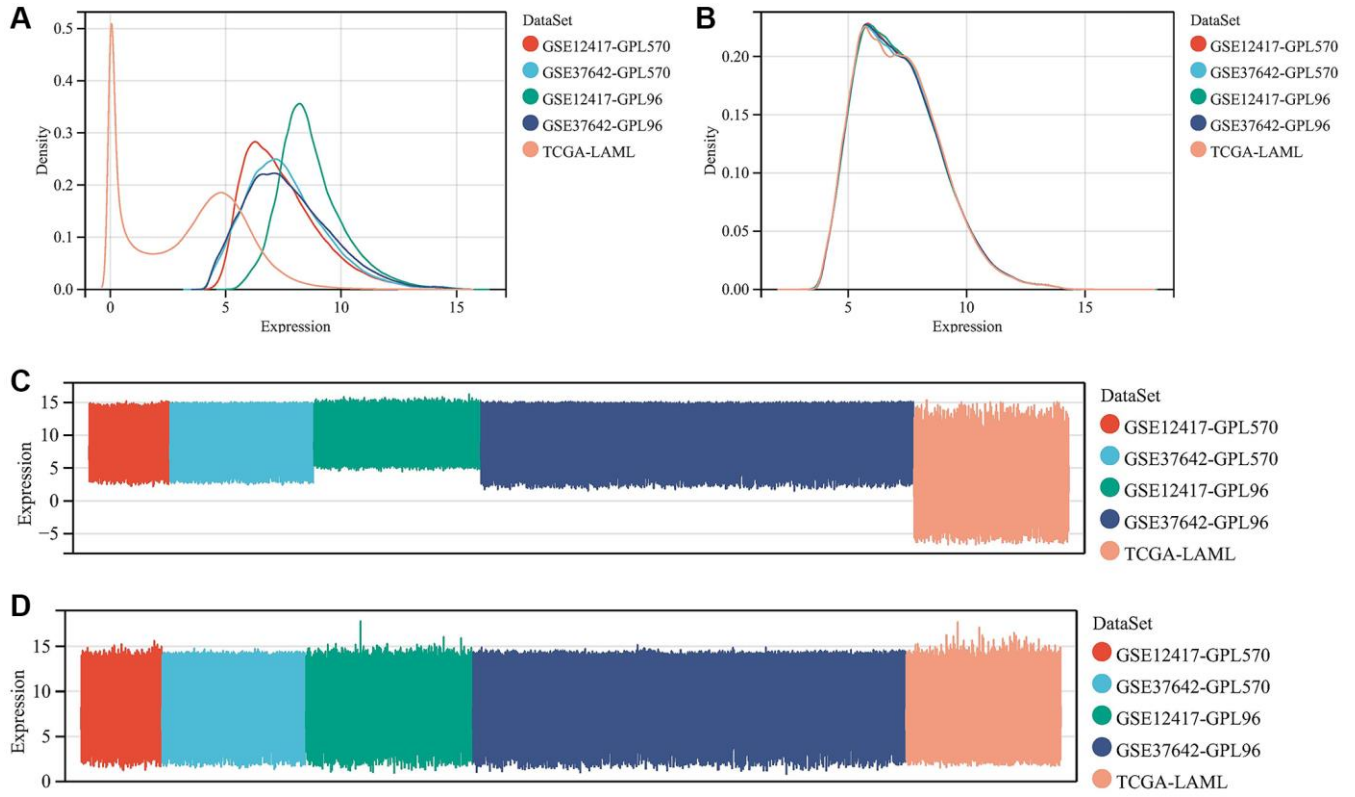
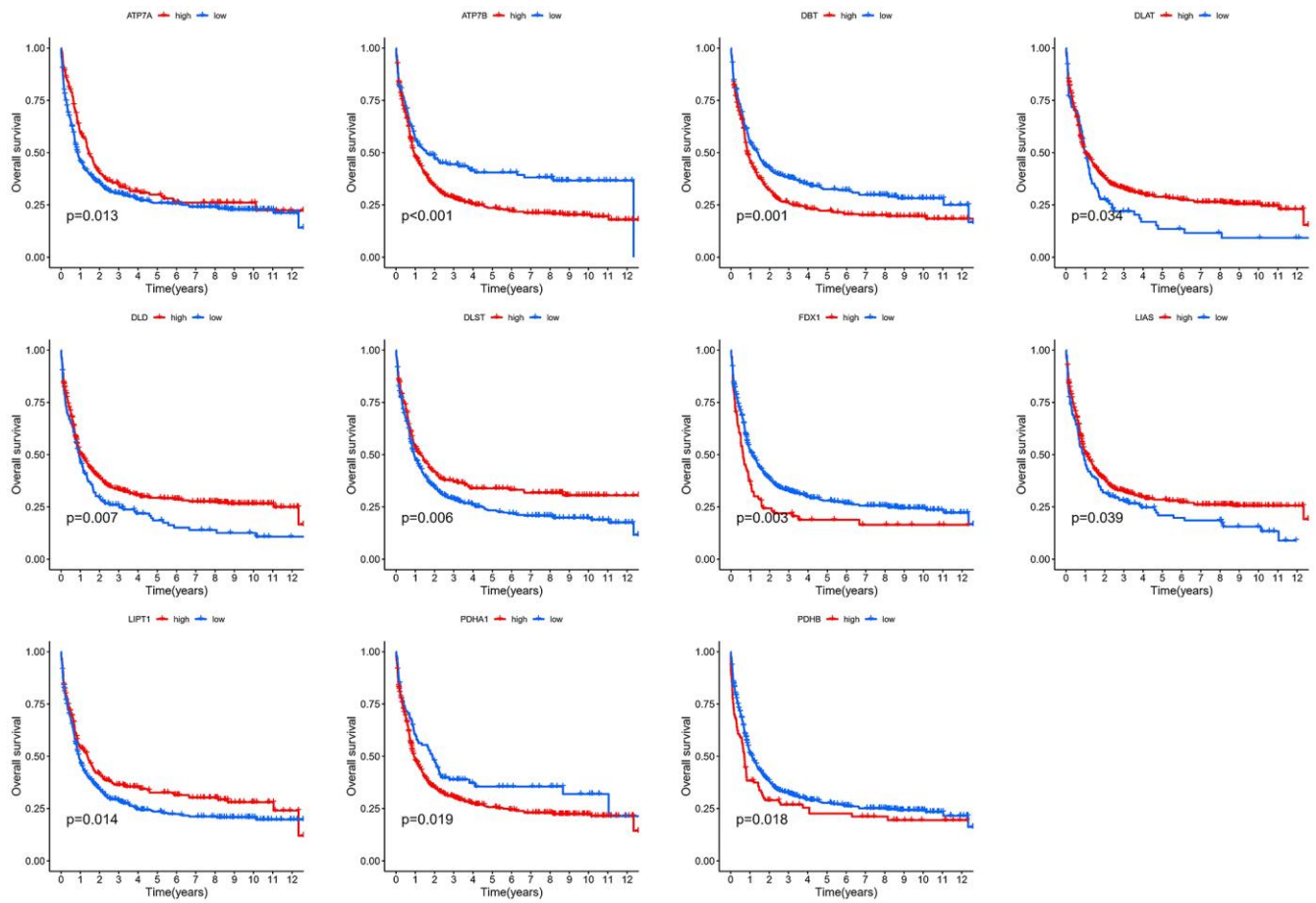


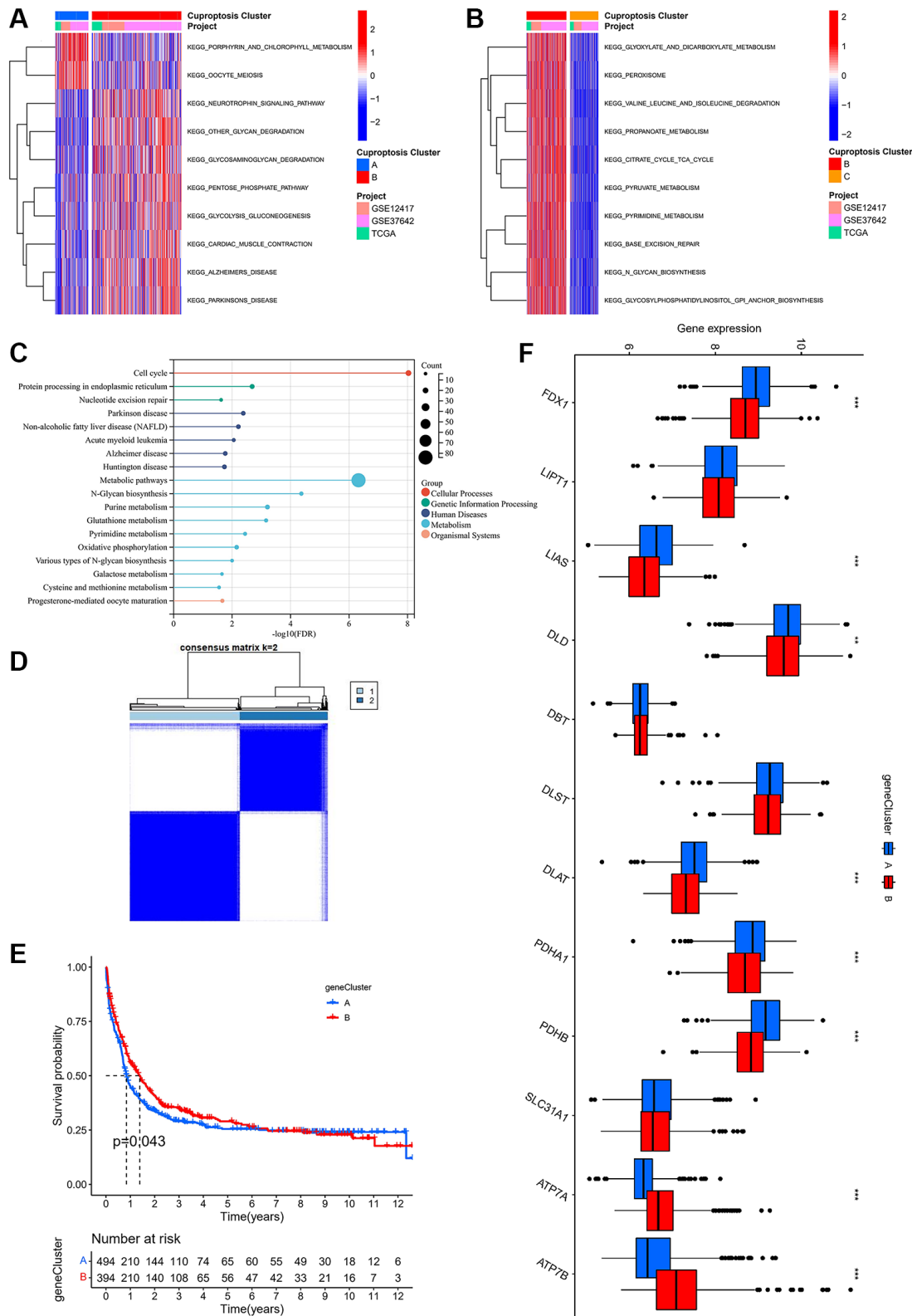
SUPPLEMENTARY FIGURES



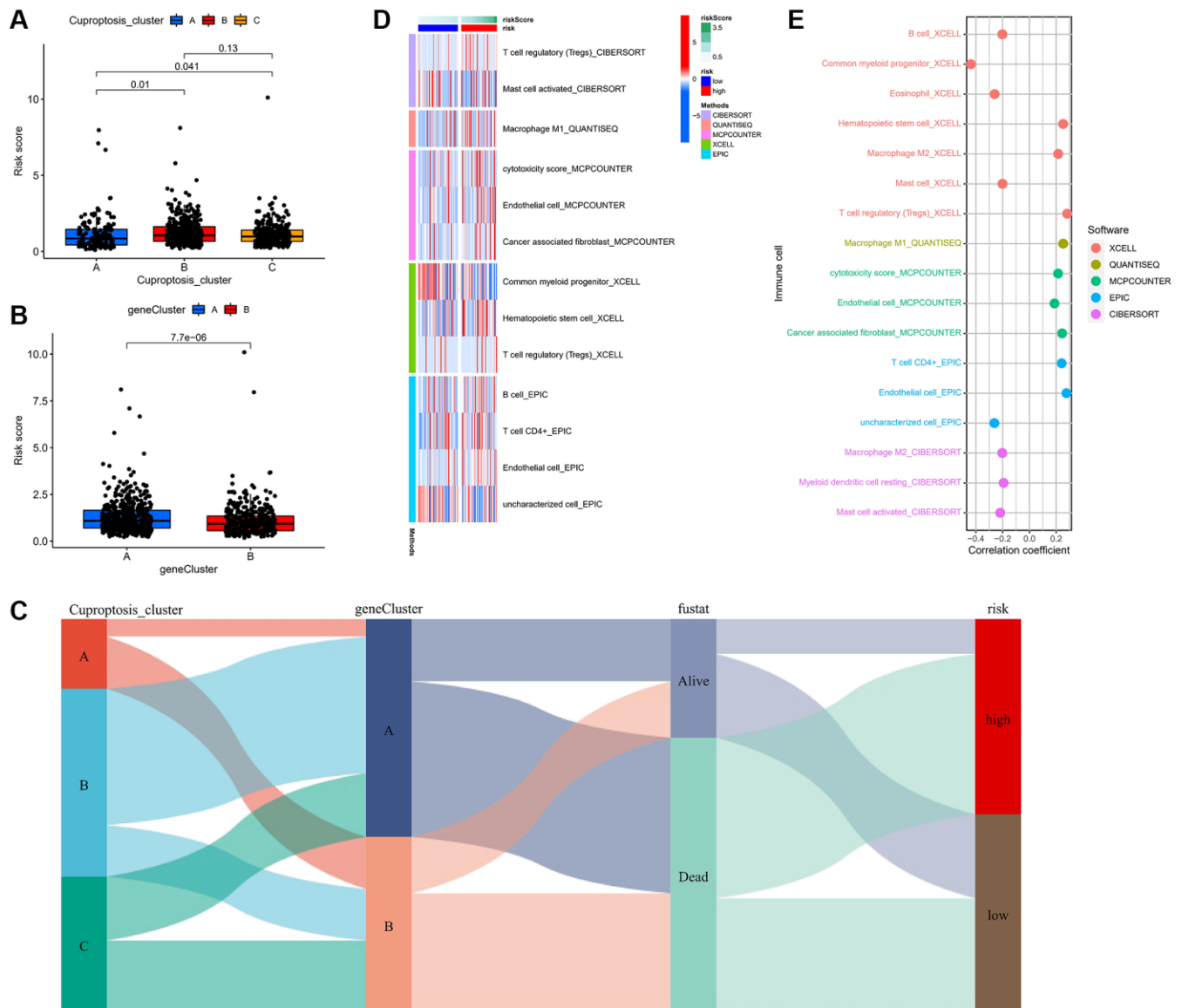
Supplementary Figure 1. Normalization of multiple cohorts. (A, C) Data characteristics before normalization of the five cohorts. (B, D) Data characteristics after normalization of the five cohorts.



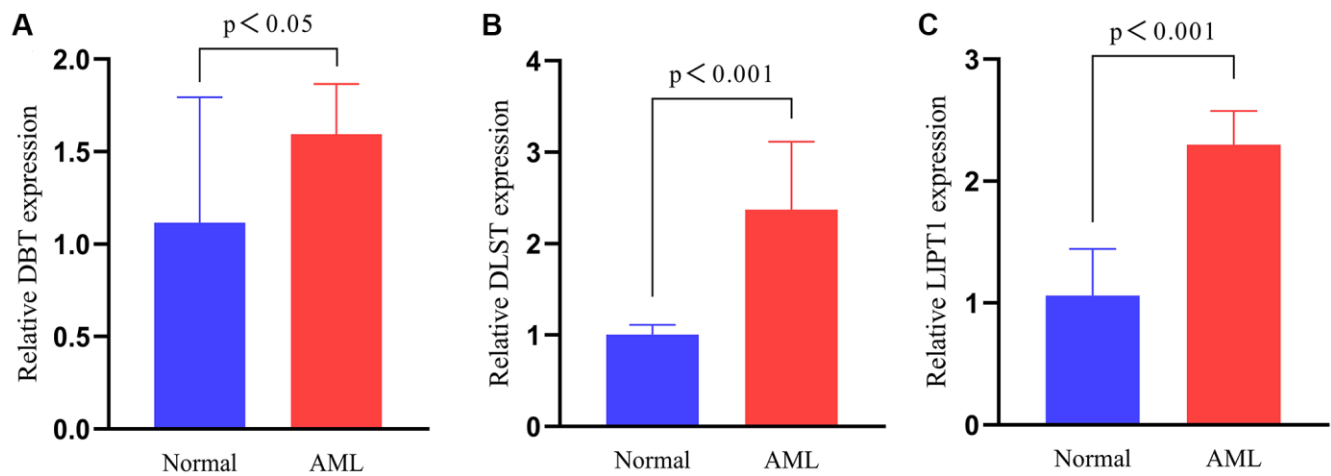
Supplementary Figure 2. Kaplan-Meier analysis of 11 cuprotosis-related genes.



Supplementary Figure 3. Characterization of different cuproptosis-regulatory subtypes. (A) Heat map showing KEGG enrichment analysis of cuproptosis subtypes A and B. (B) Heat map showing KEGG enrichment analysis of cuproptosis subtypes B and C. (C) Functional enrichment analysis of DEGs. (D) Heat map of unsupervised clustering analysis. (E) Kaplan-Meier analysis of overall survival curves for different cuproptosis-regulatory subtypes. (F) Box plot of cuproptosis-related genes expression in different cuproptosis-regulatory subtypes ($^*P < 0.05$, $^{**}P < 0.01$, $^{***}P < 0.001$).



Supplementary Figure 4. TME characteristics of risk score and their relevance with molecular subtypes. (A) Risk scores for different cuproptosis subtypes. (B) Risk scores for different cuproptosis-regulatory subtypes. (C) The relevance in cuproptosis subtypes, cuproptosis-regulatory subtypes, risk score, and survival status. (D) Heat map showing the relationship between different risk score groups and immune cells. (E) Bubble plots showing the relationship between different risk score groups and immune cells.



Supplementary Figure 5. Expression of three cuproptosis-related genes in clinical samples. (A) Expression of DBT gene in normal human and AML patients. (B) Expression of DLST gene in normal human and AML patients. (C) Expression of LIPT1 gene in normal human and AML patients.