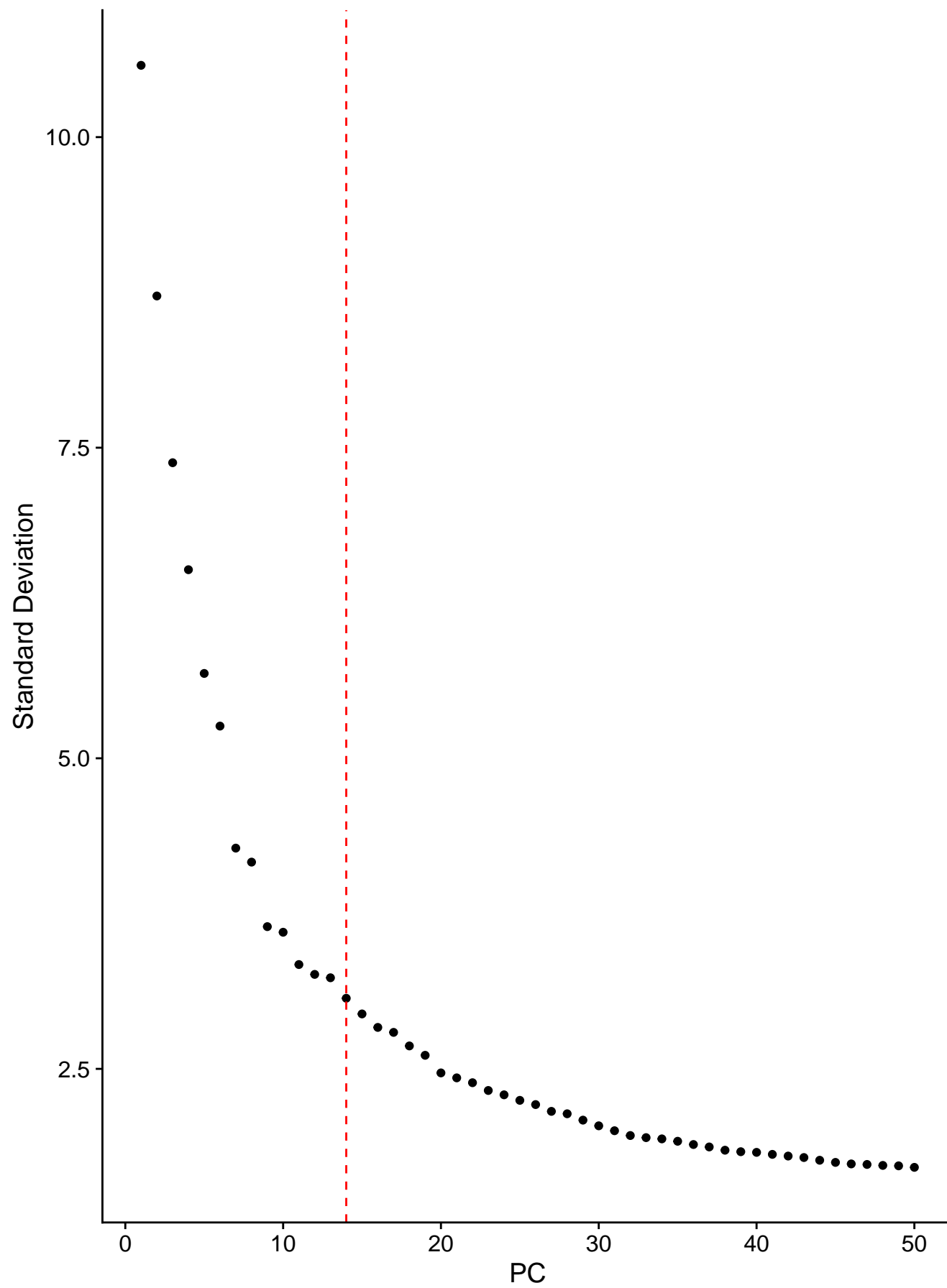
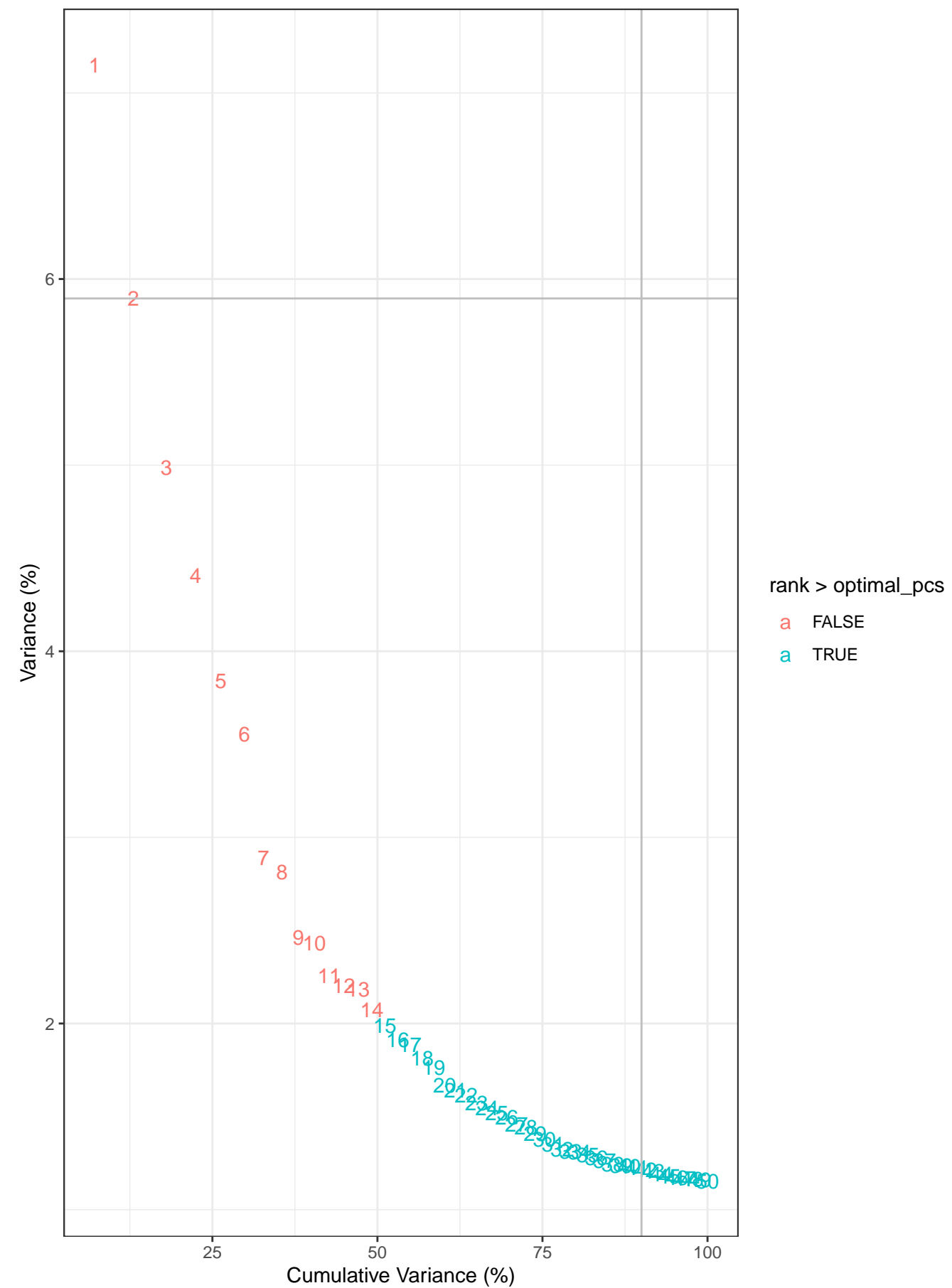


# 1M\_Org – PCA Elbow Analysis (Pre-Integration)

1M\_Org: Elbow Plot (Optimal PCs = 14)

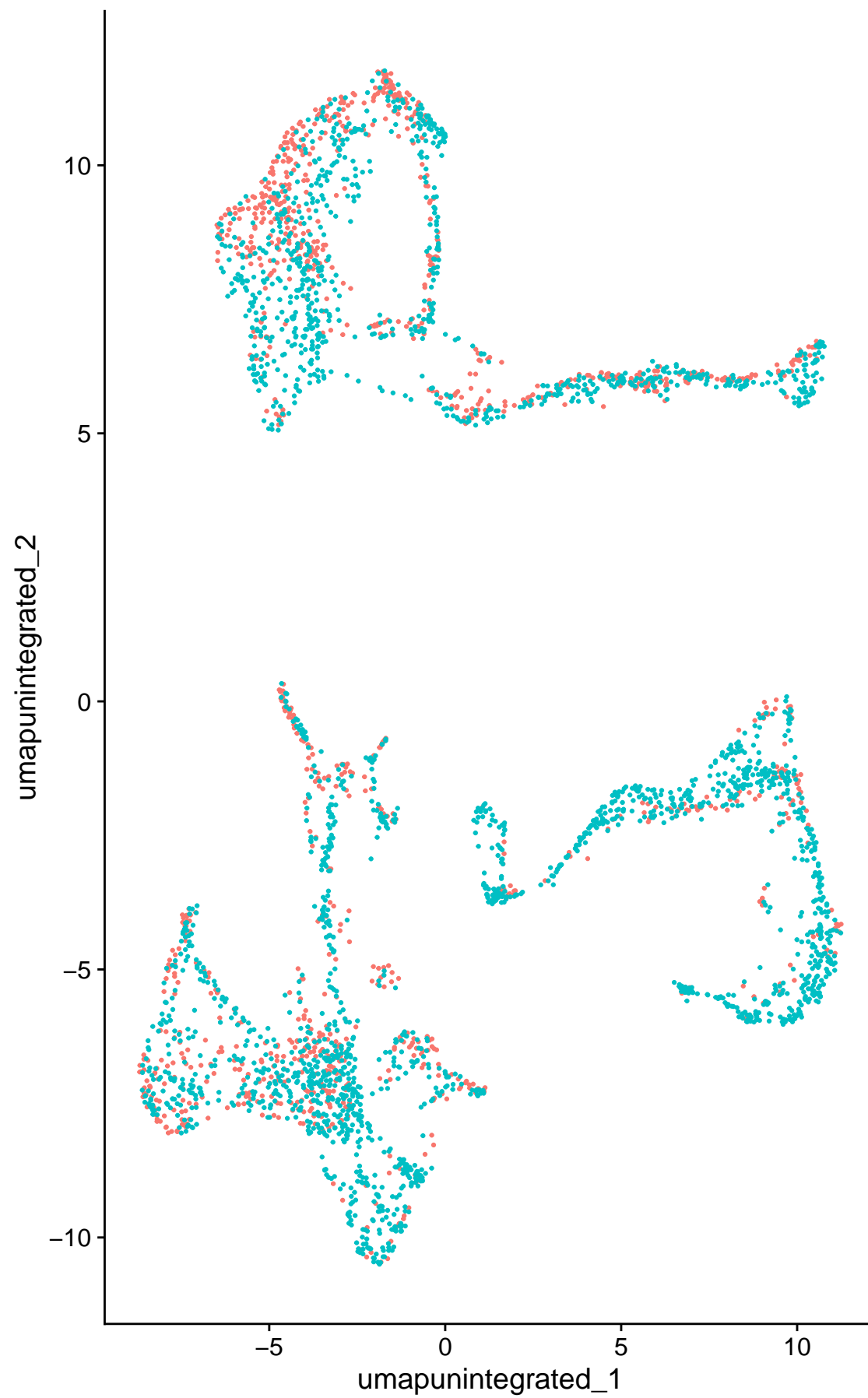


1M\_Org: Quantitative PC Selection

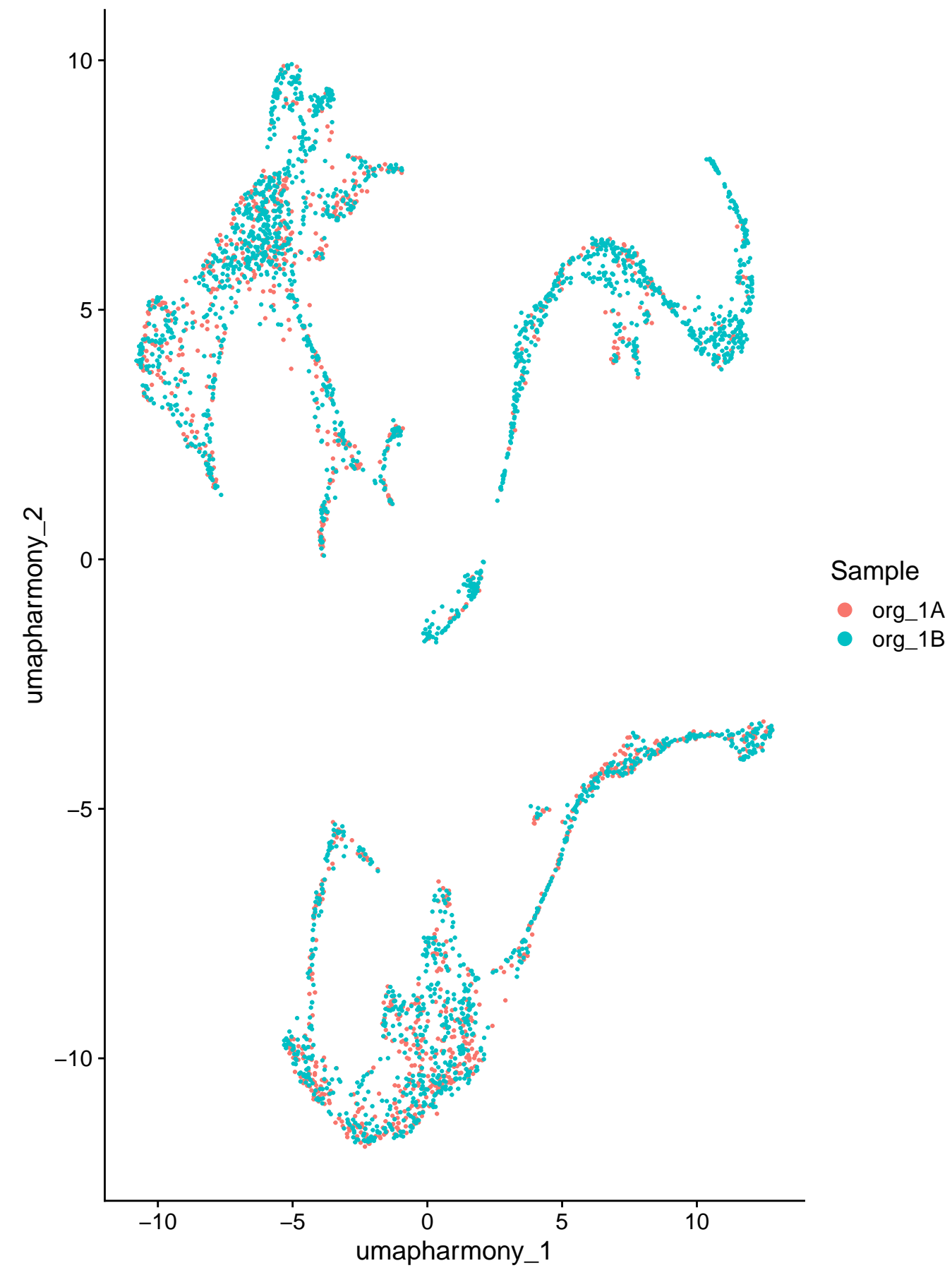


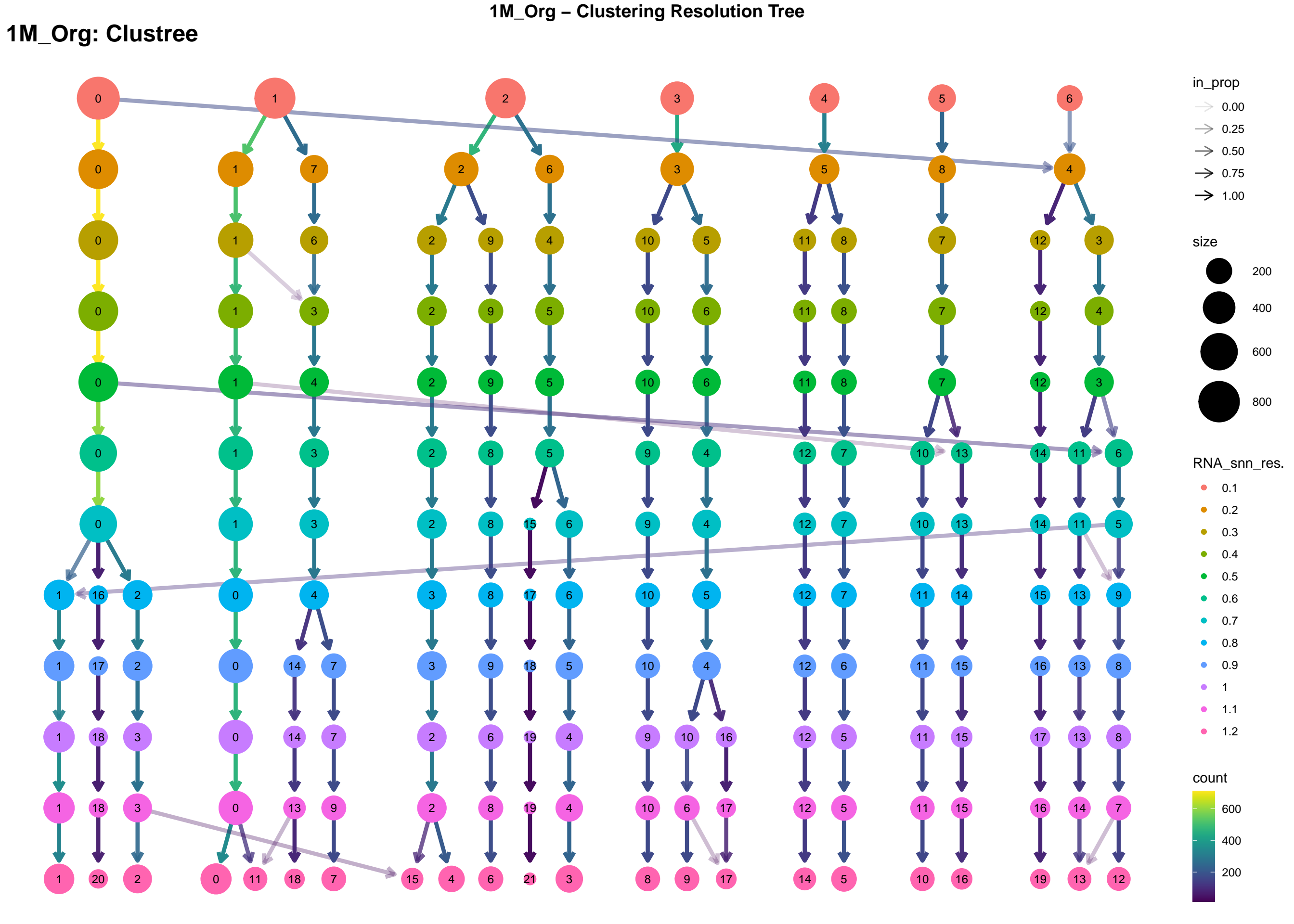
# 1M\_Org – Harmony Integration Comparison

## 1M\_Org: Before Integration



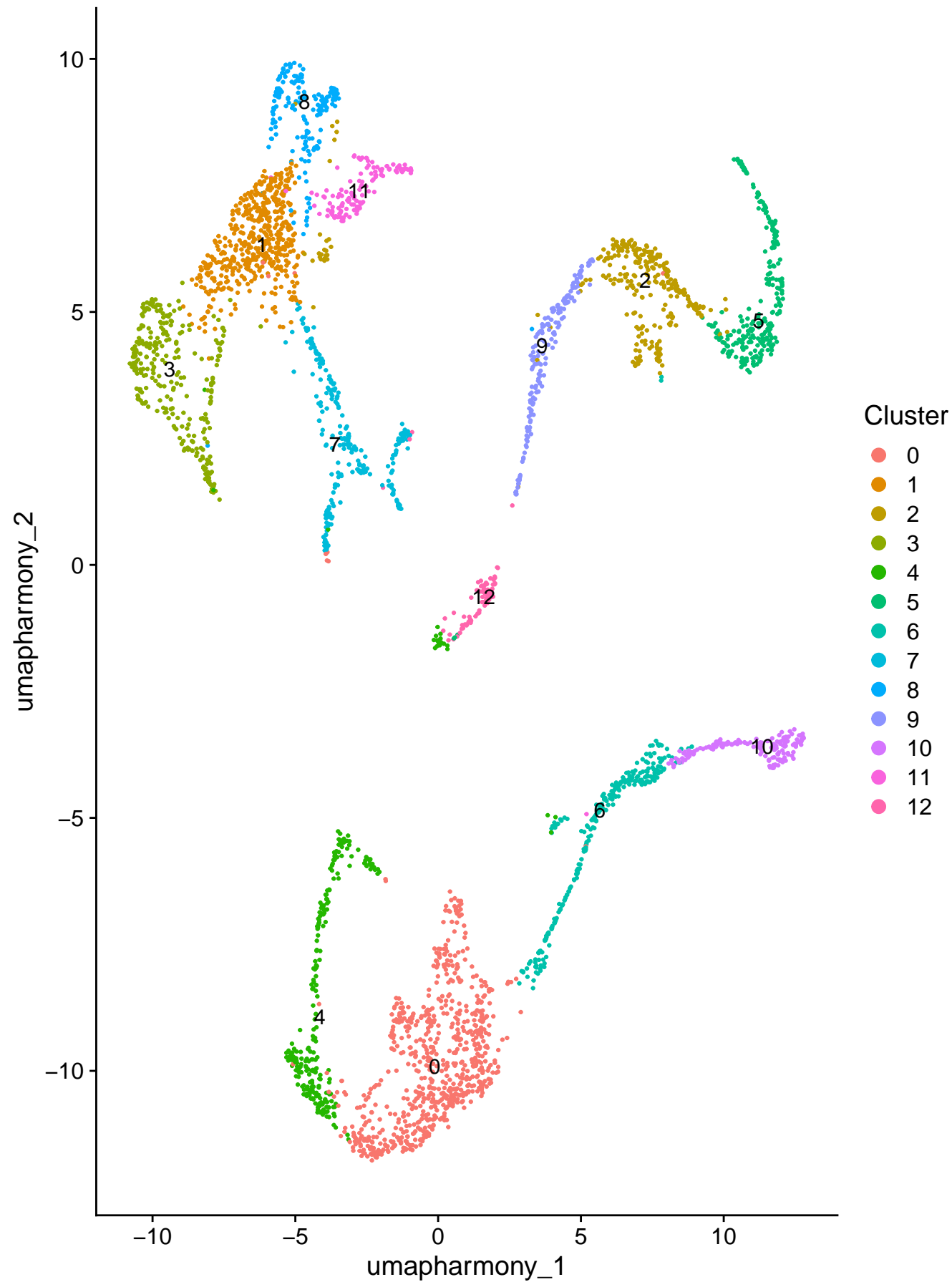
## 1M\_Org: After Harmony Integration





# 1M\_Org – Final Clustering Results

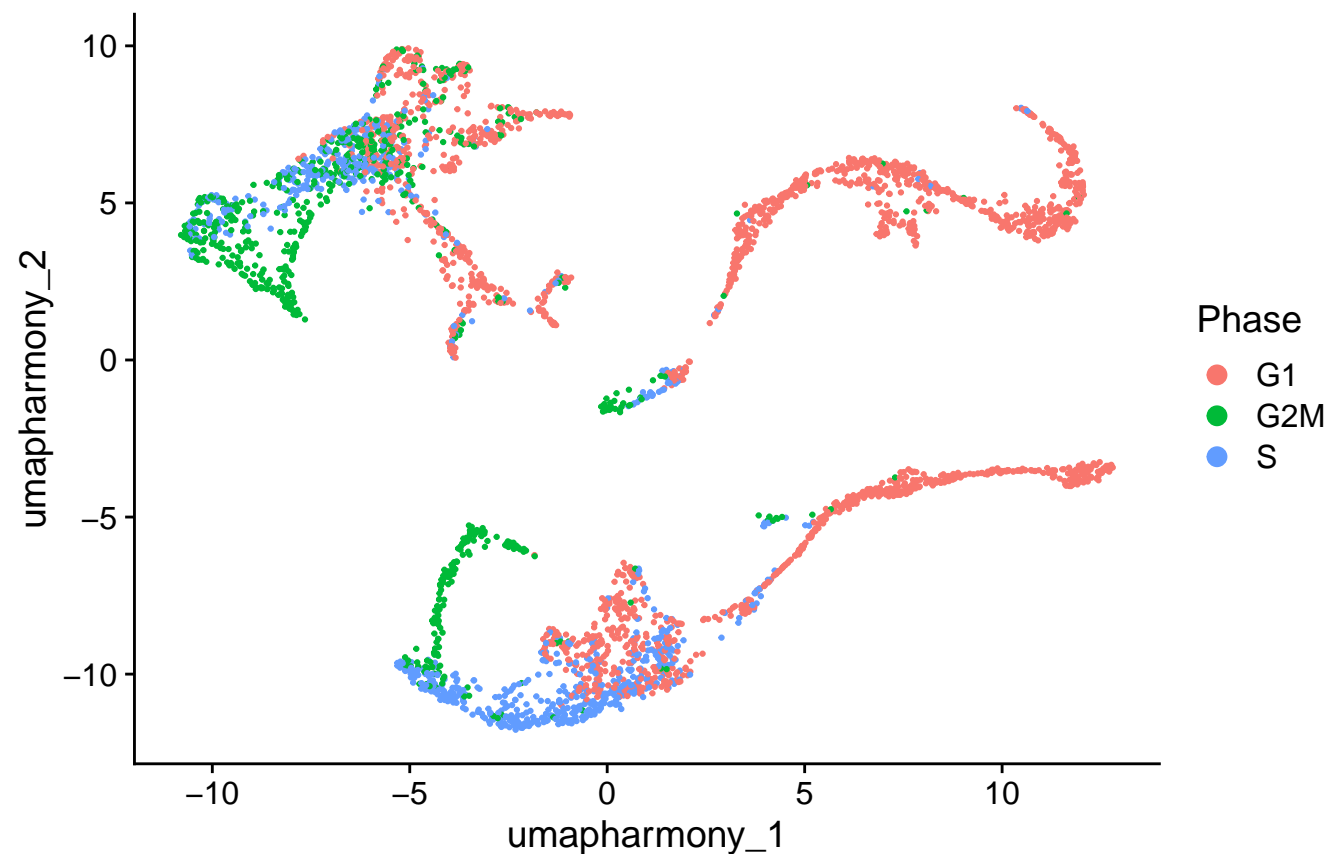
1M\_Org: Final Clusters



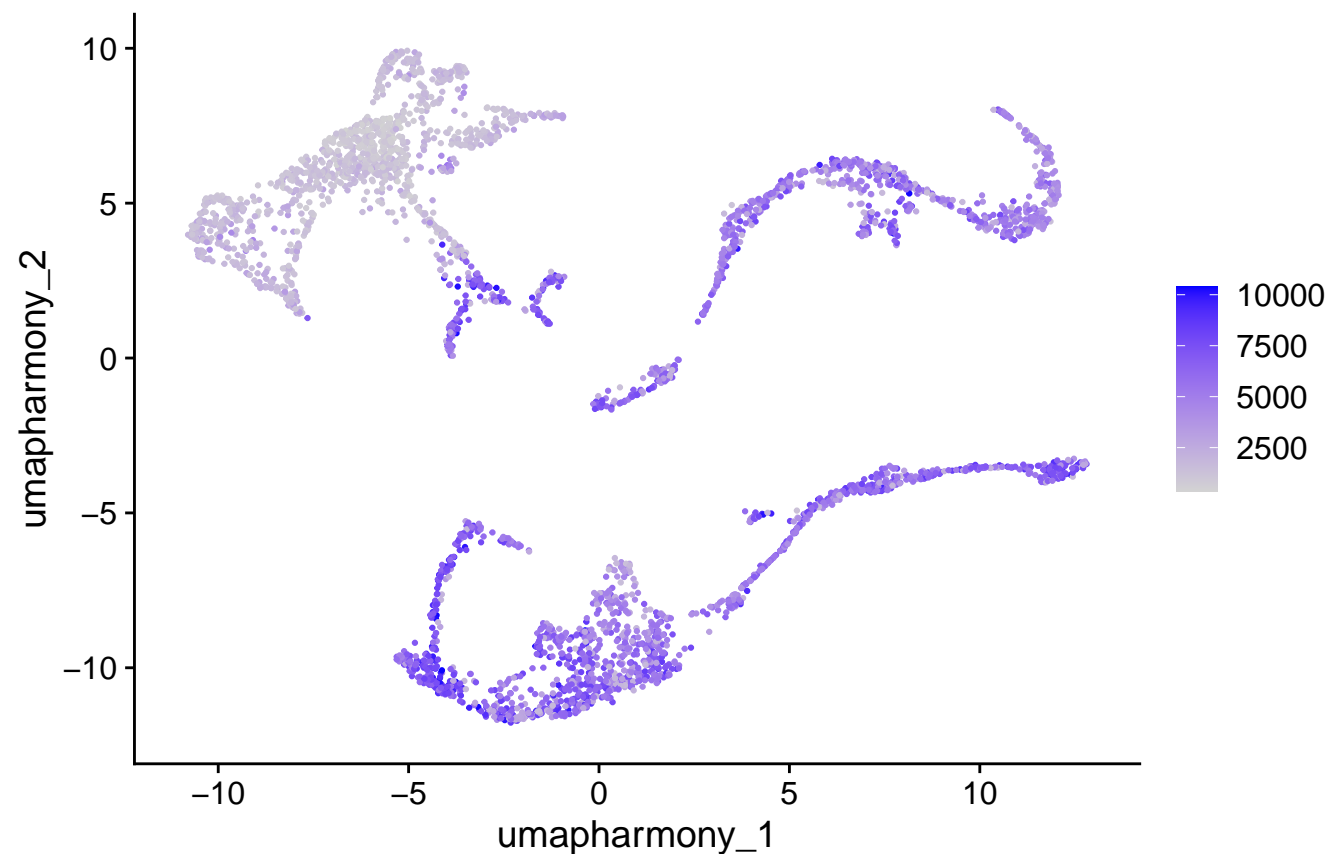
	res_vals	num_clusters	avg_sil_vals
1	0.4	13	0.306880963239079
2	0.7	16	0.292759656502037
3	0.6	15	0.292212875815006
4	1.1	20	0.262816418715783
5	0.8	18	0.261319796541482
6	0.9	19	0.253443563785026
7	0.2	9	0.250258206846109
8	0.1	7	0.243703688686436
9	1.2	22	0.231464727213263

# 1M\_Org – QC Metrics on Integrated Data

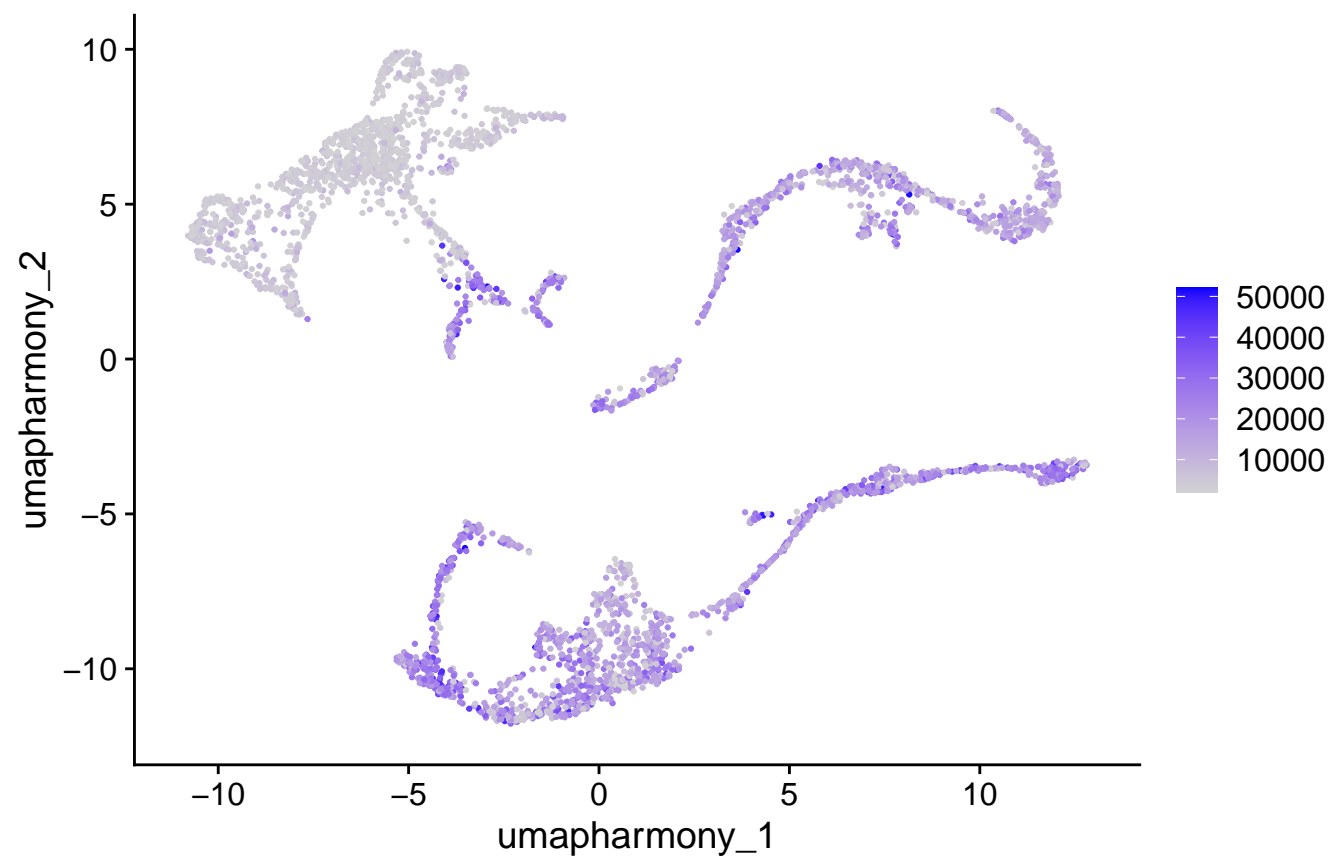
## 1M\_Org: Cell Cycle Phase



## 1M\_Org: nFeature\_RNA



## 1M\_Org: nCount\_RNA



## 1M\_Org: Final Clusters

