



**Fig. S1 Gene expression analysis of OvCa samples.** **A.** Multidimensional Scaling (MDS) plot of expression data comparing patient samples and their matching PDX samples. Patient samples and PDX samples originating from the same patient cluster together. **B-D.** Deconvolution analysis of OvCa normalized gene expression data. Normalized gene expression data was analyzed using the Carcinoma Ecotyper software (<https://ecotyper.stanford.edu/carcinoma>) that assigns cell abundance and cell states to expression data. Distribution of states is compared between patient ascites samples (n=8) and patient tumor samples (n=14). States are determined based on gene expression clusters pre-specified by the program. The bars represent the average abundance for each state (S01-S09) +/- SEM. P-values denote significant differences in state abundance based on unpaired t-tests. **A-C.** The average estimated abundance of monocyte/macrophage (**A**), CD4+ T cell (**B**) and CD8+ T cell (**C**) states in patient ascites versus patient tumor samples.