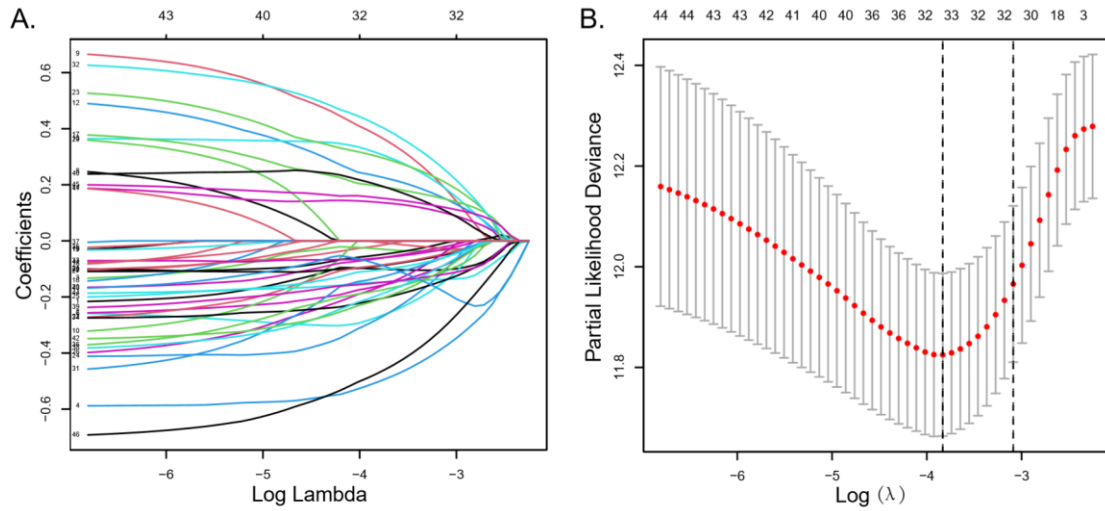
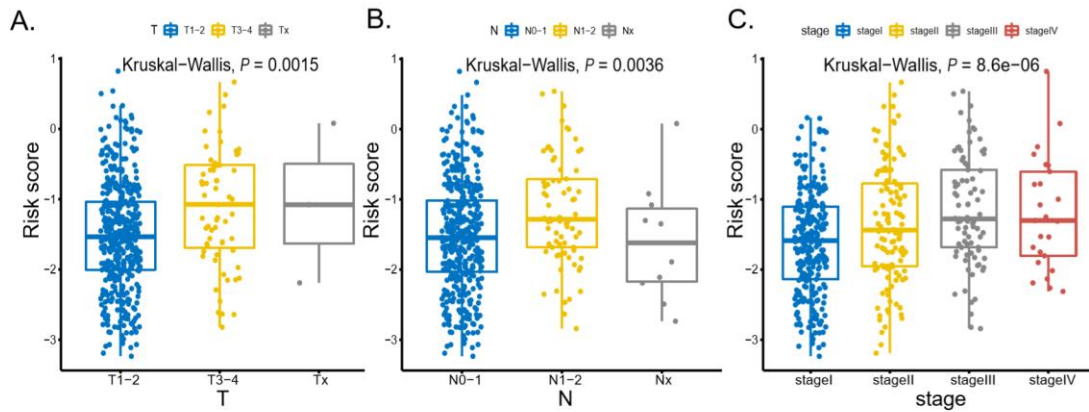


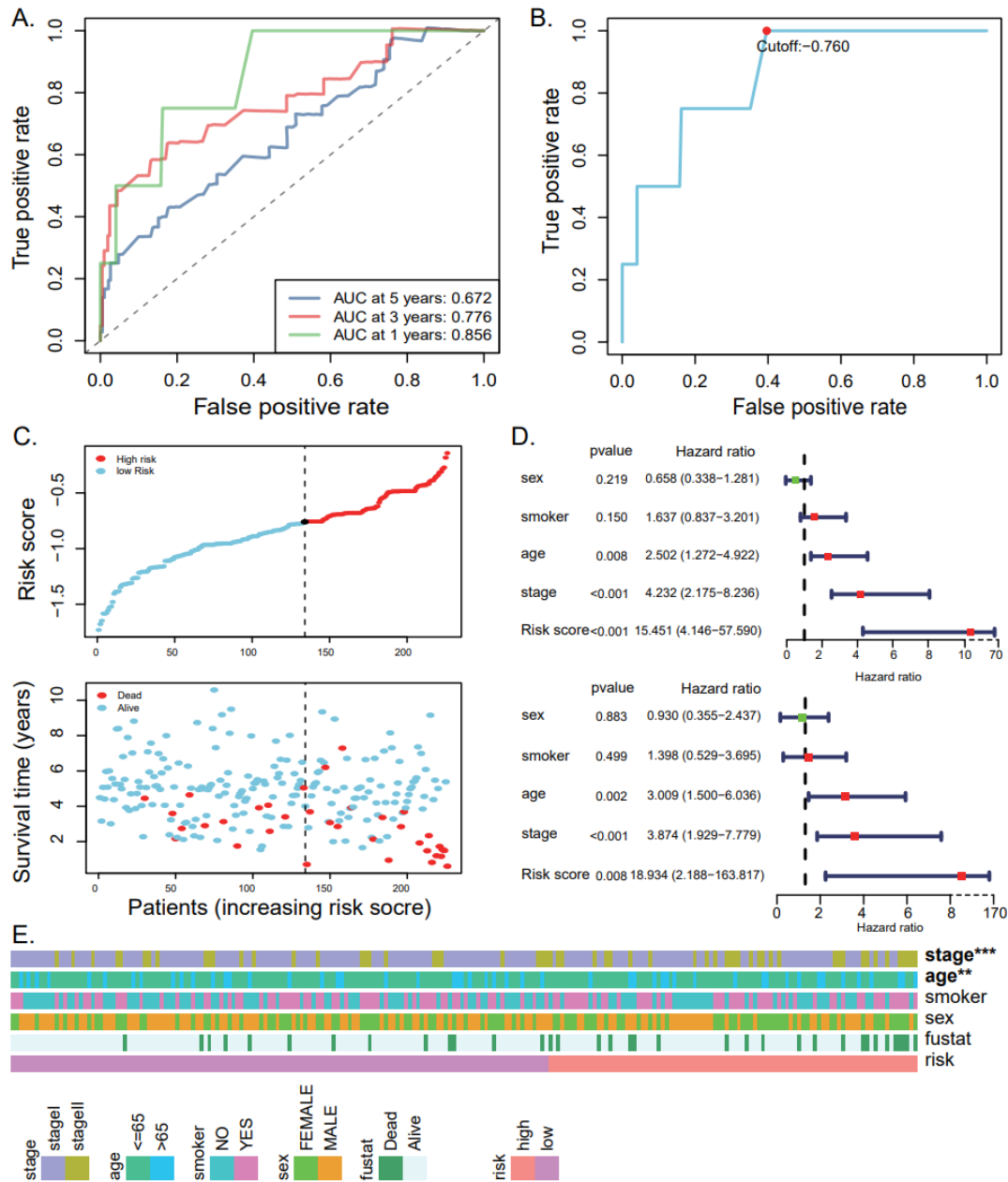
Supplemental Figure 1. Heatmap of upregulated immune-related lncRNA.



Supplemental Figure 2. The process of developing prognostic gene signature by LASSO regression analysis. (A) LASSO coefficient profiles of the 47 lincRNA pairs in TCGA-LUAD. (B) Determination of the optimal parameter (lambda) in the LASSO model for TCGA-LUAD.



Supplemental Figure 3. The association of the risk score with T, N, and stage in the TCGA-LUAD.



Supplemental Figure 4. Prognostic value of the signature of immune-related lncRNA pairs in the GSE31210 dataset. (A) The time-dependent accuracy of the risk score in predicting survival at 1, 3, and 5 years, as indicated by ROC analysis. (B) Estimation of the cutoff value with one year ROC plot. (C) Survival statuses of patients corresponding to risk score. (D) Univariate (upper panel) and multivariate (lower panel) Cox regression analysis. (E) Correlations between risk score and clinical characteristics.