Report for m84082_250614_101514_s4

Dataset details

Name: AS-266_Goetz-Pool2_HiFi_300pM-Cell4

Path: /data2/rawdata/r84082_20250614_035756/1_D01/pb_formats/m84082_250614_101514_s4.hifi_reads.consensusreadset.xml

Unique ID: b152c553-3819-4d69-ab4a-078e1cecdc0e

Created at: 2025-06-16T03:57:58.243Z

HiFi sequences: 8,055,065

HiFi bases: 52,047,263,934

Bio sample name: AS-266_Goetz-Pool2

Well sample name: AS-266_Goetz-Pool2_HiFi_300pM

Run name: Run 06.13.2025 14:38

Movie name: m84082_250614_101514_s4

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	8.1 M
HiFi reads yield	52.05 Gb
HiFi reads length (mean)	6.46 kb
HiFi reads length (median, bp)	5,704
HiFi Read Length N50 (bp)	6,894
HiFi Read Quality (median)	Q47
HiFi Read Quality (median)	47
Base Quality ≥Q30 (%)	97.53%
HiFi Number of Passes (mean)	24
Missing adapters (%)	3.25%

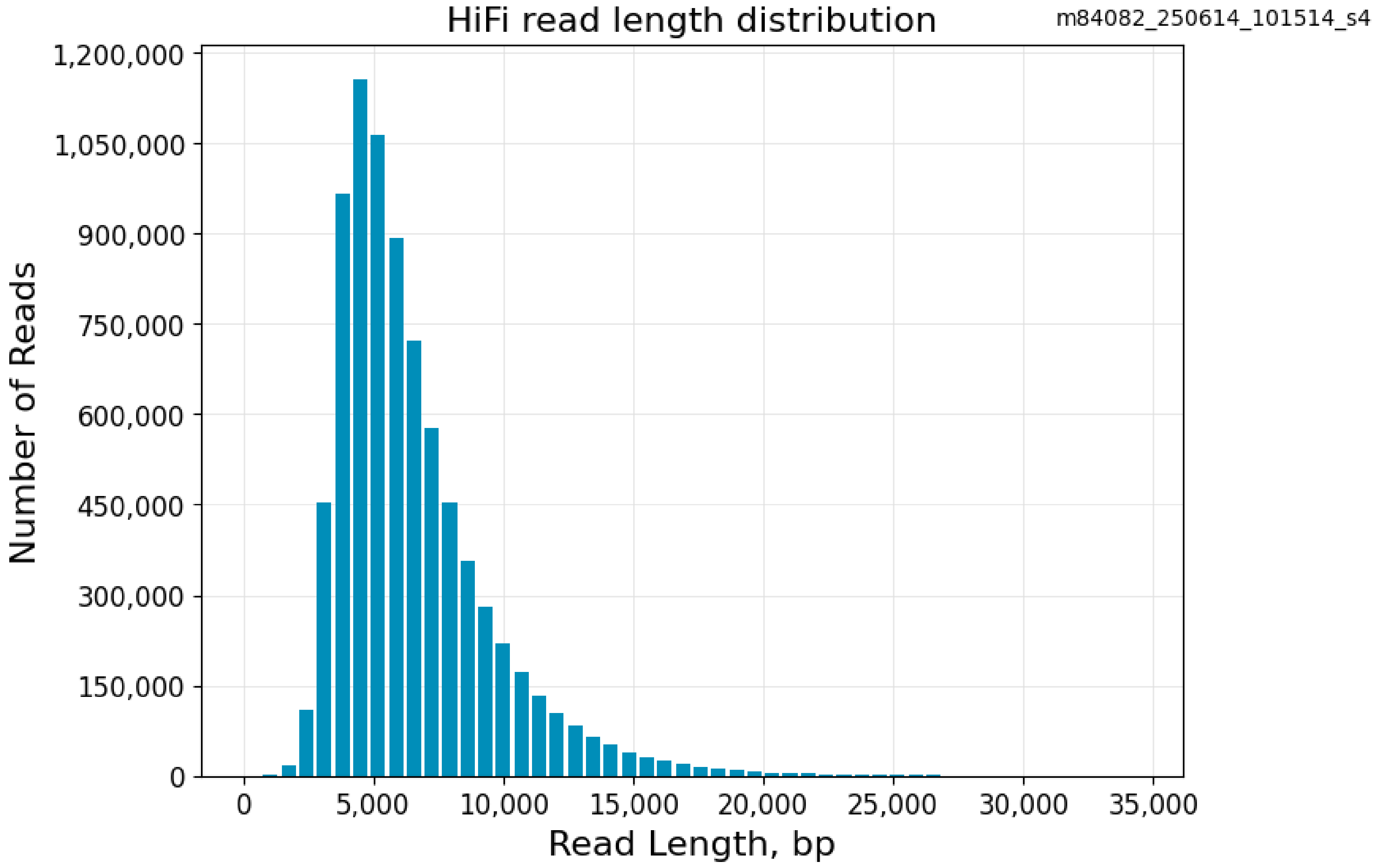
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	8,055,065	100	52.05 Gb	100
≥ 5,000	5,070,362	63	40.05 Gb	77
≥ 10,000	892,881	11	11.45 Gb	22
≥ 15,000	151,083	2	2.69 Gb	5
≥ 20,000	25,908	0	0.59 Gb	1
≥ 25,000	4,469	0	0.12 Gb	0
≥ 30,000	727	0	0.02 Gb	0
≥ 35,000	116	0	0.00 Gb	0
≥ 40,000	15	0	0.00 Gb	0

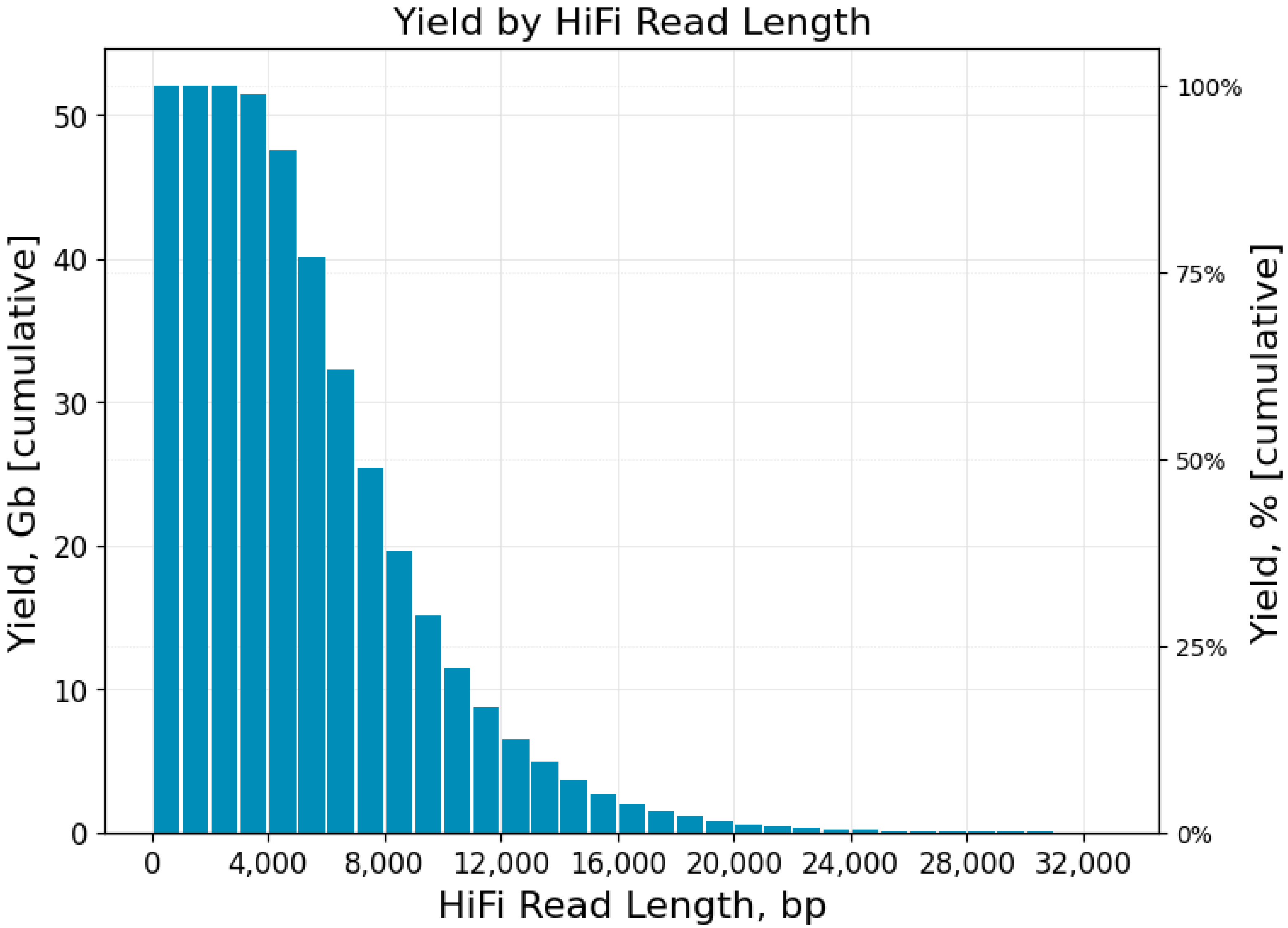
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	8,055,065	100	52.05 Gb	100
≥ Q30	6,950,903	86	44.05 Gb	85
≥ Q40	5,256,870	65	31.66 Gb	61
≥ Q50	3,421,895	42	18.94 Gb	36

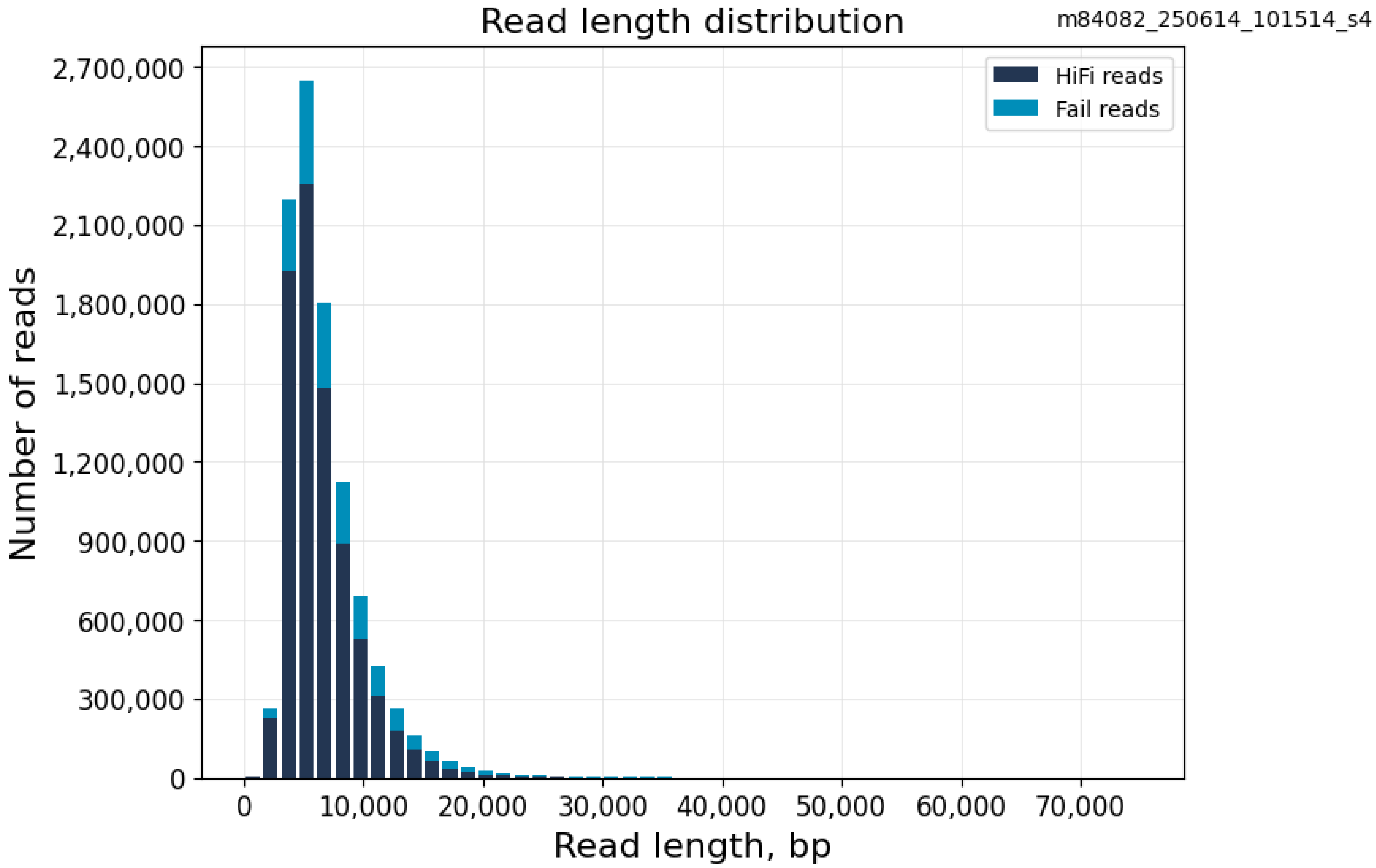
Read Length Distribution: HiFi read length distribution



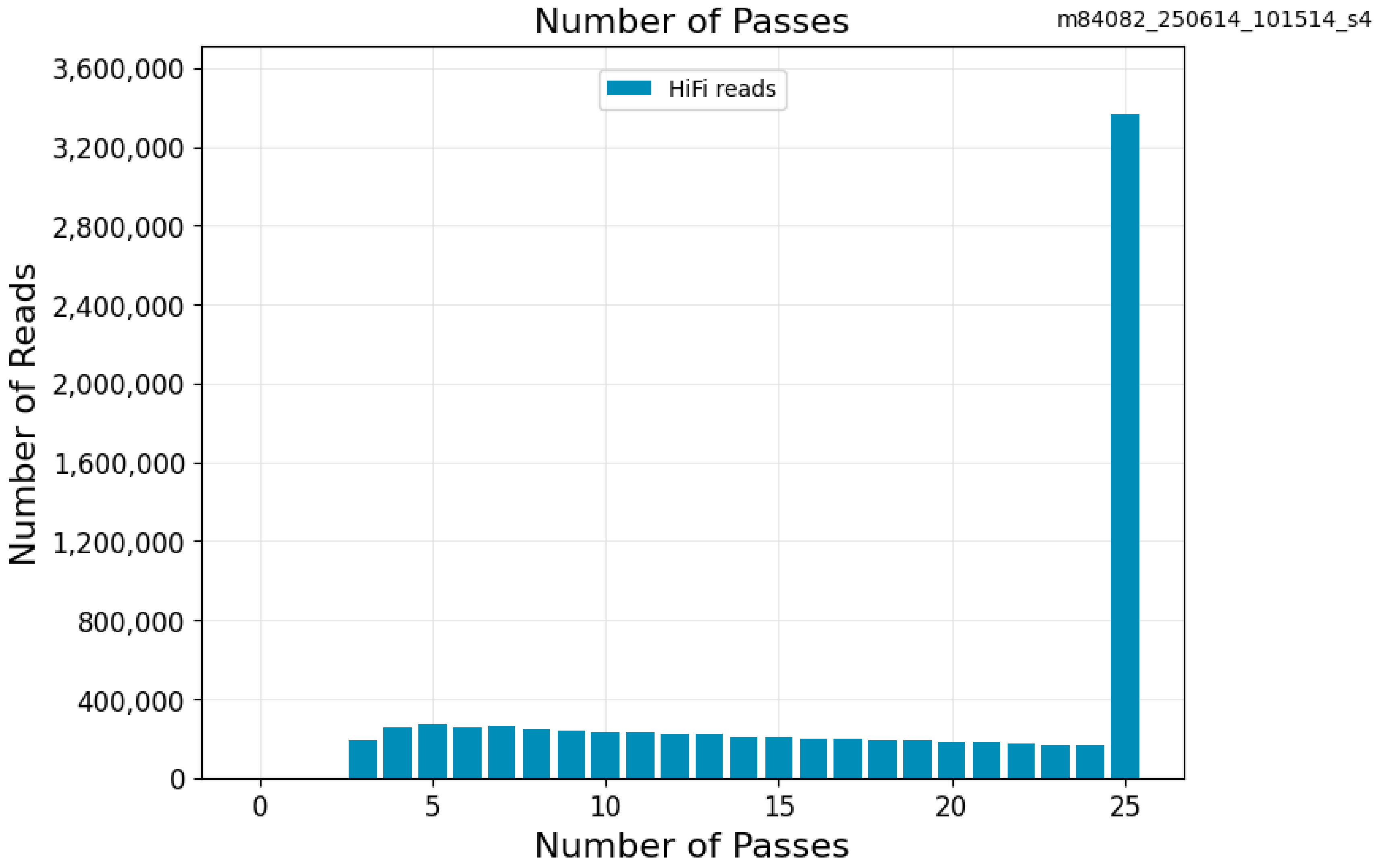
Read Length Distribution: Yield by HiFi Read Length



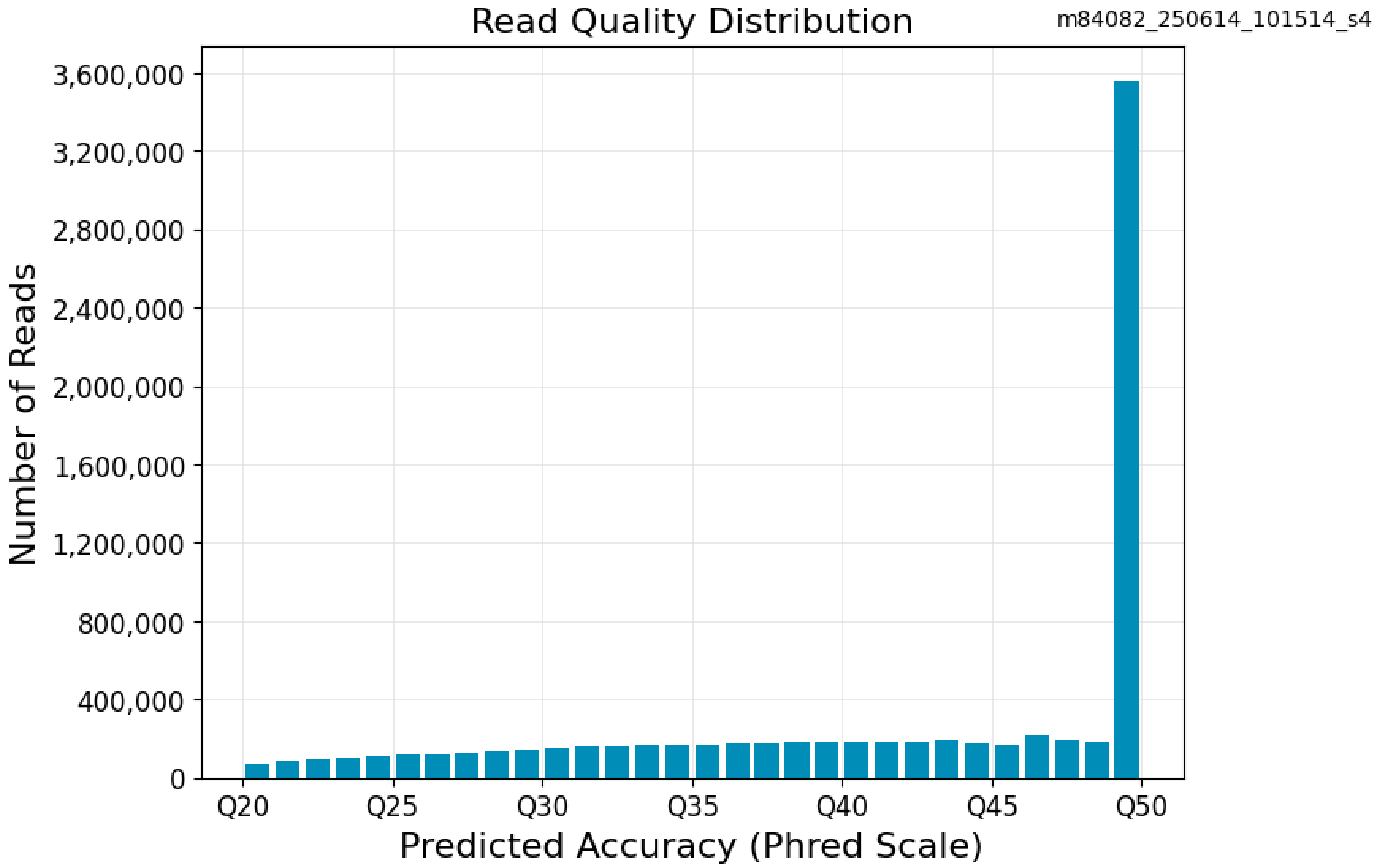
Read Length Distribution: Read length distribution



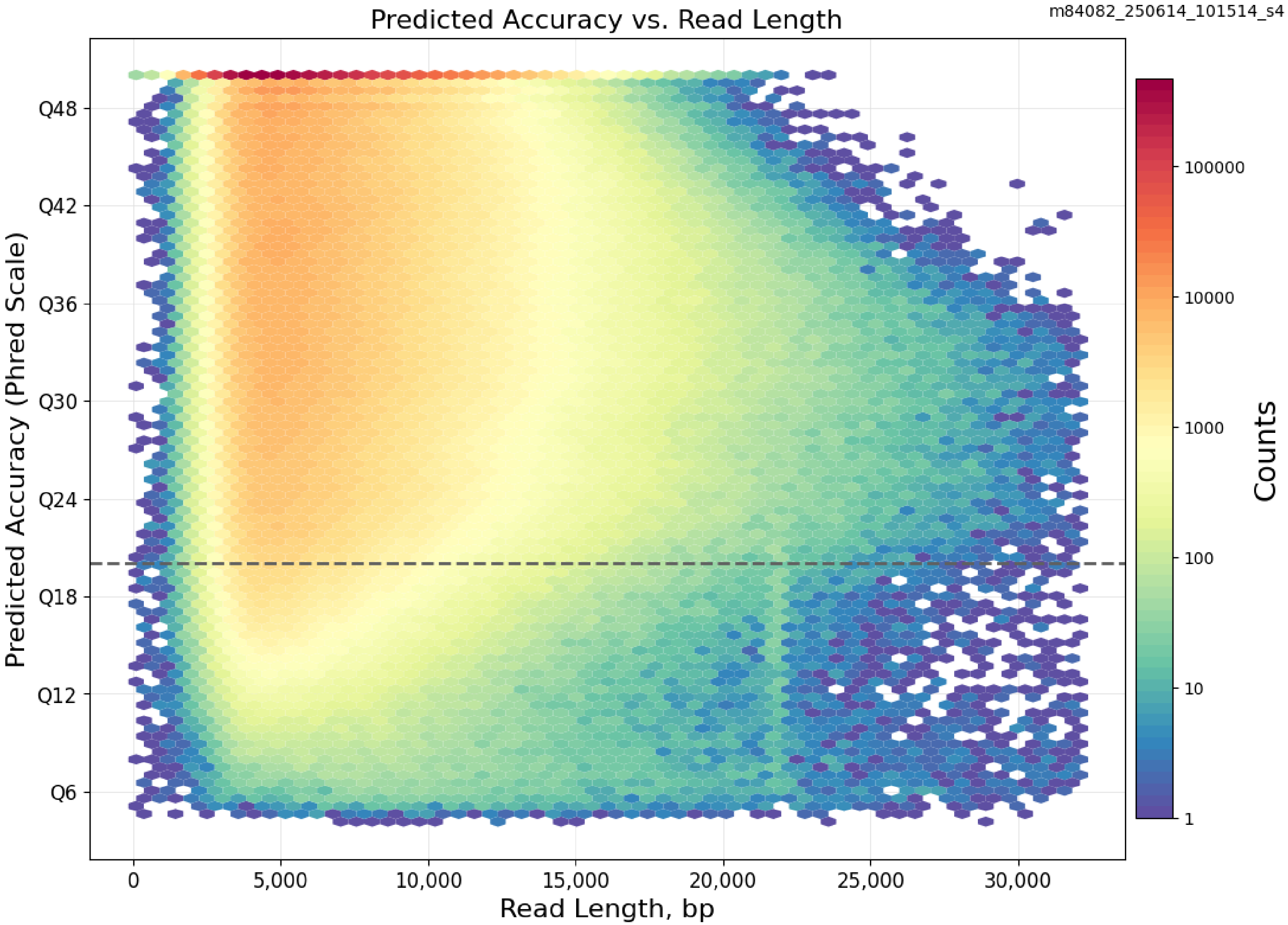
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

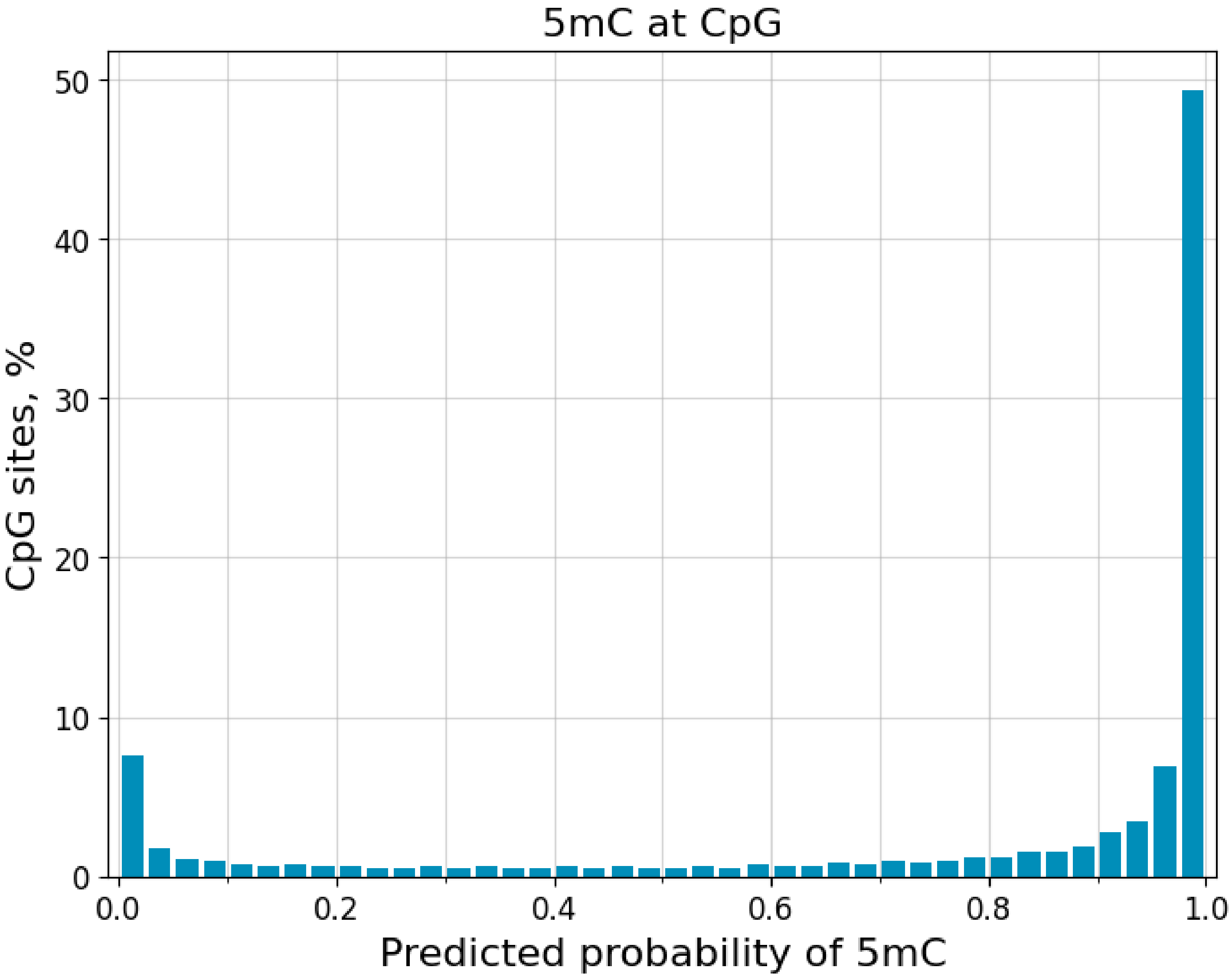


Methylation

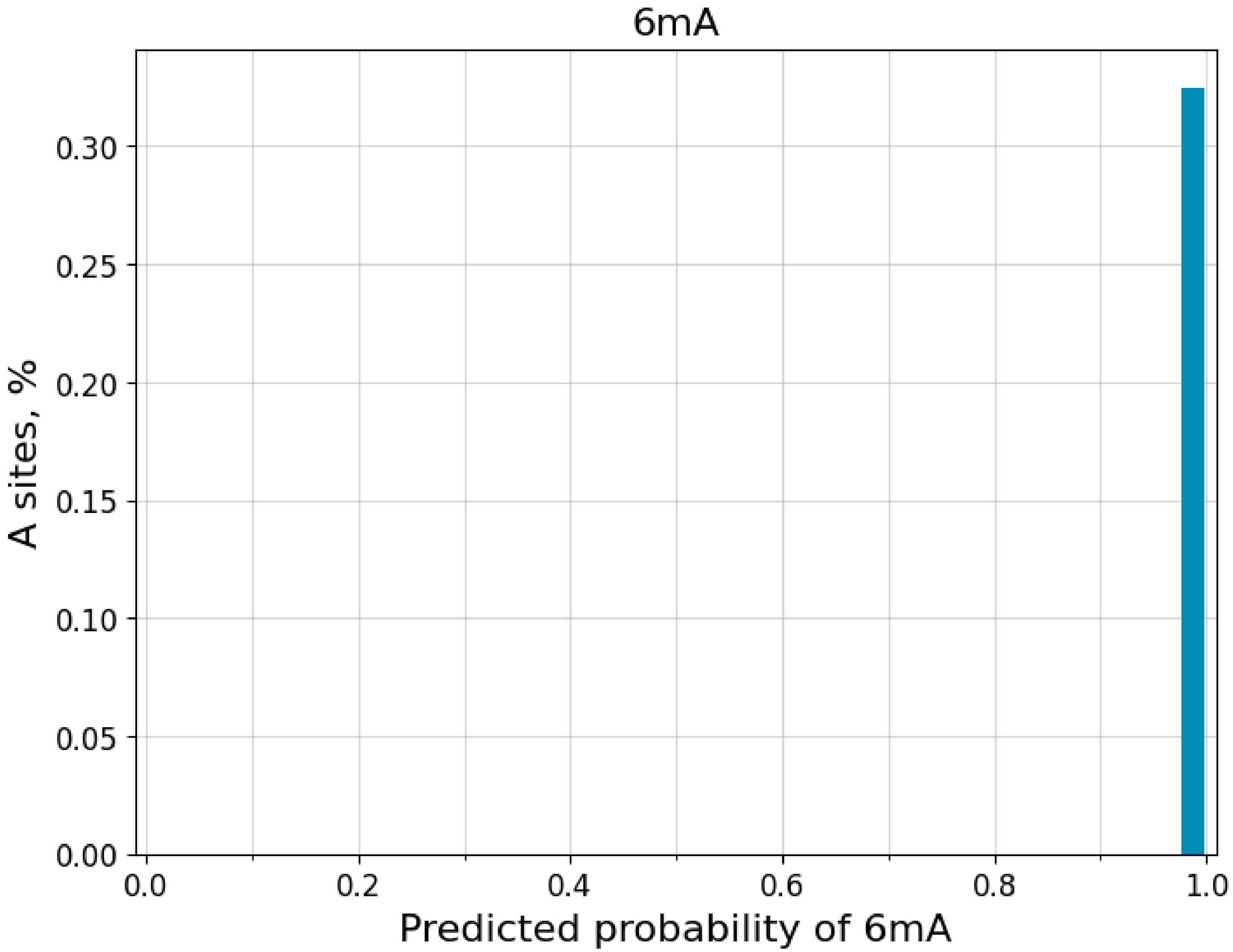
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	98.8%	77.9%
6mA	A	0.3%	0.3%

Score distributions: 5mC at CpG



Score distributions: 6mA



Loading Report

Summary Metrics

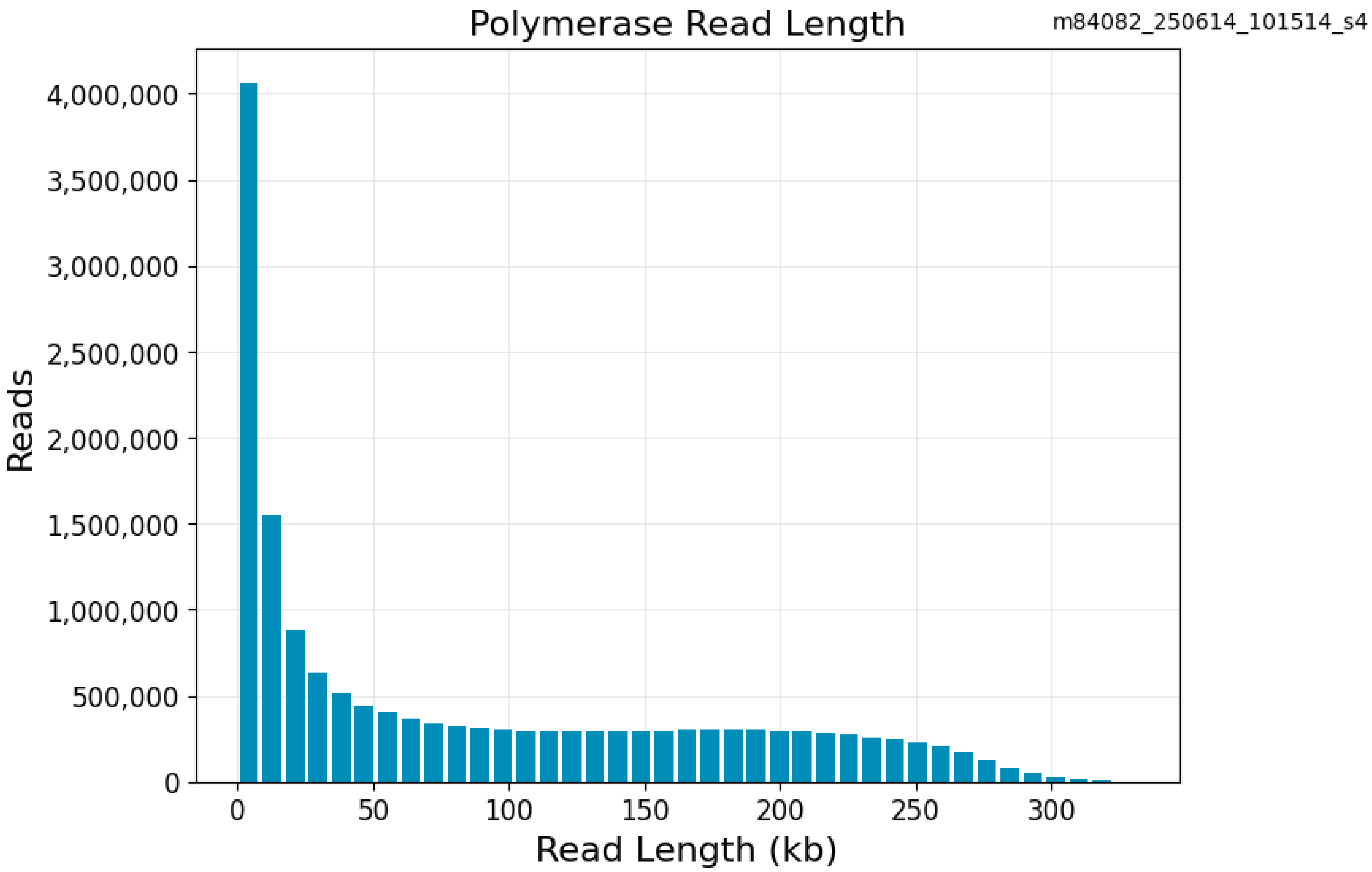
Productive ZMWs	25,165,824
Productivity 0	9,050,335
Productivity 1	15,944,614
Productivity 2	170,875

Raw Data Report

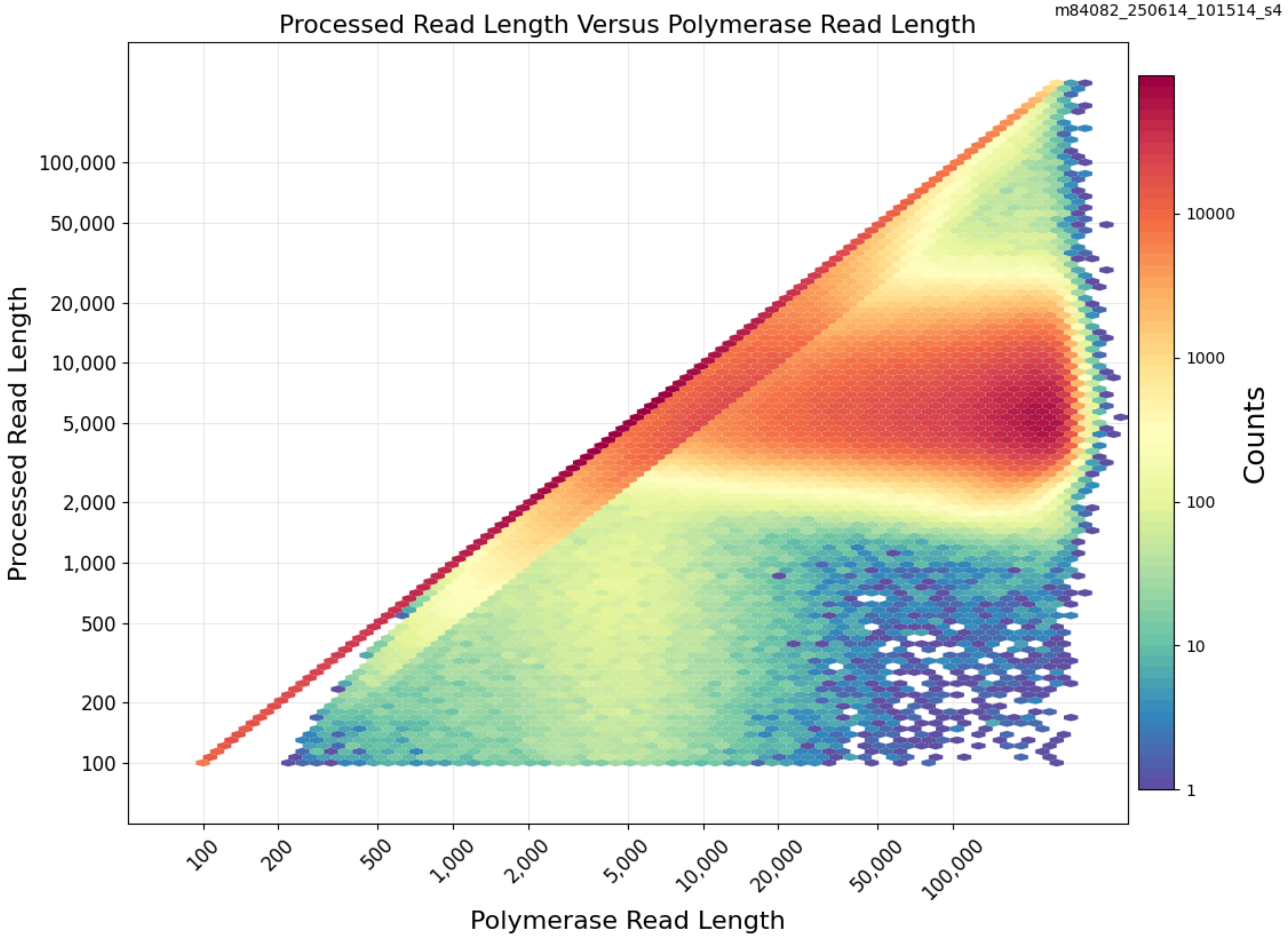
Summary Metrics

Polymerase Read Bases	1,317,609,305,789
Polymerase Reads	15,937,447
Polymerase Read Length (mean)	82.67 kb
Polymerase read length (N50)	185.25 kb
Polymerase read length longest subread length (mean)	9.62 kb
Polymerase read length longest subread length (N50)	12.75 kb
Unique Molecular Yield	129,460,207,616
Local Base Rate	2.56

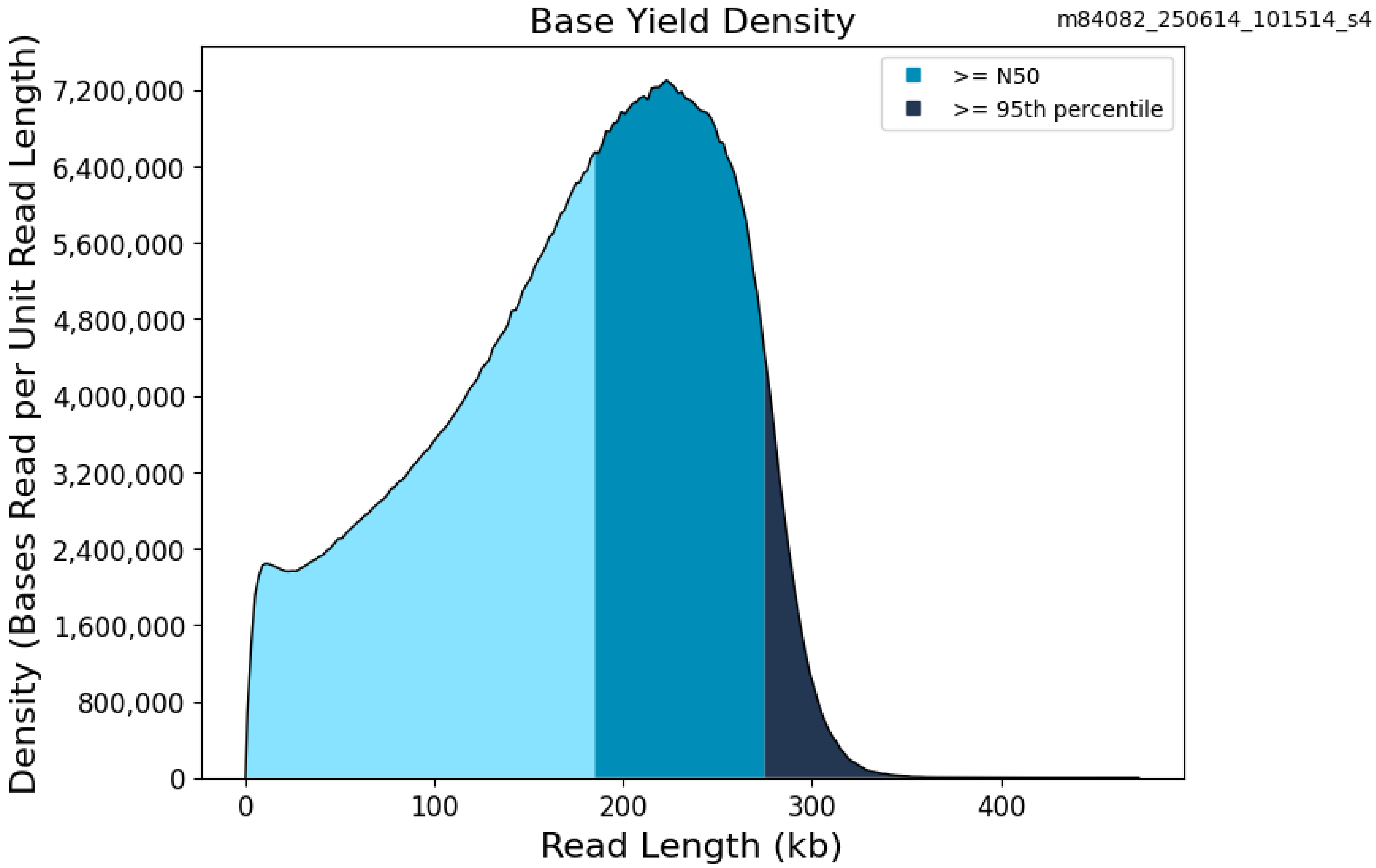
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

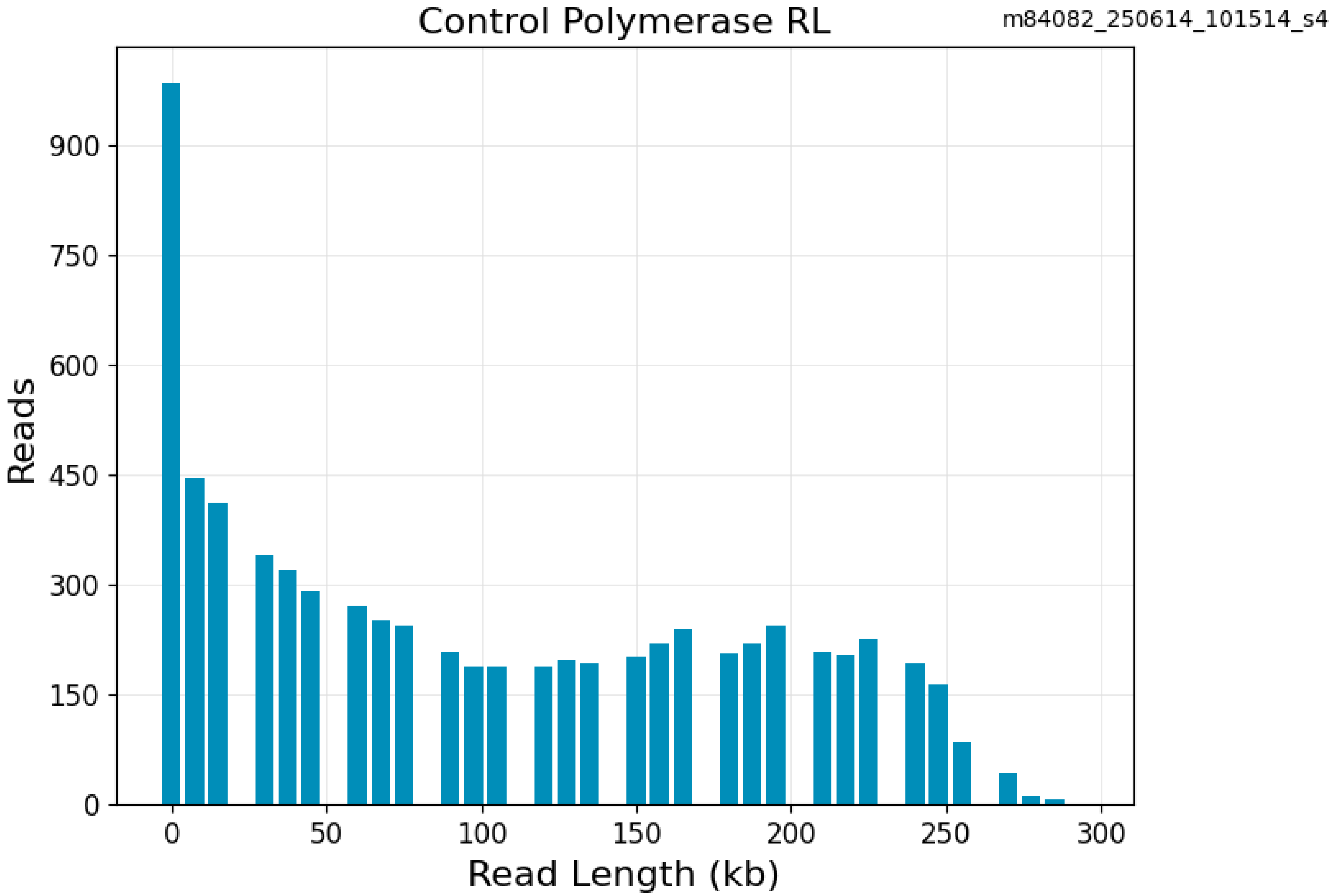


Control Report

Summary Metrics

Number of Control Reads	7,167
Control Read Length Mean	102,728
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance