

Supplementary Materials:

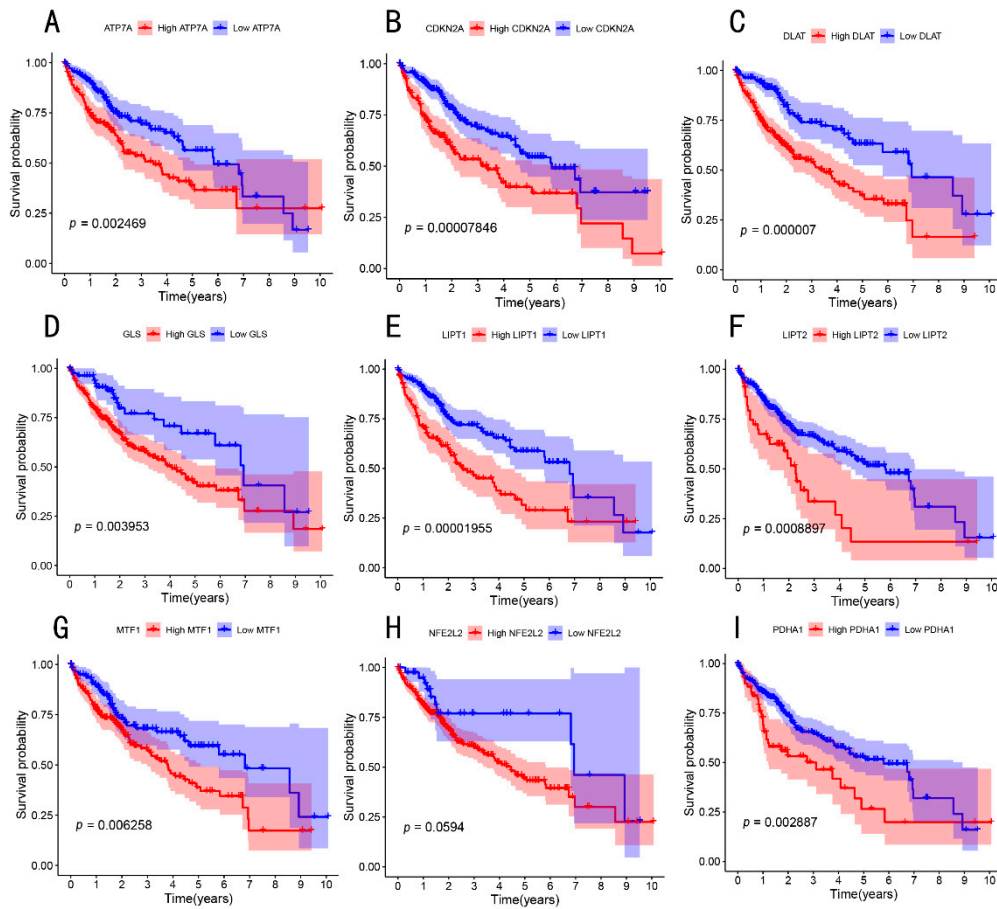


Figure S1. Survival analysis of nine cuproptosis-related prognostic genes ATP7A(A), CDKN2A(B), DLAT(C), GLS(D), LIPT1(E), LIPT2(F), MTF1(G), NFE2L2(H), PDHA1(I), obtained by univariate Cox regression analysis. The patients with high expression of ATP7A, CDKN2A, DLAT, GLS, LIPT1, LIPT2, MTF1 or PDHA1 had lower OS ($P < 0.05$).

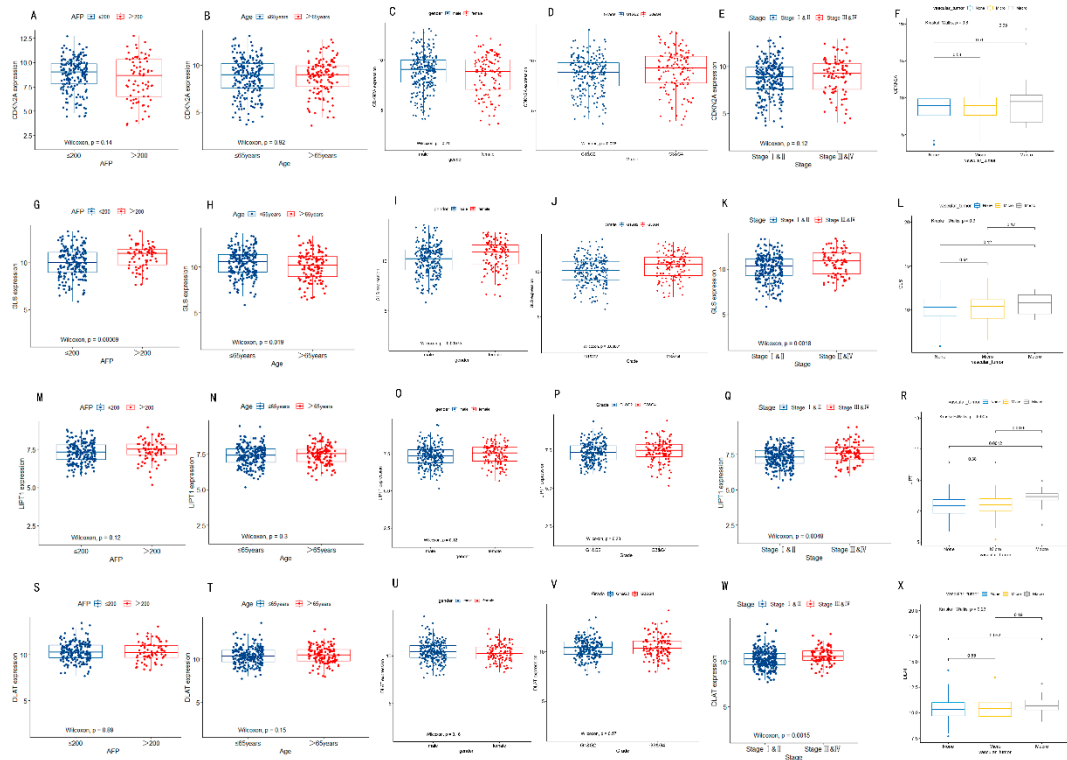


Figure S2. The relationship between clinicopathological characteristics and four genes in TCGA cohort. CDKN2A (A-F) 、GLS (G-L) 、LITP1 (M-R) 、DLAT (S-X) .

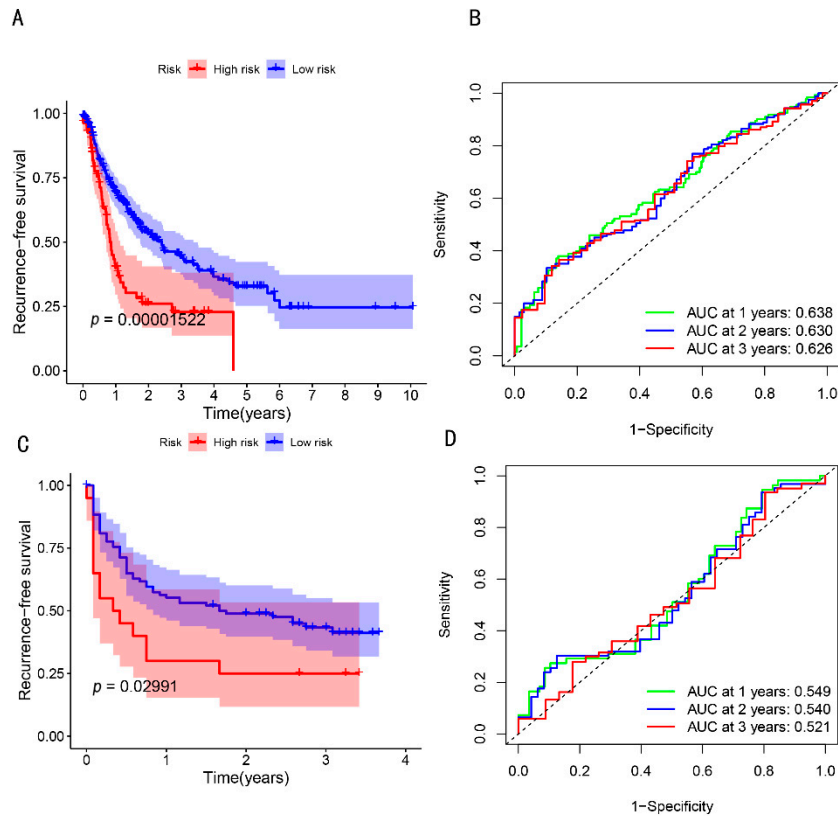


Figure S3. Four-gene signature model predicts recurrence-free survival in TCGA cohort (A) and in-house cohort data(C). Time-dependent ROC curves (B) and (D) of risk score prognostic performance.

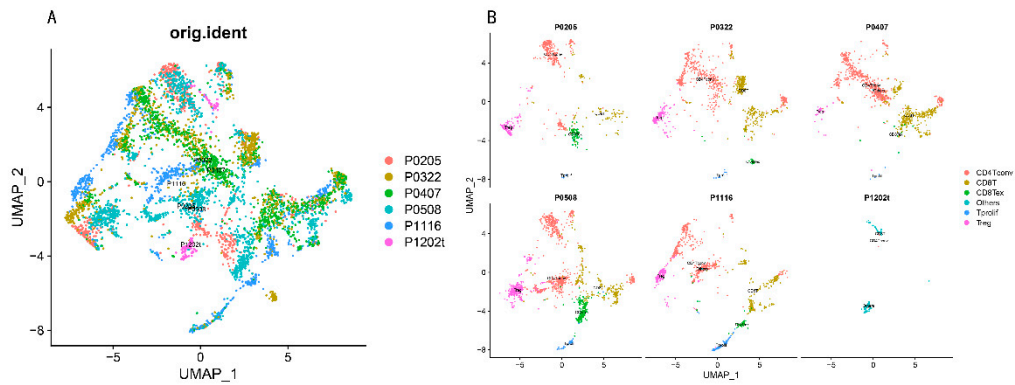


Figure S4. (A) UMAP plot showing immune cell distribution from 6 samples based on scRNA-seq. (B) UMAP plot showing the distribution of the six cell types of each sample for 6 samples