count_introns_false_4367

Alerts

The analysis detected 🛑 2 errors.

	Alert	Value	Detail
🛑	Low Fraction Reads Confidently Mapped To Transcriptome	12.9%	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	48.4%	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

3,689
Estimated Number of Cells
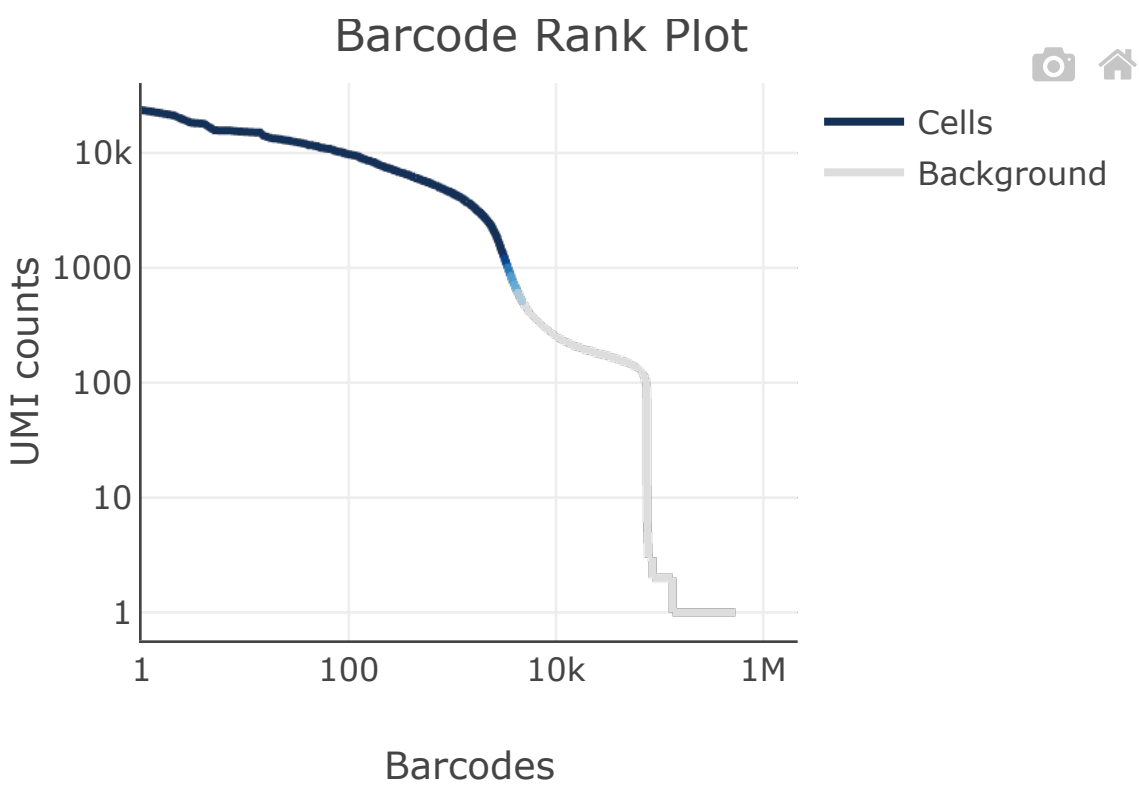
127,150
Mean Reads per Cell

1,606
Median Genes per Cell

Sequencing ⍰

Number of Reads	469,058,071
Number of Short Reads Skipped	0
Valid Barcodes	93.2%
Valid UMIs	99.8%
Sequencing Saturation	54.6%
Q30 Bases in Barcode	97.0%
Q30 Bases in RNA Read	96.4%
Q30 Bases in UMI	97.7%

Cells ⍰

Barcode Rank Plot

Estimated Number of Cells	3,689
Fraction Reads in Cells	48.4%
Mean Reads per Cell	127,150
Median UMI Counts per Cell	2,967
Median Genes per Cell	1,606
Total Genes Detected	22,574

Mapping ⍰

Reads Mapped to Genome	96.5%
Reads Mapped Confidently to Genome	94.9%
Reads Mapped Confidently to Intergenic Regions	5.7%
Reads Mapped Confidently to Intronic Regions	68.9%
Reads Mapped Confidently to Exonic Regions	20.3%
Reads Mapped Confidently to Transcriptome	12.9%
Reads Mapped Antisense to Gene	6.7%

Sample

Sample ID	count_introns_false_4367
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Reference Path	…anger_prebuilt/refdata-gex-mm10-2020-A
Transcriptome	mm10-2020-A
Pipeline Version	cellranger-7.1.0