

Report for dataset Project 6693786 Acropora pulchra-Cell2 (all samples)

Dataset 02a932ec-0bd5-44f1-9505-bf9cd67f1115

Summary

Name	Project 6693786 Acropora pulchra-Cell2 (all samples)
Created At	2024-01-29 22:02:06.307
Number of Records	5898386
Total Length	79183709778
Movie Name	m84100_240128_024355_s2
ICS Version	13.0.0.212033
Well Sample	Project 6693786 Acropora pulchra
Biological Sample	Project 6693786 Acropora pulchra
Barcode Name	bc1029--bc1029

Run Preview

Summary

Estimated HiFi Yield (Gb)	None
HiFi read quality, median	None
HiFi read length, mean	9,931
P1 (%)	4610.00%
Time (Hrs)	4
Workflow	Basic
Movie Name	m84100_240128_024355_s2_basic_preview_4hr
Movie Id	m84100_240128_024355_s2

Barcode preview

Barcode	HiFi reads	HiFi read length (mean, bp)
bc1016--bc1016	1.1%	11168
bc1029--bc1029	93.9%	9744
Other	0.2%	12982
Not Barcoded	4.8%	12267

Run Preview

Summary

Estimated HiFi Yield (Gb)	82,325,141,133
HiFi read quality, median	39
HiFi read length, mean	13,207
P1 (%)	None
Time (Hrs)	29
Workflow	Full
Movie Name	m84100_240128_024355_s2_full_preview_29hr
Movie Id	m84100_240128_024355_s2

Barcode preview

Barcode	HiFi reads	HiFi read length (mean, bp)
bc1029--bc1029	98.5%	13207
Other	0.2%	7322
Not Barcoded	1.3%	10633

CCS Processing

Summary

ZMWs input	12,926,487
ZMWs pass filters	6,044,643
ZMWs fail filters	6,881,844
ZMWs shortcut filters	0
ZMWs with tandem repeats	32,902
Below SNR threshold	182,118
Median length filter	968,273
Lacking full passes	4,083,650
Heteroduplex insertions	0
Coverage drops	0
Insufficient draft cov	0
Draft too different	0
Draft generation error	2
Draft above --max-length	0
Draft below --min-length	0
Reads failed polishing	4,388
Empty coverage windows	6,382
CCS did not converge	0
CCS adapter concatenation	8
CCS adapter palindrome	5
CCS adapter residue	35
ZMW with full-length subread	1,634,234
ZMW with control failure	2,262
ZMW with control success	485
CCS below minimum RQ	0
Unknown error	0

ZMWs missing adapters	318,248
HiFi Reads	5,919,035
HiFi Yield (bp)	79,716,779,948
HiFi Read Length (mean, bp)	13,467
HiFi Read Length (median, bp)	12,769
HiFi Read Length N50 (bp)	12,769
HiFi Read Quality (median)	39
HiFi Number of Passes (mean)	14
<Q20 Reads	125,608
<Q20 Yield (bp)	1,850,725,519
<Q20 Read Length (mean, bp)	14,734
<Q20 Read Length (median, bp)	14,172
<Q20 Read Quality (median)	17
>=Q30 Reads	4,795,554
>=Q30 Yield (bp)	61,264,178,798
>=Q30 Read Length (mean, bp)	12,775
>=Q30 Read Length (median, bp)	12,067
>=Q30 Read Quality (median)	42
Base quality >=Q30 (bp)	75,629,667,093
Base quality >=Q30 (%)	94.9

Barcodes

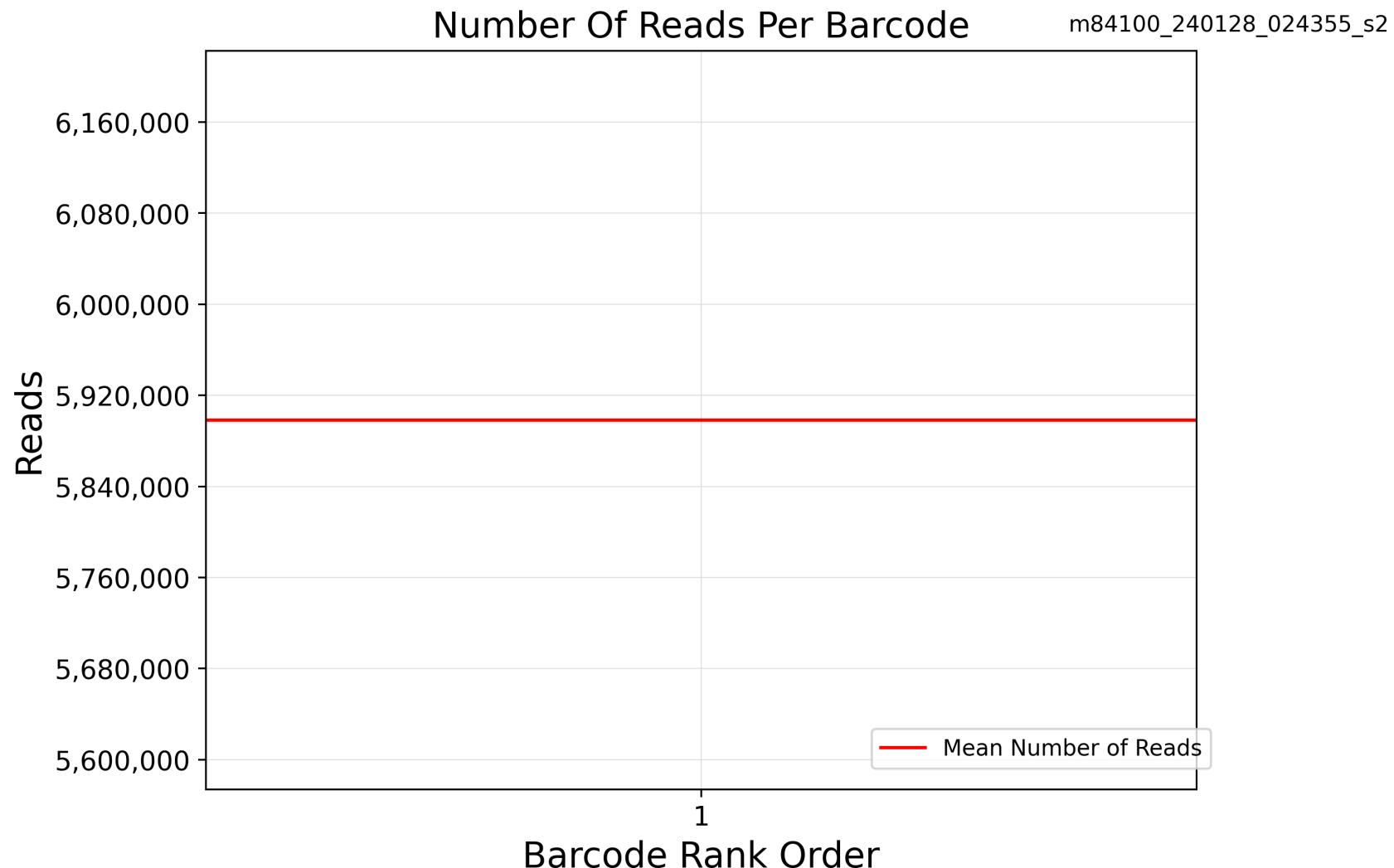
Summary

Unique Barcodes	1
Barcode HiFi Reads	5,898,386
Unbarcode HiFi Reads	20,649
Barcode HiFi Reads (%)	0.9965114245818786
Barcode HiFi yield (Gb)	79,183,709,778
Unbarcode HiFi yield (Gb)	266,119,812
Barcode HiFi Yield (%)	0.9966504671769177
Mean HiFi Reads per Barcode	5,898,386
Max. HiFi Reads per Barcode	5,898,386
Min. HiFi Reads per Barcode	5,898,386
Barcode HiFi read length (mean, kb)	13,424
Unbarcode HiFi read length (mean, kb)	12,887

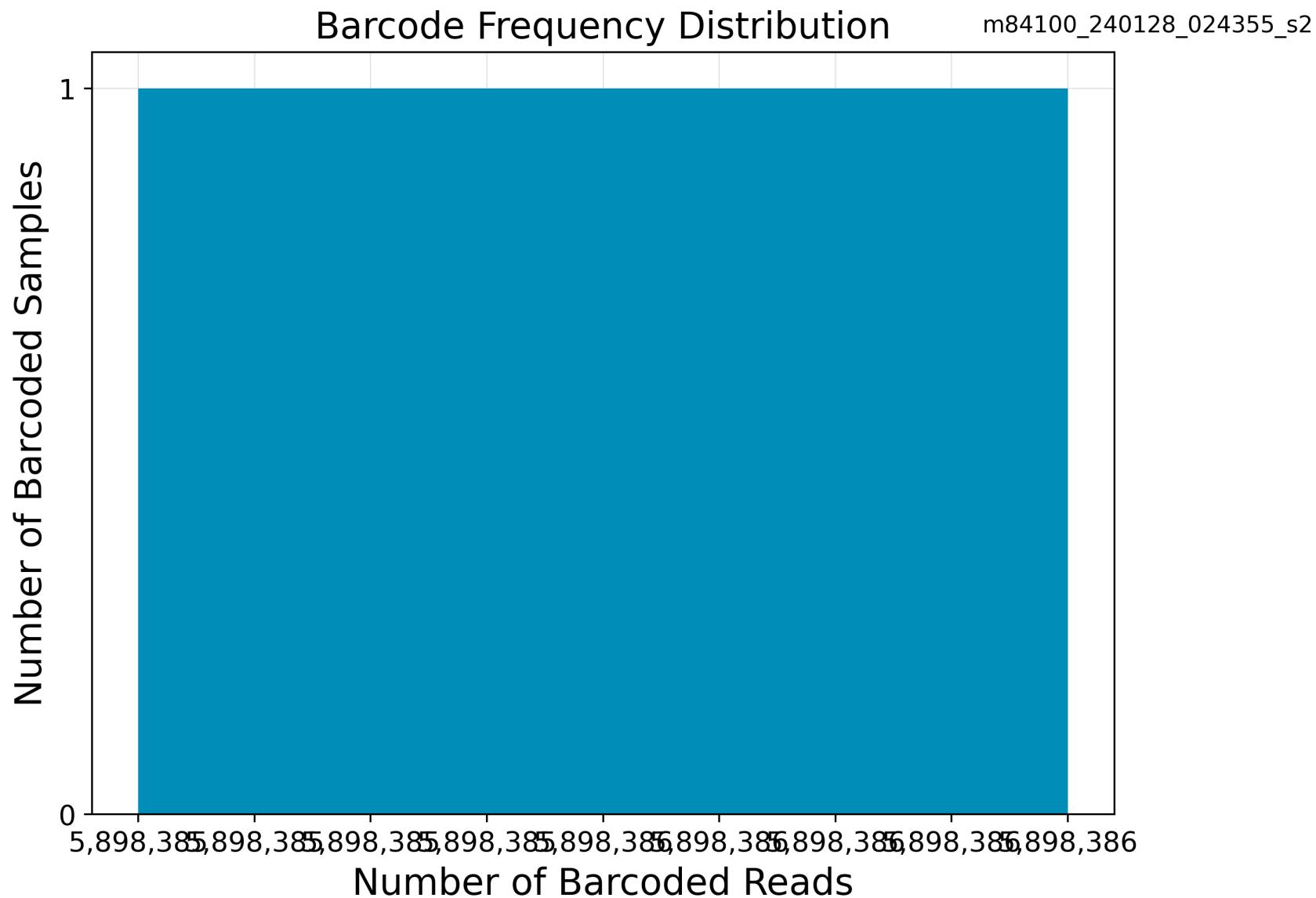
Barcode Data

Sample Name	Barcode	Barcode Quality	HiFi Reads	HiFi Read Length (mean, bp)	HiFi Read Quality (median, QV)	HiFi Yield (bp)	Polymerase Read Length (mean, bp)
Project 6693786 Acropora pulchra	bc1029--bc1029	98.2	5898386	13424	Q39	79183709778	169536
No Name	Not Barcoded	0.0	20649	12887	Q29	266119812	159034

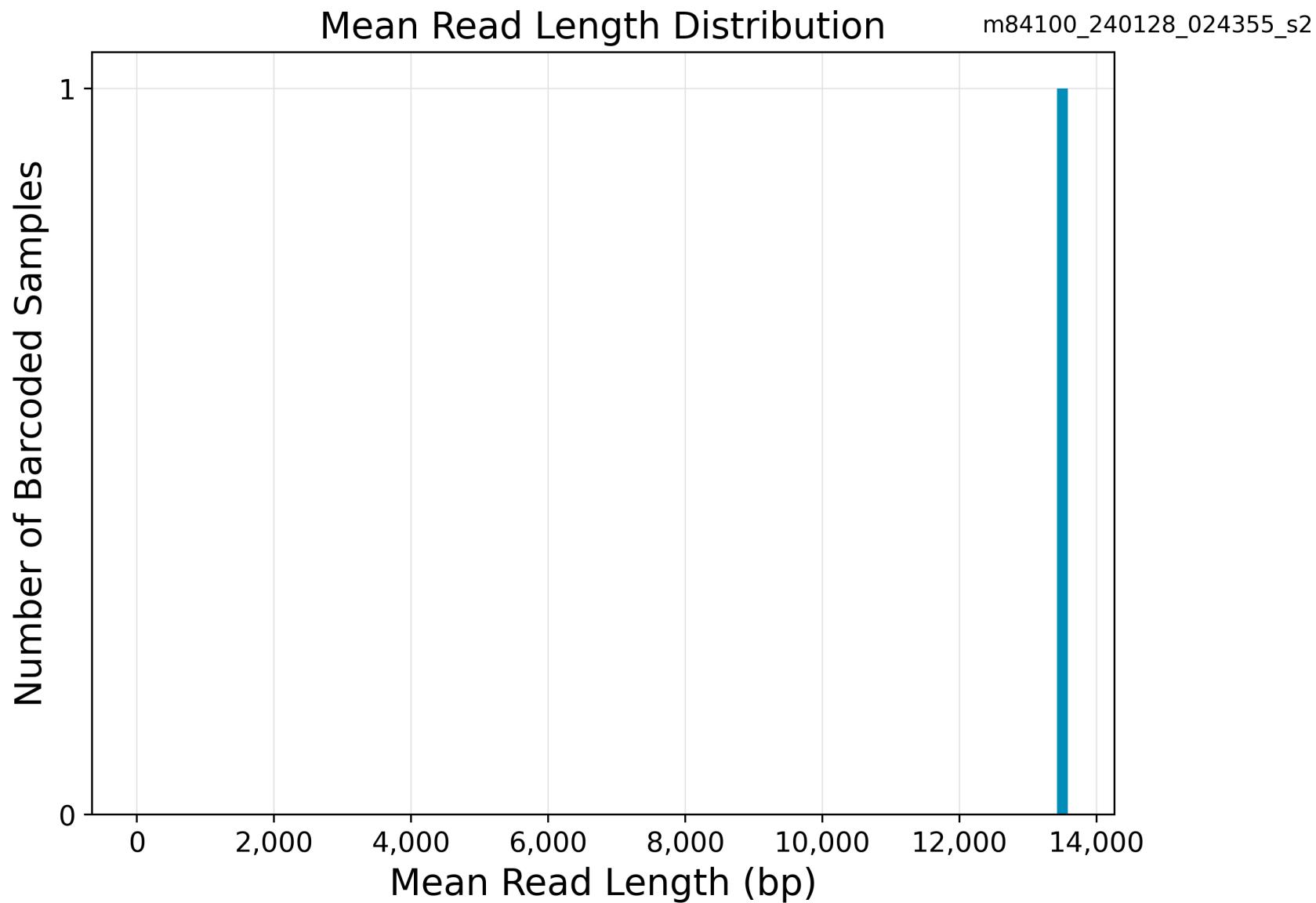
Number Of Reads Per Barcode



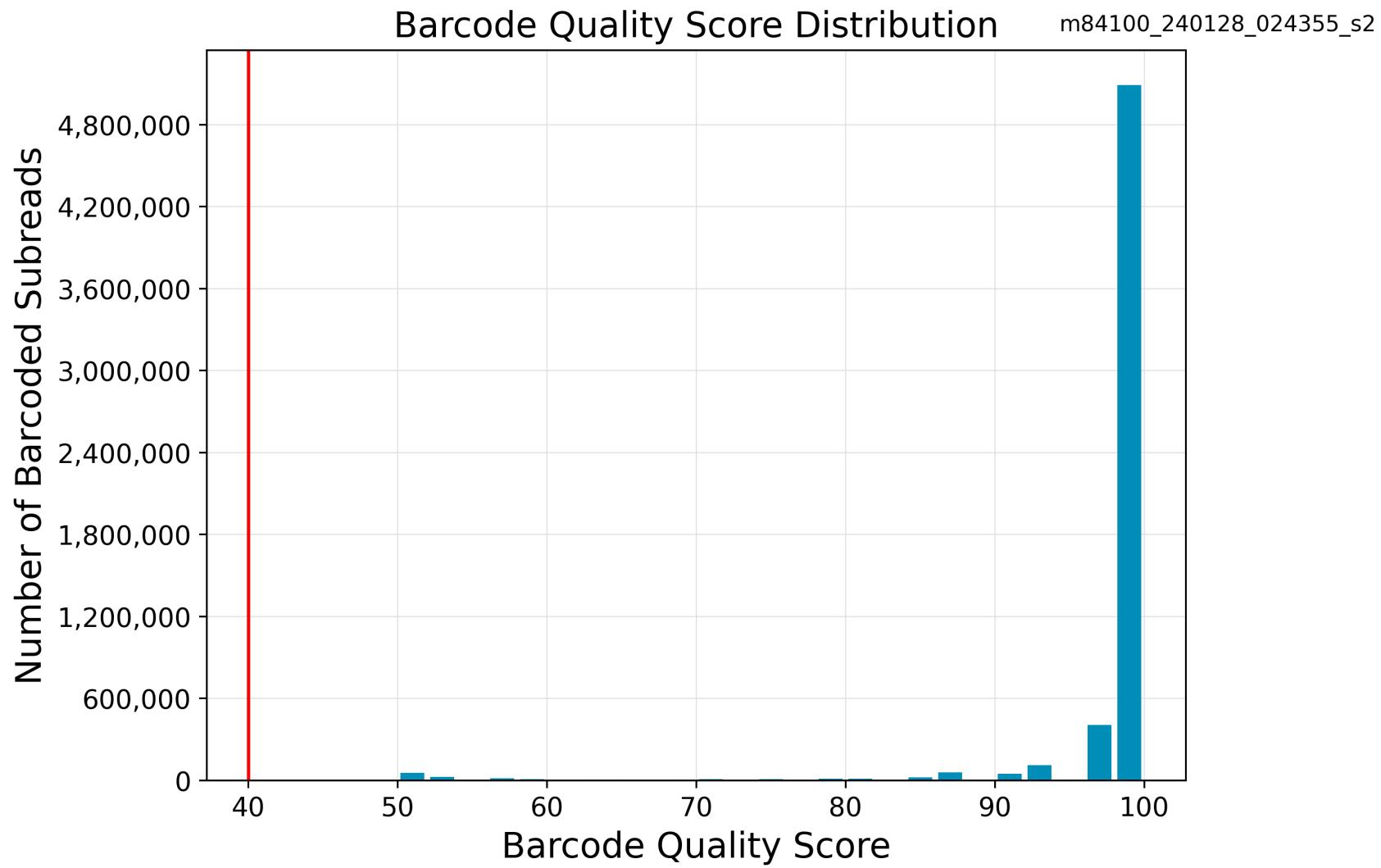
Barcode Frequency Distribution



Mean Read Length Distribution



Barcode Quality Score Distribution



Adapter Report

Summary

Adapter Dimers (0-10bp) %	0
Short Inserts (11-100bp) %	0
Local Base Rate	2.53

Loading Report

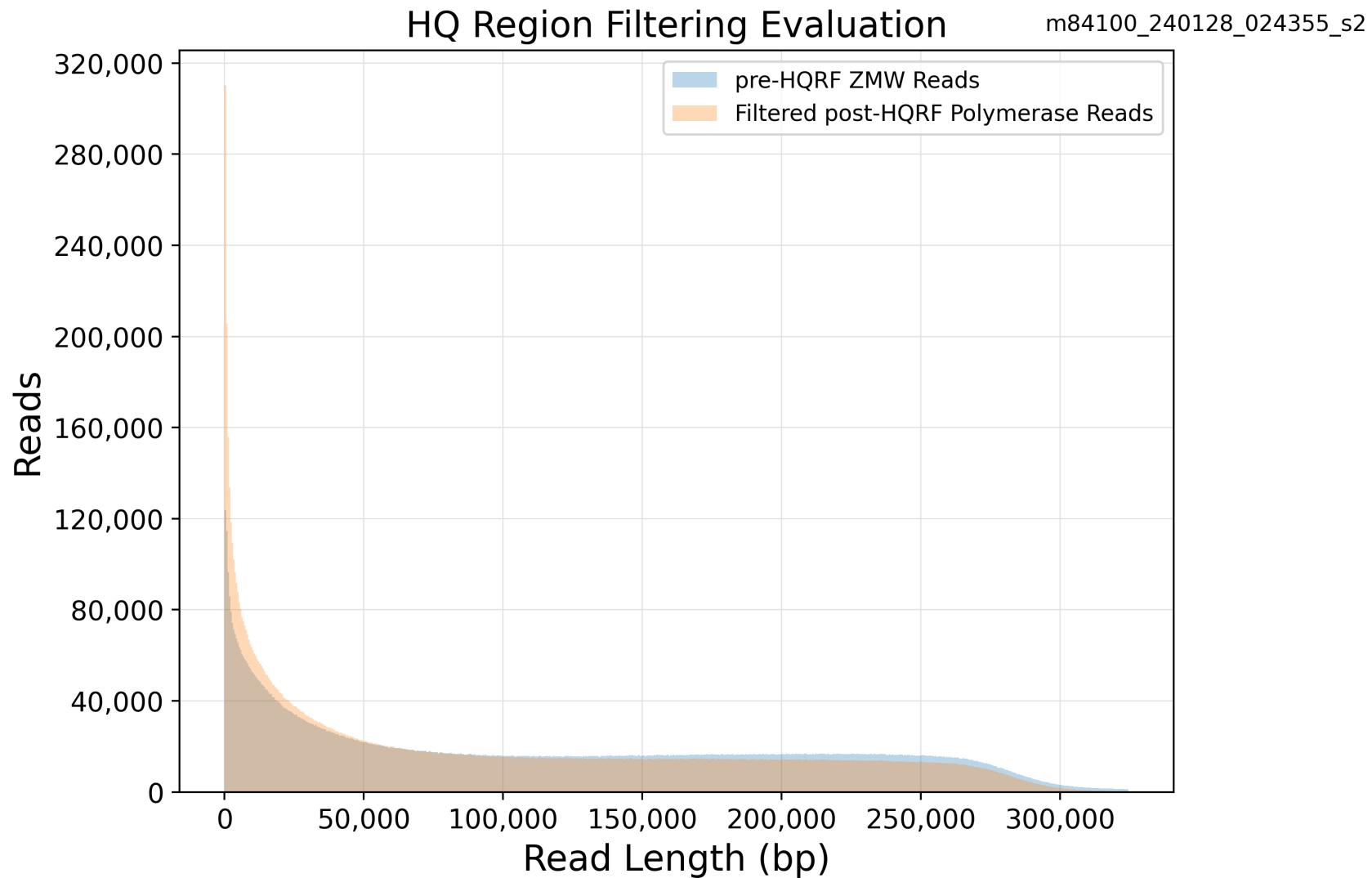
Summary

Productive ZMWs	25,165,824
Productivity 0	13,050,180
Productivity 1	12,011,121
Productivity 2	104,523

Loading Statistics

Collection Context	Total ZMWs	Productivity 0	P0 (%)	Productivity 1	P1 (%)	Productivity 2	P2 (%)	Loading type
m84100_240128_024355_s2	25165824	13050180	51.86	12011121	47.73	104523	0.42	Workflow_Kestrel.py

HQ Region Filtering Evaluation



CCS Analysis Report

Summary

HiFi reads	5,919,035
HiFi reads yield	79,449,829,590
HiFi reads length (mean)	13,422
HiFi reads length (median, bp)	12,724
HiFi Read Length N50 (bp)	16,547
HiFi Read Quality (median)	Q39
HiFi Read Quality (median)	39
Base Quality Q30 (%)	94.87%
HiFi Number of Passes (mean)	15

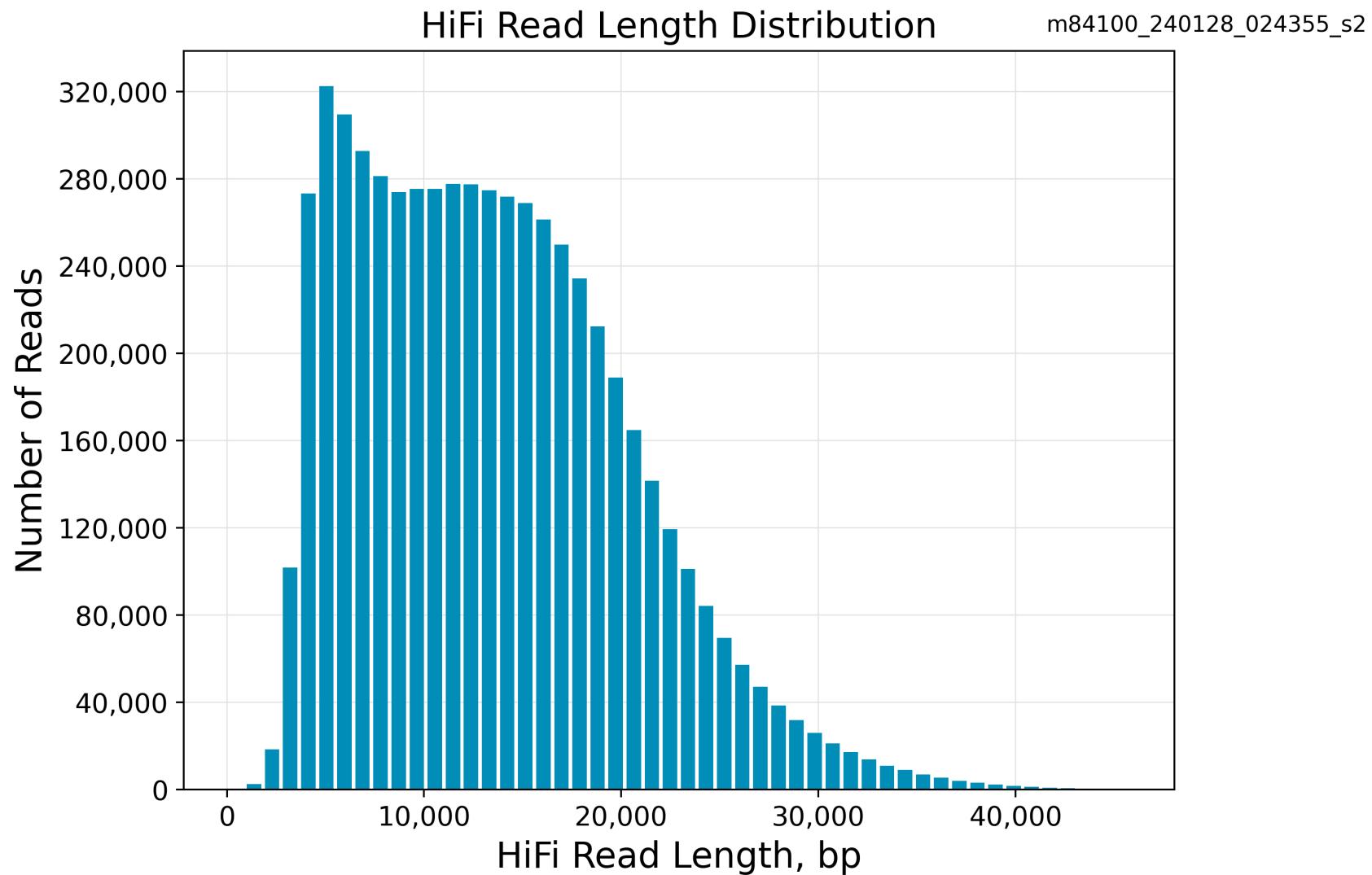
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
0	5919035	100	79449829590 Gb	100
5,000	5361604	91	77172562085 Gb	97
10,000	3781279	64	65442668746 Gb	82
15,000	2282342	39	46720114737 Gb	59
20,000	1003027	17	24538123626 Gb	31
25,000	344106	6	9960087695 Gb	13
30,000	103346	2	3445360546 Gb	4
35,000	24353	0	916532705 Gb	1
40,000	3602	0	151238252 Gb	0

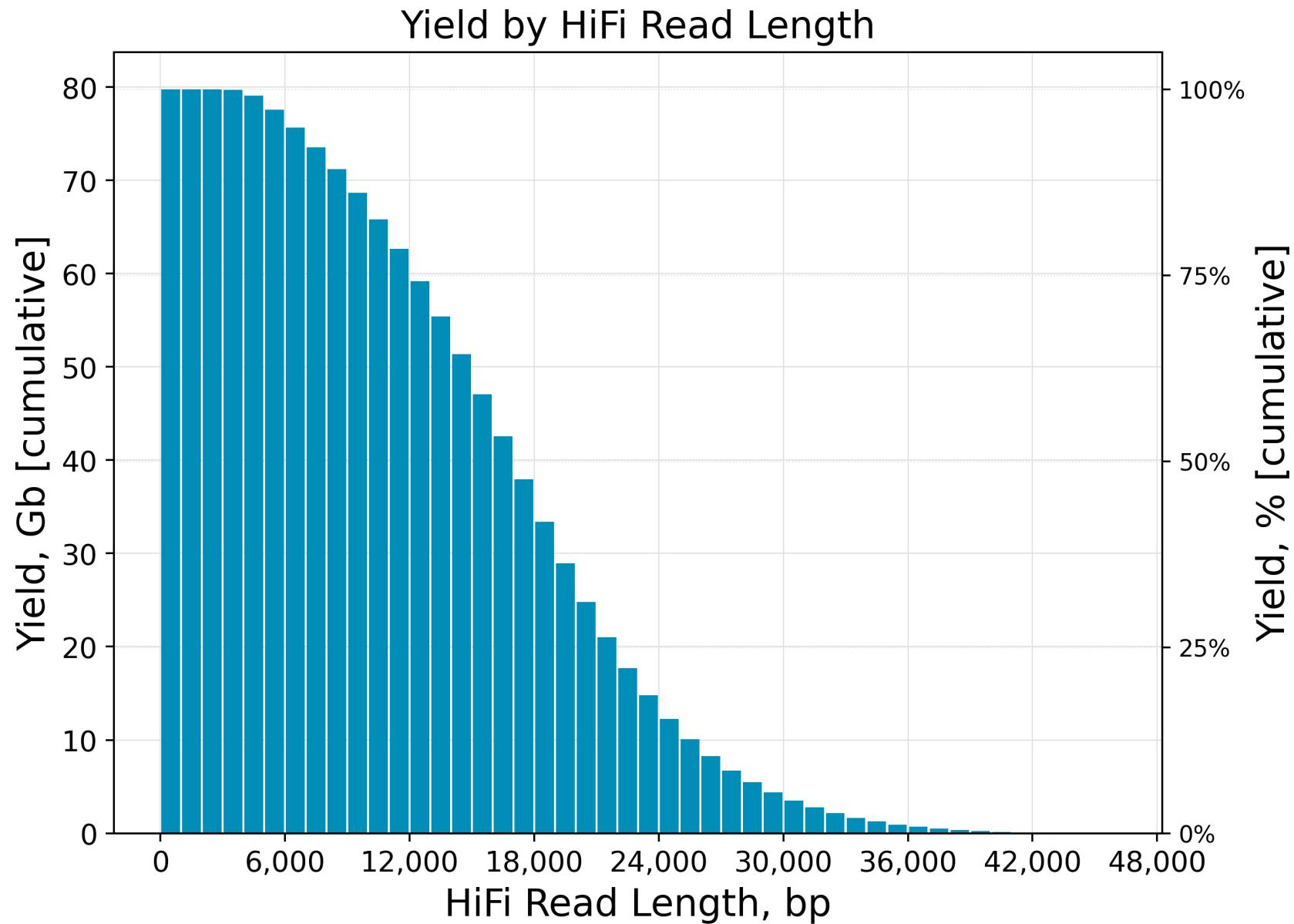
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
Q20	5919035	100	79.45 Gb	100
Q30	4795568	81	61.04 Gb	77
Q40	2781495	47	28.81 Gb	36
Q50	1157955	20	8.50 Gb	11

HiFi Read Length Distribution



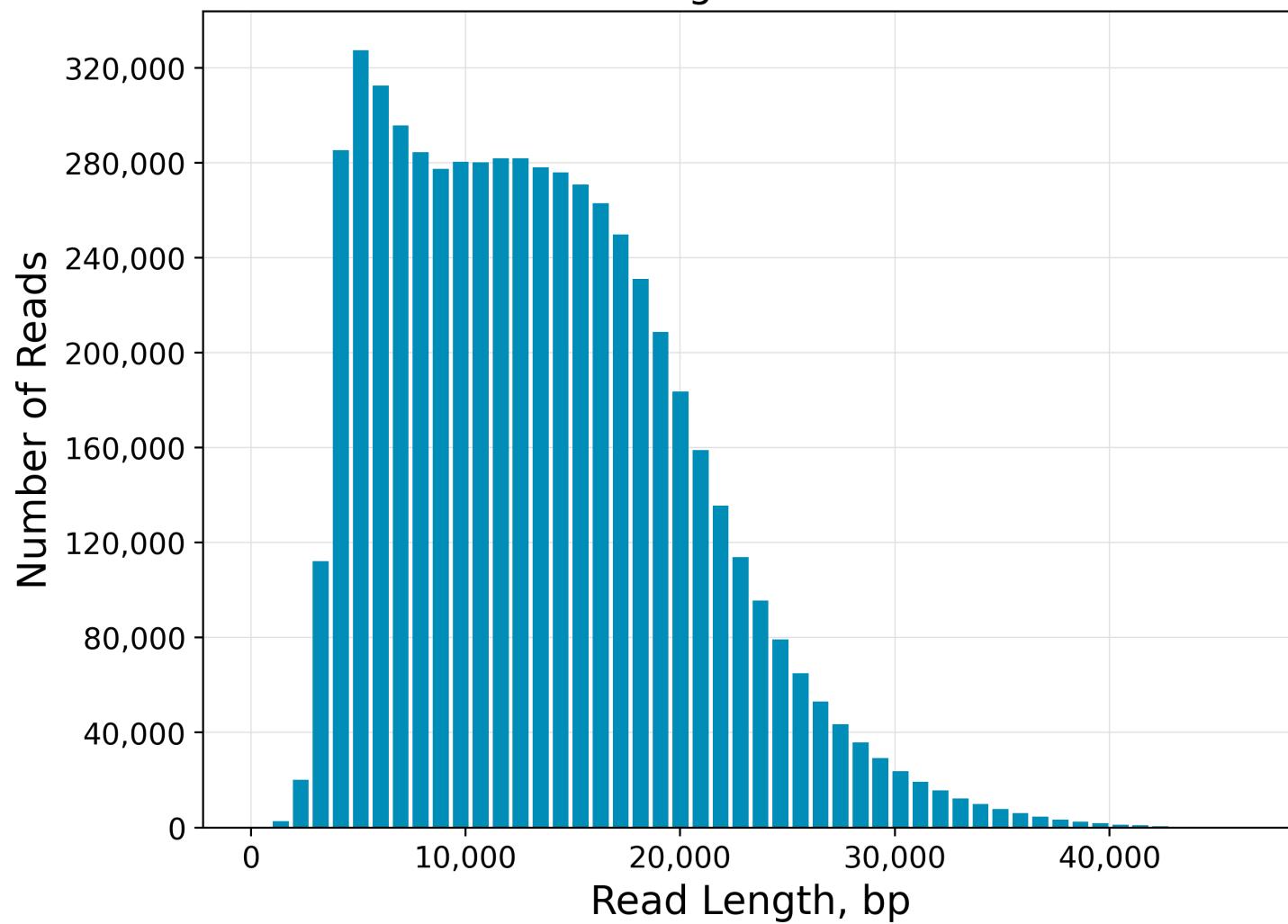
Yield by HiFi Read Length



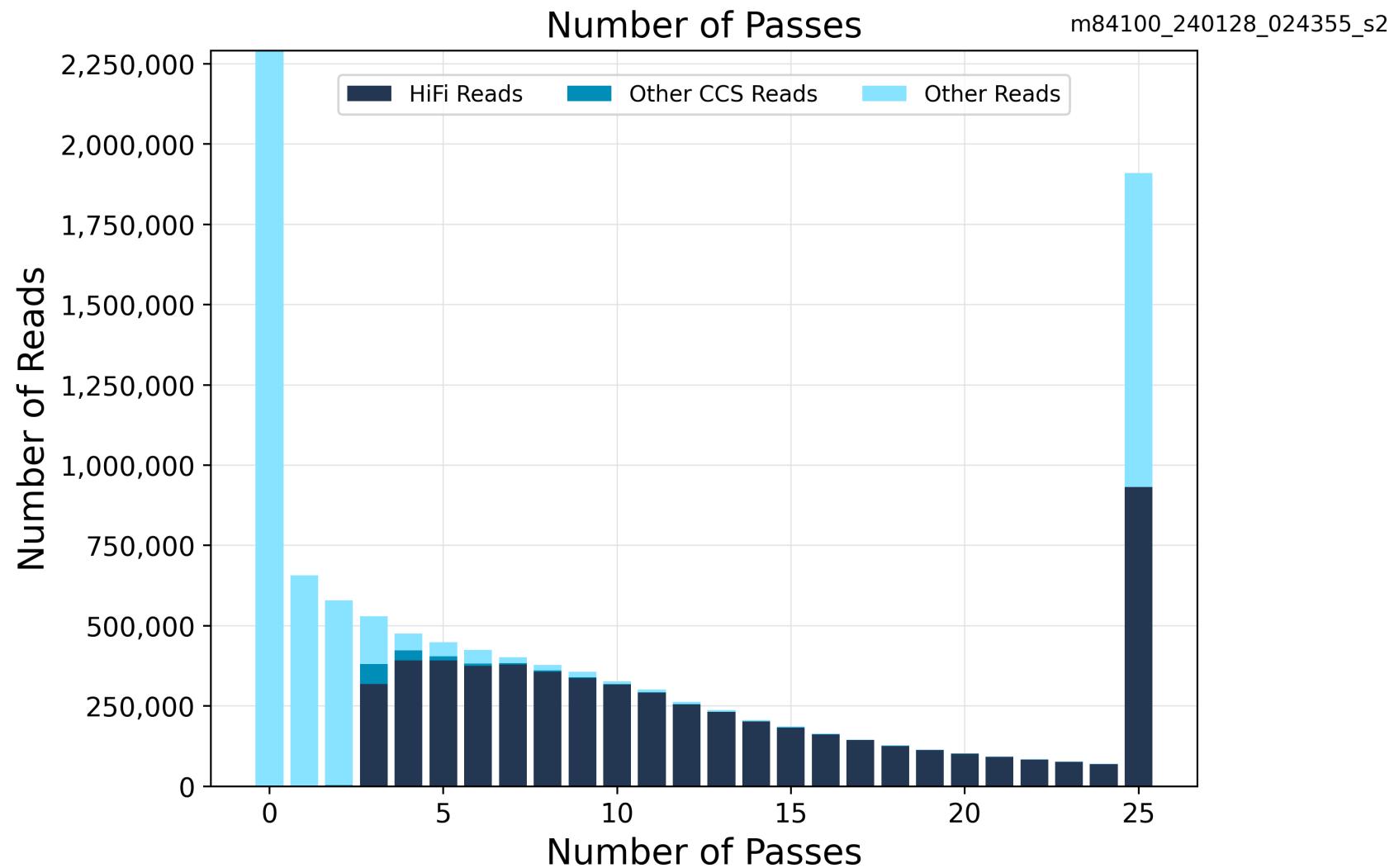
Read Length Distribution

Read Length Distribution

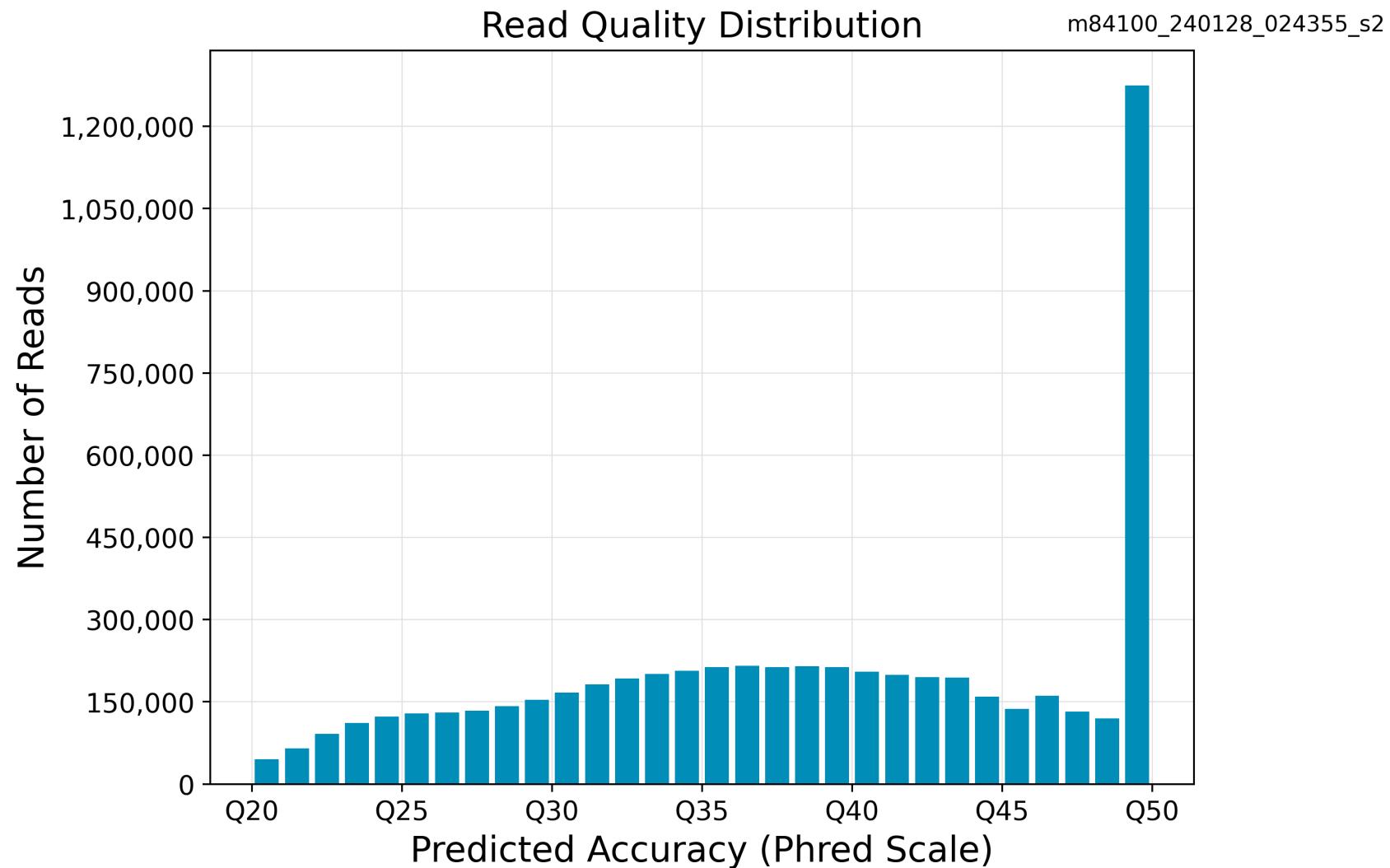
m84100_240128_024355_s2



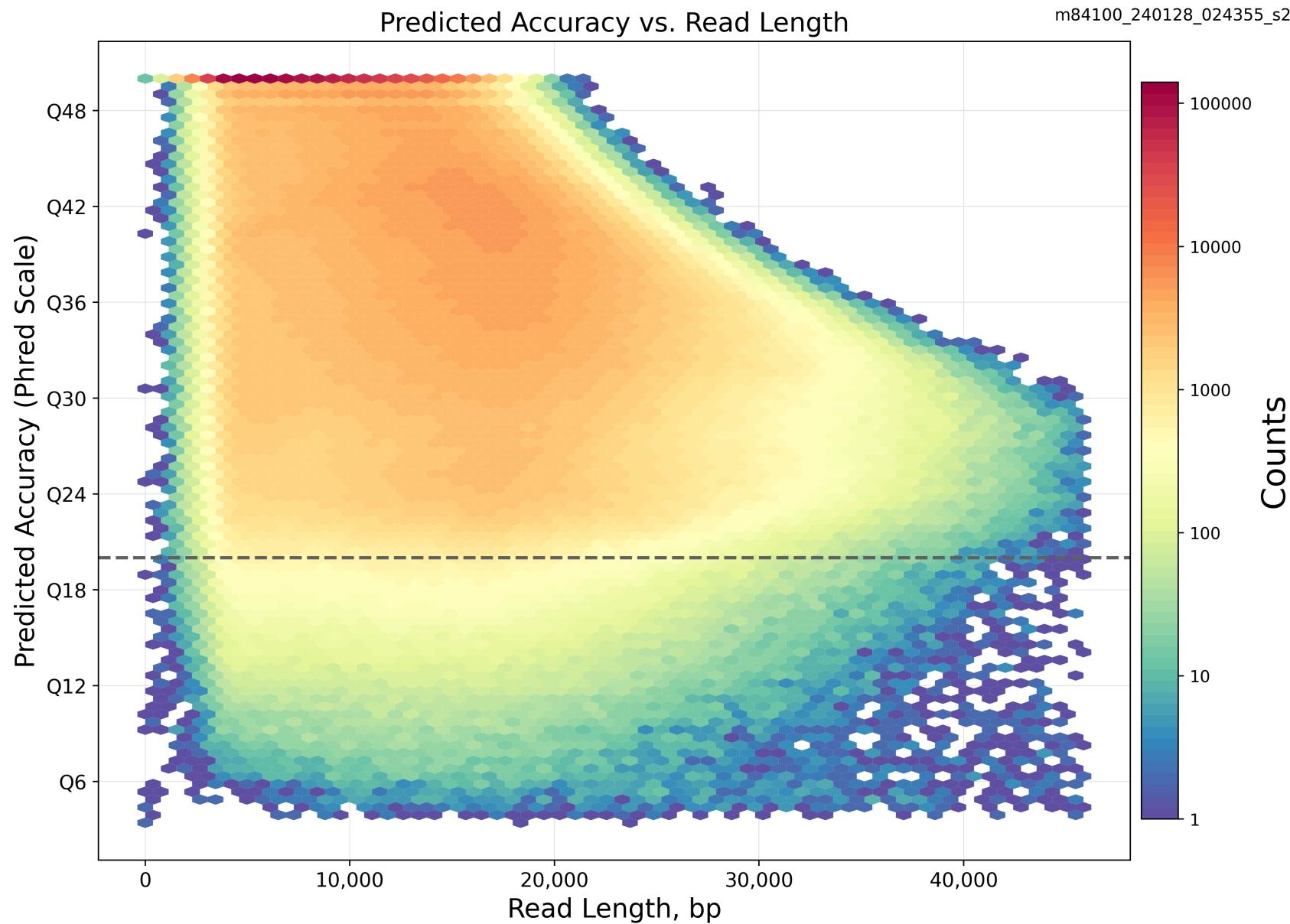
Number of Passes



Read Quality Distribution



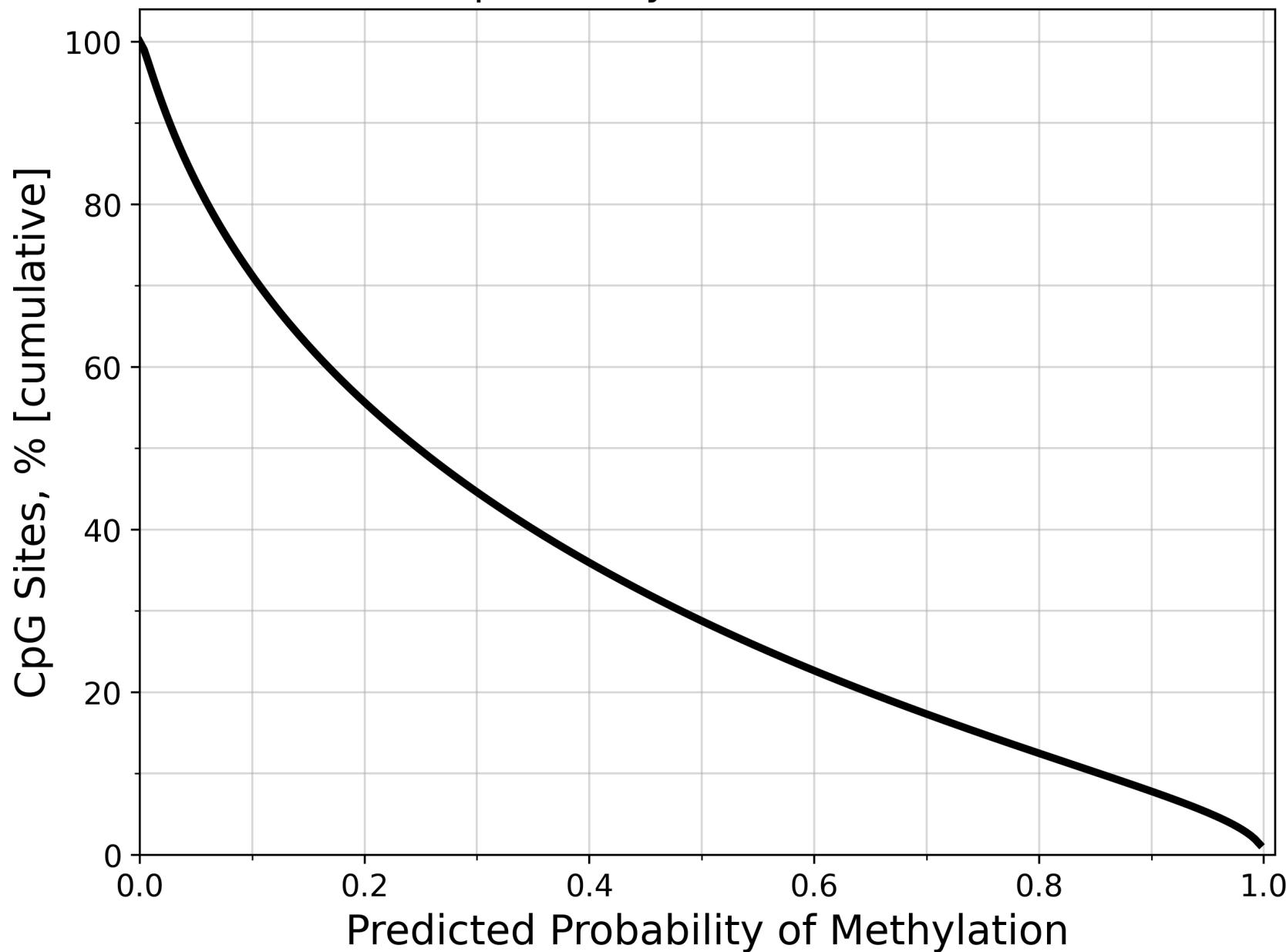
Predicted Accuracy vs. Read Length



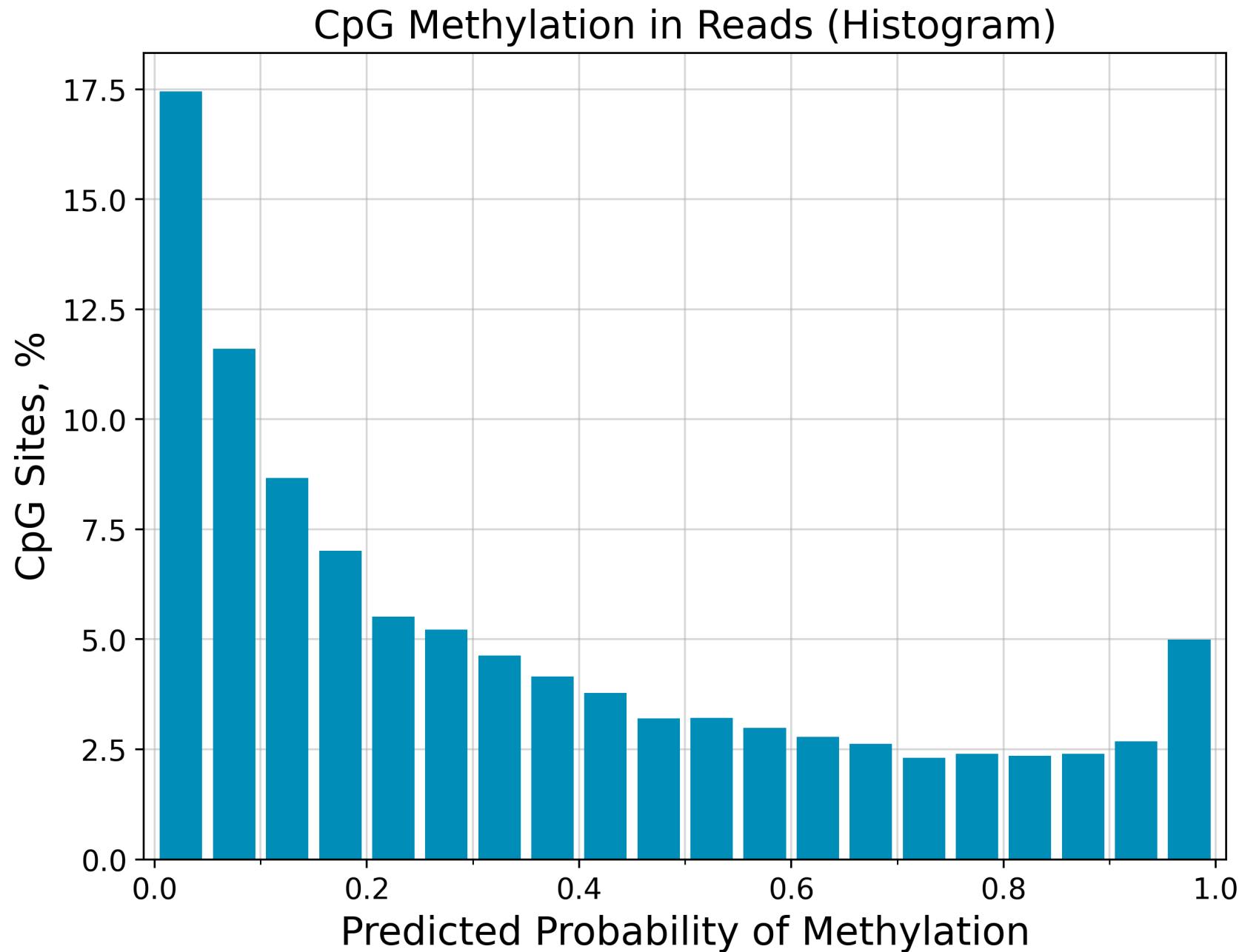
5mC CpG Report

CpG Methylation in Reads

CpG Methylation in Reads



CpG Methylation in Reads (Histogram)

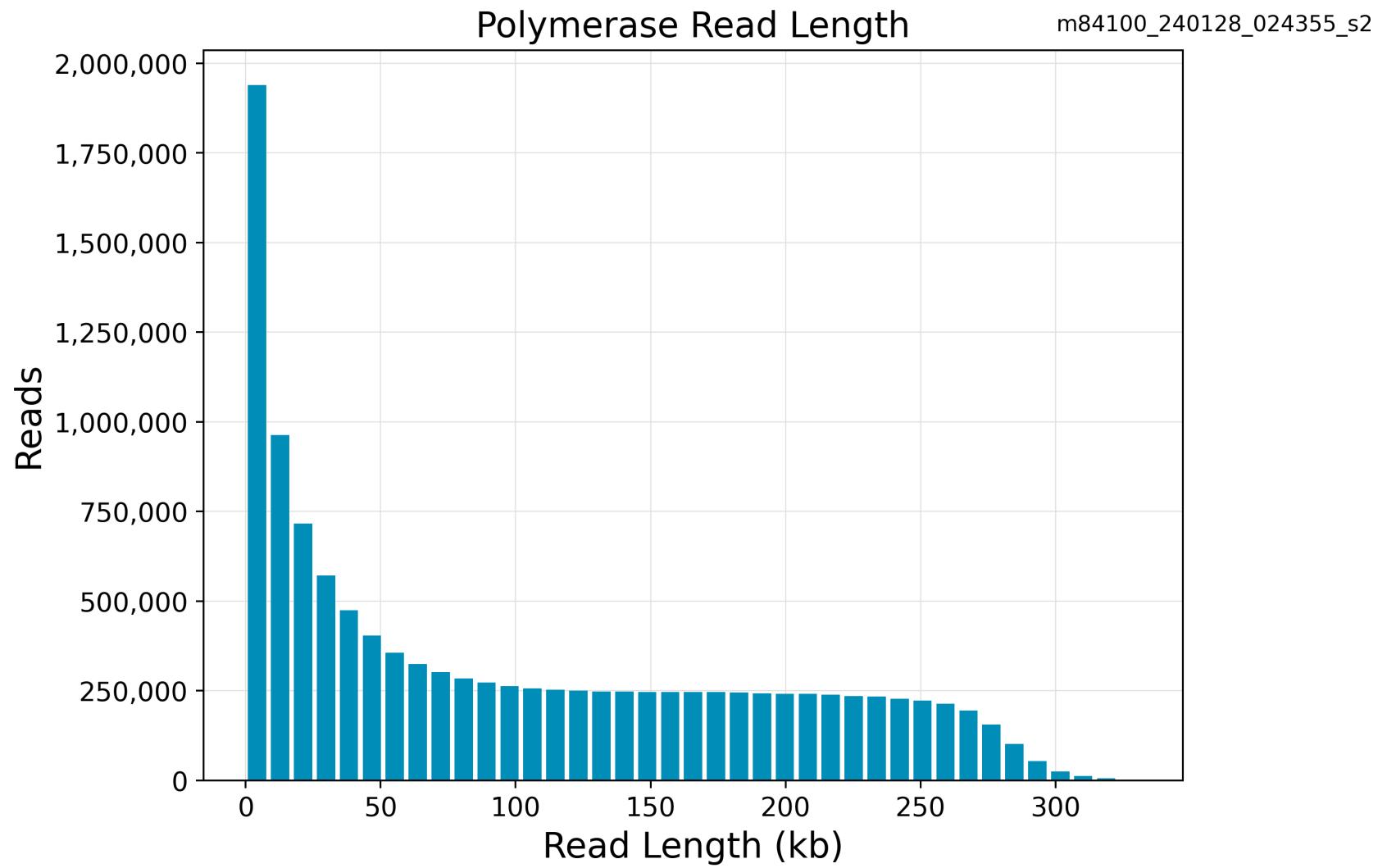


Raw Data Report

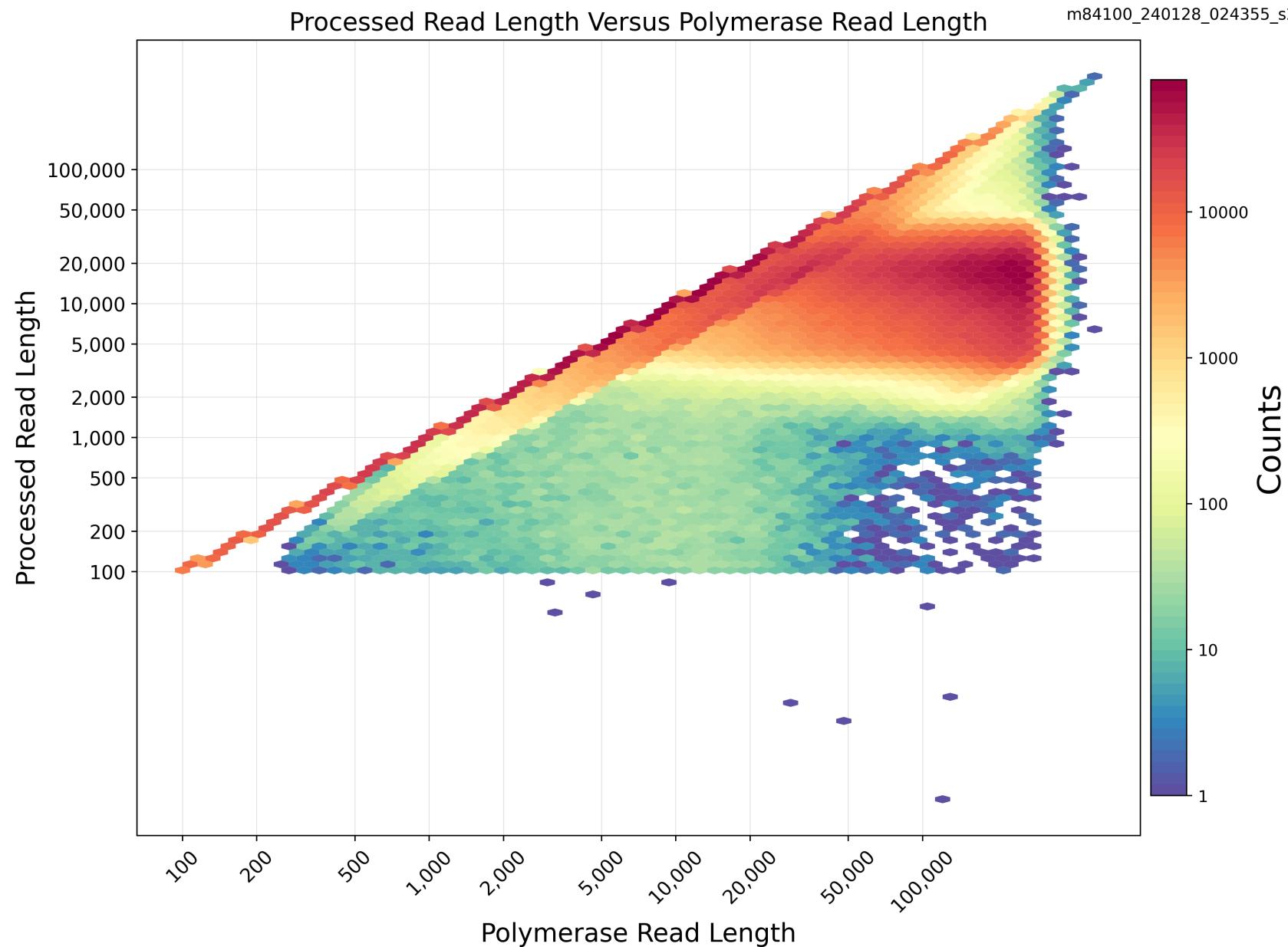
Summary

Polymerase Read Bases	1,185,658,815,264
Polymerase Reads	12,008,374
Polymerase Read Length (mean)	98,736
Polymerase read length (N50)	190,750
Polymerase read length longest subread length (mean)	16,465
Polymerase read length longest subread length (N50)	21,250
Unique Molecular Yield	181,473,165,312

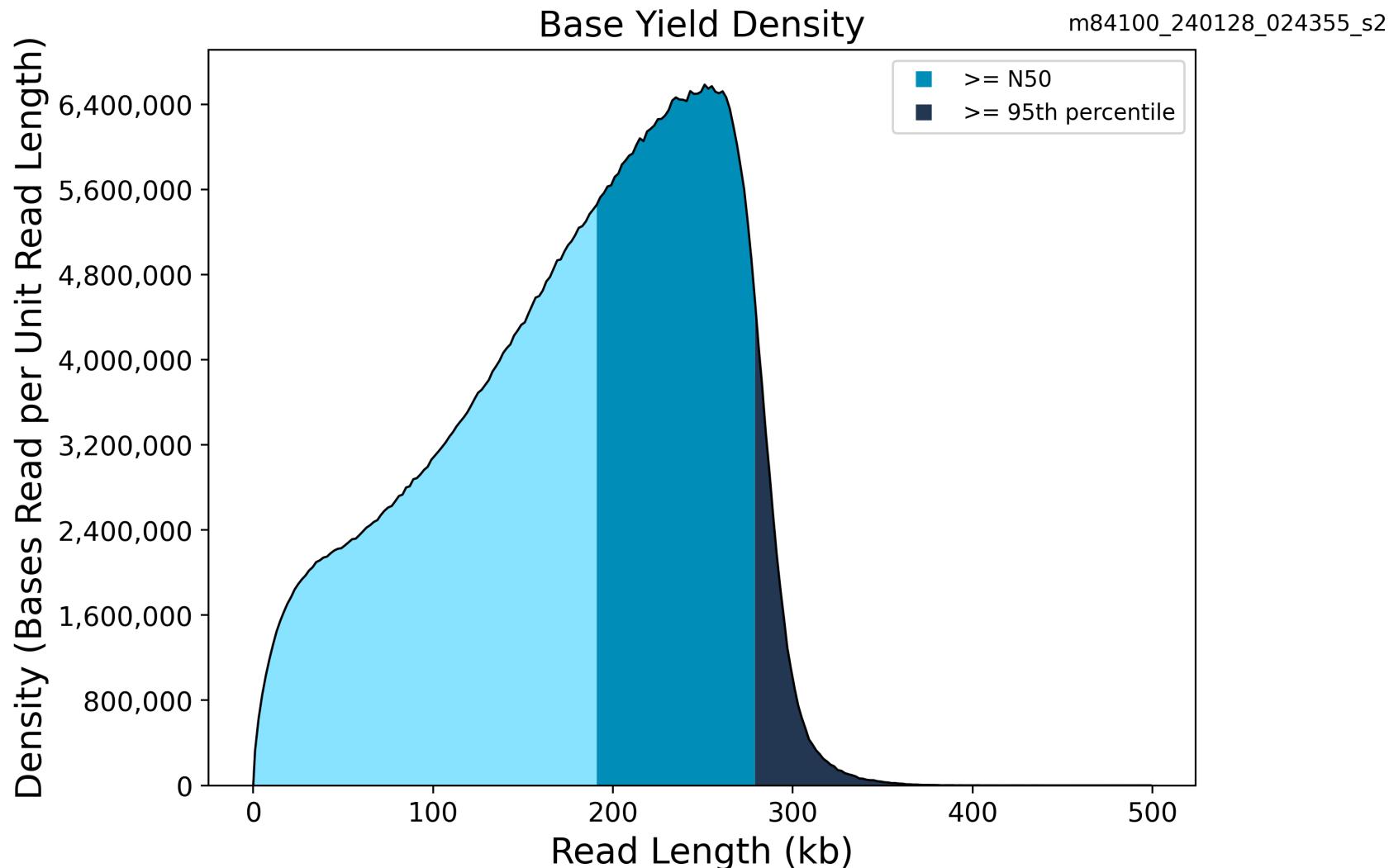
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density



Control Report

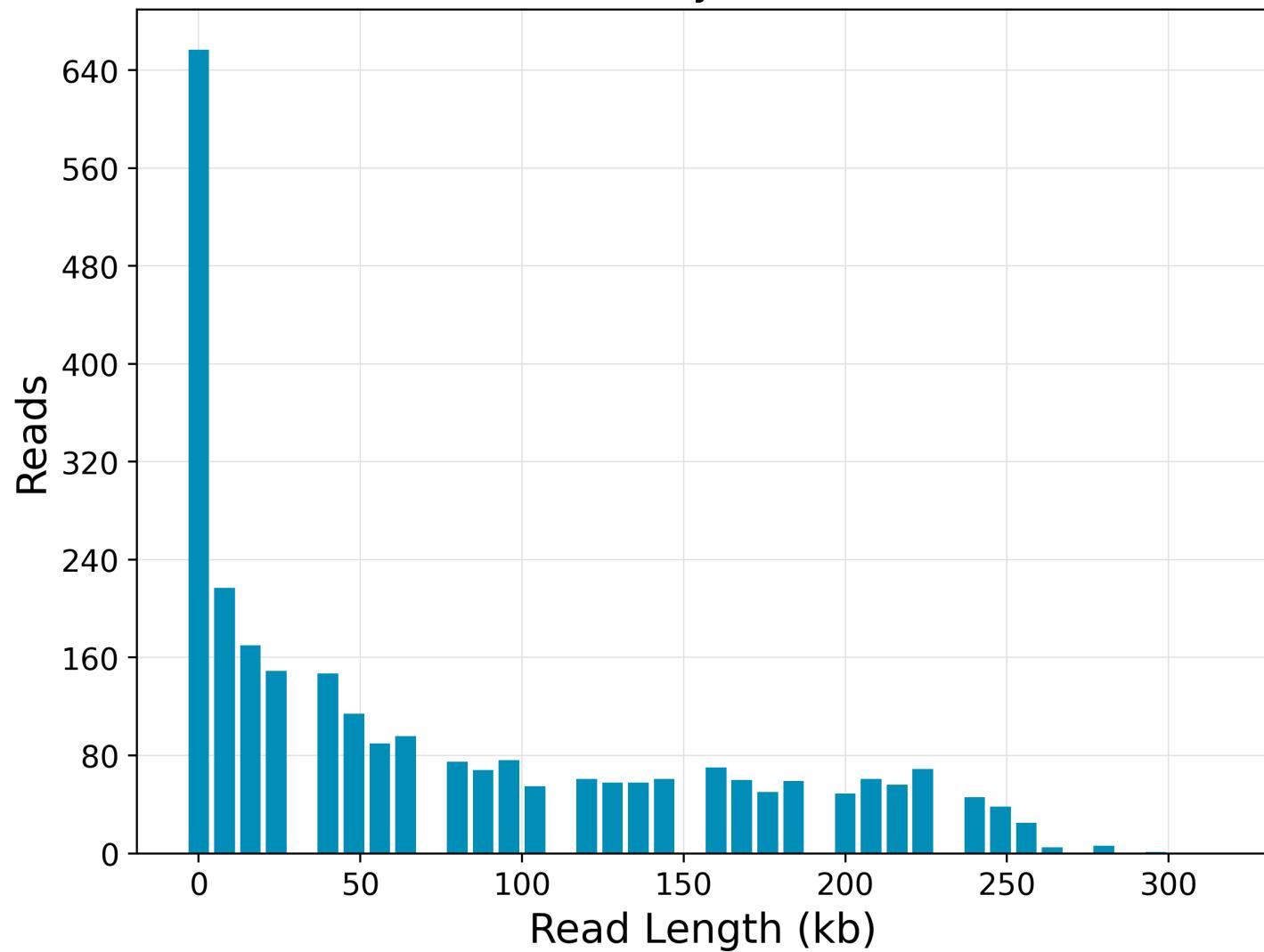
Summary

Number of Control Reads	2,747
Control Read Length Mean	78,451
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Polymerase RL

Control Polymerase RL

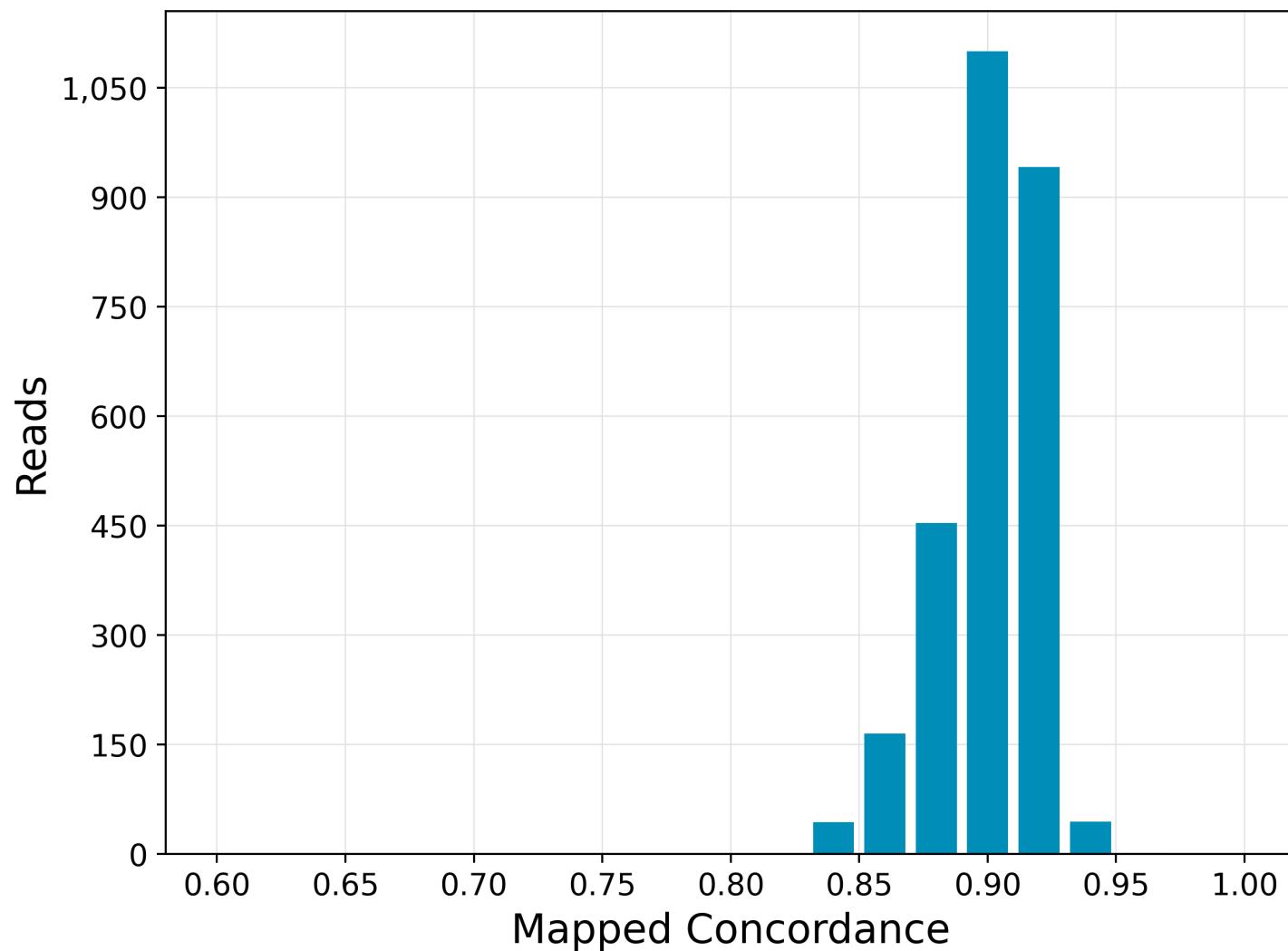
m84100_240128_024355_s2



Control Concordance

Control Concordance

m84100_240128_024355_s2



No Sample Setup found

Instrument run(s)

Run 61f164d0-6266-4197-a068-f6fbe1788292

Summary

Name	Run 01.27.2024 16:49
Status	COMPLETE
Created	2024-01-27 23:55:58.853
Started	2024-01-28 00:42:05.385
Completed	2024-01-29 16:58:11.185
Context	r84100_20240128_004145
Instrument Name	84100
Instrument Serial Number	84100
ICS Version	13.0.0.212033
Primary Analysis Version	13.0.0.212033
Chemistry Version	13.0.0.205983

Parent jobs (1)

Job 6698

Summary

Job Type	import-dataset
Name	import-dataset
Comments	Description for job Import PacBio DataSet
Created At	2024-01-29 22:16:23.361
SMRT Link Version	13.0.0.207600

No child jobs found