count_Col01mMR1

Alerts

The analysis detected ❗ 1 error.

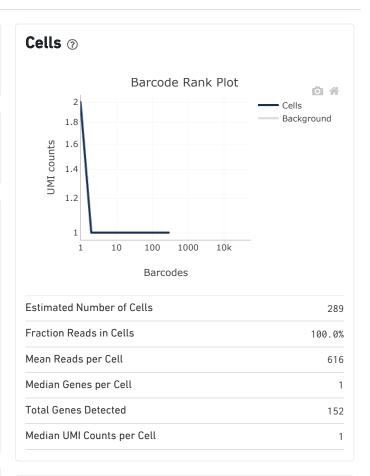|	Alert	Value	Detail
❗	Low Fraction Reads Confidently Mapped To Transcriptome	0.2%	Ideal > 30%. This can indicate use of the wrong reference transcriptome, a reference transcriptome with overlapping genes, poor library quality, poor sequencing quality, or reads shorter than the recommended minimum. Application performance may be affected.

Summary   Analysis

<table>
<tr><td align="center">289
Estimated Number of Cells</td></tr>
</table>

616	**1**
Mean Reads per Cell	Median Genes per Cell

Sequencing ⍰

Number of Reads	178,160
Number of Short Reads Skipped	0
Valid Barcodes	91.2%
Valid UMIs	99.9%
Sequencing Saturation	0.3%
Q30 Bases in Barcode	99.1%
Q30 Bases in RNA Read	84.1%
Q30 Bases in UMI	99.4%

Cells ⍰

Barcode Rank Plot

Estimated Number of Cells	289
Fraction Reads in Cells	100.0%
Mean Reads per Cell	616
Median Genes per Cell	1
Total Genes Detected	152
Median UMI Counts per Cell	1

Mapping ⍰

Reads Mapped to Genome	4.6%
Reads Mapped Confidently to Genome	2.2%
Reads Mapped Confidently to Intergenic Regions	1.7%
Reads Mapped Confidently to Intronic Regions	0.3%
Reads Mapped Confidently to Exonic Regions	0.3%
Reads Mapped Confidently to Transcriptome	0.2%
Reads Mapped Antisense to Gene	0.1%

Sample

Sample ID	count_Col01mMR1
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Reference Path	…Solanum_lycopersicum.52
Transcriptome	Solanum_lycopersicum.52-
Pipeline Version	cellranger-6.0.1