

Figure S1 Flow chart of this study. CIRC, cuproptosis- and immune-related gene; TCGA, The Cancer Genome Atlas; HCC, hepatocellular carcinoma; CIRGs, cuproptosis- and immune-related genes; ICGC, International Cancer Genome Consortium; GEO, Gene Expression Omnibus.

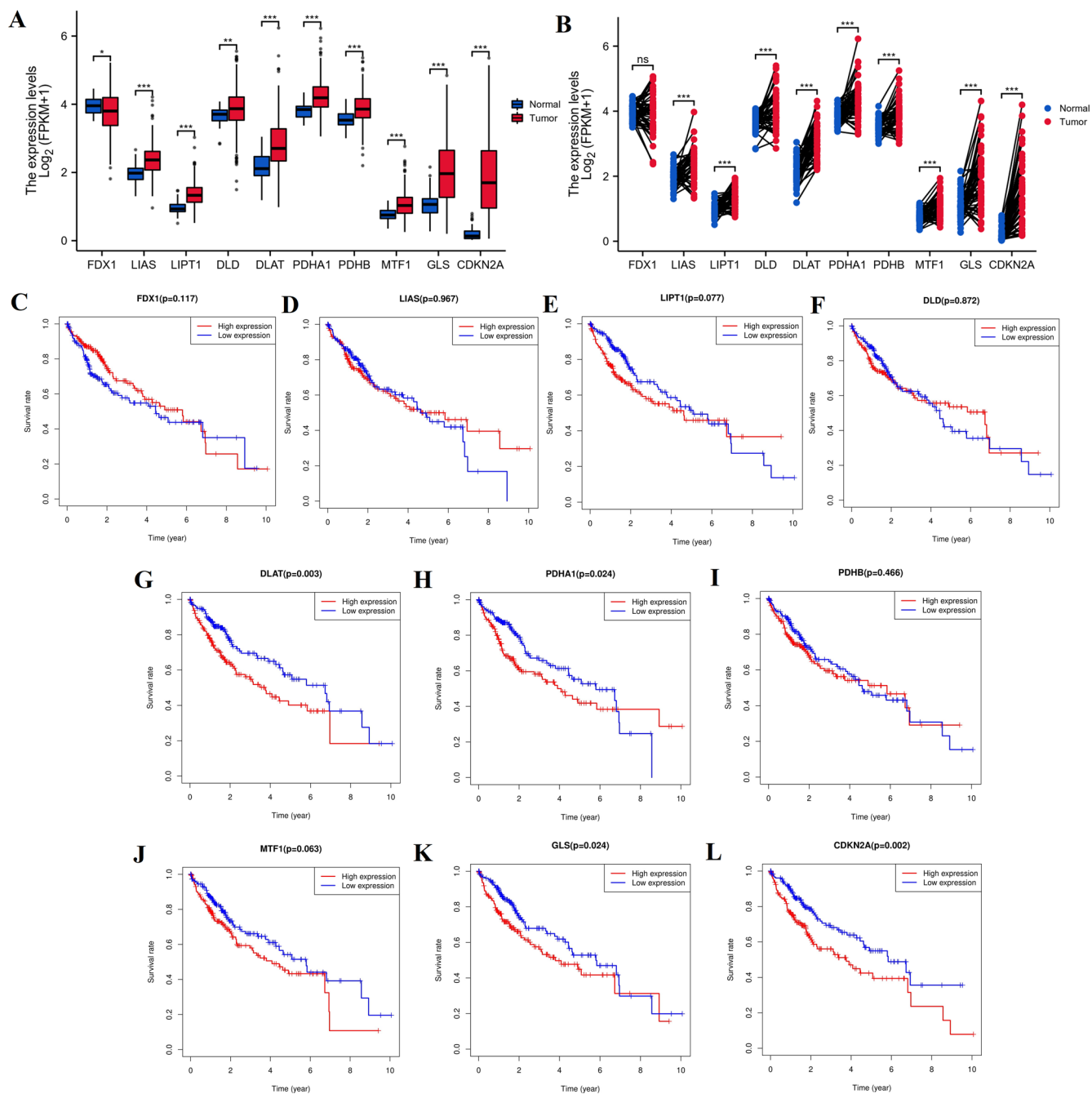


Figure S2 Expression of ten CRGs in HCC tissues. (A) Differential expression profiles of ten CRGs in HCC and normal tissues. (B) Differential expression profiles of ten CRGs in HCC and corresponding paracancerous normal tissues. (C-L) Prognostic analyses of ten CRGs in HCC samples. *, P<0.05; **, P<0.01; ***, P<0.001; ns, P>0.05. CRGs, cuproptosis-related genes; HCC, hepatocellular carcinoma.

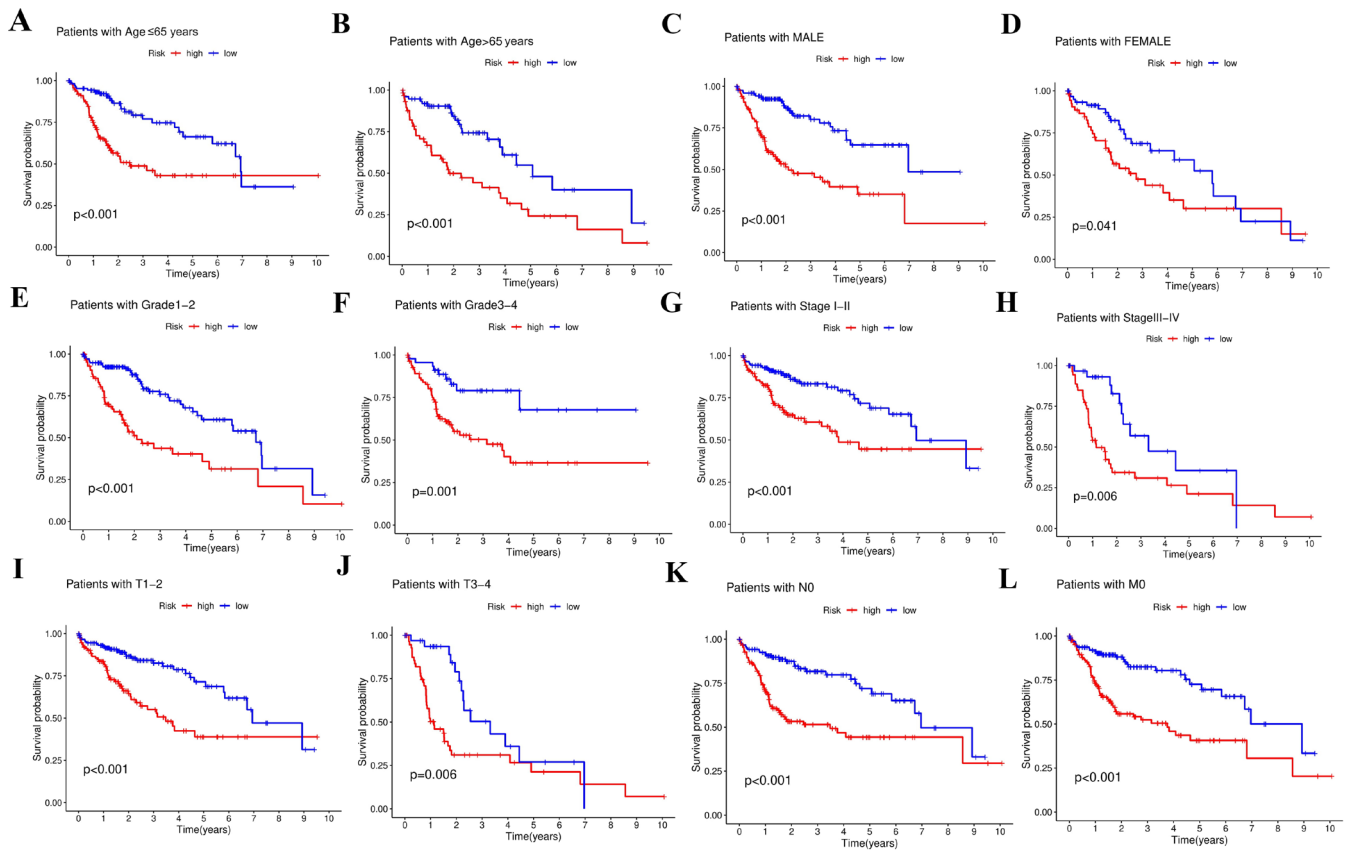


Figure S3 Prognostic analysis of HCC patients with different risk scores in different clinical subgroups. (A-L) K-M survival curves of the different risk cohorts in various clinical subgroups. HCC, Hepatocellular carcinoma; K-M, Kaplan-Meier.

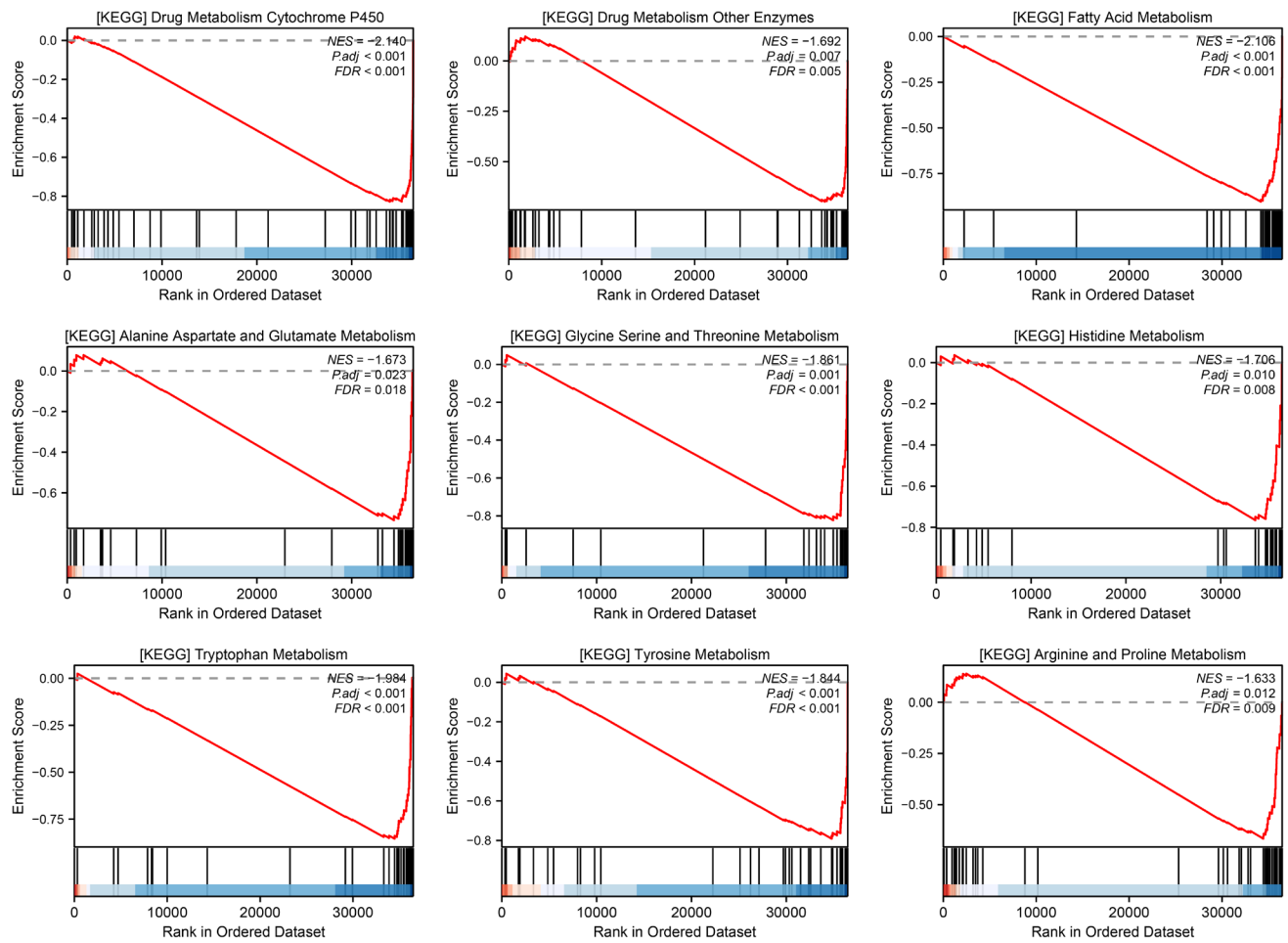


Figure S4 Metabolism-related GSEA pathways in HCC. GSEA, gene set enrichment analysis; HCC, hepatocellular carcinoma.