcoglycan epsilon
ILMN_1666502	SOBP	0.667445	0.0004	0.0004	4.065752	Up	sine oculis binding protein homolog
ILMN_2316386	GPBAR1	0.828862	0.000402	0.000402	4.063058	Up	G protein-coupled bile acid receptor 1
ILMN_2377900	MAP1B	1.140578	0.000411	0.000411	4.055336	Up	microtubule associated protein 1B
ILMN_2232177	ACTN1	0.63592	0.000419	0.000419	4.047935	Up	actinin alpha 1
ILMN_1795679	STMN2	1.434038	0.000434	0.000434	4.033809	Up	stathmin 2
ILMN_1771261	SYNC	1.004439	0.000455	0.000455	4.015841	Up	syncoilin, intermediate filament protein
ILMN_2413644	TM4SF19	0.839844	0.00046	0.00046	4.011693	Up	transmembrane 4 L six family member 19
ILMN_1781626	C1S	1.250935	0.00046	0.00046	4.011381	Up	complement C1s

ILMN_2115862	ESPNL	0.592832	0.000461	0.000461	4.011043	Up	espin like
ILMN_2202915	FAR2	0.717943	0.000463	0.000463	4.008904	Up	fatty acyl-CoA reductase 2
ILMN_1730416	CYCS	0.538013	0.000473	0.000473	4.000795	Up	cytochrome c, somatic
ILMN_1733288	C1RL	0.569636	0.000479	0.000479	3.996304	Up	complement C1r subcomponent like
ILMN_2187746	EMX2	0.526956	0.000491	0.000491	3.986382	Up	empty spiracles homeobox 2
ILMN_1737163	SH3BGL3	0.572465	0.000492	0.000492	3.985522	Up	SH3 domain binding glutamate rich protein like 3
ILMN_1670870	ALCAM	0.68422	0.000506	0.000506	3.975	Up	activated leukocyte cell adhesion molecule
ILMN_1669362	IGFBP6	1.927527	0.000529	0.000529	3.958008	Up	insulin like growth factor binding protein 6
ILMN_1773865	HSPA5	0.542294	0.000535	0.000535	3.953083	Up	heat shock protein family A (Hsp70) member 5
ILMN_1791494	SYNPO2	0.555068	0.000563	0.000563	3.933878	Up	synaptopodin 2
ILMN_1727709	GPBAR1	0.738312	0.000582	0.000582	3.920655	Up	G protein-coupled bile acid receptor 1
ILMN_1766914	MFAP4	1.402644	0.000585	0.000585	3.91908	Up	microfibril associated protein 4
ILMN_2059689	TMEM54	0.718887	0.000587	0.000587	3.917919	Up	transmembrane protein 54
ILMN_1653161	SNCG	1.257281	0.000602	0.000602	3.908096	Up	synuclein gamma
ILMN_2370208	CMTM3	0.671258	0.000625	0.000625	3.893215	Up	CKLF like MARVEL transmembrane domain containing 3
ILMN_1712545	S100A3	0.548387	0.000634	0.000634	3.888169	Up	S100 calcium binding protein A3
ILMN_1719316	TMED3	1.118639	0.000674	0.000674	3.864212	Up	transmembrane p24 trafficking protein 3
ILMN_1789196	TPM2	0.999608	0.000674	0.000674	3.864171	Up	tropomyosin 2
ILMN_1676663	TNFRSF11B	0.737053	0.000674	0.000674	3.863984	Up	TNF receptor superfamily member 11b
ILMN_1752802	CLPTM1L	0.538557	0.000681	0.000681	3.860129	Up	CLPTM1 like
ILMN_1776953	MYL9	0.73886	0.000694	0.000694	3.853141	Up	myosin light chain 9
ILMN_1688295	ZNF219	0.693667	0.000695	0.000695	3.852426	Up	zinc finger protein 219
ILMN_1653006	CSN1S1	1.490032	0.000707	0.000707	3.845789	Up	casein alpha s1
ILMN_1788955	PDLIM1	0.78358	0.000725	0.000725	3.836228	Up	PDZ and LIM domain 1
ILMN_1696048	MEDAG	1.372503	0.000746	0.000746	3.825101	Up	mesenteric estrogen dependent adipogenesis
ILMN_1667081	CCND2	1.194174	0.000754	0.000754	3.82061	Up	cyclin D2
ILMN_1791447	CXCL12	1.463874	0.000764	0.000764	3.815507	Up	C-X-C motif chemokine ligand 12
ILMN_1773650	LRRN3	0.857534	0.000772	0.000772	3.81182	Up	leucine rich repeat neuronal 3
ILMN_1788098	LHCGR	0.89169	0.000777	0.000777	3.80896	Up	luteinizing hormone/choriogonadotropin receptor
ILMN_1726245	TGFB2	0.593243	0.000793	0.000793	3.801026	Up	transforming growth factor beta receptor 2
ILMN_1711748	PLTP	0.575848	0.000794	0.000794	3.800825	Up	phospholipid transfer protein
ILMN_2067656	CCND2	1.120476	0.000809	0.000809	3.79331	Up	cyclin D2
ILMN_1695423	CD9	0.740259	0.000811	0.000811	3.792273	Up	CD9 molecule
ILMN_1689734	IL1RN	0.603248	0.000826	0.000826	3.785204	Up	interleukin 1 receptor antagonist
ILMN_1682226	CLDN15	0.574303	0.000834	0.000834	3.781751	Up	claudin 15
ILMN_1651354	SPP1	1.473099	0.000848	0.000848	3.775351	Up	secreted phosphoprotein 1
ILMN_1701827	CADM3	0.906754	0.000855	0.000855	3.771972	Up	cell adhesion molecule 3
ILMN_1762606	AQP11	0.606742	0.000856	0.000856	3.77143	Up	aquaporin 11
ILMN_1752294	PCDH9	0.795465	0.000895	0.000895	3.754302	Up	protocadherin 9
ILMN_1757604	TPM2	1.097432	0.000924	0.000924	3.741629	Up	tropomyosin 2
ILMN_1846517	ZNF404	0.539851	0.000927	0.000927	3.74066	Up	zinc finger protein 404
ILMN_1733756	COL12A1	0.856512	0.000957	0.000957	3.728149	Up	collagen type XII alpha 1 chain
ILMN_1775330	CCDC9B	0.541531	0.00096	0.00096	3.72698	Up	coiled-coil domain containing 9B

ILMN_1727194	CALU	0.528913	0.001017	0.001017	3.704368	Up	calumenin
ILMN_1689004	TNFRSF12A	0.747228	0.001026	0.001026	3.700896	Up	TNF receptor superfamily member 12A
ILMN_1681983	RSPO3	0.686707	0.001033	0.001033	3.698195	Up	R-spondin 3
ILMN_1659895	MSN	0.625448	0.001043	0.001043	3.694419	Up	moesin
ILMN_2368318	FGR	0.658653	0.001059	0.001059	3.68866	Up	FGR proto-oncogene, Src family tyrosine kinase
ILMN_1688780	S100A4	1.113275	0.001085	0.001085	3.679083	Up	S100 calcium binding protein A4
ILMN_2326273	CHI3L2	0.994947	0.001109	0.001109	3.670674	Up	chitinase 3 like 2
ILMN_1656910	TRIM6	0.874617	0.00114	0.00114	3.65994	Up	tripartite motif containing 6
ILMN_1690464	SLC35G1	0.621139	0.001146	0.001146	3.657985	Up	solute carrier family 35 member G1
ILMN_1680154	MAP1B	0.767967	0.001168	0.001168	3.650234	Up	microtubule associated protein 1B
ILMN_1695432	TPST2	0.631332	0.001178	0.001178	3.647137	Up	tyrosylproteinsulfotransferase 2
ILMN_1769556	NPR3	1.277963	0.001204	0.001204	3.638396	Up	natriuretic peptide receptor 3
ILMN_1709630	CCDC107	0.580296	0.001213	0.001213	3.635726	Up	coiled-coil domain containing 107
ILMN_1719938	FGF11	0.526074	0.001215	0.001215	3.634907	Up	fibroblast growth factor 11
ILMN_1705442	CMTM3	0.862194	0.001216	0.001216	3.634754	Up	CKLF like MARVEL transmembrane domain containing 3
ILMN_1809101	STEAP2	0.596209	0.001232	0.001232	3.629353	Up	STEAP2 metalloreductase
ILMN_2126038	STMN2	1.000711	0.001248	0.001248	3.624508	Up	stathmin 2
ILMN_1716246	FRZB	1.171067	0.001249	0.001249	3.624283	Up	frizzled related protein
ILMN_1765109	TNFRSF25	0.935143	0.00125	0.00125	3.623681	Up	TNF receptor superfamily member 25
ILMN_1686116	THBS1	0.92544	0.001267	0.001267	3.618613	Up	thrombospondin 1
ILMN_1703374	NAV1	0.572426	0.001331	0.001331	3.599306	Up	neuron navigator 1
ILMN_2120247	SLC2A10	0.724743	0.001347	0.001347	3.594626	Up	solute carrier family 2 member 10
ILMN_1774602	FBLN2	0.732902	0.001389	0.001389	3.582362	Up	fibulin 2
ILMN_1720303	OSTM1	0.544277	0.001419	0.001419	3.574118	Up	osteoclastogenesis associated transmembrane protein 1
ILMN_1728262	SAA2	1.626006	0.001484	0.001484	3.556403	Up	serum amyloid A2
ILMN_1684306	S100A4	1.095809	0.00154	0.00154	3.542006	Up	S100 calcium binding protein A4
ILMN_1767135	SOS1	0.669373	0.001554	0.001554	3.538311	Up	SOS Ras/Rac guanine nucleotide exchange factor 1
ILMN_2311166	ITGB5	0.677959	0.001588	0.001588	3.529759	Up	integrin subunit beta 5
ILMN_1780349	PRG4	1.243154	0.001623	0.001623	3.521134	Up	proteoglycan 4
ILMN_1865764	ZMAT3	0.587479	0.001638	0.001638	3.517465	Up	zinc finger matrin-type 3
ILMN_2049672	ANO3	0.733106	0.00164	0.00164	3.517198	Up	anoctamin 3
ILMN_1723481	CHST3	0.61328	0.001697	0.001697	3.503528	Up	carbohydrate sulfotransferase 3
ILMN_1730670	FSTL3	0.886754	0.001749	0.001749	3.491738	Up	folliculin like 3
ILMN_1677603	C1S	0.559371	0.001764	0.001764	3.488236	Up	complement C1s
ILMN_2389501	HSD11B1	1.150839	0.001819	0.001819	3.476139	Up	hydroxysteroid 11-beta dehydrogenase 1
ILMN_2129505	CYB561A3	0.524082	0.001892	0.001892	3.460542	Up	cytochrome b561 family member A3
ILMN_2385672	ELN	0.691623	0.001931	0.001931	3.452532	Up	elastin
ILMN_1750790	GSTM5	0.915719	0.002019	0.002019	3.434939	Up	glutathione S-transferase mu 5
ILMN_1691410	BAMBI	0.527637	0.002035	0.002035	3.431697	Up	BMP and activin membrane bound inhibitor
ILMN_1761941	FAM198B	1.004094	0.002161	0.002161	3.407852	Up	family with sequence similarity 198 member B
ILMN_1813561	SCIN	0.841973	0.002249	0.002249	3.392005	Up	scinderin
ILMN_1874901	MYMX	1.099779	0.002337	0.002337	3.376776	Up	myomixer, myoblast fusion factor
ILMN_2359907	CD68	0.6105	0.00241	0.00241	3.364459	Up	CD68 molecule

ILMN_1768940	COL15A1	0.737179	0.002477	0.002477	3.35347	Up	collagen type XV alpha 1 chain
ILMN_2208903	CD52	1.060026	0.002573	0.002573	3.338374	Up	CD52 molecule
ILMN_1791280	HSPB8	0.744974	0.002774	0.002774	3.308162	Up	heat shock protein family B (small) member 8
ILMN_2374449	SPP1	1.225401	0.0028	0.0028	3.304459	Up	secreted phosphoprotein 1
ILMN_1667893	TNS3	0.580577	0.002814	0.002814	3.302498	Up	tensin 3
ILMN_2405642	DHDDS	0.75152	0.002815	0.002815	3.30234	Up	dehydrololichyldiphosphate synthase subunit
ILMN_1672124	FAM198B	0.855847	0.002832	0.002832	3.299928	Up	family with sequence similarity 198 member B
ILMN_1675386	CES1	1.290413	0.00284	0.00284	3.298759	Up	carboxylesterase 1
ILMN_1675797	EPDR1	0.778794	0.002842	0.002842	3.298553	Up	ependymin related 1
ILMN_2302757	FCGBP	0.736052	0.002851	0.002851	3.297263	Up	Fc fragment of IgG binding protein
ILMN_1662932	LCP1	1.204997	0.002892	0.002892	3.291554	Up	lymphocyte cytosolic protein 1
ILMN_1762294	ADAMTSL4	0.530835	0.002915	0.002915	3.288379	Up	ADAMTS like 4
ILMN_2207505	LEP	0.926283	0.002934	0.002934	3.285758	Up	leptin
ILMN_1801710	APBB1IP	0.636573	0.002939	0.002939	3.285044	Up	amyloid beta precursor protein binding family B member 1 interacting protein
ILMN_1688480	CCND1	1.306118	0.002988	0.002988	3.278393	Up	cyclin D1
ILMN_1711566	TIMP1	1.341538	0.003021	0.003021	3.274039	Up	TIMP metalloproteinase inhibitor 1
ILMN_2118663	ERV3-1	0.661689	0.003035	0.003035	3.272124	Up	endogenous retrovirus group 3 member 1, envelope
ILMN_1660691	RAB31	0.709054	0.003132	0.003132	3.259457	Up	RAB31, member RAS oncogene family
ILMN_2329679	TPST2	0.55545	0.003374	0.003374	3.229456	Up	tyrosylproteinsulfotransferase 2
ILMN_1789535	DHDDS	0.745734	0.003401	0.003401	3.226338	Up	dehydrololichyldiphosphate synthase subunit
ILMN_1795963	OSGIN1	0.67904	0.003407	0.003407	3.225533	Up	oxidative stress induced growth inhibitor 1
ILMN_1807925	GNG2	0.834543	0.003615	0.003615	3.201662	Up	G protein subunit gamma 2
ILMN_2167915	DSEL	0.710109	0.003624	0.003624	3.200638	Up	dermatansulfateepimerase like
ILMN_1774874	IL1RN	0.859928	0.003639	0.003639	3.198924	Up	interleukin 1 receptor antagonist
ILMN_1689111	CXCL12	0.954243	0.003689	0.003689	3.193422	Up	C-X-C motif chemokine ligand 12
ILMN_1779875	THY1	1.139729	0.003871	0.003871	3.17396	Up	Thy-1 cell surface antigen
ILMN_1720282	NQO1	1.254269	0.003892	0.003892	3.171678	Up	NAD(P)H quinone dehydrogenase 1
ILMN_2132982	IGFBP5	0.905666	0.003894	0.003894	3.171544	Up	insulin like growth factor binding protein 5
ILMN_1667948	SPATA18	0.587846	0.003905	0.003905	3.170399	Up	spermatogenesis associated 18
ILMN_1729117	COL5A2	0.640357	0.004082	0.004082	3.152419	Up	collagen type V alpha 2 chain
ILMN_1668629	C4orf48	0.583778	0.004123	0.004123	3.148274	Up	chromosome 4 open reading frame 48
ILMN_1661755	FAM129B	0.559501	0.004167	0.004167	3.144004	Up	family with sequence similarity 129 member B
ILMN_1815205	LYZ	0.888701	0.004176	0.004176	3.143076	Up	lysozyme
ILMN_1676563	HTRA1	0.717816	0.00422	0.00422	3.138853	Up	HtrA serine peptidase 1
ILMN_1739161	PLPP1	0.659073	0.004346	0.004346	3.126844	Up	phospholipid phosphatase 1
ILMN_1718198	NPY5R	0.680103	0.004442	0.004442	3.117994	Up	neuropeptide Y receptor Y5
ILMN_1700268	QPRT	0.699906	0.004533	0.004533	3.109706	Up	quinolinatephosphoribosyltransferase
ILMN_1754795	FAT1	0.577636	0.00456	0.00456	3.107242	Up	FAT atypical cadherin 1
ILMN_2070521	BHMT2	0.720849	0.004718	0.004718	3.093369	Up	betaine-homocysteine S-methyltransferase 2
ILMN_2408748	SLC22A12	0.712622	0.004807	0.004807	3.085718	Up	solute carrier family 22 member 12
ILMN_1808732	SAA1	1.188117	0.004821	0.004821	3.084499	Up	serum amyloid A1
ILMN_1676213	SRPX2	0.800783	0.005117	0.005117	3.060079	Up	sushi repeat containing protein X-linked 2
ILMN_2359945	CES1	1.12408	0.005165	0.005165	3.056273	Up	carboxylesterase 1
ILMN_1681886	ADAMTS5	0.669885	0.005448	0.005448	3.034336	Up	ADAM metalloproteinase with thrombospondin type

							1 motif 5
ILMN_2198413	MYEOV	0.990449	0.005456	0.005456	3.033789	Up	myeloma overexpressed
ILMN_1772821	KIAA1671	0.625167	0.0056	0.0056	3.02307	Up	KIAA1671
ILMN_1735877	EFEMP1	0.530826	0.005622	0.005622	3.021426	Up	EGF containing fibulin extracellular matrix protein 1
ILMN_1769282	FRMD6	0.590922	0.005627	0.005627	3.021047	Up	FERM domain containing 6
ILMN_1671337	SLC2A5	0.819888	0.005673	0.005673	3.01771	Up	solute carrier family 2 member 5
ILMN_1745954	CORO1C	0.555758	0.005891	0.005891	3.00216	Up	coronin 1C
ILMN_1813043	BHMT2	0.656478	0.005947	0.005947	2.998245	Up	betaine-homocysteine S-methyltransferase 2
ILMN_2413816	GRB14	0.547963	0.006056	0.006056	2.990752	Up	growth factor receptor bound protein 14
ILMN_1696187	PYGL	0.644613	0.006112	0.006112	2.986947	Up	glycogen phosphorylase L
ILMN_2288483	CEP19	0.554845	0.006145	0.006145	2.984691	Up	centrosomal protein 19
ILMN_1792409	AMOT	0.816144	0.006593	0.006593	2.95555	Up	angiomin
ILMN_1704656	PPP2R1B	0.907097	0.00667	0.00667	2.950717	Up	protein phosphatase 2 scaffold subunit Abeta
ILMN_1663519	SLC24A3	0.633922	0.006681	0.006681	2.950063	Up	solute carrier family 24 member 3
ILMN_1785272	COL1A2	1.193362	0.006691	0.006691	2.949439	Up	collagen type I alpha 2 chain
ILMN_1743130	PTGFRN	0.524934	0.006893	0.006893	2.937051	Up	prostaglandin F2 receptor inhibitor
ILMN_1684554	COL16A1	0.61773	0.006913	0.006913	2.935844	Up	collagen type XVI alpha 1 chain
ILMN_1912662	#N/A	0.754156	0.006937	0.006937	2.934422	Up	NA
ILMN_1750324	IGFBP5	0.747781	0.006964	0.006964	2.93278	Up	insulin like growth factor binding protein 5
ILMN_2389506	HSD11B1	0.984125	0.007022	0.007022	2.929321	Up	hydroxysteroid 11-beta dehydrogenase 1
ILMN_1743836	MXRA7	0.631725	0.007077	0.007077	2.926107	Up	matrix remodeling associated 7
ILMN_1810172	SFRP4	1.030645	0.007248	0.007248	2.91613	Up	secreted frizzled related protein 4
ILMN_1901314	MIR3188	0.733061	0.007283	0.007283	2.91414	Up	microRNA 3188
ILMN_1779182	TMEM98	0.794433	0.007292	0.007292	2.913633	Up	transmembrane protein 98
ILMN_1790859	PLAC9	1.050248	0.00741	0.00741	2.906899	Up	placenta specific 9
ILMN_1711092	KCNB1	0.551283	0.007446	0.007446	2.904916	Up	potassium voltage-gated channel subfamily B member 1
ILMN_2090105	TAGLN2	0.596354	0.007534	0.007534	2.900001	Up	transgelin 2
ILMN_2183409	SCARB1	0.663206	0.007717	0.007717	2.889966	Up	scavenger receptor class B member 1
ILMN_2104356	COL1A2	1.147573	0.007881	0.007881	2.881147	Up	collagen type I alpha 2 chain
ILMN_1764109	C1R	0.857406	0.007884	0.007884	2.881016	Up	complement C1r
ILMN_1773389	PLTP	0.698948	0.007931	0.007931	2.878531	Up	phospholipid transfer protein
ILMN_2317364	CSN1S1	0.754633	0.008037	0.008037	2.872918	Up	casein alpha s1
ILMN_1811370	HSD11B1	0.987491	0.008232	0.008232	2.862873	Up	hydroxysteroid 11-beta dehydrogenase 1
ILMN_1715748	FLNC	0.938831	0.008274	0.008274	2.860761	Up	filamin C
ILMN_1702487	SGK1	0.776167	0.008467	0.008467	2.85108	Up	serum/glucocorticoid regulated kinase 1
ILMN_1785732	TNFAIP6	0.814063	0.008644	0.008644	2.842376	Up	TNF alpha induced protein 6
ILMN_1752968	LAMB2	0.525558	0.00872	0.00872	2.838678	Up	laminin subunit beta 2
ILMN_1739428	IFIT2	0.526187	0.008742	0.008742	2.837639	Up	interferon induced protein with tetratricopeptide repeats 2
ILMN_1795930	PTGER4	0.559346	0.008844	0.008844	2.832708	Up	prostaglandin E receptor 4
ILMN_2207504	LEP	0.982719	0.009035	0.009035	2.823736	Up	leptin
ILMN_1680948	LMOD1	0.695953	0.009262	0.009262	2.813224	Up	leiomodlin 1
ILMN_2361862	VLDLR	0.854371	0.009369	0.009369	2.808386	Up	very low density lipoprotein receptor
ILMN_1677723	ANGPT1	0.555038	0.009564	0.009564	2.799696	Up	angiopoietin 1

ILMN_1779841	PPP2R1B	0.853222	0.00961	0.00961	2.797666	Up	protein phosphatase 2 scaffold subunit Abeta
ILMN_2086890	ANGPT1	0.538832	0.009689	0.009689	2.794185	Up	angiopoietin 1
ILMN_1668345	OAF	0.706992	0.009694	0.009694	2.793955	Up	out at first homolog
ILMN_1712639	AIFM2	0.528075	0.009914	0.009914	2.784441	Up	apoptosis inducing factor, mitochondria associated 2
ILMN_2175912	ITGB2	0.995891	0.009957	0.009957	2.782636	Up	integrin subunit beta 2
ILMN_2304512	SAA1	1.23664	0.010239	0.010239	2.770776	Up	serum amyloid A1
ILMN_1803213	MXRA5	1.316927	0.010301	0.010301	2.768192	Up	matrix remodeling associated 5
ILMN_2128770	CDR2L	0.648047	0.010378	0.010378	2.765041	Up	cerebellar degeneration related protein 2 like
ILMN_1699829	CTGF	1.157229	0.010714	0.010714	2.751485	Up	connective tissue growth factor
ILMN_1668065	ELMOD3	0.623974	0.011063	0.011063	2.737816	Up	ELMO domain containing 3
ILMN_2400935	TAGLN	1.014014	0.012046	0.012046	2.701368	Up	transgelin
ILMN_1814917	TLE2	0.597486	0.012167	0.012167	2.69709	Up	transducin like enhancer of split 2
ILMN_2085862	SLC15A3	0.636791	0.01239	0.01239	2.689276	Up	solute carrier family 15 member 3
ILMN_1733094	STEAP1	0.592088	0.012408	0.012408	2.688656	Up	STEAP family member 1
ILMN_1791759	CXCL10	0.657731	0.012449	0.012449	2.687253	Up	C-X-C motif chemokine ligand 10
ILMN_1776936	KANK4	0.876463	0.012729	0.012729	2.677674	Up	KN motif and ankyrin repeat domains 4
ILMN_1800078	LMO2	0.63765	0.012879	0.012879	2.672643	Up	LIM domain only 2
ILMN_2115125	CTGF	1.120845	0.012951	0.012951	2.670237	Up	connective tissue growth factor
ILMN_1654396	ITGB2	0.895679	0.013318	0.013318	2.658192	Up	integrin subunit beta 2
ILMN_1701017	SAA1	1.464529	0.013581	0.013581	2.64974	Up	serum amyloid A1
ILMN_2285713	TDP1	0.644122	0.013593	0.013593	2.649359	Up	tyrosyl-DNA phosphodiesterase 1
ILMN_1735453	FAM98A	0.663756	0.013712	0.013712	2.645589	Up	family with sequence similarity 98 member A
ILMN_1803094	PDGFD	0.783158	0.014521	0.014521	2.620732	Up	platelet derived growth factor D
ILMN_2048591	LRRN3	0.742029	0.014574	0.014574	2.619167	Up	leucine rich repeat neuronal 3
ILMN_1665033	NPR3	0.645778	0.014643	0.014643	2.617101	Up	natriuretic peptide receptor 3
ILMN_1780663	KLHL30	0.558729	0.014833	0.014833	2.611491	Up	kelch like family member 30
ILMN_1657697	SAR1A	0.634135	0.014959	0.014959	2.607818	Up	secretion associated Ras related GTPase 1A
ILMN_1778668	TAGLN	0.906221	0.015205	0.015205	2.600719	Up	transgelin
ILMN_1715189	LHX6	0.565688	0.015316	0.015316	2.597543	Up	LIM homeobox 6
ILMN_1714861	CD68	0.675226	0.015872	0.015872	2.582001	Up	CD68 molecule
ILMN_2150095	CES1	0.984298	0.015943	0.015943	2.580041	Up	carboxylesterase 1
ILMN_2214473	ARHGEF35	0.811545	0.016232	0.016232	2.572178	Up	Rho guanine nucleotide exchange factor 35
ILMN_2376859	PDGFD	0.719127	0.016976	0.016976	2.552558	Up	platelet derived growth factor D
ILMN_1686664	MT2A	0.710372	0.017665	0.017665	2.535057	Up	metallothionein 2A
ILMN_1756071	MFGE8	0.547292	0.017825	0.017825	2.531091	Up	milk fat globule-EGF factor 8 protein
ILMN_1672660	MBP	0.589996	0.018136	0.018136	2.523473	Up	myelin basic protein
ILMN_2390919	FBLN2	0.618463	0.018757	0.018757	2.508612	Up	fibulin 2
ILMN_2129161	LRRC32	0.633777	0.019006	0.019006	2.50277	Up	leucine rich repeat containing 32
ILMN_2077952	GALNT16	0.693338	0.019332	0.019332	2.495234	Up	polypeptide N-acetylgalactosaminyltransferase 16
ILMN_2188264	CYR61	0.614752	0.019359	0.019359	2.49463	Up	cysteine rich angiogenic inducer 61
ILMN_2081087	HSPA12A	0.712069	0.019366	0.019366	2.494464	Up	heat shock protein family A (Hsp70) member 12A
ILMN_1731374	CPE	0.684523	0.019703	0.019703	2.486818	Up	carboxypeptidase E
ILMN_1790529	LUM	1.011109	0.019825	0.019825	2.484067	Up	lumican
ILMN_1690170	CRABP2	0.621015	0.019878	0.019878	2.482893	Up	cellular retinoic acid binding protein 2

ILMN_2112638	SVEP1	0.620822	0.020031	0.020031	2.479476	Up	sushi, von Willebrand factor type A, EGF and pentraxin domain containing 1
ILMN_1745356	CXCL9	0.621326	0.020666	0.020666	2.465596	Up	C-X-C motif chemokine ligand 9
ILMN_1707337	MSTO1	0.52744	0.020761	0.020761	2.463566	Up	misato 1, mitochondrial distribution and morphology regulator
ILMN_1677198	C1R	0.747849	0.020785	0.020785	2.46305	Up	complement C1r
ILMN_1773567	LAMA5	0.597756	0.021626	0.021626	2.445353	Up	laminin subunit alpha 5
ILMN_1880143	#N/A	1.313752	0.022328	0.022328	2.431054	Up	NA
ILMN_1778977	TYROBP	0.880575	0.023449	0.023449	2.409065	Up	TYRO protein tyrosine kinase binding protein
ILMN_1789639	FMOD	0.551304	0.023716	0.023716	2.403955	Up	fibromodulin
ILMN_1767113	AOX1	0.568405	0.023837	0.023837	2.401671	Up	aldehyde oxidase 1
ILMN_1743199	EGR2	0.837499	0.024408	0.024408	2.391003	Up	early growth response 2
ILMN_2137789	KLF4	0.69295	0.024585	0.024585	2.387746	Up	Kruppel like factor 4
ILMN_1656920	CRIP1	0.949702	0.024669	0.024669	2.386203	Up	cysteine rich protein 1
ILMN_1750100	TUBB8	0.542127	0.024671	0.024671	2.386169	Up	tubulin beta 8 class VIII
ILMN_2143795	CYTOR	0.653327	0.025094	0.025094	2.37848	Up	cytoskeleton regulator RNA
ILMN_1773313	ATP5MD	0.888141	0.025158	0.025158	2.377325	Up	ATP synthase membrane subunit DAPIT
ILMN_1807042	MARCKS	0.527377	0.025383	0.025383	2.373296	Up	myristoylated alanine rich protein kinase C substrate
ILMN_1750974	S100A9	0.533811	0.025625	0.025625	2.369003	Up	S100 calcium binding protein A9
ILMN_2134538	FTH1	0.660487	0.02646	0.02646	2.354446	Up	ferritin heavy chain 1
ILMN_1742332	KCTD12	0.622266	0.027085	0.027085	2.343832	Up	potassium channel tetramerization domain containing 12
ILMN_1810910	CFH	0.588853	0.027275	0.027275	2.340649	Up	complement factor H
ILMN_1667796	HBA1	1.236166	0.027548	0.027548	2.336103	Up	hemoglobin subunit alpha 1
ILMN_2073235	FTH1	0.608036	0.028444	0.028444	2.321488	Up	ferritin heavy chain 1
ILMN_1774287	CFB	0.599443	0.029185	0.029185	2.309725	Up	complement factor B
ILMN_2125010	SKAP2	0.539815	0.029275	0.029275	2.308306	Up	src kinase associated phosphoprotein 2
ILMN_2173835	FTH1P3	0.662782	0.029605	0.029605	2.303169	Up	ferritin heavy chain 1 pseudogene 3
ILMN_1734276	PMEPA1	0.531815	0.030569	0.030569	2.288446	Up	prostate transmembrane protein, androgen induced 1
ILMN_1797776	PRSS23	0.559654	0.031299	0.031299	2.277572	Up	serine protease 23
ILMN_2100437	HBB	1.198522	0.032716	0.032716	2.257103	Up	hemoglobin subunit beta
ILMN_1730906	FILIP1L	0.558741	0.03308	0.03308	2.251975	Up	filamin A interacting protein 1 like
ILMN_1746525	FTH1	0.659996	0.033776	0.033776	2.242313	Up	ferritin heavy chain 1
ILMN_2412192	CFH	0.617233	0.0349	0.0349	2.227088	Up	complement factor H
ILMN_1699665	CLIC6	1.048527	0.035707	0.035707	2.216421	Up	chloride intracellular channel 6
ILMN_1663490	ZNF541	0.56762	0.036403	0.036403	2.207405	Up	zinc finger protein 541
ILMN_2207328	TPGS2	0.6484	0.036764	0.036764	2.202786	Up	tubulin polyglutamylase complex subunit 2
ILMN_1725090	CTHRC1	0.710406	0.038042	0.038042	2.186755	Up	collagen triple helix repeat containing 1
ILMN_2105573	CCL3L3	0.989332	0.039486	0.039486	2.169215	Up	C-C motif chemokine ligand 3 like 3
ILMN_1668055	SAA4	0.818678	0.040036	0.040036	2.162689	Up	serum amyloid A4, constitutive
ILMN_2203950	HLA-A	0.552025	0.040908	0.040908	2.152498	Up	major histocompatibility complex, class I, A
ILMN_1803033	MGST1	0.565499	0.041608	0.041608	2.144465	Up	microsomal glutathione S-transferase 1
ILMN_1801205	GPNUMB	0.87457	0.041612	0.041612	2.144418	Up	glycoprotein numb
ILMN_1748840	CALB2	0.575885	0.044509	0.044509	2.112392	Up	calbindin 2

ILMN_1696911	FTH1	0.76525	0.044581	0.044581	2.111618	Up	ferritin heavy chain 1
ILMN_2309156	PMEPA1	0.578206	0.044785	0.044785	2.10944	Up	prostate transmembrane protein, androgen induced 1
ILMN_1661196	CSF2RA	0.652935	0.046014	0.046014	2.096479	Up	colony stimulating factor 2 receptor alpha subunit
ILMN_2376455	CSF2RA	0.670921	0.046639	0.046639	2.090007	Up	colony stimulating factor 2 receptor alpha subunit
ILMN_2391150	FILIP1L	0.541279	0.048499	0.048499	2.071199	Up	filamin A interacting protein 1 like
ILMN_1738578	FILIP1L	0.649489	0.048772	0.048772	2.068499	Up	filamin A interacting protein 1 like
ILMN_1705676	MRAP	0.740128	0.048781	0.048781	2.06841	Up	melanocortin 2 receptor accessory protein
ILMN_1706013	FTH1	0.538663	0.049065	0.049065	2.065608	Up	ferritin heavy chain 1
ILMN_1764714	ANGPTL8	0.674487	0.049616	0.049616	2.060209	Up	angiopoietin like 8
ILMN_1700183	APLNR	0.60085	0.049861	0.049861	2.057827	Up	apelin receptor
ILMN_1682176	CLEC3B	0.756039	0.049876	0.049876	2.057683	Up	C-type lectin domain family 3 member B
ILMN_1684227	GPR146	-0.83595	1.71E-09	1.71E-09	-9.06509	Down	G protein-coupled receptor 146
ILMN_1821176	RNF125	-1.20288	2.73E-09	2.73E-09	-8.85291	Down	ring finger protein 125
ILMN_1694514	ZDHHC11	-1.16835	1.08E-08	1.08E-08	-8.24436	Down	zinc finger DHHC-type containing 11
ILMN_2298818	RPS29	-0.68843	6.63E-08	6.63E-08	-7.46988	Down	ribosomal protein S29
ILMN_1662188	WNT11	-0.68384	7.34E-08	7.34E-08	-7.42761	Down	Wnt family member 11
ILMN_1705346	NBEA	-0.72037	9.33E-08	9.33E-08	-7.32789	Down	neurobeachin
ILMN_1881960	HDAC9	-1.17786	2.12E-07	2.12E-07	-6.9912	Down	histone deacetylase 9
ILMN_1725787	RFX1	-0.40524	2.68E-07	2.68E-07	-6.89627	Down	regulatory factor X1
ILMN_2396287	RFX2	-0.56092	2.76E-07	2.76E-07	-6.88354	Down	regulatory factor X2
ILMN_2175465	RSL24D1	-0.46858	3.6E-07	3.6E-07	-6.77716	Down	ribosomal L24 domain containing 1
ILMN_1730794	SERTAD4	-0.89762	1.28E-06	1.28E-06	-6.27275	Down	SERTA domain containing 4
ILMN_1752810	LARP6	-0.78114	2.04E-06	2.04E-06	-6.08902	Down	La ribonucleoprotein domain family member 6
ILMN_2184966	ZHX2	-0.82429	2.19E-06	2.19E-06	-6.06085	Down	zinc fingers and homeoboxes 2
ILMN_2352563	CLDND1	-0.40042	2.91E-06	2.91E-06	-5.95008	Down	claudin domain containing 1
ILMN_1691559	ELF2	-0.65194	3.12E-06	3.12E-06	-5.92228	Down	E74 like ETS transcription factor 2
ILMN_1749821	MED28	-0.52157	3.69E-06	3.69E-06	-5.85719	Down	mediator complex subunit 28
ILMN_2389347	NR3C1	-0.55108	3.74E-06	3.74E-06	-5.85196	Down	nuclear receptor subfamily 3 group C member 1
ILMN_1789508	GTF3C3	-0.5818	4.23E-06	4.23E-06	-5.8044	Down	general transcription factor IIIC subunit 3
ILMN_2295252	C9orf72	-0.46781	4.56E-06	4.56E-06	-5.77509	Down	chromosome 9 open reading frame 72
ILMN_1757183	ZFHx4-AS1	-0.70437	5.53E-06	5.53E-06	-5.70054	Down	ZFHx4 antisense RNA 1
ILMN_2346727	MTUS1	-0.62796	5.6E-06	5.6E-06	-5.69632	Down	microtubule associated scaffold protein 1
ILMN_1666208	MIS18BP1	-0.42342	6.97E-06	6.97E-06	-5.61133	Down	MIS18 binding protein 1
ILMN_1722829	HLF	-1.04562	7.13E-06	7.13E-06	-5.60276	Down	HLF, PAR bZIP transcription factor
ILMN_1790973	CDS2	-0.45775	7.13E-06	7.13E-06	-5.6027	Down	CDP-diacylglycerol synthase 2
ILMN_1694106	GPD1L	-1.21248	7.83E-06	7.83E-06	-5.56674	Down	glycerol-3-phosphate dehydrogenase 1 like
ILMN_1735743	FBLN7	-0.70811	8.05E-06	8.05E-06	-5.55624	Down	fibulin 7
ILMN_1792951	ZHX2	-0.59218	1.03E-05	1.03E-05	-5.46294	Down	zinc fingers and homeoboxes 2
ILMN_1746658	RORB	-1.44876	1.04E-05	1.04E-05	-5.45785	Down	RAR related orphan receptor B
ILMN_1747119	FBXO46	-0.49642	1.11E-05	1.11E-05	-5.43233	Down	F-box protein 46
ILMN_1722329	CASQ2	-1.56426	1.14E-05	1.14E-05	-5.42341	Down	calsequestrin 2
ILMN_1706706	DCAF7	-0.42387	1.21E-05	1.21E-05	-5.39933	Down	DDB1 and CUL4 associated factor 7
ILMN_1730907	ZFAND1	-0.60649	1.26E-05	1.26E-05	-5.38283	Down	zinc finger AN1-type containing 1
ILMN_1735038	MARCH3	-0.53104	1.4E-05	1.4E-05	-5.34512	Down	membrane associated ring-CH-type finger 3

ILMN_1681780	MKX	-1.37991	1.44E-05	1.44E-05	-5.33293	Down	mohawkhomeobox
ILMN_1797154	AZGP1	-1.37572	1.72E-05	1.72E-05	-5.26426	Down	alpha-2-glycoprotein 1, zinc-binding
ILMN_1726547	MAP3K5	-0.8941	1.77E-05	1.77E-05	-5.2531	Down	mitogen-activated protein kinase kinasekinase 5
ILMN_1799289	MRPL55	-0.4503	1.83E-05	1.83E-05	-5.24231	Down	mitochondrial ribosomal protein L55
ILMN_1782609	STAG2	-0.41892	1.88E-05	1.88E-05	-5.23192	Down	stromal antigen 2
ILMN_1800451	MED16	-0.60494	1.96E-05	1.96E-05	-5.21497	Down	mediator complex subunit 16
ILMN_1778523	KLF9	-0.92493	2.2E-05	2.2E-05	-5.17137	Down	Kruppel like factor 9
ILMN_1708059	USP13	-0.51604	2.49E-05	2.49E-05	-5.12403	Down	ubiquitin specific peptidase 13
ILMN_1760727	ANG	-0.78319	2.55E-05	2.55E-05	-5.11517	Down	angiogenin
ILMN_1751143	TMEM243	-0.63607	2.56E-05	2.56E-05	-5.11254	Down	transmembrane protein 243
ILMN_1760490	ACVR1	-0.62337	2.65E-05	2.65E-05	-5.09947	Down	activin A receptor type 1
ILMN_1790782	MED16	-0.63172	2.75E-05	2.75E-05	-5.08654	Down	mediator complex subunit 16
ILMN_1748578	RAD21	-0.71483	3.08E-05	3.08E-05	-5.04321	Down	RAD21 cohesin complex component
ILMN_1662935	C1QTNF7	-0.56926	3.72E-05	3.72E-05	-4.97056	Down	C1q and TNF related 7
ILMN_1660451	STARD13	-0.4495	3.89E-05	3.89E-05	-4.95347	Down	StAR related lipid transfer domain containing 13 [
ILMN_1655497	EIF4B	-0.52825	3.95E-05	3.95E-05	-4.94802	Down	eukaryotic translation initiation factor 4B
ILMN_2076640	KHDRBS1	-0.45183	3.96E-05	3.96E-05	-4.94687	Down	KH RNA binding domain containing, signal transduction associated 1
ILMN_1770247	HOXA10	-0.51668	3.97E-05	3.97E-05	-4.94619	Down	homeobox A10
ILMN_1652549	DTNA	-0.6919	4.46E-05	4.46E-05	-4.90175	Down	dystrobrevin alpha
ILMN_1811367	MAT2B	-0.4369	4.69E-05	4.69E-05	-4.88274	Down	methionine adenosyltransferase 2B
ILMN_1730201	DTNA	-0.89589	4.73E-05	4.73E-05	-4.87937	Down	dystrobrevin alpha
ILMN_1810628	PRUNE2	-0.98344	5.62E-05	5.62E-05	-4.81407	Down	prune homolog 2
ILMN_1677396	NDFIP2	-0.46666	5.7E-05	5.7E-05	-4.80812	Down	Nedd4 family interacting protein 2
ILMN_1738095	PER2	-0.92194	6.05E-05	6.05E-05	-4.78554	Down	period circadian regulator 2
ILMN_2103841	AIP	-0.45066	6.73E-05	6.73E-05	-4.74505	Down	aryl hydrocarbon receptor interacting protein
ILMN_1724349	RGS3	-0.74322	6.74E-05	6.74E-05	-4.74458	Down	regulator of G protein signaling 3
ILMN_1654268	HMGB2	-0.80135	7.07E-05	7.07E-05	-4.72659	Down	high mobility group box 2
ILMN_1740996	CA3	-1.83227	7.42E-05	7.42E-05	-4.70796	Down	carbonic anhydrase 3
ILMN_1763311	SPX	-1.62598	7.43E-05	7.43E-05	-4.70777	Down	spexin hormone
ILMN_2262288	EEF1G	-0.60713	7.48E-05	7.48E-05	-4.70498	Down	eukaryotic translation elongation factor 1 gamma
ILMN_2347349	CCNB1IP1	-0.62741	7.53E-05	7.53E-05	-4.70247	Down	cyclin B1 interacting protein 1
ILMN_1807514	ZNF394	-0.39537	7.9E-05	7.9E-05	-4.68415	Down	zinc finger protein 394
ILMN_1672908	TWIST1	-0.85589	8.24E-05	8.24E-05	-4.66846	Down	twist family bHLH transcription factor 1
ILMN_1808157	RUNDC3B	-0.49287	8.27E-05	8.27E-05	-4.66671	Down	RUN domain containing 3B
ILMN_1729180	GATM	-0.51604	9.08E-05	9.08E-05	-4.63121	Down	glycine amidinotransferase
ILMN_1722811	CDKN1B	-0.64659	9.65E-05	9.65E-05	-4.60803	Down	cyclin dependent kinase inhibitor 1B
ILMN_1738047	FAM170B	-0.56504	9.94E-05	9.94E-05	-4.59684	Down	family with sequence similarity 170 member B
ILMN_1804735	CBS	-0.52494	0.0001	0.0001	-4.59345	Down	cystathionine-beta-synthase
ILMN_1691611	HNRNPA1P10	-0.7512	0.000101	0.000101	-4.58978	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10
ILMN_1654543	MED6	-0.42696	0.000102	0.000102	-4.58768	Down	mediator complex subunit 6
ILMN_1749447	RPS9	-0.54354	0.000104	0.000104	-4.57948	Down	ribosomal protein S9
ILMN_1798164	PHF3	-0.57458	0.000109	0.000109	-4.5601	Down	PHD finger protein 3
ILMN_1781560	ST3GAL6	-0.8137	0.000109	0.000109	-4.5601	Down	ST3 beta-galactoside alpha-2,3-sialyltransferase 6

ILMN_1655422	RPL17	-0.52633	0.000122	0.000122	-4.51945	Down	ribosomal protein L17
ILMN_1795228	ZFAND5	-0.72934	0.000127	0.000127	-4.50466	Down	zinc finger AN1-type containing 5
ILMN_1690386	KAT14	-0.43942	0.000133	0.000133	-4.48521	Down	lysine acetyltransferase 14
ILMN_1736510	FOXN2	-0.49204	0.000133	0.000133	-4.48497	Down	forkhead box N2
ILMN_1804798	BEX4	-0.6225	0.000143	0.000143	-4.45813	Down	brain expressed X-linked 4
ILMN_1769277	RPL9	-0.41195	0.000148	0.000148	-4.44428	Down	ribosomal protein L9
ILMN_1799642	TRIM24	-0.39819	0.000149	0.000149	-4.44385	Down	tripartite motif containing 24
ILMN_2294976	ANG	-0.79076	0.000159	0.000159	-4.41709	Down	angiogenin
ILMN_1805996	SIN3A	-0.56259	0.00016	0.00016	-4.41525	Down	SIN3 transcription regulator family member A
ILMN_2175075	SRSF4	-0.44136	0.000163	0.000163	-4.40778	Down	serine and arginine rich splicing factor 4
ILMN_1793616	RNF38	-0.44936	0.000167	0.000167	-4.39862	Down	ring finger protein 38
ILMN_1677962	GPHN	-0.65151	0.000168	0.000168	-4.39736	Down	gephyrin
ILMN_1902658	LINC01278	-0.40063	0.000179	0.000179	-4.37307	Down	long intergenic non-protein coding RNA 1278
ILMN_2401258	FAM13A	-0.9418	0.000181	0.000181	-4.36775	Down	family with sequence similarity 13 member A
ILMN_1678504	RHOT1	-0.57537	0.000189	0.000189	-4.35223	Down	ras homolog family member T1
ILMN_1696974	ANG	-0.71006	0.000199	0.000199	-4.33318	Down	angiogenin
ILMN_2124951	RBMX	-0.5553	0.000203	0.000203	-4.32423	Down	RNA binding motif protein X-linked
ILMN_1720745	HNRNPA1P58	-0.72079	0.000205	0.000205	-4.32093	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 58
ILMN_1660986	PER3	-0.81664	0.000205	0.000205	-4.32037	Down	period circadian regulator 3
ILMN_1682864	SPSB3	-0.45379	0.000222	0.000222	-4.29046	Down	splA/ryanodine receptor domain and SOCS box containing 3
ILMN_1723212	SRSF3	-0.50378	0.000228	0.000228	-4.28117	Down	serine and arginine rich splicing factor 3
ILMN_1707965	ZFHx4-AS1	-0.58402	0.000228	0.000228	-4.28102	Down	ZFHx4 antisense RNA 1
ILMN_1695276	MAPRE2	-0.63141	0.00024	0.00024	-4.26121	Down	microtubule associated protein RP/EB family member 2
ILMN_1809139	AHCTF1	-0.5111	0.000242	0.000242	-4.25724	Down	AT-hook containing transcription factor 1
ILMN_1795678	POLR3C	-0.43557	0.000251	0.000251	-4.24422	Down	RNA polymerase III subunit C
ILMN_1663489	UBR2	-0.39554	0.000253	0.000253	-4.24027	Down	ubiquitin protein ligase E3 component n-recognin 2
ILMN_1734317	DPF2	-0.5493	0.000256	0.000256	-4.2369	Down	double PHD fingers 2
ILMN_1747192	RNF125	-0.39931	0.000256	0.000256	-4.23562	Down	ring finger protein 125
ILMN_1752510	FAM13A	-0.99837	0.000257	0.000257	-4.23415	Down	family with sequence similarity 13 member A
ILMN_2394777	DTNA	-0.61549	0.000264	0.000264	-4.22394	Down	dystrobrevin alpha
ILMN_2157219	AASS	-0.55808	0.000265	0.000265	-4.2237	Down	aminoadipate-semialdehyde synthase
ILMN_2042595	PCM1	-0.40898	0.000265	0.000265	-4.2224	Down	pericentriolar material 1
ILMN_1740024	NAALAD2	-1.17474	0.000266	0.000266	-4.2222	Down	N-acetylated alpha-linked acidic dipeptidase 2
ILMN_1682316	TRIM33	-0.40627	0.000266	0.000266	-4.22211	Down	tripartite motif containing 33
ILMN_1734897	SLC4A4	-0.62874	0.000268	0.000268	-4.21926	Down	solute carrier family 4 member 4
ILMN_2276952	TSC22D3	-0.78215	0.000272	0.000272	-4.21282	Down	TSC22 domain family member 3
ILMN_2294978	ANG	-0.79321	0.000276	0.000276	-4.20706	Down	angiogenin
ILMN_2080751	ADNP2	-0.4253	0.00028	0.00028	-4.20216	Down	ADNP homeobox 2
ILMN_1735979	BCKDHA	-0.54967	0.000283	0.000283	-4.19813	Down	branched chain keto acid dehydrogenase E1, alpha polypeptide
ILMN_1761560	PHF13	-0.58385	0.000285	0.000285	-4.1947	Down	PHD finger protein 13
ILMN_1810436	DNAJC27	-0.40591	0.000295	0.000295	-4.18259	Down	DnaJ heat shock protein family (Hsp40) member C27

ILMN_1690586	HNRNPA1P4	-0.57304	0.000296	0.000296	-4.18026	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 4
ILMN_1683660	EIF3H	-0.40346	0.000309	0.000309	-4.16481	Down	eukaryotic translation initiation factor 3 subunit H
ILMN_2327795	RERE	-0.42563	0.000312	0.000312	-4.16001	Down	arginine-glutamic acid dipeptide repeats
ILMN_1802096	ABTB1	-0.52379	0.000328	0.000328	-4.14094	Down	ankyrin repeat and BTB domain containing 1
ILMN_2325978	HDGFL2	-0.53491	0.00034	0.00034	-4.12766	Down	HDGF like 2
ILMN_1746929	DNAH17	-0.47091	0.000342	0.000342	-4.12492	Down	dynein axonemal heavy chain 17
ILMN_2348975	NASP	-0.40415	0.000344	0.000344	-4.12336	Down	nuclear autoantigenic sperm protein
ILMN_2207539	RPS17	-0.42621	0.000344	0.000344	-4.12328	Down	ribosomal protein S17
ILMN_1727633	NECTIN3	-0.40189	0.000351	0.000351	-4.11545	Down	nectin cell adhesion molecule 3
ILMN_1768575	SFTPD	-0.72081	0.000351	0.000351	-4.11531	Down	surfactant protein D
ILMN_1795856	ELF2	-0.47007	0.000357	0.000357	-4.10893	Down	E74 like ETS transcription factor 2
ILMN_1756417	ANKRD37	-0.4384	0.000361	0.000361	-4.10435	Down	ankyrin repeat domain 37
ILMN_1767422	POLR1D	-0.54704	0.000365	0.000365	-4.10011	Down	RNA polymerase I and III subunit D
ILMN_1707339	BTG3	-0.44002	0.000377	0.000377	-4.08847	Down	BTG anti-proliferation factor 3
ILMN_1800461	CSNK2B	-0.39465	0.000385	0.000385	-4.08031	Down	casein kinase 2 beta
ILMN_1654060	MKNK2	-0.51063	0.000401	0.000401	-4.06434	Down	MAP kinase interacting serine/threonine kinase 2
ILMN_1671603	MED30	-0.42207	0.000408	0.000408	-4.05791	Down	mediator complex subunit 30
ILMN_1652846	PCYT2	-0.58494	0.000424	0.000424	-4.04302	Down	phosphate cytidylyltransferase 2, ethanolamine
ILMN_1672743	ZNF334	-0.44795	0.000426	0.000426	-4.04083	Down	zinc finger protein 334
ILMN_1789809	RPL13AP6	-0.5148	0.000429	0.000429	-4.03806	Down	ribosomal protein L13a pseudogene 6
ILMN_1740960	MACROD1	-0.48775	0.000432	0.000432	-4.03593	Down	MACRO domain containing 1
ILMN_1652409	SPATA7	-0.59601	0.000433	0.000433	-4.03481	Down	spermatogenesis associated 7
ILMN_1741881	C9orf72	-0.57025	0.000471	0.000471	-4.00247	Down	chromosome 9 open reading frame 72
ILMN_1699644	MARCH3	-0.5546	0.000472	0.000472	-4.00193	Down	membrane associated ring-CH-type finger 3
ILMN_1714170	SPSB1	-0.58359	0.000477	0.000477	-3.99765	Down	splA/ryanodine receptor domain and SOCS box containing 1
ILMN_1655796	MARCH3	-0.61363	0.000496	0.000496	-3.98239	Down	membrane associated ring-CH-type finger 3
ILMN_1711069	YPEL5	-0.40328	0.000501	0.000501	-3.97844	Down	yippee like 5
ILMN_2194627	GMCL1	-0.68208	0.000505	0.000505	-3.97585	Down	germ cell-less, spermatogenesis associated 1
ILMN_2110167	POLR1E	-0.39568	0.000531	0.000531	-3.95636	Down	RNA polymerase I subunit E
ILMN_2305112	CTH	-0.79808	0.000544	0.000544	-3.94675	Down	cystathionine gamma-lyase
ILMN_2182148	CNRIP1	-0.71975	0.000557	0.000557	-3.93763	Down	cannabinoid receptor interacting protein 1
ILMN_1793410	SNTB1	-0.48614	0.000561	0.000561	-3.9354	Down	syntrophin beta 1
ILMN_1708098	LIX1L	-0.48995	0.000563	0.000563	-3.93347	Down	limb and CNS expressed 1 like
ILMN_1780132	PELI2	-0.68127	0.00058	0.00058	-3.92231	Down	pellino E3 ubiquitin protein ligase family member 2
ILMN_1702821	TTLL7	-0.41216	0.000586	0.000586	-3.91858	Down	tubulin tyrosine ligase like 7
ILMN_1723843	CSNK2A2	-0.47468	0.000595	0.000595	-3.91234	Down	casein kinase 2 alpha 2
ILMN_1801441	RFTN2	-0.62656	0.000596	0.000596	-3.91203	Down	raftlin family member 2
ILMN_2311278	ADD3	-0.52845	0.000603	0.000603	-3.9073	Down	adducin 3
ILMN_1729142	CENPV	-0.58292	0.000624	0.000624	-3.89406	Down	centromere protein V
ILMN_2038772	RPS9	-0.51676	0.00063	0.00063	-3.89034	Down	ribosomal protein S9
ILMN_1722059	SAFB	-0.45526	0.000656	0.000656	-3.87472	Down	scaffold attachment factor B
ILMN_1656682	AZIN1	-0.42329	0.000656	0.000656	-3.87459	Down	antizyme inhibitor 1
ILMN_1794875	GPAT3	-1.48566	0.000664	0.000664	-3.87013	Down	glycerol-3-phosphate acyltransferase 3

ILMN_1717420	UBE2W	-0.51123	0.000689	0.000689	-3.8557	Down	ubiquitin conjugating enzyme E2 W
ILMN_1662318	CCDC59	-0.44764	0.000697	0.000697	-3.85146	Down	coiled-coil domain containing 59
ILMN_1786242	RPL14	-0.39564	0.000698	0.000698	-3.85088	Down	ribosomal protein L14
ILMN_1814661	PHLPP1	-0.45914	0.000699	0.000699	-3.84995	Down	PH domain and leucine rich repeat protein phosphatase 1
ILMN_1665132	CD36	-0.92302	0.000708	0.000708	-3.84519	Down	CD36 molecule
ILMN_1685357	RTN2	-0.46378	0.000709	0.000709	-3.84451	Down	reticulin 2
ILMN_1670532	GMCL1	-0.63244	0.000711	0.000711	-3.84355	Down	germ cell-less, spermatogenesis associated 1
ILMN_2376403	TSC22D3	-0.93577	0.000745	0.000745	-3.82526	Down	TSC22 domain family member 3
ILMN_1771734	GMPS	-0.40677	0.000751	0.000751	-3.82208	Down	guanine monophosphate synthase
ILMN_1777660	RNF144A	-0.66466	0.000765	0.000765	-3.81523	Down	ring finger protein 144A
ILMN_1677228	TMLHE	-0.41087	0.000781	0.000781	-3.80705	Down	trimethyllysine hydroxylase, epsilon
ILMN_1683447	RPL35	-0.40252	0.000798	0.000798	-3.7986	Down	ribosomal protein L35
ILMN_1749081	AUTS2	-0.61612	0.000799	0.000799	-3.79821	Down	AUTS2, activator of transcription and developmental regulator
ILMN_1679949	SLC25A23	-0.55426	0.0008	0.0008	-3.79792	Down	solute carrier family 25 member 23
ILMN_1655557	INTS6	-0.50525	0.000801	0.000801	-3.79754	Down	integrator complex subunit 6
ILMN_1797893	N4BP2L2	-0.43567	0.000802	0.000802	-3.79699	Down	NEDD4 binding protein 2 like 2
ILMN_1746819	C5	-0.6768	0.000805	0.000805	-3.79521	Down	complement C5
ILMN_1683575	TMLHE	-0.49273	0.000814	0.000814	-3.79109	Down	trimethyllysine hydroxylase, epsilon
ILMN_1792885	CTSC	-0.91588	0.000842	0.000842	-3.77782	Down	cathepsin C
ILMN_1804679	KAT8	-0.45615	0.000842	0.000842	-3.77777	Down	lysine acetyltransferase 8
ILMN_1713682	FBXO11	-0.39613	0.000844	0.000844	-3.7772	Down	F-box protein 11
ILMN_1695110	BCAT2	-0.55233	0.000881	0.000881	-3.76017	Down	branched chain amino acid transaminase 2
ILMN_1791097	RSBN1	-0.43263	0.000887	0.000887	-3.75766	Down	round spermatid basic protein 1
ILMN_1782543	EEF1D	-0.44289	0.000891	0.000891	-3.75596	Down	eukaryotic translation elongation factor 1 delta
ILMN_1757338	PLSCR4	-0.48847	0.000891	0.000891	-3.75577	Down	phospholipid scramblase 4
ILMN_1701134	PTEN	-0.5057	0.000927	0.000927	-3.74036	Down	phosphatase and tensin homolog
ILMN_2228732	CCNG2	-0.68275	0.000933	0.000933	-3.7381	Down	cyclin G2
ILMN_1713764	#N/A	-0.58118	0.000935	0.000935	-3.73719	Down	NA
ILMN_1796962	PPP3R1	-0.45421	0.000939	0.000939	-3.7357	Down	protein phosphatase 3 regulatory subunit B, alpha
ILMN_1700316	RPS12	-0.51024	0.000943	0.000943	-3.73387	Down	ribosomal protein S12
ILMN_1756999	RBL2	-0.42764	0.000953	0.000953	-3.72994	Down	RB transcriptional corepressor like 2
ILMN_1697510	ACSS2	-0.43839	0.000958	0.000958	-3.72791	Down	acyl-CoA synthetase short chain family member 2
ILMN_1697448	TXNIP	-0.41817	0.000968	0.000968	-3.72371	Down	thioredoxin interacting protein
ILMN_1681703	FOXO3	-0.40924	0.00097	0.00097	-3.72296	Down	forkhead box O3
ILMN_2347193	GSDMB	-0.87834	0.00097	0.00097	-3.72284	Down	gasdermin B
ILMN_1666739	RBM15	-0.39717	0.000973	0.000973	-3.72161	Down	RNA binding motif protein 15
ILMN_1778836	SRSF7	-0.63062	0.000988	0.000988	-3.71565	Down	serine and arginine rich splicing factor 7
ILMN_1732074	#N/A	-0.74016	0.001026	0.001026	-3.70082	Down	NA
ILMN_1661173	TRIP4	-0.40095	0.001026	0.001026	-3.70082	Down	thyroid hormone receptor interactor 4
ILMN_1681634	PXMP2	-0.83494	0.001028	0.001028	-3.70021	Down	peroxisomal membrane protein 2
ILMN_1733305	EIF2A	-0.41666	0.001029	0.001029	-3.69992	Down	eukaryotic translation initiation factor 2A
ILMN_2318638	TGIF1	-0.45231	0.001031	0.001031	-3.69897	Down	TGFB induced factor homeobox 1
ILMN_1660847	PFKFB3	-0.98614	0.001042	0.001042	-3.69509	Down	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3

ILMN_1767142	ZNF280D	-0.6049	0.001066	0.001066	-3.68608	Down	zinc finger protein 280D
ILMN_2401253	FAM13A	-0.67261	0.001092	0.001092	-3.67663	Down	family with sequence similarity 13 member A
ILMN_1677607	SC5D	-0.81449	0.001095	0.001095	-3.67563	Down	sterol-C5-desaturase
ILMN_1810864	PMP22	-0.63497	0.001096	0.001096	-3.67519	Down	peripheral myelin protein 22
ILMN_1709132	ELP2	-0.43637	0.001107	0.001107	-3.6712	Down	elongatoracetyltransferase complex subunit 2
ILMN_1726250	CPAMD8	-0.45219	0.001127	0.001127	-3.6644	Down	C3 and PZP like, alpha-2-macroglobulin domain containing 8
ILMN_2278433	LOC285074	-0.54057	0.001137	0.001137	-3.66096	Down	anaphase promoting complex subunit 1 pseudogene
ILMN_1719205	FBL	-0.43794	0.001168	0.001168	-3.65035	Down	fibrillarin
ILMN_1751785	DMRT2	-0.75395	0.001185	0.001185	-3.64476	Down	doublesex and mab-3 related transcription factor 2
ILMN_1760714	RPS3	-0.44835	0.001187	0.001187	-3.64418	Down	ribosomal protein S3
ILMN_2264681	LETMD1	-0.51143	0.001207	0.001207	-3.63751	Down	LETM1 domain containing 1
ILMN_1789171	EEF2K	-0.63414	0.00123	0.00123	-3.63021	Down	eukaryotic elongation factor 2 kinase
ILMN_1704537	PHGDH	-1.18282	0.001241	0.001241	-3.62676	Down	phosphoglycerate dehydrogenase
ILMN_2146761	FABP5	-0.51494	0.001249	0.001249	-3.62413	Down	fatty acid binding protein 5
ILMN_1657373	P3H2	-0.6377	0.001252	0.001252	-3.62331	Down	prolyl 3-hydroxylase 2
ILMN_1695598	RPL18	-0.46798	0.001256	0.001256	-3.62204	Down	ribosomal protein L18
ILMN_1773964	H1FX	-0.41349	0.00127	0.00127	-3.61761	Down	H1 histone family member X
ILMN_1748124	TSC22D3	-0.77823	0.001316	0.001316	-3.60369	Down	TSC22 domain family member 3
ILMN_1769319	CNBP	-0.47448	0.001332	0.001332	-3.59896	Down	CCHC-type zinc finger nucleic acid binding protein
ILMN_1703565	NOP53	-0.42352	0.001341	0.001341	-3.59639	Down	NOP53 ribosome biogenesis factor
ILMN_1772876	ZNF395	-0.44848	0.00136	0.00136	-3.59063	Down	zinc finger protein 395
ILMN_2351638	BEX4	-0.53061	0.001378	0.001378	-3.5857	Down	brain expressed X-linked 4
ILMN_2338480	RHOT1	-0.58486	0.001382	0.001382	-3.58439	Down	ras homolog family member T1
ILMN_1719696	PLD1	-0.47509	0.001387	0.001387	-3.58296	Down	phospholipase D1
ILMN_2325168	ARRB1	-0.39681	0.001494	0.001494	-3.5538	Down	arrestin beta 1
ILMN_1813530	AGT	-0.5035	0.001525	0.001525	-3.54573	Down	angiotensinogen
ILMN_1799015	PXMP2	-0.84383	0.001573	0.001573	-3.53362	Down	peroxisomal membrane protein 2
ILMN_2334042	THYN1	-0.57793	0.001587	0.001587	-3.53007	Down	thymocyte nuclear protein 1
ILMN_1744347	AL590609.1	-0.45678	0.001595	0.001595	-3.52796	Down	ribosomal protein L36 (RPL36) pseudogene
ILMN_1657515	RPS6KA5	-0.52375	0.001607	0.001607	-3.52518	Down	ribosomal protein S6 kinase A5
ILMN_2054607	CYP4V2	-0.59585	0.001635	0.001635	-3.51834	Down	cytochrome P450 family 4 subfamily V member 2
ILMN_2323801	MOCOS1	-0.7044	0.001651	0.001651	-3.51439	Down	molybdenum cofactor synthesis 1
ILMN_1695034	HNRNPA1P37	-0.71138	0.001653	0.001653	-3.51391	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 37
ILMN_1666206	GSDMB	-1.03517	0.001664	0.001664	-3.51145	Down	gasdermin B
ILMN_1749834	SMIM1	-0.53971	0.001697	0.001697	-3.50354	Down	small integral membrane protein 1 (Vel blood group)
ILMN_1698934	CMTM7	-0.59983	0.001701	0.001701	-3.5028	Down	CKLF like MARVEL transmembrane domain containing 7
ILMN_1754149	LETMD1	-0.40275	0.001741	0.001741	-3.4934	Down	LETM1 domain containing 1
ILMN_1710885	RPSAP12	-0.39686	0.001827	0.001827	-3.47443	Down	ribosomal protein SA pseudogene 12
ILMN_1788689	PHIP	-0.52812	0.001853	0.001853	-3.46884	Down	pleckstrin homology domain interacting protein
ILMN_2407346	LDHD	-0.78788	0.001859	0.001859	-3.46766	Down	lactate dehydrogenase D
ILMN_1654289	ELK1	-0.4093	0.001901	0.001901	-3.45883	Down	ELK1, ETS transcription factor

ILMN_1719661	MSRB1	-0.42174	0.001905	0.001905	-3.45788	Down	methionine sulfoxidereductase B1
ILMN_1676091	HNRNPA1P7	-0.58631	0.001975	0.001975	-3.44365	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 7
ILMN_1765500	NDUFV3	-0.47187	0.001982	0.001982	-3.44214	Down	NADH:ubiquinoneoxidoreductase subunit V3
ILMN_1765032	MUC20-OT1	-0.54689	0.002004	0.002004	-3.4379	Down	MUC20 overlapping transcript
ILMN_1702363	SULF1	-1.08556	0.002014	0.002014	-3.43577	Down	sulfatase 1
ILMN_1743620	RARRES1	-0.52985	0.002029	0.002029	-3.43282	Down	retinoic acid receptor responder 1
ILMN_1657760	SYT17	-0.47881	0.002082	0.002082	-3.42268	Down	synaptotagmin 17
ILMN_1655163	STK24	-0.52056	0.002104	0.002104	-3.4184	Down	serine/threonine kinase 24
ILMN_1722089	RNF217	-0.49485	0.002117	0.002117	-3.41611	Down	ring finger protein 217
ILMN_2402817	ZBTB16	-0.77388	0.002137	0.002137	-3.41224	Down	zinc finger and BTB domain containing 16
ILMN_1783956	ATP8B4	-0.6446	0.00214	0.00214	-3.41172	Down	ATPase phospholipid transporting 8B4 (putative)
ILMN_2183938	LEMD3	-0.53026	0.002156	0.002156	-3.40882	Down	LEM domain containing 3
ILMN_1698685	MATN2	-0.40191	0.002157	0.002157	-3.40864	Down	matrilin 2
ILMN_1654690	HDHD5	-0.39979	0.00217	0.00217	-3.40619	Down	haloaciddehalogenase like hydrolase domain containing 5
ILMN_1700831	SLC27A2	-1.11722	0.002174	0.002174	-3.40554	Down	solute carrier family 27 member 2
ILMN_1679041	SLC3A2	-0.49613	0.002178	0.002178	-3.40467	Down	solute carrier family 3 member 2
ILMN_1776363	ANK2	-0.6836	0.002187	0.002187	-3.40315	Down	ankyrin 2
ILMN_1786197	NR2F1	-0.50821	0.00219	0.00219	-3.40251	Down	nuclear receptor subfamily 2 group F member 1
ILMN_1678323	AASS	-0.51408	0.002208	0.002208	-3.39938	Down	aminoadipate-semialdehyde synthase
ILMN_1657810	PPM1M	-0.50248	0.002231	0.002231	-3.39512	Down	protein phosphatase, Mg2+/Mn2+ dependent 1M
ILMN_1695590	ADRB2	-0.86384	0.002236	0.002236	-3.39424	Down	adrenoceptor beta 2
ILMN_1807554	EYA1	-0.45309	0.00224	0.00224	-3.39358	Down	EYA transcriptional coactivator and phosphatase 1
ILMN_1844692	FOXO3	-0.4053	0.002262	0.002262	-3.38971	Down	forkhead box O3
ILMN_1701947	GPR34	-0.63372	0.002273	0.002273	-3.38773	Down	G protein-coupled receptor 34
ILMN_1765208	GLUL	-0.48308	0.002351	0.002351	-3.37425	Down	glutamate-ammonia ligase
ILMN_1747244	CCNG2	-0.46567	0.002393	0.002393	-3.36729	Down	cyclin G2
ILMN_1798624	MOCS1	-0.55467	0.002445	0.002445	-3.35871	Down	molybdenum cofactor synthesis 1
ILMN_1680196	LAPTM4B	-0.44371	0.002502	0.002502	-3.34953	Down	lysosomal protein transmembrane 4 beta
ILMN_1737025	PLCL2	-0.47585	0.002545	0.002545	-3.34262	Down	phospholipase C like 2
ILMN_1810433	FAM207A	-0.40305	0.002599	0.002599	-3.33437	Down	family with sequence similarity 207 member A
ILMN_2083588	TTC32	-0.40982	0.002602	0.002602	-3.33388	Down	tetratricopeptide repeat domain 32
ILMN_1880406	PTEN	-0.44058	0.002689	0.002689	-3.32067	Down	phosphatase and tensin homolog
ILMN_2348367	FGFRL1	-0.62279	0.002736	0.002736	-3.31382	Down	fibroblast growth factor receptor like 1
ILMN_1683263	TSPAN8	-0.61312	0.002774	0.002774	-3.30821	Down	tetraspanin 8
ILMN_1742788	PKD1L2	-1.01131	0.002779	0.002779	-3.30747	Down	polycystin 1 like 2 (gene/pseudogene)
ILMN_1780236	PMM1	-0.63809	0.00282	0.00282	-3.30165	Down	phosphomannomutase 1
ILMN_1791467	PLIN5	-0.41569	0.002865	0.002865	-3.29524	Down	perilipin 5
ILMN_2290808	RPL21	-0.59943	0.002867	0.002867	-3.29498	Down	ribosomal protein L21
ILMN_1710124	CMTM8	-0.80058	0.002943	0.002943	-3.28454	Down	CKLF like MARVEL transmembrane domain containing 8
ILMN_1779486	FAM126B	-0.47129	0.002978	0.002978	-3.2797	Down	family with sequence similarity 126 member B
ILMN_2255310	RPS15A	-0.63234	0.002987	0.002987	-3.27853	Down	ribosomal protein S15a
ILMN_1653496	GLUL	-0.72238	0.00305	0.00305	-3.27012	Down	glutamate-ammonia ligase
ILMN_1758281	CALCRL	-0.78586	0.003177	0.003177	-3.25369	Down	calcitonin receptor like receptor

ILMN_2049303	ECI1	-0.55796	0.003187	0.003187	-3.25251	Down	enoyl-CoA delta isomerase 1
ILMN_1854349	RNF217	-0.51519	0.003187	0.003187	-3.25248	Down	ring finger protein 217
ILMN_1798654	MCM6	-0.45891	0.003246	0.003246	-3.2451	Down	minichromosome maintenance complex component 6
ILMN_1781638	HDDC3	-0.42977	0.003264	0.003264	-3.2429	Down	HD domain containing 3
ILMN_1753534	RPS18	-0.4732	0.003407	0.003407	-3.22559	Down	ribosomal protein S18
ILMN_1692177	TSC22D1	-0.54834	0.003461	0.003461	-3.21918	Down	TSC22 domain family member 1
ILMN_1801795	RPL18A	-0.47586	0.003522	0.003522	-3.21216	Down	ribosomal protein L18a
ILMN_1715024	LSS	-0.48264	0.003722	0.003722	-3.18981	Down	lanosterol synthase
ILMN_1761322	FHOD3	-0.85631	0.003793	0.003793	-3.18216	Down	formin homology 2 domain containing 3
ILMN_1779751	FMC1	-0.45529	0.003804	0.003804	-3.18097	Down	formation of mitochondrial complex V assembly factor 1 homolog
ILMN_1785284	ALDH6A1	-0.6169	0.003926	0.003926	-3.16823	Down	aldehyde dehydrogenase 6 family member A1
ILMN_1660832	RPL18A	-0.42124	0.003963	0.003963	-3.16437	Down	ribosomal protein L18a
ILMN_1653001	CABLES1	-0.40265	0.004025	0.004025	-3.15807	Down	Cdk5 and Abl enzyme substrate 1
ILMN_2384807	LRRCC1	-0.44474	0.004046	0.004046	-3.15595	Down	leucine rich repeat and coiled-coil centrosomal protein 1
ILMN_1675460	RPL29	-0.39808	0.004048	0.004048	-3.15575	Down	ribosomal protein L29
ILMN_1654609	EPB41L4A-AS1	-0.51803	0.004077	0.004077	-3.15286	Down	EPB41L4A antisense RNA 1
ILMN_1787248	SIVA1	-0.41798	0.004263	0.004263	-3.13477	Down	SIVA1 apoptosis inducing factor
ILMN_1773119	CCNF	-0.43811	0.004344	0.004344	-3.12704	Down	cyclin F
ILMN_1740717	ADH1C	-0.588	0.004462	0.004462	-3.11609	Down	alcohol dehydrogenase 1C (class I), gamma polypeptide
ILMN_2305407	ZBTB16	-0.68894	0.004508	0.004508	-3.11199	Down	zinc finger and BTB domain containing 16
ILMN_1670134	FADS1	-1.09346	0.004556	0.004556	-3.10763	Down	fatty acid desaturase 1
ILMN_1783684	RBBP4	-0.40939	0.00479	0.00479	-3.08718	Down	RB binding protein 4, chromatin remodeling factor
ILMN_1671478	CKB	-0.63338	0.004827	0.004827	-3.08404	Down	creatine kinase B
ILMN_1755909	GID8	-0.40117	0.005017	0.005017	-3.06817	Down	GID complex subunit 8 homolog
ILMN_1813456	PCBD1	-0.64387	0.005022	0.005022	-3.06778	Down	pterin-4 alpha-carbinolaminatedehydratase 1
ILMN_1694840	MATN2	-0.49009	0.005145	0.005145	-3.05787	Down	matrilin 2
ILMN_1692464	TTC38	-0.48834	0.005183	0.005183	-3.05487	Down	tetratricopeptide repeat domain 38
ILMN_1664014	STOX1	-0.81909	0.005378	0.005378	-3.03966	Down	storkhead box 1
ILMN_1731064	COQ8A	-0.67616	0.005413	0.005413	-3.03698	Down	coenzyme Q8A
ILMN_1700733	FAM214A	-0.45812	0.005537	0.005537	-3.0277	Down	family with sequence similarity 214 member A
ILMN_1662174	ORMDL3	-0.74365	0.00558	0.00558	-3.02449	Down	ORMDL sphingolipid biosynthesis regulator 3
ILMN_1716797	CD302	-0.55642	0.005698	0.005698	-3.01591	Down	CD302 molecule
ILMN_2340131	MAPK10	-0.45954	0.005724	0.005724	-3.014	Down	mitogen-activated protein kinase 10
ILMN_1718629	NRIP1	-0.63132	0.005777	0.005777	-3.01023	Down	nuclear receptor interacting protein 1
ILMN_1757467	H1FO	-0.43213	0.00612	0.00612	-2.98641	Down	H1 histone family member 0
ILMN_1773063	OSBPL1A	-0.39462	0.006163	0.006163	-2.98347	Down	oxysterol binding protein like 1A
ILMN_2305116	CTH	-0.39952	0.006295	0.006295	-2.97474	Down	cystathionine gamma-lyase
ILMN_1736911	TMOD1	-0.55465	0.006324	0.006324	-2.97281	Down	tropomodulin 1
ILMN_1696347	CTSC	-0.63671	0.006354	0.006354	-2.97085	Down	cathepsin C
ILMN_1835017	GLUL	-0.52146	0.006647	0.006647	-2.95216	Down	glutamate-ammonia ligase
ILMN_1707062	REV1	-0.4136	0.006976	0.006976	-2.93207	Down	REV1, DNA directed polymerase

ILMN_1714384	PCCA	-0.42758	0.007366	0.007366	-2.90939	Down	propionyl-CoA carboxylase subunit alpha
ILMN_1738207	CISH	-0.82272	0.007368	0.007368	-2.90929	Down	cytokine inducible SH2 containing protein
ILMN_1783598	CAB39L	-0.51195	0.00786	0.00786	-2.88226	Down	calcium binding protein 39 like
ILMN_1653494	S100A1	-0.75357	0.008027	0.008027	-2.87347	Down	S100 calcium binding protein A1
ILMN_2218277	RPS2	-0.45343	0.008061	0.008061	-2.87169	Down	ribosomal protein S2
ILMN_1754272	GINS3	-0.55926	0.008196	0.008196	-2.86473	Down	GINS complex subunit 3
ILMN_1783149	CDH23	-0.49907	0.008324	0.008324	-2.85821	Down	cadherin related 23
ILMN_1721580	TBX15	-0.52139	0.00849	0.00849	-2.8499	Down	T-box 15
ILMN_1703123	CSRNP1	-0.48515	0.008494	0.008494	-2.84975	Down	cysteine and serine rich nuclear protein 1
ILMN_1691966	LINC02076	-0.50304	0.008554	0.008554	-2.84675	Down	long intergenic non-protein coding RNA 2076
ILMN_1695311	HLA-DMA	-0.73553	0.00856	0.00856	-2.84645	Down	major histocompatibility complex, class II, DM alpha
ILMN_1750496	ZBTB16	-0.61415	0.008644	0.008644	-2.84236	Down	zinc finger and BTB domain containing 16
ILMN_1739083	SIRT1	-0.43004	0.008765	0.008765	-2.83651	Down	sirtuin 1
ILMN_1770085	BTG2	-0.62761	0.008768	0.008768	-2.83636	Down	BTG anti-proliferation factor 2
ILMN_2401618	MLX	-0.40216	0.008865	0.008865	-2.83173	Down	MLX, MAX dimerization protein
ILMN_2305225	NDRG4	-1.14352	0.008955	0.008955	-2.82749	Down	NDRG family member 4
ILMN_1729033	RPL9	-0.44385	0.008985	0.008985	-2.82605	Down	ribosomal protein L9
ILMN_1800091	RARRES1	-0.53546	0.00924	0.00924	-2.81424	Down	retinoic acid receptor responder 1
ILMN_1791847	DAPK2	-0.52118	0.009391	0.009391	-2.8074	Down	death associated protein kinase 2
ILMN_1676159	STK26	-0.62873	0.009423	0.009423	-2.80595	Down	serine/threonine kinase 26
ILMN_1718977	GADD45B	-0.59259	0.00965	0.00965	-2.79591	Down	growth arrest and DNA damage inducible beta
ILMN_1715555	DBP	-0.53512	0.009791	0.009791	-2.78974	Down	D-box binding PAR bZIP transcription factor
ILMN_1698259	TMEM100	-0.77227	0.009942	0.009942	-2.78326	Down	transmembrane protein 100
ILMN_1684368	SMIM3	-0.53983	0.010068	0.010068	-2.7779	Down	small integral membrane protein 3
ILMN_1735367	HSD17B11	-0.42718	0.010203	0.010203	-2.77228	Down	hydroxysteroid 17-beta dehydrogenase 11
ILMN_1679093	ZNF581	-0.4191	0.010916	0.010916	-2.74352	Down	zinc finger protein 581
ILMN_1707649	MPDZ	-0.44065	0.01123	0.01123	-2.7314	Down	multiple PDZ domain crumbs cell polarity complex component
ILMN_1671092	SOX17	-0.54376	0.011244	0.011244	-2.73088	Down	SRY-box 17
ILMN_2328776	STK26	-0.49827	0.011334	0.011334	-2.72746	Down	serine/threonine kinase 26
ILMN_1728083	EIF4EBP2	-0.4121	0.011407	0.011407	-2.72471	Down	eukaryotic translation initiation factor 4E binding protein 2
ILMN_1709486	SRPX	-0.59773	0.011581	0.011581	-2.71826	Down	sushi repeat containing protein X-linked
ILMN_1706660	HYI	-0.47577	0.011645	0.011645	-2.71588	Down	hydroxypyruvate isomerase (putative)
ILMN_1738816	FOXO1	-0.50839	0.011736	0.011736	-2.71257	Down	forkhead box O1
ILMN_1678535	ESR1	-0.48298	0.011741	0.011741	-2.71236	Down	estrogen receptor 1
ILMN_1652246	NACAD	-0.56561	0.012028	0.012028	-2.702	Down	NAC alpha domain containing
ILMN_1791222	GLYCK	-0.6914	0.012173	0.012173	-2.69688	Down	glycerate kinase
ILMN_1729749	HERC5	-0.74104	0.012635	0.012635	-2.68089	Down	HECT and RLD domain containing E3 ubiquitin protein ligase 5
ILMN_1781819	PAPSS1	-0.41286	0.012711	0.012711	-2.67828	Down	3'-phosphoadenosine 5'-phosphosulfate synthase 1
ILMN_2229214	STOX1	-0.6532	0.01281	0.01281	-2.67495	Down	storkhead box 1
ILMN_1900520	#N/A	-0.47028	0.013101	0.013101	-2.66528	Down	NA
ILMN_1811933	SHMT1	-0.57643	0.013105	0.013105	-2.66513	Down	serine hydroxymethyltransferase 1
ILMN_1700546	ELOVL6	-0.64894	0.013212	0.013212	-2.66164	Down	ELOVL fatty acid elongase 6
ILMN_1814464	RAMP2	-0.44254	0.01341	0.01341	-2.65519	Down	receptor activity modifying protein 2

ILMN_1781010	ARHGEF3	-0.67277	0.013631	0.013631	-2.64813	Down	Rho guanine nucleotide exchange factor 3
ILMN_1778444	FKBP5	-1.05059	0.013648	0.013648	-2.64759	Down	FK506 binding protein 5
ILMN_2220283	HNRNPA1P10	-0.47457	0.013952	0.013952	-2.63806	Down	heterogeneous nuclear ribonucleoprotein A1 pseudogene 10
ILMN_1660635	LACTB2	-0.47503	0.014165	0.014165	-2.63149	Down	lactamase beta 2
ILMN_1776213	RGMB	-0.52099	0.014885	0.014885	-2.60998	Down	repulsive guidance molecule BMP co-receptor b
ILMN_2061452	ORC2	-0.47703	0.015166	0.015166	-2.60185	Down	origin recognition complex subunit 2
ILMN_1743784	SHMT1	-0.47754	0.01575	0.01575	-2.58537	Down	serine hydroxymethyltransferase 1
ILMN_1695299	PDLIM3	-0.42944	0.016438	0.016438	-2.56668	Down	PDZ and LIM domain 3
ILMN_2131861	SOCS2	-0.64331	0.016571	0.016571	-2.56315	Down	suppressor of cytokine signaling 2
ILMN_2242463	CTSC	-0.54644	0.016581	0.016581	-2.56289	Down	cathepsin C
ILMN_1794914	UBTD1	-0.46864	0.01716	0.01716	-2.54783	Down	ubiquitin domain containing 1
ILMN_1787567	TSC22D1	-0.41504	0.017272	0.017272	-2.54497	Down	TSC22 domain family member 1
ILMN_2051972	GPC3	-0.47873	0.01777	0.01777	-2.53246	Down	glypican 3
ILMN_1728799	FBP1	-0.43121	0.018124	0.018124	-2.52375	Down	fructose-bisphosphatase 1
ILMN_1811598	ADH1B	-0.64322	0.018502	0.018502	-2.51465	Down	alcohol dehydrogenase 1B (class I), beta polypeptide
ILMN_1690096	PPP1R1B	-0.39748	0.018632	0.018632	-2.51157	Down	protein phosphatase 1 regulatory inhibitor subunit 1B
ILMN_1781256	LEFTY2	-0.42676	0.01877	0.01877	-2.5083	Down	left-right determination factor 2
ILMN_1799280	BDH1	-0.43115	0.019319	0.019319	-2.49554	Down	3-hydroxybutyrate dehydrogenase 1
ILMN_1793543	CIART	-0.50833	0.019494	0.019494	-2.49156	Down	circadian associated repressor of transcription
ILMN_1727087	GJA1	-0.62741	0.019563	0.019563	-2.48998	Down	gap junction protein alpha 1
ILMN_1652955	RPS27	-0.51384	0.02033	0.02033	-2.47289	Down	ribosomal protein S27
ILMN_1709613	IGF1	-0.5613	0.02055	0.02055	-2.46811	Down	insulin like growth factor 1
ILMN_1702168	HSD17B12	-0.40602	0.021038	0.021038	-2.45765	Down	hydroxysteroid 17-beta dehydrogenase 12
ILMN_1768534	BHLHE40	-0.47888	0.021039	0.021039	-2.45763	Down	basic helix-loop-helix family member e40
ILMN_2230025	PDLIM3	-0.58435	0.022514	0.022514	-2.42734	Down	PDZ and LIM domain 3
ILMN_1742917	NXNL1	-0.44529	0.022528	0.022528	-2.42705	Down	nucleoredoxin like 1
ILMN_2331636	ACACA	-0.54723	0.022716	0.022716	-2.42333	Down	acetyl-CoA carboxylase alpha
ILMN_1756928	RTN1	-0.52782	0.023225	0.023225	-2.41338	Down	reticulon 1
ILMN_1725791	HACD1	-0.48778	0.023407	0.023407	-2.40987	Down	3-hydroxyacyl-CoA dehydratase 1
ILMN_1814526	ADD3	-0.54021	0.023431	0.023431	-2.4094	Down	adducin 3
ILMN_2359345	NET1	-0.66813	0.023703	0.023703	-2.40421	Down	neuroepithelial cell transforming 1
ILMN_2221006	RAD21	-0.67963	0.023956	0.023956	-2.39942	Down	RAD21 cohesin complex component
ILMN_1757882	PPP1R16A	-0.52488	0.024408	0.024408	-2.39099	Down	protein phosphatase 1 regulatory subunit 16A
ILMN_2326324	LDHC	-0.46033	0.024413	0.024413	-2.39091	Down	lactate dehydrogenase C
ILMN_1694780	GCHFR	-0.57882	0.024843	0.024843	-2.38302	Down	GTP cyclohydrolase I feedback regulator
ILMN_2186061	PFKFB3	-0.53663	0.025098	0.025098	-2.3784	Down	6-phosphofructo-2-kinase/fructose-2,6-biphosphatase 3
ILMN_1694776	SCP2	-0.39618	0.025742	0.025742	-2.36693	Down	sterol carrier protein 2
ILMN_1816634	AC004160.1	-0.47774	0.025816	0.025816	-2.36563	Down	novel transcript, antisense to THSD7A
ILMN_1763852	ACACB	-0.42465	0.026406	0.026406	-2.35538	Down	acetyl-CoA carboxylase beta
ILMN_1749875	AC141557.1	-0.58299	0.026502	0.026502	-2.35372	Down	ovostatin (OVOS) pseudogene
ILMN_1772910	GAS1	-0.59307	0.027065	0.027065	-2.34416	Down	growth arrest specific 1
ILMN_1701173	KCNK6	-0.465	0.027711	0.027711	-2.33342	Down	potassium two pore domain channel subfamily K

							member 6
ILMN_1768505	IL13RA1	-0.39597	0.027731	0.027731	-2.33309	Down	interleukin 13 receptor subunit alpha 1
ILMN_1772123	ACACA	-0.5172	0.028001	0.028001	-2.32866	Down	acetyl-CoA carboxylase alpha
ILMN_1676765	RPL18A	-0.45199	0.028068	0.028068	-2.32756	Down	ribosomal protein L18a
ILMN_1789558	ZC2HC1A	-0.4103	0.028262	0.028262	-2.32443	Down	zinc finger C2HC-type containing 1A
ILMN_1743445	FAM107A	-0.57785	0.028483	0.028483	-2.32086	Down	family with sequence similarity 107 member A
ILMN_1760574	RAI2	-0.44939	0.028548	0.028548	-2.31981	Down	retinoic acid induced 2
ILMN_1800540	CD55	-0.49697	0.02916	0.02916	-2.31011	Down	CD55 molecule (Cromer blood group)
ILMN_1660890	ACADL	-0.42123	0.02924	0.02924	-2.30885	Down	acyl-CoA dehydrogenase long chain
ILMN_1665510	ERRFI1	-0.49543	0.029318	0.029318	-2.30764	Down	ERBB receptor feedback inhibitor 1
ILMN_1676822	C2orf40	-0.51359	0.029379	0.029379	-2.30669	Down	chromosome 2 open reading frame 40
ILMN_1755808	RPS27	-0.59398	0.029664	0.029664	-2.30225	Down	ribosomal protein S27
ILMN_1715401	MT1G	-0.61901	0.029679	0.029679	-2.30202	Down	metallothionein 1G
ILMN_1782305	NR4A2	-0.66741	0.030329	0.030329	-2.29206	Down	nuclear receptor subfamily 4 group A member 2
ILMN_1703102	ST13P15	-0.42368	0.030763	0.030763	-2.28553	Down	ST13, Hsp70 interacting protein pseudogene 15
ILMN_2403237	CHN2	-0.42851	0.030784	0.030784	-2.28522	Down	chimerin 2
ILMN_1797793	BLVRB	-0.47037	0.031521	0.031521	-2.27431	Down	biliverdinreductase B
ILMN_2408572	RNASE4	-0.4736	0.035171	0.035171	-2.22348	Down	ribonuclease A family member 4
ILMN_1684982	PDK4	-0.42956	0.038313	0.038313	-2.18341	Down	pyruvate dehydrogenase kinase 4
ILMN_2371055	EFNA1	-0.49597	0.039014	0.039014	-2.17488	Down	ephrin A1
ILMN_2267535	NET1	-0.48927	0.039057	0.039057	-2.17437	Down	neuroepithelial cell transforming 1
ILMN_1776490	C17orf53	-0.39414	0.041169	0.041169	-2.14949	Down	chromosome 17 open reading frame 53
ILMN_1652466	WNT3	-0.60148	0.045134	0.045134	-2.10573	Down	Wnt family member 3
ILMN_1698554	AACS	-0.50824	0.045299	0.045299	-2.10398	Down	acetoacetyl-CoA synthetase
ILMN_1722156	RWDD2A	-0.42053	0.045756	0.045756	-2.09917	Down	RWD domain containing 2A
ILMN_2111187	ELOVL6	-0.7318	0.049464	0.049464	-2.06169	Down	ELOVL fatty acid elongase 6

Table 3 The enriched pathway terms of the up-regulated differentially expressed genes

BIOCYC				
Pathway ID	Pathway Name	LogP	Gene Count	Genes
545361	thyroid hormone metabolism II (via conjugation and/or degradation)	2.643466898	02	SULT1A1,SULT1A2
545353	serotonin degradation	2.25690676	02	SULT1A1,SULT1A2
545356	melatonin degradation I	1.802432827	02	SULT1A1,SULT1A2
545359	superpathway of melatonin degradation	1.720921143	02	SULT1A1,SULT1A2
142378	L-serine degradation	1.695428398	01	SDSL
142400	lactose degradation III	1.695428398	01	GLB1
835392	superpathway of tryptophan utilization	1.605692623	03	QPRT,SULT1A1,SULT1A2
545334	histamine degradation	1.407410907	01	HNMT
547502	glutamine degradation/glutamate biosynthesis	1.407410907	01	GLS
545306	dolichol and dolichyl phosphate biosynthesis	1.407410907	01	DHDDS
KEGG				
83068	ECM-receptor interaction	10	11	COL1A2,COL6A1,COL6A2,DAG1,ITGAV,ITGB5,LAMA5,LAMB2,LAMB3,SPP1,THBS1
83067	Focal adhesion	10	18	ACTN1,CCND1,CCND2,COL1A2,COL6A1,COL6A2,ERBB2,FLNC,ITGAV,ITGB5,LAMA5,LAM
692234	PI3K-Akt signaling pathway	4.828155946	20	ANGPT1,CCND1,CCND2,COL1A2,COL6A1,COL6A2,FGF11,GNG2,ITGAV,ITGB5,LAMA5,LA
172847	Protein digestion and absorption	4.157653601	09	COL11A1,COL12A1,COL15A1,COL1A2,COL3A1,COL5A2,COL6A1,COL6A2,ELN
673221	Chemical carcinogenesis	3.67876368	08	ALDH1A3,GSTM5,HSD11B1,MGST1,SULT1A1,SULT1A2,SULT1A3,SULT1A4
153910	Phagosome	3.620143426	11	C1R,HLA-A,ITGAV,ITGB2,ITGB5,RAB7B,SCARB1,THBS1,TUBB2A,TUBB2B,TUBB8
167324	Amoebiasis	3.21097747	08	ACTN1,COL1A2,COL3A1,ITGB2,LAMA5,LAMB2,LAMB3,RAB7B
782000	Proteoglycans in cancer	3.14746694	12	CCND1,ERBB2,FLNC,GPC1,ITGAV,ITGB5,LUM,MMP9,MSN,SOS1,STAT3,THBS1
83115	Bladder cancer	2.916353651	05	CCND1,ERBB2,MMP9,THBS1,TYMP
169642	Toxoplasmosis	2.748907163	08	CYCS,HSPA8,IRAK1,LAMA5,LAMB2,LAMB3,STAT1,STAT3
Pathway Interaction Database				
137932	IL6-mediated signaling events	2.821528426	05	LBPSOS1,STAT1,STAT3,TIMP1
138010	Glypican 1 network	2.801555589	04	FGR,GPC1,SLIT2,TGFR2
138009	Plasma membrane estrogen receptor signaling	2.801555589	04	GNG2,MMP9,MSN,SOS1
137945	amb2 Integrin signaling	2.6061022	05	FGR,HP,ITGB2,MMP9,THY1
138064	Syndecan-4-mediated signaling events	2.511901482	04	ACTN1,CXCL12,MMP9,THBS1
137910	CXCR4-mediated signaling events	2.41318701	06	CXCL12,FGR,GNG2,MMP9,STAT1,STAT3
169348	Signaling events mediated by focal adhesion kinase	2.381190903	05	ACTN1,CCND1,ITGAV,ITGB5,SOS1
138011	CXCR3-mediated signaling events	2.363501461	04	CXCL10,CXCL9,GNG2,ITGB2

169349	Validated transcriptional targets of AP1 family members Fra1 and Fra2	2.363501461	04	CCND1,COL1A2,HMOX1,MMP9
169352	Regulation of Wnt-mediated beta catenin signaling and target gene transcription	2.33010021	06	CCND1,CCND2,KLF4,MMP9,TLE2,YWHAH
REACTOME				
1270245	Collagen formation	10	14	COL11A1,COL12A1,COL15A1,COL16A1,COL1A2,COL3A1,COL5A2,COL6A1,COL6A2,CRT
1269897	Binding and Uptake of Ligands by Scavenger Receptors	10	09	COL1A2,COL3A1,FTH1,HBA1,HBB,HP,SAA1,SCARB1,SPARC
1270244	Extracellular matrix organization	10	34	ACTN1,ADAMTS5,COL11A1,COL12A1,COL15A1,COL16A1,COL1A2,COL3A1,COL5A2,CO
1270251	Elastic fibre formation	5.863438649	08	EFEMP1,ELN,FBLN2,ITGAV,ITGB5,LOX,MFAP4,MFAP5
1470923	Interleukin-4 and 13 signaling	5.599166845	12	CCND1,COL1A2,HMOX1,HSPA8,ITGB2,LAMA5,LBP,MMP9,SAA1,STAT1,STAT3,TIMP1
1270254	Non-integrin membrane-ECM interactions	5.548528425	08	ACTN1,DAG1,ITGAV,ITGB5,LAMA5,LAMB2,LAMB3,THBS1
1269310	Cytokine Signaling in Immune system	5.166203341	34	ANGPT1,APBB1IP,CCL3L3,CCND1,COL1A2,CSF2RA,CXCL10,ERBB2,GRIN2B,HAVCR2,HL
1457780	Neutrophil degranulation	4.840148593	25	CD68,CST3,FGR,FTH1,GLB1,GNS,HBB,HLA-A,HP,HSPA8,ITGAV,ITGB2,LYZ,MGST1,MMP9
1270256	ECM proteoglycans	4.82830206	08	DAG1,FMOD,ITGAV,ITGB5,LAMA5,LAMB2,LUM,SPARC
1269318	Signaling by Interleukins	4.289720048	25	ANGPT1,APBB1IP,CCL3L3,CCND1,COL1A2,CSF2RA,CXCL10,ERBB2,GRIN2B,HAVCR2,HM
GenMAPP				
MAP00140	C21 Steroid hormone metabolism	1.802432827	02	CYP11A1,HSD11B1
MAP00531	Glycosaminoglycan degradation	1.802432827	02	GLB1,GNS
MAP00510	N Glycans biosynthesis	1.462554363	02	B4GALT5,MGAT3
MSigDB C2 BIOCARTA				
M3005	Genes encoding collagen proteins	10	09	COL11A1,COL12A1,COL15A1,COL16A1,COL1A2,COL3A1,COL5A2,COL6A1,COL6A2
M3008	Genes encoding structural ECM glycoproteins	10	21	CTHRC1,EFEMP1,ELN,FBLN2,IGFBP5,IGFBP6,LAMA5,LAMB2,LAMB3,MFAP4,MFAP5,MF
M5889	Ensemble of genes encoding extracellular matrix and extracellular matrix-associated proteins	10	63	ADAMTS5,ADAMTSL4,ANGPT1,CCL3L3,CLEC3B,COL11A1,COL12A1,COL15A1,COL16A
M5884	Ensemble of genes encoding core extracellular matrix including ECM glycoproteins, collagens and proteoglycans	10	32	COL11A1,COL12A1,COL15A1,COL16A1,COL1A2,COL3A1,COL5A2,COL6A1,COL6A2,CTF
M5885	Ensemble of genes encoding ECM-associated proteins including ECM-affiliated proteins, ECM regulators and secreted factors	4.474941666	32	ADAMTS5,ADAMTSL4,ANGPT1,CCL3L3,CLEC3B,CST3,CXCL10,CXCL12,CXCL9,EGFL6,F
M5883	Genes encoding secreted soluble factors	4.27355877	19	ANGPT1,CCL3L3,CXCL10,CXCL12,CXCL9,EGFL6,FGF11,FRZB,FSTL3,IL1RN,INHBB,LEP,F

M5887	Genes encoding structural components of basement membranes	3.91235413	06	COL15A1,COL6A1,COL6A2,LAMA5,LAMB2,LAMB3
M6778	IL-10 Anti-inflammatory Signaling Pathway	2.37453478	03	HMOX1,STAT1,STAT3
M18342	G alpha i Pathway	2.317474526	04	CFB,DAG1,SOS1,STAT3
M917	Complement Pathway	2.233353975	03	C1R,C1S,CFB
PantherDB				
P00034	Integrin signalling pathway	10	19	ACTN1,COL11A1,COL12A1,COL15A1,COL16A1,COL1A2,COL3A1,COL5A2,COL6A1,COL6A2
P00008	Axon guidance mediated by Slit/Robo	2.301673714	03	CXCL12,RHOC,SLIT2
P00049	Parkinson disease	2.127254382	06	FGR,HSPA5,HSPA8,SNCG,UCHL1,YWHAH
P00005	Angiogenesis	2.006215782	08	ANGPT1,FRZB,GRB14,PDGFD,RHOC,SOS1,STAT1,STAT3
P00031	Inflammation mediated by chemokine and cytokine signaling pathway	1.864244118	09	CCL3L3,COL12A1,COL6A1,COL6A2,CXCL10,GNG2,RHOC,SOS1,STAT3
P04395	Vasopressin synthesis	1.720921143	02	CPE,OXT
P00038	JAK/STAT signaling pathway	1.410153707	02	STAT1,STAT3
P04393	Ras Pathway	1.343390185	04	RHOC,SOS1,STAT1,STAT3
P00016	Cytoskeletal regulation by Rho GTPase	1.323968148	04	RHOC,TUBB2A,TUBB2B,TUBB8
Pathway Ontology				
PW:0000021	hypertension	4.522214868	03	HMOX1,LOX,SOD2
PW:0000286	integrin signaling	2.188340257	04	APBB1IP,ITGAV,ITGB2,ITGB5
PW:0000498	reverse cholesterol transport	1.802432827	02	PLTP,SCARB1
PW:0000378	oxidative stress responses	1.695428398	01	NQO1
PW:0000138	Vitamin B6 metabolic	1.695428398	01	AOX1
PW:0000346	CADASIL	1.695428398	01	NOTCH3
PW:0000300	renal disease, renal disorder	1.695428398	01	SPP1
PW:0000413	heme catabolic	1.695428398	01	HMOX1
PW:0000169	nerve growth factor signaling	1.695428398	01	SOS1
PW:0000238	insulin-like growth factor signaling	1.647369002	02	IGFBP5,IGFBP6
SMPDB				
SMP00101	Suprofen Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00109	Mefanamic acid Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00104	Indomethacin Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00077	Piroxicam Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00093	Diclofenac Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00120	Naproxen Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00085	Ketoprofen Pathway	2.116454504	02	AKR1C3,PTGDS
SMP00130	Steroidogenesis	1.997182265	02	CYP11A1,HSD11B1
SMP00371	Congenital Lipoid	1.695428398	01	CYP11A1

	Adrenal Hyperplasia (CLAH) or Lipoid CAH			
SMP00202	MNGIE (Mitochondrial Neurogastrointestinal Encephalopathy)	1.695428398	01	TYMP

Table 4 The enriched pathway terms of the down-regulated differentially expressed genes

BIOCYC				
Pathway ID	Pathway Name	LogP	Gene Count	Genes
142373	superpathway of methionine degradation	4.000296992	04	BCKDHA,CBS,MAT2B,PCCA
142421	fatty acid beta-oxidation	3.86108057	04	ACADL,ECI1,SCP2,SLC27A2
KEGG				
83036	Ribosome	10	18	RPL14,RPL17,RPL18,RPL18A,RPL21,RPL29,RPL35,RPL9,RPS12,RPS15A,RPS
83004	Propanoate metabolism	5.564719729	07	ACACA,ACACB,ACSS2,ALDH6A1,BCKDHA,LDHC,PCCA
989139	AMPK signaling pathway	4.488377132	11	ACACA,ACACB,CAB39L,CD36,EEF2K,FBP1,FOXO1,FOXO3,IGF1,PFKFB3,SIRT1
82949	Glycine, serine and threonine metabolism	3.864500032	06	CBS,CTH,GATM,GLYCTK,PHGDH,SHMT1
83002	Glyoxylate and dicarboxylate metabolism	3.667203873	05	GLUL,GLYCTK,HYI,PCCA,SHMT1
921162	FoxOsignaling pathway	3.474041745	10	CCNG2,CDKN1B,FOXO1,FOXO3,GADD45B,IGF1,MAPK10,PTEN,RBL2,SIRT1
377873	Herpes simplex infection	3.430846606	12	C5,CSNK2A2,CSNK2B,EEF1D,HLA-DMA,MAPK10,NOP53,PER2,PER3,SRSF3,SF
868084	Fatty acid metabolism	3.41818559	07	ACACA,ACADL,ELOVL6,FADS1,HACD1,HSD17B12
132956	Metabolic pathways	3.326019848	43	AASS,ACACA,ACACB,ACADL,ACSS2,ADH1B,ADH1C,ALDH6A1,BCAT2,BCKDHA
790012	Biosynthesis of amino acids	3.113855172	07	BCAT2,CBS,CTH,GLUL,MAT2B,PHGDH,SHMT1
Pathway Interaction Database				
138036	FoxO family signaling	4.344156036	07	CDKN1B,FOXO1,FOXO3,MAPK10,RBL2,SIRT1,ZFAND5
137956	HIF-2-alpha transcription factor network	3.258024576	05	BHLHE40,EFNA1,ELK1,SIRT1,TWIST1
137963	Regulation of nuclear SMAD2/3 signaling	3.045281998	07	ESR1,FOXO1,FOXO3,NR3C1,RBBP4,SIN3A,TGIF1
137972	Signaling events mediated by HDAC Class III	2.977804515	05	ACSS2,FOXO1,FOXO3,HOXA10,SIRT1
137979	FOXA1 transcription factor network	2.782996939	05	CDKN1B,ESR1,NDUFV3,NRIP1,SFTPD
138020	Class I PI3K signaling events mediated by Akt	2.332504648	04	CDKN1B,FOXO1,FOXO3,MAP3K5
138027	Regulation of Androgen receptor activity	1.744963151	04	FOXO1,NR3C1,SIRT1,TRIM24
137916	Regulation of retinoblastoma protein	1.582589283	04	CDKN1B,RBBP4,SFTPD,SIRT1
138062	Signaling events mediated by HDAC Class II	1.514289673	03	ESR1,HDAC9,NR3C1
137997	Signaling events mediated by HDAC Class I	1.356649762	04	HDAC9,RBBP4,SIN3A,SIRT1
REACTOME				
1268690	Eukaryotic Translation Elongation	10	19	EEF1D,EEF1G,RPL14,RPL17,RPL18,RPL18A,RPL21,RPL29,RPL35,RPL9,RPS12
1270158	Metabolism of amino acids and derivatives	10	34	AASS,ALDH6A1,AZIN1,BCAT2,BCKDHA,CBS,CKB,CTH,GATM,GLUL,NAALAD2,F
1270010	Fatty acid, triacylglycerol, and ketone body metabolism	10	19	AACS,ACACA,ACADL,AGT,BDH1,CD36,ECI1,ELOVL6,FADS1,GPAT3,GPD1L,HAC
1270001	Metabolism of lipids and lipoproteins	4.373325922	34	AACS,ACACA,ACACB,ACADL,AGT,BDH1,CD36,CDS2,CSNK2A2,CSNK2B,ECI1,EI
1270161	Branched-chain amino acid catabolism	4.002640203	05	ALDH6A1,BCAT2,BCKDHA,SHMT1,TMLHE
1268854	Disease	2.588390587	30	ACACA,ARRB1,CCDC59,CD36,CDKN1B,FOXO1,FOXO3,GPC3,HDAC9,PAPSS1,P
1269871	Circadian Clock	2.518155723	06	BHLHE40,DBP,NR3C1,NRIP1,PER2,SIRT1
1269652	Nuclear Receptor transcription pathway	2.452176105	05	ESR1,NR2F1,NR3C1,NR4A2,RORB

1270168	Carnitine synthesis	2.410152815	02	SHMT1,TMLHE
1270029	Regulation of lipid metabolism by Peroxisome proliferator-activated receptor alpha (PPARalpha)	2.380171215	08	AGT,CD36,FADS1,MED16,MED28,MED30,MED6,SIN3A
GenMAPP				
MAP00640	Propanoate metabolism	4.411975751	05	ACACA,ACACB,ALDH6A1,LDHC,PCCA
MAP00450	Selenoamino acid metabolism	2.239863267	02	CBS,CTH
MAP00910	Nitrogen metabolism	2.08446222	03	CA3,CTH,GLUL
MAP00271	Methionine metabolism	1.980370918	02	CBS,CTH
MAP00272	Cysteine metabolism	1.87699911	02	CTH,LDHC
MAP00280	Valineleucine and isoleucine degradation	1.825387093	03	ALDH6A1,BCKDHA,PCCA
MAP00100	Sterol biosynthesis	1.785852022	02	LSS,SC5D
MAP00010	Glycolysis Gluconeogenesis	1.688196341	04	ADH1B,ADH1C,FBP1,LDHC
MAP00620	Pyruvate metabolism	1.619507881	03	ACACA,ACACB,LDHC
MAP00310	Lysine degradation	1.394254793	02	AASS,SHMT1
MSigDB C2 BIOCARTA				
M6682	CDK Regulation of DNA Replication	2.277315691	03	CDKN1B,MCM6,ORC2
M10145	PTEN dependent cell cycle arrest and apoptosis	2.277315691	03	CDKN1B,FOXO3,PTEN
M12012	p38 MAPK Pathway	2.199389482	04	EEF2K,ELK1,MAP3K5,MKNK2
M4170	Interferon gamma pathway.	1.785852022	02	CISH,ELP2
M5374	The SARS-coronavirus Life Cycle	1.785852022	02	FBL,LDHC
M287	Erk1/Erk2 MapkSignaling pathway	1.737787907	03	ELK1,MKNK2,RPS6KA5
M13863	MAPKinaseSignaling Pathway	1.507327629	05	ELK1,MAP3K5,MAPK10,MKNK2,RPS6KA5
M2499	CARM1 and Regulation of the Estrogen Receptor	1.481705587	03	ESR1,HDAC9,NRIP1
M13158	The IGF-1 Receptor and Longevity	1.446542824	02	FOXO3,IGF1
M14532	PI3K Pathway	1.419841166	03	CD55,FOXO1,PTEN
PantherDB				
P05918	p38 MAPK pathway	3.140376991	05	EEF2K,ELK1,MAP3K5,MKNK2,RPS6KA5
P02776	Serine glycine biosynthesis	2.410152815	02	PHGDH,SHMT1
P00015	Circadian clock system	1.87699911	02	PER2,PER3
P00035	Interferon-gamma signaling pathway	1.737787907	03	CISH,MAPK10,SOCS2
P00032	Insulin/IGF pathway-mitogen activated protein kinase kinase/MAP kinase cascade	1.696738708	03	ELK1,IGF1,RPS6KA5
P02737	Cysteine biosynthesis	1.68650448	01	CBS
P00033	Insulin/IGF pathway-protein kinase B signaling cascade	1.514289673	03	FOXO3,IGF1,PTEN
P05911	Angiotensin II-stimulated signaling through G proteins and beta-arrestin	1.481705587	03	AGT,ARRB1,ELK1
P00036	Interleukin signaling pathway	1.417751205	05	CDKN1B,ELK1,FOXO3,IL13RA1,MKNK2
P02724	Alanine biosynthesis	1.398756651	01	BCAT2
Pathway Ontology				

PW:0000047	glycine, serine and threonine metabolic	5.257885042	05	CBS,CTH,GATM,PHGDH,SHMT1
PW:0000400	transulfuration of homocysteine metabolism	3.383735276	02	CBS,CTH
PW:0000198	p38 MAPK signaling	3.052433182	04	IGF1,MAP3K5,MKNK2,RPS6KA5
PW:0000427	molybdenum cofactor biosynthetic	2.626189633	02	GPHN,MOCS1
PW:0000510	altered insulin-like growth factor signaling	1.68650448	01	IGF1
PW:0000371	calcium homeostasis	1.68650448	01	S100A1
PW:0000250	peptidoglycan biosynthetic	1.68650448	01	GLUL
PW:0000076	pathway of urea cycle and metabolism of amino groups	1.564200004	02	CKB,GATM
PW:0000008	Wntsignaling	1.548065942	03	MAPK10,WNT11,WNT3
PW:0000440	glycine metabolic	1.398756651	01	SHMT1
SMPDB				
SMP00004	Glycine, Serine and Threonine Metabolism	5.090440722	06	CBS,CTH,GATM,GLYCTK,PHGDH,SHMT1
SMP00029	Selenoamino Acid Metabolism	3.206449708	02	CBS,CTH,PAPSS1
SMP00033	Methionine Metabolism	2.511627198	03	CBS,CTH,SHMT1
SMP00071	Ketone Body Metabolism	2.410152815	02	BDH1,CTH
SMP00384	MethylmalonateSemialdehyde Dehydrogenase Deficiency	1.68650448	01	ALDH6A1
SMP00239	Saccharopinuria/Hyperlysinemia II	1.68650448	01	AASS
SMP00362	Arginine: Glycine Amidinotransferase Deficiency (AGAT Deficiency)	1.68650448	01	GATM
SMP00177	Cystathionine Beta-Synthase Deficiency	1.68650448	01	CBS
SMP00032	Valine, Leucine and Isoleucine Degradation	1.657349818	03	ALDH6A1,BCKDHA,PCCA
SMP00016	Propanoate Metabolism	1.631017126	02	ALDH6A1,PCCA

Table 5 The enriched GO terms of the up-regulated differentially expressed genes

GO ID	CATEGORY	GO Name	logP	Gene Count	Genes
GO:0048514	BP	blood vessel morphogenesis	10	32	AMOT,ANGPT1,CCDC80,COL15A1,COL3A1,CXCL10,CXCL12,ERBB2,HMOX1,I
GO:0072358	BP	cardiovascular system development	10	45	AMOT,ANGPT1,APLNR,CCDC80,COL11A1,COL15A1,COL1A2,COL3A1,CPE,CR
GO:0051241	BP	negative regulation of multicellular organismal process	10	47	AMOT,ANGPT1,COL3A1,COL5A2,CORO1C,CPE,CST3,CXCL10,EFEMP1,ERBB2
GO:0072359	BP	circulatory system development	10	45	AMOT,ANGPT1,APLNR,CCDC80,COL11A1,COL15A1,COL1A2,COL3A1,CPE,CR
GO:0001944	BP	vasculature development	10	35	AMOT,ANGPT1,CCDC80,COL15A1,COL1A2,COL3A1,CXCL10,CXCL12,ERBB2,I
GO:0040012	BP	regulation of locomotion	10	42	AMOT,ANGPT1,CARMIL1,COL3A1,CORO1C,CXCL10,CXCL12,CXCL9,DAG1,EF
GO:0043062	BP	extracellular structure organization	10	36	ADAMTS5,ADAMTSL4,CCDC80,COL11A1,COL12A1,COL16A1,COL1A2,COL3
GO:0016477	BP	cell migration	10	69	AMOT,ANGPT1,BAMBI,CARMIL1,CCL3L3,CD248,COL1A2,COL3A1,CORO1C,C
GO:0033993	BP	response to lipid	10	42	AKR1C3,ALPL,CCND1,CXCL10,CXCL9,GNG2,HAVCR2,HMOX1,HNMT,IL1RN,IN
GO:0031589	BP	cell-substrate adhesion	10	21	ACTN1,ANGPT1,CARMIL1,CCDC80,COL16A1,COL3A1,CORO1C,DAG1,EGFL6,
GO:0031012	CC	extracellular matrix	10	41	ADAMTS5,ADAMTSL4,ALPL,CCDC80,CD248,CLEC3B,COL11A1,COL12A1,CO
GO:0044420	CC	extracellular matrix component	10	21	CCDC80,COL11A1,COL12A1,COL15A1,COL1A2,COL3A1,COL5A2,COL6A1,CS
GO:0005615	CC	extracellular space	10	87	ACTN1,ADAMTS5,AIFM2,ALPL,ANGPT1,C1R,C1RL,C1S,CCL3L3,CD9,CES1,CF A,HMOX1,HPHSPA8,HTRA1,IGFBP5,IGFBP6,IL1RN,INHBB,LAMA5,LBP,LCP1,L
GO:0005788	CC	endoplasmic reticulum lumen	10	19	ADAMTS5,ADAMTSL4,CALU,CES1,COL11A1,COL12A1,COL15A1,COL16A1,C
GO:0005581	CC	collagen trimer	10	12	COL11A1,COL12A1,COL15A1,COL16A1,COL1A2,COL3A1,COL5A2,COL6A1,C
GO:0005912	CC	adherens junction	5.456429066	25	ACTN1,ALCAM,APBB1IP,CADM3,CD9,CORO1C,DAG1,FAM129B,FAT1,FLNC,H
GO:0005925	CC	focal adhesion	5.418442901	22	ACTN1,ALCAM,APBB1IP,CD9,CORO1C,DAG1,FAT1,FLNC,HSPA5,HSPA8,ITGA
GO:0005604	CC	basement membrane	5.289701566	11	CCDC80,COL15A1,CST3,DAG1,EFEMP1,EGFL6,LAMA5,LAMB2,LAMB3,SPAR
GO:0071682	CC	endocytic vesicle lumen	4.986142167	05	HBA1,HBB,HPSAA1,SPARC
GO:0048471	CC	perinuclear region of cytoplasm	3.401186527	27	CST3,DOCK6,ERBB2,FAT1,GLB1,HMOX1,HSPA8,INF2,INHBB,MAP1B,MSN,MT
GO:0019838	MF	growth factor binding	10	15	COL1A2,COL3A1,COL6A1,ERBB2,GPC1,HTRA1,IGFBP5,IGFBP6,IL1RN,ITGA
GO:0005178	MF	integrin binding	10	13	ACTN1,ADAMTS5,CD9,COL16A1,COL3A1,EGFL6,GNPMB,ITGB5,LAMA5,LAM
GO:0050839	MF	cell adhesion molecule binding	10	19	ACTN1,ADAMTS5,CADM3,CD9,COL16A1,COL3A1,CPE,EGFL6,GNPMB,GRIN2
GO:0050840	MF	extracellular matrix binding	10	11	ADAMTS5,CD248,COL11A1,DAG1,FBLN2,GPC1,ITGA,SLIT2,SPARC,SPP1,TH
GO:0005201	MF	extracellular matrix structural constituent	5.80617847	10	COL11A1,COL12A1,COL15A1,COL1A2,COL3A1,COL5A2,ELN,FBLN2,LUM,MF
GO:0005509	MF	calcium ion binding	5.576968244	32	ACTN1,C1R,C1S,CALB2,CALU,CD248,CLEC3B,DAG1,EFEMP1,EGFL6,EPDR1,F
GO:0005539	MF	glycosaminoglycan binding	4.874249306	15	ADAMTS5,CCDC80,CFH,CLEC3B,CXCL10,FMOD,GNS,GNPMB,NRP2,RSPO3,S
GO:0003779	MF	actin binding	4.582186708	21	ACTN1,CORO1C,DAG1,ENC1,FLNC,INF2,LCP1,LMOD1,MAP1B,MARCKS,MSN
GO:0001968	MF	fibronectin binding	4.577634254	06	CCDC80,FSTL3,IGFBP5,ITGA,MMP9,THBS1
GO:0001786	MF	phosphatidylserine binding	4.577634254	06	HSPA8,MARCKS,MFGE8,SCARB1,SCIN,THBS1

Table 6 The enriched GO terms of the down-regulated differentially expressed genes

GO ID	CATEGORY	GO Name	logP	Gene Count	Genes
GO:0016053	BP	organic acid biosynthetic process	10	25	ACACA,ACACB,ACADL,ACSS2,AGT,BCAT2,CBS,CTH,ELOVL6,FADS1,GATM,GL
GO:0043603	BP	cellular amide metabolic process	10	45	ABTB1,ACACA,ACACB,AGT,ANG,BTG2,CTH,EEF1D,EEF1G,EEF2K,EIF2A,EIF3H
GO:0072599	BP	establishment of protein localization to endoplasmic reticulum	10	17	RPL14,RPL17,RPL18,RPL18A,RPL21,RPL29,RPL35,RPL9,RPS12,RPS15A,RP
GO:0072330	BP	monocarboxylic acid biosynthetic process	10	18	ACACA,ACACB,ACADL,ACSS2,AGT,ELOVL6,FADS1,HACD1,HSD17B12,LDHC,I
GO:0006412	BP	translation	10	37	ABTB1,ANG,BTG2,EEF1D,EEF1G,EEF2K,EIF2A,EIF3H,EIF4B,EIF4EBP2,ESR1,F
GO:0006413	BP	translational initiation	10	22	EIF2A,EIF3H,EIF4B,EIF4EBP2,KHDRBS1,RPL14,RPL17,RPL18,RPL18A,RPL21
GO:0019752	BP	carboxylic acid metabolic process	10	43	AACS,AASS,ACACA,ACACB,ACADL,ACSS2,ADH1C,AGT,ALDH6A1,AZIN1,BCA1
GO:0009057	BP	macromolecule catabolic process	4.553158507	45	ARRB1,AZIN1,BTG2,C2orf40,CCNF,CDKN1B,CSNK2A2,CTSC,EIF4B,FBX011,F
GO:0006633	BP	fatty acid biosynthetic process	4.538876498	12	ACACA,ACACB,ACADL,ACSS2,AGT,ELOVL6,FADS1,HACD1,HSD17B12,PDK4,S
GO:1903507	BP	negative regulation of nucleic acid-templated transcription	4.521620083	47	ARRB1,BHLHE40,BTG2,CD36,CDKN1B,CIART,EFNA1,ELF2,ELP2,ESR1,FOXO1
GO:0022627	CC	cytosolic small ribosomal subunit	10	09	RPS12,RPS15A,RPS17,RPS18,RPS2,RPS27,RPS29,RPS3,RPS9
GO:0005840	CC	ribosome	10	19	MRPL55,RPL14,RPL17,RPL18,RPL18A,RPL21,RPL29,RPL35,RPL9,RPS12,RP
GO:0005730	CC	nucleolus	4.057557776	34	ABTB1,ACACA,ANG,BHLHE40,EEF1D,FBL,FBX011,GTFC3,H1F0,H1FX,HMGI
GO:0000785	CC	chromatin	2.602659466	19	AHCTF1,ARRB1,DPF2,ESR1,H1F0,H1FX,HMGB2,NASP,NRIP1,ORC2,RAD21,R
GO:0044451	CC	nucleoplasm part	2.467015328	25	CIART,ELP2,FBL,HDAC9,INTS6,KAT14,KAT8,MED16,MED28,MED30,MED6,M
GO:0017053	CC	transcriptional repressor complex	2.414075613	06	ELP2,N4BP2L2,RBBP4,SIN3A,TBX15,ZBTB16
GO:1902494	CC	catalytic complex	2.343912583	33	ACVR1,ARRB1,BCKDHA,CCNF,CDKN1B,DCAF7,DNAH17,ELP2,FBX011,GPD1I
GO:1990234	CC	transferase complex	2.245632262	24	ACVR1,CCNF,CDKN1B,DCAF7,ELP2,FBX011,HDAC9,INTS6,KAT14,KAT8,MAP
GO:0042383	CC	sarcolemma	2.070467563	08	ADRB2,ANK2,CD36,DTNA,ESR1,PPP3R1,RTN2,SNTB1
GO:0005694	CC	chromosome	1.671134405	27	ADD3,AHCTF1,ARRB1,CCNB1IP1,CENPV,DPF2,ESR1,FBL,FBX011,H1F0,H1F
GO:0003735	MF	structural constituent of ribosome	10	20	MRPL55,RPL14,RPL17,RPL18,RPL18A,RPL21,RPL29,RPL35,RPL9,RPS12,RP
GO:0008134	MF	transcription factor binding	5.500226582	29	AIP,ARRB1,BHLHE40,CSNK2B,EEF1D,ELK1,ESR1,FBL,FOXO1,FOXO3,HDAC9,I
GO:0044212	MF	transcription regulatory region DNA binding	4.619830311	35	ARRB1,BHLHE40,CIART,DBP,DMRT2,DPF2,ELK1,ESR1,FOXO3,HMGB2,HOXA1
GO:0016829	MF	lyase activity	3.979976654	13	BCKDHA,CA3,CBS,CENPV,CTH,GLUL,HACD1,MACROD1,MOCS1,PCBD1,RPS3
GO:0043565	MF	sequence-specific DNA binding	3.820984116	39	CIART,CSRNP1,DBP,DMRT2,DPF2,ELF2,ELK1,ESR1,FOXN2,FOXO1,FOXO3,HL
GO:0016874	MF	ligase activity	3.787075306	20	AACS,ACACA,ACACB,ACSS2,CCNB1IP1,GLUL,GMPS,HERC5,MARCH3,PCCA,F
GO:0000981	MF	DNA-binding transcription factor activity, RNA polymerase II-specific	3.202034757	26	BHLHE40,BTG2,CSRNP1,DBP,ELF2,ELK1,ESR1,FOXO1,FOXO3,HOXA10,KLF9
GO:0003700	MF	DNA-binding transcription factor activity	2.896608329	40	AHCTF1,BHLHE40,BTG2,CNBP,CSRNP1,DBP,DMRT2,ELF2,ELK1,ESR1,FOXN2

GO:1990837	MF	sequence-specific double-stranded DNA binding	2.677080807	26	CIART,DBP,DMRT2,DPF2,ELK1,ESR1,HMGB2,HOXA10,KLF9,MKX,MLX,NR3C1
GO:0046914	MF	transition metal ion binding	2.551740448	43	ADH1B,ADH1C,ANG,CA3,CCNB1IP1,CNBPCYP4V2,DPF2,DTNA,ESR1,FBXO11

Table 7 Topology table for up and down regulated genes

Category	Node	Degree	Betweenness	Stress	Closeness	Clustering Coefficient
Up	HSPA8	646	0.131757	1.63E+08	0.3772	0.002313
Up	HSPA5	516	0.099887	1.14E+08	0.376106	0.004142
Up	ERBB2	292	0.063535	48663168	0.356491	0.003339
Up	STAT3	264	0.05522	47126446	0.354335	0.004008
Up	YWHAH	264	0.045286	37963446	0.341753	0.001872
Up	LMO2	233	0.044111	33426870	0.33642	0.001101
Up	HLA-A	220	0.014824	11862288	0.326107	0.003636
Up	ADAMTSL4	209	0.038316	19994762	0.327888	0.019089
Up	STAT1	180	0.028372	23747148	0.343822	0.006094
Up	SPTAN1	177	0.024448	27747372	0.350321	0.009156
Up	RAB9A	165	0.028366	16595428	0.322962	0.001848
Up	NEK6	156	0.020457	28448632	0.313392	0
Up	ACTN1	148	0.020209	23472660	0.328689	0.004818
Up	CEP19	141	0.023639	25737074	0.304756	3.04E-04
Up	TUBB2A	137	0.015254	18211616	0.33286	0.005474
Up	IRAK1	124	0.015303	12259430	0.341367	0.008806
Up	CALU	122	0.018218	12821024	0.339628	0.006774
Up	TAGLN2	122	0.015529	11548640	0.335163	0.013548
Up	AMOT	117	0.014715	21956260	0.319553	0.001373
Up	MSN	117	0.014992	11814740	0.333839	0.011799
Up	FLNC	116	0.016791	14264076	0.327062	0.004813
Up	CCND1	115	0.017274	10796534	0.331599	0.005631
Up	VASN	112	0.016584	11691916	0.320385	0.01287
Up	S100A9	110	0.013508	13323590	0.323624	0.003288
Up	TPM2	107	0.013762	11390822	0.313825	0.004579
Up	PPP2R1B	107	0.015219	10094554	0.313122	0.002015
Up	HOXC8	107	0.01648	15471342	0.31475	0.004585
Up	TUBB8	104	0.012767	8605522	0.307178	0.004759
Up	FTH1	103	0.01708	14706820	0.312194	5.94E-04
Up	SGK1	99	0.011615	13595420	0.313136	4.30E-04
Up	CORO1C	96	0.012278	9996916	0.3286	0.002632
Up	APLNR	95	0.017519	18213738	0.28924	0
Up	TGFBR2	94	0.014661	11193844	0.314627	0.004061
Up	PLIN3	93	0.014305	8824500	0.31656	0.003419
Up	SERPINH1	93	0.010233	10810052	0.333793	0.009584
Up	SPP1	92	0.015326	7687964	0.318447	0.001954
Up	SAR1A	90	0.016122	14074460	0.317113	9.99E-04
Up	MVP	89	0.013541	10850118	0.333486	0.007752
Up	TUBB2B	83	0.006011	10710364	0.306893	0.002351
Up	EFEMP1	83	0.013576	7822462	0.317002	0.006323
Up	FAM189A2	78	0.012518	23336552	0.286627	0
Up	IGFBP5	76	0.01285	6614978	0.288941	0.001053
Up	UCHL1	72	0.009707	7499836	0.333196	0.016499

Up	MAP1B	69	0.004895	4706194	0.319961	0.017903
Up	VGLL3	69	0.007203	18517996	0.262443	0
Up	NOTCH3	68	0.009978	10388152	0.307543	0
Up	SOD2	67	0.007596	13310940	0.290512	0
Up	ITGAV	66	0.008412	5317186	0.319863	0.012121
Up	CYCS	66	0.009031	4242804	0.312087	0.00373
Up	HAVCR2	64	0.009241	5323290	0.302763	0.003472
Up	ITGB5	63	0.006615	5660860	0.311658	0.009217
Up	CDR2L	62	0.008588	10276842	0.286469	0
Up	NAV1	61	0.007818	7186322	0.305705	0.001093
Up	HBB	60	0.009359	4158840	0.308837	0.008475
Up	NCKAP5L	60	0.005732	7955376	0.288953	0
Up	GLS	58	0.007723	6913514	0.293433	0.00242
Up	MBP	58	0.005048	8226944	0.292618	0
Up	SOS1	57	0.004934	5230050	0.304182	0.003759
Up	DAG1	56	0.007357	5343410	0.309113	0.005591
Up	S100A4	56	0.006973	9715070	0.299345	0
Up	HMOX1	54	0.008308	5623900	0.291807	0.005279
Up	KIAA1671	54	0.0045	5540890	0.289033	0.013976
Up	QPRT	53	0.006138	4832362	0.293599	0.003922
Up	CXCL9	52	0.006983	6107104	0.260505	0
Up	TAGLN	51	0.003826	2401428	0.299099	0.003137
Up	OSGIN1	50	0.004118	5186448	0.291351	0
Up	IFIT2	50	0.003562	6888492	0.28333	0
Up	SMYD2	49	0.005556	7843036	0.28708	0
Up	GLB1	47	0.005936	5981072	0.297555	0.009251
Up	RAB6B	46	0.00547	4701204	0.301094	0.002899
Up	ZNF219	46	0.005238	3326716	0.286277	0.004831
Up	PCBP3	45	0.004574	3845082	0.288815	0.00101
Up	SULT1A1	45	0.005119	2944316	0.296571	0.019192
Up	LYZ	44	0.003086	5138132	0.302058	0
Up	PALLD	44	0.003814	2660068	0.311993	0.013742
Up	THBS1	44	0.00823	4538560	0.305757	0.015856
Up	CD9	43	0.005751	2964190	0.298239	0.007752
Up	AEN	43	0.004667	7111924	0.272267	0
Up	COPG2	43	0.004913	4775648	0.313082	0
Up	FAT1	42	0.00404	5889734	0.276326	0
Up	WWC1	42	0.003429	2836442	0.307386	0.022067
Up	IGFBP6	42	0.004231	3088344	0.288082	0.005128
Up	ITGB2	41	0.005357	4411146	0.303395	0.003659
Up	NUP188	41	0.003108	4907892	0.290617	0
Up	COL1A2	40	0.005029	5099026	0.285883	0.002564
Up	HSPB8	40	0.003647	4517138	0.278775	0
Up	SYNC	40	0.004315	7896734	0.276295	0

Up	PYGL	39	0.003197	2471758	0.299901	0.003003
Up	PRSS23	39	0.004248	4905244	0.290966	0
Up	PDLIM1	39	0.003659	2786872	0.299876	0.012012
Up	SFRP4	39	0.003767	2048128	0.298877	0.002699
Up	FAM98A	37	0.00261	4955160	0.28916	0
Up	RHOC	37	0.004285	3441322	0.293599	0.004505
Up	TM4SF19	37	0.00657	2728698	0.298582	0.003003
Up	MARCKS	35	0.003247	3052972	0.309508	0.008403
Up	DLGAP4	35	0.00253	4101184	0.292783	0
Up	KLF4	34	0.002104	3387628	0.296499	0
Up	FRMD6	34	0.003547	2173770	0.30067	0.010695
Up	INF2	34	0.001906	3741376	0.28604	0
Up	NMT2	34	0.004925	5082380	0.285804	0
Up	CYB561	34	0.004216	2892542	0.26327	0.008913
Up	PLTP	33	0.003576	3913370	0.266437	0
Up	GNG2	33	0.00334	8521644	0.258991	0
Up	STMN2	33	0.002979	3380914	0.280173	0.00947
Up	RAB31	33	0.003188	4366610	0.279064	0
Up	FAM129B	31	0.00205	1963278	0.294946	0.002151
Up	LAMB2	31	0.002316	1445266	0.300434	0.002151
Up	S100A11	31	0.001135	1884242	0.294504	0
Up	GNS	31	0.003232	3132614	0.290048	0.008602
Up	FGR	31	0.002564	1608758	0.306595	0.04086
Up	SNCG	31	0.002583	1761424	0.285445	0.010753
Up	LHX6	30	0.004005	4295336	0.246849	0
Up	MMP9	29	0.003533	1643986	0.276106	0.022792
Up	SCARB1	29	0.002413	3830600	0.280985	0
Up	CCPG1	29	0.004637	5110776	0.259472	0
Up	COL6A2	29	0.002815	3690848	0.252537	0
Up	GRIN2B	29	0.002302	1122488	0.285838	0.004926
Up	CRIP1	28	0.001512	1100488	0.275102	0.005291
Up	LOX	28	0.003132	2234520	0.288769	0.018519
Up	THY1	28	0.001582	2195824	0.270061	0
Up	CCND2	28	0.001204	1179300	0.283695	0
Up	HP	28	0.003646	2155794	0.295847	0.010582
Up	LAMA5	27	0.002587	1793790	0.277859	0.002849
Up	TNFAIP6	27	0.006221	4007336	0.269101	0.011396
Up	EPDR1	27	0.003089	1767128	0.292819	0.025641
Up	KCTD12	26	0.001742	1864764	0.281377	0
Up	CRTAP	26	0.001485	1239886	0.280562	0.058462
Up	NQO1	25	0.001997	3076618	0.283352	0
Up	TMEM189	25	0.002319	1489396	0.29263	0.013333
Up	HSPA12A	25	0.00251	2745446	0.270302	0
Up	CCDC107	25	0.002939	2945106	0.271718	0

Up	CDK14	25	0.002145	1096846	0.290978	0.019763
Up	CD68	25	0.002914	1383318	0.282131	0.003333
Up	PLXNA1	24	9.97E-04	1385474	0.270766	0
Up	CSN1S1	24	0.003031	1574476	0.289355	0.018116
Up	TLE2	24	0.002913	4771720	0.250017	0
Up	TNS3	24	0.001733	1610768	0.300832	0.025362
Up	ZMAT3	24	0.002518	3853494	0.282	0
Up	CMTM3	24	0.003041	1808232	0.276495	0
Up	FBLN2	23	0.001502	1075964	0.266359	0.009524
Up	COL6A1	23	0.001413	1973664	0.27114	0
Up	S100A3	23	0.003098	2878998	0.266975	0
Up	NABP1	23	0.00259	2546540	0.287888	0
Up	TMEM54	23	0.003244	2905042	0.268504	0
Up	SLC2A5	23	0.003375	3974418	0.245913	0
Up	ELN	22	0.002632	2145182	0.257094	0.026316
Up	LAMB3	22	0.001502	3046028	0.266681	0
Up	SLIT2	22	0.00217	1500762	0.276895	0.031579
Up	IRF8	22	0.001595	2777354	0.276022	0
Up	STK38L	22	0.001104	2534630	0.285075	0
Up	PLEKH02	22	0.002217	2540732	0.280259	0
Up	GPC1	21	0.002734	2130592	0.265163	0
Up	PTGDS	21	0.001473	2337746	0.283131	0.005848
Up	GRB14	21	0.001711	2329784	0.283242	0
Up	KANK4	21	0.001599	1521196	0.263061	0.038095
Up	TYMP	21	0.001517	1727486	0.26495	0
Up	CYB561A3	20	0.002132	1166162	0.238198	0
Up	HTRA1	20	0.002054	1885686	0.274614	0
Up	B4GALT5	20	0.00169	2081630	0.25831	0
Up	LCP1	20	9.58E-04	807902	0.287466	0.026316
Up	CPE	20	0.001095	1580024	0.254127	0
Up	KCNB1	20	0.00263	3492512	0.248759	0
Up	OAF	20	0.002196	1509446	0.24643	0
Up	SYNPO2	20	0.0017	928102	0.313487	0.042105
Up	ENC1	20	0.001007	2393036	0.267545	0
Up	DOCK6	20	0.002214	2355528	0.264247	0
Up	STC2	19	0.001811	1655032	0.277233	0.005848
Up	MT2A	19	0.002237	959090	0.268902	0
Up	CTGF	19	0.001764	1325662	0.294456	0
Up	MYL9	19	0.001619	2835070	0.268912	0
Up	SPARC	18	8.80E-04	597658	0.277001	0.013072
Up	CLPTM1L	18	0.001824	833924	0.285512	0.006536
Up	RND3	18	0.001204	1106966	0.265677	0
Up	PDGFD	18	0.001355	1414168	0.243393	0
Up	CFH	17	0.001731	2152476	0.272994	0.007353

Up	SKAP2	17	9.81E-04	1151386	0.283396	0
Up	NRP2	17	9.07E-04	486396	0.251654	0
Up	PTGFRN	17	0.001198	1067934	0.269121	0.022059
Up	LUM	17	0.001227	656762	0.25121	0.044118
Up	MSTO1	17	0.002208	3259790	0.257149	0
Up	SULT1A4	17	6.90E-04	583300	0.273363	0.038095
Up	EGR2	17	0.00263	3566970	0.248682	0
Up	HSD11B1	16	0.002065	1911100	0.262538	0
Up	CLEC3B	16	0.001399	1548088	0.268039	0
Up	SPATA18	16	5.71E-04	672478	0.253799	0
Up	LBP	16	0.002333	1568590	0.268952	0.016667
Up	SLC15A3	15	4.37E-04	457084	0.256794	0
Up	TNMD	15	0.001379	1792380	0.231387	0
Up	SULT1A3	15	6.90E-04	583300	0.273363	0.038095
Up	EGFL6	15	0.001449	606972	0.282801	0.009524
Up	TIMP1	14	9.63E-04	966968	0.260048	0
Up	PCDH9	14	0.00128	1242150	0.259472	0
Up	SCIN	14	0.001524	2668388	0.272329	0
Up	PPFIBP2	13	5.69E-04	812444	0.271941	0
Up	CFB	13	0.001023	696242	0.267703	0
Up	MGST1	13	0.00132	678514	0.284306	0.038462
Up	FAR2	13	8.79E-04	732968	0.218776	0
Up	SUSD1	13	0.001025	1337044	0.270887	0
Up	TPGS2	13	0.001458	2285296	0.267575	0
Up	TDP1	13	9.31E-04	1584550	0.265415	0
Up	CRABP2	13	8.82E-04	942492	0.267536	0
Up	OSTM1	13	7.99E-04	999584	0.26442	0
Up	TMED3	13	0.001768	1105754	0.265813	0
Up	COL3A1	12	2.61E-04	160032	0.26087	0.060606
Up	CXCL12	12	0.00126	1131608	0.249862	0.044444
Up	ALCAM	12	7.48E-04	562268	0.281934	0.045455
Up	PLBD2	12	0.001267	1342160	0.26394	0
Up	VLDLR	12	9.88E-04	542830	0.238456	0
Up	RARRES3	12	9.30E-04	856238	0.279161	0.015152
Up	CLIP3	12	6.70E-04	1115216	0.261593	0
Up	TYROBP	12	0.002505	2860066	0.223185	0
Up	C1S	11	6.79E-04	608832	0.25209	0.055556
Up	APBB1IP	11	9.33E-04	1638836	0.25223	0
Up	AKR1C3	11	0.001423	2534148	0.227205	0
Up	GSTM5	11	8.52E-04	1238616	0.242426	0
Up	PMEPA1	11	4.35E-04	769218	0.259983	0
Up	CES1	11	6.23E-04	347800	0.256233	0
Up	CST3	10	3.63E-04	602294	0.240246	0
Up	C1R	10	7.52E-04	640506	0.24426	0.071429

Up	TPST2	10	0.001334	791042	0.240063	0
Up	IL1RN	10	8.27E-04	447858	0.264161	0
Up	FAM171A1	10	7.80E-04	810132	0.259472	0
Up	WISP2	10	0.00128	834384	0.252994	0
Up	BAMBI	10	5.81E-04	1266400	0.209461	0
Up	CYR61	10	4.24E-04	263992	0.274127	0.022222
Up	TRIM6	10	4.51E-04	534944	0.26087	0
Up	ALPL	10	5.55E-04	721174	0.261057	0
Up	ITIH5	10	6.43E-04	776104	0.254243	0
Up	LRRC32	10	0.001144	585708	0.29736	0
Up	RAB7B	10	7.26E-04	844758	0.254278	0
Up	TNFRSF25	9	2.85E-04	685356	0.24732	0
Up	MRAP	9	7.09E-05	25240	0.224052	0.285714
Up	ABCC3	9	8.71E-04	1216854	0.26163	0
Up	SULT1A2	9	6.57E-04	314992	0.251924	0.111111
Up	TMEM98	9	2.61E-04	155616	0.243727	0
Up	OXT	8	2.82E-04	94820	0.270736	0
Up	ALDH1A3	8	4.74E-04	503556	0.264468	0
Up	FRZB	8	9.85E-04	1157822	0.241556	0
Up	NRCAM	8	5.47E-04	264746	0.26952	0
Up	MXRA7	8	6.15E-04	756206	0.27286	0
Up	CCL3L3	7	5.89E-04	701756	0.221863	0
Up	GALNT16	7	8.61E-04	688996	0.20576	0
Up	MFGE8	7	6.10E-05	57244	0.275666	0
Up	NANOS3	7	0.00111	1372154	0.223116	0
Up	SLC43A2	7	2.34E-04	412138	0.263023	0
Up	SH3BGRL3	7	5.99E-04	384954	0.294528	0.047619
Up	GLIPR2	7	4.84E-04	529920	0.264719	0
Up	SLC35G1	7	4.45E-04	474316	0.250595	0
Up	AIFM2	7	4.98E-04	235562	0.277424	0
Up	GPR137B	7	8.43E-04	898792	0.225708	0
Up	MSC	7	6.42E-05	82488	0.258337	0
Up	CHST3	6	1.06E-04	160442	0.256785	0
Up	CSF2RA	6	8.28E-04	886838	0.247733	0
Up	HNMT	6	3.42E-05	17242	0.256052	0.133333
Up	GPNUMB	6	3.16E-04	277798	0.209758	0
Up	FMOD	6	2.06E-04	211588	0.256667	0
Up	LHCGR	6	2.88E-04	385926	0.236786	0
Up	AOX1	6	3.09E-04	272424	0.24166	0
Up	PLAC9	6	6.27E-04	222890	0.244531	0
Up	SVEP1	6	1.77E-04	275960	0.229465	0
Up	TNFRSF12A	6	4.39E-04	734164	0.234017	0
Up	ARHGEF35	6	6.12E-04	505012	0.261838	0
Up	COL12A1	6	5.77E-04	302930	0.236917	0

Up	ANO3	6	3.43E-04	145774	0.283884	0
Up	CYP11A1	6	4.21E-04	468402	0.22961	0
Up	INHBB	6	8.26E-04	1475316	0.197768	0
Up	MFAP4	5	1.82E-04	253934	0.269101	0
Up	PTGER4	5	8.66E-05	176032	0.251593	0
Up	EMX2	5	8.39E-04	557038	0.207446	0
Up	SGCE	5	8.61E-05	130332	0.240437	0
Up	COL15A1	5	3.88E-05	52870	0.252441	0
Up	SDSL	5	3.32E-06	14564	0.243034	0
Up	MEDAG	5	5.76E-04	526934	0.245531	0
Up	DHDDS	5	3.63E-04	153640	0.237443	0
Up	CXCL10	4	1.67E-05	16262	0.195302	0
Up	CCDC80	4	1.46E-05	25932	0.2422	0
Up	BHMT2	4	2.82E-04	426448	0.252204	0
Up	RSP03	4	5.54E-04	508130	0.214551	0
Up	ELMOD3	4	5.58E-04	492186	0.252739	0
Up	FCGBP	4	3.13E-05	39280	0.239952	0
Up	MYEOV	4	5.54E-04	423866	0.216025	0
Up	CALB2	4	5.57E-06	11274	0.217571	0
Up	CLIC6	4	8.26E-04	476328	0.205133	0
Up	SLC22A12	4	3.13E-04	225200	0.230308	0
Up	SAA2	3	2.46E-04	227126	0.206321	0
Up	NPR3	3	5.50E-04	508058	0.198411	0
Up	LRRN3	3	4.02E-05	40314	0.248776	0
Up	FSTL3	3	5.50E-04	207682	0.203296	0
Up	MN1	3	5.03E-05	16738	0.263547	0
Up	NPY5R	3	5.50E-04	624054	0.23441	0
Up	LEP	3	2.00E-05	6786	0.240079	0
Up	TNFRSF11B	3	5.50E-04	350406	0.174996	0
Up	FGF11	3	5.50E-04	761782	0.20555	0
Up	ESPNL	3	1.27E-06	498	0.203478	0
Up	CLCA2	3	3.05E-04	367670	0.228075	0
Up	PEMT	3	1.59E-04	62928	0.243646	0
Up	IRX2	3	2.77E-04	309966	0.21852	0
Up	STEAP1	3	4.53E-04	352508	0.215429	0
Up	ZNF541	3	2.77E-04	274356	0.247572	0
Up	SOBP	3	2.77E-04	316828	0.222188	0
Up	C1RL	3	1.77E-04	66534	0.262557	0
Up	COL16A1	2	2.04E-05	16970	0.239115	0
Up	PLA2G7	2	2.75E-04	335702	0.24376	0
Up	SAA1	2	2.75E-04	148902	0.195675	0
Up	CTHRC1	2	6.09E-06	4436	0.211849	0
Up	PRG4	2	2.46E-06	14846	0.264835	0
Up	COL5A2	2	6.90E-07	1504	0.240955	0

Up	MXRA5	2	1.03E-06	2100	0.230945	0
Up	TRAM2	2	3.17E-05	31874	0.246623	0
Up	SLC46A3	2	1.00E-05	7956	0.229255	0
Up	CHI3L2	2	3.90E-06	1466	0.215327	0
Up	SAA4	2	4.85E-05	50948	0.190364	0
Up	SEMA3G	2	2.75E-04	257800	0.19568	0
Up	ANGPT1	2	2.61E-06	808	0.214406	0
Up	MGAT3	2	3.91E-05	29366	0.244383	0
Up	ANKDD1A	2	9.60E-07	1688	0.2118	0
Up	CD248	2	6.52E-06	10130	0.239873	0
Up	HOXB8	2	4.46E-06	1564	0.202876	0
Up	AQP11	1	0	0	0.203752	0
Up	STEAP2	1	0	0	1	0
Up	ZCCHC24	1	0	0	0.195664	0
Up	ZNF404	1	0	0	0.216269	0
Up	CADM3	1	0	0	0.193111	0
Up	ADAMTS5	1	0	0	0.183304	0
Up	CLDN15	1	0	0	0.189782	0
Up	FILIP1L	1	0	0	0.203216	0
Up	ERV3-1	1	0	0	0.205306	0
Up	SRPX2	1	0	0	0.200165	0
Up	COL11A1	1	0	0	1	0
Up	DSEL	1	0	0	0.24154	0
Up	CD52	1	0	0	0.213939	0
Down	ESR1	806	0.153485	2.1E+08	0.391884	0.005195
Down	FBL	381	0.043577	81882548	0.346337	0.006492
Down	CSNK2B	292	0.043492	62952016	0.346503	0.003676
Down	ARRB1	284	0.043293	53941490	0.351245	0.003976
Down	PCM1	259	0.045751	77483406	0.325315	2.10E-04
Down	RPS2	258	0.021334	29889924	0.362321	0.041768
Down	NR3C1	253	0.03159	46690102	0.34422	0.002364
Down	ADRB2	250	0.03968	53808532	0.340109	0.001104
Down	RAD21	248	0.03088	38413802	0.337972	0.008732
Down	RPS3	245	0.017178	35272712	0.36097	0.047307
Down	SIRT1	244	0.034146	31338754	0.355876	0.005544
Down	PTEN	241	0.037893	32252050	0.360594	0.011462
Down	RPL14	226	0.013916	21099462	0.354002	0.052738
Down	CSNK2A2	222	0.028742	33637672	0.343584	0.00481
Down	RBBP4	207	0.023381	32706132	0.348164	0.006285
Down	SIN3A	205	0.025789	23294856	0.343942	0.007413
Down	RPL18	200	0.010425	18789086	0.348548	0.0399
Down	EEF1G	198	0.024334	40864084	0.340859	0.004804
Down	RPL18A	180	0.009178	15465286	0.337579	0.031409
Down	EEF1D	170	0.017304	24337902	0.342257	0.008768

Down	KHDRBS1	169	0.021941	22978510	0.341725	0.007448
Down	TSC22D1	165	0.023146	19501674	0.327648	0.002121
Down	ZBTB16	162	0.0213	20359632	0.339647	0.005818
Down	RPS18	160	0.006517	12825590	0.353588	0.103575
Down	FKBP5	159	0.025477	16402018	0.340811	0.002309
Down	RPS9	156	0.008163	14334452	0.355127	0.071795
Down	RBMX	154	0.015786	19978510	0.343454	0.014291
Down	SRSF3	147	0.012702	20302456	0.34695	0.015376
Down	CNBP	143	0.008966	10463900	0.329148	0.030927
Down	GMCL1	142	0.026139	13929296	0.325213	0.001747
Down	DCAF7	133	0.015646	19452348	0.330181	0.005436
Down	RPS27	130	0.006414	10432460	0.333287	0.0774
Down	ANG	125	0.012754	12253912	0.329746	0.005032
Down	RPS15A	122	0.003647	7958980	0.346387	0.091316
Down	RPL21	119	0.003241	7186482	0.343114	0.105541
Down	MCM6	115	0.011128	16694928	0.318021	0.00547
Down	PHGDH	114	0.0116	16787514	0.340651	0.005589
Down	BHLHE40	111	0.016058	12746680	0.327767	0.006116
Down	SRSF7	110	0.005523	11199958	0.334546	0.017515
Down	EIF3H	100	0.007885	9251336	0.3279	0.013662
Down	PCBD1	99	0.013565	10286996	0.325169	0.004296
Down	ERRFI1	98	0.014097	15392316	0.321384	8.77E-04
Down	TRIM33	97	0.009891	16723318	0.319153	0.002464
Down	ZNF581	95	0.01075	17787620	0.300492	0
Down	SAFB	94	0.006963	9017284	0.340875	0.024937
Down	CDKN1B	94	0.00783	14212380	0.324008	6.86E-04
Down	RPL35	94	0.002448	5082406	0.323994	0.07784
Down	RPL17	91	0.003522	6092462	0.336593	0.063004
Down	MAP3K5	91	0.008997	9878956	0.322655	0.005363
Down	EIF4B	89	0.006598	9945562	0.327811	0.009088
Down	MED28	85	0.004511	6219300	0.311861	0.027917
Down	UBE2W	82	0.010803	7628448	0.314508	0.001298
Down	RPS17	82	0.002298	4799800	0.332905	0.080699
Down	RPS12	80	0.002825	4036378	0.339934	0.148734
Down	ACACA	80	0.009068	7691876	0.325782	0.005193
Down	CKB	78	0.006241	16771888	0.309839	0
Down	GTF3C3	74	0.007225	7434672	0.321883	0.011477
Down	SLC3A2	73	0.009036	10552728	0.326294	0.006088
Down	STK24	72	0.007434	10153518	0.312344	4.14E-04
Down	PLSCR4	72	0.010452	7631318	0.296772	3.91E-04
Down	POLR3C	68	0.006634	7596830	0.30519	0.005268
Down	FBX011	68	0.008173	17787740	0.308326	0
Down	RBL2	67	0.005282	4511324	0.319729	0.007237
Down	FOXO3	67	0.004241	7009168	0.320378	0.006731

Down	ORC2	66	0.004554	4837818	0.305152	0.011905
Down	CBS	66	0.006855	10225996	0.306349	9.92E-04
Down	HSD17B11	65	0.012449	11836966	0.310927	0.002404
Down	POLR1D	64	0.00273	1440872	0.29313	0.002016
Down	H1FX	64	0.002945	6401706	0.319223	0.005952
Down	UBR2	63	0.008831	13796534	0.289738	0
Down	INTS6	63	0.005834	15502722	0.296311	0
Down	CCDC59	62	0.004589	3595682	0.314781	0.003702
Down	TRIM24	62	0.006498	4516452	0.324515	0.014689
Down	GLYCTK	62	0.00675	11693046	0.283838	0
Down	NASP	60	0.004695	4623040	0.316744	0.008475
Down	PMP22	60	0.011787	10774698	0.287604	0.00452
Down	FOXO1	60	0.004278	3088194	0.319125	0.02381
Down	RPL29	60	0.001898	2789638	0.330301	0.10113
Down	HDAC9	60	0.00473	3277096	0.320958	0.024436
Down	NRIP1	59	0.004763	3915702	0.331371	0.016949
Down	DPF2	59	0.004275	10395394	0.305408	0
Down	GJA1	57	0.007603	9578982	0.29055	0
Down	MED16	56	0.002612	1962778	0.316648	0.043506
Down	LEMD3	56	0.007232	9603698	0.301829	0
Down	AIP	56	0.006796	11292940	0.298577	0
Down	FABP5	55	0.004222	5751334	0.308588	0.001347
Down	GID8	54	0.006384	5854498	0.309693	0.014329
Down	RPS6KA5	53	0.005533	4215266	0.320053	0.011611
Down	SYT17	52	0.0054	4982314	0.307829	0.004525
Down	MED6	52	0.001798	1731700	0.31349	0.060332
Down	USP13	52	0.004671	3189134	0.31589	0.003771
Down	SRSF4	51	0.001223	4103844	0.29794	0
Down	PPP1R16A	51	0.005746	8058742	0.284528	8.50E-04
Down	MAPRE2	50	0.003825	4616696	0.314468	0.007092
Down	SMIM3	50	0.008337	3707366	0.254227	0.007979
Down	RSBN1	49	0.003391	3832346	0.300418	0.017857
Down	HMGB2	49	0.00357	6132900	0.324501	0.005952
Down	TMOD1	48	0.003984	8904450	0.296299	0
Down	MED30	48	0.001878	1464014	0.312626	0.092754
Down	CTH	47	0.006011	3830276	0.296348	0.00202
Down	HSD17B12	47	0.005085	5578098	0.313937	0.007401
Down	RGS3	47	0.005772	3327954	0.303786	0.004625
Down	TSC22D3	47	0.005191	6455444	0.317965	0.00404
Down	FBP1	46	0.005464	7243238	0.290526	0
Down	HERC5	46	0.002437	2306250	0.315383	0.024313
Down	MAPK10	46	0.004248	3264596	0.315986	0.015504
Down	MLX	46	0.005762	3878434	0.314863	0.008457
Down	RBM15	45	0.002883	3510776	0.316372	0.023256

Down	GINS3	45	0.004967	3943546	0.295371	0.005051
Down	POLR1E	45	0.00356	2068300	0.309074	0.014799
Down	MRPL55	45	0.001429	1326326	0.296215	0.059596
Down	TWIST1	44	0.003116	2544250	0.307347	0.011614
Down	MKNK2	44	0.002816	4837732	0.305216	0
Down	STAG2	44	0.00376	3789932	0.303088	0.019027
Down	LDHD	44	0.006194	16854336	0.276069	0
Down	SMIM1	44	0.004525	9485444	0.238897	0.001057
Down	CASQ2	44	0.004898	4308174	0.281473	0.004228
Down	SCP2	43	0.005135	6506708	0.296869	0
Down	PHLPP1	43	0.004994	3038530	0.311848	0.011074
Down	TRIP4	42	0.001657	1529960	0.313815	0.042973
Down	GMPS	42	0.003893	7262370	0.309693	0.002323
Down	SHMT1	42	0.003936	8051056	0.287866	0
Down	TXNIP	42	0.003899	3198328	0.311567	0.010256
Down	SLC27A2	41	0.004286	7953682	0.281615	0
Down	PLD1	41	0.004575	8671384	0.277281	0
Down	STARD13	41	0.004088	7680918	0.28168	0
Down	H1FO	39	0.002026	5049202	0.307725	0
Down	RPS29	39	0.00166	1696418	0.30281	0.052632
Down	KAT8	39	0.002294	2594188	0.308562	0.009009
Down	PPP3R1	39	0.00613	3752894	0.303013	0.00135
Down	SIVA1	39	0.004978	8423944	0.300654	0
Down	NDRG4	39	0.005926	3321224	0.2663	0.006748
Down	GLUL	38	0.003974	7950262	0.297806	0
Down	YPEL5	38	0.003258	3190842	0.303418	0.027027
Down	NDUFV3	38	0.005051	10700788	0.277578	0
Down	TMEM243	38	0.003169	7642644	0.240719	0
Down	AHCTF1	36	0.003267	9927400	0.285996	0
Down	MPDZ	36	0.004815	7322830	0.289785	0
Down	PELI2	36	0.004349	8786880	0.283738	0
Down	EIF2A	35	0.002235	4455856	0.301228	0
Down	RERE	35	0.002532	3260444	0.288495	0.005042
Down	FAM107A	35	0.001685	2737530	0.280538	0
Down	ADD3	34	0.002352	3903388	0.29566	0
Down	ACVR1	34	0.002812	1540502	0.281615	0.040323
Down	DTNA	34	0.0046	6493716	0.268238	0
Down	BCKDHA	33	0.004981	3209648	0.297989	0.003788
Down	GPHN	33	0.003321	1994352	0.29105	0.004301
Down	ORMDL3	33	0.005211	6879928	0.295263	0
Down	ANK2	32	0.003754	5707286	0.299847	0
Down	LAPTM4B	32	0.004378	5216260	0.279943	0
Down	CMTM7	32	0.003893	6019606	0.23971	0
Down	ELP2	31	0.002629	4968302	0.277706	0

Down	LETMD1	31	0.003704	7124402	0.291132	0
Down	N4BP2L2	30	0.00334	4389434	0.264371	0
Down	ELK1	30	0.002079	2769152	0.300667	0.010582
Down	NR2F1	29	0.002065	959324	0.312505	0.022167
Down	NR4A2	29	0.002998	2829956	0.296215	0.014778
Down	MACROD1	29	0.001235	3532516	0.281375	0
Down	TMEM100	29	0.003454	6768494	0.24397	0
Down	RFX1	28	0.002666	2779366	0.290352	0
Down	TGIF1	28	0.001931	2216518	0.309048	0.011396
Down	RNF38	28	0.001869	2323162	0.295467	0
Down	EEF2K	27	0.001709	1732296	0.300754	0.002849
Down	CENPV	27	7.64E-04	916218	0.300791	0.011396
Down	GPD1L	27	0.0038	2065944	0.287764	0
Down	RTN1	27	0.003472	3693402	0.24963	0.005698
Down	RNF144A	26	0.001768	2193532	0.263097	0
Down	PCCA	26	0.002139	1140242	0.295756	0.003333
Down	AZGP1	26	0.001528	3469730	0.282975	0
Down	CISH	26	0.002792	5275460	0.291085	0
Down	CDS2	26	0.002017	4473790	0.243055	0
Down	UBTD1	26	0.003129	5391322	0.274297	0
Down	CD55	26	0.002437	2011446	0.272956	0.007246
Down	PHIP	25	5.08E-04	1172608	0.287912	0
Down	CD36	25	0.003914	7406080	0.276006	0
Down	S100A1	25	0.002661	2518130	0.289058	0
Down	REV1	25	0.001251	2934360	0.289912	0
Down	MTUS1	25	6.89E-04	974254	0.279404	0
Down	PAPSS1	24	0.002838	1647244	0.29396	0.003623
Down	RSL24D1	24	3.60E-04	545300	0.29578	0.021739
Down	BDH1	24	0.004104	2618626	0.283285	0
Down	PER2	24	0.001282	946214	0.309997	0.039855
Down	GADD45B	24	0.002817	1193404	0.27519	0.007246
Down	RNF125	23	0.001332	1162624	0.296396	0.004762
Down	SOCS2	23	0.001435	940792	0.281702	0.011858
Down	SPSB1	23	0.001434	2592614	0.297867	0
Down	CLDND1	22	0.003682	3938544	0.227122	0
Down	LDHC	22	0.001828	1166582	0.280019	0.004329
Down	MAT2B	22	0.001968	1498338	0.307243	0.004329
Down	SPSB3	21	0.002693	1276008	0.293284	0
Down	FAM207A	21	9.49E-04	884202	0.279835	0
Down	NDFIP2	21	0.002063	1524792	0.302357	0.019048
Down	LSS	20	0.00202	2696762	0.281954	0
Down	FBXO46	20	9.35E-04	2293462	0.275263	0
Down	RHOT1	20	0.001825	2280866	0.282942	0
Down	GPC3	20	0.002147	2749372	0.254762	0

Down	LRRCC1	20	0.002064	854052	0.274826	0.026316
Down	AUTS2	20	9.02E-04	504644	0.298406	0.173684
Down	ZC2HC1A	20	8.63E-04	1221736	0.296784	0
Down	WNT11	20	0.001522	5218644	0.229389	0
Down	EYA1	20	0.001835	2780896	0.275849	0
Down	IGF1	19	0.001837	818638	0.268694	0.006536
Down	CTSC	19	0.001819	3214564	0.267329	0
Down	NBEA	19	0.001923	1417408	0.27439	0
Down	ALDH6A1	19	0.00243	3499248	0.246982	0
Down	FGFRL1	19	0.001946	3042038	0.258913	0
Down	LACTB2	19	0.002624	4365370	0.250026	0
Down	ACACB	18	0.00102	942534	0.30749	0.019608
Down	FADS1	18	0.002153	2374440	0.235818	0
Down	ZFAND5	18	0.001584	2970634	0.287752	0
Down	HOXA10	18	8.32E-04	1820868	0.273049	0
Down	SLC25A23	18	0.003186	2107154	0.292233	0
Down	PXMP2	18	0.001454	638106	0.254905	0
Down	BTG2	18	0.001432	2446066	0.273398	0
Down	HDDC3	18	0.00212	2271936	0.264207	0
Down	ELF2	17	0.00103	1487840	0.297599	0
Down	SNTB1	17	0.001109	1816642	0.234311	0
Down	ZHX2	17	0.001792	2313992	0.272823	0
Down	OSBPL1A	17	8.03E-04	1264296	0.274732	0
Down	AZIN1	17	0.002061	845410	0.287172	0
Down	AGT	17	0.001628	2370886	0.290294	0
Down	BLVRB	16	0.001054	1899696	0.266154	0
Down	PFKFB3	16	7.87E-04	486422	0.305113	0.021978
Down	RTN2	16	0.001709	1185784	0.252319	0.016667
Down	CCNB1IP1	16	7.78E-04	750980	0.293984	0.010989
Down	PDLIM3	15	0.001191	1801652	0.250968	0
Down	MIS18BP1	15	0.002176	783488	0.296553	0.019048
Down	RORB	15	9.28E-04	516190	0.278334	0.038095
Down	PMM1	15	0.001477	1129998	0.249236	0
Down	BCAT2	15	0.001308	1601362	0.275222	0
Down	TBX15	15	0.001199	1804722	0.241335	0
Down	CHN2	14	0.001172	1488748	0.258535	0
Down	GCHFR	14	0.001199	1748870	0.272148	0
Down	MATN2	14	0.001676	2457288	0.229636	0
Down	SERTAD4	14	0.00115	1587264	0.289484	0
Down	CCNF	14	5.90E-04	950744	0.272536	0
Down	TMLHE	14	7.34E-04	588780	0.285422	0
Down	NACAD	14	0.0013	1098172	0.288095	0
Down	PCYT2	14	0.001419	1597954	0.257765	0
Down	C5	14	0.002009	3259876	0.225088	0

Down	ECI1	13	8.42E-04	694090	0.286153	0.012821
Down	ARHGEF3	13	4.02E-04	892554	0.275483	0
Down	FOXN2	13	0.001323	710658	0.293533	0
Down	RFX2	13	0.00122	697206	0.250353	0
Down	BTG3	13	8.16E-04	1023508	0.264323	0
Down	SC5D	12	0.001169	1802206	0.205851	0
Down	PHF3	12	4.47E-04	280086	0.291869	0
Down	EIF4EBP2	12	5.49E-04	527474	0.279147	0
Down	CNRIP1	12	0.001496	1776000	0.258388	0
Down	ZDHHC11	12	8.57E-04	1377474	0.234728	0
Down	CDH23	11	0.0014	2519498	0.242649	0
Down	CCNG2	11	9.91E-04	1771946	0.255013	0
Down	NET1	11	6.54E-04	395582	0.286537	0
Down	TTC32	11	8.95E-04	1167886	0.251716	0
Down	DBP	11	0.001232	1420266	0.250026	0
Down	HYI	11	1.59E-04	237420	0.25304	0
Down	PER3	11	7.84E-04	578572	0.256572	0.036364
Down	MOCS1	10	0.002204	4112338	0.213425	0
Down	IL13RA1	10	0.001567	1617998	0.261449	0
Down	ZNF394	10	9.41E-04	1269642	0.24557	0
Down	CSRNP1	10	7.20E-04	882450	0.280181	0
Down	AASS	10	3.71E-04	610398	0.269382	0
Down	ADNP2	10	5.77E-04	864076	0.283971	0
Down	RFTN2	10	0.001209	2171452	0.231739	0
Down	RAI2	10	7.37E-04	851334	0.268814	0
Down	CAB39L	10	0.001142	1670150	0.243414	0
Down	PRUNE2	9	3.27E-04	759154	0.260885	0
Down	THYN1	9	5.05E-04	704092	0.285523	0
Down	PLCL2	9	0.00111	3025490	0.25565	0
Down	ABTB1	9	4.22E-04	232970	0.282843	0.083333
Down	EFNA1	9	0.001128	792906	0.268555	0.027778
Down	SPATA7	9	6.10E-04	551960	0.275545	0
Down	MKX	9	8.77E-05	153692	0.292587	0.083333
Down	CD302	9	5.79E-05	82832	0.208678	0
Down	STOX1	9	6.94E-04	829352	0.242901	0
Down	DAPK2	9	0.001145	1532140	0.255049	0
Down	GSDMB	8	8.86E-04	639468	0.264602	0
Down	MSRB1	8	5.94E-04	1094210	0.253712	0
Down	PPP1R1B	8	3.53E-04	586750	0.260501	0
Down	FAM214A	8	1.01E-04	112368	0.250595	0
Down	TTLL7	8	1.93E-04	116868	0.28749	0
Down	FAM13A	8	8.98E-04	849488	0.248929	0
Down	CABLES1	7	4.14E-04	563884	0.267773	0
Down	NAALAD2	7	4.58E-04	222398	0.216867	0.047619

Down	ADH1B	7	0.00125	1783716	0.261204	0
Down	CALCRL	7	0.00111	437762	0.187489	0
Down	ZNF395	7	4.70E-05	69798	0.28017	0
Down	PDK4	7	8.39E-04	1826048	0.236833	0
Down	FAM126B	7	3.34E-04	570254	0.284439	0
Down	ST3GAL6	6	8.55E-04	1152862	0.256581	0
Down	RUNDC3B	6	4.17E-04	520596	0.25848	0
Down	FBLN7	6	3.05E-04	519984	0.261195	0
Down	SULF1	6	1.72E-04	242586	0.2663	0
Down	LIX1L	6	3.11E-04	615256	0.253358	0
Down	CIART	6	5.63E-04	638684	0.259311	0
Down	PLIN5	6	8.30E-04	1453450	0.21646	0
Down	RAMP2	6	4.80E-04	195708	0.197799	0
Down	ACSS2	5	2.81E-04	453366	0.241728	0
Down	RNF217	5	2.85E-04	487428	0.239844	0
Down	SRPX	5	2.61E-05	35474	0.269192	0
Down	ACADL	5	3.59E-04	454718	0.258812	0
Down	SFTPD	5	0.001101	1022596	0.195741	0
Down	CYP4V2	5	5.82E-04	277440	0.261515	0
Down	RWDD2A	5	4.43E-05	98420	0.251193	0
Down	TTC38	4	5.49E-06	6228	0.22522	0
Down	GAS1	4	1.09E-04	69102	0.272802	0.166667
Down	ZNF280D	4	6.05E-06	14918	0.242414	0
Down	AACS	4	3.19E-04	524692	0.216847	0
Down	KLF9	4	3.18E-05	25494	0.279544	0.166667
Down	NXNL1	4	3.36E-06	9678	0.242252	0
Down	HLF	4	5.51E-04	279718	0.212831	0
Down	CA3	4	6.16E-05	104110	0.244413	0
Down	PHF13	4	1	12	1	0
Down	SOX17	4	9.55E-06	16194	0.23657	0
Down	LARP6	3	1.86E-05	10288	0.256137	0
Down	FHOD3	3	2.12E-06	5676	0.252284	0
Down	HLA-DMA	3	2.75E-04	1237430	0.181505	0
Down	DMRT2	3	6.54E-06	12390	0.230291	0
Down	LEFTY2	3	5.51E-04	526654	0.2086	0
Down	ELOVL6	3	2.78E-04	223110	0.201097	0
Down	PKD1L2	2	1.32E-06	3454	0.235963	0
Down	GATM	2	2.75E-04	550962	0.189267	0
Down	BEX4	2	2.75E-04	248730	0.202544	0
Down	ZNF334	2	3.94E-06	6896	0.23337	0
Down	ANKRD37	2	7.60E-07	164	0.206471	0
Down	CMTM8	2	1.07E-05	39428	0.259719	0
Down	ADH1C	2	2.75E-04	372628	0.207125	0
Down	SLC4A4	2	1.07E-06	826	0.210456	0

Down	MT1G	2	2.32E-06	1756	0.199533	0
Down	ZFAND1	1	0	0	0.259942	0
Down	DNAJC27	1	0	0	0.217653	0
Down	WNT3	1	0	0	0.204258	0
Down	RNASE4	1	0	0	0.222959	0
Down	DNAH17	1	0	0	0.21384	0
Down	C1QTNF7	1	0	0	0.218748	0

Table 8 Target gene - miRNA interaction table

Regulation	Target gene	Degree	MicroRNA	Regulation	Target gene	Degree	MicroRNA
Up	SOD2	257	hsa-mir-3144-3p	Down	BTG2	247	hsa-mir-6075
Up	CCND1	251	hsa-mir-7706	Down	TXNIP	228	hsa-mir-3194-3p
Up	TUBB2A	193	hsa-mir-7162-3p	Down	MED28	203	hsa-mir-6861-5p
Up	CCND2	179	hsa-mir-5692c	Down	CNBP	197	hsa-mir-4651
Up	TMEM189	146	hsa-mir-548z	Down	MKNK2	195	hsa-mir-3650
Up	SAR1A	145	hsa-mir-3929	Down	DCAF7	174	hsa-mir-550b-2-5p
Up	ZMAT3	145	hsa-mir-5009-3p	Down	CDKN1B	146	hsa-mir-2355-5p
Up	IGFBP5	144	hsa-mir-548az-3p	Down	FAM126B	141	hsa-mir-7703
Up	CYCS	137	hsa-mir-6836-5p	Down	GLUL	126	hsa-mir-7160-5p
Up	CCDC80	135	hsa-mir-6126	Down	HSD17B12	126	hsa-mir-6840-3p
Up	TGFBR2	110	hsa-mir-6758-5p	Down	PTEN	125	hsa-mir-217
Up	MSN	108	hsa-mir-4739	Down	ZNF394	122	hsa-mir-4649-3p
Up	NAV1	108	hsa-mir-7150	Down	KCNK6	117	hsa-mir-4731-5p
Up	CPE	98	hsa-mir-7160-5p	Down	SRSF7	108	hsa-mir-30c-2-3p
Up	THBS1	95	hsa-mir-6825-5p	Down	MED16	104	hsa-mir-30c-1-3p
Up	HOXC8	95	hsa-mir-7111-5p	Down	CCNF	102	hsa-mir-3155b
Up	FAM129B	92	hsa-mir-6855-3p	Down	FOXN2	101	hsa-mir-3133
Up	OSTM1	90	hsa-mir-4794	Down	NR3C1	100	hsa-mir-3609
Up	STC2	90	hsa-mir-206	Down	IGF1	98	hsa-mir-299-3p
Up	HSPA8	86	hsa-mir-5697	Down	SHMT1	97	hsa-mir-4477a
Up	SUSD1	86	hsa-mir-4728-5p	Down	RPS6KA5	95	hsa-mir-4423-5p
Up	DSEL	85	hsa-mir-7977	Down	CBS	94	hsa-mir-6883-5p
Up	STAT3	80	hsa-mir-6833-3p	Down	RNF125	92	hsa-mir-4257
Up	VLDLR	77	hsa-mir-548ad-5p	Down	LDHD	91	hsa-mir-6512-5p
Up	SERPINH1	77	hsa-mir-6808-5p	Down	NDUFV3	91	hsa-mir-548an
Up	BAMBI	76	hsa-mir-3649	Down	RPL14	90	hsa-mir-3960
Up	KCNB1	74	hsa-mir-5695	Down	HMGB2	89	hsa-mir-6894-3p
Up	ERBB2	73	hsa-mir-3921	Down	FKBP5	88	hsa-mir-6852-5p
Up	SLC43A2	70	hsa-mir-6852-5p	Down	ACACA	86	hsa-mir-378d
Up	MAP1B	68	hsa-mir-5697	Down	RPL18A	85	hsa-mir-6784-5p
Up	CALU	67	hsa-mir-1537-5p	Down	RBBP4	84	hsa-mir-5696
Up	BHMT2	67	hsa-mir-520h	Down	HOXA10	83	hsa-mir-7113-3p
Up	CRTAP	67	hsa-mir-1273h-5p	Down	PER2	82	hsa-mir-4433a-3p
Up	RHOC	65	hsa-mir-591	Down	ELP2	80	hsa-mir-7111-3p
Up	GNS	64	hsa-mir-6808-5p	Down	EIF4EBP2	78	hsa-mir-944
Up	WWC1	63	hsa-mir-5697	Down	RPS15A	73	hsa-mir-6720-5p
Up	MXRA7	61	hsa-mir-203a-3p	Down	ESR1	72	hsa-mir-3668
Up	PMEPA1	59	hsa-mir-6879-5p	Down	CD55	71	hsa-mir-6813-3p
Up	AEN	59	hsa-mir-4725-3p	Down	FOXO1	68	hsa-mir-4753-3p
Up	PLXNA1	58	hsa-mir-940	Down	FADS1	68	hsa-mir-3189-5p
Up	GRIN2B	58	hsa-mir-4469	Down	RGMB	67	hsa-mir-5681a
Up	C1RL	57	hsa-mir-3663-3p	Down	RTN2	66	hsa-mir-4680-5p

Up	SGK1	57	hsa-mir-3646	Down	LIX1L	65	hsa-mir-4421
Up	TAGLN2	57	hsa-mir-1972	Down	TGIF1	65	hsa-mir-7-2-3p
Up	YWHAH	55	hsa-mir-6865-3p	Down	FOXO3	64	hsa-mir-5590-3p
Up	SLC35G1	55	hsa-mir-6854-5p	Down	EEF2K	64	hsa-mir-4728-5p
Up	GPR137B	54	hsa-mir-520c-3p	Down	ZNF581	63	hsa-mir-6877-5p
Up	B4GALT5	54	hsa-mir-4306	Down	EFNA1	62	hsa-mir-6893-5p
Up	PTGFRN	53	hsa-mir-6828-3p	Down	RSBN1	57	hsa-mir-548as-5p
Up	SLC2A5	51	hsa-mir-6893-5p	Down	PHF13	55	hsa-mir-7977
Up	PPP2R1B	48	hsa-mir-8082	Down	GMPS	54	hsa-mir-4267
Up	SCIN	48	hsa-mir-3163	Down	ALDH6A1	54	hsa-mir-6847-3p
Up	ZCCHC24	48	hsa-mir-4290	Down	ELK1	54	hsa-mir-4704-3p
Up	HMOX1	47	hsa-mir-4443	Down	H1FO	52	hsa-mir-548ah-5p
Up	PLIN3	45	hsa-mir-4701-3p	Down	DNAH17	51	hsa-mir-4658
Up	AIFM2	44	hsa-mir-6826-5p	Down	BTG3	50	hsa-mir-4509
Up	NABP1	43	hsa-mir-3666	Down	GATM	49	hsa-mir-548bb-3p
Up	STEAP2	43	hsa-mir-6501-3p	Down	TWIST1	49	hsa-mir-4672
Up	TRAM2	43	hsa-mir-3065-3p	Down	DMRT2	48	hsa-mir-1253
Up	HSPA5	42	hsa-mir-4650-3p	Down	PPP3R1	48	hsa-mir-548as-3p
Up	MARCKS	41	hsa-mir-4687-3p	Down	MLX	48	hsa-mir-6747-5p
Up	ADAMTS5	40	hsa-mir-548am-3p	Down	RNF38	47	hsa-mir-3166
Up	SRPX2	40	hsa-mir-3178	Down	RFTN2	46	hsa-mir-3689b-3p
Up	HLA-A	39	hsa-mir-2110	Down	TMEM100	45	hsa-mir-302c-3p
Up	FSTL3	39	hsa-mir-6085	Down	ANG	45	hsa-mir-6839-5p
Up	LYZ	38	hsa-mir-661	Down	LETMD1	45	hsa-mir-6885-3p
Up	QPRT	38	hsa-mir-4755-5p	Down	SPSB1	45	hsa-mir-3924
Up	MFRP	36	hsa-mir-6842-5p	Down	SC5D	44	hsa-mir-4793-3p
Up	KCTD12	35	hsa-mir-6754-3p	Down	SIN3A	44	hsa-mir-1343-5p
Up	SKAP2	35	hsa-mir-4778-5p	Down	MTUS1	43	hsa-mir-4266
Up	CDK14	35	hsa-mir-4533	Down	ZBTB16	43	hsa-mir-6749-3p
Up	KIAA1671	34	hsa-mir-6895-3p	Down	N4BP2L2	43	hsa-mir-3149
Up	CYB561	34	hsa-mir-1827	Down	PFKFB3	43	hsa-mir-4644
Up	CYR61	33	hsa-mir-6516-5p	Down	PDLIM3	43	hsa-mir-4755-3p
Up	EMX2	33	hsa-mir-6867-3p	Down	TMLHE	43	hsa-mir-548ac
Up	ALDH1A3	32	hsa-mir-1185-2-3p	Down	NRIP1	42	hsa-mir-6511a-3p
Up	THY1	32	hsa-mir-4685-3p	Down	ACADL	42	hsa-mir-3689c
Up	CXCL10	31	hsa-mir-767-5p	Down	TRIM33	41	hsa-mir-4768-5p
Up	CCPG1	31	hsa-mir-558	Down	ELOVL6	41	hsa-mir-4252
Up	TAGLN	31	hsa-mir-6785-5p	Down	CABLES1	40	hsa-mir-548t-3p
Up	SOBP	31	hsa-mir-487b-3p	Down	ORMDL3	40	hsa-mir-5695
Up	TPM2	30	hsa-mir-4801	Down	PHIP	38	hsa-mir-4729
Up	CTGF	30	hsa-mir-133b	Down	RNF217	38	hsa-mir-5190
Up	COL1A2	30	hsa-mir-5010-5p	Down	ARRB1	38	hsa-mir-3934-5p
Up	RAB31	30	hsa-mir-3117-5p	Down	SIRT1	37	hsa-mir-4474-5p
Up	HOXB8	30	hsa-mir-129-1-3p	Down	NOP53	36	hsa-mir-3617-5p

Up	RAB9A	30	hsa-mir-6511b-5p	Down	TSC22D3	35	hsa-mir-4639-3p
Up	HAVCR2	30	hsa-mir-1273h-5p	Down	GAS1	35	hsa-mir-5692a
Up	TPST2	29	hsa-mir-7151-3p	Down	CLDND1	35	hsa-mir-1178-5p
Up	COL12A1	28	hsa-mir-6079	Down	AIP	35	hsa-mir-6870-5p
Up	MSC	28	hsa-mir-4745-5p	Down	BHLHE40	34	hsa-mir-7113-5p
Up	CEP19	27	hsa-mir-5688	Down	EIF2A	34	hsa-mir-6790-3p
Up	KLF4	26	hsa-mir-130a-3p	Down	AZIN1	34	hsa-mir-6780b-5p
Up	FRMD6	26	hsa-mir-2276-5p	Down	ERRFI1	34	hsa-mir-3922-5p
Up	SOS1	26	hsa-mir-5571-5p	Down	ZNF395	34	hsa-mir-548o-5p
Up	CORO1C	26	hsa-mir-6751-3p	Down	THYN1	33	hsa-mir-4500
Up	TMEM54	26	hsa-mir-4472	Down	CCDC59	33	hsa-mir-1972
Up	MFAP5	26	hsa-mir-5692b	Down	P3H2	33	hsa-mir-6851-5p
Up	DHDDS	26	hsa-mir-4710	Down	ACVR1	32	hsa-mir-3666
Up	CYB561A3	25	hsa-mir-4433b-3p	Down	ZFAND5	31	hsa-mir-4459
Up	PALLD	24	hsa-mir-1298-5p	Down	MKX	31	hsa-mir-548g-5p
Up	LOX	24	hsa-mir-3591-5p	Down	EIF3H	31	hsa-mir-3187-5p
Up	SAA1	24	hsa-mir-4441	Down	RUNDC3B	31	hsa-mir-5088-3p
Up	S100A11	24	hsa-mir-1207-5p	Down	CDS2	30	hsa-mir-6852-3p
Up	AMOT	23	hsa-mir-6806-3p	Down	LAPTM4B	30	hsa-mir-548x-5p
Up	FTH1	23	hsa-mir-6126	Down	WNT3	30	hsa-mir-6130
Up	VASN	23	hsa-mir-449a	Down	PRUNE2	29	hsa-mir-518a-5p
Up	FBLN2	23	hsa-mir-548am-3p	Down	CCNB1IP1	29	hsa-mir-6770-5p
Up	KLHL30	23	hsa-mir-4695-3p	Down	TTC38	29	hsa-mir-4770
Up	NCKAP5L	22	hsa-mir-4640-5p	Down	PHF3	28	hsa-mir-4530
Up	TIMP1	22	hsa-mir-8059	Down	USP13	28	hsa-mir-548aw
Up	ELN	22	hsa-mir-2115-3p	Down	RFX1	28	hsa-mir-6801-5p
Up	CDR2L	22	hsa-mir-1295b-5p	Down	FAM107A	28	hsa-mir-6749-3p
Up	MMP9	21	hsa-mir-211-5p	Down	RPS9	28	hsa-mir-7111-3p
Up	SNCG	21	hsa-mir-6838-5p	Down	GINS3	28	hsa-mir-3155a
Up	TRIM6	21	hsa-mir-5186	Down	RAD21	27	hsa-mir-4428
Up	SPARC	21	hsa-mir-7855-5p	Down	RPS3	27	hsa-mir-6844
Up	SH3BGRL3	21	hsa-mir-4794	Down	MSRB1	27	hsa-mir-216b-5p
Up	RAB6B	21	hsa-mir-6797-5p	Down	TRIM24	26	hsa-mir-548ap-3p
Up	CYP11A1	21	hsa-mir-6766-5p	Down	PHLPP1	26	hsa-mir-1307-3p
Up	INF2	20	hsa-mir-4646-3p	Down	NASP	26	hsa-mir-3127-3p
Up	CXCL12	20	hsa-mir-7152-3p	Down	NECTIN3	26	hsa-mir-548b-5p
Up	LHX6	20	hsa-mir-5690	Down	RPL9	25	hsa-mir-4729
Up	TMEM98	20	hsa-mir-5590-3p	Down	RPS2	25	hsa-mir-196a-5p
Up	HSPB8	20	hsa-mir-4657	Down	MAPK10	25	hsa-mir-6737-5p
Up	CLIC6	20	hsa-mir-3689e	Down	RWDD2A	25	hsa-mir-548at-3p
Up	EPDR1	19	hsa-mir-374a-5p	Down	RPS27	24	hsa-mir-1260a
Up	STAT1	19	hsa-mir-1183	Down	PER3	24	hsa-mir-4700-5p
Up	IRAK1	18	hsa-mir-1226-3p	Down	SLC25A23	24	hsa-mir-4441
Up	FAM98A	18	hsa-mir-3158-5p	Down	STARD13	24	hsa-mir-219a-1-3p

Up	VGLL3	18	hsa-mir-4252	Down	ADH1B	24	hsa-mir-300
Up	PRSS23	18	hsa-mir-4672	Down	KLF9	23	hsa-mir-6750-3p
Up	PLA2G7	18	hsa-mir-4524b-3p	Down	NDFIP2	23	hsa-mir-664b-3p
Up	CD68	18	hsa-mir-7113-3p	Down	FAM13A	23	hsa-mir-3679-3p
Up	FAR2	18	hsa-mir-3924	Down	MAPRE2	23	hsa-mir-3140-3p
Up	MN1	17	hsa-mir-3667-3p	Down	SRSF3	23	hsa-mir-6860
Up	PLEKH02	17	hsa-mir-6515-3p	Down	UBE2W	22	hsa-mir-5197-3p
Up	ITIH5	17	hsa-mir-4753-3p	Down	SOX17	22	hsa-mir-3118
Up	KANK4	17	hsa-mir-1290	Down	GJA1	21	hsa-mir-1298-5p
Up	TNS3	16	hsa-mir-6071	Down	HLF	21	hsa-mir-664a-3p
Up	DBNDD1	16	hsa-mir-4300	Down	DPF2	20	hsa-mir-5088-3p
Up	SLC46A3	16	hsa-mir-6796-3p	Down	FGFRL1	20	hsa-mir-6790-5p
Up	CHST3	16	hsa-mir-6131	Down	POLR1D	20	hsa-mir-1273e
Up	LRRC32	16	hsa-mir-6779-3p	Down	MAP3K5	20	hsa-mir-4775
Up	SLC22A12	16	hsa-mir-3189-5p	Down	CYP4V2	20	hsa-mir-4324
Up	PCDH9	14	hsa-mir-4635	Down	SNTB1	20	hsa-mir-199b-5p
Up	SMYD2	14	hsa-mir-4516	Down	TTLL7	20	hsa-mir-4677-3p
Up	SCARB1	14	hsa-mir-5091	Down	CD36	20	hsa-mir-6516-3p
Up	MYL9	14	hsa-mir-6764-5p	Down	RPL35	20	hsa-mir-7157-3p
Up	CST3	13	hsa-mir-4768-5p	Down	DNAJC27	19	hsa-mir-27a-3p
Up	NRP2	13	hsa-mir-374c-5p	Down	SERTAD4	19	hsa-mir-6883-3p
Up	CD9	13	hsa-mir-4727-3p	Down	POLR1E	19	hsa-mir-6893-5p
Up	TPGS2	12	hsa-mir-1252-3p	Down	SLC4A4	19	hsa-mir-939-3p
Up	DLGAP4	12	hsa-mir-4768-3p	Down	PCYT2	18	hsa-mir-3960
Up	CRABP2	12	hsa-mir-449b-5p	Down	ADD3	18	hsa-mir-4776-3p
Up	SPATA18	12	hsa-mir-6840-3p	Down	CTH	18	hsa-mir-548s
Up	MFGE8	12	hsa-mir-4442	Down	MARCH3	18	hsa-mir-4715-3p
Up	COL3A1	11	hsa-mir-29c-3p	Down	RSL24D1	18	hsa-mir-4274
Up	MT2A	11	hsa-mir-6823-5p	Down	GTF3C3	17	hsa-mir-6760-5p
Up	ANKDD1A	11	hsa-mir-4695-5p	Down	BDH1	17	hsa-mir-298
Up	PPDPF	11	hsa-mir-5096	Down	PLIN5	17	hsa-mir-6890-3p
Up	LAMA5	11	hsa-mir-1909-3p	Down	PHGDH	17	hsa-mir-4257
Up	SLC24A3	11	hsa-mir-7845-5p	Down	MED30	17	hsa-mir-6130
Up	EGR2	10	hsa-mir-20a-5p	Down	ZFAND1	17	hsa-mir-3622b-5p
Up	PTGER4	10	hsa-mir-20b-5p	Down	SRSF4	17	hsa-mir-6761-5p
Up	ENC1	10	hsa-mir-6733-5p	Down	HDGFL2	17	hsa-mir-2682-5p
Up	C1S	10	hsa-mir-548s	Down	RPL18	16	hsa-mir-4661-3p
Up	SVEP1	10	hsa-mir-6888-5p	Down	RPS17	16	hsa-mir-4433b-5p
Up	TNFRSF12A	9	hsa-mir-92a-1-5p	Down	NR4A2	16	hsa-mir-7157-5p
Up	DAG1	9	hsa-mir-3676-3p	Down	STAG2	16	hsa-mir-3651
Up	GNG2	9	hsa-mir-4713-5p	Down	RORB	16	hsa-mir-4282
Up	SEMA3G	9	hsa-mir-4287	Down	DAPK2	16	hsa-mir-7161-5p
Up	NOTCH3	9	hsa-mir-206	Down	GPR146	16	hsa-mir-660-3p
Up	OAF	9	hsa-mir-6868-3p	Down	SYT17	16	hsa-mir-4311

Up	IRX2	9	hsa-mir-1305	Down	SIVA1	15	hsa-mir-581
Up	FCMR	9	hsa-mir-1260a	Down	TSC22D1	15	hsa-mir-590-3p
Up	CTHRC1	8	hsa-mir-548l	Down	ACACB	15	hsa-mir-6797-3p
Up	RND3	8	hsa-mir-200c-3p	Down	NDRG4	15	hsa-mir-1299
Up	NUP188	8	hsa-mir-7847-3p	Down	PLSCR4	14	hsa-mir-1178-3p
Up	CLPTM1L	8	hsa-mir-4694-3p	Down	SCP2	14	hsa-mir-4776-3p
Up	FAM198B	8	hsa-mir-1273e	Down	GID8	14	hsa-mir-340-5p
Up	TMED3	8	hsa-mir-1260b	Down	SLC3A2	13	hsa-mir-8068
Up	ITGAV	8	hsa-mir-548c-3p	Down	FBXO11	13	hsa-mir-4453
Up	ALCAM	8	hsa-mir-148a-3p	Down	OSBPL1A	13	hsa-mir-5003-3p
Up	GSTM5	8	hsa-mir-6793-3p	Down	MIS18BP1	13	hsa-mir-3679-5p
Up	C1R	8	hsa-mir-6824-3p	Down	FMC1	13	hsa-mir-5095
Up	COL5A2	7	hsa-mir-767-5p	Down	RERE	13	hsa-mir-4763-5p
Up	CD248	7	hsa-mir-4436b-5p	Down	ARHGEF3	13	hsa-mir-4793-5p
Up	LCP1	7	hsa-mir-520a-3p	Down	PMP22	12	hsa-mir-4769-5p
Up	S100A9	7	hsa-mir-4252	Down	ADNP2	12	hsa-mir-5004-5p
Up	ZNF219	7	hsa-mir-7845-5p	Down	STK24	12	hsa-mir-766-3p
Up	TUBB8	7	hsa-mir-5680	Down	BEX4	12	hsa-mir-5580-3p
Up	COL6A1	6	hsa-mir-1301-3p	Down	CKB	11	hsa-mir-551a
Up	ACTN1	6	hsa-let-7e-5p	Down	SLC27A2	11	hsa-mir-7113-3p
Up	HTRA1	6	hsa-mir-6774-5p	Down	RPL21	11	hsa-mir-218-5p
Up	TUBB2B	6	hsa-mir-186-5p	Down	NBEA	11	hsa-mir-9-5p
Up	SPP1	6	hsa-mir-146a-5p	Down	CD302	11	hsa-mir-4690-3p
Up	SYNC	6	hsa-mir-3122	Down	ORC2	11	hsa-mir-6728-3p
Up	CADM3	6	hsa-mir-5689	Down	GMCL1	11	hsa-mir-6864-3p
Up	NEK6	5	hsa-mir-1307-3p	Down	ELF2	11	hsa-mir-190a-3p
Up	UCHL1	5	hsa-mir-181a-5p	Down	AACS	10	hsa-mir-1470
Up	TDP1	5	hsa-mir-320a	Down	LEFTY2	10	hsa-mir-660-3p
Up	LEP	5	hsa-mir-7856-5p	Down	ATP8B4	10	hsa-mir-208b-5p
Up	COL6A2	5	hsa-mir-10a-5p	Down	TRIP4	10	hsa-mir-4728-3p
Up	GPC1	5	hsa-mir-140-3p	Down	RBL2	9	hsa-mir-106a-5p
Up	IFIT2	5	hsa-mir-645	Down	REV1	9	hsa-mir-20b-5p
Up	PLBD2	5	hsa-mir-3607-3p	Down	PCCA	9	hsa-mir-1273e
Up	NPR3	4	hsa-mir-16-5p	Down	RFX2	9	hsa-mir-3131
Up	TNFRSF11B	4	hsa-mir-181a-5p	Down	PCBD1	9	hsa-mir-5584-5p
Up	FGF11	4	hsa-mir-193b-3p	Down	TBX15	9	hsa-mir-5582-5p
Up	CMTM3	4	hsa-mir-24-3p	Down	ZC2HC1A	9	hsa-mir-1914-3p
Up	ANO3	4	hsa-mir-186-5p	Down	EIF4B	8	hsa-mir-423-3p
Up	COL15A1	4	hsa-mir-29b-3p	Down	RPS12	8	hsa-mir-181b-5p
Up	SFRP4	4	hsa-mir-103a-3p	Down	STK26	8	hsa-mir-5000-5p
Up	PDLIM1	4	hsa-mir-504-5p	Down	INTS6	8	hsa-mir-4317
Up	PYGL	4	hsa-mir-155-5p	Down	KHDRBS1	8	hsa-mir-27b-3p
Up	FAM171A1	4	hsa-mir-124-3p	Down	PELI2	8	hsa-mir-151a-5p
Up	ABCC3	4	hsa-mir-197-3p	Down	RPL29	8	hsa-mir-92a-1-5p

Up	SPTAN1	4	hsa-mir-128-3p	Down	MAT2B	7	hsa-mir-377-3p
Up	FAT1	4	hsa-mir-222-3p	Down	ST3GAL6	7	hsa-mir-6868-3p
Up	NMT2	4	hsa-mir-181d-5p	Down	FBXO46	7	hsa-mir-513a-5p
Up	STK38L	4	hsa-mir-130a-3p	Down	SAFB	6	hsa-mir-1229-3p
Up	FRZB	4	hsa-mir-30b-5p	Down	PDK4	6	hsa-mir-182-5p
Up	TM4SF19	4	hsa-mir-550a-3p	Down	RPL17	6	hsa-mir-519d-3p
Up	TNFAIP6	4	hsa-mir-19b-2-5p	Down	LEMD3	6	hsa-mir-10b-5p
Up	C3orf14	4	hsa-mir-6072	Down	CAB39L	6	hsa-mir-10a-5p
Up	ITGB5	3	hsa-let-7b-5p	Down	MCM6	6	hsa-mir-1180-3p
Up	LAMB3	3	hsa-mir-218-5p	Down	RHOT1	5	hsa-mir-15a-5p
Up	PLPP1	3	hsa-mir-124-3p	Down	HDHD5	5	hsa-mir-484
Up	LBP	3	hsa-mir-22-3p	Down	NET1	5	hsa-mir-320a
Up	GLS	3	hsa-mir-7-5p	Down	KAT14	5	hsa-mir-5196-3p
Up	ITGB2	3	hsa-mir-146a-5p	Down	RPS18	5	hsa-mir-421
Up	CXCL9	3	hsa-mir-34a-5p	Down	LSS	5	hsa-mir-30a-5p
Up	RAB7B	3	hsa-mir-92b-3p	Down	BCAT2	5	hsa-mir-615-3p
Up	CFB	3	hsa-mir-210-5p	Down	FAM214A	5	hsa-mir-222-3p
Up	MSTO1	3	hsa-mir-10b-5p	Down	CCNG2	5	hsa-mir-93-3p
Up	DOCK6	3	hsa-mir-361-5p	Down	CTSC	5	hsa-mir-199a-5p
Up	SYNPO2	3	hsa-mir-144-5p	Down	SOCS2	4	hsa-mir-16-5p
Up	CCDC107	3	hsa-mir-5193	Down	GPD1L	4	hsa-mir-210-3p
Up	GLB1	2	hsa-mir-155-5p	Down	RNF144A	4	hsa-mir-24-3p
Up	APLNR	2	hsa-mir-16-5p	Down	RGS3	4	hsa-mir-133a-3p
Up	FMOD	2	hsa-mir-21-5p	Down	CISH	4	hsa-mir-150-5p
Up	FILIP1L	2	hsa-mir-335-5p	Down	S100A1	4	hsa-mir-138-5p
Up	PDGFD	2	hsa-mir-145-5p	Down	RPS29	4	hsa-mir-652-3p
Up	HSD11B1	2	hsa-mir-26b-5p	Down	EEF1D	4	hsa-mir-149-5p
Up	GPNMB	2	hsa-mir-508-5p	Down	CNRIP1	4	hsa-mir-3977
Up	PCBP3	2	hsa-mir-26b-5p	Down	ANK2	4	hsa-mir-122-5p
Up	HSPA12A	2	hsa-mir-339-5p	Down	ZNF280D	4	hsa-mir-505-5p
Up	MGST1	2	hsa-mir-652-3p	Down	TMOD1	4	hsa-mir-1185-1-3p
Up	AKR1C3	2	hsa-mir-98-5p	Down	WNT11	4	hsa-mir-5580-3p
Up	FAM189A2	2	hsa-mir-192-5p	Down	LACTB2	3	hsa-mir-30c-5p
Up	INHBB	2	hsa-mir-34a-5p	Down	FBL	3	hsa-mir-20a-5p
Up	SLIT2	2	hsa-mir-330-3p	Down	PLD1	3	hsa-mir-638
Up	FLNC	2	hsa-mir-1-3p	Down	AUTS2	3	hsa-mir-21-5p
Up	SHTN1	2	hsa-mir-106b-5p	Down	PCM1	3	hsa-mir-8055
Up	MFAP4	2	hsa-mir-449a	Down	H1FX	3	hsa-mir-1-3p
Up	WISP2	2	hsa-mir-124-3p	Down	MED6	3	hsa-mir-199a-3p
Up	GLIPR2	2	hsa-mir-155-5p	Down	RNASE4	3	hsa-mir-215-5p
Up	CYTOR	2	hsa-mir-376c-3p	Down	RBMX	3	hsa-mir-196a-5p
Up	GALNT16	2	hsa-mir-140-5p	Down	GPC3	3	hsa-mir-1271-5p
Up	LHCGR	2	hsa-mir-513a-3p	Down	HDAC9	3	hsa-mir-29a-5p
Up	LAMB2	2	hsa-mir-196b-5p	Down	PAPSS1	2	hsa-mir-100-5p

Up	IRF8	2	hsa-mir-646	Down	GPHN	2	hsa-let-7b-5p
Up	NRCAM	2	hsa-mir-4282	Down	AHCTF1	2	hsa-mir-186-5p
Up	SULT1A1	1	hsa-mir-631	Down	CENPV	2	hsa-mir-28-5p
Up	CLCA2	1	hsa-let-7b-5p	Down	RAI2	2	hsa-let-7e-5p
Up	AOX1	1	hsa-mir-26b-5p	Down	EEF1G	2	hsa-mir-218-5p
Up	GRB14	1	hsa-mir-26b-5p	Down	ECI1	2	hsa-mir-155-5p
Up	TYMP	1	hsa-mir-92a-3p	Down	BLVRB	2	hsa-mir-127-5p
Up	HBB	1	hsa-mir-92a-3p	Down	MPDZ	2	hsa-mir-26b-5p
Up	CES1	1	hsa-mir-197-3p	Down	HSD17B11	2	hsa-mir-1-3p
Up	MYEOV	1	hsa-mir-7-5p	Down	EYA1	2	hsa-mir-101-3p
Up	COL16A1	1	hsa-mir-181a-5p	Down	LRRCC1	2	hsa-mir-215-5p
Up	LRRN3	1	hsa-mir-181a-5p	Down	C5	2	hsa-mir-10a-5p
Up	S100A4	1	hsa-mir-187-3p	Down	NR2F1	2	hsa-mir-149-5p
Up	ALPL	1	hsa-mir-204-5p	Down	CA3	2	hsa-mir-1-3p
Up	CCL3L3	1	hsa-mir-215-5p	Down	CSNK2A2	2	hsa-mir-1228-3p
Up	LMO2	1	hsa-mir-223-3p	Down	HERC5	2	hsa-mir-3529-3p
Up	ADAMTSL4	1	hsa-mir-1-3p	Down	PXMP2	2	hsa-mir-15b-5p
Up	TNFRSF25	1	hsa-mir-124-3p	Down	SULF1	2	hsa-mir-516a-3p
Up	MVP	1	hsa-mir-124-3p	Down	ABTB1	2	hsa-mir-125b-5p
Up	PEMT	1	hsa-mir-124-3p	Down	IL13RA1	2	hsa-mir-143-3p
Up	UNC13C	1	hsa-mir-128-3p	Down	BCKDHA	2	hsa-mir-29c-3p
Up	IL1RN	1	hsa-mir-125a-5p	Down	ZDHHC11	2	hsa-mir-375
Up	CFH	1	hsa-mir-146a-5p	Down	UBR2	2	hsa-mir-5580-3p
Up	CARMIL1	1	hsa-mir-149-5p	Down	GSDMB	2	hsa-mir-5692a
Up	RARRES3	1	hsa-mir-30e-3p	Down	AASS	2	hsa-mir-591
Up	AQP11	1	hsa-mir-375	Down	AGT	1	hsa-mir-26b-5p
Up	ESPNL	1	hsa-mir-375	Down	SRPX	1	hsa-mir-26b-5p
Up	ZNF404	1	hsa-mir-375	Down	C17orf53	1	hsa-mir-26b-5p
Up	CALB2	1	hsa-mir-335-5p	Down	GCHFR	1	hsa-mir-92a-3p
Up	CHI3L2	1	hsa-mir-335-5p	Down	TTC32	1	hsa-mir-92a-3p
Up	COL11A1	1	hsa-mir-335-5p	Down	FAM207A	1	hsa-mir-107
Up	MGAT3	1	hsa-mir-335-5p	Down	ZHX2	1	hsa-mir-139-5p
Up	PLTP	1	hsa-mir-335-5p	Down	PLCL2	1	hsa-mir-181a-5p
Up	PTGDS	1	hsa-mir-335-5p	Down	MACROD1	1	hsa-mir-1-3p
Up	CLEC3B	1	hsa-mir-335-5p	Down	HYI	1	hsa-mir-1-3p
Up	LMOD1	1	hsa-mir-335-5p	Down	PPP1R16A	1	hsa-mir-1-3p
Up	CLIP3	1	hsa-mir-335-5p	Down	CALCRL	1	hsa-mir-124-3p
Up	SLC2A10	1	hsa-mir-335-5p	Down	CMTM7	1	hsa-mir-124-3p
Up	RSP03	1	hsa-mir-335-5p	Down	AZGP1	1	hsa-mir-128-3p
Up	TMEM178A	1	hsa-mir-335-5p	Down	CASQ2	1	hsa-mir-128-3p
Up	GPBAR1	1	hsa-mir-335-5p	Down	C9orf72	1	hsa-mir-142-3p
Up	SULT1A3	1	hsa-mir-18a-3p	Down	MOCS1	1	hsa-mir-320a
Up	MBP	1	hsa-mir-127-5p	Down	FBLN7	1	hsa-mir-377-3p
Up	EFEMP1	1	hsa-mir-338-5p	Down	GPR34	1	hsa-mir-335-5p

	Down	HLA-DMA	1	hsa-mir-335-5p
	Down	SFTPD	1	hsa-mir-335-5p
	Down	NAALAD2	1	hsa-mir-335-5p
	Down	CPAMD8	1	hsa-mir-335-5p
	Down	YPEL5	1	hsa-mir-335-5p
	Down	ZNF334	1	hsa-mir-335-5p
	Down	ACSS2	1	hsa-mir-335-5p
	Down	STOX1	1	hsa-mir-335-5p
	Down	COQ8A	1	hsa-mir-484
	Down	TMEM243	1	hsa-mir-484
	Down	HACD1	1	hsa-mir-652-3p
	Down	LARP6	1	hsa-mir-652-3p
	Down	PPM1M	1	hsa-mir-744-5p
	Down	CMTM8	1	hsa-mir-877-5p
	Down	GLYCTK	1	hsa-mir-940
	Down	FHOD3	1	hsa-mir-1303
	Down	HDDC3	1	hsa-mir-4708-3p
	Down	DTNA	1	hsa-mir-8485

Degree – No of miRNA interact with target gene. We taken any one miRNA in table.

Table 9 Target gene - miRNA interaction table

	TF	Degree		TF	Degree		
Regulation			Target gene	Regulation		Target gene	
Up	MAZ	70	YWHAH	Down	TFDP1	91	EFNA1
Up	TFDP1	62	LYZ	Down	MAZ	85	MED16
Up	KLF9	60	HP	Down	KDM5B	82	RWDD2A
Up	KLF16	54	TRAM2	Down	SAP30	82	ADD3
Up	EZH2	51	CCND1	Down	PHF8	82	AIP
Up	MXD4	49	OAF	Down	SMAD5	77	CCNF
Up	SAP30	49	CCDC107	Down	ZNF76	72	ANG
Up	PHF8	49	CEP19	Down	ZNF580	69	DBP
Up	KDM5B	49	HOXB8	Down	SP1	68	BCKDHA
Up	HBP1	48	TNFRSF12A	Down	ZNF24	66	HMGB2
Up	ZNF580	48	BAMBI	Down	ELF1	65	GADD45B
Up	ZNF76	48	CRABP2	Down	GTF2E2	65	ZFAND1
Up	SIN3A	47	STAT3	Down	ZFP2	60	SERTAD4
Up	ZNF24	47	SH3BGR13	Down	POLR2A	60	KHDRBS1
Up	NR2F6	45	NRCAM	Down	KLF16	59	FBXO46
Up	MXD3	45	OSGIN1	Down	HBP1	58	LSS
Up	ATF1	44	LEP	Down	CREB3L1	58	KAT8
Up	ZBTB11	44	HSPA8	Down	CHD1	58	EIF4B
Up	ZNF423	44	TUBB2B	Down	KLF7	57	CTH
Up	NRF1	43	DBNDD1	Down	REST	56	MIS18BP1
Up	SSRP1	42	PLTP	Down	ATF1	56	CCNB1IP1
Up	TGIF2	42	FAM98A	Down	IRF1	56	TRIM24
Up	GLIS2	42	TAGLN2	Down	ZNF501	55	HNRNPA1P10
Up	ZBTB7A	41	ADAMTSL4	Down	MYNN	55	FOXO3
Up	ELF1	41	NCKAP5L	Down	ZBTB11	54	MOCS1
Up	ZBTB26	40	MT2A	Down	ZBTB7A	54	FOXO1
Up	SMAD5	40	MYEOV	Down	KLF11	53	HLF
Up	ARID4B	39	TLE2	Down	ZNF71	53	NR2F1
Up	KLF11	38	PLEKH02	Down	SSRP1	52	HLA-DMA
Up	RXRB	38	CFB	Down	TAF7	52	ZNF581
Up	ZBTB33	38	CD68	Down	NR2F6	52	ANKRD37
Up	NR4A1	38	FTH1	Down	HMGN3	51	BCAT2
Up	TFE3	38	B4GALT5	Down	ZFX	51	H1F0
Up	ZFX	38	NEK6	Down	ZNF324	51	PTEN
Up	SOX13	37	INF2	Down	ZEB1	51	GCHFR
Up	HIC1	37	AIFM2	Down	MXD3	50	LETMD1
Up	DMAP1	36	ABCC3	Down	TGIF2	50	H1FX
Up	SP2	36	FGF11	Down	KLF8	50	KLF8
Up	THRB	36	AEN	Down	NRF1	49	ORMDL3
Up	NR2F1	36	NANOS3	Down	BCL11B	49	HOXA10
Up	KLF1	36	ELMOD3	Down	BCL11A	48	FBL
Up	IRF1	36	RHOC	Down	MXD4	47	LDHD

Up	GATAD1	36	SULT1A1	Down	KLF1	47	KLF9
Up	ZFP37	36	LOX	Down	ZFP37	47	BCKDHA
Up	BCOR	36	ERV3-1	Down	ZNF335	45	AASS
Up	ZFP64	35	HNMT	Down	WT1	45	ELF2
Up	MYNN	34	MARCKS	Down	ZNF423	45	MRPL55
Up	CHD1	34	IRX2	Down	SMARCA5	45	NASP
Up	DRAP1	34	QPRT	Down	E2F5	45	FADS1
Up	BCL11B	34	TYMP	Down	SP2	45	MSRB1
Up	HDGF	34	S100A3	Down	NFRKB	45	CDKN1B
Up	ZNF2	34	VLDLR	Down	ZNF610	44	HDHC3
Up	HMG20B	33	SOS1	Down	NFYC	44	TTC38
Up	MBD1	33	ZNF219	Down	ID3	43	EPB41L4A-AS1
Up	GTF2E2	33	TM4SF19	Down	ETV4	43	ERRFI1
Up	WRNIP1	33	LRRC32	Down	DMAP1	42	RNF125
Up	MLLT1	33	CCND2	Down	EGR1	42	FOXN2
Up	SP1	33	SLC7A4	Down	SP3	42	EYA1
Up	CTCF	33	ALCAM	Down	IRF4	42	SIN3A
Up	KLF8	33	NOTCH3	Down	FOXM1	42	RFX1
Up	ETV4	33	MXRA7	Down	WRNIP1	42	ST3GAL6
Up	TEAD1	32	NCKAP5L	Down	FOXJ2	42	UBR2
Up	SMAD4	32	CD248	Down	NR2C2	41	UBE2W
Up	REST	32	CDR2L	Down	ZBTB26	41	ZHX2
Up	NR2C2	32	CCPG1	Down	INSM2	41	S100A1
Up	EGR1	32	FSTL3	Down	ZNF639	40	LIX1L
Up	ZNF610	32	LMOD1	Down	SP7	40	LAPTM4B
Up	IRF4	32	CLIP3	Down	PPARG	40	MARCH3
Up	FOXM1	32	COL16A1	Down	GABPA	40	INTS6
Up	GATA4	32	AQP11	Down	YY1	39	PER2
Up	KLF7	32	CALU	Down	HCFC1	39	ORC2
Up	ZNF501	32	RSPO3	Down	BCOR	39	MED28
Up	ELK1	32	TPM2	Down	ARID4B	39	PCM1
Up	ZFP2	32	CD9	Down	GATAD1	38	TXNIP
Up	KDM1A	31	KIAA1671	Down	CTCF	38	WNT11
Up	E2F5	31	DOCK6	Down	CREM	38	MLX
Up	POLR2A	31	HBB	Down	ELF3	38	NR3C1
Up	SMARCA5	31	GPNMB	Down	CCNT2	38	RBMX
Up	FOSL1	31	LAMB2	Down	NR4A1	37	CISH
Up	CREB3L1	31	ZCCHC24	Down	RFXANK	37	LDHD
Up	TFAP4	30	DLGAP4	Down	KLF6	37	CD55
Up	RCOR2	30	GLS	Down	NCOR1	37	RBM15
Up	ZNF341	30	KLHL30	Down	HMG20B	36	CABLES1
Up	ZNF175	30	CXCL10	Down	ZNF101	36	PCCA
Up	ZEB1	30	EMX2	Down	SMAD4	36	SIVA1
Up	BCL11A	30	C4orf48	Down	GTF2F1	36	STAG2

Up	SOX5	29	ERBB2	Down	POLR2H	36	RBBP4
Up	ZNF644	29	LBP	Down	TFAP4	35	DCAF7
Up	ZNF589	29	HSD11B1	Down	GATA4	35	CSNK2B
Up	ZNF197	29	DAG1	Down	TRIM28	35	ZC2HC1A
Up	RERE	29	ENC1	Down	MBD1	35	DNAJC27
Up	PPARG	29	CRABP2	Down	HIC1	35	ECI1
Up	NFRKB	29	SKAP2	Down	KDM5A	35	GMPS
Up	RAD21	29	SULT1A2	Down	RXRB	35	MT1G
Up	RFXANK	29	DLGAP4	Down	GMEB2	35	YPEL5
Up	INSM2	29	MVP	Down	ZNF644	35	CD302
Up	TEAD3	28	WWC1	Down	KLF13	35	ZNF394
Up	HMG3	27	PPDPF	Down	ZNF18	35	ZNF334
Up	CBFB	27	LCP1	Down	GLIS2	33	PPP1R1B
Up	SP3	27	GPR137B	Down	ZBTB33	33	STOX1
Up	ZNF639	27	HSPA5	Down	L3MBTL2	33	THYN1
Up	ID3	27	MMP9	Down	ZBTB40	33	RNF144A
Up	RARA	26	MFAP4	Down	ESRRA	33	ZFAND5
Up	IKZF1	26	S100A4	Down	CBFB	33	CBFB
Up	ZNF71	26	MN1	Down	NCOA1	33	ZNF280D
Up	NFYC	26	SOD2	Down	TFE3	33	C17orf53
Up	CEBPG	26	CDK14	Down	TEAD3	32	RPS2
Up	NFIA	25	LAMA5	Down	TARDBP	32	RPS3
Up	EED	25	IRF8	Down	MLLT1	32	STARD13
Up	MTA2	25	SAA1	Down	HDGF	32	RPS12
Up	SP7	25	HOXC8	Down	ETV1	32	SRSF4
Up	GABPA	25	C3orf14	Down	ZNF2	32	AUTS2
Up	NFIL3	25	NQO1	Down	ATF3	31	RHOT1
Up	SIRT6	24	TNFRSF12A	Down	SOX13	31	GPHN
Up	SMARCA4	24	SMYD2	Down	ZNF341	31	RPS9
Up	GATAD2A	24	DBNDD1	Down	RNF2	31	SOCS2
Up	ELF3	23	SLX1A-SULT1A3	Down	SOX5	31	PCYT2
Up	FOSL2	23	PALLD	Down	MEF2D	31	RTN2
Up	MLX	23	PLTP	Down	GLI4	31	NDUFV3
Up	NCOR1	23	LCP1	Down	EZH2	31	TWIST1
Up	ZNF394	23	TYROBP	Down	ZFP64	30	DCAF7
Up	EBF1	23	VASN	Down	TRIM22	30	FAM207A
Up	WT1	23	NAV1	Down	ETS1	30	SPSB3
Up	TAF7	23	CYR61	Down	TSHZ1	30	NR2F1
Up	ZNF324	23	RAB9A	Down	THRB	29	PPM1M
Up	CTBP2	23	FAT1	Down	LEF1	29	CSRNP1
Up	HDAC1	23	SH3BGR13	Down	DDX20	29	DBP
Up	HMG20A	22	SAA4	Down	CEBPG	29	POLR1E
Up	ZKSCAN1	22	SPARC	Down	USF2	29	RPS27
Up	ETV1	22	SDSL	Down	NFIA	29	SPATA7

Up	ZNF584	22	RARRES3	Down	DRAP1	29	RNASE4
Up	GTF2F1	22	RND3	Down	ZNF589	28	MOCS1
Up	L3MBTL2	22	AMOT	Down	ZNF384	28	USP13
Up	BCL6	22	HLA-A	Down	ZNF83	28	SRSF3
Up	ATF3	21	CFH	Down	GATAD2A	28	TTC32
Up	YY1	21	BHMT2	Down	KDM1A	27	ACSS2
Up	SMARCE1	21	MGST1	Down	BCL6	27	INTS6
Up	LEF1	21	LMO2	Down	FOSL1	27	RPL29
Up	ZBTB40	21	HBA1	Down	RAD21	27	TMEM100
Up	DPF2	20	PLBD2	Down	ZNF263	27	RPL35
Up	ADNP	20	COL15A1	Down	RARA	27	FKBP5
Up	TRIM28	20	CYCS	Down	GLIS1	27	RUNDC3B
Up	CREM	20	CTHRC1	Down	SMARCE1	27	UBR2
Up	KLF6	20	LCP1	Down	ZNF366	26	TMOD1
Up	ARID1B	20	SLC35G1	Down	ZNF175	26	TXNIP
Up	FOXA3	19	HAVCR2	Down	ZNF382	26	NASP
Up	GLIS1	19	FGF11	Down	RCOR2	26	ORMDL3
Up	SUZ12	19	SFRP4	Down	PRDM10	26	AZIN1
Up	NR2F2	19	INF2	Down	SIRT6	25	TGIF1
Up	THAP1	19	MYL9	Down	SMARCA4	25	BLVRB
Up	ZNF335	19	EGR2	Down	RERE	25	RPL29
Up	BHLHE40	19	TAGLN2	Down	ZNF197	25	GMPS
Up	TRIM22	19	CHI3L2	Down	MTA1	25	CNBP
Up	GATA2	19	TRAM2	Down	ADNP	25	FBL
Up	ESRRA	19	TLE2	Down	ZKSCAN1	24	RPL18
Up	POLR2H	18	TDP1	Down	NFIL3	24	AHCTF1
Up	FOXJ2	18	APLNR	Down	JUND	24	DTNA
Up	ZNF18	18	HOXC8	Down	ARID1B	23	GLUL
Up	CUX1	18	TMED3	Down	PBX2	22	MRPL55
Up	GFI1B	18	RAB31	Down	ARNT	22	FADS1
Up	ETS1	18	NRP2	Down	HDAC1	22	TSC22D3
Up	ZHX2	18	GLS	Down	IKZF1	22	RPL18A
Up	MEF2D	18	DBNDD1	Down	GATA2	22	GMCL1
Up	ZNF121	17	TYROBP	Down	MYBL2	21	MT1G
Up	TBX21	17	MSC	Down	MBD4	21	GPHN
Up	ZNF263	16	TIMP1	Down	HNF4G	21	ACACB
Up	PRDM1	16	RND3	Down	CREB1	21	ERRFI1
Up	CREB1	16	PYGL	Down	SIN3B	21	ALDH6A1
Up	ZNF623	16	ZNF404	Down	EED	21	AIP
Up	ZNF382	15	RSPO3	Down	CTBP2	21	SOX17
Up	MTA1	15	KLF4	Down	IRF2	21	CCDC59
Up	SUPT5H	15	HMOX1	Down	GTF2A2	21	H1FX
Up	MBD2	15	WISP2	Down	FOXA3	21	EEF2K
Up	RNF2	15	PPP2R1B	Down	STAT1	21	RSL24D1

Up	JUND	15	OXT	Down	SCRT1	20	ORC2
Up	PBX2	15	PPFIBP2	Down	GFI1B	20	EYA1
Up	HNF4G	14	OAF	Down	ZNF146	20	LARP6
Up	MYBL2	14	LBP	Down	MXI1	20	ANKRD37
Up	MBD4	14	SAA4	Down	MBD2	20	BTG2
Up	TRIM24	14	MYEOV	Down	MIXL1	20	HNRNPA1P10
Up	RELA	14	DLGAP4	Down	CREB3	20	BHLHE40
Up	DDX20	14	MIR3188	Down	BACH1	20	CISH
Up	GTF2A2	14	CCDC80	Down	ZNF623	20	HLA-DMA
Up	SMC3	14	CYB561	Down	ZNF207	20	YPEL5
Up	TSHZ1	14	CRIP1	Down	SUZ12	20	FAM107A
Up	TARDBP	14	MIR3188	Down	SUPT5H	19	RPL35
Up	PKNOX1	13	TM4SF19	Down	MAX	19	RPL18
Up	KLF13	13	TRAM2	Down	JUNB	19	RPL14
Up	TCF7	13	FLNC	Down	HES1	19	RHOT1
Up	PRDM10	13	FILIP1L	Down	TBX21	18	ARHGEF3
Up	BACH1	13	RARRES3	Down	TEAD1	18	FOXN2
Up	MIXL1	13	TM4SF19	Down	ZBTB17	18	HOXA10
Up	CREB3	13	NUP188	Down	HMBX1	18	RBMX
Up	GLI4	13	MXRA7	Down	ZNF584	18	MOCS1
Up	HCFC1	13	PMEP1A	Down	ZNF121	18	SRSF7
Up	CCNT2	12	LAMA5	Down	ZNF143	17	ADD3
Up	HMBX1	12	FAM189A2	Down	PRDM1	17	PTEN
Up	GMEB2	12	TDP1	Down	ATF4	17	N4BP2L2
Up	ARNT	11	CLDN15	Down	HMG20A	17	NET1
Up	ZNF143	11	ERV3-1	Down	RAD51	17	PHF3
Up	KDM5A	11	MMP9	Down	RELA	17	LEFTY2
Up	ZNF366	11	IGFBP6	Down	MYC	17	EIF4B
Up	RCOR1	11	AQP11	Down	EGR2	16	TGIF1
Up	MXI1	11	DLGAP4	Down	EBF1	16	GPR146
Up	ZNF207	11	ZNF219	Down	ZNF239	16	BLVRB
Up	DEK	11	S100A4	Down	PML	16	CSNK2B
Up	ZNF101	11	CD68	Down	THRAP3	16	ELOVL6
Up	HDAC6	11	CXCL12	Down	ZBTB1	16	LSS
Up	HDAC2	11	ESPNL	Down	THAP1	15	AGT
Up	NCOA1	11	CRTAP	Down	NR2F2	15	KLF9
Up	ZNF558	11	TUBB2B	Down	KLF4	15	WNT11
Up	USF2	11	KCNB1	Down	MTA2	15	STARD13
Up	ZNF7	11	ITGB5	Down	ZNF558	15	BCAT2
Up	ZNF384	10	LYZ	Down	SMC3	15	C17orf53
Up	SREBF2	10	LAMB3	Down	CDC5L	15	RPS27
Up	RUNX3	10	PLEKH02	Down	PKNOX1	14	ZNF394
Up	SPI1	10	SH3BGL3	Down	TCF7	14	PHF13
Up	ZBTB1	10	COL6A1	Down	NFE2	14	BHLHE40

Up	MAFK	10	MVP	Down	SREBF2	13	KHDRBS1
Up	ZNF83	10	RHOC	Down	FOXA2	13	BEX4
Up	MYC	10	VASN	Down	CEBPD	13	RNF144A
Up	NFIC	10	HNMT	Down	TEAD4	13	RPS9
Up	RAD51	10	LEP	Down	MITF	13	NR4A2
Up	CTBP1	9	SOBP	Down	ZNF7	12	GSDMB
Up	ZBTB17	9	BAMBI	Down	RFX3	12	MED16
Up	CEBPA	9	TUBB2A	Down	DNMT1	12	DBP
Up	ATF4	9	C1S	Down	FOSL2	12	RSBN1
Up	TAL1	9	SLC7A4	Down	CTBP1	11	FOXO3
Up	RFX1	9	STAT3	Down	HDAC6	11	PCM1
Up	MAX	9	CCND2	Down	HDAC2	11	GADD45B
Up	STAT1	9	FSTL3	Down	RCOR1	11	RPS27
Up	RFX3	9	TAGLN2	Down	TBP	11	ANG
Up	SCRT1	8	MAP1B	Down	ZNF641	11	SIN3A
Up	THRAP3	8	HBB	Down	ZNF407	11	NXNL1
Up	HHEX	8	ELMOD3	Down	CUX1	11	CKB
Up	GATA1	8	RAB6B	Down	MAFK	11	LAPTM4B
Up	PRDM2	8	C1R	Down	EP300	11	RBMX
Up	NFE2	8	SH3BGRL3	Down	CEBPA	11	LEMD3
Up	FOXK2	8	ERBB2	Down	GTF2B	11	RPS29
Up	JUNB	7	TMEM98	Down	CBX8	10	PELI2
Up	DNMT1	7	TNFRSF12A	Down	FOXK2	10	KLF9
Up	ZNF146	7	TUBB2B	Down	GATA1	10	PLCL2
Up	CDC5L	7	TUBB2A	Down	PRDM2	10	PCYT2
Up	TBX3	7	HNMT	Down	HHEX	9	CTH
Up	FOS	7	VGLL3	Down	ZHX1	9	MKNK2
Up	CEBPB	6	AIFM2	Down	ZNF217	8	TRIM33
Up	ZNF407	6	APLNR	Down	TAL1	8	CD55
Up	CEBPD	6	TRIM6	Down	HDAC8	8	HDDC3
Up	FOXA2	6	SPTAN1	Down	E2F6	8	PFKFB3
Up	TEAD4	6	BAMBI	Down	MNT	8	SIVA1
Up	GATAD2B	6	STC2	Down	DIDO1	8	LEFTY2
Up	MAFF	6	ENC1	Down	DEK	7	RPL35
Up	MITF	6	FTH1	Down	SCRT2	7	HSD17B12
Up	SIN3B	6	MVP	Down	CEBPB	7	REV1
Up	HES1	6	LAMB3	Down	PTRF	7	SLC3A2
Up	ZNF512	6	SCARB1	Down	ZNF512	7	CTSC
Up	SCRT2	6	PLEKH02	Down	SPI1	7	PPM1M
Up	GATA3	5	HSPA5	Down	RUNX3	7	ELOVL6
Up	E2F4	5	MT2A	Down	MAFF	7	IGF1
Up	ZNF239	5	DBNDD1	Down	GATAD2B	7	ZFAND1
Up	NONO	5	MYEOV	Down	RUNX1	6	KHDRBS1
Up	JUN	5	HSPB8	Down	SREBF1	6	DPF2

Up	IRF2	5	IFIT2	Down	PYG02	6	MRPL55
Up	ZNF217	5	MGST1	Down	STAT3	6	NDFIP2
Up	TEAD2	5	RARRES3	Down	GATA3	6	ZHX2
Up	POU5F1	4	ANGPT1	Down	ZNF547	6	GPHN
Up	ZNF641	4	CCDC107	Down	POU2F2	6	CLDND1
Up	POU2F2	4	TAGLN2	Down	TBX3	6	PER2
Up	PYG02	4	CHST3	Down	ZNF202	5	RWDD2A
Up	PTRF	4	NRCAM	Down	HNF4A	5	ORMDL3
Up	SIX4	4	PMEPA1	Down	E2F4	5	MIS18BP1
Up	EP300	4	FLNC	Down	CHD4	5	RFX1
Up	NFATC1	4	NAV1	Down	MAFG	5	UBR2
Up	MTA3	4	MIR3188	Down	PTTG1	5	BHLHE40
Up	ZNF16	4	DOCK6	Down	ZNF585B	5	NR3C1
Up	NFE2L2	3	PRSS23	Down	ZNF8	5	FBL
Up	ZNF488	3	HOXC8	Down	NFYB	5	DBP
Up	PML	3	CD68	Down	NFE2L2	5	NDUFV3
Up	ZHX1	3	SLC7A4	Down	POU5F1	4	AASS
Up	BCL3	3	CHI3L2	Down	ATF2	4	RBM15
Up	ZNF547	3	CDR2L	Down	NFIC	4	CTSC
Up	DIDO1	3	COL6A1	Down	IRF3	4	BLVRB
Up	ZC3H11A	3	LAMA5	Down	USF1	4	EEF2K
Up	UBTF	3	CRIP1	Down	ZNF16	4	SRSF3
Up	HLF	3	IGFBP6	Down	ETS2	3	TRIM24
Up	USF1	3	STC2	Down	TBL1XR1	3	SOCS2
Up	ZNF264	3	SOBP	Down	TEAD2	3	PHF13
Up	YBX1	3	SLC22A12	Down	ETV6	3	ORC2
Up	CBX8	2	CCND2	Down	CHD2	3	PTEN
Up	HNF4A	2	CFB	Down	ZFP41	3	GADD45B
Up	MYB	2	MYEOV	Down	TCF3	3	LAPTM4B
Up	ZNF202	2	TNFRSF12A	Down	STAT5A	3	RNF144A
Up	RBBP5	2	GNG2	Down	SETDB1	3	RNF217
Up	RXRA	2	PLTP	Down	RBBP5	3	RPL9
Up	ZNF8	2	DBNDD1	Down	CEBPZ	3	SIN3A
Up	SREBF1	2	DHDDS	Down	POLR3A	2	ANG
Up	ATF2	2	EMX2	Down	BDP1	2	RNASE4
Up	ZNF140	2	FGF11	Down	BRF1	2	ANG
Up	MCM3	2	FGR	Down	GTF3C2	2	RNASE4
Up	KAT2A	2	SGK1	Down	MCM7	2	KCNK6
Up	GTF2B	2	SOS1	Down	NANOG	2	C17orf53
Up	CHD7	2	SLC2A5	Down	JUN	2	POLR1D
Up	PTTG1	2	HSPA5	Down	ZNF138	2	GINS3
Up	EHMT2	2	KCNB1	Down	NFYA	2	RGMB
Up	RUNX1	2	MIR3188	Down	TAF1	2	HNRNPA1P10
Up	ZNF274	2	RHOC	Down	SP4	2	ZNF394

Up	AEBP2	2	SGCE	Down	PRDM12	2	RPL17
Up	NANOG	2	SH3BGRL3	Down	YBX1	1	BCAT2
Up	HDAC8	2	SLC7A4	Down	HSF1	1	CCDC59
Up	ZNF585B	2	TYMP	Down	PPARGC1A	1	CCDC59
Up	MEF2A	1	CHI3L2	Down	NONO	1	CD55
Up	MEF2C	1	CHI3L2	Down	FOS	1	CD55
Up	ZNF292	1	COL12A1	Down	SIX4	1	DCAF7
Up	NFE2L1	1	DBNDD1	Down	TCF7L2	1	ELK1
Up	IRF3	1	DHDDS	Down	MYB	1	FOXO1
Up	SRF	1	EGR2	Down	ZNF707	1	GCHFR
Up	TBP	1	FTH1	Down	ZC3H11A	1	GCHFR
Up	TBL1XR1	1	FTH1	Down	UBTF	1	GCHFR
Up	NR3C1	1	MYEOV	Down	KAT2A	1	H1FX
Up	TCF7L2	1	SERPINH1	Down	CHD7	1	LDHC
Up	ETS2	1	SLC7A4	Down	SRF	1	MRPL55
Up	MCM5	1	SLC7A4	Down	ZZZ3	1	NR2F1
Up	E2F6	1	SLC7A4	Down	RXRA	1	ORMDL3
Up	TSC22D4	1	SLC7A4	Down	ZNF264	1	PTEN
Up	MCM7	1	SLC7A4	Down	ZNF274	1	RAMP2
Up	ETV6	1	SOS1	Down	BRCA1	1	RPS2
Up	STAT5A	1	SPTAN1	Down	FOXA1	1	UBR2
Up	TCF3	1	SPTAN1	Down	NFE2L1	1	ZFAND5
Up	MAFG	1	TPGS2	Down	BCL3	1	ZNF581
Up	TAF1	1	TUBB2B	Down	BCLAF1	1	ZNF581
Up	CHD4	1	TYROBP	Down			
Up	MNT	1	VASN	Down			
Up	SETDB1	1	ZNF404	Down			

Degree – No of target gene interact with TF. We taken any one target gene in table. TF transcription factors

Figures

A**B** **Figure 1**

Box plots of the gene expression data before (A) and after normalization (B). Horizontal axis represents the sample symbol and the vertical axis represents the gene expression values. The black line in the box plot represents the median value of gene expression. (A1-A12 = adipocytes from lean persons; B1-B12 = adipocytes from obese patients)

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Figure 2

Heat map of up regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1-A12 = adipocytes from lean persons; B1-B12 = adipocytes from obese patients)

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Figure 3

Heat map of down regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1-A12 = adipocytes from lean persons; B1-B12 = adipocytes from obese patients)

Figure 3

Heat map of down regulated differentially expressed genes. Legend on the top left indicate log fold change of genes. (A1-A12 = adipocytes from lean persons; B1-B12 = adipocytes from obese patients)

Figure 4

Volcano plot of differentially expressed genes. Genes with a significant change of more than two-fold were selected.

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Figure 5
 Protein–protein interaction network of up regulated genes. Green nodes denotes up regulated genes.

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Figure 6

Scatter plot for up regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; D-Closeness centrality; E- Clustering coefficient)

Figure 6

Scatter plot for up regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; D-Closeness centrality; E- Clustering coefficient)

Figure 7

Protein–protein interaction network of down regulated genes. Red nodes denotes down regulated genes.

Figure 7

Protein–protein interaction network of down regulated genes. Red nodes denotes down regulated genes.

Figure 8

Scatter plot for down regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; Closeness centrality; E- Clustering coefficient)

Figure 8

Scatter plot for down regulated genes. (A- Node degree; B- Betweenness centrality; C- Stress centrality ; Closeness centrality; E- Clustering coefficient)

Module 12

Module 17

Module 26

Module 68

Figure 9

Modules in PPI network. The green nodes denote the up regulated genes.

Module 12

Module 17

Module 26

Module 68

Figure 9

Modules in PPI network. The green nodes denote the up regulated genes.

Module 15

Module 28

Module 60

Module 86

Figure 10

Modules in PPI network. The Red nodes denote the down regulated genes.

[illegible]

A network diagram illustrating the regulatory interactions between ESR1 and other transcription factors. ESR1 is represented by a large red circle at the center. It is connected to several smaller cyan circles representing other transcription factors. The connections are shown as black lines. The transcription factors include SRPK2, JUN, EED, SRRM1, HNRNPF, HNRNP60, HNRNPH2, MAP1LC3B, HNRNPA1, PPP2R1A, CUL3, CLK3, YBX1, STAU1, PTPN19, SAFB, SORBS3, KHDRBS1, SRSF3, CAND1, MATR3, CIRBP, CTNNB1, SAFB2, ESR2, HNRNPK, SRRM2, DDX5, RBMX, PPP1CC, RPSA, MCM2, RB1CC1, EIF4A3, NR2F6, HDAC5, U2AF2, OBSL1, MAP1LC3A, TUBA1A, ELAVL2, FUS, RBM14, and DHX15.

Network diagram showing ESR1 as a central hub gene connected to various other genes. The size of the circles represents the degree of connectivity. ESR1 is the largest circle in the center. Other large circles include FBL, RPL18, RPL18A, and RPL21. Smaller circles include SAFB, SIN3A, HDAC9, RPS18, RPS25, MRPS9, RPS24, SAFB2, ZBTB16, MRPS27, RPS3A, IGF1R, RPS2, RPL14, RPL18A, RPL21, FBL, TP53, RPS27, KHDRBS1, PTEN, RBBP4, RPS3, TRIM24, RPS9, SIRT1, RPS26, MRPS2, RPS27A, and RPS3A.

Network diagram illustrating interactions between CSNK2A2, CSNK2B, and DCAF7. The diagram shows a central cluster of nodes, with CSNK2A2 and CSNK2B being the largest and most central. DCAF7 is also a prominent node. Other nodes include VCP, CBX7, TP53, RYBP, CBX4, PPP1CA, RING1, PCGF3, CSNK2A1, TFAP2A, PCGF6, CBX8, YAF2, PCGF5, JUN, WWOX, AUTS2, CEP170, and RNF2. The nodes are connected by edges, representing interactions.

Modules in PPI network. The Red nodes denote the down regulated genes.

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The network of down regulated genes and their related miRNAs. The red circles nodes are the down regulated genes, and chocolate diamond nodes are the miRNAs

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Figure 13

TF - gene network of predicted target up regulated genes.. (Blue triangle - TFs and green circles- target up regulated genes)

Figure 14

TF-gene network of predicted target down regulated genes. (Blue triangle - TFs and red circles- target down regulated genes)

Figure 14

TF-gene network of predicted target down regulated genes. (Blue triangle - TFs and red circles- target up regulated genes)

Figure 15

Immunohistochemical IHC analyses of hub genes were produced using the human protein atlas (HPA) online platform. A) STAT3 B) CORO1C C) SERPINH1 D) MVP E) ITGB5 F) PCM1 G) SIRT1 H) EEF1G I) PTEN J) RPS2

Figure 15

Immunohisto chemical I(IHC) analyses of hub genes were produced using the human protein atlas (HPA) online platform. A) STAT3 B) CORO1C C) SERPINH1 D) MVP E) ITGB5 F) PCM1 G) SIRT1 H) EEFG I) PTEN J) RPS2

Figure 16

ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for obesity prognosis. A) STAT3 B) CORO1C C) SERPINH1 D) MVP E) ITGB5 F) PCM1 G) SIRT1 H) EEFG I) PTEN J) RPS2

Figure 16

ROC curve validated the sensitivity, specificity of hub genes as a predictive biomarker for obesity prognosis. A) STAT3 B) CORO1C C) SERPINH1 D) MVP E) ITGB5 F) PCM1 G) SIRT1 H) EEF1G I) PTEN J) RPS2

Figure 17

Validation of microarray data by RT-PCR. A) STAT3 B) CORO1C C) SERPINH1 D) MVP E) ITGB5 F) PCM1 G) SIRT1 H) EEF1G I) PTEN J) RPS2

Figure 17