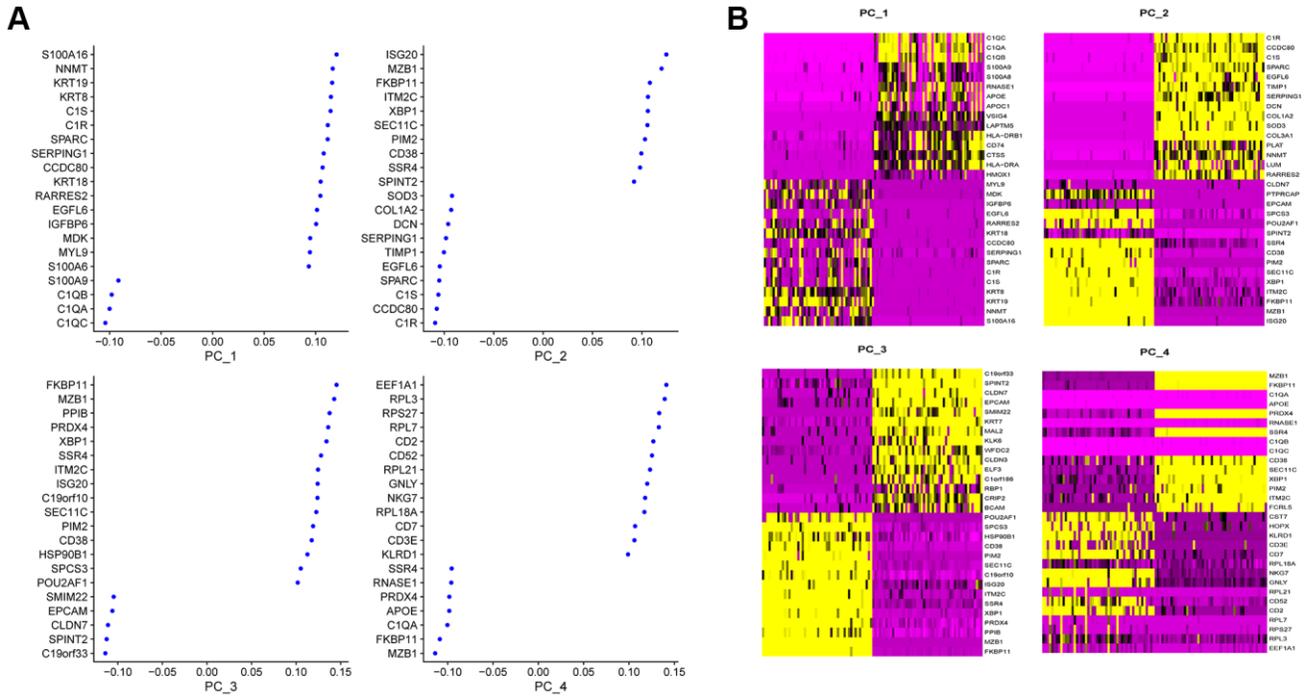
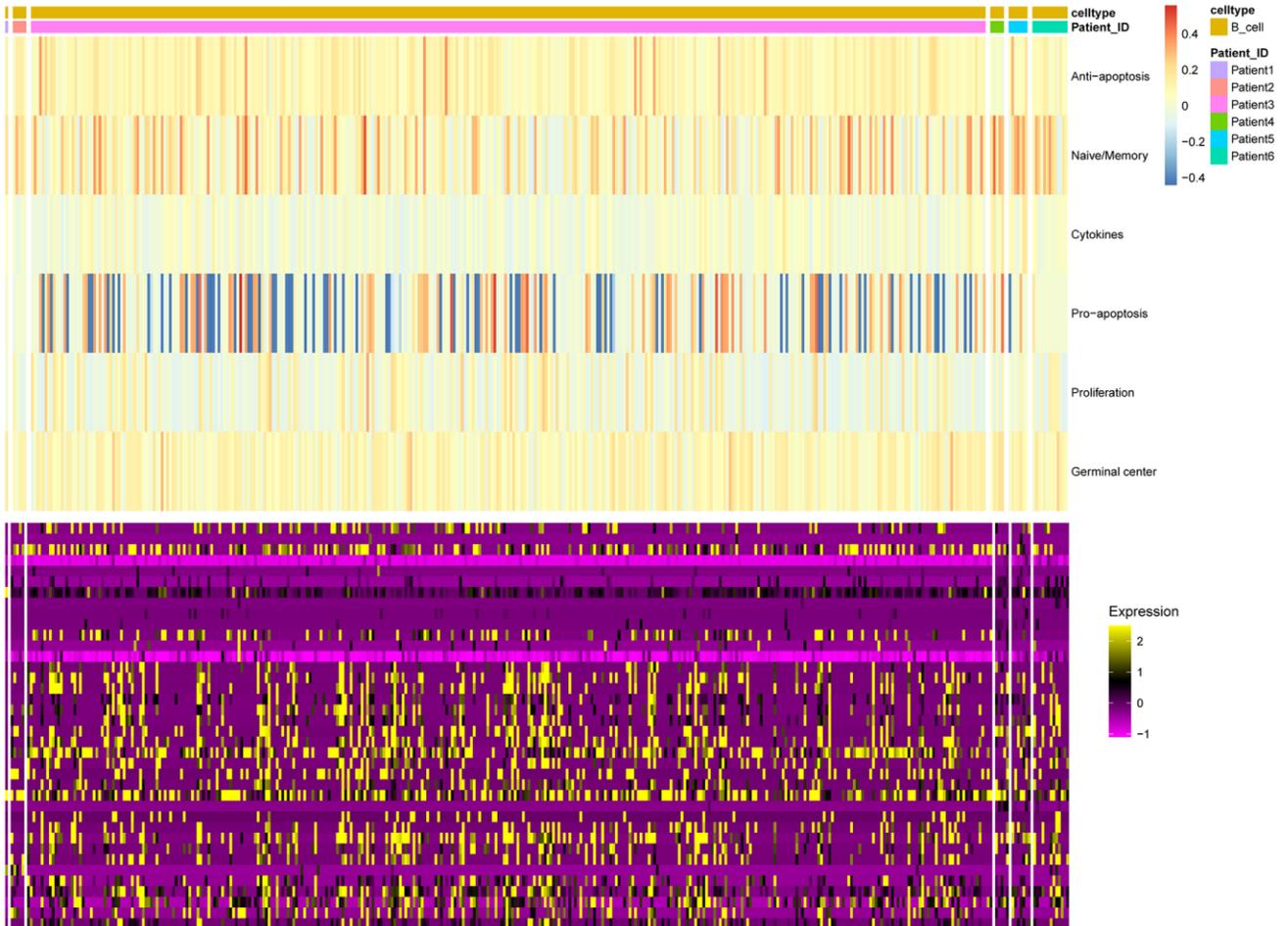


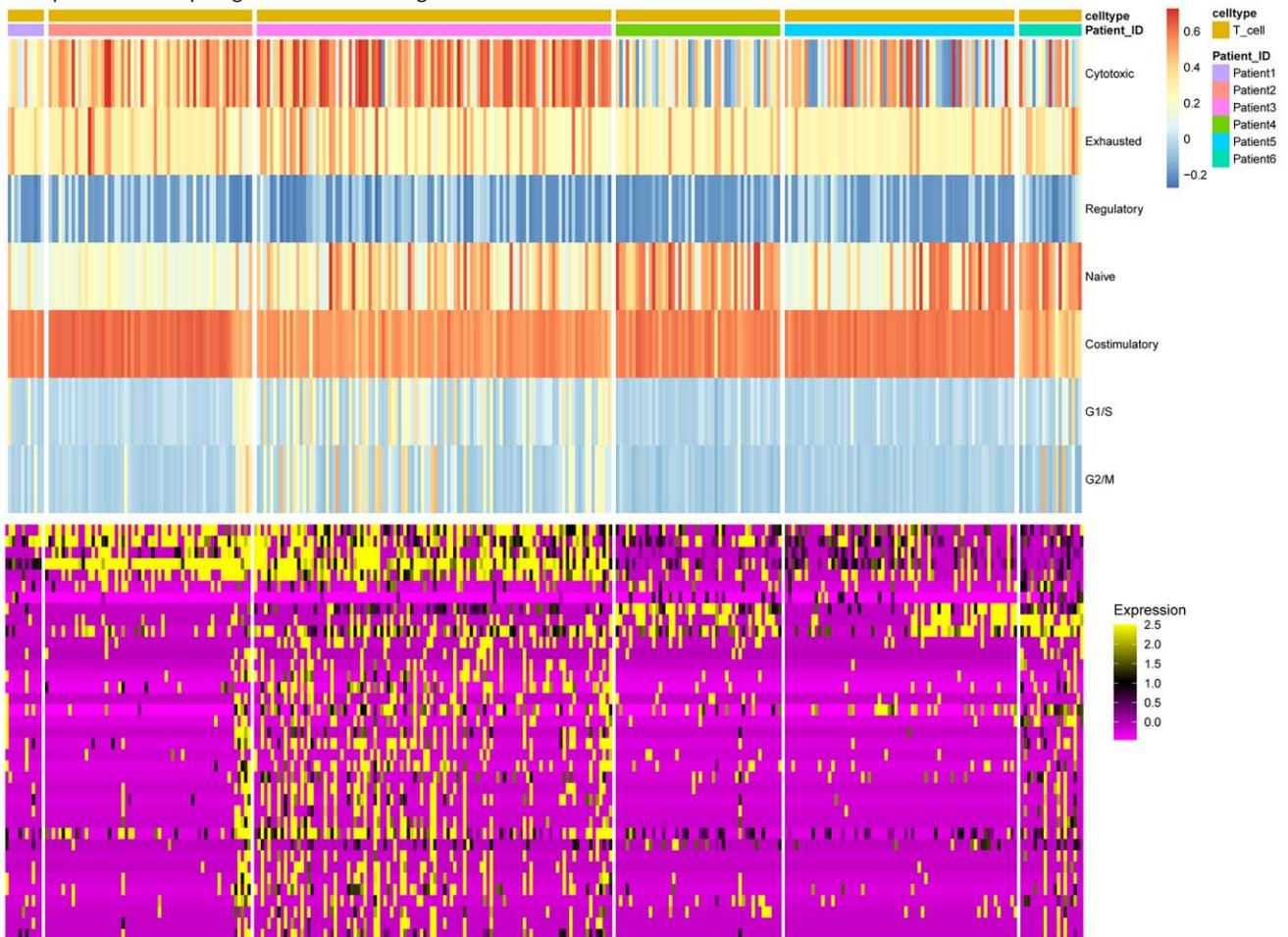
SUPPLEMENTARY FIGURES



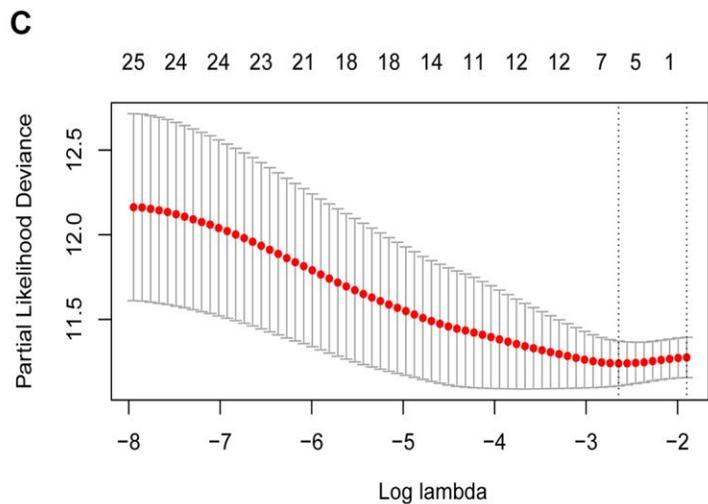
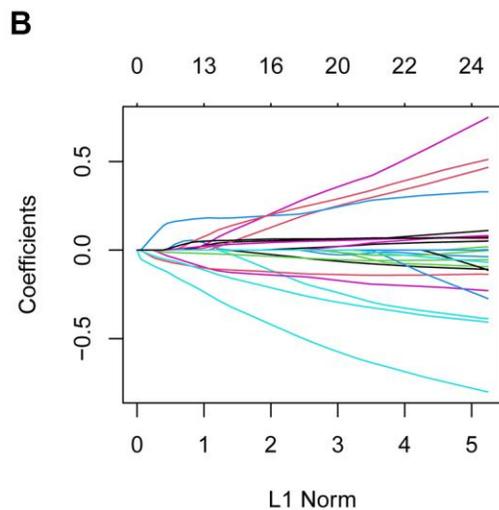
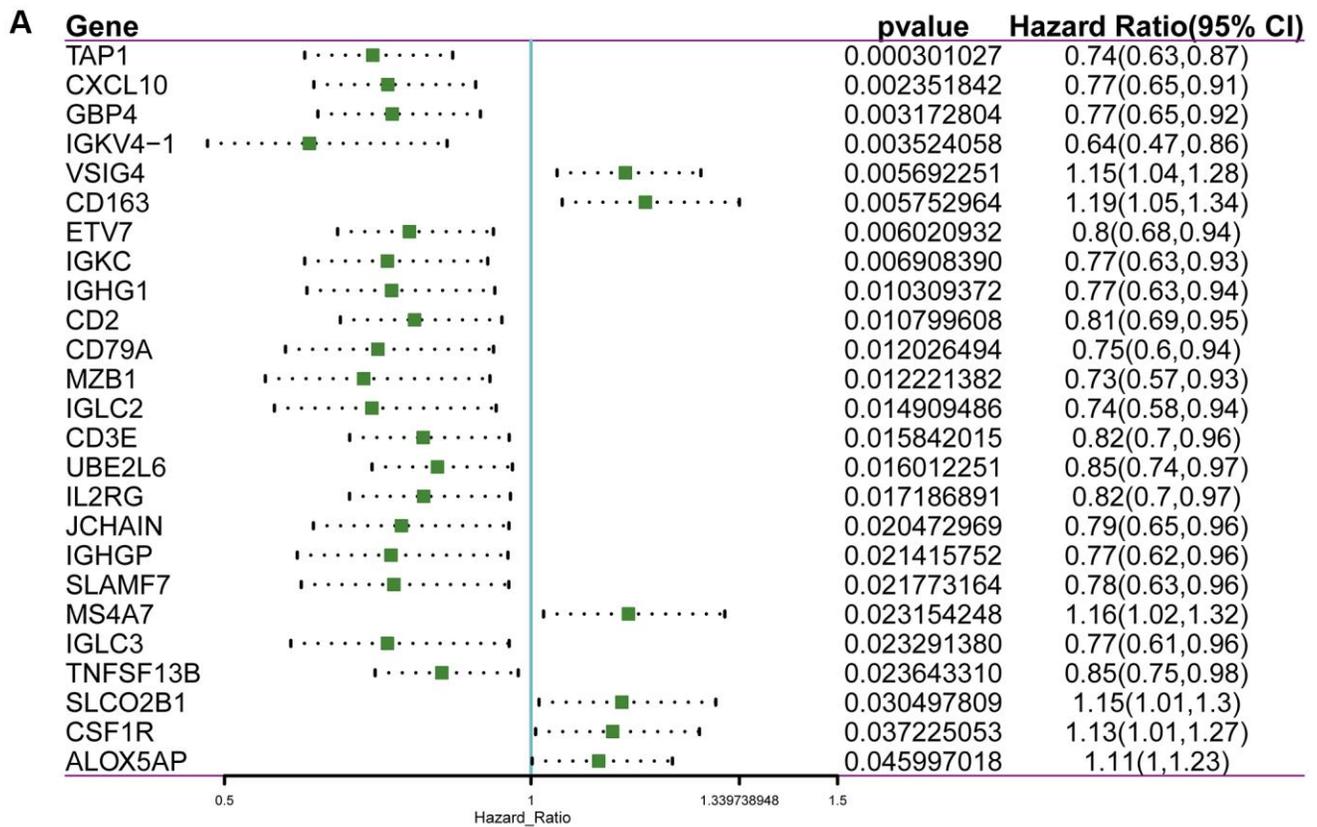
Supplementary Figure 1. Dot plots (A) and heatmaps (B) display the top 20 highly correlated genes in PC1 to PC4.



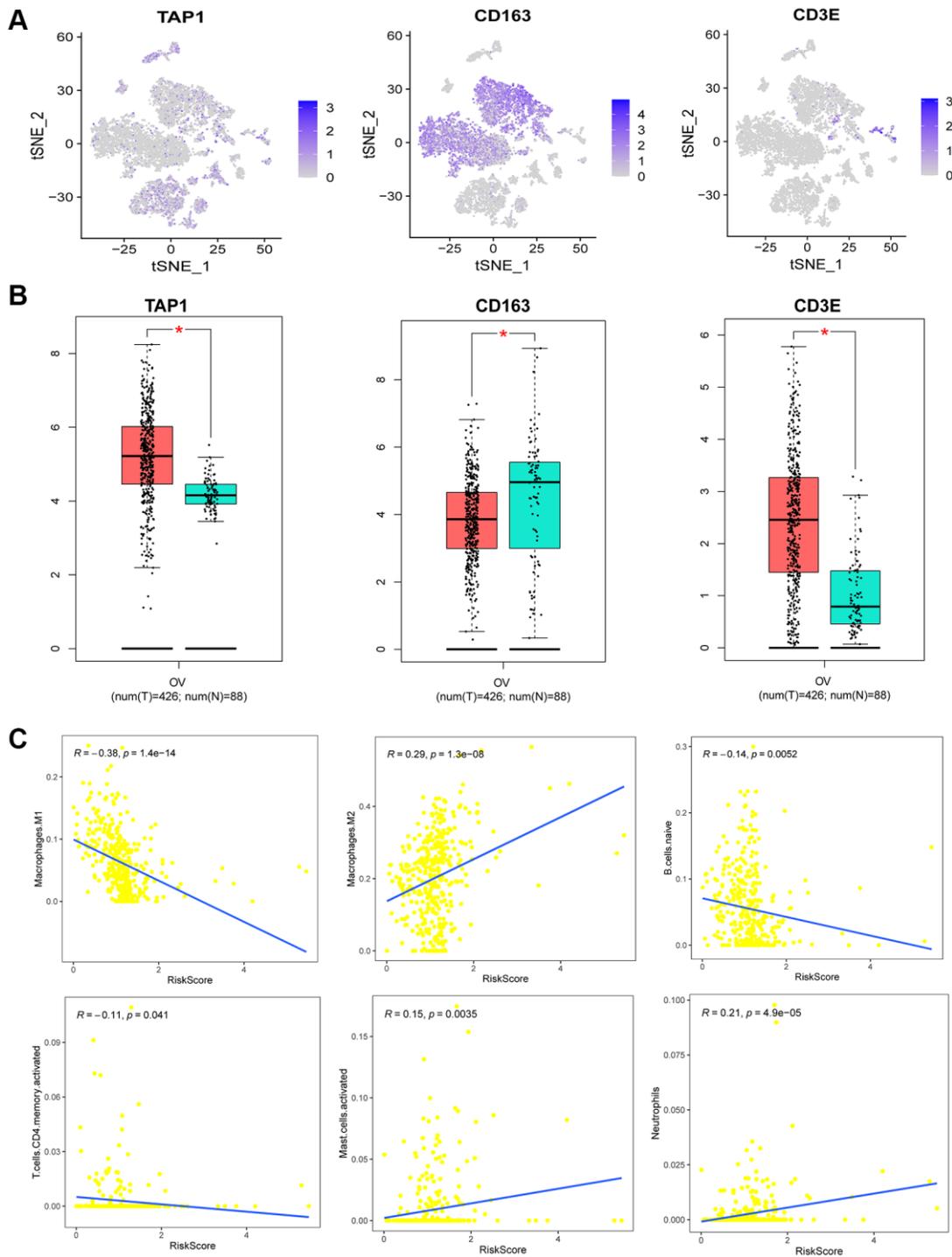
Supplementary Figure 2. B-cell signatures in OC samples. Upper panel: GSVA enrichment scores of B cells in functional status. Bottom panel: heatmap of genes in the above gene sets.



Supplementary Figure 3. T-cell signatures in OC samples. Upper panel: GSVA enrichment scores of T cells in functional status. Bottom panel: heatmap of genes in the above gene sets.



Supplementary Figure 4. (A) Univariate Cox regression analysis of 25 prognostic genes from 219 TAMRG. (B) LASSO coefficient profiles of 25 genes. (C) LASSO regression with 10-fold cross-validation resulted in six prognostic genes using an optimal lambda value.



Supplementary Figure 5. (A) The expression of *TAP1*, *CD163*, and *CD3E* in scRNA-seq set. (B) The expression of *TAP1*, *CD163*, and *CD3E* in 426 OV (TCGA) samples and 88 normal (GTEx) samples. (C) The relationship between the proportion of six infiltrating immune cell types and the risk score.