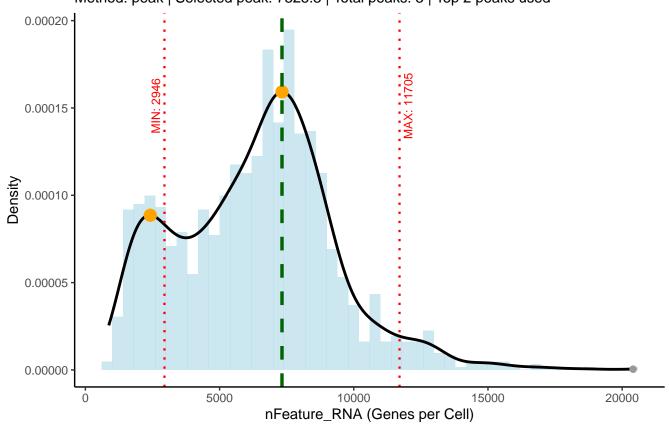
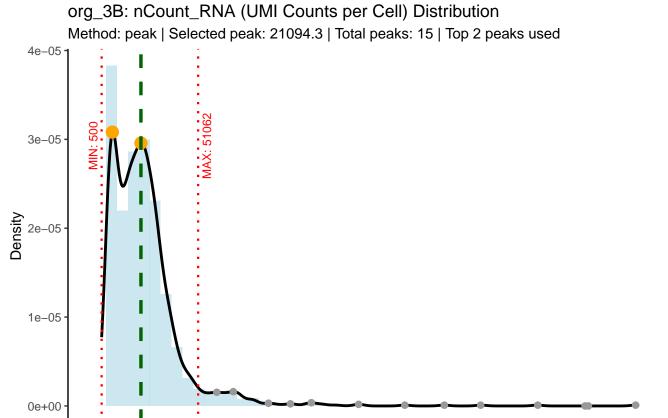
org_3B - Adaptive Threshold Determination

org_3B: nFeature_RNA (Genes per Cell) Distribution

Method: peak | Selected peak: 7325.3 | Total peaks: 3 | Top 2 peaks used



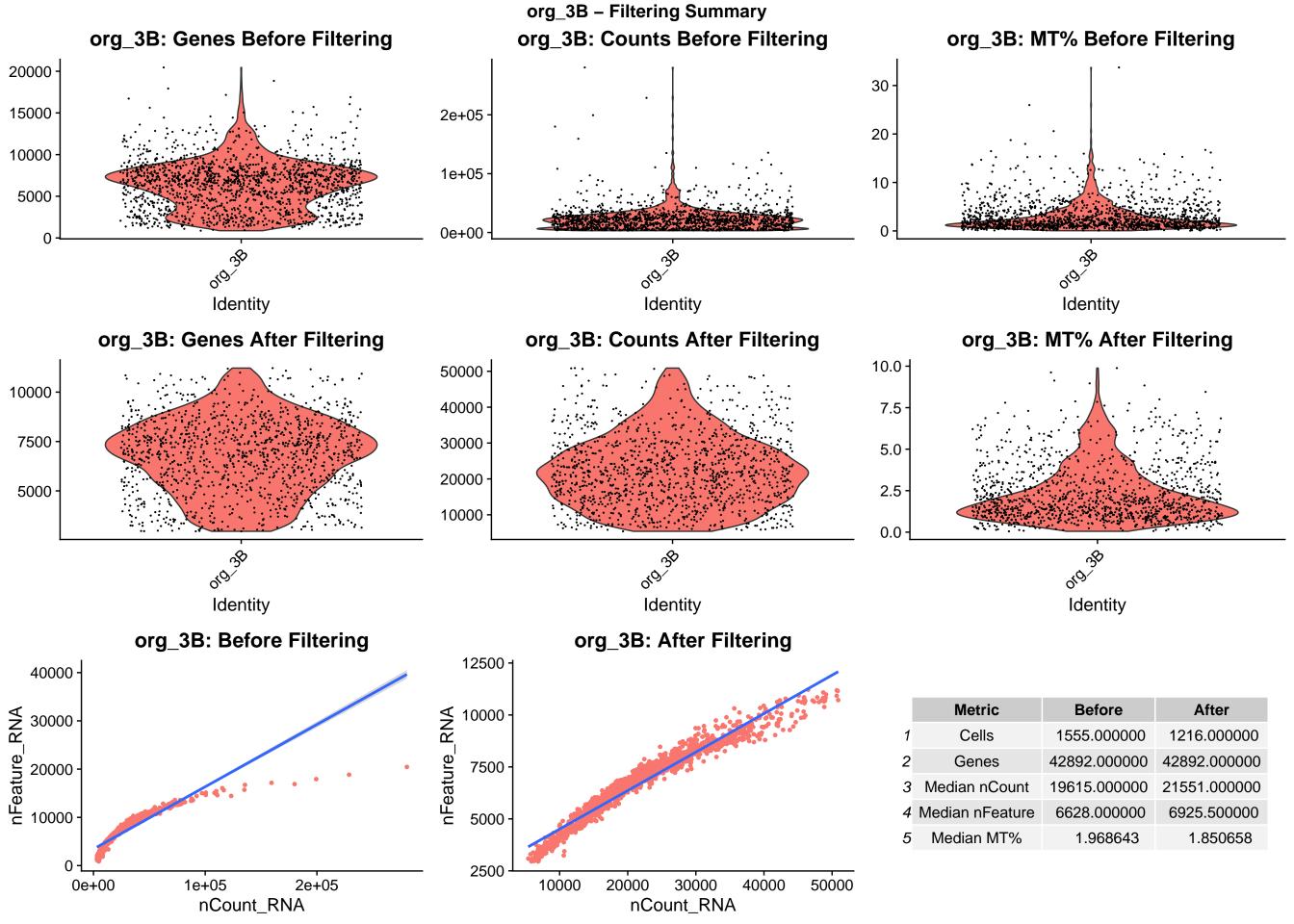


1e+05

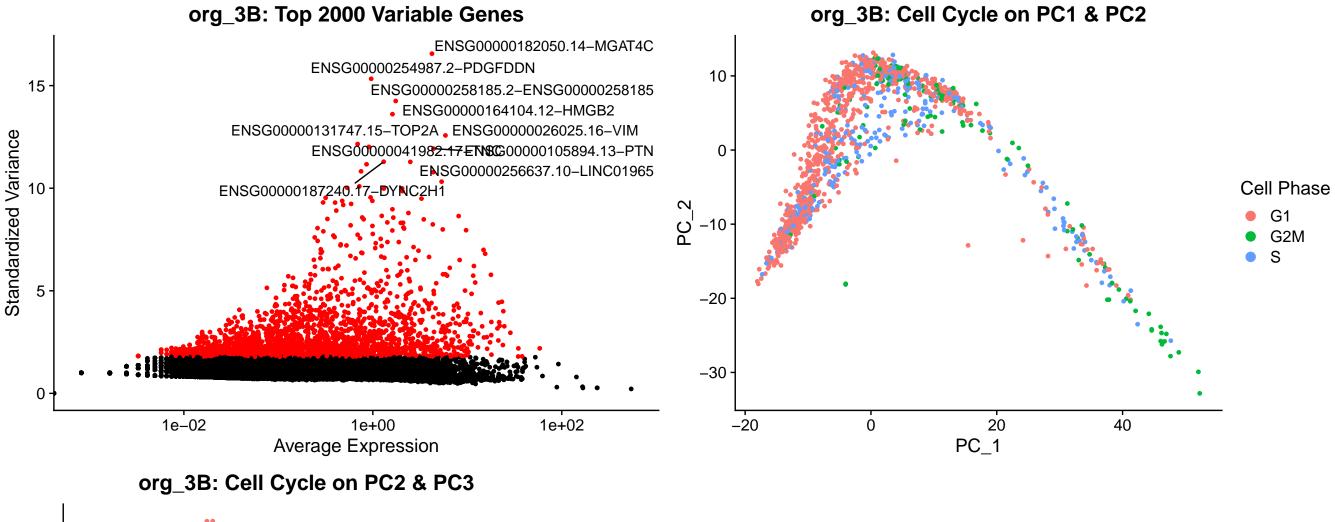
nCount_RNA (UMI Counts per Cell)

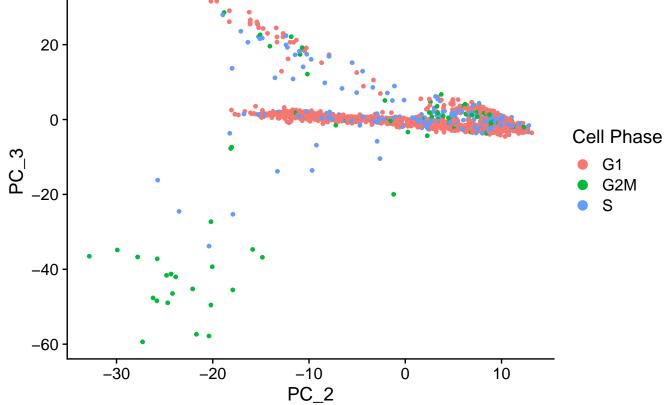
2e+05

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
ature_RNA	peak	7325	3	7325, 2420	2920	2946	11705
ount_RNA	peak	21094	15	6115, 21094	19978	500	51062



org_3B - Variable Features & Cell Cycle

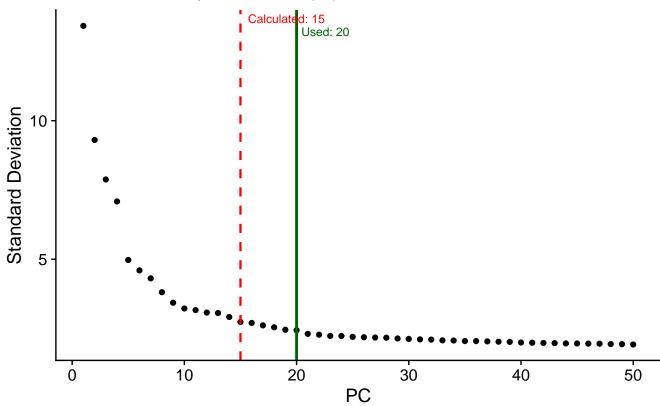




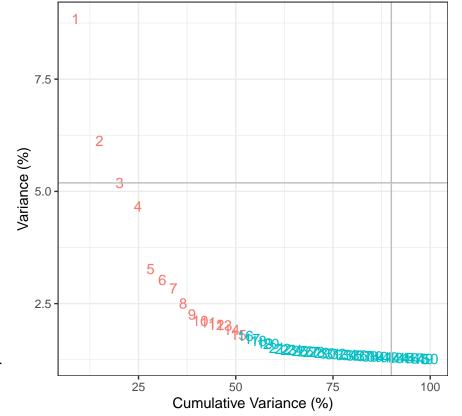
org_3B - PCA Selection & Silhouette Analysis

org_3B: Elbow Plot

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



org_3B: Quantitative PC Selection Calculated: 15 PCs | Used: 20 PCs (+5)

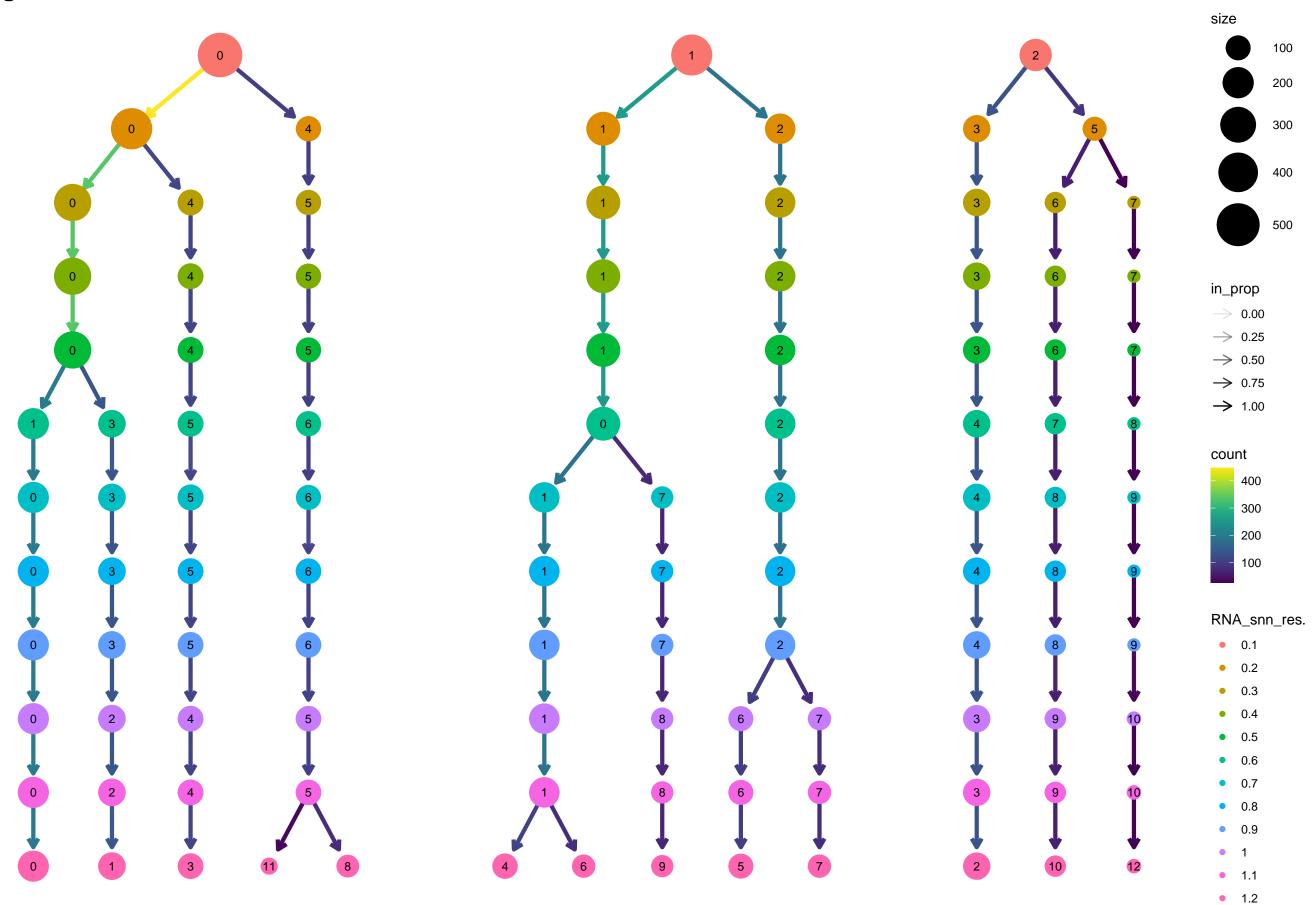


rank > optimal_pcs_calculated

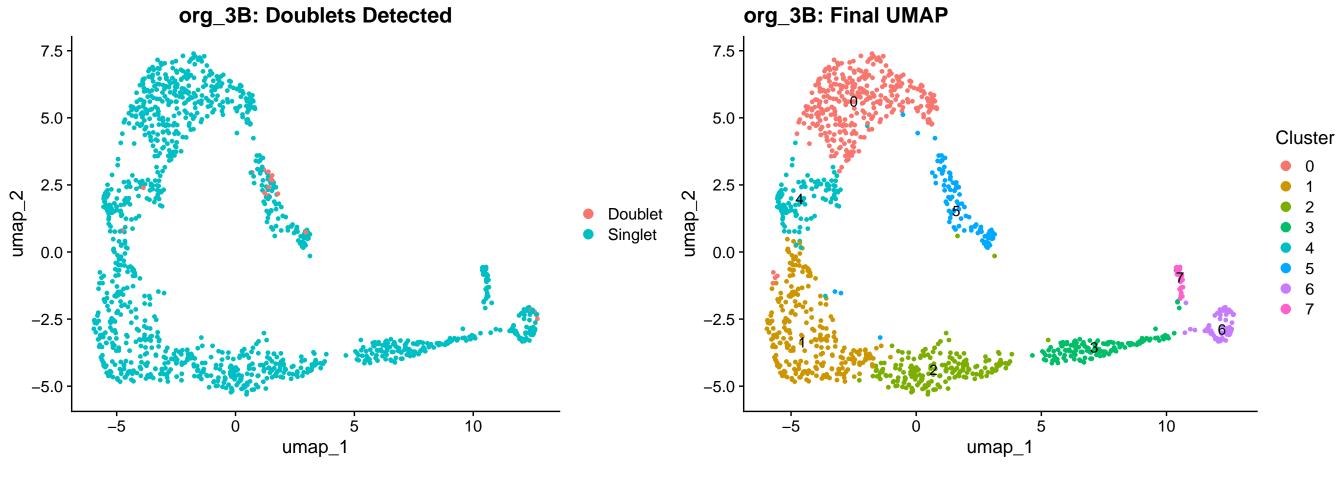
- a FALSE
- a TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.3	8	0.35283655820304
2	0.2	6	0.348179323151582
3	0.7	10	0.319829422723608
4	0.6	9	0.31419744781651
5	1.2	13	0.281863564983331
6	0.1	3	0.269638582523755
7	1	11	0.263192596847039

org_3B: Clustree



org_3B - UMAP & Doublet Removal



	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	37923	10079	16
2	Singlet	21408	6897	1200

org_3B - QC Metrics & Cell Cycle on UMAP org_3B: nFeature_RNA org_3B: nCount_RNA 8 -11000 50000 umap_2 umap_2 40000 9000 30000 7000 20000 5000 10000 3000 10 10 -5 -5 0 0 umap_1 umap_1 org_3B: Cell Cycle Phase org_3B: Final UMAP 7.5 -7.5 -5.0 5.0 Cluster Phase 2.5 2.5 umap_2 0.0 -2.5 · -2.5 -5.0 --5.0 · 10 <u>-</u>5 <u>-</u>5 10 5 5 0 0 umap_1 umap_1