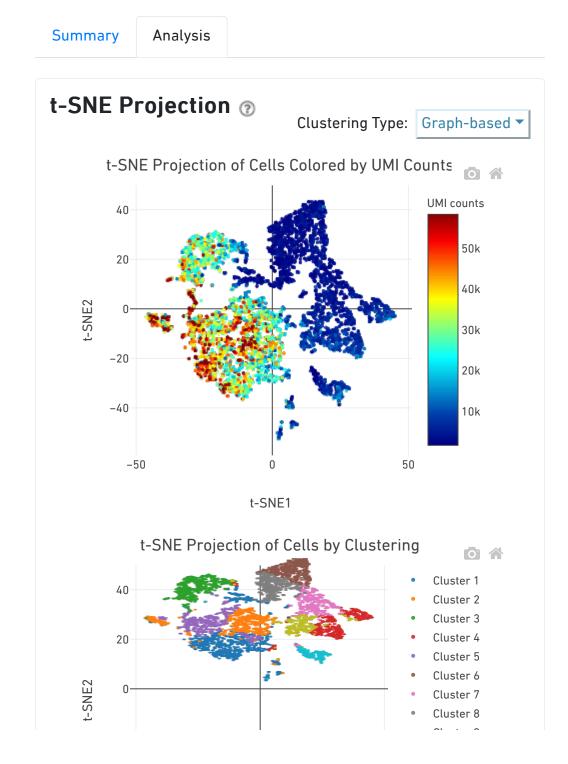
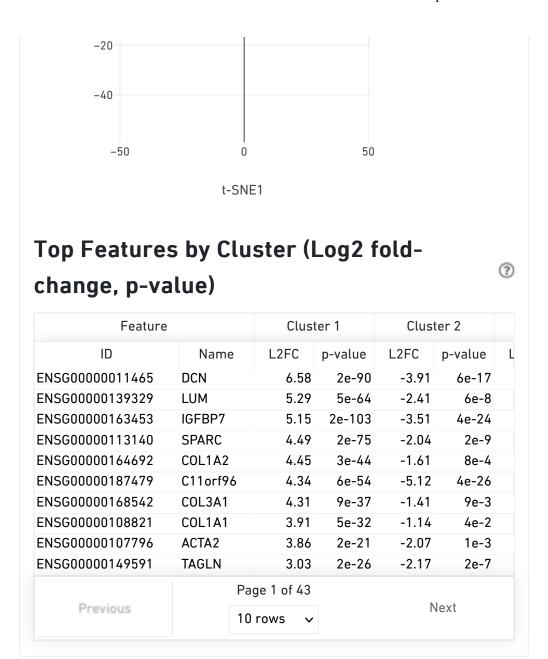
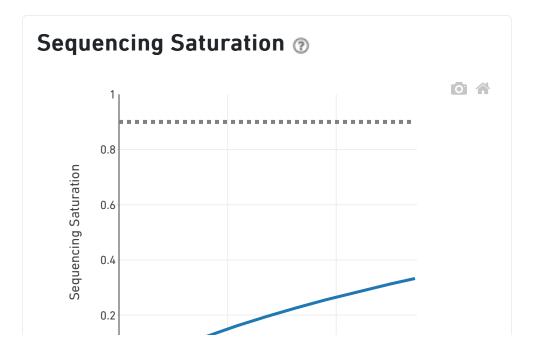


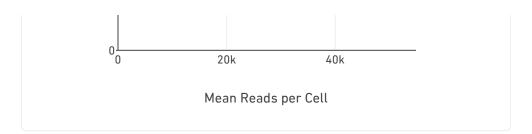
Breast_Cancer_3p - Sorted cells from Human Invasive Ductal Carcinoma, 3' v3.1

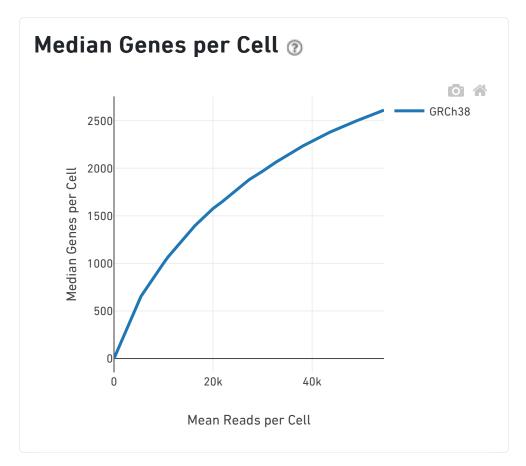


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Breast_Cancer_3p - Sorted cells from Human Invasive Ductal Carcinoma, 3' v3.1

Summary

Analysis

5,680

Estimated Number of Cells

54,504

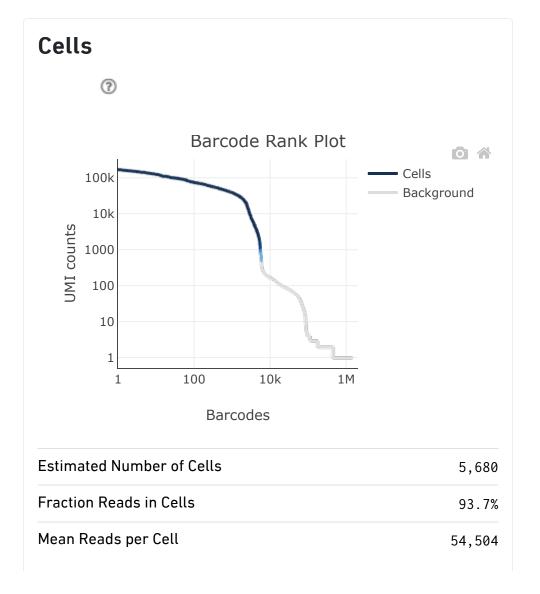
2,610

Mean Reads per Cell

Median Genes per Cell

Sequencing ②		
Number of Reads	309,585,432	
Number of Short Reads Skipped	0	
Valid Barcodes	98.2%	
Valid UMIs	100.0%	
Sequencing Saturation	33.3%	
Q30 Bases in Barcode	95.7%	
Q30 Bases in RNA Read	93.5%	
Q30 Bases in UMI	94.2%	

Mapping		
②		
Reads Mapped to Genome	96.8%	
Reads Mapped Confidently to Genome	94.0%	
Reads Mapped Confidently to Intergenic Regions	8.7%	
Reads Mapped Confidently to Intronic Regions	21.9%	
Reads Mapped Confidently to Exonic Regions	63.4%	
Reads Mapped Confidently to Transcriptome	60.8%	
Reads Mapped Antisense to Gene	1.4%	



26,156
11,498

Sample	
Sample ID	Breast_Cancer_3p
Sample Description	Sorted cells from Human Invasive Ductal Carcinoma, 3' v3.1
Chemistry	Single Cell 3' v3
Include introns	False
Reference Path	references/refdata-gex-GRCh38-2020-A
Transcriptome	GRCh38-2020-A
Pipeline Version	cellranger-6.0.0