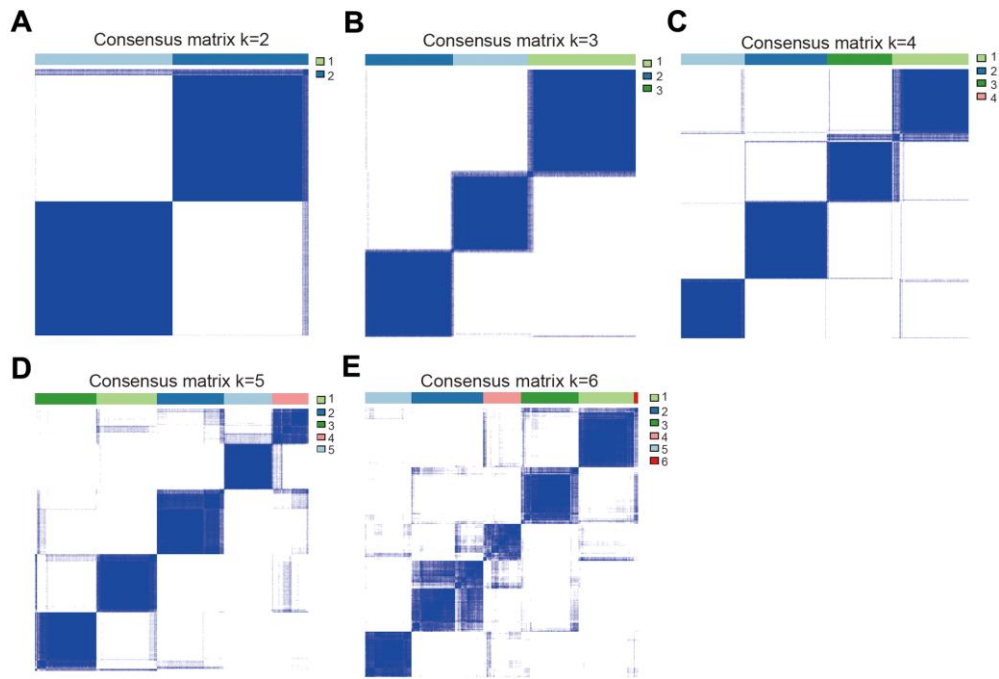
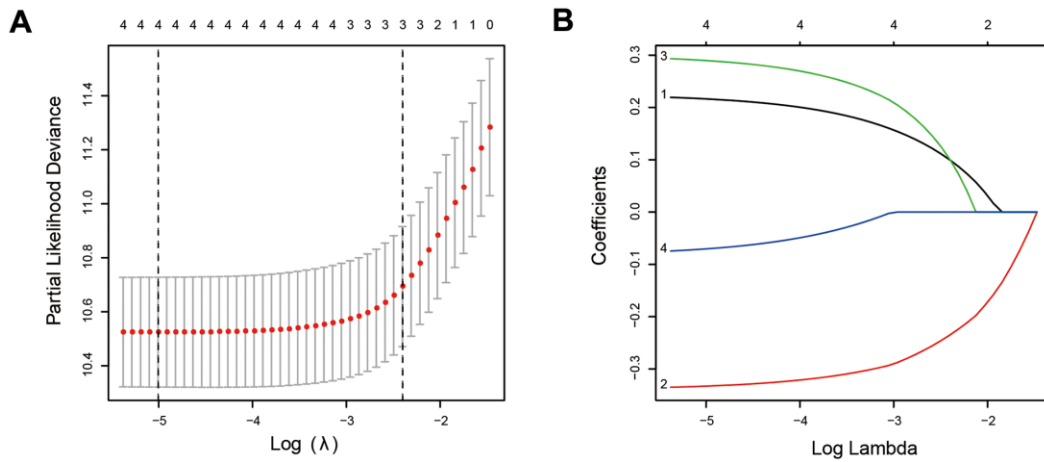


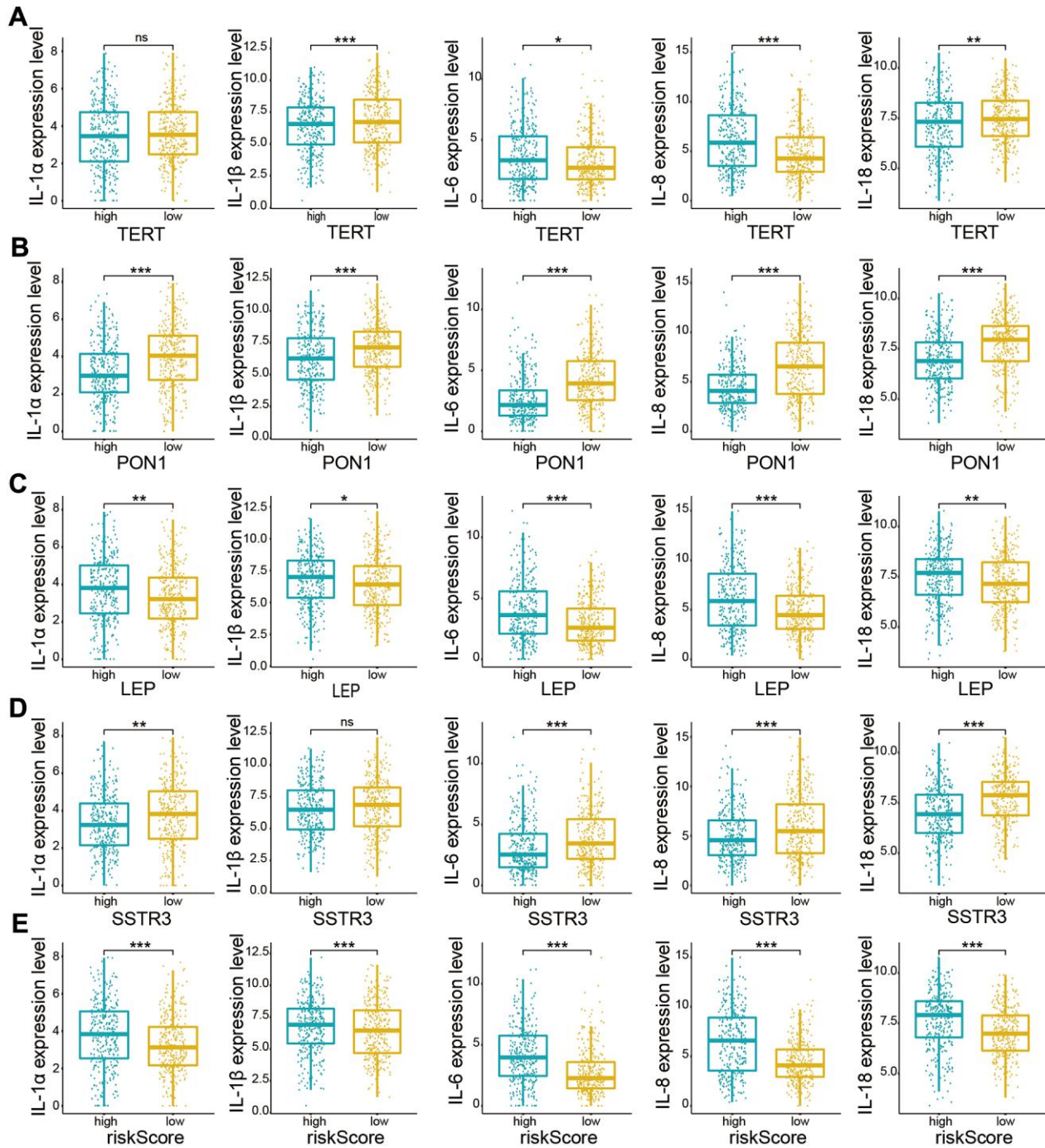
SUPPLEMENTARY FIGURES



Supplementary Figure 1. The consensus score matrix of the four survival-associated AGs expression in glioma samples based on TCGA datasets. The consensus score matrix of the four survival-associated AGs expression in glioma samples based on TCGA datasets. (A–E) at K = 2 (A), 3 (B), 4 (C), 5 (D), and 6 (E), the correlation between groups, the consensus score matrix for the four selected AGs in the TCGA datasets.



Supplementary Figure 2. Risk model derived from expression patterns of four survival-associated AGs. (A) Partial likelihood deviance for tuning the parameter selection in the Lasso regression model in the TCGA datasets. (B) Lasso coefficient profiles of the four survival-associated AGs in the TCGA datasets.



Supplementary Figure 3. The expressing features of interferons and chemokines based on expression levels of the four selected AGs and the risk score. (A–E) Distribution of interferons and chemokines (IL-1 α , IL-1 β , IL-6, IL-8, and IL-18) expression levels based on expression levels of the four selected AGs (TERT (A), PON1(B), LEP (C), and SSTR3 (D)) of patients with glioma and the risk score (E) in the TCGA datasets.