

Copy of Kinnex-SingleCell-Release-PBMC-10x3p

SUCCESSFUL

Copy

Delete

▼ Analysis Overview
Status
Thumbnails
Display All
► Read Segmentation
► Read Statistics
► Cell Statistics
► Transcript Statistics
► Data

Display All

Status

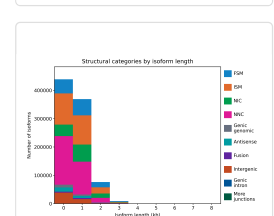
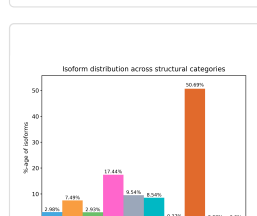
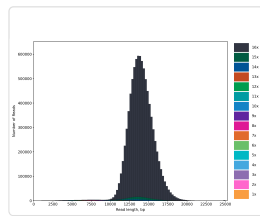
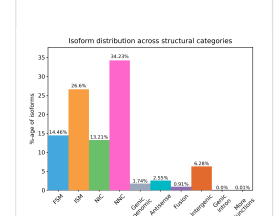
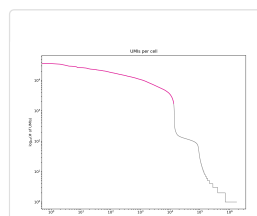
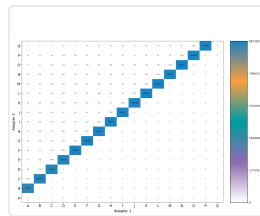
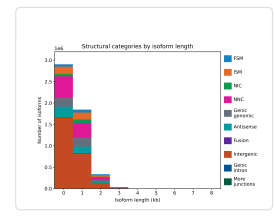
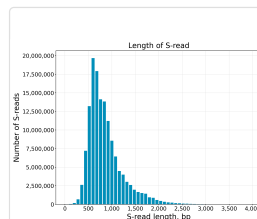
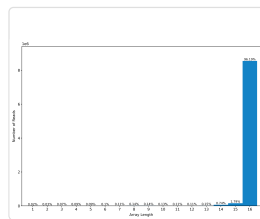
Analysis	Copy of Kinnex-SingleCell-Release-PBMC-10x3p
Analysis ID	110684
Status	SUCCESSFUL: 14 tasks finished
Created By	etseng
Date Created	2024-02-14, 11:14:49 AM
Date Updated	2024-02-14, 11:05:47 PM
Application	Read Segmentation and Single-Cell Iso-Seq
SMRT Link Version	13.1.0.218252

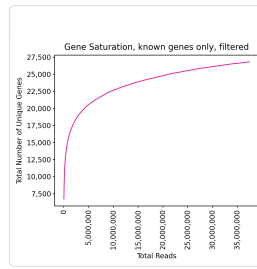
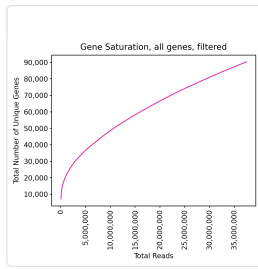
Inputs

Data Type	Name	Import Com
BarcodeSet	Barcode Sets: 10x Chromium single cell 3' c...	Yes
BarcodeSet	Barcode Sets: MAS-Seq Adapter v1 (MAS16)	Yes
ConsensusReadSet	HiFi Reads: 3pPBMC-Cell8 (Bio Sample 3)	Yes
ReferenceSet	References: Human Genome hg38, with Ge...	Yes

► Analysis Parameters

Thumbnails

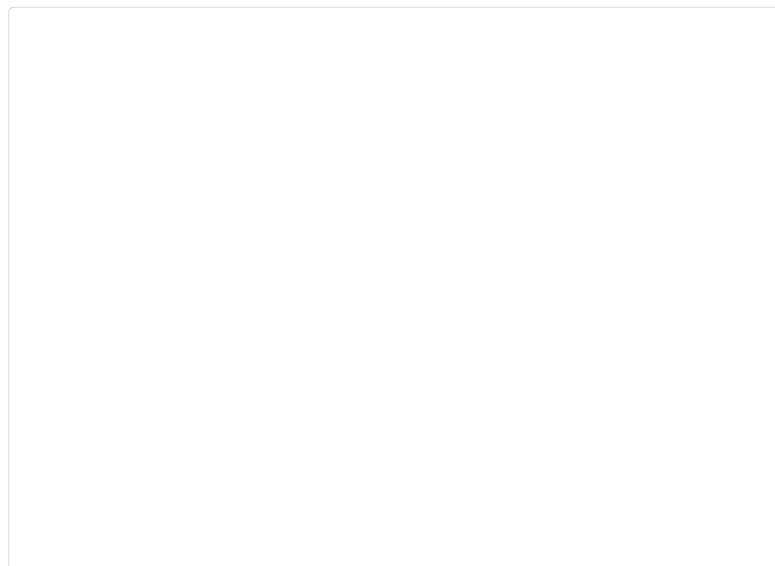
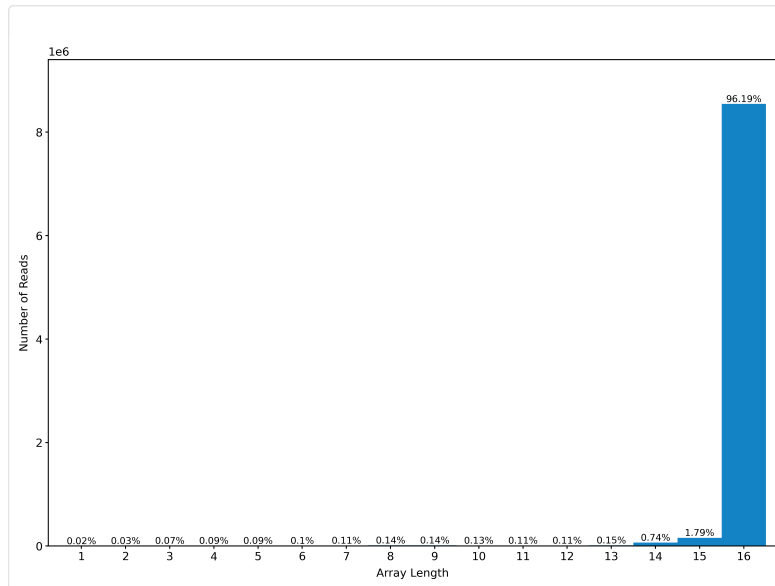


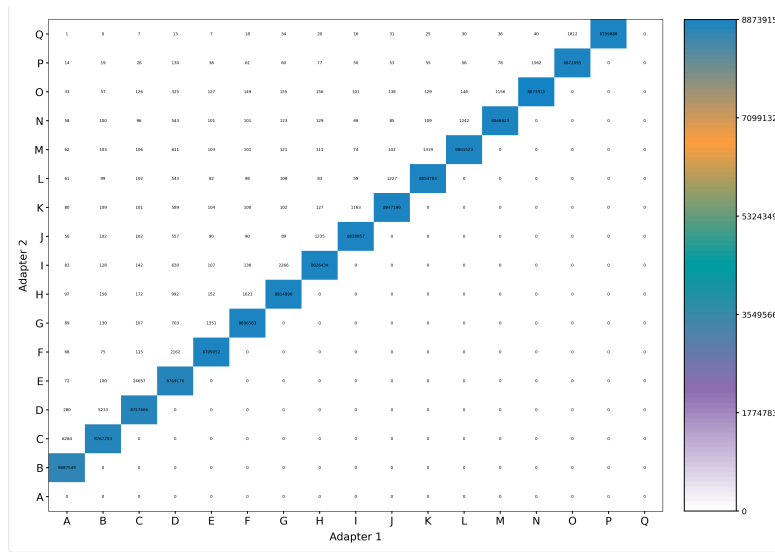


Read Segmentation

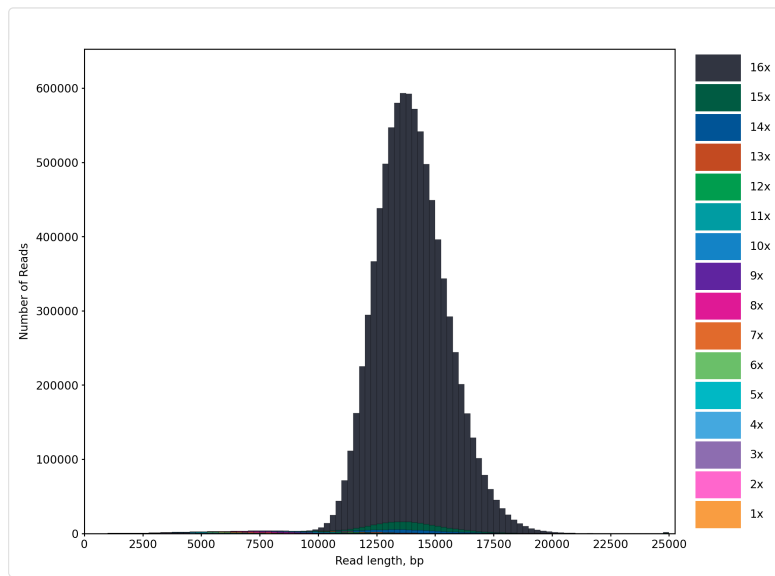
Value	Analysis Metric
8,889,073	Reads
141,045,827	Segmented reads (S-reads)
860	Mean length of S-reads
96.18 %	Percent of reads with full arrays
15.87	Mean array size (concatenation factor)

Segmentation Statistics

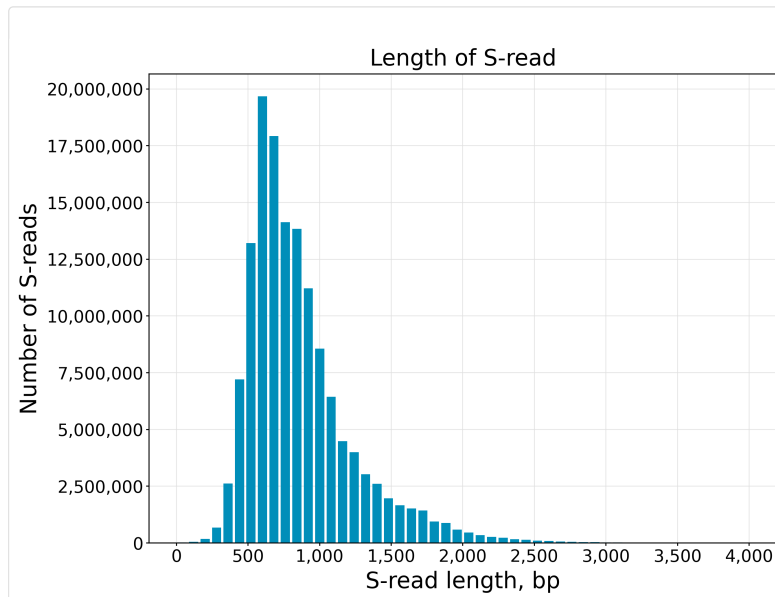




Length of Reads



S-read Length Distribution



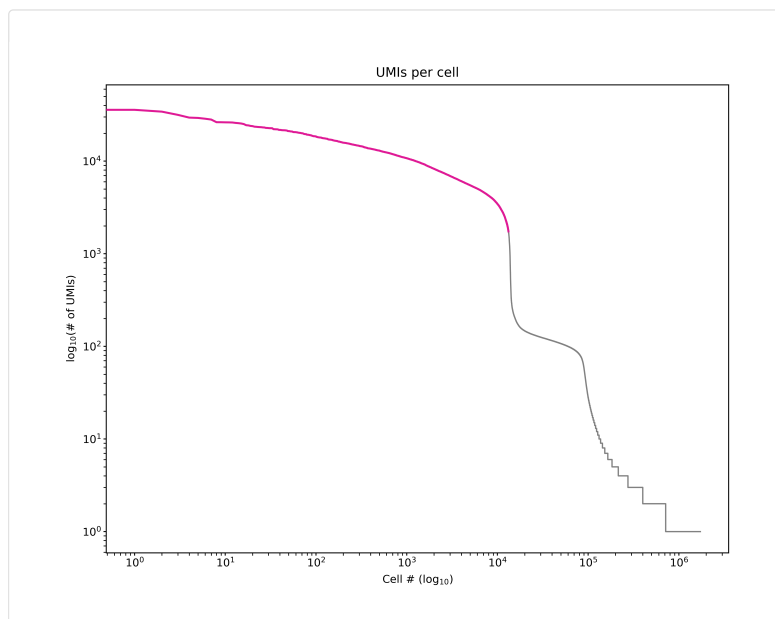
Read Statistics

Value	Analysis Metric
141,045,827	Reads
SEGMENT	Read Type
140,183,884	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
134,236,764	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
131,936,982	FLNC Reads with Valid Barcodes
134,118,572	FLNC Reads with Valid Barcodes, corrected
81,678,354	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
12,840	Estimated Number of Cells
84.67%	Reads in Cells
8,852	Mean Reads per Cell
4,884	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
101,499,129	FLNC Reads Mapped Confidently to Genome
50,707,902	FLNC Reads Mapped Confidently to Transcriptome

Value	Analysis Metric
2,664,088	Total Unique Genes
90,294	Total Unique Genes, filtered
36,615	Total Unique Genes, known genes only
26,813	Total Unique Genes, filtered, known genes only
4,686,331	Total Unique Transcripts
610,357	Total Unique Transcripts, filtered
96,468	Total Unique Transcripts, known transcripts only
83,246	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Value ↑	Analysis Metric ↑
2,396	Median Genes per Cell
1,359	Median Genes per Cell, known genes only
2,719	Median Transcripts per Cell
1,012	Median Transcripts per Cell, known transcripts only
2,664,088	Total Unique Genes
36,615	Total Unique Genes, known genes only
4,686,331	Total Unique Transcripts
96,468	Total Unique Transcripts, known transcripts only

Transcript Summary, filtered

Value ↑	Analysis Metric ↑
912	Median Genes per Cell
897	Median Genes per Cell, known genes only
1,060	Median Transcripts per Cell
845	Median Transcripts per Cell, known transcripts only
90,294	Total Unique Genes
26,813	Total Unique Genes, known genes only
610,357	Total Unique Transcripts
83,246	Total Unique Transcripts, known transcripts only

Transcript Classification

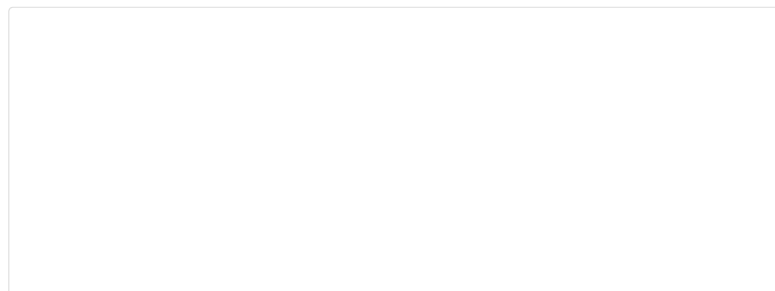
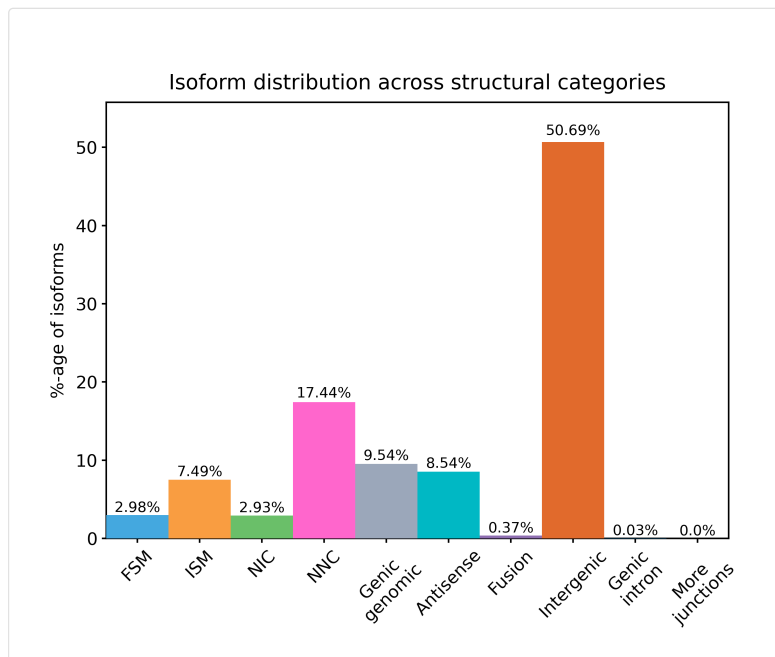
Category ↑	Count ↑	CAGE Detected ↑	CAGE Detected ... ↑	polyA Motif Det... ↑
FSM	152712	88244	57.78%	46781
ISM	383733	160256	41.76%	111539
NIC	150099	104666	69.73%	48939

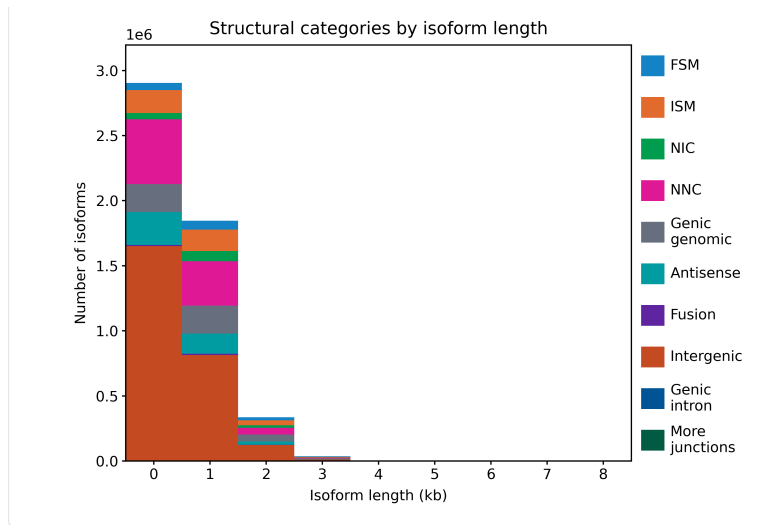
NNC	893989	538189	60.20%	356247
Antisense	437730	6339	1.44%	106296
Fusion	18893	10675	56.50%	7643
More junctions	122	63	51.63%	34
Genic intron	1641	8	0.48%	497
Genic genomic	488919	111842	22.87%	145673
Intergenic	2598470	11685	0.44%	831630

Transcript Classification, filtered

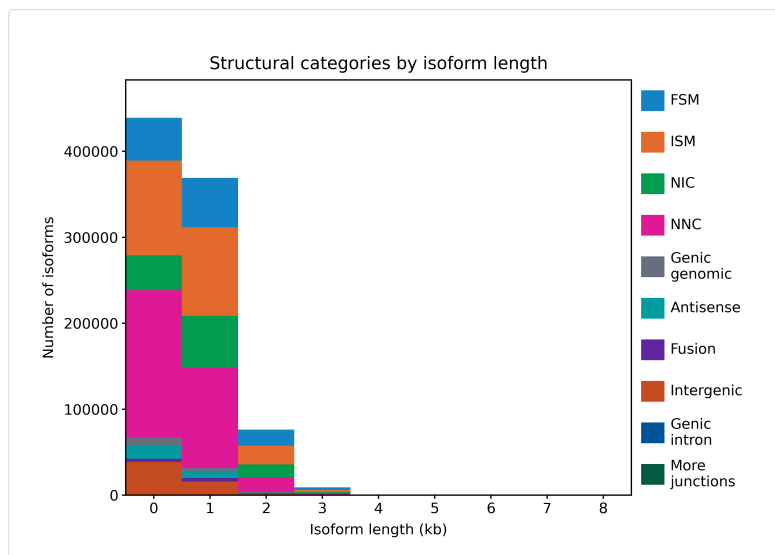
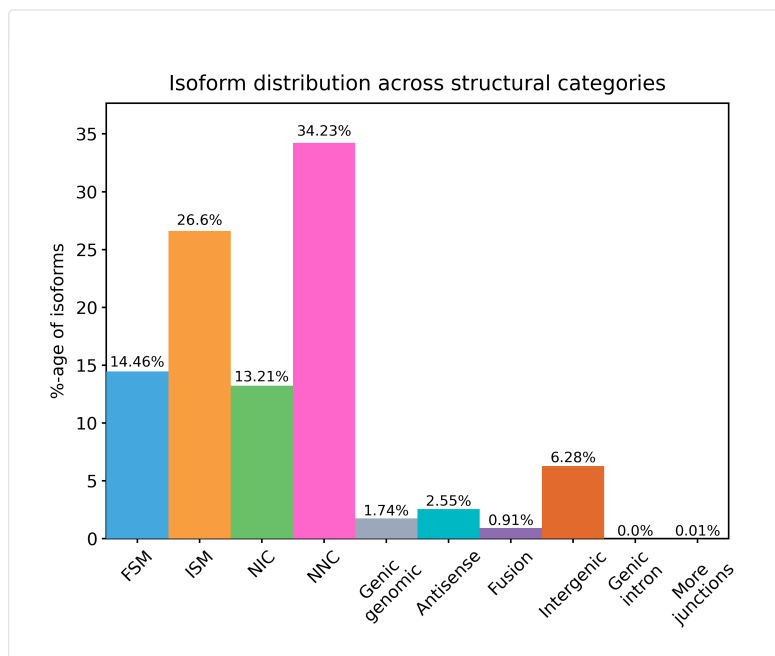
Category ↓	Count ↓	CAGE Detected ↓	CAGE Detected, ... ↓	polyA Detected ↓	p
FSM	129358	77272	59.73%	46781	
ISM	237949	123756	52.00%	82063	
NIC	118188	82457	69.76%	48355	
NNC	306169	193527	63.20%	147027	
Antisense	22839	1350	5.91%	14590	
Fusion	8136	4787	58.83%	4067	
More junctions	80	39	48.75%	29	
Genic intron	1	0	0.00%	0	
Genic genomic	15539	8144	52.41%	6256	
Intergenic	56159	1557	2.77%	35526	

Transcript Classification Plots





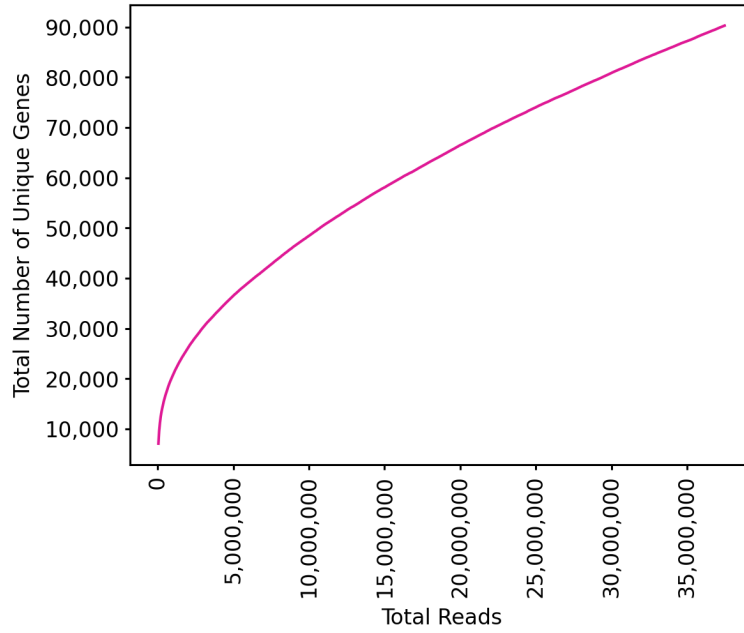
Transcript Classification Plots, filtered



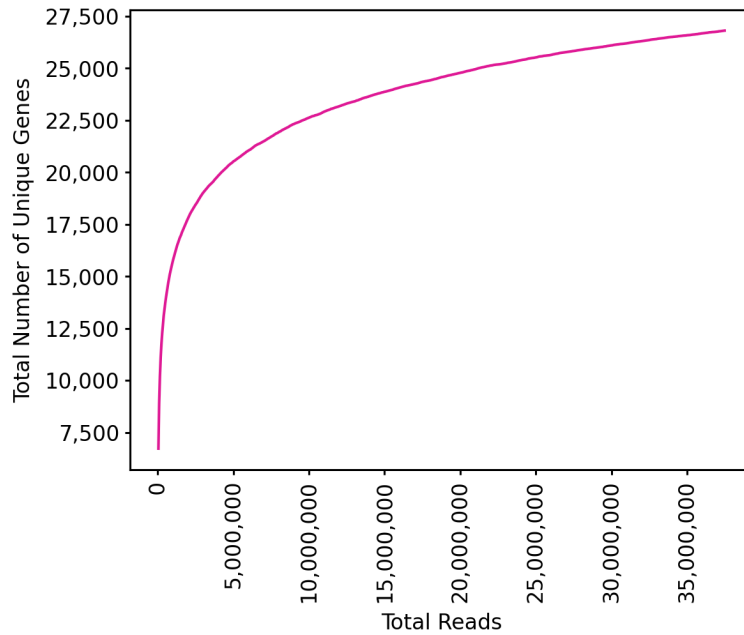
Gene Saturation



Gene Saturation, all genes, filtered









Gene Saturation, known genes only, filtered



File Downloads

Edit Output File Name Prefix

Example:analysis-Bio Sample 3-110684

File ↕	Size ↕	Type ↕
3pPBMC-Cell8 (Bio Sample 3) Segmented Reads	21 KB	ConsensusRead
 Report read segmentation	3 KB	JsonReport
 Deduplicated reads after cell barcode correction, unmapped, BAM	19 GB	bam
 Single-cell isoform and gene matrix, tar-gzipped	2 GB	tgz
 Segmented Reads, passing, unaligned	73 GB	bam
 Non-passing reads, unaligned	2 GB	bam
 Unique mapped transcripts, GFF	2 GB	gff