

KinnexRelease-10x-3pGEX-PBMC-10k-Revio-largeMem

SUCCESSFUL

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► Transcript Statistics

► Data

Display All

Status

Analysis	KinnexRelease-10x-3pGEX-PBMC-10k-Revio-largeMem
Analysis ID	124624
Status	SUCCESSFUL: 14 tasks finished
Created By	etseng
Date Created	2025-08-02, 06:22:21 AM
Date Updated	2025-08-02, 11:15:12 PM
Application	Read Segmentation and Single-Cell Iso-Seq
SMRT Link Version	25.3.0.273777

Inputs

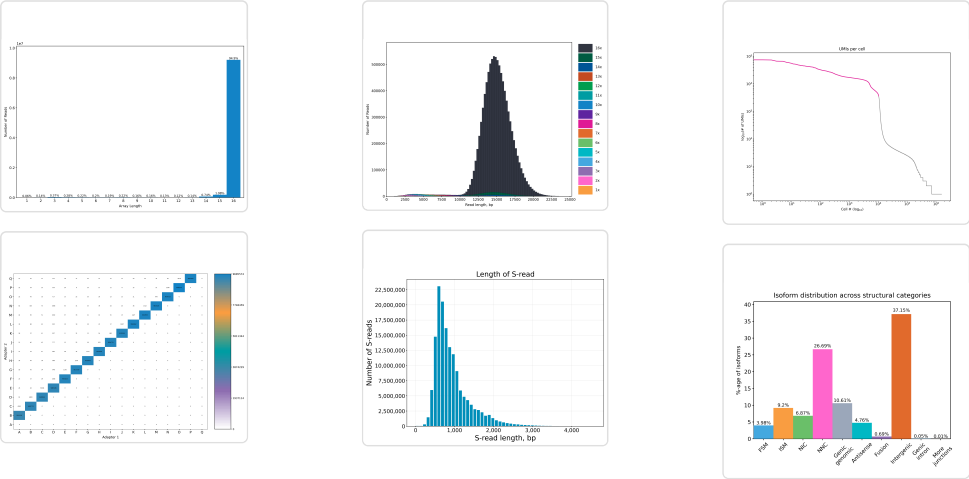
Data Type	Name
BarcodeSet	Barcodes: 10x Chromium single cell 3' cDN
BarcodeSet	Barcodes: MAS-Seq Adapter v1 (MAS16)
ConsensusReadSet	HiFi reads: 3prime v4_GEX_hPBMCs_10k_
ReferenceSet	References: Human Genome hg38, with Ge

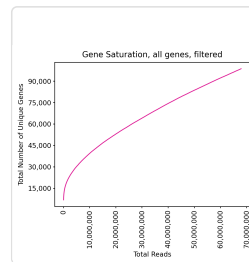
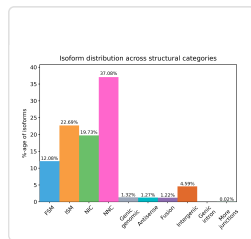
Path

/pbi/flash/smrtlink/smrtlink-alpha/smrtlink/userdata/jobs_root/0000/0000124/0000124624

► Analysis Parameters

Thumbnails

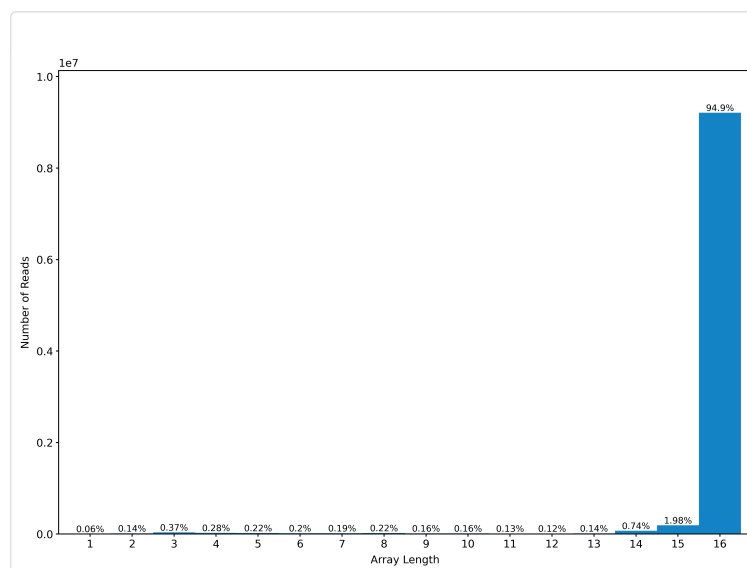


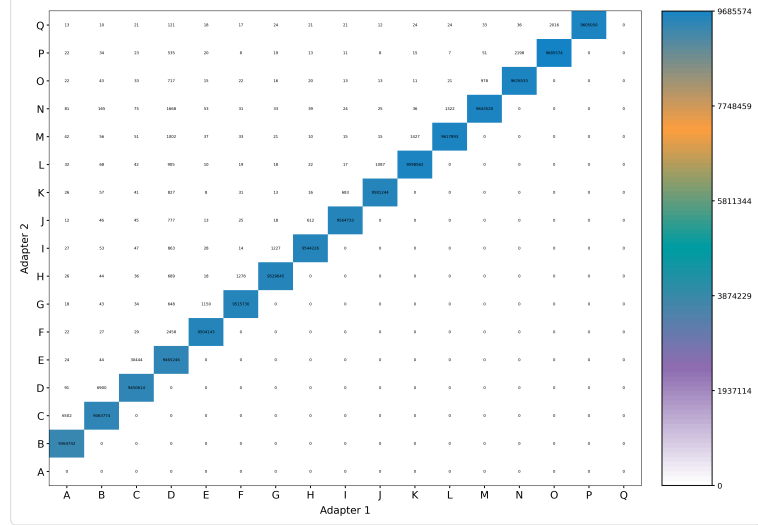


Read Segmentation

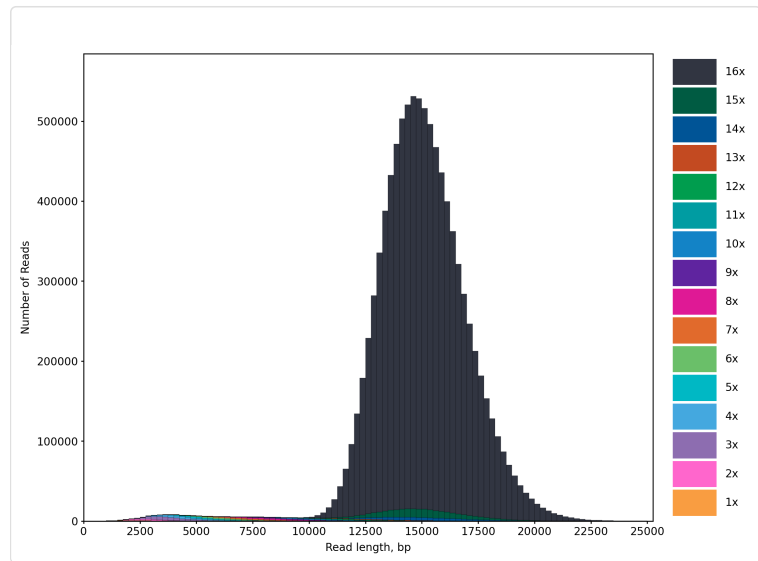
Value	Analysis Metric
9,709,186	Reads
152,811,229	Segmented reads (S-reads)
928	Mean length of S-reads
94.89 %	Percent of reads with full arrays
15.74	Mean array size (concatenation factor)

Segmentation Statistics

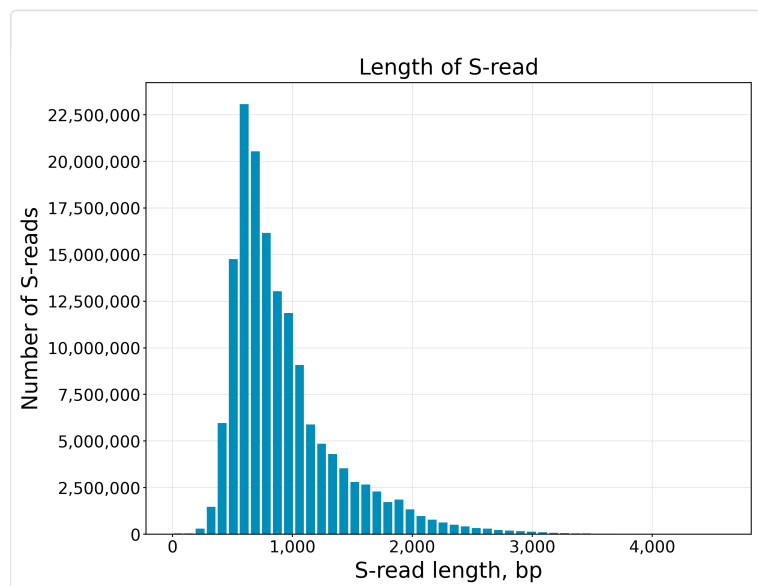




Length of Reads



S-read Length Distribution



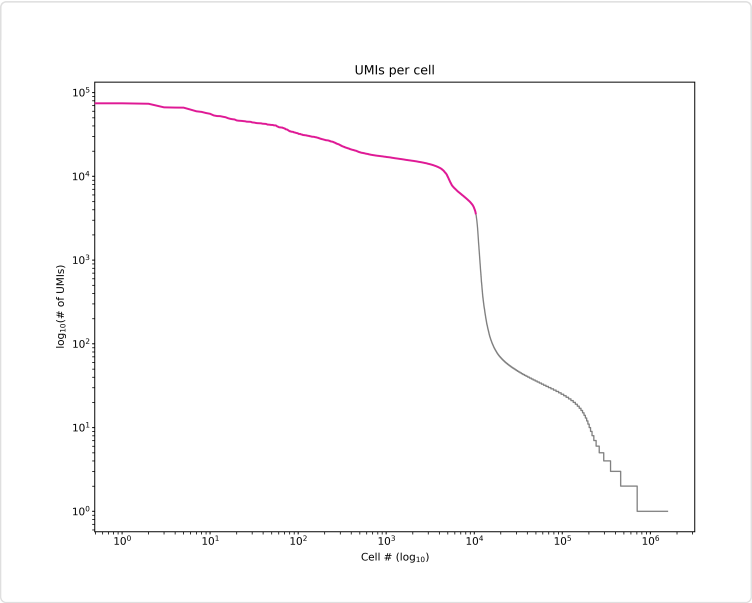
Read Statistics

Value	Analysis Metric
152,811,229	Reads
SEGMENT	Read Type
151,565,748	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
147,805,910	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
144,807,139	FLNC Reads with Valid Barcodes
147,466,710	FLNC Reads with Valid Barcodes, corrected
110,681,049	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
10,324	Estimated Number of Cells
90.65%	Reads in Cells
12,978	Mean Reads per Cell
9,194	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
120,736,189	FLNC Reads Mapped Confidently to Genome
79,264,395	FLNC Reads Mapped Confidently to Transcriptome
1,902,966	Total Unique Genes
98,700	Total Unique Genes, filtered
37,474	Total Unique Genes, known genes only
28,955	Total Unique Genes, filtered, known genes only
4,399,569	Total Unique Transcripts
999,042	Total Unique Transcripts, filtered
103,849	Total Unique Transcripts, known transcripts only
93,952	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Search ...

Value ⬆️⬆️	Analysis Metric ⬆️⬆️
3,369	Median Genes per Cell
2,476	Median Genes per Cell
4,522	Median Transcripts per
2,145	Median Transcripts per
1,902,966	Total Unique Genes
37,474	Total Unique Genes, kr
4,399,569	Total Unique Transcrip
103,849	Total Unique Transcrip

Transcript Summary, filtered

Search ...

Value ⬆️⬆️	Analysis Metric ⬆️⬆️
1,822	Median Genes per Cell
1,787	Median Genes per Cell
2,222	Median Transcripts per

2,389	Median Transcripts per
1,839	
98,700	Total Unique Genes
28,955	Total Unique Genes, kr
999,042	Total Unique Transcrip
93,952	Total Unique Transcrip

Transcript Classification

Search ...

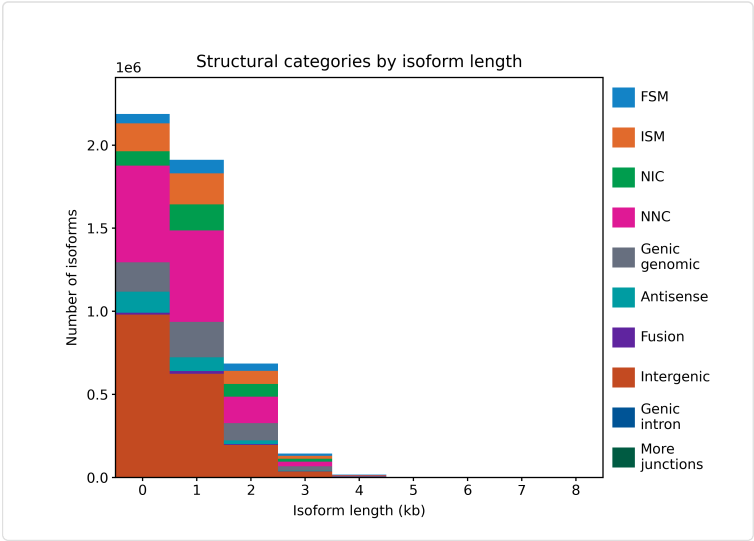
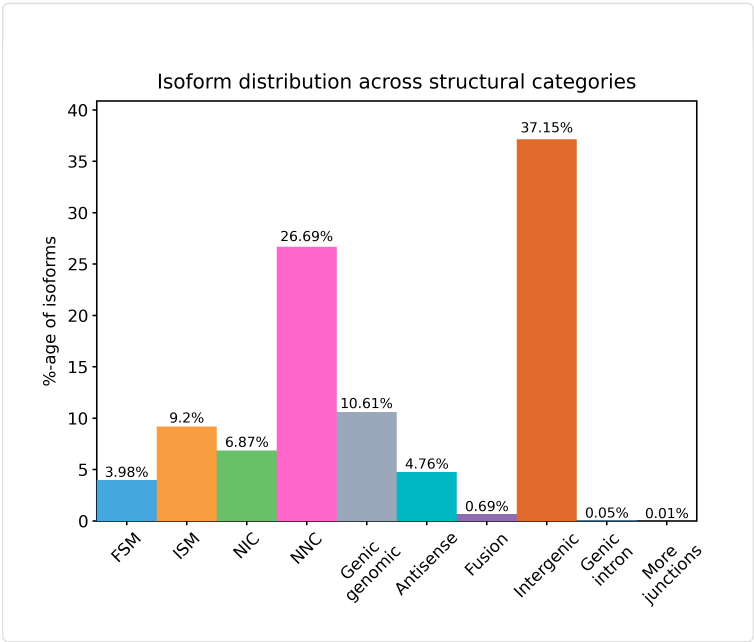
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕
FSM	196828	119402	60.66%
ISM	455016	204144	44.86%
NIC	339815	235082	69.17%
NNC	1320505	874184	66.20%
Antisense	235426	10877	4.62%
Fusion	34017	20041	58.91%
More junctions	457	246	53.82%
Genic intron	2254	12	0.53%
Genic genomic	525027	138280	26.33%
Intergenic	1838219	21953	1.19%

Transcript Classification, filtered

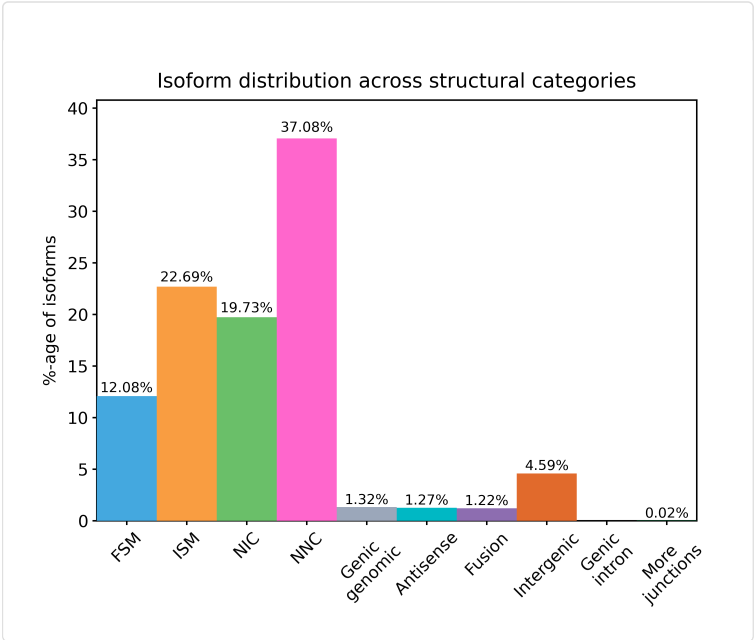
Search ...

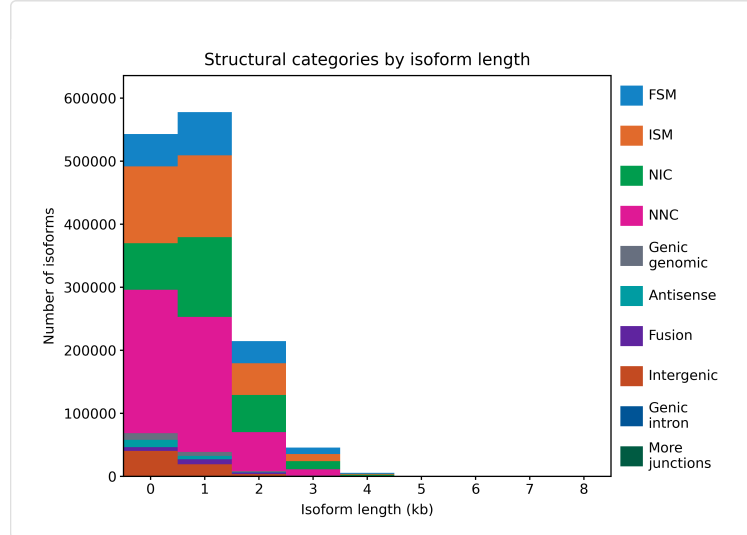
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕
FSM	167573	103997	62.06%
ISM	314765	158530	50.36%
NIC	273808	190384	69.53%
NNC	514400	345302	67.12%
Antisense	17604	2071	11.76%
Fusion	16945	10215	60.28%
More junctions	282	158	56.02%
Genic intron	0	0	0.00%
Genic genomic	18361	9601	52.29%
Interaenic	63690	2479	3.89%

Transcript Classification Plots



Transcript Classification Plots, filtered





Gene Saturation





File Downloads

Edit Output File Name
Prefix

Example:analysis-3prime_v4_GEX_hPBMCs_10k_Rep1-124624

File ↕	Type ↕	Size	Path
Report read_seg m	JsonReport	3 KB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam	31 GB	 /pbi/dept/secondary/siv/sn
Single-cell isoform	tgz	3 GB	 /pbi/dept/secondary/siv/sn
Segmented Reads	bam	95 GB	 /pbi/dept/secondary/siv/sn
Non-passing read s	bam	3 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr anscripts	gff	2 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr anscripts	gff	889 MB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam	16 GB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam_bai	21 MB	 /pbi/dept/secondary/siv/sn

Related Datasets

Data Set ↕	Type ↕
3prime_v4_GEX_hPBMCs_10k_Rep1-Cell1(all samples)_Segmented Re...	ccsreads