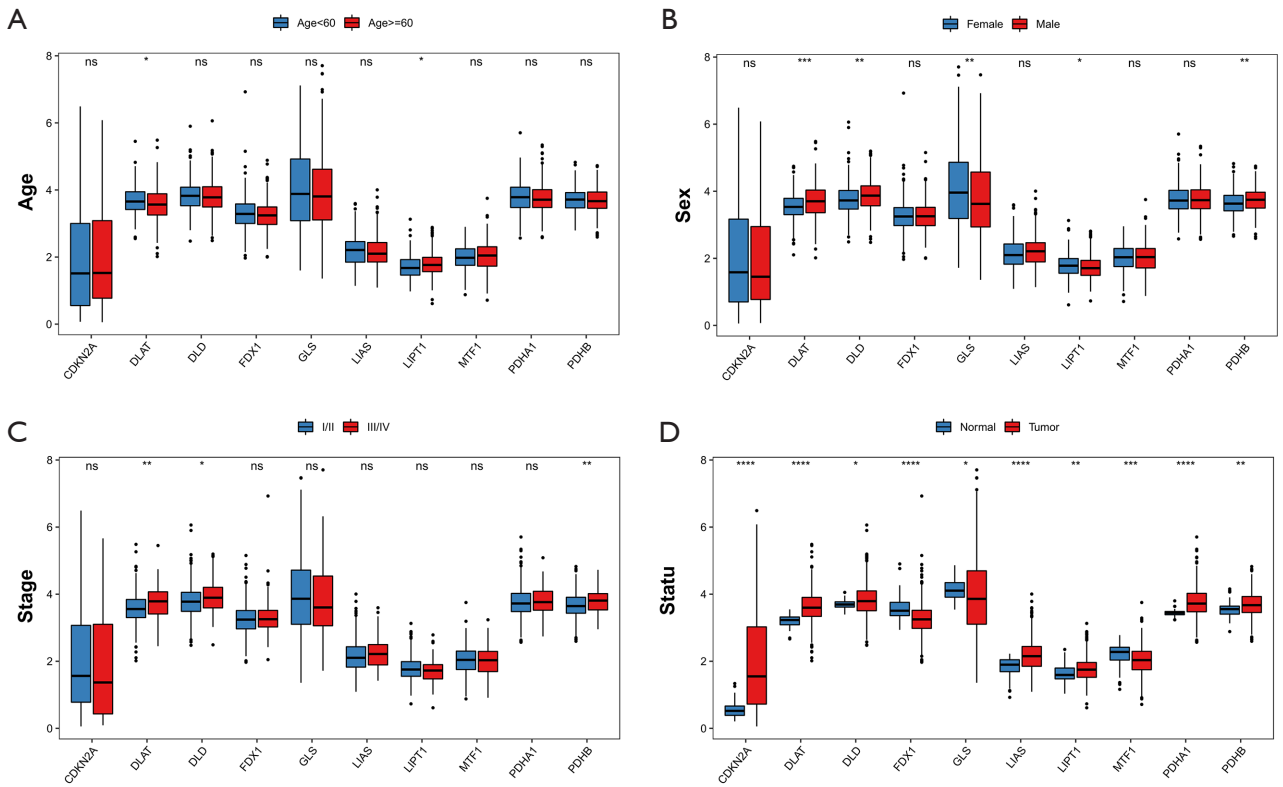

Figure S1 Association between the expression of 10 cuproptosis genes and clinical characteristics. The expression distribution of cuproptosis genes in different (A) age, (B) sex, (C) tumor stage, and (D) tumor status groups in TCGA-LUAD cohort. ns: not significant; *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001.

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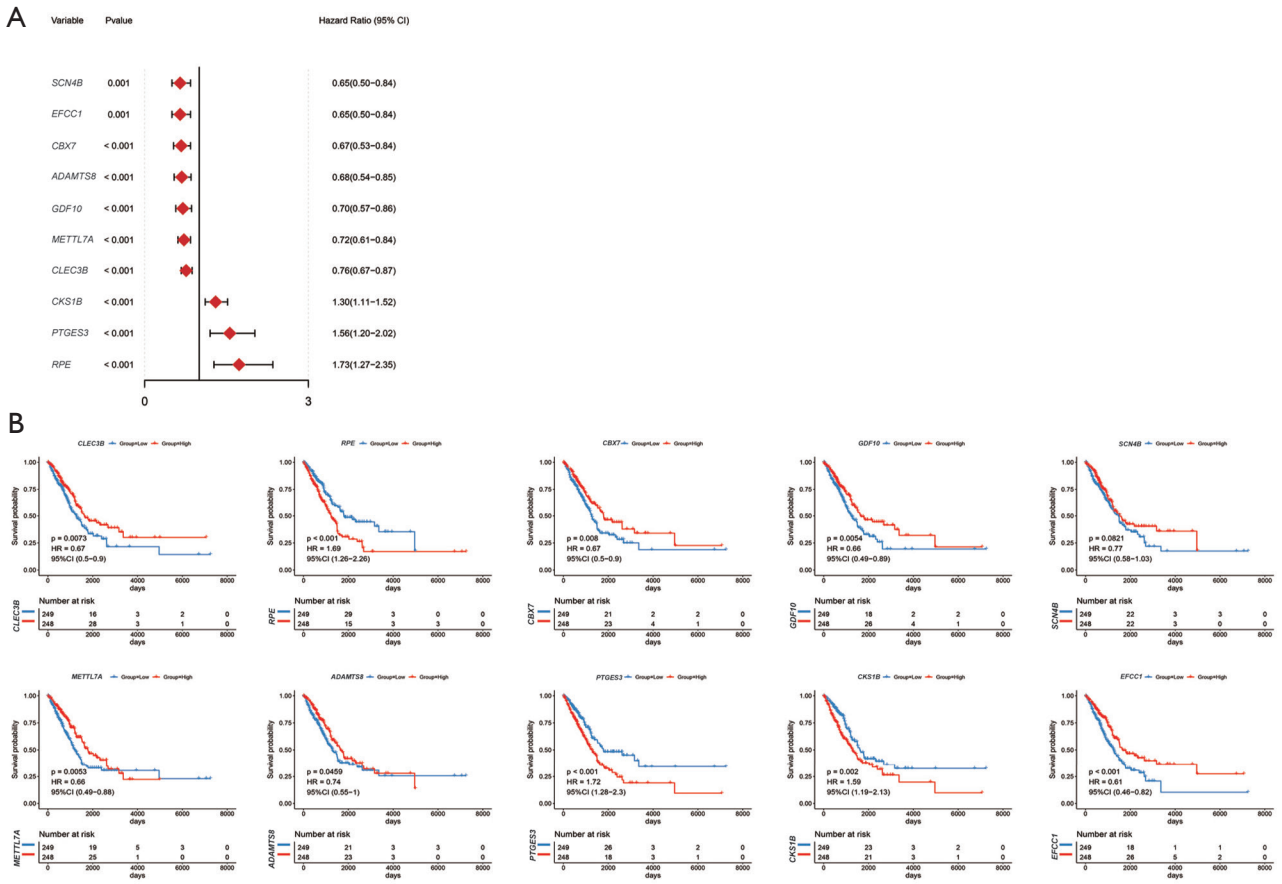

Figure S2 Identification of the prognosis-related genes. (A) The forest plot of the top 10 prognosis-related genes. (B) Survival curves for the high- and low-expression groups of the top 10 prognosis-related genes.

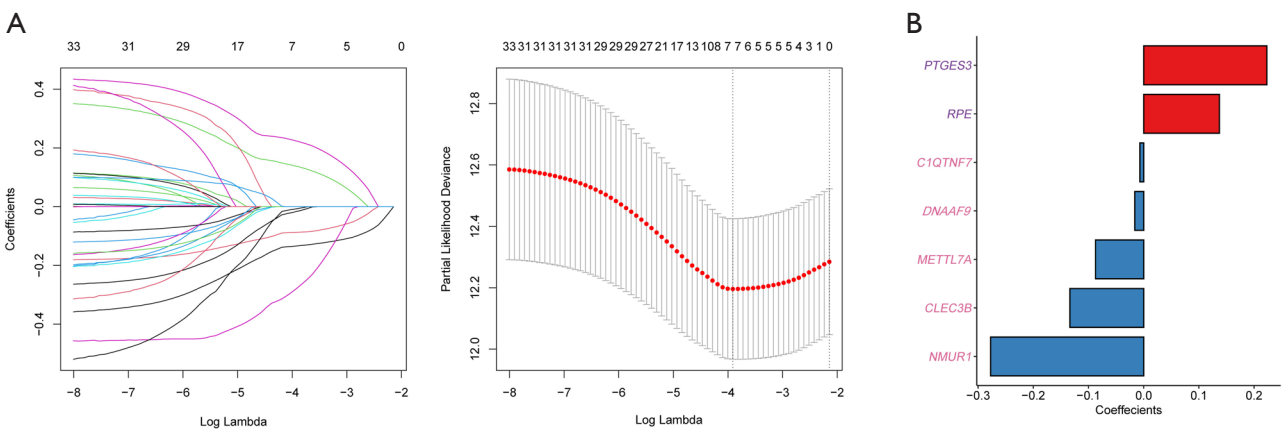

Figure S3 Establishment of the prognostic signature. (A) Selection of tuning parameter (λ) in the LASSO Cox regression using 10-fold cross-validation via minimum criteria (Each curve represents the change of each gene coefficient with the increase of penalty value. The larger the lambda, the more severely the linear model is punished.). (B) LASSO regression coefficients for the 7 prognostic genes. The color of the gene names indicated the key module they belong to.

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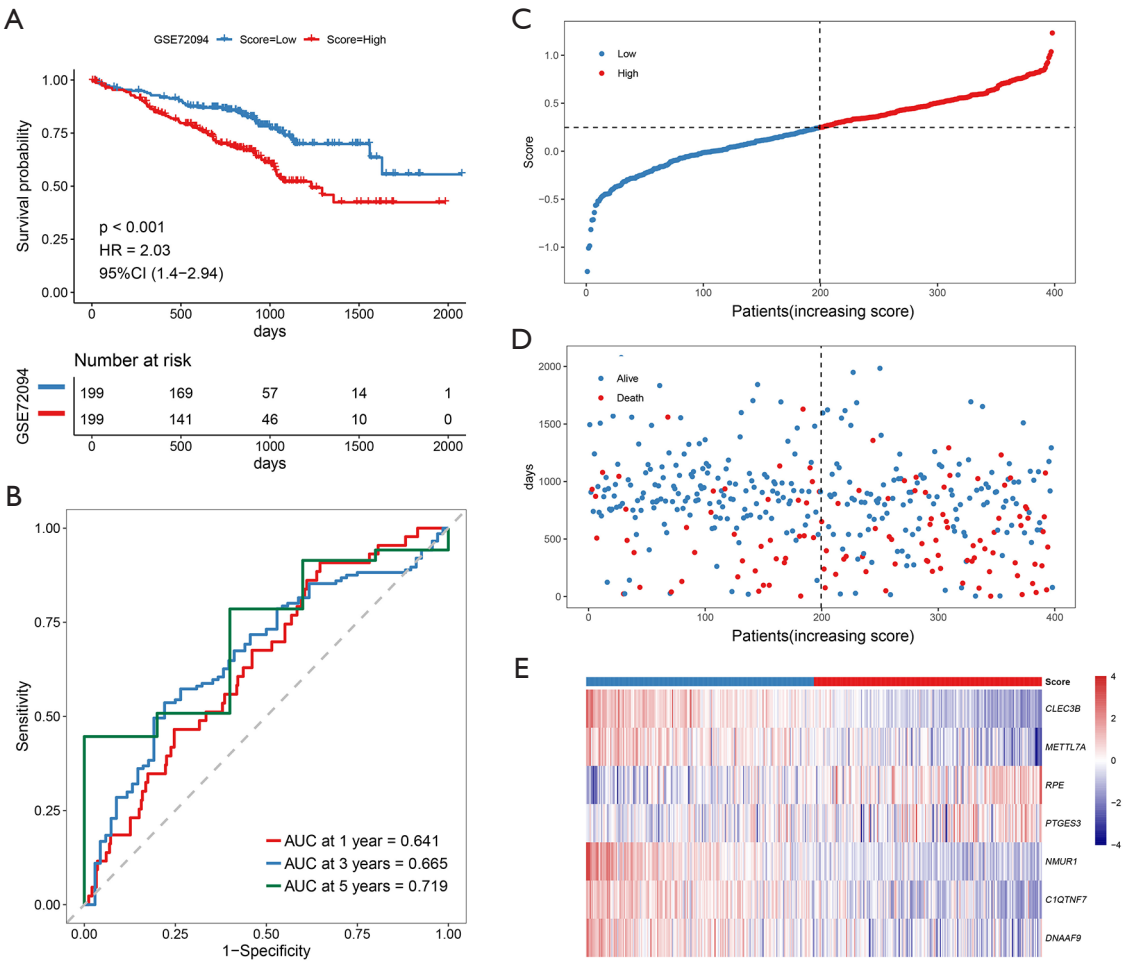

Figure S4 Validation of the prognostic risk model in GSE72094. (A) Kaplan-Meier curves for overall survival (OS) of the low-risk and high-risk groups. (B) Time-dependent ROC analysis of the prognostic signature. (C) Distribution of risk scores for patients in the GSE72094 data set. (D) Survival status of each sample in the validation set. (E) Heatmap of mRNA expression of 7 prognostic genes.

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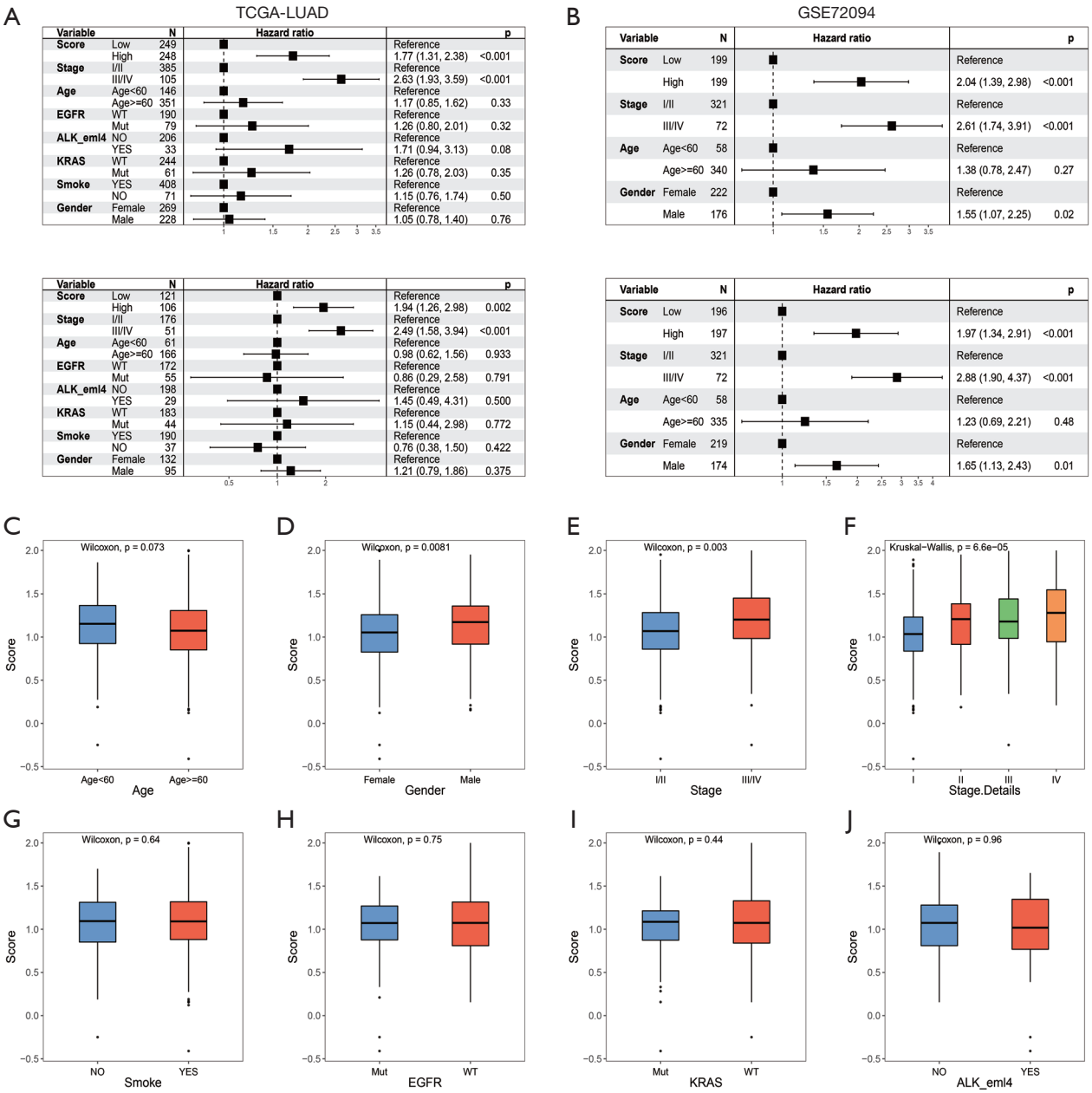

Figure S5 Independence of the risk score. (A) Univariate and multivariate Cox regression analyses of risk score and clinical factors in TCGA-LUAD cohort and (B) in the GSE72094 data set. (C-J) Distribution of risk scores in the different clinical characteristic groups.

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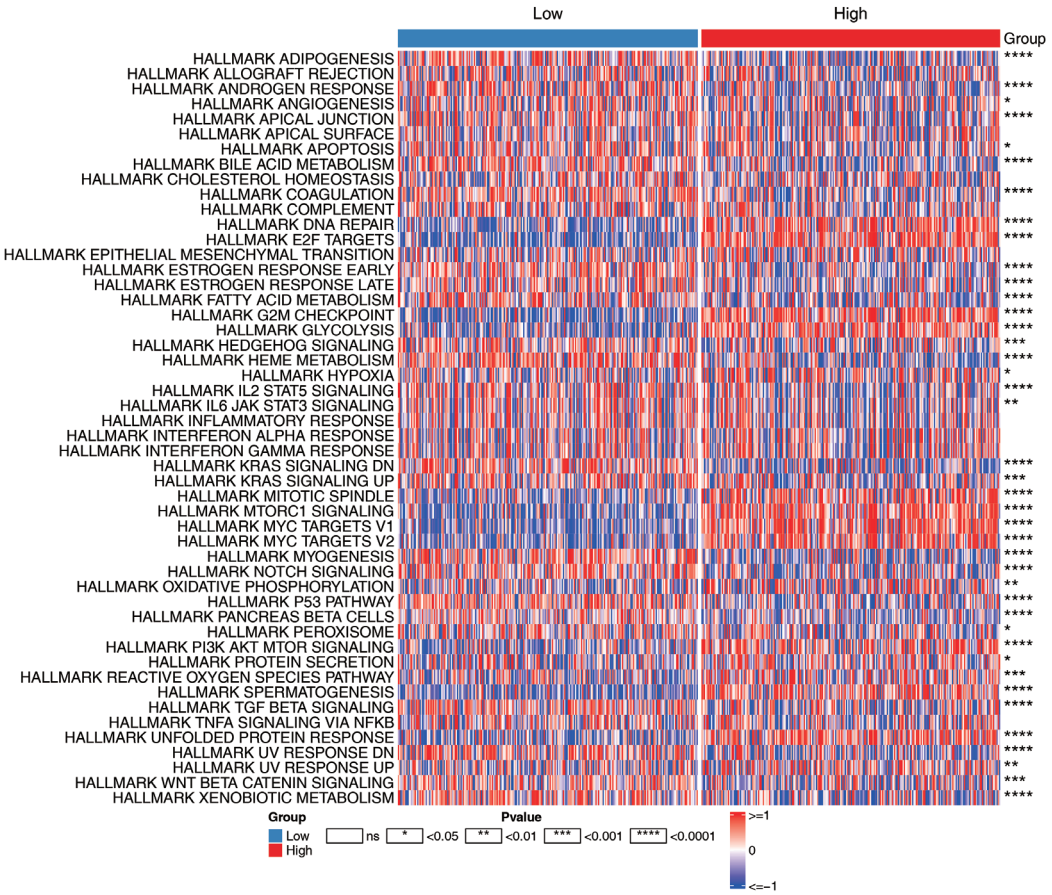

Figure S6 Heatmap of GSVA enrichment analysis. Enrichment score of hallmark gene sets between the high-risk and low-risk groups in TCGA-LUAD. ns: not significant; *, P<0.05; **, P<0.01; ***, P<0.001; ****, P<0.0001.

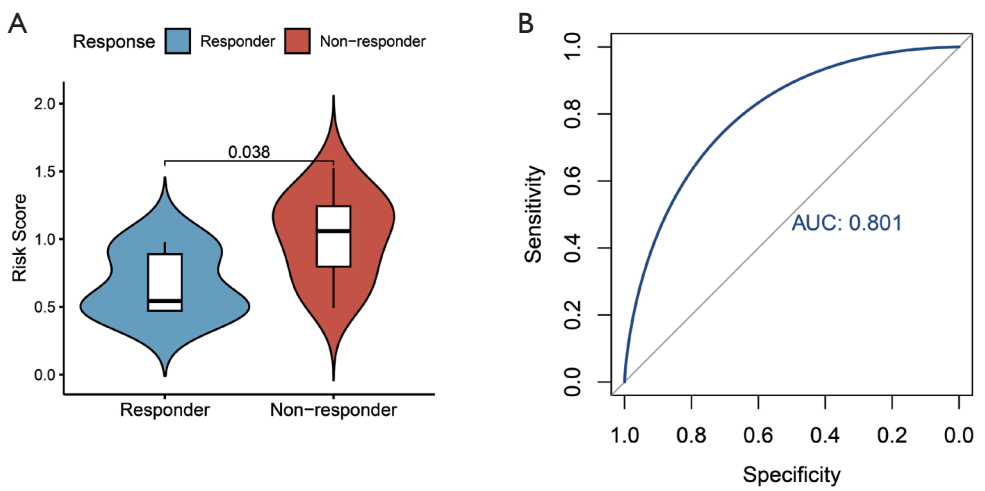

Figure S7 The risk score predicted immunotherapy response. (A) Comparison of the risk score between responders and non-responders. Wilcoxon rank-sum test was used. (B) AUC indicated the predictive potential of risk score.

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