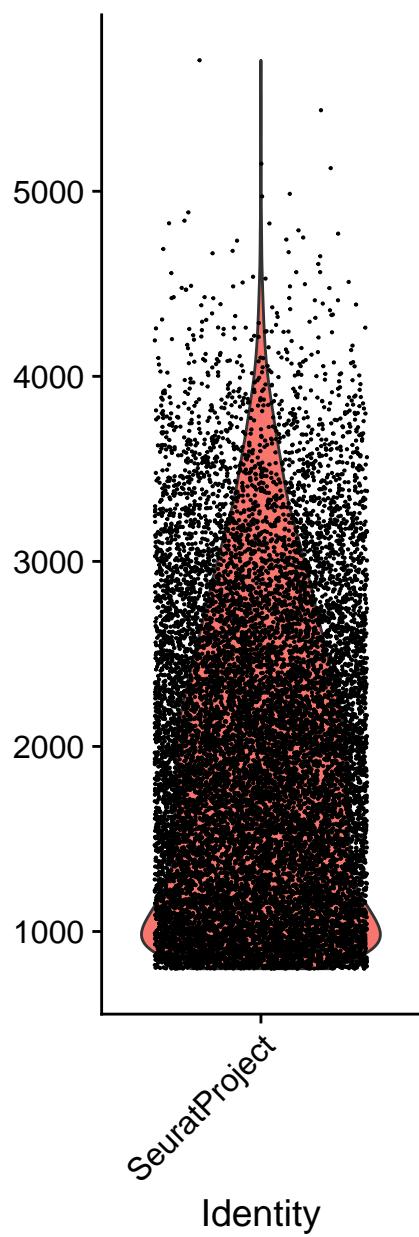
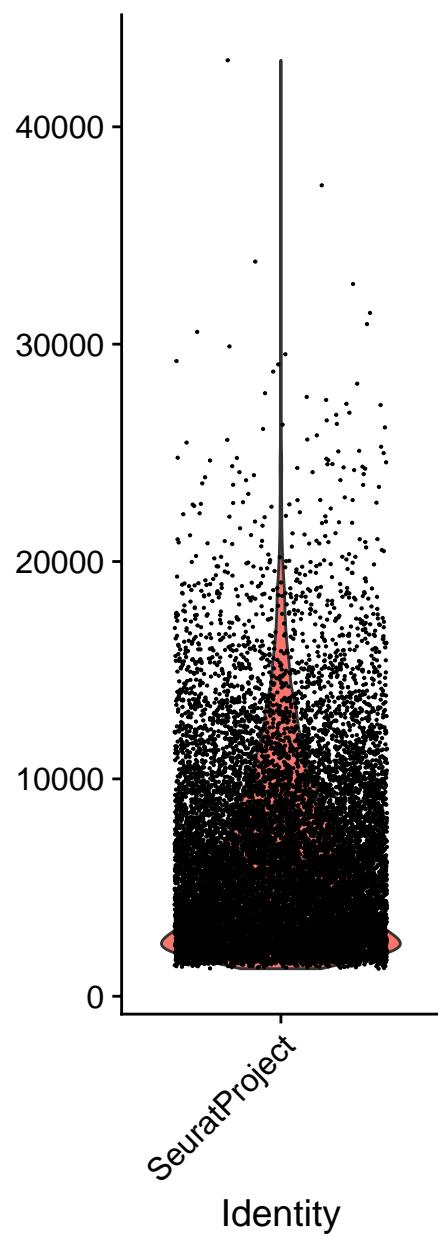


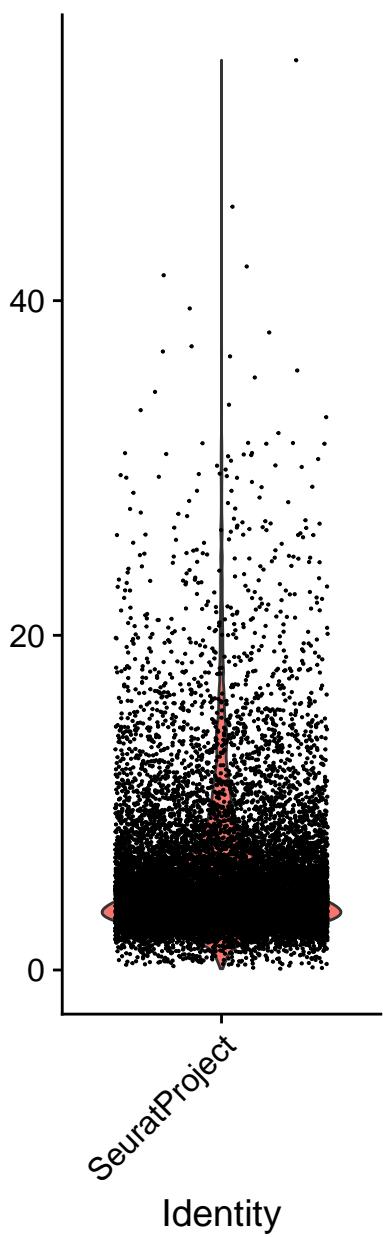
nFeature_RNA



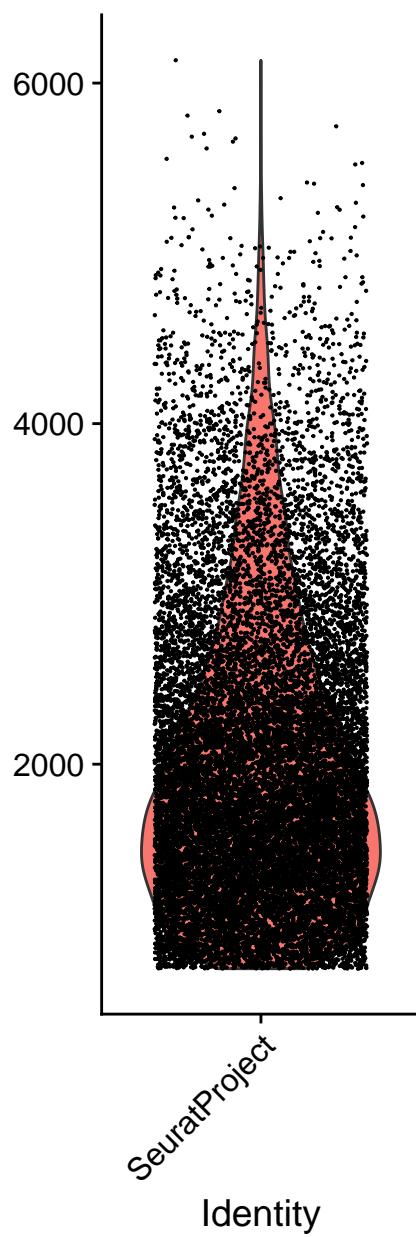
nCount_RNA



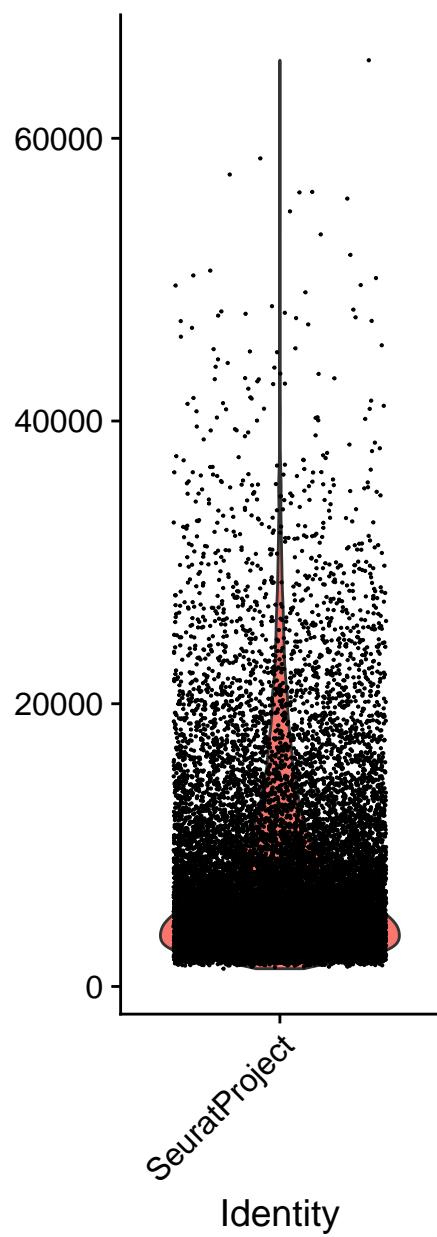
percent.mt



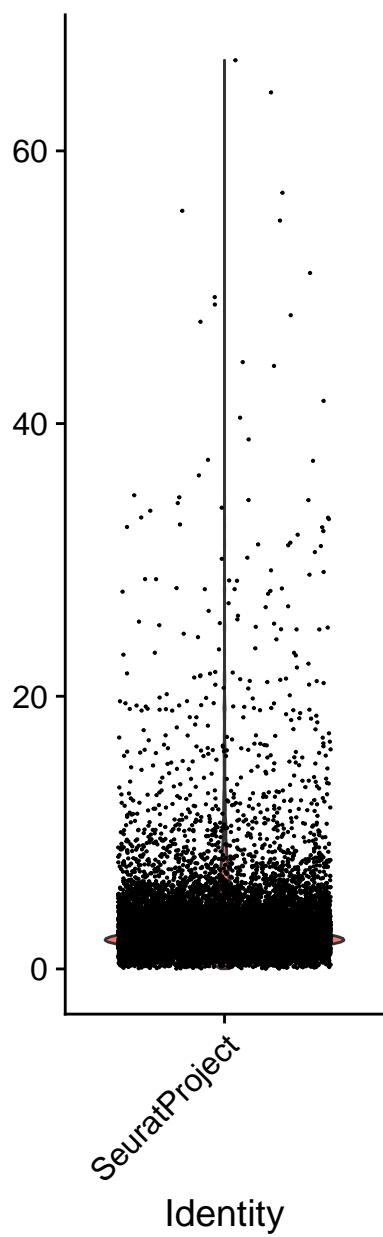
nFeature_RNA



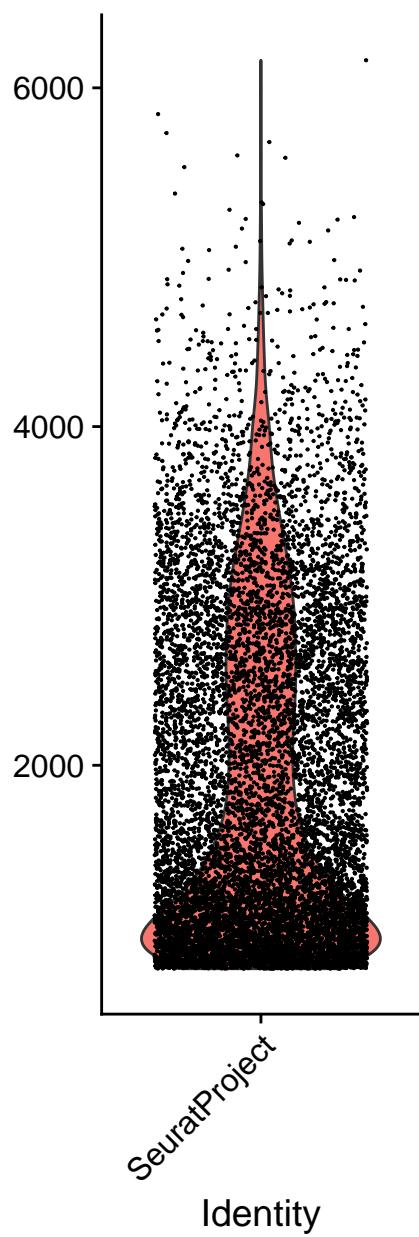
nCount_RNA



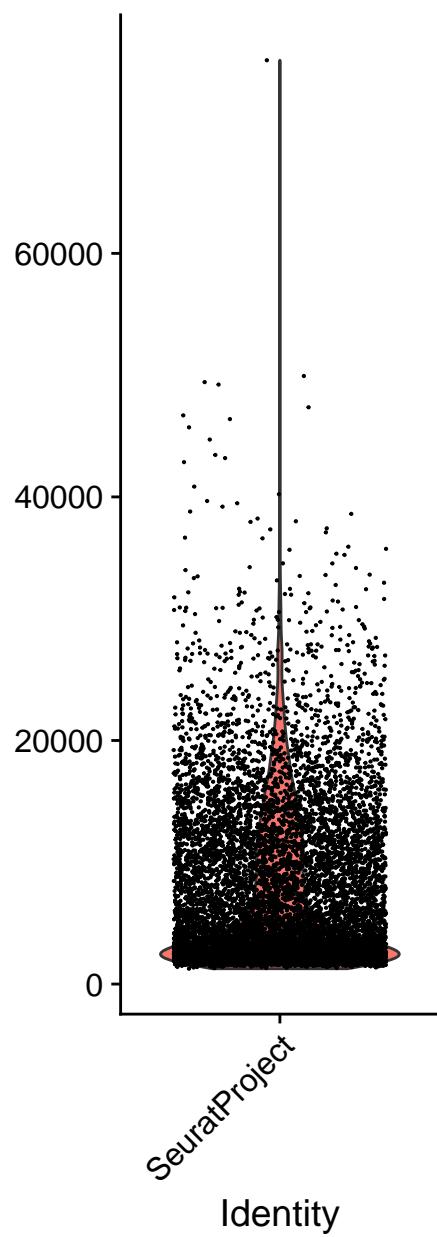
percent.mt



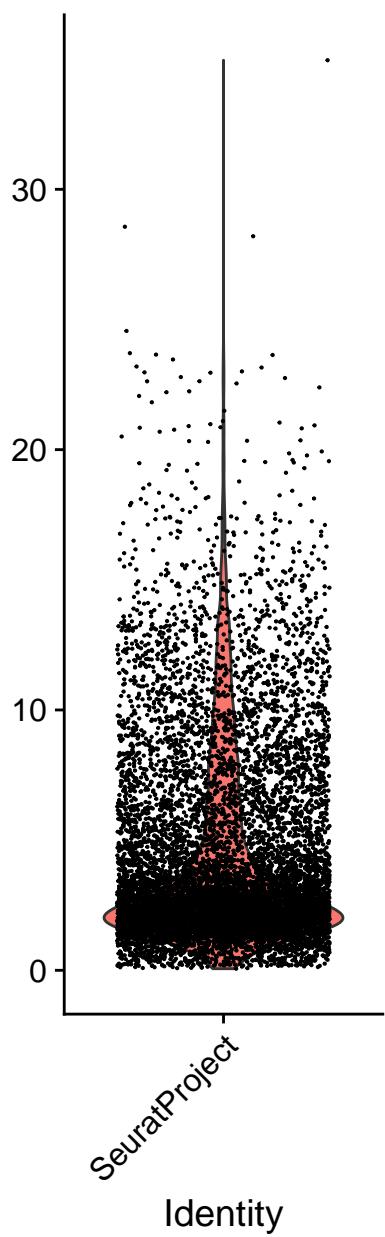
nFeature_RNA

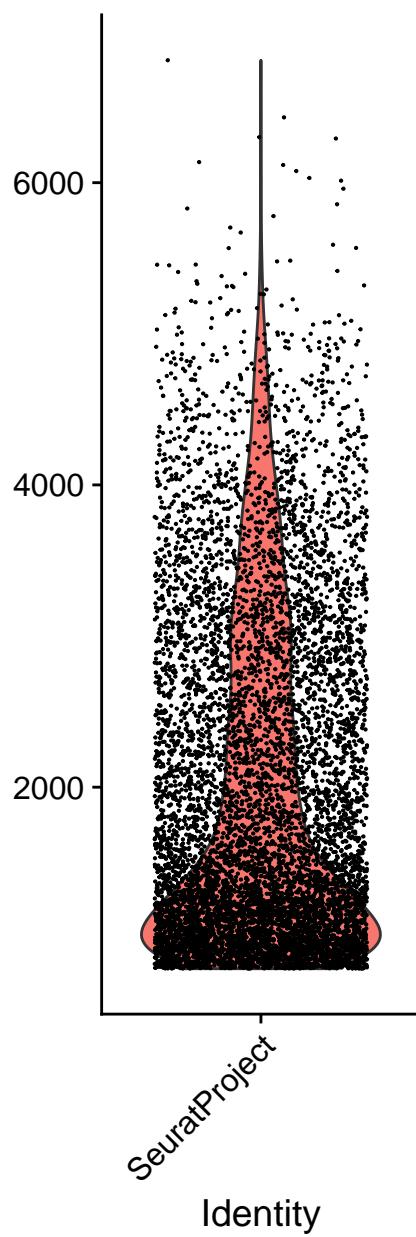
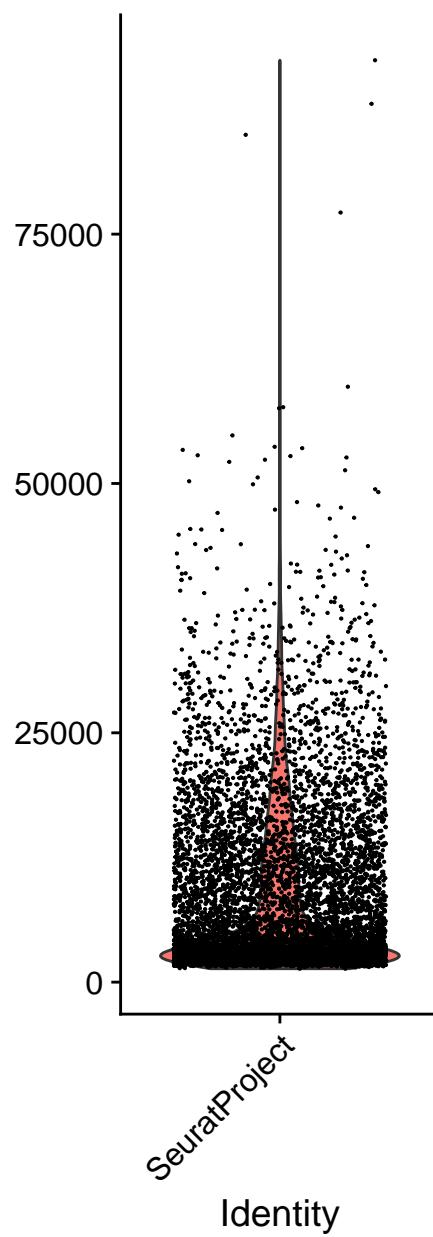
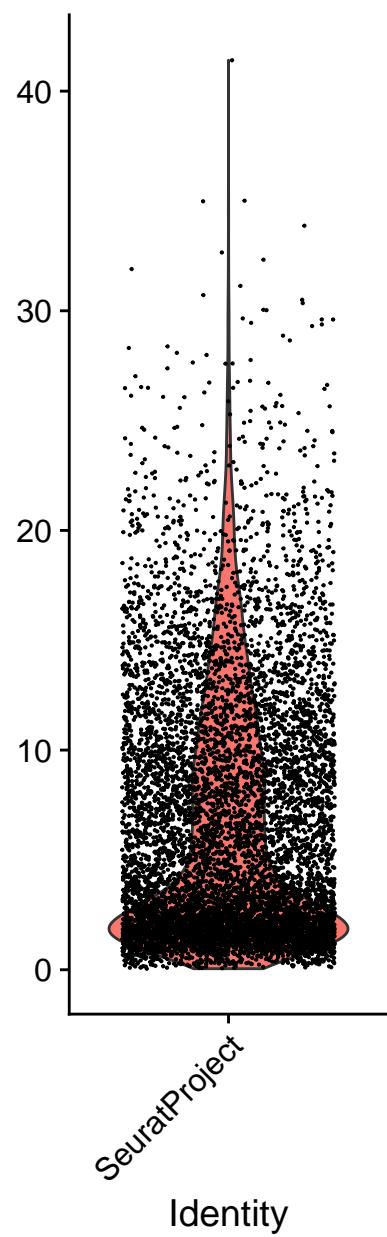


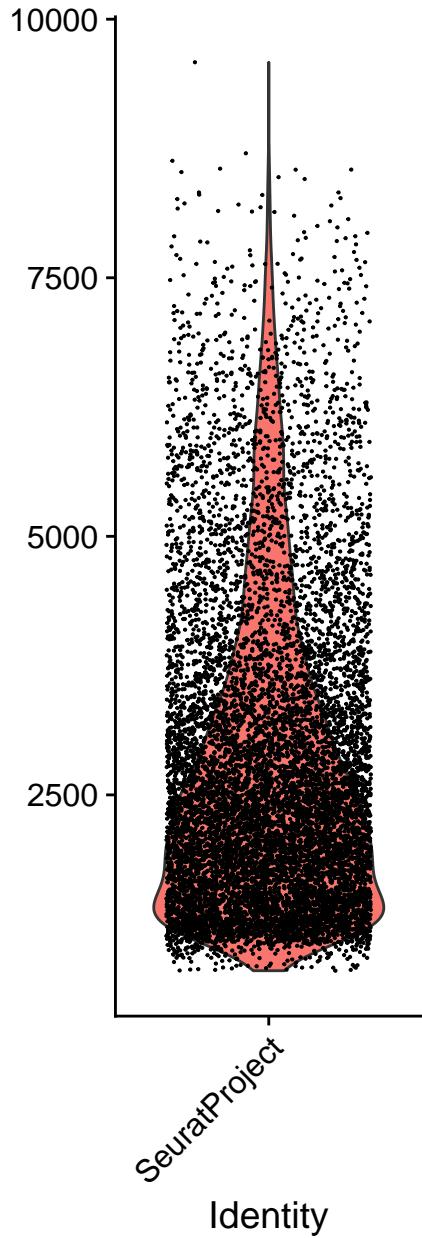
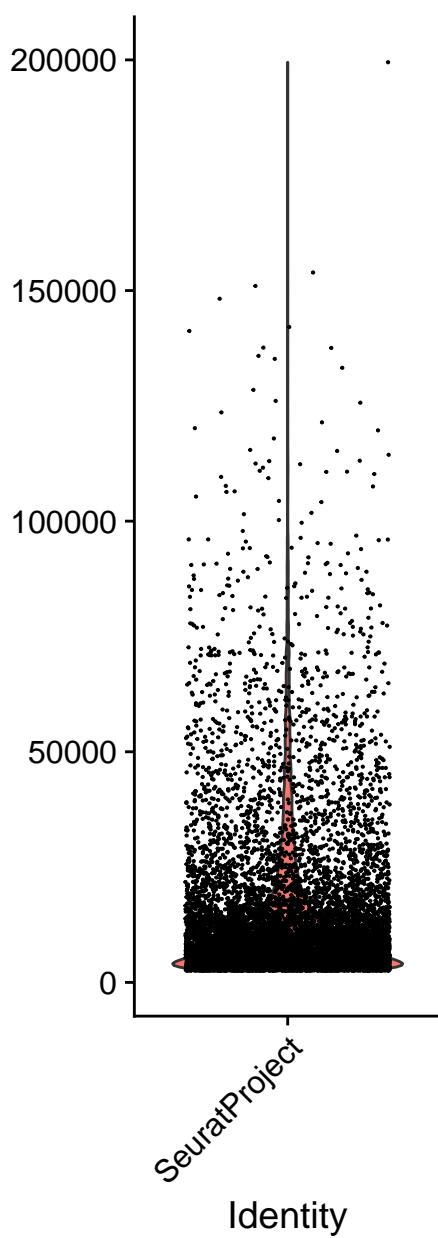
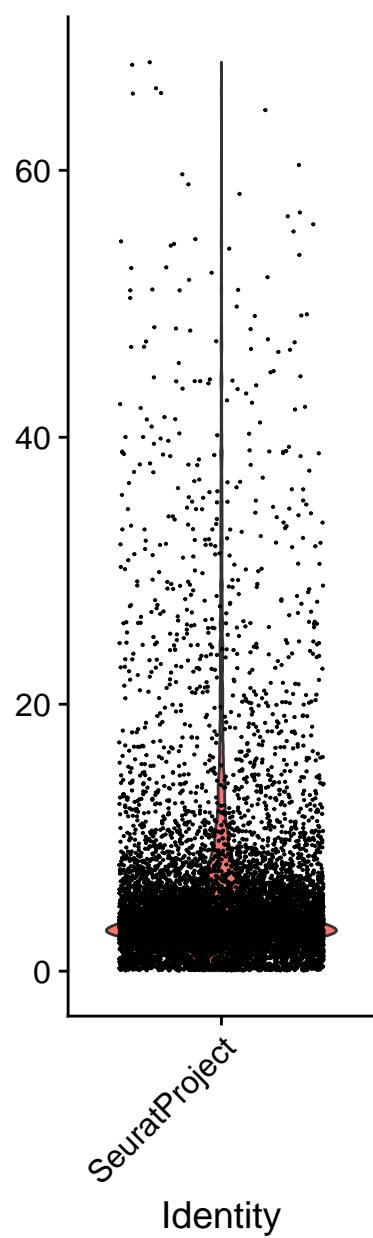
nCount_RNA

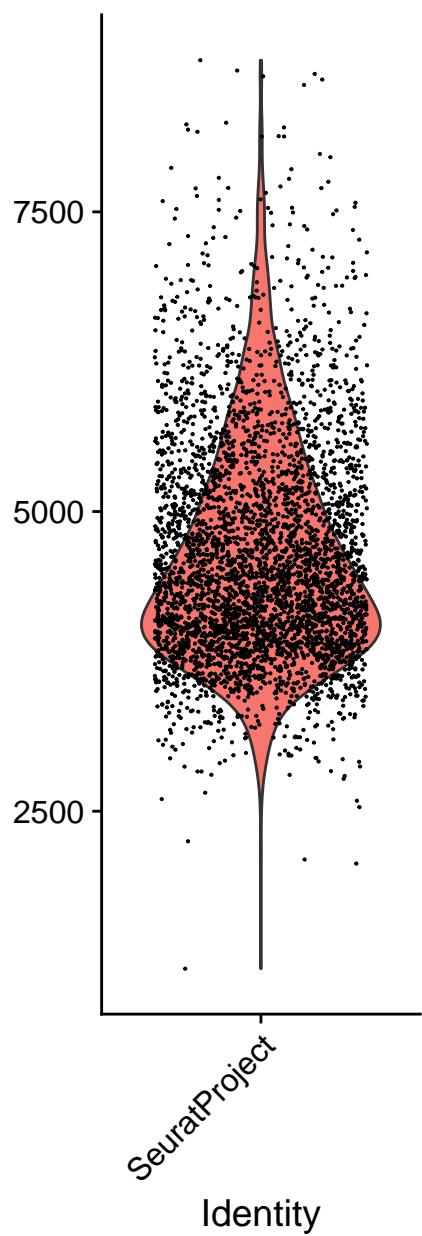
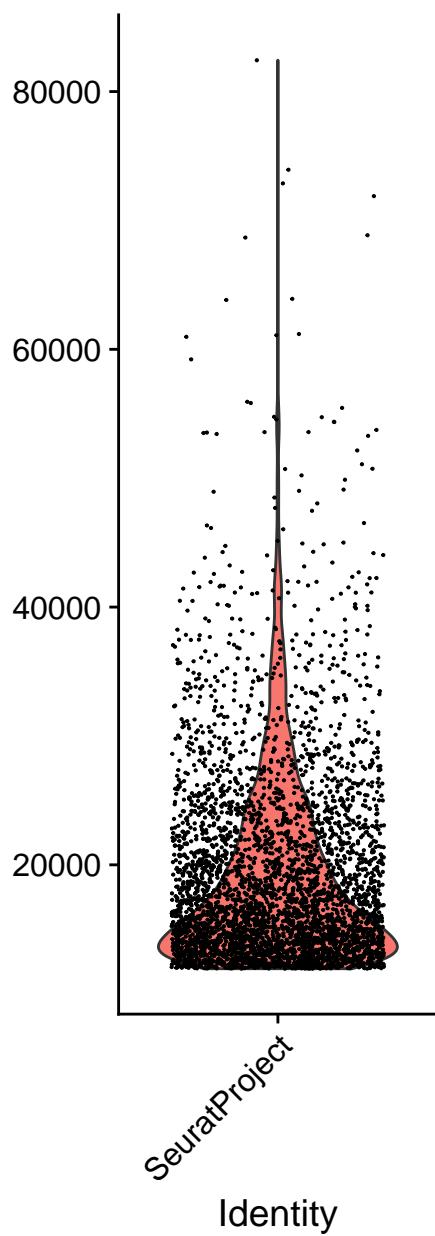
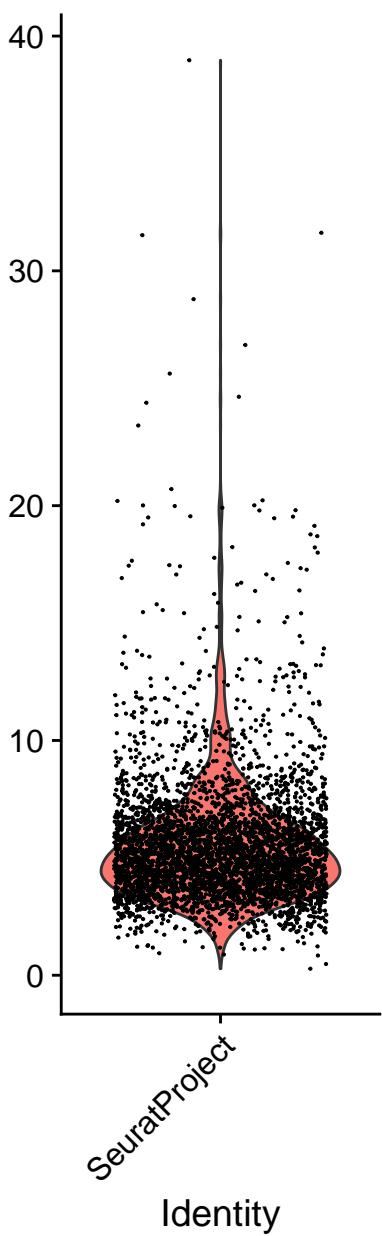


percent.mt

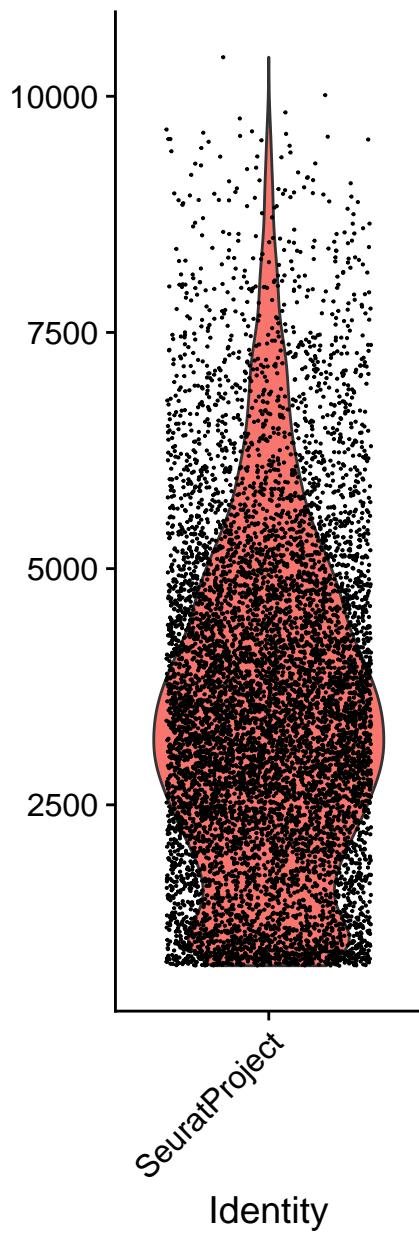


nFeature_RNA**nCount_RNA****percent.mt**

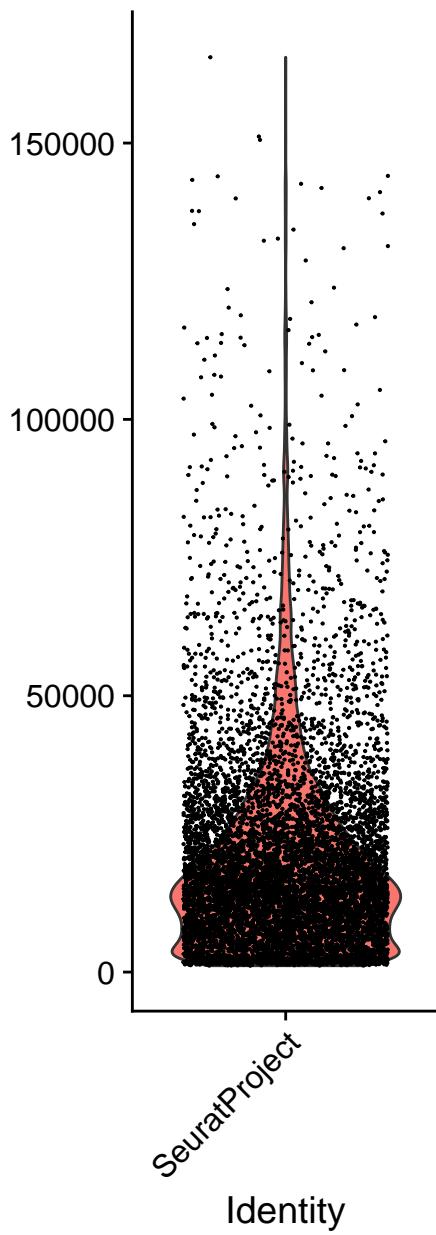
nFeature_RNA**nCount_RNA****percent.mt**

nFeature_RNA**nCount_RNA****percent.mt**

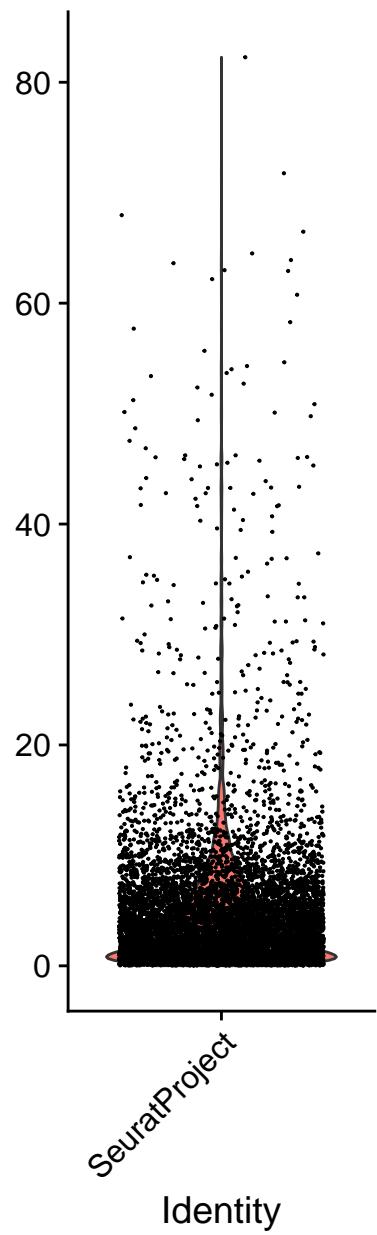
nFeature_RNA



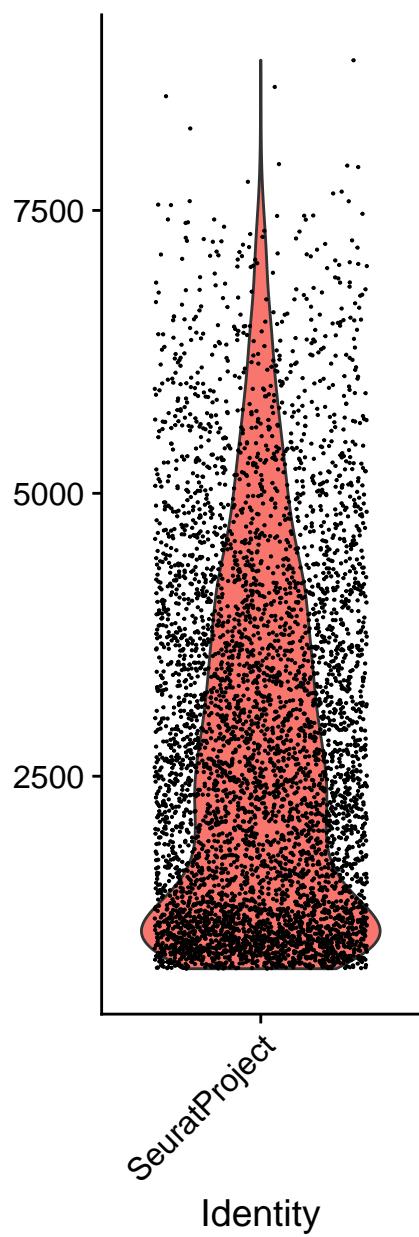
nCount_RNA



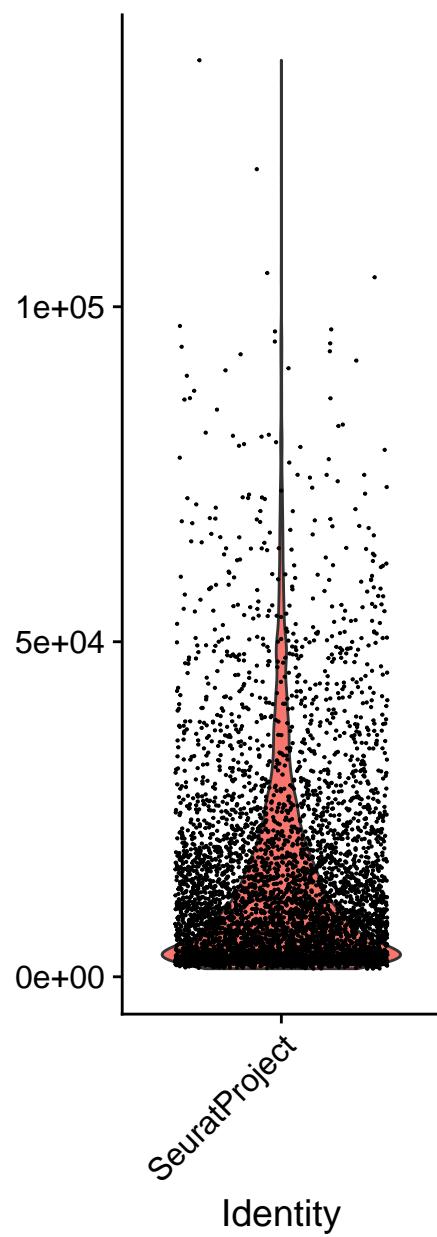
percent.mt



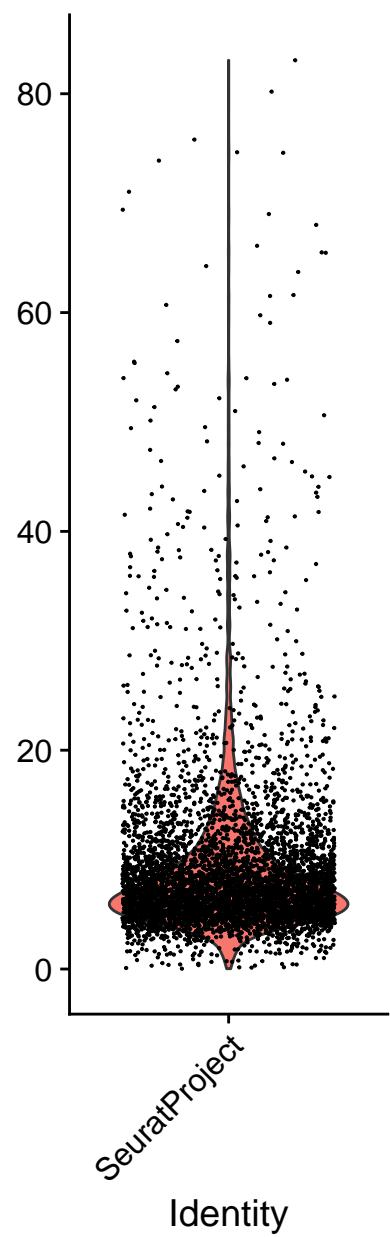
nFeature_RNA

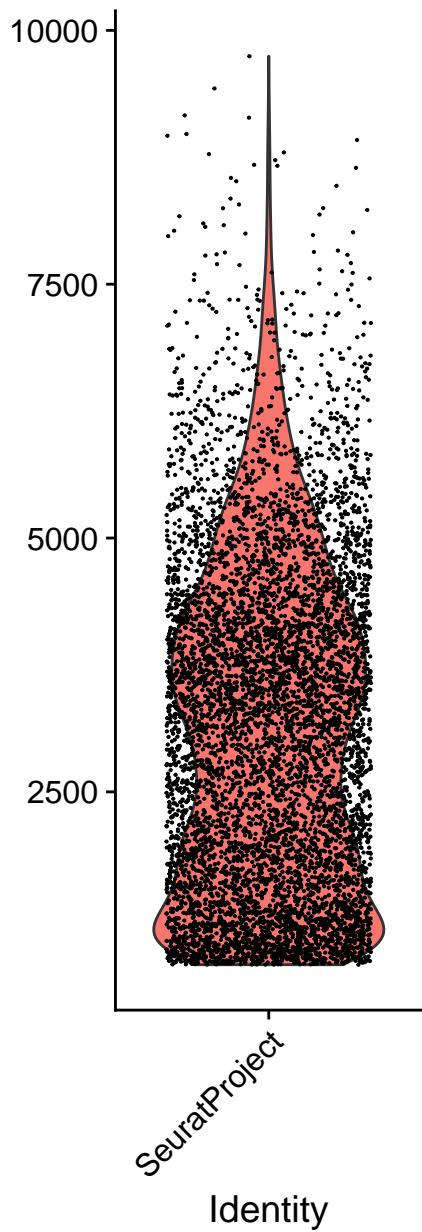
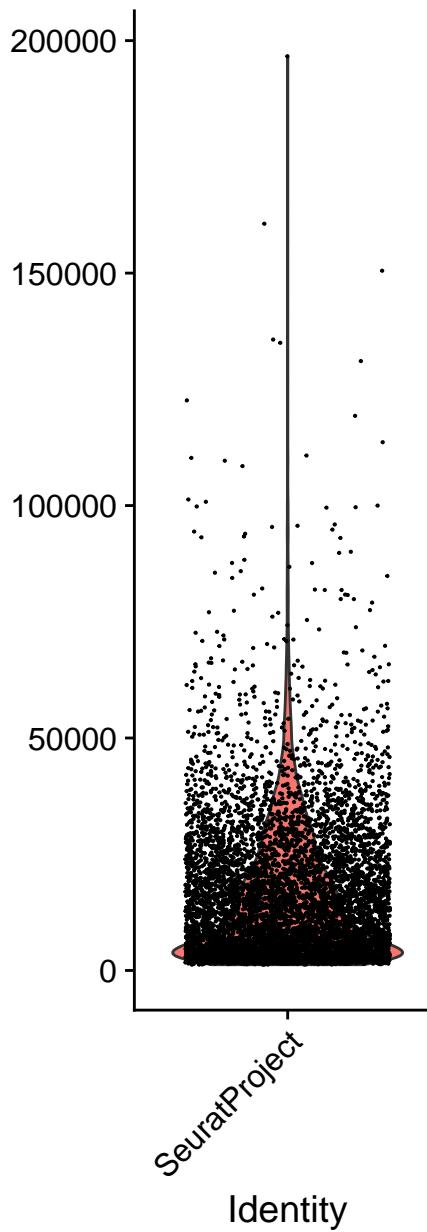
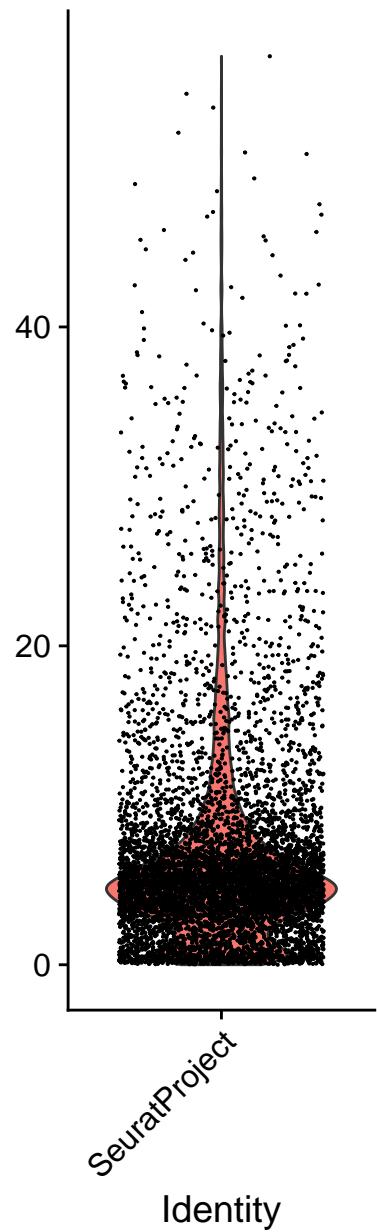


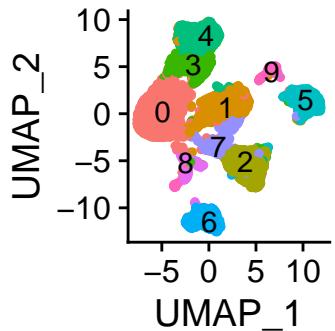
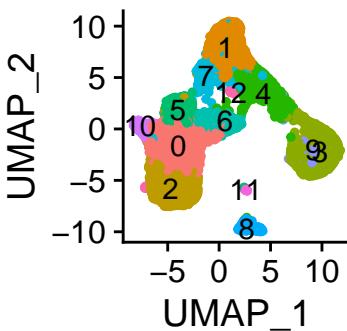
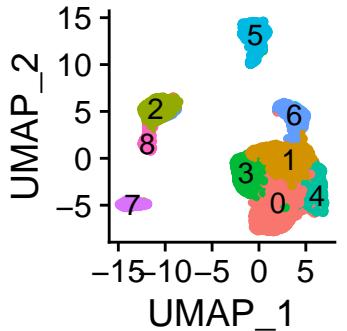
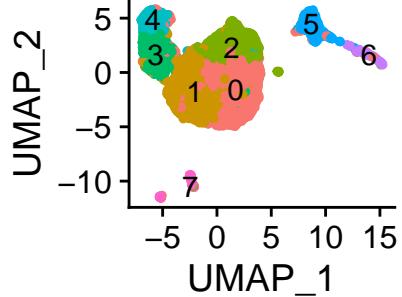
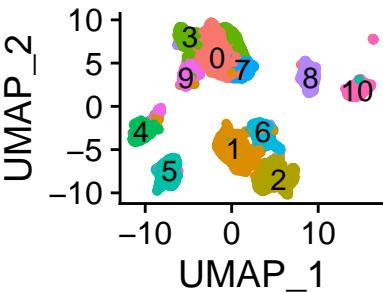
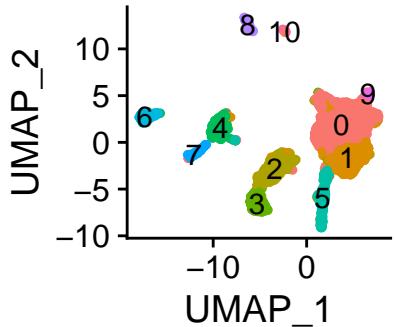
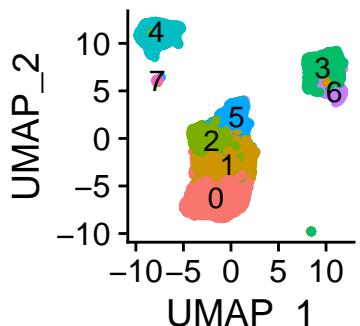
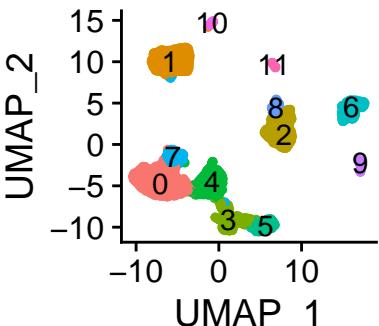
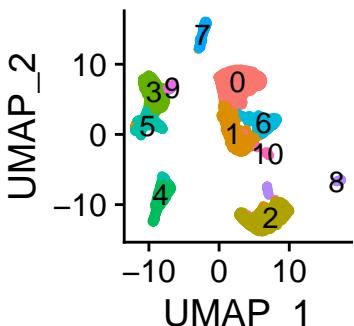
nCount_RNA

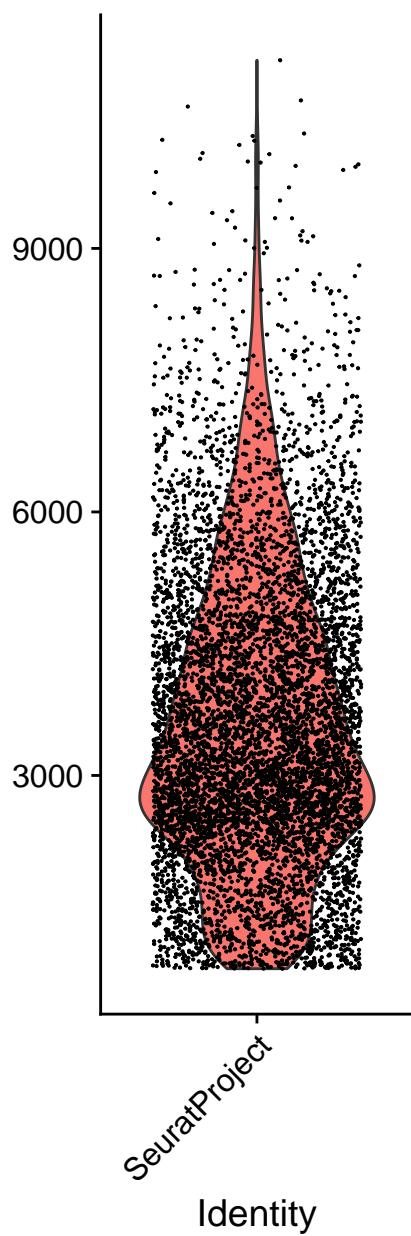
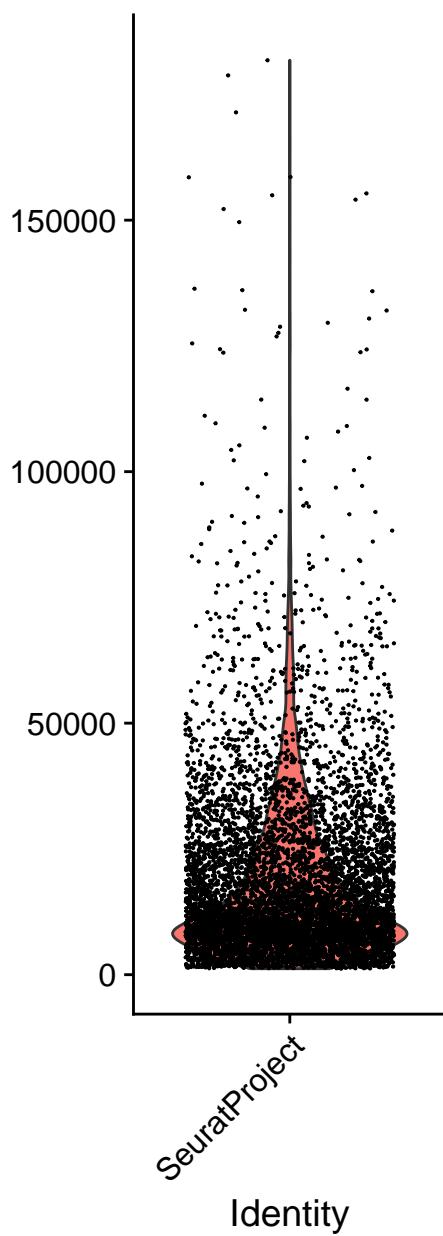
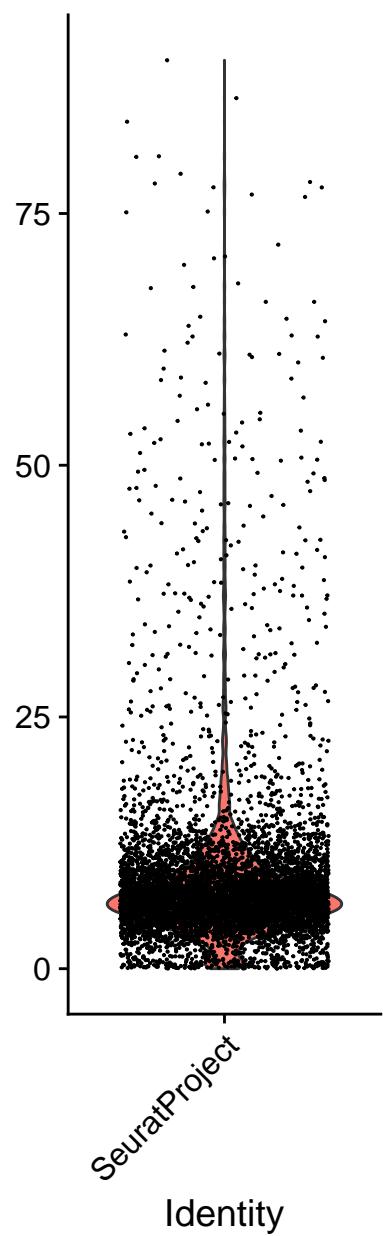


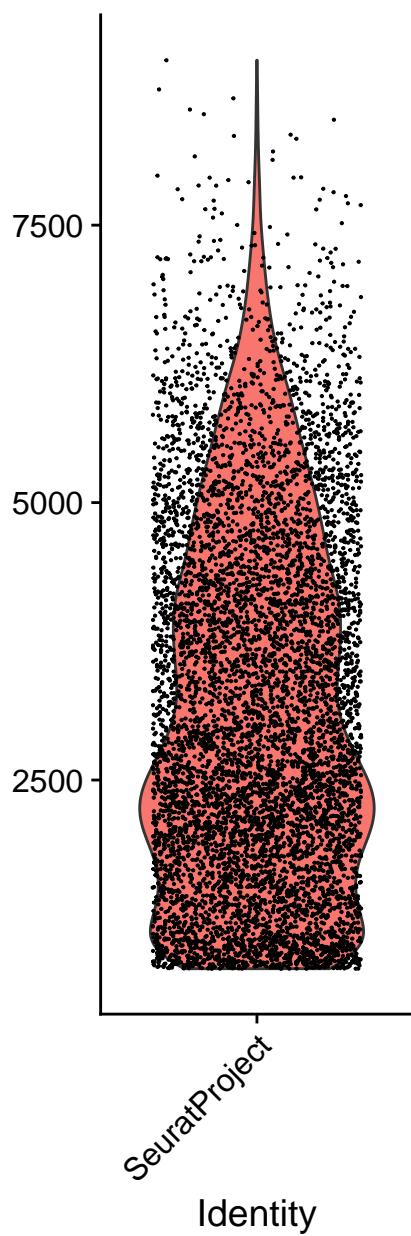
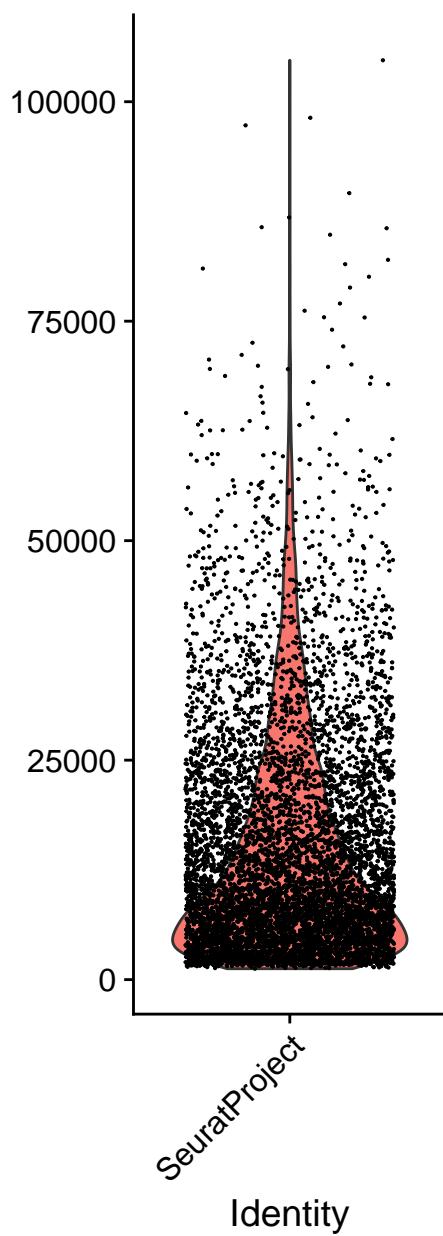
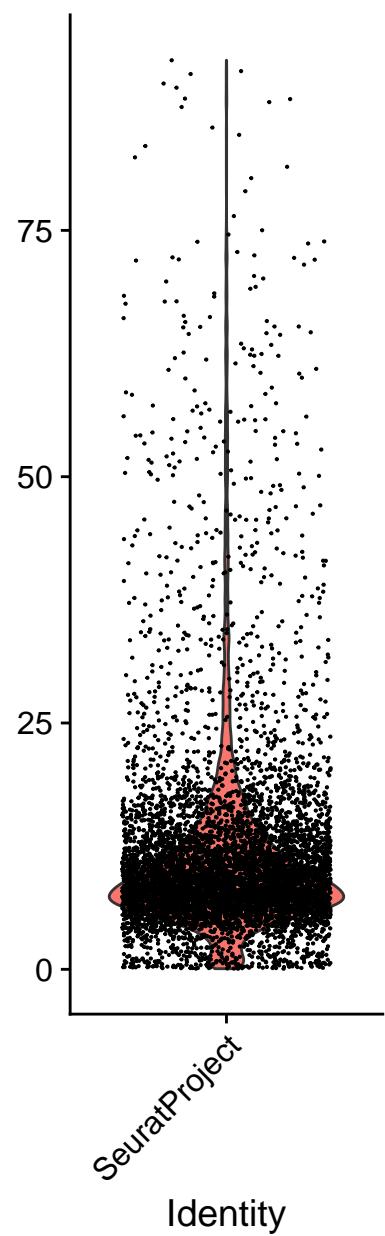
percent.mt



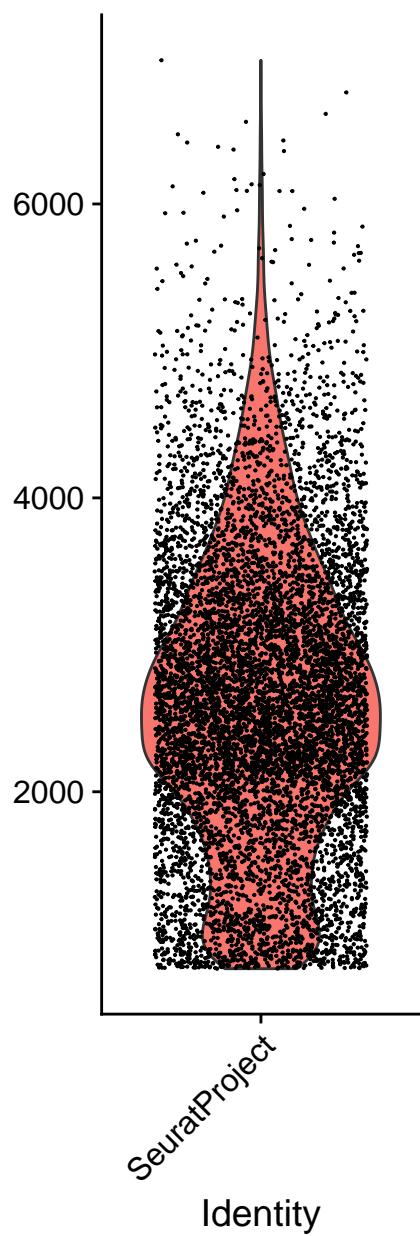
nFeature_RNA**nCount_RNA****percent.mt**

BC5 basic clu**BC6 basic clus****BC10 basic clu****BC11 basic clu****BC16 basic clu****BC17 basic clu****BC20 basic clu****BC21 basic clus****BC22 basic clu**

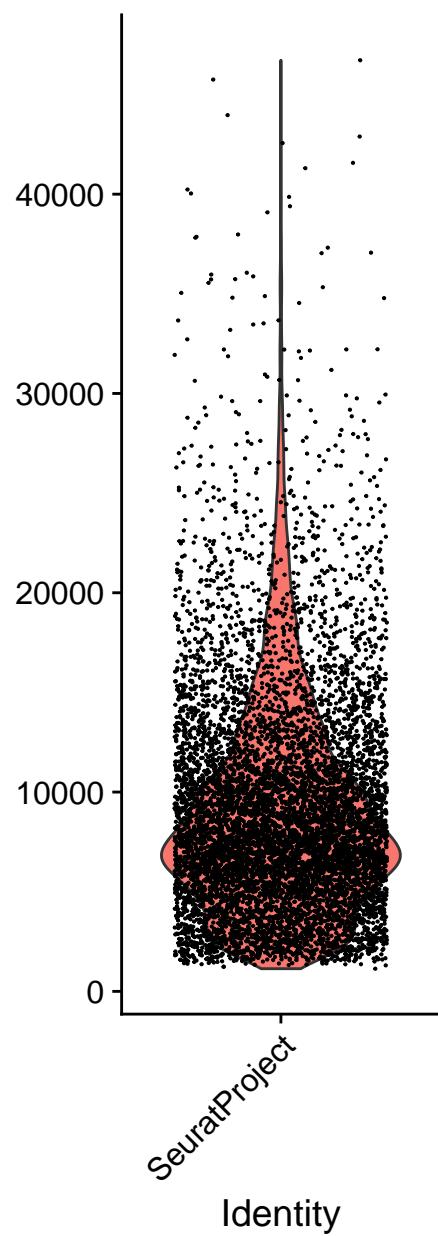
nFeature_RNA**nCount_RNA****percent.mt**

nFeature_RNA**nCount_RNA****percent.mt**

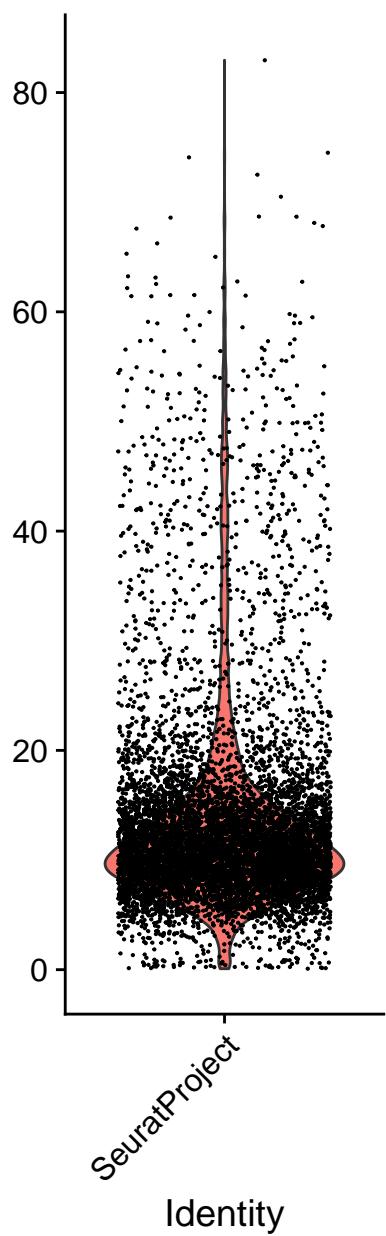
nFeature_RNA

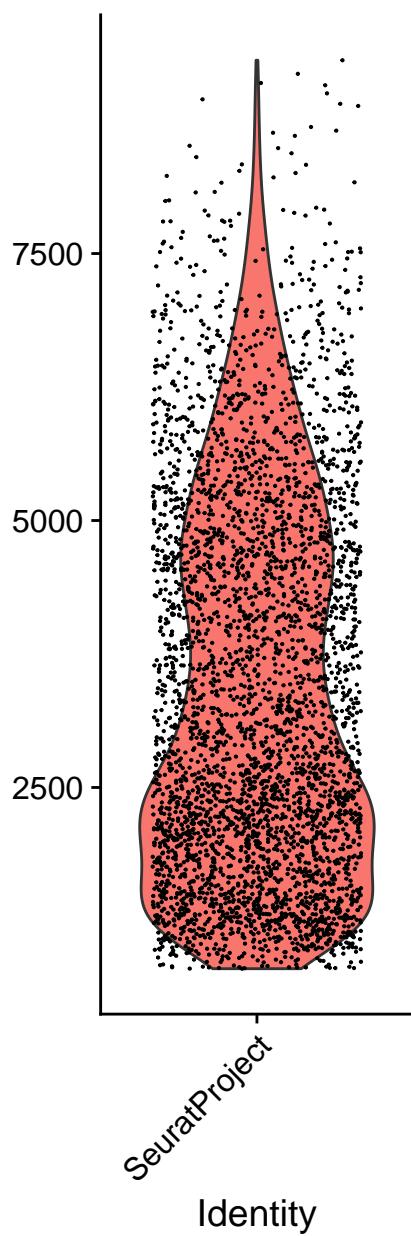
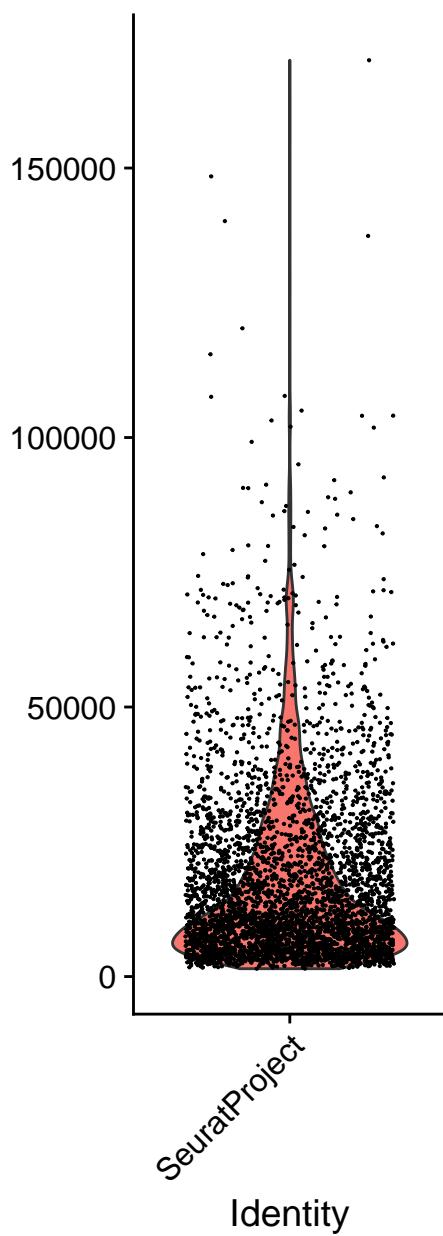
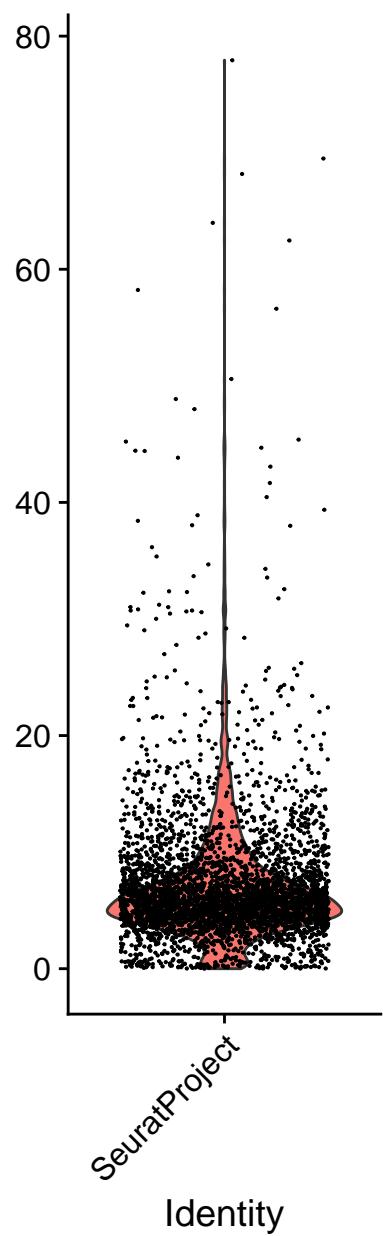


nCount_RNA

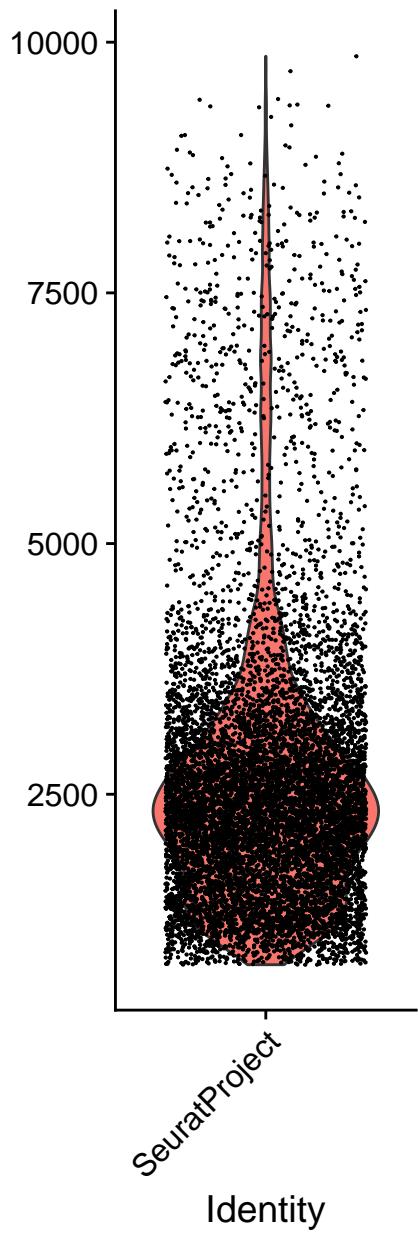


percent.mt

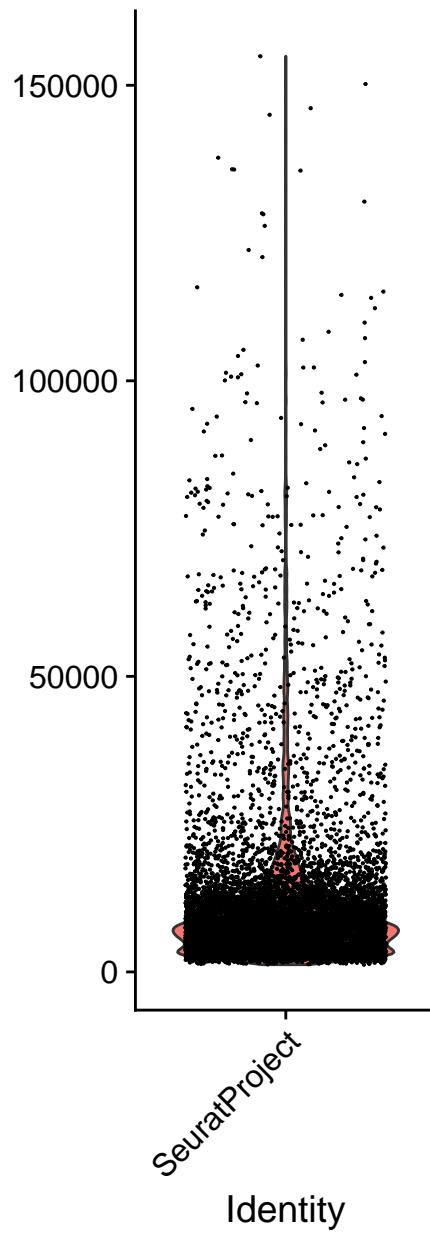


nFeature_RNA**nCount_RNA****percent.mt**

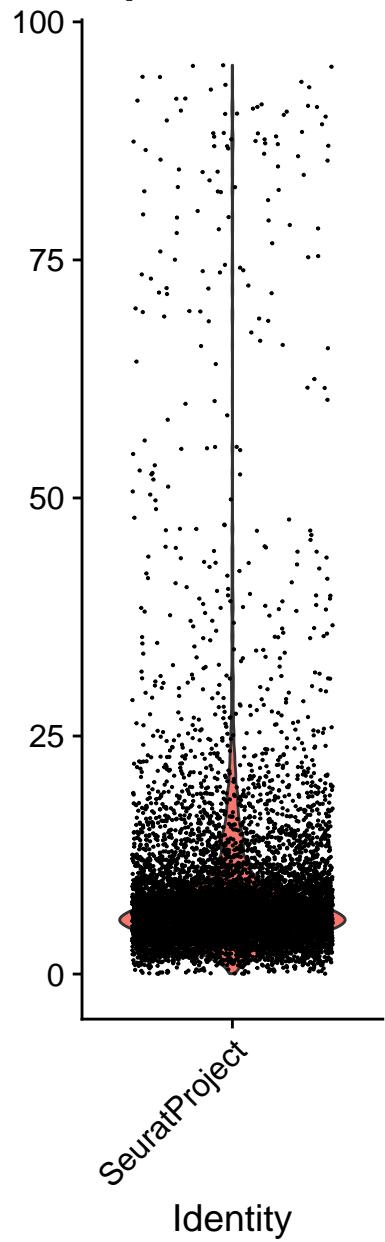
nFeature_RNA



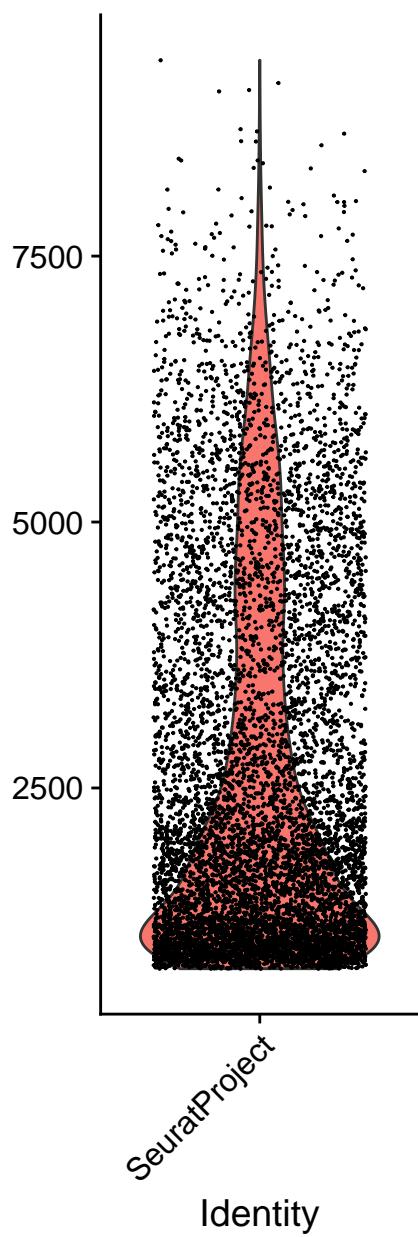
nCount_RNA



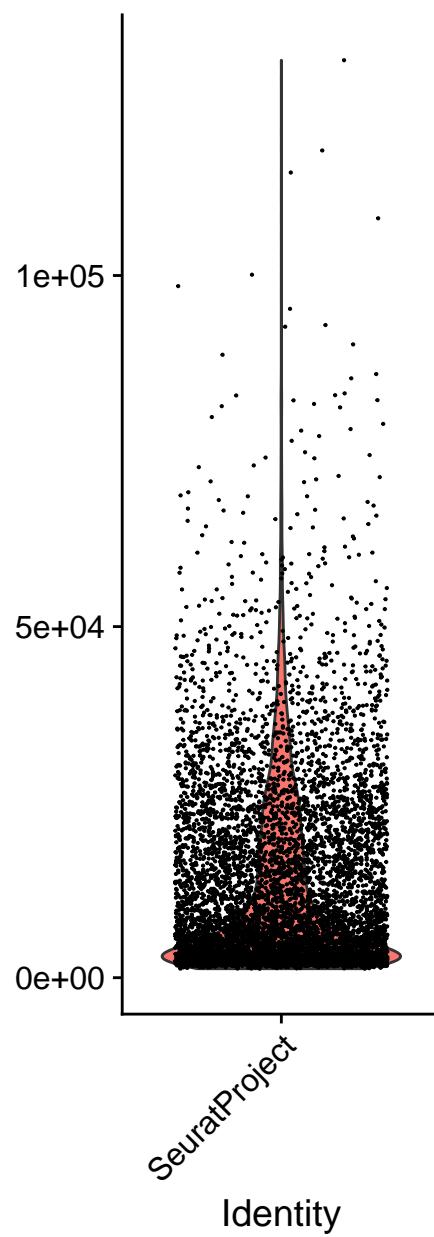
percent.mt



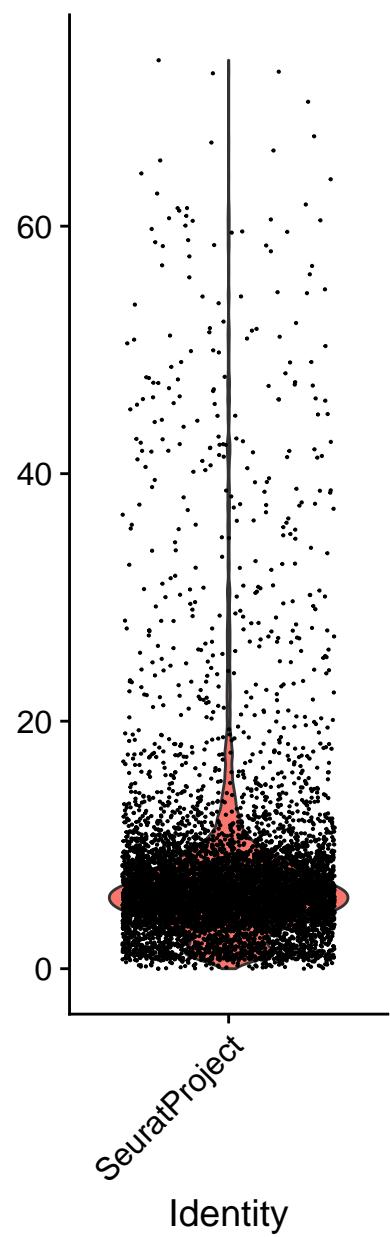
nFeature_RNA

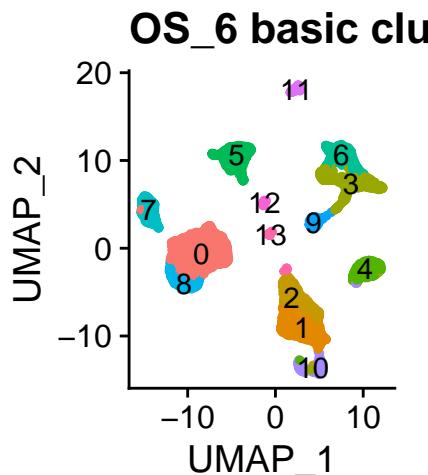
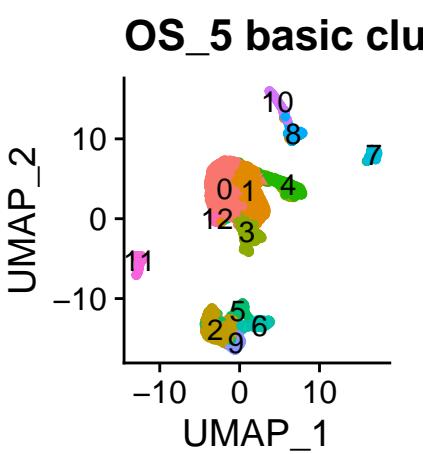
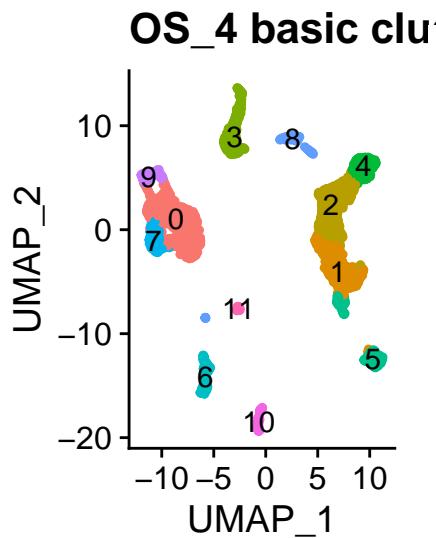
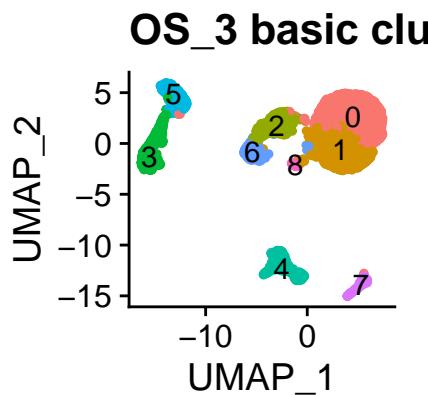
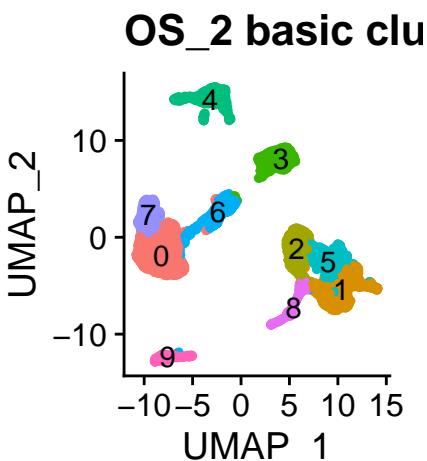
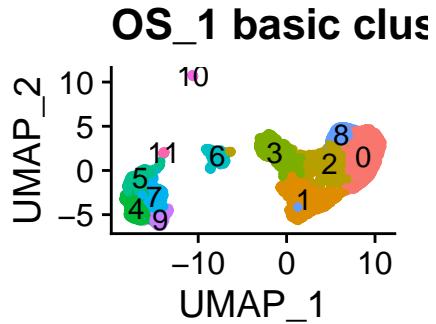


nCount_RNA

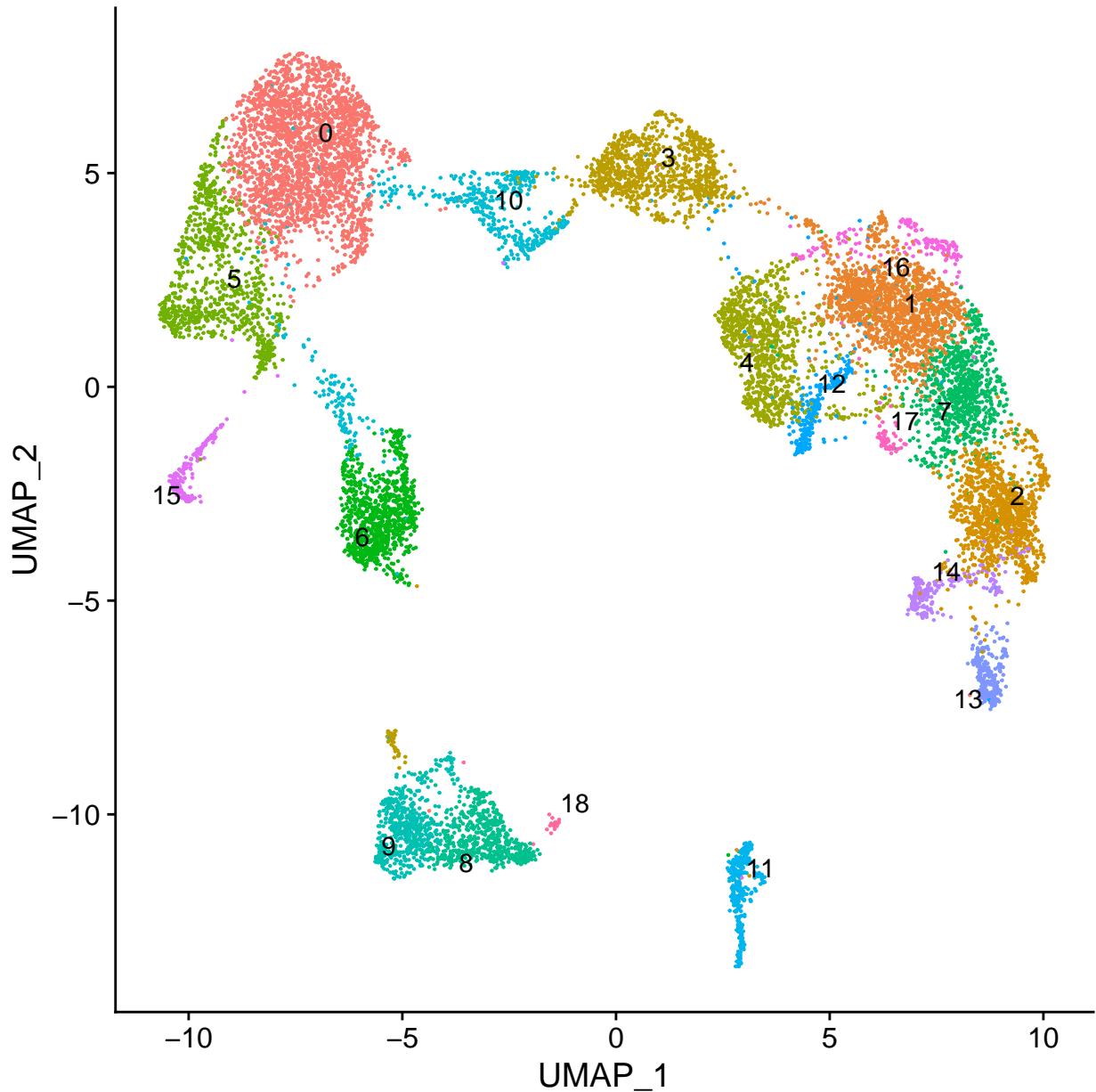


percent.mt

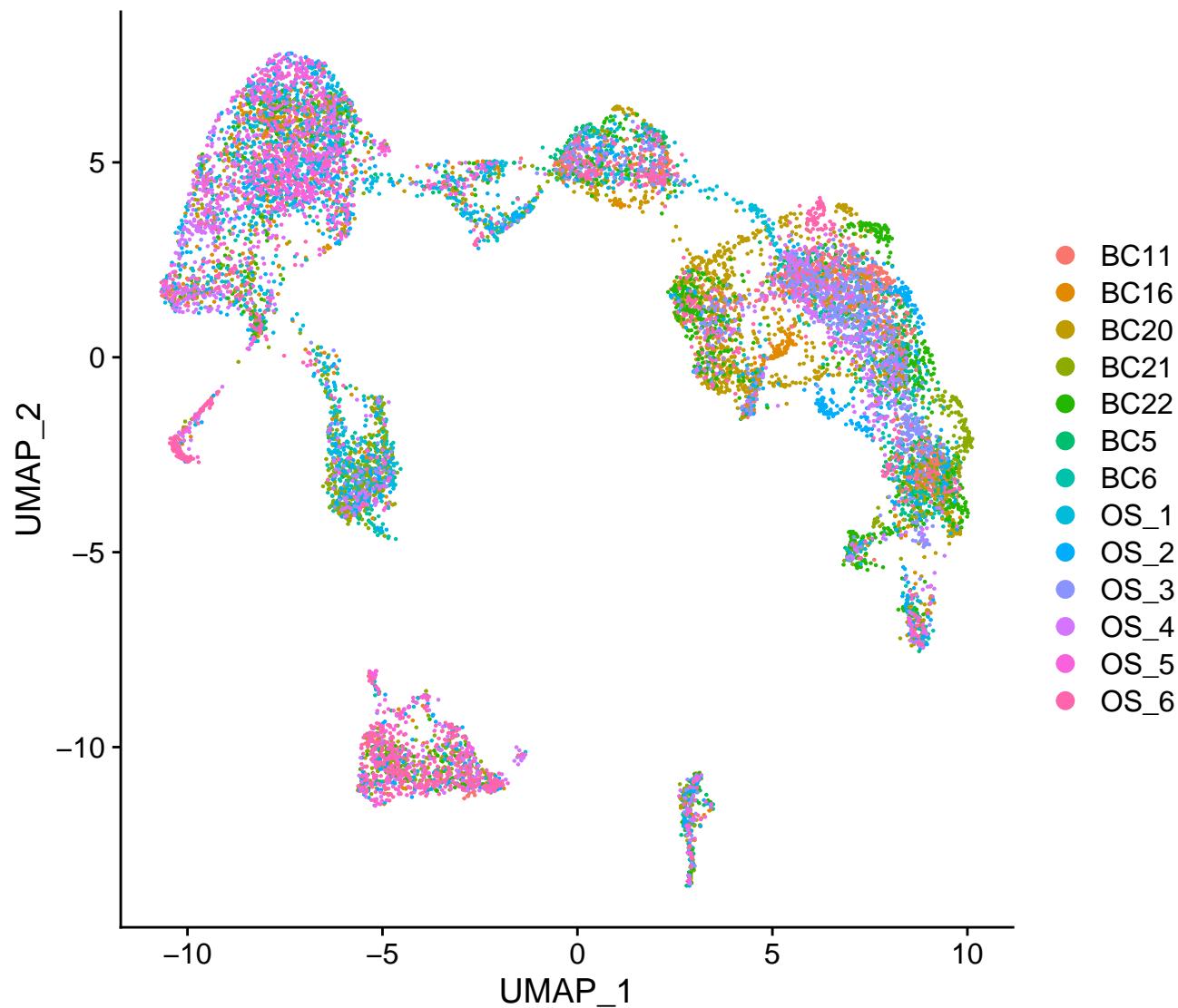




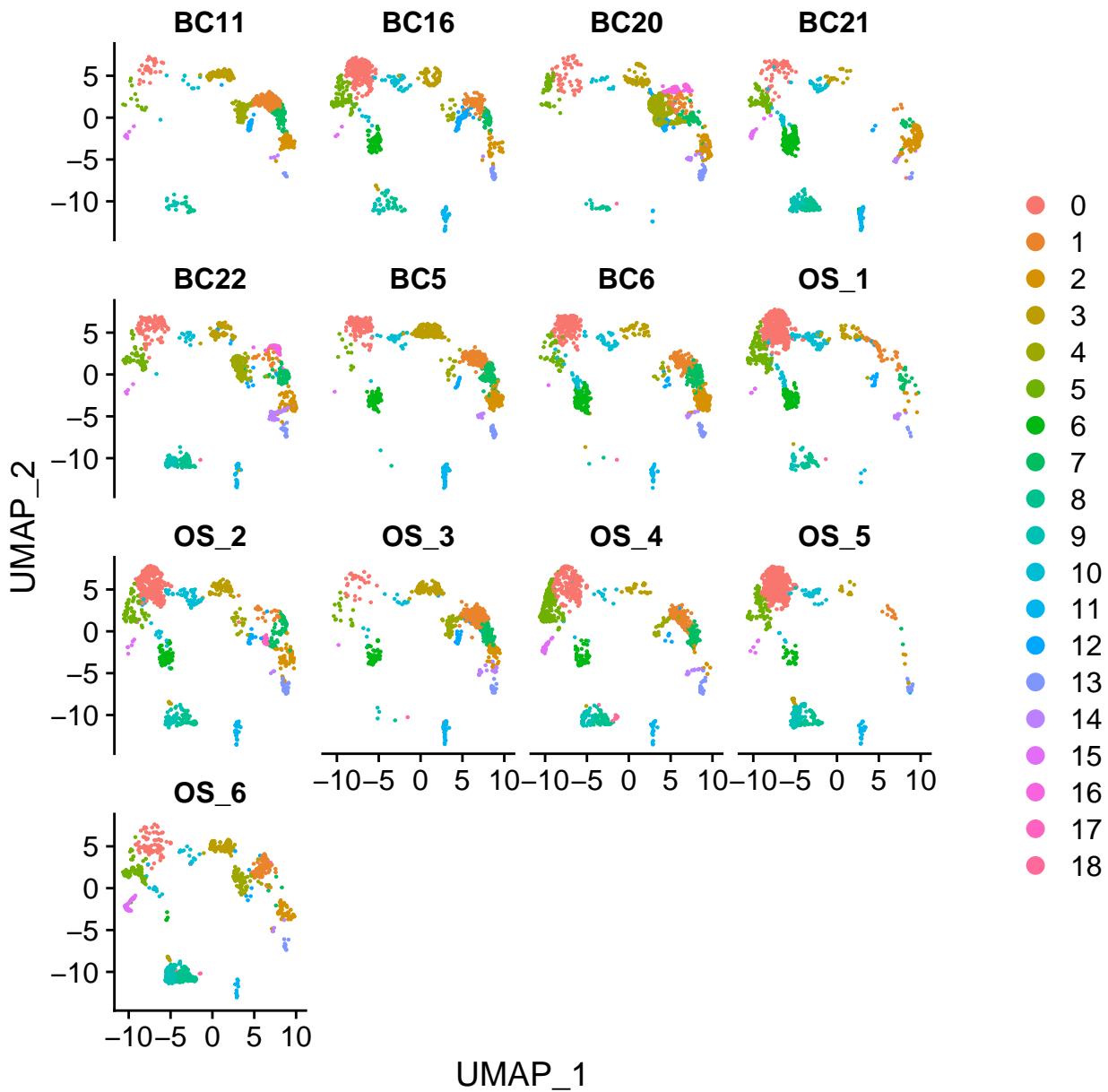
Primary Tumors (integrated)



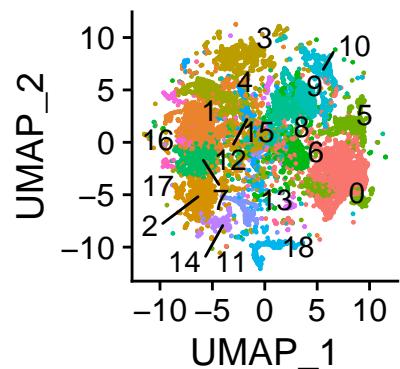
Primary Tumors (integrated)



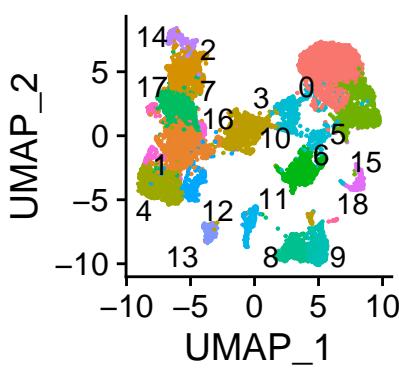
Primary Tumors (integrated)



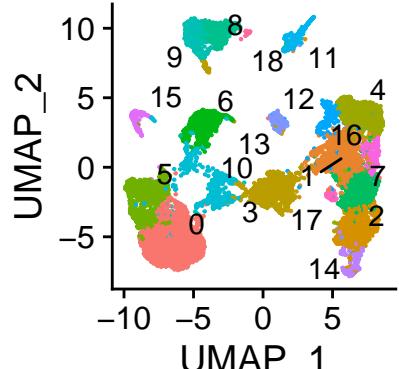
set.op.mix.ratio



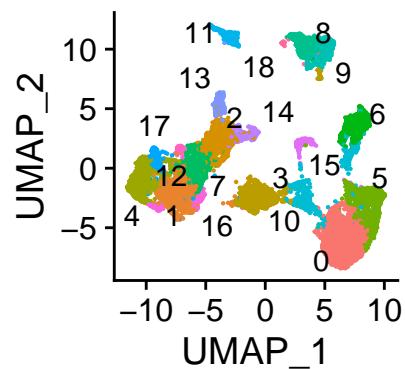
set.op.mix.ratio



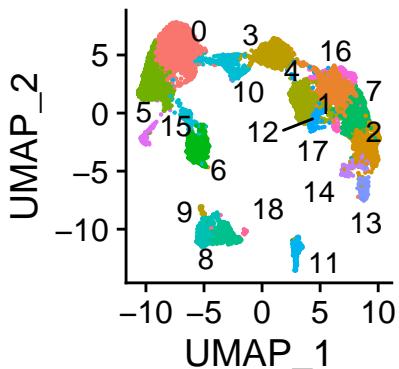
set.op.mix.ratio



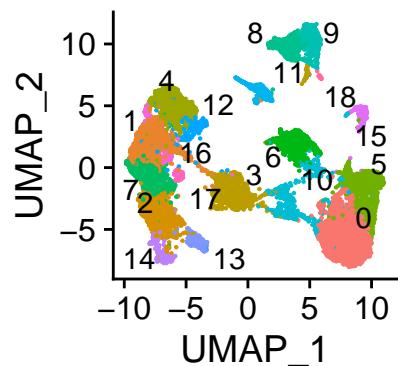
set.op.mix.ratio



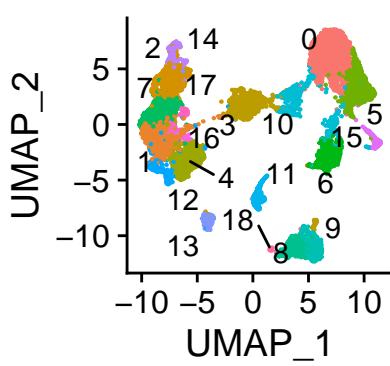
set.op.mix.ratio = 1



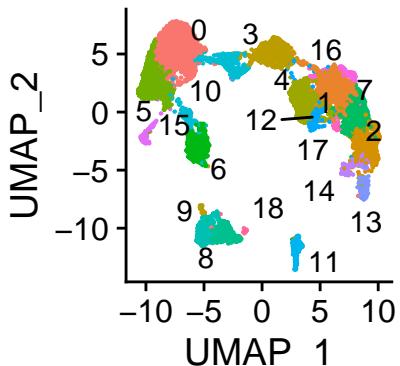
n.neighbors = 1



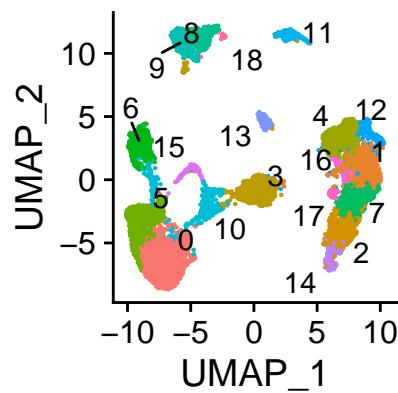
n.neighbors = 2



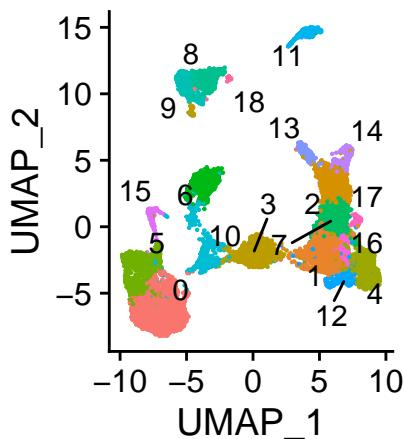
n.neighbors = 3



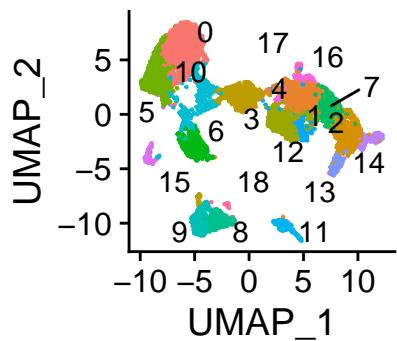
n.neighbors = 4



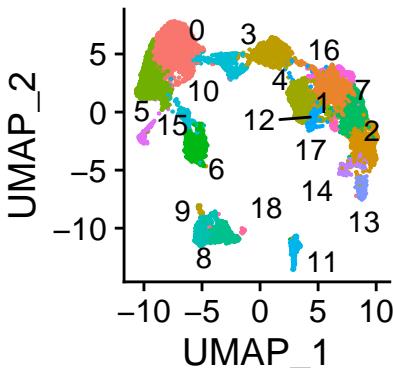
n.neighbors = 50



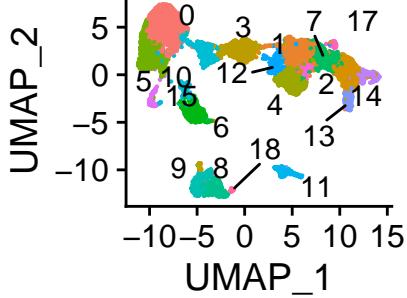
n.epochhs = 100



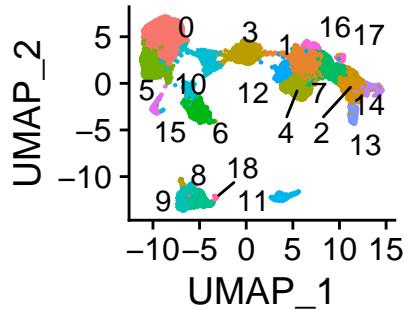
n.epochhs = 200



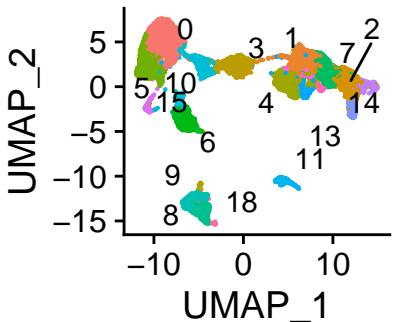
n.epochhs = 300



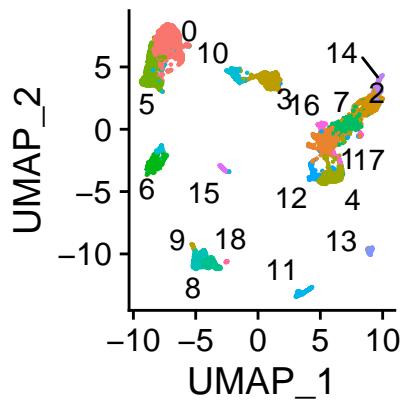
n.epochhs = 400



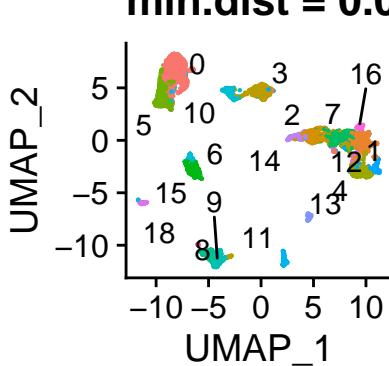
n.epochhs = 500



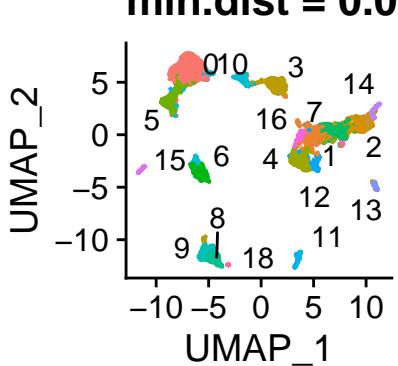
min.dist = 0.00



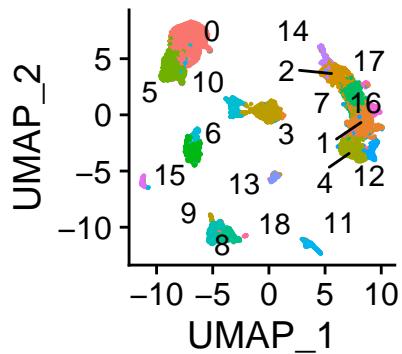
min.dist = 0.00



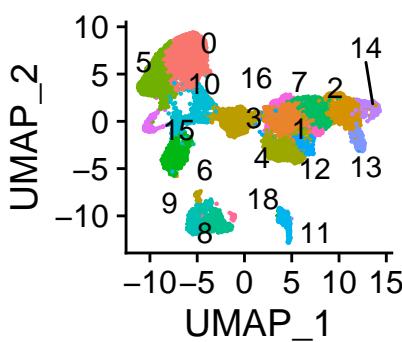
min.dist = 0.02

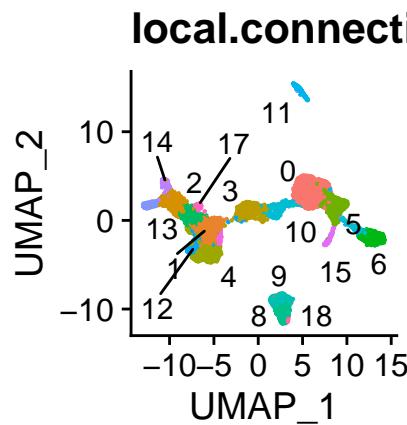
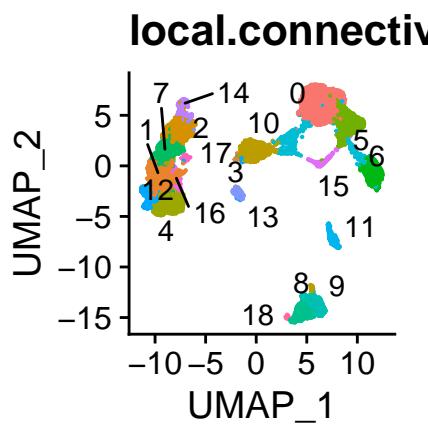
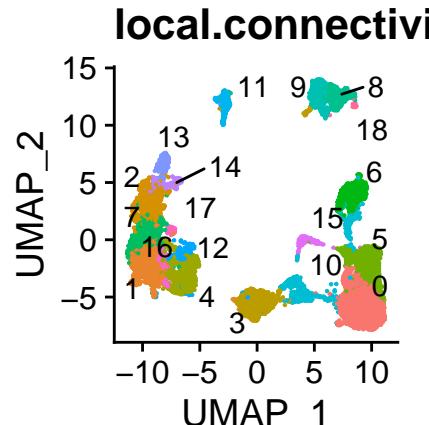
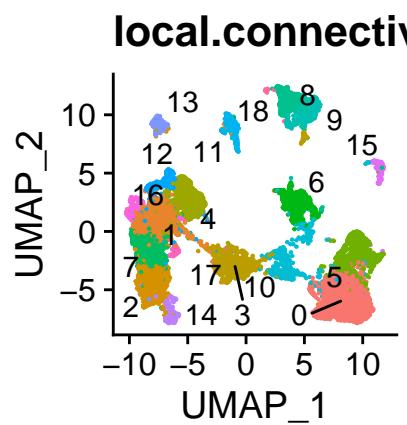
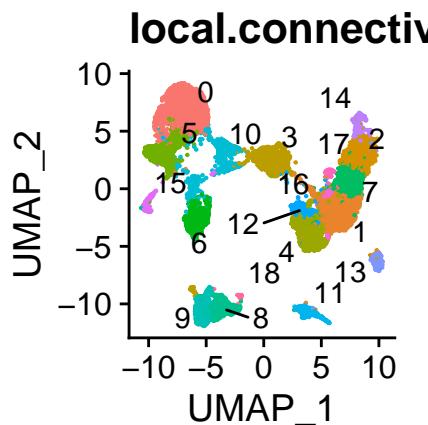


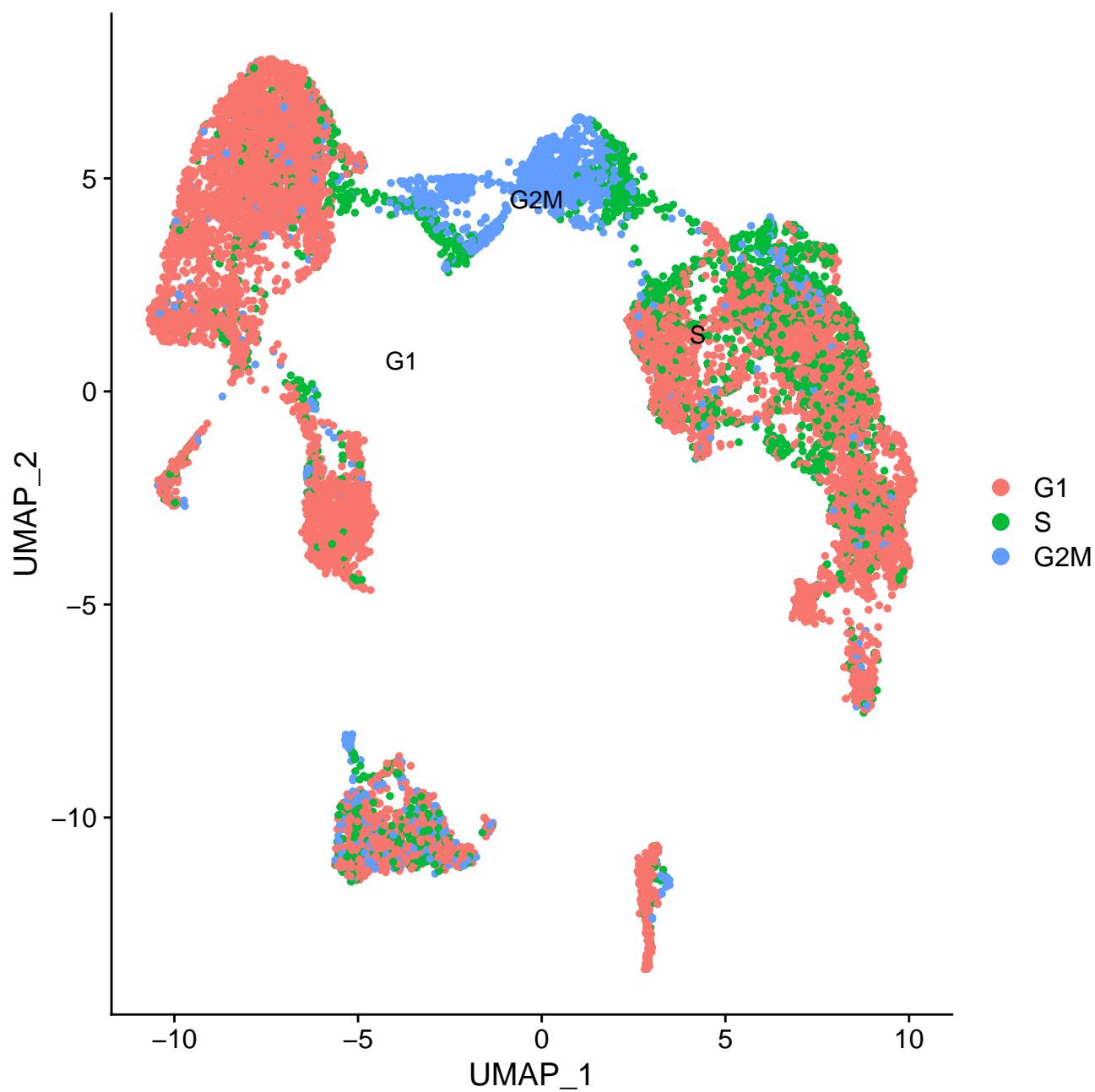
min.dist = 0.11

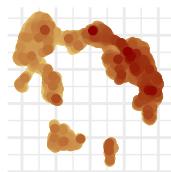


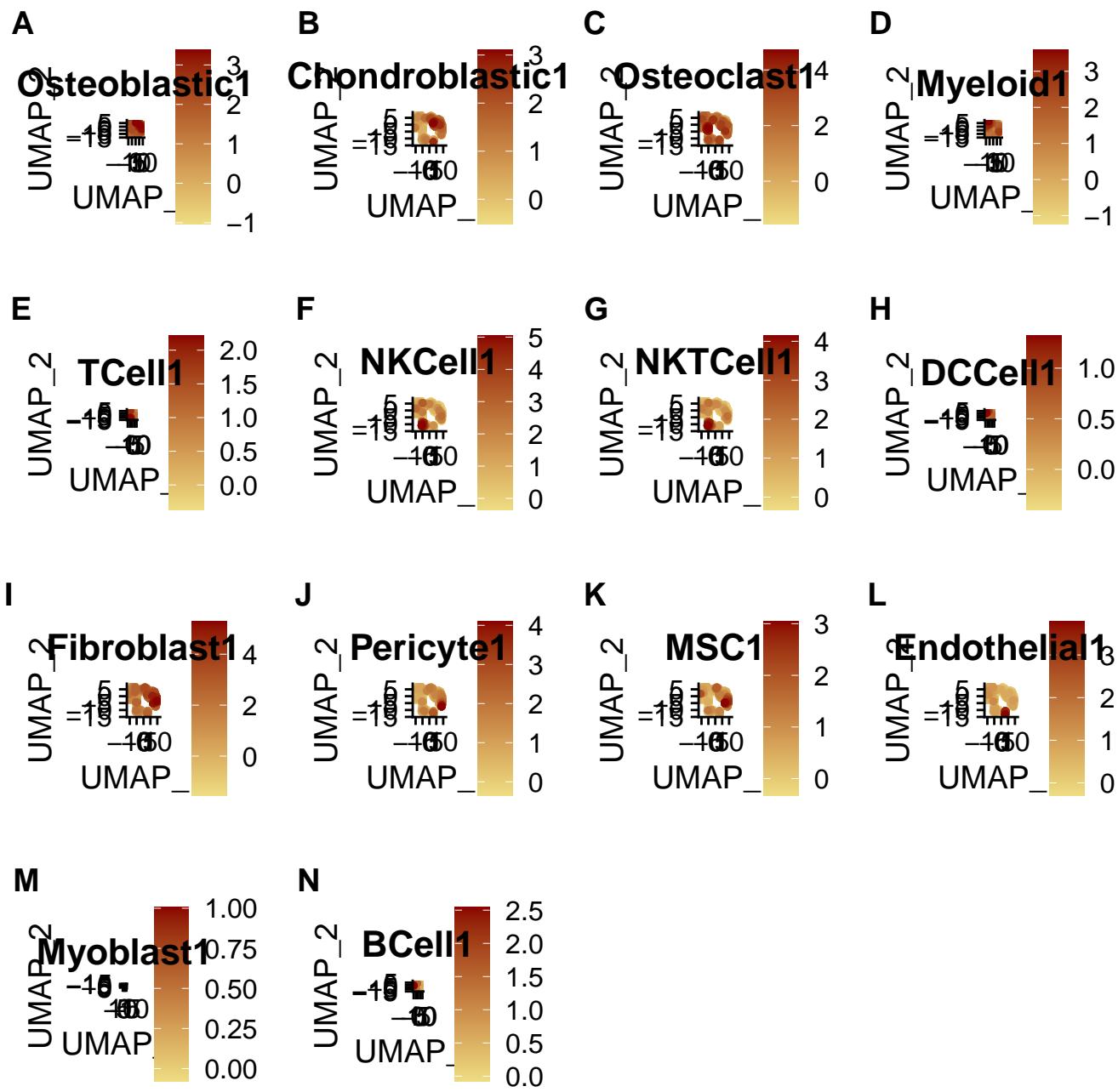
min.dist = 0.4608



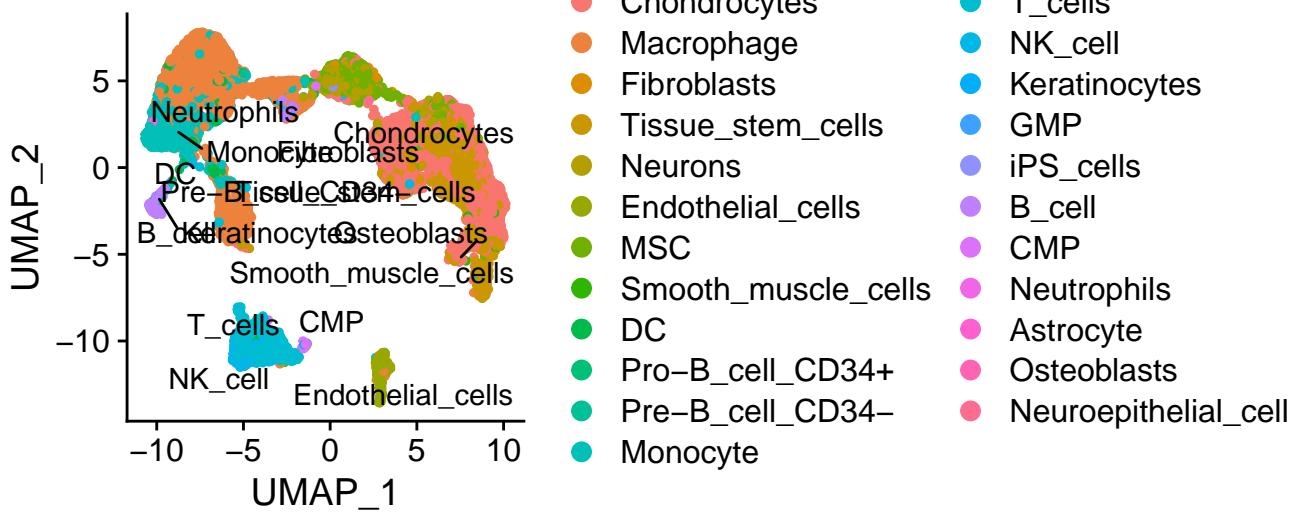


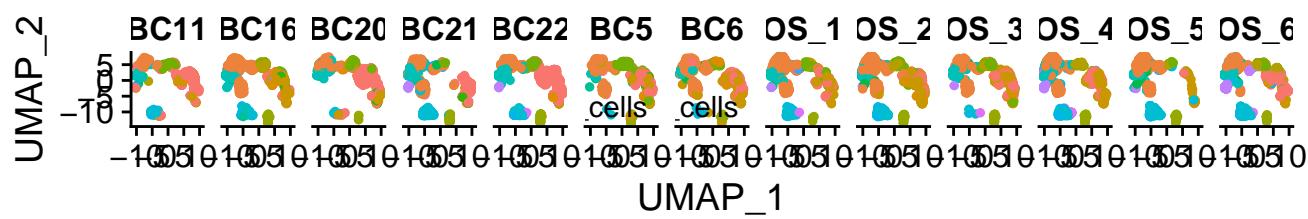






Cell Type Predictions (Human Primary Cell Atlas)





Cell Type Predictions (Blueprint/ENCODE)

