count_nlp711mMR1

Alerts

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

	Alert	Value	Detail
0	Low Fraction Reads Confidently Mapped To Transcriptome	1.7%	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

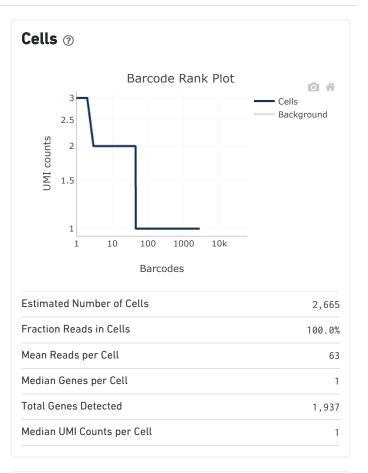
Analysis

2,665
Estimated Number of Cells

63	1
Mean Reads per Cell	Median Genes per Cell

Sequencing ②				
168,280				
0				
90.9%				
99.9%				
0.3%				
99.1%				
84.1%				
99.4%				

Mapping ③				
Reads Mapped to Genome	5.5%			
Reads Mapped Confidently to Genome	3.9%			
Reads Mapped Confidently to Intergenic Regions	1.3%			
Reads Mapped Confidently to Intronic Regions	0.6%			
Reads Mapped Confidently to Exonic Regions	2.0%			
Reads Mapped Confidently to Transcriptome	1.7%			
Reads Mapped Antisense to Gene	0.1%			



Sample				
Sample ID	count_nlp711mMR1			
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			