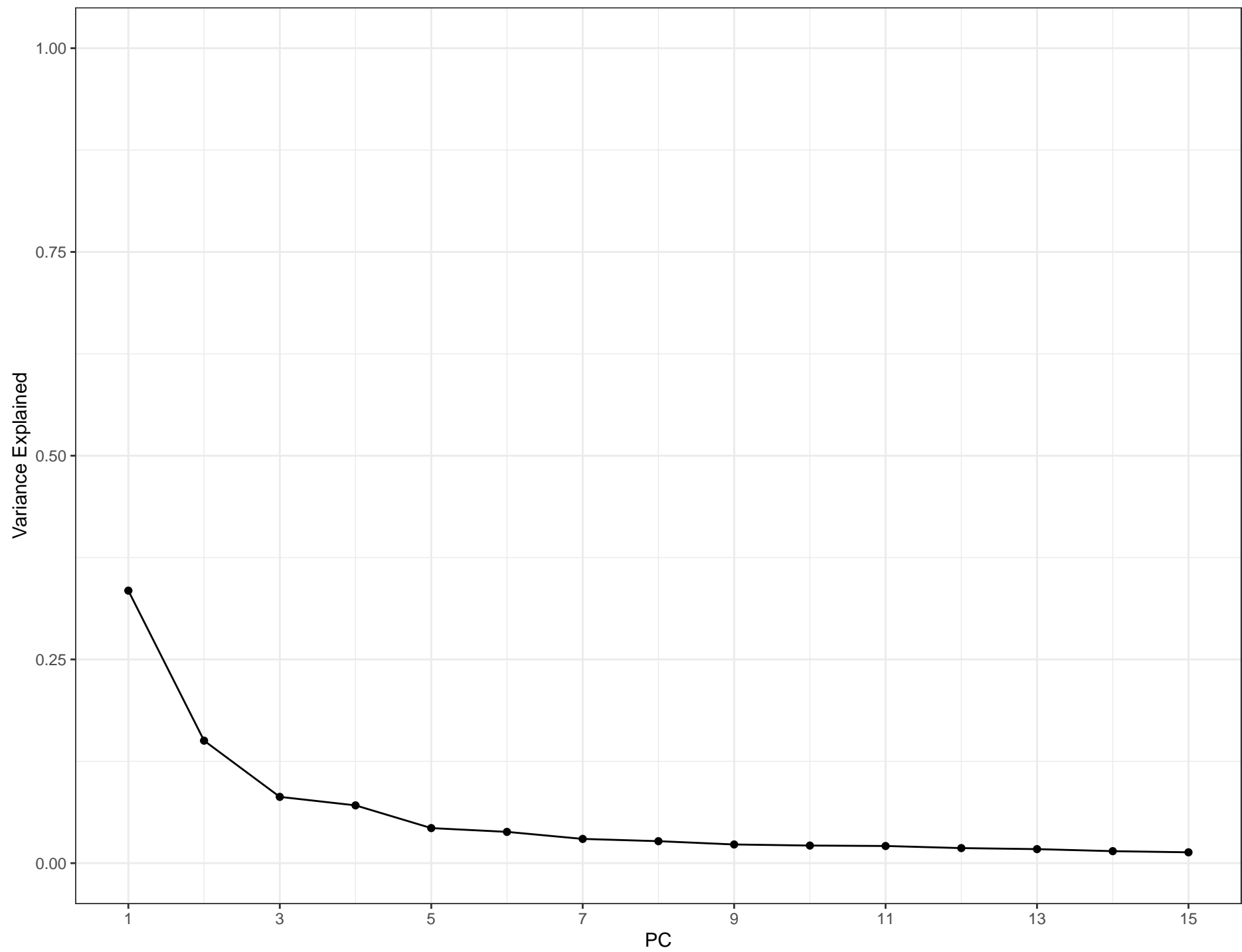
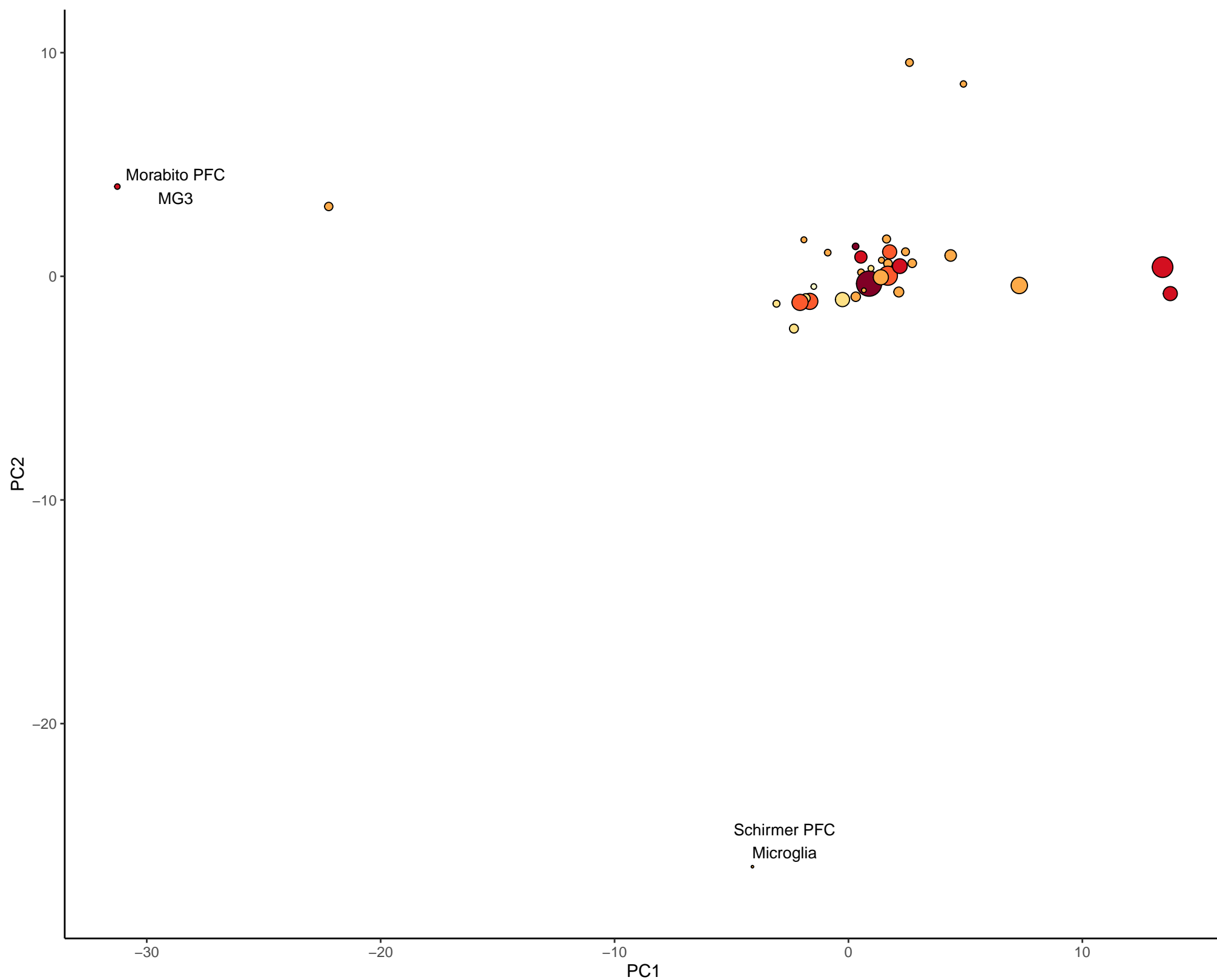


**MIC Subtypes**  
**Normalized Counts Mean Expression Scree Plot**  
26 cell types, 29 datasets, 8,723 genes



# Microglia Batch Corrected Mean Expression

26 cell types found in 29 datasets from 18 studies  
8,723 genes



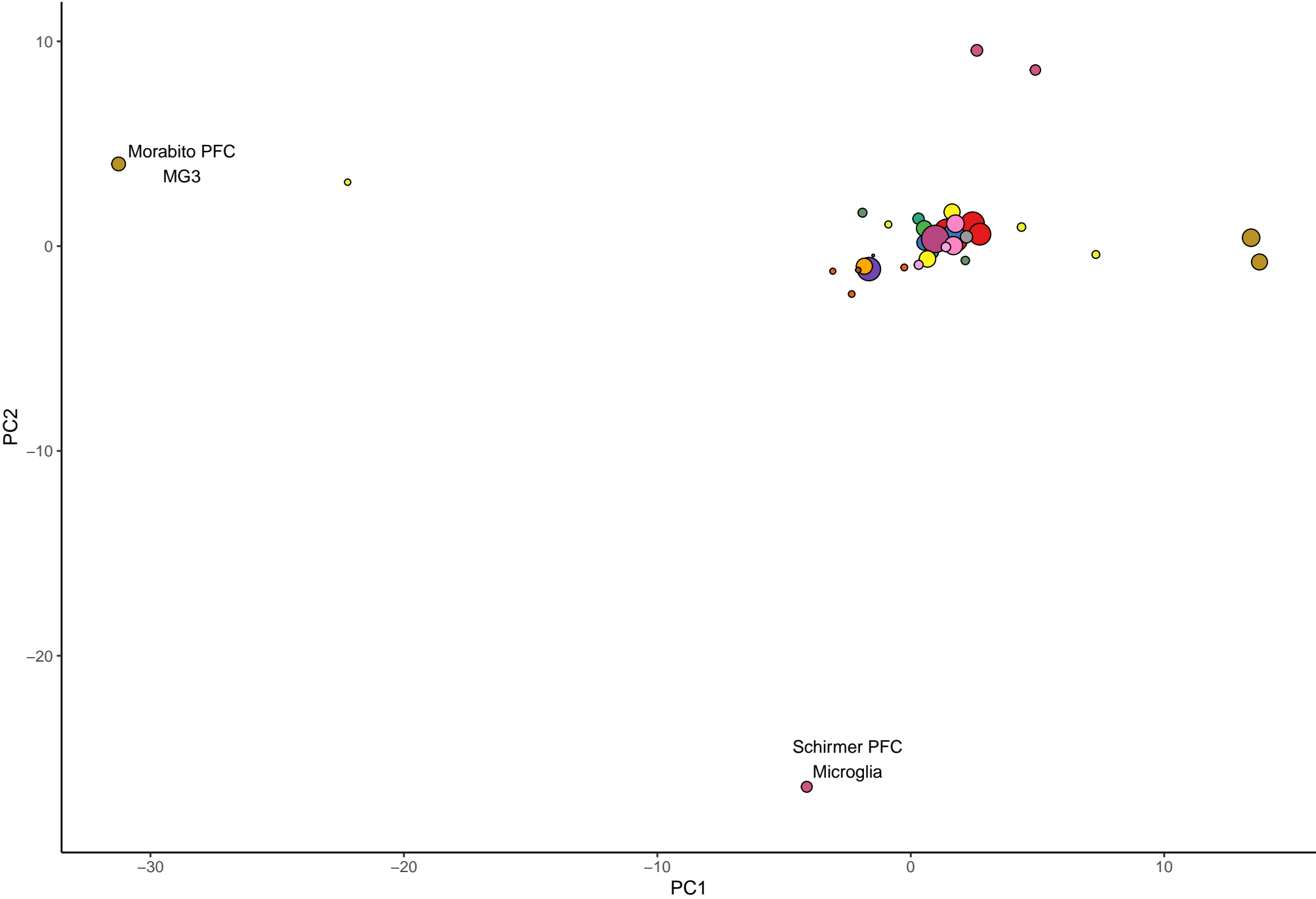
# Nuclei

• 6 • 100 • 500 • 1,000 • 1,000

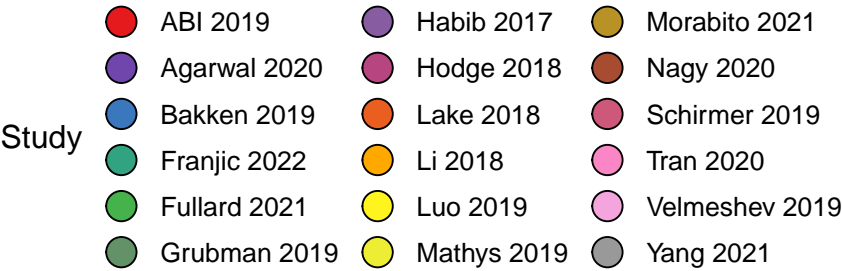
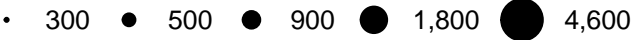
Year 2017 2018 2019 2020 2021 2022

Microglia Batch Corrected Mean Expression

26 cell types found in 29 datasets from 18 studies  
8,723 genes

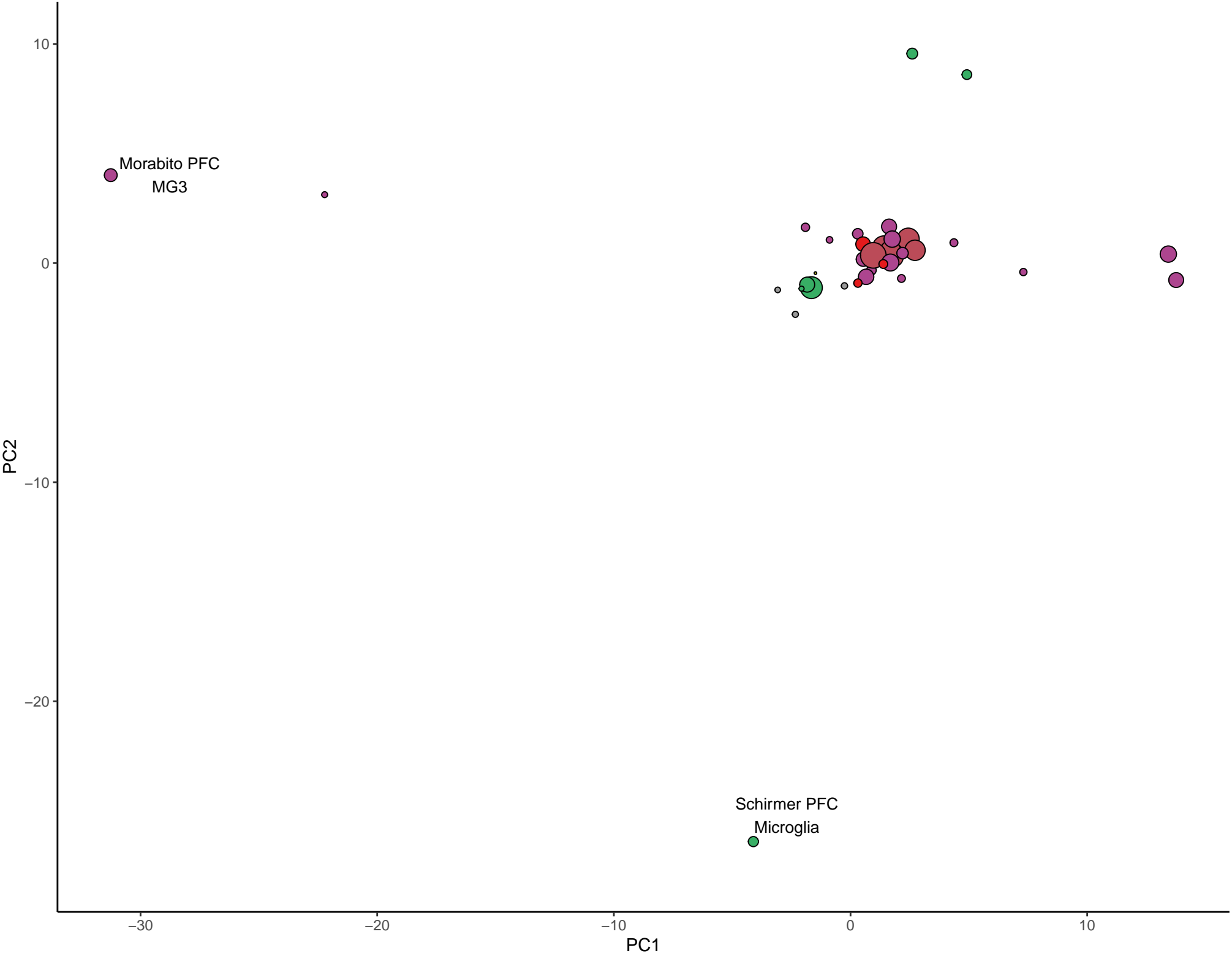


Median # Unique Genes



Microglia Batch Corrected Mean Expression

26 cell types found in 29 datasets from 18 studies  
8,723 genes



Median # Unique Genes

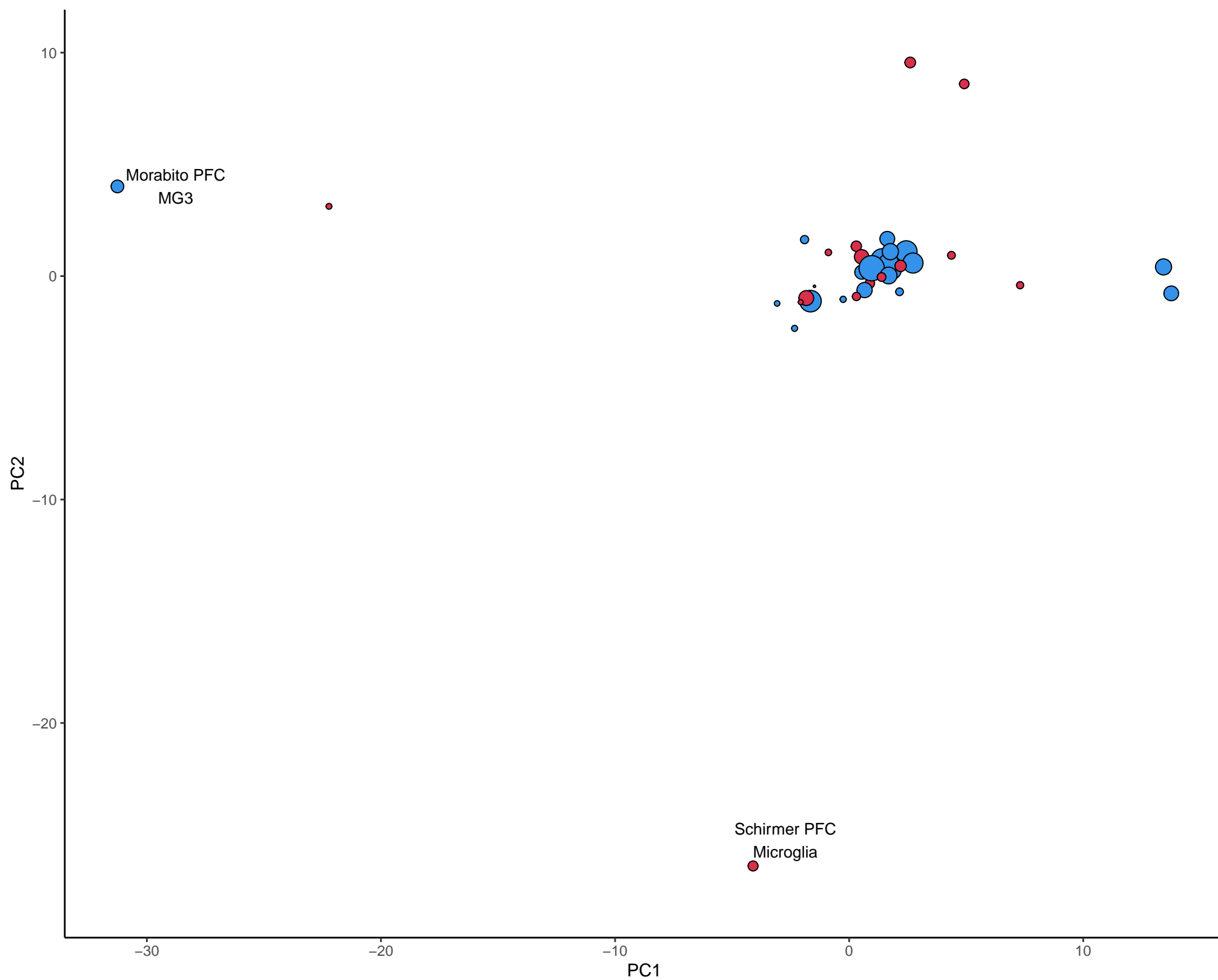
• 400 • 1,000 • 3,000 • 4,000

Platform

10x Chromium	10x Chromium V3	SMART-Seq v4
10x Chromium V2	DroNc-seq	snDrop-seq

# Microglia Batch Corrected Mean Expression

26 cell types found in 29 datasets from 18 studies  
8,723 genes



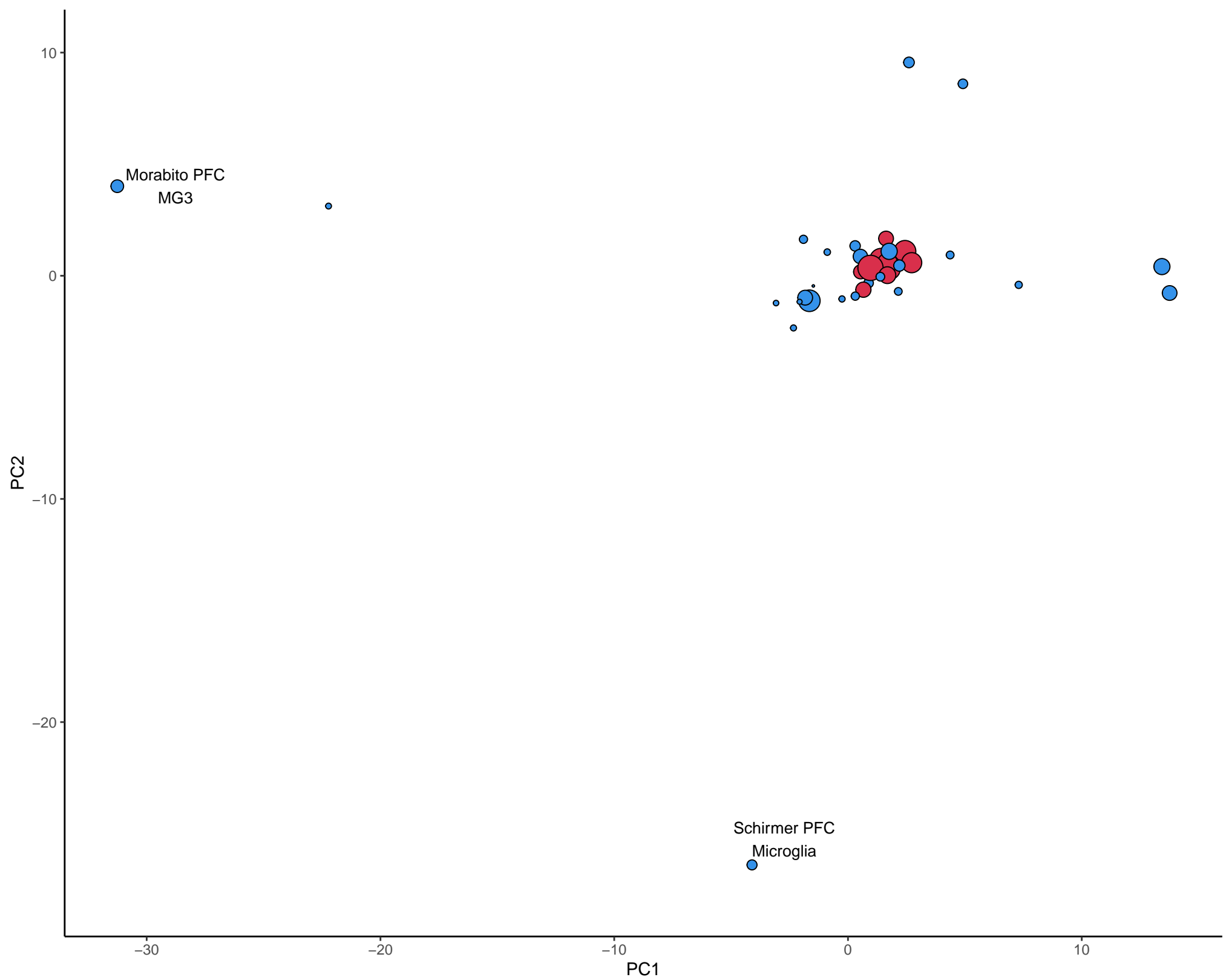
Median # Unique Genes

• 315 • 500 • 1,000 • 4,000

FACS Y N

# Microglia Batch Corrected Mean Expression

26 cell types found in 29 datasets from 18 studies  
8,723 genes



Median # Unique Genes

• 315 • 500 • 1,000 • 4,000

Unbiased Sampling Y N