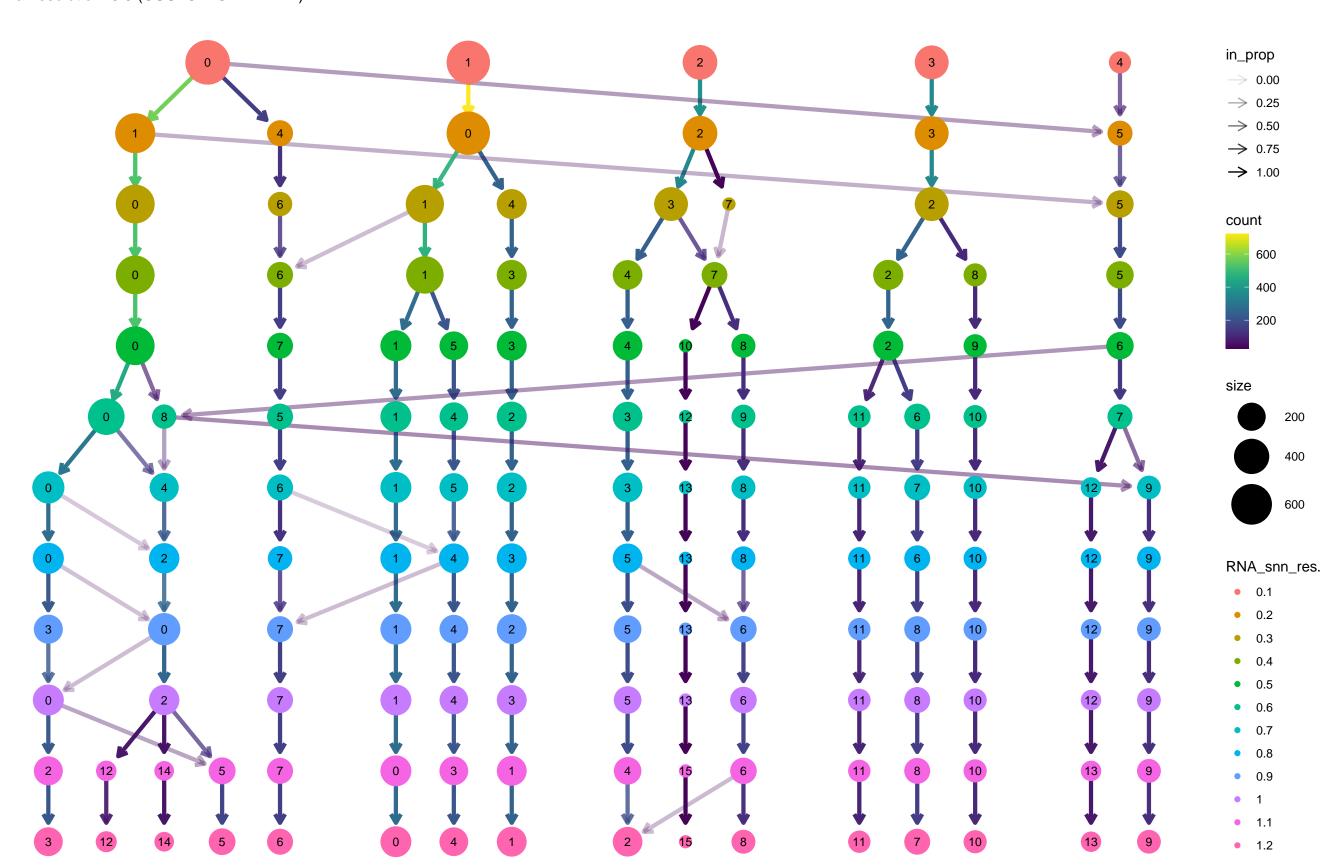
**6M\_Org - PCA Elbow Analysis (Pre-Integration)** 6M\_Org: Quantitative PC Selection **6M\_Org: Elbow Plot** Calculated: 16 PCs | Used: 21 PCs (+5) Calculated: 16 PCs | Used: 21 PCs (+5) Calculated: 16 Used: 21 10 -Standard Deviation rank > optimal\_pcs\_calculated a FALSE TRUE a 5 5 10 20 30 40 50 0 25 75 50 100 PC Cumulative Variance (%)

## **6M\_Org: Clustree**

Final resolution: 0.5 (CUSTOM OVERRIDE)

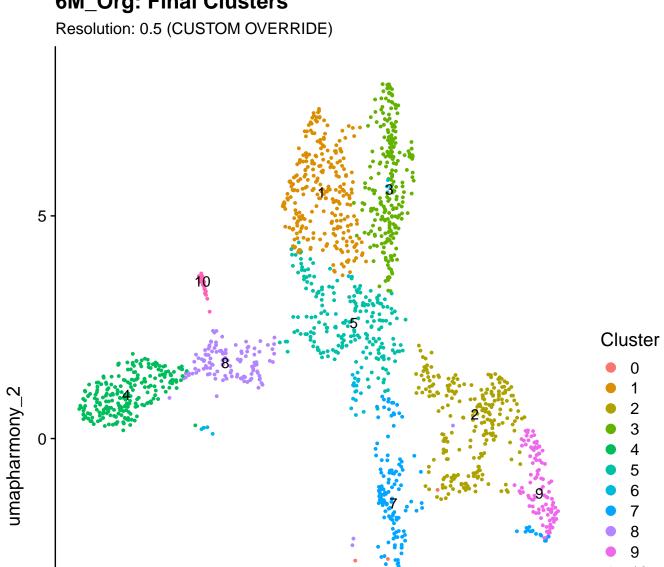


## **6M\_Org – Final Clustering Results**

10

5

## **6M\_Org: Final Clusters**



0 umapharmony\_1

-5

-10

	res_vals	num_clusters	avg_sil_vals
1	0.1	5	0.376925713688954
2	0.2	6	0.375046143243745
3	0.5	11	0.250178195967382
4	8.0	14	0.238711125692361
5	1.2	16	0.232045964561219
6	0.4	9	0.231815356092906
7	0.6	13	0.208620999238172
8	0.3	8	0.184144235381265

6M\_Org - QC Metrics on Integrated Data 6M\_Org: Cell Cycle Phase 6M\_Org: nFeature\_RNA 5 umapharmony\_2 umapharmony\_2 Phase 10000 G1 7500 G2M 5000 -5 -5 10 -10 **-**5 -10 -5 10 5 umapharmony\_1 umapharmony\_1 6M\_Org: nCount\_RNA 6M\_Org: Final Clusters Resolution: 0.5 (CUSTOM OVERRIDE) 5 Cluster umapharmony\_2 umapharmony\_2 60000 40000 20000 **-5** -10 <u>-</u>5 10 -<del>1</del>0 <u>-</u>5 10 5 umapharmony\_1 umapharmony\_1