Immagine che contiene testo, schermata, Policromia, Carattere

Descrizione generata automaticamente

**Fig. S1** Plot of the top marker genes for each cluster. It represents the expression level (color) and the percentage of cells (dot dimension) for each cluster. It is clear how some genes are strongly correlated to specific cluster, allowing a first understanding of the cellular heterogeneity of the dataset.

Immagine che contiene testo, schermata, numero, diagramma

Descrizione generata automaticamente

**Fig. S2** Plot of the top most differentially accessible peaks per cluster. It is immediate that the peaks accessibility is less remarkable than gene expression to represent specific clusters. First of all, the peaks appear in very low percentage of clusters’ cells, questioning their strength as markers of cell types. Moreover, the peaks are not uniquely identified features (like genes), making it difficult to generalize the found peaks as markers.