

# count\_nlp711mMR1

## Alerts

The analysis detected 1 error.

Alert	Value	Detail
<span style="color: red;">1</span> Low Fraction Reads Confidently Mapped To Transcriptome	0.3%	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
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524

Estimated Number of Cells

321

Mean Reads per Cell

1

Median Genes per Cell

### Sequencing ?

Number of Reads	168,280
Number of Short Reads Skipped	0
Valid Barcodes	90.9%
Valid UMIs	99.9%
Sequencing Saturation	0.0%
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	524
Fraction Reads in Cells	100.0%
Mean Reads per Cell	321
Median Genes per Cell	1
Total Genes Detected	87
Median UMI Counts per Cell	1

### Mapping ?

Reads Mapped to Genome	6.2%
Reads Mapped Confidently to Genome	3.2%
Reads Mapped Confidently to Intergenic Regions	2.4%
Reads Mapped Confidently to Intronic Regions	0.2%
Reads Mapped Confidently to Exonic Regions	0.6%
Reads Mapped Confidently to Transcriptome	0.3%
Reads Mapped Antisense to Gene	0.2%

### Sample

Sample ID	count_nlp711mMR1
Sample Description	
Chemistry	Single Cell 3' v3
Include introns	False
Reference Path	...idopsis_thaliana.TAIR10
Transcriptome	Arabidopsis_thaliana.TAIR10-
Pipeline Version	cellranger-6.0.1