org_1A – Adaptive Threshold Determination
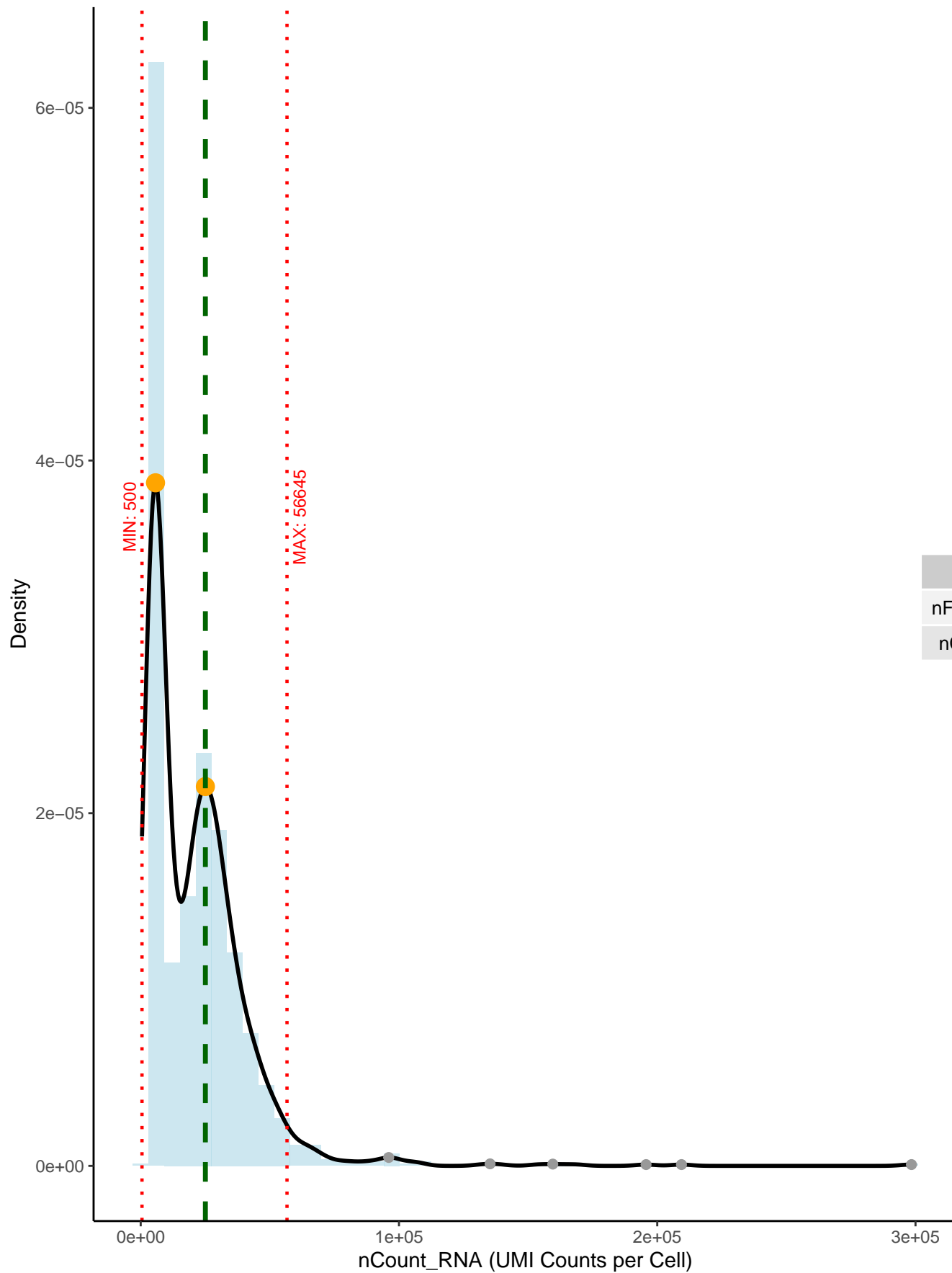
org_1A: nCount_RNA (UMI Counts per Cell) Distribution

Method: peak | Selected peak: 25041.8 | Total peaks: 8 | Top 2 peaks used
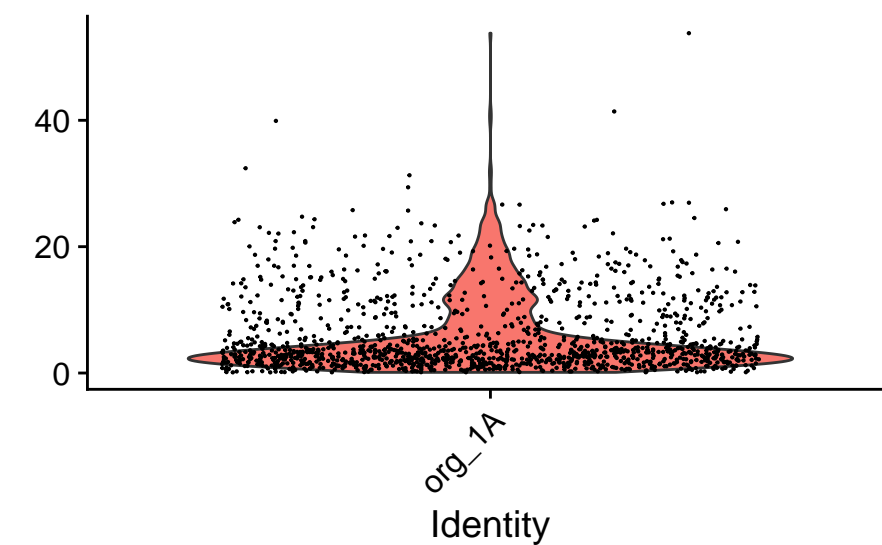
Density

MIN: 500

MAX: 56645

6e−05

4e−05

2e−05

0e+00

0e+00   1e+05   2e+05   3e+05

nCount_RNA (UMI Counts per Cell)

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Thresh
nFeature_RNA	custom	NA	NA	NA	NA	4000	12525
nCount_RNA	peak	25042	8	5735, 25042	21069	500	56645

org_1A – Filtering Summary
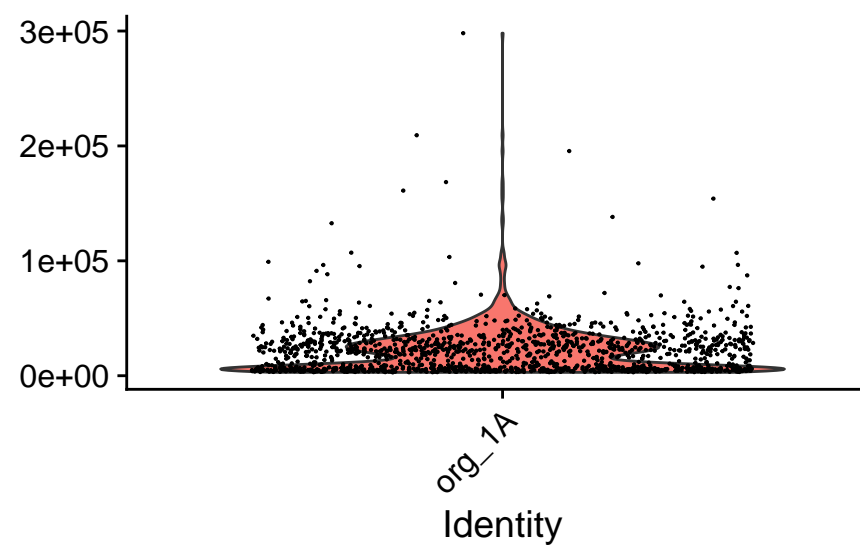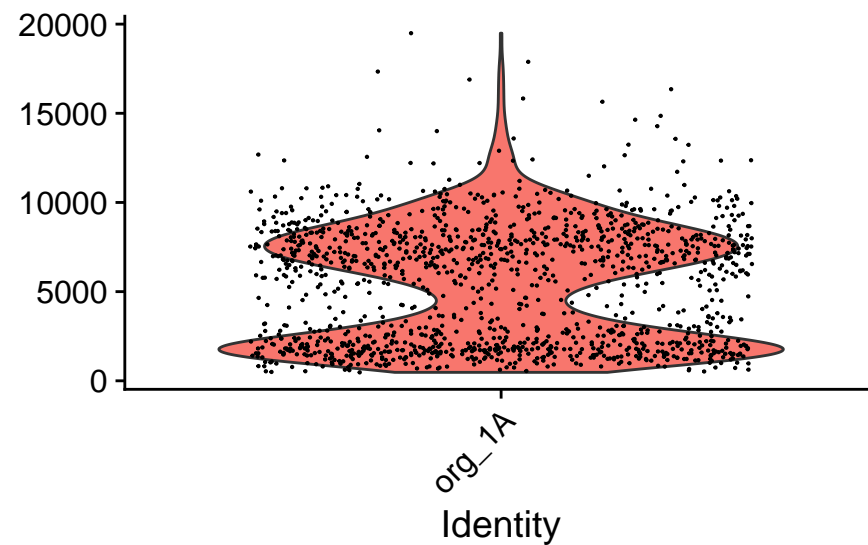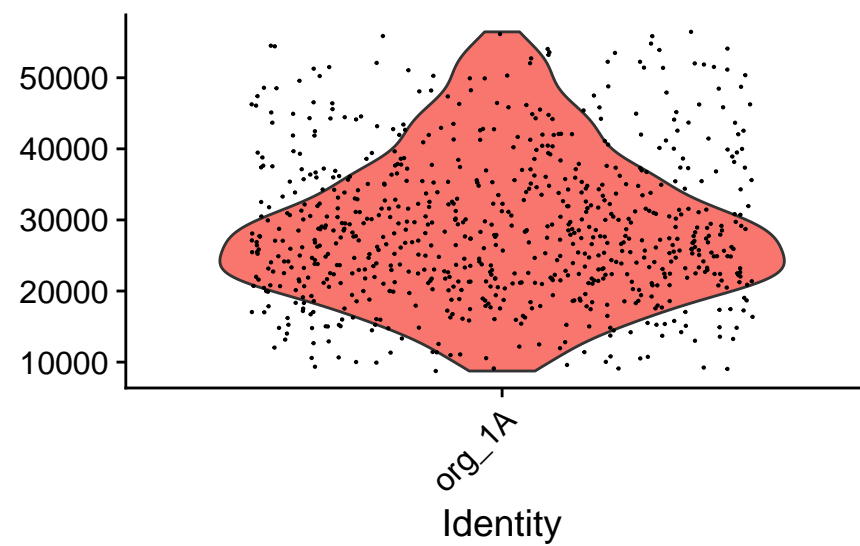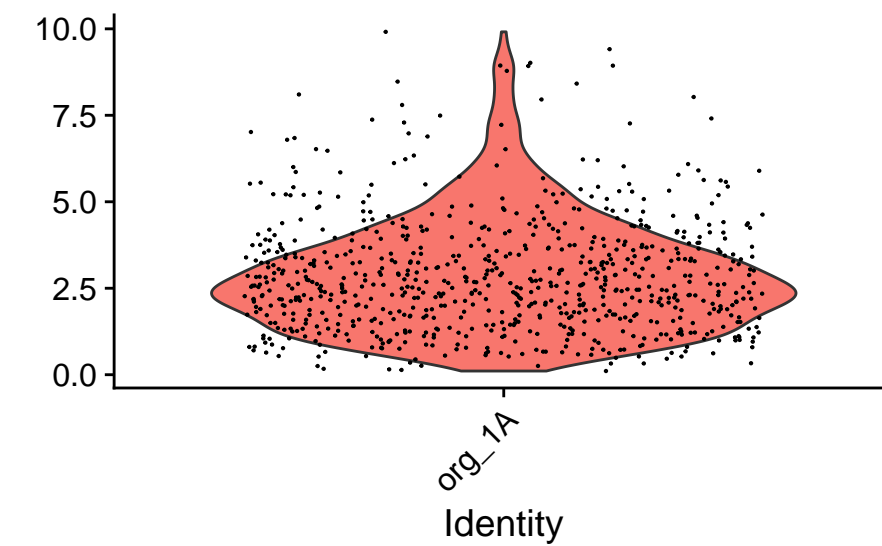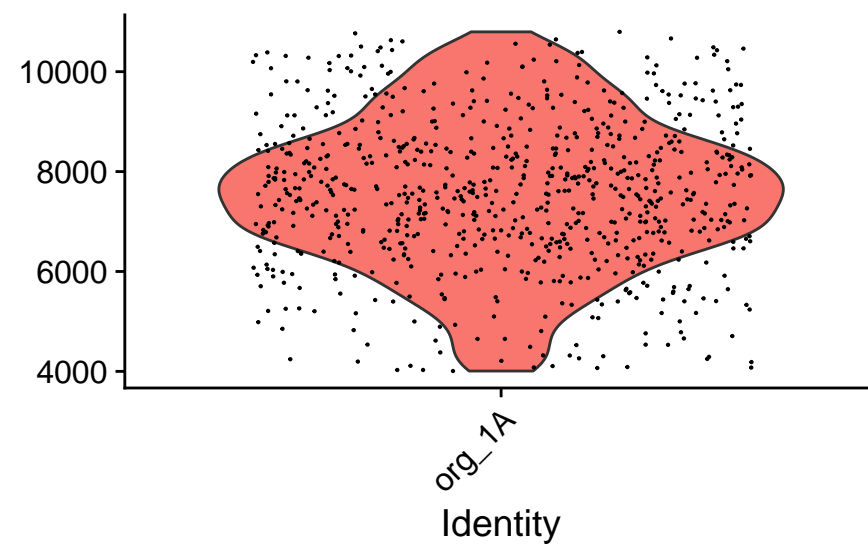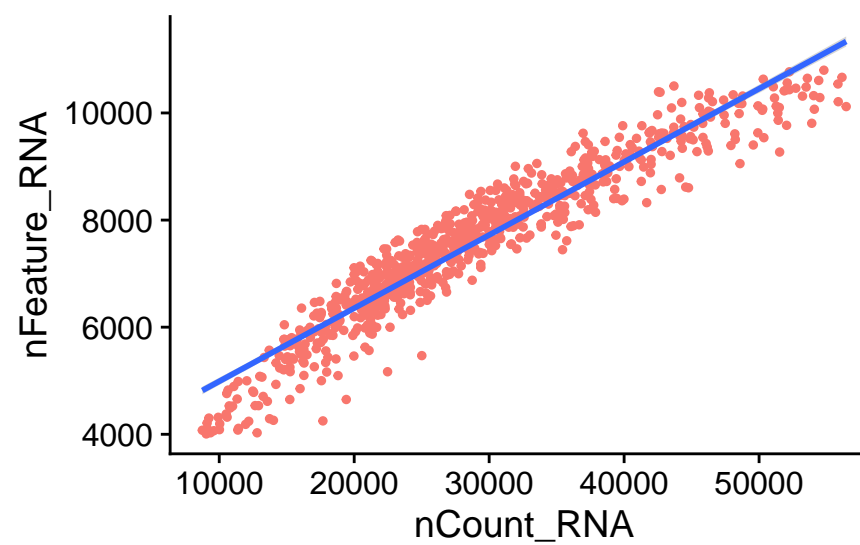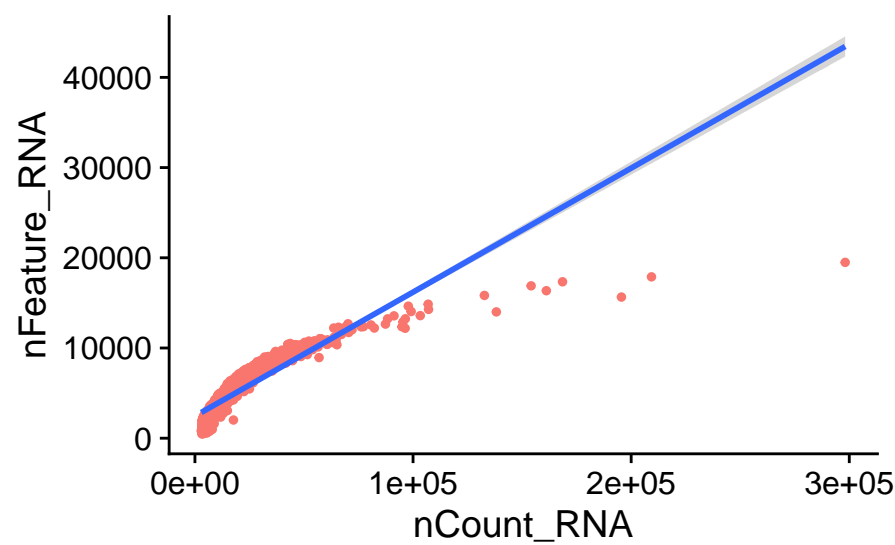
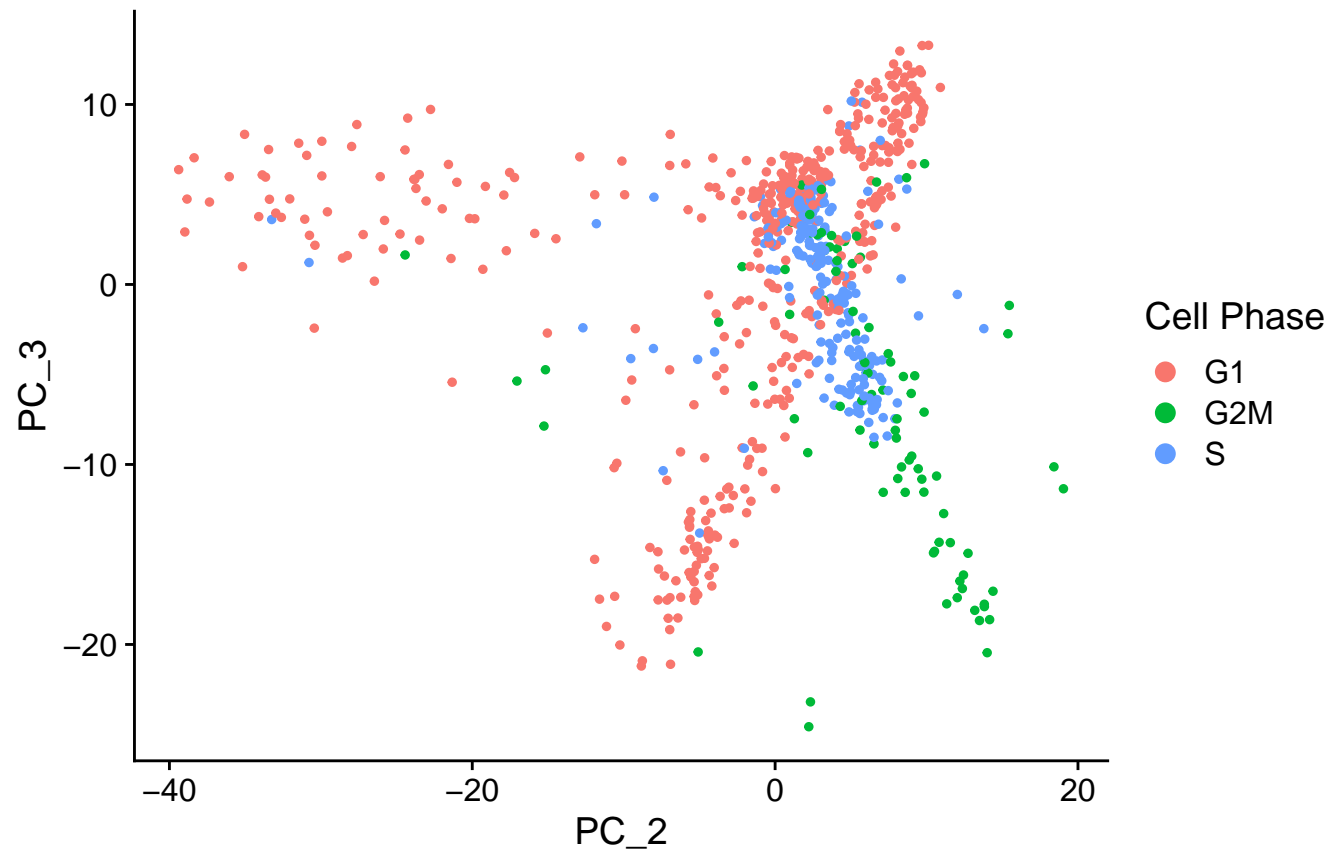|	Metric	Before	After
1	Cells	1398.000000	763.000000
2	Genes	42431.000000	42431.000000
3	Median nCount	18656.500000	27493.000000
4	Median nFeature	6038.500000	7572.000000
5	Median MT%	3.384393	2.585652

org_1A – Variable Features & Cell Cycle

org_1A: Top 2000 Variable Genes

ENSG00000147655.12–RSPO2
ENSG00000083067.27–TRPM3
ENSG00000157168.22–NRG1
ENSG00000152208.13–GRID2
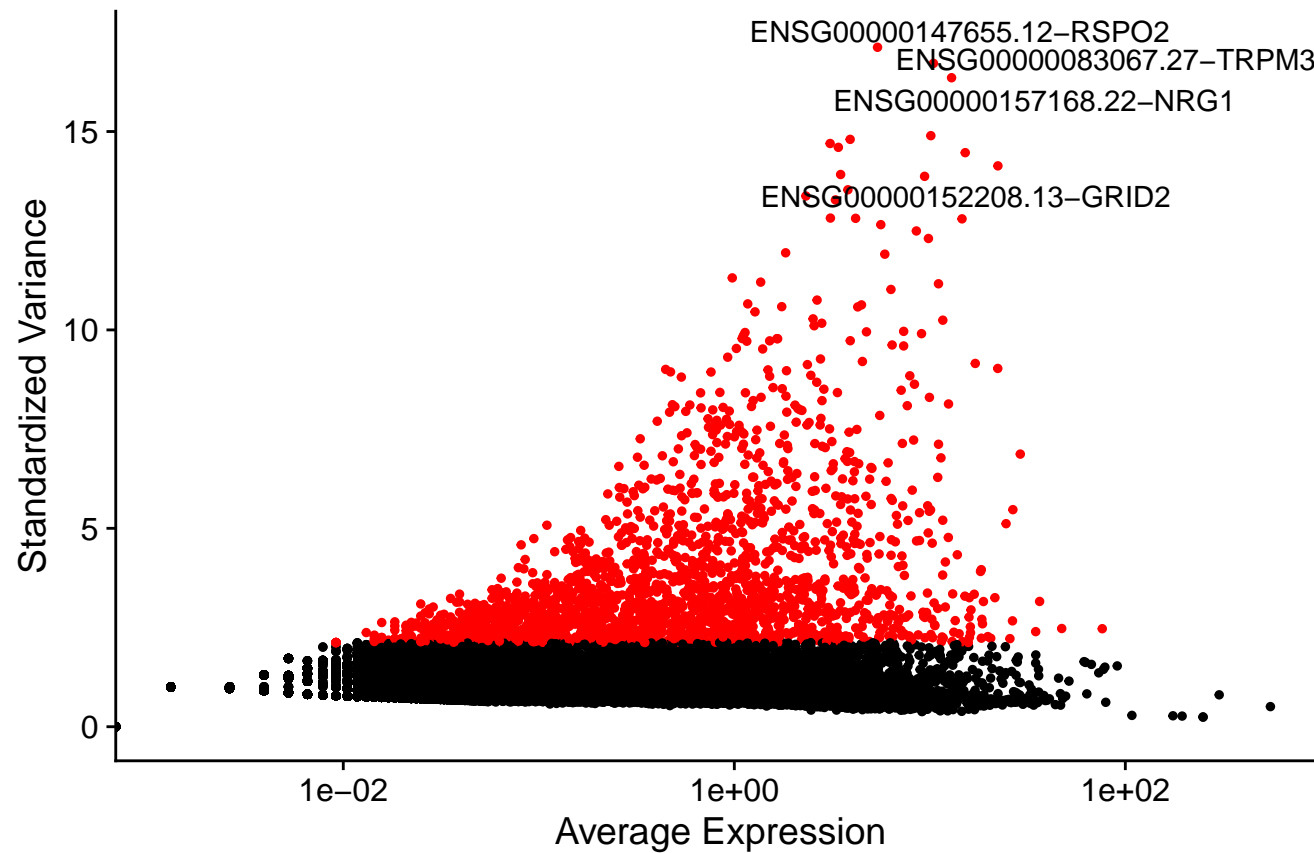
org_1A: Cell Cycle on PC1 & PC2

Cell Phase
G1
G2M
S
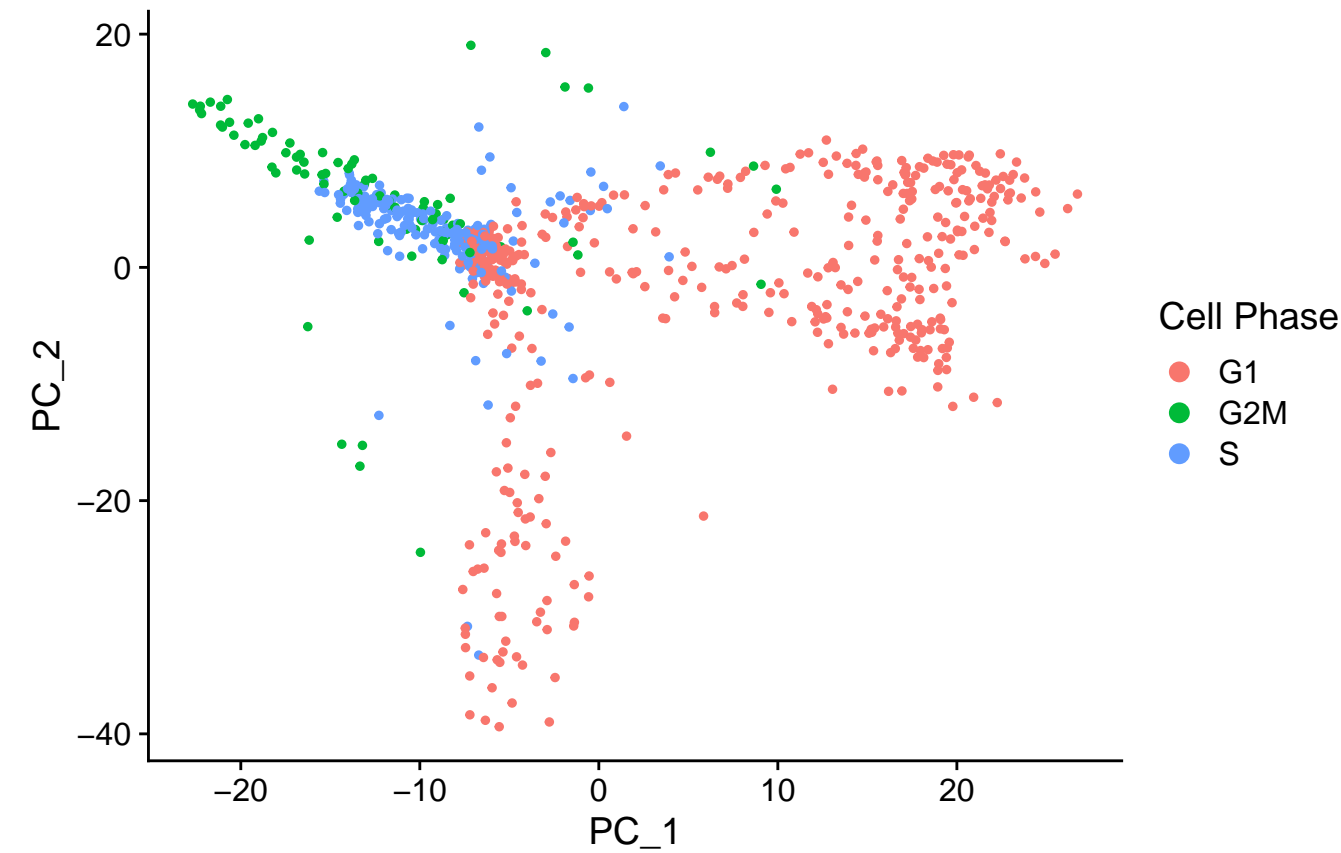
org_1A: Cell Cycle on PC2 & PC3
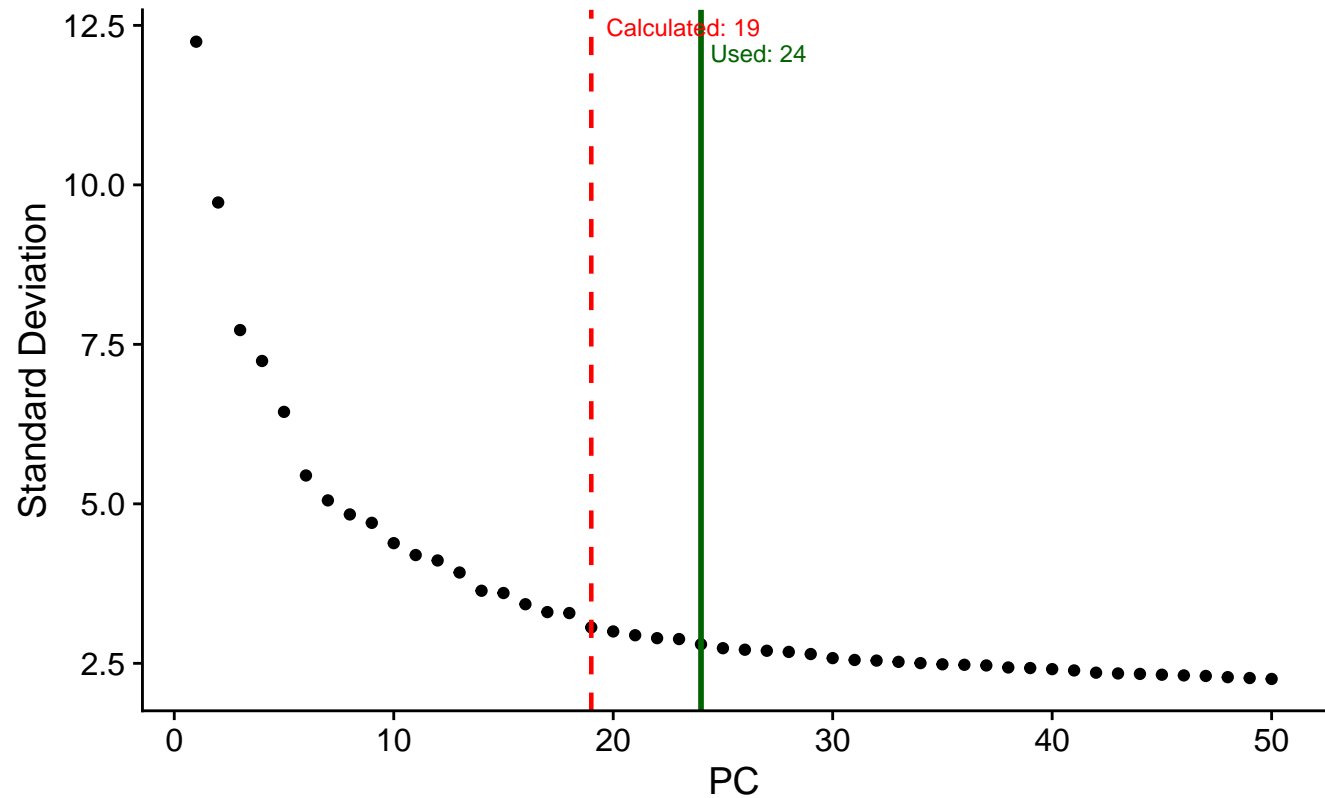
Cell Phase
G1
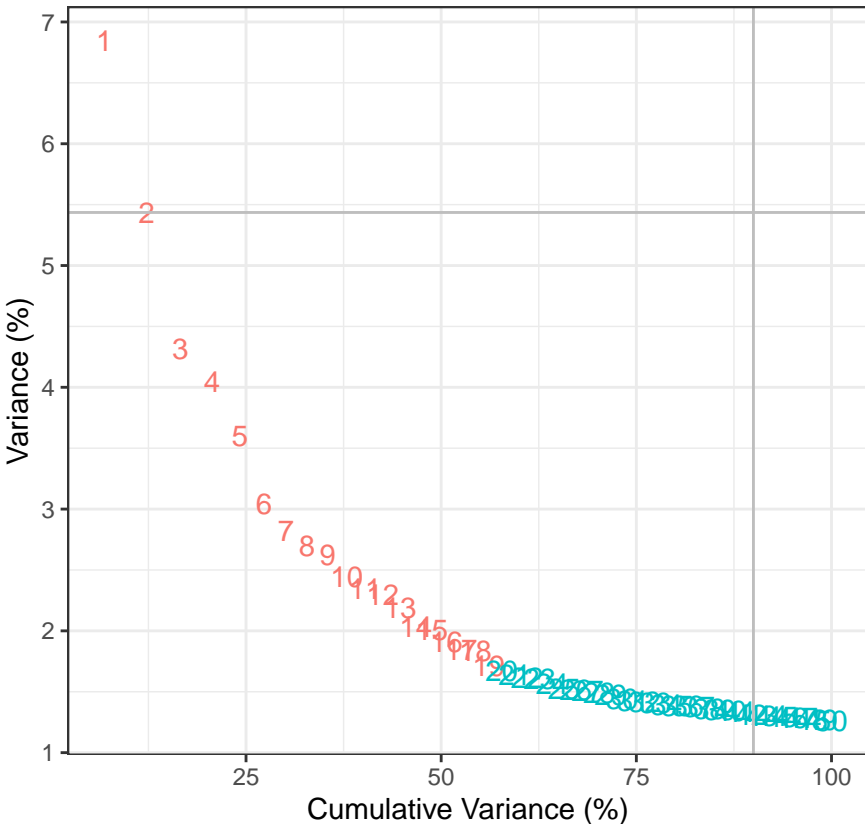G2M
S

org_1A – PCA Selection & Silhouette Analysis

org_1A: Elbow Plot

Calculated: 19 PCs | Used: 24 PCs (+5)

org_1A: Quantitative PC Selection

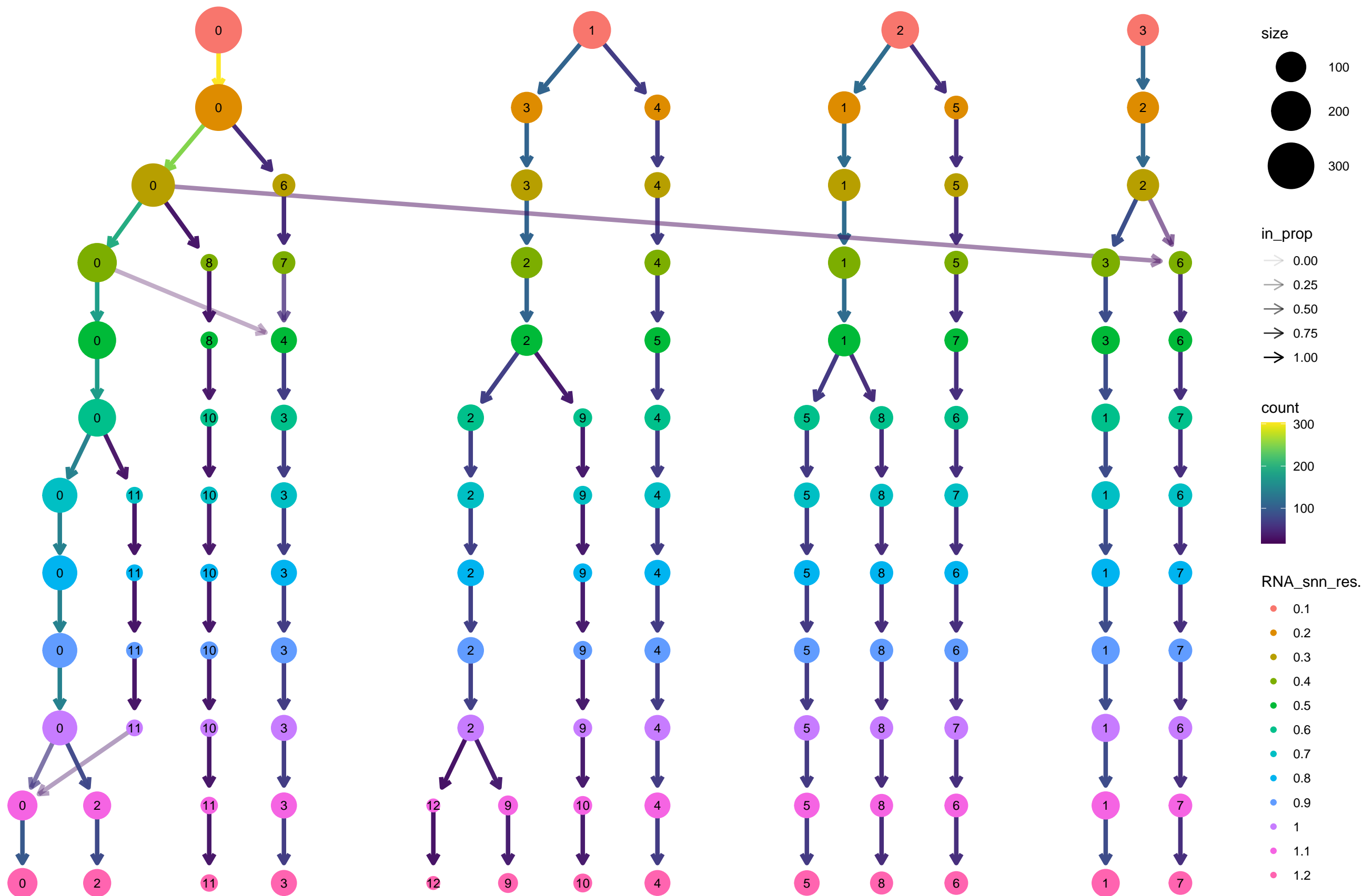Calculated: 19 PCs | Used: 24 PCs (+5)

rank > optimal_pcs_calculated

a   FALSE

a   TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.2	6	0.350247347540968
2	0.3	7	0.321188591456401
3	0.1	4	0.271809106417426
4	0.6	11	0.260225169105883
5	0.4	9	0.2442963090576
6	0.7	12	0.243360950036212
7	1.1	13	0.240452176175489

org_1A – Clustering Resolution Tree
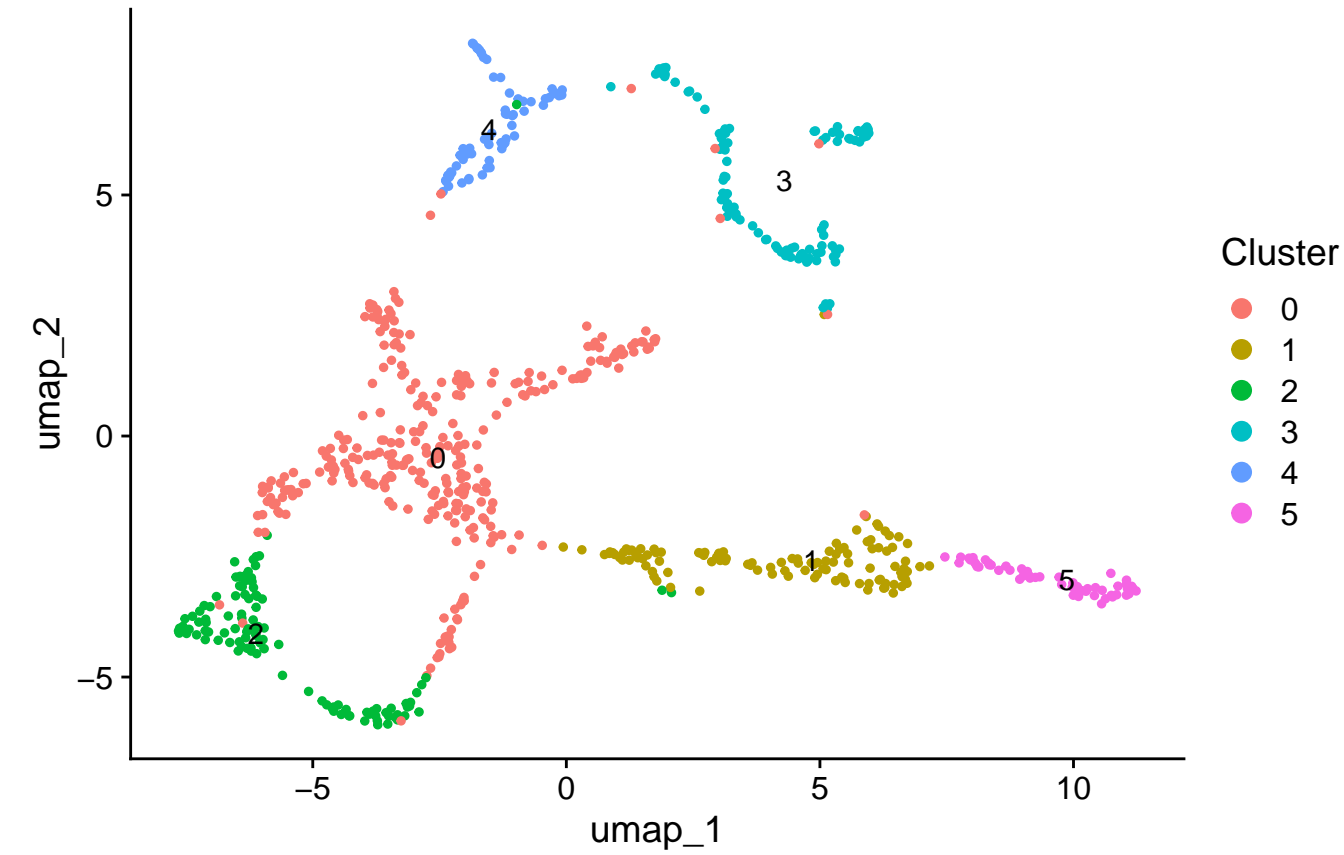
org_1A: Clustree

org_1A – UMAP & Doublet Removal

org_1A: Doublets Detected
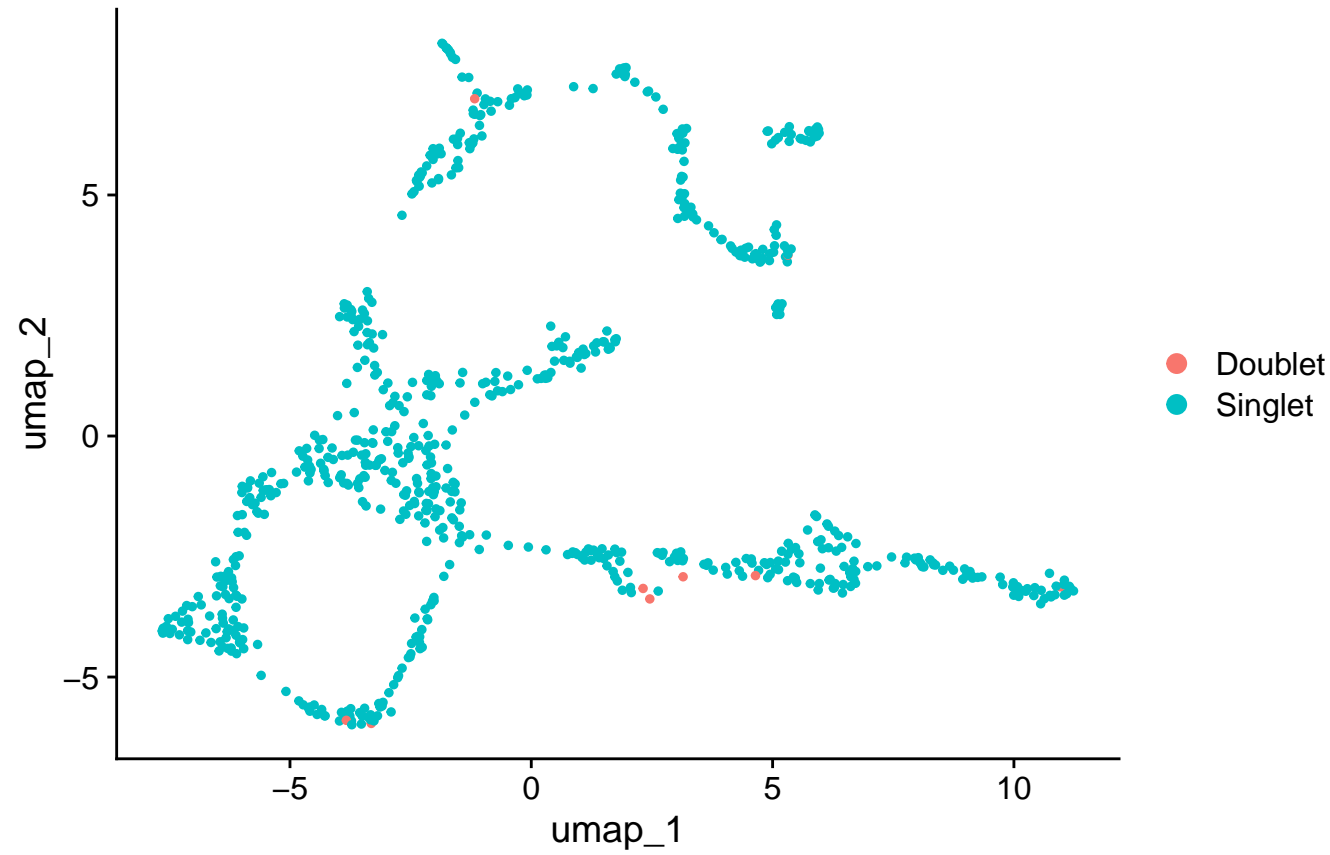
org_1A: Final UMAP

	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	42051.0	9290.0	9
2	Singlet	27371.5	7556.5	754

org_1A – QC Metrics & Cell Cycle on UMAP