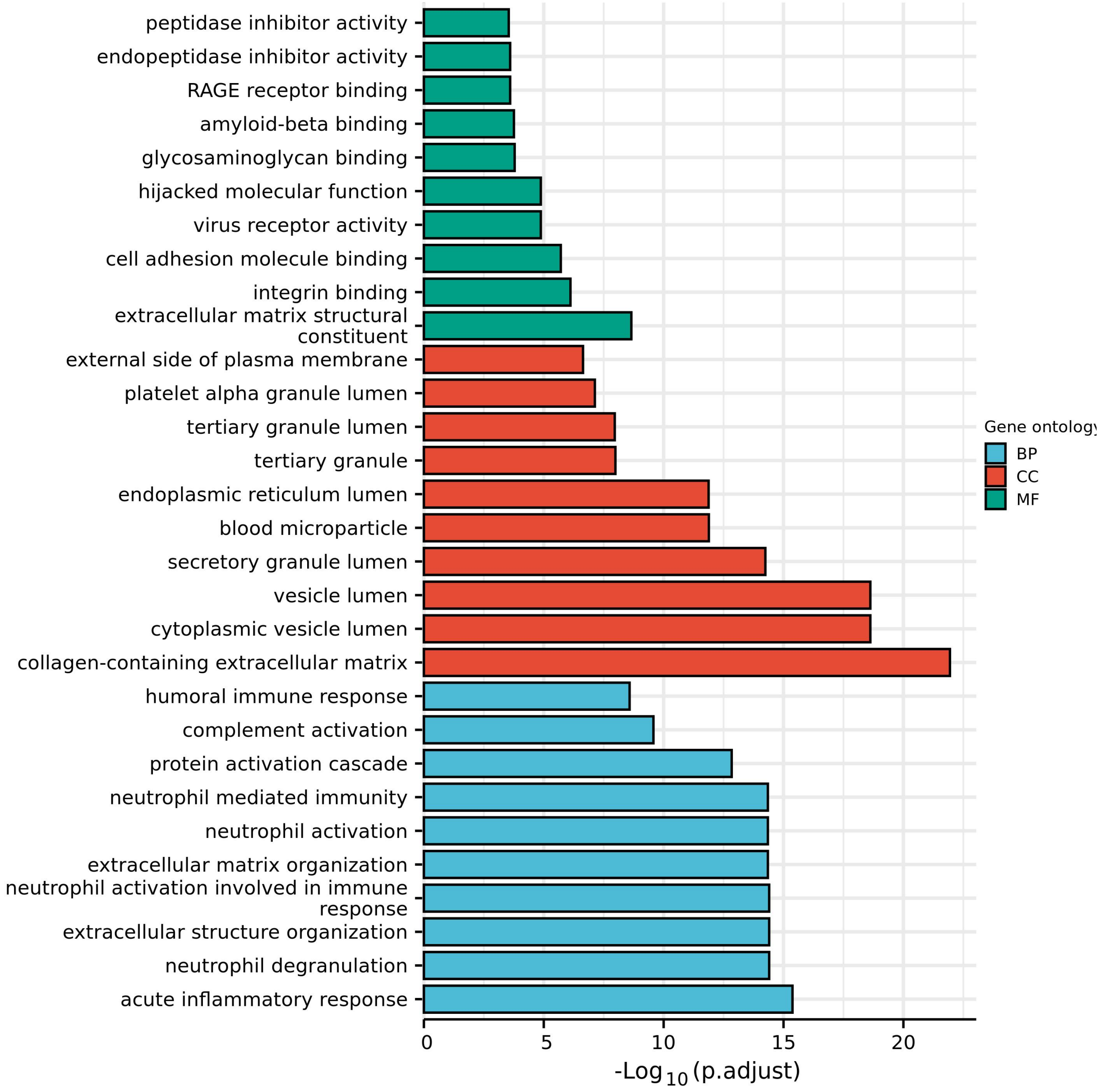
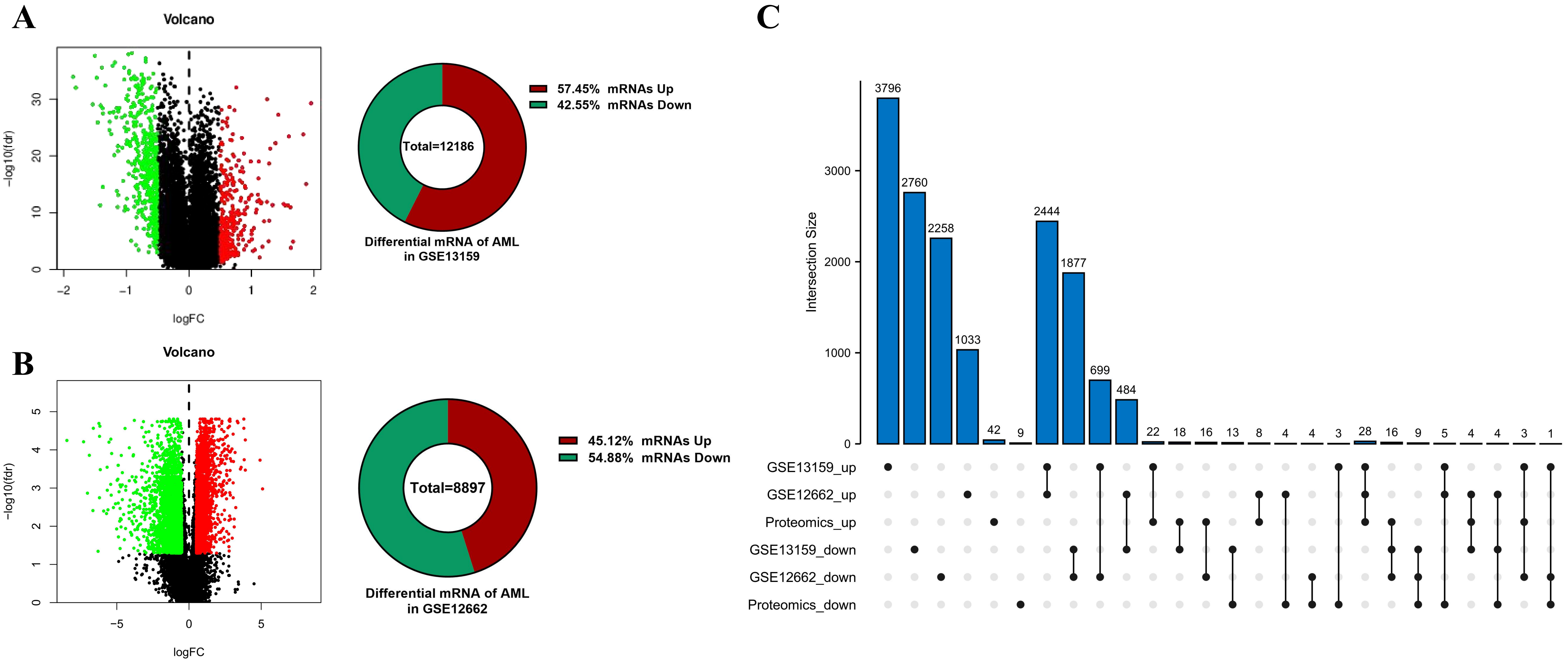
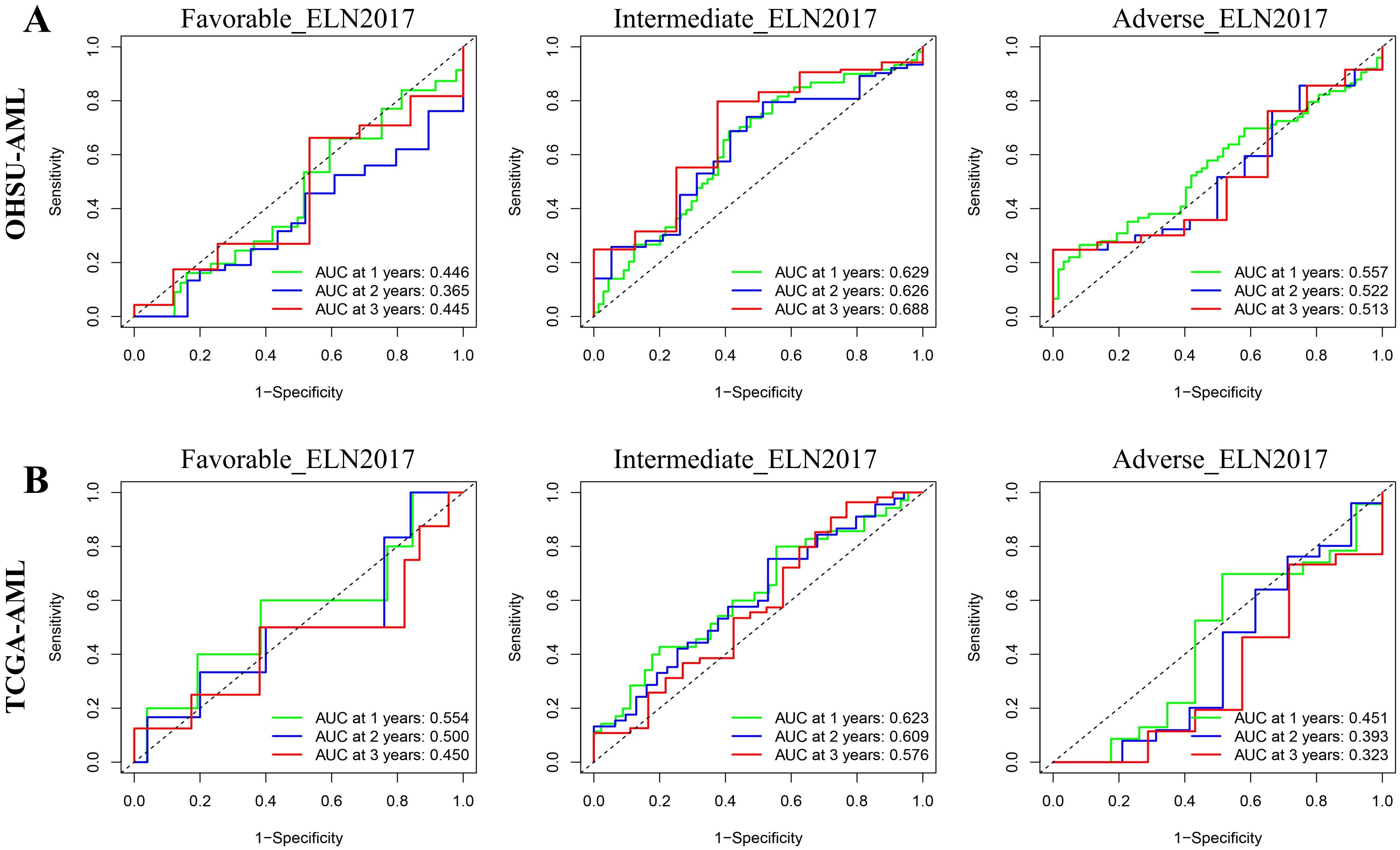


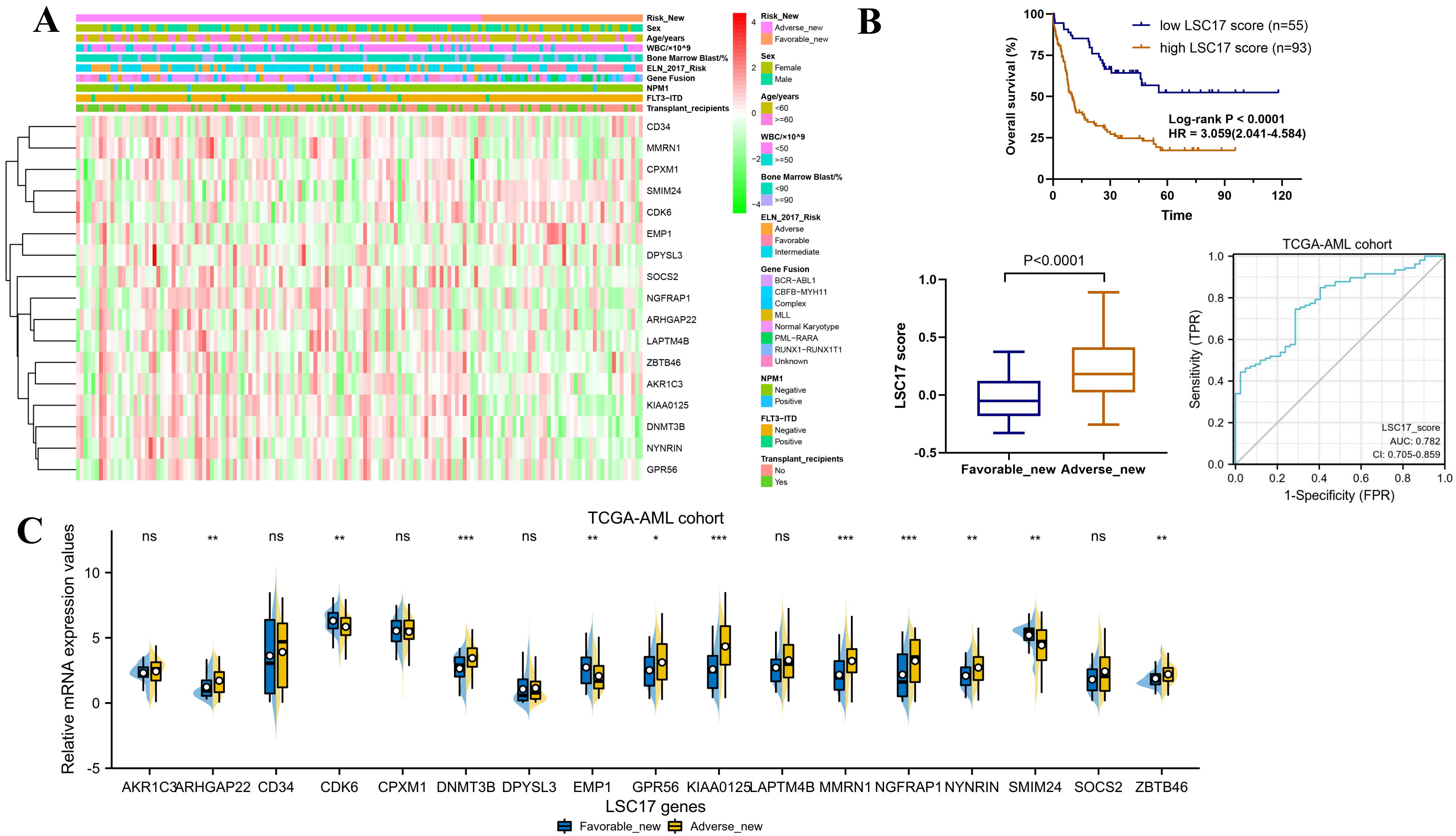
Supplemental Figure S1. The Gene Ontology (GO) enrichment analysis (Top 10) of all differentially expressed serum proteins in AML.



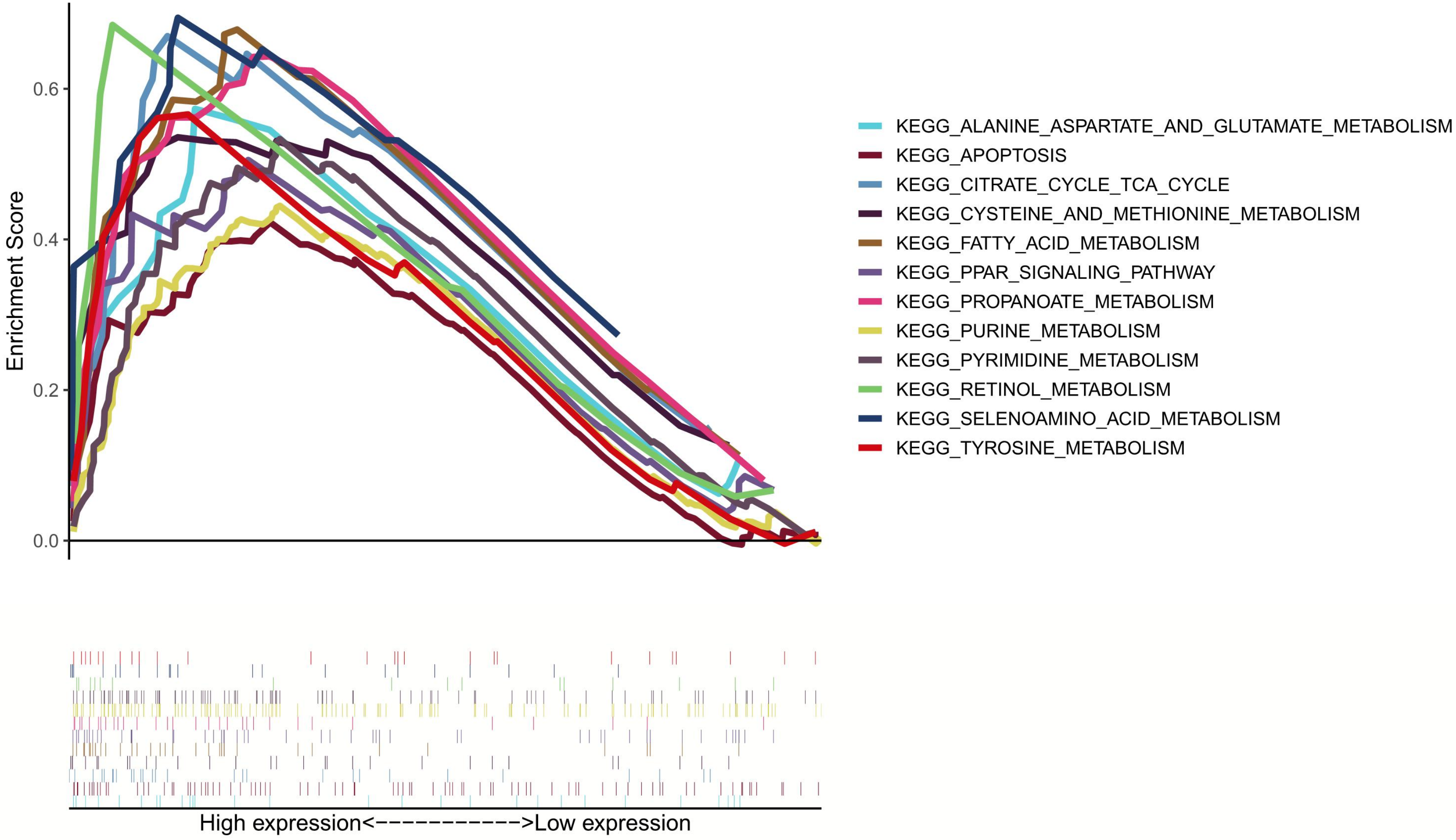
Supplemental Figure S2. Differential analysis of combined proteome and transcriptome data. (A-B) Volcano plots of differentially expressed mRNA in the transcriptome of the GEO dataset (accession number GSE12662 and GSE13159). (C) The UpSet diagrams of differentially expressed genes in the three source platforms were drawn.



Supplemental Figure S3. Time dependent receiver operating characteristic (ROC) curves of overall survival at 1, 3- and 5- years, the prediction value of AML in intermediate-risk group was higher. (A) In the OHSU-AML cohort, the area under ROC curve of overall survival of favorable, intermediate, and adverse group in the ELN-2017 risk stratification. (B) Validation of the area under the ROC curve for each risk stratification in the TCGA-AML cohort.



Supplemental Figure S4. The TCGA dataset validated the association of new ICAM2-based risk stratification with clinical information. (A)Heatmap of the correlation between identified new_risk and clinical features. (B) The subgroup with higher leukemia stem cell score in AML had worse prognosis and higher LSC17 score in the new_risk stratification. (C)Differentially expressed LSC17-related genes in the new_risk stratification.



Supplemental Figure S5. GSEA delineates biological pathways correlated with ICAM2 expression. Some enrichment results showed that there was a significant correlation between high- and low- ICAM2 expression groups.