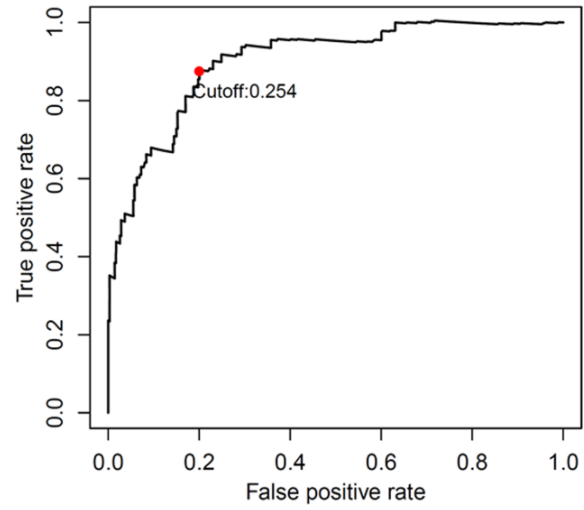
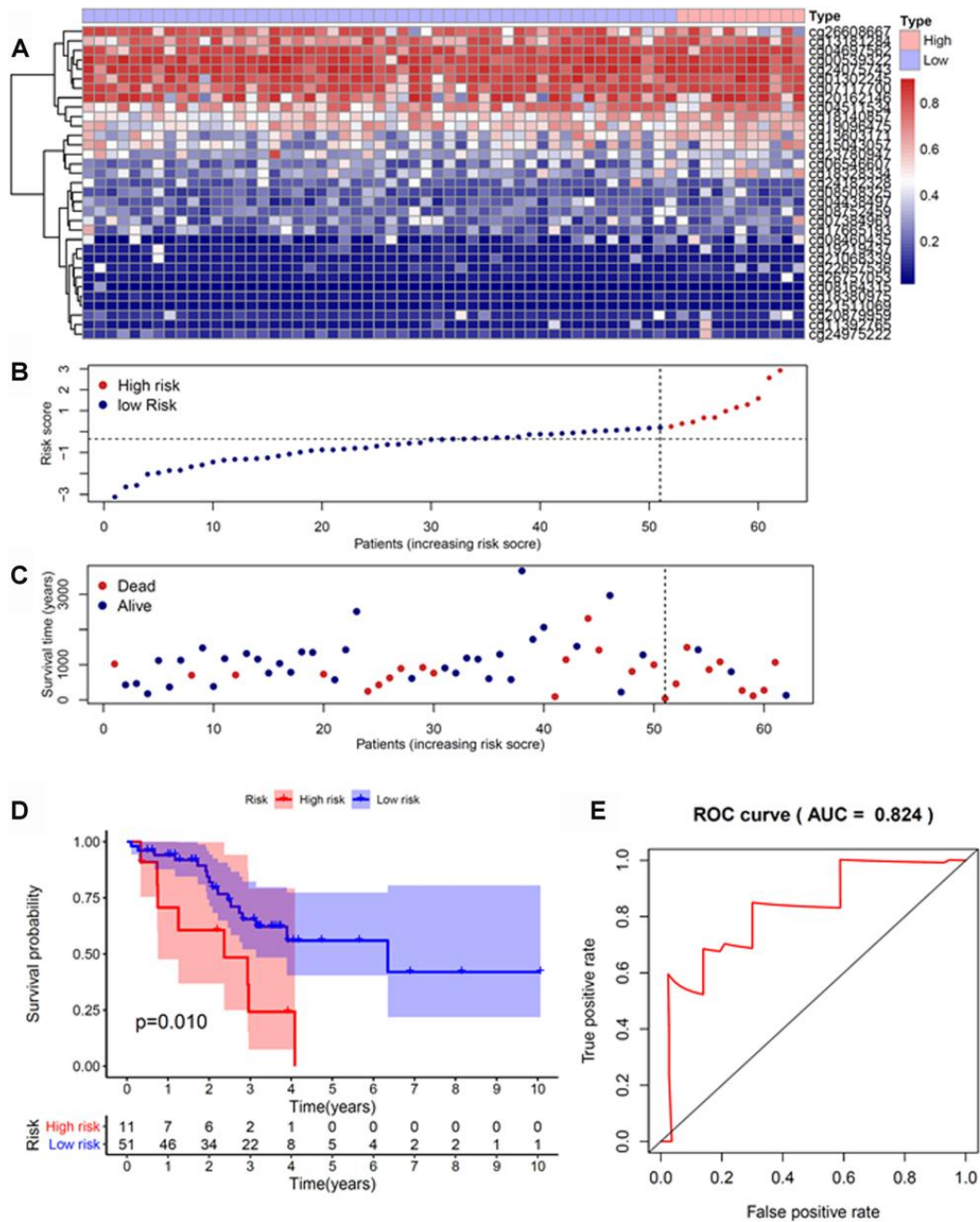


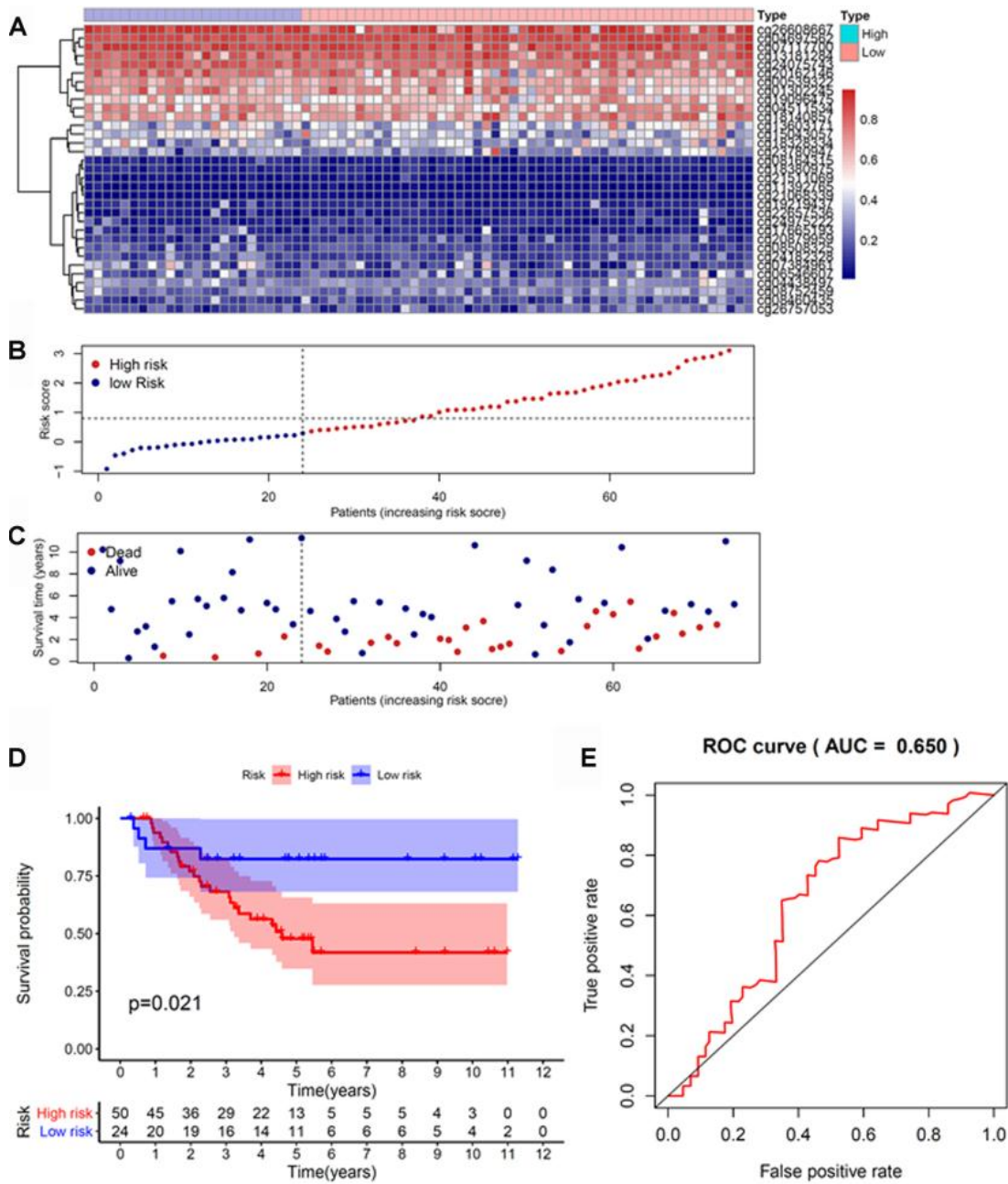
SUPPLEMENTARY FIGURES



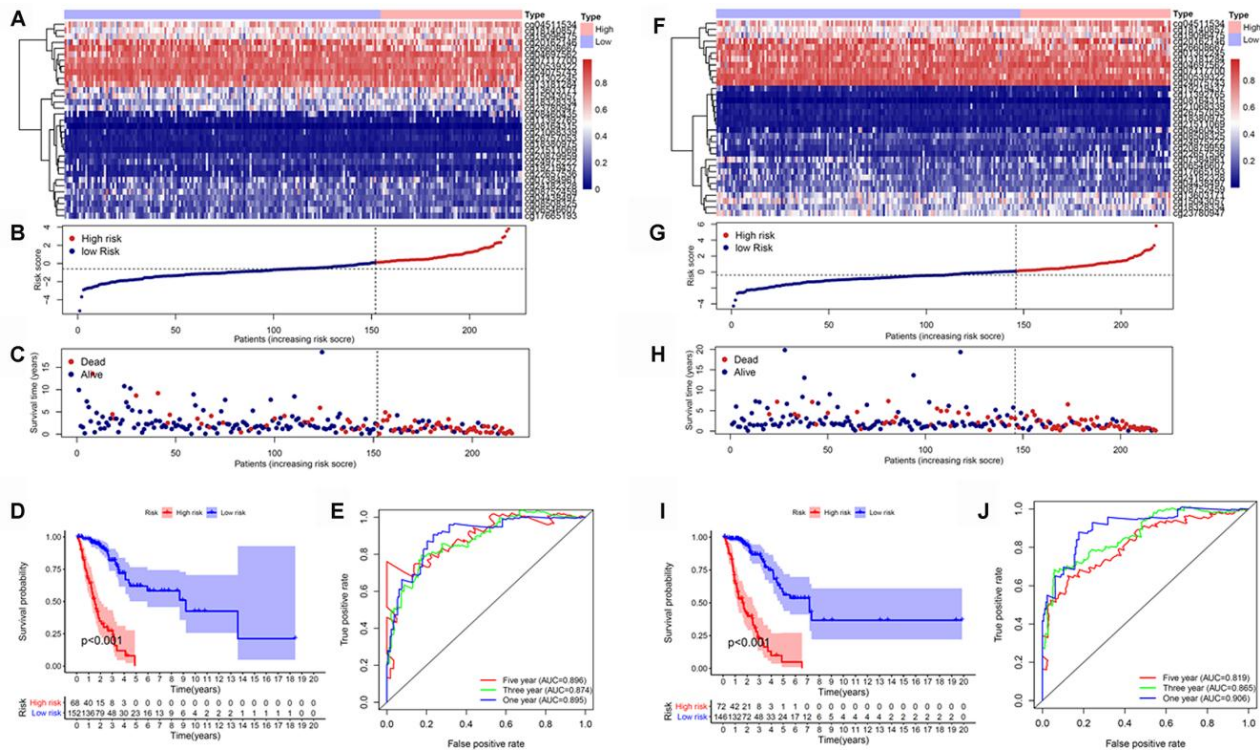
Supplementary Figure 1. Optimal cut-off value for the risk score.



Supplementary Figure 2. Validation of the prognostic methylation model for patients with LUAD using the HM27K dataset. (A) The clustering analysis heatmap of methylation profile in DNA methylation signature sites. (B) Distribution of the DNA methylation-based risk score. (C) Vital status of patients in the high- and low-risk groups. (D) Kaplan–Meier survival curves of the relative overall survival of patients in the high- and low-risk groups. (E) Accuracy of the prognostic model in predicting survival time by ROC curve analysis. LUAD, lung adenocarcinoma; HM27K, HumanMethylation 27K; ROC, receiver operating characteristic.



Supplementary Figure 3. Validation of the prognostic methylation model for patients with LUAD using the meta-GEO dataset. (A) The clustering analysis heatmap of methylation profile in DNA methylation signature sites. (B) The distribution of the DNA methylation-based risk score. (C) Vital status of patients in the high- and low-risk groups. (D) Kaplan–Meier survival curves of the relative overall survival of patients in high- and low-risk groups. (E) Accuracy of the prognostic model in predicting survival time by ROC curve analysis. LUAD, lung adenocarcinoma; GEO, Gene Expression Omnibus; ROC, receiver operating characteristic.



Supplementary Figure 4. Validation of the prognostic methylation model for patients with LUAD using TCGA internal validation. (A) The clustering analysis heatmap of methylation profile in the DNA methylation signature sites for the training set. (B) Distribution of the DNA methylation-based risk score for the training set. (C) Vital status of patients in the high- and low-risk groups for the training set. (D) Kaplan–Meier survival curves of the relative overall survival of patients in high- and low-risk groups for the training set. (E) Accuracy of the prognostic model in predicting survival time by ROC curve analysis for the training set. (F) The clustering analysis heatmap of methylation profile in DNA methylation signature sites for the testing set. (G) Distribution of the DNA methylation-based risk score for testing set. (H) Vital status of patients in the high- and low-risk groups for the testing set. (I) Kaplan–Meier survival curves of the relative overall survival of patients in the high- and low-risk groups for the testing set. (J) Accuracy of the prognostic model in predicting survival time by ROC curve analysis for the testing set. LUAD, lung adenocarcinoma; ROC, receiver operating characteristic; TCGA, The Cancer Genome Atlas.