test Mini Summary

Overall Statistics

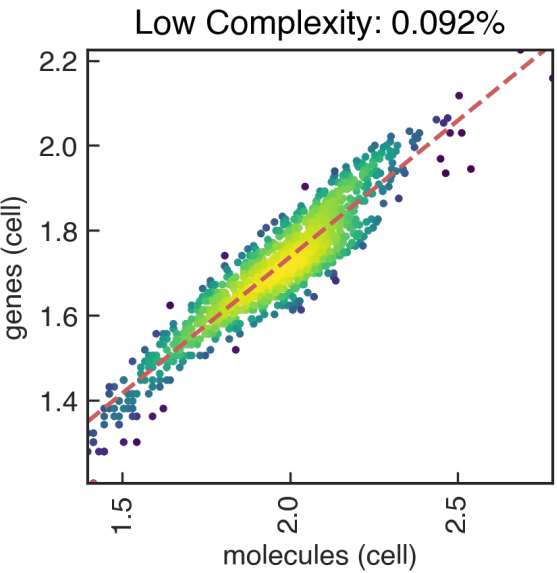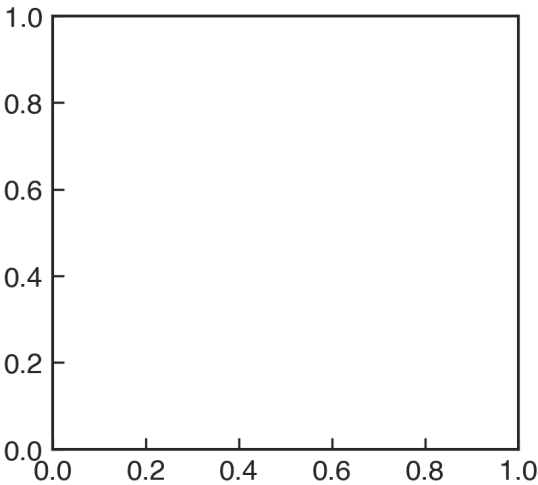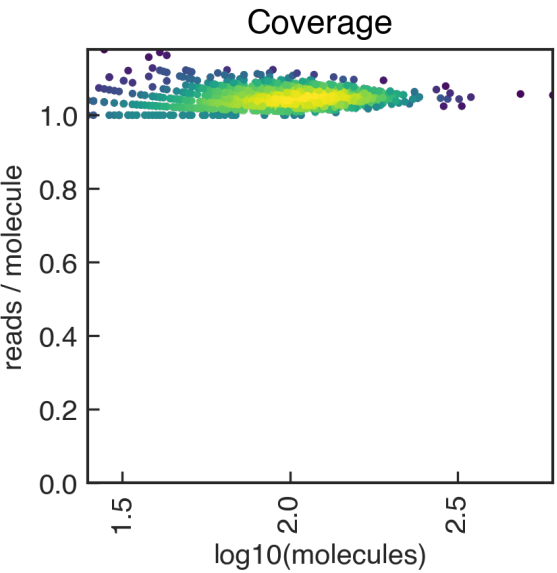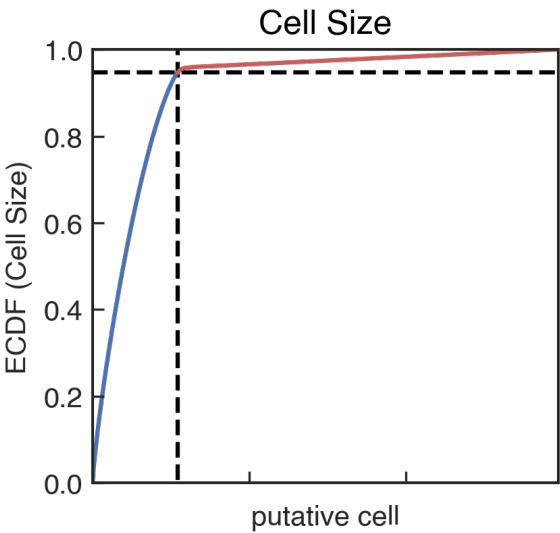|	
# Reads:	1673159
% of uniquely mapped reads:	12.80%
% of multi-mapped reads:	2.31%
% of unmapped reads:	84.58%
% of filtered reads mapping to genome:	48.99%
Sequencing saturation rate:	4.55%
# Cells:	1087
Median molecules per cell:	95
Average reads per cell:	111
Average reads per molecule:	1.05

Cell Size Distribution
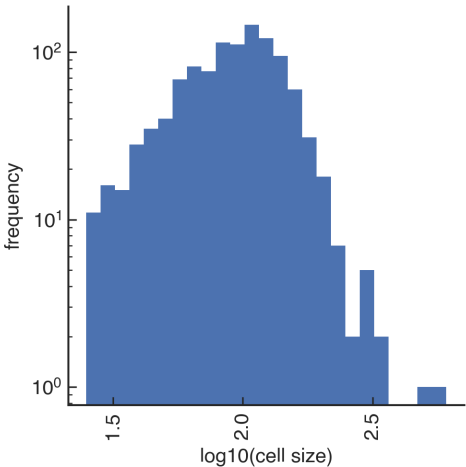
Filtering

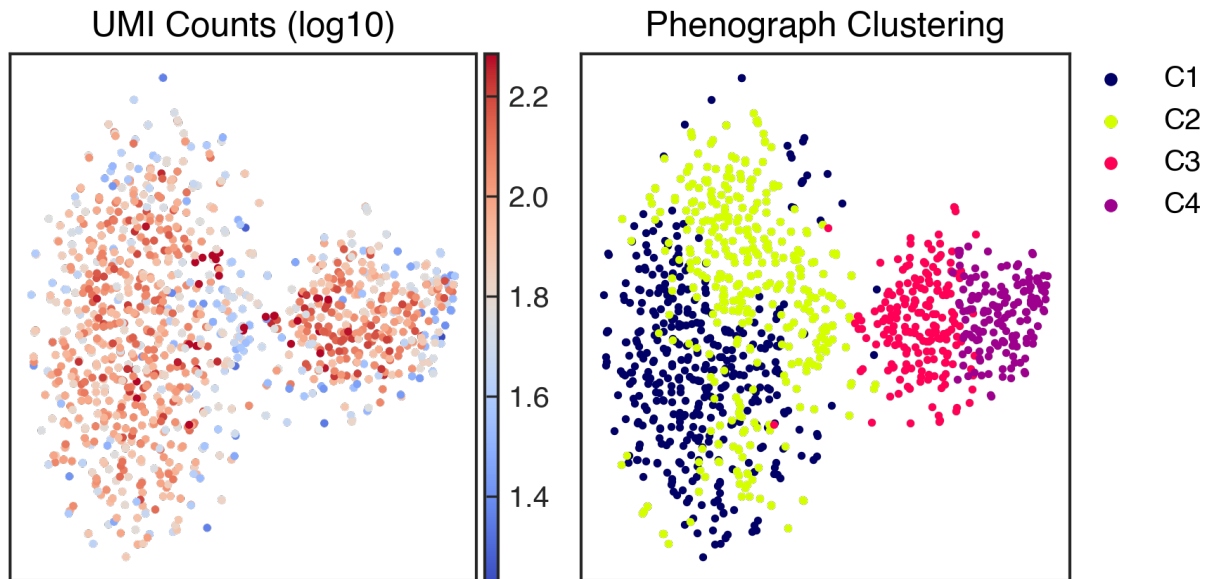Indian red indicates cells that have been filtered

PCA Components
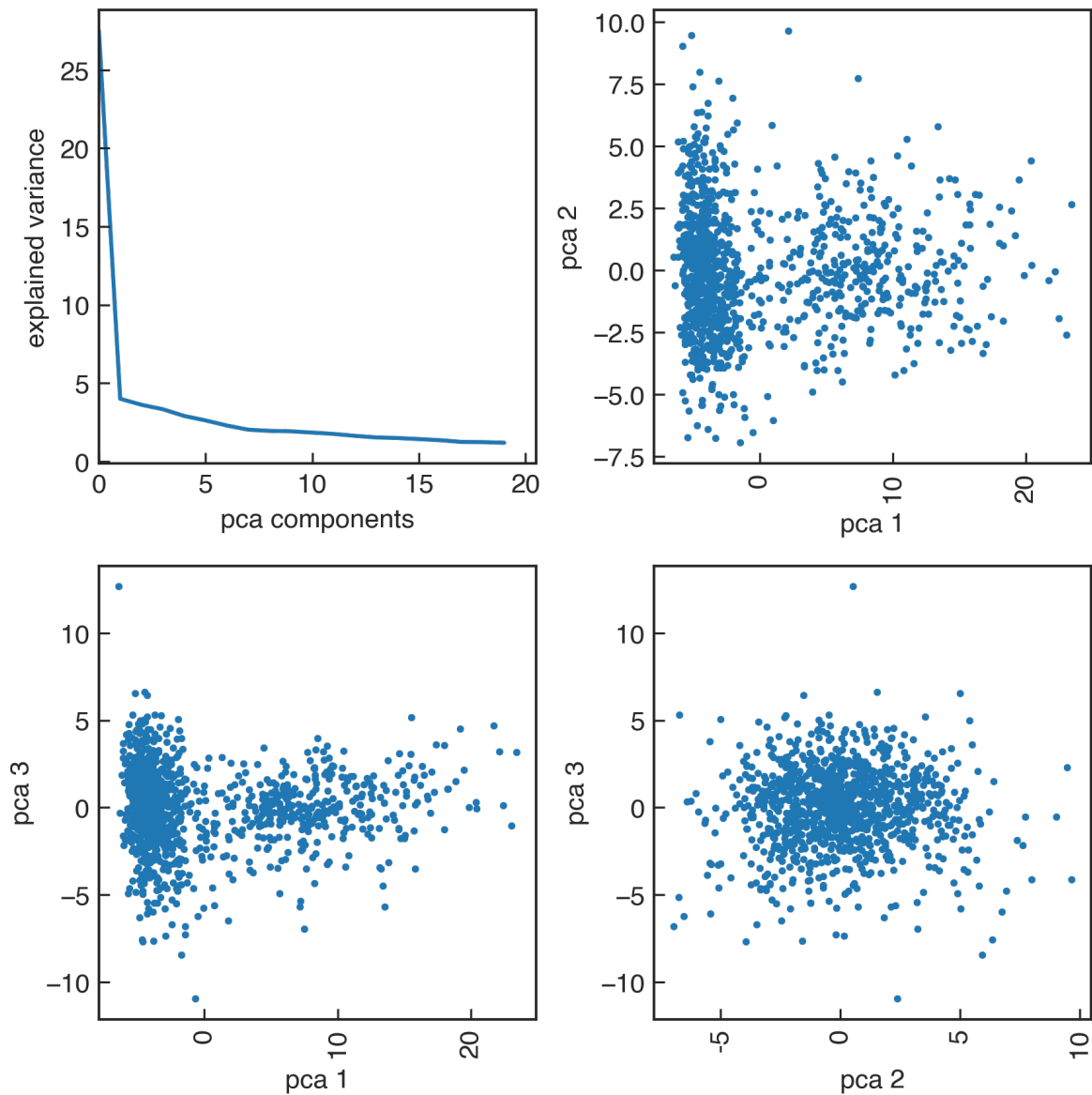
Phenograph Clustering

Library size has been regressed out of all PCA components. We ran Phenograph clustering algorithm on the dataset with revised PCA components and with 80 nearest neighbors.

Warnings

High percentage of cell death: No
Noisy first few principle components: No
Low sequencing saturation rate: Yes (4.55%)