

Report for dataset SNAM-1-Cell1 (all samples)

Dataset 3de2de6c-5886-41ba-a937-2cb2e0b95141

Summary

Name	SNAM-1-Cell1 (all samples)
Created At	2025-09-14 21:29:05.603
Number of Records	8,197,233
Total Length	130,430,852,645
Movie Name	m84039_250913_082427_s3
ICS Version	13.3.0.253824
Well Sample	SNAM-1
Biological Sample	SNAM-1
Barcode Name	bcM0001--bcM0001

Loading Report

Summary

Productive ZMWs	25,165,824
Productivity 0	9,575,365
Productivity 1	15,519,464
Productivity 2	70,995

Barcodes

Summary

Unique Barcodes	1
Barcoded HiFi Reads	8,197,233
Unbarcoded HiFi Reads	11,071
Barcoded HiFi Reads (%)	99.87 %
Barcoded HiFi yield (Gb)	130.43 Gb
Unbarcoded HiFi yield (Gb)	0.14 Gb
Barcoded HiFi Yield (%)	99.89 %
Mean HiFi Reads per Barcode	8,197,233
Max. HiFi Reads per Barcode	8,197,233
Min. HiFi Reads per Barcode	8,197,233
Barcoded HiFi read length (mean, kb)	15.91 kb
Unbarcoded HiFi read length (mean, kb)	12.62 kb

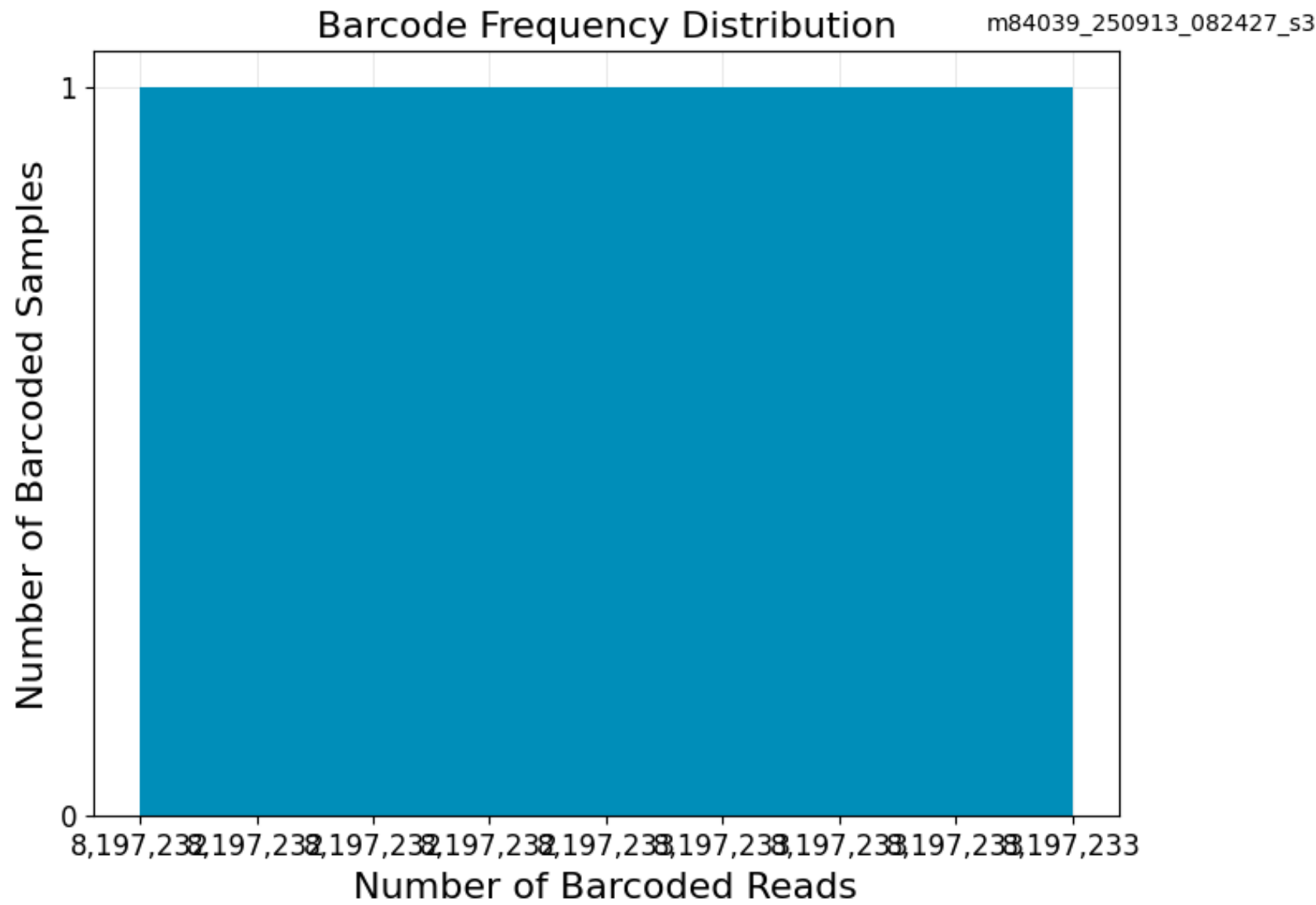
Barcode Data

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)
SNAM-1	bcM0001--bcM0001	97.7	8197233	15911	Q32	130430852645	150360
No Name	Not Barcoded	0.0	11071	12621	Q27	139732856	121716

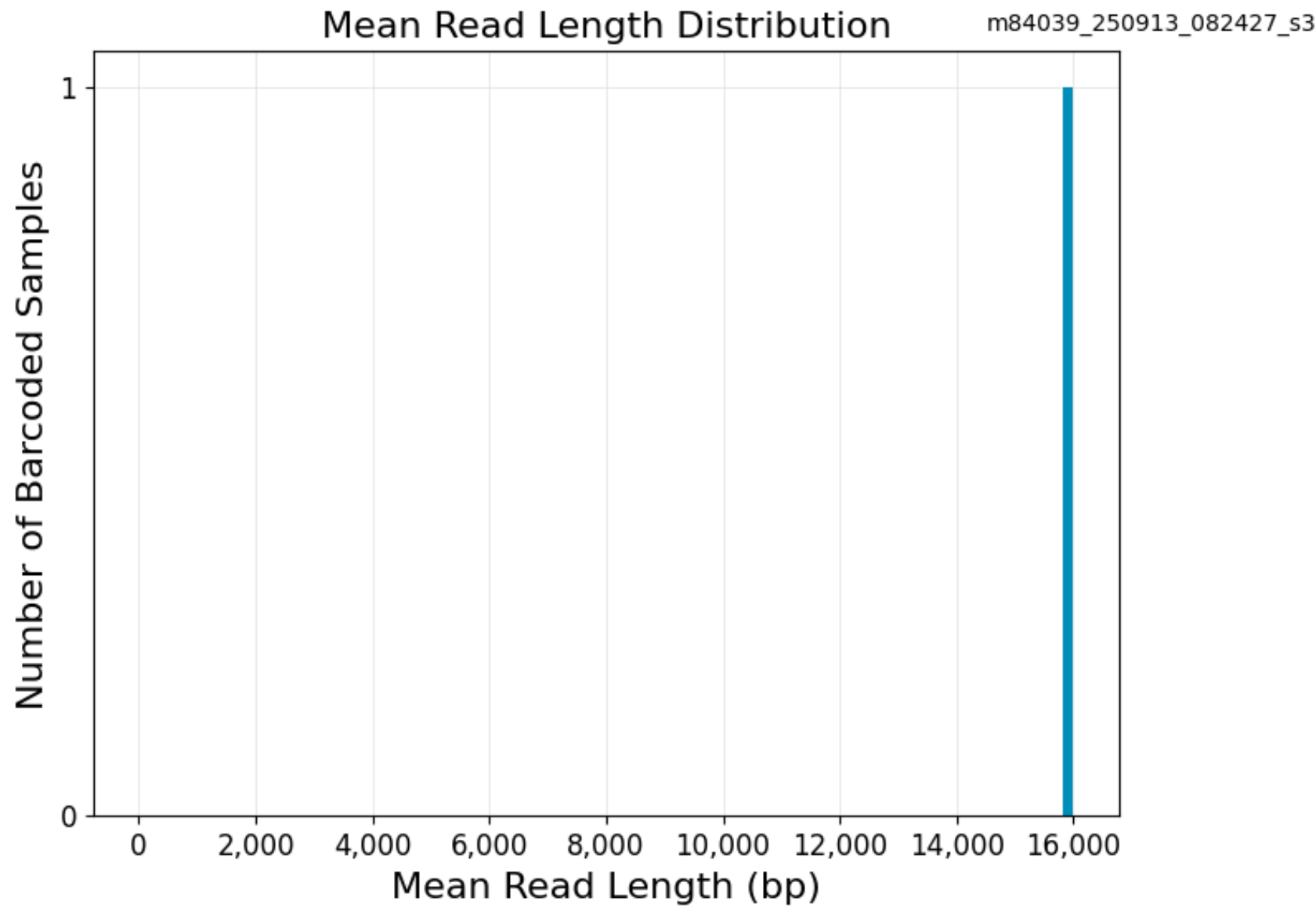
Number Of Reads Per Barcode



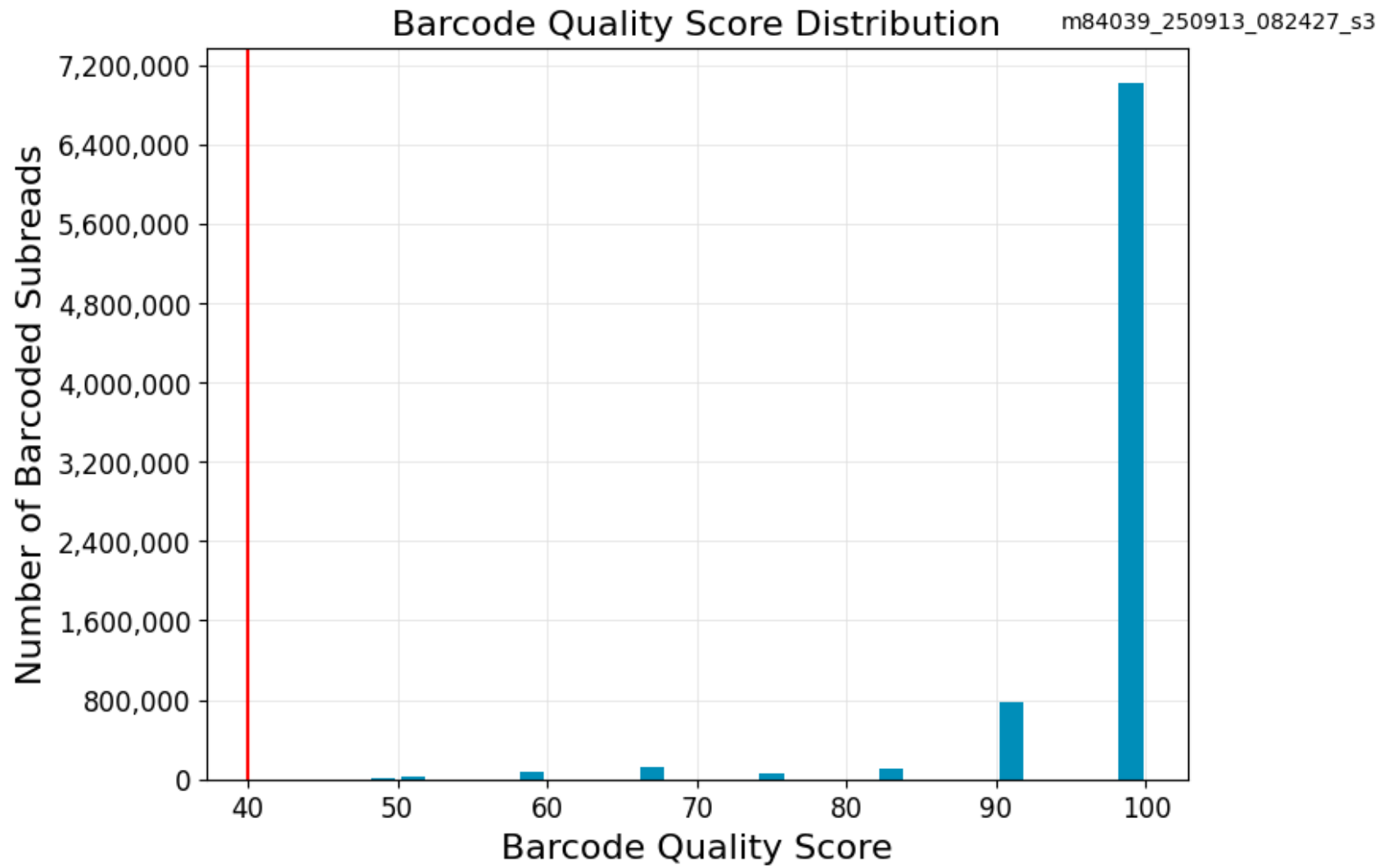
Barcode Frequency Distribution



Mean Read Length Distribution



Barcode Quality Score Distribution

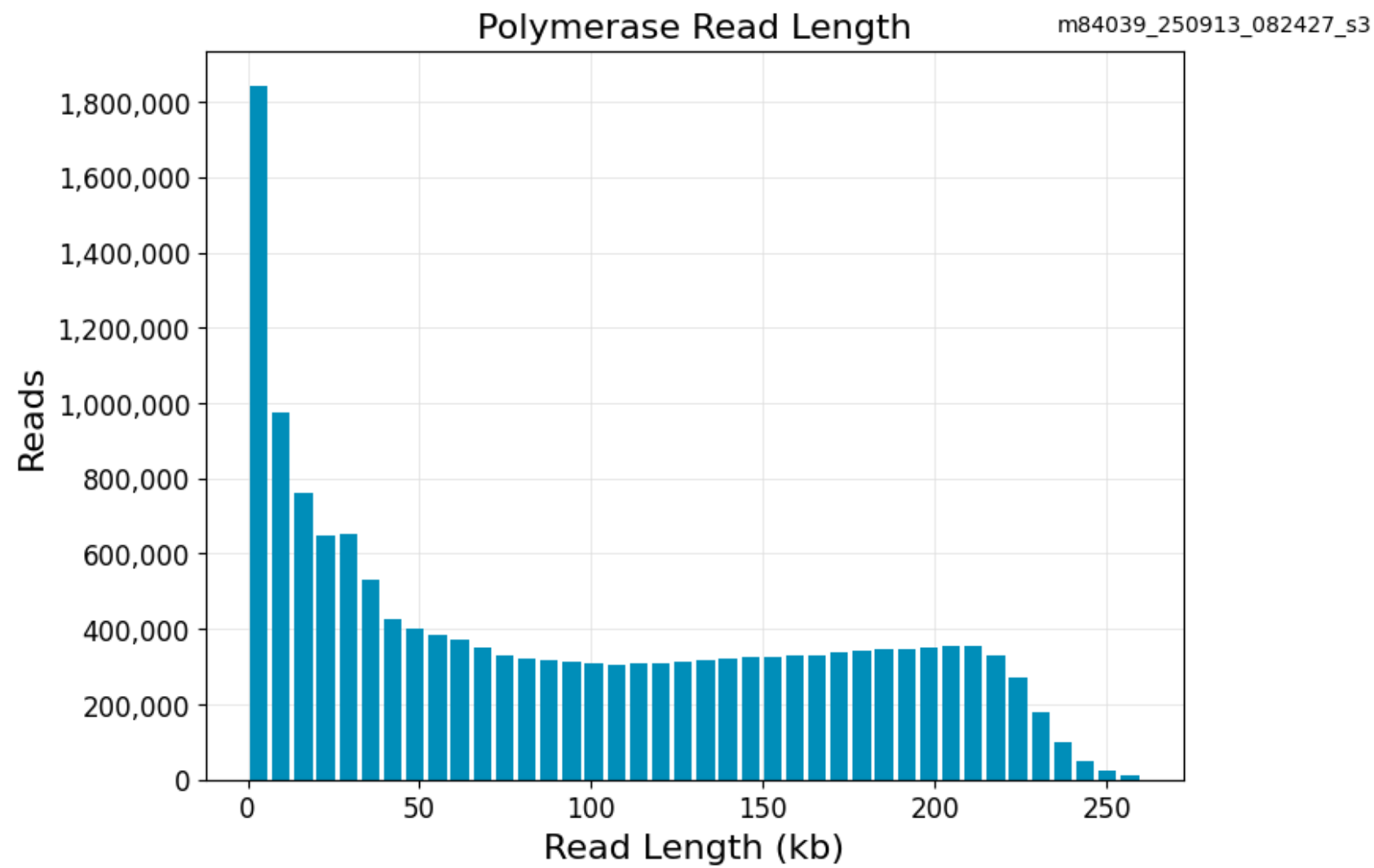


Raw Data Report

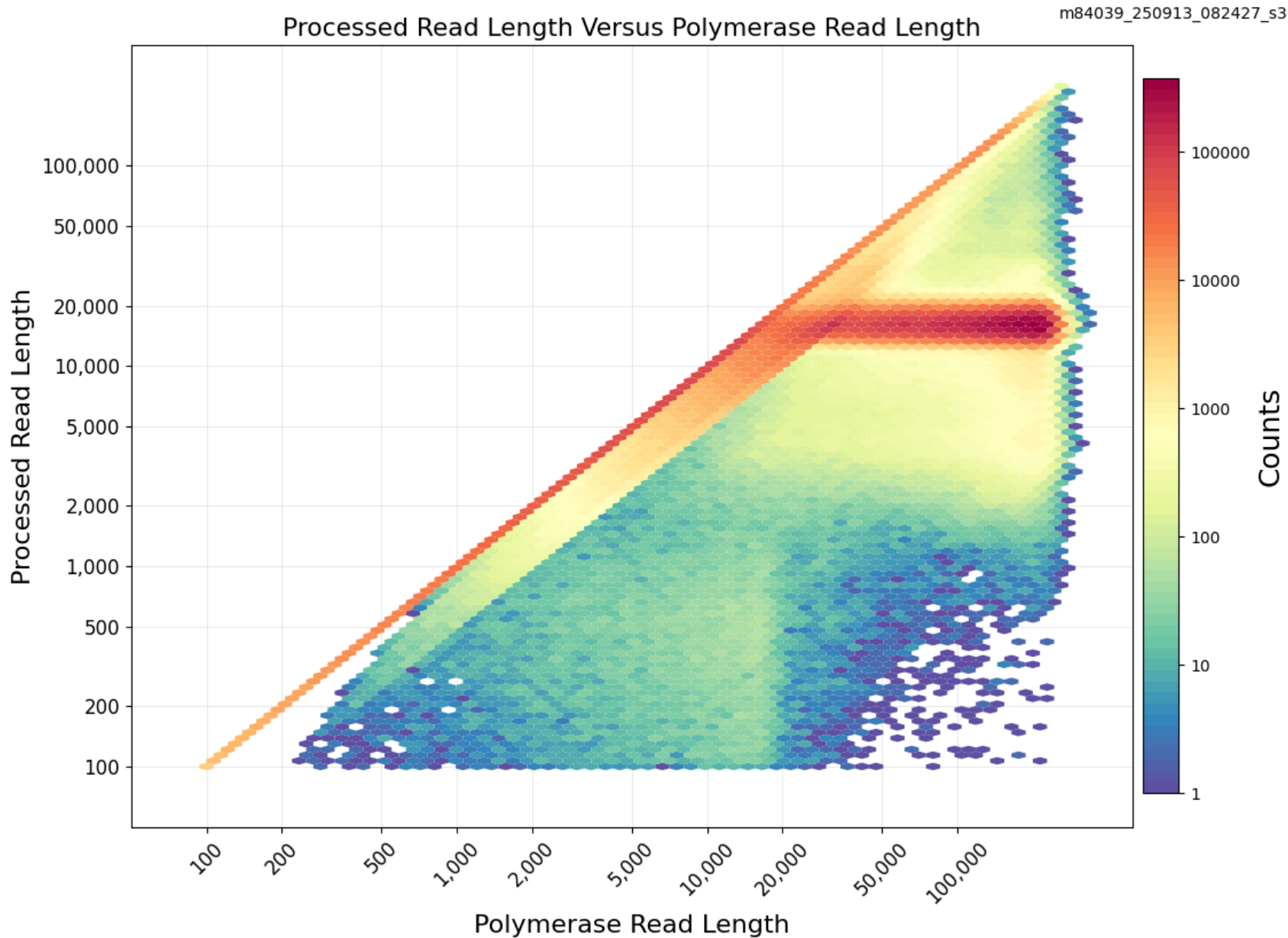
Summary

Polymerase Read Bases	1,409,230,754,024
Polymerase Reads	15,515,583
Polymerase Read Length (mean)	90.83 kb
Polymerase read length (N50)	164.75 kb
Polymerase read length longest subread length (mean)	16.40 kb
Polymerase read length longest subread length (N50)	16.75 kb
Unique Molecular Yield	243,119,177,728
Local Base Rate	2.78

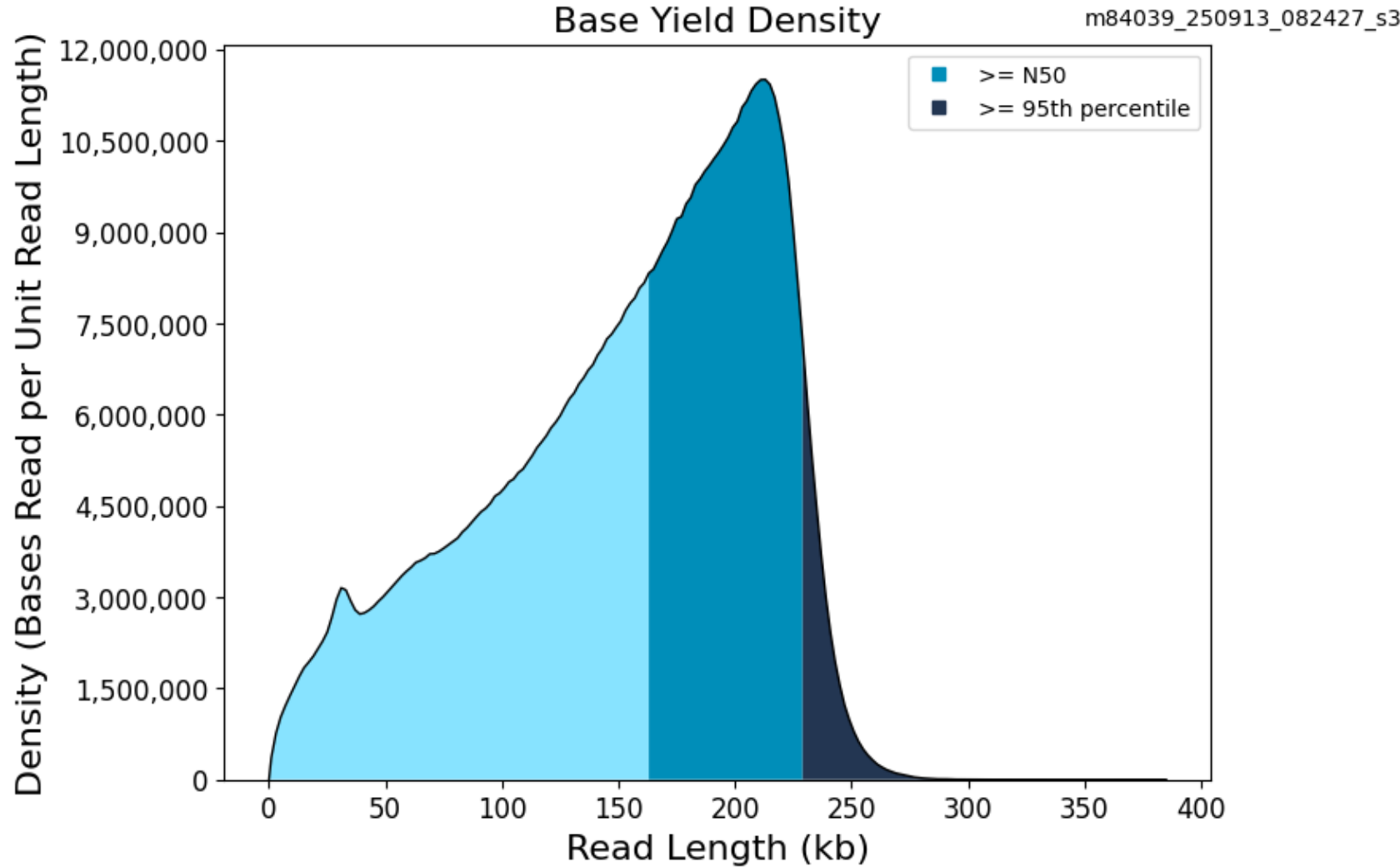
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density



Run Preview

Summary

Estimated HiFi Yield (Gb)	127,452,008,489
HiFi read quality, median	31
HiFi read length, mean	15,917
P1 (%)	None
Time (Hrs)	23
Workflow	Full
Movie Name	m84039_250913_082427_s3_full_preview_23hr
Movie Id	m84039_250913_082427_s3

Barcode preview

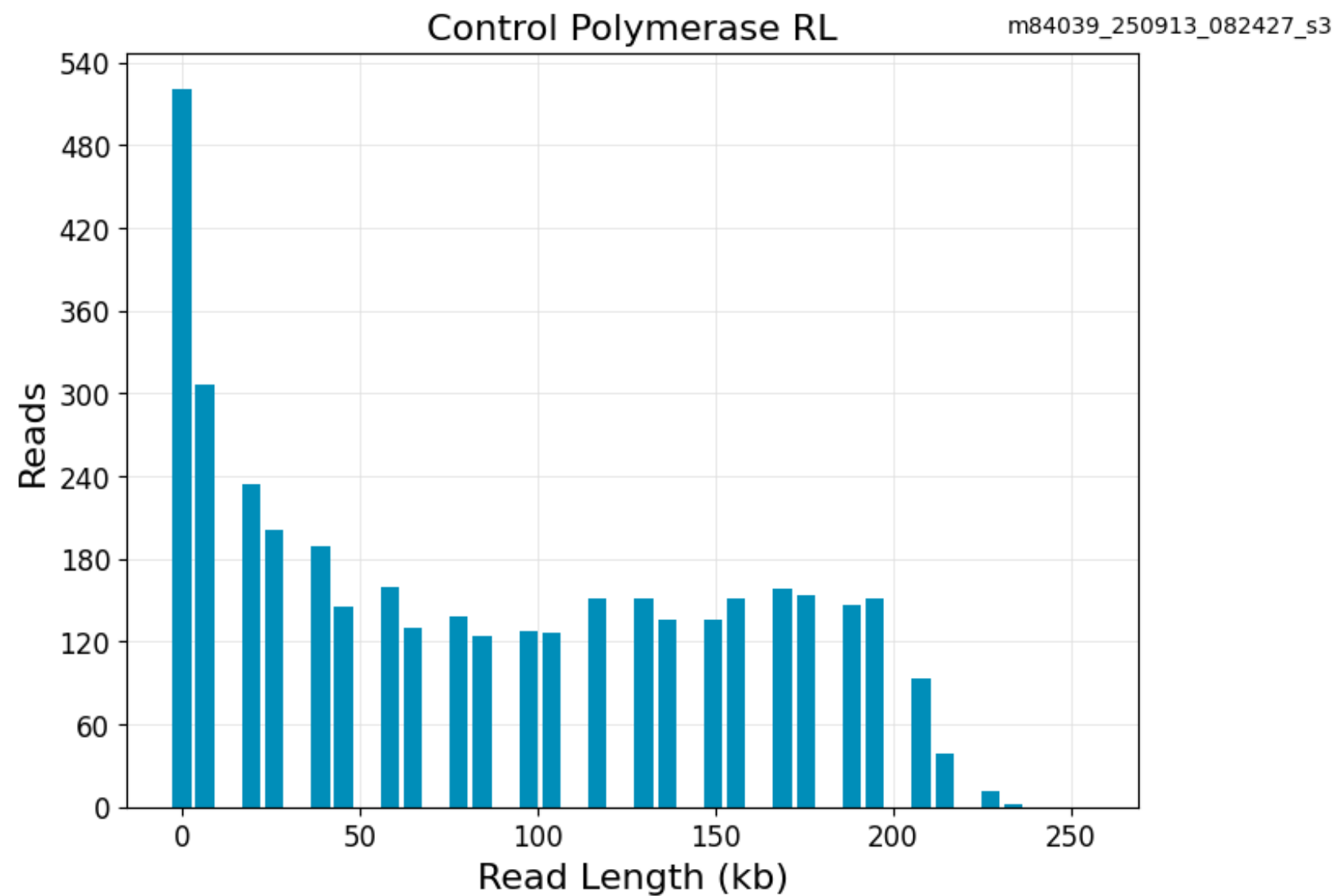
Barcode	HiFi reads	HiFi read length (mean, bp)
bcM0001--bcM0001	99.9%	15920
Not Barcoded	0.1%	4706

Control Report

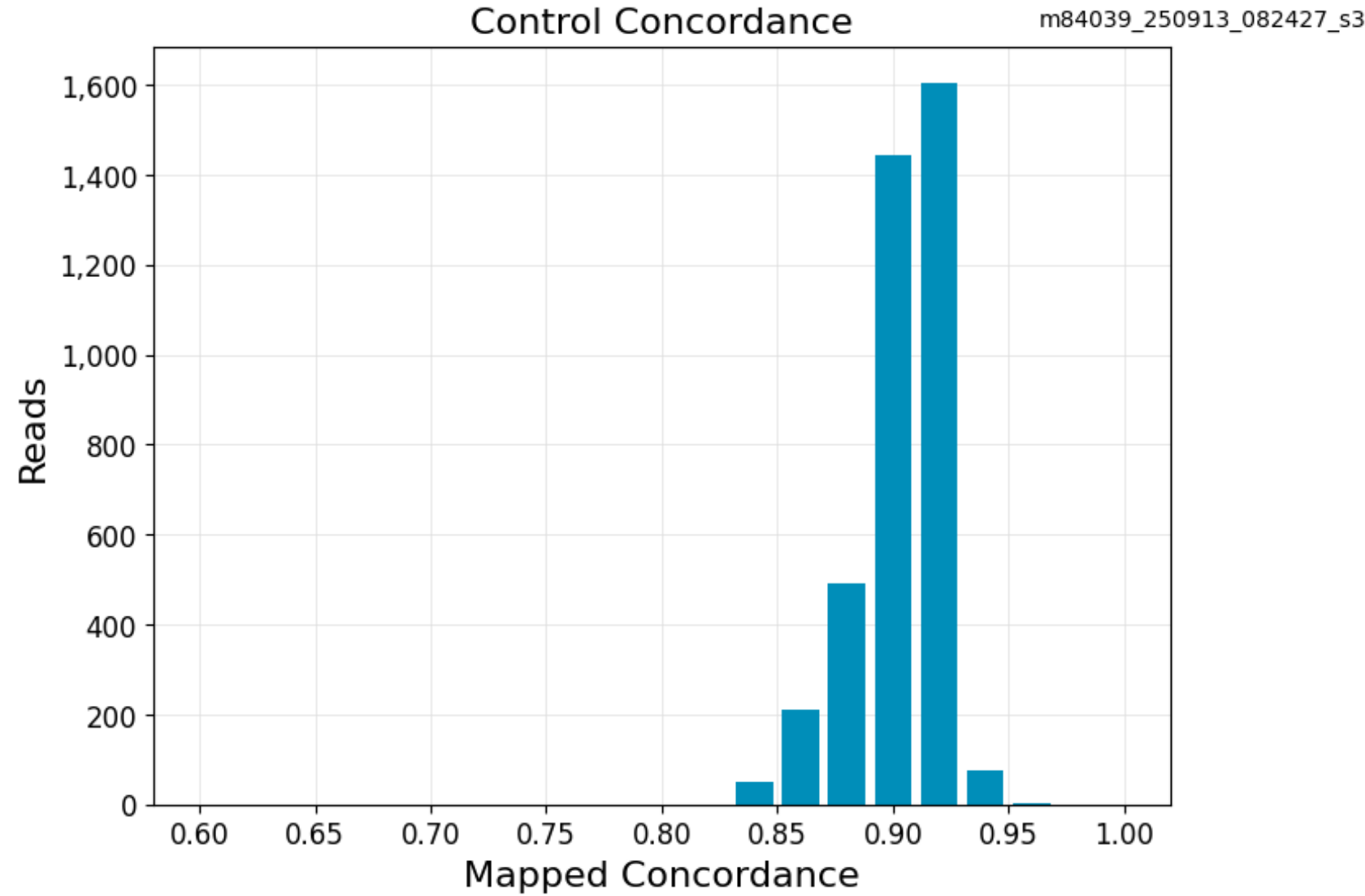
Summary

Number of Control Reads	3,881
Control Read Length Mean	88,358
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.93

Control Polymerase RL



Control Concordance



CCS Analysis Report

Summary

HiFi reads	8.2 M
HiFi reads yield	130.57 Gb
HiFi reads length (mean)	15.91 kb
HiFi reads length (median, bp)	15,951
HiFi Read Length N50 (bp)	16,118
HiFi Read Quality (median)	Q32
HiFi Read Quality (median)	32
Base Quality Q30 (%)	95.29%
HiFi Number of Passes (mean)	9
Missing adapters (%)	2.19%

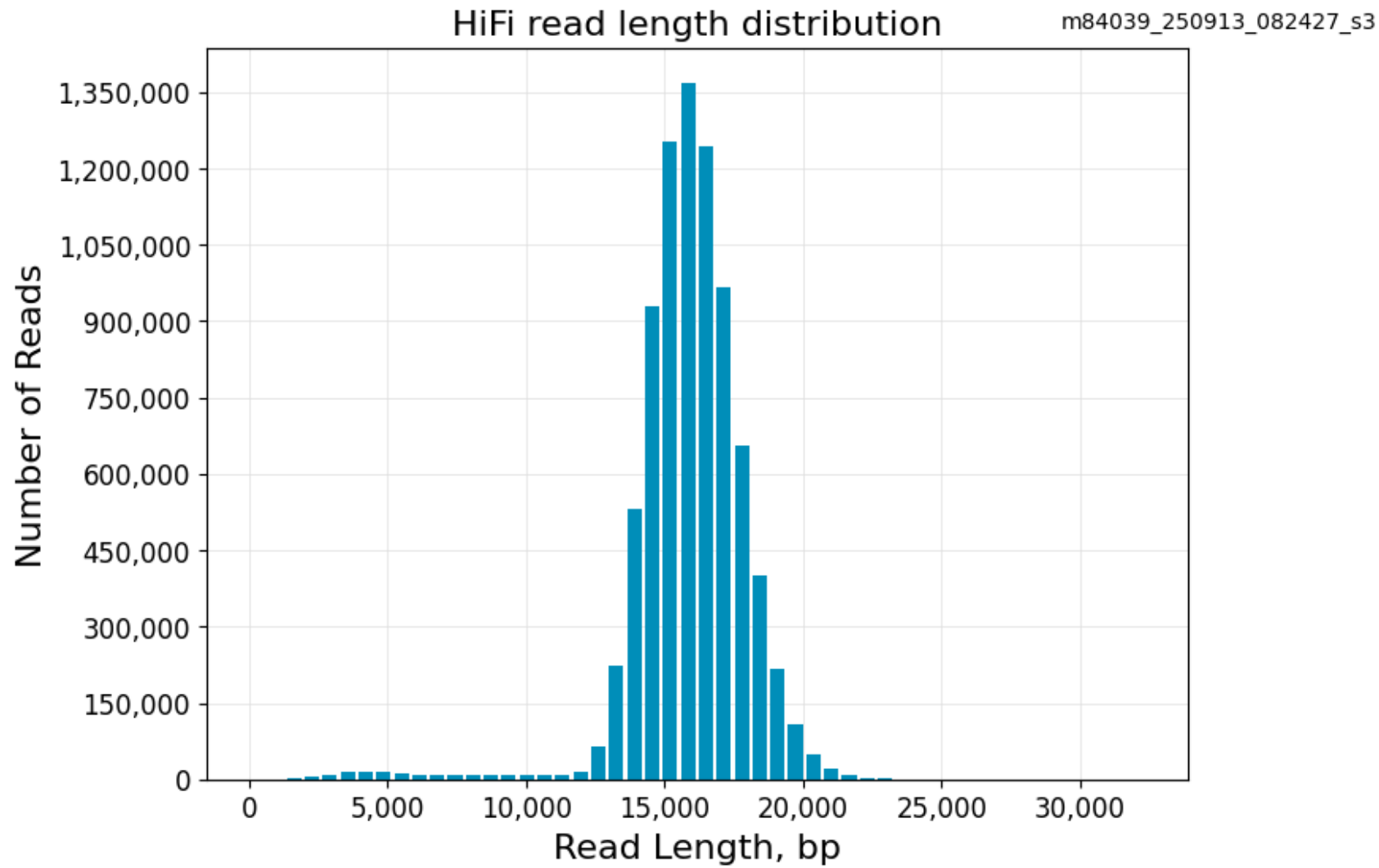
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
0	8208304	100	130.57 Gb	100
5,000	8149104	99	130.36 Gb	100
10,000	8080862	98	129.85 Gb	99
15,000	6054381	74	101.10 Gb	77
20,000	87609	1	1.81 Gb	1
25,000	174	0	0.00 Gb	0
30,000	48	0	0.00 Gb	0
35,000	9	0	0.00 Gb	0
40,000	1	0	0.00 Gb	0

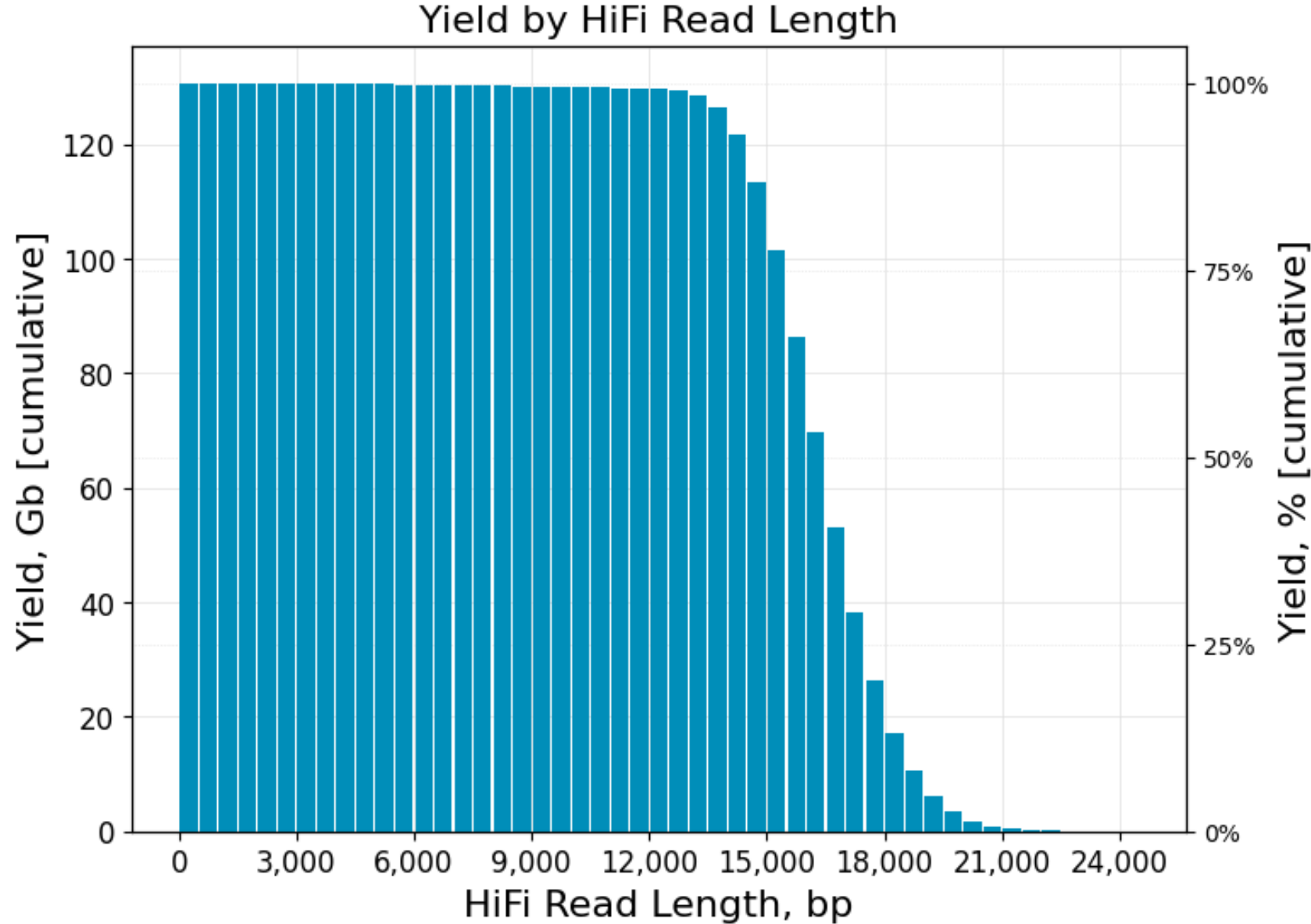
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
Q20	8208304	100	130.57 Gb	100
Q30	5240873	64	83.09 Gb	64
Q40	105344	1	1.17 Gb	1
Q50	11965	0	0.04 Gb	0

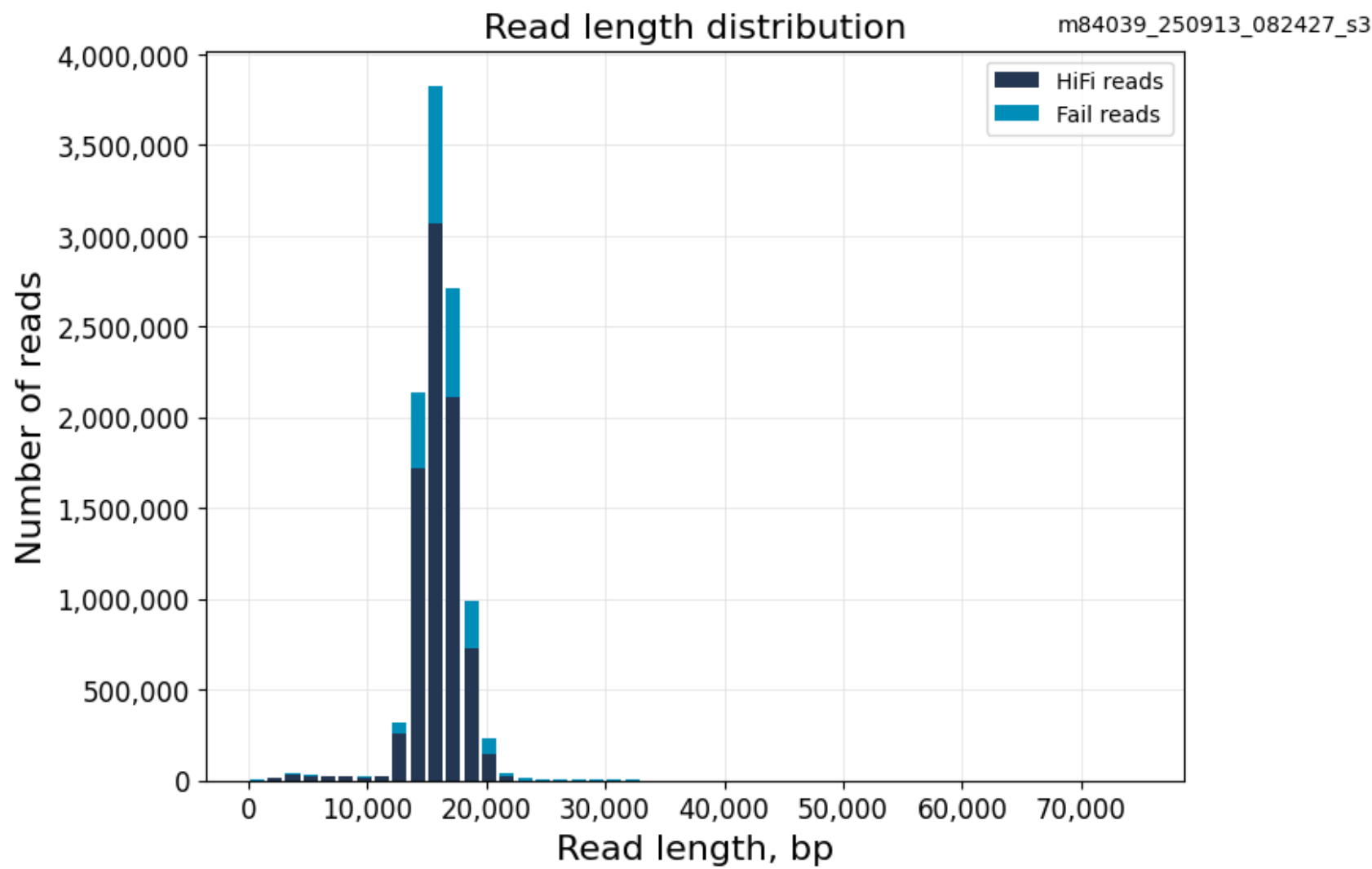
HiFi read length distribution



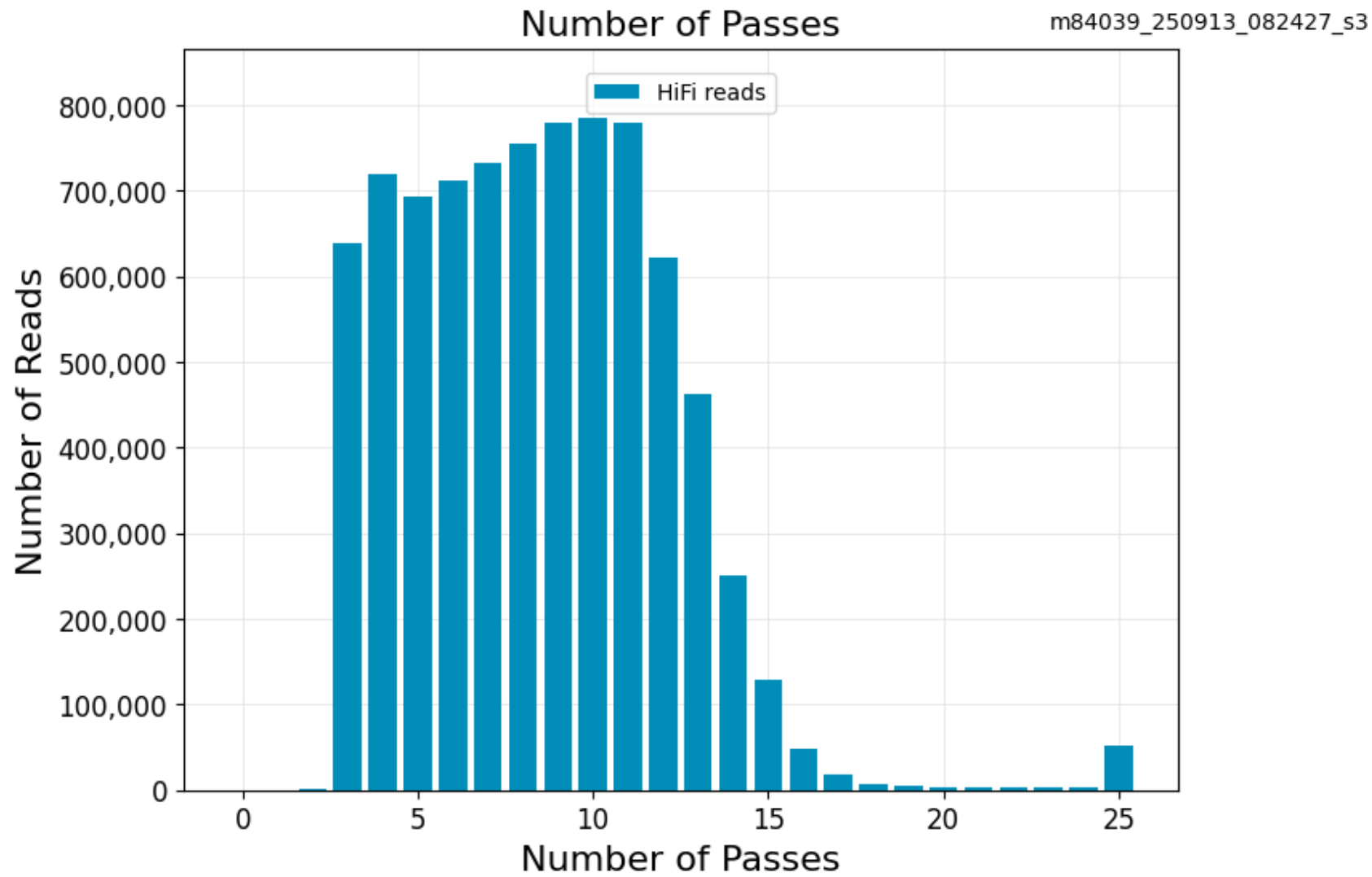
Yield by HiFi Read Length



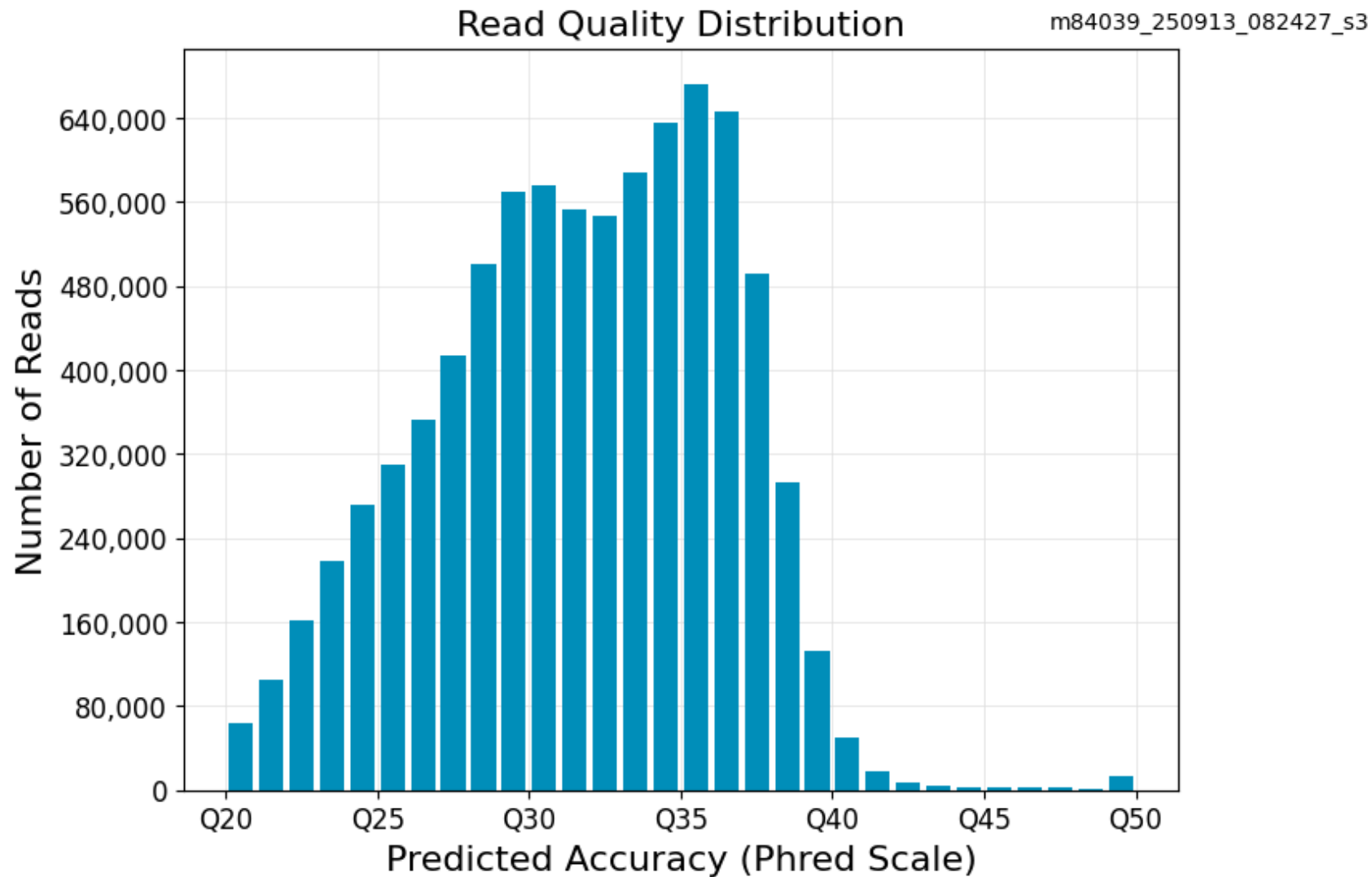
Read length distribution



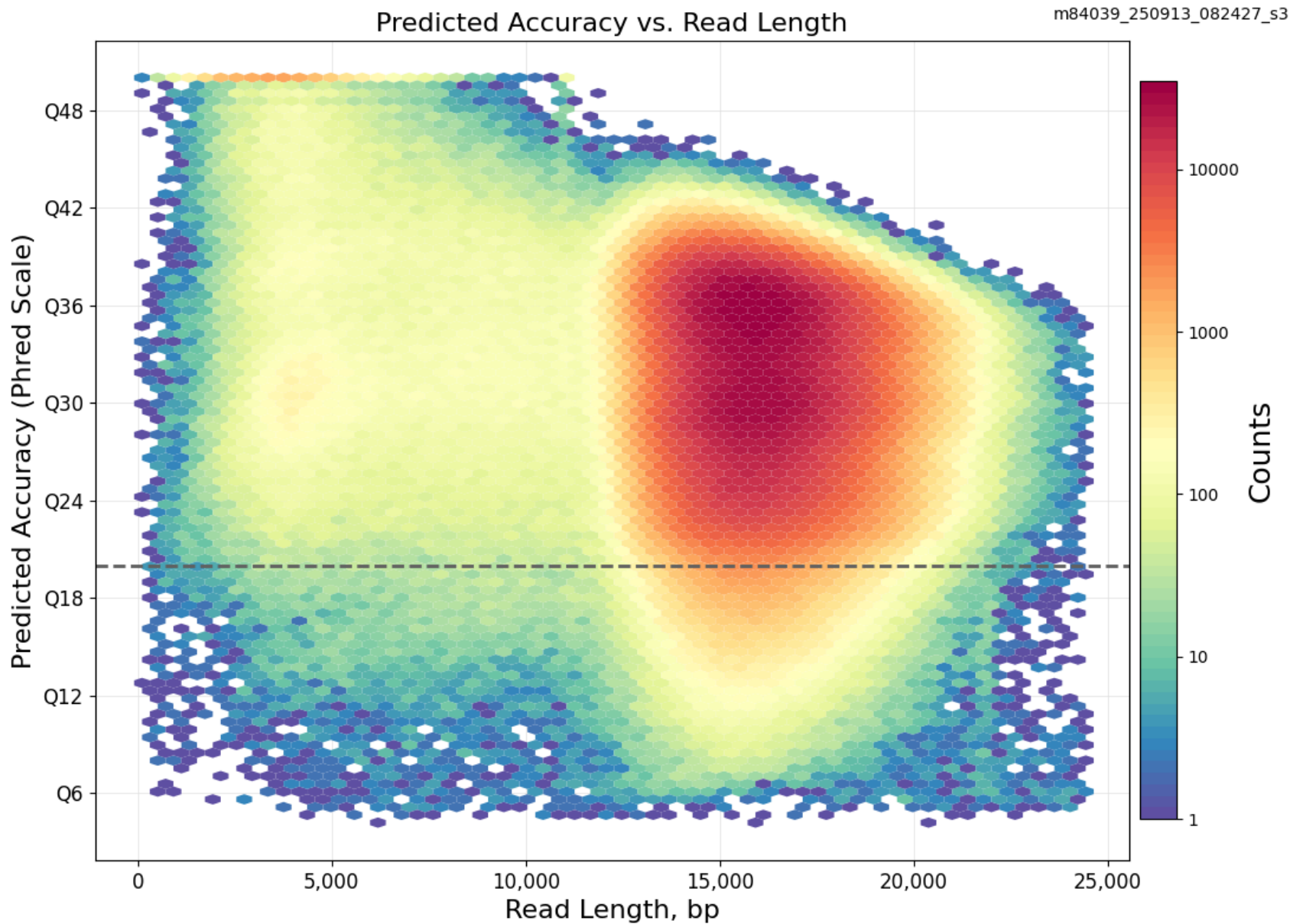
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length



Run Preview

Summary

Estimated HiFi Yield (Gb)	None
HiFi read quality, median	None
HiFi read length, mean	15,395
P1 (%)	57.20 %
Time (Hrs)	4
Workflow	Basic
Movie Name	m84039_250913_082427_s3_basic_preview_4hr
Movie Id	m84039_250913_082427_s3

Barcode preview

Barcode	HiFi reads	HiFi read length (mean, bp)
bcM0001--bcM0001	93.8%	15414
Other	1.0%	14618
Not Barcoded	5.2%	14966

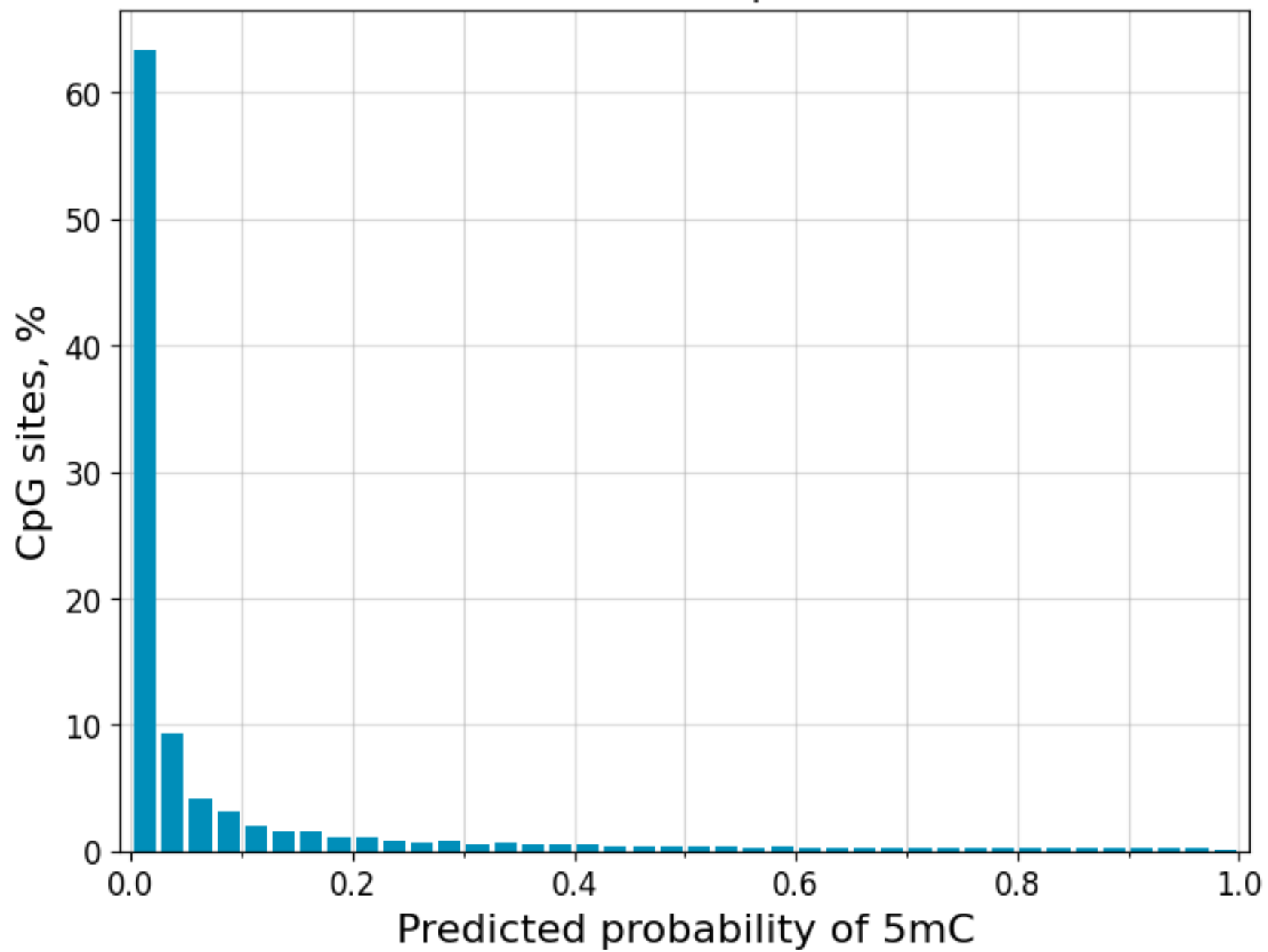
Methylation

Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	98.8%	5.2%
6mA	A	0.6%	0.6%

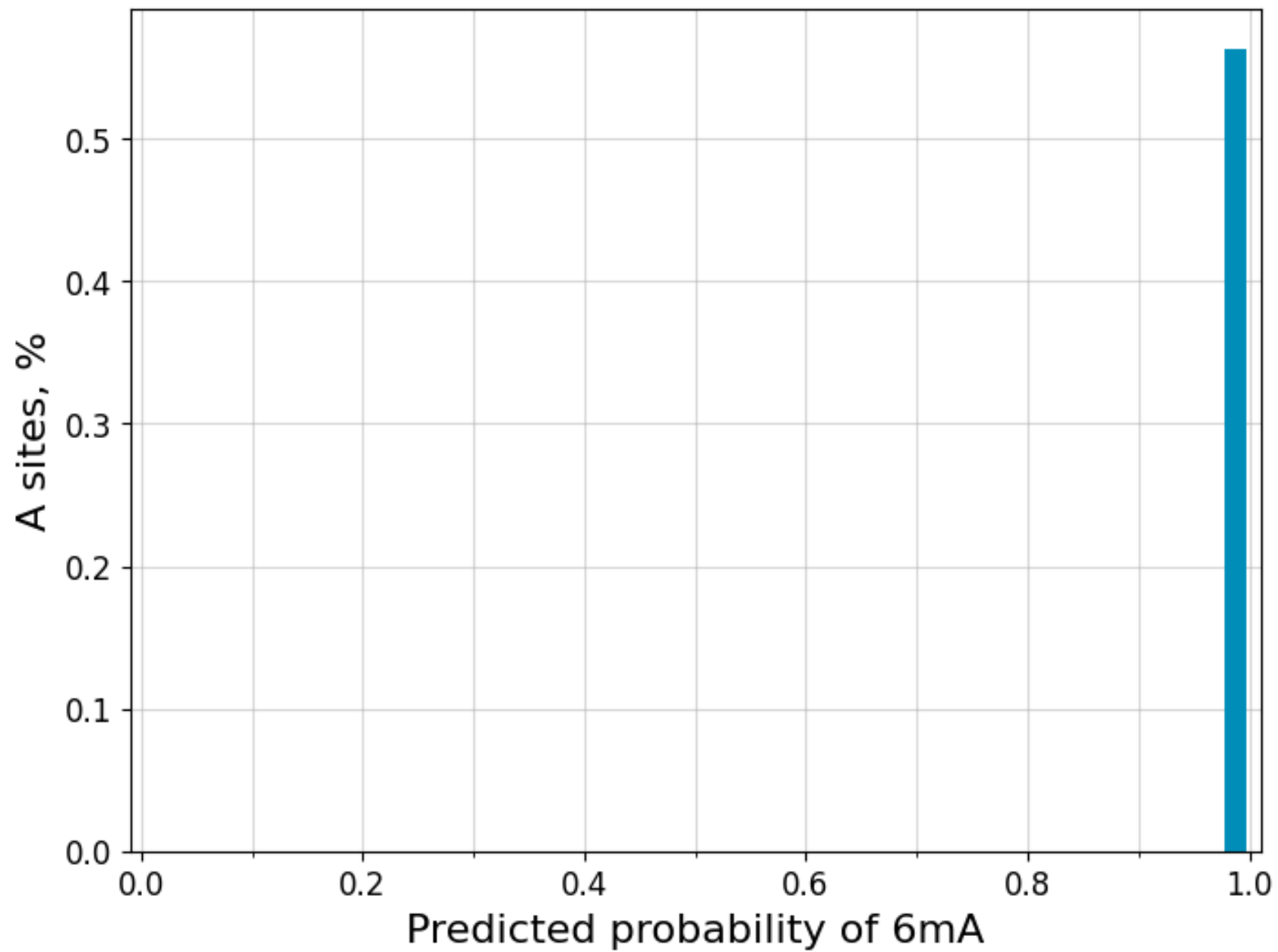
5mC methylation at CpG in reads

5mC at CpG



6mA methylation in reads

6mA



No Sample Setup found

Instrument run(s)

Run 0d8115db-908b-443f-b68f-bcb3d322b933

Summary

Name	20250912_10X_Fiberseq_Quest_CSVsetup1
Status	COMPLETE
Created	2025-09-12 01:12:39.919
Started	2025-09-12 17:57:47.593
Completed	2025-09-16 00:37:19.663
Context	r84039_20250912_175724
Instrument Name	84039
Instrument Serial Number	84039
ICS Version	13.3.0.253824
Primary Analysis Version	13.3.0.253824
Chemistry Version	13.3.0.249246

Parent jobs (1)

Job 12237

Summary

Job Type	import-collection
Name	import-collection
Comments	Description for job Import Collection
Created At	2025-09-14 21:39:33.608
SMRT Link Version	25.3.0.273777

No child jobs found