

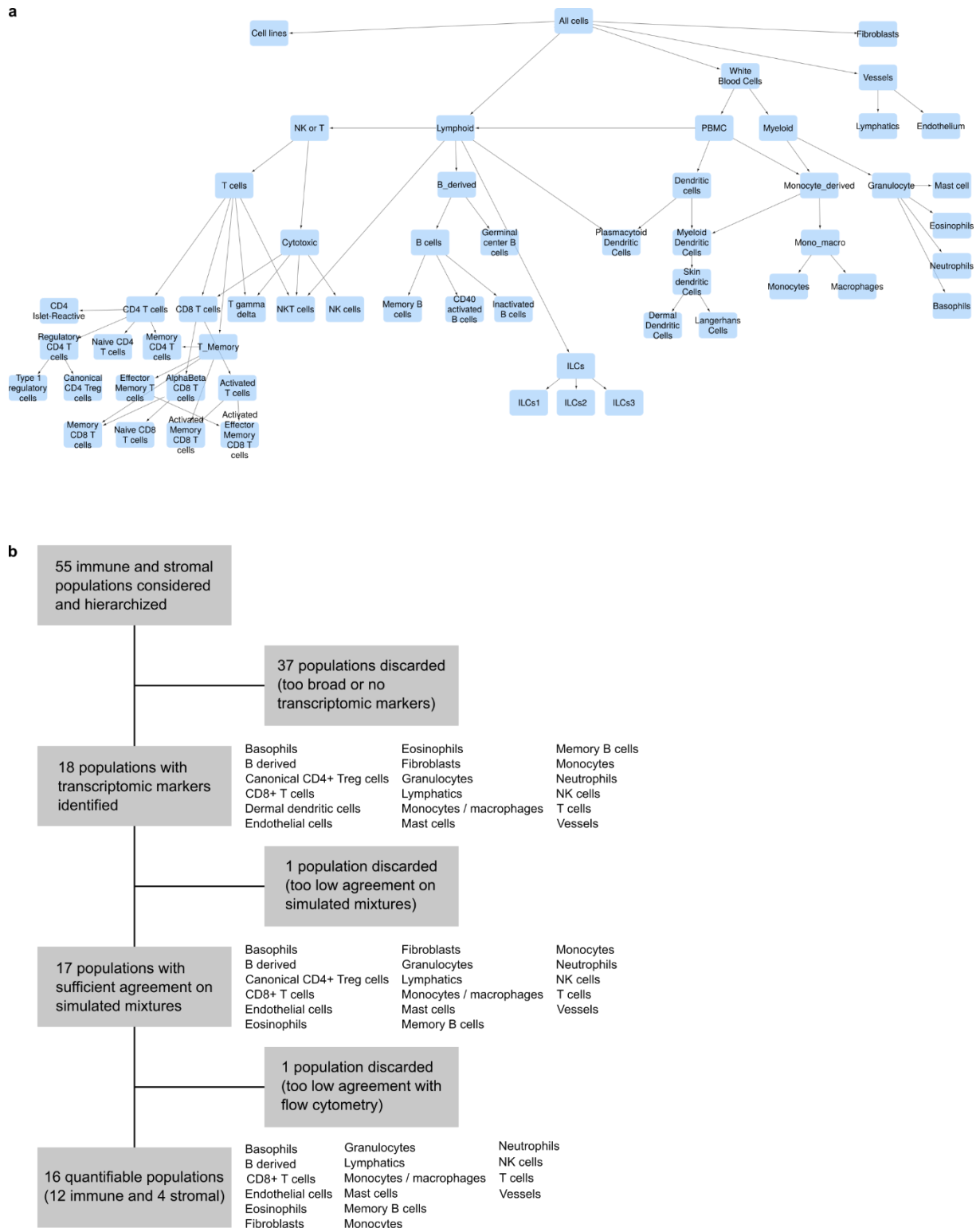


Fig S1: Cell populations and signatures

a Cell populations hierarchy used in the present study. **b** Counts of the number of signatures identified and discarded during the various validation steps.

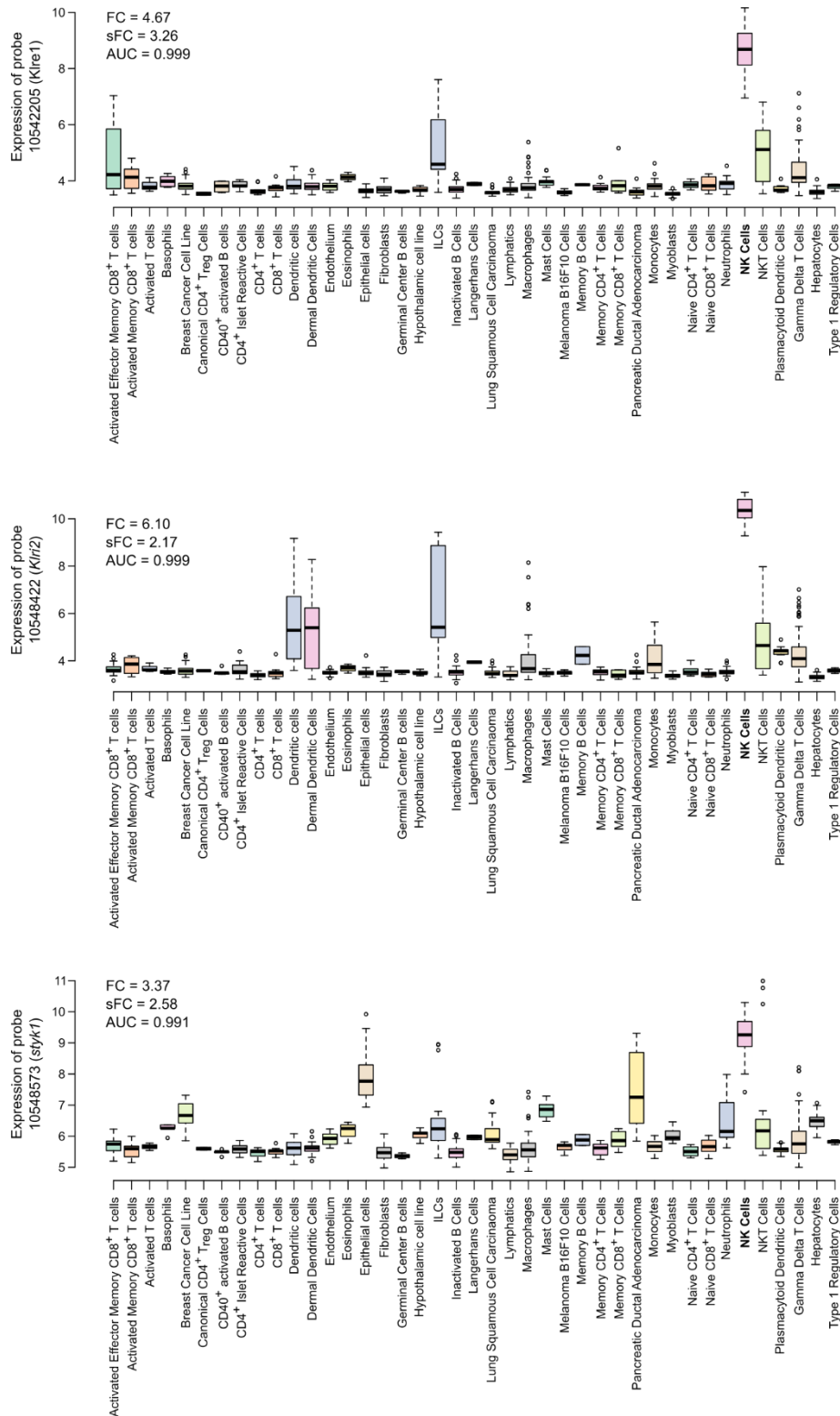


Fig S2: Examples of discarded transcriptomic markers

The three markers presented here satisfied the criteria to be considered as transcriptomic markers for NK cells, but they were discarded during manual curation due to insufficient specificity.

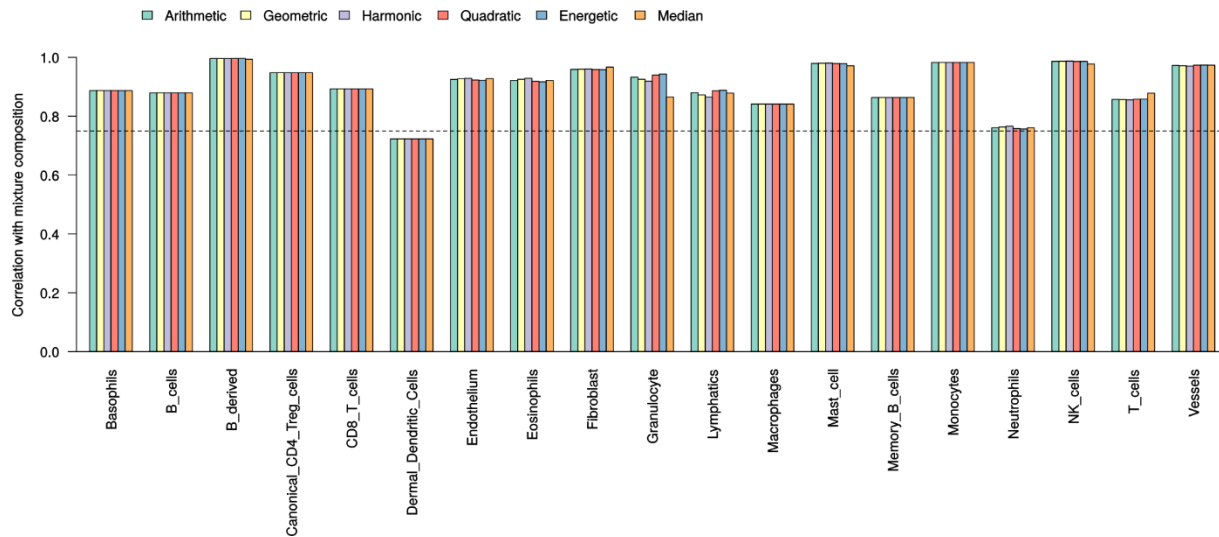


Fig S4: Comparison of different scoring methods.

This figure relates to in silico simulated RNA mixtures. For each cell population, the correlation between the mixtures' compositions and the expression the of the signature was compared for various scoring methods.

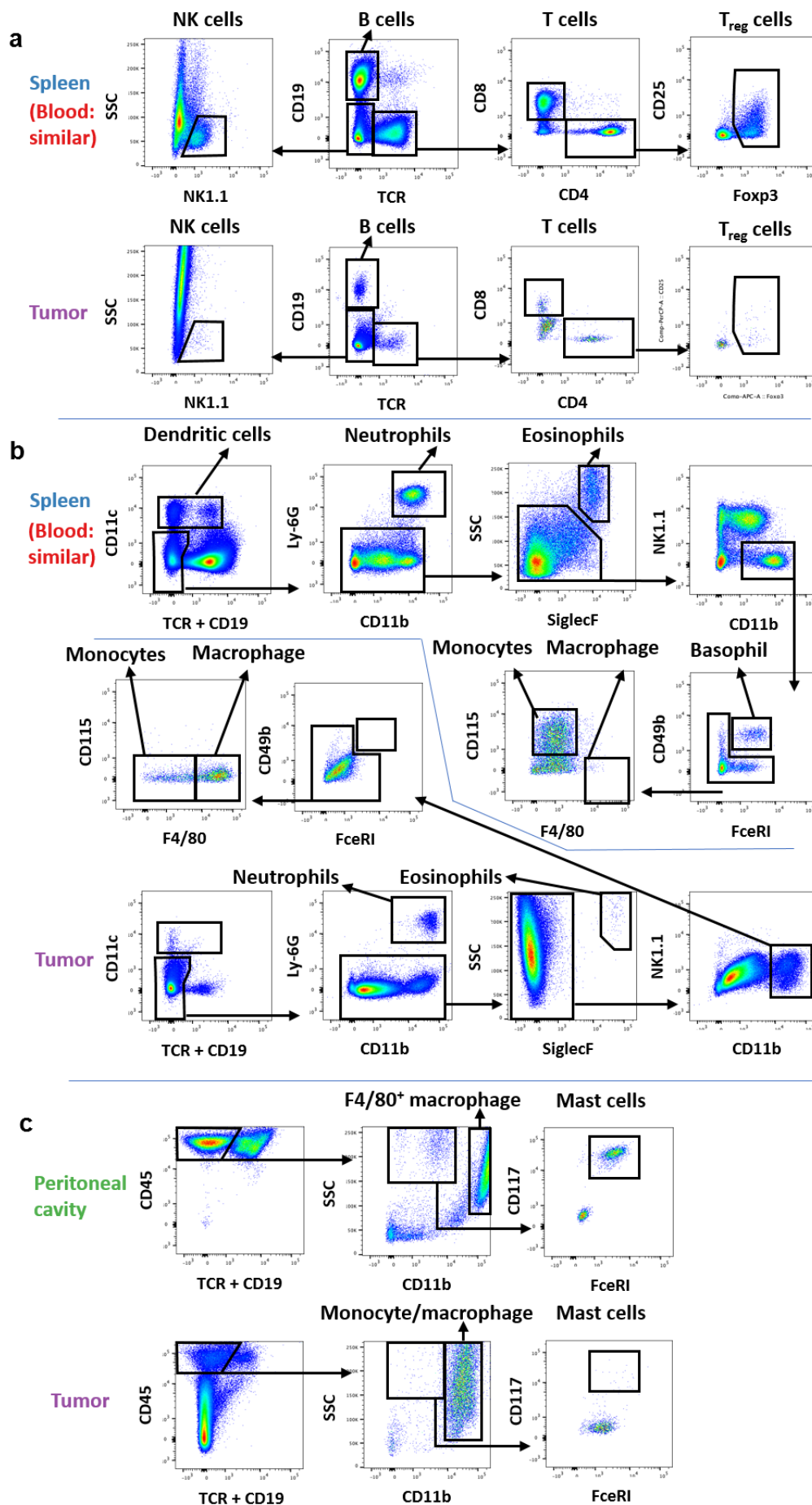


Fig S5: Representative gating strategy of flow cytometry analyses for **a.** T cells, B cells and NK cells; **b.** dendritic cells, granulocytes, monocytes and macrophages; and **c.** mast cells and peritoneal macrophages. Blood samples were not shown due to high similarity of the gating strategy to splenocytes

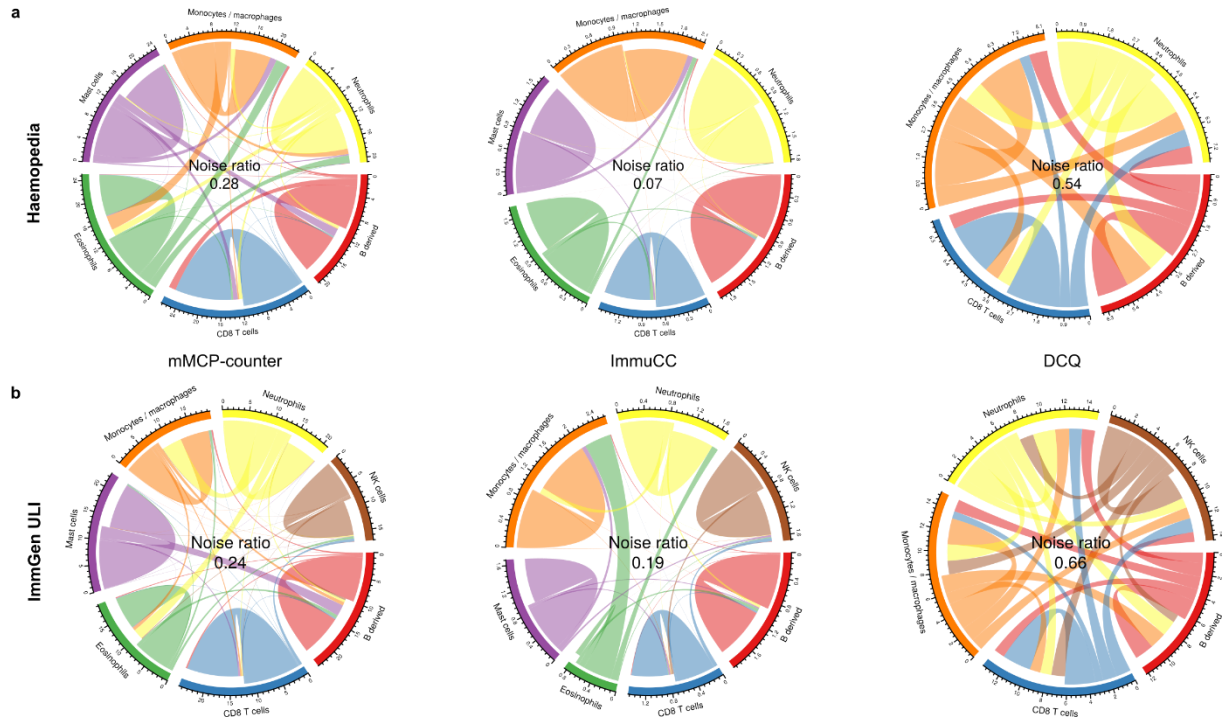


Fig S6: Spillover analysis and noise ratio for the three methods on the Haemopedia (**a**) and ImmGen ULI (**b**) datasets. The circo plots indicate spillover experiment outputs. Each color corresponds to a cell population, and the estimates for pure profiles are represented by the arcs inside the plot. These arcs are color-coded according to the true cell type that was given as an input to the method, and their size represents the weight given to other cell types by the methods.

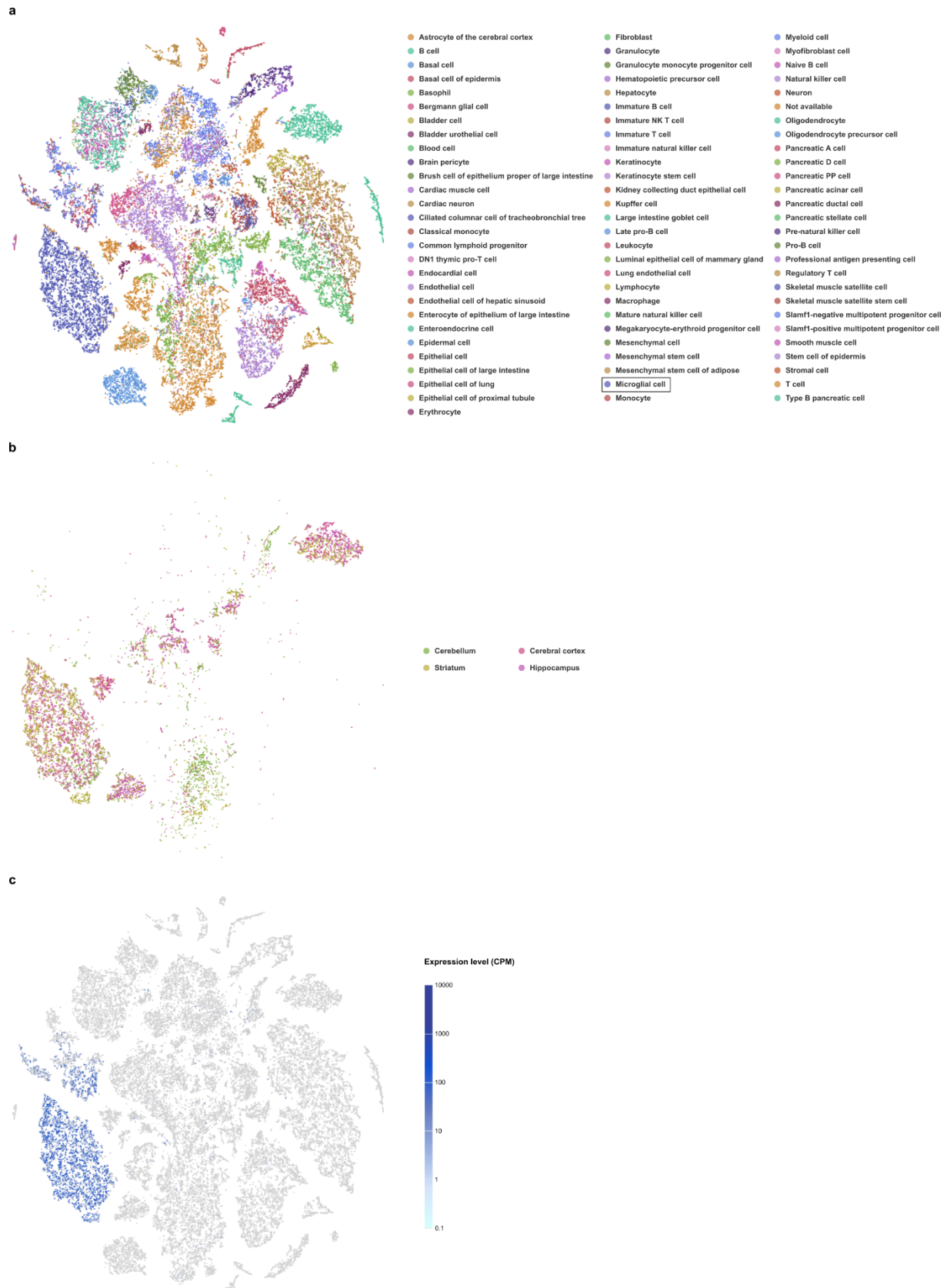


Fig S7: The mMCP-counter signature for monocytes / macrophages is also expressed in microglial cells in the brain

This figure was generated using the Elixir platform from single-cell RNA-seq data from the Tabula Muris consortium.

- a.** t-SNE representation of the full dataset, colored by inferred cell type. This notably shows a cluster of microglial cells, dark blue, left of the plot.
- b.** Position of brain cells in the same t-SNE plot, colored by region of origin.
- c.** Expression level of the mMCP-counter signature for monocytes/macrophages, showing a strong expression in several cell clusters, including the microglial cell cluster.