

Figure S1. (A) Kaplan-Meier curve showed the prognosis of high- and low-risk patients. (B) Calibration curves showed the prediction accuracy of the predictive risk model.

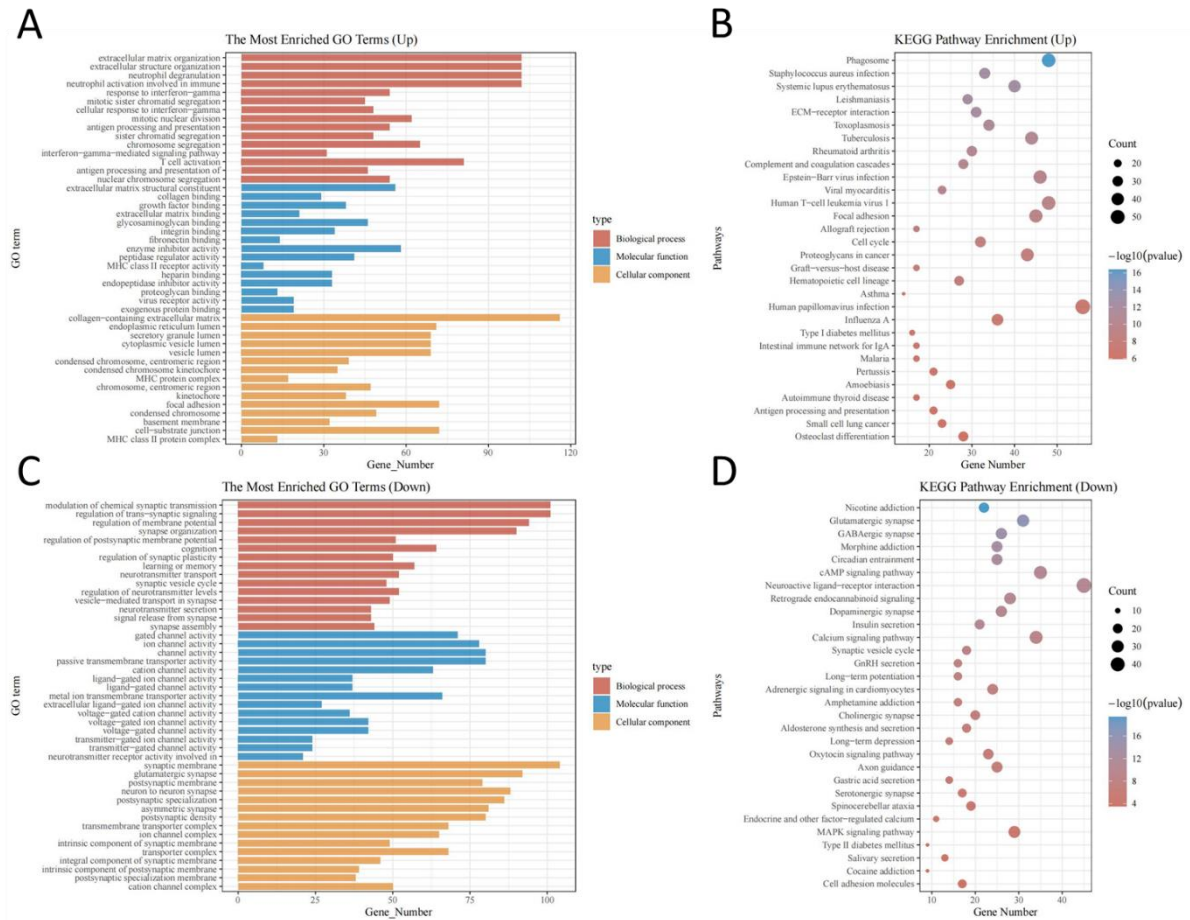


Figure S2. GO and KEGG analysis of DEGs in the group (Tumor vs Normal). (A-B) GO and KEGG analysis of 5,961 upregulated DEGs. (C-D) GO and KEGG analysis of 920 downregulated

DEGs.

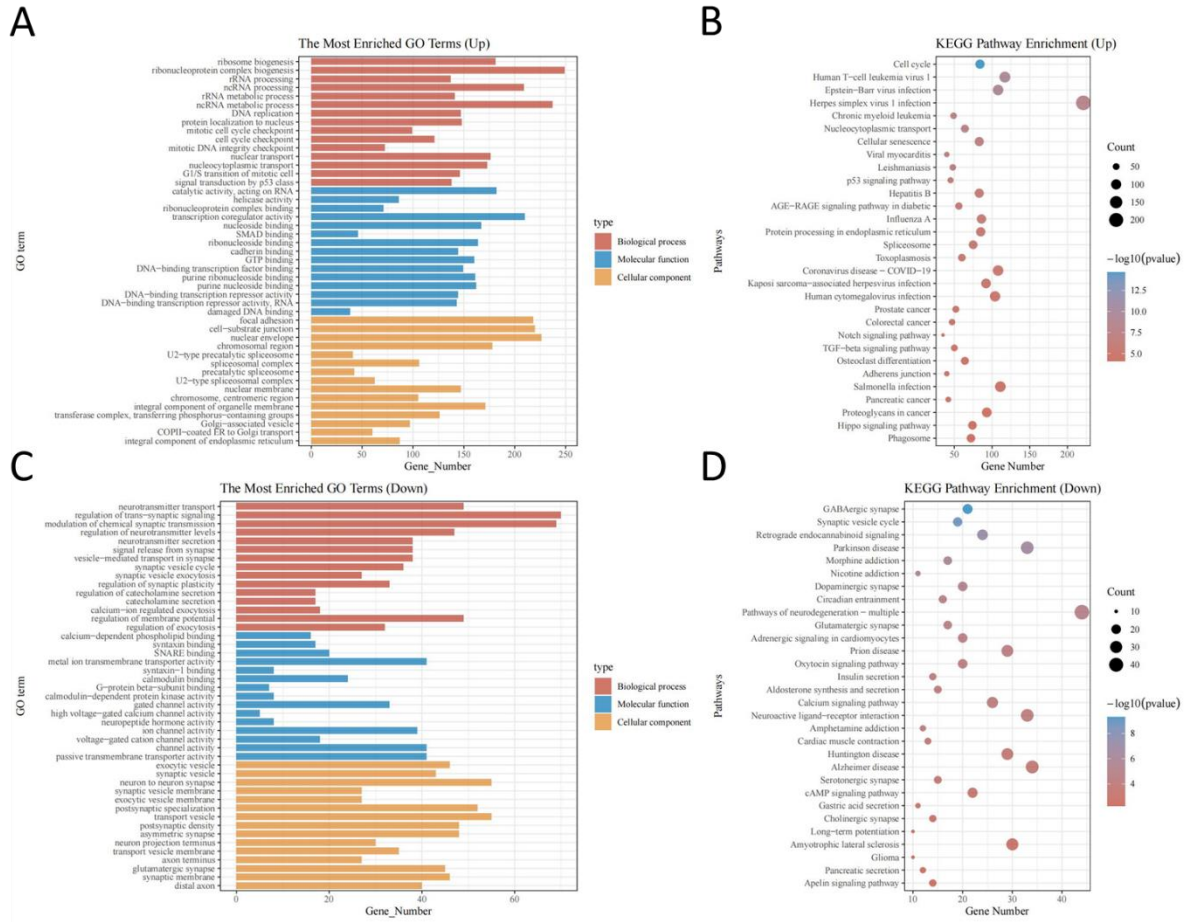
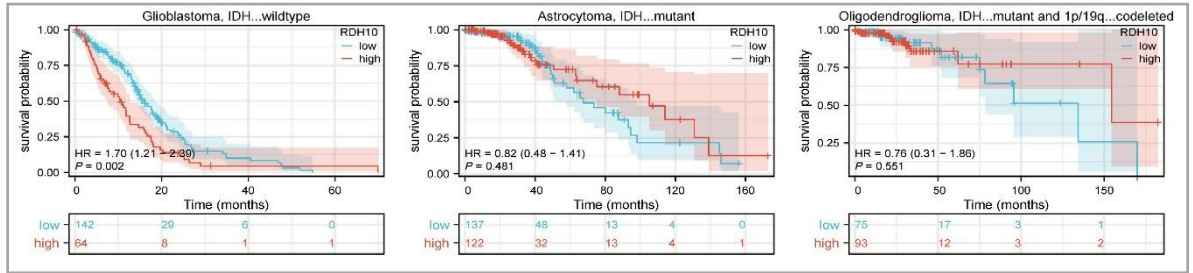
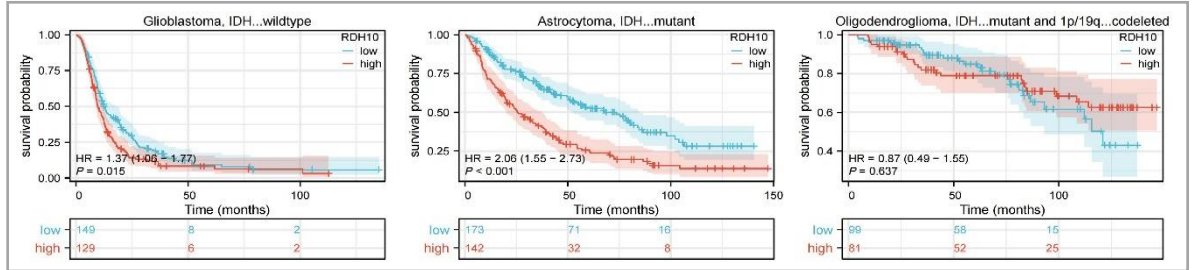


Figure S3. GO and KEGG analysis of DEGs in the group (GBM vs LGG). (A-B) GO and KEGG analysis of 1,349 upregulated DEGs. (C-D) GO and KEGG analysis of 905 downregulated DEGs. GBM: glioblastoma multiforme. LGG: low-grade glioma.

TCGA



CGGA



Gravendeel

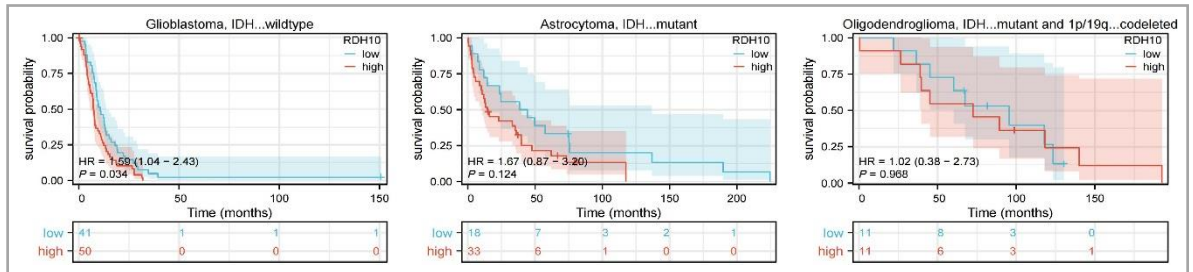
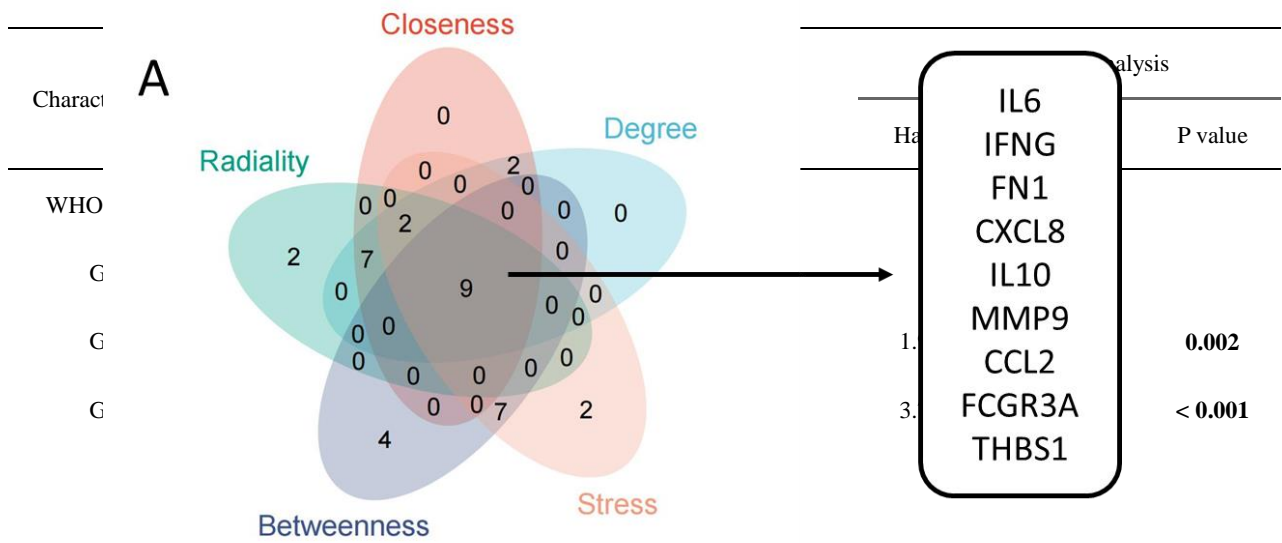


Figure S4. Survival analysis of RDH10 in different glioma subtypes in TCGA, CGGA and Gravendeel cohorts.



B

Gene name	Degree	Closeness	Radiality	Betweenness	Stress
IL6	177	385.6929	8.68296	36265.43	563116
IFNG	156	370.7929	8.60872	26989.09	404730
FN1	136	365.3095	8.62765	35568.08	459630
CXCL8	134	356.4262	8.53739	19670.32	297844
IL10	130	355.0429	8.52721	11001.38	235448
MMP9	126	352.1929	8.52138	12705.56	244502
CCL2	121	346.1762	8.4748	10147.26	199106
FCGR3A	94	326.0929	8.37436	9750.798	171016
THBS1	74	320.3929	8.38164	10659.18	187860

Figure S5. Identification of hub genes for the functions of RDH10. (A) The Venn diagram showed the overlapping genes of the top 20 genes using 5 different algorithms: Degree, Closeness, Radiality, Betweenness, and Stress. (B) The scores of Degree, Closeness, Radiality, Betweenness, and Stress in the 9 hub genes.

Age	698	1.066 (1.057 - 1.076)	< 0.001	1.035 (1.023 - 1.047)	< 0.001
IDH status	688				
WT	246	Reference		Reference	
Mut	442	0.116 (0.089 - 0.151)	< 0.001	0.388 (0.249 - 0.604)	< 0.001
1p/19q codeletion	691				
Non-codel	520	Reference		Reference	
Codel	171	0.225 (0.147 - 0.346)	< 0.001	0.518 (0.310 - 0.864)	0.012
RDH10	698	1.535 (1.437 - 1.640)	< 0.001	1.022 (0.910 - 1.149)	0.710

Table S1. Univariate and multivariate Cox analysis of RDH10 and clinical features in TCGA glioma cohort.