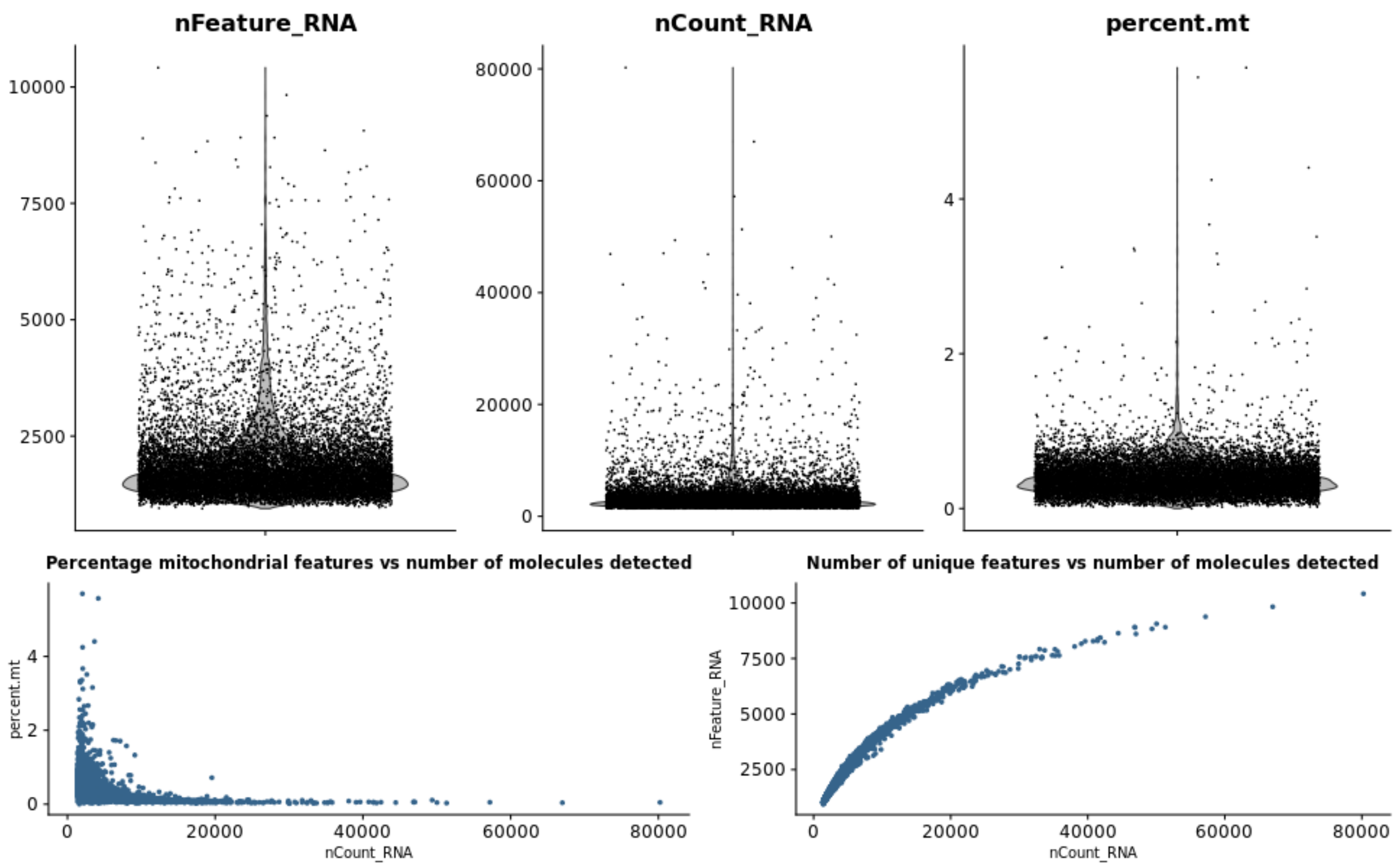


Script options

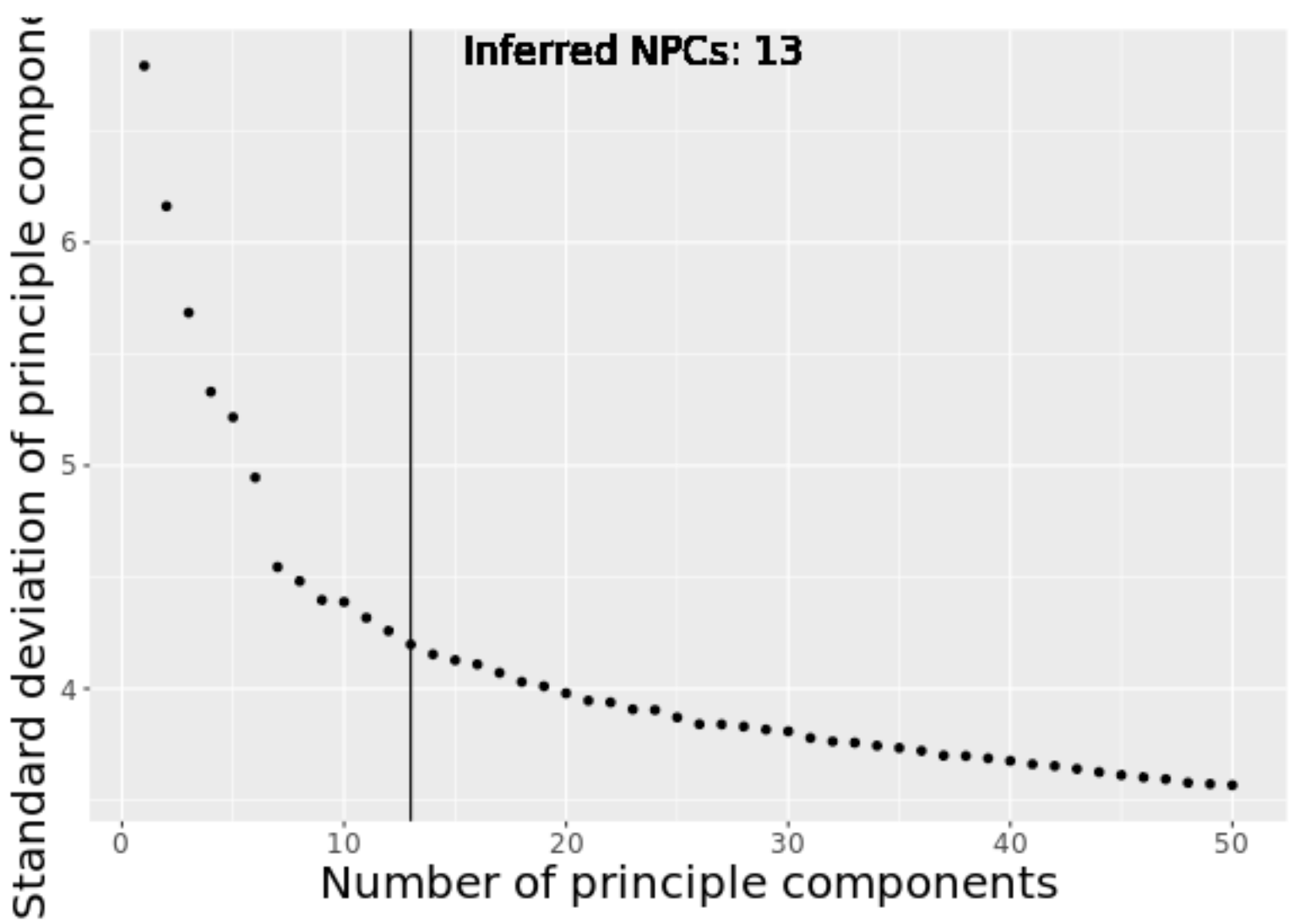
Input Directory: ... /badsample/  
Output Directory: ... /badsample//pipeline\_output  
Minimum Cells Filter: 3  
Minimum Features Filter: 200  
Maximum Features Filter: 2500  
Maximum Percentage MT Filter: 5

	Pre-filtering	Post-filtering	Singlets
Number of cells	13932	12205	179
Median nCount_RNA	2634	2487	2345
Minimum nCount_RNA	1376	1376	1377
Maximum nCount_RNA	80225	5557	5179
Median nFeature_RNA	1654	1590	1500
Minimum nFeature_RNA	942	942	1008
Maximum nFeature_RNA	10415	2500	2500
Median percent.mt	0	0	0
Minimum percent.mt	0	0	0
Maximum percent.mt	6	4	4

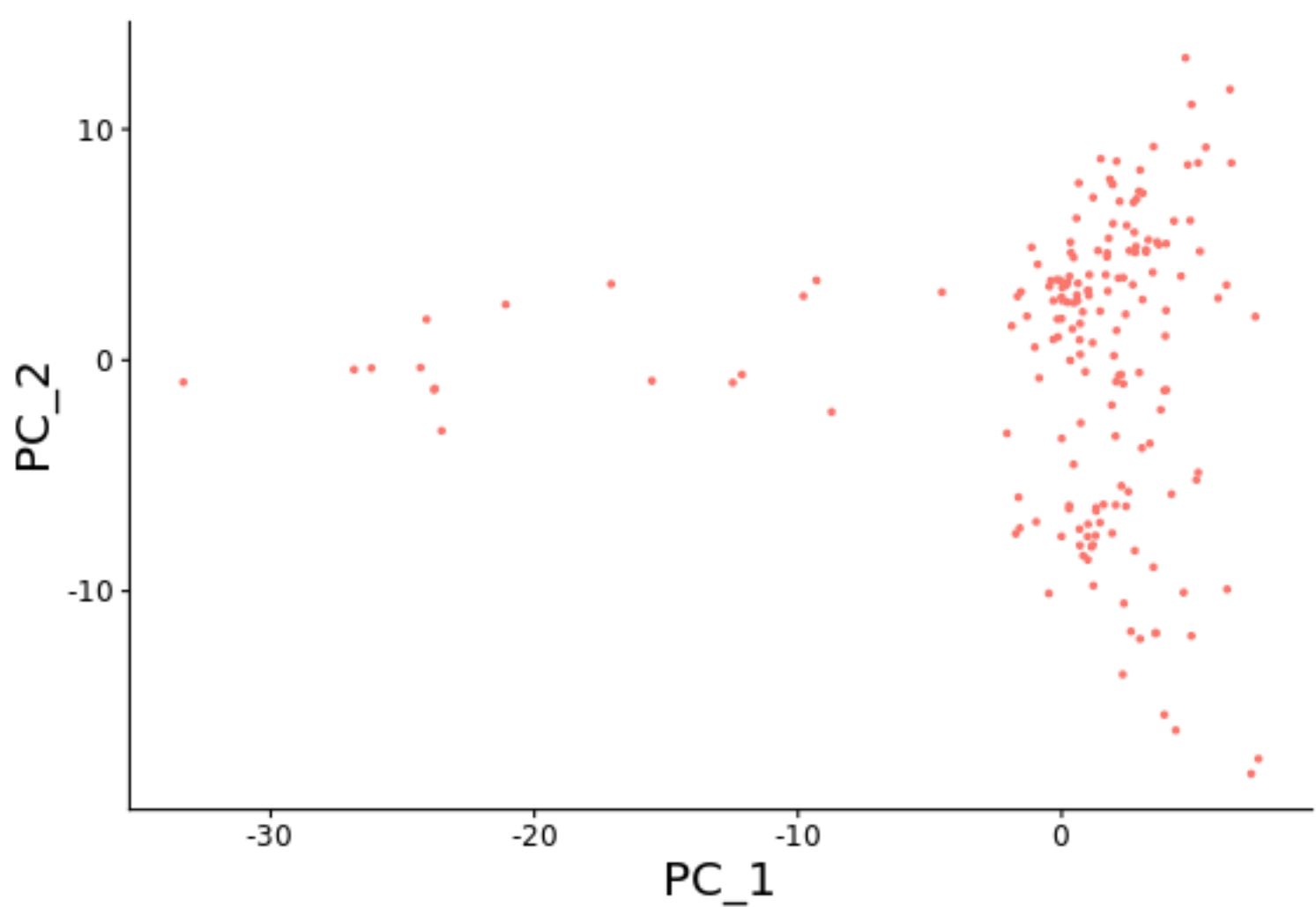
Quality Control Plots



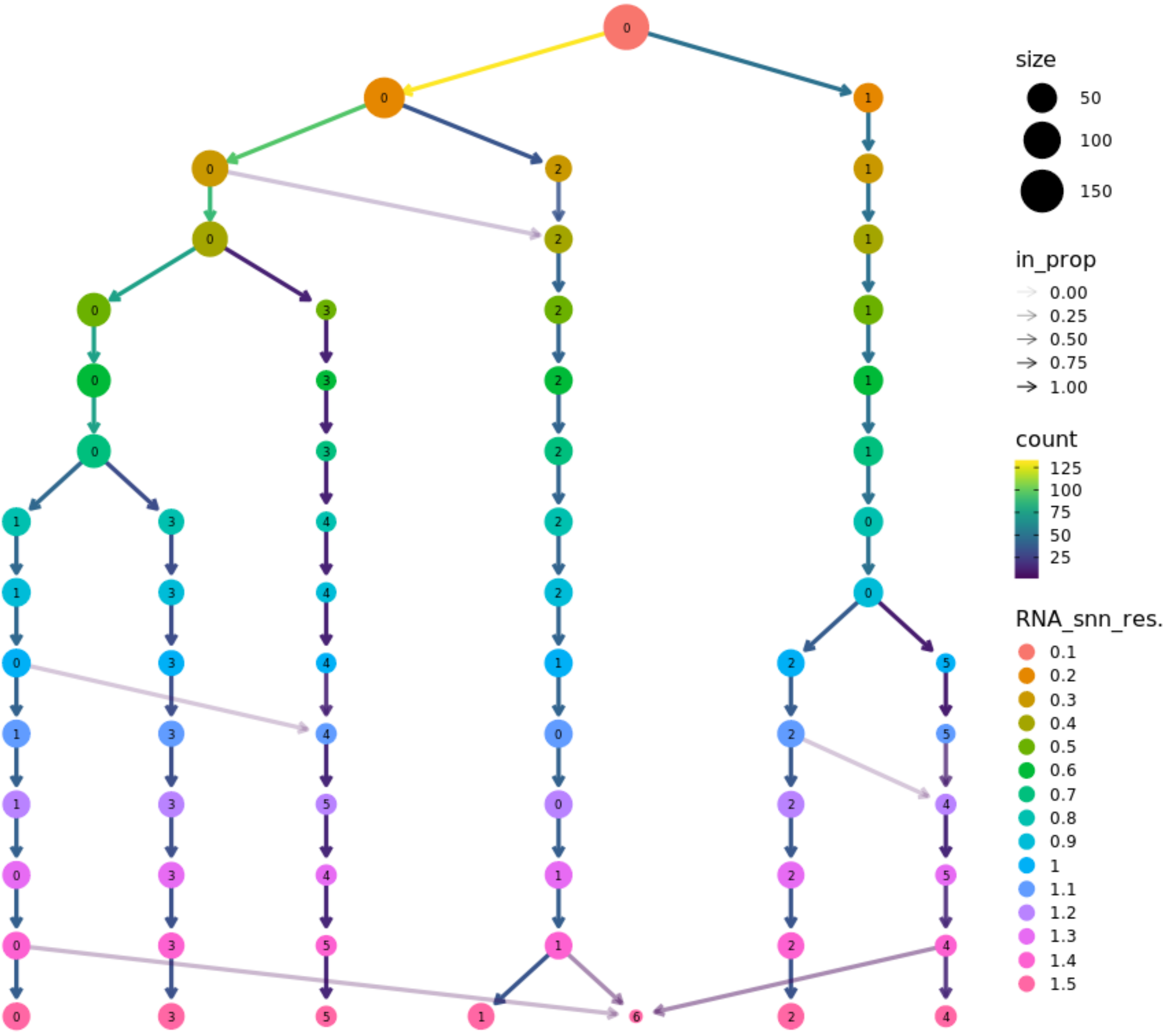
Selection of Principle Components



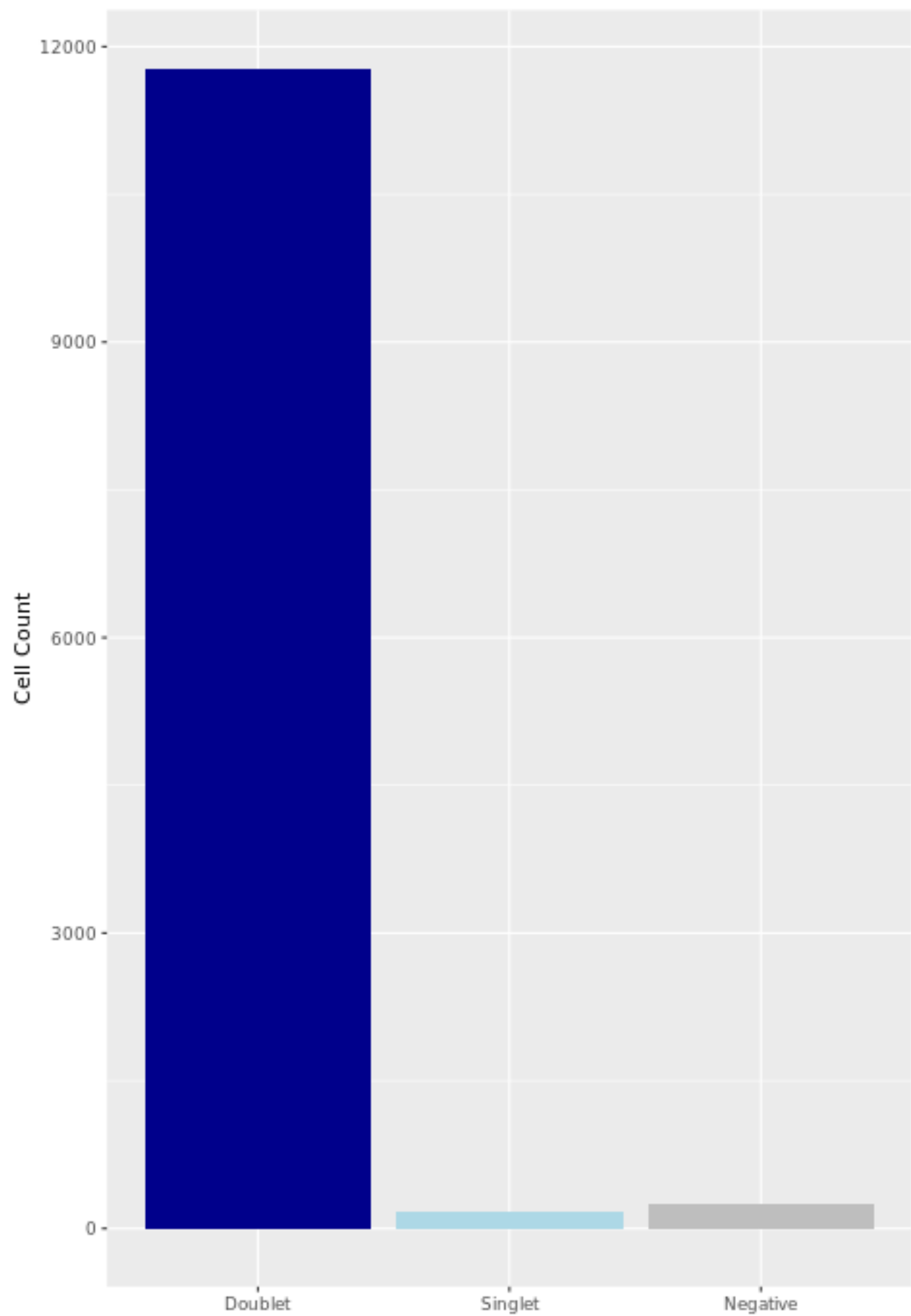
Plotting Principle Components



Selection of K from Clustree



Number of Doublets Identified



Expression Counts Over Hashtags

