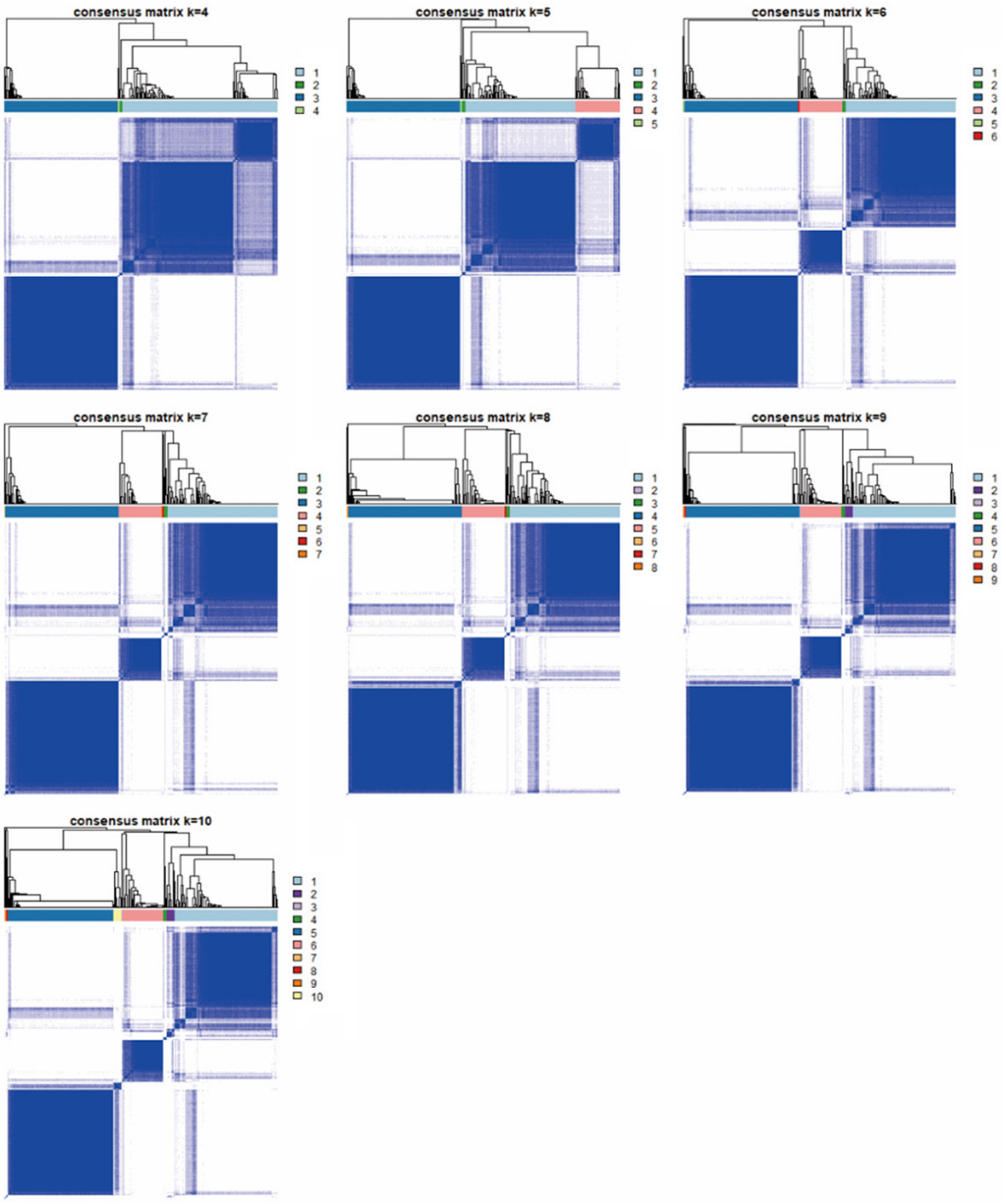


Figure S1. Consensus clustering matrix of 309 CGGA samples for k = 4 to k = 10.

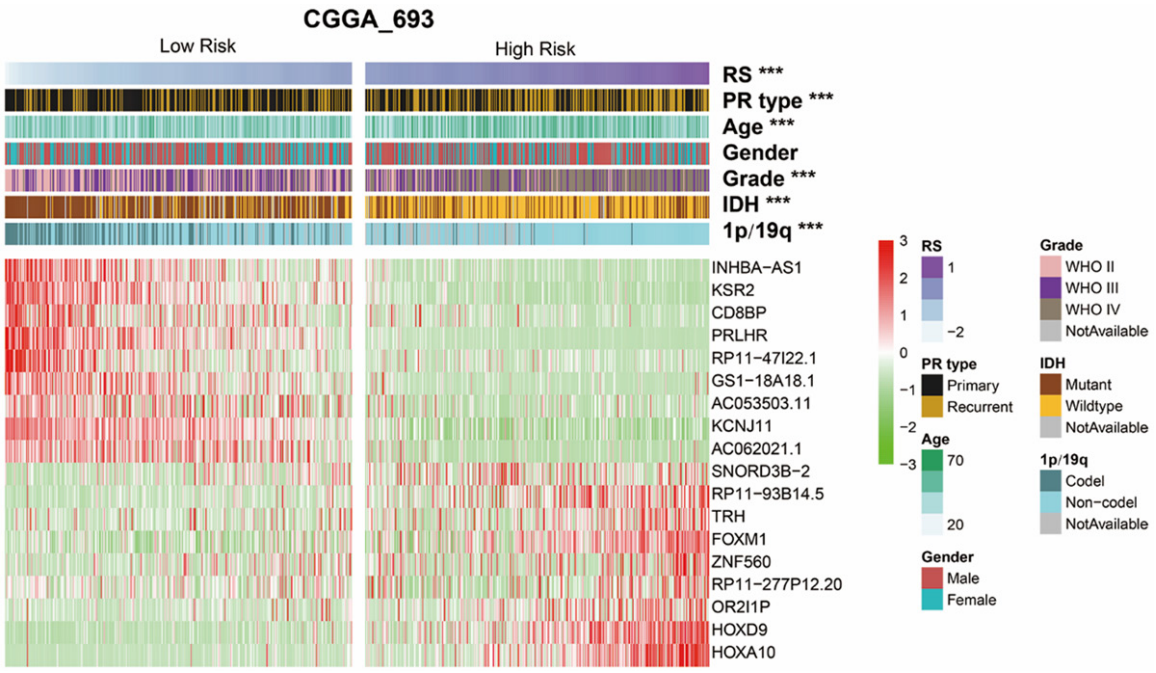
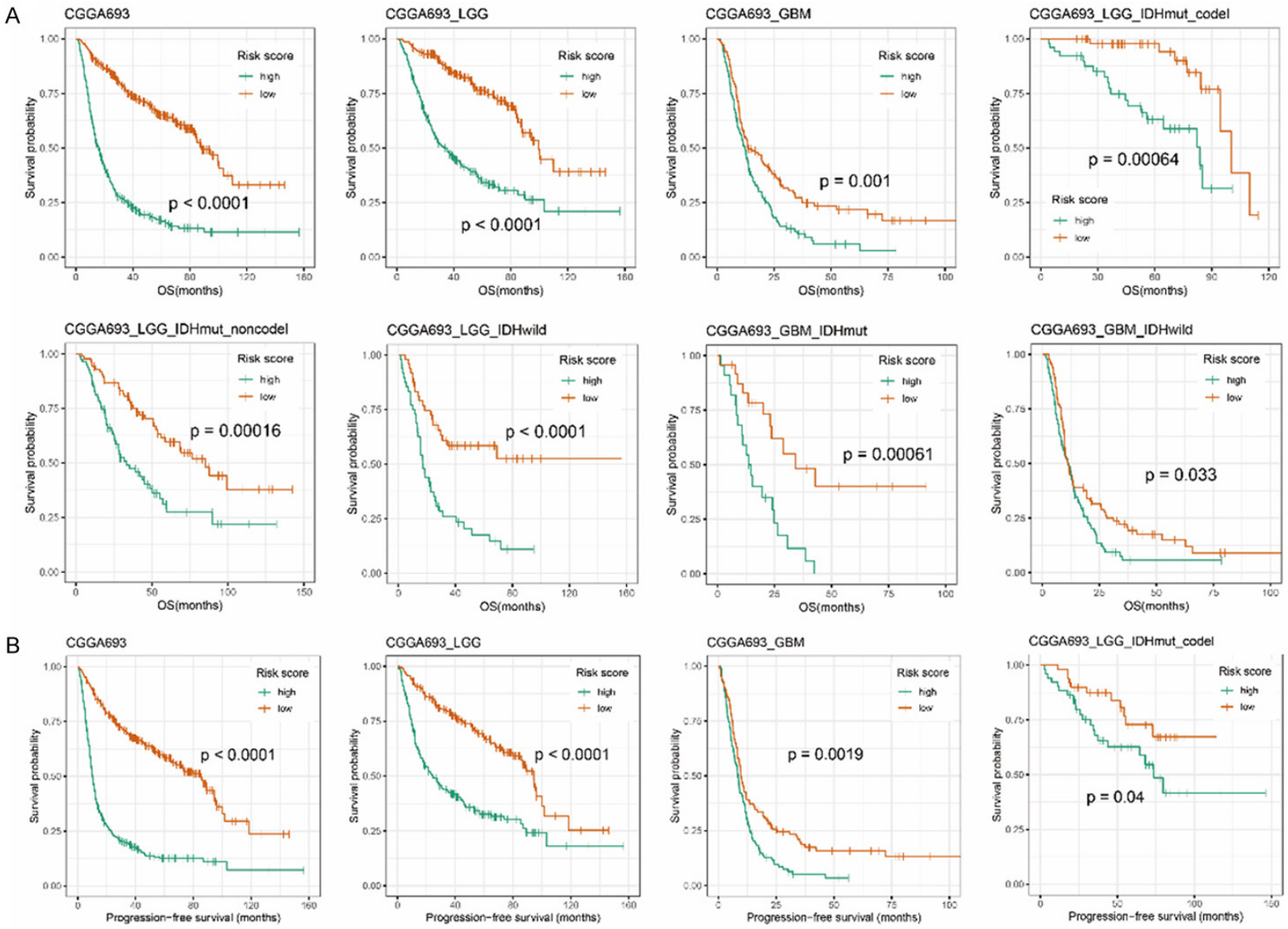


Figure S2. Heatmap and clinicopathological features of low- and high-risk group based on recurrence-related signature in CGGA_693 dataset.


A
CGGA693
CGGA693_LGG
CGGA693_GBM
CGGA693_LGG_IDHmut_codel
CGGA693_LGG_IDHmut_noncodel
CGGA693_LGG_IDHwild
CGGA693_GBM_IDHmut
CGGA693_GBM_IDHwild
Risk score
high
low
Survival probability
OS(months)
p < 0.0001
p = 0.001
p = 0.00064
p = 0.00016
p < 0.0001
p = 0.00061
p = 0.033
B
CGGA693
CGGA693_LGG
CGGA693_GBM
CGGA693_LGG_IDHmut_codel
Progression−free survival (months)
p < 0.0001
p < 0.0001
p = 0.0019
p = 0.04

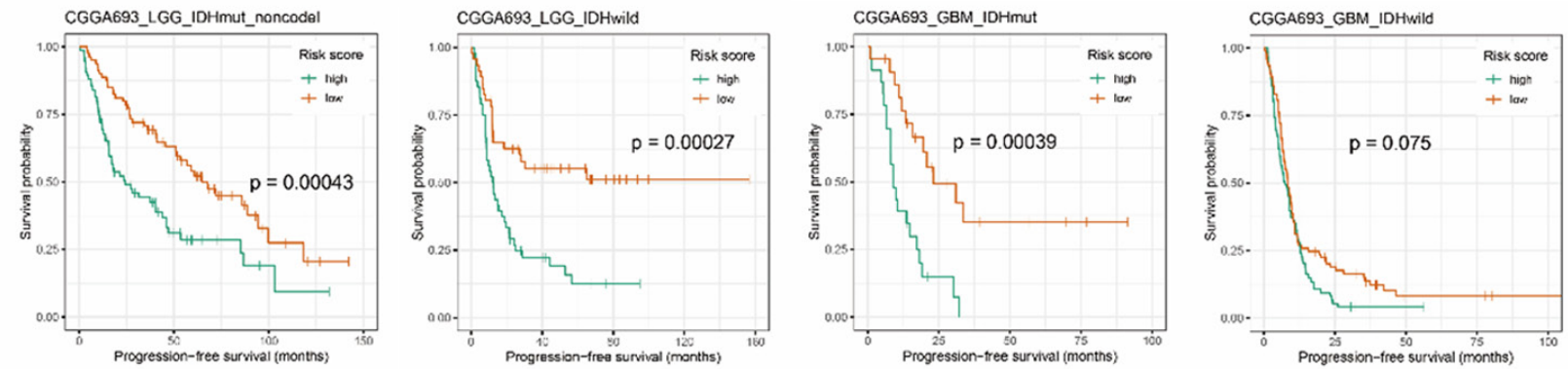


Figure S3. Survival prediction of the recurrence-related signature in CGGA_693 dataset. A. Overall survival prediction of the signature in all grade gliomas, lower grade gliomas (LGG, grade II and III), glioblastoma (GBM, grade IV), LGG with IDH-mutant and 1p/19q-codeleted, LGG with IDH-mutant and 1p/19q-intact, LGG with IDH-wildtype, GBM with IDH-mutant, GBM with IDH-wildtype. B. Progression free survival prediction of the signature in all grade gliomas, lower grade gliomas (LGG, grade II and III), glioblastoma (GBM, grade IV), LGG with IDH-mutant and 1p/19q-codeleted, LGG with IDH-mutant and 1p/19q-intact, LGG with IDH-wildtype, GBM with IDH-mutant, GBM with IDH-wildtype. Survival difference was determined by a log-rank test.

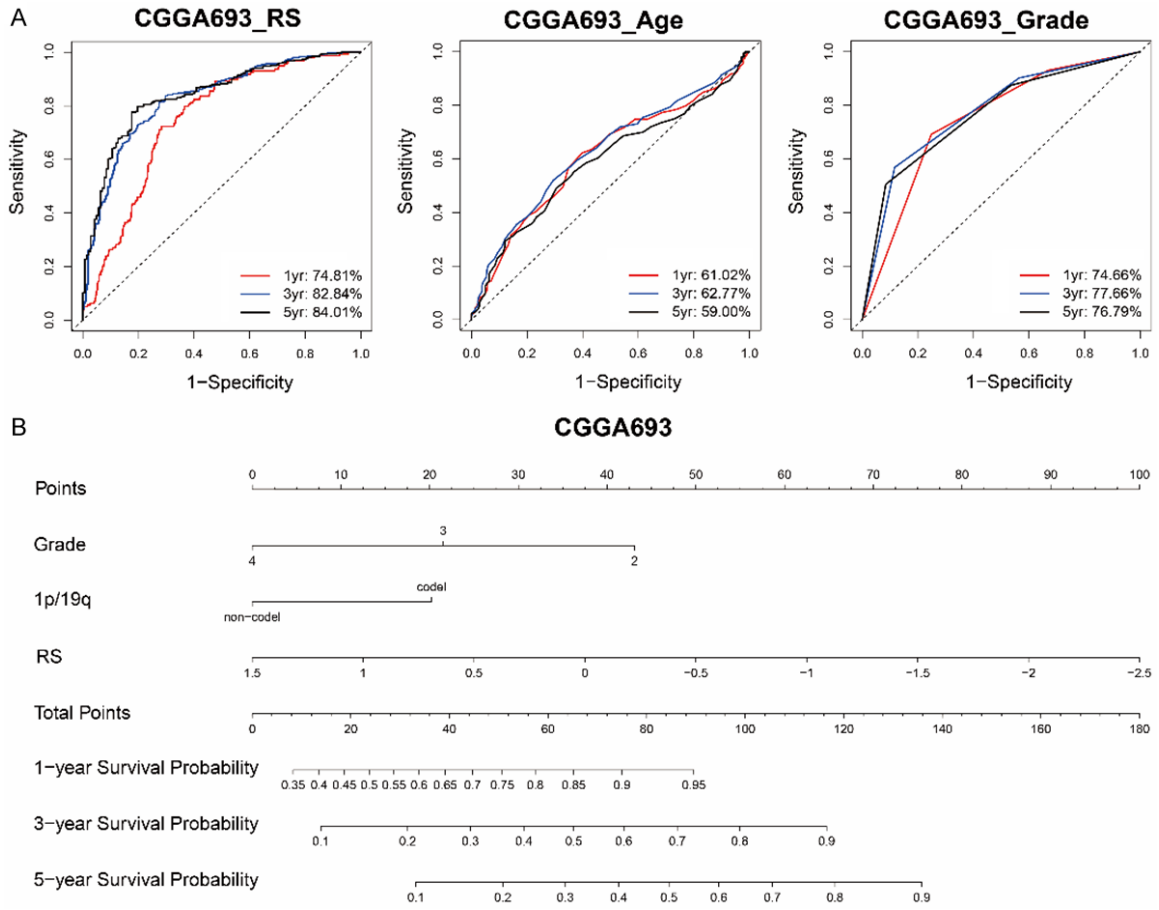
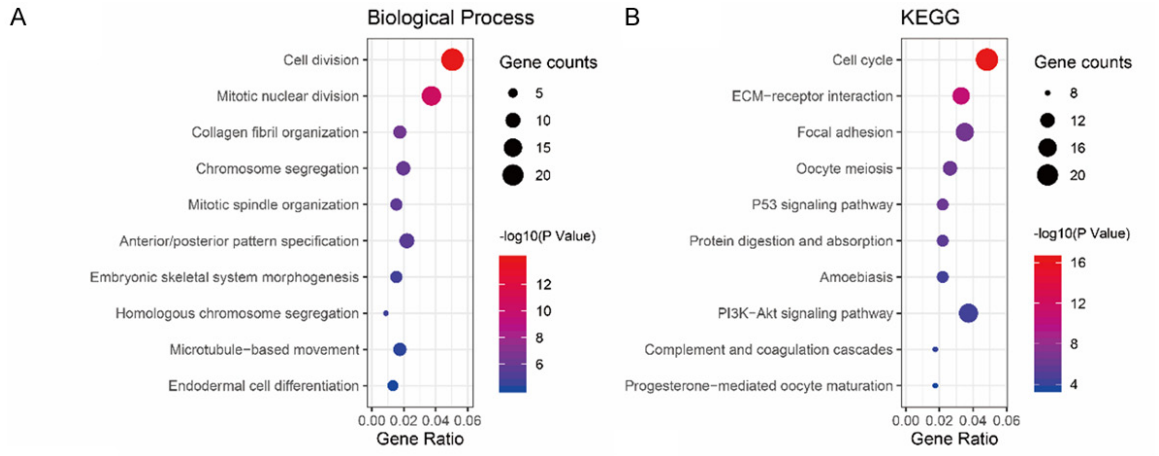


Figure S4. A survival prediction model for glioma patients based on recurrence-related signature. A. 1-year, 3-year and 5-year ROC curves indicated the sensitivity and specificity of signature risk score, age and grade in CGGA_693 dataset. B. A nomogram prediction model was developed by integrating the signature RS with the pathologic features in the CGGA_693 dataset.



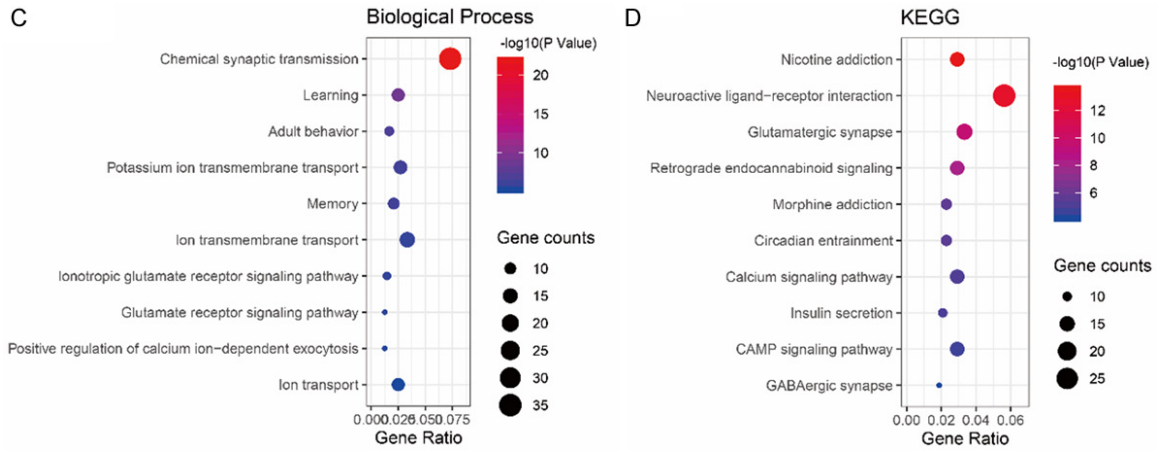


Figure S5. Functional annotation of recurrence-related signature in CGGA_693 dataset. With Gene Ontology (GO) analysis in DAVID, we analyzed biological processes of signature positively related genes (A) and negatively related genes (C). With KEGG pathway analysis in DAVID, we also revealed the enrichment pathways of genes that were positively (B) or negatively (D) associated with signature.

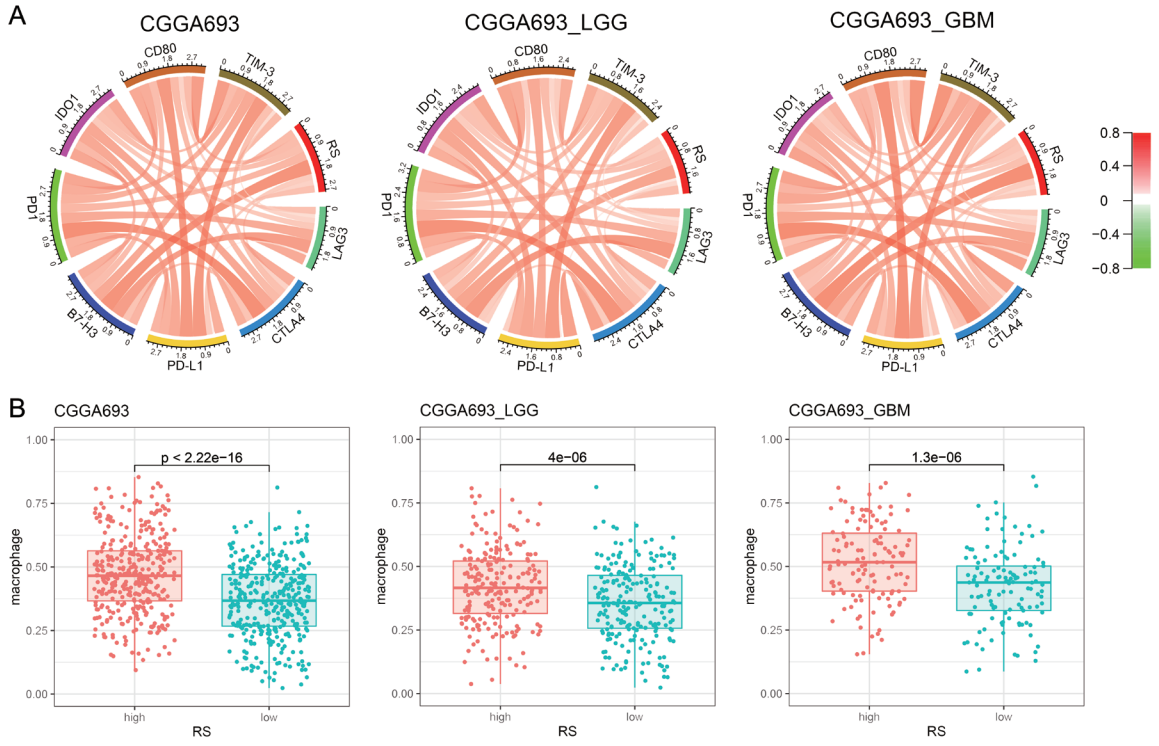


Figure S6. Recurrence-related signature and immune microenvironment in CGGA693 dataset. A. Pearson correlation of eight immune checkpoint genes and signature in all grade gliomas, lower grade gliomas (LGG) and glioblastoma multiforme (GBM). B. Tumor-associated macrophages in high-risk patients compared to low-risk patients by CIBERSORT.