

Appendix

Figure legends of supplementary figures.

Supplementary Figure S1 | The relative abundance of 22 distinct immune cell types in the (A) TCGA-OV cohort and GSE140082 cohort.

Supplementary Figure S2 | Weighted gene co-expression network analysis in the TCGA-OV cohort. (A) Sample dendrogram with trait heatmap. (B) Dendrogram of differentially expressed genes clustered based on different metrics.

Supplementary Figure S3 | Weighted gene co-expression network analysis in the GSE140082 cohort. (A) Sample dendrogram with trait heatmap. (B) Analysis of the scale-free fit index and the average connectivity of various soft threshold power. (C) Dendrogram of differentially expressed genes clustered based on different metrics.

Supplementary Figure S4 | Consensus maps showed the correlation profiling of OC patients derived from 2 to 10 sub-consensuses.

Supplementary Figure S5 | Verification of the subclass distribution. (A) PCA and (B) t-SNE analyses supported the classification of OC into two subtypes.

Supplementary Figure S6 | The violin plots showed (A) the immune score, (B) the stromal score, (C) the ESTIMATE score, and (D) the tumor purity in different OC subtypes.

Supplementary Figure S7 | The boxplots showed the gene expression (log) of 148 immunomodulators in different OC subtypes: (A) chemokine; (B) receptor; (C) MHC; (D) immunostimulatory; (E) immunoinhibitory.

Supplementary Figure S8 | Functional enrichment analyses of OC clusters. (A) GO and (B) KEGG pathway analyses of DEGs between CD8⁺ T cell-based molecular subtypes. Oncological signatures were significantly enriched in (C) Cluster 1 and (D) Cluster 2 identified by gene set enrichment analysis (GSEA).

Supplementary Figure S9 | The survival curves of the remaining 9 genes in the TCGA-OV cohort. (A) BATF2; (B) CCR7; (C) CD3G; (D) CD40LG; (E) CLEC5A; (F) CXCL9; (G) ETV7; (H) HLA_DOB; (I) HLA_F.

Supplementary Figure S10 | The survival curves of the remaining 9 genes in the GSE140082 cohort. (A) BATF2; (B) CCR7; (C) CD3G; (D) CD40LG; (E) CLEC5A; (F) CXCL9; (G) ETV7; (H) HLA_DOB; (I) HLA_F.

Supplementary Figure S11 | The survival curves of the remaining 9 genes in the GSE32062 cohort. (A) BATF2; (B) CCR7; (C) CD3G; (D) CD40LG; (E) CLEC5A; (F) CXCL9; (G) ETV7; (H) HLA_DOB; (I) HLA_F.

Supplementary Figure S12 | The lollipop charts showed the correlation between the immune infiltrates and (A) CD38 and (B) CXCL13 expression in the TCGA-OV cohort.