

10x-ALSmice-SingleNucleiExomeEnrichment-SNAM-justReadSeg - SNAM-2

SUCCESSFUL

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▼Analysis Overview

Status

Thumbnails

Display All

➤Read Segmentation

➤Data

Display All

Status

Analysis

10x-ALSmice-SingleNucleiExomeEnrichment-SNAM-justReadSeg - SNAM-2

Analysis ID

13171

From Multi-Job

[13169](#)

Status

SUCCESSFUL: 4 tasks finished

Created By

etseng

Date Created

2025-11-18, 02:00:16 PM

Date Updated

2025-11-18, 03:04:47 PM

Application

Read Segmentation

SMRT Link Version

25.4.0.278749

Inputs

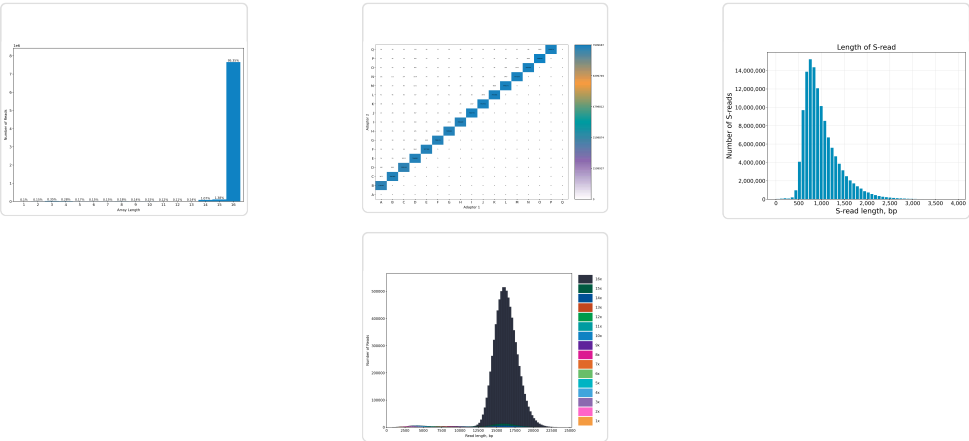
Data Type	Name
BarcodeSet	Barcodes: MAS-Seq Adapter v1 (MAS16)
ConsensusReadSet	HiFi reads: SNAM-2-Cell2 (all samples)

Path

/pbi/flash/smartlink/smartlink-appslabht/smartlink/userdata/jobs_root/0000/0000013/0000013171

➤ Analysis Parameters

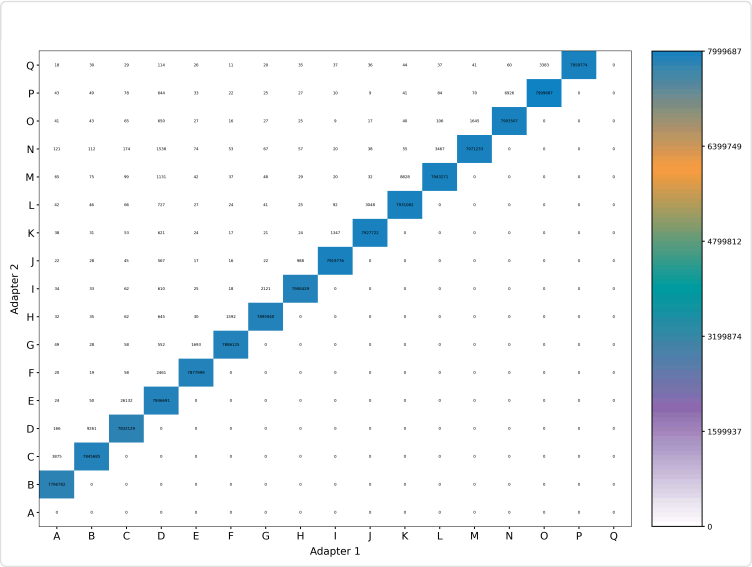
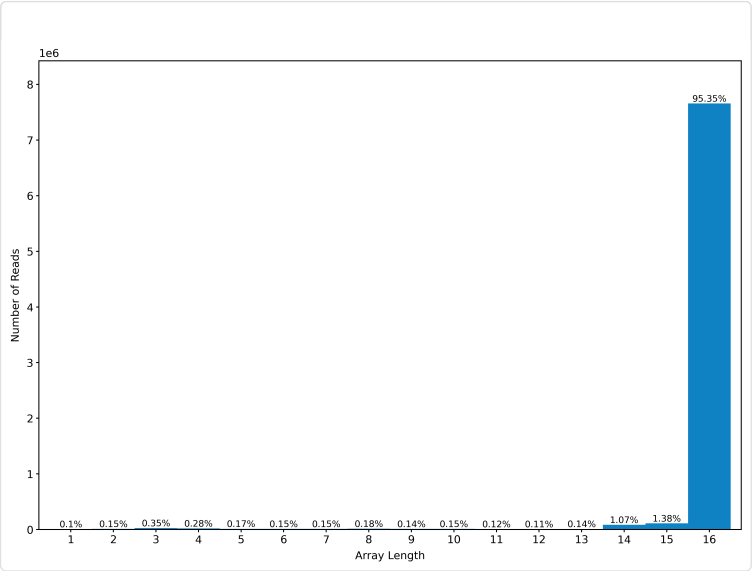
Thumbnails



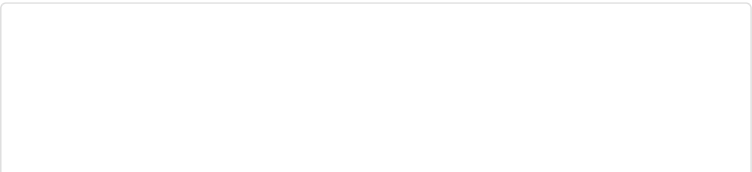
Read Segmentation

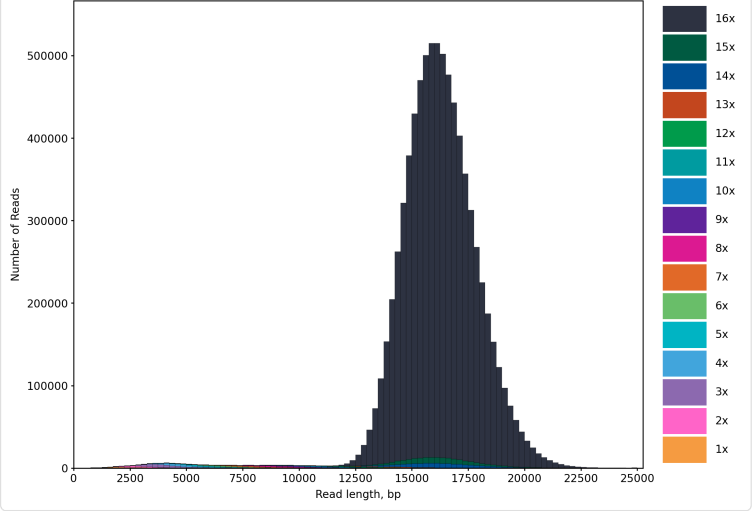
Value	Analysis Metric
8,033,810	Reads
126,533,832	Segmented reads (S-reads)
1,001	Mean length of S-reads
95.33 %	Percent of reads with full arrays
15.75	Mean array size (concatenation factor)

Segmentation Statistics

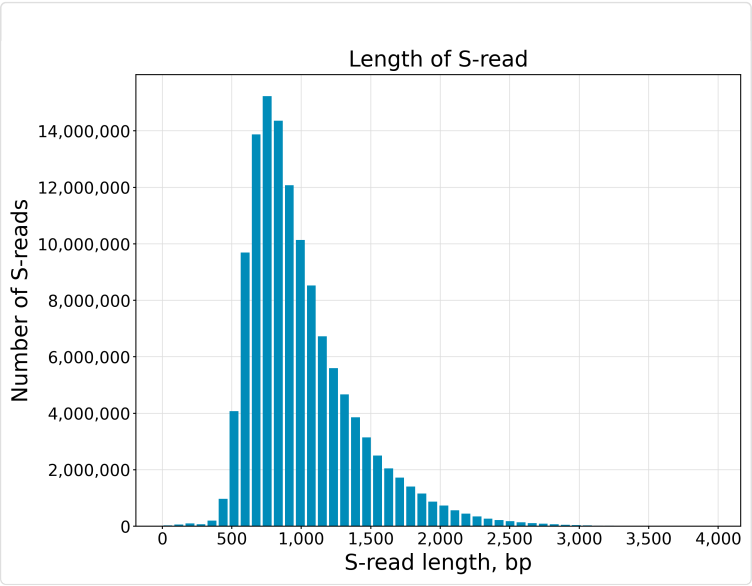


Length of Reads





S-read Length Distribution



File Downloads

Edit Output File Name Prefix

Example:analysis-SNAM-2-13171

File ↕	Type ↕	Size	Path
Non-passing read:	bam	3 GB	 /pbi/dept/secondary/siv/smr
Segmented Reads	bam	85 GB	 /pbi/dept/secondary/siv/smr
Analysis Log	log	15 KB	 /pbi/flash/smrtlink/smrtlink- <i>...</i>
SMRT Link Log	log	13 KB	 /pbi/flash/smrtlink/smrtlink- <i>...</i>