

Description of Additional Supplementary Files:

Supplementary Data 1: Differentially expressed genes for each respective cell-type.

Differential expression (DE) analysis between clusters/two groups of cells was performed using the non-parametric Wilcoxon Rank Sum test implemented in the FindMarkers() functions from the Seurat R package. DE testing was limited to genes which show, on average, at least 0.1 log-fold change between the two groups of cells and on genes that are detected in a minimum fraction of 0.01 cells in either of the two populations. A gene was defined as differentially expressed if the absolute average log fold-change (avg_logFC) was >0.25 and the Bonferroni-adjusted p-value <0.01 .

Supplementary Data 2: List of genes used for macrophage phenotyping in Figure 5

Genelist_m1: list of pro-inflammatory (“M1-like”) genes adapted from Xue *et al.* (manuscript reference 26)

Genelist_m2: list of anti-inflammatory (“M2-like”) adapted from Xue *et al.* (manuscript reference 26)