Report for m84031_260504_231011_s1

Dataset details

Name: Acq13-Cell1 (all samples)

Path: /collections/appslabvast/r84031/r84031_20260504_230217/1_A01/pb_formats/m84031_260504_231011_s1.hifi_reads.consensusreadset.xml

Unique ID: 3bd380ef-b6bc-4bc7-87c9-819f8c0fc430

Created at: 2026-05-06T13:46:53.814Z

HiFi sequences: 8,907,432

HiFi bases: 144,621,006,554

Bio sample name: RRV-52

Well sample name: Acq13

Run name: 20260504_RRV_Run03_84031

Movie name: m84031_260504_231011_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	8.9 M
HiFi reads yield	145.00 Gb
HiFi reads length (mean)	16.23 kb
HiFi reads length (median, bp)	16,092
HiFi Read Length N50 (bp)	17,752
HiFi Read Quality (median)	Q34
HiFi Read Quality (median)	34
Base Quality ≥Q30 (%)	94.21%
HiFi Number of Passes (mean)	9
Missing adapters (%)	2.81%

HiFi Read Length Summary

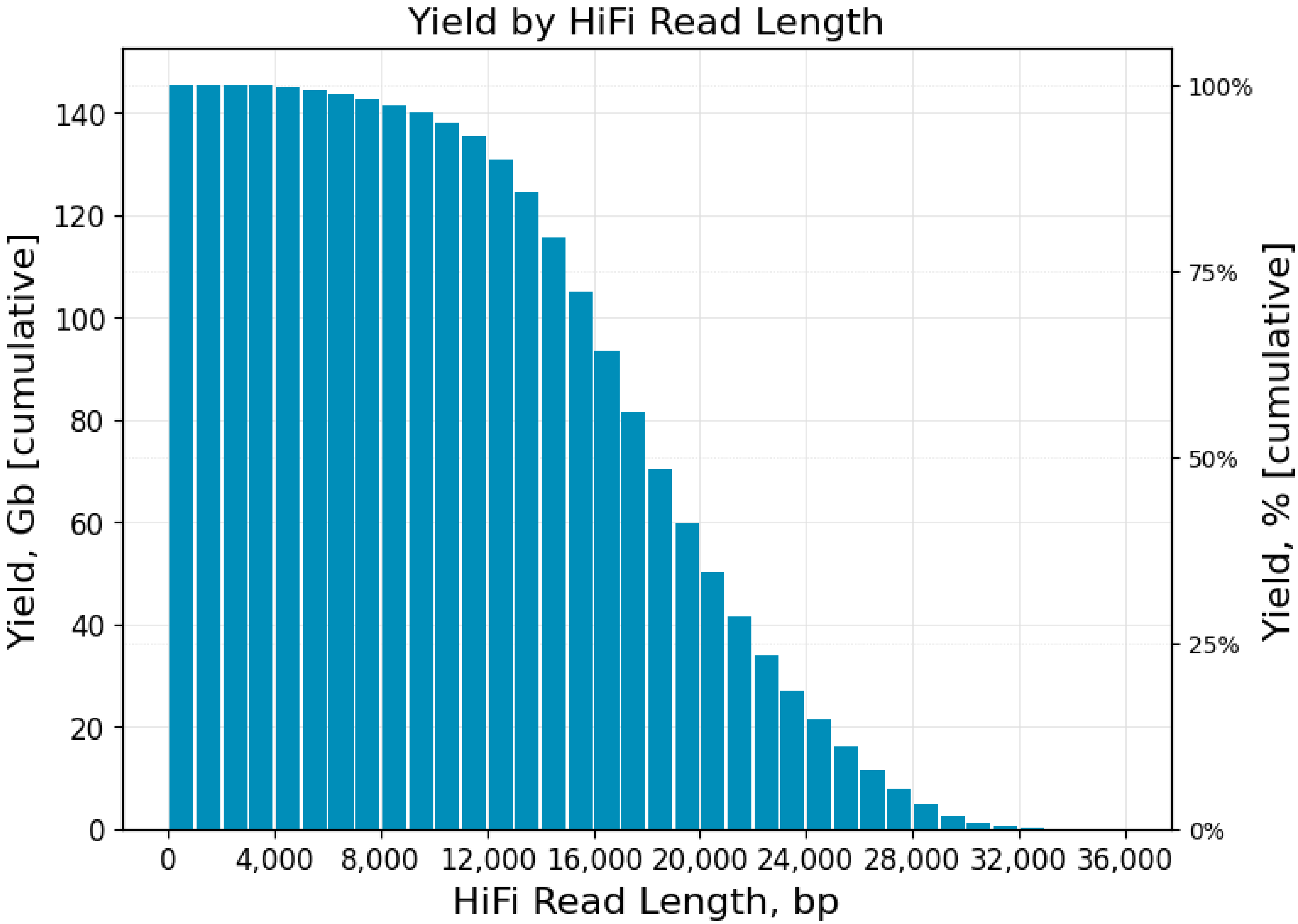
Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	8,931,824	100	145.00 Gb	100
≥ 5,000	8,651,999	97	143.91 Gb	99
≥ 10,000	7,844,156	88	137.73 Gb	95
≥ 15,000	5,280,373	59	104.47 Gb	72
≥ 20,000	2,111,715	24	49.70 Gb	34
≥ 25,000	583,255	7	15.85 Gb	11
≥ 30,000	40,221	0	1.25 Gb	1
≥ 35,000	317	0	0.01 Gb	0
≥ 40,000	96	0	0.00 Gb	0

HiFi Read Quality Summary

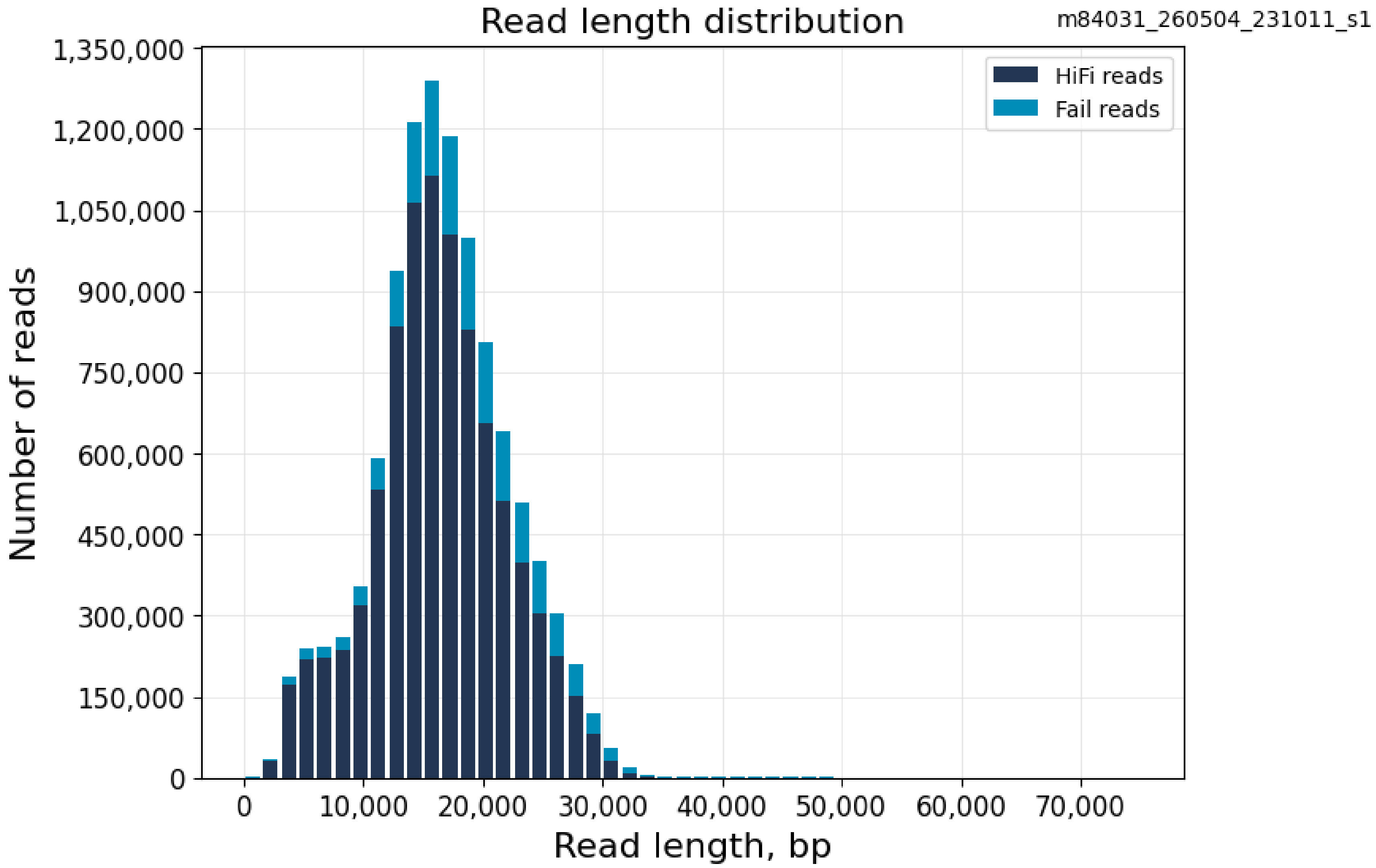
Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	8,931,824	100	145.00 Gb	100
≥ Q30	6,122,408	69	93.34 Gb	64
≥ Q40	1,779,286	20	19.64 Gb	14
≥ Q50	412,567	5	2.79 Gb	2

Read Length Distribution: HiFi read length distribution

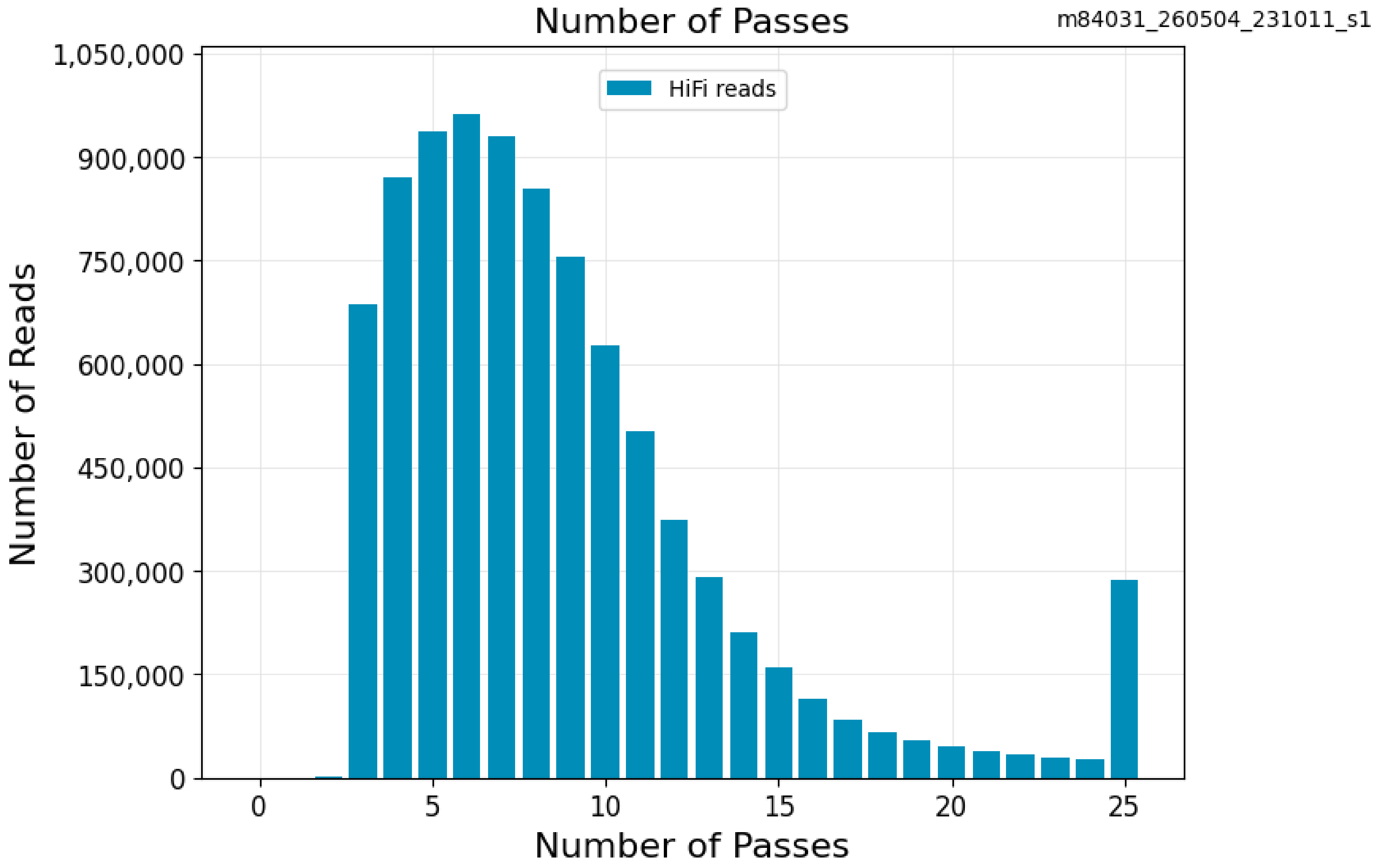
Read Length Distribution: Yield by HiFi Read Length



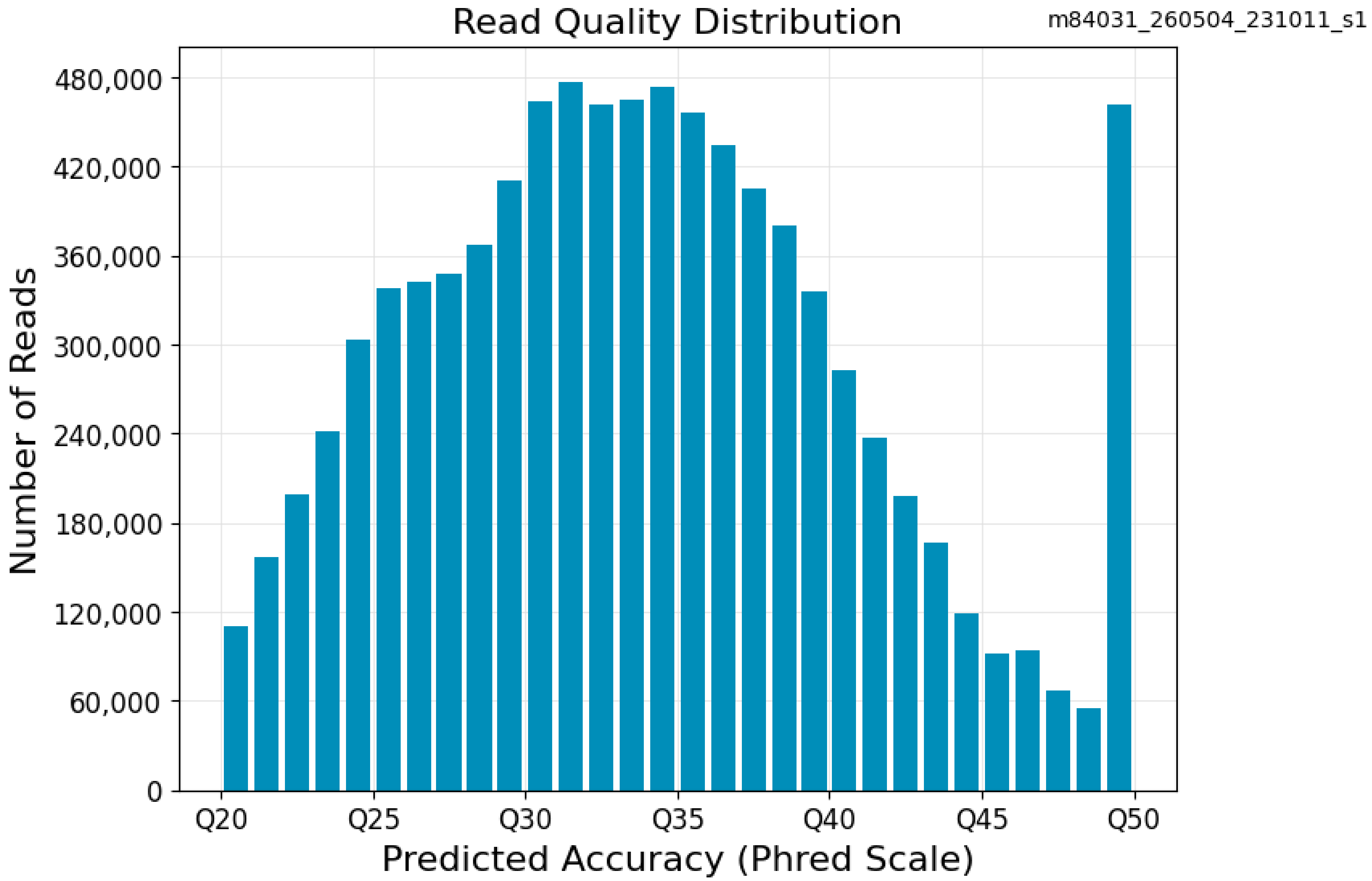
Read Length Distribution: Read length distribution



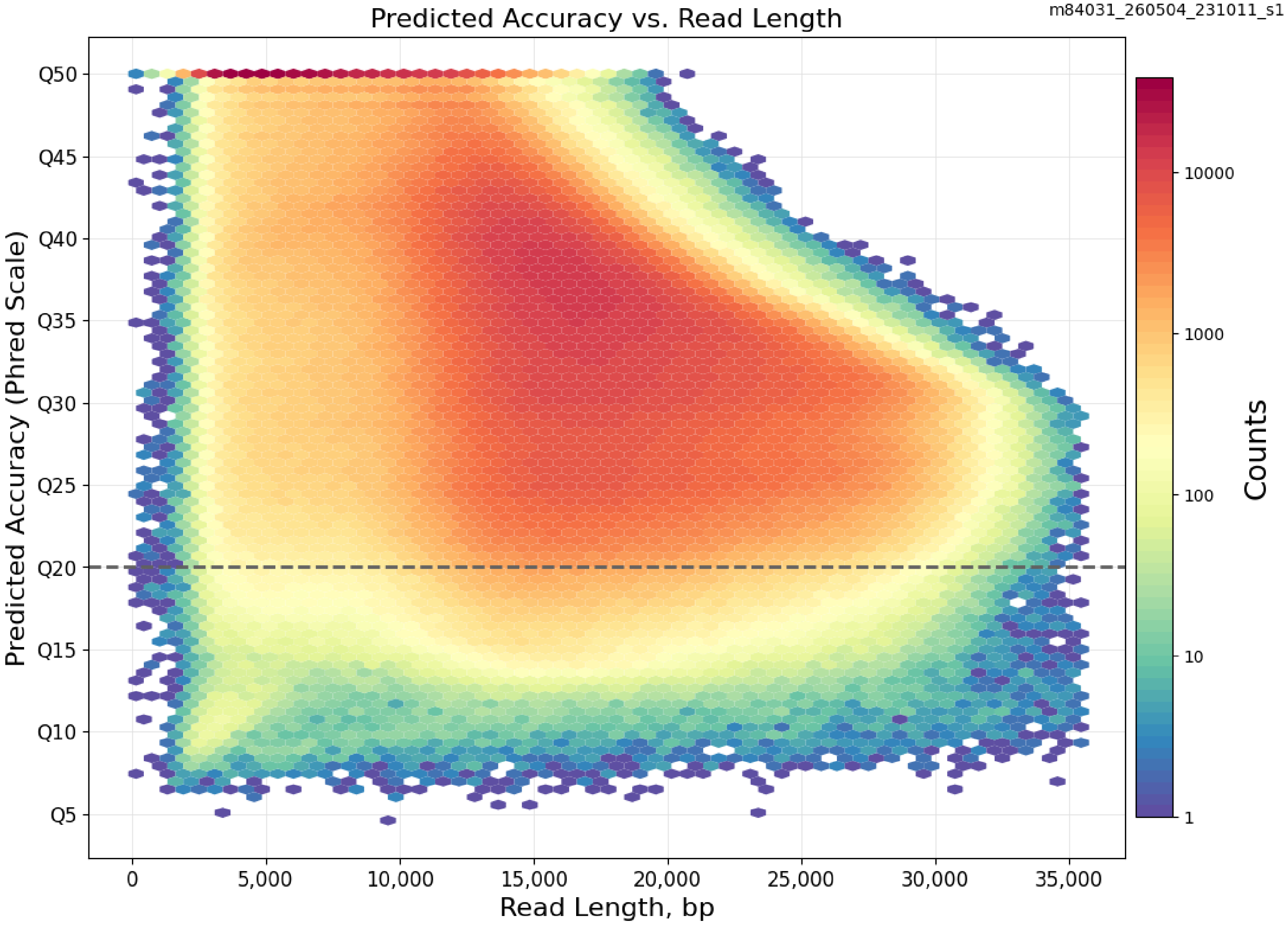
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

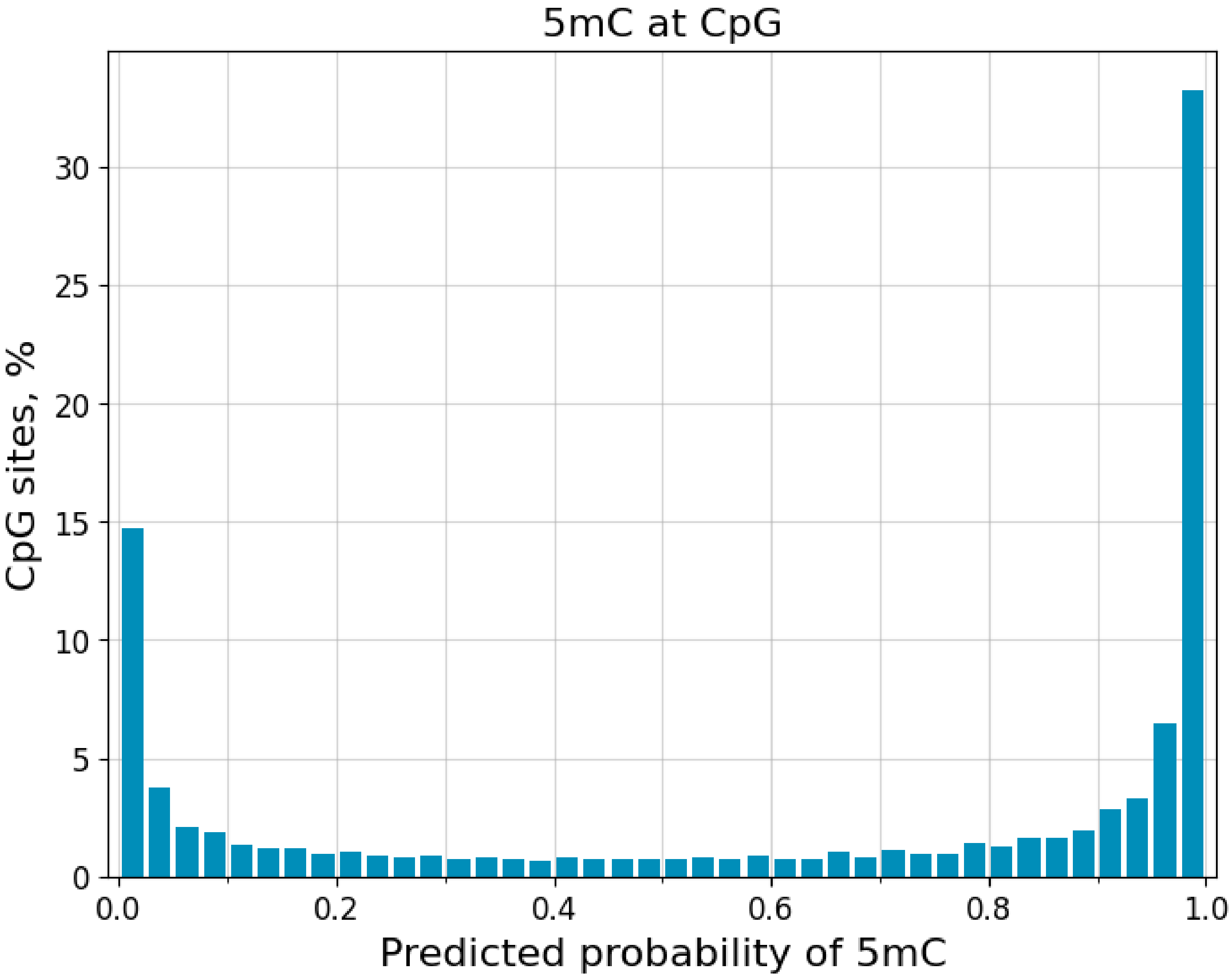


Methylation

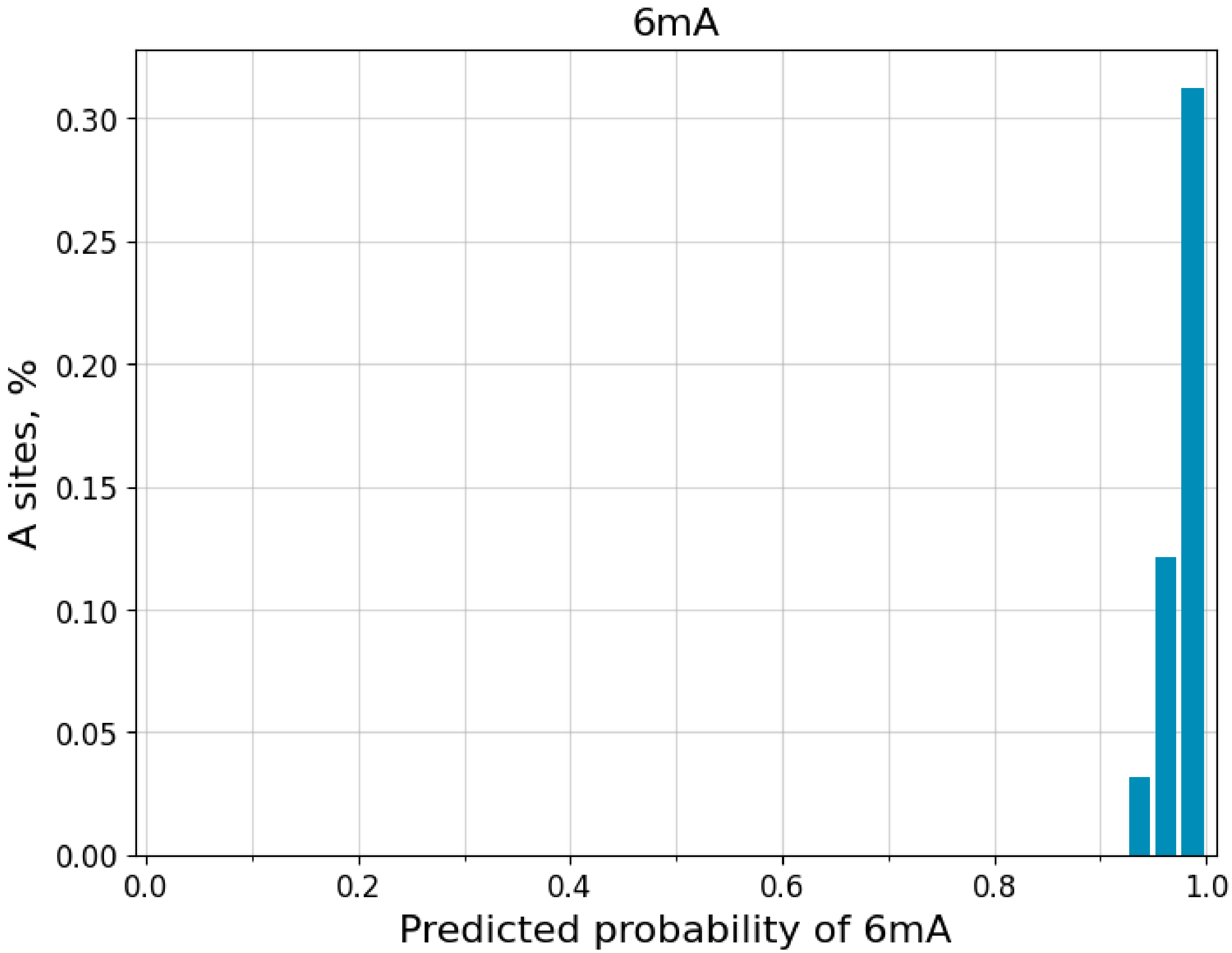
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	100.0%	63.2%
6mA	A	0.5%	0.5%
5hmC	CpG	0.5%	0.5%

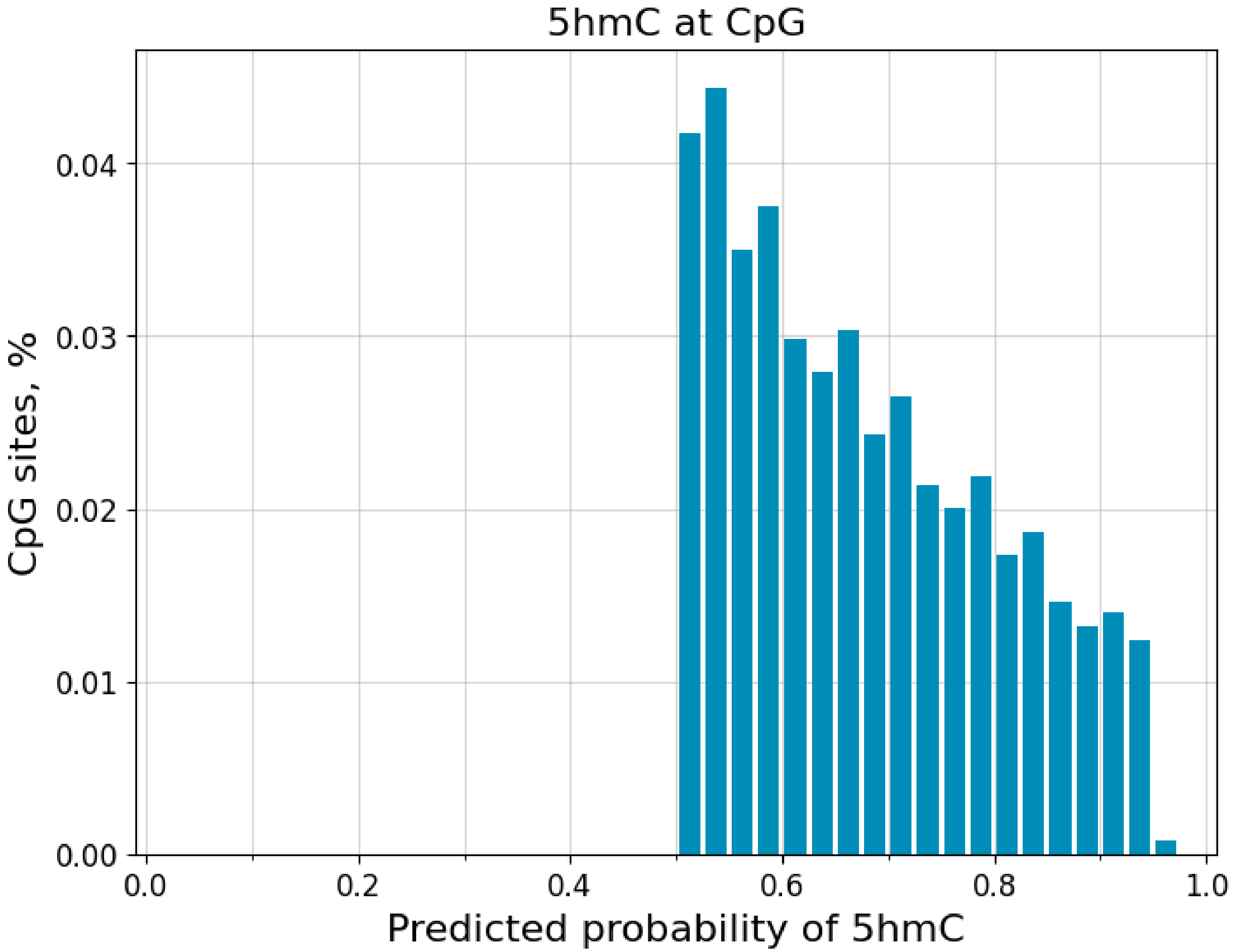
Score distributions: 5mC at CpG



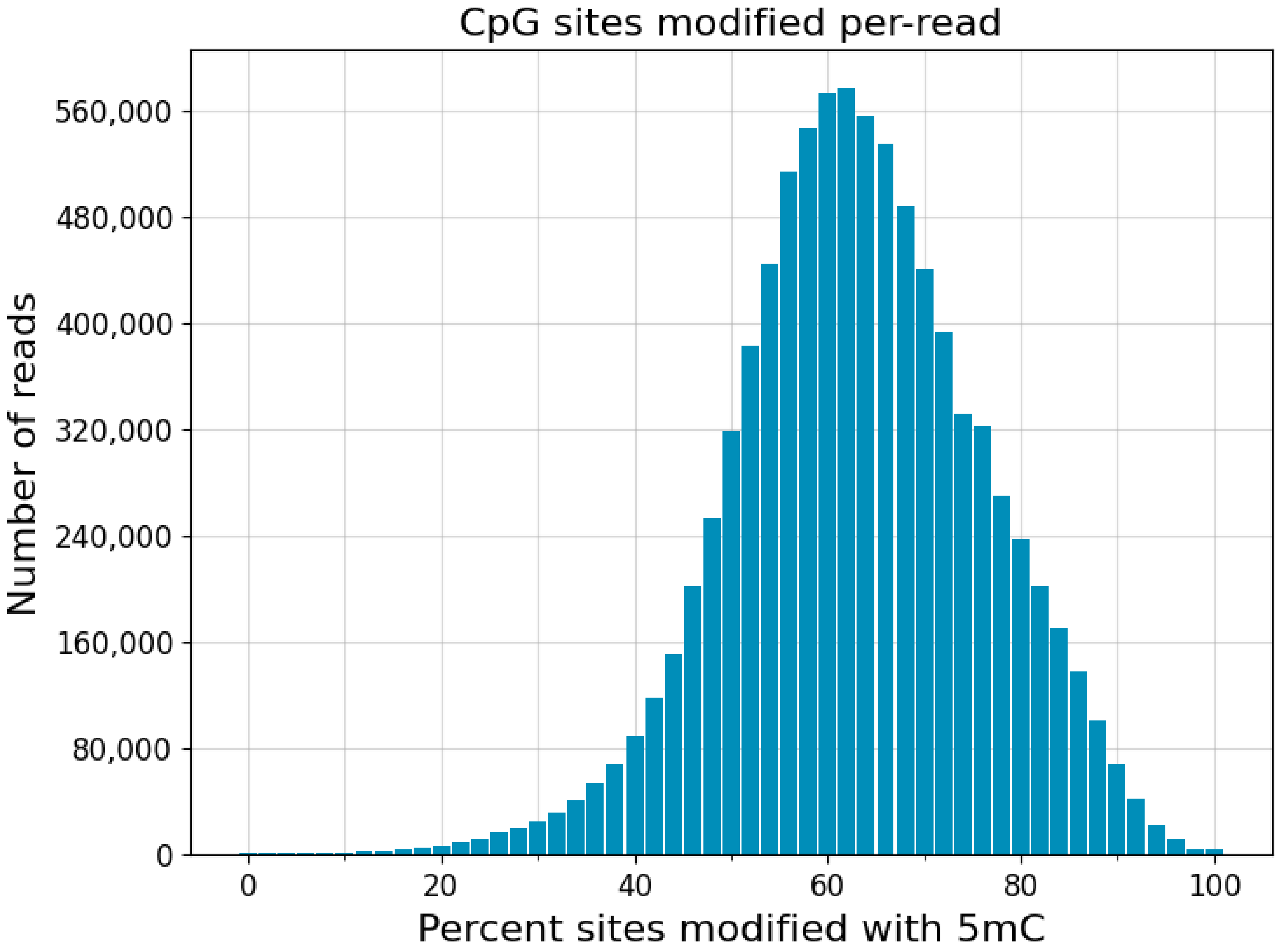
Score distributions: 6mA



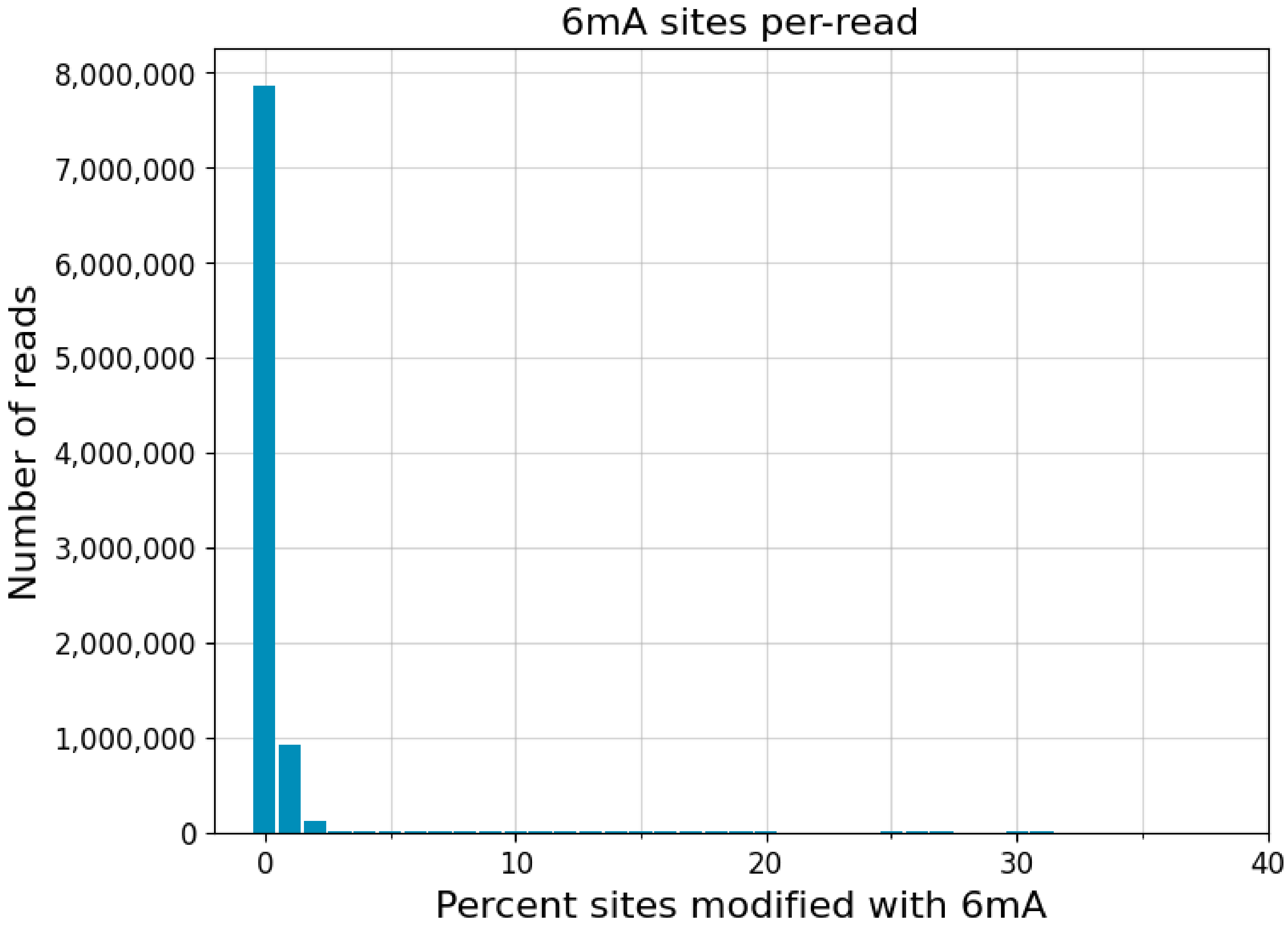
Score distributions: 5hmC at CpG



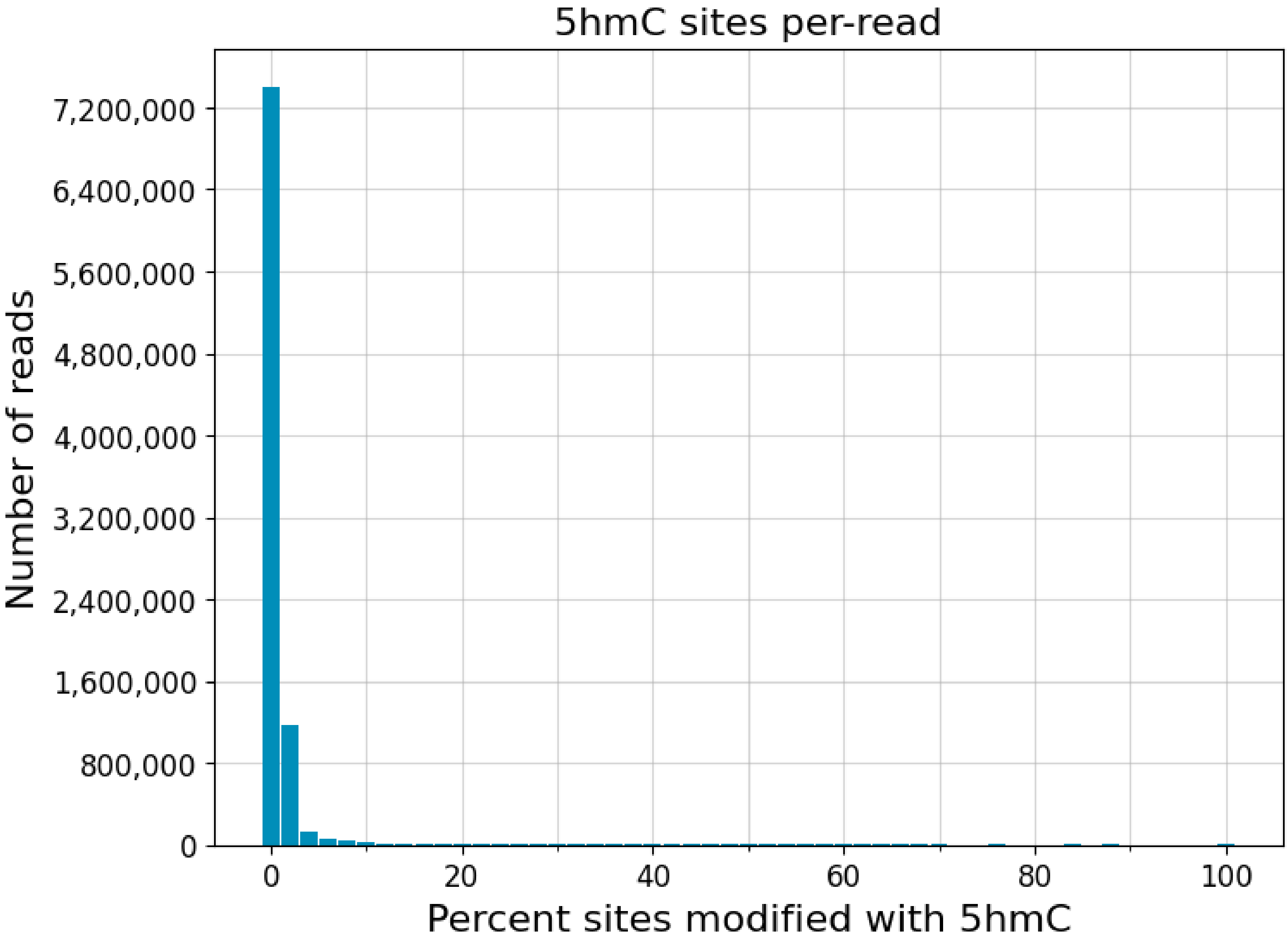
Per-read distributions: CpG sites modified per-read



Per-read distributions: 6mA sites per-read



Per-read distributions: 5hmC sites per-read



Barcodes

Summary Metrics

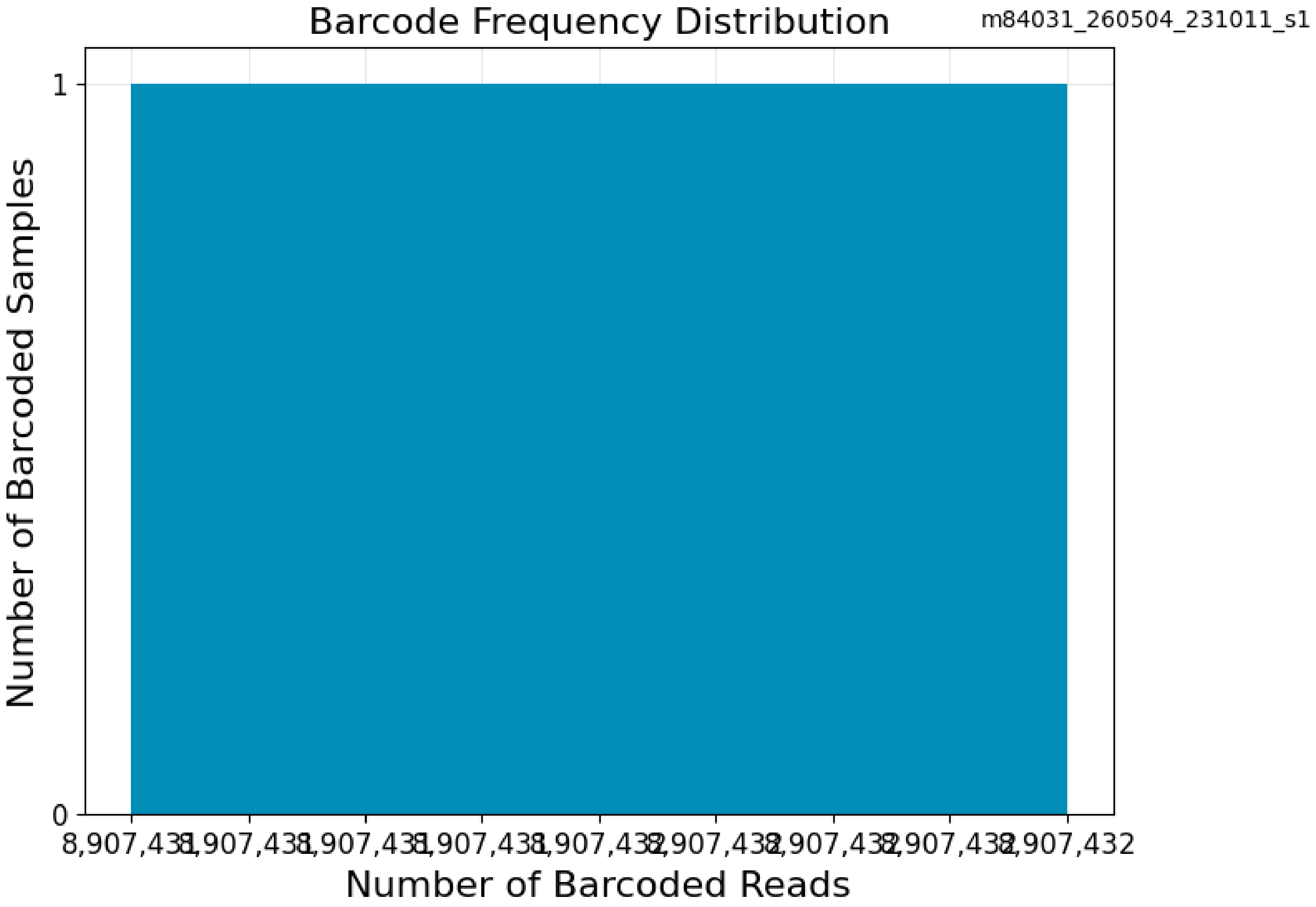
Unique Barcodes	1
Barcoded HiFi Reads	8,907,432
Unbarcoded HiFi Reads	24,392
Barcoded HiFi Reads (%)	99.73 %
Barcoded HiFi yield (Gb)	144.62 Gb
Unbarcoded HiFi yield (Gb)	0.38 Gb
Barcoded HiFi Yield (%)	99.74 %
Mean HiFi Reads per Barcode	8,907,432
Max. HiFi Reads per Barcode	8,907,432
Min. HiFi Reads per Barcode	8,907,432
Barcoded HiFi read length (mean, kb)	16.23 kb
Unbarcoded HiFi read length (mean, kb)	15.69 kb

Barcode Data

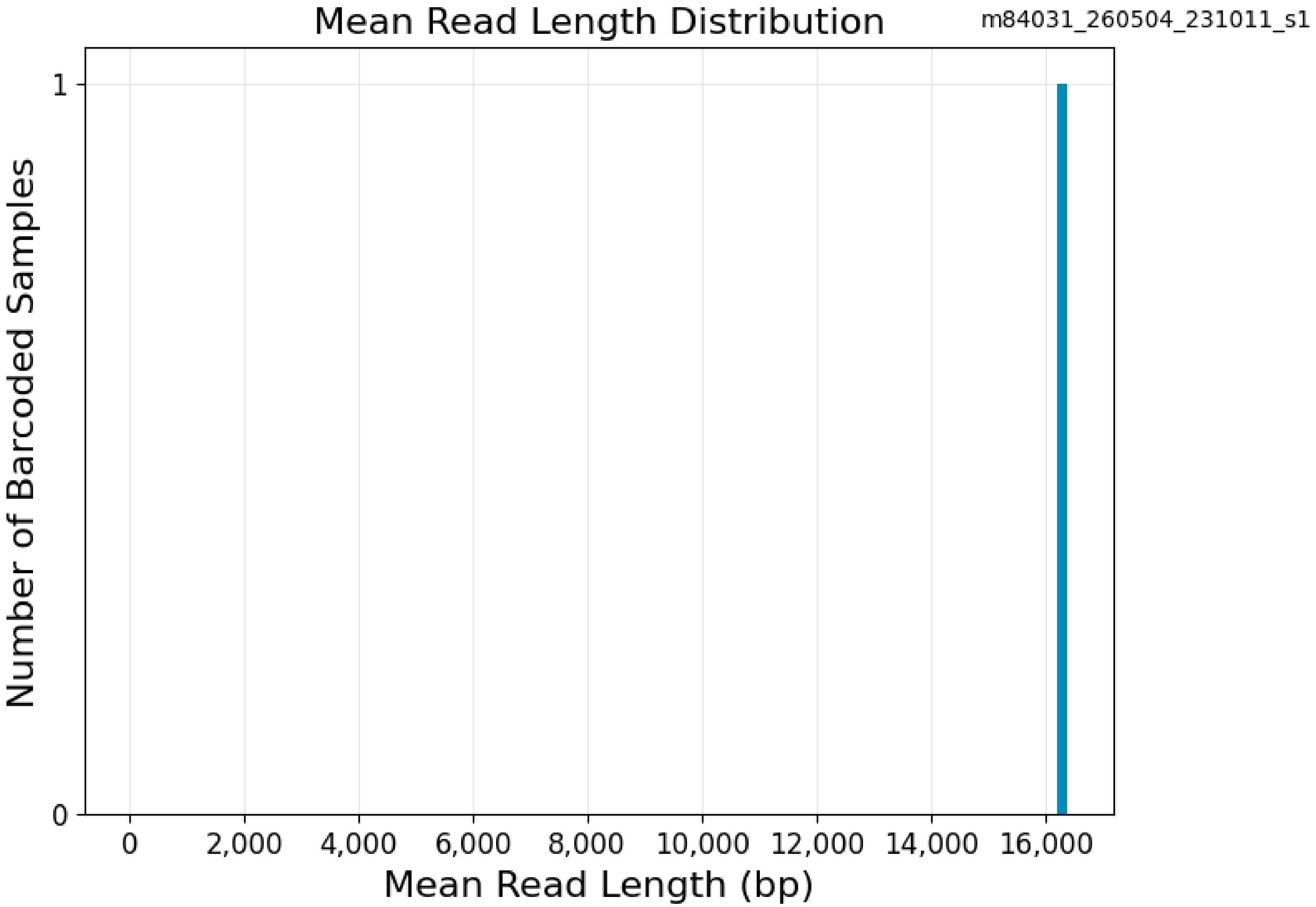
Sample Name	Barcode	Barcode Quality	HiFi Reads	HiFi Read Length (mean, bp)	HiFi Read Quality (median, QV)	HiFi Yield (bp)	Polymerase Read Length (mean, bp)
RRV-52	bc2002--bc2002	96.6	8,907,432	16,235	Q34	144,621,006,554	144,894
No Name	Not Barcoded	0.0	24,392	15,692	Q25	382,775,404	129,924

Barcoded Read Statistics: Number Of Reads Per Barcode

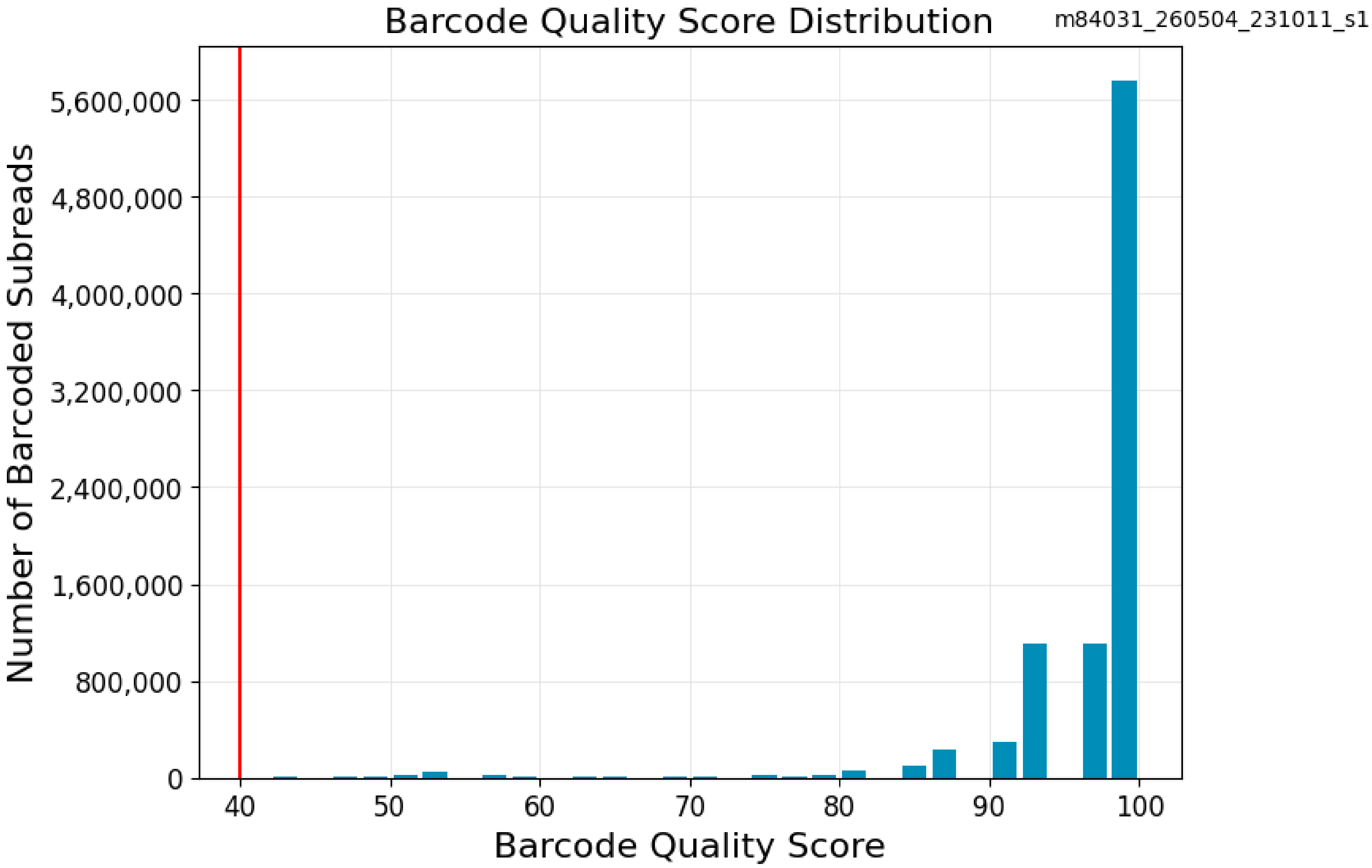
Barcoded Read Statistics: Barcode Frequency Distribution



Barcoded Read Statistics: Mean Read Length Distribution



Barcode Quality Scores: Barcode Quality Score Distribution



Loading Report

Summary Metrics

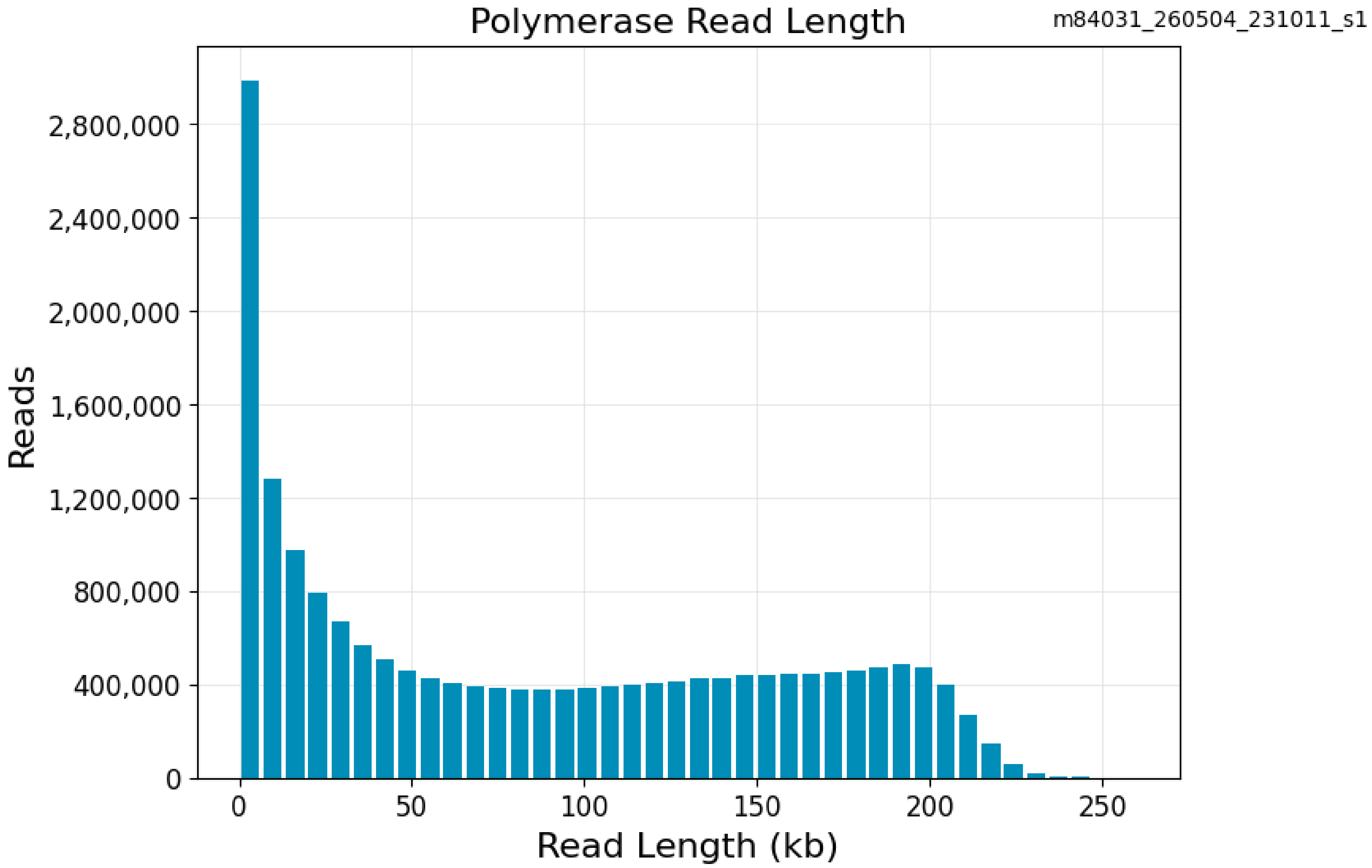
Productive ZMWs	25,165,824
Productivity 0	6,024,471
Productivity 1	18,854,709
Productivity 2	286,644

Raw Data Report

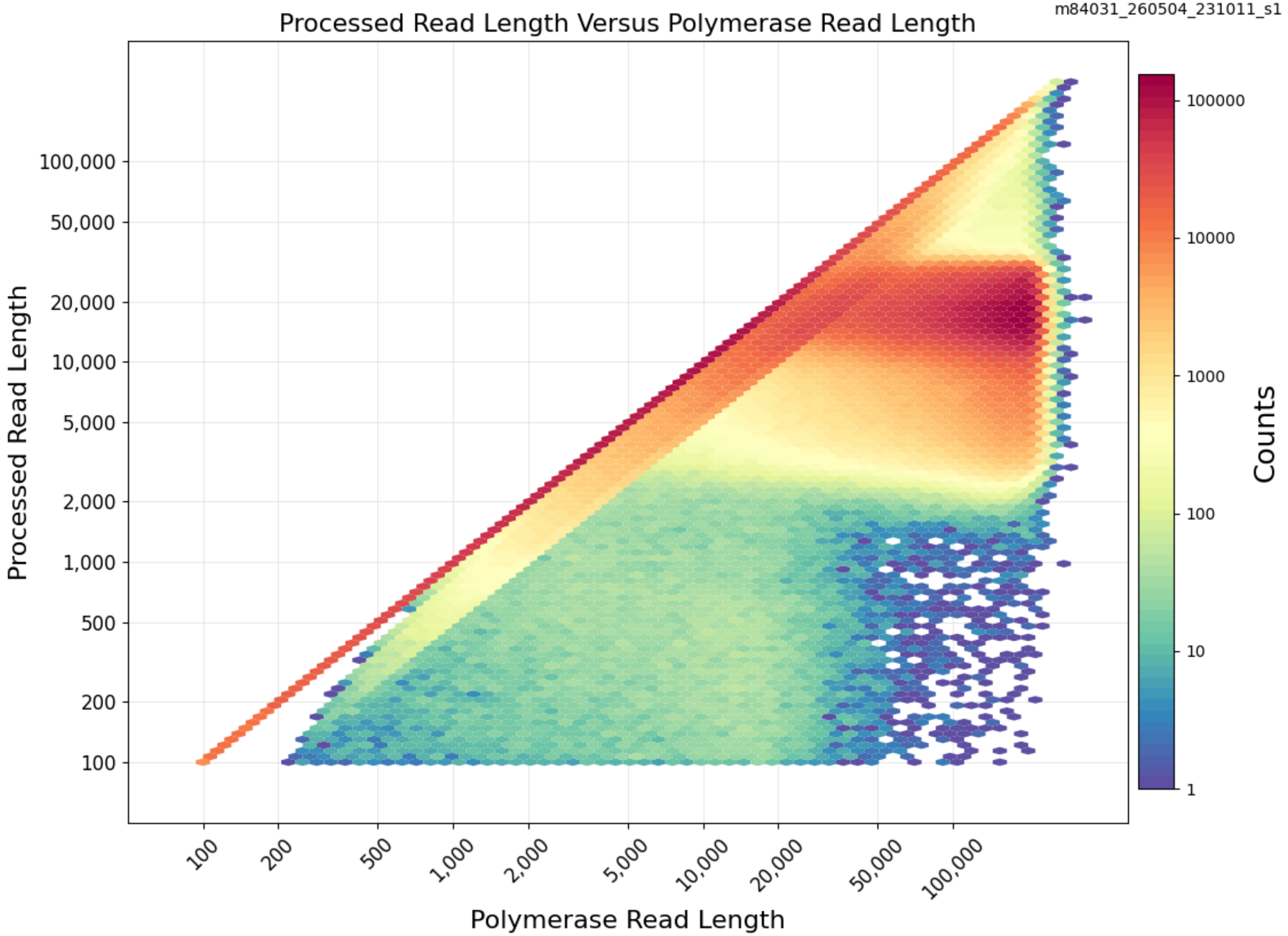
Summary Metrics

Polymerase Read Bases	1,526,709,634,492
Polymerase Reads	18,849,547
Polymerase Read Length (mean)	80.99 kb
Polymerase read length (N50)	153.75 kb
Polymerase read length longest subread length (mean)	16.94 kb
Polymerase read length longest subread length (N50)	20.75 kb
Unique Molecular Yield	304,454,926,336
Local Base Rate	2.33

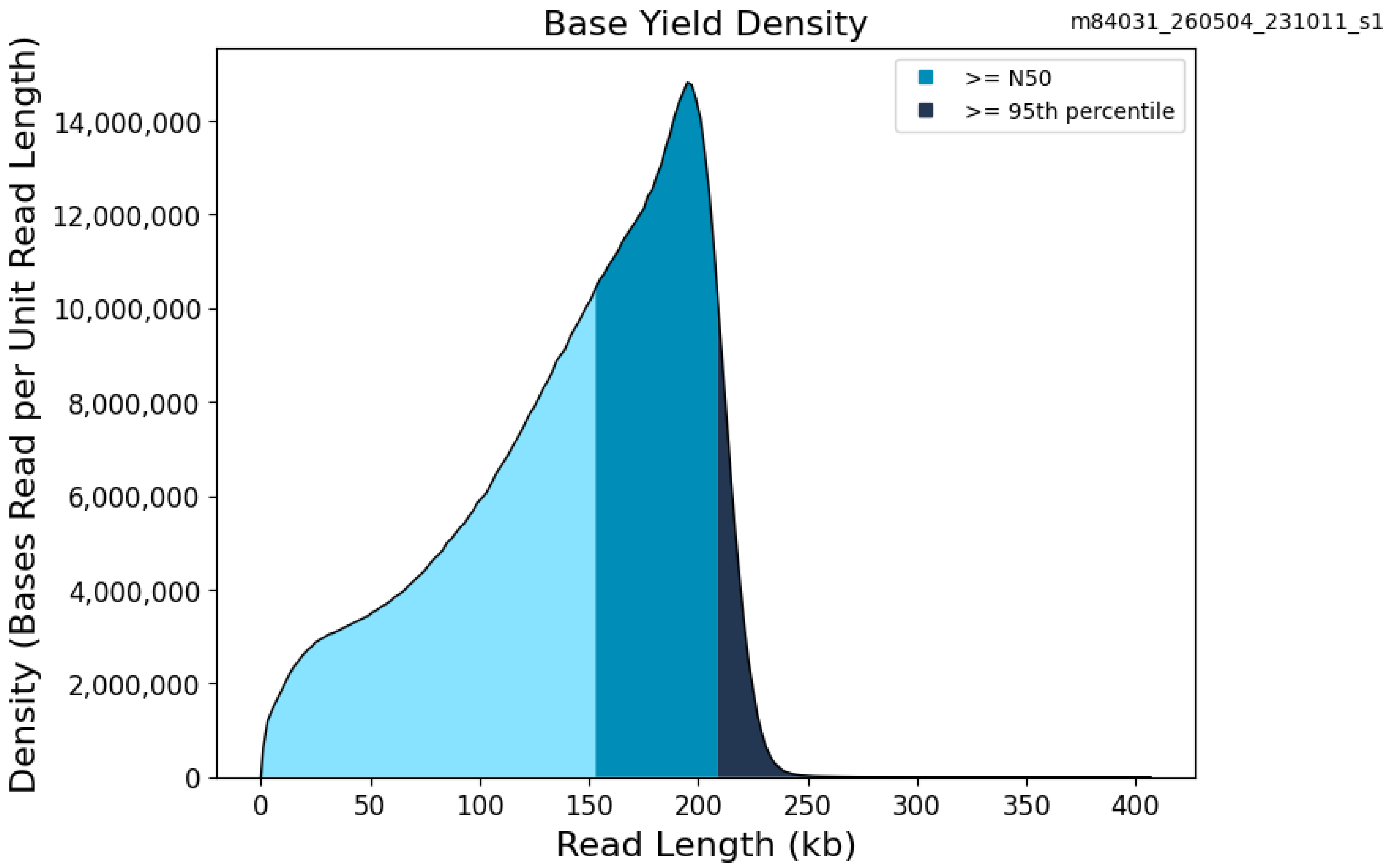
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

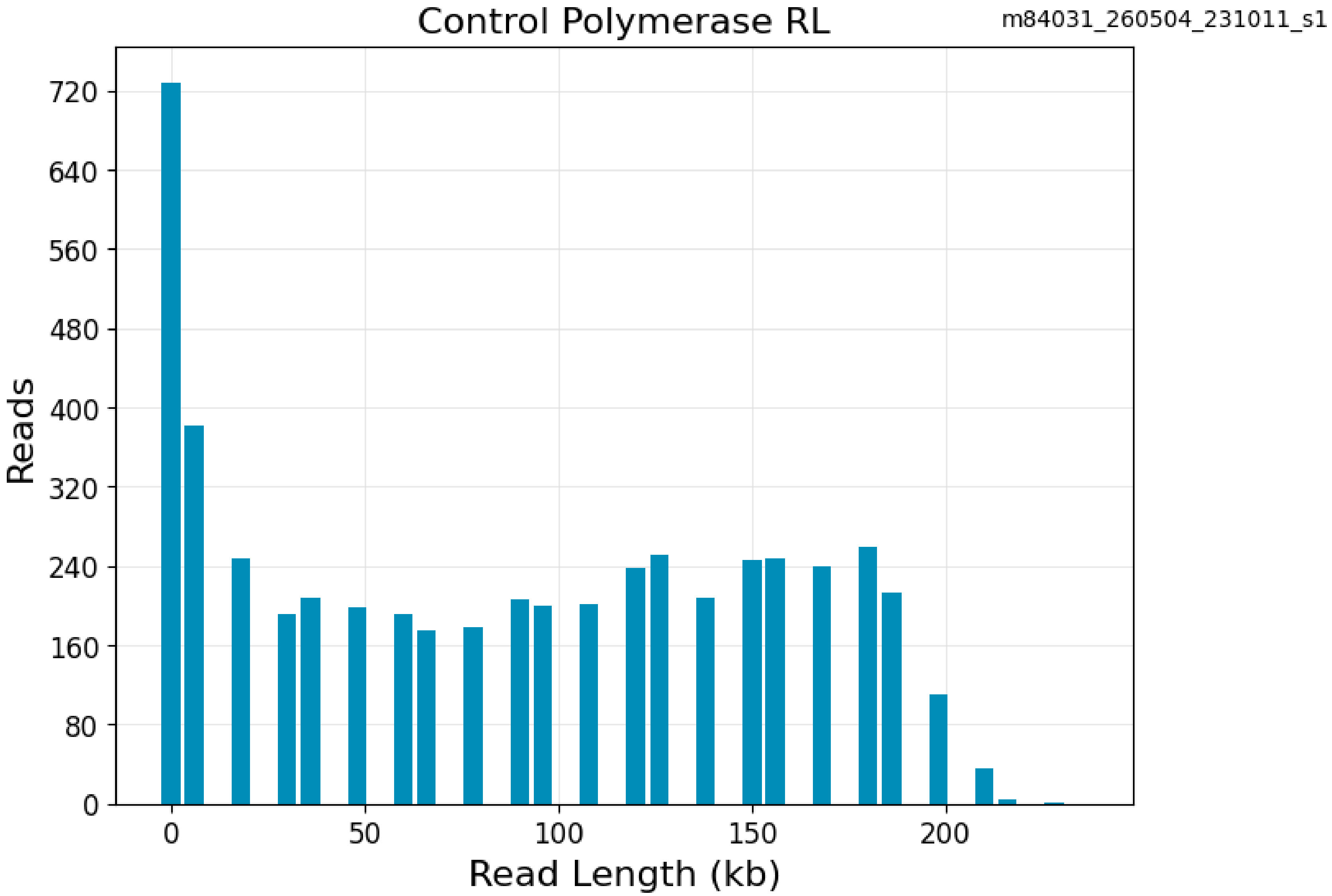


Control Report

Summary Metrics

Number of Control Reads	5,162
Control Read Length Mean	88,950
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance