Report for m84031_260507_084733_s1

Dataset details

Name: Acq15-Cell1 (all samples)

Path: /collections/appslabvast/r84031/r84031_20260506_220223/1_A01/pb_formats/m84031_260507_084733_s1.hifi_reads.consensusreadset.xml

Unique ID: bde72dbe-e759-4303-9af8-efb1e65544fb

Created at: 2026-05-08T22:54:05.137Z

HiFi sequences: 7,104,977

HiFi bases: 127,204,451,242

Bio sample name: RRV-54

Well sample name: Acq15

Run name: 20260506_RRV_Run06_84031

Movie name: m84031_260507_084733_s1

Instrument name: 84031

Instrument software: 13.5.0.286960

Number of child datasets: 1

Number of HiFi BAM files: 1

CCS Analysis Report

Summary Metrics

HiFi reads	7.1 M
HiFi reads yield	127.49 Gb
HiFi reads length (mean)	17.90 kb
HiFi reads length (median, bp)	17,588
HiFi Read Length N50 (bp)	19,182
HiFi Read Quality (median)	Q35
HiFi Read Quality (median)	35
Base Quality ≥Q30 (%)	95.17%
HiFi Number of Passes (mean)	9
Missing adapters (%)	2.25%

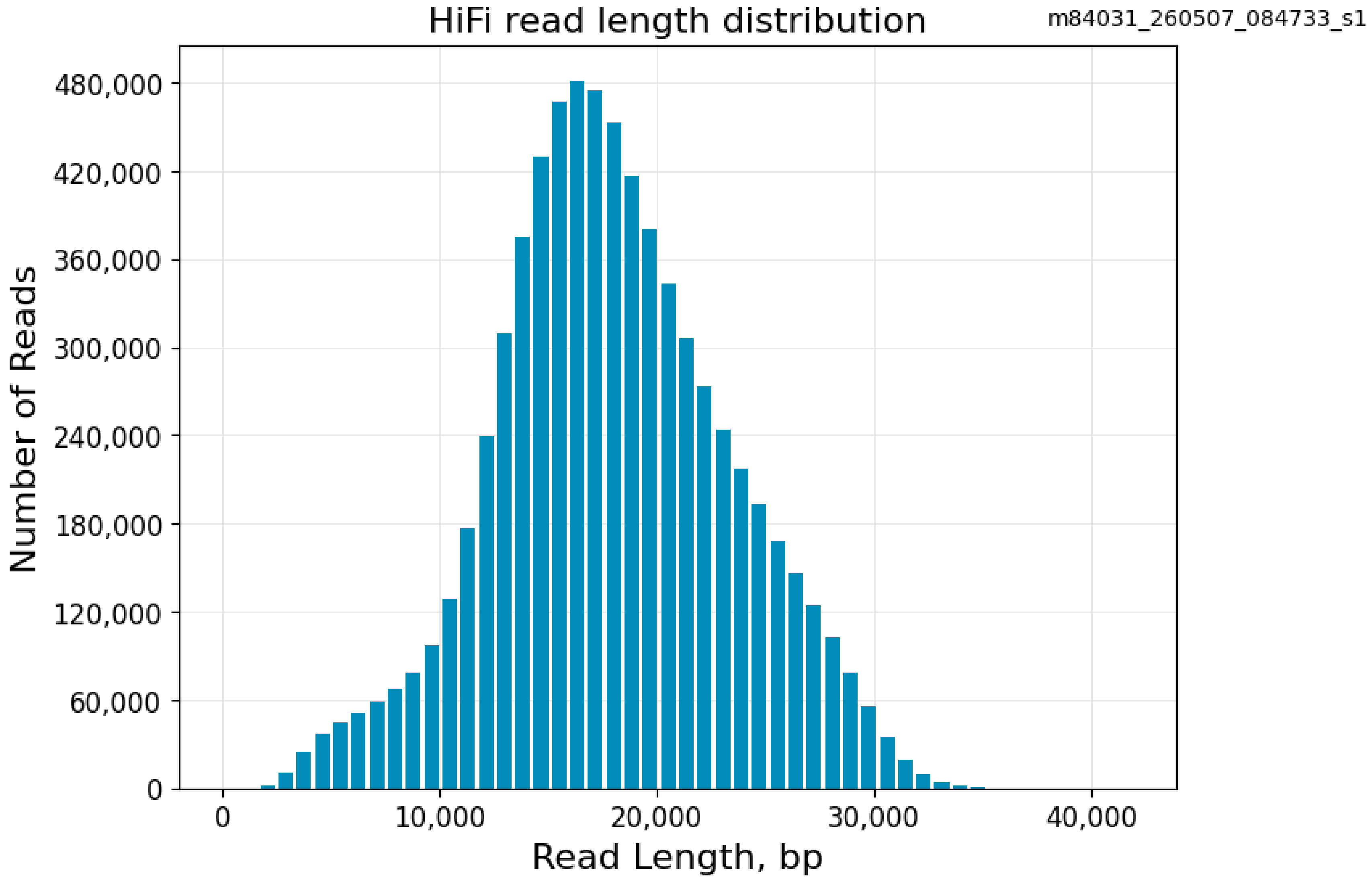
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	7,121,629	100	127.49 Gb	100
≥ 5,000	7,047,575	99	127.19 Gb	100
≥ 10,000	6,653,750	93	124.08 Gb	97
≥ 15,000	5,022,130	71	102.77 Gb	81
≥ 20,000	2,357,974	33	56.41 Gb	44
≥ 25,000	769,963	11	21.13 Gb	17
≥ 30,000	78,289	1	2.44 Gb	2
≥ 35,000	656	0	0.03 Gb	0
≥ 40,000	191	0	0.01 Gb	0

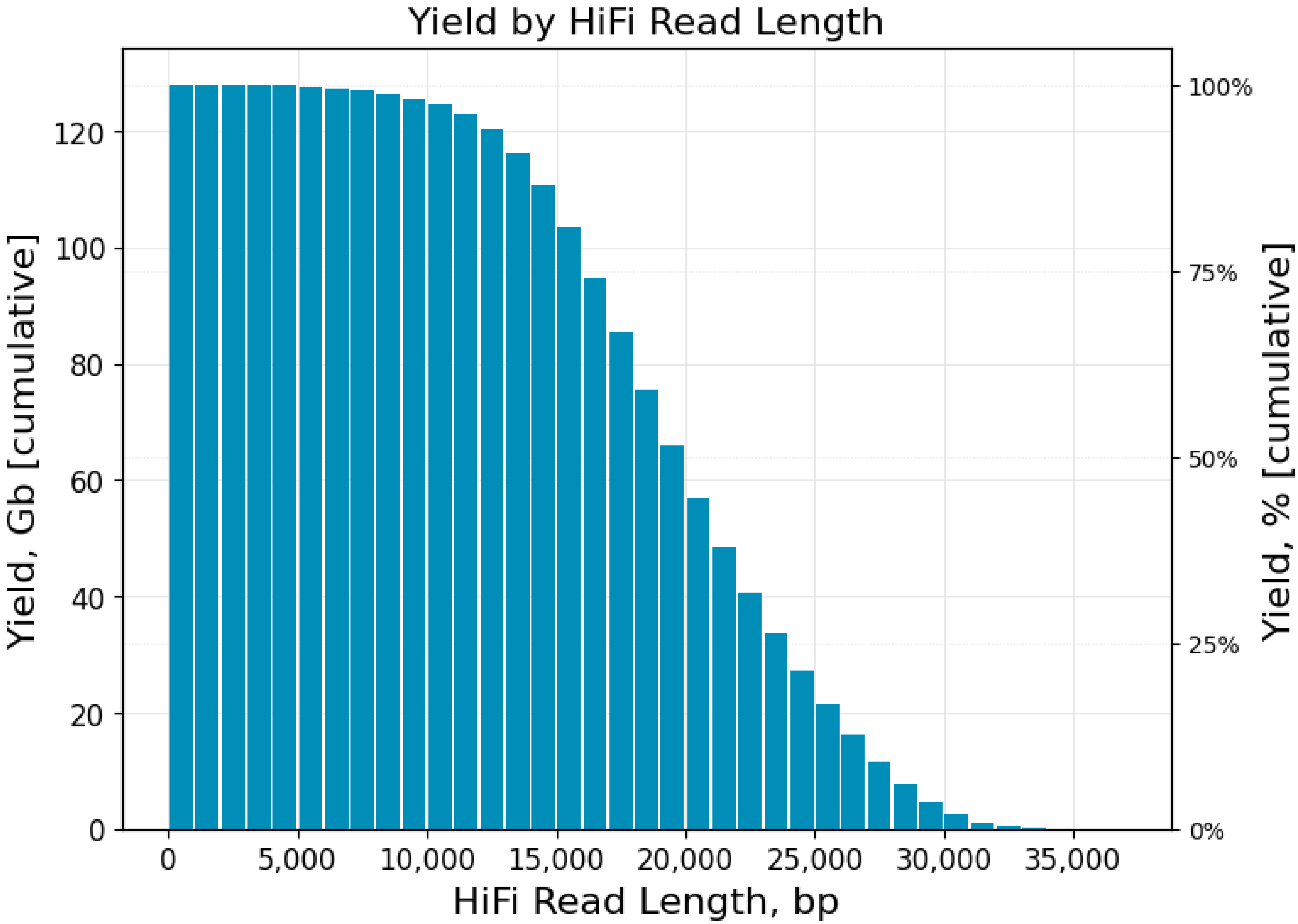
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	7,121,629	100	127.49 Gb	100
≥ Q30	5,251,424	74	90.75 Gb	71
≥ Q40	1,638,659	23	21.98 Gb	17
≥ Q50	276,375	4	2.49 Gb	2

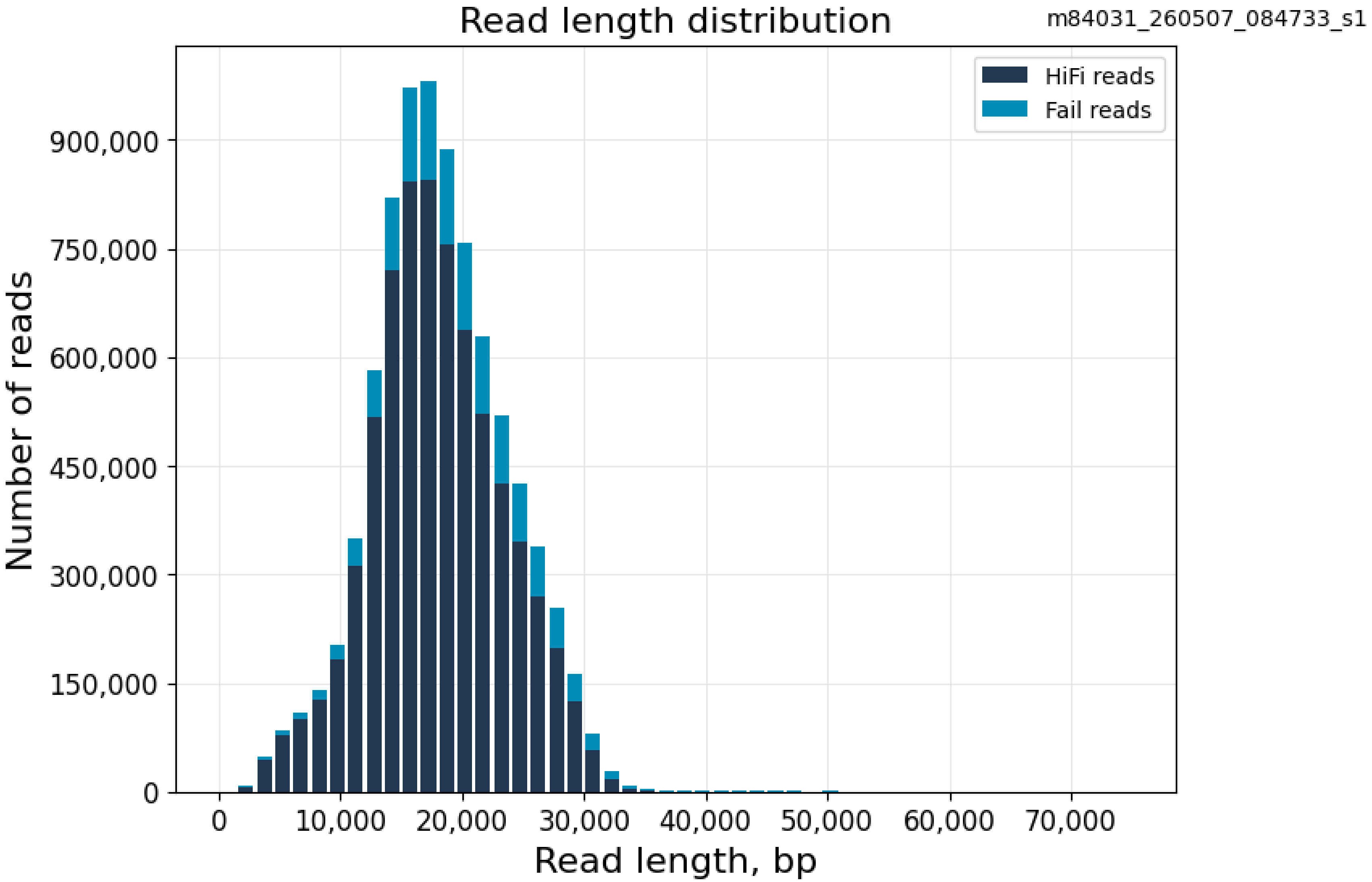
Read Length Distribution: HiFi read length distribution



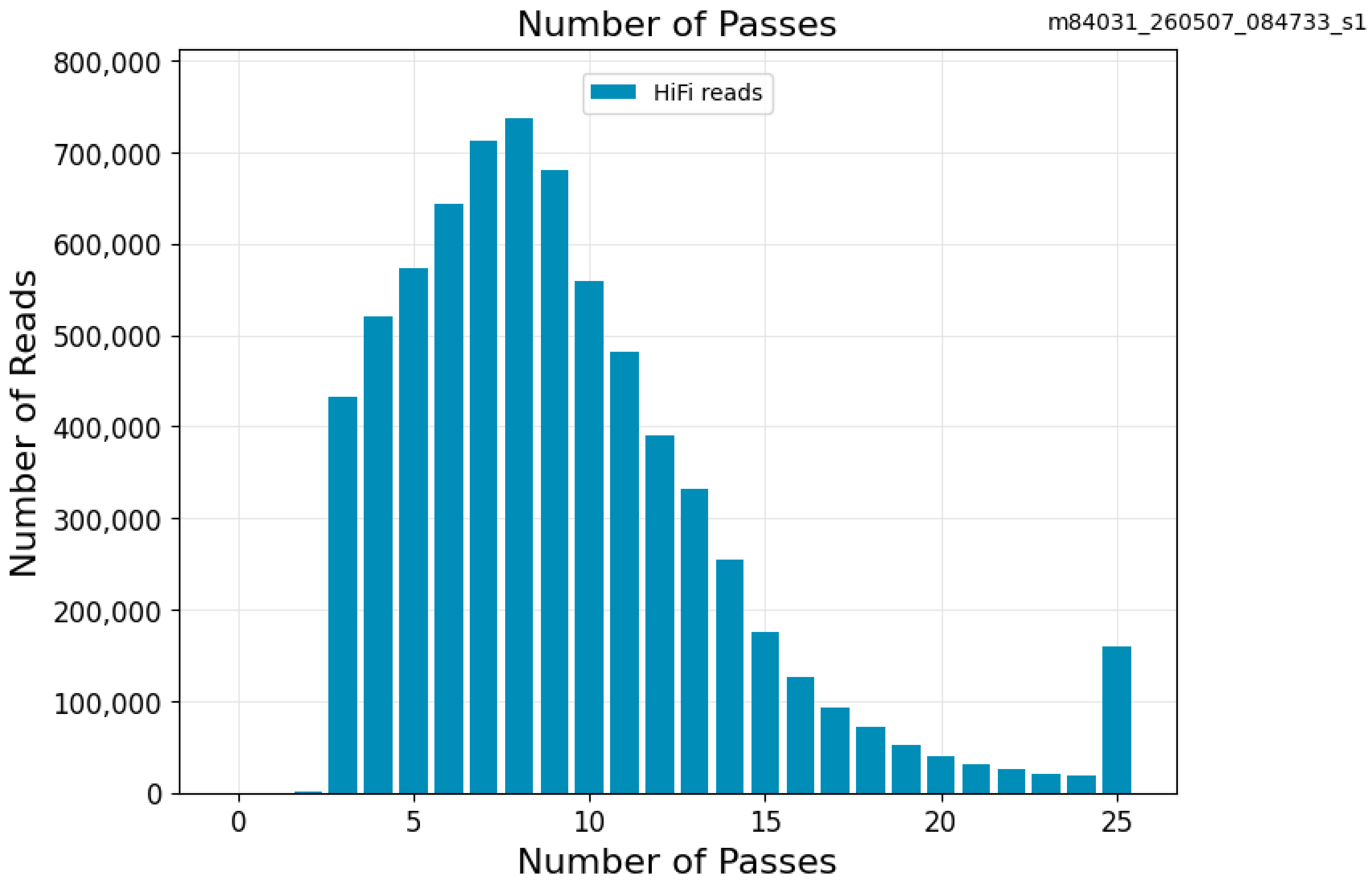
Read Length Distribution: Yield by HiFi Read Length



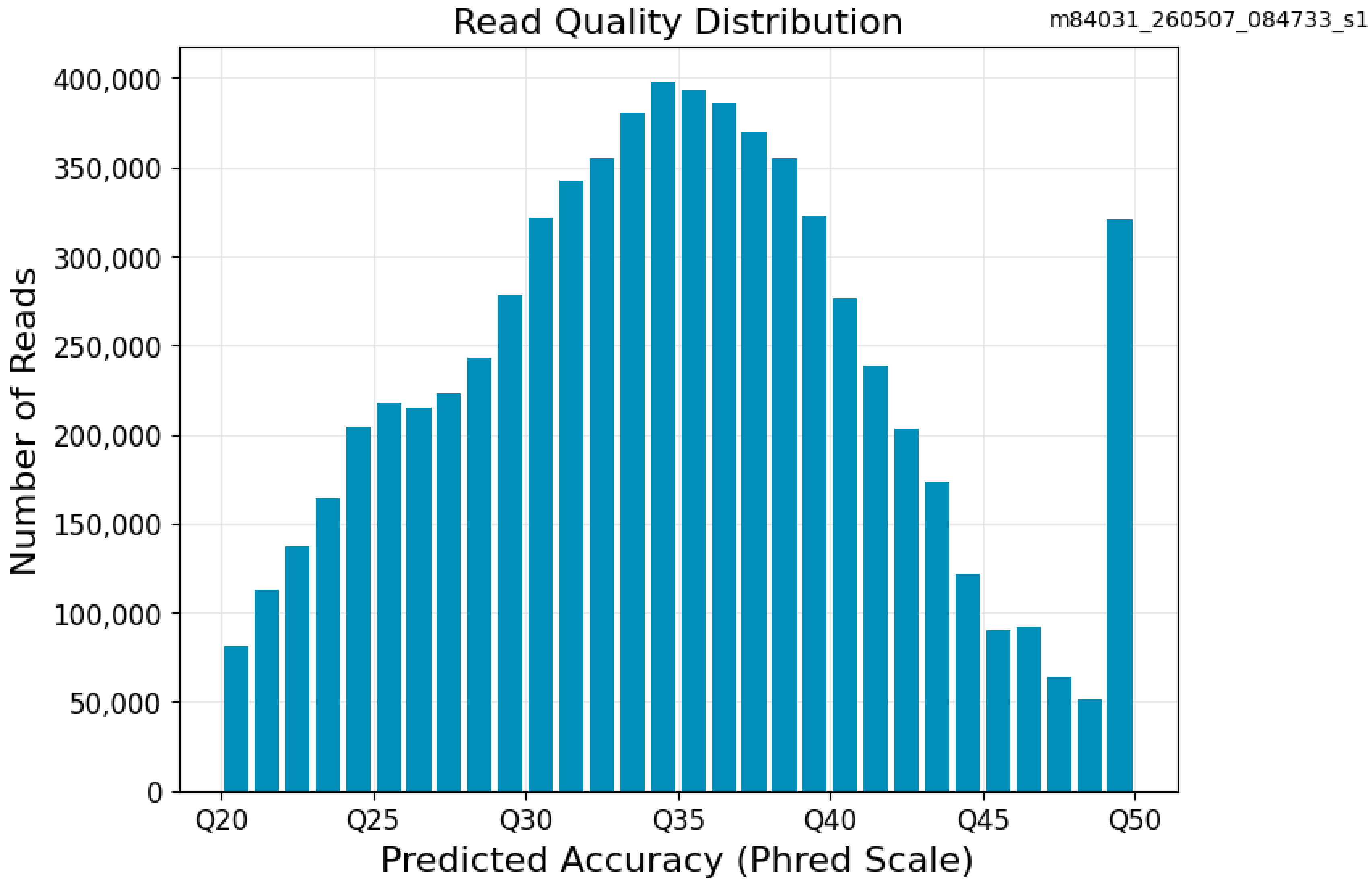
Read Length Distribution: Read length distribution



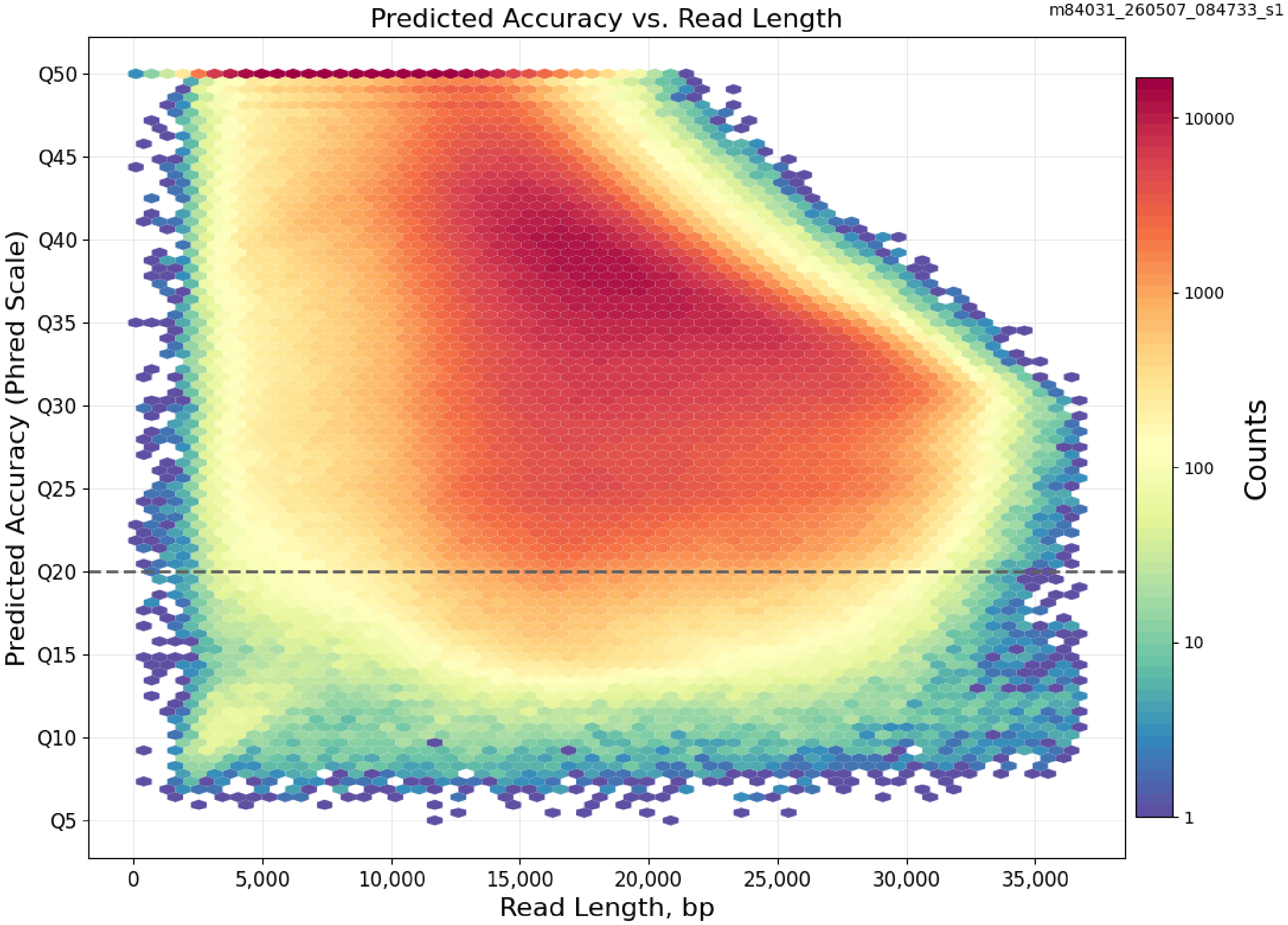
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

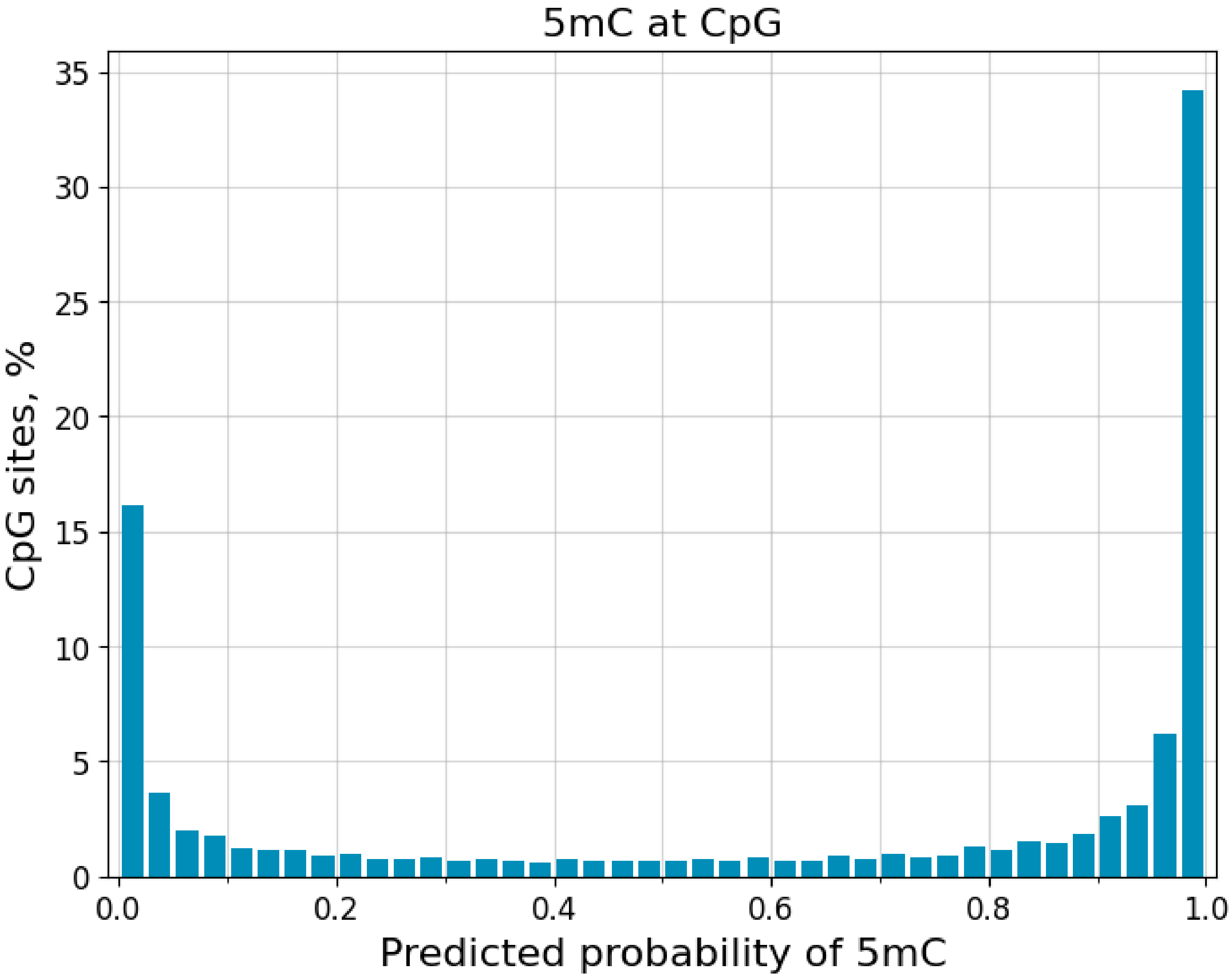


Methylation

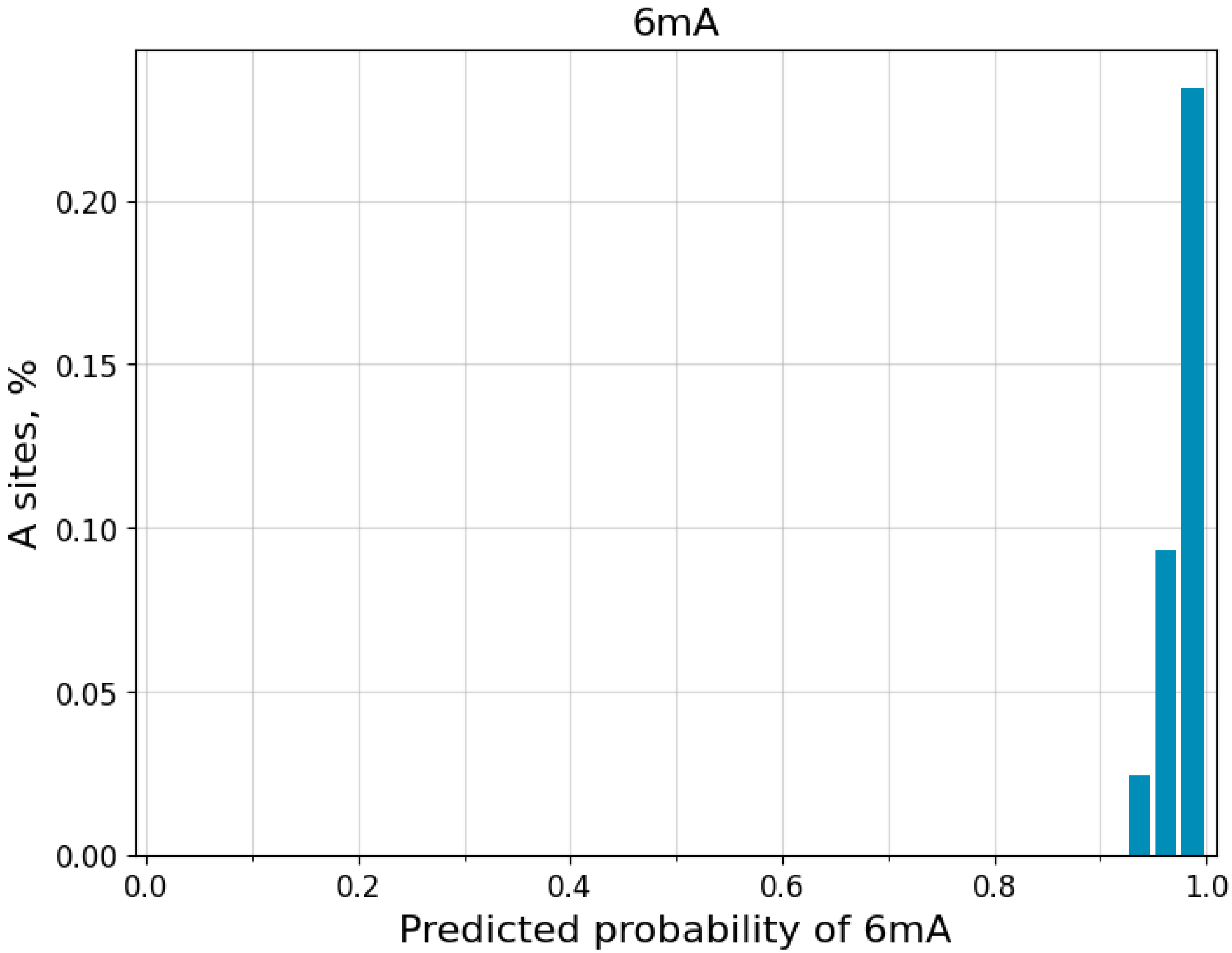
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	98.9%	62.1%
6mA	A	0.4%	0.4%
5hmC	CpG	0.5%	0.5%

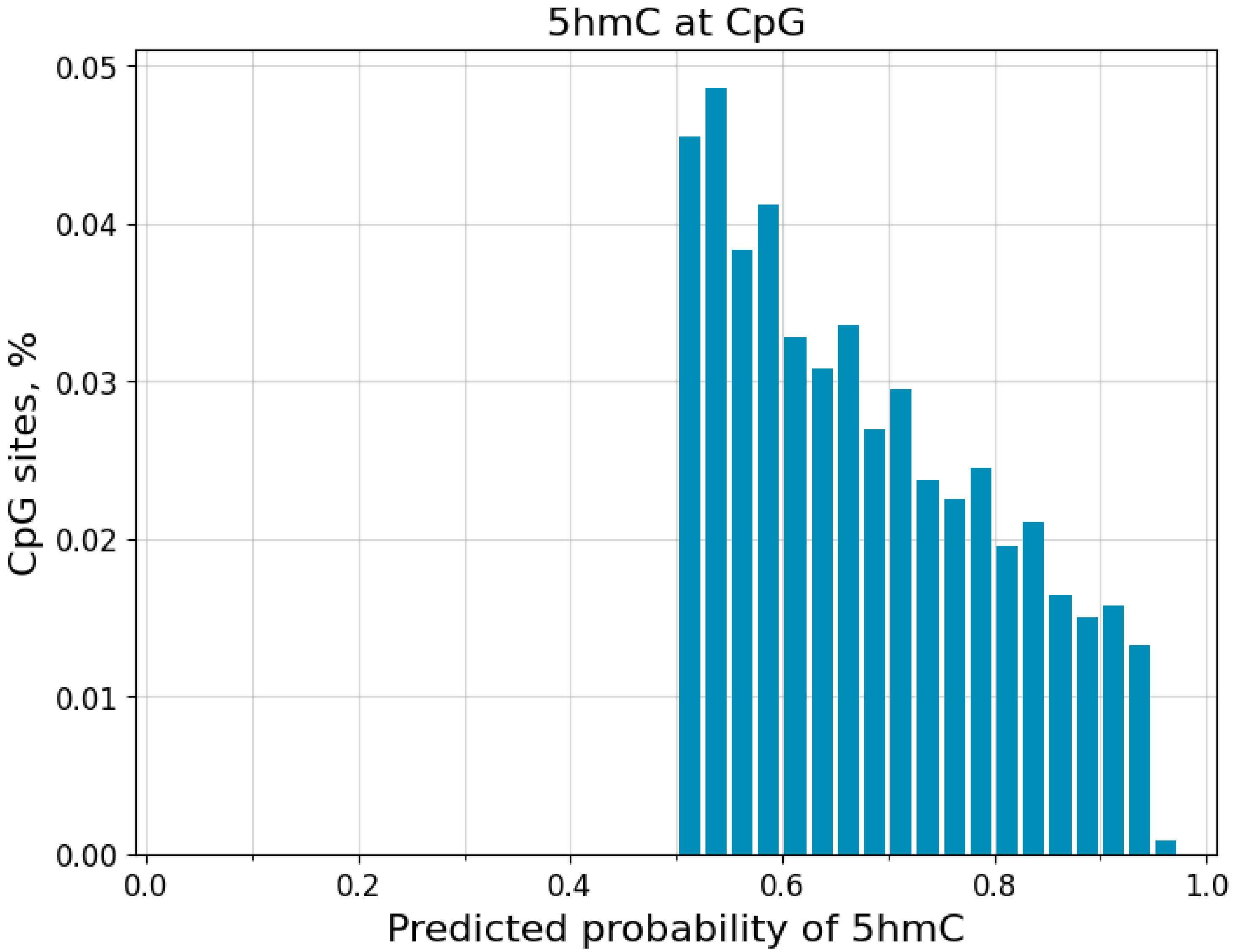
Score distributions: 5mC at CpG



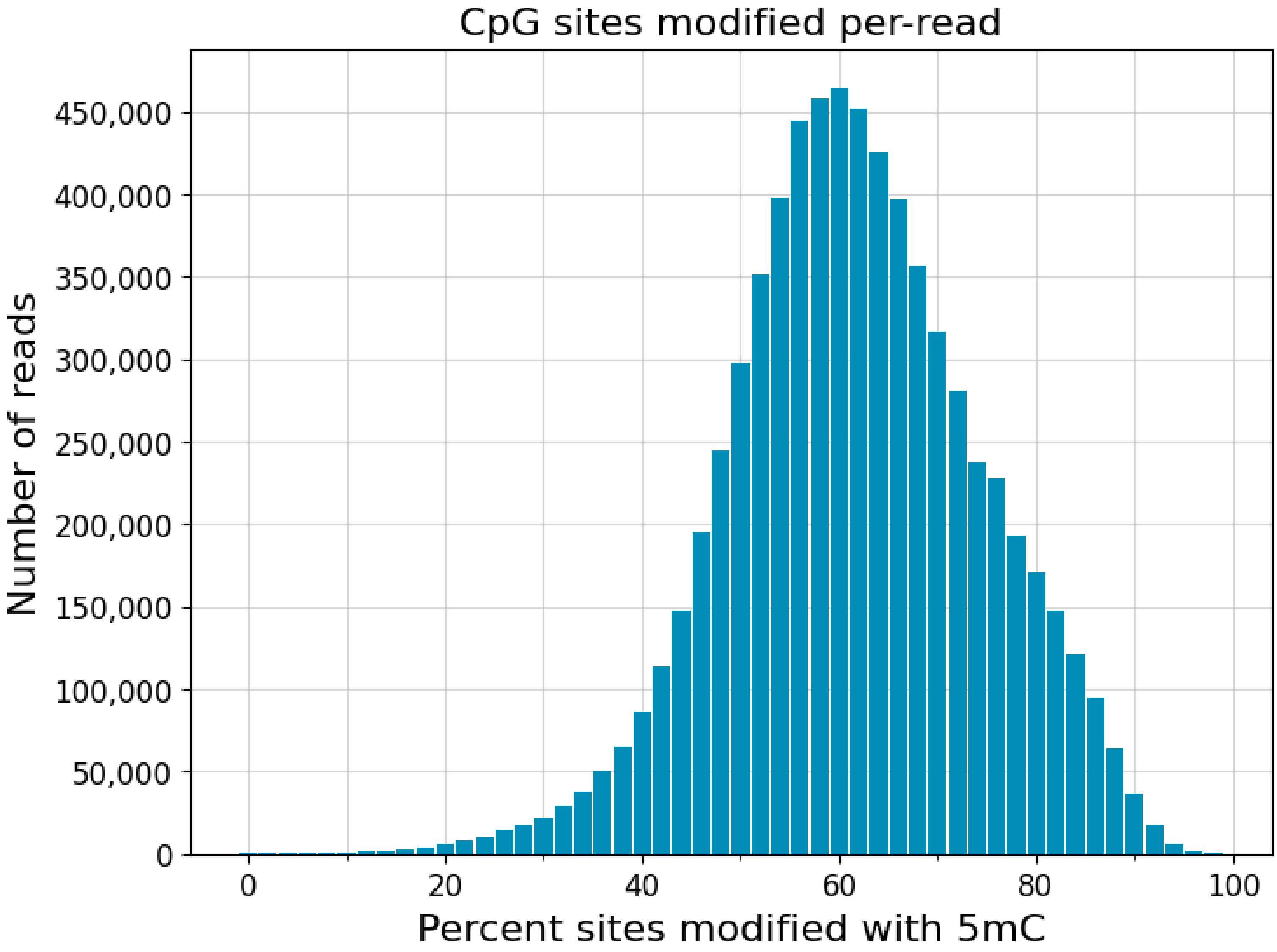
Score distributions: 6mA



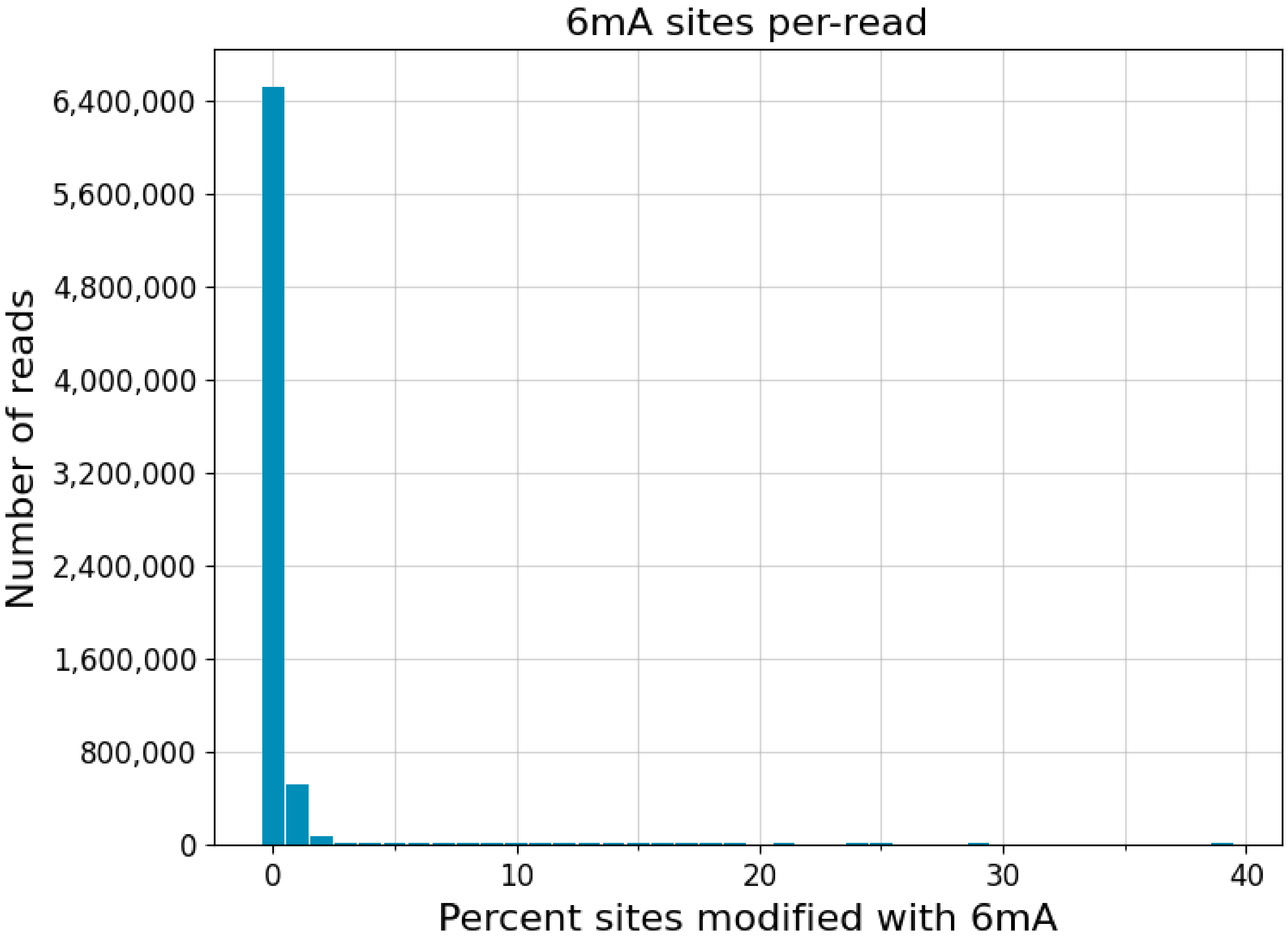
Score distributions: 5hmC at CpG



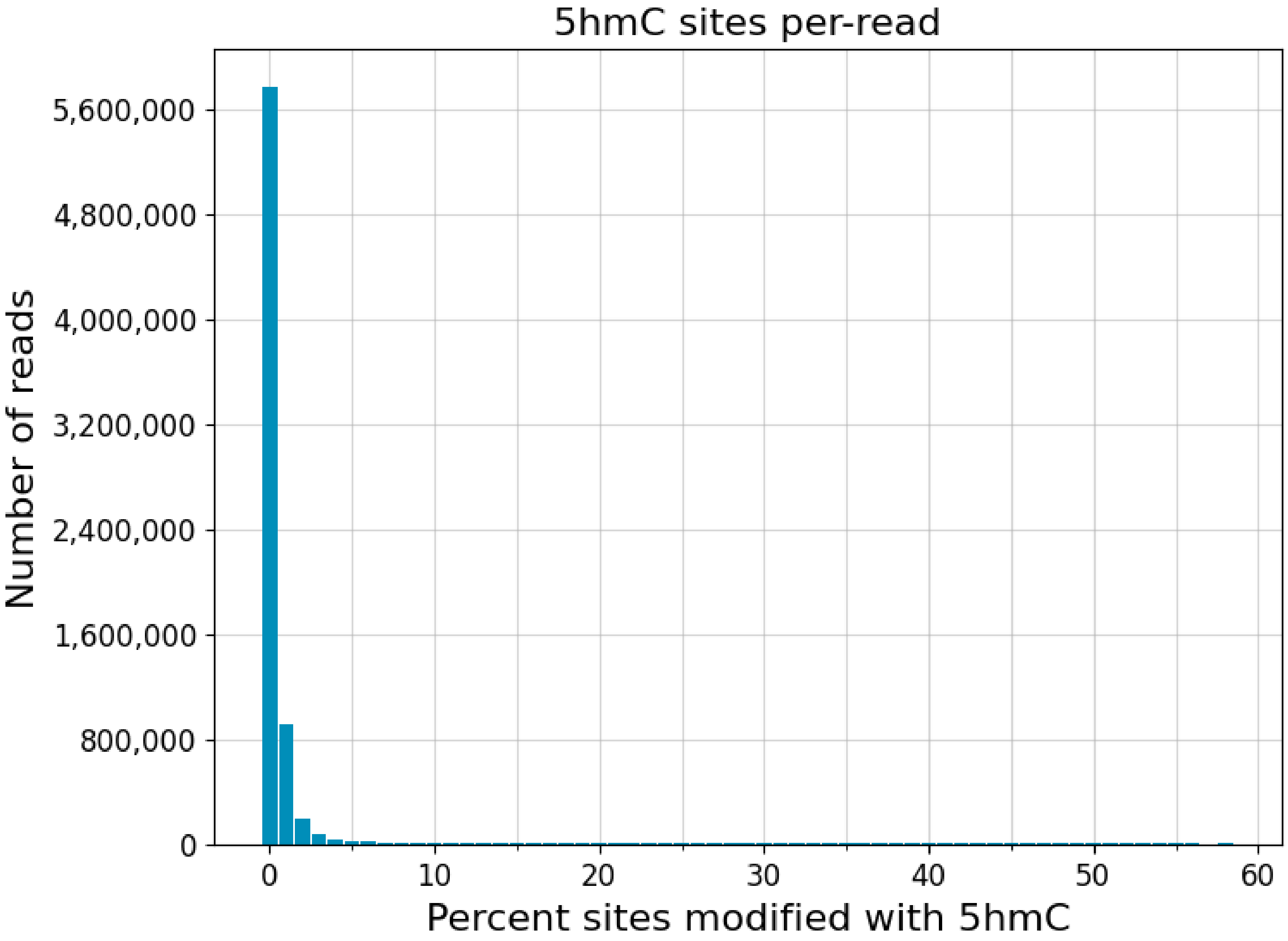
Per-read distributions: CpG sites modified per-read



Per-read distributions: 6mA sites per-read



Per-read distributions: 5hmC sites per-read



Barcodes

Summary Metrics

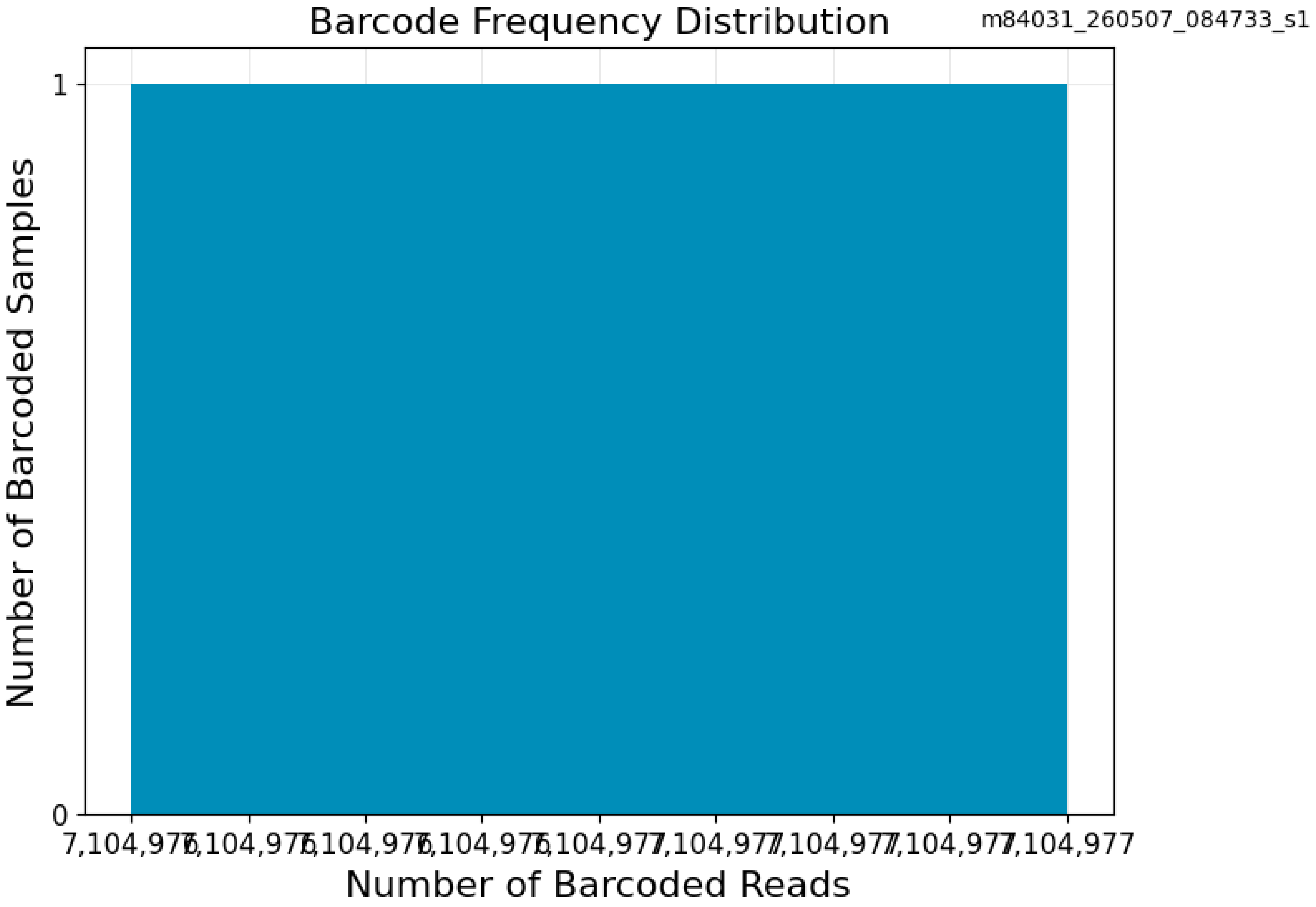
Unique Barcodes	1
Barcoded HiFi Reads	7,104,977
Unbarcoded HiFi Reads	16,652
Barcoded HiFi Reads (%)	99.77 %
Barcoded HiFi yield (Gb)	127.20 Gb
Unbarcoded HiFi yield (Gb)	0.28 Gb
Barcoded HiFi Yield (%)	99.78 %
Mean HiFi Reads per Barcode	7,104,977
Max. HiFi Reads per Barcode	7,104,977
Min. HiFi Reads per Barcode	7,104,977
Barcoded HiFi read length (mean, kb)	17.90 kb
Unbarcoded HiFi read length (mean, kb)	16.86 kb

Barcode Data

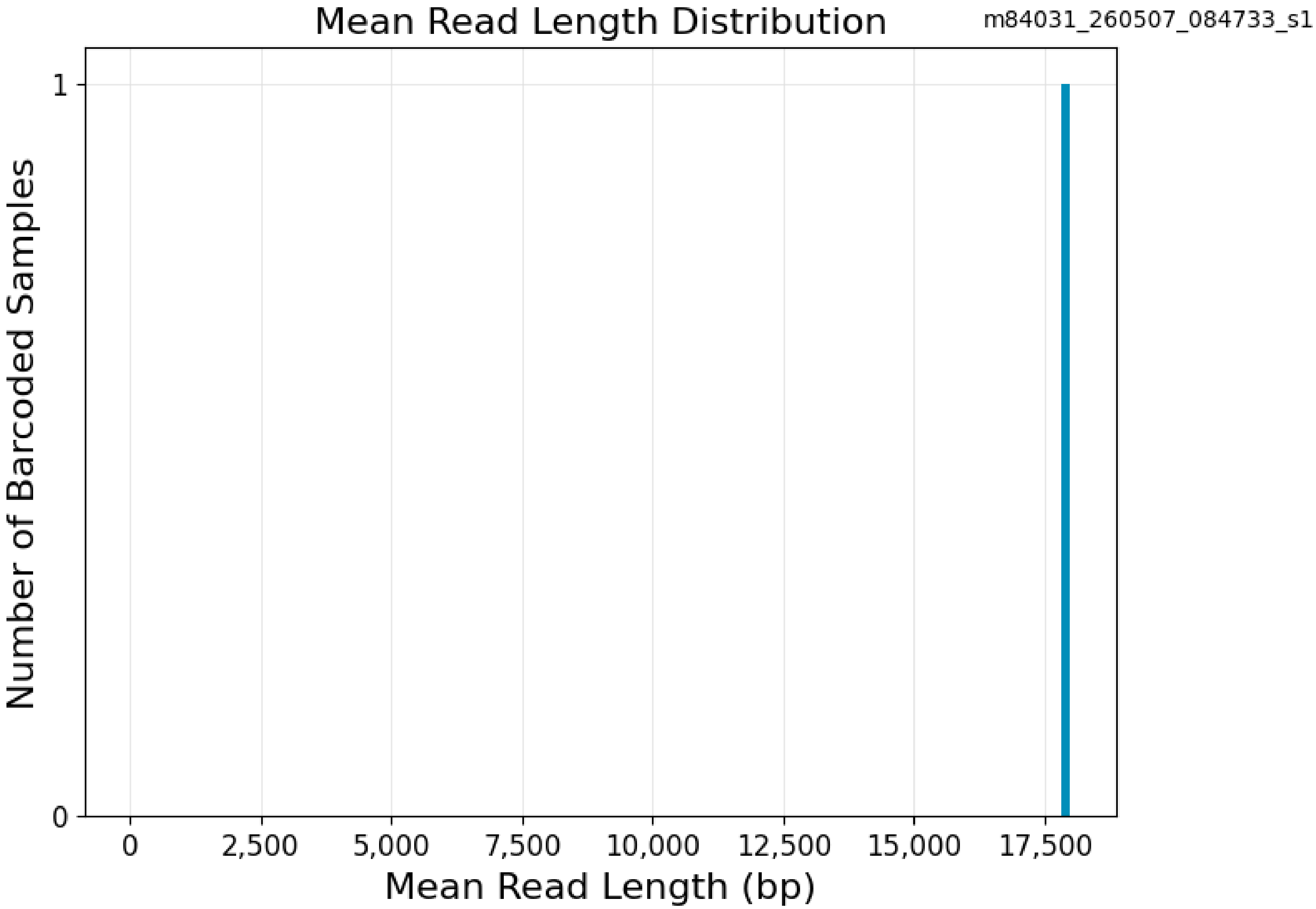
Sample Name	Barcode	Barcode Quality	HiFi Reads	HiFi Read Length (mean, bp)	HiFi Read Quality (median, QV)	HiFi Yield (bp)	Polymerase Read Length (mean, bp)
RRV-54	bc2004--bc2004	96.7	7,104,977	17,903	Q35	127,204,451,242	170,723
No Name	Not Barcoded	0.0	16,652	16,855	Q26	280,679,486	155,546

Barcoded Read Statistics: Number Of Reads Per Barcode

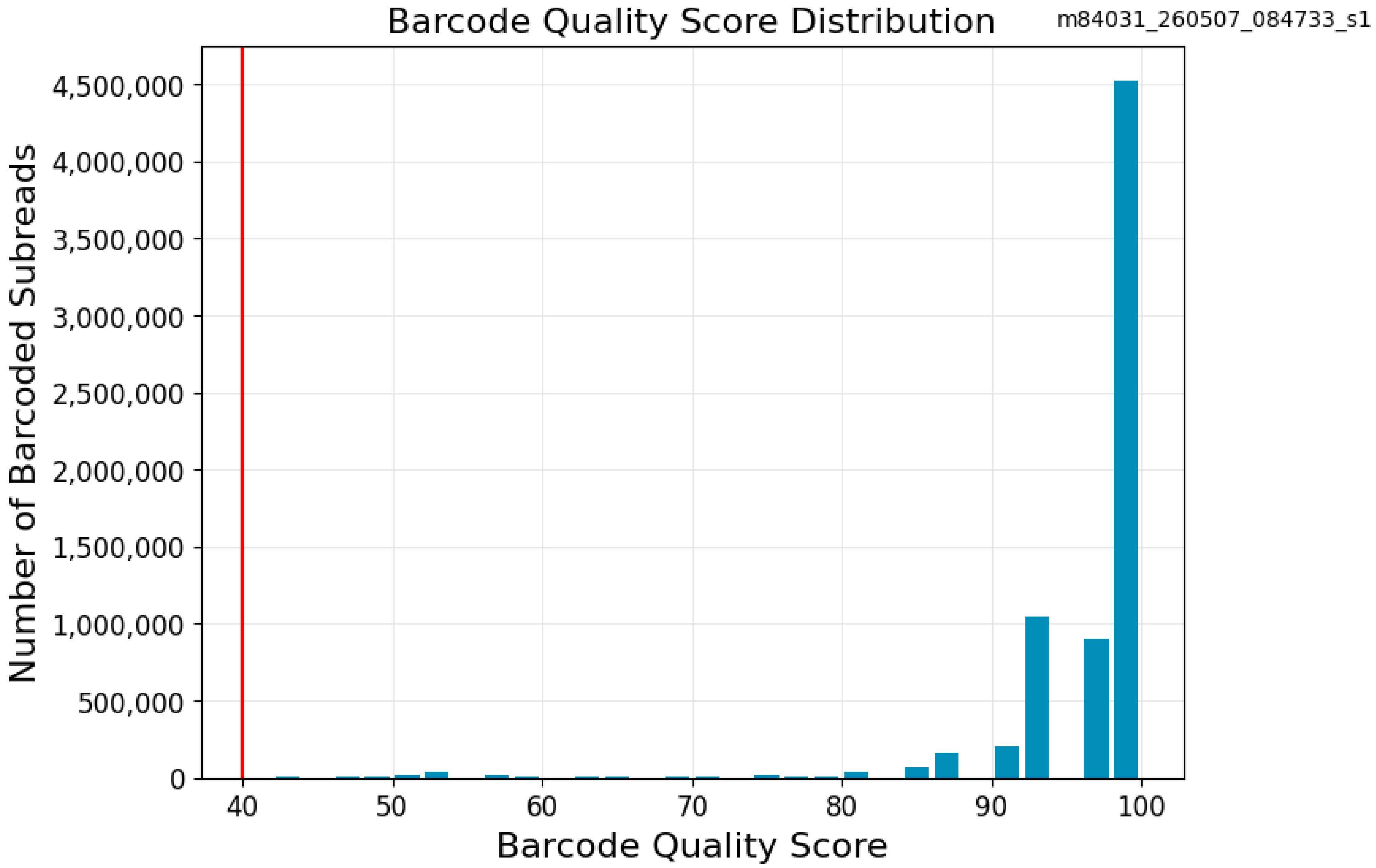
Barcoded Read Statistics: Barcode Frequency Distribution



Barcoded Read Statistics: Mean Read Length Distribution



Barcode Quality Scores: Barcode Quality Score Distribution



Loading Report

Summary Metrics

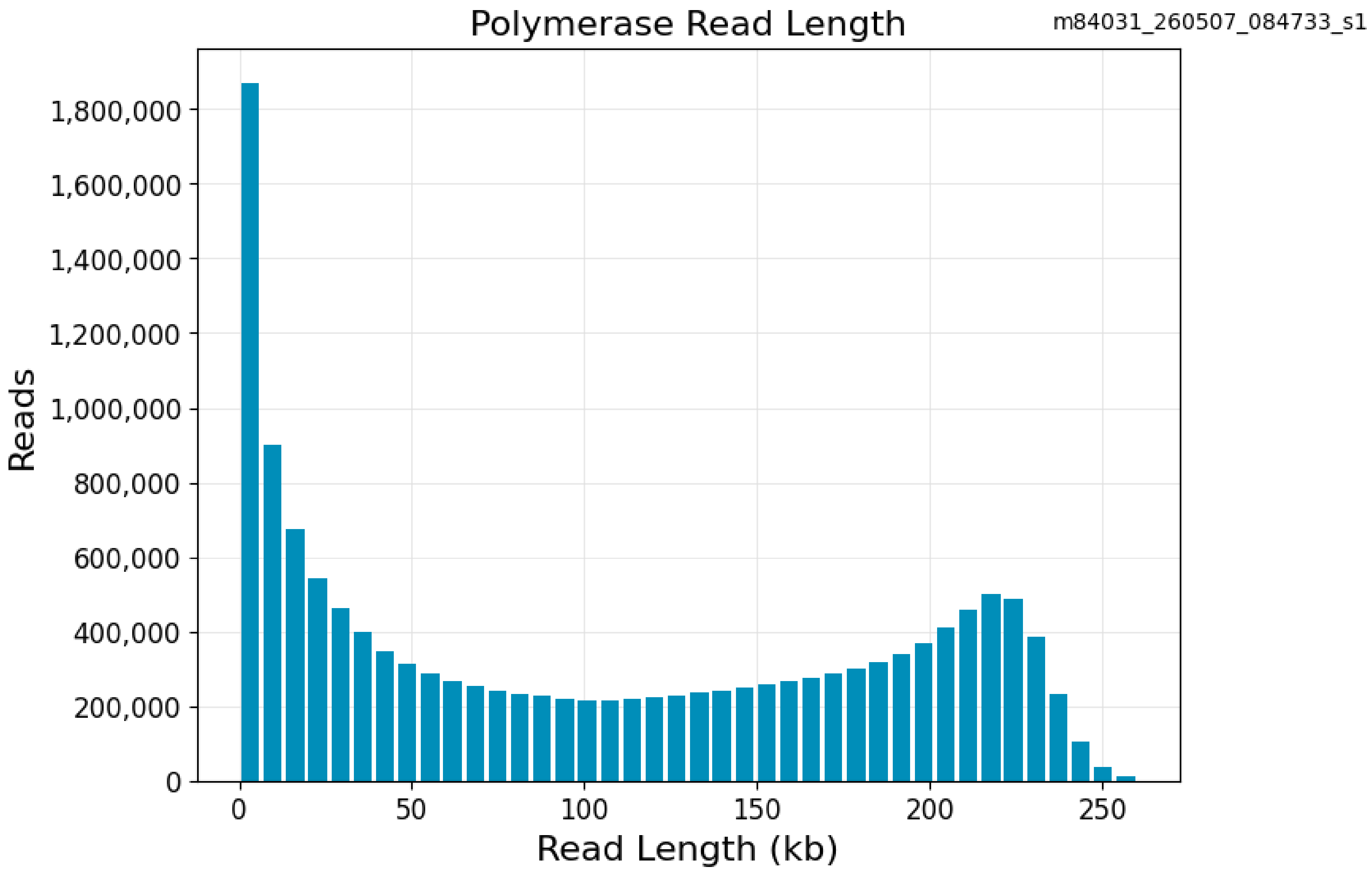
Productive ZMWs	25,165,824
Productivity 0	10,748,900
Productivity 1	14,124,863
Productivity 2	292,061

Raw Data Report

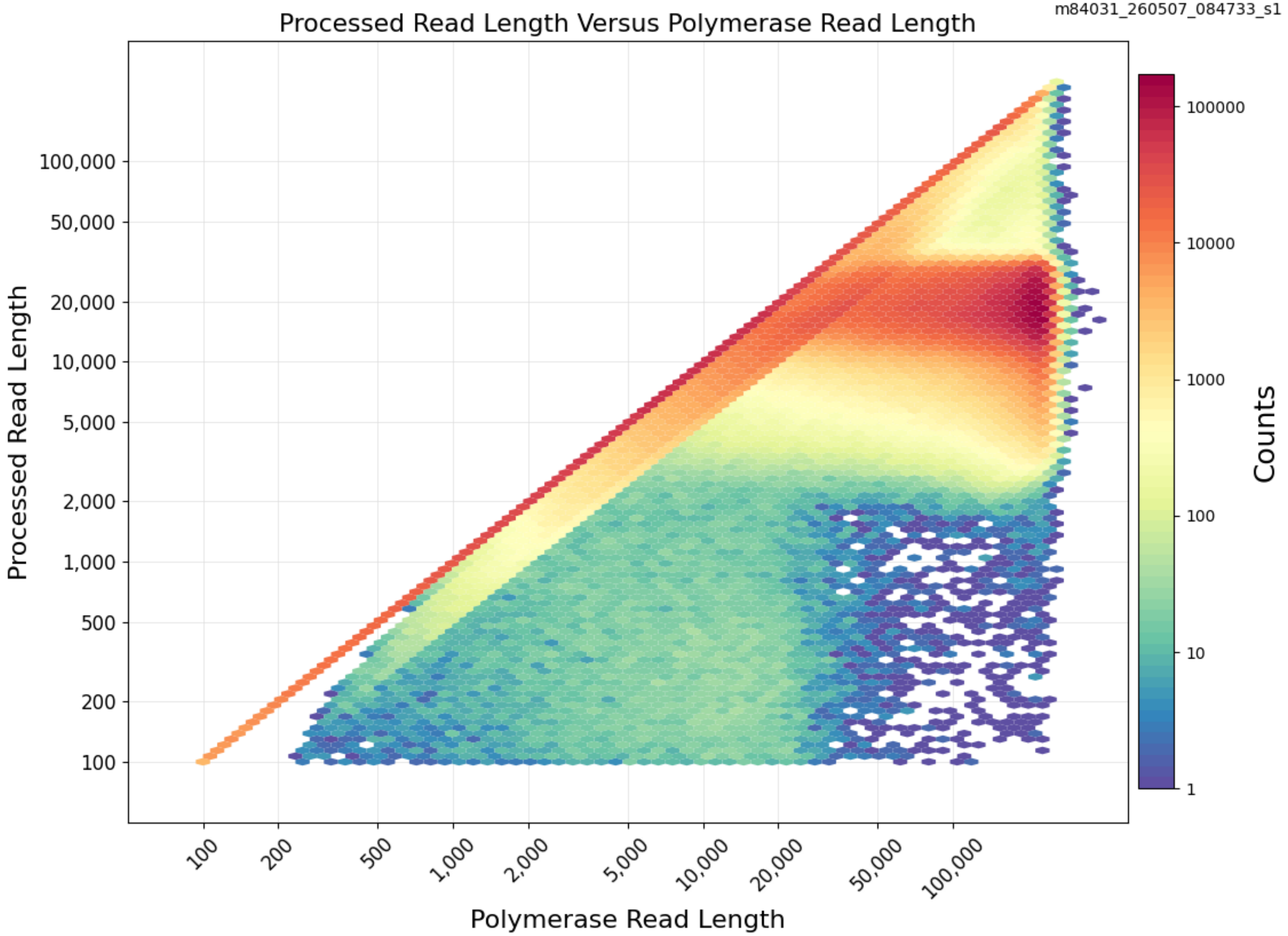
Summary Metrics

Polymerase Read Bases	1,439,666,527,884
Polymerase Reads	14,121,854
Polymerase Read Length (mean)	101.95 kb
Polymerase read length (N50)	187.75 kb
Polymerase read length longest subread length (mean)	19.74 kb
Polymerase read length longest subread length (N50)	22.75 kb
Unique Molecular Yield	266,072,735,744
Local Base Rate	2.57

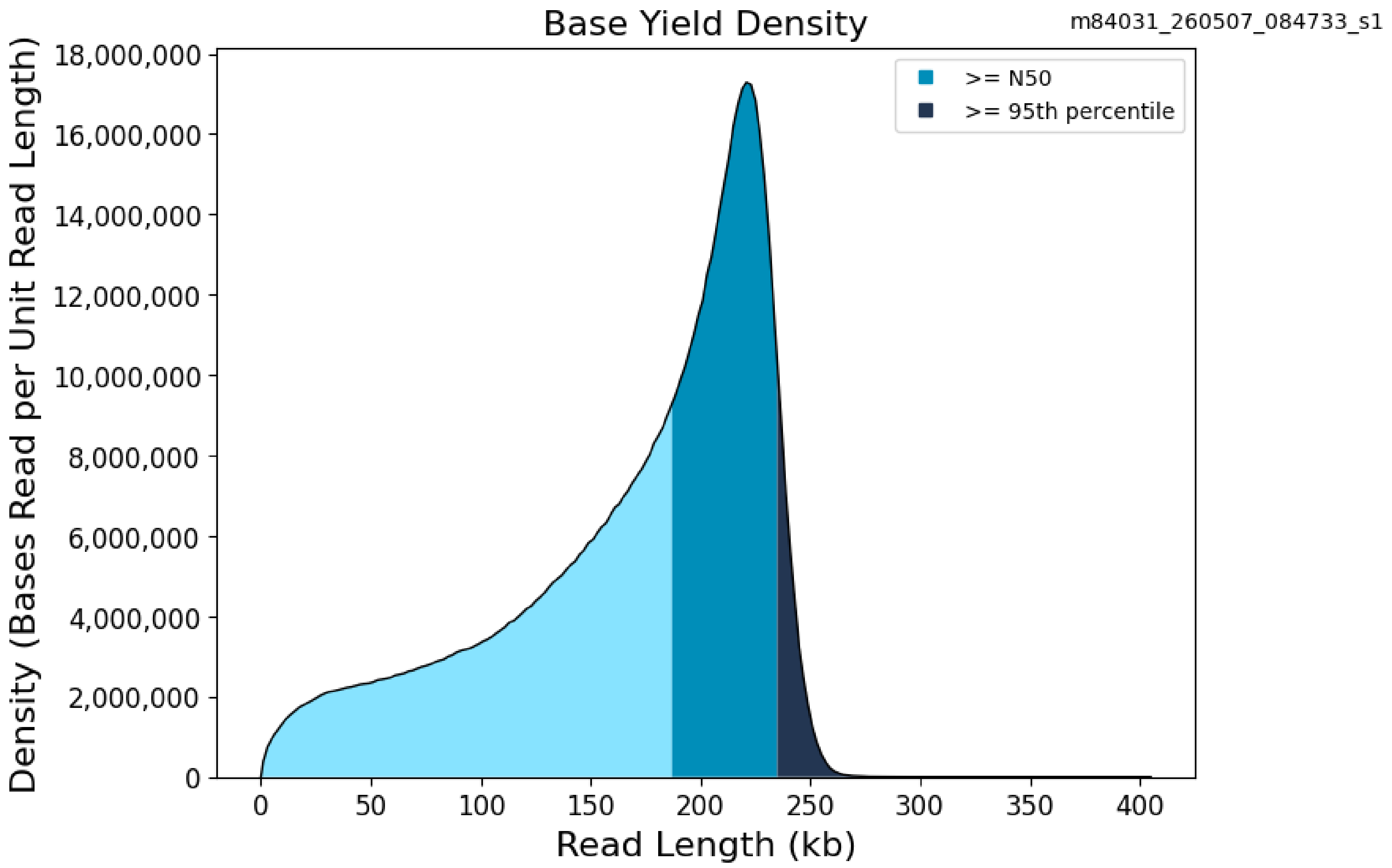
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

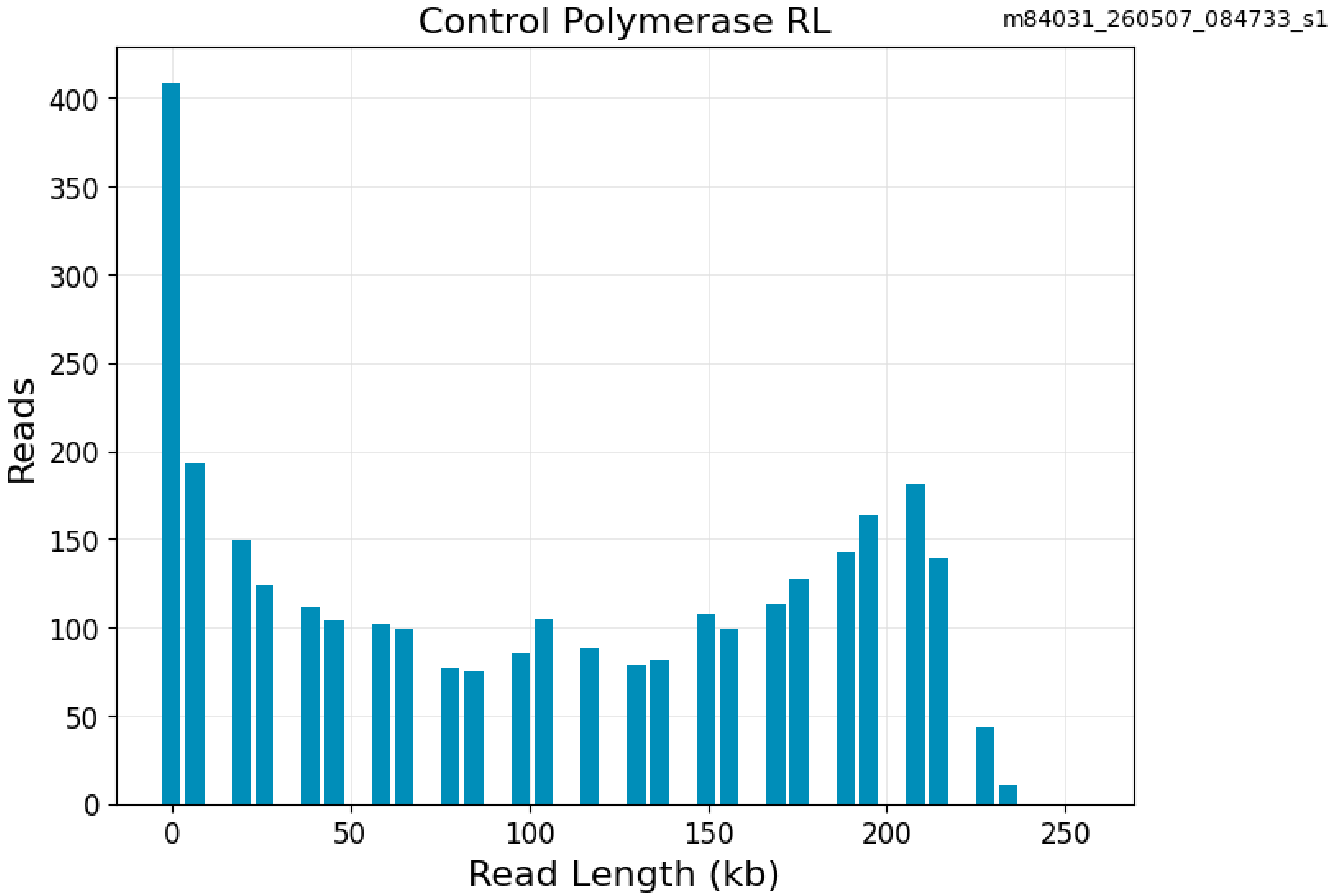


Control Report

Summary Metrics

Number of Control Reads	3,009
Control Read Length Mean	103,943
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance