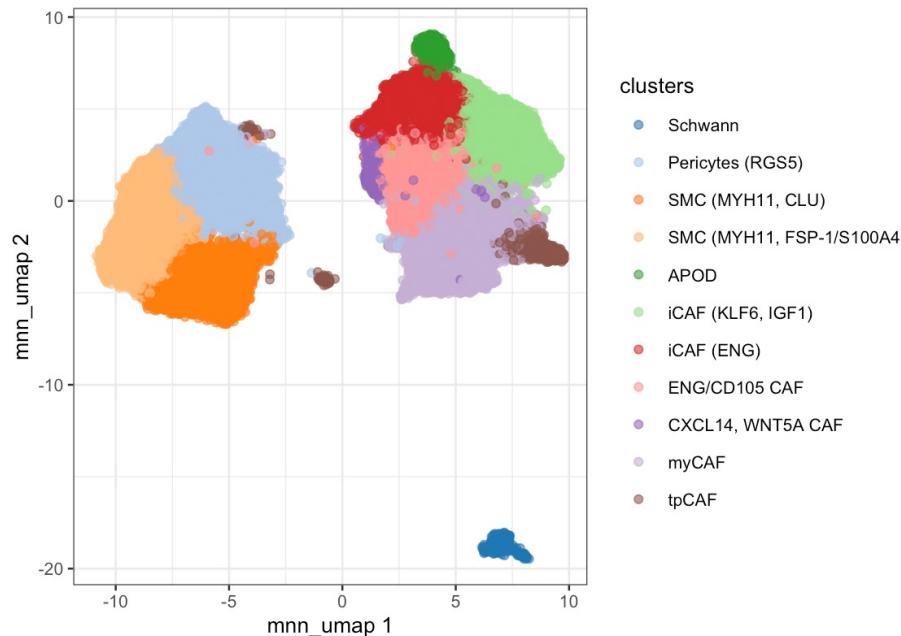
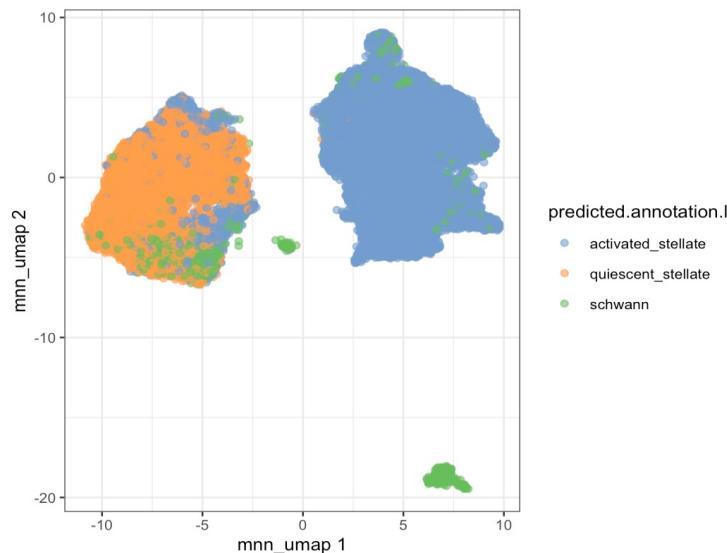


- I picked everything that was annotated by Azimuth as 'activated_stellate', 'quiescent stellate' or 'schwann'
- Then I removed all cells outside of the REF.UMAP region shown here; this removes KRT19+, VWF+ and CDH5+ cells

Note: I can leave out step 1 and get similar results for clustering

I did this for each cohort, did batch correction using fastMNN, and then used their corrected gene expression to do UMAP/Leiden

- Have been meaning to do SCVI or Harmony and compare – for sure when I incorporate met data

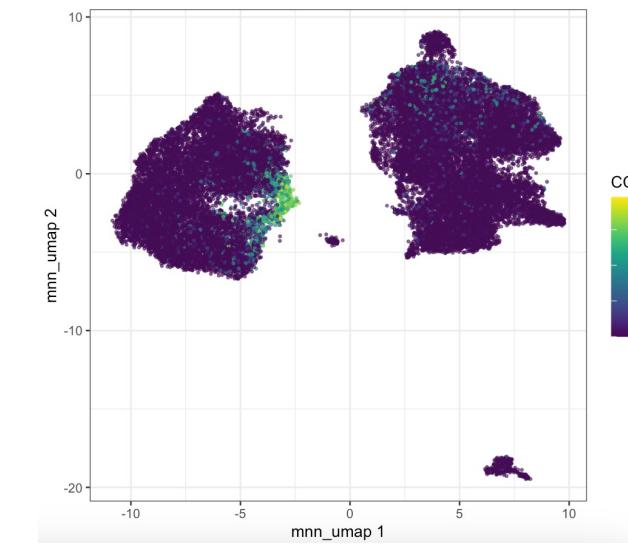
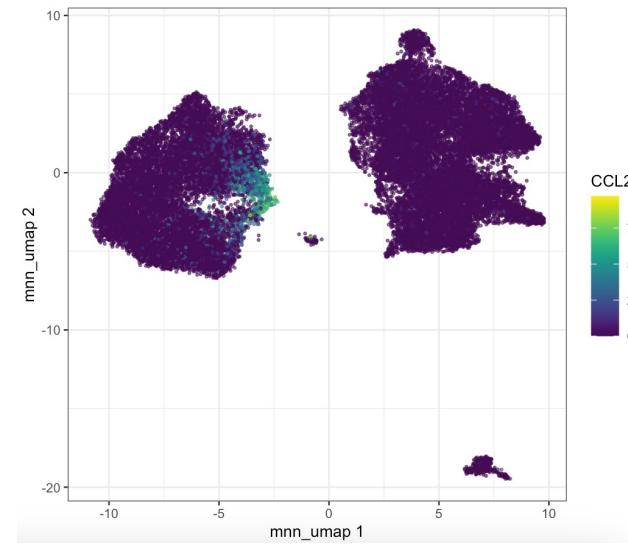
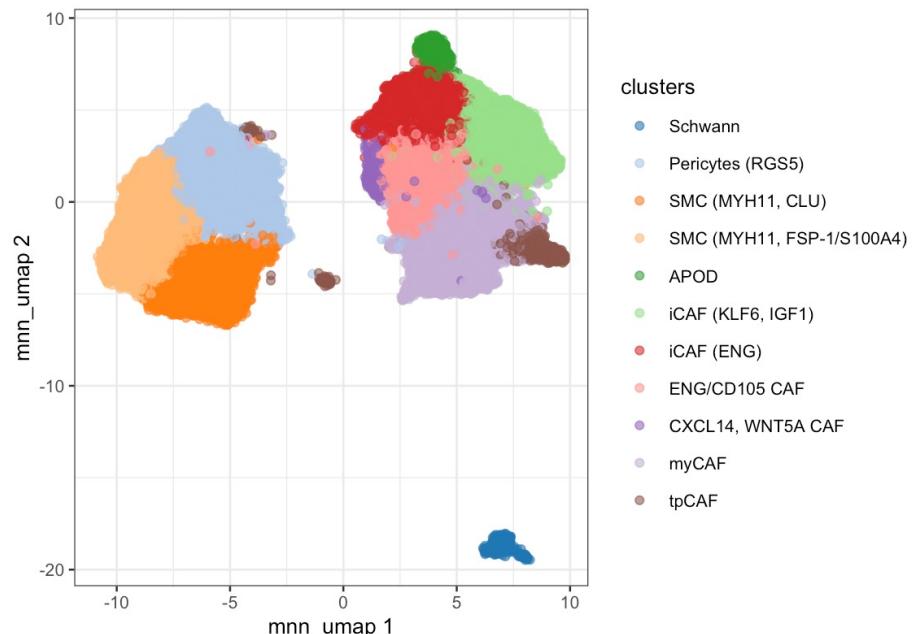


The one population that I don't appear to get a cluster for (though the cells group together in MNN-UMAP space) is the reticular CAFs.

Markers: CCL21/CCL19

Schumacher & Thommen, Science, 2022

Cords et al., Biorxiv, 2022

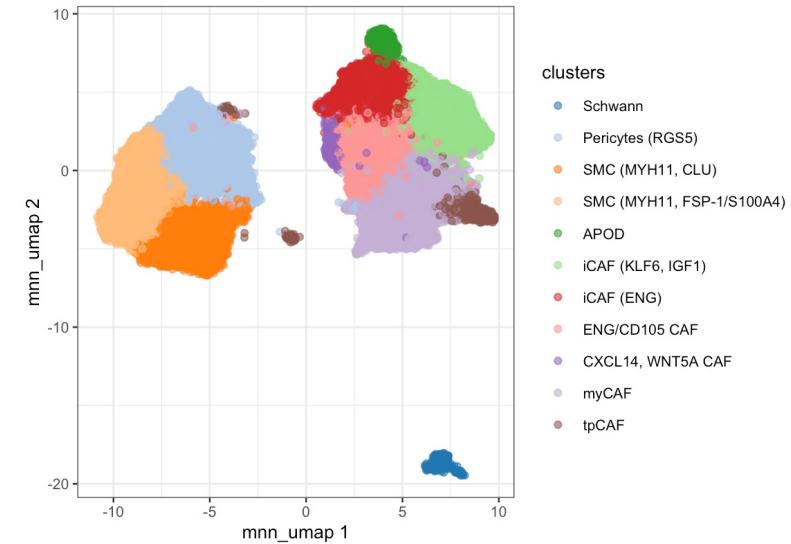
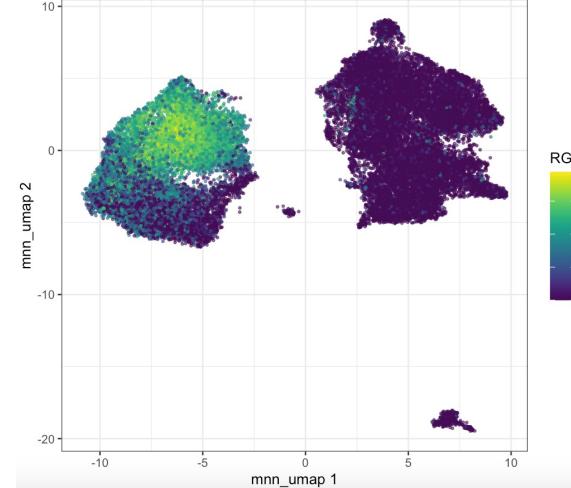
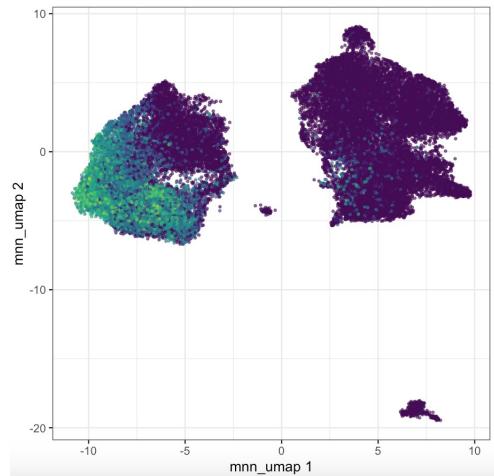


Mural cells:

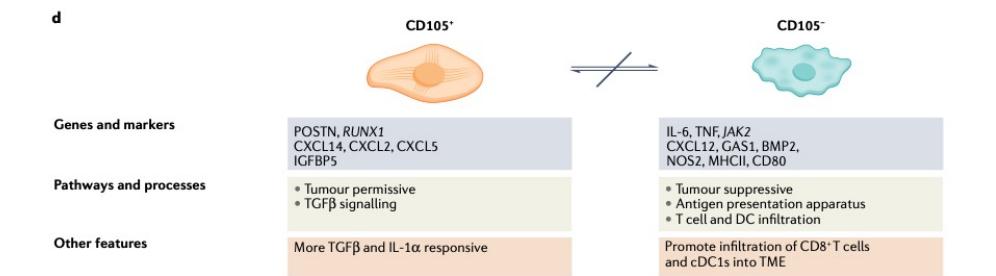
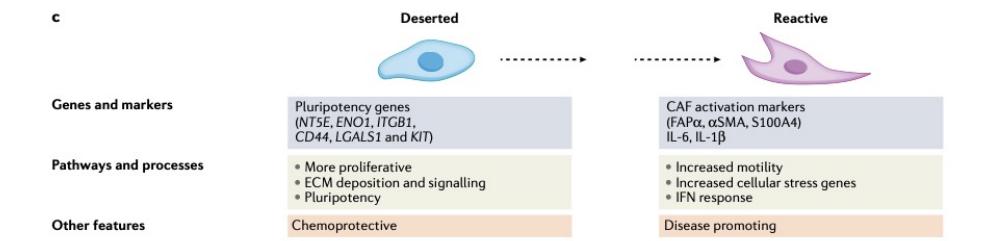
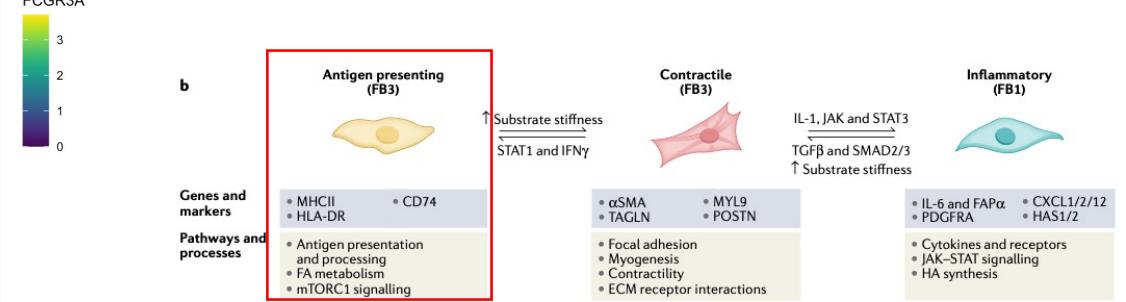
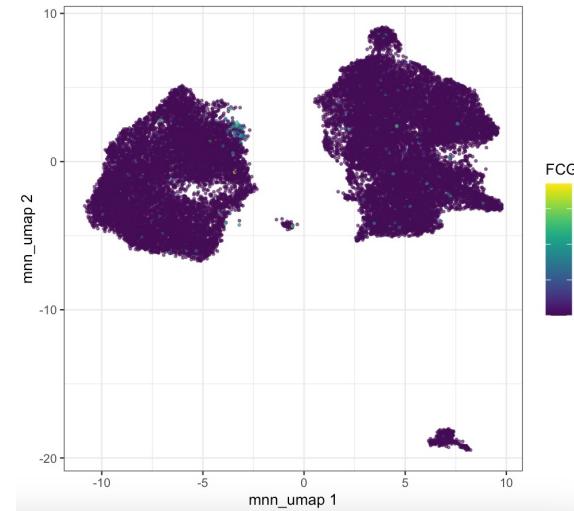
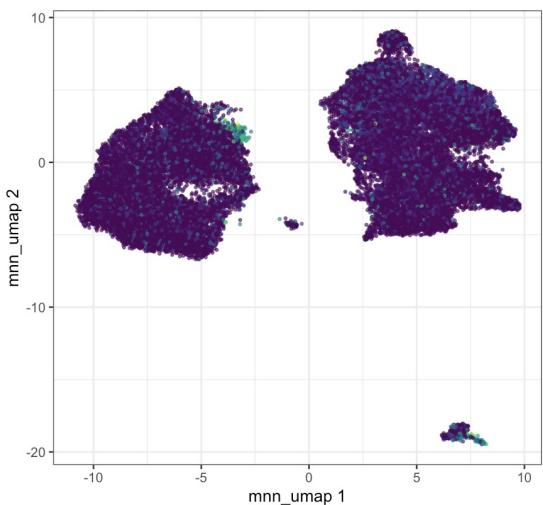
SMC = MYH11

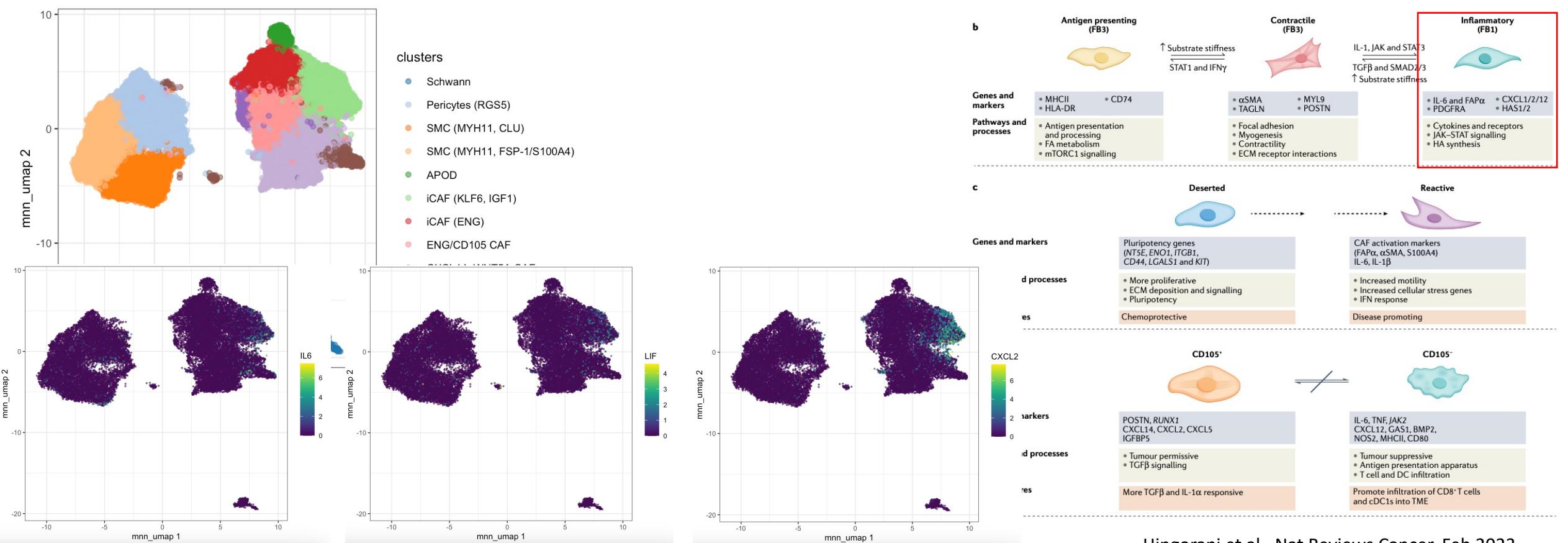
pericytes = RGS5

Markers from Buechler et al., Nature, 2021

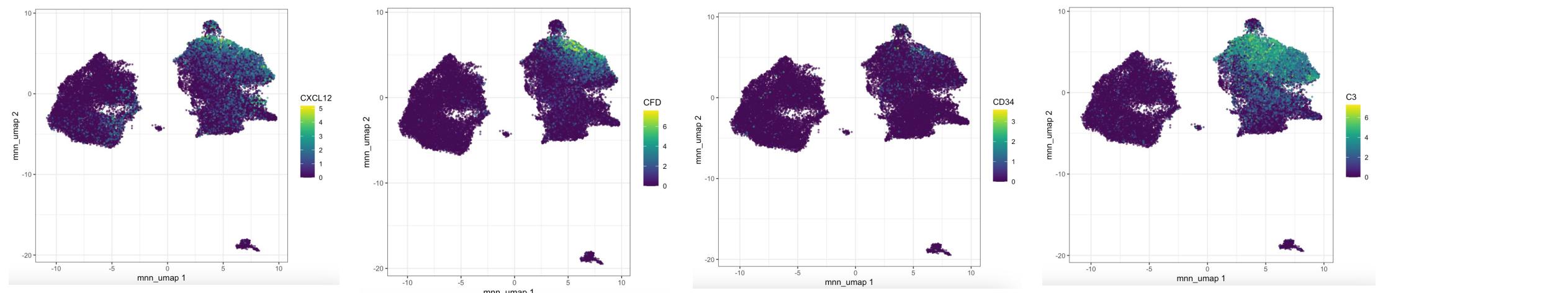


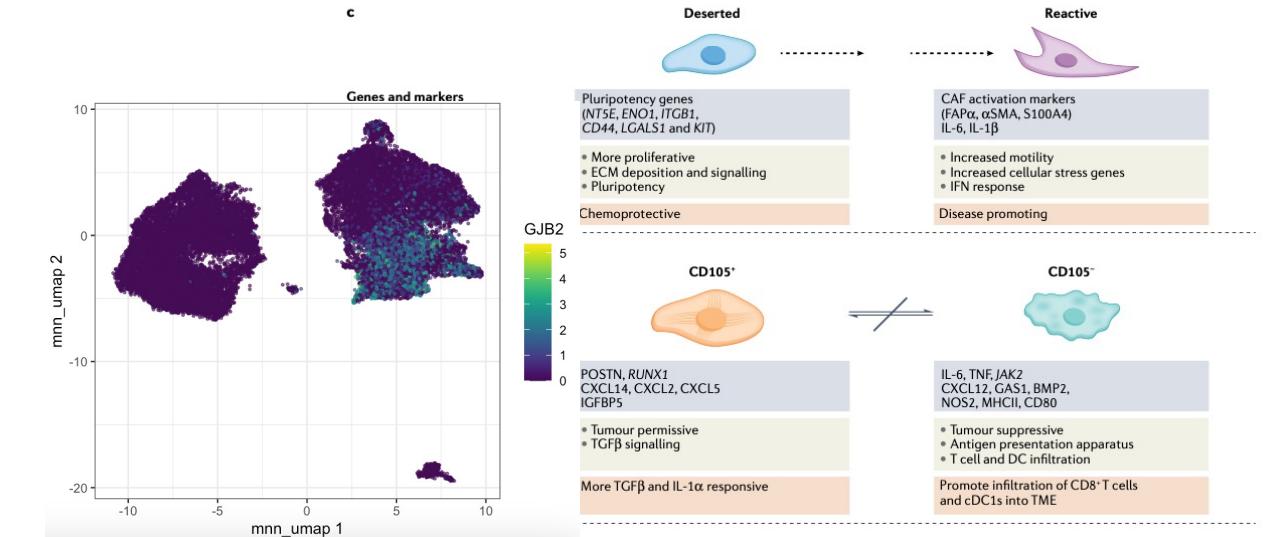
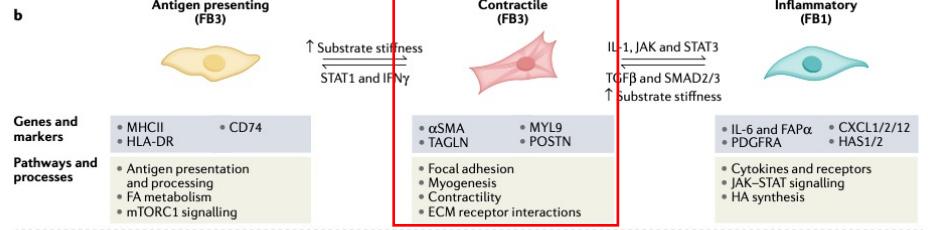
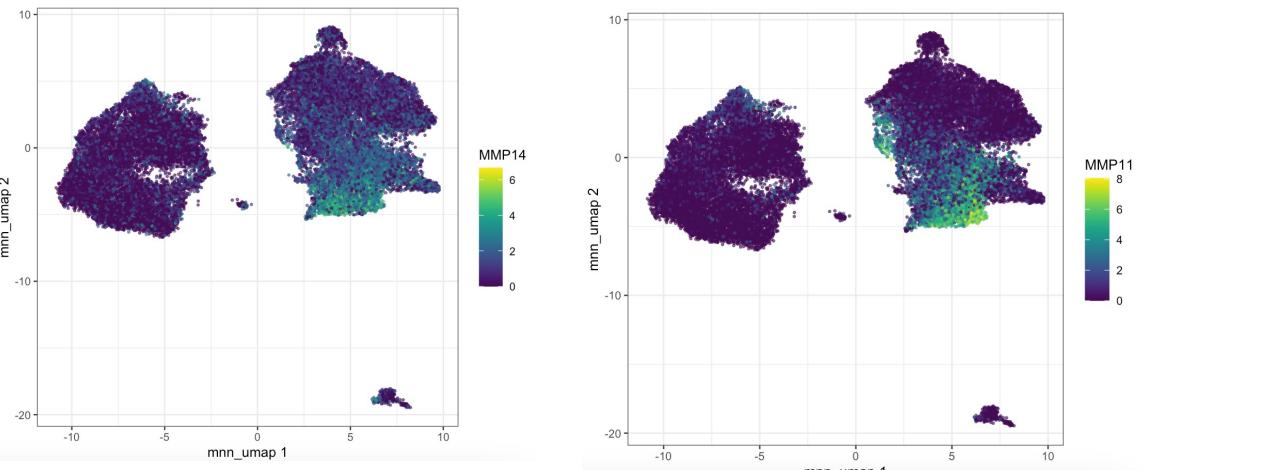
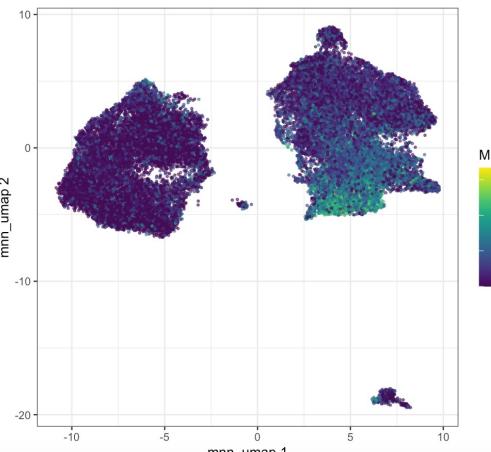
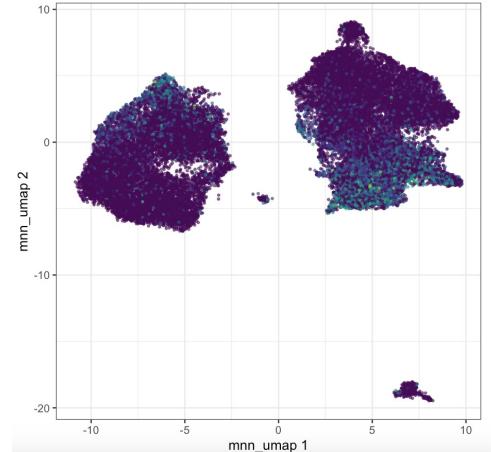
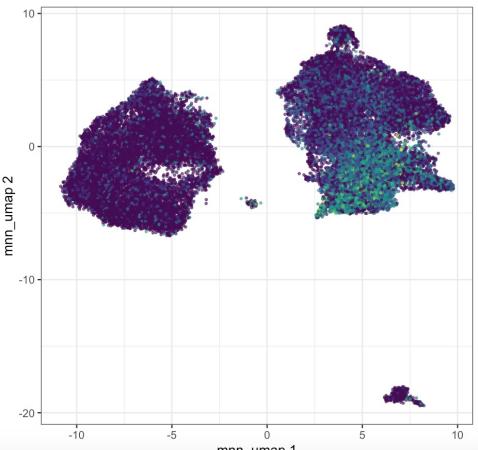
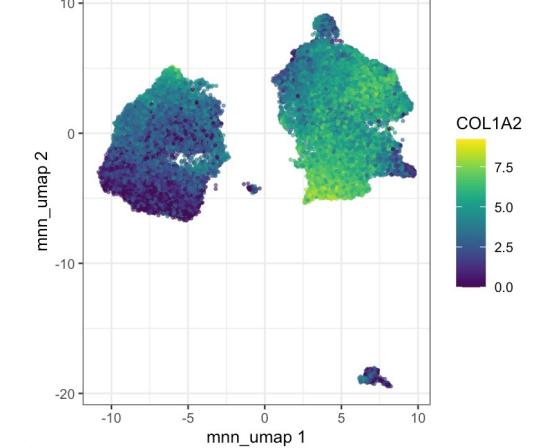
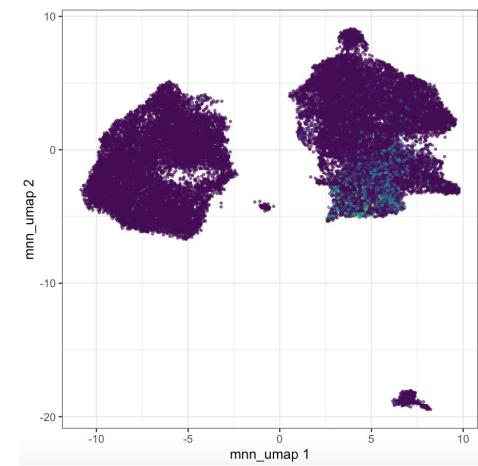
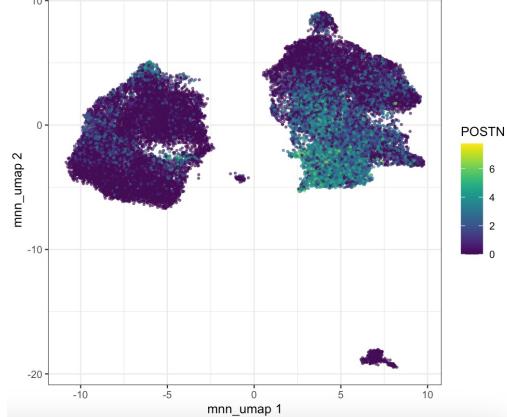
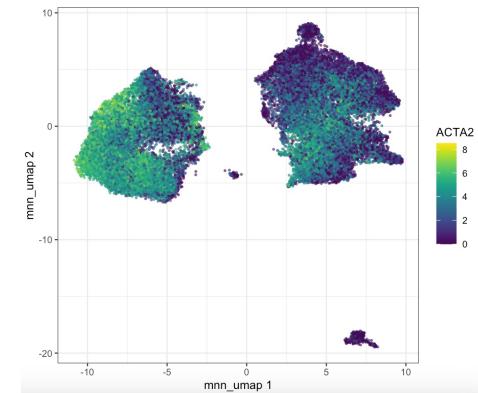
- I don't see an apCAF population
- In this scRNA-seq data, CD74 and HLA-D* genes are really mainly expressed in the Schwann cells and a little immune cluster (PTPRC, S100A8/9, ITGAM(CD11b), CD68)

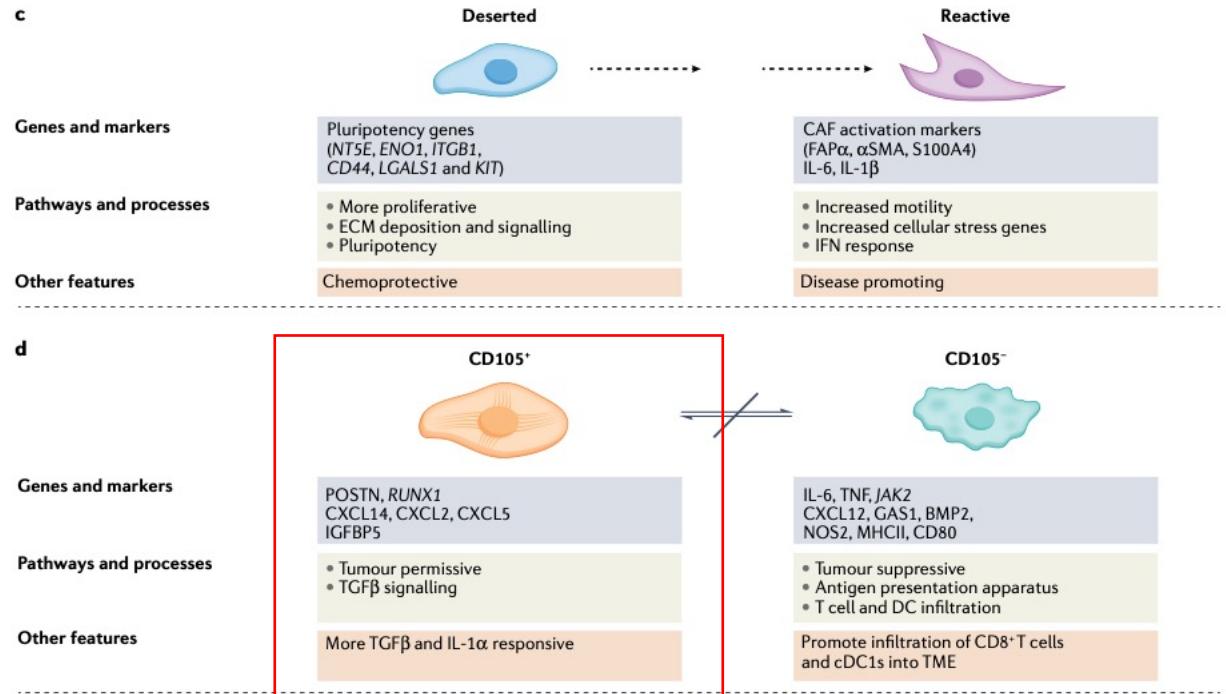
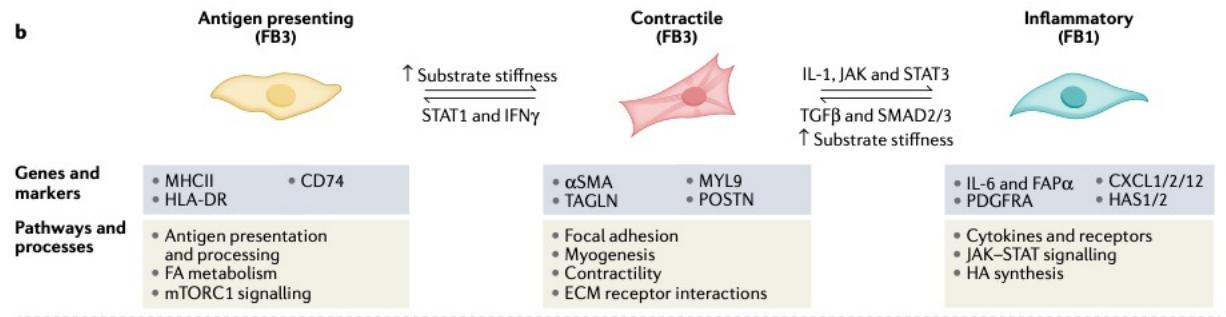
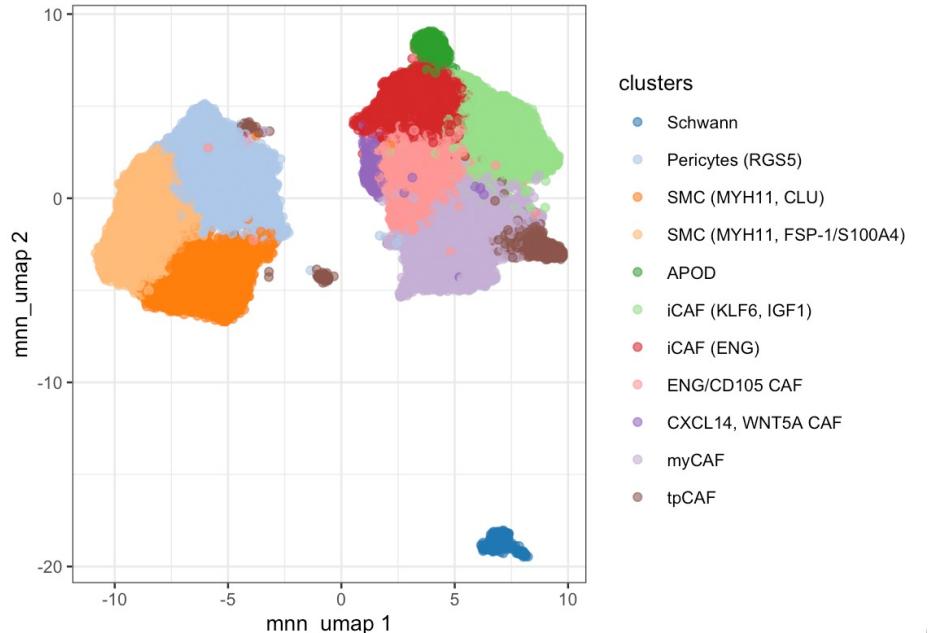
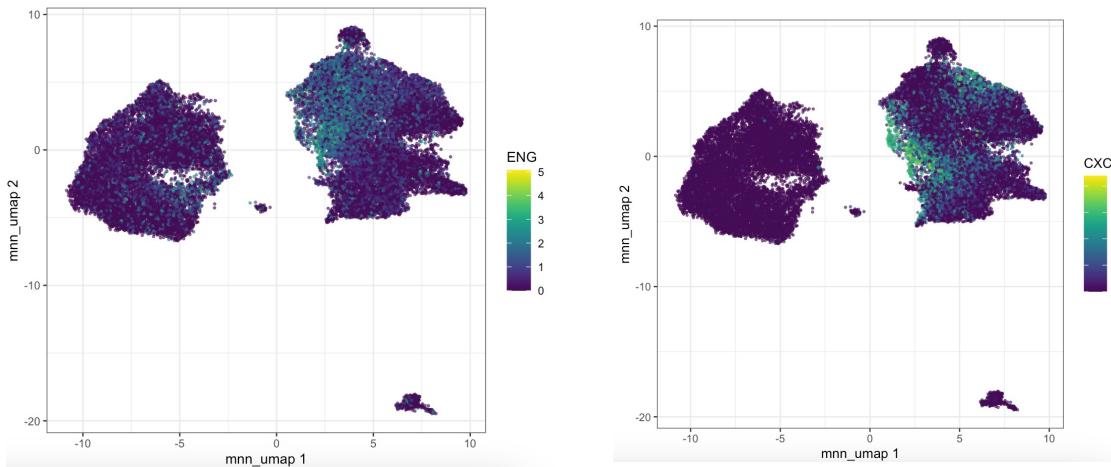


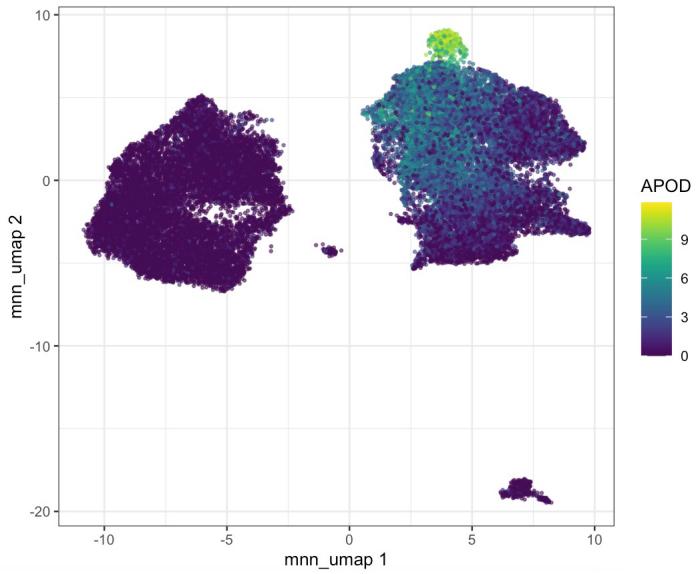


Hingorani et al., Nat Reviews Cancer, Feb 2023

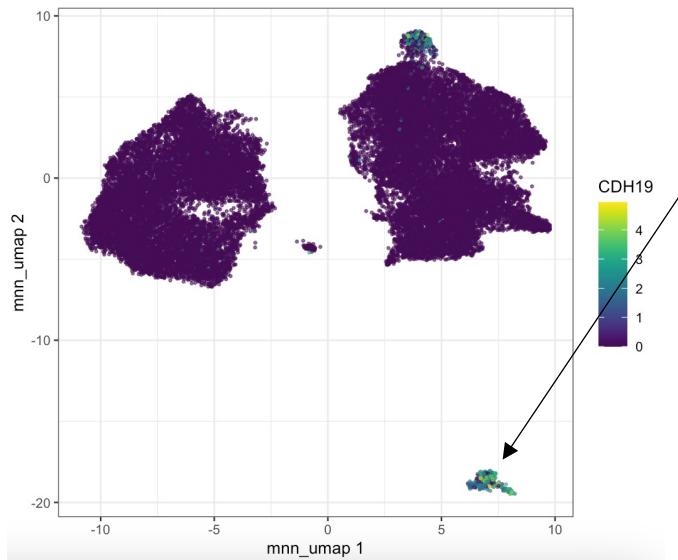






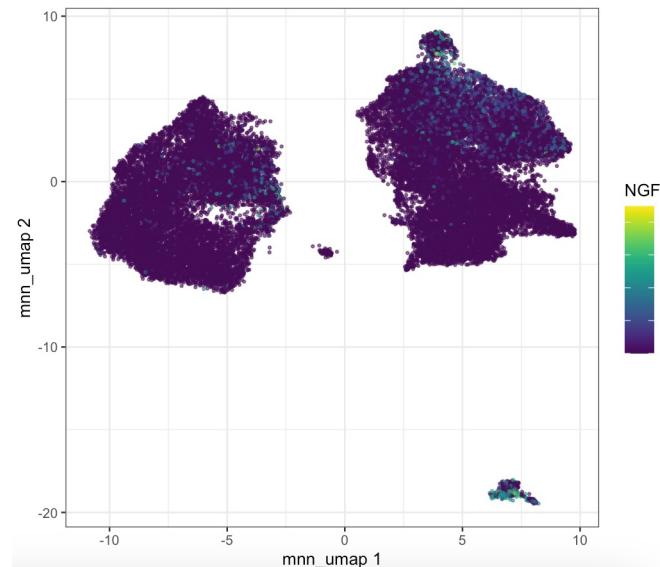


- Not sure what this is; Doesn't really look like fat
- Marker (DE) genes for this cluster: APOD, DCN, GSN, ABCA8, GPC3, CFH, CYP1B1, ITM2A, SERPINF1, LUM, CDH19, PI16, ANGPTL7, BAMBI
- In healthy tissue scRNA-seq (not many cells), I do see APOD expressed in some of the “activated stellate cells”



This cluster is the **Schwann Cells**

Marker (DE) genes: CRYAB, GPM6B, S100B, CD74, CDH19, PLP1, HLA-DRA



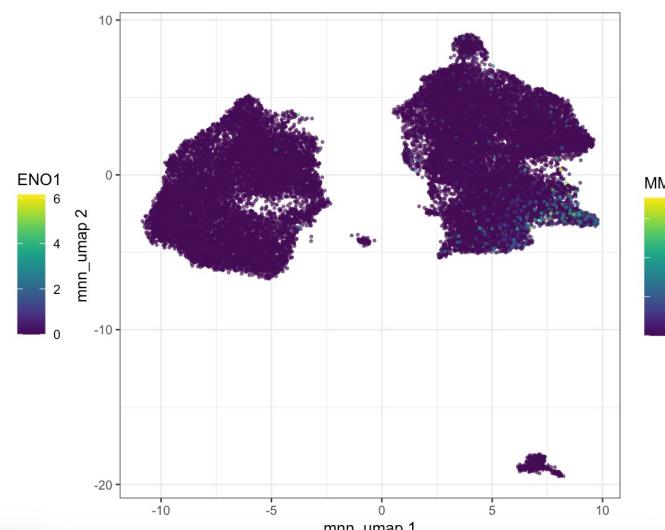
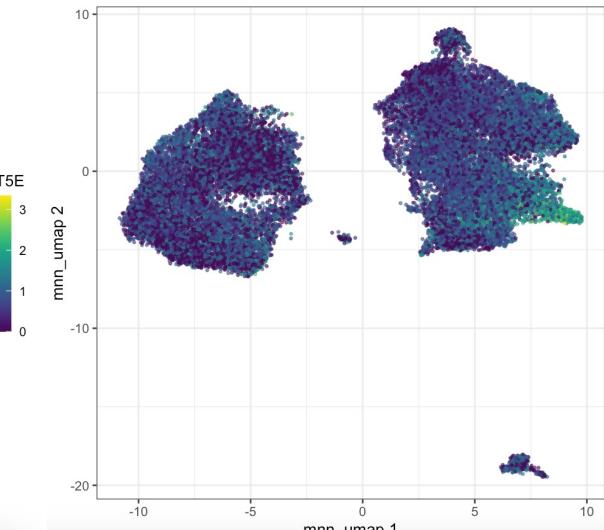
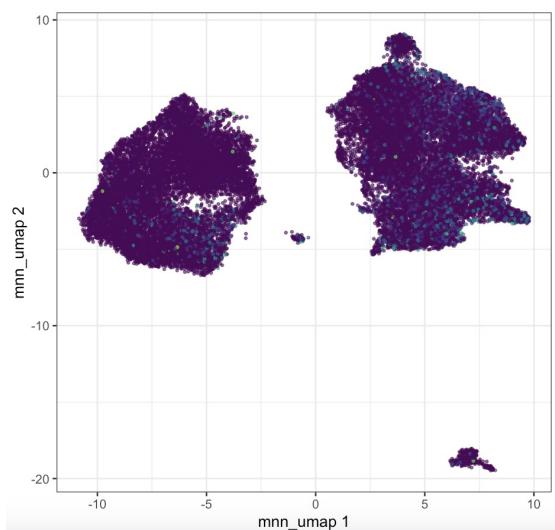
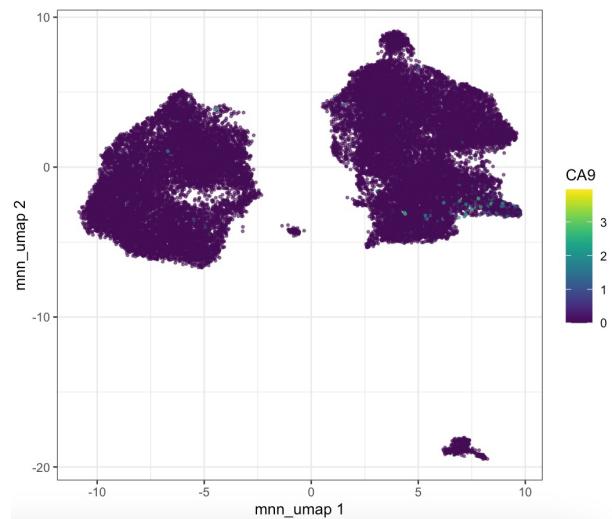
Potentially? tpCAF (L. Cords) and "Deserted" (B. Gruenwald) phenotype?

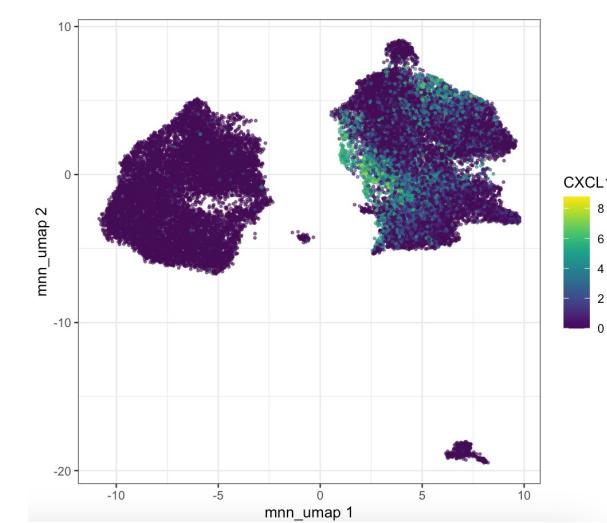
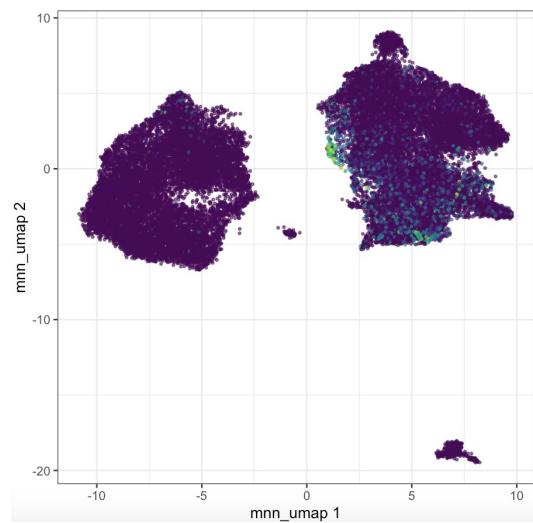
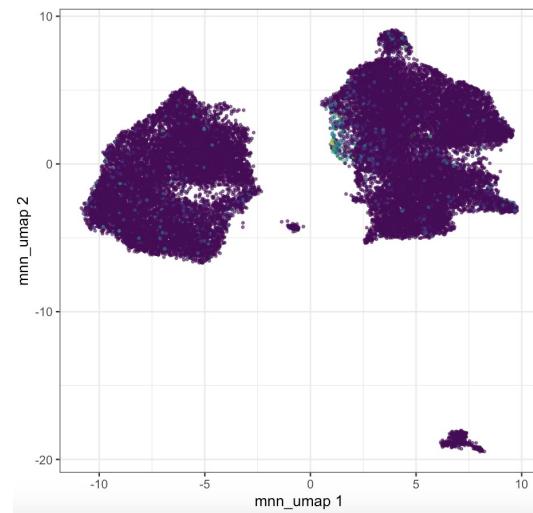
Highly enriched in ribosomal genes

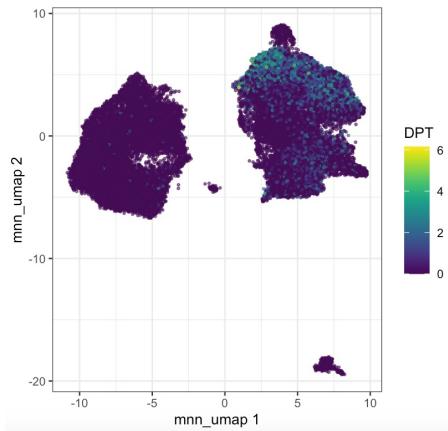
This looks a lot like the tpCAF population from Lena Cord's panel:

- MME = CD10; NT5E = CD73
- Note; in this clustering data NT5E doesn't look that enriched in this cluster, but if I subcluster the CAFs sometimes I do see it appear
- ENO1 and NT5E are in the DE genes sufficiently enriched in the "deserted" phenotype from Barbara's publication
- Note2: None of these genes are unique to mesenchymal cells. In fact, Lena Cords called them tpCAFs "Since this gene expression signature resembles that of tumour cells"

Note: the hypoxic CAF overlaps best with this tpCAF, maybe?







DPT and CD34 (which DPT overlaps well with) have been reported to be markers for a stemlike population that exists in steady-state tissue

Buechler et al, 2021 / Krishnamurty, Nature, 2022
Foster et al ,Cancer Cell, Nov 2022

