

Supplemental Figures

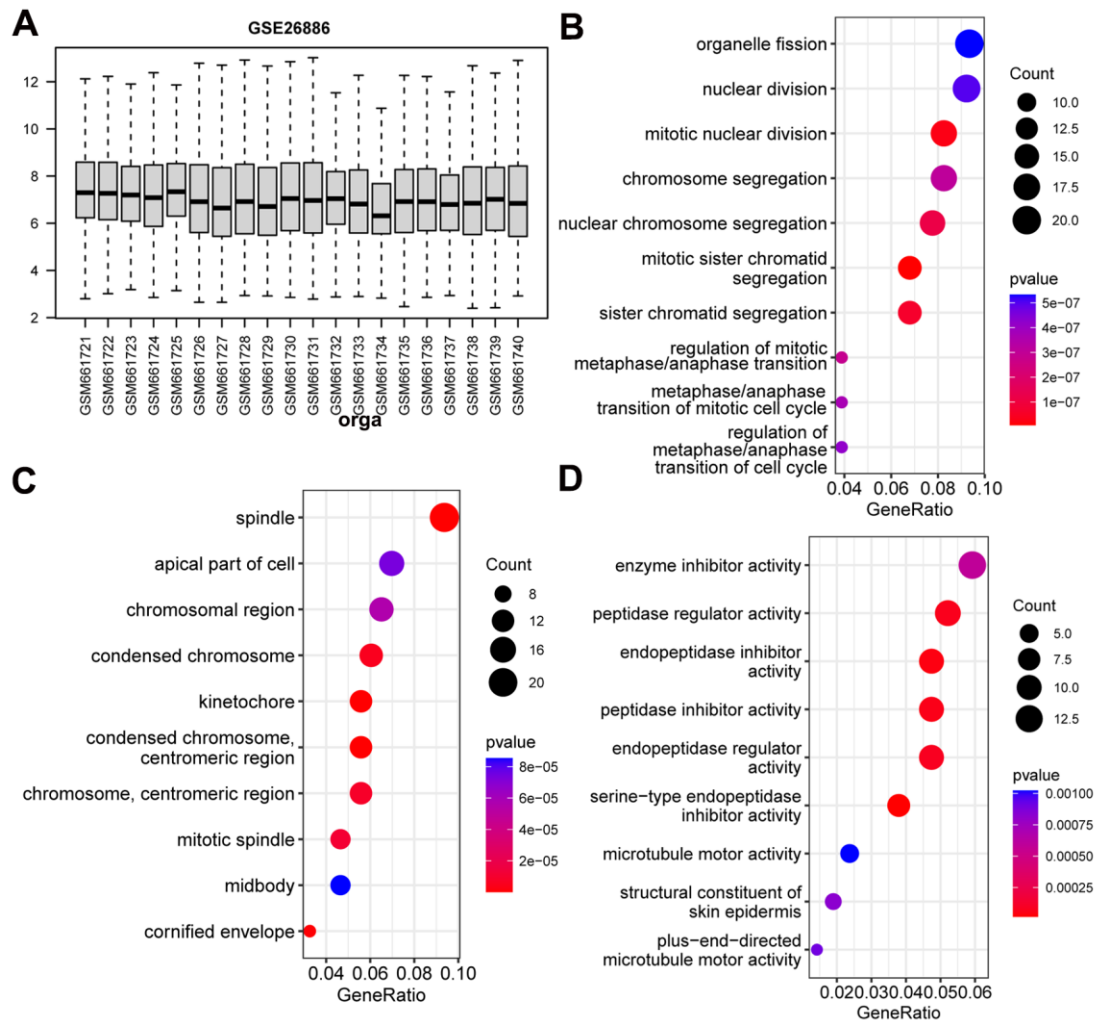


Figure S1. Normalization and functional enrichment of data. (A) Normalization of database information. (B-D) Gene function enrichment analysis showed that it was mainly enriched in cell cycle and G2M checkpoint.

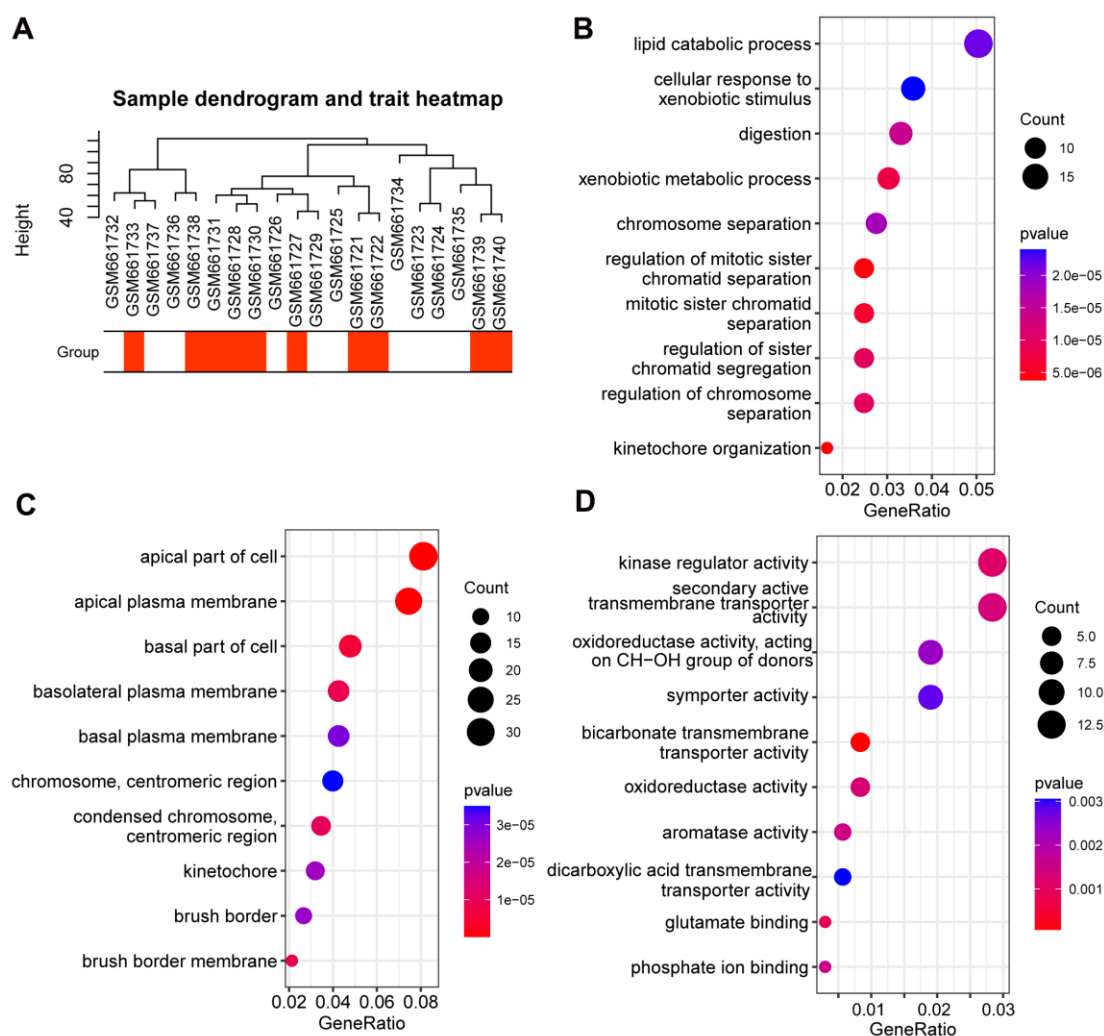


Figure S2. Clustering and functional enrichment analysis of BE with scores related to copper poisoning. (A) A dendrogram of all BE samples with cuproptosis-related score was clustered using average linkage. (B-D) After three gene models (MEsalmon, MEgreen, MEcyan) were corrected by copper-copper correlation scores, all genes were analyzed for functional enrichment.

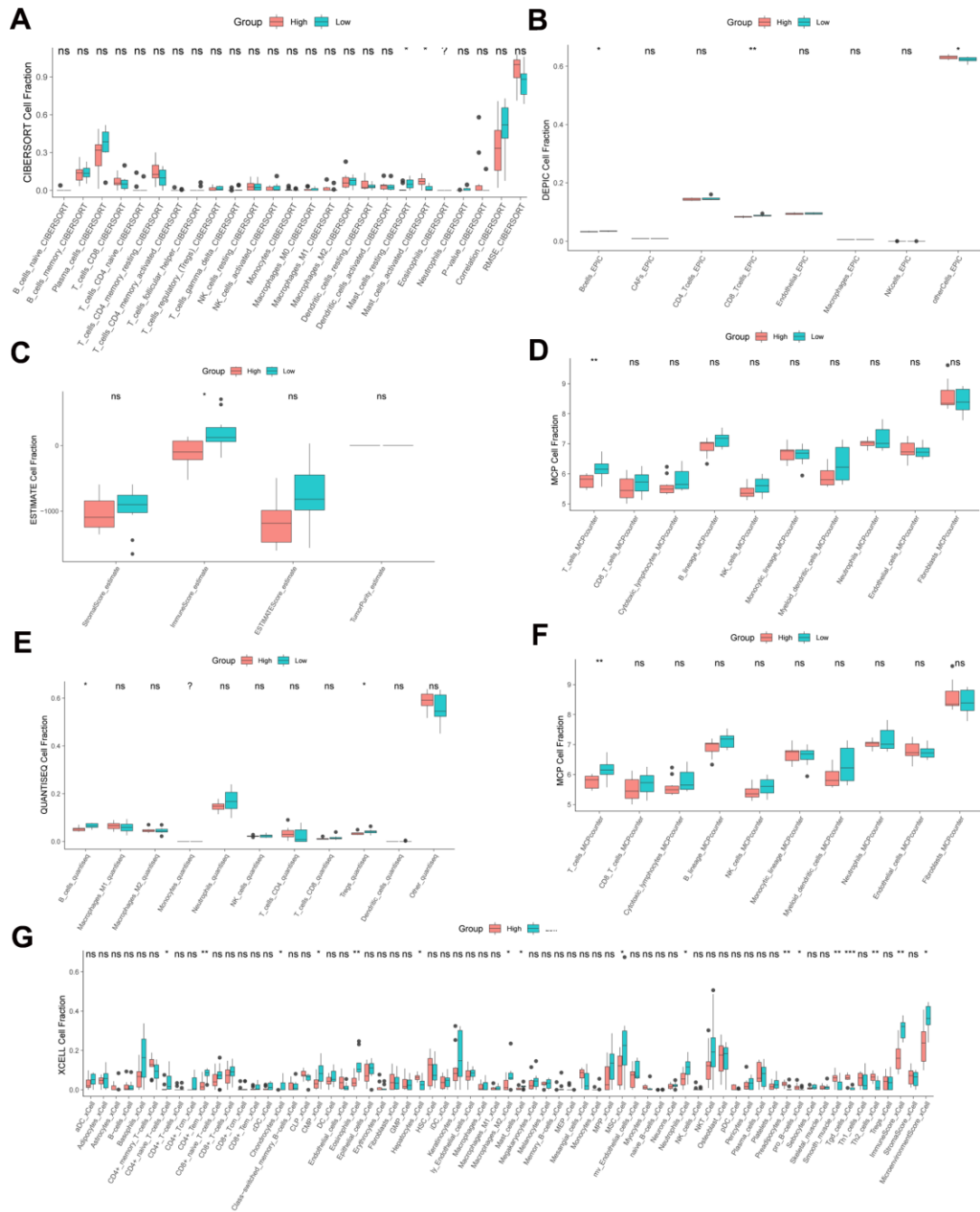


Figure S3. Seven different immune infiltration algorithms were utilized to calculate the immune infiltration landscape.

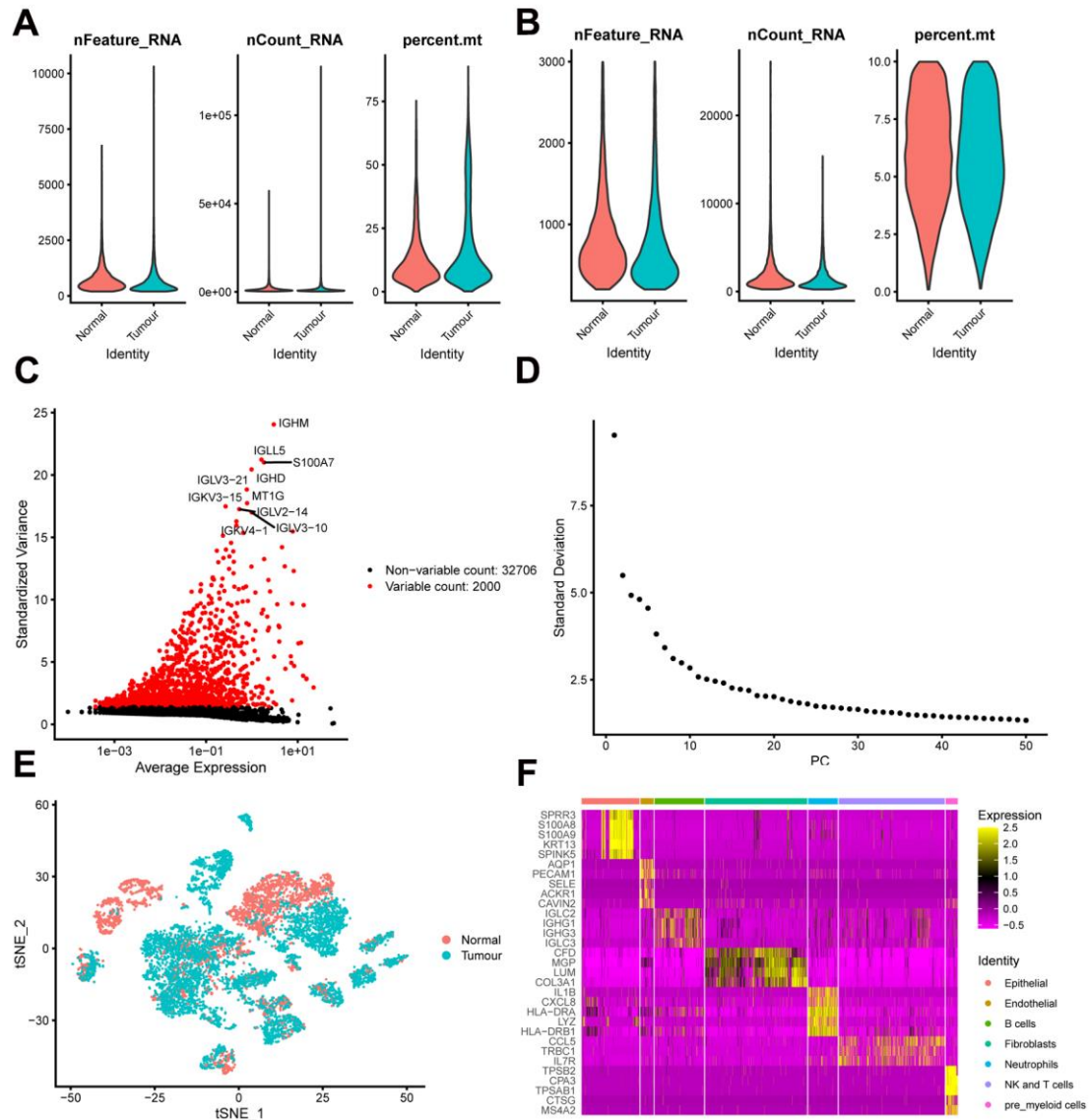


Figure S4. Quality control and marker genes. (A-E) The single cell sequence data were used for quality control of the functional analysis of CENPE and SHCBP1. **(F)** All 34,706 cells were used for marker gene t-SNE analysis.