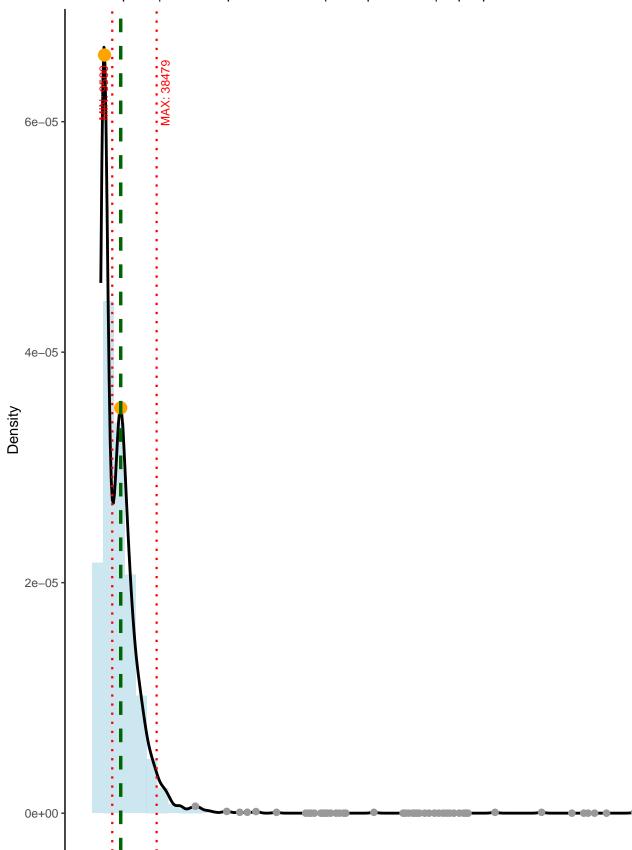
org\_1B - Adaptive Threshold Determination

org\_1B: nCount\_RNA (UMI Counts per Cell) Distribution

Method: peak | Selected peak: 15038.8 | Total peaks: 49 | Top 2 peaks used



0e+00

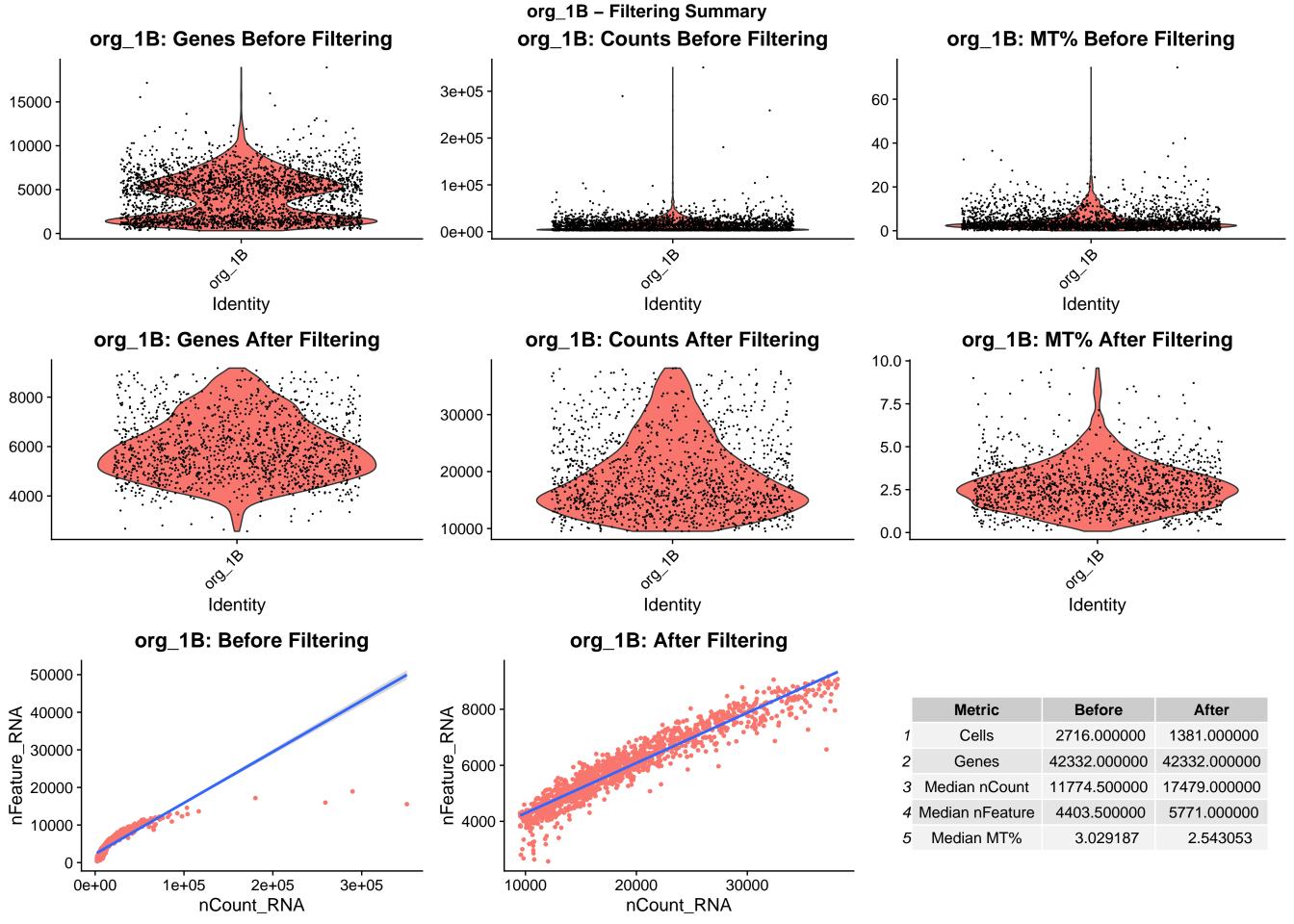
1e+05

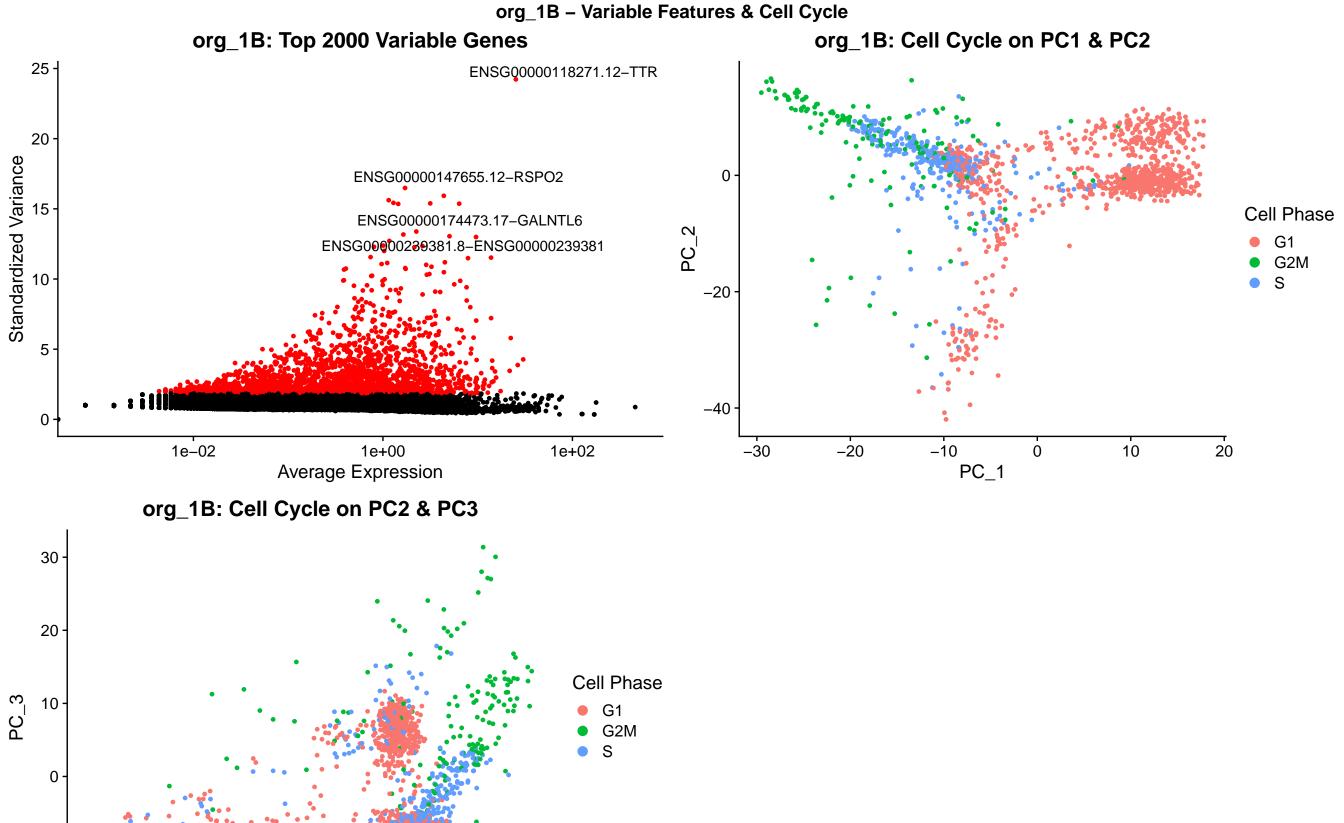
2e+05

nCount\_RNA (UMI Counts per Cell)

3e+05

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threst
nFeature_RNA	custom	NA	NA	NA	NA	2500	9326
nCount_RNA	peak	15039	49	4444, 15039	15627	9500	38479





-10

<del>-4</del>0

<del>-</del>20

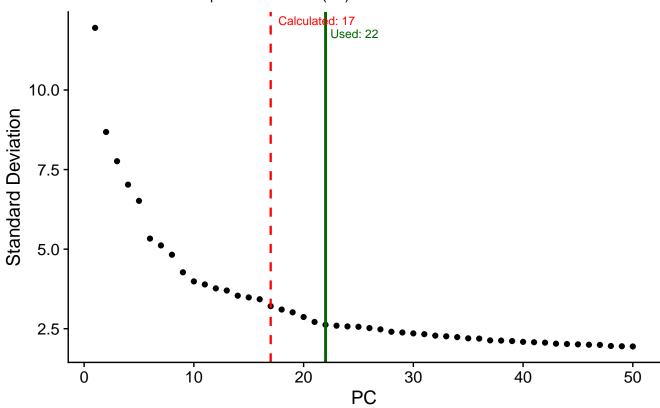
PC\_2

0

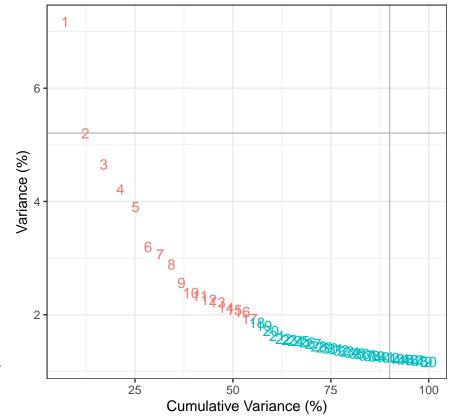
org\_1B - PCA Selection & Silhouette Analysis

org\_1B: Elbow Plot

Calculated: 17 PCs | Used: 22 PCs (+5)



org\_1B: Quantitative PC Selection Calculated: 17 PCs | Used: 22 PCs (+5)

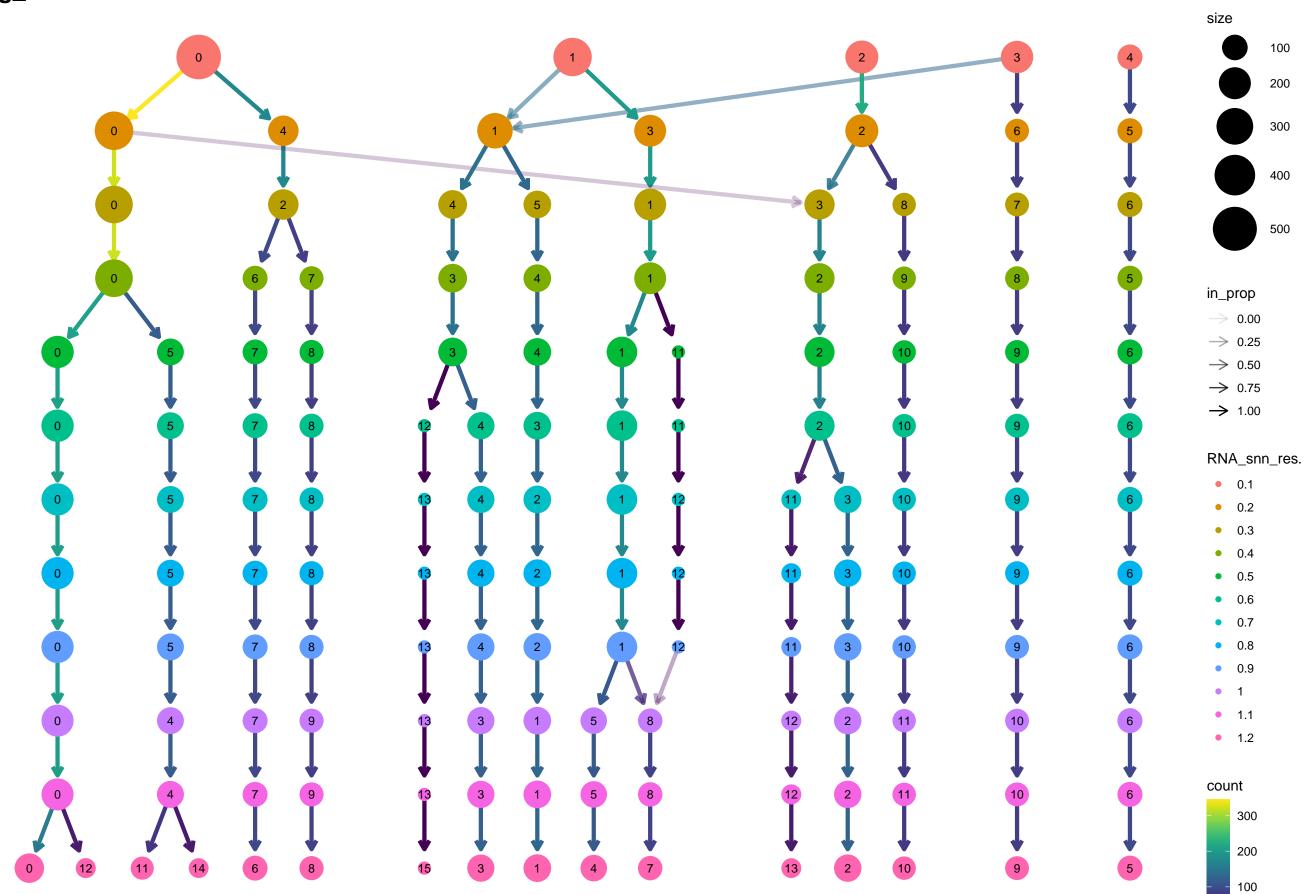


rank > optimal\_pcs\_calculated

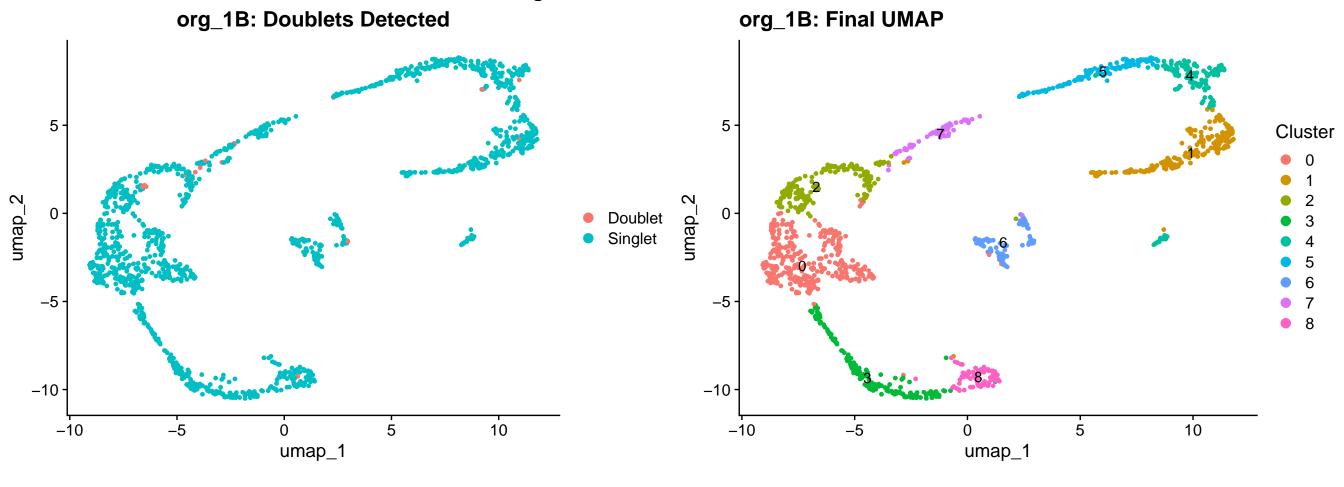
- a FALSE
  - TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.3	9	0.369902796929745
2	0.4	10	0.361363869214392
3	0.2	7	0.353373351080964
4	0.1	5	0.332409255973207
5	0.5	12	0.281168823931882
6	0.7	14	0.259750677046559
7	0.6	13	0.25002087727607
8	1.2	16	0.233673131821511

org\_1B: Clustree



org\_1B - UMAP & Doublet Removal



	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	26568	7163	19
2	Singlet	17427	5753	1362

org\_1B - QC Metrics & Cell Cycle on UMAP org\_1B: nFeature\_RNA org\_1B: nCount\_RNA 10 ¬ ر 10 5 -5 -8000 umap\_2 umap\_2 30000 0 -6000 20000 4000 10000 -5 -5 **-10** -**-10** -10 10 **-**5 **–**10 <del>-</del>5 **–**10 Ó 5 Ó umap\_1 umap\_1 org\_1B: Cell Cycle Phase org\_1B: Final UMAP 5 -Cluster Phase umap\_2 umap\_2 0 --5· **-5 -10** -**-10** --10 <u>-</u>5 5 10 -10 -5 5 10 umap\_1 umap\_1