# Report for m84039_241001_220042_s2

## Dataset details

**Name**: HG2_BC18-Cell1 (all samples)

**Path**: /collections/appslabvast/r84039/r84039_20241001_215320/1_A01/pb_formats/m84039_241001_220042_s2.hifi_reads.consensusreadset.xml

**Unique ID**: 6736dea5-f88a-4554-b77a-6e06271371d1

**Created at**: 2024-10-03T10:13:32.428Z

**HiFi sequences**: 8,080,358

**HiFi bases**: 114,900,164,232

**Bio sample name**: HG2-bc18

**Well sample name**: HG2_BC18

**Run name**: 20241001_Kudo_FINAL-HG2-HG3-HG4-HG2-500

**Movie name**: m84039_241001_220042_s2

**Instrument name**: 84039

**ICS version**: 13.3.0.249820

**Number of child datasets**: 1

**Number of HiFi BAM files**: 1

## CCS Analysis Report

### Summary Metrics

| | |
|---|---:|
| **HiFi reads** | 8.1 M |
| **HiFi reads yield** | 115.17 Gb |
| **HiFi reads length (mean)** | 14.22 kb |
| **HiFi reads length (median, bp)** | 14,717 |
| **HiFi Read Length N50 (bp)** | 16,985 |
| **HiFi Read Quality (median)** | Q35 |
| **HiFi Read Quality (median)** | 35 |
| **Base Quality ≥Q30 (%)** | 93.50% |
| **HiFi Number of Passes (mean)** | 11 |
| **Missing adapters (%)** | 4.89% |

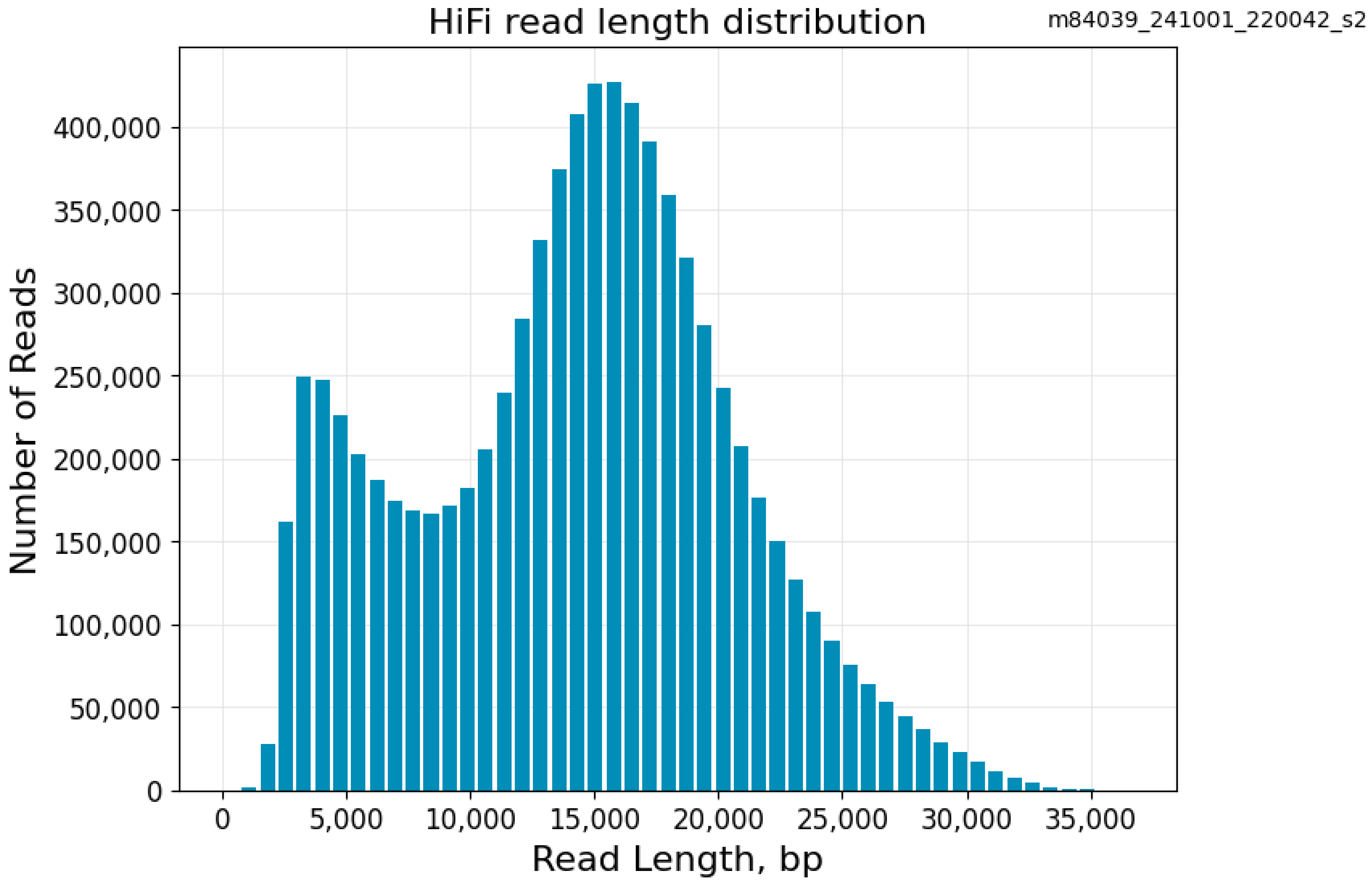
## HiFi Read Length Summary

| Read Length (kb) | Reads | Reads (%) | Yield (Gb) | Yield (%) |
|---|---|---|---|---|
| ≥ 0 | 8,099,799 | 100 | 115.17 Gb | 100 |
| ≥ 5,000 | 7,217,054 | 89 | 111.98 Gb | 97 |
| ≥ 10,000 | 5,993,845 | 74 | 102.90 Gb | 89 |
| ≥ 15,000 | 3,886,758 | 48 | 75.79 Gb | 66 |
| ≥ 20,000 | 1,396,299 | 17 | 32.75 Gb | 28 |
| ≥ 25,000 | 360,631 | 4 | 9.93 Gb | 9 |
| ≥ 30,000 | 46,092 | 1 | 1.44 Gb | 1 |
| ≥ 35,000 | 362 | 0 | 0.01 Gb | 0 |
| ≥ 40,000 | 17 | 0 | 0.00 Gb | 0 |

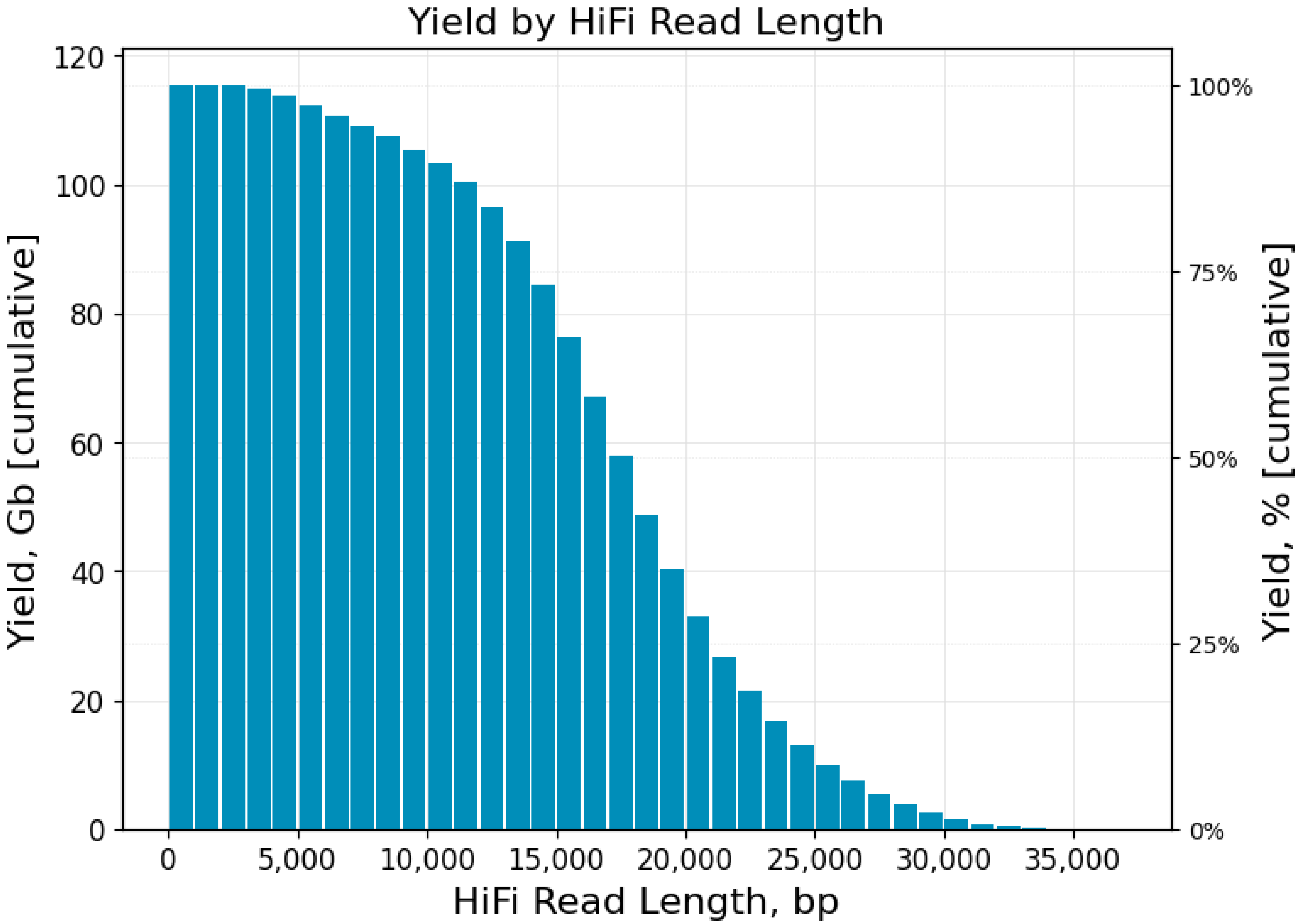
## HiFi Read Quality Summary

| Read Quality (Phred) | Reads | Reads (%) | Yield (Gb) | Yield (%) |
|---|---|---|---|---|
| ≥ Q20 | 8,099,799 | 100 | 115.17 Gb | 100 |
| ≥ Q30 | 6,040,937 | 75 | 79.27 Gb | 69 |
| ≥ Q40 | 2,236,410 | 28 | 19.34 Gb | 17 |
| ≥ Q50 | 781,588 | 10 | 4.09 Gb | 4 |

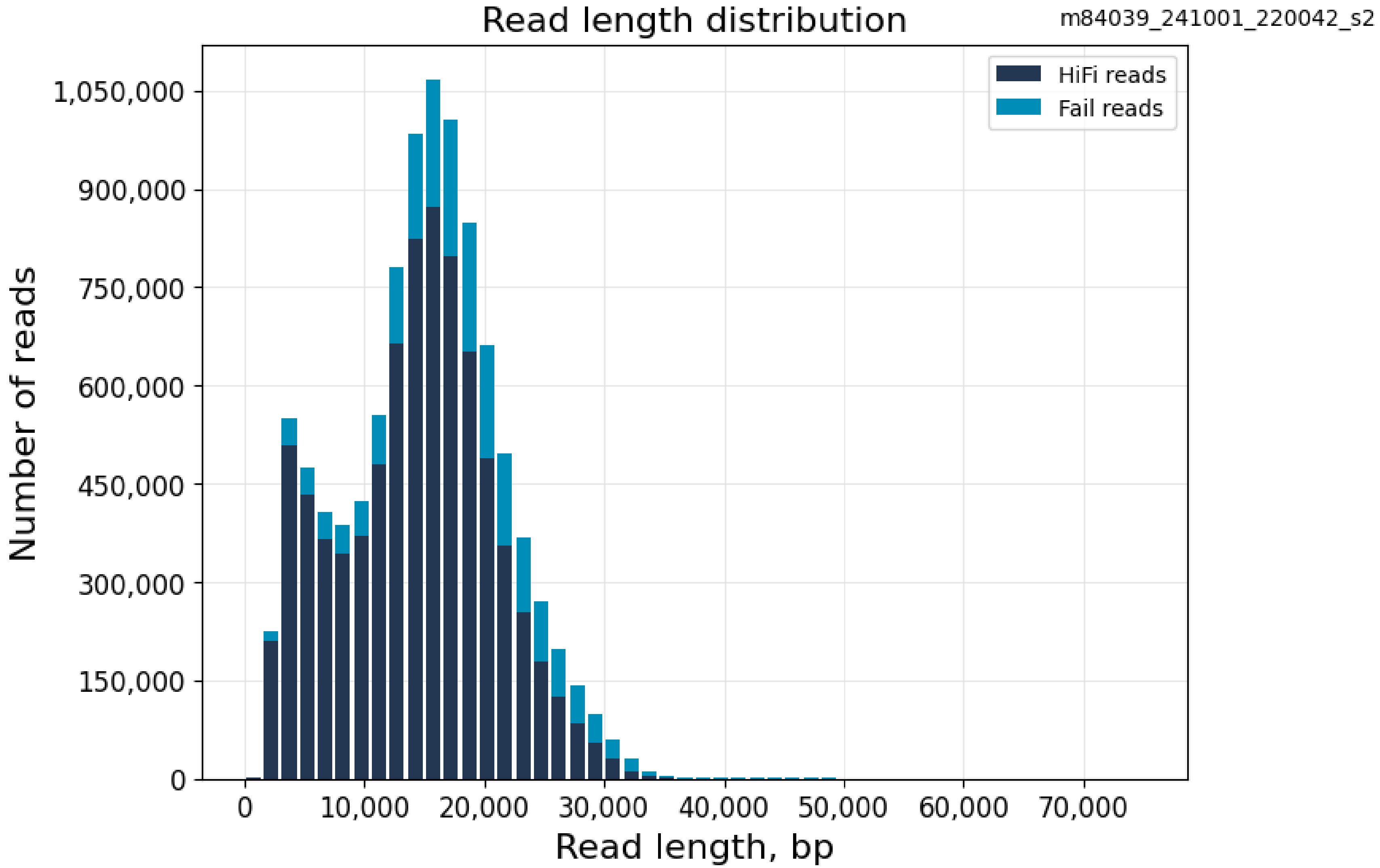
### Read Length Distribution: HiFi read length distribution



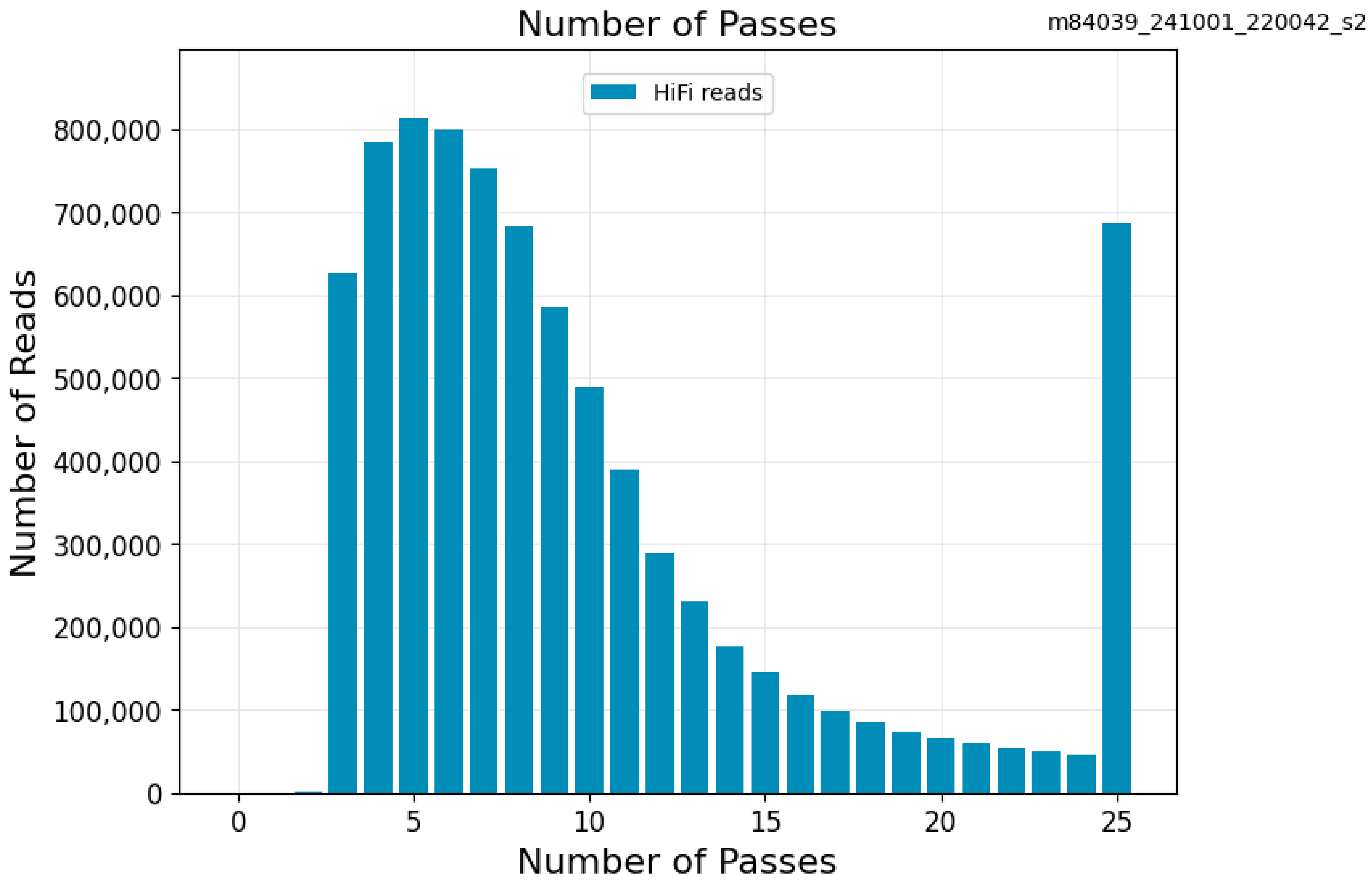
## Read Length Distribution: Yield by HiFi Read Length



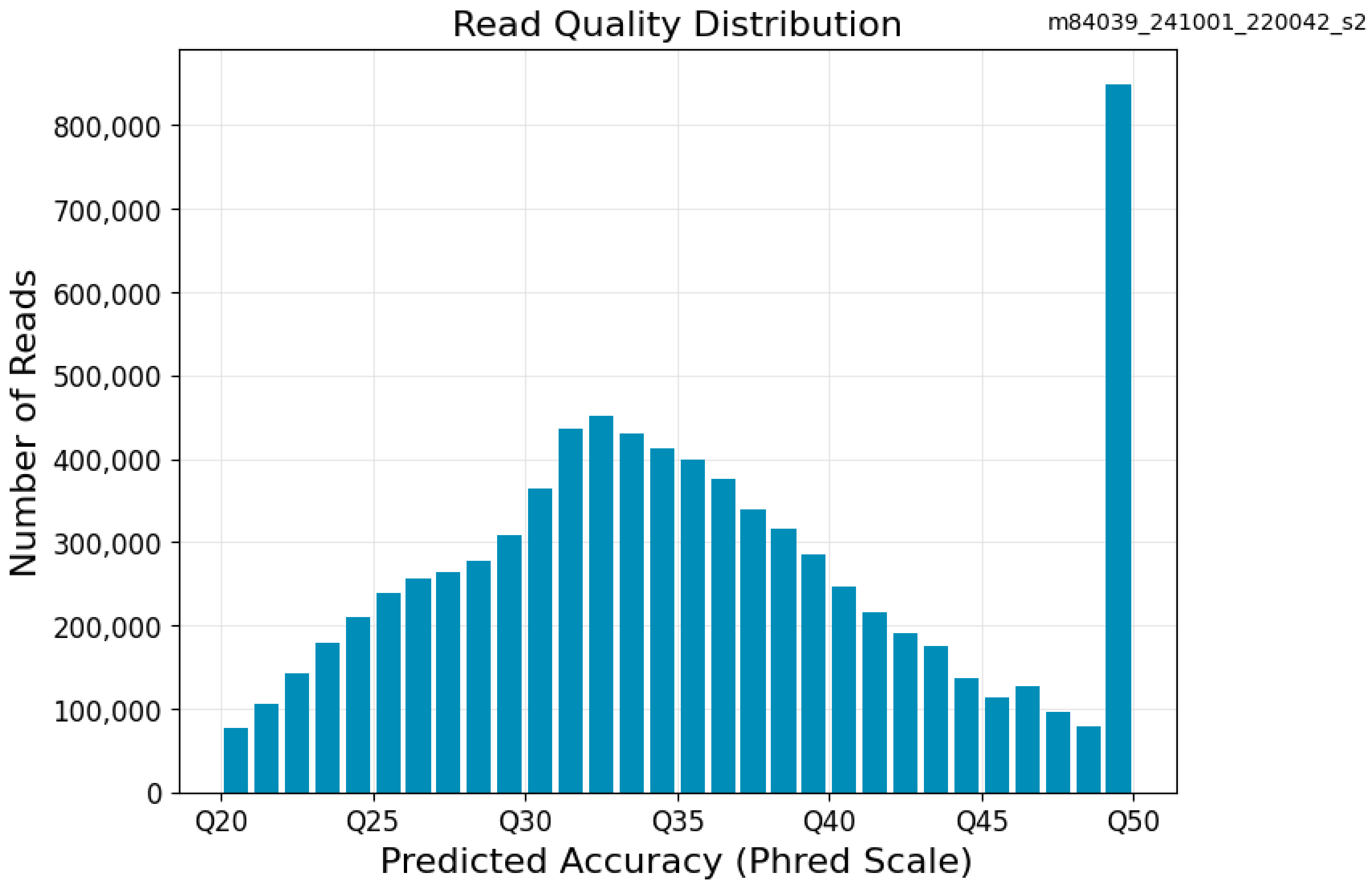
## Read Length Distribution: Read length distribution



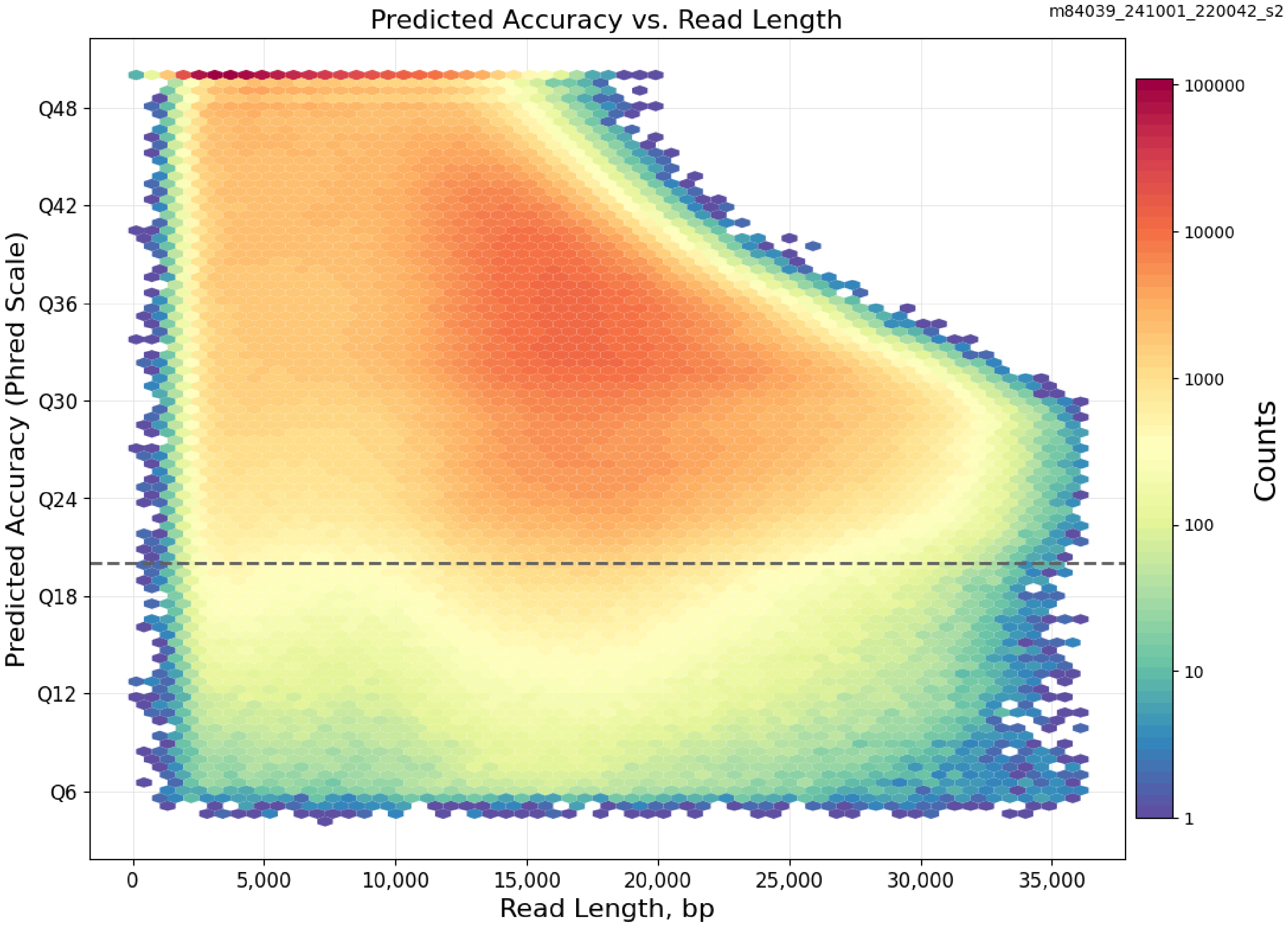
## Number of Passes



### Read Quality Distribution



## Predicted Accuracy vs. Read Length

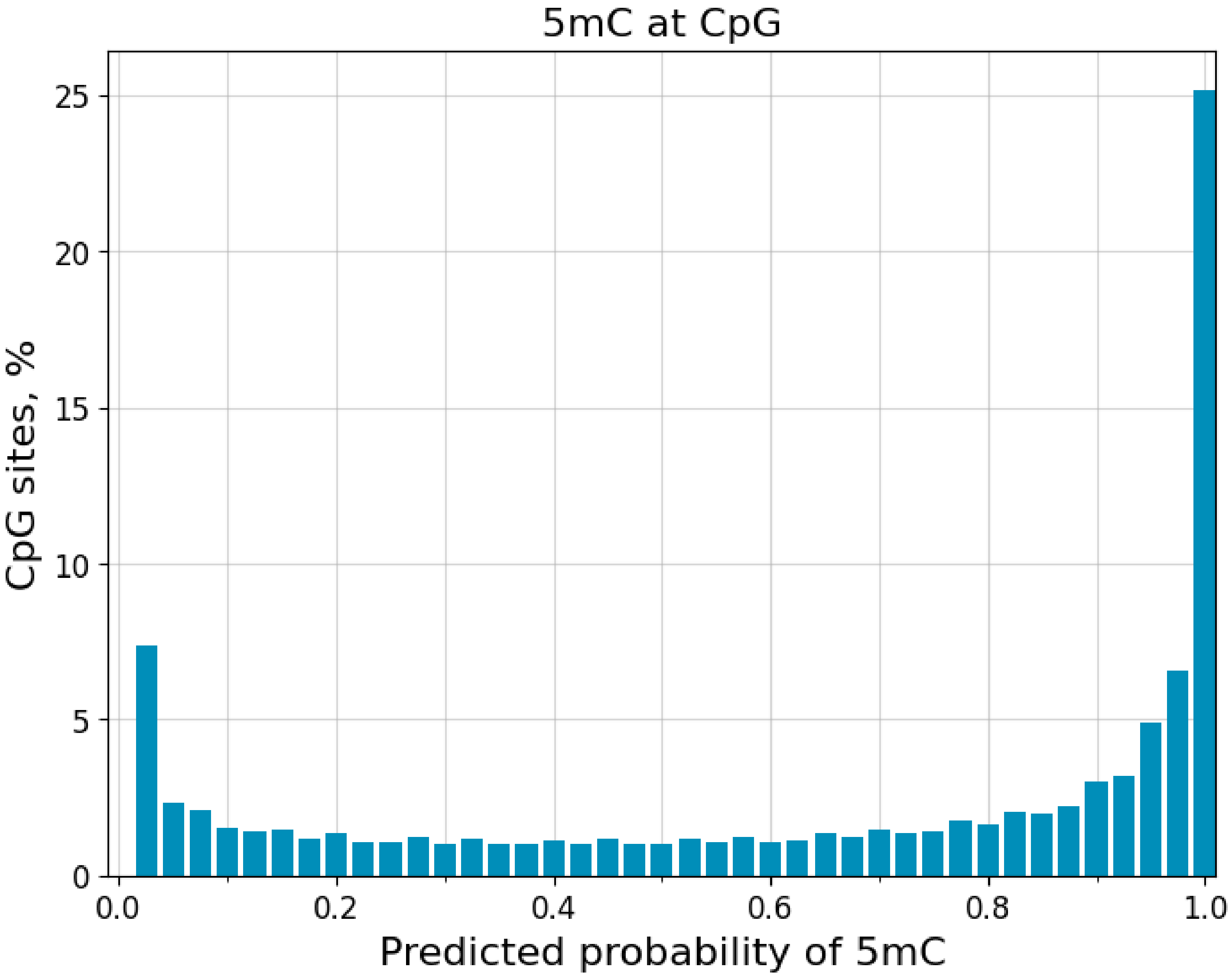


## Methylation

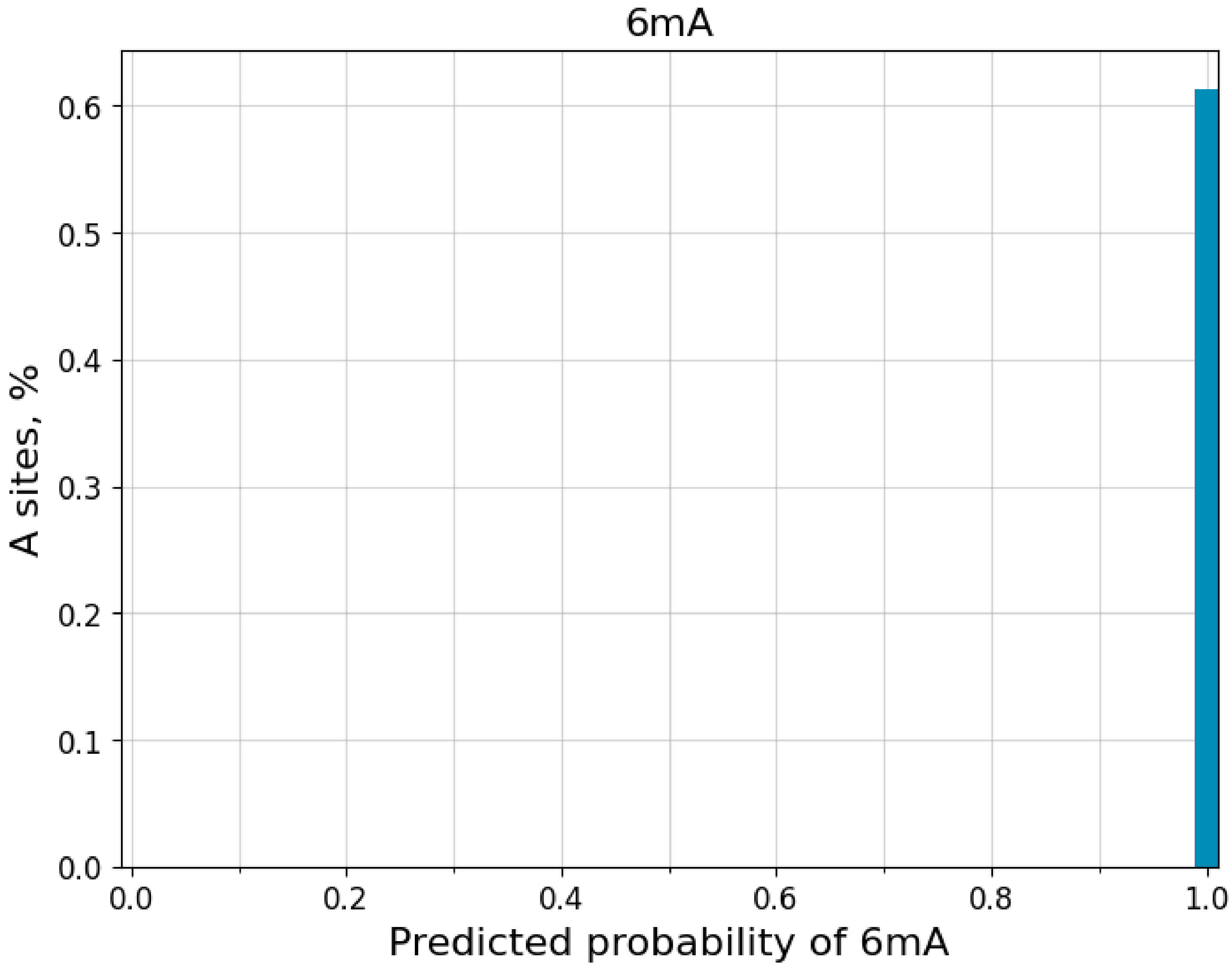
### Summary

| Modification | Motif | Scored sites | Modified sites (Pr > 0.5) |
|---:|---:|---:|---:|
| 5mC | CpG | 96.6% | 64.9% |
| 6mA | A | 0.6% | 0.6% |

### Score distributions: 5mC at CpG



## Score distributions: 6mA



## Barcodes

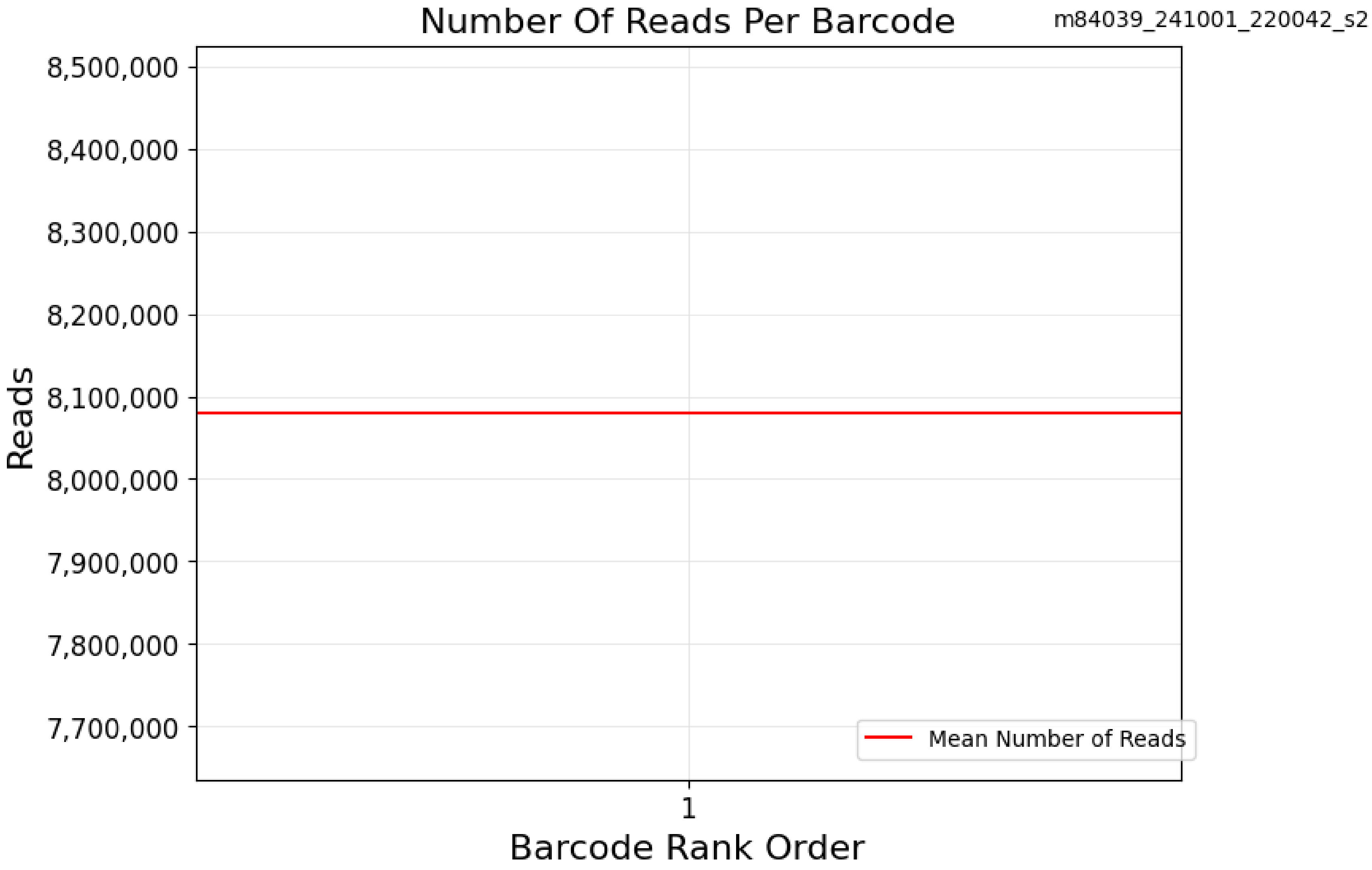
### Summary Metrics

| | |
|---|---:|
| **Unique Barcodes** | 1 |
| **Barcoded HiFi Reads** | 8,080,358 |
| **Unbarcoded HiFi Reads** | 19,452 |
| **Barcoded HiFi Reads (%)** | 99.76 % |
| **Barcoded HiFi yield (Gb)** | 114.90 Gb |
| **Unbarcoded HiFi yield (Gb)** | 0.27 Gb |
| **Barcoded HiFi Yield (%)** | 99.76 % |
| **Mean HiFi Reads per Barcode** | 8,080,358 |
| **Max. HiFi Reads per Barcode** | 8,080,358 |
| **Min. HiFi Reads per Barcode** | 8,080,358 |
| **Barcoded HiFi read length (mean, kb)** | 14.22 kb |
| **Unbarcoded HiFi read length (mean, kb)** | 14.06 kb |

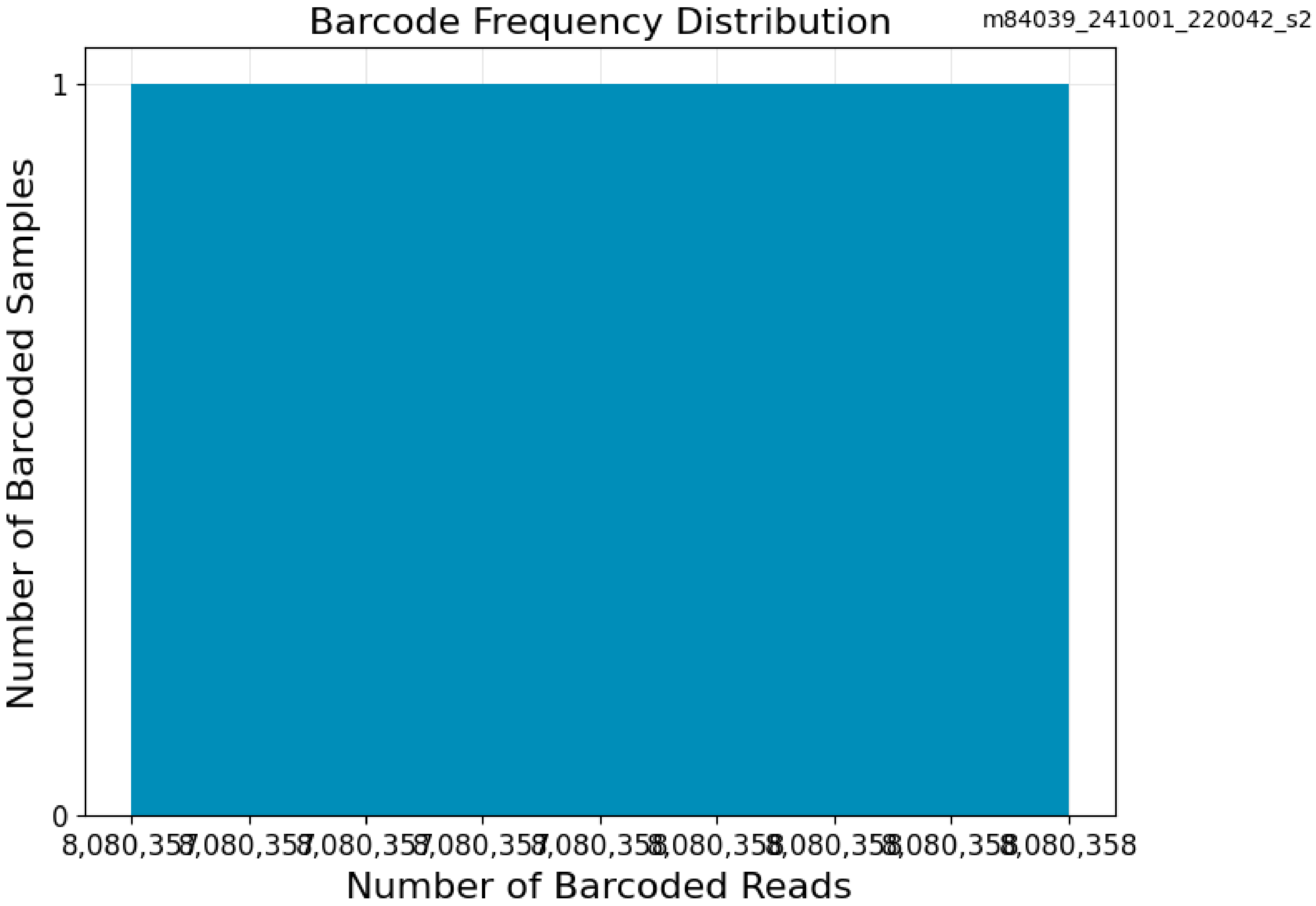
## Barcode Data

| 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) |
|---|---|---|---|---|---|---|---|
| HG2-bc18 | bc2018--bc2018 | 97.7 | 8,080,358 | 14,219 | Q0 | 114,900,164,232 | 135,066 |
| No Name | Not Barcoded | 0.0 | 19,452 | 14,057 | Q29 | 273,440,095 | 119,472 |

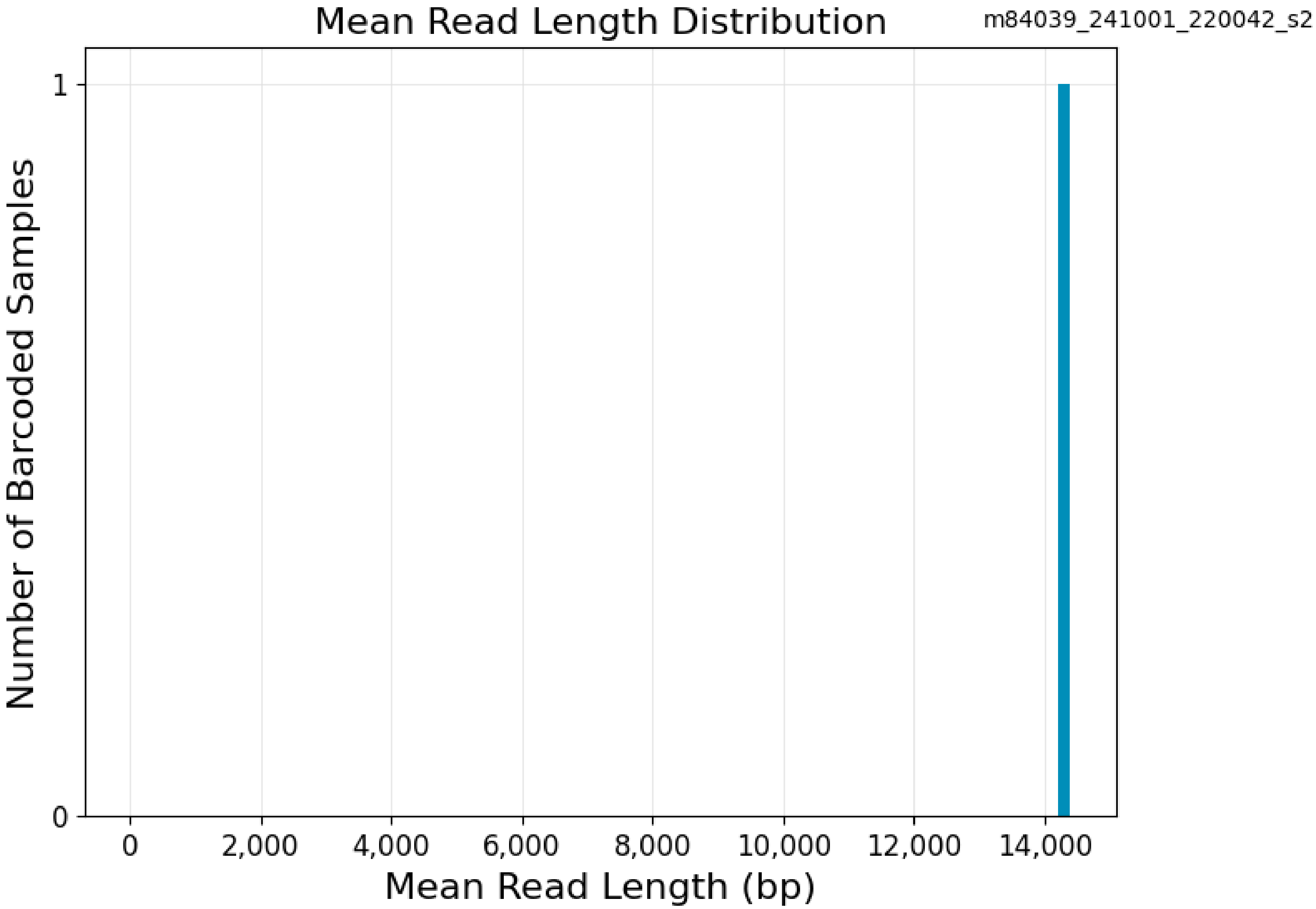
## Barcoded Read Statistics: Number Of Reads Per Barcode



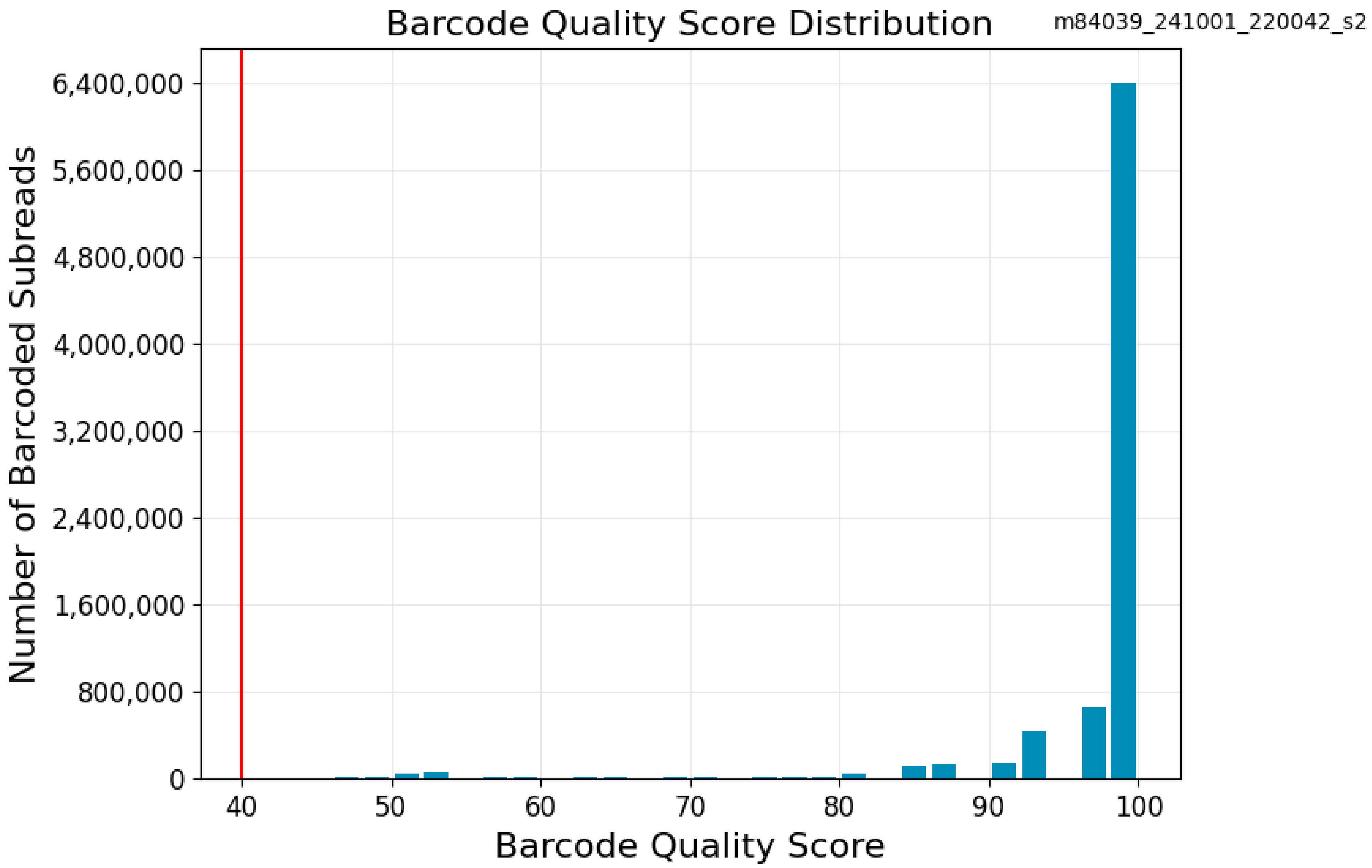
## Barcoded Read Statistics: Barcode Frequency Distribution



## Barcoded Read Statistics: Mean Read Length Distribution



## Barcode Quality Scores: Barcode Quality Score Distribution



## Loading Report

### Summary Metrics

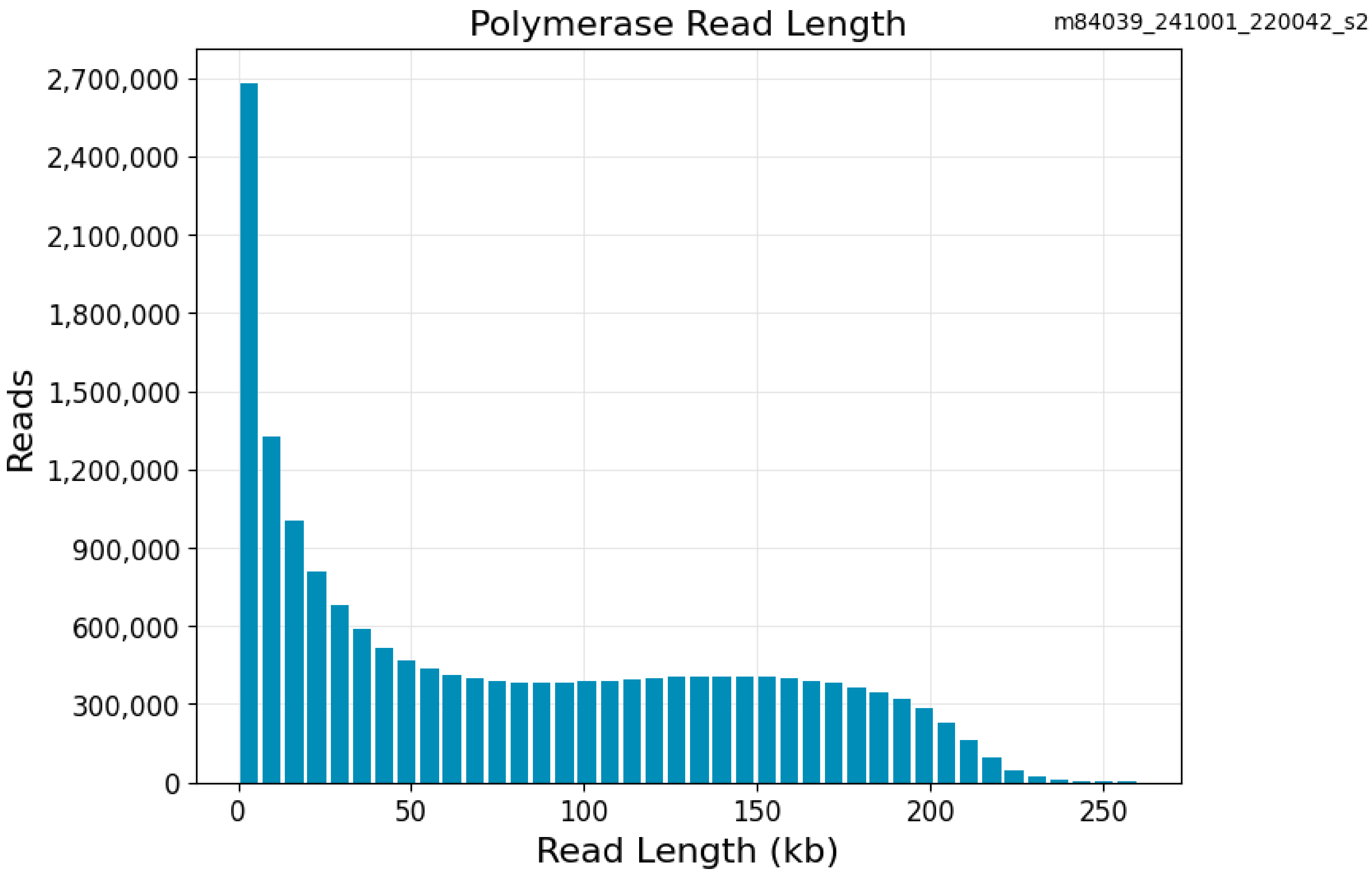
| | |
|---|---|
| **Productive ZMWs** | 25,165,824 |
| **Productivity 0** | 7,475,767 |
| **Productivity 1** | 17,553,440 |
| **Productivity 2** | 136,617 |

## Raw Data Report

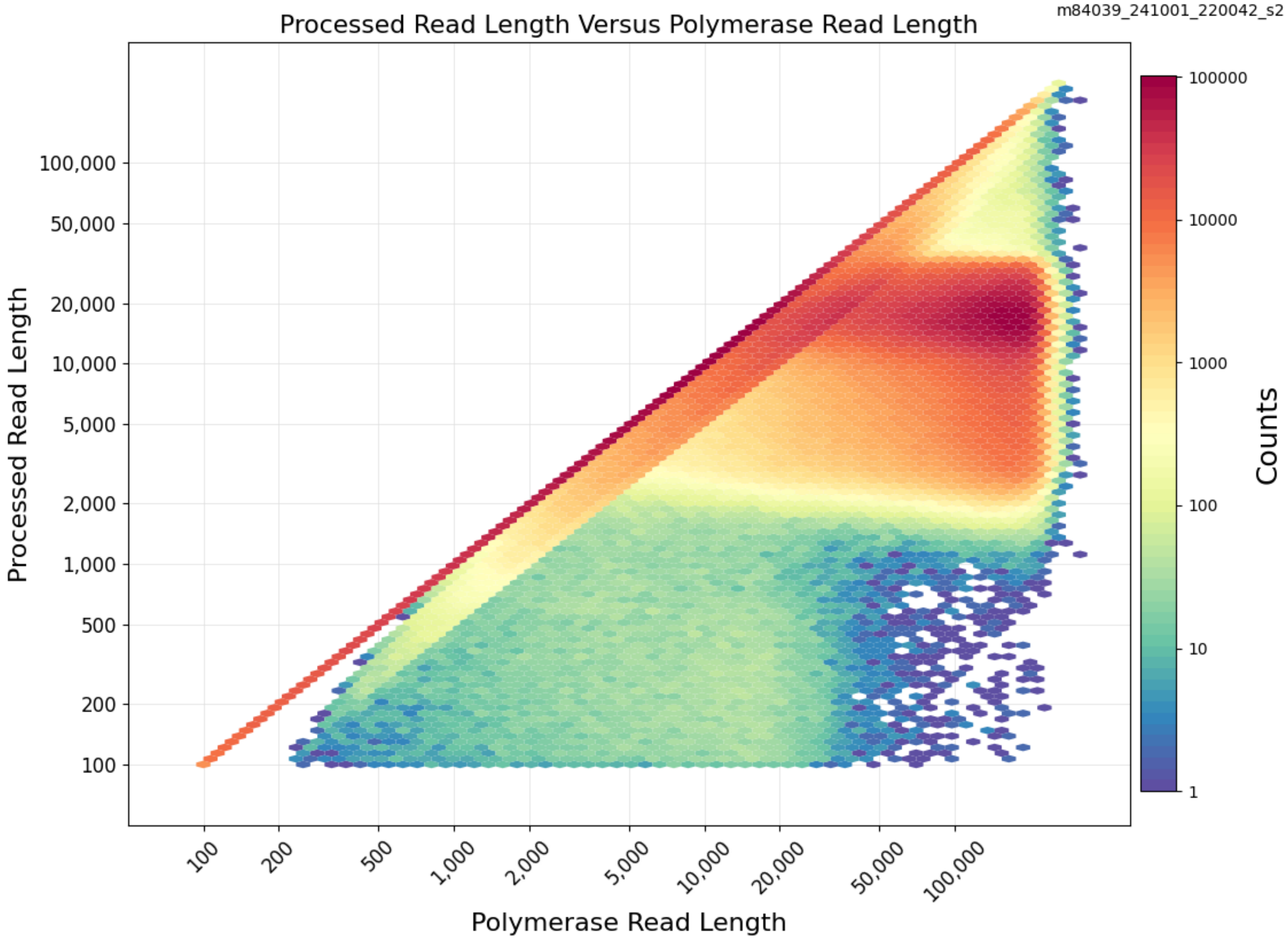
### Summary Metrics

| | |
|---|---:|
| **Polymerase Read Bases** | 1,322,928,468,949 |
| **Polymerase Reads** | 17,547,146 |
| **Polymerase Read Length (mean)** | 75.39 kb |
| **Polymerase read length (N50)** | 143.25 kb |
| **Polymerase read length longest subread length (mean)** | 15.51 kb |
| **Polymerase read length longest subread length (N50)** | 19.75 kb |
| **Unique Molecular Yield** | 258,927,591,424 |
| **Local Base Rate** | 2.32 |

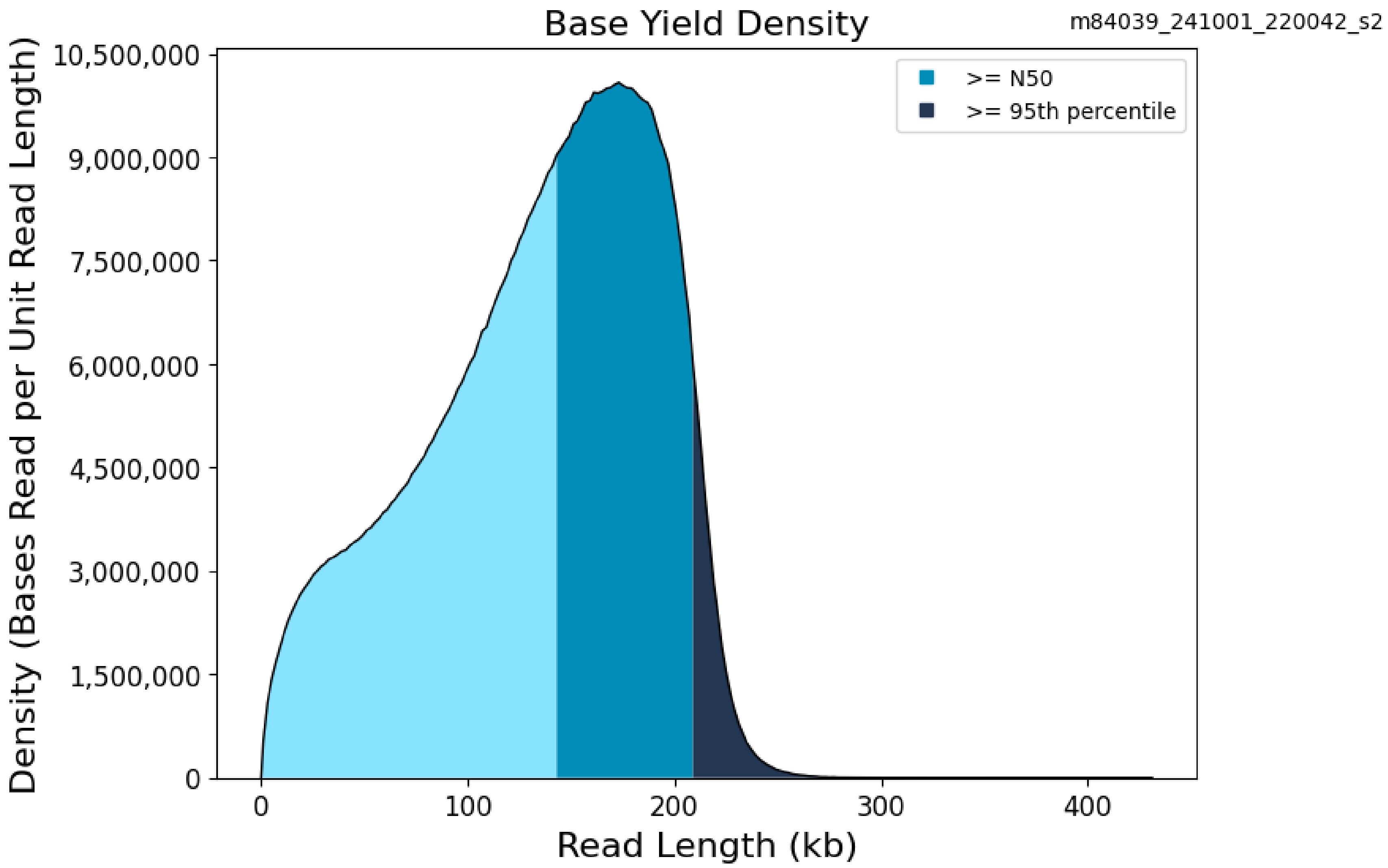
## Polymerase Read Length



## Longest Subread Length Versus Polymerase Read Length



## Base Yield Density

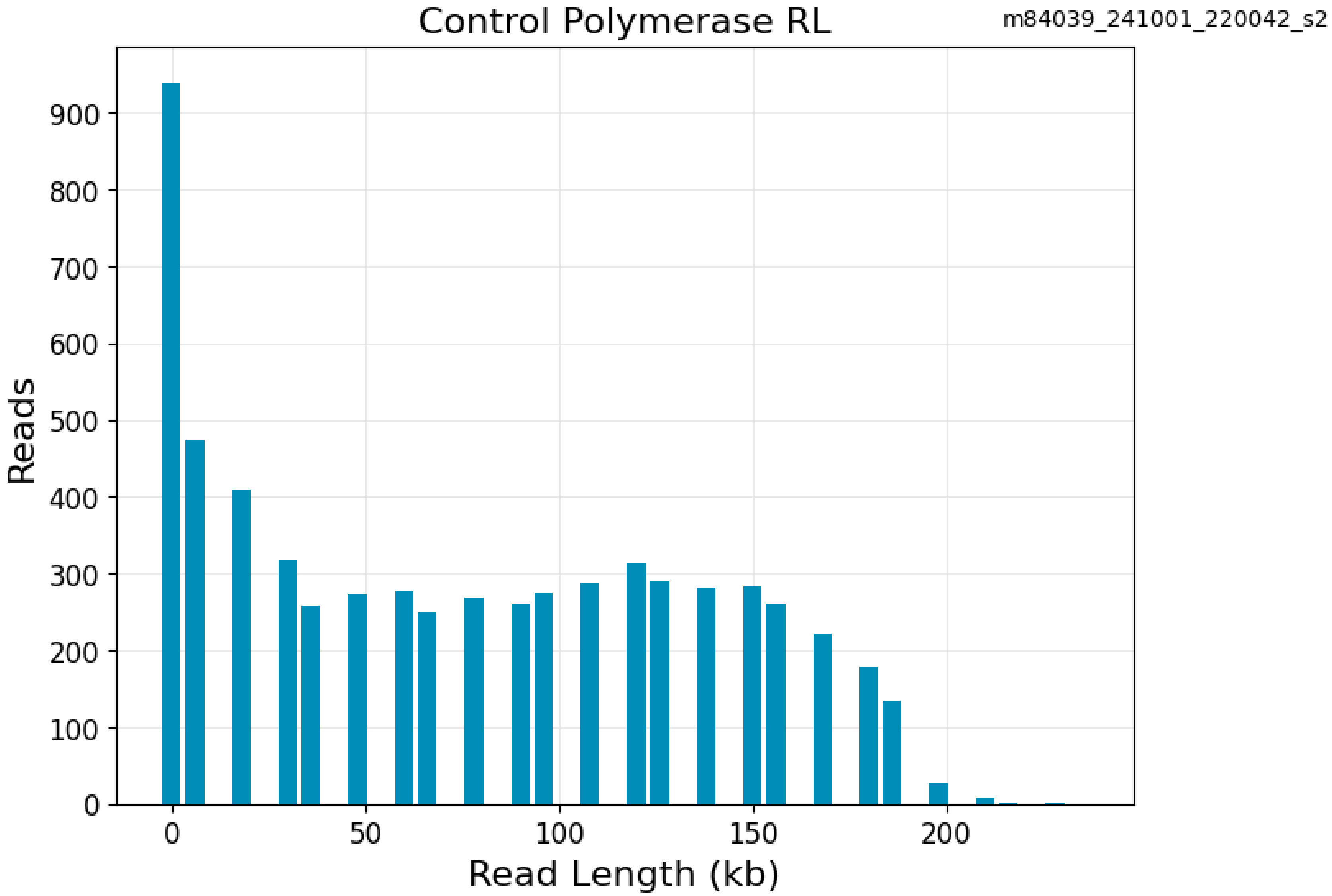


## Control Report

### Summary Metrics

| | |
|---|---:|
| **Number of Control Reads** | 6,294 |
| **Control Read Length Mean** | 77,774 |
| **Control Read Concordance Mean** | 0.91 |
| **Control Read Concordance Mode** | 0.93 |

## Control Read Length: Control Polymerase RL



## Control Read Quality: Control Concordance