Report for m84082_251001_025627_s2

Dataset details

Name: AS-306_Goetz-Pool3_FA253-FA092_Amplicon_300pM-Cell2 (all samples)

Path:
/data2/rawdata/r84082_20251001_004552/1_B01/pb_formats/m84082_251001_025627_s2.hifi_reads.consensusreadset.xml

Unique ID: db0f4407-9c8a-4ad7-a9a4-4929b50de503

Created at: 2025-10-02T22:09:03.220Z

HiFi sequences: 9,187,090

HiFi bases: 51,264,010,702

Bio sample name: [multiple]

Well sample name: AS-306_Goetz-Pool3_FA253-FA092_Amplicon_300pM

Run name: Run 09.30.2025 14:49

Movie name: m84082_251001_025627_s2

Instrument name: Revio

ICS version: 13.3.0.253824

Number of child datasets: 2

Number of HiFi BAM files: 2

CCS Analysis Report

Summary Metrics

HiFi reads	9.3 M
HiFi reads yield	51.70 Gb
HiFi reads length (mean)	5.58 kb
HiFi reads length (median, bp)	4,594
HiFi Read Length N50 (bp)	6,214
HiFi Read Quality (median)	Q47
HiFi Read Quality (median)	47
Base Quality ≥Q30 (%)	97.36%
HiFi Number of Passes (mean)	27
Missing adapters (%)	3.23%

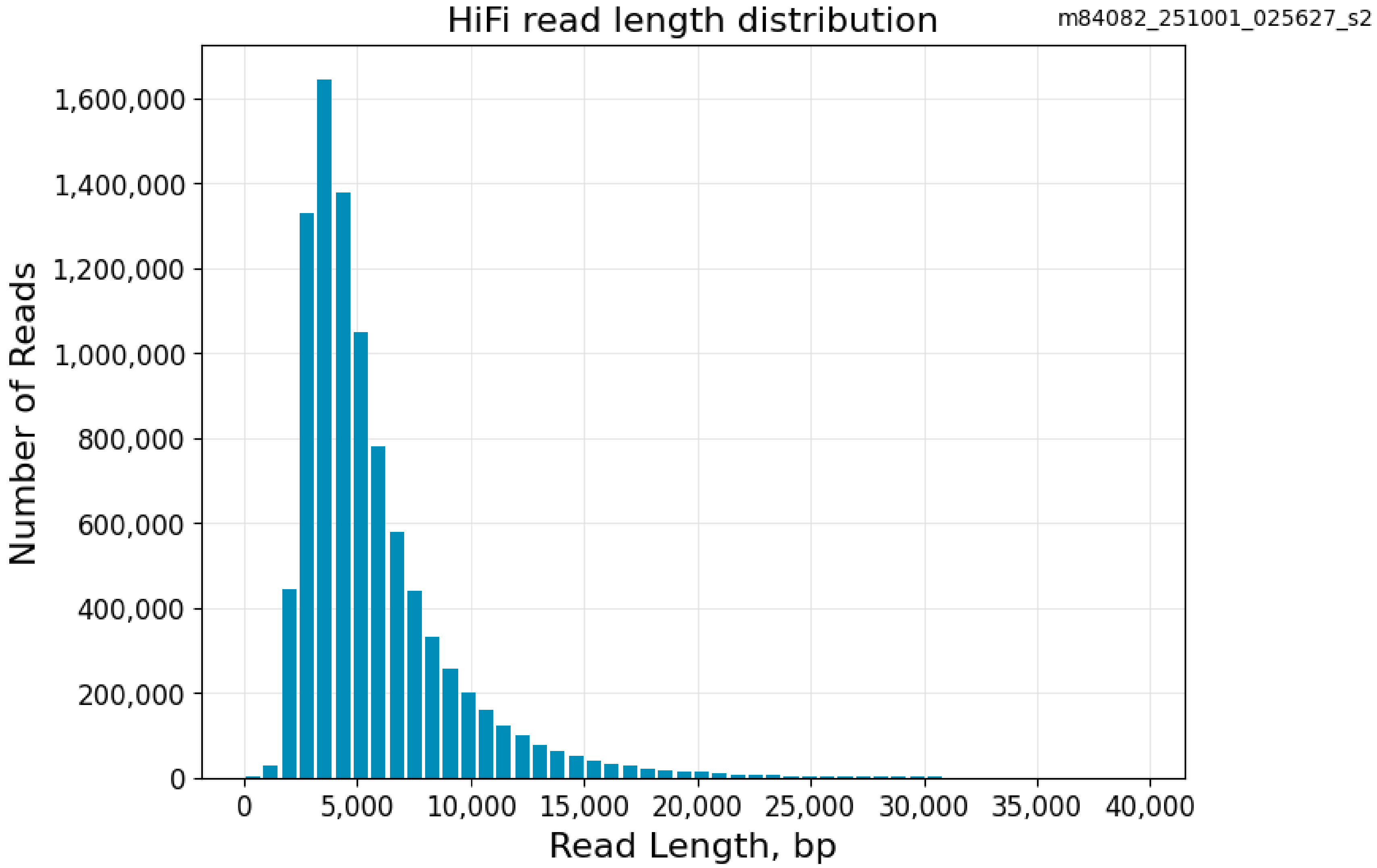
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	9,259,367	100	51.70 Gb	100
≥ 5,000	4,026,652	43	33.34 Gb	64
≥ 10,000	857,595	9	11.79 Gb	23
≥ 15,000	224,380	2	4.24 Gb	8
≥ 20,000	62,963	1	1.51 Gb	3
≥ 25,000	17,771	0	0.51 Gb	1
≥ 30,000	4,893	0	0.17 Gb	0
≥ 35,000	1,323	0	0.05 Gb	0
≥ 40,000	307	0	0.01 Gb	0

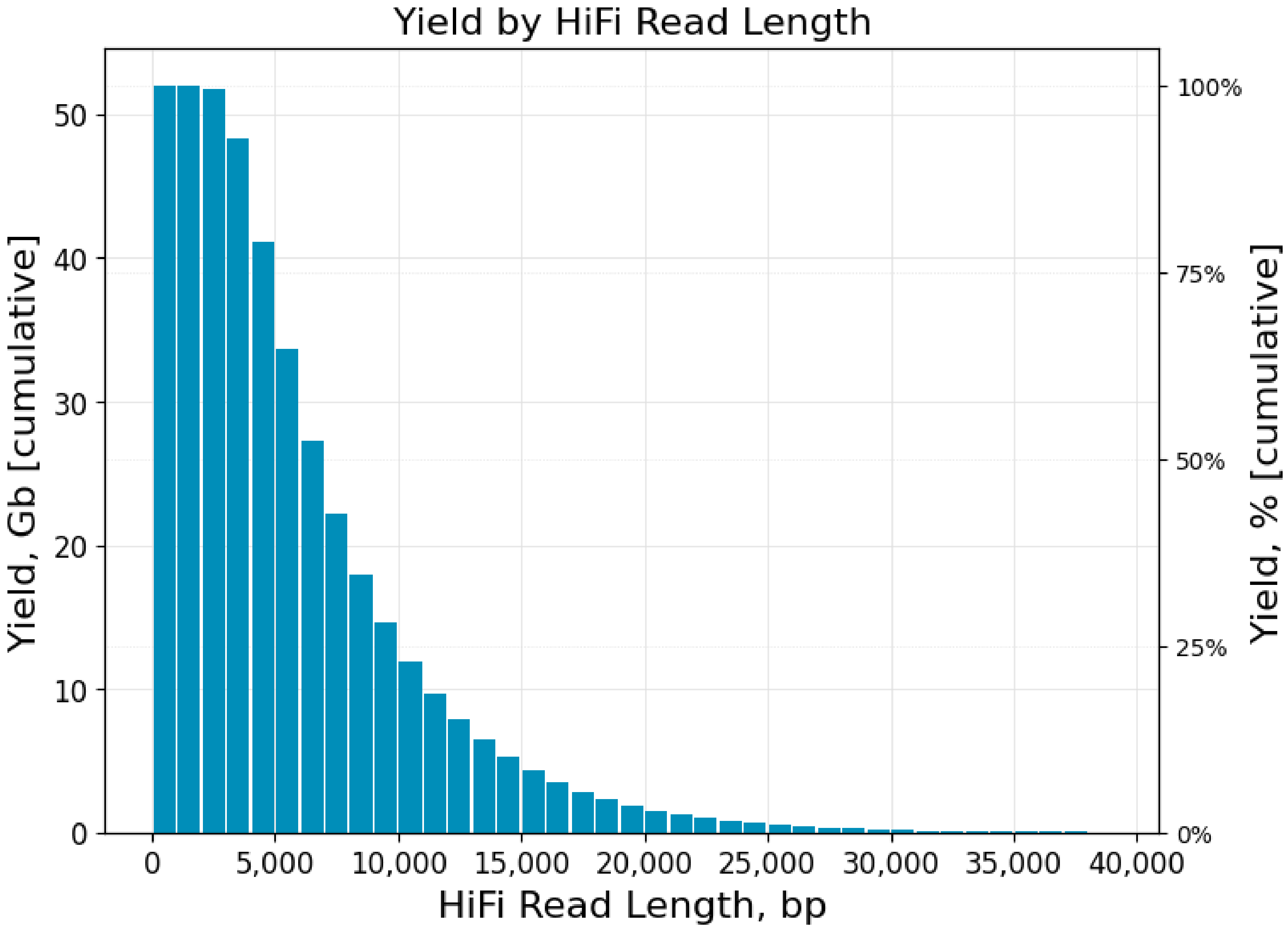
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	9,259,367	100	51.70 Gb	100
≥ Q30	7,935,719	86	42.82 Gb	83
≥ Q40	5,968,774	64	29.66 Gb	57
≥ Q50	3,922,408	42	17.45 Gb	34

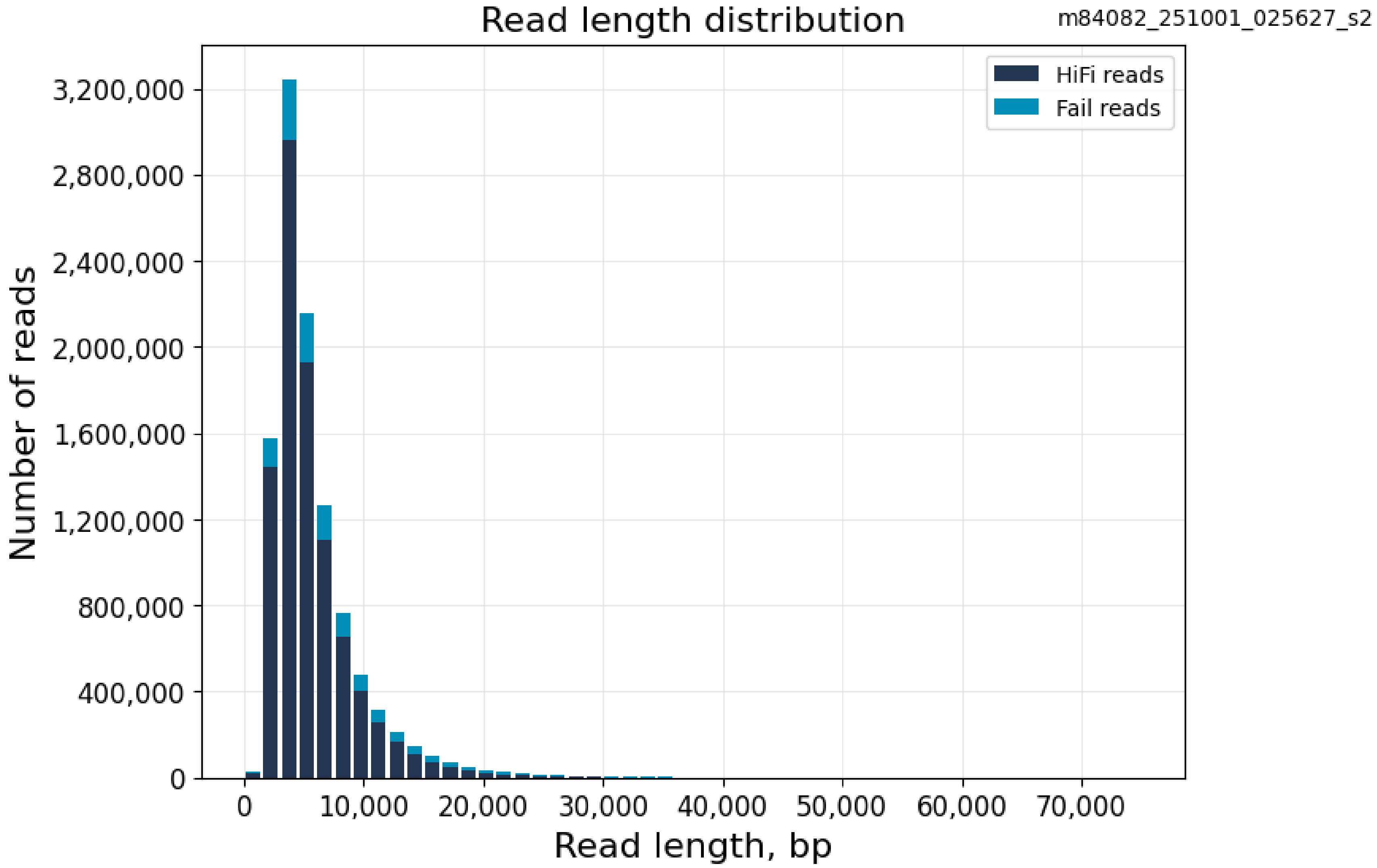
Read Length Distribution: HiFi read length distribution



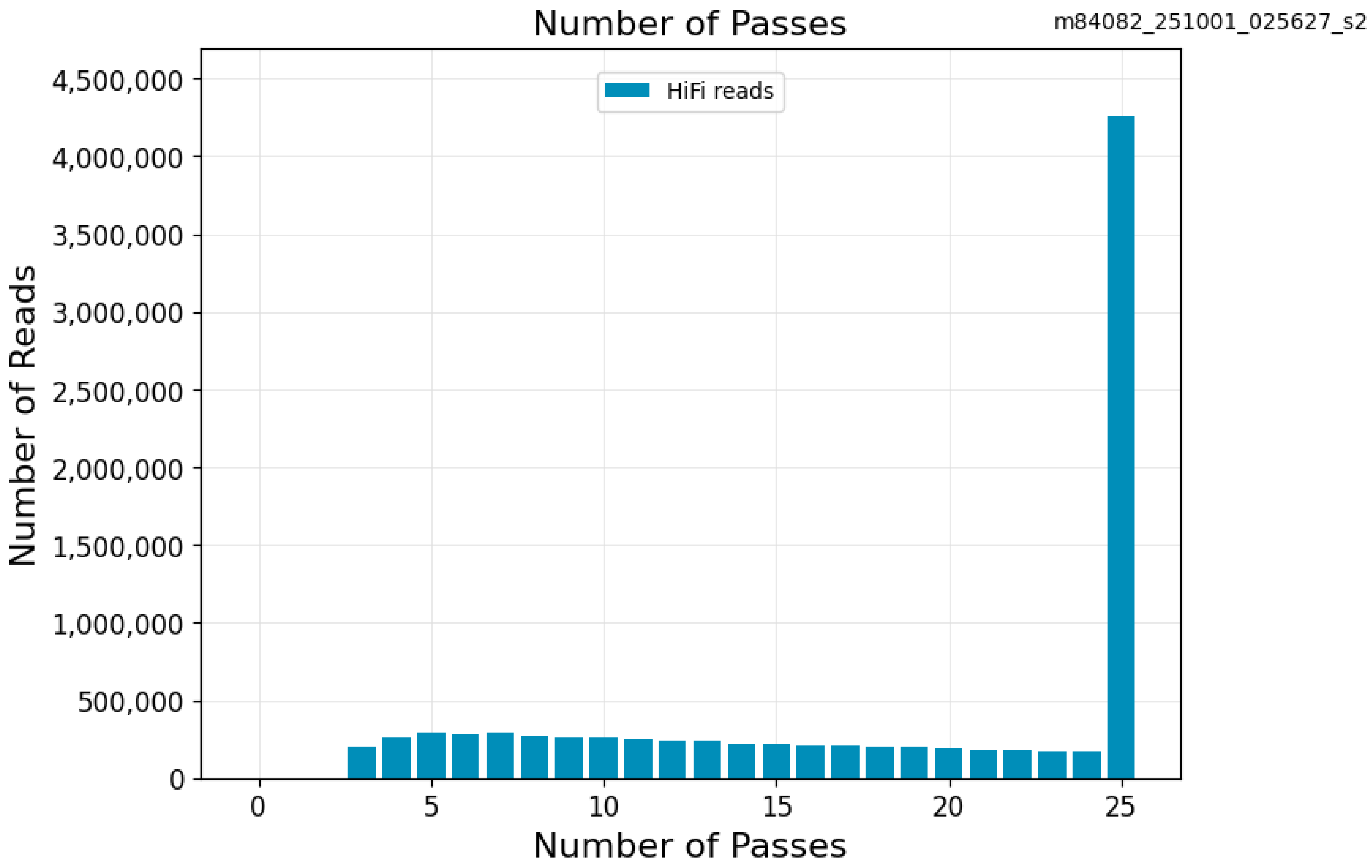
Read Length Distribution: Yield by HiFi Read Length



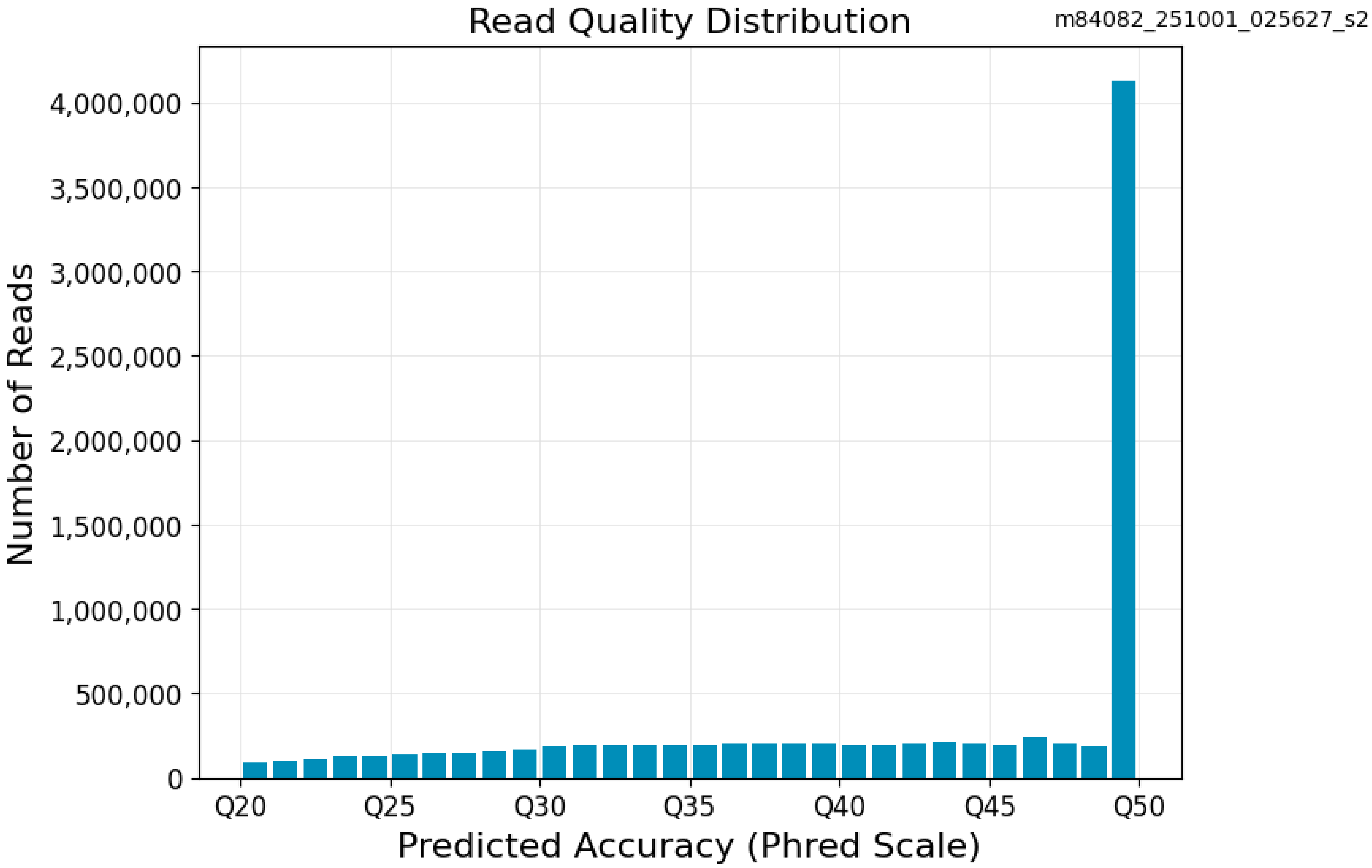
Read Length Distribution: Read length distribution



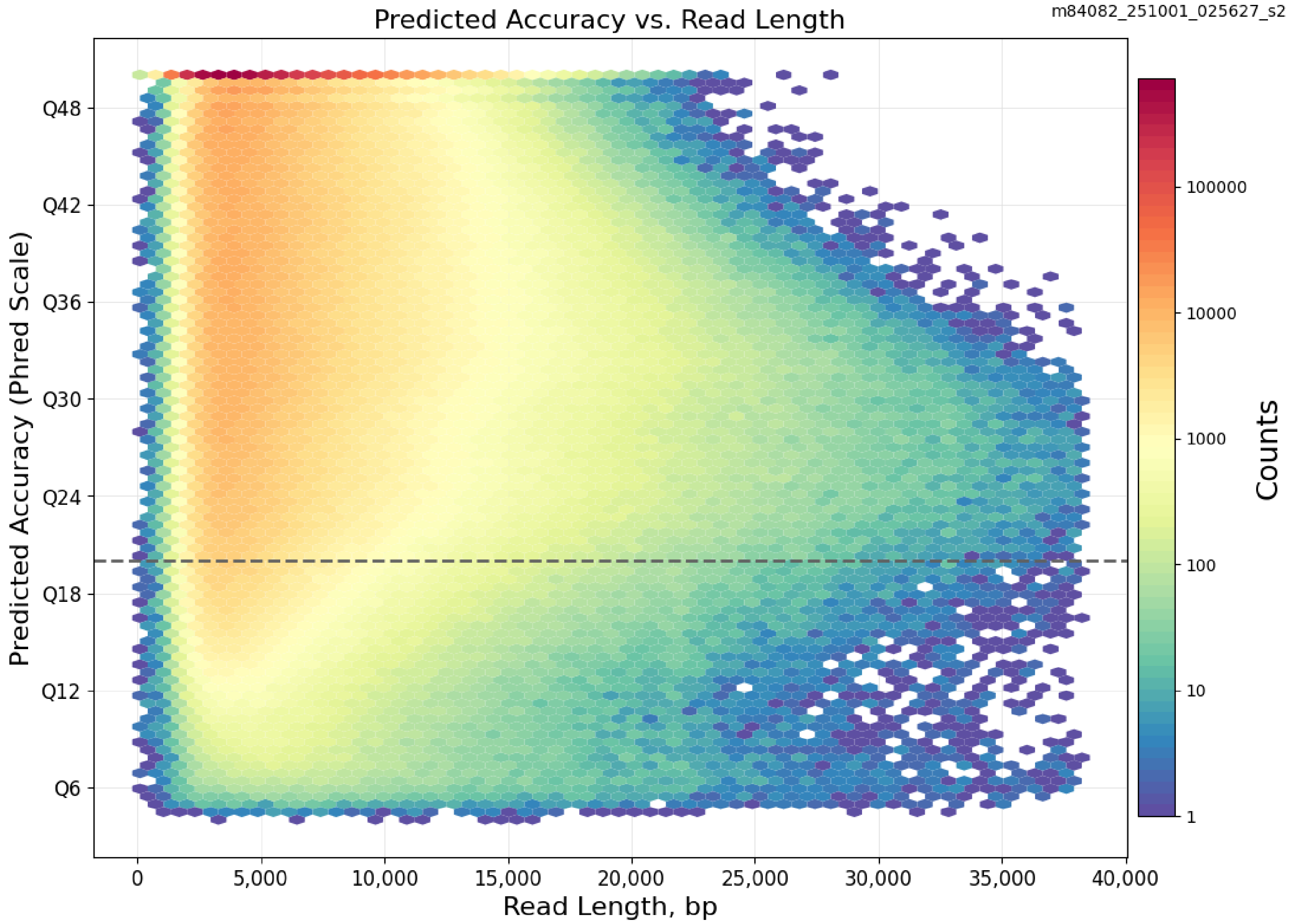
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

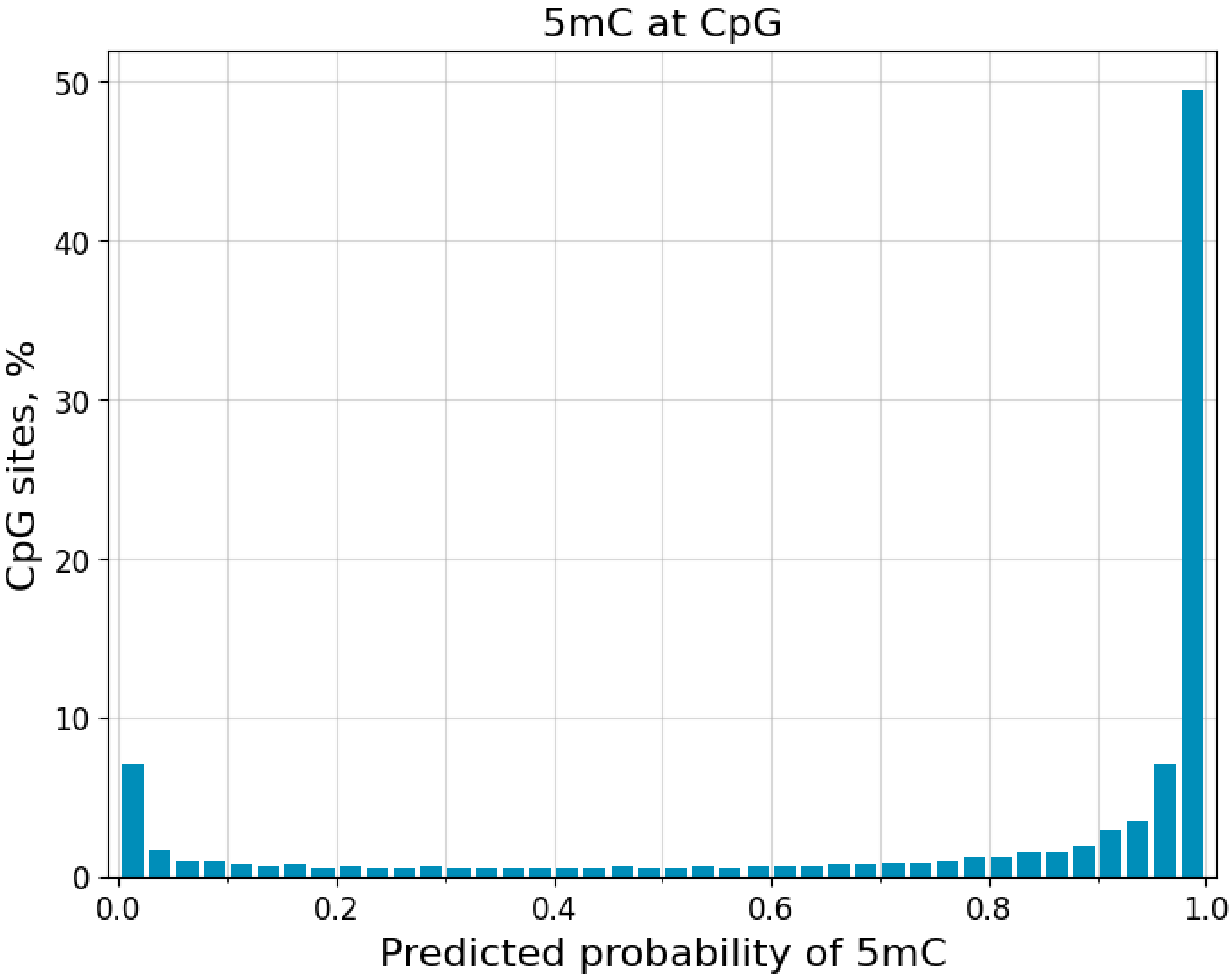


Methylation

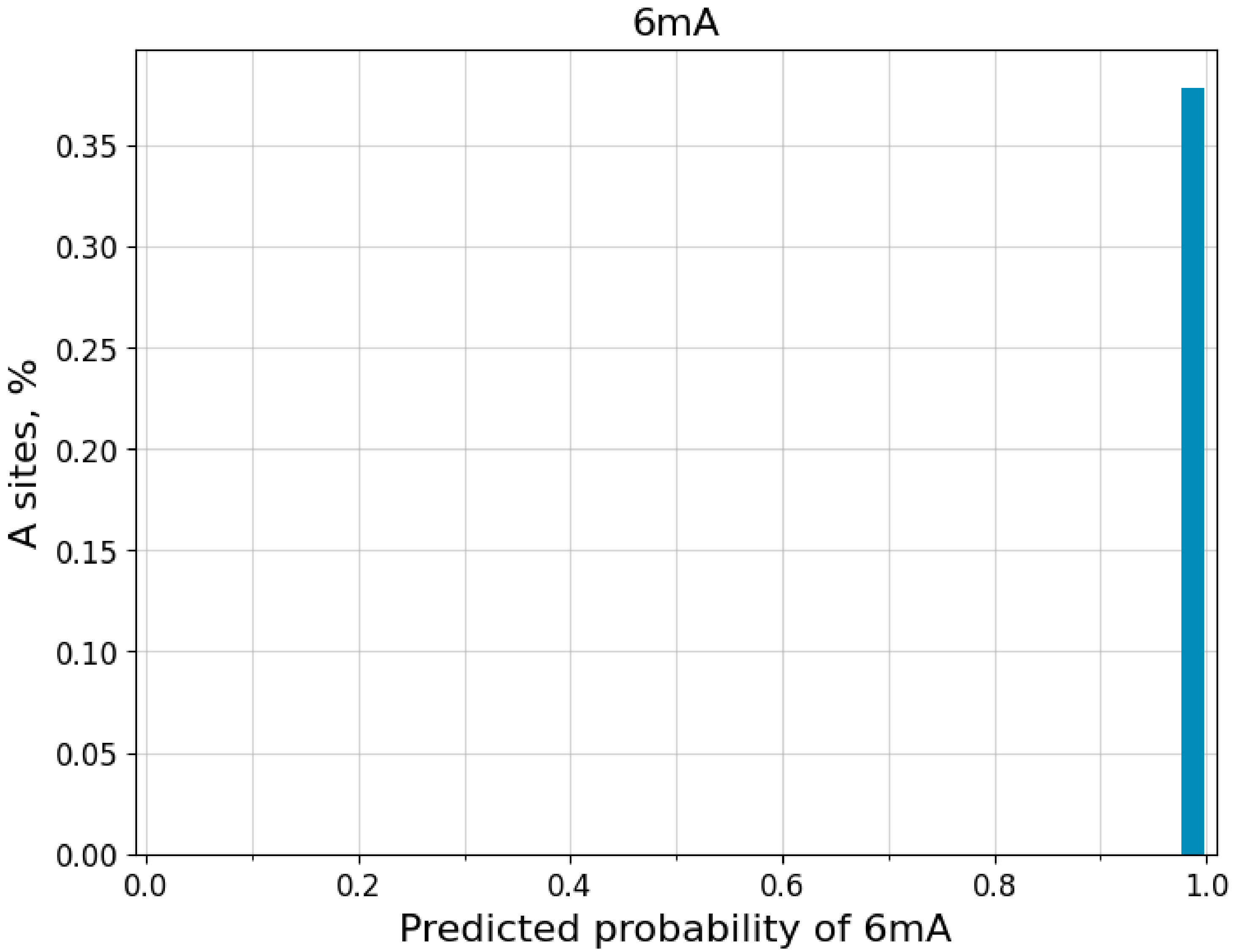
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	98.2%	78.2%
6mA	A	0.4%	0.4%

Score distributions: 5mC at CpG



Score distributions: 6mA



Barcodes

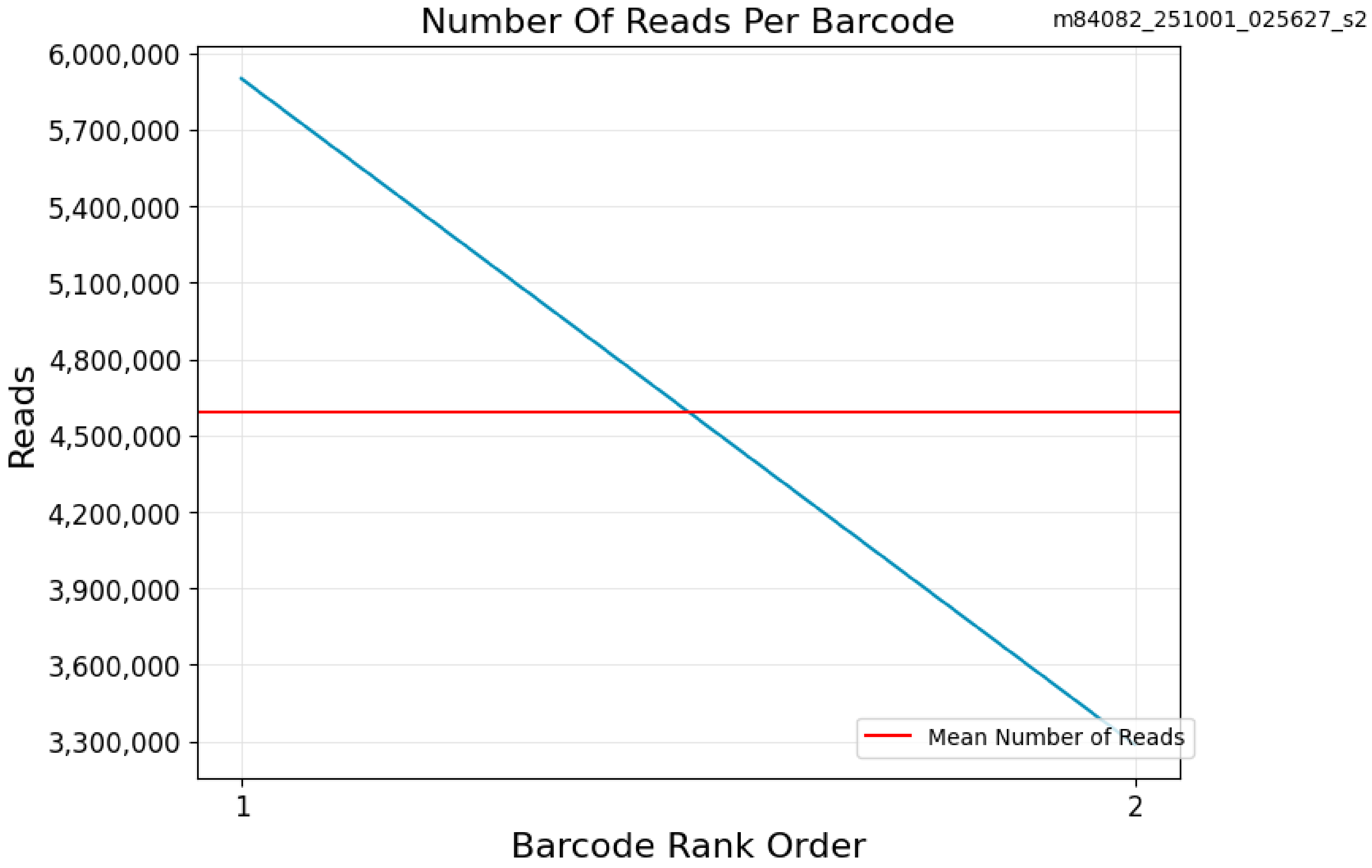
Summary Metrics

Unique Barcodes	2
Barcoded HiFi Reads	9,187,090
Unbarcoded HiFi Reads	72,277
Barcoded HiFi Reads (%)	99.22 %
Barcoded HiFi yield (Gb)	51.26 Gb
Unbarcoded HiFi yield (Gb)	0.44 Gb
Barcoded HiFi Yield (%)	99.16 %
Mean HiFi Reads per Barcode	4,593,545
Max. HiFi Reads per Barcode	5,899,468
Min. HiFi Reads per Barcode	3,287,622
Barcoded HiFi read length (mean, kb)	5.58 kb
Unbarcoded HiFi read length (mean, kb)	6.04 kb

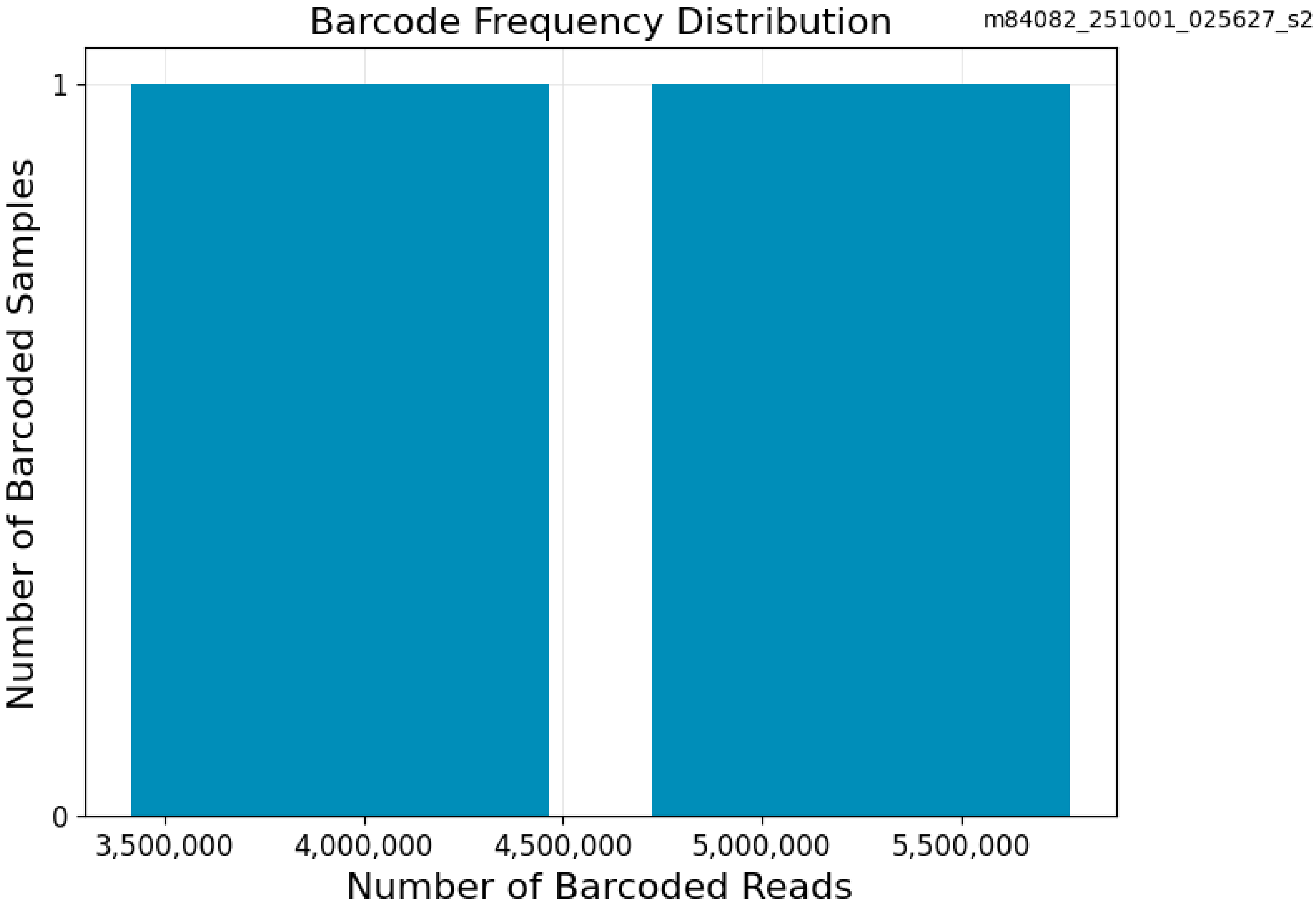
Barcode Data

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)
AS-306_Goetz-Pool3_FA092	bc2068--bc2068	97.1	3,287,622	4,224	Q49	13,887,000,171	134,213
AS-306_Goetz-Pool3_FA253	bc2096--bc2096	96.1	5,899,468	6,335	Q45	37,377,010,531	140,657
No Name	Not Barcoded	0.0	72,277	6,039	Q29	436,490,816	133,053

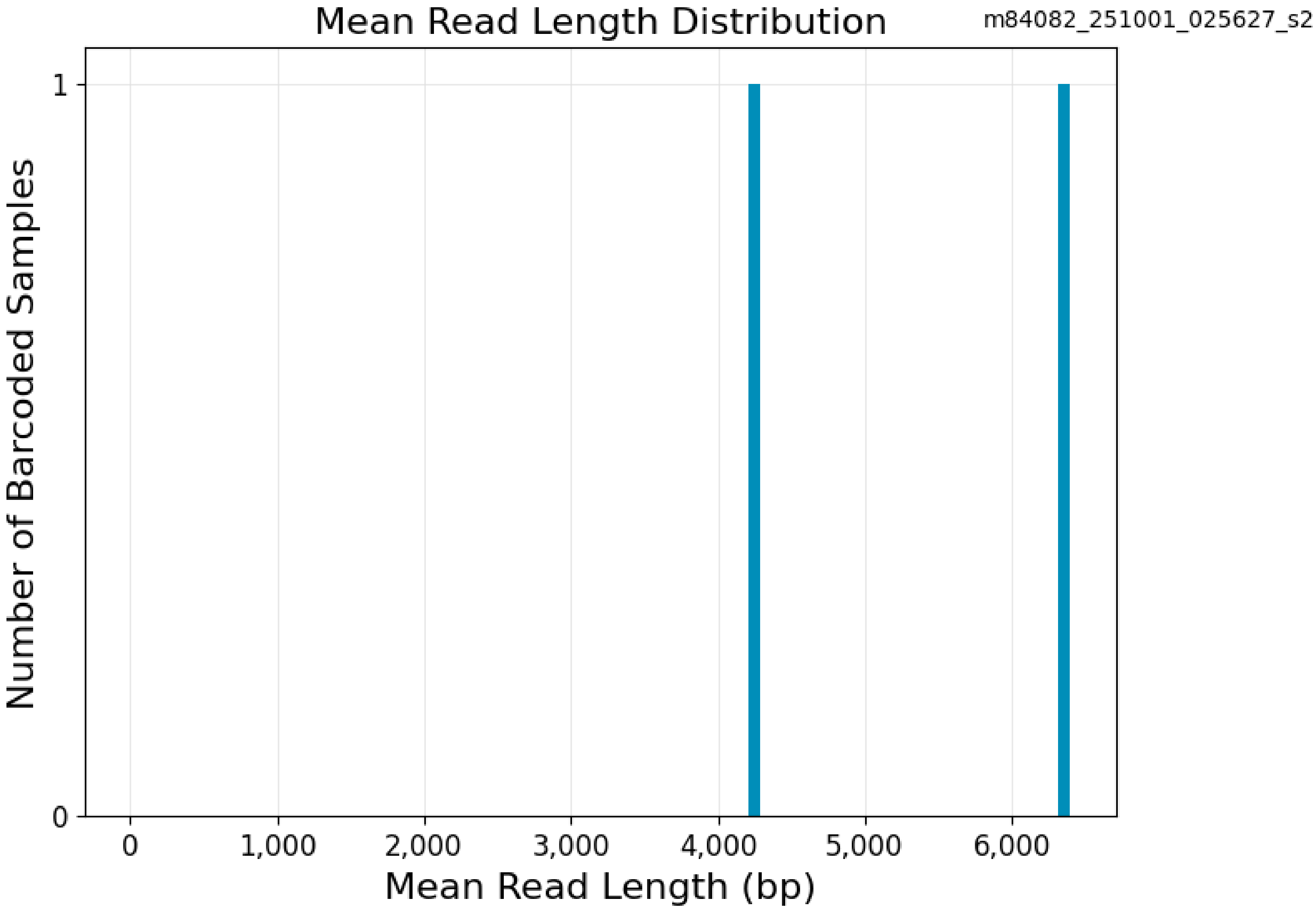
Barcoded Read Statistics: Number Of Reads Per Barcode



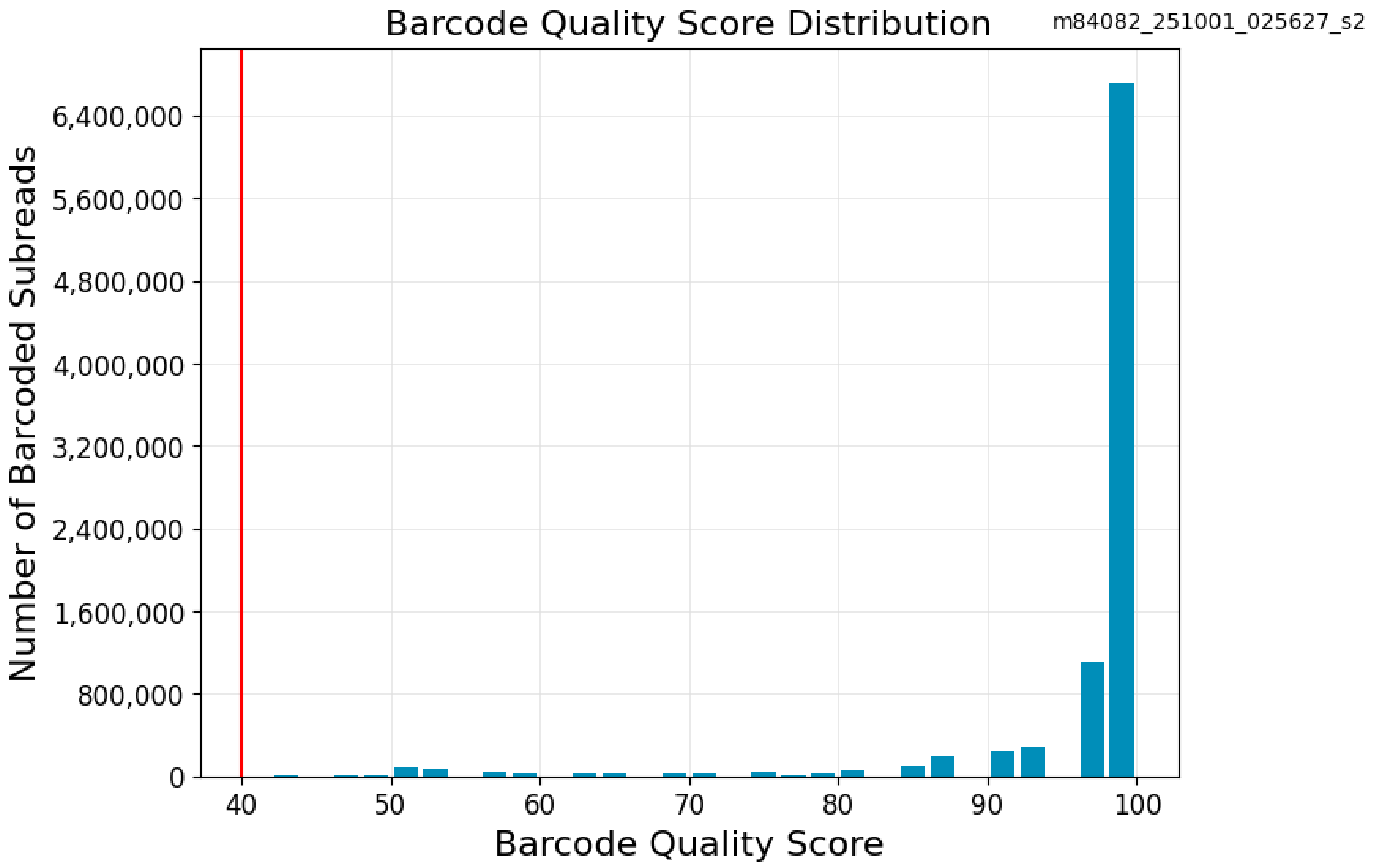
Barcoded Read Statistics: Barcode Frequency Distribution



Barcoded Read Statistics: Mean Read Length Distribution



Barcode Quality Scores: Barcode Quality Score Distribution



Loading Report

Summary Metrics

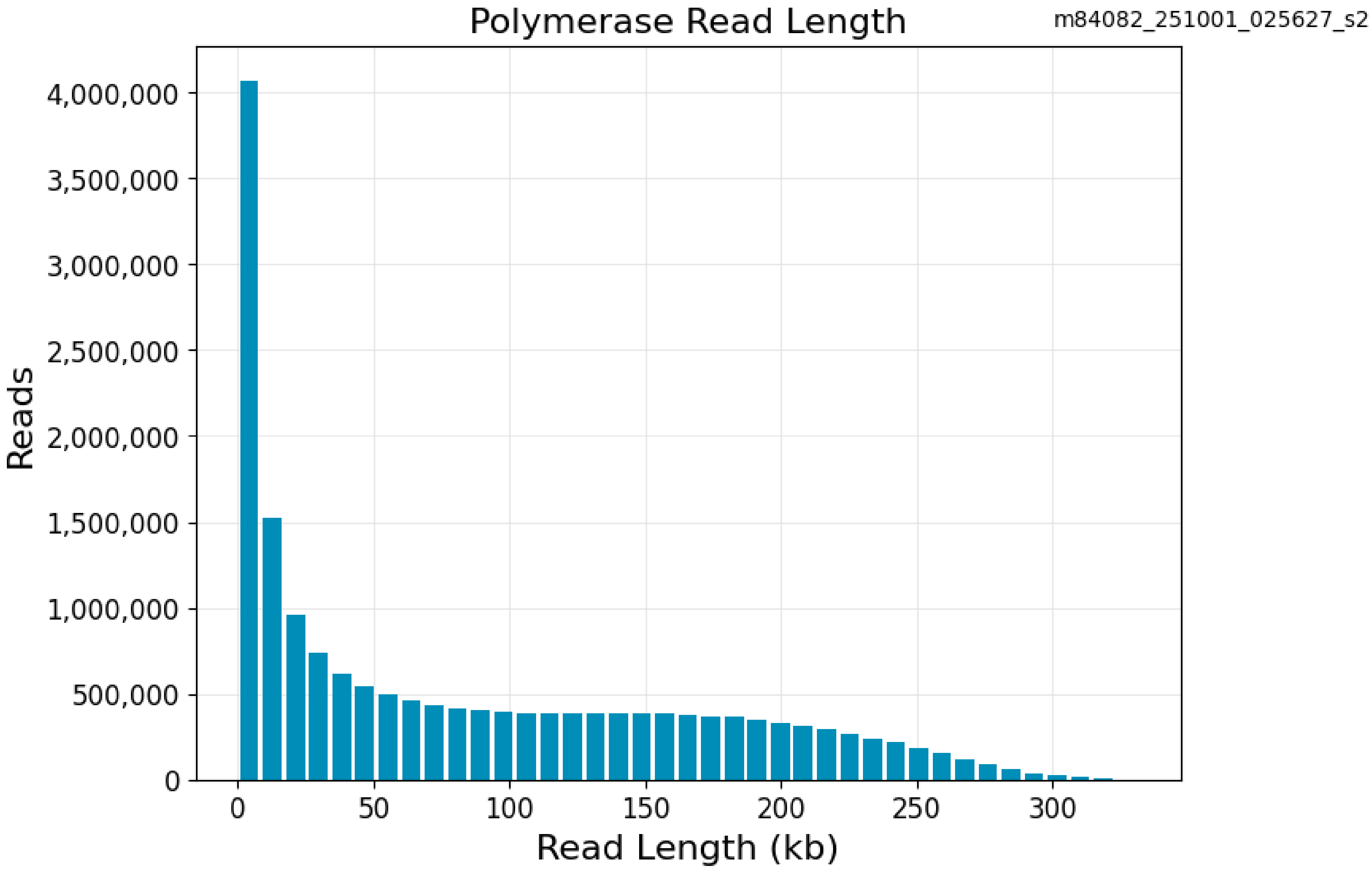
Productive ZMWs	25,165,824
Productivity 0	7,367,761
Productivity 1	17,589,857
Productivity 2	208,206

Raw Data Report

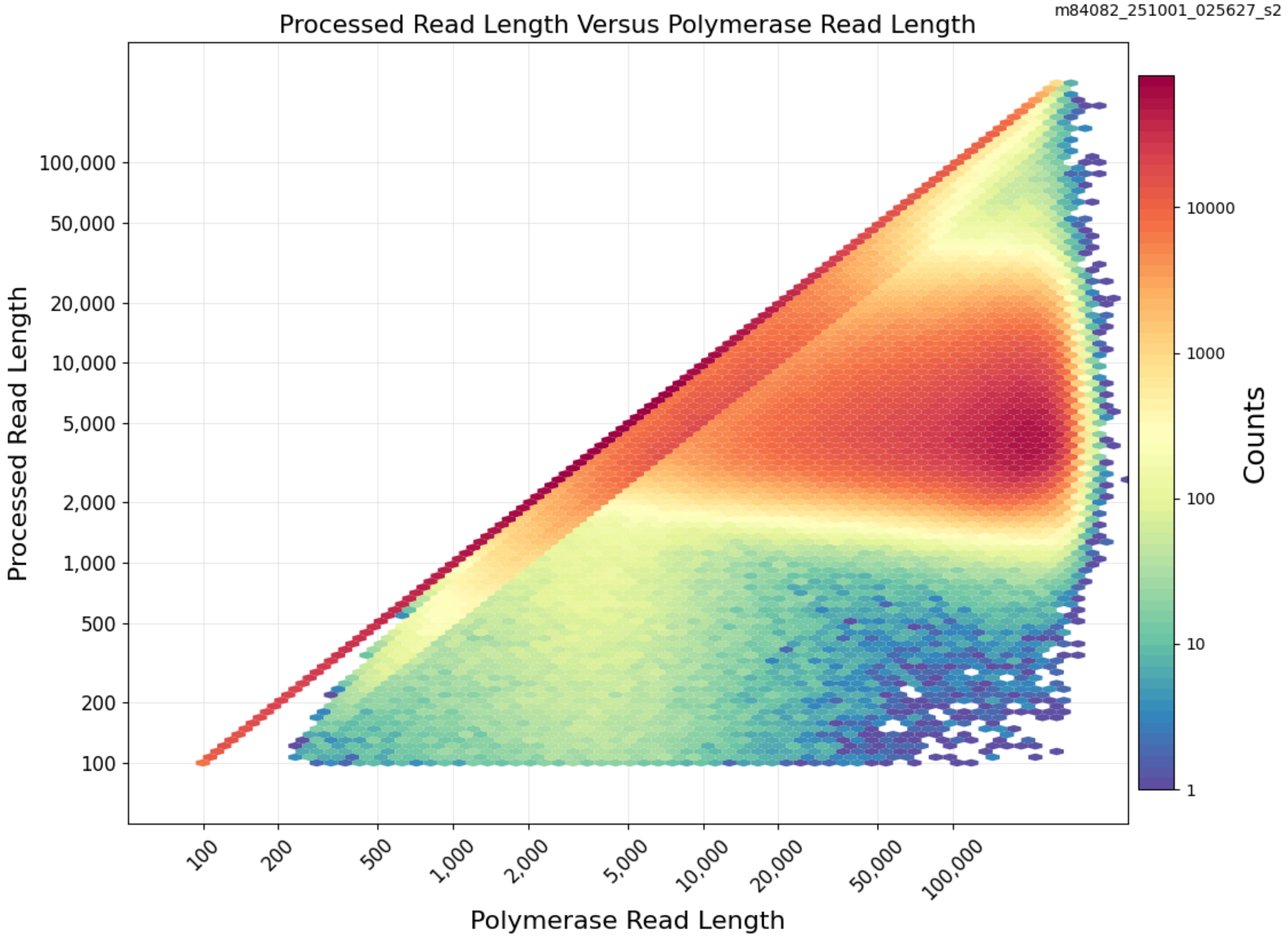
Summary Metrics

Polymerase Read Bases	1,442,086,707,762
Polymerase Reads	17,584,965
Polymerase Read Length (mean)	82.01 kb
Polymerase read length (N50)	170.75 kb
Polymerase read length longest subread length (mean)	9.78 kb
Polymerase read length longest subread length (N50)	16.25 kb
Unique Molecular Yield	139,333,615,616
Local Base Rate	2.42

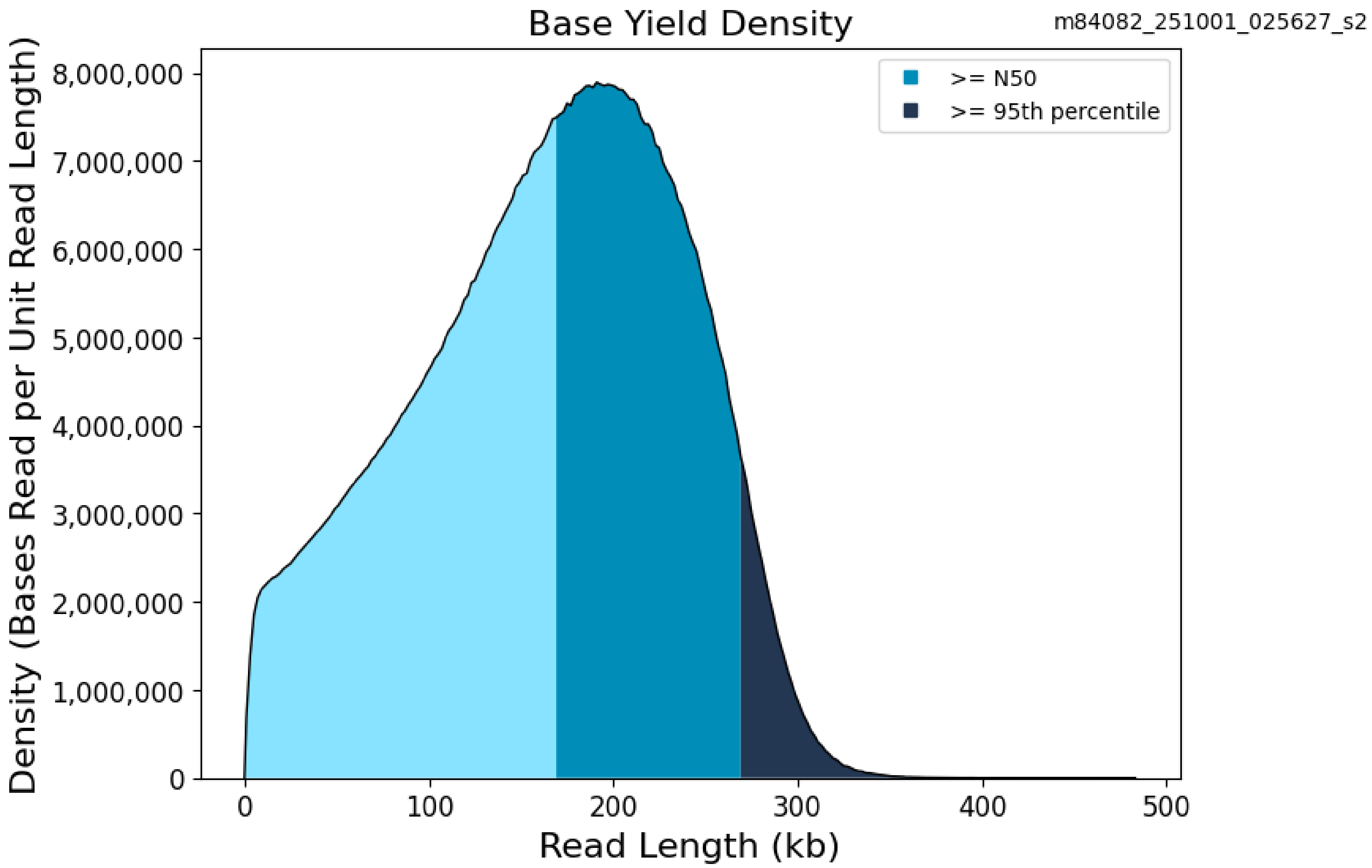
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

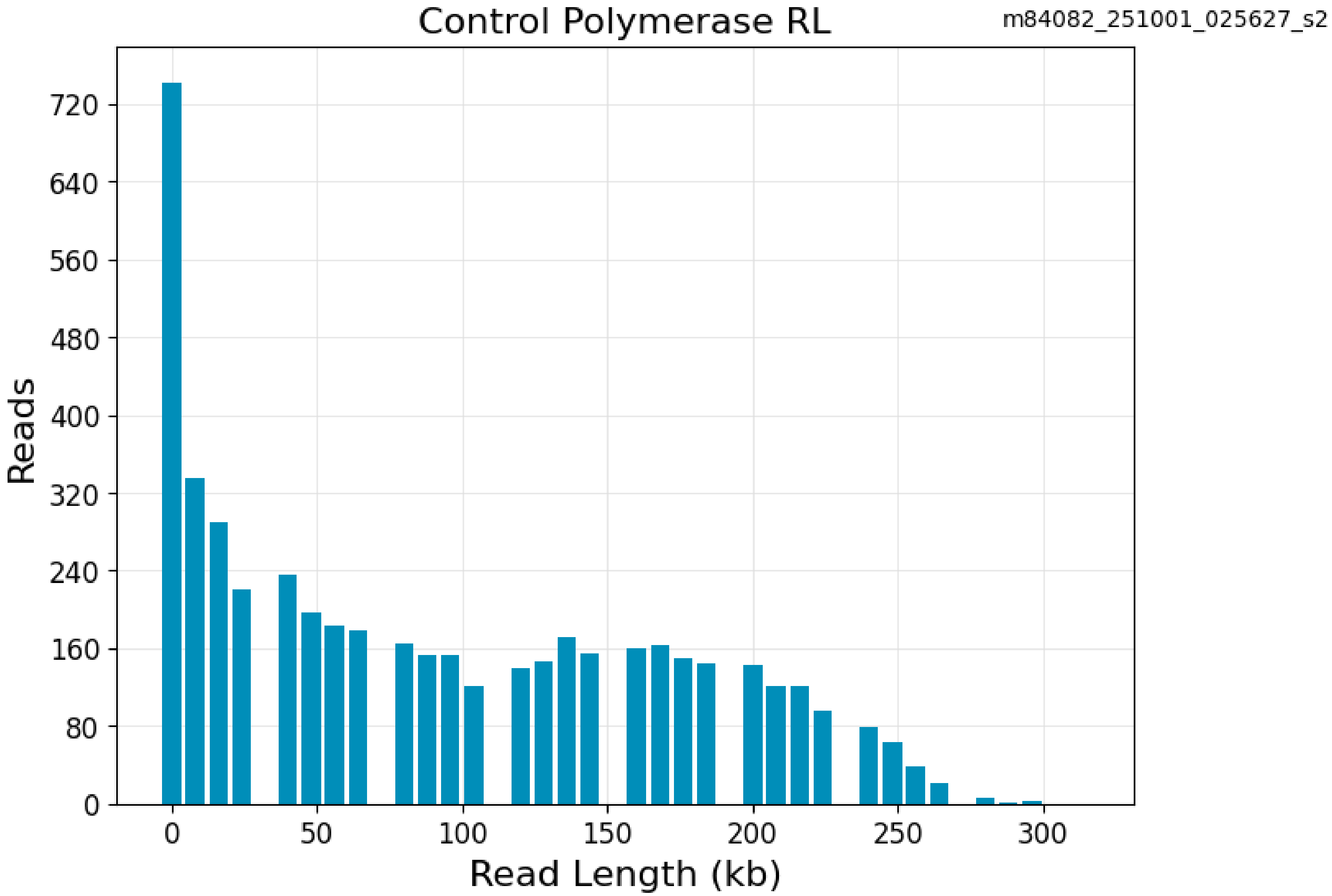


Control Report

Summary Metrics

Number of Control Reads	4,892
Control Read Length Mean	94,606
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance