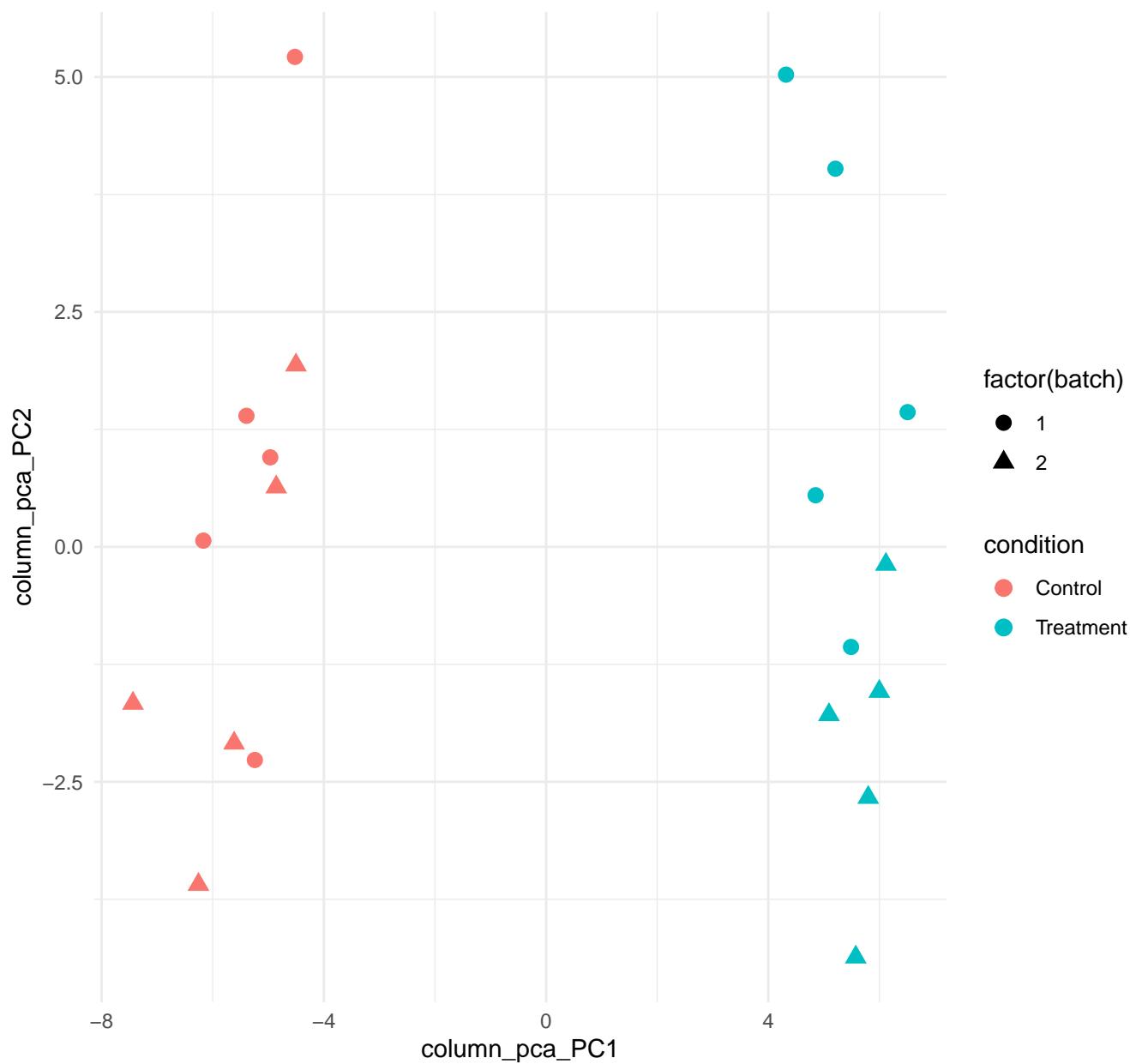


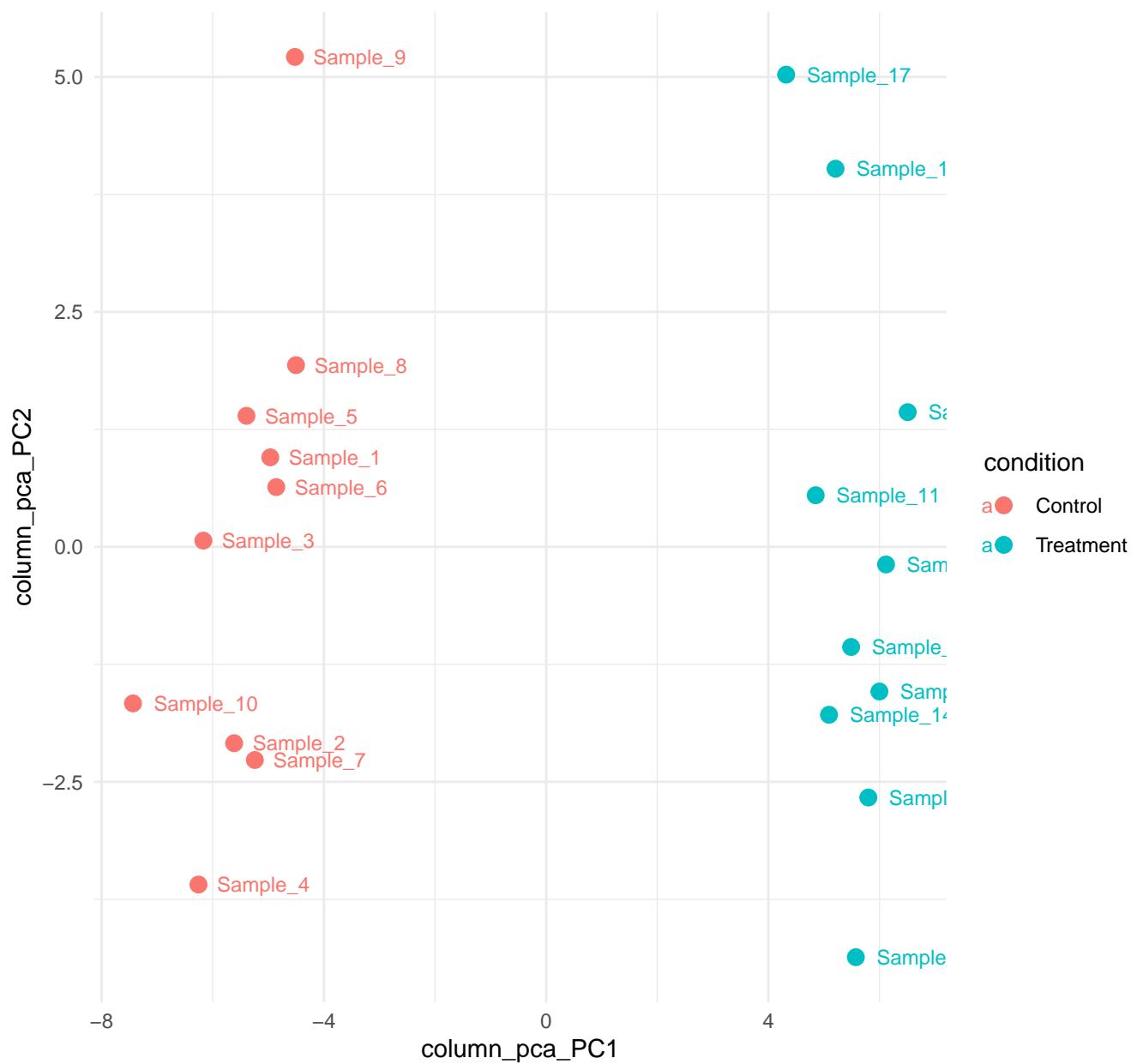
PCA of Samples

Using pull_active() to extract column metadata



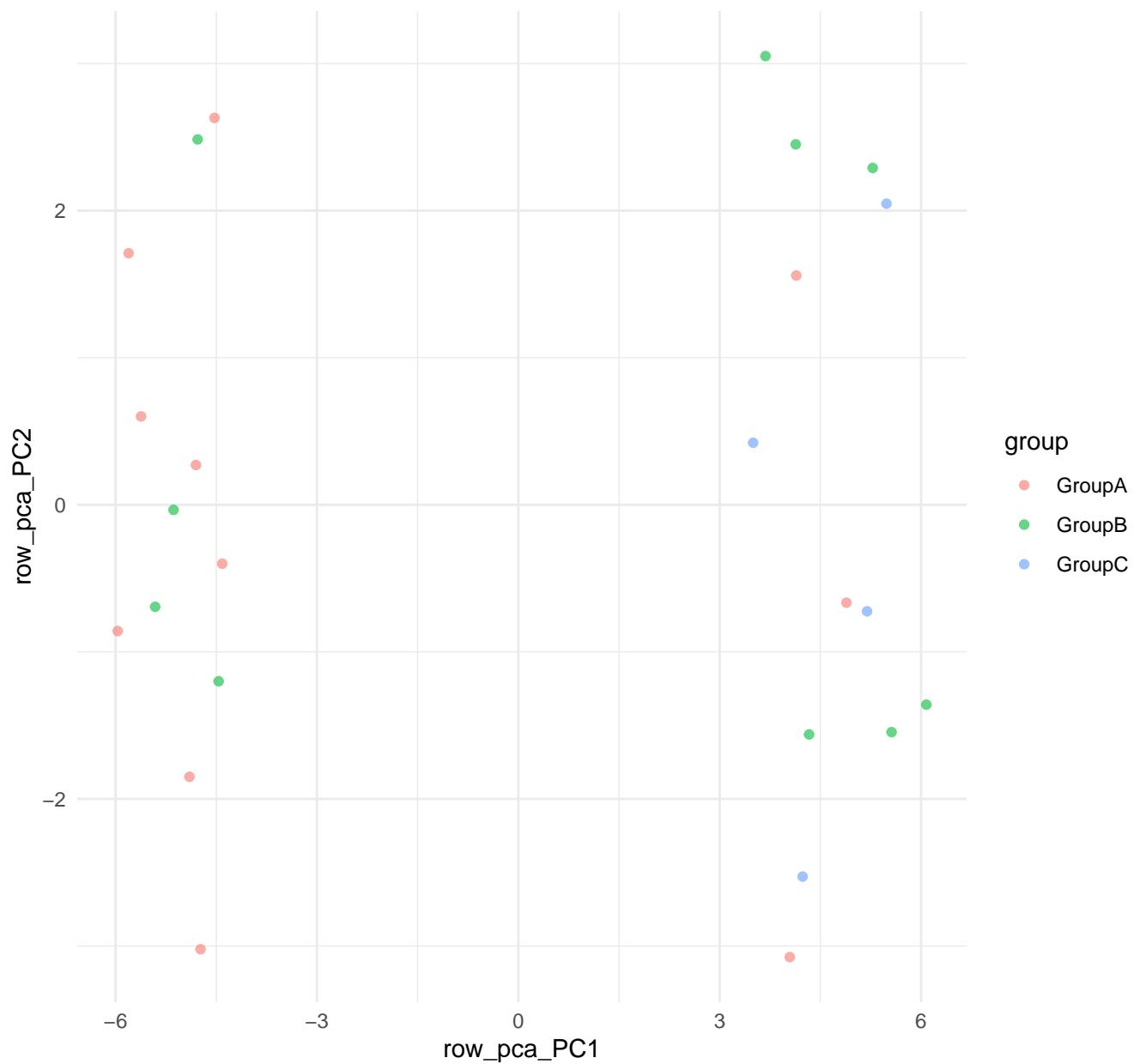
PCA of Samples with Labels

Using `as_tibble()` for cleaner tibble output



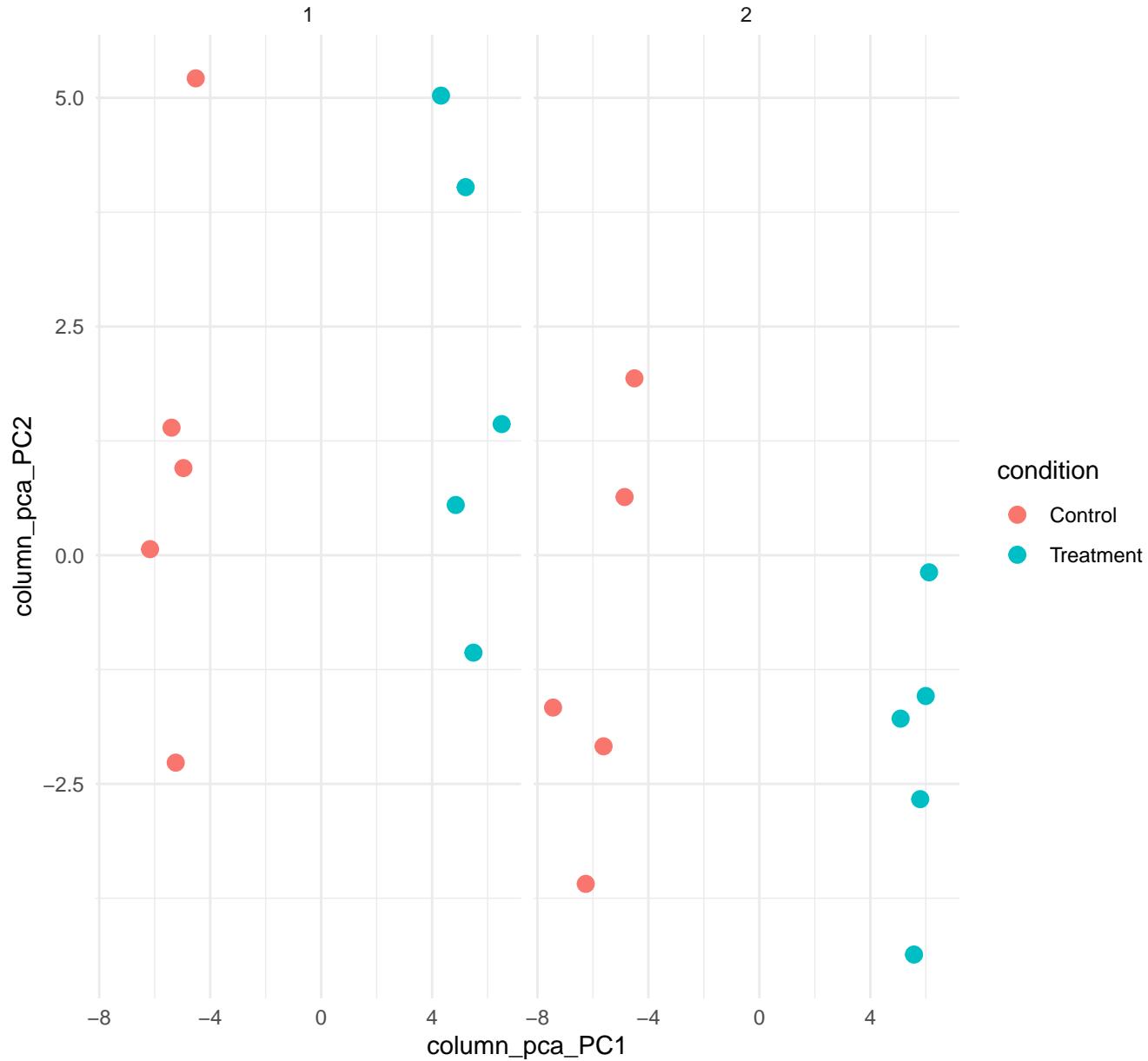
PCA of High-Variance Genes

Filtered to top 25% most variable genes

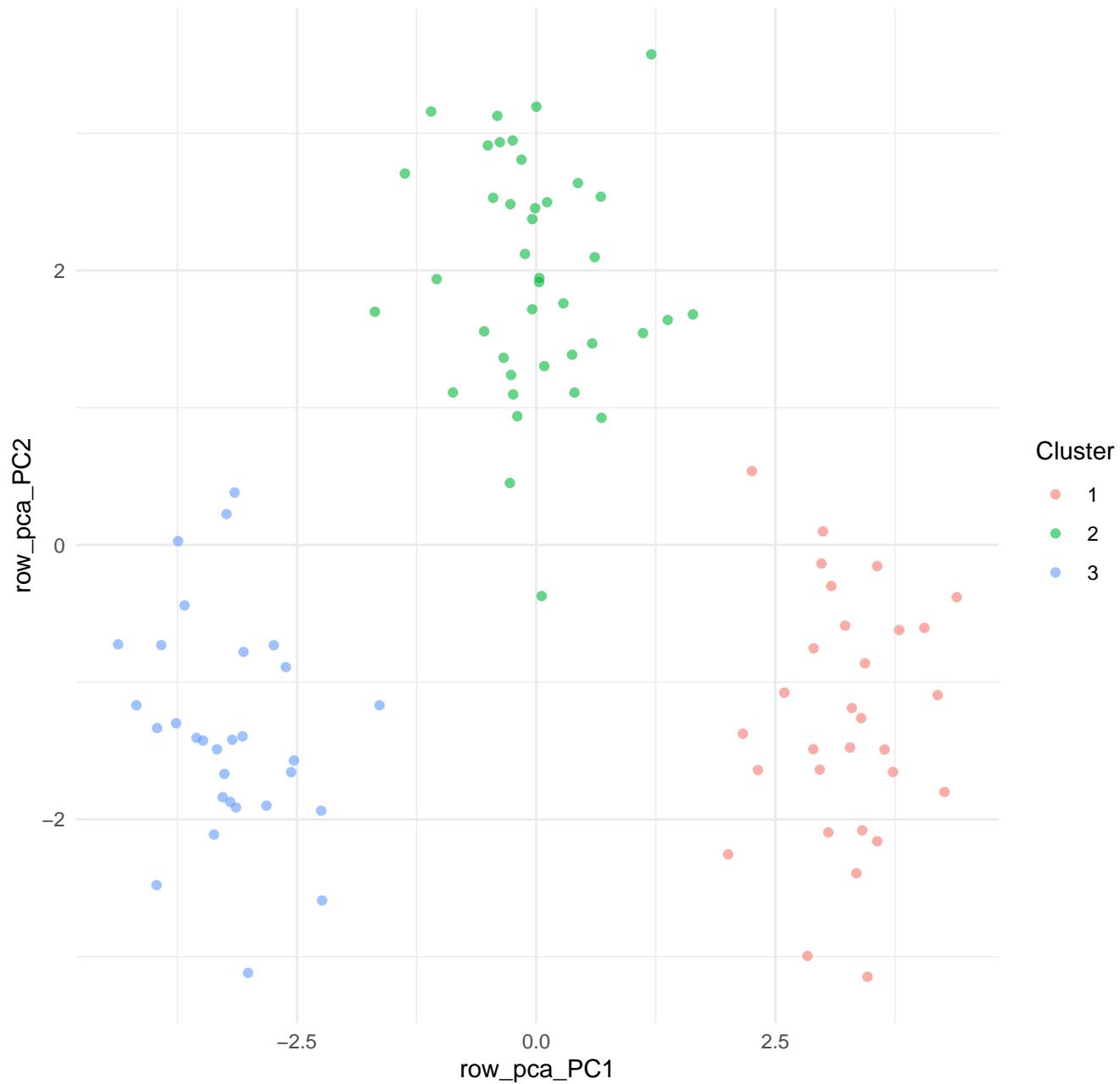


PCA by Batch

Faceted plot showing batch effects



Gene Clusters in PCA Space



PCA using base R

