Report for m84031_260506_033729_s1

Dataset details

Name: Acq14-Cell5 (all samples)

Path: /collections/appslabvast/r84031/r84031_20260504_230217/2_A01/pb_formats/m84031_260506_033729_s1.hifi_reads.consensusreadset.xml

Unique ID: bb760677-ba7e-44bd-8c36-f064bb17bd60

Created at: 2026-05-07T18:54:03.159Z

HiFi sequences: 8,243,356

HiFi bases: 143,715,487,802

Bio sample name: RRV-53

Well sample name: Acq14

Run name: 20260504_RRV_Run03_84031

Movie name: m84031_260506_033729_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	8.3 M
HiFi reads yield	144.19 Gb
HiFi reads length (mean)	17.43 kb
HiFi reads length (median, bp)	17,228
HiFi Read Length N50 (bp)	18,924
HiFi Read Quality (median)	Q35
HiFi Read Quality (median)	35
Base Quality ≥Q30 (%)	95.03%
HiFi Number of Passes (mean)	10
Missing adapters (%)	2.65%

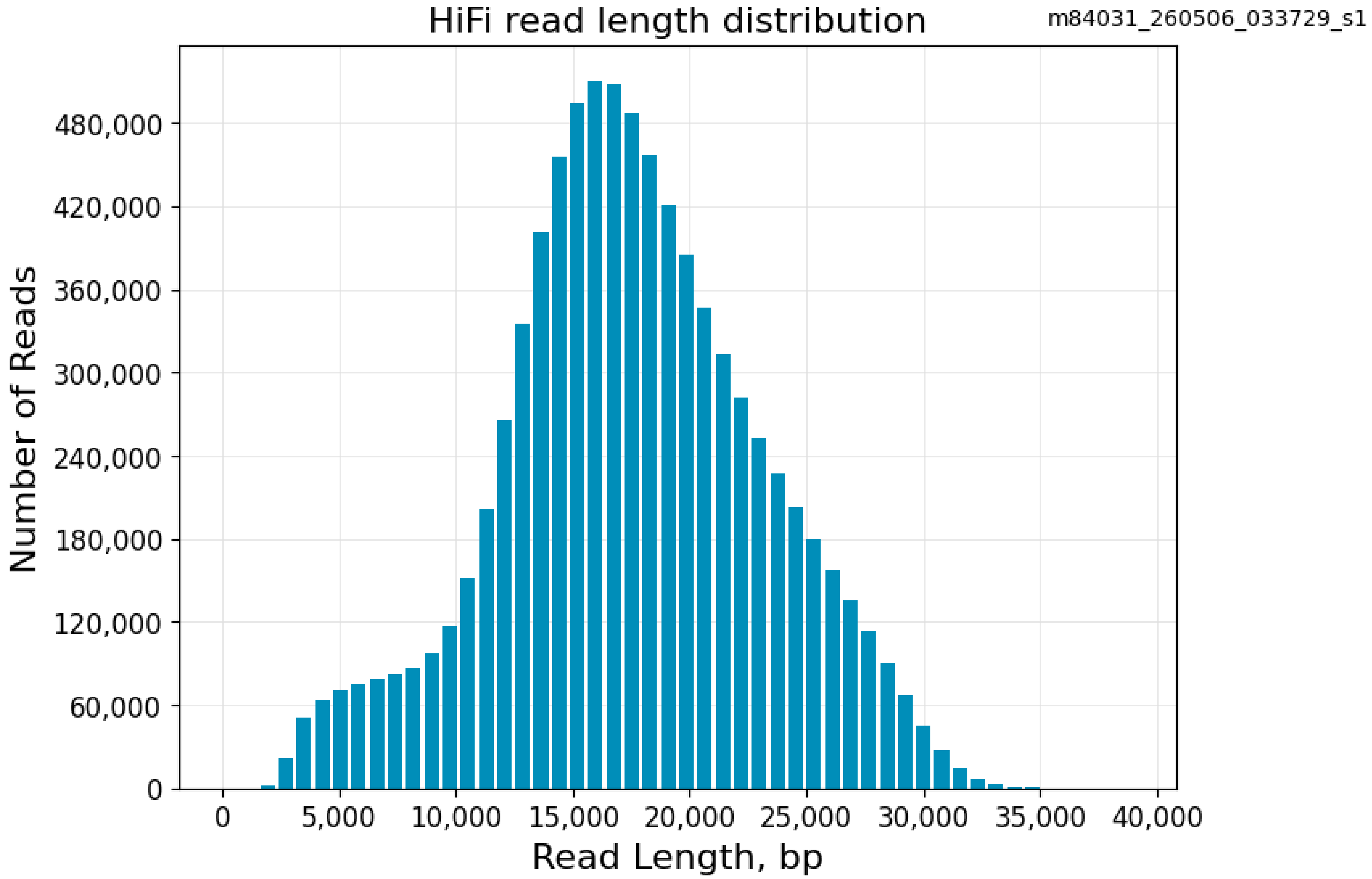
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	8,272,123	100	144.19 Gb	100
≥ 5,000	8,103,232	98	143.53 Gb	100
≥ 10,000	7,544,403	91	139.22 Gb	97
≥ 15,000	5,580,688	67	113.62 Gb	79
≥ 20,000	2,571,530	31	61.32 Gb	43
≥ 25,000	817,049	10	22.34 Gb	15
≥ 30,000	71,477	1	2.22 Gb	2
≥ 35,000	472	0	0.02 Gb	0
≥ 40,000	141	0	0.01 Gb	0

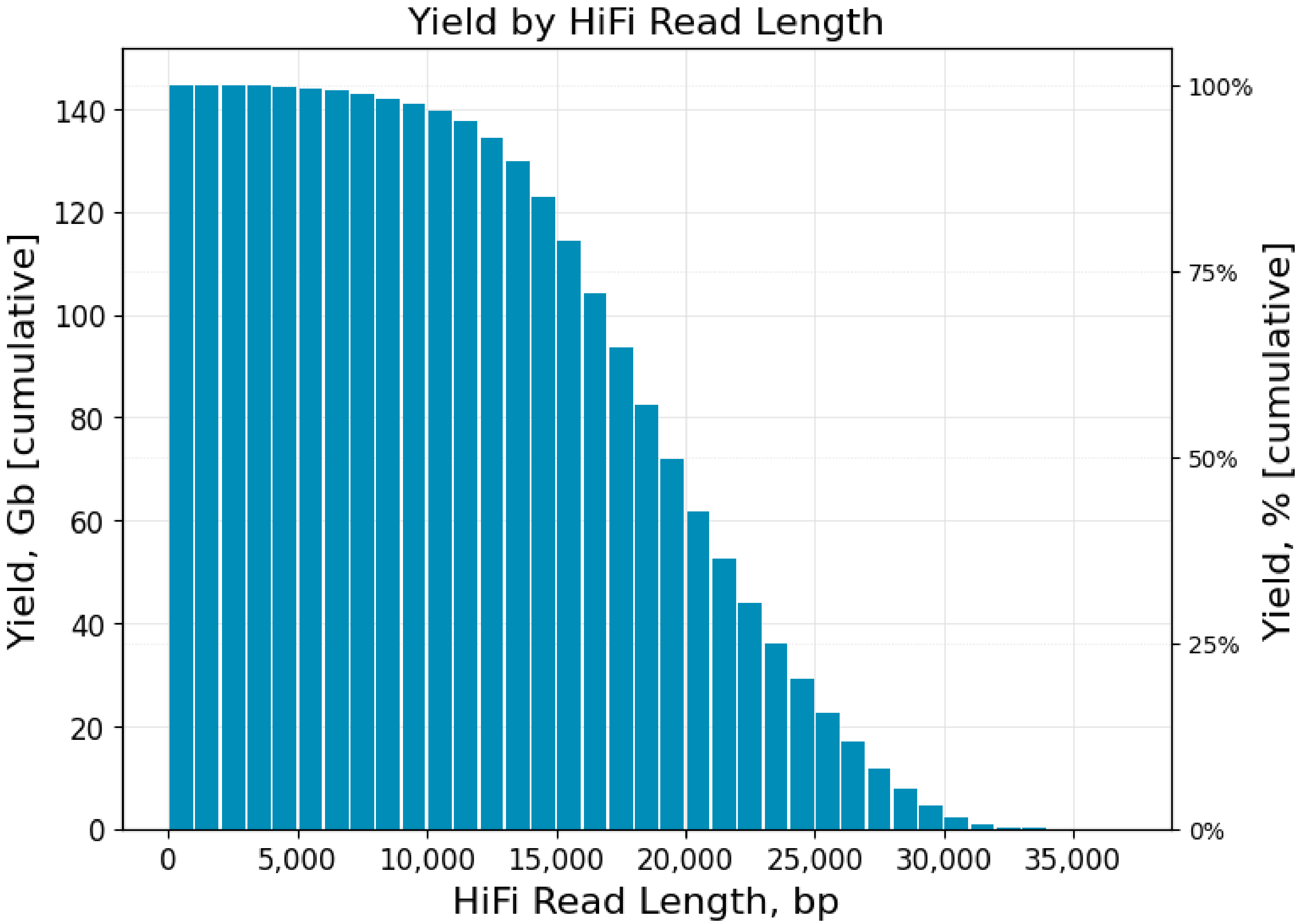
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	8,272,123	100	144.19 Gb	100
≥ Q30	6,040,007	73	101.12 Gb	70
≥ Q40	1,897,793	23	24.01 Gb	17
≥ Q50	381,442	5	3.04 Gb	2

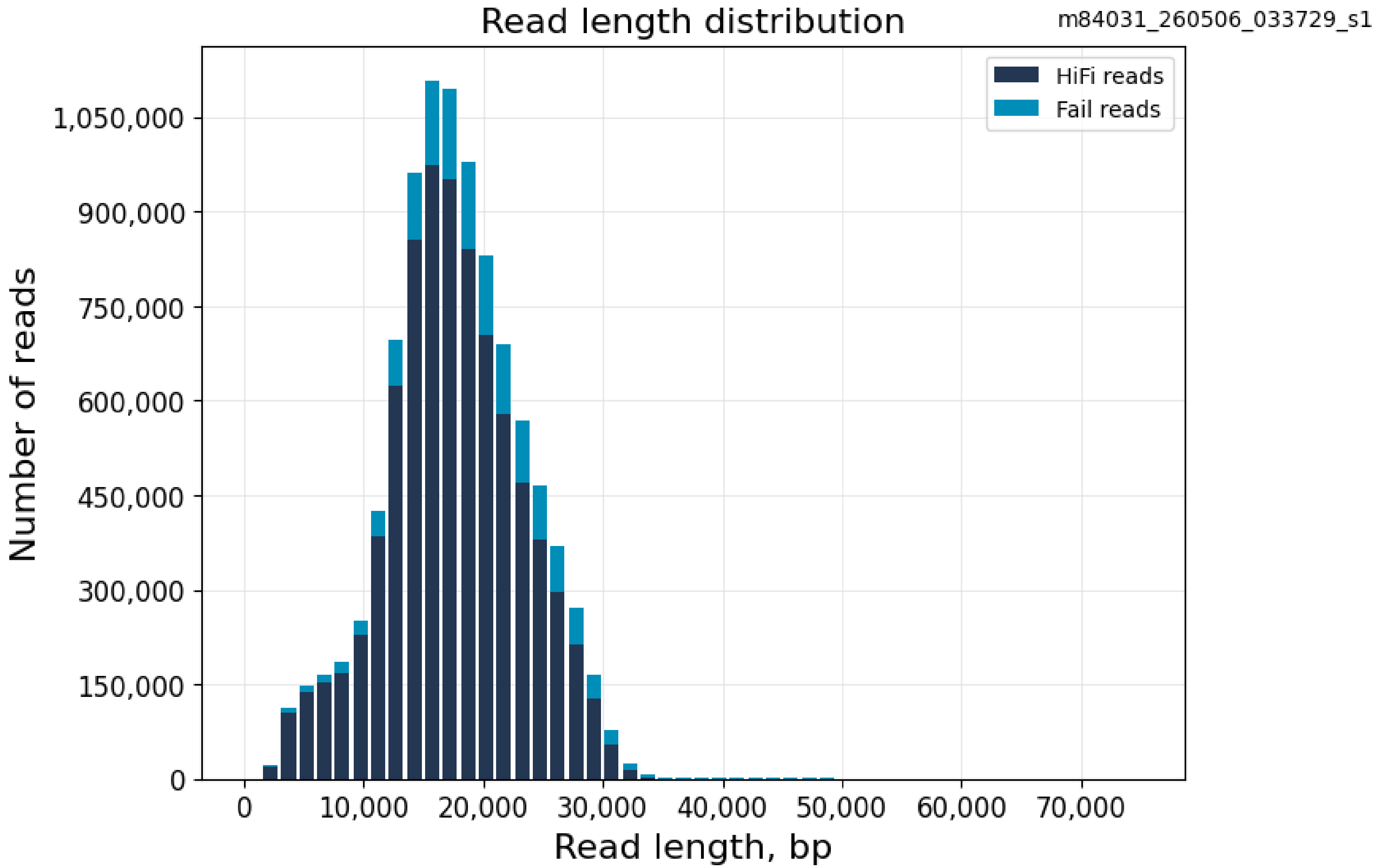
Read Length Distribution: HiFi read length distribution



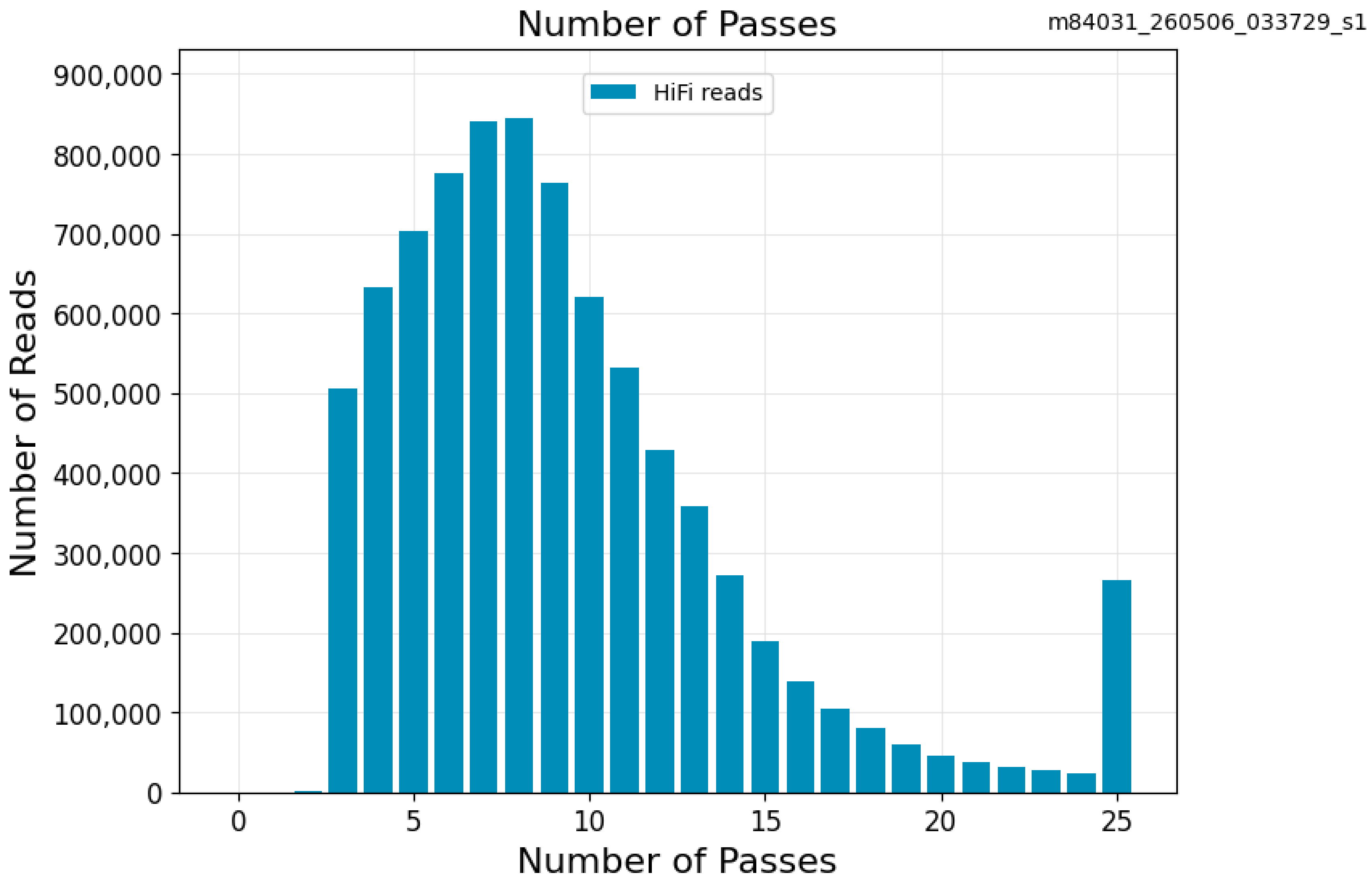
Read Length Distribution: Yield by HiFi Read Length



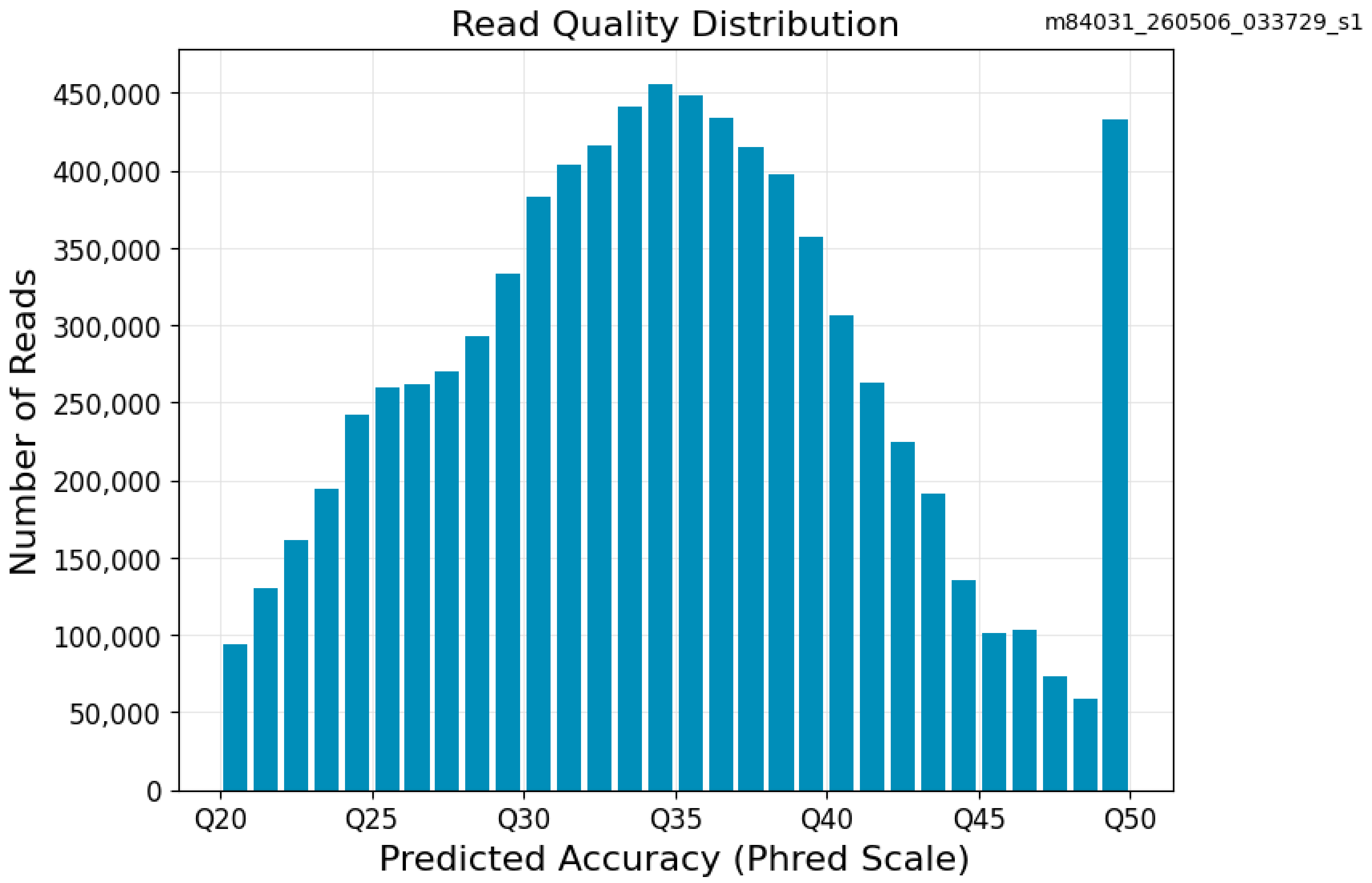
Read Length Distribution: Read length distribution



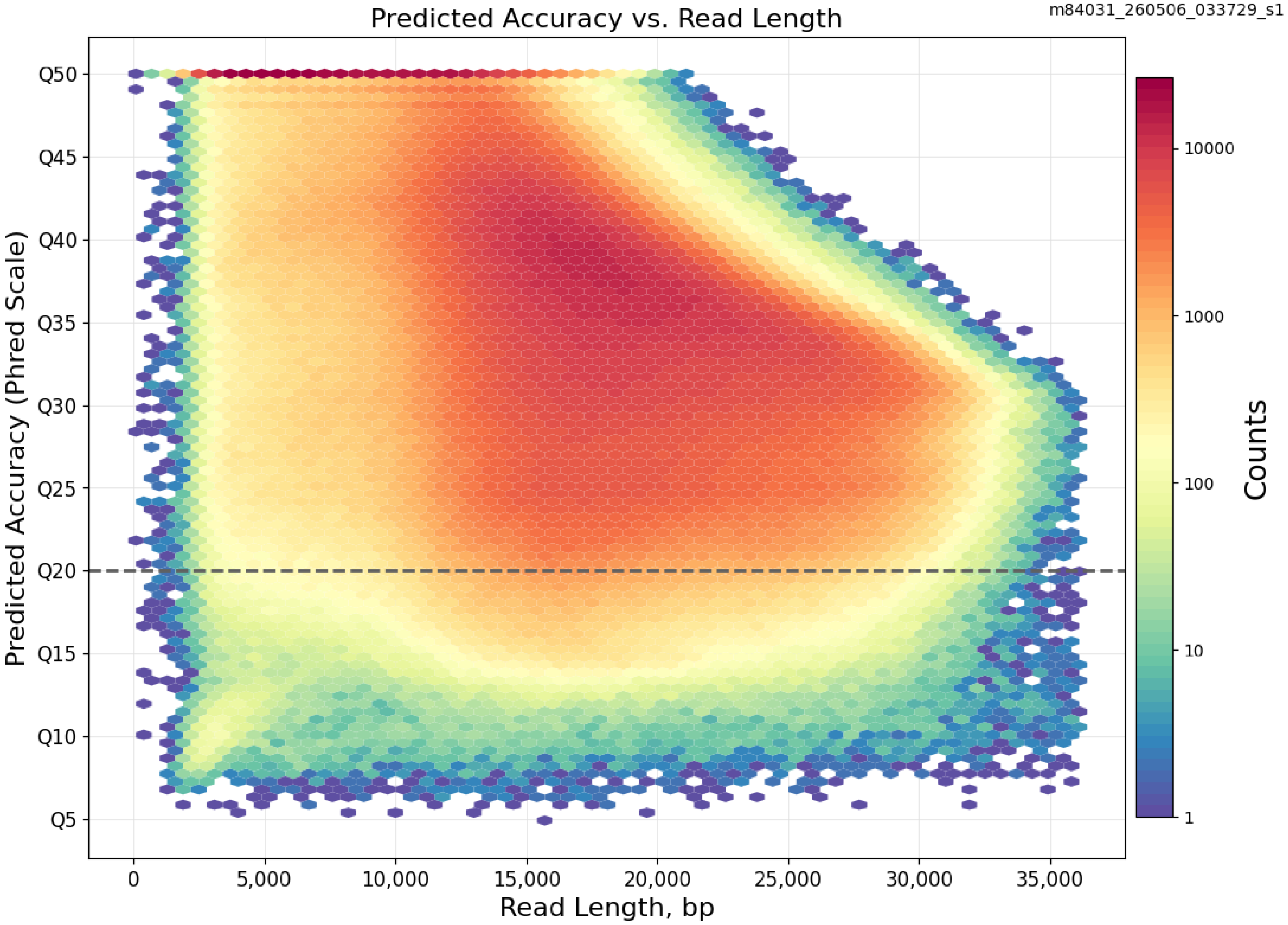
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

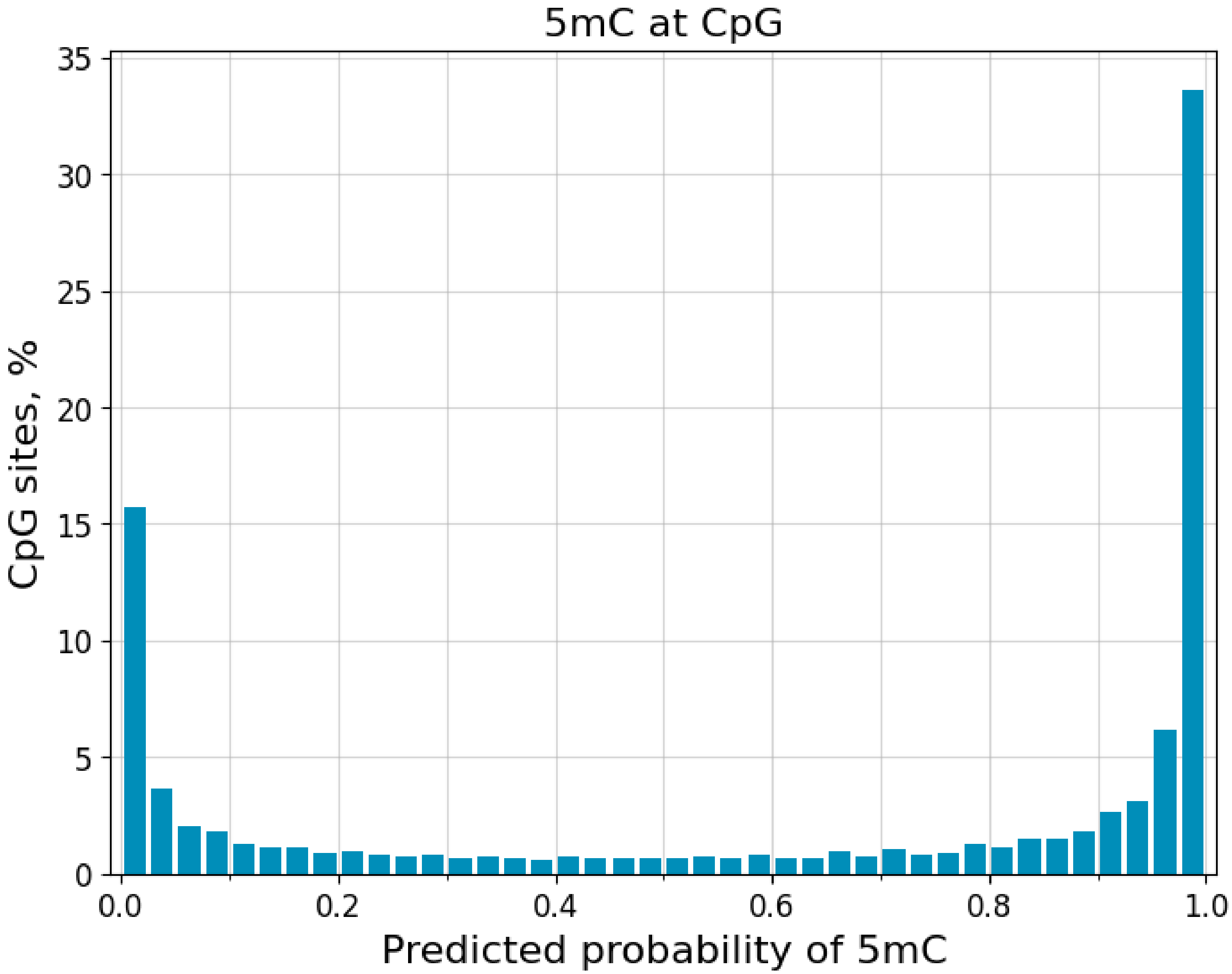


Methylation

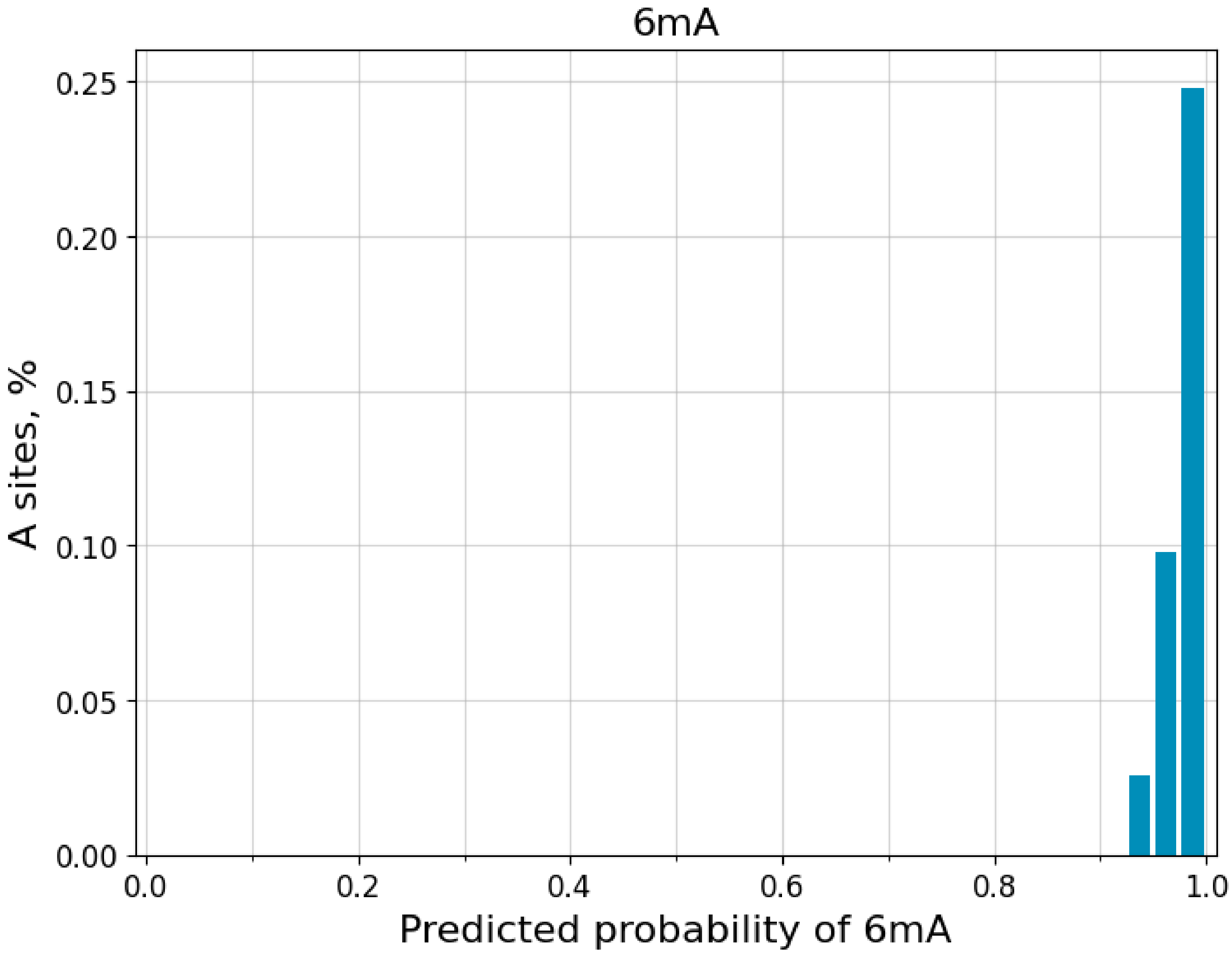
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	97.9%	61.5%
6mA	A	0.4%	0.4%
5hmC	CpG	0.5%	0.5%

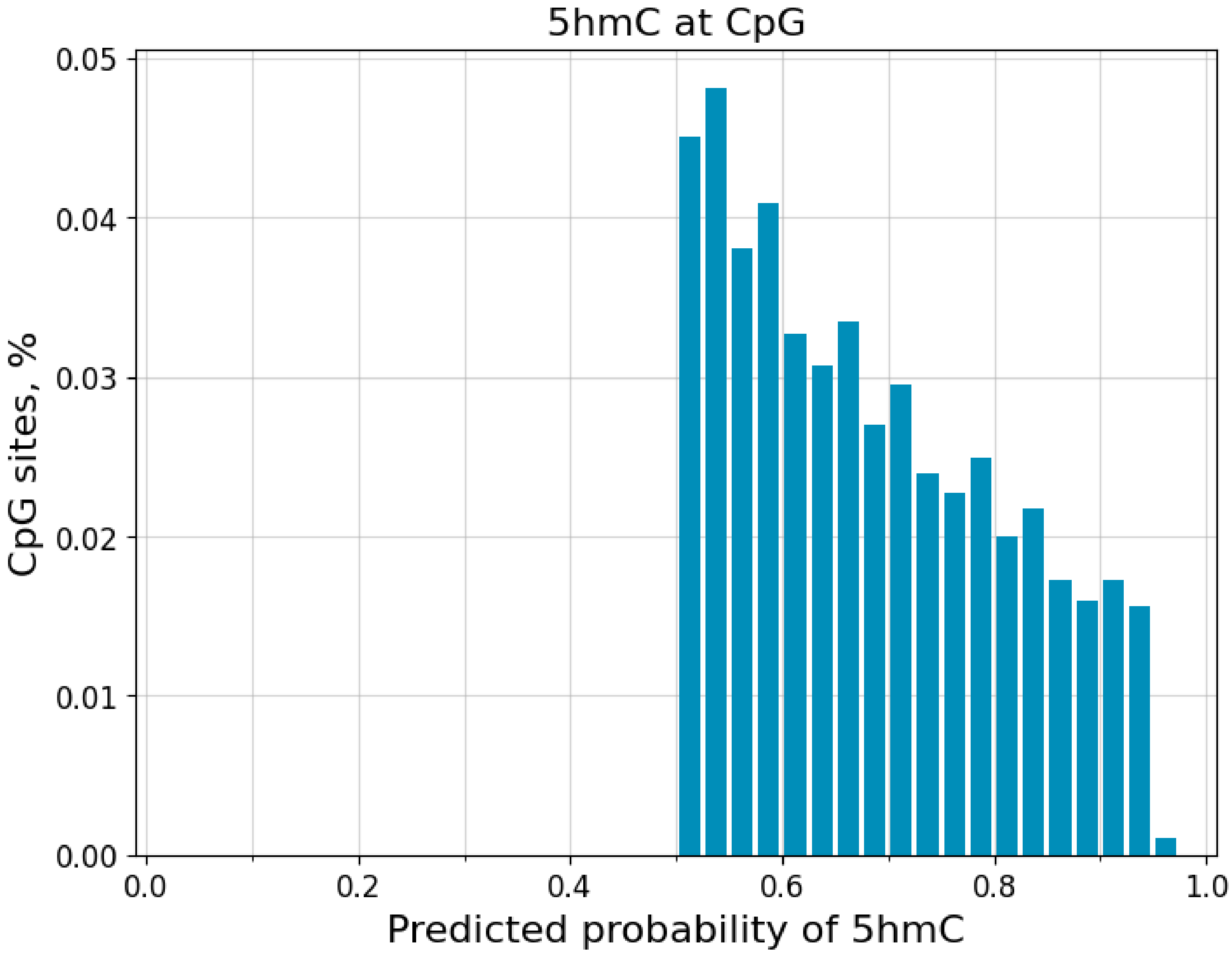
Score distributions: 5mC at CpG



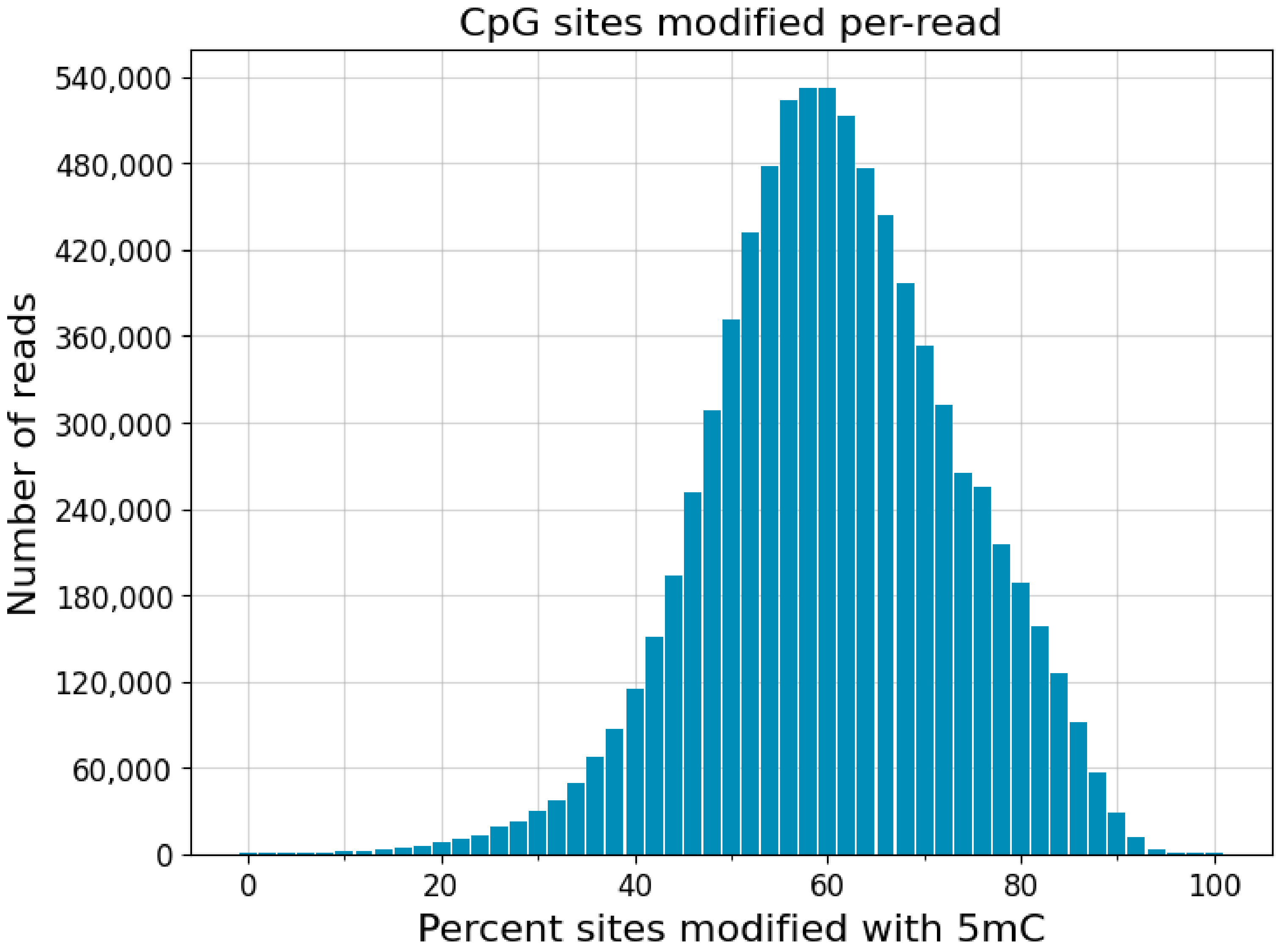
Score distributions: 6mA



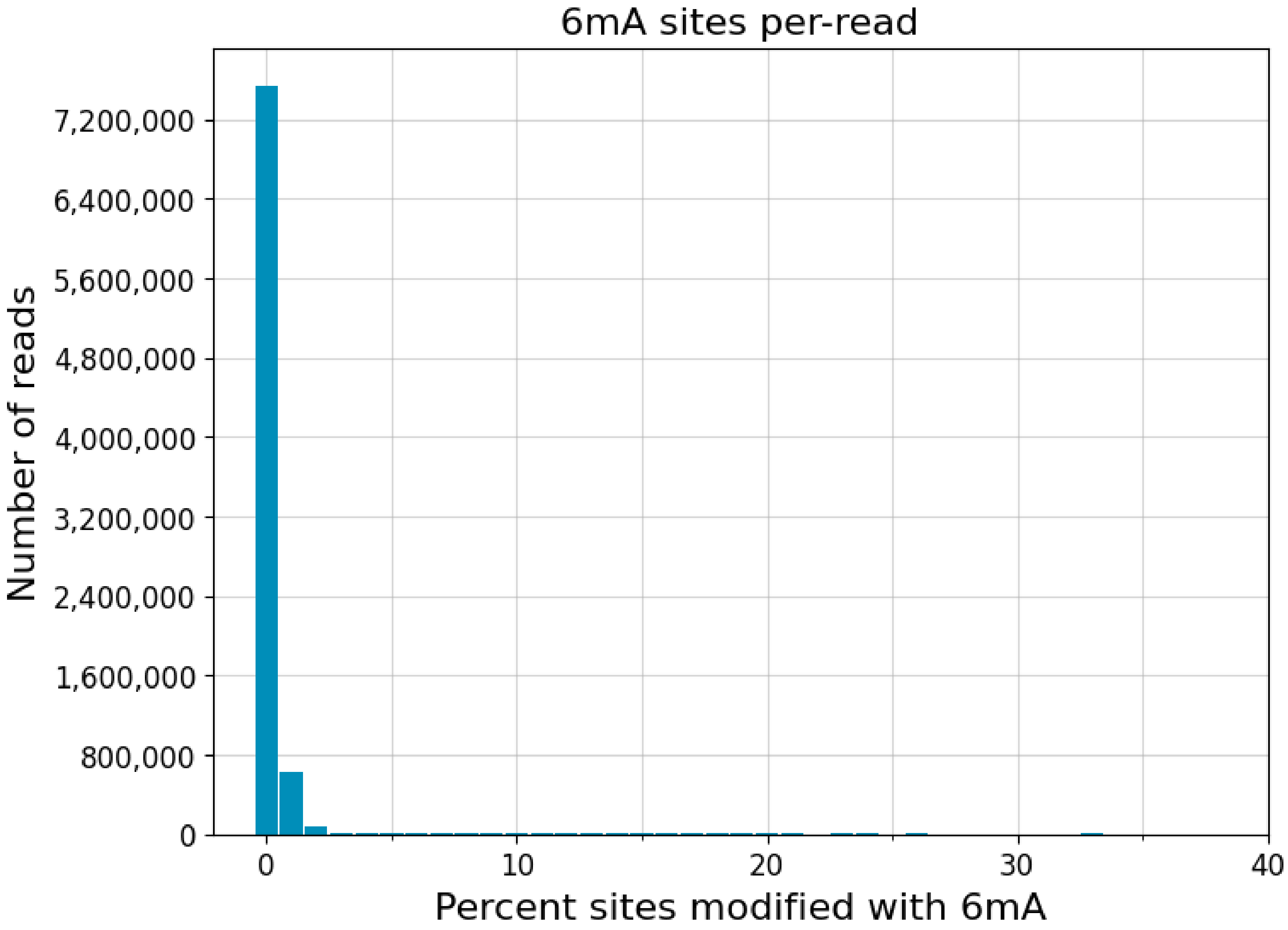
Score distributions: 5hmC at CpG



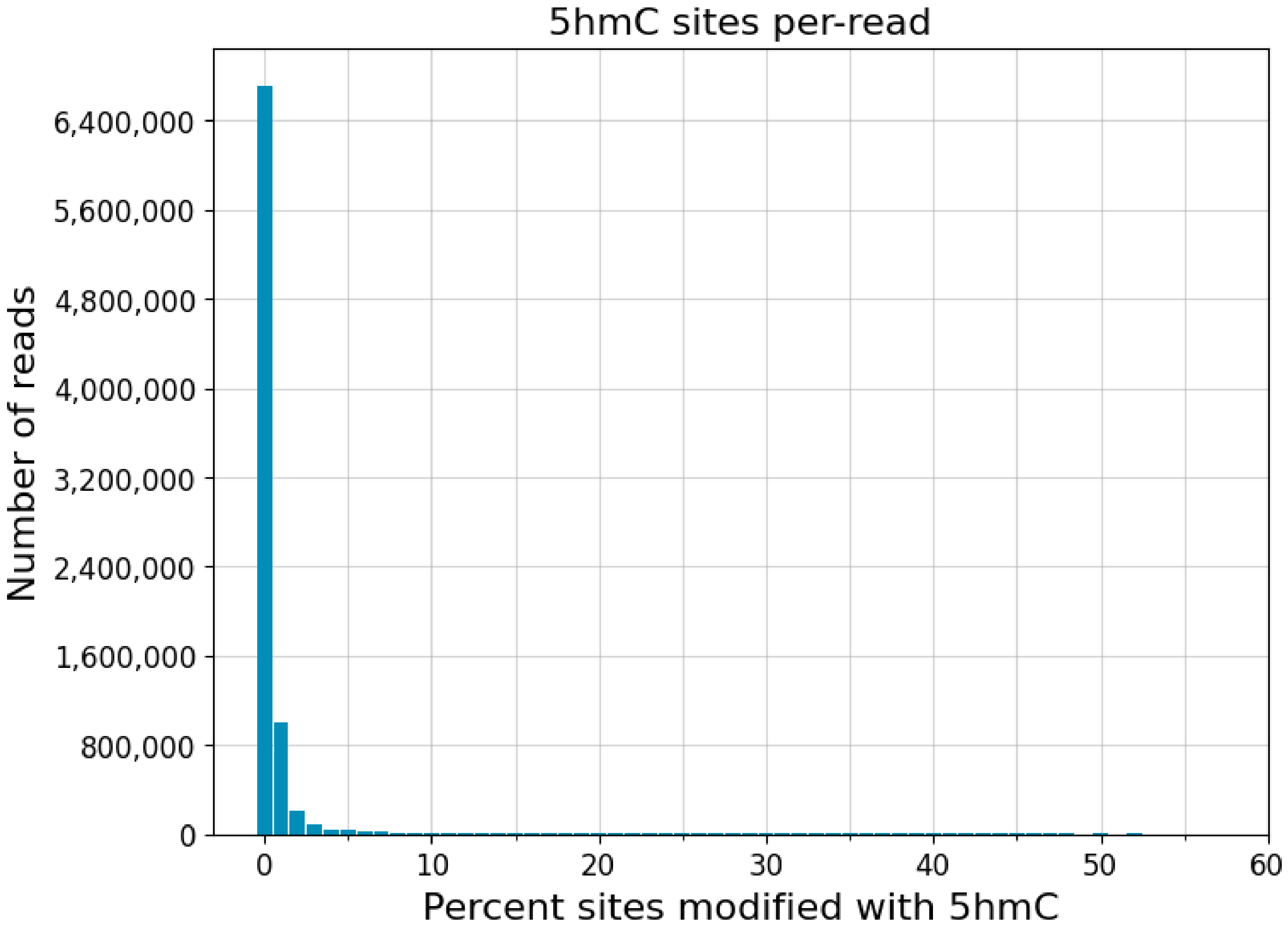
Per-read distributions: CpG sites modified per-read



Per-read distributions: 6mA sites per-read



Per-read distributions: 5hmC sites per-read



Barcodes

Summary Metrics

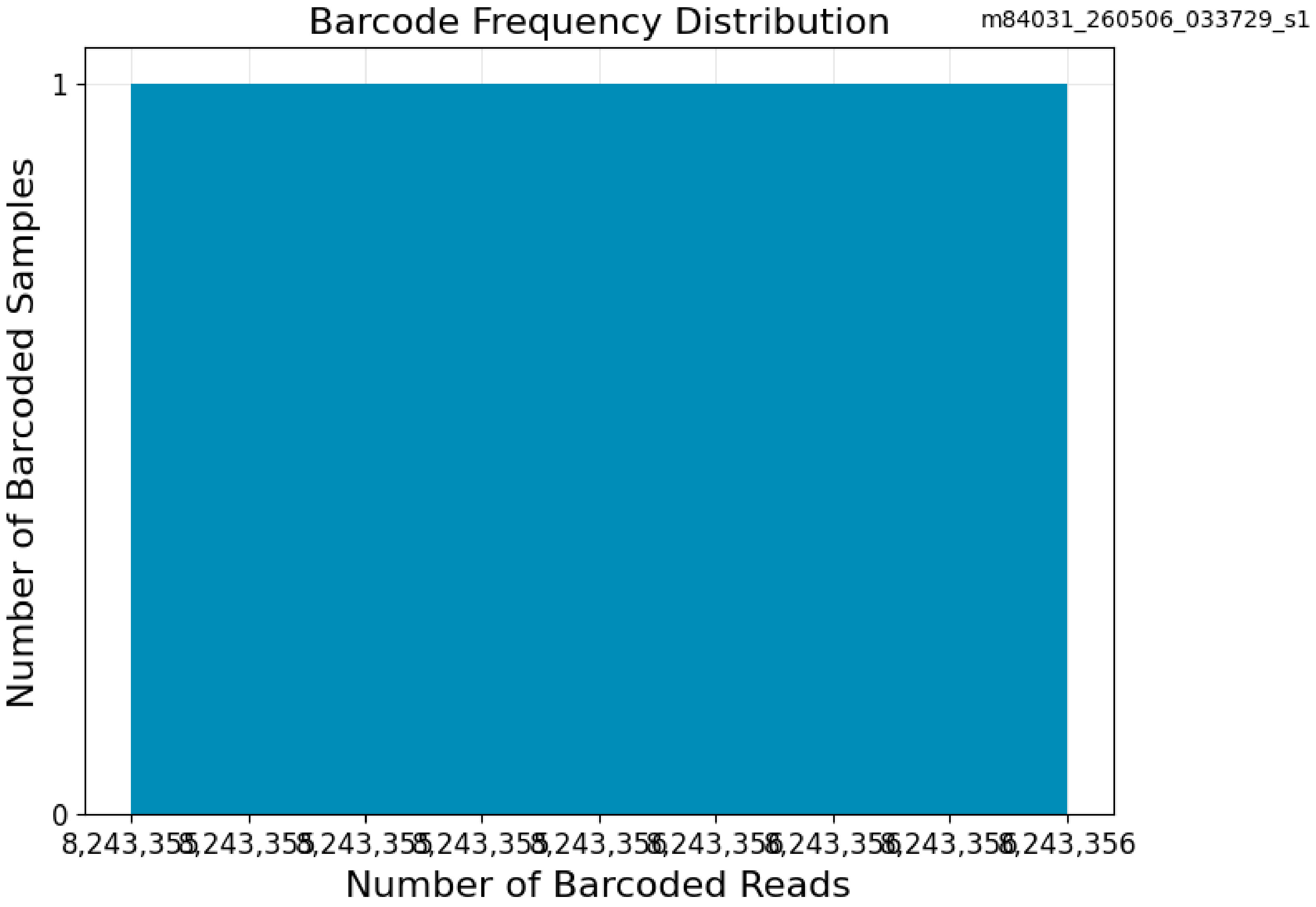
Unique Barcodes	1
Barcoded HiFi Reads	8,243,356
Unbarcoded HiFi Reads	28,767
Barcoded HiFi Reads (%)	99.65 %
Barcoded HiFi yield (Gb)	143.72 Gb
Unbarcoded HiFi yield (Gb)	0.47 Gb
Barcoded HiFi Yield (%)	99.67 %
Mean HiFi Reads per Barcode	8,243,356
Max. HiFi Reads per Barcode	8,243,356
Min. HiFi Reads per Barcode	8,243,356
Barcoded HiFi read length (mean, kb)	17.43 kb
Unbarcoded HiFi read length (mean, kb)	16.46 kb

Barcode Data

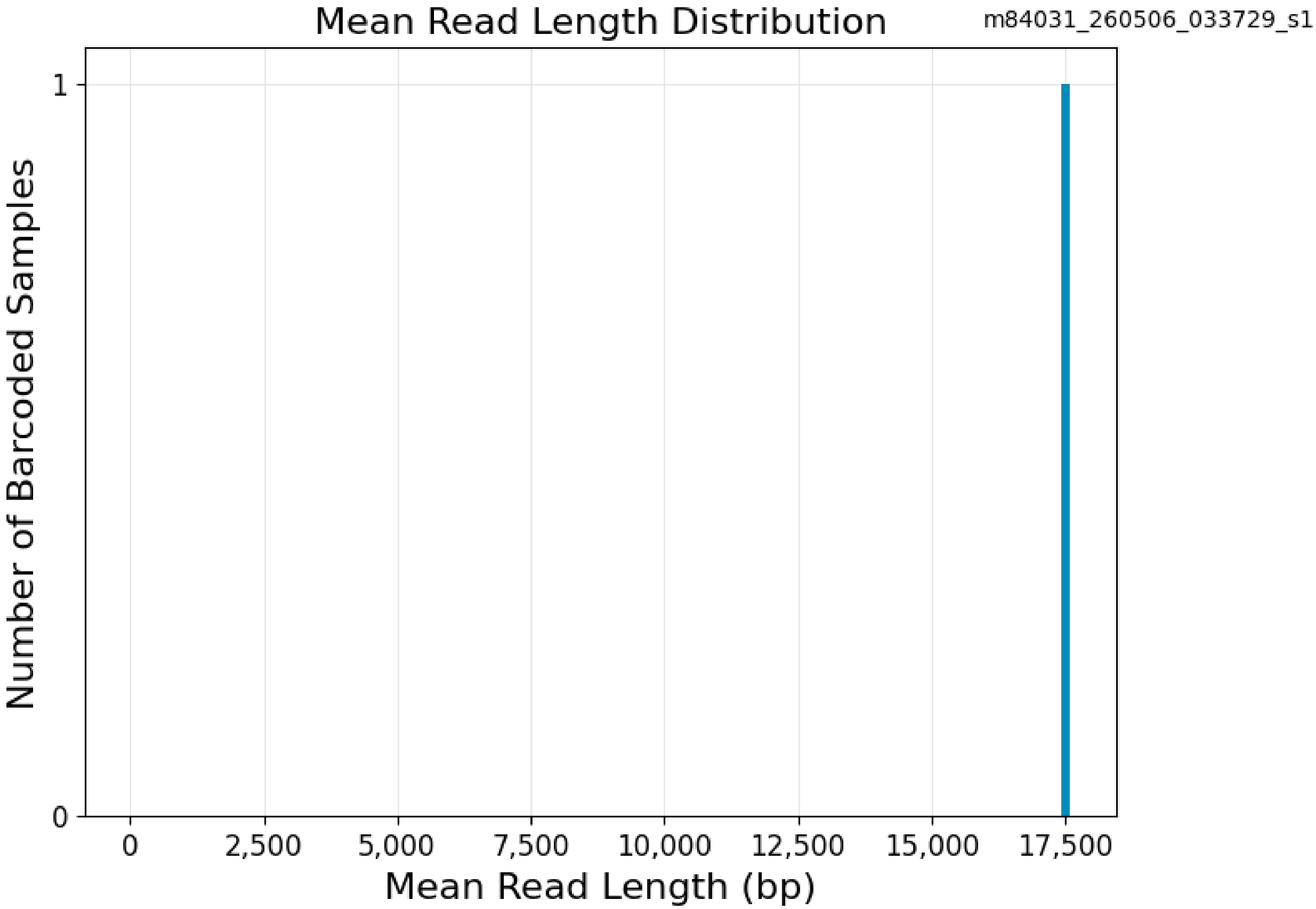
Sample Name	Barcode	Barcode Quality	HiFi Reads	HiFi Read Length (mean, bp)	HiFi Read Quality (median, QV)	HiFi Yield (bp)	Polymerase Read Length (mean, bp)
RRV-53	bc2003--bc2003	97.7	8,243,356	17,434	Q35	143,715,487,802	165,831
No Name	Not Barcoded	0.0	28,767	16,461	Q26	473,537,639	146,381

Barcoded Read Statistics: Number Of Reads Per Barcode

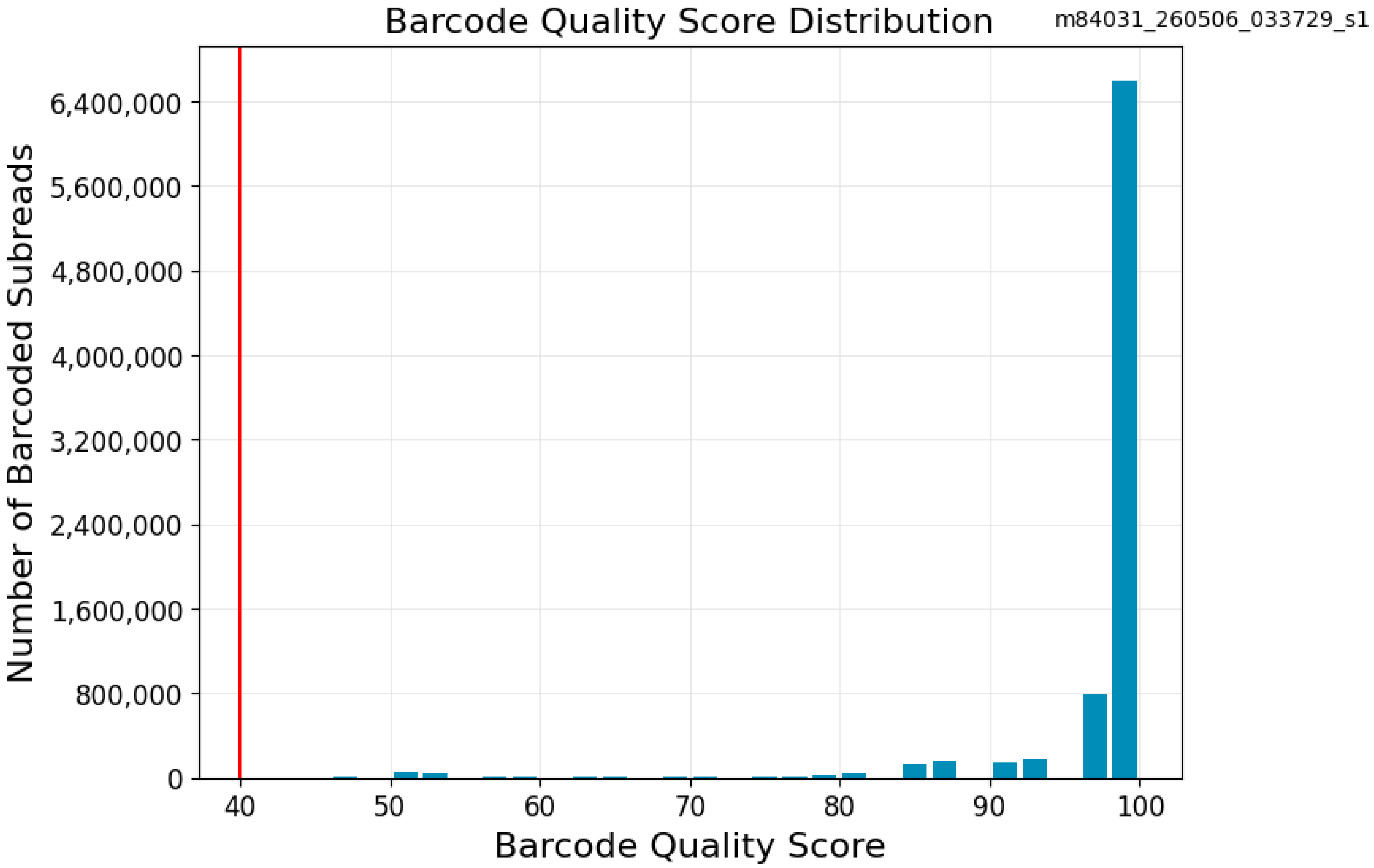
Barcoded Read Statistics: Barcode Frequency Distribution



Barcoded Read Statistics: Mean Read Length Distribution



Barcode Quality Scores: Barcode Quality Score Distribution



Loading Report

Summary Metrics

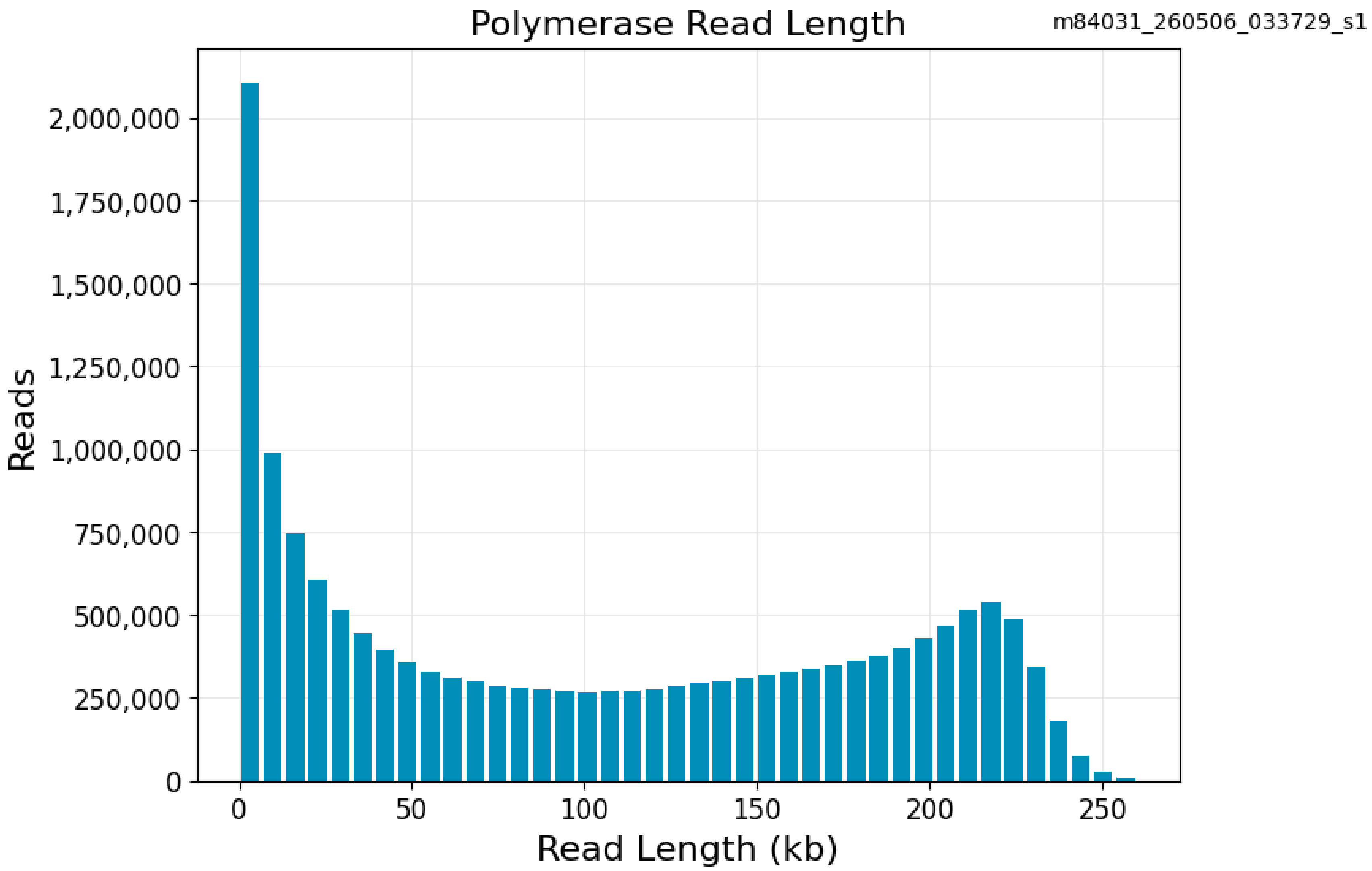
Productive ZMWs	25,165,824
Productivity 0	8,850,220
Productivity 1	16,040,349
Productivity 2	275,255

Raw Data Report

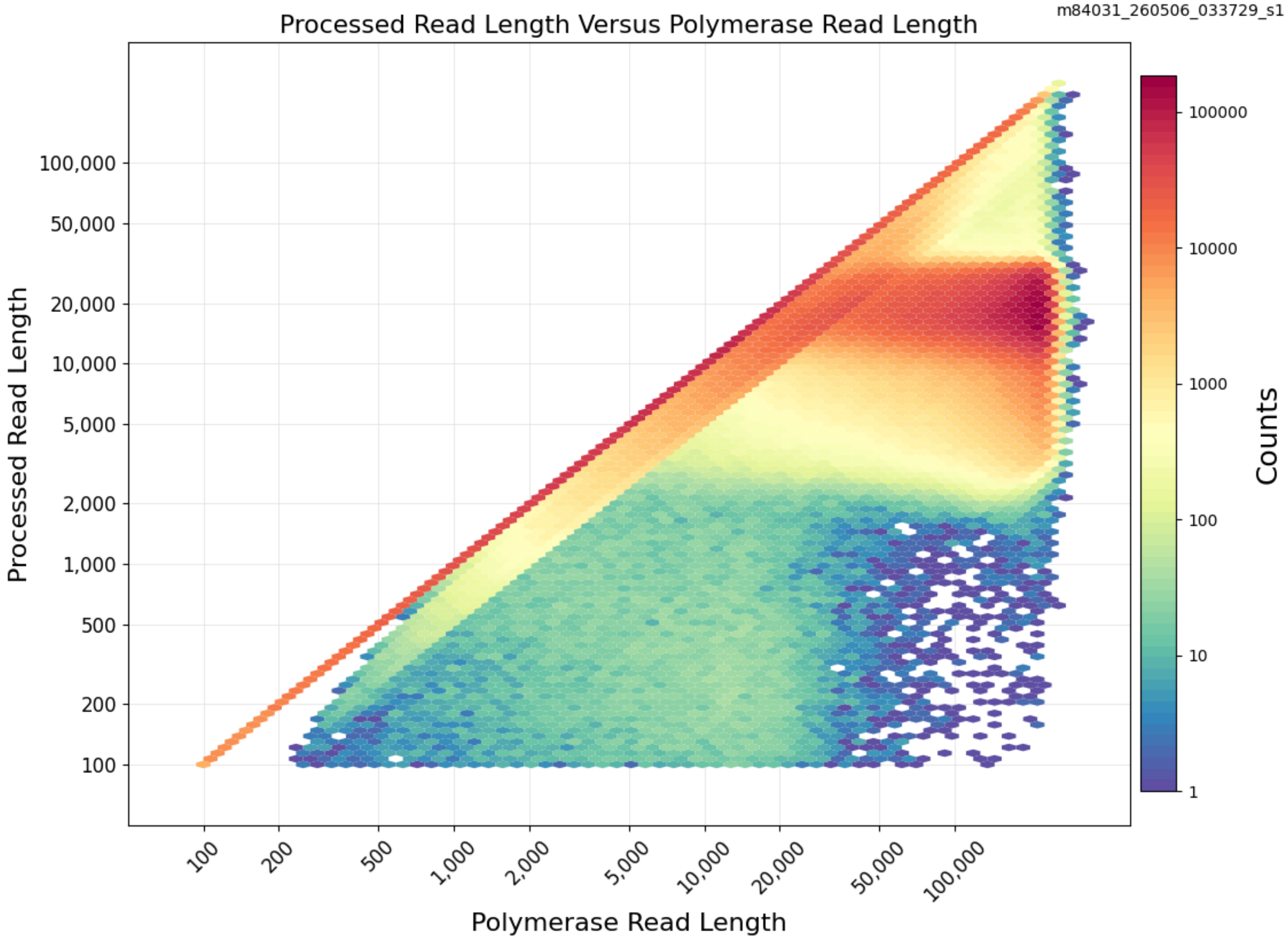
Summary Metrics

Polymerase Read Bases	1,606,762,478,082
Polymerase Reads	16,036,674
Polymerase Read Length (mean)	100.19 kb
Polymerase read length (N50)	181.25 kb
Polymerase read length longest subread length (mean)	18.92 kb
Polymerase read length longest subread length (N50)	22.25 kb
Unique Molecular Yield	288,434,946,048
Local Base Rate	2.54

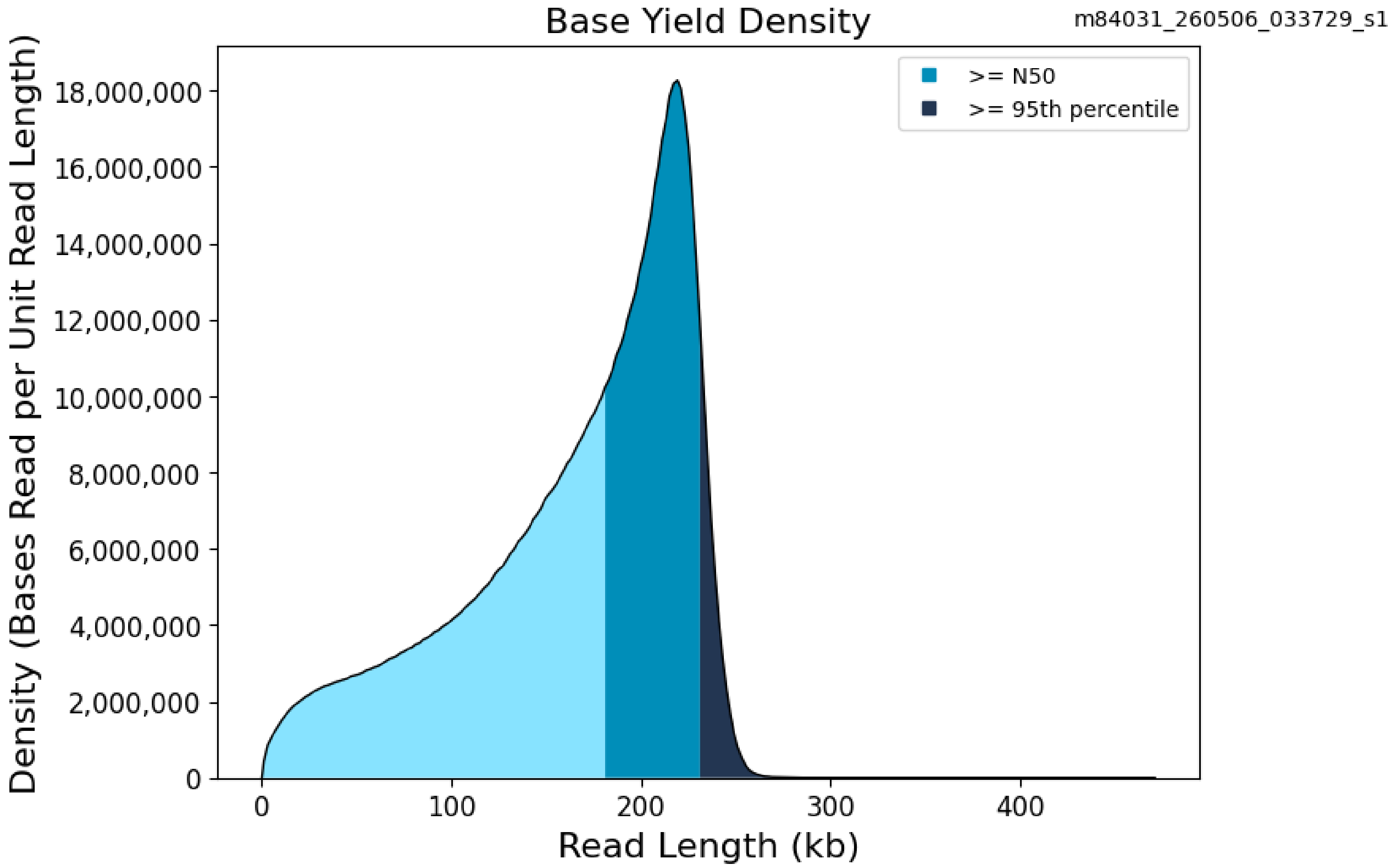
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

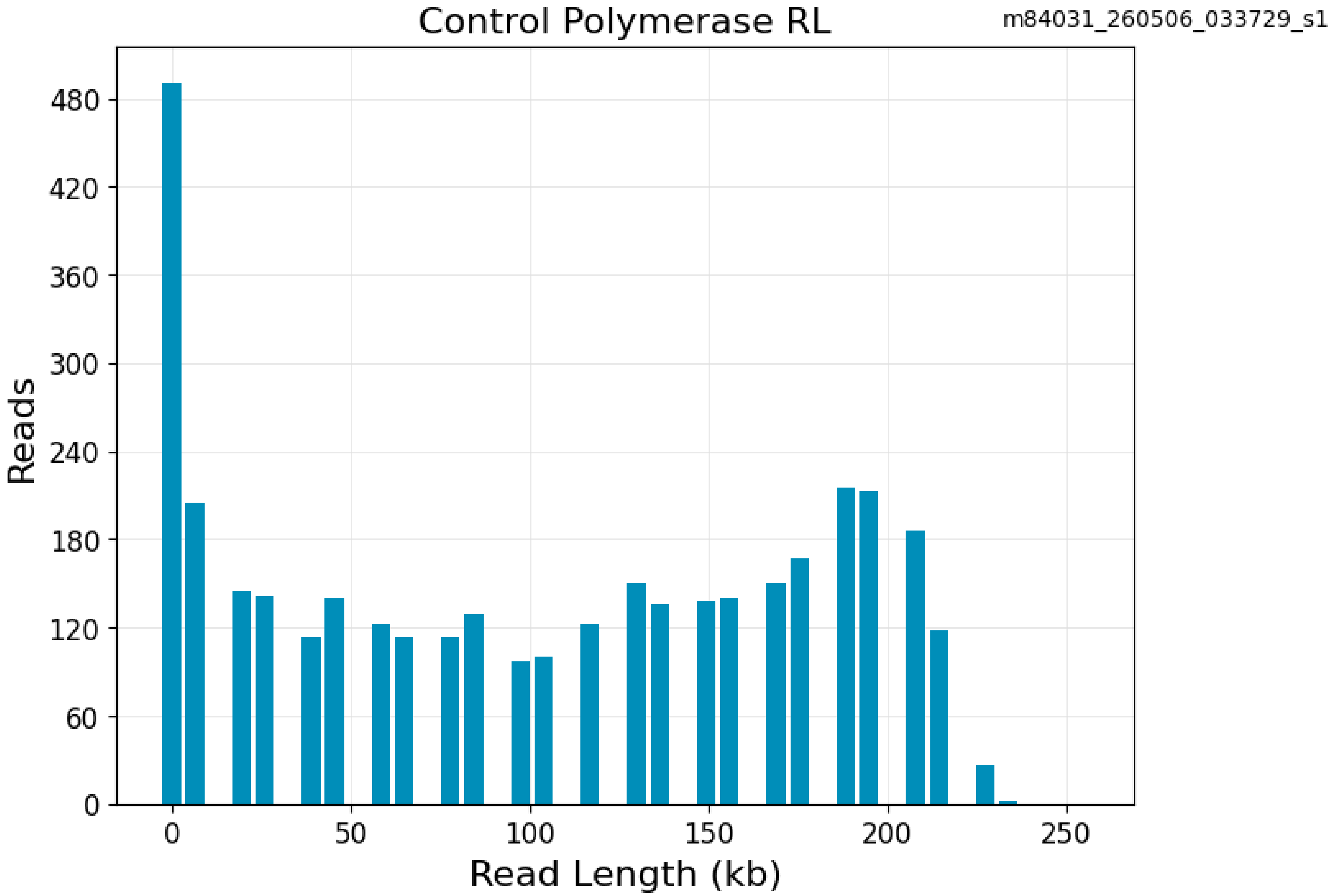


Control Report

Summary Metrics

Number of Control Reads	3,675
Control Read Length Mean	104,988
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance