Ardighieri et al. Infiltration by CXCL10 secreting macrophages is associated with antitumor immunity and response to therapy in ovarian cancer subtypes

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Supplementary Figure S1. Digital image analysis of T-cells, tumor-associated macrophages (TAMs) and Plasmacytoid dendritic cells (PDCs) in ovarian carcinoma. Sections are from one representative HGSC case. A, D, G: digitalized immunostained slides (200x magnification; scale bar 200 um) recognizing CD3⁺ T-cells (A), CD163⁺ TAMs (D) and BDCA2⁺ PDCs (G). B, C, E, F, H, I: absolute immune cells count performed with Tissue Studio 2.0, based on segmentation of nucleus objects (B, E, H) and recognition of positive intraepithelial and stromal immune cells (C, F, I), with different staining intensity (yellow mild, red moderate and brown strong).

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Supplementary Figure S2. **Distribution of immune cell variables.** Q-Q plots of CD3⁺, log₂CD3⁺, CD163⁺ and log₂CD163⁺ cells densities showing that both immune populations densities follow log-normal distributions.



Supplementary Figure S3. **Progression free survival and immune contexture.** Univariable analysis of progression free survival estimates (Kaplan-Meier method) according to high density of CD3⁺ T-cells (**A**), high density of CD163⁺ TAMs (**B**) or Immunoscore classes (**C**). P values estimated with log-rank test (**A**, **B**), pairwise comparisons p-values adjusted with FDR (**C**). Forest-plot reporting H.R. with CI_{95%} of multivariable progression free survival analysis with Cox-model (**D**).



Supplementary Figure S4. Differential gene expression analysis. Volcano plots showing differentially expressed genes in patients affected by ovarian cancer, compared to healthy ovarian controls (A), and differentially expressed genes in HGSC compared to EC or CCC (B). Light blue dots representing significant different expressed genes by FDR adjustment.



Supplementary Figure S5. Limited infiltration of plasmacytoid dendritic cells in OCs. Violin plots of immune cells distribution in OCs sections, p value estimated by ANOVA (A); representative sections from OCs cases immunostained for BDCA2 showing the rare presence of BDCA2⁺ PDCs (B). Magnification 200x.



Supplementary Figure S6. Clinical correlates of OC-IS³⁰. Box plots showing OC-IS³⁰ score in different tumor stages groups (**A**), BRCA1 and BRCA2 mutational status groups (**B**) and scatter plot showing no correlation between OC-IS³⁰ score and TMB (**C**). P values estimated by Wilcoxon unpaired test in A, B and Spearman test in C.



Supplementary Figure S7. Macrophage polarization in OCs. In A, B and G the IL6, COX2 and CXCL10 genes expression was measured by qRT-PCR on polarized monocyte-derived M ϕ , IFNa (100 U/mL) unstimulated or stimulated with IFN- γ (50 ng/mL) or IFN- γ (20 ng/mL) + LPS (100 ng/mL) or IL-4 (20 ng/mL) or IL-10 (20 ng/mL) for 4 or 18 hours. The mRNA relative expression (- Δ Ct) was normalized to the housekeeping gene using the comparative Ct method. The mean and SD of technical replicates (n = 3) are shown. The statistical significance was calculated by a Student's t test. * p < 0.05; ** p < 0.01; **** p < 0.001; **** p < 0.0001. In C sections from cell-block preparations of polarized monocyte-derived M ϕ subjected to *in situ* hybridization as labeled. Magnification 400X. Western blot analysis performed on polarized monocyte-derived M ϕ illustrate the protein expression of IRF1, pSTAT1Y701 and IRF4 as labeled (D, E). Sections from cell-block preparations of polarized monocyte-derived M ϕ subjected to *in situ* hybridization as labeled to *in situ* hybridization as labeled. Magnification 400X. (F).



Supplementary Figure S8. M1-type M ϕ polarization across cancer types. Sections from various cancer types (A, B) immunostained as labeled. Magnification 200X (B: a-h; scale bar 100 um) and 400X (A, B: i-l, scale bar 50 um). Sections from various cancer types showing the presence of CD163⁺pSTAT1Y701⁺ (A, a melanomas, b colorectal carcinoma, c endometrial carcinoma, d lung carcinoma, e oral squamous cell carcinomas, f laryngeal carcinoma, g triple negative breast carcinoma, h HER2⁺ breast carcinoma, d lung carcinoma, e oral squamous cell carcinomas, f laryngeal carcinoma, g triple negative breast carcinoma, c endometrial carcinoma, d lung carcinoma, e oral squamous cell carcinomas, f laryngeal carcinoma, g triple negative breast carcinoma, c endometrial carcinoma, h HER2⁺ breast carcinoma, and it is expression is detected in CD163⁺ TAMs (B: i and k melanoma; j colorectal carcinoma).



Supplementary Figure S9: scRNAseq analysis of myeloid cells across cancer types. Heatmap showing normalized expression of the top 25 most variable genes in cluster 9, as defined in Figure 9A.

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