



Figure S5. Pro-inflammatory macrophages are decreased, and M2-like macrophages are increased in advanced/metastatic disease, related to **Figure 5**. **(A)** tSNE representation of scRNA-seq data, with labeling of individual myeloid cell populations after sub-clustering. **(B)** Heatmap of myeloid cell lineage and functional markers provides phenotypic information for individual myeloid cell populations. **(C)** Representation of each sample within each myeloid cell cluster, colored by tissue of origin. **(D)** Volcano plot of differentially expressed genes (edgeR) between macrophages (defined from trajectory analysis, right lineage after the bifurcation) from metastatic disease vs those from early and locally advanced disease (thresholds: at least 1.5-fold change, and q value less than 10^{-10}). TradeSeq plots showing both the average expression pattern and individual cell expression values for **(E)** inflammatory cytokines, and **(F)** M2-like macrophage markers.