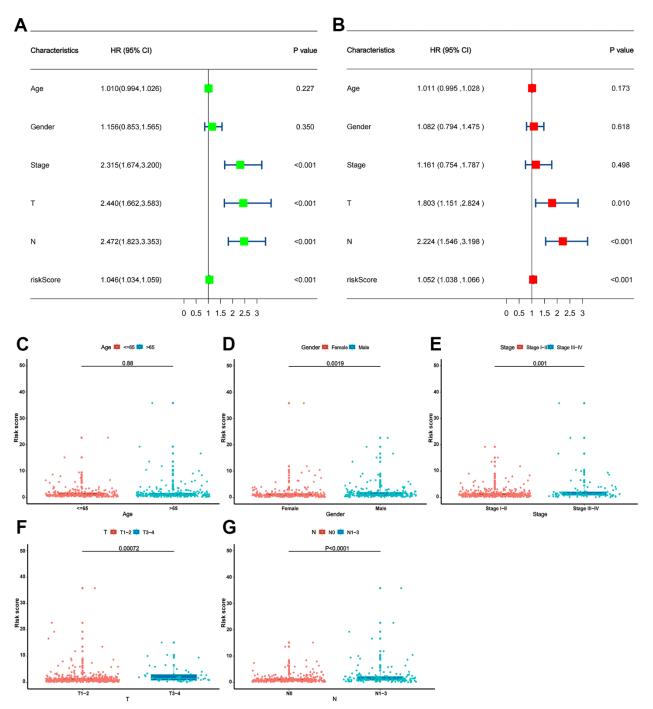
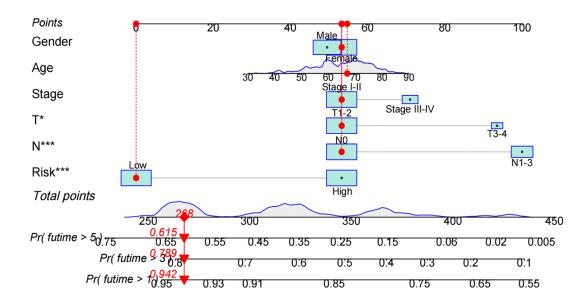
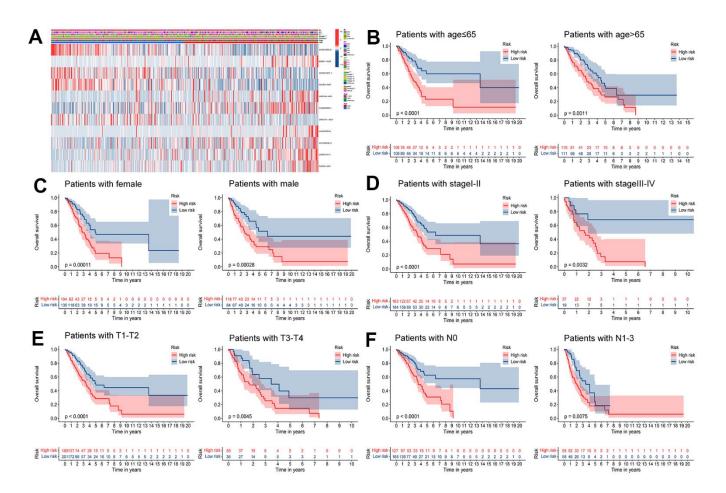
SUPPLEMENTARY FIGURES



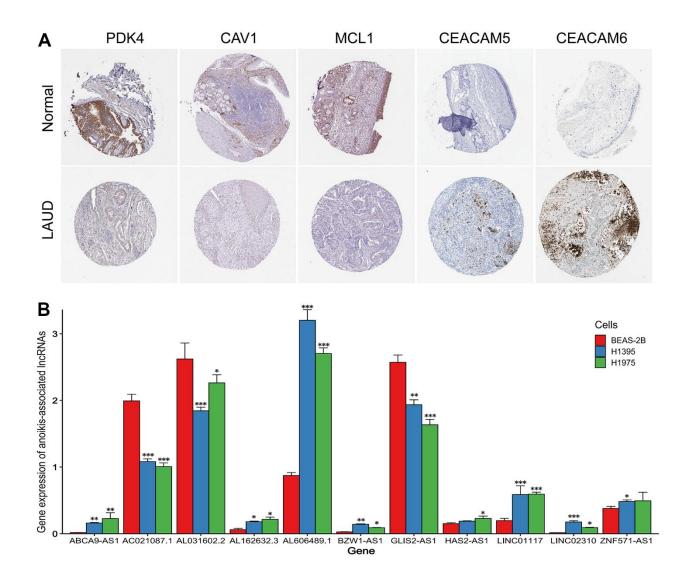
Supplementary Figure 1. Independent prognostic analysis of the prognostic signature. (A) Univariate and (B) Multivariate Cox regression analysis to examine the value of clinical characteristics and risk score as independent prognostic predictors. Correlation analysis of risk score with age (C), gender (D), stage (E), T stage (F) and N stage (G).



Supplementary Figure 2. Nomograms for predicting 1-, 3-, 5-year overall survival for a randomly selected patient in test cohort.



Supplementary Figure 3. Subgroup validation based on clinical features. (A) Heatmap for expression levels and correlation of risk signature with clinical factors. Kaplan-Meier survival analysis between high- and low-risk groups stratified by clinical characteristics: (B) age (≤65 and >65), (C) gender (female and male), (D) stage (I-II and III-IV), (E) T stage (T1-2 and T3-4) and (F) N stage (N0 and N1-3).



Supplementary Figure 4. Validation of apoptosis-related genes and ARIncRNAs expression levels. (A) Protein expression map of the top 5 differential apoptosis-related genes in normal and tumor tissues. (B) Expression levels of 11 ARIncRNAs in high and low risk groups.