**Supplementary Data** **Figure Legends**

**Supplementary Fig. S1.** Treatment schedule for the ten ovarian cancer patients who received at least five cycles of chemotherapy. Color scale of the grey bar represents the relative CA125 level for each individual patient. Patients labeled in black are CA125 complete responders and patients in red are CA125 incomplete responders. NED, no evidence of disease; NA, not acquired.

**Supplementary Fig. S2.** Circulating T cell responses to viral antigens throughout chemotherapy in CA125 complete responders and CA125 incomplete responders. **A and B**, IFNγ ELISpot responses of CA125 complete responders (**A**) and CA125 incomplete responders (**B**) over the course of chemotherapy. ELISpot data were background (OVA)-subtracted with n = 3 biologically independent samples. Each data point represents the mean ± standard error of the mean (s.e.m.). Repeated-measures regression model was used for generating *P*-values.

**Supplementary Fig. S3. A and B,** Relative changes of ELISpot response to FluA (**A**) and CEF (**B**) at each timepoint after chemotherapy compared to baseline. Values were set to 3x the control (OVA) if the average of 3 replicates was smaller than this limit before normalization. (Thus, a flat line at 1.0 represents values smaller than 3x the control.) The black lines represent CA125 complete responders while the red lines represent CA125 incomplete responders.

**Supplementary Fig. S4.** Percent positive ELISpot responses to FluA and CEF of healthy donors (n = 10) and patients at baseline (n = 6), C3 (n = 7), C6 (n = 7) and post-chemotherapy (n = 7). Positivity was defined as SFC responses at least 3x higher than paired negative controls.

**Supplementary Fig. S5.** TCR repertoire dynamics across primary treatment for ovarian cancer. **A,** Heatmap of read counts for samples of the 8 patients (Pts. 1, 2, 4, 5, 6, 7, 8, and 10). **B,** Dynamics of clonotype diversity for Patients 1-10 before and after chemotherapy (initial cohort, left), 5 additional patients (Patients A-E) before and after chemotherapy + surgery (middle), and 2 healthy donors with longitudinal blood draws (right). Black lines represent CA125 complete responders, red lines represent CA125 incomplete responders, and blue lines represent two healthy blood donors. **C**, Clonotype diversity by normalized Shannon Index of 12 healthy donors (including 10 healthy donors at baseline, and day 1 blood draw of the 2 healthy donors with longitudinal data), Patients 1-10 (left), and 5 additional patients (Patients A-E, right) as in **B**. Bars represent the median value for each group. **D,** Proportions of the top 100 clonotypes over the course of chemotherapy treatment in patient 1. Top 100 clonotypes were ranked according to the clonotype proportion at Baseline. Total UMIs at Baseline, C3, C6, and Post were 17040, 22351, 51254, and 41719, respectively.

**Supplementary Fig. S6.** Transcriptional profile of integrated PBMCs for cell type identification. Feature plots of selected marker genes for the integrated clusters of patients 1, 2, 3, 6, and 7.

**Supplementary Fig. S7. A-E**, Quantification of the percentage, by single cell RNAseq, of B cells (**A**), NK cells (**B**), DCs (**C**), CD4+ T cells (**D**), and CD8+ T cells (**E**) before chemotherapy (Baseline) and after the third cycle of chemotherapy (C3). *P*-value between Baseline and C3 was calculated using a two-sided one-sample t-test. Black lines represented CA125 complete responders and the red line represents the CA125 incomplete responder.

**Supplementary Fig. S8.** Flow cytometric analysis of monocytes and T cells before and after chemotherapy. **A-B**, Quantification of the percentage of CD14+ monocytes (**A**) and CD3+ T cells (**B**) pre-chemotherapy (Baseline) and after the third cycle of chemotherapy (C3) for the 5 patients from single cell RNAseq analyses (Pts. 1, 2, 3, 6, and 7). *P*-values were calculated using a two-sided one-sample t-test for each of the 5 patients (Pts. 1, 2, 3, 6, and 7).

**Supplementary Fig. S9.** Transcriptional profile of CD8+ and CD4+ T cell sub-clusters. **A and B**, Expression heat map for the indicated gene signatures (lineage, naïve or memory, inhibitory, activation, effector, transcription factor, and NK/γδ-like) by CD8+ (**A**) and CD4+ (**B**) T cell sub-clusters. T cell subclusters are denoted by color keys across the top of each heat map, which correspond to legends on the right: TCM: central memory T; TEM: effector memory T; MAIT: Mucosal-associated invariant T; CTL: cytotoxic T; Treg: regulatory T cells.

**Supplementary Fig. S10.** Stability of T cell subpopulations following chemotherapy. **A-D**, Clonotype dynamics in CD8+ T cells. **A,** UMAP of the CD8+ T cell subpopulations of 5 patients (Pts. 1, 2, 3, 6, and 7). **B,** Distribution of multitons (TCR clonotypes with multiple clones) and singletons (TCR clonotypes with a single clone) for the CD8+ TCR clonotypes. **C,** Frequency map of CD8+ TCR clonotypes. The frequency of each TCR clonotype was calculated within each sample. **D,** Summary table of the number of CD8+ T cells and TCR clonotypes in each of the 5 patients pre- (Baseline) and after 3 cycles of chemotherapy (C3). Pie charts represent percentages of multitons and singletons in each CD8+ T cell states; colors correspond to legends in **A** and **B**. **E-H**, Clonotype dynamics in CD4+ T cells. **E,** UMAP of the CD4+ T cell subpopulations of the 5 patients (Pts. 1, 2, 3, 6, and 7). **F,** Distribution of the multitons and singletons of the CD4+ TCR clonotypes. **G,** Frequency map of the CD4+ TCR clonotypes. The frequency of each TCR clonotype was calculated within each sample. **H,** Summary table of the number of CD4+ T cells and TCR clonotypes in each of the 5 patients at Baseline and C3. Pie charts represent percentages of multitons and singletons in each CD4+ T cell state; colors correspond to legends in **E** and **F**.

**Supplementary Fig. S11.** Intersection of TCR clonotypes and T cell subclusters. **A**, Proportion of clonotypes belonging to proliferating, naïve, effector memory (TEM), central memory (TCM) CD8+ T cell and Mucosal-associated invariant T (MAIT) subclusters in each of the 5 patients (Pts. 1, 2, 3, 6, and 7), before and after the third cycle of chemotherapy. **B**, Changes in percent clonotype of the 5 patients in each CD8+ subcluster after the third cycle of chemotherapy. **C**, Proportion of clonotypes belonging proliferating, naïve, TCM, TEM, cytotoxic (CTL) CD4+ T cells, and regulatory T cell (Treg) subclusters in each of the 5 patients before and after the third cycle of chemotherapy. **D**, Changes in percent clonotype of the 5 patients in each CD4+ subcluster after the third cycle of chemotherapy. *P*-values were calculated using a two-sided one-sample t-tests. Black lines represent CA125 complete responders and the red lines represent a CA125 incomplete responder.

**Supplementary Fig. S12.** Complete blood count (CBC) absolute monocyte values. Bars represent the median monocyte number at the corresponding time point. Statistical testing using a Wilcoxon rank-sum test.

**Supplementary Fig. S13.** Analysis of complete blood count (CBC) monocyte values in a cohort of 27 ovarian cancer patients undergoing neoadjuvant chemotherapy. **A**, CBC absolute monocyte count density (i.e. distribution of monocyte counts) for the cohort of patients pre-treatment and after three cycles of neoadjuvant chemotherapy (on treatment). **B**, CBC monocyte percentage pretreatment and after three cycles of neoadjuvant chemotherapy. Box plots represent the median and 25th and 75th percentiles. Dots represent individual patients, with grey lines connecting pre- and on-treatment values. Statistical testing using a paired T test.

**Supplementary Fig. S14.** Identification of monocyte subpopulations. **A**, UMAP of monocyte subpopulations from the integrated PBMC samples of patients 1, 2, 3, 6, and 7. Subpopulations were categorized using marker genes identified by Villani and colleagues1. **B**, Average expression (color) and percent cells expressing (dot size) of 5 top signature genes for each monocyte subpopulation. **C**, Relative percentage of monocyte subpopulations from Patients 1, 2, 3, 6, and 7, at the indicated timepoints. **D**, Relative monocyte sub-population frequency pre-chemotherapy (Base) and after the third cycle of chemotherapy (C3). Black lines represent CA125 complete responders, and the red line represents the CA125 incomplete responder.

**Supplementary Fig. S15.** HLA class II expression in monocyte populations after chemotherapy. **A**, Average expression (color) and percent expressing cells (dot size) for HLA class II genes in each monocyte subpopulation. **B**, Heatmap of the average expression of the 8 HLA class II genes in CD14++CD16- classical (left) and cytotoxic (right) monocyte subpopulations at baseline and C3. Patients labeled in black were CA125 complete responders and the patient labeled in red was a CA125 incomplete responder.

**Supplementary Fig. S16.** Identification of DC subpopulations. **A**, UMAP of DC subpopulations from the integrated PBMC samples from patients 1, 2, 3, 6, and 7. Subpopulations were categorized using marker genes identified by Villani and colleagues1. **B**, Average expression (color) and percent cells expressing (dot size) each of the top 2 signature genes for the indicated DC subpopulations. **C**. Quantification of the percentage of each DC subpopulation pre-chemotherapy (Base) and after the third cycle of chemotherapy (C3). Black lines represent CA125 complete responders, and the red line represents the CA125 incomplete responder. pDC: plasmacytoid dendritic cell.

**Supplementary Fig. S17.** Gene set enrichment analysis of all the upregulated genes (listed across the top) in the monocyte population after the third cycle of chemotherapy, compared to baseline (pre-chemotherapy) for 5 patients (Pts. 1, 2, 3, 6, and 7). Shaded boxes indicate the presence of a specific gene in the indicated gene set on the left.

**Reference**

1. Villani AC, Satija R, Reynolds G, Sarkizova S, Shekhar K, Fletcher J*, et al.* Single-cell RNA-seq reveals new types of human blood dendritic cells, monocytes, and progenitors. *Science* 2017;**356**(6335) doi 10.1126/science.aah4573.