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Supplemental Information

Mouse Ovarian Cancer Models Recapitulate

the Human Tumor Microenvironment

and Patient Response to Treatment

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Tumor Stage 2009 IIA IIB IIC IIIA IIIB IIIC IV - No data

Figure S1. Histological and molecular characterisation of murine HGSOC models, related

to Figure 1. A-F Tissue sections were derived from mouse model tumors and stained with hematoxylin and eosin A: HGS2, representation of tumour cells organised in sheets, scale bar set to 200μm; B: HGS3, representation of spindle-like morphology, scale bar set to 200μm; C: 60577, representation of tumour cells organized in nests, scale bar set to 200μm; D: HGS2, representation of pleomorphic cells with nuclei with prominent nucleoli, scale bar set to 50μm; E: HGS2, necrotic area, scale bar set to 200μm; F: HGS2, calcification, scale bar set to 200μm. G, Hierarchical cluster analysis of murine sample transcriptomes. H, Overlap of differentially-expressed genes (FDR < 0.05) in murine tumours vs normal omental samples. I, OncoPrint showing list of genes with high mutation frequency in TCGA and present in CNA regions in mouse models. Annotation of tumour stage has been included.

COL11A1



RUNX2



VDR



FOLR1



Figure S2. Concordance of murine and human HGSOC tumor-associated proteins, related to Figure 2. **A**, IHC for COL11A1, RUNX2, VDR and FOLR1 staining. Representative images for HGS2 and HuHGS are depicted. For FOLR1, staining on the 30200 model, in which we observed the highest expression of the marker, has been included. Scale bars,100µm (COL11A1) and 50µm, (RUNX2, VDR, FOLR1).



Figure S3. ICGC and TCGA consensus WGCNA, related to Figure 3. A, WGCNA consensus analysis was performed using the ovarian ICGC and TCGA expression datasets and consensus clusters of co-regulated genes are presented as a dendrogram. Colors show different modules (gene programs). **B**, Cluster dendrogram of consensus module eigenvalues (ME) illustrates clustering of programs associated with ECM (MEblue) and immune response (MEgreen) pathways. **C**, Heatmap of consensus ME across TCGA samples (N = 593). **D**, Heatmap of association of C1–C5 classification. Positive associations are shown in red and negative are shown in blue. Pearson's r and p-values are indicated in the fields where a significant association was observed (p < 0.05). **E**, Heatmap of associations are shown in red and negative are shown in blue. Pearson's r and p-values are indicated in the fields where a significant association was observed (p < 0.05). **E**, Heatmap of associations are shown in red and negative are shown in blue. Pearson's r and p-values are indicated in the fields where a significant association was observed (p < 0.05). **E**, Heatmap of associations are shown in red and negative are shown in blue. Pearson's r and p-values are indicated in the fields where a significant association was observed (p < 0.05).



Figure S4, related to Figure 4. Heatmap illustrating expression of angiogenesis-associated

genes (N = 93) across primary HGSOC tumors in the ICGC dataset.



HGS3

HGS3

HGS4

HGS4

Figure S5. Matrix index proteins in HGSOC murine models, related to Figure 5. IHC for

VCAN, FN1, COMP, CTSB, COL11A1, COL1A1. Representative images all six HGSOC murine models and normal omental tissues is shown. Scale bars,100µm. Barplots illustrate the result of digital analysis and quantification of % positive area by Definiens Tissue Studio[®]. Pvalues correspond to one-way ANOVA. Each dot represents a tumor from an individual mouse.

60577



Figure S6. Anti-IL6 treatment of the 60577 murine model, related to Figure 6. Mice

injected with 60577 cells were treated with isotype control or anti-IL-6 2 mg/kg i.p. twice weekly, starting 10 days after cell injection until endpoint. The immune infiltrates were analyzed by flow cytometry. Student's t-test values are depicted on the barplots. Each dot represents a tumor from an individual mouse.