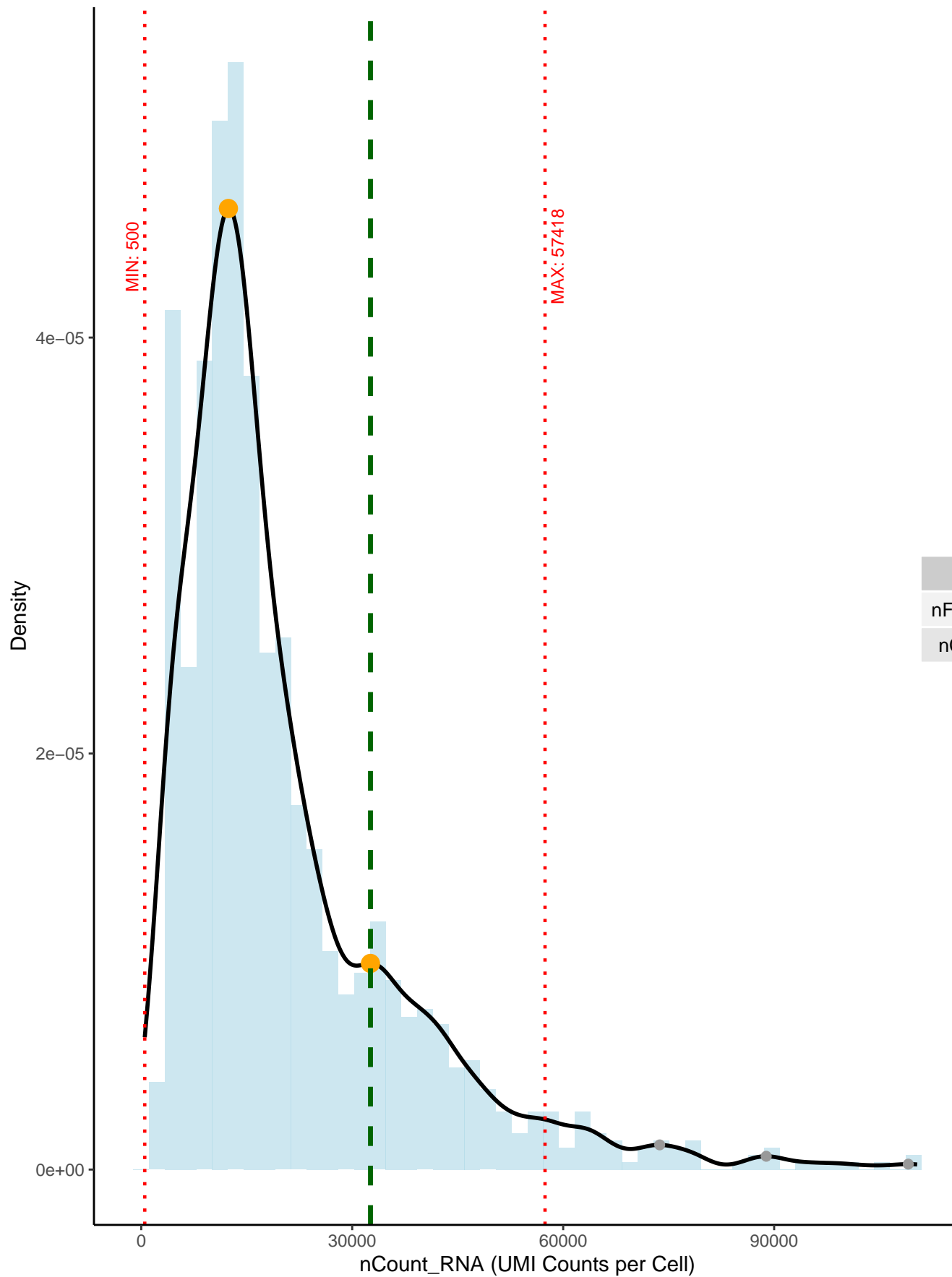# org_6C – Adaptive Threshold Determination

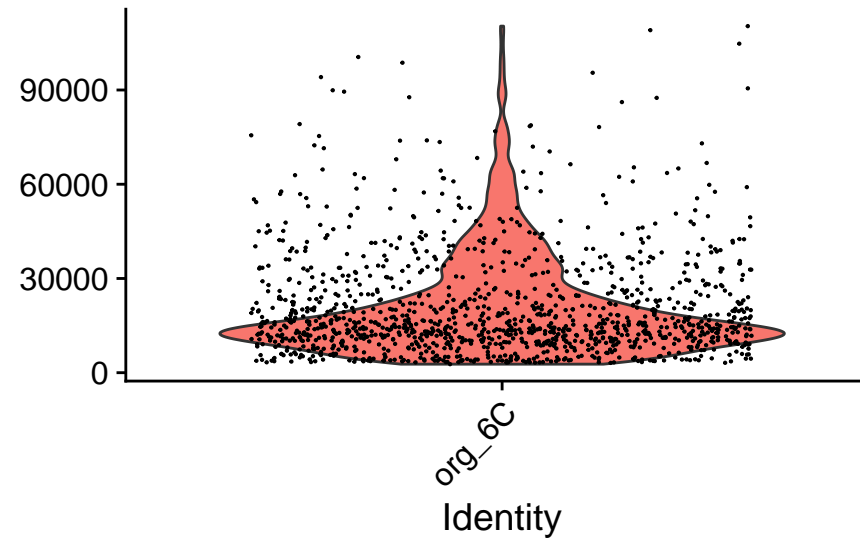## org_6C: nCount_RNA (UMI Counts per Cell) Distribution

Method: peak | Selected peak: 32599.3 | Total peaks: 5 | Top 2 peaks used
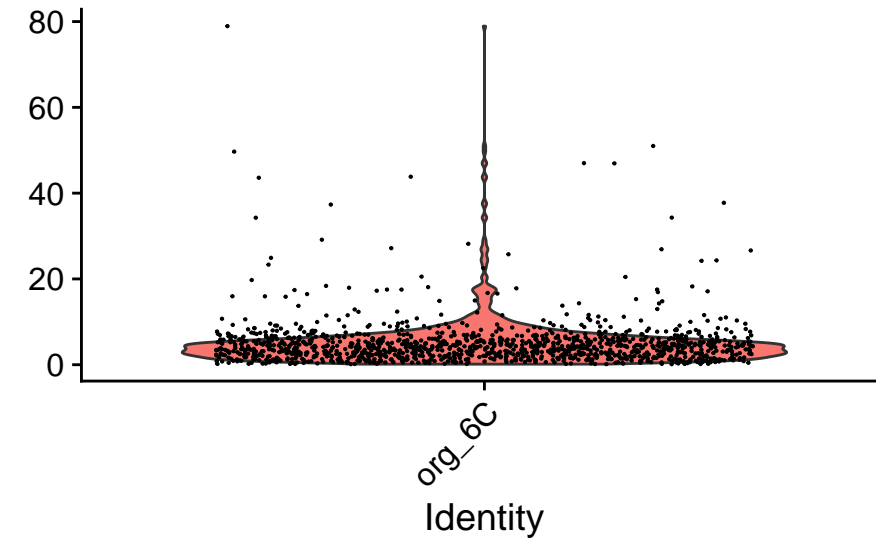

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Thres
nFeature_RNA	custom	NA	NA	NA	NA	2500	10000
nCount_RNA	peak	32599	5	12398, 32599	16546	500	57418

org_6C – Filtering Summary
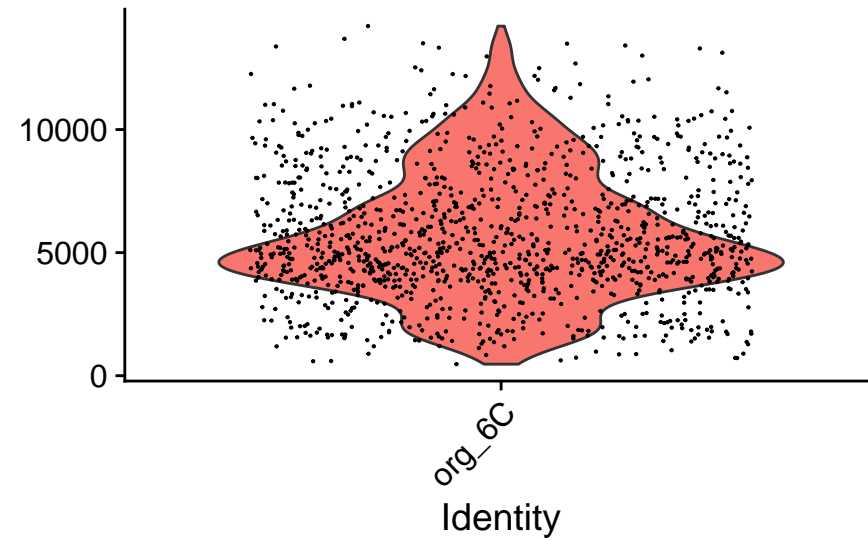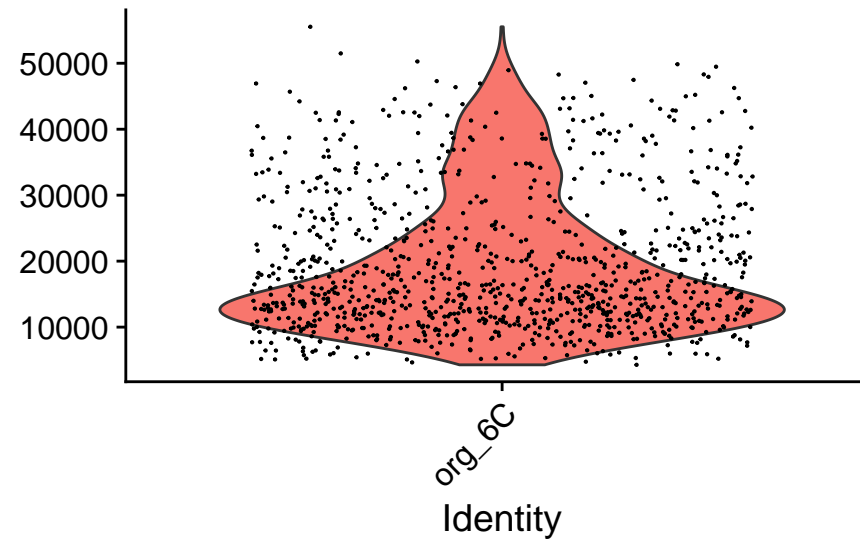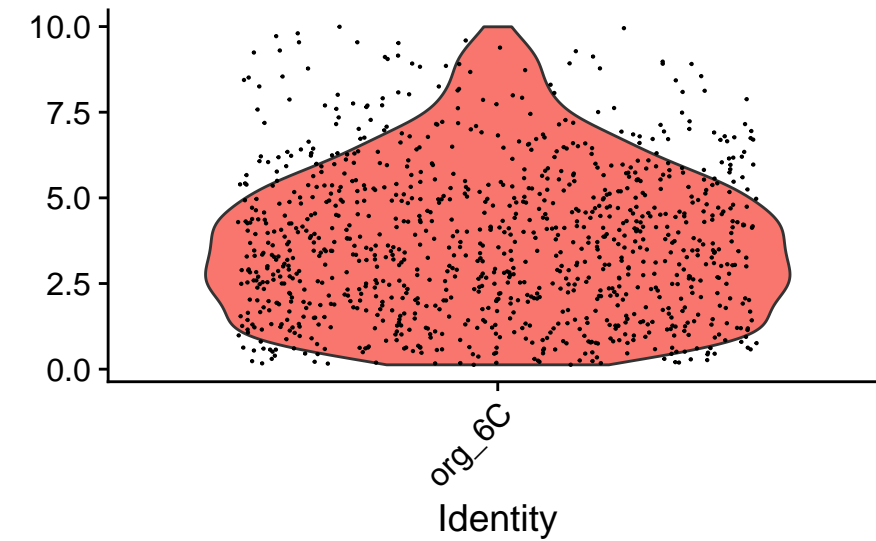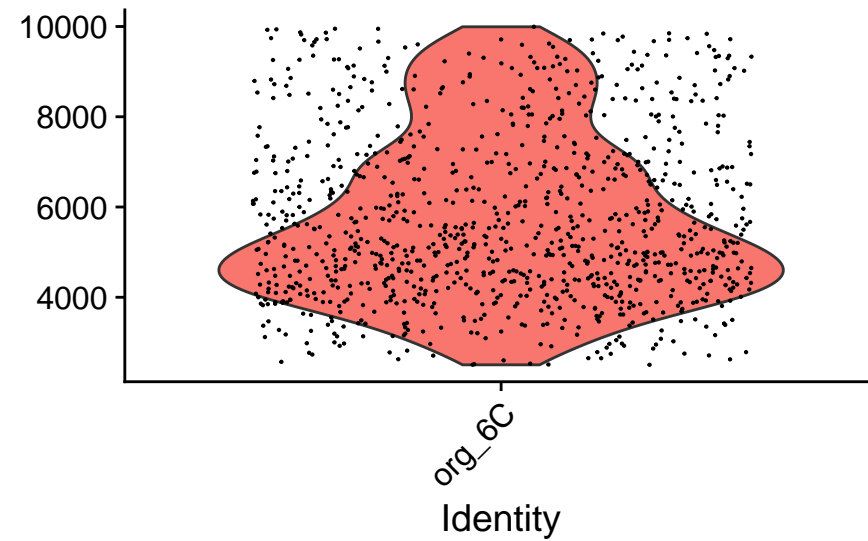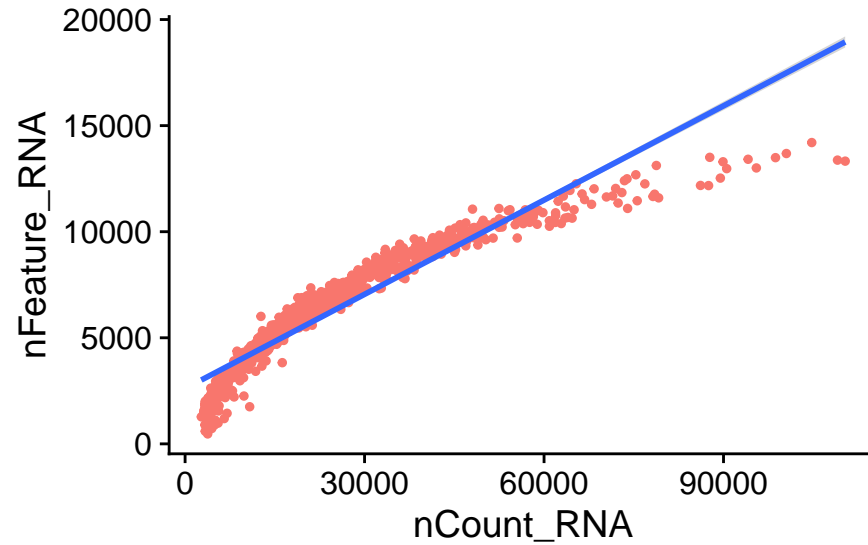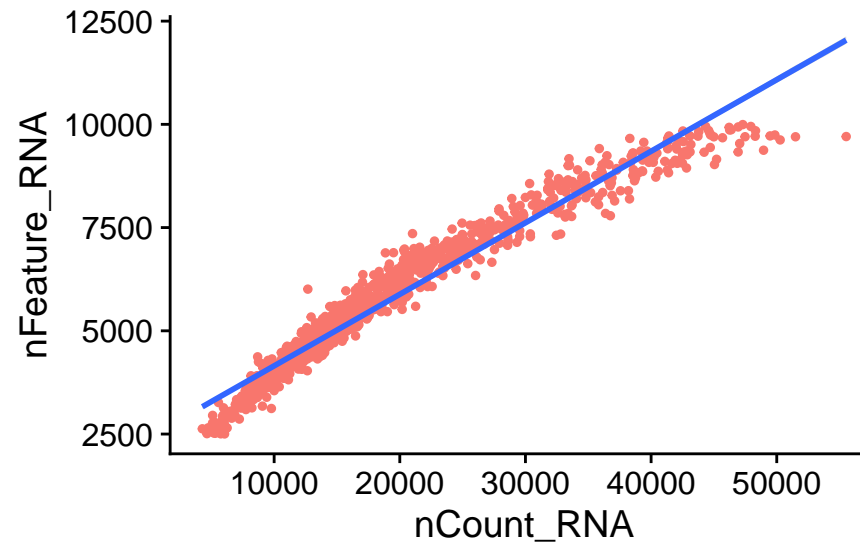
	Metric	Before	After
1	Cells	1274.000000	1031.000000
2	Genes	40115.000000	40115.000000
3	Median nCount	15290.500000	15708.000000
4	Median nFeature	5169.500000	5301.000000
5	Median MT%	3.975554	3.497476

org_6C – Variable Features & Cell Cycle

org_6C: Top 2000 Variable Genes

ENSG00000297311.1–ENSG00000297311   ENSG00000109846.9–CRYAB
ENSG00000178568.16–ERBB4
ENSG00000117724.15–CENPF
ENSG00000169220–GRIK2
ENSG00000136208.14–IL1RAPL2
ENSG00000183117.20–CSMD1
ENSG00000183690.16–NKAIN2
ENSG00000175497.17–DPP10
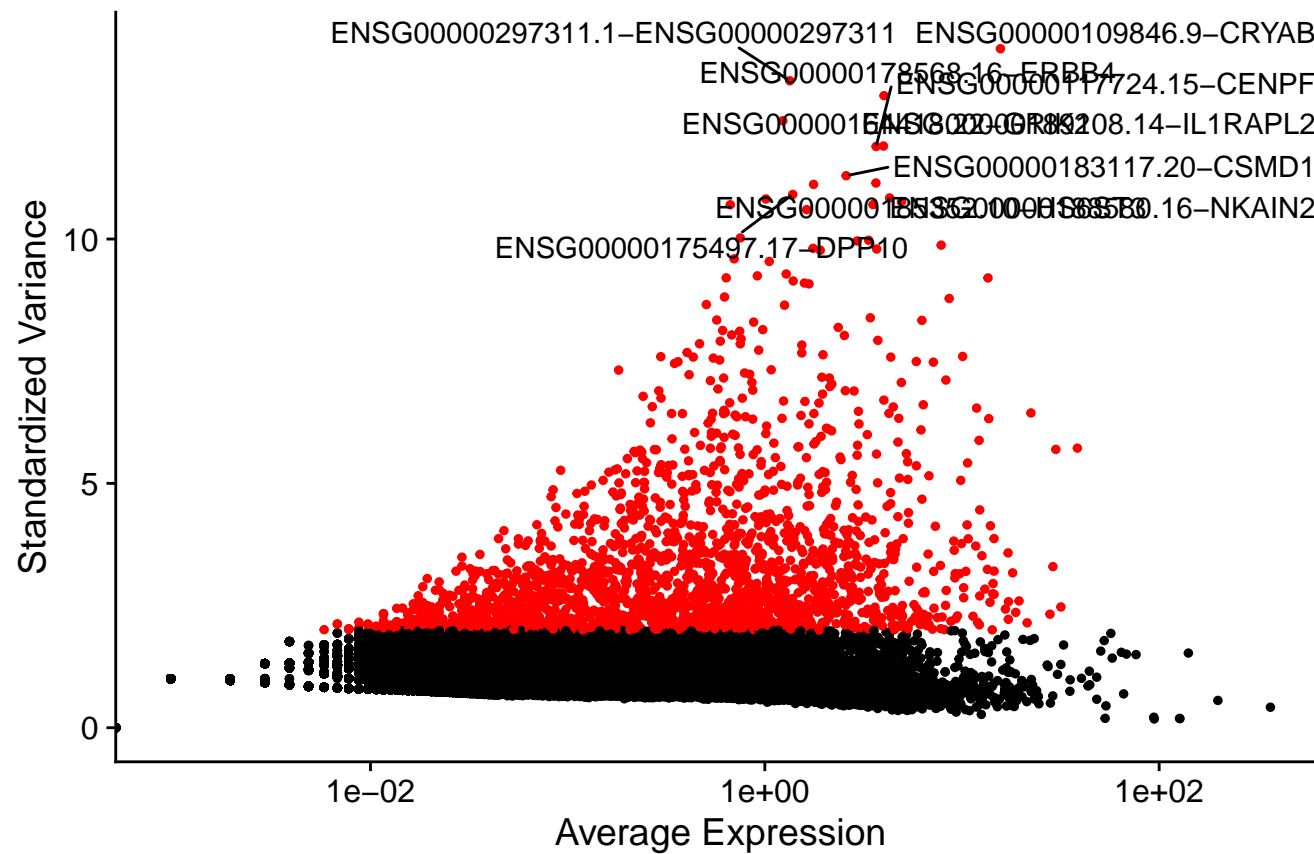
org_6C: Cell Cycle on PC1 & PC2

Cell Phase
- G1
- G2M
- S
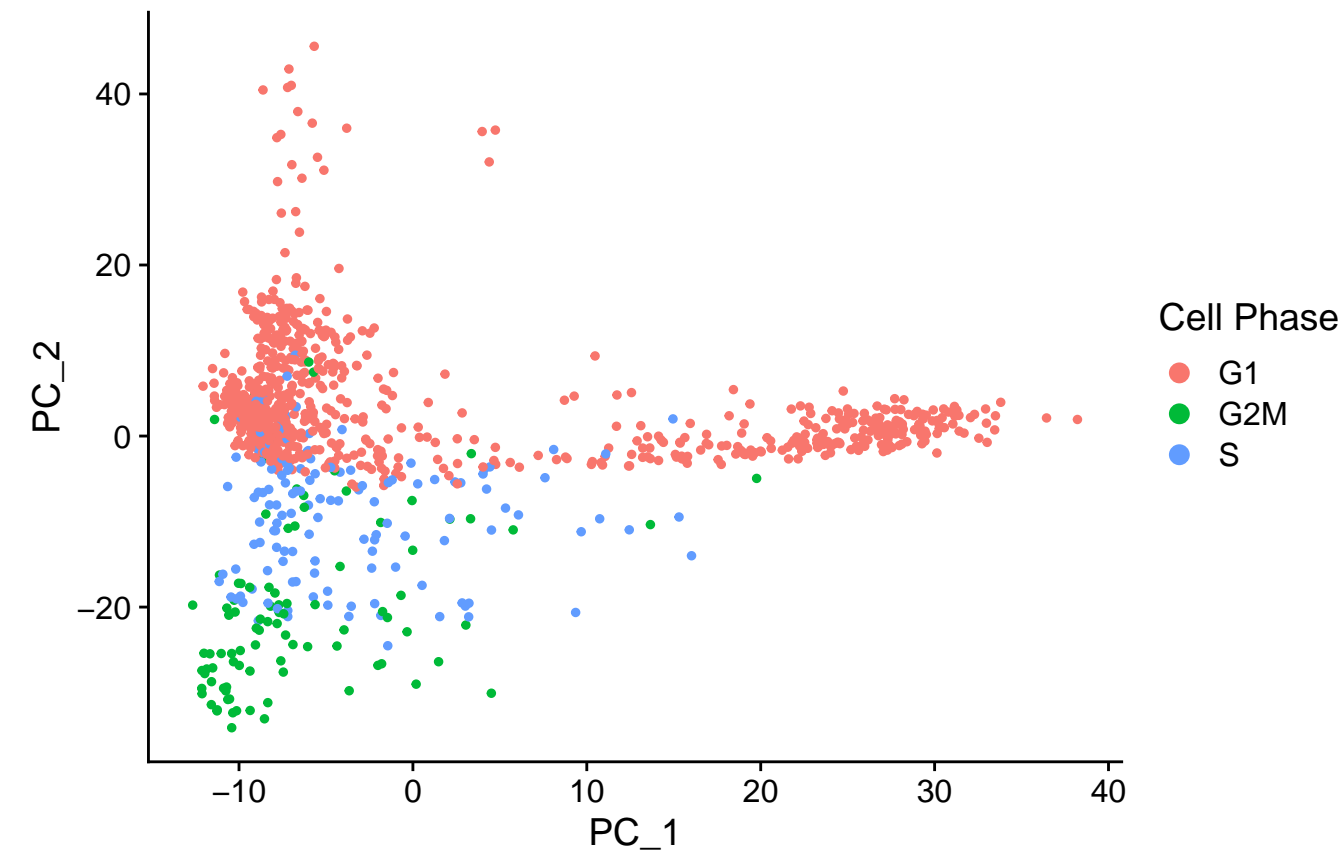
org_6C: Cell Cycle on PC2 & PC3

Cell Phase
- G1
- G2M
- S
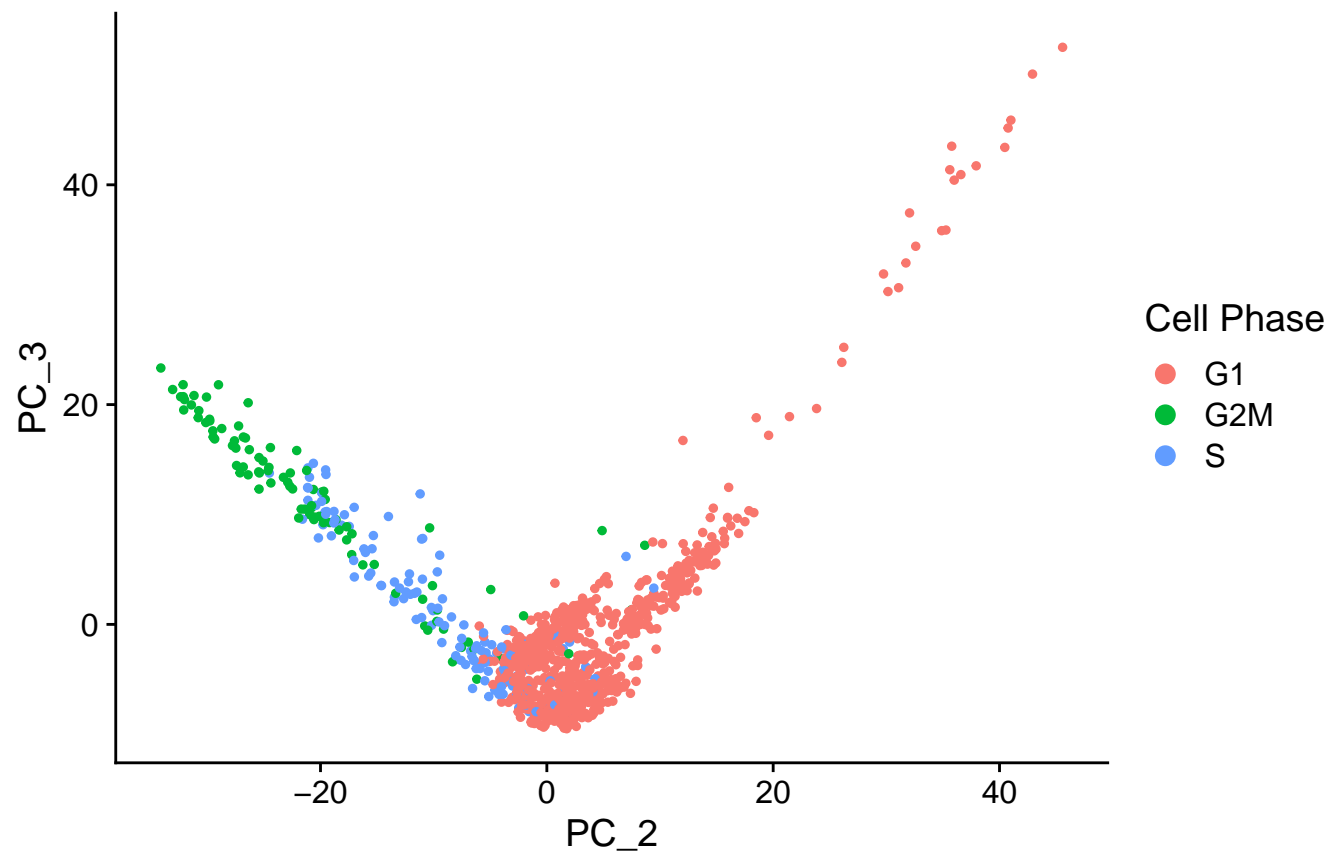
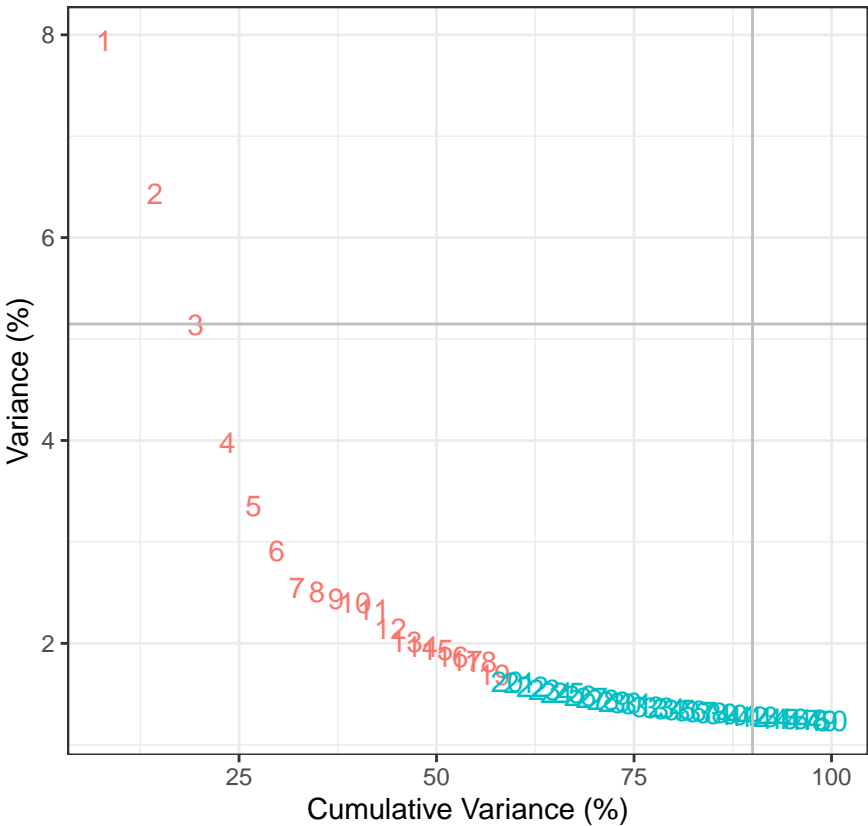# org_6C – PCA Selection & Silhouette Analysis

org_6C: Elbow Plot
Calculated: 19 PCs | Used: 24 PCs (+5)
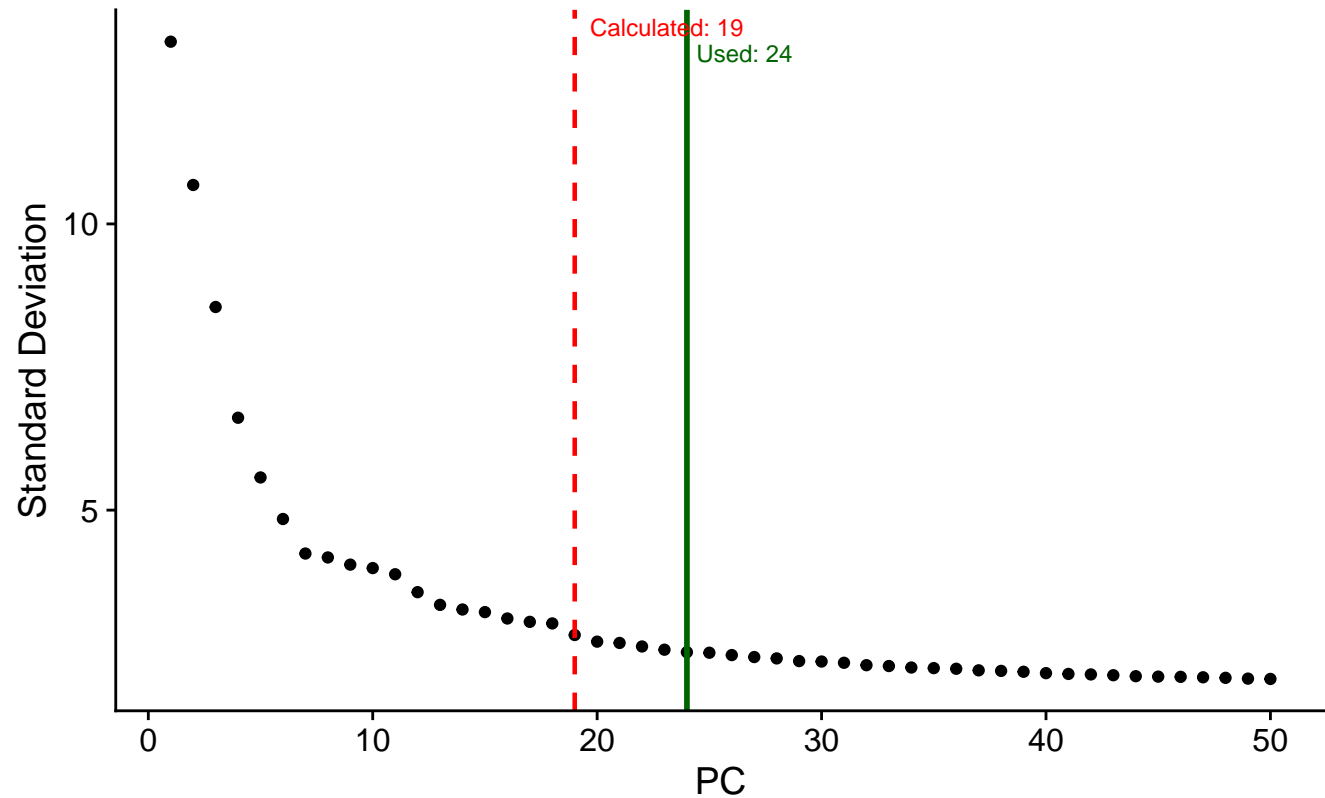
org_6C: Quantitative PC Selection
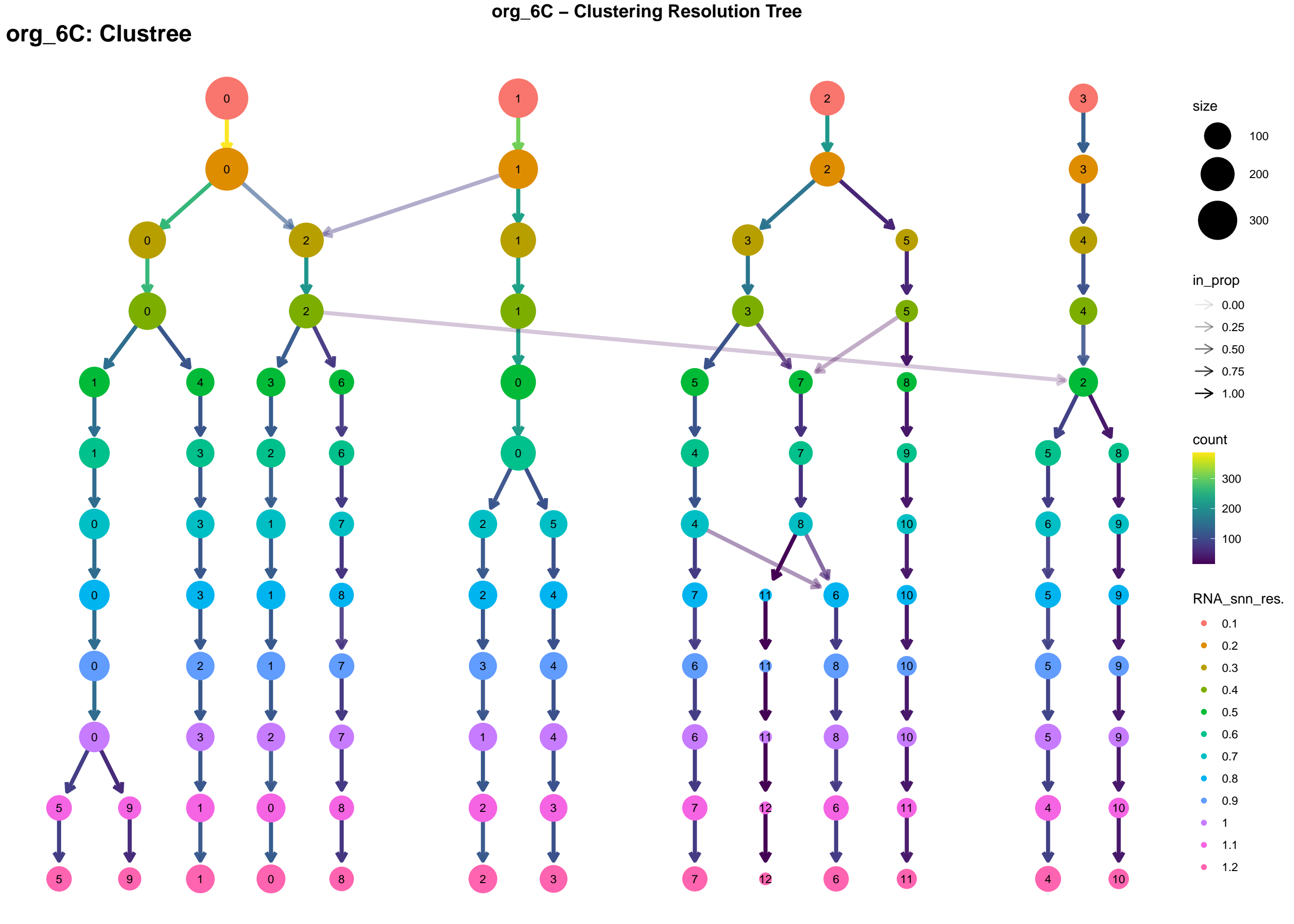Calculated: 19 PCs | Used: 24 PCs (+5)
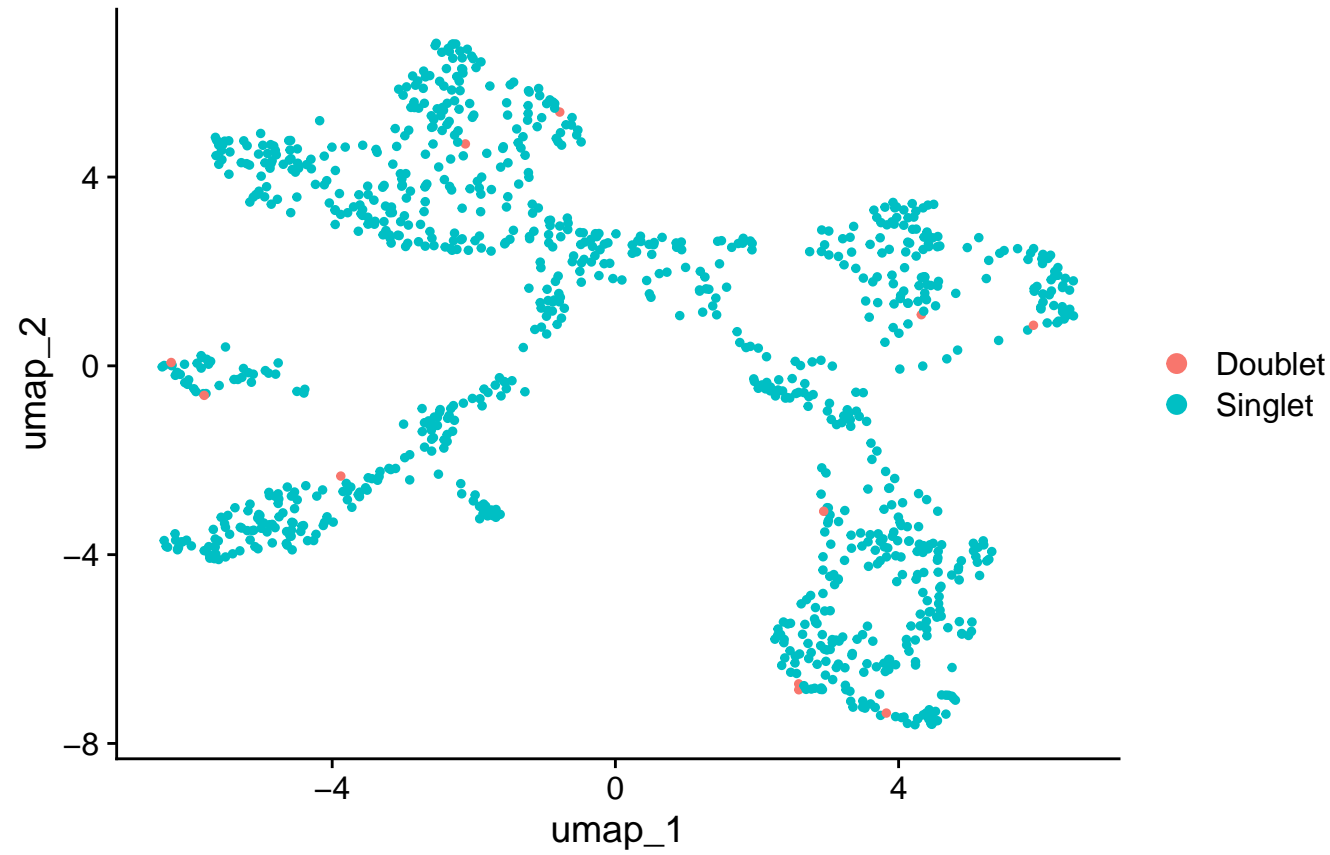

rank > optimal_pcs_calculated

a FALSE

a TRUE

	res_vals	num_clusters	avg_sil_vals
1	0.1	4	0.357559678208044
2	0.4	6	0.3368018801232
3	0.6	10	0.2726413631018
4	0.5	9	0.259807083457976
5	0.7	11	0.258822211095107
6	0.8	12	0.254756488557545
7	1.1	13	0.237340006269029

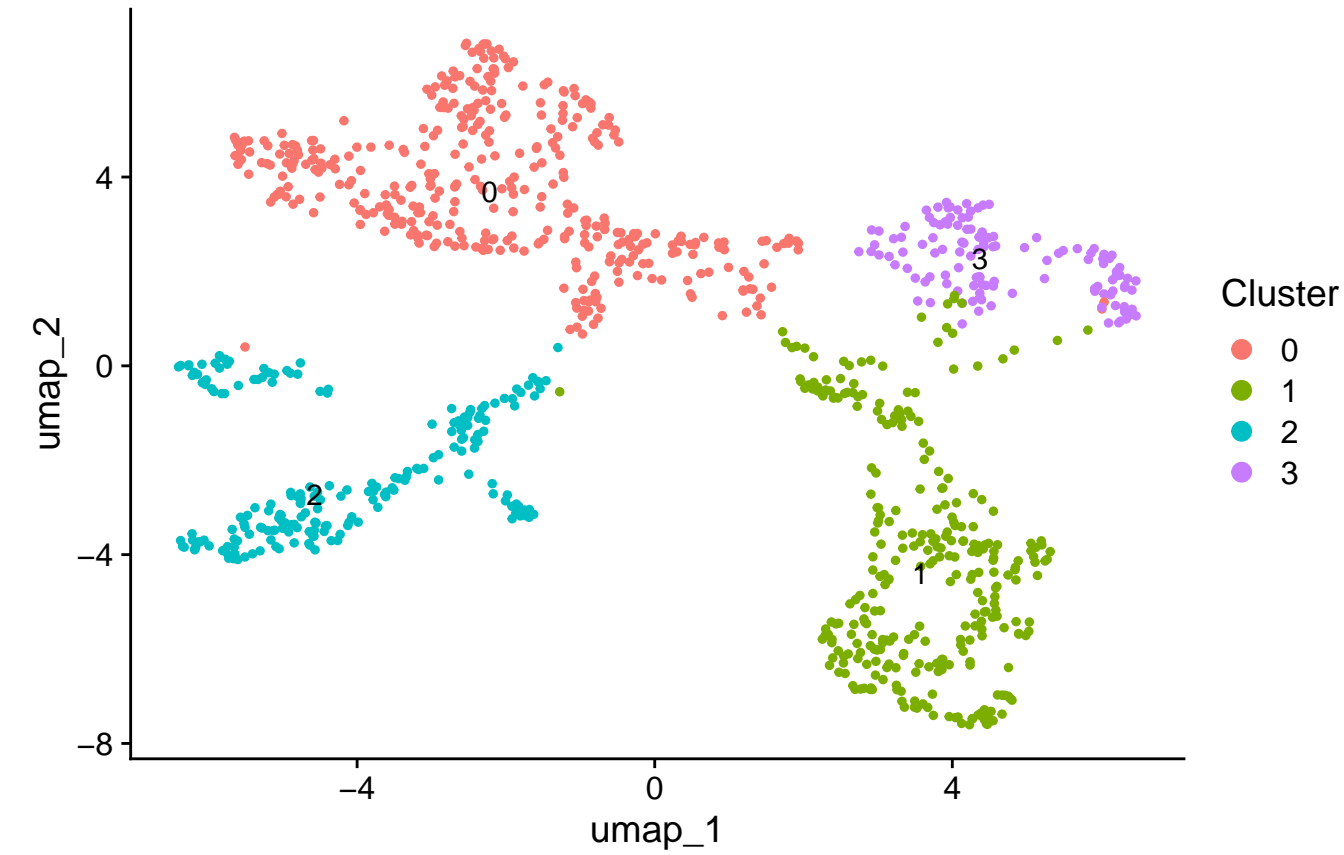org_6C – Clustering Resolution Tree

org_6C: Clustree

org_6C – UMAP & Doublet Removal

org_6C: Doublets Detected

org_6C: Final UMAP

	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	35880.0	8828	11
2	Singlet	15678.5	5288	1020

org_6C – QC Metrics & Cell Cycle on UMAP