

KinnexRelease-10x-3pGEX-PBMC-10k-Vega

SUCCESSFUL

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▼ Analysis Overview

Status

Thumbnails

Display All

► Read Segmentation

► Read Statistics

► Cell Statistics

► Transcript Statistics

► Data

Display All

Status

Analysis KinnexRelease-10x-3pGEX-PBMC-10k-Vega

Analysis ID 124496

Status SUCCESSFUL: 14 tasks finished

Created By etseng

Date Created 2025-08-01, 07:07:17 AM

Date Updated 2025-08-01, 02:52:20 PM

Application Read Segmentation and Single-Cell Iso-Seq

SMRT Link Version 25.3.0.273777

Inputs

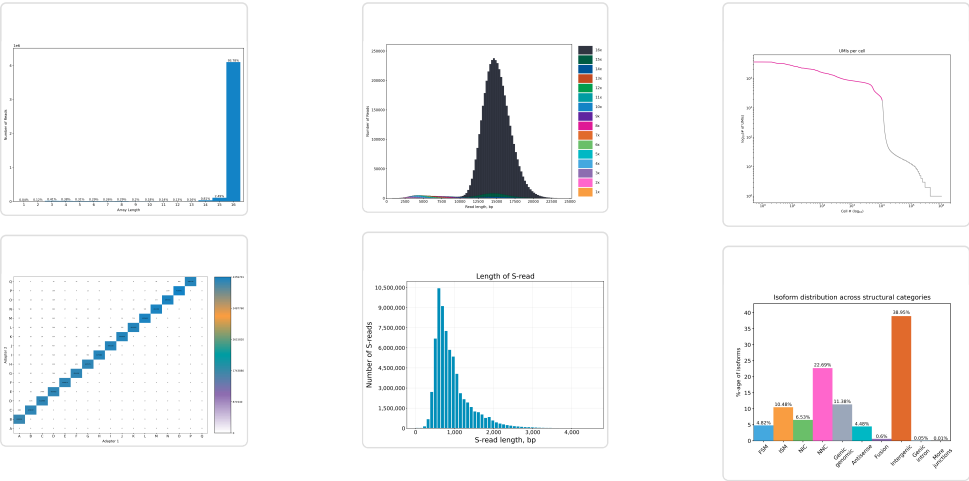
Data Type	Name
BarcodeSet	Barcodes: 10x Chromium single cell 3' cDN
BarcodeSet	Barcodes: MAS-Seq Adapter v1 (MAS16)
ConsensusReadSet	HiFi reads: 3prime v4_GEX_hPBMCs_10k_
ReferenceSet	References: Human Genome hg38, with Ge

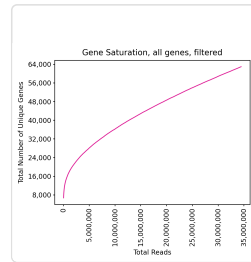
Path

/pbi/flash/smrtlink/smrtlink-alpha/smrtlink/userdata/jobs_root/0000/0000124/0000124496

► Analysis Parameters

Thumbnails

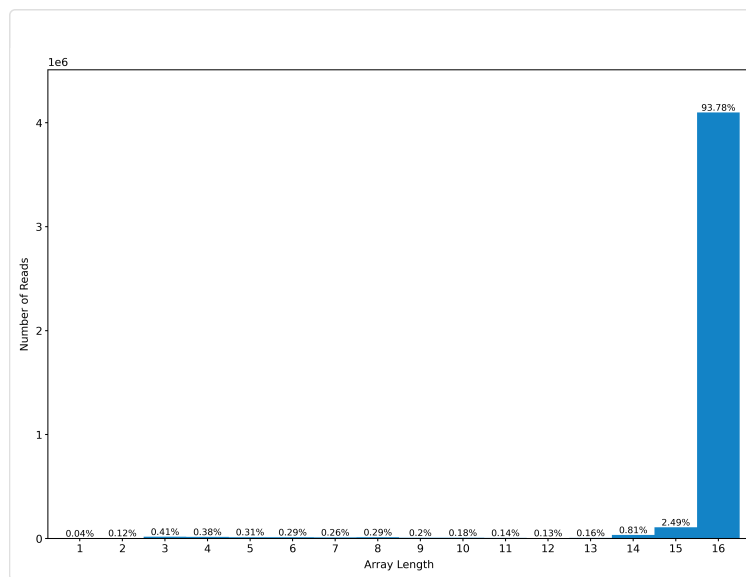


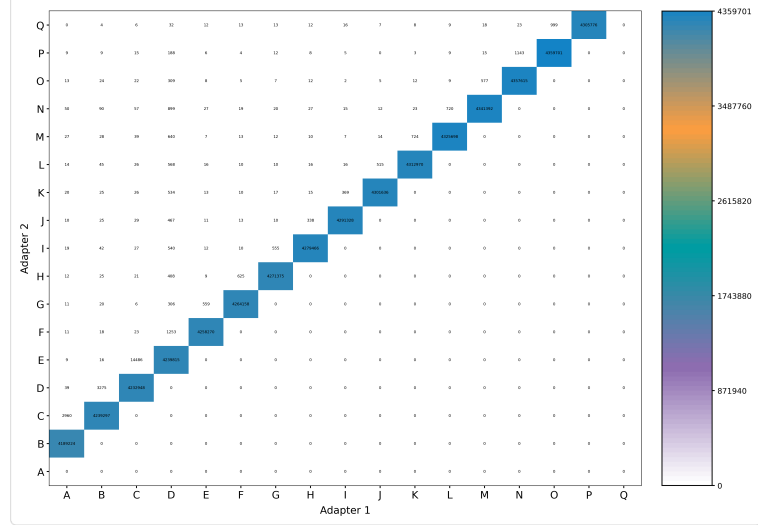


Read Segmentation

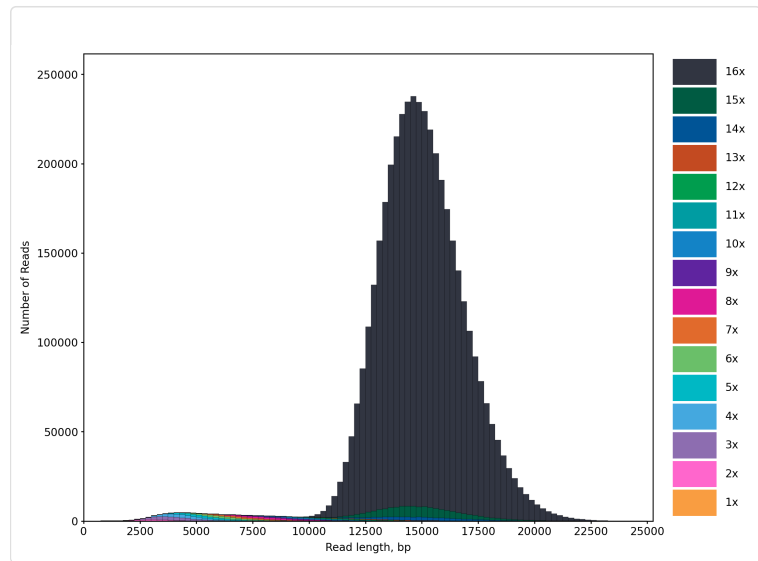
Value	Analysis Metric
4,372,029	Reads
68,570,669	Segmented reads (S-reads)
924	Mean length of S-reads
93.78 %	Percent of reads with full arrays
15.68	Mean array size (concatenation factor)

Segmentation Statistics

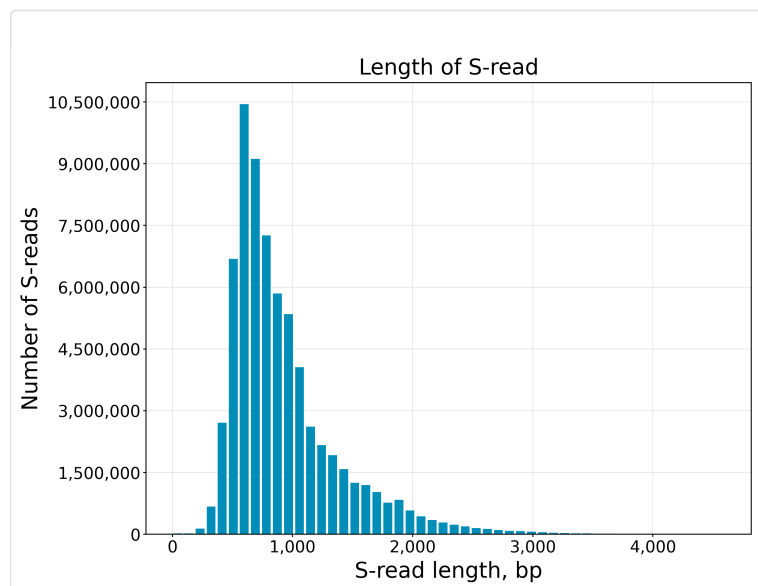




Length of Reads



S-read Length Distribution



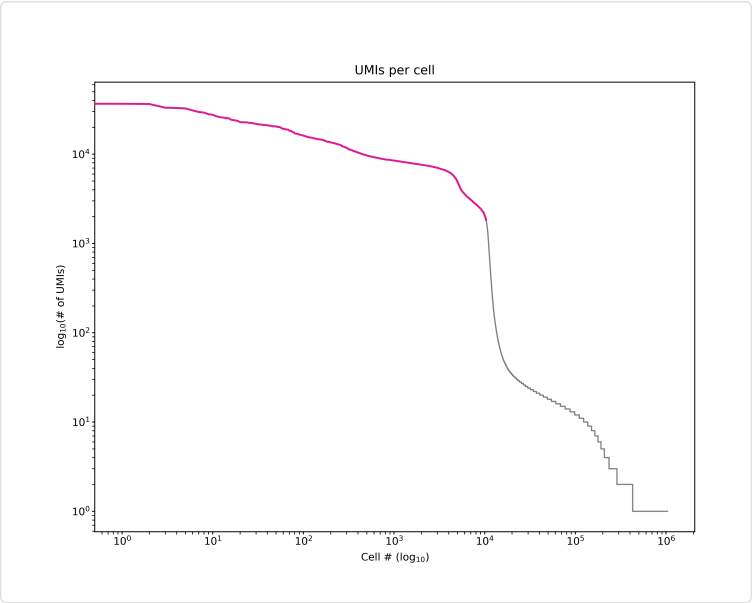
Read Statistics

Value	Analysis Metric
68,570,669	Reads
SEGMENT	Read Type
68,007,729	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
66,266,566	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
64,948,820	FLNC Reads with Valid Barcodes
66,113,774	FLNC Reads with Valid Barcodes, corrected
54,980,296	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
10,329	Estimated Number of Cells
90.69%	Reads in Cells
5,818	Mean Reads per Cell
4,561	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
54,152,125	FLNC Reads Mapped Confidently to Genome
35,486,110	FLNC Reads Mapped Confidently to Transcriptome
1,310,725	Total Unique Genes
62,925	Total Unique Genes, filtered
33,435	Total Unique Genes, known genes only
25,832	Total Unique Genes, filtered, known genes only
2,819,731	Total Unique Transcripts
604,684	Total Unique Transcripts, filtered
92,696	Total Unique Transcripts, known transcripts only
82,608	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Search ...

Value 	Analysis Metric 
2,002	Median Genes per Cell
1,510	Median Genes per Cell
2,466	Median Transcripts per
1,253	Median Transcripts per
1,310,725	Total Unique Genes
33,435	Total Unique Genes, kr
2,819,731	Total Unique Transcrip
92,696	Total Unique Transcrip

Transcript Summary, filtered

Search ...

Value 	Analysis Metric 
1,108	Median Genes per Cell
1,095	Median Genes per Cell
1,310	Median Transcripts per

1,348	Median Transcripts per
1,086	Median Transcripts per
62,925	Total Unique Genes
25,832	Total Unique Genes, kr
604,684	Total Unique Transcrip
82,608	Total Unique Transcrip

Transcript Classification

Search ...

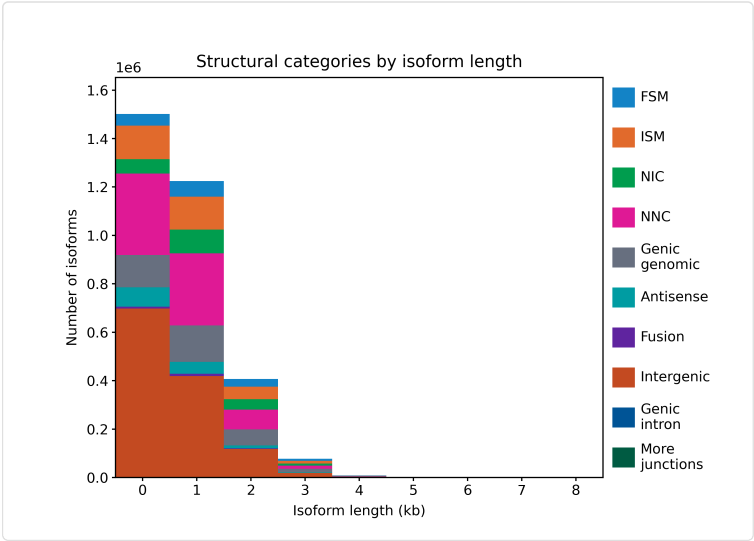
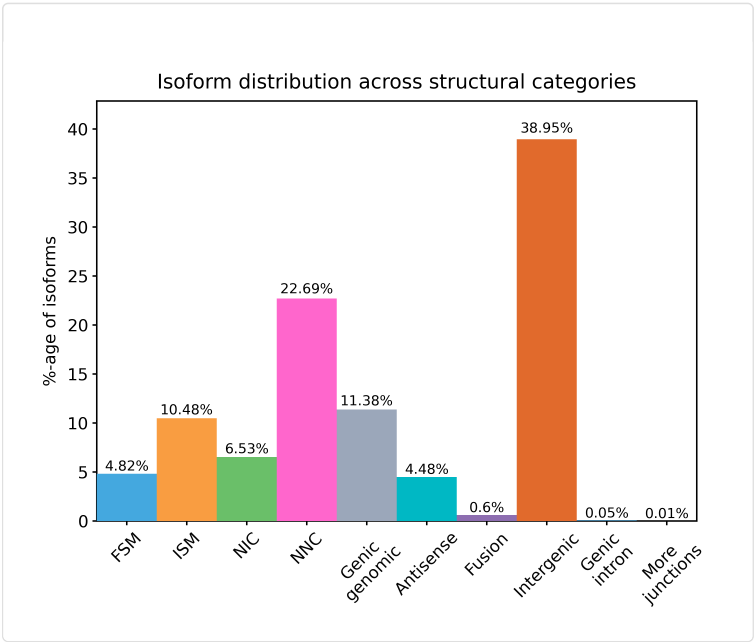
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕
FSM	155050	97462	62.85%
ISM	337549	155273	46.00%
NIC	210362	147978	70.34%
NNC	730606	489006	66.93%
Antisense	144203	7403	5.13%
Fusion	19435	11682	60.10%
More junctions	239	122	51.04%
Genic intron	1694	12	0.70%
Genic genomic	366435	97488	26.60%
Intergenic	1254061	15628	1.24%

Transcript Classification, filtered

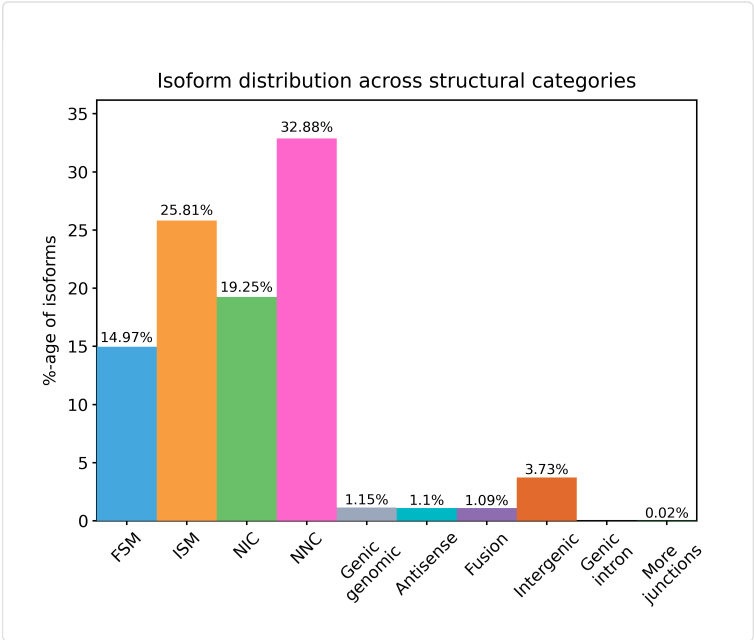
Search ...

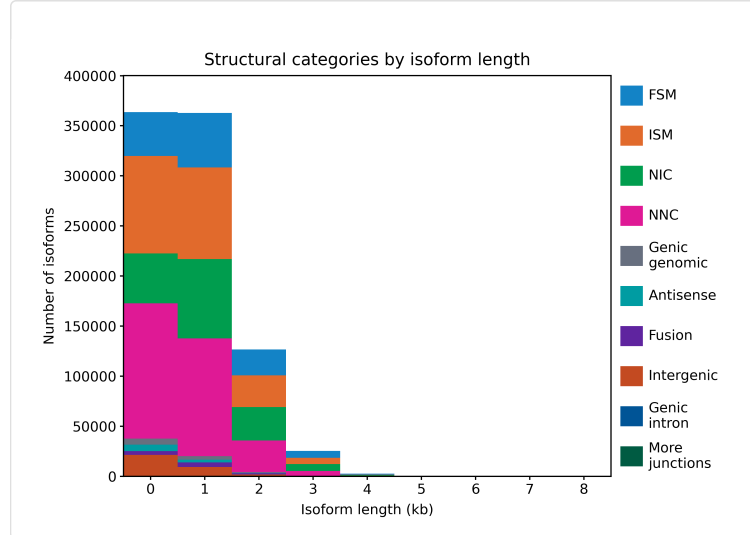
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕
FSM	131927	84716	64.21%
ISM	227511	120138	52.80%
NIC	169708	120081	70.75%
NNC	289868	196647	67.84%
Antisense	9729	1259	12.94%
Fusion	9621	5876	61.07%
More junctions	167	83	49.70%
Genic intron	0	0	0.00%
Genic genomic	10112	5517	54.55%
Interaenic	32871	1412	4.29%

Transcript Classification Plots

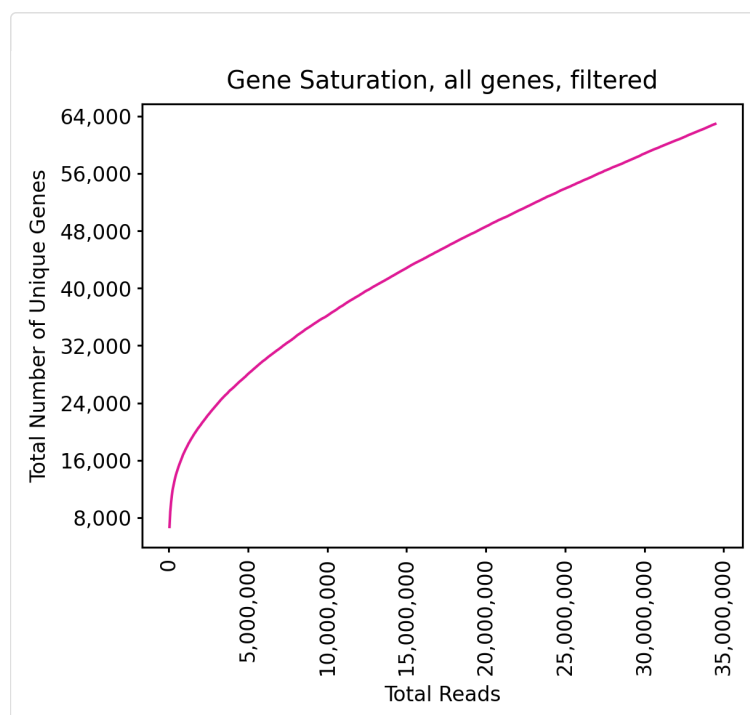


Transcript Classification Plots, filtered





Gene Saturation





File Downloads

Edit Output File Name
Prefix

Example:analysis-3prime_v4_GEX_hPBMCs_10k_Rep1-124496

File ↕	Type ↕	Size	Path
Report read_seg m	JsonReport	3 KB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam	15 GB	 /pbi/dept/secondary/siv/sn
Single-cell isoform	tgz	2 GB	 /pbi/dept/secondary/siv/sn
Segmented Reads	bam	42 GB	 /pbi/dept/secondary/siv/sn
Non-passing read s	bam	2 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr anscripts	gff	1 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr anscripts	gff	558 MB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam	8 GB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam_bai	11 MB	 /pbi/dept/secondary/siv/sn

Related Datasets

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