Supplementary Tables

Supplementary Table S1 - Differentially expressed genes between cells in integrated single-cell RNA seq dataset

Supplementary Table S2 - 3000 most variable genes used to identify cNMF modules, their cNMF weight in each programme, and which programme they are associated with

Supplementary Table S3 - Gene sets used to score cells for each biological process in figure 1 radar plot

Supplementary Table S4 - Cell type frequency for initial broad cell type annotation by sample

Supplementary Table S5 - Assignment of cNMF programmes to all CosMx cancer cells and breakdown of ambiguous cancer cells after threshold removal

Supplementary Table S6 - Moran's I spatial autocorrelation test scores

Supplementary Table S7 - cNMF scores before and after chemotherapy

Supplementary Table S8 - Differences in cNMF score after correction for sample sizes/cell numbers

Supplementary Table S9 - Percentage of cell types within given distances of a cancer cell

Supplementary Table S10 - Mean percentage of cell types within 50uM intervals of a cancer cell

Supplementary Table S11 - Difference in immune cell frequency in tri cell niche with MyoCAF and Cancer compared to M2 macrophages (adjusted for cell abundance)

Supplementary Table S12 - Percentage of cancer immune cells in a niche (radius of 50uM) with a cancer cell and fibroblast subtype (corrected for cell type abundance)

Supplementary Table S13 - Number of differentially expressed genes between niche cancer cells and non-niche cancer cells at 5μm radius increments