

## Dataset details

**Name:** 2009093\_Gfrim-Head-Cell3

**Path:** /PACBIO/r84286\_20250616\_221216/1\_C01/pb\_formats/m84286\_250617\_022601\_s1.hifi\_reads.consensusreadset.xml

**Unique ID:** 80ca32a6-f3d8-44dc-9c49-7dbd80ddd0db

**Created at:** 2025-06-18T12:16:05.521Z

**HiFi sequences:** 4,601,075

**HiFi bases:** 66,765,938,649

**Bio sample name:** 2009093\_Gfrim-Head

**Well sample name:** 2009093\_Gfrim-Head

**Run name:** R6002976

**Movie name:** m84286\_250617\_022601\_s1

**Instrument name:** 84286

**ICS version:** 13.3.0.253824

**Number of child datasets:** 0

**Number of HiFi BAM files:** 1

## CCS Analysis Report

### Summary Metrics

HiFi reads	4.6 M
HiFi reads yield	66.71 Gb
HiFi reads length (mean)	14.50 kb
HiFi reads length (median, bp)	14,151
HiFi Read Length N50 (bp)	14,624
HiFi Read Quality (median)	Q34
HiFi Read Quality (median)	34
Base Quality $\geq$ Q30 (%)	94.08%
HiFi Number of Passes (mean)	9
Missing adapters (%)	15.38%

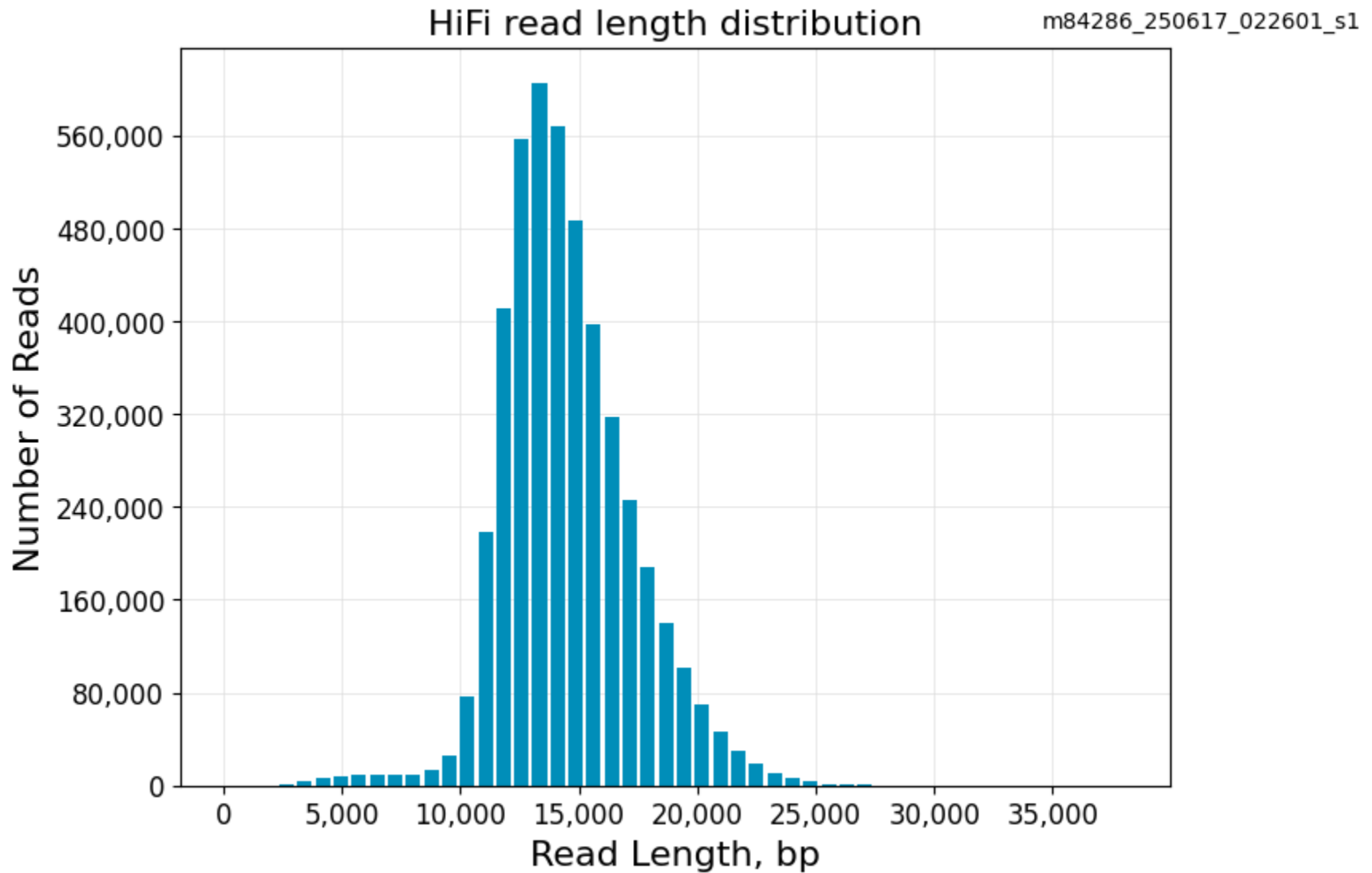
## HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	4,601,074	100	66.71 Gb	100
≥ 5,000	4,583,946	100	66.64 Gb	100
≥ 10,000	4,498,150	98	65.94 Gb	99
≥ 15,000	1,723,295	37	29.77 Gb	45
≥ 20,000	170,152	4	3.66 Gb	5
≥ 25,000	4,121	0	0.11 Gb	0
≥ 30,000	219	0	0.01 Gb	0
≥ 35,000	41	0	0.00 Gb	0
≥ 40,000	10	0	0.00 Gb	0

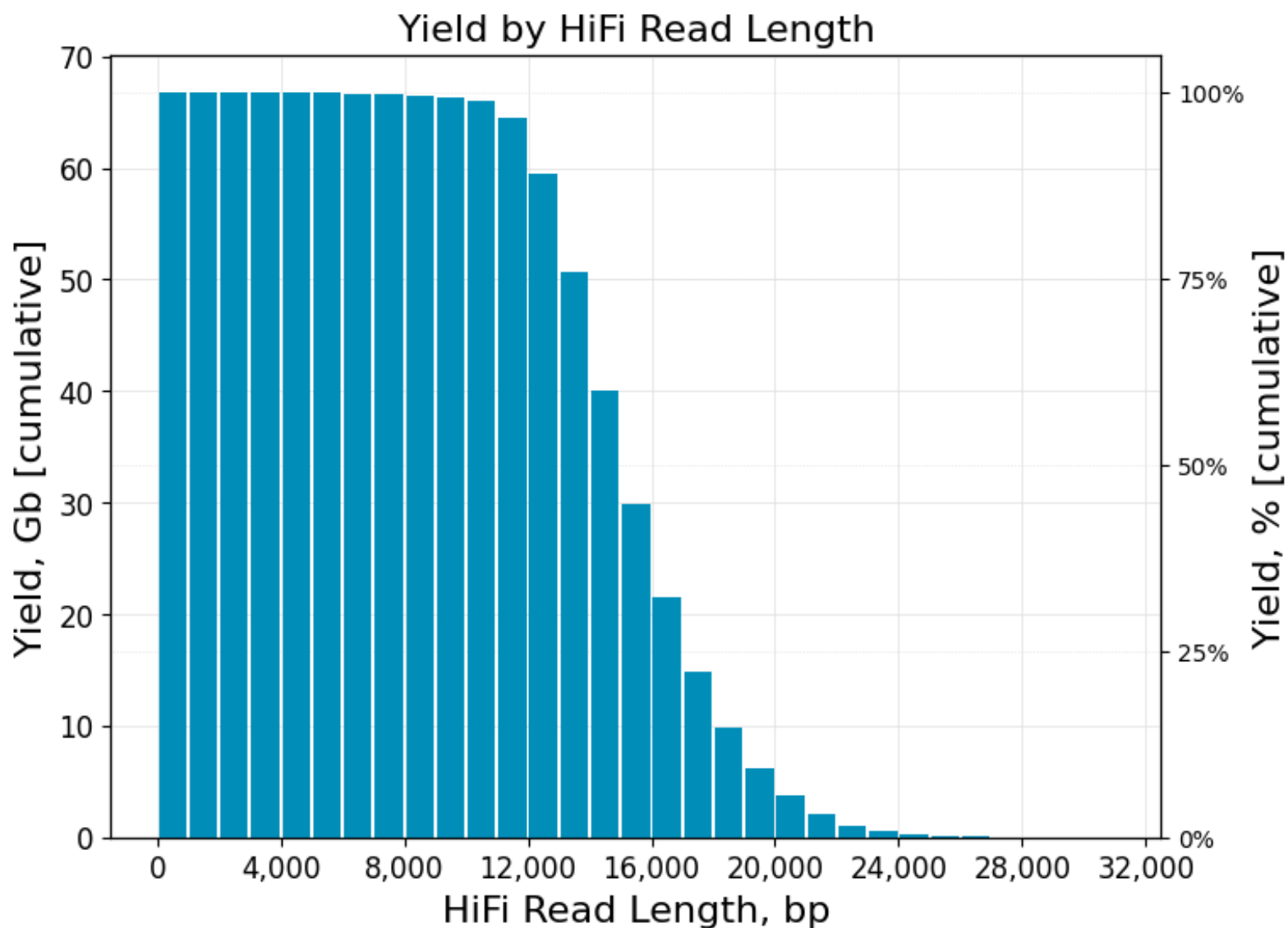
## HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
$\geq Q20$	4,601,074	100	66.71 Gb	100
$\geq Q30$	3,144,508	68	44.94 Gb	67
$\geq Q40$	922,913	20	12.06 Gb	18
$\geq Q50$	66,927	1	0.69 Gb	1

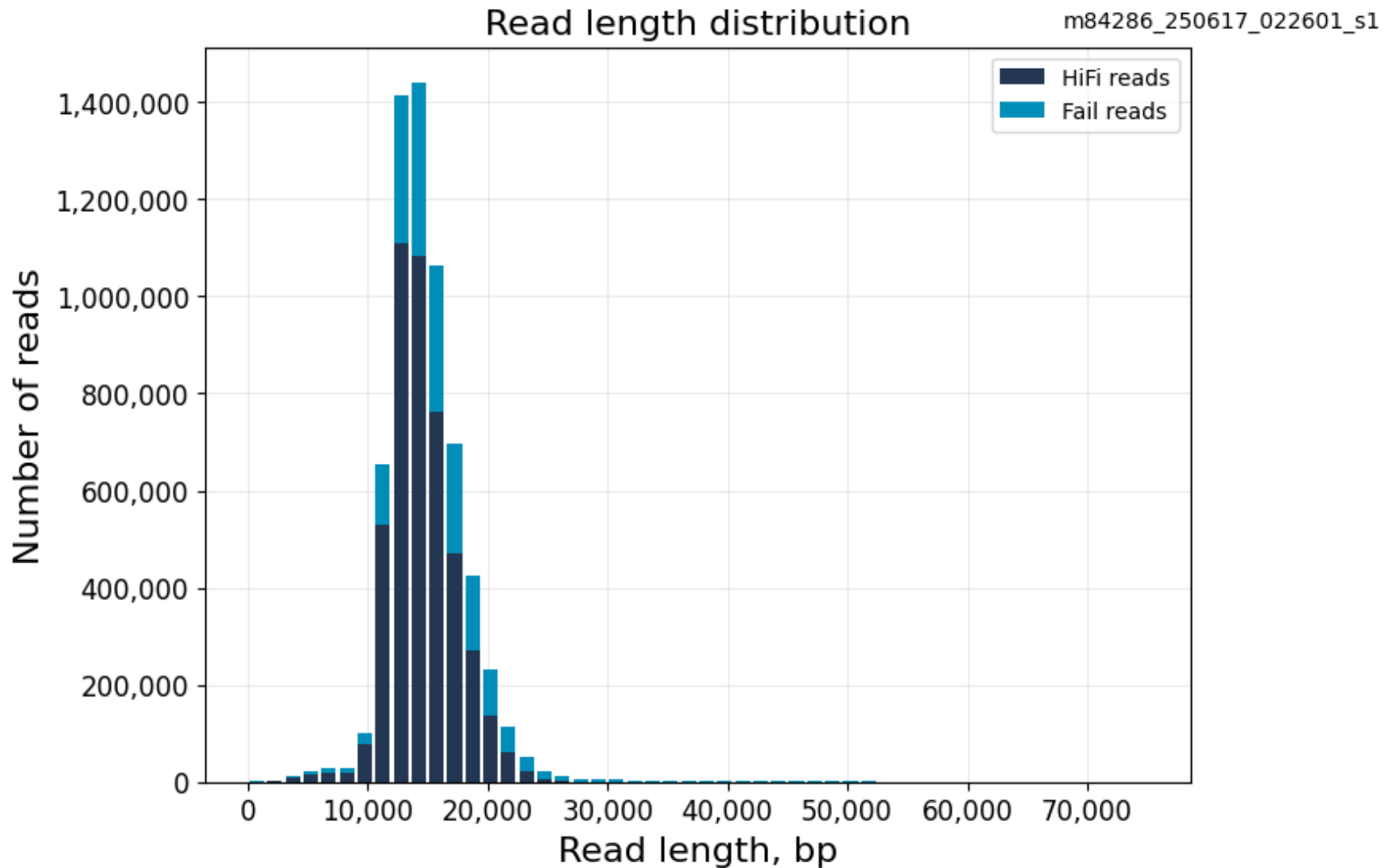
## Read Length Distribution: HiFi read length distribution



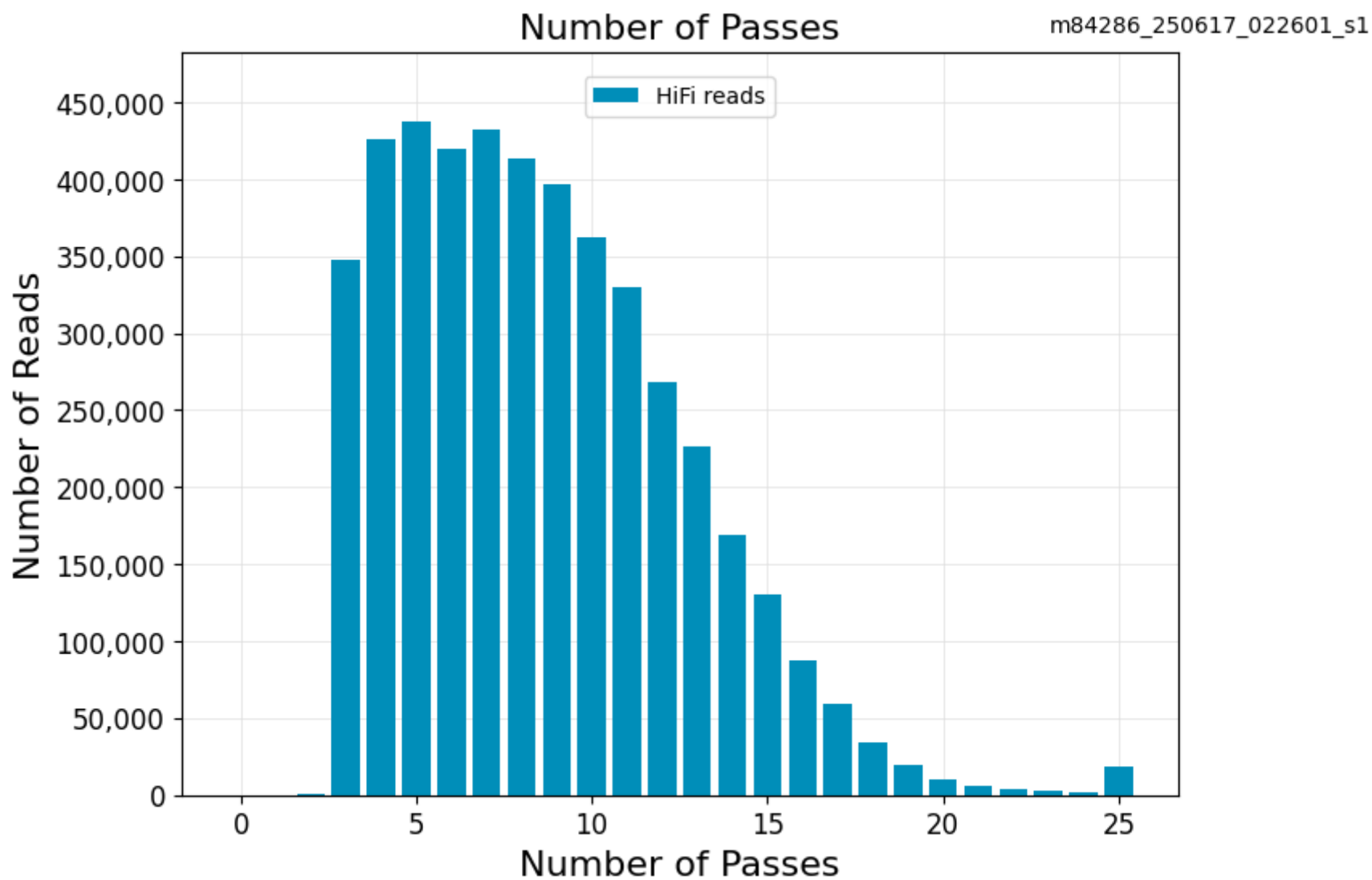
## Read Length Distribution: Yield by HiFi Read Length



## Read Length Distribution: Read length distribution

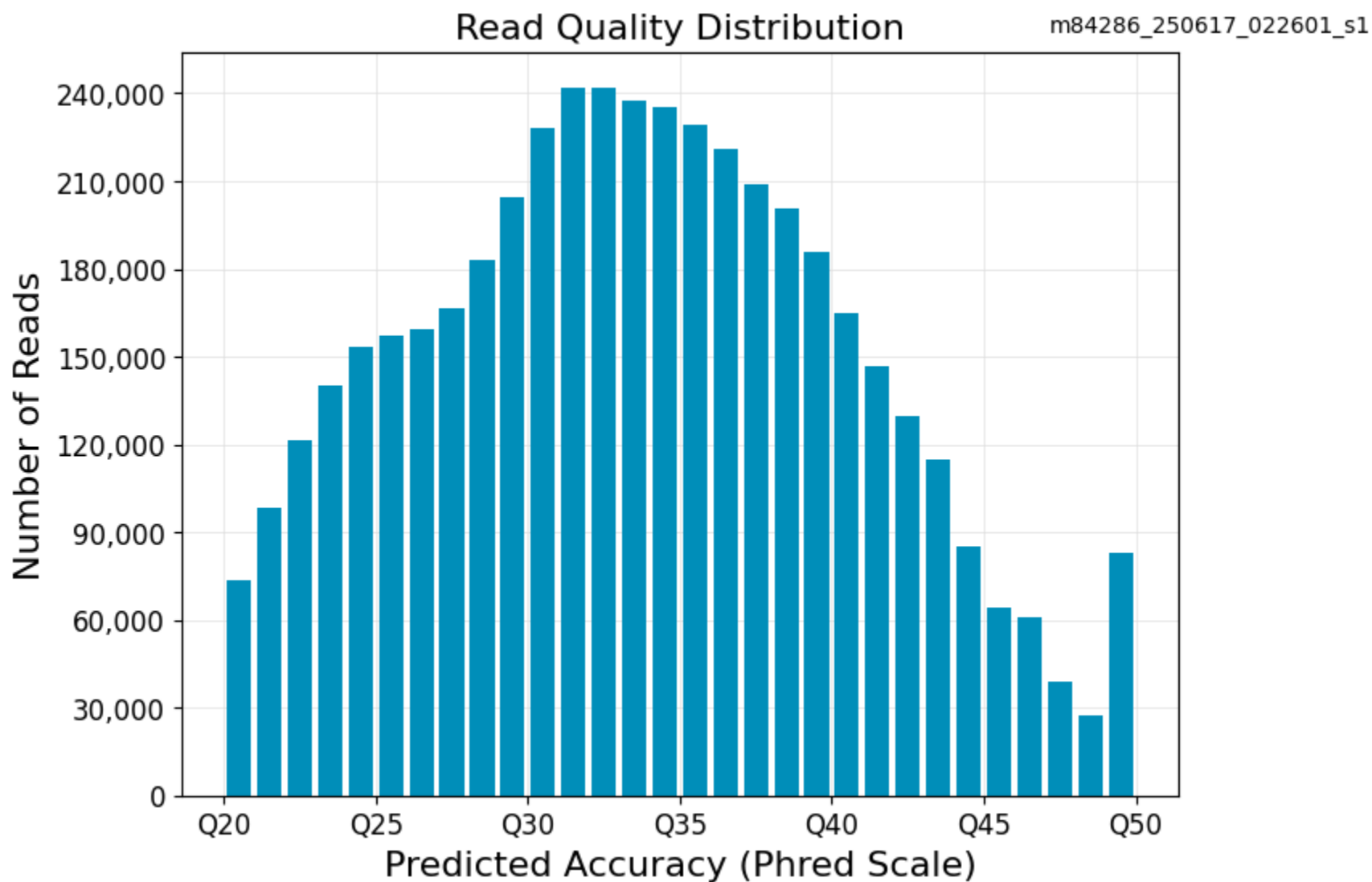


## Number of Passes

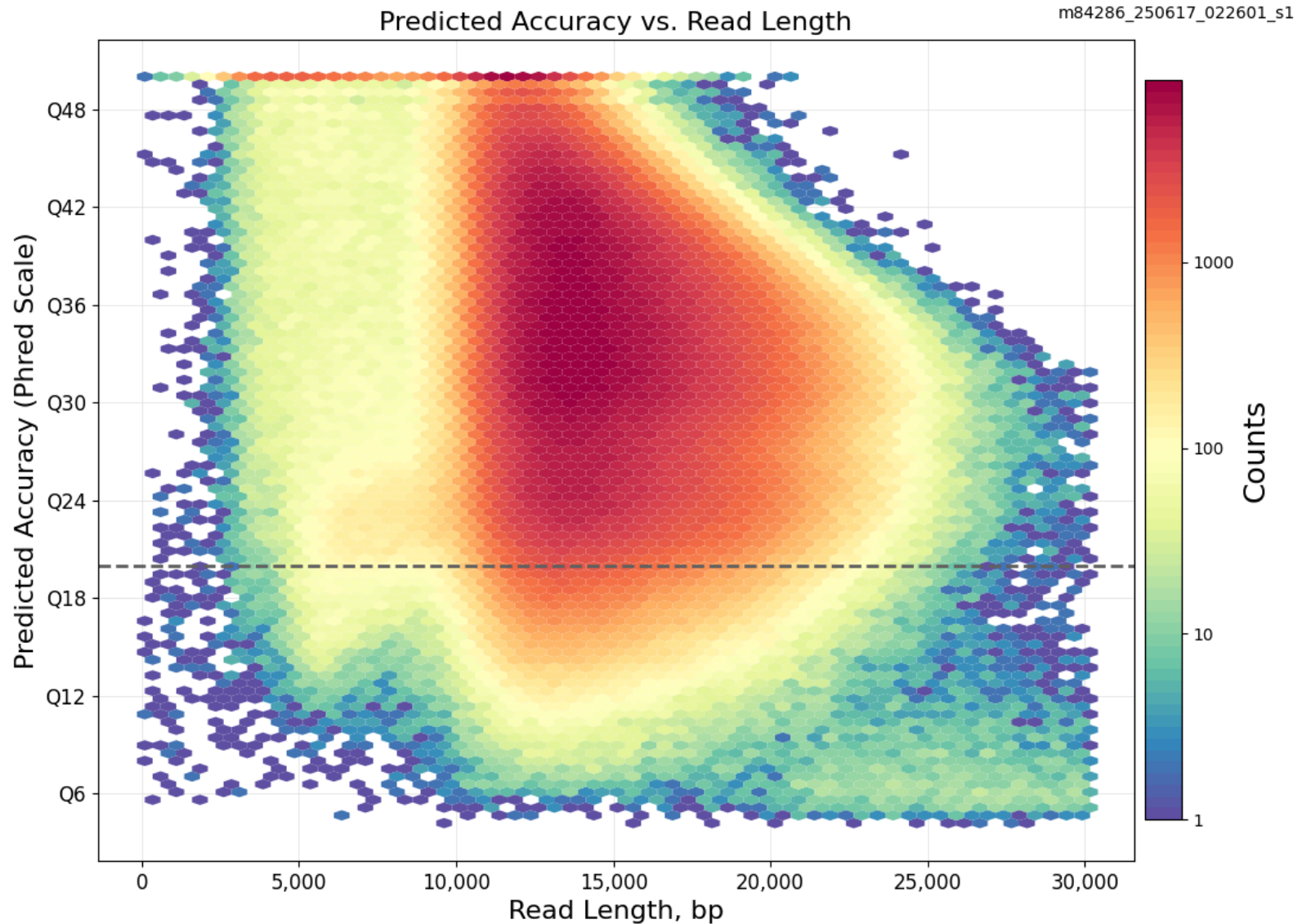




## Read Quality Distribution



## Predicted Accuracy vs. Read Length

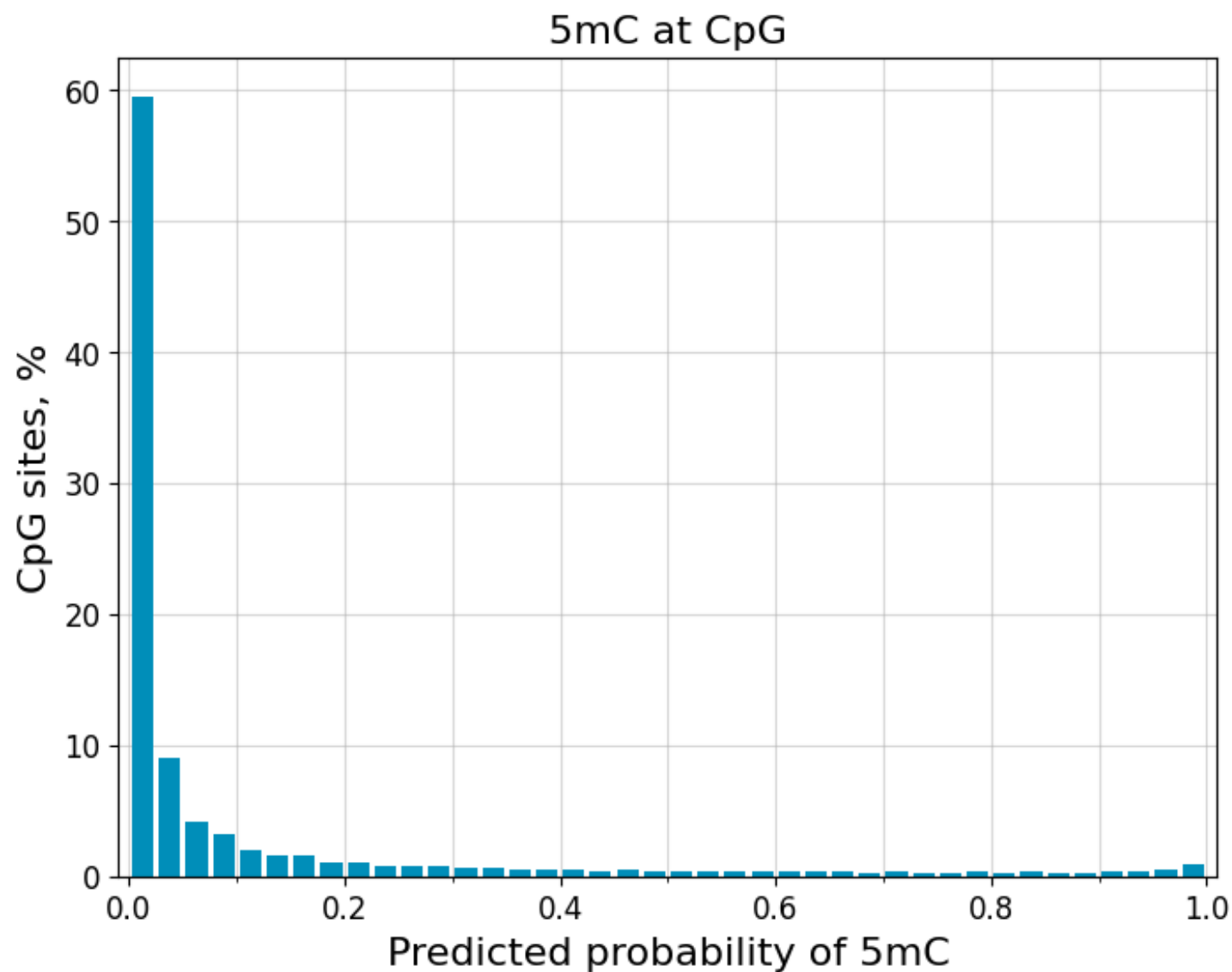


## Methylation

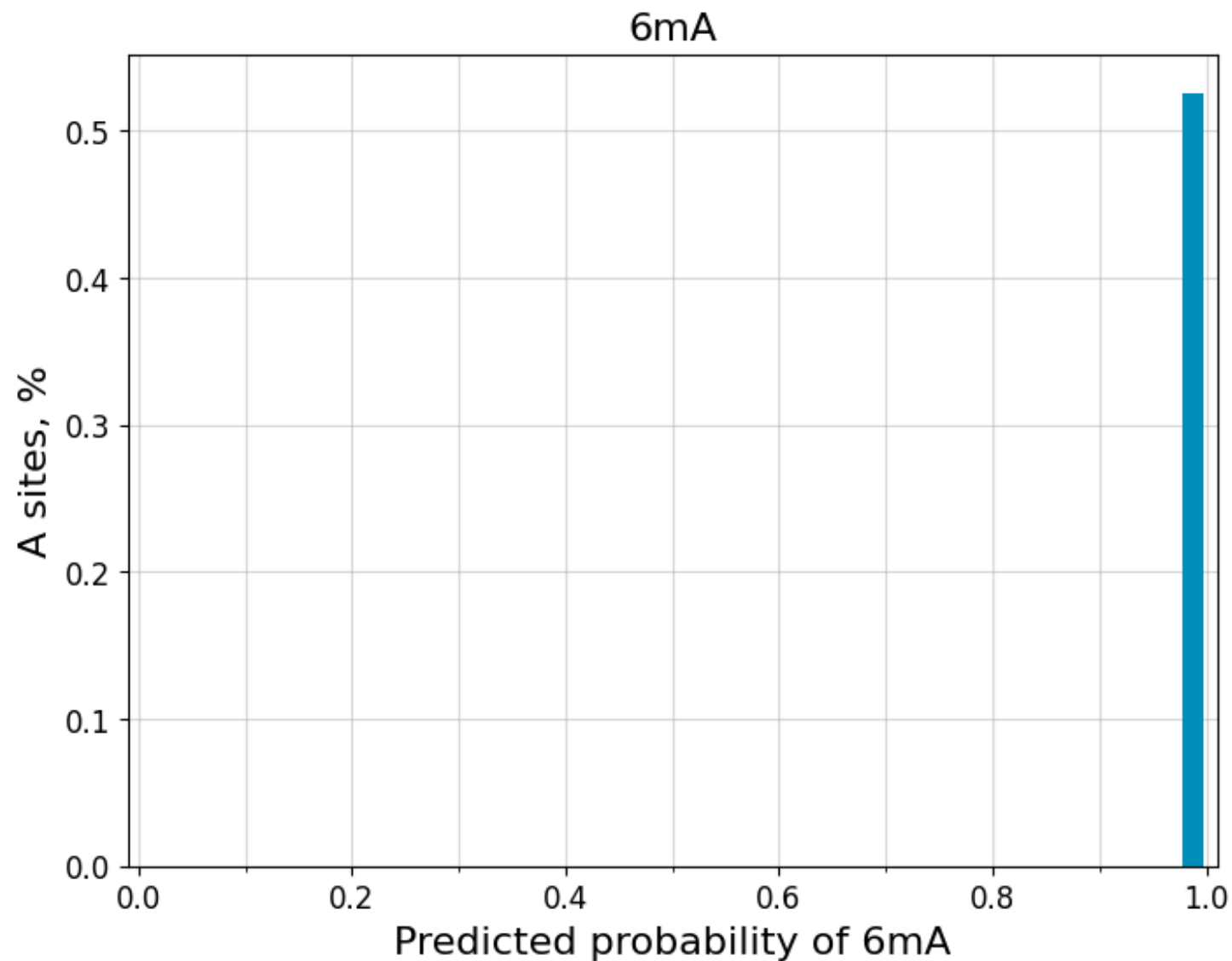
### Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	96.7%	7.1%
6mA	A	0.5%	0.5%

## Score distributions: 5mC at CpG



## Score distributions: 6mA



## Loading Report

### Summary Metrics

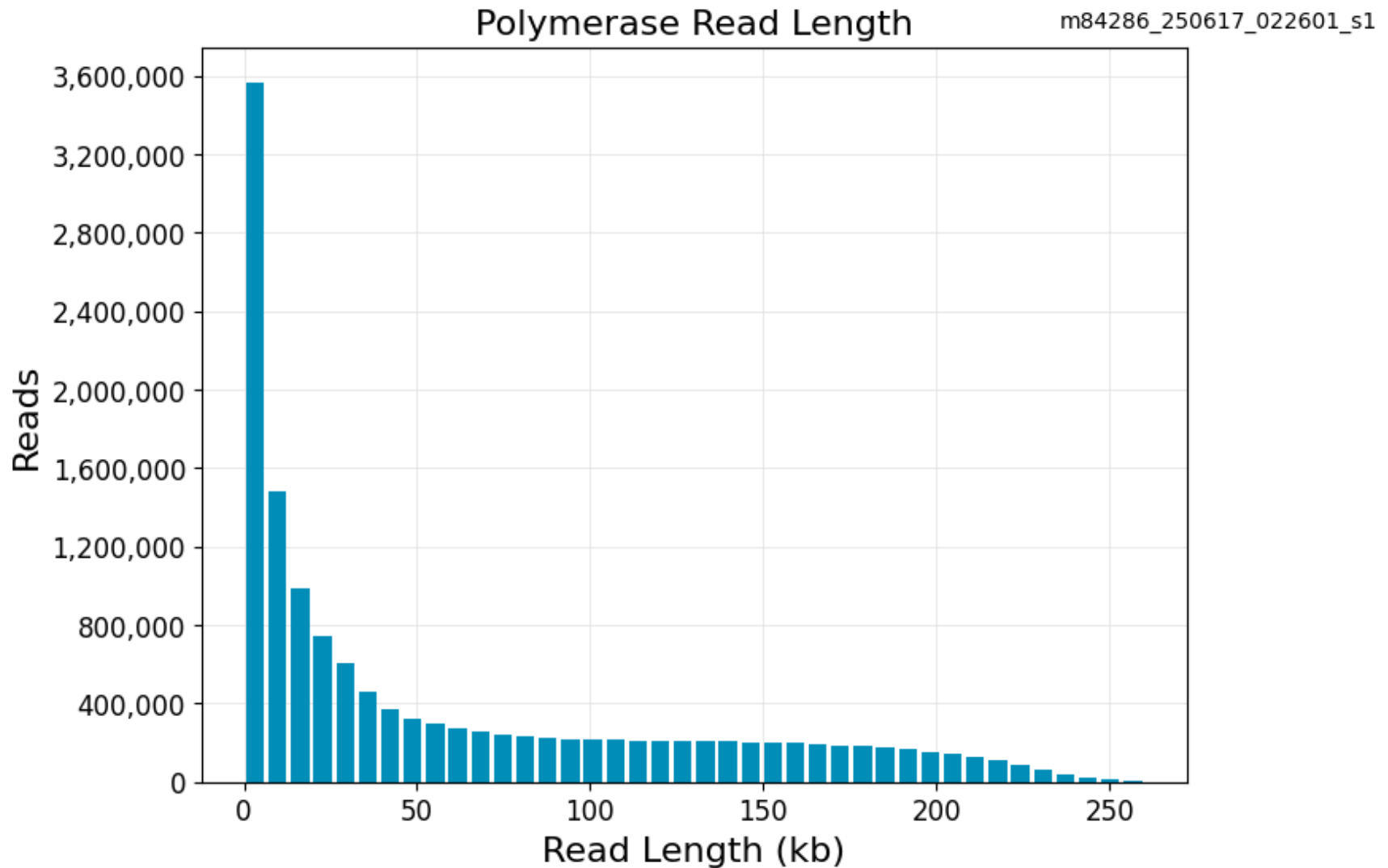
<b>Productive ZMWs</b>	25,165,824
<b>Productivity 0</b>	11,031,725
<b>Productivity 1</b>	14,020,538
<b>Productivity 2</b>	113,561

## Raw Data Report

### Summary Metrics

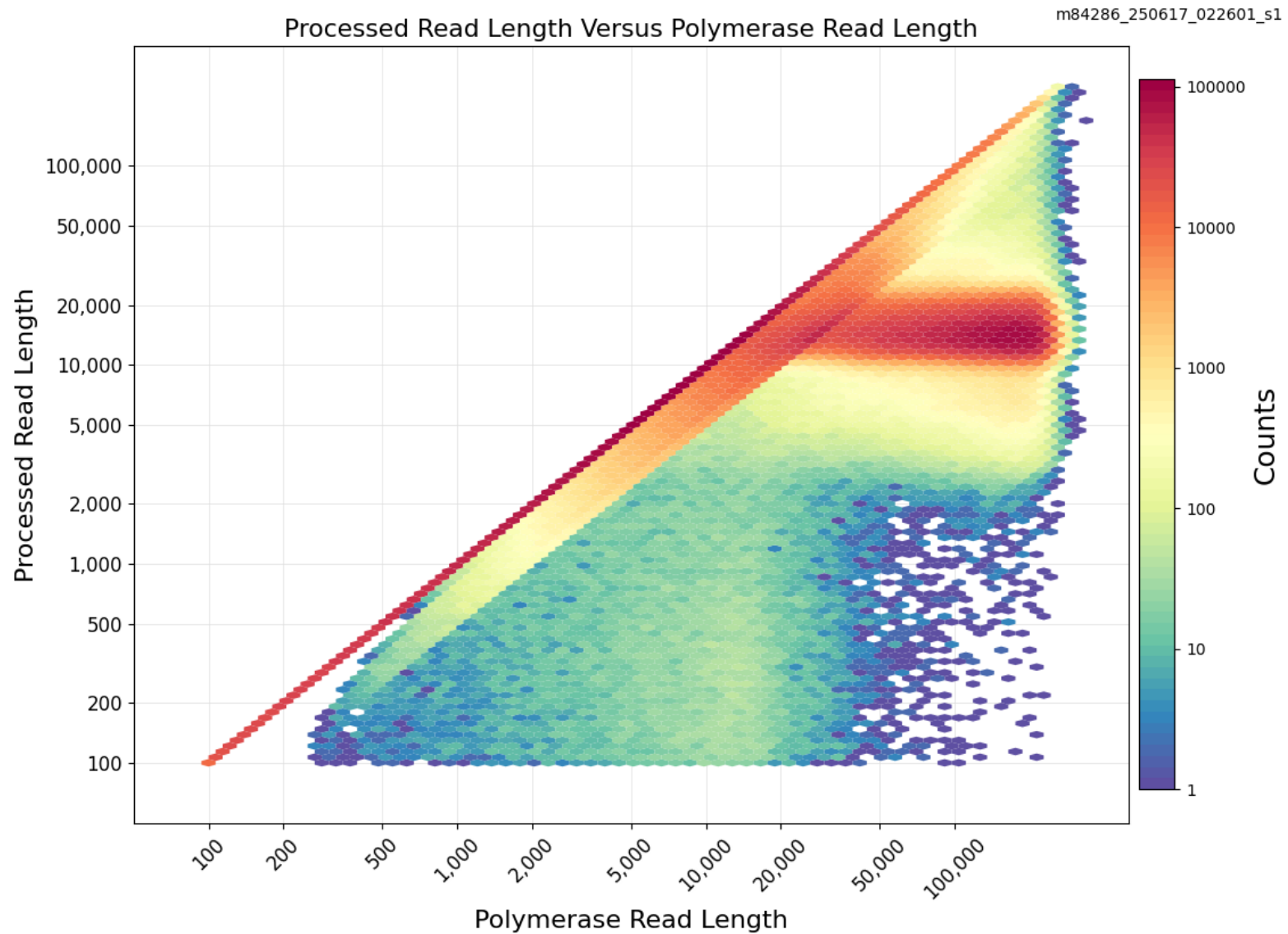
<b>Polymerase Read Bases</b>	818,059,615,192
<b>Polymerase Reads</b>	14,017,303
<b>Polymerase Read Length (mean)</b>	58.36 kb
<b>Polymerase read length (N50)</b>	141.75 kb
<b>Polymerase read length longest subread length (mean)</b>	14.07 kb
<b>Polymerase read length longest subread length (N50)</b>	17.25 kb
<b>Unique Molecular Yield</b>	188,291,727,360
<b>Local Base Rate</b>	2.29

## Polymerase Read Length

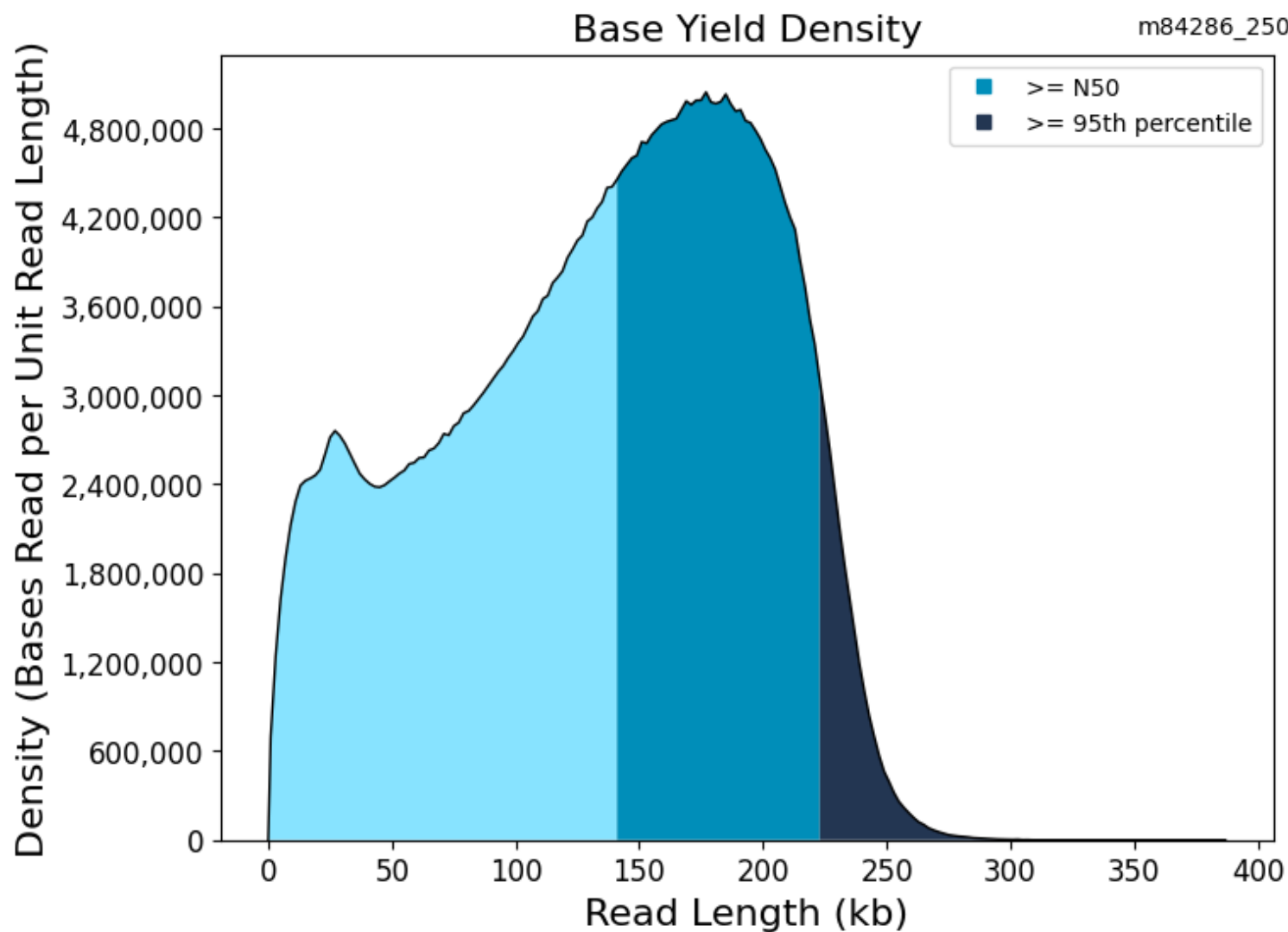




## Longest Subread Length Versus Polymerase Read Length



## Base Yield Density

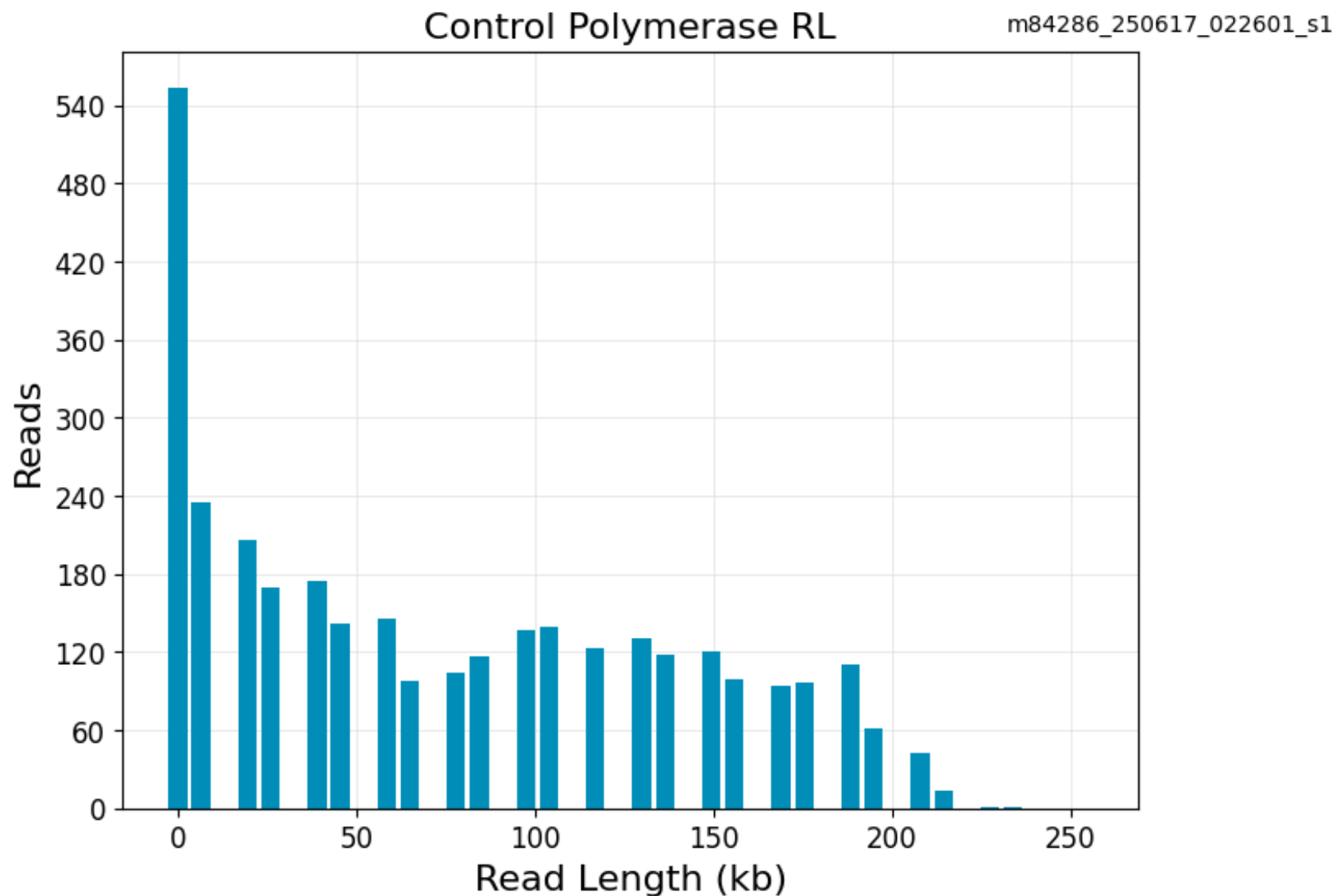


## Control Report

### Summary Metrics

<b>Number of Control Reads</b>	3,235
<b>Control Read Length Mean</b>	77,805
<b>Control Read Concordance Mean</b>	0.91
<b>Control Read Concordance Mode</b>	0.91

## Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance

