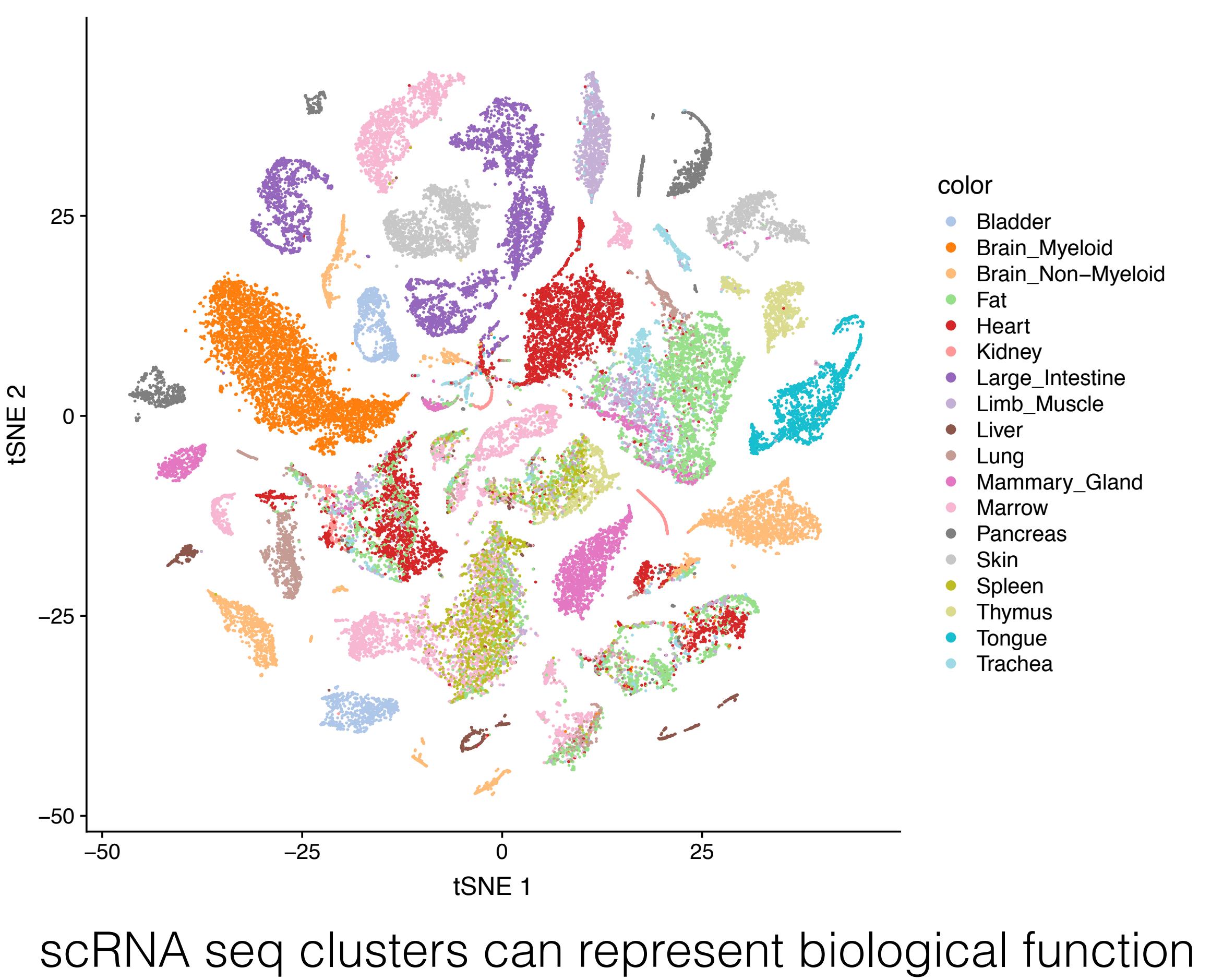
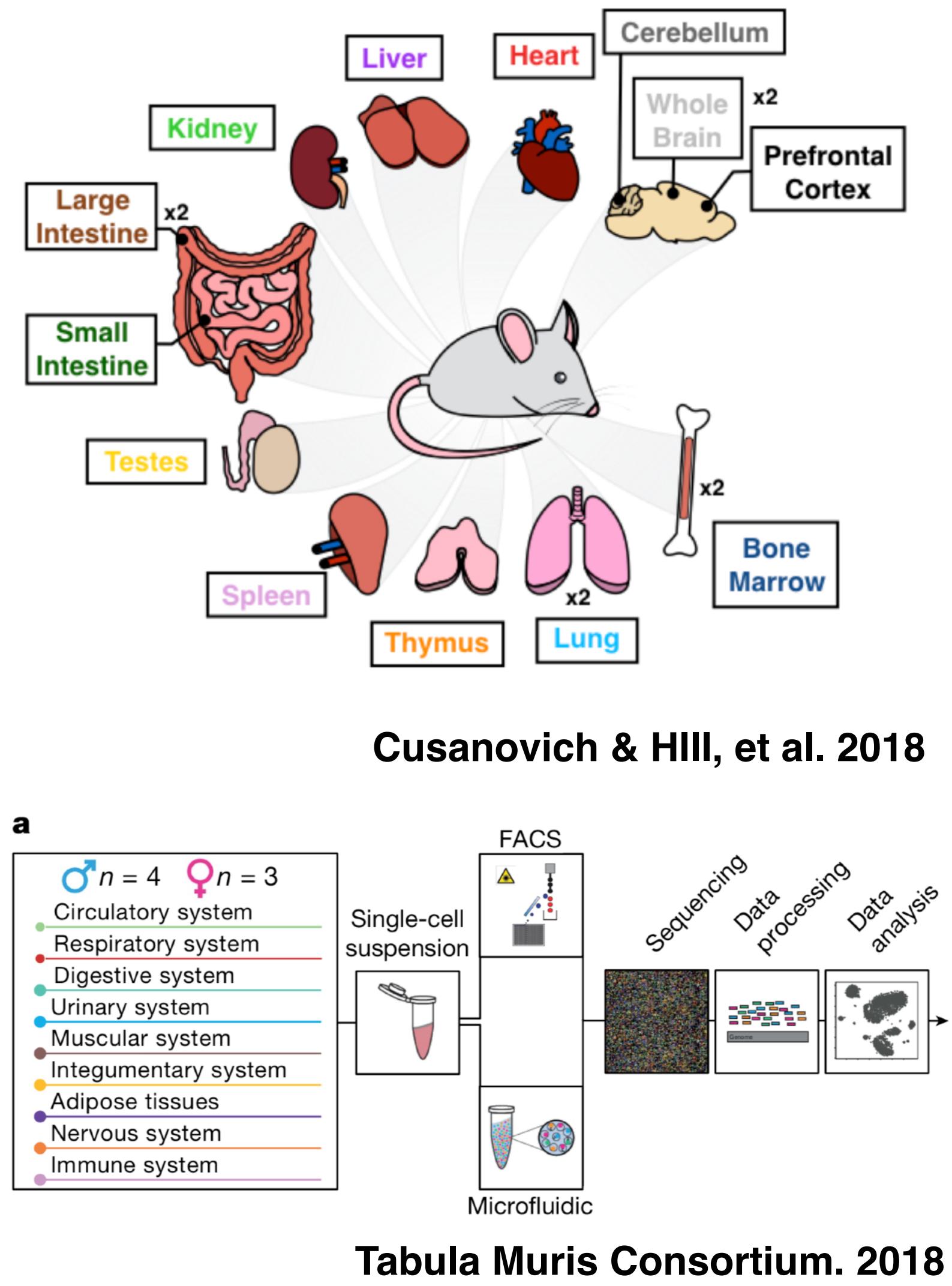
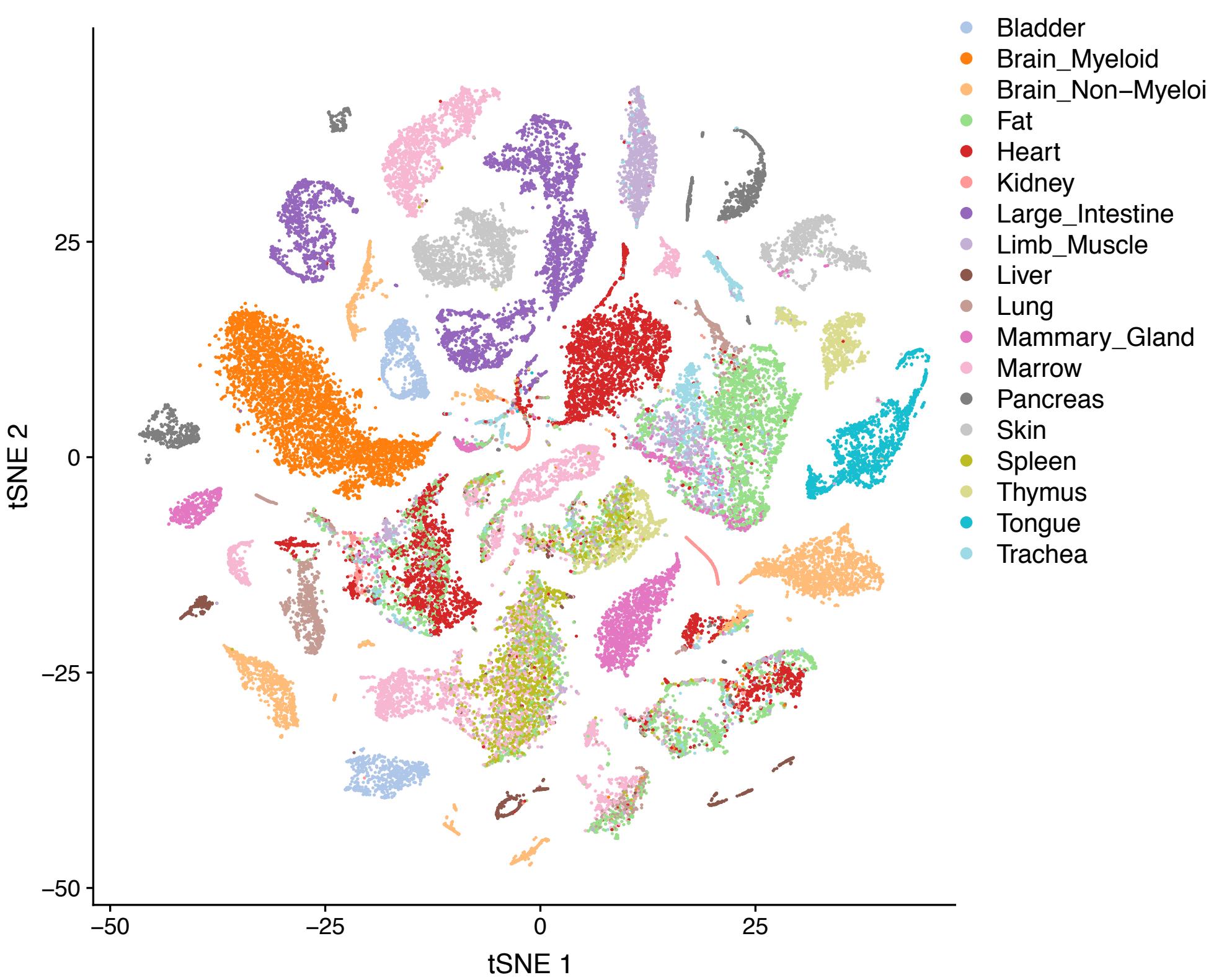


Cell atlas dataset provides an opportunity to explore the identity of cell types

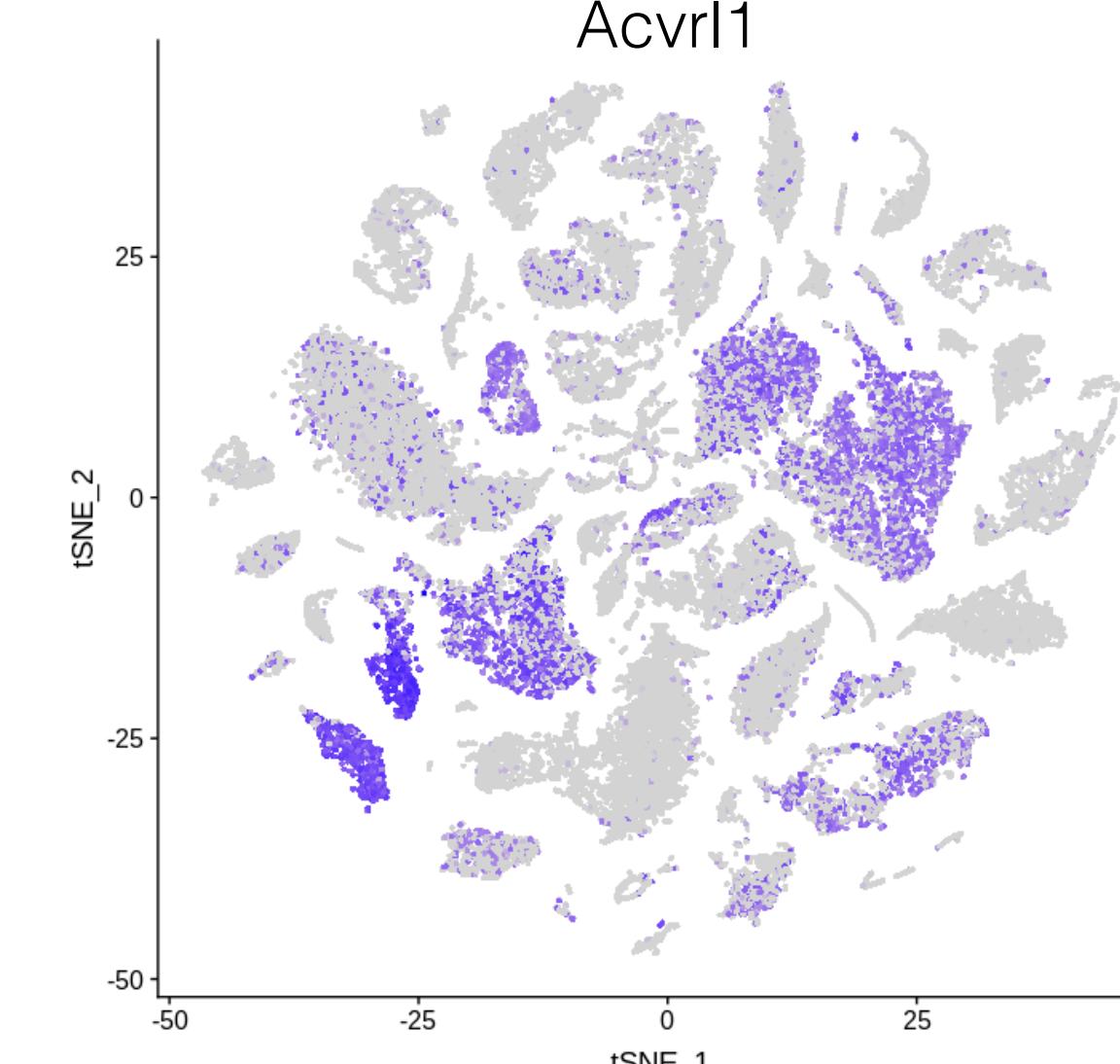
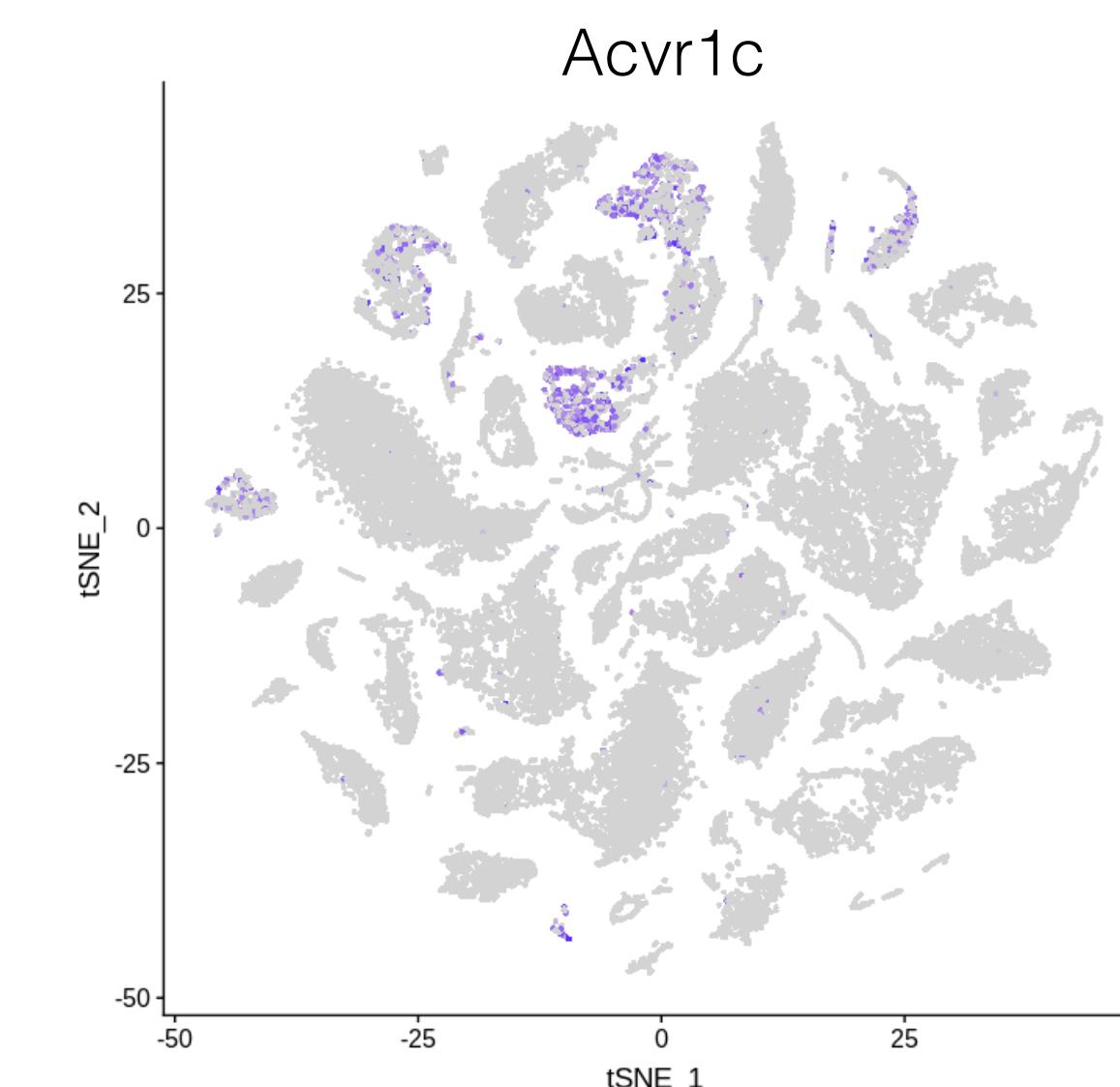
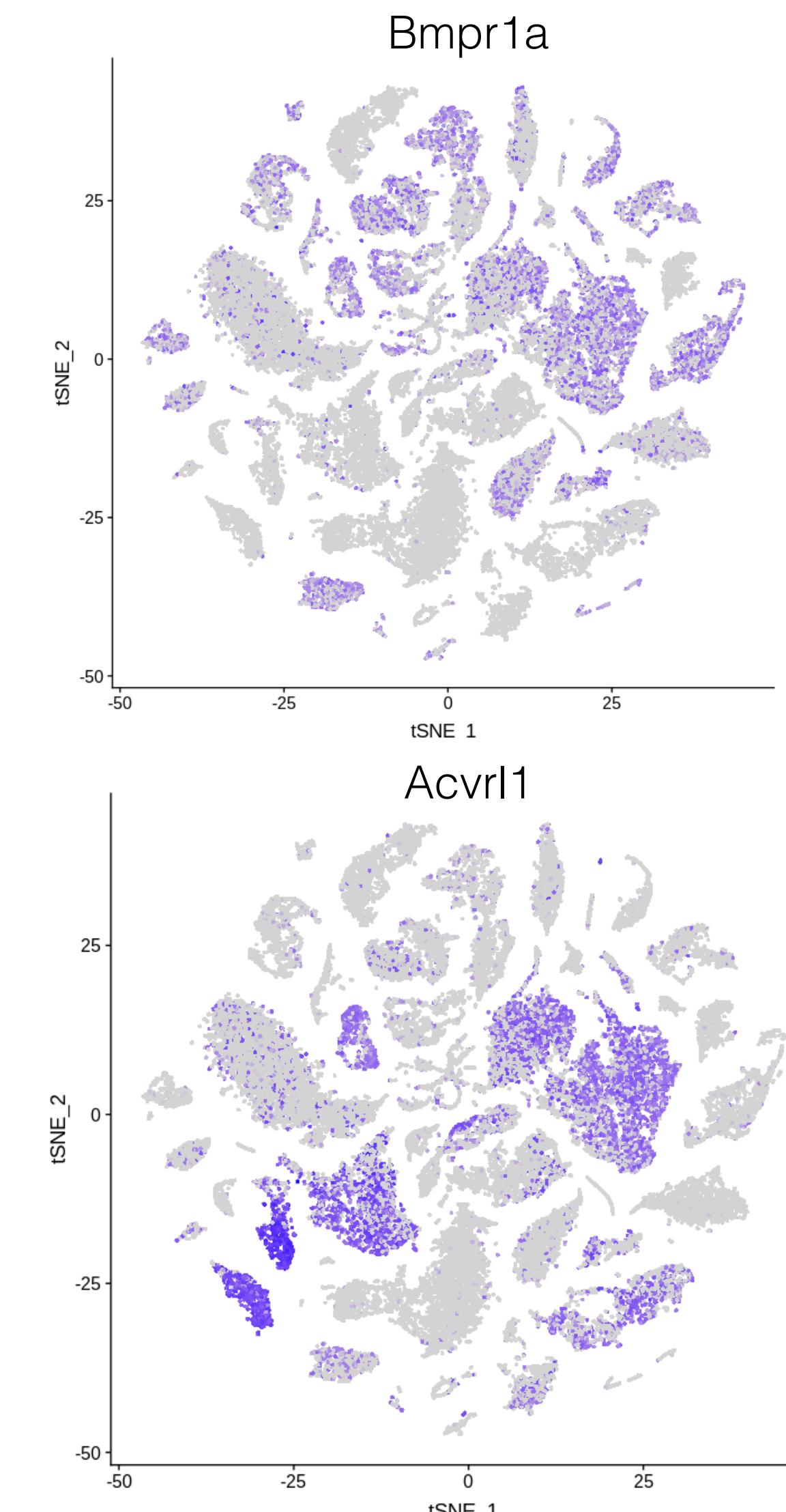
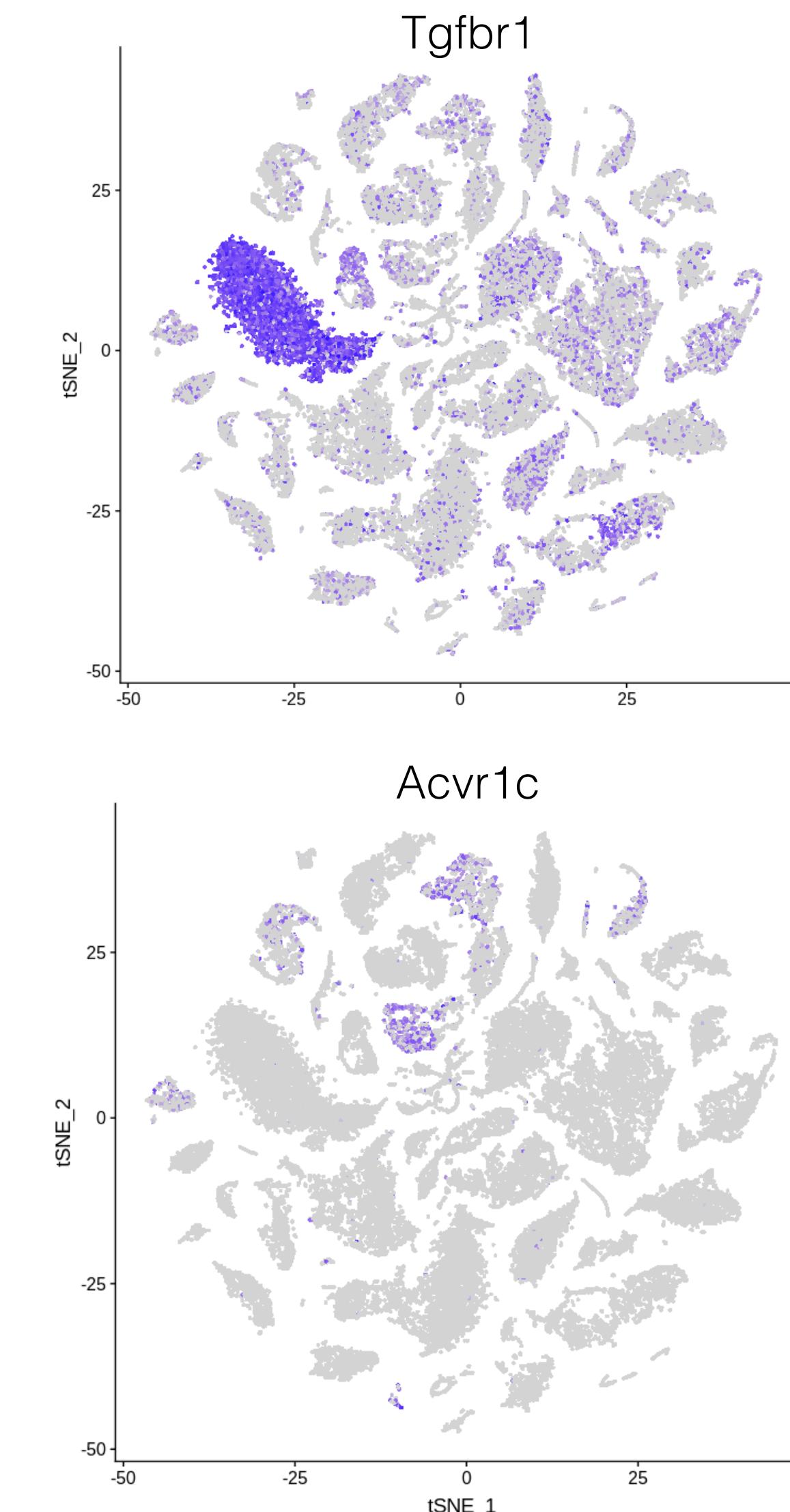


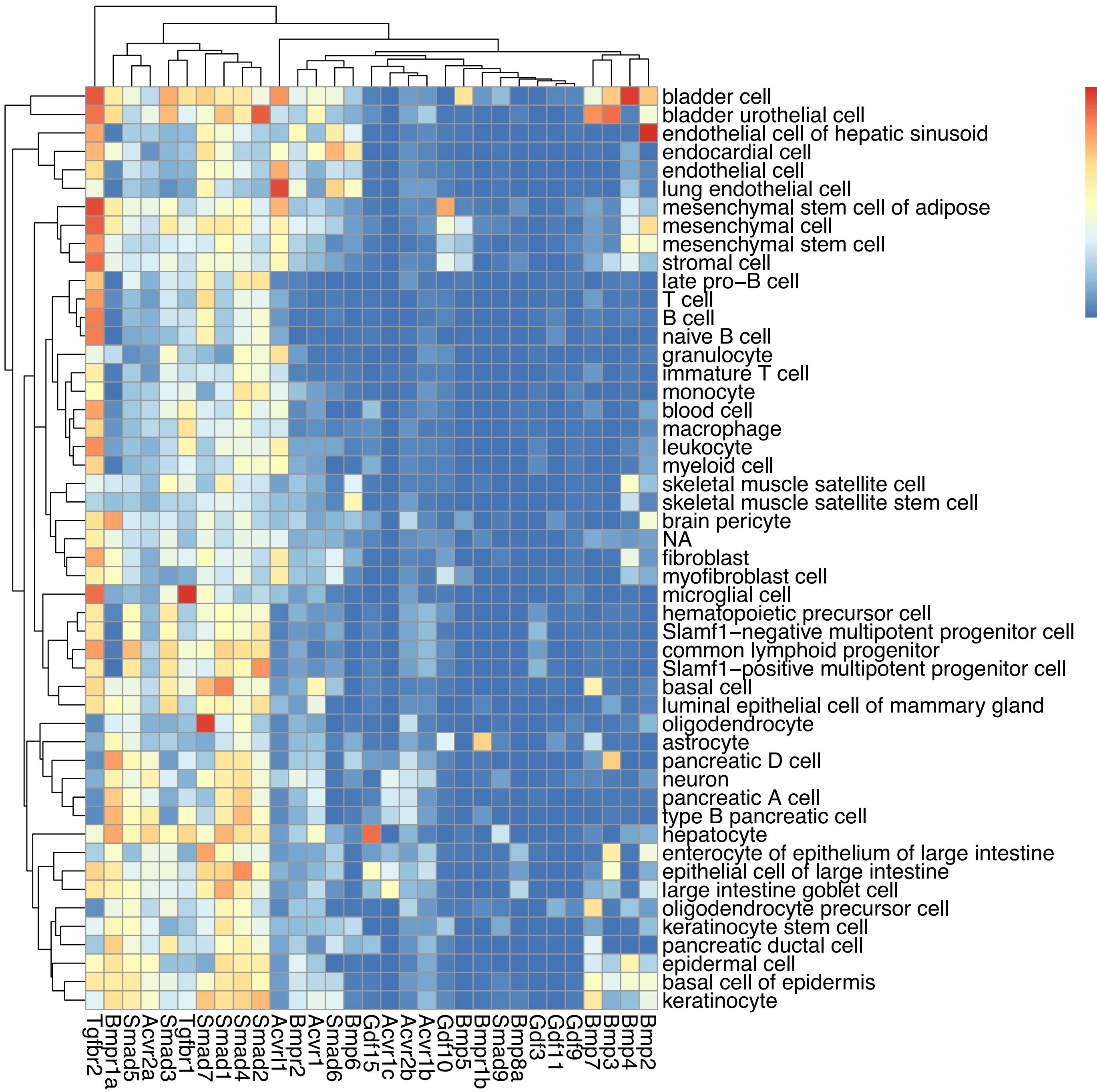
Components of signalling pathways show heterogeneous expression across cell types and tissues

Clustering 44k cells. Full transcriptome



Location of cells expressing BMP genes

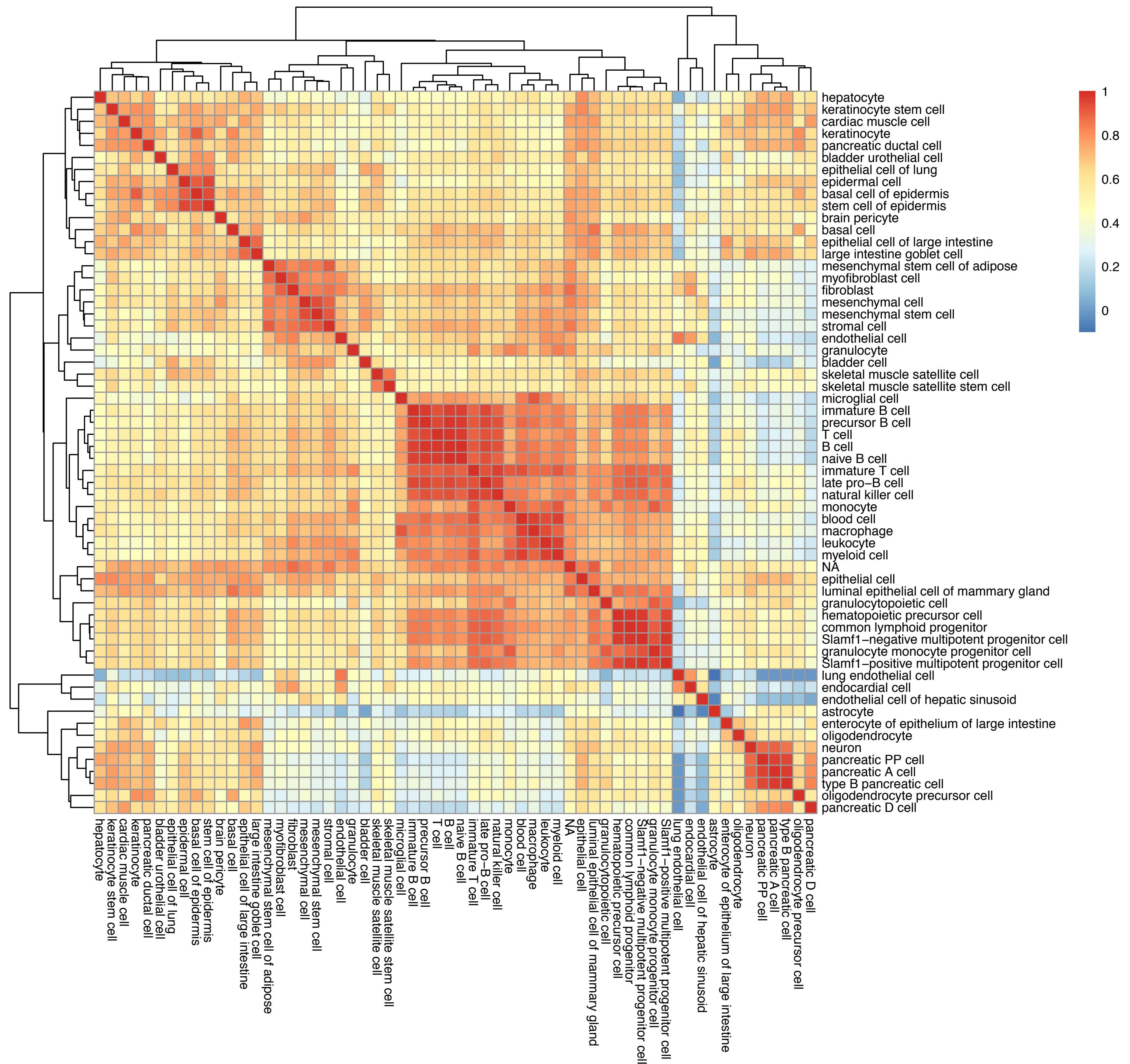




Percentage of cells expressing
BMP genes on each of the annotated
cell types in the tabula munis data set

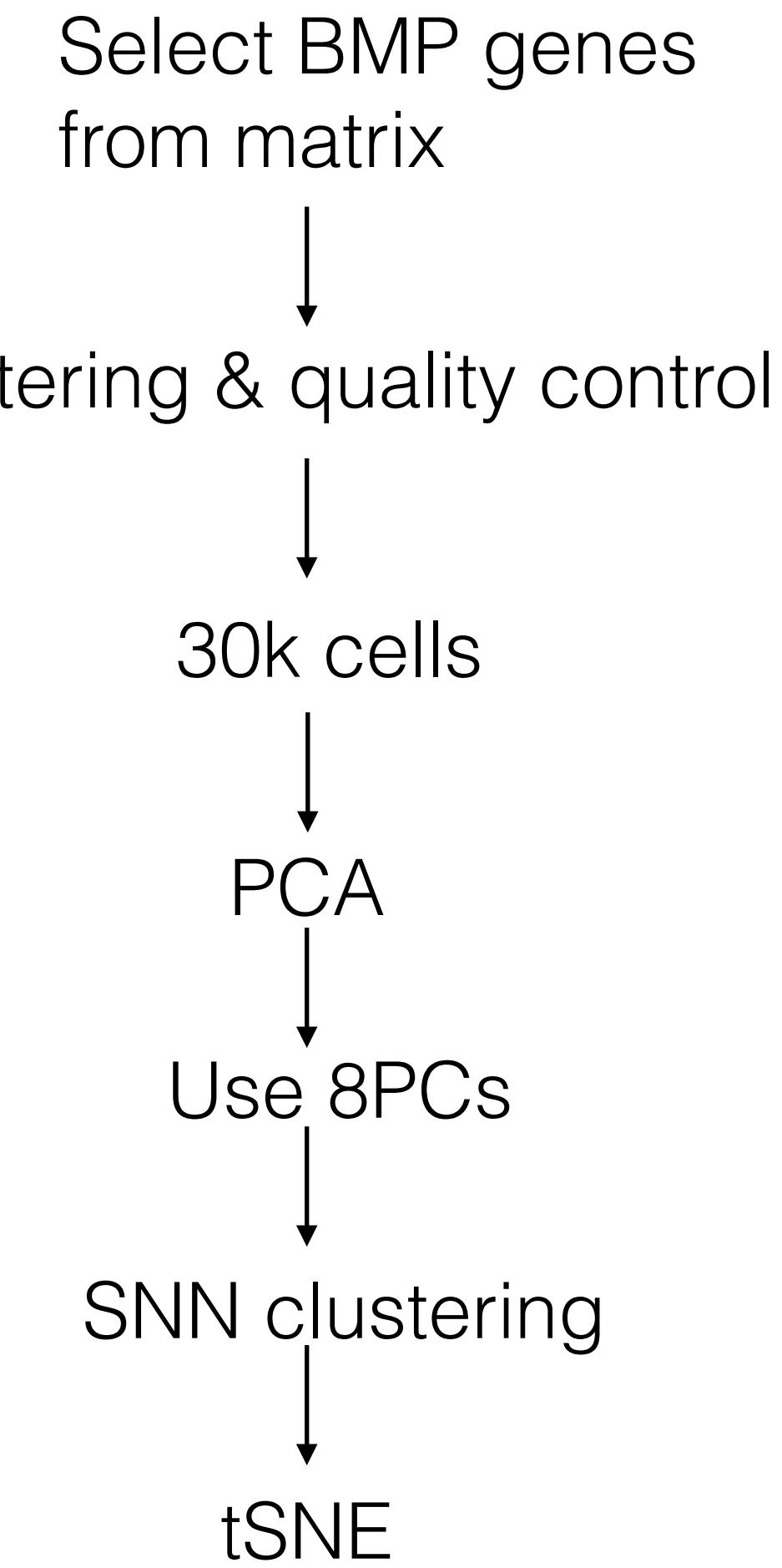
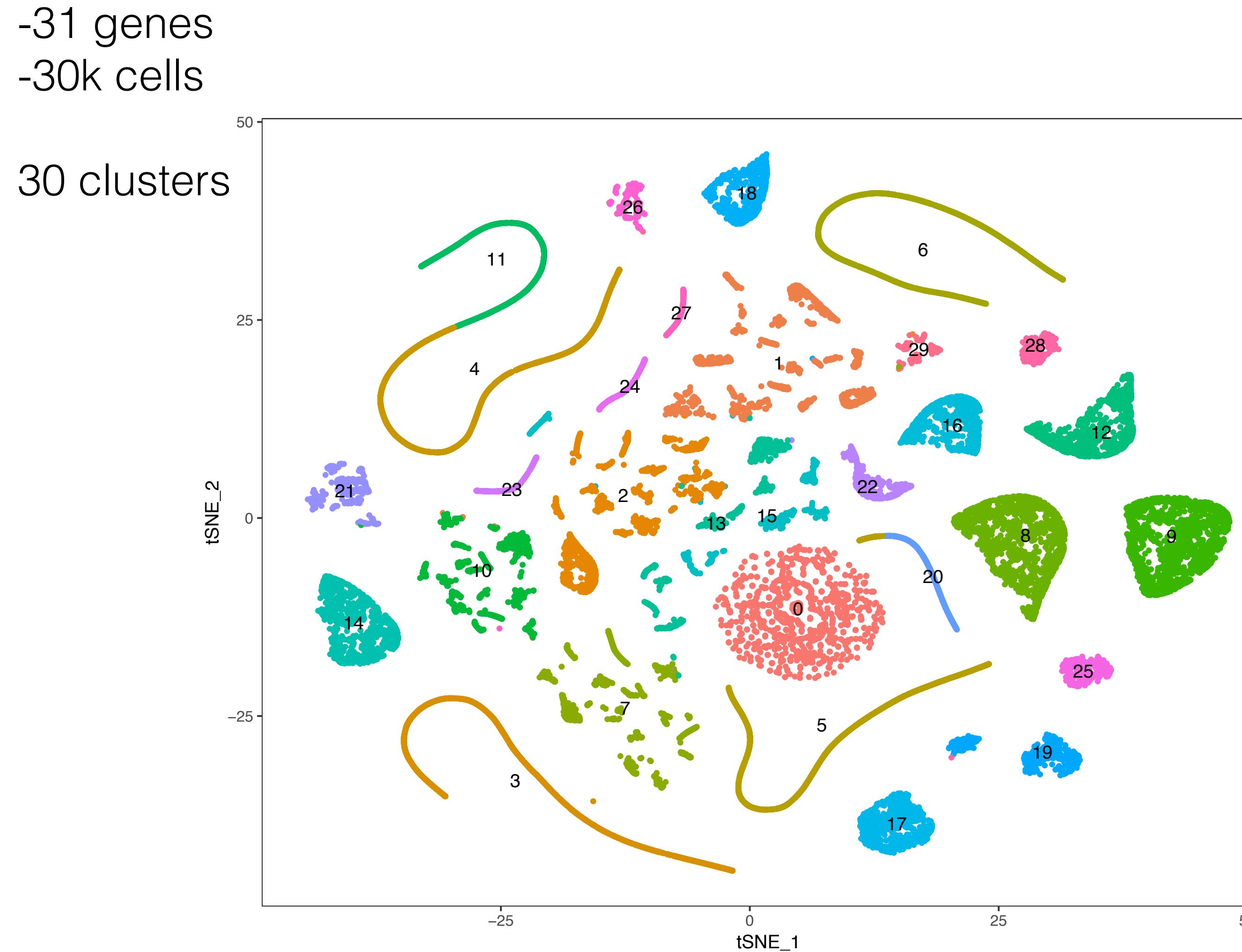
Cell types are annotated manually based on expression of known markers.

Only cell types with more than 50 cells in the dataset are considered (60 types)

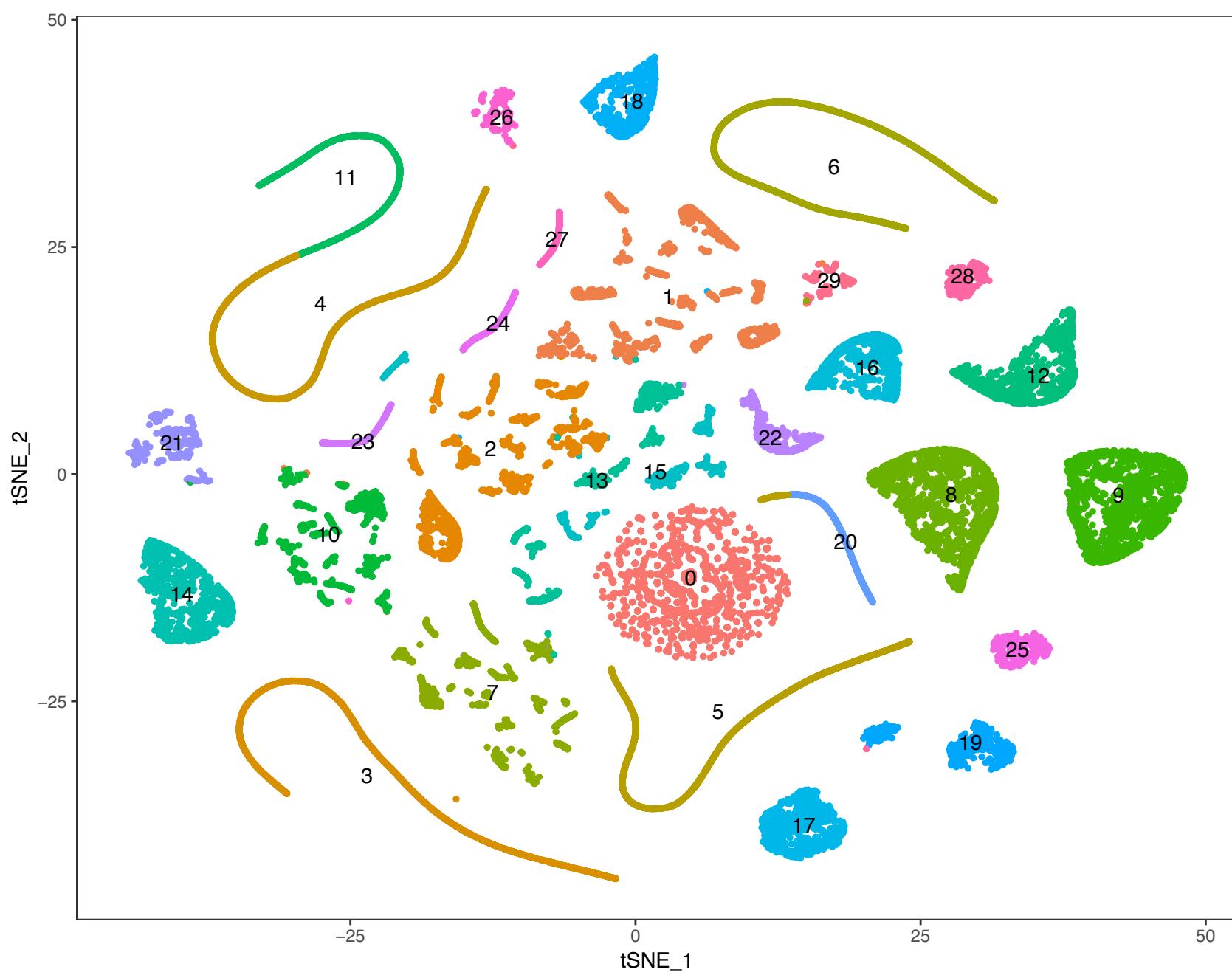


Correlation matrix of all cell types based on their BMP expression profiles

Clustering single cells using only the BMP genes generates defined clusters

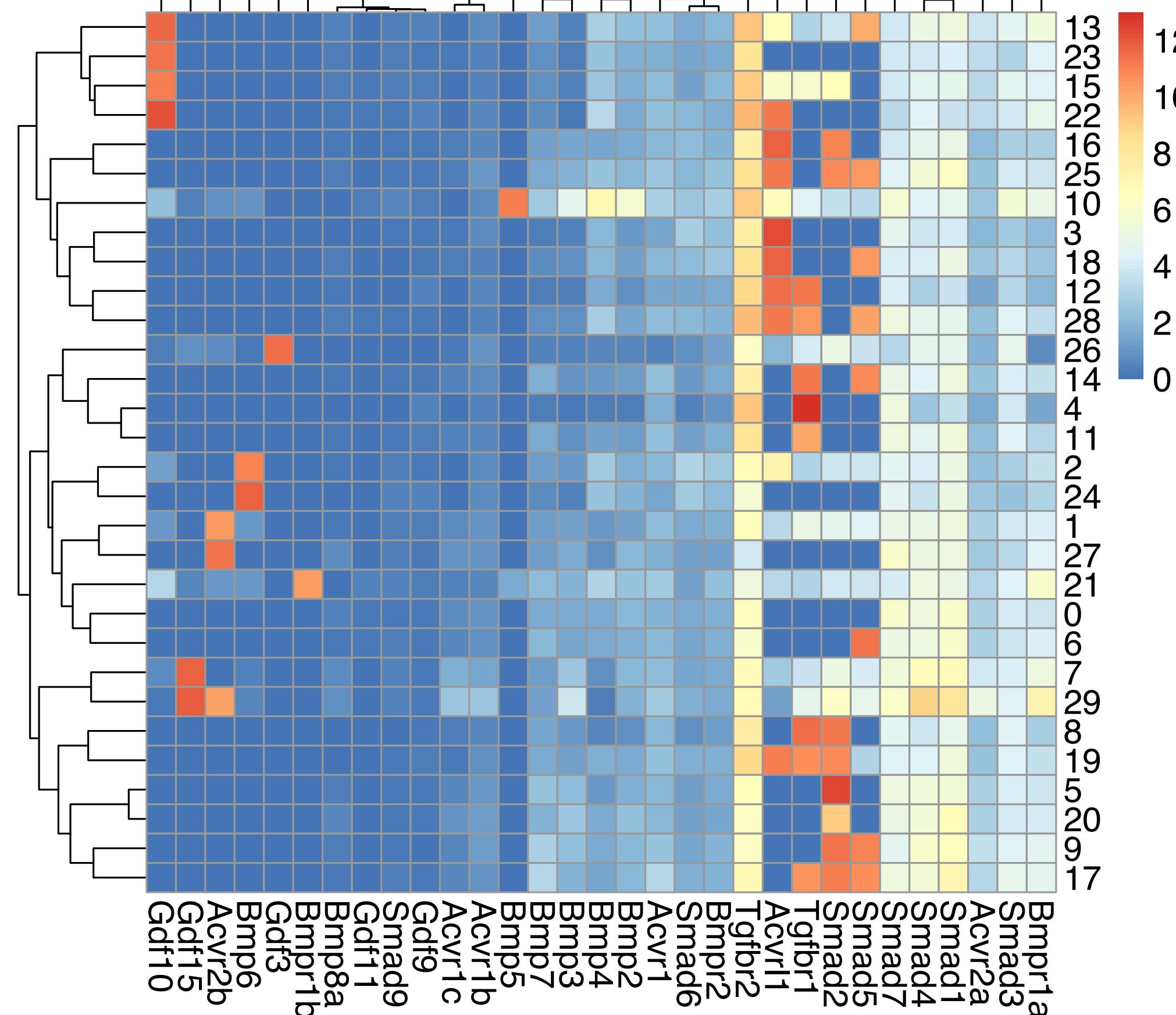


BMP expression profiles of main clusters

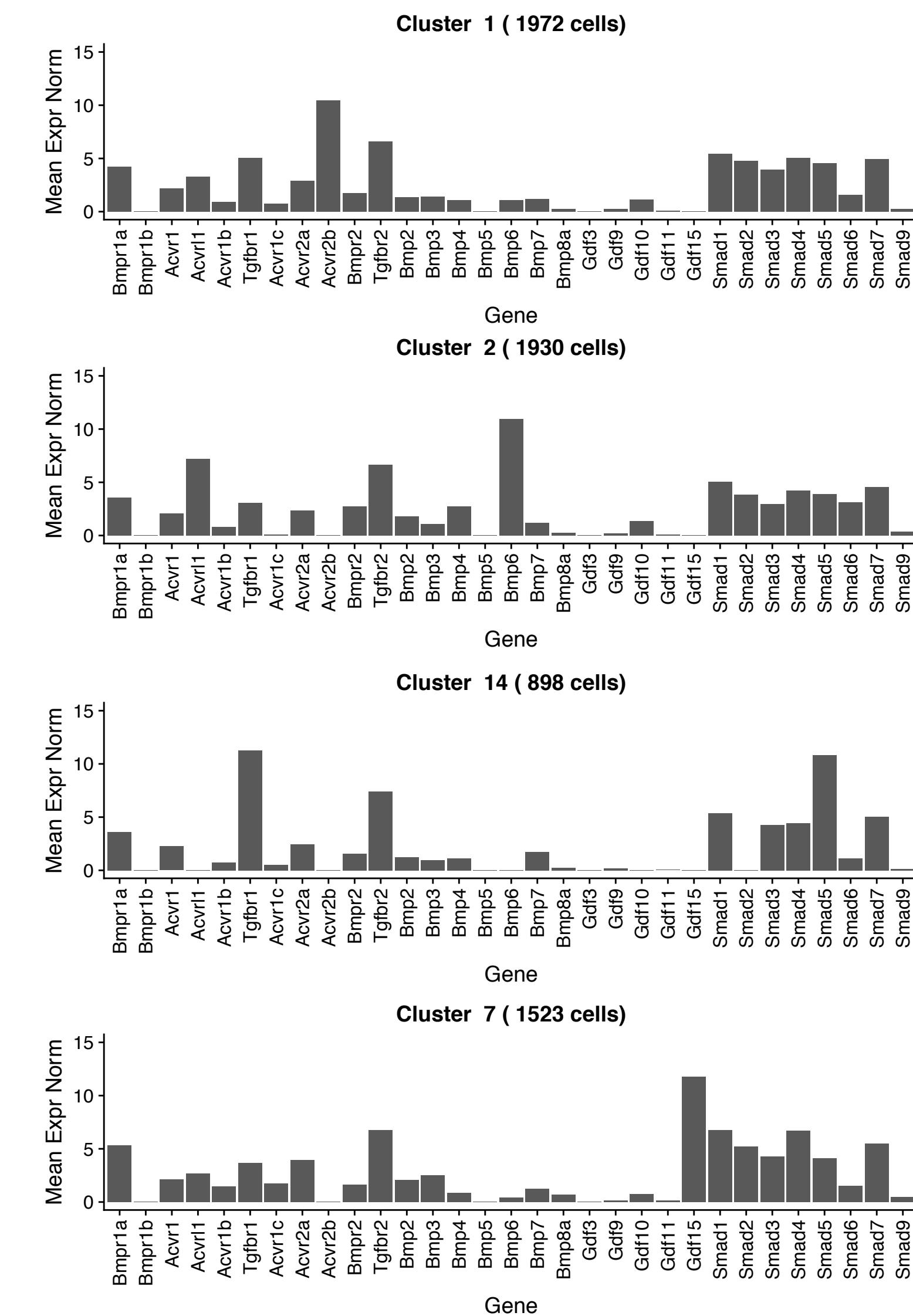
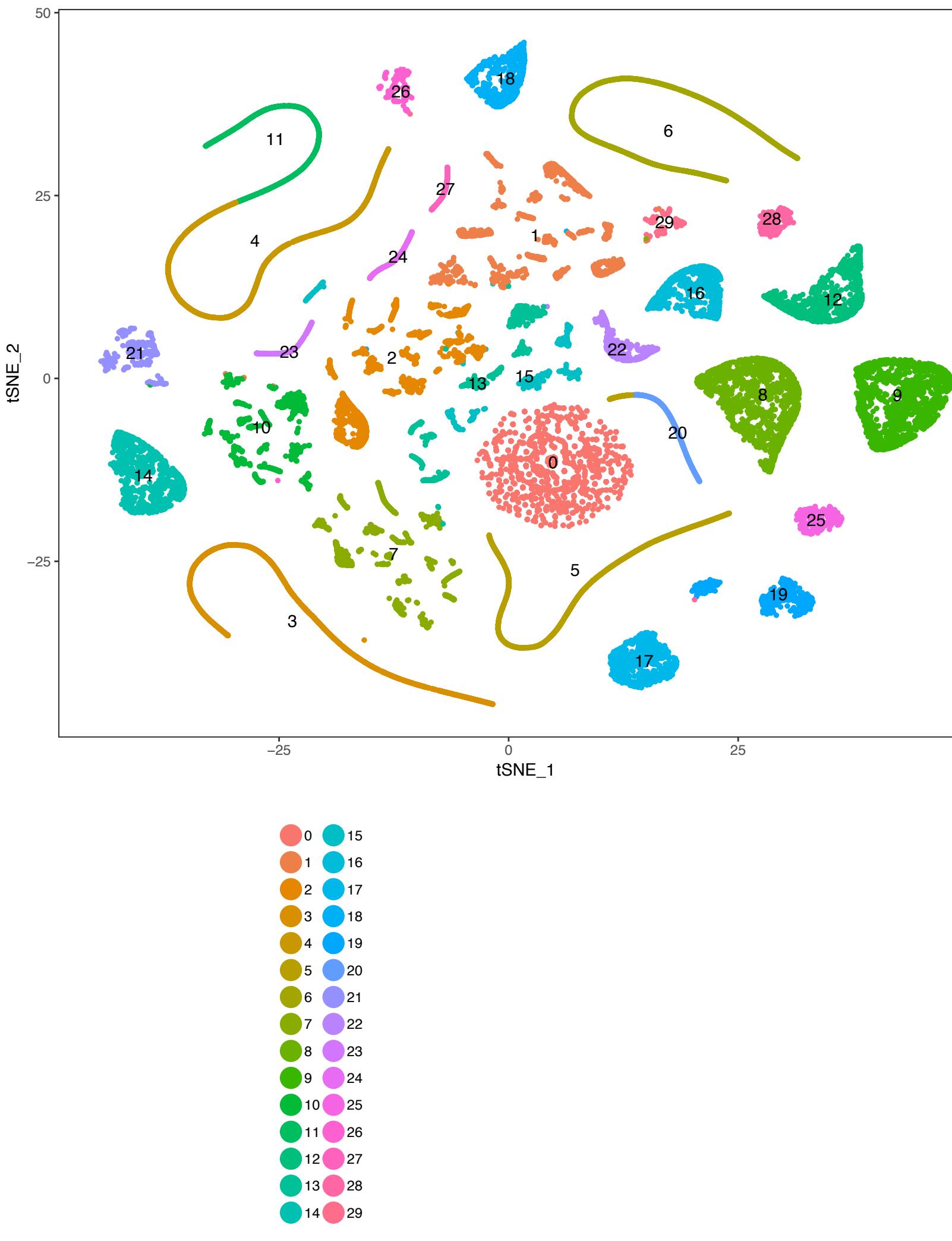


30 clusters found by SNN on
the PCA space

11 highly variable genes:



BMP expression profiles of main clusters



BMP expression profiles of main clusters

