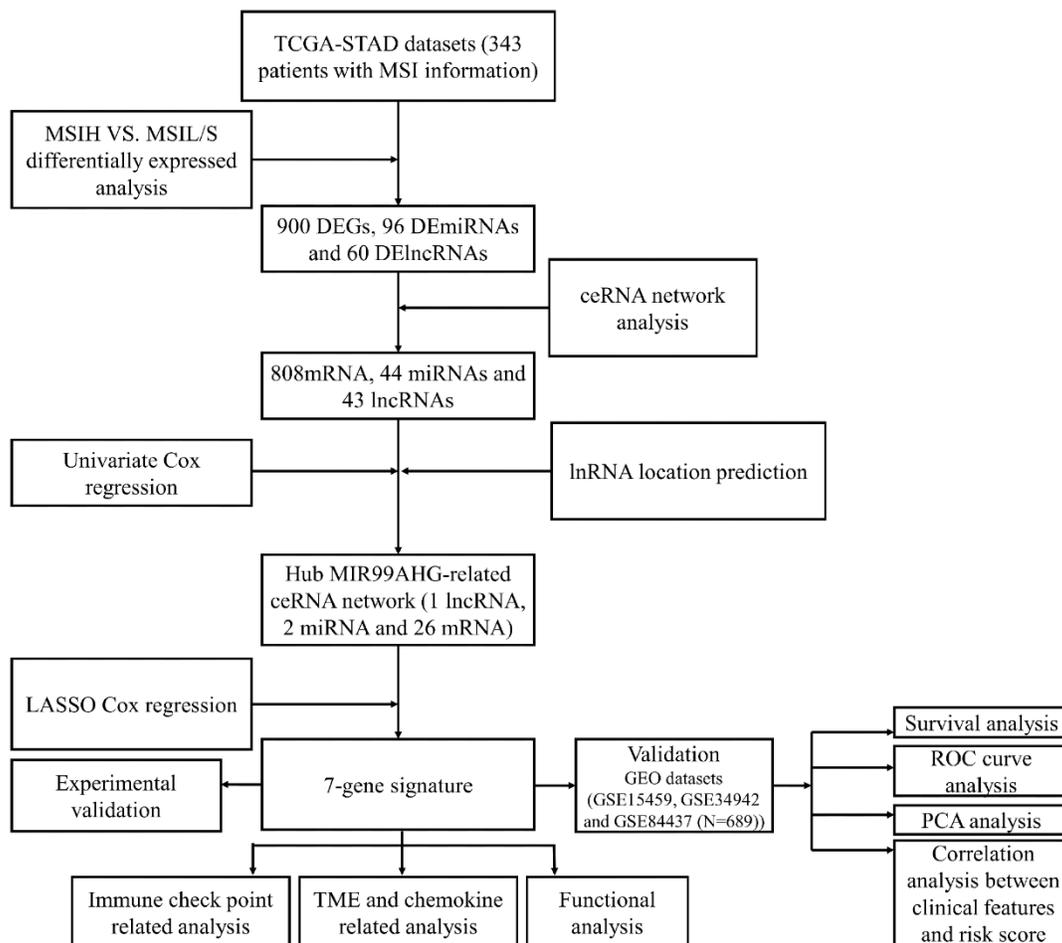
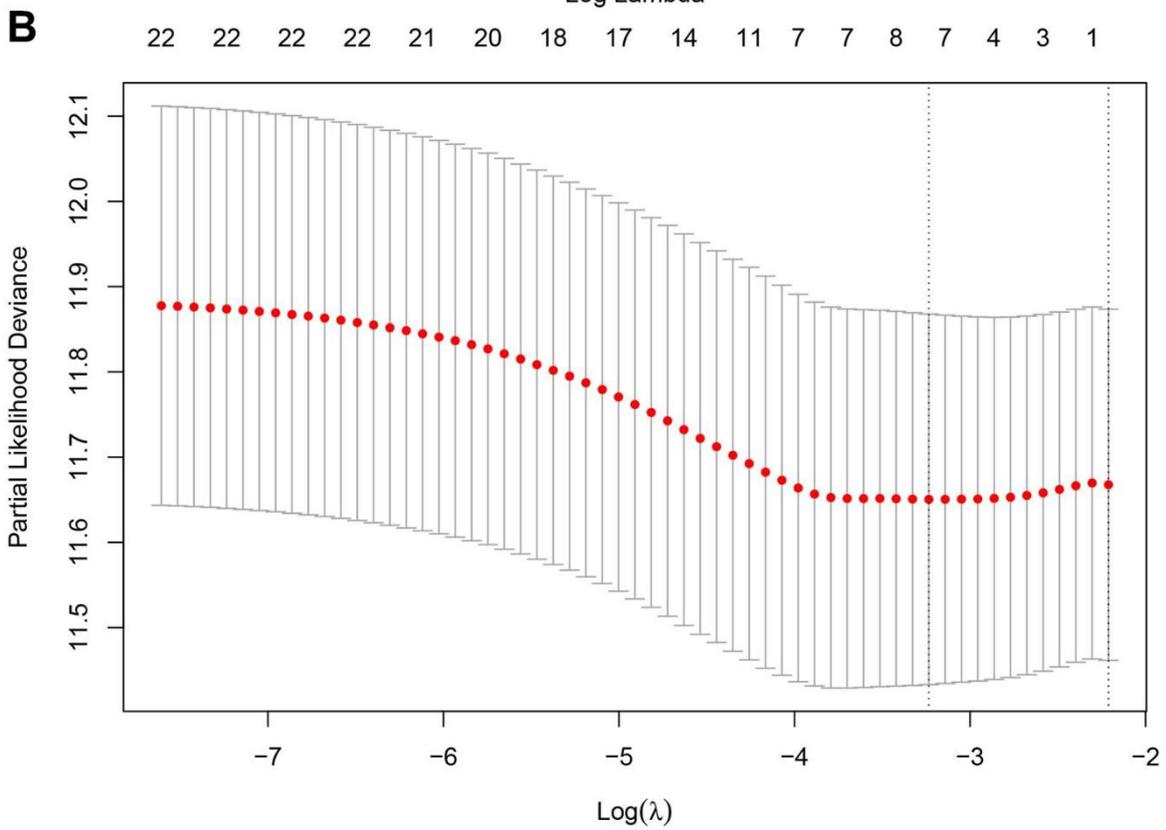
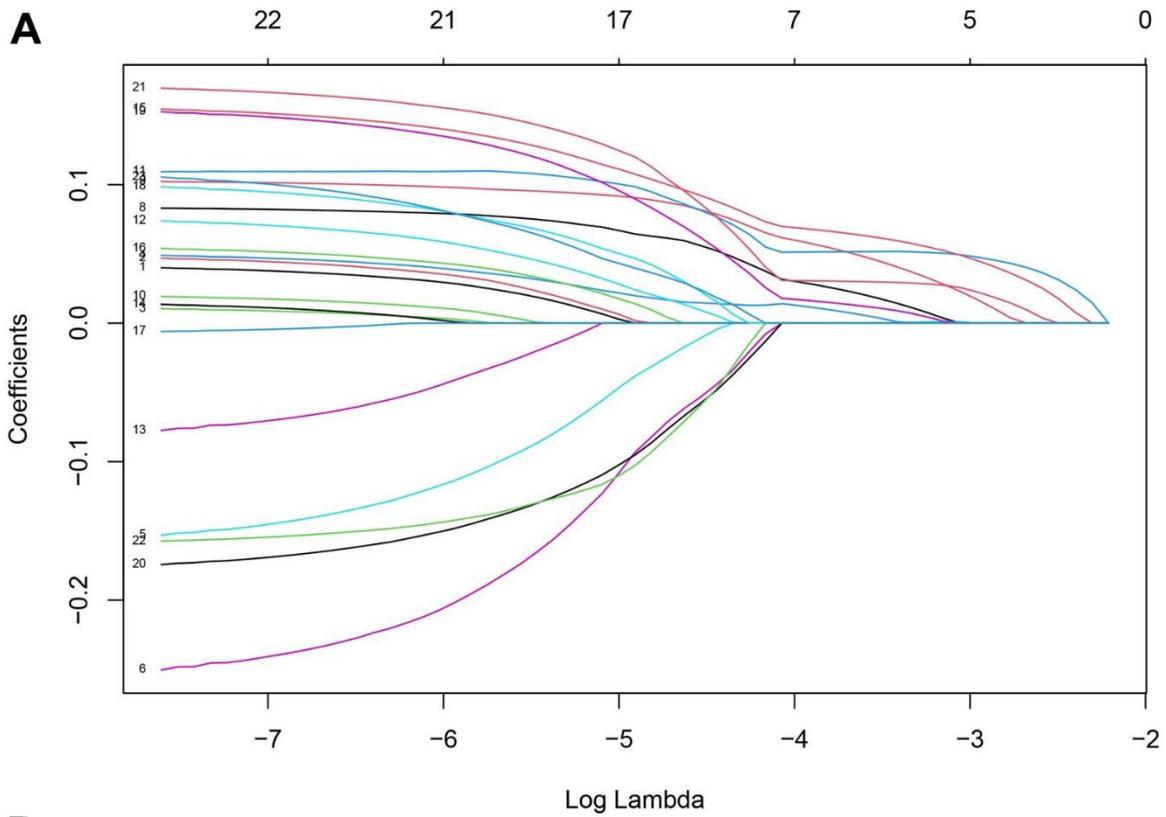


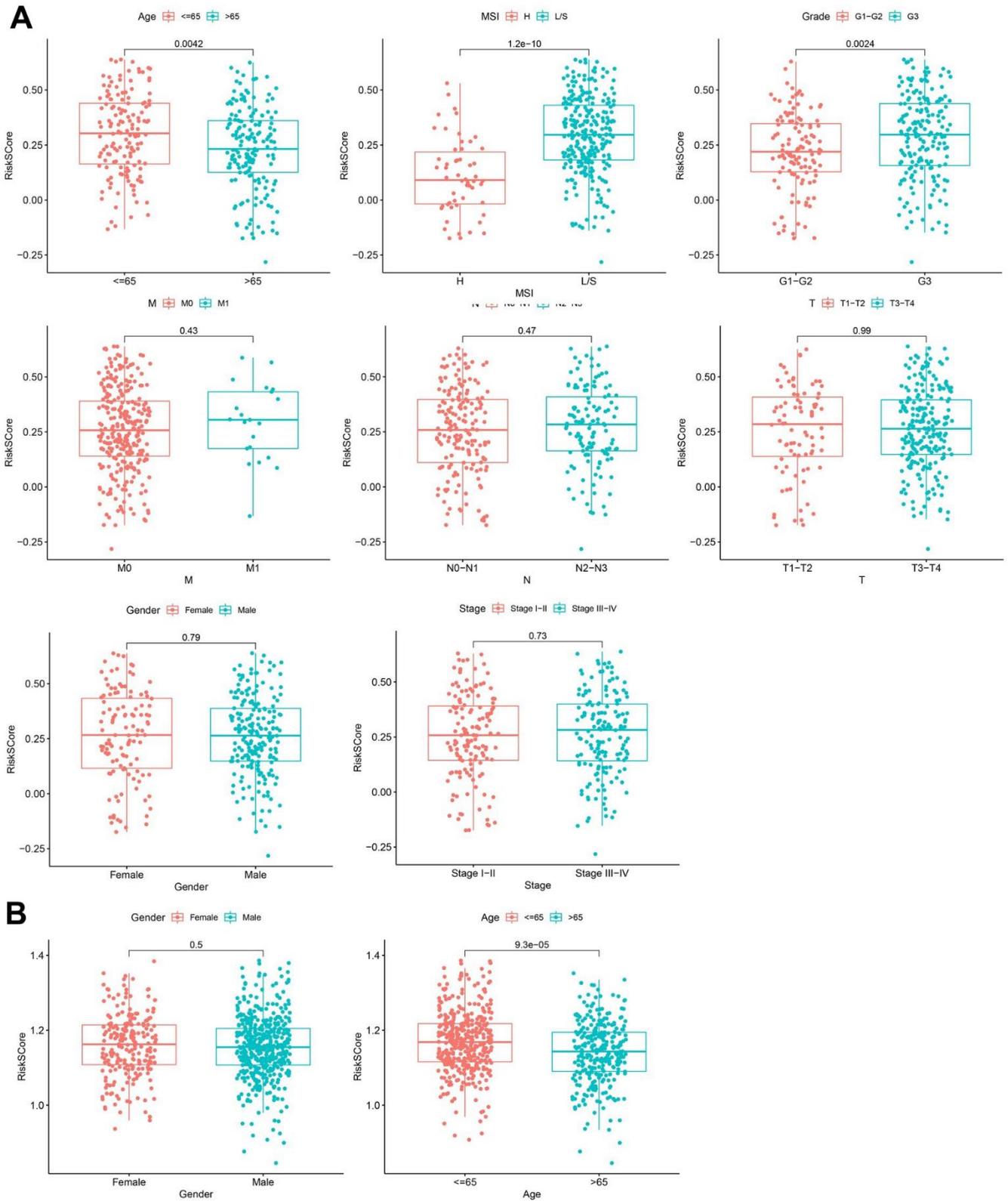
## SUPPLEMENTARY FIGURES



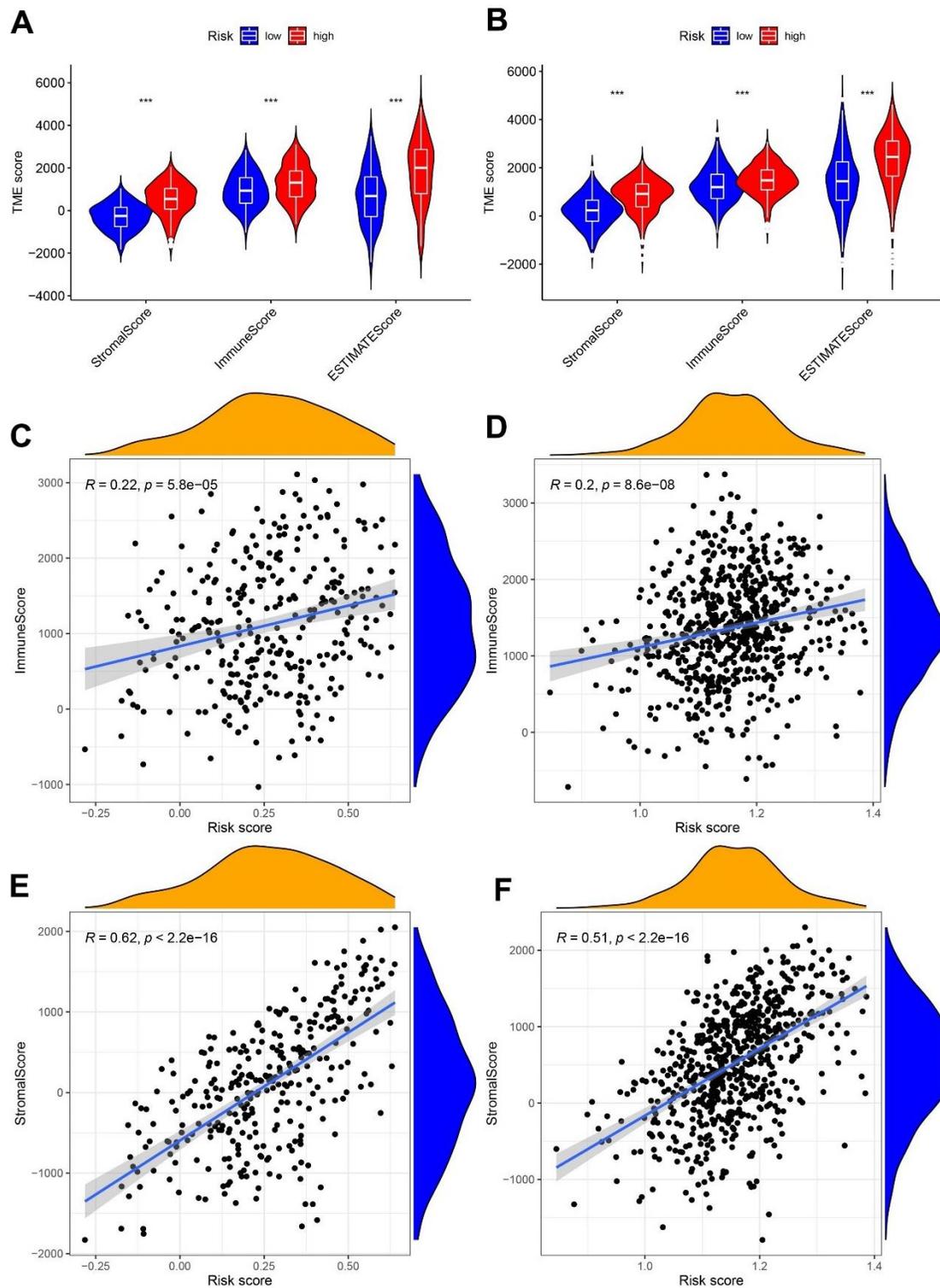
Supplementary Figure 1. The flow diagram of the study.



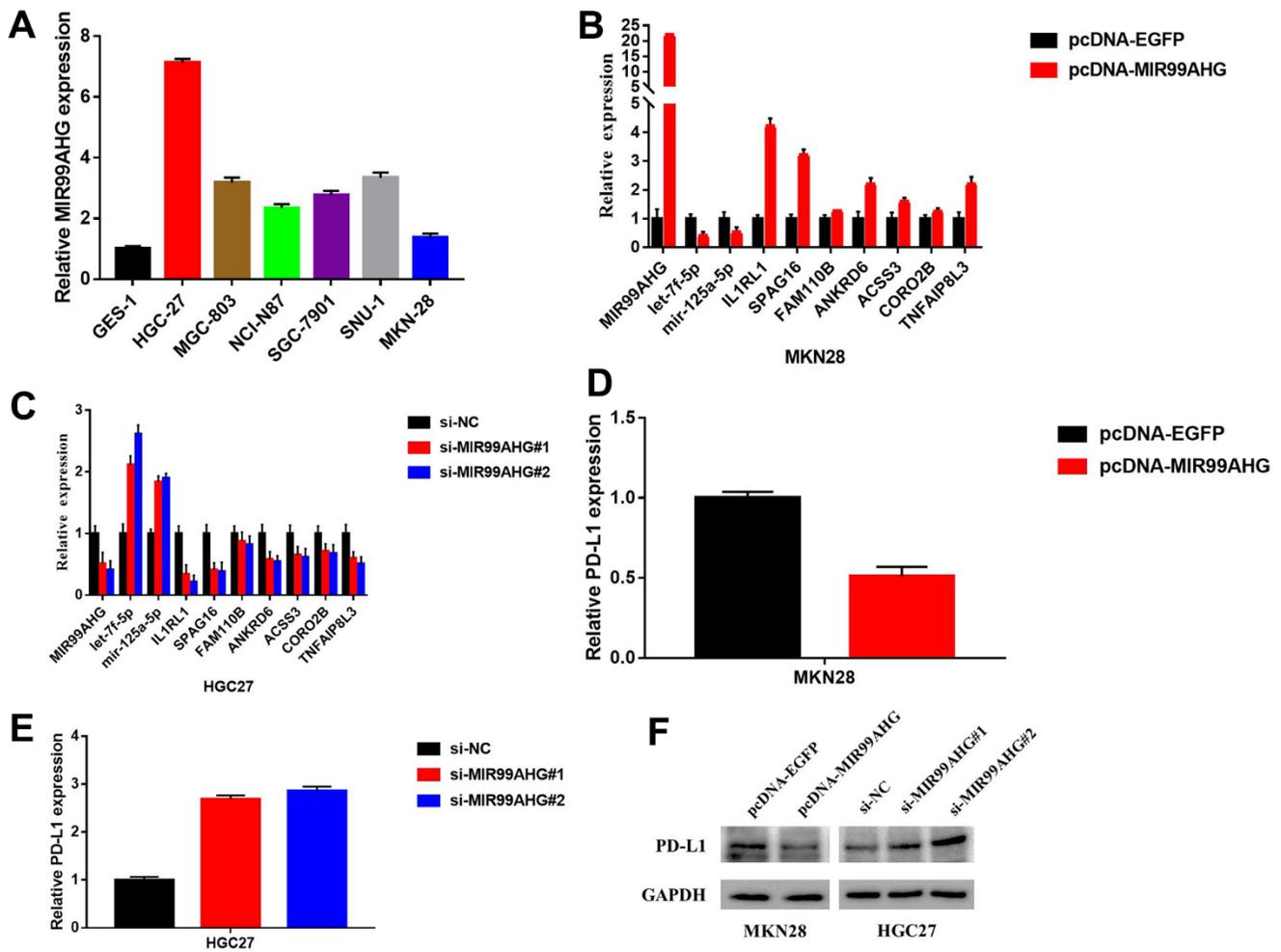
**Supplementary Figure 2. Prognostic model constructed using LASSO algorithm. (A)** LASSO coefficient profiles of the expression of 26 candidate RBPs. **(B)** Selection of the penalty parameter ( $\lambda$ ) in the LASSO model via cross-validation.



**Supplementary Figure 3. Correlation between predicted risk score and clinical features. (A) TCGA database results. (B) GEO database results.**



**Supplementary Figure 4. Signature-related immune landscape based on the stromal, immune and ESTIMATE scores. (A, B)** Differences in the TME score between the two risk groups in the TCGA and GEO datasets, respectively. **(C, D)** The relationship between the immune score and risk score in the TCGA and GEO datasets, respectively. **(E, F)** The relationship between the stromal score and risk score in the TCGA and GEO datasets, respectively.



**Supplementary Figure 5. Experimental validation.** (A) Relative expression of MIR99AHG in six gastric cancer cell lines (hgc27, MGC803, NCI-N87, SGC7901, SNU-1 and MKN45) and human normal gastric epithelial cell line (GES1) analyzed by quantitative RT-PCR. (B, C) Effect of MIR99AHG overexpression or knockdown on the ceRNA network molecules expression. (D–F) Effect of MIR99AHG overexpression or knockdown on PD-L1 expression.