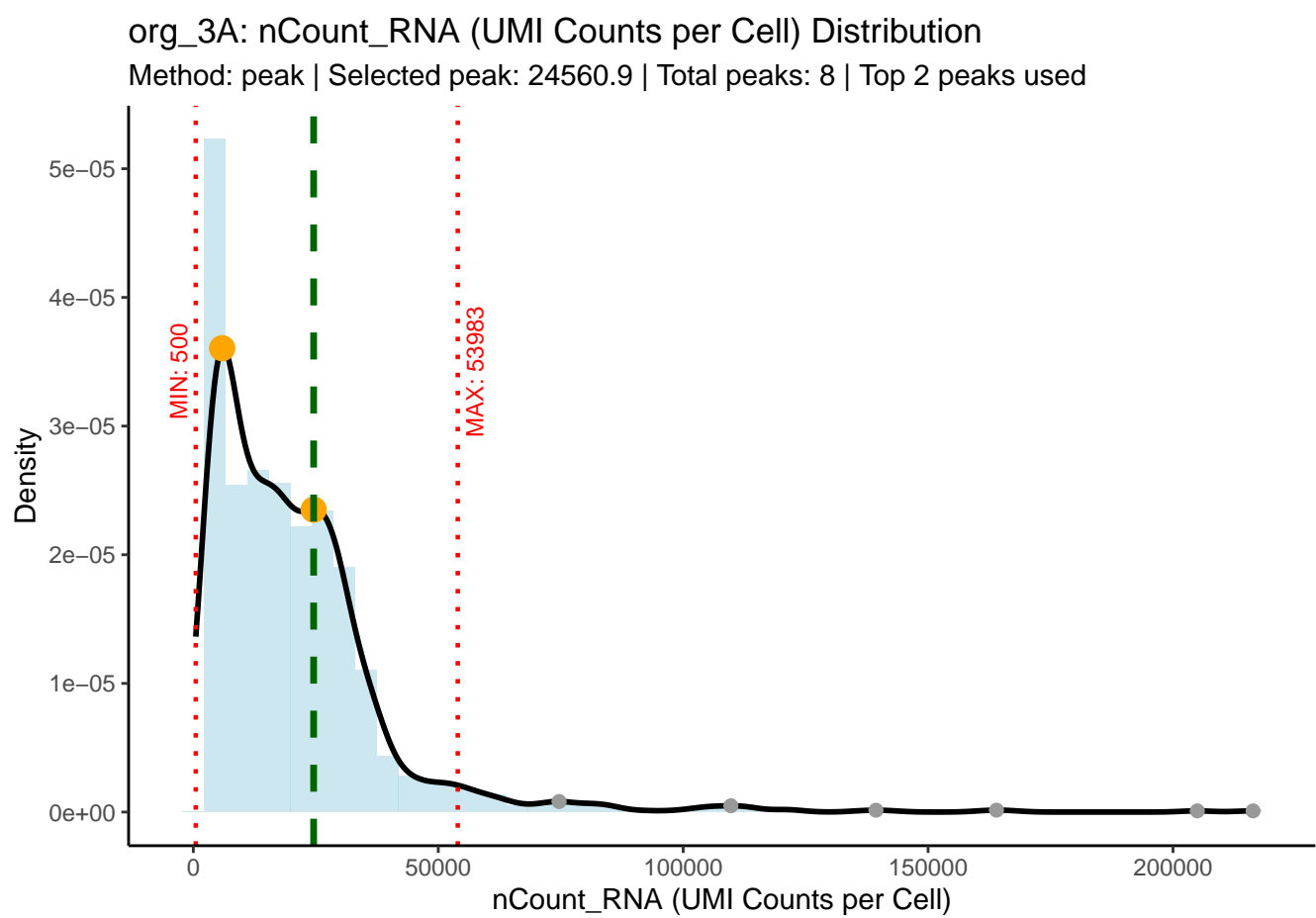
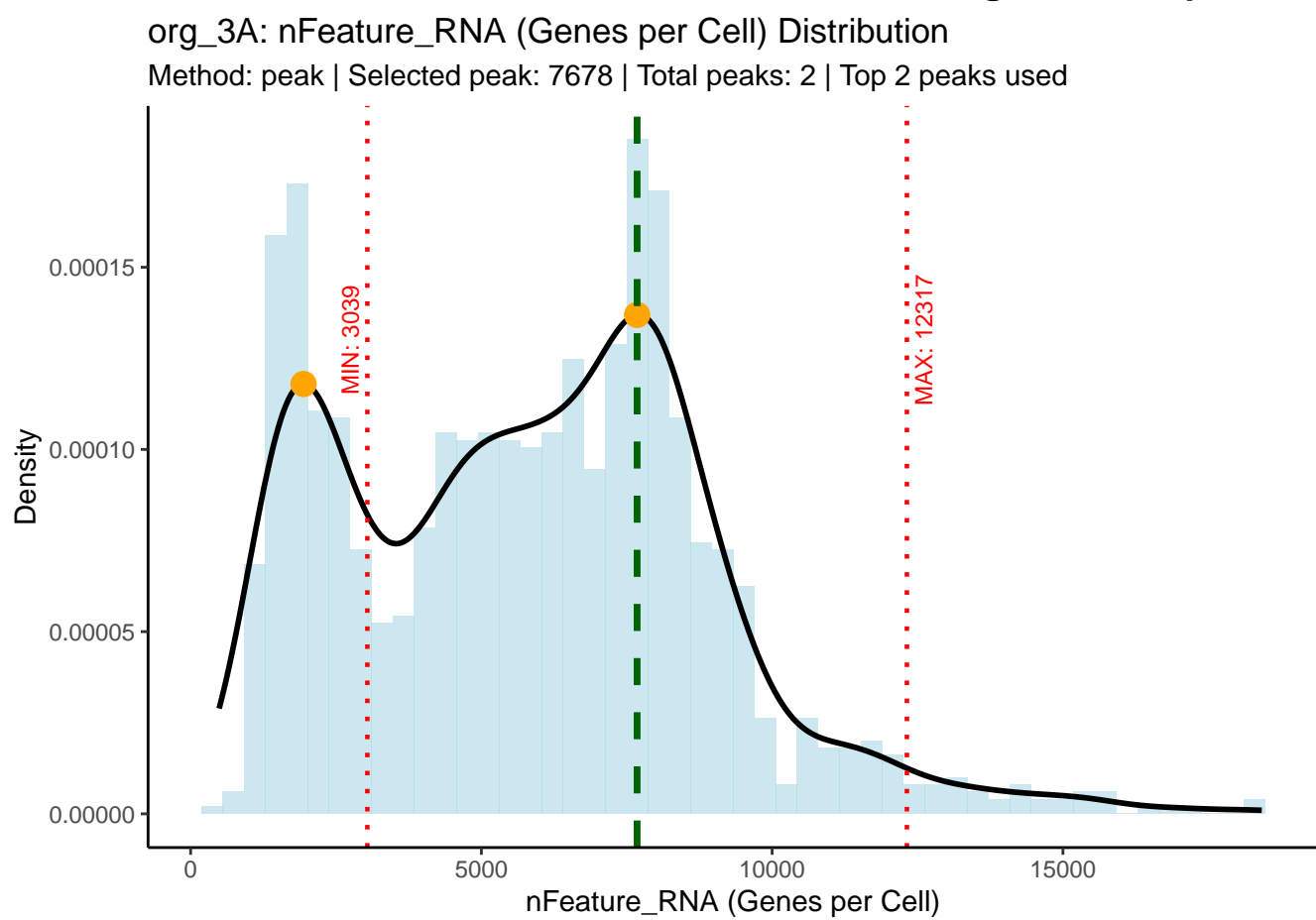
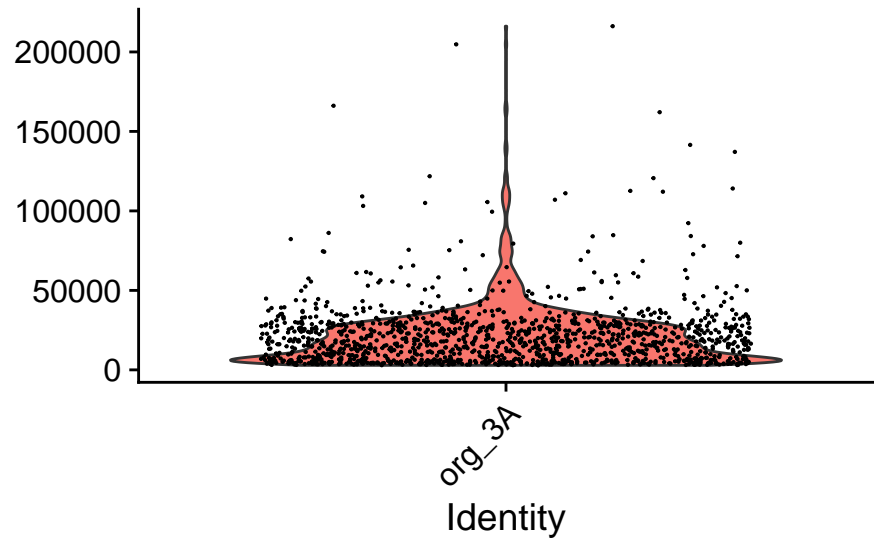


org_3A – Adaptive Threshold Determination

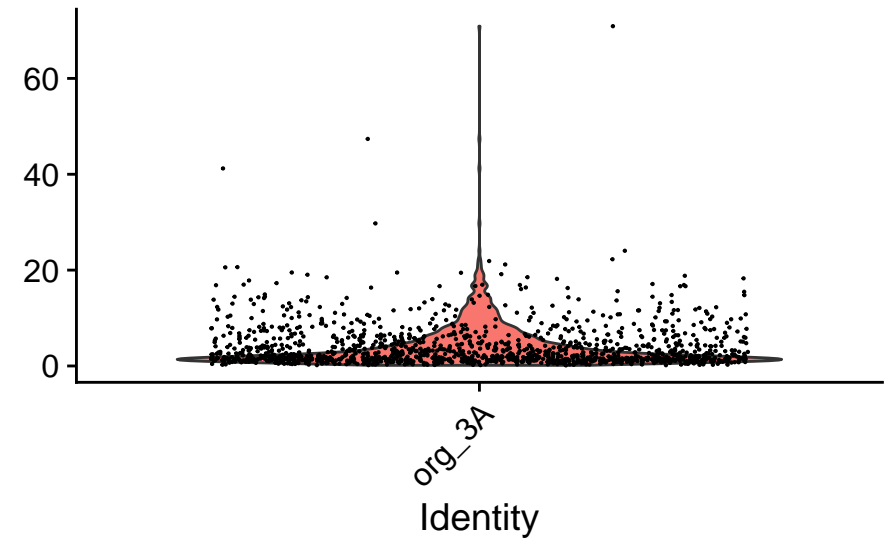


Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
nFeature_RNA	peak	7678	2	7678, 1942	3093	3039	12317
nCount_RNA	peak	24561	8	5883, 24561	19615	500	53983

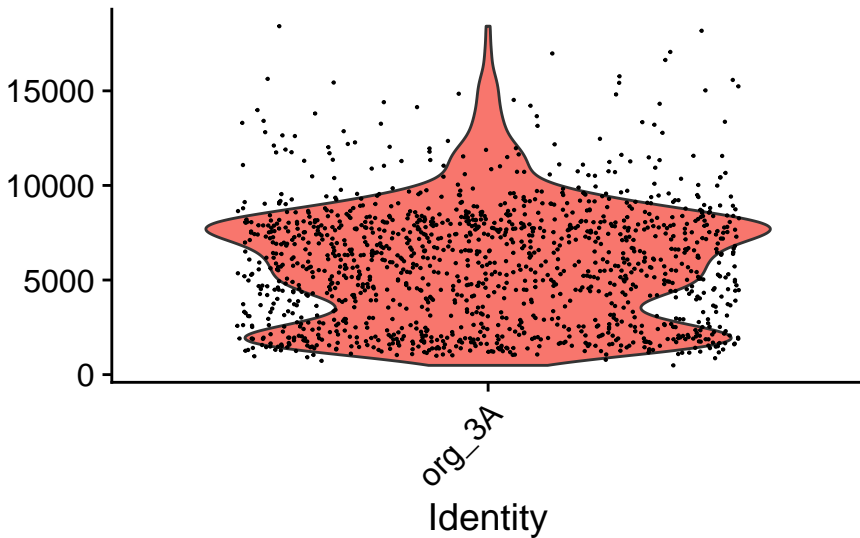
org_3A – Filtering Summary
org_3A: Counts Before Filtering



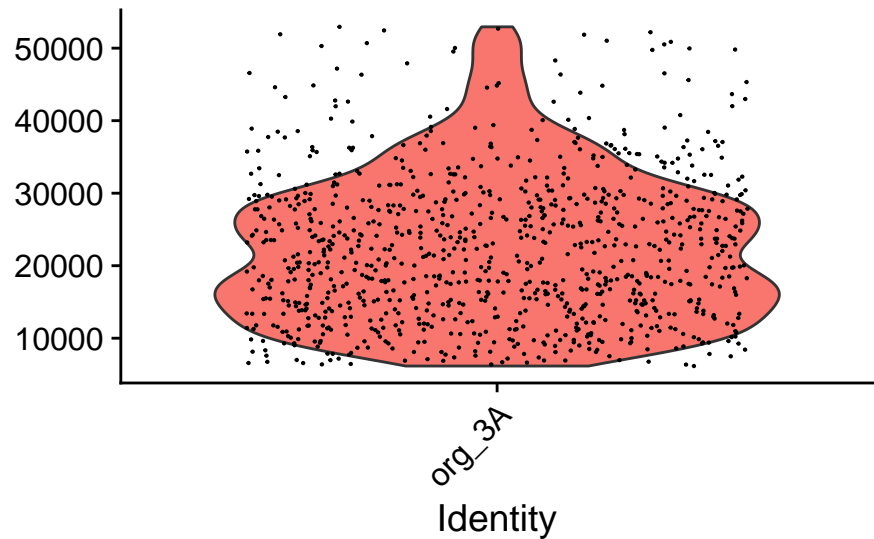
org_3A: MT% Before Filtering



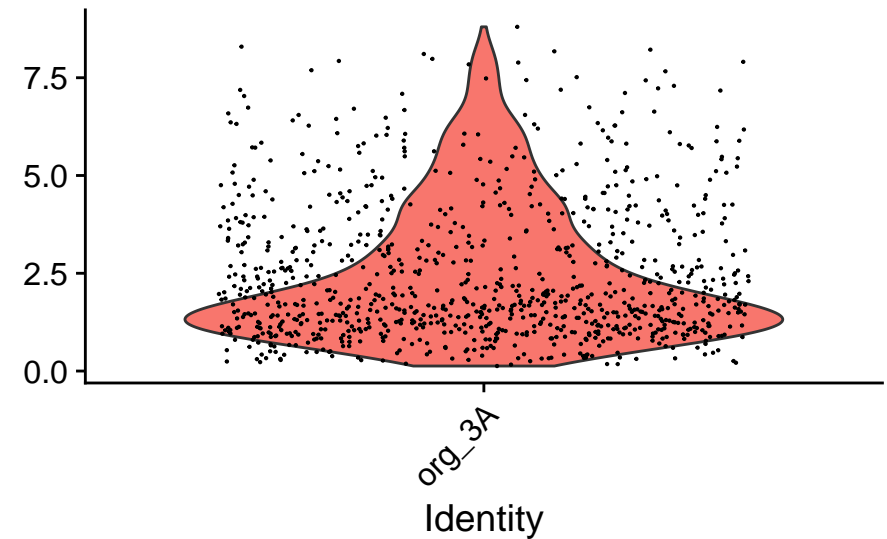
org_3A: Genes Before Filtering



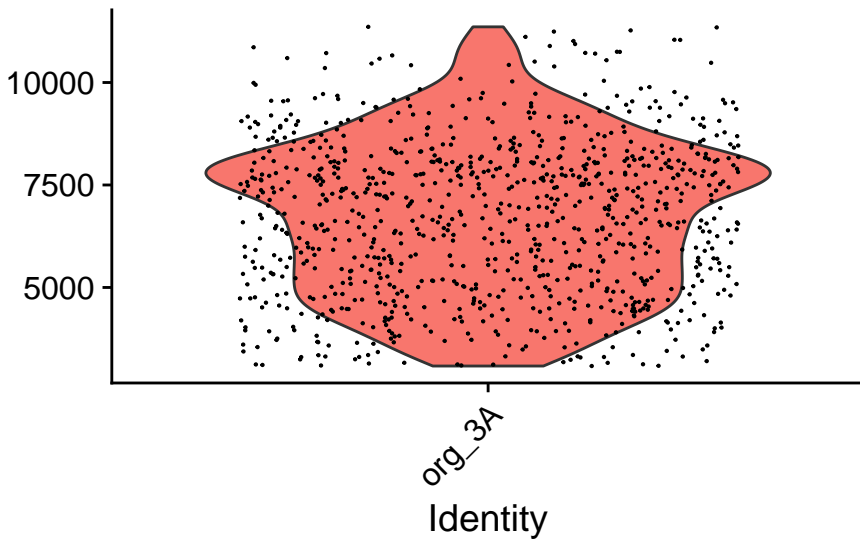
org_3A: Counts After Filtering



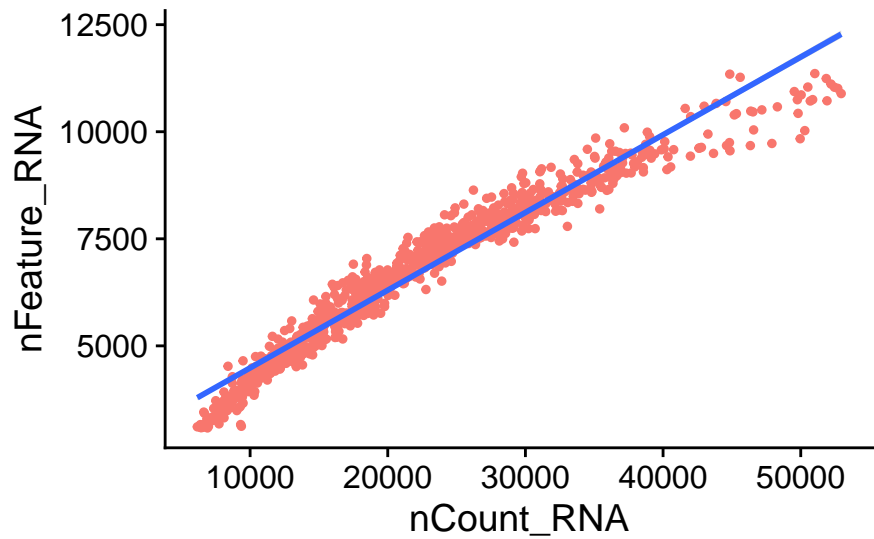
org_3A: MT% After Filtering



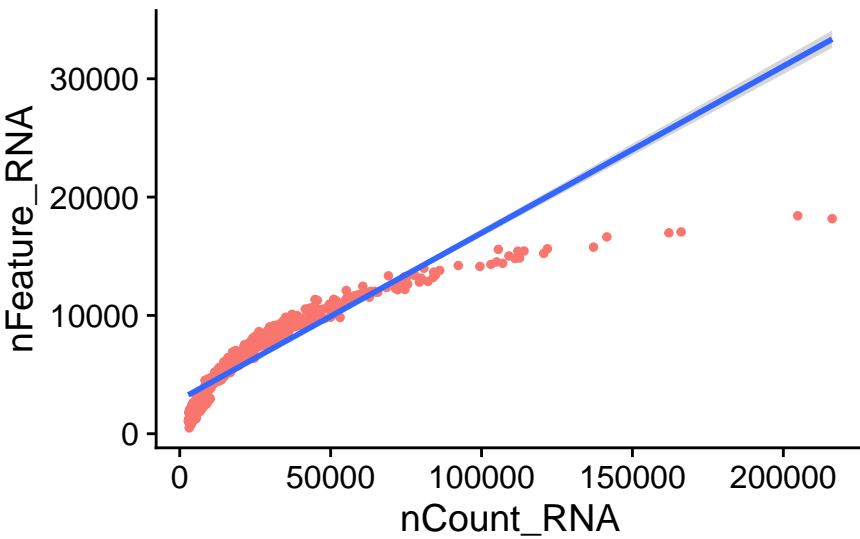
org_3A: Genes After Filtering



org_3A: After Filtering



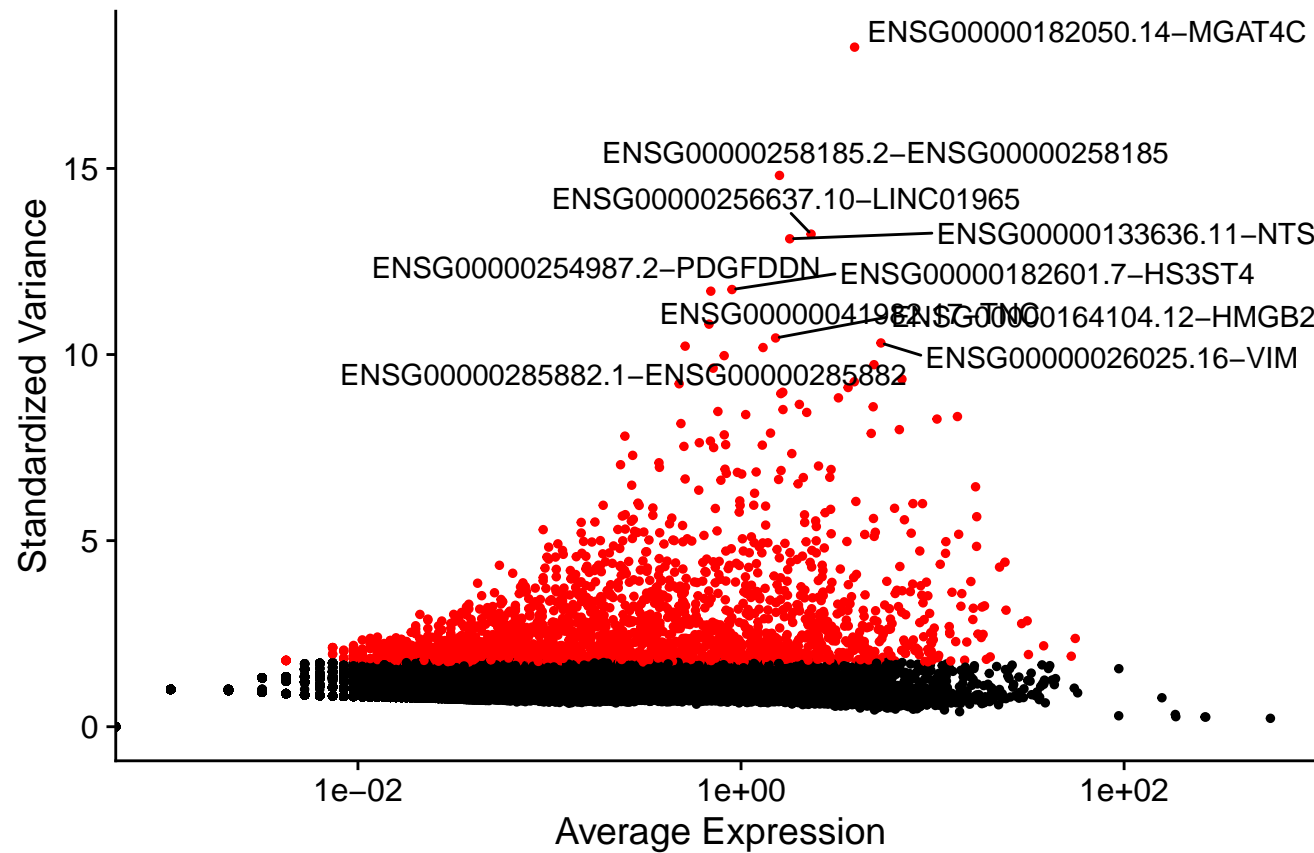
org_3A: Before Filtering



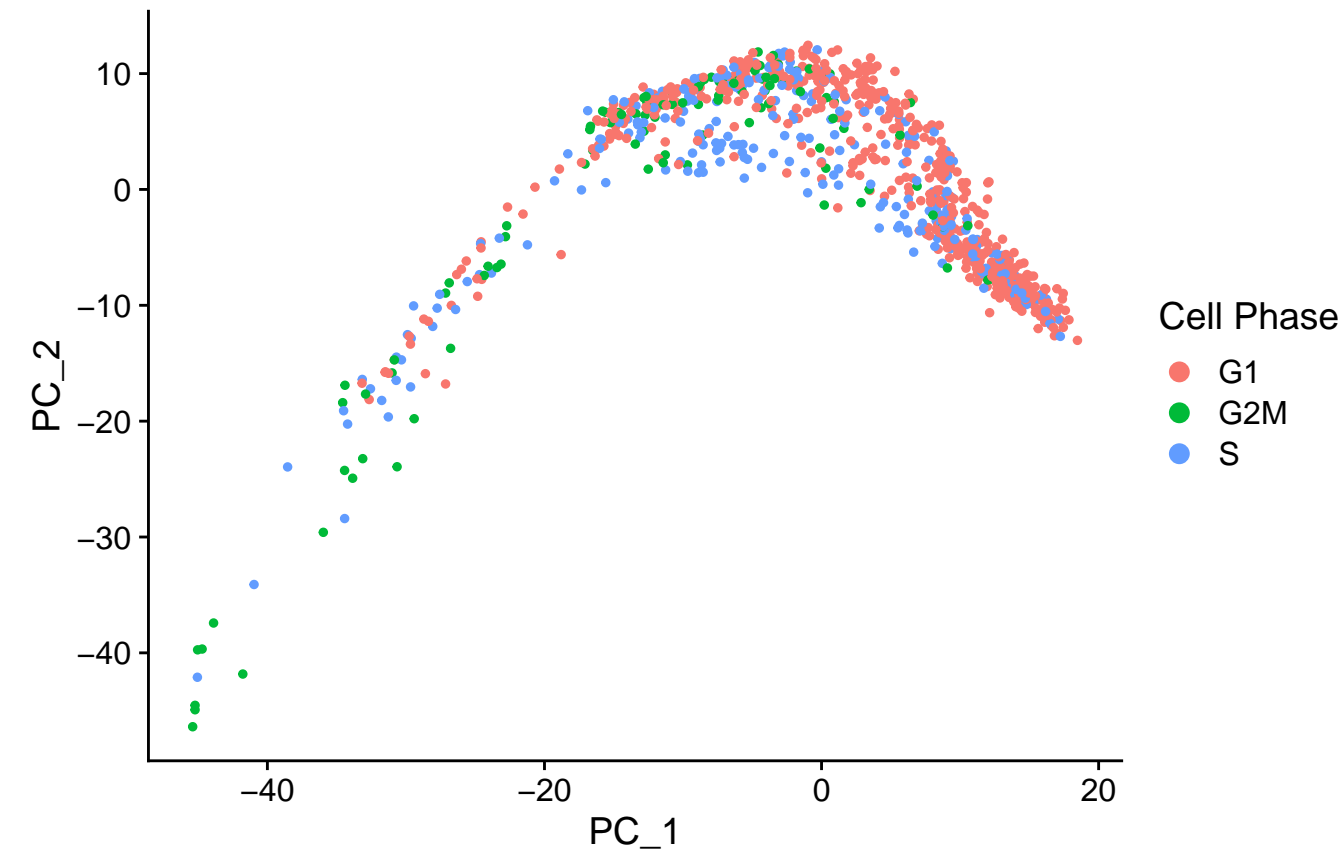
	Metric	Before	After
1	Cells	1359.00000	949.000000
2	Genes	41616.00000	41616.000000
3	Median nCount	17279.00000	21424.000000
4	Median nFeature	5907.00000	6877.000000
5	Median MT%	2.26399	1.873642

org_3A – Variable Features & Cell Cycle

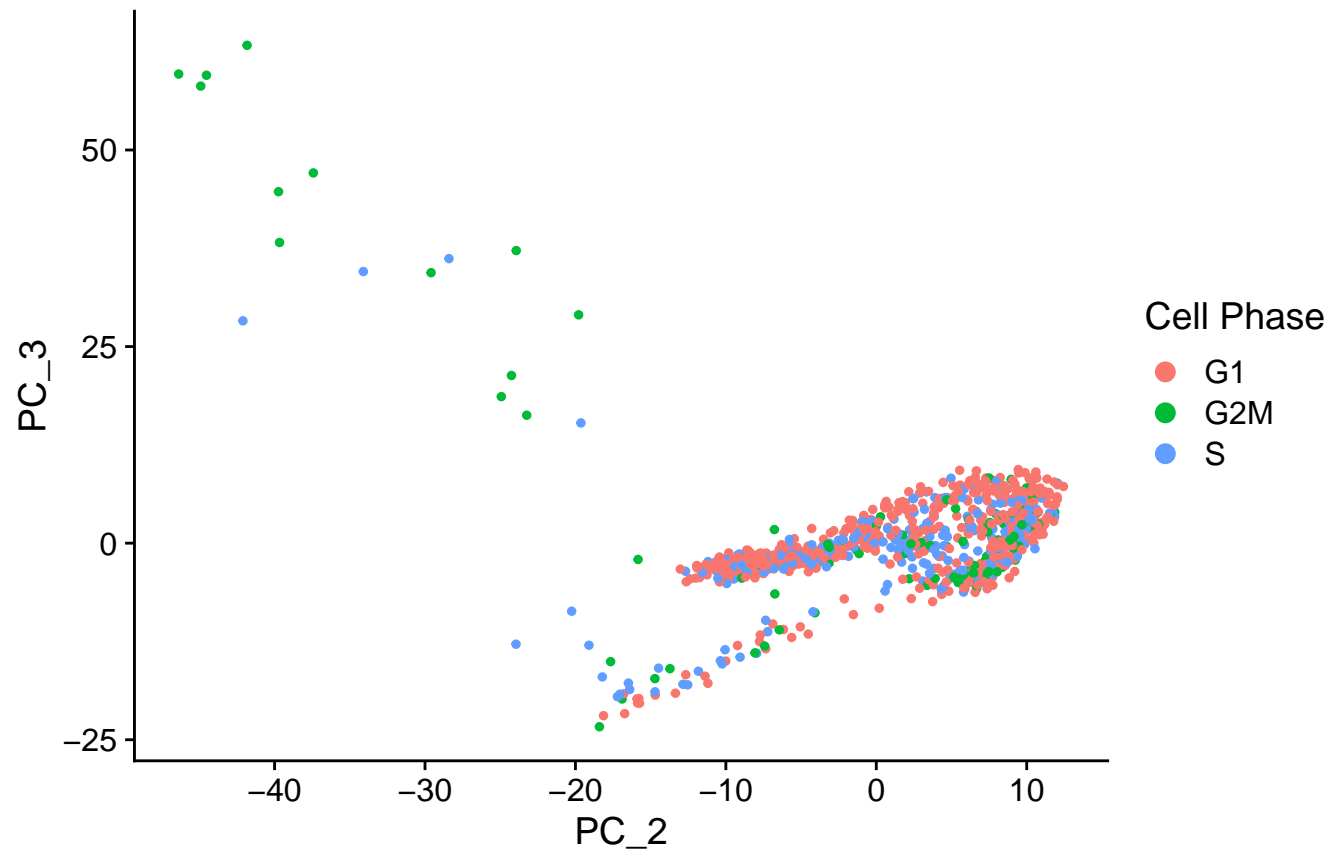
org_3A: Top 2000 Variable Genes



org_3A: Cell Cycle on PC1 & PC2



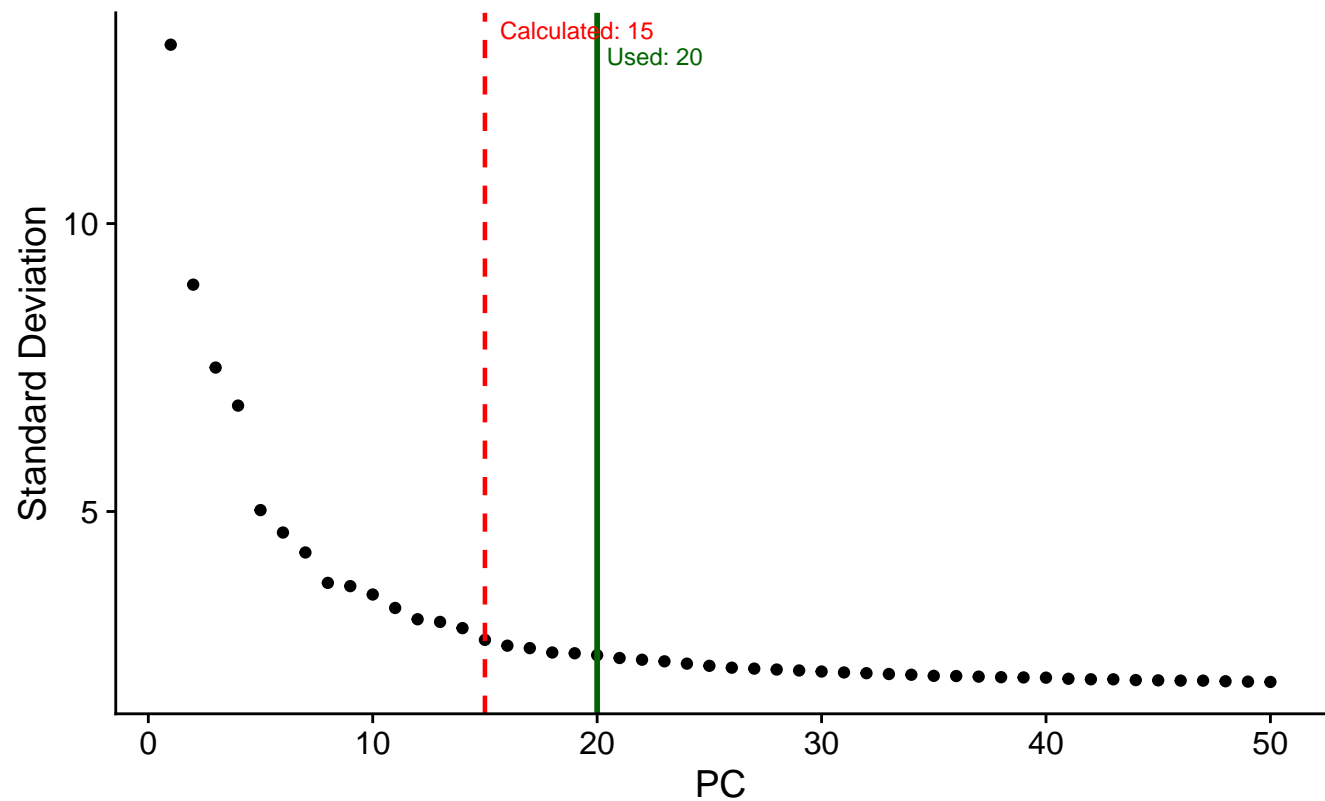
org_3A: Cell Cycle on PC2 & PC3



org_3A – PCA Selection & Silhouette Analysis

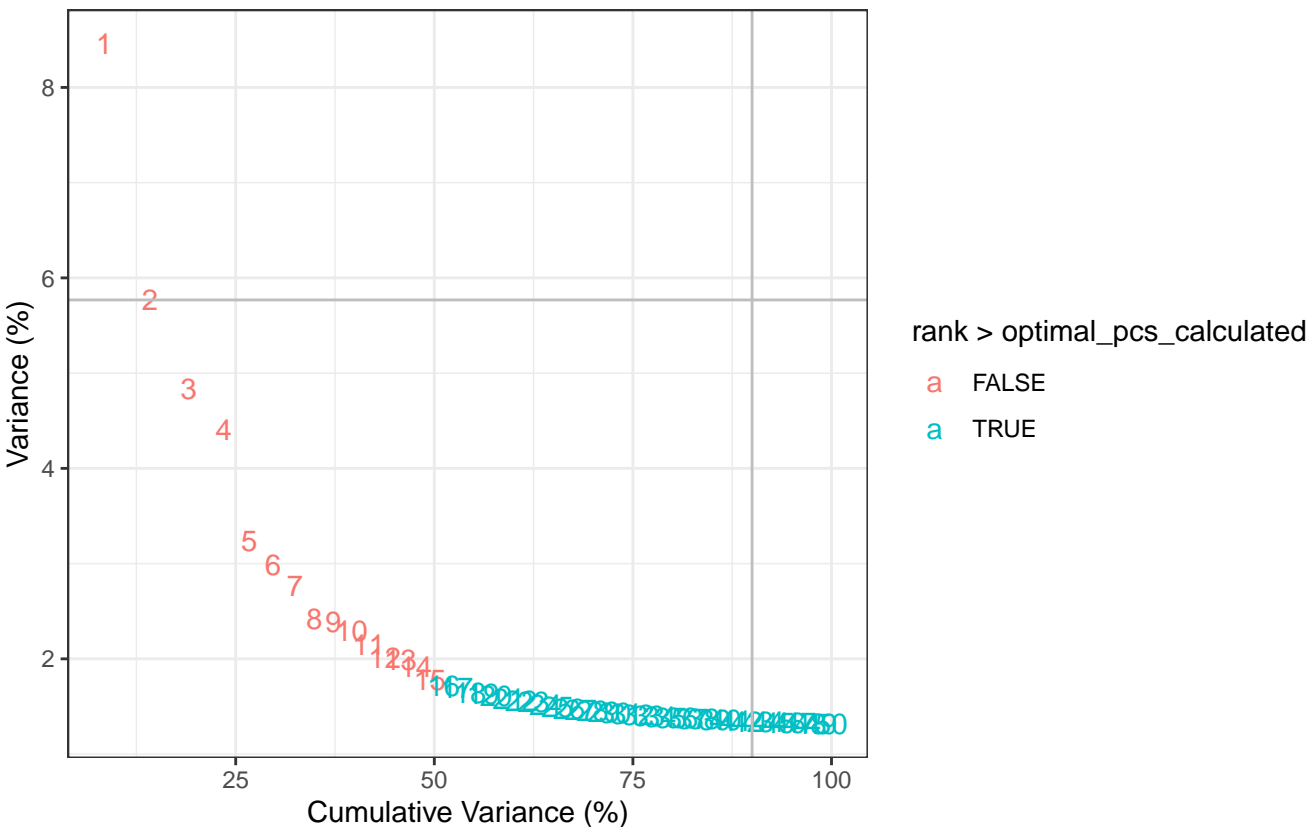
org_3A: Elbow Plot

Calculated: 15 PCs | Used: 20 PCs (+5)

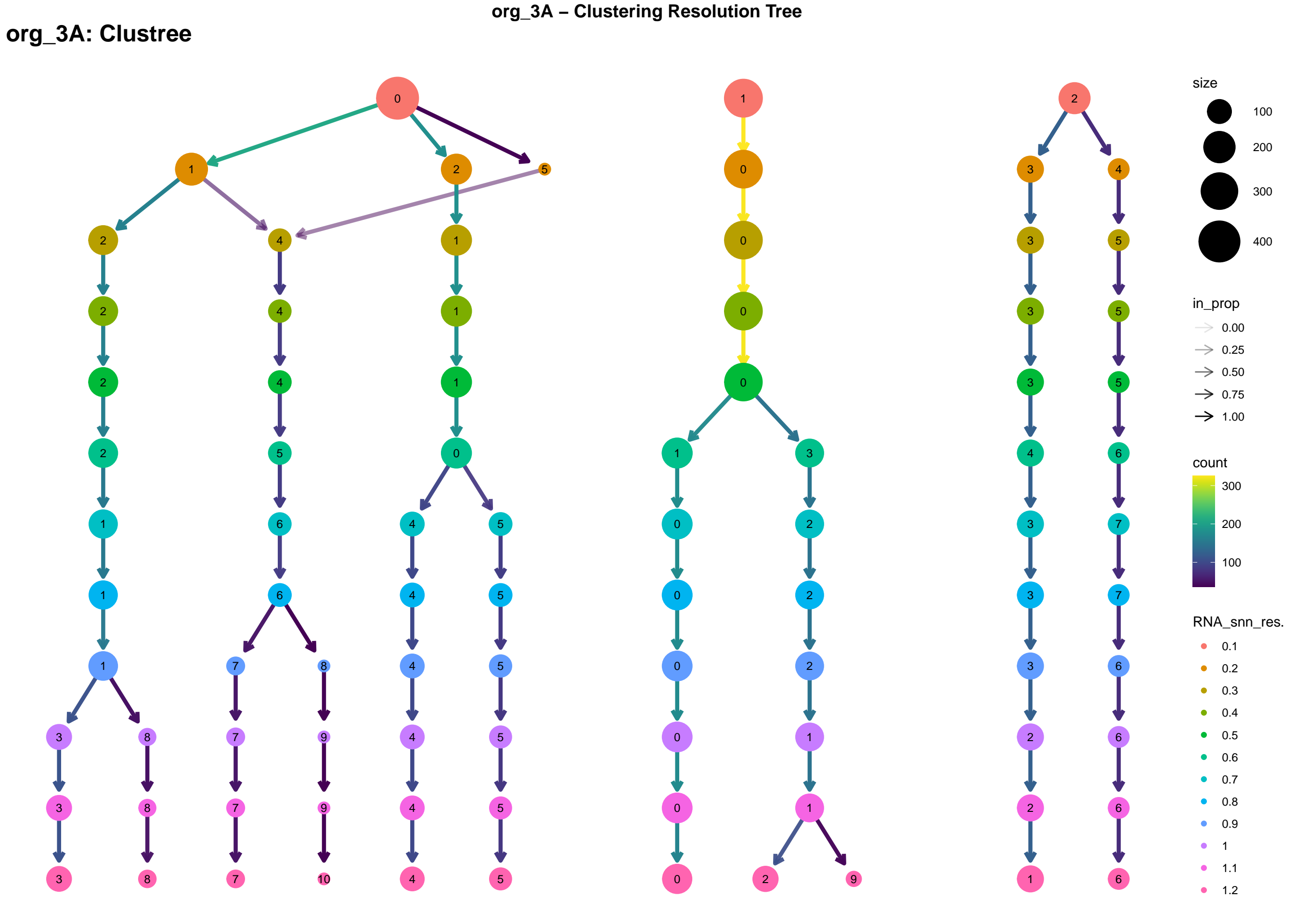


org_3A: Quantitative PC Selection

Calculated: 15 PCs | Used: 20 PCs (+5)

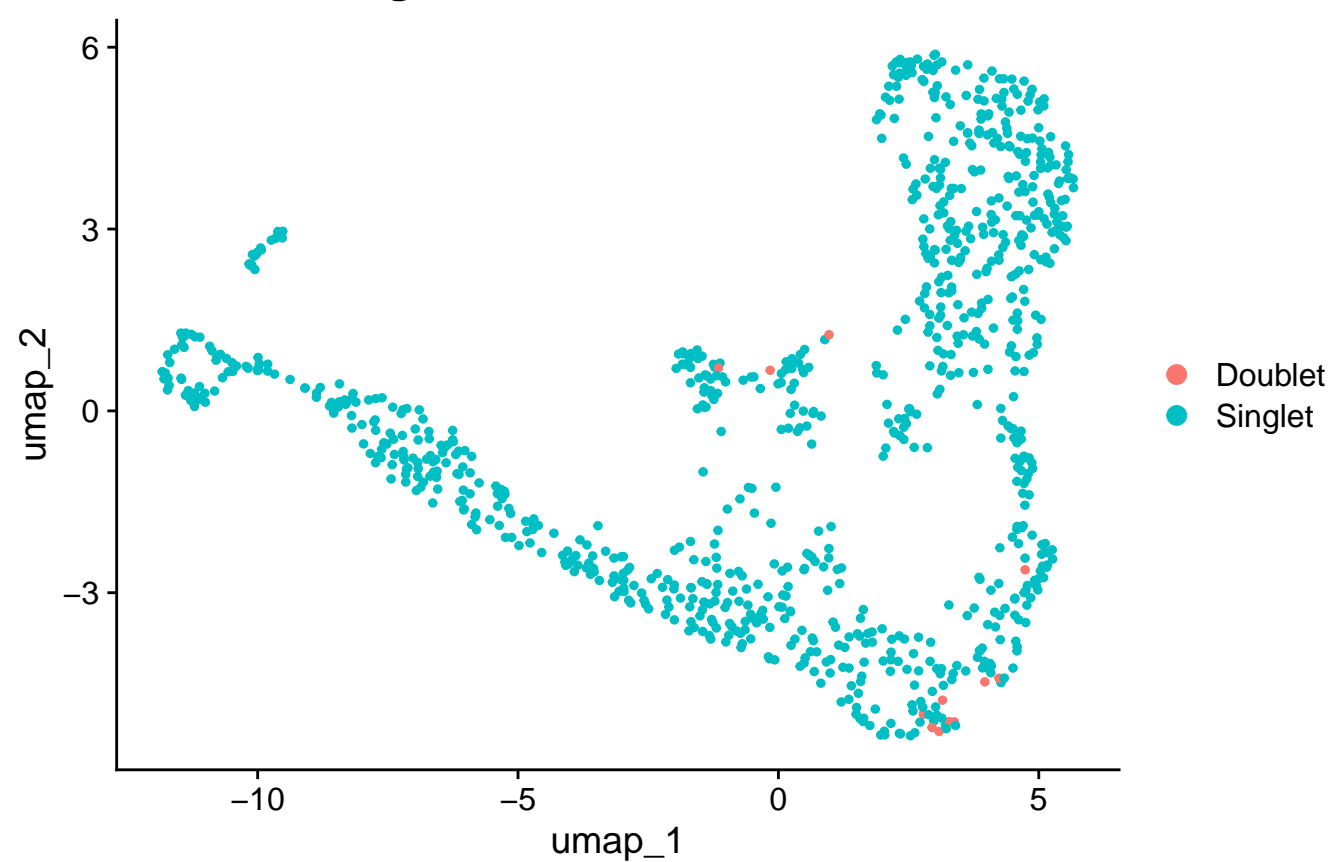


	res_vals	num_clusters	avg_sil_vals
1	0.3	6	0.380173021781017
2	0.1	3	0.305961906145535
3	0.9	9	0.29822098429095
4	0.6	7	0.298004981545512
5	0.7	8	0.288914061904453
6	1.2	11	0.25865767037393
7	1	10	0.252564791595052

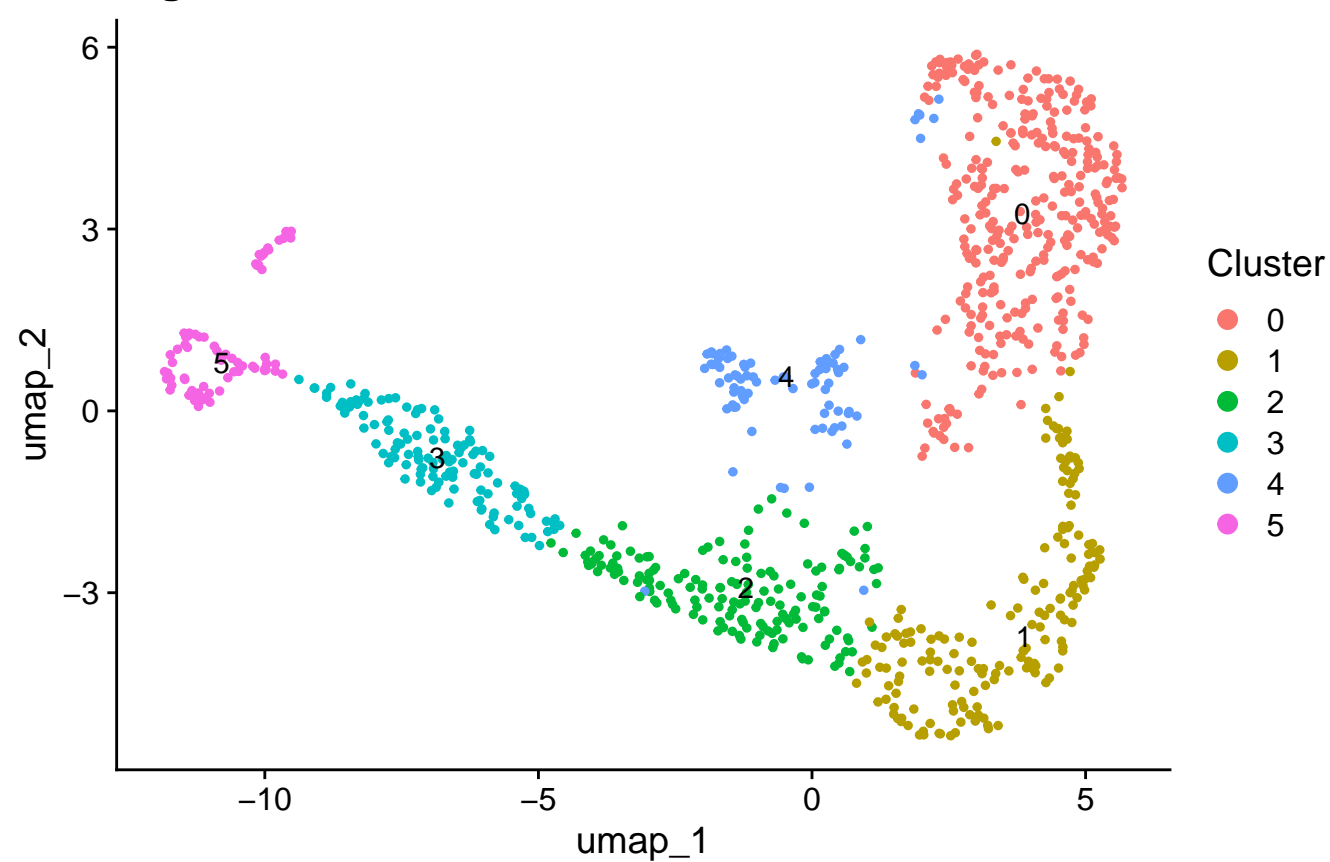


org_3A – UMAP & Doublet Removal

org_3A: Doublets Detected



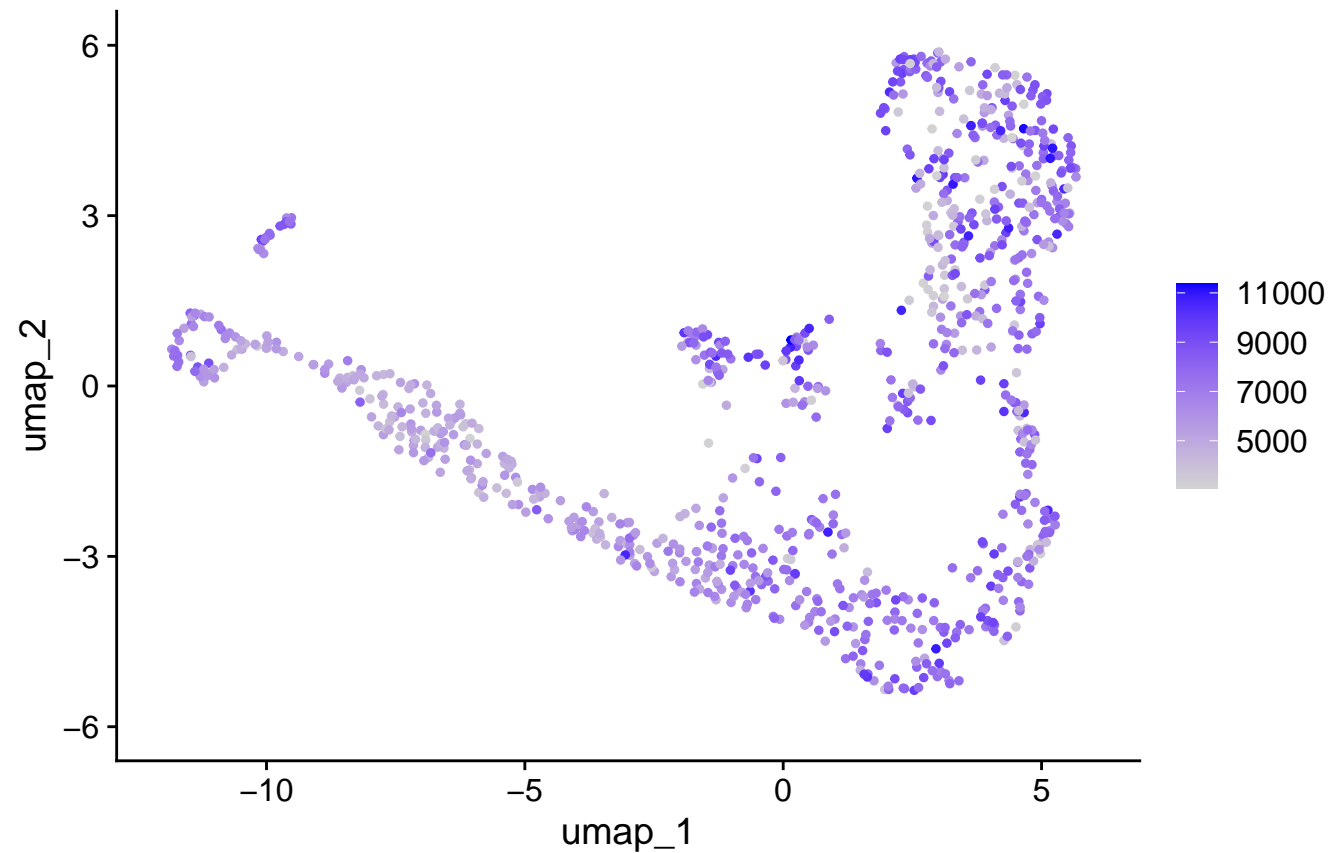
org_3A: Final UMAP



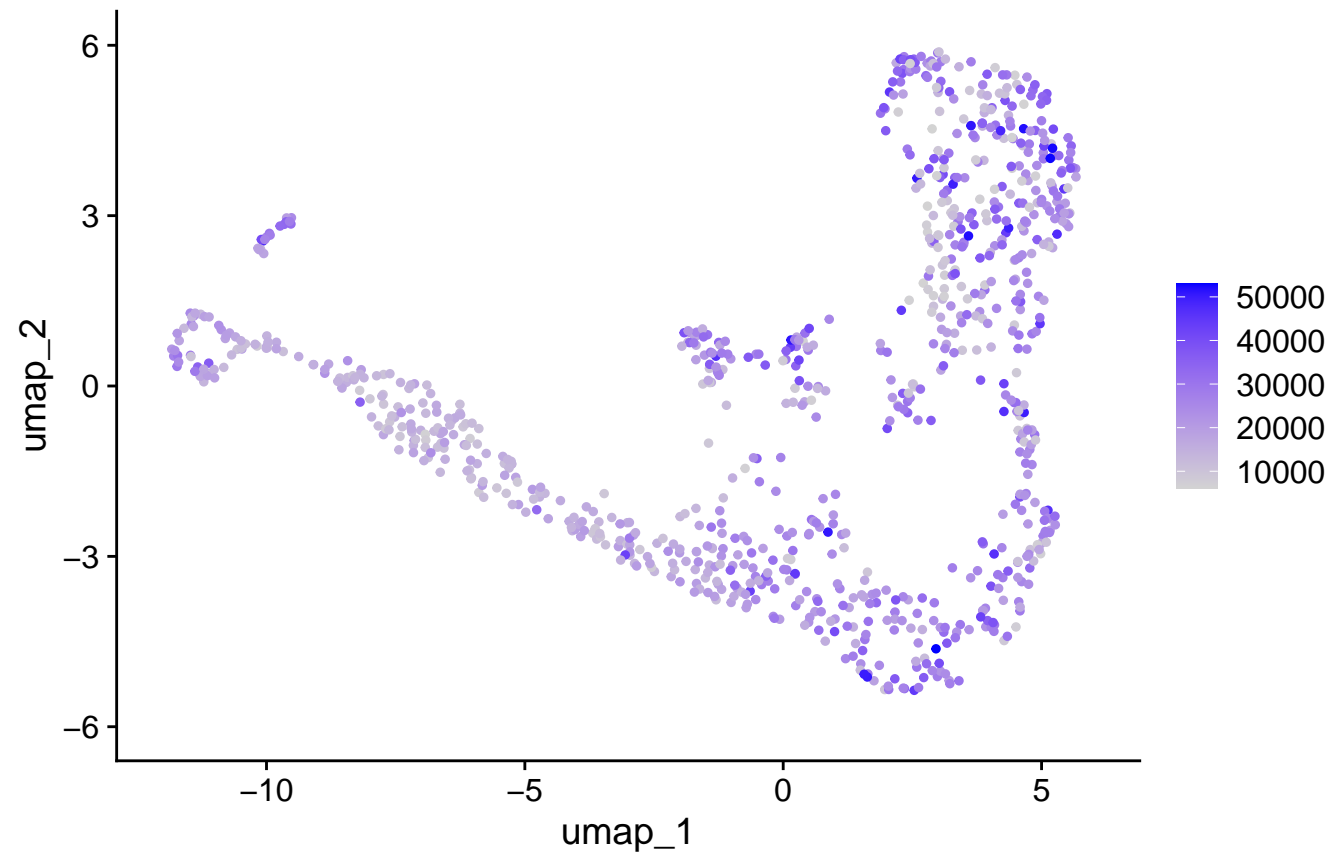
	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	36682	9182.5	12
2	Singlet	21207	6799.0	937

org_3A – QC Metrics & Cell Cycle on UMAP

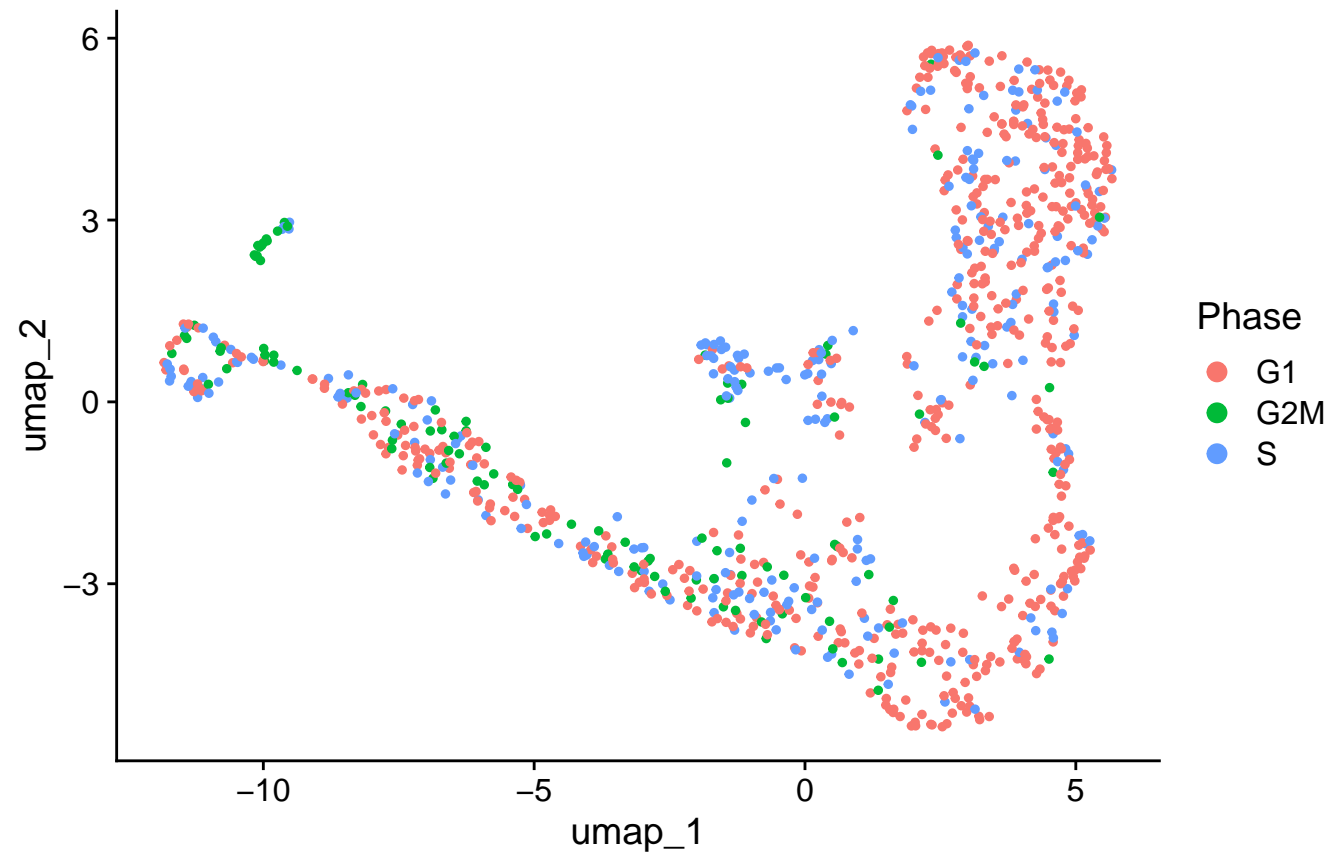
org_3A: nFeature_RNA



org_3A: nCount_RNA



org_3A: Cell Cycle Phase



org_3A: Final UMAP

