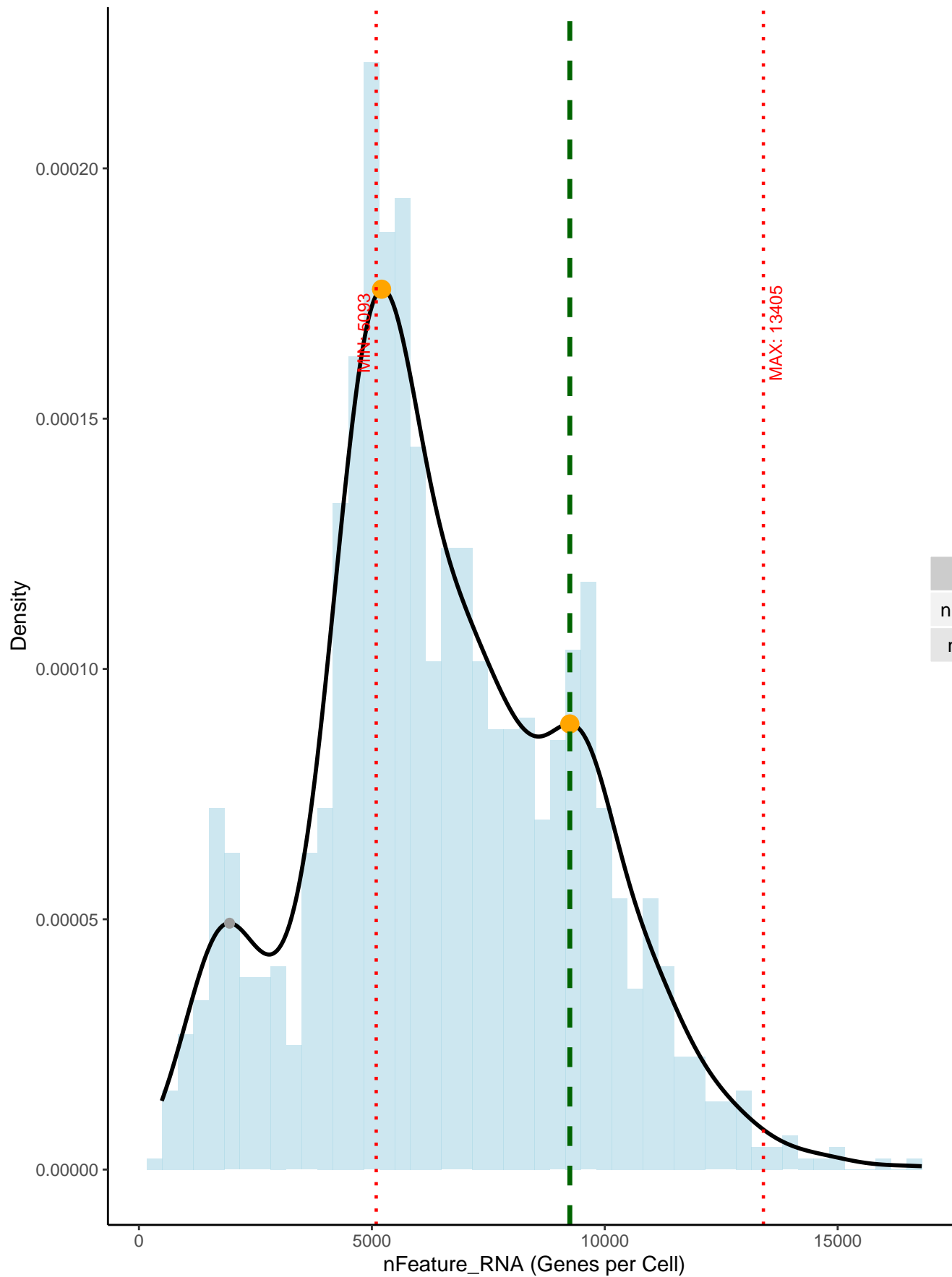


org_6B – Adaptive Threshold Determination

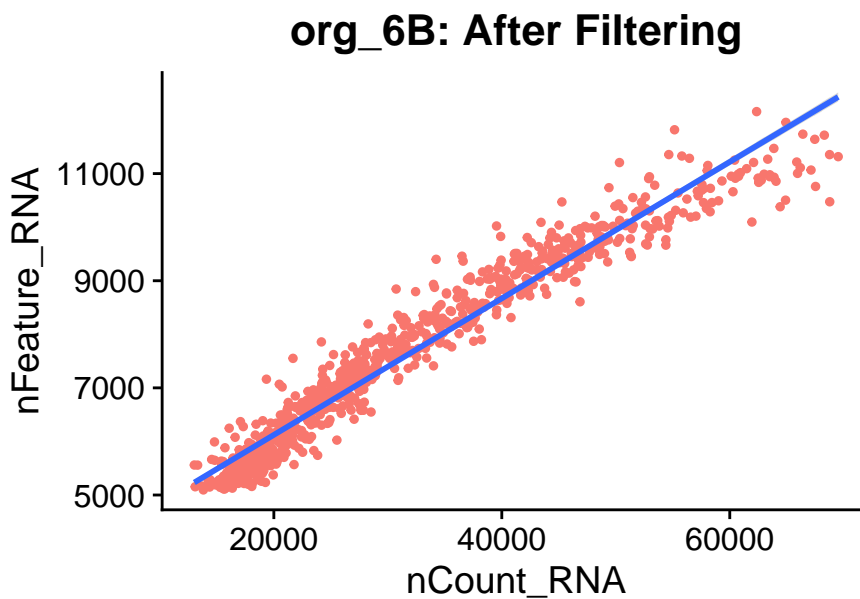
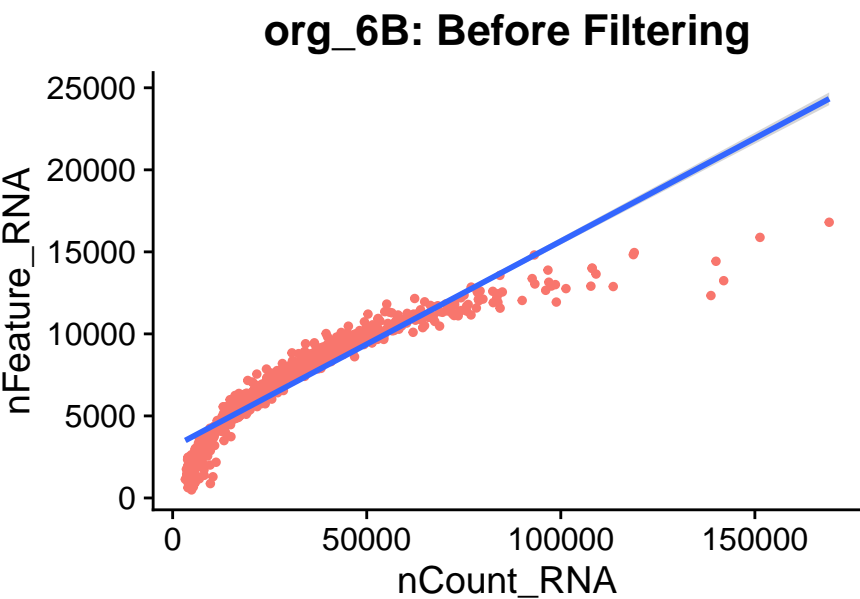
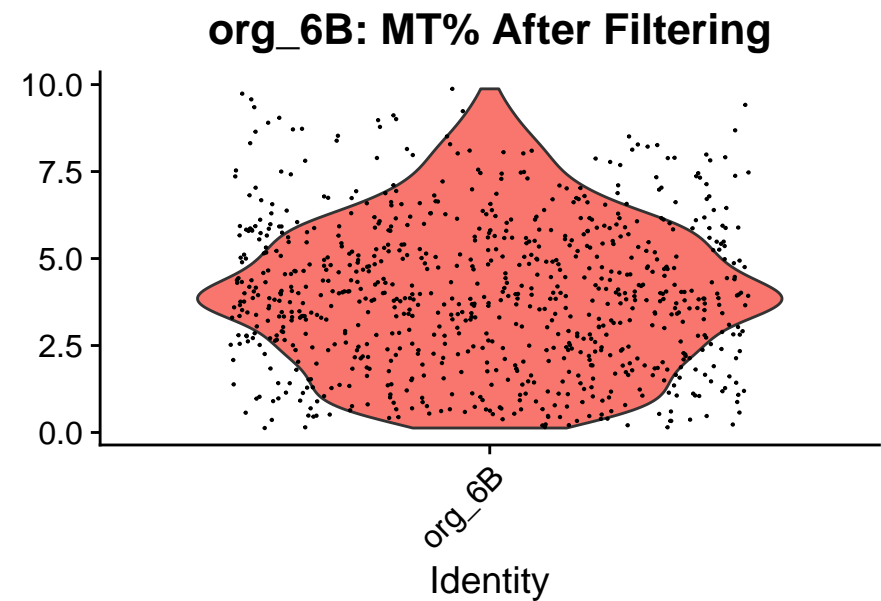
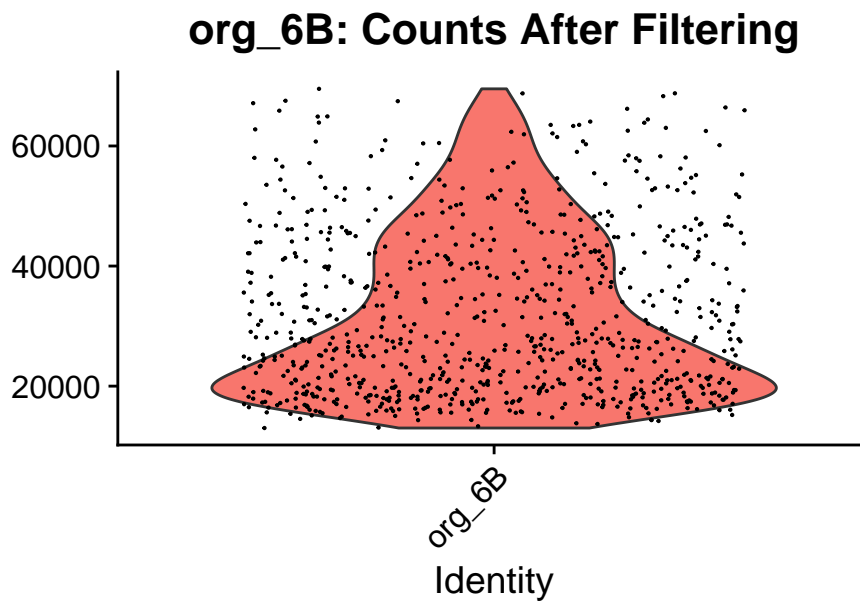
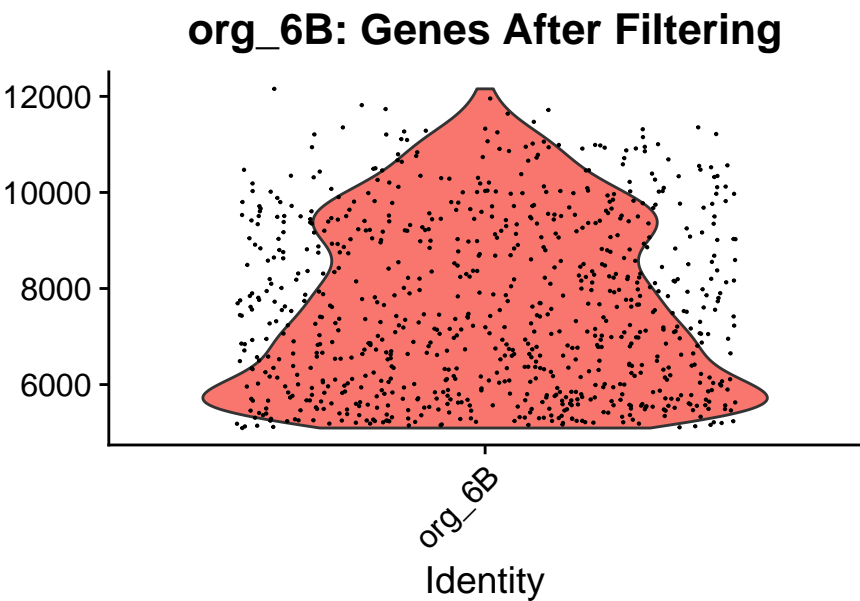
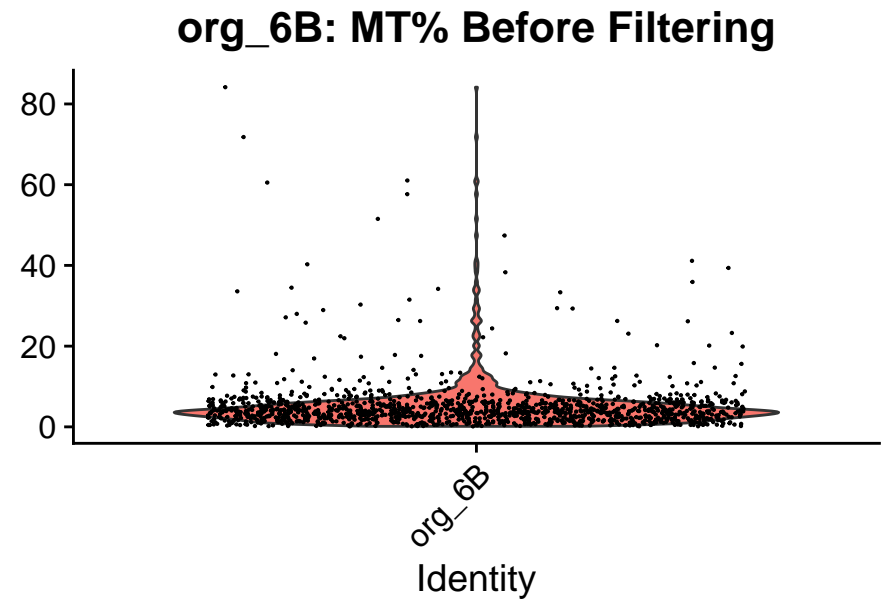
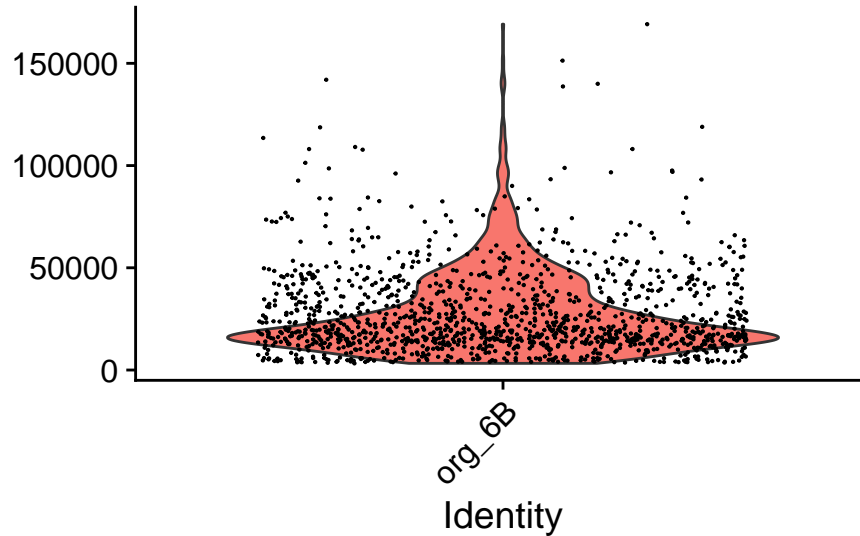
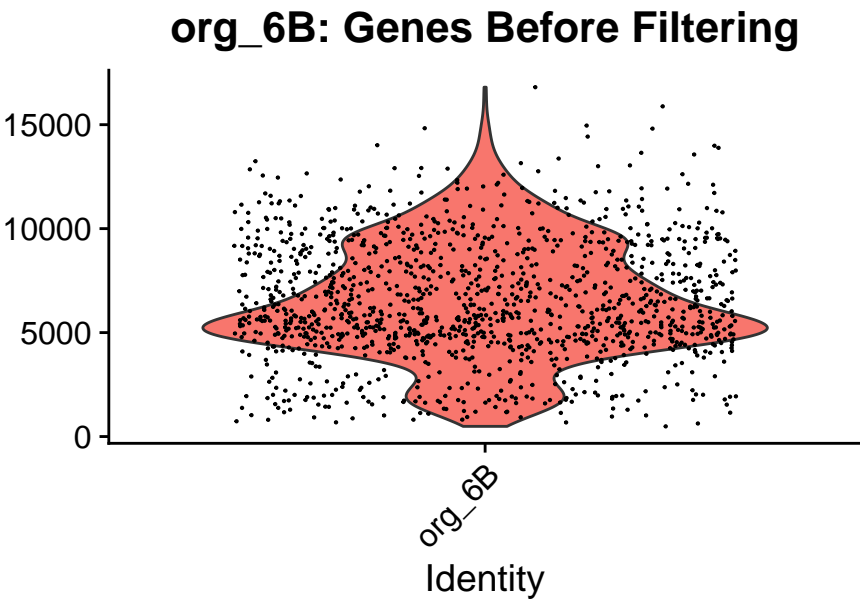
org_6B: nFeature_RNA (Genes per Cell) Distribution

Method: peak | Selected peak: 9249.2 | Total peaks: 3 | Top 2 peaks used



Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Thresh
nFeature_RNA	peak	9249	3	5208, 9249	2771	5093	13405
nCount_RNA	custom	NA	NA	NA	NA	500	70000

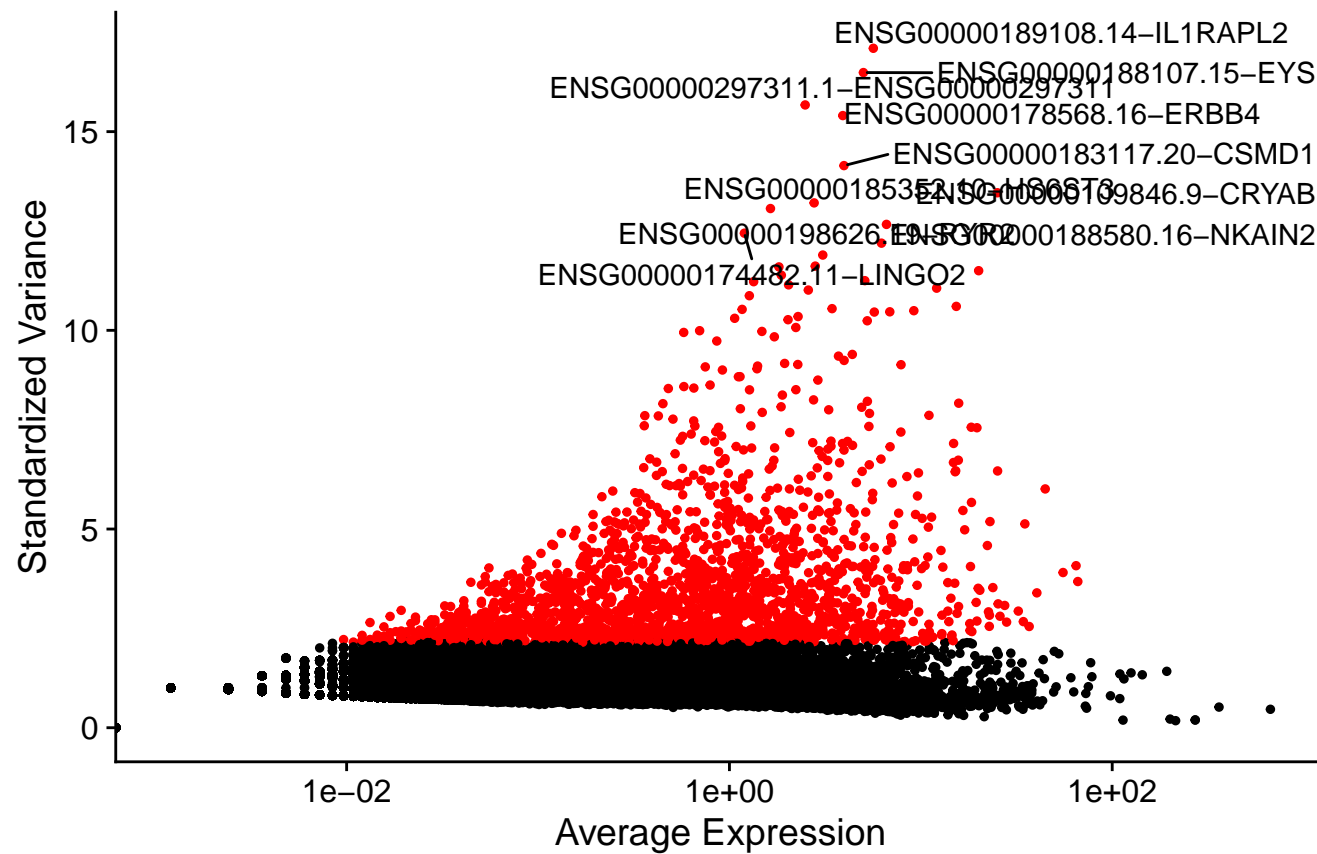
org_6B – Filtering Summary
org_6B: Counts Before Filtering



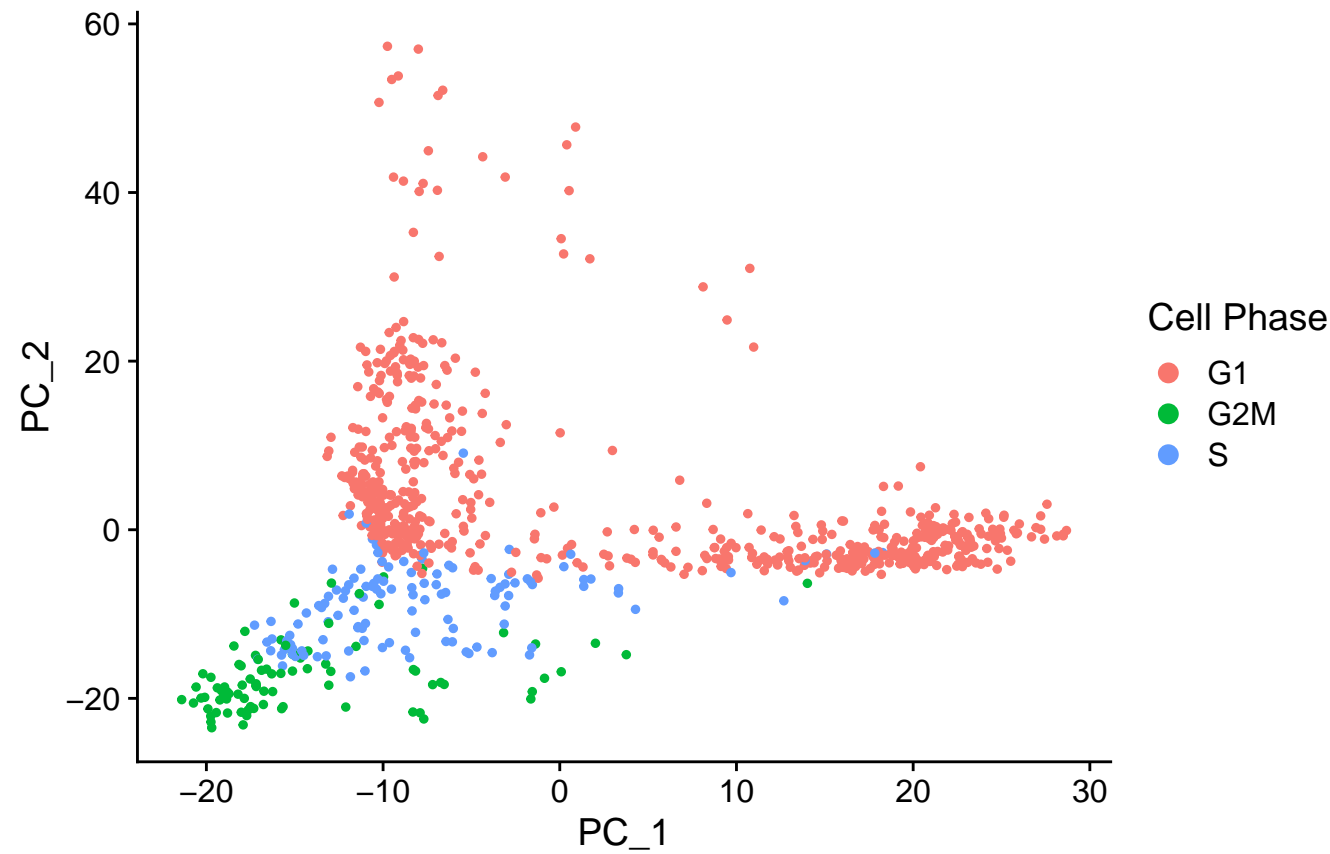
	Metric	Before	After
1	Cells	1331.000000	830.000000
2	Genes	42303.000000	42303.000000
3	Median nCount	20622.000000	27654.000000
4	Median nFeature	6085.000000	7320.000000
5	Median MT%	3.840036	3.861832

org_6B – Variable Features & Cell Cycle

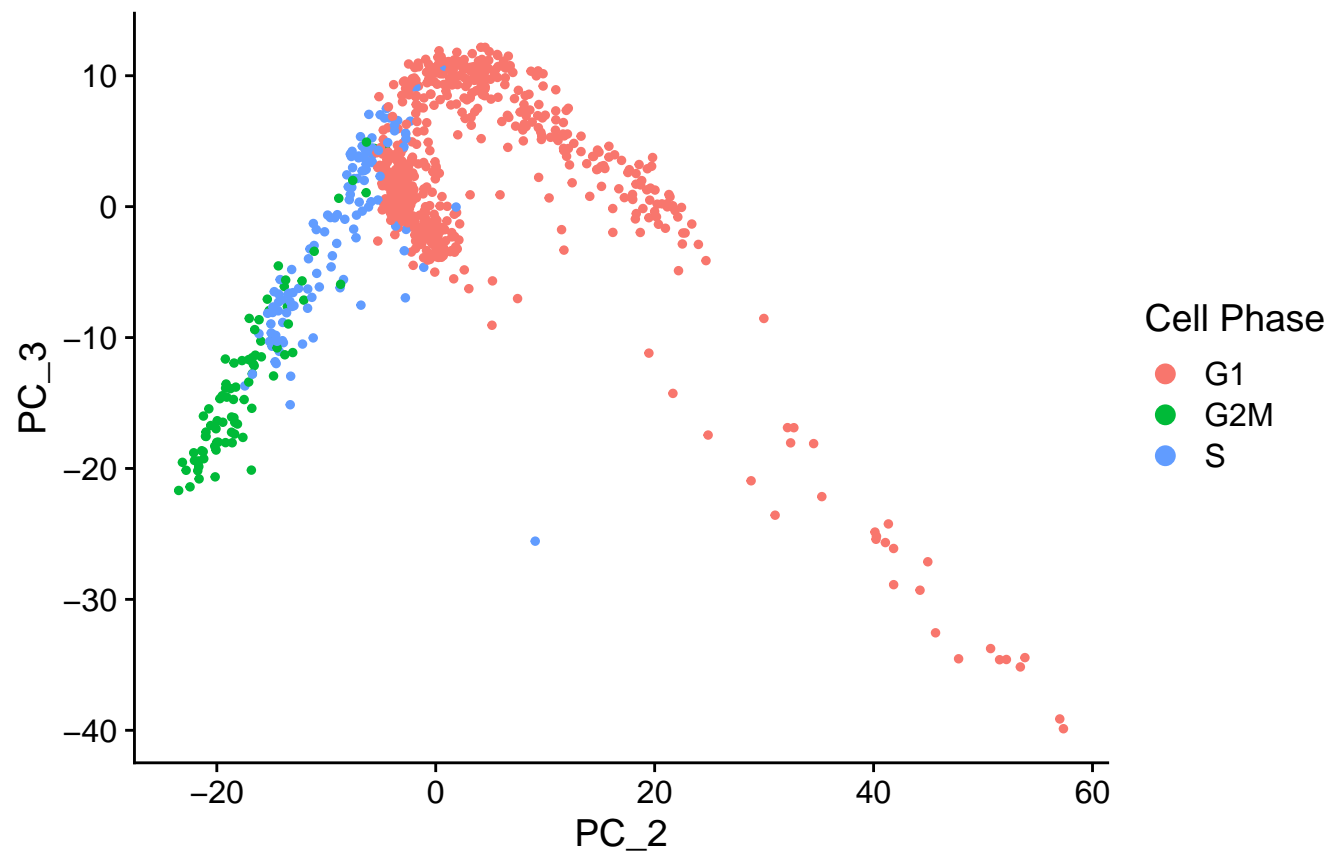
org_6B: Top 2000 Variable Genes



org_6B: Cell Cycle on PC1 & PC2



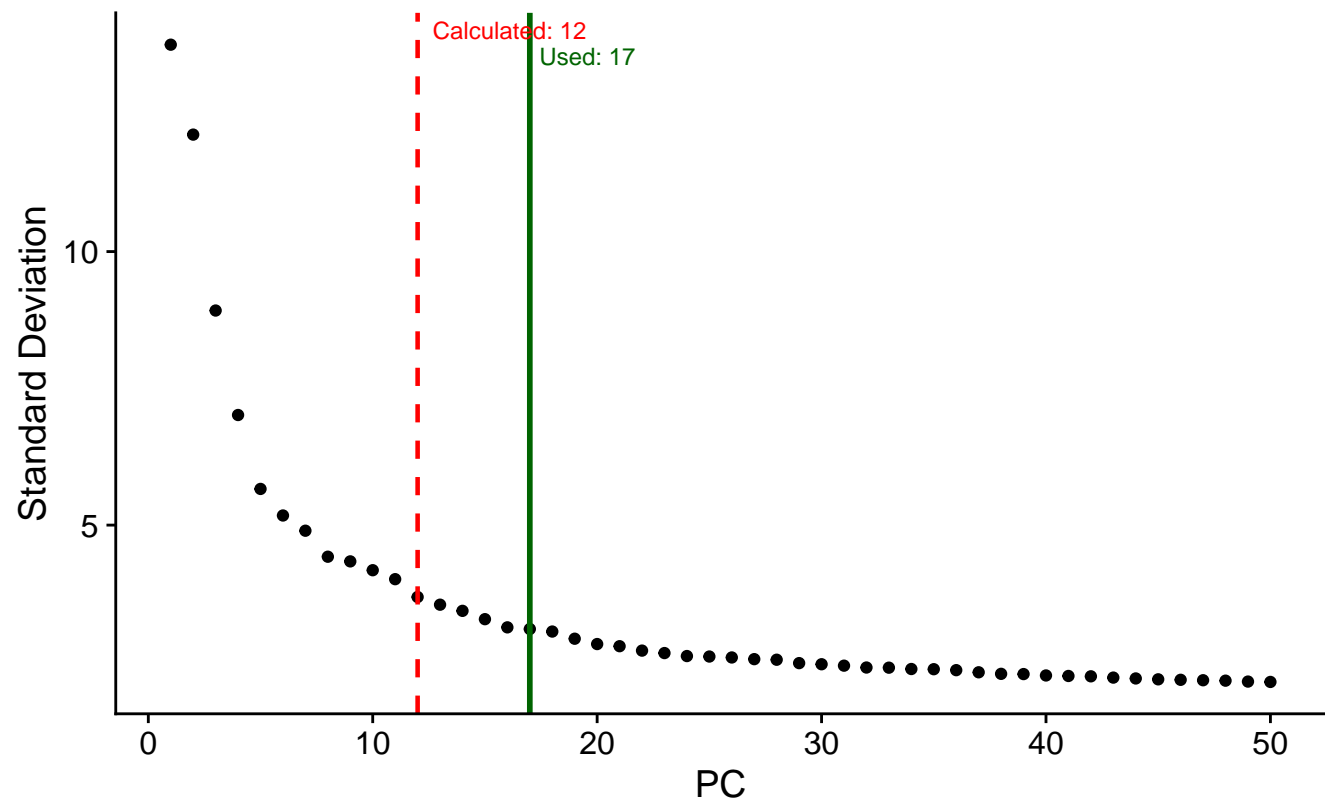
org_6B: Cell Cycle on PC2 & PC3



org_6B – PCA Selection & Silhouette Analysis

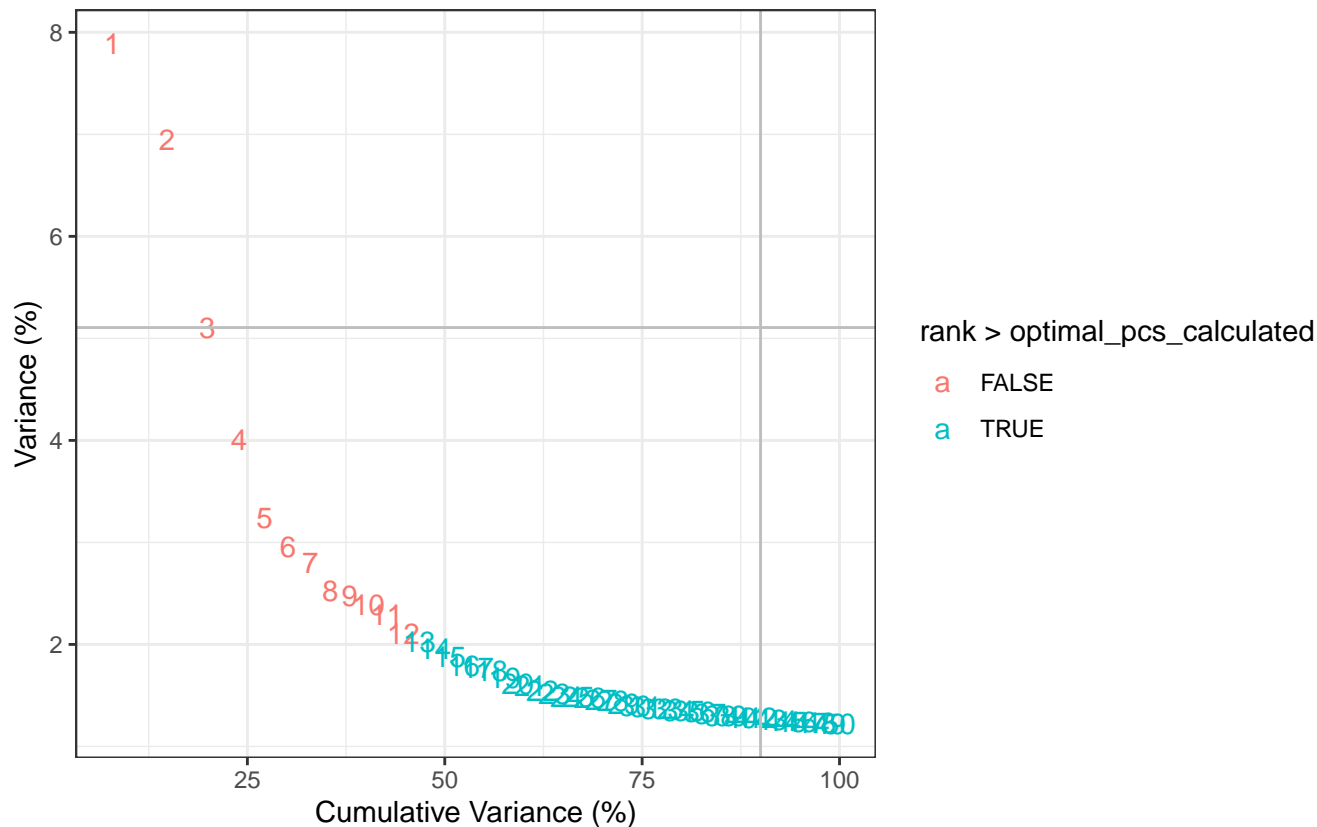
org_6B: Elbow Plot

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



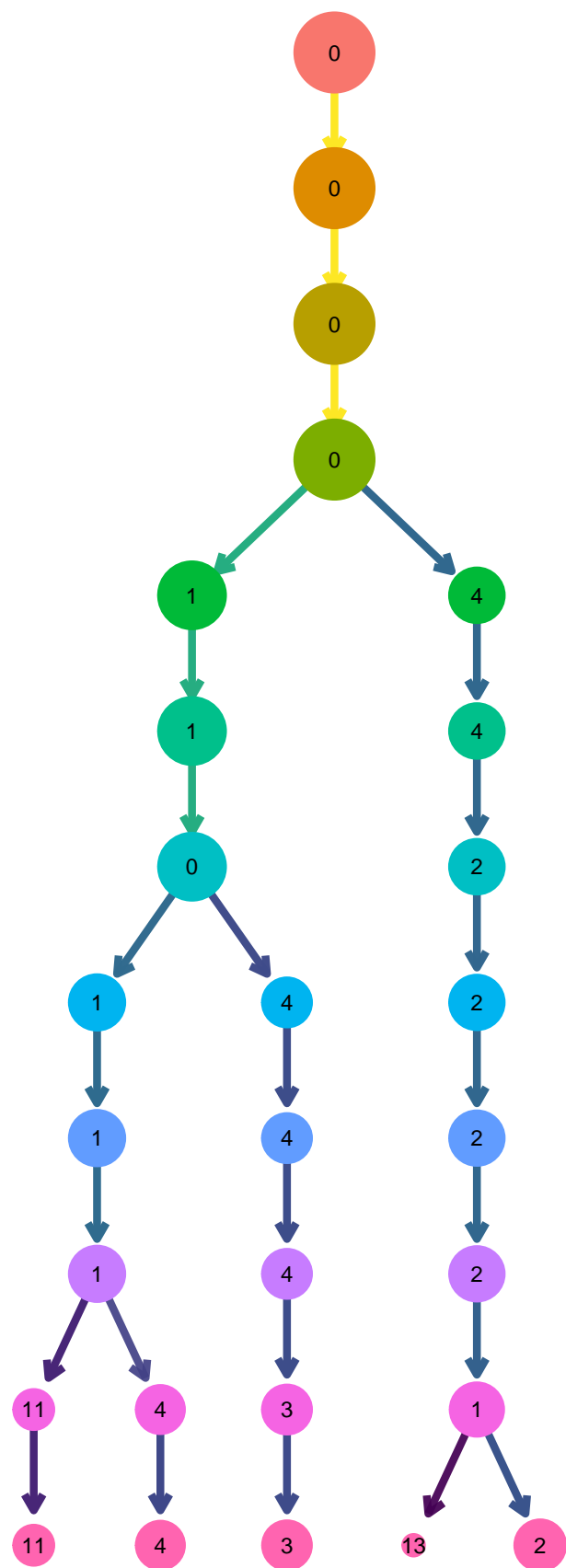
org_6B: Quantitative PC Selection

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

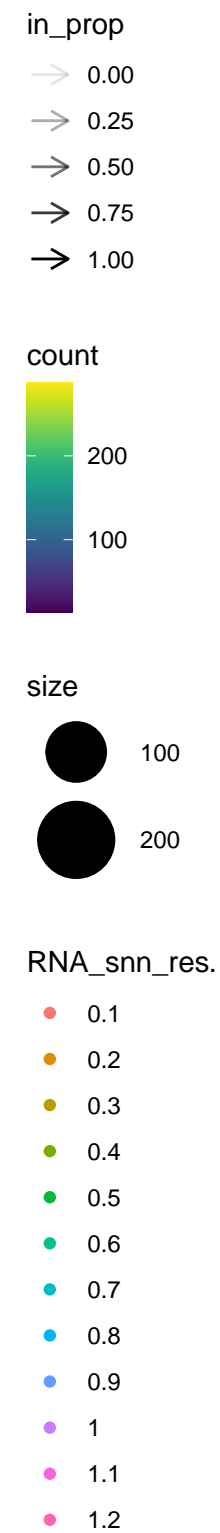
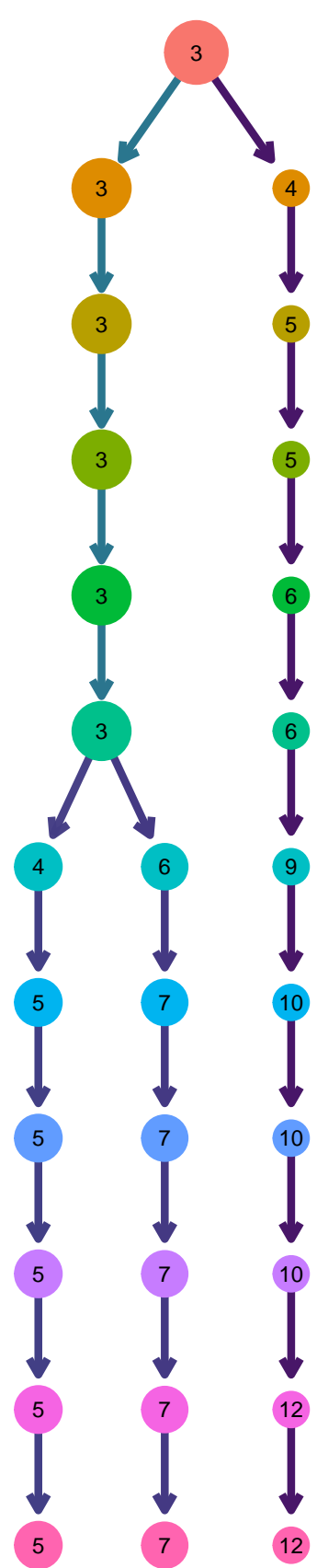
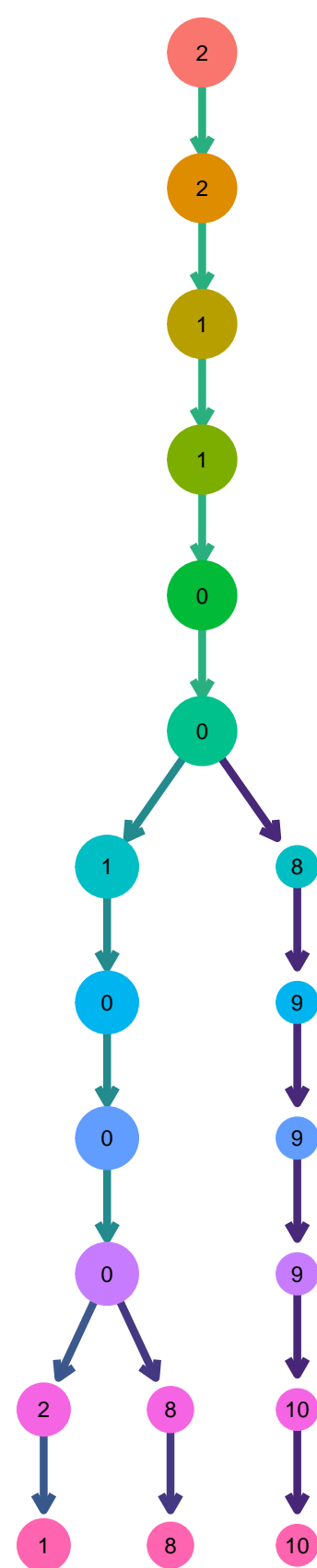
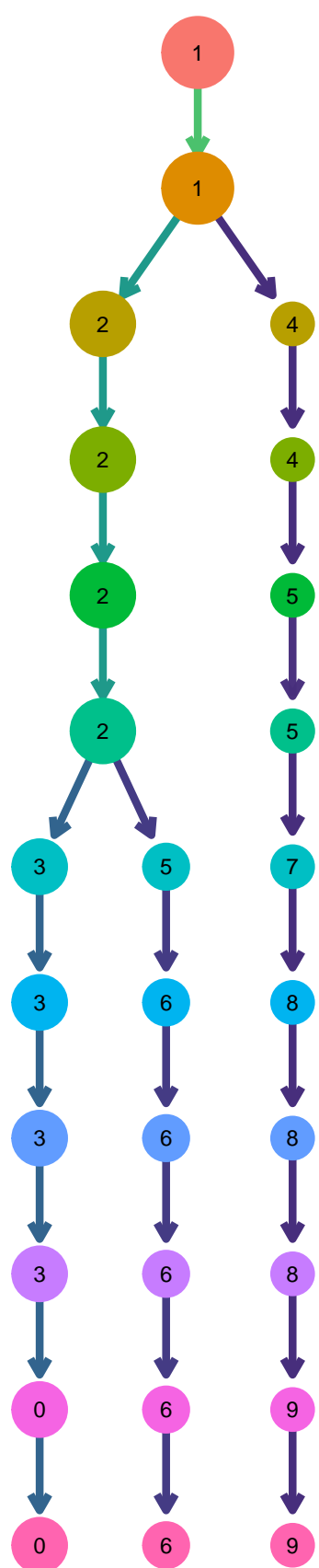


	res_vals	num_clusters	avg_sil_vals
1	0.2	5	0.365112703569581
2	0.3	6	0.343077246428305
3	0.6	7	0.32679351238759
4	0.1	4	0.326373845167903
5	0.7	10	0.298304459522128
6	0.8	11	0.28801665490873
7	1.2	14	0.255695826507696
8	1.1	13	0.254679429839651

org_6B: Clustree

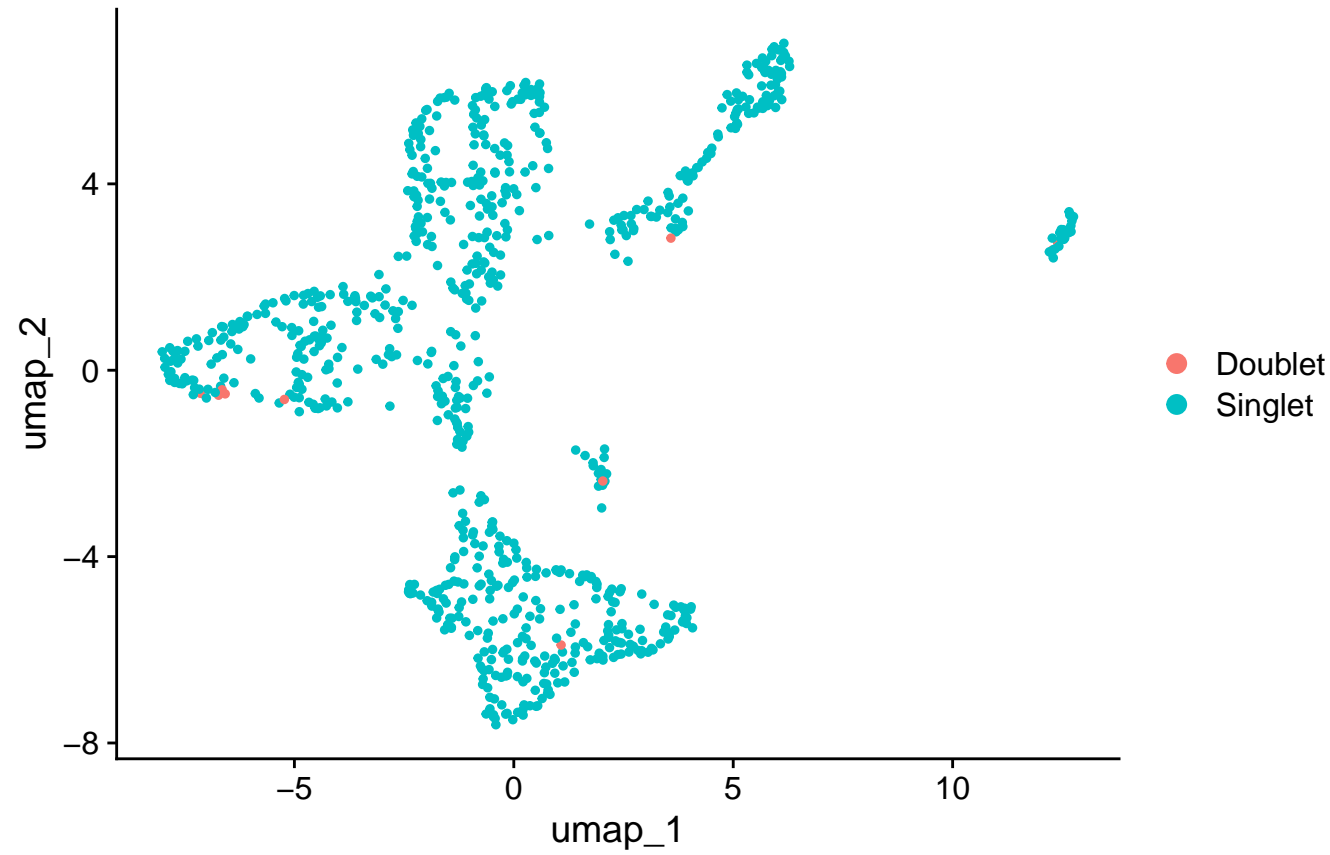


org_6B – Clustering Resolution Tree

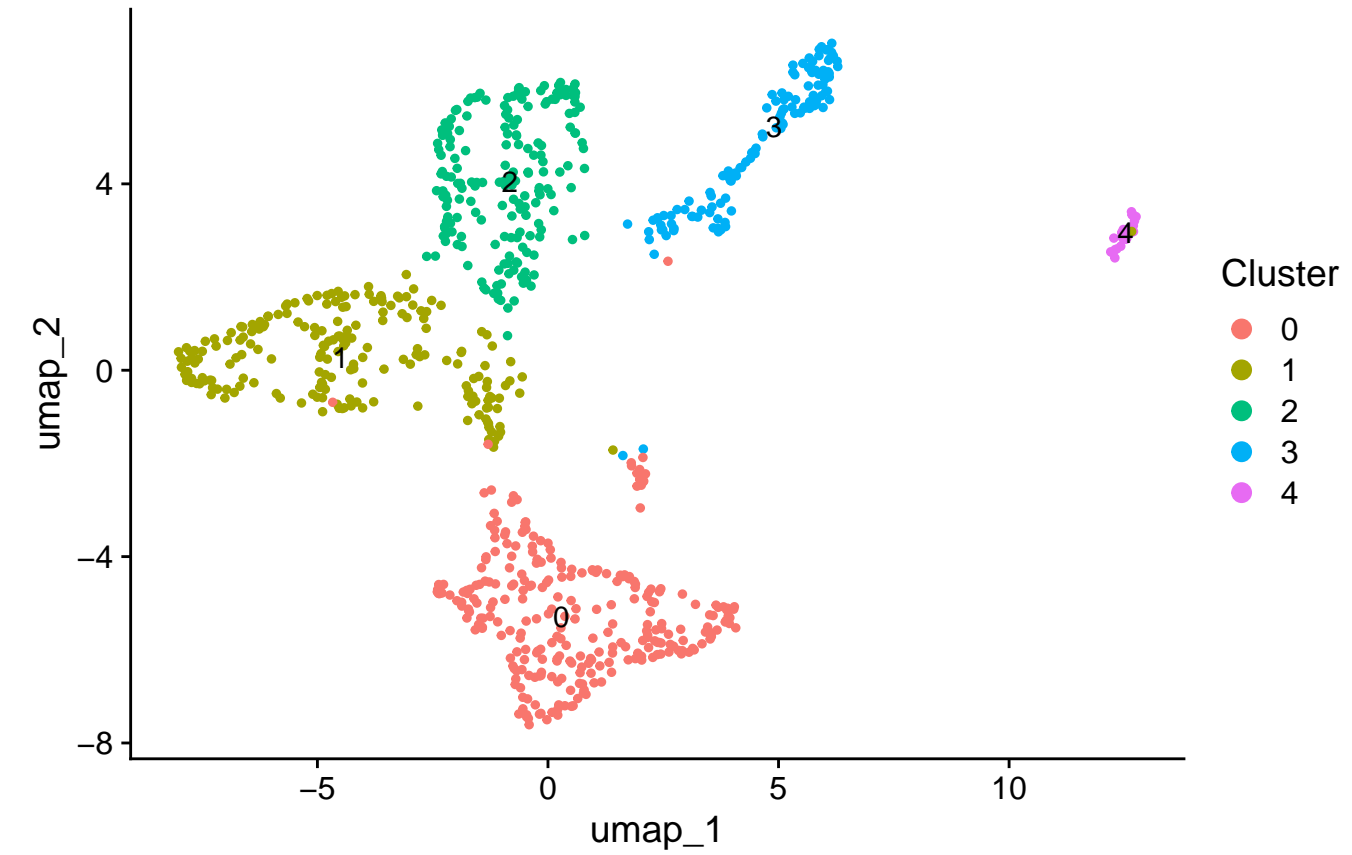


org_6B – UMAP & Doublet Removal

org_6B: Doublets Detected



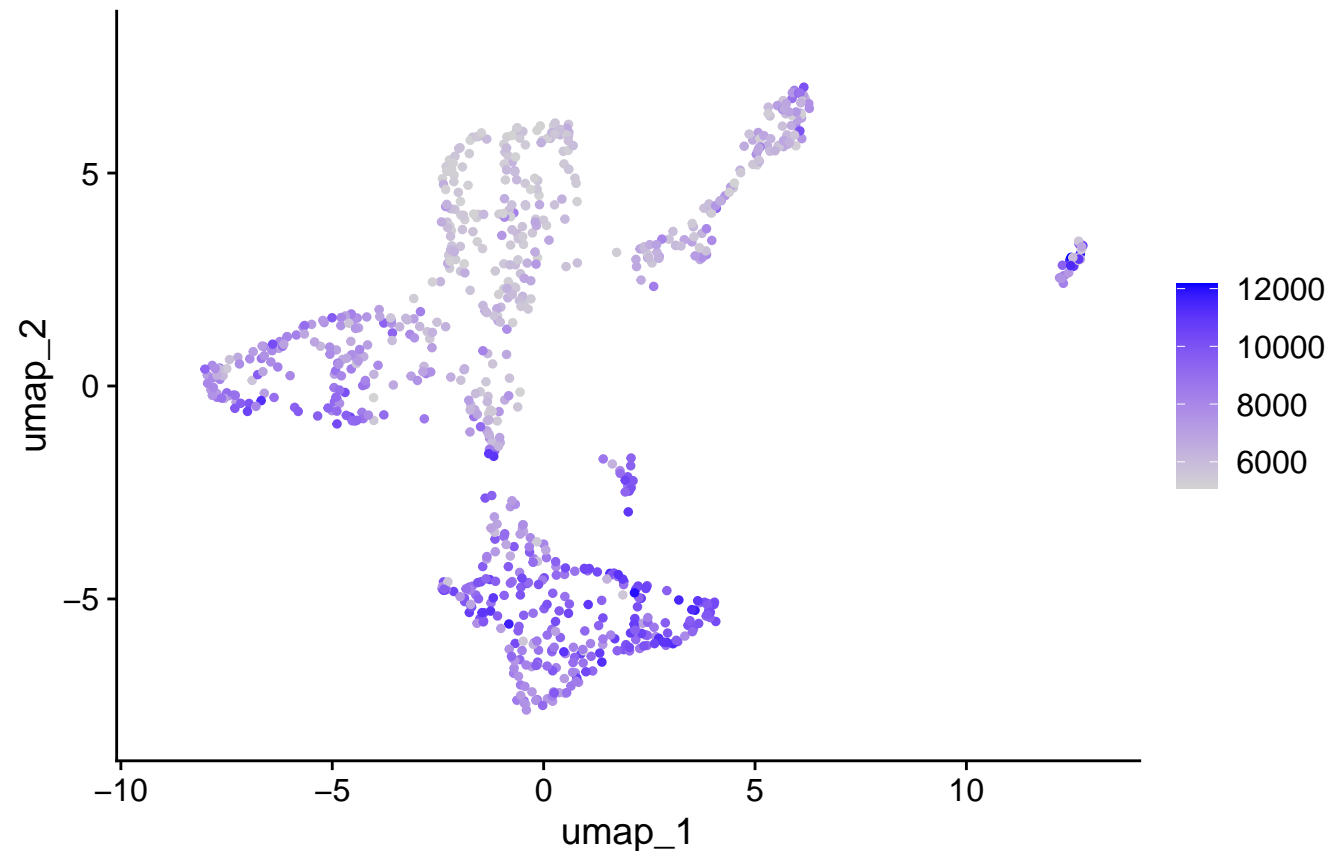
org_6B: Final UMAP



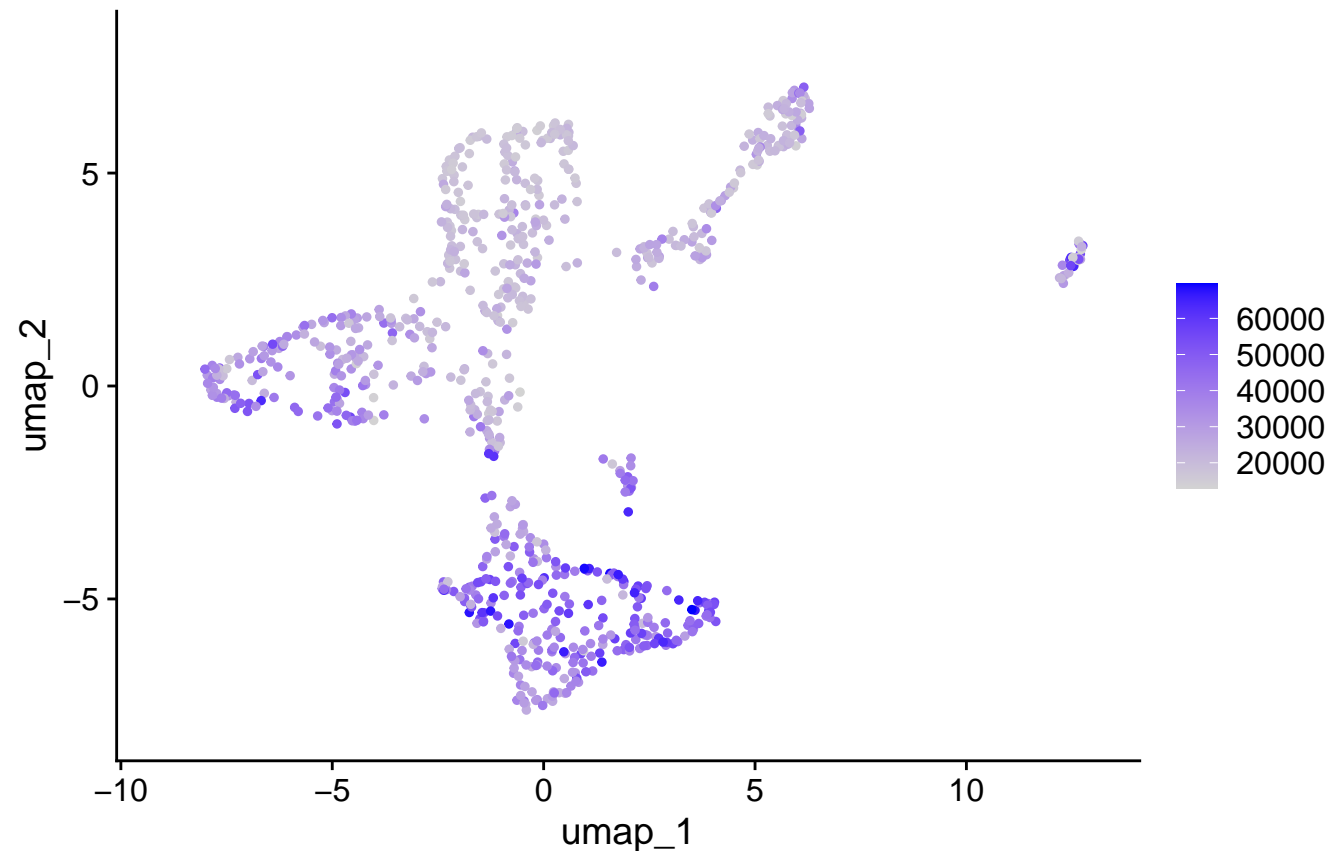
	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	54010	10667	10
2	Singlet	27490	7277	820

org_6B – QC Metrics & Cell Cycle on UMAP

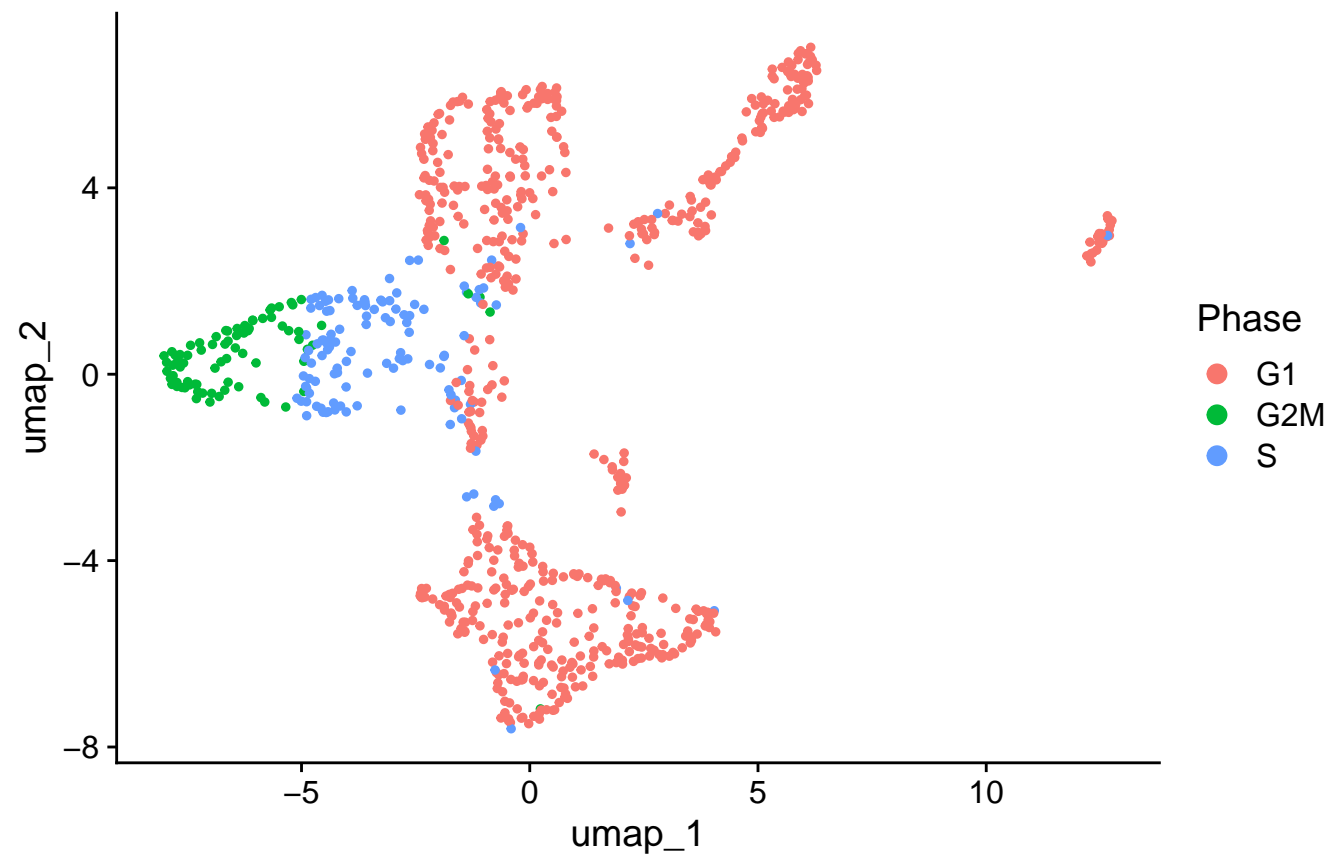
org_6B: nFeature_RNA



org_6B: nCount_RNA



org_6B: Cell Cycle Phase



org_6B: Final UMAP

