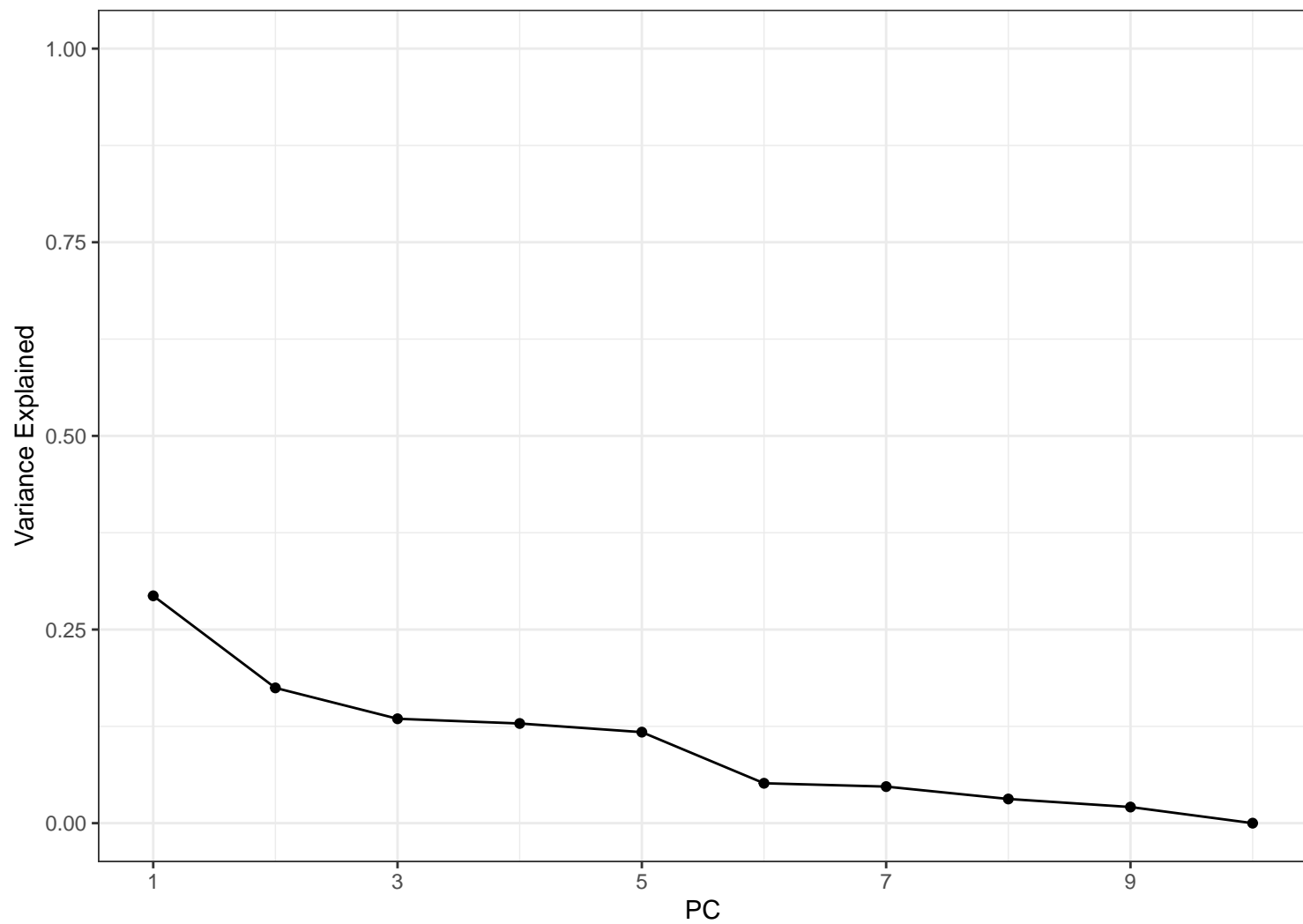
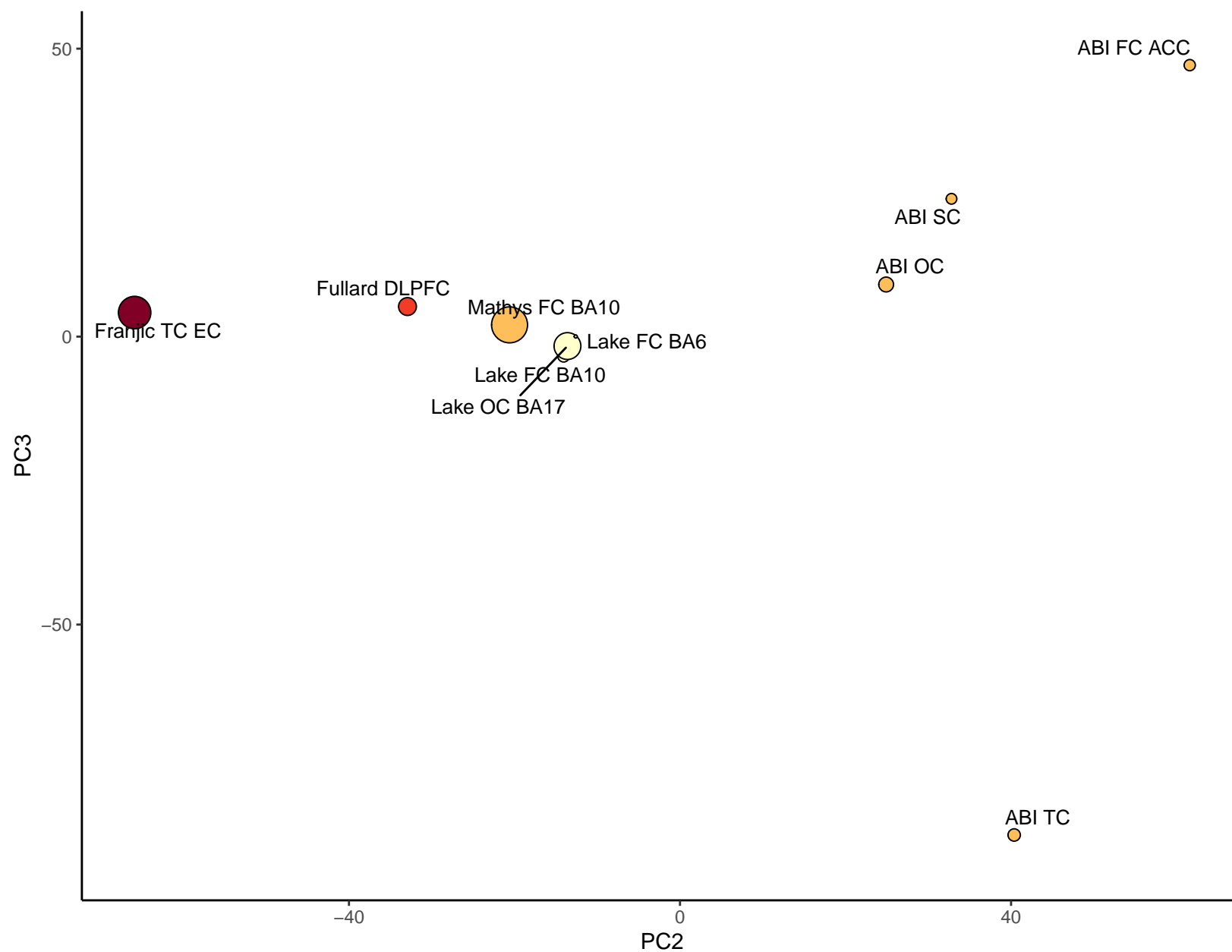


PER Subtypes  
Normalized Counts Mean Expression Scree Plot  
10 datasets, 8,596 genes



# Dataset Pericyte Mean Expression Projections

8,596 protein coding genes



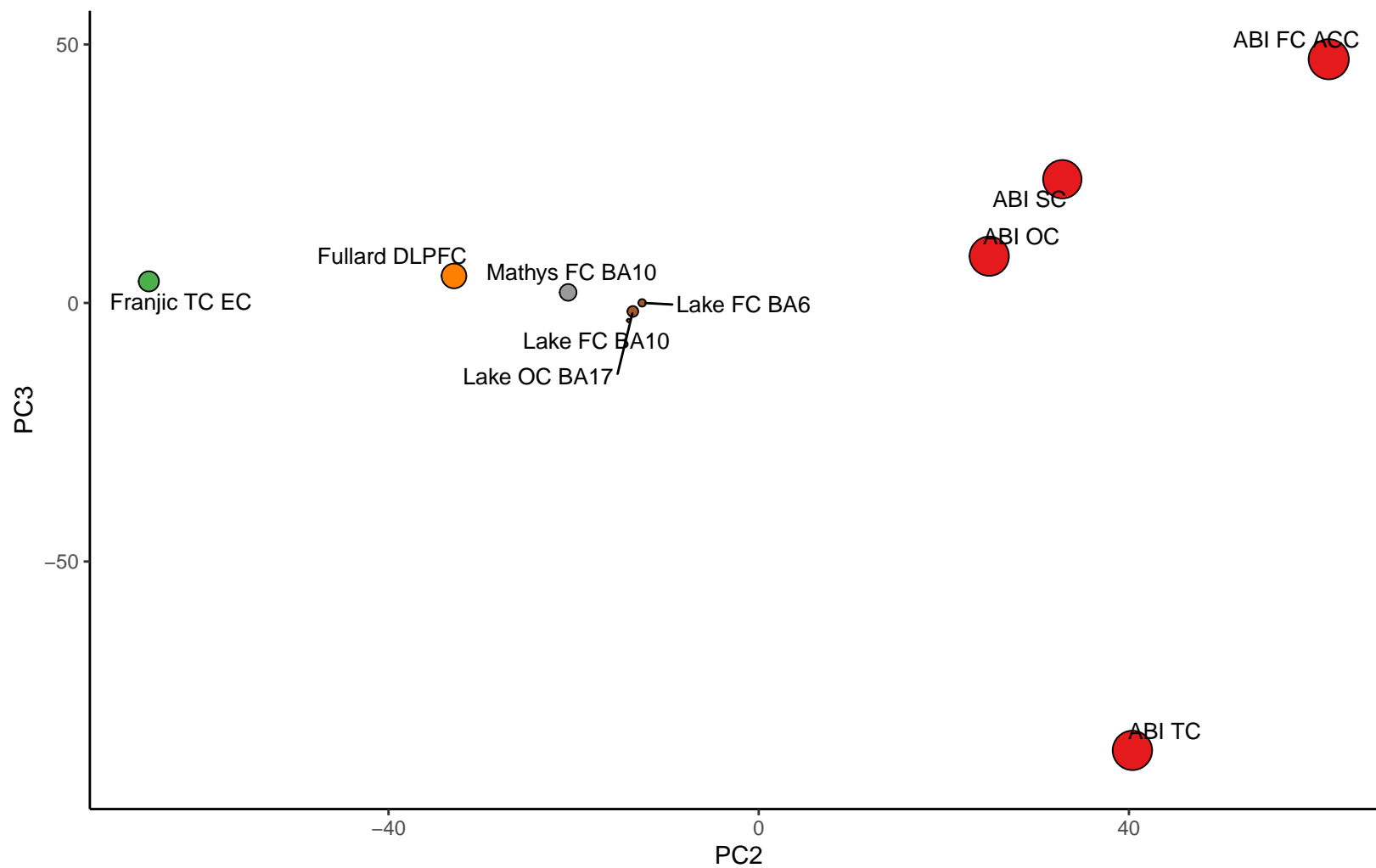
# Nuclei

• 4,100 • 5,900 • 7,100 • 19,300 • 33,300

Year 2018 2019 2021 2022

# Dataset Pericyte Mean Expression Projections

8,596 protein coding genes



Median # Unique Genes

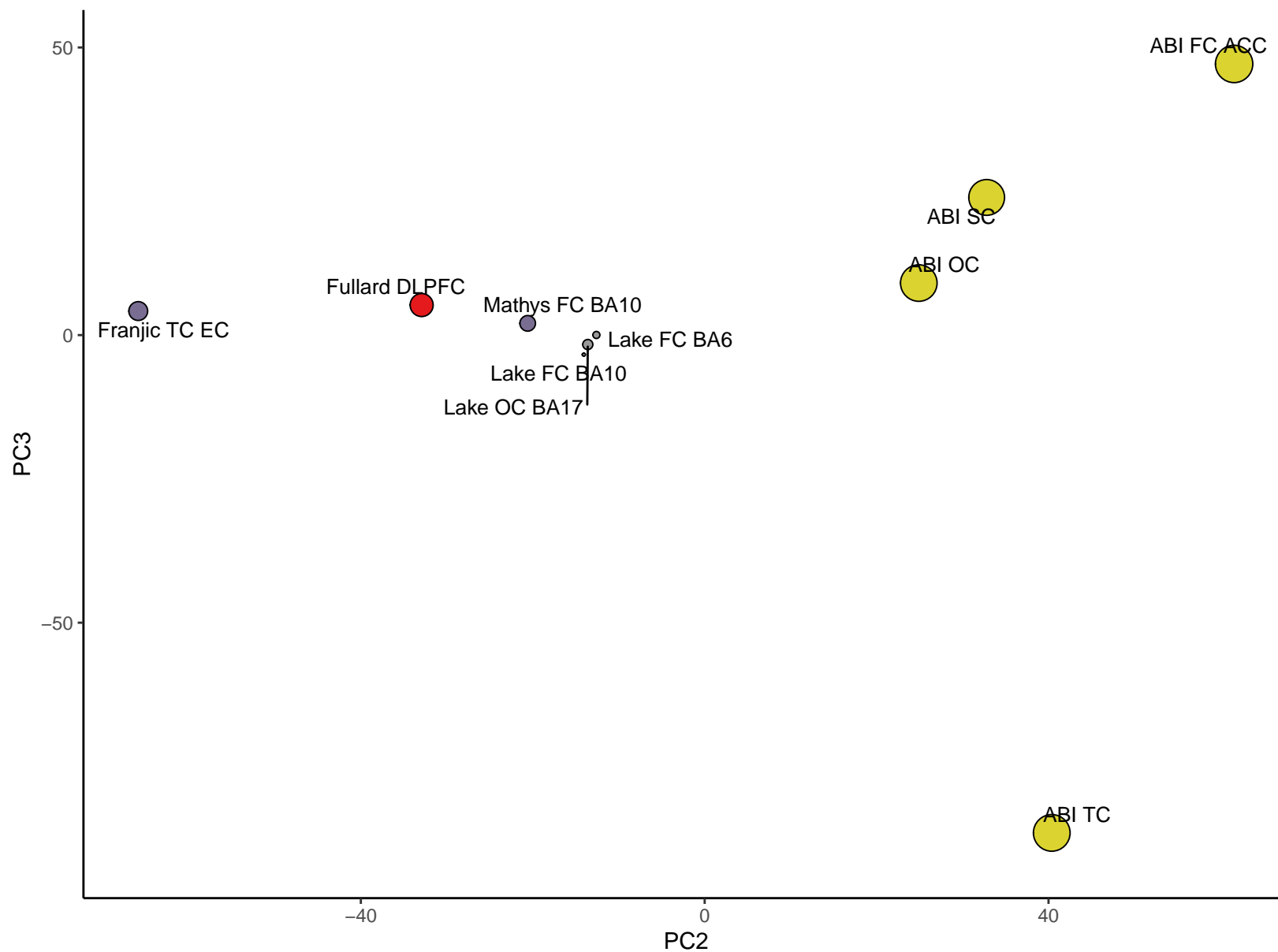
• 500 • 800 • 2,100 • 6,100 • 6,400

Study

- ABI 2019
- Franjic 2022
- Fullard 2021
- Lake 2018
- Mathys 2019

# Dataset Pericyte Mean Expression Projections

8,596 protein coding genes



Median # Unique Genes

• 600 • 1,000 • 3,000 • 6,000 • 6,000

Platform

10x Chromium

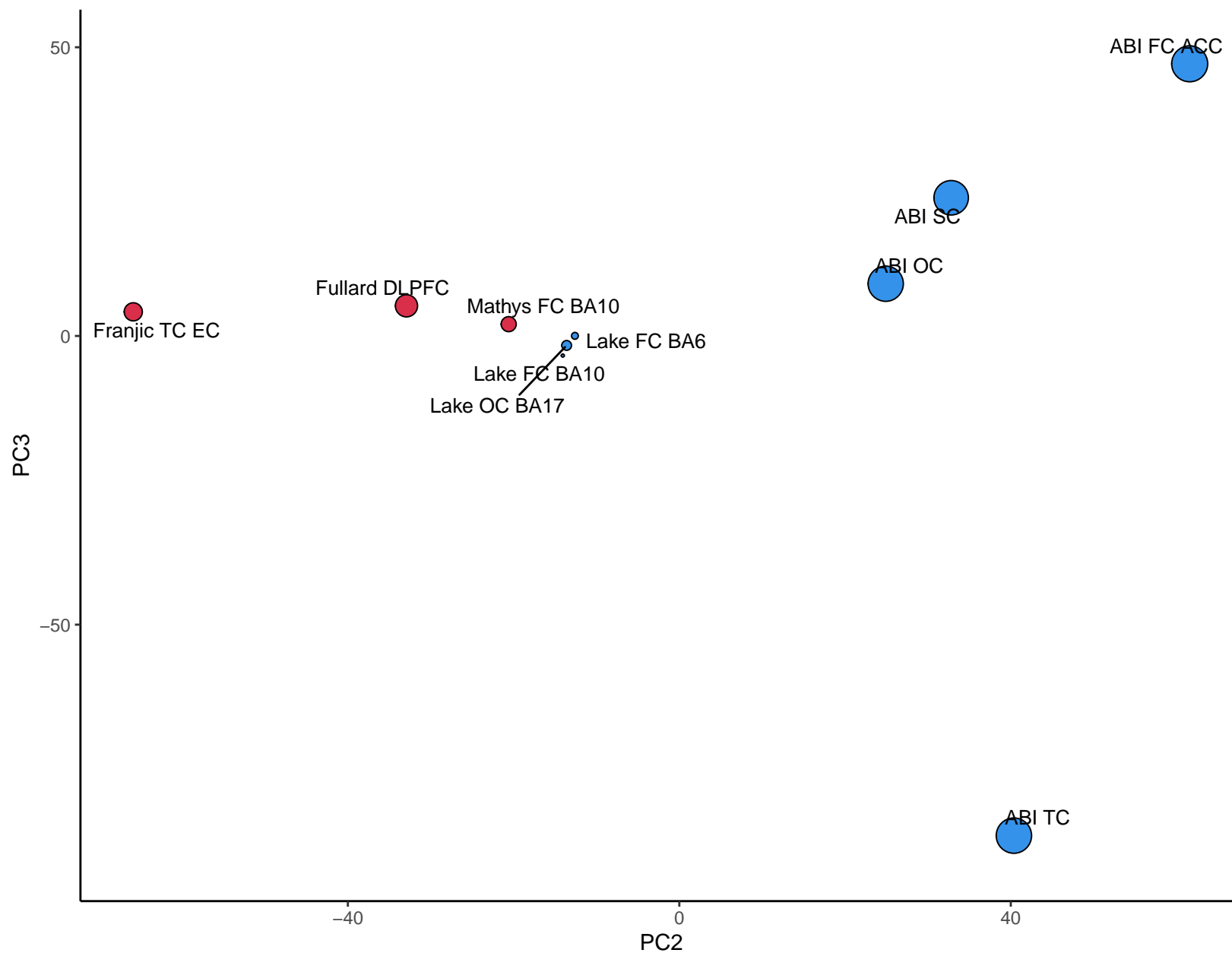
10x Chromium V3

SMART-Seq v4

snDrop-seq

# Dataset Pericyte Mean Expression Projections

8,596 protein coding genes



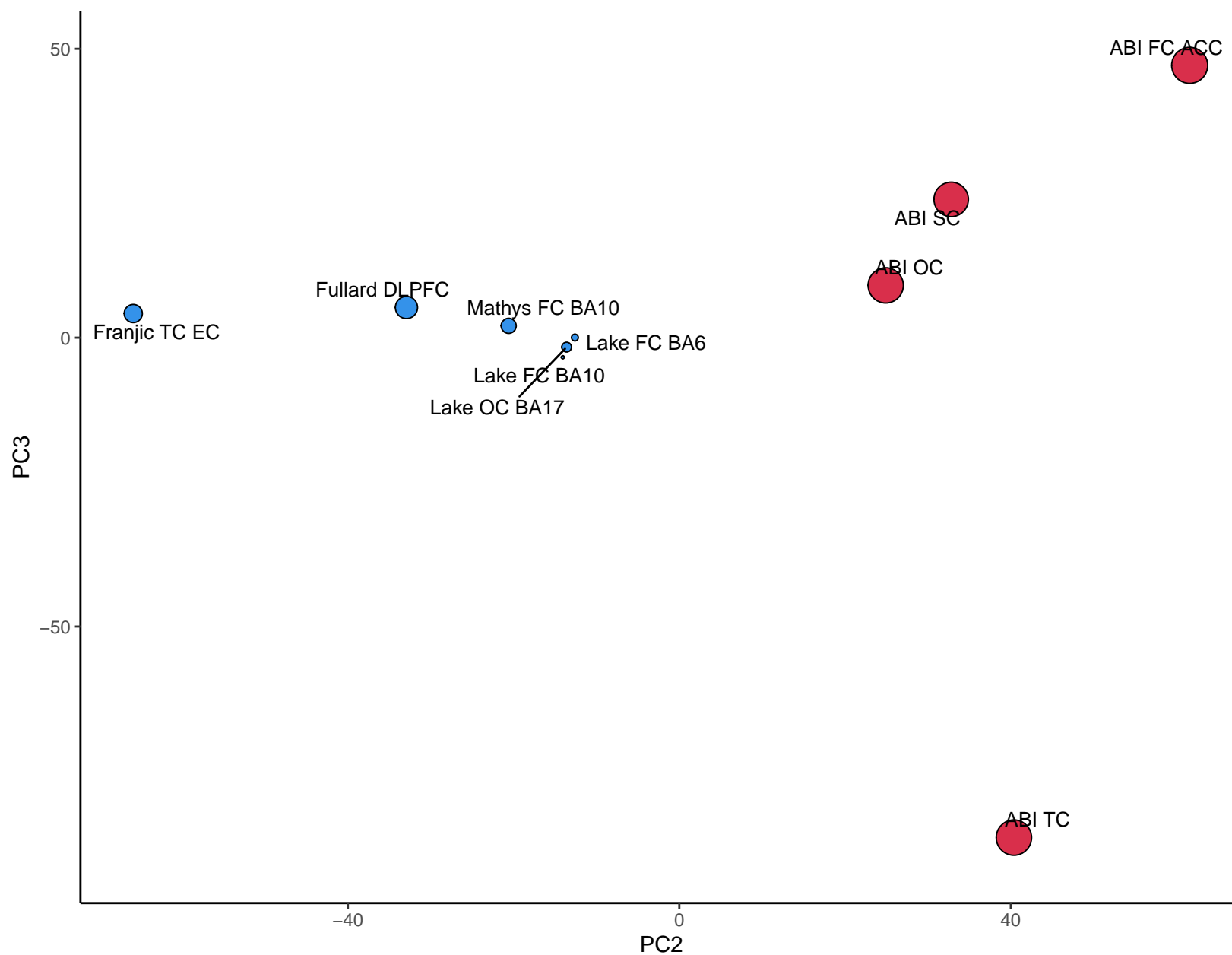
Median # Unique Genes

• 539 • 1,000 • 5,000 • 6,000

FACS Y N

# Dataset Pericyte Mean Expression Projections

8,596 protein coding genes



Median # Unique Genes

• 539 • 1,000 • 5,000 • 6,000

Unbiased Sampling Y N