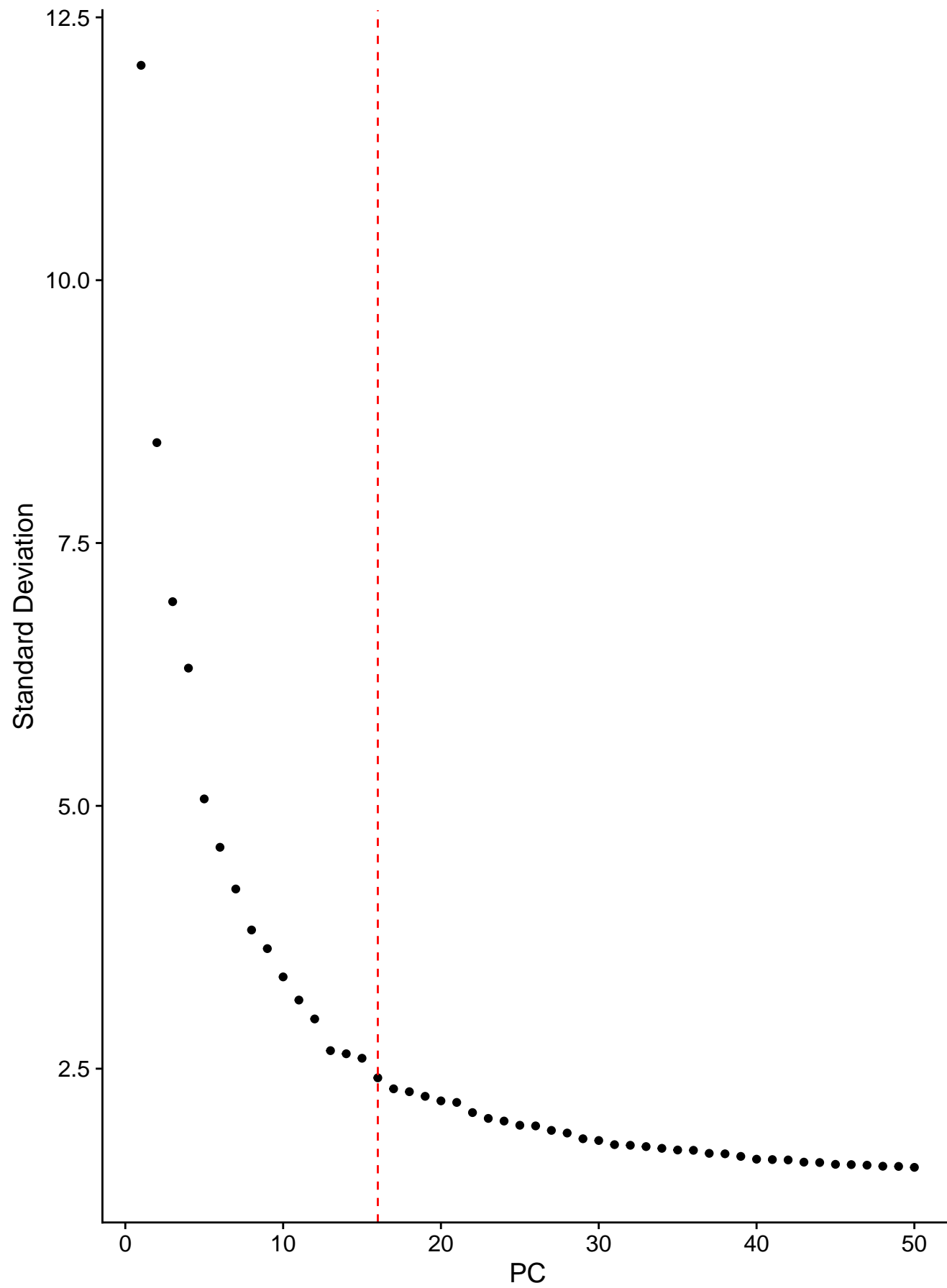
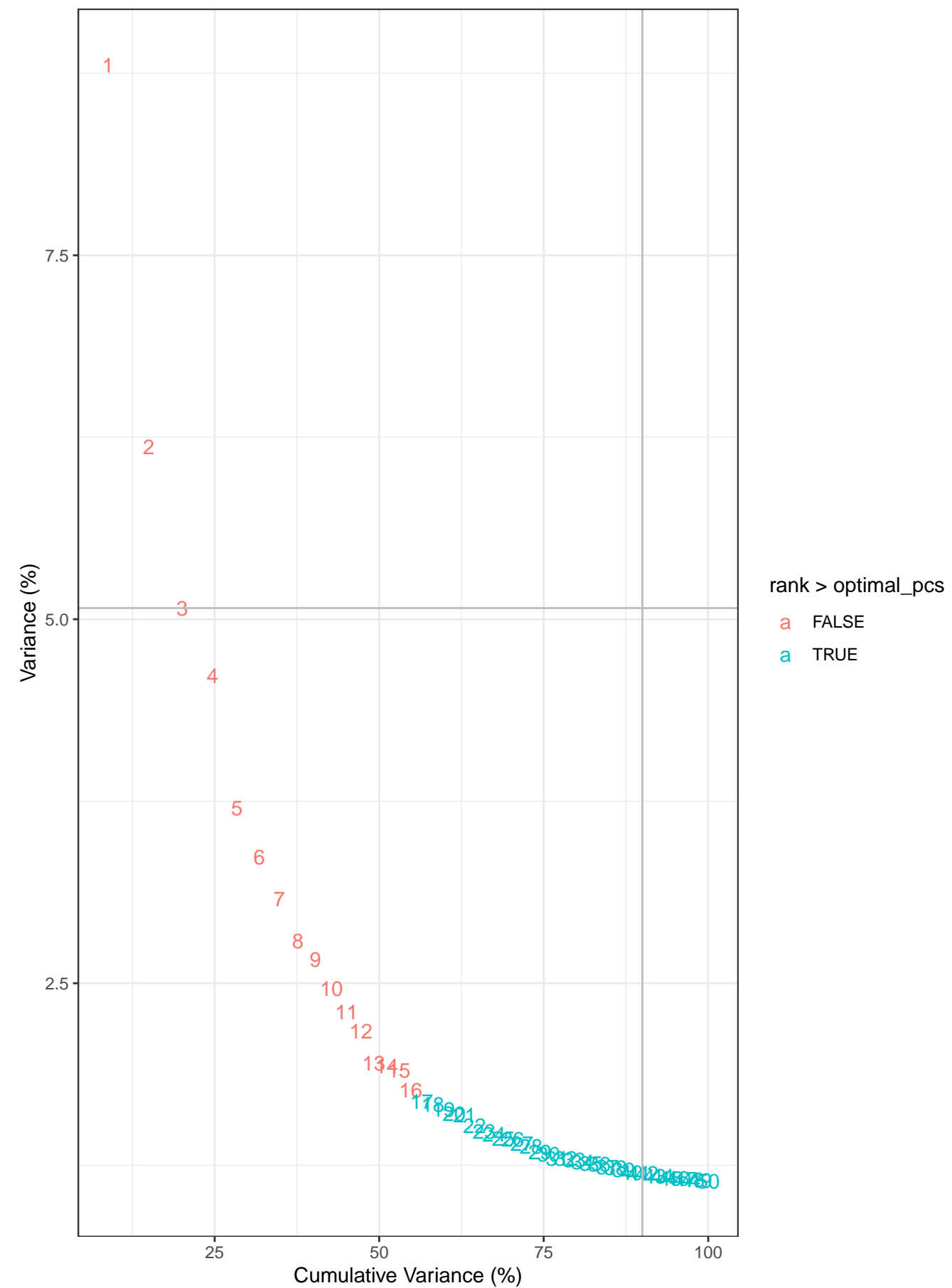


# 3M\_Org – PCA Elbow Analysis (Pre-Integration)

## 3M\_Org: Elbow Plot (Optimal PCs = 16)

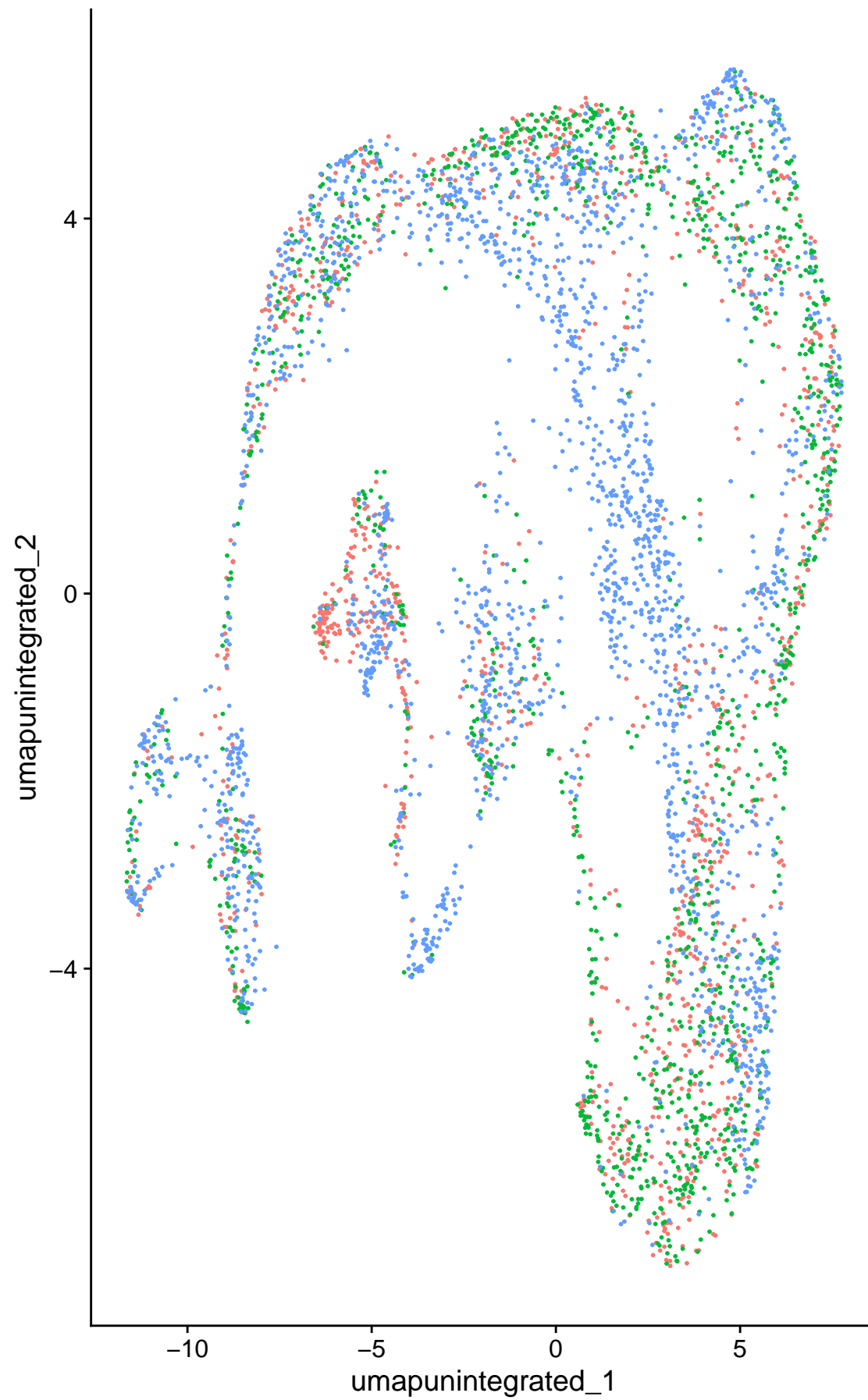


## 3M\_Org: Quantitative PC Selection

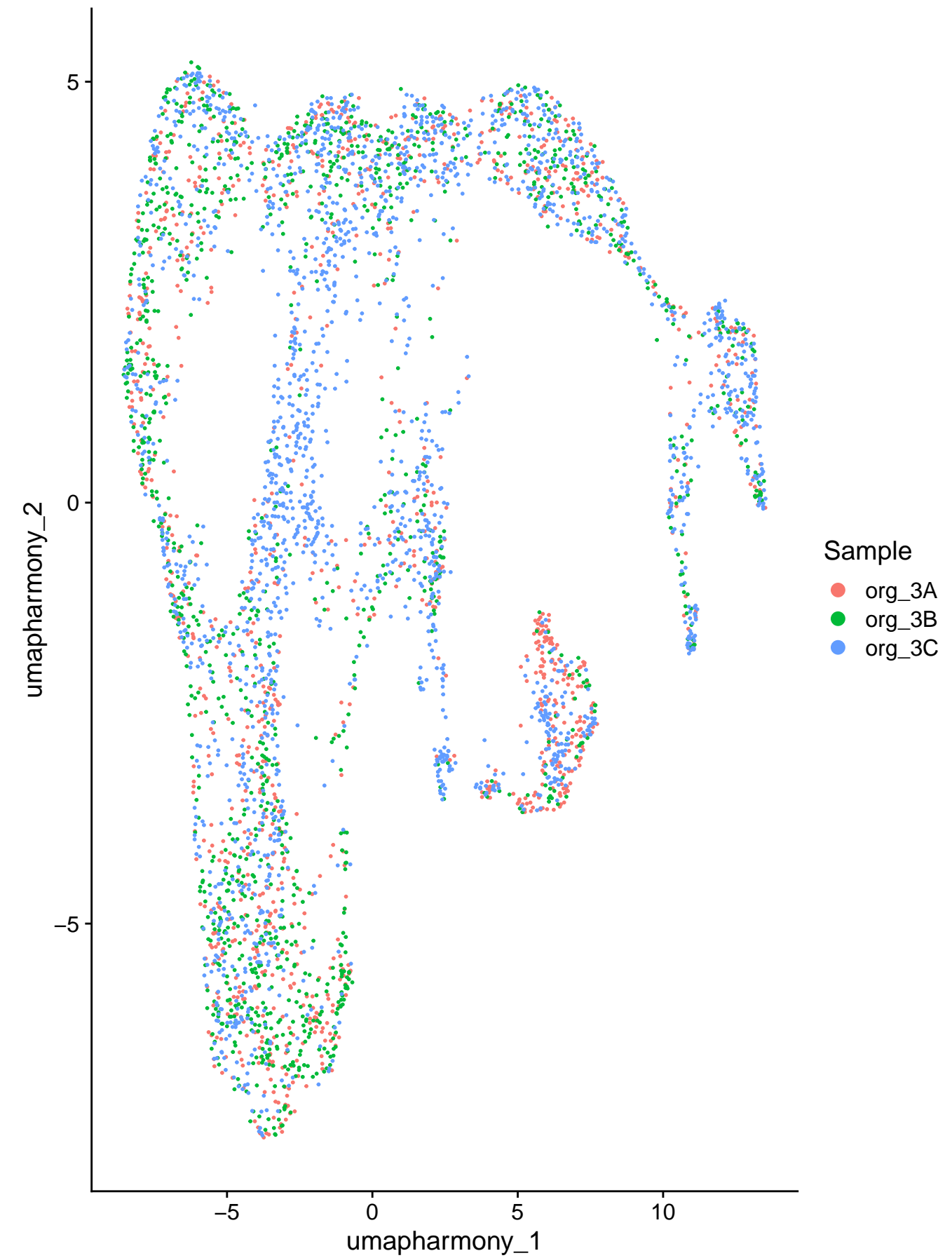


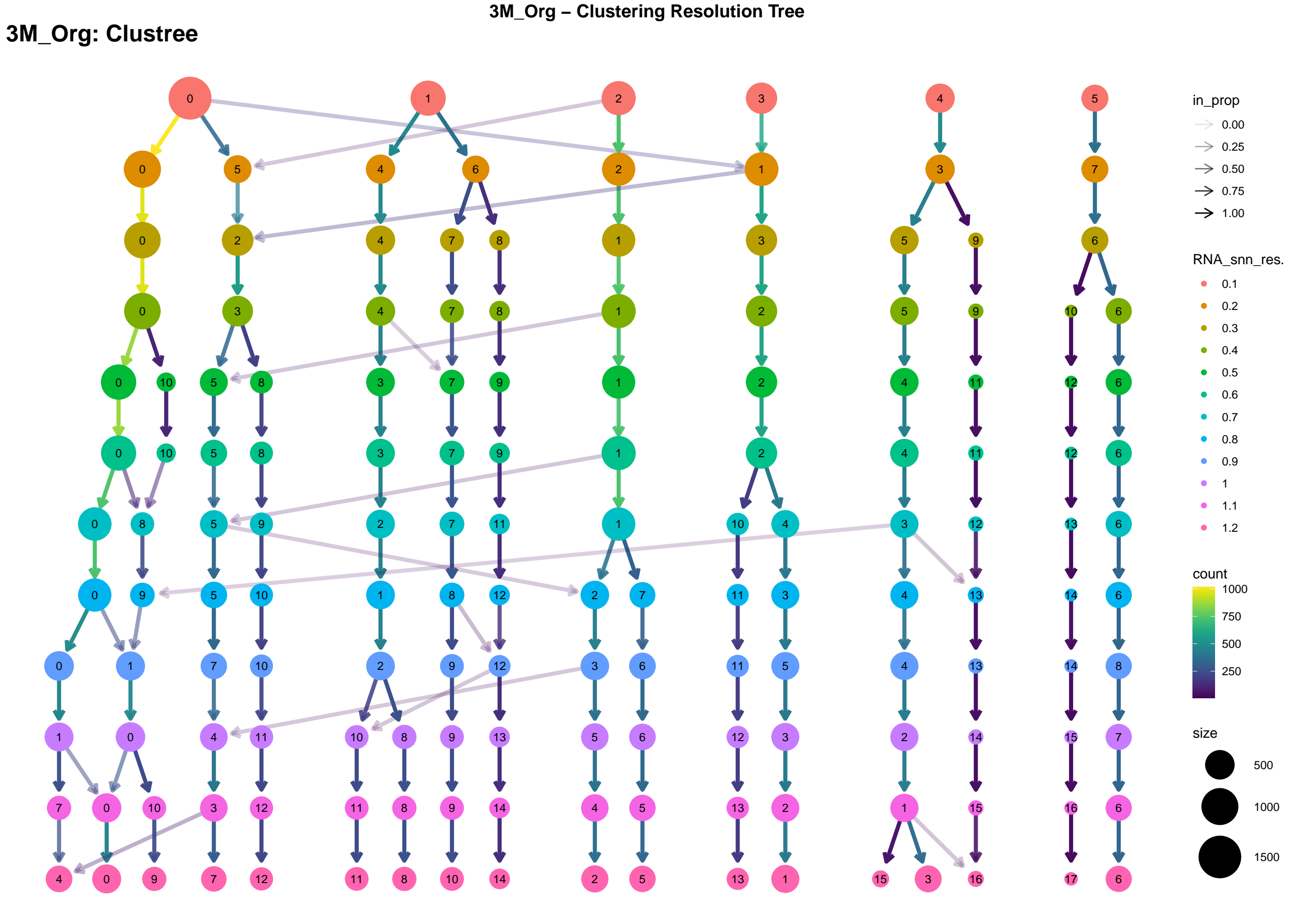
# 3M\_Org – Harmony Integration Comparison

## 3M\_Org: Before Integration

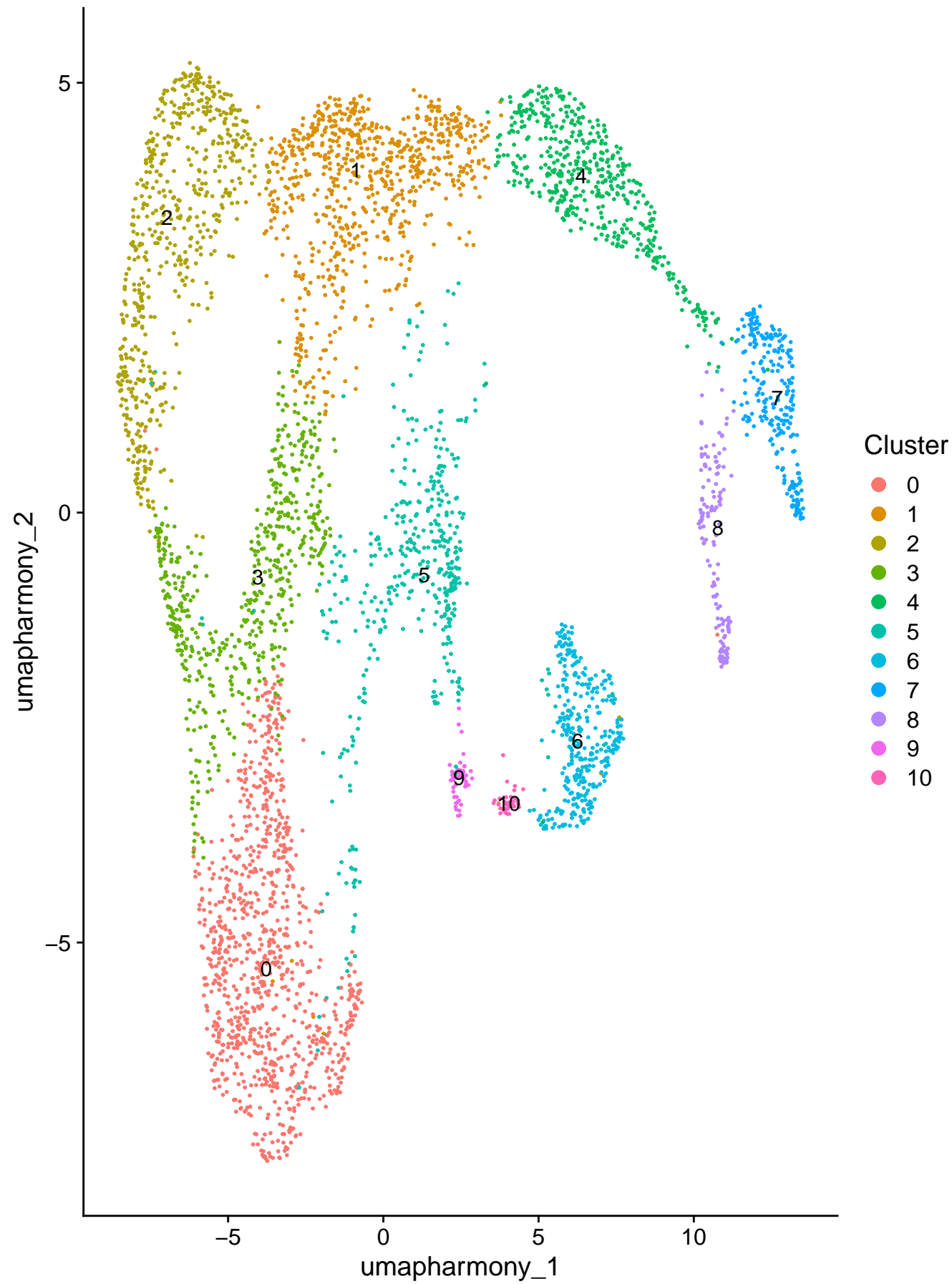


## 3M\_Org: After Harmony Integration





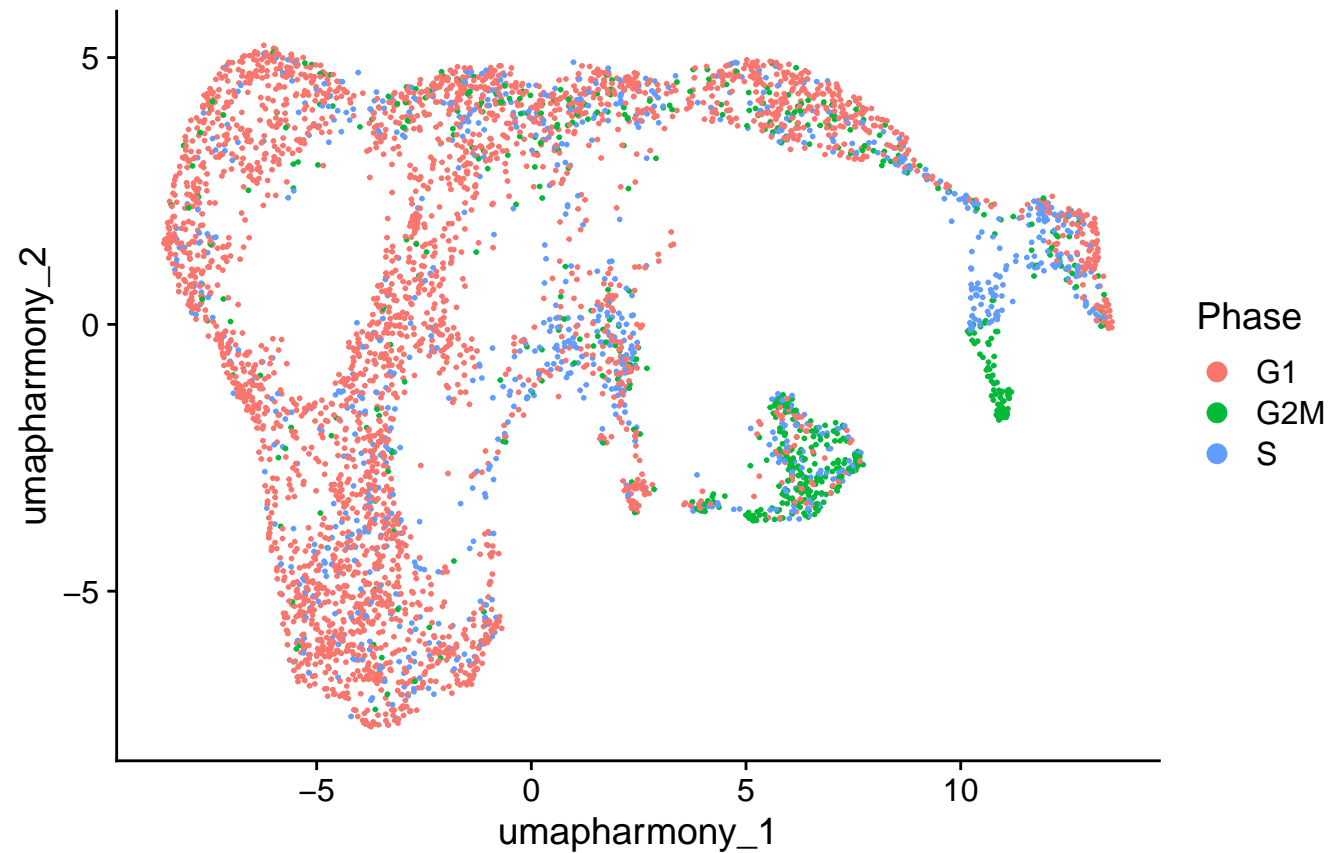
3M\_Org: Final Clusters



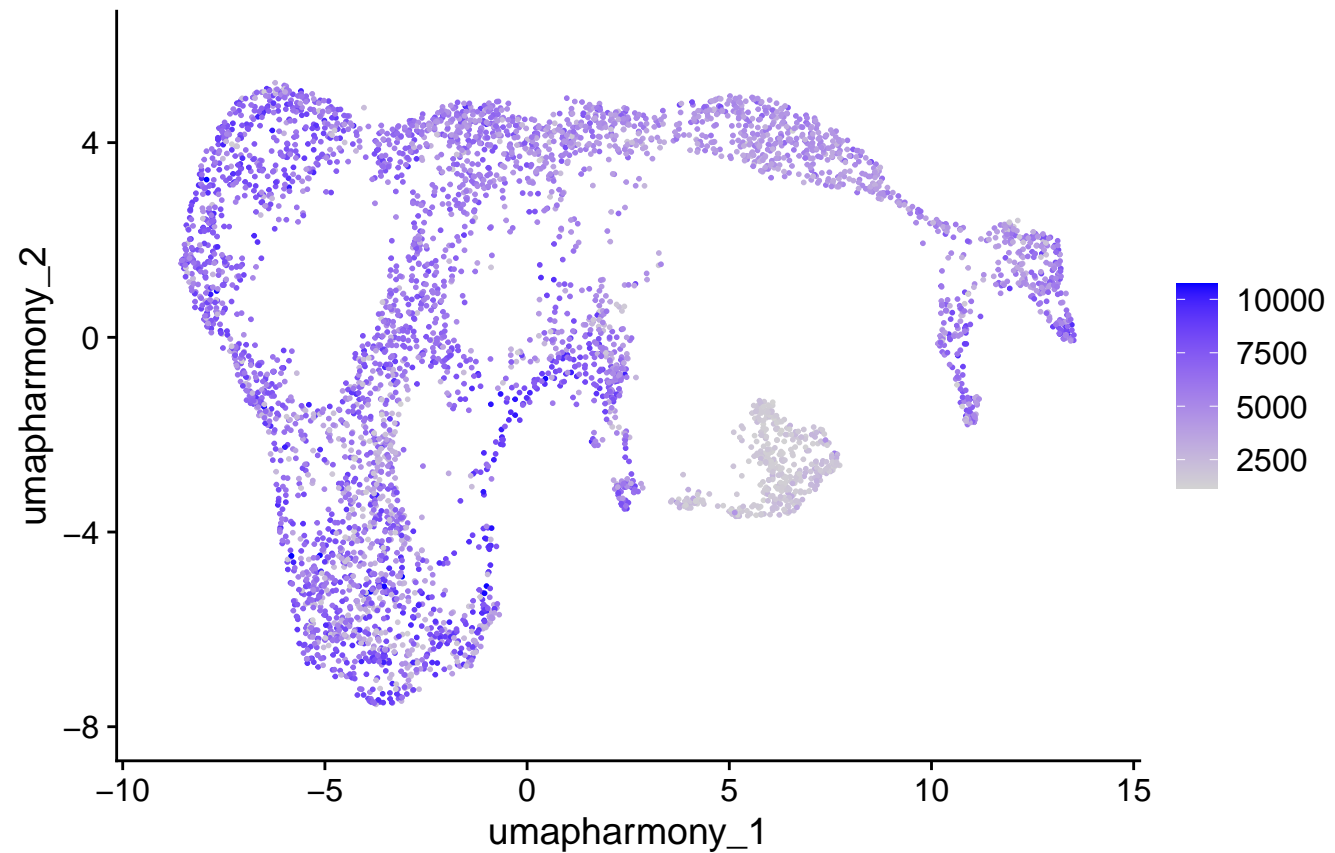
	res_vals	num_clusters	avg_sil_vals
1	0.4	11	0.379971491839363
2	0.3	10	0.379920557899472
3	0.2	8	0.336260498765787
4	0.6	13	0.321513053501275
5	0.7	14	0.313644831909305
6	0.9	15	0.287896986706524
7	0.1	6	0.279413865891652
8	1	16	0.264329016484654
9	1.1	17	0.239157312578938
10	1.2	18	0.238128419489758

### 3M\_Org – QC Metrics on Integrated Data

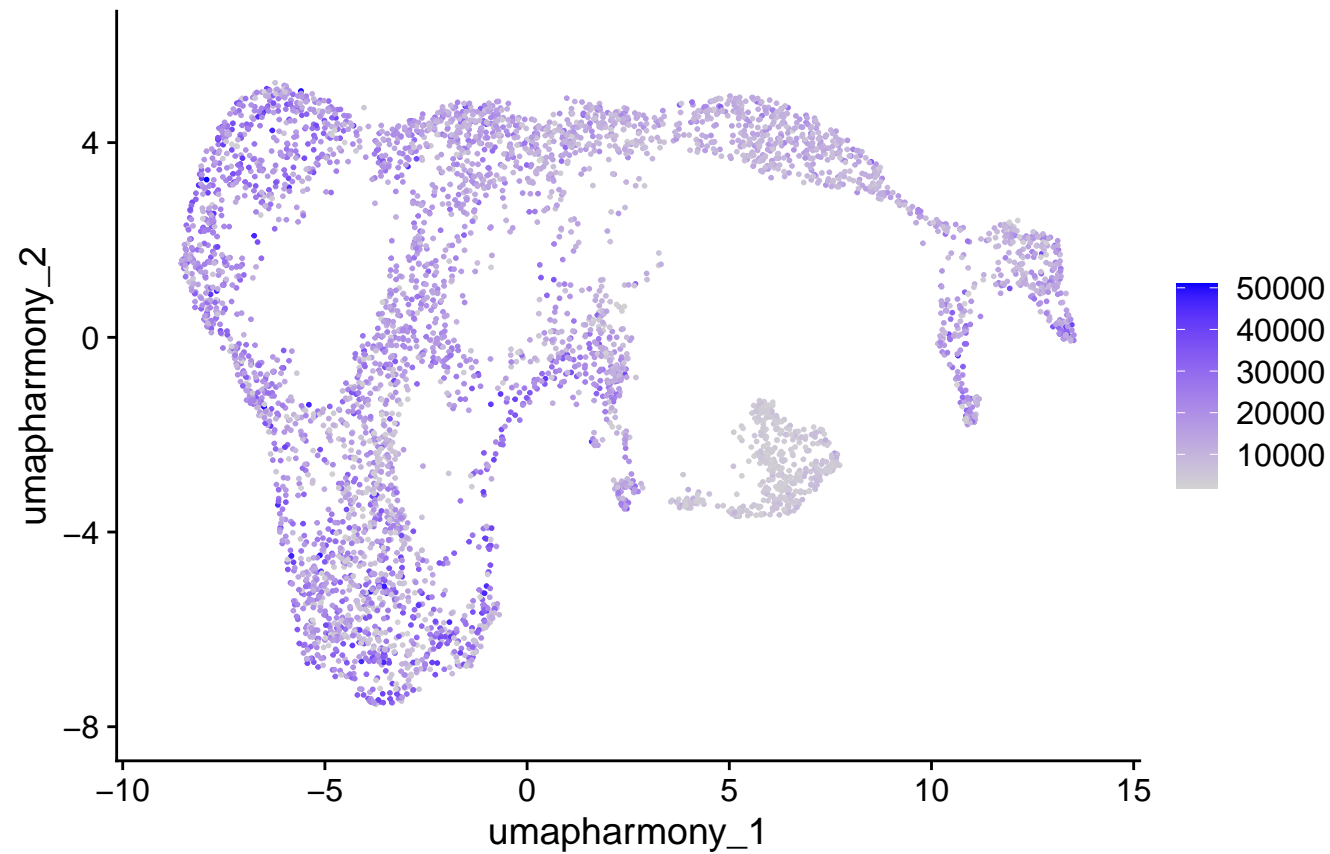
#### 3M\_Org: Cell Cycle Phase



#### 3M\_Org: nFeature\_RNA



#### 3M\_Org: nCount\_RNA



#### 3M\_Org: Final Clusters

