count_

Alerts

The analysis detected ❗1 error and ⓘ 1 informational notice.

	Alert	Value	Detail
❗	High Fraction of Reads Mapped Antisense to Genes	58.2%	Ideal < 20%. Rates of up to 40% are common for single nuclei samples. Higher fraction of antisense reads may indicate use of an incorrect chemistry type, or an issue with the reference transcriptome.
ⓘ	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

3,731
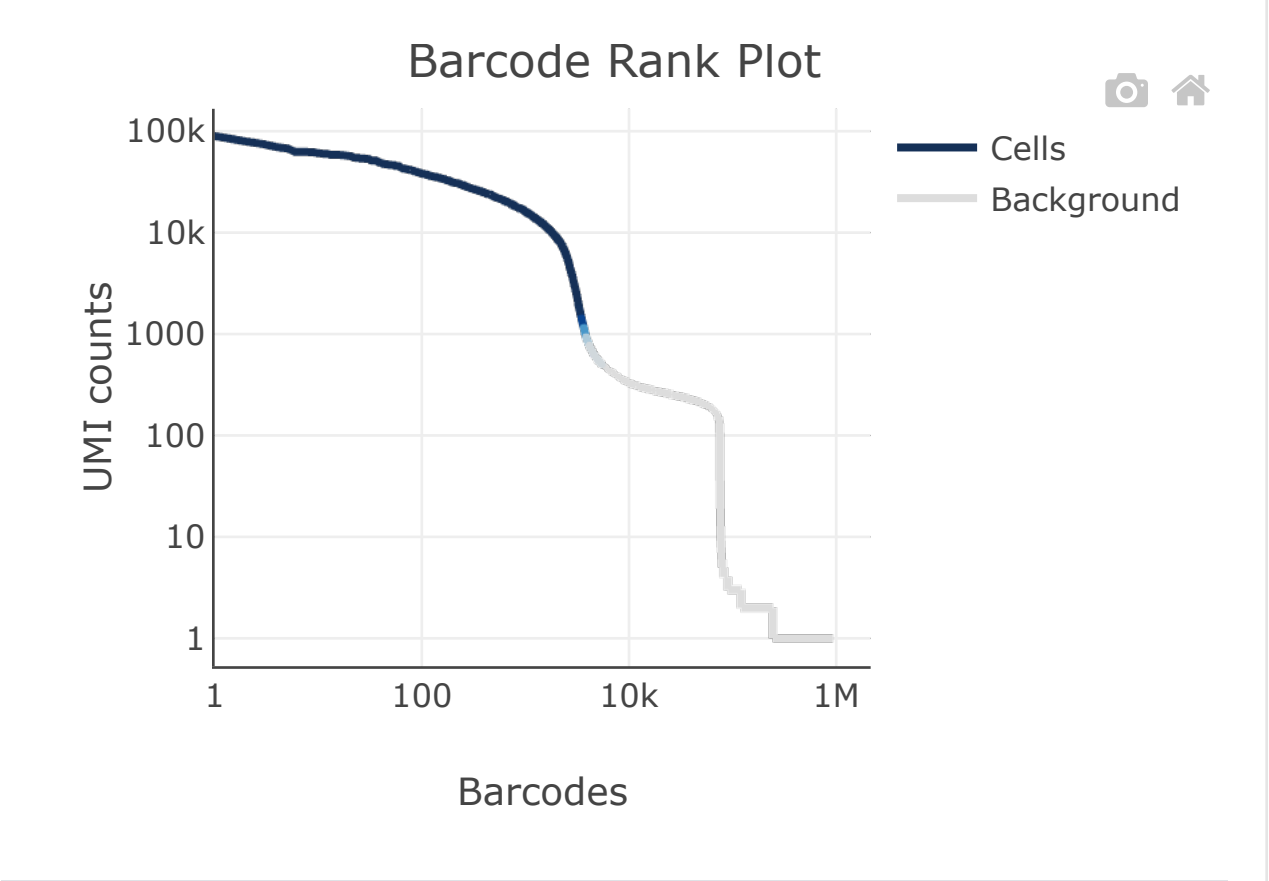Estimated Number of Cells

125,719
Mean Reads per Cell

3,407
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	54.3%
Q30 Bases in Barcode	97.0%
Q30 Bases in RNA Read	96.4%
Q30 Bases in UMI	97.7%

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	30.8%
Reads Mapped Antisense to Gene	58.2%

Cells ⓘ

Barcode Rank Plot

Estimated Number of Cells	3,731
Fraction Reads in Cells	70.0%
Mean Reads per Cell	125,719
Median UMI Counts per Cell	9,420
Median Genes per Cell	3,407
Total Genes Detected	25,808

Sample

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