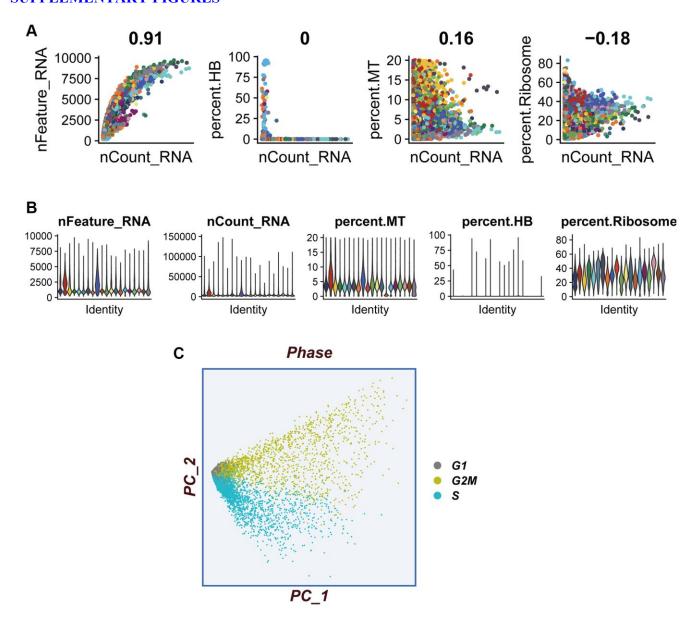
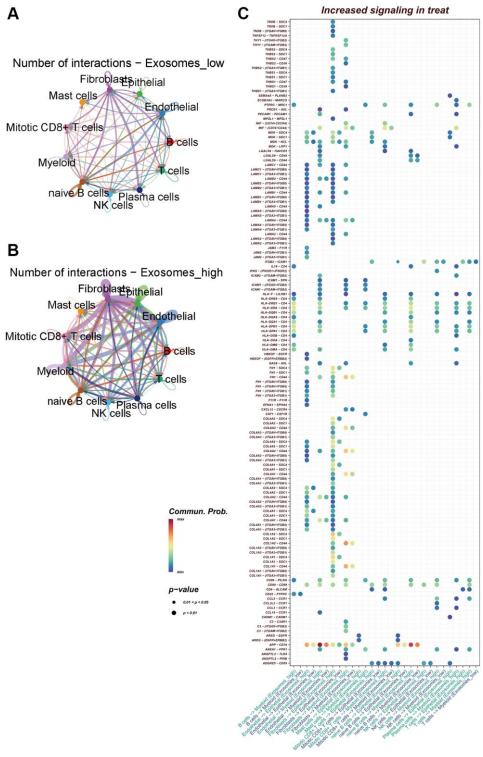
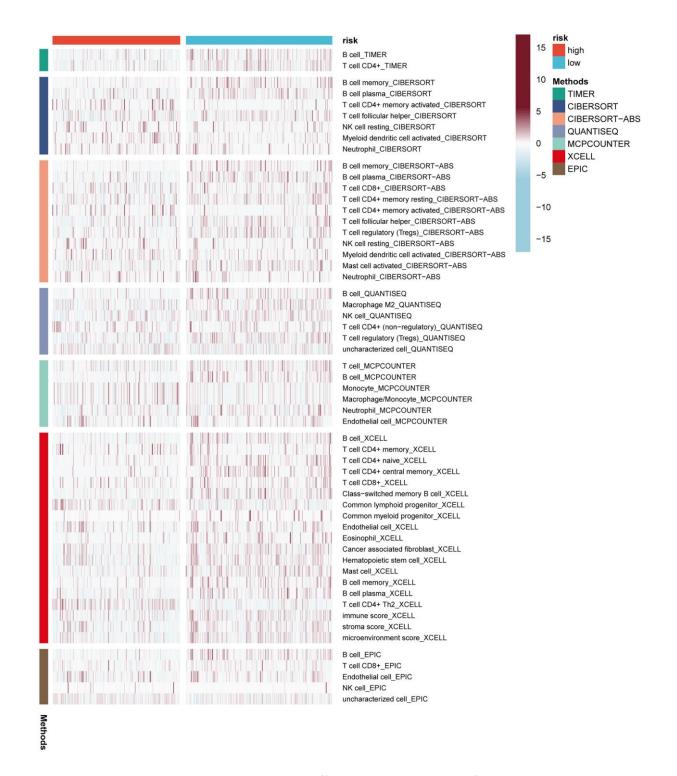
SUPPLEMENTARY FIGURES



Supplementary Figure 1. Quality control and dimensionality reduction analysis of single cell sequencing data. (A) Sequencing depth is significantly and positively correlated with total intracellular sequence (R = 0.91). (B) Removal of non-compliant cells by restricting the ratio of mitochondrial genes, hemoglobin genes and ribosomal genes. (C) PCA analysis did not show any significant cell cycle changes.



Supplementary Figure 2. Cell-to-cell communication. (A, B) Differences in the number of cellular communications between groups with high and low expression of EA. (C) Differential expression of ligand-receiving pairs between the high- and low-EA expression groups.



Supplementary Figure 3. Heat map demonstrating the differences in immune cell infiltration between high- and low-risk groups assessed using seven algorithms.