

sc-org figures (AB) to pdf

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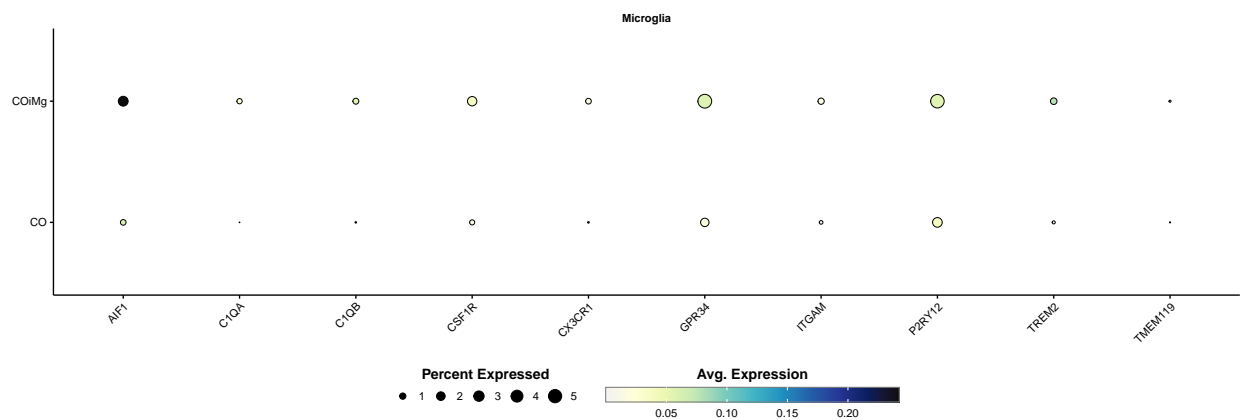
02/15/2024

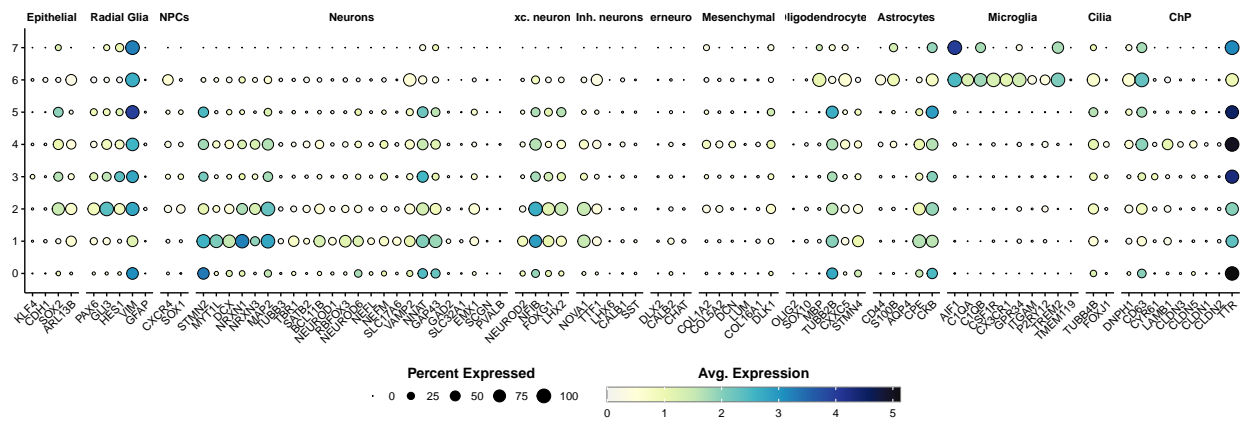
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Single-cell RNA-seq analysis of COs vs COiMG

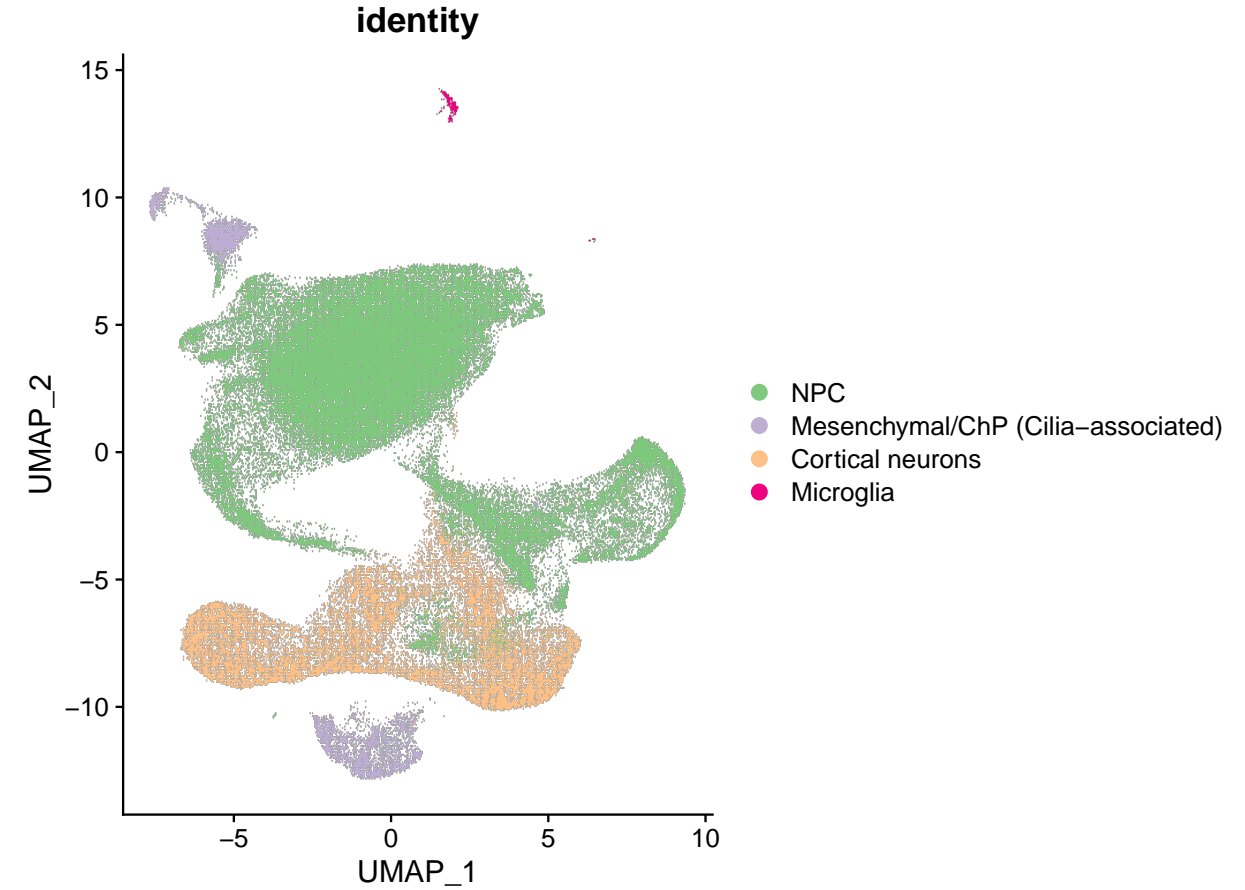
Annotation

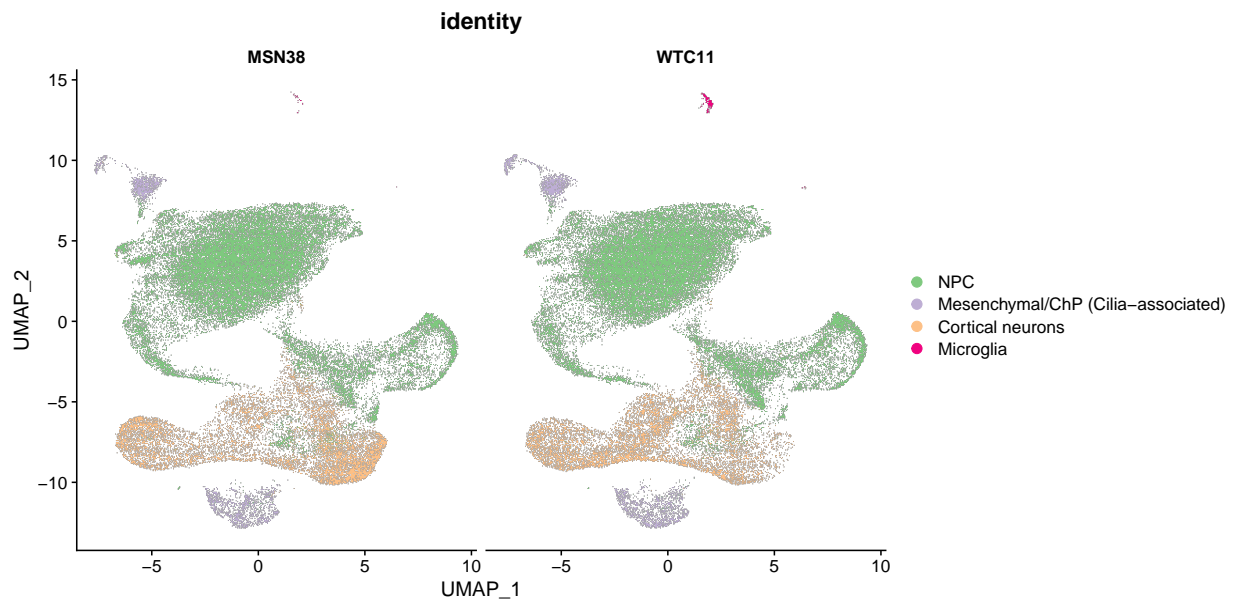
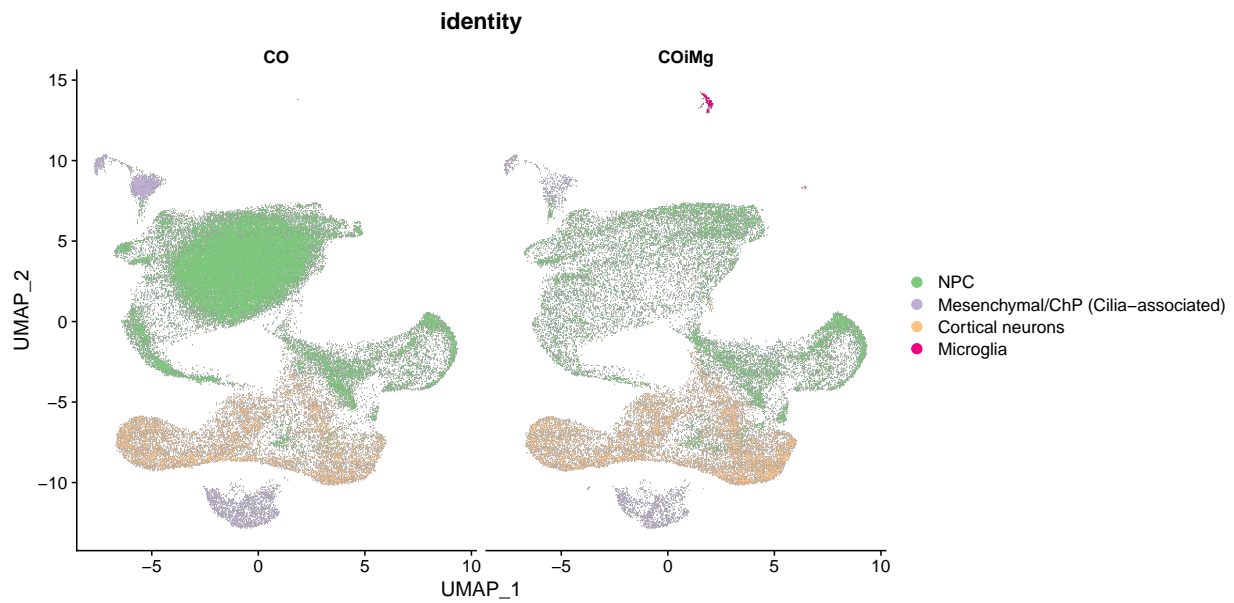




UMAPs

```
##
##                               NPC                               Cortical neurons
##                               79480                             22070
## Mesenchymal/ChP (Cilia-associated)                             Microglia
##                               5588                               282
```





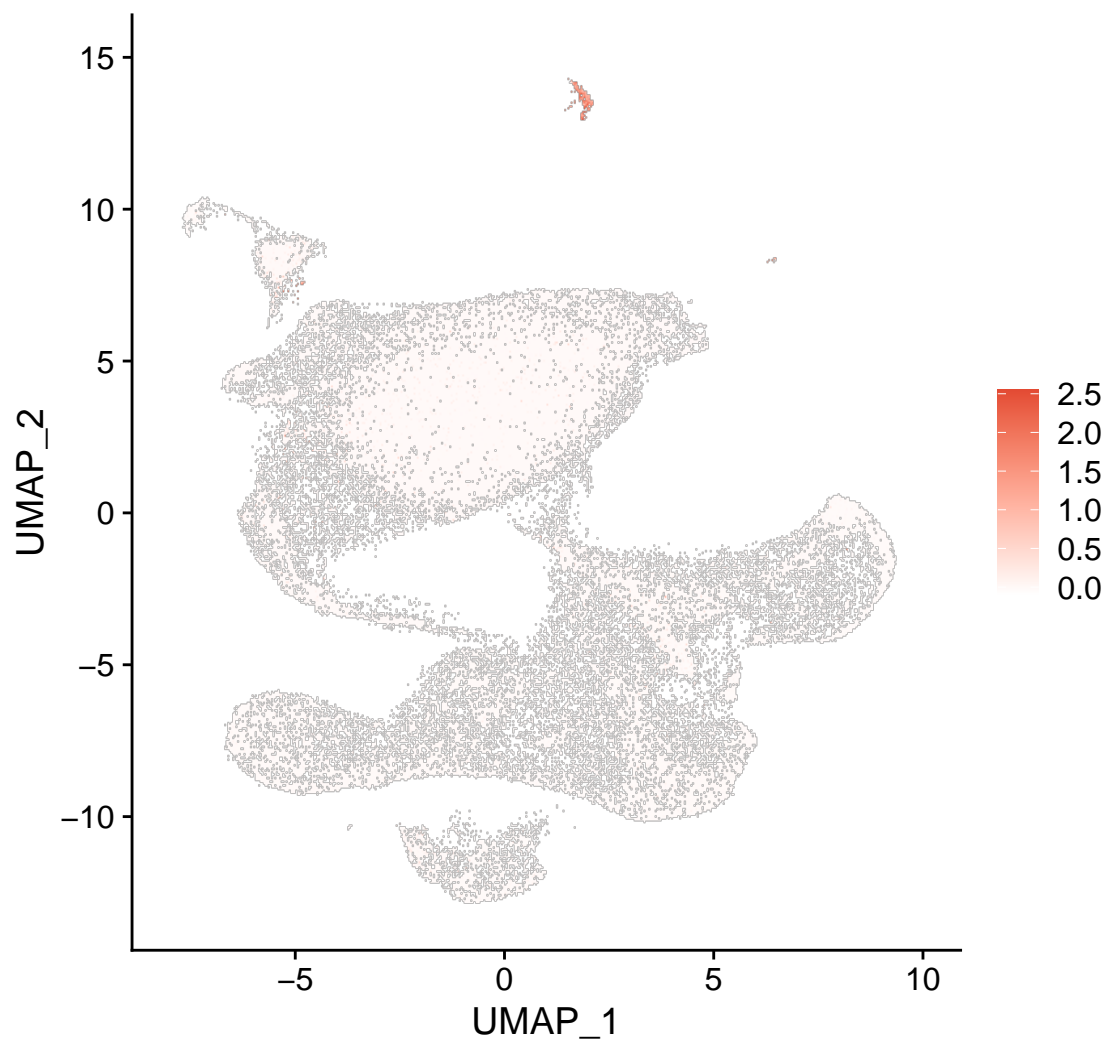
```
##
##           NPC Mesenchymal/ChP (Cilia-associated) Cortical neurons Microglia
##  MSN38 38690                                2603           11712         26
##  WTC11 40790                                2985           10358        256
```

Feature plots - marker scores

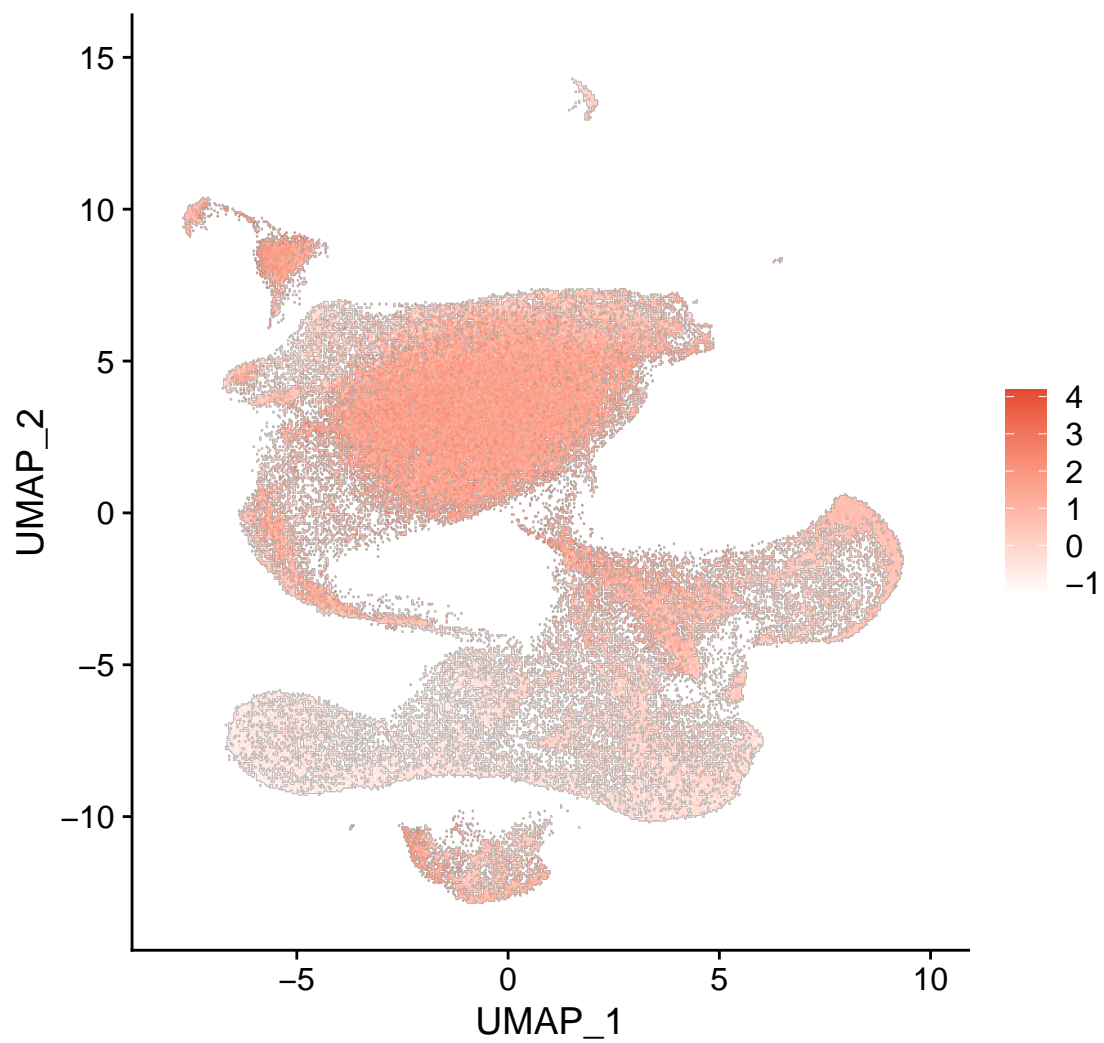
Concatenated marker lists

Here I simply filtered the genes inside these gene sets based on their raw rowMeans(expression) > 1

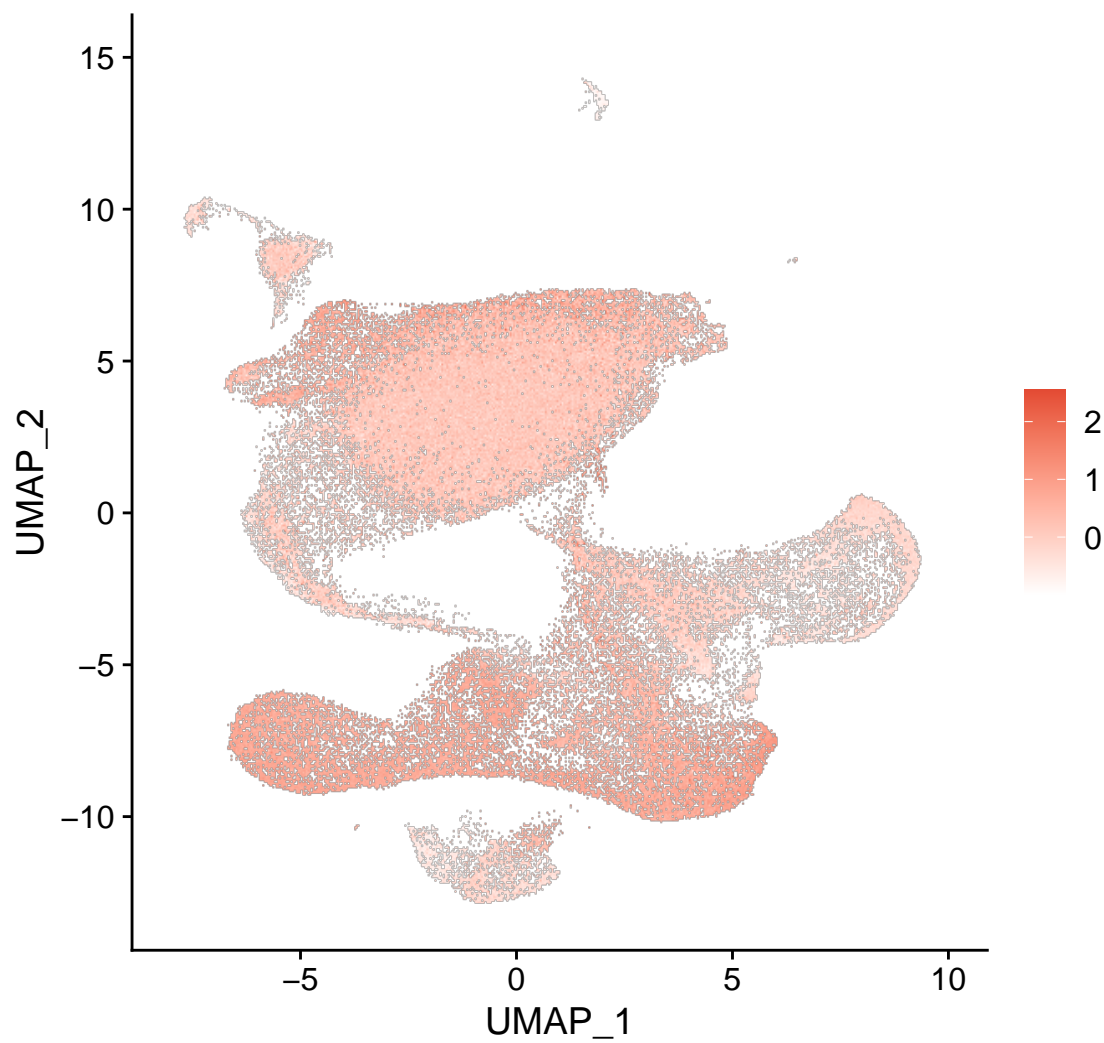
Microglia markers

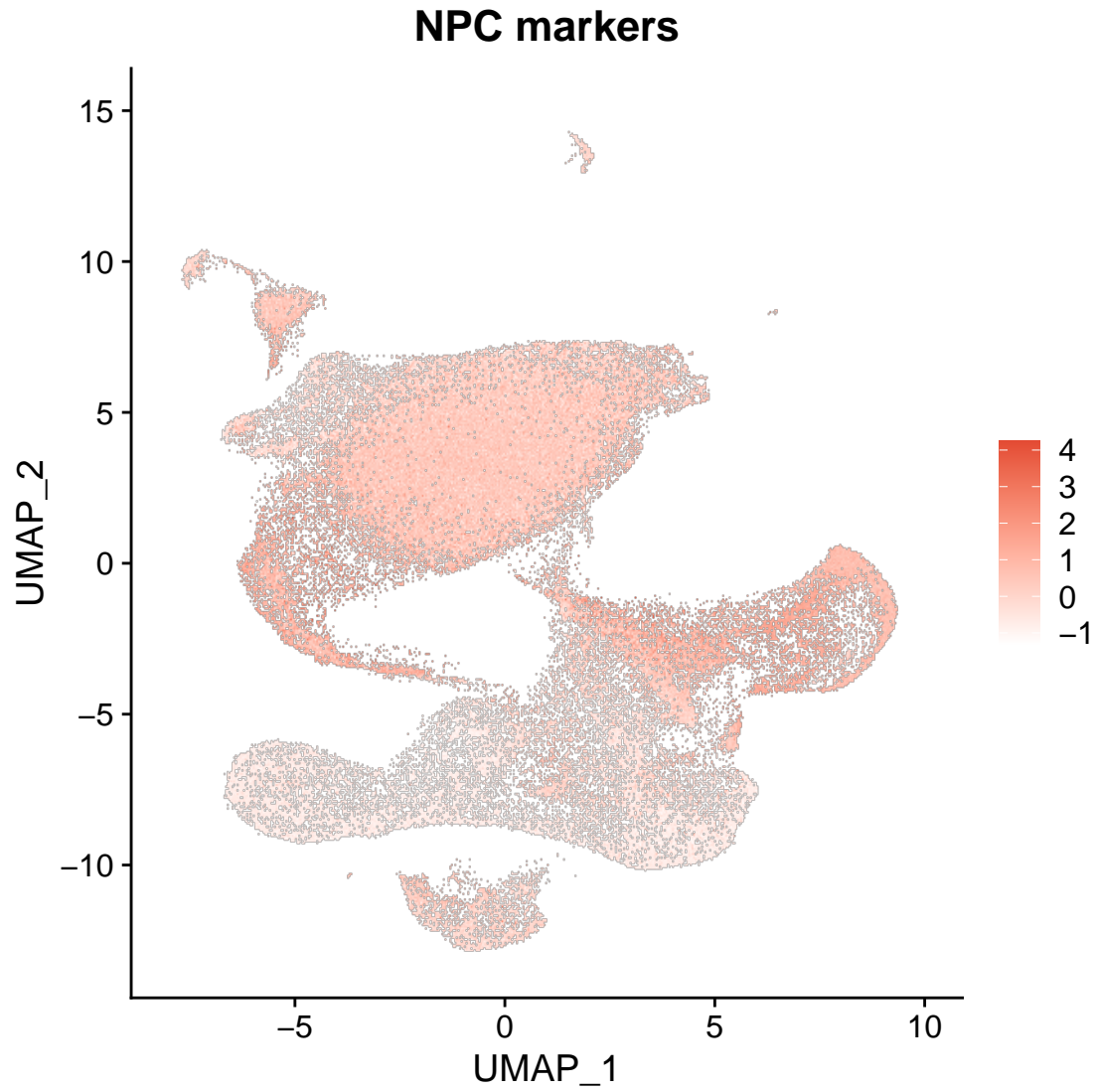


Mesenchymal/ChP markers



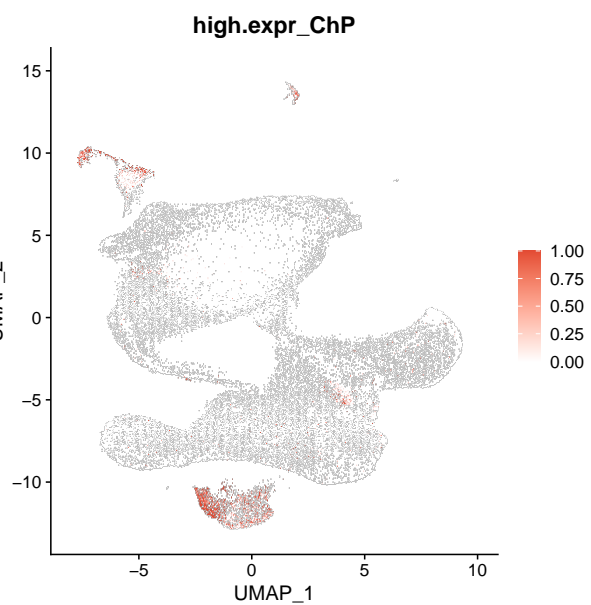
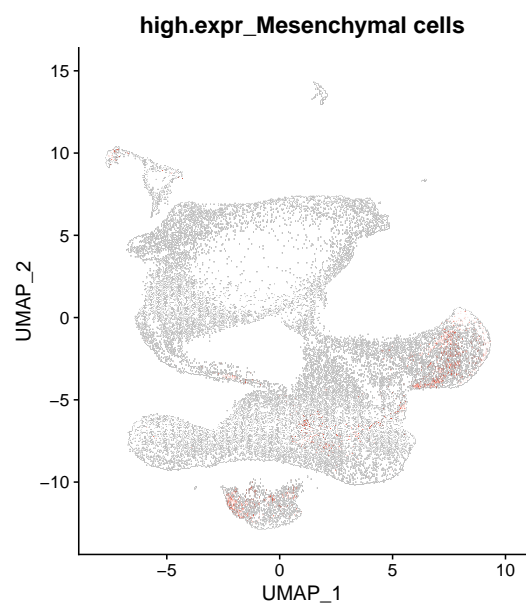
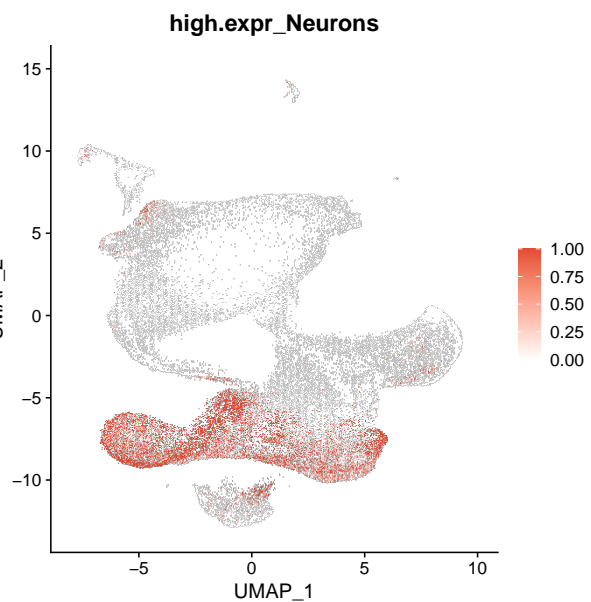
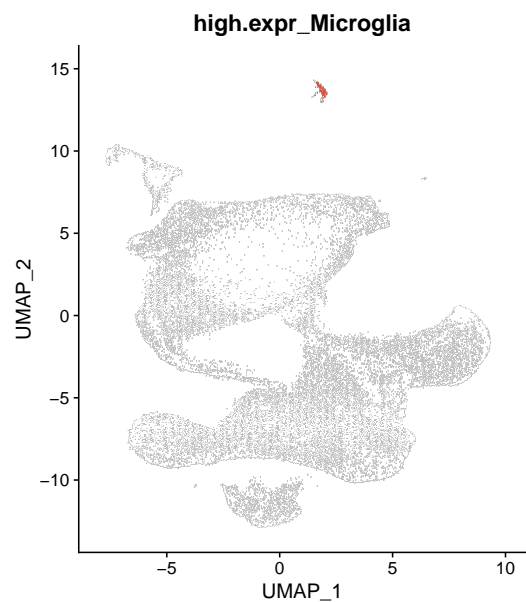
Neuron markers

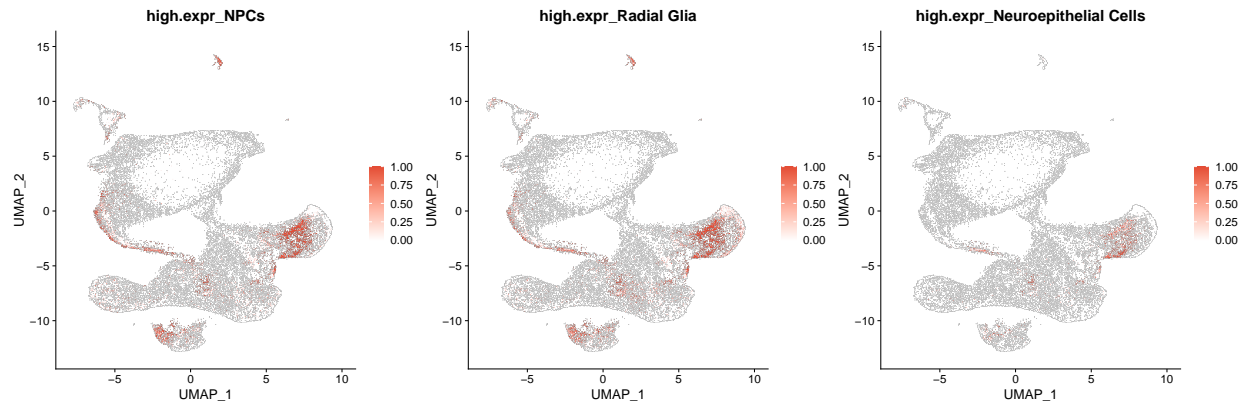




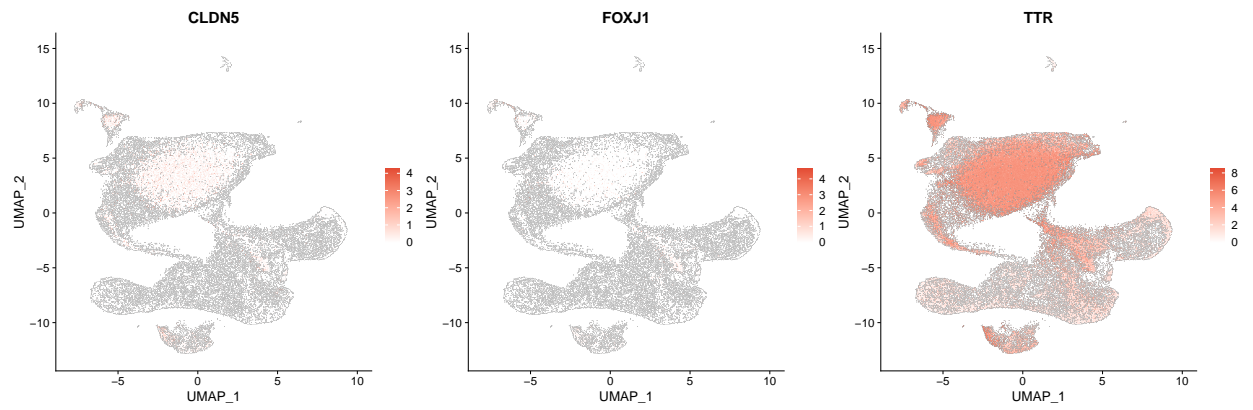
Filtered list

Then I said that any cell must express at least fulfill $\text{colMeans}(\text{expression}) > 5$ to be considered a high expression cell. These I annotated with 1, the other cells with 0. The results is a gradient between 0-1, colored.

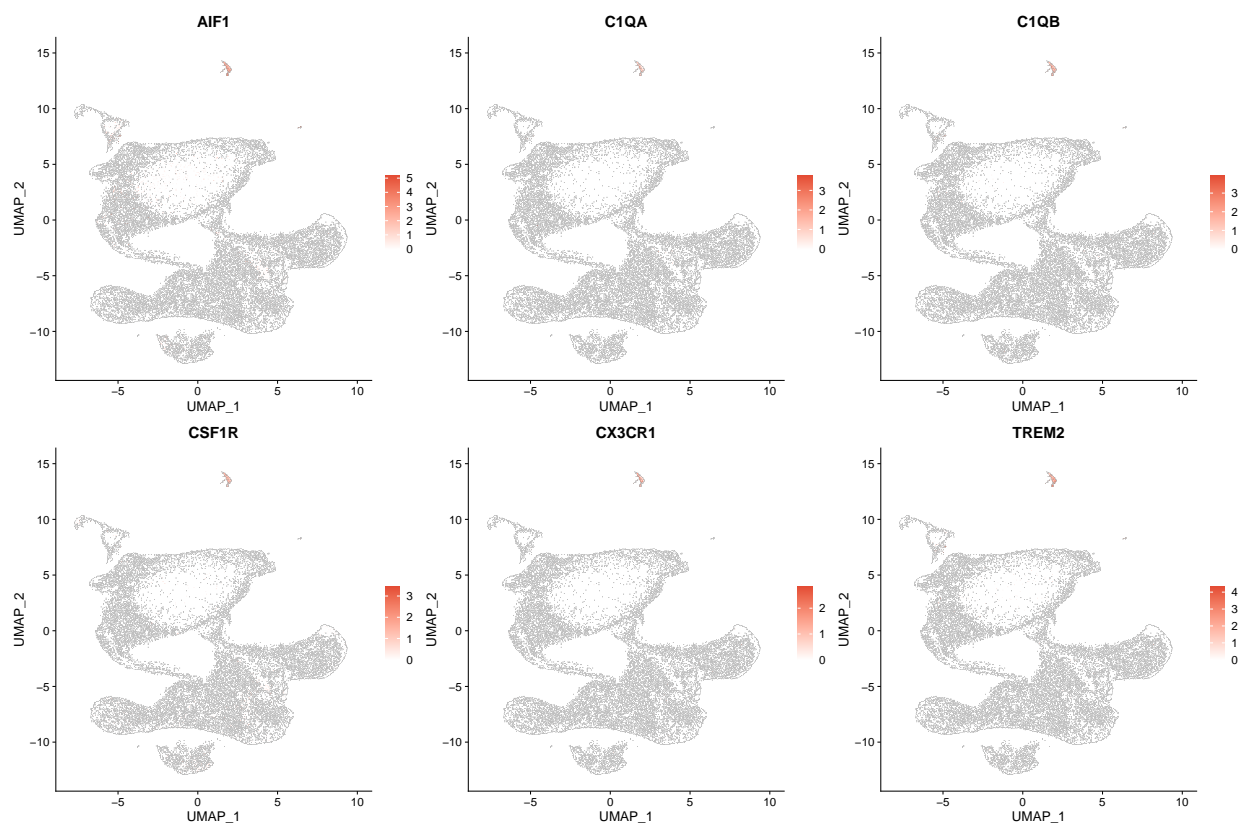




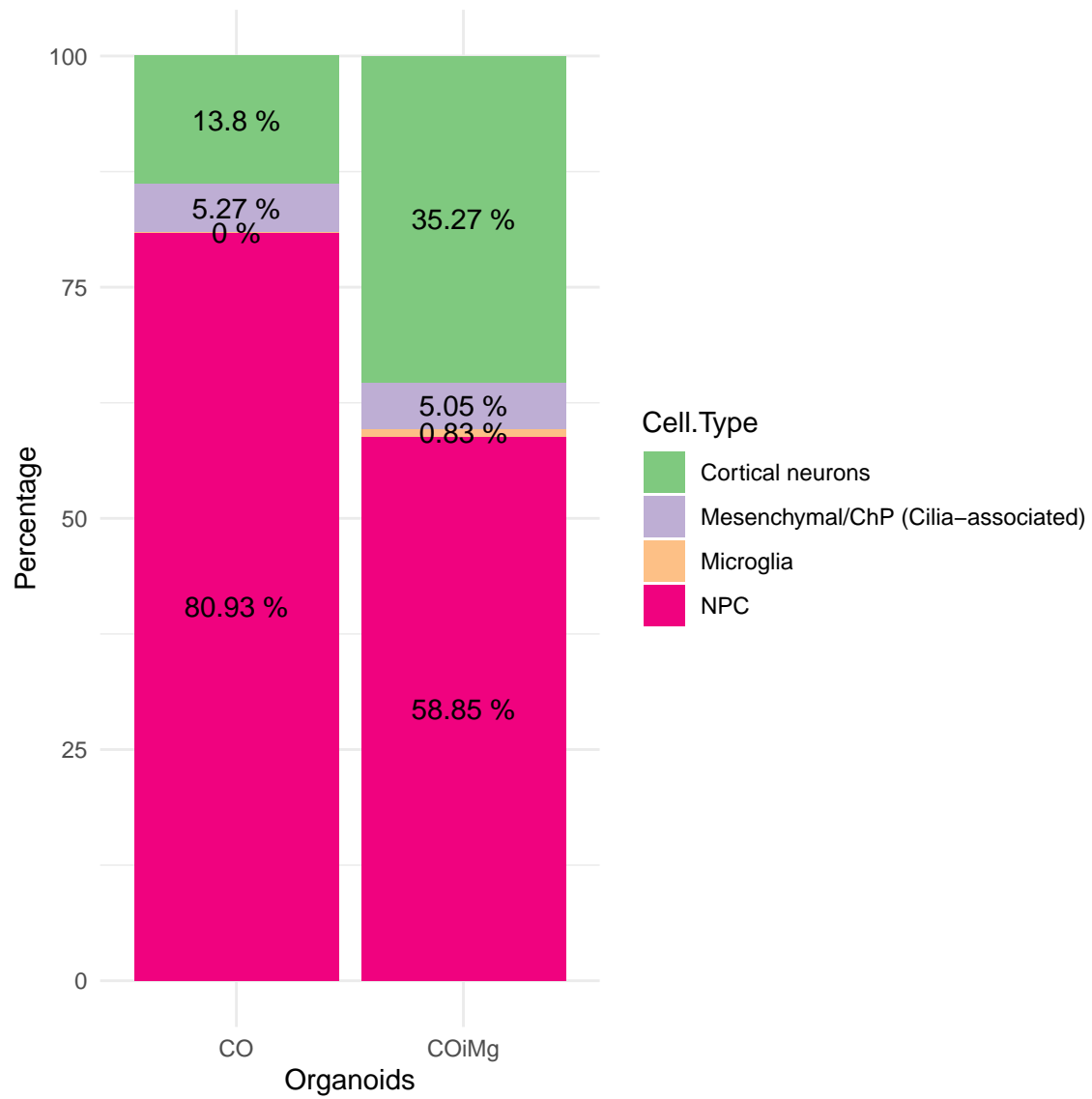
Feature Plots - Cilia genes



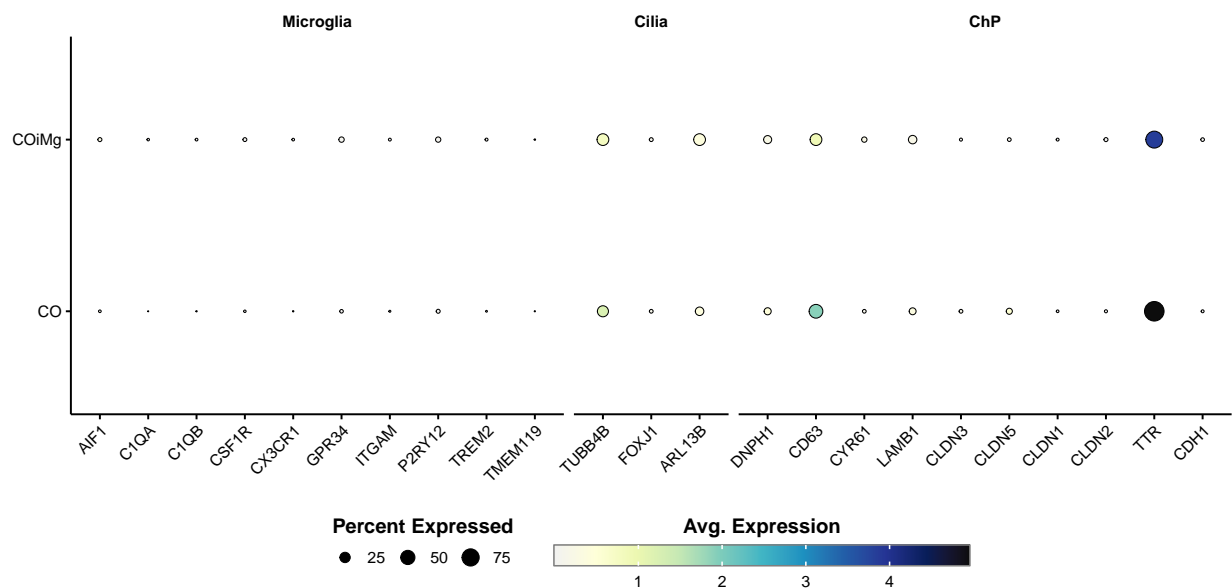
Feature Plots - Microglia genes



Proportions



Cilia genes CO vs COiMg



Bulk DEGs across clusters

