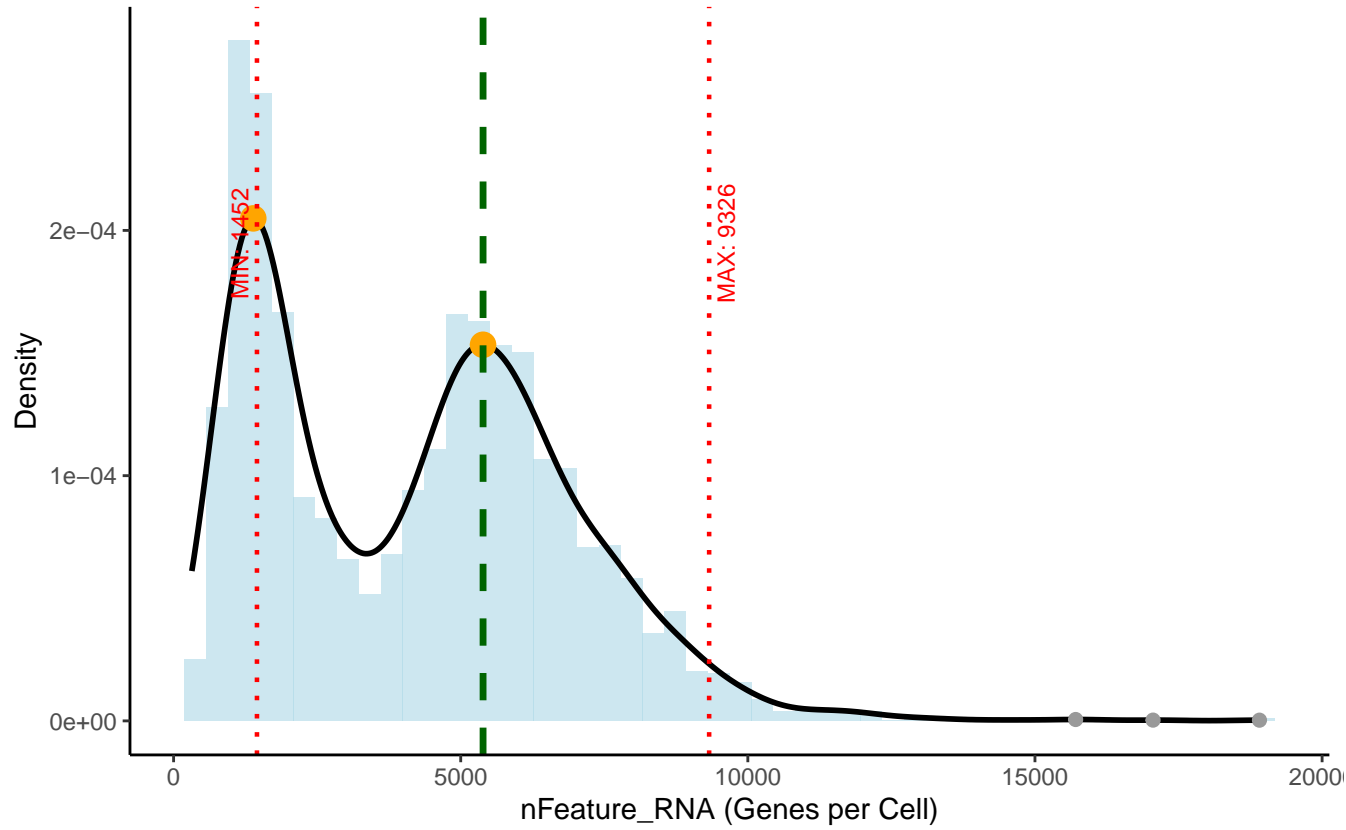


## org\_1B – Adaptive Threshold Determination

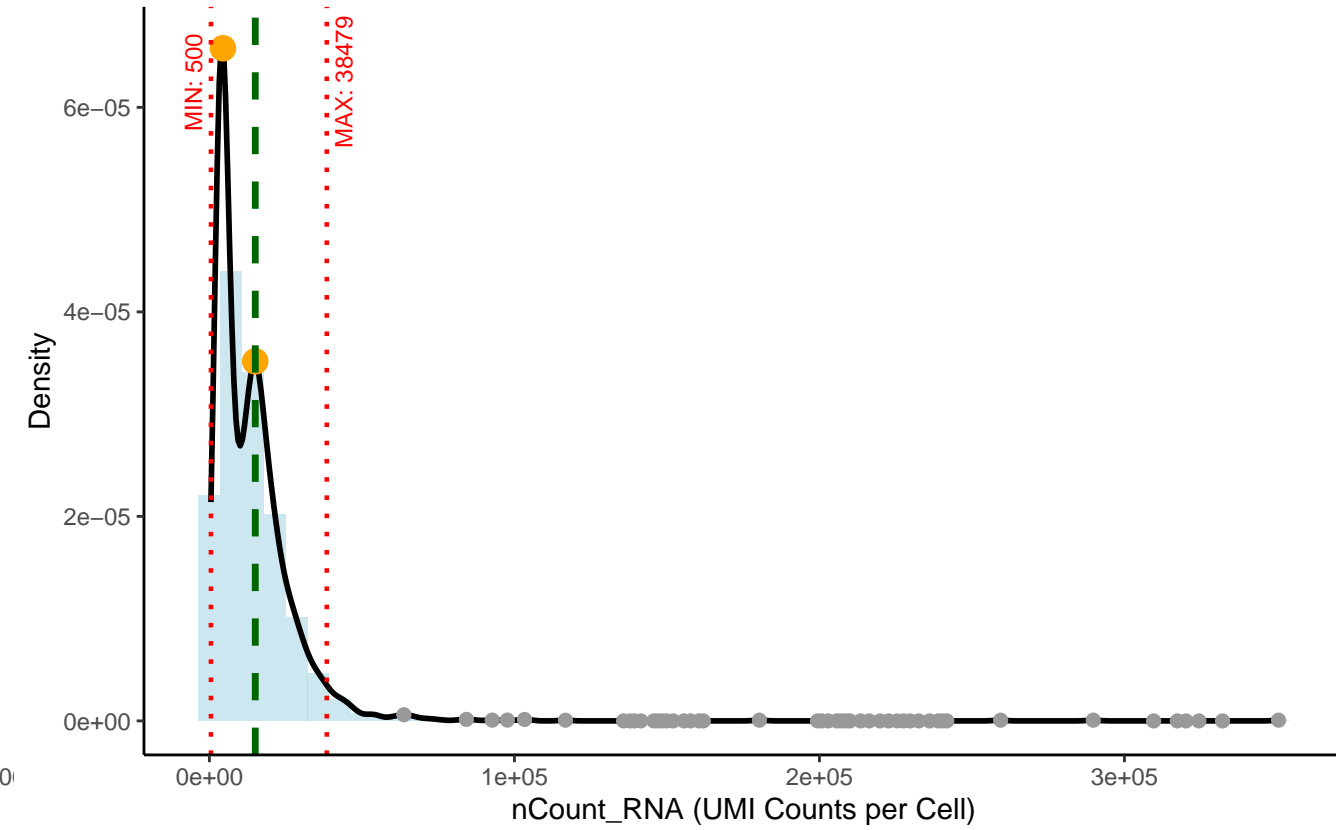
org\_1B: nFeature\_RNA (Genes per Cell) Distribution

Method: peak | Selected peak: 5389 | Total peaks: 5 | Top 2 peaks used



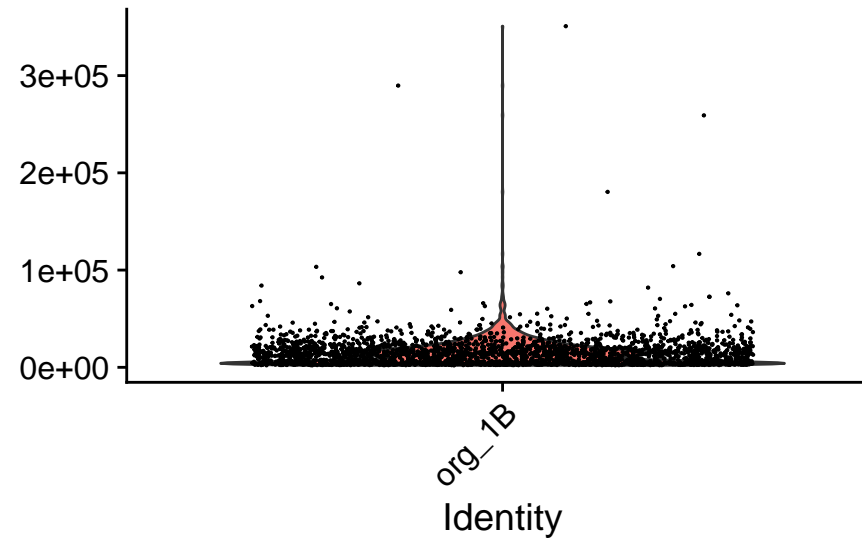
org\_1B: nCount\_RNA (UMI Counts per Cell) Distribution

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

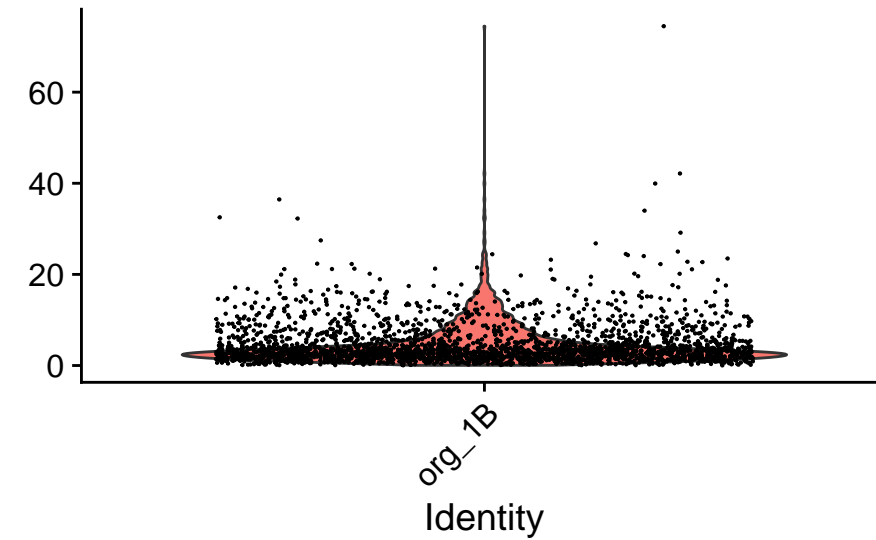


Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
nFeature_RNA	peak	5389	5	1388, 5389	2624	1452	9326
nCount_RNA	peak	15039	49	4444, 15039	15627	500	38479

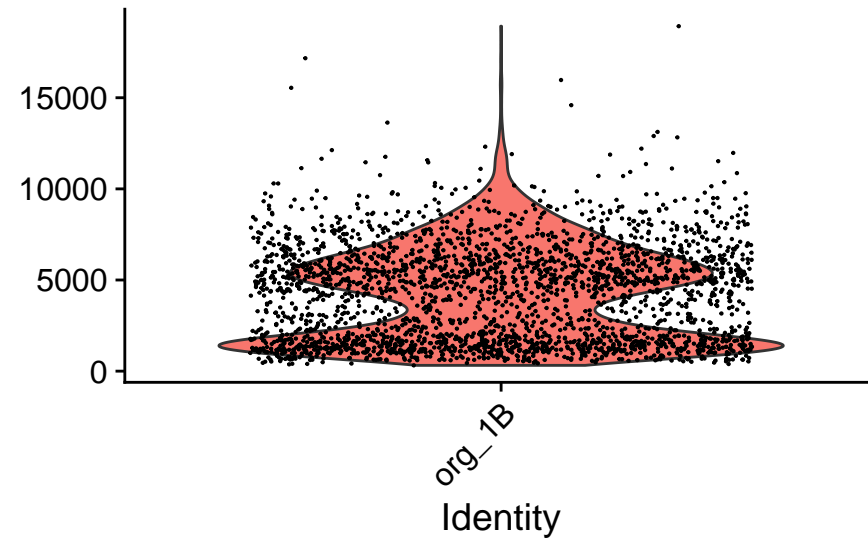
org\_1B – Filtering Summary  
org\_1B: Counts Before Filtering



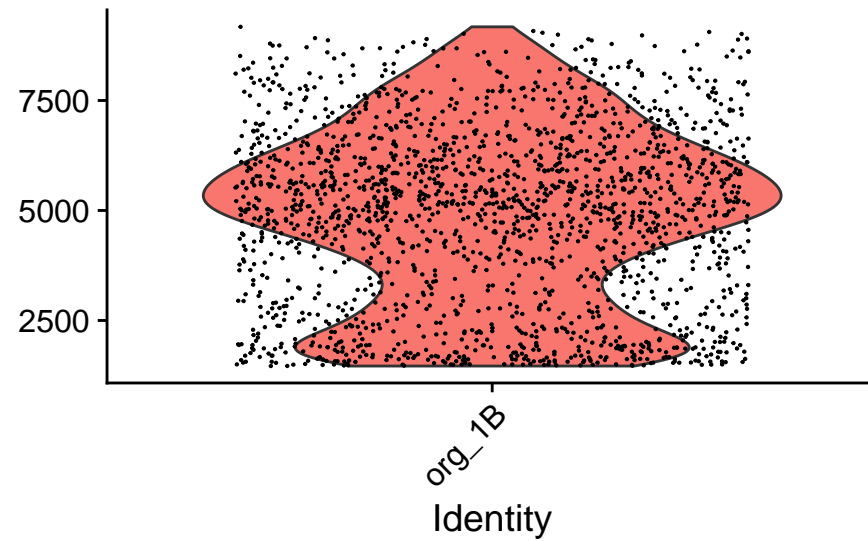
org\_1B: MT% Before Filtering



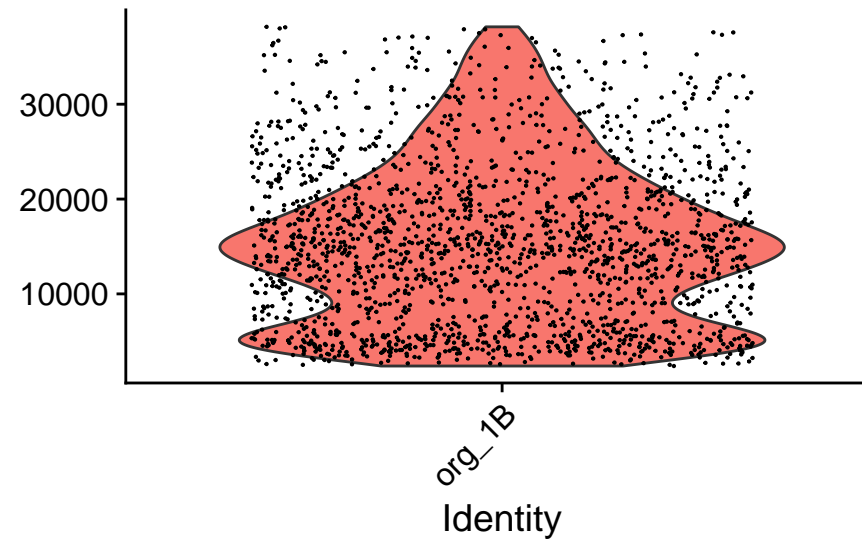
org\_1B: Genes Before Filtering



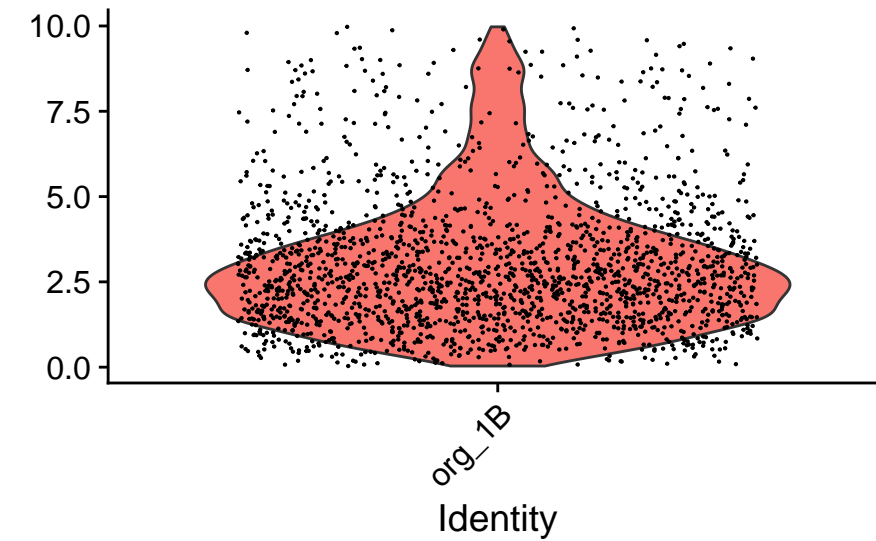
org\_1B: Genes After Filtering



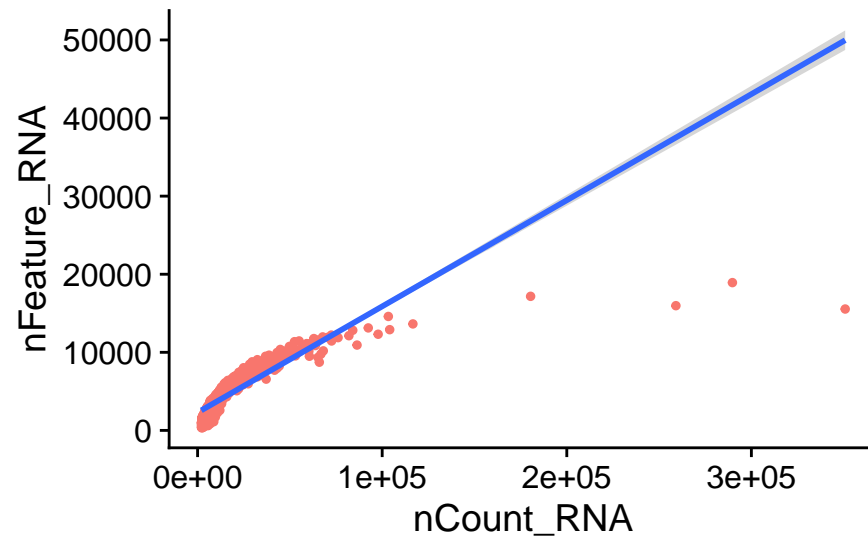
org\_1B: Counts After Filtering



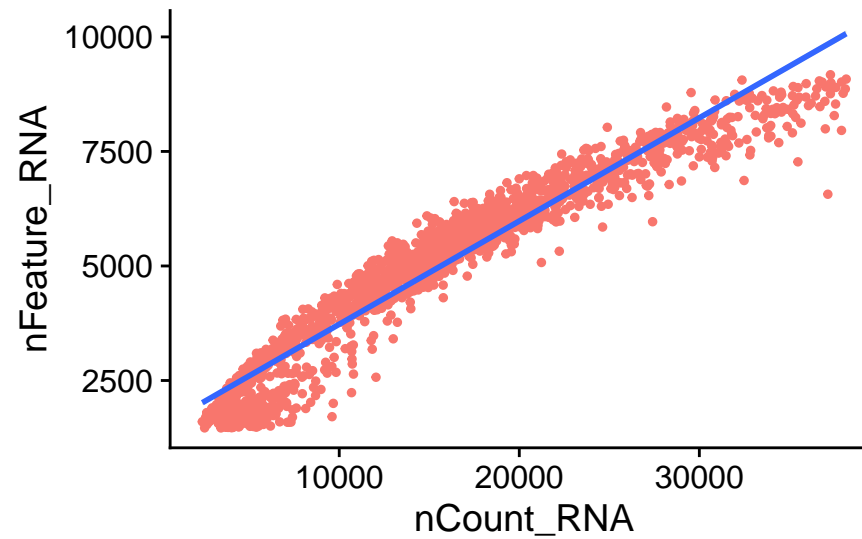
org\_1B: MT% After Filtering



org\_1B: Before Filtering



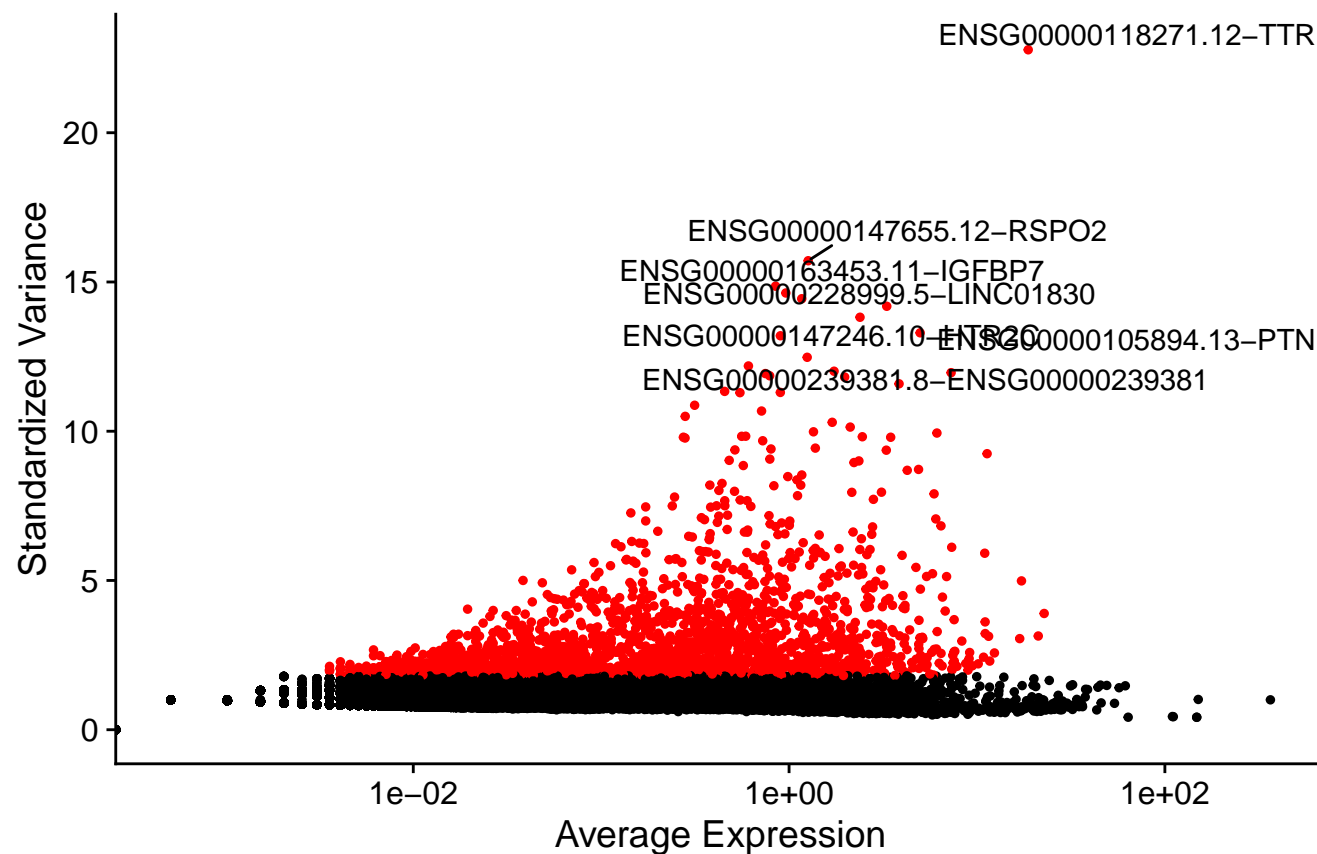
org\_1B: After Filtering



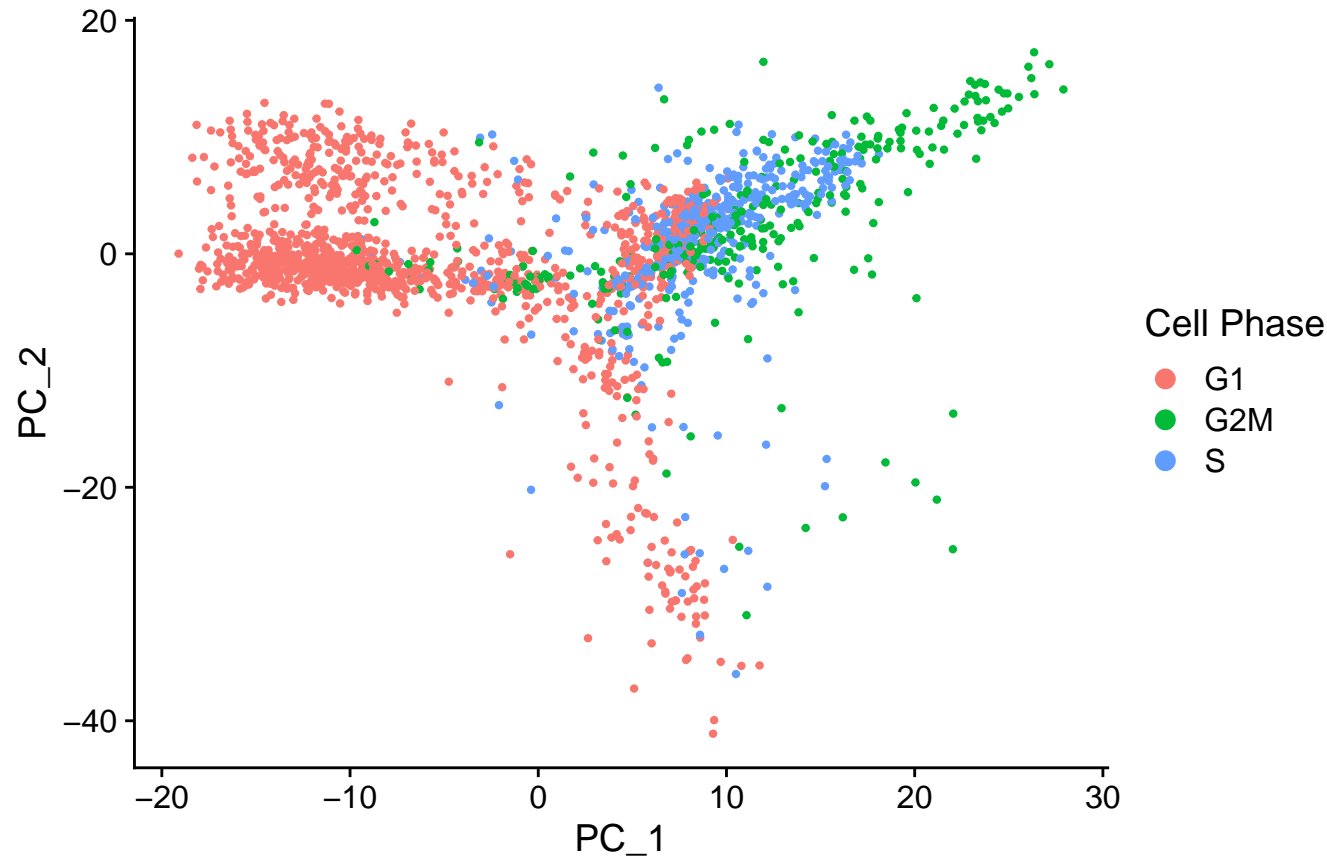
	Metric	Before	After
1	Cells	2716.000000	1953.000000
2	Genes	42332.000000	42332.000000
3	Median nCount	11774.500000	14677.000000
4	Median nFeature	4403.500000	5119.000000
5	Median MT%	3.029187	2.637941

# org\_1B – Variable Features & Cell Cycle

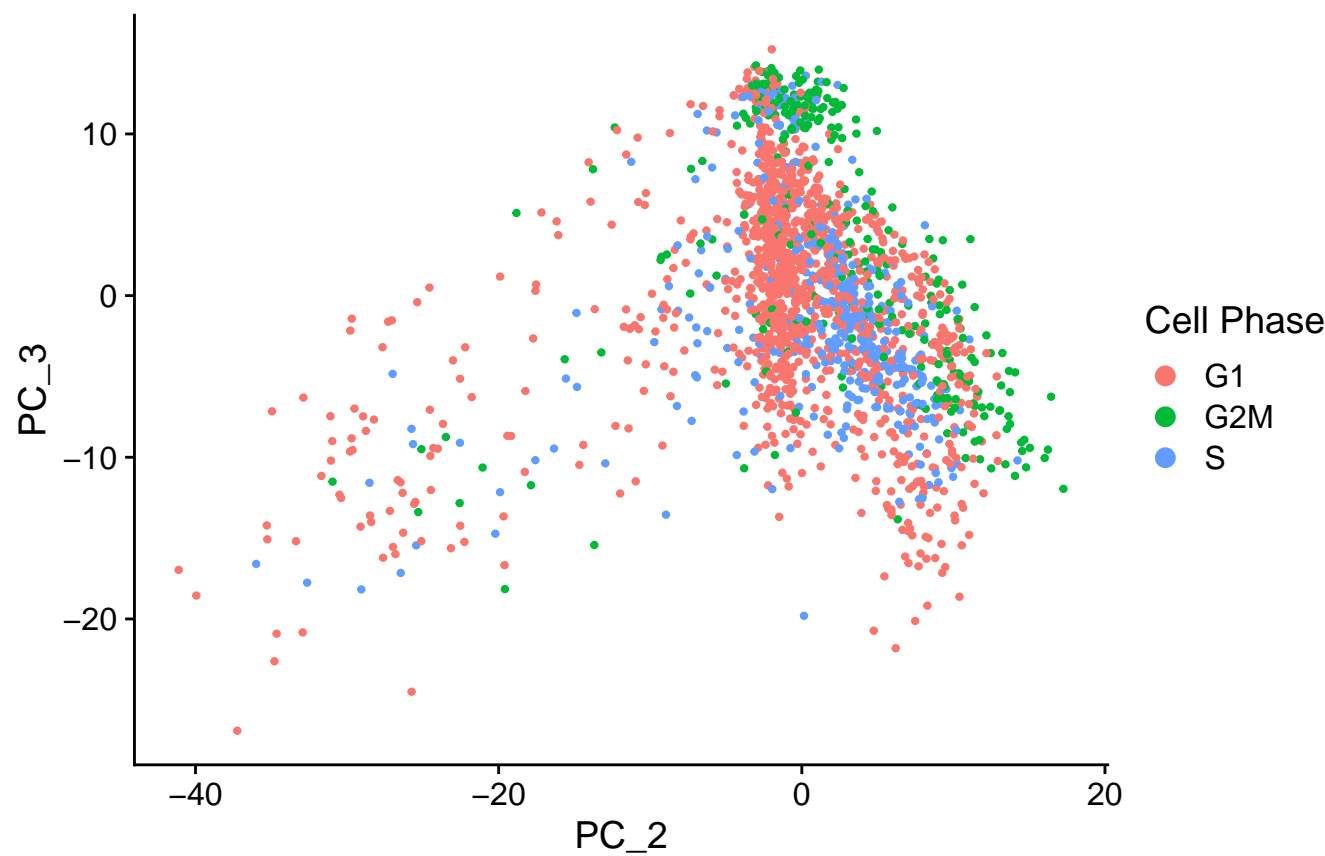
## org\_1B: Top 2000 Variable Genes



## org\_1B: Cell Cycle on PC1 & PC2



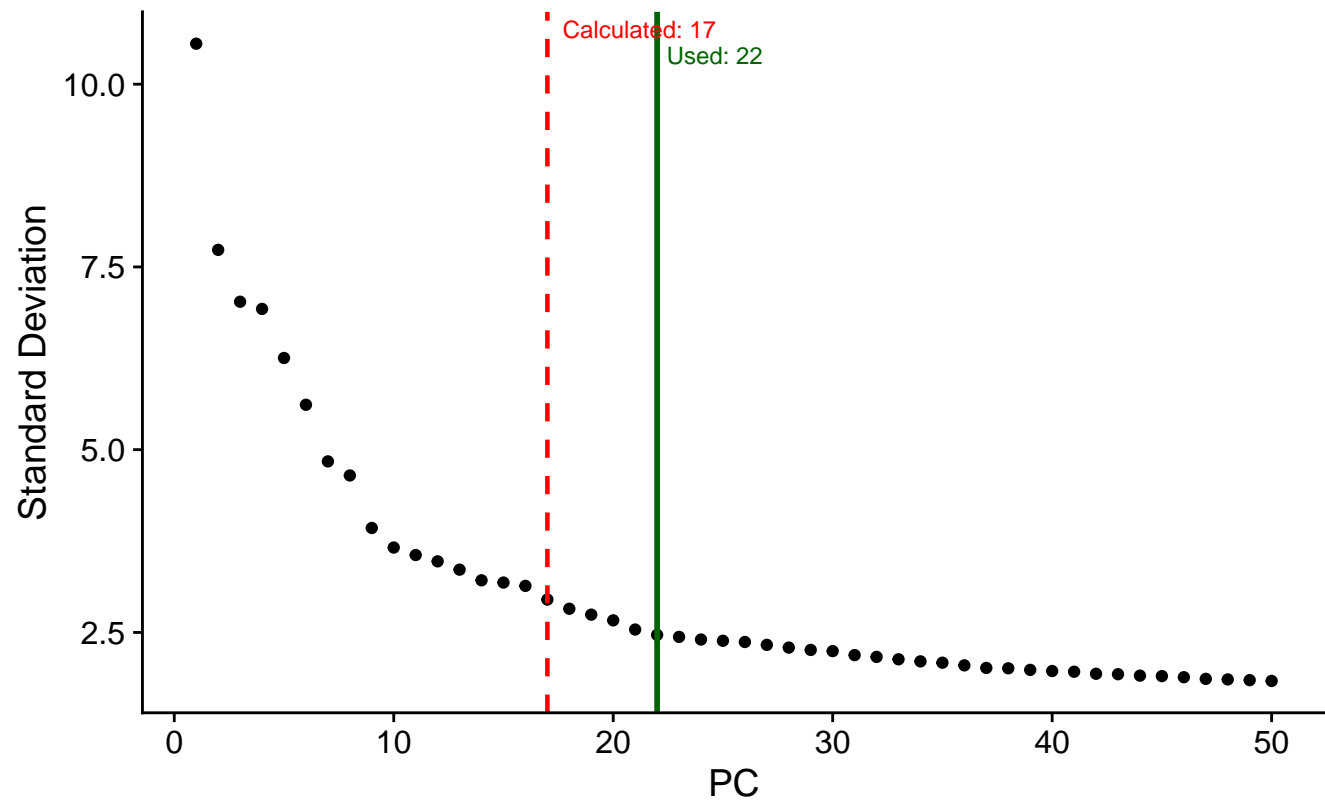
## org\_1B: Cell Cycle on PC2 & PC3



org\_1B – PCA Selection & Silhouette Analysis

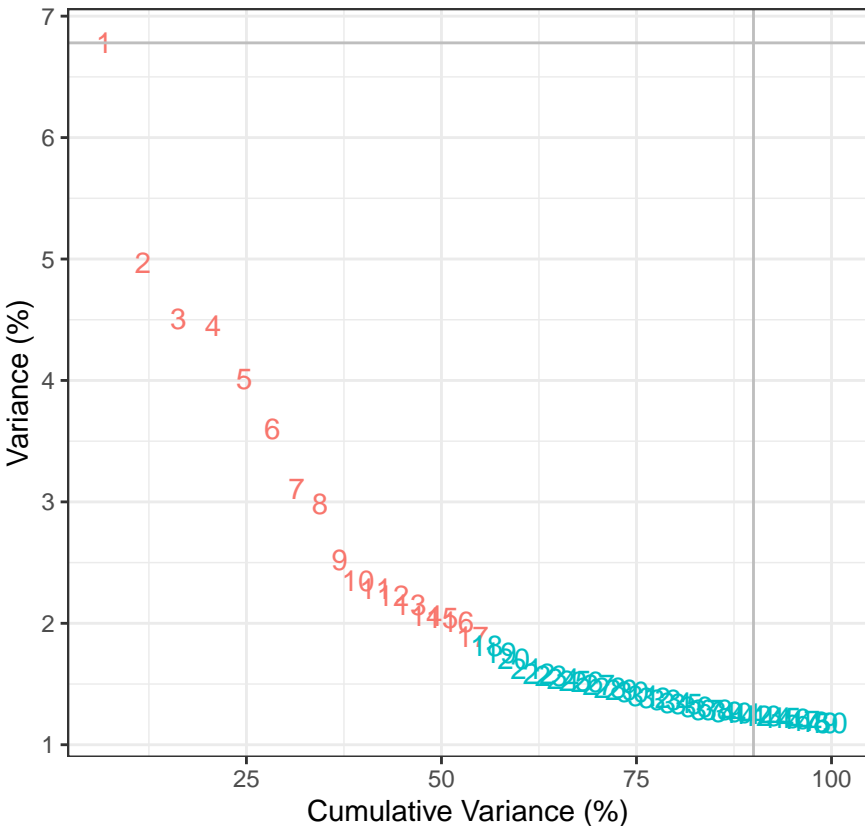
org\_1B: Elbow Plot

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



org\_1B: Quantitative PC Selection

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

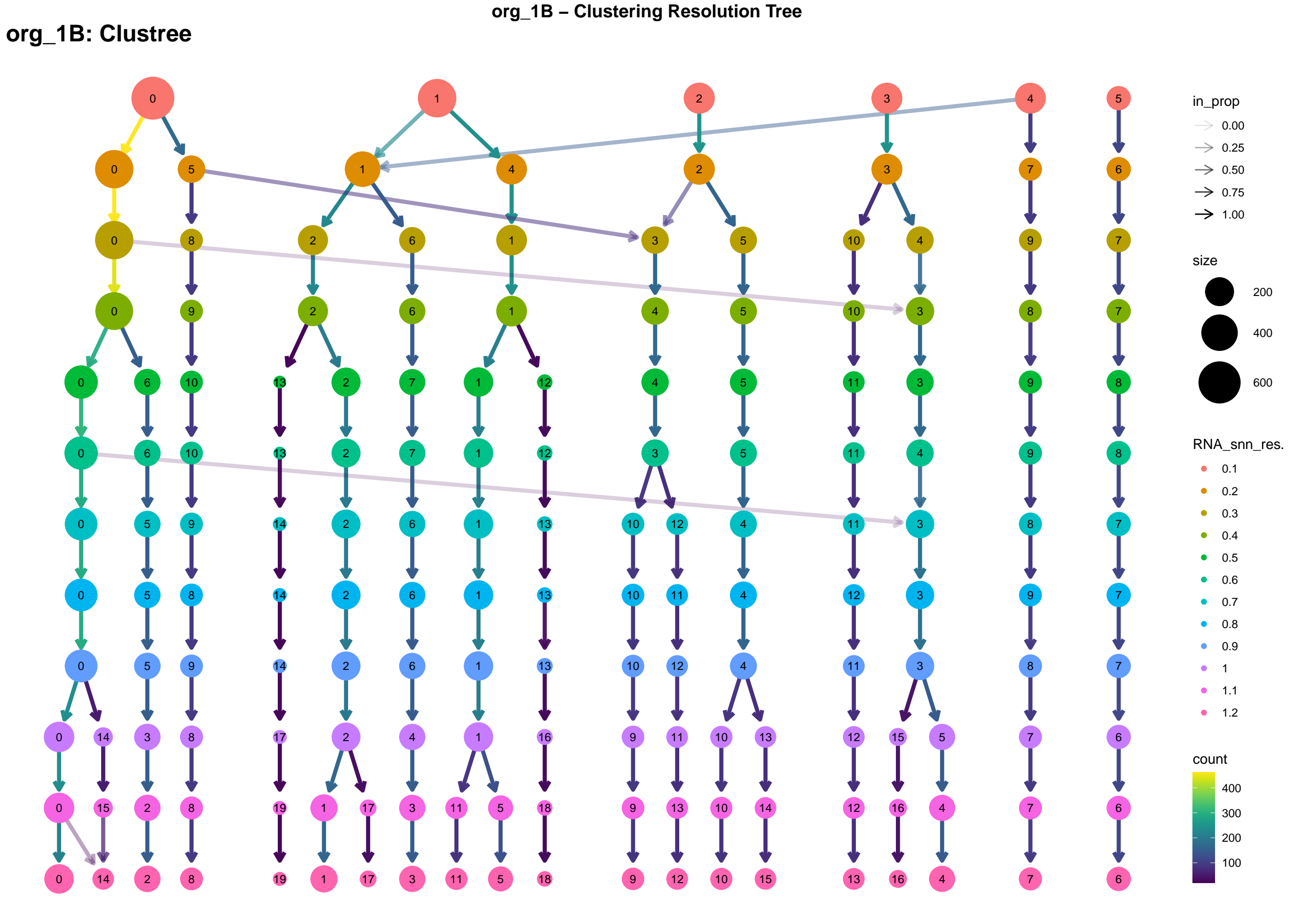


rank > optimal\_pcs\_calculated

a FALSE

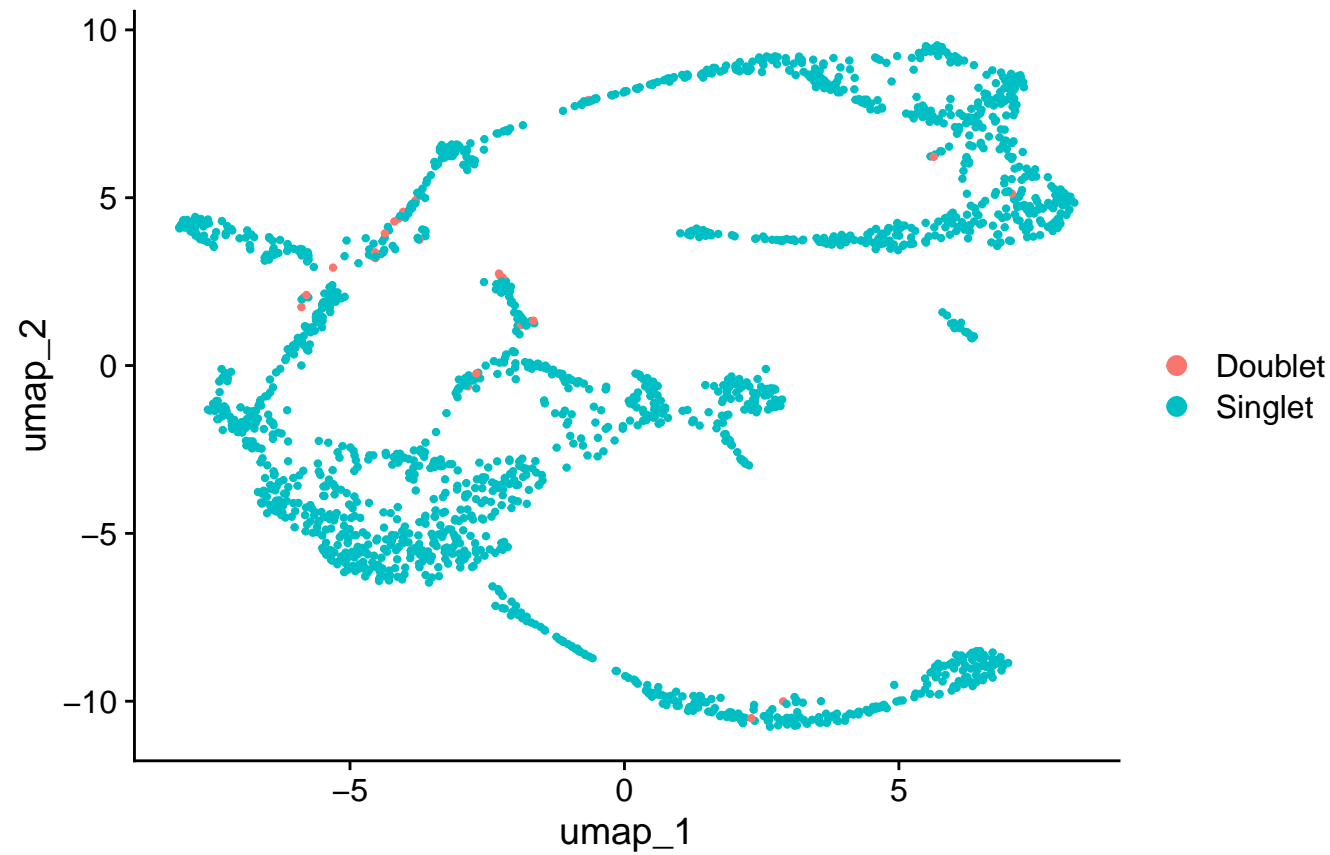
a TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.2	8	0.334133604767285
2	0.3	11	0.318688948210646
3	0.1	6	0.288694479619635
4	0.9	15	0.242037619722552
5	0.6	14	0.22489564080046
6	1	18	0.215307045181525
7	1.1	20	0.188478017106846

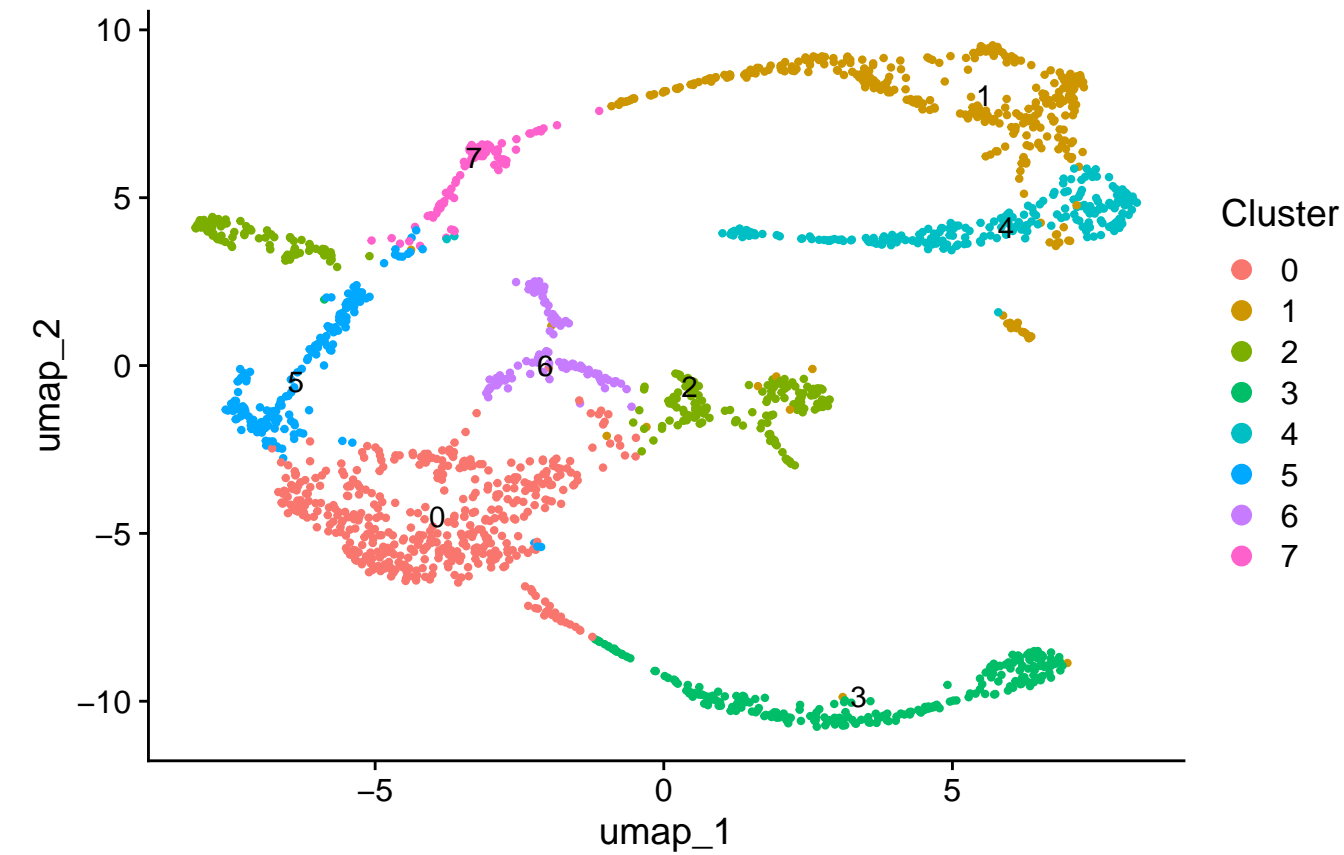


# org\_1B – UMAP & Doublet Removal

org\_1B: Doublets Detected



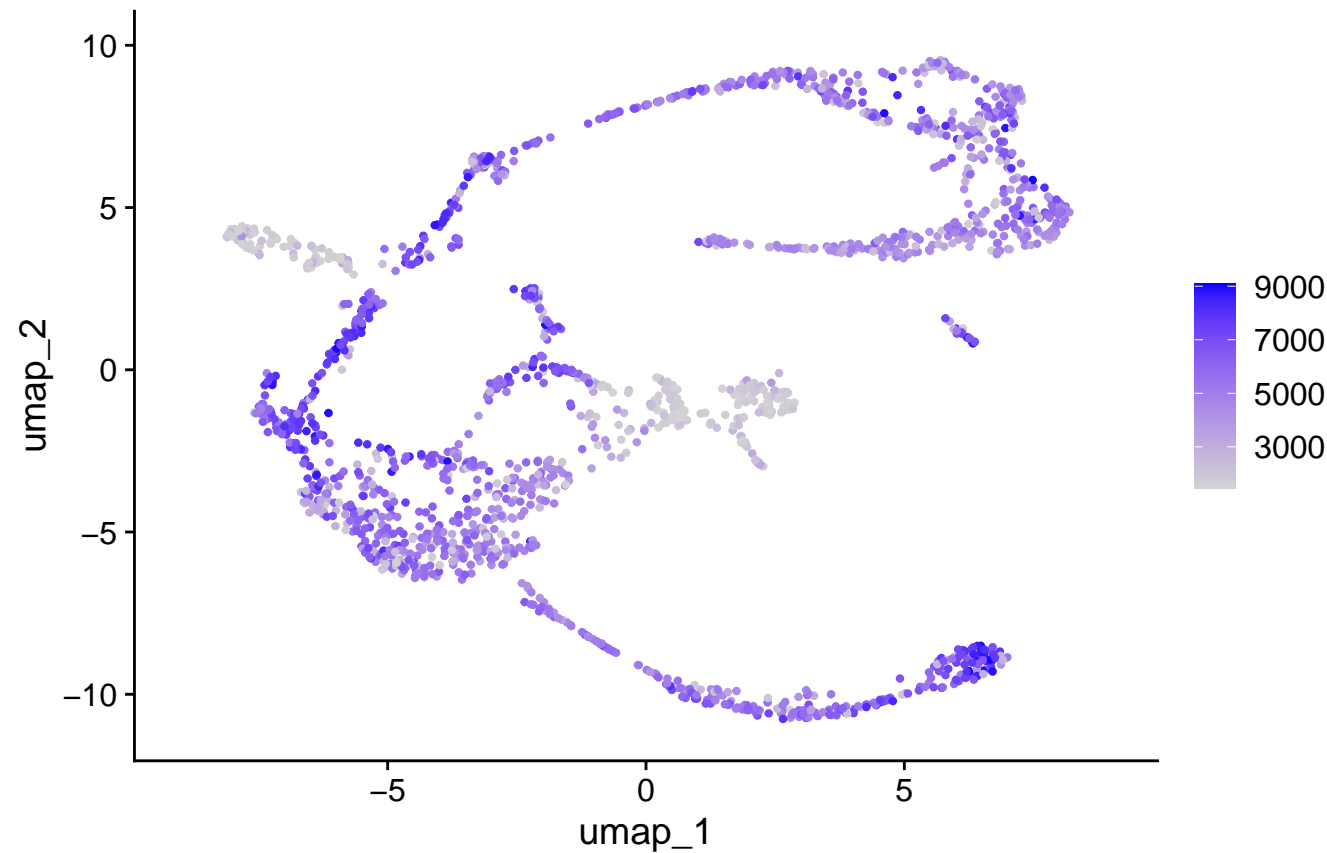
org\_1B: Final UMAP



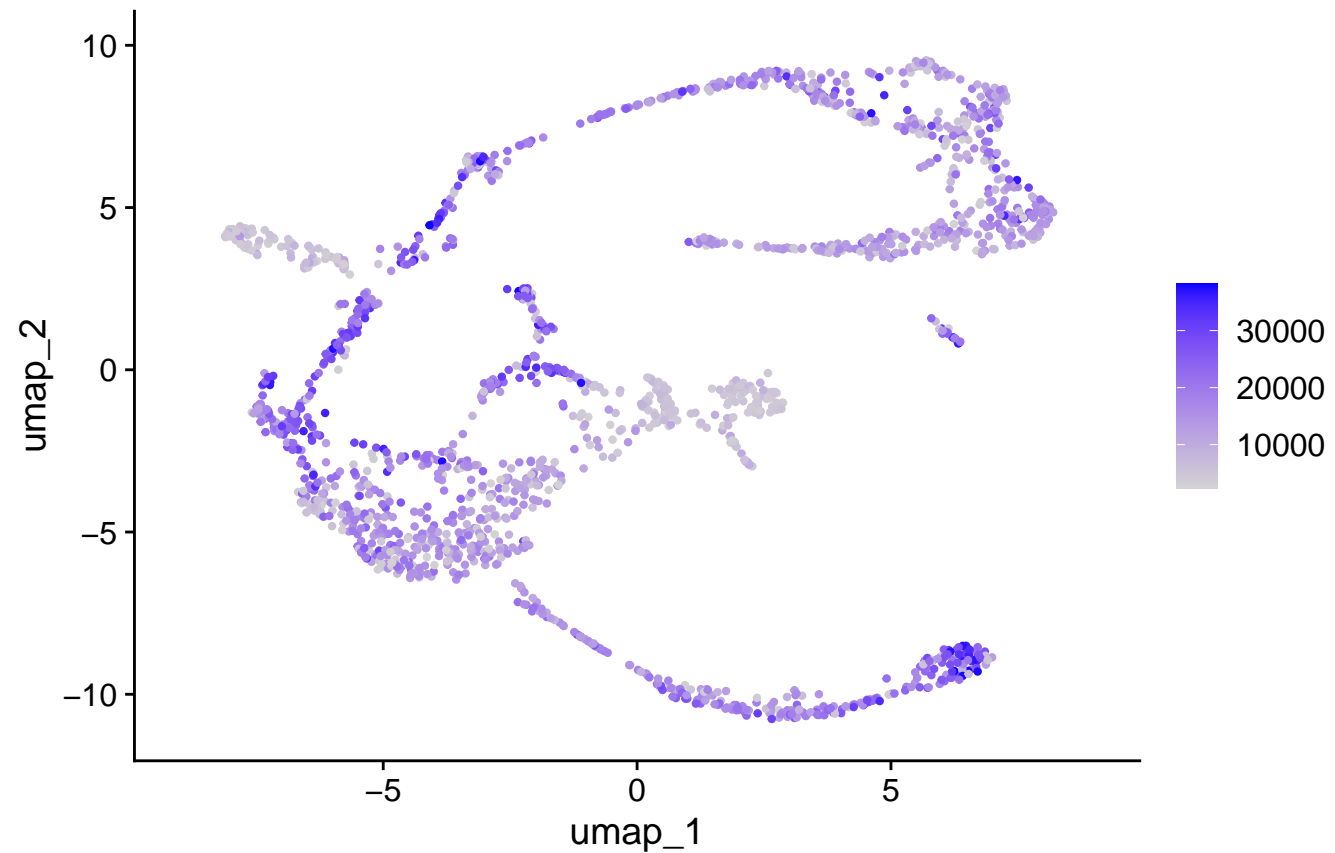
	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	30762.5	7833.5	26
2	Singlet	14559.0	5094.0	1927

# org\_1B – QC Metrics & Cell Cycle on UMAP

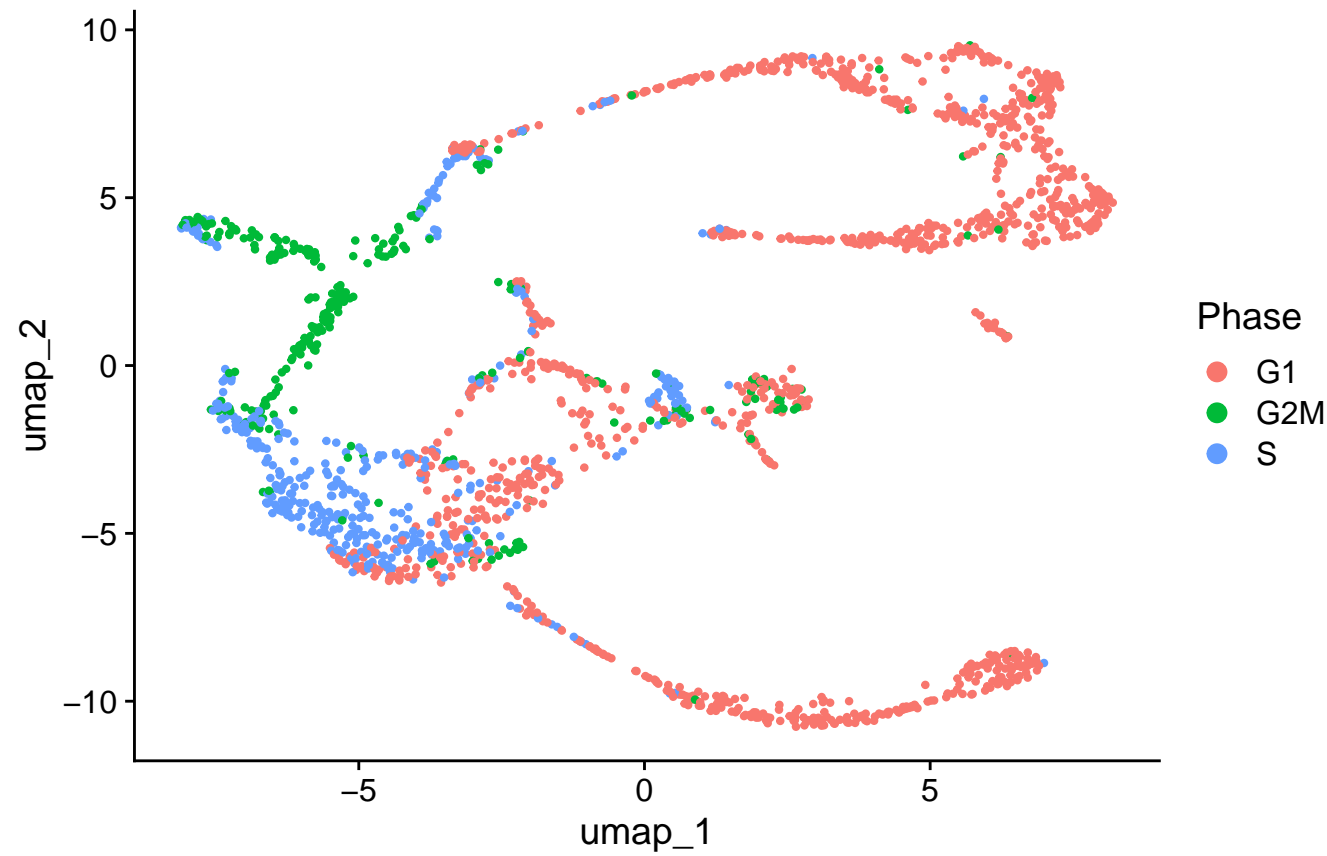
## org\_1B: nFeature\_RNA



## org\_1B: nCount\_RNA



## org\_1B: Cell Cycle Phase



## org\_1B: Final UMAP

