org_6A - Adaptive Threshold Determination

Method: peak | Selected peak: 5374.9 | Total peaks: 1 | Top 2 peaks used

0.00025

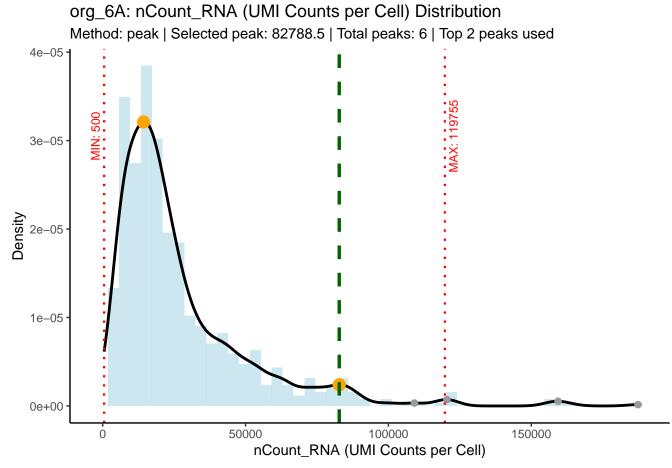
0.00015

0.00005

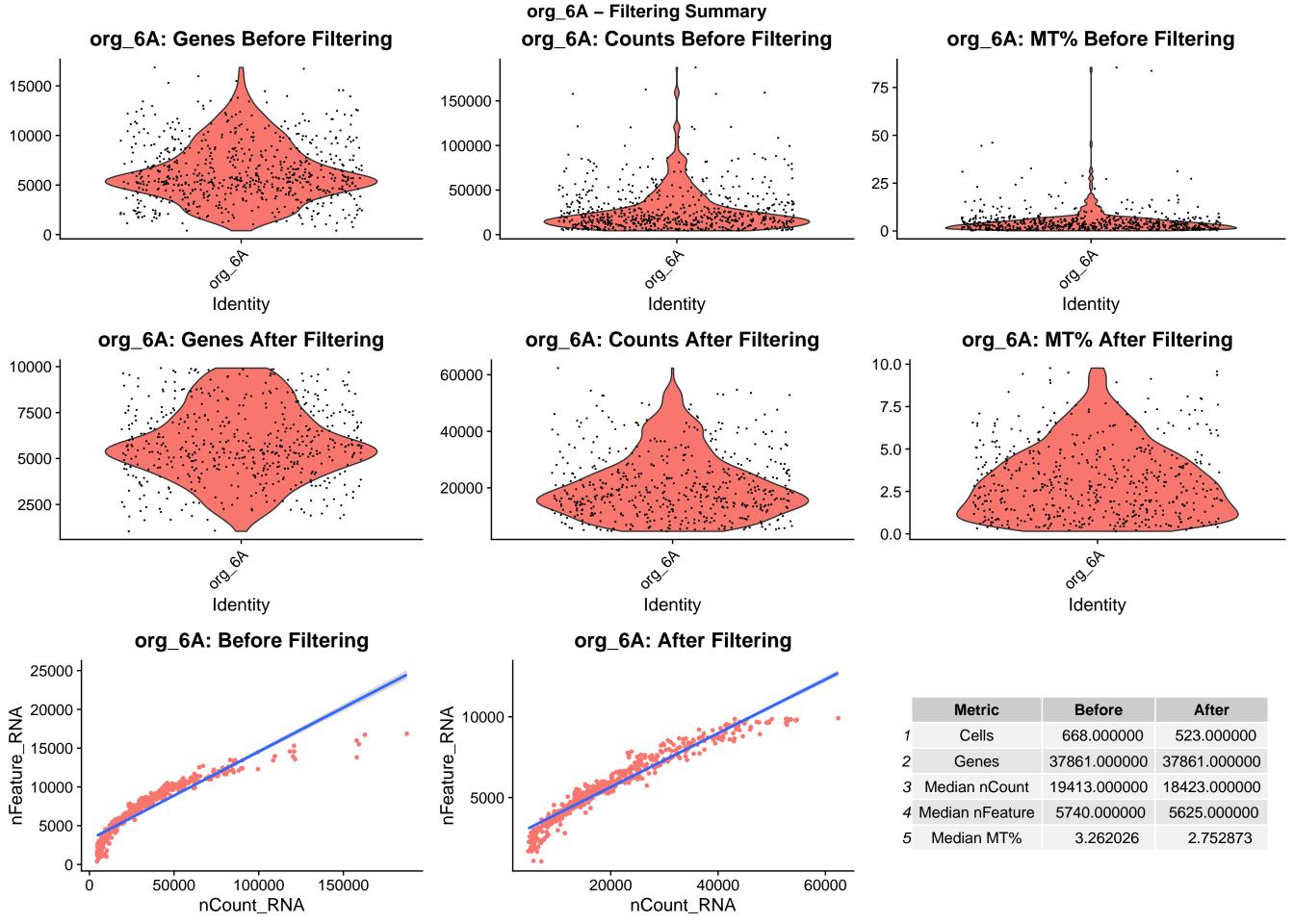
0.00000

nFeature_RNA (Genes per Cell)

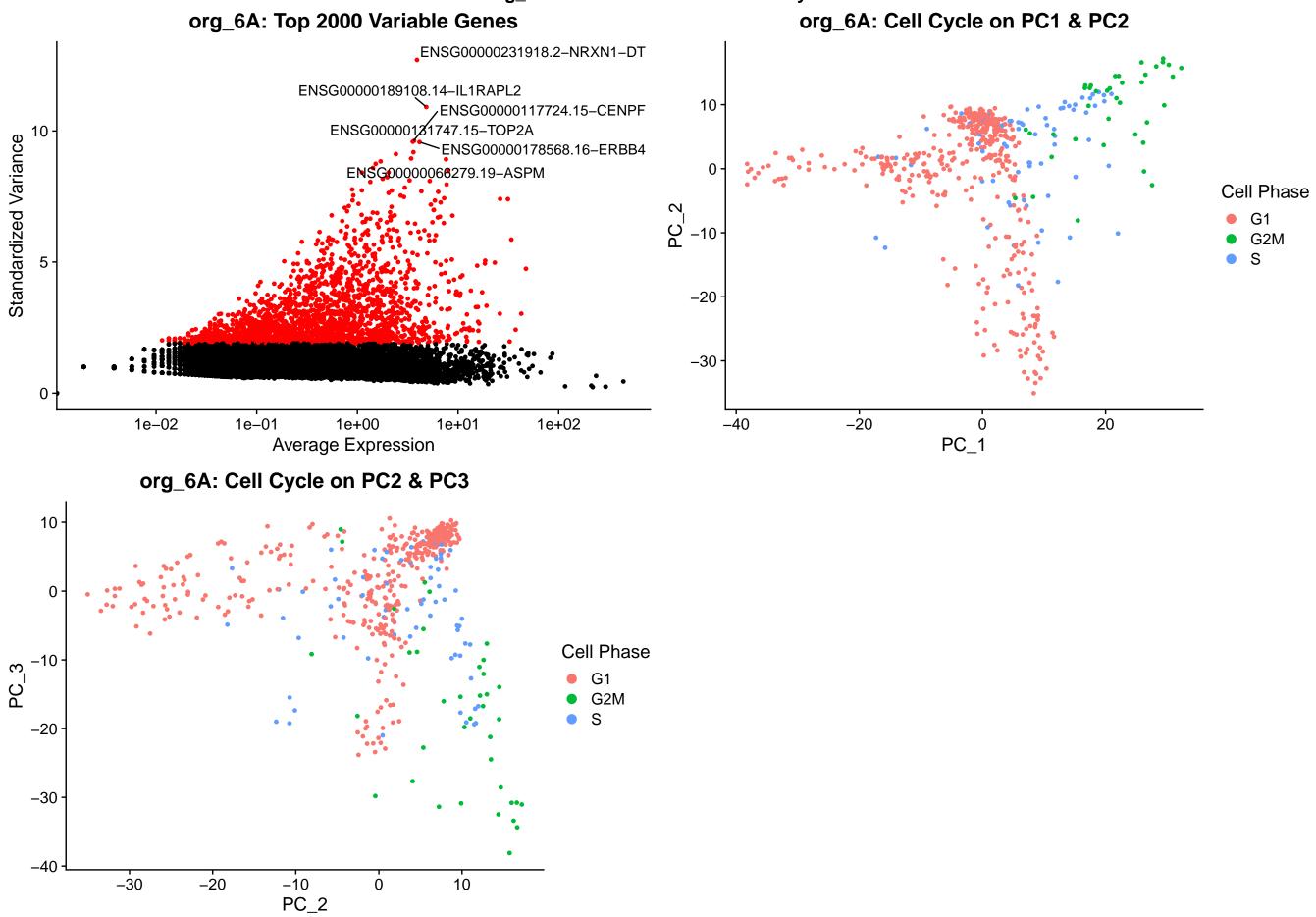
org_6A: nFeature_RNA (Genes per Cell) Distribution



Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
ture_RNA	peak	5375	1	5375	3031	829	9921
unt_RNA	peak	82789	6	14297, 82789	24644	500	119755



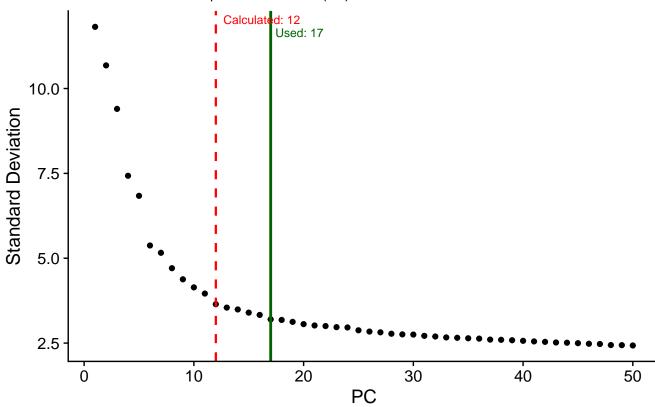
org_6A - Variable Features & Cell Cycle



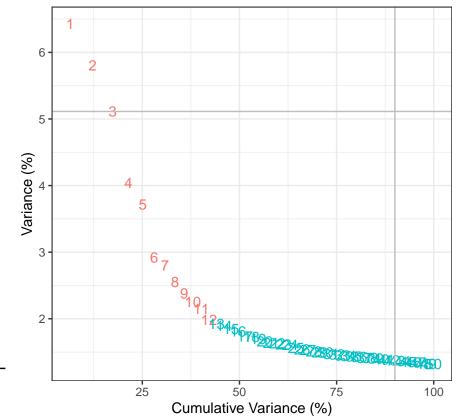
org_6A - PCA Selection & Silhouette Analysis

org_6A: Elbow Plot

Calculated: 12 PCs | Used: 17 PCs (+5)



org_6A: Quantitative PC Selection Calculated: 12 PCs | Used: 17 PCs (+5)

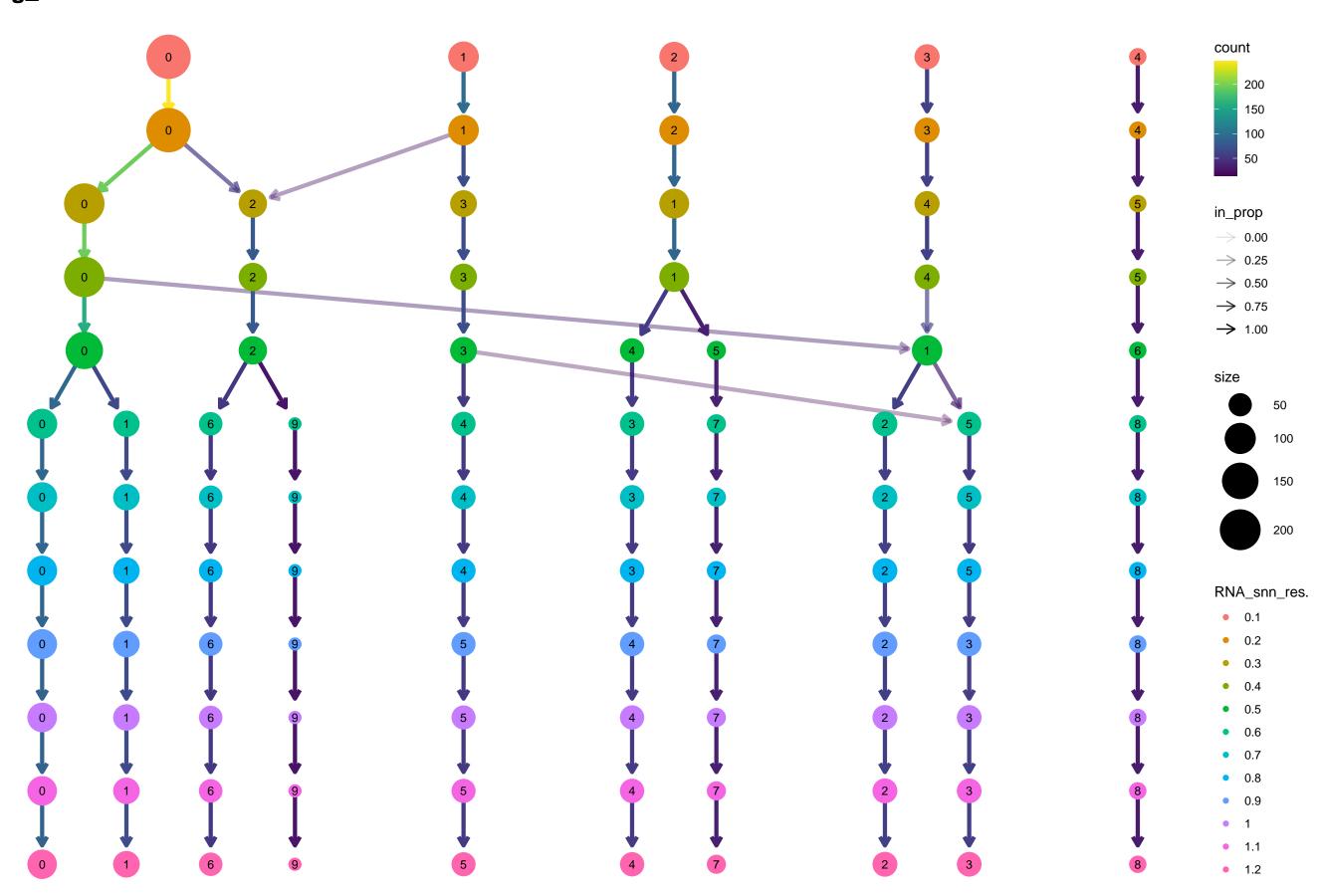


rank > optimal_pcs_calculated

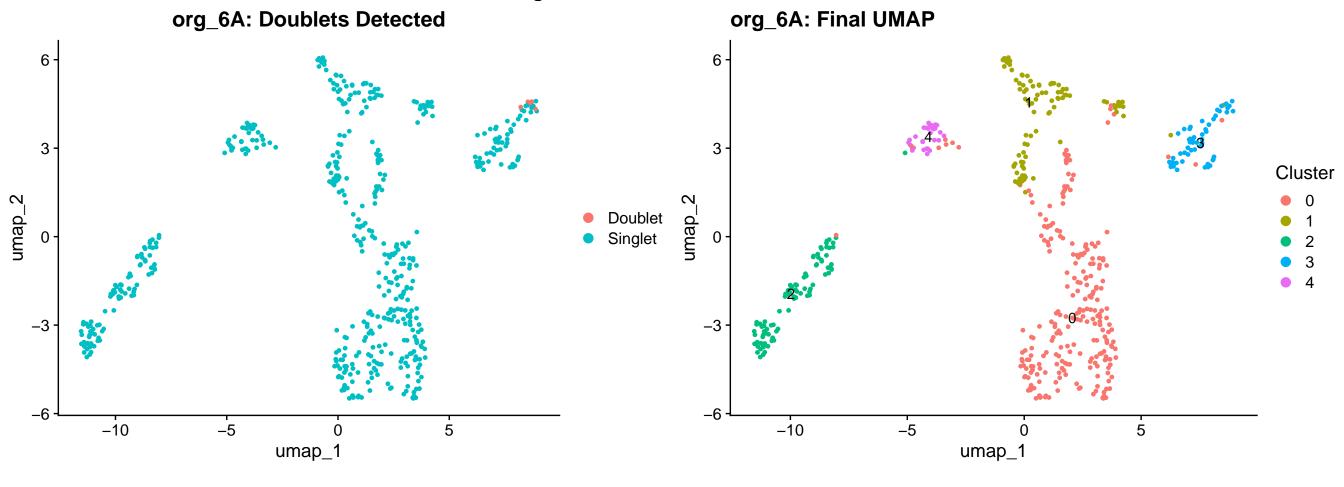
- a FALSE
 - TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.1	5	0.397534255240846
2	0.3	6	0.359222476002996
3	0.5	7	0.312007422553343
4	0.7	10	0.206836834107449

org_6A: Clustree



org_6A - UMAP & Doublet Removal



	DF. classifications	median_nCount	median_nFeature	count
1	Doublet	45551.5	9397.5	6
2	Singlet	18221.0	5577.0	517

org_6A - QC Metrics & Cell Cycle on UMAP org_6A: nFeature_RNA org_6A: nCount_RNA 60000 umap_2 7500 40000 5000 20000 2500 10 10 **-**5 -10 **-**5 -10 umap_1 umap_1 org_6A: Cell Cycle Phase org_6A: Final UMAP 6 -3 Cluster Phase umap_2 -3 -10 <u>-</u>5 5 **–**10 -5 5 0 umap_1 umap_1