Epigenetically Profiling Human Brain Cell Types Utilizing ATAC-Seq

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Introduction

- The human brain contains many distinct cell types with differing morphological, electrophysiological, and connectional properties.

- We wish to identify enhancer elements that distinguish these cell types.

Aims:

- Identification of cell type-specific enhancers using ATAC-seq

- Integration of epigenetic data and transcriptomic data to identify of distinct cell class/type-specific regulators

# Epigenetic Landscapes of Neuronal Classes/Type Using ATAC-seq

Vibratome sections
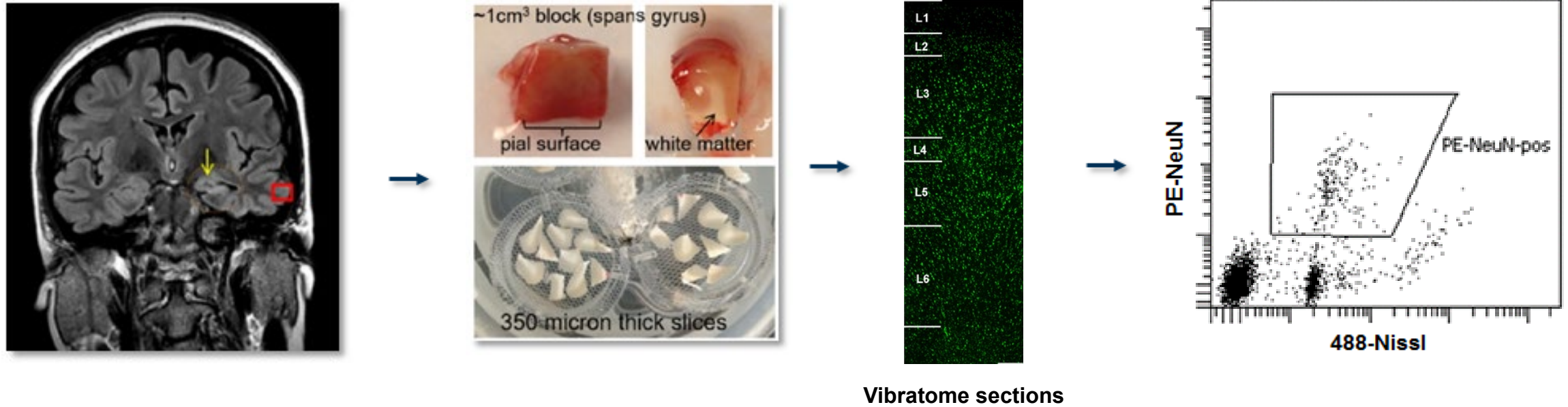
Each sample is:

→ Sliced and dissected into layers (1 through 6)

→ Dounced to isolate the nuclei

→ Stained with PE-NeuN antibody

→ Single nuclei are sorted as $NeuN^+$ and $NeuN^-$ from each layer using FACS

→ Tn5 tagmentation

→ Indexed and amplified by PCR

→ MiSeq

ATAC-seq data revealing the epigenetic landscape of neuronal classes/types
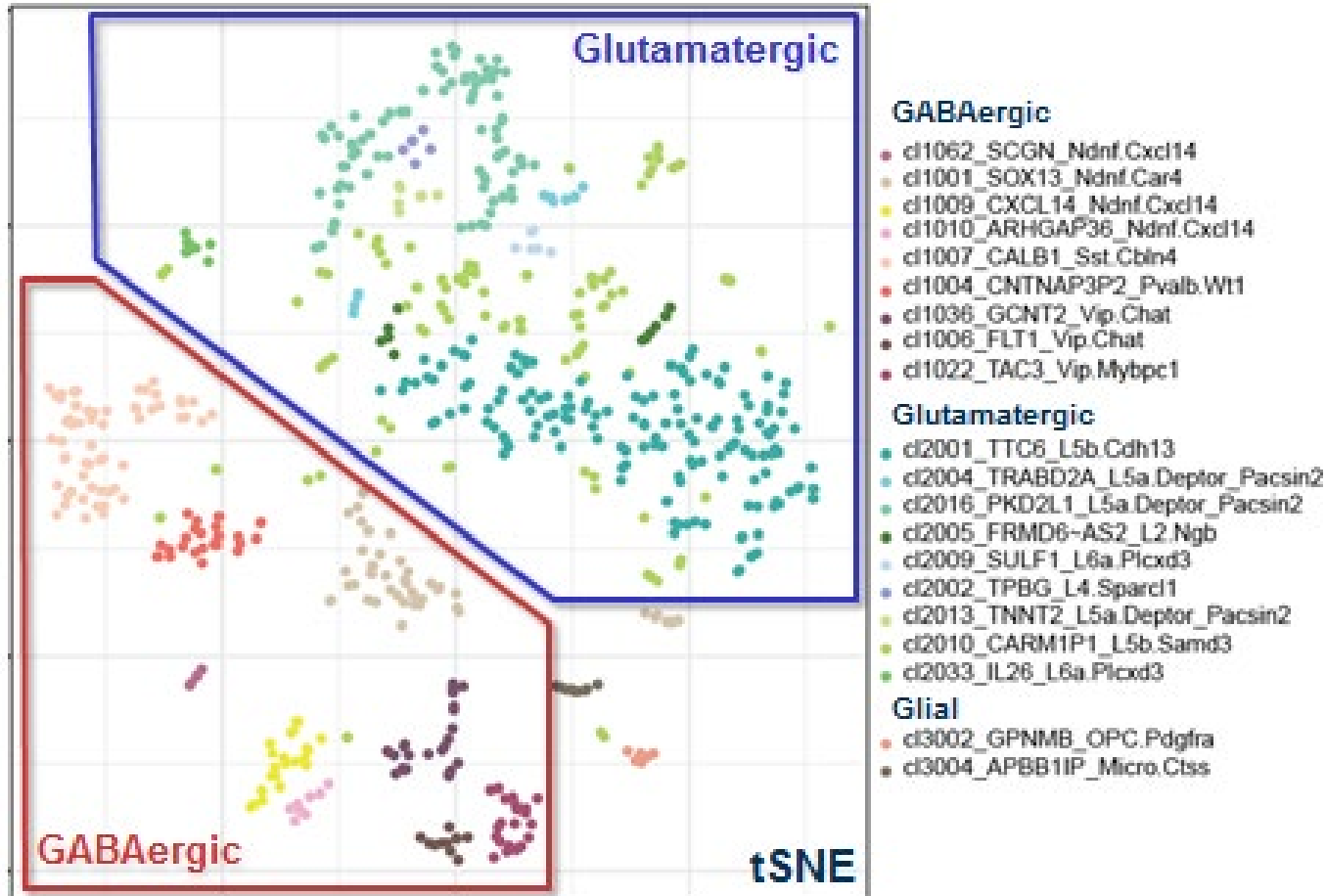

- Current clustered data from different cases of human brain tissues

- Reads are used to compute Jaccard distances among cells, which are used to cluster cells into like groups

- We observe major neuronal classes (excitatory and inhibitory), as well as subclass specificity in inhibitory cells

ATAC-seq results generated during internship
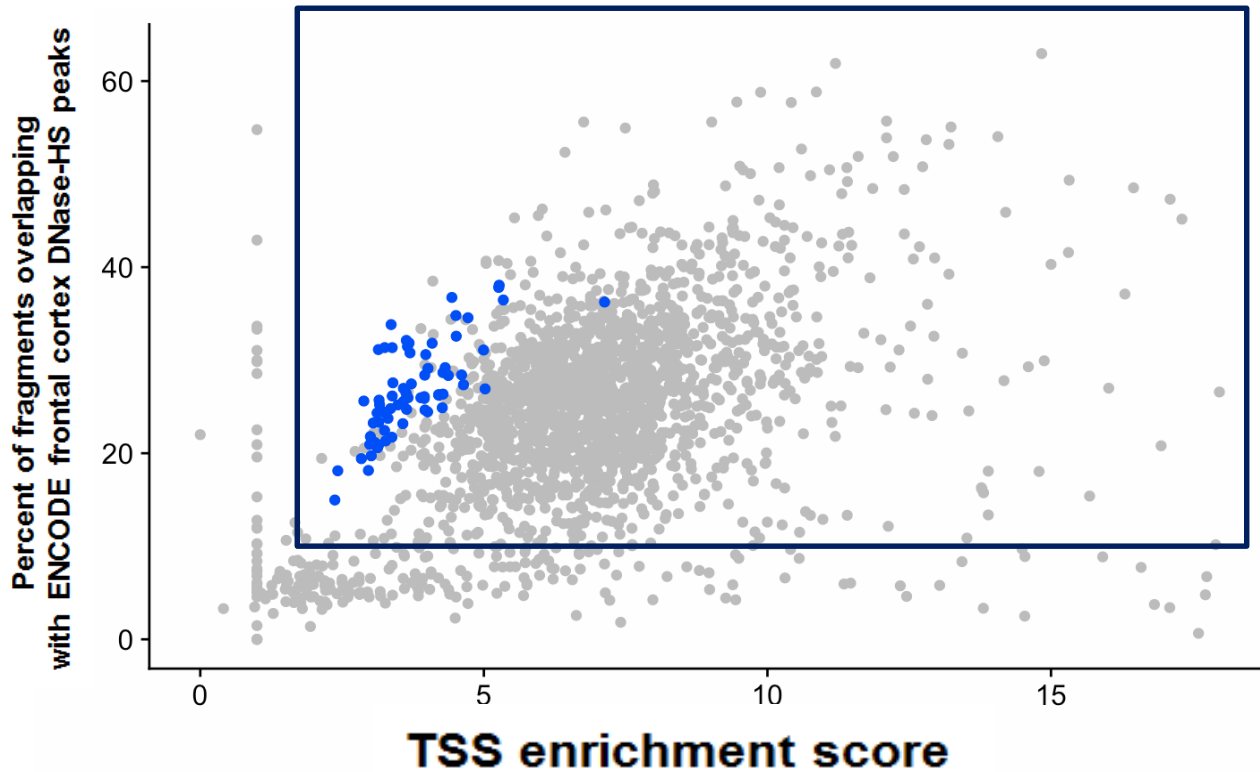
Comparison of single cell QC metrics with known data set
→ **Demonstrates high quality cells**
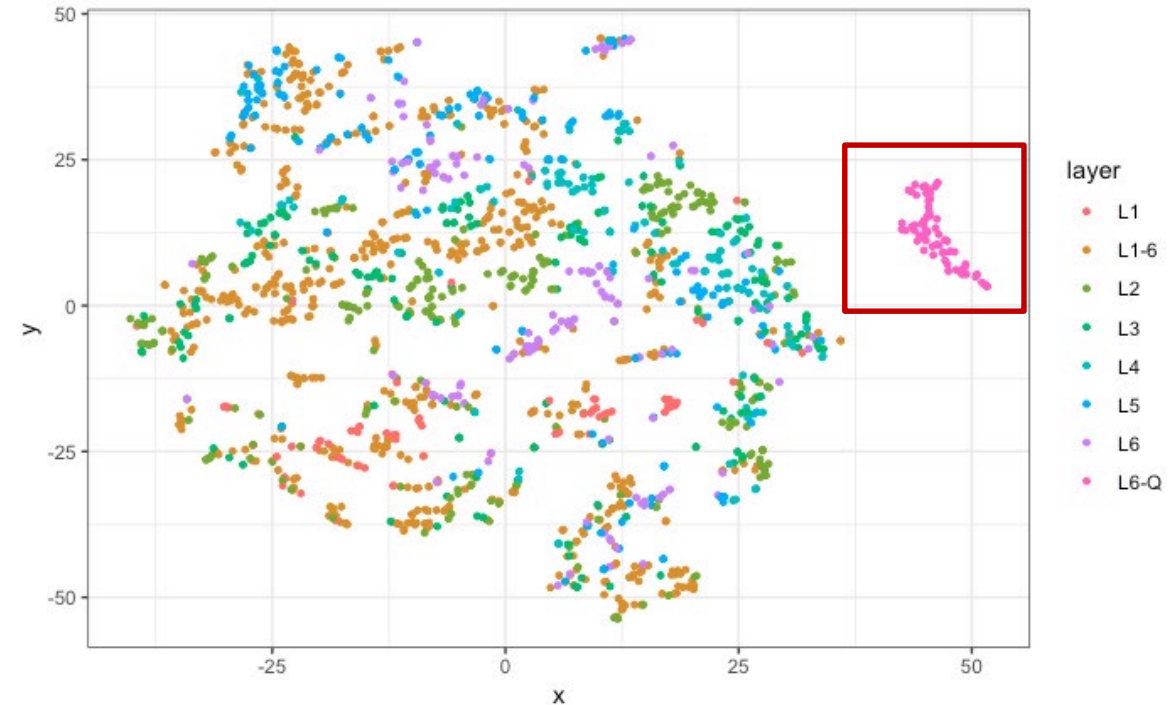
Clustering nuclei with tSNE separates distinct neuron classes
→ **Cells cluster together (as expected)**
→ **Cells cluster apart from previous cells (not as expected)**
→ **Unclear whether this is sample-specific or operator-specific**

Using these epigenomic elements to create viral tools for prospective marking of mouse and human cell types

Inhibitory neuron-specific enhancer in AAV viral vector
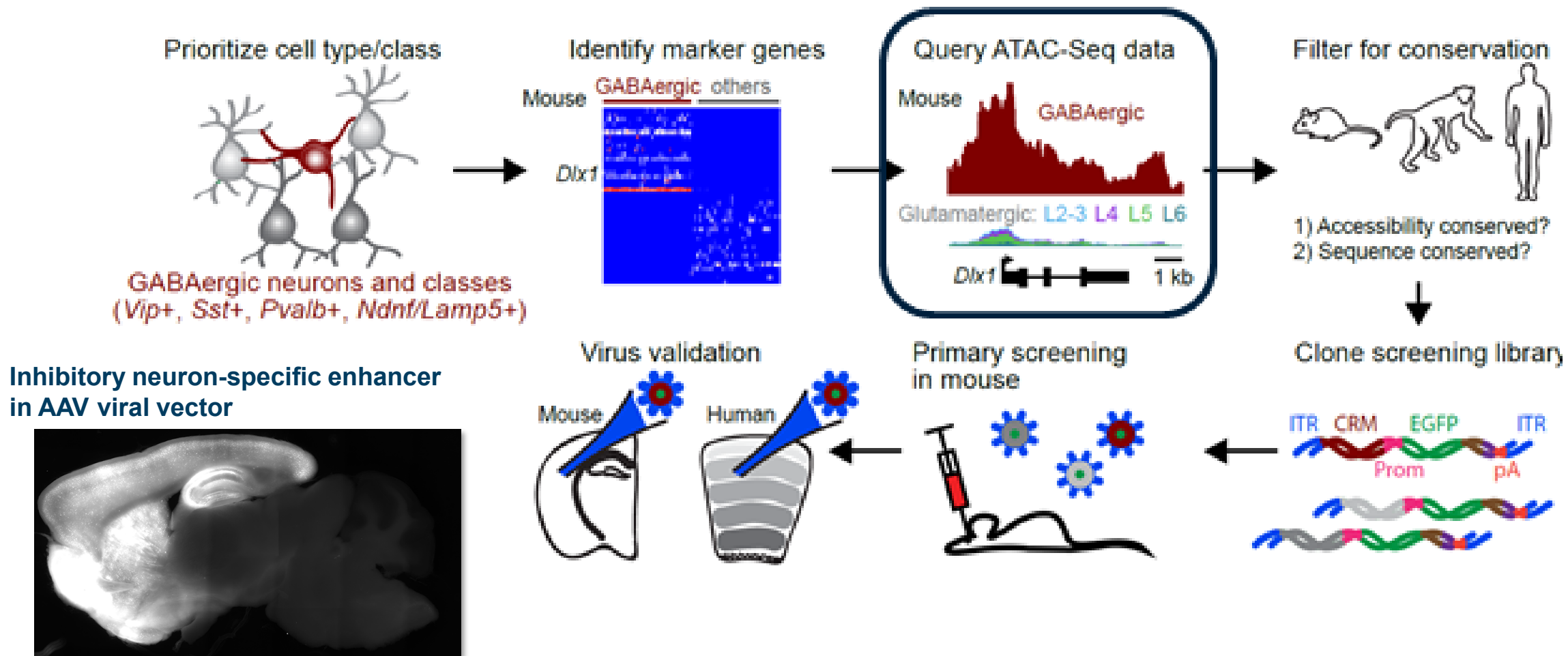
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