

count_Arab1rep1

Alerts

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

Alert	Value	Detail
⚠️	Low Fraction Reads in Cells	56.3% 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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10,185

Estimated Number of Cells

38,356

Mean Reads per Cell

1,373

Median Genes per Cell

Sequencing ?	
Number of Reads	390,656,728
Number of Short Reads Skipped	0
Valid Barcodes	94.4%
Valid UMIs	100.0%
Sequencing Saturation	45.7%
Q30 Bases in Barcode	97.7%
Q30 Bases in RNA Read	95.3%
Q30 Bases in UMI	97.4%

Mapping ?	
Reads Mapped to Genome	97.4%
Reads Mapped Confidently to Genome	74.8%
Reads Mapped Confidently to Intergenic Regions	7.1%
Reads Mapped Confidently to Intronic Regions	0.3%
Reads Mapped Confidently to Exonic Regions	67.4%
Reads Mapped Confidently to Transcriptome	66.4%
Reads Mapped Antisense to Gene	1.2%

Cells ?

Barcode Rank Plot

Estimated Number of Cells	10,185
Fraction Reads in Cells	56.3%
Mean Reads per Cell	38,356
Median UMI Counts per Cell	2,535
Median Genes per Cell	1,373
Total Genes Detected	23,312

Sample	
Sample ID	count_Arab1rep1
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	True
Reference Path	...ana/TAIR10/Arabidopsis_thaliana.TAIR10
Transcriptome	Arabidopsis_thaliana.TAIR10-
Pipeline Version	cellranger-7.1.0