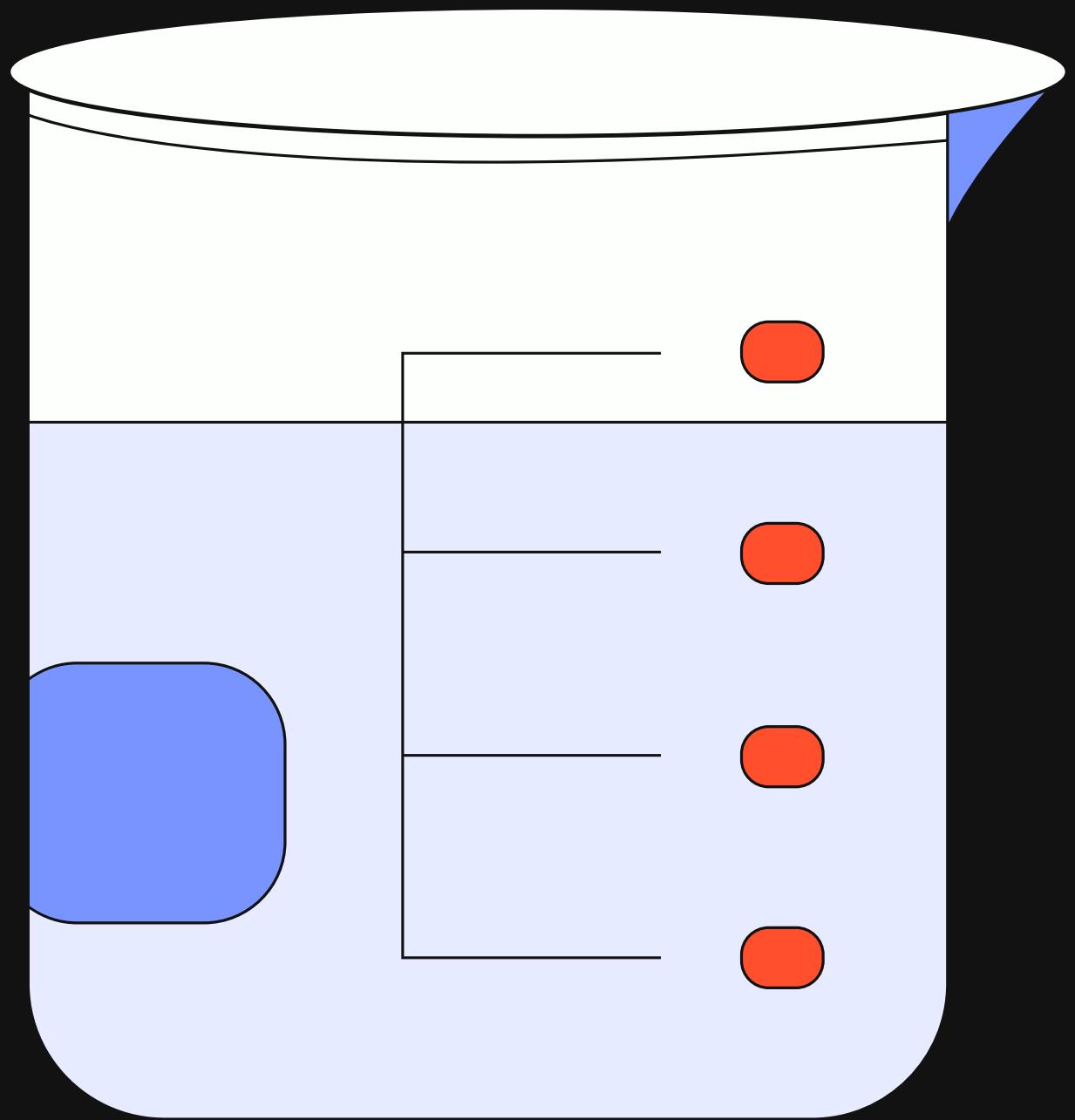


SPATIAL TRANSCRIPTOMIC ANALYSIS

JACINTA & KIAN
W/ DR. MATTHEW ROSE
& NIMA SHIROONI

August 2023

UC IRVINE



PRESENTATION OUTLINE

- INTRO & BACKGROUND
- SINGLE CELL SAMPLE COLLECTION
- ANALYSIS OF SCRNA-SEQ
- SLIDE-SEQ SAMPLE COLLECTION
- ANALYSIS OF SLIDE-SEQ
- RESULTS

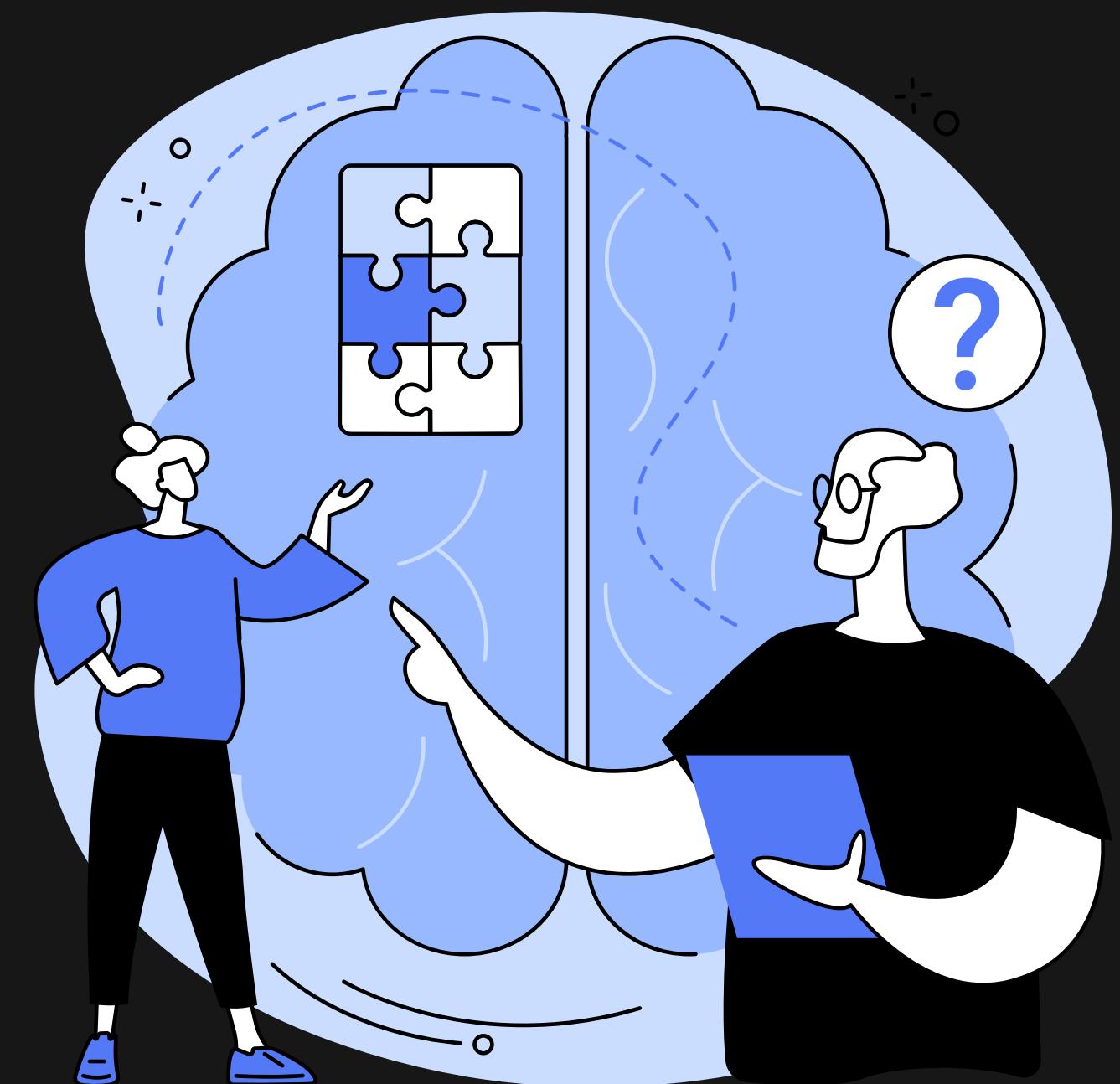


“

OUR GOALS & RESEARCH

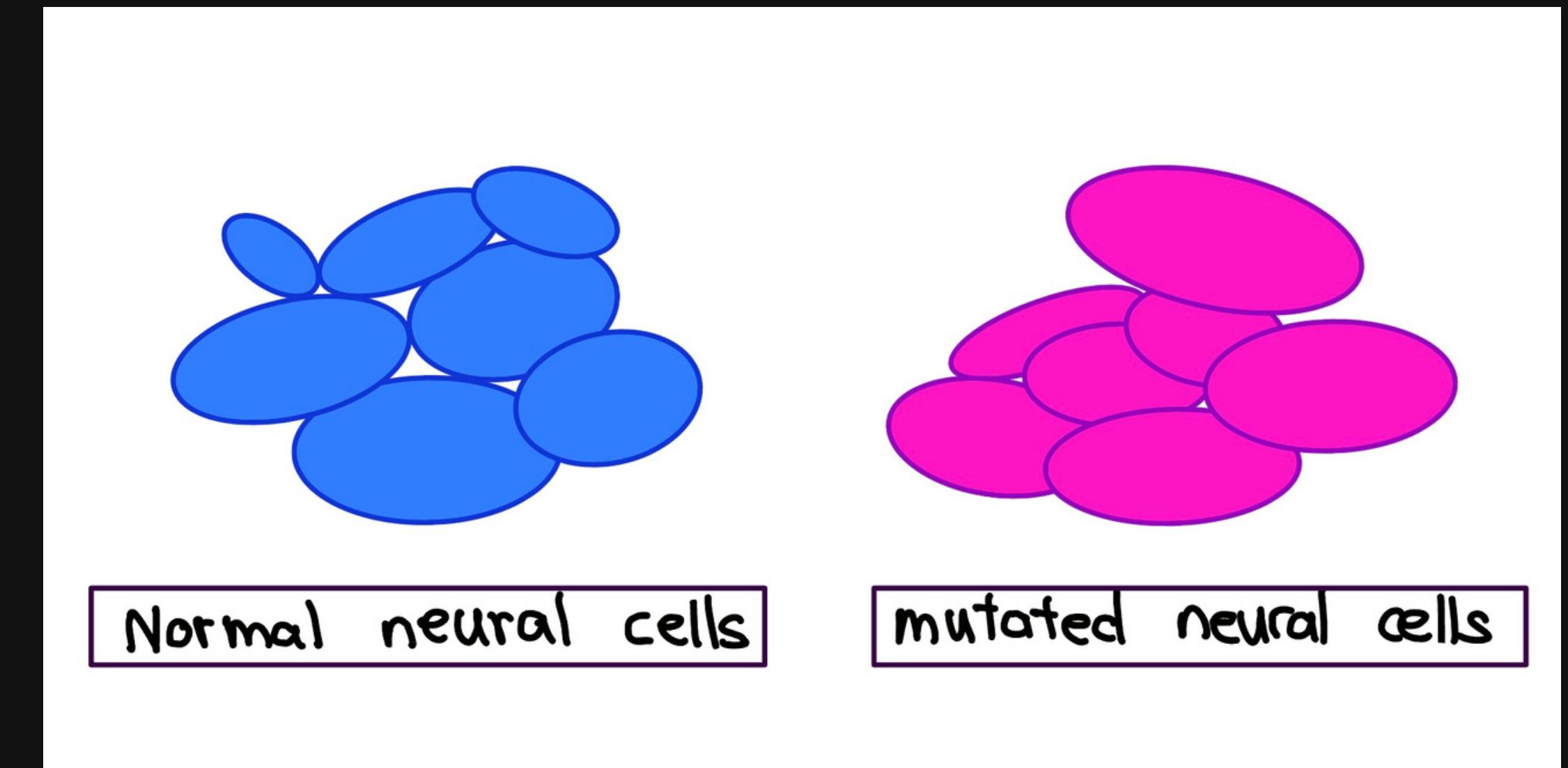
We want to find out why neurological diseases only affect certain groups of cells.

We use single-cell and spatial RNA sequencing data to identify genetic patterns in different developing motor neuron subgroups.



RNA-SEQUENCING

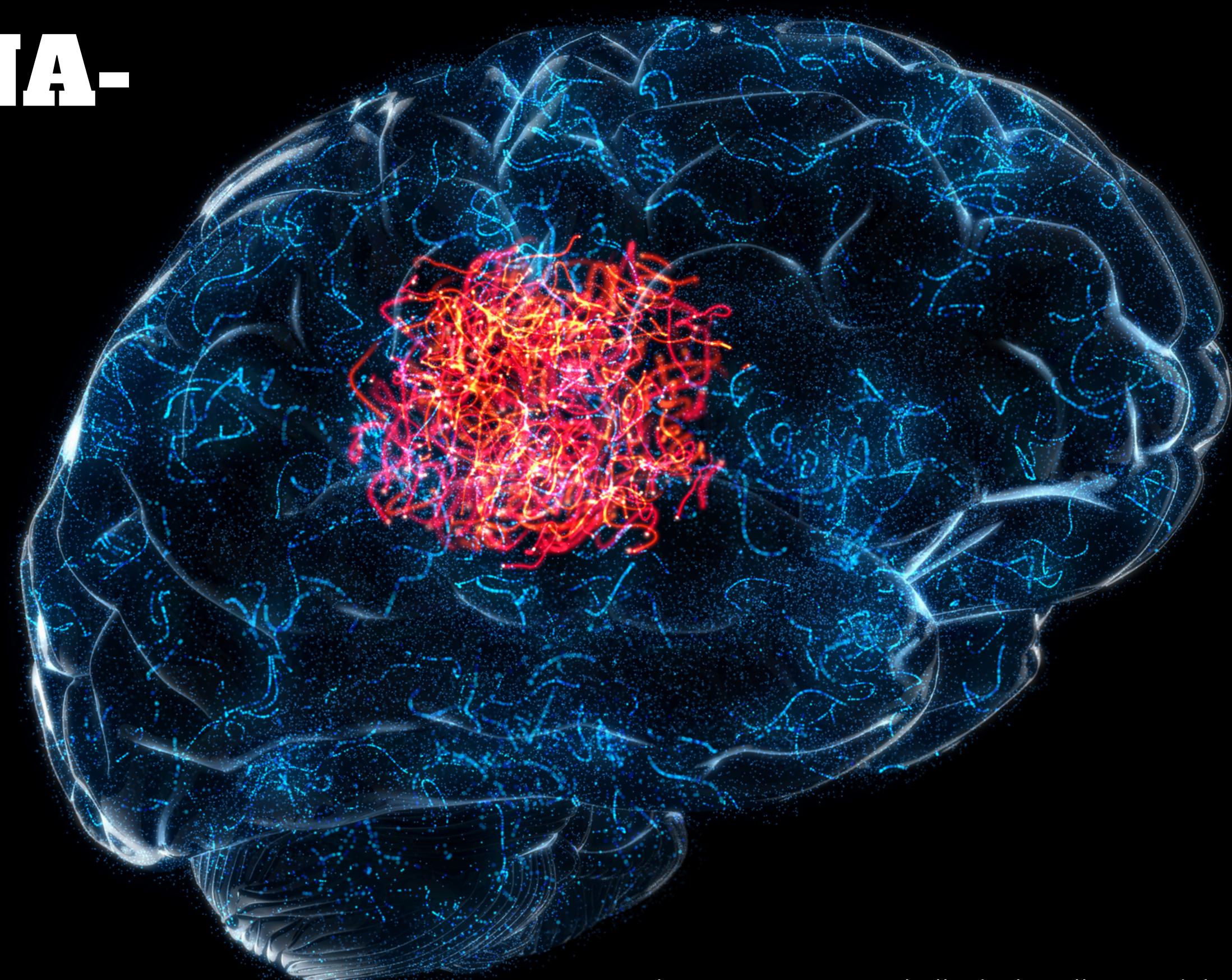
- Gene expression
- Identify RNA transcripts present
- Disease mechanisms, new treatment strategies



Jacinta, Kian, 2023

Application of RNA-Sequencing

- Identification of cancer subtypes and stages of development
- Understanding the cancer's molecular mechanisms can help us develop prevention and treatment strategies



SINGLE CELL SAMPLE COLLECTION

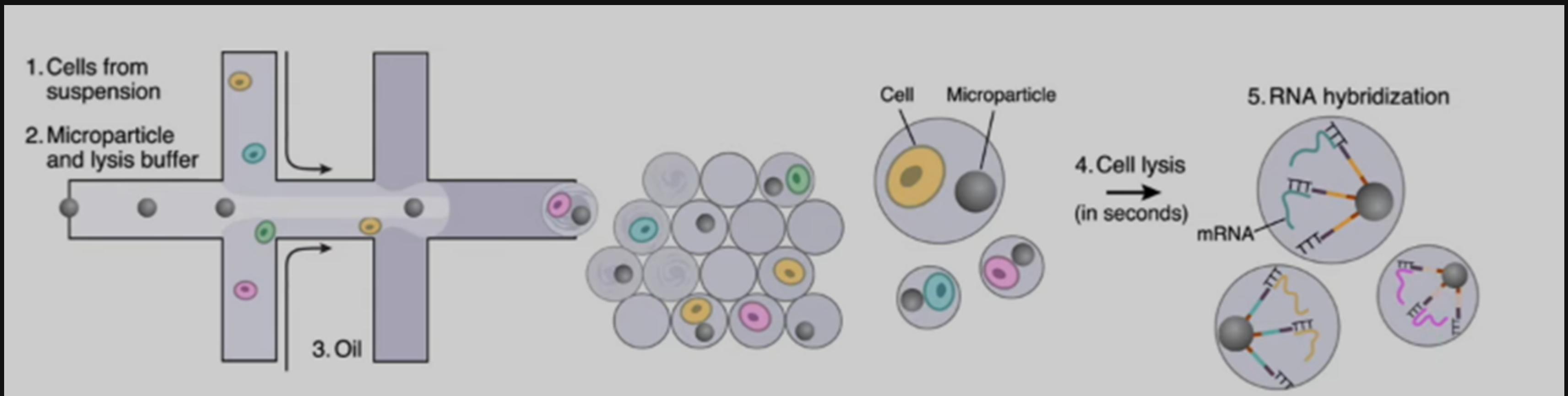


Sample

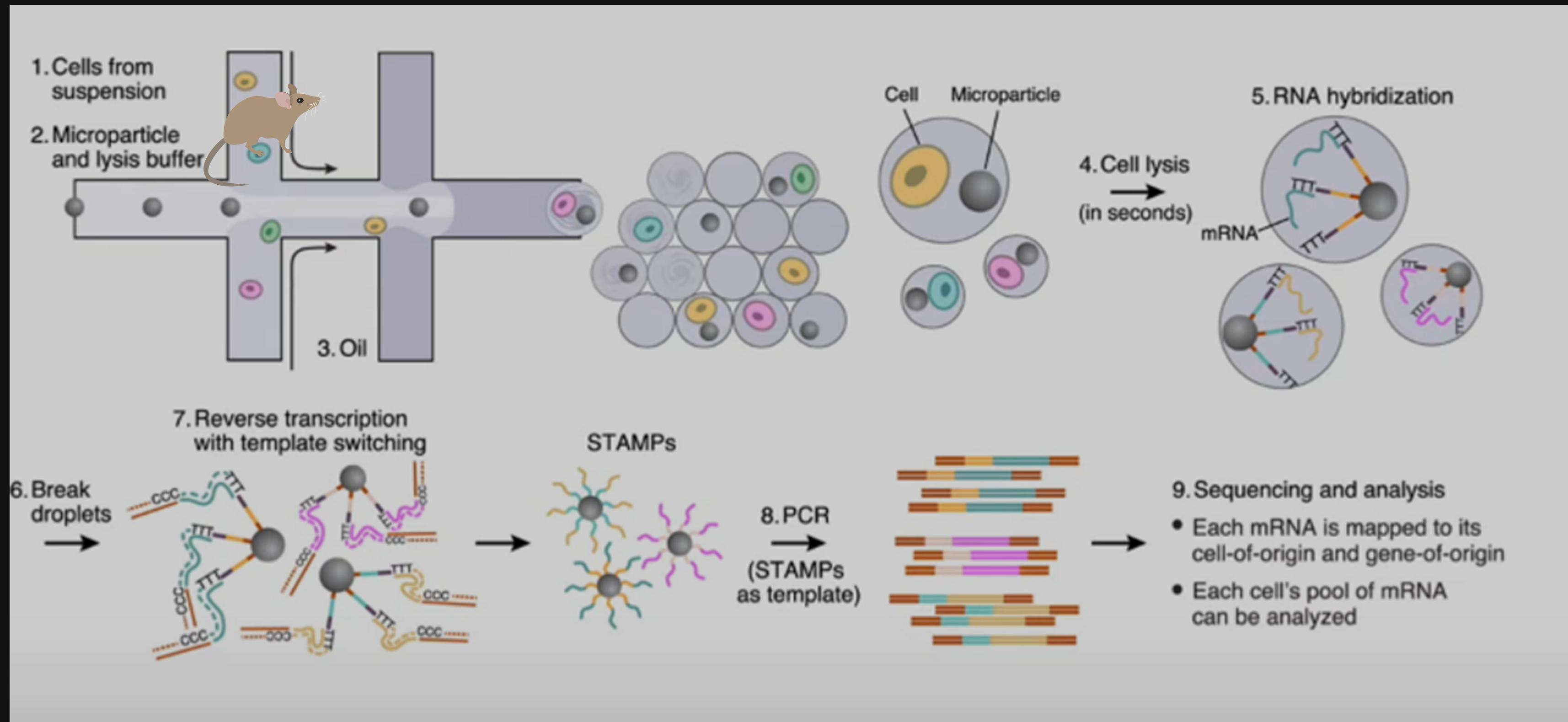




PROCESS OVERVIEW

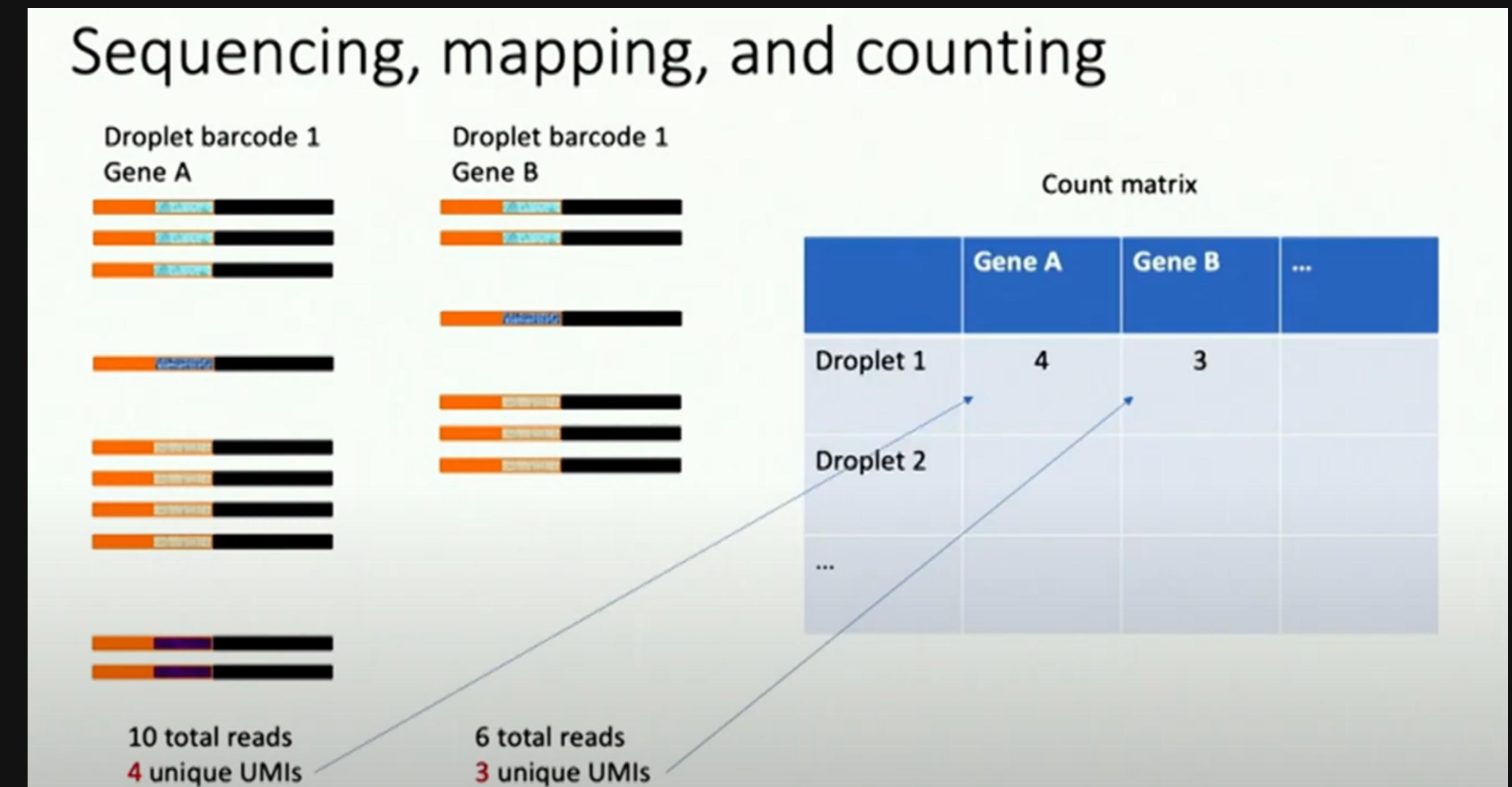


PROCESS OVERVIEW



PLATFORM & DATA

- R platform with Seurat
- High dimensional data
- Count Matrix (cell by gene)
- Unique Molecular Identifiers (UMIs) are attached to each RNA molecule





ANALYSIS OF scRNA-SEQ

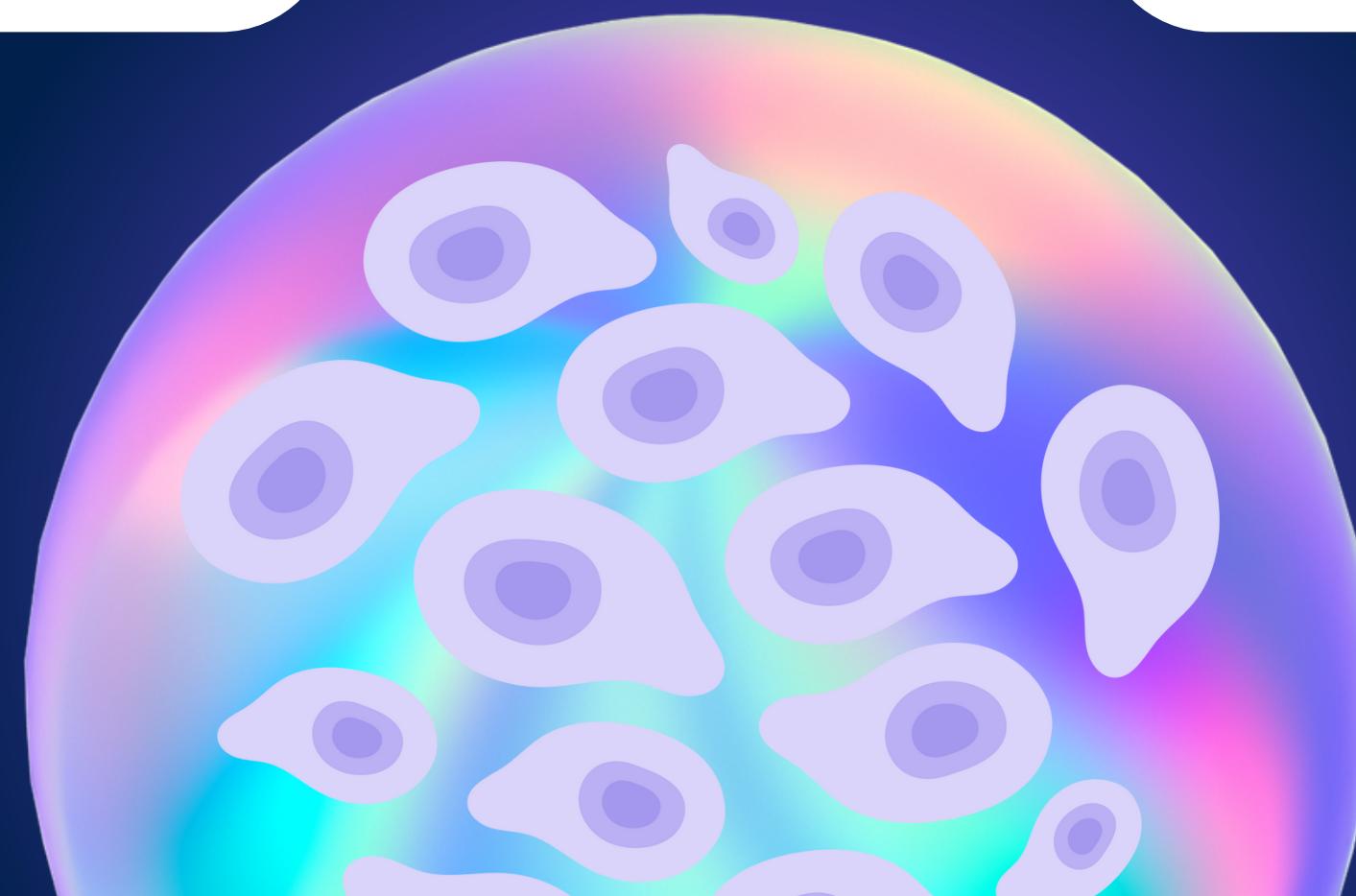
COVARIATES

- 1 Ambient RNA
- 2 Low Quality Cells
- 3 Doublets

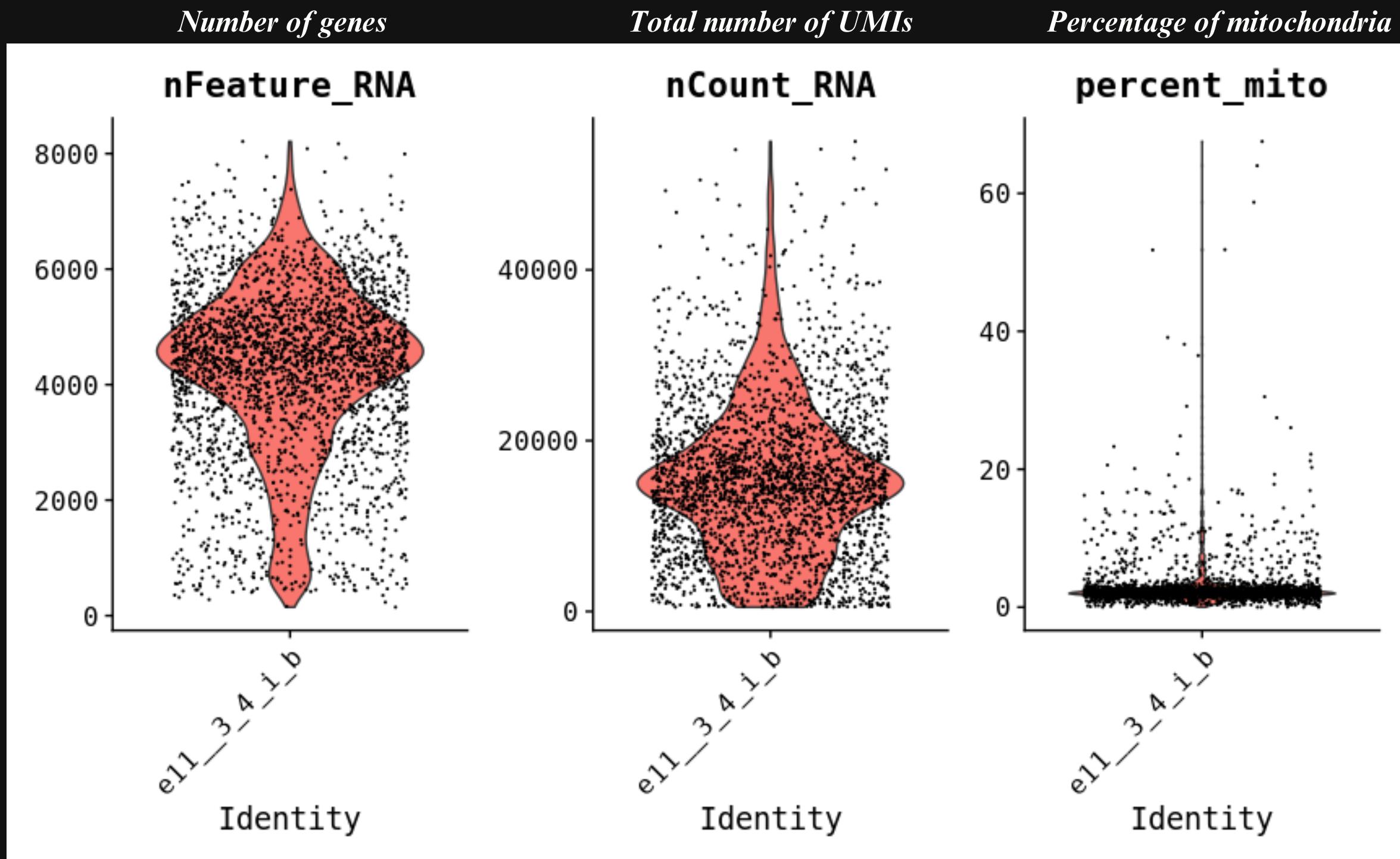
Quality control process

FILTERING

DOUBLEFINDER

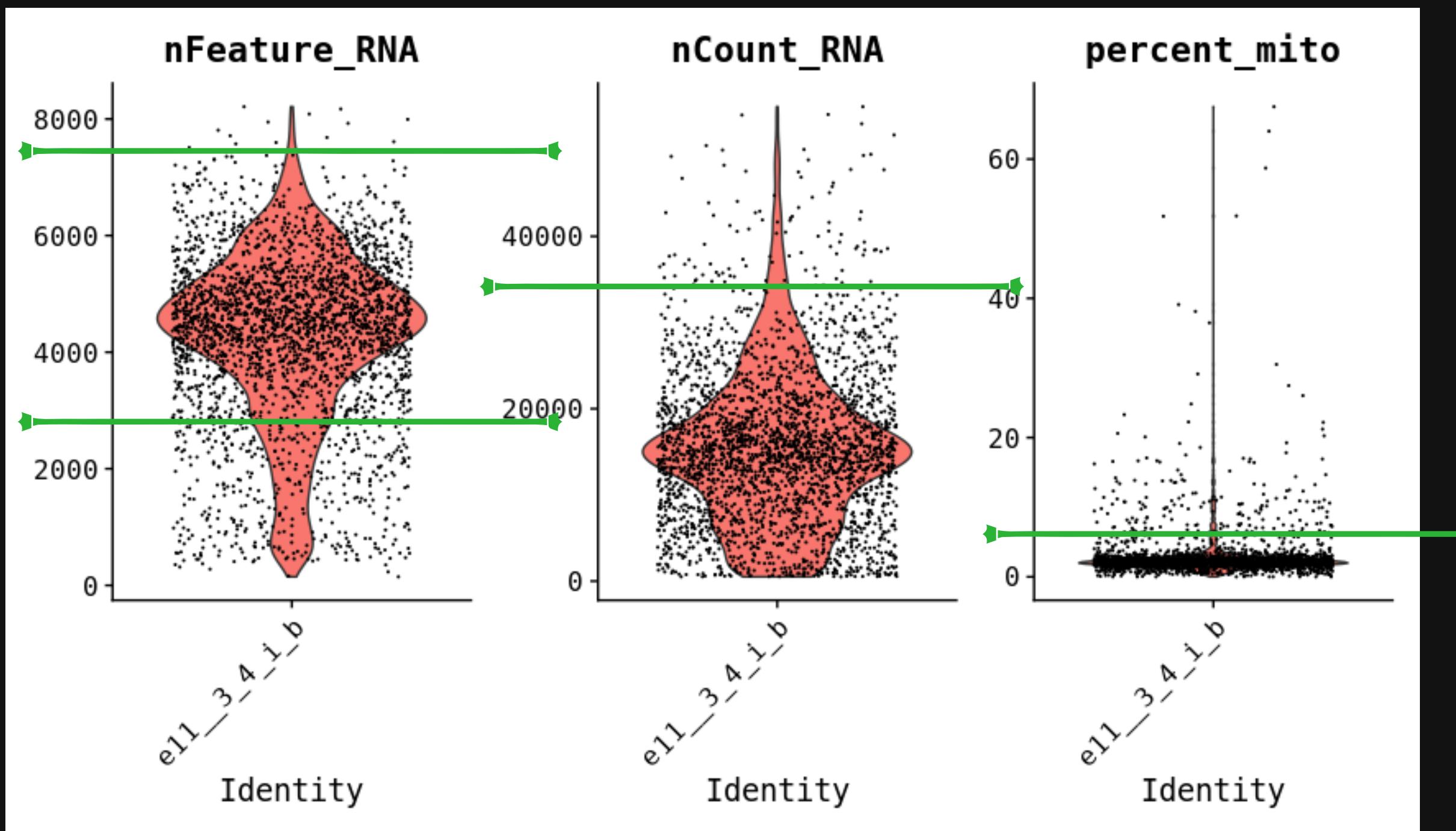


FILTERING



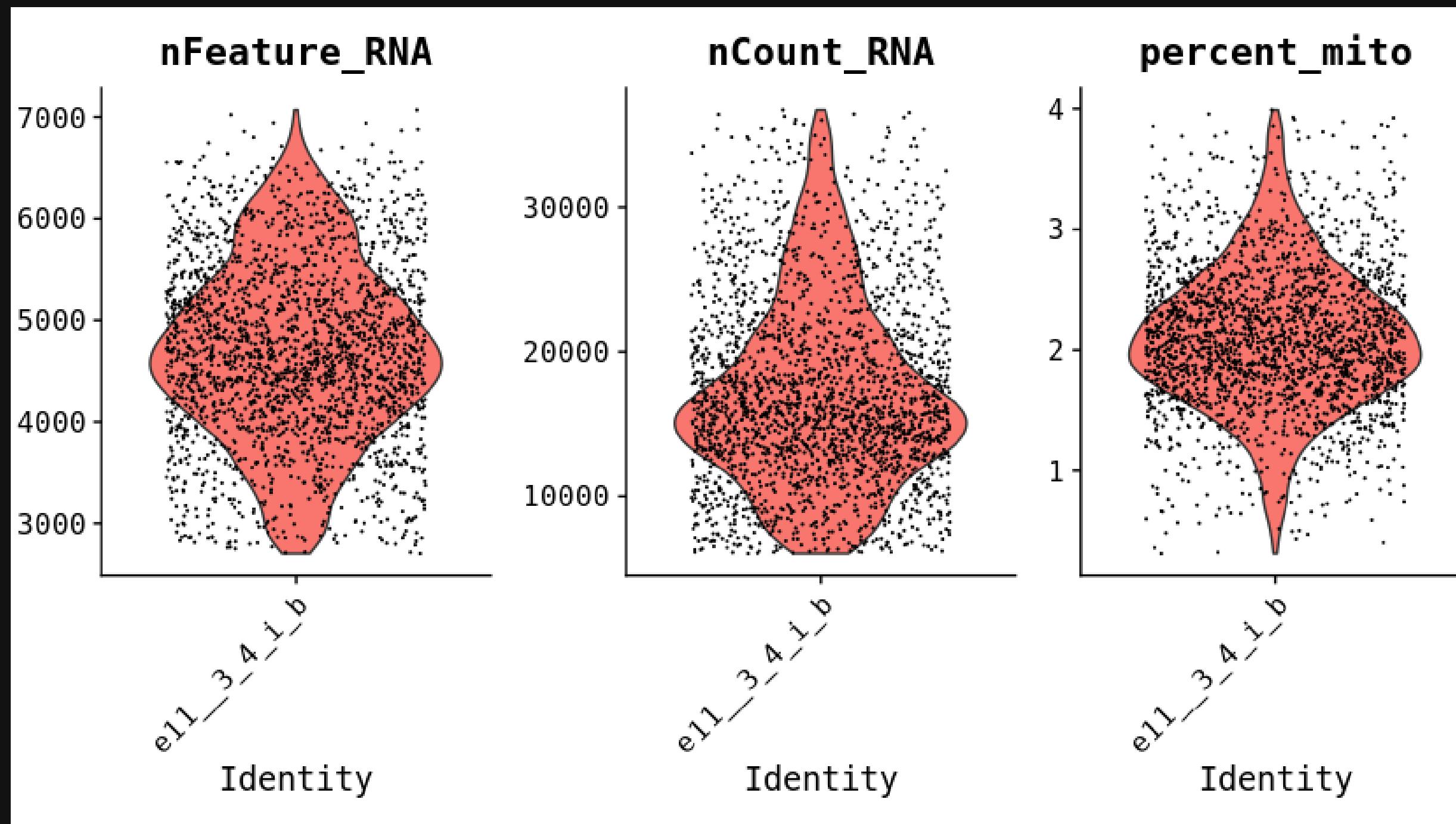
**VIOLIN PLOT BEFORE
FILTERING**

FILTERING



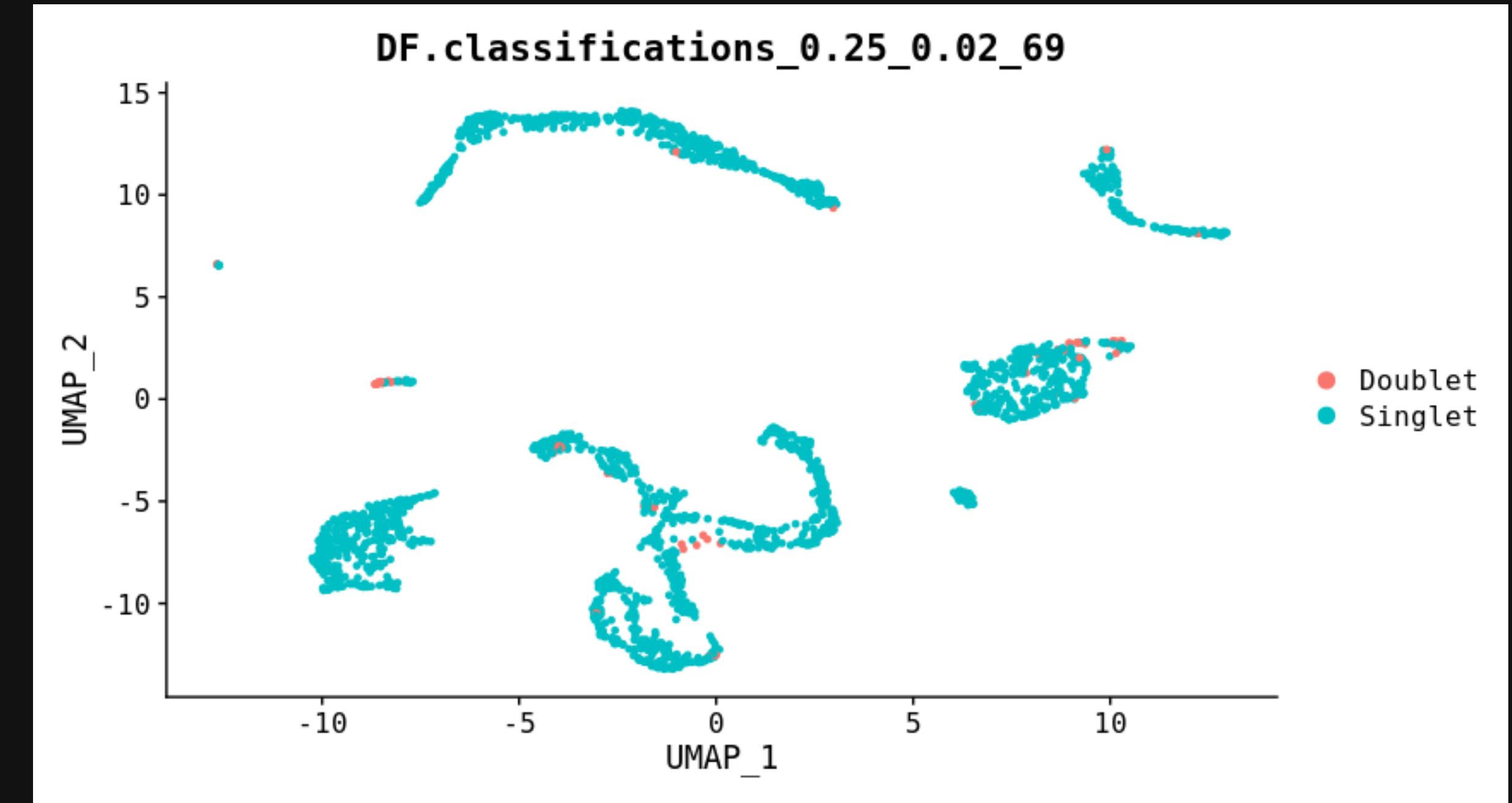
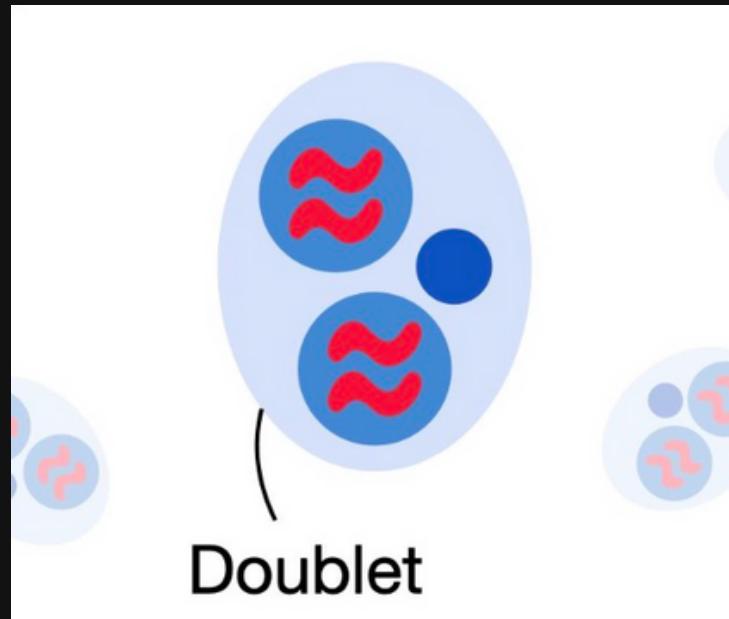
VIOLIN PLOT BEFORE
FILTERING

FILTERING



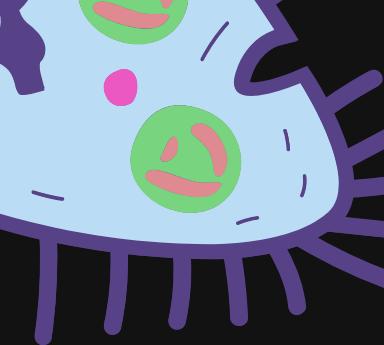
**VIOLIN PLOT AFTER
FILTERING**

DOUBLET FINDER

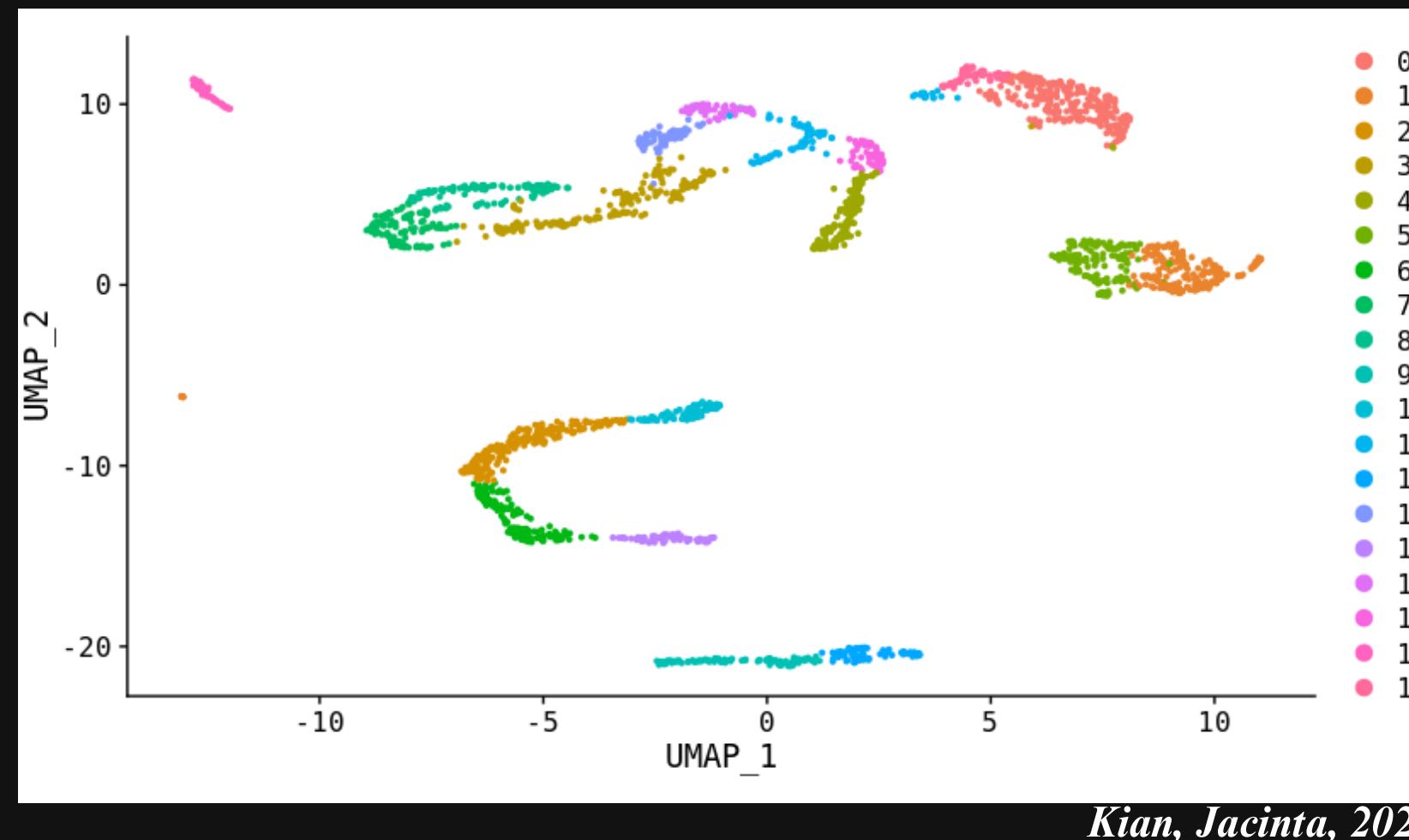


Kian, Jacinta, 2023

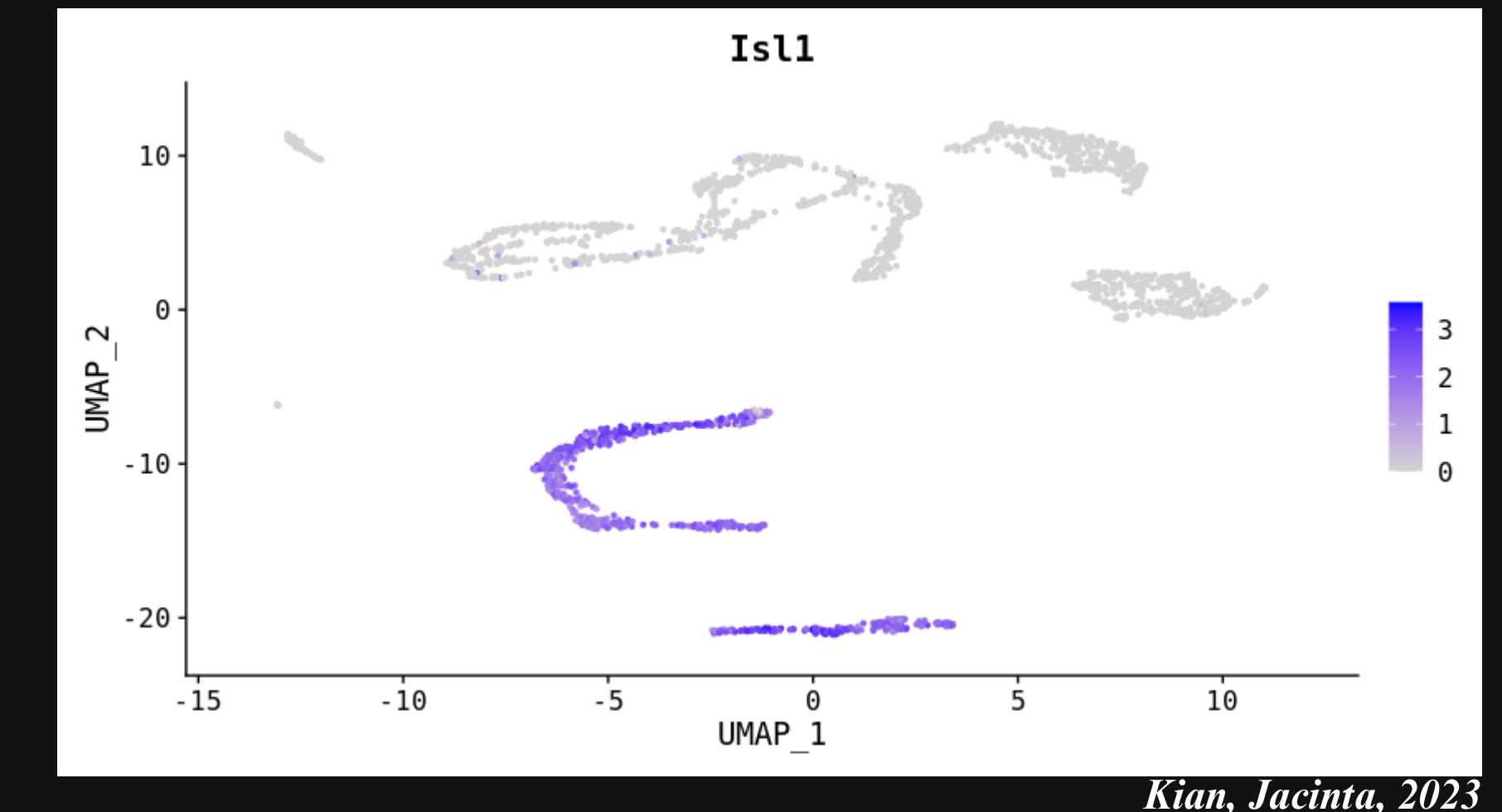
Simulated Doublets based on sample size



CLUSTERING AND DIFFERENTIAL GENE EXPRESSION



Each cluster represents a cell type.

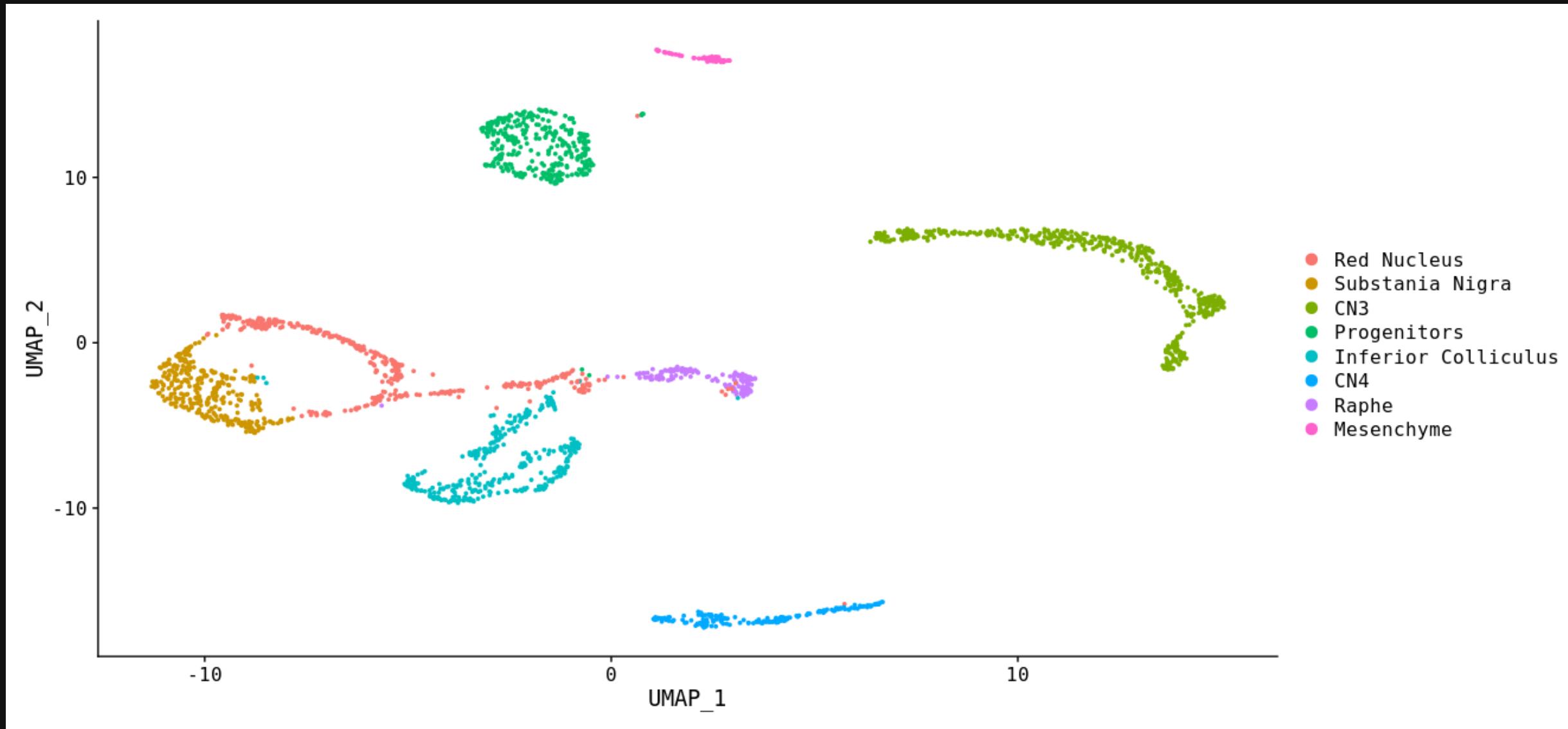


Can identify cell type based on gene expression.



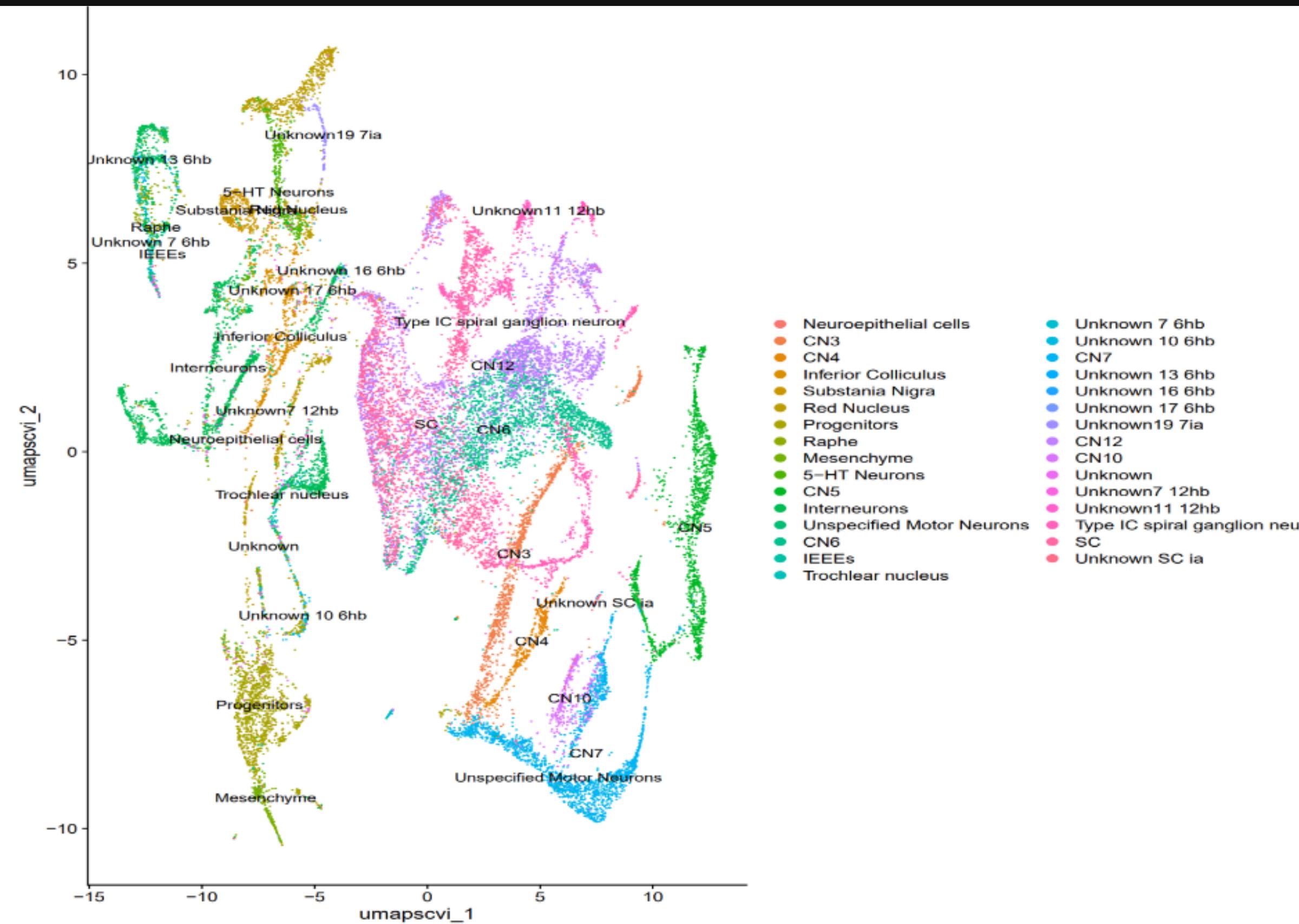


ANNOTATION



Identify and classify the cell types present in the dataset

INTEGRATION

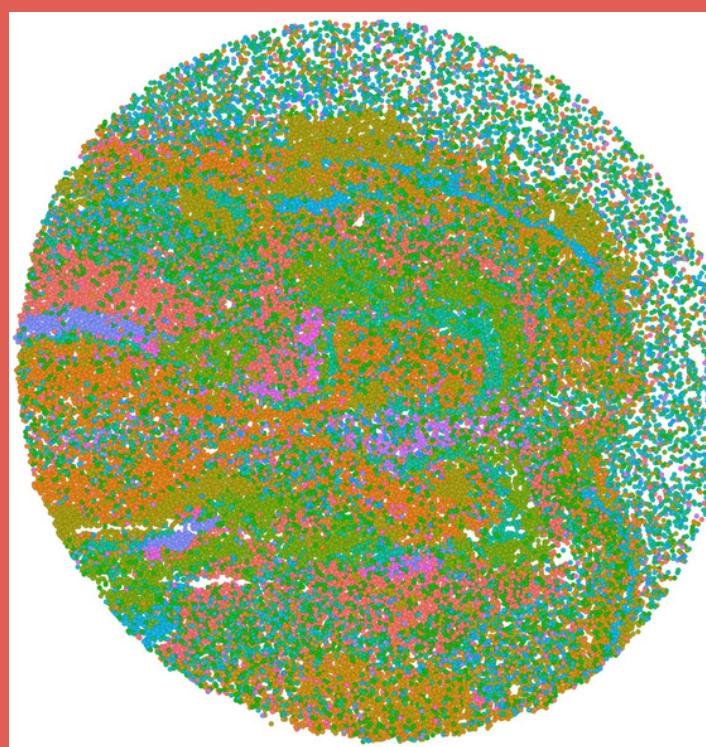
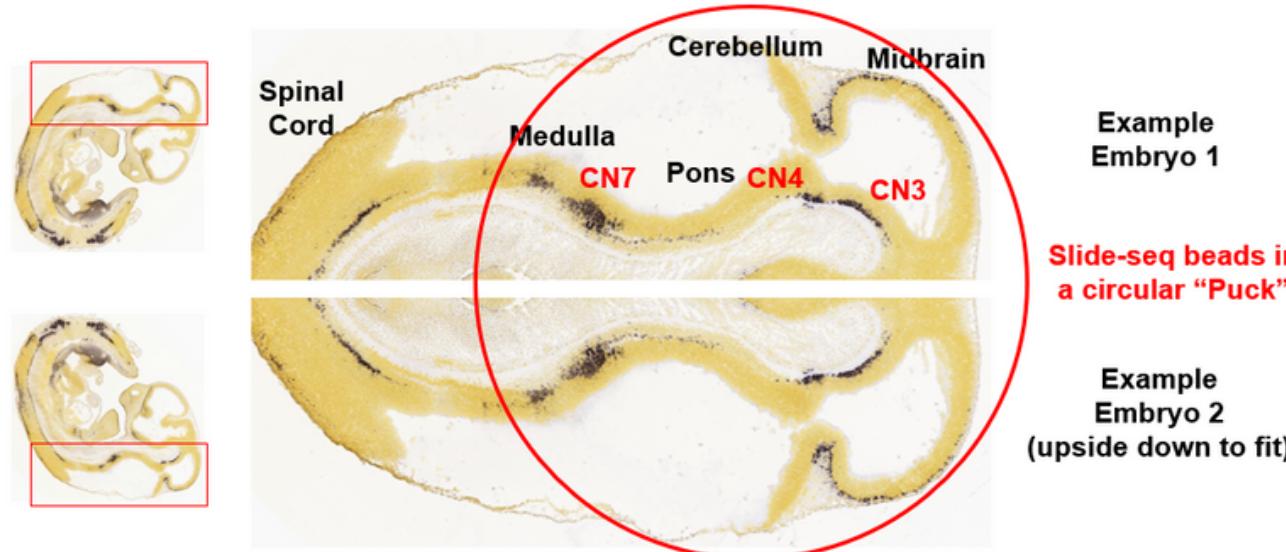


10 scRNA datasets
(e11 developing mouse brain)
layered on top of each other

SLIDE-SEQ SAMPLE COLLECTION

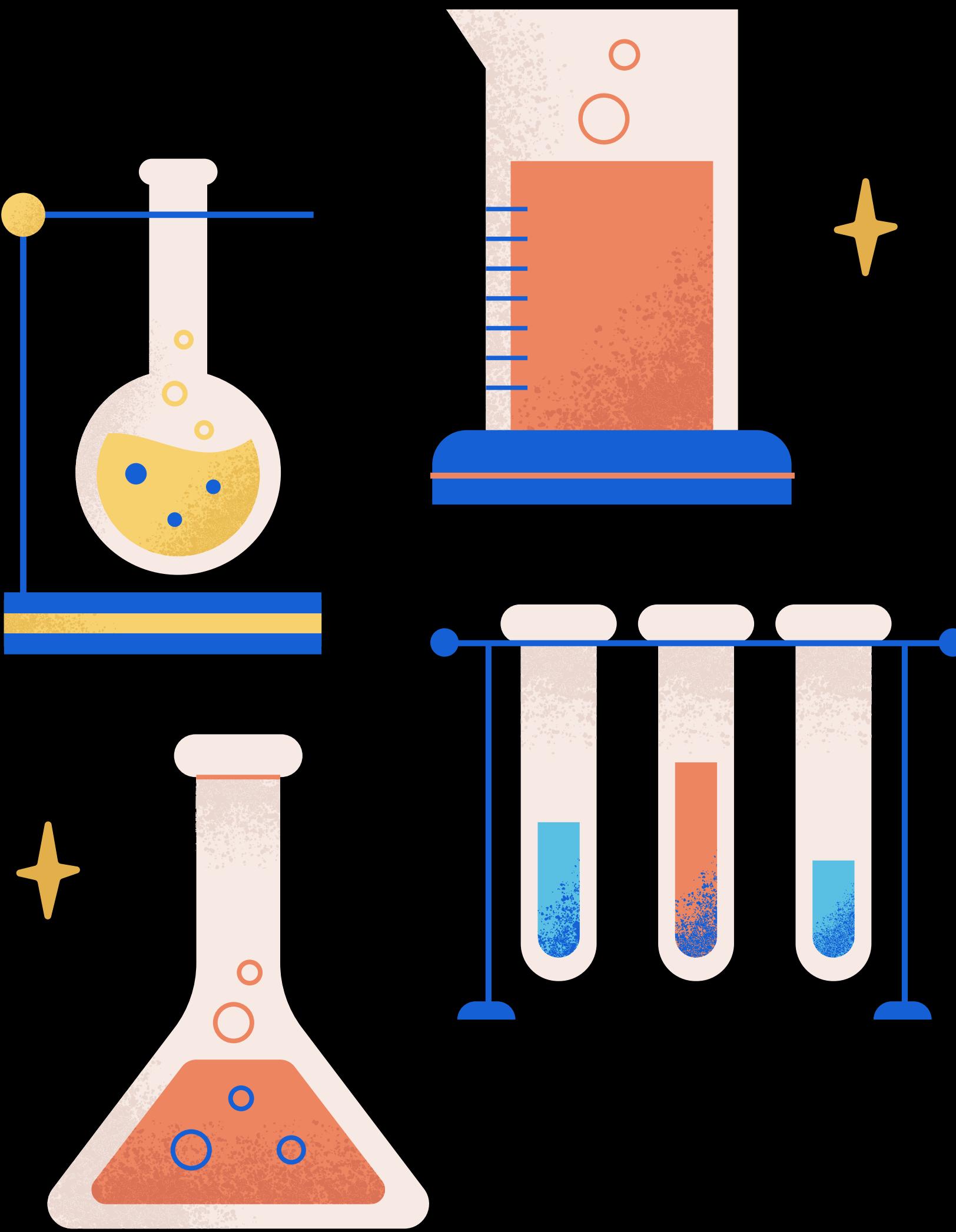
SLIDE-SEQ PROCESS

Two E11.5 mouse brainstems fit on single “puck”



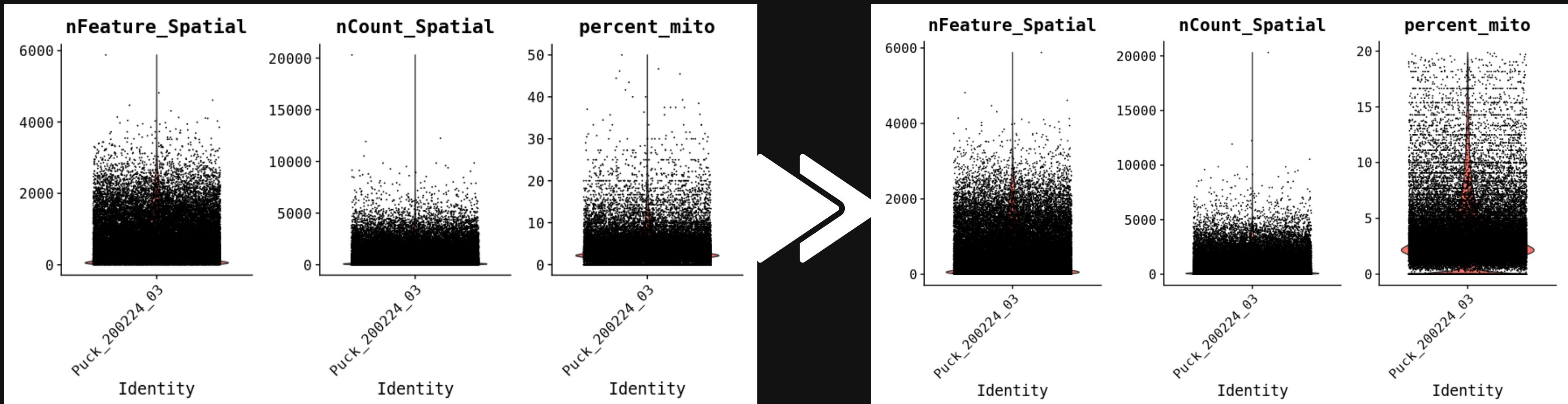
Dr. Rose, 2021

Slide-seq differs from single cell RNA-seq in
that it can give us insight into
the spatial orientation of the cells on
the tissue.



ANALYSIS OF SLIDE- SEQ

SIMILAR QC PROCESS FOR SLIDE-SEQ

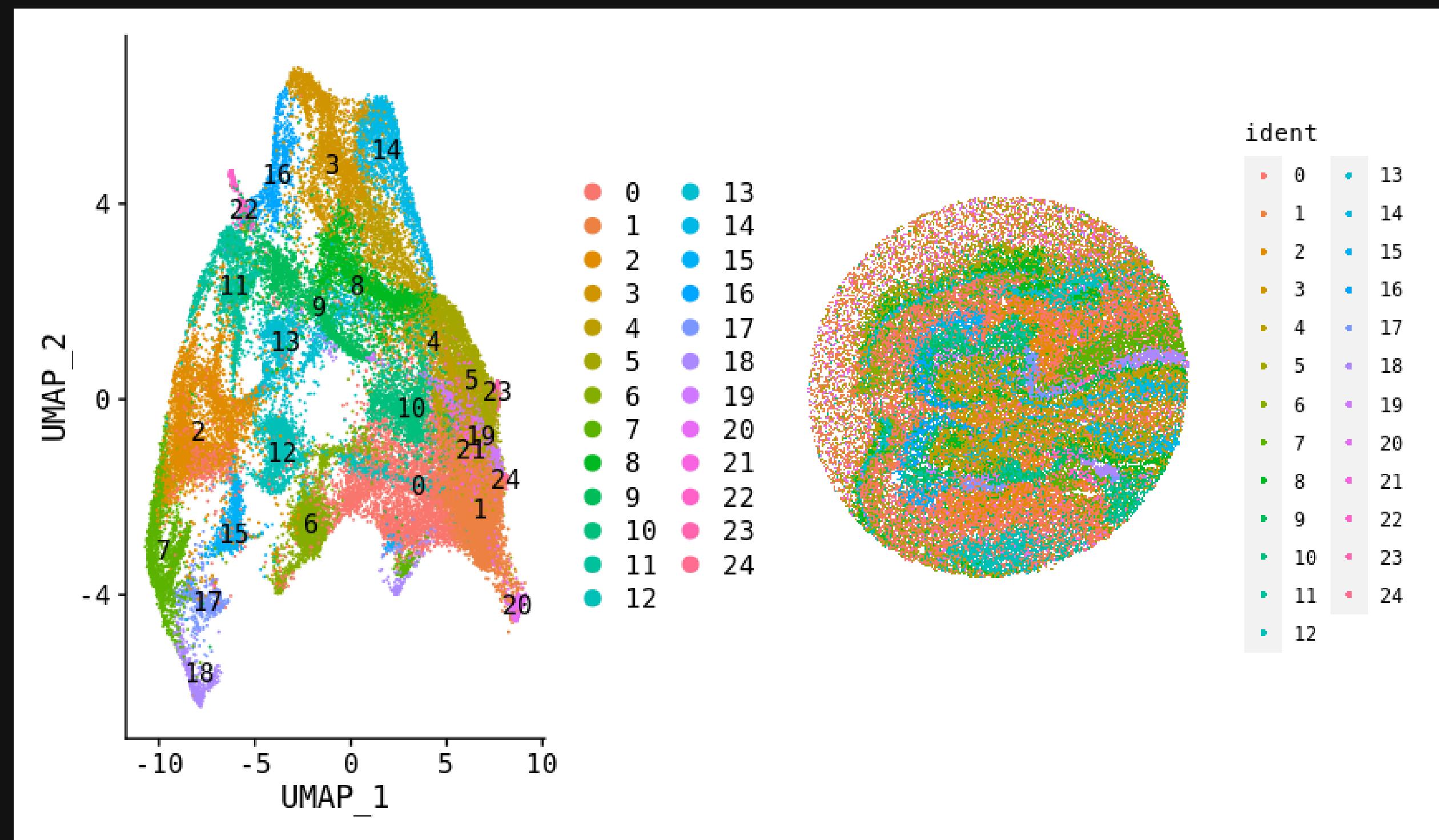


Jacinta, Kian, 2023

PRE-FILTERING

POST-FILTERING

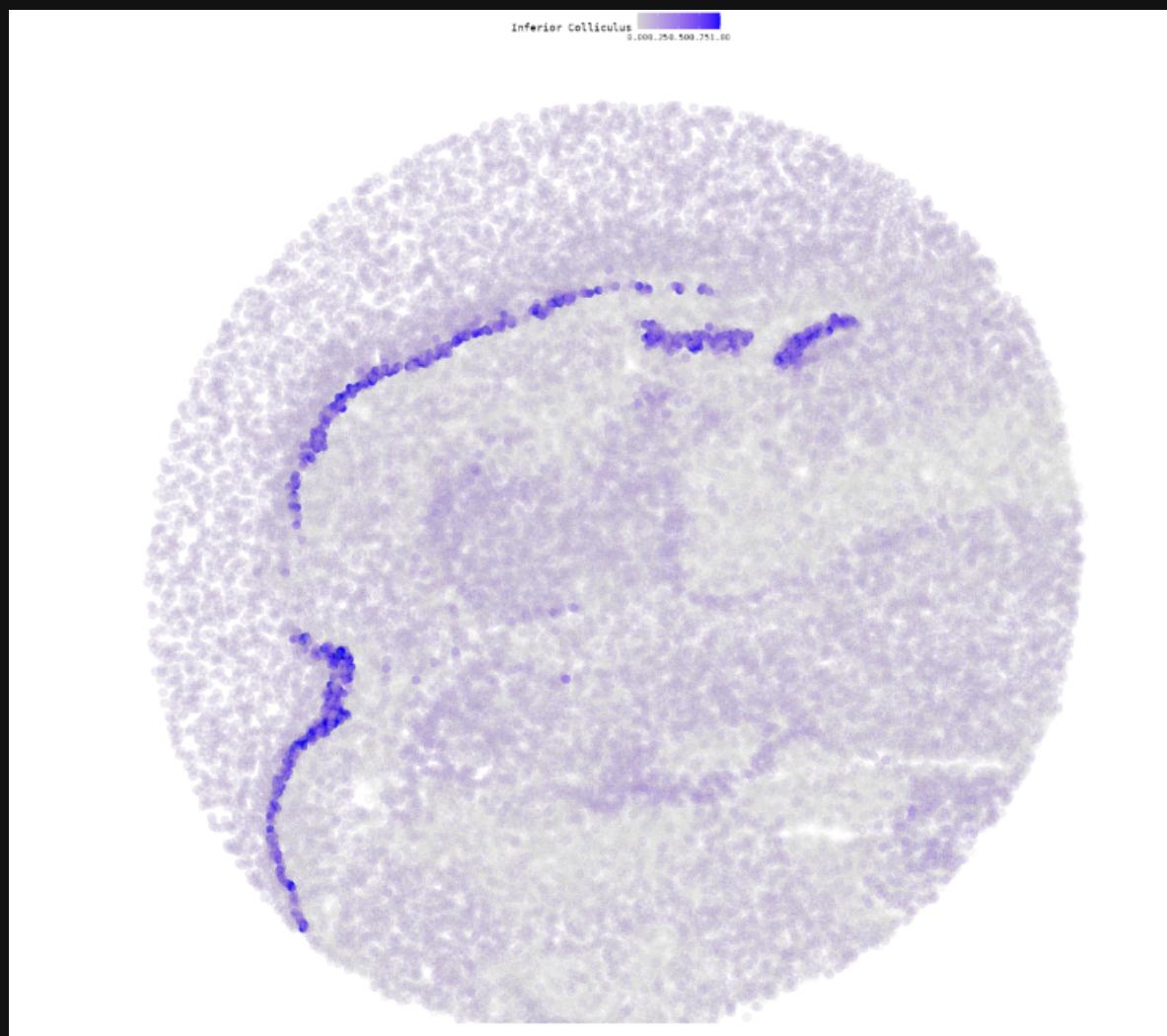
CLUSTERING



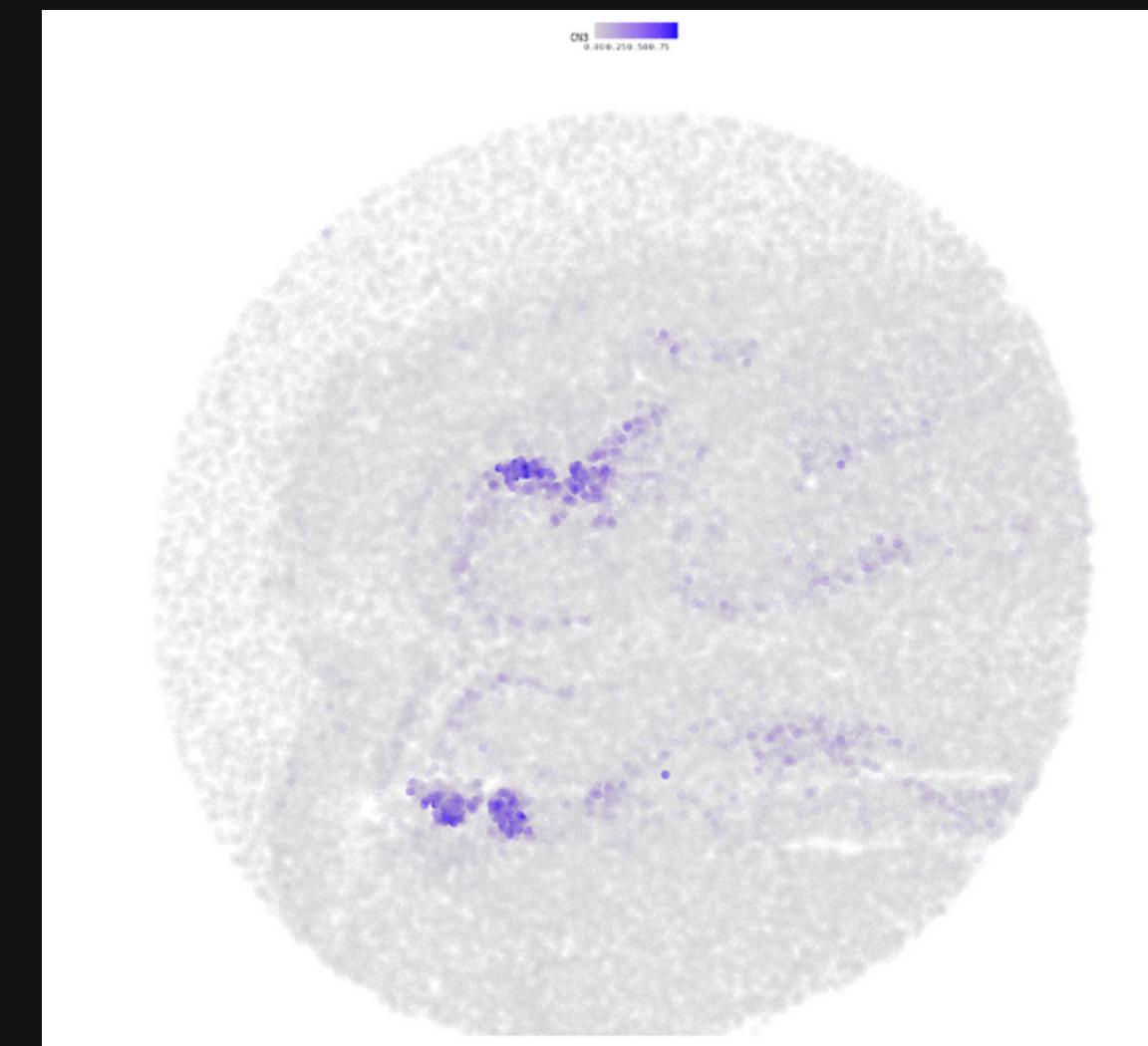
Jacinta, Kian, 2023

REFERENCE MAPPING USING THE SC-RNA DATA

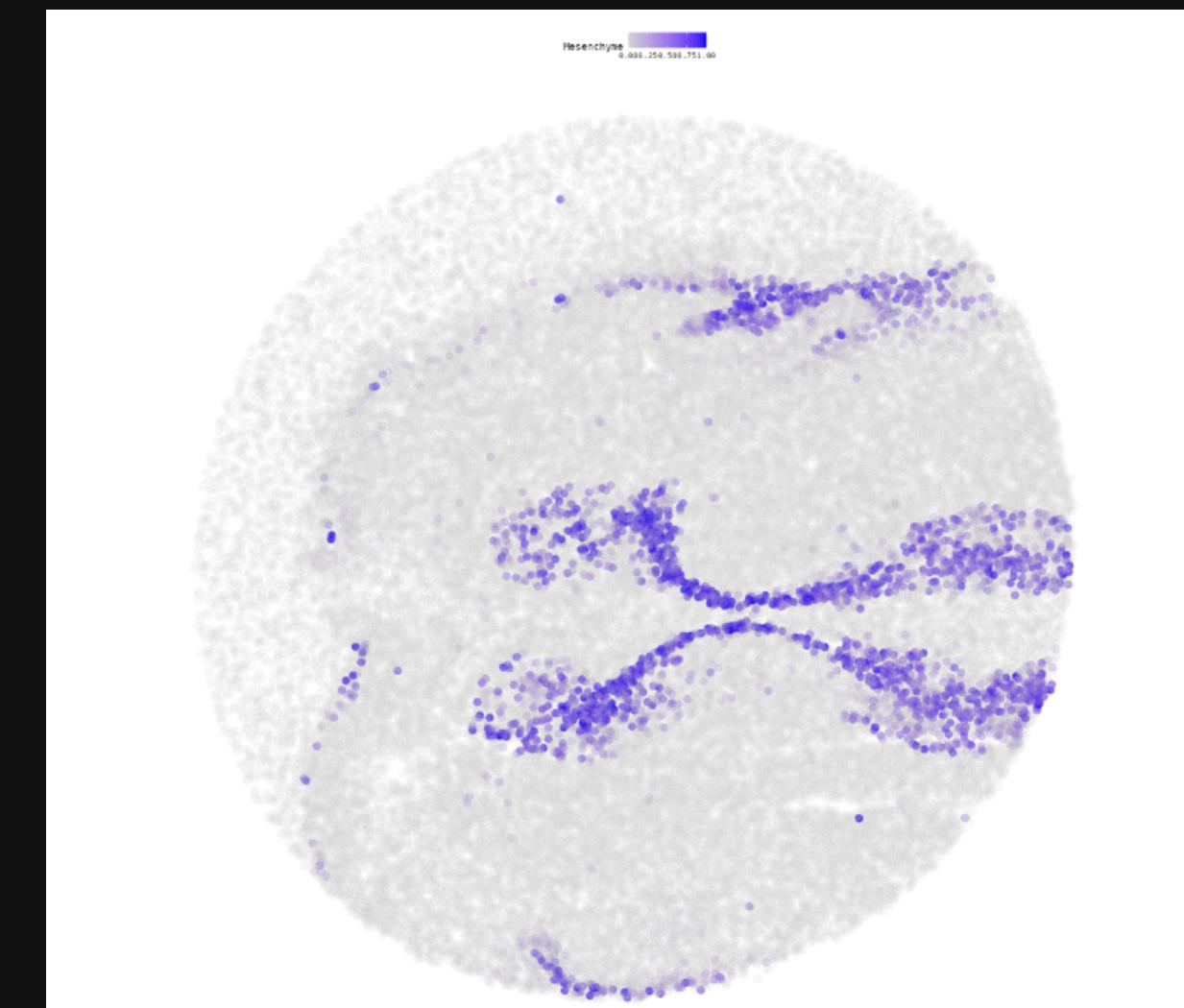
Inferior Colliculus



CN3



Mesenchyme

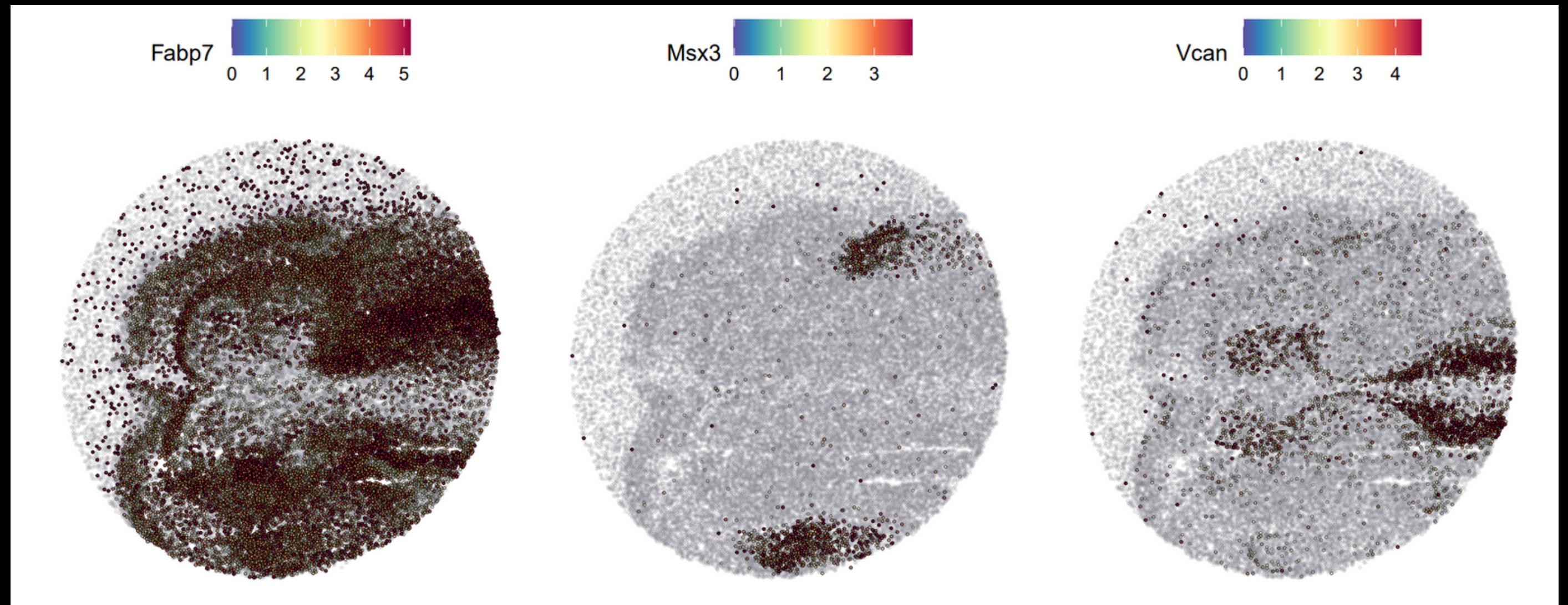


Kian, Jacinta, 2023

Kian, Jacinta, 2023

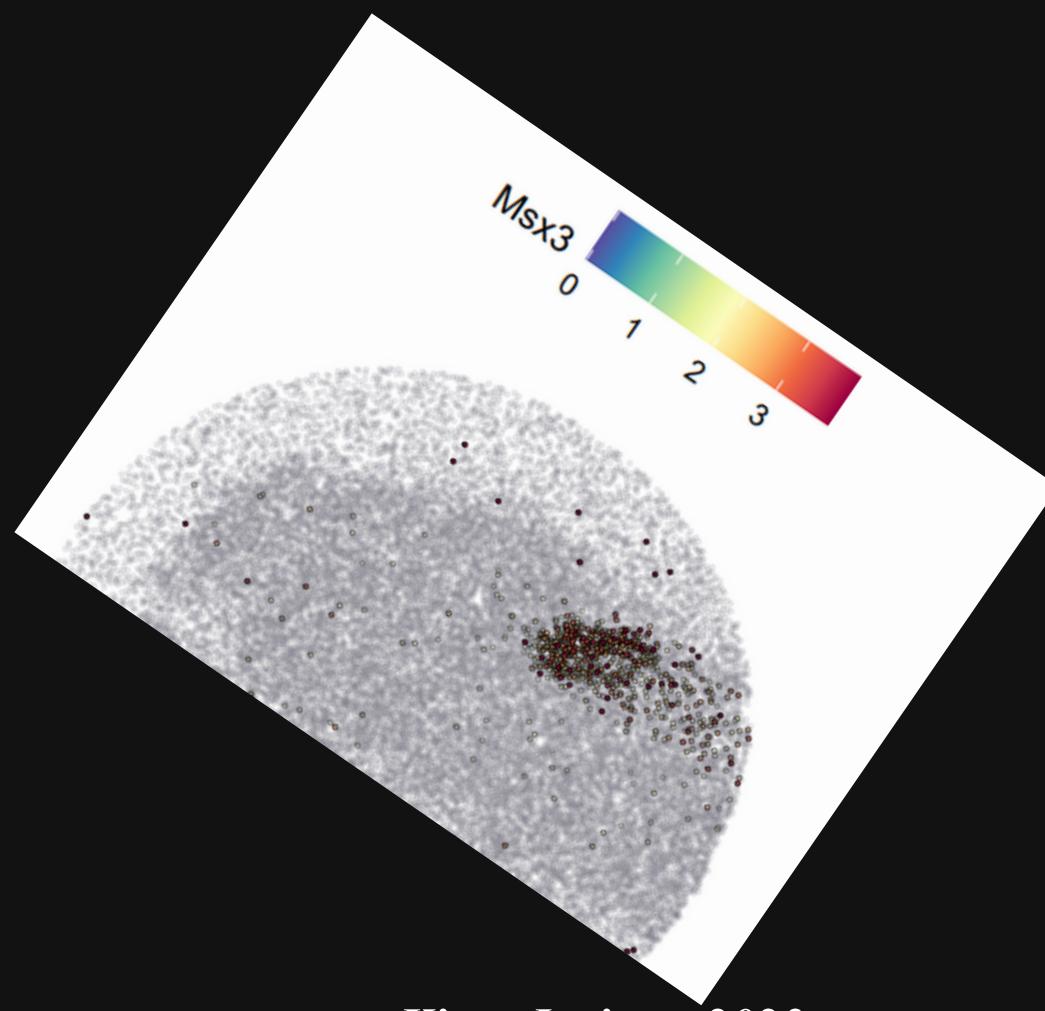
Kian, Jacinta, 2023

DIFERENTIAL GENE EXPRESSION

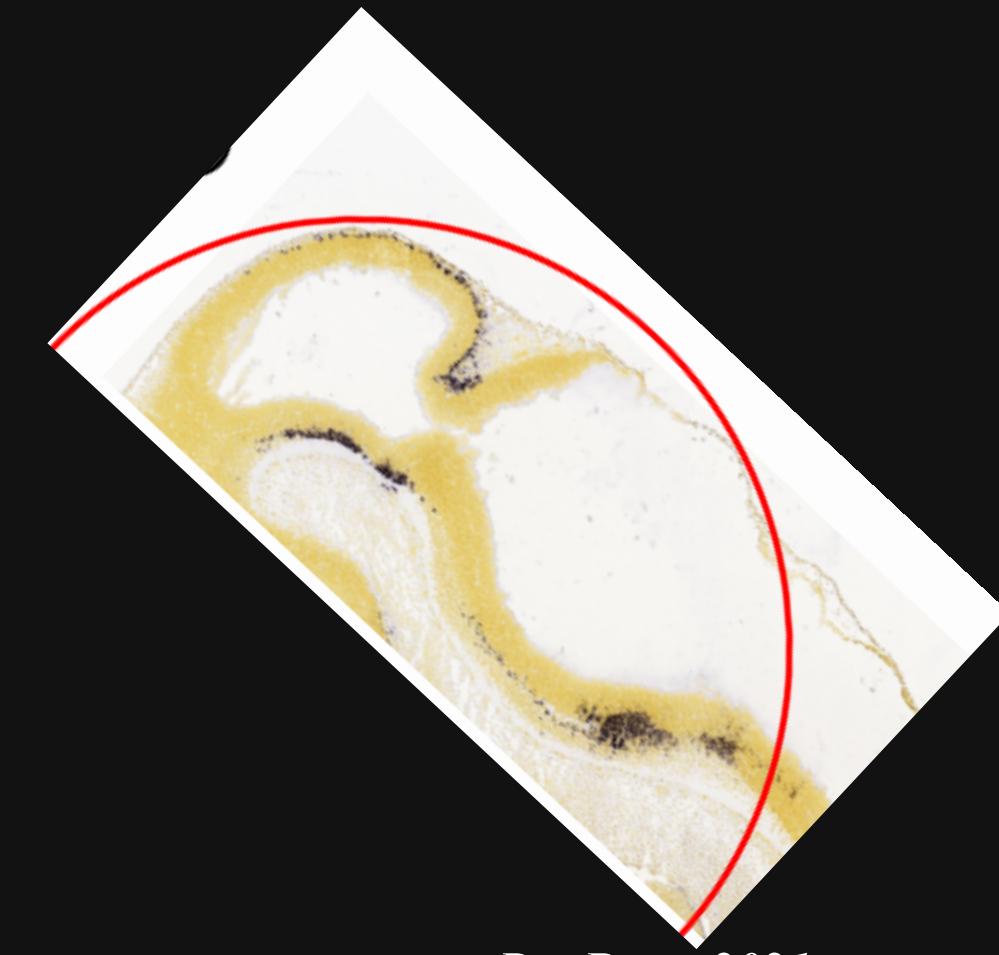


Kian, Jacinta, 2023

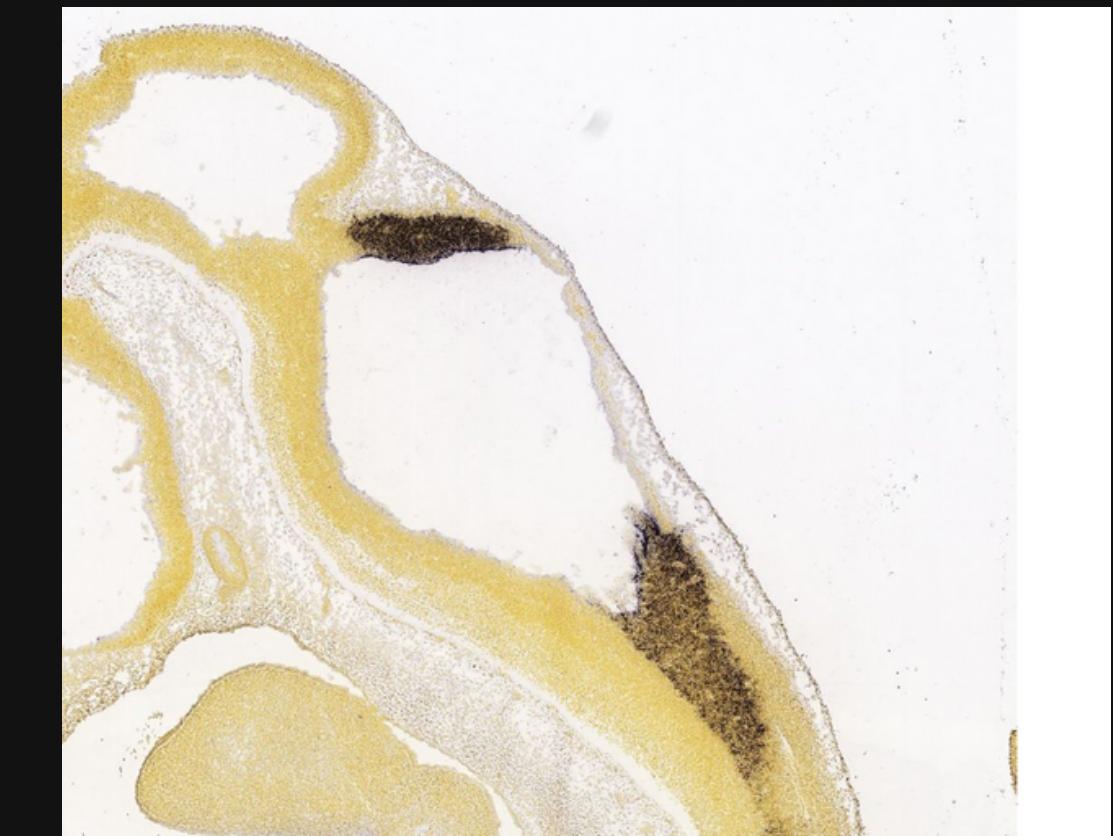
COMPARISON TO BIOLOGICAL GROUND TRUTH



Kian, Jacinta, 2023



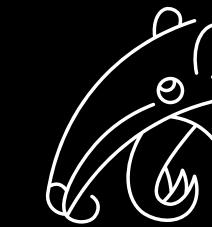
Dr. Rose, 2021



**How our sample is oriented
on the puck**



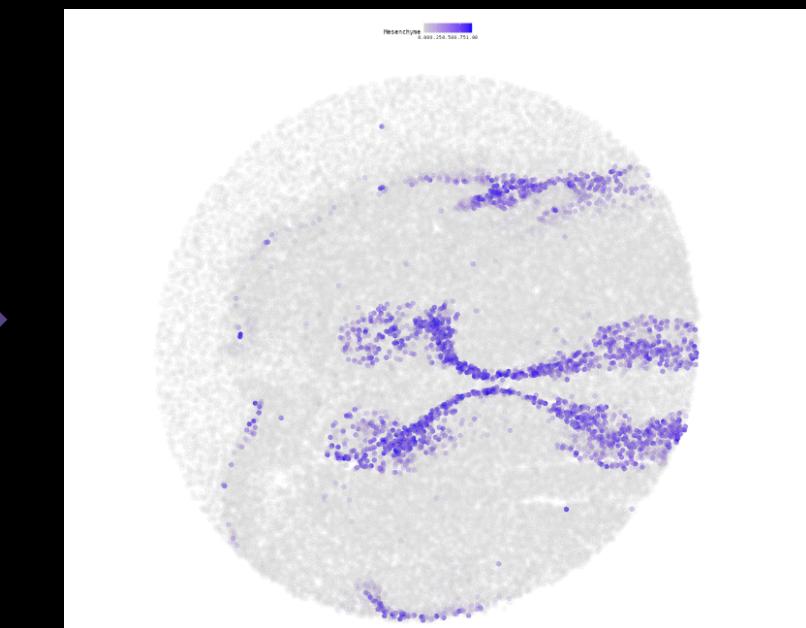
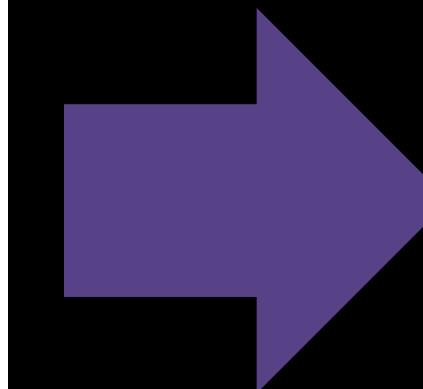
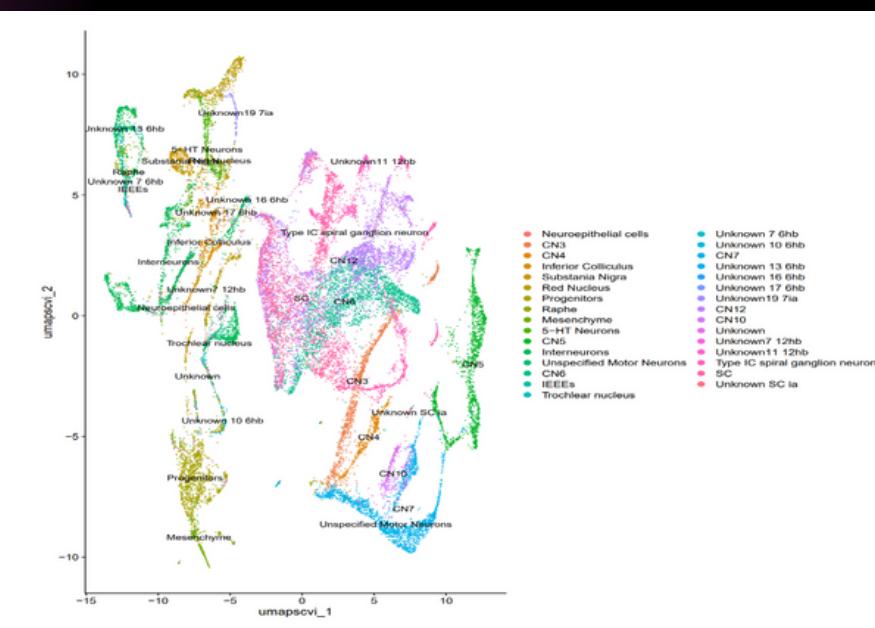
**Msx3 expression according to
the Allen Brain Atlas**

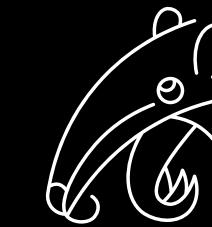


UC Irvine

Results & Recap

Fully integrated scRNA data mapped onto Slide-seq

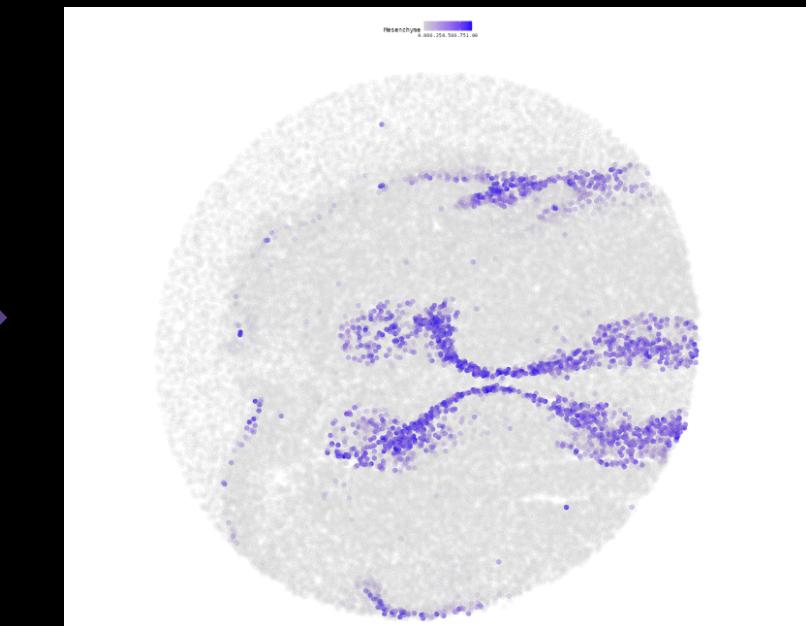
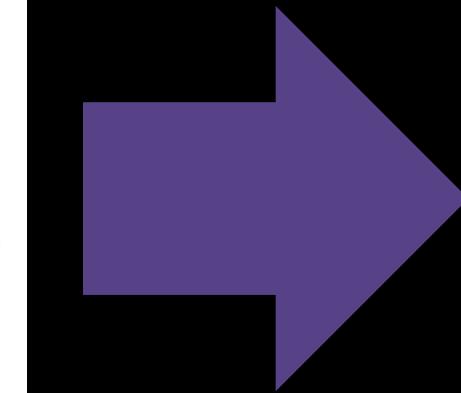
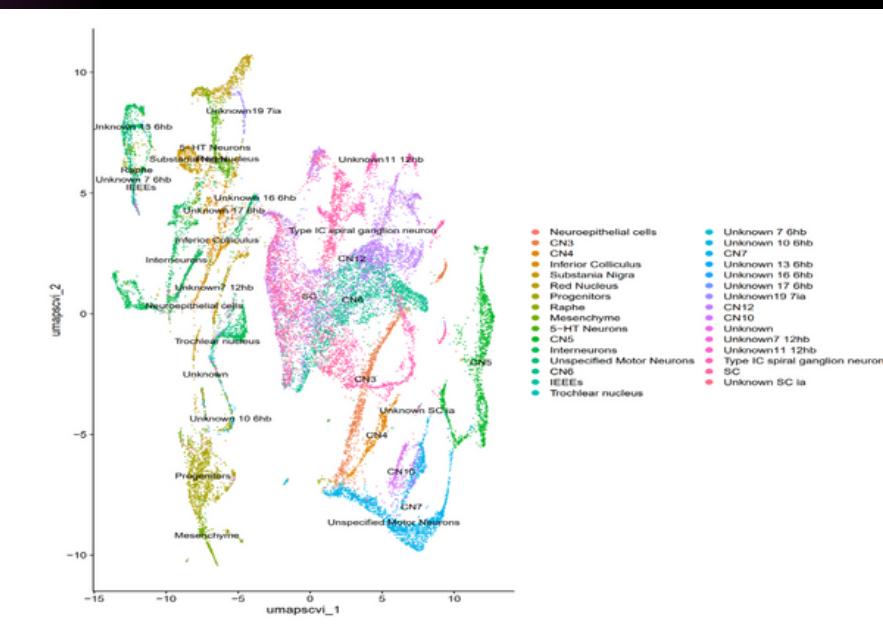


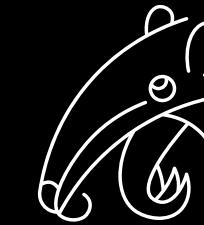


UC Irvine

Results & Recap

Several unknown populations

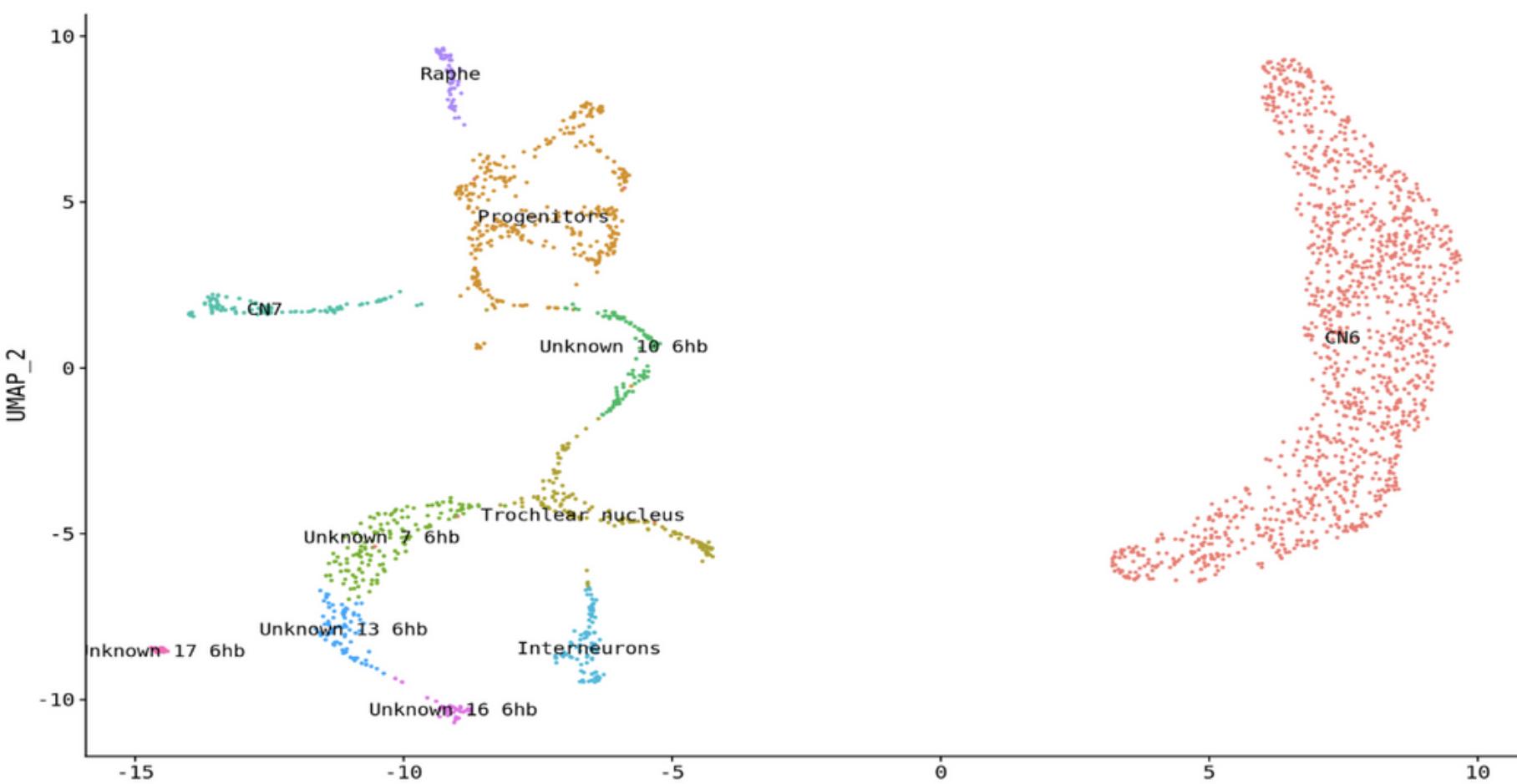




UC Irvine

Results & Recap

Finding CN7 in CN6 Sample





Results & Recap

Why should we care about these results?



THANK YOU FOR LISTENING! AND THANK YOU MENTORS

DON'T HESITATE TO ASK ANY QUESTIONS!