

KinnexRelease-10x-5pGEX-20k-Revio2cell-largeMem

SUCCESSFUL

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Display All

Status

Analysis KinnexRelease-10x-5pGEX-20k-Revio2cell-largeMem

Analysis ID 124627

Status SUCCESSFUL: 15 tasks finished

Created By etseng

Date Created 2025-08-02, 06:32:20 AM

Date Updated 2025-08-04, 03:19:00 AM

Application Read Segmentation and Single-Cell Iso-Seq

SMRT Link Version 25.3.0.273777

Inputs

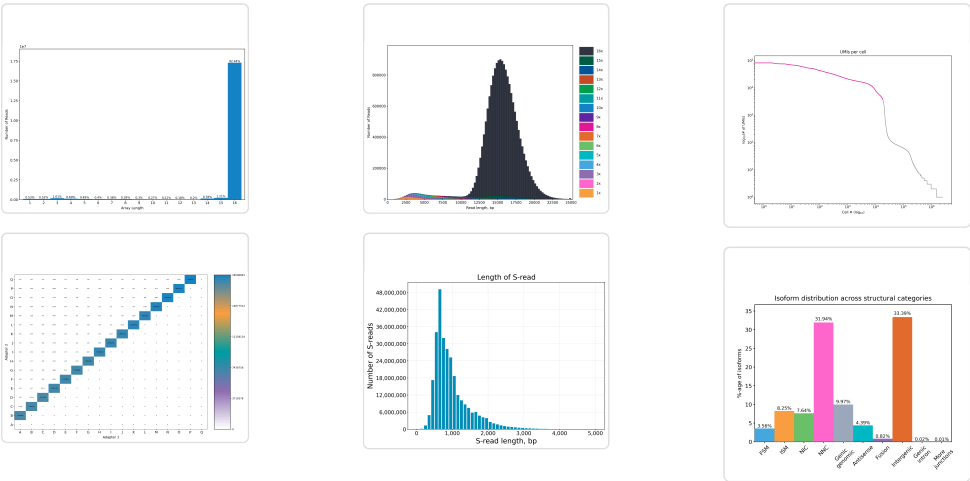
Data Type	Name
BarcodeSet	Barcodes: MAS-Seq Adapter v1 (MAS16)
BarcodeSet	Barcodes: 10X Chromium single cell 5' cDN
ConsensusReadSet	HiFi reads: 5prime v4_GEX_hPBMCs_20k
ConsensusReadSet	HiFi reads: 5prime v4_GEX_hPBMCs_20k
ReferenceSet	References: Human Genome hg38, with Ge

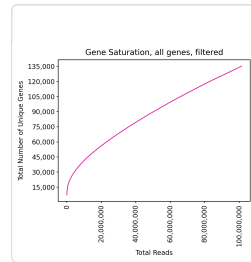
Path

/pbi/flash/smrtlink/smrtlink-alpha/smrtlink/userdata/jobs_root/0000/0000124/0000124627

► Analysis Parameters

Thumbnails

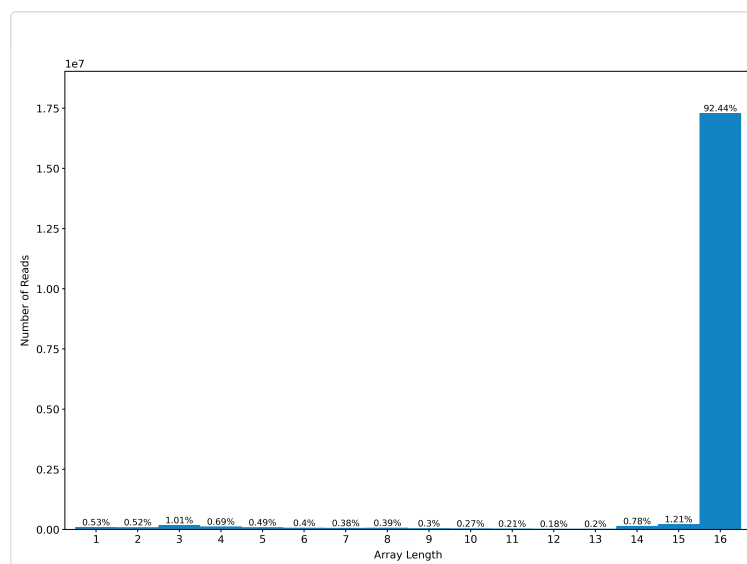


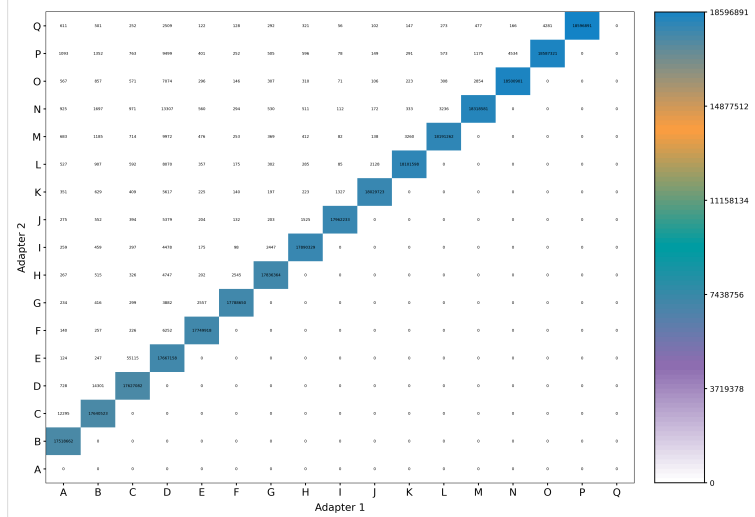


Read Segmentation

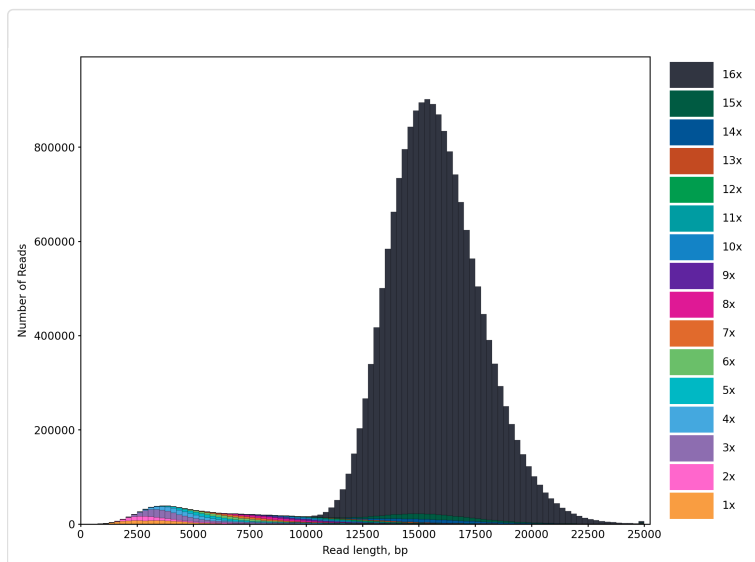
Value	Analysis Metric
18,767,390	Reads
288,007,196	Segmented reads (S-reads)
970.006	Mean length of S-reads
92.20 %	Percent of reads with full arrays
15.35	Mean array size (concatenation factor)

Segmentation Statistics

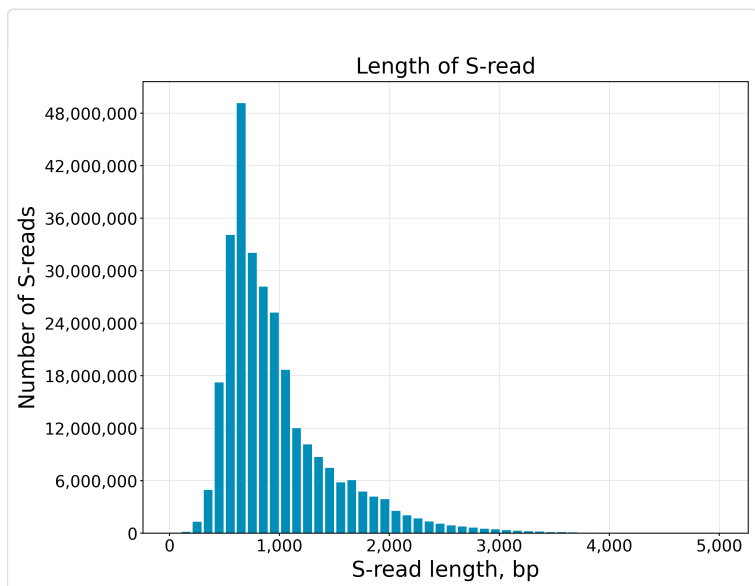




Length of Reads



S-read Length Distribution



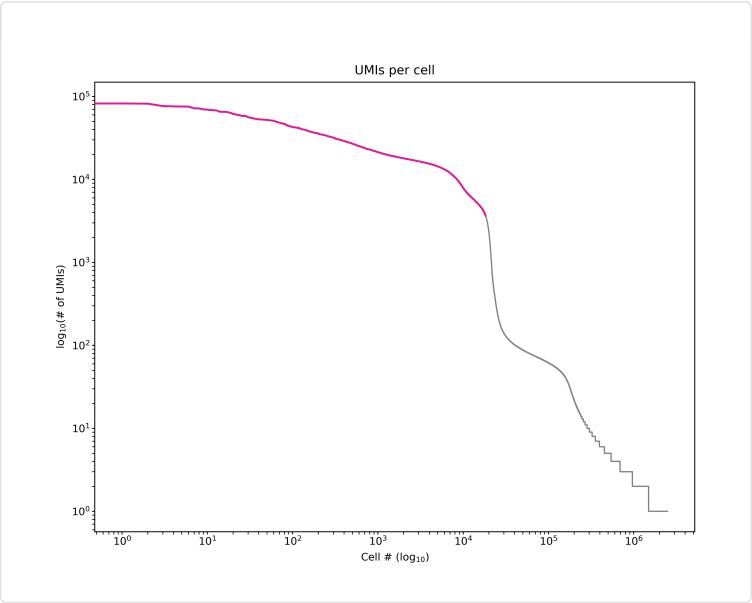
Read Statistics

Value	Analysis Metric
288,007,196	Reads
SEGMENT	Read Type
285,630,076	Reads with 5' and 3' Primers with extracted UMIs and Barcodes
283,891,388	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail (FLNC reads)
271,375,072	FLNC Reads with Valid Barcodes
280,263,363	FLNC Reads with Valid Barcodes, corrected
197,544,312	Reads after Barcode Correction and UMI Deduplication

Cell Statistics

Value	Analysis Metric
17,654	Estimated Number of Cells
87.12%	Reads in Cells
14,011	Mean Reads per Cell
9,524	Median UMIs per Cell

Barcode Rank Plot



Transcript Statistics

Value	Analysis Metric
191,189,865	FLNC Reads Mapped Confidently to Genome
119,177,062	FLNC Reads Mapped Confidently to Transcriptome
2,160,147	Total Unique Genes
135,011	Total Unique Genes, filtered
39,976	Total Unique Genes, known genes only
31,071	Total Unique Genes, filtered, known genes only
5,637,804	Total Unique Transcripts
1,384,709	Total Unique Transcripts, filtered
108,978	Total Unique Transcripts, known transcripts only
99,281	Total Unique Transcripts, filtered, known transcripts only

Transcript Summary

Search ...

Value 	Analysis Metric 
3,154	Median Genes per Cell
2,407	Median Genes per Cell
4,137	Median Transcripts per
1,950	Median Transcripts per
2,160,147	Total Unique Genes
39,976	Total Unique Genes, kr
5,637,804	Total Unique Transcrip
108,978	Total Unique Transcrip

Transcript Summary, filtered

Search ...

Value 	Analysis Metric 
1,772	Median Genes per Cell
1,743	Median Genes per Cell
2,255	Median Transcripts per

2,255	Median Transcripts per
1,670	Median Transcripts per
135,011	Total Unique Genes
31,071	Total Unique Genes, kr
1,384,709	Total Unique Transcrip
99,281	Total Unique Transcrip

Transcript Classification

Search ...

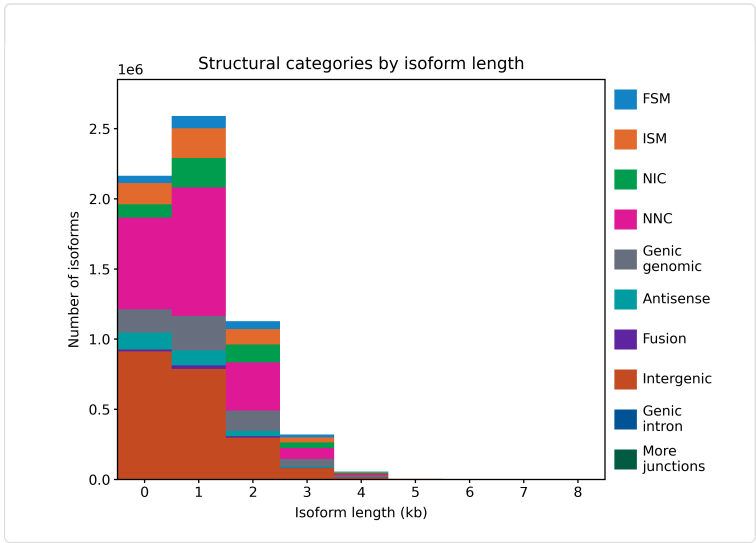
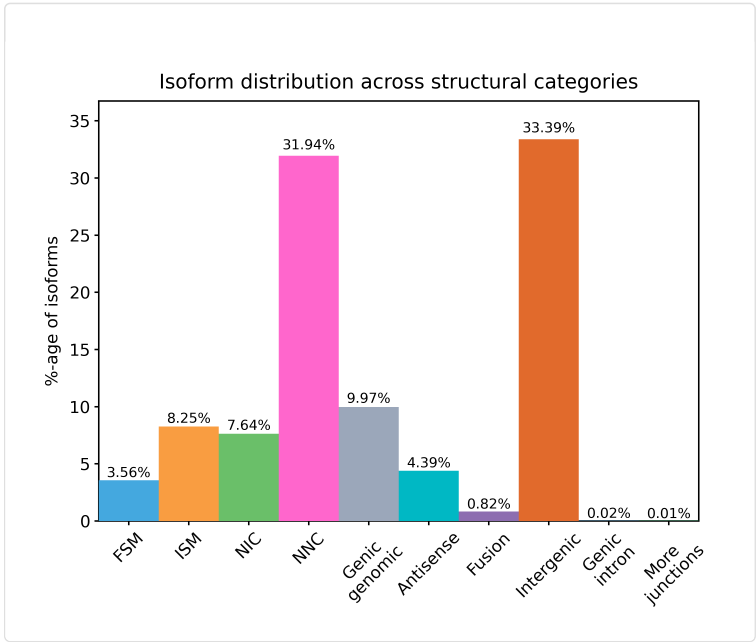
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected (%) ↕
FSM	222891	128967	57.86%
ISM	517523	212697	41.09%
NIC	478879	308184	64.35%
NNC	2002321	1231439	61.50%
Antisense	275513	12153	4.41%
Fusion	51581	28536	55.32%
More junctions	857	418	48.77%
Genic intron	1099	6	0.54%
Genic genomic	625205	149505	23.91%
Intergenic	2093371	21491	1.02%

Transcript Classification, filtered

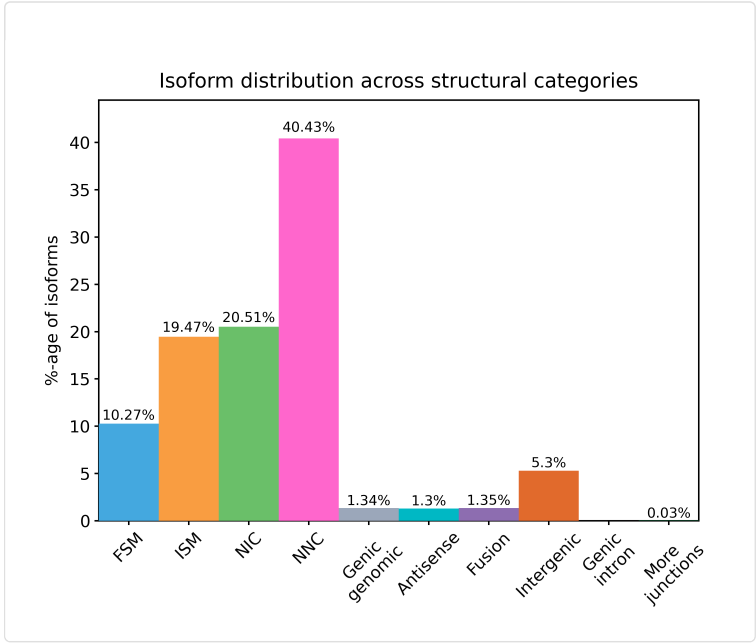
Search ...

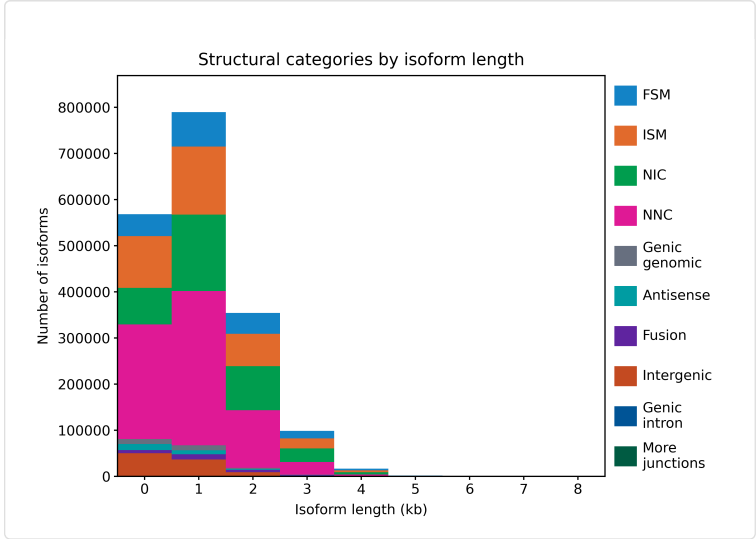
Category ↕	Count ↕	CAGE Detected ↕	CAGE Detected, (%) ↕
FSM	187860	111558	59.38%
ISM	356165	161074	45.22%
NIC	375188	243279	64.84%
NNC	739730	466058	63.00%
Antisense	23799	2438	10.24%
Fusion	24723	14126	57.13%
More junctions	490	252	51.42%
Genic intron	0	0	0.00%
Genic genomic	24507	10487	42.79%
Interaenic	96991	2584	2.66%

Transcript Classification Plots



Transcript Classification Plots, filtered





Gene Saturation





File Downloads

Edit Output File Name
Prefix

Example:analysis-5prime_v4_GEX_hPBMCs_20k_Rep1-124627

File ↕	Type ↕	Size	Path
Report read_seg	JsonReport	3 KB	 /pbi/dept/secondary/siv/sn
Deduplicated read	bam	59 GB	 /pbi/dept/secondary/siv/sn
Single-cell isoform	tgz	5 GB	 /pbi/dept/secondary/siv/sn
Segmented Reads	bam	94 GB	 /pbi/dept/secondary/siv/sn
Segmented Reads	bam	93 GB	 /pbi/dept/secondary/siv/sn
Non-passing read:	bam	4 GB	 /pbi/dept/secondary/siv/sn
Non-passing read:	bam	3 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr:	gff	3 GB	 /pbi/dept/secondary/siv/sn
Unique mapped tr:	gff	1 GB	 /pbi/dept/secondary/siv/sn

Related Datasets

Data Set ↕	Type ↕
KinnexRelease-10x-5pGEX-20k-Revio2cell-largeMem Segmented Reads	ccsreads