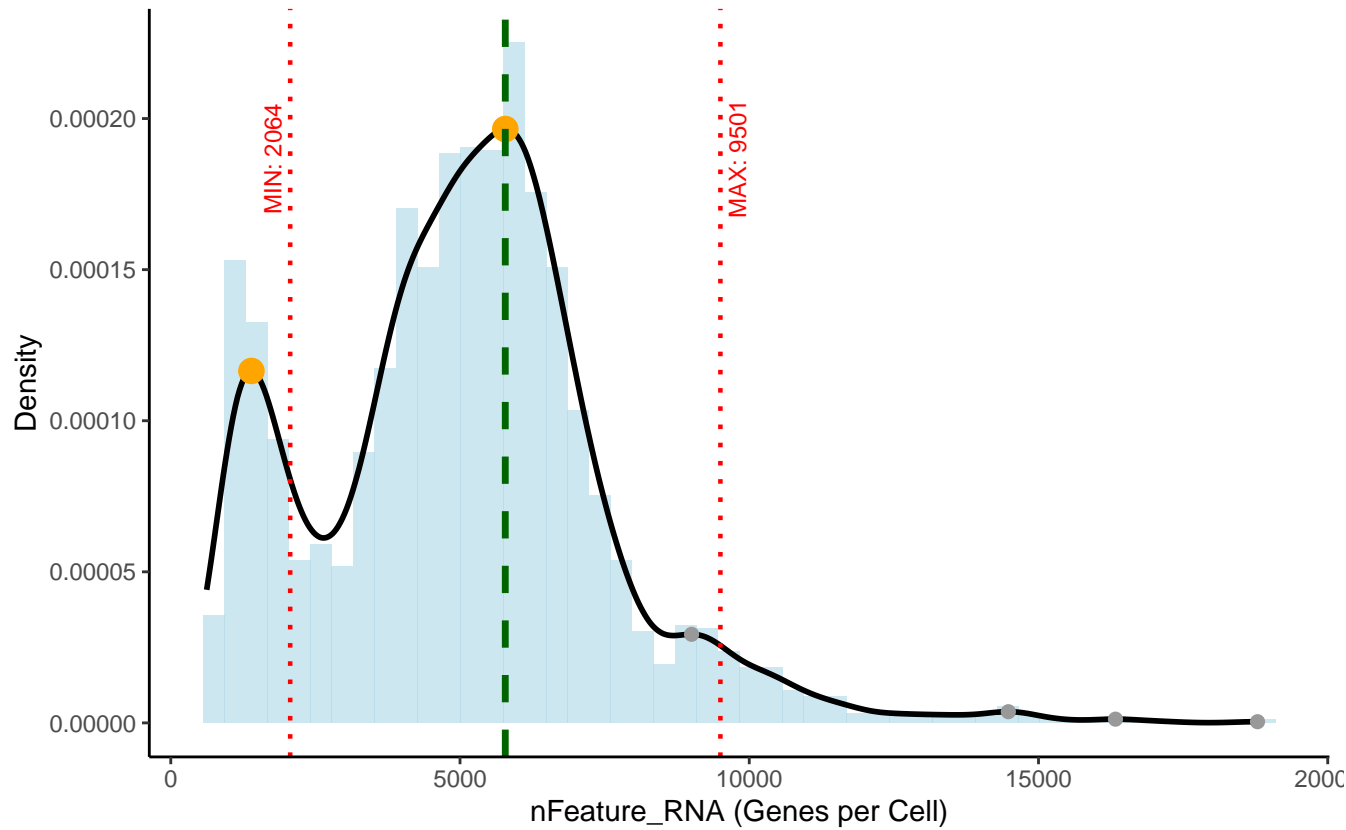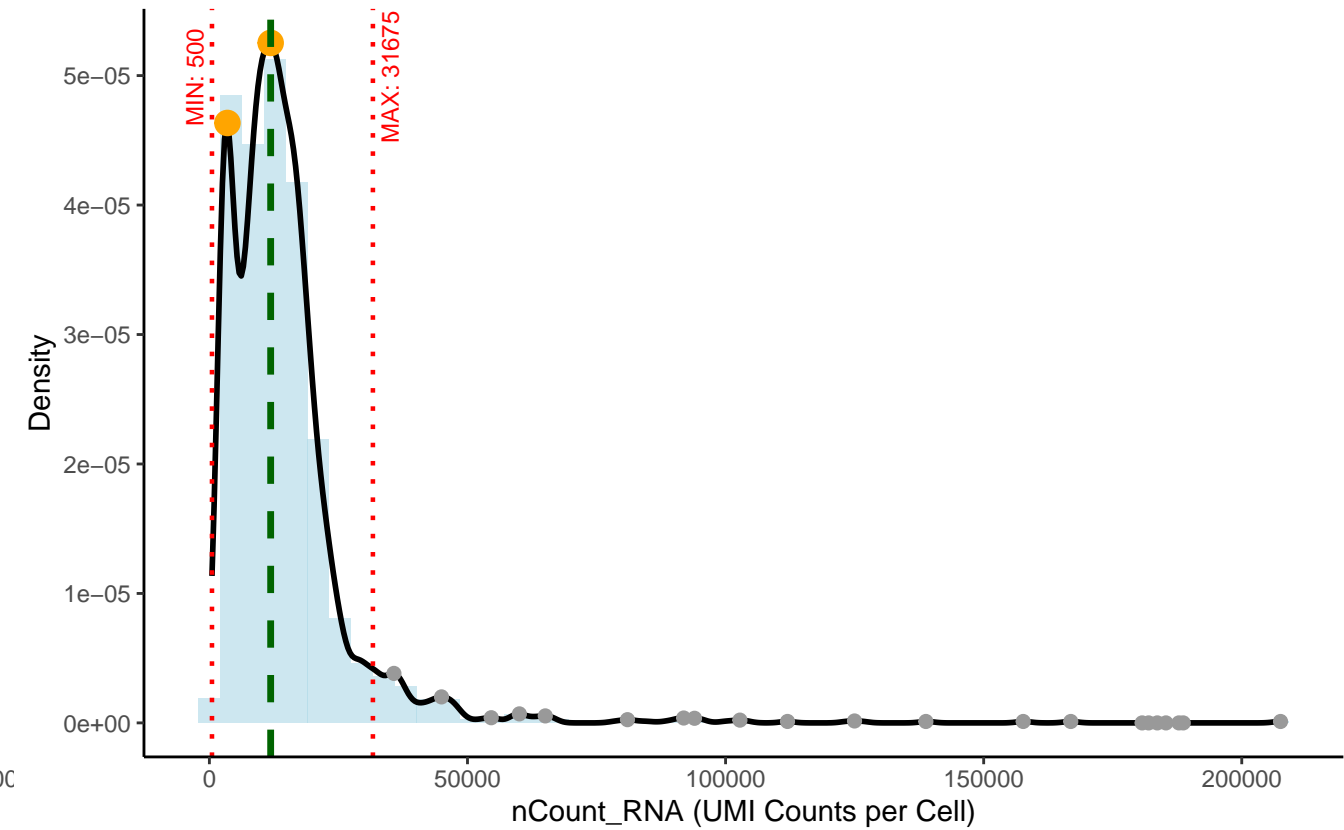# org_3C – Adaptive Threshold Determination

org_3C: nFeature_RNA (Genes per Cell) Distribution
Method: peak | Selected peak: 5782.6 | Total peaks: 6 | Top 2 peaks used

org_3C: nCount_RNA (UMI Counts per Cell) Distribution
Method: peak | Selected peak: 11870.8 | Total peaks: 23 | Top 2 peaks used

| Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
ature_RNA	peak	5783	6	5783, 1394	2479	2064	9501
ount_RNA	peak	11871	23	11871, 3492	13203	500	31675

org_3C – Filtering Summary

org_3C: Genes Before Filtering | org_3C: Counts Before Filtering | org_3C: MT% Before Filtering
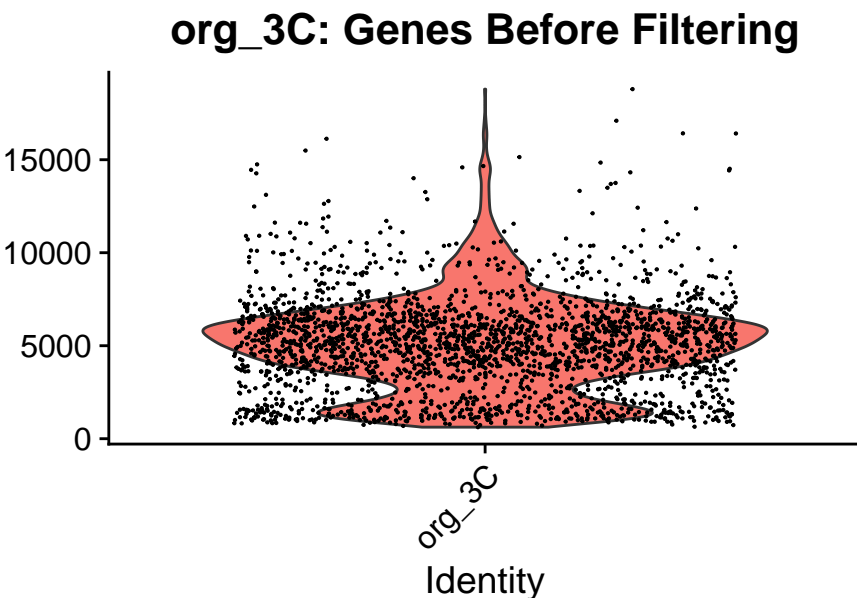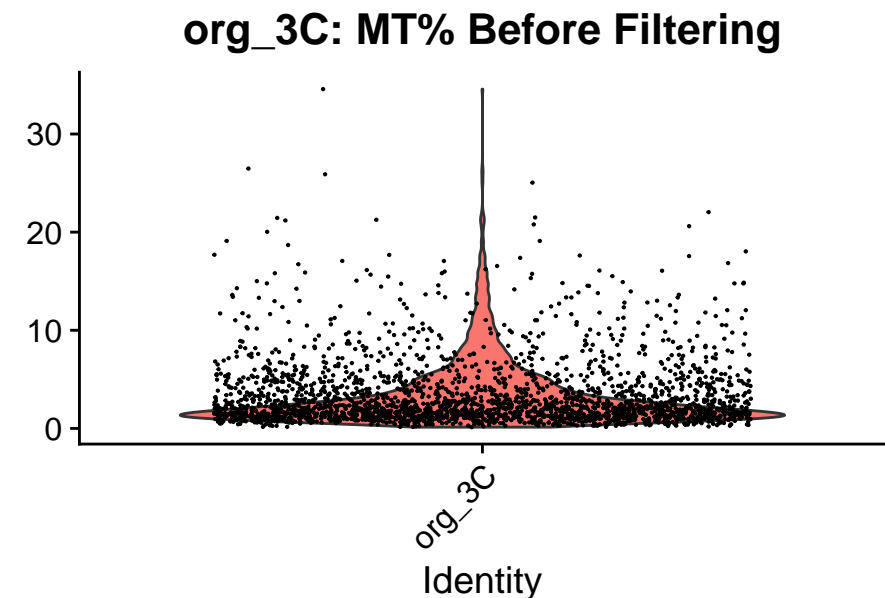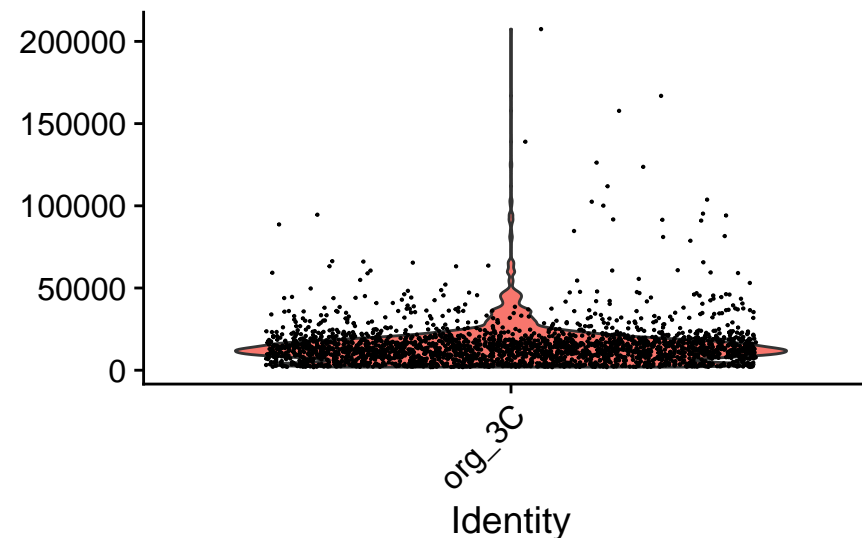
org_3C: Genes After Filtering | org_3C: Counts After Filtering | org_3C: MT% After Filtering
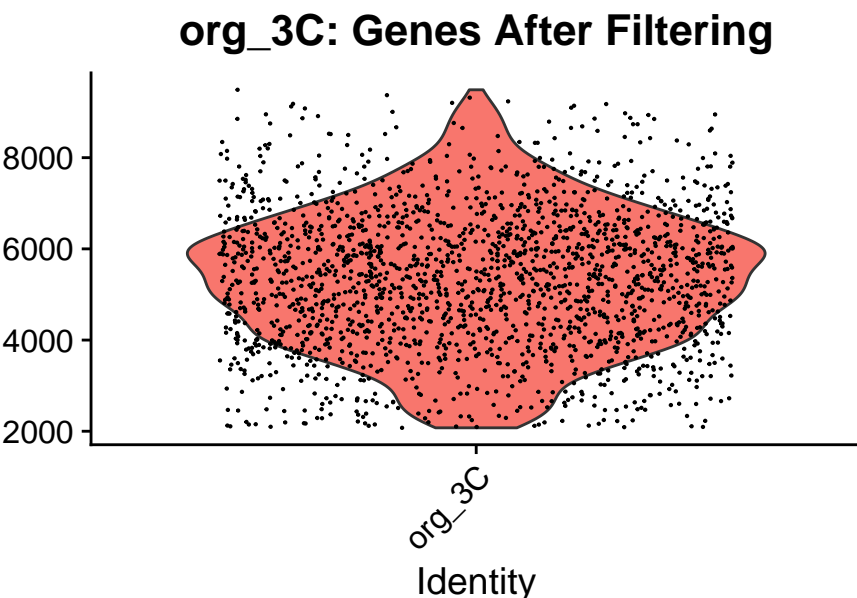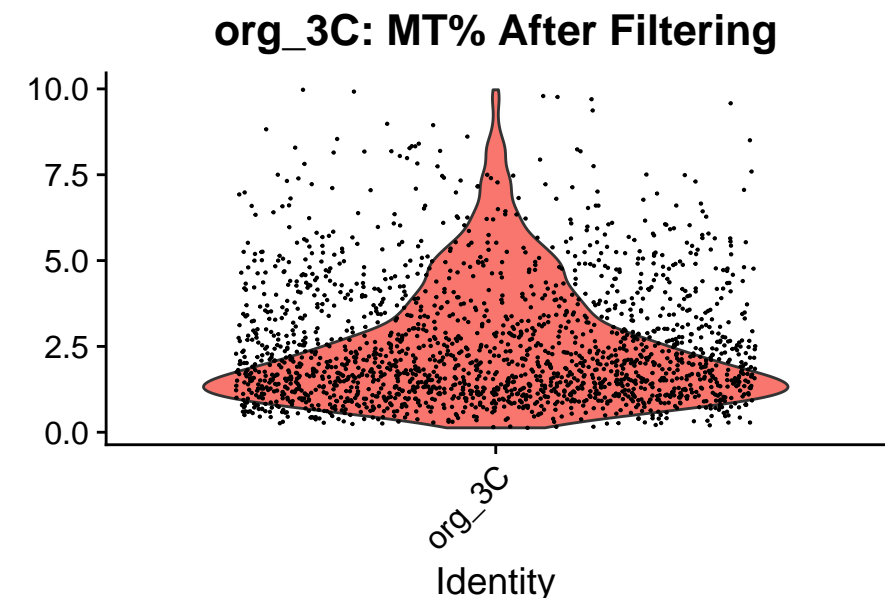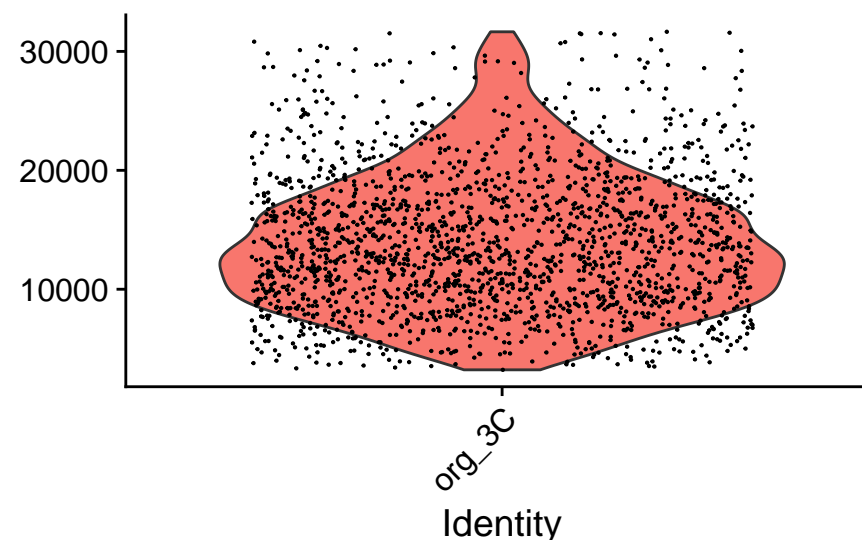
org_3C: Before Filtering | org_3C: After Filtering
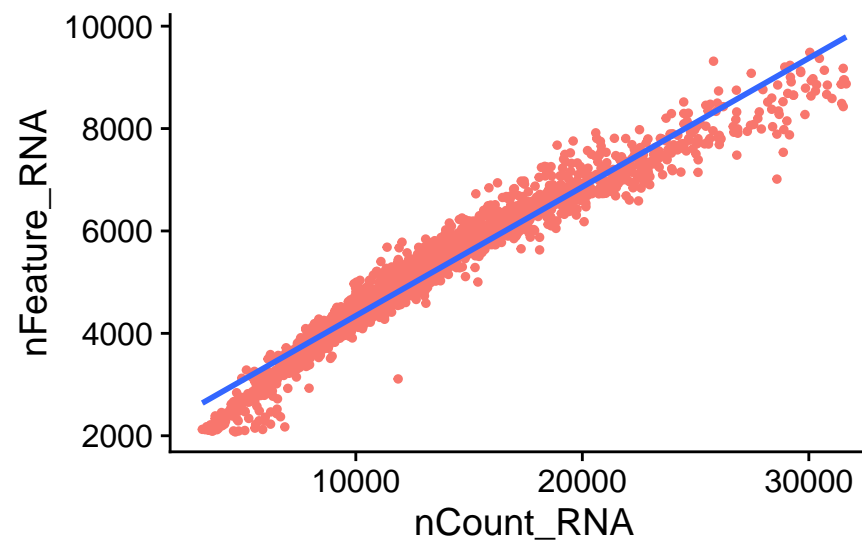
	Metric	Before	After
1	Cells	2504.00000	1961.000000
2	Genes	44412.00000	44412.000000
3	Median nCount	12433.50000	13282.000000
4	Median nFeature	5107.00000	5362.000000
5	Median MT%	2.18771	2.004686
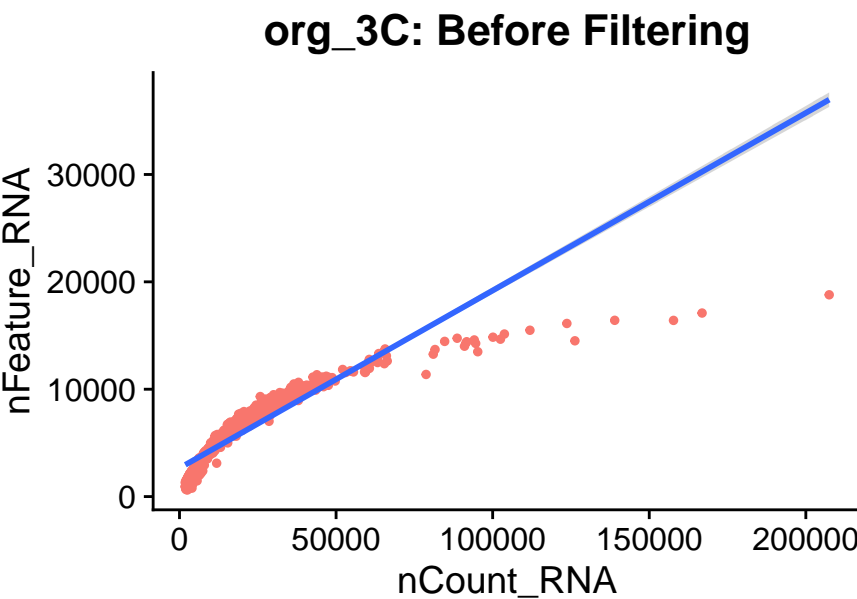
org_3C – Variable Features & Cell Cycle
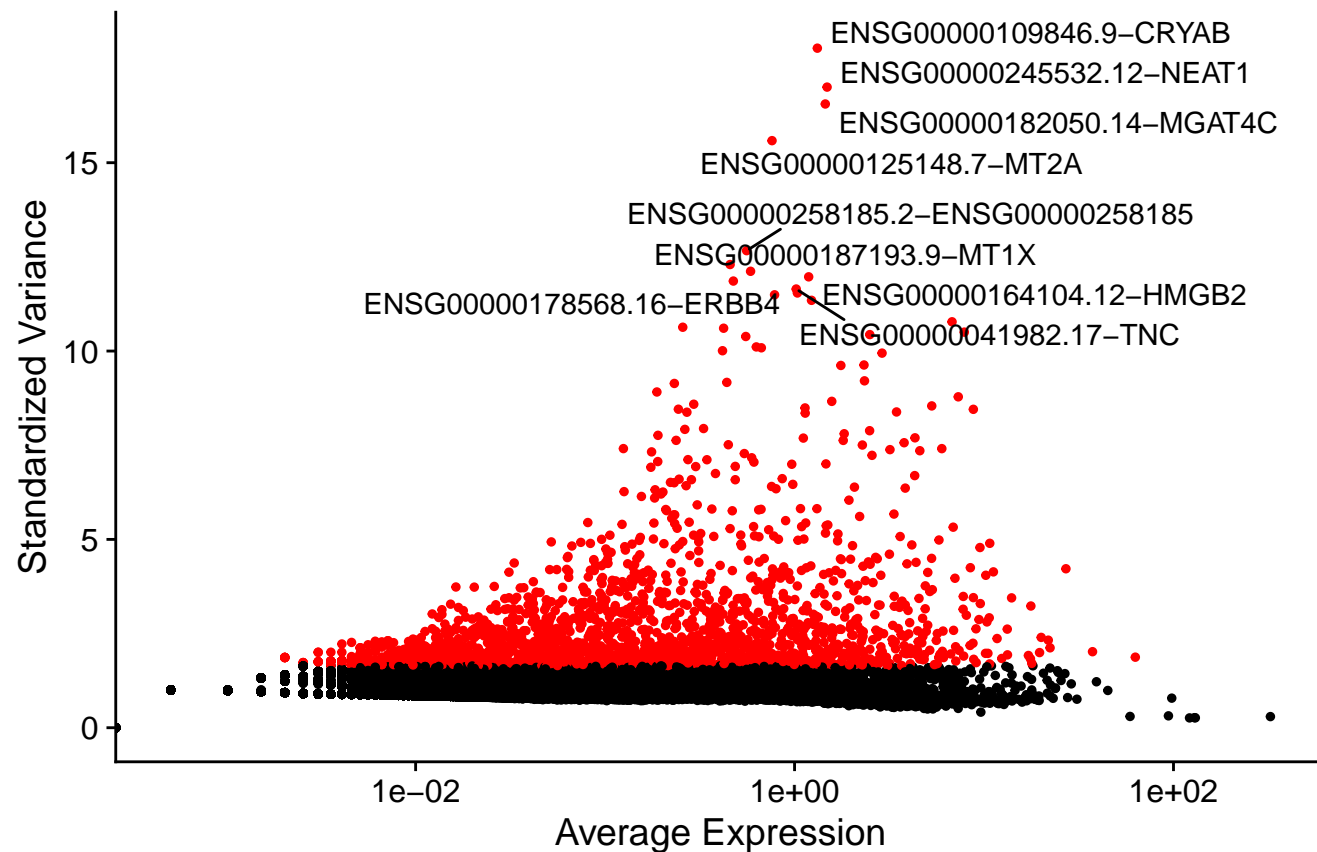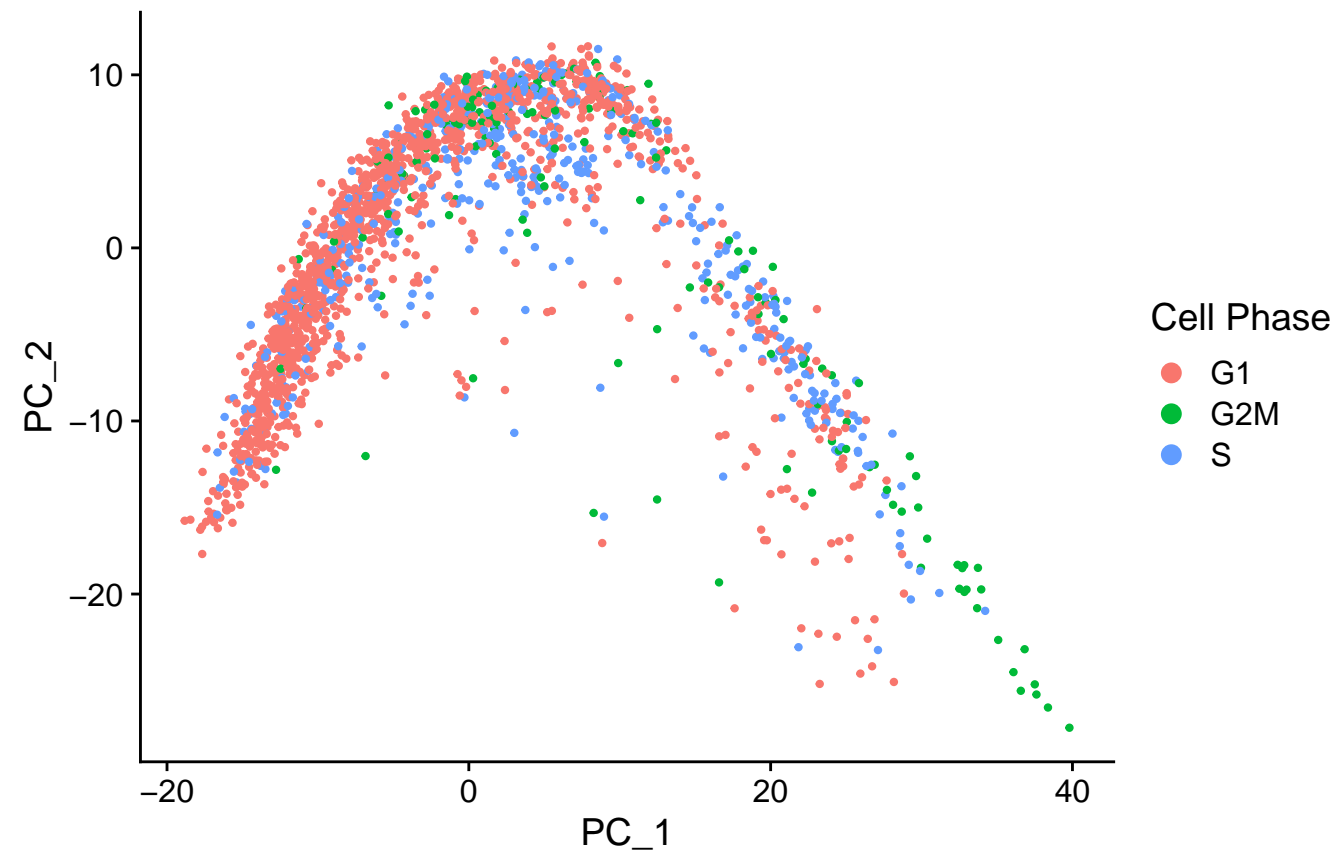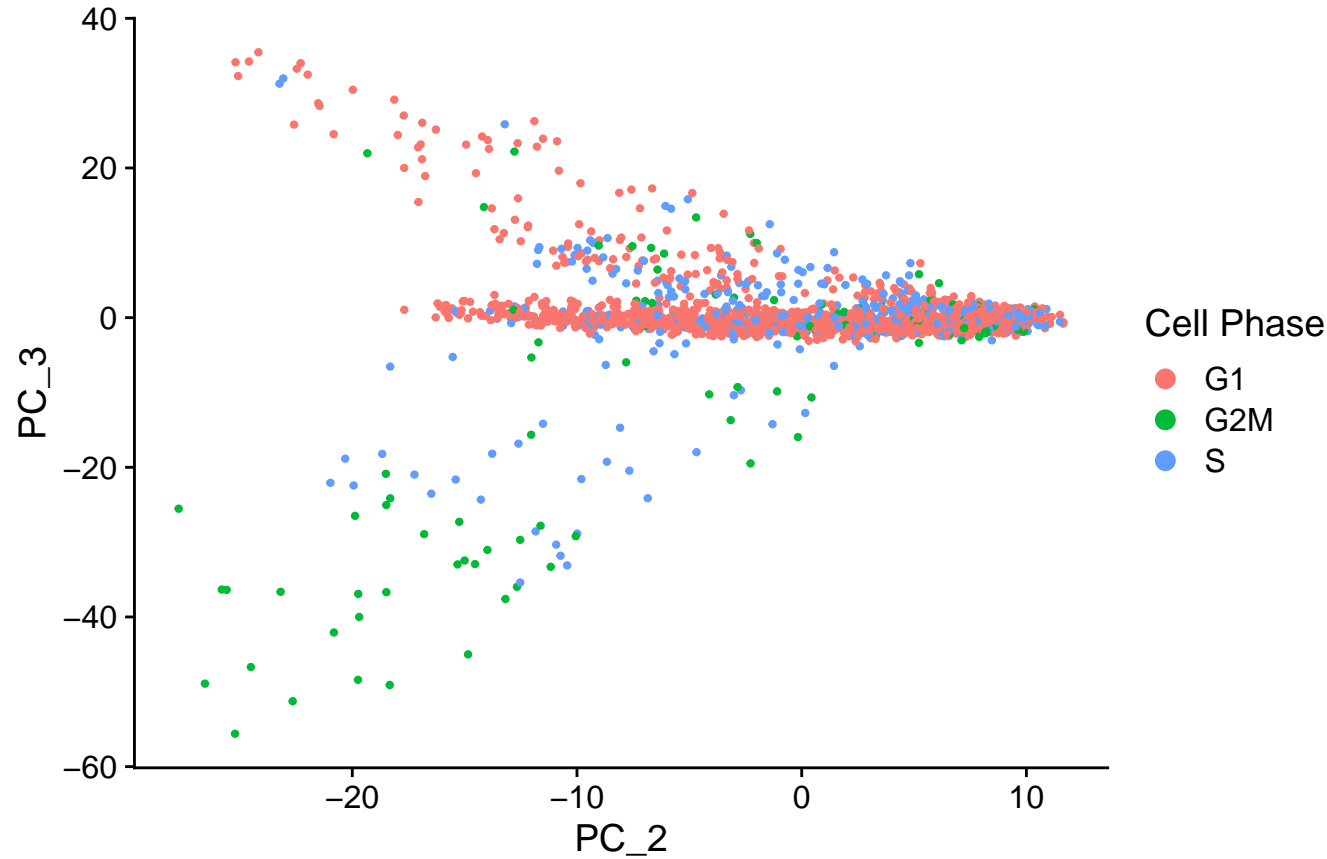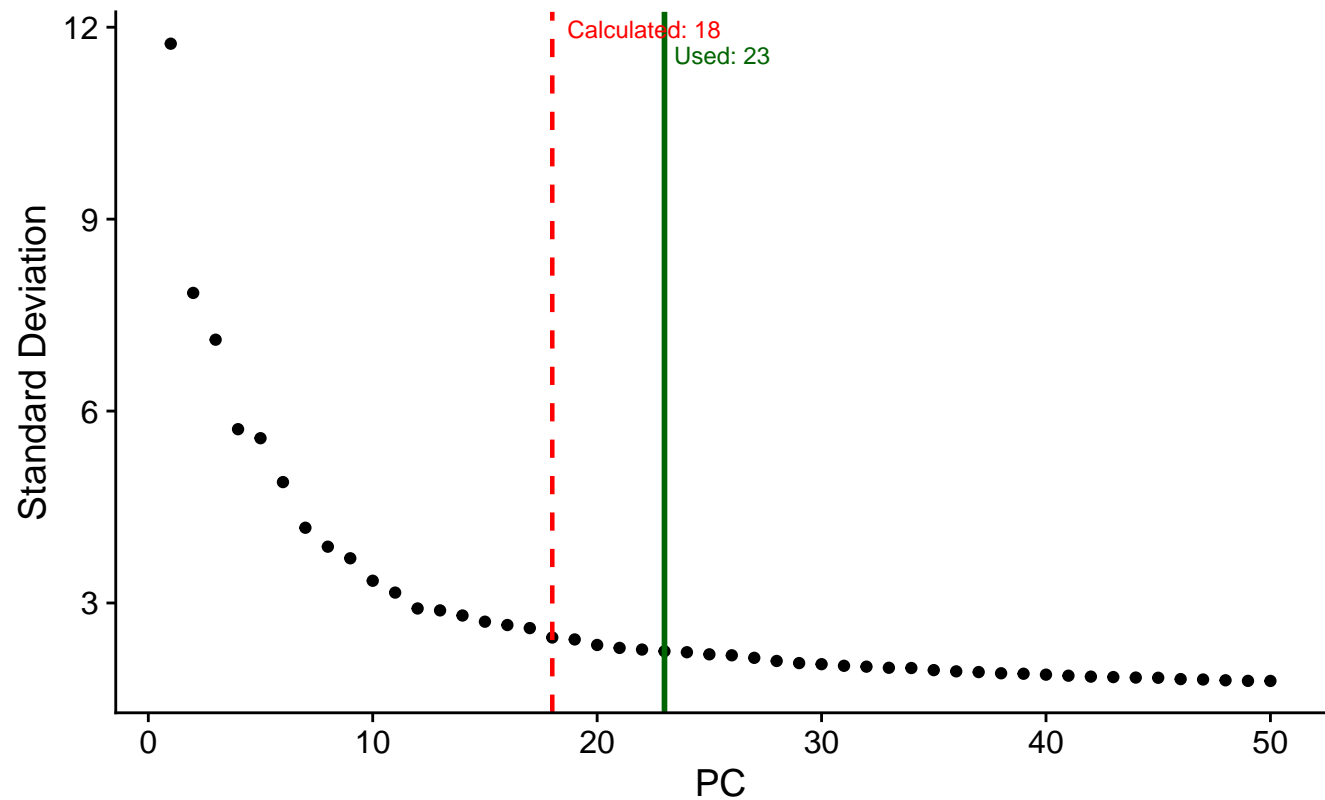
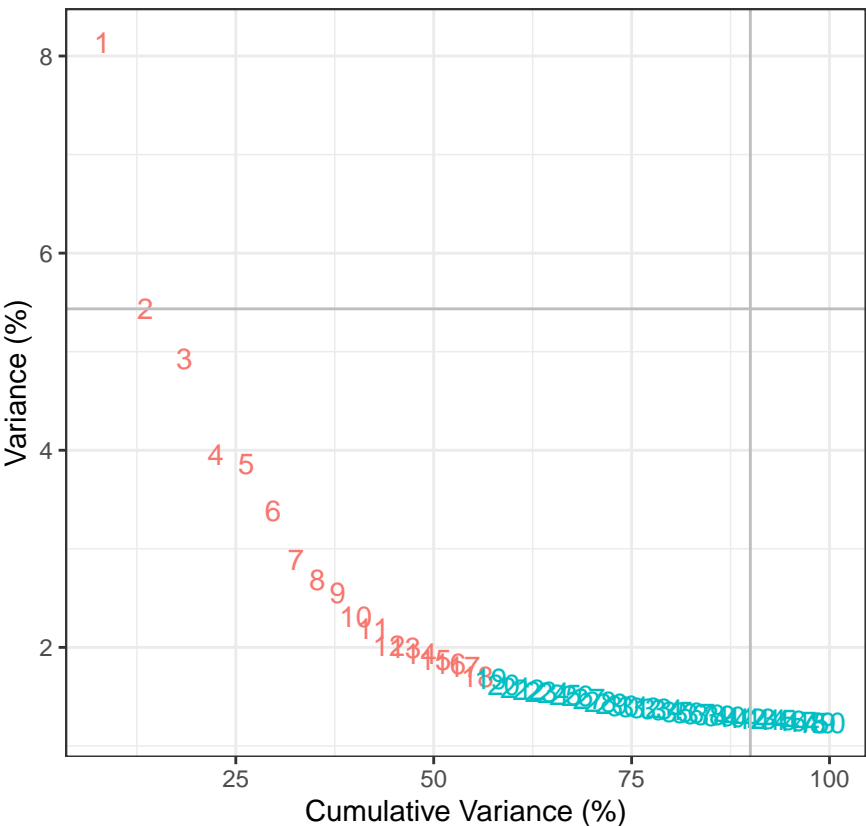# org_3C – PCA Selection & Silhouette Analysis

org_3C: Elbow Plot
Calculated: 18 PCs | Used: 23 PCs (+5)

org_3C: Quantitative PC Selection
Calculated: 18 PCs | Used: 23 PCs (+5)
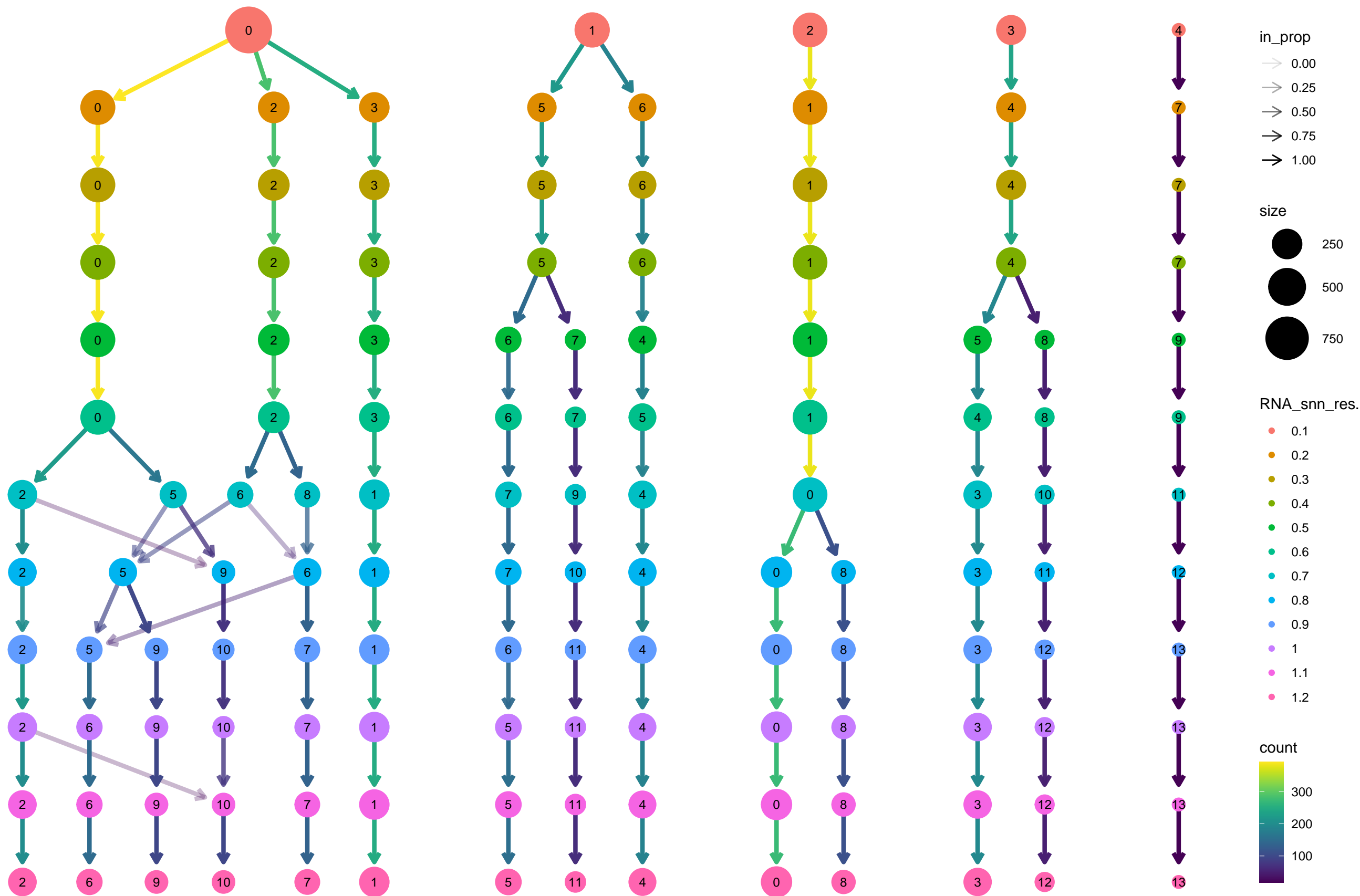

rank > optimal_pcs_calculated

a FALSE

a TRUE

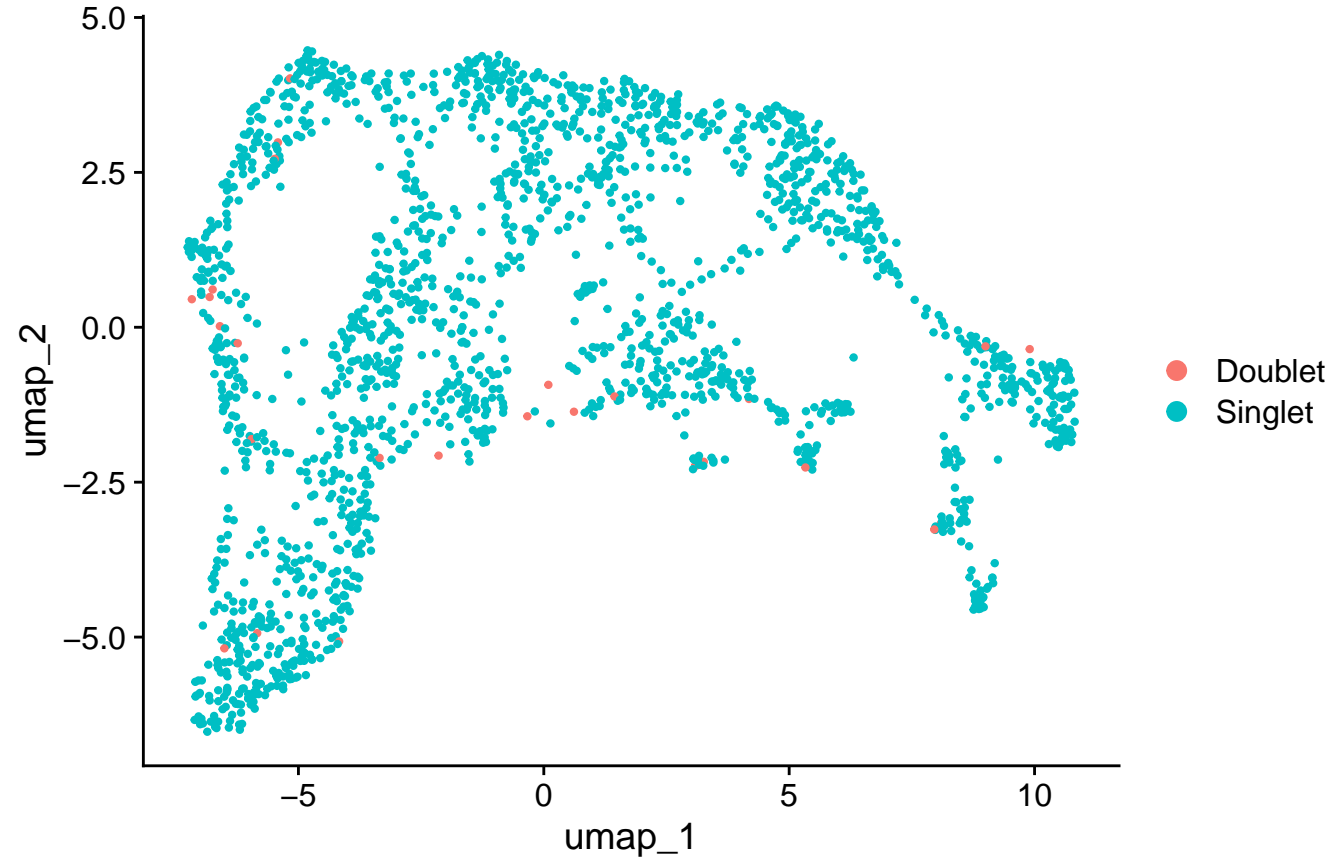|	res_vals	num_clusters	avg_sil_vals
1	0.5	10	0.300247569870767
2	0.7	12	0.266991612243595
3	0.8	13	0.238277368511831
4	0.9	14	0.235781557851224
5	0.2	8	0.233219503997527
6	0.1	5	0.0828500818707492

org_3C: Clustree

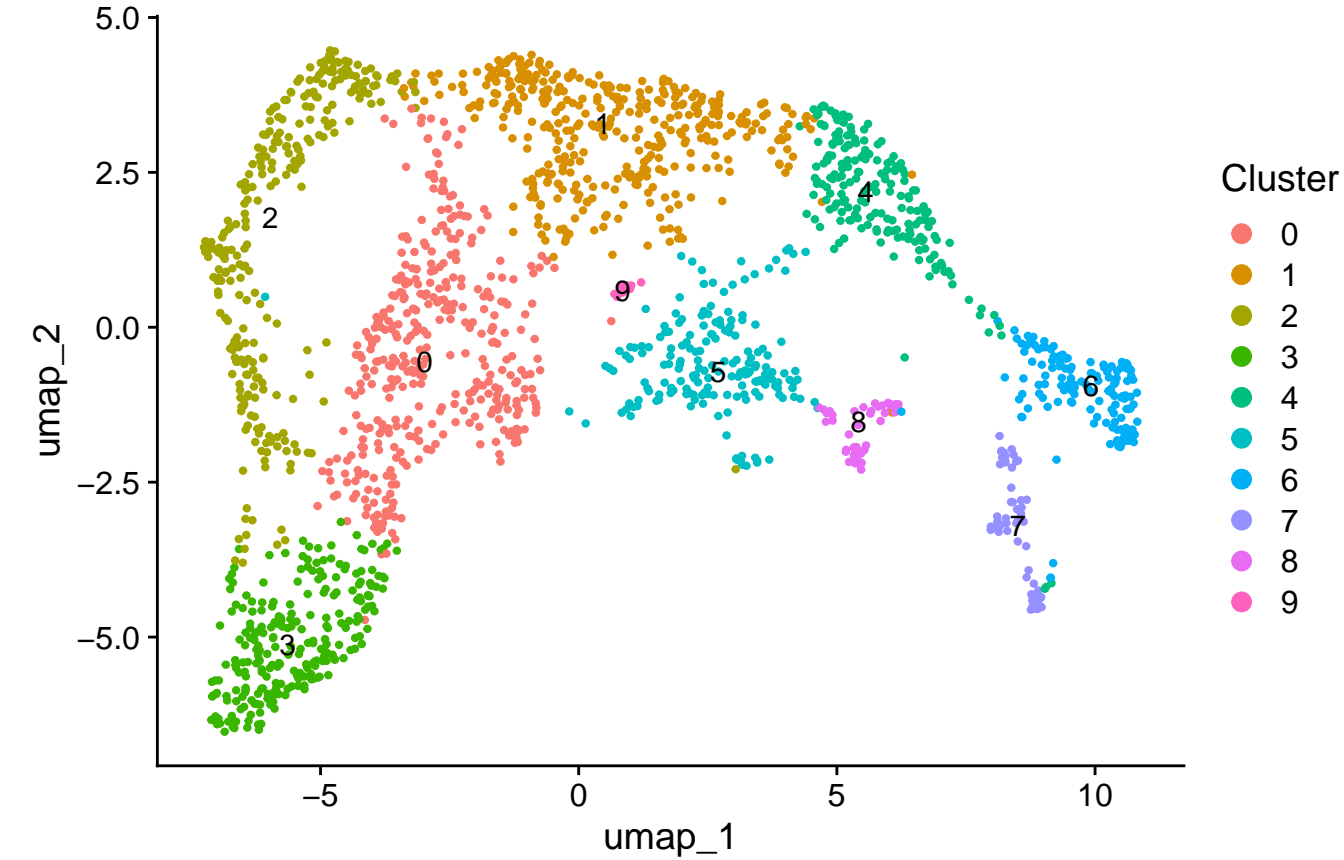org_3C – Clustering Resolution Tree

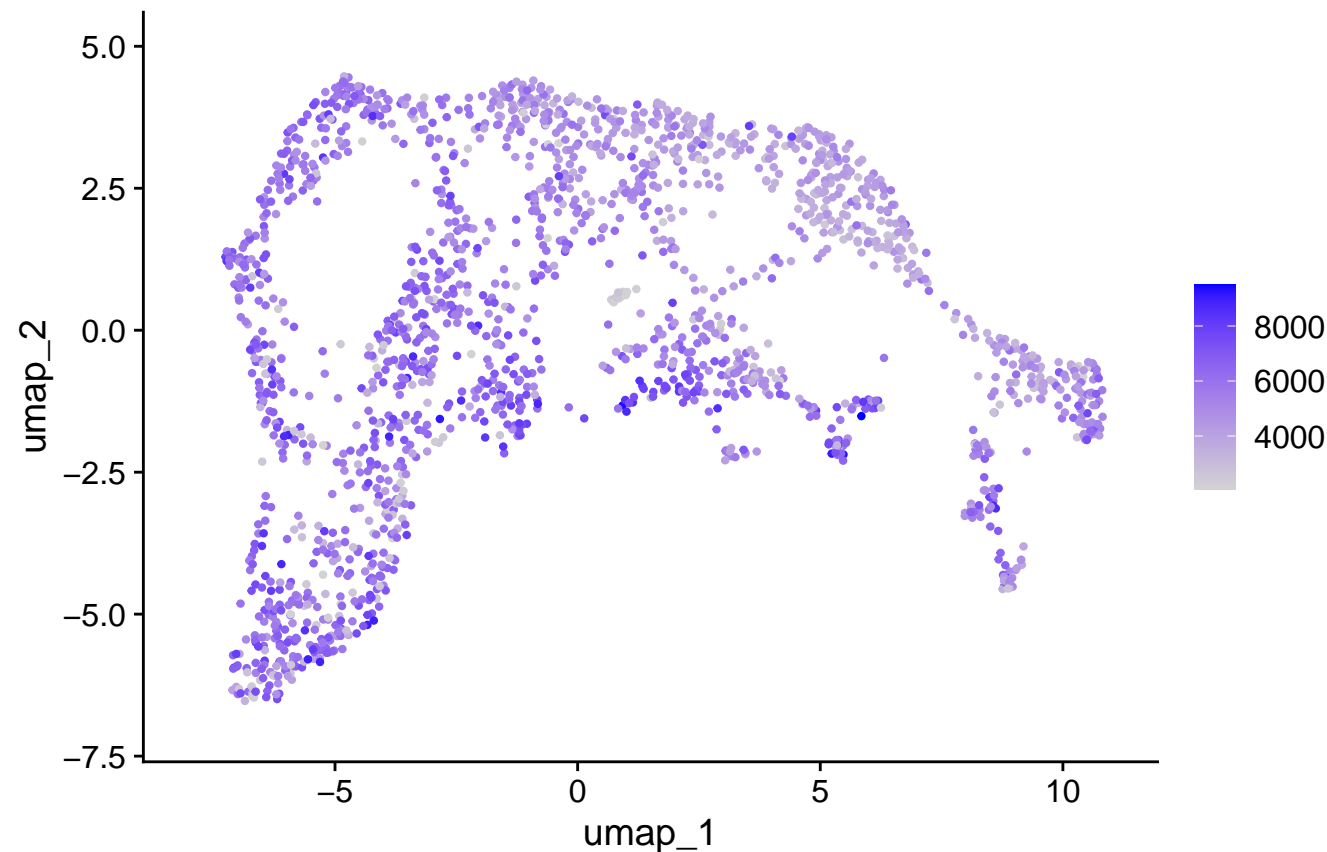# org_3C – UMAP & Doublet Removal
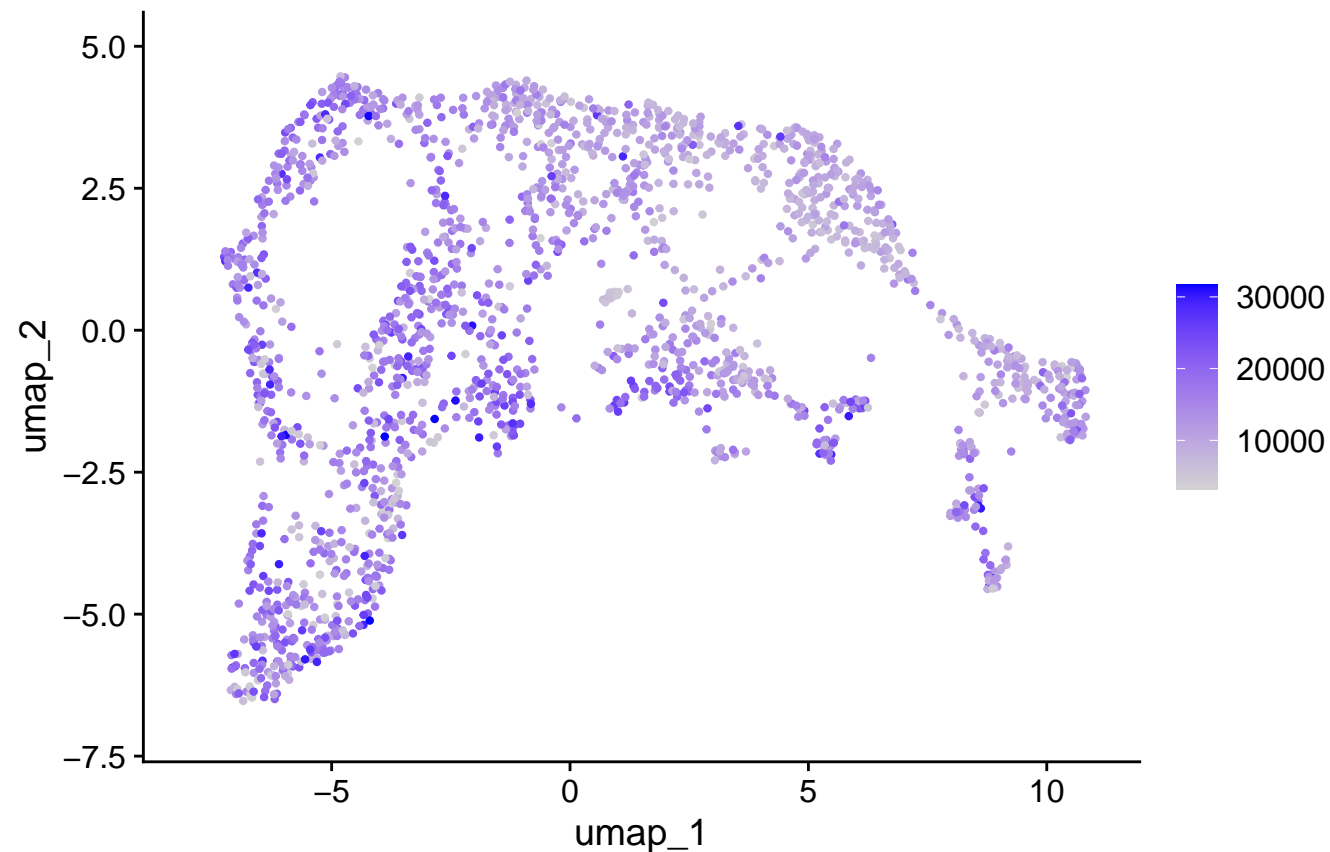
org_3C: Doublets Detected

org_3C: Final UMAP

	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	26815	8344.0	27
2	Singlet	13139	5331.5	1934

org_3C – QC Metrics & Cell Cycle on UMAP