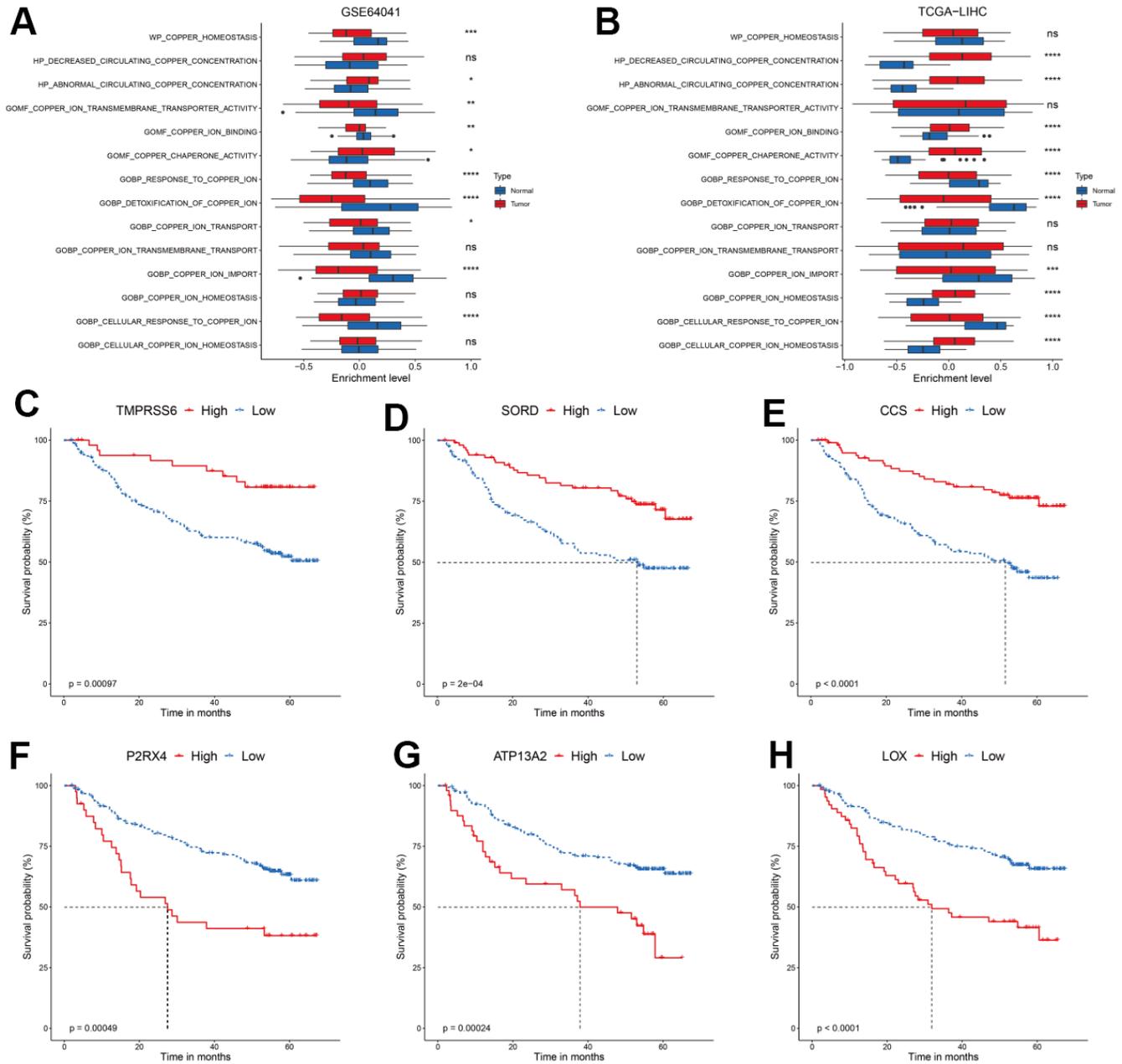
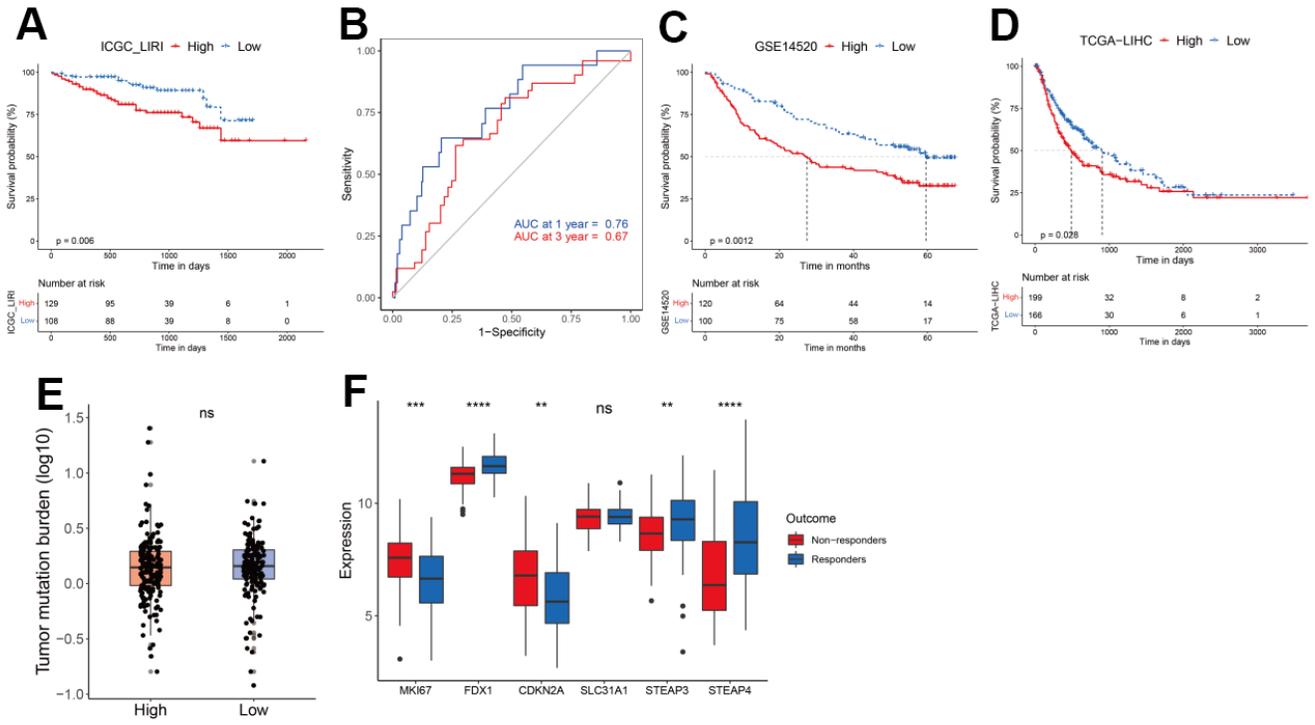


SUPPLEMENTARY FIGURES



Supplementary Figure 1. Copper metabolism was aberrantly expressed in HCC and might affect prognosis of HCC patients. (A, B) The box plot showing the enrichment level of 14 copper metabolism in tumor and corresponding normal tissues from GSE64041 (A) and TCGA-LIHC (B) dataset. (C–H) Prognosis analyses of HCC patients stratified by the expression of TMPRSS6 (C), SORD (D), CCS (E), P2RX4 (F), ATP13A2 (G) and LOX (H). P-values were shown as *p < 0.05, **p < 0.01, ***p < 0.001, and ****p < 0.0001.



Supplementary Figure 2. Prognosis and TMB analyses in CMscore stratified HCC subgroups. (A) The prognostic significance of CMscore in the ICGC-LIRI dataset. The Kaplan-Meier method was used for prognosis analysis. (B) Time-dependent ROC analyses of the CMscore regarding the OS and survival status in the ICGC-LIRI dataset. (C, D) PFS analyses of HCC patients with high and low CMscore in the GSE14520 (C) and TCGA-LIHC (D) cohorts. (E) Box and dot plot showing the TMB of HCC patients from high- and low-CMscore subgroups. Wilcoxon test was used for data analyses. (F) The boxplot showing the expression of MKI67, cuproptosis-related genes, and copper ion related genes between responders and non-responders to TACE.