Figure S1

Overlap of genes upregulated in ovarian cancer TAMs relative to non-polarized MDMs (M0) (Schumann *et al.,* 2015 and present study) with genes upregulated in MDMs polarized with LPS+INFγ (M1), IL-13 (M2a), ultrapure LPS + immune complexes (M2b) or IL-10 (M2c) (Xue *et al.,* 2014).

A total of 1710 genes were upregulated (fold change >1.5) in TAMs versus non-polarized MDMs (median TPM>3 in TAMs).

Analysis of the MDM data sets published by Xue *et al.* (2014) yielded the following groups (minimum fold change 1.5):
M1, n=871; M2a, n=464; M2b, n=428; M2c, n= 179.

The overlaps of these groups with genes upregulated in TAMs were as follows:
M1, n=138 (8.1%); M2a, n=47 (2.7%); M2b, n=101 (5.9%); M2c, n= 35 (2.0%).
No overlap ("other") was detectable for the majority of genes upregulated in TAMs (81%).

References

Schumann T, Adhikary T, Wortmann A, Finkernagel F, Lieber S, Schnitzer E, Legrand N, Schober Y, Nockher WA, Toth PM, et al: **Deregulation of PPARβ/δ target genes in tumor-associated macrophages by fatty acid ligands in the ovarian cancer microenvironment.** *Oncotarget* 2015, **6:**13416-13433.

Xue J, Schmidt SV, Sander J, Draffehn A, Krebs W, Quester I, De Nardo D, Gohel TD, Emde M, Schmidleithner L, et al: **Transcriptome-based network analysis reveals a spectrum model of human macrophage activation.** *Immunity* 2014, **40:**274-288.
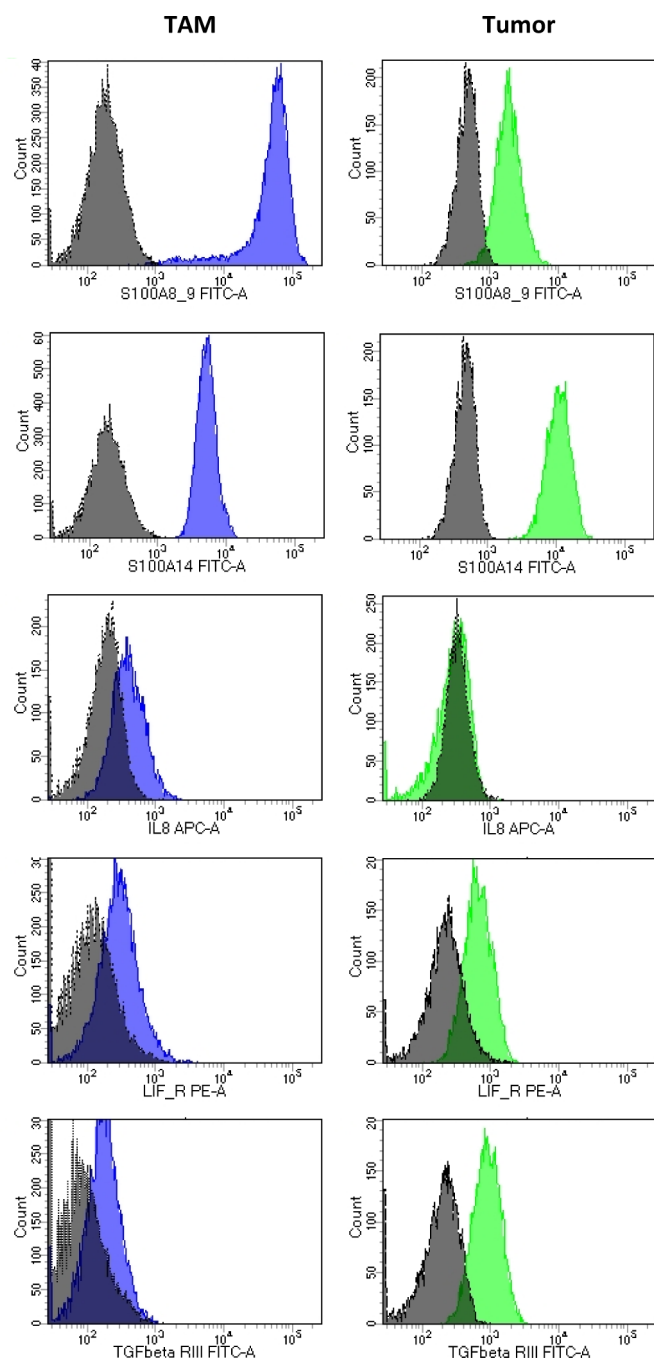
Figure S2

FACS histograms of intracellular cytokine expression (S100A8/A9, S100A14, IL-8) and surface receptor exposure (LIFR, TGFBR3) by TAMs (blue peaks) and tumor cells (green).

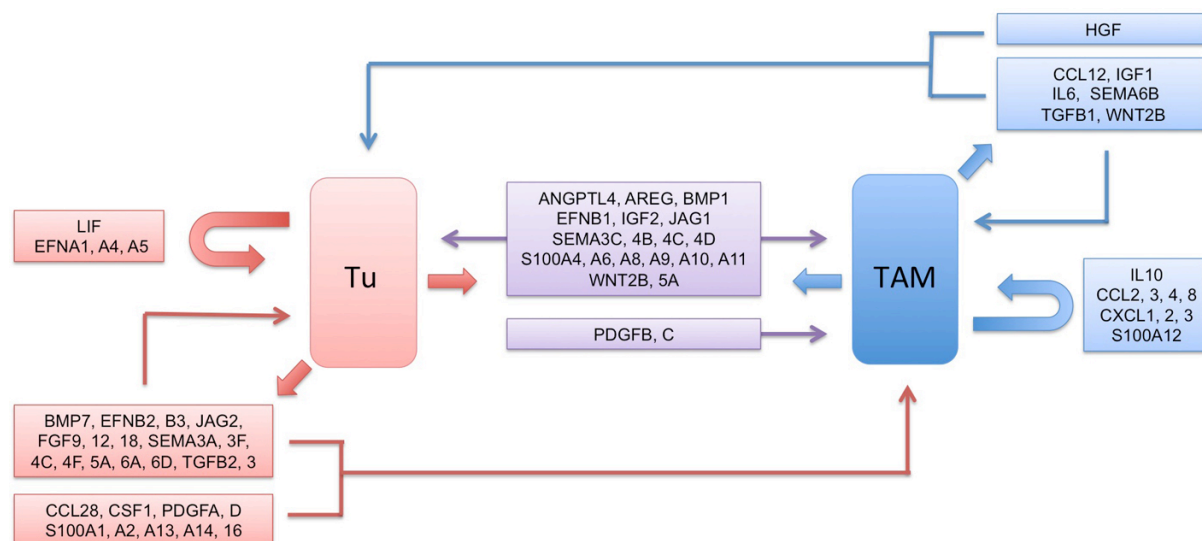Grey areas show the staining with matched isotype control antibodies.

Figure S3

Cellular origins and targets of cytokines and growth factors in the ovarian cancer microenviroment.

The model is based on the RNA-Seq data in Figure 2 and the scheme in Figure 4. Gene names are explained in Dataset S1.

Red: ligands mainly expressed by tumor cells; blue: ligands mainly expressed by TAMs; purple: ligands expressed by both cell types.

Thin arrows point to the direction of the major target cell; straight broad arrows indicate the origin of the ligands; bend arrows show autocrine mechanisms.
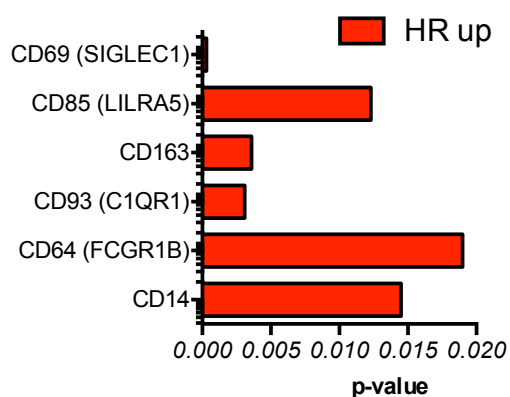
Figure S4

Association of relapse-free survival (RFS) with the expression of macrophage genes.

Summary of RFS analyses for 1018 serous ovarian carcinoma patients depicting the results of logrank P tests and the directions of the respective hazard ratio (HR), using the KM plotter database and online tool [37]. Significant instances (for 'JetSet best probe') are shown in red (HR>1) or green (HR<1); grey bars indicate lack of significant associations (p≥0.5) or p > Benjamini-Hochberg critical value for FDR=0.10.