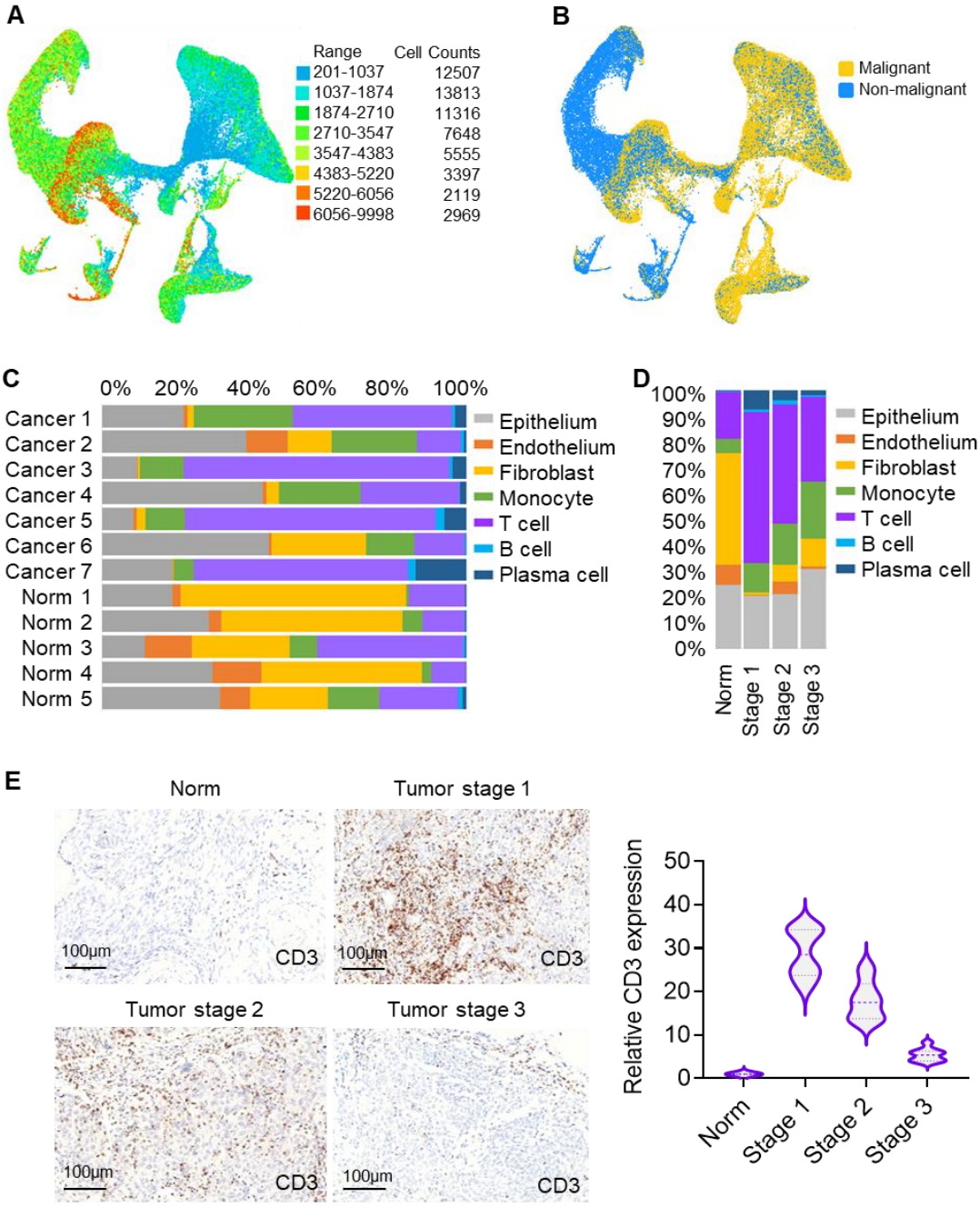
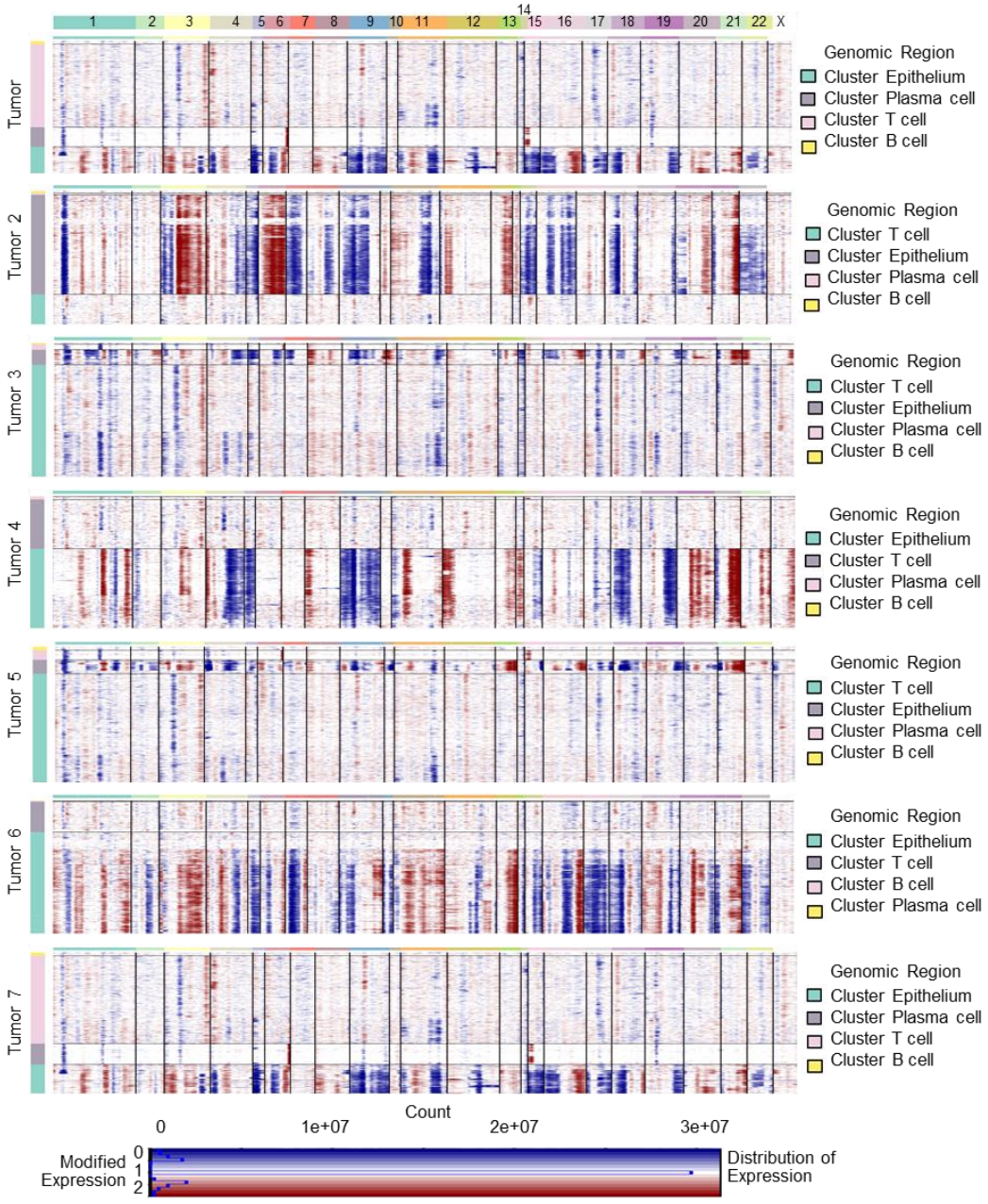
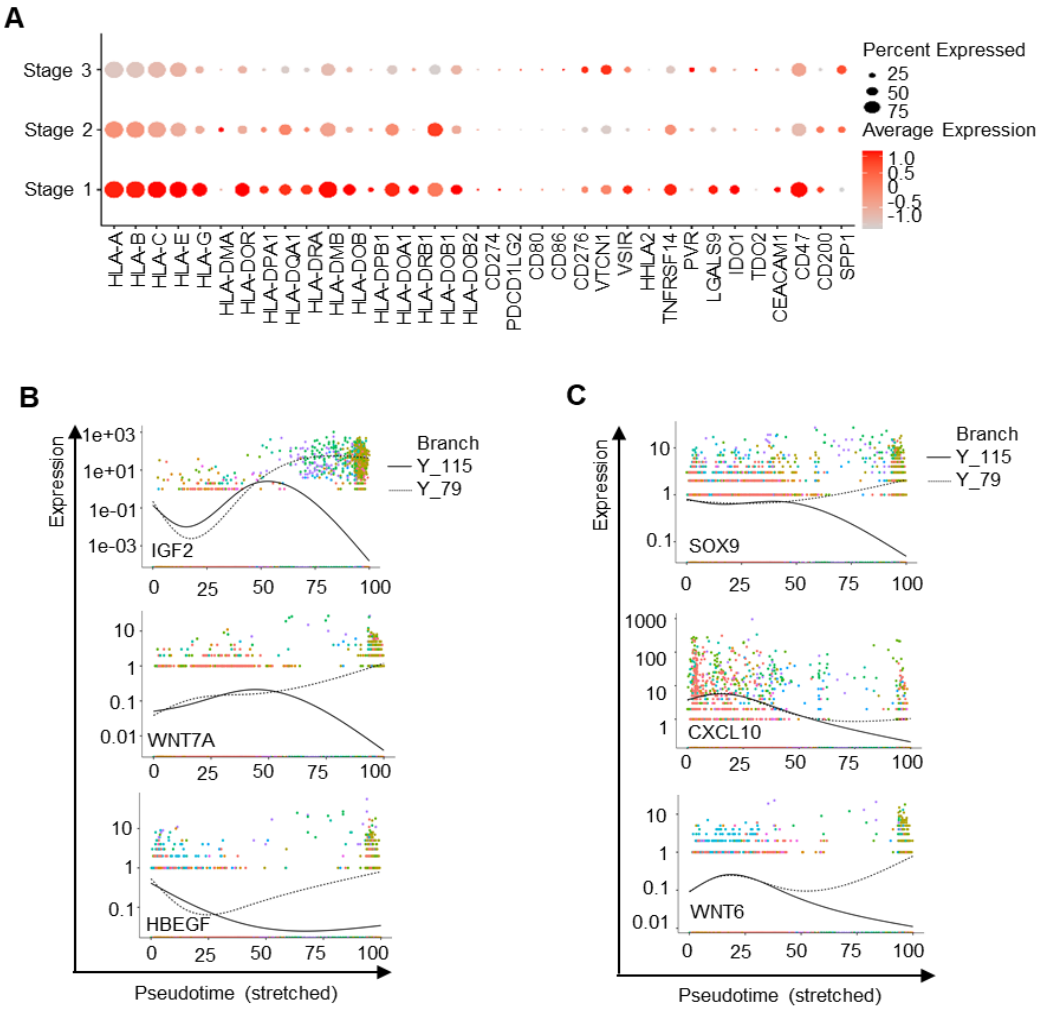


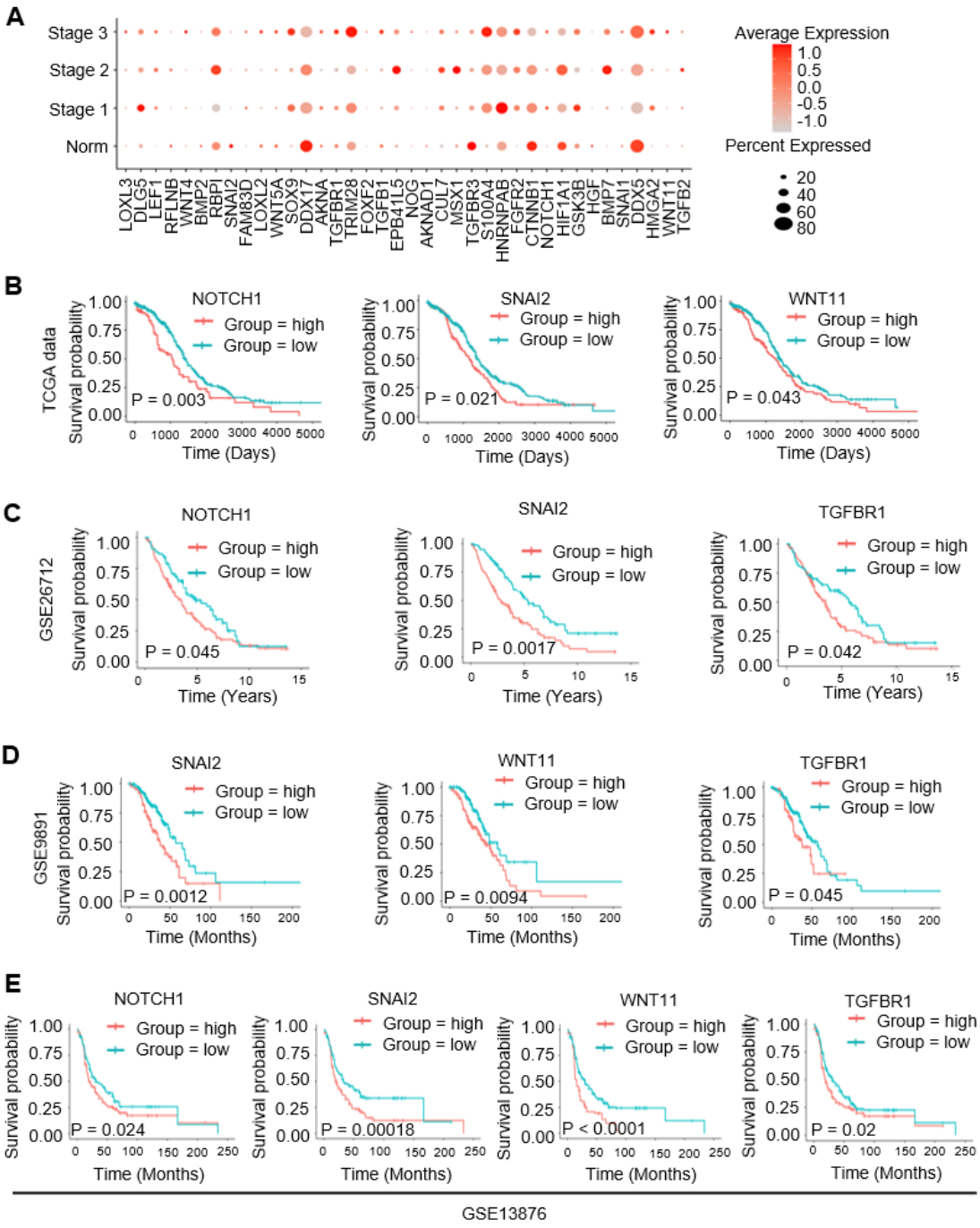
Supplementary Fig. S1. Overview of the 59,324 single cells form HGSOC and nonmalignant ovarian samples. (A) UMAP plot of the 59,324 cells profiled here with each cell color coded for the number of transcripts detected in that cell. (B) UMAPs plots demonstrate cells from malignant (Yellow) and non-malignant (Blue) patients. (C) The fractions of seven cell types in each patient. (D) The percentages of seven cell types in different stages of HGSOC. (E) The validation of CD3 expression in different tumor-stage HGSOC ovarian tissues and non-malignant ovarian tissues using IHC staining.



Supplementary Fig. S2. Copy-number variation analysis of HGSOC cells. Inferred large-scale copy number variations (CNVs) help identify malignant and non-malignant cells. Epithelial and spike in control cells are included in the y axis and chromosomal regions on the x axis. Deletions (blue) or amplifications (red) were inferred by averaging expression on the respective chromosomes.

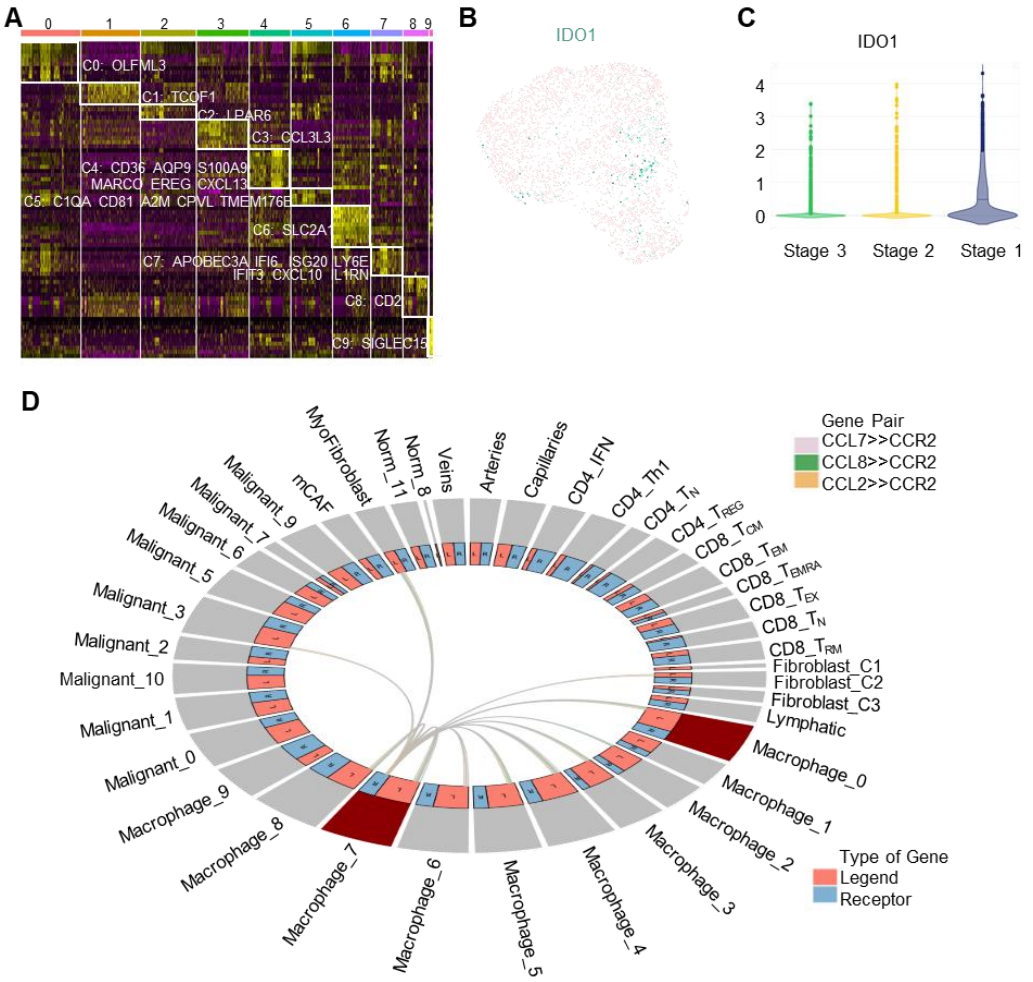


Supplementary Fig. S3. Features of epithelial cells. (A) The features of immune checkpoint inhibition ligand genes expressed in different stages of HGSOC tumor cells. (B and C) Expression of stage 3- (B) and stage 1-specific (C) marker genes across pseudospace in HGSOC epithelial cells. Cells are colored according to the fraction from which they were isolated.

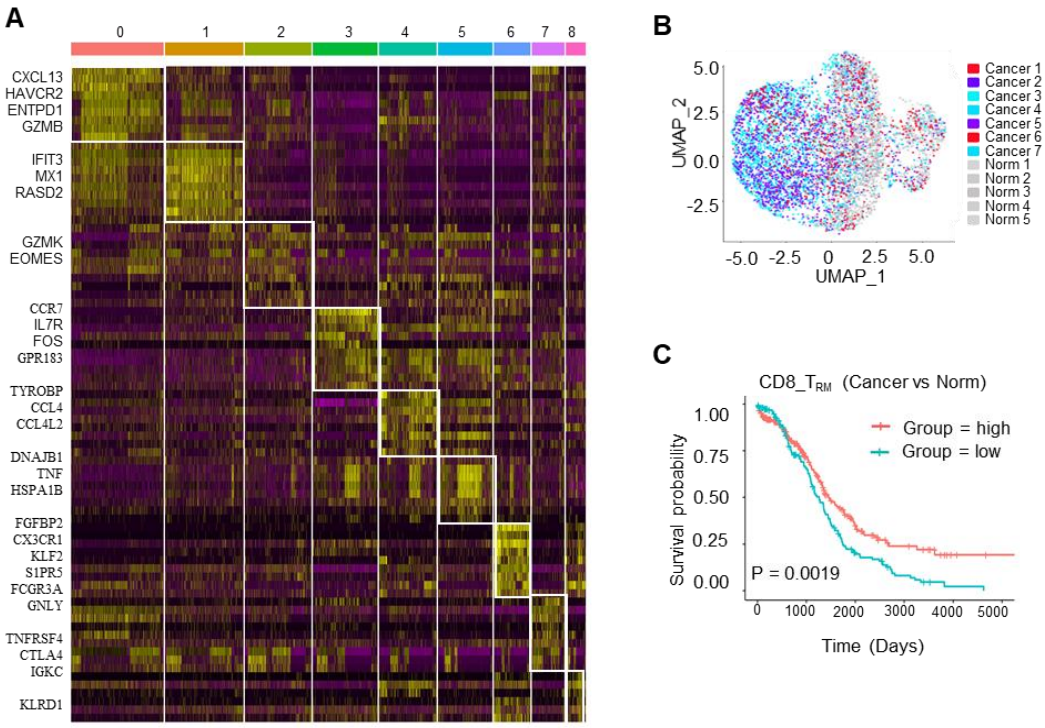


Supplementary Fig. S4. The prognostic value of EMT markers in TCGA and GEO HGSOC tumors. (A) Dot plots showing the expression levels of specific EMT-associated genes in different stages of HGSOC and nonmalignant ovarian tissues. (B) The Kaplan–Meier curves show the overall survival of 373 TCGA HGSCO patients stratified by specific EMT-associated genes. P value was calculated by log-rank test. (C) The Kaplan–Meier overall survival curves of GEO HGSOC patients (GSE26712, n = 185) grouped by specific EMT-associated genes. P value was calculated by log-

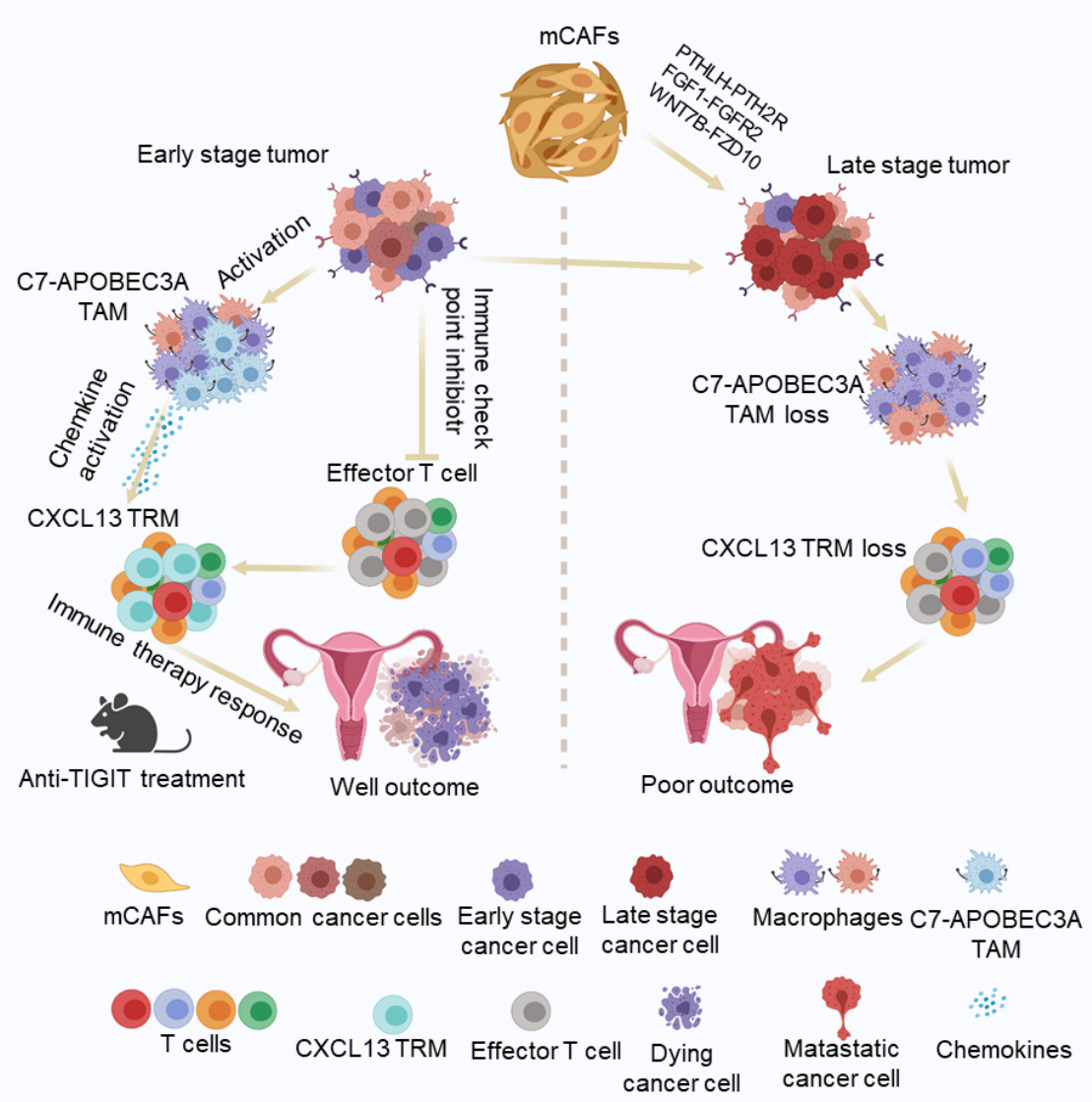
rank test. (D) The Kaplan–Meier overall survival curves of GEO HGSOC patients (GSE9891, n = 229) grouped by specific EMT-associated genes. (E) The Kaplan–Meier overall survival curves of GEO HGSOC patients (GSE13876, n = 415) grouped by specific EMT-associated genes. P value was calculated by log-rank test.



Supplementary Fig. S5. Features of macrophages. (A) Heatmap of the macrophage clusters with unique signature genes. (B) UMAP plot color-coded for expression (Pink to Green) of IDO1 for the macrophages. (C) Violin plots with the fraction of IDO positive cells relative to the total macrophage count grouped by tumor stages. (D) Model of the cross-compartment chemokine ligand-receptor interactions among macrophage_0, macrophage_7 and TME.



Supplementary Fig. S6. Features of CD8$^+$ T cells. (A) Heatmap showing expression levels of specific marker genes in each CD8$^+$ T cell cluster. (B) The UMAP plot demarcated by colors showing the different stages of HGSOC tumors and non-malignant ovarian samples. (C) Kaplan–Meier survival curves for overall survival from TCGA HGSOCs showing significant prognostic separation according to differentially expressed CD8$^+$ T_{RM} marker gene signature (Cancer vs Norm) derived from single-cell data. Log-rank P value is shown.



Supplementary Fig. S7. scRNA-seq signatures reveal the clinical-stage-specific features of the HGSOC cellular ecosystem. Features shared in early-stage tumors are shown on the left side and features shared in late-stage tumors are shown on the right side of the figure.