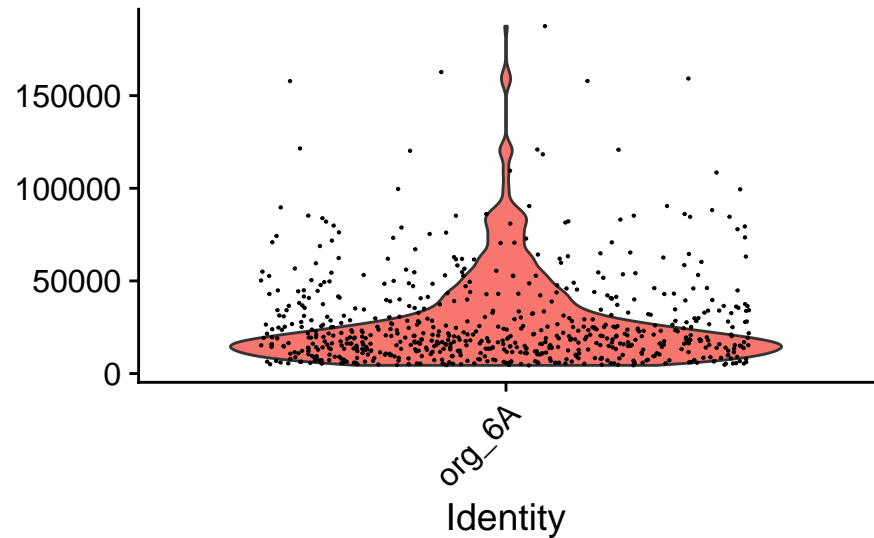
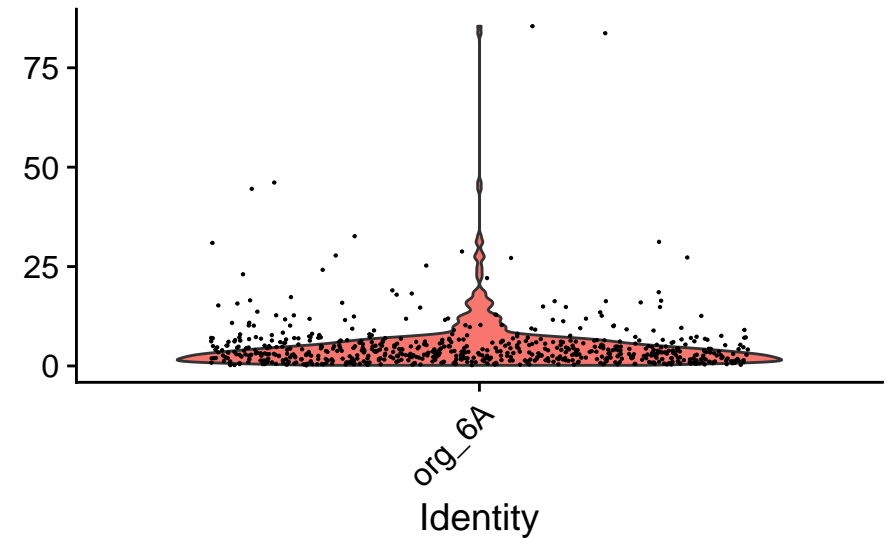


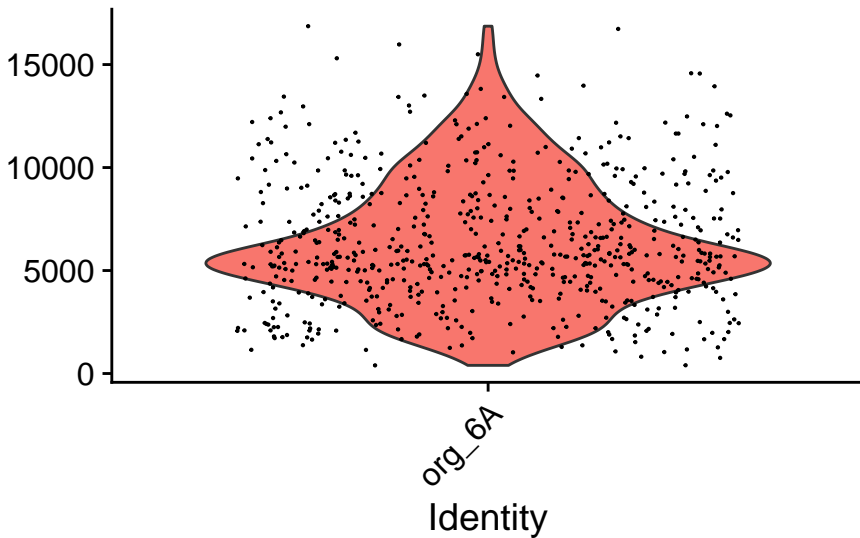
org_6A – Filtering Summary
org_6A: Counts Before Filtering



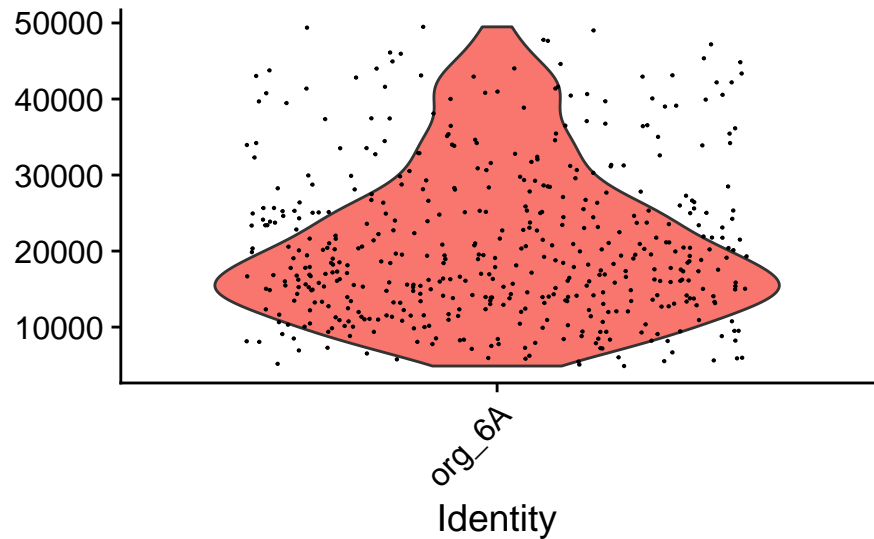
org_6A: MT% Before Filtering



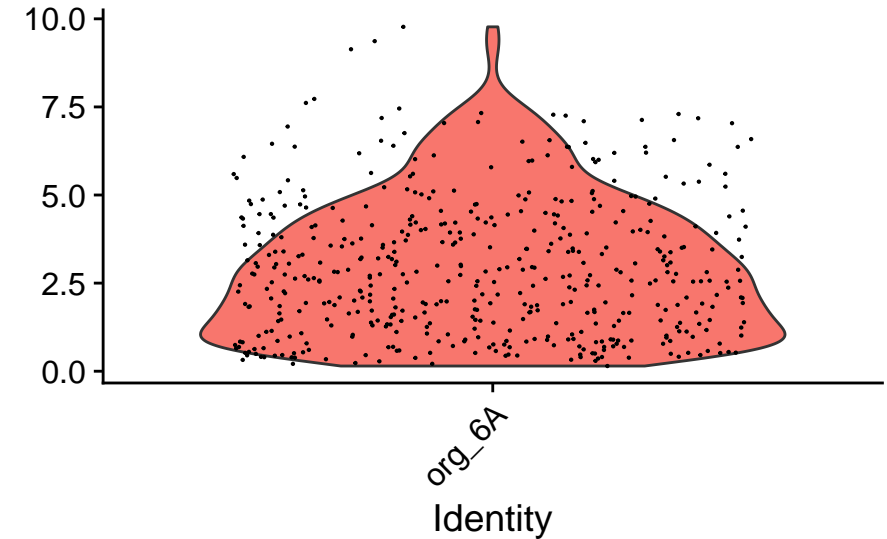
org_6A: Genes Before Filtering



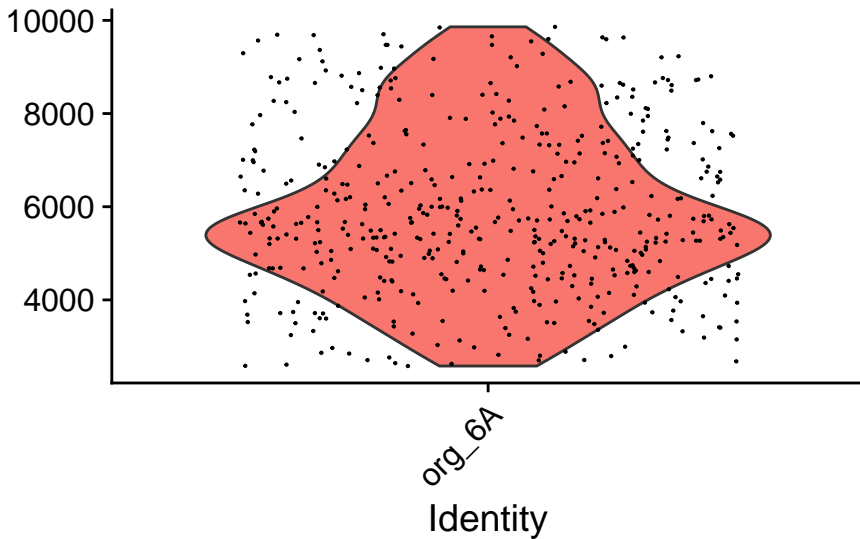
org_6A: Counts After Filtering



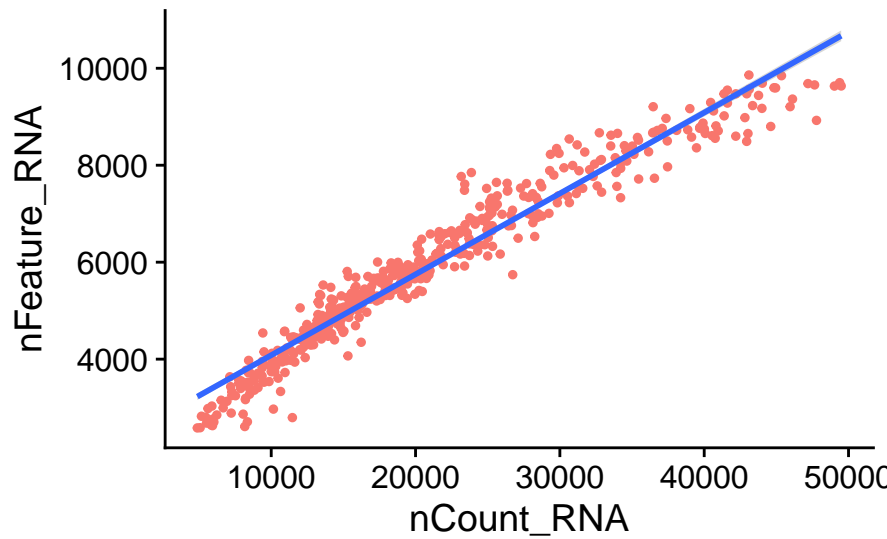
org_6A: MT% After Filtering



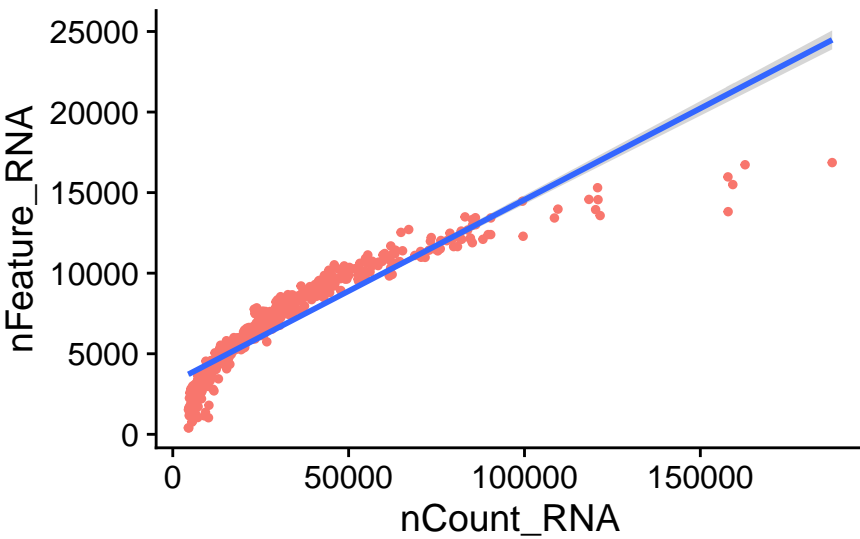
org_6A: Genes After Filtering



org_6A: After Filtering



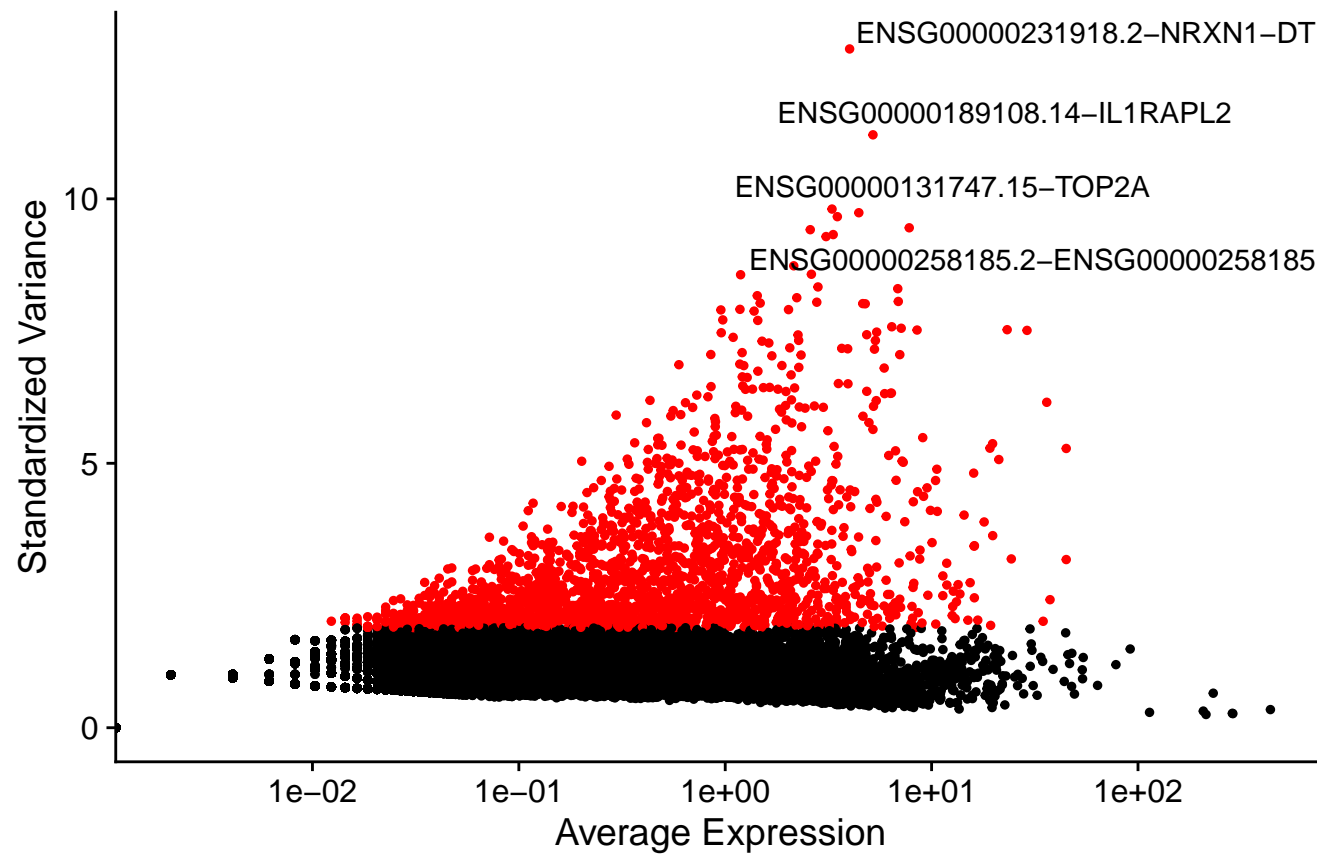
org_6A: Before Filtering



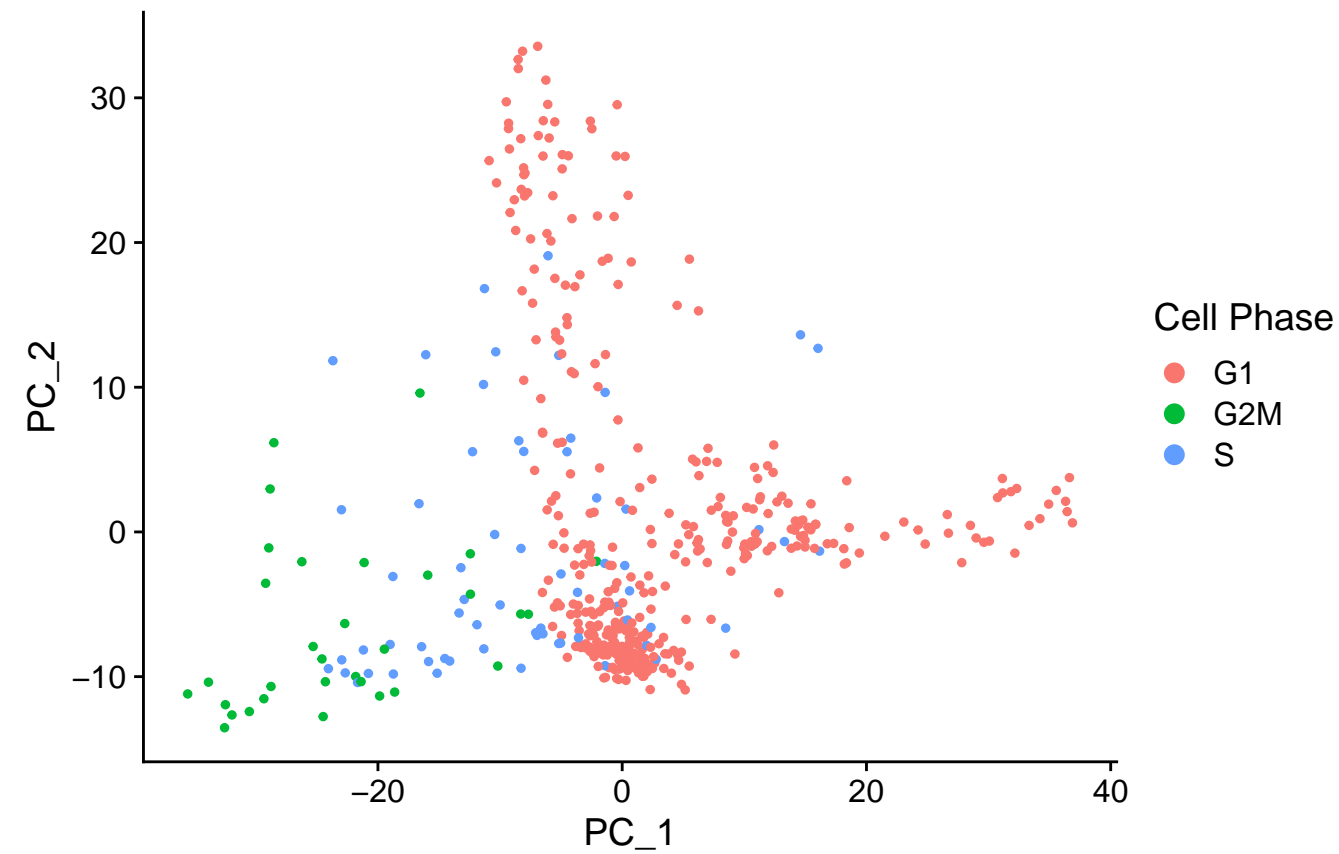
	Metric	Before	After
1	Cells	668.000000	486.000000
2	Genes	37861.000000	37861.000000
3	Median nCount	19413.000000	18807.500000
4	Median nFeature	5740.000000	5663.000000
5	Median MT%	3.262026	2.648337

org_6A – Variable Features & Cell Cycle

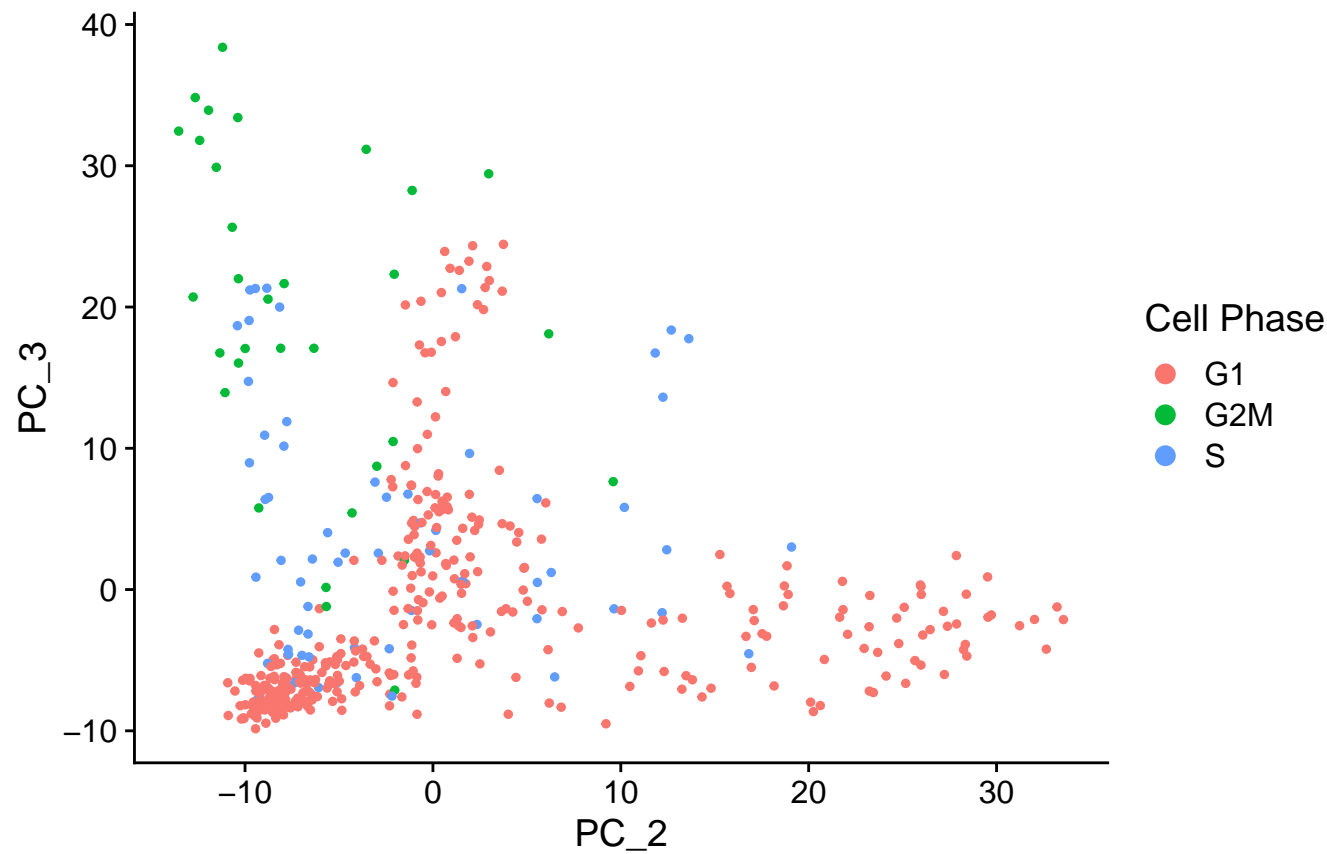
org_6A: Top 2000 Variable Genes



org_6A: Cell Cycle on PC1 & PC2



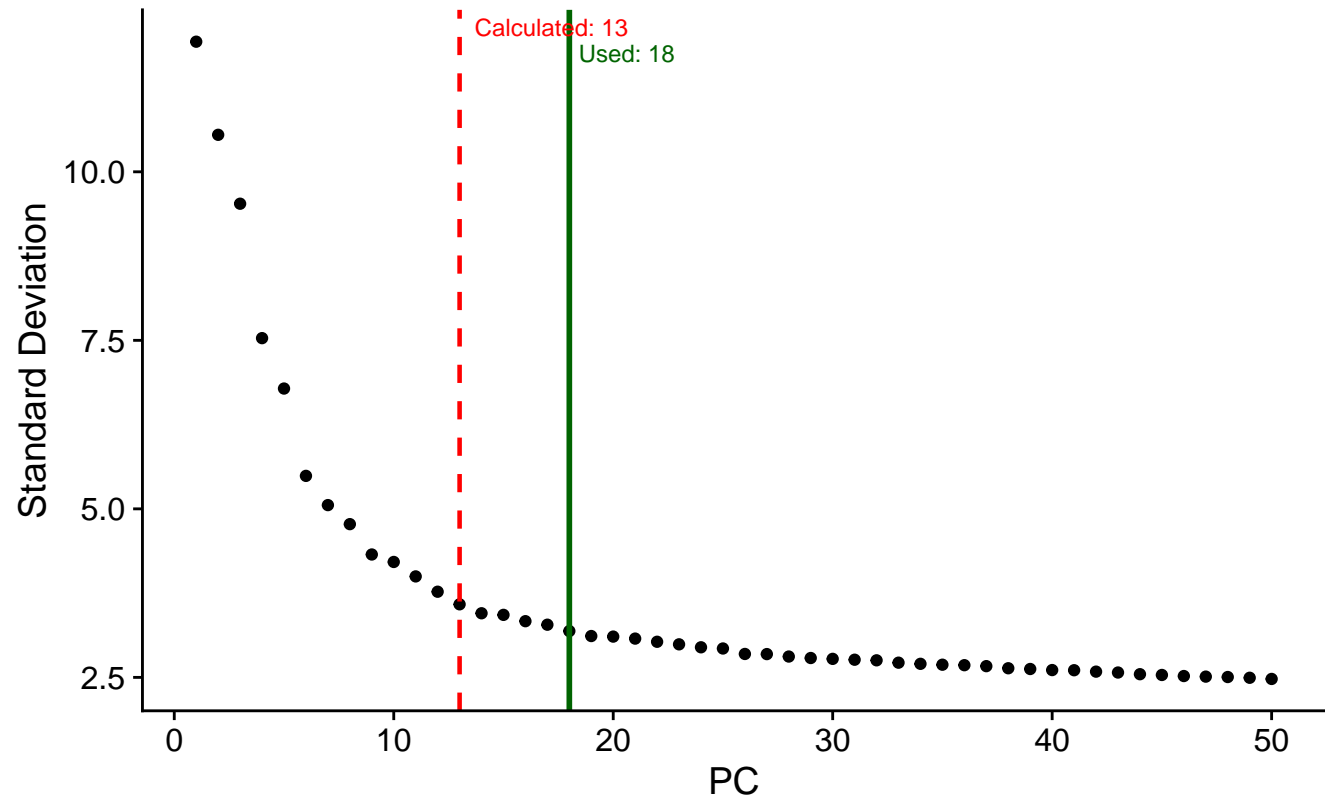
org_6A: Cell Cycle on PC2 & PC3



org_6A – PCA Selection & Silhouette Analysis

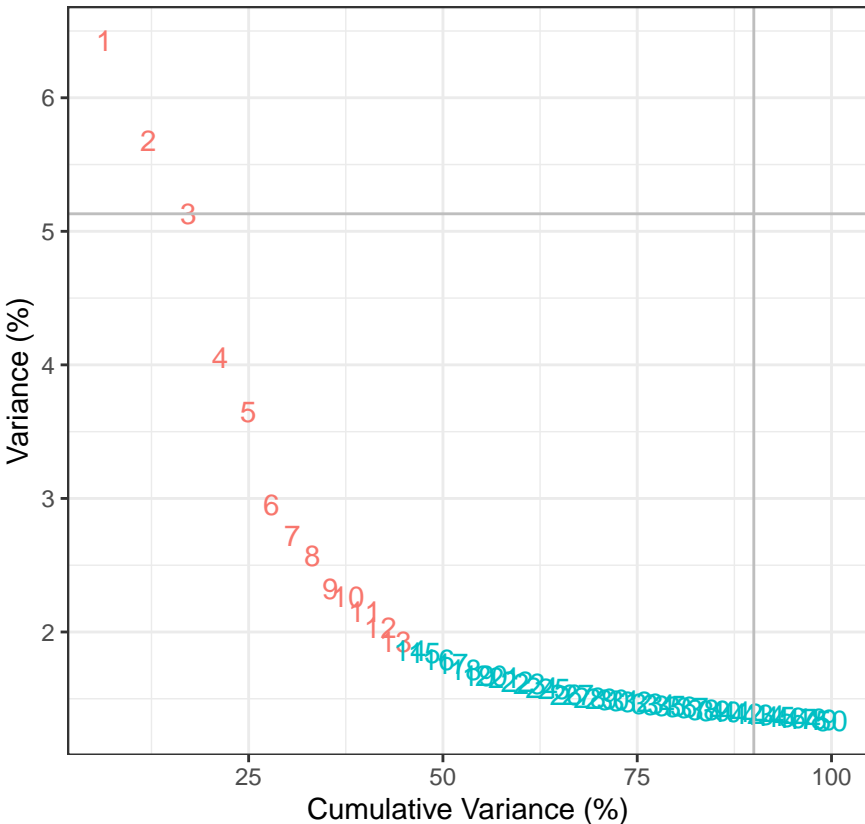
org_6A: Elbow Plot

Calculated: 13 PCs | Used: 18 PCs (+5)



org_6A: Quantitative PC Selection

Calculated: 13 PCs | Used: 18 PCs (+5)



rank > optimal_pcs_calculated

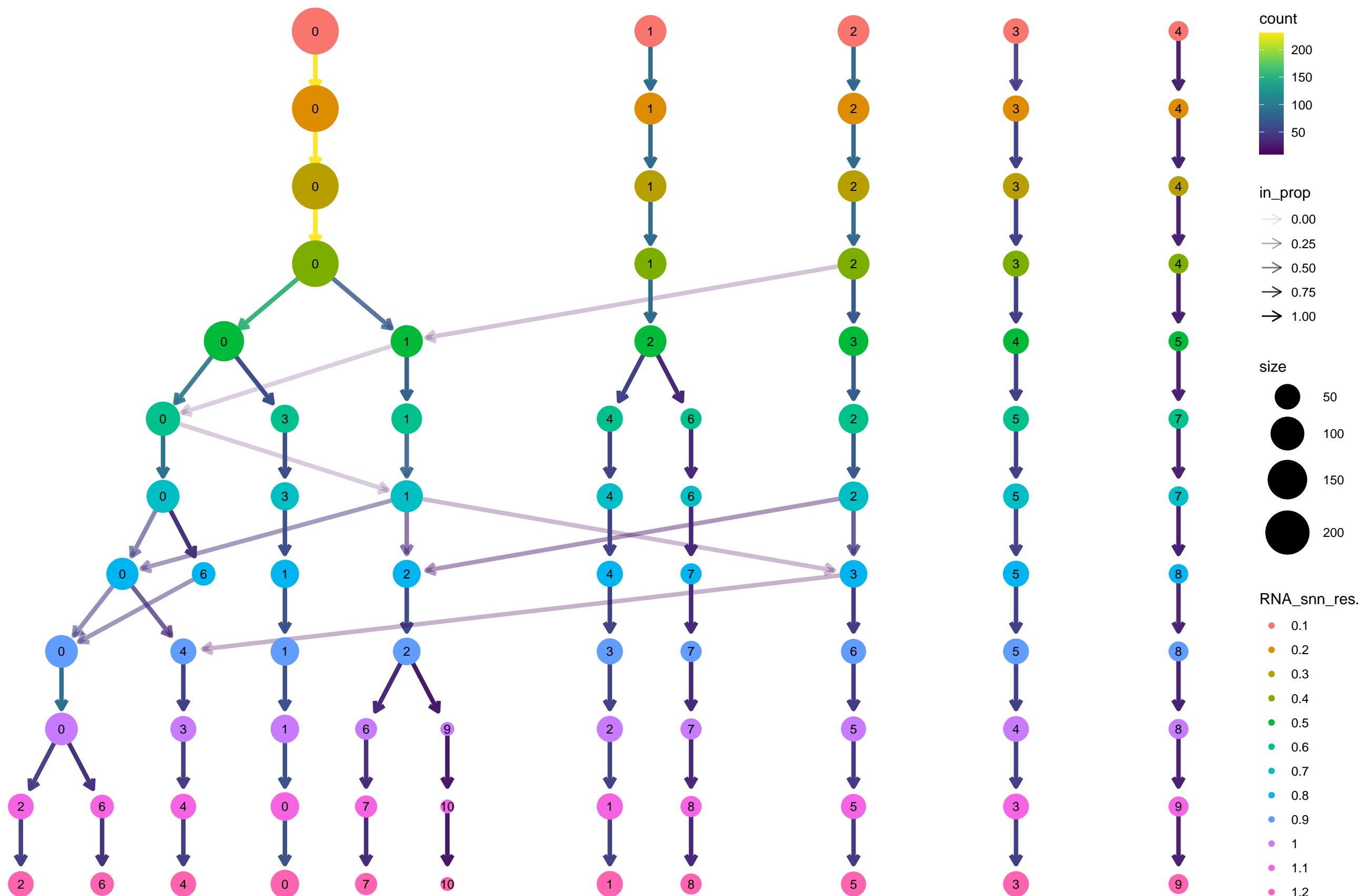
a FALSE

a TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.2	5	0.414886220856559
2	0.5	6	0.314351377724674
3	1	10	0.203244672708833
4	1.1	11	0.187827674134369
5	0.9	9	0.179300251087355
6	0.6	8	0.167499663878492

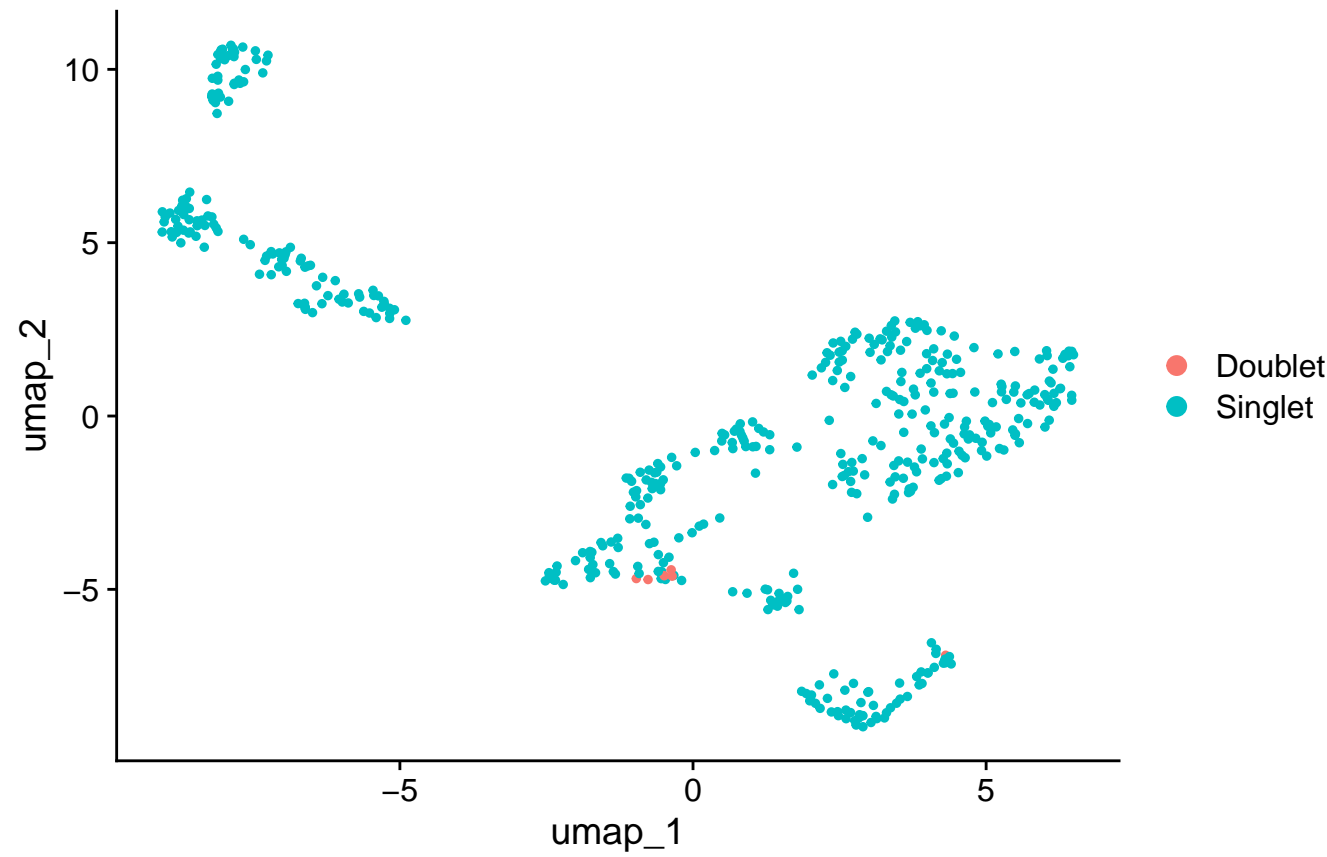
org_6A: Clustree

org_6A – Clustering Resolution Tree

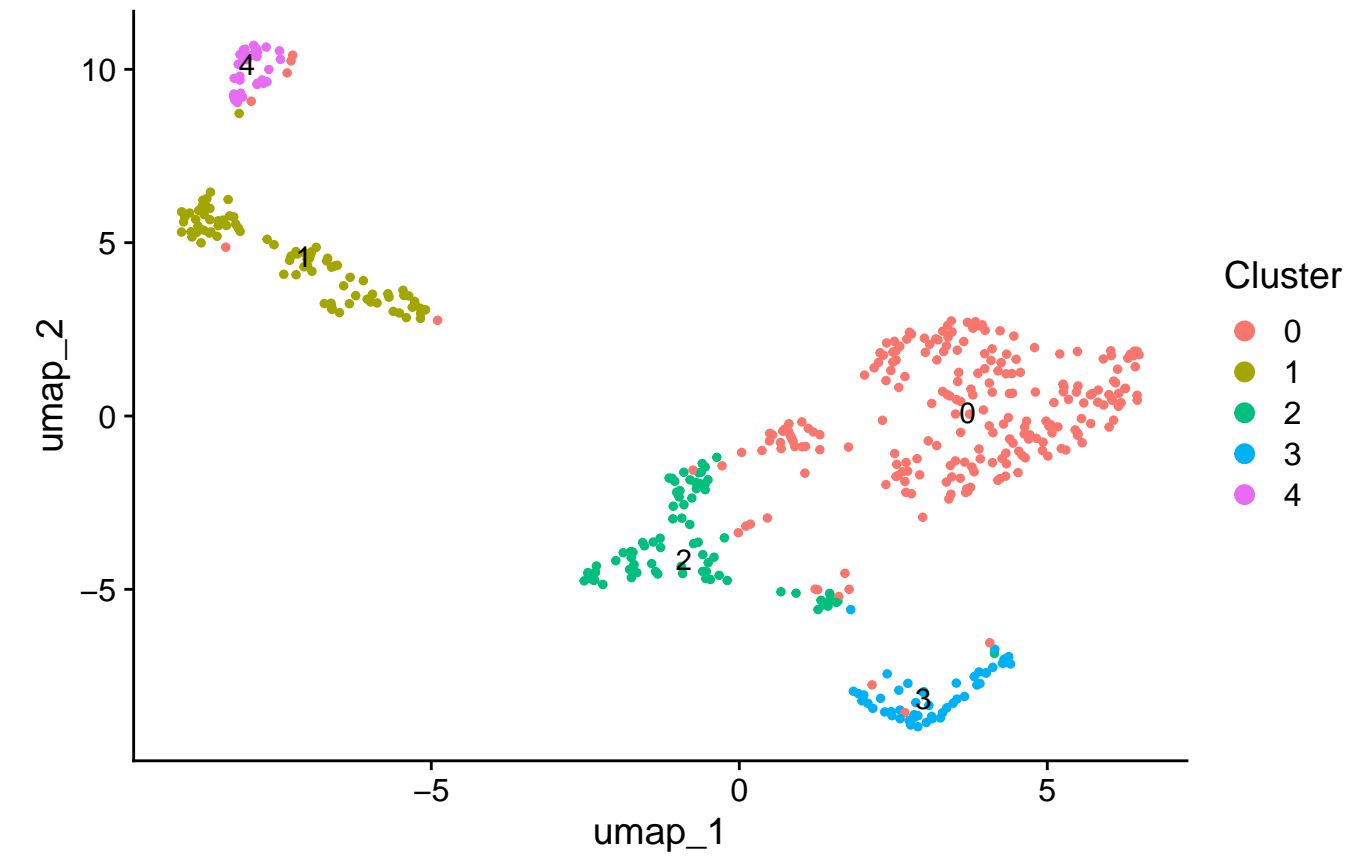


org_6A – UMAP & Doublet Removal

org_6A: Doublets Detected



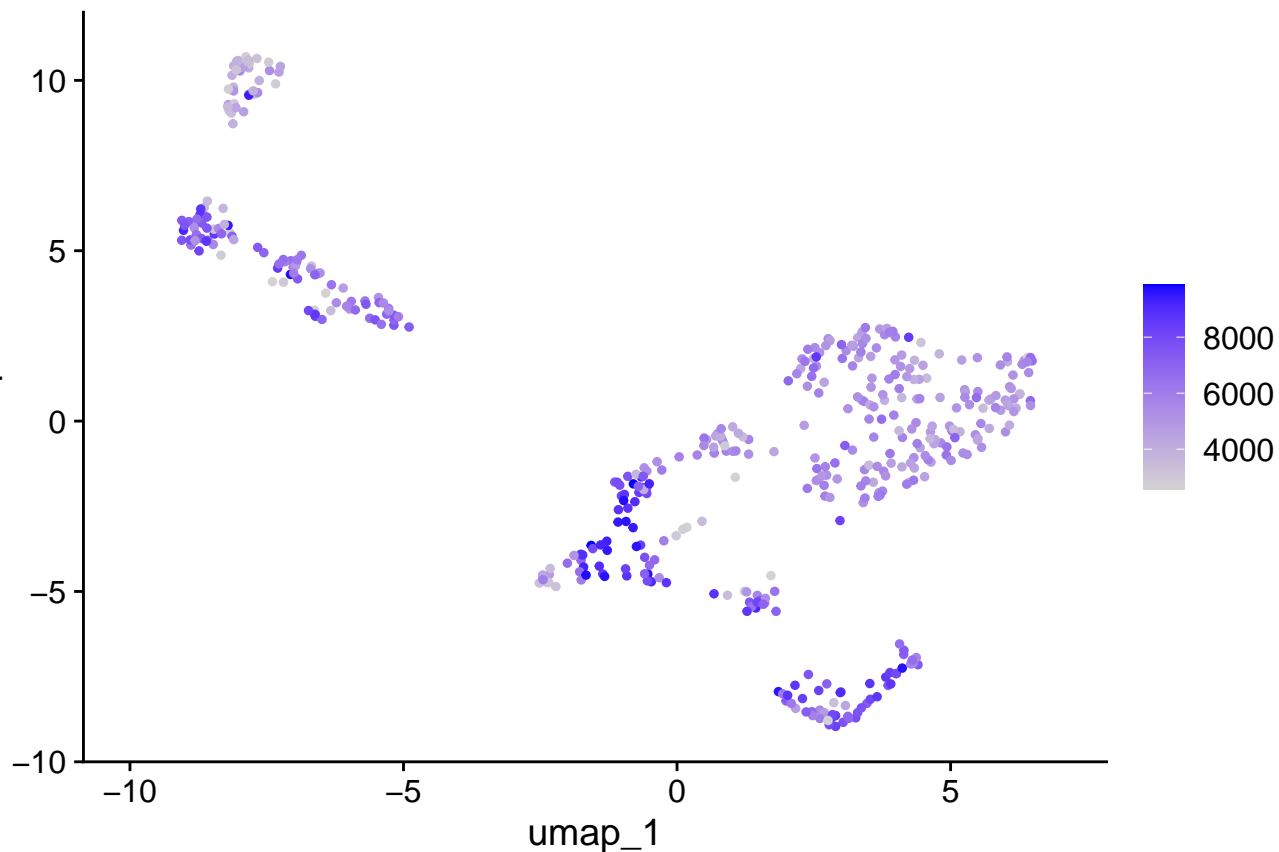
org_6A: Final UMAP



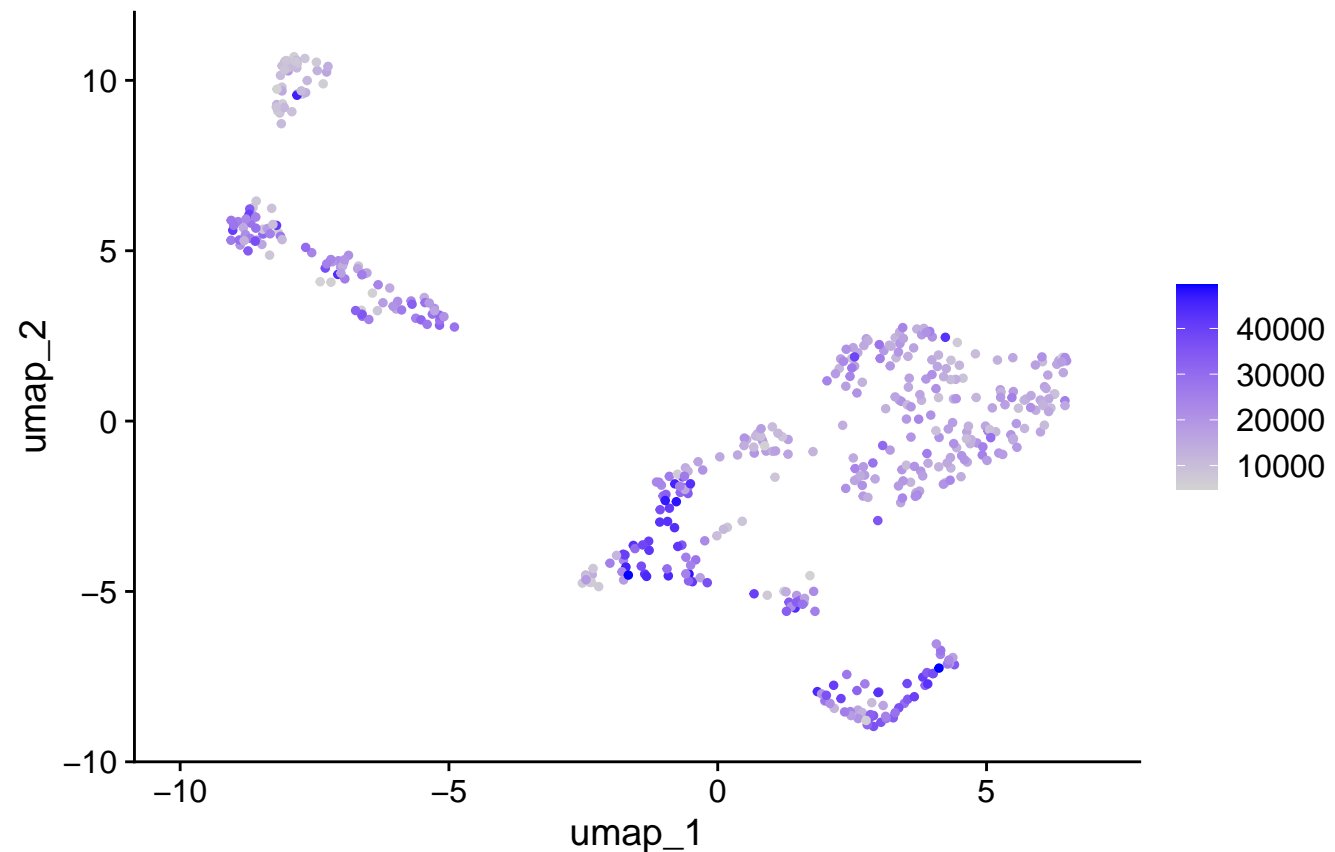
	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	35583.5	8363	6
2	Singlet	18578.5	5657	480

org_6A – QC Metrics & Cell Cycle on UMAP

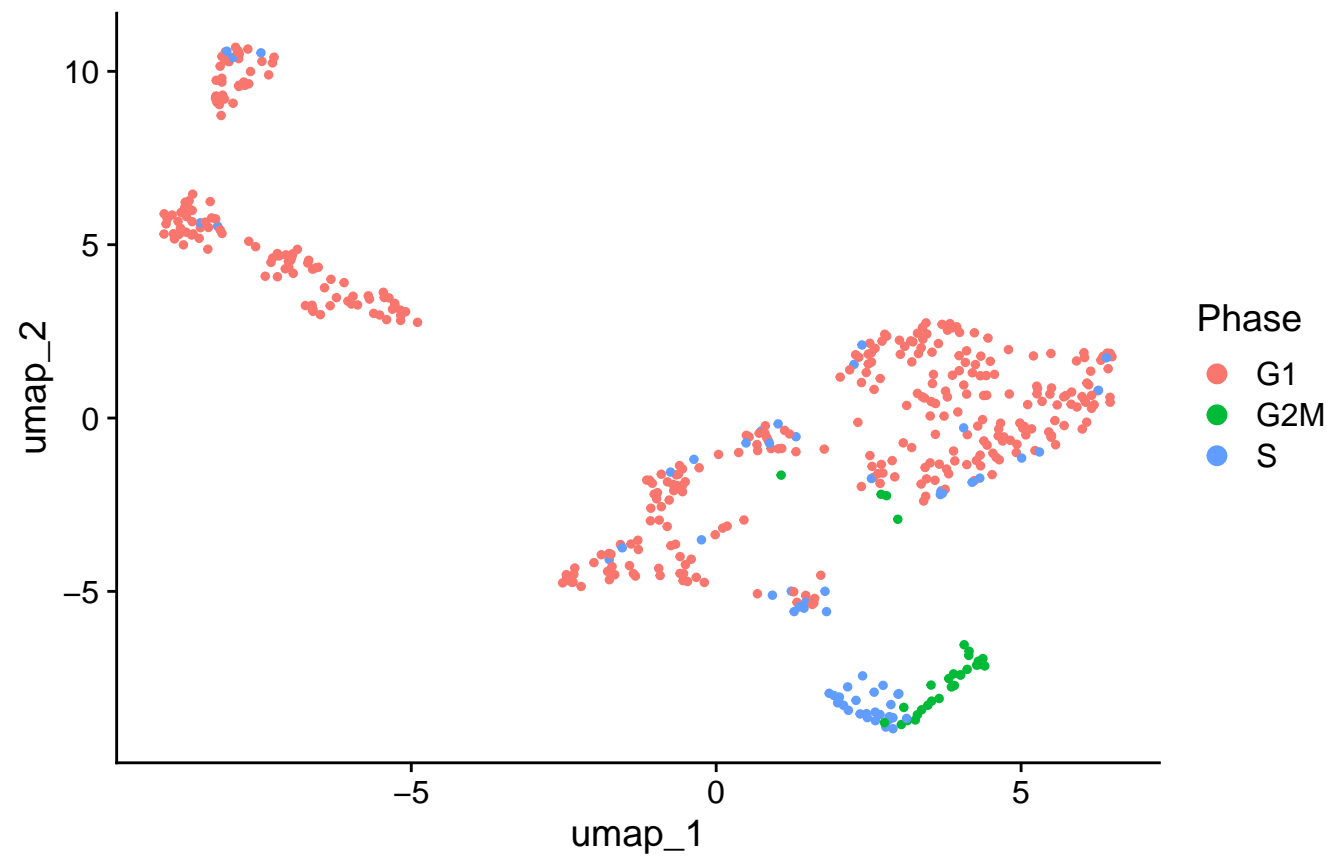
org_6A: nFeature_RNA



org_6A: nCount_RNA



org_6A: Cell Cycle Phase



org_6A: Final UMAP

