Report for m84082_250614_081210_s3

Dataset details

Name: AS-266_Goetz-Pool1_HiFi_300pM-Cell3

Path: /data2/rawdata/r84082_20250614_035756/1_C01/pb_formats/m84082_250614_081210_s3.hifi_reads.consensusreadset.xml

Unique ID: ea368156-7d09-425d-9228-52a09dc68d5a

Created at: 2025-06-16T02:53:24.248Z

HiFi sequences: 9,035,911

HiFi bases: 60,762,649,081

Bio sample name: AS-266_Goetz-Pool1

Well sample name: AS-266_Goetz-Pool1_HiFi_300pM

Run name: Run 06.13.2025 14:38

Movie name: m84082_250614_081210_s3

Instrument name: Revio

ICS version: 13.3.0.253824

Number of child datasets: 0

Number of HiFi BAM files: 1

CCS Analysis Report

Summary Metrics

HiFi reads	9.0 M
HiFi reads yield	60.76 Gb
HiFi reads length (mean)	6.72 kb
HiFi reads length (median, bp)	5,831
HiFi Read Length N50 (bp)	7,212
HiFi Read Quality (median)	Q47
HiFi Read Quality (median)	47
Base Quality ≥Q30 (%)	97.42%
HiFi Number of Passes (mean)	23
Missing adapters (%)	2.82%

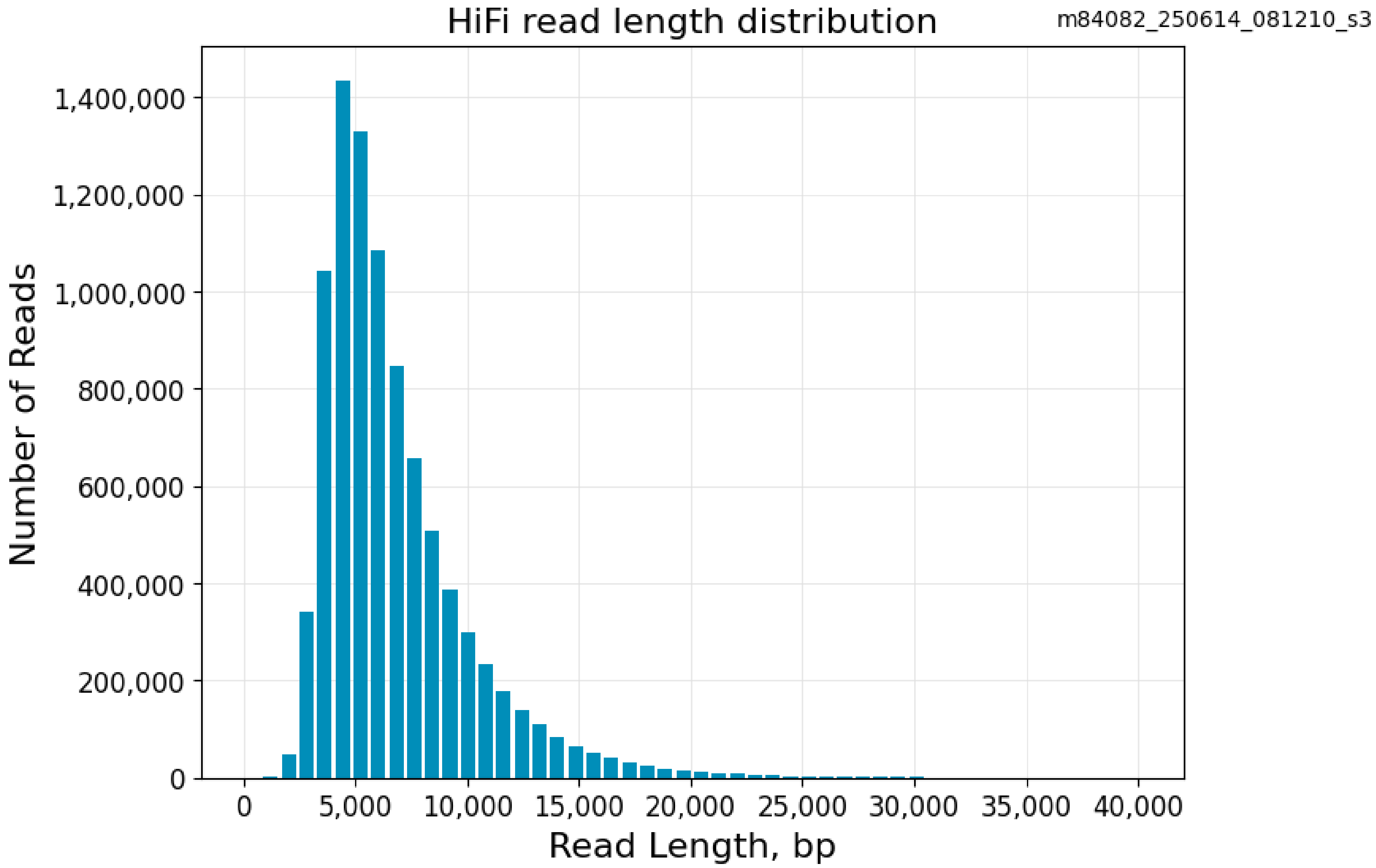
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	9,035,907	100	60.76 Gb	100
≥ 5,000	5,837,365	65	47.91 Gb	79
≥ 10,000	1,204,236	13	16.05 Gb	26
≥ 15,000	264,462	3	4.89 Gb	8
≥ 20,000	63,221	1	1.49 Gb	2
≥ 25,000	15,900	0	0.46 Gb	1
≥ 30,000	4,139	0	0.14 Gb	0
≥ 35,000	1,109	0	0.04 Gb	0
≥ 40,000	282	0	0.01 Gb	0

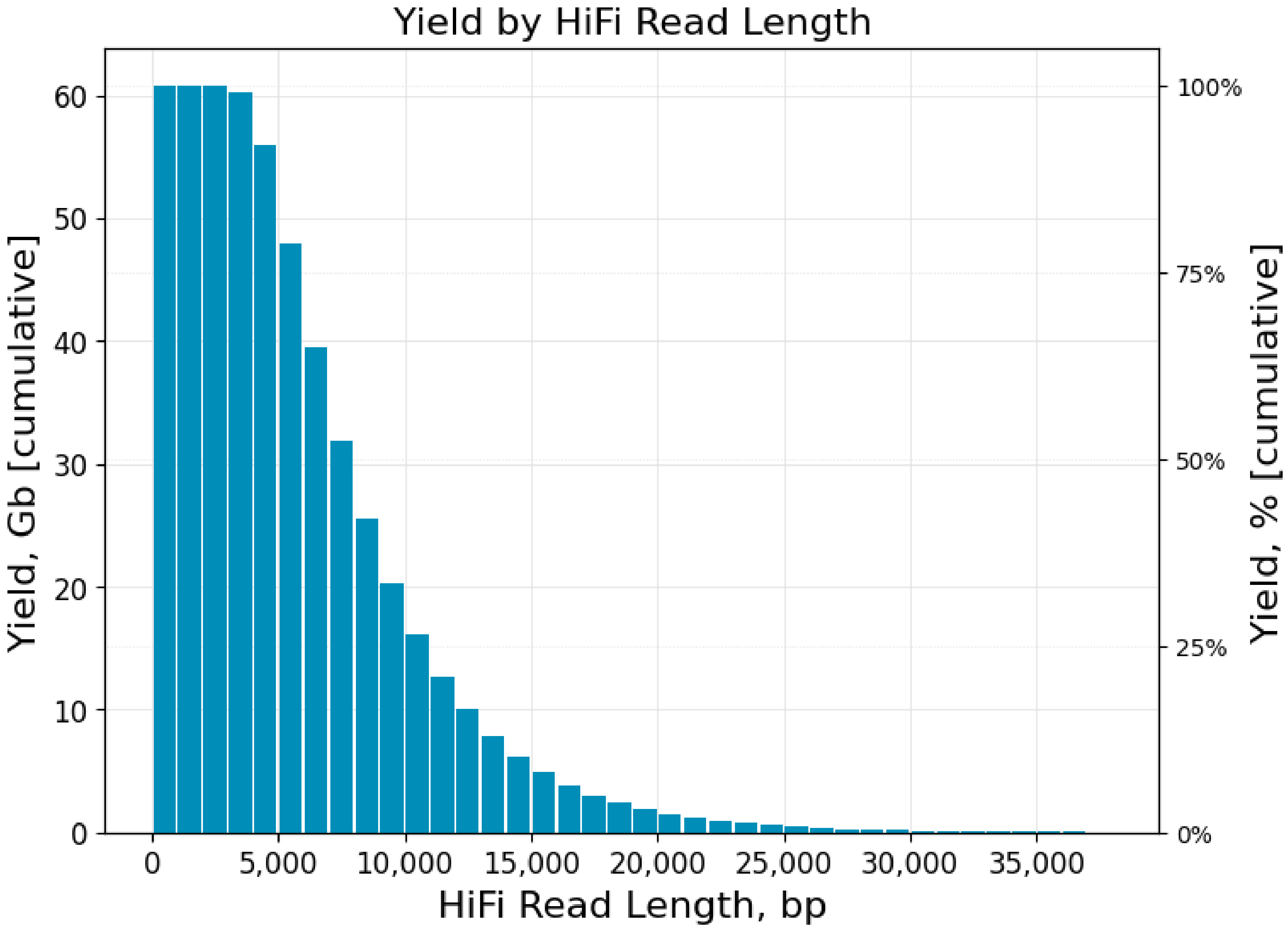
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	9,035,907	100	60.76 Gb	100
≥ Q30	7,813,971	86	51.40 Gb	85
≥ Q40	5,921,643	66	36.75 Gb	60
≥ Q50	3,913,336	43	22.20 Gb	37

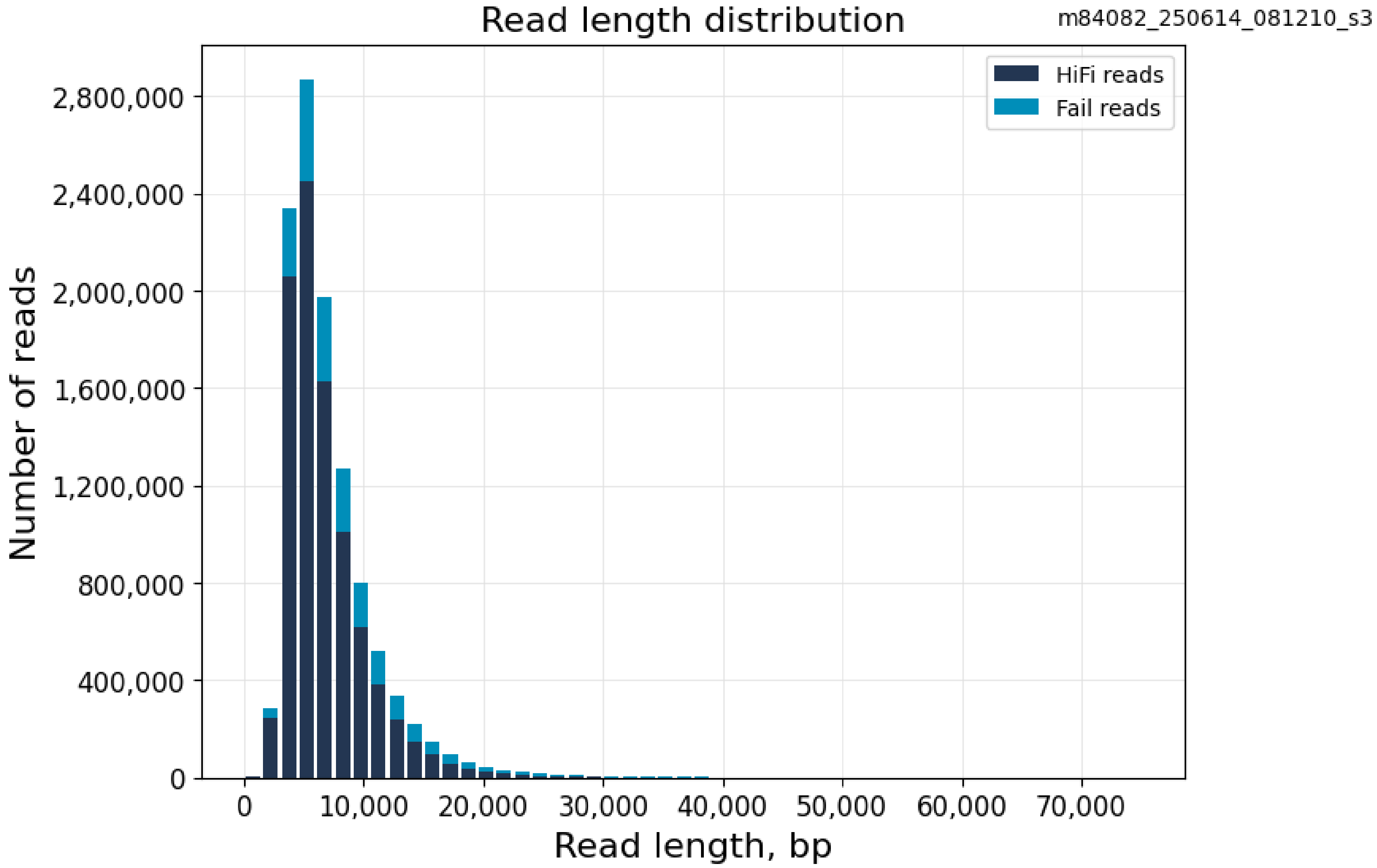
Read Length Distribution: HiFi read length distribution



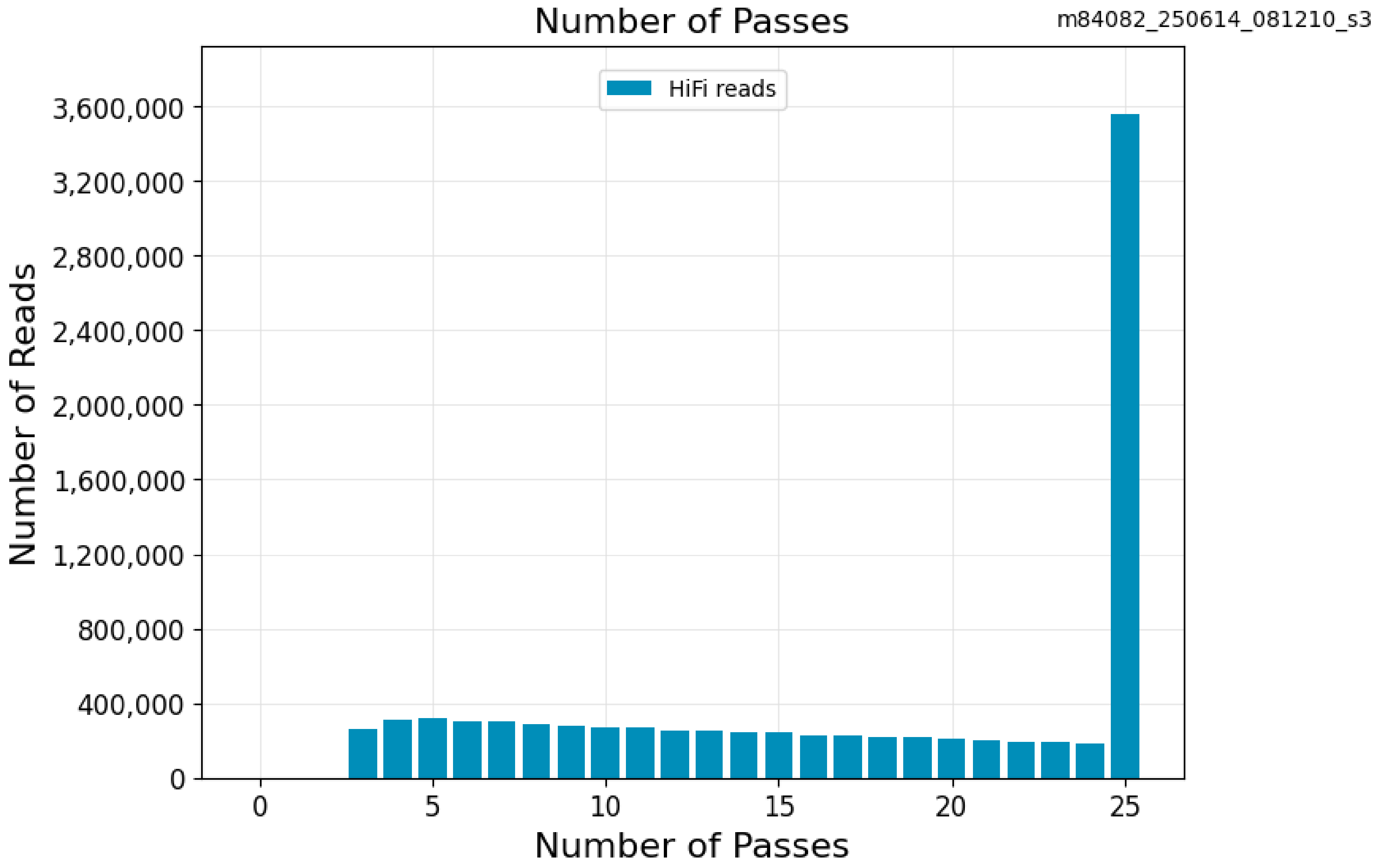
Read Length Distribution: Yield by HiFi Read Length



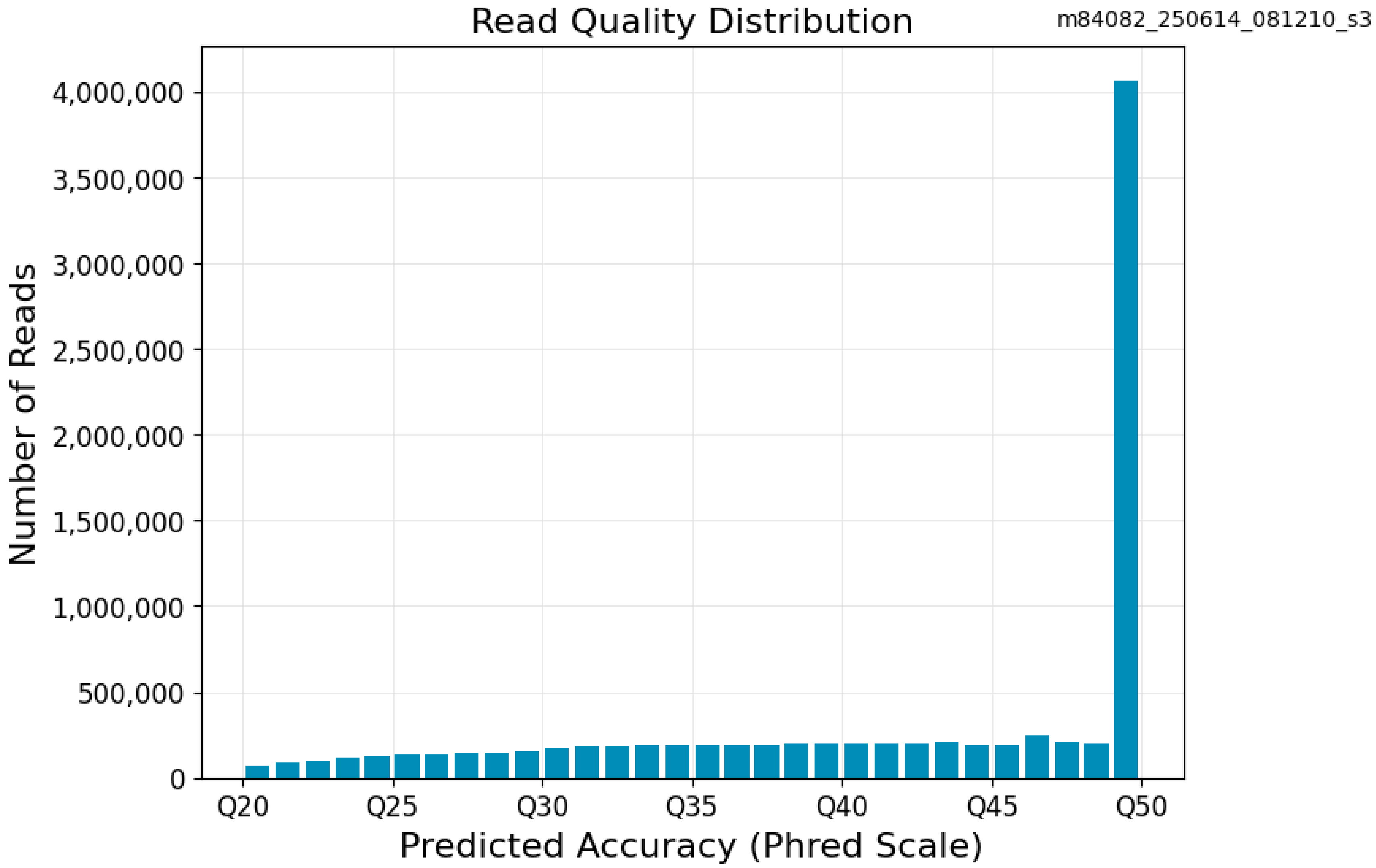
Read Length Distribution: Read length distribution



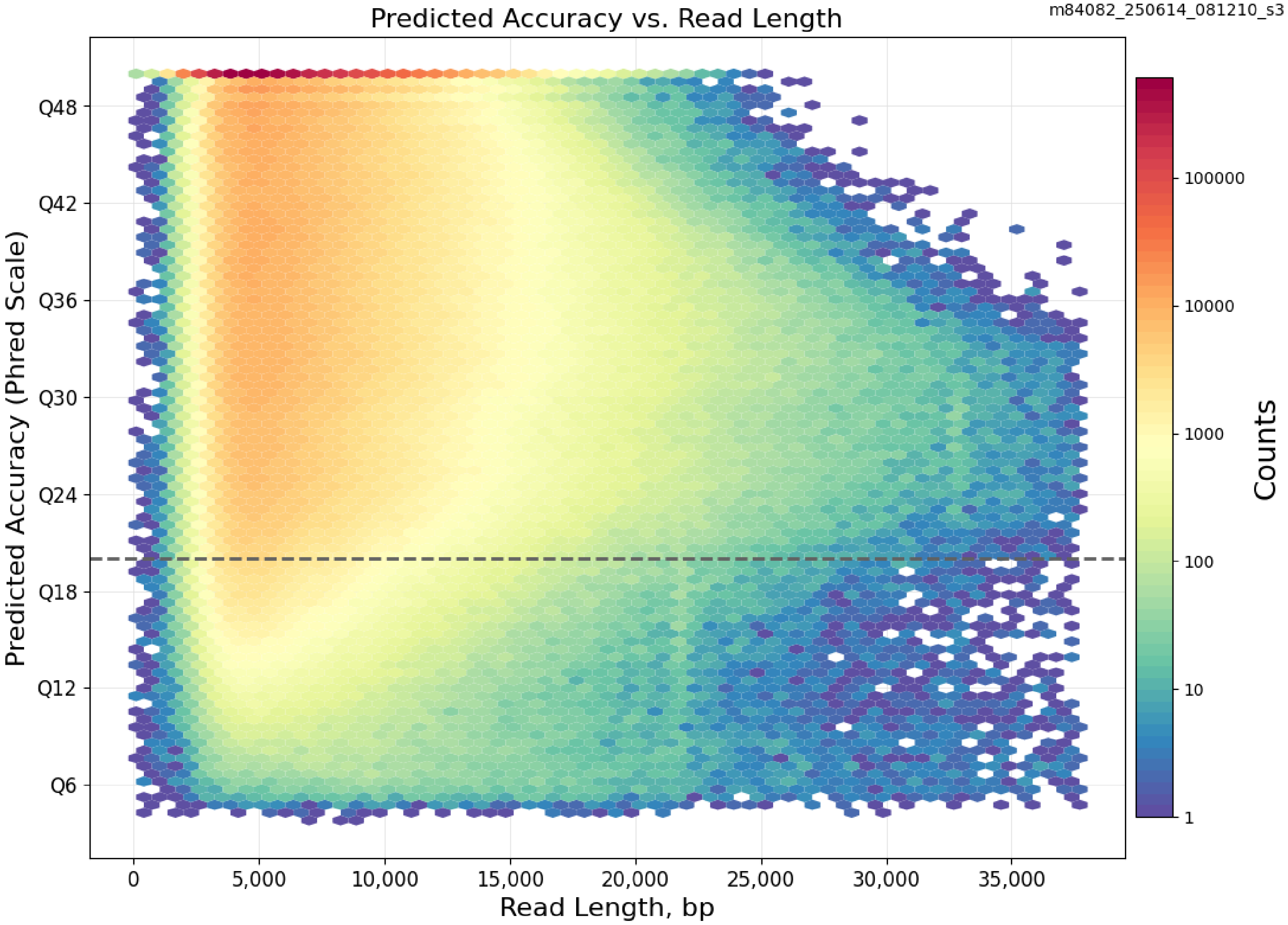
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

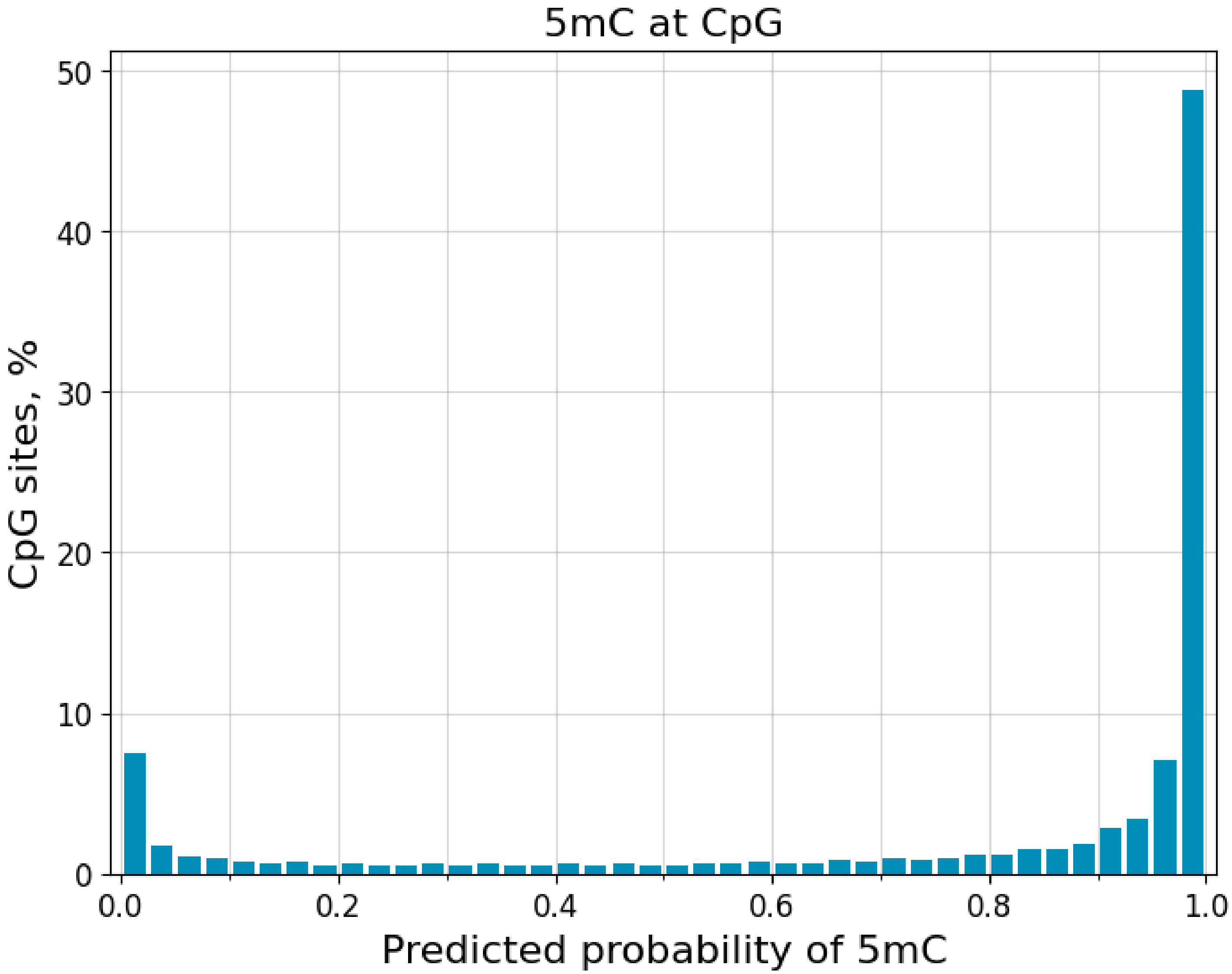


Methylation

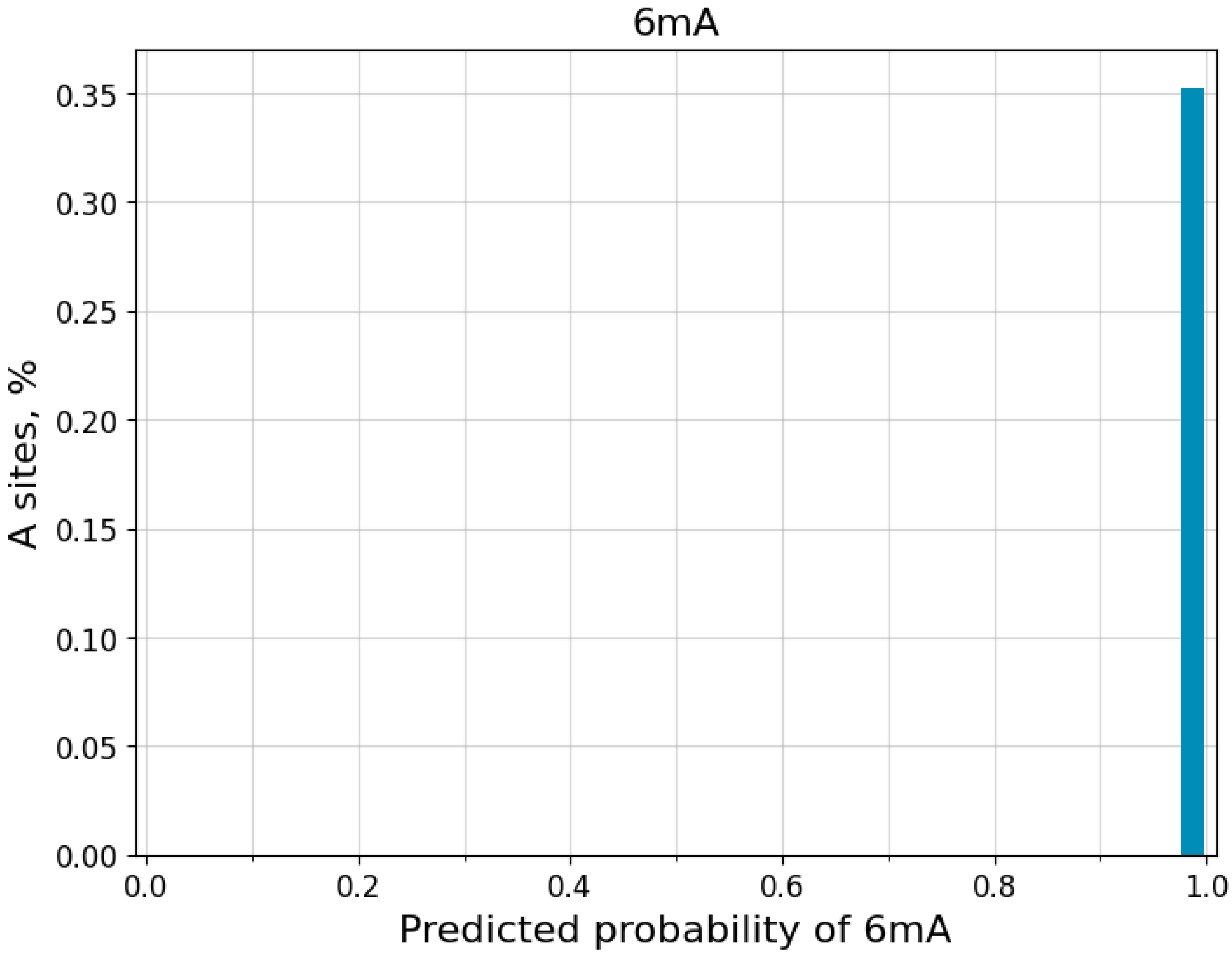
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	98.1%	77.6%
6mA	A	0.4%	0.4%

Score distributions: 5mC at CpG



Score distributions: 6mA



Loading Report

Summary Metrics

Productive ZMWs	25,165,824
Productivity 0	8,582,296
Productivity 1	16,463,320
Productivity 2	120,208

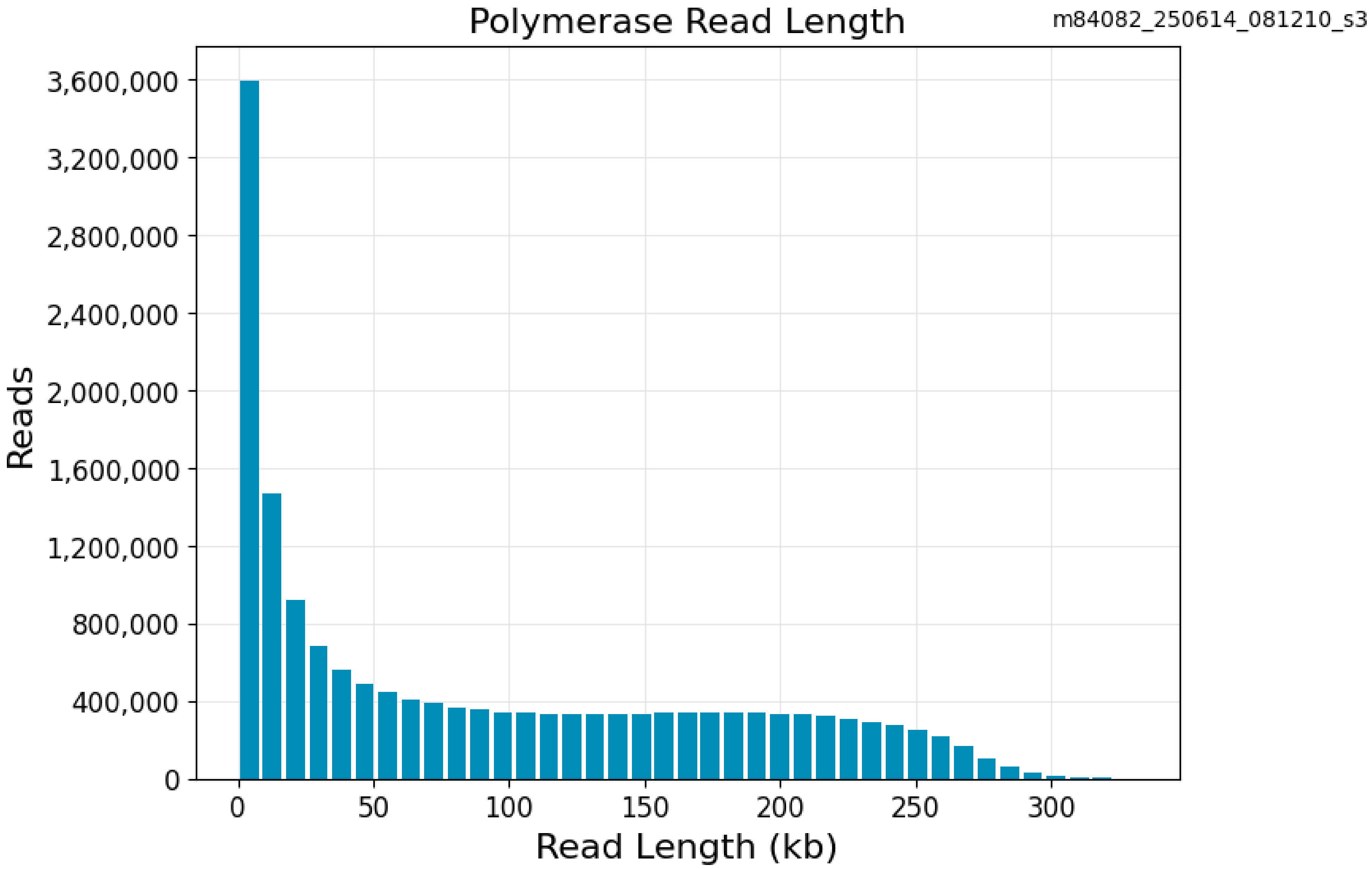
Report for m84082_250614_081210_s3

Raw Data Report

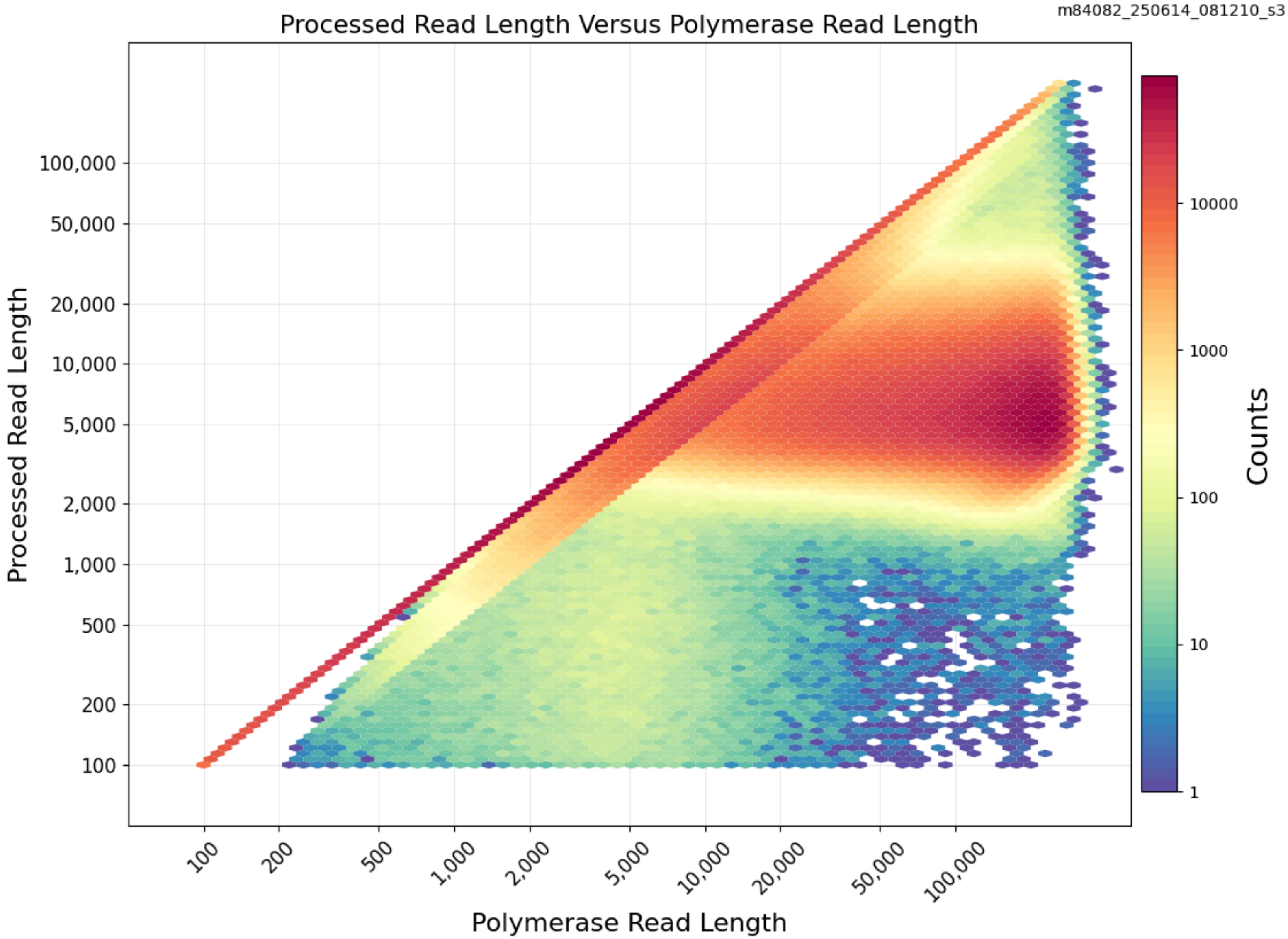
Summary Metrics

Polymerase Read Bases	1,438,500,444,295
Polymerase Reads	16,457,064
Polymerase Read Length (mean)	87.41 kb
Polymerase read length (N50)	182.25 kb
Polymerase read length longest subread length (mean)	9.62 kb
Polymerase read length longest subread length (N50)	12.75 kb
Unique Molecular Yield	136,956,985,344
Local Base Rate	2.52

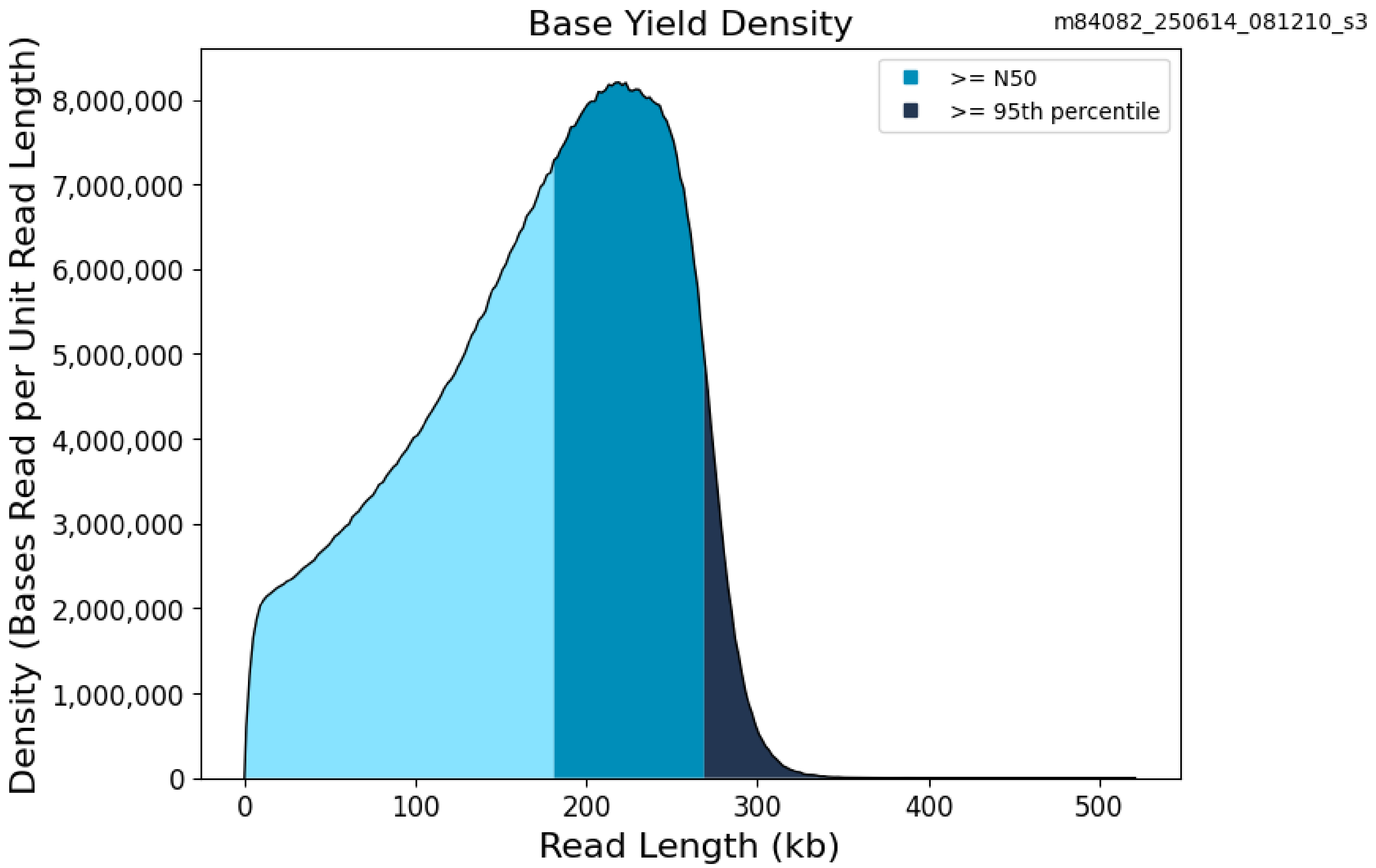
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

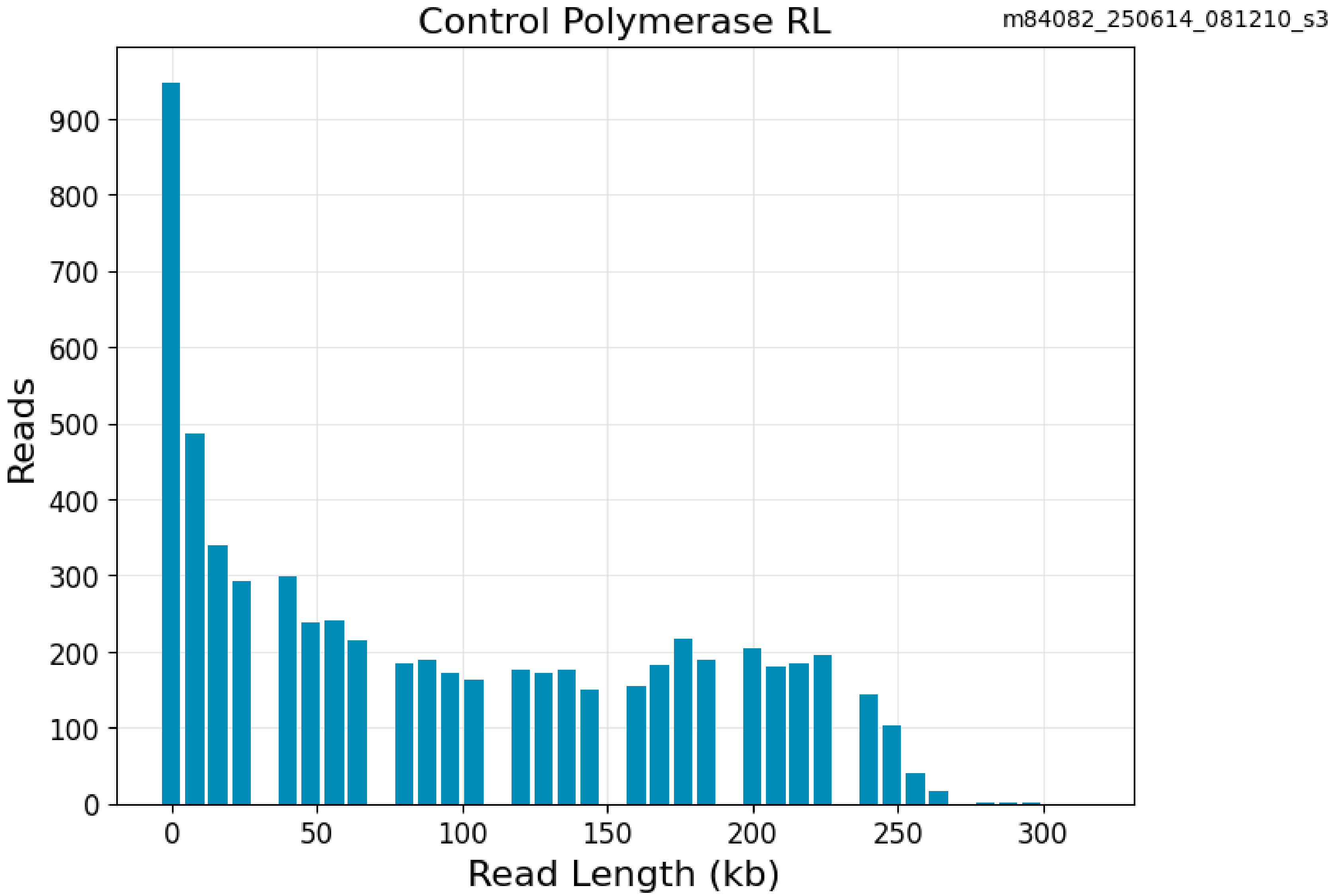


Control Report

Summary Metrics

Number of Control Reads	6,256
Control Read Length Mean	96,704
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.93

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance