

Cell Ranger analysis of all samples

1. *Plasmodium yoelii* 17XNL were treated with artemether for 6 h in mice

C: Control group

A: Test group

2. *Plasmodium yoelii* 17XNL were treated with artemether for 0, 3, 9, and 24 h in mice

Zero_h: *P. yoelii* 17XNL were treated with artemether for 0 h

Three_h: *P. yoelii* 17XNL were treated with artemether for 3 h

Nine_h: *P. yoelii* 17XNL were treated with artemether for 9 h

Twenty_four_h: *P. yoelii* 17XNL were treated with artemether for 24 h

3. *Plasmodium falciparum* 3D7 were treated with desferrioxamine (DFO), dihydroartemisinin (DHA) and dihydroartemisinin + iron sucrose for 3, 9, and 24 h in vitro

CH_no_drug_3: *P. falciparum* 3D7 were treated without any drug

DFO_3: *P. falciparum* 3D7 were treated with DFO for 3 h

DHA_3: *P. falciparum* 3D7 were treated with DHA for 3 h

DHA_Fe_3: *P. falciparum* 3D7 were treated with DHA and iron sucrose for 3 h

DFO_9: *P. falciparum* 3D7 were treated with DFO for 9 h

DHA_9: *P. falciparum* 3D7 were treated with DHA for 9 h

DHA_Fe_9: *P. falciparum* 3D7 were treated with DHA and iron sucrose for 9 h

DFO_24: *P. falciparum* 3D7 were treated with DFO for 24 h

DHA_24: *P. falciparum* 3D7 were treated with DHA for 24 h

DHA_Fe_24: *P. falciparum* 3D7 were treated with DHA and iron sucrose for 24 h

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

CH_no_drug_3

Summary

Gene Expression

11,162

Estimated Number of Cells

30,747

Mean Reads per Cell

1,109

Median Genes per Cell

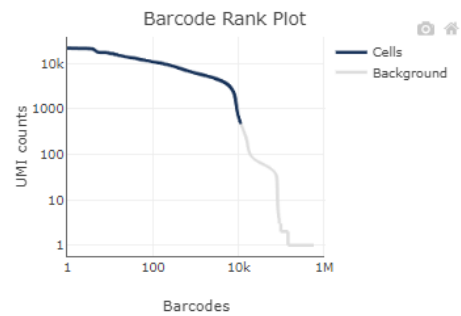
Sequencing ⓘ

Number of Reads	343,203,551
Number of Short Reads Skipped	0
Valid Barcodes	97.3%
Valid UMIs	99.9%
Sequencing Saturation	75.7%
Q30 Bases in Barcode	96.7%
Q30 Bases in RNA Read	91.5%
Q30 Bases in UMI	96.3%

Mapping ⓘ

Reads Mapped to Genome	89.9%
Reads Mapped Confidently to Genome	72.2%
Reads Mapped Confidently to Intergenic Regions	11.6%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	60.4%
Reads Mapped Confidently to Transcriptome	55.5%
Reads Mapped Antisense to Gene	2.7%

Cells ⓘ



Estimated Number of Cells	11,162
Fraction Reads in Cells	92.8%
Mean Reads per Cell	30,747
Median UMI Counts per Cell	3,472
Median Genes per Cell	1,109
Total Genes Detected	5,558

Sample

Sample ID	CH_no_drug_3
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DFO_3

Summary

Gene Expression

7,823

Estimated Number of Cells

44,082

Mean Reads per Cell

1,207

Median Genes per Cell

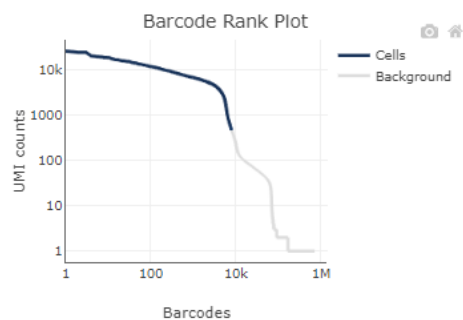
Sequencing ⓘ

Number of Reads	344,857,181
Number of Short Reads Skipped	0
Valid Barcodes	97.2%
Valid UMIs	99.9%
Sequencing Saturation	79.9%
Q30 Bases in Barcode	96.6%
Q30 Bases in RNA Read	91.0%
Q30 Bases in UMI	96.2%

Mapping ⓘ

Reads Mapped to Genome	87.7%
Reads Mapped Confidently to Genome	70.7%
Reads Mapped Confidently to Intergenic Regions	11.3%
Reads Mapped Confidently to Intronic Regions	0.3%
Reads Mapped Confidently to Exonic Regions	59.1%
Reads Mapped Confidently to Transcriptome	54.3%
Reads Mapped Antisense to Gene	2.5%

Cells ⓘ



Estimated Number of Cells	7,823
Fraction Reads in Cells	93.2%
Mean Reads per Cell	44,082
Median UMI Counts per Cell	3,897
Median Genes per Cell	1,207
Total Genes Detected	5,568

Sample

Sample ID	DFO_3
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DHA_3

Summary Gene Expression

6,838

Estimated Number of Cells

50,243

Mean Reads per Cell

1,550

Median Genes per Cell

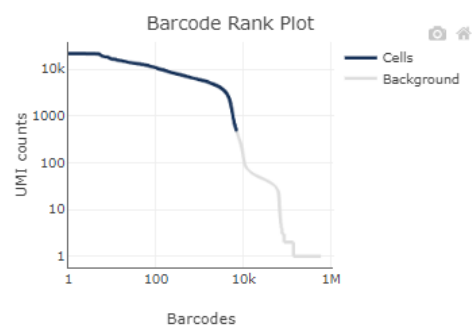
Sequencing ?

Number of Reads	343,564,319
Number of Short Reads Skipped	0
Valid Barcodes	97.8%
Valid UMIs	99.9%
Sequencing Saturation	86.1%
Q30 Bases in Barcode	96.7%
Q30 Bases in RNA Read	92.6%
Q30 Bases in UMI	96.4%

Mapping ?

Reads Mapped to Genome	92.5%
Reads Mapped Confidently to Genome	83.6%
Reads Mapped Confidently to Intergenic Regions	14.8%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	68.6%
Reads Mapped Confidently to Transcriptome	62.9%
Reads Mapped Antisense to Gene	2.8%

Cells ?



Estimated Number of Cells	6,838
Fraction Reads in Cells	93.6%
Mean Reads per Cell	50,243
Median UMI Counts per Cell	3,654
Median Genes per Cell	1,550
Total Genes Detected	5,604

Sample

Sample ID	DHA_3
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DHA_Fe_3

Summary

Gene Expression

6,979

Estimated Number of Cells

49,636

Mean Reads per Cell

1,558

Median Genes per Cell

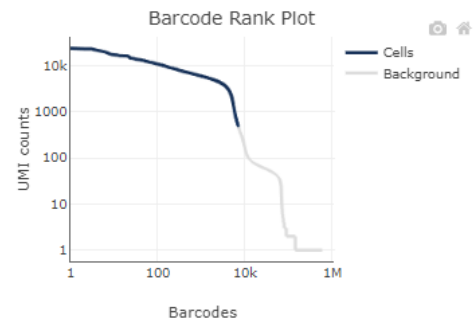
Sequencing ?

Number of Reads	346,410,390
Number of Short Reads Skipped	0
Valid Barcodes	97.8%
Valid UMIs	99.9%
Sequencing Saturation	84.7%
Q30 Bases in Barcode	96.7%
Q30 Bases in RNA Read	93.1%
Q30 Bases in UMI	96.3%

Mapping ?

Reads Mapped to Genome	90.2%
Reads Mapped Confidently to Genome	81.3%
Reads Mapped Confidently to Intergenic Regions	15.8%
Reads Mapped Confidently to Intronic Regions	0.3%
Reads Mapped Confidently to Exonic Regions	65.2%
Reads Mapped Confidently to Transcriptome	59.5%
Reads Mapped Antisense to Gene	3.0%

Cells ?



Estimated Number of Cells	6,979
Fraction Reads in Cells	93.2%
Mean Reads per Cell	49,636
Median UMI Counts per Cell	3,703
Median Genes per Cell	1,558
Total Genes Detected	5,601

Sample

Sample ID	DHA_Fe_3
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DFO_9

Summary

Gene Expression

5,560

Estimated Number of Cells

57,076

Mean Reads per Cell

1,088

Median Genes per Cell

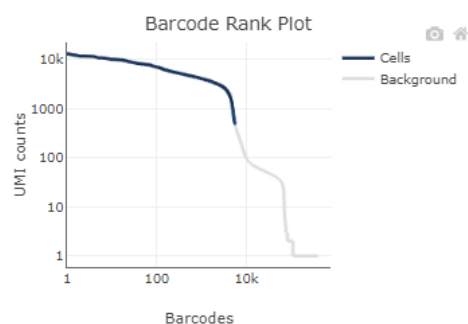
Sequencing

Number of Reads	317,340,986
Number of Short Reads Skipped	0
Valid Barcodes	97.5%
Valid UMIs	99.9%
Sequencing Saturation	88.7%
Q30 Bases in Barcode	96.2%
Q30 Bases in RNA Read	92.8%
Q30 Bases in UMI	95.7%

Mapping

Reads Mapped to Genome	89.8%
Reads Mapped Confidently to Genome	74.8%
Reads Mapped Confidently to Intergenic Regions	11.4%
Reads Mapped Confidently to Intronic Regions	0.4%
Reads Mapped Confidently to Exonic Regions	63.0%
Reads Mapped Confidently to Transcriptome	58.6%
Reads Mapped Antisense to Gene	2.1%

Cells



Estimated Number of Cells	5,560
Fraction Reads in Cells	92.0%
Mean Reads per Cell	57,076
Median UMI Counts per Cell	2,905
Median Genes per Cell	1,088
Total Genes Detected	5,566

Sample

Sample ID	DFO_9
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DHA_9

Summary

Gene Expression

4,909

Estimated Number of Cells

59,093

Mean Reads per Cell

944

Median Genes per Cell

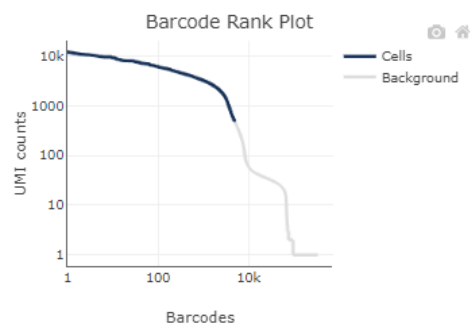
Sequencing ?

Number of Reads	290,086,667
Number of Short Reads Skipped	0
Valid Barcodes	97.1%
Valid UMIs	99.9%
Sequencing Saturation	89.8%
Q30 Bases in Barcode	96.3%
Q30 Bases in RNA Read	93.1%
Q30 Bases in UMI	95.9%

Mapping ?

Reads Mapped to Genome	87.7%
Reads Mapped Confidently to Genome	64.6%
Reads Mapped Confidently to Intergenic Regions	11.4%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	53.0%
Reads Mapped Confidently to Transcriptome	48.5%
Reads Mapped Antisense to Gene	2.5%

Cells ?



Estimated Number of Cells	4,909
Fraction Reads in Cells	88.6%
Mean Reads per Cell	59,093
Median UMI Counts per Cell	1,945
Median Genes per Cell	944
Total Genes Detected	5,599

Sample

Sample ID	DHA_9
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DHA_Fe_9

Summary Gene Expression

5,211

Estimated Number of Cells

54,936

Mean Reads per Cell

923

Median Genes per Cell

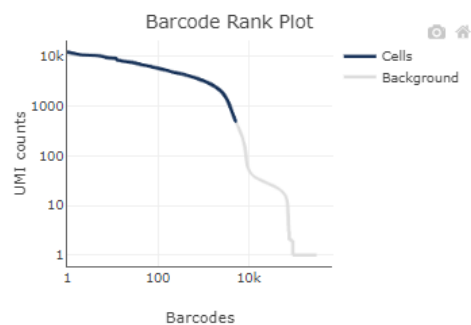
Sequencing ?

Number of Reads	286,273,308
Number of Short Reads Skipped	0
Valid Barcodes	96.9%
Valid UMIs	99.9%
Sequencing Saturation	86.6%
Q30 Bases in Barcode	96.3%
Q30 Bases in RNA Read	91.5%
Q30 Bases in UMI	95.9%

Mapping ?

Reads Mapped to Genome	70.8%
Reads Mapped Confidently to Genome	50.8%
Reads Mapped Confidently to Intergenic Regions	9.0%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	41.5%
Reads Mapped Confidently to Transcriptome	37.9%
Reads Mapped Antisense to Gene	2.0%

Cells ?



Estimated Number of Cells	5,211
Fraction Reads in Cells	87.9%
Mean Reads per Cell	54,936
Median UMI Counts per Cell	1,913
Median Genes per Cell	923
Total Genes Detected	5,600

Sample

Sample ID	DHA_Fe_9
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DFO_24

Summary

Gene Expression

7,786

Estimated Number of Cells

34,118

Mean Reads per Cell

918

Median Genes per Cell

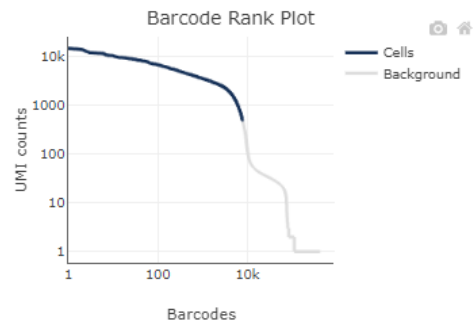
Sequencing ?

Number of Reads	265,641,171
Number of Short Reads Skipped	0
Valid Barcodes	97.7%
Valid UMIs	99.9%
Sequencing Saturation	83.3%
Q30 Bases in Barcode	96.3%
Q30 Bases in RNA Read	93.0%
Q30 Bases in UMI	95.8%

Mapping ?

Reads Mapped to Genome	74.3%
Reads Mapped Confidently to Genome	61.8%
Reads Mapped Confidently to Intergenic Regions	10.3%
Reads Mapped Confidently to Intronic Regions	0.5%
Reads Mapped Confidently to Exonic Regions	51.0%
Reads Mapped Confidently to Transcriptome	46.0%
Reads Mapped Antisense to Gene	2.8%

Cells ?



Estimated Number of Cells	7,786
Fraction Reads in Cells	92.6%
Mean Reads per Cell	34,118
Median UMI Counts per Cell	1,948
Median Genes per Cell	918
Total Genes Detected	5,595

Sample

Sample ID	DFO_24
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DHA_24

Alerts

The analysis detected ⚠ 2 warnings.

Alert	Value	Detail
⚠ Low Fraction Reads Confidently Mapped To Transcriptome	21.3%	Ideal > 30%. This can indicate use of the wrong reference transcriptome, a reference transcriptome with overlapping genes, poor library quality, poor sequencing quality, or reads shorter than the recommended minimum. Application performance may be affected.
⚠ Low Fraction Reads in Cells	61.8%	Ideal > 70%. Application performance may be affected. Many of the reads were not assigned to cell-associated barcodes. This could be caused by high levels of ambient RNA or by a significant population of cells with a low RNA content, which the algorithm did not call as cells. The latter case can be addressed by inspecting the data to determine the appropriate cell count and using --force-cells.

Summary

Gene Expression

1,659

Estimated Number of Cells

177,792

Mean Reads per Cell

438

Median Genes per Cell

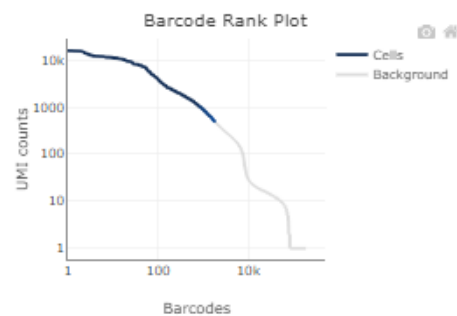
Sequencing ⓘ

Number of Reads	294,956,429
Number of Short Reads Skipped	0
Valid Barcodes	96.5%
Valid UMIs	99.9%
Sequencing Saturation	91.5%
Q30 Bases in Barcode	96.3%
Q30 Bases in RNA Read	92.6%
Q30 Bases in UMI	95.9%

Mapping ⓘ

Reads Mapped to Genome	58.6%
Reads Mapped Confidently to Genome	28.6%
Reads Mapped Confidently to Intergenic Regions	5.0%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	23.4%
Reads Mapped Confidently to Transcriptome	21.3%
Reads Mapped Antisense to Gene	1.1%

Cells ⓘ



Estimated Number of Cells	1,659
Fraction Reads in Cells	61.8%
Mean Reads per Cell	177,792
Median UMI Counts per Cell	1,033
Median Genes per Cell	438
Total Genes Detected	5,559

Sample

Sample ID	DHA_24
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0

DHA_Fe_24

Alerts

The analysis detected 1 error and 1 warning.

Alert	Value	Detail
Low Fraction Reads Confidently Mapped To Transcriptome	14.0%	Ideal > 30%. This can indicate use of the wrong reference transcriptome, a reference transcriptome with overlapping genes, poor library quality, poor sequencing quality, or reads shorter than the recommended minimum. Application performance may be affected.
Low Fraction Reads in Cells	57.8%	Ideal > 70%. Application performance may be affected. Many of the reads were not assigned to cell-associated barcodes. This could be caused by high levels of ambient RNA or by a significant population of cells with a low RNA content, which the algorithm did not call as cells. The latter case can be addressed by inspecting the data to determine the appropriate cell count and using --force-cells.

Summary

Gene Expression

1,739

Estimated Number of Cells

168,298

Mean Reads per Cell

443

Median Genes per Cell

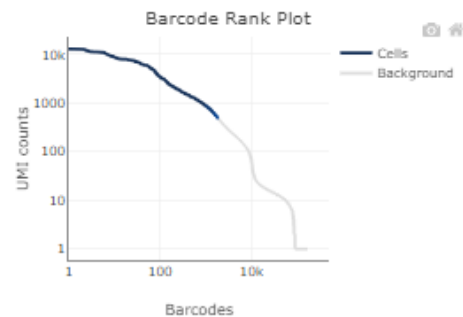
Sequencing

Number of Reads	292,670,577
Number of Short Reads Skipped	0
Valid Barcodes	97.3%
Valid UMIs	99.9%
Sequencing Saturation	87.1%
Q30 Bases in Barcode	96.2%
Q30 Bases in RNA Read	92.5%
Q30 Bases in UMI	95.7%

Mapping

Reads Mapped to Genome	38.0%
Reads Mapped Confidently to Genome	19.8%
Reads Mapped Confidently to Intergenic Regions	4.2%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	15.5%
Reads Mapped Confidently to Transcriptome	14.0%
Reads Mapped Antisense to Gene	0.8%

Cells



Estimated Number of Cells	1,739
Fraction Reads in Cells	57.8%
Mean Reads per Cell	168,298
Median UMI Counts per Cell	986
Median Genes per Cell	443
Total Genes Detected	5,549

Sample

Sample ID	DHA_Fe_24
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Transcriptome	plasmodium_falciparum-
Pipeline Version	cellranger-7.0.0