

KinnexRelease-10x-3pGEX-PBMC-20k -rep1-2RevioCell-largeMem

SUCCESSFUL

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▼ Analysis Overview

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► Read Statistics

► Cell Statistics

► Transcript Statistics

► Data

Display All

Status

Analysis	KinnexRelease-10x-3pGEX-PBMC-20k-rep1-2RevioCell-largeMem
Analysis ID	124625
Status	SUCCESSFUL: 15 tasks finished
Created By	etseng
Date Created	2025-08-02, 06:23:49 AM
Date Updated	2025-08-03, 09:26:27 PM
Application	Read Segmentation and Single-Cell Iso-Seq
SMRT Link Version	25.3.0.273777

Inputs

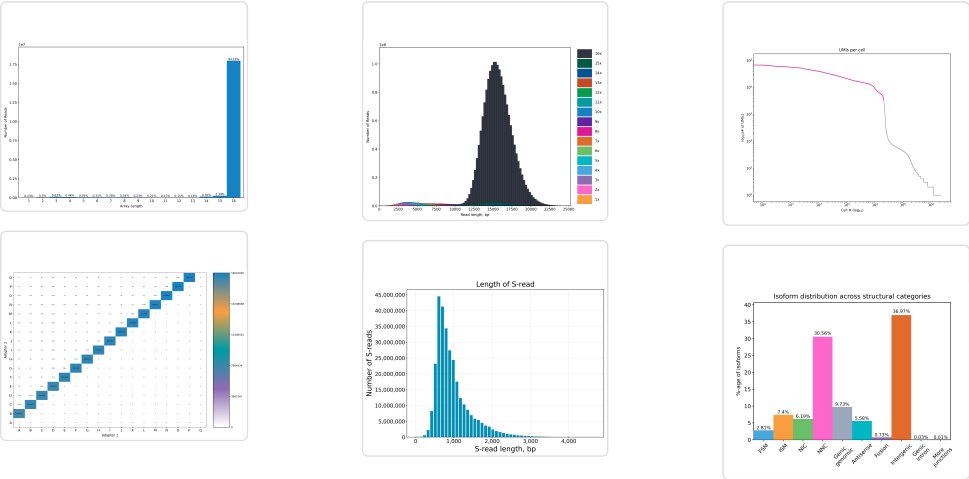
Data Type	Name
BarcodeSet	Barcodes: MAS-Seq Adapter v1 (MAS16)
BarcodeSet	Barcodes: 10x Chromium single cell 3' cDN
ConsensusReadSet	HiFi reads: 3prime v4_GEX_hPBMCs_20k
ConsensusReadSet	HiFi reads: 3prime v4_GEX_hPBMCs_20k
ReferenceSet	References: Human Genome hg38, with Ge

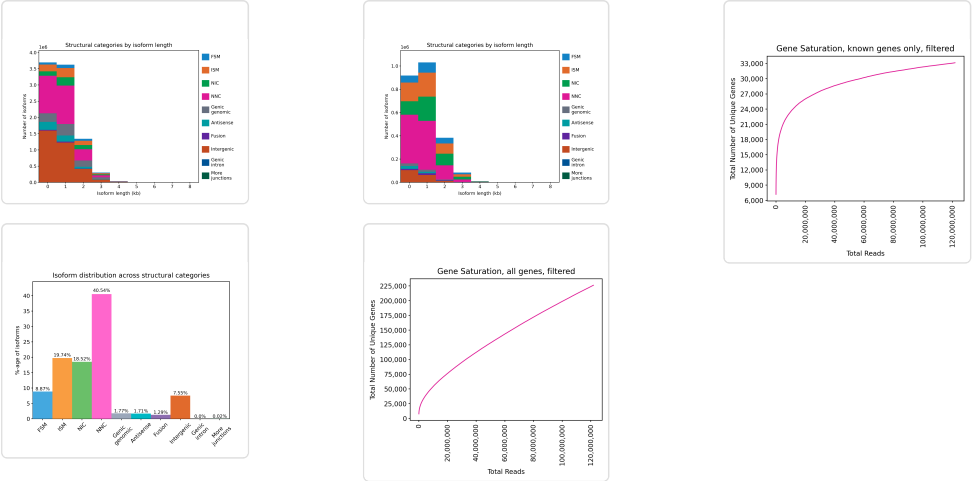
Path

/pbi/flash/smrtlink/smrtlink-alpha/smrtlink/userdata/jobs_root/0000/0000124/0000124625

► Analysis Parameters

Thumbnails

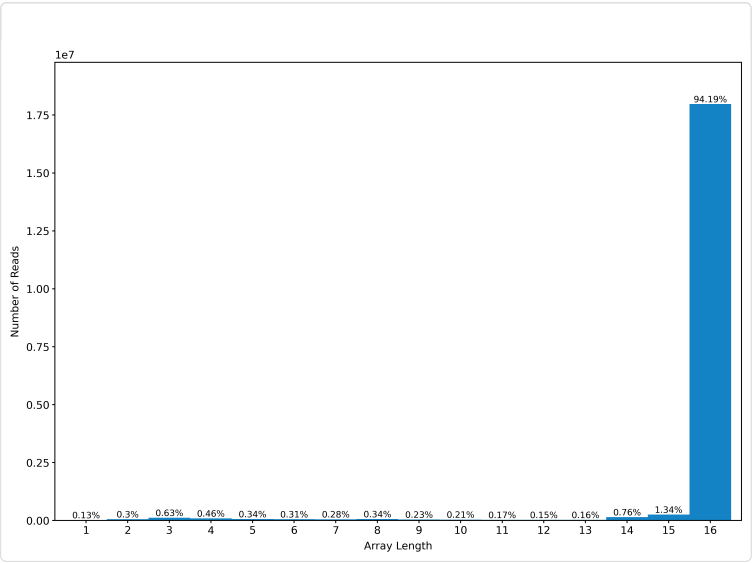


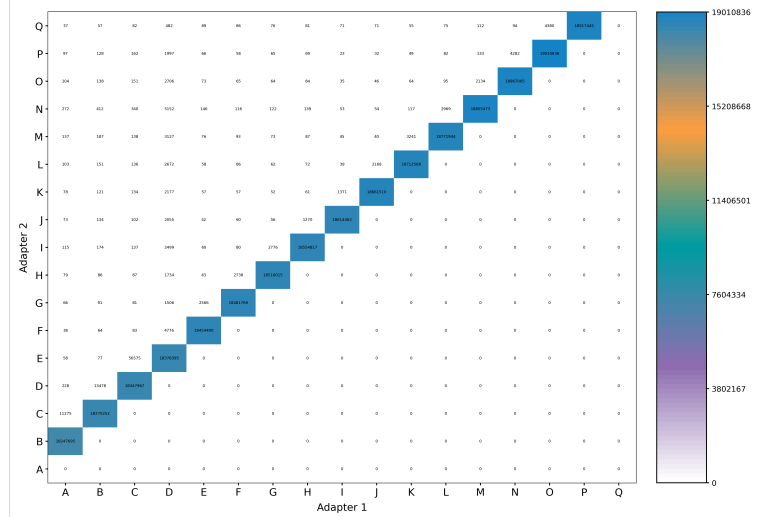


Read Segmentation

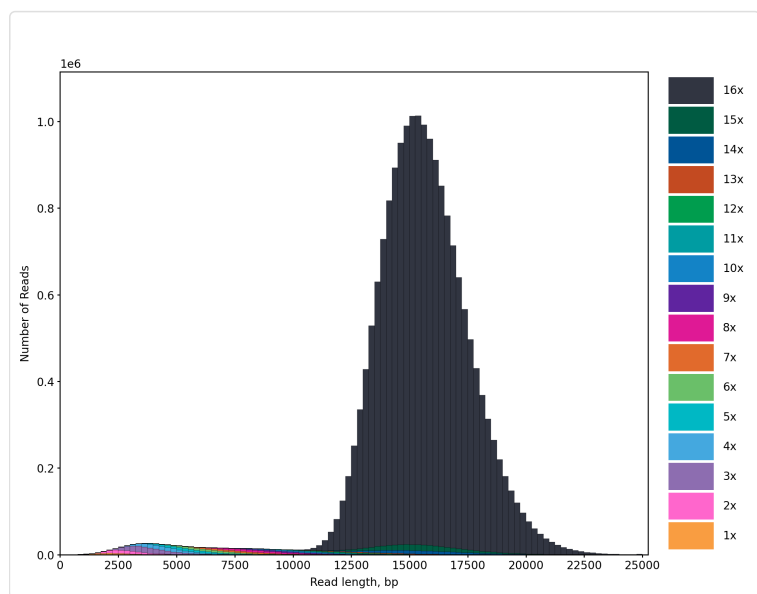
Value	Analysis Metric
19,094,849	Reads
297,862,553	Segmented reads (S-reads)
963	Mean length of S-reads
94.17 %	Percent of reads with full arrays
15.60	Mean array size (concatenation factor)

Segmentation Statistics

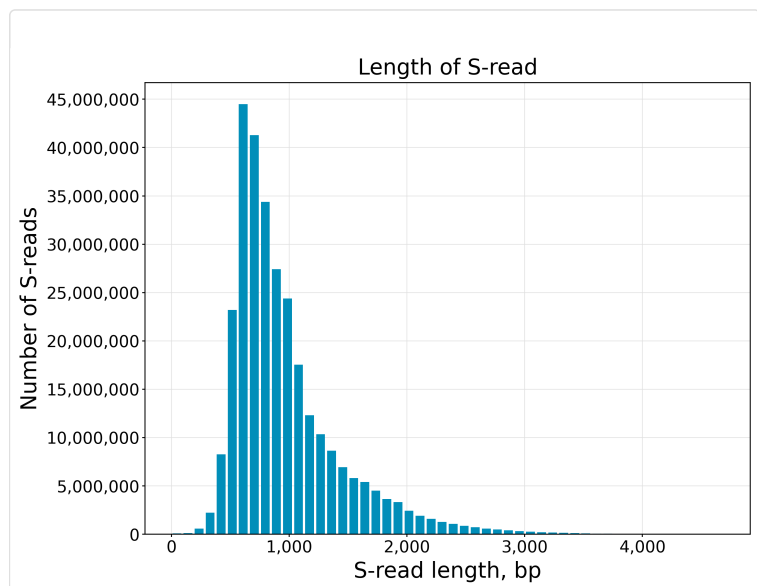




Length of Reads



S-read Length Distribution



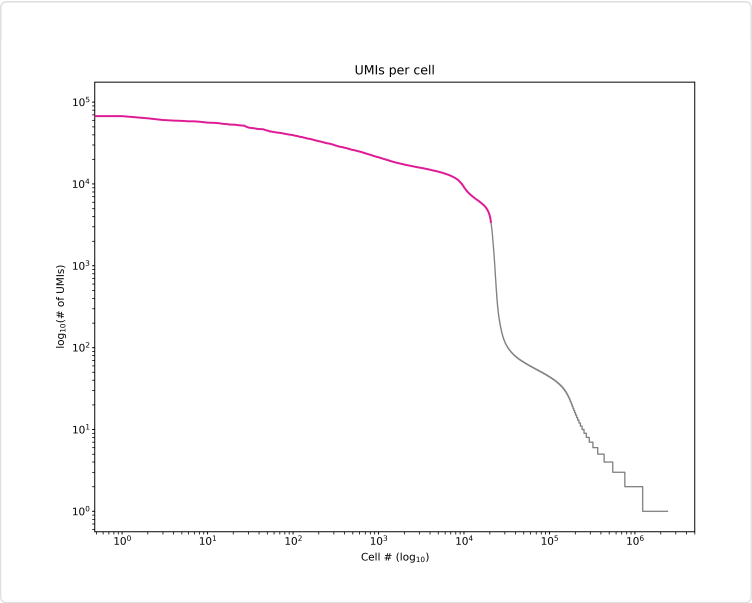
Read Statistics

Value	Analysis Metric
297,862,553	Reads
SEGMENT	Read Type
295,436,944	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
288,569,391	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
282,849,411	FLNC Reads with Valid Barcodes
287,921,294	FLNC Reads with Valid Barcodes, corrected
218,678,519	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
20,426	Estimated Number of Cells
91.76%	Reads in Cells
12,964	Mean Reads per Cell
8,882	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
233,818,089	FLNC Reads Mapped Confidently to Genome
141,208,760	FLNC Reads Mapped Confidently to Transcriptome
3,404,460	Total Unique Genes
226,088	Total Unique Genes, filtered
43,407	Total Unique Genes, known genes only
33,141	Total Unique Genes, filtered, known genes only
8,203,385	Total Unique Transcripts
1,841,952	Total Unique Transcripts, filtered
117,310	Total Unique Transcripts, known transcripts only
107,850	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Search ...

Value ⬆️⬆️	Analysis Metric ⬆️⬆️
3,557	Median Genes per Cell
2,504	Median Genes per Cell
4,725	Median Transcripts per
2,024	Median Transcripts per
3,404,460	Total Unique Genes
43,407	Total Unique Genes, kr
8,203,385	Total Unique Transcrip
117,310	Total Unique Transcrip

Transcript Summary, filtered

Search ...

Value ⬆️⬆️	Analysis Metric ⬆️⬆️
1,806	Median Genes per Cell
1,764	Median Genes per Cell
2,251	Median Transcripts per

2,351	Median Transcripts per
1,742	
226,088	Total Unique Genes
33,141	Total Unique Genes, kr
1,841,952	Total Unique Transcrip
107,850	Total Unique Transcrip

Transcript Classification

Search ...

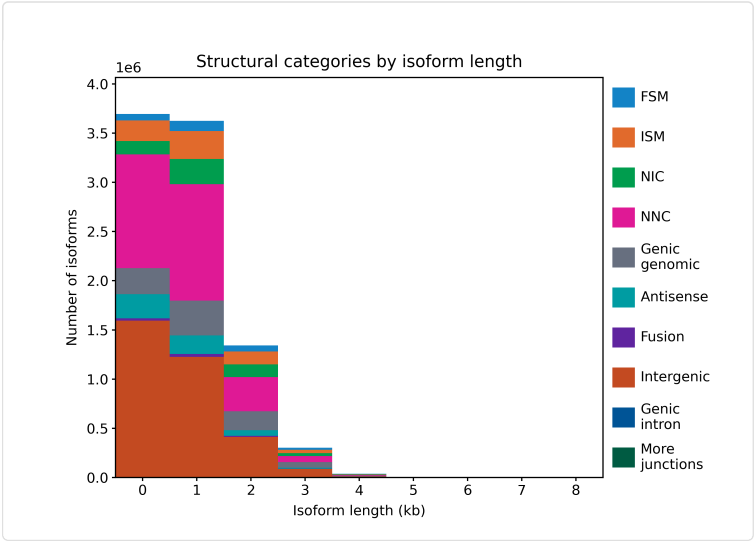
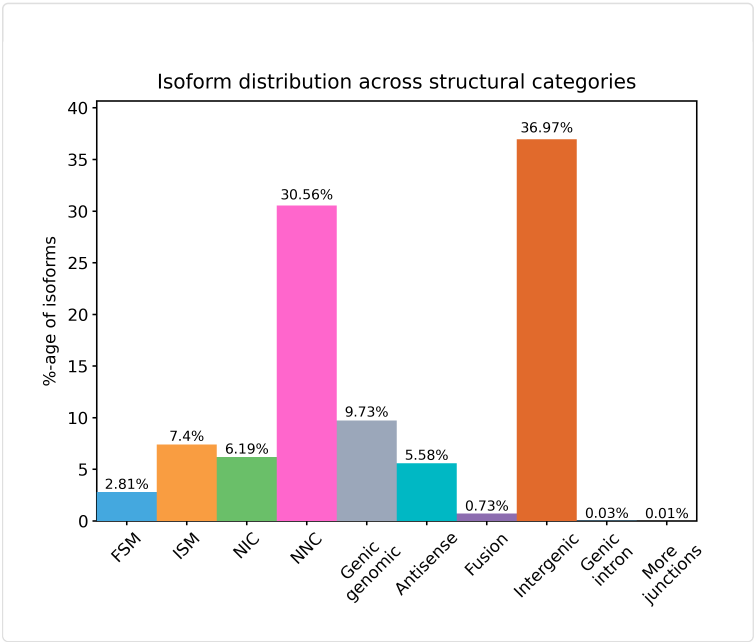
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕
FSM	252662	142005	56.20%
ISM	666164	267482	40.15%
NIC	557760	357644	64.12%
NNC	2751523	1694810	61.59%
Antisense	502622	17401	3.46%
Fusion	66138	37016	55.96%
More junctions	930	423	45.48%
Genic intron	2437	8	0.32%
Genic genomic	875737	213170	24.34%
Intergenic	3328928	31057	0.93%

Transcript Classification, filtered

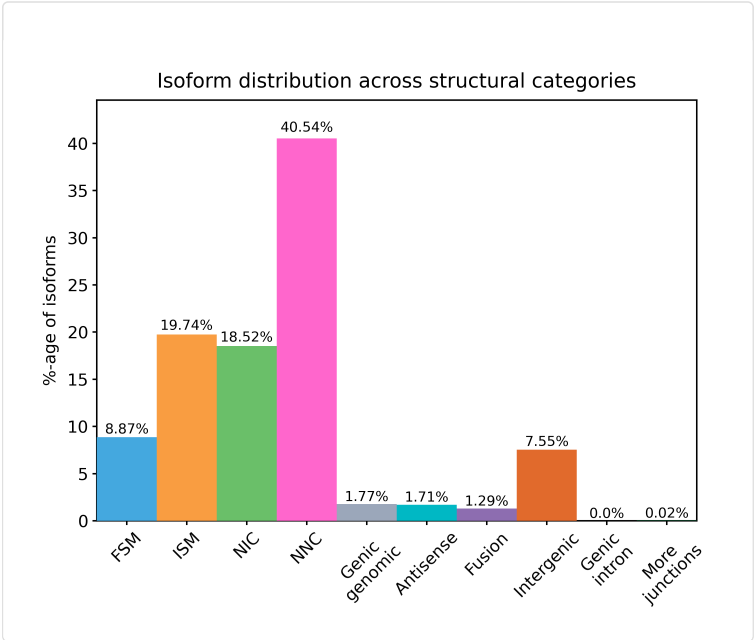
Search ...

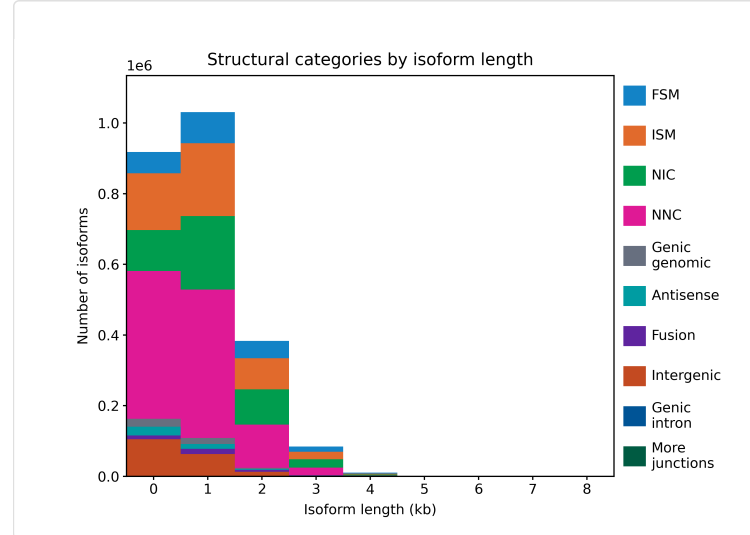
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕
FSM	215414	124039	57.58%
ISM	479344	211772	44.17%
NIC	449764	290143	64.51%
NNC	984611	622549	63.22%
Antisense	41574	3747	9.01%
Fusion	31312	18086	57.76%
More junctions	566	261	46.11%
Genic intron	2	0	0.00%
Genic genomic	42998	19202	44.65%
Interaenic	183275	4338	2.36%

Transcript Classification Plots

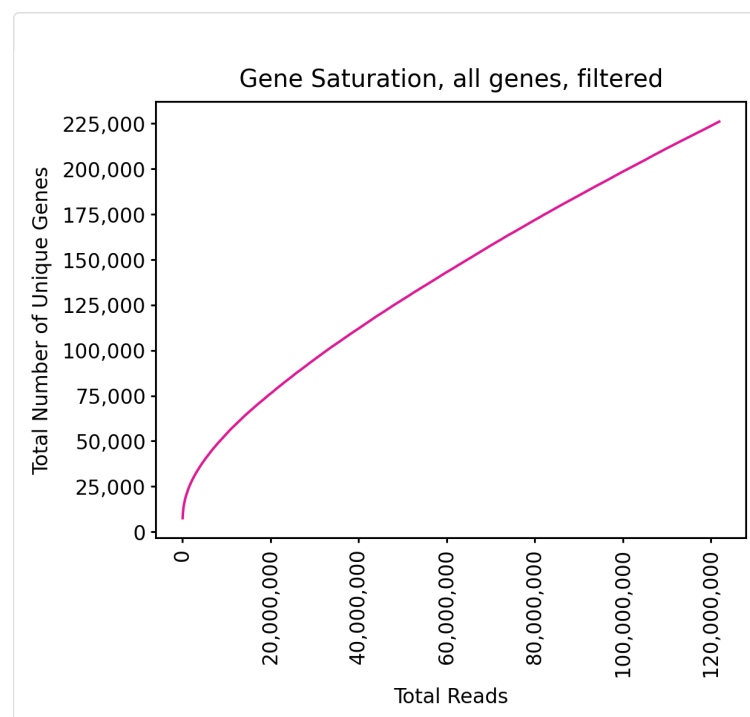


Transcript Classification Plots, filtered





Gene Saturation





File Downloads

Edit Output File Name
Prefix

Example:analysis-3prime_v4_GEX_hPBMCs_20k_Rep1-124625

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	96 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-rep1-2RevioCell-largeMem Seg...	ccsreads