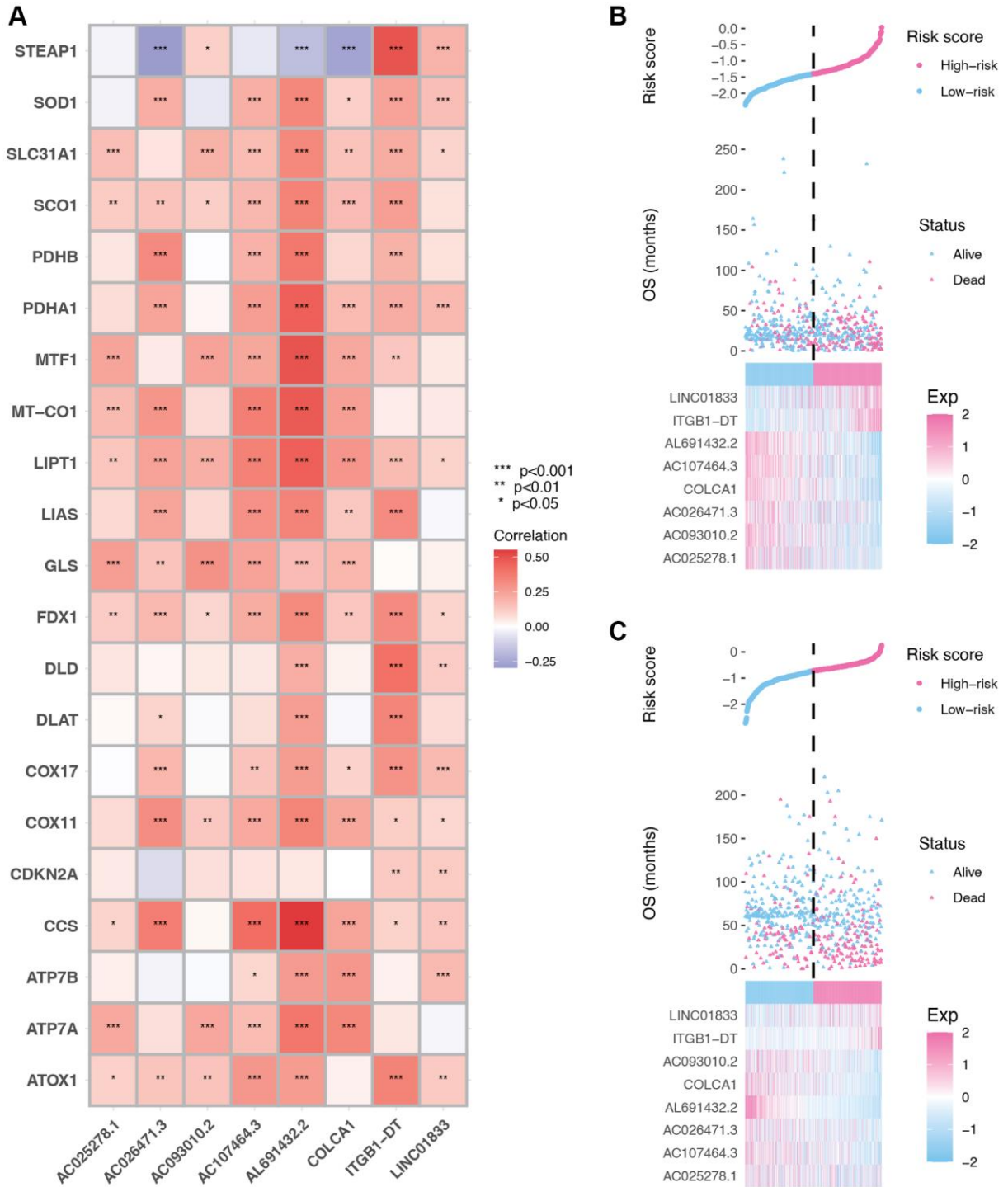


SUPPLEMENTARY FIGURES



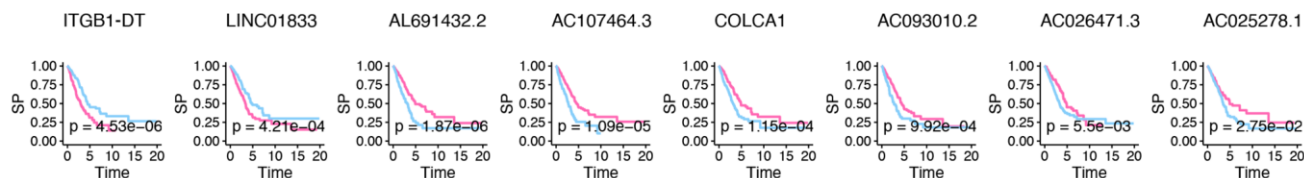
Supplementary Figure 1. The profile of the signature lncRNAs. (A) The heatmap shows the signature's eight lncRNAs' correlations with 21 copper homeostasis/cuproptosis-regulated genes. (B, C) The distributions of the risk score, survival status, survival time, and eight lncRNAs' levels for LUAD cases in the training cohort and validation cohort.

A

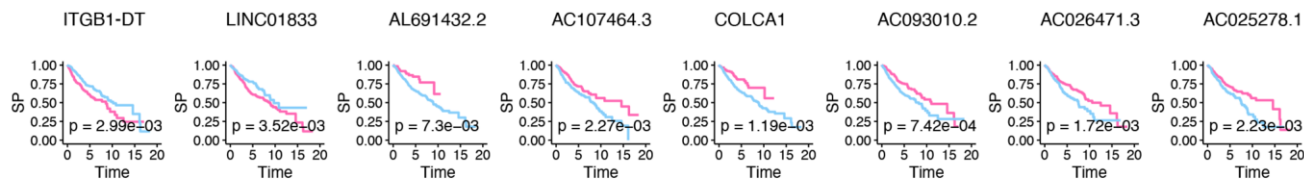
Kaplan–Meier estimator

Level — High — Low

Training cohort

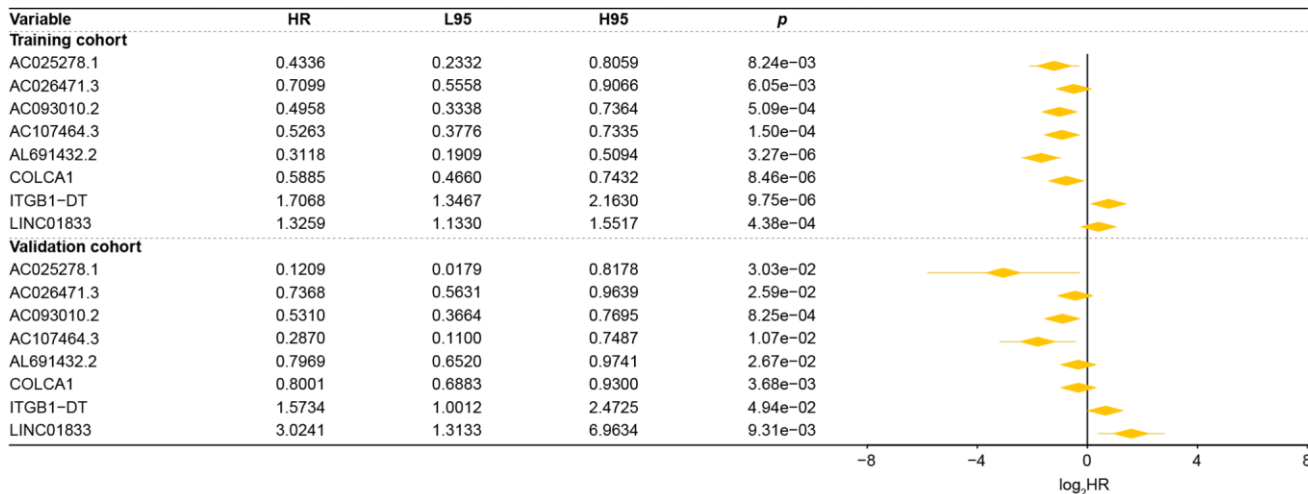


Validation cohort



B

Univariate Cox regression



Supplementary Figure 2. The Kaplan-Meier analysis (A) and univariate Cox models (B) established in the studied cohorts testing the predictive ability of each of the eight signature lncRNAs. Patients were grouped based on their median risk score. The Kaplan-Meier method compared the survival difference between high and low-risk patients, and the log-rank test examined the significance.