A CSF-cytokine code predicts macrophage response polarity and tumor outcomes

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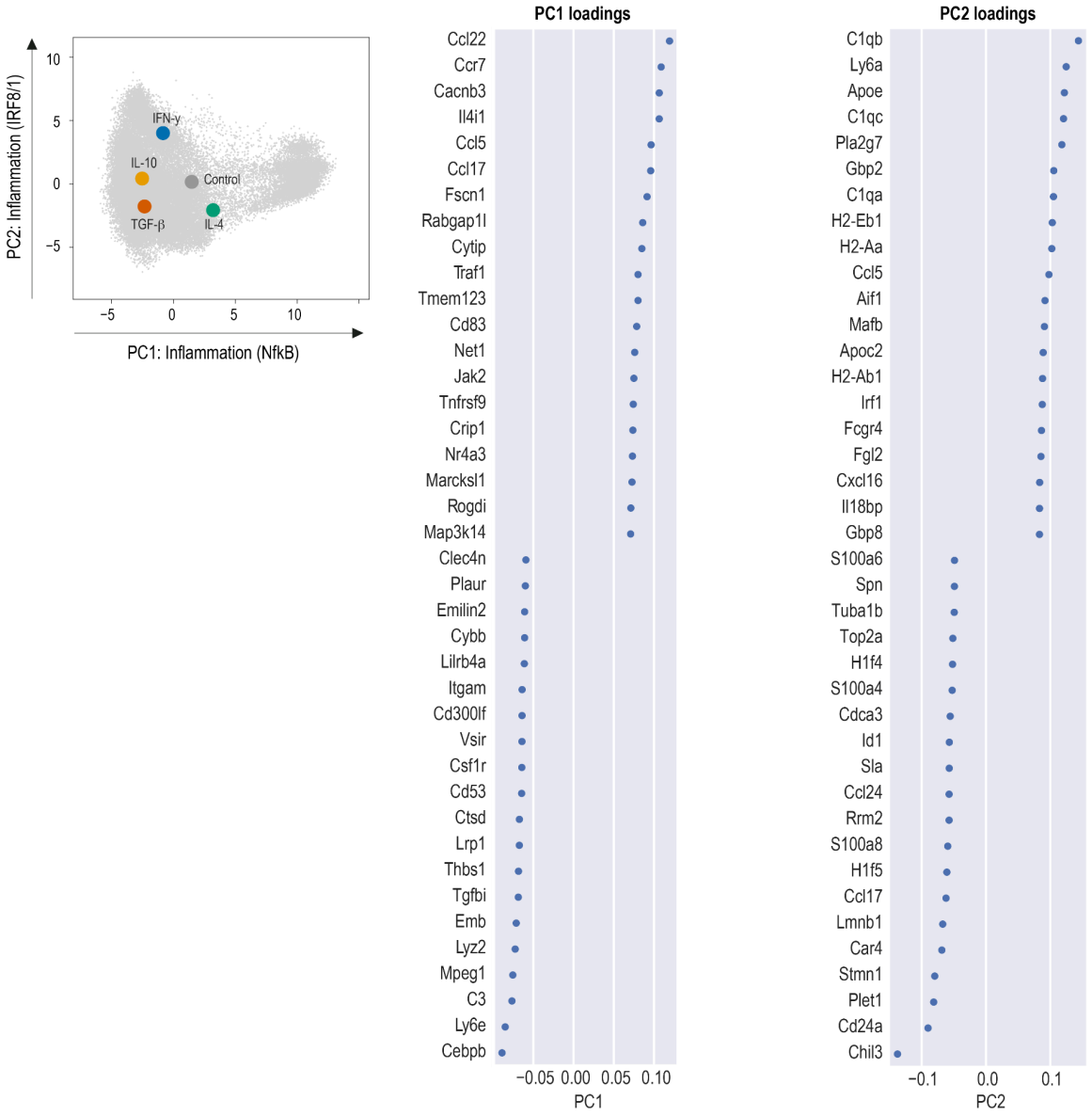
Supplementary Figures

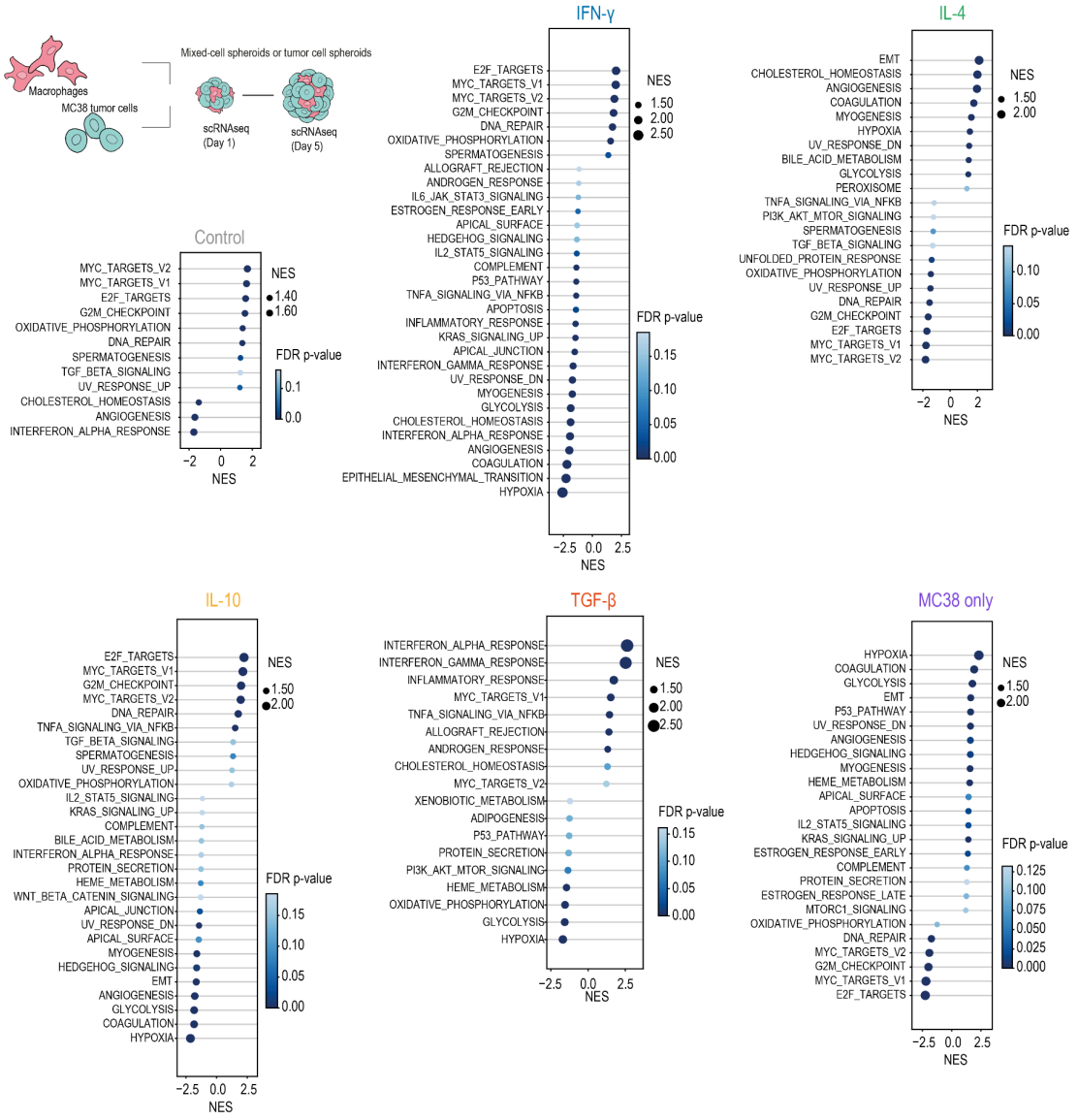
Supplementary Figure 1



Supplementary Figure 1

BM precursors were cultured with GM-CSF alone or in combination with IFN-γ, IL-4, IL-10, or TGF-β and analyzed by multiplexed scRNA-seq (see Fig. 2). Principal-component analysis (PCA) identified two dominant axes of variation. The 20 genes with the highest positive and negative loadings for PC1 and PC2 are listed.

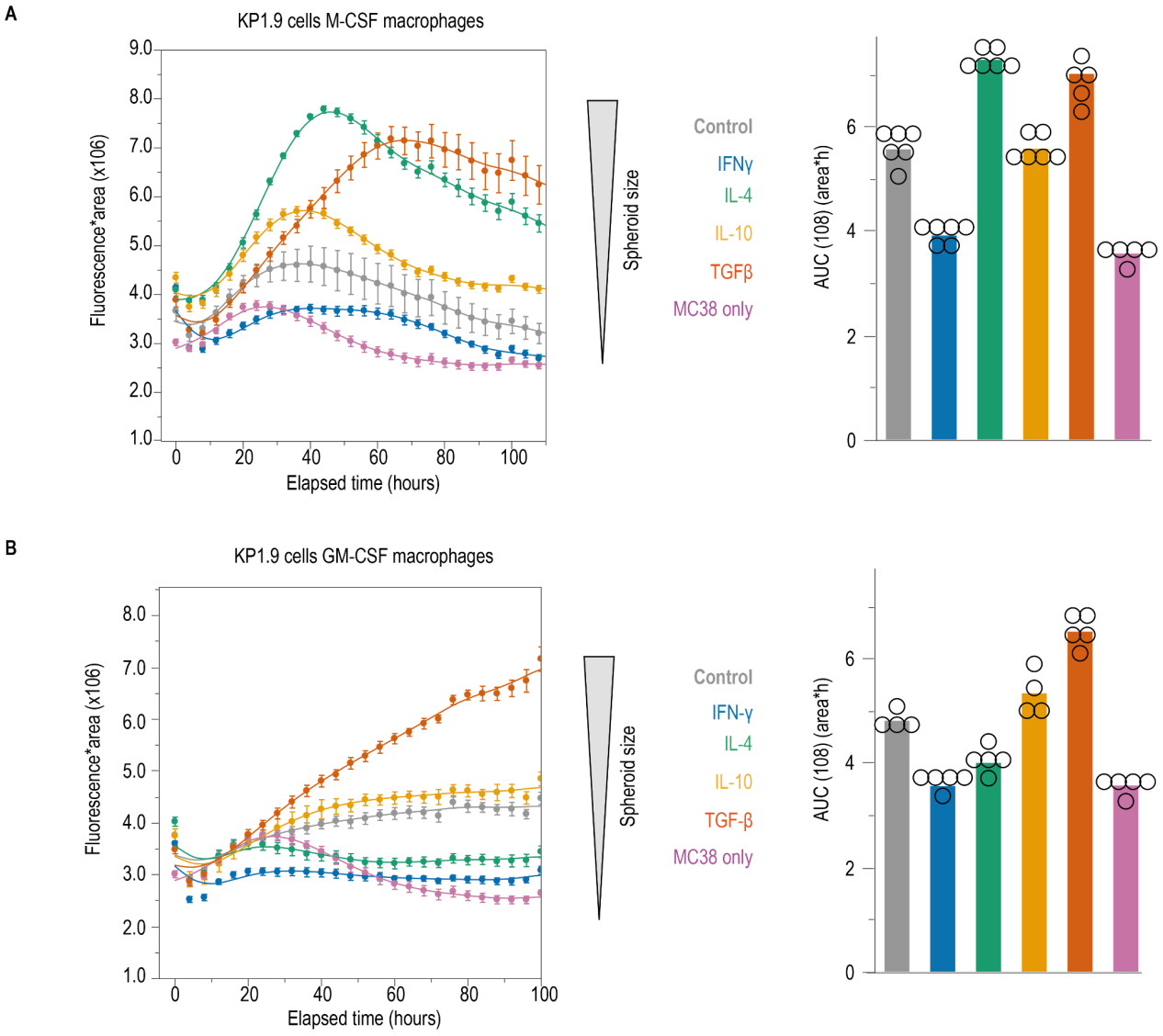
Supplementary Figure 2



Supplementary Figure 2

Time-resolved, multiplexed scRNA-seq experiment of mixed cell spheroids composed of M-CSF macrophages and MC38 cancer cells (see Fig. 4). Cells per treatment were functionally annotated according to GSEA (Hallmark gene sets).

Supplementary Figure 3



Supplementary Figure 3

A. GFP-KP1.9 cells were cultured alone or mixed 1:2 with cytokine-polarised M-CSF or GM-CSF macrophages in ultra-low-attachment plates and imaged for five days.

B. M-CSF macrophages**:** Integrated GFP fluorescence intensities across the spheroid area over time, demonstrating enhanced spheroid growth in the presence of anti-inflammatory macrophages. Data are the mean ± SE of five replicates analyzed within one representative experiment. AUC quantification, one-way ANOVA Dunnett posttest corrected for multiple comparisons (control vs IFN-γ p = <0.0001, control vs IL-4 p<0.0001, control vs IL-10 p >0.999 (ns), control vs TGF-β p<0.0001, control vs TC <0.0001).

C. GM-CSF macrophages: Analysis as in B (Control vs IFN-γ p<0.0001, control vs IL-4 p 0.0002, control vs IL-10 p 0.0234, control vs TGF-β p<0.0001, control vs TC p<0.0001).