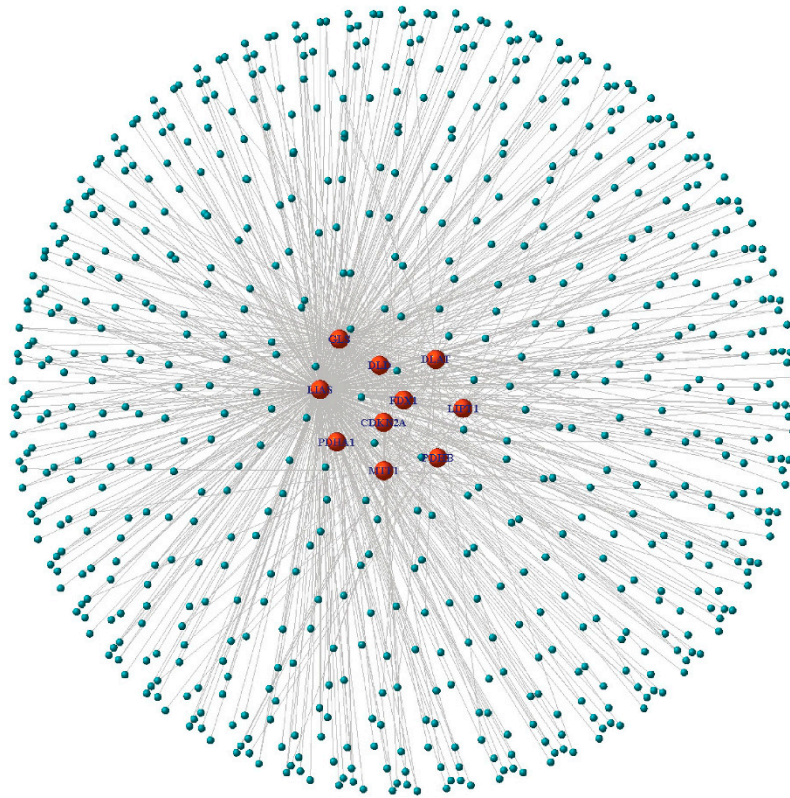
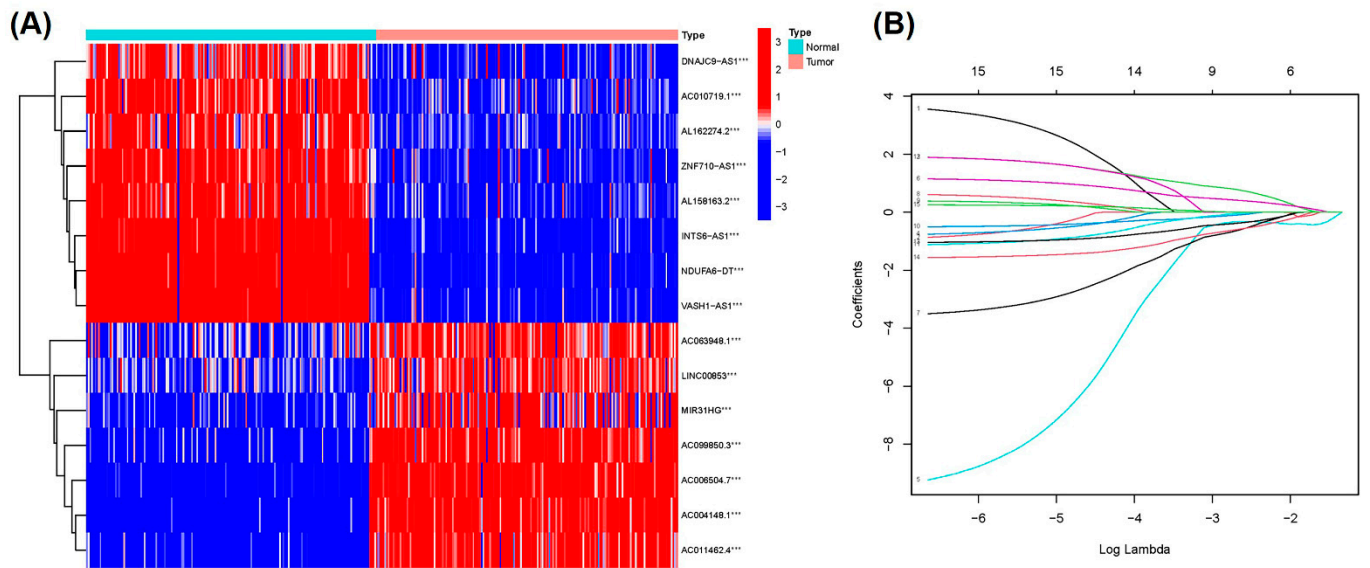


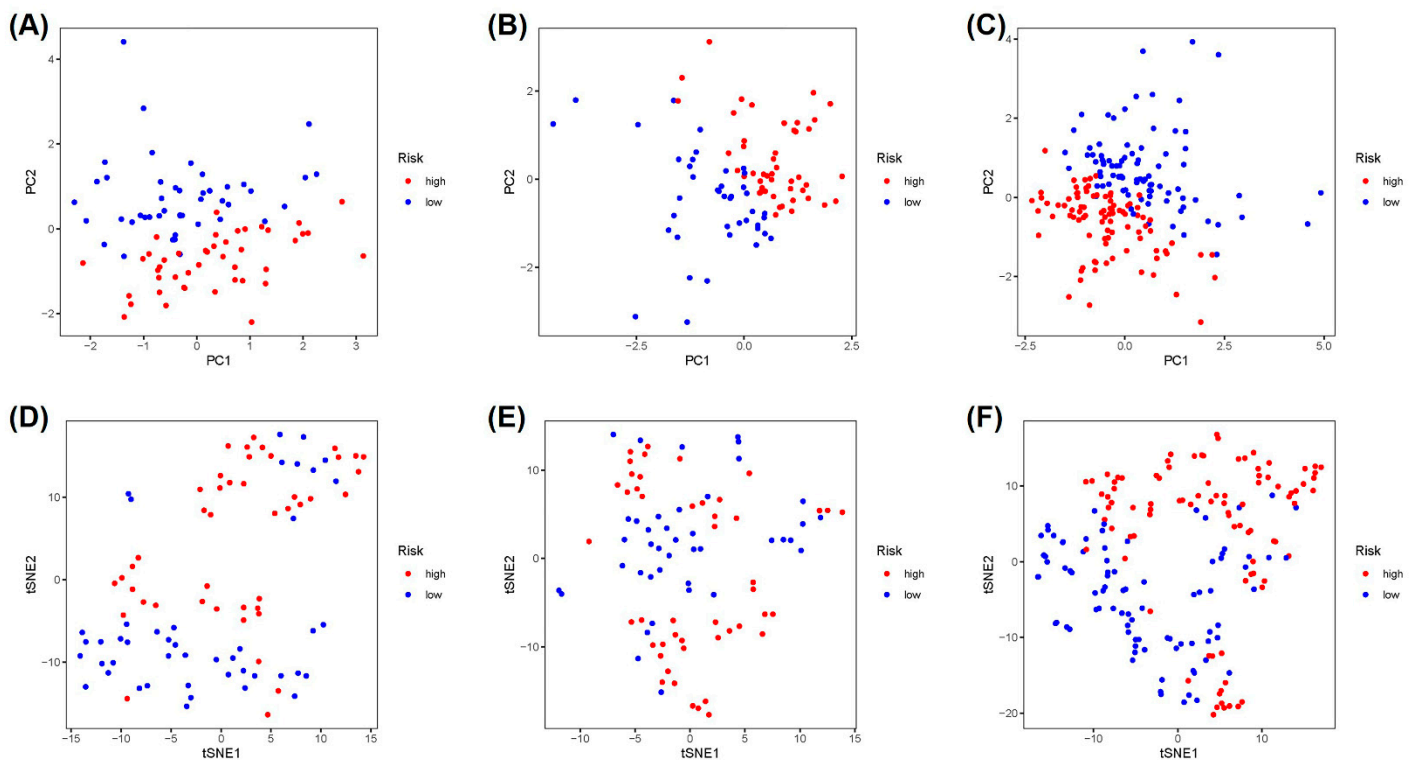
● lncRNA ● Cuproptosis-related gene



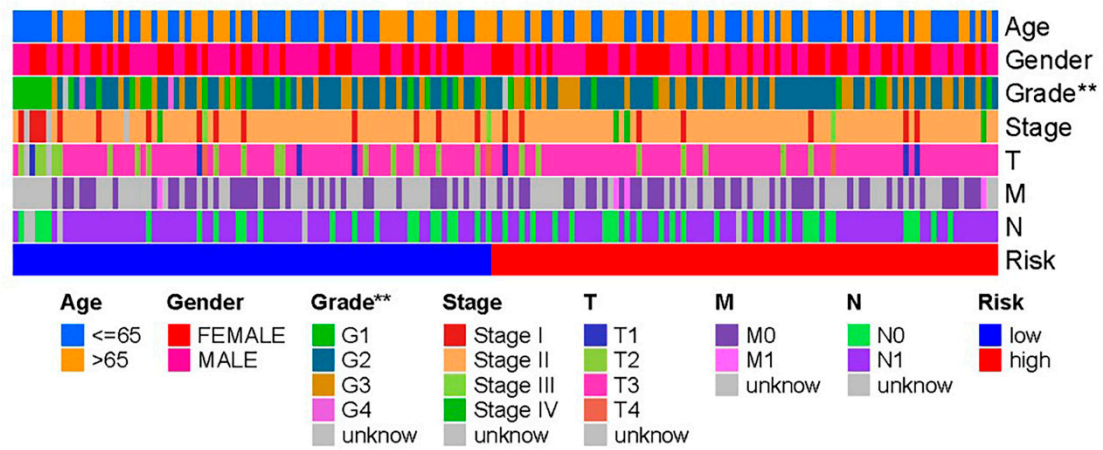
**Figure S1.** The network between cuproptosis-related genes and lncRNAs (correlation coefficients  $> 0.4$  and  $p < 0.001$ ).



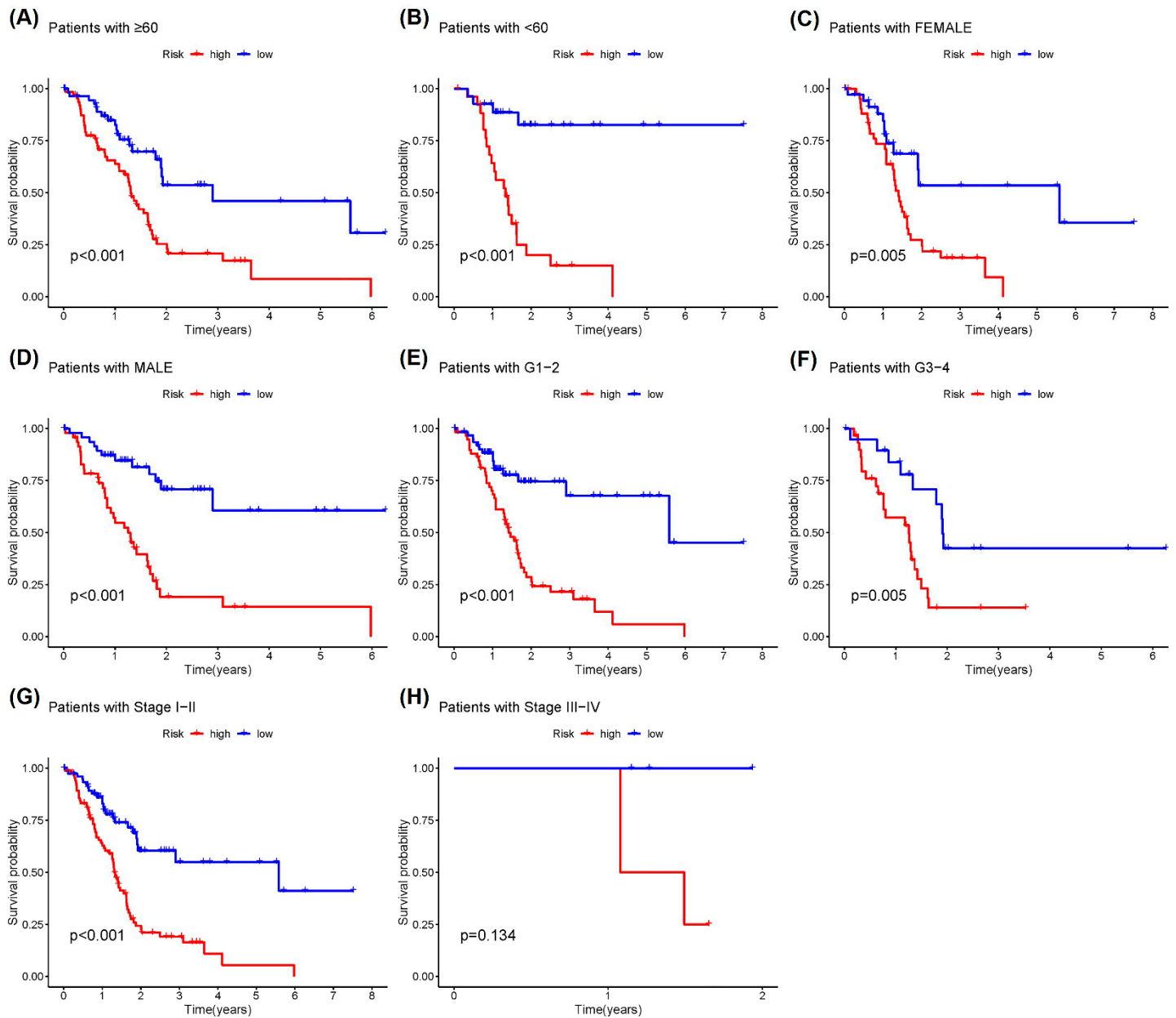
**Figure S2.** (A) The heatmap of the 15 differentially expressed cuproptosis-related lncRNA with prognostic value. (B) Distribution of LASSO coefficients. \*\*\*  $p < 0.001$ .



**Figure S3.** PCA and t-SNE scatter plot for the expression of 4 cuproptosis-related lncRNAs distinguishing the low- and high-risk cohorts. (A and D) the train cohort, (B and E) test cohort, and (C and F) entire cohort.

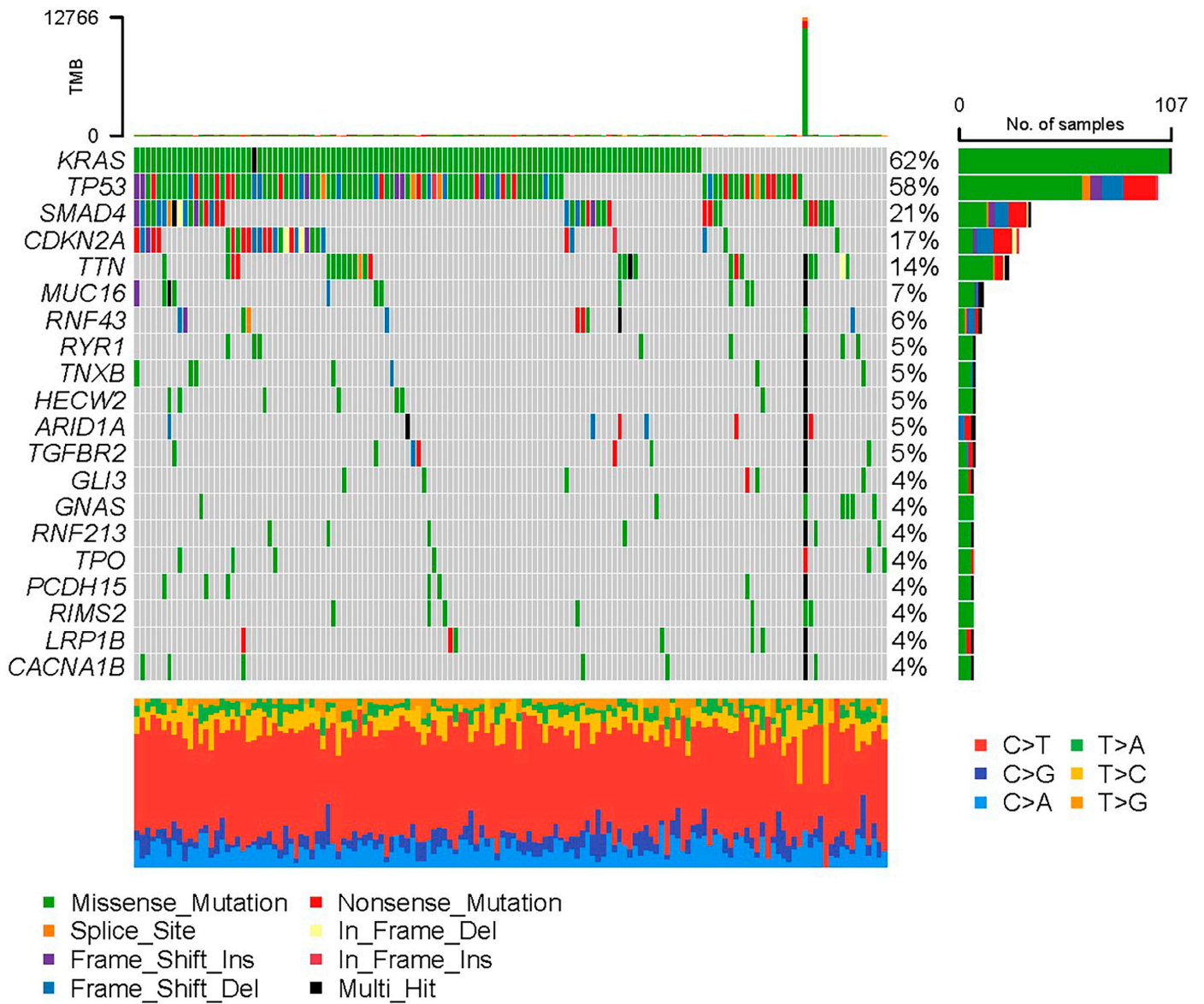


**Figure S4.** Strip chart showing relationships between clinical characteristics and cuproptosis-related lncRNA signature score.\*\*  $p < 0.01$ .



**Figure S5.** The subgroup analysis of overall survival of PAAD patients in the low- and high-risk groups by **(A and B)** age, **(C and D)** sex, **(E and F)** tumor grade, and **(G and H)** clinical stage.

Altered in 142 (82.08%) of 173 samples.



**Figure S6.** Waterfall plots of the 20 most frequently mutated genes in PAAD patients.



