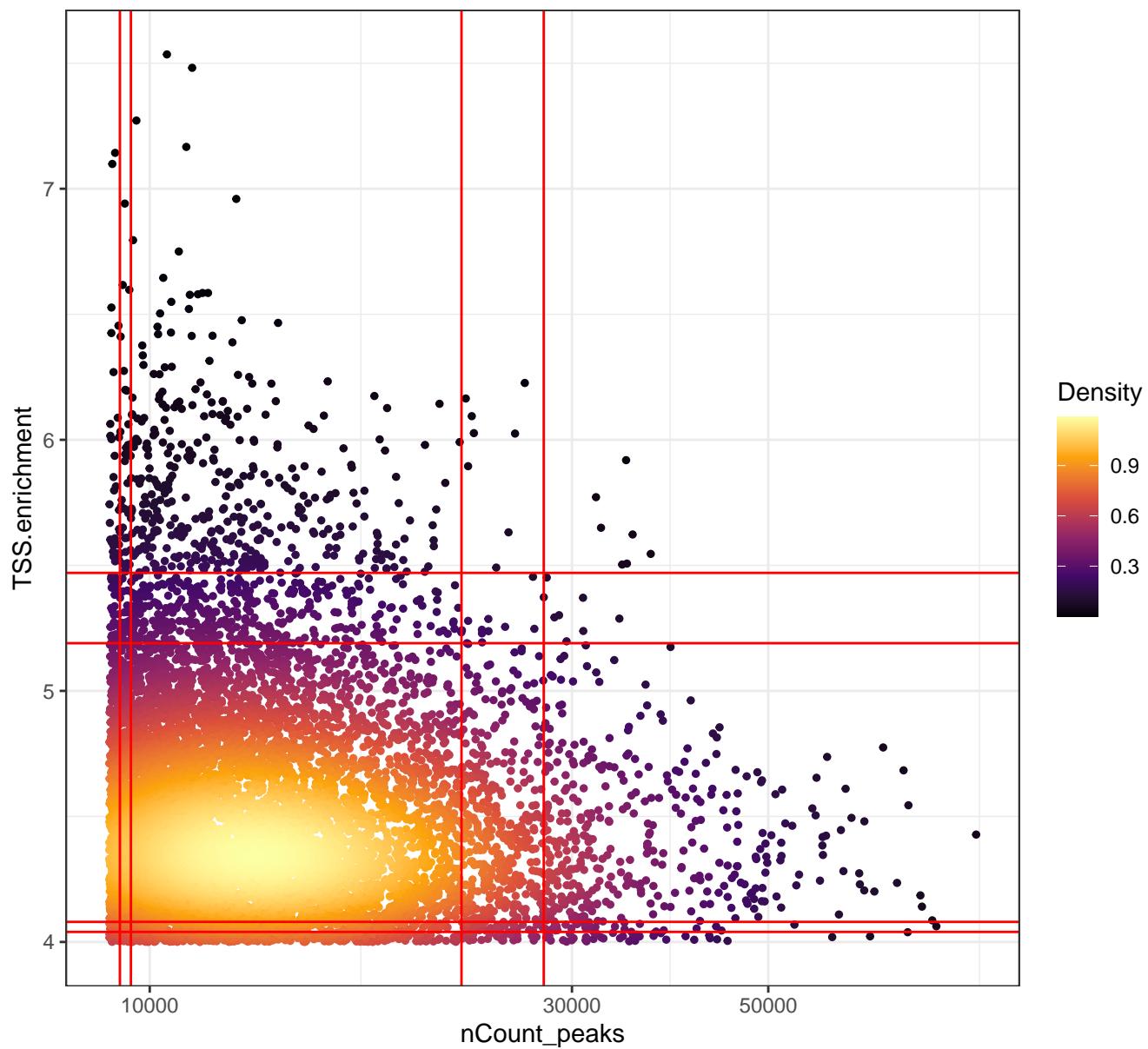


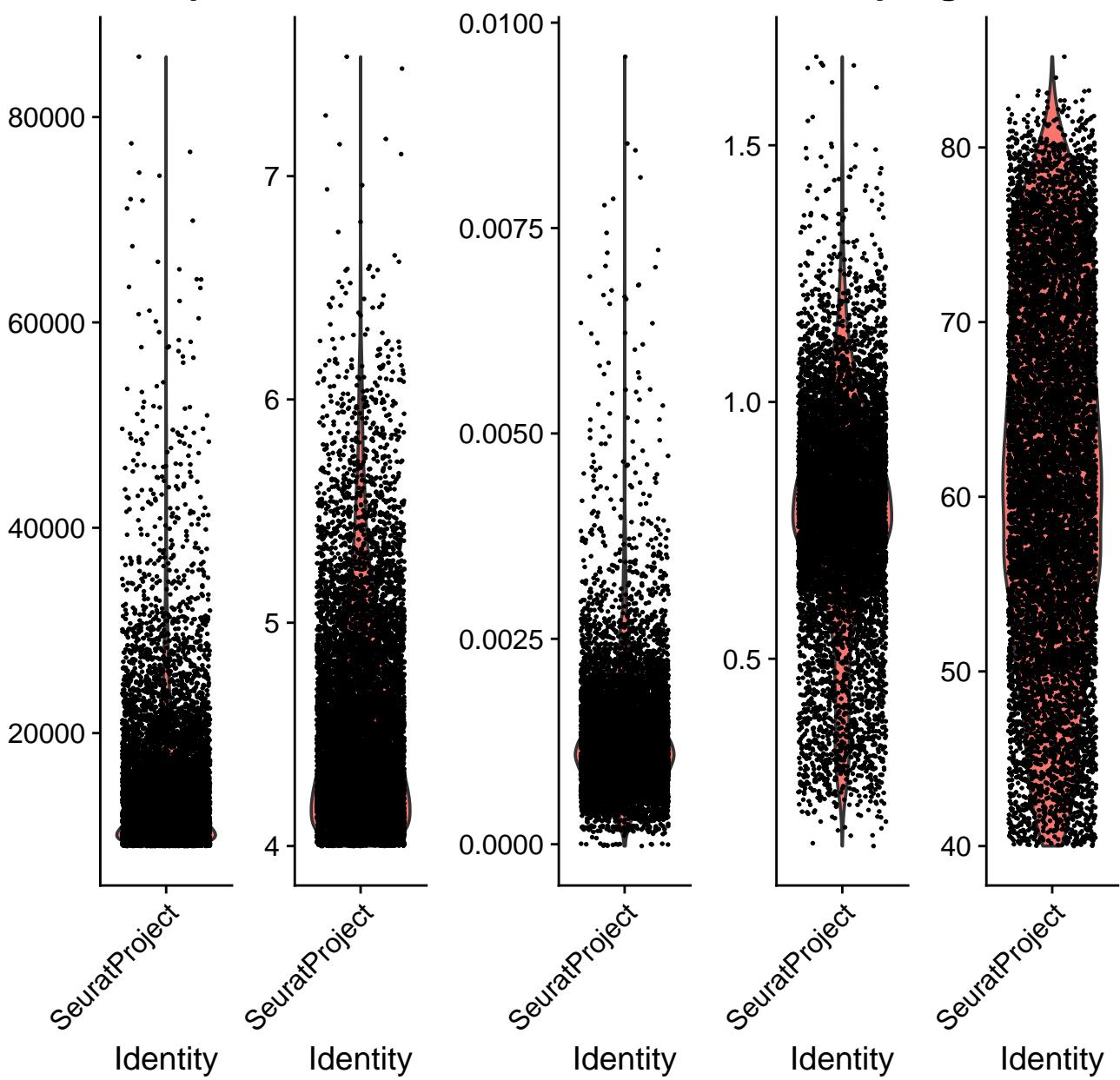
## Quantiles

nCount\_peaks: 5%:9253.05 10%:9522 90%:22505.3 95%:27878.65

TSS.enrichment: 5%:4.04 10%:4.08 90%:5.19 95%:5.47

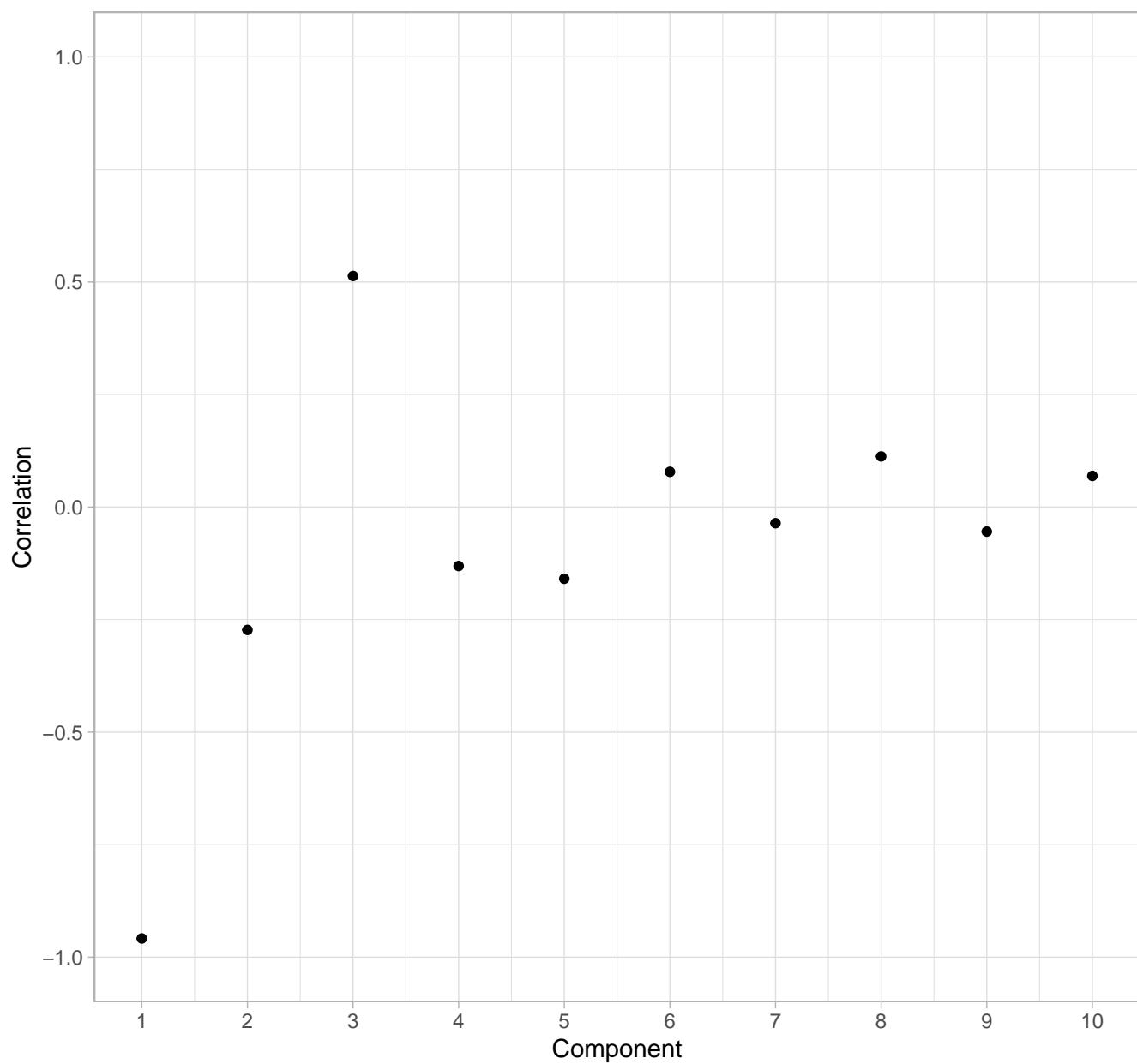


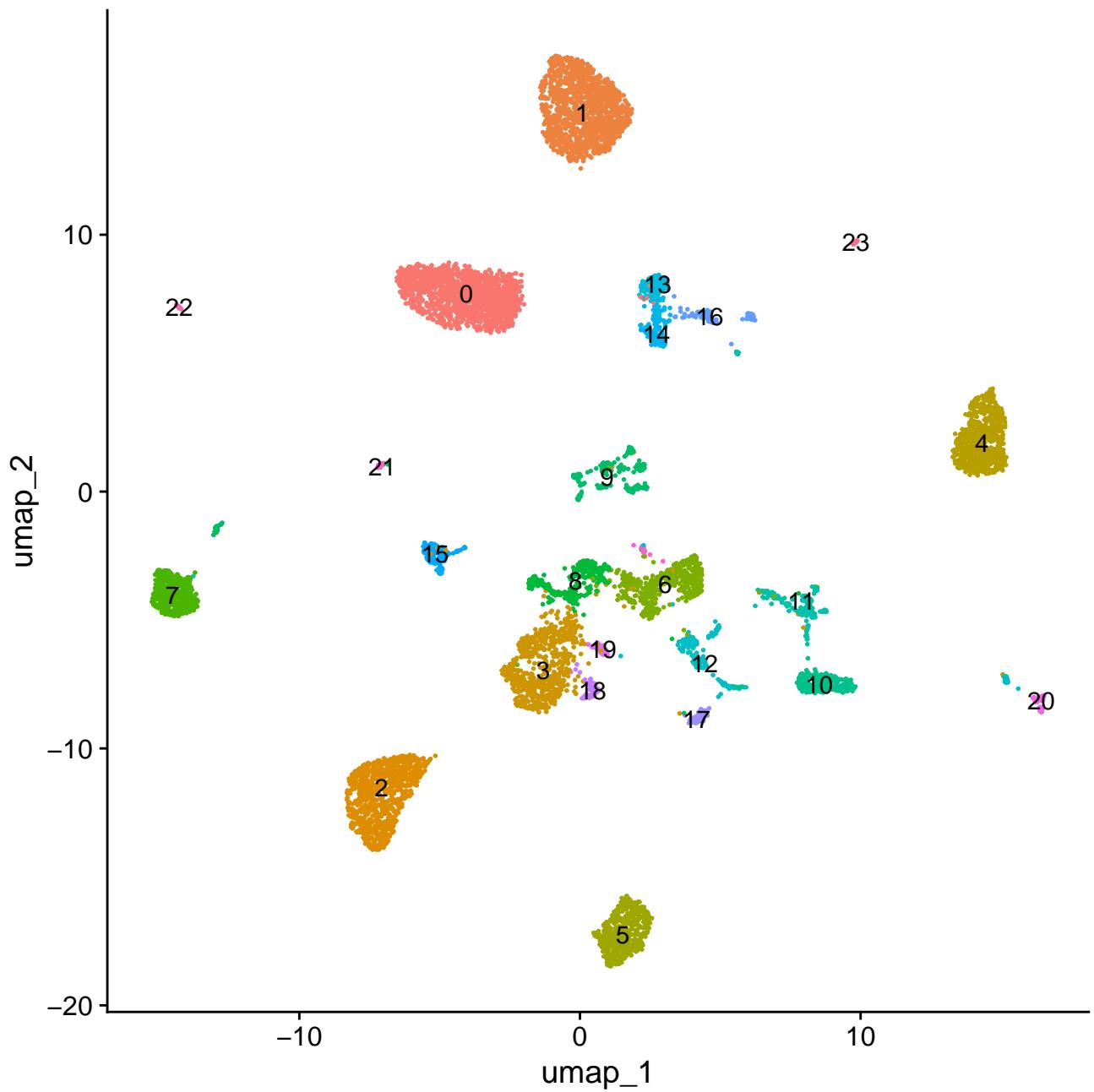
nCount\_peaks.enrichmentblacklist\_ratioeosomeoptigenes\_in\_p



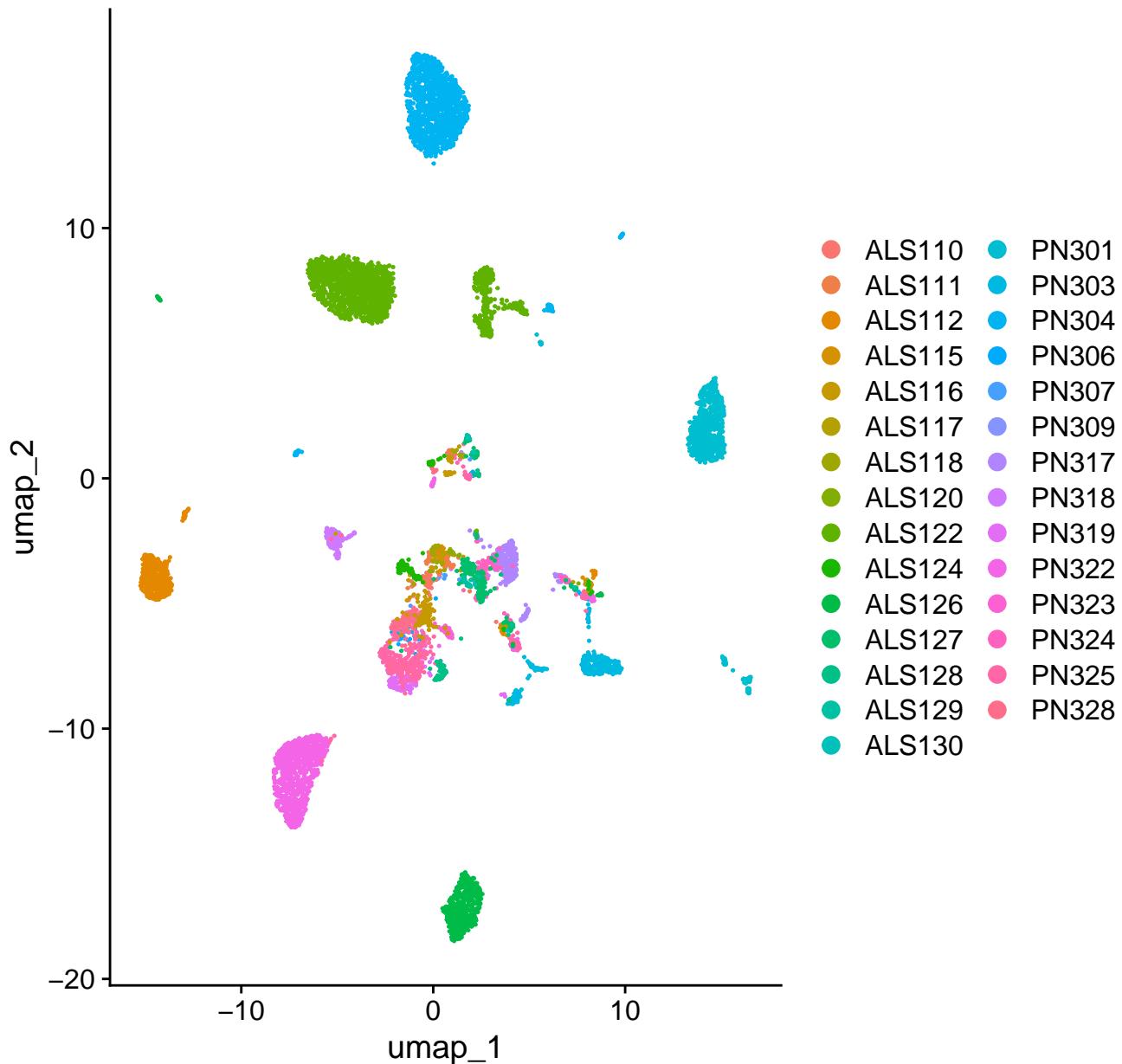
# Correlation between depth and reduced dimension components

Assay: peaks Reduction: lsi

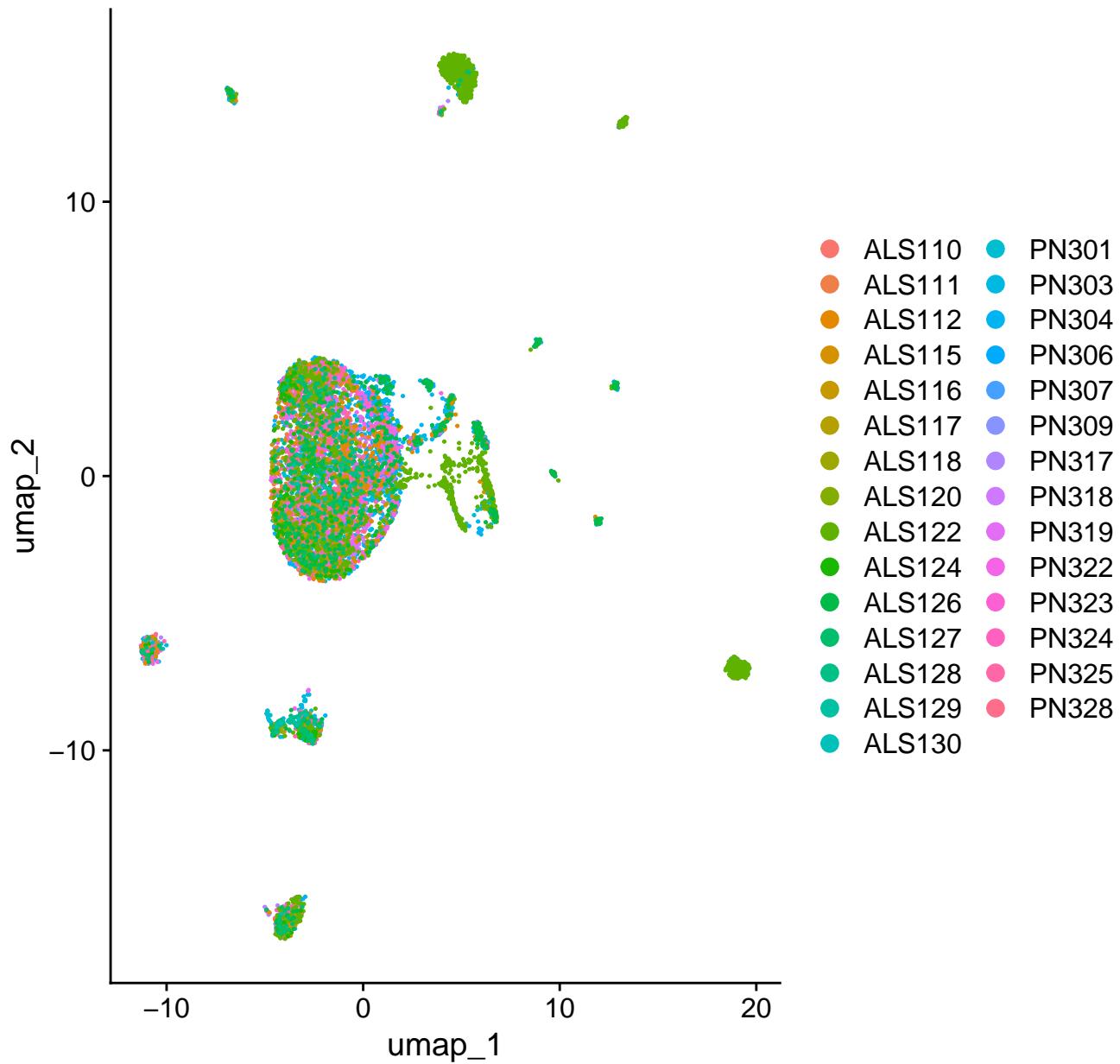


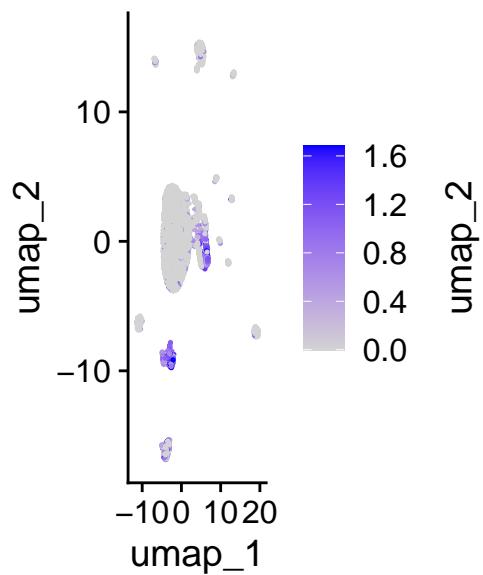
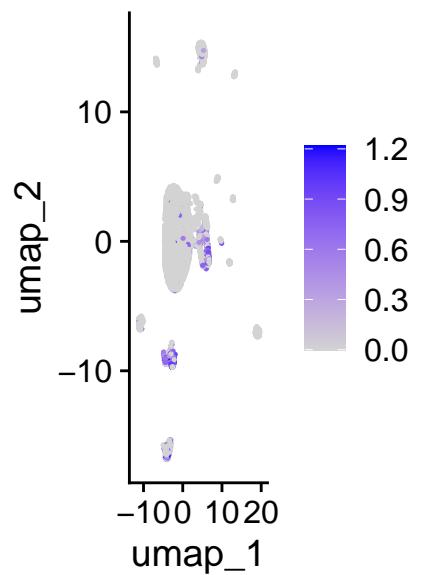
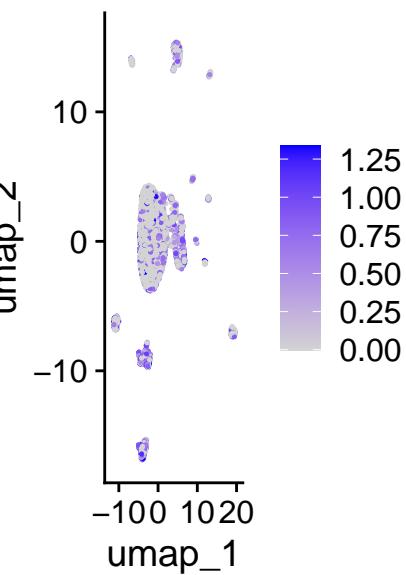
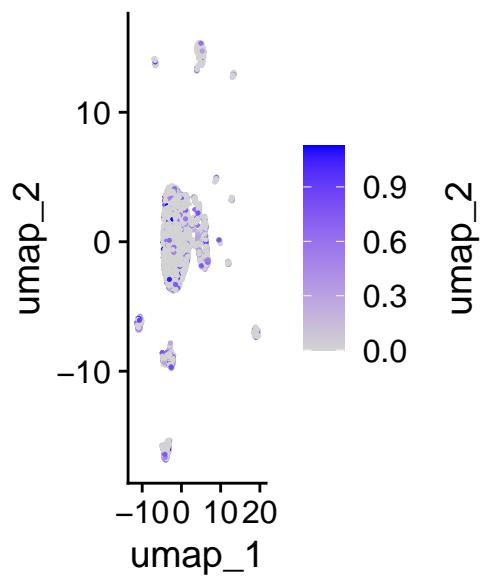
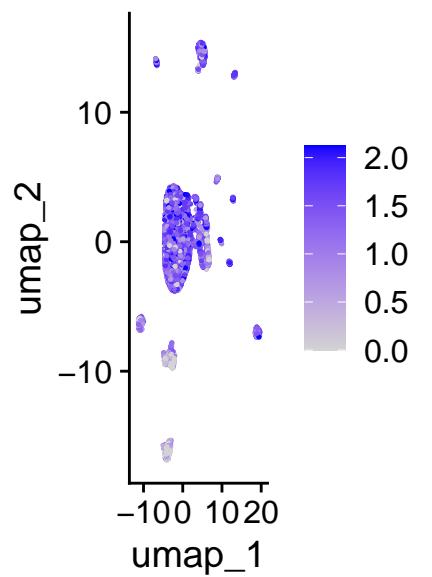


dataset

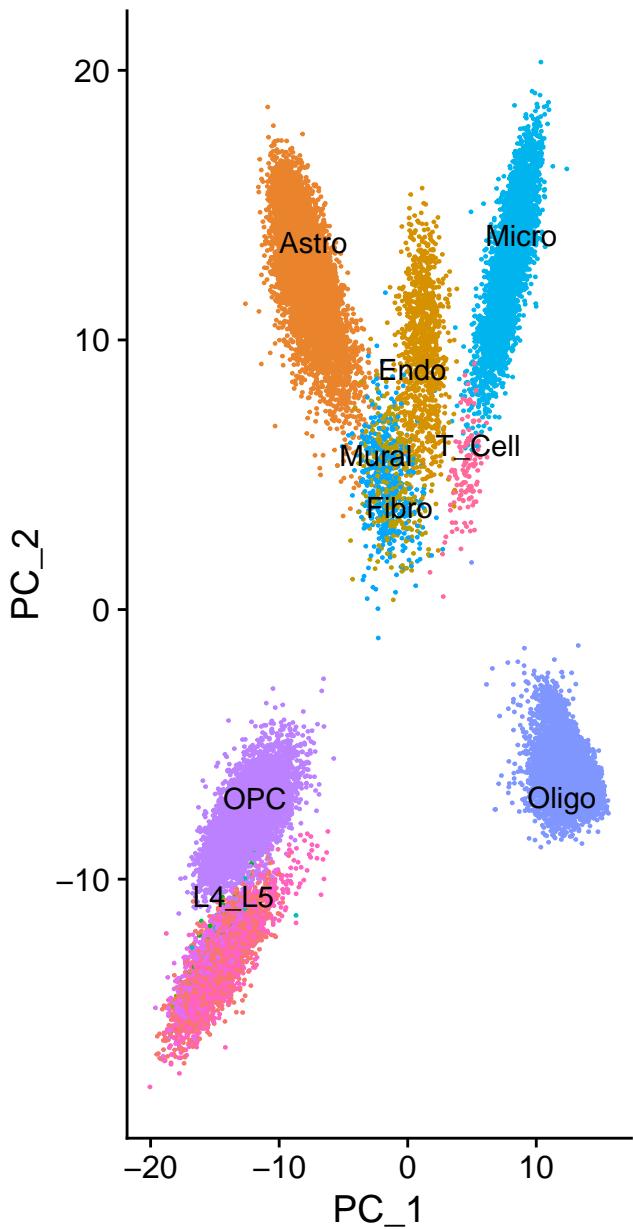


# dataset

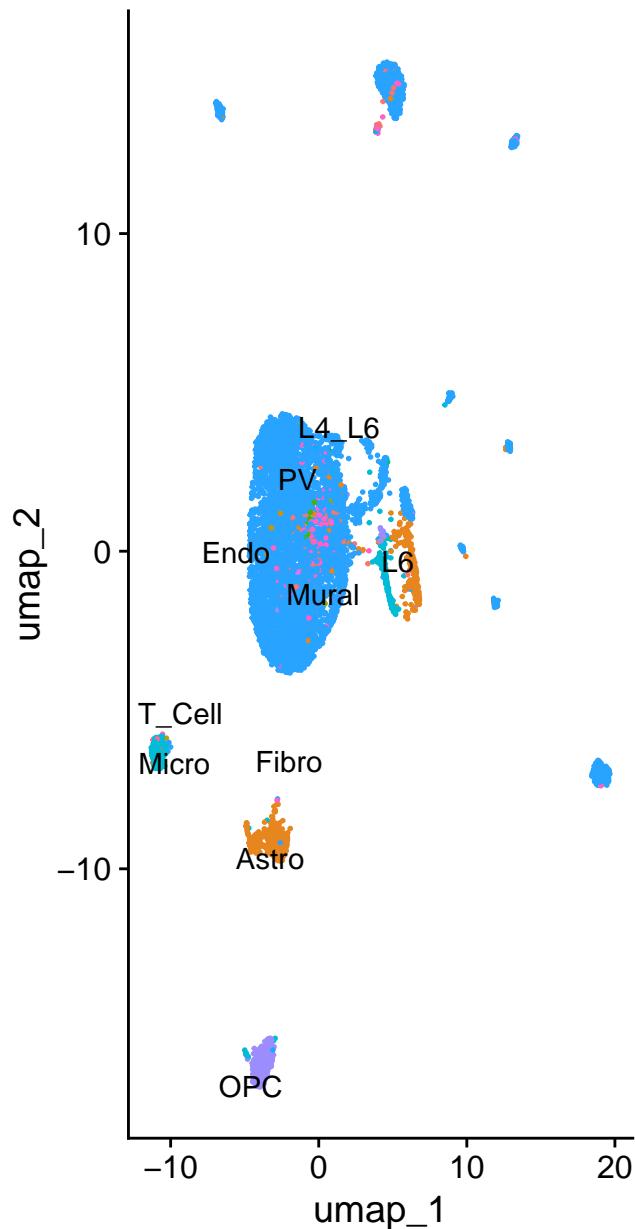


**GFAP****AQP4****VEGFA****VEGFB****SHTN1**

### scRNA-seq



### scATAC-seq



# **prediction.score.max**

