

Copy of Iso-Seq_MT_Pool.MG.IS

SUCCESSFUL

Copy

Delete

<p>▼ Analysis Overview</p>
Status
Thumbnails
Display All
<p>► CCS Analysis Read Classification</p>
<p>► Transcript Clustering</p>
<p>► Data</p>

Display All

Status

Analysis	Copy of Iso-Seq_MT_Pool.MG.IS
Analysis ID	11605
Status	SUCCESSFUL: 17 tasks finished
Created By	kmiyamot
Date Created	2023-06-06, 01:42:53 PM
Date Updated	2023-06-06, 08:44:51 PM
Application	Iso-Seq Analysis
SMRT Link Version	12.0.0.176214

Inputs

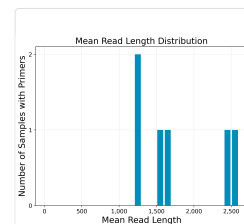
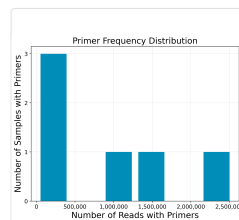
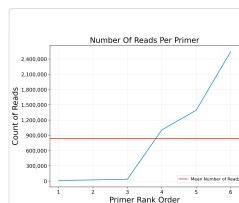
Data Type ↑	Name ↑	Import
BarcodeSet	Barcode Sets: 230606_IS_bc	Yes
ConsensusReadSet	HiFi Reads: MT_Pool.MG.IS-Cell1	Yes

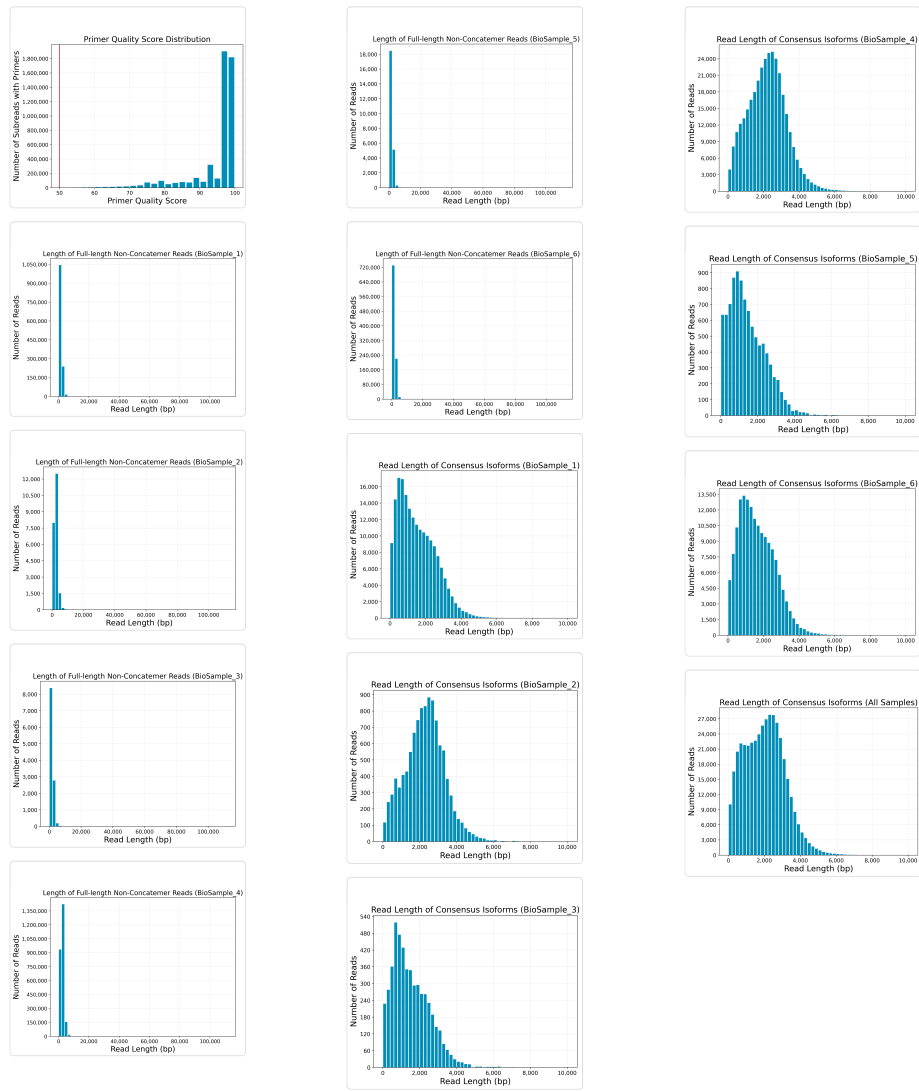
Path /net/eichler/vol28/projects/sequencing/pacbio/smt-link/userdata/jobs_root/0000/0000011/0000011605

▼ Analysis Parameters

Add task memory (MB)	0
Cluster Barcoded Samples Separately	false
Filters to Add to the Data Set	
Min. CCS Predicted Accuracy (Phred Scale)	10
Maximum Fuzzy Junction Difference (bp)	5
Minimum Gap-Compressed Identity (%)	95
Minimum Mapped Coverage (%)	99
Minimum Mapped Length (bp)	50
Advanced pbmm2 Options	
Require and Trim Poly(A) Tail	true
Run Clustering	true

Thumbnails





CCS Analysis Read Classification

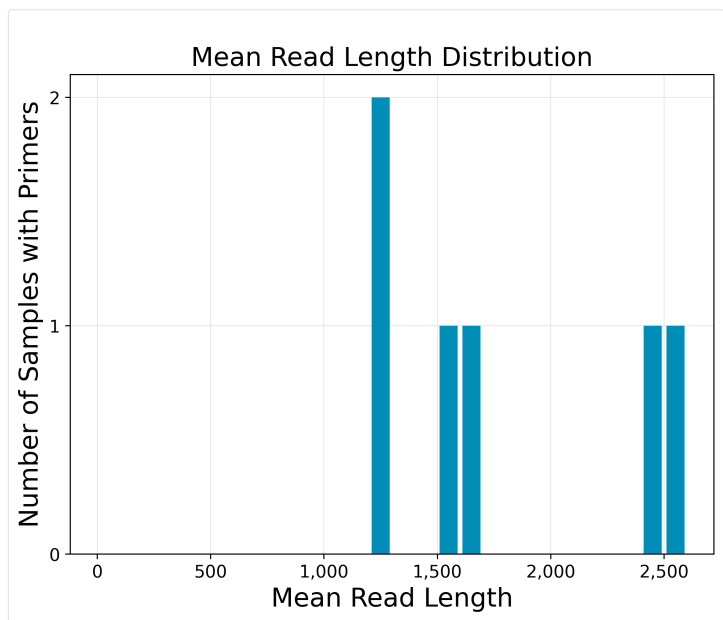
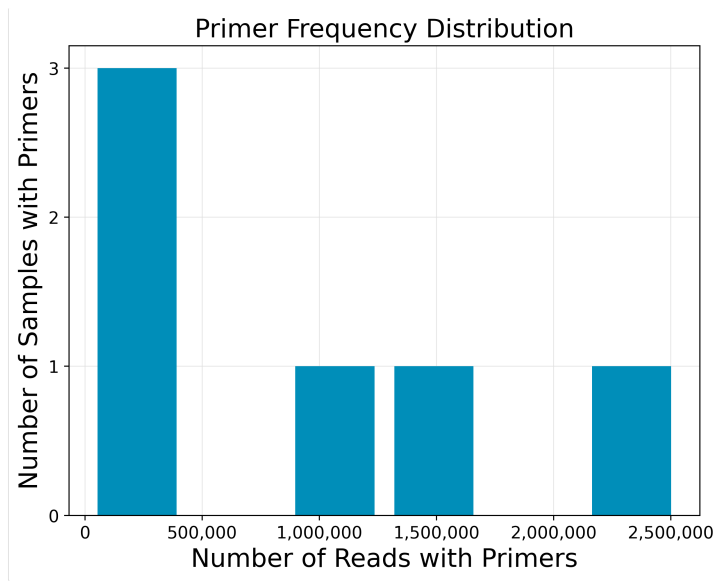
Value	Analysis Metric
7,426,132	Reads
5,012,206	Reads with 5' and 3' Primers
4,849,473	Non-Concatamer Reads with 5' and 3' Primers
4,844,793	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail
1,899	Mean Length of Full-Length Non-Concatamer Reads
6	Unique Primers
835,367	Mean Reads per Primer
2,542,894	Max. Reads per Primer
11,955	Min. Reads per Primer
2,413,926	Reads without Primers
30.98%	Percent Bases in Reads with Primers
67.49%	Percent Reads with Primers

Primer Data

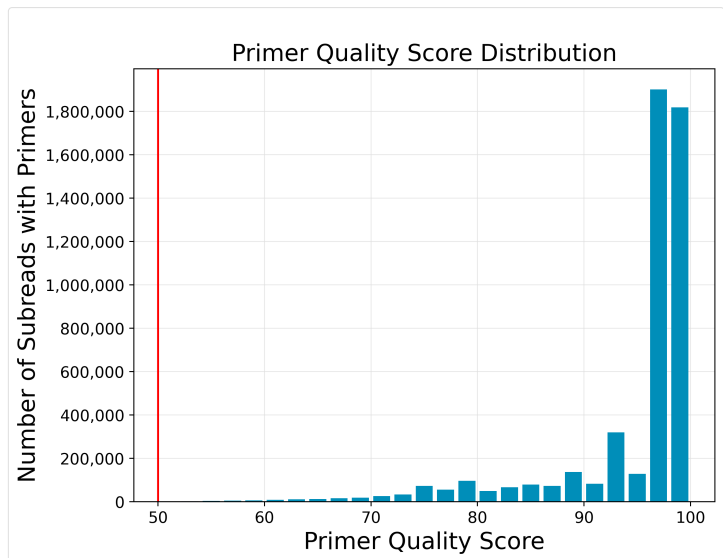
Bio Sample Name	Primer Name	CCS Reads	Mean Primer Quality	Reads with 5' and 3' Primers	Non-Concatamer Reads with 5' and 3' Primers	Non-Concatamer Reads with 5' and 3' Primers and Poly-A Tail
BioSample_1	bc1012_MTF_2_5p--bc1012_MTF_2_3p	1,393,520	94.0	1,393,520	1,298,206	1,297,327
BioSample_2	bc1012_MTF_2_5p--bc1020_MTG_3p	22,711	76.0	22,711	22,248	22,218
BioSample_3	bc1012_MTF_2_5p--bc1023_MTF_3p	11,955	77.0	11,955	11,403	11,383
BioSample_4	bc1020_MTG_5p--bc1020_MTG_3p	2,542,894	95.0	2,542,894	2,530,035	2,527,226
BioSample_5	bc1023_MTF_5p--bc1012_MTF_2_3p	36,389	75.0	36,389	23,941	23,924
BioSample_6	bc1023_MTF_5p--bc1023_MTF_3p	1,004,737	94.0	1,004,737	963,640	962,715
MT_Pool	No Primer	2,413,926	0.0	0	0	0

Primer Read Statistics

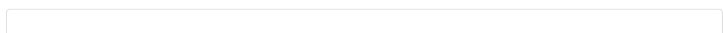


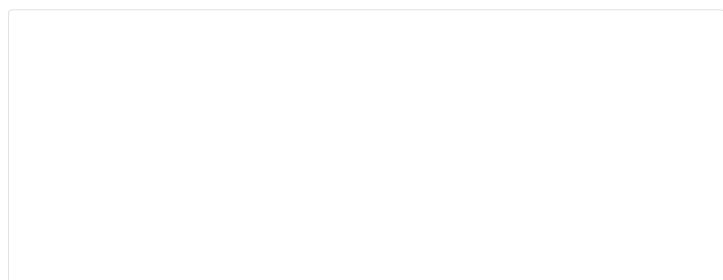
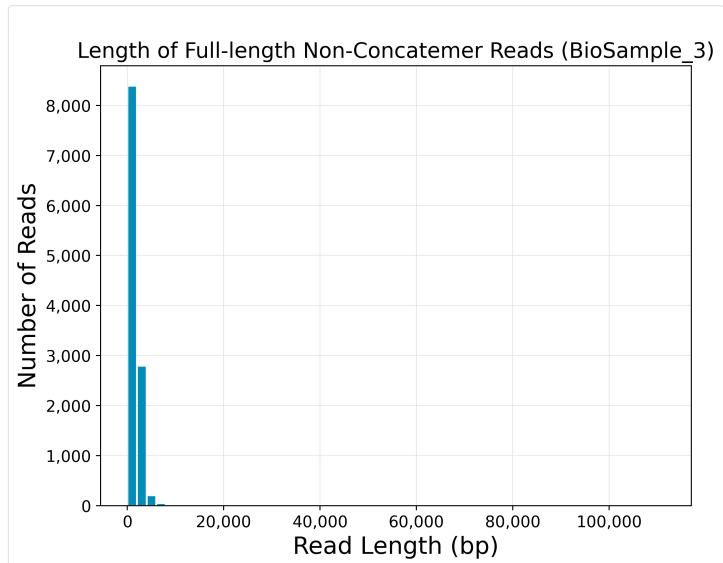
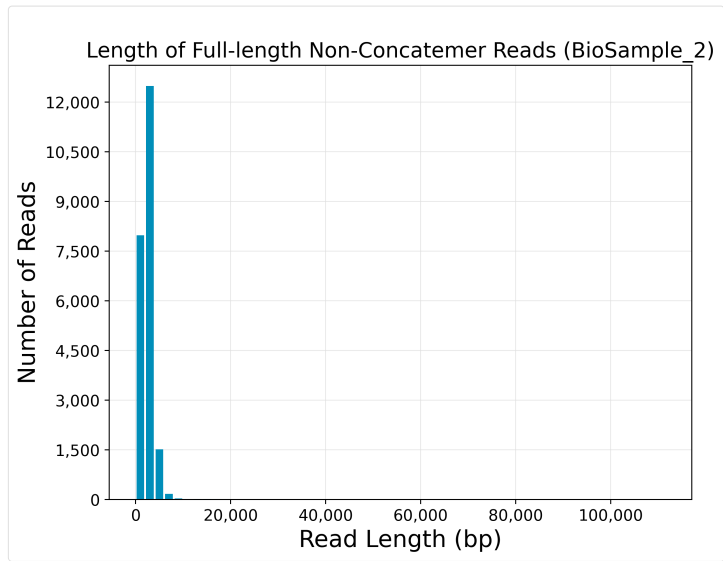
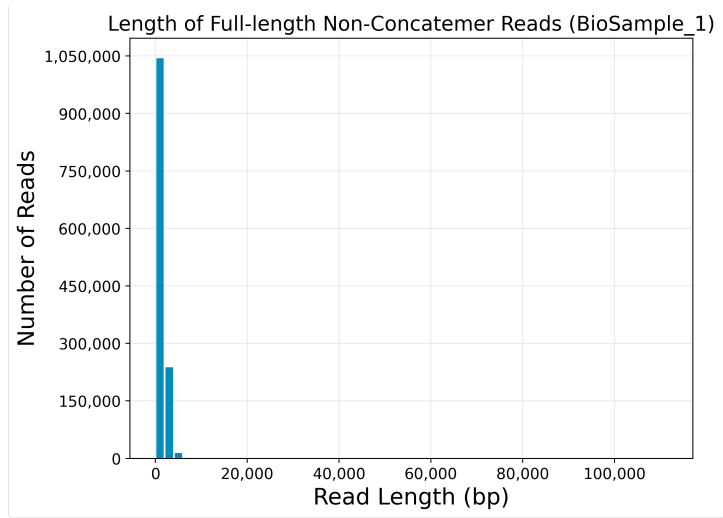


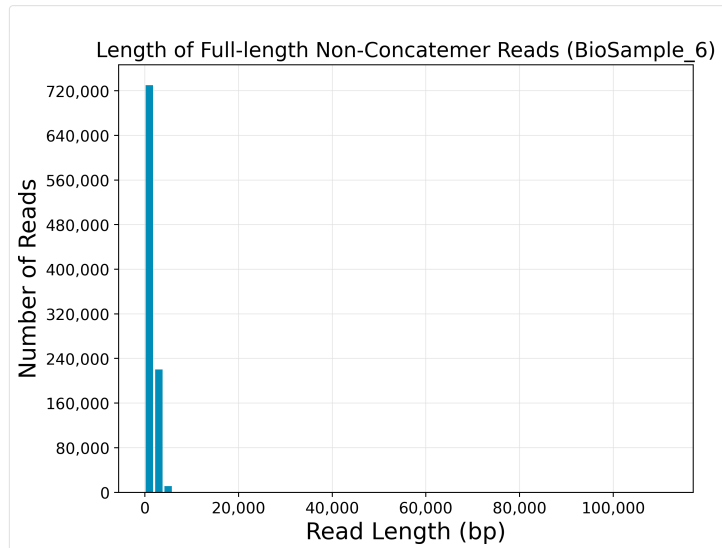
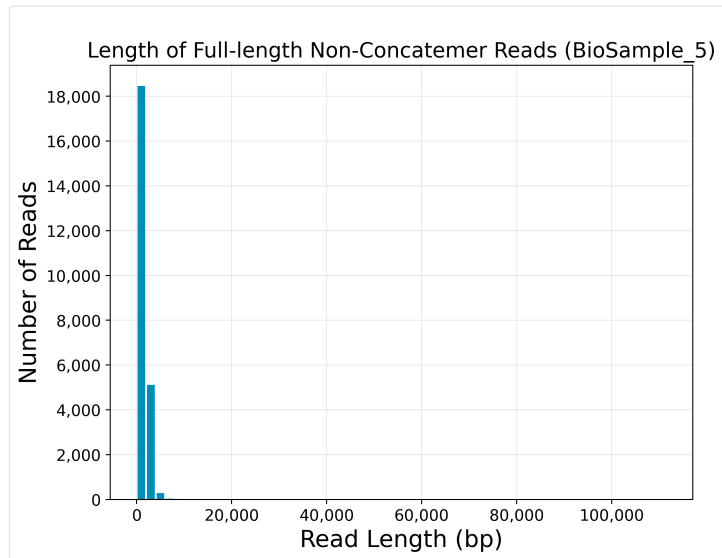
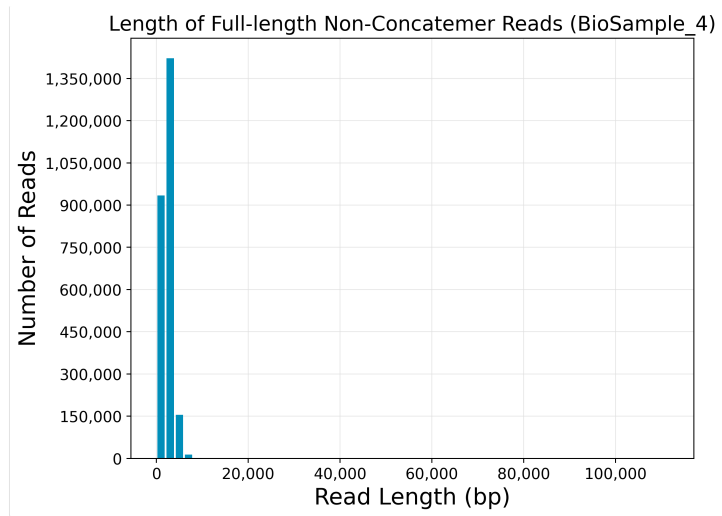
Primer Quality Scores



Length of Full-length Non-Concatemer Reads





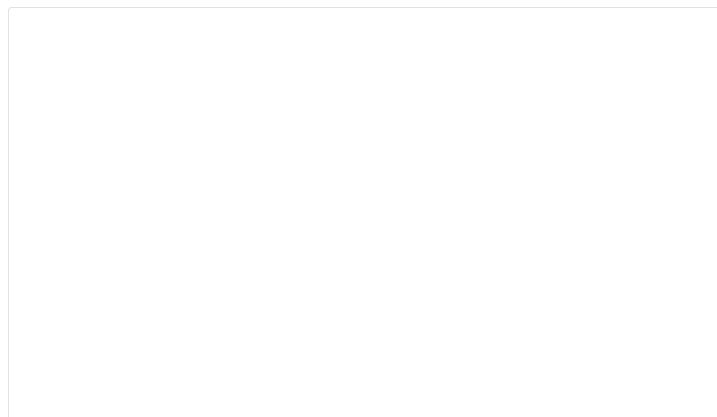
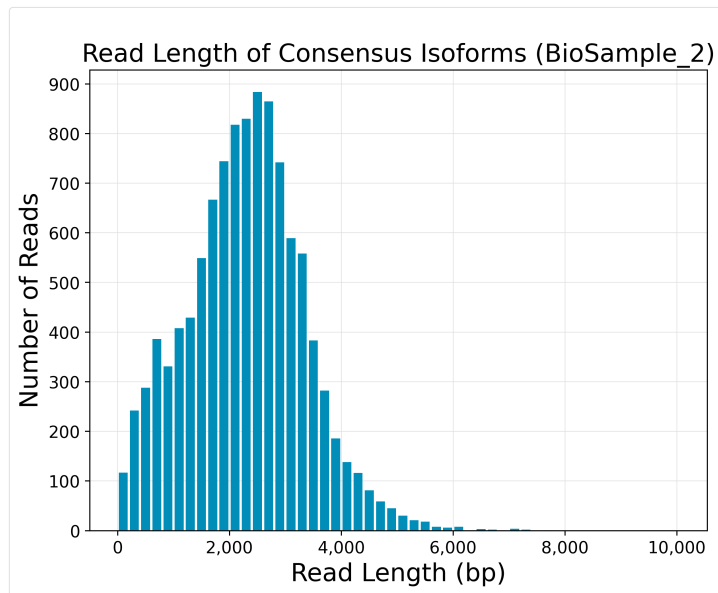
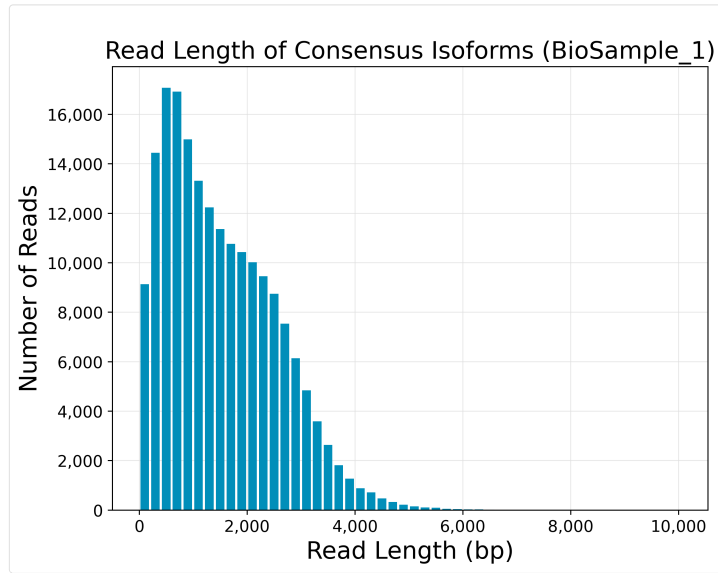


Summary Metrics

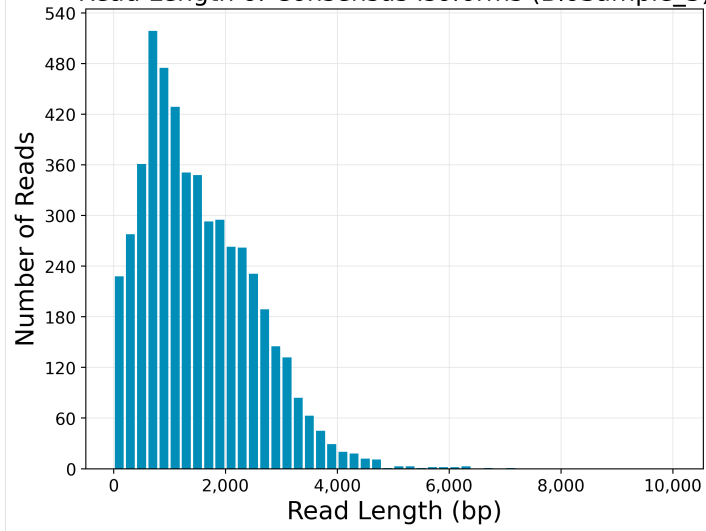
Sample Name	Number of High-Quality Isoforms	Number of Low-Quality Isoforms
BioSample_1	188,270	1,646
BioSample_2	10,811	31
BioSample_3	5,094	6

Sample Name	Number of High-Quality Isoforms	Number of Low-Quality Isoforms
BioSample_4	327,736	3,428
BioSample_5	9,556	21
BioSample_6	159,632	1,513
All Samples	411,251	4,721

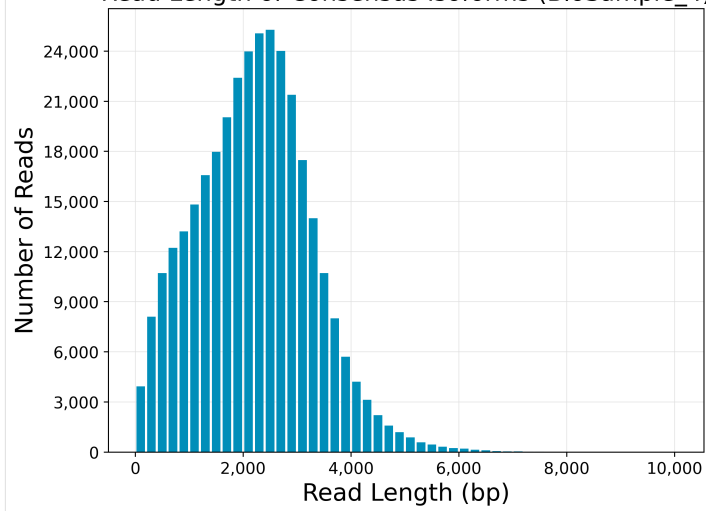
Length of Consensus Isoforms



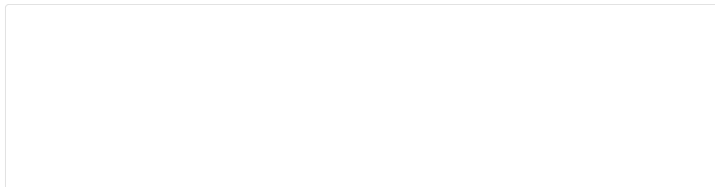
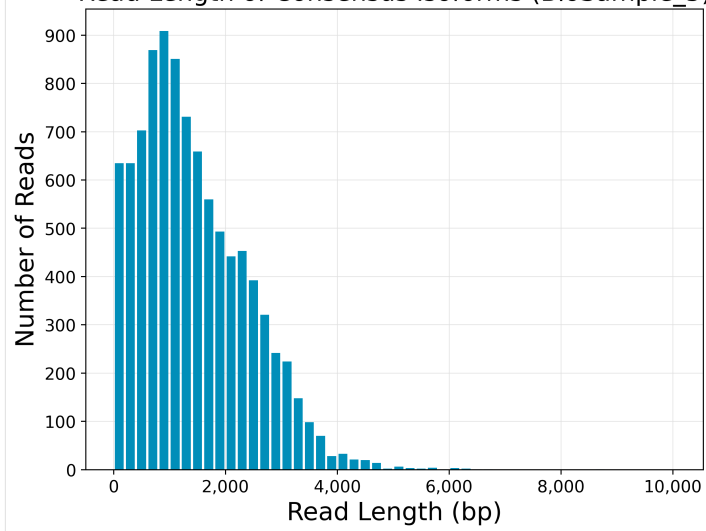
Read Length of Consensus Isoforms (BioSample_3)

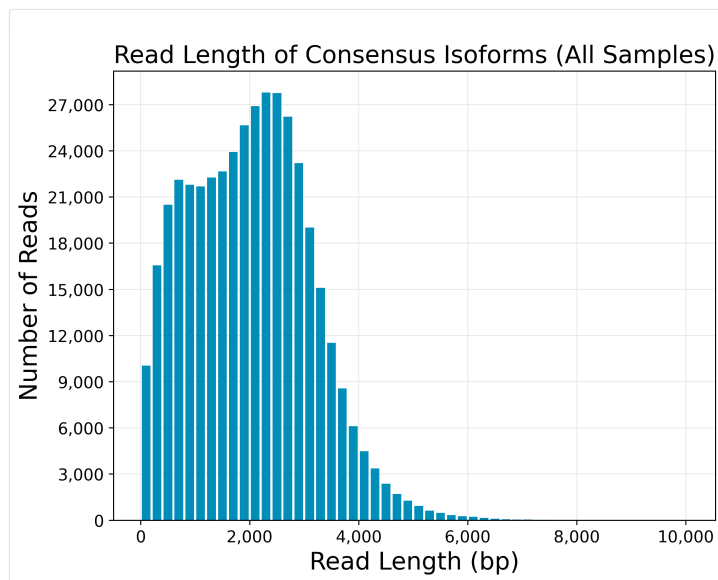
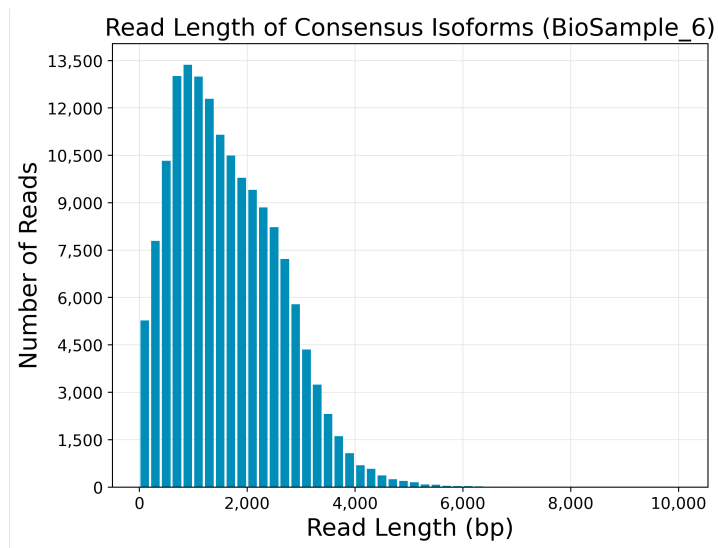


Read Length of Consensus Isoforms (BioSample_4)



Read Length of Consensus Isoforms (BioSample_5)





File Downloads

Example:analysis-MT_Pool-11605

File	Size	Type
Full-Length Non-Concatemer Report (BioSample_6)	73 MB	csv
Full-Length Non-Concatemer Reads (BioSample_6)	942 MB	bam
Full-Length Non-Concatemer Report (BioSample_5)	2 MB	csv
Full-Length Non-Concatemer Reads (BioSample_5)	22 MB	bam
Full-Length Non-Concatemer Report (BioSample_4)	191 MB	csv
Full-Length Non-Concatemer Reads (BioSample_4)	4 GB	bam
Full-Length Non-Concatemer Report (BioSample_3)	903 KB	csv
Full-Length Non-Concatemer Reads (BioSample_3)	11 MB	bam
Full-Length Non-Concatemer Report (BioSample_2)	2 MB	csv
Full-Length Non-Concatemer Reads (BioSample_2)	34 MB	bam
Full-Length Non-Concatemer Report (BioSample_1)	103 MB	csv