Interferon signaling in ascites-associated macrophages is associated with a favorable clinical outcome in a subgroup of ovarian carcinoma patients

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Figure S1.

Multidimensional scaling analysis of TAM samples.

Clusters A and B refer to the clusters identified by PCA in Fig. 2A. Analysis was performed as for PCA except that the `sklearn.manifold.MDS` function `mds.fit_transform()` was used.
Inverse association of \textit{PCOLCE2} expression with high-grade serous ovarian cancer survival (RFS).

The Kaplan-Meier plot was generated by the KM plotter online tool (http://kmplot.com).

Reference

Figure S3.

Venn diagram showing the overlaps of the upstream regulators gene sets identified in Fig. 3C.
Figure S4.

Subgroup-selective expression of signature genes.

Expression of the ECM-associated genes of signature A identified by GO enrichment analysis (Fig. 3C) in subgroup A and B TAMs. Boxes show the upper and lower quartiles, whiskers the 95% CI, and horizontal lines the median.
Hierarchical clustering was performed with all TAM samples (n=18) using the `scipy.cluster.hierarchy` functions `linkage (method="weighted", metric="correlation")` and `dendrogram (truncate_mode = "none", color_threshold=1)`.

Green: cluster I; red: cluster II; cyan: cluster III.
Figure S6.

Association of signature A (top) and signature B (bottom) with ovarian cancer survival (OS).

Data (z-scores) were obtained from the PRECOG database, which contains the results of a meta-analysis of 1763 patients from 12 studies.

Reference

Figure S7.

Association of the ECM remodeling-linked genes of signature A with high-grade serous ovarian cancer survival.

PRECOG data, details in Figure S5.
Figure S8.

Association of tumor-infiltrating host cells with high-grade serous ovarian cancer survival (OS).

Host cell infiltration inferred from RNA expression data using CIBERSORT was associated with OS. The data show no significant association of OS with myeloid cells, but a trend towards a shorter OS for monocytes.

Reference
Expression of type I IFN genes in different cell types present in ovarian cancer ascites.

Expression of type I IFN genes showing a significant association with OS (Fig. 6A; blue bars) in TAM (n=33), tumor cell (n=22) and TAT (n=5) samples from ovarian carcinoma ascites, and in CD3+ T cells from healthy donors (n=2). Each dot represents an individual sample (see Dataset S1 for details).