Research Article

Novel Pathology-Related Hub Genes in Focal Segmental Glomerulosclerosis

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Abstract

Objectives: Focal Segmental Glomerulosclerosis (FSGS) is a progressive glomerular disease. The pathogenesis of this disease, however, remains unclear. Here, we attempted to identify key candidate genes in FSGS through stringent bioinformatic analysis.

Methods: We systematically searched the Gene Expression Omnibus database for gene expression microarrays derived from human glomeruli tissues with FSGS. First, we identified differentially expressed genes (DEGs) by using the Limma package in R. Then, we subjected these DEGs to Gene Ontology (GO) analysis for further analysis. Finally, we constructed Protein–Protein Interaction networks (PPI) through four different methods and performed intersection analysis to further refine our results.

Results: A total of 627 DEGs were identified between the FSGS and control groups, among which 534 were up-regulated and 93 were down-regulated. GO analysis revealed that the DEGs were enriched in mRNA processing, cell adhesion molecule binding, and cadherin binding. Furthermore, via PPI, 7 DEGs overlapped in the four groups constructed through different analytical approaches. We also validated the overlapped 7 hub genes in in vitro experiments, including RBM5 and HNRNPF, with potentially important roles in the development of FSGS.

Conclusion: Our study provides a valuable resource for novel biomarkers and therapeutic targets for FSGS.

Keywords: Focal segmental glomerulosclerosis; Bioinformatic analysis; RBM5; HNRNPF

Introduction

Focal Segmental Glomerulosclerosis (FSGS) is a primary glomerular disease that manifests with heavy proteinuria [1]. It is the leading cause of the development of end-stage renal disease. Typically, FSGS lesions present a segmental manifestation that includes parietal cell migration, hyaline deposition, capillary collapse, and intracapillary thrombi. Recent studies suggest that podocyte injury may play a key role in FSGS lesions [2]. Injury and loss of podocytes result in foot process effacement and protein loss [3]. However, the pathogenesis of FSGS remains unclear, and the present diagnostic and therapeutic methods for this disease remain inadequate. Oxidative stress has been implicated in the development and progression of this FSGS [4,5]. Nuclear factor E2-related factor 2 (Nrf2) is a transcription factor that can potently induce the production of numerous antioxidants and prevent the generation of oxidative stress in renal fibrosis and inflammation [6–8]. Furthermore, apoptosis and the renin–angiotensin system are strongly involved in FSGS-related injury [9–12]. Nevertheless, a considerable amount of important FSGS genes remain unidentified given the lack of global analysis.

With the development of bioinformatic analysis technology, gene expression profiling analysis has been increasingly used to explore molecular mechanisms and identify novel biomarkers in various diseases [13–16]. Bioinformatic analysis is mainly used to predict novel diagnostic biomarkers and therapeutic targets associated with tumors, such as bladder cancer [17], meningioma [18], and hepatocellular carcinoma [19]. The application of bioinformatic analysis in renal diseases, such as renal cell carcinoma [20], lupus nephritis [21], IgA nephropathy [22], and chronic kidney disease [23], has begun to develop gradually. However, up to now, no study has subjected FSGS to bioinformatic analysis. Thus, exploring the underlying crucial genes and effective therapeutic targets for FSGS through bioinformatic analysis is necessary.

In this study, we downloaded the gene expression profile datasets of FSGS from the Gene Expression Omnibus (GEO) database and investigated Differentially Expressed Genes (DEGs) between FSGS and control samples by using the Limma package in R. We performed Gene Ontology (GO) enrichment analysis for all DEGs. In addition, we constructed protein–protein interaction (PPI) networks, identified novel hub genes, and validated them in in vitro experiments. Our study aimed to predict novel diagnostic biomarkers and potential therapeutic targets for FSGS.

Materials and Methods

Data collection

Gene expression profiles were retrieved from NCBI's GEO database (http://www.ncbi.nlm.nih.gov/geo/) by using the key words "focal segmental glomerulosclerosis" with the following criteria: 1) the study type is expression profiling by array, 2) the attribute name is tissue, 3) the organism of interest is *Homo sapiens*, and 4) the platform used is the Affymetrix Human Genome U133A Array. Ultimately, on the basis of the above criteria, we selected dataset GSE47185 of FSGS. Original CEL files were used for further bioinformatic analysis.

Data preprocessing

CEL files were normalized and converted to expression profiles by using the Affy package of R [24]. In brief, the original data were read using the Affy Bioconductor package and preprocessed for normalization through the robust multiarray analysis method, which includes background correction, normalization, expression calculation and batch effects removal. After obtaining the gene expression value, genes were annotated with the hgu133A.db and annotate software packages.

DEG analysis

The Limma package of R [25] was used to analyze DEGs after preprocessing. The linear fit method, Bayesian analysis, and *t*-test algorithm were used to calculate the P and FC values. DEGs were screened by setting a cut-off value of |log 2 Fold Change (FC)| > 1 and P < 0.05. The ggplot2 software package was used to visualize results. Moreover, to identify and visualize the DEGs between FSGS and normal samples, we generated a heat map of the top 10% DEGs by using the heatmap package (Version 1.0.8).

GO enrichment analysis for DEGs

The GO consortium includes three independent branches: Biological Process (BP), Cellular Component (CC), and Molecular Function (MF). In this study, we subjected the identified DEGs to GO enrichment analysis by using R and the clusterProfiler package [26]. P < 0.05 was used as the threshold for the identification of significant GO terms.

PPI Network Construction

To explore the relationships among the top 30% DEGs, we used the online tool STRING (Search Tool for the Retrieval of Interacting Genes/Proteins; http://string.embl.de/) database for the construction of PPI networks. The minimum required interaction score of 0.4 was used as the significant cut-off threshold. Then, the obtained PPI interaction networks were visualized by using Cytoscape software (version 6.3).

Hub-gene screening

On the basis of the STRING results, we introduced the four methods Degree, EPC, Maximal Clique Centrality (MCC), and DMNC [27] to rank the importance of nodes in the PPI networks and to further identify hub genes from the top 30% DEGs. Nodes with high centrality scores were considered hub genes. We applied the R package Venn diagram (version1.6.17, https://cran.r-project.org/web/packages/VennDiagram/) [28] to identify overlapping DEGs among these hub genes.

Degree ($Deg(v) = |N(v)|$) is a computing tool in Cytoscape software [29]. The default filter "in and out" was between 7 and 42 in the present study.

MCC is a topological analysis method in CytoHubba [27]. Given a node v, the MCC of v is defined as $MCC(v) = \Sigma C \in S(v)(|C|-1)!$.

Maximum Neighborhood Component (MNC) is another computing tool in cytoHubba. $MNC(v) = |V(MC(v))|$, where $MC(v)$ is a maximum connected component of $G[N(v)]$, and $G[N(v)]$ is the induced subgraph of G by $N(v)$. On the basis of MNC, Lin et al. proposed that $DMNC(v) = |E(MC(v))|/|V(MC(v))| \varepsilon$, where $\varepsilon = 1.7$.

Cell culture

Conditionally immortalized human podocytes (LY893) were kindly provided by Dr. Lan Ni and Moin Saleem(Bristol, U.K.). Podocytes were cultured in RPMI 1640 medium(Gibco)supplemented with 10% Fetal Bovine Serum (Gibco) and 1% Insulin-Transferrin-Selenium(Invitrogen) at 33°C under 5% CO2 for propagation, then were thermo switched to 37°C under 5% CO2 when at 60% confluency for differentiation. The differentiated podocytes were incubated with adriamycin to construct an in vitro model for FSGS [30].

Quantitative Real-Time PCR

Total RNA was extracted using the RNeasy Plus Mini Kit (BioTeke RP1202) in accordance with the manufacturer's instructions. The cDNA was obtained by reverse transcription, amplified and detected using a SYBR Green Supermix kit (Takara). Then, a BIO-RAD CFX-96 Real-Time PCR system (Bio-Rad) was used for PCR analysis under the following conditions: 95 °C for 3 min, followed by 40 cycles of 95 °C for 10 s and 51 °C for 30 s. The primer sequences used for PCR are listed in Table 1. Statistical differences were determined by Student's t-test using R "ggpubr" package(version 0.1.8, https://CRAN.R-project.org/package=ggpubr).

Results

DEGs identification

This dataset GSE47185 contains the mRNA expression profiles of 13 FSGS samples and 14 control samples (normal tissue of renal tumor excision). Under the threshold of |log 2 fold change (FC)| > 1 and adj.P value < 0.05, 627 DEGs were identified between the FSGS and control groups. These DEGs included 534 up-regulated and 93 down-regulated DEGs. The results of expression-level analysis are presented as a volcano plot in Fig. 1A. As shown in Table 2, RPS4Y1, PLPP3, DDX3Y, SART3, TCF4, TROVE2, IQGAP1, MBP, CALD1, and RBFOX2 are the 10 most significantly up-regulated genes, whereas CYP4A11, FOSB, EGR1, G6PC, ALB, CTSZ, PPP3R1, XIST, PCK1, and HPGD are the 10 most significantly down-regulated genes. The more information of all DEGs is listed in supplementary Table 1.

The heatmaps of the top 10% DEGs are shown in Fig. 1B. The data are presented in a matrix format, in which rows represent individual

genes, and columns represent individual samples. The purple and green colors indicate up-regulated and down-regulated genes, respectively. The hierarchy cluster analysis indicated that FSGS and control groups could be distinguished from each other on the basis of their different expression patterns.

Functional enrichment analysis

To reveal the biological functions of DEGs, we used the clusterProfiler package for GO analysis. We set adj.P value < 0.01 to identify significantly enriched GO terms. The top eight GO terms

for the DEGs enriched in the BP, CC, and MF are shown in Figure 2.The DEGs were mainly involved in GO terms that included mRNA processing, regulation of mRNA metabolic process, antigen processing and presentation of exogenous antigen, focal adhesion, cell adhesion molecule binding, cadherin binding, and actin binding. Among these terms, the MFs related to focal adhesion (GO:0005925) [31,32], cell adhesion molecule (GO:0050839) [33,34], cadherin (GO:0045296) [35], and actin binding (GO:0003779) [36] were all confirmed to be involved in glomerulosclerosis. Detailed information on the top eight GO terms is shown in Table 3.

Table 1. Primer sequences for RT-PCR.

Gene	Forward primer	Reverse primer
FUS	5' GCAGGAGTTTGTGGAGTG 3'	5' TGAGTACAGGCAGGATGTG 3'
DHX15	5' CTTTACAAGCAGGGACTA 3'	5' TCAAGAACAGTAGAGGGAT 3'
PRPF31	5' TGTCGGGCTTCTCGTCTA 3'	5' CACCTTCCCTTCTGTGCTCT 3'
PQBP1	5' CAAGAAGGCAGTAAGCCGAAAG 3'	5' TGTGGTGTCAGCGCCAGTC 3'
RBM5	5' GGTGCGAAATGGAGATGA 3'	5' AGAGTTGCTGGTGCCTGA 3'
HNRNPR	5' AAGTCCCACAGAACCGAGAT 3'	5' AACCCTGAGAAGAACTGAACAA 3'
TRA2B	5' CACATACGCCAACACCAG 3'	5' TCCTCCACCTCCTCCTCT 3'
GAPDH	5' CTTTGGTATCGTGGAAGGACTC 3'	5' GTAGAGGCAGGGATGATGTTCT 3'
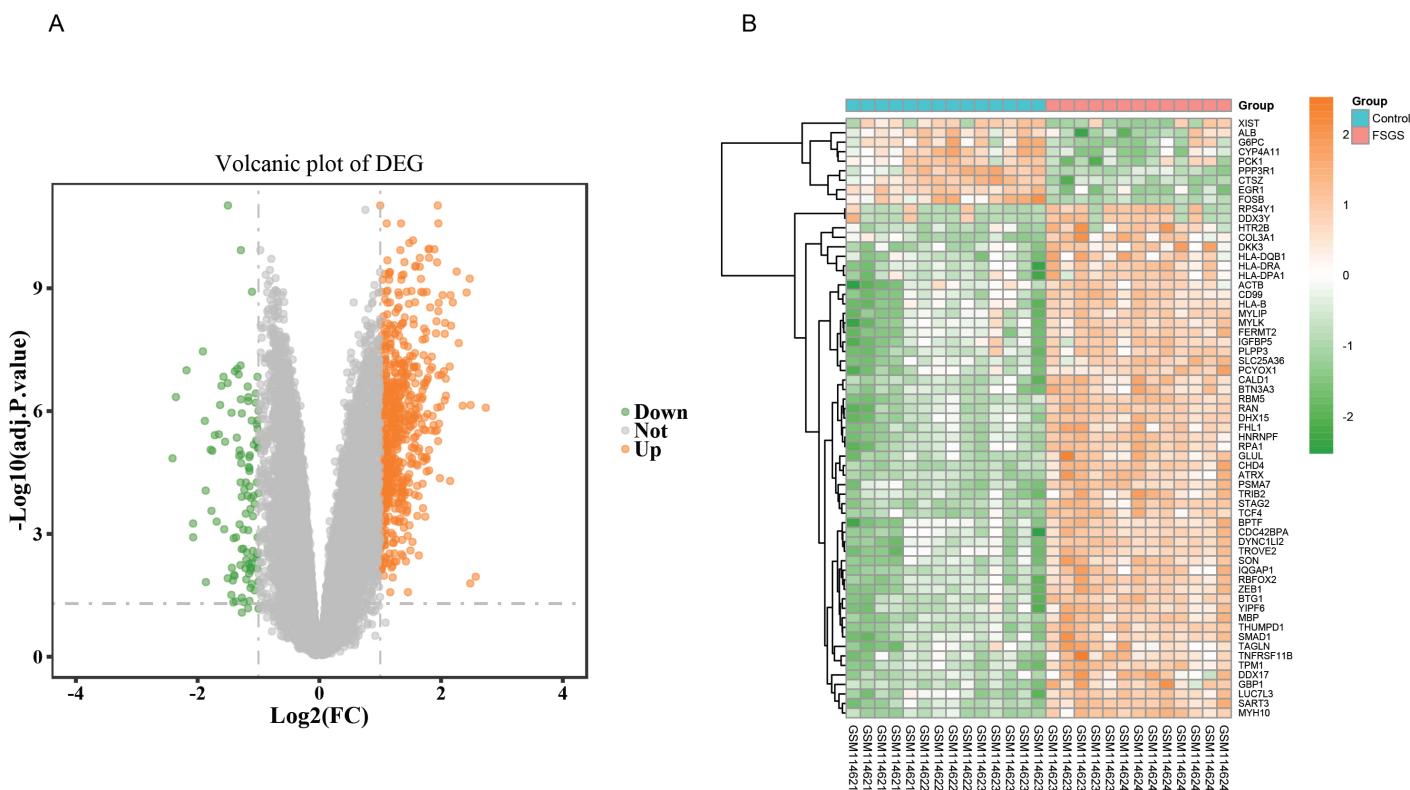
Figure 1. Visualization of DEGs

A, The volcano plot of differentially expressed genes between FSGS and healthy tissues. The red plots represent up-regulated genes, green plots represent down-regulated genes, while grey plots represent non-significant genes. The volcano plot was constructed using the ggplot2 package of the R language; B, A heatmap of the top 10% DEGs. The horizontal axis denotes the different samples, and the vertical axis denotes different DEGs.blue, normal samples; red, FSGS samples; purple clusters represent up-regulated DEGs and green clusters represent down-regulated DEGs. Color key represents the Z-score based on the Gene expression value.

The Most Enriched GO Terms
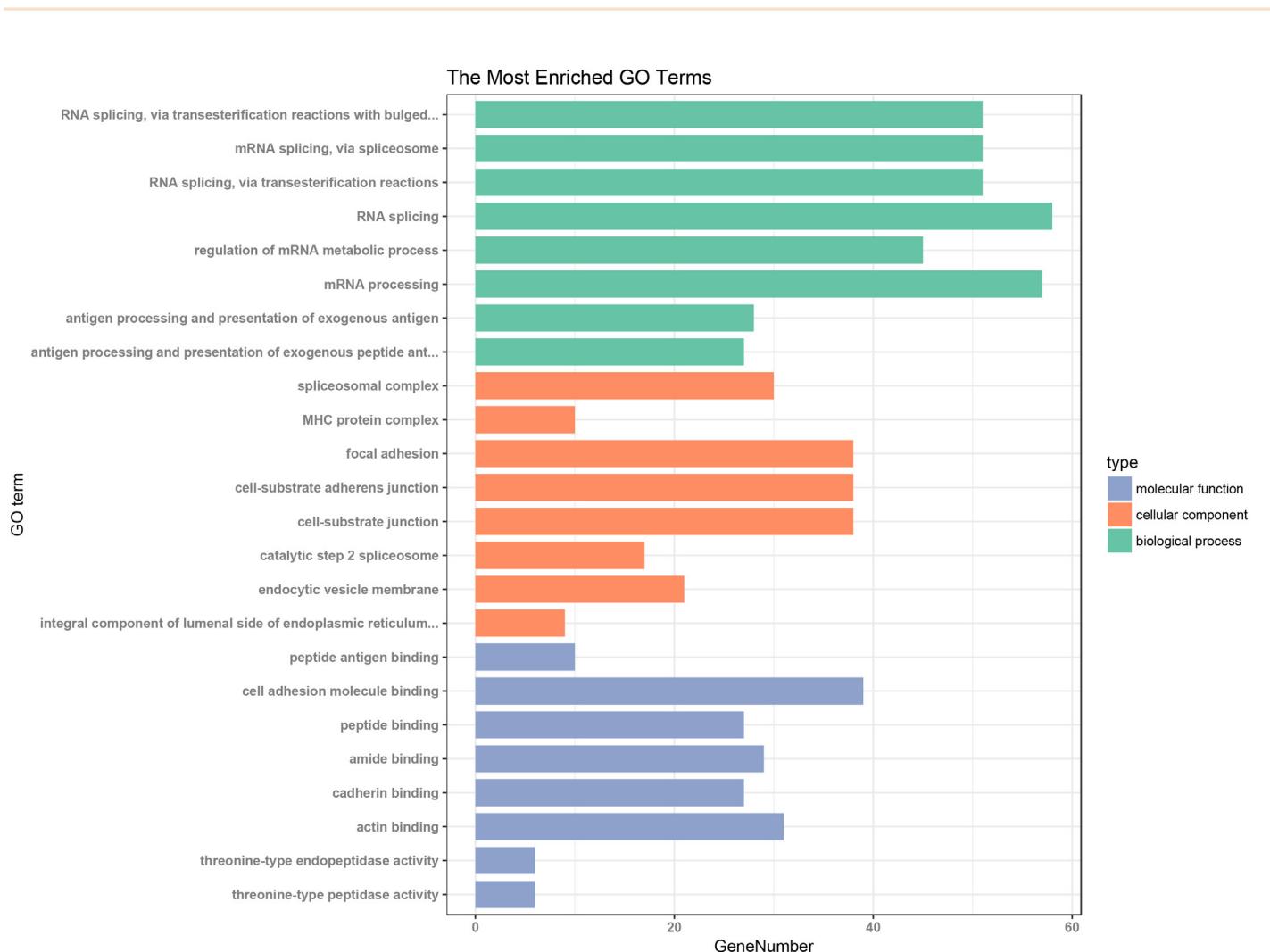
Figure 2. The 8 most significant enriched GO terms of DEGs

The adj.P value< 0.01 was used as the threshold for the identification of significant GO terms. The Gene ontology covers the biological process, cellular component, and molecular function. The horizontal axis represents the gene counts, the vertical axis represents GO terms.Green column graphs represent biological process(BP) GO term; orange column graphs represent cellular component(CC) GO term; and blue column graphs represent molecular function (MF) GO term.

Table 2. The Most Significant 10 Up-Regulated Genes And Down-Regulated Genes.

Gene Symbols	Log FC	Average Expression level	Adj.P. Value
RPS4Y1	2.569009	9.570289	1.11E-02
PLPP3	2.485089	9.251834	7.13E-07
DDX3Y	2.478844	7.003028	1.62E-02
SART3	2.470577	7.660357	5.82E-10
TCF4	2.41899	7.335133	1.27E-09
TROVE2	2.355365	9.457713	7.39E-07
IQGAP1	2.290646	8.145384	2.19E-08
MBP	2.255968	7.587945	3.91E-10
CALD1	2.192563	8.074506	2.21E-09
RBFOX2	2.164463	8.698168	8.22E-09

Gene Symbols	Log FC	Average Expression level	Adj.P. Value
CYP4A11	-2.41227	9.128665	1.42E-05
FOSB	-2.35626	8.074382	4.53E-07
EGR1	-2.18278	10.28014	1.01E-07
G6PC	-2.07454	6.566343	5.57E-04
ALB	-2.0735	9.571928	1.21E-03
CTSZ	-1.91281	8.256097	3.49E-08
PPP3R1	-1.88153	7.627366	1.74E-06
XIST	-1.86386	7.615666	1.50E-02
PCK1	-1.7723	10.99439	2.73E-04
HPGD	-1.7174	10.07267	3.87E-06

Table 3. The Most Significantly Enriched GO Terms In BP ,CC and MF.

ID	Description	Adj.P.Value	Gene ID	Category
GO:0000377	RNA splicing, via transesterification reactions with bulged adenosine as nucleophile	1.19E-16	SART3/RBFOX2/LUC7L3/HNRNPF/DDX17/SON/RBM5/DHX15/SCAF11/HNRNPM/FUS/ RBM25/MBNL2/HNRNPR/PRPF31/TRA2B/PQBP1/HNRNPD/SRRM2/DDX39A/DDX41/ DHX9/SRSF3/TIA1/HNRNPA2B1/PNN/PRPF4B/HNRNPC/JMJD6/SRRM1/SYNCRIP/ DNAJC8/SNRPB/PAPOLA/METTL3/SRSF7/SF3B4/GPKOW/C1QBP/DHX35/CSTF1/SART1/ RBM8A/LSM4/USP39/POLR2E/PRPF19/SRPK2/HNRNPA3/PRMT5/POLR2A	BP
GO:0000398	mRNA splicing, via spliceosome	1.19E-16	SART3/RBFOX2/LUC7L3/HNRNPF/DDX17/SON/RBM5/DHX15/SCAF11/HNRNPM/FUS/ RBM25/MBNL2/HNRNPR/PRPF31/TRA2B/PQBP1/HNRNPD/SRRM2/DDX39A/DDX41/ DHX9/SRSF3/TIA1/HNRNPA2B1/PNN/PRPF4B/HNRNPC/JMJD6/SRRM1/SYNCRIP/ DNAJC8/SNRPB/PAPOLA/METTL3/SRSF7/SF3B4/GPKOW/C1QBP/DHX35/CSTF1/SART1/ RBM8A/LSM4/USP39/POLR2E/PRPF19/SRPK2/HNRNPA3/PRMT5/POLR2A	BP
GO:0000375	RNA splicing, via transesterification reactions	1.20E-16	SART3/RBFOX2/LUC7L3/HNRNPF/DDX17/SON/RBM5/DHX15/SCAF11/HNRNPM/FUS/ RBM25/MBNL2/HNRNPR/PRPF31/TRA2B/PQBP1/HNRNPD/SRRM2/DDX39A/DDX41/ DHX9/SRSF3/TIA1/HNRNPA2B1/PNN/PRPF4B/HNRNPC/JMJD6/SRRM1/SYNCRIP/ DNAJC8/SNRPB/PAPOLA/METTL3/SRSF7/SF3B4/GPKOW/C1QBP/DHX35/CSTF1/SART1/ RBM8A/LSM4/USP39/POLR2E/PRPF19/SRPK2/HNRNPA3/PRMT5/POLR2A	BP
GO:0008380	RNA splicing	2.97E-16	SART3/RBFOX2/LUC7L3/HNRNPF/DDX17/SON/RBM5/DHX15/PPIG/SCAF11/HNRNPM/ FUS/RBM25/MBNL2/HNRNPR/PRPF31/TRA2B/PQBP1/HNRNPD/SRRM2/DDX39A/DDX41/ DHX9/SRSF3/TIA1/AKAP8L/LGALS3/HNRNPA2B1/PNN/PRPF4B/HNRNPC/JMJD6/ SRRM1/RRAGC/SYNCRIP/DNAJC8/SNRPB/WT1/IK/PAPOLA/METTL3/SRSF7/SF3B4/ GPKOW/C1QBP/DHX35/TMBIM6/CSTF1/SART1/RBM8A/LSM4/USP39/POLR2E/PRPF19/ SRPK2/HNRNPA3/PRMT5/POLR2A	BP
GO:1903311	regulation of mRNA metabolic process	2.24E-15	RBFOX2/DDX17/SON/RBM5/PSMA7/PSMB8/RBM25/PSMC3/TNPO1/SERBP1/MBNL2/ HNRNPR/YWHAB/TRA2B/SET/HNRNPD/PSMA3/PUM1/PSMB4/DHX9/EIF4G1/SRSF3/ PSMD4/TIA1/PSMD13/AHCYL1/HNRNPA2B1/HNRNPC/JMJD6/PSME3/PSMB9/SYNCRIP/ PAPOLA/METTL3/SRSF7/SF3B4/C1QBP/CNOT8/TMBIM6/RBM8A/BTG2/PRPF19/PSMB10/ SRPK2/ZFP36	BP
GO:0006397	mRNA processing	5.38E-13	SART3/RBFOX2/LUC7L3/HNRNPF/DDX17/SON/RBM5/DHX15/SCAF11/HNRNPM/FUS/ RBM25/MBNL2/HNRNPR/PRPF31/TRA2B/PQBP1/HNRNPD/SRRM2/DDX39A/DDX41/ DHX9/SRSF3/TIA1/AKAP8L/AHCYL1/LGALS3/HNRNPA2B1/PNN/PRPF4B/HNRNPC/ JMJD6/SRRM1/SYNCRIP/DNAJC8/SNRPB/IK/PAPOLA/METTL3/SRSF7/SF3B4/GPKOW/ C1QBP/DHX35/TMBIM6/CSTF1/CHTOP/SART1/RBM8A/LSM4/USP39/POLR2E/PRPF19/ SRPK2/HNRNPA3/PRMT5/POLR2A	BP
GO:0019884	antigen processing and presentation of exogenous antigen	1.68E-08	HLA-DRA/DYNC1LI2/HLA-DQB1/HLA-B/PSMA7/HLA-DPA1/PSMB8/PSMC3/HLA-DMB/ HLA-G/CALR/PSMA3/KLC1/HLA-DMA/PSMB4/PSMD4/TAP1/HLA-F/PSMD13/AP3D1/ AP1S2/HLA-C/VAMP3/HLA-DPB1/PSME3/PSMB9/OSBPL1A/PSMB10	BP
GO:0002478	antigen processing and presentation of exogenous peptide antigen	2.89E-08	HLA-DRA/DYNC1LI2/HLA-DQB1/HLA-B/PSMA7/HLA-DPA1/PSMB8/PSMC3/HLA-DMB/ HLA-G/CALR/PSMA3/KLC1/HLA-DMA/PSMB4/PSMD4/TAP1/HLA-F/PSMD13/AP1S2/ HLA-C/VAMP3/HLA-DPB1/PSME3/PSMB9/OSBPL1A/PSMB10	BP
GO:0005681	spliceosomal complex	1.85E-10	LUC7L3/HNRNPF/RBM5/DHX15/HNRNPM/RBM25/HNRNPR/PRPF31/TRA2B/SRRM2/ DDX39A/DDX41/WAC/LGALS3/HNRNPA2B1/PNN/PRPF4B/HNRNPC/SRRM1/SYNCRIP/ SNRPB/IK/SF3B4/DHX35/SART1/RBM8A/LSM4/USP39/PRPF19/HNRNPA3	CC
GO:0042611	MHC protein complex	4.84E-07	HLA-DRA/HLA-DQB1/HLA-B/HLA-DPA1/HLA-DMB/HLA-G/HLA-DMA/HLA-F/HLA-C/ HLA-DPB1	CC
GO:0005925	focal adhesion	4.84E-07	IQGAP1/FERMT2/CD99/FHL1/ACTB/HCK/PALLD/EZR/ZFYVE21/PDPK1/YWHAB/GDI2/ DLC1/ITGA8/CALR/ACTR3/KRAS/NRP1/ARPC1B/CAT/FLRT3/PTPRC/EFNB2/EPB41L5/ PPFIBP1/EGFR/CAV1/DAB2/LAP3/HSP90B1/CAP1/P4HB/NFASC/PTK2/DST/RAC1/ TSPAN4/SNTB2	CC
GO:0005924	cell-substrate adherens junction	4.84E-07	IQGAP1/FERMT2/CD99/FHL1/ACTB/HCK/PALLD/EZR/ZFYVE21/PDPK1/YWHAB/GDI2/ DLC1/ITGA8/CALR/ACTR3/KRAS/NRP1/ARPC1B/CAT/FLRT3/PTPRC/EFNB2/EPB41L5/ PPFIBP1/EGFR/CAV1/DAB2/LAP3/HSP90B1/CAP1/P4HB/NFASC/PTK2/DST/RAC1/ TSPAN4/SNTB2	CC
GO:0030055	cell-substrate junction	5.47E-07	IQGAP1/FERMT2/CD99/FHL1/ACTB/HCK/PALLD/EZR/ZFYVE21/PDPK1/YWHAB/GDI2/ DLC1/ITGA8/CALR/ACTR3/KRAS/NRP1/ARPC1B/CAT/FLRT3/PTPRC/EFNB2/EPB41L5/ PPFIBP1/EGFR/CAV1/DAB2/LAP3/HSP90B1/CAP1/P4HB/NFASC/PTK2/DST/RAC1/ TSPAN4/SNTB2	CC

ID	Description	Adj.P.Value	Gene ID	Category
GO:0071013	catalytic step 2 spliceosome	1.38E-06	HNRNPF/HNRNPM/HNRNPR/SRRM2/DDX41/HNRNPA2B1/PNN/PRPF4B/HNRNPC/ SRRM1/SYNCRIP/SNRPB/DHX35/SART1/RBM8A/PRPF19/HNRNPA3	CC
GO:0030666	endocytic vesicle membrane	1.27E-05	HLA-DRA/HLA-DQB1/HLA-B/HLA-DPA1/RAB31/CD163/PICALM/ATG12/HLA-G/CALR/ TAP1/HLA-F/TYRP1/AP1S2/HLA-C/VAMP3/HLA-DPB1/EGFR/CAV1/GPR161/ATP6V0E2	CC
GO:0071556	integral component of lumenal side of endoplasmic reticulum membrane	1.27E-05	HLA-DRA/HLA-DQB1/HLA-B/HLA-DPA1/HLA-G/CALR/HLA-F/HLA-C/HLA-DPB1	CC
GO:0042605	peptide antigen binding	4.99E-06	HLA-DRA/HLA-DQB1/HLA-B/HLA-DPA1/SLC7A8/HLA-G/TAP1/HLA-F/HLA-C/HLA-DPB1	MF
GO:0050839	cell adhesion molecule binding	6.24E-05	IQGAP1/CALD1/RAN/COL3A1/FN1/EZR/SERBP1/RAB1A/PKN2/PICALM/LYN/KIF5B/ IGF1/YWHAB/ICAM2/SNX1/HSP90AB1/SWAP70/MYO6/CALR/STAT1/LRRFIP1/COL4A3/ NUDC/EPB41L1/EIF5/ZC3H15/EIF4G1/KTN1/ENO1/ITGB2/SNX2/PCMT1/PPFIBP1/EGFR/ P4HB/DST/TSPAN4/CXADR	MF
GO:0042277	peptide binding	6.24E-05	HLA-DRA/HLA-DQB1/PPP3R1/HLA-B/HLA-DPA1/PPIG/NPEPPS/TNPO1/CRHBP/EDNRB/ SLC7A8/KPNB1/HSP90AB1/CD14/HLA-G/TNPO3/CALR/KPNA2/TAP1/HLA-F/ITGB2/PPIC/ HLA-C/HLA-DPB1/NKTR/PPARG/NPR3	MF
GO:0033218	amide binding	6.24E-05	HLA-DRA/HLA-DQB1/PPP3R1/HLA-B/HLA-DPA1/PPIG/NPEPPS/TNPO1/CRHBP/EDNRB/ SLC7A8/KPNB1/HSP90AB1/CD14/HLA-G/TNPO3/CALR/KPNA2/TAP1/HLA-F/ITGB2/ FOLR1/PPIC/HLA-C/HLA-DPB1/NKTR/COL4A3BP/PPARG/NPR3	MF
GO:0045296	cadherin binding	9.40E-04	IQGAP1/CALD1/RAN/EZR/SERBP1/RAB1A/PKN2/PICALM/KIF5B/YWHAB/SNX1/ HSP90AB1/SWAP70/MYO6/STAT1/LRRFIP1/NUDC/EPB41L1/EIF5/ZC3H15/EIF4G1/KTN1/ ENO1/SNX2/PCMT1/PPFIBP1/EGFR	MF
GO:0003779	actin binding	3.00E-03	CALD1/TPM1/MYH10/GBP1/TAGLN/MYLK/ENC1/PHACTR2/PALLD/EZR/LIMCH1/ MYO6/CXCR4/HCLS1/ACTR3/EPB41L1/GMFG/GC/ADD3/ARPC1B/PLS1/YWHAH/EGFR/ WDR1/KLHL20/CAP1/PTK2/DST/ARPC1A/COBL/SNTB2	MF
GO:0004298	threonine-type endopeptidase activity	5.19E-03	PSMA7/PSMB8/PSMA3/PSMB4/PSMB9/PSMB10	MF
GO:0070003	threonine-type peptidase activity	5.19E-03	PSMA7/PSMB8/PSMA3/PSMB4/PSMB9/PSMB10	MF

PPI Network Construction and Hub-Gene Screening

The major part of the constructed PPI network is presented in Figure 3A. To further reduce the scope for analysis, we analyzed the PPI network by using the four analysis methods in CytoHubba based on the R package Venn diagram. We used the top ranked 20 DEGs to identify seven overlapping hub genes screened through the four CytoHubba methods (Degree, EPC, MCC, and DMNC) in cytoscape software (Figure 3B–F). The seven overlapping hub genes included FUS, DHX15, PRPF31, PQBP1, RBM5, HNRNPR, and TRA2B. Strikingly, the identified hub DEGs in our study have never been reported in literature related to FSGS. In addition, these genes simultaneously ranked to the high position by the four different CytoHubba methods suggests they may play important roles in the development of FSGS.

Gene Expression Validation in *In-Vitro* Experiments

We validated the 7 top ranked hub genes expression in the FSGS model in vitro (Figure 4). Quantitative real-time PCR indicated that the mRNA levels of FUS, DHX15, PQBP1, RBM5, and HNRNPR were up-regulated after they were stimulated by adriamycin (ADR). The changes in PRPF31 and TRA2B mRNA were statistically insignificant.

Except for PRPF31 and TRA2B, the changes in all of the other gene expression levels were consistent with the bioinformatic analysis results (Supplementary Table 1), with the accordance rate reaching 70% approximately.

Extended information on Potential Hub Genes

On the basis of the above results, we used the abbreviations of the seven hub genes and FSGS as keywords to search the NCBI database for identifying the potential relationship between these hub genes and FSGS. Search results revealed that the seven hub genes have never been reported in literature related to FSGS. Then, we carefully collated information relevant to the biological functions and signaling pathways that involve these hub genes on *Gene Cards* website (https:// www.genecards.org). The results indicate that heterogeneous nuclear ribonucleoprotein F (HNRNPF) is closely related to Nrf2 gene expression, renal angiotensinogen gene expression, the TGF-β1 signaling pathway, and oxidative stress. Moreover, RNA-binding motif protein 5 (RBM5) is involved in apoptosis induction in many tumors. Ultimately, in accordance with the accepted pathogenesis of FSGS, we selected HNRNPF and RBM5 as representative targets for further discussion. Extended information on HNRNPF and RBM5 are shown in Table 4.
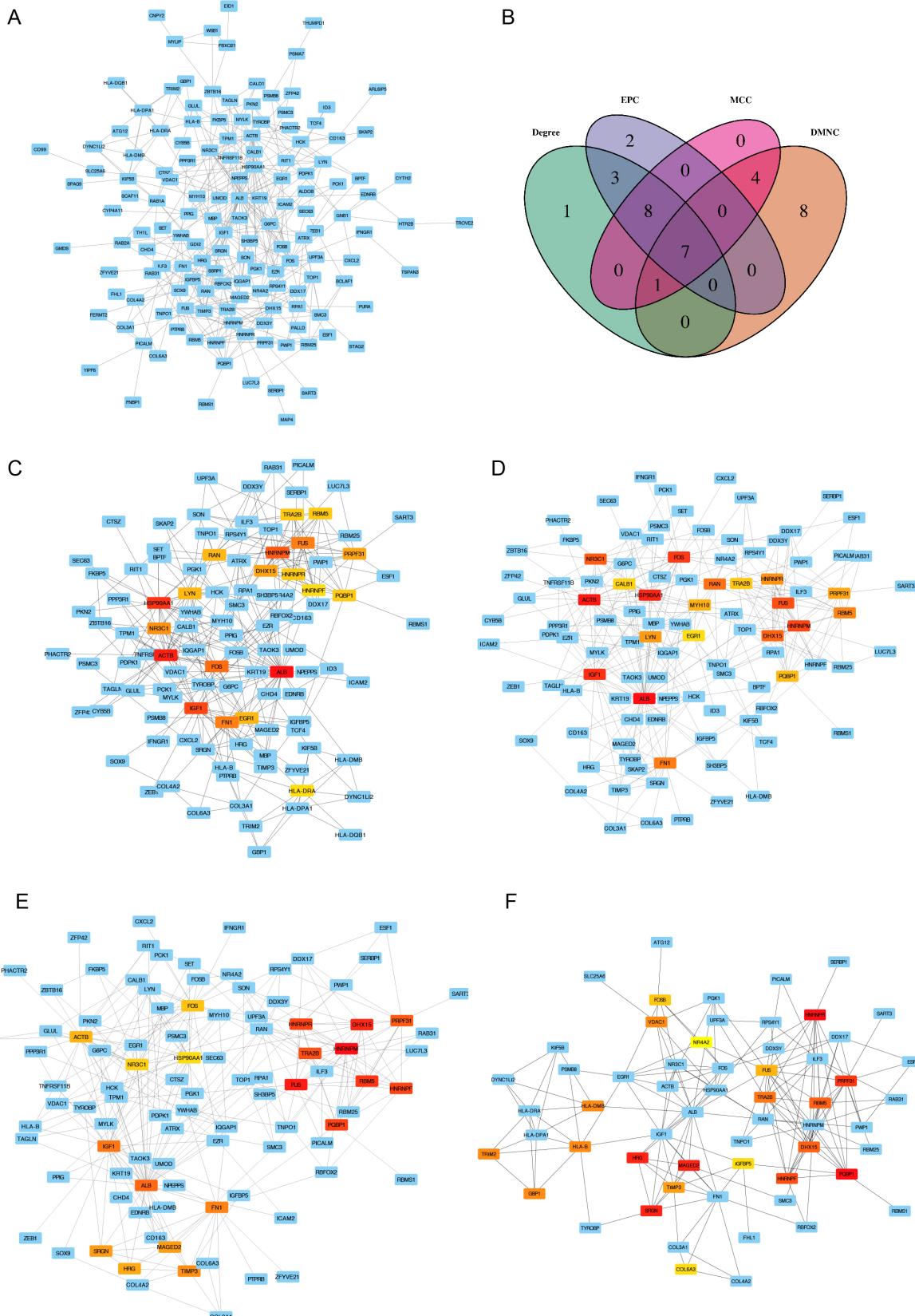
Figure 3: Protein-protein interaction (PPI) networks of DEGs and screening of hub genes

A: The major part of PPI network; B: Venn diagram of differentially expressed genes based on four screening methods including "Degree", "EPC", "MCC", and "DMNC"; C: PPI of DEGs screened by the method "Degree" in Cytohubba; D: PPI of DEGs screened by the method "EPC" in Cytohubba; E: PPI of DEGs screened by the method "MCC" in Cytohubba; F: PPI of DEGs screened by the method "DMNC" in Cytohubba. The depth of red represents the rank of the hub genes.
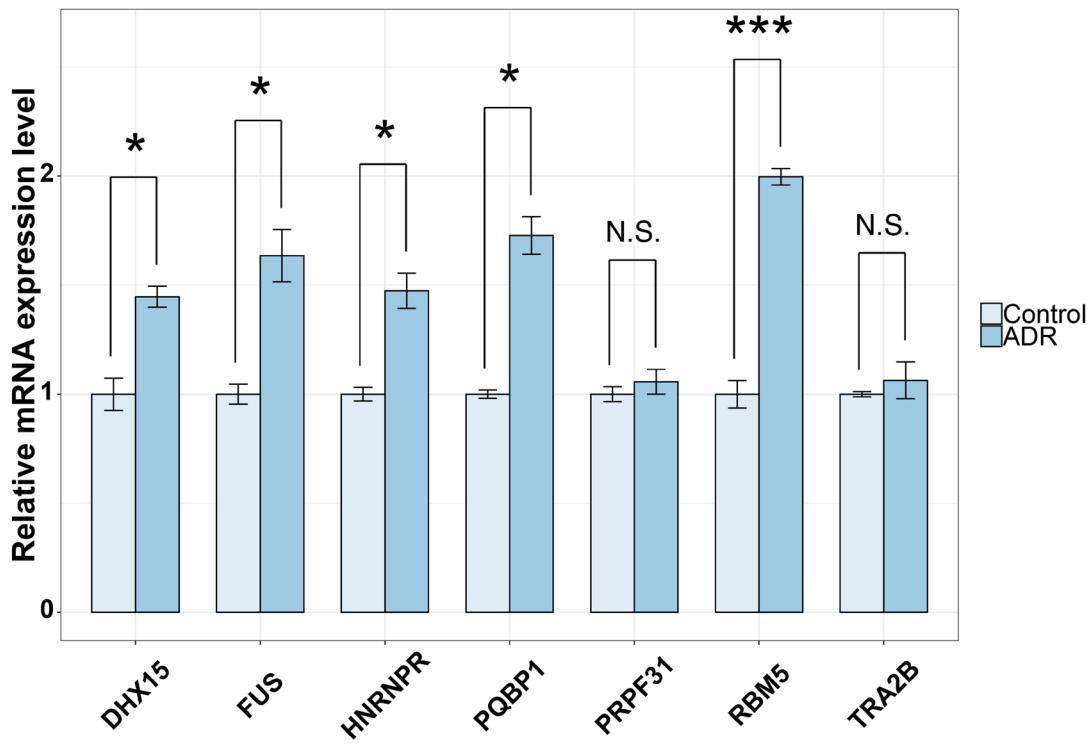
Figure 4. In vitro validation for the novel hub genes

Adriamycin (ADR) (0.125 ug/ml) was used to stimulate confluent conditionally immortalized human podocytes (LY893) for 0 (control) and 48 h. The mRNA expression levels of 7 novel top hub genes were measured by quantitative real-time PCR. The mRNA expression levels of the target genes were normalized to that of GAPDH. The data in three separate experiments were presented as mean ± SD (n=3). *Significantly changed expression levels in ADR-stimulated cells compared with the controls (P<0.05). N.S., no significant difference (P>0.05)

Table 4. Extended Information of The Potential MN-Related Hub Genes.

Gene	Function	Disease/Cells	DOI	Authors
HNRNPF	Stimulates renal Ace-2 gene expression and prevents TGF-β1-induced kidney injury	Diabetes	10.1007/s00125-015-3700-y	Lo CS, Shi Y, Chang SY
	Mediate renal angiotensinogen gene expression and prevention of hypertension and kidney injury	Diabetes	10.1007/s00125-013-2910-4	Abdo S, Lo CS, Chenier I
	Inhibits Nrf2 Gene Expression	Diabetic mice	10.1210/en.2016-1576	Ghosh A, Abdo S, Zhao S
	Against oxidative stress	Diabetic mice	10.2337/db16-1588	Lo CS, Shi Y, Chenier
	Suppresses angiotensinogen gene expression	Diabetic mice	10.2337/db11-1349	Lo CS, Chang SY, Chenier I
	Modulate the alternative splicing of the apoptotic mediator Bcl-x	Human HeLa cells	10.1074/jbc.M501070200	GarneauD,Revil T, Fisette JF
	Modulates angiotensinogen gene expression	Diabetes	10.1681/ASN.2004080715	Wei CC, Guo DF, Zhang SL
RBM5	Inhibition of Wnt/β-catenin signaling and induction of apoptosis	Gliomas	10.1186/s12957-016-1084-1	Jiang Y, Sheng H, Meng L
	Impacts cell proliferation and apoptosis	Lung cancer	10.1615/JEnvironPatholToxicolOncol.2017019366	Prabhu VV, Devaraj N
	Regulates the activity of Wnt/β-catenin signaling	Alveolar epithelial injury	10.3892/or.2015.3828	Hao YQ, Su ZZ, Lv XJ
	Promotes caspase activation	Human neuronal cells	10.1038/jcbfm.2014.242	Jackson TC, Du L,Janesko-Feldman K
	Promotes neuronal apoptosis	Spinal cord injury	10.1016/j.biocel.2014.12.020	Zhang J, Cui Z, Feng G
	Inhibits cell growth and induces apoptosis	Lung adenocarcinoma	10.1186/1477-7819-10-160	Shao C, Zhao L, Wang K

Discussion

Bioinformatics is a newly developed interdisciplinary subject that combines biological science and computer science. Over the past few years, a growing body of research has used gene expression profiles to explore key genes in the pathogenesis of numerous diseases [15,16,40,41]. To our knowledge, our study is the first work that subjected FSGS to bioinformatic analysis. We identified 627 DEGs between the FSGS and control groups. These DEGs included numerous DEGs that have not been previously reported to be involved in FSGS. Then, we predicted DEG functions on the basis of GO annotations. The GO terms we identified included focal adhesion [31,32], cell adhesion molecule [33,34], cadherin [35], and actin binding [36]. These processes are associated with glomerulosclerosis. For example, the genetic deletion of Epb41l5, a podocyte-specific focal adhesome component, results in podocyte detachment, severe proteinuria, and focal segmental glomerulosclerosis development [31]. In immortalized human podocytes, the overexpression of R431C mutant ANLN, an F-actin binding cell cycle gene, enhances podocyte motility [36]. Next, we identified seven overlapping hub genes by constructing PINs through four different analytical methods. Through an accurate search of the NCBI database, we identified HNRNPF and RBM5 as the representative targets for further elaboration.

HNRNPF is a protein-coding gene associated with gene expression. However, no research has been conducted on the role and mechanisms of HNRNPF in FSGS. In this work, we found that HNRNPF is an important DEG among the seven overlapping hub genes in the PPI networks. In addition, HNRNPF is deeply involved with Nrf2 [42], a renal angiotensinogen gene that is expressed in the kidney [43]. Furthermore, in diabetic mice, HNRNPF participates in the TGF-β1 signaling pathway [44] and oxidative stress [45]. These genes and pathways have been confirmed to play vital roles in the pathogenesis of FSGS [4,11,46]. One research suggested that osthole could improve FSGS by activating the Nrf2 antioxidant pathway [47]. TGF-β1 reduces WT1 expression in mouse podocytes and cultured human podocytes before overt glomerulosclerosis begins [46]. In addition, damage to podocytes stimulates TGF-β1 and TGF-βIIR expression in glomerular epithelial cells; this effect eventually leads to extracellular matrix overproduction [48]. On the basis of our analytical results, we conclude that HNRNPF likely participates in FSGS through oxidative stress-associated genes and pathways and is a potential biomarker for this disease.

RBM5 is a nuclear RNA-binding protein that is often genetically deleted in renal cancer[49]. Unfortunately, the role of RBM5 in FSGS remains unreported. In our study, we identified RBM5 as an up-regulated hub gene in FSGS. Moreover, RBM5 actively participates in apoptosis induction in tumors [50,51]. Apoptosis-induced podocyte damage is a key factor in the pathogenesis of FSGS [12,52]. On the basis of previous findings combined with our present bioinformatic analysis results, we speculate that RBM5 may participate in apoptosis promotion during FSGS progression.

Conclusion

Our study provides a fast, powerful, and effective strategy for the discovery of novel diagnostic biomarkers and therapeutic targets for FSGS. Our results suggest that HNRNPF and RBM5 are molecular candidates for the diagnosis and treatment of FSGS. However, our results are preliminary, and further work is needed to decipher these candidate genes.

Author contributions

Q.M and Z.H designed the research; Z.H analyzed the data and performed the research; D.Z wrote the manuscript. All authors read and approved the final manuscript.

Qianhong Ma and Dongmei Zhang contributed equally to this work and should be considered co-first authors.

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Supplementary Table 1

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
RPS4Y1	2.569009422	9.570289361	3.101358611	0.004371381	0.011115768	-2.711721859
PLPP3	2.485089122	9.251833831	7.62668606	2.66E-08	7.13E-07	9.068379301
DDX3Y	2.478844353	7.003027727	2.920309189	0.006843408	0.016208722	-3.132862184
SART3	2.470577198	7.660356798	12.25209245	9.40E-13	5.82E-10	19.16340462
TCF4	2.418989646	7.335132517	11.59356528	3.44E-12	1.27E-09	17.89787797
CYP4A11	-2.412274749	9.12866545	-6.123580669	1.33E-06	1.42E-05	5.192258061
FOSB	-2.356258176	8.074381933	-7.877904555	1.42E-08	4.53E-07	9.690625188
TROVE2	2.355365338	9.457713493	7.605950945	2.80E-08	7.39E-07	9.016659035
IQGAP1	2.290645788	8.14538406	9.69432624	1.94E-10	2.19E-08	13.93671972
MBP	2.255967535	7.587944516	12.62989302	4.56E-13	3.91E-10	19.86587003
CALD1	2.192562666	8.074505734	11.18804096	7.85E-12	2.21E-09	17.09171526
EGR1	-2.182777112	10.2801361	-8.747798502	1.72E-09	1.01E-07	11.78050827
RBFOX2	2.164462681	8.69816763	10.33705244	4.72E-11	8.22E-09	15.33081151
IGFBP5	2.148130254	9.995294632	5.537086859	6.45E-06	5.09E-05	3.626766637
CDC42BPA	2.079395261	9.770721553	7.925115034	1.26E-08	4.20E-07	9.806647308
SMAD1	2.076607382	7.949965987	8.465377555	3.38E-09	1.61E-07	11.11324049
G6PC	-2.074536589	6.566342687	-4.459033616	0.000121983	0.000557225	0.736400459
ALB	-2.073497949	9.571928342	-4.114808392	0.000309678	0.001209773	-0.171567409
ZEB1	2.066318697	8.614493251	10.45925661	3.63E-11	7.03E-09	15.5895635
TPM1	2.060897076	9.232448331	10.04753441	8.88E-11	1.30E-08	14.70977983
FERMT2	2.05930113	7.350506265	7.771402732	1.85E-08	5.49E-07	9.427823748
LUC7L3	2.047718235	8.759118544	8.718232863	1.85E-09	1.06E-07	11.71116708
RAN	2.025548667	10.29196832	11.46235083	4.49E-12	1.47E-09	17.63930778
SLC25A36	2.003665861	8.269066322	8.586494779	2.53E-09	1.31E-07	11.40073865
HLA-DRA	1.992802428	11.12961293	7.574703865	3.03E-08	7.84E-07	8.938615772
HTR2B	1.980142562	6.49870054	5.606952454	5.34E-06	4.35E-05	3.814138409
PCYOX1	1.966411418	7.433879894	7.068593108	1.10E-07	2.03E-06	7.65787493
ATRX	1.961414528	6.588331245	11.16381872	8.25E-12	2.27E-09	17.04289981
DYNC1LI2	1.955508721	9.605304116	10.85559765	1.57E-11	3.64E-09	16.41511633
CD99	1.9554319	9.927197771	8.57318363	2.61E-09	1.33E-07	11.36923982
CHD4	1.94490416	8.814477542	16.59170115	5.35E-16	9.51E-12	26.31762235
MYLIP	1.938154662	9.419703765	7.548038454	3.24E-08	8.23E-07	8.871918527
HNRNPF	1.934376435	8.42993207	13.0216741	2.19E-13	2.32E-10	20.57678872
HLA-DQB1	1.933559554	9.283173095	6.877515473	1.81E-07	2.96E-06	7.16657257
FHL1	1.916965148	7.704294928	10.06888924	8.47E-11	1.27E-08	14.75597408
CTSZ	-1.912814074	8.256096924	-9.422794947	3.59E-10	3.49E-08	13.3308037
DDX17	1.900816911	7.156016292	6.849768897	1.94E-07	3.11E-06	7.094896981
THUMPD1	1.891011353	7.141971356	13.73428793	6.01E-14	1.12E-10	21.82576576
PPP3R1	-1.881530742	7.627366273	-7.148865697	8.96E-08	1.74E-06	7.863044486
TNFRSF11B	1.87836792	7.853323079	7.02736233	1.23E-07	2.20E-06	7.552206366
XIST	-1.863860797	7.615665673	-2.956875261	0.006256155	0.015025427	-3.048847061
SON	1.851258175	7.997946847	8.840334385	1.39E-09	8.53E-08	11.99675806

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
GLUL	1.846739708	7.937765075	9.235752198	5.51E-10	4.67E-08	12.90751377
DKK3	1.838529383	7.235094143	6.88002716	1.80E-07	2.95E-06	7.173056725
BTG1	1.820054032	7.907833291	11.00485807	1.15E-11	2.94E-09	16.72066783
TRIB2	1.81921404	8.182950746	8.768912824	1.64E-09	9.74E-08	11.82995473
RBM5	1.808667325	8.306181873	13.85226391	4.87E-14	1.09E-10	22.02721576
HLA-B	1.803285216	12.34984324	6.340923899	7.42E-07	8.94E-06	5.766672368
MYH10	1.802983311	6.632652763	13.31027341	1.29E-13	1.80E-10	21.08934934
STAG2	1.793115173	5.860191501	13.76494033	5.69E-14	1.12E-10	21.87824888
GBP1	1.783205635	6.97780633	8.494851598	3.15E-09	1.53E-07	11.18338801
RPA1	1.779726763	9.056001662	9.084532378	7.82E-10	5.91E-08	12.56176241
BPTF	1.776426474	7.907083176	7.356751223	5.27E-08	1.17E-06	8.390867161
PCK1	-1.772301574	10.99438749	-4.775458625	5.15E-05	0.000272763	1.580947098
BTN3A3	1.772184439	6.173764331	8.425121851	3.73E-09	1.74E-07	11.01724161
TAGLN	1.764332395	9.007016683	5.779780851	3.34E-06	3.00E-05	4.276795382
PSMA7	1.763068956	6.889044422	11.69687487	2.80E-12	1.22E-09	18.09994223
HLA-DPA1	1.762375082	10.82315093	6.098738113	1.42E-06	1.50E-05	5.126369472
MYLK	1.75861114	10.39524956	6.152944852	1.23E-06	1.34E-05	5.270080435
YIPF6	1.747988074	9.294461389	8.337256865	4.61E-09	2.03E-07	10.80694239
COL3A1	1.741079028	10.03488916	6.880350494	1.80E-07	2.95E-06	7.173891393
ACTB	1.739818254	10.62946301	4.630671948	7.64E-05	0.000379292	1.193646749
DHX15	1.737775319	10.02003843	9.85519139	1.36E-10	1.72E-08	14.29091385
PPIG	1.731145889	7.407036172	7.251707604	6.89E-08	1.43E-06	8.124803038
SCAF11	1.721893208	9.371324456	10.2275776	5.99E-11	9.60E-09	15.09731143
HPGD	-1.717401682	10.07266901	-6.740627536	2.59E-07	3.87E-06	6.812168581
DPP8	1.715249149	9.638588643	8.318534824	4.82E-09	2.09E-07	10.76199707
WSB1	1.714938423	8.596432117	6.91877743	1.62E-07	2.75E-06	7.273007517
ENC1	1.714016384	6.351234133	9.286980973	4.90E-10	4.30E-08	13.02392792
FN1	1.713084538	9.852710944	6.048869862	1.62E-06	1.68E-05	4.993973035
UPF3A	1.706676789	8.950115438	11.59802708	3.41E-12	1.27E-09	17.90663237
KRT19	1.703164941	8.133804492	4.840602977	4.31E-05	0.000235133	1.755562232
BCLAF1	1.697469525	8.139217001	9.830297038	1.44E-10	1.80E-08	14.23633277
FBXO21	1.697287783	9.28818289	5.462538041	7.90E-06	5.94E-05	3.426663378
IFNGR1	1.695558168	9.158556204	8.094628782	8.32E-09	3.11E-07	10.22081389
HCK	1.695111511	7.690905947	7.857688804	1.49E-08	4.67E-07	9.640854784
CXCL2	-1.686811585	6.477878156	-4.50798237	0.000106777	0.000500487	0.866554554
PHACTR2	1.679845963	7.782456361	7.807529456	1.69E-08	5.14E-07	9.517134367
HNRNPM	1.673764753	11.0821542	11.69753948	2.80E-12	1.22E-09	18.10123784
CAMK2N1	-1.651602298	10.19208306	-6.765897326	2.42E-07	3.70E-06	6.877740372
FUS	1.650968802	9.619854977	13.27029455	1.39E-13	1.82E-10	21.01889984
PLPBP	1.650135185	5.59234436	12.81694912	3.21E-13	2.98E-10	20.20749556
PSMB8	1.646543823	10.456135	7.886039857	1.39E-08	4.48E-07	9.71063892
SEC63	1.640469887	7.954060099	6.382735607	6.64E-07	8.19E-06	5.876729688
PALLD	1.635448714	8.943061698	7.556440719	3.17E-08	8.09E-07	8.892944454

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
ZBTB16	1.635125895	7.66230392	3.653696968	0.001057166	0.003348994	-1.358707431
RBM25	1.63291277	6.324655258	8.650201845	2.17E-09	1.18E-07	11.5511557
TYROBP	1.630051539	7.893243583	5.141218255	1.90E-05	0.00012023	2.563038692
DACH1	1.623091259	7.101855154	6.801703043	2.20E-07	3.44E-06	6.970537686
PSMC3	1.612543512	9.366600505	5.93353245	2.21E-06	2.14E-05	4.68711502
RBMS1	1.6103609	8.650805194	4.65105936	7.23E-05	0.000362333	1.248105923
PGK1	1.607870056	10.36413941	5.403307466	9.28E-06	6.73E-05	3.267574125
NPEPPS	1.606521068	8.421329051	7.835158094	1.58E-08	4.88E-07	9.585322216
PTPRB	1.604906513	9.444331687	7.330988837	5.62E-08	1.23E-06	8.325736785
TNPO1	1.599343907	9.775968964	8.87594367	1.27E-09	8.10E-08	12.07966014
EZR	1.591497713	8.757810465	5.97334531	1.98E-06	1.97E-05	4.793136085
MAGED2	1.586605561	10.30790428	12.89378949	2.78E-13	2.81E-10	20.3466641
ANKRD12	1.580638115	7.392354398	6.693843176	2.92E-07	4.26E-06	6.690596121
FNBP1	1.575997647	8.157390697	8.31499427	4.86E-09	2.10E-07	10.75349206
NR4A2	-1.57481871	6.24079609	-8.527861329	2.91E-09	1.45E-07	11.26180965
SERBP1	1.573844316	8.951883468	11.22792569	7.23E-12	2.19E-09	17.17193154
SPAG9	1.573771613	5.928584131	12.82512531	3.16E-13	2.98E-10	20.22233593
SCAMP1	1.572326984	7.135740239	7.680340099	2.32E-08	6.50E-07	9.201956772
RAB1A	1.571530153	8.448144883	6.477980274	5.16E-07	6.71E-06	6.126856918
TAOK3	1.570396428	7.085559648	9.345798665	4.28E-10	3.85E-08	13.15714066
SRGN	1.568368396	9.423138514	5.18175814	1.70E-05	0.000109899	2.672037194
ZFYVE21	1.5676445	6.846082627	7.262978403	6.69E-08	1.40E-06	8.153414092
HRG	-1.562922635	8.320562127	-4.315974661	0.000179859	0.000770138	0.357348521
PWP1	1.561834997	8.446947472	8.857117309	1.33E-09	8.24E-08	12.03585221
SKAP2	1.561530224	9.277742191	7.33501641	5.57E-08	1.22E-06	8.335924267
UBXN4	1.551349919	9.105993907	6.390043816	6.51E-07	8.06E-06	5.895950838
PECAM1	1.550870521	9.054536986	6.663178499	3.17E-07	4.53E-06	6.610791348
MBNL2	1.550572397	7.066502239	10.39994319	4.12E-11	7.62E-09	15.46422432
SOX9	-1.548564432	8.004071342	-6.562764085	4.13E-07	5.60E-06	6.348811078
TRIM2	1.546572067	8.578770031	8.831695492	1.41E-09	8.68E-08	11.97661948
HNRNPR	1.545721471	9.080452193	10.58685737	2.76E-11	5.70E-09	15.85761598
MYOF	1.54258444	8.617870178	7.043673577	1.18E-07	2.13E-06	7.594032778
NR3C1	1.537314952	8.658438842	7.183782173	8.20E-08	1.62E-06	7.95205499
TFPI2	1.530489929	8.411366859	3.999919431	0.000421606	0.001565513	-0.471022596
TMEM47	1.524753951	8.263583054	6.004266035	1.83E-06	1.84E-05	4.875407299
PURA	1.522929493	7.624254878	6.128405127	1.31E-06	1.41E-05	5.20504847
RAB31	1.519313807	8.597342752	6.411935462	6.15E-07	7.72E-06	5.95349937
CYB5B	1.515075529	7.815221603	11.7624269	2.46E-12	1.16E-09	18.22746762
RIT1	1.514871553	7.235874533	7.407198303	4.63E-08	1.07E-06	8.518169631
PRPF31	1.51015233	6.970023854	7.948526057	1.19E-08	4.05E-07	9.864072564
ALDOB	-1.504568555	8.472159452	-3.061872507	0.004824275	0.012090824	-2.80464753
MAP4	1.503555867	8.031894594	5.975611845	1.97E-06	1.96E-05	4.799168802
RAB2A	-1.502751043	8.315889782	-16.2138848	9.61E-16	9.51E-12	25.7672033

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
BTN3A2	1.502705438	7.877942556	6.982291597	1.38E-07	2.40E-06	7.436477371
GMDS	1.497770885	9.599429406	7.605970724	2.80E-08	7.39E-07	9.016708396
CD163	1.496518651	7.363641477	3.780358703	0.000756817	0.002538255	-1.036824644
PKN2	1.492252244	7.396561746	9.26254208	5.18E-10	4.46E-08	12.96843728
PICALM	1.48883338	7.452309182	7.882640103	1.40E-08	4.50E-07	9.702276208
LYN	1.48458898	7.748906756	6.995137981	1.33E-07	2.35E-06	7.469486452
ARL6IP5	1.481819394	9.42435093	6.181264534	1.14E-06	1.26E-05	5.345073096
SH3BP5	1.480757339	9.948617496	7.175018224	8.38E-08	1.65E-06	7.929726958
CYTH2	1.478569815	8.695293012	14.0977443	3.17E-14	7.84E-11	22.44167418
HSP90AA1	1.475101446	10.7822491	5.488461362	7.36E-06	5.62E-05	3.49626449
PDPK1	1.474624621	8.188917333	5.243240876	1.44E-05	9.60E-05	2.837346192
SMC3	1.470872089	7.133595994	11.12401077	8.96E-12	2.41E-09	16.96251038
MBTPS1	1.465393655	8.496997806	7.766899015	1.87E-08	5.53E-07	9.416678054
TIMP3	1.463150322	9.290336056	7.335248955	5.56E-08	1.22E-06	8.336512413
SSRP1	1.462015221	7.615804716	9.043612741	8.60E-10	6.37E-08	12.46766016
NAA35	1.458486577	6.726259229	8.092465915	8.37E-09	3.11E-07	10.21555345
KIF5B	1.454182588	8.394875765	5.616323045	5.20E-06	4.27E-05	3.839255868
DHRS7	1.454116053	7.744616405	9.572938924	2.56E-10	2.65E-08	13.66709981
CNPY2	1.453764841	8.534477403	8.634059418	2.26E-09	1.20E-07	11.51309488
FKBP5	1.452723718	7.291698701	4.149986734	0.000281682	0.001116854	-0.079470163
COL6A3	1.447501816	7.827000817	4.905985588	3.61E-05	0.000203504	1.930987853
COL4A2	1.446665268	7.456526747	6.876736022	1.81E-07	2.96E-06	7.164560203
CALB1	-1.44533189	9.757638848	-2.605850418	0.01452899	0.030801016	-3.831208449
IGF1	-1.437115619	9.406113438	-3.336824653	0.002407335	0.006723822	-2.146238464
NELFCD	1.434489749	9.91051469	11.67139035	2.95E-12	1.22E-09	18.0502204
YWHAB	1.431615777	8.640142735	5.544355542	6.32E-06	5.00E-05	3.646268215
RGCC	1.429769752	7.679603868	4.732902335	5.78E-05	0.000299666	1.466986783
SLC25A6	1.428984166	11.61631244	9.101576376	7.52E-10	5.75E-08	12.60089001
ID3	1.428233521	10.14589451	8.266105018	5.47E-09	2.29E-07	10.63587854
TRA2B	1.424948669	9.497698712	8.624014607	2.31E-09	1.22E-07	11.48939306
GDI2	1.424531564	9.161869349	6.615965347	3.59E-07	4.97E-06	6.48773575
CRHBP	1.423223574	10.85750131	3.501852173	0.001572242	0.004679346	-1.739506163
EID1	1.422600712	9.21370437	7.376173329	5.01E-08	1.13E-06	8.439915301
SET	1.420718447	10.19887727	8.55531067	2.73E-09	1.37E-07	11.32690802
FOS	-1.420440832	9.273302043	-3.000916158	0.005612259	0.013756238	-2.946942453
VDAC1	1.415009019	8.172894871	7.118018567	9.71E-08	1.85E-06	7.784289799
WASHC4	1.412990786	7.331446343	8.01490027	1.01E-08	3.56E-07	10.02649009
UMOD	-1.412526572	11.37016849	-2.38566243	0.024069305	0.047104894	-4.291378203
SERTAD2	1.411604795	8.175798374	8.513812449	3.01E-09	1.48E-07	11.22845173
PQBP1	1.411256434	7.748400335	6.769612323	2.40E-07	3.68E-06	6.887374717
CEP350	1.409862497	6.337432566	7.135793044	9.27E-08	1.79E-06	7.829682626
GLYAT	-1.407015938	9.579743485	-4.089844356	0.000331191	0.001276585	-0.236812106
ICAM2	1.406910331	9.771163793	5.247150209	1.42E-05	9.52E-05	2.84785686

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
GNB1	1.402945544	9.130430125	10.649444	2.42E-11	5.13E-09	15.98830239
HLA-DMB	1.401194865	10.17298113	8.848947598	1.36E-09	8.38E-08	12.01682652
EDNRB	1.398466757	8.373823696	4.94196731	3.27E-05	0.000188026	2.02759004
ESF1	1.398047621	7.471743775	13.05457765	2.06E-13	2.30E-10	20.63569798
AIDA	1.397041007	7.692499594	8.873300307	1.28E-09	8.11E-08	12.07351212
TOP1	1.396150489	8.310821776	7.122657614	9.59E-08	1.83E-06	7.796140615
SNX1	1.393315129	7.77005298	9.617845685	2.31E-10	2.46E-08	13.76708049
CLDND1	1.389278478	8.356235731	7.353059136	5.32E-08	1.18E-06	8.381538064
TSPAN3	1.38922393	9.719295375	4.512799487	0.000105387	0.000495607	0.879374553
SLC7A8	1.388681022	9.335582412	4.354999431	0.000161804	0.000706402	0.460535324
ARHGAP5	-1.388500976	8.373041869	-8.710601093	1.88E-09	1.07E-07	11.69324854
ILF3	1.386329503	6.940492403	8.230768777	5.97E-09	2.45E-07	10.55066888
ATG12	1.384776561	7.242819619	7.607340868	2.79E-08	7.39E-07	9.020127669
ZNF148	1.382618168	8.099582442	12.45022932	6.42E-13	4.62E-10	19.53391159
DLC1	1.379754481	9.408529743	8.406044121	3.90E-09	1.80E-07	10.97166939
MYDGF	1.379051924	8.854924998	9.767015768	1.65E-10	1.97E-08	14.09720669
PSD3	1.379024578	6.766600545	5.210698818	1.57E-05	0.000103008	2.749850991
CDC37	1.377078992	9.468182931	10.45472383	3.67E-11	7.04E-09	15.58000157
KPNB1	1.376929789	9.458847188	9.024827414	8.99E-10	6.56E-08	12.4243824
FOXN3	1.375967793	6.83901797	8.165674647	6.99E-09	2.76E-07	10.39326148
LIMCH1	1.375409137	9.097684708	5.56555133	5.97E-06	4.77E-05	3.703125677
MLEC	1.374524107	9.243909884	6.009168559	1.80E-06	1.82E-05	4.888445732
FABP5	1.370563815	7.473351905	3.638781888	0.001099405	0.003461152	-1.396367326
SCNN1A	-1.367945371	9.167955994	-4.114464255	0.000309965	0.001210427	-0.172467464
TPR	1.367879082	8.216314258	4.77899159	5.10E-05	0.000270724	1.590412014
HSP90AB1	1.36640902	9.19132412	5.419142441	8.89E-06	6.51E-05	3.310113519
ABCF2	1.364898619	7.12749747	8.687031396	1.99E-09	1.11E-07	11.63785903
HNRNPD	1.36405605	9.094619756	8.738208165	1.76E-09	1.02E-07	11.75802893
TGFBR2	1.362070619	7.153715484	5.381838143	9.84E-06	7.03E-05	3.209890462
CD14	1.361767811	8.618764289	5.636868061	4.92E-06	4.09E-05	3.894313936
FRZB	1.361170602	9.126704666	5.082735903	2.22E-05	0.000137296	2.405816869
BBS4	1.360150632	7.202996413	8.971308938	1.02E-09	7.08E-08	12.30081903
HLA-G	1.359808391	10.72098347	5.244182836	1.43E-05	9.58E-05	2.839878762
SWAP70	1.359427598	9.113593244	5.306026158	1.21E-05	8.33E-05	3.006138059
TNPO3	1.358231729	7.693616767	10.42872351	3.88E-11	7.26E-09	15.52510066
LACTB2	-1.355852383	7.530616	-6.671617676	3.10E-07	4.45E-06	6.632763722
CEP57	1.352993373	5.052119046	12.37324173	7.44E-13	4.88E-10	19.39050197
MYO6	1.352421261	9.176047271	5.255177235	1.39E-05	9.36E-05	2.869438127
EPRS	1.351852256	8.607022753	8.649814499	2.17E-09	1.18E-07	11.55024283
LRBA	-1.349799955	8.811192382	-8.795602403	1.54E-09	9.30E-08	11.8923698
CXCR4	1.347649061	8.222517485	3.684201964	0.000975644	0.003135087	-1.281519314
SRRM2	1.347568684	8.460042382	5.001654871	2.78E-05	0.000165066	2.187913815
RPLP0	1.34749233	11.59881981	12.16742107	1.11E-12	6.17E-10	19.00364445

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
ITGA8	1.343209501	8.187995584	5.506346749	7.01E-06	5.43E-05	3.544273858
DDX39A	1.342371076	8.373749992	14.91487814	7.84E-15	2.61E-11	23.77683811
SSBP2	1.341694376	8.032258834	10.36379012	4.46E-11	8.01E-09	15.38759602
HMGCR	1.340708611	7.991412194	7.949010066	1.19E-08	4.05E-07	9.865259037
STX11	1.338253755	6.131744045	8.963225837	1.04E-09	7.12E-08	12.28212241
TTF1	1.335503511	7.454129952	7.565990872	3.10E-08	7.95E-07	8.916832104
AZIN1	1.331515063	6.892036517	13.60307467	7.59E-14	1.17E-10	21.59996308
OAS1	1.328744906	7.180037476	4.581369291	8.74E-05	0.000424389	1.062067683
PLEKHB1	-1.325016546	7.570574431	-8.601436826	2.44E-09	1.27E-07	11.43606785
TMEM230	1.322637972	8.978392691	6.664841119	3.15E-07	4.52E-06	6.615120736
BMPR2	1.321446254	6.459157792	7.530440342	3.39E-08	8.48E-07	8.827852131
ZNF207	1.320509797	9.748881671	7.924554461	1.27E-08	4.20E-07	9.805271384
RAD21	1.320165778	7.728846175	7.217996731	7.51E-08	1.53E-06	8.039137581
HCLS1	1.318686529	9.088478783	7.557331729	3.17E-08	8.09E-07	8.895173607
COG7	1.318315987	7.957007308	6.947663903	1.51E-07	2.60E-06	7.34740937
TSPAN5	1.317168741	7.574432985	7.172334408	8.44E-08	1.66E-06	7.922887565
CALR	-1.316887257	9.46952319	-6.187797543	1.12E-06	1.24E-05	5.362364282
CASP1	1.315406814	7.280061706	6.917554285	1.63E-07	2.75E-06	7.269855086
CD53	1.314626339	9.310209635	4.82374315	4.51E-05	0.000244358	1.710352793
STAT1	1.311254404	7.989702392	8.164628307	7.01E-09	2.76E-07	10.39072663
NASP	1.311023485	8.658422087	8.195333579	6.50E-09	2.59E-07	10.46505182
ATF3	-1.309777911	9.32422844	-4.436888056	0.000129551	0.000586505	0.677587657
LRRFIP1	1.308595239	9.842768068	6.02460185	1.73E-06	1.77E-05	4.929480606
BLVRA	1.307890164	7.463070636	7.883905699	1.40E-08	4.49E-07	9.705389497
TRAM2	1.307573251	8.603172154	6.048923045	1.62E-06	1.68E-05	4.994114324
SPTLC1	1.306960571	7.365444445	8.208877143	6.29E-09	2.54E-07	10.49779515
COL4A3	1.303589773	10.63769098	5.004570724	2.75E-05	0.000164118	2.195748058
DDX41	1.303536766	9.473571199	11.00669283	1.14E-11	2.94E-09	16.72440575
ACTR3	1.302268329	10.75060111	7.097878642	1.02E-07	1.93E-06	7.732811998
ACLY	1.302204054	8.910503391	7.337433307	5.53E-08	1.22E-06	8.342036709
FNTA	1.301806985	9.235960273	8.985880851	9.85E-10	6.90E-08	12.33450181
FCN1	1.301737217	7.825729707	4.507676388	0.000106866	0.000500799	0.865740298
GPM6B	1.30102056	7.554873441	5.23789948	1.46E-05	9.70E-05	2.822985149
NUDC	1.299825767	10.1129032	9.124297995	7.13E-10	5.57E-08	12.65298921
PHB	1.299280352	9.036698753	8.34467426	4.52E-09	2.00E-07	10.82473593
USP1	1.299122208	5.712328518	6.903628133	1.69E-07	2.81E-06	7.233951504
UGCG	1.299100428	7.637255196	6.564098659	4.11E-07	5.59E-06	6.352299401
NUP88	1.298049189	7.778731314	11.63242519	3.19E-12	1.26E-09	17.97404068
LEPROT	1.297113978	11.60207857	4.961828441	3.10E-05	0.000180137	2.080928206
SORD	-1.296373291	9.712182519	-3.408042698	0.002004522	0.00576643	-1.971684138
RNASEH1	1.296211957	8.062974187	7.743815272	1.98E-08	5.73E-07	9.359509858
BGN	-1.293749031	10.83426956	-5.497336355	7.19E-06	5.53E-05	3.520088593
EPB41L1	-1.293565904	8.131970301	-8.910275853	1.18E-09	7.65E-08	12.15942346

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
NT5DC2	1.290854598	7.006657669	5.49509333	7.23E-06	5.55E-05	3.514067608
EIF5	1.290509517	9.992535565	5.777169499	3.37E-06	3.01E-05	4.26981525
JUND	-1.288819693	11.17357526	-13.61921949	7.38E-14	1.17E-10	21.62784642
PLK2	1.287415552	7.339410911	5.759288171	3.53E-06	3.14E-05	4.222009283
M6PR	1.286522924	7.51082701	7.771500991	1.85E-08	5.49E-07	9.428066888
DHRS7B	1.286003609	9.123234779	8.514469828	3.01E-09	1.48E-07	11.23001323
TCF7L1	-1.284417857	9.471134171	-6.21840816	1.03E-06	1.16E-05	5.443338468
TMEM140	1.284344829	9.254354193	10.94233816	1.31E-11	3.20E-09	16.59303621
CYP27B1	-1.28385958	8.032205684	-5.997251595	1.86E-06	1.87E-05	4.856749376
KRAS	1.281495706	8.377790663	6.362344392	7.01E-07	8.55E-06	5.823074564
GMFG	1.279945687	9.288317601	7.459463711	4.06E-08	9.68E-07	8.64973168
PSMA3	1.279565875	10.16490647	5.83933803	2.85E-06	2.64E-05	4.435894253
CNOT2	1.279300816	8.782442522	6.434254514	5.79E-07	7.35E-06	6.01212757
KLC1	1.277054189	9.104980272	7.524681574	3.44E-08	8.56E-07	8.813423521
PLPPR1	-1.276165848	8.240622771	-3.816088742	0.000688405	0.002344447	-0.945391009
ABCG1	1.275777921	7.186008684	6.811441439	2.15E-07	3.37E-06	6.995753313
DAZAP2	1.274142925	9.739018005	7.637559175	2.59E-08	7.01E-07	9.095478672
ERLIN2	-1.273846883	9.305200067	-7.370850264	5.08E-08	1.14E-06	8.426477123
GC	-1.272445074	6.332951466	-2.524545429	0.017546408	0.036095513	-4.004098064
RNF13	1.268534955	10.26760703	5.355043954	1.06E-05	7.48E-05	3.137888261
COL1A2	1.266974585	7.179573515	3.501641194	0.001573104	0.004681133	-1.740031084
ZC3H15	1.266150743	9.172149178	5.200299793	1.61E-05	0.000105414	2.721890801
KMT5B	1.265913904	8.649285188	7.46494521	4.00E-08	9.61E-07	8.663510146
PUM1	1.263073454	8.134411951	6.955641137	1.48E-07	2.55E-06	7.367939869
ADD3	1.258422615	8.997988364	5.947988367	2.12E-06	2.08E-05	4.725622462
KPNA2	1.255126625	8.907075287	6.720095976	2.73E-07	4.03E-06	6.758843409
HLA-DMA	1.254424027	10.37397051	5.785073702	3.29E-06	2.96E-05	4.290942076
THEMIS2	1.253798071	7.019422688	6.789113515	2.28E-07	3.53E-06	6.937924834
GNL3L	1.252325393	7.124510447	10.81838227	1.69E-11	3.89E-09	16.33847971
PSMB4	1.249957625	10.72159802	9.265970538	5.14E-10	4.44E-08	12.97622687
AGMAT	-1.248270761	10.8536785	-3.824270959	0.000673611	0.002304987	-0.924415444
GIPC2	-1.247317538	7.723359098	-4.309932572	0.000182827	0.000781047	0.341387838
DHX9	1.246849962	6.351974134	7.128339548	9.45E-08	1.81E-06	7.810652181
EWSR1	1.246648172	8.535866582	10.08327007	8.21E-11	1.24E-08	14.78704752
SETD5	1.245898909	7.482287092	7.89652774	1.36E-08	4.40E-07	9.736427478
EIF4G1	1.244109972	7.486954023	8.936556557	1.10E-09	7.39E-08	12.22037107
SRSF3	1.243986139	9.803111657	7.286475154	6.30E-08	1.34E-06	8.21301214
ILF2	1.243442066	9.552958146	6.68055437	3.03E-07	4.37E-06	6.656023645
CYP26B1	-1.242450416	8.634347541	-2.397548309	0.02343442	0.046015965	-4.26720407
SERPINE1	1.240736407	6.725458286	4.521128924	0.000103025	0.000486376	0.901546668
PSMD4	1.240423225	10.38557871	10.02544818	9.32E-11	1.33E-08	14.66193831
PDLIM3	1.239425245	7.796445864	8.153301921	7.21E-09	2.81E-07	10.36327807
TMEM87A	1.238174918	8.636838914	8.683893986	2.01E-09	1.12E-07	11.63048026

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
PRRC2C	1.238003417	7.756011399	7.200125227	7.86E-08	1.58E-06	7.993668362
SNX4	1.237495753	7.321680798	7.530106662	3.39E-08	8.48E-07	8.827016208
NRP1	1.236313178	9.129569229	5.883209216	2.53E-06	2.39E-05	4.552965336
WAC	1.235001654	7.03036538	7.197894999	7.90E-08	1.58E-06	7.98799151
SASH1	1.234739955	8.294239034	7.261823684	6.71E-08	1.40E-06	8.15048352
TAP1	1.234734308	9.251835212	8.342764658	4.55E-09	2.01E-07	10.82015571
CHMP2A	1.234514701	10.38085677	5.726260811	3.86E-06	3.38E-05	4.133668805
ARPC1B	1.23312388	9.847594921	6.629826451	3.46E-07	4.86E-06	6.523885973
C1QA	1.232874166	7.267276992	3.49242546	0.001611225	0.004776231	-1.762948256
ZFPM2	-1.231930712	8.037949772	-5.308203625	1.20E-05	8.29E-05	3.011991311
APLP2	1.231910612	10.32603877	7.606109272	2.80E-08	7.39E-07	9.017054163
UTP14A	1.231347458	7.661719061	7.121605911	9.62E-08	1.84E-06	7.793454173
CAT	1.229093195	8.87973752	6.872999304	1.83E-07	2.99E-06	7.15491194
TIA1	1.227747542	7.247584903	9.010951208	9.29E-10	6.61E-08	12.39238301
NAGK	1.22754899	9.926020105	10.36793433	4.42E-11	8.00E-09	15.39638877
TM9SF1	1.227465595	8.623773028	8.253859905	5.64E-09	2.34E-07	10.60636978
GLG1	1.226621678	9.826971817	5.632513248	4.98E-06	4.12E-05	3.882644978
XPNPEP1	1.225389014	8.466825777	7.86771117	1.46E-08	4.60E-07	9.665536137
HYAL2	1.22355501	9.281267332	6.500981316	4.86E-07	6.40E-06	6.18713754
ASF1A	1.223294692	7.739507727	7.51950823	3.48E-08	8.66E-07	8.80045816
WARS	1.221822477	9.608411649	7.31487298	5.86E-08	1.27E-06	8.284953181
TMCO3	1.22011721	9.102616418	4.979257633	2.95E-05	0.000173536	2.127743623
KTN1	1.218156632	6.898784102	5.40406927	9.26E-06	6.72E-05	3.269620769
NNT	1.215568091	6.952880722	5.386246015	9.72E-06	6.96E-05	3.221734225
XPNPEP2	-1.215559549	8.851730714	-3.325159474	0.002480356	0.006893212	-2.174682385
FLRT3	1.210792751	10.14839181	4.168211768	0.000268176	0.001070866	-0.031686858
FADS3	1.209980177	7.375563699	8.103163063	8.15E-09	3.06E-07	10.24156454
ENO1	1.209953356	7.883385651	6.223548255	1.01E-06	1.15E-05	5.45692833
HLA-F	1.209909743	11.83477086	8.124091232	7.74E-09	2.96E-07	10.29240912
PTPRC	1.208351307	5.832030673	8.047207456	9.35E-09	3.38E-07	10.10533478
SYT1	-1.208255658	7.30889895	-4.705882758	6.23E-05	0.000319624	1.394681992
COMT	1.206977299	9.312304131	7.752820425	1.94E-08	5.66E-07	9.381819803
PLS1	-1.206303455	8.261543055	-5.496977729	7.19E-06	5.53E-05	3.519125937
ITGB2	1.205909695	7.91890843	5.254326121	1.39E-05	9.37E-05	2.867149862
SMARCE1	1.205666484	8.972747998	7.373668132	5.04E-08	1.13E-06	8.433591315
SEC14L1	1.205033056	7.939442936	6.08339441	1.48E-06	1.55E-05	5.085651874
POSTN	1.201856865	10.82658185	3.379886179	0.00215532	0.006130585	-2.040877409
DEFB1	-1.200644494	10.99447884	-3.02989907	0.005223435	0.012932645	-2.879463619
TYRP1	-1.200351272	6.207994431	-3.539545898	0.001425307	0.004302374	-1.645531253
IMP3	1.199878035	9.403506224	8.37029393	4.25E-09	1.92E-07	10.88613742
SMARCA2	1.199515299	6.947329006	7.267526219	6.61E-08	1.38E-06	8.164954491
AKAP8L	1.199316813	6.916908369	7.807966077	1.69E-08	5.14E-07	9.518212724
PSMD13	1.198610121	8.052040062	10.25115059	5.69E-11	9.46E-09	15.14772671

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
COPS8	1.1970076	9.204275007	7.044000749	1.17E-07	2.13E-06	7.594871427
AKAP13	1.19666266	7.792140231	6.987365814	1.36E-07	2.38E-06	7.449517889
RRAD	1.196066763	6.953293655	7.077275531	1.08E-07	2.01E-06	7.680102108
PLEKHO1	1.195459638	7.723639306	7.159751859	8.72E-08	1.70E-06	7.89081119
FOLR1	-1.193436488	6.956916716	-3.734922458	0.000853477	0.002814152	-1.152704059
PPIC	1.192607632	8.477886659	6.960597292	1.46E-07	2.53E-06	7.380691668
SNX2	1.192127734	8.610500524	6.157301546	1.21E-06	1.33E-05	5.281621255
MBD4	1.185770843	8.009202546	7.069175367	1.10E-07	2.03E-06	7.659365794
AP3D1	1.18500723	8.6135603	7.725903422	2.07E-08	5.94E-07	9.315102851
HBB	1.184947119	11.93377932	3.343143234	0.002368653	0.006631573	-2.130813886
RNF114	1.183206283	9.30418479	9.465288756	3.26E-10	3.26E-08	13.42629734
ABHD17A	1.181106471	9.170196843	8.329715797	4.69E-09	2.06E-07	10.78884453
LRRC42	1.180209467	7.573503367	8.941836312	1.09E-09	7.34E-08	12.23260386
DDAH1	-1.180008114	11.46433716	-5.151767722	1.84E-05	0.000117466	2.591402158
TSC22D3	1.179816234	8.262843013	4.224652868	0.000230275	0.000942027	0.116582968
GYG1	1.177529499	9.834468492	6.016373152	1.77E-06	1.80E-05	4.907603688
UQCRC2	1.176924599	9.899057439	7.23706376	7.15E-08	1.47E-06	8.087606913
FKBP11	1.176919235	8.727123226	6.266120256	9.06E-07	1.04E-05	5.569402926
TM4SF1	1.176815697	8.331708401	5.239153764	1.45E-05	9.68E-05	2.826357468
AHCYL1	1.176691914	8.745386211	5.330391797	1.13E-05	7.91E-05	3.071632149
SLC28A1	-1.176464801	6.772070338	-8.212773139	6.23E-09	2.52E-07	10.50720966
LGALS3	1.176104581	9.941755013	7.549802161	3.23E-08	8.21E-07	8.876332784
CAVIN2	1.174754505	6.982038785	5.495846891	7.22E-06	5.54E-05	3.516090419
SERPINH1	1.174275681	9.648430496	6.407521754	6.22E-07	7.79E-06	5.941900078
ACTA2	1.173648029	10.38204081	5.932733912	2.21E-06	2.15E-05	4.684987509
HNRNPA2B1	1.173592582	11.06475641	9.665793594	2.07E-10	2.28E-08	13.87352619
AP1S2	1.172535127	8.523906337	5.252624432	1.40E-05	9.41E-05	2.862574763
PNN	1.17087381	7.970795555	7.747188801	1.97E-08	5.70E-07	9.367868879
HLA-C	1.169664398	10.16761106	7.595608208	2.88E-08	7.54E-07	8.990840477
PRPF4B	1.169551009	6.935475927	5.67669604	4.42E-06	3.75E-05	4.000998961
USP48	-1.168630772	9.038096545	-7.747244509	1.97E-08	5.70E-07	9.368006903
MCM7	1.168505141	8.351995021	8.050385686	9.28E-09	3.36E-07	10.11308366
TUG1	1.168335892	9.165666062	6.054292701	1.60E-06	1.66E-05	5.008378733
CASP4	1.167446728	7.679803702	10.35532363	4.54E-11	8.03E-09	15.36962558
FOXO3	1.167411973	8.567526997	5.725633219	3.87E-06	3.38E-05	4.131989636
VAMP2	-1.166211897	7.442364851	-7.873871112	1.43E-08	4.56E-07	9.680699271
PDIA6	1.165260403	10.67248004	5.899377478	2.42E-06	2.31E-05	4.596082594
DDOST	1.164865434	10.9394614	6.470185623	5.27E-07	6.83E-06	6.10641779
PYCARD	1.163566225	7.46929959	5.864762597	2.66E-06	2.50E-05	4.503753551
ZNF24	1.162861739	7.210438195	7.357297992	5.26E-08	1.17E-06	8.392248586
TYRO3	1.161757961	8.189575049	5.5953718	5.51E-06	4.46E-05	3.783092394
ADH6	-1.16166635	8.207644366	-3.436207702	0.001863907	0.005412229	-1.902237878
ACSL3	1.16124775	8.408959315	3.546281515	0.001400494	0.004237233	-1.628698861

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
PARP2	1.161143625	8.581427075	11.19875359	7.68E-12	2.21E-09	17.11328056
MCCC2	-1.160816294	10.45719644	-5.897428416	2.43E-06	2.32E-05	4.590885687
ZNF22	1.159131186	7.261181636	12.5812987	5.00E-13	4.05E-10	19.77645675
RALBP1	1.158724753	8.274230454	7.859219723	1.49E-08	4.66E-07	9.644625716
NUP85	1.156176785	8.422135666	9.538080515	2.77E-10	2.81E-08	13.5892997
CPD	1.156112532	6.819716927	8.154881627	7.18E-09	2.81E-07	10.36710738
HCP5	1.155541743	8.967916149	5.892526241	2.47E-06	2.34E-05	4.577813709
AGTR1	1.155149645	6.968562585	5.121576314	2.00E-05	0.000125603	2.510230811
LIN37	1.155105526	6.577595527	9.667828073	2.06E-10	2.28E-08	13.87803581
CCT6A	1.154913313	9.14834035	7.235166054	7.18E-08	1.48E-06	8.08278478
HNRNPC	1.154717025	8.873047157	6.813932366	2.13E-07	3.35E-06	7.002201462
SLC13A1	-1.15376563	7.5476979	-3.18681201	0.003526296	0.009294589	-2.508681404
VAMP3	1.152730555	7.405947549	4.957816762	3.13E-05	0.000181512	2.070153776
MAP4K3	-1.150486671	7.339441604	-6.152728191	1.23E-06	1.34E-05	5.269506464
JMJD6	1.150291091	7.191119689	12.55420458	5.27E-13	4.05E-10	19.726484
HLA-DPB1	1.150218342	11.36426215	5.525706581	6.65E-06	5.21E-05	3.596230432
SRRM1	-1.149363305	9.137180405	-5.391189648	9.59E-06	6.88E-05	3.235017125
RRAGC	1.149352733	8.837854366	6.475336686	5.20E-07	6.75E-06	6.119925528
ZNF804A	-1.149172983	8.504688414	-5.863390141	2.67E-06	2.50E-05	4.500091338
PSME3	-1.148471143	9.262437167	-5.79437545	3.21E-06	2.90E-05	4.315800219
RBP4	-1.148117964	8.285701455	-2.430483745	0.021754392	0.043227525	-4.199808903
NMD3	1.147678273	7.096738478	5.993365837	1.88E-06	1.89E-05	4.846412134
PSMB9	1.144615141	10.39353049	6.638465727	3.38E-07	4.76E-06	6.546407914
SYNCRIP	1.144133474	7.533673599	5.254346869	1.39E-05	9.37E-05	2.867205645
YWHAH	1.142268582	8.609758108	3.448365406	0.001806203	0.005267323	-1.872190252
DNAJC8	1.141702145	9.890908337	12.41268851	6.90E-13	4.67E-10	19.46406954
ARF4	1.141135381	9.861513946	4.629461092	7.67E-05	0.000380207	1.190413168
CYP1B1	1.139251767	8.983971841	6.038927934	1.66E-06	1.71E-05	4.967557162
FGL2	1.139176467	10.00389177	5.396769049	9.45E-06	6.81E-05	3.250007688
TAX1BP1	1.137965	10.06609394	7.996955328	1.06E-08	3.69E-07	9.982636271
DNAJC7	1.136922569	8.975904344	5.350564296	1.07E-05	7.55E-05	3.125849226
SNRPB	1.13575687	10.70918168	8.092302578	8.37E-09	3.11E-07	10.21515617
WT1	1.132916354	9.05457011	4.948629513	3.21E-05	0.000185305	2.045480572
SLC13A3	-1.132662093	10.63519462	-3.356064493	0.002291407	0.006445268	-2.099233019
EFNB2	1.132430918	8.078269009	5.104816376	2.09E-05	0.000130601	2.465173592
GATM	-1.132347483	9.378659276	-4.820073926	4.56E-05	0.000246052	1.700515384
CNIH4	1.131683601	8.479595575	5.273080806	1.32E-05	8.97E-05	2.917571743
EPHX1	-1.131399427	8.499935775	-2.800395449	0.00915647	0.020779471	-3.404434478
SLC12A1	-1.131269099	9.982695474	-3.262062692	0.002913818	0.007915227	-2.327789665
DDX18	1.12754023	7.44385403	6.968940574	1.43E-07	2.48E-06	7.402152136
ALAS1	1.125667398	9.259205057	10.4312198	3.86E-11	7.26E-09	15.5303756
PIPOX	-1.123197227	9.810383723	-3.323828884	0.002488819	0.006915008	-2.177924155
TMEM204	1.123075986	10.94367823	5.734623996	3.78E-06	3.30E-05	4.156043341

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
IFI16	1.121716104	6.377629496	6.221519431	1.02E-06	1.15E-05	5.451564585
FDPS	1.121519611	9.476641456	5.462769647	7.89E-06	5.94E-05	3.427285292
ADSL	1.120968528	9.354870139	11.7975847	2.29E-12	1.13E-09	18.29564463
C21orf59	1.120241495	9.349721825	8.079662341	8.63E-09	3.19E-07	10.18440035
PLXDC2	1.119961822	6.674408432	6.694948461	2.91E-07	4.25E-06	6.693470854
IK	1.119516839	11.08344752	11.17279646	8.10E-12	2.26E-09	17.06100157
EPB41L5	1.119432184	8.719882514	5.112636291	2.05E-05	0.000128284	2.486196259
PAPOLA	1.11940591	9.203346945	6.556215488	4.20E-07	5.67E-06	6.331691821
BABAM1	1.118621088	9.799168898	13.13465146	1.78E-13	2.09E-10	20.77854969
EIF3A	1.118546997	8.851059563	7.373548512	5.05E-08	1.13E-06	8.433289332
10-Sep	1.11477609	7.162778757	5.1308438	1.95E-05	0.000123054	2.535146373
METTL3	1.114576495	9.512185519	10.75712554	1.93E-11	4.32E-09	16.21193997
RYBP	1.114362488	8.074681305	5.558649075	6.08E-06	4.84E-05	3.684612117
SRSF7	1.114068517	7.812810523	6.78434274	2.31E-07	3.57E-06	6.925561917
SPCS2	1.113642182	10.67916436	10.02665475	9.29E-11	1.33E-08	14.66455361
IL6ST	1.112439922	7.249378474	5.2191725	1.53E-05	0.000101131	2.772634323
CASP3	1.112233366	7.060212477	6.02808801	1.71E-06	1.75E-05	4.938747575
SLC22A8	-1.111645351	8.172587127	-2.906495713	0.007078547	0.016675257	-3.164457325
SLC34A1	-1.111436435	8.827172212	-3.462040019	0.001743365	0.005105454	-1.838343558
SLCO3A1	1.110078679	7.643092094	5.674934307	4.44E-06	3.76E-05	3.996281323
H2AFZ	1.109787786	10.36972324	7.309395678	5.94E-08	1.29E-06	8.271084918
TRAM1	1.109674164	9.330891829	5.475848882	7.62E-06	5.78E-05	3.462403688
CPM	1.108350817	6.344952054	4.511146811	0.000105862	0.000497192	0.874975993
SF3B4	-1.106855958	8.447412686	-11.66922686	2.96E-12	1.22E-09	18.04599558
GPKOW	1.105821203	9.402386711	15.05894645	6.17E-15	2.61E-11	24.00537577
COMMD4	1.105582864	8.633374558	9.573721267	2.55E-10	2.65E-08	13.66884399
NKTR	1.105103578	7.436472493	6.31627032	7.93E-07	9.41E-06	5.701708637
GZMB	1.104615964	6.213304274	4.943201366	3.26E-05	0.000187539	2.030903852
PRKAR1A	1.103349619	9.085496498	6.930113803	1.58E-07	2.69E-06	7.302217123
GAR1	1.103322681	8.867905942	11.69566488	2.81E-12	1.22E-09	18.09758328
PCMT1	1.10293129	9.090122013	8.57858399	2.58E-09	1.32E-07	11.38202189
OSBPL1A	1.101591227	7.294578344	6.029552935	1.71E-06	1.75E-05	4.942641418
CSNK1A1	1.101429726	9.136865726	8.271107725	5.41E-09	2.27E-07	10.64792844
FRY	1.101325533	7.416761028	4.840073415	4.32E-05	0.000235359	1.75414204
ETS2	1.10079836	9.955899787	6.80950633	2.16E-07	3.38E-06	6.990743531
C1QBP	1.099436575	9.443174021	7.90432057	1.33E-08	4.35E-07	9.755579866
CAMK1	1.098714967	7.277320139	8.659802769	2.12E-09	1.16E-07	11.57377593
TIGAR	1.098198376	7.2916035	5.49588839	7.21E-06	5.54E-05	3.516201816
ELF1	1.097652061	9.011134077	8.423523203	3.74E-09	1.74E-07	11.01342471
PPFIBP1	1.096172641	6.181551302	6.404621461	6.27E-07	7.83E-06	5.934277118
TCF25	1.096054149	8.091775108	6.227690486	1.00E-06	1.13E-05	5.467878422
CDC27	1.095817747	8.505153326	4.91940844	3.48E-05	0.000197882	1.967020368
SLA	1.094863831	8.203268999	6.487175988	5.04E-07	6.58E-06	6.150962717

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
NEU1	1.093178847	8.947170302	7.96855995	1.13E-08	3.91E-07	9.913156724
MTDH	1.092673248	9.333952516	4.191473779	0.000251861	0.001016156	0.029369908
RALYL	-1.091884713	8.179522241	-3.770225925	0.0007774	0.002597903	-1.062705647
EGR2	-1.090102058	6.469861827	-4.641895549	7.41E-05	0.000369589	1.223623989
SELENOW	1.089407334	10.83413383	8.564446583	2.67E-09	1.35E-07	11.34855174
DHX35	1.088913326	7.875257997	8.366012273	4.30E-09	1.94E-07	10.87588196
H2AFY	1.088300954	8.945648275	7.534738013	3.35E-08	8.41E-07	8.838617254
FEZ2	1.088132355	9.829802339	6.601202262	3.73E-07	5.13E-06	6.449212407
CXCL1	-1.08797836	7.890182363	-3.583978395	0.001269183	0.003906784	-1.534276712
TUBG1	1.086695059	8.745692451	9.151344631	6.70E-10	5.33E-08	12.71491244
EGFR	1.086214902	6.754578363	6.745928219	2.55E-07	3.84E-06	6.82592863
DERL1	1.086001096	6.89012709	6.279613636	8.74E-07	1.01E-05	5.605021567
CAV1	1.084584181	7.441861966	7.66312002	2.43E-08	6.70E-07	9.159125496
IDH3G	1.082946039	9.572242915	4.996077021	2.82E-05	0.000166977	2.172927883
DDIT4	1.082694616	9.431563963	4.287981287	0.000194025	0.000818704	0.283437599
MT1G	-1.082597887	12.96743712	-5.150025681	1.85E-05	0.000117877	2.586718443
TUBB3	1.081470203	10.81289795	9.271887653	5.07E-10	4.40E-08	12.98966696
EFHC1	1.08144924	8.498565098	9.503313964	2.99E-10	3.03E-08	13.51153807
MPHOSPH8	1.081120204	8.222430403	6.647821917	3.30E-07	4.67E-06	6.570790457
SLC39A6	1.080520811	8.612275262	5.321066886	1.16E-05	8.09E-05	3.046567941
GMPR2	1.080419808	10.1835269	9.982494926	1.02E-10	1.40E-08	14.56870652
PLPP1	1.079549675	12.22298887	4.588629924	8.57E-05	0.000417251	1.081433867
C3AR1	1.079533021	7.464575983	4.520362847	0.00010324	0.000487288	0.899507206
PKP4	1.078988705	7.219341697	4.508110069	0.00010674	0.000500419	0.86689438
SCG5	1.078692914	6.420091104	3.471874341	0.001699488	0.00500128	-1.81396971
CNOT8	1.078685586	8.779292263	6.264621562	9.09E-07	1.05E-05	5.565445885
MKNK2	1.07867287	9.762189026	11.32712576	5.91E-12	1.88E-09	17.37056083
ZNF721	1.077745797	8.69368259	4.543383862	9.70E-05	0.000462503	0.960815239
STK32B	-1.076764142	8.278102207	-6.487474074	5.03E-07	6.58E-06	6.151743993
DAB2	1.076679738	9.010118077	5.160270103	1.80E-05	0.000115318	2.614262168
WDR1	1.075060578	10.70569774	12.48277575	6.04E-13	4.48E-10	19.59432742
DDX50	1.072849739	10.42516752	5.249666541	1.41E-05	9.46E-05	2.854622248
CLDN3	1.07236717	6.08859028	4.843722356	4.27E-05	0.000233435	1.763928086
ZBTB20	1.071588517	9.17400408	4.031253406	0.000387637	0.001460553	-0.389561913
ASNA1	1.071351132	9.062987359	4.634014168	7.58E-05	0.000376438	1.202572636
COL4A3BP	1.069228532	7.496292481	6.771068462	2.39E-07	3.67E-06	6.891150626
DBT	1.068894976	10.81364504	6.479610391	5.14E-07	6.70E-06	6.131130702
KLF6	1.068595042	8.694058607	3.923383883	0.000517366	0.001851367	-0.669284058
KLHL20	1.068504768	7.038412418	10.21355215	6.17E-11	9.83E-09	15.06727982
EED	1.06808641	8.464217814	7.919227461	1.28E-08	4.24E-07	9.792194251
MTF2	1.067468895	7.289425208	9.731404613	1.79E-10	2.08E-08	14.01867335
USE1	1.067373964	8.080264229	8.78600915	1.57E-09	9.41E-08	11.86994673
DIP2C	-1.064411186	8.287020133	-4.950915171	3.19E-05	0.000184439	2.051618708

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
GUCY1A3	1.064369955	8.391717113	7.722954073	2.09E-08	5.98E-07	9.307786878
FABP1	-1.063475899	8.139323754	-2.732116105	0.010784021	0.023903519	-3.556239515
NMI	1.063418627	8.913174785	6.061674729	1.56E-06	1.63E-05	5.027985704
FNDC3B	1.062680278	7.298362048	6.320892845	7.83E-07	9.33E-06	5.713893204
C21orf33	1.062481266	7.988234956	3.425838621	0.001914528	0.005546208	-1.92783153
LAP3	1.062459662	10.15323608	5.869684864	2.62E-06	2.47E-05	4.516887066
HSP90B1	1.06186157	8.503549506	5.777879179	3.36E-06	3.01E-05	4.271712257
ING3	1.061456364	7.638573932	4.825058581	4.50E-05	0.000243541	1.71387968
C1QB	1.061188708	6.688390333	3.127770653	0.004091421	0.010523969	-2.649244412
TMBIM6	1.060676668	12.20049452	4.027508929	0.00039155	0.001473553	-0.39930522
GPR161	1.059734032	6.501724924	6.01425427	1.78E-06	1.81E-05	4.901969665
NAA15	1.057880748	6.432962831	6.629466788	3.46E-07	4.86E-06	6.522948198
SULF1	1.05757773	9.843063851	6.231652537	9.93E-07	1.12E-05	5.478350927
WIPI1	1.056510973	8.27825346	6.246765604	9.54E-07	1.09E-05	5.518286309
ZBTB38	1.056169824	7.302859849	7.766411617	1.87E-08	5.53E-07	9.415471696
CSTF1	1.055434663	7.337081595	10.68718219	2.23E-11	4.83E-09	16.06685271
CX3CR1	1.055309203	8.117188378	3.623156632	0.001145417	0.003583227	-1.435762734
NFYC	1.054756655	6.448423523	8.20428046	6.36E-09	2.56E-07	10.48668483
APOL3	1.054037856	10.02998628	7.311646662	5.91E-08	1.28E-06	8.276784737
PALMD	1.053740224	7.735488403	6.012628847	1.78E-06	1.81E-05	4.897647525
CHTOP	1.052486772	7.220378721	6.679260814	3.04E-07	4.38E-06	6.652657347
SEC11A	1.051884002	10.29217746	4.251936424	0.000213903	0.000885124	0.188406866
VAMP5	1.050721926	10.52172068	4.438313791	0.00012905	0.000584474	0.681372633
ANKLE2	1.05042763	7.196105217	8.876060405	1.27E-09	8.10E-08	12.07993162
CAP1	1.050024945	10.95712377	7.506067683	3.61E-08	8.86E-07	8.766758041
P4HB	1.049010802	10.47300414	4.458270788	0.000122236	0.000558178	0.734373822
PLEKHA1	1.048977766	7.19454498	7.575881532	3.02E-08	7.84E-07	8.941559368
SART1	1.047328783	8.1137404	8.376187797	4.19E-09	1.90E-07	10.90025038
ERBB4	-1.046679912	10.46327143	-7.702647823	2.20E-08	6.23E-07	9.257386132
CPQ	1.046010336	10.54802267	5.912742818	2.33E-06	2.24E-05	4.631713331
FXR1	1.045839377	7.714915221	6.751506073	2.51E-07	3.80E-06	6.840405057
NFASC	-1.043772901	11.00079661	-7.995409742	1.06E-08	3.70E-07	9.978857179
RBM8A	1.043747898	7.545132469	4.96501949	3.07E-05	0.00017886	2.089498913
AATF	1.043262199	9.350762714	7.721186391	2.10E-08	6.00E-07	9.303401537
RNF146	1.042920236	7.254295397	5.404368353	9.25E-06	6.72E-05	3.270424275
PTK2	1.042474572	7.441602272	7.416573273	4.52E-08	1.05E-06	8.541792951
NSFL1C	1.042373942	7.852911437	6.47816252	5.16E-07	6.71E-06	6.127334735
FBXW7	1.041338605	7.484615862	5.840734365	2.83E-06	2.63E-05	4.439622073
NSDHL	1.040858898	7.542287566	9.071986684	8.06E-10	6.00E-08	12.53293586
LSM4	1.040785139	7.644681813	7.310557642	5.92E-08	1.28E-06	8.274027254
FBXO9	1.038692099	7.796898194	5.341521258	1.10E-05	7.71E-05	3.101545225
PPARG	1.037896309	6.88201037	7.302296857	6.05E-08	1.30E-06	8.253105673
GLT8D1	1.037533949	8.106135801	7.178182333	8.31E-08	1.64E-06	7.937789238

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
HMGN4	-1.03747284	9.403636016	-6.593807899	3.80E-07	5.22E-06	6.429909286
PTGER4	1.037231193	6.884584114	5.215070337	1.55E-05	0.000102088	2.761604788
MED6	1.035682324	5.366963402	7.930582401	1.25E-08	4.18E-07	9.820064745
DST	1.034952212	8.875164537	5.651911373	4.72E-06	3.95E-05	3.934617402
IFT27	1.034430229	8.164343121	9.736350061	1.77E-10	2.08E-08	14.02958994
MTUS1	1.033651385	7.914456679	6.513891394	4.69E-07	6.21E-06	6.220950438
ACO2	1.033548604	10.80339959	5.484032163	7.45E-06	5.68E-05	3.484373888
SP3	-1.031245916	9.087202589	-3.605371867	0.001200071	0.003731848	-1.480530029
VDAC3	1.030703765	8.940345624	6.468148347	5.30E-07	6.84E-06	6.101074729
USP39	1.029451601	8.677413981	9.982258621	1.02E-10	1.40E-08	14.56819292
CMTM6	1.02805724	9.525157136	4.774766756	5.16E-05	0.000273084	1.579093631
XYLT1	-1.027723777	8.518221821	-5.498716221	7.16E-06	5.52E-05	3.523792515
ARHGAP19	1.02763613	9.56426488	7.028513894	1.22E-07	2.19E-06	7.55516027
POLR2E	1.027421342	7.924388244	3.308300088	0.002589674	0.00715863	-2.215716541
BTG2	-1.026399219	10.23337218	-7.052038998	1.15E-07	2.10E-06	7.615472284
PRPF19	1.026183615	8.826847728	8.122731764	7.77E-09	2.96E-07	10.2891081
ANKRD11	1.025729915	7.978900966	7.642598687	2.56E-08	6.94E-07	9.108033698
PSMB10	1.024330336	9.421279003	3.339953151	0.002388107	0.006680164	-2.138602883
SRPK2	1.024123484	9.338732967	5.693785151	4.22E-06	3.62E-05	4.04675383
COL4A1	1.024118647	8.992245418	5.104326235	2.10E-05	0.000130711	2.46385594
NRN1	1.024086017	9.095218377	4.759145776	5.38E-05	0.000282366	1.537252436
RSRC2	1.023758956	8.613657235	6.01119626	1.79E-06	1.82E-05	4.893838006
RAC1	1.0232867	11.63257747	4.154851659	0.000278012	0.001103875	-0.066719657
HADHA	1.022601138	10.74473959	6.326166993	7.72E-07	9.21E-06	5.727793185
AUP1	1.021101769	9.246258609	11.719411	2.68E-12	1.22E-09	18.14384431
TXNIP	1.02026765	11.46235662	5.062303643	2.35E-05	0.000143623	2.350896021
TUBB	1.019856466	11.1030305	5.384868531	9.76E-06	6.98E-05	3.218033023
LPL	-1.019304987	9.954464295	-3.318786443	0.002521146	0.006987401	-2.190204228
NPR3	1.019147185	7.765826952	6.380158117	6.69E-07	8.24E-06	5.869949575
GNA11	1.018301382	7.135455751	3.567078203	0.001326501	0.00405132	-1.576653085
ARPC1A	1.018110026	10.05733879	5.427722254	8.68E-06	6.39E-05	3.333160252
TSPAN4	1.017903455	9.153133398	3.286599685	0.002737228	0.007501373	-2.268400912
HNRNPA3	1.017675658	7.627507212	5.584619489	5.67E-06	4.57E-05	3.75426261
JUN	-1.01630629	10.14683512	-8.526608216	2.92E-09	1.45E-07	11.25883533
COBL	-1.016074994	9.359404055	-7.163224111	8.64E-08	1.68E-06	7.899664761
EIF3B	1.015917612	7.916407277	7.295506558	6.16E-08	1.32E-06	8.235902161
COPS6	1.01571967	10.73984087	6.871235397	1.84E-07	3.00E-06	7.150356983
PTPRO	-1.015461858	12.12826016	-4.113981359	0.000310368	0.001211407	-0.173730401
ZFP36	-1.015055803	9.582243452	-6.92601257	1.59E-07	2.71E-06	7.2916514
BUD23	1.014932236	9.485752254	6.221938523	1.02E-06	1.15E-05	5.452672596
PBLD	-1.014740962	10.58094791	-3.724016801	0.000878415	0.002881032	-1.180450248
SNTB2	1.014417654	7.961457348	6.282527181	8.67E-07	1.01E-05	5.612710524
CTDSPL	1.01439347	10.43635804	4.266936434	0.000205397	0.000857252	0.22793438

gene.symbols	logFC	AveExpr	ts	P.Value	adj.P.Val	B
RNF7	1.01409318	9.590065207	9.476640922	3.18E-10	3.19E-08	13.45176623
PTPRN2	1.013187332	9.817821348	9.100558946	7.54E-10	5.75E-08	12.59855544
ZBTB18	-1.012739735	9.549857266	-6.564108062	4.11E-07	5.59E-06	6.352323976
SERINC3	1.012252699	9.515098643	5.004169961	2.76E-05	0.000164243	2.194671288
EPHA4	1.012059148	7.692051937	8.221126207	6.11E-09	2.48E-07	10.52738762
EXPH5	-1.011374294	9.267532038	-6.395702776	6.42E-07	7.99E-06	5.910831112
SLC14A1	1.010232523	8.216419273	4.925155609	3.42E-05	0.00019565	1.982449863
AMPH	-1.008900528	7.734124024	-3.684116541	0.000975864	0.003135087	-1.281735767
HLA-J	1.00871551	10.19609554	8.597452642	2.46E-09	1.28E-07	11.42665058
PRMT5	1.007933207	9.428092233	7.939886786	1.22E-08	4.11E-07	9.842889558
PON2	1.007800835	10.09079366	3.81949425	0.000682209	0.002328987	-0.936662463
FBXW2	1.007654936	7.868340028	7.861953607	1.48E-08	4.63E-07	9.651359007
STX18	1.006898222	10.37920307	10.5061697	3.28E-11	6.42E-09	15.68836623
MRPL9	1.00575951	8.56785435	10.39823871	4.14E-11	7.62E-09	15.4606155
NCOA1	1.005421619	9.05825609	6.916782293	1.63E-07	2.76E-06	7.267865336
EIF3D	1.004960463	10.76774901	9.588105769	2.47E-10	2.61E-08	13.70089836
ZNF45	1.004939996	5.556368284	6.771883066	2.38E-07	3.67E-06	6.893262879
RBL2	1.004173461	7.21346767	8.632505051	2.27E-09	1.21E-07	11.50942809
PTP4A2	1.003941839	7.140081341	8.279182405	5.30E-09	2.24E-07	10.66737061
CXADR	1.003893604	9.64625798	3.484927272	0.001642901	0.004854007	-1.781577202
TTC37	1.001622392	7.444769781	5.465907256	7.83E-06	5.91E-05	3.435710333
ATP6V0E2	-1.001198901	9.83254098	-7.451280242	4.14E-08	9.82E-07	8.629154547
UROD	1.001043527	9.325183612	16.03116183	1.28E-15	9.51E-12	25.49653811
THSD7A	1.001019085	9.626288581	3.889413906	0.00056643	0.001995535	-0.756941013
NFIL3	-1.000765264	8.473403841	-5.219220674	1.53E-05	0.000101131	2.77276385
POLR2A	-1.000463151	8.643383429	-6.408934128	6.20E-07	7.77E-06	5.945612006