org\_1A - Adaptive Threshold Determination

org\_1A: nFeature\_RNA (Genes per Cell) Distribution
Method: peak | Selected peak: 7552.2 | Total peaks: 2 | Top 2 peaks used

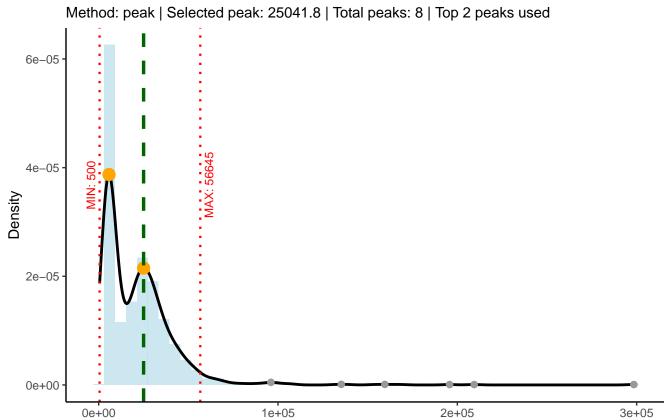
0.00025

0.00005

0.00005

0.00000

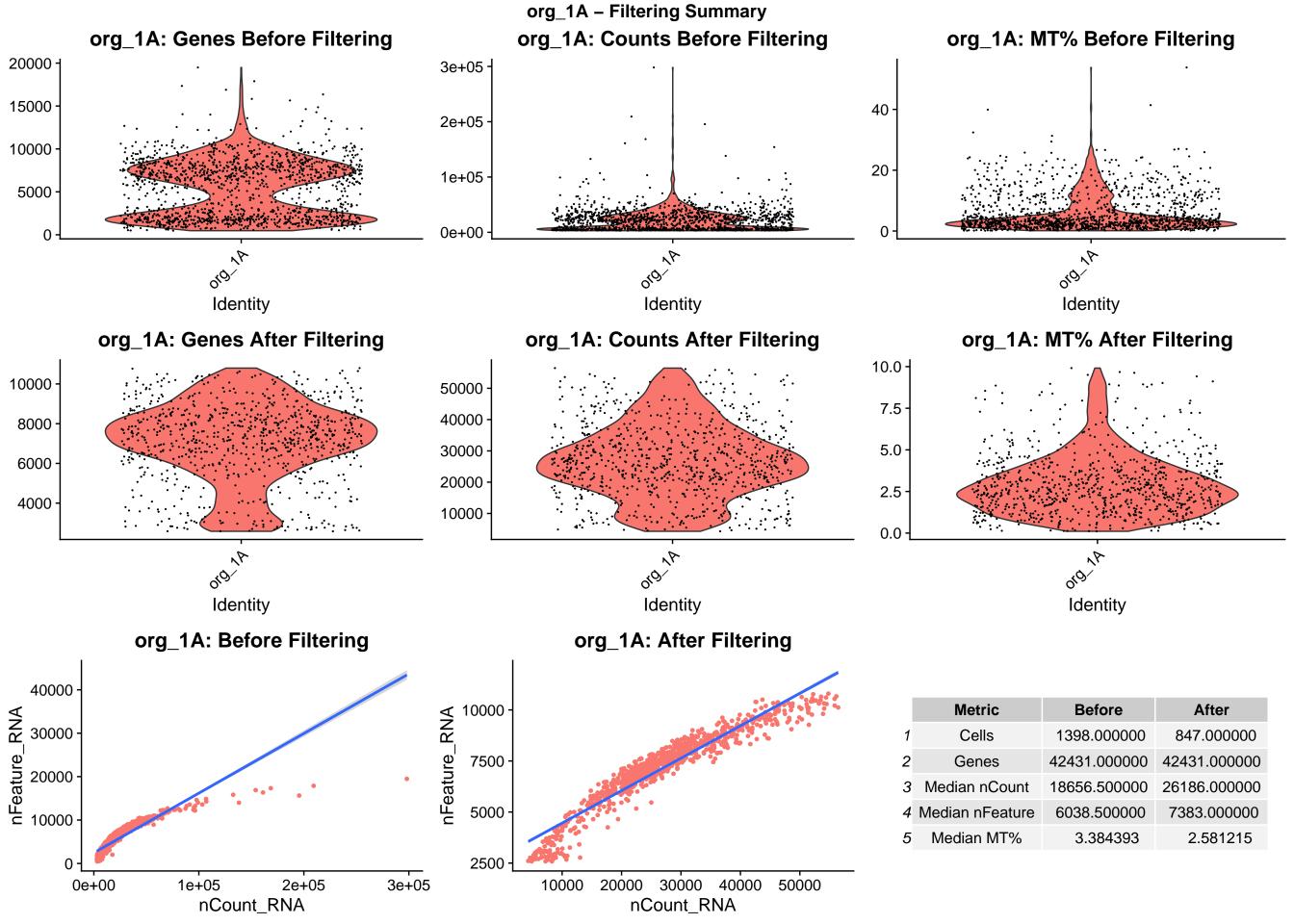
nFeature\_RNA (Genes per Cell)



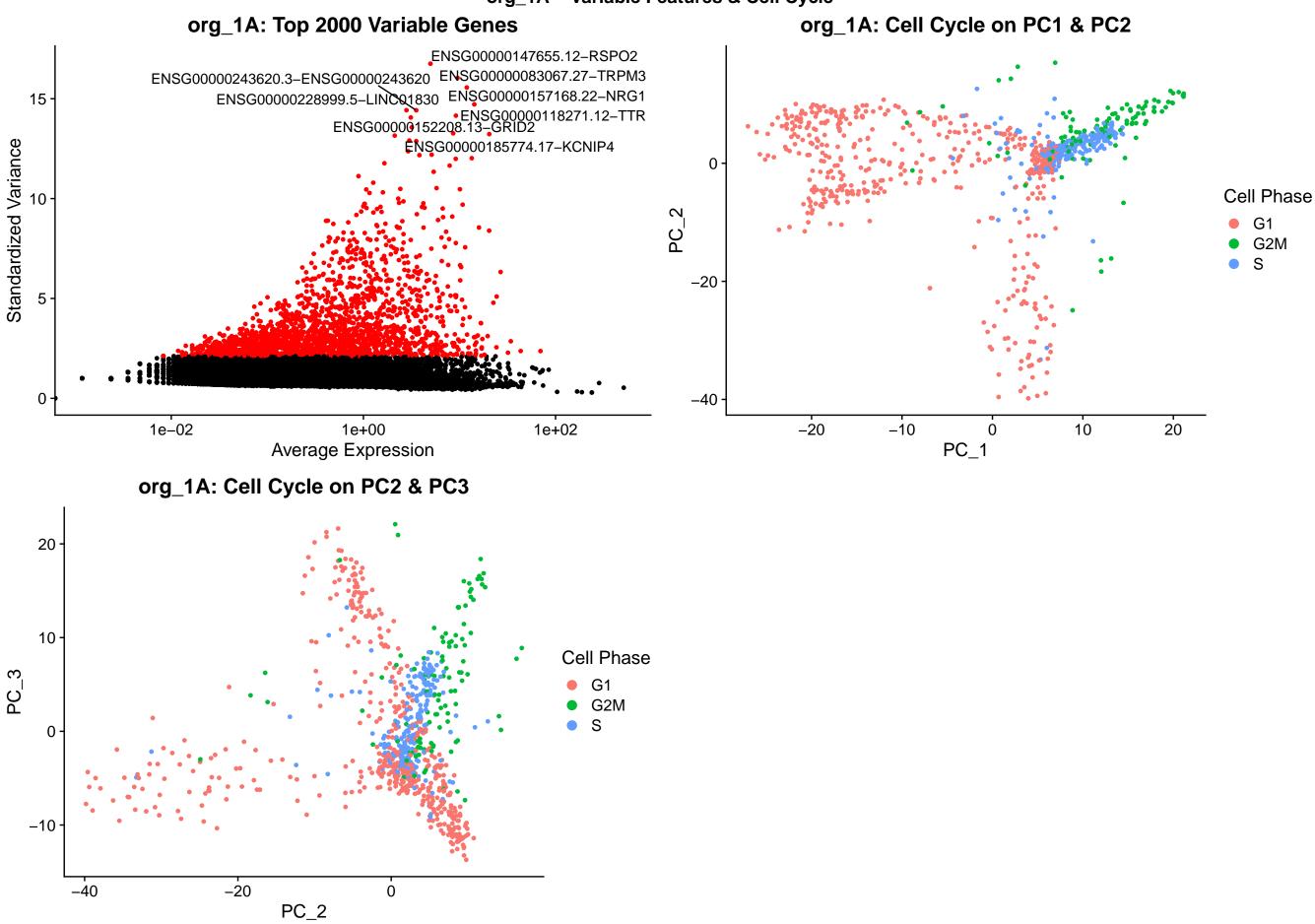
nCount\_RNA (UMI Counts per Cell)

org\_1A: nCount\_RNA (UMI Counts per Cell) Distribution

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
ature_RNA	peak	7552	2	1781, 7552	3315	2579	12525
ount_RNA	peak	25042	8	5735, 25042	21069	500	56645



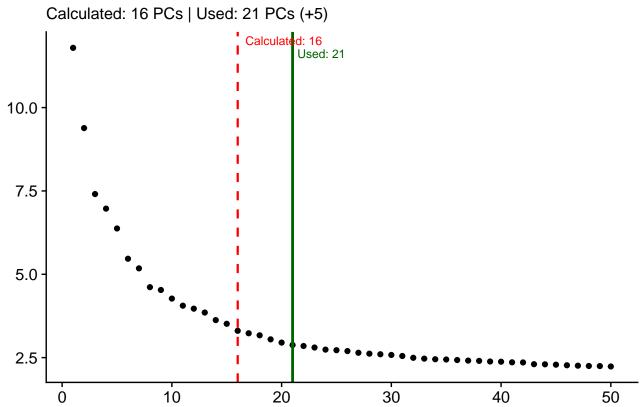
org\_1A - Variable Features & Cell Cycle



org\_1A - PCA Selection & Silhouette Analysis

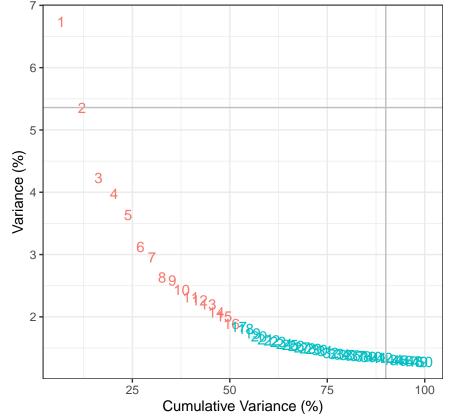
org\_1A: Elbow Plot

Standard Deviation



PC

org\_1A: Quantitative PC Selection Calculated: 16 PCs | Used: 21 PCs (+5)

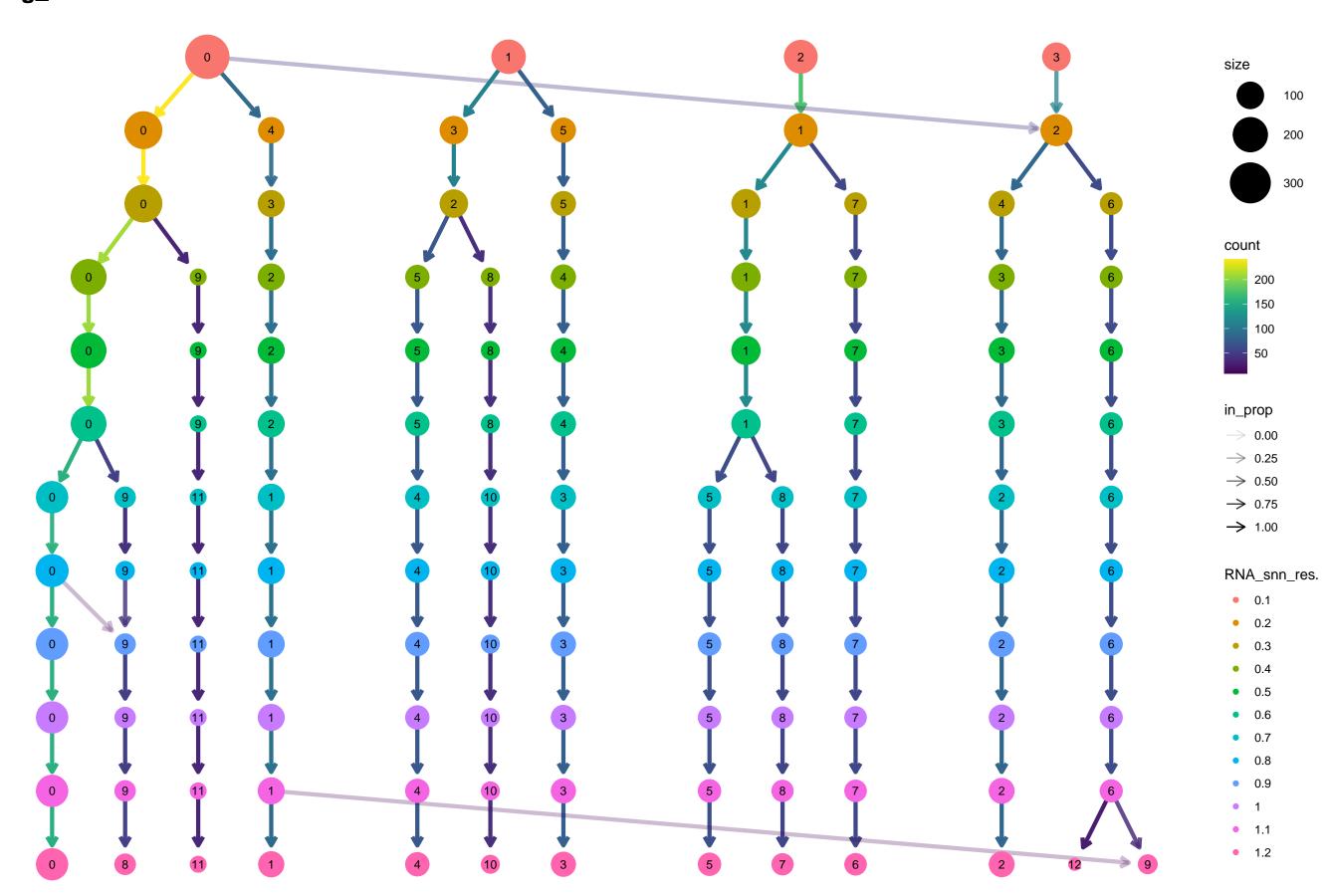


rank > optimal\_pcs\_calculated

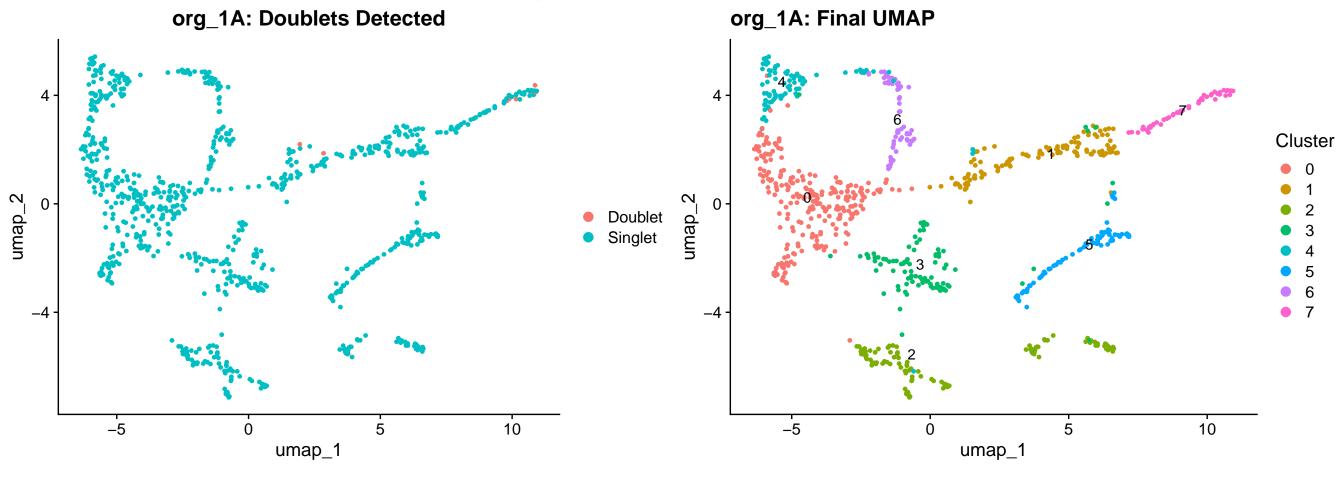
- a FALSE
- a TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.3	8	0.300965368622129
2	1.2	13	0.269978582814319
3	0.2	6	0.256689741570076
4	0.7	12	0.247993881199659
5	0.1	4	0.246381755878222
6	0.4	10	0.238072738149021

org\_1A: Clustree



org\_1A - UMAP & Doublet Removal



	<b>DF.</b> classifications	median_nCount	median_nFeature	count
1	Doublet	36964.5	8742.5	12
2	Singlet	25924.0	7355.0	835

org\_1A - QC Metrics & Cell Cycle on UMAP org\_1A: nFeature\_RNA org\_1A: nCount\_RNA 10000 50000 umap\_2 40000 8000 30000 6000 20000 10000 4000 **-4** --8 --8 -**-**5 10 10 <u>-</u>5 0 umap\_1 umap\_1 org\_1A: Final UMAP org\_1A: Cell Cycle Phase Cluster Phase umap\_2 umap\_2 10 -5 -<del>5</del> 5 10 5 umap\_1 umap\_1