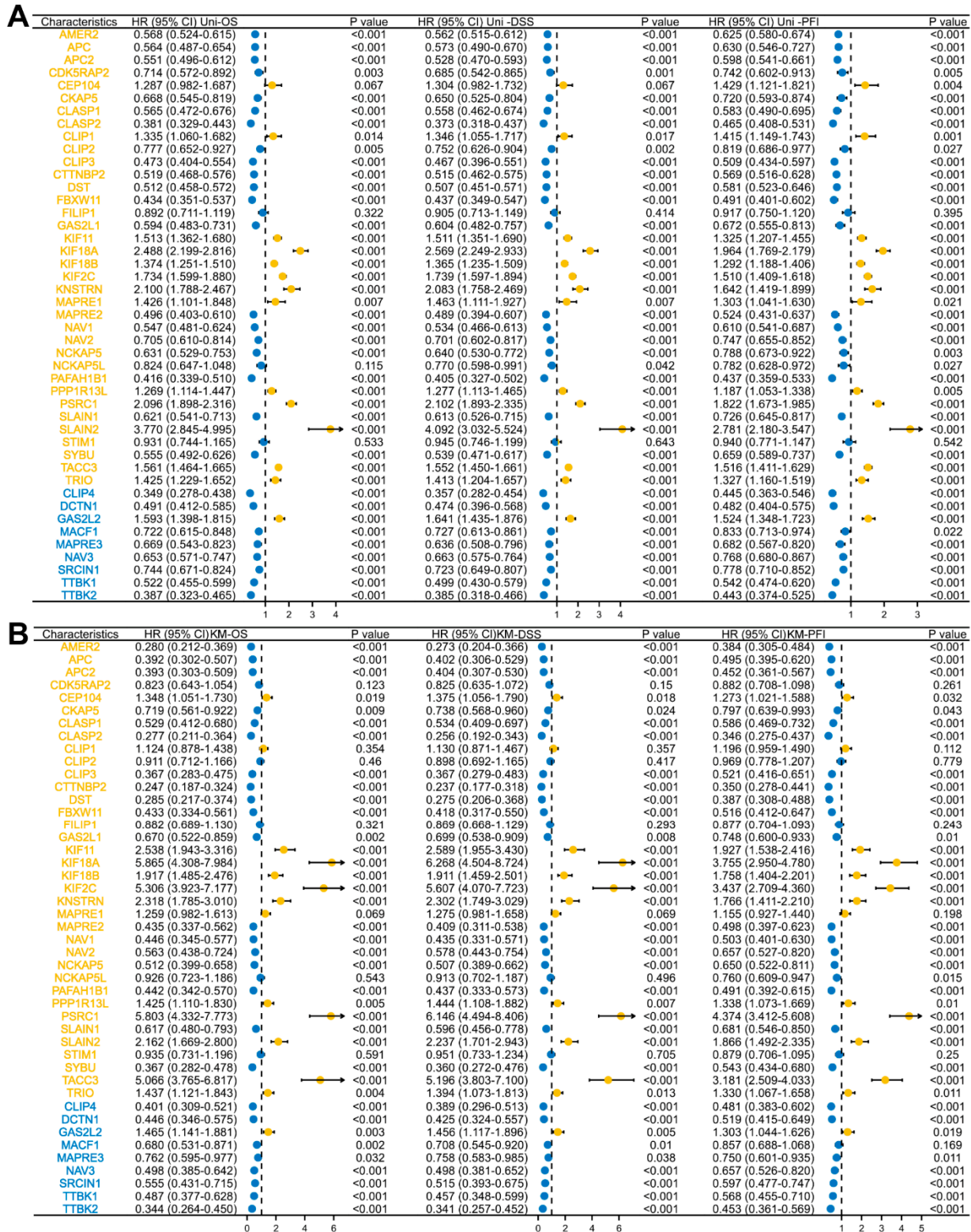
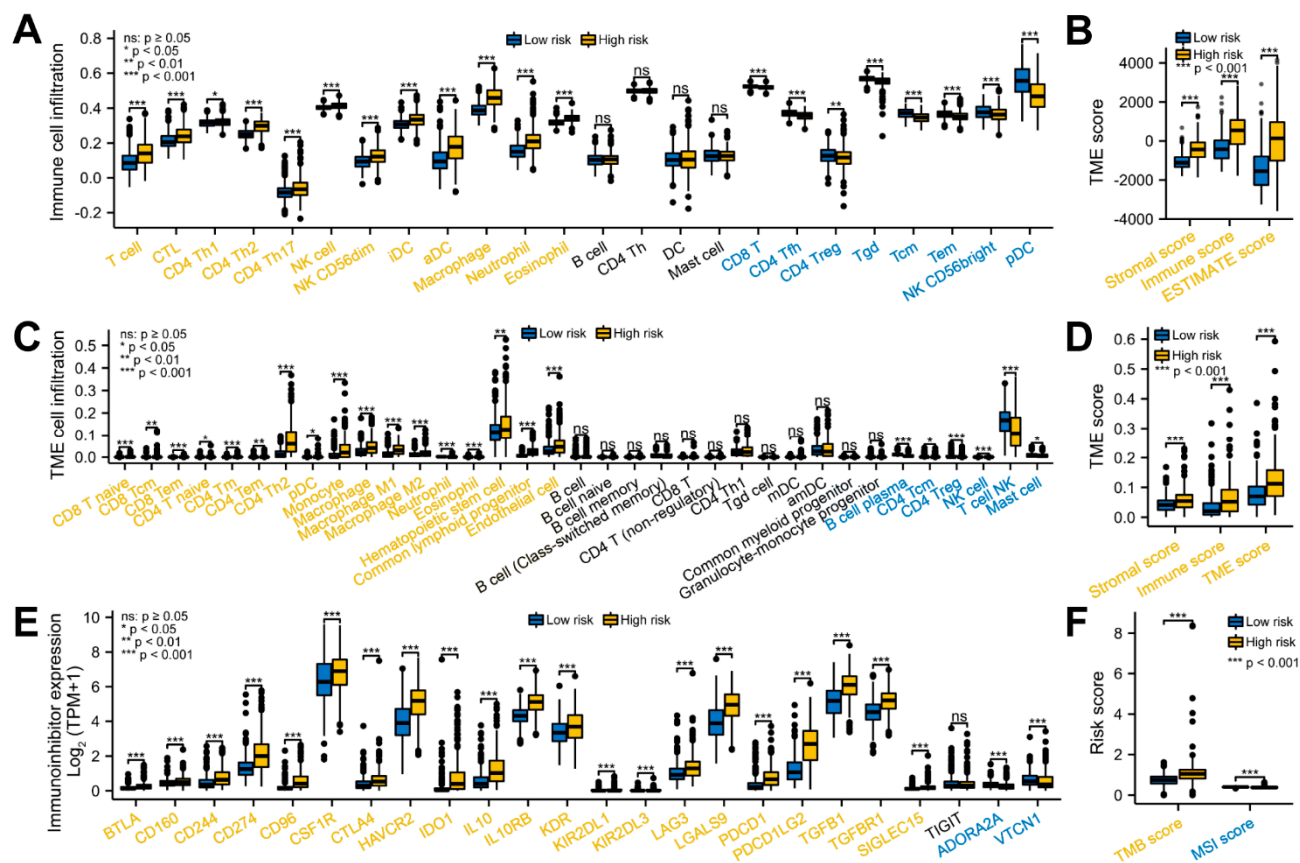


**Figure S1.** Glioma patients with DEMPERGs were distinguished into three subgroups by unsupervised consensus clustering. Related to Figure 4. (A) Complex heatmap of DEMPERG expression. (B) PCA plot. (C) KM OS plot.



**Figure S2.** Identification of prognostic-related DEMPERGs in glioma. Related to Figure 6A. (A,B) Forest plots of univariate Cox (A) and KM analyses (B) of DEMPEAGs with OS, DSS, and PFI. Yellow and blue words represented upregulated and downregulated genes in normal and glioma tissues, and yellow and blue dots represented risky and protective genes in glioma, respectively.



**Figure S3.** Different TME infiltrations between the two risk groups in glioma. Related to Figure 8. (A,B) Histograms of immune cell infiltration (A) and TME scores (B) using ssGSEA and ESTIMATE algorithm between the two risk groups. (C,D) Histograms of TME cell infiltration (C) and TME scores (D) using the xCell algorithm between the two risk groups. (E,F) Histograms of immunoinhibitor expression (E), TMB and MSI score (F) between the two risk groups.