

count_Tomato10rep1

Alerts

The analysis detected ⚠️ 1 warning and ℹ️ 1 informational notice.

Alert	Value	Detail
⚠️	Low Fraction Reads in Cells	63.5% 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.
ℹ️	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
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6,693

Estimated Number of Cells

58,523

Mean Reads per Cell

852

Median Genes per Cell

Sequencing ?	
Number of Reads	391,696,259
Number of Short Reads Skipped	0
Valid Barcodes	97.7%
Valid UMIs	100.0%
Sequencing Saturation	85.9%
Q30 Bases in Barcode	97.6%
Q30 Bases in RNA Read	96.1%
Q30 Bases in UMI	97.2%

Mapping ?	
Reads Mapped to Genome	95.3%
Reads Mapped Confidently to Genome	72.7%
Reads Mapped Confidently to Intergenic Regions	32.4%
Reads Mapped Confidently to Intronic Regions	4.8%
Reads Mapped Confidently to Exonic Regions	35.4%
Reads Mapped Confidently to Transcriptome	36.3%
Reads Mapped Antisense to Gene	3.8%

Cells ?

Barcode Rank Plot

Estimated Number of Cells	6,693
Fraction Reads in Cells	63.5%
Mean Reads per Cell	58,523
Median UMI Counts per Cell	1,127
Median Genes per Cell	852
Total Genes Detected	24,244

Sample	
Sample ID	count_Tomato10rep1
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	True
Reference Path	...persicum/SL3.0/Solanum_lycopersicum.52
Transcriptome	Solanum_lycopersicum.52-
Pipeline Version	cellranger-7.1.0