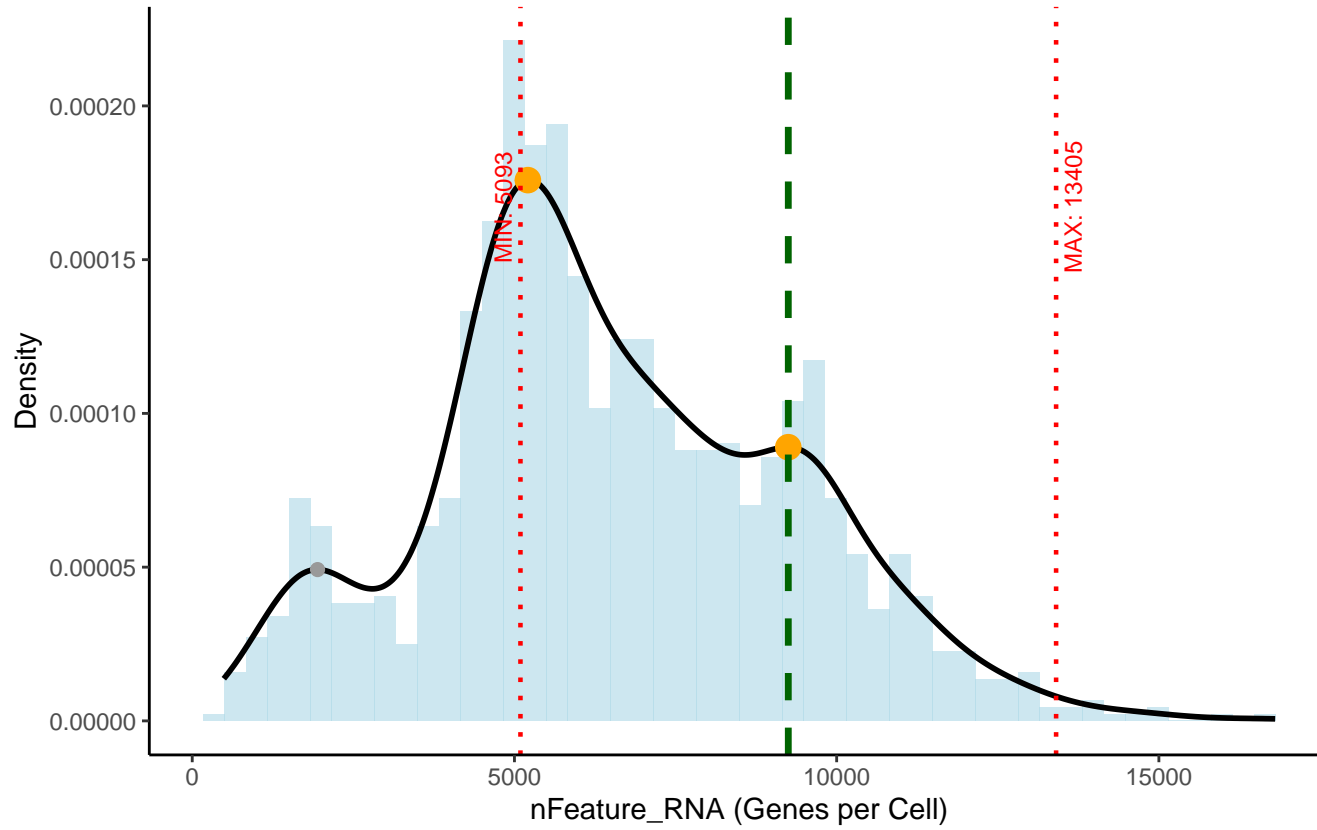# org_6B – Adaptive Threshold Determination

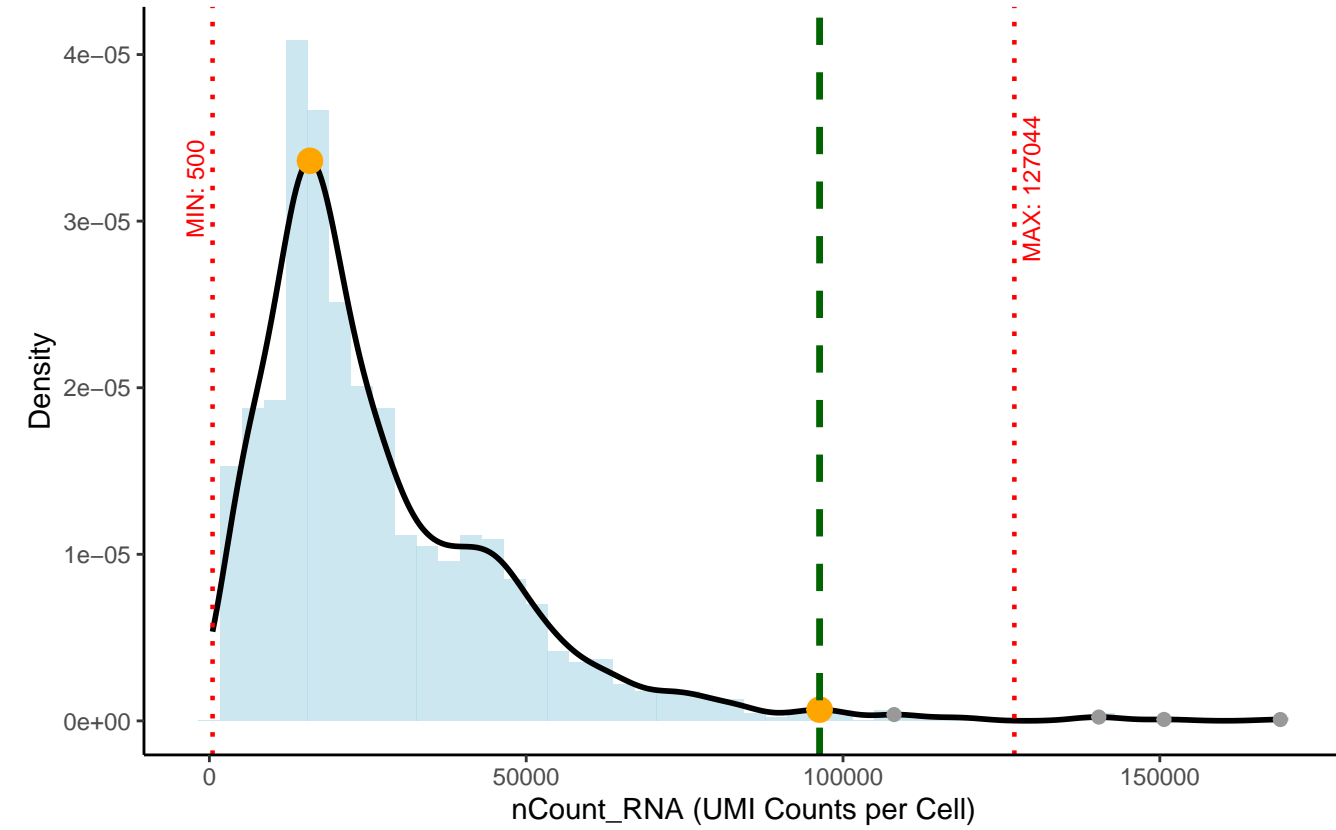## org_6B: nFeature_RNA (Genes per Cell) Distribution
Method: peak | Selected peak: 9249.2 | Total peaks: 3 | Top 2 peaks used

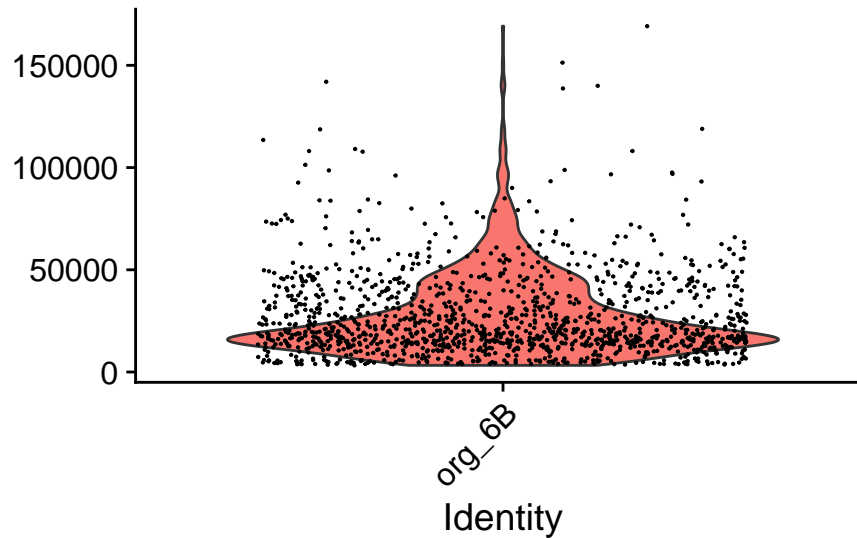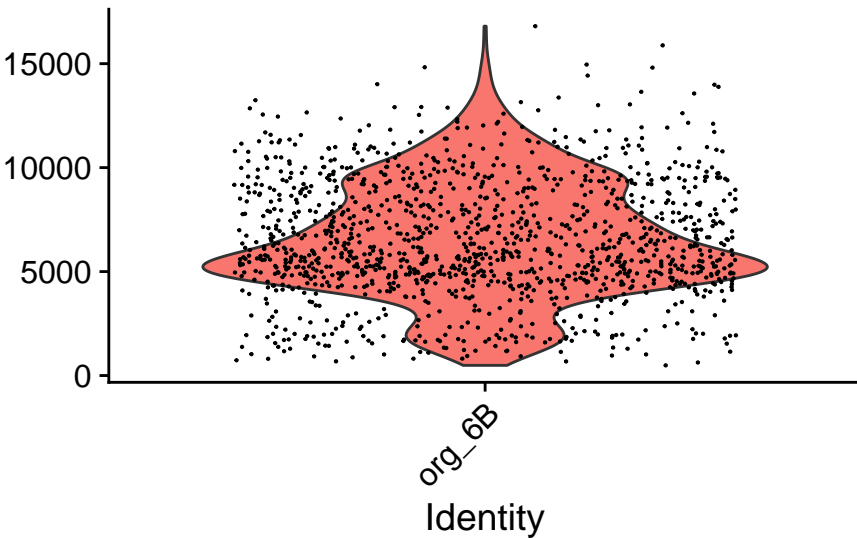## org_6B: nCount_RNA (UMI Counts per Cell) Distribution
Method: peak | Selected peak: 96306.6 | Total peaks: 6 | Top 2 peaks used
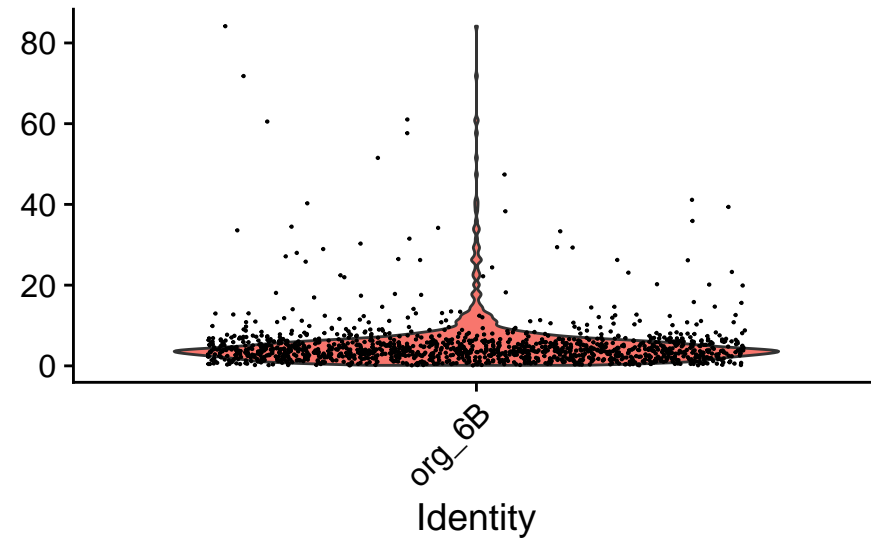

Metric	Method	Selected_Peak	Total_Peaks	Top2_Peaks	SD	MIN_Threshold	MAX_Threshold
ature_RNA	peak	9249	3	5208, 9249	2771	5093	13405
ount_RNA	peak	96307	6	15873, 96307	20492	500	127044

org_6B – Filtering Summary

org_6B: Genes Before Filtering — Identity: org_6B

org_6B: Counts Before Filtering — Identity: org_6B

org_6B: MT% Before Filtering — Identity: org_6B

org_6B: Genes After Filtering — Identity: org_6B
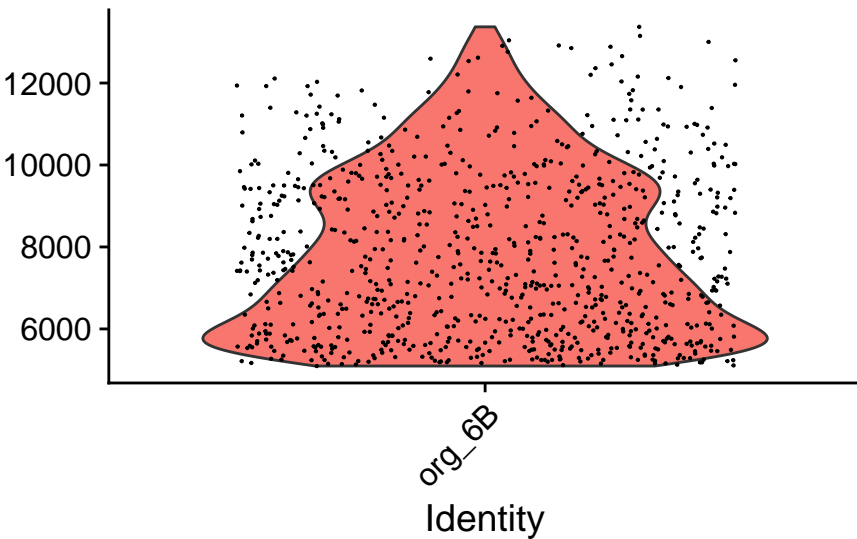
org_6B: Counts After Filtering — Identity: org_6B
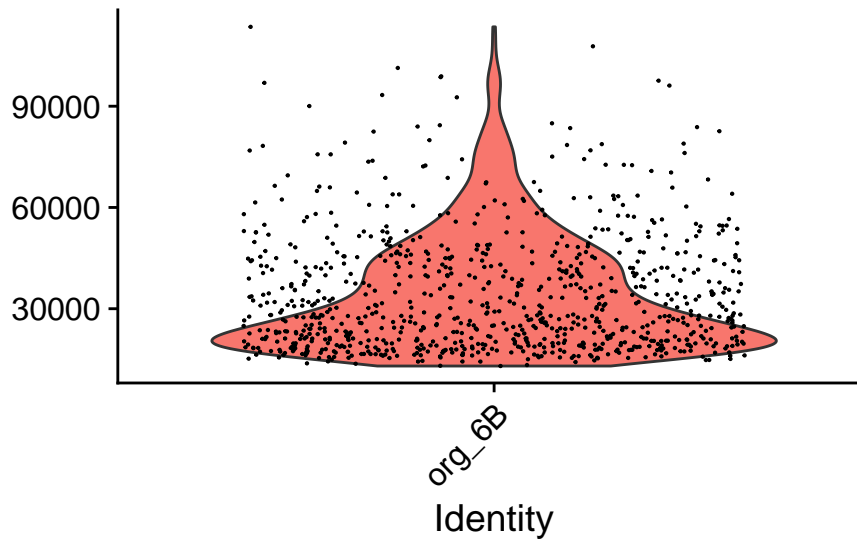
org_6B: MT% After Filtering — Identity: org_6B

org_6B: Before Filtering — nCount_RNA vs nFeature_RNA
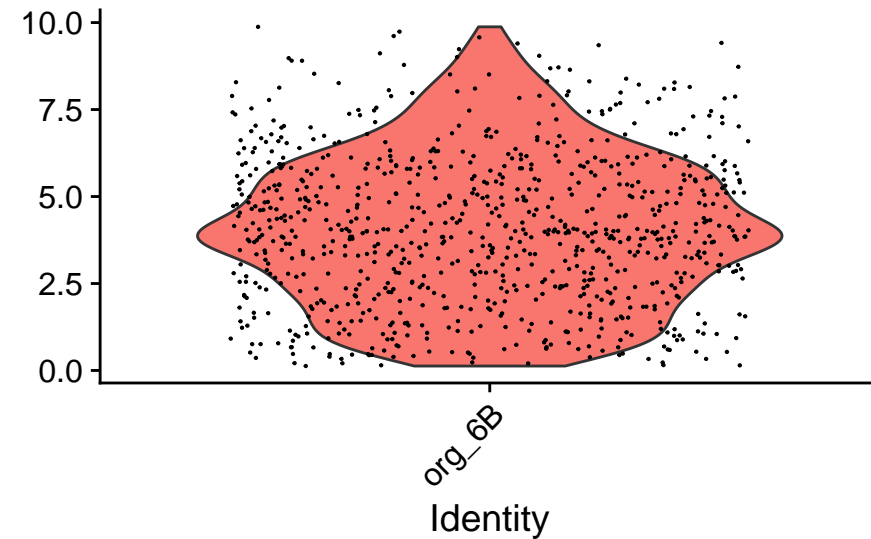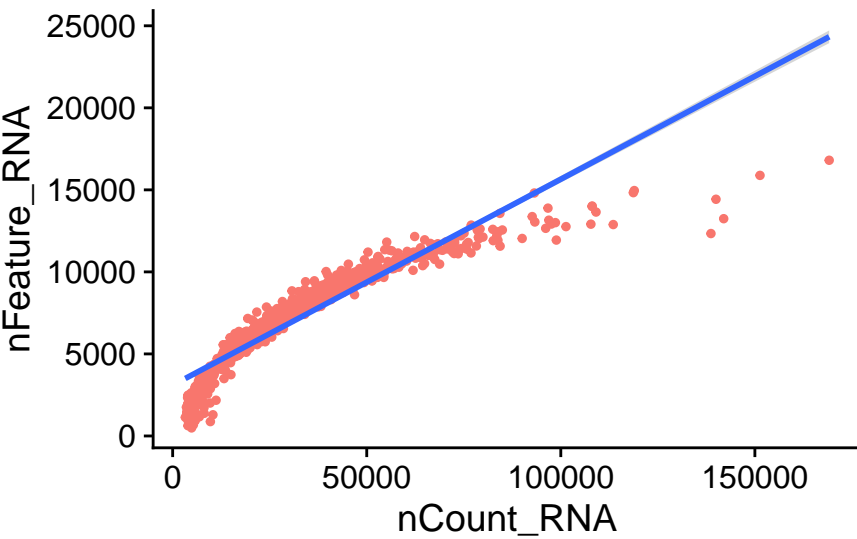
org_6B: After Filtering — nCount_RNA vs nFeature_RNA
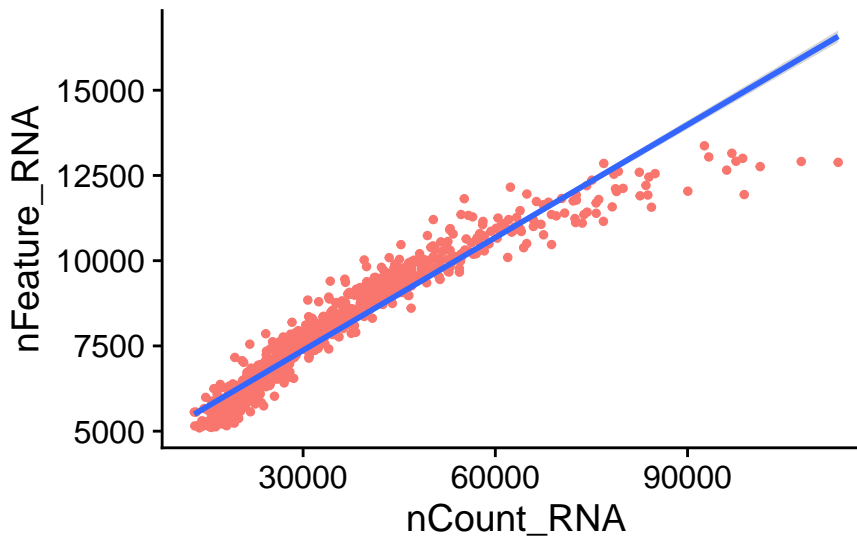
	Metric	Before	After
1	Cells	1331.000000	871.00000
2	Genes	42303.000000	42303.00000
3	Median nCount	20622.000000	28278.00000
4	Median nFeature	6085.000000	7463.00000
5	Median MT%	3.840036	3.97616

org_6B – Variable Features & Cell Cycle
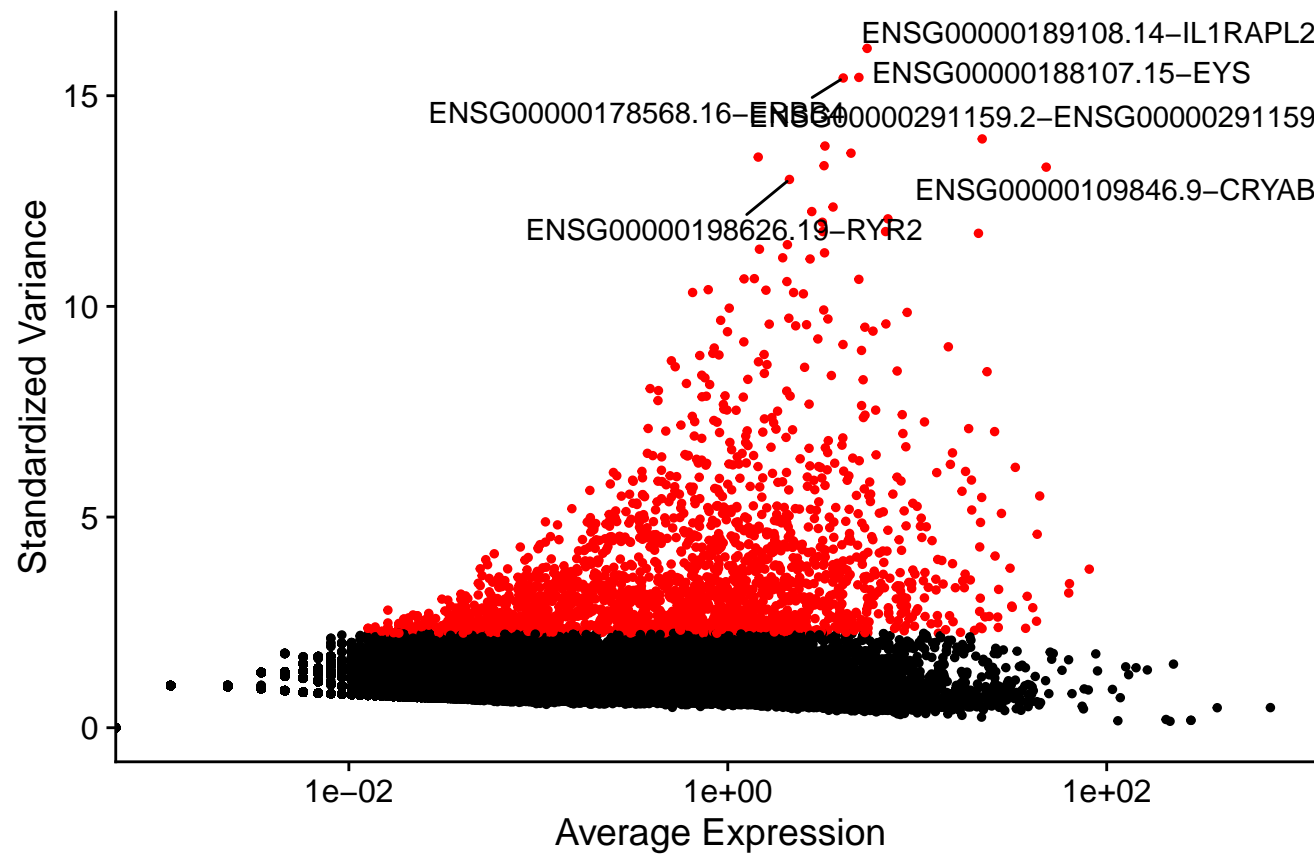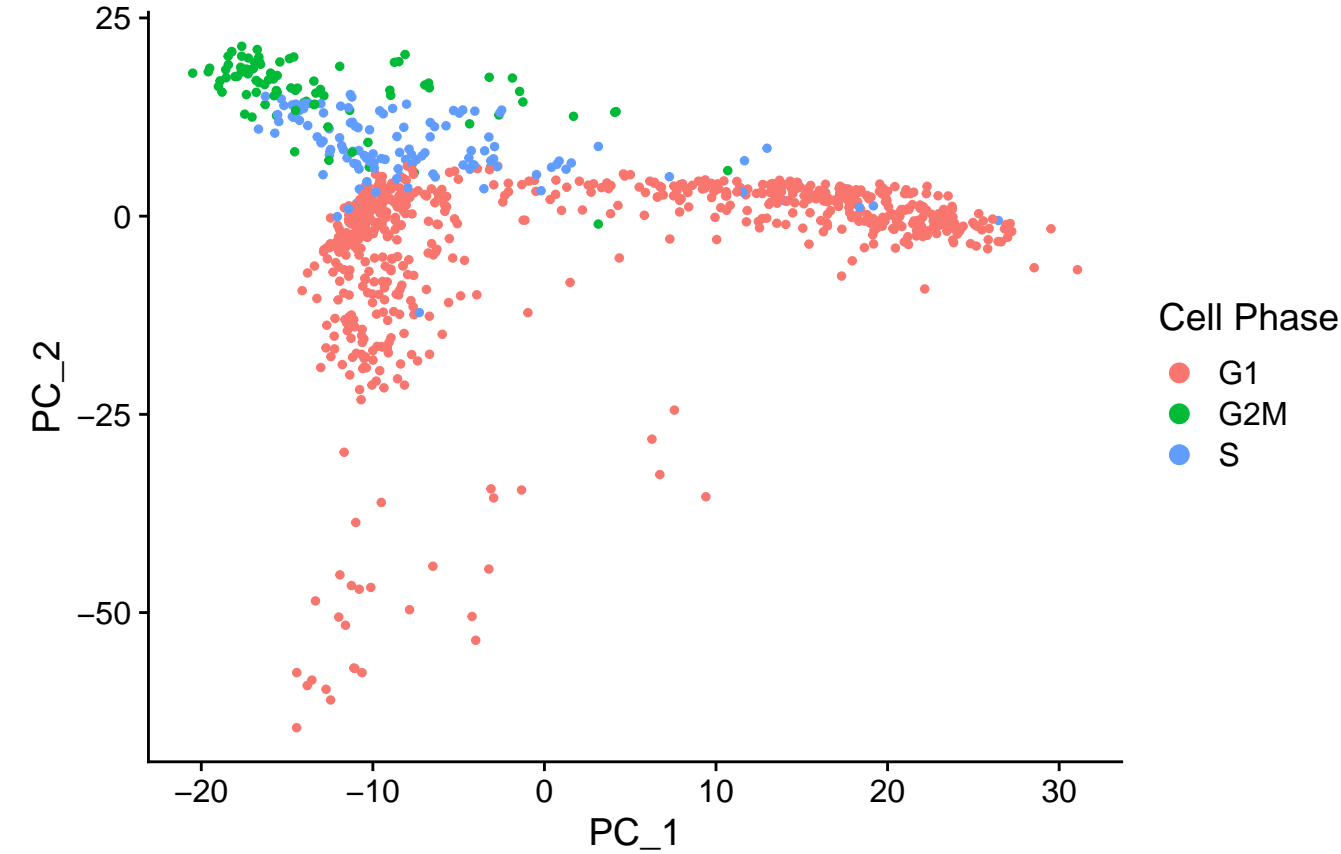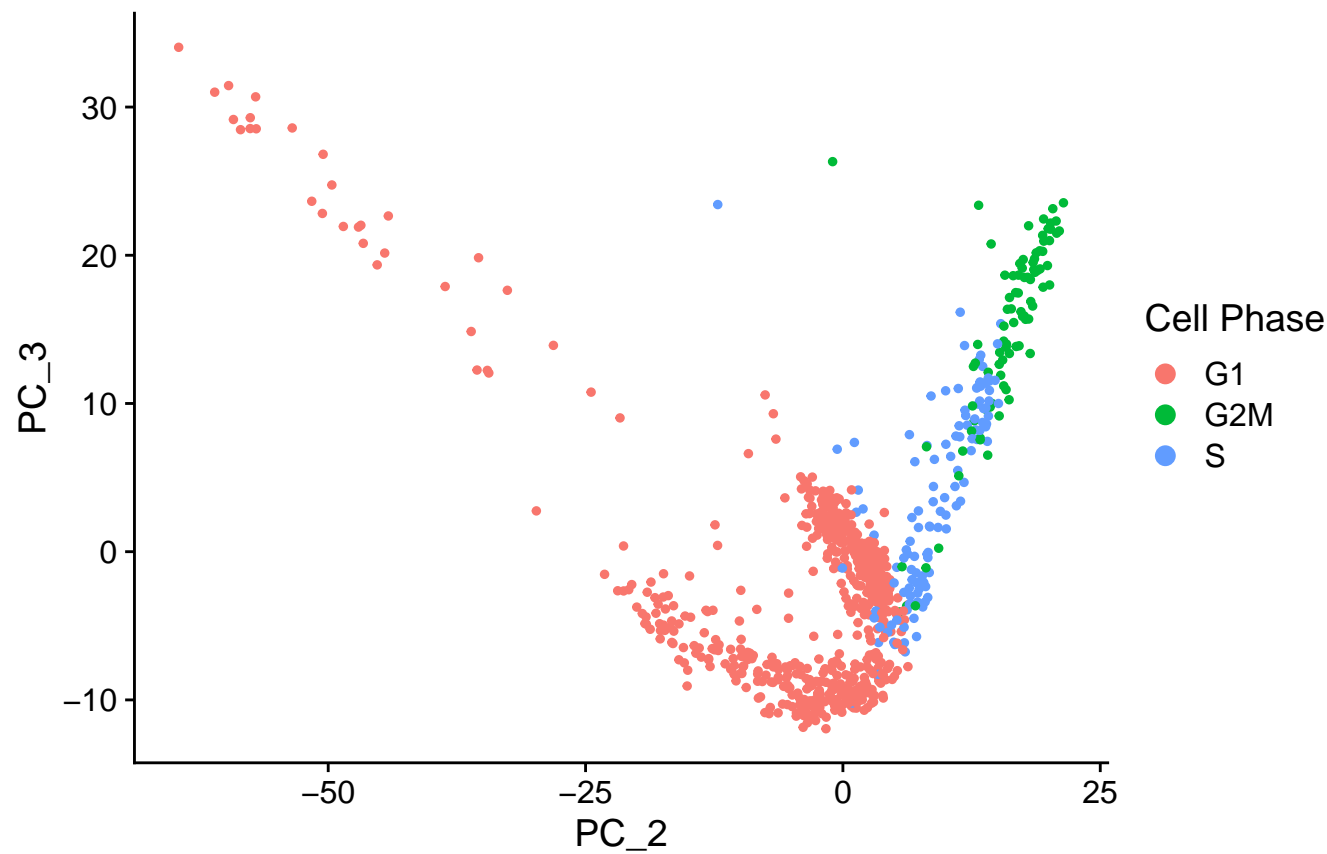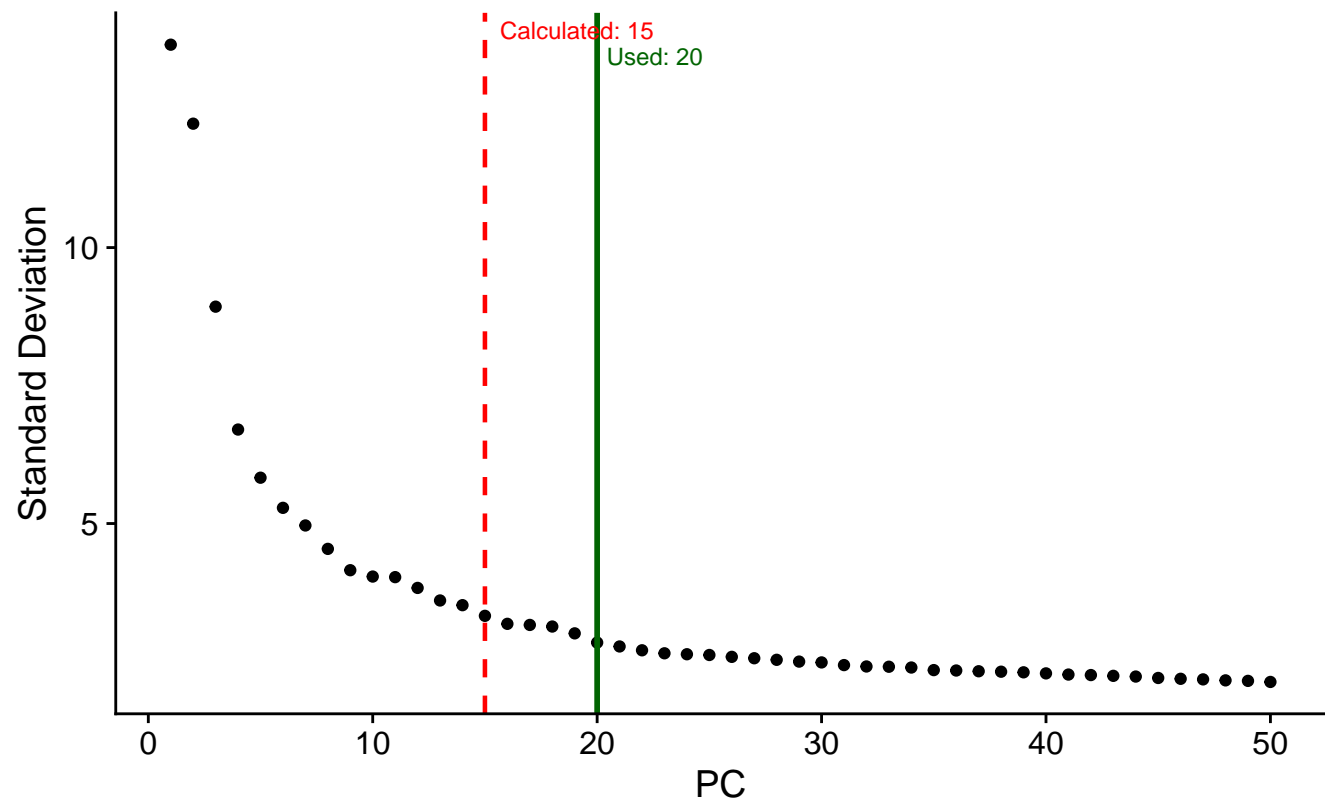
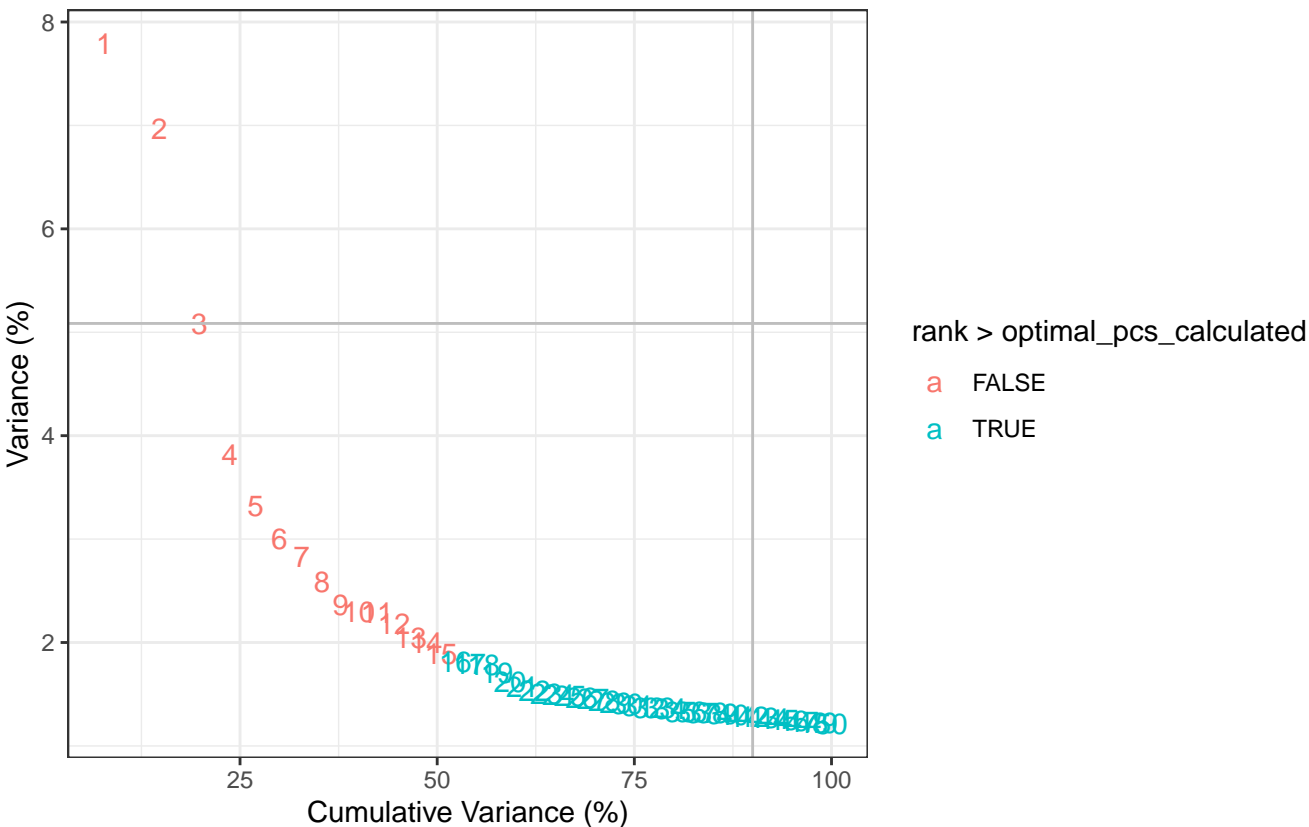# org_6B – PCA Selection & Silhouette Analysis

org_6B: Elbow Plot

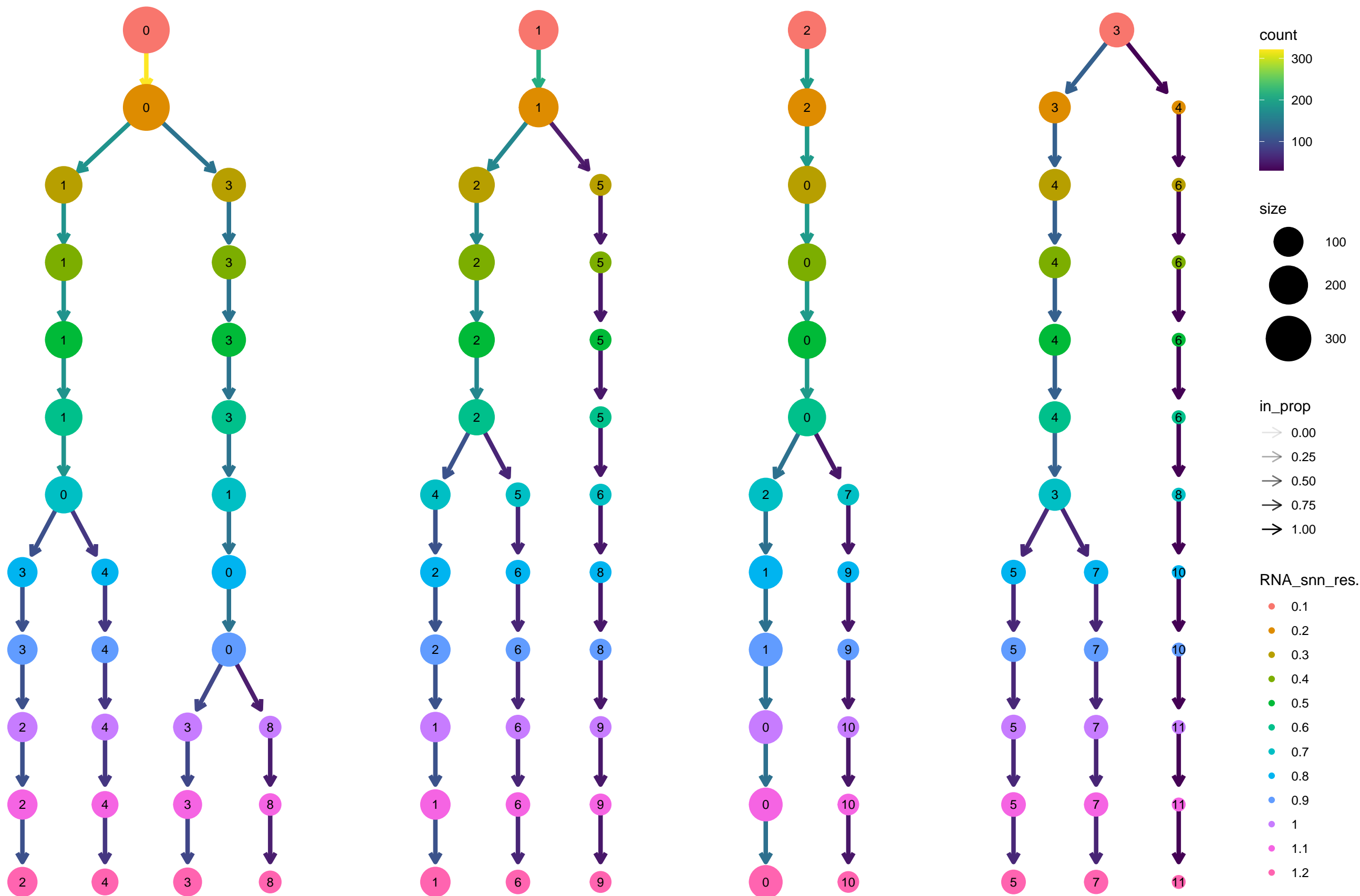Calculated: 15 PCs | Used: 20 PCs (+5)

org_6B: Quantitative PC Selection

Calculated: 15 PCs | Used: 20 PCs (+5)

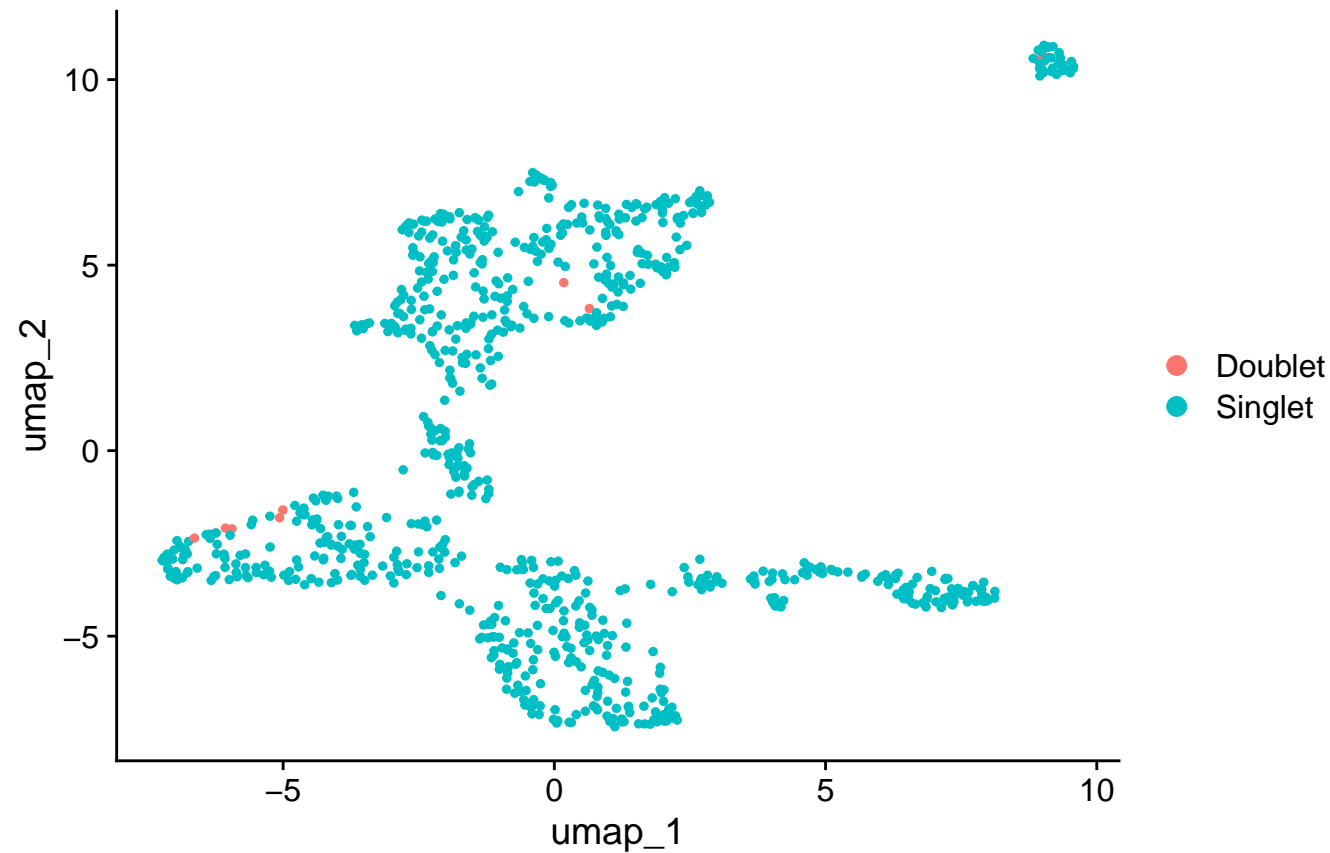|	res_vals	num_clusters	avg_sil_vals
1	0.2	5	0.358965114547919
2	0.3	7	0.324173651387618
3	0.1	4	0.314929461574948
4	0.7	9	0.2976305914547
5	1	12	0.278875154045644
6	0.9	11	0.261163338761591

org_6B: Clustree

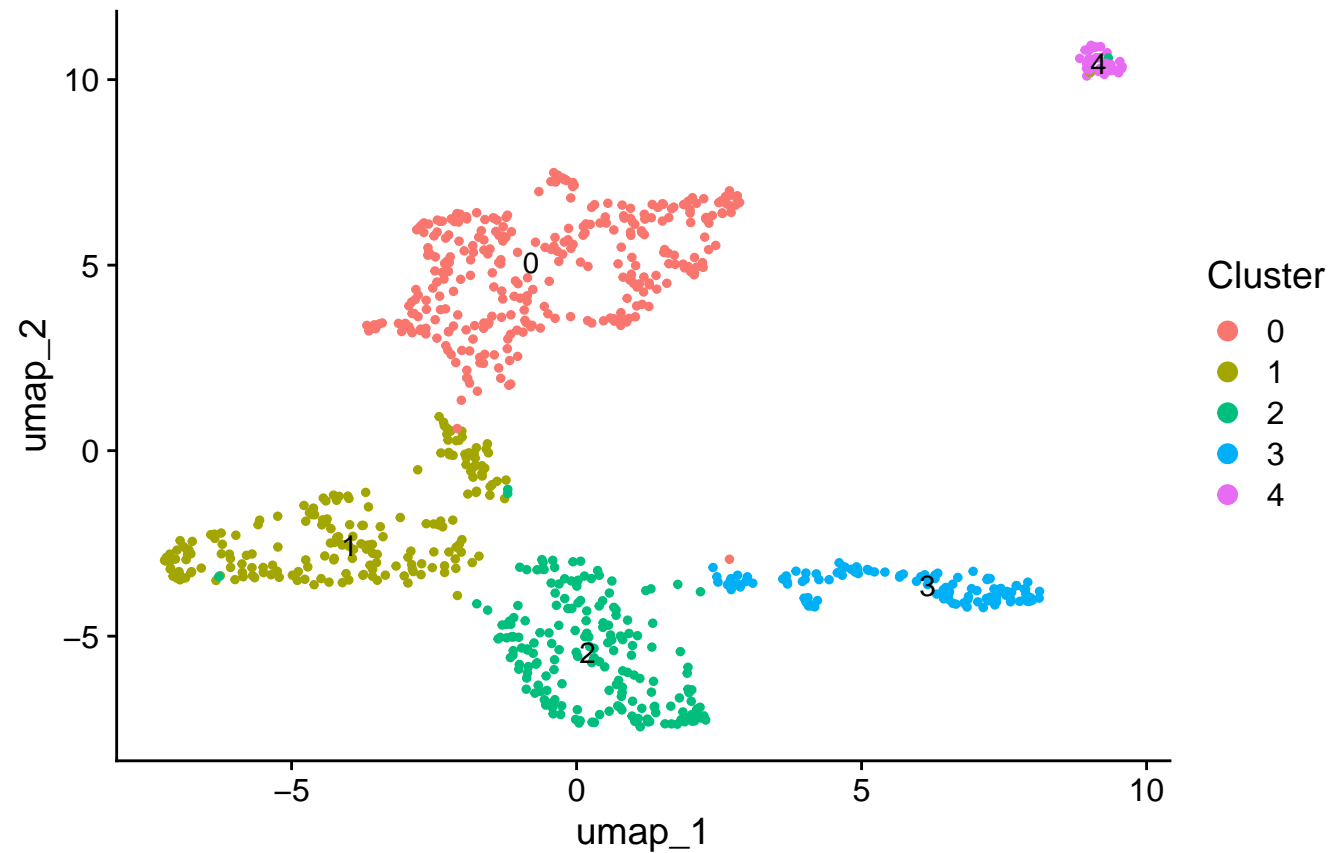org_6B – Clustering Resolution Tree

org_6B – UMAP & Doublet Removal
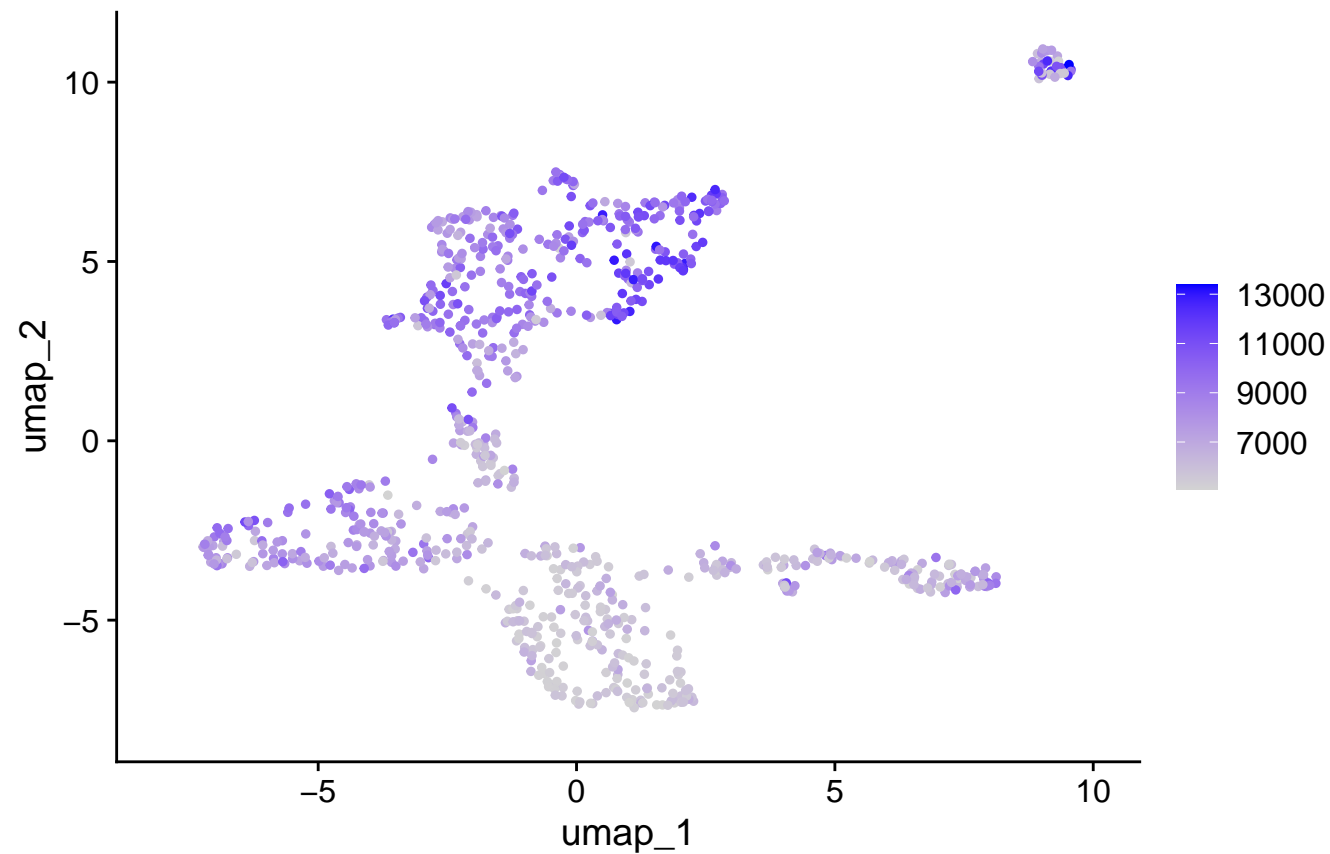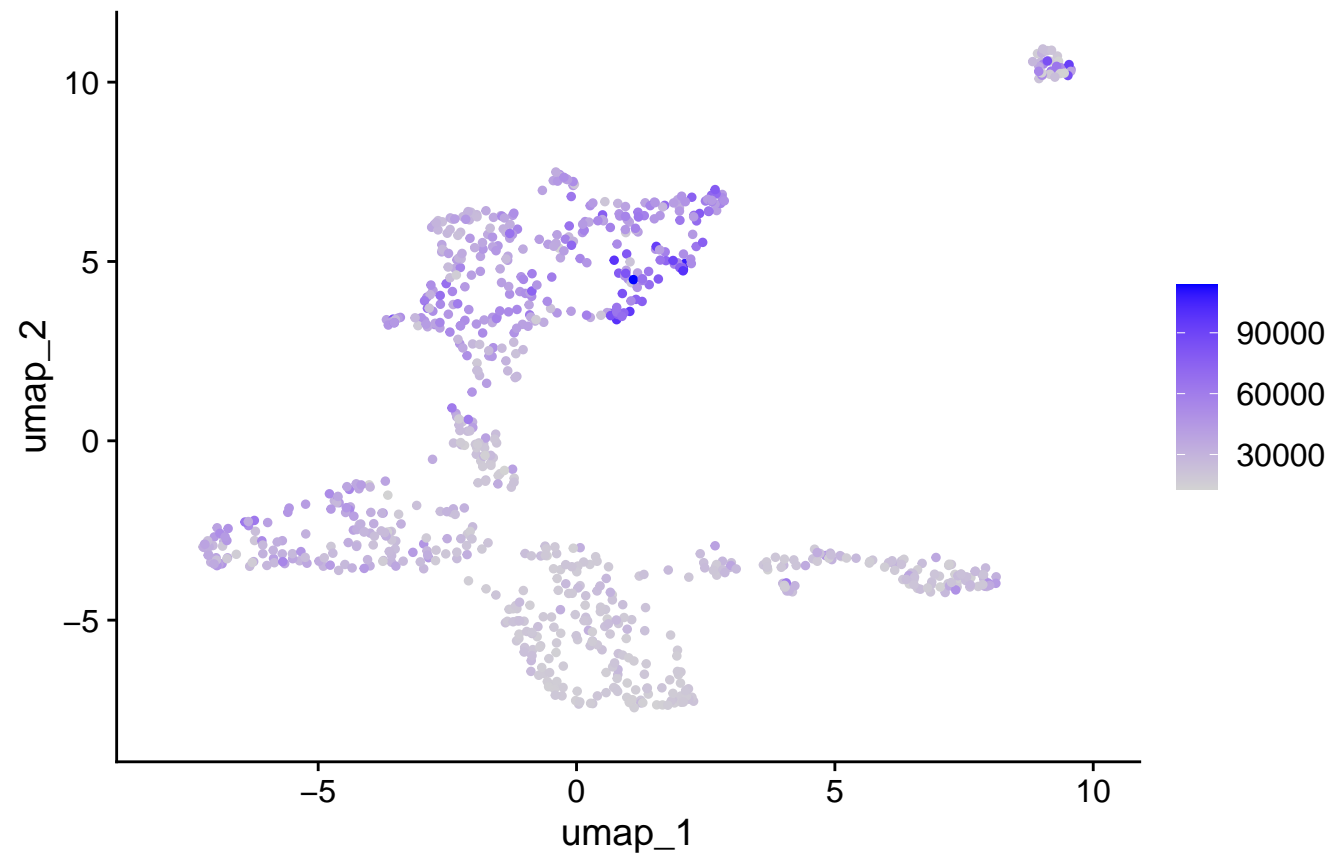
org_6B: Doublets Detected

org_6B: Final UMAP

	DF.classifications	median_nCount	median_nFeature	count
1	Doublet	59892.5	10880	10
2	Singlet	28050.0	7433	861

org_6B – QC Metrics & Cell Cycle on UMAP