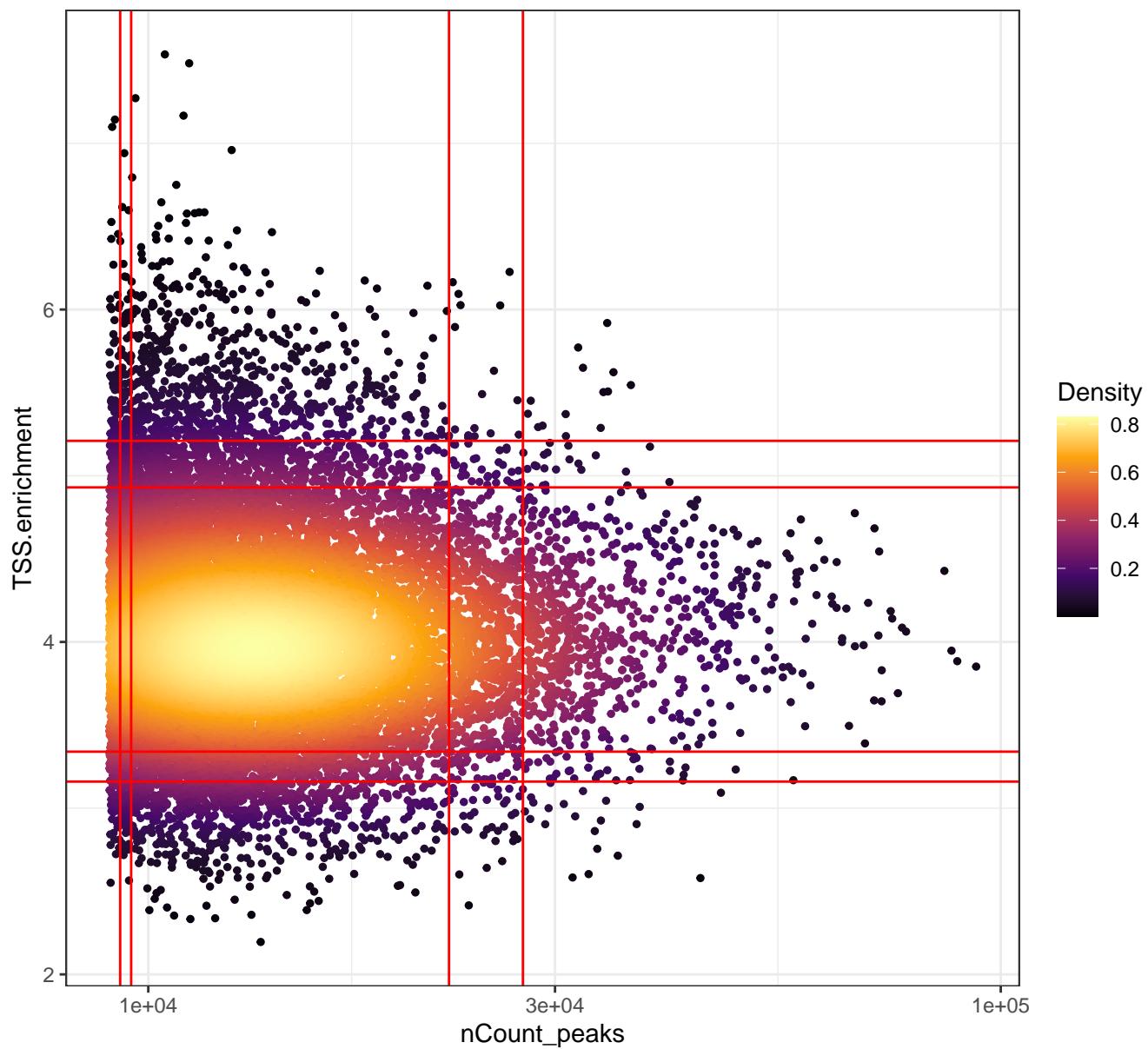


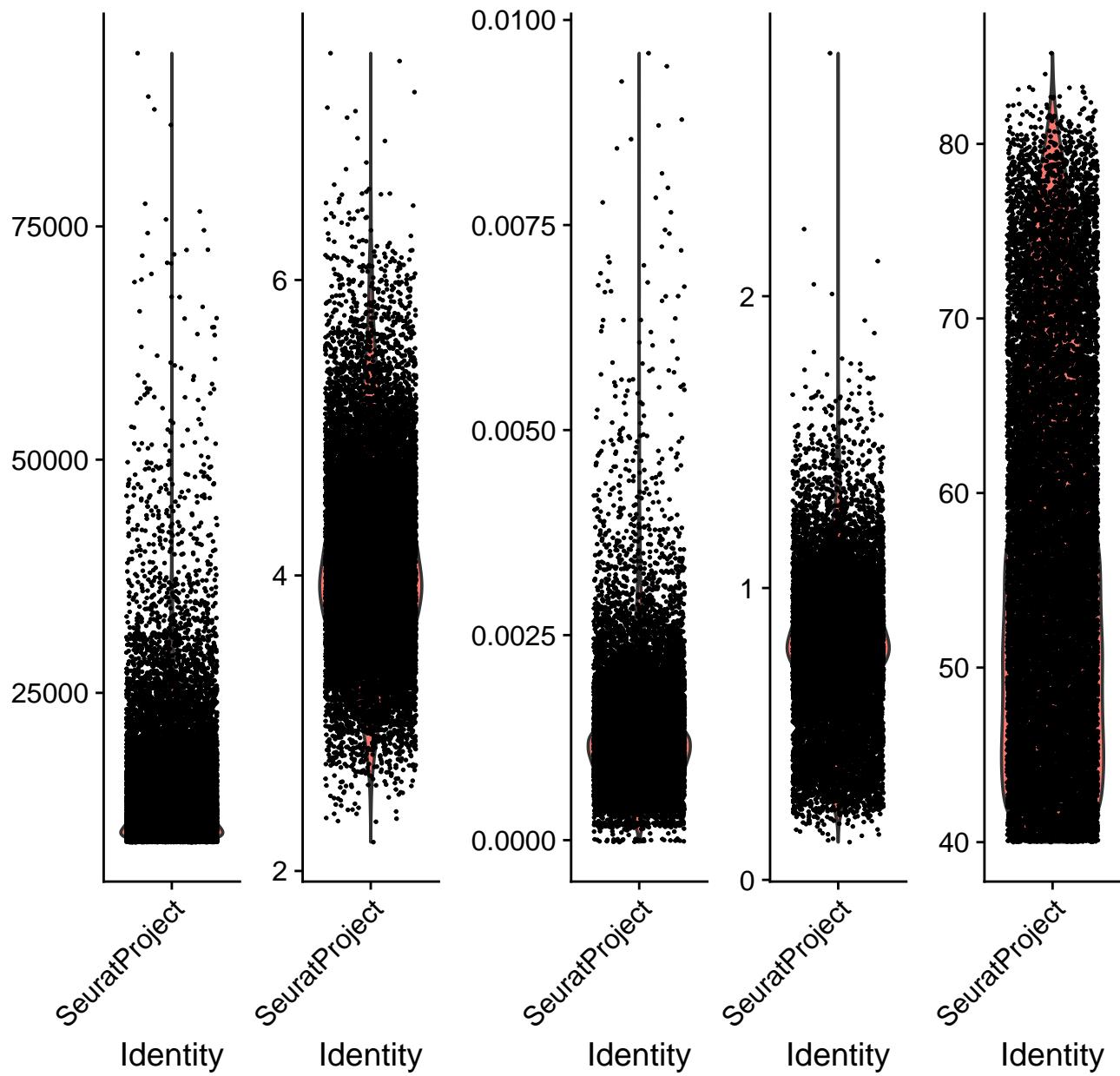
Quantiles

nCount_peaks: 5%:9269 10%:9548 90%:22530.6 95%:27509

TSS.enrichment: 5%:3.16 10%:3.34 90%:4.93 95%:5.21

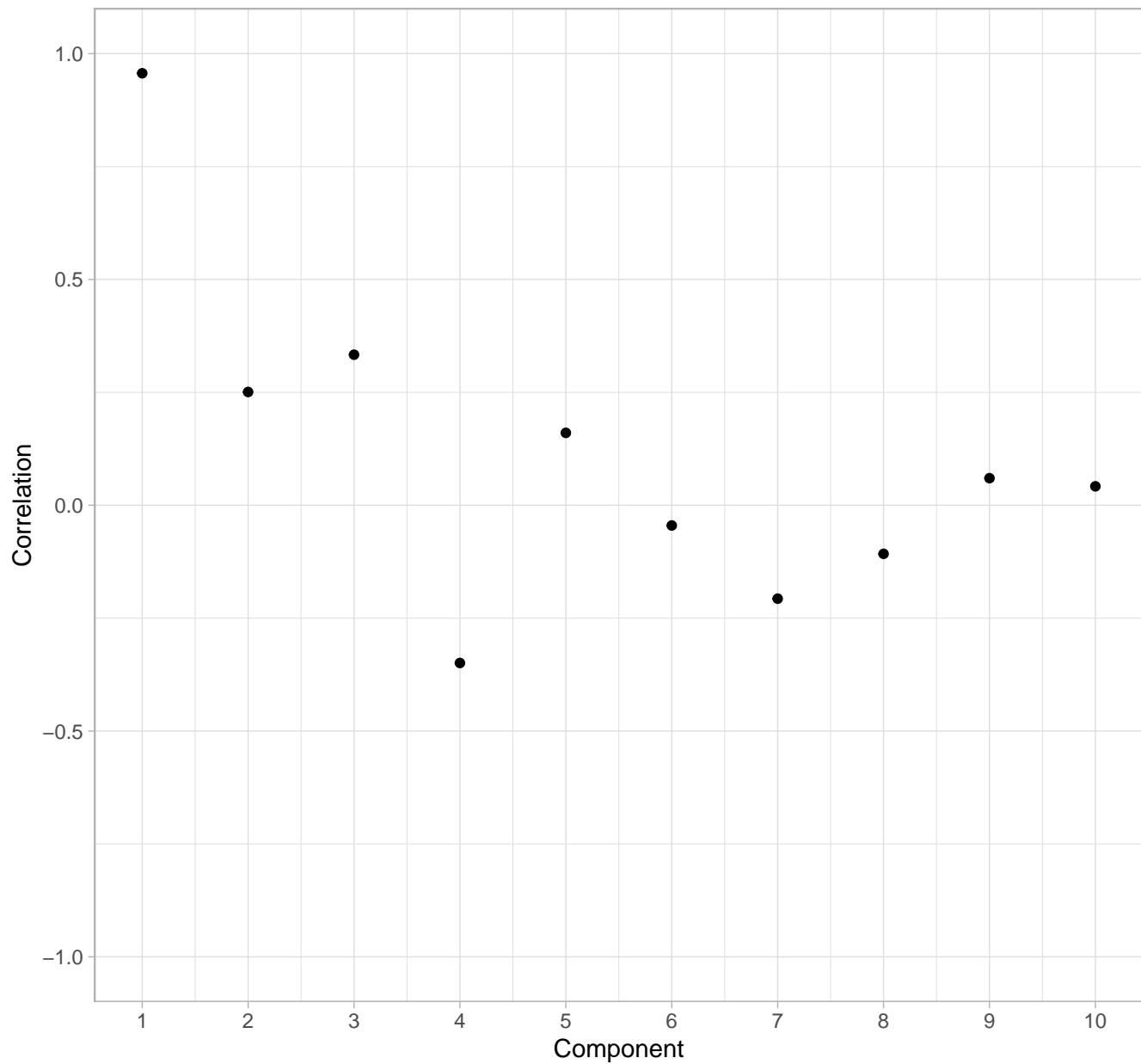


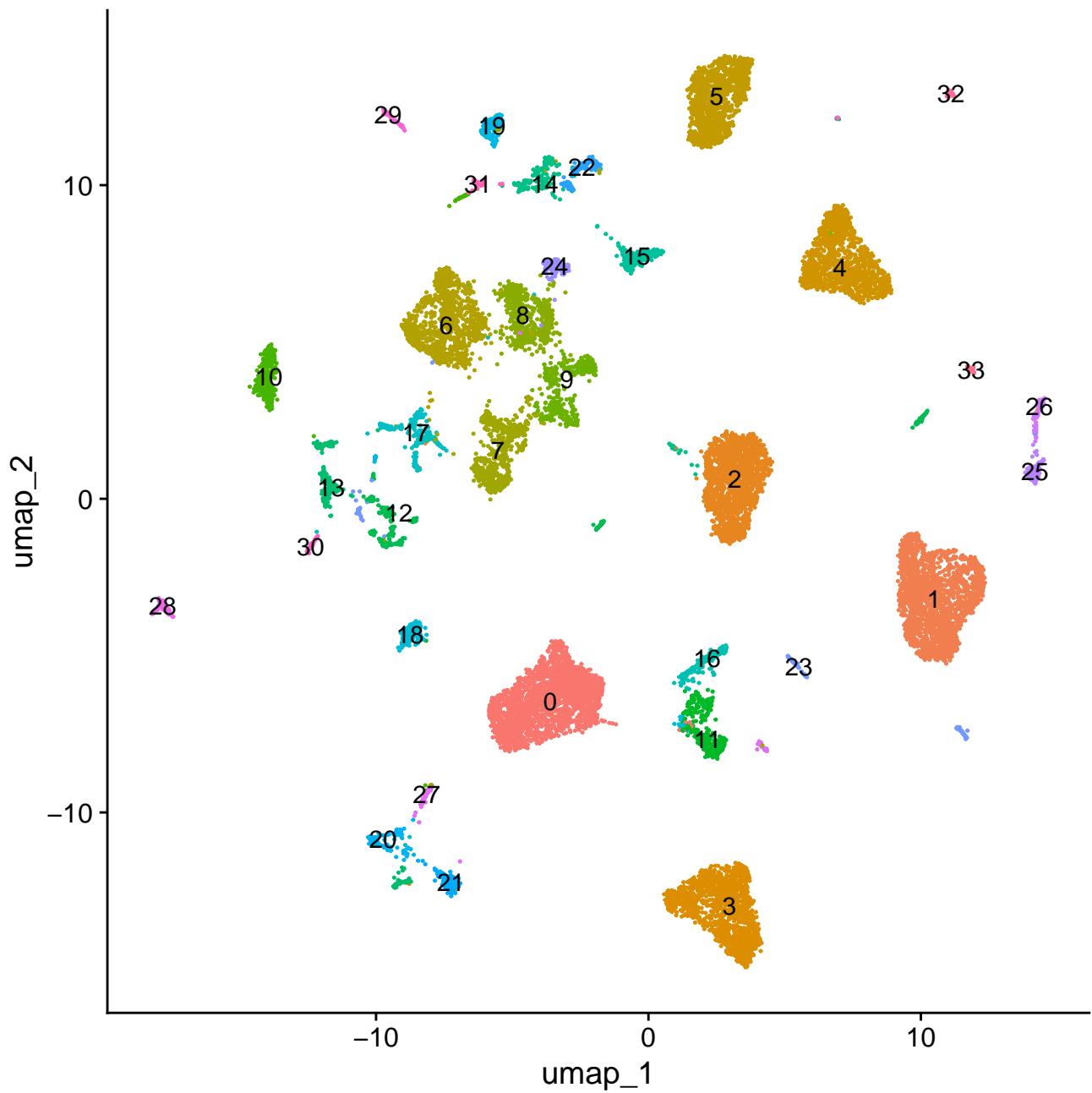
nCount_p <= 8. enrichment blacklist nuleosome psig reads_in_p



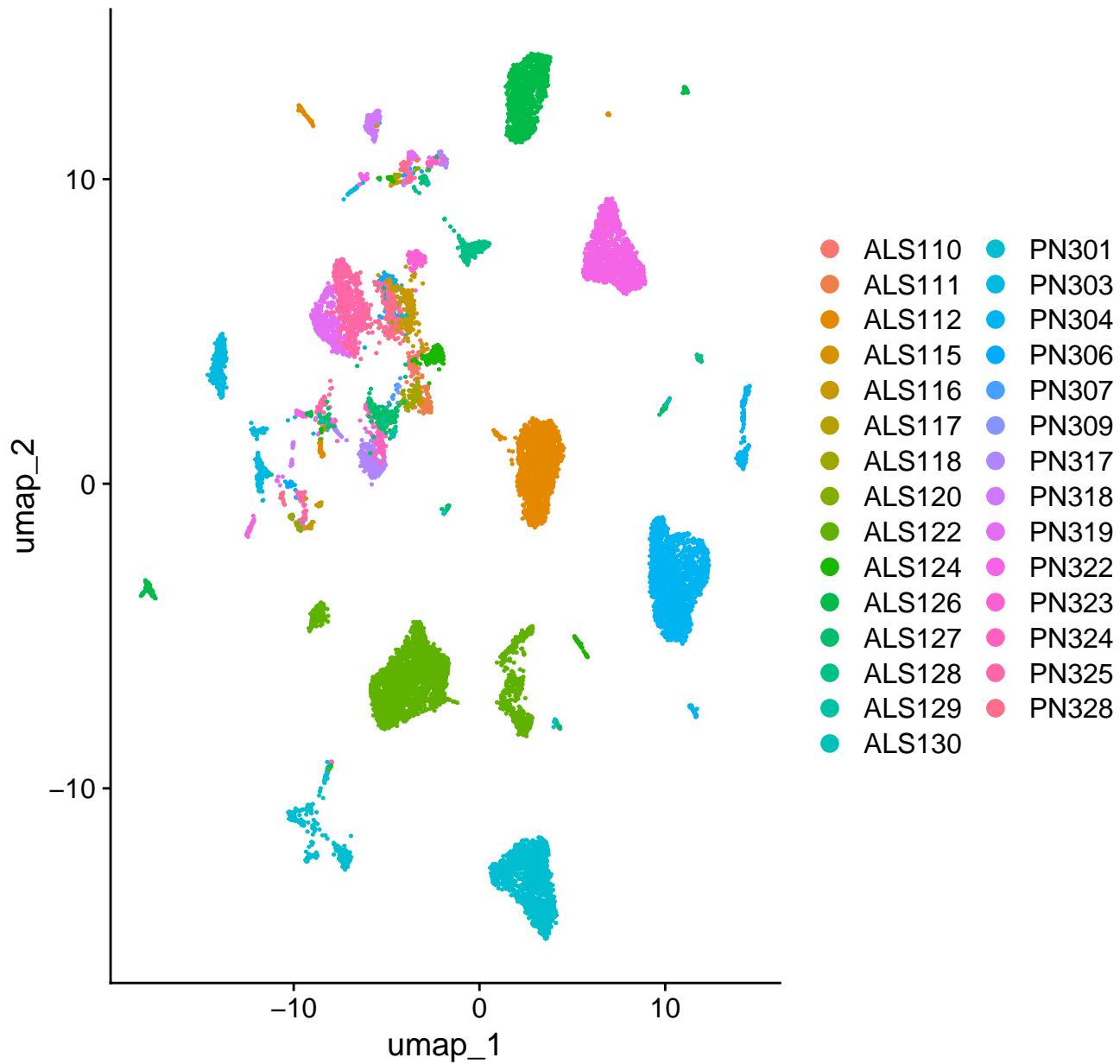
Correlation between depth and reduced dimension components

Assay: peaks Reduction: lsi

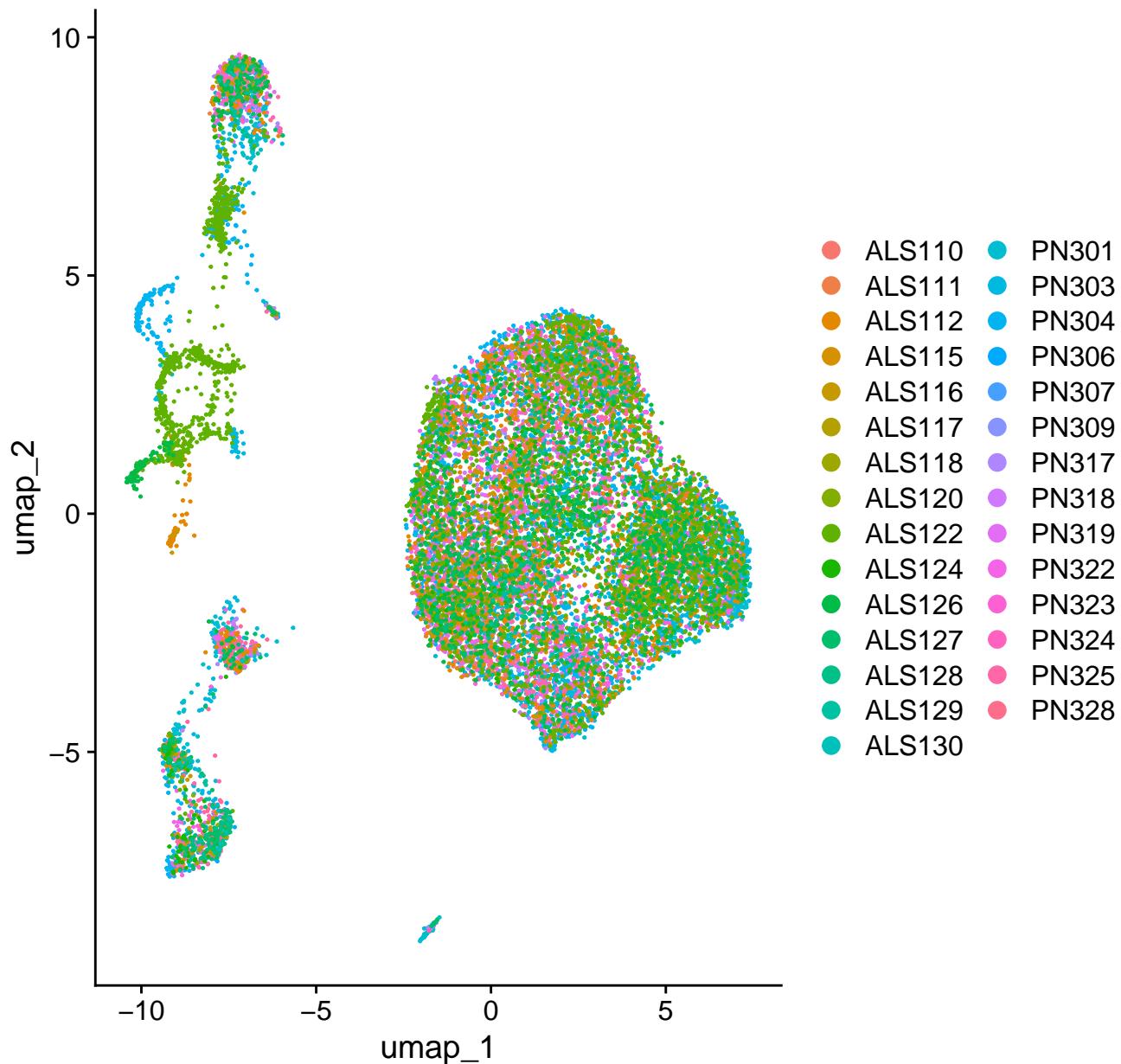


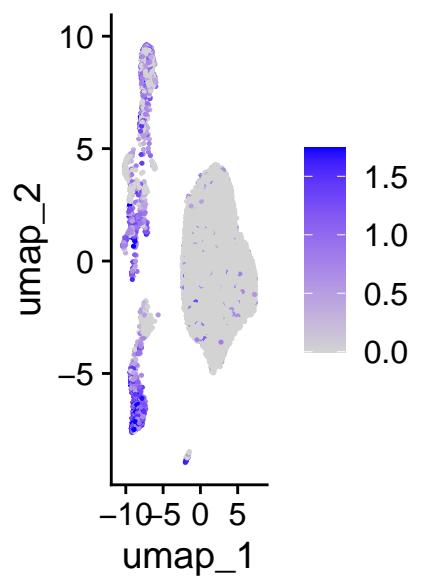
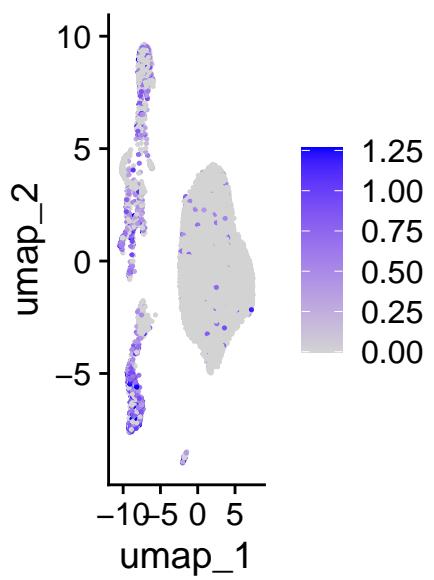
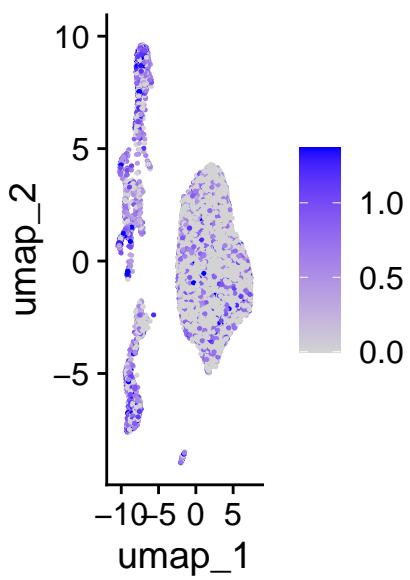
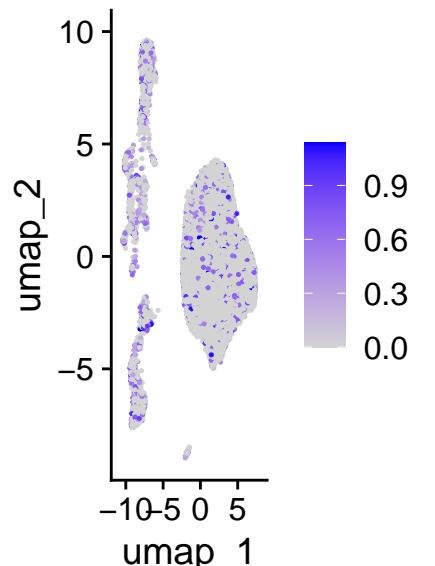
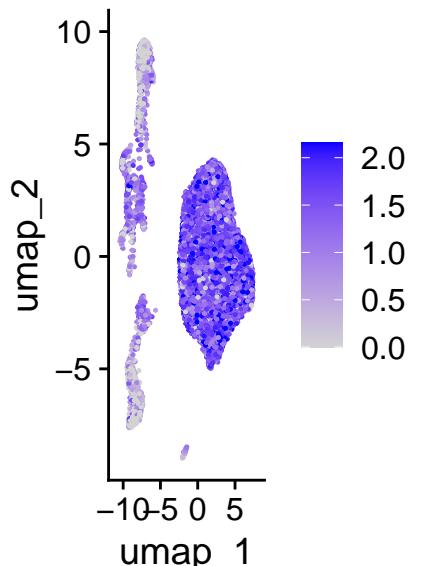


dataset

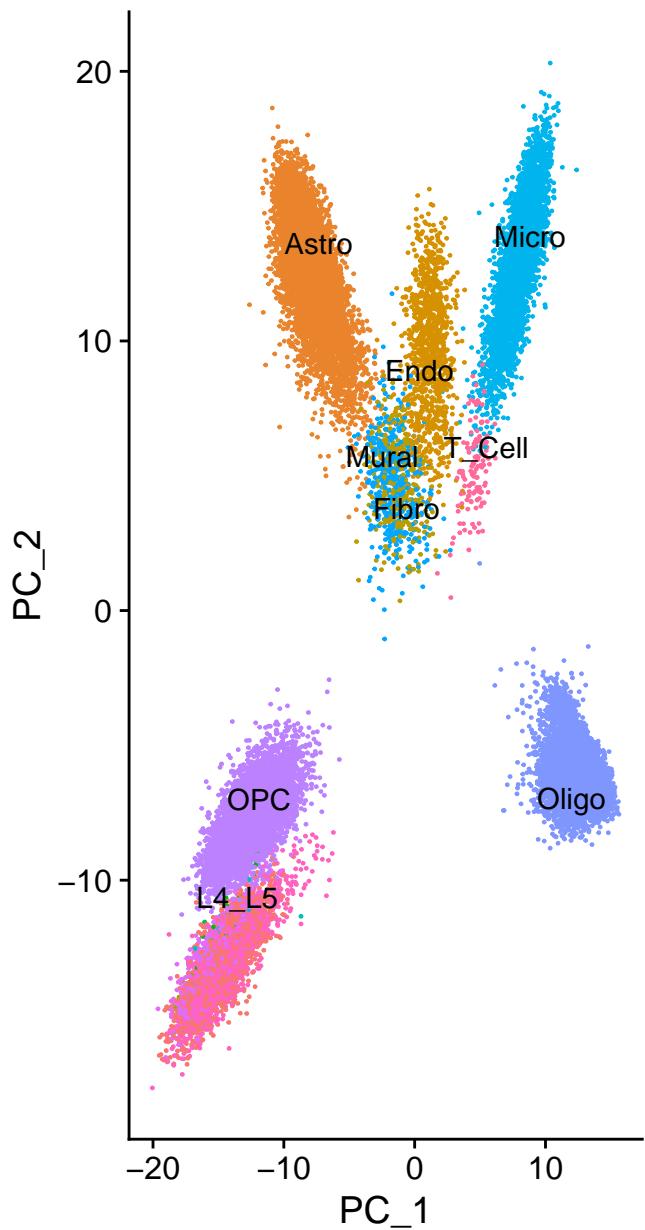


dataset

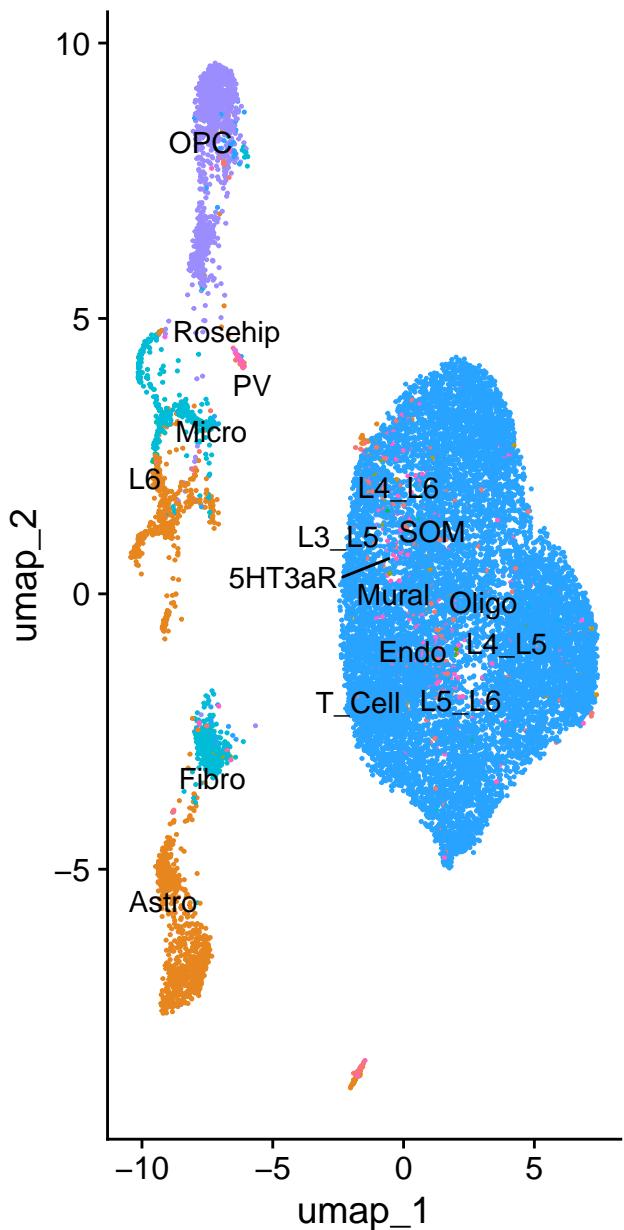


GFAP**AQP4****VEGFA****VEGFB****SHTN1**

scRNA-seq



scATAC-seq



prediction.score.max

