

Table S1 Cuproptosis-related genes

Genes

NFE2L2

NLRP3

ATP7B

ATP7A

SLC31A1

FDX1

LIAS

LIPT1

LIPT2

DLD

DLAT

PDHA1

PDHB

MTF1

GLS

CDKN2A

DBT

GCSH

DLST

Table S2 Demographic and clinical characteristics between the training and testing cohort

Characteristics	Total	Train	Test	P-value*
Age, years				0.1464
<=65	237 (47.4%)	128 (51.2%)	109 (43.6%)	
>65	253 (50.6%)	119 (47.6%)	134 (53.6%)	
unknow	10 (2%)	3 (1.2%)	7 (2.8%)	
Gender				0.2434
Female	270 (54%)	128 (51.2%)	142 (56.8%)	
Male	230 (46%)	122 (48.8%)	108 (43.2%)	
Stage				0.2969
Stage I	268 (53.6%)	124 (49.6%)	144 (57.6%)	
Stage II	119 (23.8%)	66 (26.4%)	53 (21.2%)	
Stage III	80 (16%)	43 (17.2%)	37 (14.8%)	
Stage IV	25 (5%)	11 (4.4%)	14 (5.6%)	
unknow	8 (1.6%)	6 (2.4%)	2 (0.8%)	

*Chi-square test.

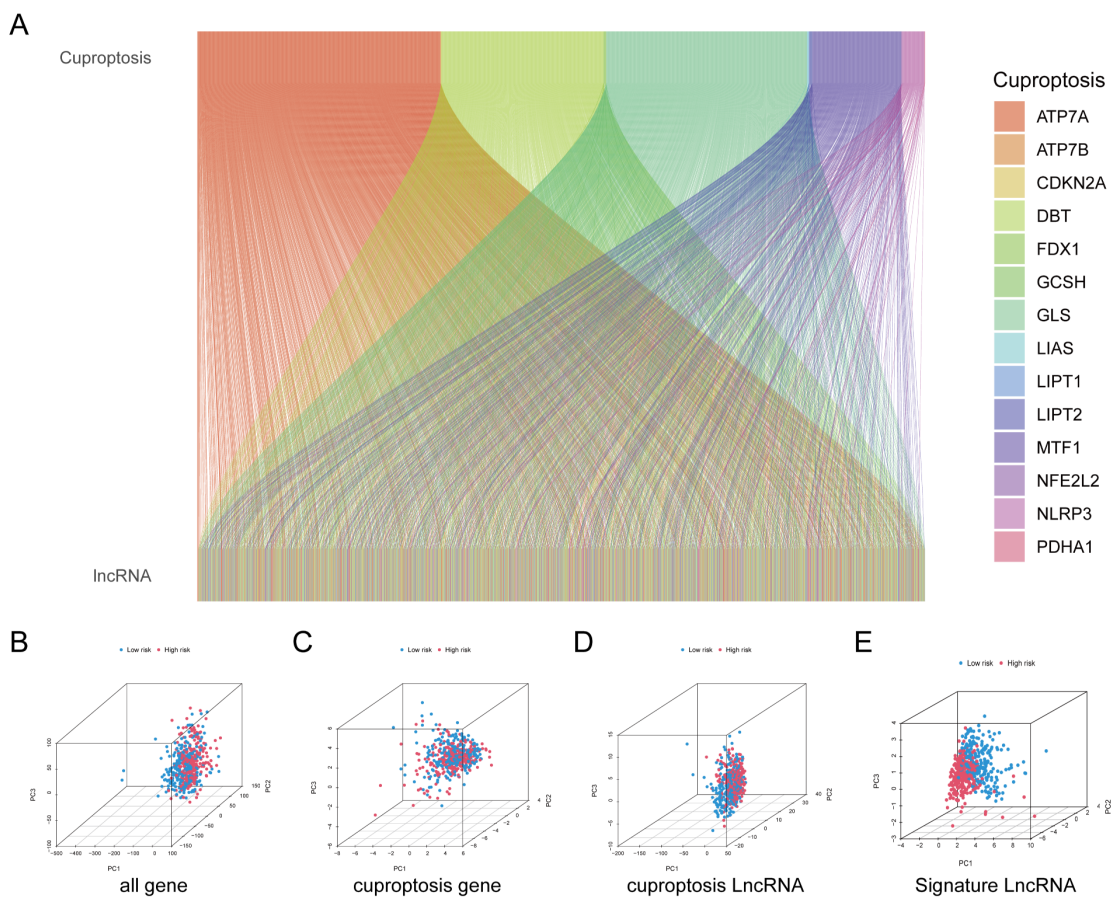


Figure S1 Identification of cuproptosis-related lncRNAs and principal component analysis (PCA) in the entire LUAD cohort. (A) Sankey diagram for cuproptosis-related genes and lncRNAs. (B-E) PCA analysis based on (B) all gene, (C) cuproptosis-related gene, (D) cuproptosis-related lncRNAs and (E) signature lncRNAs, respectively.

Table S3 The cuproptosis-related lncRNAs risk signature

LncRNAs	coefficient
AC090541.1	0.425683724
LINC02390	-1.102861115
NIFK-AS1	-0.766522002
AC026355.2	-0.40311251
AC107021.2	1.174579099
MIR34AHG	-0.944282562
LINC01215	-0.560092802

Table S4 Risk score for patients in the training cohort

Table with 10 columns: Id, AC090541.1, LINC02390, NIFK-AS1, AC026355.2, AC107021.2, MIR34A4HG, LINC01215, Risk score, Risk group*. Rows list various patient IDs like TCGA-MP-A4T6, TCGA-49-4510, etc., with corresponding values for each feature and a risk group classification.

* The training cohort patients were divided into high-risk and low-risk groups using the median risk score as the cut-off.

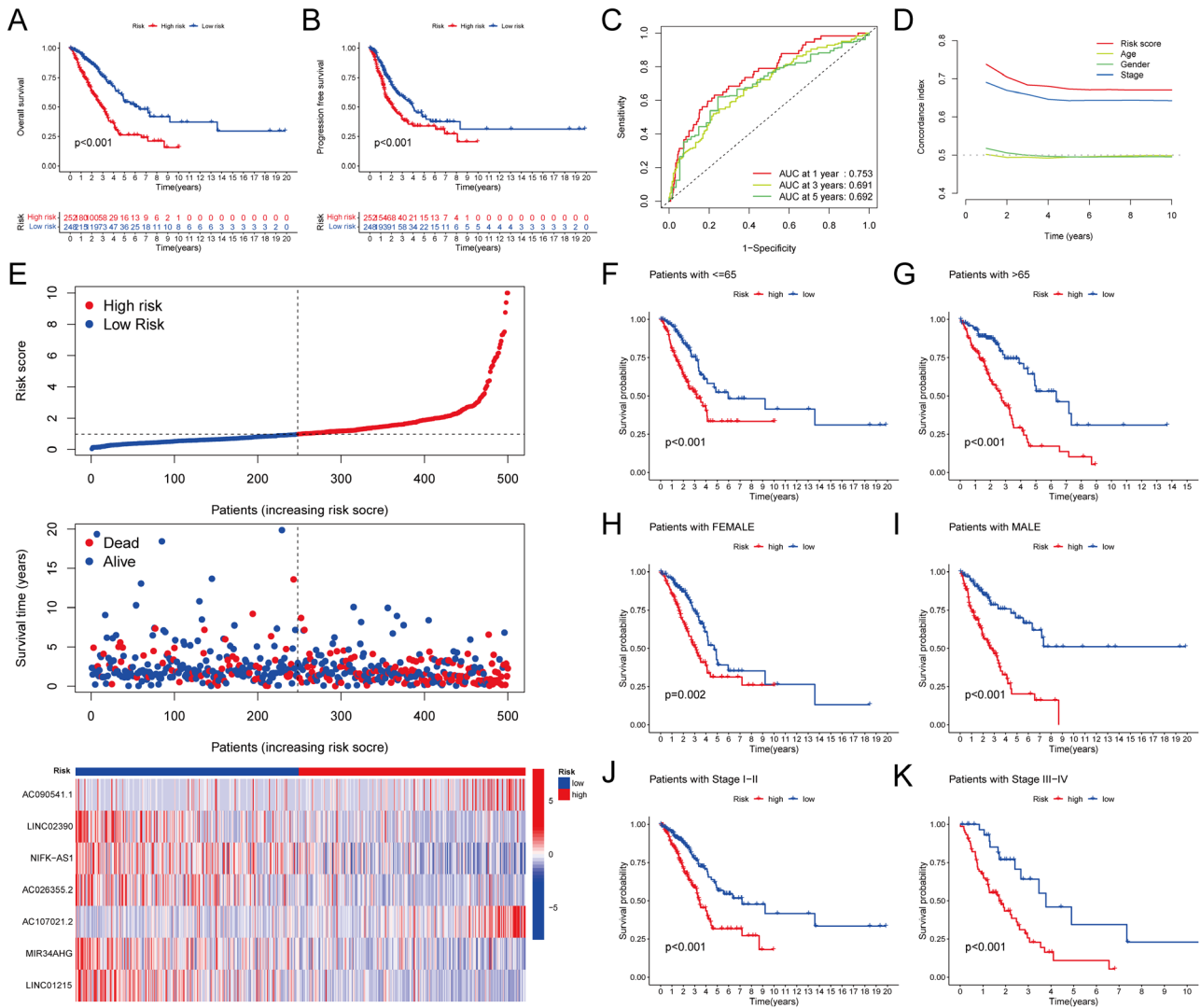


Figure S2 Survival analysis of the CLPS in the entire LUAD cohort. Kaplan-Meier curves of (A) OS and (B) PFS in the entire cohort. (C) ROC curves for the risk signature at 1, 3, and 5 years in the entire cohort. (D) The C-index of the CLPS risk score and other clinical characteristics in the entire cohort. (E) Survival state (the middle section) of the patients sorted according to the risk scores (the top section) and the differences in the CLPS lncRNAs between the high and low-risk groups (the bottom section) in the entire cohort. (F-K) Kaplan-Meier curves of OS in distinct subgroups with different clinical characteristics: (F) age ≤ 65 , (G) age > 65 , (H) female, (I) male, (J) Stage I-II, and (K) Stage III-IV. CLPS, cuproptosis-related lncRNAs prognostic signature; LUAD, lung adenocarcinoma; OS, overall survival; PFS, progression-free survival; ROC, receiver operating characteristic; lncRNAs, long non-coding RNAs; AUC, area under the curve.

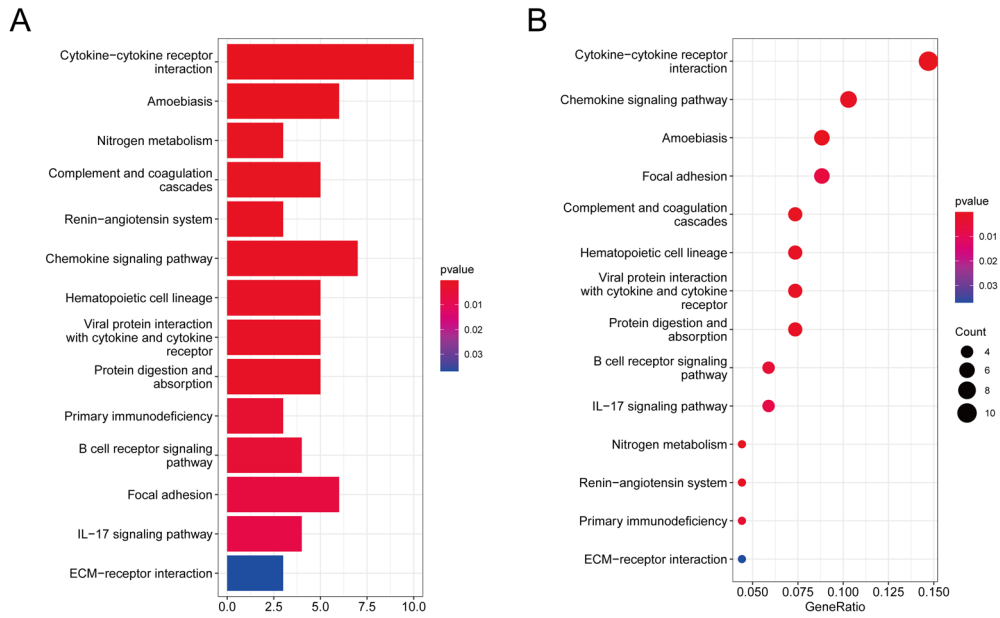


Figure S3 Functional annotation for DEGS between the high-risk and low-risk groups using KEGG pathway analysis. (A) Bar plot and (B) bubble plot showing the significantly enriched KEGG pathways. Bubble color representing the P value, and the bubble size representing the number of genes in the relevant pathway.

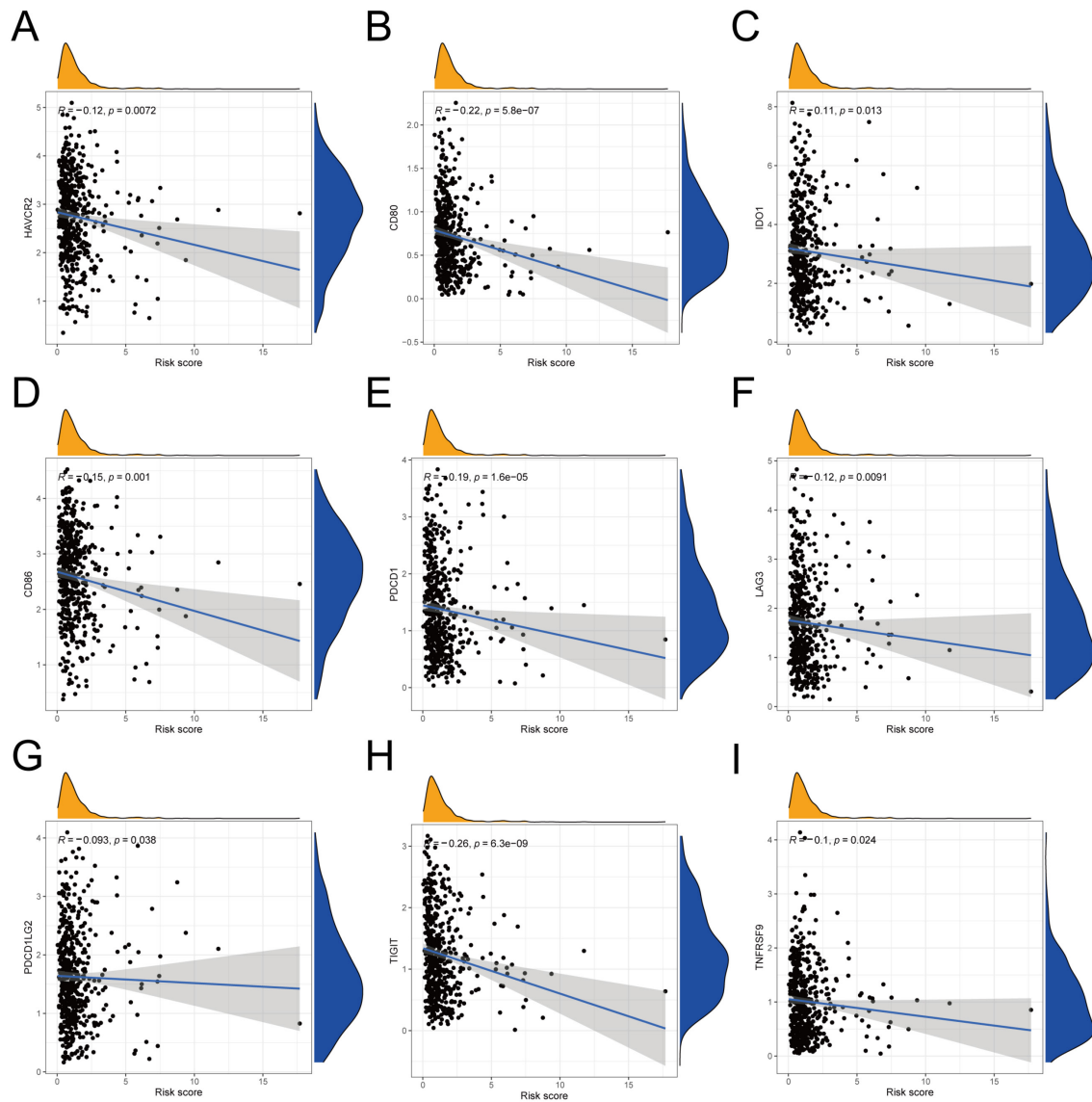


Figure S4 Correlation between the risk score and immune-checkpoint related gene expression: (A) HAVCR2, (B) CD80, (C) IDO1, (D) CD86, (E) PDCD1, (F) LAG3, (G) PDCD1LG2, (H) TIGIT, (I) TNFRSF9.