count_run1

Alerts

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

	Alert	Value	Detail
0	Low Fraction Reads Confidently Mapped To Transcriptome	6.3%	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

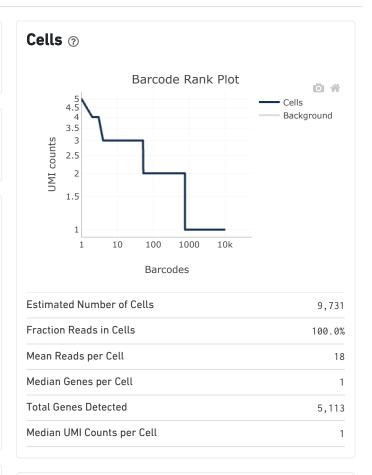
Analysis

9,731 Estimated Number of Cells

18	1		
Mean Reads per Cell	Median Genes per Cell		

Sequencing ③			
Number of Reads	178,160		
Number of Short Reads Skipped	0		
Valid Barcodes	91.2%		
Valid UMIs	99.9%		
Sequencing Saturation	0.2%		
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	16.9%			
Reads Mapped Confidently to Genome	11.5%			
Reads Mapped Confidently to Intergenic Regions	4.2%			
Reads Mapped Confidently to Intronic Regions	0.4%			
Reads Mapped Confidently to Exonic Regions	6.9%			
Reads Mapped Confidently to Transcriptome	6.3%			
Reads Mapped Antisense to Gene	0.4%			



Sample				
count_run1				
Single Cell 3' v3				
False				
idopsis_thaliana.TAIR10				
Arabidopsis_thaliana.TAIR10-				
cellranger-6.0.1				