10x GENOMICS   Cell Ranger • count

Tumour_1

Alerts

The analysis detected ⓘ 1 informational notice.

	Alert	Value	Detail
ⓘ	Intron mode used		This data has been analyzed with intronic reads included in the count matrix. This behavior is different from previous Cell Ranger versions. If you would not like to count intronic reads, please rerun with the "include-introns" option set to "false". Please contact support@10xgenomics.com for any further questions.

Summary	Gene Expression

3,472
Estimated Number of Cells

31,846
Mean Reads per Cell

3,011
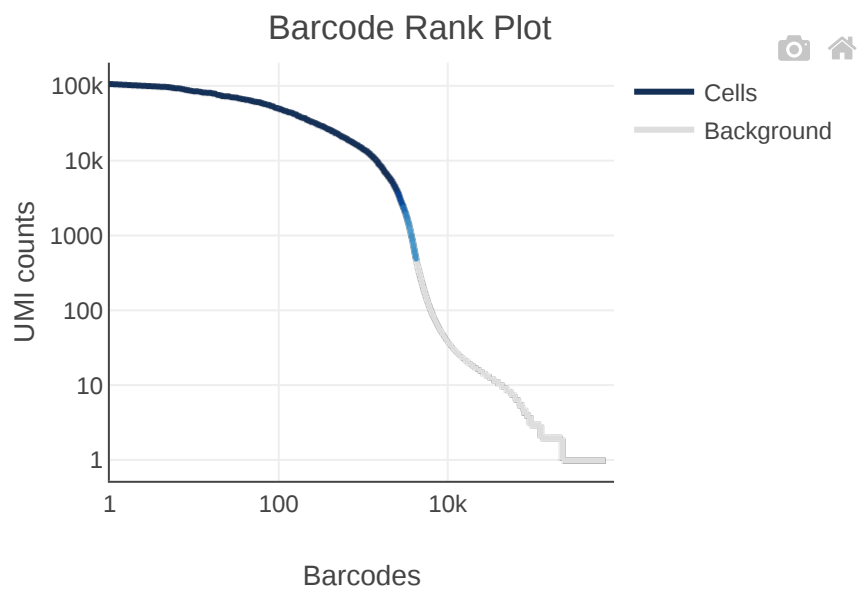Median Genes per Cell

Sequencing ⓘ

Number of Reads	110,568,588
Number of Short Reads Skipped	0
Valid Barcodes	96.4%
Valid UMIs	99.9%
Sequencing Saturation	42.7%
Q30 Bases in Barcode	94.7%

Q30 Bases in RNA Read	92.9%
Q30 Bases in UMI	94.7%

Mapping ⍰

Reads Mapped to Genome	96.7%
Reads Mapped Confidently to Genome	93.5%
Reads Mapped Confidently to Intergenic Regions	6.5%
Reads Mapped Confidently to Intronic Regions	25.9%
Reads Mapped Confidently to Exonic Regions	61.1%
Reads Mapped Confidently to Transcriptome	76.3%
Reads Mapped Antisense to Gene	9.9%

Cells ⍰

Barcode Rank Plot

Estimated Number of Cells	3,472
Fraction Reads in Cells	92.6%
Mean Reads per Cell	31,846
Median UMI Counts per Cell	7,928
Median Genes per Cell	3,011

Total Genes Detected	29,604

Sample

Sample ID	Tumour_1
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	True
Reference Path	…/10xgenomics/refdata-gex-GRCh38-2020-A
Transcriptome	GRCh38-2020-A
Pipeline Version	cellranger-7.1.0