

General status reporting:

Single sample analysis:

Control

Summary

Analysis

4,004

Estimated Number of Cells

49,575

Mean Reads per Cell

3,408

Median Genes per Cell

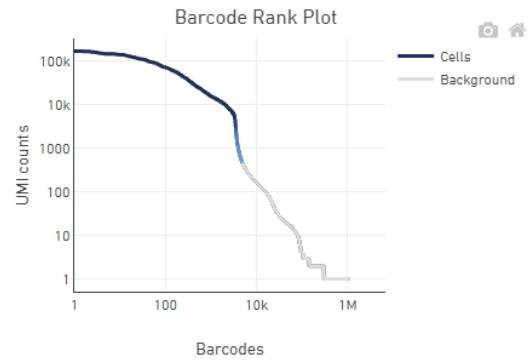
Sequencing

Number of Reads	198,498,394
Valid Barcodes	98.2%
Valid UMIs	100.0%
Sequencing Saturation	48.6%
Q30 Bases in Barcode	97.8%
Q30 Bases in RNA Read	96.2%
Q30 Bases in UMI	97.8%

Mapping

Reads Mapped to Genome	93.3%
Reads Mapped Confidently to Genome	88.5%
Reads Mapped Confidently to Intergenic Regions	5.1%
Reads Mapped Confidently to Intronic Regions	14.0%
Reads Mapped Confidently to Exonic Regions	69.4%
Reads Mapped Confidently to Transcriptome	66.2%
Reads Mapped Antisense to Gene	1.6%

Cells



Estimated Number of Cells	4,004
Fraction Reads in Cells	92.7%
Mean Reads per Cell	49,575
Median Genes per Cell	3,408
Total Genes Detected	22,378
Median UMI Counts per Cell	10,214

Sample

Sample ID	Roy_Control
Sample Description	
Chemistry	Single Cell 3' v3
Reference Path	...iu/ref/refdata-cellranger-mm10-3.0.0
Transcriptome	mm10-3.0.0
Pipeline Version	cellranger-4.0.0

Aggregation status:

AGG

Count Summary

Count Analysis

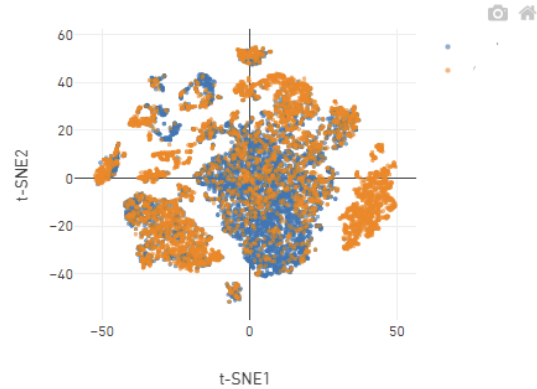
15,418

Estimated Number of Cells

Aggregation ?

Pre-Normalization Total Number of Reads	826,033,422
Post-Normalization Total Number of Reads	818,833,696
Pre-Normalization Mean Reads per Cell	53,576
Post-Normalization Mean Reads per Cell	53,109
Fraction of Reads Kept ()	100.0%
Fraction of Reads Kept ()	98.2%
Pre-Normalization Total Reads per Cell ()	54,035
Pre-Normalization Total Reads per Cell ()	53,090
Pre-Normalization Confidently Mapped Barcoded Reads per Cell ()	31,475
Pre-Normalization Confidently Mapped Barcoded Reads per Cell ()	32,055

t-SNE Projection Colored by Library ID



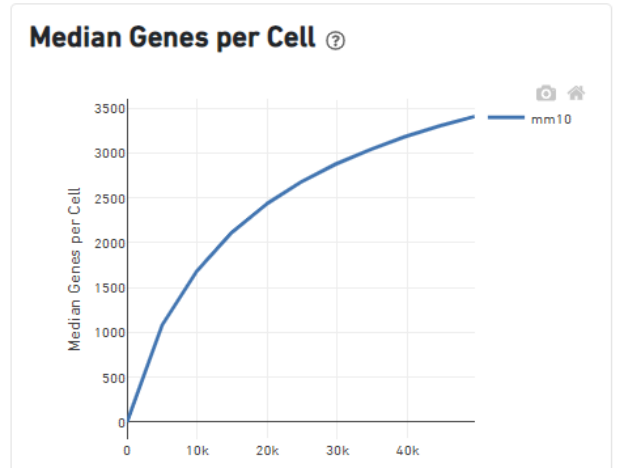
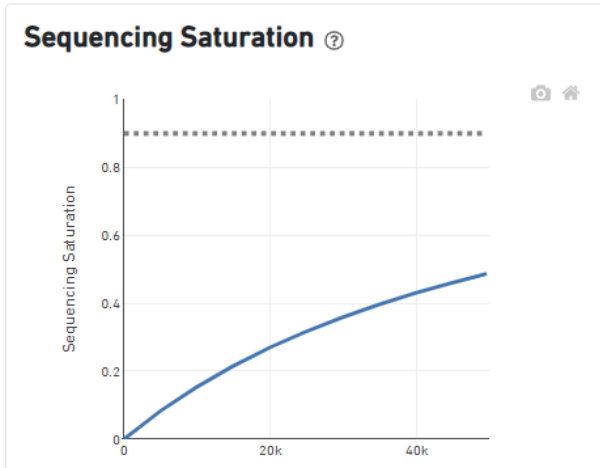
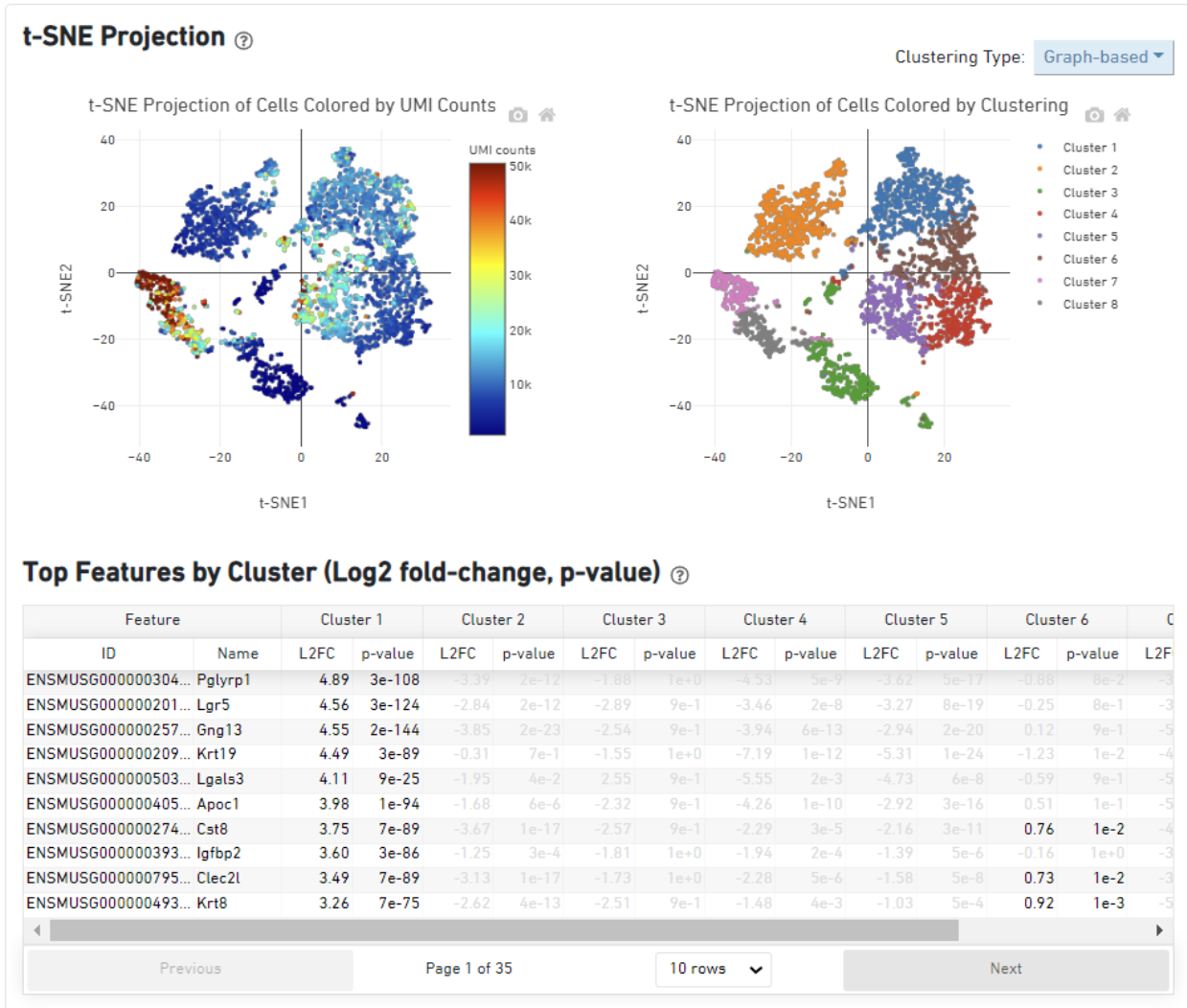
Cells ?

Estimated Number of Cells	15,418
Fraction Reads in Cells	94.4%
Median Genes per Cell	1,757
Median UMI Counts per Cell	5,837

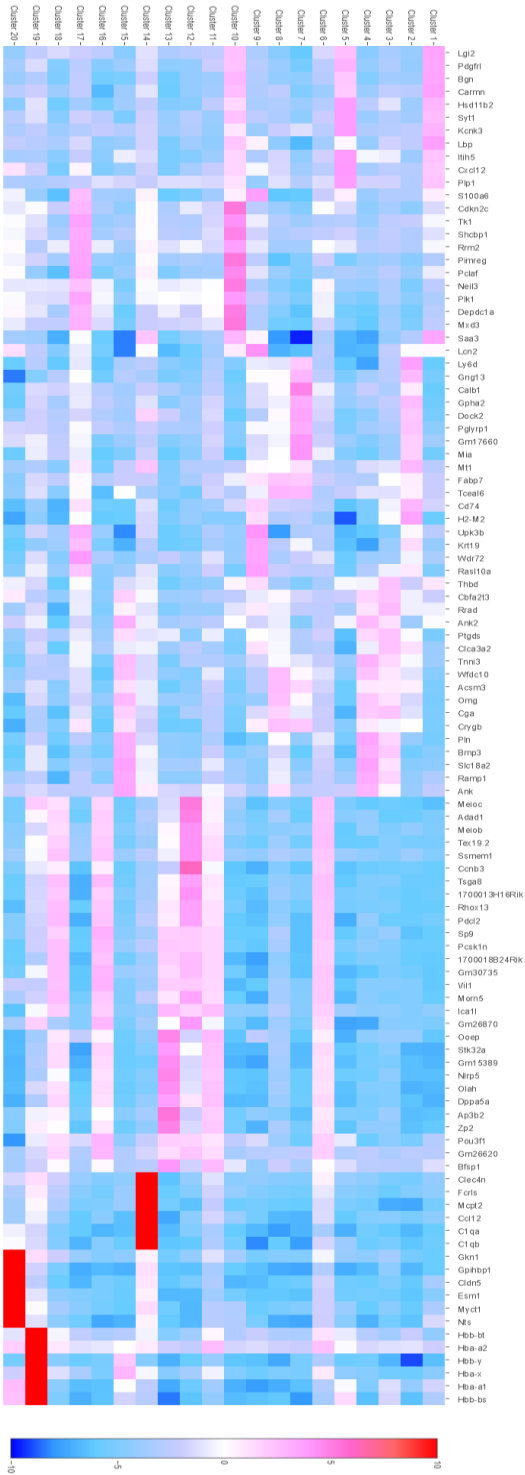
Sample

Sample ID	AGG
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	mm10
Pipeline Version	cellranger-5.0.1

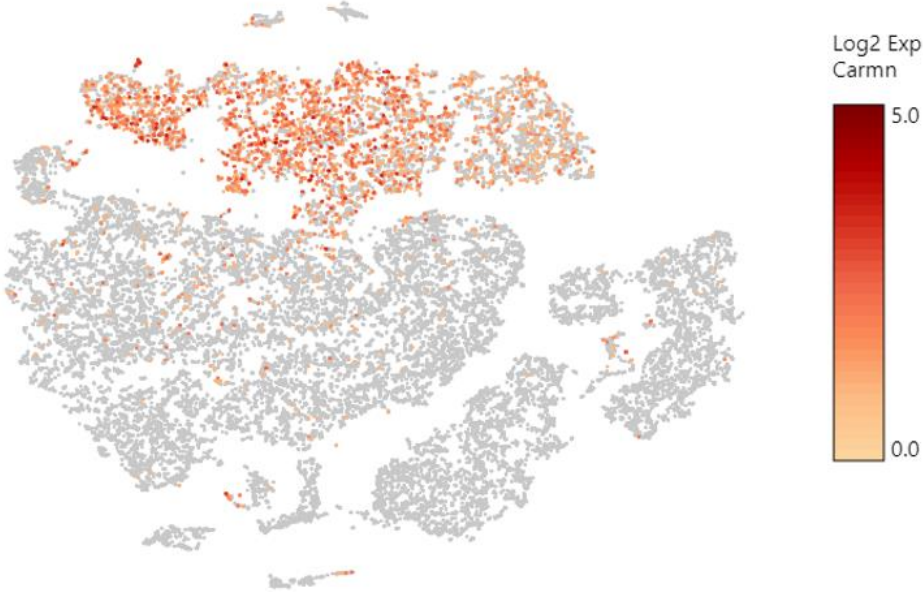
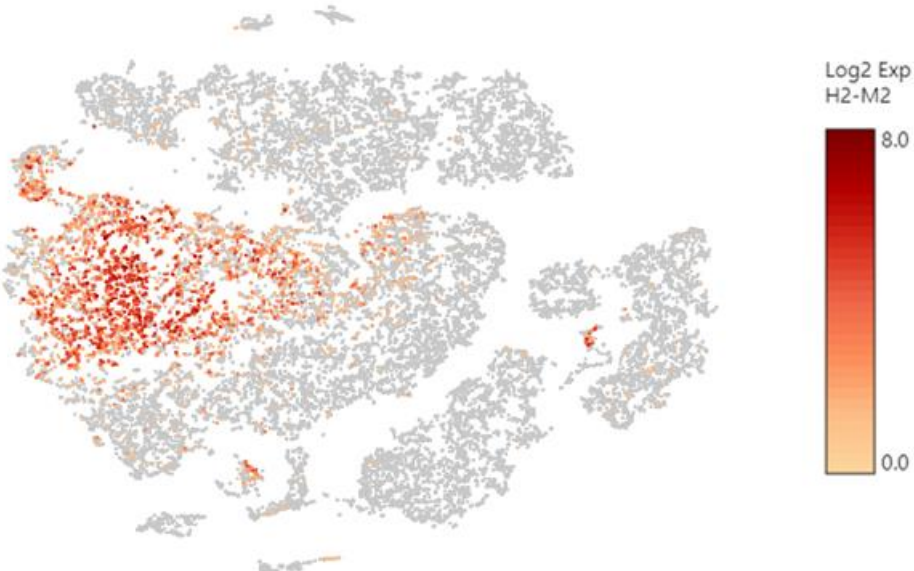
Analysis report (clustering + markers per cluster):



Heatmap:

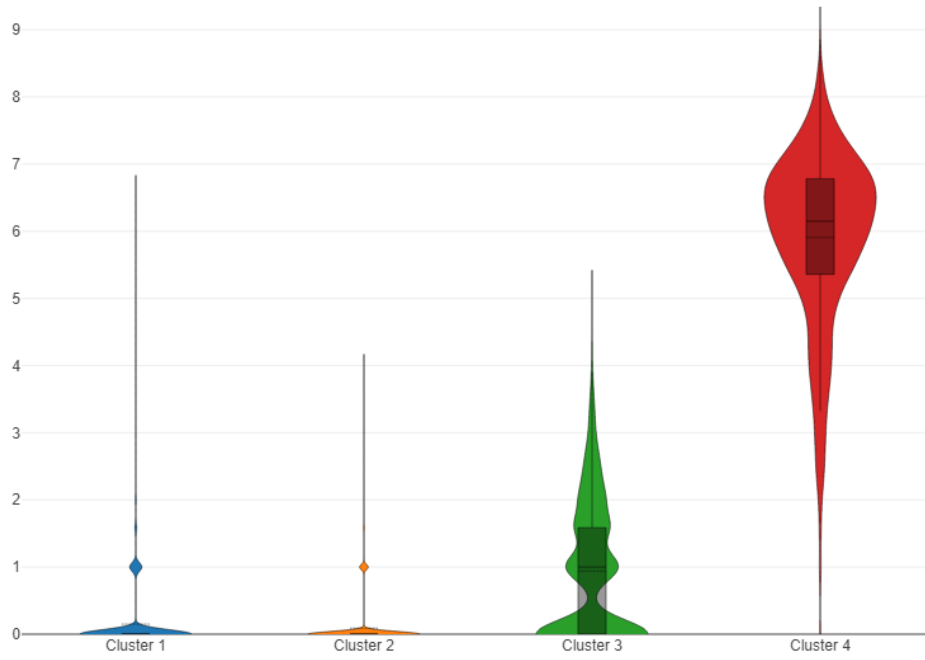


Marker gene identification



Violin plots:

Log2 Exp - Sycp3 (K-Means 4)



Log2 Exp - Foxl2 (K-Means 4)

