org_6C - Adaptive Threshold Determination

org_6C: nFeature_RNA (Genes per Cell) Distribution
Method: peak | Selected peak: 4616.6 | Total peaks: 3 | Top 2 peaks used

0.00025

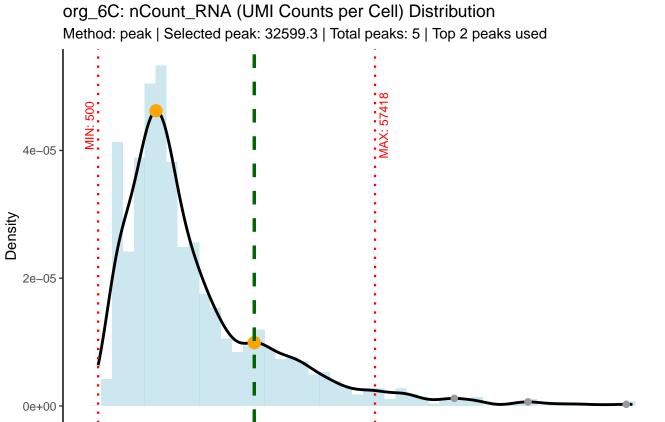
0.00015

0.00005

0.00005

0.00000

nFeature_RNA (Genes per Cell)



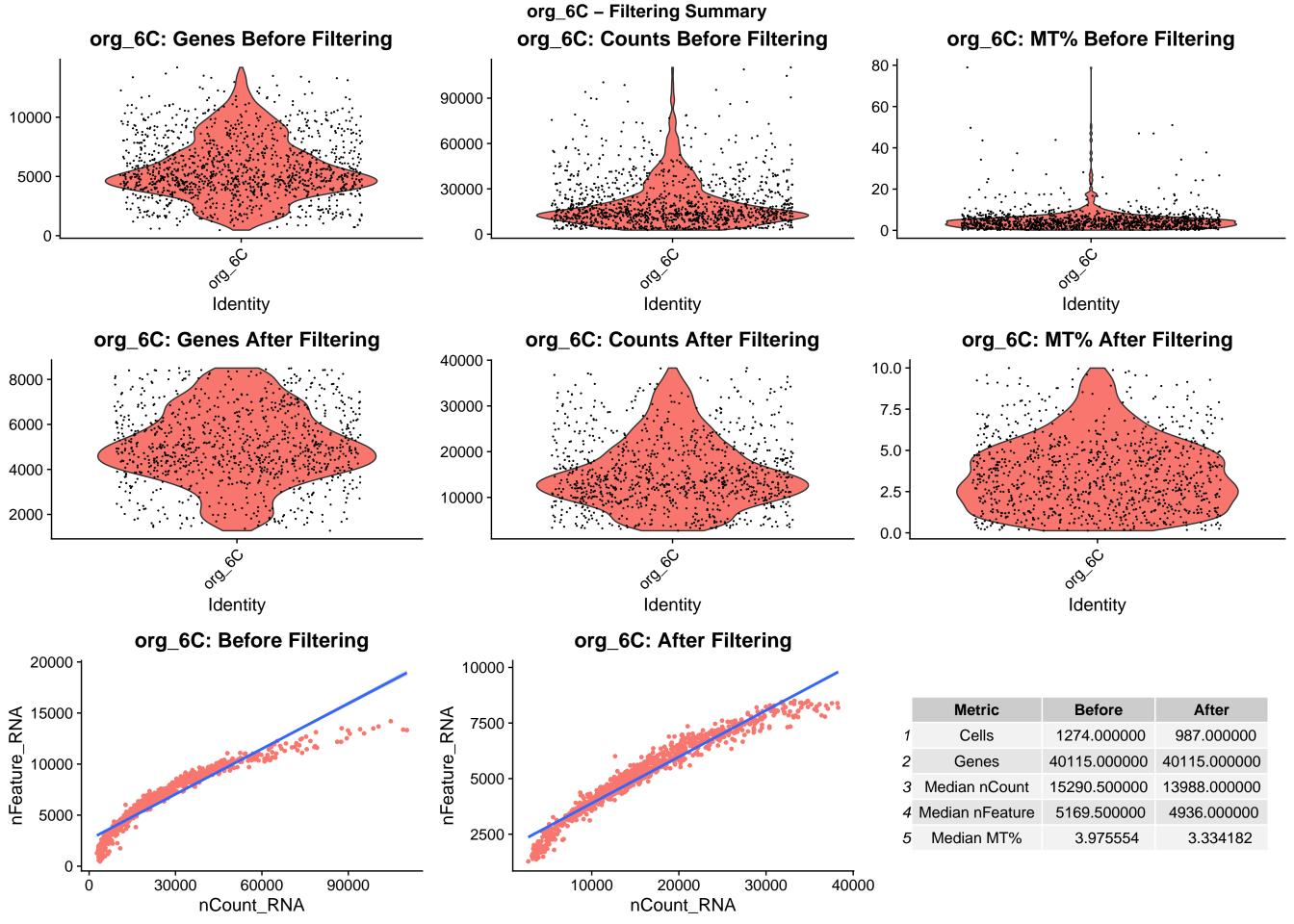
30000

60000

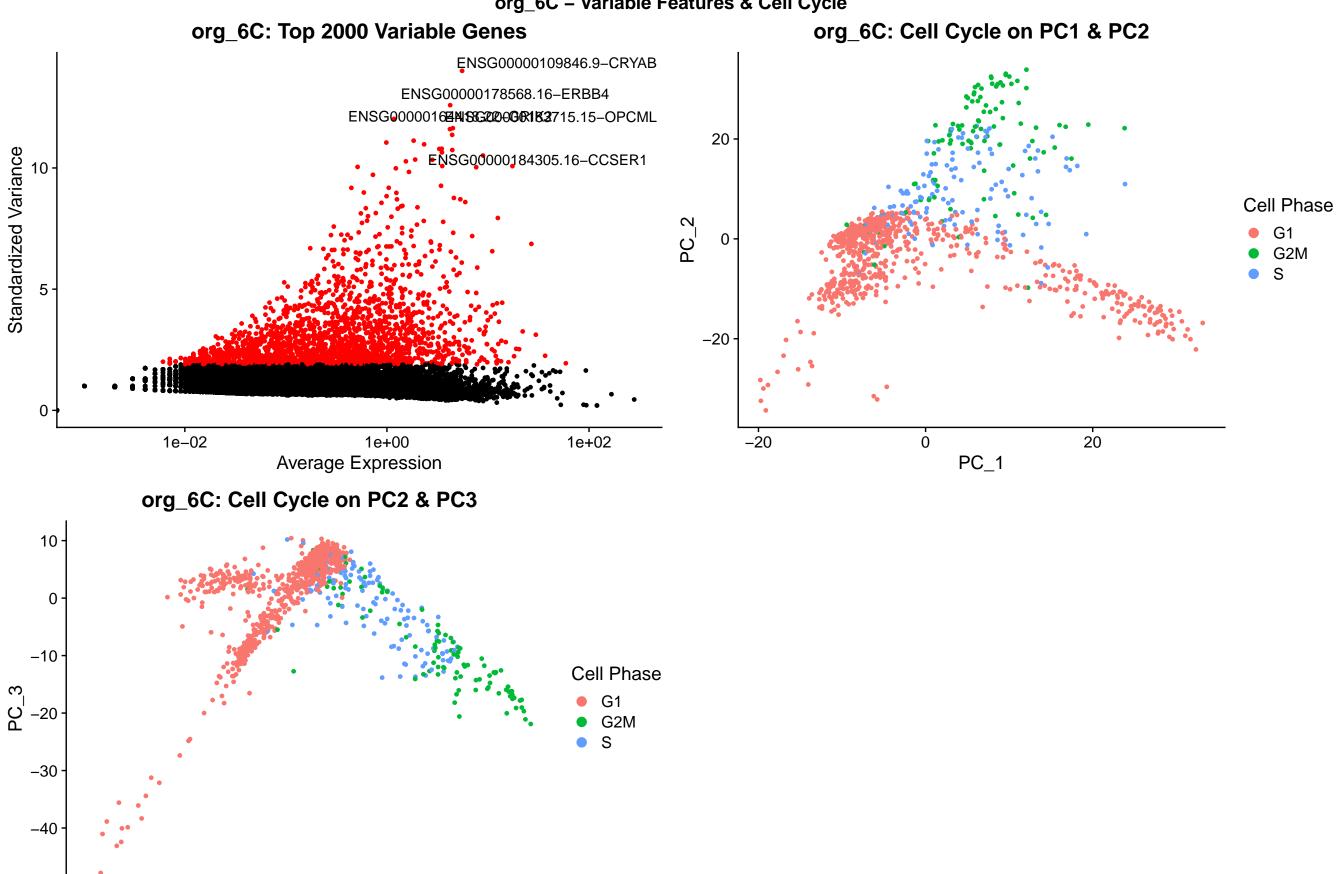
nCount_RNA (UMI Counts per Cell)

90000

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
ture_RNA	peak	4617	3	4617, 2178	2597	722	8512
unt_RNA	peak	32599	5	12398, 32599	16546	500	57418



org_6C - Variable Features & Cell Cycle



-50

0 PC_2

20

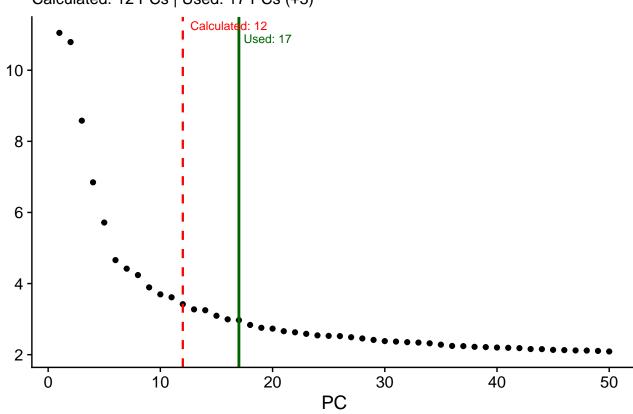
-20

org_6C - PCA Selection & Silhouette Analysis

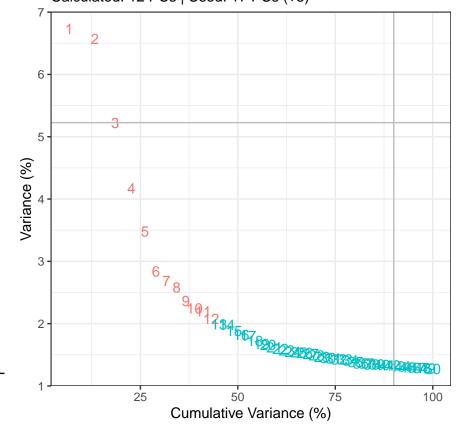
org_6C: Elbow Plot

Standard Deviation

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



org_6C: Quantitative PC Selection Calculated: 12 PCs | Used: 17 PCs (+5)

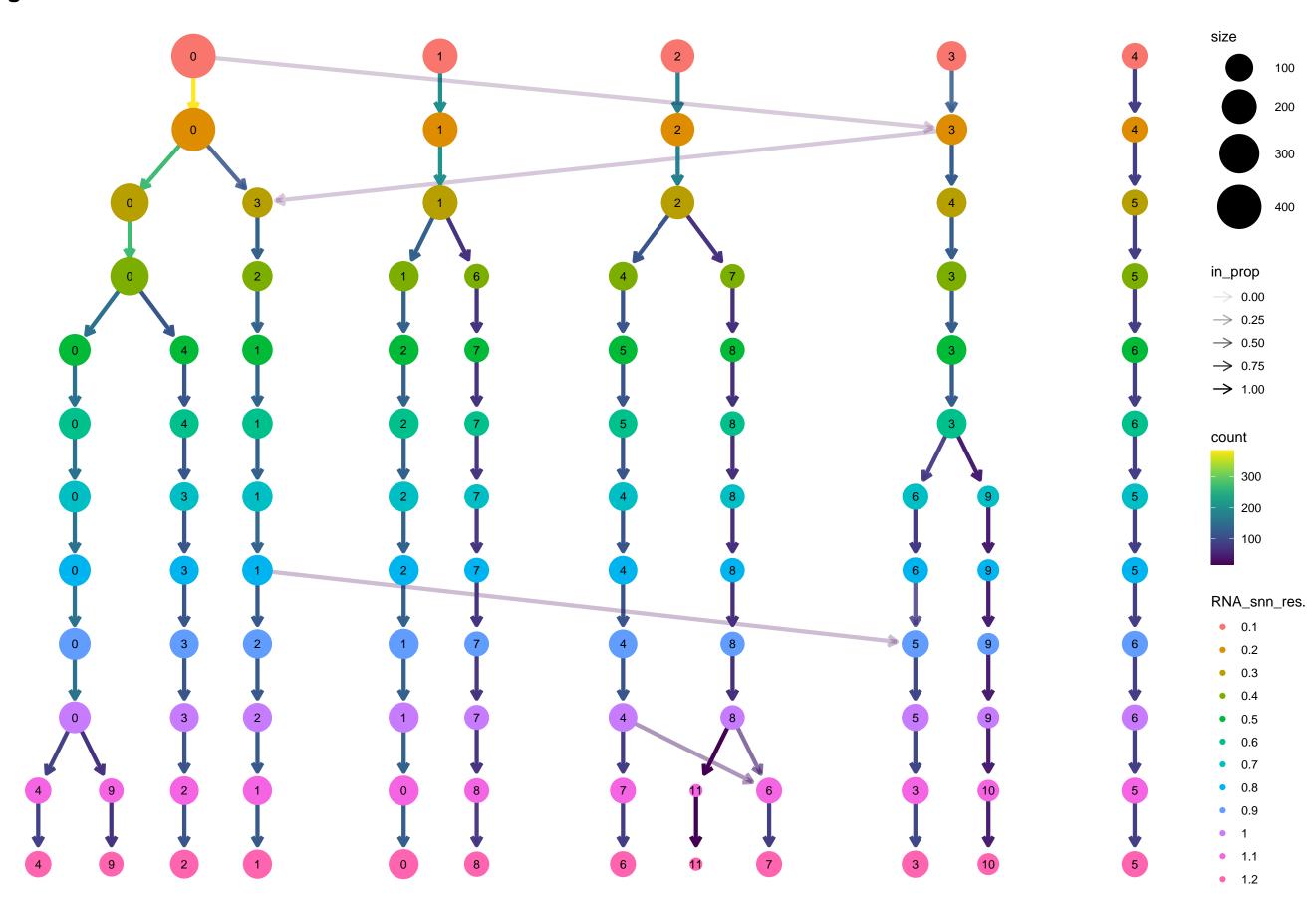


rank > optimal_pcs_calculated

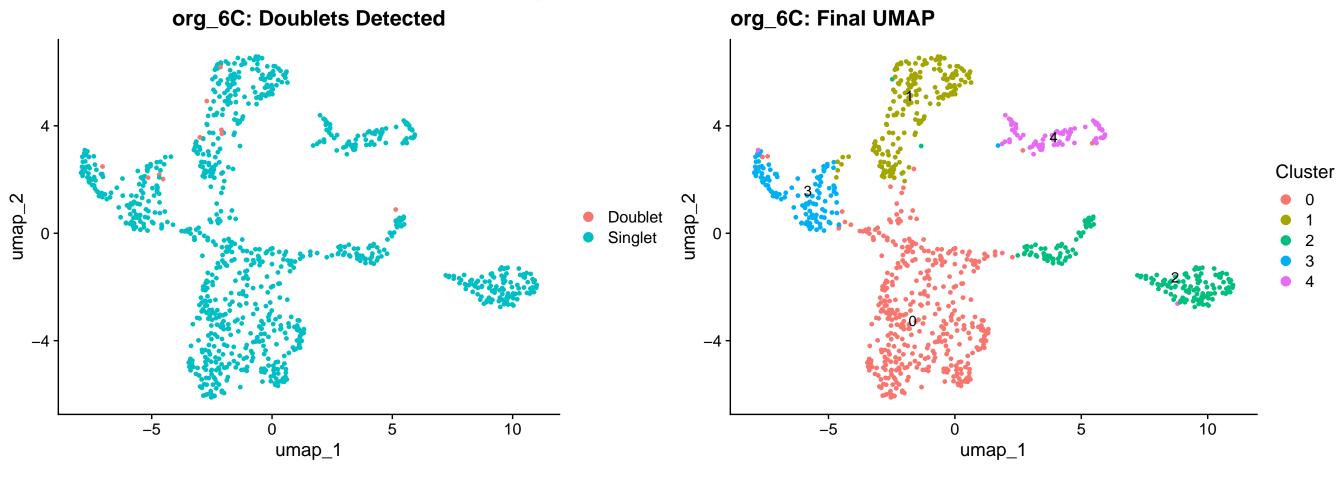
- a FALSE
- a TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.1	5	0.361599100507883
2	0.4	8	0.319985082064438
3	0.3	6	0.260047577472373
4	0.7	10	0.251962219464654
5	0.5	9	0.241354071545283
6	1.1	12	0.22117873436575

org_6C: Clustree



org_6C - UMAP & Doublet Removal



	DF. classifications	median_nCount	median_nFeature	count
1	Doublet	26597	7411.5	12
2	Singlet	13914	4924.0	975

org_6C - QC Metrics & Cell Cycle on UMAP org_6C: nCount_RNA org_6C: nFeature_RNA 4 -8000 umap_2 umap_2 30000 6000 20000 4000 10000 2000 **-**5 10 <u>-</u>5 10 umap_1 umap_1 org_6C: Final UMAP org_6C: Cell Cycle Phase Cluster Phase umap_2 <u>-</u>5 5 10 -5 10 5 0 umap_1 umap_1