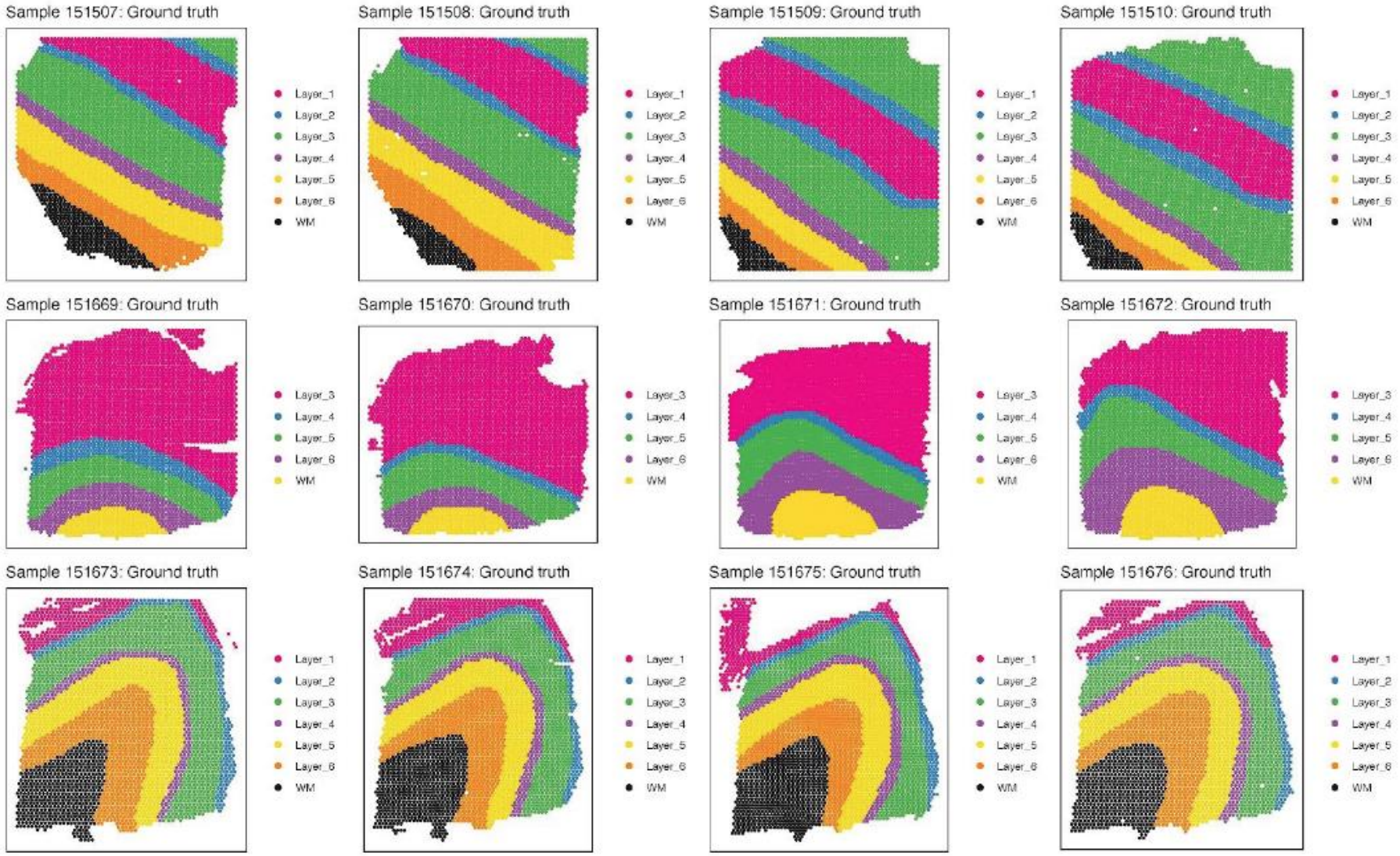
Analysis of Maynard et al., 2020 brain spatial transcriptomic data

4/13

12 samples with layer annotation

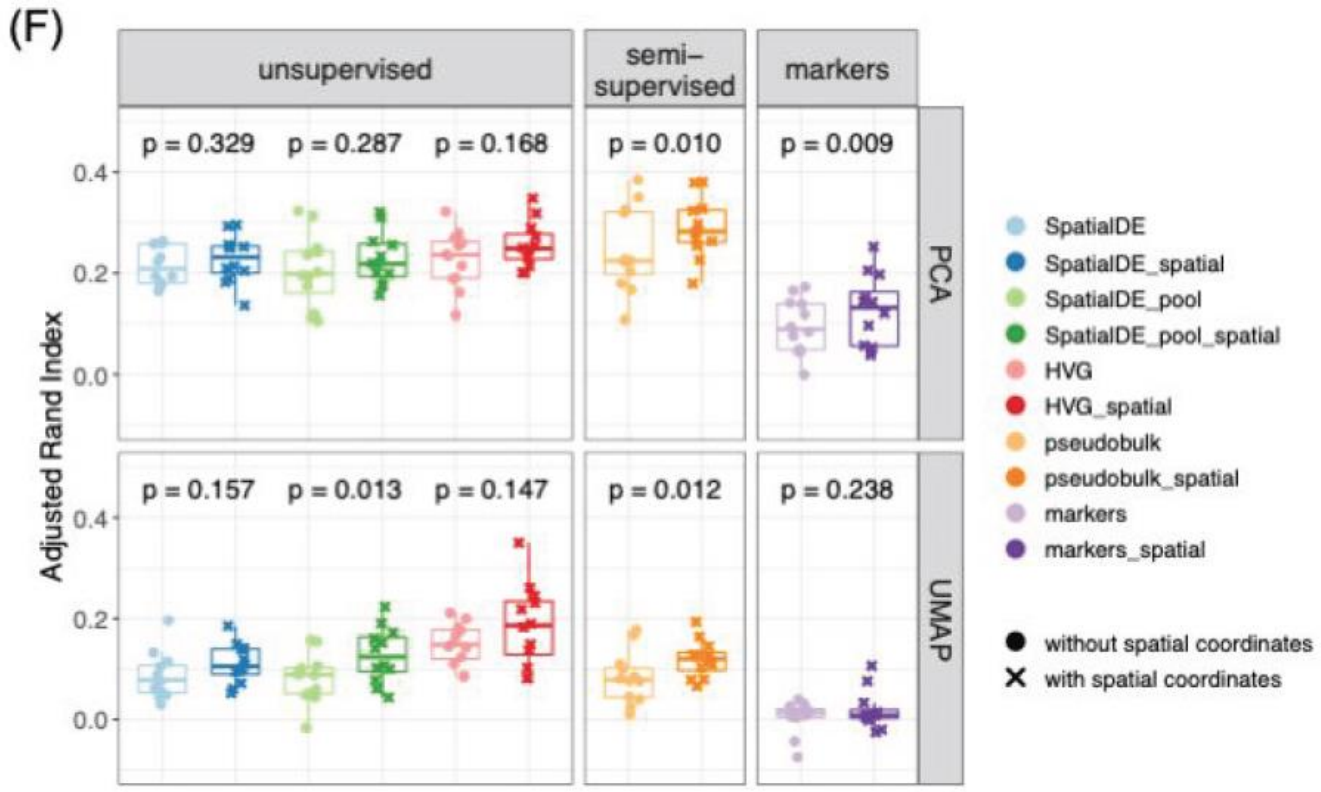
3 donors



10 µm apart 300 µm apart 10 µm apart

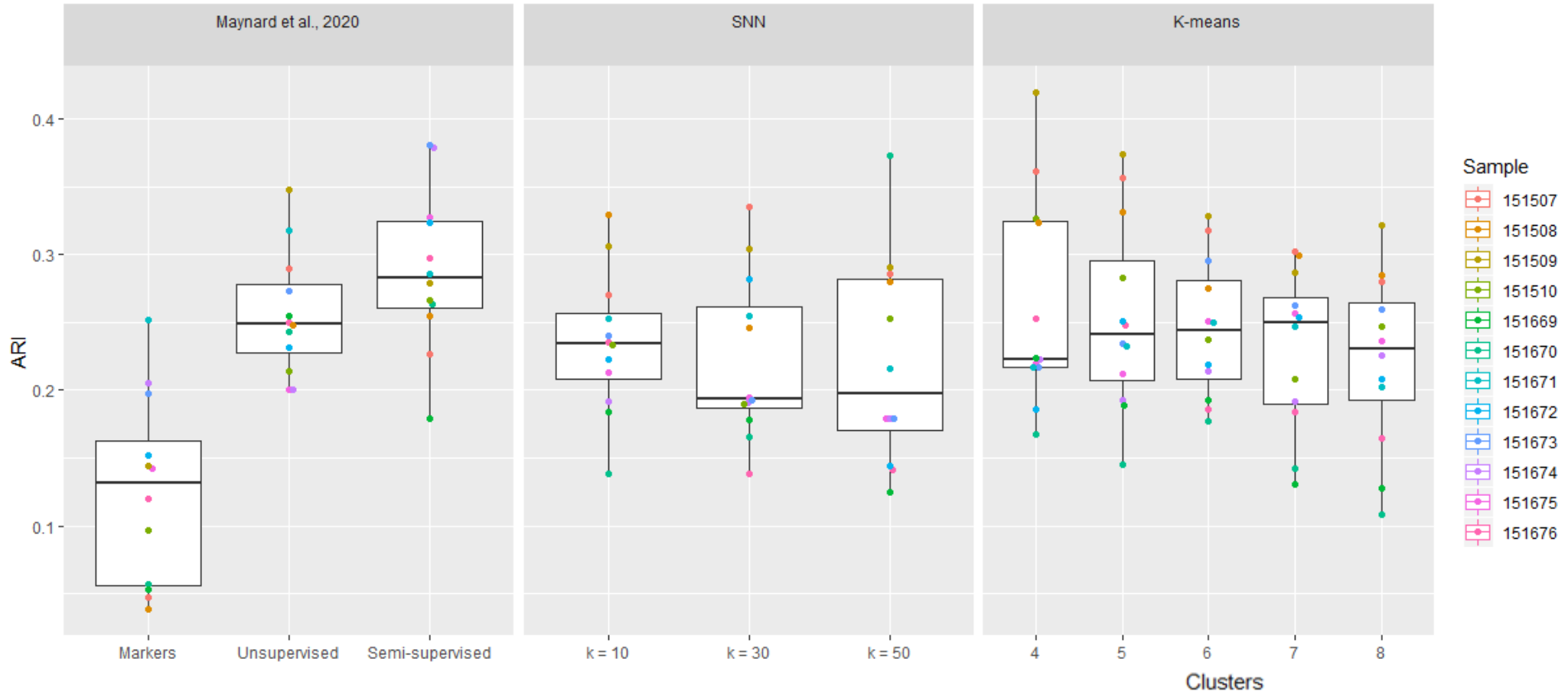
Maynard et al., 2020

Maynard et al., 2020 clustering analysis



Maynard et al., 2020

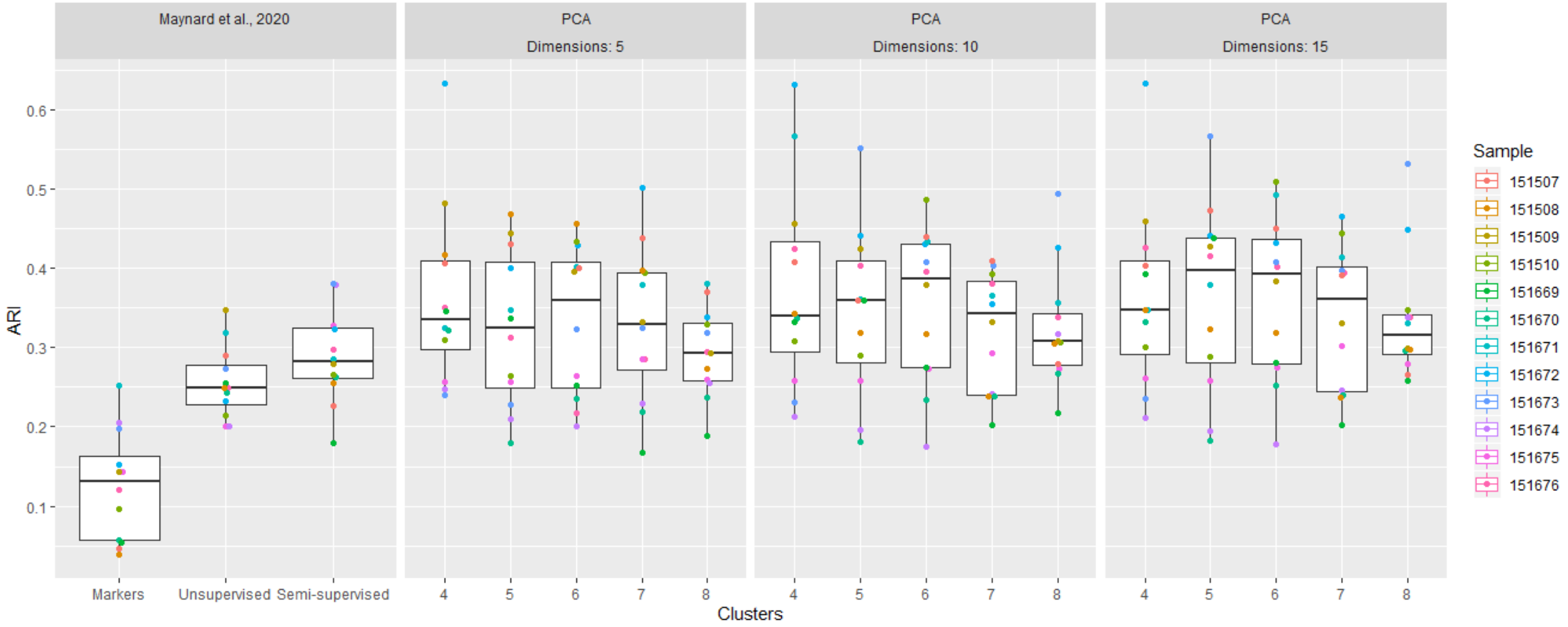
SNN and K-means clustering performance



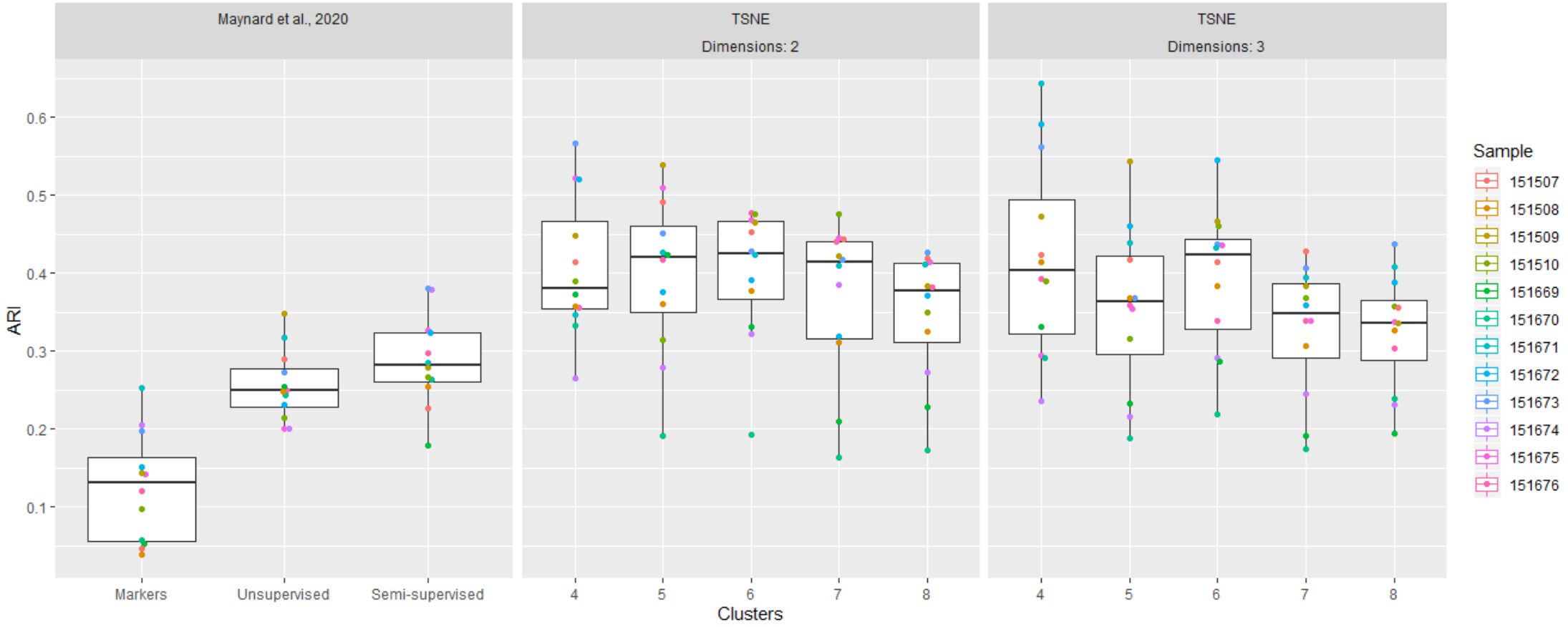
Spatial clustering method

- Each spot $i \in \{1, \ldots, n\}$ has a latent state z (i.e. cell type) where $z \in \{1, \ldots, q\}$
  - Potts model prior encourages neighboring spots to have the same state: $\pi(z) = \sum_{\langle i\ j \rangle} I(z_i = z_j)$
- Model low d-dimensional representation of expression Y (i.e. top PCs, t-SNE) as MVN(μ_z, Λ^{-1})
- Estimate parameters $\boldsymbol{z}_{n\times 1}, \boldsymbol{\mu}_{\mathbf{1},d\times 1}, \ldots, \boldsymbol{\mu}_{\boldsymbol{q},d\times 1}, \boldsymbol{\Sigma}_{d\times d}$ using MCMC
  - Initialize with k-means clustering
  - Update z using Metropolis-Hastings
  - Take predicted cluster of each spot to be modal state of chain

PCA spatial clustering performance



t-SNE spatial clustering performance



Model comparison