

KinnexRelease-10x-3pGEX-PBMC-20k -rep2-2RevioCell-largeMem

SUCCESSFUL

Send Log Files

Copy

Delete

▼ Analysis Overview

Status

Thumbnails

Display All

► Read Segmentation

► Read Statistics

► Cell Statistics

► Transcript Statistics

► Data

Display All

Status

Analysis	KinnexRelease-10x-3pGEX-PBMC-20k-rep2-2RevioCell-largeMem
Analysis ID	124626
Status	SUCCESSFUL: 15 tasks finished
Created By	etseng
Date Created	2025-08-02, 06:27:51 AM
Date Updated	2025-08-03, 03:41:44 PM
Application	Read Segmentation and Single-Cell Iso-Seq
SMRT Link Version	25.3.0.273777

Inputs

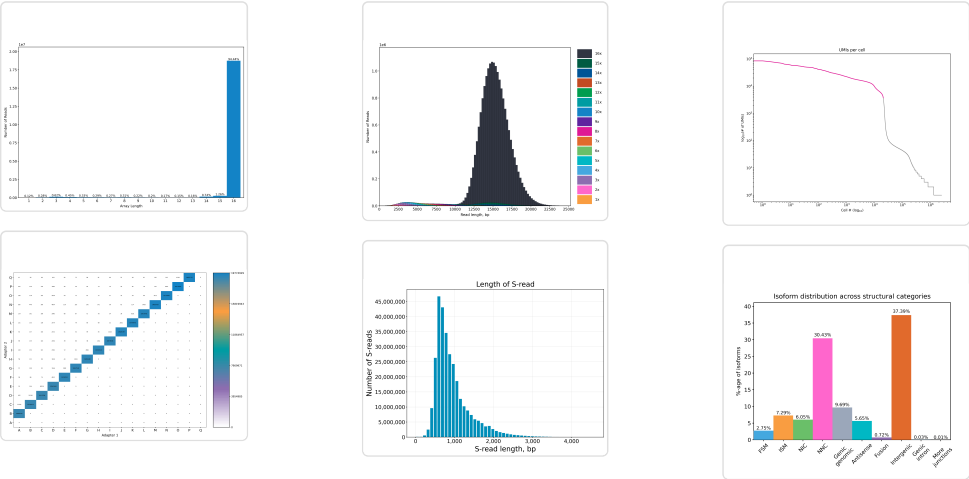
Data Type	Name
BarcodeSet	Barcodes: MAS-Seq Adapter v1 (MAS16)
BarcodeSet	Barcodes: 10x Chromium single cell 3' cDNA
ConsensusReadSet	HiFi reads: 3prime v4 GEX hPBMCs 20k
ConsensusReadSet	HiFi reads: 3prime v4 GEX hPBMCs 20k
ReferenceSet	References: Human Genome hg38, with Ge

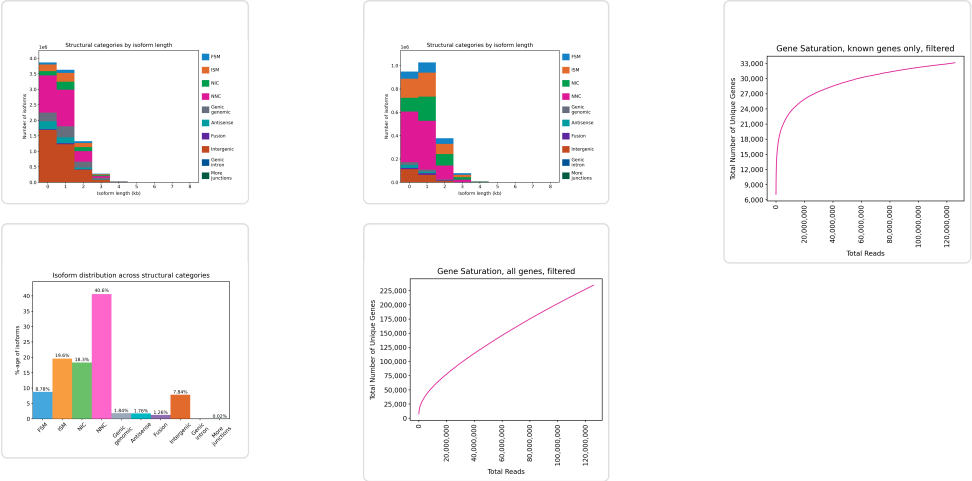
Path

/pbi/flash/smrtlink/smrtlink-alpha/smrtlink/userdata/jobs_root/0000/0000124/0000124626

► Analysis Parameters

Thumbnails

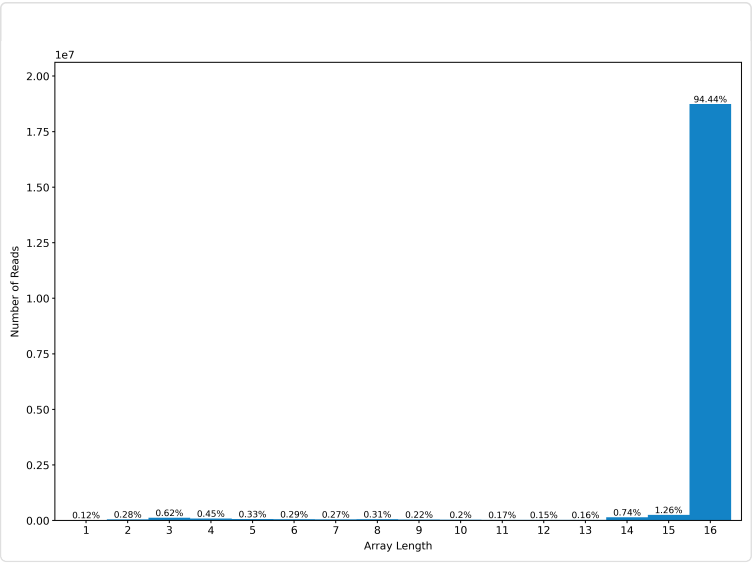


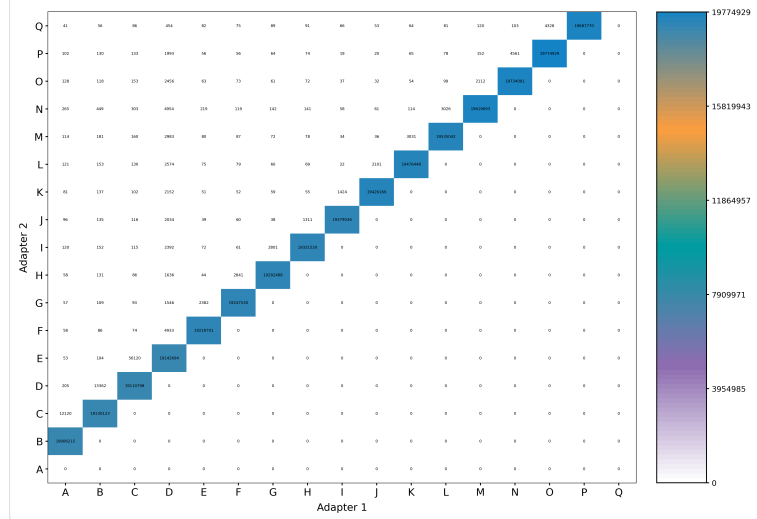


Read Segmentation

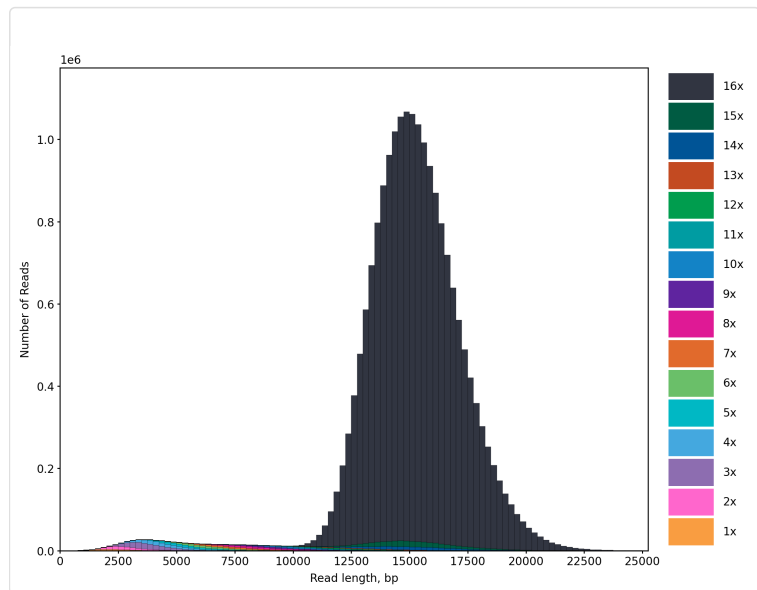
Value	Analysis Metric
19,856,760	Reads
310,092,557	Segmented reads (S-reads)
941.5	Mean length of S-reads
94.42 %	Percent of reads with full arrays
15.62	Mean array size (concatenation factor)

Segmentation Statistics

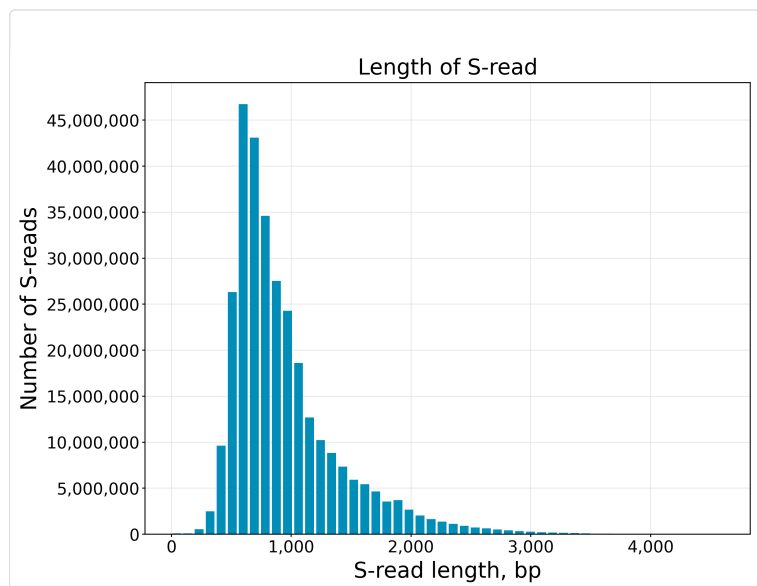




Length of Reads



S-read Length Distribution



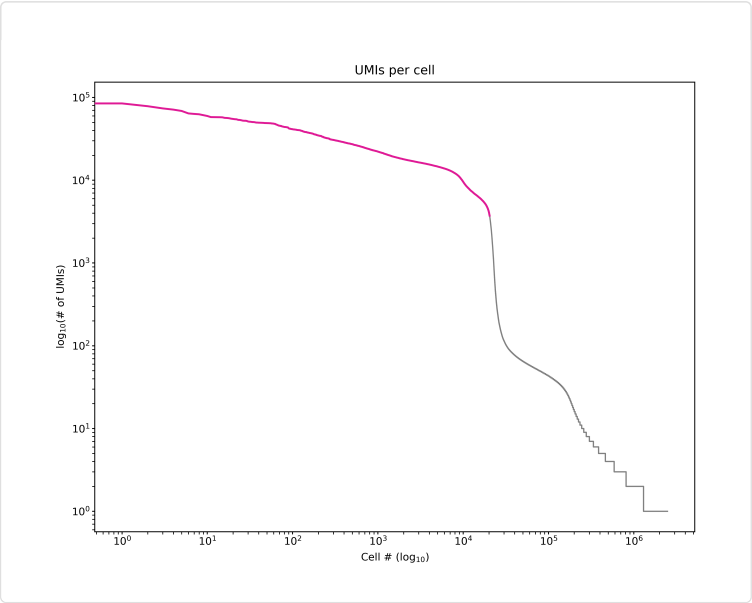
Read Statistics

Value	Analysis Metric
310,092,557	Reads
SEGMENT	Read Type
307,623,491	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
300,266,603	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
294,426,429	FLNC Reads with Valid Barcodes
299,602,036	FLNC Reads with Valid Barcodes, corrected
225,778,491	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
20,218	Estimated Number of Cells
91.79%	Reads in Cells
13,632	Mean Reads per Cell
9,397	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
242,519,132	FLNC Reads Mapped Confidently to Genome
147,827,734	FLNC Reads Mapped Confidently to Transcriptome
3,494,509	Total Unique Genes
234,431	Total Unique Genes, filtered
43,472	Total Unique Genes, known genes only
33,117	Total Unique Genes, filtered, known genes only
8,344,200	Total Unique Transcripts
1,858,418	Total Unique Transcripts, filtered
117,728	Total Unique Transcripts, known transcripts only
108,246	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Search ...

Value 	Analysis Metric 
3,729	Median Genes per Cell
2,586	Median Genes per Cell
5,003	Median Transcripts per
2,105	Median Transcripts per
3,494,509	Total Unique Genes
43,472	Total Unique Genes, kr
8,344,200	Total Unique Transcrip
117,728	Total Unique Transcrip

Transcript Summary, filtered

Search ...

Value 	Analysis Metric 
1,863	Median Genes per Cell
1,816	Median Genes per Cell
2,444	Median Transcripts per

2,444	Median Transcripts per
1,802	
234,431	Total Unique Genes
33,117	Total Unique Genes, kr
1,858,418	Total Unique Transcrip
108,246	Total Unique Transcrip

Transcript Classification

Search ...

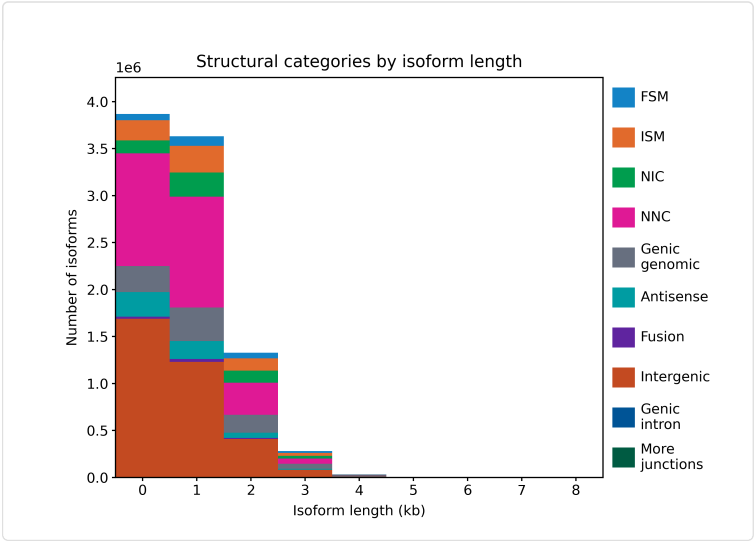
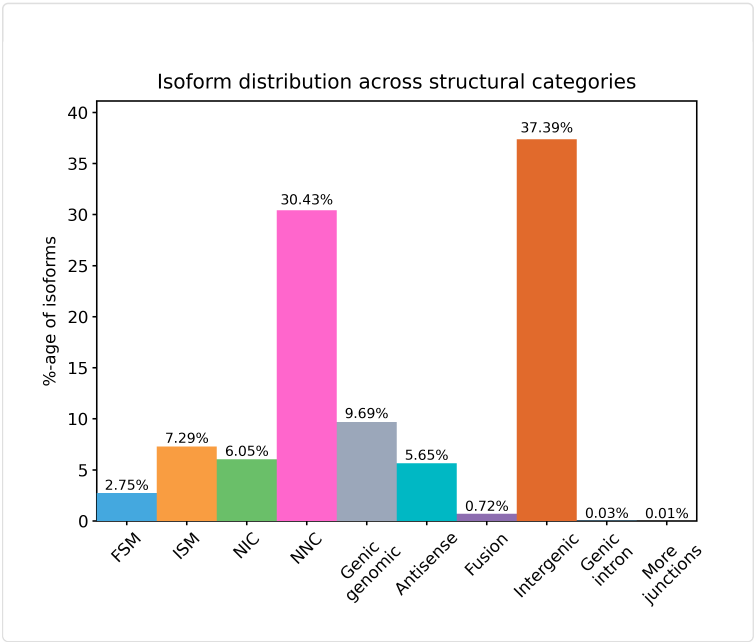
Category ⬆️⬆️	Count ⬆️⬆️	CAGE Detected ⬆️⬆️	CAGE Detected (%) ⬆️⬆️
FSM	251486	141312	56.19%
ISM	666493	266062	39.91%
NIC	553284	354213	64.02%
NNC	2782904	1713835	61.58%
Antisense	517075	17598	3.40%
Fusion	65406	36305	55.50%
More junctions	912	436	47.80%
Genic intron	2390	6	0.25%
Genic genomic	885675	217877	24.60%
Intergenic	3418826	31704	0.92%

Transcript Classification, filtered

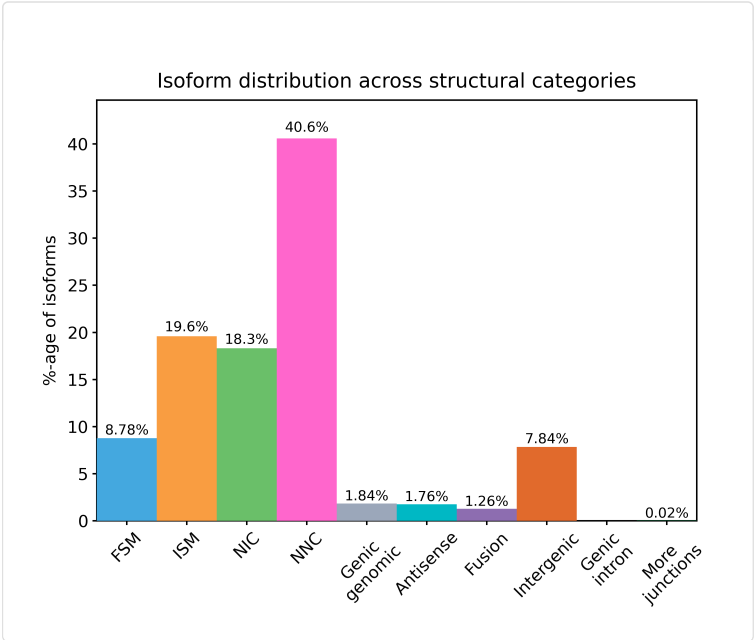
Search ...

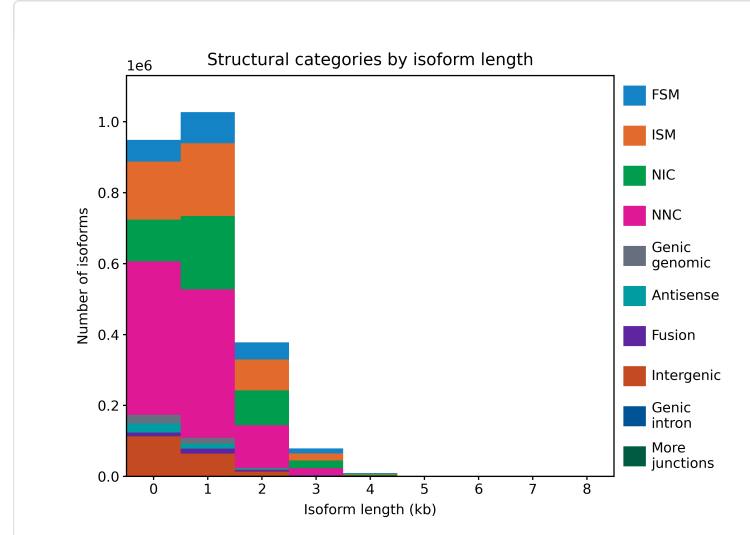
Category ⬆️⬆️	Count ⬆️⬆️	CAGE Detected ⬆️⬆️	CAGE Detected, (%) ⬆️⬆️
FSM	214619	123903	57.73%
ISM	479019	211101	44.06%
NIC	447260	288119	64.41%
NNC	992116	626669	63.16%
Antisense	42994	3803	8.84%
Fusion	30875	17615	57.05%
More junctions	547	262	47.89%
Genic intron	0	0	0.00%
Genic genomic	44856	20221	45.07%
Interaenic	191524	4418	2.30%

Transcript Classification Plots



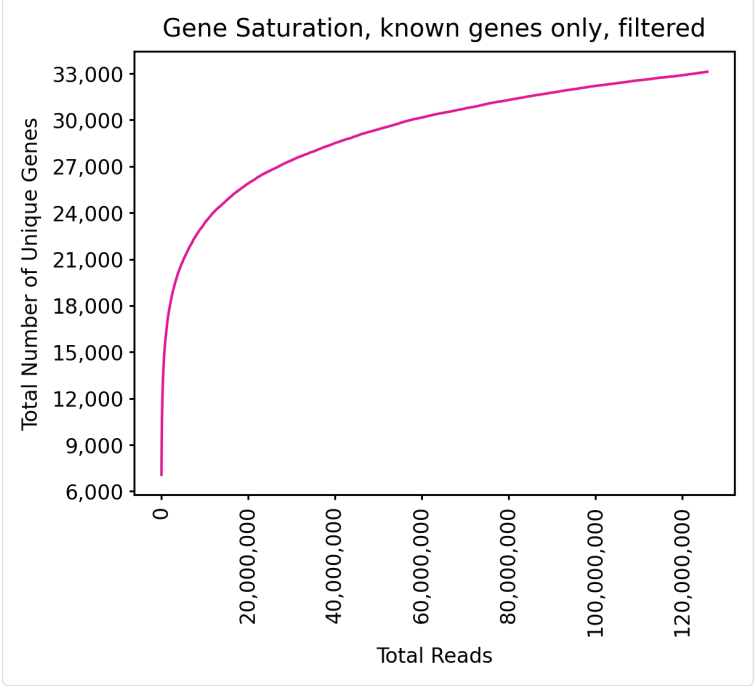
Transcript Classification Plots, filtered





Gene Saturation





File Downloads

Edit Output File Name
Prefix

Example:analysis-3prime_v4_GEX_hPBMCs_20k_Rep2-124626

File ⬆	Type ⬆	Size	Path
Report read_seg	JsonReport	3 KB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam	66 GB	 /pbi/dept/secondary/siv/sn
Single-cell isoform	tgz	6 GB	 /pbi/dept/secondary/siv/sn
Segmented Reads	bam	97 GB	 /pbi/dept/secondary/siv/sn
Segmented Reads	bam	97 GB	 /pbi/dept/secondary/siv/sn
Non-passing read:	bam	3 GB	 /pbi/dept/secondary/siv/sn
Non-passing read:	bam	3 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr:	gff	4 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr:	gff	2 GB	 /pbi/dept/secondary/siv/sn

Related Datasets

Data Set ⬆	Type ⬆
KinnexRelease-10x-3pGEX-PBMC-20k-rep2-2RevioCell-largeMem Seg...	ccsreads