

Report for dataset SNAM-2-Cell2 (all samples)

Dataset f228aa30-a1ed-43c5-8487-461689069625

Summary

Name	SNAM-2-Cell2 (all samples)
Created At	2025-09-14 23:26:02.562
Number of Records	8,033,810
Total Length	129,430,283,449
Movie Name	m84039_250913_102724_s4
ICS Version	13.3.0.253824
Well Sample	SNAM-2
Biological Sample	SNAM-2
Barcode Name	bcM0002--bcM0002

Run Preview

Summary

Estimated HiFi Yield (Gb)	None
HiFi read quality, median	None
HiFi read length, mean	15,678
P1 (%)	55.30 %
Time (Hrs)	4
Workflow	Basic
Movie Name	m84039_250913_102724_s4_basic_preview_4hr
Movie Id	m84039_250913_102724_s4

Barcode preview

Barcode	HiFi reads	HiFi read length (mean, bp)
bcM0002--bcM0002	92.0%	15695
Other	1.5%	14709
Not Barcoded	6.6%	15494

Run Preview

Summary

Estimated HiFi Yield (Gb)	128,201,645,004
HiFi read quality, median	31
HiFi read length, mean	16,053
P1 (%)	None
Time (Hrs)	23
Workflow	Full
Movie Name	m84039_250913_102724_s4_full_preview_23hr
Movie Id	m84039_250913_102724_s4

Barcode preview

Barcode	HiFi reads	HiFi read length (mean, bp)
bcM0002--bcM0002	98.9%	16043
Not Barcoded	1.1%	15889

Barcodes

Summary

Unique Barcodes	1
Barcoded HiFi Reads	8,033,810
Unbarcoded HiFi Reads	24,888
Barcoded HiFi Reads (%)	99.69 %
Barcoded HiFi yield (Gb)	129.43 Gb
Unbarcoded HiFi yield (Gb)	0.34 Gb
Barcoded HiFi Yield (%)	99.74 %
Mean HiFi Reads per Barcode	8,033,810
Max. HiFi Reads per Barcode	8,033,810
Min. HiFi Reads per Barcode	8,033,810
Barcoded HiFi read length (mean, kb)	16.11 kb
Unbarcoded HiFi read length (mean, kb)	13.69 kb

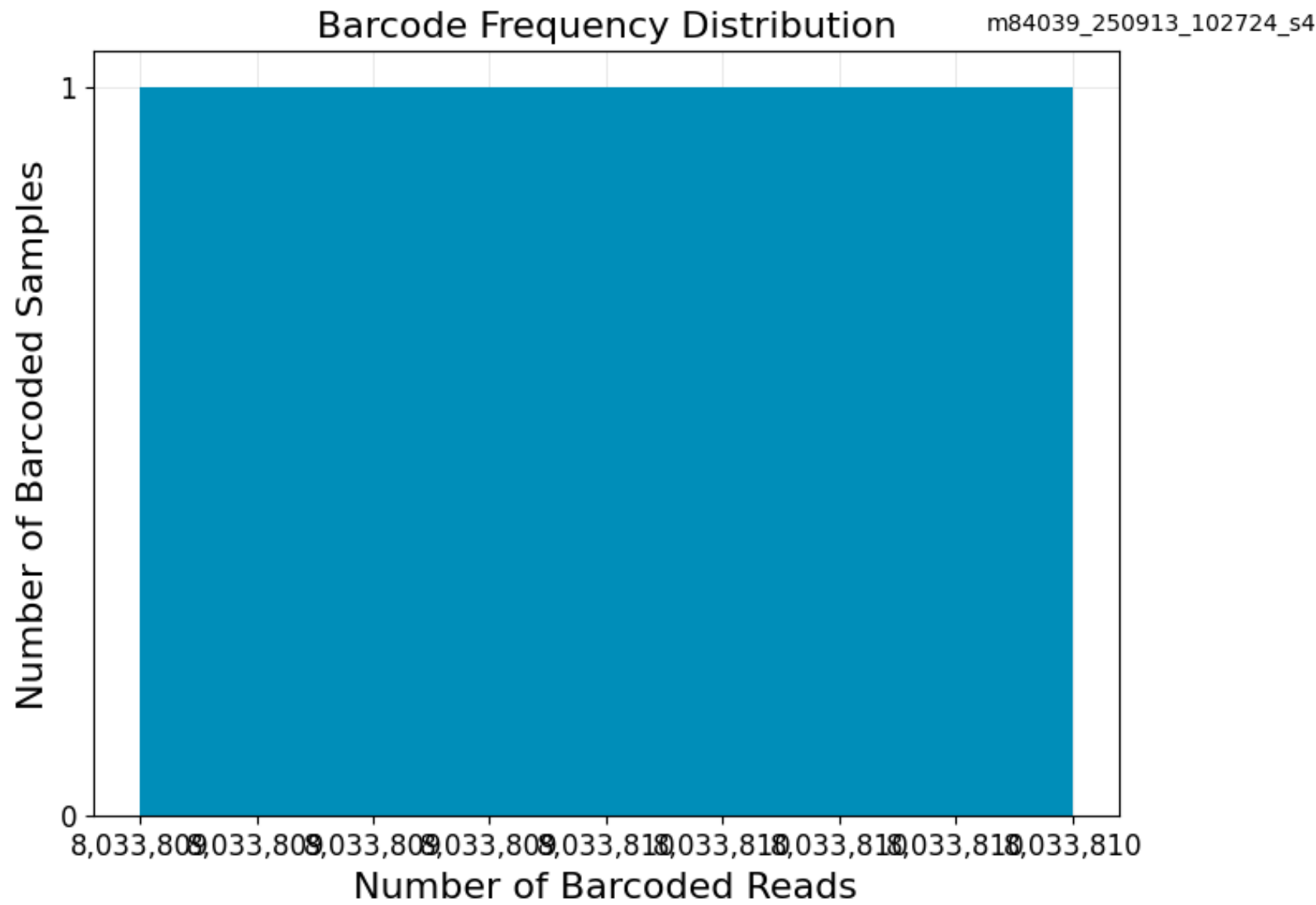
Barcode Data

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-2	bcM0002--bcM0002	97.0	8033810	16110	Q32	129430283449	152048
No Name	Not Barcoded	0.0	24888	13693	Q27	340811653	123891

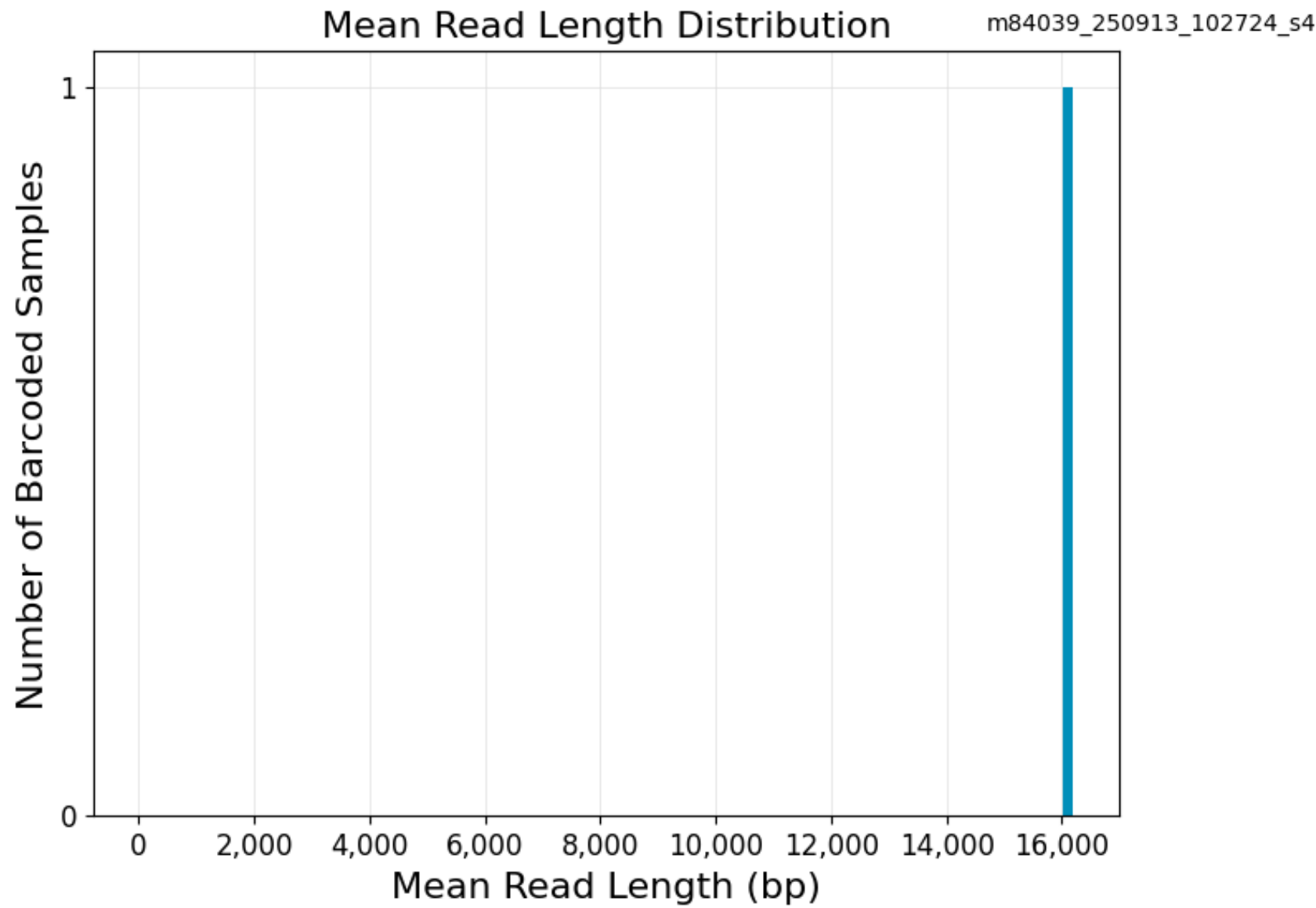
Number Of Reads Per Barcode



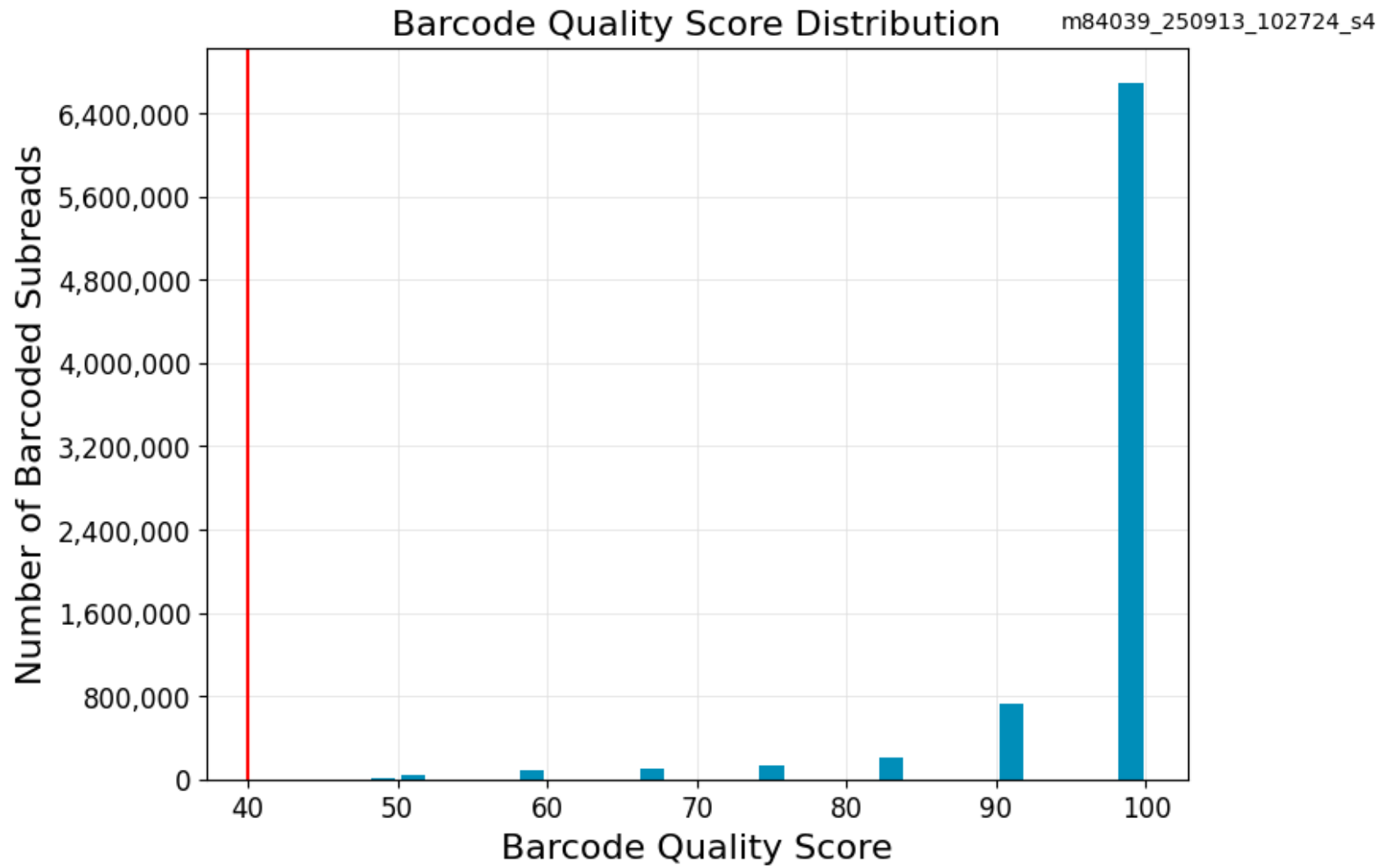
Barcode Frequency Distribution



Mean Read Length Distribution



Barcode Quality Score Distribution

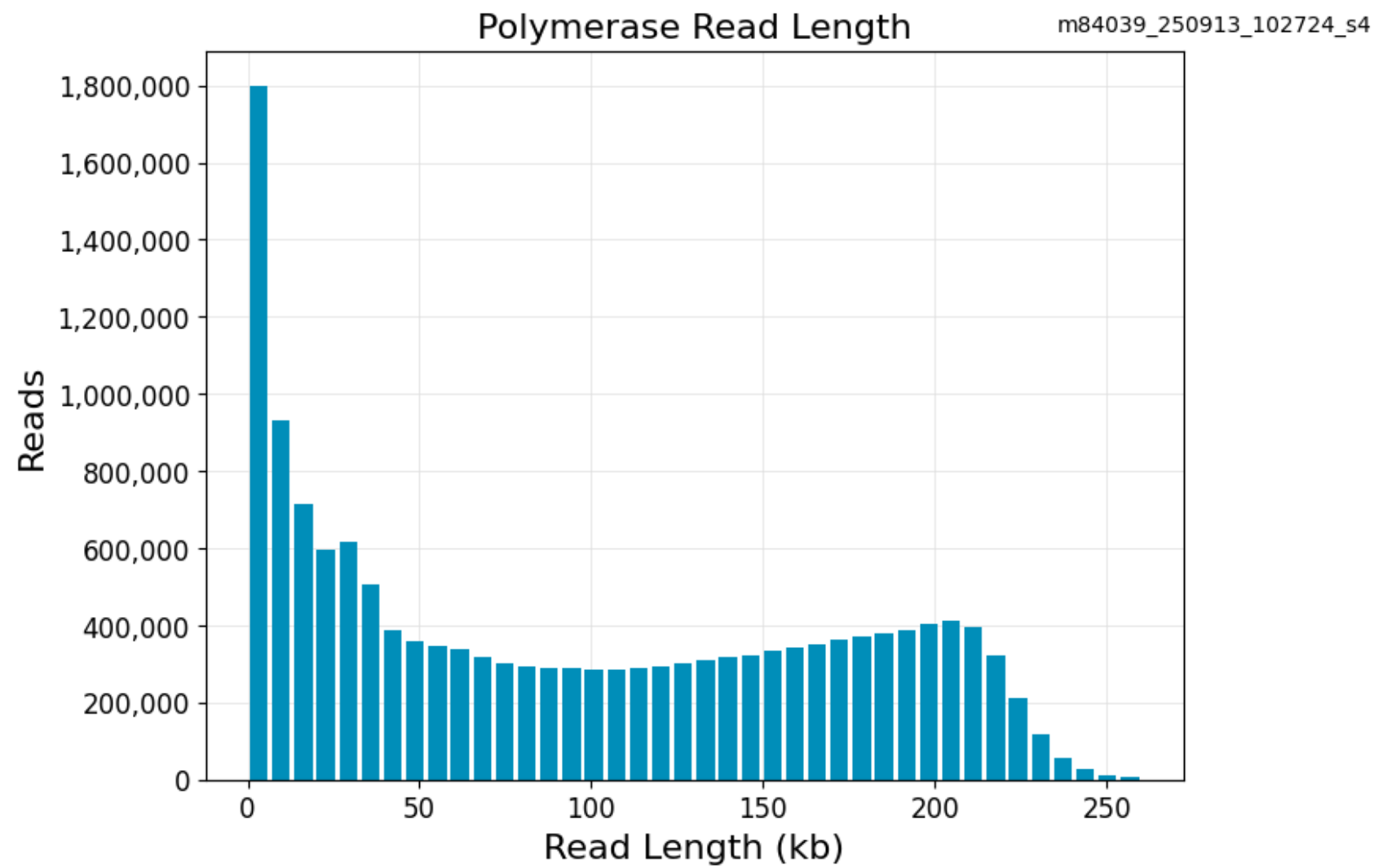


Raw Data Report

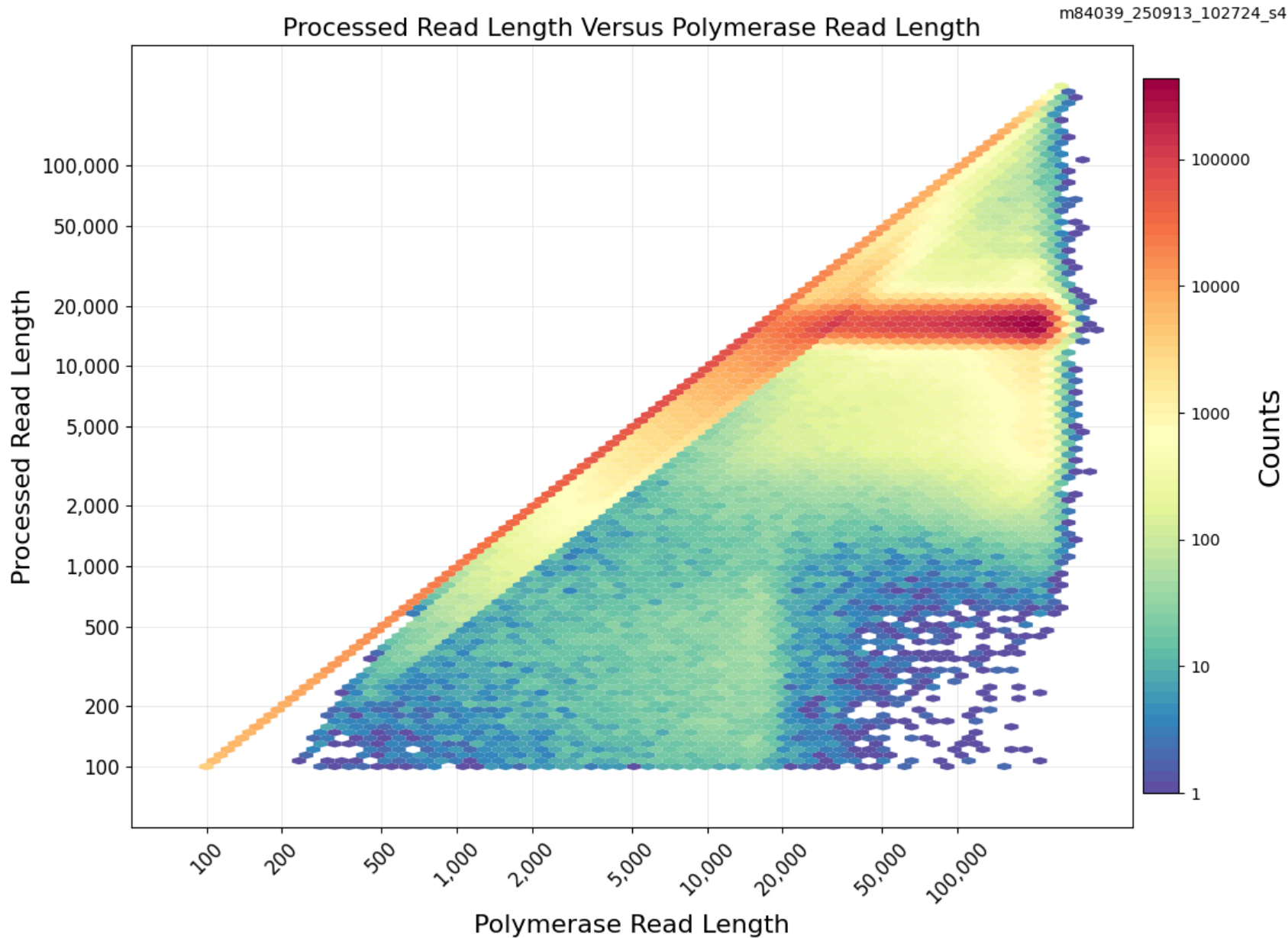
Summary

Polymerase Read Bases	1,385,027,155,278
Polymerase Reads	14,986,633
Polymerase Read Length (mean)	92.42 kb
Polymerase read length (N50)	166.75 kb
Polymerase read length longest subread length (mean)	16.17 kb
Polymerase read length longest subread length (N50)	17.25 kb
Unique Molecular Yield	231,987,396,608
Local Base Rate	2.69

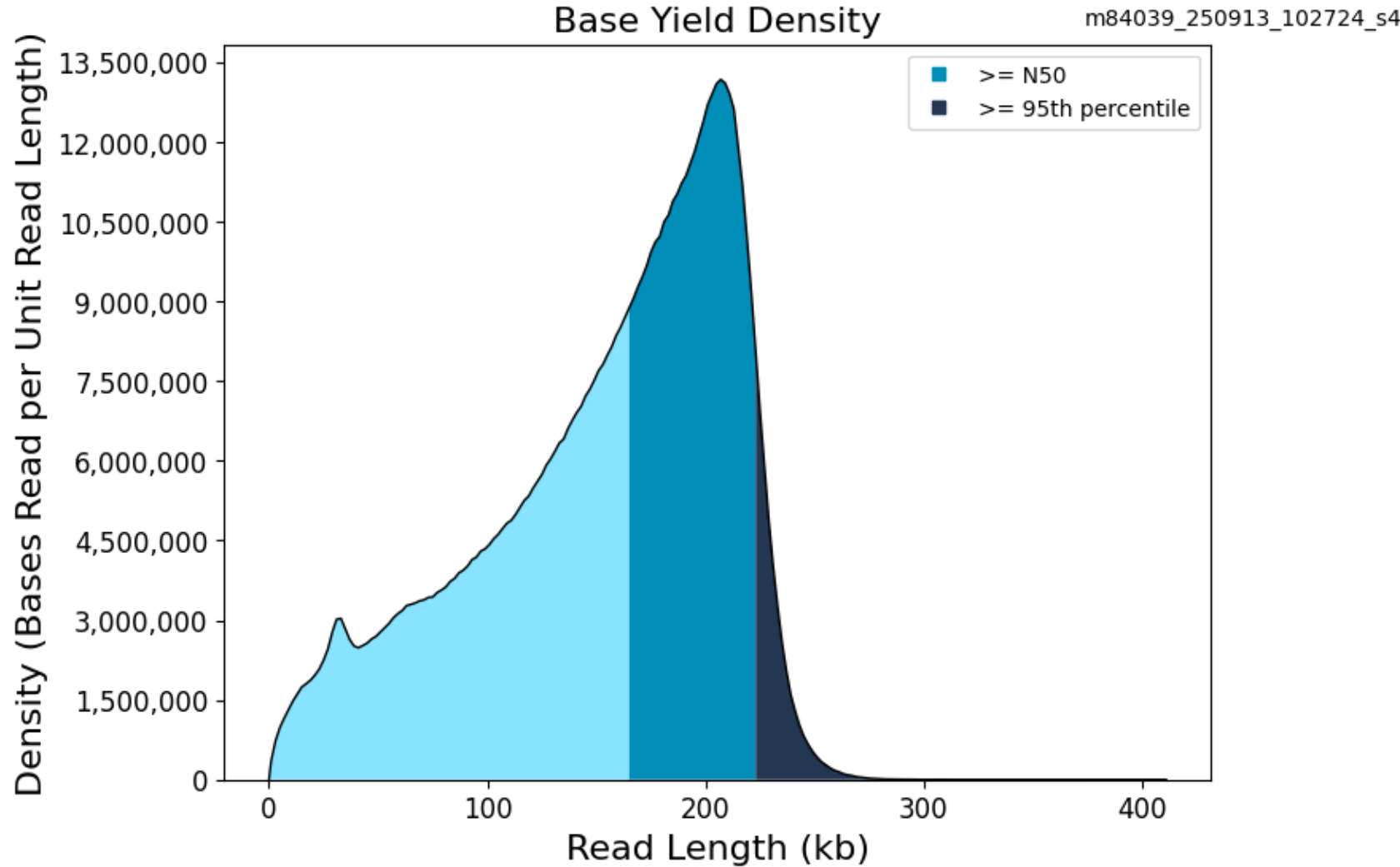
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density



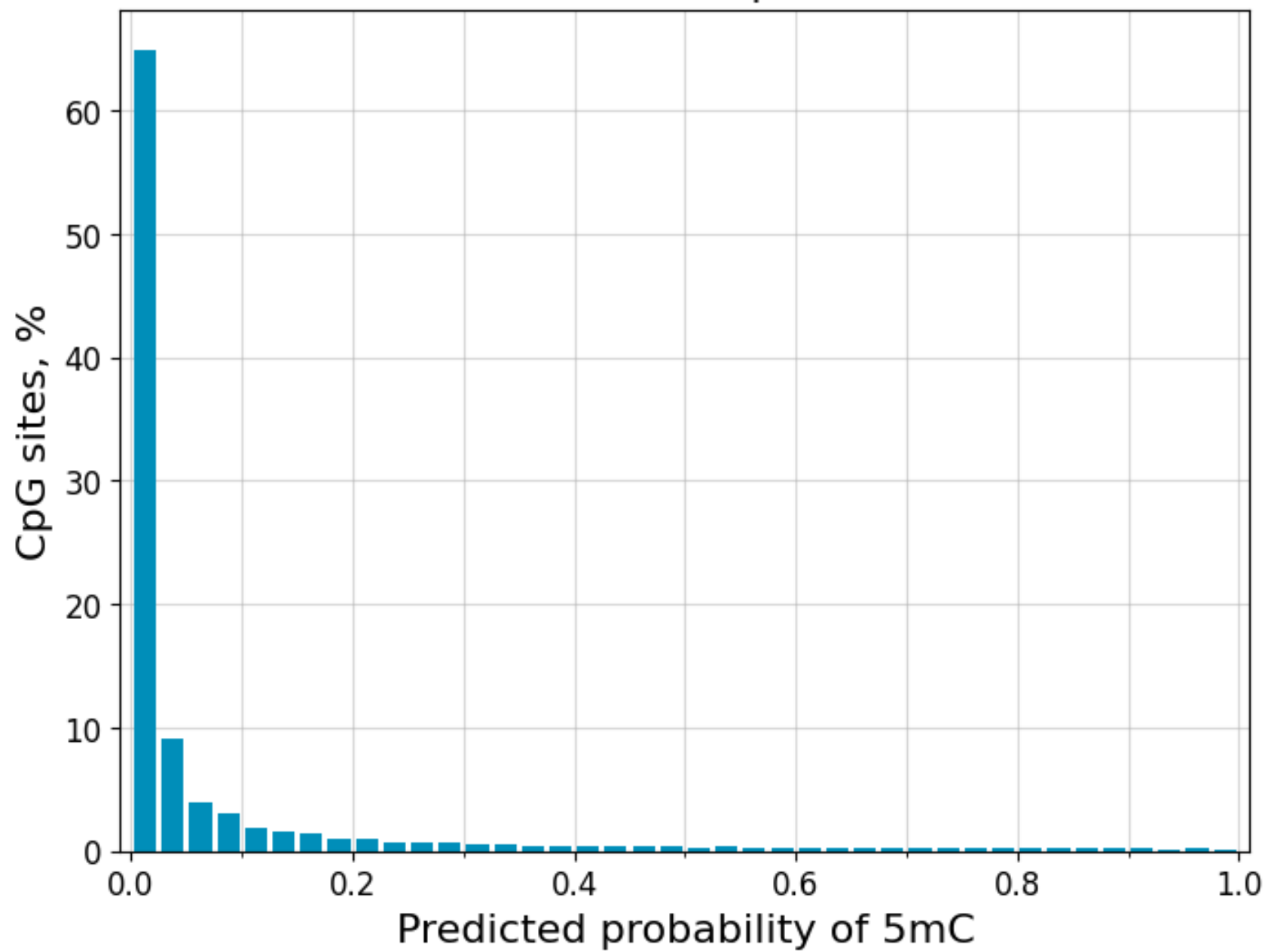
Methylation

Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	98.4%	4.7%
6mA	A	0.6%	0.6%

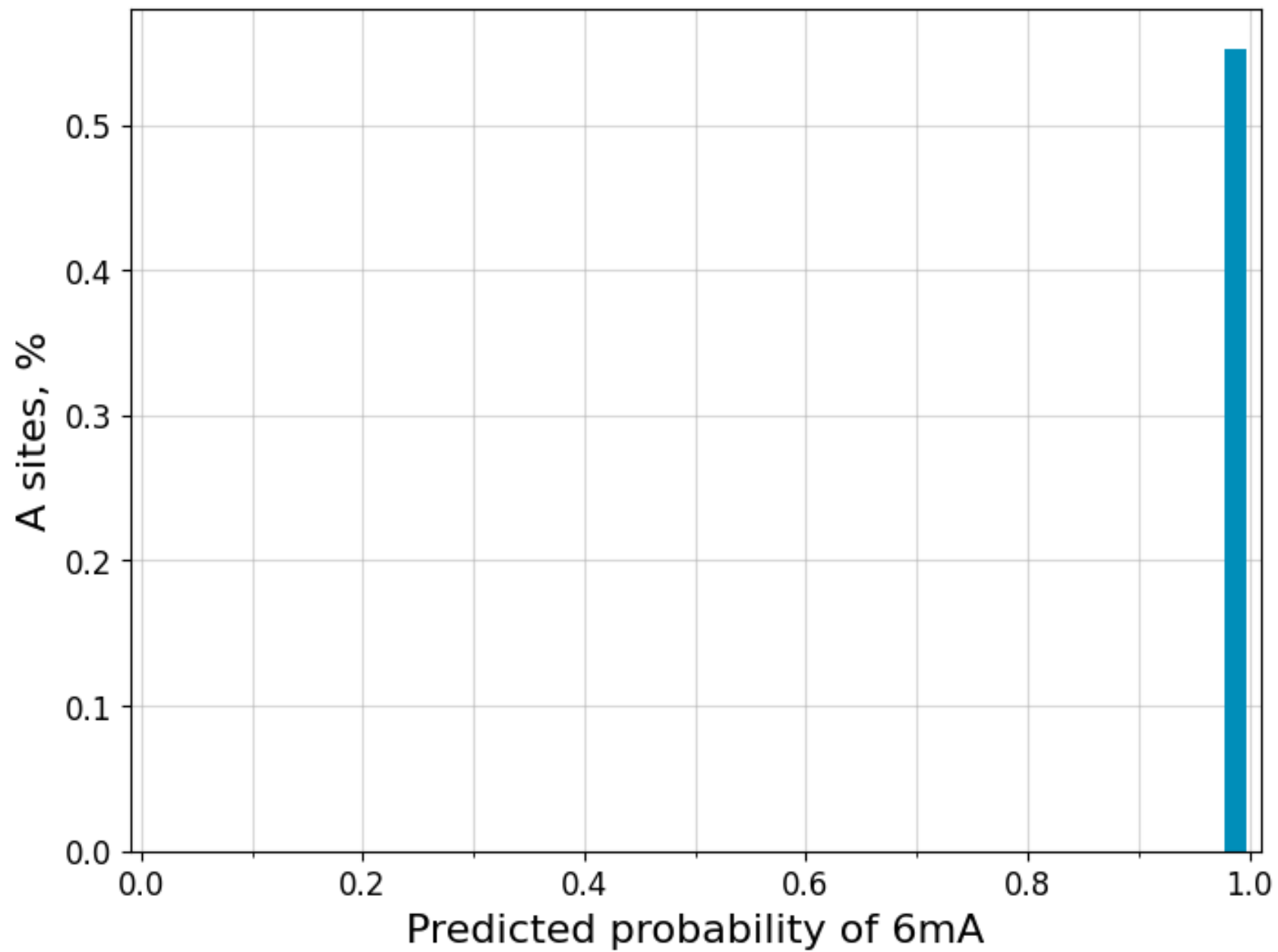
5mC methylation at CpG in reads

5mC at CpG



6mA methylation in reads

6mA



Loading Report

Summary

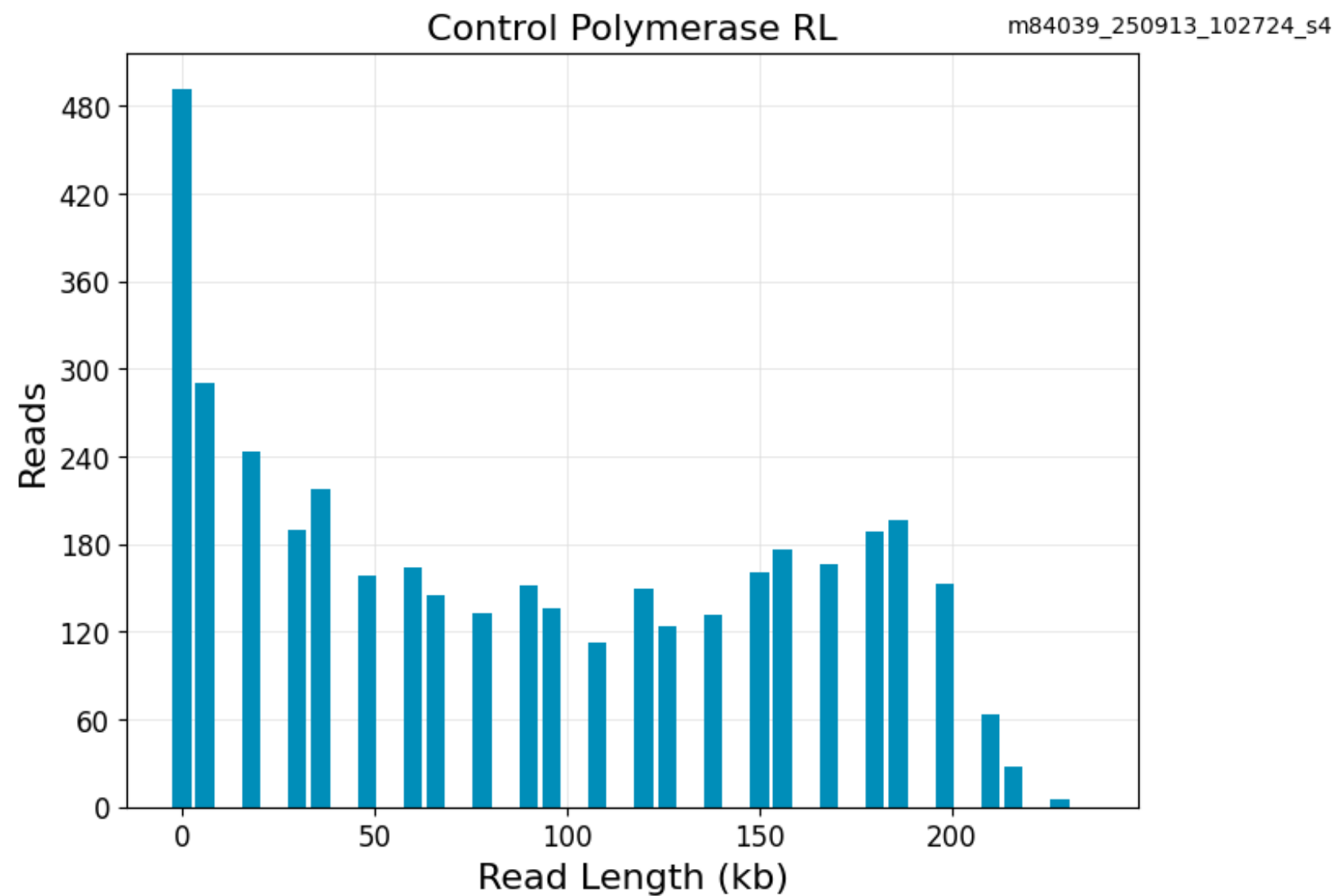
Productive ZMWs	25,165,824
Productivity 0	10,109,737
Productivity 1	14,990,610
Productivity 2	65,477

Control Report

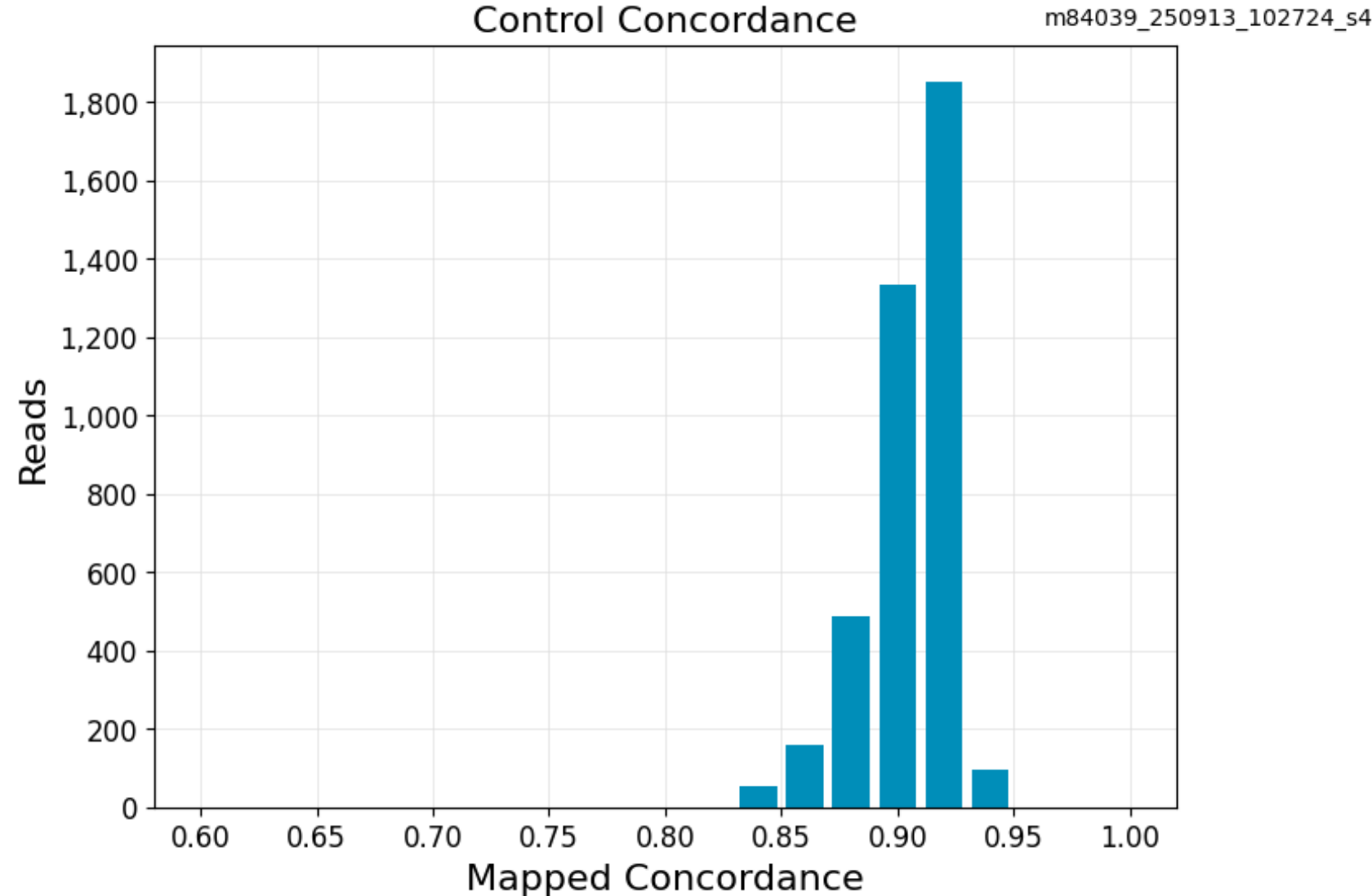
Summary

Number of Control Reads	3,977
Control Read Length Mean	89,871
Control Read Concordance Mean	0.92
Control Read Concordance Mode	0.93

Control Polymerase RL



Control Concordance



CCS Analysis Report

Summary

HiFi reads	8.1 M
HiFi reads yield	129.77 Gb
HiFi reads length (mean)	16.10 kb
HiFi reads length (median, bp)	16,163
HiFi Read Length N50 (bp)	16,332
HiFi Read Quality (median)	Q32
HiFi Read Quality (median)	32
Base Quality Q30 (%)	95.52%
HiFi Number of Passes (mean)	9
Missing adapters (%)	2.42%

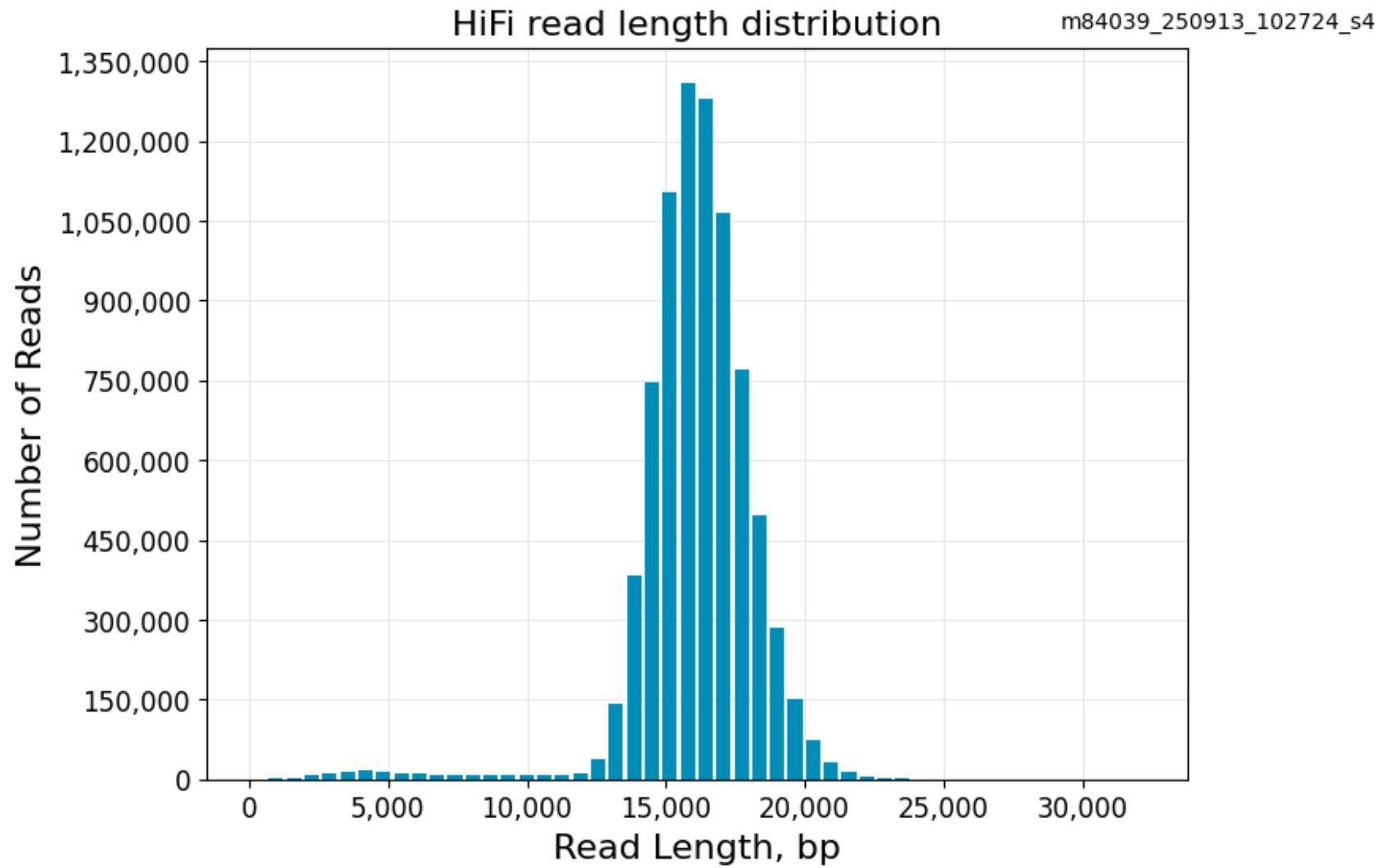
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
0	8058698	100	129.77 Gb	100
5,000	7994980	99	129.55 Gb	100
10,000	7922870	98	129.02 Gb	99
15,000	6287631	78	105.76 Gb	81
20,000	119483	1	2.48 Gb	2
25,000	403	0	0.01 Gb	0
30,000	117	0	0.00 Gb	0
35,000	10	0	0.00 Gb	0
40,000	1	0	0.00 Gb	0

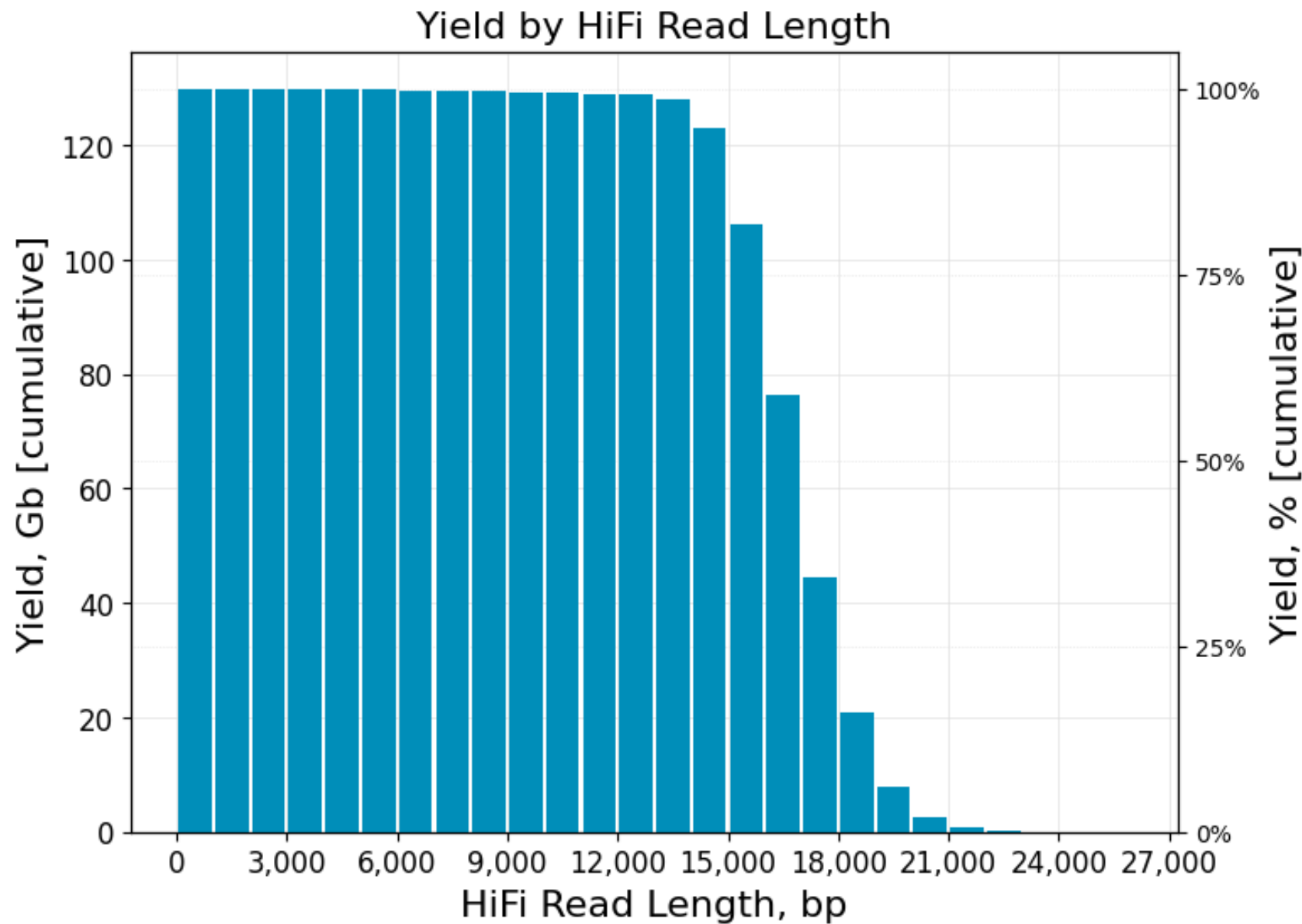
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
Q20	8058698	100	129.77 Gb	100
Q30	5119202	64	82.12 Gb	63
Q40	94355	1	0.95 Gb	1
Q50	14733	0	0.05 Gb	0

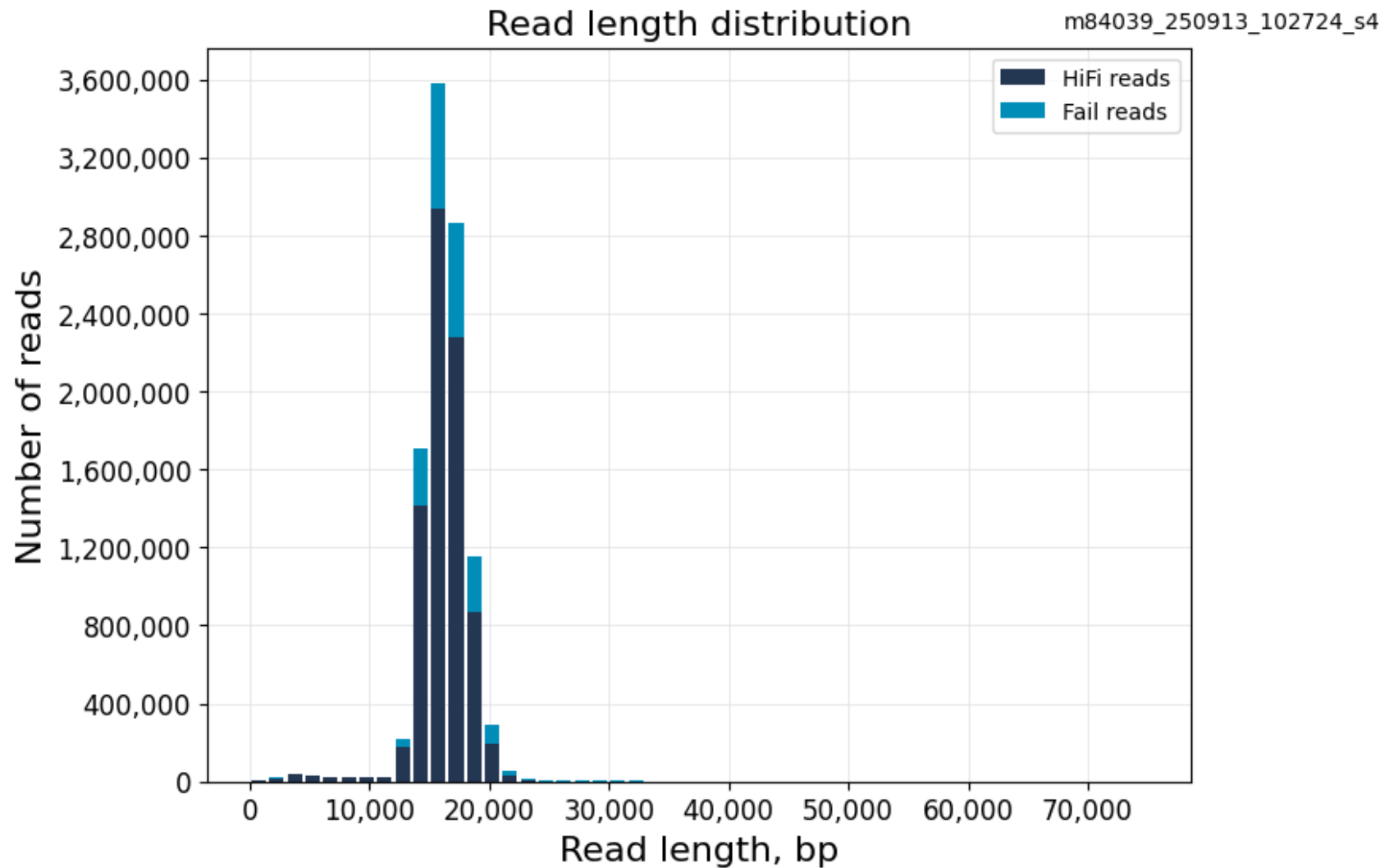
HiFi read length distribution



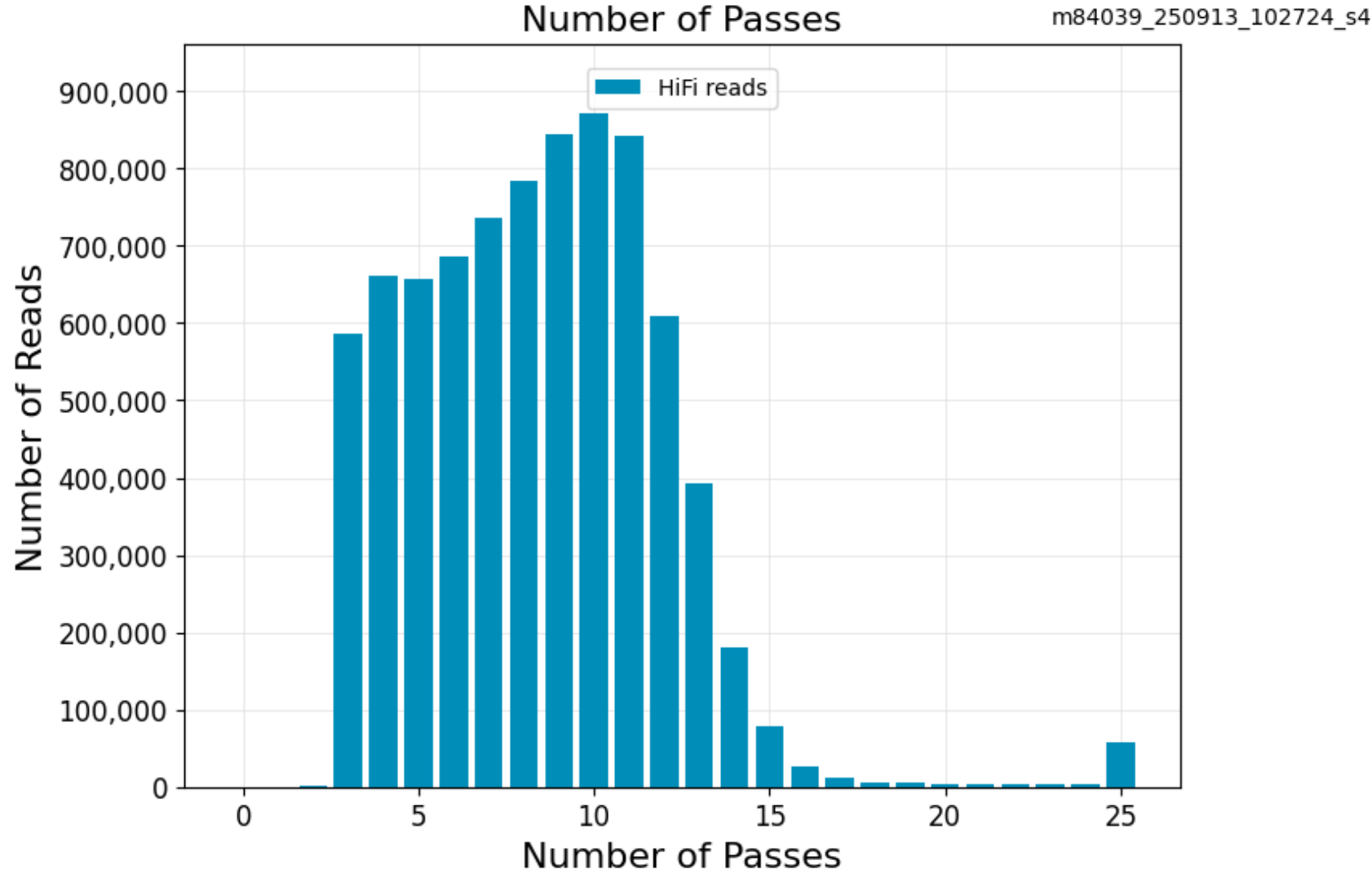
Yield by HiFi Read Length



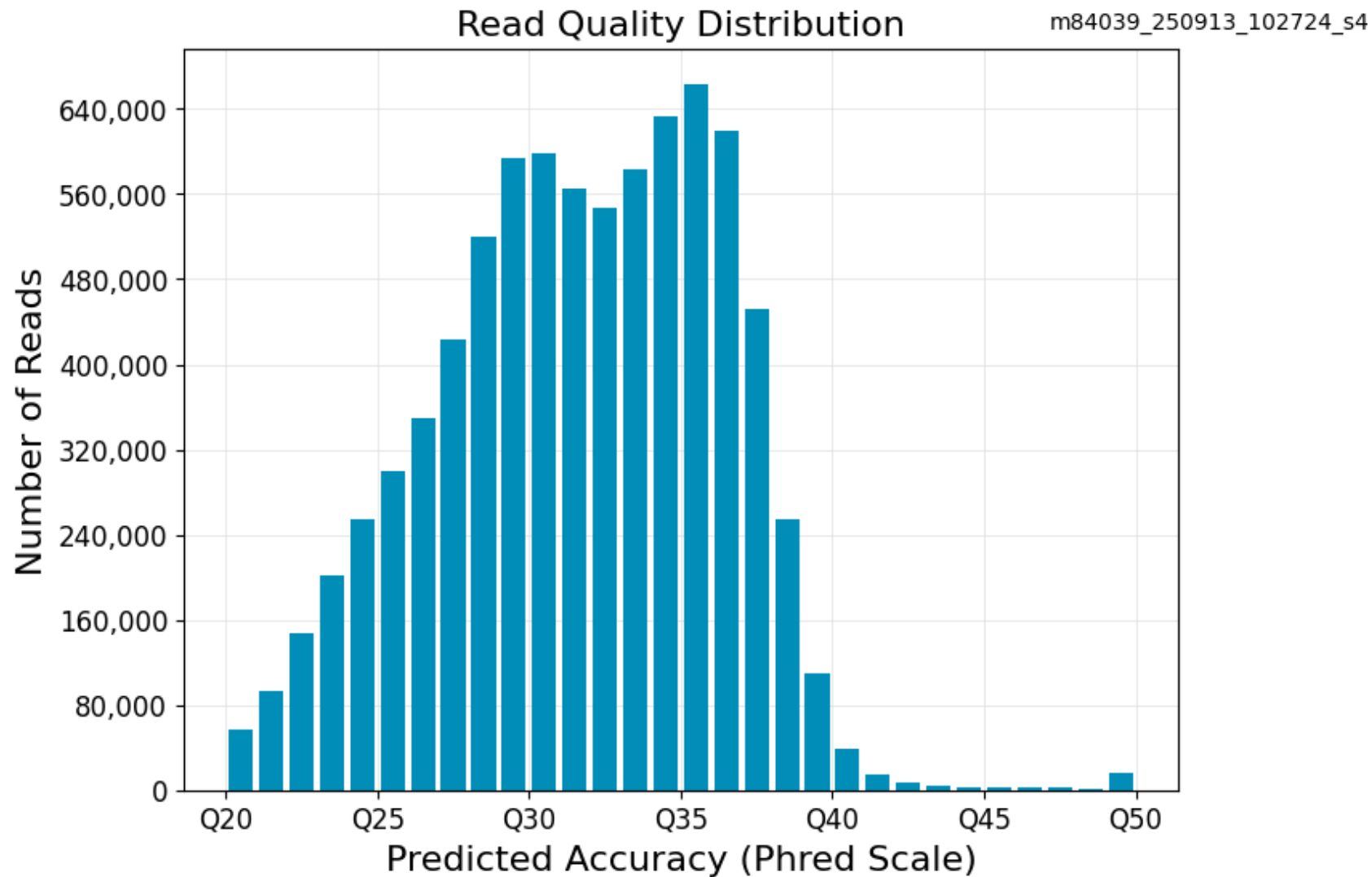
Read length distribution



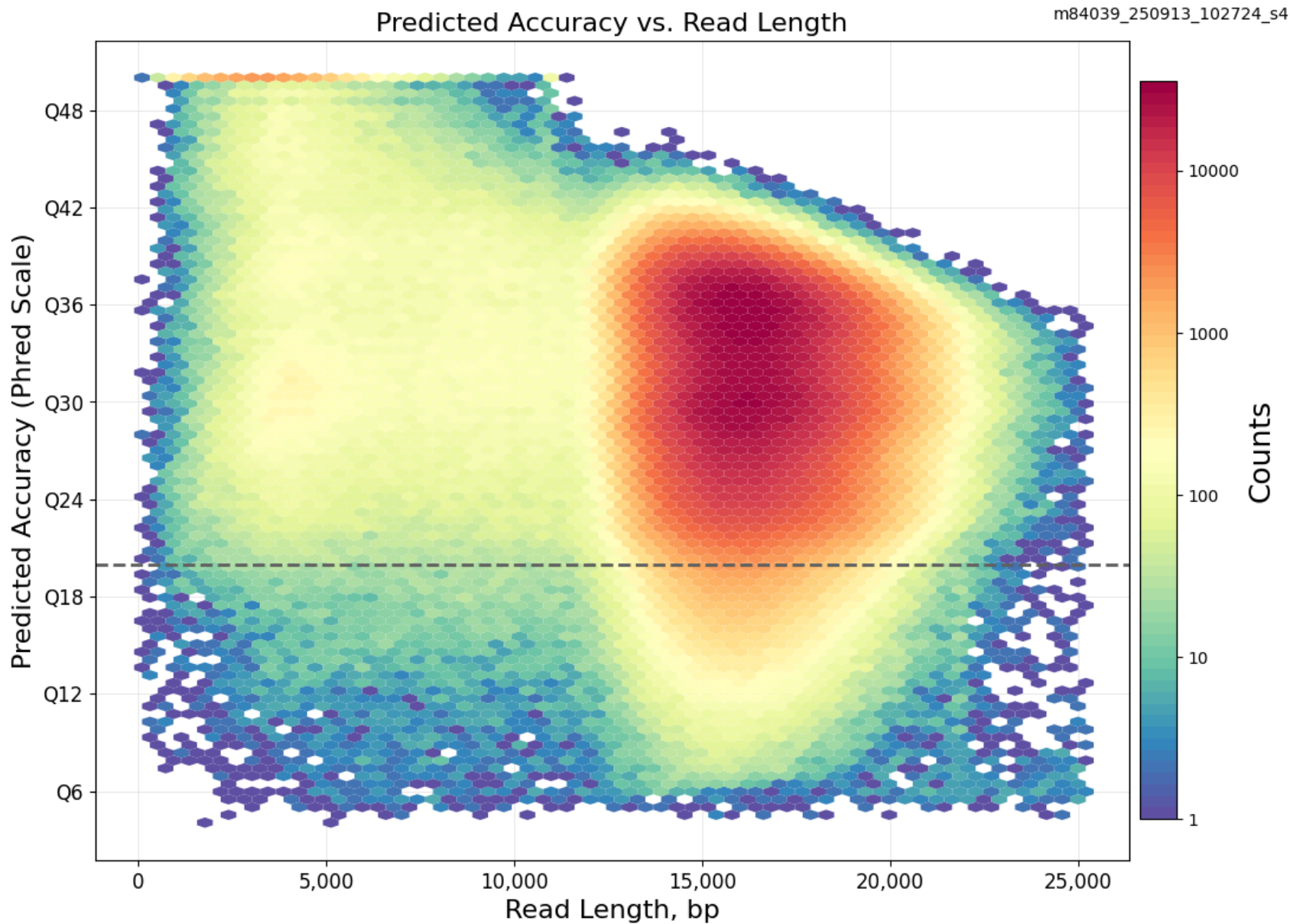
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length



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 12238

Summary

Job Type	import-collection
Name	import-collection
Comments	Description for job Import Collection
Created At	2025-09-14 23:36:02.101
SMRT Link Version	25.3.0.273777

No child jobs found