

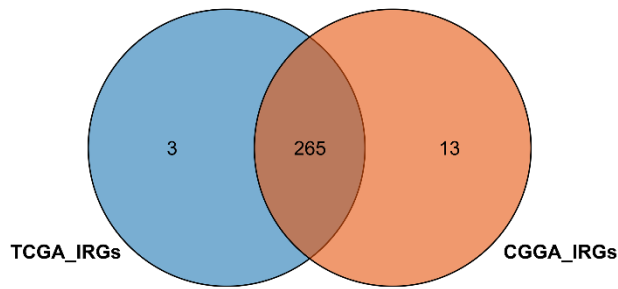
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**Supplemental Information**

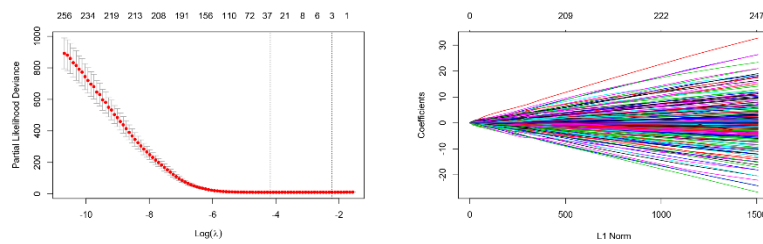
**Immune-related genes with APA  
in microenvironment indicate risk stratification  
and clinical prognosis in grade II/III gliomas**

**Shengchao Xu, Lu Tang, Gan Dai, Chengke Luo, and Zhixiong Liu**

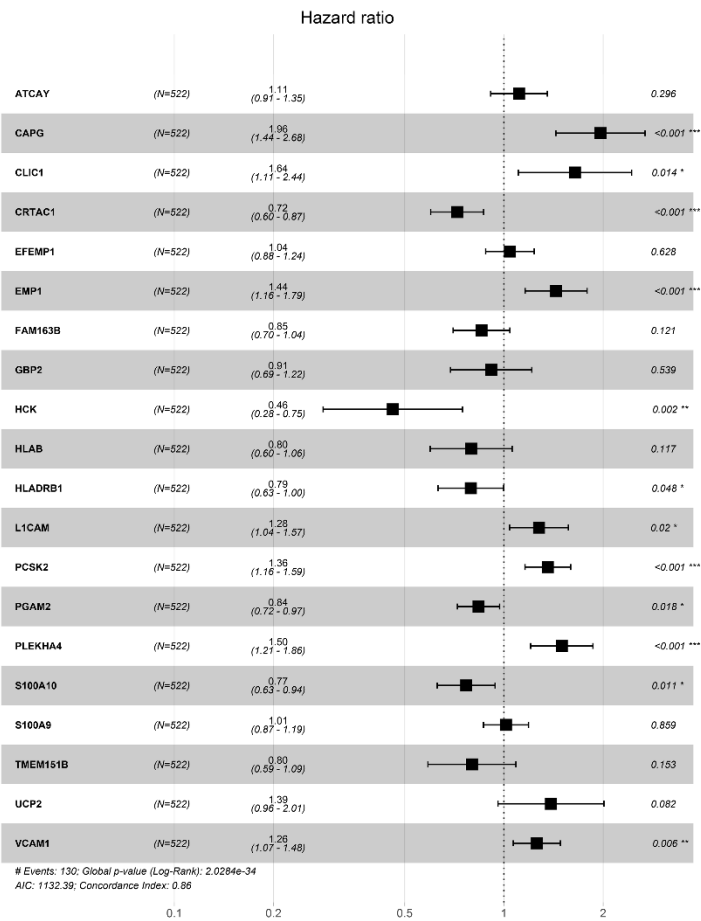
## Supplemental Figures



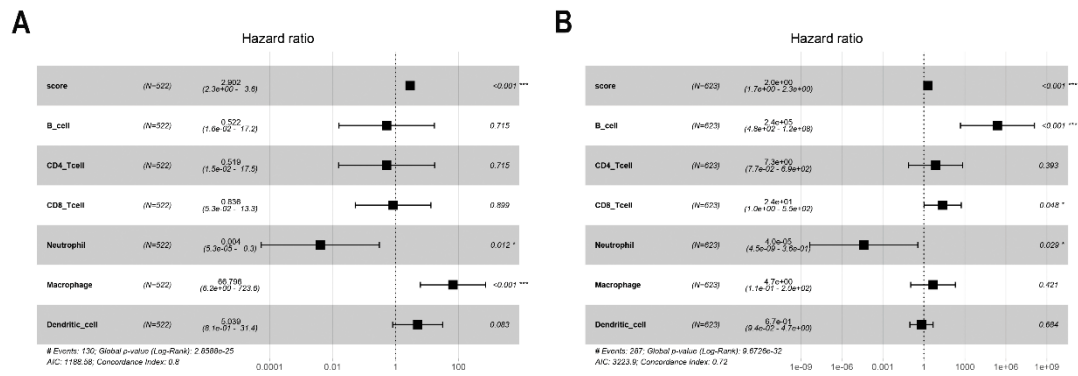
**Figure S1.** Identification of immune-related genes.



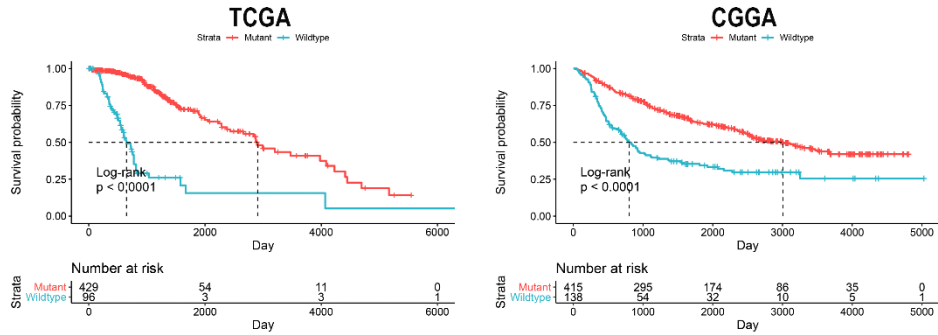
**Figure S2.** LASSO analysis of prognostic immune-related genes.



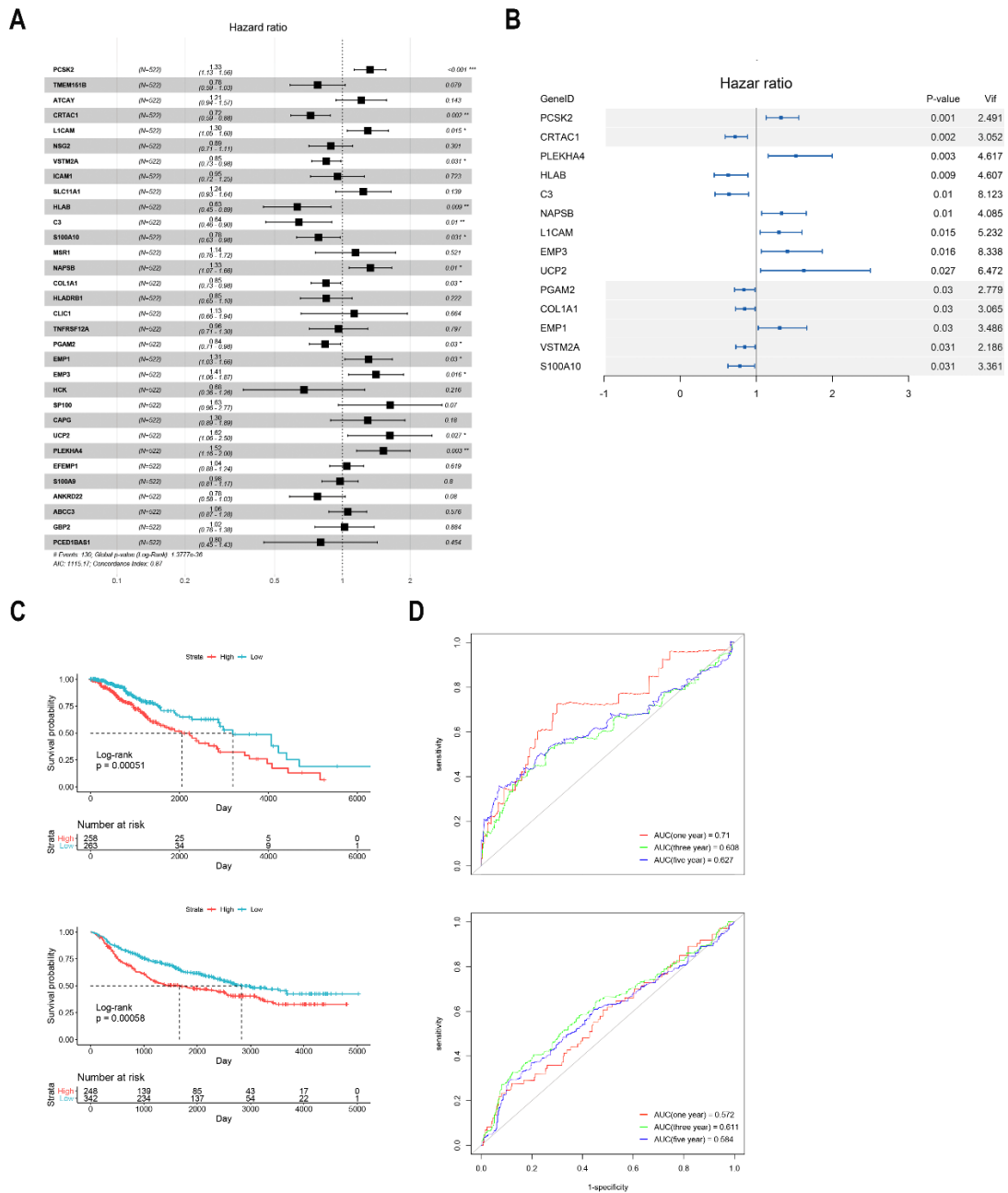
**Figure S3.** Multivariate Cox analysis of immune-related genes with alternative polyadenylation.



**Figure S4.** Multivariate Cox analysis of risk score and infiltrated immune cells. **A-B.** Multivariate Cox analysis of risk score and infiltrated immune cells in TCGA (A) and CGGA (B) datasets.



**Figure S5.** Kaplan-Meier analysis of IDH mutant and wildtype lower-grade gliomas.



**Figure S6.** Construction of risk signature of immune-related genes without the screening of alternative polyadenylation. **A.** Multivariate Cox analysis of included immune-related genes. **B.** Selection of candidate immune-related genes. **C.** Survival analysis of patients in the low-risk and high-risk groups. **D.** ROC analysis of risk score in predicting one-, three-, and five-year survival.

### Supplemental Tables

**Table S1.** ESTIMATE score of TCGA and CGGA datasets.

**Table S2.** Differentially expressed genes in stromal and immune groups.

**Table S3.** Gene list of identified immune-related genes.