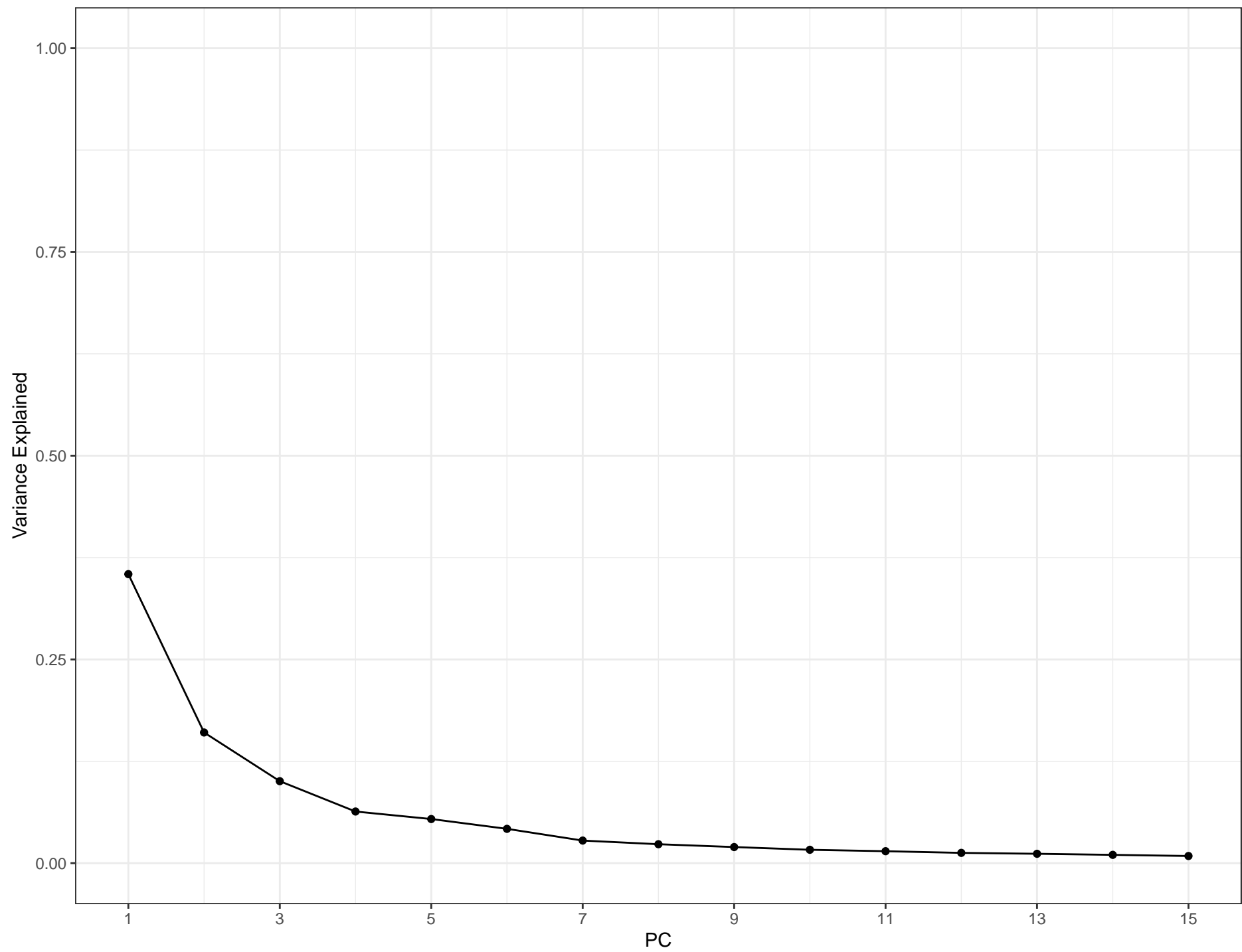
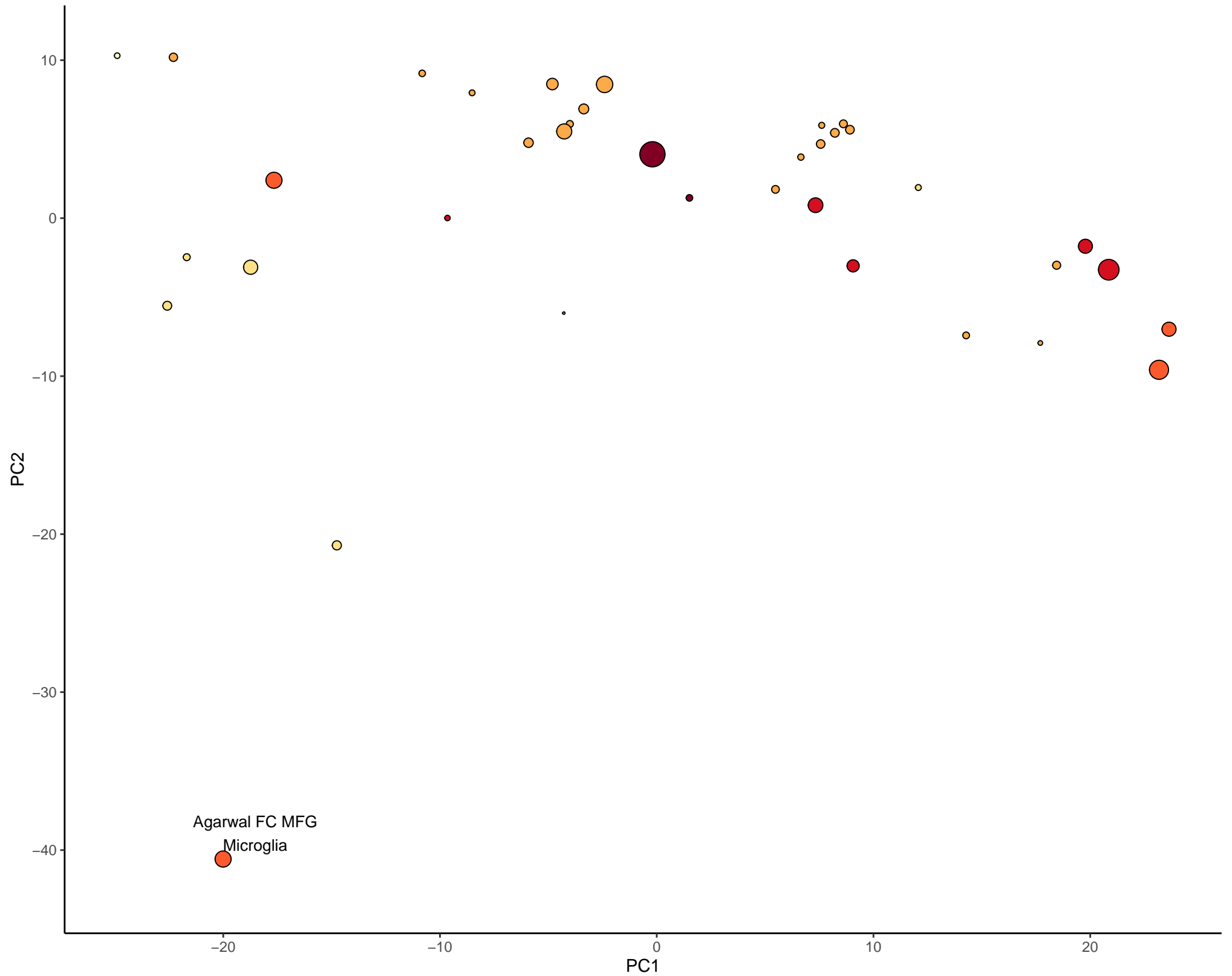


**MIC Subtypes**  
**Normalized Counts Mean Expression Scree Plot**  
26 cell types, 29 datasets, 8,723 genes



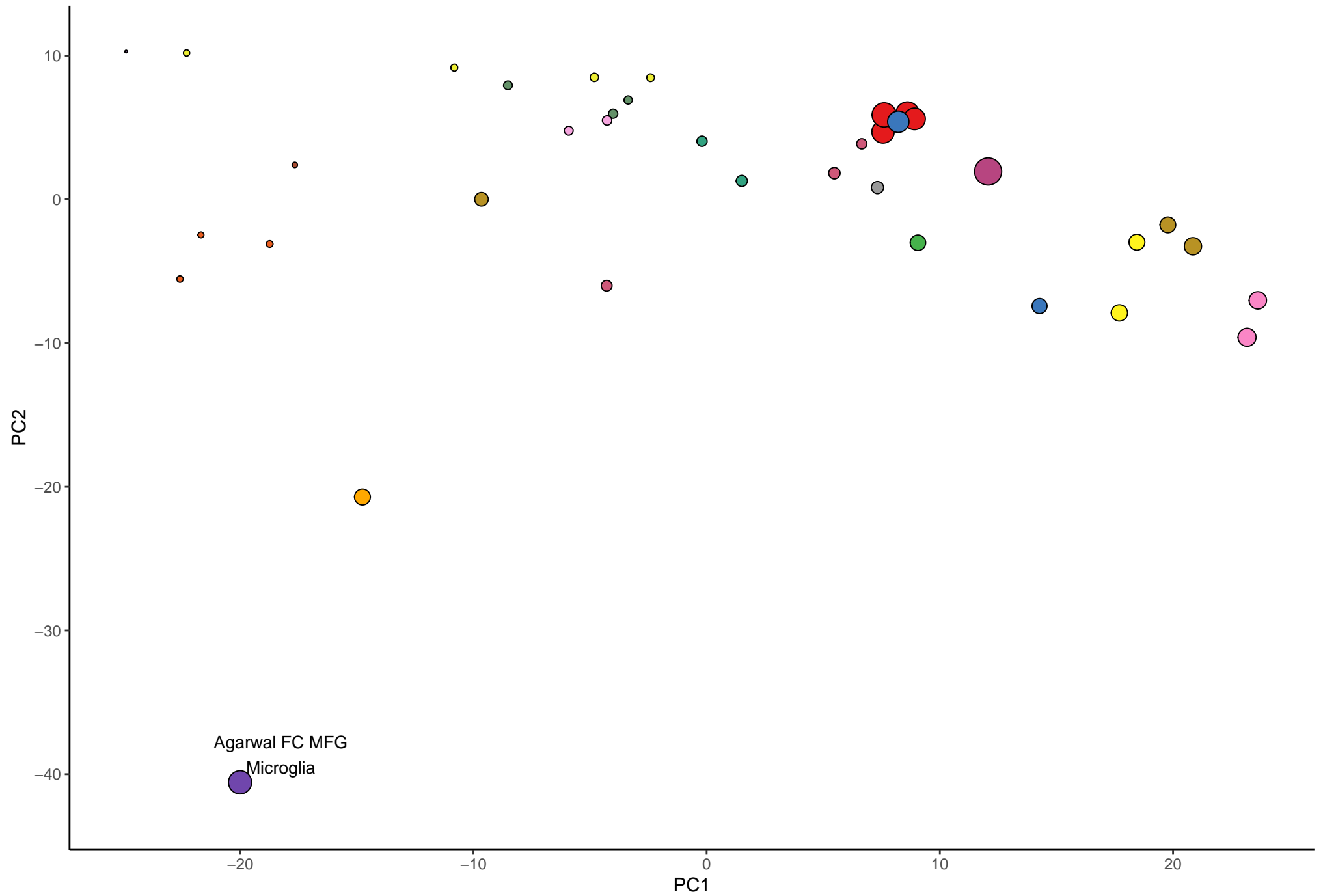
# Microglia Mean Expression

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



# Microglia Mean Expression

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



Median # Unique Genes

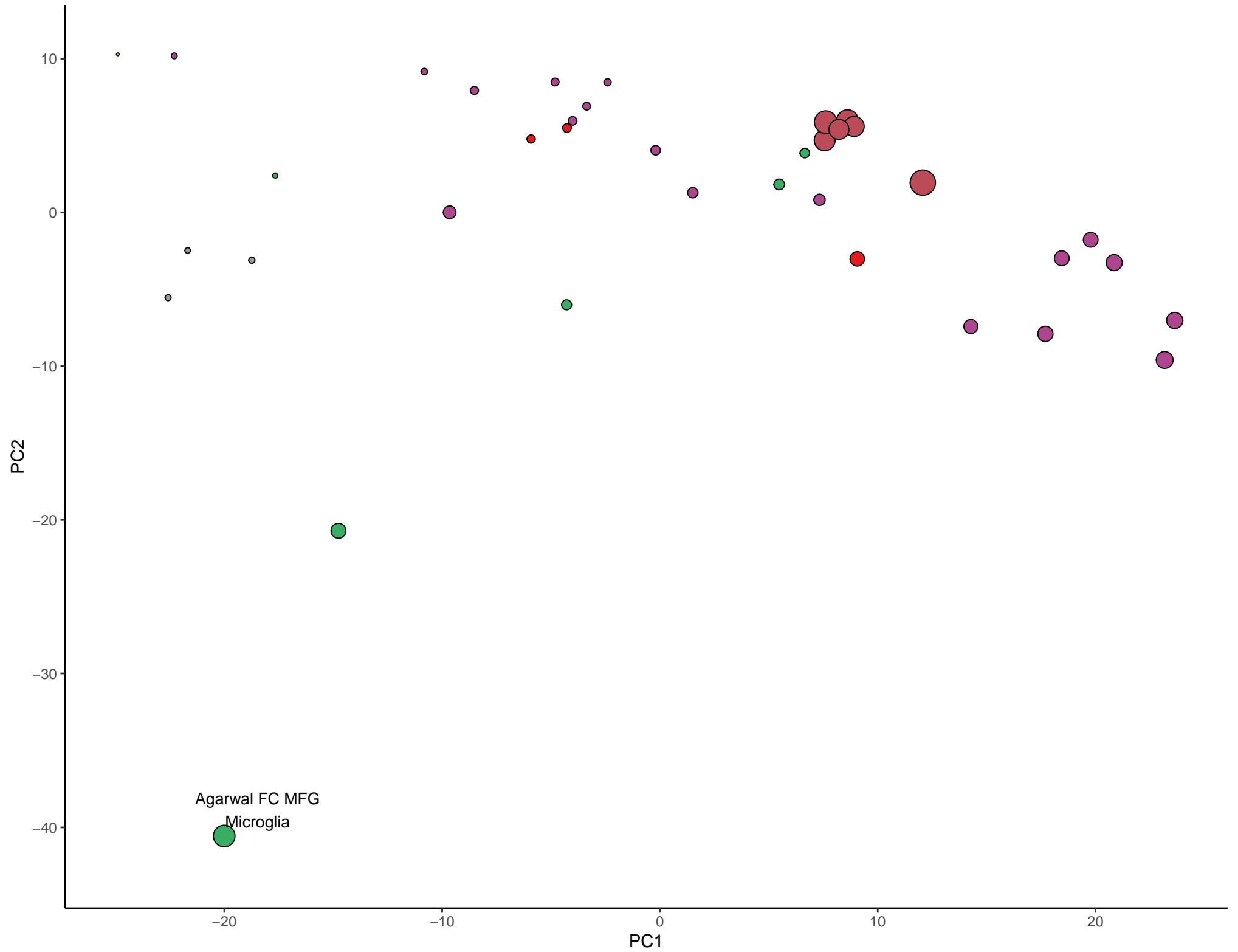
• 300 • 500 • 900 • 1,800 • 4,600

Study

- |              |             |                |
|--------------|-------------|----------------|
| ABI 2019     | Habib 2017  | Morabito 2021  |
| Agarwal 2020 | Hodge 2018  | Nagy 2020      |
| Bakken 2019  | Lake 2018   | Schirmer 2019  |
| Franjic 2022 | Li 2018     | Tran 2020      |
| Fullard 2021 | Luo 2019    | Velmeshev 2019 |
| Grubman 2019 | Mathys 2019 | Yang 2021      |

# Microglia Mean Expression

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



Median # Unique Genes

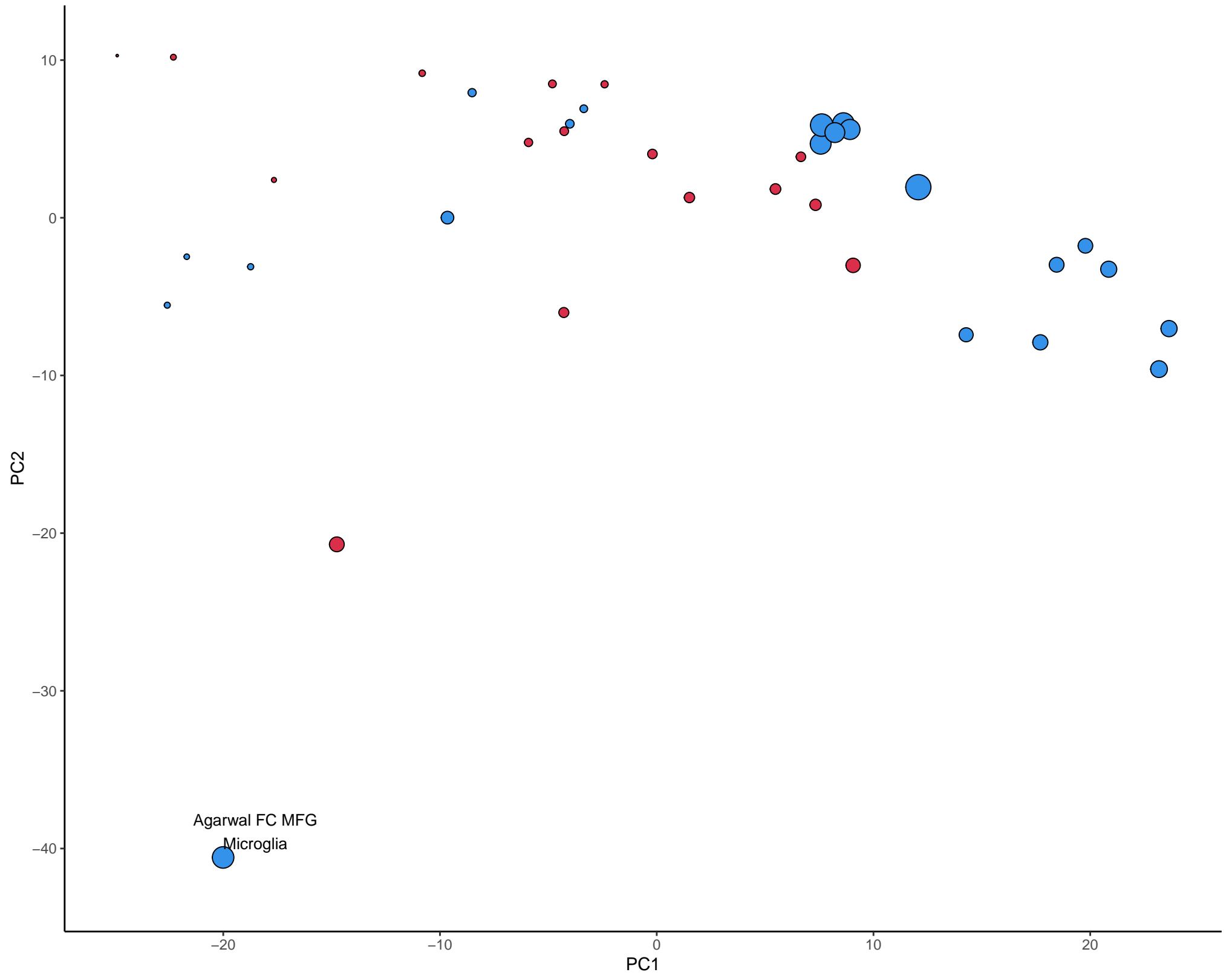
• 400 • 1,000 • 3,000 • 4,000

Platform

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

# Microglia Mean Expression

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



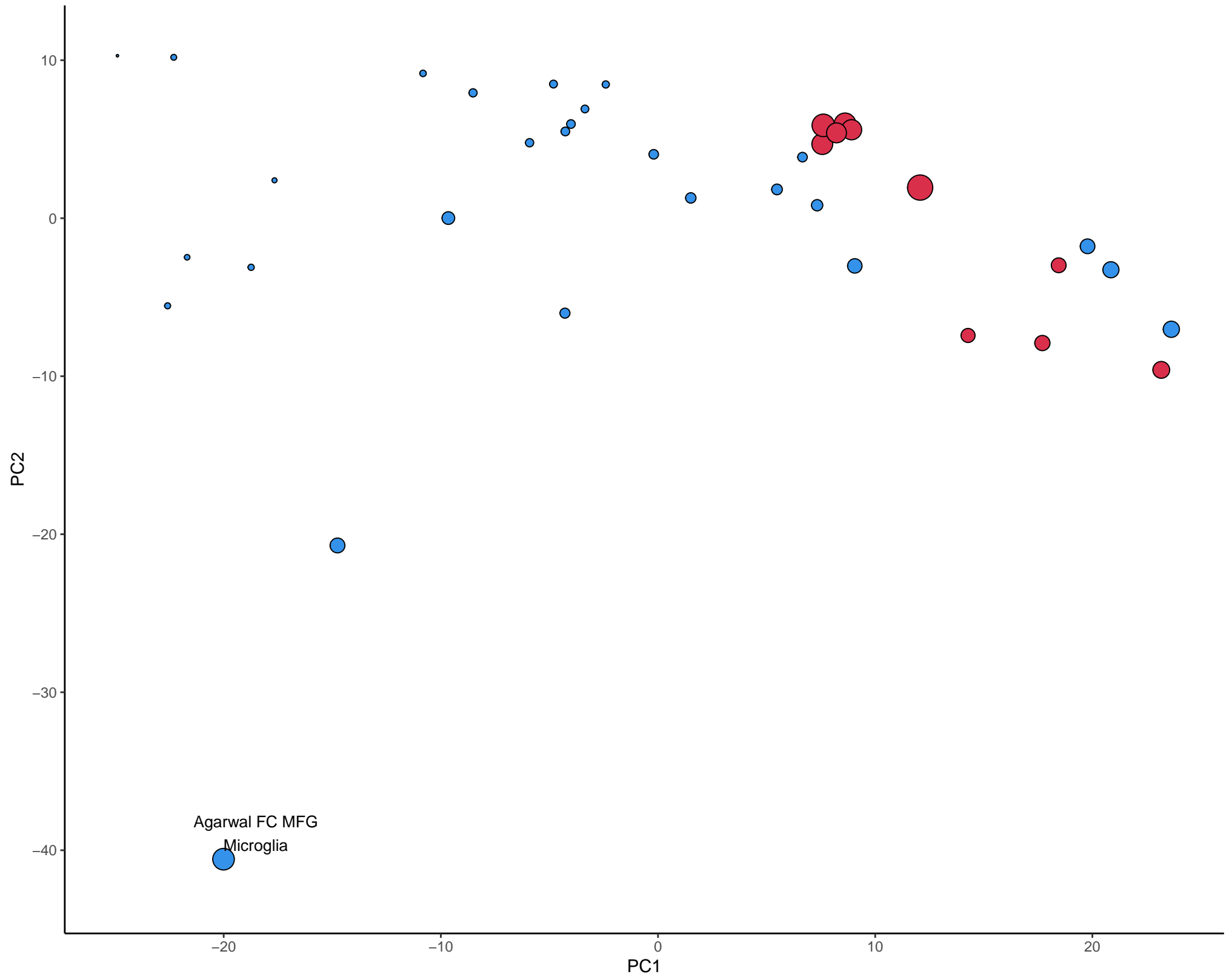
Median # Unique Genes

• 315 • 500 • 1,000 • 4,000

FACS Y N

# Microglia 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