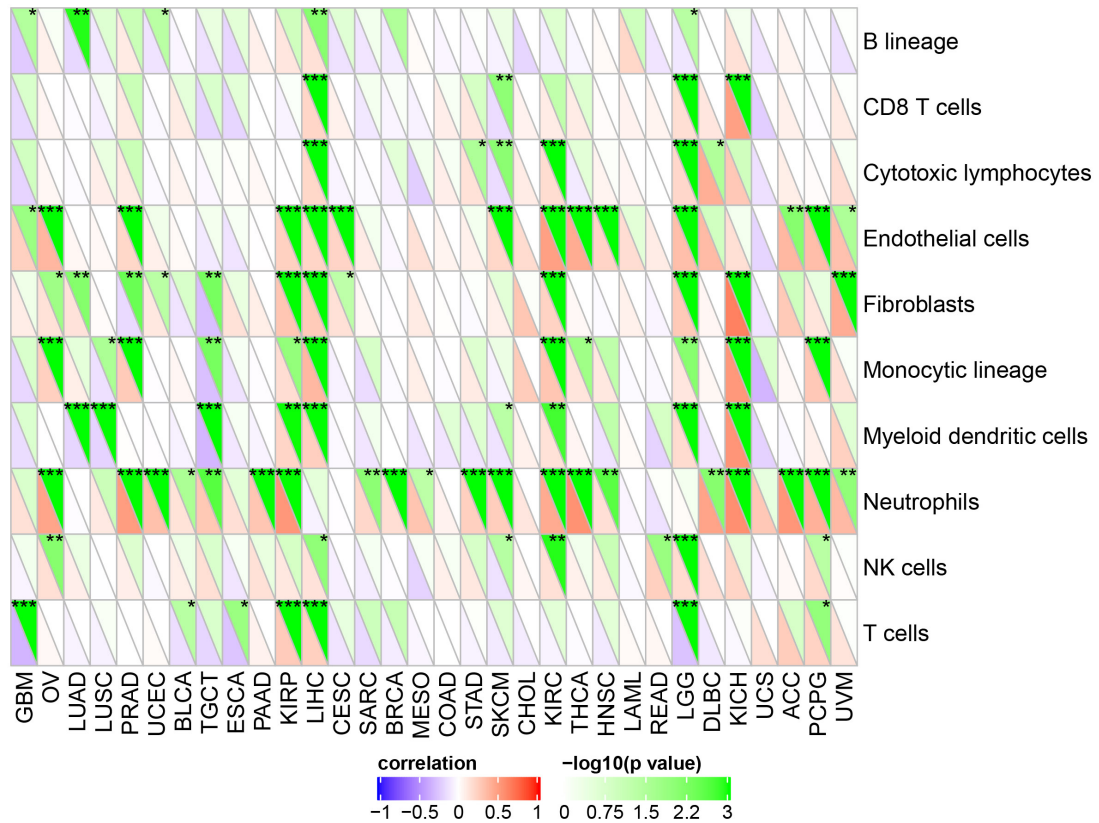
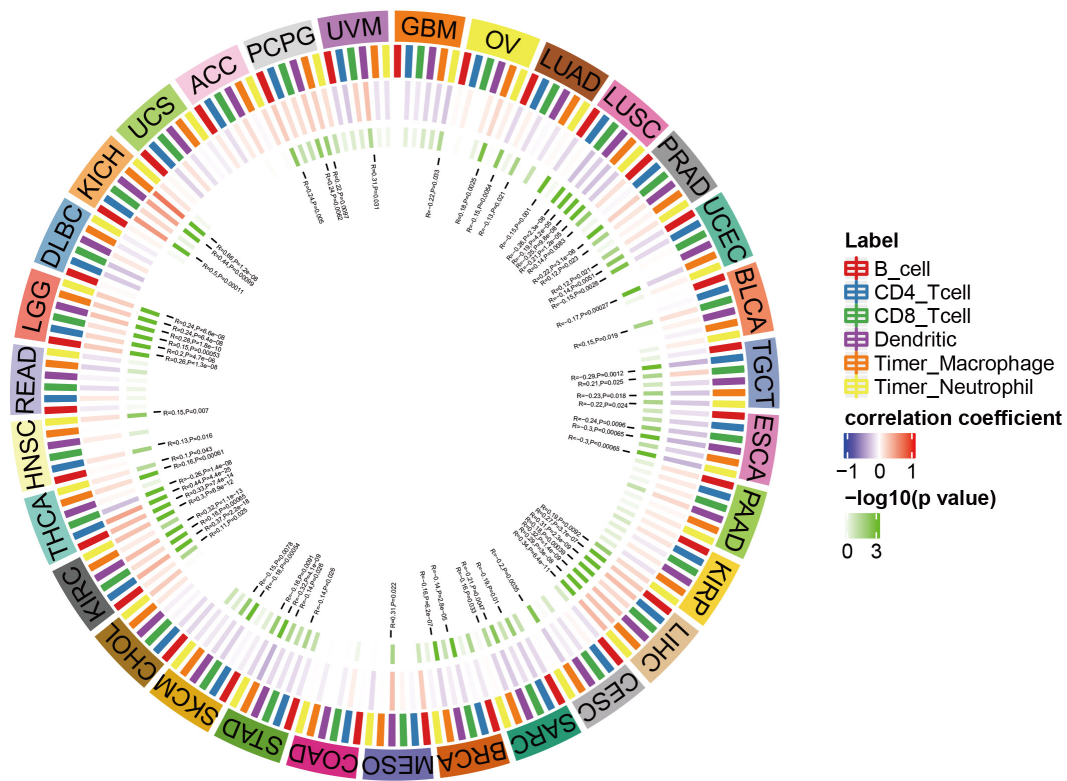


**Figure S1.** The Pearson correlation between the immune scores of 33 cancers in the TCGA database obtained by the ESTIMATE algorithm and the PTBP1 expression.

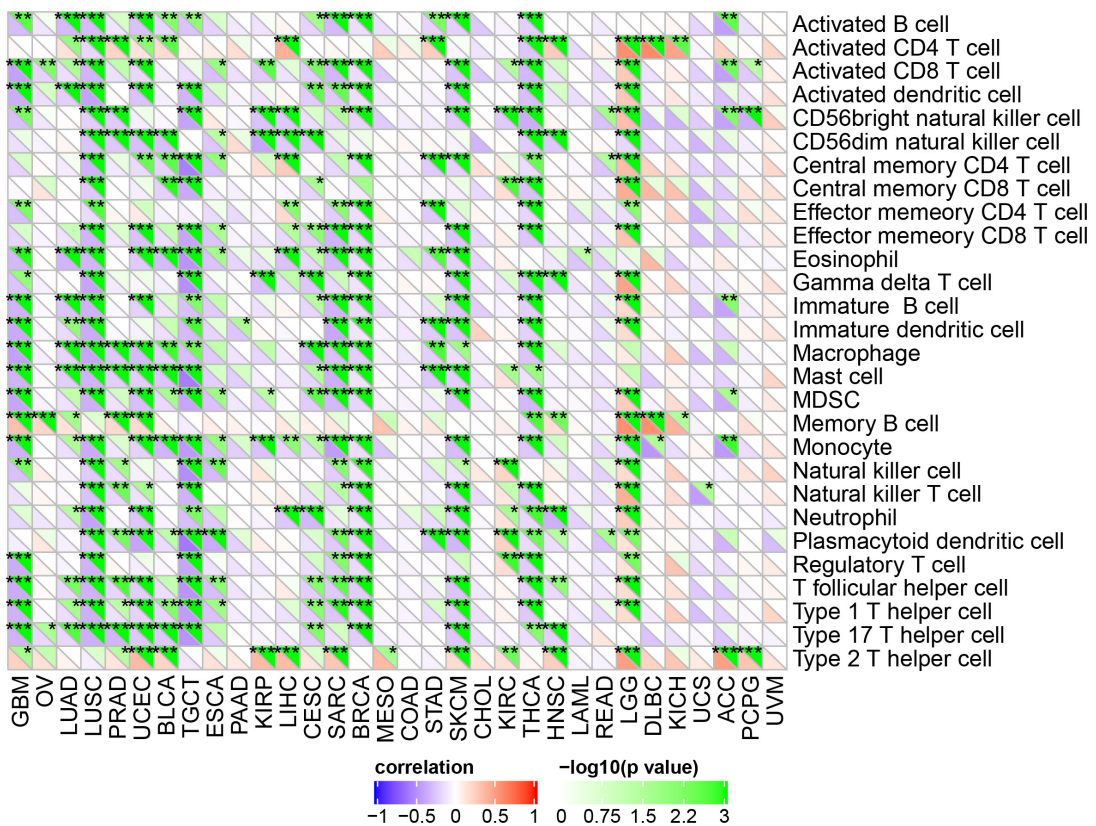


**Figure S2.** The Pearson correlation between the immune scores of 33 cancers in the

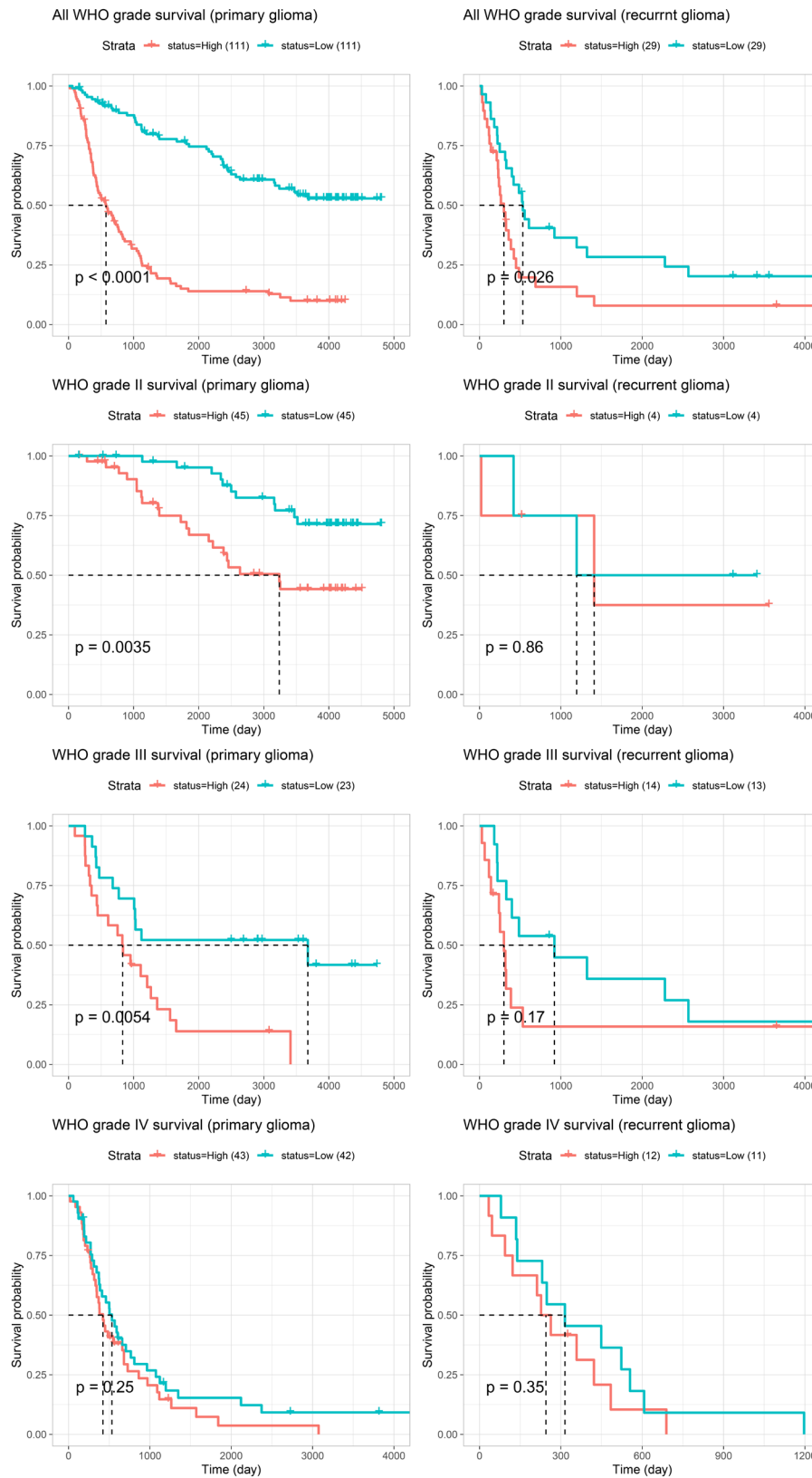
TCGA database obtained by the MCPcounter algorithm and the PTBP1 expression.



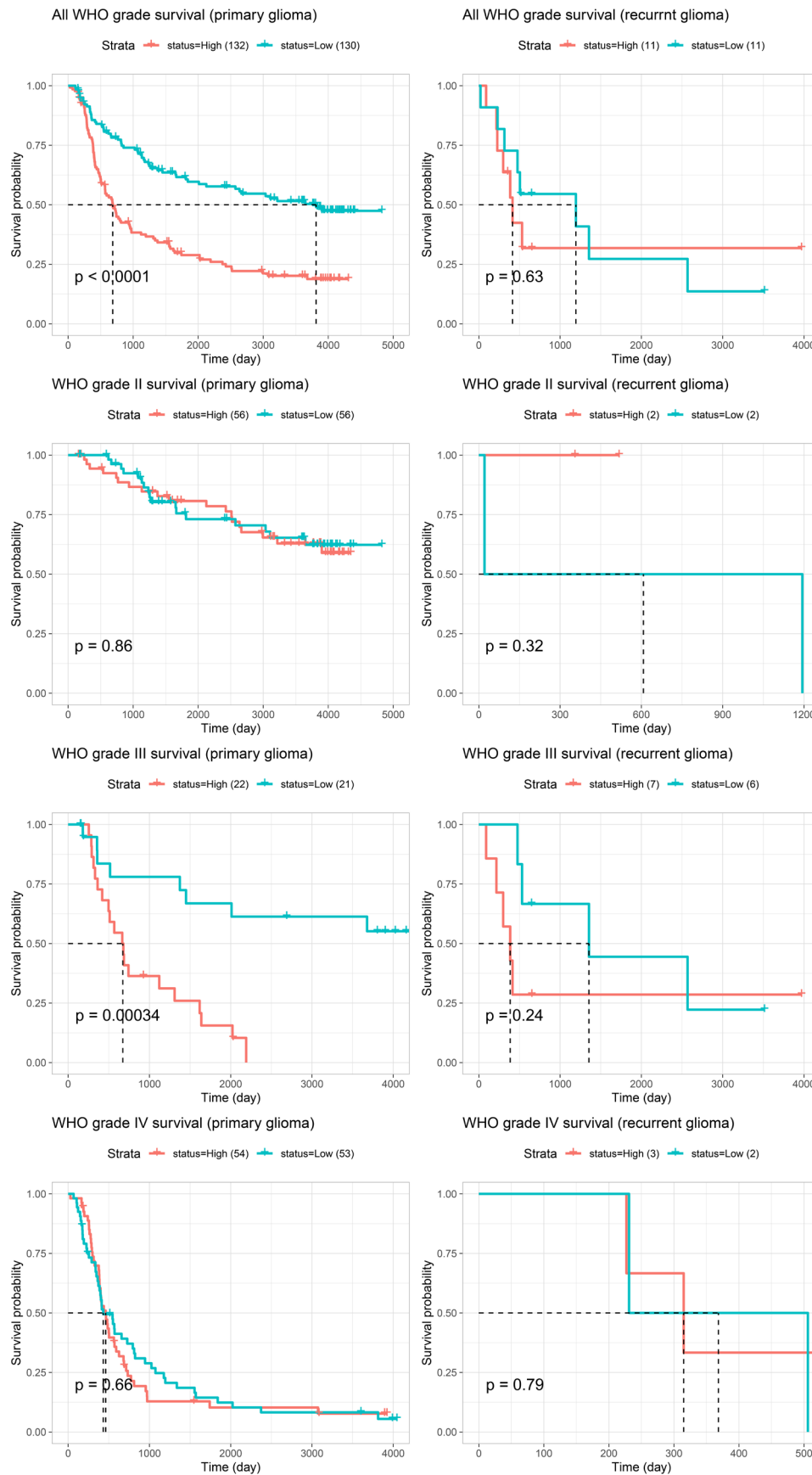
**Figure S3.** The Pearson correlation between the immune scores of 33 cancers in the TCGA database obtained by the TIMER database and the PTBP1 expression.



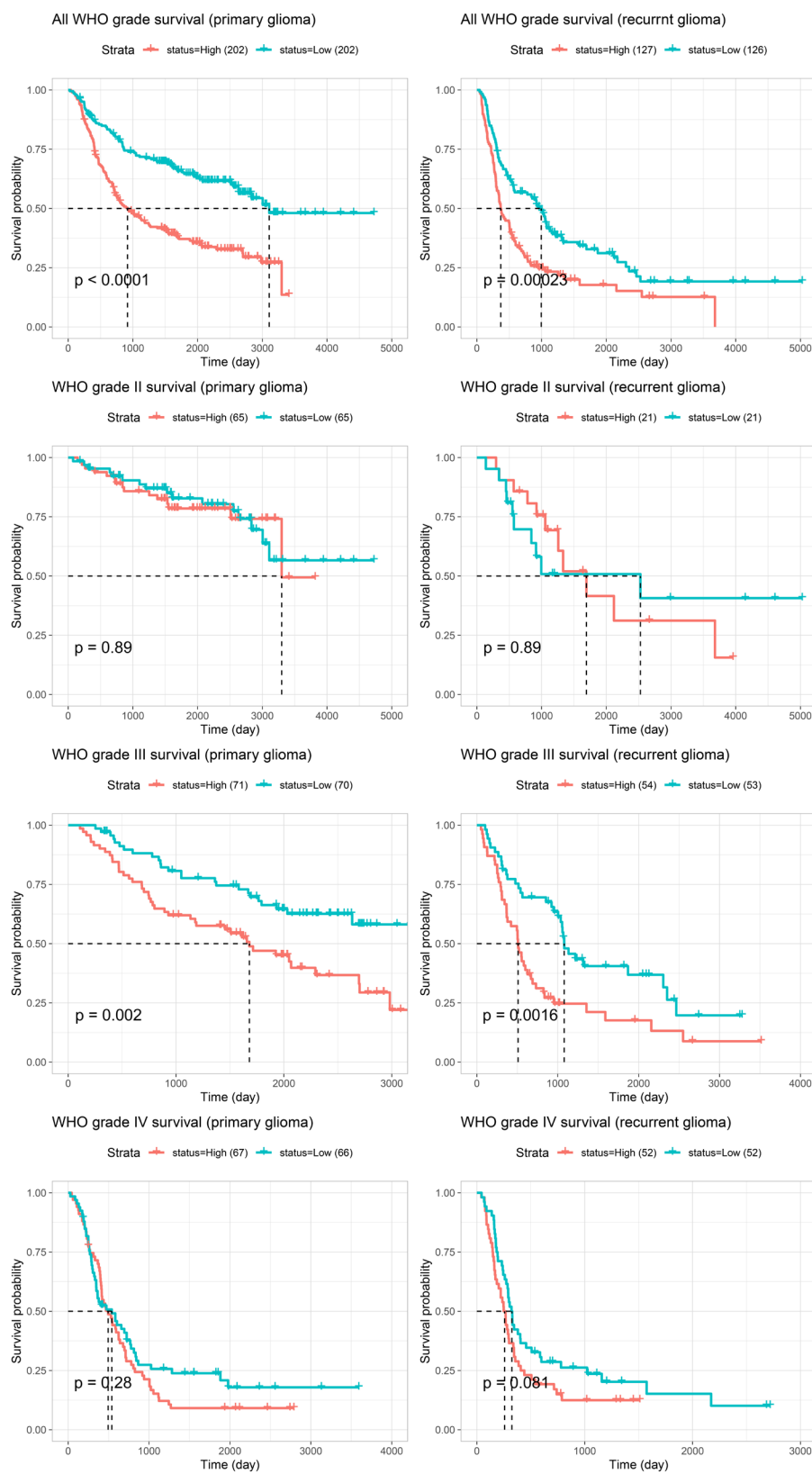
**Figure S4.** The Pearson correlation between the immune scores of 33 cancers in the TCGA database obtained by the CIBERSORT algorithm and the the PTBP1 expression.



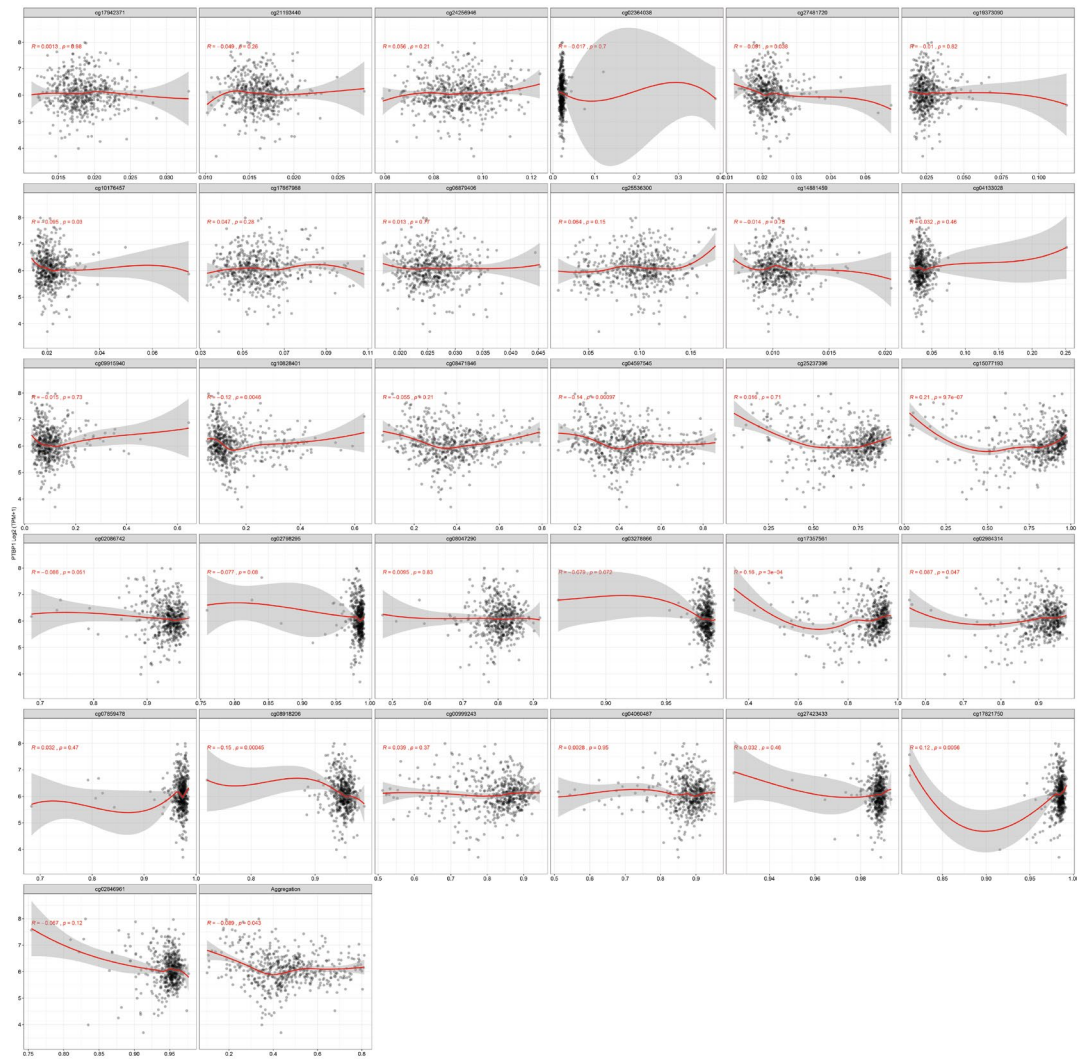
**Figure S5.** Relationship between PTBP1 expression and prognosis for the mRNA\_325 dataset in the CGGA database.



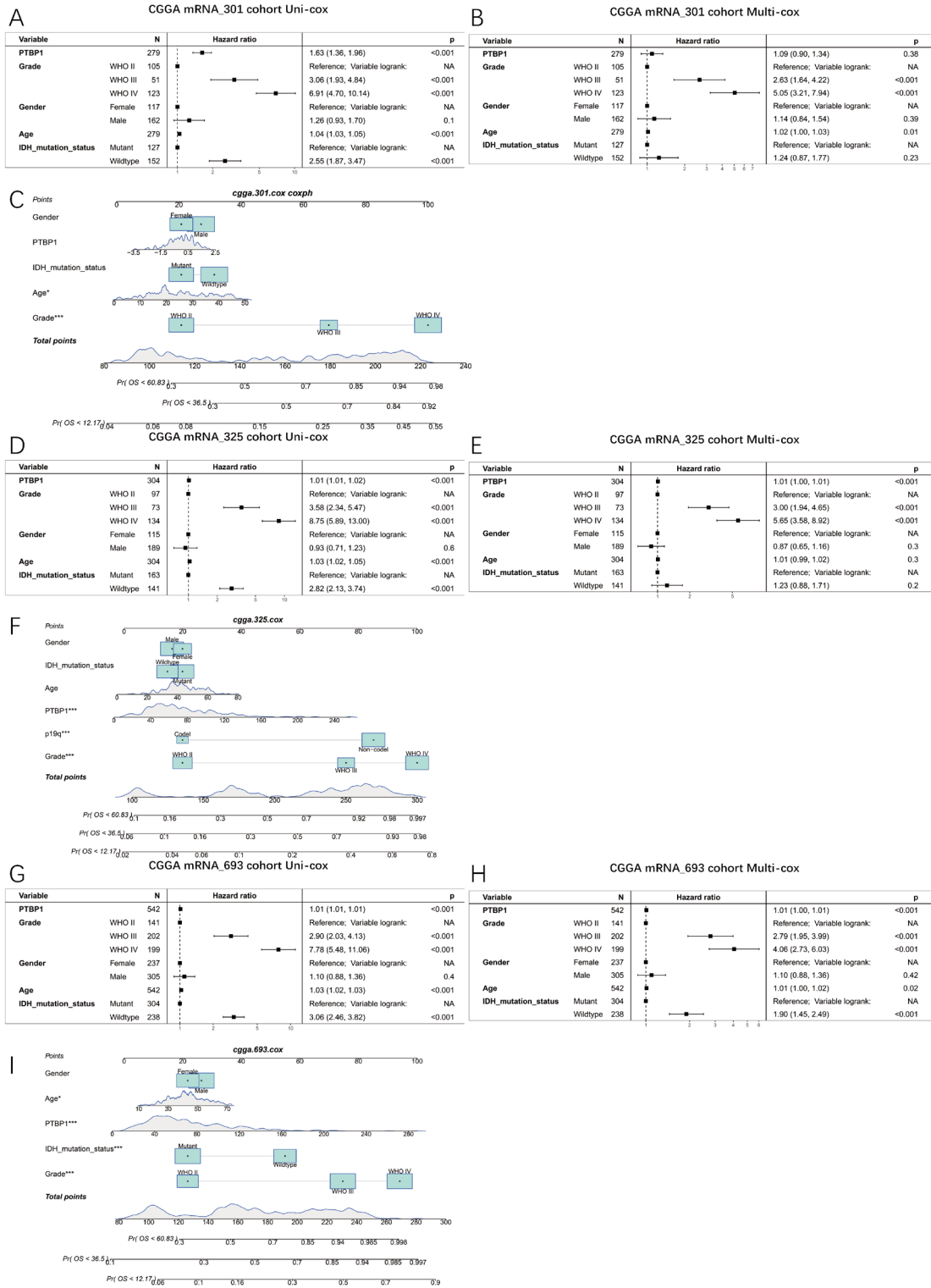
**Figure S6.** Relationship between PTBP1 expression and prognosis for the mRNA\_301 dataset.



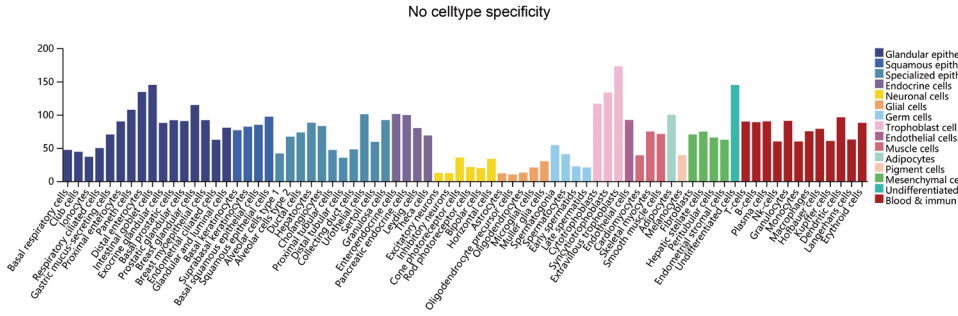
**Figure S7.** Relationship between PTBP1 expression and prognosis in the mRNA\_693 dataset in the CGGA database.



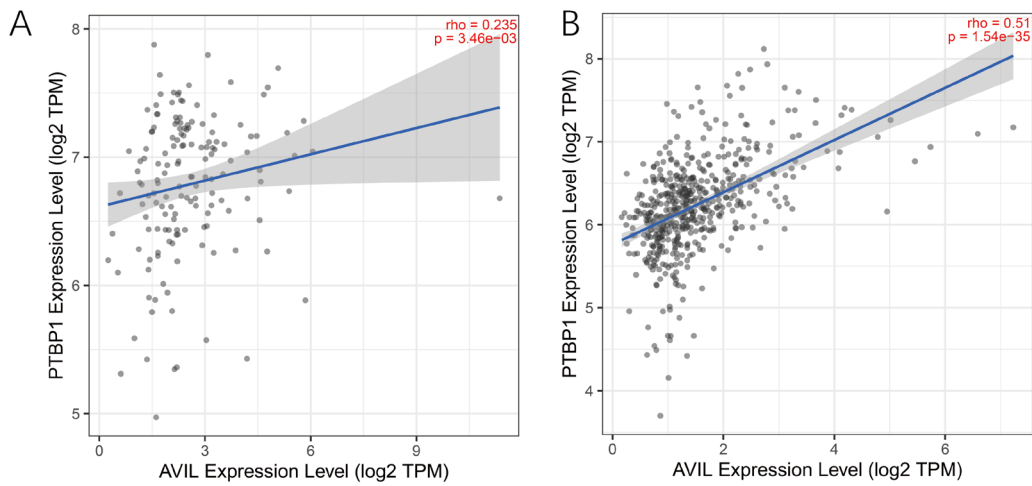
**Figure S8.** Analysis of the correlation between the PTBP1 expression and the methylation of its 31 methylation sites.



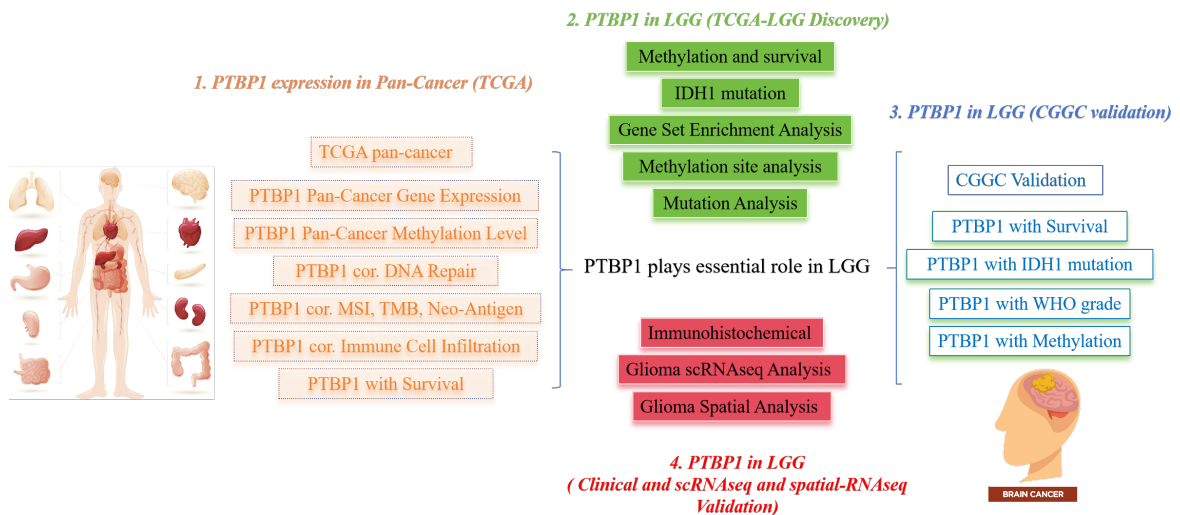
**Figure S9.** Validation of PTBP1 as an independent prognostic factor for glioma in three independent cohorts of CGGA mRNA\_301, CGGA mRNA\_325, CGGA mRNA\_693. (A-C) unicon, multicox forest plot and nomogram of CGGA mRNA\_301 cohort. (D-F) Unicon, multicox forest plot and nomogram of CGGA mRNA\_325 cohort. (G-I) CGGA mRNA\_693 cohort of unicon, multicox forest plots and nomogram.



**Figure S10.** The expression of PTBP1 in a variety of cell types was obtained on the The human protein atlas website. The results indicate that PTBP1 is not cell type specific.



**Figure S11.** Correlation of AVIL with PTBP1 expression.



**Figure S12.** The workflow of the research.