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Original Article

Integrative analyses reveal prognostic and immunogenic characteristics of m7G methylation regulators in patients with glioma

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Abstract: Objectives: The expression profiles, biological mechanisms, and clinical relevance of m7G regulators in glioma were studied in this research. Methods: Based on the Chinese Glioma Genome Atlas (CGGA) and The Cancer Genome Atlas (TCGA) datasets, glioma patients, can be categorized into three groups according to 29 m7G regulators, and different subtypes of glioma show different immune cell infiltration characteristics, function enrichment, and clinical prognosis. Three gene clusters were confirmed by utilizing the differentially expressed genes (DEGs) across the three m7G clusters. Results: A prognostic signature based on 12 m7G regulators was established and validated, producing an effective tool for predicting overall survival (OS) in glioma patients. High m7G scores indicated elevated tumor mutation burden and activation of immunity, suggesting an inflamed tumor microenvironment phenotype with poor overall survival. Low m7G scores characterized by a lack of immune infiltration and low mutation burden indicated a non-inflamed phenotype with a favorable clinical prognosis. It was also found that the m7G risk scores can affect chemotherapy sensitivity and prognosis of patients who received immunotherapy. The hub gene *EIF4E1B* of m7G regulators can inhibit the *in vitro* progression of glioma cells by regulating PD-L1 expression through p53 signaling pathway-related inactivation. Conclusions: The m7G prognostic signature can be a biomarker of the overall survival of patients with glioma. An initial *in-vitro* experiment suggested the potential biological mechanisms of immune regulation, with m7G regulators affecting glioma progression by modulating immune responses. The present research provides a better understanding of how m7G regulators function in glioma progression as well as the impact on clinical outcomes, which can provide new insights that might be beneficial for precision therapy of glioma.

Keywords: m7G methylation, glioma, immunotherapy, immune infiltration, prognosis

Introduction

One of the most prevalent malignancies of the central nervous system is human glioma, which accounts for about 80% of primary intracranial malignant tumors [1]. More than 50% of cases of glioma are those of glioblastoma, which is highly malignant [2]. The conventional treatment is maximum tumor resection based on functional area preservation, combined with temozolomide administration, radiotherapy, and standard adjuvant treatment [3]. However, glioma patients typically show high recurrence rates and short overall survival after surgery. Furthermore, the prognosis of glioma patients differs between molecular subtypes [4]. The lack of understanding of the underlying mechanism and regulation networks of associated genes is the primary obstacle to prognosis improvement and the development of effective glioma treatment strategies. Therefore, exploration of the potential molecular mechanisms and gene regulation pathways in individuals with glioma from different perspectives is vital.

Previous studies have explored the effects of various genes on glioma tumorigenesis [5-8]. However, the respective gene regulatory landscapes and mechanisms are not comprehensively elucidated. Methylation is one of the most common modification pathways of transfer ribose nucleic acid (tRNA), including m1A, m5U, M5C, m1G, m2G, and 7-methyguanosine (m7G) [9]. The most prevalent form of tRNA methylation is S-adenosyl-L-methionine (AdoMet)-dependent methylation through AdoMet-dependent methyltransferases. A lot of prior research highlighted the involvement of RNA methylation in tumor advancement [10-12]. m7G RNA methylation is a very conserved modified nucleoside affecting tumor treatment. Knockout of *NSUN2* and *METTL1* can increase the 5-fluorouracil sensitivity of HeLa cells. Methyltransferase-like 1 suppresses colon cancer via the mechanism of activating the m7G-regulated let-7e miRNA/HMGA2 axis [13]. The m7G tRNA methylome also affects the translation of cell cycle genes [14]. However, the function of m7G RNA methylation regulators in glioma remains unclear.

The immune response of tumors is an important process in tumor development [15]. The expression profiles, biological mechanisms, and clinical relevance of m7G regulators in glioma were studied during this research. Subsequently, three m7G clusters and gene clusters were identified, followed by the construction and validation of a prognostic model incorporating several m7G regulators. Moreover, the association of m7G risk scores with chemotherapy and immunotherapy outcomes was also investigated. Furthermore, genetic mutations and immune infiltration levels of varying molecular subtypes and risk population categories were explored, followed by screening potential small-molecule compounds for chemotherapy. In addition, the tumor suppressor effect of hub gene *EIF4E1B* on the progression of glioma was validated via the regulation of programmed cell death protein ligand 1 (PD-L1). The comprehensive findings of the analytical procedures conducted in this study provide new insights into how m7G regulators mediate the clinical prognosis and immune treatment of glioma.

Materials and methods

Patients and samples

Training and validation datasets were provided by the Chinese Glioma Genome Atlas (CGGA) and the Cancer Genome Atlas (TCGA). Both datasets were normalized before further analyses, and samples without follow-up or clinical data were excluded. Through the literature review, 29 m7G RNA methylation regulators were identified (Table S1). There was no need to obtain ethical approval because the data acquisition was from public databases.

Bioinformatic analyses

The following methods were used: (1) The STRING database (https://cn.string-db.org/) was used to perform protein-protein interaction (PPI) analyses. Then, a tabular text file was downloaded and processed using the Cytoscape software (Version 3.9.1). A PPI network was constructed, and the hub genes were identified using the maximum clade credibility method (MCC). (2) The "ConsensusClustering" package was utilized for consensus analysis for the purpose of identifying the potential molecular subtypes. Data dimension reduction was done using a principal component analysis (PCA). (3) The differentially expressed genes (DEGs) were identified by the "limma" package in R software. (4) The gene set enrichment analysis (GSEA) was conducted using GSEA v4.2.3. (5) The R package "GSVA" was utilized to perform gene-set variation analysis (GSVA). (6) Gene Ontology (GO) functional enrichment and Kyoto Encyclopedia of Genes and Genomes (KEGG) analyses were conducted by the R package "clusterProfiler".

The least absolute shrinkage and selection operator (LASSO) regression was used for the construction and validation of a model and selection of the final gene number, followed by multivariate cox regression modeling. The formula used for the calculation of the risk score of each sample was as follows: $coef_1*gene_{Expresion1} + ... + coef_n*gene_n$. Using the median value of risk score, glioma patients were classified into two groups, i.e., a high-risk and a low-risk group. The survival curves of these groups were compared through Kaplan-Meier (KM) analyses, and their predictive ability was assessed using a receiver operating characteristic curve (ROC). PCA was employed to establish a risk classification. A nomograph was produced for individual risk assessment. Subsequently, tumor microenvironment and immune infiltration levels were compared across both risk groups. The correlation between signature genes and drug IC50 values was assessed by Pearson's correlation.

Cell lines and western blotting

Human astrocytes were purchased from BIO-NEED (Beijing, China), and U251 and LN229 were purchased from the BeNa Culture Collection (Beijing). All cells were cultured in DMEM (Sigma-Aldrich, USA) with 10% fetal bovine serum (FBS) at 37°C with 5% CO_2. EIF4E1B and negative control (NC) were synthesized by Santa Cruz Biotechnology (USA). Cell transfection was done using 40 nM *EIF4E1B* RNA or vector for 24 hours. The cell proteins were extracted using RIPA buffer. Protein concentrations were detected using a BCA kit. Incubation of the membranes was done with rabbit anti-human primary antibodies against EIF4E1B (Cell Signaling Technology, USA), E-cadherin, N-cadherin, and Vimentin (Cell Signaling Technology) or β-tubulin (Cell Signaling Technology) as a loading control.

Reverse-transcription quantitative polymerase chain reaction (RT-qPCR)

RT-qPCR was performed as per the guidelines provided by the manufacturer (Takara Bio, Japan). TRIzol kit (Invitrogen, USA) was utilized for total RNA extraction, and cDNA was formed by reverse transcription of 1,000 ng RNA in 20 μL reaction volume. Santa-Cruz Biotechnology designed the following qPCR primer sequences: reverse 3'-AGTGGGAGGAGGAGGAGAAG-5' and forward 5'-GTCCTCCACAGTGTCCACCT-3'. SYBR premix Taq and a CFX96 Real-Time PCR Detection System (Bio-Rad, USA) were employed to perform RT-qPCR. For the relative expression quantification of EIF4E1B, the $2^{-\Delta\Delta CT}$ method was utilized.

Cell migration assay

We utilized 24-well transwell chambers to conduct cell migration assays with 600 μL DMEM and 10% FBS at the bottom. NC and glioma (U251 and LN229) cells (1×10^5) with transfection of EIF4E1B were seeded into the upper chambers with 100 μL serum-free medium. Cotton swabs were utilized to remove cells on the upper surface of the filter following a whole day of culture. In addition, 4% formaldehyde was utilized to fix lower-surface invading cells, followed by their staining using Giemsa solution.

Cell scratchy assay

Horizontal lines were drawn across the back of a six-well plate using a marker at approximately 0.5-1 cm distance from each other. Approximately 1×10^5 NC shRNA and U251 and LN229 EIF4E1B-overexpressing cells were seeded into the six-well plate. A sterile 200-μL pipette tip was employed to scrape the cell monolayer after two days. This was followed by cell washing thrice using PBS to remove loose cells and adding the serum-free medium, after which cell incubation was done at 37°C with 5% CO_2. Photographs were recorded at 0 and 48 hours.

Clonogenic assay

NCs and U251 and LN229 EIF4E1B-overexpressing cells were seeded in six-well plates (1×10^5 cells per well). PBS was employed to wash the cells thrice after a period of 14 days, and then they were stained using 0.2% crystal violet. The surviving colonies were identified as those with a cell number greater than 50. Viability data were standardized based on the NC treatment.

Statistical analyses

A Chi-squared test tested the differences (variations) in categorical variables, and a *t*-test was performed to compare the means. One-way ANOVA was conducted to make a comparison across more than two groups, and multiple comparisons were performed using Dunnett's method. Spearmen correlation analysis was conducted for the purpose of testing correlations between two respective continuous variables. Univariate and multivariate cox regression was employed for the computation of the hazard ratio (HR) and their 95% confidence intervals (CIs). R version 4.0.1 was utilized for conducting all statistical analytical procedures, and statistical significance was reported at $P < 0.05$.

Results

Landscapes of m7G regulators in glioma cases

In total, 29 m7G regulators were identified according to previous studies. Initially, the expression levels of these m7G regulators were compared across tumor and healthy samples, and ten genes (*METTL1*, *NSUN2*, *DCPS*, *CYFIP1*, *GEMIN5*, *NCBP1*, *NCBP2*, *EFIF3D*, *IFIT5*, and *LSM1*) were significantly up-regulated in tumor samples, whereas six genes (*EIF4E*, *EIF4E1B*, *EIF4E3*, *LARP1*, *EIF4G3*, and *NCBP2L*) were significantly down-regulated (**Figure 1A**, **1B**). Furthermore, the gene alteration levels of m7G regulators were evaluated, and overall, the m7G gene alteration rate was 2.6% (23/885). Only *GEMIN5*, *EIF4A1*, and *EIF4G3* had 1% gene alterations, and no gene alterations were found in the other genes (**Figure 1C**). A copy number variation analysis indicated that several m7G genes had high loss frequencies. Furthermore, several genes had high gain frequencies (*METTL1*, *AGO2*, *LSM1*, and *WDR4*; **Figure 1D** and **1E**).

Identification of m7G clusters and their characteristics

Initially, the correlations among the identified m7G regulators were explored. Most m7G regulators showed positive associations with other regulators, whereas EIF4E1B, AGO2, EIF4E3, and DCP2 showed negative correlations with other m7G regulators (**Figure 2A**). A PPI network of m7G regulators was constructed using the STRING database. The top 10 hub genes were identified by means of the MCC method, including *EIF4E*, *EIF4A1*, *AGO2*, *NCBP2*, *EIFE1B*, *NCBP1*, *DCP2*, *EIFE3*, *EIF4G3*, and *EIF4E2* (**Figure 2B**). A network plot showed that *DCPS*, *DCP2*, *NSUN2*, *WDR4*, *METTL1*, *NCHP2L*, *NSNUPN*, *LSM1*, *EIF4A1*, *NCBP3*, *NCBP1*, *GEMIN5*, *EIF4E2*, *EIF4E*, *CYFIP1*, *NUDT4B*, and *NUDT16* were risk factors, whereas other genes were favorable factors with respect to OS (**Figure 2C**). Subsequently, consensus clustering analyses were conducted to explore glioma-related molecular subtypes. The results indicated three molecular subtypes based on m7G RNA methylation regulators. The identified optimal k value was 3, according to the estimated comprehensive correlation coefficient. A consensus matrix indicated three distinct clusters with definite boundaries, suggesting that the clustering was stable and robust (**Figure 2D**). Furthermore, the PCA indicated that three components were distinctly separated (**Figure 2E**). The overall survival curves of the three clusters and KM analyses showed significant differences among the clusters. Cluster 2 showed the best OS, cluster 2 was in second place, and cluster 3 showed the worst OS (**Figure 2F**).

Subtypes based on m7G regulators had different patterns

Functional and expression characteristics of different clusters were also explored. GSVA analysis indicated differences in pathway enrichment among the three subtypes. Upregulation and downregulation of the oxidative phosphorylation, arachidonic and linoleic acid metabolism, sphingolipid, and glycosylate and dicarboxylate metabolism pathways were observed in cluster 2 and cluster 1, respectively (**Figure 2G**). The pyruvate, glyoxylate, dicarboxylate, critical TCA cycle, and pentose phosphate pathways were downregulated in cluster 3 (**Figure 2H**). The metabolism of the xenobiotics-based drug by cytochrome P450 was significantly up-regulated in cluster 1 (**Figure 2I**). Therefore, these findings suggest differences in pathway enrichment, clinical characteristics, and m7G expression profiling between subtypes.

Immune landscape in three m7G clusters

To explore the immune landscape of three m7G clusters, the tumor microenvironment levels among three m7G clusters were compared. Cluster 3 and cluster 1 had higher immune scores. However, no significant variations in stromal, estimate, and tumor purity occurred between the three clusters (**Figure 2J-M**). Furthermore, expression levels of most immune cells varied remarkably across the three molecular subtypes. T, B memory, activated NK, and plasma cells were up-regulated in cluster 1 and cluster 3, whereas M2 macrophages were downregulated (**Figure 2N**, **2O**). Cluster 2 showed upregulation of T cells resting CD4 memory cells and M0 macrophages. Significant variations in immune checkpoint-related genes were observed (**Figure 2P**), and *PD-L1* was highly expressed in clusters 3 and 1 (Figure S1). Clusters 1 and 3 had higher immune content, which may be referred to as the immune-flamed phenotype, defined as a “hot” tumor, whereas cluster 2 may be termed the immune-excluded phenotype, which was considered to comprise “cold” tumors. Coupled with the prognosis and immune content of glioma patients, m7G clustering can effectively classify glioma patients.

Identification of gene clusters based on DEG overlap among m7G clusters

The DEG overlap among three m7G clusters was examined, and 487 DEGs were identified

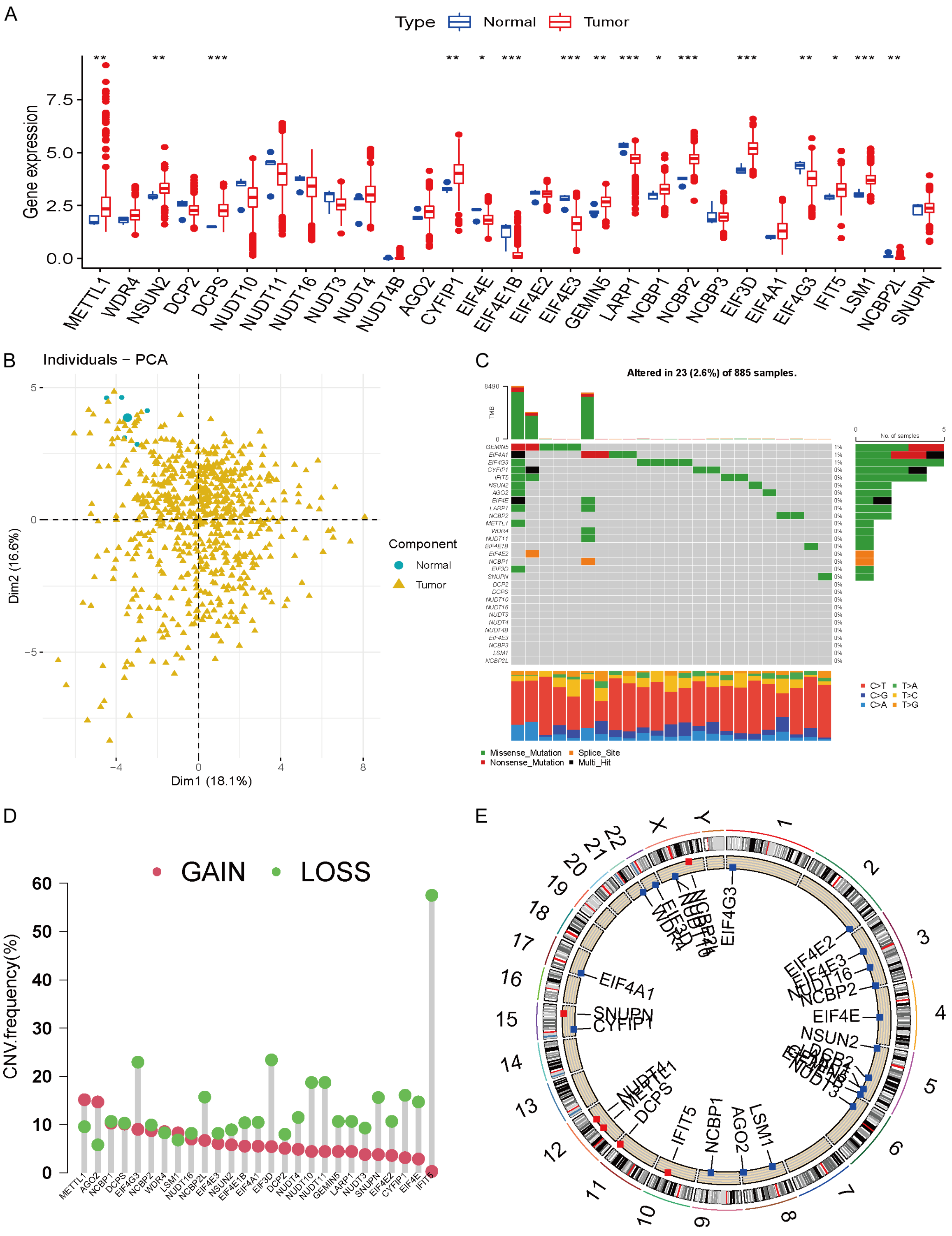


Figure 1. The landscape of m7G regulators in glioma. A: Expression levels of m7G regulators between tumor and healthy samples. B: PCA of m7G regulators between tumor and healthy samples. C: The gene alterations of m7G regulators in glioma. D and E: Copy number variation frequencies of m7G regulators in glioma.

(**Figure 3A**). Consensus clustering was performed, which identified the optimal number of consensus matrices as 3 (**Figure 3B**). PCA and tSNE analysis also confirmed the gene clusters

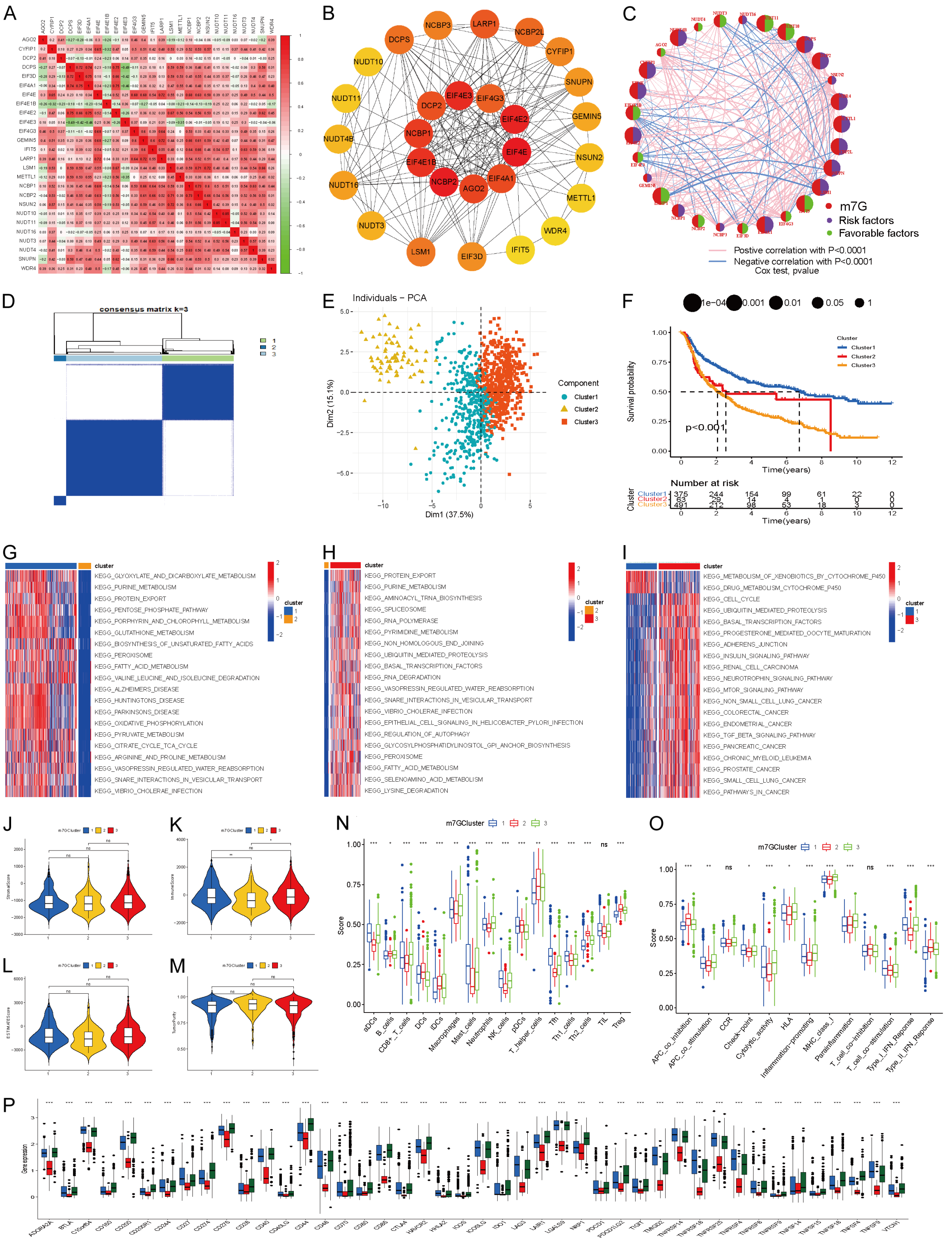


Figure 2. Molecular subtypes of glioma based on m7G RNA methylation regulators. A: Correlation heatmap of m7G regulators in CGGA. B: Protein-protein interaction showing the associations among m7G regulators. C: The correlations of m7G regulators with prognosis. D: Consensus clustering identified the optimal number of subtypes (K = 3). E: PCA showed three distinct clusters. F: Kaplan-Meier analysis indicated significant differences in overall survival among three subtypes. G-I: GSVA indicated the enriched pathways in three m7G clusters. J-M: The differences in stromal, immune, estimate, and tumor purity across three m7G clusters. N and O: Comparisons of immune cell infiltrations and immune function among three m7G clusters. P: Differentially expressed immune checkpoint-related genes among three m7G clusters.

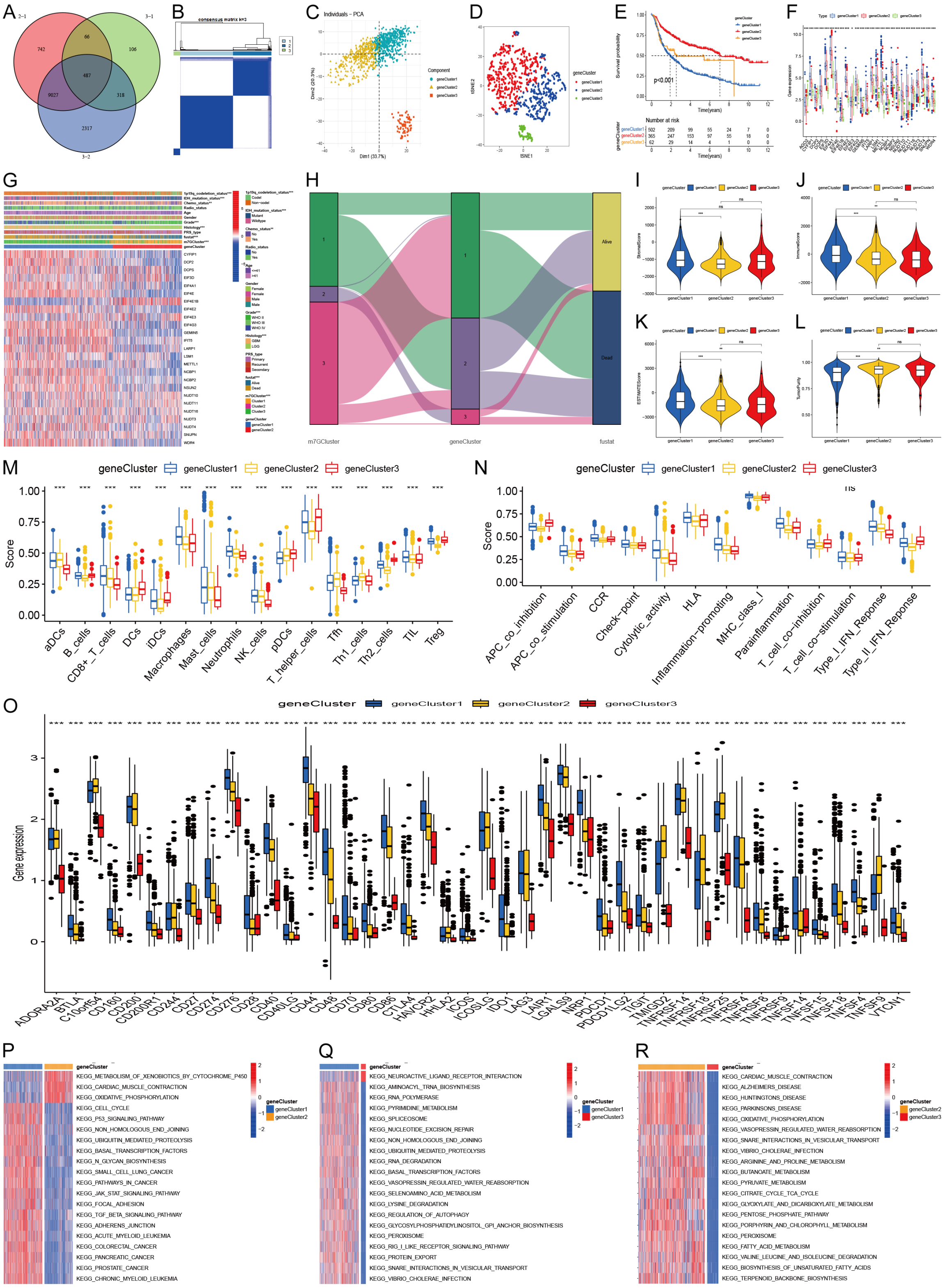


Figure 3. Identification of gene clusters-based DEGs among three m7G clusters. A: A Venn diagram indicating 487 DEGs among three m7G clusters. B: Consensus matrix identified the number of gene clustering. C and D: PCA and tSEN indicated three distinct gene clusters. E: Kaplan-Meier analysis indicated significant differences in overall survival among three gene clusters. F: Expression levels of m7G regulators. G: Expression profiling and clinical features. H: ggalluvial analysis indicated changes from m7G clusters to survival outcomes. I-L: Differences in stromal, immune, estimate, and tumor purity. M and N: Comparisons of immune cell infiltrations and immune functions. O: Differentially expressed immune checkpoint-related genes. P-R: GSVA indicated the enriched pathways.

(**Figure 3C**, **3D**). The KM curve indicated the worst OS exhibited by cluster 1, followed by gene cluster 3, whereas gene cluster 2 had better overall survival (**Figure 3E**). m7G regulators showed markedly different expression among the three gene clusters (**Figure 3F**). The gene clusters were associated with 1p19q, IDH mutation, chemotherapy, tumor grade, histology, and m7G clusters (**Figure 3G** and **3H**). Tumor microenvironment analysis indicated high stromal, immune, and estimate scores in gene cluster 1. Gene clusters 2 and 3 showed similar stromal, immune, estimate, and tumor purity scores (**Figure 3I-L**). Similarly, greater immune cell infiltration scores were presented by gene cluster 1 (with respect to aDCs, B cells, CD8+ T cells, macrophages, mast cells, neutrophils, NK cells, TIL, Treg) and immune function score (APC stimulation, CCR, checkpoint, cytolytic activity, HLA, inflammation-promoting, MHC class I, parainflammation, T cell inhibition, type I IFN, and type II IFN). Gene cluster 3 showed higher DCs, T helper cells, TH2 cells, and APC_co_inhibition (**Figure 3M** and **3N**). Immune checkpoint-related genes showed higher expression levels in gene clusters 1 and 2 than in gene cluster 3 (**Figure 3O**). The GSVA indicated the primary enrichment of gene cluster 1 in the cell cycle, P53 and JAK-STAT signaling, and TGF beta signaling pathways, and gene cluster 2 was predominantly enriched in oxidative phosphorylation, pyruvate metabolism, citrate cycle TCA cycle, and energy metabolism pathways. Gene cluster 1 was enriched with regard to RNA polymerase degradation, lysine degradation, regulation of autophagy, and protein export, among others (**Figure 3P-R**).

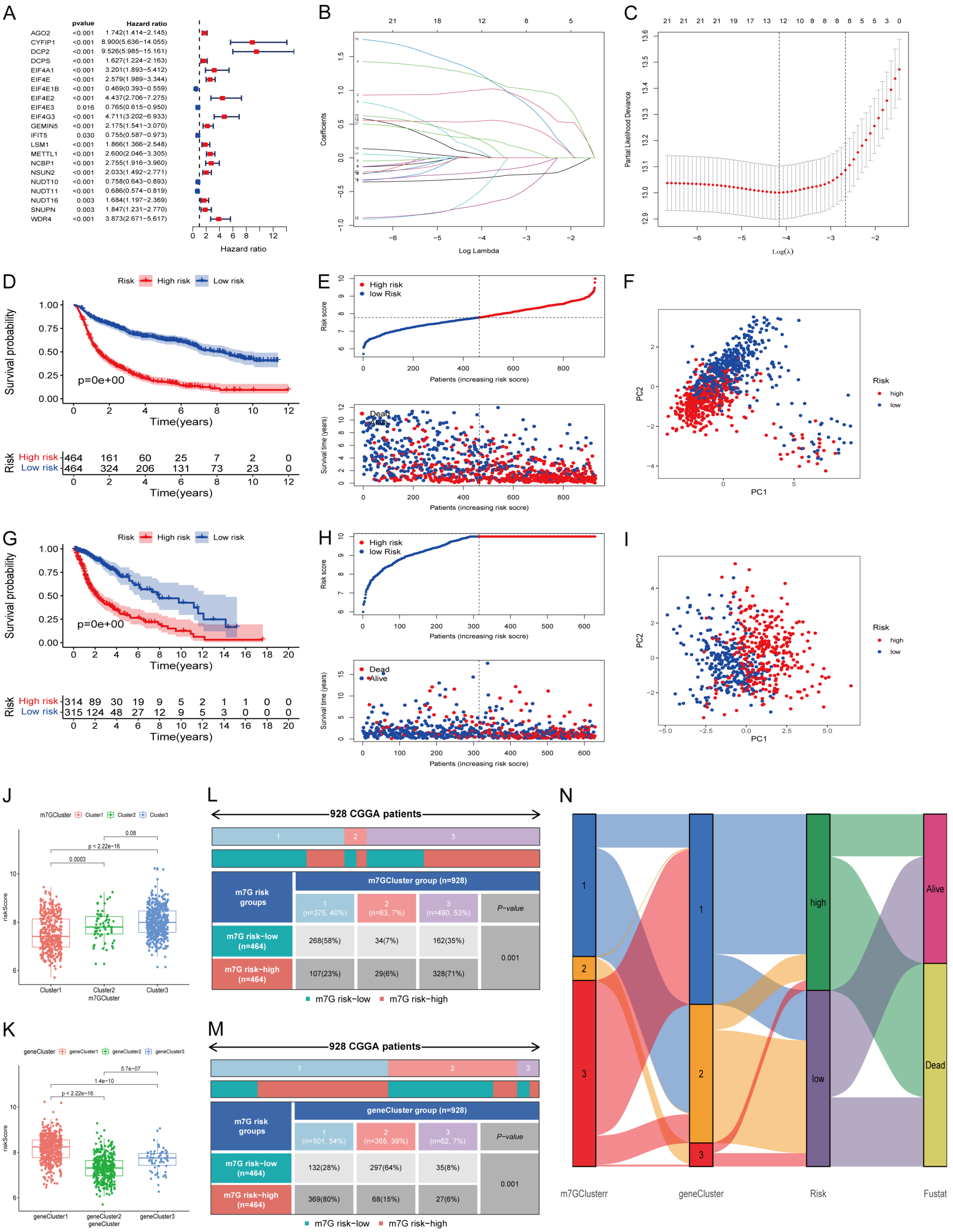
Development and validation of m7G regulator-based predictive model

Univariate cox regression analyses for m7G regulators were conducted, and 21 prognosis-related m7G genes in glioma cases were identified, including 16 risk genes and five protection genes (*FIF4E1B*, *EIF4E3*, *IFIT5*, *NUDT10*, and *NUTD11*; **Figure 4A**). Then LASSO regression analyses were conducted, and 12 m7G genes were identified for the development of a prediction model (**Figure 4B** and **4C**, Table S2). Among these 12 genes, *CYFIP1*, *DCP2*, *EIF4A1*, *EIF4G3*, *LSM1*, *METTL1*, *NCBP1*, and *WDR4* were risk genes, and *EIF4E1B*, *GEMIN5*, *IFIT5*, and *NUDT11* were protective genes for glioma. For the CGGA training dataset, glioma patients were classified into high- and low-risk groups as per their median risk scores. KM analyses indicated a poorer OS of high-risk patients compared to the others ($P < 0.001$; **Figure 4D**, **4E**). The PCA indicated two markedly separated components in glioma individuals (**Figure 4F**). In the TCGA validation dataset, similar survival trends (**Figure 4G**, **4H**) and risk components were identified (**Figure 4I**). The model's prediction ability was further assessed using the training and validation datasets. For CGGA, the one-, two- and three-year area under the curve (AUC) values were 0.712, 0.783, and 0.779, respectively. The one-, two-, three-year AUC values were 0.778, 0.782, and 0.750, respectively. The model validation was done with the help of the TCGA dataset, showing comparably high prediction ability.

To validate the stability of the model, stratified analyses were further performed with different clinical parameters (Figure S2A-T). Age group, gender, WHO stage, 1p19q codeletion status, IDH mutation type, and radiotherapy and chemotherapy status did not affect poorer survival of the high-risk group ($P < 0.001$). No differences in the OS were seen among patients with GBM, WHO IV, and secondary type ($P > 0.05$). The risk scores of m7G clusters and gene clusters were also compared, and the results found that m7G cluster 3 had the highest risk scores, followed by cluster 2, and m7G cluster 1 had the lowest risk scores (**Figure 4J**, **4K**). By contrast, gene clusters ranked by risk scores from highest group to lowest were gene clusters 1, 3, and 2. The population distributions of m7G clusters and gene clusters differed significantly (**Figure 4L-N**).

Tumor microenvironment and immune landscape of different risk groups

The individuals with high risk exhibited higher stroma, immune, and estimate scores in contrast with the other group, whereas tumor purity was lower in individuals with high risk (**Figure 5A-D**). To explore the effects of the risk group on immune infiltration, immune cells and components in both risk groups were investigated. Most immune cells exhibited elevated levels in the high-risk groups (**Figure 5E**), apart from neutrophils and Tfh cells. All immune-related functions were significantly elevated in individuals with greater risk scores (**Figure 5F**). Regulatory T cells and M0, M1, and M2 macro-



m7G risk groups	m7GCluster group (n=928)			
	1 (n=375, 40%)	2 (n=63, 7%)	3 (n=490, 53%)	*P−value*
m7G risk−low (n=464)	268(58%)	34(7%)	162(35%)	0.001
m7G risk−high (n=464)	107(23%)	29(6%)	328(71%)	

■ m7G risk−low ■ m7G risk−high

m7G risk groups	geneCluster group (n=928)			
	1 (n=501, 54%)	2 (n=365, 39%)	3 (n=62, 7%)	*P−value*
m7G risk−low (n=464)	132(28%)	297(64%)	35(8%)	0.001
m7G risk−high (n=464)	369(80%)	68(15%)	27(6%)	

■ m7G risk−low ■ m7G risk−high

Figure 4. Development and validation of m7G regulator-based prognostic signatures. A: Forest plot of univariate cox regression in CGGA. B and C: Parameter selection tuning by cross-validation using LASSO regression. D: Kaplan-Meier curves of risk groups in CGGA. E: Distribution of risk score and patients as per the risk score in CGGA. F: Display of two components by PCA in CGGA. G: Kaplan-Meier curves of two risk groups in TCGA. H: Distribution of risk score and patients as per the risk score in TCGA. I: Display of two components by PCA in TCGA. J and K: Risk scores in different m7G and gene clusters. L and M: Risk distributions in different m7G and gene clusters. N: ggalluvial analysis indicated changes of m7G clusters, gene clusters, greater and smaller risk, and survival outcomes.

phages showed positive correlations with risk scores, whereas a negative correlation was observed for activated NK cells, monocytes, activated mast cells, and eosinophils with risk scores (**Figure 5G-N**). Furthermore, the correlations of signature genes with immune subtypes were explored, and 12 signature genes involved in three immune subtypes (C3, C4, and C5) were identified. These signature genes showed significant differences in expression levels among immune subtypes ($P < 0.001$; **Figure 5O**). A greater tumor mutation burden was observed for patients with high risk in comparison to the others (**Figure 5P**), and the TMB showed a positive link to risk score ($R = 0.44$, $P < 0.001$; **Figure 5Q**). In addition, the differences in immune checkpoint-related genes were compared for the two groups, and all immune checkpoint-associated genes were significantly expressed in individuals with greater risk (**Figure 5R**). Moreover, the correlations of signature gene expression with cancer stem cell-like properties were compared (RNAss, DNAss) and the TME (stromal score, immune score, and ESTIMATE score). WDR4, SCP2, NUDT11, EIF4E1B, GEMIN5, NCBP1, EFI4G3, and IFIT5 were positively associated with RNAss levels, whereas CYFIP1, EIF4A1, and LSM showed negative correlations with RNAs. METTL1, WDR4, DCP2, CYFIP1, EIF4A1, and LSM1 were positively associated with DNA levels. Positive-related genes (*METTL1*, *CYFIP1*, *WDR4*, *EIF4E1B*, *LSM1*) and the negative-related genes *IFIT5*, *DCP2*, *NUDT11*, and *LSM1* showed similar trends with respect to stromal, immune, and estimated scores (Figure S3).

Functional and pathway enrichment analysis

To study possible mechanisms in different risk groups, GO functional enrichment and KEGG pathways analyses was conducted. A total of 320 DEGs were identified (152 down-regulated and 168 up-regulated genes; Table S3) in the CGGA dataset and 1,461 DEGs (322 down-regulated and 1,139 up-regulated genes; Table S4) in the TCGA dataset. GO analysis indicated remarkable enrichment of extracellular structure and organization, presynapitc, collagen-containing, and GABA receptor complexes in individuals with high-risk scores (**Figure 6A**). KEGG analysis showed that ECM-receptor interaction, cell cycle, p53 signaling pathway, PI3K-Akt signaling pathway, protein digestion, and absorption were also enriched in the high-risk group (**Figure 6B**).

Gene alterations and methylation changes in different risk groups

A waterfall plot was produced, showing that IDH1 mutation was 38% and 90% in the high- and low-risk group, respectively. Some genes showed high mutation frequencies in individuals with greater risk, such as *EGFR*, *PTEN*, *RYR2*, *FLG*, and *PKHD1* (**Figure 6C**). The low-risk group showed high mutation frequencies with respect to *CIC*, *IDH2*, and *APOB* (**Figure 6D**). The two groups had similar trends in variant type, classification, and SNV class (**Figure 6E**, **6F**). Several co-occurrence pairs were identified: LRP2-TP53, SPTA1, DNAH17; HYDIN-TTN, EGFR-COL6A3 in individuals with greater risk, and MYH1-DNMT3A, NIPBL-IDH2 in individuals with lower risk (**Figure 6G**, **6H**). The methylation levels of m7G regulators were remarkably increased in individuals with greater risk, apart from NUDT11, NCBP2, LSM1, and NCNP2L (**Figure 6I**).

Clinical correlation, independent analysis, and risk assessment

The high-risk group tended to be GBM, recurrent type, advanced WHO stage, aged, and treated without chemotherapy or radiotherapy (**Figure 7A**). The 1p19q non-codeletion ratio and wildtype ratio were also greater in individuals with elevated risk scores compared to the others ($P < 0.001$, **Figure 7B**).

In the CGGA training set, univariate cox regression depicted a positive association of elevated risk scores with poor OS (HR: 3.154, 95% CI: 2.739-3.631, $P < 0.001$; **Figure 7C**), and multivariate cox regression identified the role of the risk score in independently predicting OS in glioma patients (HR: 1.769, 95% CI: 1.473-2.125, $P < 0.001$; **Figure 7D**). Furthermore, risk score independence was validated in the TCGA dataset and its significant association was observed with OS (univariate: HR: 1.574, 95% CI: 1.447-1.711, $P < 0.001$; **Figure 7E**; multivariate: HR: 1.332, 95% CI: 1.027-1470, $P < 0.001$; **Figure 7F**). Moreover, it was found that age, grade, primary-recurrent-secondary type, IDH, 1p19q status, and chemotherapy also affected the OS of individuals with glioma. In addition, the model stability was assessed using

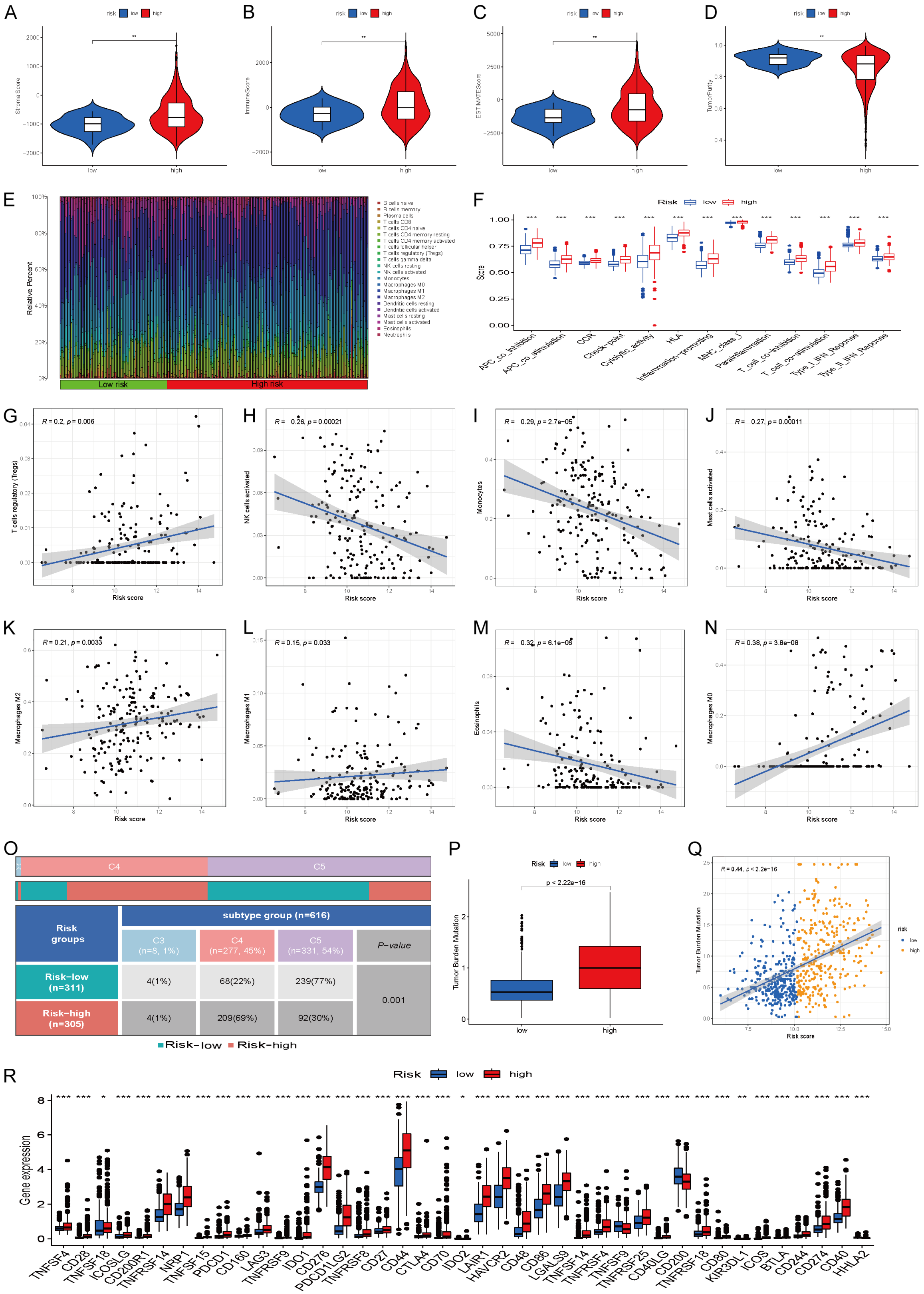


Figure 5. Immune infiltration analysis of two risk groups. A-D: Boxplot showing the comparative analysis of stromal, immune, Estimation scores, and tumor purity between two risk groups. E and F: Comparisons of immune-related cells and functions of two risk groups. G-N: Scatter plot showing risk score's association with regulatory T cells, activated NK cells, monocytes, activated mast cells, M0, M1, and M2 macrophages, and eosinophils. O: The immune

subtype distributions of risk groups. P and Q: The correlation of risk score with tumor mutation burden. R: Differentially expressed immune checkpoint-related genes in both risk groups.

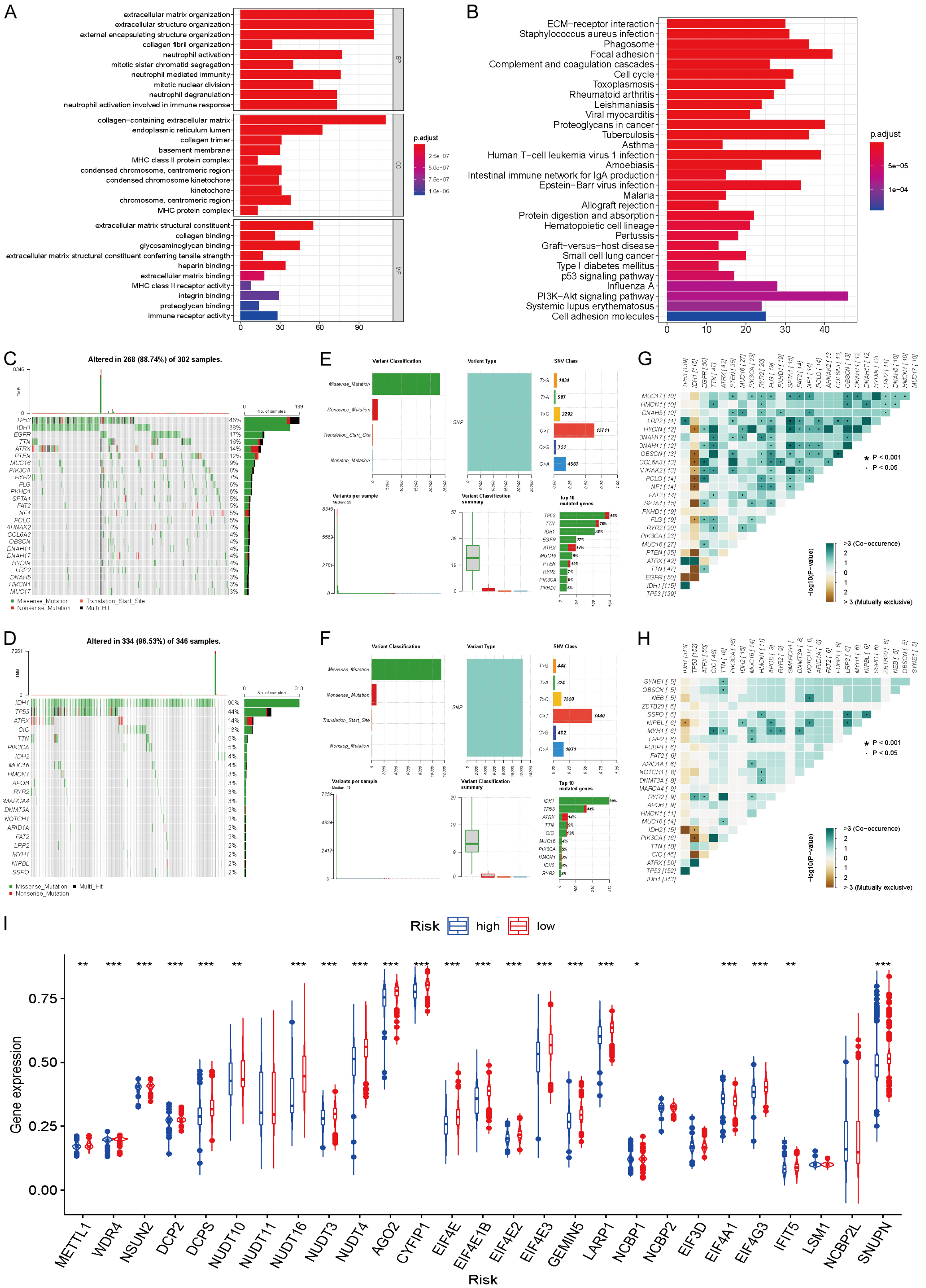


Figure 6. Functional enrichment, pathways analysis, gene alterations, and methylation changes in different risk groups. A and B: GO enrichment analysis of differentially expressed genes between high- and low-risk groups. C-E: Gene alteration levels in the high-risk group. F-H: Gene alteration levels in the low-risk group. I: Methylation levels of m7G regulators between both risk groups.

the calibration curve in training and validation sets. The one-, two- and three-year calibration curves were scattered around the reference line (**Figure 7G-I**). An OS probability prediction tool with clinical parameters and risk score was developed (**Figure 7J**). The C-index was high (0.802, 95% CI: 0.782-0.820). The multi-ROC indicated that the risk score achieved the best prediction ability for the five-year OS of individuals with glioma (**Figure 7K**).

Chemotherapy sensitivity and immunotherapy

The IC50 level of several conventional chemotherapeutic agents was compared between the two risk groups. Those of ACAR and AKT inhibitor VIII were greater in subjects with elevated risk scores, suggesting that glioma may be resistant to these two drugs (**Figure 8A**, **8B**). The IC50 values of Vinblastine, Tipifarnib, Rapamycin, Pyrimethamine, Pazopanib, JNK inhibitor VIII, Gemcitabine, Docetaxel, Vinorelbine, and Cisplatin were lower in subjects with greater risk showing their sensitivity to these drugs (**Figure 8C-L**). Pearson correlation tests were conducted between identified signature genes and several drugs to identify small-molecular compounds. *CYFIP1* was correlated with 13 compounds, and *DCP2, METTL1*, and *WDR4* were correlated with one compound (Figure S4). The details are shown in Table S5.

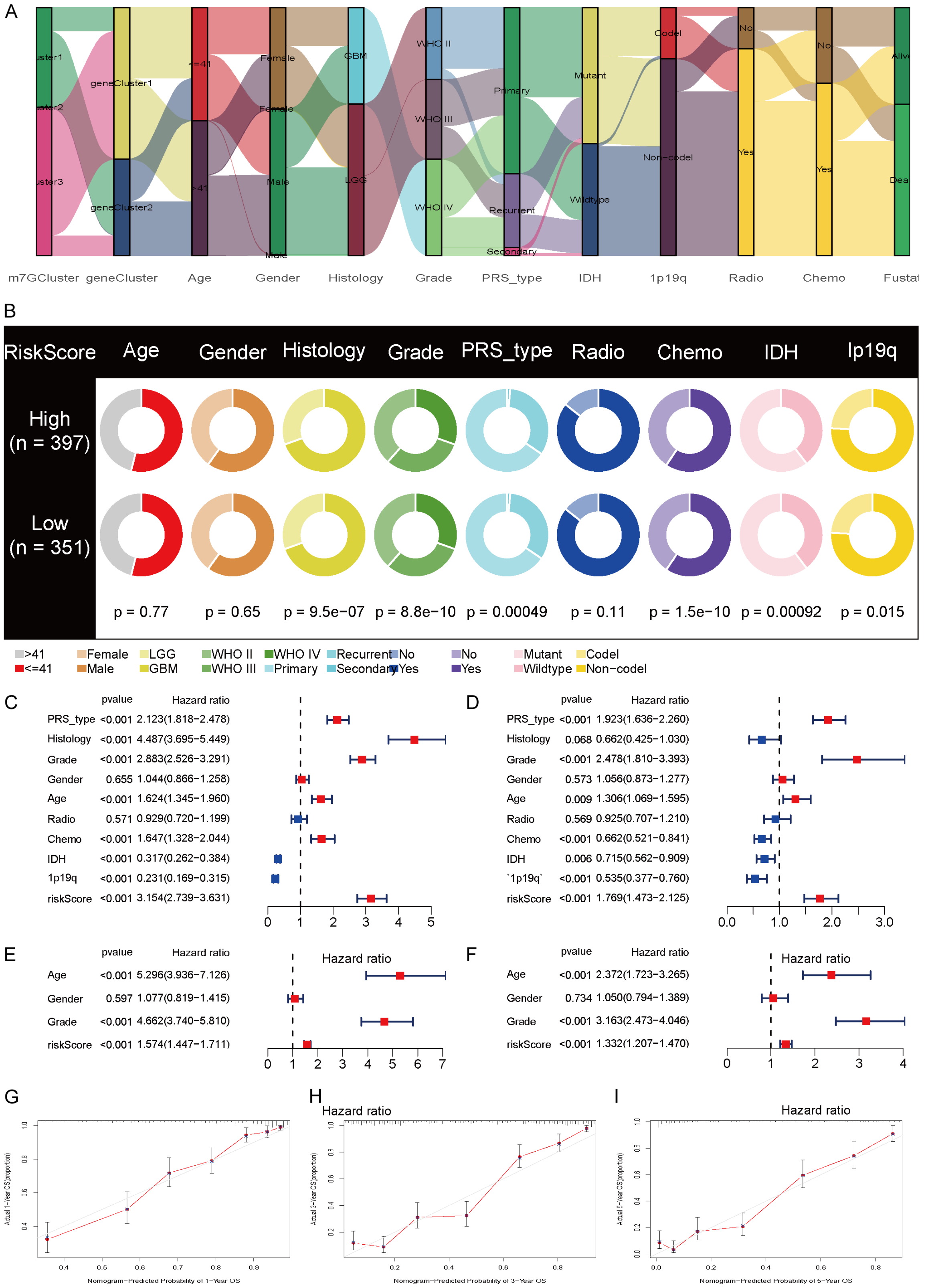
The influence of m7G risk score on immunotherapy was also assessed, and it was observed that the TIDE, MSI, and exclusion were elevated, and immune dysfunction was lowered in subjects with greater risk (**Figure 8M-P**). Using an IMigor dataset, m7G risk scores were produced, and the SD/PD group showed greater risk scores (**Figure 8Q**). The SD/PD ratio was higher in the high-risk group ($P < 0.001$; **Figure 8R**). Furthermore, a worse overall prognosis was observed for subjects with greater risk in contrast with the others ($P < 0.001$; **Figure 8S**).

Inhibition of PD-L1 expression by overexpression of hub gene EIF4E1B through the p53 signaling pathway in glioma

To explore the function of m7G regulators on the progression of glioma, the DEGs between cancerous and healthy samples were screened, and the overlap of the top 10 hub genes was examined. *EIF4E1B* was identified for *in vitro* validation. *EIF4E1B* was expressed at lower levels in glioma tissues (**Figures 9A**, S5). Its expression decreased with increasing tumor grade (**Figure 9B**), and elevated *EIF4E1B* expression indicated a better prognosis for glioma patients (**Figure 9C**). Univariate and multivariate cox regression indicated EIF4E1B as an independent prognosis predictor in subjects with glioma (HR: 0.745, 95% CI: 0.647-0.858; **Figure 9D**, **9E**).

EIF4E1B overexpression in glioma cells was established (**Figure 9F**). The clonogenic assay suggested that *EIF4E1B* overexpression inhibited glioma cell growth *in vitro* (**Figure 9G**). The scratch assay indicated that *EIF4E1B* overexpression inhibited the migration ability of glioma cells (**Figure 9H**). Similarly, the migration and invasion abilities were also suppressed owing to *EIF4E1B* overexpression (**Figure 10A**, **10B**). m7G regulators were involved in immune infiltration in glioma, and EIF4E1B expression showed a negative link to PD-L1 expression (**Figure 10C**). KEGG pathway analysis indicated that the p53 signaling pathway was significantly and negatively enriched when *EIF4E1B* was highly expressed (**Figure 10D**). p53 is a tumor-suppressing gene, and prior research indicated that the frequencies of p53 mutation are very high, which are associated with tumorigenesis and immune escape [16-18]. The association of *TP53* expression with tumor mutation burden in glioma patients was studied, and expression of the key gene *TP53* of the p53 signaling pathway was positively associated with TMB (Figure S6).

Furthermore, *EIF4E1B* expression showed a negative link to *TP53* expression in glioma cases (**Figure 10E**). Western blotting indicated that *TP53* and *PD-L1* expression was reduced when *EIF4E1B* was overexpressed (**Figure 10F** and **10G**). qPCR results also indicated that relative mRNA levels of *TP53* and *PD-L1* were significantly decreased during elevated *EIF4E1B* expression (**Figure 10H** and **10I**). These findings were indicative of the role of *EIF4E1B*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High (n = 397)
Low (n = 351)
p = 0.77
p = 0.65
p = 9.5e−07
p = 8.8e−10
p = 0.00049
p = 0.11
p = 1.5e−10
p = 0.00092
p = 0.015
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PRS_type <0.001 2.123(1.818−2.478)
Histology <0.001 4.487(3.695−5.449)
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Gender 0.655 1.044(0.866−1.258)
Age <0.001 1.624(1.345−1.960)
Radio 0.571 0.929(0.720−1.199)
Chemo <0.001 1.647(1.328−2.044)
IDH <0.001 0.317(0.262−0.384)
1p19q <0.001 0.231(0.169−0.315)
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PRS_type <0.001 1.923(1.636−2.260)
Histology 0.068 0.662(0.425−1.030)
Grade <0.001 2.478(1.810−3.393)
Gender 0.573 1.056(0.873−1.277)
Age 0.009 1.306(1.069−1.595)
Radio 0.569 0.925(0.707−1.210)
Chemo <0.001 0.662(0.521−0.841)
IDH 0.006 0.715(0.562−0.909)
`1p19q` <0.001 0.535(0.377−0.760)
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Gender 0.734 1.050(0.794−1.389)
Grade <0.001 3.163(2.473−4.046)
riskScore <0.001 1.332(1.207−1.470)
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Actual 1−Year OS(proportion)
Nomogram−Predicted Probability of 1−Year OS
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Hazard ratio
Actual 3−Year OS(proportion)
Nomogram−Predicted Probability of 3−Year OS
0.2
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1.0
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Hazard ratio
Actual 5−Year OS(proportion)
Nomogram−Predicted Probability of 5−Year OS
0.0
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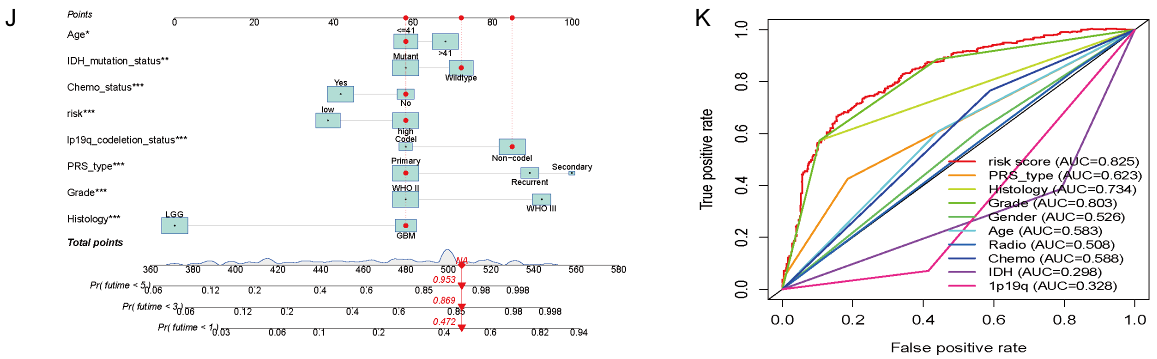


Figure 7. Independent prognosis analysis of risk score. A: Changes of m7G clusters, gene clusters, clinical characteristics, and survival outcomes. B: Correlation of risk groups with clinical characteristics. C and D: Univariate and multivariate cox forest plot of the risk score in CGGA. E and F: Univariate and multivariate cox forest plot of the risk score in TCGA. G-I: Calibration plots of the nomogram to predict OS over one, three, and five years in the CGGA. J: Nomograph predicting one, three, and five-year OS probabilities as per the m7G prognostic signature. K: Multi ROCs of the prognostic capability of risk score and clinical parameters for 5-year OS.

as a tumor suppressor gene through the activation of immune responses in glioma cells.

Discussion

This study produced several key findings. (1) Using expression profiling of m7G regulators, six hub genes were identified in glioma (*EIF4E*, *NCBP2*, *EIF4E1B*, *NCBP1*, *EIF4E2*, *EIF4E3*). (2) Glioma patients can be divided according to three molecular subtypes using m7G regulators, and different molecular subtypes show divergent biological function and pathway enrichment, clinical characteristics, survival prognosis, and immune infiltration patterns. (3) A prognostic signature model was constructed based on 12 m7G regulators, which was validated through an independent cohort dataset. The risk assessment tool based on prognostic risk score can accurately predict the survival probability of glioma patients. (4) Three gene clusters based on DEGs among three m7G clusters were obtained, and different immune phenotypes were confirmed. (5) The signature genes were closely associated with immune subtypes. Different risk groups also showed different immune infiltration levels and immune functioning, especially about eosinophils, M0 macrophages, activated NK cells, activated memory T cells, and regulatory T cells. The function and pathway enrichment and gene alteration levels were also different. (6) Several small-molecular compounds associated with m7G regulators were also identified, which may provide insights for treatment strategies. The m7G risk score affected the prognosis of patients who received immunotherapy. (7) Expression of the tumor suppressor gene *EIF4E1B* can inhibit the progression of glioma cells via inhibiting *PD-L1* expression *in vitro*, and this process is achieved through the regulation of the p53 signaling pathways in glioma cells. Therefore, this study produced new insights regarding biological mechanisms and immune treatment of glioma.

Covalent modification after the synthesis of biomolecules is a key aspect of intracellular signal transduction and is vital for numerous physiological mechanisms. RNA molecules, like proteins, undergo extensive post-synthetic covalent modifications that constitute the transcriptome [19]. RNA modifications can affect RNA processes and characteristics such as splicing, stability, and location [20]. Numerous RNA modifications have been identified through mass spectrometry. However, such approaches merely provide snapshots of the RNA modification landscape, and the number of discovered modifications is steadily increasing [21, 22]. m7G is present in eukaryotic mRNA5' caps and at defined internal positions in tRNAs and rRNAs across all domains of life [23]. However, there are few studies on the role of m7G methylation modification. Considering the potential effect of some similar modifications on many diseases, including tumors, it was assumed that m7G methylation modification might also be vital for the biological mechanisms and clinical relevance of tumors. Initially, the molecular subtypes of glioma were studied using the observed m7G regulators, resulting in three

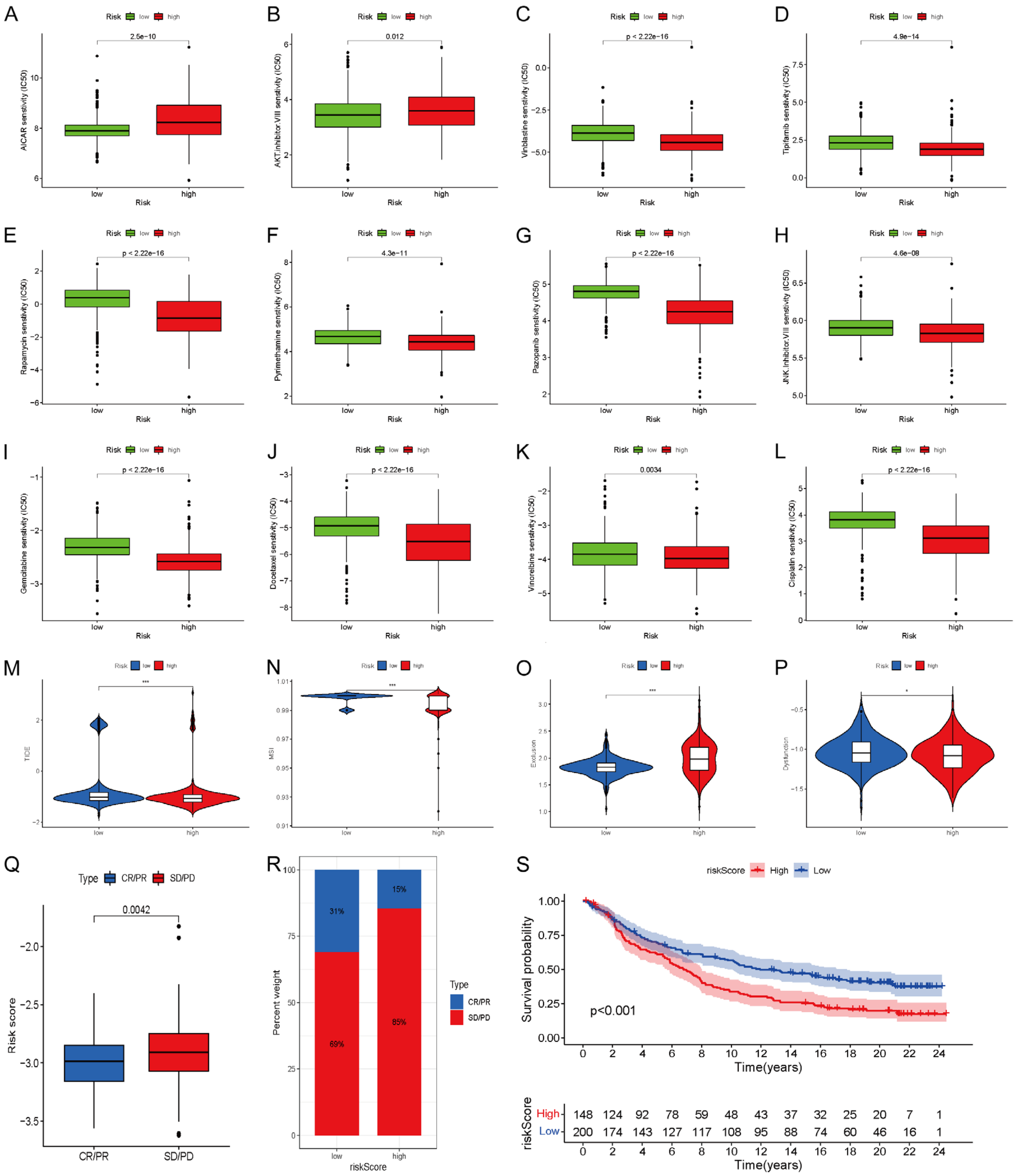


Figure 8. Effect of m7G risk score on chemotherapy sensitivity and immune therapy. A, B: Chemotherapy resistance drugs in high-risk groups. C-L: Chemotherapy-sensitive drugs in high-risk groups. M-P: The TIDE score indicated that the high-risk group showed better immune response. Q: SD/PD group receiving immune therapy had higher risk scores. R: The rate of CR/PR is higher in the low-risk group. S: The high-risk group had a worse prognosis after immune therapy in IMigor.

clusters with markedly different expression profiles and clinical characteristics. Significant expression differences in m7G regulators were observed. These clusters also showed significant differences in some basic clinical characteristics such as tumor grade, histology, IDH mutation, and 1p19 codeletion status.

Furthermore, different subtypes had different clinical prognoses, which suggested the potential use of m7G regulators for molecular clustering. Subsequently, using 12 m7G regulators, a prognostic signature capable of predicting the OS of subjects with glioma was developed and thoroughly validated using an independent

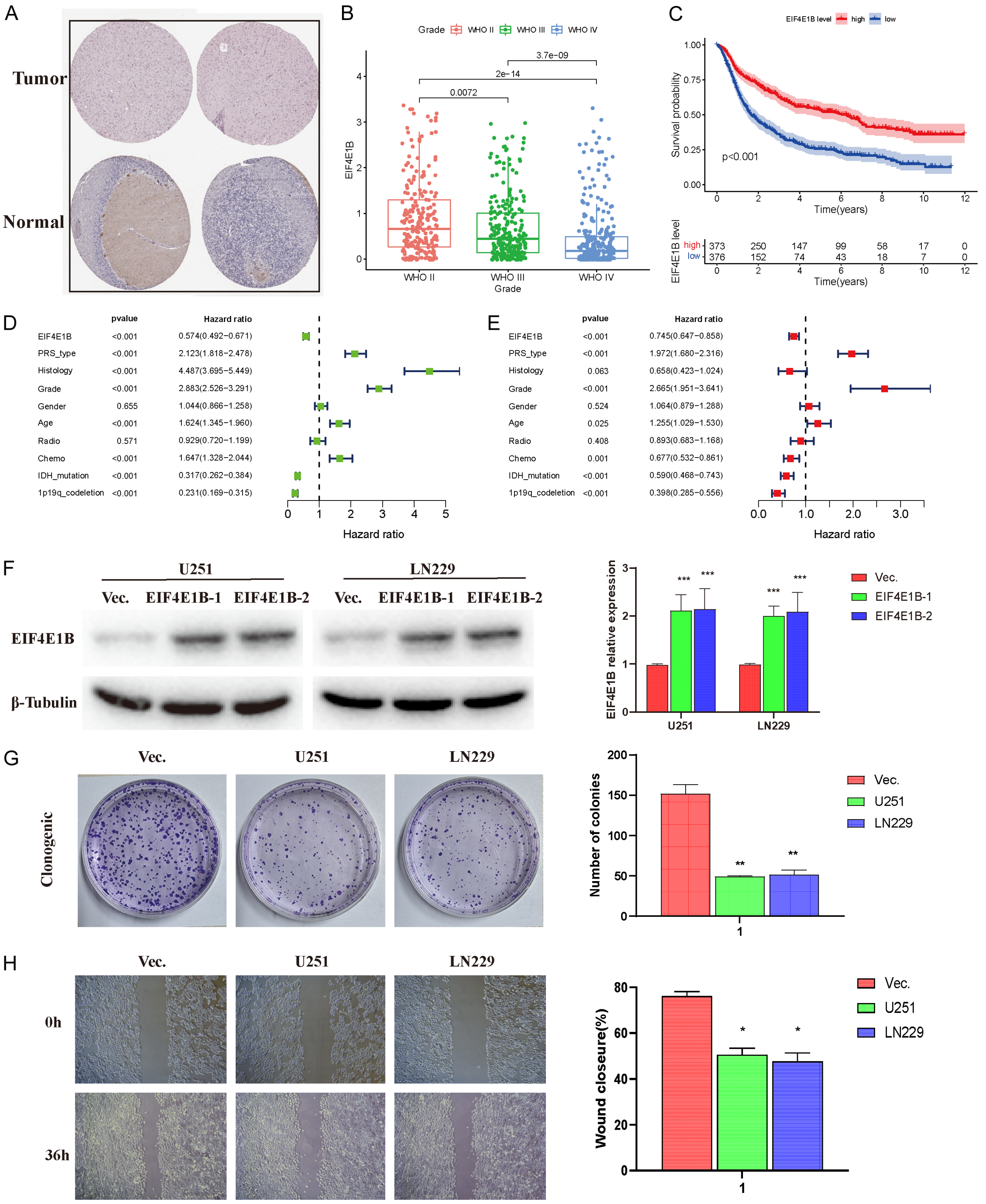
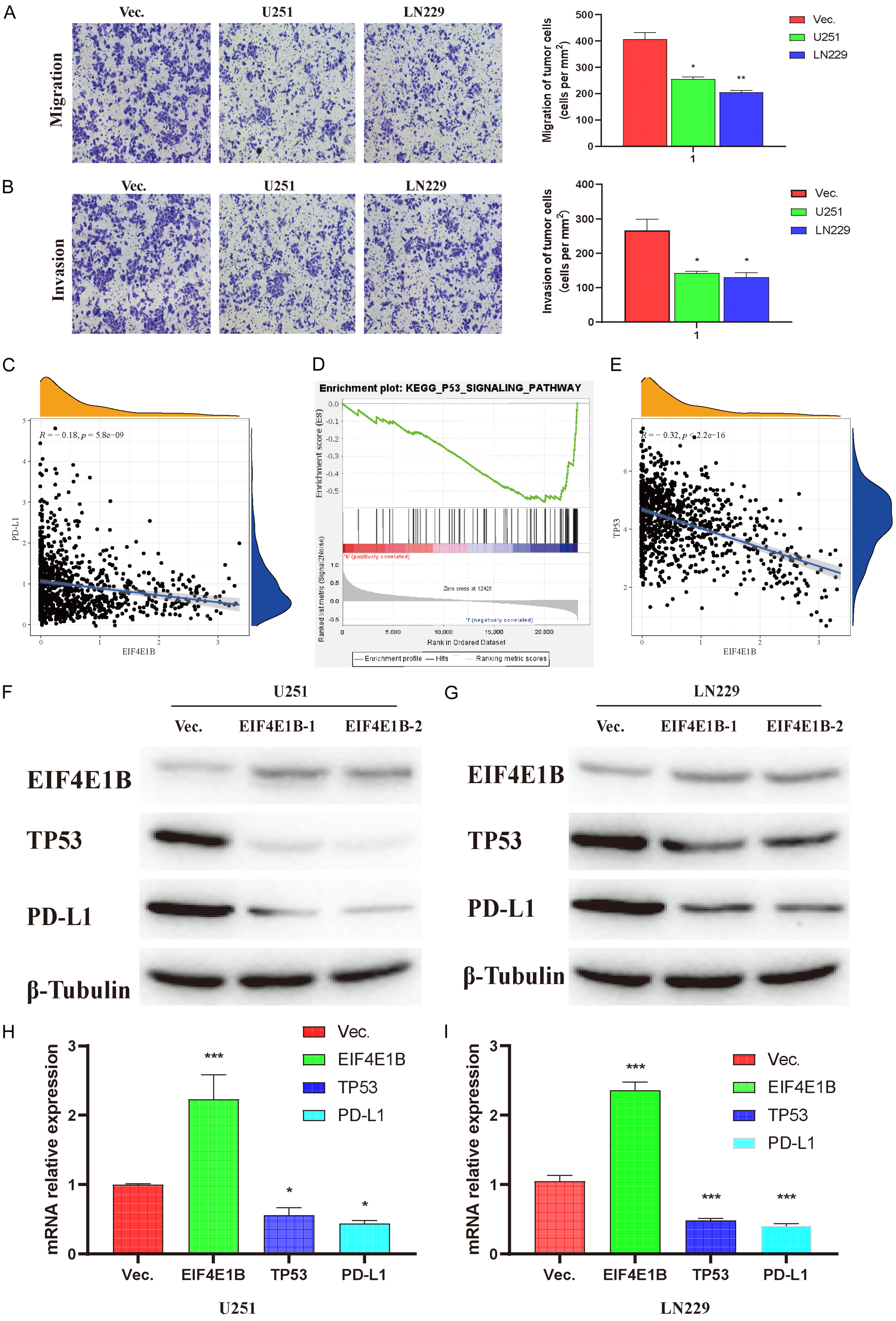


Figure 9. The Hub gene *EIF4E1B* overexpression inhibited growth and migration in glioma cells. A: *EIF4E1B* is lowly expressed in glioma. B: *EIF4E1B* expression is associated with glioma grade. C: Highly expressed *EIF4E1B* favored prognosis in glioma patients. D and E: *EIF4E1B* is an independent predictor of overall survival in glioma. F: Construction of Overexpressed EIF4E1B in glioma cell lines. G: *EIF4E1B* overexpression reduced the clonogenic formation ability of glioma cells. H: *EIF4E1B* overexpression inhibited glioma cell migration, according to a scratch assay.

cohort. The predictive ability of prognostic signature was 0.825 at five-year OS, which is a relatively high level.

The m7G regulators showed an association with immune infiltration in glioma. Cluster 3 depicted the lowest immune infiltration level,


A
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Migration
Migration of tumor cells (cells per mm^2)
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U251
LN229
Invasion
Invasion of tumor cells (cells per mm^2)
400
300
200
100
0
*
*
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Vec.
U251
LN229
C
R = − 0.18, p = 5.8e−09
PD-L1
EIF4E1B
D
Enrichment plot: KEGG_P53_SIGNALING_PATHWAY
Enrichment score (ES)
Ranked list metric (Signal2Noise)
'N' (positively correlated)
Zero cross at 12426
'T' (negatively correlated)
Rank in Ordered Dataset
Enrichment profile
Hits
Ranking metric scores
E
R = − 0.32, p < 2.2e−16
TP53
EIF4E1B
F
U251
Vec.
EIF4E1B-1
EIF4E1B-2
EIF4E1B
TP53
PD-L1
β-Tubulin
G
LN229
Vec.
EIF4E1B-1
EIF4E1B-2
EIF4E1B
TP53
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β-Tubulin
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Figure 10. *EIF4E1B* overexpression inhibited *PD-L1* expression via the p53 signaling pathway. A: *EIF4E1B* overexpression inhibited migration of glioma cells. B: *EIF4E1B* overexpression inhibited invasion of glioma cells. C: *EIF4E1B* expression is negatively associated with *PD-L1* expression. D: p53 signaling pathway is negatively enriched with highly expressed *EIF4E1B*. E: *EIF4E1B* expression is negatively correlated to *TP53* expression in glioma. F and G: Western blotting showed *EIF4E1B* overexpression inhibited *TP53* and *PD-L1* expression. H and I: mRNA levels of *TP53* and *PD-L1* were decreased after *EIF4E1B* overexpression.

whereas subtype 1 had the highest level. In addition, remarkable variations in the expression levels of immune checkpoints were observed across the three subtypes. The tumor microenvironment contains stromal, tumor, and immune cells. The greater the stromal and immune scores, the lower the purity of the tumor [24]. The findings of this study showed that subtype 3 had the lowest matrix score, the lowest immune score, and the highest tumor purity. PD-L1 on the cancer cell surface can disrupt the immune functions of tumor-infiltrating lymphocytes, while the PD1/PDL1 signaling pathway reduces the sensitivity of tumor cells to T cell-mediated apoptosis, suggesting that PDL1 is ubiquitous in tumor cells [25, 26]. Therefore, antibodies targeting PD1/PDL1 can enhance the cytotoxic effect of tumor-infiltrating lymphocytes [27]. m7G regulators can present different immune characteristics that is indirect for immune regulation. Previous study reported YTHDF1 (m6A methylation regulator) protein is involved in antigen delivery from dendritic cells to CD8+ T cells, promoting the translation of protease cathepsins in lysozymes, inhibiting the cross-presentation of neoantigens and promoting immune escape. Knockout of YTHDF1 can promote the activation of DC and CD8+ T cells, inhibit tumors and increase the therapeutic effect of immune checkpoint inhibitors. This result suggested that RNA methylation may be directly involved in immune regulation. We added these descriptions.

Our results found 10 (METTL1, NSUN2, DCPS, CYFIP1, GEMIN5, NCBP1, NCBP2, EFIF3D, IFIT5, LSM1) genes were significantly up-regulated in tumors while 6 (EIF4E, EIF4E1B, EIF4E3, LARP1, EIF4G3, NCBP2L) genes were significantly down-regulated as gene alteration levels of m7G regulators, and found the overall m7G gene alteration rate was 2.6% (23/885). Only GEMIN5, EIF4A1, and EIF4G3 had a 1% level of gene alteration. EIF4A1 is an important type of eukaryotic translation initiation factor in eukaryotic cells. It has ATP-dependent RNA helicase activity and RNA-dependent ATPase activity, and its main role is to participate in the recruitment of ribosomes in the initial stage of protein translation. It has been found that in some tumors, the expression levels of many translation-initiating factors, including EIF4A1, are altered, leading to uncontrolled initiation of gene translation and the development and progression of cancer [28]. EIF4A1 plays an oncogenic role in liver cancer, breast cancer, stomach cancer, colon cancer and other tumors, so it is speculated that the expression of EIF4A1 may play an important role in the occurrence and development of tumors.

About glioma research, *PDL1* is mainly expressed in glioma cells and microglia, and *PD1* is expressed in tumor-infiltrating lymphocytes [29]. Changes in *PDL1* expression are linked to the pathological grade of glioma. The expression level of *PDL1* in IDH wildtype patients is significantly higher than that in IDH mutant patients, and changes in *PDL1* expression show an inverse link to the prognosis of patients with glioma [30]. It was found that *PD-L1* expression had a positive link to many m7G regulators, suggesting that m7G regulators are involved in immune regulation processes. Further, subtype 3 had the highest PD-L1 expression level, which may explain why subtype 3 had the worst prognosis. Furthermore, the high-risk score group affects the efficiency of immunotherapy according to the IMigor dataset, which further confirms the role of m7G regulators in immune responses.

The glioma patients were classified into high- and low-risk groups based on their median risk score, showing marked variations in immune infiltration levels. Stromal, immune, and estimate scores were higher in subjects with greater risk compared to the others. The risk score had a positive association with M0 macrophages, resting NK cells, activated CD4 memory T cells, and regulatory T cells. Furthermore, glioma patients can be categorized into three immune subtypes (C3, C4, C5), and the subjects with greater risk represented a higher proportion in C4 and a lower proportion in C5 compared to the other group. The expression of immune checkpoint-related genes in different risk groups was also compared, and they showed a high-expressed trend in the subjects with greater risk.

These findings were further indicative of the involvement of m7G regulators in immune regulation processes. To validate the immune regulatory role of m7G regulators in glioma, the hub gene *EIF4E1B* was chosen for conducting *in vitro* experiments. *EIF4E1B* is a protein-coding gene, and its related GO annotations are RNA binding and translation initiation factor activity [31]. It was found that *EIF4E1B* was lowly expressed in glioma, and it was an independent predictor in glioma patients. The *in-vitro* experiment indicated that high expression EI4E1B could inhibit the invasion and migration of glioma. *EIF4E1B* expression was strongly and negatively correlated with *PD-L1* expression in glioma cases. It was hypothesized that *EIF4E1B* would affect the immune functioning in gliomas. Pathway enrichment analyses depicted significant and negative enrichment of the p53 signaling pathway in the *EIF4E1B* high-expression group. A previous study confirmed that p53 is a suppressor gene in many tumors [32]. However, the key molecular TP53 was inhibited in the *EIF4E1B* high-expression group, and a negative correlation between *EIF4E1B* and *TP53* expression was observed. It was assumed that the p53 mutation might be tumorigenic in gliomas because *TP53* mutation frequencies were very high (46%).

Further, *TP53* expression was positively associated with TMB levels in gliomas. Western blotting and qPCR further indicated that *TP53* and *PD-L1* expression was decreased in *EIF4E1B* high-expression glioma cells. These results indicated that *EIF4E1B* inhibited glioma progression through the p53 signaling pathway, which affected the immune function in glioma cells. A previous study also found that p53 mutation can increase PD-L1 and CD8+ cell levels, which leads to increased immune responses in tumors [33, 34]. The findings of this research highlight that m7G regulators may be immune treatment targets in glioma patients.

This research has certain limitations. First, although the training and validation datasets consisted of a relatively large sample size, more external cohort data are required for validating the constructed model's accuracy and stability. Second, the TCGA dataset only included several clinical parameters (age, gender, and grade), while adding further clinical characteristics may affect the outcome. Third, the present experiments were performed *in vitro*. Therefore, *in vivo* results would be required for confirmation. Overall, the mechanisms underlying the development and progression of gliomas are very complex, and multiple regulation pathways and networks may exist. Consequently, these findings require confirmation through further *in vivo* and *in vitro* observations.

In conclusion, this is innovative scientific research on m7G regulator expression patterns in glioma and analysis of their effects on survival. The m7G prognostic signature may be a biomarker of overall survival in glioma patients and may affect immunotherapy. Comprehensive analyses and preliminary *in vitro* experiments suggested that m7G regulators function in glioma progression by the regulation of immune responses. The present study enhances understanding of the role of m7G regulators in glioma progression as well as the impact on clinical outcomes, which can provide new insights regarding precision therapy of glioma.

Acknowledgements

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Disclosure of conflict of interest

None.

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Table S1. The 29 m7G genes used for classification

Genesymbol	Entrez Gene ID	Description
METTL1	4234	Methyltransferase 1
WDR4	10785	WD Repeat Domain 4
NSUN2	54888	NOP2/Sun RNA Methyltransferase 2
DCP2	167227	Decapping MRNA 2
DCPS	28960	Decapping Enzyme, Scavenger
NUDT10	170685	Nudix Hydrolase 10
NUDT11	55190	Nudix Hydrolase 11
NUDT16	131870	Nudix Hydrolase 16
NUDT3	11165	Nudix Hydrolase 3
NUDT4	11163	Nudix Hydrolase 4
NUDT4B	440672	Nudix Hydrolase 4B
AGO2	27161	Argonaute RISC Catalytic Component 2
CYFIP1	23191	Cytoplasmic FMR1 Interacting Protein 1
EIF4E	1977	Eukaryotic Translation Initiation Factor 4E
EIF4E1B	253314	Eukaryotic Translation Initiation Factor 4E Family Member 1B
EIF4E2	9470	Eukaryotic Translation Initiation Factor 4E Family Member 2
EIF4E3	317649	Eukaryotic Translation Initiation Factor 4E Family Member 3
GEMIN5	25929	Gem Nuclear Organelle Associated Protein 5
LARP1	23367	La Ribonucleoprotein 1
NCBP1	4686	Nuclear Cap Binding Protein Subunit 1
NCBP2	22916	Nuclear Cap Binding Protein Subunit 2
NCBP3	55421	Nuclear Cap Binding Protein Subunit 3
EIF3D	8664	Eukaryotic Translation Initiation Factor 3 Subunit D
EIF4A1	1973	Eukaryotic Translation Initiation Factor 4A1
EIF4G3	8672	Eukaryotic Translation Initiation Factor 4 Gamma 3
IFIT5	24138	Interferon Induced Protein With Tetratricopeptide Repeats 5
LSM1	27257	LSM1 Homolog
NCBP2L	392517	Nuclear Cap Binding Protein Subunit 2 Like
SNUPN	10073	Snurportin 1

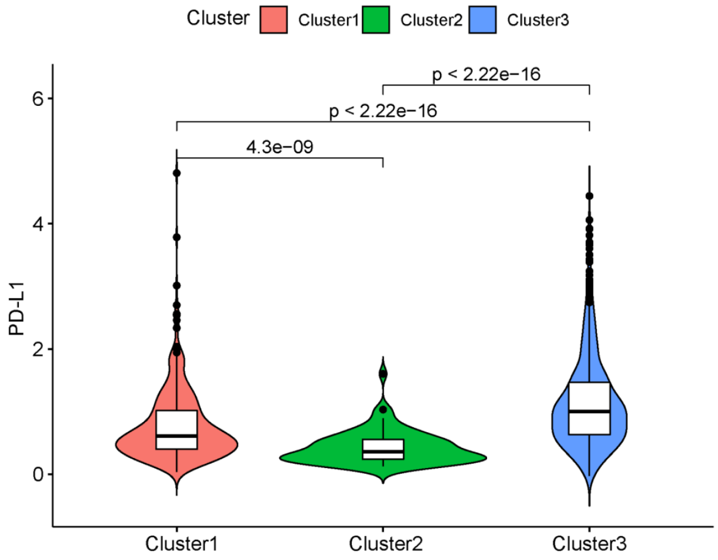
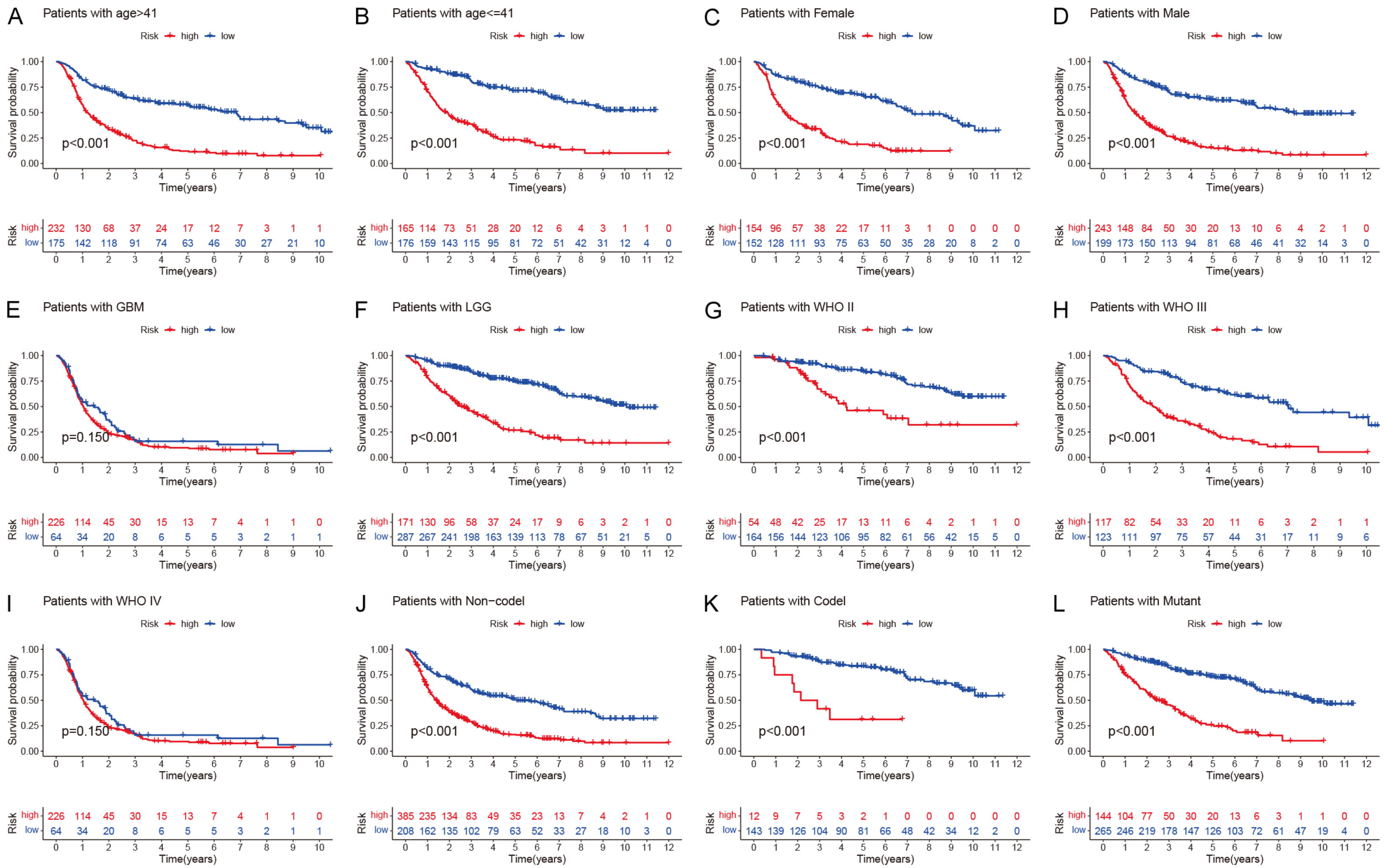


Figure S1. Comparisons of PD-L1 expression among three clusters.

Table S2. 12 identified m7G signature genes in prognostic model

Gene	Coef	HR
CYFIP1	1.000038732	2.7183871
DCP2	1.224698856	3.4031411
EIF4A1	0.136948211	1.1467688
EIF4E1B	-0.304430755	0.7375431
EIF4G3	1.287634601	3.6242037
GEMIN5	-0.557281291	0.5727641
IFIT5	-0.712077184	0.4906240
LSM1	0.063024982	1.0650534
METTL1	0.541934725	1.7193301
NCBP1	0.294588036	1.3425732
NUDT11	-0.218614752	0.8036313
WDR4	0.289880058	1.3362672


A Patients with age>41
p<0.001
high 232 130 68 37 24 17 12 7 3 1 1
low 175 142 118 91 74 63 46 30 27 21 10
B Patients with age<=41
p<0.001
high 165 114 73 51 28 20 12 6 4 3 1 1 0
low 176 159 143 115 95 81 72 51 42 31 12 4 0
C Patients with Female
p<0.001
high 154 96 57 38 22 17 11 3 1 0 0 0 0
low 152 128 111 93 75 63 50 35 28 20 8 2 0
D Patients with Male
p<0.001
high 243 148 84 50 30 20 13 10 6 4 2 1 0
low 199 173 150 113 94 81 68 46 41 32 14 3 0
E Patients with GBM
p=0.150
high 226 114 45 30 15 13 7 4 1 1 0
low 64 34 20 8 6 5 5 3 2 1 1
F Patients with LGG
p<0.001
high 171 130 96 58 37 24 17 9 6 3 2 1 0
low 287 267 241 198 163 139 113 78 67 51 21 5 0
G Patients with WHO II
p<0.001
high 54 48 42 25 17 13 11 6 4 2 1 1 0
low 164 156 144 123 106 95 82 61 56 42 15 5 0
H Patients with WHO III
p<0.001
high 117 82 54 33 20 11 6 3 2 1 1
low 123 111 97 75 57 44 31 17 11 9 6
I Patients with WHO IV
p=0.150
high 226 114 45 30 15 13 7 4 1 1 0
low 64 34 20 8 6 5 5 3 2 1 1
J Patients with Non−codel
p<0.001
high 385 235 134 83 49 35 23 13 7 4 2 1 0
low 208 162 135 102 79 63 52 33 27 18 10 3 0
K Patients with Codel
p<0.001
high 12 9 7 5 3 2 1 0 0 0 0 0 0
low 143 139 126 104 90 81 66 48 42 34 12 2 0
L Patients with Mutant
p<0.001
high 144 104 77 50 30 20 13 6 3 1 1 0 0
low 265 246 219 178 147 126 103 72 61 47 19 4 0
Risk high low
Survival probability
Time(years)

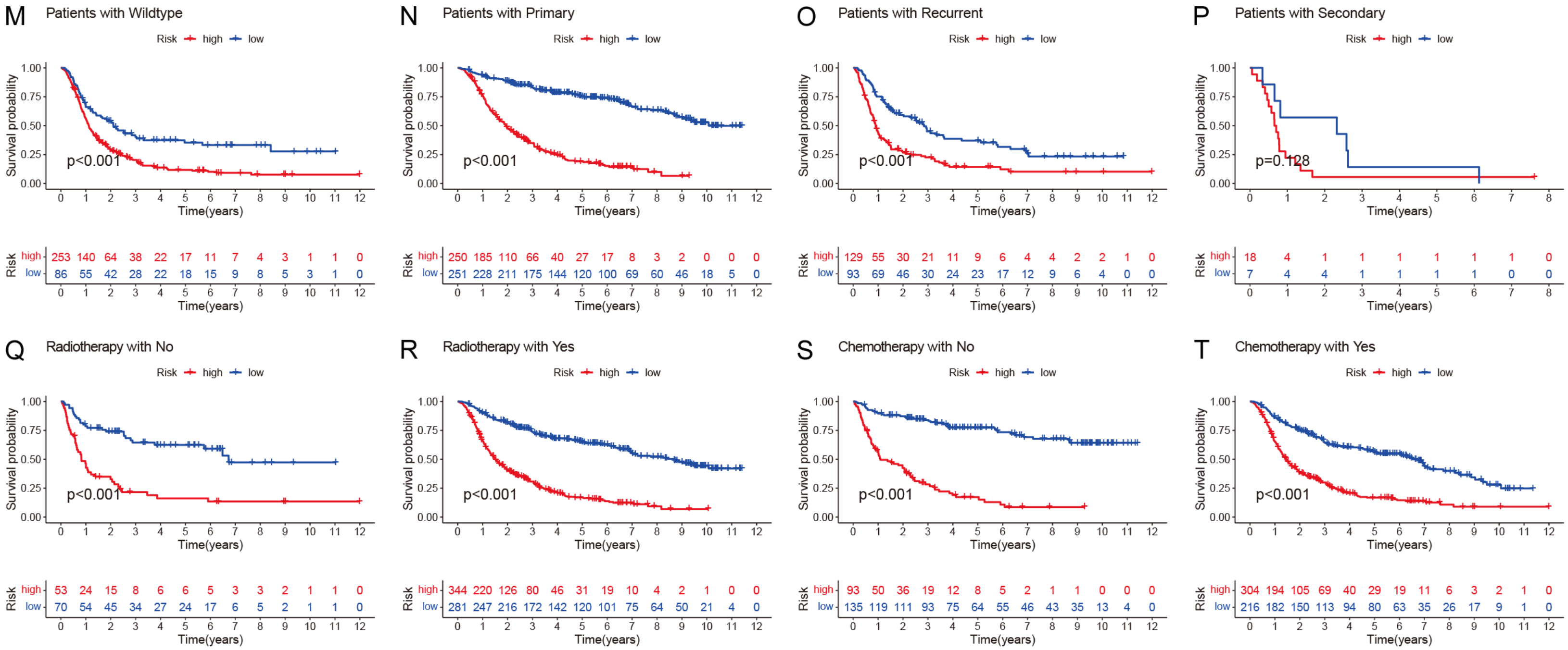


Figure S2. Stratified analyses of high- and low-risk group. A and B: Age. C and D: Gender. E and F: Histology. G-I: WHO stage. J and K: 1p19q codeletion status. L and M: IDH mutation status. N-P: Primary vs Recurrent vs Secondary. Q and R: Radiotherapy. S and T: Chemotherapy.

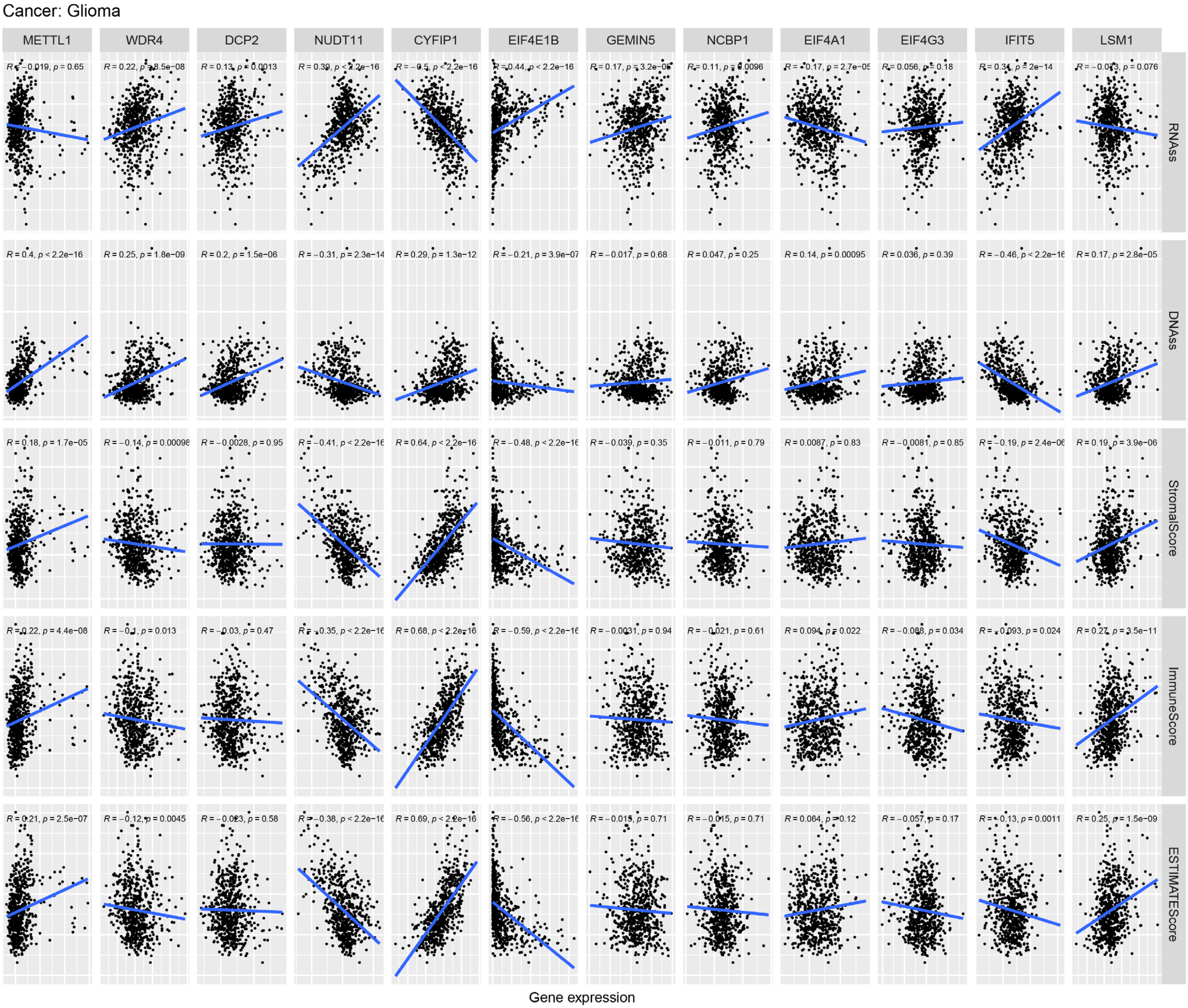


Figure S3. Association between signature genes and RNAss, DNAss, stromal, immune, and estimated scores.

Table S3. Differentially expressed genes from CGGA based on risk score

gene	lowMean	highMean	logFC	*p*Value	fdr
RP1-293L6.1	1.909253885	0.502836849	-1.924846676	2.55E-70	2.18E-68
CACNG3	1.895397916	0.513851118	-1.883078434	8.81E-53	1.55E-51
SLC6A7	1.650195359	0.469349305	-1.813902899	3.13E-41	2.68E-40
AC062021.1	2.578419509	0.749796499	-1.781916014	5.04E-56	1.15E-54
SOHLH1	1.913326239	0.56471742	-1.760481848	2.23E-49	3.10E-48
HRH3	2.802787164	0.828085181	-1.759011111	2.16E-84	2.06E-81
SYCE1	1.651533997	0.492794683	-1.744748072	4.31E-48	5.52E-47
RP11-82C23.2	1.87147169	0.559909423	-1.74090786	2.79E-31	1.42E-30
NGB	1.674968213	0.505254134	-1.72905259	4.88E-38	3.51E-37
HAR1A	1.682205177	0.509580116	-1.722972791	1.77E-80	7.95E-78
RP5-1119A7.17	2.878093375	0.888172134	-1.696202185	2.58E-80	1.13E-77
KCNC2	2.337156486	0.76171767	-1.617426066	1.14E-62	4.57E-61
AMER3	1.60889297	0.526567462	-1.611378074	7.37E-75	1.16E-72
CACNG2	1.873406413	0.621747684	-1.591262775	5.28E-65	2.71E-63
WSCD2	1.819696446	0.606943668	-1.584063278	5.96E-73	6.93E-71
MAL2	1.894216475	0.633585157	-1.579990772	2.60E-43	2.52E-42
GABRA1	2.258249259	0.75738864	-1.576099049	1.22E-45	1.34E-44
GJB6	2.077558103	0.697802434	-1.573998291	4.61E-42	4.14E-41
FAM19A1	1.530200207	0.51427988	-1.573094804	3.96E-56	9.09E-55
RP11-227B21.2	2.543876386	0.855649965	-1.571935933	1.29E-59	3.93E-58
GABRG2	2.702756259	0.910524321	-1.569661953	5.05E-63	2.09E-61
SLC26A4-AS1	2.105373101	0.726631383	-1.534780338	3.54E-46	4.02E-45
CHRM1	2.765360735	0.963662695	-1.520867526	5.05E-76	9.06E-74
RP11-192H23.5	3.362025258	1.173136671	-1.518959465	9.27E-37	6.24E-36
TNNT2	2.150385549	0.753554987	-1.512810653	2.15E-36	1.42E-35
SVOP	3.483528098	1.224299655	-1.50859249	4.13E-76	7.49E-74
DACH2	1.581953011	0.56286323	-1.490850437	4.83E-59	1.39E-57
AC013268.5	1.629741083	0.580276953	-1.489829246	9.22E-30	4.35E-29
RP11-1263C18.1	1.871129769	0.67090594	-1.479727195	6.48E-55	1.33E-53
AC112229.7	1.754581556	0.635654936	-1.464811288	6.36E-35	3.89E-34
PRKCG	2.353377111	0.856171814	-1.458760274	1.52E-49	2.13E-48
CCKBR	1.654481853	0.604027552	-1.453693204	3.97E-42	3.58E-41
SRRM4	1.523255846	0.561872689	-1.438843096	1.68E-61	6.14E-60
PVALB	2.715503778	1.011777141	-1.42432832	5.04E-40	4.06E-39
EMX1	1.753502362	0.668574871	-1.391078337	3.29E-33	1.84E-32
TESPA1	1.596326787	0.609066388	-1.390084623	7.74E-16	1.91E-15
GABRG1	2.033420719	0.781024811	-1.380468458	2.37E-57	5.93E-56
GABRB2	1.721975988	0.666804154	-1.368730028	1.83E-37	1.28E-36
SSTR1	1.556332343	0.604351068	-1.364691409	1.25E-51	2.03E-50
TRIM67	1.87172705	0.729221919	-1.359940233	5.08E-43	4.82E-42
CLEC2L	2.666531602	1.042620954	-1.354749667	8.73E-49	1.16E-47
RTN4RL1	1.604000886	0.631062678	-1.345819731	3.29E-42	2.97E-41
TMEM155	1.779287303	0.700441179	-1.344963674	4.43E-27	1.83E-26
SLC32A1	1.981331896	0.780187768	-1.344577283	6.41E-39	4.84E-38
SYNPR	2.507231653	0.992171425	-1.337433986	4.33E-40	3.50E-39
CBLN2	2.087598568	0.832099662	-1.32701608	1.90E-48	2.50E-47
GABRA5	2.371776316	0.952472073	-1.316219257	4.23E-42	3.81E-41

ATP2B3	1.64043421	0.662061466	-1.309040667	8.59E-49	1.15E-47
CPNE9	1.55067316	0.625913135	-1.308860279	6.62E-39	4.99E-38
HBQ1	2.408364668	0.972939458	-1.307631918	1.10E-46	1.28E-45
SYT13	2.628607746	1.061953586	-1.307578159	5.09E-54	9.89E-53
RP11-307B6.3	2.720020405	1.099028845	-1.307388222	3.75E-40	3.04E-39
RTBDN	1.940456516	0.788605737	-1.299019992	4.76E-44	4.83E-43
LRTM2	1.897830922	0.771536416	-1.298545311	5.27E-49	7.17E-48
CUX2	1.764395606	0.722958605	-1.287189123	3.38E-52	5.74E-51
TBR1	1.663455709	0.683728082	-1.282688868	9.07E-31	4.48E-30
NEUROD2	2.000558426	0.82480583	-1.278276327	5.51E-34	3.20E-33
CTD-2380F24.1	1.892961389	0.780848246	-1.277530884	2.46E-58	6.63E-57
PACSIN1	3.743233798	1.556529742	-1.265952016	6.04E-53	1.08E-51
SLC6A17	2.500080808	1.040222842	-1.265082103	3.03E-46	3.46E-45
SV2B	2.15523486	0.897673437	-1.263582482	1.83E-39	1.42E-38
GRIN1	5.626466152	2.348343869	-1.260585406	1.88E-72	2.08E-70
KIAA1644	2.125375244	0.887932625	-1.259195461	1.38E-55	2.98E-54
MPPED1	2.436940077	1.020874312	-1.255265521	7.56E-40	6.02E-39
PRMT8	1.835350879	0.769761984	-1.253571572	4.70E-47	5.65E-46
MYT1L	2.799977963	1.175463737	-1.25218544	4.51E-58	1.19E-56
SLC30A3	2.139135506	0.899890919	-1.249205834	2.25E-30	1.09E-29
CACNA1B	1.57246835	0.662428675	-1.247193949	5.23E-44	5.28E-43
CDH18	2.219195087	0.935220183	-1.246658528	1.88E-63	8.28E-62
KCNA1	1.804079212	0.76368508	-1.24021294	2.69E-35	1.68E-34
KCNK4	2.127638377	0.902918327	-1.236585565	4.90E-62	1.87E-60
FSTL5	1.485441491	0.630841545	-1.235542201	4.80E-45	5.14E-44
ATP8A2	1.455325925	0.620976123	-1.228732583	3.20E-48	4.15E-47
WNT10B	1.688859042	0.723815834	-1.222354348	5.68E-34	3.29E-33
CKMT1A	3.32453592	1.425302505	-1.221884817	5.34E-67	3.31E-65
KCNT1	2.363667449	1.013858175	-1.22117122	1.76E-51	2.82E-50
WIF1	1.532269546	0.659100803	-1.217099076	2.69E-17	7.09E-17
SYT4	2.845003263	1.22662855	-1.213731872	1.11E-57	2.84E-56
CPLX3	1.612199882	0.696435719	-1.210968518	5.02E-42	4.49E-41
IQSEC3	3.201373829	1.386211258	-1.207544013	3.22E-65	1.67E-63
4-Mar	1.79900132	0.779443384	-1.206680106	5.85E-54	1.13E-52
SPHKAP	1.54361777	0.670042749	-1.203990509	1.14E-47	1.43E-46
SCRT1	3.231376814	1.409574897	-1.196888857	9.38E-67	5.73E-65
MIR7-3HG	2.475494999	1.080480369	-1.196044175	1.09E-44	1.15E-43
KCNJ3	1.452205352	0.634588628	-1.194351901	7.08E-41	5.95E-40
CAMK1G	1.898409153	0.831179767	-1.191558521	2.65E-29	1.22E-28
RP11-1C8.7	2.120057963	0.929612729	-1.189401981	1.95E-37	1.36E-36
EPHA10	1.888009195	0.830495911	-1.184820821	6.19E-69	4.43E-67
SYN2	3.652420832	1.61289181	-1.179203334	1.40E-55	3.02E-54
ST8SIA3	3.852538207	1.703325474	-1.177455131	1.34E-60	4.51E-59
RP11-357K6.1	1.954643445	0.864602138	-1.176797154	8.26E-44	8.21E-43
CYP17A1-AS1	2.303425751	1.023556576	-1.170190247	7.01E-56	1.57E-54
DDN	3.443648317	1.532224799	-1.168309838	3.04E-48	3.95E-47
RBFOX3	3.29757929	1.471300495	-1.16431542	6.29E-53	1.12E-51
GDA	2.501595206	1.117995667	-1.161933763	6.76E-35	4.12E-34
CREG2	2.181640274	0.975892177	-1.160619576	1.35E-31	6.98E-31

VSTM2A	3.290217509	1.473260885	-1.159170035	6.65E-55	1.36E-53
PPP4R4	1.562683644	0.703116526	-1.152190033	1.62E-38	1.21E-37
RASAL1	2.774140736	1.250472641	-1.149567487	2.60E-43	2.52E-42
AC131056.3	1.678094058	0.757341628	-1.147807446	1.83E-42	1.67E-41
GAD2	1.833130031	0.827597354	-1.147308189	6.00E-33	3.32E-32
PTPRT	1.974732374	0.893497483	-1.144121575	1.58E-55	3.38E-54
KIAA1045	2.519220744	1.147450427	-1.134545716	3.56E-46	4.04E-45
HS3ST4	1.620339911	0.741244021	-1.128276022	4.87E-36	3.16E-35
RFPL1S	2.087601112	0.961877034	-1.117921698	6.15E-50	8.83E-49
SLC8A2	2.90304961	1.338553138	-1.116894813	1.01E-62	4.08E-61
RP11-21A7A.4	1.648000967	0.760925334	-1.114890288	1.93E-42	1.76E-41
CDH22	2.868170902	1.328640606	-1.110180079	9.56E-70	7.80E-68
GS1-72M22.1	1.558683774	0.72323833	-1.10778522	3.20E-47	3.90E-46
TNNT1	3.79139837	1.76410319	-1.103795099	4.13E-57	1.02E-55
SLC1A6	2.564599187	1.195154985	-1.101535654	1.78E-55	3.80E-54
NELL1	1.586488811	0.740768086	-1.098743496	8.90E-32	4.65E-31
CXXC11	3.838402701	1.79263625	-1.098423302	3.18E-62	1.24E-60
CALN1	2.107736802	0.985684625	-1.096496699	1.14E-50	1.72E-49
SLC17A7	4.468444119	2.096875791	-1.091531177	3.00E-42	2.72E-41
CCK	4.781881594	2.253438338	-1.085450434	5.83E-46	6.54E-45
CACNA2D3	1.912355911	0.902585647	-1.083215309	1.13E-56	2.69E-55
RP11-143K11.1	2.816157763	1.329562154	-1.082776936	9.02E-60	2.77E-58
NEFL	3.45030438	1.6336075	-1.078662244	8.53E-35	5.17E-34
KCNJ11	3.042525708	1.442075293	-1.077122961	2.29E-75	3.81E-73
CPLX2	5.590030933	2.652010464	-1.075769798	3.16E-77	6.98E-75
GLT1D1	1.748865537	0.830210175	-1.074870853	2.08E-34	1.24E-33
HMGCLL1	1.609258637	0.764167419	-1.074435559	3.75E-46	4.25E-45
RPRML	2.426050126	1.152208634	-1.074207385	1.34E-33	7.63E-33
CKMT1B	3.577681192	1.708231013	-1.066521743	2.94E-63	1.27E-61
MCF2	1.56913702	0.749814293	-1.065366104	7.68E-48	9.70E-47
RBFOX1	2.582932972	1.235668102	-1.063718915	1.58E-35	9.99E-35
NEFM	3.538779603	1.695224042	-1.061775959	3.30E-38	2.40E-37
FAM163B	3.745057824	1.794079051	-1.061744535	2.37E-47	2.91E-46
KCNK3	2.061221247	0.989369404	-1.058918179	9.98E-58	2.58E-56
WNT7B	2.733370532	1.312219805	-1.058671642	4.80E-57	1.18E-55
NEURL	2.973658567	1.42971015	-1.056516313	3.22E-58	8.59E-57
LRFN2	1.400693193	0.674818593	-1.053569356	1.63E-38	1.21E-37
FAM19A2	2.374347855	1.146058553	-1.050850559	1.42E-58	3.92E-57
CALY	5.303023188	2.561431992	-1.049864469	7.55E-60	2.34E-58
RP11-268P4.5	1.694285912	0.820727119	-1.045702822	5.83E-37	3.97E-36
SH2D5	1.958049118	0.949330909	-1.044433994	5.28E-30	2.53E-29
TAC1	2.316121703	1.123554324	-1.043641183	7.43E-31	3.69E-30
GDF10	1.663490632	0.808493105	-1.040906367	2.19E-41	1.89E-40
CHGA	5.301266374	2.582105779	-1.03778893	6.98E-77	1.44E-74
PRSS3	2.68965568	1.312826986	-1.034744697	3.57E-43	3.43E-42
RLTPR	3.230843906	1.577847762	-1.033953037	5.92E-69	4.28E-67
KCNK12	1.697438663	0.830139357	-1.031933995	2.08E-53	3.83E-52
RP11-74E22.4	1.74056198	0.852012564	-1.030606578	5.40E-43	5.12E-42
SCN3B	3.936342974	1.929895593	-1.028333128	1.00E-78	3.06E-76

CTD-2339F6.1	1.912619612	0.941606414	-1.022353921	3.29E-15	7.87E-15
KCTD4	2.016181764	0.998355012	-1.014000877	8.41E-47	9.92E-46
CRYM	3.569045098	1.768448775	-1.013053701	6.83E-33	3.76E-32
GABRD	4.220268242	2.091639912	-1.012700196	1.36E-68	9.47E-67
RP11-320H14.1	2.244764222	1.116775359	-1.007224905	2.30E-23	8.00E-23
RAB3C	2.58512342	1.28778846	-1.005337533	1.14E-52	1.99E-51
SLC25A41	1.400312307	0.699572977	-1.001202157	2.26E-53	4.16E-52
ITPRIPL1	0.82732845	1.655624166	1.000843112	7.84E-68	5.11E-66
NOX4	0.957079116	1.917703331	1.002669459	3.87E-47	4.67E-46
C11orf82	0.679531241	1.362695679	1.003851628	3.06E-56	7.10E-55
GAPT	0.745485288	1.495728407	1.00459645	1.61E-47	2.00E-46
ADAMTS15	0.928148092	1.867363028	1.008575505	1.87E-42	1.71E-41
PTGES3P1	1.032392153	2.085374014	1.014315074	5.57E-47	6.68E-46
MMP19	1.029263272	2.079198019	1.014415113	3.81E-35	2.35E-34
OSM	0.883441853	1.785424352	1.015059922	6.91E-29	3.11E-28
MMP11	1.014829724	2.054751715	1.017726396	2.65E-48	3.46E-47
EXO1	0.726665555	1.471393358	1.017819557	7.23E-48	9.14E-47
DKK1	0.71578971	1.450287431	1.018731146	2.53E-12	5.28E-12
COL5A2	1.735383093	3.516378715	1.018836278	4.60E-73	5.49E-71
HOXD3	0.787000189	1.59769723	1.021558151	4.48E-31	2.25E-30
TFPI	1.498649428	3.045390085	1.022964095	4.88E-71	4.54E-69
LRRN4CL	0.958014788	1.94742689	1.023449337	2.13E-47	2.62E-46
RP4-792G4.2	1.322734976	2.693459138	1.025936148	8.09E-36	5.18E-35
CCNB2	1.401385041	2.862676188	1.030511088	3.74E-55	7.80E-54
PDGFD	0.699869036	1.429679185	1.030534562	3.03E-41	2.60E-40
SDC1	1.155907116	2.363160567	1.031692185	1.13E-55	2.47E-54
BCL2A1	1.164744799	2.381292458	1.031730928	1.30E-42	1.20E-41
KIAA0040	1.229920684	2.516811102	1.033031658	6.00E-72	6.19E-70
DPEP1	1.037387831	2.128494456	1.036877981	6.41E-36	4.13E-35
FOSL1	0.967695531	1.987731076	1.038497481	2.33E-45	2.53E-44
STEAP3	1.588853227	3.279927308	1.045677982	2.11E-69	1.64E-67
RRM2	1.509809758	3.119266465	1.046840026	3.56E-69	2.69E-67
CD93	1.46171976	3.021528211	1.047611666	6.85E-79	2.22E-76
ESPL1	0.935061684	1.940147405	1.053032822	1.11E-55	2.44E-54
COL14A1	0.740598682	1.537453416	1.053778811	1.89E-44	1.96E-43
ST14	1.077221103	2.237269193	1.054424457	3.31E-59	9.76E-58
NUAK2	0.669303111	1.392782938	1.057238808	5.27E-66	2.92E-64
ARHGAP11B	0.760078665	1.582174962	1.057688502	6.27E-74	8.78E-72
SLC47A2	0.969307695	2.01794234	1.057858342	6.10E-34	3.53E-33
TNFAIP8	0.870852297	1.816219584	1.060438684	4.40E-69	3.24E-67
COL4A1	2.5085004	5.234385598	1.061195038	3.57E-84	3.21E-81
FPR3	0.961350133	2.010450751	1.06438512	1.13E-55	2.48E-54
CTHRC1	1.42878785	2.988403878	1.064583422	2.34E-53	4.29E-52
HJURP	1.082841026	2.267667098	1.06638741	3.71E-58	9.87E-57
HOXB-AS1	0.698315405	1.463878339	1.067844954	1.79E-23	6.27E-23
BUB1B	1.03152723	2.167919156	1.071529052	4.34E-60	1.38E-58
GTSE1	1.114368973	2.349416681	1.07607561	1.04E-63	4.67E-62
IGLC1	1.249133621	2.638335633	1.078700296	1.99E-21	6.34E-21
CENPK	1.137695197	2.405700088	1.080342704	3.71E-73	4.53E-71

ACTG2	1.076520338	2.2791255	1.082104793	2.15E-40	1.76E-39
RP11-61L23.2	0.94155669	1.997087786	1.084777885	1.32E-51	2.13E-50
PTPN7	0.807778568	1.717926081	1.088636188	2.35E-70	2.04E-68
RNASE2	1.060204464	2.258473313	1.091005347	4.19E-45	4.51E-44
CENPF	1.421547134	3.041846496	1.097485416	6.78E-65	3.41E-63
DRAXIN	0.943568525	2.019595724	1.097867328	3.12E-56	7.22E-55
SERPINE1	1.768496053	3.799129918	1.103146049	1.06E-56	2.52E-55
LILRB3	0.674046563	1.452583323	1.107700761	4.28E-40	3.46E-39
LUM	1.441487621	3.108962754	1.108874886	3.91E-51	6.07E-50
MFAP2	1.231830652	2.661663493	1.111524255	9.39E-52	1.54E-50
GDF15	1.37900183	2.982335219	1.112818057	9.29E-51	1.41E-49
IGLC3	1.346522047	2.912132649	1.112838221	5.26E-24	1.89E-23
VAV3	0.687667319	1.48728106	1.112894618	2.35E-50	3.47E-49
SOCS3	1.922836181	4.160185227	1.113411909	2.30E-69	1.77E-67
HTRA3	0.925451995	2.006601634	1.116524168	2.05E-46	2.38E-45
CISH	0.696217848	1.513009739	1.119810569	4.23E-63	1.78E-61
HOTAIRM1	1.313485178	2.855027809	1.120104877	7.17E-44	7.17E-43
KIF2C	1.275881103	2.775039663	1.121014498	6.95E-75	1.10E-72
EMR2	0.633500649	1.378245375	1.121414757	2.41E-63	1.05E-61
SLAMF8	0.895551289	1.94915819	1.122003218	7.11E-61	2.44E-59
ITGA4	0.678863519	1.478575721	1.123014664	1.19E-55	2.60E-54
COL1A1	2.058900244	4.489076132	1.124544632	7.46E-67	4.59E-65
PDPN	2.108700722	4.627597599	1.133909063	2.64E-74	3.95E-72
PRF1	0.65136067	1.43011997	1.13460766	1.63E-41	1.42E-40
CDC25C	0.643885559	1.41488627	1.135809894	8.70E-50	1.24E-48
FMOD	1.093237624	2.404870348	1.137352101	5.81E-37	3.96E-36
ELF4	0.656362104	1.445796551	1.139300703	8.71E-78	2.22E-75
ARSJ	0.690706558	1.523722523	1.141455377	1.62E-37	1.13E-36
CA9	1.03935153	2.295200316	1.142936387	3.98E-24	1.44E-23
G0S2	1.13933495	2.521589723	1.146141617	1.79E-30	8.74E-30
SPINK8	0.659435751	1.463914227	1.150527018	1.30E-30	6.36E-30
IGHG3	0.880062056	1.96449186	1.158479028	8.07E-22	2.62E-21
NEK2	0.824644992	1.840945608	1.158601921	1.11E-53	2.10E-52
KYNU	0.635098006	1.424383956	1.165286945	6.71E-62	2.52E-60
RP11-155G14.5	0.80851733	1.813489038	1.165417422	1.98E-43	1.93E-42
FAM129A	0.988268435	2.216732311	1.165459696	1.56E-80	7.21E-78
APOL4	1.094889877	2.468916824	1.173092461	8.98E-64	4.09E-62
HOXB7	0.623266818	1.405980082	1.173654343	1.40E-32	7.57E-32
HMMR	0.670229541	1.514510232	1.176124143	3.39E-60	1.09E-58
COL5A1	1.28862221	2.931680857	1.185898694	6.09E-59	1.72E-57
PLAU	1.594459061	3.630645054	1.187158837	1.42E-78	4.10E-76
THBD	0.777648148	1.770966428	1.187347412	4.16E-52	7.00E-51
HOXD4	0.668270651	1.522429616	1.187871112	2.72E-35	1.69E-34
HSPA6	1.183403425	2.703514389	1.19189406	1.28E-63	5.73E-62
COL15A1	0.609374905	1.395800101	1.195690347	3.49E-47	4.23E-46
IGHG2	1.13465345	2.603471483	1.198184873	2.24E-27	9.36E-27
KDELR3	0.70965216	1.62878457	1.198611842	7.66E-56	1.71E-54
IGHM	0.710698647	1.631322705	1.198732344	1.12E-21	3.62E-21
NCAPG	0.907961025	2.093556538	1.205253604	9.48E-66	5.17E-64

CENPA	0.924973073	2.139276133	1.209639441	3.69E-63	1.57E-61
TMEM71	0.649443145	1.503415422	1.210968571	5.01E-66	2.79E-64
LEFTY2	0.714591516	1.654526991	1.211228136	1.97E-41	1.70E-40
IGLC2	1.01618208	2.352919014	1.211292737	6.77E-23	2.31E-22
BUB1	0.879824686	2.044945601	1.21677448	1.33E-71	1.31E-69
NDC80	1.013933536	2.362163303	1.22014562	1.31E-70	1.16E-68
CTD-3049M7.1	0.959911611	2.244216806	1.225238583	3.37E-37	2.33E-36
DEPDC1B	0.632268625	1.479101152	1.226111183	4.22E-61	1.48E-59
SPOCD1	1.943115278	4.548201275	1.226924607	9.46E-68	6.14E-66
IL13RA2	1.022810458	2.398206367	1.229416991	2.29E-33	1.29E-32
IQGAP3	0.768869902	1.816109593	1.240039853	9.36E-70	7.68E-68
COL3A1	1.871067638	4.426770997	1.242393031	2.68E-73	3.32E-71
IGHA2	0.624079533	1.476625051	1.242501736	1.13E-18	3.18E-18
HSPA7	1.303097984	3.084294294	1.24299486	6.52E-55	1.34E-53
KIF23	0.931599559	2.210937055	1.246876091	4.69E-78	1.23E-75
FAM183A	0.65094585	1.549261089	1.250970854	2.00E-19	5.79E-19
FAM111B	0.594718129	1.420524792	1.256146051	2.16E-60	7.14E-59
IGJ	0.589938288	1.411191742	1.258278072	4.12E-27	1.70E-26
FAM83D	0.714950275	1.713062945	1.260663353	1.70E-61	6.19E-60
HAS2	0.80934027	1.940023191	1.261255613	3.51E-69	2.68E-67
FCGR2B	1.000747526	2.413278591	1.269916423	5.39E-45	5.76E-44
CXCL10	0.845244773	2.038880692	1.270336262	2.63E-48	3.45E-47
SGOL1	0.620596054	1.500414864	1.273635032	2.01E-58	5.45E-57
KIF4A	0.847270118	2.054861695	1.278147402	2.78E-70	2.35E-68
CSTA	0.815705943	1.992603313	1.28853346	4.44E-53	7.95E-52
CDCA8	0.873663601	2.135114072	1.28916336	1.75E-77	4.10E-75
CKAP2L	0.628215651	1.542183931	1.29564305	2.36E-62	9.27E-61
C6orf141	0.6947163	1.711098453	1.300426919	1.61E-22	5.39E-22
GPR65	0.731154832	1.805495973	1.304146349	3.08E-70	2.59E-68
TTK	0.638471024	1.578306217	1.305684087	8.92E-61	3.04E-59
MELK	0.89776814	2.237950786	1.317763507	2.20E-73	2.77E-71
CYP27B1	0.601613508	1.504009441	1.321904758	1.42E-55	3.07E-54
IL8	0.892639515	2.243929709	1.329877907	7.99E-29	3.59E-28
ABCC3	1.215643255	3.075395487	1.339052034	4.83E-57	1.19E-55
TNFAIP6	0.814479179	2.06328109	1.340990657	2.06E-50	3.06E-49
SERPINA5	0.580210152	1.473941142	1.345031473	1.33E-50	1.99E-49
RAB42	0.743523759	1.891937255	1.347413494	1.17E-76	2.31E-74
HOXB2	0.776418203	1.991747533	1.35912894	1.74E-45	1.90E-44
NAMPTL	0.619720542	1.594571562	1.36347915	9.75E-60	2.99E-58
FCGR2C	1.060496605	2.736783769	1.367741451	2.36E-62	9.27E-61
KIF20A	0.811712914	2.095738905	1.368417521	9.17E-74	1.26E-71
LTF	1.531700183	3.959688987	1.370253189	3.50E-38	2.54E-37
ENPEP	0.578842097	1.49672287	1.370565366	6.27E-69	4.47E-67
GAS2L3	0.692493521	1.799912007	1.3780539	5.79E-86	8.03E-83
CA3	0.827692585	2.263465465	1.451366356	4.50E-56	1.03E-54
HOXB3	0.729910983	2.023906531	1.47135023	4.04E-39	3.08E-38
CELSR1	0.544631532	1.515465596	1.476408685	1.26E-61	4.68E-60
SRPX2	0.914596623	2.567426586	1.489115527	5.26E-74	7.43E-72
CEP55	0.573644552	1.627736797	1.504638458	2.92E-79	1.04E-76

COL6A3	0.75466528	2.157646279	1.515549565	6.62E-54	1.27E-52
ADAM12	0.660096057	1.934972215	1.551564965	5.11E-74	7.29E-72
LOX	0.713678529	2.098578711	1.5560663	8.37E-64	3.82E-62
PTX3	0.89665161	2.65129428	1.564077364	1.96E-68	1.34E-66
DLGAP5	0.553917061	1.661669932	1.58489196	8.09E-72	8.29E-70
HOXD9	0.641741346	1.941066674	1.596785833	1.55E-44	1.62E-43
TRDC	0.504088161	1.527870225	1.59977403	5.09E-39	3.86E-38
ASPM	0.498009289	1.52465721	1.614240358	3.72E-72	3.94E-70
CLCF1	0.653418575	2.001541474	1.615032138	7.96E-79	2.48E-76
HIST1H2BH	0.490755972	1.509640721	1.621127514	2.58E-37	1.79E-36
TREM1	0.804493684	2.481393387	1.624997472	3.77E-59	1.11E-57
DMRTA2	0.5180082	1.603156159	1.629868121	7.30E-36	4.70E-35
ESM1	0.784324109	2.437030884	1.635602681	8.63E-56	1.92E-54
GPX8	0.650485349	2.051185984	1.656869841	3.63E-71	3.39E-69
LIF	0.591142618	1.912315048	1.693742082	6.45E-64	2.97E-62
MMP9	0.983326099	3.227412808	1.71463628	5.93E-51	9.13E-50
COL8A1	0.588772488	1.949381637	1.727234395	4.85E-57	1.19E-55
CLEC5A	0.480902037	1.593353305	1.728251259	1.55E-50	2.32E-49
IGF2BP2	0.50984665	1.725772019	1.759106602	4.26E-67	2.67E-65
EN1	0.495227122	1.735931265	1.809547591	2.40E-50	3.54E-49
HOXA7	0.429580052	1.578466755	1.877524969	1.43E-36	9.50E-36
PI3	0.485056726	1.84704507	1.928993689	4.90E-22	1.61E-21
IGF2BP3	0.495401349	1.917433502	1.952506843	1.44E-76	2.76E-74
HOXA10	0.398487211	1.635383644	2.037023789	1.89E-57	4.79E-56
POSTN	0.657781093	2.765512358	2.071867344	1.06E-46	1.24E-45
SAA1	0.553706269	2.348029239	2.084257612	1.41E-32	7.64E-32
PLA2G2A	0.477138361	2.489181674	2.383191945	2.09E-42	1.91E-41
IBSP	0.301801238	1.752273064	2.537556985	2.86E-55	6.01E-54

Table S4. Differentially expressed genes from TCGA based on risk score

gene	lowMean	highMean	logFC	*p*Value	fdr
TRIM67	8.655723498	1.077292267	-3.006244711	3.63E-31	3.51E-30
LHX5-AS1	5.48796946	0.746463336	-2.878129146	6.61E-34	8.19E-33
AC104051.2	20.02564809	2.76609175	-2.855928017	3.26E-13	8.49E-13
AC023421.1	2.046973952	0.316794255	-2.691874664	1.79E-30	1.63E-29
LINC01602	13.84812132	2.321234644	-2.576725998	8.14E-14	2.21E-13
LHX5	1.972944751	0.347800746	-2.504017622	6.72E-26	4.17E-25
F5	5.572057191	1.008854526	-2.465491908	3.44E-33	4.02E-32
AL122019.1	3.383273647	0.689706588	-2.294365219	2.26E-25	1.34E-24
GRIN3A	2.640896808	0.541017912	-2.287279666	6.91E-36	1.06E-34
PRLHR	5.296434439	1.087040343	-2.28461598	5.59E-49	4.61E-47
AL049749.1	3.529093572	0.73898861	-2.255673649	5.98E-45	2.73E-43
KCNIP2	24.99429285	5.495199246	-2.185355013	1.76E-51	2.32E-49
SLC17A8	2.8031148	0.629610198	-2.154500016	1.81E-12	4.48E-12
CACNG2	4.005211014	0.914628515	-2.13062045	1.15E-41	3.40E-40
AC062021.1	11.10650771	2.570823634	-2.111102706	1.22E-36	2.02E-35
KCNJ11	11.19277175	2.590973148	-2.111001377	1.64E-49	1.51E-47
AL513217.1	2.300632064	0.533717616	-2.10788174	3.76E-47	2.28E-45

AL022313.4	10.4881585	2.636003191	-1.992337371	1.85E-43	6.98E-42
BCYRN1	3.213168887	0.812939852	-1.982776293	1.67E-31	1.67E-30
AL355916.1	10.6809797	2.706015402	-1.980802026	7.56E-33	8.51E-32
HMGA1P7	2.088798478	0.535762535	-1.963007707	2.16E-27	1.49E-26
ABCC8	8.237984926	2.14660573	-1.940234252	5.53E-43	1.97E-41
MIR6071	4.570465814	1.208606966	-1.918996047	1.14E-36	1.89E-35
CORO6	3.049980177	0.823364051	-1.8891975	6.45E-33	7.28E-32
AC027130.1	2.310843567	0.625659093	-1.884970914	1.33E-54	3.15E-52
AC012213.4	2.978403961	0.823373176	-1.854921087	5.25E-35	7.32E-34
AC122707.1	2.8318185	0.793335401	-1.835725969	7.75E-38	1.45E-36
HRH3	5.064851715	1.423777796	-1.830796024	2.81E-38	5.54E-37
SELL	44.8764744	12.64910726	-1.826923772	2.19E-24	1.20E-23
RGR	5.57291018	1.571108586	-1.826648006	3.31E-33	3.88E-32
XKR7	1.920658662	0.543082827	-1.822357	6.90E-30	5.93E-29
4-Mar	4.254459462	1.215670463	-1.807223642	9.49E-27	6.24E-26
CHGB	37.38452739	10.80836416	-1.790293107	9.03E-38	1.68E-36
ADARB2	4.194870761	1.221503539	-1.77996832	1.55E-45	7.55E-44
CRTAC1	26.36653495	7.714306667	-1.773099583	2.95E-46	1.58E-44
L1CAM	16.92744752	4.99484418	-1.760852869	1.62E-24	8.95E-24
ATOH8	16.24758131	4.877367225	-1.736050463	4.45E-48	3.22E-46
ZFR2	1.797738244	0.5419501	-1.729951048	3.59E-21	1.54E-20
AC109439.2	2.3268307	0.708795345	-1.71492521	1.95E-35	2.83E-34
USH1C	13.03824209	3.985271236	-1.709999546	3.17E-34	4.06E-33
CALN1	7.567113743	2.315238097	-1.708582565	1.87E-37	3.34E-36
SCRT1	9.67801638	2.967688086	-1.705371913	4.11E-33	4.76E-32
AMER3	2.487769186	0.771177882	-1.68971706	1.21E-35	1.79E-34
SVOP	6.487666816	2.02931433	-1.676707382	9.37E-35	1.27E-33
KCNK3	4.552613717	1.439107221	-1.661520969	1.21E-29	1.02E-28
SLC24A4	2.859496703	0.905597274	-1.658819721	2.44E-40	6.20E-39
SNORC	9.663788621	3.065116153	-1.656647153	5.65E-24	2.98E-23
NOG	11.02695881	3.510195921	-1.651411495	5.94E-40	1.42E-38
MYH7	9.041464048	2.87879851	-1.651089585	9.01E-27	5.93E-26
RTP5	16.38222897	5.266684619	-1.637164689	1.33E-34	1.78E-33
CARTPT	1.95033847	0.641339138	-1.604565161	0.007285904	0.009208168
CRLF1	18.53253777	6.121234731	-1.598165854	6.45E-28	4.62E-27
SLC7A14	5.689730035	1.890079731	-1.589913108	2.01E-39	4.51E-38
GDF10	5.020552926	1.677699668	-1.581361785	3.08E-31	3.01E-30
TLX1	1.826385947	0.619948746	-1.558770813	4.30E-20	1.73E-19
HAR1A	1.771282738	0.603218117	-1.554042854	8.19E-41	2.21E-39
DUSP9	2.706106401	0.932242056	-1.537442062	6.50E-37	1.10E-35
SSTR2	6.789018464	2.355926791	-1.5269083	4.30E-35	6.05E-34
MCF2	1.572676023	0.549049862	-1.518212423	9.20E-39	1.92E-37
TMEM151B	11.65696654	4.082165148	-1.513785955	9.42E-36	1.41E-34
TNNT1	2.407419591	0.845041543	-1.51039344	5.18E-30	4.52E-29
LINC00836	5.484388671	1.92647484	-1.509367472	5.25E-33	5.98E-32
INA	33.44736306	11.75708968	-1.508361492	2.13E-33	2.53E-32
PLN	3.399889659	1.195302953	-1.508111606	0.000223924	0.000319307
AC053503.1	11.42585855	4.040489016	-1.499700758	8.73E-30	7.43E-29
AC074286.1	1.52118369	0.538538088	-1.498074087	9.09E-35	1.24E-33

UNC79	4.764207713	1.707843095	-1.480060878	7.32E-34	9.01E-33
WNT7B	6.594422027	2.366862409	-1.478270378	3.21E-31	3.12E-30
NSG2	67.42313719	24.28651731	-1.473088135	1.44E-36	2.36E-35
FAM19A2	1.934850854	0.700929892	-1.464880306	3.29E-34	4.19E-33
SLC22A6	2.45341941	0.891652432	-1.460240522	3.09E-39	6.81E-38
GJB6	5.479789967	1.992452883	-1.459574989	1.33E-10	2.92E-10
FAM133A	3.25807104	1.185933266	-1.457995232	8.61E-48	5.93E-46
AC092162.3	1.655687926	0.603725615	-1.455465852	1.06E-26	6.92E-26
SLC25A48	6.380225281	2.331851146	-1.452131669	1.35E-36	2.22E-35
DAPL1	4.159157075	1.523788622	-1.448628383	1.38E-12	3.44E-12
MSX2	2.3369703	0.859644675	-1.442827034	1.98E-17	6.71E-17
ACTL6B	14.55398439	5.373730434	-1.437418311	7.59E-32	7.80E-31
PVALB	3.146192318	1.165794791	-1.432293001	1.48E-13	3.94E-13
CHGA	27.58843682	10.2339129	-1.430705856	7.86E-31	7.37E-30
ETNPPL	59.11840653	21.96273293	-1.428549796	3.72E-33	4.33E-32
GABRG2	9.432693671	3.512076476	-1.425345556	5.66E-28	4.08E-27
MMD2	18.6306453	6.946554398	-1.423308185	4.53E-28	3.29E-27
FAM155A	6.110553893	2.2785871	-1.42316364	3.51E-38	6.84E-37
ZDHHC22	45.46184991	17.04840348	-1.415019749	5.05E-40	1.23E-38
SLC14A1	18.20543896	6.838927403	-1.412527546	7.18E-11	1.60E-10
LINC02440	3.629904301	1.378241893	-1.397102398	1.99E-28	1.50E-27
SRRM3	5.860556347	2.237416202	-1.389203977	3.24E-27	2.20E-26
CPLX2	37.23723929	14.2389103	-1.386907377	4.24E-29	3.38E-28
WSCD2	2.039427586	0.78034758	-1.38597551	3.21E-30	2.86E-29
RIMS2	2.416776834	0.927657142	-1.381420665	6.67E-29	5.22E-28
HPSE2	7.474401851	2.881501098	-1.375137561	4.30E-29	3.43E-28
TNR	75.46131064	29.10872107	-1.374285704	1.07E-34	1.44E-33
BRINP1	16.38438756	6.328774855	-1.372323596	9.70E-41	2.59E-39
GFRA1	7.307717588	2.826372673	-1.370469175	3.84E-31	3.70E-30
DACH2	1.803848864	0.698017922	-1.369742483	5.21E-25	3.00E-24
CSDC2	32.70640282	12.65827861	-1.369491868	6.87E-34	8.48E-33
TESPA1	3.275332667	1.270133238	-1.366661601	0.013046998	0.016096253
RASL10A	16.32996163	6.36724067	-1.358781199	7.85E-34	9.64E-33
DGCR6	5.699362659	2.224495655	-1.357322316	2.70E-43	9.97E-42
GABBR1	78.90581221	30.84887029	-1.354913915	1.88E-48	1.44E-46
SYT4	9.148383283	3.611658843	-1.340855188	3.48E-23	1.73E-22
CDHR1	9.122914959	3.612534416	-1.336483537	6.47E-32	6.69E-31
SCG3	217.6837943	86.54640534	-1.330688205	6.33E-46	3.26E-44
ASIC4	27.63567319	11.01592712	-1.326940837	5.45E-24	2.88E-23
ENHO	173.6287957	69.2159589	-1.326829615	2.25E-52	3.85E-50
GRIN1	17.08384477	6.821155547	-1.324544628	2.86E-27	1.95E-26
HIP1R	46.65220356	18.67725379	-1.320662883	3.72E-39	8.09E-38
SCN3B	12.21935384	4.921675008	-1.311946697	2.69E-32	2.90E-31
CSMD3	2.352293417	0.947827641	-1.311371389	4.18E-32	4.40E-31
SFRP2	64.59321614	26.0497015	-1.310115814	7.80E-21	3.27E-20
AL354798.1	2.255091459	0.909913061	-1.309385334	5.36E-33	6.10E-32
PPP1R1A	7.435286481	3.011217519	-1.304041403	9.86E-39	2.05E-37
CNNM1	1.68742078	0.683699273	-1.303385976	9.02E-31	8.43E-30
AC005696.4	7.733829095	3.14470748	-1.298257059	8.78E-38	1.64E-36

GPR17	57.39094009	23.35124602	-1.297323472	4.45E-20	1.78E-19
AMZ1	2.780060531	1.134373208	-1.293220932	3.74E-31	3.62E-30
PCDHGA3	1.944868485	0.794260081	-1.2919892	1.10E-07	2.00E-07
ALDOC	448.8128937	183.7037813	-1.2887328	3.91E-53	7.81E-51
ACSL6	7.525173339	3.081256359	-1.288206095	2.46E-42	8.07E-41
LINC00634	22.61803346	9.263649495	-1.287820926	1.59E-57	7.82E-55
CUX2	3.163092377	1.297384287	-1.285729819	6.77E-26	4.20E-25
AC124798.1	2.294645945	0.944564262	-1.280550712	1.89E-32	2.06E-31
MRVI1	14.74188477	6.07012713	-1.28012235	9.91E-48	6.66E-46
NRSN1	12.80239711	5.291120751	-1.274768717	5.65E-32	5.88E-31
SLC25A21-AS1	2.585956121	1.072630814	-1.269544191	7.06E-40	1.66E-38
CACNA2D3	2.780228287	1.153543618	-1.269130793	1.21E-33	1.46E-32
GDAP1L1	21.21527274	8.802766669	-1.269074294	3.22E-34	4.12E-33
RHBDL3	15.79987489	6.558608649	-1.268451437	8.32E-35	1.14E-33
TPTE2P1	1.736105411	0.721417177	-1.266948868	1.16E-37	2.11E-36
MYT1L	3.026037147	1.258980795	-1.265173423	1.05E-23	5.42E-23
GABRG1	6.43090247	2.680547256	-1.262493641	3.05E-32	3.28E-31
CABP1	4.736567498	1.982154354	-1.256772632	7.66E-24	3.99E-23
LINC00599	4.529425155	1.902720837	-1.251264057	5.48E-25	3.15E-24
SNCB	44.12197554	18.54836755	-1.250205168	1.60E-24	8.87E-24
MIR124-2HG	2.087557534	0.881603733	-1.243613721	2.14E-29	1.75E-28
CLVS2	2.602985374	1.099585612	-1.243207271	2.02E-21	8.84E-21
PCDHGA10	5.926985669	2.513125065	-1.237816101	0.000573707	0.000794208
NEFM	13.84850993	5.908319388	-1.228911033	2.43E-13	6.39E-13
JPH3	13.19230844	5.63028914	-1.228416117	1.73E-34	2.29E-33
LINC01411	1.655707932	0.706775452	-1.228124365	4.58E-06	7.43E-06
KCNC2	2.337229658	1.000248866	-1.224440508	8.11E-20	3.20E-19
PSD	22.05144495	9.440495665	-1.223938679	6.76E-34	8.35E-33
ACBD7	11.57800913	4.957943957	-1.223573331	1.09E-24	6.14E-24
MRO	19.82640103	8.496848783	-1.222423022	2.52E-42	8.23E-41
SMOC1	178.4272428	76.50204915	-1.221765611	2.96E-32	3.18E-31
SUSD5	9.516407806	4.088944588	-1.218688585	5.03E-23	2.46E-22
IQSEC3	4.905108136	2.110075711	-1.216990177	2.70E-23	1.35E-22
NTSR2	26.52716472	11.46822256	-1.209828678	3.90E-18	1.39E-17
FXYD7	12.17124237	5.264957236	-1.20898272	3.00E-16	9.46E-16
CBLN2	1.870799885	0.811934828	-1.20421941	4.24E-22	1.96E-21
YPEL4	5.387340384	2.340705814	-1.202629596	8.71E-42	2.64E-40
CBLN1	3.783600829	1.645526827	-1.201210345	4.02E-30	3.56E-29
GABRB3	6.932674698	3.026680113	-1.19567586	5.04E-32	5.27E-31
KCNJ9	16.46081547	7.191886164	-1.194593718	2.90E-35	4.15E-34
AC015540.1	3.624329866	1.584554138	-1.193637316	2.38E-29	1.94E-28
CAMK4	2.378590207	1.040492718	-1.192839872	4.23E-18	1.50E-17
SHISAL1	5.604354931	2.460811839	-1.187413977	6.53E-22	2.97E-21
GABRD	17.30752837	7.623646306	-1.18284662	1.43E-28	1.08E-27
DUSP26	29.98415461	13.21335434	-1.182203542	4.04E-48	2.95E-46
KCNK7	2.073226092	0.914018022	-1.18158294	4.22E-26	2.66E-25
ST8SIA3	5.416328335	2.388372182	-1.181287527	4.24E-26	2.68E-25
SEZ6L	61.78017644	27.24433351	-1.181187793	6.88E-22	3.12E-21
CHRM1	6.779054088	2.990858429	-1.180524359	4.39E-27	2.96E-26

SCD	311.2818258	137.3689515	-1.180165388	6.39E-43	2.24E-41
SGSM1	3.325613414	1.468552612	-1.17922552	1.70E-39	3.89E-38
ASPHD1	20.06523727	8.871845747	-1.177392029	5.03E-33	5.75E-32
TUNAR	1.584729399	0.700934346	-1.176885289	3.90E-16	1.22E-15
AL450311.2	2.332117778	1.03198809	-1.176214329	2.01E-28	1.50E-27
DDN	14.11930875	6.248878887	-1.176000175	2.79E-15	8.31E-15
TMEM271	5.054431397	2.243747572	-1.171638426	9.77E-25	5.52E-24
AP006333.2	1.821154058	0.8087338	-1.171116157	4.62E-33	5.30E-32
SMIM18	6.207797092	2.760806895	-1.16899142	2.16E-26	1.38E-25
LCNL1	4.947829103	2.200717498	-1.16882171	2.02E-22	9.49E-22
LINC01532	3.944125616	1.756576757	-1.166938881	1.95E-23	9.89E-23
RFPL1S	2.831375626	1.261822435	-1.165994251	2.30E-21	1.00E-20
PCBP3	2.939259085	1.310199567	-1.165665956	7.07E-37	1.19E-35
MYOM1	2.620269467	1.170953406	-1.162031515	1.39E-35	2.05E-34
TMEM100	40.32940581	18.05107967	-1.15974702	4.32E-26	2.72E-25
SPHKAP	5.194966241	2.334650231	-1.153907947	2.42E-25	1.43E-24
RUNDC3A	33.38402809	15.03899614	-1.15044977	6.30E-40	1.50E-38
INSYN2B	1.843348769	0.830861578	-1.149649013	4.10E-25	2.39E-24
SHISA6	5.806528372	2.617290441	-1.149601828	4.83E-14	1.33E-13
CAMK2A	35.39559782	15.97278216	-1.147954317	2.07E-09	4.20E-09
MIR7158	2.432546588	1.098447083	-1.147002065	2.53E-14	7.11E-14
KCNIP3	12.78323158	5.785335586	-1.143780041	2.85E-32	3.07E-31
GALNT13	26.86778116	12.18327691	-1.140974958	2.15E-32	2.34E-31
SNAP91	16.56790606	7.513145151	-1.140902399	3.50E-35	4.95E-34
AL139246.5	1.926570825	0.875490861	-1.1378712	8.58E-14	2.32E-13
LRRTM4	4.329907697	1.97147535	-1.135060599	2.04E-31	2.02E-30
PARD3-AS1	1.829706462	0.833333955	-1.134645546	3.24E-28	2.38E-27
OLMALINC	10.34056187	4.713228709	-1.133526984	2.90E-51	3.68E-49
PACSIN1	19.7610866	9.007604609	-1.133446872	5.22E-13	1.34E-12
CPLX1	22.98714646	10.48374524	-1.132673186	2.72E-28	2.01E-27
SHC3	16.62708494	7.584458798	-1.132417114	1.68E-08	3.20E-08
GABRA3	9.864460202	4.506976972	-1.130080028	5.12E-26	3.21E-25
AC025211.1	1.758633072	0.804004706	-1.129178654	3.19E-21	1.37E-20
BTBD17	26.91500311	12.35853116	-1.122903306	2.23E-22	1.05E-21
PDZD4	74.4660172	34.23835024	-1.12096901	2.40E-40	6.12E-39
CDH18	2.244514165	1.032921157	-1.119673064	2.21E-26	1.42E-25
CCKBR	1.734161008	0.799051971	-1.117876606	2.21E-11	5.08E-11
CDK5R2	12.06579577	5.577134451	-1.113327112	2.94E-22	1.37E-21
DKFZp779M0652	2.856755143	1.320534296	-1.113255615	4.80E-33	5.49E-32
TSPYL2	32.25117155	14.91766201	-1.112330124	9.10E-46	4.59E-44
BMP2	21.37169177	9.887233401	-1.112062321	7.75E-26	4.78E-25
CHRNA4	2.55084786	1.180244862	-1.111890652	6.93E-26	4.30E-25
CHADL	21.04226664	9.739119025	-1.111426937	1.51E-36	2.47E-35
LINC02058	1.488340829	0.689792986	-1.109469576	6.46E-26	4.02E-25
RTN1	70.27756023	32.58333245	-1.108929945	1.11E-41	3.29E-40
SNAP25	120.1369937	55.71614198	-1.1085132	2.46E-20	1.00E-19
AL391834.1	4.554084509	2.114326328	-1.106963002	7.07E-35	9.74E-34
MPPED1	2.860184058	1.32794792	-1.106909422	1.00E-13	2.70E-13
LINC00844	99.86106411	46.42854894	-1.104910088	4.10E-35	5.78E-34

FGFBP3	13.70147016	6.371315202	-1.104667585	2.32E-19	8.91E-19
AL359764.1	2.32254468	1.081707267	-1.102396223	4.02E-18	1.43E-17
SPX	9.147217853	4.260464691	-1.102322217	2.29E-20	9.35E-20
NRGN	152.2483323	71.06249612	-1.099266154	2.87E-06	4.72E-06
FAM163B	15.93168455	7.442555938	-1.098028755	1.35E-23	6.92E-23
CELF4	6.829452873	3.191182752	-1.097678774	1.73E-23	8.80E-23
CLEC2L	2.533264481	1.183841907	-1.097521274	1.23E-12	3.08E-12
CACNG3	4.499248803	2.103710119	-1.096748227	8.61E-16	2.65E-15
SCN2B	6.832606743	3.196448998	-1.095966019	3.96E-32	4.19E-31
ATP6V1G2	62.67507001	29.34024354	-1.095010856	1.16E-43	4.52E-42
PLIN1	1.925101999	0.90129465	-1.094864155	1.18E-18	4.34E-18
ATCAY	52.48881918	24.60450239	-1.093087803	5.86E-24	3.08E-23
PHYHIP	28.97685468	13.58877174	-1.092485945	9.79E-22	4.38E-21
DGCR10	1.706260699	0.800281399	-1.092258809	9.56E-29	7.38E-28
SNCG	24.99047788	11.72539798	-1.091741598	6.91E-22	3.13E-21
HMGCLL1	1.509122989	0.708112358	-1.091660187	6.10E-24	3.20E-23
AL359091.1	9.723810873	4.562965994	-1.091549931	4.88E-27	3.27E-26
AL121908.1	1.58433996	0.743718253	-1.09105385	3.65E-29	2.94E-28
SSTR1	4.47587991	2.102844063	-1.089829458	2.53E-24	1.37E-23
RAB3C	5.418069882	2.548610871	-1.088067886	2.42E-23	1.22E-22
GNAL	4.385376002	2.064501584	-1.086907019	1.79E-33	2.14E-32
VSNL1	32.53006619	15.32001295	-1.086356241	9.29E-09	1.80E-08
NMNAT2	14.17133988	6.675065224	-1.08612233	6.49E-30	5.60E-29
LRP4	41.9450825	19.75985413	-1.085929387	1.26E-38	2.57E-37
TNK2	38.98278238	18.37474577	-1.085112777	1.44E-31	1.45E-30
PHYHIPL	82.12159297	38.72003332	-1.084681419	1.42E-45	6.97E-44
GPR27	9.777453951	4.613707145	-1.083532404	2.76E-26	1.76E-25
AC124854.1	1.51322703	0.714068132	-1.083494813	3.54E-26	2.24E-25
IFITM10	17.54407612	8.280076829	-1.083267917	3.33E-28	2.45E-27
NAP1L2	15.6834137	7.404484201	-1.082768469	4.86E-41	1.34E-39
SLIT1	34.09247752	16.13608024	-1.079163281	2.60E-25	1.54E-24
LINC01088	14.50254273	6.865567544	-1.078854979	5.12E-12	1.23E-11
LIMS2	17.58028688	8.324341318	-1.078550587	9.63E-22	4.31E-21
UNC80	3.972636065	1.883635508	-1.07657681	3.53E-28	2.59E-27
SLC6A7	1.724055118	0.817830186	-1.07593268	6.33E-08	1.16E-07
SLC6A1	55.28658228	26.22609239	-1.075926523	7.63E-44	3.03E-42
NEUROD6	1.693570451	0.803461285	-1.075767589	1.96E-12	4.85E-12
AC092681.1	2.282952945	1.083550446	-1.075134802	3.56E-22	1.65E-21
NDRG2	267.8128776	127.2381534	-1.073693993	6.62E-48	4.65E-46
SYN1	40.65340665	19.3309618	-1.072462832	3.05E-25	1.79E-24
RBFOX3	2.46358997	1.171594032	-1.07228941	3.95E-19	1.49E-18
ATP2B3	2.53754297	1.208570332	-1.070130821	3.18E-20	1.29E-19
TMEM130	16.48752911	7.864045492	-1.068031634	1.50E-16	4.82E-16
SLC25A18	27.13202098	12.94792574	-1.067275518	1.34E-40	3.52E-39
GPIHBP1	8.862450386	4.23289626	-1.066060515	1.01E-23	5.24E-23
NGB	1.86955124	0.893266703	-1.065529121	1.49E-06	2.49E-06
CDH22	3.839648491	1.835051363	-1.065153797	7.46E-26	4.61E-25
SHD	51.7111835	24.72899315	-1.064272823	1.31E-21	5.81E-21
CCDC92B	2.170230731	1.039653511	-1.061745636	8.56E-32	8.75E-31

CCK	11.88634923	5.697274206	-1.060961925	2.24E-11	5.16E-11
SAPCD2	20.86222477	9.99991431	-1.060905379	1.19E-15	3.63E-15
HTR2A	2.095901873	1.005067171	-1.06027925	1.06E-25	6.48E-25
PTGDS	293.8997228	140.9503119	-1.060137328	2.47E-31	2.43E-30
AC007938.1	1.5363924	0.736982692	-1.05984409	5.83E-32	6.05E-31
AL157700.1	5.609220343	2.695997823	-1.056980925	6.56E-30	5.65E-29
FAM57B	8.878838301	4.269485966	-1.056308544	5.45E-36	8.39E-35
GPR158	9.812053966	4.719593803	-1.055892471	1.38E-30	1.27E-29
GRAMD1B	9.265264736	4.458387903	-1.055310055	1.23E-44	5.42E-43
SULT4A1	16.2850926	7.838512526	-1.05490011	2.73E-13	7.14E-13
MEGF11	9.128562851	4.406049087	-1.05090218	5.95E-22	2.71E-21
CA10	13.35198718	6.447841249	-1.050166345	2.36E-20	9.61E-20
DGKG	5.950331201	2.875510692	-1.04915177	1.14E-24	6.41E-24
CKMT1B	1.532617924	0.743631328	-1.043338629	4.85E-26	3.04E-25
P2RX6	3.402139687	1.650768658	-1.043304425	2.73E-28	2.02E-27
ARHGDIG	12.09678524	5.870105938	-1.043165253	1.27E-26	8.26E-26
SHANK2	2.066342588	1.00363944	-1.041838394	1.02E-27	7.18E-27
PID1	37.18542741	18.07571853	-1.040684357	4.82E-34	6.03E-33
AKR1C3	7.664744014	3.726476909	-1.04042529	5.15E-35	7.19E-34
ARPP21	6.549262159	3.190464361	-1.037565963	4.06E-34	5.12E-33
FHDC1	3.783241133	1.844038055	-1.036754304	3.45E-14	9.60E-14
JPH4	27.88866141	13.59601866	-1.036494443	3.58E-34	4.55E-33
FAIM2	79.88948674	38.96115674	-1.035969149	2.86E-47	1.78E-45
CAMSAP3	4.219415038	2.061017235	-1.033686434	2.84E-30	2.54E-29
PSTPIP1	3.430791559	1.677623572	-1.032122439	7.50E-26	4.63E-25
KIAA1755	8.390392259	4.104881283	-1.031397761	5.64E-40	1.36E-38
ADGRV1	6.763219541	3.309062954	-1.031287447	8.81E-19	3.26E-18
PPP4R4	2.411868368	1.180077702	-1.031269315	4.62E-26	2.90E-25
HAPLN1	5.699285046	2.789657073	-1.030693165	7.61E-19	2.82E-18
AF131216.3	5.180923014	2.53684496	-1.030173795	2.72E-30	2.44E-29
CRY2	19.10695232	9.363627301	-1.02895826	1.19E-51	1.69E-49
TUB	24.75145451	12.14040311	-1.027696982	3.88E-42	1.24E-40
PRKCG	6.634639992	3.254565044	-1.027553437	3.27E-10	6.98E-10
PTPRN	13.32200881	6.535117548	-1.02752655	2.96E-17	9.93E-17
FA2H	12.91207816	6.334901191	-1.027327195	1.92E-17	6.52E-17
HOGA1	2.644854248	1.299164628	-1.025603962	1.12E-29	9.40E-29
CALY	6.577672982	3.233301653	-1.024569173	3.59E-16	1.13E-15
AC012558.1	1.544300226	0.759386754	-1.024046514	5.51E-13	1.41E-12
SLC8A2	6.908744797	3.400046752	-1.022869037	2.29E-28	1.71E-27
HPCAL4	21.00714174	10.34759195	-1.021584812	7.32E-26	4.53E-25
GABRB2	3.199116291	1.576499744	-1.020948501	1.06E-11	2.48E-11
MYL3	2.501440821	1.233678827	-1.019792466	2.82E-31	2.77E-30
MTMR7	2.787445884	1.374752254	-1.019772145	2.10E-31	2.09E-30
RIPPLY2	6.85758733	3.385243471	-1.018441491	3.64E-38	7.06E-37
PDE2A	12.78256322	6.310429207	-1.018367122	1.28E-30	1.18E-29
GRIN2C	3.352822242	1.656313604	-1.017400141	1.37E-27	9.58E-27
ALDH2	37.04208057	18.30020865	-1.017305036	1.59E-52	2.82E-50
ANK1	1.84139067	0.90976706	-1.017226636	5.43E-20	2.16E-19
AL731533.2	2.715732223	1.341798776	-1.017172901	1.07E-35	1.60E-34

LINC00320	6.1657213	3.04890183	-1.01597998	1.08E-27	7.64E-27
KLHL32	8.457931625	4.195097519	-1.01160055	4.21E-40	1.04E-38
GOLGA7B	6.821009948	3.383982702	-1.011263173	1.48E-29	1.23E-28
NECAB2	11.1281531	5.522042596	-1.010940252	8.83E-32	9.01E-31
ADHFE1	8.58254728	4.259911445	-1.01058246	7.02E-42	2.16E-40
LINC01105	5.116255154	2.540199051	-1.010146664	3.09E-20	1.25E-19
RGS7	6.313233749	3.136261342	-1.009333385	3.54E-24	1.90E-23
CALB1	1.727941668	0.85910923	-1.008141039	3.79E-14	1.05E-13
PNMA3	5.907857034	2.942806859	-1.005442055	9.44E-24	4.89E-23
FRRS1L	6.369872625	3.179261005	-1.002573063	1.41E-25	8.51E-25
SLC1A2	98.45505606	49.17449421	-1.001555083	1.98E-28	1.48E-27
ADA2	4.229530074	8.46215385	1.000527535	3.78E-33	4.39E-32
CYBA	9.88800944	19.78915957	1.000958318	2.55E-34	3.31E-33
FUCA2	7.812128515	15.63823582	1.001290181	1.95E-36	3.15E-35
RPL39P3	20.16731786	40.39143544	1.002030191	6.09E-13	1.55E-12
SKP1P1	1.675772221	3.357432185	1.002532195	1.97E-17	6.66E-17
IGFBP7-AS1	1.414996385	2.837401704	1.003772046	3.69E-08	6.89E-08
EVA1C	2.407423387	4.829454092	1.004370233	6.14E-25	3.52E-24
ANGPT1	0.843619408	1.692616007	1.004590524	1.13E-10	2.48E-10
SIGLEC14	1.852489708	3.719087636	1.005483217	1.76E-25	1.05E-24
EPHB4	2.601809548	5.22468794	1.005829509	1.91E-23	9.69E-23
STK40	6.922481561	13.90107015	1.00583474	1.54E-63	2.73E-60
SLC1A5	4.049840305	8.140142508	1.007189031	5.39E-34	6.73E-33
FERMT3	4.856255731	9.762358247	1.007385299	6.88E-35	9.49E-34
ARC	15.42618709	31.03531572	1.008529309	5.71E-15	1.67E-14
RPL23P8	0.729056688	1.466927254	1.008694427	3.00E-11	6.84E-11
OAS2	2.873669576	5.786234123	1.009730513	2.43E-30	2.19E-29
TNFRSF10D	0.792008641	1.595355879	1.010290209	3.68E-27	2.50E-26
PSPH	12.99397773	26.17810681	1.010517629	7.18E-19	2.66E-18
SLC30A7	1.546778813	3.117225263	1.010995505	3.26E-68	2.31E-64
FGFRL1	6.079820497	12.2630924	1.012222197	2.07E-19	7.96E-19
YBX3	4.546903837	9.189896955	1.015164192	7.14E-30	6.13E-29
BTBD19	0.865772223	1.75026389	1.015513036	4.18E-33	4.83E-32
SDK1	0.726290624	1.46879795	1.016017088	2.22E-21	9.71E-21
MS4A7	5.216128408	10.55244945	1.016526628	1.06E-25	6.45E-25
DSN1	3.428401927	6.935857823	1.016538072	2.38E-41	6.75E-40
TMEM51	4.1887524	8.474100041	1.016539552	1.80E-50	2.00E-48
C4orf47	1.355502804	2.742750173	1.016795121	6.18E-14	1.69E-13
ITGB1	11.27342905	22.81600093	1.017119538	1.87E-43	7.05E-42
COL18A1	5.581182028	11.29571452	1.017132927	3.01E-24	1.62E-23
SPRED3	1.326478147	2.685859332	1.017782839	3.96E-13	1.02E-12
TMEM106A	1.05198707	2.13024709	1.017903808	2.26E-37	3.97E-36
PTAFR	3.307865348	6.701249937	1.018529708	2.34E-31	2.31E-30
ACP5	1.227558668	2.488109699	1.019258118	1.84E-08	3.49E-08
RNF122	4.488823441	9.102985611	1.020002448	2.59E-35	3.70E-34
PCED1B	1.077881285	2.186236536	1.020251207	2.75E-38	5.42E-37
ZNF436	6.31404218	12.80728138	1.020328462	4.10E-57	1.71E-54
TMSB10	632.8658324	1284.196583	1.020894479	7.52E-32	7.73E-31
DUSP6	7.136633721	14.48480895	1.021225021	7.30E-20	2.89E-19

ABI3	4.937151457	10.02125985	1.021313083	3.29E-37	5.70E-36
PLEKHG2	2.931856092	5.955147169	1.02232287	1.39E-47	9.22E-46
LTBR	1.83778637	3.733936669	1.022728385	2.85E-39	6.34E-38
RCAN1	13.79389055	28.02675628	1.022775356	1.40E-25	8.48E-25
ARHGDIB	27.80805057	56.50553905	1.022889686	5.35E-40	1.29E-38
NCAPG2	2.444098788	4.968351536	1.023464656	5.14E-42	1.61E-40
AC107075.1	0.826282969	1.680094532	1.023834573	2.05E-08	3.87E-08
AL136454.1	2.281444634	4.642084098	1.024825016	7.75E-08	1.42E-07
RPS7P1	5.709116189	11.61801761	1.025024593	8.23E-14	2.23E-13
GNG5	33.48473341	68.18456352	1.025941679	3.96E-47	2.36E-45
PKMYT1	1.286886883	2.620684157	1.026058244	1.90E-20	7.79E-20
GSDMD	2.852705082	5.809676501	1.026127226	2.92E-25	1.72E-24
SLC47A2	0.908246503	1.849962494	1.026340211	1.47E-13	3.91E-13
CD84	1.597377222	3.253663542	1.026360025	1.45E-26	9.38E-26
MYO1F	2.246941128	4.578698904	1.026975371	1.03E-38	2.12E-37
AP001453.2	0.793357738	1.617258822	1.027507131	7.35E-24	3.84E-23
ECM2	3.402245775	6.938032954	1.028039329	2.30E-25	1.36E-24
SLC26A2	1.504004653	3.067118434	1.028074845	1.24E-42	4.19E-41
CDC7	2.804738966	5.721309566	1.0284789	1.46E-42	4.92E-41
PLOD1	14.72844412	30.0529225	1.028900258	9.44E-51	1.07E-48
GGH	4.630724101	9.453408956	1.029596864	5.27E-36	8.16E-35
MTND5P11	0.710164284	1.450276278	1.03010305	7.48E-07	1.28E-06
SNORD17	1.082088265	2.210026774	1.030245664	7.22E-11	1.61E-10
DCBLD2	2.033146141	4.154674541	1.031021548	4.85E-35	6.80E-34
SLC16A4	3.57215676	7.300098447	1.031120527	2.09E-24	1.15E-23
NRM	5.063222852	10.35192841	1.031771657	8.16E-39	1.71E-37
COX20P1	1.937635471	3.963145665	1.032348814	0.015559872	0.019059164
LINC01150	0.920581375	1.883405238	1.032726288	2.54E-32	2.75E-31
CYTH4	2.196236306	4.494003243	1.032967875	1.49E-34	1.98E-33
ZDHHC12	2.715837394	5.559639603	1.033594262	6.56E-39	1.39E-37
RPL10AP6	2.133624326	4.369436901	1.03414119	4.70E-12	1.13E-11
COLEC12	2.531224068	5.18624396	1.034854849	3.90E-17	1.30E-16
HCK	4.54721145	9.318331528	1.035089567	8.65E-32	8.84E-31
CALM2P2	1.307146487	2.680305177	1.035976447	9.88E-15	2.84E-14
MYO5C	0.723269118	1.483903626	1.03679294	4.29E-09	8.50E-09
YBX1P10	2.469980594	5.070462171	1.037617548	7.98E-41	2.16E-39
AJUBA	0.892966577	1.83351206	1.037931672	3.23E-38	6.33E-37
SERPINB1	5.088081023	10.45339986	1.03877869	9.90E-35	1.34E-33
PSPHP1	20.71202437	42.57285198	1.039465172	3.71E-07	6.49E-07
AC016739.1	8.850369298	18.19329797	1.039597529	3.87E-12	9.40E-12
TLR7	1.535979109	3.157673948	1.039703616	1.92E-28	1.44E-27
CD40	1.541063331	3.168564398	1.039903186	7.32E-34	9.01E-33
NPM1P27	2.565307775	5.274605476	1.039931264	1.34E-08	2.57E-08
HOXD8	1.293713688	2.661963409	1.04097237	1.32E-17	4.52E-17
TMEM45A	1.494860086	3.078049841	1.042006133	2.48E-21	1.08E-20
KIRREL1	2.402928999	4.94998563	1.042630316	7.94E-36	1.20E-34
RPS6KA1	3.385434094	6.976159149	1.043092119	6.35E-44	2.55E-42
PROSER3	0.980889685	2.021947491	1.043582733	3.52E-59	2.63E-56
FAM181A	3.2790796	6.761983444	1.04415556	2.30E-17	7.76E-17

SYDE1	4.248648653	8.76305185	1.044429352	6.09E-45	2.78E-43
PIFO	3.14671616	6.492150626	1.044849422	1.10E-21	4.92E-21
FCGR1CP	1.409867084	2.90907729	1.045002469	3.83E-24	2.05E-23
TMSB4X	472.0752612	974.2787649	1.04531774	1.49E-43	5.68E-42
CFAP77	0.733352129	1.514486727	1.046250934	4.59E-05	6.90E-05
VCAM1	6.064079561	12.52691005	1.046670009	5.00E-20	2.00E-19
AL139100.1	0.952594068	1.968119971	1.046884695	7.39E-14	2.01E-13
TAGLN	12.1204039	25.04171201	1.046895421	6.25E-13	1.59E-12
BST2	36.85928903	76.16337044	1.04706908	1.38E-25	8.37E-25
MTTP	0.782316598	1.617278487	1.047743646	4.15E-07	7.21E-07
PLOD2	4.902420269	10.13503224	1.047784606	2.03E-31	2.01E-30
TNFRSF1A	15.06667819	31.15022761	1.04788133	1.66E-30	1.52E-29
AL355974.2	10.0409251	20.76083794	1.047972479	3.12E-15	9.27E-15
TTF2	0.712271405	1.472770176	1.04803334	7.78E-64	1.58E-60
NMNAT3	1.399777855	2.895198871	1.048464561	6.94E-21	2.92E-20
GADD45A	16.81960901	34.79023522	1.048538264	1.83E-25	1.09E-24
RCC1	4.115121742	8.513532745	1.0488228	3.26E-52	5.41E-50
LCP2	2.14853568	4.44733897	1.049588633	2.41E-40	6.14E-39
TRIM38	0.740338442	1.534347353	1.051368278	9.42E-43	3.24E-41
CXCR4	11.67018398	24.2068867	1.052590238	2.79E-24	1.51E-23
ELK3	4.51042266	9.359470344	1.053164258	9.68E-47	5.51E-45
COLGALT1	9.367514604	19.44340347	1.053542551	1.63E-56	5.25E-54
GDPD2	4.081501168	8.47280443	1.053739699	5.71E-19	2.14E-18
SLC10A4	1.966158717	4.083925659	1.054576817	2.36E-05	3.63E-05
ANXA2R	1.059266743	2.201079163	1.055145101	1.02E-28	7.82E-28
ZNF468	1.108844977	2.304165225	1.05518649	8.03E-55	2.00E-52
LHFPL2	4.55778216	9.483154001	1.057034992	7.90E-51	9.26E-49
AC104692.1	2.345954612	4.882148087	1.057340955	5.14E-06	8.31E-06
S100A10	44.47764857	92.57739727	1.057579485	3.63E-20	1.46E-19
TNFAIP3	1.840493591	3.832711323	1.058272614	7.28E-31	6.84E-30
DBF4	1.706278469	3.55376019	1.058493213	4.94E-39	1.06E-37
SIGLEC10	5.043764149	10.50507494	1.058513733	3.49E-27	2.38E-26
SLC37A2	1.392479774	2.900857817	1.058823213	2.59E-33	3.07E-32
RPL13AP5	17.80937682	37.10292119	1.058895742	7.78E-17	2.54E-16
IGLV1-47	0.941507096	1.962221519	1.059444046	0.001319885	0.001777728
RPS7P11	1.37739459	2.872098136	1.06016313	1.54E-12	3.82E-12
MAOB	34.64613968	72.24304799	1.060164148	6.81E-17	2.24E-16
ISLR	4.718609019	9.839401005	1.060208855	0.001243451	0.001677648
RCN3	3.671875362	7.657614941	1.060378028	2.24E-26	1.43E-25
TGFB1I1	2.598066321	5.41845114	1.060442258	1.33E-29	1.11E-28
RPL22P1	2.293986225	4.797353365	1.064381982	2.73E-18	9.80E-18
MIS18BP1	1.135441256	2.374602212	1.064432789	6.14E-55	1.58E-52
COX6A1P2	4.717354185	9.873002551	1.065510976	2.40E-09	4.84E-09
DUSP10	2.175513669	4.555319474	1.066196155	1.28E-38	2.62E-37
MYD88	4.730633684	9.908361286	1.066613024	9.14E-38	1.69E-36
S1PR3	3.889587706	8.150500516	1.067271418	4.30E-34	5.42E-33
PSME2P2	0.678649824	1.422167739	1.067352379	6.68E-19	2.49E-18
NETO2	2.778263149	5.82209235	1.06735447	8.30E-24	4.32E-23
EHD2	9.708780728	20.34998188	1.067665478	7.99E-28	5.68E-27

HAVCR2	5.89099095	12.35537798	1.068556904	1.51E-35	2.22E-34
FAM181A-AS1	0.702628778	1.473669195	1.068578137	1.91E-17	6.46E-17
FTH1P16	1.752053605	3.676747709	1.06938327	2.40E-09	4.84E-09
ECHDC2	1.124878819	2.361445472	1.069900631	1.87E-17	6.33E-17
CHIC2	7.139843332	14.99312785	1.070337065	6.15E-41	1.68E-39
AC090114.1	1.024923126	2.153968356	1.07148135	3.30E-15	9.79E-15
CEBPD	12.62545964	26.53477691	1.071548508	6.32E-24	3.31E-23
EPSTI1	1.178227338	2.47727484	1.072136004	4.13E-32	4.36E-31
TMEM37	1.343125935	2.824813531	1.072561055	2.83E-30	2.53E-29
DPY19L1	9.739456522	20.48705011	1.072799094	5.93E-38	1.13E-36
NXPH4	1.872756711	3.940011838	1.073036472	2.28E-06	3.77E-06
CPM	3.798385006	7.993464038	1.073434698	2.68E-13	7.03E-13
MYL9	9.165702762	19.29287556	1.073750784	4.49E-14	1.24E-13
WDR76	1.855357632	3.907695491	1.074620746	2.13E-30	1.93E-29
FOSL2	5.74807973	12.10646526	1.074625722	1.26E-25	7.64E-25
AC015922.2	2.467655332	5.197985467	1.074811699	6.73E-25	3.84E-24
GPR183	2.988539242	6.303210491	1.076646354	3.57E-28	2.62E-27
NCKAP1L	2.337536561	4.930564739	1.07676397	3.89E-36	6.09E-35
ST8SIA5	1.110194745	2.34276753	1.077401035	0.000302512	0.00042699
C1QTNF6	1.22416416	2.583674885	1.077627505	3.80E-32	4.04E-31
TMEM159	1.873254	3.956283666	1.078599339	7.82E-30	6.68E-29
UBBP1	0.997475228	2.108899835	1.080137656	1.27E-10	2.79E-10
RPS2P46	4.226229432	8.941961779	1.08122029	7.27E-21	3.05E-20
CIP2A	0.857176866	1.814085125	1.081577336	4.86E-41	1.34E-39
GAL3ST4	7.904151778	16.73281315	1.081997459	1.48E-51	2.00E-49
IL10RA	2.245136453	4.753685473	1.082243321	5.81E-29	4.58E-28
SPATA6	3.121976857	6.610270755	1.082249523	2.04E-37	3.61E-36
MORN3	0.642856538	1.361184536	1.082293944	1.38E-16	4.44E-16
AC079140.2	0.797200036	1.688941513	1.083105689	1.97E-12	4.87E-12
C8orf88	1.191828227	2.525369089	1.083317935	5.15E-30	4.50E-29
CALD1	10.41950085	22.0815442	1.0835549	6.54E-38	1.24E-36
LRRN4CL	1.601387322	3.395560727	1.084327544	1.19E-21	5.30E-21
MRPS17	6.342031865	13.45236344	1.08484263	3.93E-18	1.40E-17
LIPG	0.670051825	1.421782507	1.085356199	6.21E-23	3.02E-22
LMO1	2.531856748	5.381847474	1.087905725	3.53E-10	7.52E-10
RBBP8	3.339339469	7.102695124	1.088803799	3.75E-45	1.75E-43
EEF1A1P4	0.701171166	1.491953542	1.089364037	5.74E-11	1.29E-10
IGHM	1.247718096	2.655778524	1.089842825	2.38E-12	5.86E-12
IGLV2-23	1.015709447	2.162309011	1.090084945	7.73E-11	1.72E-10
CRB2	4.003966648	8.526339724	1.090496582	5.22E-15	1.53E-14
LYN	3.43658535	7.321318674	1.091127732	1.59E-44	6.88E-43
AL034379.1	0.654257163	1.394468931	1.091786072	3.75E-11	8.52E-11
PDGFA	7.1607805	15.26678867	1.092207876	2.65E-15	7.92E-15
PCDH18	1.889728519	4.032833788	1.093614957	1.34E-36	2.20E-35
AC005000.1	0.890246317	1.900608797	1.094185145	1.23E-11	2.87E-11
FOXD1	1.915321218	4.089116148	1.094202676	3.54E-29	2.86E-28
PCED1B-AS1	1.693147346	3.616245425	1.094785063	7.21E-34	8.89E-33
CD44	21.72653797	46.42296006	1.09538021	1.18E-21	5.24E-21
AC009902.3	0.824091591	1.761921942	1.096273416	7.97E-10	1.66E-09

RPL39L	2.174343498	4.652673555	1.097480095	8.12E-10	1.69E-09
CDT1	2.285841231	4.892797974	1.097934513	3.48E-24	1.87E-23
PRSS23	1.964174758	4.206567697	1.098720266	1.96E-27	1.35E-26
FAM111A	2.476374599	5.304055944	1.098866426	2.89E-49	2.47E-47
ACSS3	1.182867884	2.53570499	1.100097962	8.58E-12	2.03E-11
PIK3AP1	2.334326138	5.006690846	1.100851234	2.55E-34	3.31E-33
WWTR1	7.273413877	15.6043861	1.101247024	6.66E-30	5.73E-29
HIST1H4E	0.909206989	1.951090505	1.101600023	1.76E-08	3.34E-08
CHEK1	1.24012858	2.662633233	1.102364005	8.14E-35	1.11E-33
CDCA3	1.010861007	2.170478383	1.102428414	4.56E-32	4.80E-31
AC098613.1	0.737085301	1.583282022	1.103014764	3.41E-29	2.76E-28
TKTL1	0.656679491	1.411996696	1.104475409	1.24E-05	1.94E-05
AC131235.1	1.597360448	3.434920151	1.104586665	1.12E-09	2.32E-09
VOPP1	16.62969223	35.76109613	1.10462949	4.47E-22	2.06E-21
EVA1B	3.302731135	7.104877126	1.10515017	4.76E-32	4.99E-31
E2F1	4.682892322	10.08055438	1.106103211	2.26E-23	1.14E-22
RNU4-1	3.103811774	6.684155282	1.106704179	6.12E-06	9.83E-06
LGI2	0.953206412	2.053349558	1.107118689	6.25E-09	1.23E-08
CXCL3	0.638385051	1.375703753	1.107671056	0.023999168	0.028842924
SAMSN1	2.77486264	5.980004103	1.107730117	4.44E-36	6.93E-35
SLA	2.813753937	6.064021138	1.107778612	1.39E-29	1.16E-28
HLX	0.66986307	1.443823582	1.107956352	7.08E-23	3.43E-22
FAAP24	0.63808381	1.375391276	1.108024266	1.99E-50	2.17E-48
TRAM2	2.02477675	4.365768559	1.108472805	2.41E-52	4.07E-50
RNU4-2	8.554467737	18.47927028	1.111157791	0.004251972	0.005482724
TIFA	0.790951794	1.71012047	1.112436284	1.49E-28	1.13E-27
AC092718.4	2.52527331	5.461717487	1.112915152	1.40E-29	1.17E-28
AC079250.1	1.321912079	2.859636461	1.113205526	1.79E-11	4.14E-11
SAMD9	1.637343822	3.542387199	1.113364612	1.19E-35	1.76E-34
AL355472.2	1.48953084	3.224628832	1.114275116	7.49E-12	1.78E-11
CD302	1.130991484	2.449139413	1.114686833	8.17E-41	2.21E-39
TTYH3	23.33469525	50.54017318	1.114953982	2.23E-35	3.22E-34
TCIRG1	3.253782078	7.050137958	1.115533859	1.10E-36	1.83E-35
C1QA	86.65133091	187.9676969	1.117190936	3.24E-30	2.88E-29
LAMC3	1.349174079	2.927521011	1.117603019	7.06E-24	3.69E-23
LRRC32	1.740462104	3.782817	1.119990584	1.62E-21	7.15E-21
TMEM158	10.74843329	23.36372601	1.120143987	1.88E-10	4.08E-10
RN7SL4P	0.886988296	1.930285213	1.121827057	4.50E-10	9.51E-10
AC027309.2	4.124175475	8.979808636	1.122578983	6.99E-11	1.56E-10
ACTA2	9.608721164	20.92329885	1.122693991	1.17E-13	3.14E-13
IGFBP4	20.51381516	44.69630933	1.123559881	3.12E-19	1.19E-18
ARHGAP18	2.216161568	4.828944372	1.12364478	5.73E-30	4.96E-29
AL080243.2	1.780378808	3.884297605	1.125469507	3.54E-14	9.86E-14
MTND4LP30	0.794300433	1.733039924	1.125548195	3.66E-08	6.83E-08
PDGFRL	0.706598586	1.541755079	1.125610831	1.84E-05	2.85E-05
LAPTM5	53.60847118	117.011469	1.126117046	1.95E-37	3.47E-36
PABPC1L	2.229175377	4.866301712	1.126315648	6.00E-18	2.10E-17
KCNK13	0.789290035	1.725837973	1.128669586	6.60E-40	1.56E-38
CLEC7A	1.322762667	2.892425627	1.12872563	3.72E-32	3.96E-31

AC080038.1	0.802464492	1.755160967	1.129093886	1.06E-23	5.48E-23
RPL35P5	2.041176489	4.466604497	1.129777585	4.74E-11	1.07E-10
LAMA2	1.786355061	3.911677705	1.130768644	4.66E-24	2.48E-23
RPL26P19	2.687877407	5.886060155	1.130834948	5.69E-13	1.45E-12
FAM126A	1.417746738	3.104809588	1.130904957	1.97E-43	7.36E-42
PLEK	3.780659621	8.283147003	1.131541026	2.87E-36	4.54E-35
SPAG5	1.997736683	4.377569693	1.13176371	9.00E-25	5.10E-24
MCM8	0.877380628	1.92352635	1.132478836	7.59E-51	8.97E-49
ANG	1.040820962	2.283110871	1.133278997	1.13E-32	1.25E-31
AC024940.2	0.957885134	2.104250238	1.135381711	3.25E-13	8.47E-13
IGHG2	2.679022501	5.886977354	1.13582038	1.24E-11	2.89E-11
PDLIM7	3.869434536	8.507507165	1.136613709	1.01E-37	1.87E-36
LY96	6.092626026	13.40144867	1.137252868	5.73E-30	4.96E-29
AQP1	124.5688719	274.207137	1.138322519	6.01E-13	1.53E-12
LINC01503	1.766751025	3.890369255	1.13880835	3.22E-22	1.50E-21
CD300LF	0.727976555	1.603055198	1.13886021	2.30E-30	2.08E-29
ARPC1B	9.963701379	21.96175103	1.140239398	3.56E-44	1.48E-42
ANTXR2	1.199942271	2.645507001	1.140579236	2.16E-38	4.30E-37
RINL	0.935552693	2.063346023	1.141094963	5.08E-42	1.60E-40
SLC27A3	2.285401579	5.042725193	1.141755916	2.66E-23	1.34E-22
PROS1	5.822535898	12.84968933	1.142013945	5.74E-27	3.82E-26
NKG7	0.97182555	2.144840495	1.142101096	3.21E-22	1.49E-21
RPL23AP65	0.839195859	1.852894523	1.142701293	9.32E-12	2.20E-11
HIST1H2AE	1.474730319	3.256193859	1.142735438	2.97E-16	9.39E-16
ARSD	1.87397171	4.139401129	1.143322886	6.97E-22	3.15E-21
GLIPR1	2.46927851	5.456131474	1.143788841	4.24E-32	4.47E-31
MILR1	1.919103087	4.241722045	1.144217876	1.80E-36	2.91E-35
CDH6	1.167268674	2.580077204	1.144277567	1.19E-21	5.28E-21
CNN1	0.710950841	1.572742031	1.14546034	5.40E-06	8.71E-06
IER5L	2.693299202	5.961202944	1.14622898	3.40E-26	2.16E-25
SHC1	7.580749137	16.78847965	1.147059258	5.03E-39	1.08E-37
RAB27A	0.839383131	1.859462376	1.147484183	5.55E-37	9.46E-36
CD53	15.35752243	34.0355844	1.14809839	2.18E-38	4.32E-37
EMILIN3	3.545343598	7.861089383	1.1488038	5.10E-29	4.03E-28
ADPRH	1.092134119	2.422194997	1.149164976	1.15E-48	9.01E-47
F2RL1	1.494198623	3.313926343	1.1491696	2.66E-26	1.69E-25
CCT6A	42.21254548	93.64915719	1.149594182	3.94E-38	7.62E-37
RPL9P7	0.960478449	2.131517345	1.150055646	3.73E-12	9.07E-12
RPL41P2	1.942486339	4.313000451	1.150787414	4.69E-13	1.21E-12
IL1R1	1.291820636	2.868705426	1.150994061	9.62E-08	1.75E-07
LCP1	5.577701927	12.38974515	1.151403768	4.03E-38	7.77E-37
EMP1	13.25056156	29.44298959	1.151870665	6.87E-28	4.91E-27
KNTC1	0.873676094	1.941629951	1.152097848	4.06E-43	1.47E-41
FZD6	1.302586154	2.896170857	1.152767919	1.18E-20	4.90E-20
AL162151.2	4.618322568	10.27102107	1.153138764	1.13E-07	2.04E-07
NIPSNAP2	19.69626435	43.80935973	1.1533171	1.14E-12	2.87E-12
FZD8	1.127606322	2.512491253	1.155855102	2.47E-16	7.83E-16
BST1	0.634110134	1.413773539	1.156745707	6.00E-38	1.14E-36
SAMD9L	2.61339041	5.827257639	1.156894435	3.08E-34	3.96E-33

P3H1	2.043775012	4.55724125	1.156924359	1.70E-52	2.94E-50
CYR61	19.2665646	42.99178186	1.157961557	4.23E-21	1.81E-20
AMIGO2	1.109375492	2.475568069	1.158011859	7.49E-19	2.78E-18
HCP5	2.253331693	5.028665833	1.15811599	8.00E-25	4.55E-24
EIF1AXP1	0.709098149	1.582624759	1.158261997	2.67E-20	1.08E-19
TMEM176A	6.626754214	14.79602294	1.158835126	5.84E-17	1.93E-16
PTMAP5	1.091945325	2.438108901	1.158861946	1.08E-19	4.23E-19
ADAMTS15	1.523397217	3.401565491	1.158906701	3.42E-19	1.30E-18
MFAP4	8.97114848	20.03663282	1.159275487	6.95E-13	1.76E-12
NFAM1	1.250842962	2.79375951	1.159307161	3.85E-41	1.07E-39
ADAMTS1	2.531400604	5.654477326	1.159457836	4.26E-21	1.82E-20
DCN	5.125562527	11.45113532	1.159708388	1.22E-08	2.35E-08
ZWILCH	1.340755114	2.99548838	1.159745481	5.86E-53	1.11E-50
CD274	0.630646965	1.409535354	1.160315146	8.32E-23	4.02E-22
CD300C	1.028980383	2.299925624	1.160371729	1.51E-37	2.72E-36
CLEC2B	1.195641014	2.672455225	1.160381485	8.37E-25	4.76E-24
LAMA4	3.034017188	6.783404633	1.160780294	3.92E-35	5.53E-34
FGL2	2.979850458	6.664892182	1.161341605	5.66E-34	7.03E-33
RNF135	2.209896109	4.944734037	1.161914377	1.11E-43	4.34E-42
AC011495.1	0.982717403	2.199982868	1.162643779	3.79E-14	1.05E-13
MEIS3P1	1.324870917	2.966115311	1.162722882	1.34E-28	1.02E-27
FILIP1L	2.076131129	4.649308478	1.163118583	5.97E-28	4.29E-27
CASP6	2.085824529	4.671059243	1.163131947	3.04E-44	1.27E-42
AP000924.1	1.108766599	2.483353894	1.163334167	1.29E-21	5.70E-21
CRISPLD1	10.51900563	23.56236747	1.163486172	4.61E-30	4.04E-29
RPS2P5	32.80134512	73.47522104	1.163502816	6.40E-19	2.39E-18
KPNA2	14.28540985	32.00359629	1.163691604	4.16E-49	3.49E-47
SASH3	4.508107224	10.10524809	1.164511006	7.05E-41	1.92E-39
CD300A	3.625342474	8.133584418	1.165773991	1.12E-37	2.05E-36
ALPK3	0.754824425	1.693697838	1.165963503	1.72E-32	1.88E-31
GBP3	3.793732439	8.51329708	1.166100042	6.06E-20	2.41E-19
AC133065.3	0.75251065	1.689839711	1.167102501	6.71E-28	4.80E-27
TNFAIP2	3.443013268	7.747546209	1.170067714	4.30E-22	1.98E-21
SP100	1.128902302	2.54056795	1.170230414	2.07E-43	7.71E-42
ORC6	0.97948924	2.205118354	1.170754541	4.72E-27	3.17E-26
AC004453.1	5.125175672	11.5386901	1.170806094	1.09E-10	2.41E-10
CENPH	2.44831597	5.514229206	1.171369478	1.97E-37	3.50E-36
C1QC	109.652874	247.1273478	1.172311047	9.52E-36	1.43E-34
GBP2	5.31605856	11.99187098	1.173627864	5.50E-25	3.16E-24
NRP1	2.571288787	5.802168839	1.174100626	5.33E-31	5.08E-30
COL9A3	4.909181056	11.07885149	1.174254049	5.88E-09	1.16E-08
CD109	0.91241387	2.059706132	1.174678232	4.39E-20	1.76E-19
TIMELESS	3.171476153	7.161683564	1.175144281	1.07E-38	2.22E-37
CAPG	16.60343641	37.49492297	1.175213393	1.95E-34	2.57E-33
AL645924.1	0.647487584	1.462744796	1.175753653	4.27E-06	6.94E-06
CCR1	3.329031475	7.528498934	1.177259732	3.29E-34	4.19E-33
SLC7A7	2.312328425	5.230963331	1.177730335	9.13E-42	2.74E-40
PPIAP11	0.776769262	1.757396915	1.177882048	3.68E-21	1.58E-20
XKR8	1.869808684	4.232022821	1.178456744	1.14E-26	7.43E-26

CTSZ	27.52225565	62.3353687	1.179452258	2.85E-36	4.52E-35
GPX7	4.731745009	10.71865197	1.179679243	2.84E-56	8.58E-54
HLA-DMA	12.55337042	28.44879875	1.180292974	5.73E-36	8.80E-35
EFHC2	0.726886386	1.648810918	1.181624172	6.25E-12	1.49E-11
ZNF367	1.541403789	3.497747187	1.182181175	1.16E-32	1.29E-31
LGALS1	101.0941544	229.4048643	1.182196404	2.86E-17	9.60E-17
ITGA1	0.819789707	1.861186917	1.182897169	1.34E-29	1.12E-28
AC093673.1	9.227580441	20.95352466	1.183168631	1.38E-31	1.40E-30
KCNE4	2.221108462	5.0464626	1.183992617	2.05E-14	5.79E-14
ADAMTS14	0.65644394	1.491869591	1.184377715	1.23E-12	3.09E-12
RPL37AP1	1.688103074	3.837517295	1.184770256	1.53E-08	2.93E-08
ATP5F1EP2	1.132962218	2.577524624	1.185886459	4.84E-18	1.71E-17
ZNF217	1.746938858	3.97664572	1.186722922	1.17E-44	5.19E-43
TNFRSF19	4.235216736	9.642611935	1.186988187	1.54E-30	1.41E-29
ZWINT	3.552727283	8.089653992	1.18715105	8.87E-32	9.05E-31
CENPW	2.155142439	4.908306841	1.187442217	9.12E-34	1.12E-32
SIRPB2	0.638994785	1.456032813	1.188166806	8.83E-35	1.20E-33
PPP1R3B	1.519327133	3.462555746	1.188404762	1.77E-41	5.13E-40
UCP2	9.144332607	20.85357525	1.189344964	2.68E-41	7.52E-40
CDCA4	1.837929512	4.193579645	1.190100819	1.33E-40	3.51E-39
SCIMP	0.690037283	1.575506766	1.191069731	7.86E-40	1.84E-38
PRPS2	3.17031671	7.2417955	1.191720467	5.30E-38	1.01E-36
AC107464.1	0.754573064	1.724166171	1.192166319	9.13E-10	1.90E-09
MYBPH	0.87326859	1.995686903	1.192388044	4.02E-40	9.98E-39
FCGR1A	3.458303091	7.904087498	1.192534603	1.03E-33	1.25E-32
WDHD1	0.74776027	1.709084659	1.192576137	4.06E-52	6.55E-50
AC016700.2	0.73966915	1.6910086	1.192931987	1.63E-12	4.03E-12
TPM4	17.07831073	39.06541114	1.193726518	8.26E-47	4.78E-45
CASP8	0.638868283	1.462365249	1.194713269	2.14E-50	2.28E-48
TES	0.761150723	1.743647179	1.195854077	1.04E-35	1.55E-34
LINC02308	0.721575808	1.653247124	1.196079517	6.32E-15	1.84E-14
RPS23P8	4.655557859	10.66887181	1.196381669	4.36E-07	7.57E-07
AL512329.2	0.946527859	2.169323149	1.196528103	1.94E-12	4.80E-12
FRZB	4.111711002	9.426804604	1.197029959	3.62E-18	1.29E-17
HK2	4.079852614	9.354912315	1.197207096	1.55E-41	4.56E-40
CD48	0.652499158	1.497161716	1.198182117	1.32E-24	7.36E-24
IGLV3-25	0.753785831	1.732634829	1.200741042	2.71E-10	5.80E-10
TLR2	2.968643968	6.826762725	1.20139753	5.84E-35	8.11E-34
KIF11	1.815616765	4.176390467	1.201796887	2.62E-32	2.83E-31
HILPDA	8.306563127	19.11579452	1.20244158	2.98E-25	1.75E-24
LEFTY2	1.506817525	3.475537271	1.205731298	1.67E-31	1.67E-30
IGLV1-40	1.107515546	2.554596366	1.205768409	1.02E-08	1.97E-08
PDIA4	25.55065987	59.0347345	1.208203498	7.29E-45	3.29E-43
NEK6	9.905900881	22.90953287	1.209587952	9.24E-48	6.24E-46
CAVIN1	16.55512397	38.29001586	1.209690444	9.09E-25	5.15E-24
CDC25A	1.046332257	2.420103341	1.209727609	1.00E-26	6.56E-26
ARNTL2	0.803908742	1.860236266	1.210382223	8.62E-29	6.69E-28
MAD2L1	1.876231744	4.343763729	1.211107598	2.06E-37	3.65E-36
GRIK1	1.745255531	4.043652264	1.212220653	9.18E-13	2.31E-12

RNASE3	0.641397417	1.489805801	1.215833835	4.15E-23	2.05E-22
AC073861.1	9.996302637	23.23100884	1.216585322	1.18E-14	3.38E-14
EPHA2	1.567127763	3.648199001	1.219061624	2.86E-23	1.43E-22
ADGRL2	2.288045647	5.330985449	1.220286409	4.95E-23	2.42E-22
LATS2	1.059435097	2.469473322	1.220908175	1.76E-37	3.15E-36
PTGS2	0.817975143	1.906924147	1.22111855	1.35E-11	3.16E-11
IL2RG	0.663805399	1.547741741	1.221332492	6.05E-29	4.75E-28
CDCA7	2.265650503	5.286240188	1.222316648	4.40E-26	2.77E-25
STAB1	5.886614412	13.74705227	1.223612265	8.05E-29	6.27E-28
MYL12A	11.95224214	27.91752457	1.223889743	3.00E-34	3.86E-33
GSAP	0.914778868	2.139450919	1.225745639	5.22E-34	6.53E-33
EMB	0.907575502	2.125641062	1.22780843	4.85E-30	4.24E-29
SRP9P1	1.612135816	3.77707277	1.228295289	1.18E-11	2.77E-11
CCL5	1.596768834	3.74361465	1.229276471	7.27E-23	3.52E-22
SNHG18	1.021508792	2.396813004	1.230415735	2.69E-09	5.41E-09
PLSCR1	4.586618722	10.78250858	1.233189975	1.47E-45	7.21E-44
TEKT1	0.750879447	1.766064409	1.233884751	2.06E-05	3.18E-05
RPL35P2	0.940215694	2.211423495	1.233911666	5.12E-23	2.50E-22
CYTIP	0.644743765	1.516645869	1.23408644	1.81E-37	3.23E-36
LAIR1	2.443699861	5.748517865	1.234122933	6.28E-37	1.07E-35
FTH1P8	3.455714962	8.131143184	1.234473975	2.49E-07	4.39E-07
TMSB15A	6.289742896	14.80077897	1.234600157	0.007018261	0.008884953
Z74021.1	1.542160975	3.62974565	1.234915091	3.45E-13	8.97E-13
RHOJ	3.72916414	8.793013323	1.237505356	4.68E-27	3.14E-26
DUSP5	2.52125405	5.94514122	1.237569584	4.84E-18	1.71E-17
SERPINB8	1.378017294	3.251271687	1.238410124	3.46E-52	5.64E-50
UBE2T	5.77507463	13.62578166	1.238427499	4.73E-28	3.43E-27
MS4A4A	4.127813707	9.741133047	1.238711728	7.12E-26	4.41E-25
PRR11	1.726336485	4.075828019	1.239379486	6.53E-47	3.83E-45
RPS3AP26	3.031515105	7.159501912	1.239820211	7.06E-13	1.79E-12
TM4SF1	4.842658172	11.4374249	1.239891194	1.01E-26	6.65E-26
UBL5P2	0.743192818	1.755624345	1.240175716	1.08E-07	1.95E-07
AL133260.1	1.173901309	2.774503293	1.24091839	6.77E-15	1.97E-14
TRH	2.187910519	5.173168733	1.241494513	0.016045363	0.019626374
RPL7AP6	3.215920743	7.60605295	1.241916131	1.28E-10	2.80E-10
LZTS1	3.69434435	8.739952137	1.242307033	9.06E-17	2.96E-16
CAPN5	7.984937488	18.89100546	1.242346472	3.48E-37	6.03E-36
CFD	2.665344008	6.307203969	1.24267884	1.98E-16	6.29E-16
IQGAP1	5.106378017	12.0847732	1.242818151	3.69E-50	3.74E-48
AL645929.1	1.039131701	2.459633657	1.243064938	3.17E-21	1.37E-20
FOXD3-AS1	1.374644911	3.255362555	1.243759229	9.65E-30	8.20E-29
C1QB	102.6010561	243.2445362	1.245361818	3.22E-36	5.07E-35
NDUFA4L2	7.482915351	17.74060849	1.245383133	2.37E-12	5.83E-12
NCF1C	0.613168123	1.454066707	1.245738855	4.12E-34	5.20E-33
EFNB2	4.187822719	9.932164811	1.245907831	2.55E-36	4.07E-35
CAV1	8.5611633	20.30888753	1.246232464	4.48E-24	2.38E-23
MGP	14.89886306	35.38832321	1.248071163	5.00E-20	2.00E-19
GAS1	6.097788521	14.48962922	1.248662656	1.89E-27	1.31E-26
RPS7P10	1.059316619	2.517741077	1.248996065	4.11E-13	1.06E-12

TEX26	0.82478244	1.960600978	1.249210426	2.76E-21	1.19E-20
AC136632.1	3.32586956	7.907297232	1.249453068	6.66E-09	1.30E-08
PPIC	3.008238217	7.154604721	1.249953247	2.64E-22	1.24E-21
RAB32	5.962417428	14.18211403	1.250103314	9.51E-46	4.77E-44
ZYX	34.16644784	81.35258051	1.251607845	4.19E-38	8.07E-37
SP140L	0.697859783	1.661776513	1.251717274	1.86E-41	5.39E-40
IGFBP5	54.19496509	129.1576875	1.252902785	5.21E-24	2.75E-23
KDELC2	3.058518775	7.291568736	1.253396103	3.91E-36	6.11E-35
MTRNR2L2	0.839787355	2.002416433	1.253646065	6.77E-07	1.16E-06
FZD1	2.084759747	4.971496216	1.253798976	1.10E-35	1.64E-34
AC090692.1	1.826195806	4.355370468	1.253953979	7.87E-28	5.60E-27
CD276	8.022524177	19.16710709	1.256504468	1.67E-54	3.89E-52
ITGB2	9.225392692	22.08265366	1.259231323	1.46E-40	3.83E-39
MCAM	7.144866102	17.10754462	1.25965383	2.30E-38	4.57E-37
RAB36	1.646698232	3.94296002	1.259702886	4.76E-19	1.79E-18
UBE2S	5.564140768	13.32575076	1.259985991	3.11E-31	3.04E-30
TMEM176B	18.80047116	45.08035426	1.261730035	5.40E-23	2.63E-22
DOK3	1.292710911	3.100894531	1.262284776	5.10E-51	6.29E-49
MAN1C1	4.025686906	9.659319944	1.262686649	4.01E-29	3.21E-28
ARL4C	10.92651907	26.21763364	1.26270361	6.45E-25	3.69E-24
CBX2	1.229561286	2.951873748	1.263487373	3.00E-27	2.05E-26
FYB1	2.696780659	6.475041794	1.263651319	2.86E-37	4.99E-36
APOBEC3G	0.777450641	1.867786226	1.264506354	5.88E-39	1.25E-37
GINS1	2.042202065	4.907214057	1.264778584	1.01E-40	2.69E-39
HIST2H2AC	0.595617775	1.433742915	1.267327643	1.04E-25	6.37E-25
HLA-DRB5	30.16845764	72.65059189	1.267933611	4.17E-29	3.34E-28
HLA-DPB1	27.99966588	67.43578931	1.268104845	2.73E-33	3.22E-32
CYBB	8.777941242	21.15811999	1.269256924	3.06E-39	6.75E-38
CNGA3	2.820753237	6.803081509	1.270107912	1.35E-08	2.59E-08
MYO1B	1.718307063	4.149049541	1.271793013	1.86E-28	1.40E-27
HRH1	2.871300005	6.936087627	1.272418048	2.83E-25	1.67E-24
PSRC1	13.64663567	32.98830261	1.273409223	1.14E-34	1.54E-33
CD52	1.487294115	3.595726332	1.273593252	1.55E-17	5.29E-17
CKS2	14.37191684	34.75252408	1.273865272	4.05E-32	4.28E-31
COL8A2	1.689124258	4.088691096	1.275363609	5.39E-36	8.32E-35
AL035446.1	1.875233358	4.539481656	1.275457433	3.04E-17	1.02E-16
ITGA3	3.526620464	8.537170945	1.275471747	1.39E-17	4.76E-17
MICB	0.624491194	1.511857015	1.275568568	1.55E-40	4.04E-39
OLFML3	10.88371754	26.3600314	1.276180668	3.86E-47	2.31E-45
HLA-DRB6	5.389959927	13.05946957	1.276749848	1.68E-20	6.91E-20
TTC26	1.080717865	2.618664813	1.276841469	1.19E-53	2.51E-51
VSIG4	26.18537388	63.50297941	1.278063078	5.80E-28	4.17E-27
CTSS	7.180231778	17.43113095	1.279563856	8.93E-38	1.66E-36
FST	0.719524968	1.746984804	1.279750403	1.03E-06	1.74E-06
IKBIP	1.697441222	4.125587995	1.281238134	2.58E-47	1.62E-45
NFE2L3	1.061192277	2.580917919	1.282198179	1.94E-39	4.37E-38
AC147651.3	0.838656889	2.039905786	1.28234992	4.11E-33	4.76E-32
CYP1B1	1.523269984	3.707046452	1.283098526	0.002280857	0.003010859
LILRB1	1.123740305	2.735124263	1.283297711	2.90E-39	6.43E-38

MTCO1P2	0.658043551	1.602809997	1.284348439	3.75E-07	6.55E-07
UPP1	3.121634596	7.603548228	1.284371143	6.08E-30	5.26E-29
FOLR1	1.227101337	2.989160612	1.284486022	1.63E-08	3.11E-08
SBSPON	0.605934889	1.476042295	1.284499379	1.74E-08	3.30E-08
SKAP2	3.507424651	8.546022024	1.284840924	5.84E-37	9.92E-36
CAV2	1.478638051	3.60388352	1.285283438	4.43E-23	2.18E-22
BCL2L12	1.321852861	3.222214018	1.285490725	8.88E-46	4.53E-44
RPS11P5	2.354479833	5.743690198	1.28656957	3.97E-20	1.59E-19
FABP7	33.64103917	82.15563819	1.288137317	2.60E-13	6.83E-13
RPSAP12	0.614578862	1.501666715	1.288894598	3.51E-11	7.98E-11
ACE	0.810859002	1.98205173	1.28947164	1.01E-21	4.53E-21
FZD2	1.476269817	3.609909902	1.290006405	3.88E-39	8.40E-38
ITGAL	0.961460838	2.354557427	1.29215591	1.49E-42	5.00E-41
CPVL	6.737446516	16.50021985	1.292211427	3.31E-31	3.21E-30
OSM	0.979080274	2.398001714	1.292333634	1.07E-18	3.94E-18
AL162231.2	0.644957953	1.579707357	1.292380308	4.79E-14	1.32E-13
COL22A1	1.207904597	2.960030204	1.293105385	4.84E-18	1.71E-17
PLEKHA4	7.341654961	18.02177313	1.295563744	3.11E-39	6.84E-38
TCF19	2.692923401	6.613340228	1.29620593	8.23E-35	1.13E-33
WDR78	0.589372878	1.447596734	1.29640718	1.04E-41	3.09E-40
F3	21.05656812	51.73641533	1.296909778	1.45E-24	8.06E-24
AL122020.1	1.00507988	2.471502697	1.298078316	5.90E-13	1.50E-12
FNDC3B	1.25225772	3.079631927	1.298226427	4.85E-59	3.44E-56
OLFML2A	1.302306887	3.203546528	1.298600487	8.92E-23	4.30E-22
FAUP1	1.503373583	3.699736731	1.299219056	1.72E-07	3.07E-07
AC099850.3	2.210124247	5.440383237	1.299580806	7.04E-44	2.81E-42
EME1	0.759889121	1.872323235	1.300968691	4.67E-36	7.26E-35
RPS3AP6	3.545458903	8.736154836	1.301026053	1.80E-11	4.16E-11
LXN	1.510999473	3.724145466	1.301406269	1.67E-28	1.26E-27
CDCA5	2.411571755	5.943912897	1.301439237	4.69E-31	4.48E-30
SNRPEP4	1.58458863	3.907066863	1.301977589	1.07E-13	2.88E-13
LRRC17	3.553716872	8.768912165	1.303069134	9.09E-25	5.15E-24
FLNA	27.286965	67.34361081	1.303329138	2.34E-50	2.48E-48
RBMS1	1.303908413	3.219085988	1.303808577	6.62E-58	3.61E-55
CALHM6	1.758455032	4.342608647	1.304253502	4.00E-30	3.54E-29
NUAK2	0.767585072	1.895634599	1.30428234	6.07E-32	6.30E-31
CHEK2	0.711377651	1.757287663	1.304662819	4.49E-57	1.82E-54
TSTD1	2.969626705	7.335948977	1.304702015	1.45E-14	4.12E-14
SCX	1.493420248	3.689649839	1.30486371	0.000178974	0.000257226
LTBP2	1.071717163	2.64820941	1.305092995	1.53E-24	8.50E-24
AFAP1L1	1.795544759	4.441109025	1.306498372	6.85E-22	3.11E-21
KIF18B	1.705324449	4.223325116	1.308333064	2.46E-24	1.34E-23
C9orf64	2.267117353	5.625762116	1.311189478	5.30E-31	5.06E-30
CITED1	4.788074731	11.88568267	1.311707193	7.64E-19	2.83E-18
TENT5A	1.75863265	4.365832874	1.311802746	4.00E-36	6.24E-35
ITGA2	1.166225176	2.897099561	1.312762893	1.91E-30	1.74E-29
CCL2	11.65602914	28.95951275	1.31296094	6.05E-18	2.12E-17
ALOX5	2.642996249	6.567236256	1.31311198	3.90E-40	9.71E-39
FTH1P12	0.748812211	1.861254316	1.313599328	1.45E-08	2.77E-08

RPS29P16	0.903944697	2.248672652	1.314767241	7.45E-19	2.76E-18
ICAM1	3.094083106	7.698822654	1.31512589	3.36E-26	2.13E-25
HSPB1P1	1.543131592	3.840488268	1.315428648	3.17E-17	1.06E-16
BACE2	1.010301276	2.52088974	1.319147444	3.25E-32	3.48E-31
HLA-DMB	5.493623046	13.71756776	1.320194876	1.95E-42	6.45E-41
LRRC25	1.804993624	4.508019452	1.3205	1.02E-37	1.87E-36
AC025165.4	0.634653173	1.586061473	1.321408383	1.38E-07	2.47E-07
AC098614.1	0.800275156	2.001195463	1.322294058	6.60E-40	1.56E-38
COL6A1	29.55036751	74.18973431	1.328043501	6.45E-28	4.62E-27
FBLN5	3.248061829	8.157191799	1.328493479	8.00E-26	4.93E-25
RMI2	1.035305842	2.600692051	1.328838559	5.53E-30	4.81E-29
ADGRE5	3.322446252	8.347578371	1.329111872	2.89E-28	2.14E-27
RPL24P8	1.496125178	3.762493989	1.330458389	2.42E-08	4.55E-08
MDK	19.05975993	47.96513507	1.331456172	7.61E-17	2.49E-16
HLA-DQB1	6.174459861	15.54897079	1.332434248	1.79E-28	1.35E-27
C7	1.054504056	2.661910009	1.335897155	0.009385653	0.01173124
SLC25A24	0.690518816	1.743177408	1.335966772	1.00E-41	2.99E-40
FCER1G	24.01378081	60.62799868	1.336121636	1.36E-40	3.56E-39
AC007537.1	0.89736934	2.266930771	1.336966536	2.24E-23	1.13E-22
IGHV3-23	0.830687067	2.100926253	1.338648522	6.45E-11	1.44E-10
EPHB2	1.529341257	3.869008976	1.33905371	6.67E-44	2.67E-42
CASP1	2.090763707	5.291766616	1.339719414	2.17E-43	8.07E-42
CALU	19.48326582	49.3865166	1.341881689	1.11E-48	8.71E-47
TP73-AS1	1.616909987	4.101599601	1.342947296	3.13E-31	3.05E-30
P3H2	1.126469314	2.85883179	1.343617722	7.22E-43	2.51E-41
IGLC3	1.521037386	3.860631473	1.343781231	1.60E-12	3.97E-12
POC1A	1.769911173	4.492397048	1.343808485	2.15E-37	3.79E-36
HLA-DRB1	86.2267389	219.025885	1.344894158	6.72E-34	8.31E-33
CENPM	1.6869001	4.285839806	1.345203389	6.11E-30	5.28E-29
BGN	37.7532601	95.92559153	1.345314526	2.04E-26	1.31E-25
MYOF	2.190030192	5.570317653	1.346808842	2.26E-40	5.78E-39
CD74	211.0976919	537.6106934	1.348651029	3.79E-37	6.52E-36
RPLP0P6	7.930197189	20.2304643	1.351100786	2.25E-14	6.33E-14
CEP135	0.572935946	1.462827953	1.352314339	7.28E-59	4.92E-56
COL12A1	0.642292329	1.641241274	1.35348537	3.26E-19	1.24E-18
STK32B	1.36711272	3.496586738	1.354815094	1.20E-28	9.15E-28
AC092958.1	1.015598896	2.598278976	1.355225609	1.63E-07	2.91E-07
TCEA3	1.138890631	2.913974082	1.355358836	2.04E-23	1.03E-22
C1S	9.850264566	25.2043944	1.355440911	3.15E-17	1.06E-16
SGO2	0.750483746	1.923500431	1.357841422	8.95E-48	6.13E-46
CD58	2.700745987	6.923964976	1.358240471	1.38E-44	6.00E-43
CP	2.766398649	7.092438409	1.358272647	4.65E-21	1.98E-20
GNG12	9.107073713	23.40382379	1.361684795	2.64E-44	1.11E-42
PINLYP	0.928224141	2.386066032	1.362088844	4.85E-21	2.06E-20
CXCL1	0.996462482	2.562567677	1.362702714	0.0114746	0.014243084
GPNMB	7.147424379	18.38506795	1.363039152	1.89E-25	1.13E-24
TLR1	1.023190061	2.635223102	1.364850953	8.82E-49	7.03E-47
APOL1	3.194532377	8.233491219	1.36589954	5.12E-22	2.35E-21
BATF3	1.115601011	2.876033016	1.36625909	1.07E-36	1.79E-35

FBLN1	3.59673091	9.275220323	1.366695324	7.45E-10	1.56E-09
SULF1	2.93918296	7.584401579	1.367620187	2.63E-13	6.89E-13
KLHL4	2.408041487	6.216682793	1.36828472	6.92E-32	7.13E-31
SOCS1	0.953077319	2.461762822	1.369026609	8.26E-22	3.72E-21
ATP23	2.507701351	6.477345361	1.369037125	1.29E-22	6.16E-22
PTPRC	1.713921079	4.429344229	1.369792442	3.59E-40	8.98E-39
CD14	31.50749834	81.4304331	1.369872865	4.90E-33	5.60E-32
ZBTB42	0.867725842	2.244691286	1.371205843	2.96E-43	1.08E-41
STEAP1	0.838697314	2.174701144	1.374595014	2.63E-07	4.64E-07
EZH2	2.85372184	7.402103905	1.375090669	2.87E-39	6.36E-38
JAG1	5.010583802	13.00689791	1.376226314	4.75E-43	1.71E-41
C21orf62	2.967097	7.704520318	1.376653046	6.91E-17	2.27E-16
KCNE5	2.342055276	6.084079943	1.377263984	0.000721082	0.000990972
IGHV5-51	0.661551397	1.720511205	1.378912136	1.26E-08	2.43E-08
SEC24D	1.165693263	3.031831525	1.379001375	2.61E-51	3.34E-49
EVC	0.694494416	1.807669788	1.380096161	2.89E-24	1.56E-23
COX7CP1	0.805275061	2.09699606	1.38077059	7.72E-10	1.61E-09
PLK4	0.705450187	1.837590578	1.381199243	7.66E-38	1.44E-36
EMILIN1	6.703290732	17.4698362	1.381924669	1.33E-34	1.78E-33
AHR	2.250815599	5.870165938	1.382953419	3.57E-32	3.81E-31
SPAG4	0.575664654	1.506994377	1.388373496	4.06E-19	1.53E-18
SLC7A3	0.877883121	2.301905434	1.390727786	0.000732682	0.001006134
APOBEC3C	3.994769554	10.47647391	1.390969042	2.64E-42	8.55E-41
FAM114A1	2.125945826	5.578462622	1.391762748	5.53E-43	1.97E-41
SUSD2	0.689662835	1.815262004	1.396214665	2.42E-27	1.66E-26
PROM1	1.271662308	3.350225911	1.397542771	1.36E-18	4.95E-18
AP002784.2	0.658055975	1.734346642	1.398110066	1.03E-20	4.27E-20
SMIM3	7.998909044	21.10648899	1.399811458	2.50E-34	3.25E-33
HFE	0.597316426	1.579796579	1.403171503	7.45E-38	1.40E-36
AC025458.1	0.657455675	1.739346813	1.403580087	1.62E-10	3.52E-10
ST8SIA4	1.105917404	2.926136598	1.403753478	5.31E-55	1.40E-52
GINS2	1.653166447	4.375922052	1.404355052	8.27E-37	1.39E-35
PTMAP4	0.897558931	2.376449664	1.404729274	8.56E-24	4.45E-23
TGIF1	1.769798157	4.688182489	1.405443896	1.13E-51	1.62E-49
EIF4HP1	0.804688948	2.131904697	1.405639823	2.54E-17	8.54E-17
JAK3	0.645034542	1.710972424	1.407368184	1.75E-32	1.92E-31
SIGLEC7	0.621998484	1.650868763	1.408242467	2.90E-35	4.15E-34
APOC2	0.744761395	1.977977259	1.409175643	4.72E-37	8.06E-36
BCL3	1.993820477	5.295302365	1.40917755	6.51E-36	9.95E-35
MND1	0.706184815	1.87590727	1.40947081	5.72E-31	5.45E-30
SERPINF1	6.566459403	17.4449909	1.409625253	1.64E-27	1.14E-26
FTH1P2	2.531213857	6.728880888	1.410537181	1.18E-08	2.26E-08
GZMA	0.555700093	1.478101837	1.411367283	8.40E-22	3.78E-21
RPS29P5	1.127070701	2.998572221	1.411697702	2.48E-21	1.08E-20
RAC2	1.997870637	5.316915963	1.412126493	7.91E-44	3.14E-42
AC034102.1	0.724270599	1.928692639	1.413022534	1.63E-24	9.02E-24
C2	1.191489781	3.173958458	1.413516668	2.57E-34	3.32E-33
SIGLEC9	1.279725214	3.411166198	1.414430983	3.34E-41	9.32E-40
AC009902.2	0.930711275	2.481681751	1.414912528	5.57E-15	1.63E-14

AL049873.1	1.355725595	3.616236467	1.415423819	1.21E-07	2.18E-07
PKIB	1.618962875	4.318658128	1.415513211	2.28E-23	1.15E-22
TGFB2-AS1	1.810135781	4.828662285	1.415525645	6.39E-30	5.52E-29
MIR616	0.630268913	1.684493703	1.418275623	1.40E-09	2.87E-09
MARVELD1	2.438703646	6.527608835	1.420440156	8.83E-38	1.65E-36
SUMO2P1	0.98398139	2.634818863	1.421000848	5.03E-12	1.21E-11
FAM110C	0.589977934	1.580255663	1.421425085	1.38E-15	4.19E-15
IGHV4-39	0.670539815	1.797854385	1.422881274	3.84E-09	7.65E-09
CDKN2C	8.158551443	21.8944471	1.424180089	3.51E-27	2.39E-26
PTGFRN	6.215491609	16.6868158	1.424768274	5.27E-39	1.13E-37
MMP2	8.979446942	24.10774839	1.424798418	3.04E-37	5.28E-36
RPS2P7	0.700819968	1.883731256	1.426477369	6.26E-22	2.85E-21
LDHA	23.06871995	62.22028089	1.431446955	4.33E-40	1.07E-38
FANCD2	0.73486449	1.982717214	1.431928784	1.91E-44	8.17E-43
C3	45.57627084	123.0706559	1.433132026	9.70E-41	2.59E-39
SERPING1	17.32632499	46.80024783	1.433550486	2.97E-23	1.48E-22
AC010343.1	3.081488471	8.325582377	1.433923799	1.71E-16	5.45E-16
AC114491.1	2.326099021	6.29079003	1.435328697	1.53E-10	3.34E-10
AL031727.1	1.184033416	3.204143281	1.436228865	9.43E-17	3.07E-16
NID1	7.747864894	21.00563869	1.438905951	6.44E-35	8.90E-34
AEBP1	27.81518138	75.41918071	1.439058965	2.04E-21	8.95E-21
HAS2	1.471769199	3.992406918	1.439707324	1.15E-40	3.04E-39
RPS2P55	0.577907596	1.568816449	1.440765828	3.46E-21	1.49E-20
PRC1	2.831181183	7.725195412	1.448167349	1.14E-36	1.90E-35
C5AR1	3.074445463	8.389798002	1.448309861	1.55E-31	1.56E-30
HMGN2P3	1.555424693	4.249997086	1.450153305	5.62E-35	7.82E-34
LRRC61	1.000815091	2.734869523	1.450296557	4.20E-09	8.33E-09
HLA-DPA1	17.64704757	48.24642015	1.450995065	9.68E-35	1.32E-33
AL033519.2	0.680738944	1.862588708	1.452135586	1.94E-12	4.79E-12
PHETA2	0.993669516	2.720222459	1.452886627	4.88E-44	1.99E-42
LINC01116	1.173166689	3.212591275	1.453329432	1.18E-06	1.99E-06
S100A3	1.566631444	4.290985525	1.453643214	3.94E-31	3.79E-30
CDK6	3.01286541	8.254759385	1.454089937	1.05E-32	1.17E-31
MCM2	4.807806879	13.23230642	1.460613697	3.70E-39	8.06E-38
PLIN2	3.32610131	9.159121088	1.461377051	6.93E-26	4.30E-25
KIF15	1.13664507	3.137073455	1.464637483	4.30E-35	6.05E-34
EFEMP2	4.977069672	13.73688304	1.464686199	4.67E-23	2.29E-22
FOXJ1	5.244534823	14.47679473	1.464855494	1.92E-21	8.43E-21
SEMA3A	0.541641925	1.495272353	1.464996966	2.11E-14	5.94E-14
ELF4	0.853740611	2.359781169	1.466783366	1.40E-50	1.58E-48
B3GNT7	0.907453311	2.509877104	1.467721401	5.77E-32	6.00E-31
KCNE3	0.814965955	2.256649803	1.469370854	1.83E-47	1.18E-45
FTH1P11	1.582966053	4.385992359	1.470272982	1.25E-09	2.56E-09
SLC11A1	2.20023559	6.103578844	1.471997409	1.26E-36	2.08E-35
CDK2	2.883958565	8.002266164	1.472358178	3.91E-56	1.13E-53
MS4A6A	4.224925245	11.73996617	1.474430532	6.50E-37	1.10E-35
FBP1	1.796694077	5.004486292	1.477877203	1.21E-37	2.19E-36
COL11A1	1.857978327	5.175864367	1.478066139	8.83E-18	3.06E-17
ZMYND10	1.30267951	3.631727331	1.479173699	9.57E-08	1.74E-07

HBA1	1.249907673	3.485797389	1.479667184	5.60E-10	1.18E-09
HIST1H2BK	7.086501579	19.76494902	1.479798747	1.40E-48	1.09E-46
ECT2	1.730520874	4.827263062	1.479999105	2.11E-50	2.27E-48
TXLNB	0.542174675	1.513061496	1.480640992	2.91E-19	1.11E-18
AL139095.2	0.818024237	2.285657138	1.482393513	5.57E-10	1.17E-09
RBM47	0.616061839	1.723340474	1.48406068	1.39E-44	6.02E-43
TPT1P4	1.033536913	2.892749731	1.484851597	1.04E-15	3.18E-15
RUBCNL	0.981427126	2.755538188	1.489381068	4.67E-44	1.91E-42
MTCO2P2	1.84334383	5.176720909	1.489713345	1.70E-05	2.64E-05
PTGS1	2.643265743	7.427833752	1.490620051	2.24E-47	1.43E-45
CDCA7L	2.902300606	8.176659816	1.494314665	1.87E-34	2.46E-33
HLA-DQB2	1.040934562	2.939247895	1.497567663	3.86E-17	1.28E-16
IL4I1	0.599453218	1.697144767	1.501390558	3.22E-39	7.06E-38
AQP5	0.709632336	2.00918349	1.50146567	3.79E-12	9.22E-12
HNRNPKP4	0.529935784	1.50074696	1.501791291	3.19E-19	1.21E-18
PLA2G2A	5.710353496	16.1841718	1.502931577	7.26E-28	5.18E-27
TENT5B	0.592568526	1.679481612	1.502962096	1.97E-19	7.59E-19
SLC29A1	8.025789629	22.76737454	1.504252688	9.28E-33	1.04E-31
FTH1P4	0.542900306	1.540144835	1.504306825	1.71E-10	3.72E-10
SOD2	18.19900615	51.66933486	1.505448645	4.20E-25	2.44E-24
FANCI	1.547299789	4.401239717	1.508157206	7.68E-40	1.80E-38
AC026401.3	2.61949666	7.452511932	1.508437158	3.38E-45	1.59E-43
AC096537.1	0.580834711	1.656395609	1.511847706	3.60E-14	1.00E-13
B3GNT5	0.729563479	2.083457802	1.513874463	6.96E-47	4.05E-45
AC099560.2	2.19987256	6.28802228	1.515186379	5.39E-13	1.38E-12
HIST1H3E	0.592641127	1.69619896	1.517074751	8.09E-43	2.80E-41
TEAD3	1.178289143	3.374913128	1.518156759	2.08E-24	1.14E-23
PLVAP	5.1907106	14.89153064	1.52048809	5.76E-36	8.83E-35
LMNB1	5.123509267	14.72586036	1.523147721	1.79E-46	9.86E-45
HLA-DRA	179.8980423	517.1873001	1.523507363	1.00E-38	2.08E-37
ARSI	0.708432161	2.042146406	1.527384686	7.52E-14	2.04E-13
FAM20C	11.43570497	32.97379918	1.527774816	3.40E-42	1.09E-40
PYGL	4.311984241	12.43728692	1.528247998	1.47E-53	3.03E-51
KLHDC8A	10.53686654	30.41001495	1.529100625	3.94E-25	2.29E-24
PDIA5	0.995407544	2.873736761	1.529568689	1.78E-54	4.07E-52
IQGAP2	1.224592559	3.536721348	1.530110734	1.17E-42	3.99E-41
NPNT	2.614063644	7.550805125	1.530336217	4.37E-21	1.86E-20
NME2P1	0.789541561	2.281208878	1.530711437	2.37E-24	1.29E-23
CAVIN3	1.121512914	3.240763843	1.530887662	1.15E-18	4.24E-18
SEMA3F	0.787473876	2.276787426	1.53169563	2.69E-23	1.35E-22
THBD	1.065325744	3.083201849	1.533134712	2.14E-22	1.01E-21
RSPH4A	0.642202841	1.862732538	1.536319586	6.83E-30	5.87E-29
CTSC	2.329359318	6.761121869	1.537329451	7.60E-49	6.09E-47
RAB34	4.687874013	13.6465843	1.541534191	4.96E-31	4.74E-30
TUBBP1	0.533353613	1.557349808	1.545928776	2.29E-35	3.30E-34
ITPRIPL1	0.701246242	2.048839849	1.546814178	1.18E-45	5.87E-44
CFH	1.367827775	3.997156601	1.547087506	1.53E-27	1.07E-26
TEAD2	2.509642855	7.336752876	1.547659621	6.54E-36	1.00E-34
OIP5	0.865333295	2.529880616	1.547741487	1.49E-43	5.68E-42

FPR1	5.812041972	16.99953353	1.548378133	1.10E-37	2.02E-36
SNAI2	1.312829806	3.840442202	1.548592539	5.57E-19	2.09E-18
DDIT4L	1.519356453	4.448547285	1.54987391	8.92E-22	4.00E-21
MEST	11.96658315	35.07243734	1.551326419	4.84E-29	3.85E-28
CASP4	0.871103687	2.555455078	1.552663874	2.01E-45	9.65E-44
CARD16	1.130201462	3.31999065	1.554599218	1.74E-36	2.82E-35
NAPSB	5.179983263	15.2221873	1.555156336	4.90E-35	6.87E-34
RPS10P3	0.855538521	2.514936594	1.555617308	1.19E-13	3.20E-13
FLNC	5.103402382	15.01404276	1.556781196	9.90E-35	1.34E-33
CSTA	0.622237675	1.831450629	1.557449155	5.84E-29	4.60E-28
ST14	1.231468435	3.627593064	1.558632978	4.33E-40	1.07E-38
ARHGAP11A	0.896286534	2.641314285	1.559224049	5.17E-43	1.85E-41
HMOX1	16.26249114	48.03029168	1.562396299	9.01E-32	9.18E-31
SPINK8	1.869078139	5.52527033	1.563718168	8.86E-26	5.43E-25
NFKBIZ	0.704277029	2.083416502	1.56473635	5.33E-33	6.08E-32
ADAM19	1.140828235	3.377684702	1.565953069	2.08E-26	1.33E-25
AC008080.4	0.528154549	1.565758128	1.56782931	4.33E-09	8.59E-09
LGALS3	17.08357685	50.67780735	1.568744037	5.36E-17	1.77E-16
TRIP13	0.975924926	2.896928611	1.569682056	4.13E-44	1.70E-42
CHCHD2P6	1.909224854	5.667761887	1.569792127	1.12E-15	3.42E-15
SLC2A10	1.726468582	5.14351265	1.574929873	5.27E-38	1.00E-36
CYTL1	4.383919112	13.06296267	1.575189052	4.51E-46	2.38E-44
RPL34P18	0.727674206	2.169558441	1.576036871	7.88E-09	1.53E-08
CLIC1	25.34299693	75.95177697	1.583496578	1.34E-42	4.52E-41
CCER2	1.328965081	3.983090484	1.583585056	3.11E-16	9.80E-16
RPL37P2	0.992501866	2.976953788	1.584695107	1.49E-09	3.05E-09
HLA-DOA	3.59386493	10.78138416	1.584934315	3.10E-39	6.81E-38
TYMP	3.339191704	10.03762058	1.587846492	2.62E-40	6.62E-39
TRAC	0.641920804	1.930443757	1.588465299	2.42E-23	1.22E-22
VIM	141.9980016	427.2969572	1.589368418	1.88E-47	1.21E-45
RAD51AP1	1.288959035	3.886562182	1.592288185	2.52E-47	1.59E-45
BCL2A1	1.564236073	4.718595168	1.592899141	5.64E-30	4.90E-29
ACTN1	6.968213394	21.04640639	1.594713208	3.89E-38	7.55E-37
PLA2G5	2.540358446	7.67944737	1.595970419	1.57E-13	4.16E-13
SPRY4	4.240487734	12.83212615	1.597458114	1.16E-14	3.33E-14
RPS18P12	1.992295374	6.034894746	1.598897055	1.58E-13	4.20E-13
UBE2SP1	0.526023407	1.594570801	1.599969252	8.20E-24	4.27E-23
SPC24	1.573437543	4.773774885	1.601210623	4.54E-36	7.08E-35
AC010422.3	0.721741155	2.189953877	1.601347057	1.32E-16	4.27E-16
TUBB6	4.302849335	13.05939347	1.601723664	1.38E-42	4.64E-41
RPS2P32	0.626635476	1.902109027	1.601901589	4.34E-26	2.73E-25
SECTM1	1.107246027	3.361548836	1.602150288	5.87E-31	5.57E-30
TPT1P9	1.509823012	4.585062556	1.602561977	5.76E-09	1.13E-08
CHAF1B	0.754808189	2.293538588	1.6033932	1.02E-40	2.72E-39
PLK1	1.62278362	4.931913988	1.603676994	1.50E-40	3.91E-39
ARAP3	2.055096631	6.253484247	1.605454008	4.44E-34	5.58E-33
C1RL	2.040045527	6.220033544	1.608321012	8.14E-35	1.11E-33
FOSL1	1.221002781	3.722991906	1.608395994	1.14E-25	6.96E-25
FBLN7	0.579538406	1.770402915	1.611101554	9.91E-19	3.65E-18

CDK1	2.008513715	6.135908467	1.611148648	7.44E-39	1.56E-37
BZW1P2	0.540293656	1.653091903	1.613351286	7.75E-26	4.78E-25
SLAMF8	0.937087789	2.867739839	1.613658033	1.17E-31	1.19E-30
S100A11	48.78842224	149.4244961	1.614805943	2.22E-44	9.42E-43
WEE1	1.492080877	4.573392414	1.615938975	2.57E-47	1.62E-45
SOCS2-AS1	0.550848431	1.688612955	1.616111376	1.27E-20	5.26E-20
GBP1	5.109446044	15.66956781	1.616726598	7.72E-33	8.69E-32
CXCL10	3.776633288	11.58479984	1.617060508	1.96E-31	1.95E-30
GBP1P1	0.700511352	2.150140661	1.617950708	1.52E-23	7.74E-23
GDF15	1.394493037	4.281916685	1.618515994	4.30E-23	2.12E-22
TYMS	5.195746231	15.95517273	1.618621353	3.68E-33	4.29E-32
FCGR2A	3.408484144	10.46880793	1.618894998	1.15E-45	5.75E-44
MAP3K7CL	0.860927029	2.644539107	1.619053443	1.78E-35	2.60E-34
RGS16	3.793421852	11.67043359	1.62128644	1.48E-38	3.00E-37
TAGLN2	37.66289092	116.0003912	1.622914023	5.04E-29	3.99E-28
MKI67	1.291779571	3.984563596	1.625061814	9.79E-35	1.33E-33
TGFB2	3.584393359	11.05953743	1.62549017	2.27E-33	2.69E-32
H3F3AP4	8.843220461	27.28728172	1.625584924	2.55E-28	1.90E-27
ADAM33	0.763119392	2.357743297	1.627425958	7.75E-14	2.10E-13
MSN	22.76502741	70.35555411	1.627845123	8.89E-51	1.02E-48
AC010970.1	3.084494227	9.552859482	1.630898697	4.84E-08	8.97E-08
FKBP9	7.097990229	22.02656208	1.633761842	1.41E-38	2.86E-37
SMC4	1.217396408	3.779679549	1.63446491	4.84E-51	6.02E-49
LAMC1	5.151567056	16.02260339	1.637025321	3.30E-43	1.20E-41
SCIN	1.465491706	4.558621537	1.637212837	5.51E-36	8.48E-35
SNAI1	0.555795154	1.729453958	1.637691444	1.66E-23	8.44E-23
AURKA	1.295983557	4.036619006	1.639100011	1.74E-42	5.79E-41
TFPI	0.912474058	2.842454696	1.639281907	6.04E-44	2.44E-42
FBXO17	1.22882636	3.833246021	1.641285525	1.47E-18	5.37E-18
MRC2	7.577437543	23.68193896	1.644005246	5.87E-43	2.08E-41
HMMR	0.667072494	2.087752555	1.646035272	8.83E-38	1.65E-36
MDM2	4.688149519	14.67740545	1.646506475	1.35E-15	4.09E-15
WDR38	0.782576139	2.454095513	1.648888372	6.46E-16	2.00E-15
TCIM	6.363130277	19.96935477	1.649979154	7.24E-38	1.36E-36
SLC43A3	1.706908544	5.357164893	1.650083941	2.36E-36	3.79E-35
RPL5P34	1.002535283	3.149632869	1.651530661	4.01E-23	1.98E-22
OLFML2B	3.414459633	10.73287579	1.652307503	1.25E-43	4.84E-42
SERINC2	1.083302892	3.405793493	1.652554284	1.09E-31	1.11E-30
EGFR	36.42236994	114.7882871	1.656078735	0.000255162	0.000362066
SOCS2	2.011258027	6.339083195	1.656176023	8.37E-25	4.76E-24
PDCD1LG2	0.665627206	2.09999653	1.657600639	2.46E-41	6.94E-40
COL14A1	0.834905841	2.63574221	1.658523866	2.86E-21	1.24E-20
TNC	18.52819715	58.49475865	1.65858485	1.00E-42	3.43E-41
FPR3	1.33983241	4.237942946	1.66131161	3.67E-32	3.91E-31
ITGA5	2.521318411	8.005436043	1.666801662	1.94E-41	5.60E-40
TSPAN31	10.41698193	33.15496125	1.670287416	4.58E-07	7.94E-07
DIRAS3	3.311346539	10.53951369	1.670318396	1.14E-37	2.08E-36
CIITA	0.610569864	1.943838829	1.670680316	1.66E-44	7.16E-43
CDC42P6	0.738216366	2.35405674	1.673033467	1.73E-30	1.58E-29

GAPDHP63	0.497605176	1.588601144	1.674683551	6.71E-16	2.08E-15
GJC1	0.887634608	2.834310711	1.674960099	2.83E-54	6.38E-52
HOXB7	0.791472766	2.528092548	1.675437665	5.96E-27	3.96E-26
CCR5	0.50386548	1.610388002	1.676297804	3.44E-43	1.25E-41
HSPA7	0.91694968	2.930689644	1.676325727	1.48E-31	1.49E-30
CCDC8	1.040764882	3.32882389	1.677368359	1.23E-17	4.20E-17
ENPEP	0.479894704	1.535464539	1.677885398	1.66E-38	3.35E-37
NID2	0.772425437	2.474727412	1.679802043	9.52E-36	1.43E-34
C1R	12.36908291	39.65513898	1.680769302	9.97E-28	7.05E-27
NUF2	1.103676297	3.539870761	1.681379591	1.33E-42	4.50E-41
GAPDHP65	1.182430251	3.793401098	1.68173684	2.30E-14	6.46E-14
TK1	2.650519455	8.527312591	1.685816013	1.42E-39	3.25E-38
TUBA1C	4.198558507	13.53878596	1.68913238	1.48E-30	1.36E-29
SLC16A3	1.609104267	5.194808268	1.69081269	2.64E-46	1.43E-44
TPI1P1	2.007465739	6.481735051	1.691004684	2.63E-17	8.85E-17
SEL1L3	1.73458615	5.60095869	1.691082293	3.82E-28	2.79E-27
CRABP1	1.632357692	5.274069424	1.691959338	0.01208908	0.014967835
SNRPGP10	3.777758396	12.27261688	1.699840563	3.58E-26	2.27E-25
HLA-DQA2	2.865344127	9.321563733	1.701863577	2.46E-15	7.36E-15
DTL	0.983780074	3.204337479	1.70361836	1.40E-36	2.29E-35
HLA-DQA1	3.010216012	9.811563391	1.704616018	1.00E-33	1.22E-32
RDH10	3.226689508	10.51795701	1.704727841	1.12E-32	1.24E-31
ALOX5AP	9.60562212	31.32727853	1.705468485	6.70E-47	3.91E-45
PBK	2.994870388	9.804179768	1.71090337	3.00E-35	4.27E-34
CD93	2.736723525	8.959267988	1.710931167	2.82E-42	9.12E-41
CFI	3.572726982	11.71559801	1.713333021	1.43E-30	1.32E-29
FSTL1	7.526521263	24.69474236	1.714148802	2.96E-45	1.40E-43
MOXD1	2.989953193	9.82141888	1.715808563	1.52E-20	6.27E-20
PLBD1	0.915004933	3.006717763	1.716338024	6.59E-43	2.30E-41
HAMP	1.395690453	4.591415435	1.717959969	2.44E-34	3.19E-33
OTX1	0.486824603	1.604138238	1.720324487	4.52E-11	1.02E-10
ADM	3.729001711	12.30361455	1.722220848	2.50E-15	7.46E-15
VASN	2.098858776	6.944442651	1.726253814	1.60E-24	8.83E-24
SERPINA3	0.582936549	1.933254001	1.729620436	4.80E-25	2.78E-24
MCUB	2.162001082	7.171050316	1.729817195	2.81E-40	7.08E-39
RAD51	0.609600485	2.022023094	1.72986352	3.48E-45	1.63E-43
LYZ	5.266902391	17.47150385	1.729977165	2.53E-24	1.37E-23
CDKN3	1.329909277	4.414934195	1.731064102	5.81E-40	1.40E-38
PDGFD	0.8454309	2.810135925	1.732881166	2.59E-34	3.35E-33
RPL12P4	1.292467685	4.304786881	1.735813605	6.56E-15	1.91E-14
EIF4A1P10	0.600818773	2.004703448	1.73838704	5.27E-20	2.10E-19
ANGPT2	1.554089909	5.192431969	1.740340439	6.57E-31	6.20E-30
NAMPTP1	0.771952433	2.58218808	1.742010229	2.16E-27	1.49E-26
RHOD	0.536314228	1.794037401	1.742059535	1.93E-11	4.47E-11
PLP2	11.9284304	39.9172049	1.742606484	7.25E-30	6.21E-29
PTMAP2	1.949426738	6.528690394	1.743743689	2.30E-21	1.00E-20
GPX1P1	3.08487439	10.33161355	1.743781935	1.28E-20	5.30E-20
FTH1P10	0.61110443	2.050571874	1.746535467	9.37E-10	1.94E-09
SEC61G	51.11700338	171.5411428	1.746679467	3.78E-28	2.76E-27

LSP1	1.410216372	4.732812966	1.746781375	1.09E-36	1.81E-35
TUBAP2	1.104999424	3.713450885	1.748714879	2.45E-28	1.83E-27
HOXC4	0.597843977	2.016114689	1.753736781	6.47E-43	2.27E-41
RPS19P1	0.504529557	1.707316374	1.758719728	6.81E-17	2.24E-16
KIFC1	2.172668	7.356665851	1.759584327	9.61E-37	1.61E-35
PDLIM4	3.145993619	10.65490097	1.759929535	4.88E-15	1.44E-14
CENPU	1.702958522	5.768572261	1.760170995	1.63E-42	5.45E-41
SKA3	0.837449143	2.838007994	1.760805167	2.20E-37	3.87E-36
PTTG1	3.66259451	12.42855696	1.762720907	2.05E-40	5.24E-39
KIAA0040	2.43429434	8.270711941	1.764507901	6.03E-35	8.37E-34
RBP1	6.332413715	21.5283772	1.765412155	6.74E-16	2.08E-15
CCNB1	4.015832044	13.66705695	1.76693177	1.18E-44	5.21E-43
IL1RAP	1.535431537	5.226419103	1.767178632	3.40E-35	4.83E-34
EMILIN2	0.921300297	3.13704433	1.767662534	2.71E-34	3.50E-33
YBX1P1	1.165765875	3.970003281	1.767862124	2.10E-30	1.90E-29
APOL4	2.200194394	7.501511378	1.769550298	7.15E-36	1.09E-34
RANP1	0.50903427	1.741056313	1.774128174	7.24E-21	3.04E-20
CLEC18B	0.48943953	1.677170831	1.776827113	2.19E-43	8.15E-42
PCLAF	0.974445982	3.344496722	1.779135013	1.88E-35	2.74E-34
VAV3	0.578970511	1.988654462	1.780230848	1.55E-35	2.28E-34
TEAD4	1.158517332	3.981154509	1.780907236	2.94E-37	5.13E-36
OSMR	2.284950174	7.861120555	1.782572269	3.17E-35	4.50E-34
ARSJ	0.665822401	2.294970136	1.785266066	3.90E-17	1.30E-16
SPRY1	2.5824631	8.90384017	1.785679961	3.53E-34	4.48E-33
FAM129A	1.321446828	4.556972469	1.785957279	9.18E-48	6.23E-46
NAMPT	8.771150713	30.36079665	1.791371615	2.28E-31	2.26E-30
MSR1	2.018515846	7.042465843	1.802785749	2.52E-49	2.19E-47
DEPDC1B	0.482085626	1.682722229	1.803435728	3.09E-44	1.29E-42
PRF1	0.479271565	1.676569403	1.806596954	1.71E-24	9.42E-24
ANPEP	0.62531373	2.192227949	1.809745719	3.03E-19	1.15E-18
CCNA2	1.711777994	6.00176208	1.809890523	2.97E-47	1.82E-45
RARRES2	5.696065582	19.99985721	1.811952038	7.60E-14	2.06E-13
RNASE2	2.510799571	8.822436169	1.813030219	2.17E-39	4.87E-38
PIMREG	2.321625253	8.157944327	1.813070545	9.36E-39	1.95E-37
GPR65	0.578711888	2.034394283	1.813682128	8.89E-51	1.02E-48
NCAPH	1.160323415	4.103668723	1.82238729	8.15E-42	2.48E-40
SPP1	273.1090285	966.69152	1.823578578	7.86E-37	1.32E-35
SHCBP1	0.687819743	2.436774033	1.824870042	2.03E-50	2.20E-48
CRNDE	1.0753519	3.813475519	1.826297592	1.05E-39	2.44E-38
CHODL	0.643058802	2.283958586	1.82851392	4.90E-12	1.18E-11
CRABP2	3.144648187	11.17115273	1.828807535	3.07E-21	1.33E-20
LDHAP4	0.923573235	3.28196842	1.829263087	9.30E-41	2.49E-39
FOXM1	2.657901953	9.466184332	1.832495129	3.38E-38	6.59E-37
EN2	0.441241824	1.5736761	1.83449718	2.55E-29	2.08E-28
BIRC5	3.13183782	11.17279638	1.834908905	7.30E-41	1.98E-39
OCIAD2	4.156398833	14.84540349	1.836610303	3.50E-24	1.88E-23
MMP14	11.35663616	40.5686955	1.836831342	1.87E-49	1.68E-47
FCGR3A	14.72303117	52.82922035	1.843261396	1.44E-46	8.08E-45
CDC45	0.958109976	3.459247978	1.852195269	1.17E-37	2.12E-36

IGFBP3	13.87332549	50.21674873	1.855854976	2.35E-18	8.46E-18
9-Mar	7.141156023	25.85043323	1.855958915	3.16E-09	6.32E-09
CDC6	0.620821505	2.249645284	1.857447104	2.76E-49	2.39E-47
CLCF1	0.899664214	3.266121393	1.86011987	1.00E-35	1.50E-34
PDLIM1	2.987103687	10.84615086	1.860363921	9.65E-30	8.20E-29
SFRP4	2.793132969	10.15244268	1.861870721	9.10E-27	5.98E-26
CENPK	0.505366635	1.837843011	1.862611213	9.52E-42	2.84E-40
CXCL11	0.524476692	1.909840535	1.864501617	2.56E-27	1.75E-26
LINC01579	0.574879853	2.095838724	1.866195329	4.54E-22	2.09E-21
FTLP2	1.199315771	4.397620139	1.874511431	2.07E-25	1.23E-24
PFN1P1	0.670182234	2.457553205	1.874597304	2.29E-22	1.08E-21
NUSAP1	4.289688864	15.77265924	1.878481	6.83E-44	2.73E-42
TPX2	3.938349397	14.49428742	1.879821395	5.32E-45	2.44E-43
S100A4	5.448361825	20.10540276	1.883688816	4.47E-35	6.28E-34
HSPG2	1.232949274	4.551488344	1.88422494	1.33E-44	5.80E-43
LOXL2	2.204245625	8.153886593	1.887202895	5.28E-37	9.00E-36
ANXA1	13.80496705	51.28303268	1.893294135	3.44E-38	6.69E-37
TMSB10P1	0.877088912	3.26663037	1.897008215	3.70E-20	1.49E-19
PPIAP31	0.789394126	2.949488733	1.901647209	8.78E-18	3.04E-17
METTL1	4.369768205	16.32818138	1.901735455	1.46E-21	6.45E-21
ANXA2	7.883236869	29.56804437	1.907178798	7.81E-36	1.18E-34
GTSE1	0.840537473	3.168146694	1.914255094	1.81E-42	5.99E-41
FP671120.4	1.337233183	5.050831575	1.917269874	1.33E-14	3.80E-14
TMSB4XP4	2.105760499	7.957526099	1.917978624	8.38E-32	8.59E-31
SERPINH1	6.464848756	24.47085714	1.920376112	9.58E-45	4.27E-43
DRAXIN	1.243789303	4.71053208	1.921147915	8.36E-47	4.80E-45
FREM2	0.535651303	2.030991368	1.92281806	1.82E-36	2.93E-35
GSX2	0.427885634	1.632355281	1.931657946	2.41E-14	6.76E-14
S100A9	13.44614178	51.33054038	1.932625182	1.24E-24	6.93E-24
AURKB	1.415349385	5.422825574	1.937886534	5.24E-42	1.64E-40
RAD54L	0.530188886	2.035001597	1.940451593	5.19E-53	1.01E-50
TACC3	2.309717767	8.873955151	1.941860687	1.16E-44	5.14E-43
NKX2-5	0.436405336	1.678949649	1.94381832	9.99E-26	6.11E-25
RAB42	0.701171018	2.705748171	1.9481893	2.67E-50	2.79E-48
HS3ST3B1	0.434826794	1.68716333	1.956086897	1.57E-22	7.44E-22
DPYD	1.488744716	5.794137212	1.960497462	4.17E-42	1.33E-40
TNFRSF12A	7.004835085	27.30658186	1.962825743	9.08E-42	2.73E-40
TMSB4XP1	2.007892635	7.827970283	1.962956151	9.66E-28	6.84E-27
S100A8	3.55649933	13.86772239	1.963201065	1.74E-22	8.22E-22
PLAUR	1.309737606	5.113116543	1.9649251	1.05E-41	3.10E-40
H3F3AP6	0.499256598	1.950081046	1.965680684	2.53E-21	1.10E-20
BUB1	0.772711628	3.039256115	1.975716241	3.71E-46	1.98E-44
SERPINA1	3.193587347	12.5784172	1.977700578	1.74E-46	9.65E-45
HK3	0.475599902	1.876577592	1.98028362	3.17E-38	6.23E-37
FAM111B	0.567644316	2.241830034	1.981617772	2.50E-41	7.05E-40
CD163	6.079767601	24.11183896	1.987653604	5.37E-27	3.59E-26
NOS2	1.149835543	4.573034981	1.991724422	3.23E-06	5.30E-06
TMSB4XP2	1.177099363	4.682649283	1.99208888	1.62E-26	1.04E-25
EMP3	9.695487128	38.67026661	1.995839421	2.15E-28	1.61E-27

FN1	16.71535153	66.68034588	1.996087892	5.08E-40	1.24E-38
TMSB4XP8	31.65173625	126.4472095	1.998178654	3.55E-32	3.79E-31
TCTEX1D1	0.823112194	3.289245922	1.99859588	2.21E-23	1.12E-22
DPEP1	0.575077806	2.305820933	2.003451414	2.56E-25	1.51E-24
NNMT	5.310212558	21.33396749	2.006310774	3.58E-30	3.18E-29
IQGAP3	0.597753479	2.403244315	2.007360795	2.20E-45	1.05E-43
SAA1	7.406718843	29.89612235	2.013051894	9.75E-26	5.96E-25
NEK2	0.67733741	2.746583287	2.019691455	2.83E-43	1.04E-41
TTK	0.511258362	2.082057508	2.025885477	4.73E-44	1.93E-42
LAMB1	2.727768627	11.13942907	2.029882108	5.20E-40	1.26E-38
IL13RA2	2.562158145	10.47572652	2.031618871	3.28E-19	1.24E-18
CCNB2	1.550058213	6.351264704	2.034721502	1.67E-45	8.11E-44
CHRNA1	0.80062802	3.280660767	2.034782408	5.69E-15	1.67E-14
ORC1	0.449550927	1.845262592	2.037269669	1.47E-57	7.72E-55
EXO1	0.434527594	1.783769323	2.037409357	2.59E-42	8.44E-41
CKAP2L	0.53444407	2.197588149	2.039810152	7.43E-45	3.35E-43
FABP5	5.157468634	21.21616074	2.040428564	6.77E-26	4.20E-25
RUNX1	0.586253135	2.417620629	2.043992237	2.21E-59	1.74E-56
AVIL	1.488179412	6.145613498	2.046008573	7.00E-21	2.95E-20
FBLIM1	1.166543053	4.827707635	2.049098756	2.47E-38	4.88E-37
UBE2C	4.999499711	20.70513857	2.050133218	3.64E-43	1.32E-41
TWIST1	0.679800597	2.82160663	2.053333337	3.10E-25	1.82E-24
FTLP3	6.293098225	26.12451027	2.053561626	1.57E-24	8.68E-24
STEAP3	3.334593877	13.84506785	2.053789153	1.29E-37	2.34E-36
CENPF	1.212202421	5.040167187	2.055840961	9.45E-46	4.75E-44
C6orf15	0.609628042	2.549263082	2.064079095	5.33E-22	2.44E-21
TNFRSF11B	0.628062506	2.62914051	2.065611196	1.34E-45	6.61E-44
TNFAIP6	1.504986329	6.310812091	2.068075285	1.48E-29	1.23E-28
NCAPG	0.718479173	3.020776614	2.071901259	5.05E-46	2.63E-44
VEGFA	4.281148709	18.01917368	2.073462999	3.58E-25	2.09E-24
KIF4A	1.084337073	4.580032602	2.078544571	3.42E-47	2.08E-45
CDK4	25.34585109	107.0635585	2.078645996	1.70E-23	8.62E-23
ACTBP2	0.600786988	2.541889607	2.080975903	7.90E-21	3.31E-20
SKA1	0.464458521	1.967575242	2.082797142	6.69E-45	3.03E-43
HMGN2P5	4.061022416	17.22681346	2.084740967	1.10E-30	1.02E-29
LTF	18.24980366	77.61394636	2.088434969	1.43E-30	1.31E-29
MIR4435-2HG	0.589957433	2.509230008	2.088561953	2.86E-42	9.21E-41
CEP55	0.521529637	2.220995957	2.090385622	7.34E-50	7.08E-48
E2F2	0.411269078	1.752398581	2.091176443	1.54E-47	1.01E-45
GJB2	0.990875601	4.225472399	2.092336789	1.25E-12	3.13E-12
ASF1B	1.736399328	7.421657919	2.095642736	1.78E-45	8.54E-44
HJURP	0.769860185	3.312950249	2.105448173	2.55E-42	8.31E-41
RRM2	1.836026021	7.904153577	2.106024473	1.69E-41	4.92E-40
SOCS3	6.105636732	26.29955924	2.10682496	9.42E-29	7.28E-28
HTRA3	0.469059687	2.021508748	2.107589028	2.66E-33	3.14E-32
METTL7B	12.82127236	55.38988515	2.111083107	4.36E-33	5.03E-32
NDC80	0.820806516	3.561570563	2.117399485	1.47E-46	8.20E-45
BCAT1	1.75042523	7.607734255	2.119761415	1.04E-38	2.16E-37
TOP2A	3.849840842	16.77137273	2.123130069	1.42E-43	5.49E-42

SDC1	1.242992103	5.418989617	2.124206752	1.72E-31	1.72E-30
EEF1AKMT3	2.238734783	9.785245894	2.127924479	1.88E-39	4.25E-38
HMGN1P38	0.398677124	1.744339941	2.129388492	1.37E-26	8.90E-26
CHI3L2	13.81330743	60.49618589	2.130785391	2.75E-34	3.55E-33
CYTOR	0.759684269	3.359743209	2.144879118	4.35E-34	5.48E-33
FAM83D	0.753638493	3.335045168	2.145761742	1.23E-48	9.62E-47
CENPA	0.598350928	2.654446462	2.149347278	5.79E-47	3.42E-45
AL591846.1	2.306546021	10.28975	2.157401949	3.88E-13	1.01E-12
TROAP	0.716614856	3.199105819	2.158398857	9.59E-43	3.29E-41
FAM183A	0.757197522	3.382461598	2.159331961	1.53E-26	9.91E-26
C7orf57	0.533777844	2.417296228	2.179082952	2.29E-24	1.25E-23
BUB1B	0.786539072	3.568450747	2.181707521	4.21E-46	2.23E-44
FAM20A	0.408068346	1.876736284	2.20134323	9.40E-38	1.74E-36
SPON2	0.497198755	2.286685016	2.201363064	3.78E-31	3.65E-30
KIF2C	1.28582788	5.939921929	2.207746432	1.39E-55	3.80E-53
AC074351.1	1.777135701	8.22796407	2.210981645	0.002465719	0.00324703
HP	0.447376375	2.080944524	2.217677525	3.38E-19	1.28E-18
SRPX2	1.981403784	9.221791215	2.21852409	5.60E-34	6.97E-33
TGFBI	4.625291168	21.76745111	2.23455639	1.64E-32	1.80E-31
CDCA8	1.266979433	5.964665303	2.235048081	1.74E-57	8.22E-55
KDELR3	0.716451709	3.393828968	2.243972491	9.84E-36	1.47E-34
CD248	2.282377226	10.8338364	2.246935049	7.47E-36	1.13E-34
G0S2	1.599567585	7.62734182	2.253498405	1.48E-19	5.75E-19
DES	0.728059498	3.474160054	2.254535961	4.43E-20	1.78E-19
FCGBP	5.551966183	26.58887832	2.259752231	5.95E-50	5.86E-48
MELK	0.899977951	4.35089006	2.273349001	4.65E-46	2.44E-44
CDC20	2.503434237	12.10507473	2.273631523	1.44E-51	1.98E-49
KIF20A	0.734343805	3.596973663	2.292256028	1.48E-49	1.38E-47
KIF23	0.426628911	2.089965086	2.292425202	1.30E-49	1.23E-47
SPOCD1	1.905653715	9.466863414	2.312600523	2.32E-39	5.19E-38
MYBL2	2.455624651	12.23954271	2.317387695	1.77E-40	4.58E-39
GPX8	0.62862109	3.140379386	2.32067628	6.67E-31	6.29E-30
SERPINE1	9.322134342	46.63431277	2.322659648	4.76E-32	4.99E-31
GAS2L3	0.34028012	1.725391636	2.342129096	4.88E-61	5.32E-58
DKK1	0.653097686	3.339219119	2.354140065	0.008667812	0.010881948
CHI3L1	124.6928587	638.6425038	2.356629729	1.23E-32	1.36E-31
PLAT	2.649899906	13.62808014	2.362572565	1.80E-40	4.65E-39
COL4A2	7.86458172	40.6107651	2.368420265	6.29E-47	3.70E-45
MXRA5	0.617499087	3.200193159	2.373650077	1.19E-36	1.97E-35
AL133415.1	0.556648341	2.909861711	2.386112485	4.52E-42	1.43E-40
HOTAIRM1	0.855024635	4.494591817	2.394152208	5.11E-33	5.83E-32
ANXA2P2	0.964645598	5.077699667	2.396104154	1.68E-37	3.02E-36
IL6	0.394469739	2.079482805	2.398238219	2.45E-30	2.21E-29
HOXD9	0.522204865	2.772088156	2.408285333	3.29E-36	5.17E-35
ABCC3	0.899131367	4.83511829	2.426947366	1.10E-34	1.49E-33
COL5A2	2.412972391	13.03588202	2.433604887	2.34E-41	6.66E-40
ACTG2	0.451708088	2.448837925	2.438634641	1.51E-21	6.67E-21
CXCL9	0.393242946	2.138035998	2.442793353	1.82E-29	1.50E-28
MAP1LC3C	0.381449019	2.074856197	2.443449194	2.54E-30	2.29E-29

MET	0.742934233	4.062980701	2.451232102	5.92E-12	1.42E-11
AL354919.2	0.735360948	4.024263402	2.45220027	1.11E-39	2.59E-38
WISP1	0.477584337	2.629607864	2.461020248	4.45E-22	2.05E-21
DLGAP5	0.503075348	2.781735654	2.467138927	6.53E-52	9.96E-50
MMP19	0.354110998	1.958844654	2.467729431	7.76E-28	5.52E-27
AC064875.1	0.345637038	1.932894122	2.483432883	1.64E-30	1.50E-29
SAA2	0.424598057	2.391945883	2.494015074	1.47E-17	5.04E-17
IGFBP2	11.43934737	64.46948862	2.494611793	1.80E-38	3.61E-37
CLEC5A	0.44131274	2.519101324	2.513035852	2.50E-40	6.33E-39
CTHRC1	1.130127887	6.491754015	2.522122295	2.02E-25	1.20E-24
PHLDA2	0.400653991	2.307991356	2.526209069	1.49E-24	8.26E-24
STAC	0.355229592	2.051354973	2.529753488	3.48E-30	3.09E-29
DMRTA2	0.606283492	3.506011097	2.531766116	1.15E-24	6.44E-24
MMP7	0.449817731	2.613408203	2.538520048	1.56E-32	1.72E-31
HOXC10	0.491655229	2.868714239	2.544685371	5.70E-39	1.22E-37
LOXL1	0.612936684	3.620693428	2.562456068	1.55E-25	9.34E-25
PDPN	8.175723194	48.58994974	2.571239684	7.49E-51	8.93E-49
THBS1	1.261092852	7.616809361	2.594512285	9.07E-23	4.37E-22
PLAU	1.997655719	12.17010571	2.606961827	1.94E-49	1.73E-47
PCOLCE	2.561092781	15.65037593	2.611365888	1.55E-34	2.06E-33
LINC02587	0.96301978	5.885353306	2.61149169	2.15E-14	6.05E-14
HOXD13	0.3113508	1.9344346	2.635299062	5.29E-35	7.38E-34
HOXA10	0.308260698	1.927507125	2.644513326	3.05E-41	8.52E-40
COL4A1	6.667728561	41.89952259	2.651666526	3.10E-48	2.30E-46
TIMP1	29.10922398	183.1367597	2.653373118	1.82E-31	1.81E-30
LOX	0.930830154	5.872228113	2.65731816	5.32E-48	3.81E-46
CA9	0.994673142	6.298108934	2.662624284	1.25E-15	3.79E-15
TREM1	0.344637006	2.187307832	2.666006745	3.35E-40	8.41E-39
IGHG4	0.609776986	3.892650401	2.674399174	4.00E-10	8.48E-10
FABP5P7	0.515876976	3.303499215	2.678896037	5.47E-26	3.42E-25
CXCL8	2.416769347	15.57746443	2.688308726	1.23E-11	2.86E-11
FMOD	3.743681436	24.53589065	2.712364061	9.36E-27	6.15E-26
SHOX2	0.34548768	2.265036311	2.712828007	8.98E-38	1.67E-36
MARCO	0.443282022	2.931807938	2.725493839	6.79E-06	1.09E-05
RARRES1	0.593860539	3.928605391	2.725821186	3.85E-12	9.35E-12
COL8A1	0.43420426	2.88647604	2.732863464	2.12E-33	2.52E-32
ESM1	0.465546165	3.114982885	2.742228094	1.70E-26	1.09E-25
EN1	0.317274772	2.152383697	2.762130569	4.46E-29	3.55E-28
CHRNA9	0.307318824	2.105430012	2.776306877	2.95E-37	5.13E-36
COL6A2	5.863729846	40.66192069	2.793787821	1.98E-34	2.61E-33
AGAP2-AS1	1.690063077	11.74191838	2.796519136	1.93E-24	1.06E-23
TRDC	0.714648789	4.974509775	2.799248044	4.00E-24	2.14E-23
MFAP2	0.388540275	2.713208595	2.80386391	1.71E-45	8.29E-44
PTX3	1.740823903	12.21648755	2.810987368	1.95E-33	2.32E-32
IGF2BP2	0.415338048	2.940324908	2.823617639	5.84E-40	1.40E-38
HOXB2	0.41141609	2.943429567	2.838827985	6.69E-32	6.91E-31
HOXD10	0.272984877	1.963198357	2.846313009	1.60E-31	1.61E-30
CA3	1.815369735	13.52012795	2.896773489	9.41E-42	2.82E-40
MEOX2	1.187513406	8.893955899	2.904881451	2.20E-14	6.20E-14

STC1	0.332864965	2.608182081	2.970035656	3.06E-30	2.73E-29
ADAM12	0.31829294	2.558205966	3.00670536	3.32E-38	6.49E-37
F13A1	2.269837959	18.37291149	3.016919049	4.04E-23	1.99E-22
HOXA5	0.438181756	3.712075633	3.082624782	2.54E-41	7.15E-40
COL5A1	0.648456403	5.657639109	3.125118665	1.41E-37	2.53E-36
LUM	1.230202929	10.7815657	3.131598481	8.02E-30	6.84E-29
LIF	0.466028075	4.31454381	3.210719253	2.37E-34	3.09E-33
CYP27B1	0.259516545	2.499245315	3.267594095	4.89E-39	1.05E-37
FP671120.3	0.223064508	2.268485748	3.346196709	2.56E-15	7.64E-15
CCL18	0.610486114	6.344858068	3.377557507	0.012373452	0.015305228
COL1A2	3.726647246	38.86143303	3.382388933	7.52E-37	1.27E-35
MMP9	1.055823235	12.57017997	3.57356508	6.25E-28	4.48E-27
PI3	1.446542485	17.35767824	3.584893385	1.47E-16	4.73E-16
COL1A1	2.716547916	39.56090014	3.864228853	7.08E-38	1.33E-36
IBSP	0.516250663	7.582726531	3.87657306	3.60E-34	4.56E-33
COL3A1	3.613838569	54.11644447	3.904463088	3.19E-39	6.99E-38
COL6A3	0.260638621	4.037421848	3.953311555	7.19E-26	4.45E-25
AC004233.2	0.282598018	4.754016804	4.072323749	0.000216751	0.000309482
POSTN	1.394778644	25.79202691	4.208817069	8.37E-29	6.50E-28
H19	0.591257667	12.78413259	4.43442348	9.19E-23	4.42E-22
ELDR	0.044089327	4.602098164	6.705718484	8.19E-33	9.17E-32
14-Sep	0.017344799	4.367020829	7.976002497	9.82E-15	2.83E-14
TTR	0.081186	168.3690449	11.01810834	5.52E-08	1.02E-07

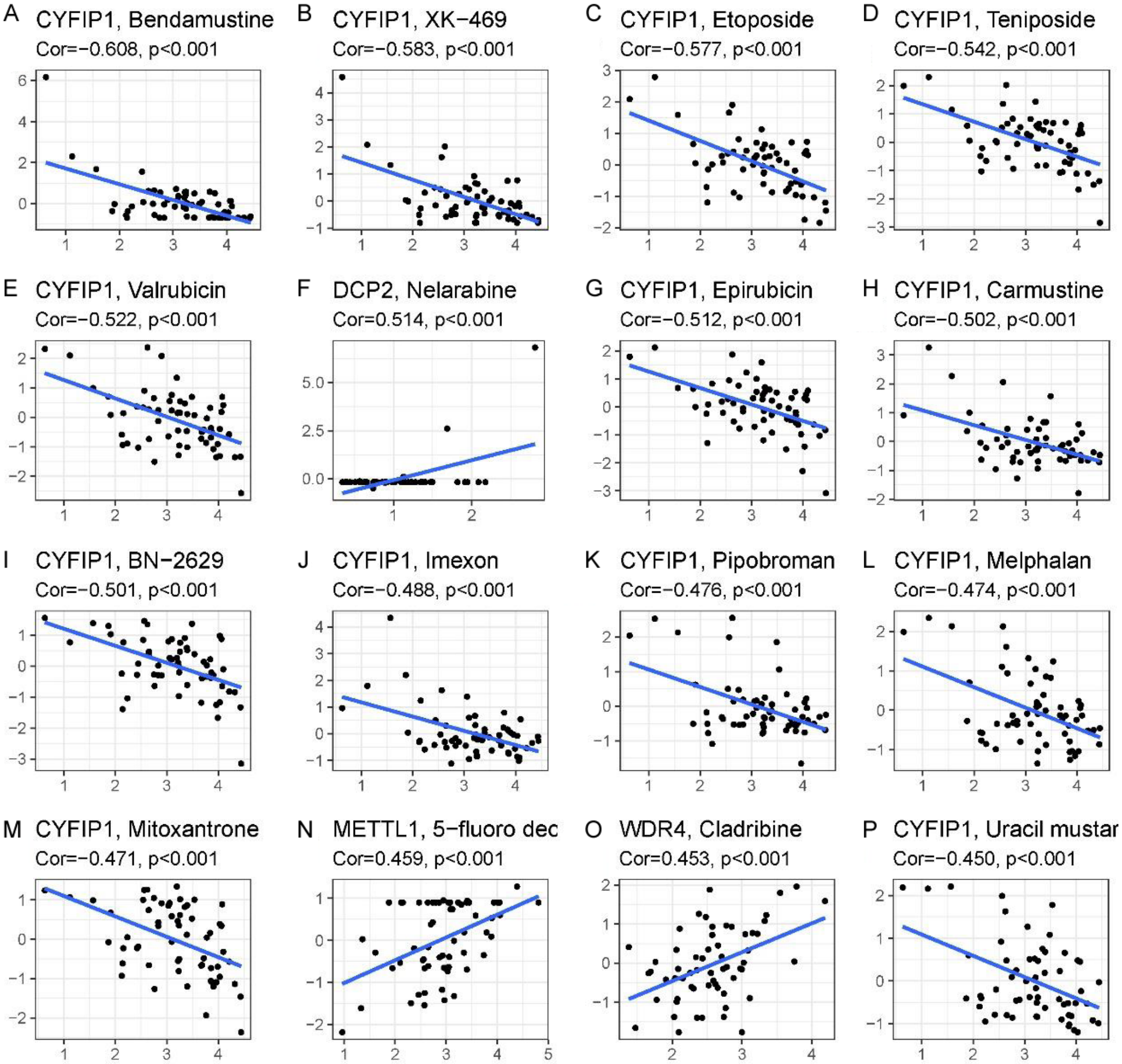


Figure S4. Drug sensitivity analysis for identified prognostic-related m7G regulators based on TCGA (Top 16). A. CYFIP1 and Bendamustine. B. CYFIP1 and XK-469. C. CYFIP1 and Etoposide. D. CYFIP1 and Teniposide. E. CYFIP1 and Valrubicin. F. DCP2 and Nelarabine. G. CYFIP1 and Epirubicin. H. CYFIP1 and Carmustine. I. CYFIP1 and BN-2629. J. CYFIP1 and Imexon. K. CYFIP1 and Pipobroman. L. CYFIP1 and Melphalan. M. CYFIP1 and Mitoxantrone. N. METTL1 and 5-fluorodec. O. WDR4 and Cladribine. P. CYFIP1 and Uracil mustar.

Table S5. Results of drug sensitivity based on 12 prognostic signature genes

Gene	Drug	cor	*p*value
CYFIP1	Bendamustine	-0.607939545	2.58E-07
CYFIP1	XK-469	-0.583256693	1.01E-06
CYFIP1	Etoposide	-0.577153942	1.38E-06
CYFIP1	Teniposide	-0.541733078	7.82E-06
CYFIP1	Valrubicin	-0.521741618	1.91E-05
DCP2	Nelarabine	0.513897826	2.67E-05
CYFIP1	Epirubicin	-0.511838979	2.92E-05
CYFIP1	Carmustine	-0.501584212	4.45E-05
CYFIP1	BN-2629	-0.501410132	4.49E-05
CYFIP1	Imexon	-0.487597636	7.77E-05
CYFIP1	Pipobroman	-0.475902404	0.000121469
CYFIP1	Melphalan	-0.473506135	0.000132857
CYFIP1	Mitoxantrone	-0.471319564	0.000144096
METTL1	5-fluoro deoxy uridine 10mer	0.459123642	0.000224417
WDR4	Cladribine	0.453216544	0.000276494
CYFIP1	Uracil mustard	-0.450046931	0.000308776
CYFIP1	Thiotepa	-0.443448619	0.000387254
CYFIP1	Hydroxyurea	-0.442886497	0.000394715
DCP2	Curcumin	0.439991984	0.000435243
WDR4	Thiotepa	0.437454341	0.000473847
CYFIP1	Daunorubicin	-0.437374122	0.000475116
CYFIP1	Chlorambucil	-0.437216405	0.000477621
WDR4	Hydroxyurea	0.435662391	0.000502952
IFIT5	Panobinostat	-0.435536042	0.000505064
WDR4	Chlorambucil	0.432509668	0.000558125
LSM1	Fenretinide	0.42982998	0.000609274
LSM1	Chelerythrine	0.427428906	0.000658673
CYFIP1	Asparaginase	-0.427165102	0.000664316
CYFIP1	Triethylenemelamine	-0.426078411	0.000688024
DCP2	Chelerythrine	0.424907898	0.000714416
WDR4	Triethylenemelamine	0.424626393	0.000720898
WDR4	Asparaginase	0.419123751	0.000858771
WDR4	Uracil mustard	0.418691592	0.000870548
CYFIP1	LMP-400	-0.418539795	0.000874719
DCP2	Fenretinide	0.414459655	0.00099381
WDR4	Vorinostat	0.412388548	0.001059689
WDR4	Raltitrexed	0.409530812	0.001157047
CYFIP1	kahalide f	0.409097959	0.001172476
NCBP1	Chelerythrine	0.406680746	0.001262087
WDR4	Cytarabine	0.401076315	0.001493974
METTL1	Hydroxyurea	0.401025664	0.001496234
WDR4	Acrichine	0.399199177	0.001579785
DCP2	Raloxifene	0.395843689	0.001744246
WDR4	Fludarabine	0.395355614	0.001769404
METTL1	Cladribine	0.395138894	0.001780678
DCP2	Fulvestrant	0.394723573	0.001802464
LSM1	Nelarabine	0.393294559	0.001879259

CYFIP1	Doxorubicin	-0.3914715	0.00198147
WDR4	kahalide f	-0.390633728	0.002030085
EIF4E1B	Fulvestrant	0.388176782	0.002178862
WDR4	Cyclophosphamide	0.381743754	0.002615523
CYFIP1	Oxaliplatin	-0.381504446	0.002633172
EIF4A1	Cladribine	0.380169184	0.00273361
WDR4	Cisplatin	0.378443766	0.002868434
CYFIP1	Batracylin	-0.378085905	0.002897127
CYFIP1	Lomustine	-0.374415682	0.00320645
WDR4	Gemcitabine	0.373812459	0.003260001
CYFIP1	Idarubicin	-0.373280546	0.003307878
CYFIP1	Paclitaxel	-0.372053559	0.003420704
WDR4	Chelerythrine	0.371926017	0.003432625
CYFIP1	Entinostat	-0.370032895	0.003613957
CYFIP1	Ifosfamide	-0.369078928	0.003708507
WDR4	Pipobroman	0.367537437	0.00386592
CYFIP1	Irinotecan	-0.366102158	0.004017771
CYFIP1	Imatinib	-0.366070834	0.004021143
NCBP1	Nelarabine	0.365412511	0.004092592
CYFIP1	Cyclophosphamide	-0.364973165	0.004140897
DCP2	Arsenic trioxide	0.364845754	0.004155
METTL1	8-Chloro-adenosine	0.364639917	0.004177872
GEMIN5	Allopurinol	0.364313836	0.004214334
METTL1	Chlorambucil	0.363143813	0.004347489
WDR4	Irinotecan	0.362935986	0.004371525
CYFIP1	Raltitrexed	-0.362561176	0.00441517
CYFIP1	Eribulin mesilate	-0.360389354	0.004675723
DCP2	SR16157	0.360033966	0.004719625
WDR4	LMP-400	0.358668756	0.00489167
CYFIP1	Fenretinide	-0.358509073	0.00491215
NCBP1	PX-316	0.358322083	0.004936228
CYFIP1	Carboplatin	-0.357378044	0.005059383
EIF4G3	AFP464	-0.355365721	0.005330963
METTL1	Vorinostat	0.352398976	0.005754725
EIF4A1	Cytarabine	0.351102218	0.005949054
EIF4A1	AP-26113	-0.351043121	0.005958045
METTL1	Parthenolide	0.349974968	0.006122635
METTL1	Gemcitabine	0.348595428	0.006341096
METTL1	Uracil mustard	0.348274237	0.006392929
EIF4A1	Gemcitabine	0.347280924	0.006555584
WDR4	Clofarabine	0.346891852	0.006620275
WDR4	Melphalan	0.346051348	0.006761937
CYFIP1	7-Hydroxystaurosporine	-0.345012875	0.006940624
WDR4	6-Mercaptopurine	0.343773017	0.00715936
WDR4	Imexon	0.343616171	0.007187456
CYFIP1	Irofulven	0.342446684	0.0074
METTL1	Triethylenemelamine	0.342032361	0.007476606
EIF4G3	Entinostat	-0.340974992	0.007675253
CYFIP1	Nelfinavir	-0.340805692	0.007707483

EIF4A1	Clofarabine	0.340449793	0.007775623
CYFIP1	Estramustine	-0.339730324	0.007914977
LSM1	Hydroxyurea	0.338498833	0.008158564
CYFIP1	Elliptinium Acetate	-0.337414017	0.008378525
NCBP1	Fenretinide	0.336080094	0.008656061
WDR4	Ifosfamide	0.334360946	0.009025526
WDR4	Dimethylaminoparthenolide	0.334335188	0.009031164
DCP2	tfdu	0.331670951	0.00963115
WDR4	Pemetrexed	0.330537909	0.009896616
WDR4	Nelarabine	0.329243393	0.010207662
EIF4A1	5-fluoro deoxy uridine 10 mer	0.328942481	0.010281167
CYFIP1	Nitrogen mustard	-0.328809781	0.010313728
METTL1	tfdu	0.328738752	0.010331193
CYFIP1	Docetaxel	-0.328616157	0.010361398
CYFIP1	Vinorelbine	-0.328195129	0.010465714
IFIT5	Tamoxifen	-0.327727786	0.01058257
CYFIP1	Arsenic trioxide	-0.327630944	0.010606925
CYFIP1	Vinblastine	-0.326534892	0.01088598
WDR4	Imatinib	0.326092092	0.011000506
DCP2	Dimethylaminoparthenolide	0.324320473	0.01146921
EIF4A1	Nelarabine	0.323953805	0.011568343
WDR4	3-Bromopyruvate (acid)	0.322442581	0.011984775
METTL1	Fludarabine	0.321800029	0.01216572
DCP2	Cyclophosphamide	0.321259764	0.012319679
CYFIP1	LDK-378	-0.32047396	0.012546609
METTL1	Melphalan	0.319123948	0.012944892
NCBP1	AT-13387	0.317631133	0.013397941
METTL1	Thiotepa	0.317405844	0.013467484
METTL1	Cytarabine	0.317345019	0.013486313
WDR4	Digoxin	0.316110351	0.013873441
LSM1	Cobimetinib (isomer 1)	-0.315529746	0.014058767
EIF4A1	tfdu	0.31523616	0.014153286
DCP2	Staurosporine	-0.314234706	0.014479817
EIF4G3	Palbociclib	-0.31344264	0.014742637
EIF4E1B	Entinostat	0.312800354	0.014958754
CYFIP1	Actinomycin D	-0.311186604	0.015513777
METTL1	Paclitaxel	-0.31044972	0.015773027
CYFIP1	Carfilzomib	-0.310211803	0.01585752
METTL1	Vinorelbine	-0.309356999	0.016164296
CYFIP1	Crizotinib	-0.309209765	0.016217645
WDR4	Triapine	0.309152029	0.016238607
WDR4	Dacarbazine	0.308367936	0.01652558
DCP2	8-Chloro-adenosine	0.308315181	0.016545043
LSM1	Ifosfamide	0.307285626	0.016928817
EIF4A1	Alectinib	-0.306581306	0.017195718
CYFIP1	Ixabepilone	-0.30602036	0.017410851
CYFIP1	Pipamperone	-0.305089874	0.017772778
CYFIP1	Dromostanolone Propionate	-0.304990812	0.017811685
METTL1	okadaic acid	-0.304921308	0.017839026

WDR4	8-Chloro-adenosine	0.304792138	0.017889934
CYFIP1	Cytarabine	-0.304725507	0.017916242
WDR4	tfdu	0.304619125	0.017958315
CYFIP1	Denileukin Diftitox Ontak	-0.303351411	0.018466197
WDR4	Carboplatin	0.300886351	0.019488873
WDR4	Carmustine	0.300529608	0.019640792
METTL1	Digoxin	0.299936154	0.019895746
EIF4A1	Methotrexate	0.299358122	0.020146774
NCBP1	8-Chloro-adenosine	0.29784917	0.020814798
LSM1	Asparaginase	0.295678725	0.021808579
DCP2	Pemetrexed	0.294116616	0.022548452
CYFIP1	Cisplatin	-0.293628744	0.022783836
EIF4G3	Aminoflavone	-0.293476812	0.022857562
CYFIP1	Dimethylaminoparthenolide	-0.292994259	0.023093063
NCBP1	Allopurinol	0.292757088	0.02320956
WDR4	Methotrexate	0.29246811	0.023352176
CYFIP1	Trametinib	0.292024865	0.023572364
WDR4	Mithramycin	-0.291769087	0.023700222
METTL1	kahalide f	-0.291269567	0.023951611
CYFIP1	Afatinib	0.29126533	0.023953753
LSM1	Trametinib	-0.290904639	0.024136685
GEMIN5	kahalide f	-0.290825888	0.024176782
NUDT11	Ethinyl estradiol	0.290449369	0.024369267
METTL1	Raltitrexed	0.29023497	0.02447945
EIF4G3	Elesclomol	-0.28995106	0.024626003
GEMIN5	Cladribine	0.289780633	0.024714331
CYFIP1	Depsipeptide	-0.289727802	0.024741766
WDR4	LMP776	0.289645879	0.02478436
WDR4	Topotecan	0.289535868	0.024841654
CYFIP1	Dexrazoxane	-0.288982994	0.025131288
EIF4G3	Lificguat	-0.287988086	0.025659662
DCP2	AFP464	0.287627949	0.025853215
EIF4A1	Pemetrexed	0.287611533	0.025862067
NUDT11	Hydrastinine HCl	0.28616807	0.026650456
EIF4E1B	AFP464	0.286145241	0.026663086
EIF4A1	Floxuridine	0.286051038	0.026715253
WDR4	Pelitrexol	0.285162337	0.027211634
WDR4	Nilotinib	0.284960329	0.02732554
CYFIP1	LMP776	-0.28487479	0.027373893
METTL1	LMP-400	0.284845605	0.027390407
METTL1	Nitrogen mustard	0.284783949	0.027425322
WDR4	Allopurinol	0.28459482	0.027532656
DCP2	Lomustine	0.284488887	0.02759293
DCP2	Pyrazoloacridine	0.282682306	0.028638008
DCP2	Ifosfamide	0.282525228	0.028730423
EIF4A1	Fludarabine	0.282476094	0.028759382
METTL1	Karenitecin	0.281571398	0.029296983
METTL1	Allopurinol	0.281298776	0.029460626
WDR4	Lomustine	0.281064993	0.029601565

METTL1	RH1	0.280716134	0.029812927
CYFIP1	Homoharringtonine	-0.280550006	0.029914022
WDR4	7-Ethyl-10-hydroxycamptothecin	0.280147616	0.030160082
WDR4	Karenitecin	0.279782971	0.030384521
LSM1	Batracylin	0.278130749	0.031419047
METTL1	7-Ethyl-10-hydroxycamptothecin	0.277394592	0.031889372
CYFIP1	Triapine	-0.277314049	0.031941185
METTL1	Triapine	0.277269532	0.031969853
DCP2	Oxaliplatin	0.276884331	0.032218811
IFIT5	geldanamycin analog	-0.276620506	0.032390255
LSM1	Selumetinib	-0.275903038	0.032860346
DCP2	XK-469	0.27575175	0.032960194
DCP2	Erlotinib	-0.275700446	0.032994112
METTL1	Pemetrexed	0.275622523	0.033045683
METTL1	Bleomycin	0.275006275	0.033455898
METTL1	Fenretinide	0.274575115	0.033745422
METTL1	XL-147	0.274306178	0.033927068
LSM1	Tanespimycin	-0.274279484	0.033945141
LSM1	Uracil mustard	0.274060436	0.034093758
METTL1	Nelarabine	0.273240216	0.034655067
EIF4A1	Celecoxib	-0.273216545	0.034671379
NUDT11	Nelfinavir	0.272667017	0.035051875
GEMIN5	8-Chloro-adenosine	0.272496388	0.035170723
LSM1	Chlorambucil	0.272290084	0.035314866
CYFIP1	Pemetrexed	-0.271375071	0.035960113
CYFIP1	Topotecan	-0.271253718	0.036046419
METTL1	Irinotecan	0.271204004	0.036081825
NCBP1	Elliptinium Acetate	-0.271149629	0.036120584
IFIT5	Tanespimycin	-0.270667674	0.036465636
WDR4	Depsipeptide	-0.270039764	0.036919284
EIF4A1	AT-13387	0.269945855	0.036987531
NCBP1	Dimethylaminoparthenolide	0.269234989	0.037507544
LSM1	kahalide f	-0.268723775	0.037885241
CYFIP1	tfdu	-0.268666125	0.037928031
EIF4E1B	SR16157	0.268457791	0.038082999
DCP2	PX-316	0.267958722	0.038456361
DCP2	Daunorubicin	0.267921289	0.038484486
METTL1	Cisplatin	0.267510034	0.038794613
IFIT5	AFP464	-0.266590668	0.039495387
DCP2	Cordycepin	0.266509009	0.039558133
LSM1	Fludarabine	0.265067849	0.040679137
NCBP1	6-Mercaptopurine	0.263952442	0.041564643
METTL1	Carboplatin	0.263632142	0.041821843
WDR4	Curcumin	0.263591714	0.041854399
DCP2	Vorinostat	0.262881271	0.042429932
GEMIN5	Fenretinide	0.261894505	0.043240116
METTL1	Dolastatin 10	-0.261859879	0.043268776
CYFIP1	Isotretinoin	-0.261798117	0.043319934
WDR4	LY-294002	-0.26165393	0.043439558

IFIT5	Tyrothricin	-0.261074535	0.043922998
CYFIP1	Chelerythrine	-0.26082803	0.044130014
WDR4	Fostamatinib	0.260079885	0.04476323
WDR4	RH1	0.259751127	0.045043835
LSM1	Imexon	0.259552973	0.045213662
NCBP1	Amonafide	0.259070568	0.045629303
DCP2	Cytarabine	0.259059473	0.045638899
METTL1	Depsipeptide	-0.258733269	0.045921779
EIF4E1B	Sunitinib	-0.257787651	0.046749942
EIF4G3	Denileukin Diftitox Ontak	-0.257780519	0.046756234
NCBP1	LY-294002	-0.257317935	0.047165842
CYFIP1	Dolastatin 10	-0.256832307	0.047599012
LSM1	XK-469	0.256595735	0.047811206
LSM1	LMP-400	0.255892156	0.048446862
CYFIP1	6-Mercaptopurine	-0.255574912	0.048735732
DCP2	Chlorambucil	0.254835838	0.049414169
GEMIN5	Pemetrexed	0.254555974	0.049673076

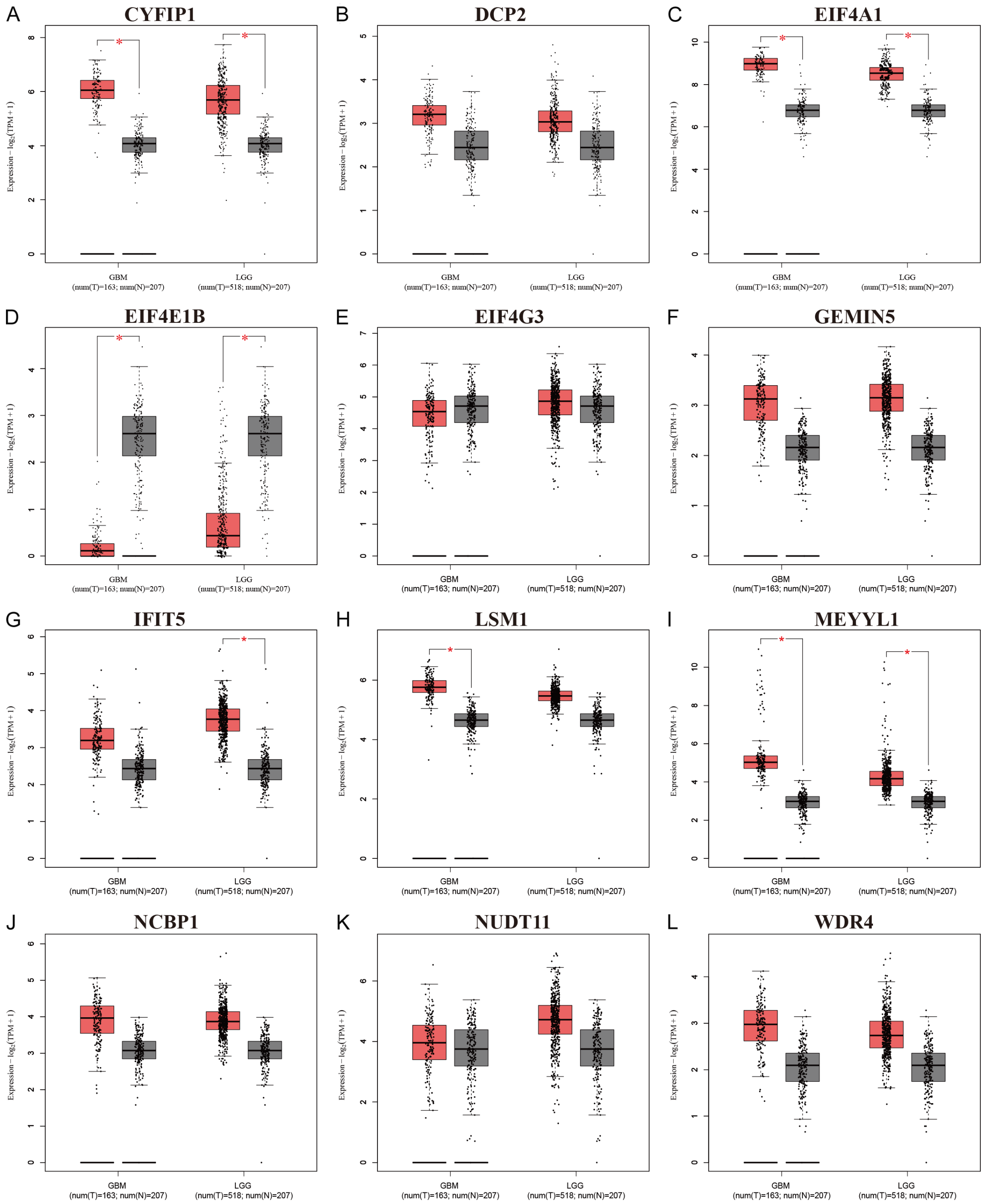


Figure S5. Expression levels of 12 prognostic signature genes between glioma and normal tissue samples (GTEx data). A-L: CYFIP1, DCP2, EIF4A1, EIF4E1B, EIF4G3, GEMIN5, IFIT5, LSM1, METTL1, NCBP1, NUDT11, and WDR4.

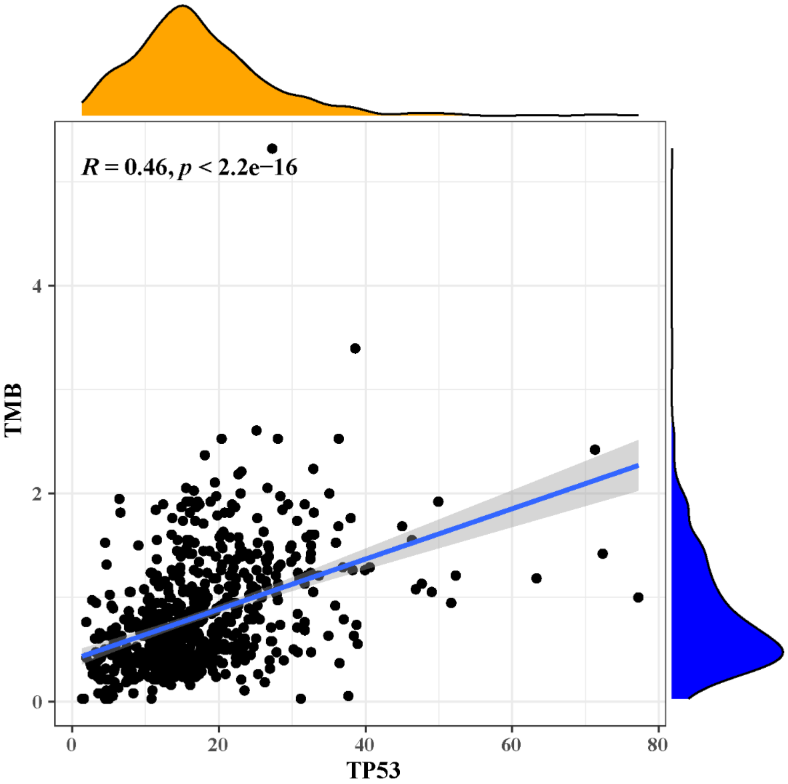


Figure S6. Correlation of TP53 expression with tumor mutation burden.