

C

Summary

Analysis

6,089

Estimated Number of Cells

49,912

Mean Reads per Cell

1,478

Median Genes per Cell

Sequencing ?

Number of Reads	303,916,080
Valid Barcodes	95.2%
Valid UMIs	100.0%
Sequencing Saturation	63.8%
Q30 Bases in Barcode	95.4%
Q30 Bases in RNA Read	94.2%
Q30 Bases in UMI	92.7%

Mapping ?

Reads Mapped to Genome	92.1%
Reads Mapped Confidently to Genome	85.5%
Reads Mapped Confidently to Intergenic Regions	33.0%
Reads Mapped Confidently to Intronic Regions	0.5%
Reads Mapped Confidently to Exonic Regions	51.9%
Reads Mapped Confidently to Transcriptome	46.0%
Reads Mapped Antisense to Gene	2.4%

Cells ?

Barcode Rank Plot

Estimated Number of Cells	6,089
Fraction Reads in Cells	81.4%
Mean Reads per Cell	49,912
Median Genes per Cell	1,478
Total Genes Detected	5,619
Median UMI Counts per Cell	4,858

Sample

Sample ID	C
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	plasmidium_yoelii-
Pipeline Version	3.1.0

A

Summary

Analysis

4,243

Estimated Number of Cells

69,462

Mean Reads per Cell

1,124

Median Genes per Cell

Sequencing

Number of Reads	294,725,759
Valid Barcodes	94.7%
Valid UMIs	100.0%
Sequencing Saturation	75.3%
Q30 Bases in Barcode	95.3%
Q30 Bases in RNA Read	94.3%
Q30 Bases in UMI	92.6%

Mapping

Reads Mapped to Genome	84.4%
Reads Mapped Confidently to Genome	76.2%
Reads Mapped Confidently to Intergenic Regions	33.1%
Reads Mapped Confidently to Intronic Regions	0.4%
Reads Mapped Confidently to Exonic Regions	42.7%
Reads Mapped Confidently to Transcriptome	37.7%
Reads Mapped Antisense to Gene	2.2%

Cells

Barcode Rank Plot

Estimated Number of Cells	4,243
Fraction Reads in Cells	75.3%
Mean Reads per Cell	69,462
Median Genes per Cell	1,124
Total Genes Detected	5,644
Median UMI Counts per Cell	2,902

Sample

Sample ID	A
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	plasmidium_yoelii-
Pipeline Version	3.1.0

zero_h

Summary

Analysis

7,175

Estimated Number of Cells

34,669

Mean Reads per Cell

973

Median Genes per Cell

Sequencing ?

Number of Reads	248,749,118
Valid Barcodes	97.9%
Valid UMIs	99.9%
Sequencing Saturation	85.0%
Q30 Bases in Barcode	96.1%
Q30 Bases in RNA Read	92.9%
Q30 Bases in UMI	94.3%

Mapping ?

Reads Mapped to Genome	96.7%
Reads Mapped Confidently to Genome	95.6%
Reads Mapped Confidently to Intergenic Regions	33.0%
Reads Mapped Confidently to Intronic Regions	0.6%
Reads Mapped Confidently to Exonic Regions	61.9%
Reads Mapped Confidently to Transcriptome	53.9%
Reads Mapped Antisense to Gene	2.2%

Cells ?

Barcode Rank Plot

Estimated Number of Cells7,175

Fraction Reads in Cells96.4%

Mean Reads per Cell34,669

Median Genes per Cell973

Total Genes Detected5,626

Median UMI Counts per Cell2,196

Sample

Sample ID	zero_h
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	plasmidium_yoelii-
Pipeline Version	cellranger-4.0.0

three_h

Summary

Analysis

8,530

Estimated Number of Cells

22,240

Mean Reads per Cell

1,038

Median Genes per Cell

Sequencing ?

Number of Reads	189,703,679
Valid Barcodes	97.8%
Valid UMIs	99.9%
Sequencing Saturation	78.2%
Q30 Bases in Barcode	96.7%
Q30 Bases in RNA Read	94.9%
Q30 Bases in UMI	95.4%

Mapping ?

Reads Mapped to Genome	96.3%
Reads Mapped Confidently to Genome	94.8%
Reads Mapped Confidently to Intergenic Regions	33.7%
Reads Mapped Confidently to Intronic Regions	0.6%
Reads Mapped Confidently to Exonic Regions	60.5%
Reads Mapped Confidently to Transcriptome	53.4%
Reads Mapped Antisense to Gene	1.7%

Cells ?

Barcode Rank Plot

Estimated Number of Cells	8,530
Fraction Reads in Cells	94.6%
Mean Reads per Cell	22,240
Median Genes per Cell	1,038
Total Genes Detected	5,613
Median UMI Counts per Cell	2,174

Sample

Sample ID	three_h
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	plasmidium_yoelii-
Pipeline Version	cellranger-4.0.0

nine_h

Summary

Analysis

5,895

Estimated Number of Cells

39,021

Mean Reads per Cell

676

Median Genes per Cell

Sequencing ?

Number of Reads	230,031,139
Valid Barcodes	97.6%
Valid UMIs	99.9%
Sequencing Saturation	88.9%
Q30 Bases in Barcode	96.1%
Q30 Bases in RNA Read	92.8%
Q30 Bases in UMI	94.2%

Mapping ?

Reads Mapped to Genome	95.4%
Reads Mapped Confidently to Genome	92.8%
Reads Mapped Confidently to Intergenic Regions	38.4%
Reads Mapped Confidently to Intronic Regions	0.7%
Reads Mapped Confidently to Exonic Regions	53.7%
Reads Mapped Confidently to Transcriptome	47.1%
Reads Mapped Antisense to Gene	1.6%

Cells ?

Barcode Rank Plot

Estimated Number of Cells	5,895
Fraction Reads in Cells	91.8%
Mean Reads per Cell	39,021
Median Genes per Cell	676
Total Genes Detected	5,587
Median UMI Counts per Cell	1,337

Sample

Sample ID	nine_h
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	plasmidium_yoelii-
Pipeline Version	cellranger-4.0.0

twenty_four_h

Summary

Analysis

3,969

Estimated Number of Cells

54,916

Mean Reads per Cell

268

Median Genes per Cell

Sequencing ?

Number of Reads	217,962,305
Valid Barcodes	96.4%
Valid UMIs	99.9%
Sequencing Saturation	93.9%
Q30 Bases in Barcode	96.2%
Q30 Bases in RNA Read	93.7%
Q30 Bases in UMI	94.2%

Mapping ?

Reads Mapped to Genome	76.6%
Reads Mapped Confidently to Genome	68.6%
Reads Mapped Confidently to Intergenic Regions	34.0%
Reads Mapped Confidently to Intronic Regions	0.8%
Reads Mapped Confidently to Exonic Regions	33.8%
Reads Mapped Confidently to Transcriptome	30.1%
Reads Mapped Antisense to Gene	1.1%

Cells ?

Barcode Rank Plot

Estimated Number of Cells	3,969
Fraction Reads in Cells	81.6%
Mean Reads per Cell	54,916
Median Genes per Cell	268
Total Genes Detected	5,423
Median UMI Counts per Cell	515

Sample

Sample ID	twenty_four_h
Sample Description	
Chemistry	Single Cell 3' v3
Transcriptome	plasmidium_yoelii-
Pipeline Version	cellranger-4.0.0