SUPPLEMENTARY FIGURES

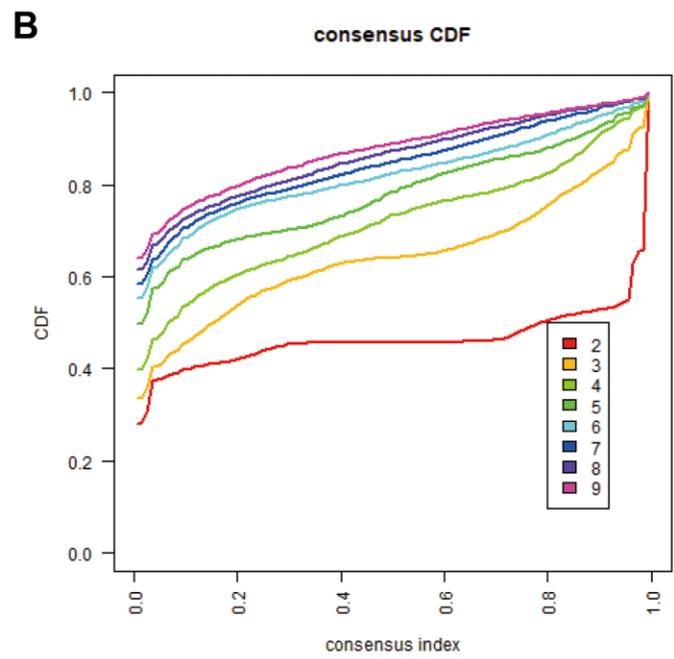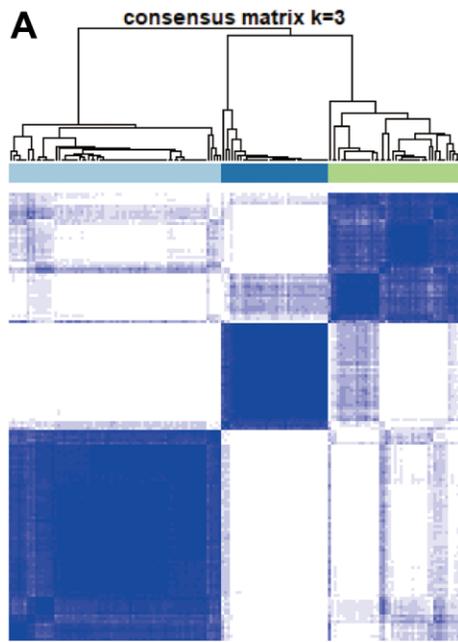Supplementary Figure 1. Characterization of necroptosis-related genes. (A) Principal component analysis of 67 necroptosis-related genes based on paired tumor samples and normal samples. (B, C) Heatmap of expression of 67 necroptosis-related genes in different types of immune cells (B) and hematological malignancies (C).
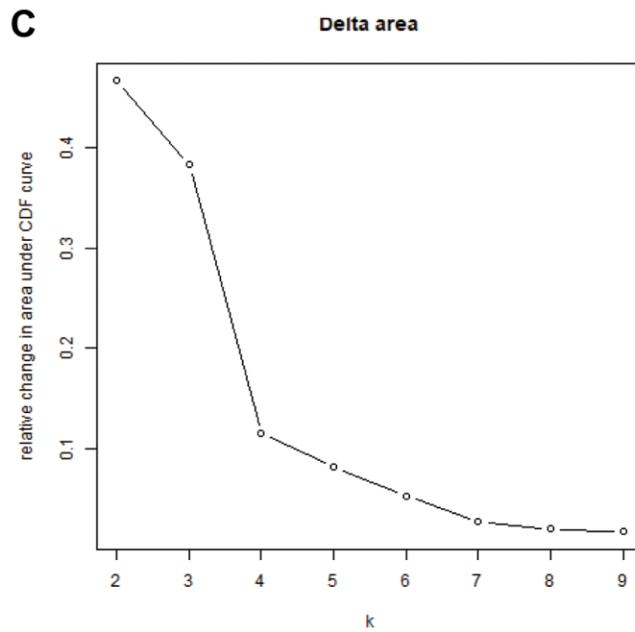
Supplementary Figure 2. Unsupervised clustering analyses of a necroptosis signature. (**A**) Concordance matrix of subtypes. (**B**, **C**) Cumulative distribution function presented as the relative change in area when k = 2–9.
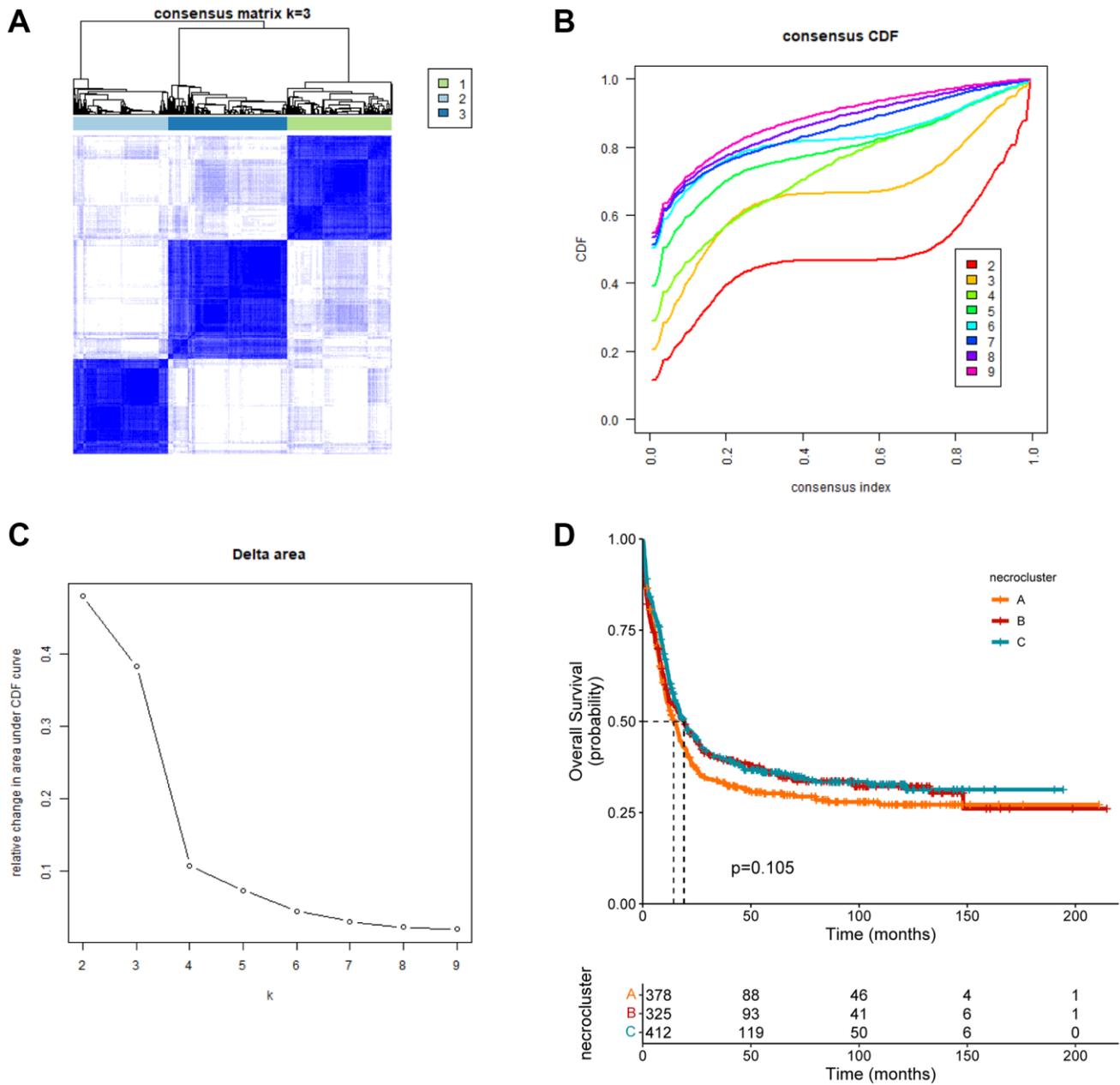
Supplementary Figure 3. Consensus clustering analysis in combined AML cohorts encompassing six datasets (1115 patients). (**A**) The concordance matrix of the subtypes was calculated. (**B**, **C**) The cumulative distribution function and relative change in area under the cumulative distribution function curve for k = 2–9. (**D**) Kaplan–Meier curves showing the overall survival for three clusters (*P* = 0.105, log-rank test).
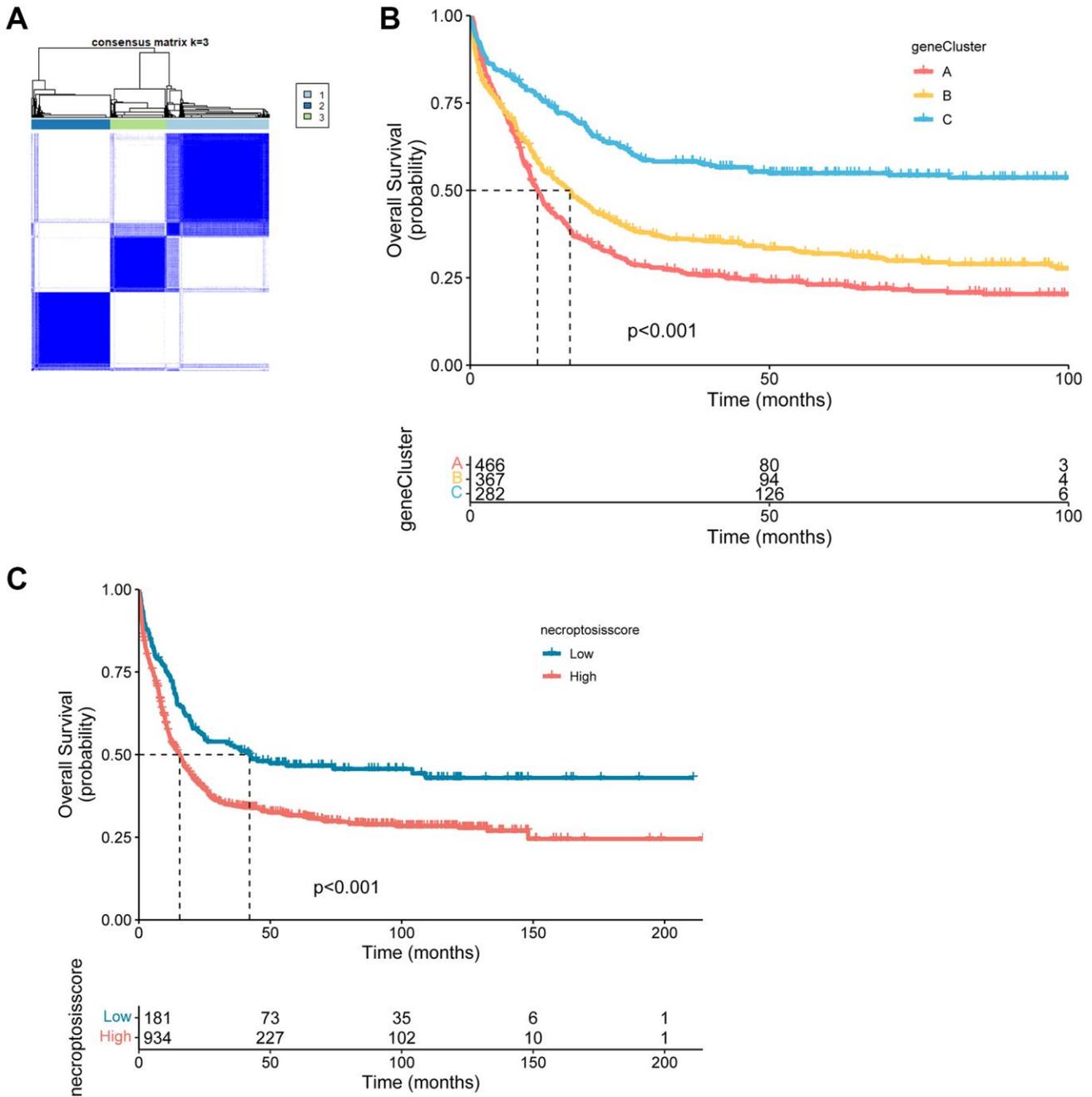
Supplementary Figure 4. Prognosis analysis of three gene clusters and the necroptosis score in combined AML cohorts encompassing six datasets (1115 patients). (**A**) Consensus matrix heatmap defining three gene clusters (k = 3). (**B**) Kaplan-Meier overall survival curves of three gene clusters ($P < 0.001$, log-rank test). (**C**) Kaplan–Meier survival analysis of high versus low necroptosis score groups ($P < 0.001$, log-rank test).