Summary of:

"An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types"

Objective: Discover cell types from datasets of mouse brain cells

The data

- 7 RNA sequence datasets

- 2 Epigenome measurement datasets

Area of brain: primary motor cortex

Conclusion: There are somewhere between ~30 and 116 cell types

1. Clusters from RNA sequence
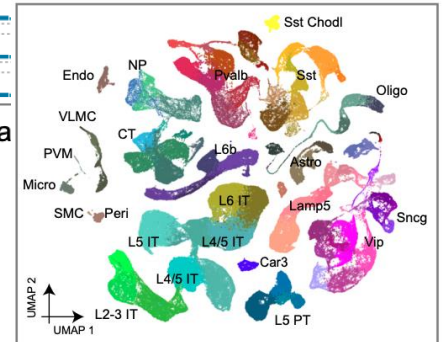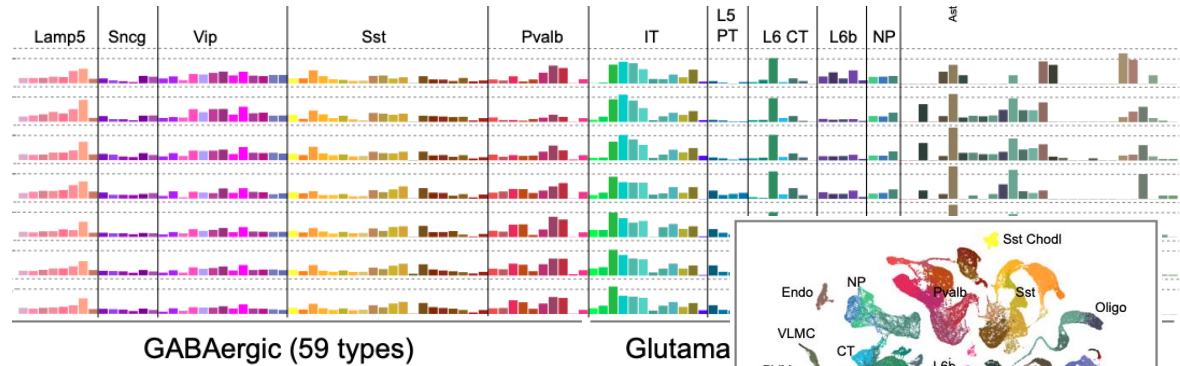
Identified 116 cell types

- Method: bootstrapped feature reduction, hierarchical clustering, nearest neighbor merging (scrattch.hicat)

About the cell type names:
Lamp5 Pax6

Second characteristic
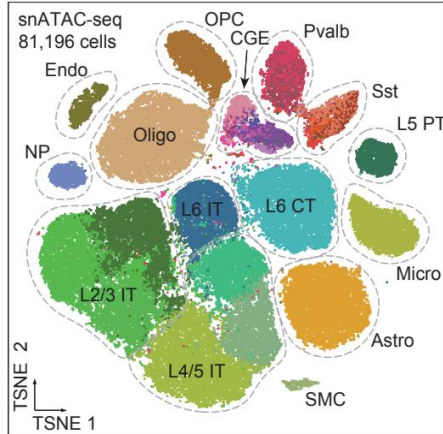
First characteristic
(marker gene or layer)

2. Clusters from epigenomic data

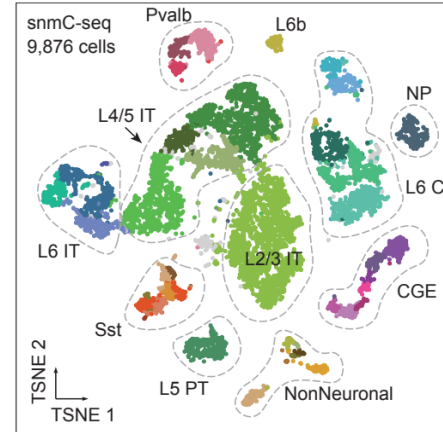## 2 methods, identified 33 and 42 cell types

Method 1:
UMAP with kNN graph or hierarchical clustering (snapATAC)

33 clusters

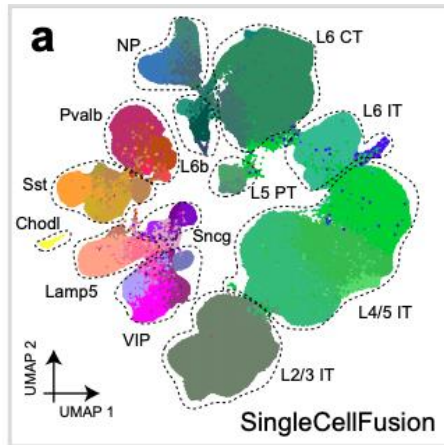Method 2:
Leiden clustering with kNN graph

42 clusters

3. Clusters from RNA and epigenomic data

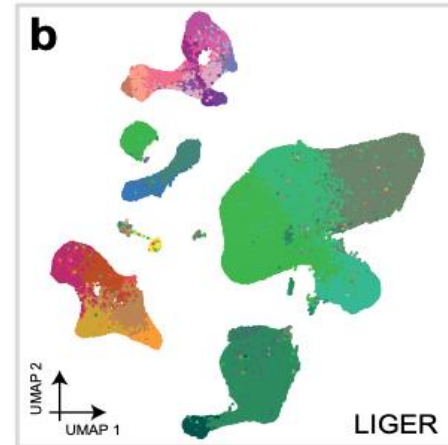**2 methods, both identified 56 cell types**

Method 1:
UMAP-based clustering (SingleCellFusion)

Method 2:
Matrix factorization-based clustering (LIGER)

References

Yao, Z. et al. An integrated transcriptomic and epigenomic atlas of mouse primary motor cortex cell types. Preprint
at *bioRxiv* https://doi.org/10.1101/2020.02.29.970558 (2020).