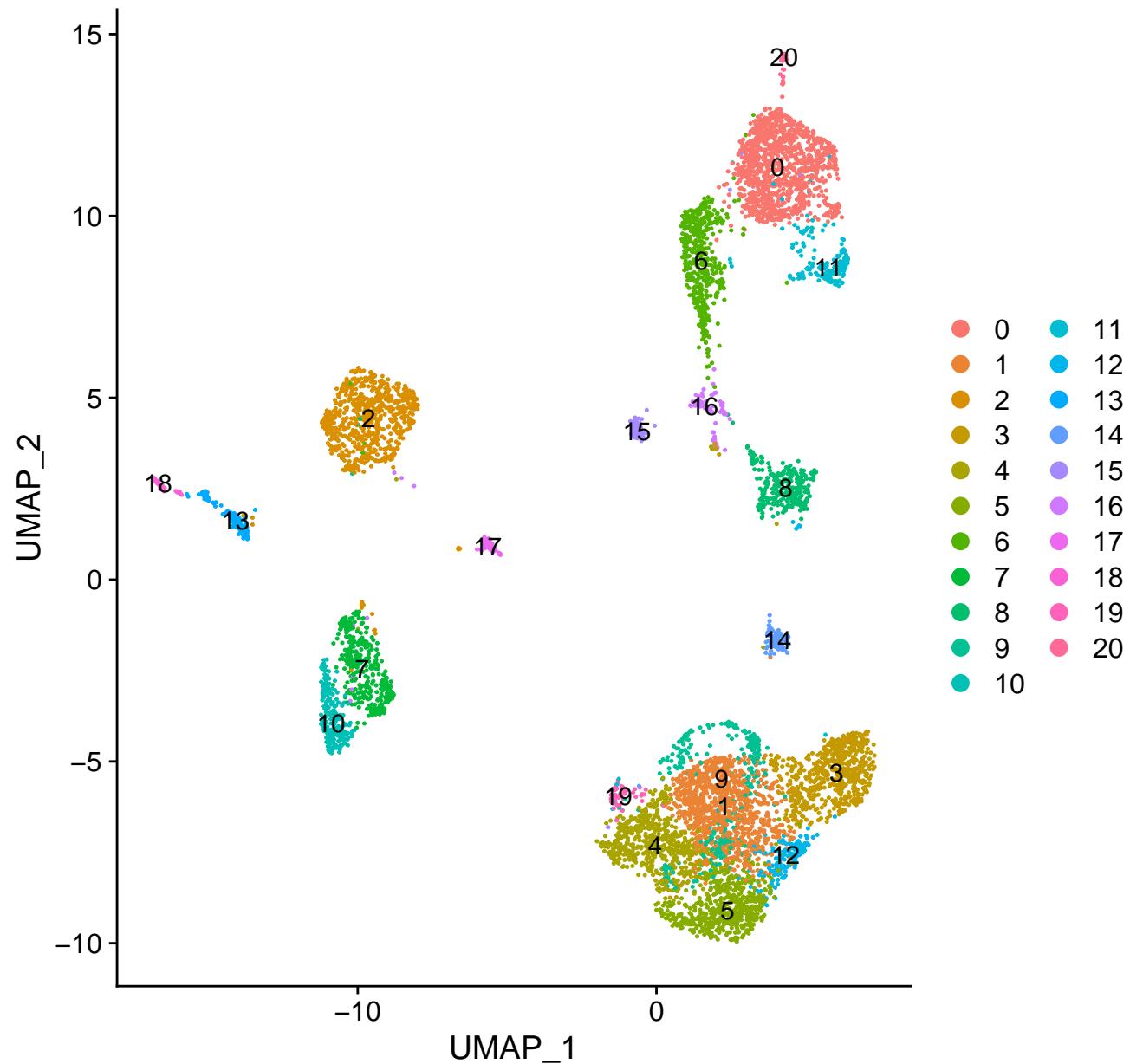
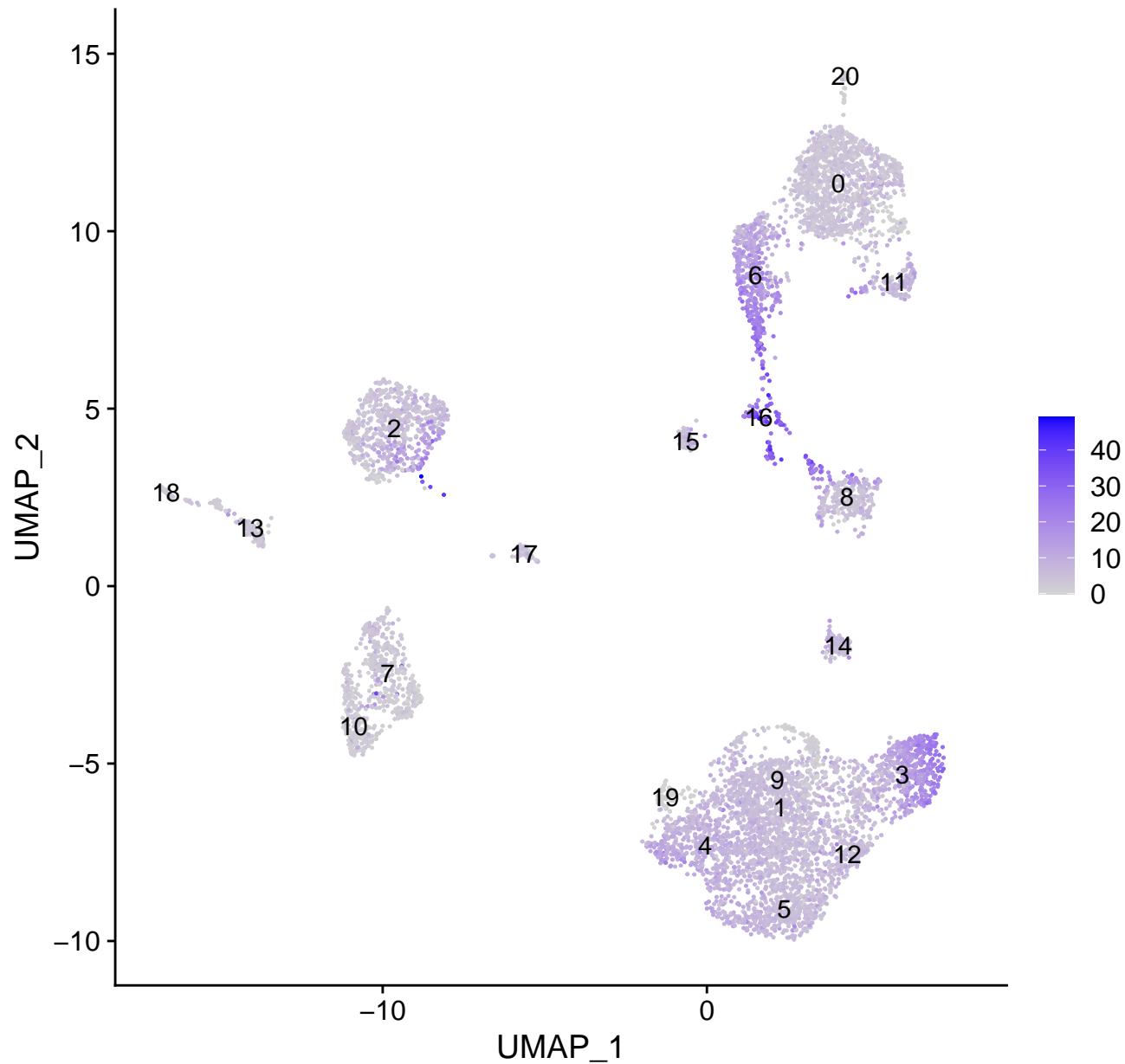


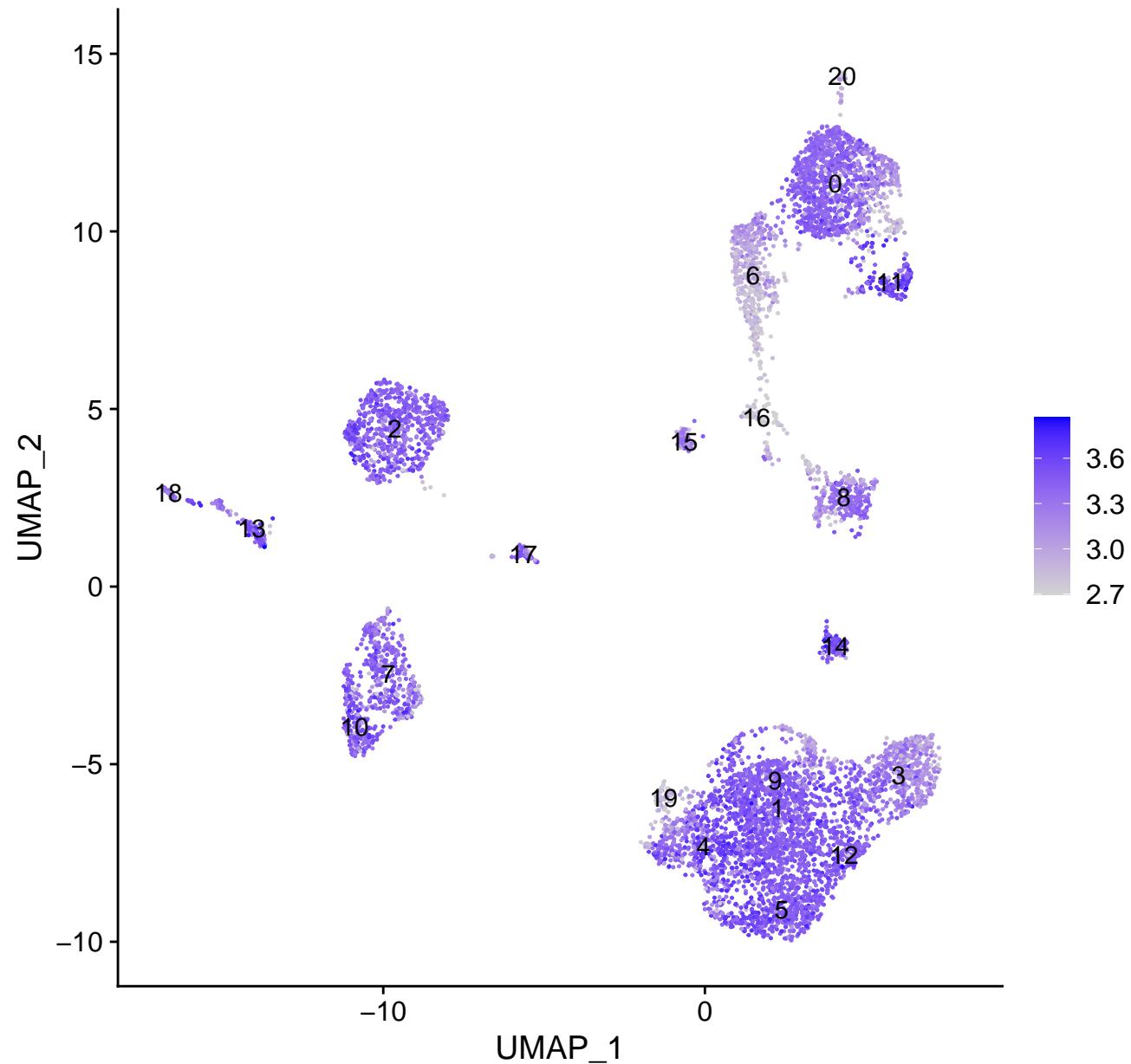
# MS18001 QC clusters



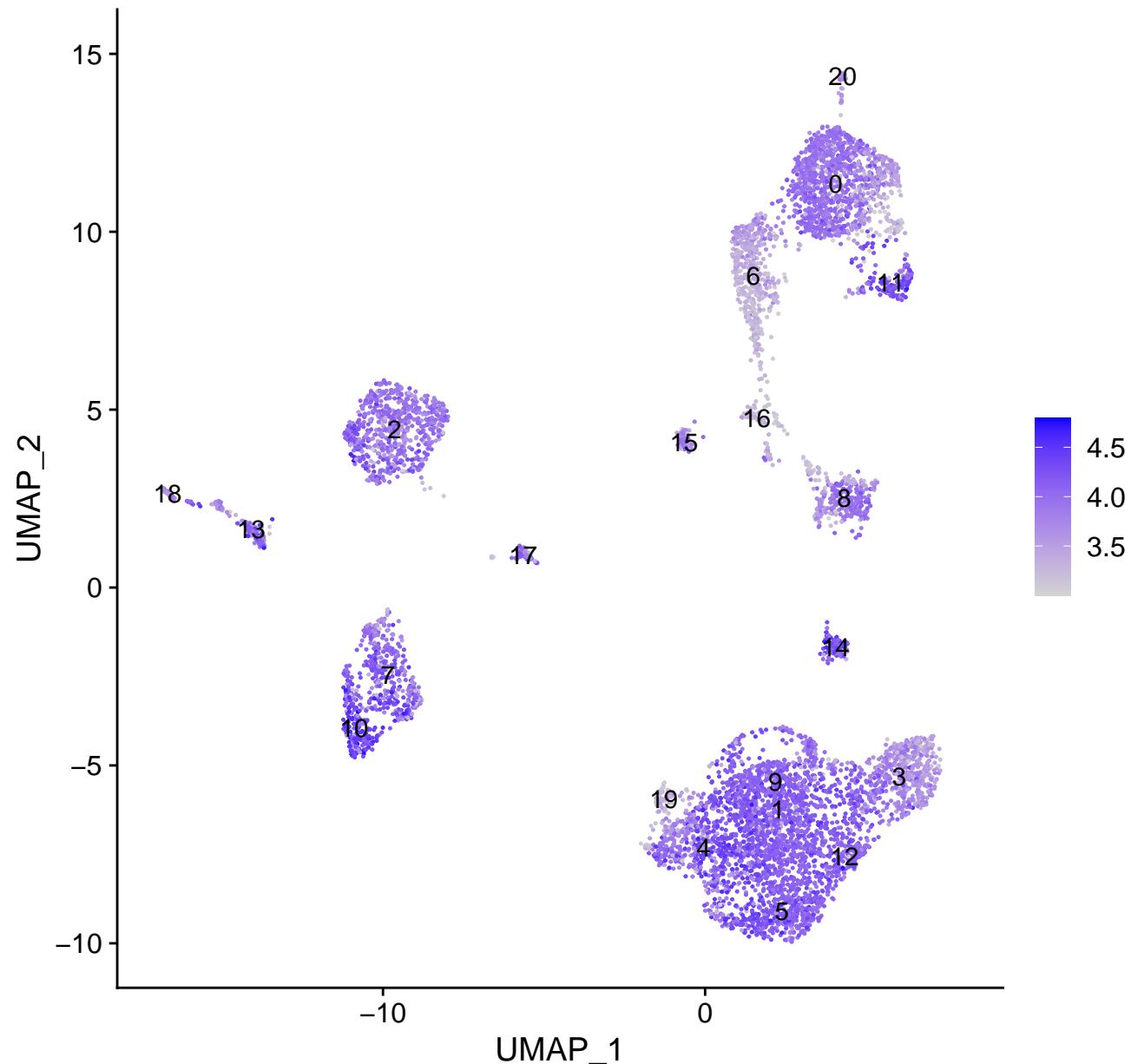
# MS18001 percent.mt



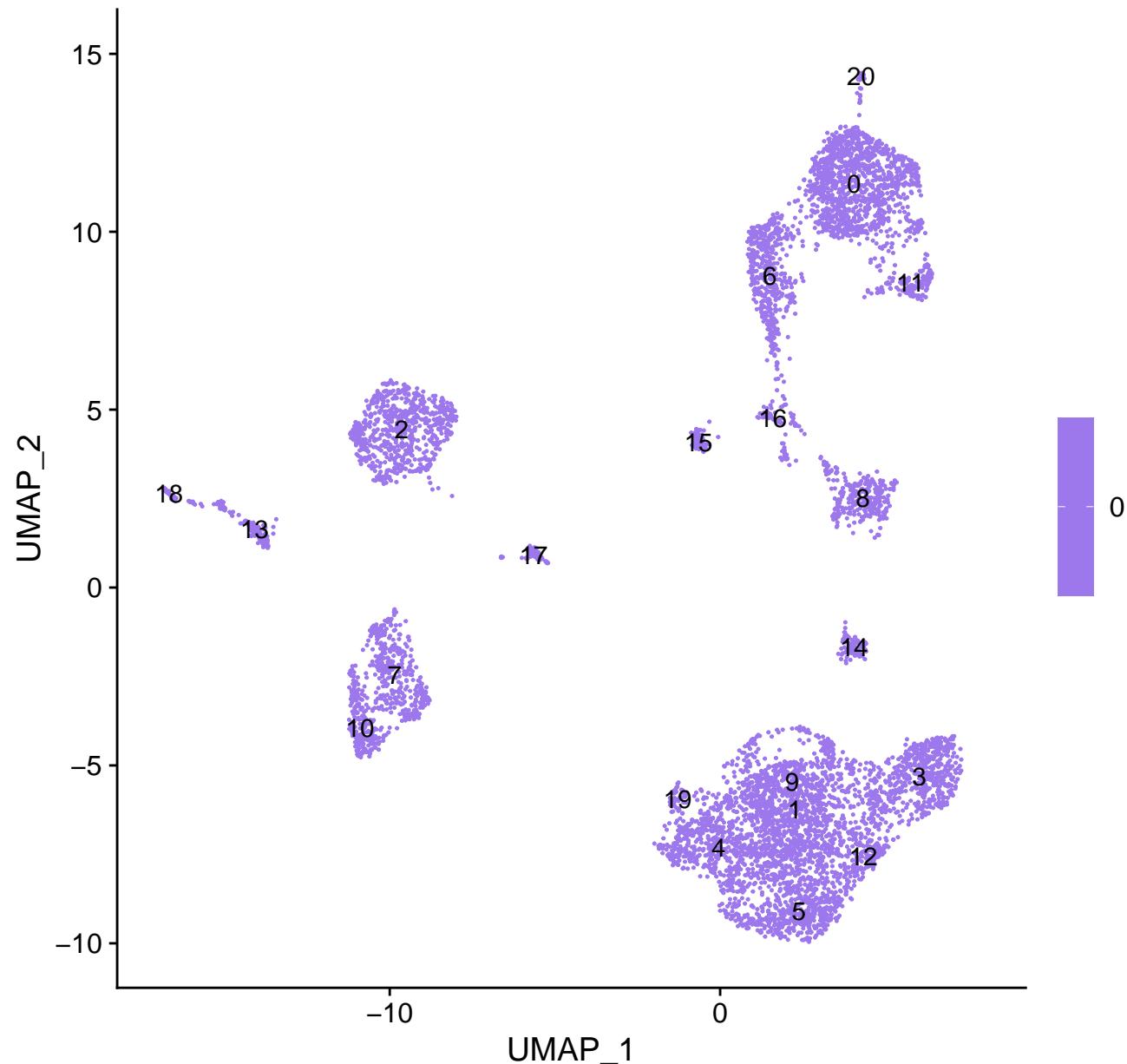
# MS18001 nFeature\_RNA



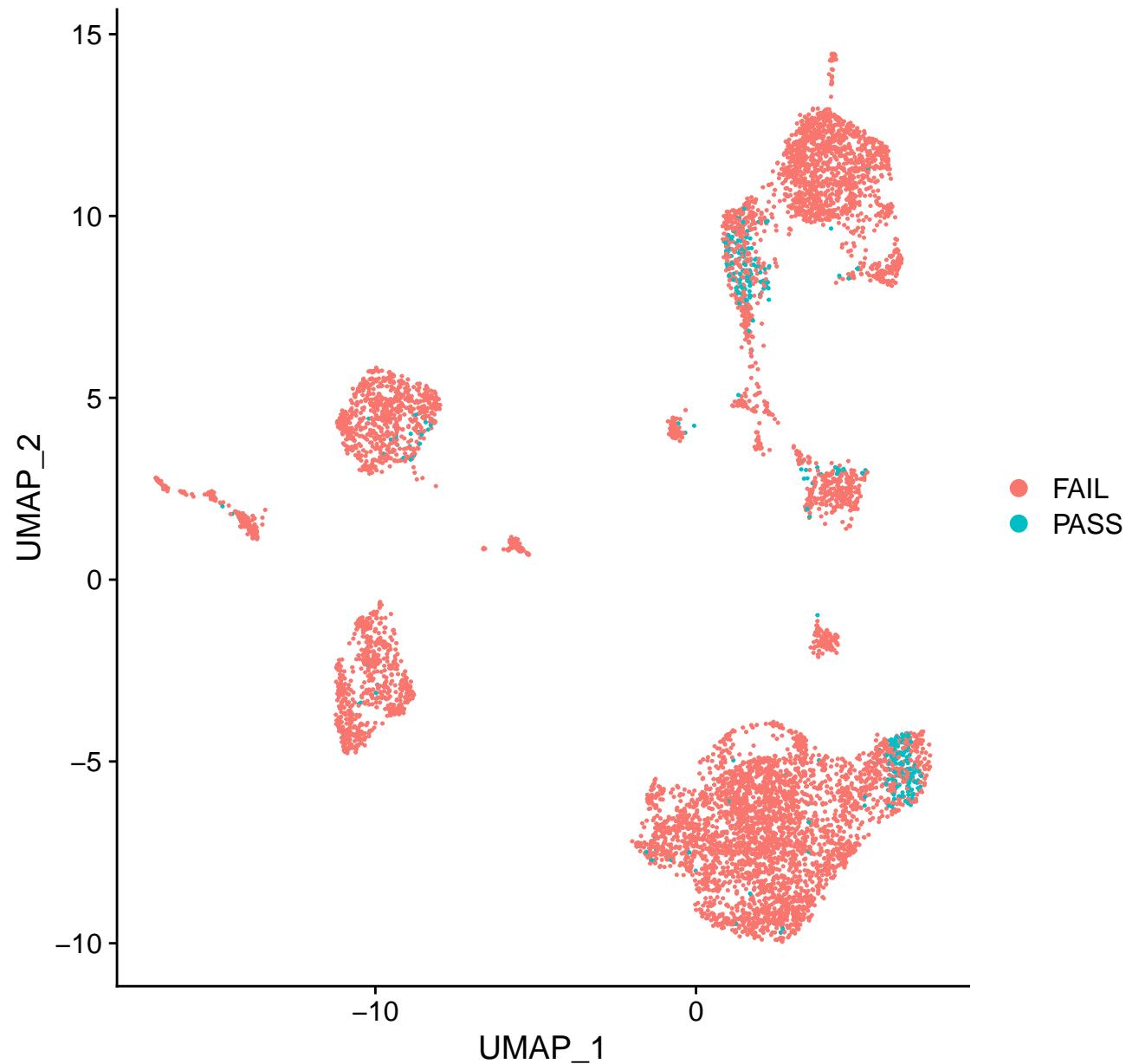
# MS18001 nCount\_RNA



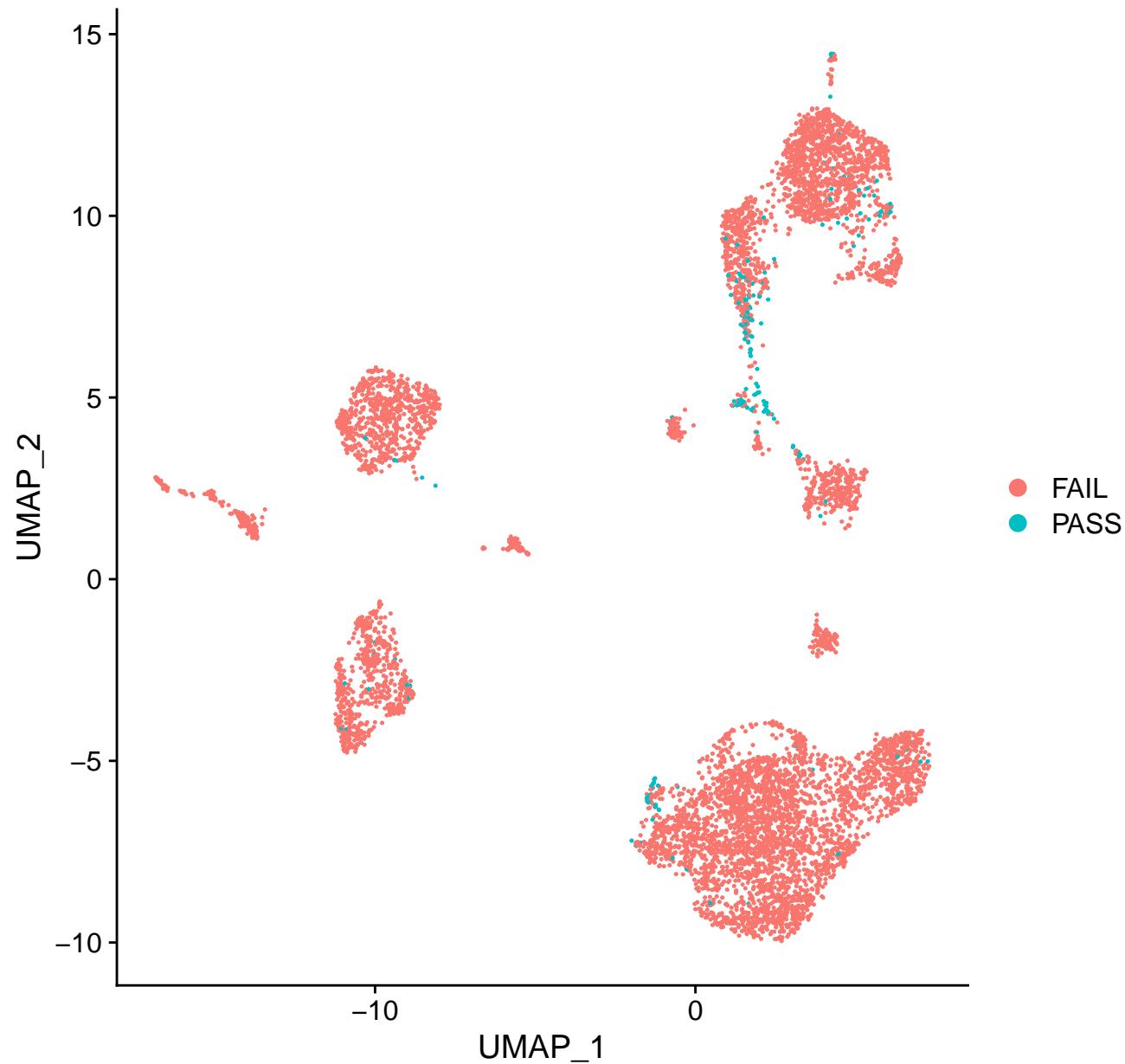
# MS18001 percent.hb



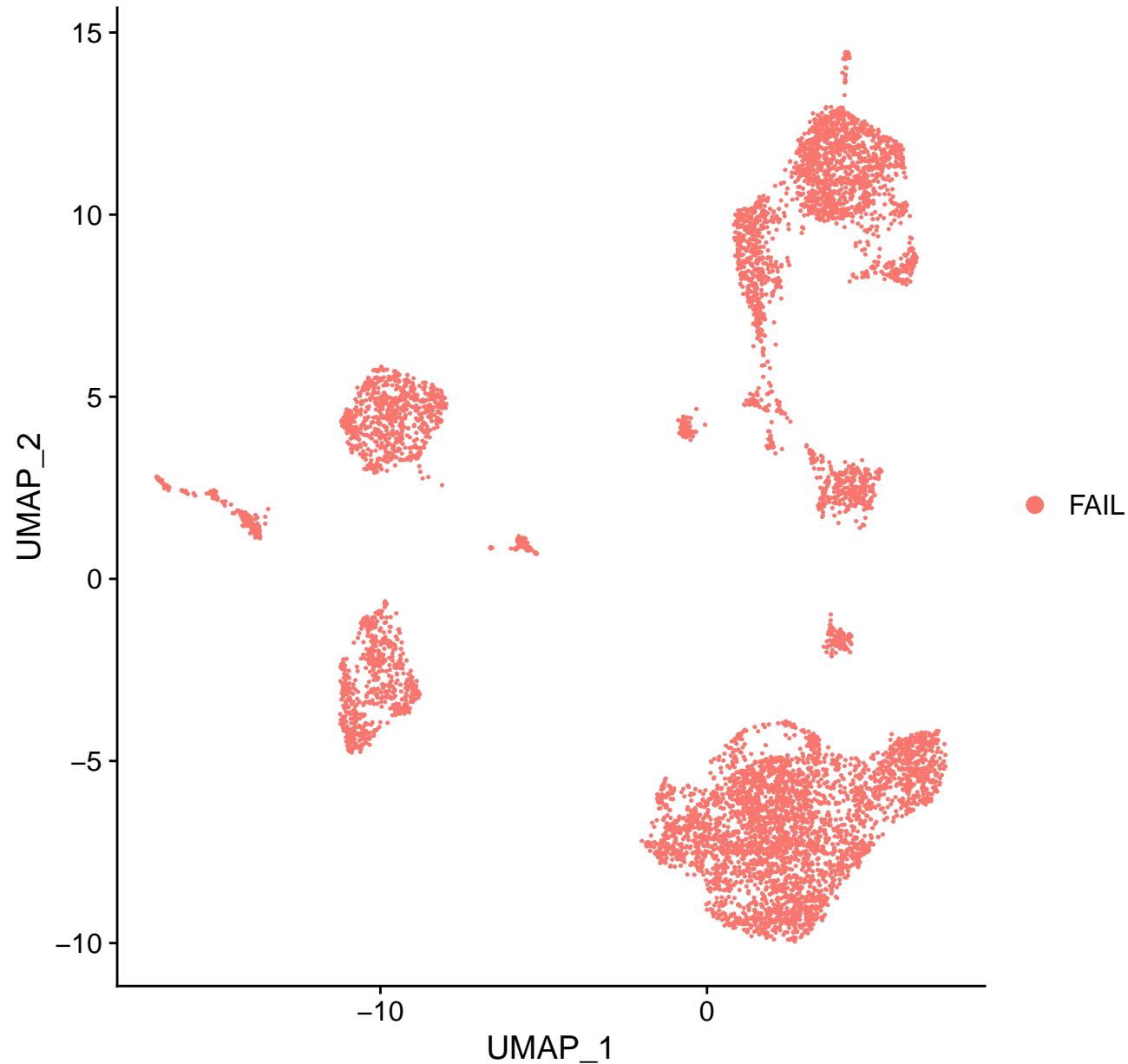
# MS18001 percent.mt (cutoffs)



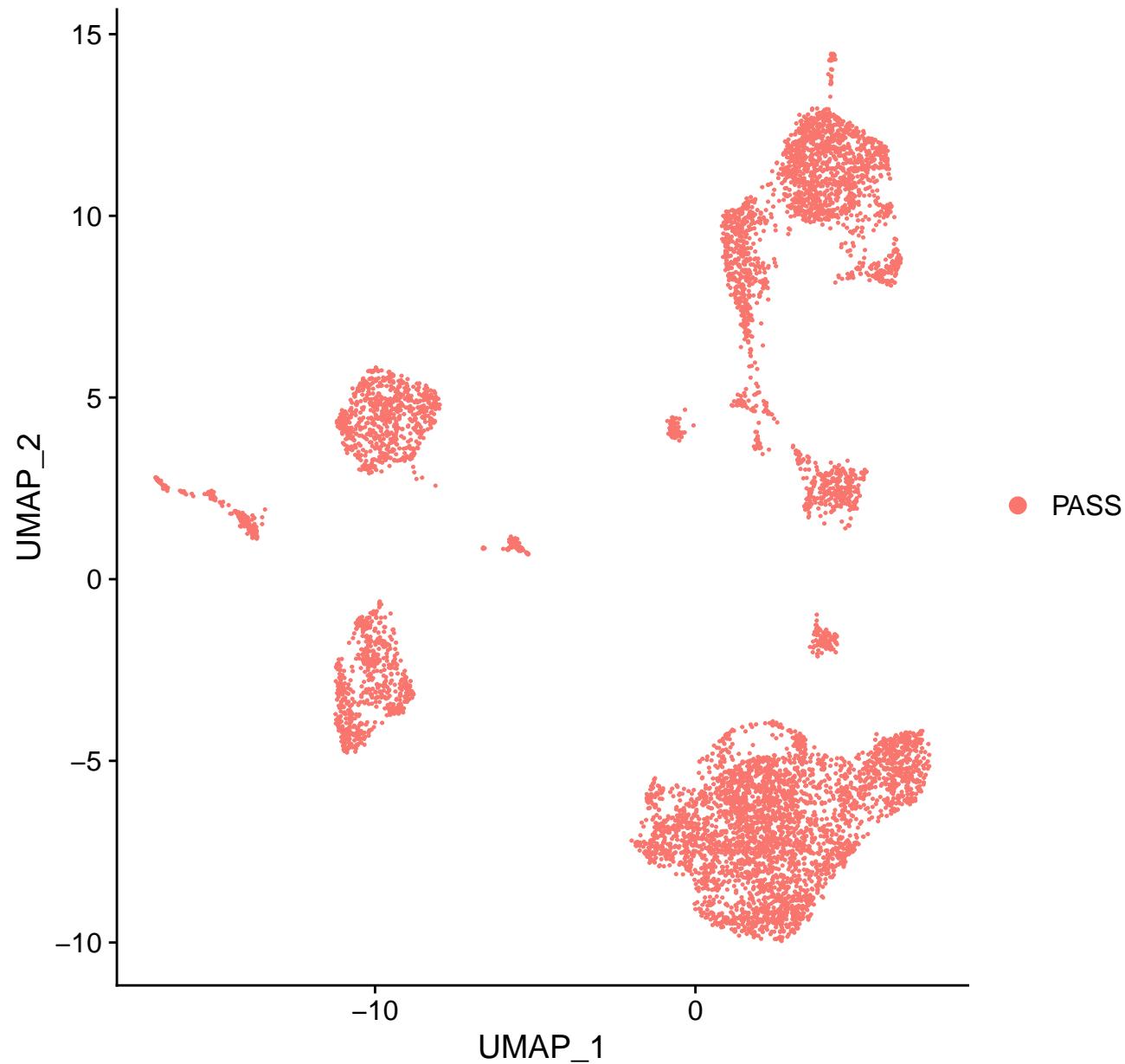
# MS18001 nFeature\_RNA (cutoffs)



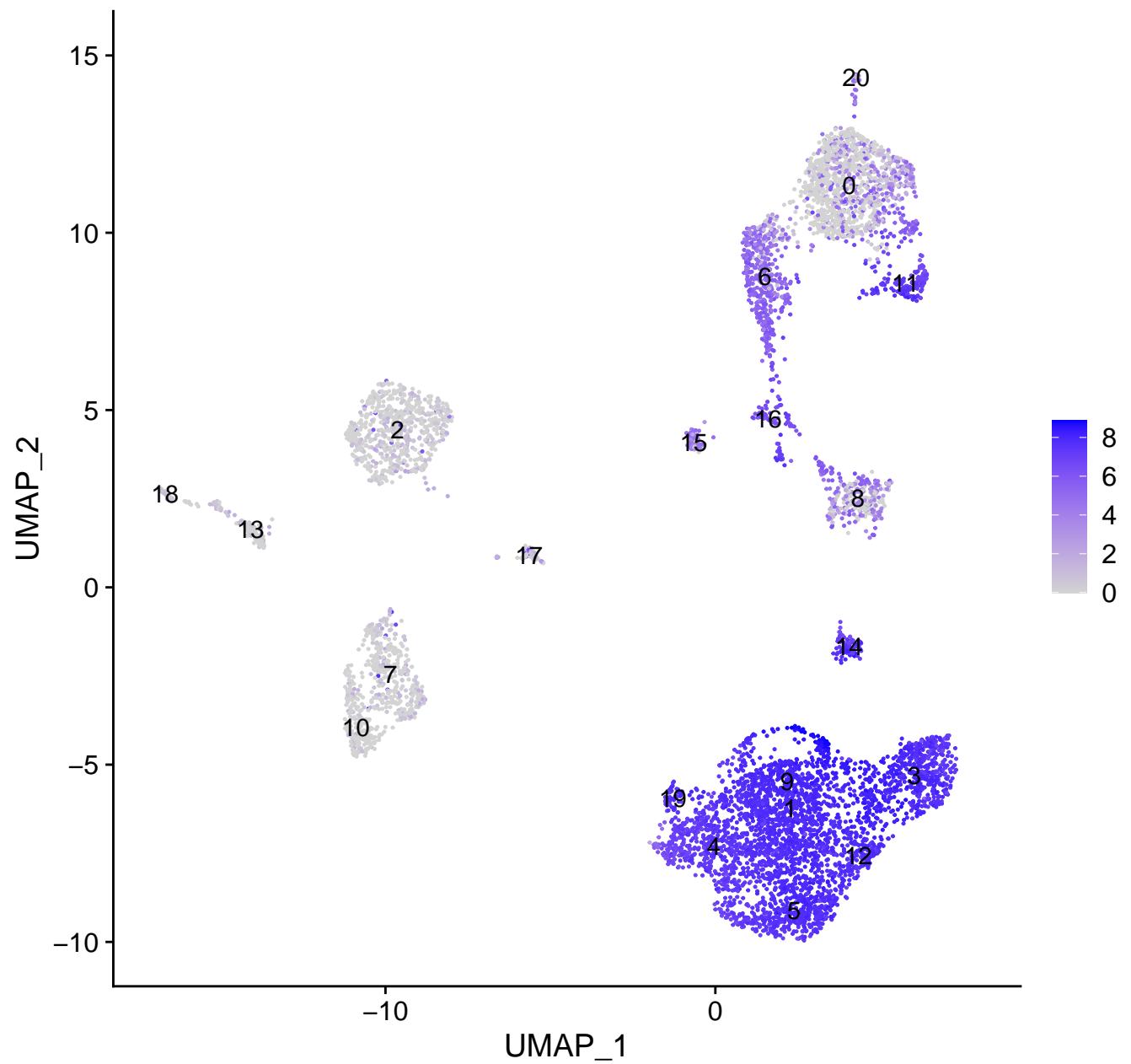
# MS18001 nCount\_RNA (cutoffs)



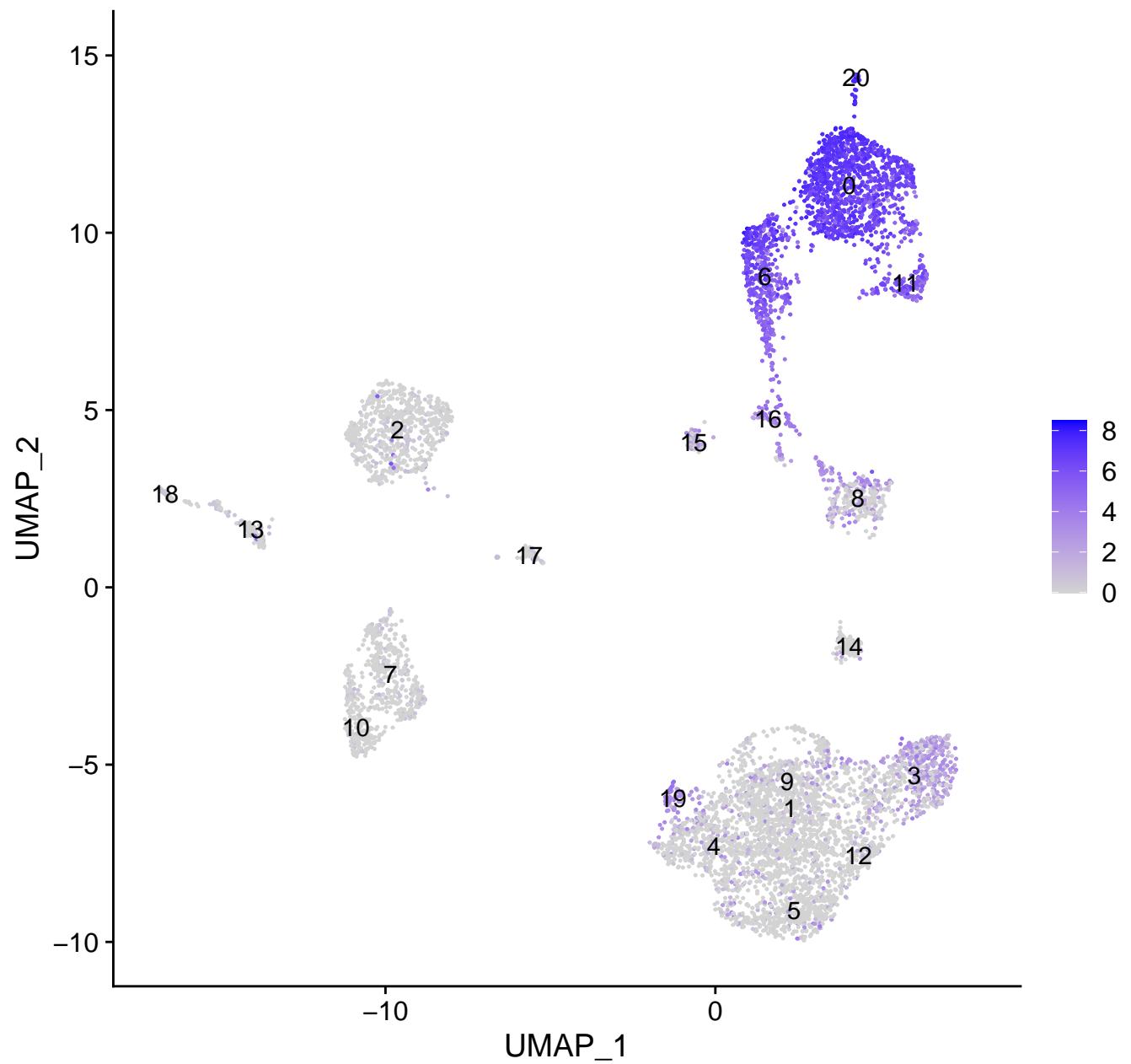
# MS18001 percent.hb (cutoffs)



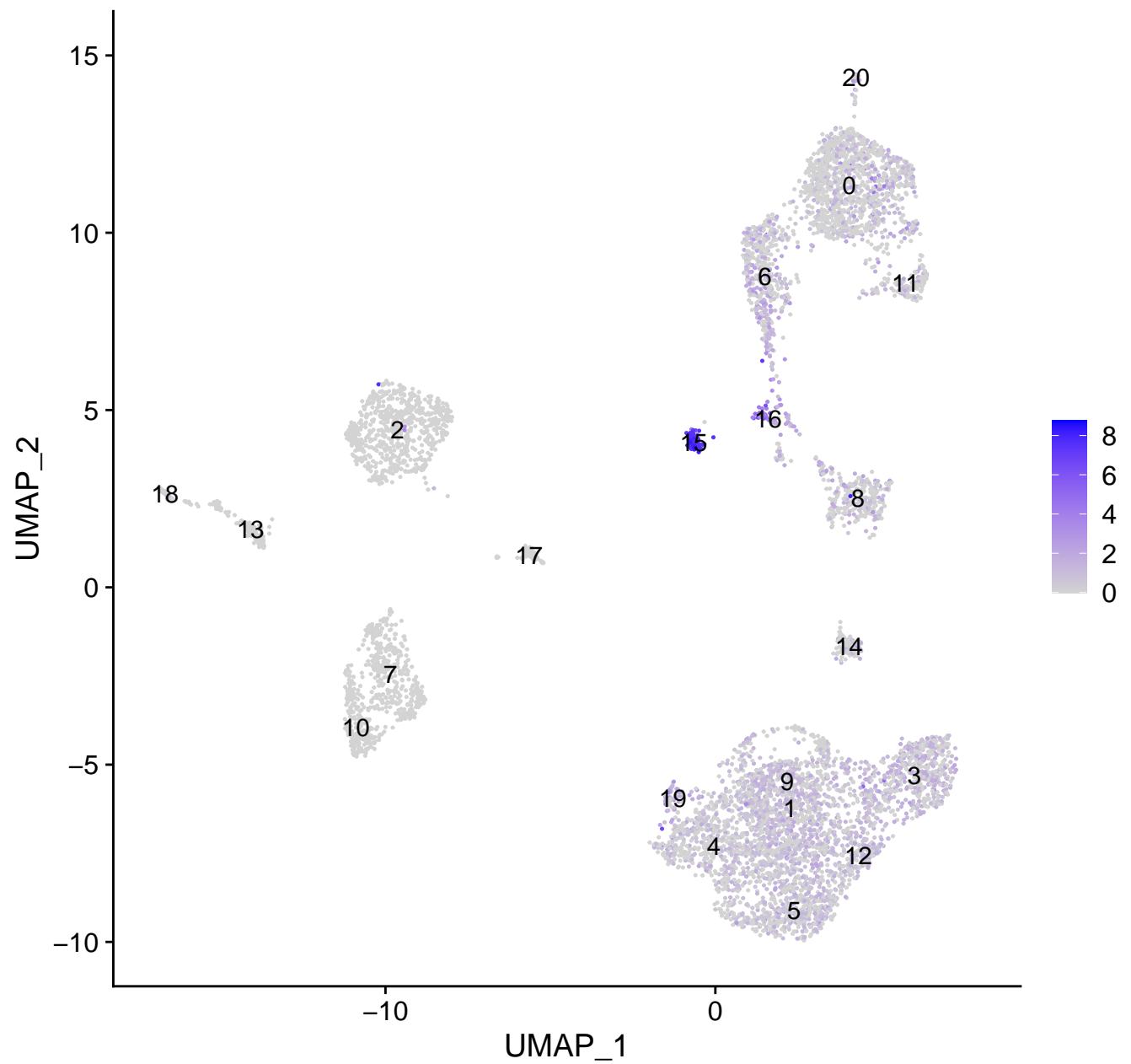
# INS



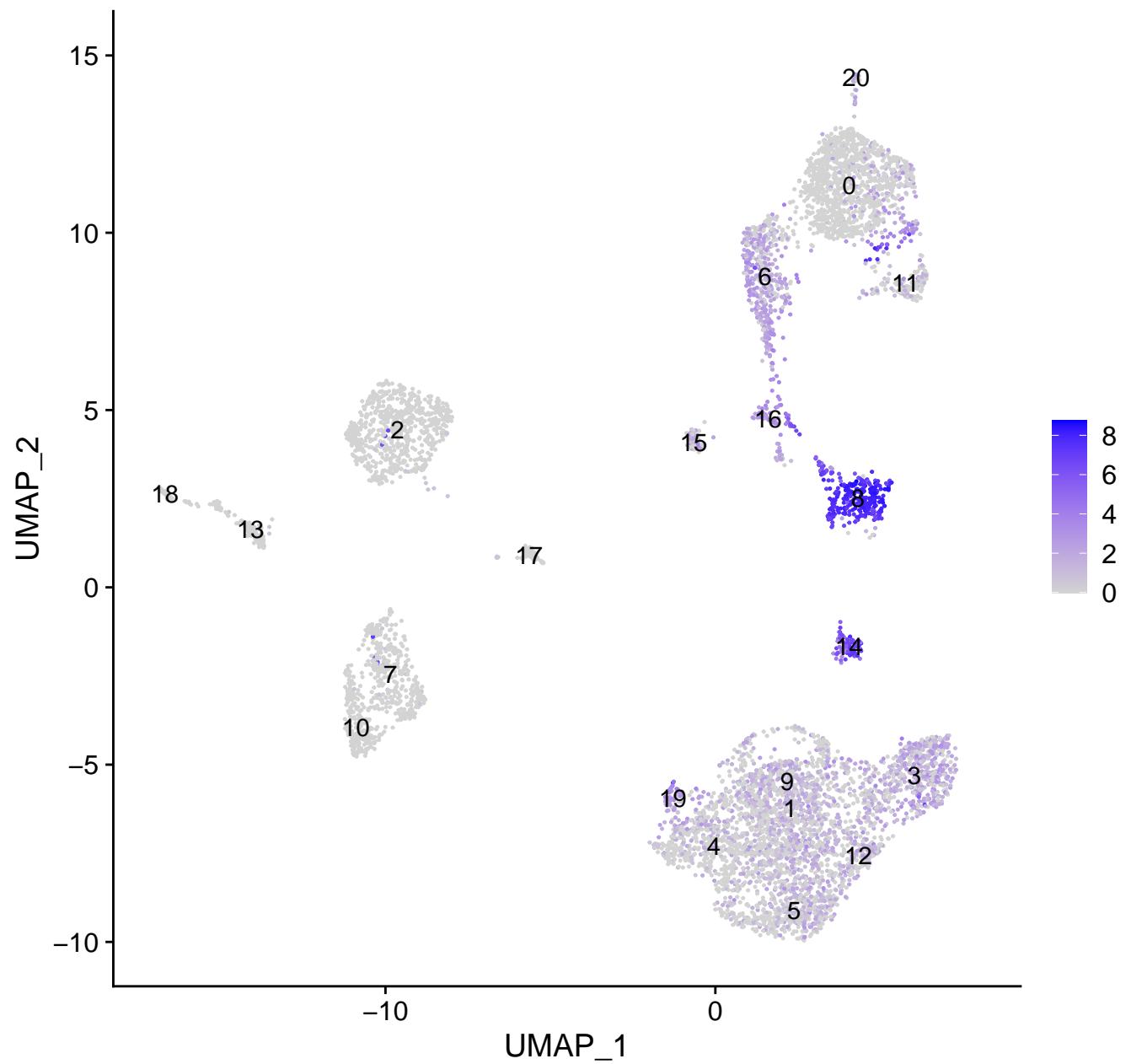
# GCG



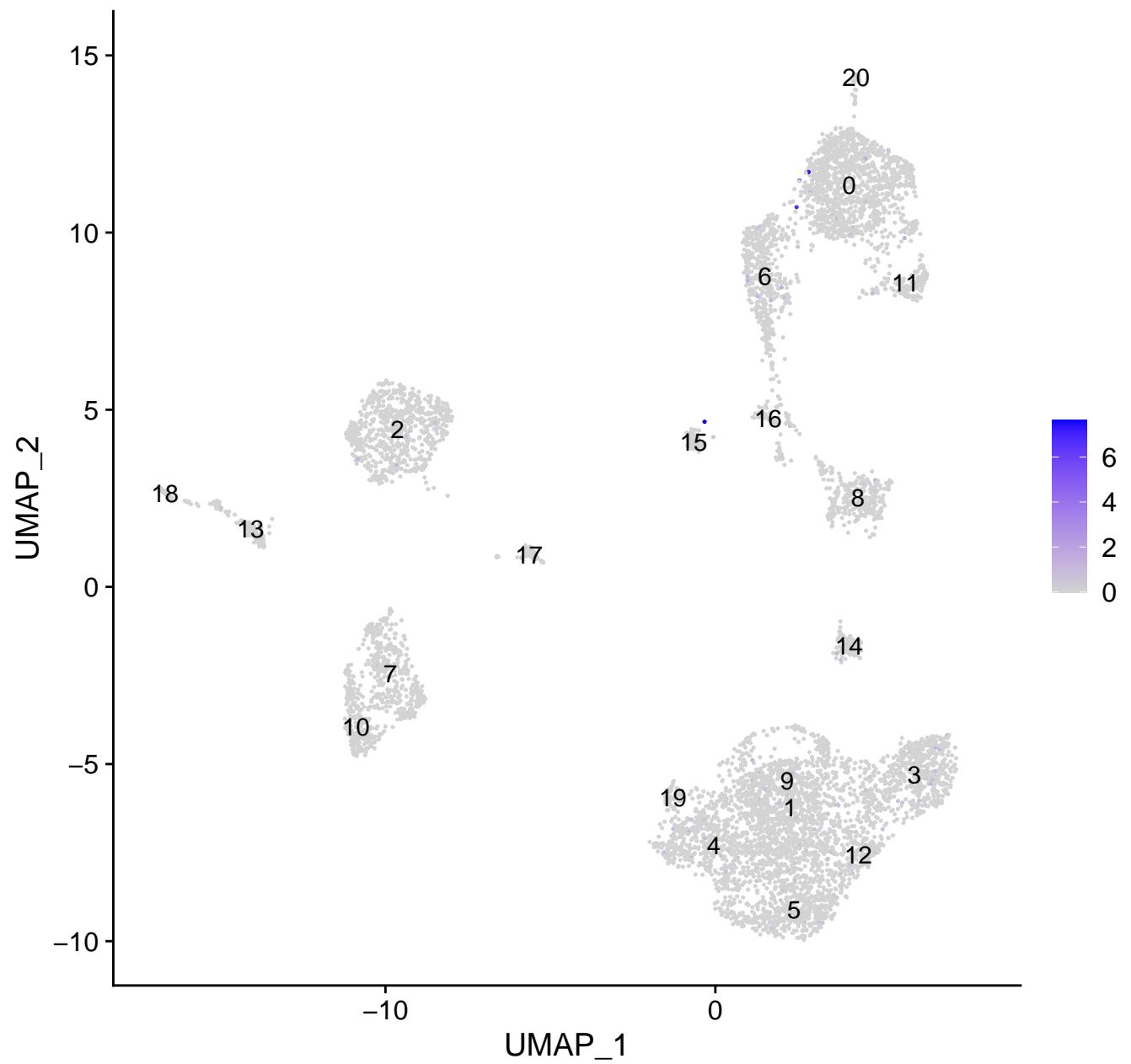
# PPY



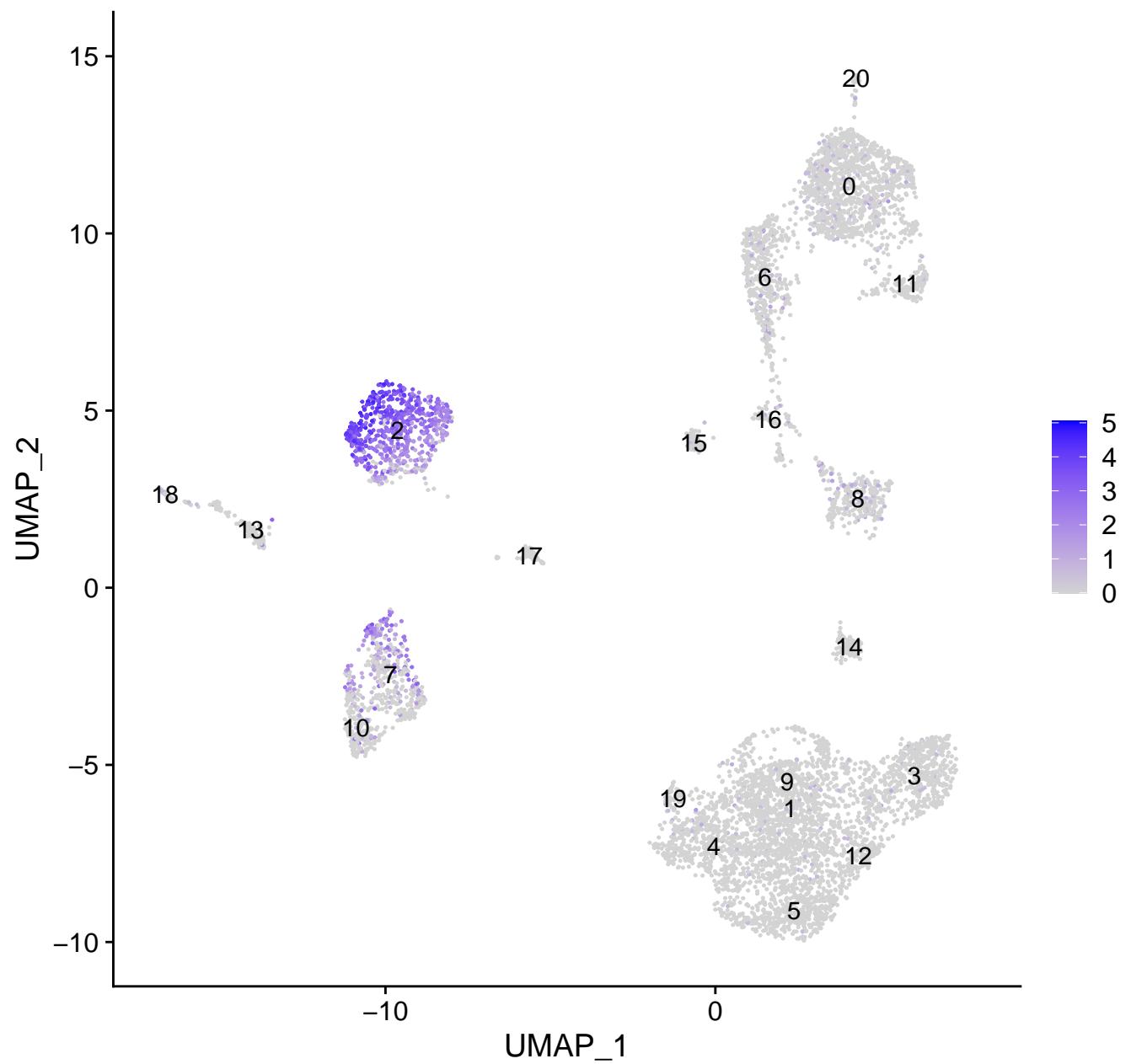
# SST



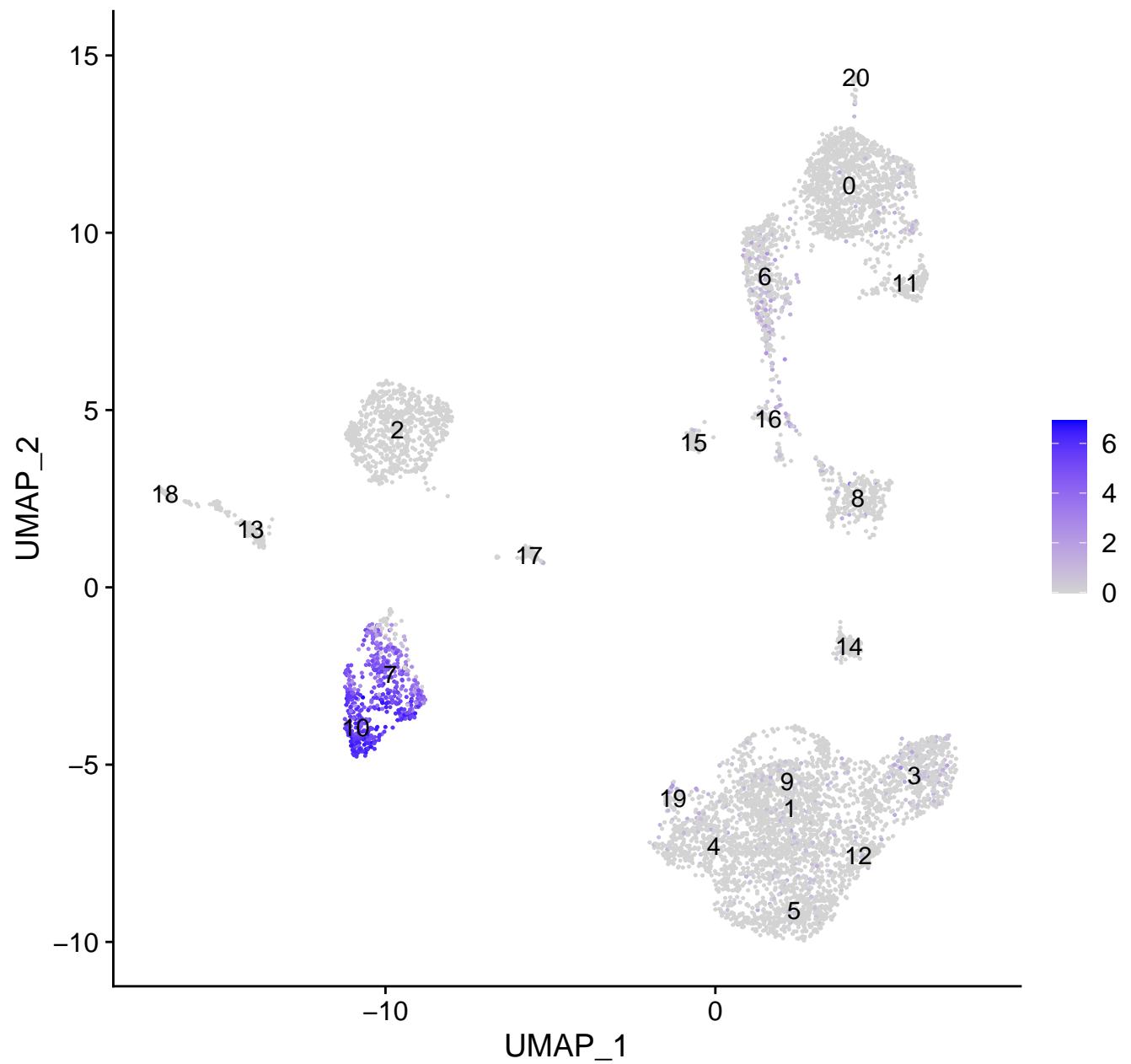
# GHRL



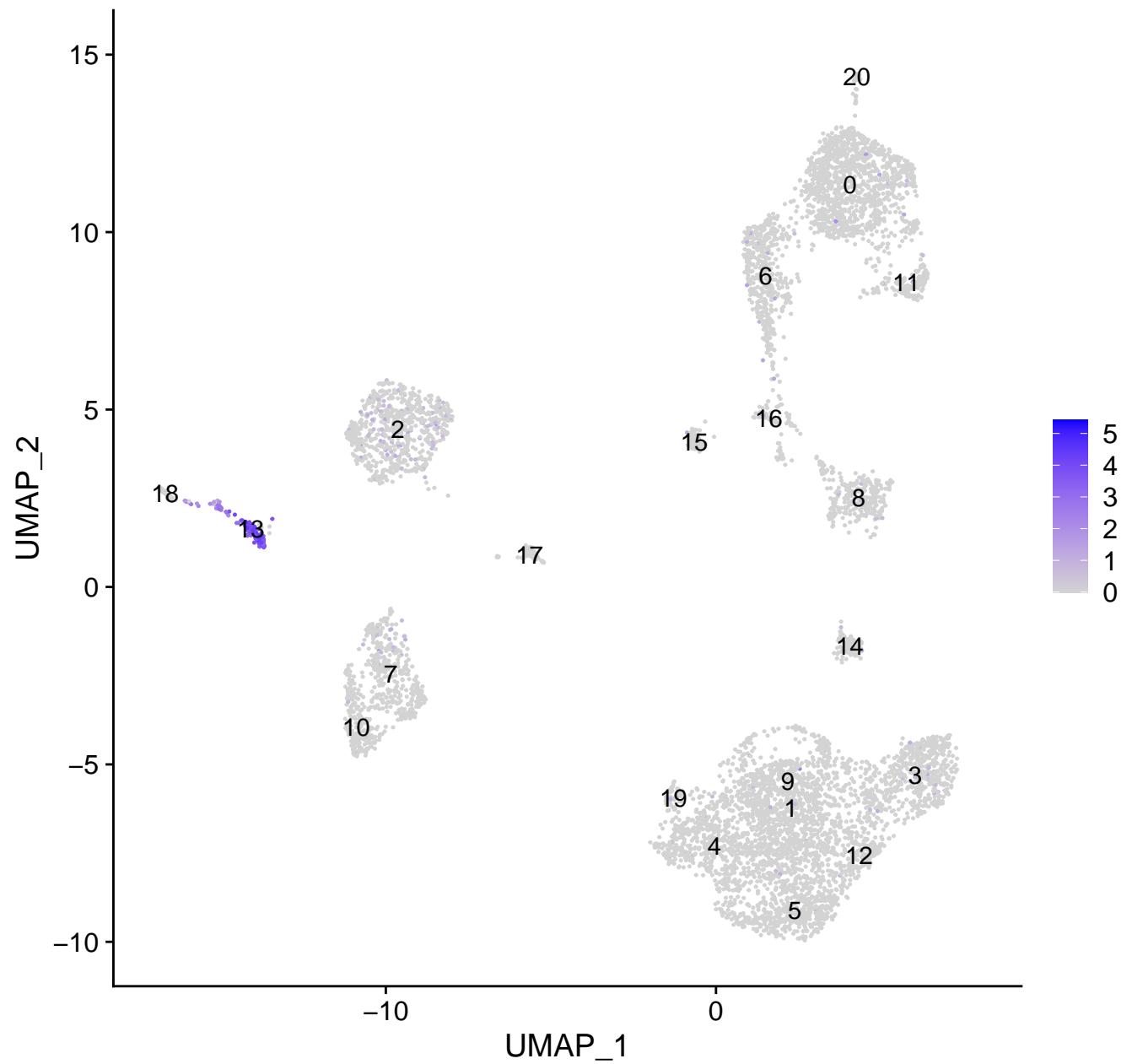
# KRT19



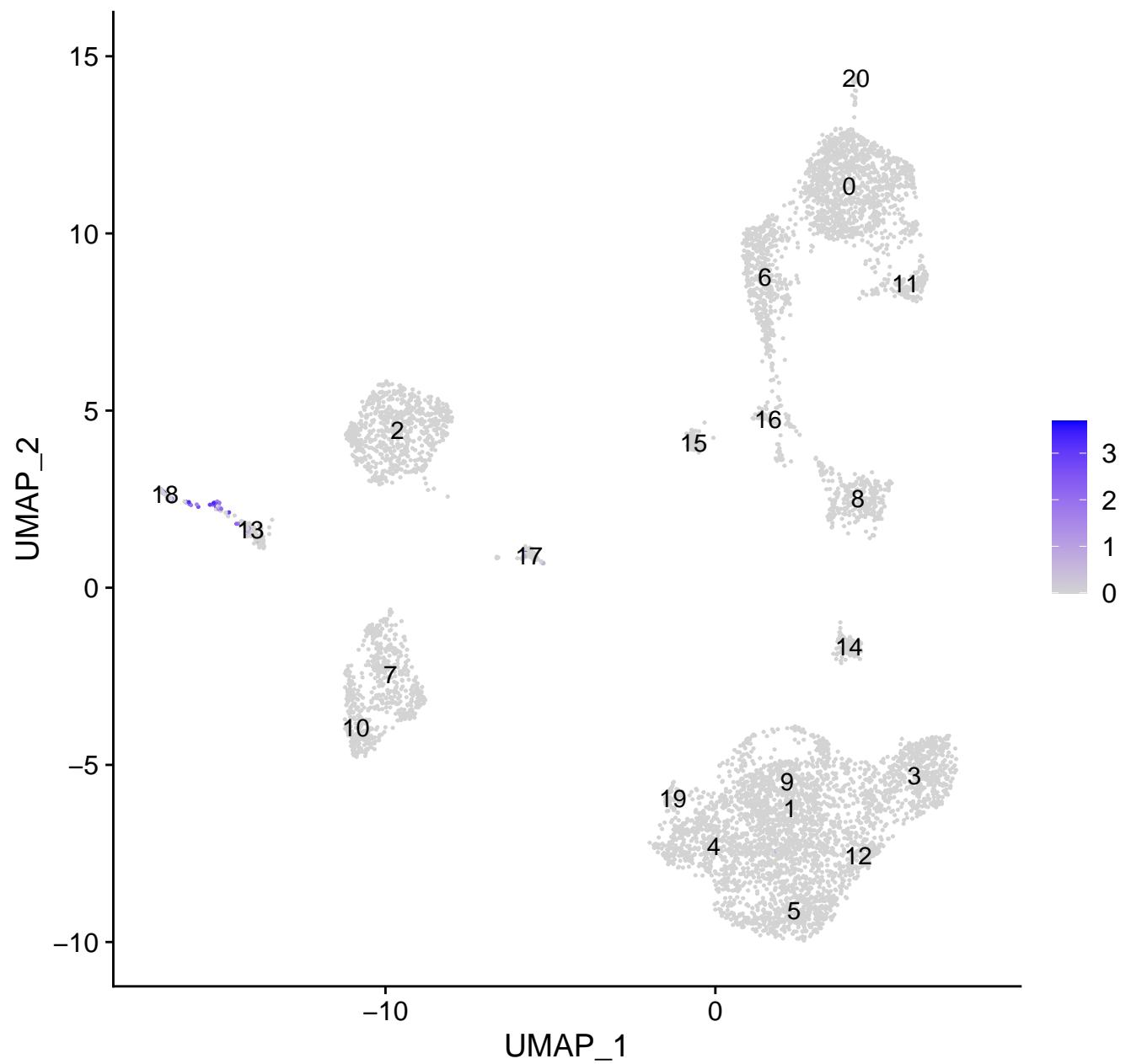
# REG1B



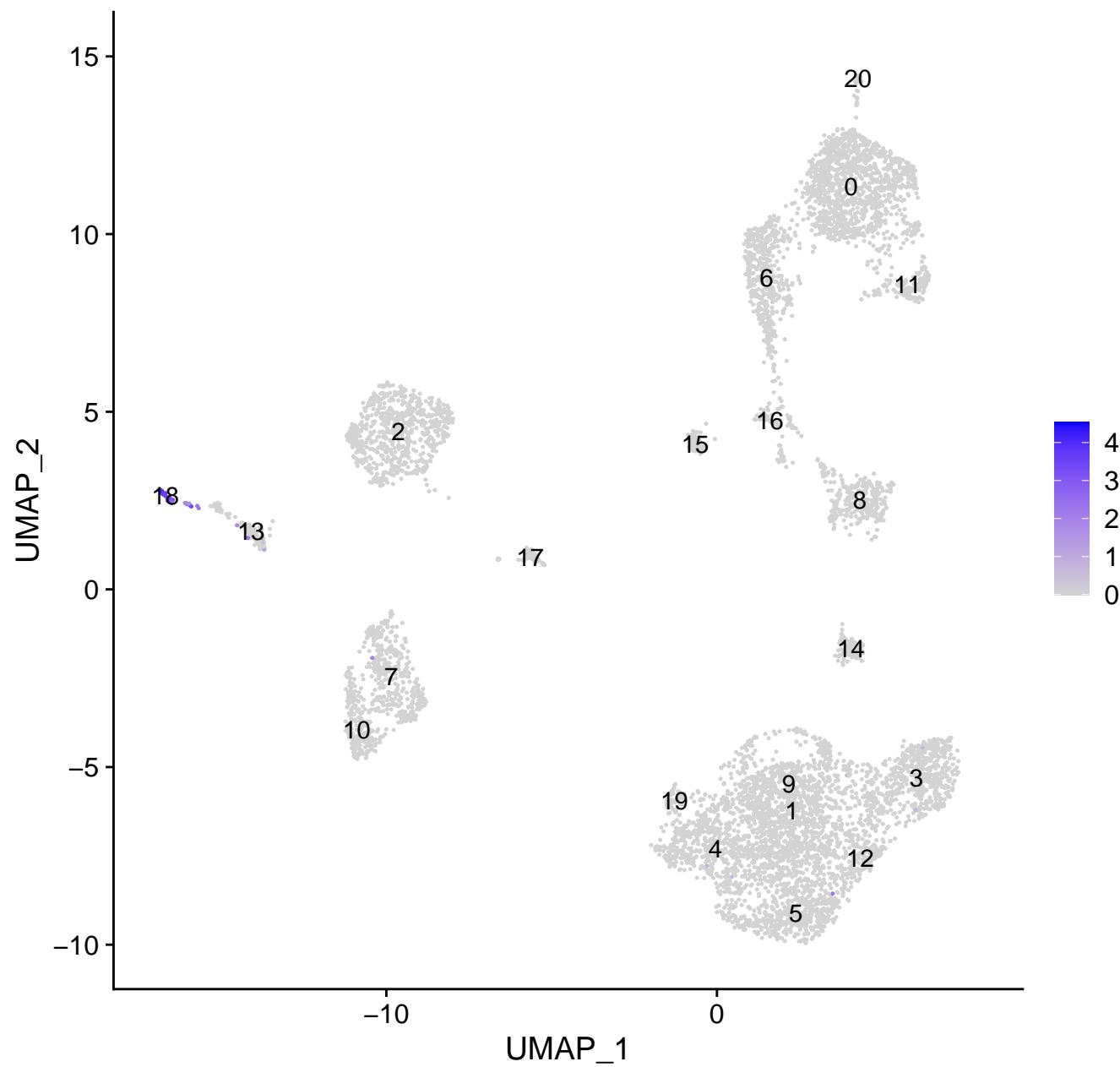
# COL1A1



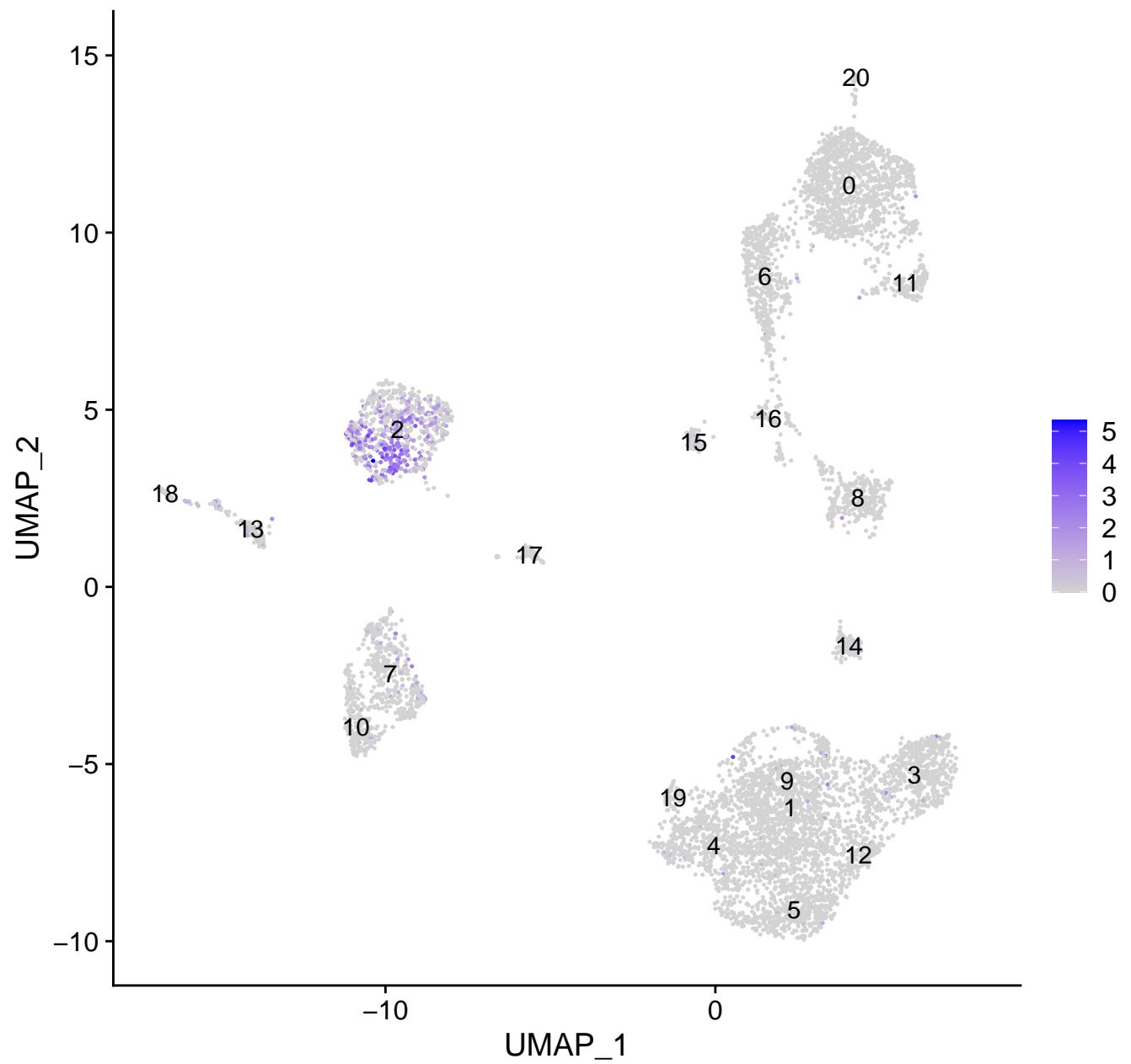
# FABP4



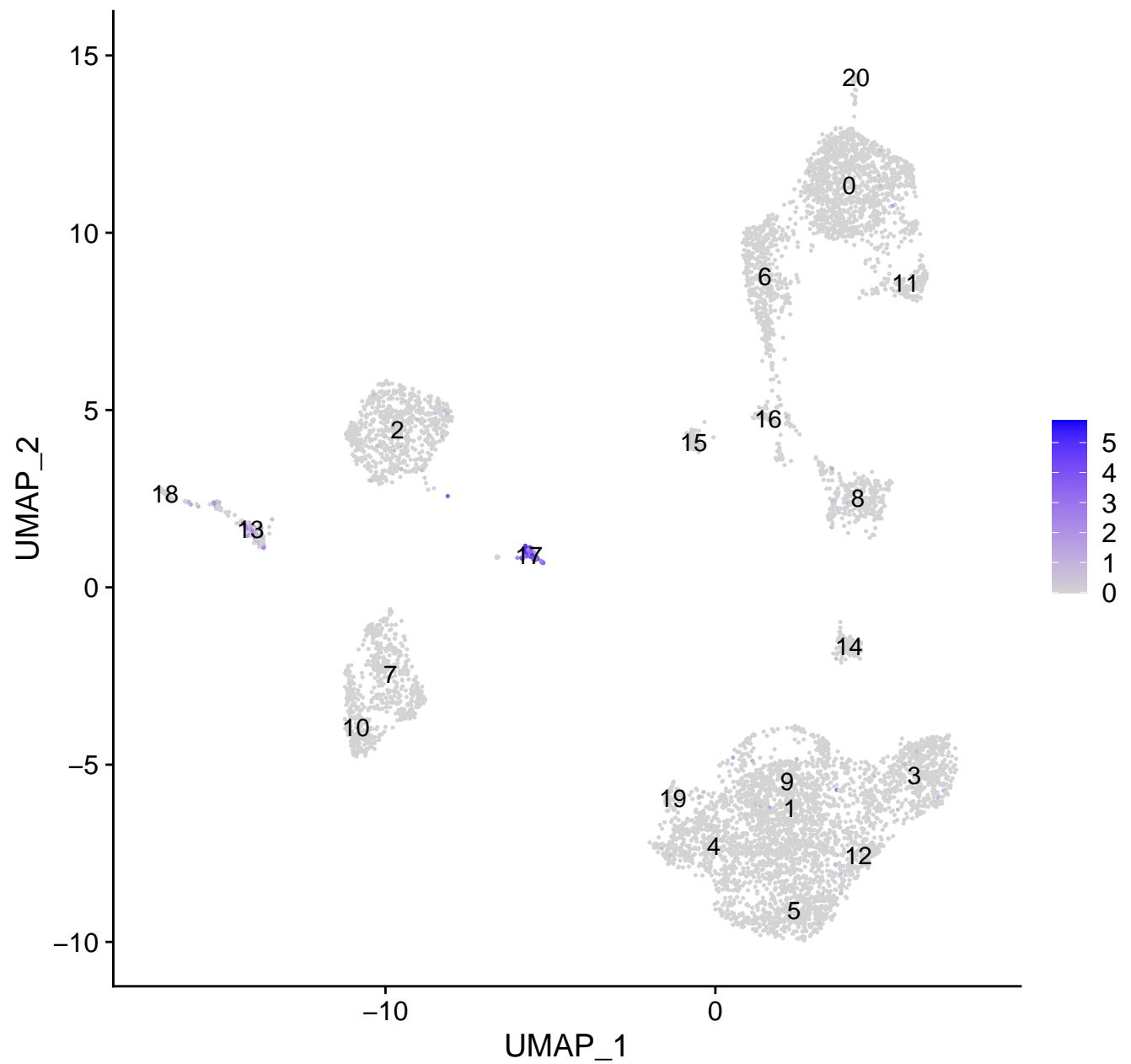
# PLVAP



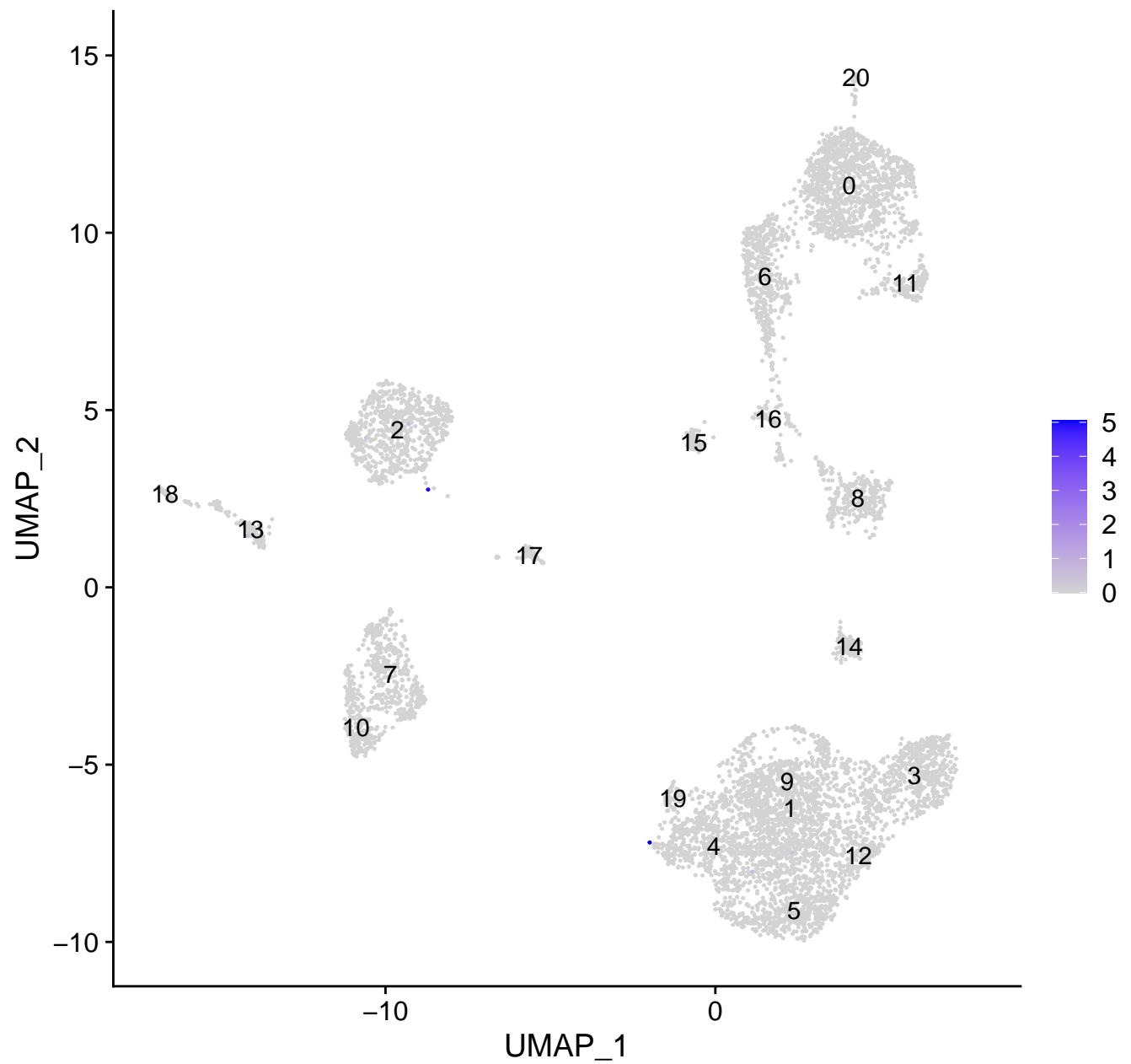
# CRYAB



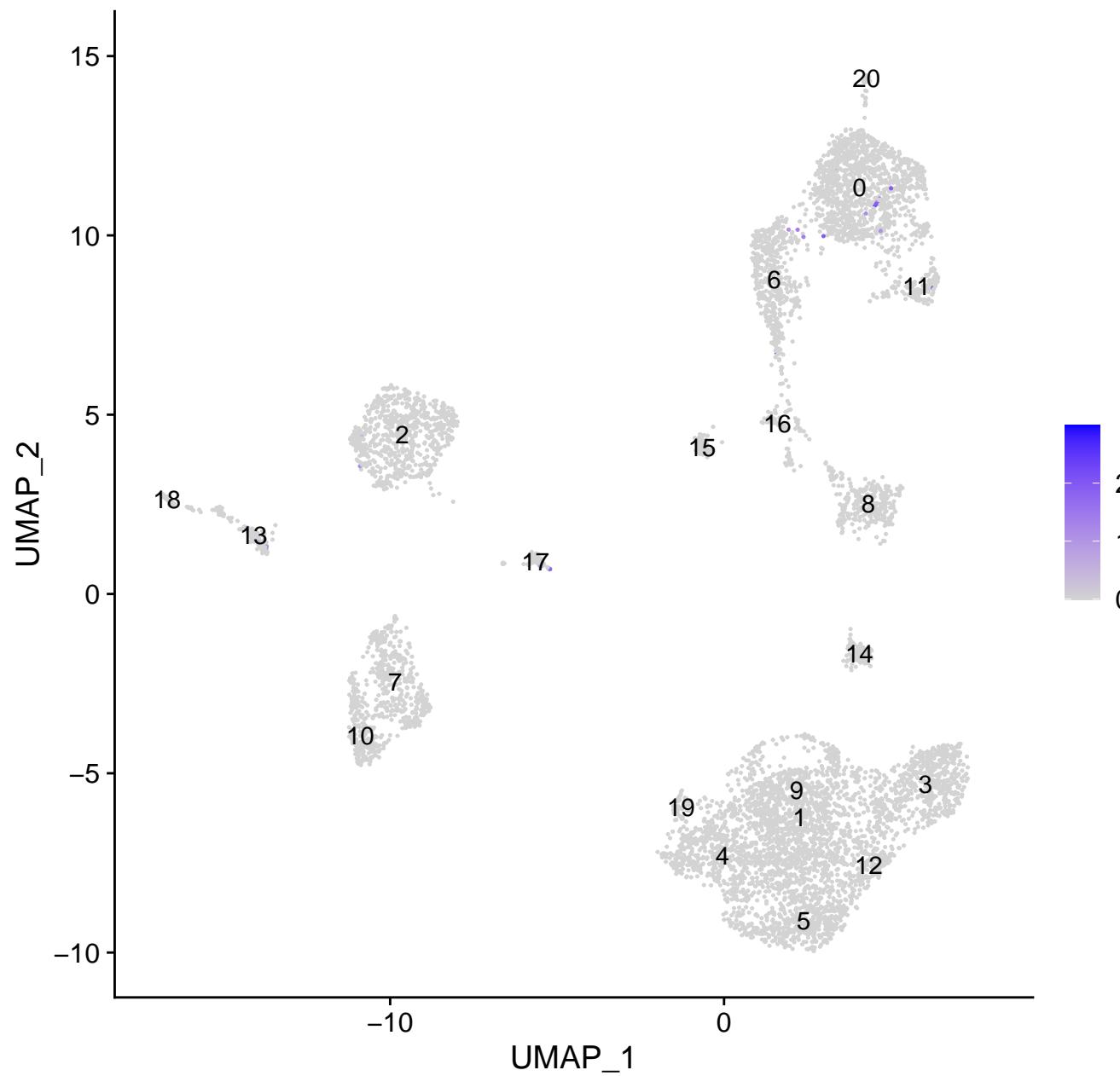
# APOE



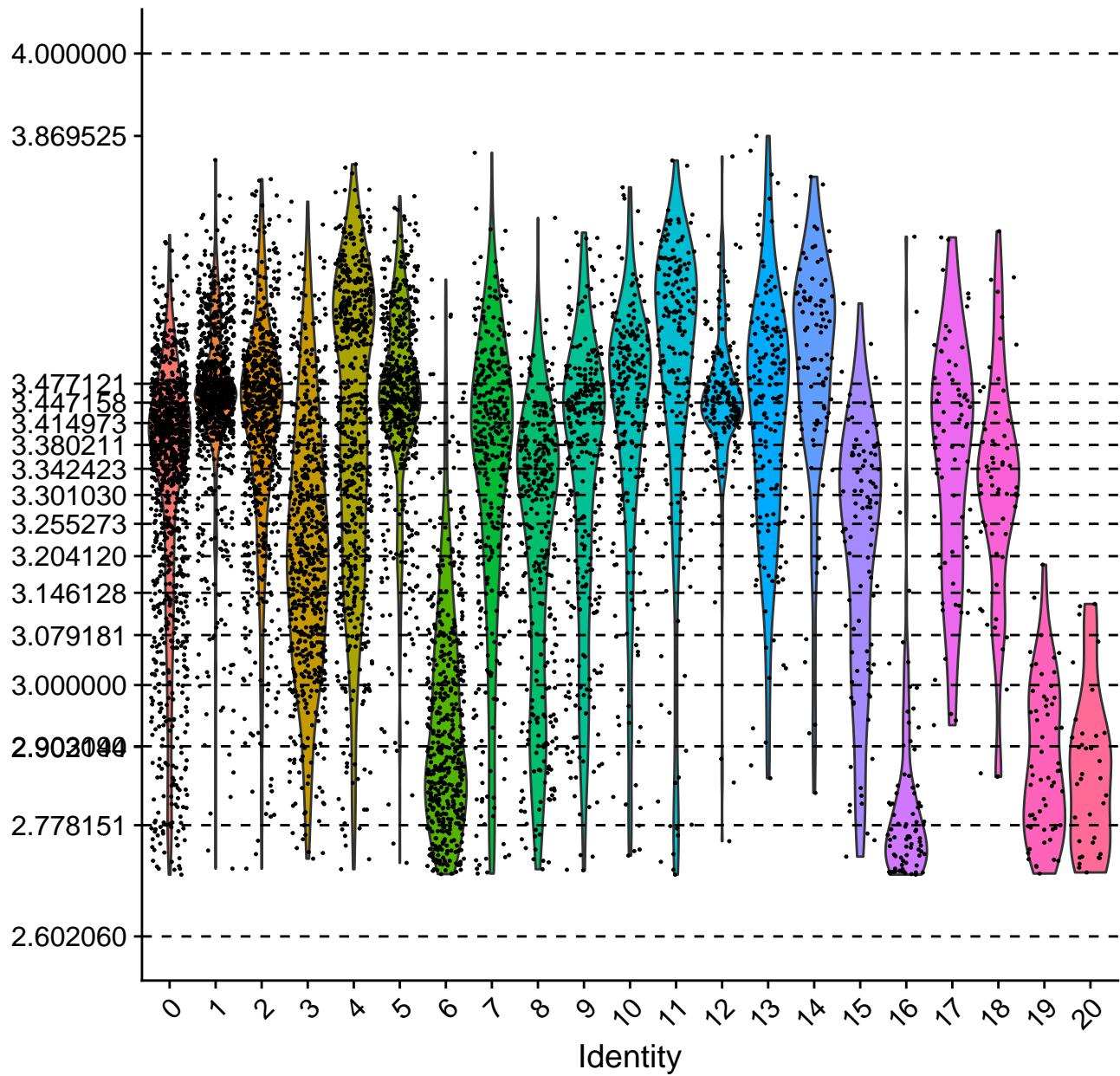
# TPSB2



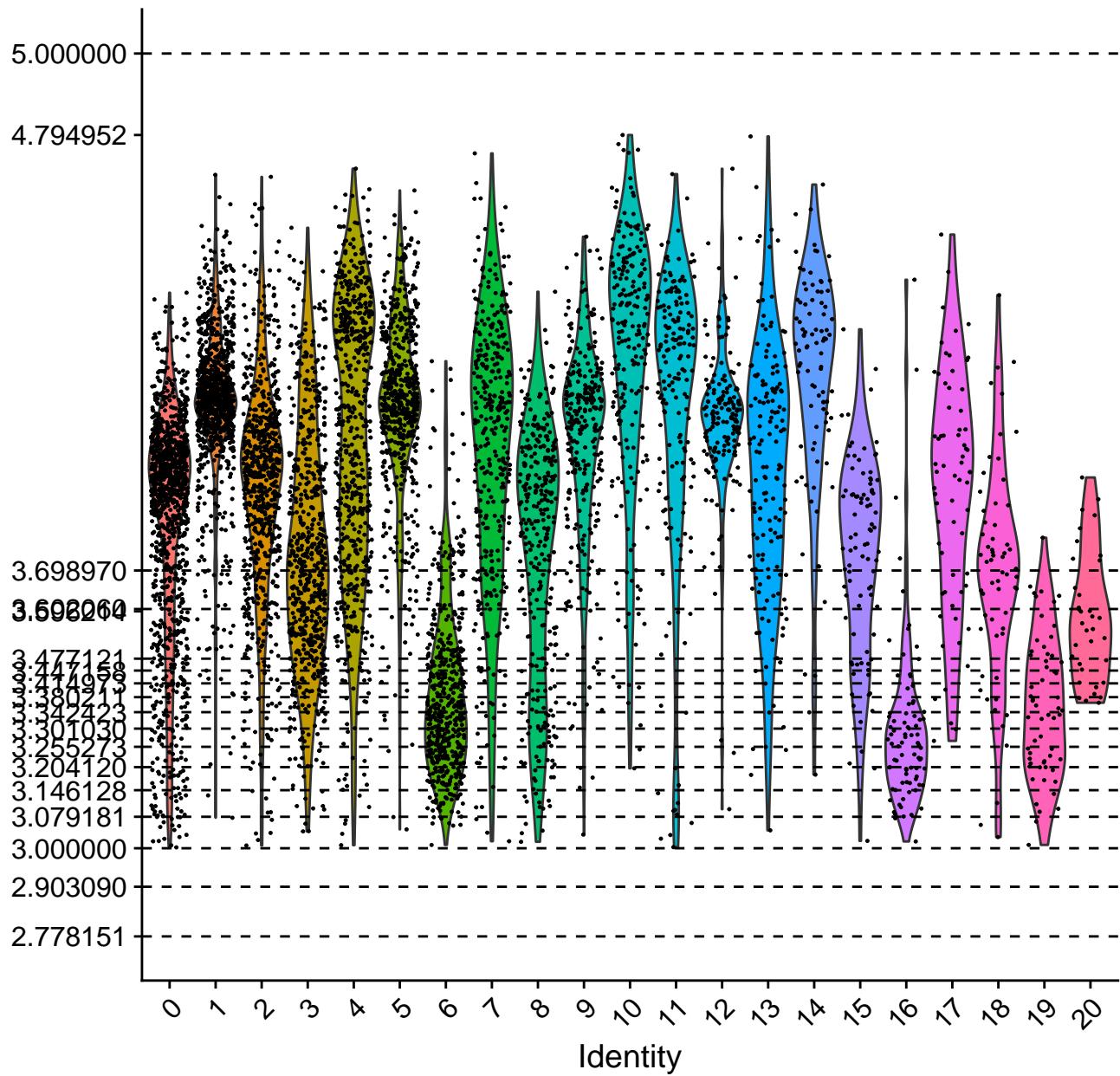
# TOP2A



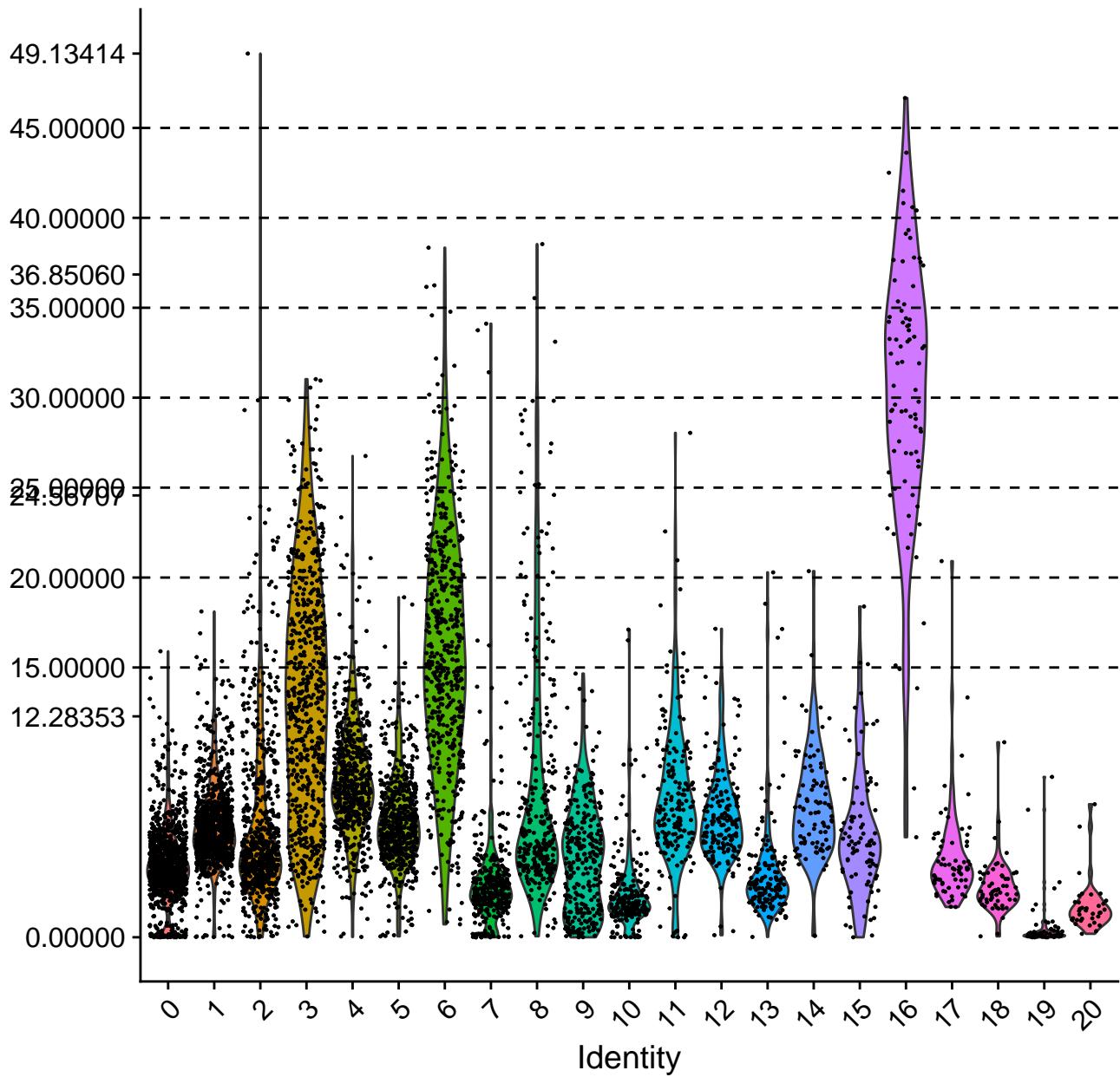
# Number of features for MS18001 per cluster



# Number of counts for MS18001 per cluster



### % of MT reads for MS18001 per cluster



### % of HB reads for MS18001 per cluster

