count_nlp711mMR1

Alerts

The analysis detected **()** 1 error.

	Alert	Value	Detail
0	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

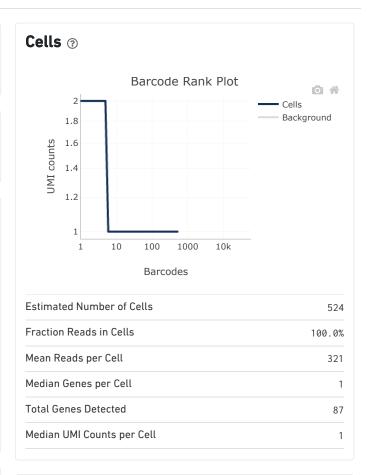
Analysis

524Estimated Number of Cells

321	1	
Mean Reads per Cell	Median Genes per Cell	

Sequencing ③				
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%			

Mapping ③				
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			