

# Report for dataset NS2778-AKawahara-Isoseq-Cell1 (CCS) (all samples)

## Dataset db425eb0-111a-4e49-a081-3f8a37a91af6

### Summary

|                   |   |
|-------------------|---|
| Name              | NS2778-AKawahara-Isoseq-Cell1 (CCS) (all samples) |
| Created At        | 2022-07-03 10:39:48.126                           |
| Number of Records | 757356  |
| Total Length      | 1598378468  |
| Movie ID          | m64219e_220701_164756                             |
| ICS Version       | 11.0.0.144466                                     |
| Well Sample       | NS2778-AKawahara-Isoseq                           |
| Biological Sample | [multiple]  |
| Barcode Name      | [multiple]  |

### Adapter Report

#### Summary

|                            |      |
|----------------------------|------|
| Adapter Dimers (0-10bp) %  | 0    |
| Short Inserts (11-100bp) % | 0    |
| Local Base Rate            | 2.28 |

# CCS Analysis Report

## Summary

|                              |               |
|------------------------------|---------------|
| HiFi Reads                   | 702,588       |
| HiFi Yield (bp)              | 1,468,883,334 |
| HiFi Read Length (mean, bp)  | 2,090         |
| HiFi Read Quality (median)   | Q38           |
| HiFi Read Quality (median)   | 38            |
| HiFi Number of Passes (mean) | 19            |
| <Q20 Reads                   | 73,626        |
| <Q20 Yield (bp)              | 178,668,434   |
| <Q20 Read Length (mean, bp)  | 2,426         |
| <Q20 Read Quality (median)   | Q16           |
| <Q20 Read Quality (median)   | 16            |

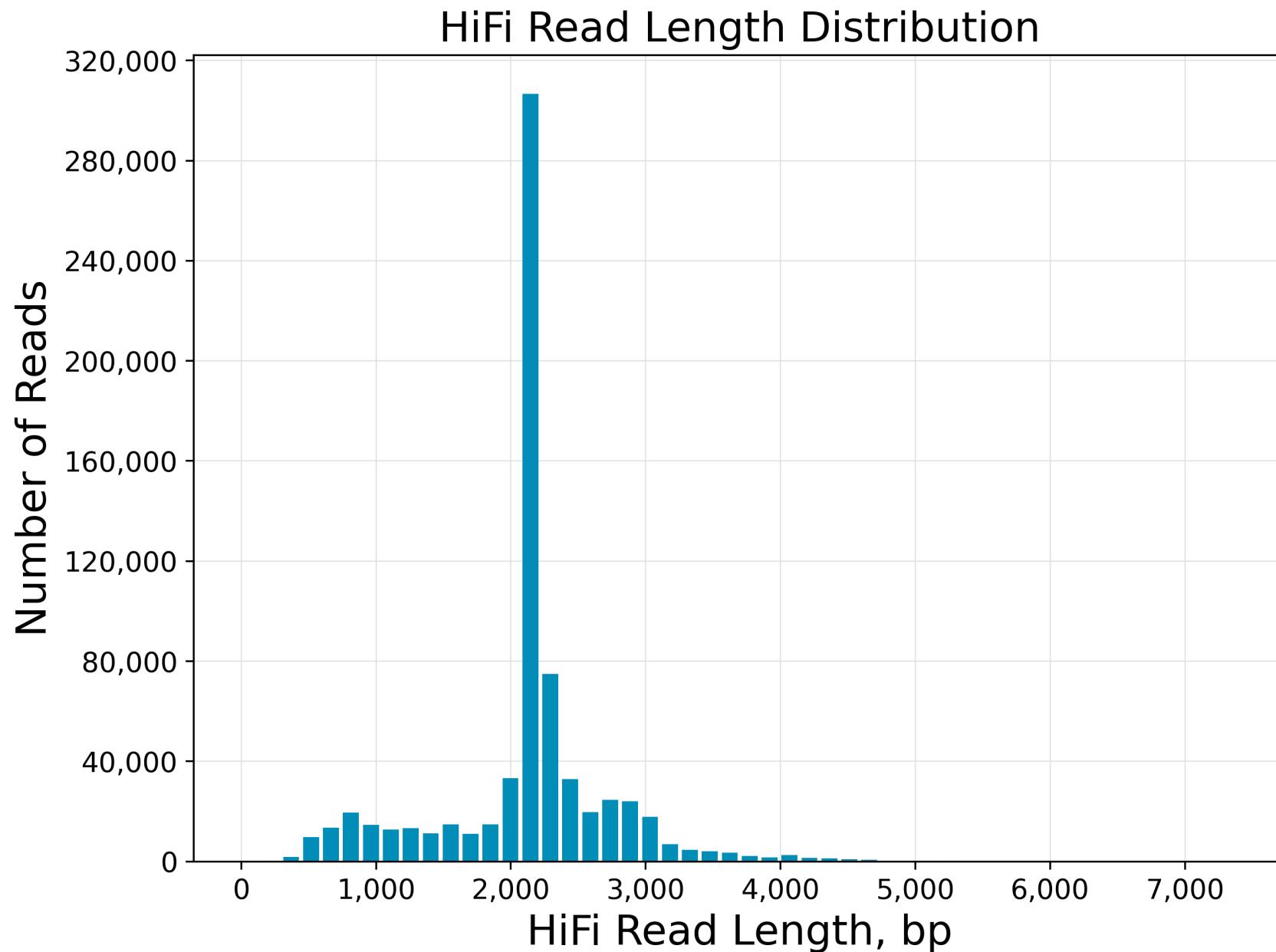
## HiFi Read Length Summary

| Read Length (bp) | Reads  | Reads (%) | Yield (bp) | Yield (%) |
|------------------|--------|-----------|------------|-----------|
| 0                | 702588 | 100       | 1468883334 | 100       |
| 5,000            | 1261   | 0         | 7184049    | 0         |
| 10,000           | 1      | 0         | 10101      | 0         |
| 15,000           | 0      | 0         | 0          | 0         |
| 20,000           | 0      | 0         | 0          | 0         |
| 25,000           | 0      | 0         | 0          | 0         |
| 30,000           | 0      | 0         | 0          | 0         |
| 35,000           | 0      | 0         | 0          | 0         |
| 40,000           | 0      | 0         | 0          | 0         |

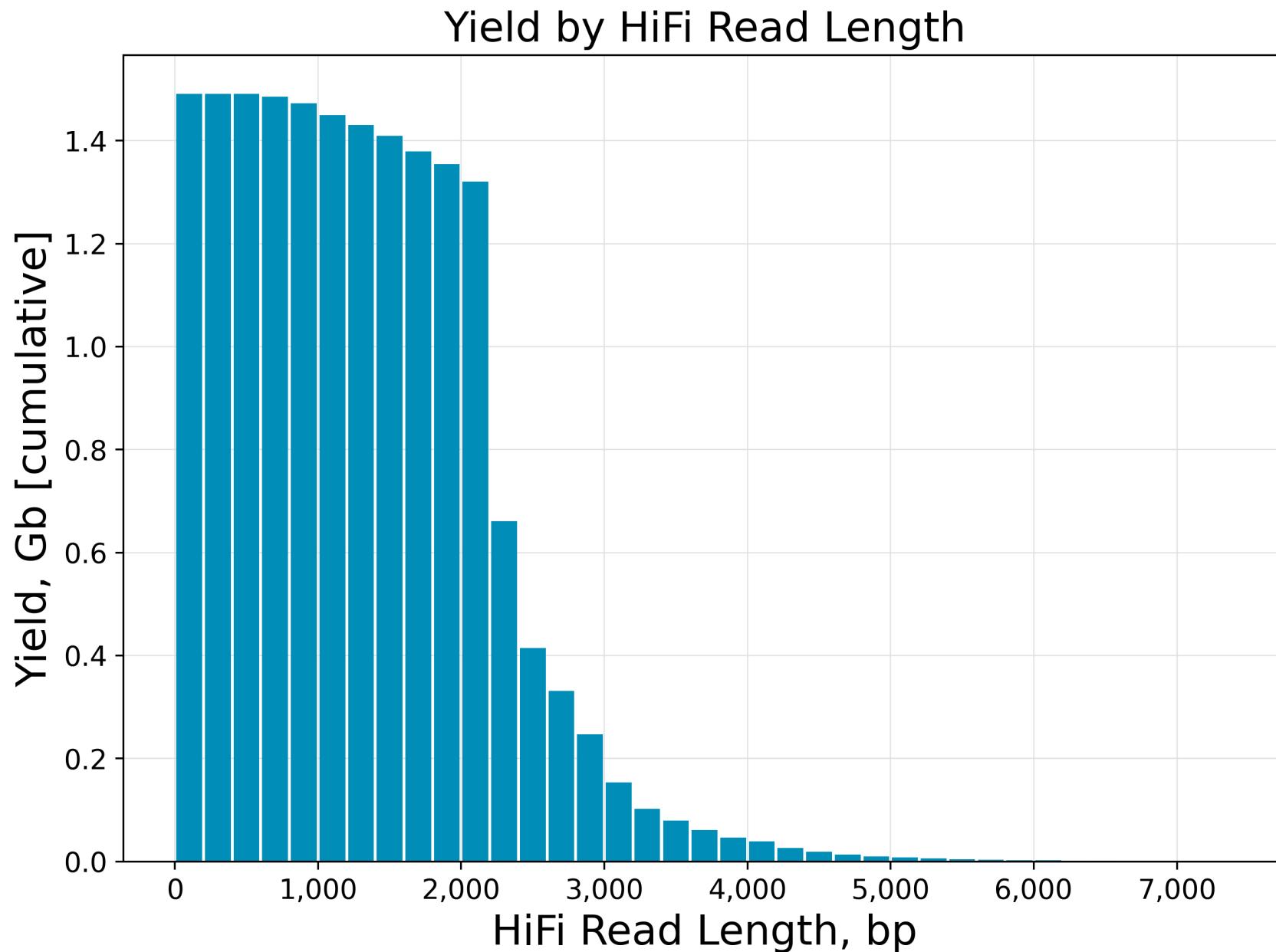
## HiFi Read Quality Summary

| Read Quality (Phred) | Reads  | Reads (%) | Yield (bp) | Yield (%) |
|----------------------|--------|-----------|------------|-----------|
| Q20                  | 702588 | 100       | 1468883334 | 100       |
| Q30                  | 572539 | 81        | 1187173061 | 81        |
| Q40                  | 282529 | 40        | 577842776  | 39        |
| Q50                  | 140894 | 20        | 277057990  | 19        |

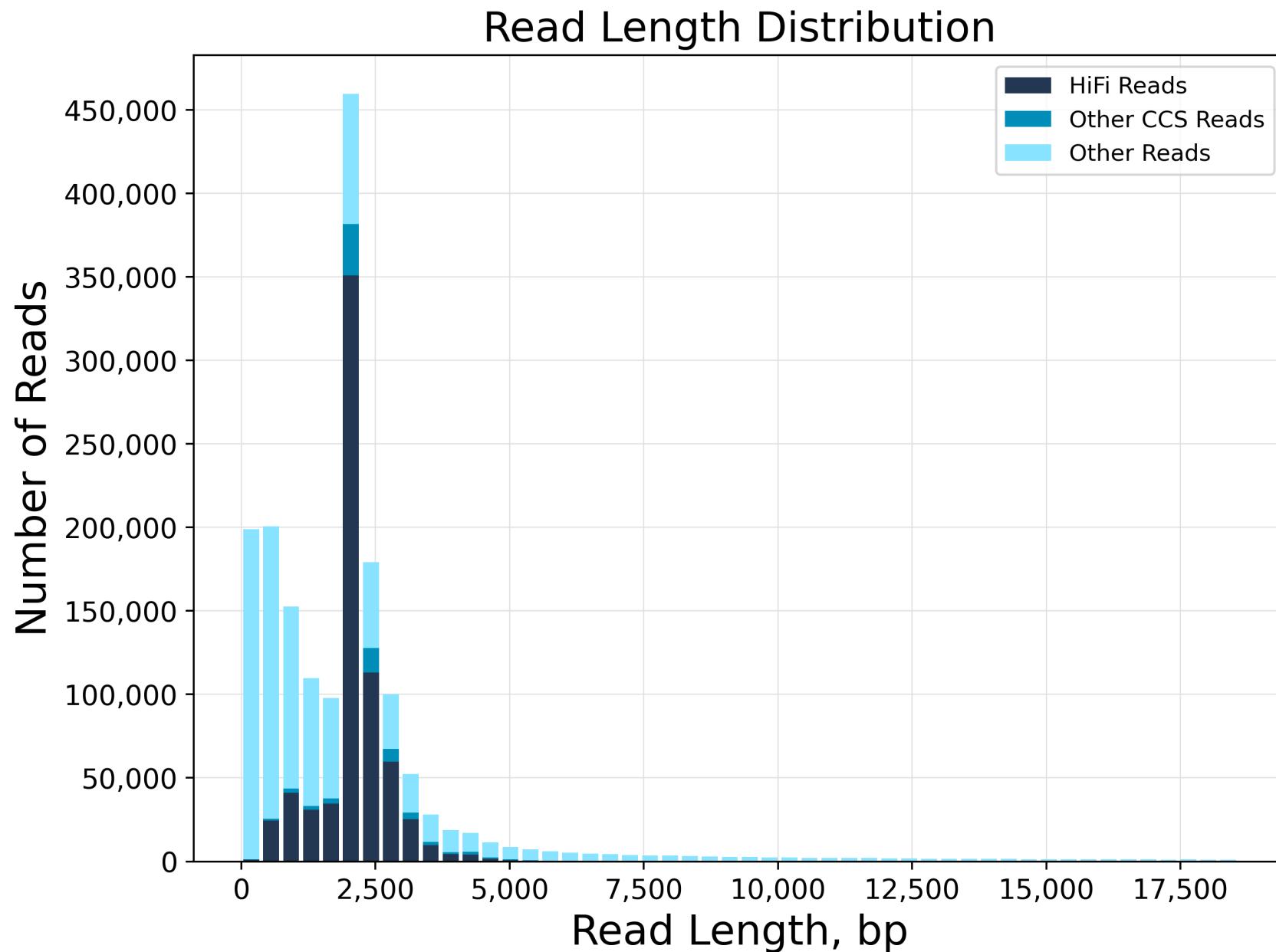
## HiFi Read Length Distribution



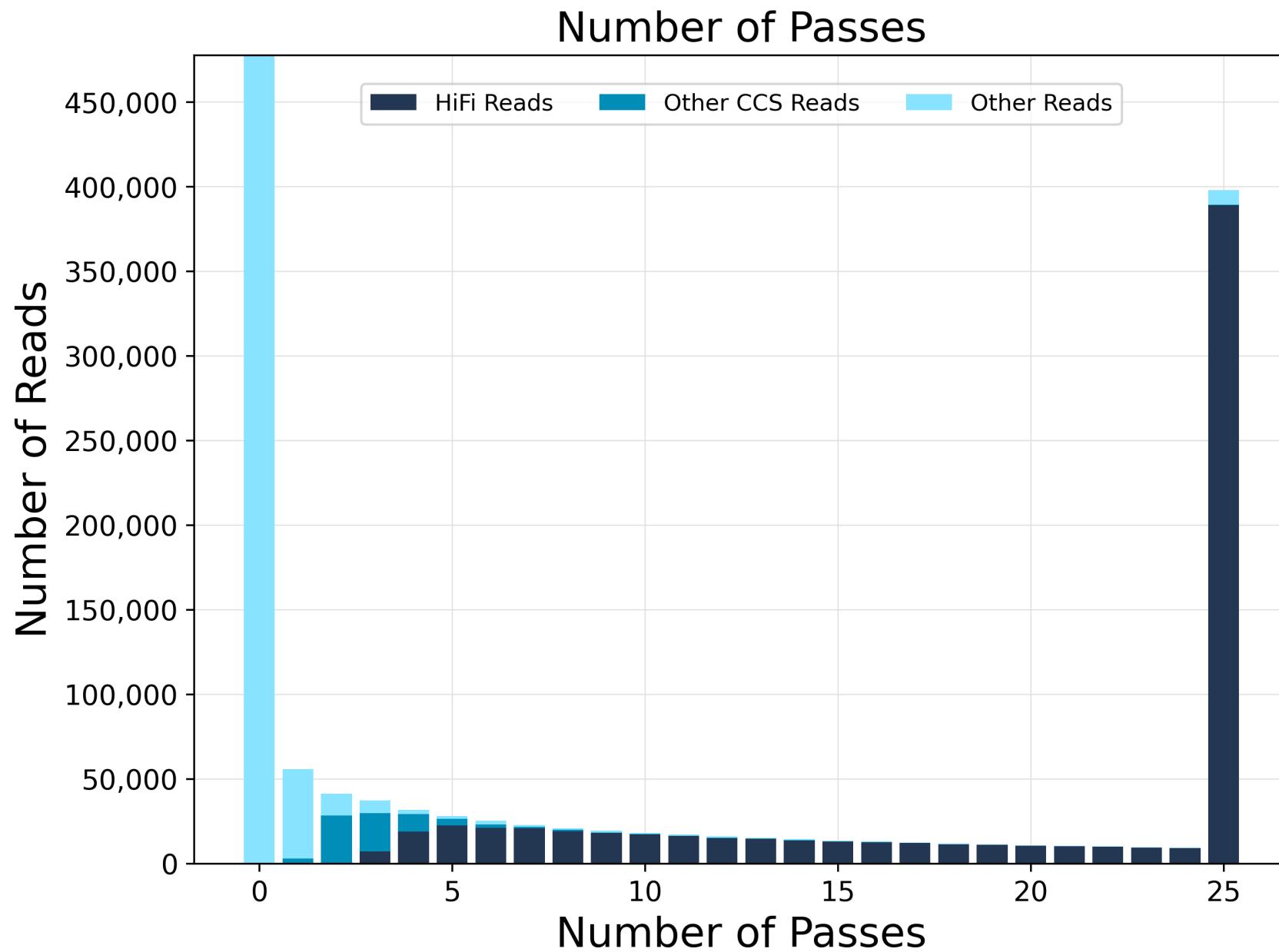
## Yield by HiFi Read Length



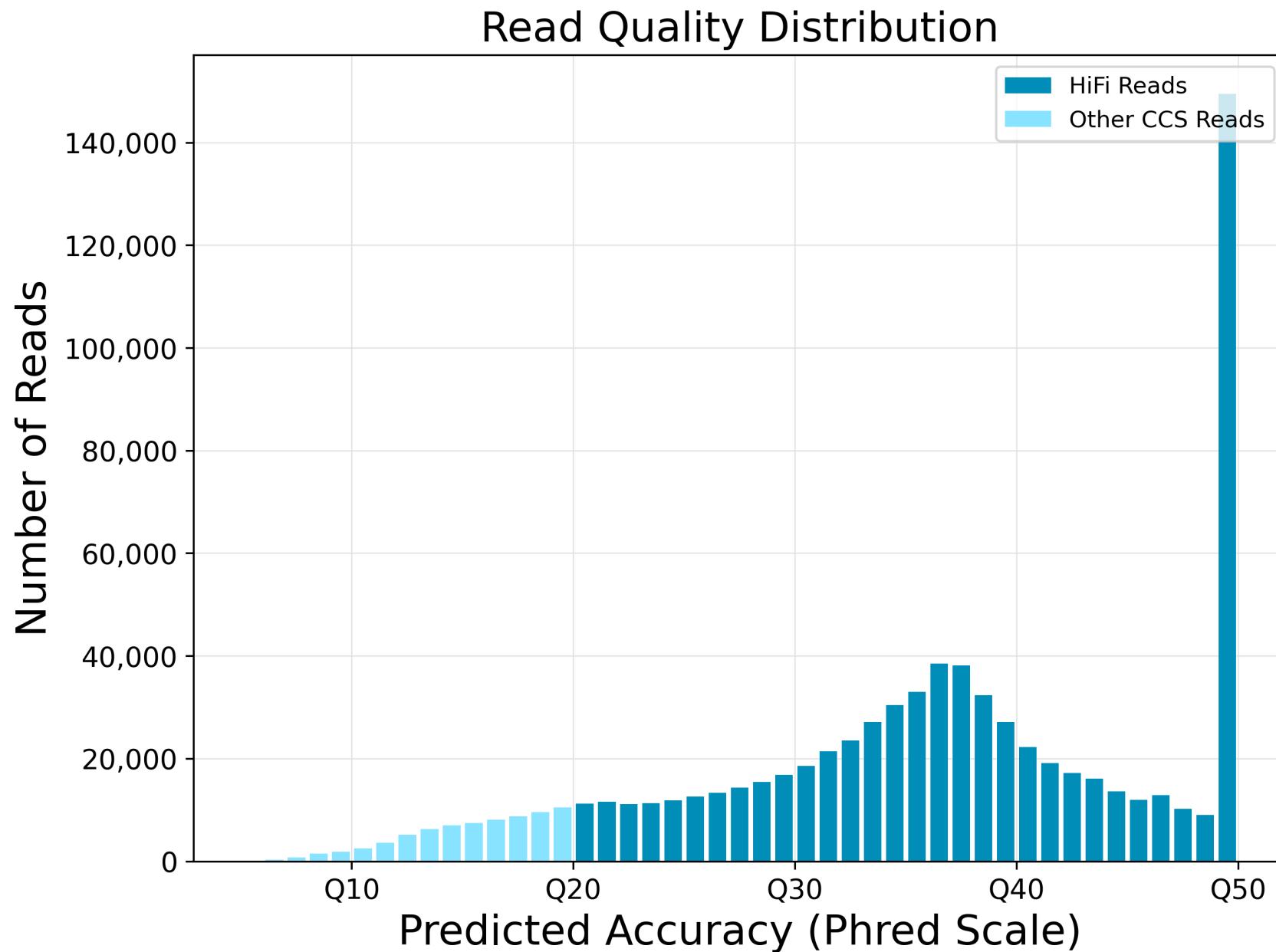
## Read Length Distribution



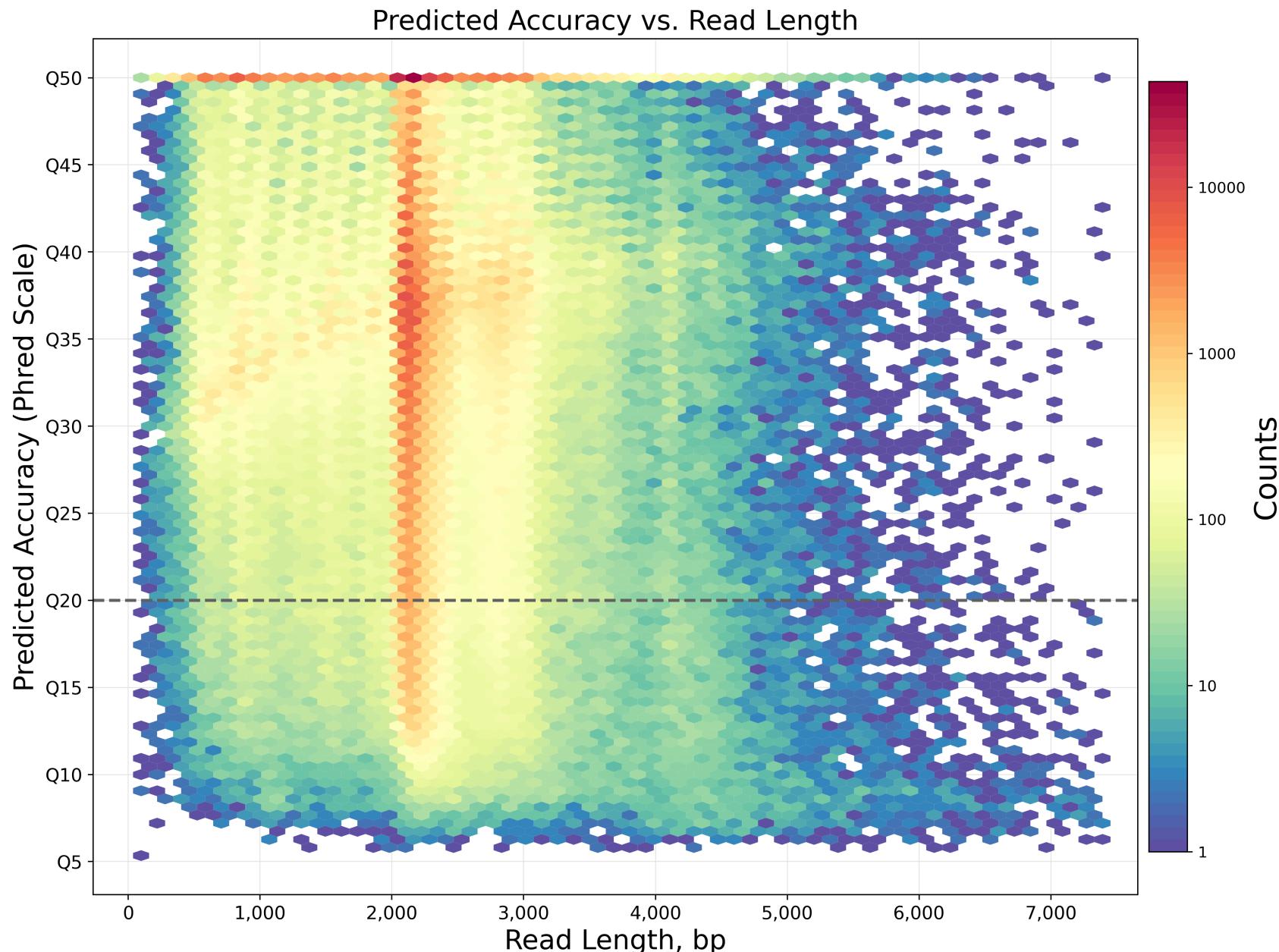
## Number of Passes



## Read Quality Distribution



## Predicted Accuracy vs. Read Length



# Barcodes

## Summary

|                                 |                     |
|---------------------------------|---------------------|
| Unique Barcodes                 | 5                   |
| Barcode Reads                   | 757,356             |
| Mean Reads                      | 151,471             |
| Max. Reads                      | 297,900             |
| Min. Reads                      | 31,684              |
| Mean Read Length                | 2,110               |
| Unbarcoded Reads                | 1,040,561           |
| Percent Bases in Barcoded Reads | 0.19999731208700267 |
| Percent Barcoded Reads          | 0.42124080255095203 |

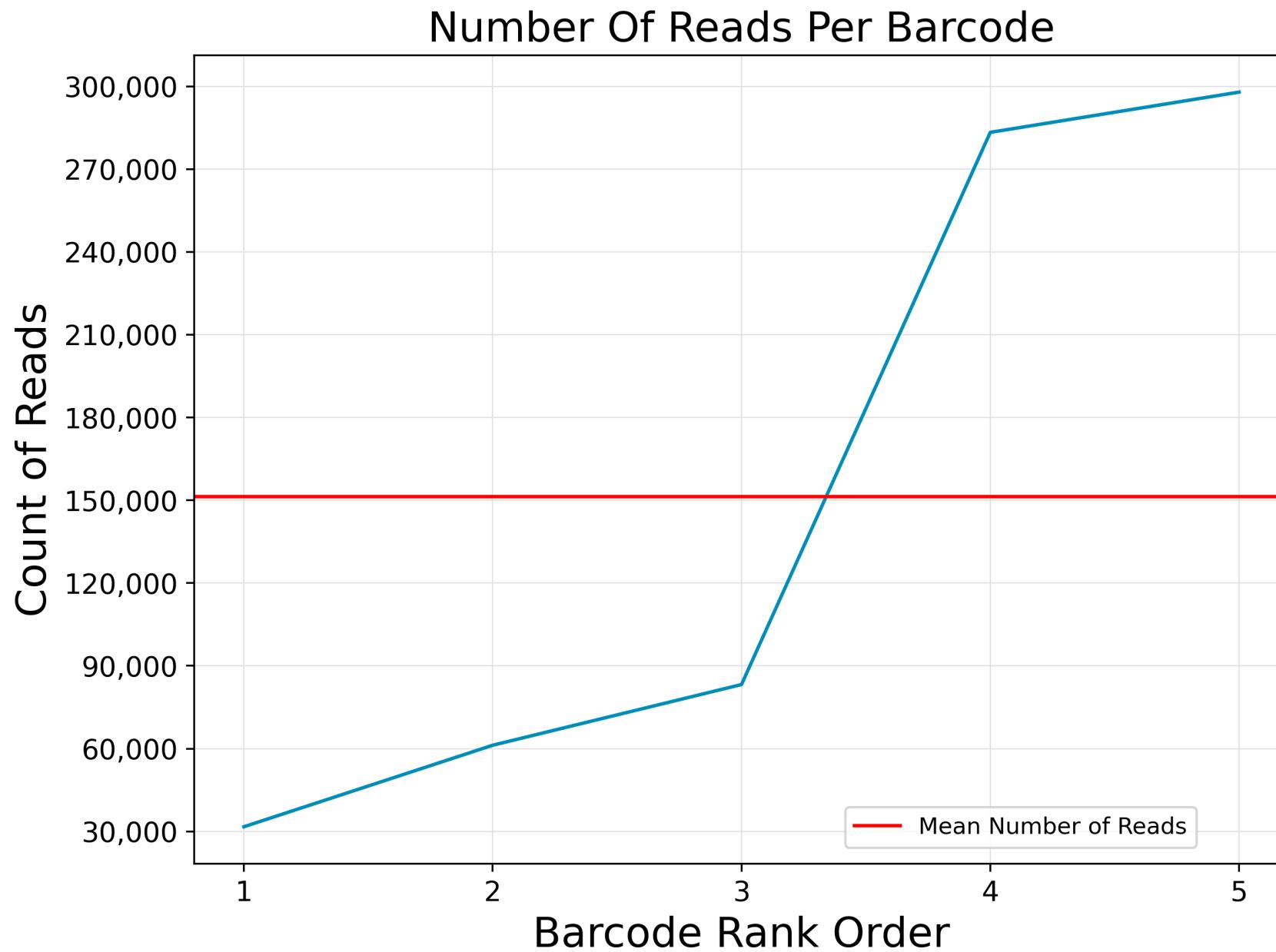
## Barcode Data

| Bio Sample Name | Barcode Name   | Polymerase Reads | Bases      | Mean Read Length | Mean Barcode Quality |
|-----------------|----------------|------------------|------------|------------------|----------------------|
| ACLU0243        | bc1001--bc1001 | 297900           | 664063131  | 2229             | 97.0                 |
| ACLU0248        | bc1002--bc1002 | 283325           | 601416023  | 2122             | 98.0                 |
| ACLU0102        | bc1003--bc1003 | 83222            | 150745711  | 1811             | 98.0                 |
| ACLU0128        | bc1008--bc1008 | 31684            | 61494671   | 1940             | 98.0                 |
| ACLU0232        | bc1009--bc1009 | 61225            | 120658932  | 1970             | 98.0                 |
| No Name         | Not Barcoded   | 1040561          | 6393621281 | 6144             | 0.0                  |

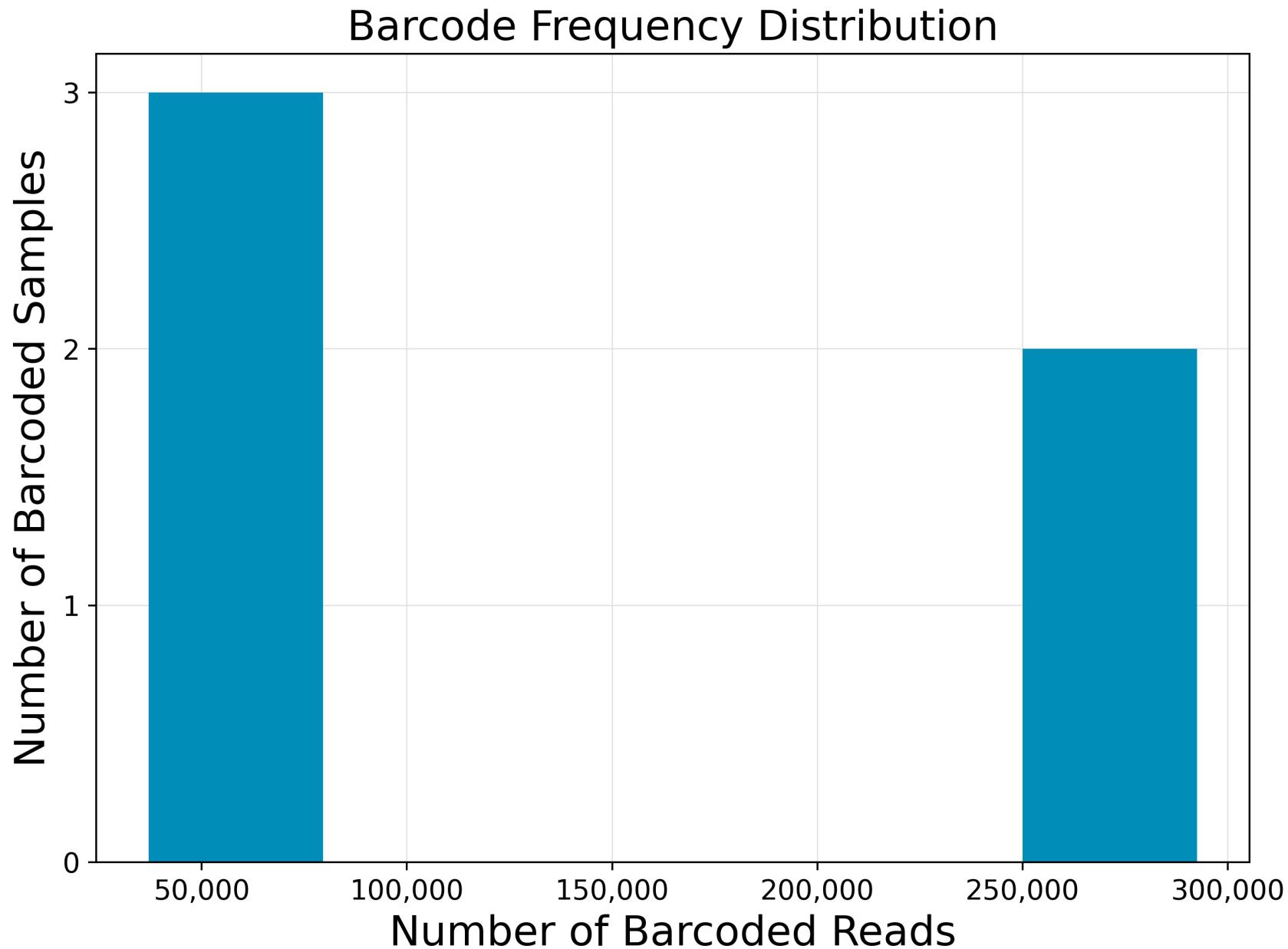
## Inferred Barcodes

| Barcode Name   | Number of ZMWs | Mean Barcode Score |
|----------------|----------------|--------------------|
| bc1001--bc1001 | 16139.0        | 97.0               |
| bc1002--bc1002 | 15483.0        | 97.0               |
| bc1003--bc1003 | 4811.0         | 98.0               |
| bc1008--bc1008 | 1776.0         | 98.0               |
| bc1009--bc1009 | 3282.0         | 98.0               |

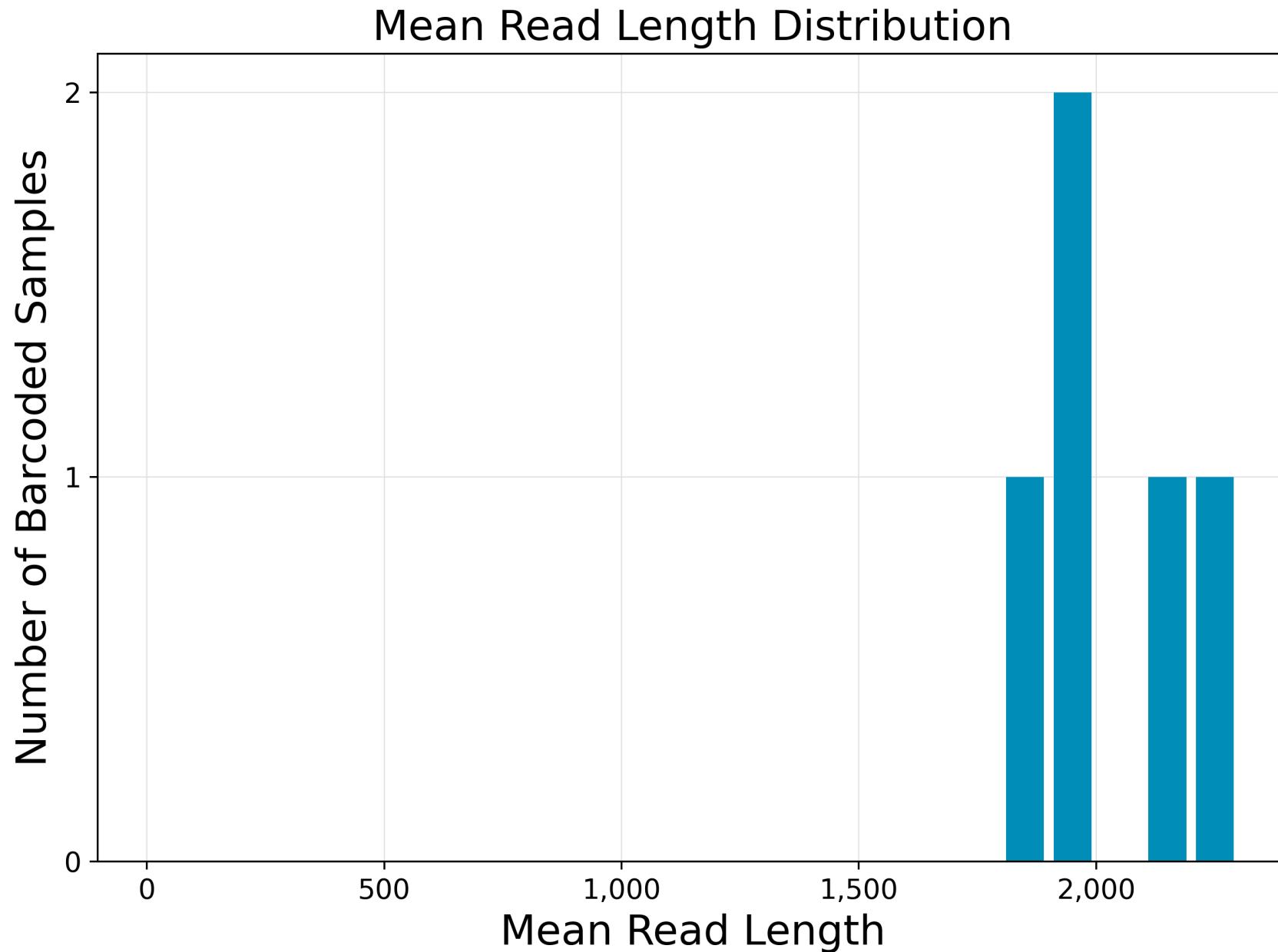
## Number Of Reads Per Barcode



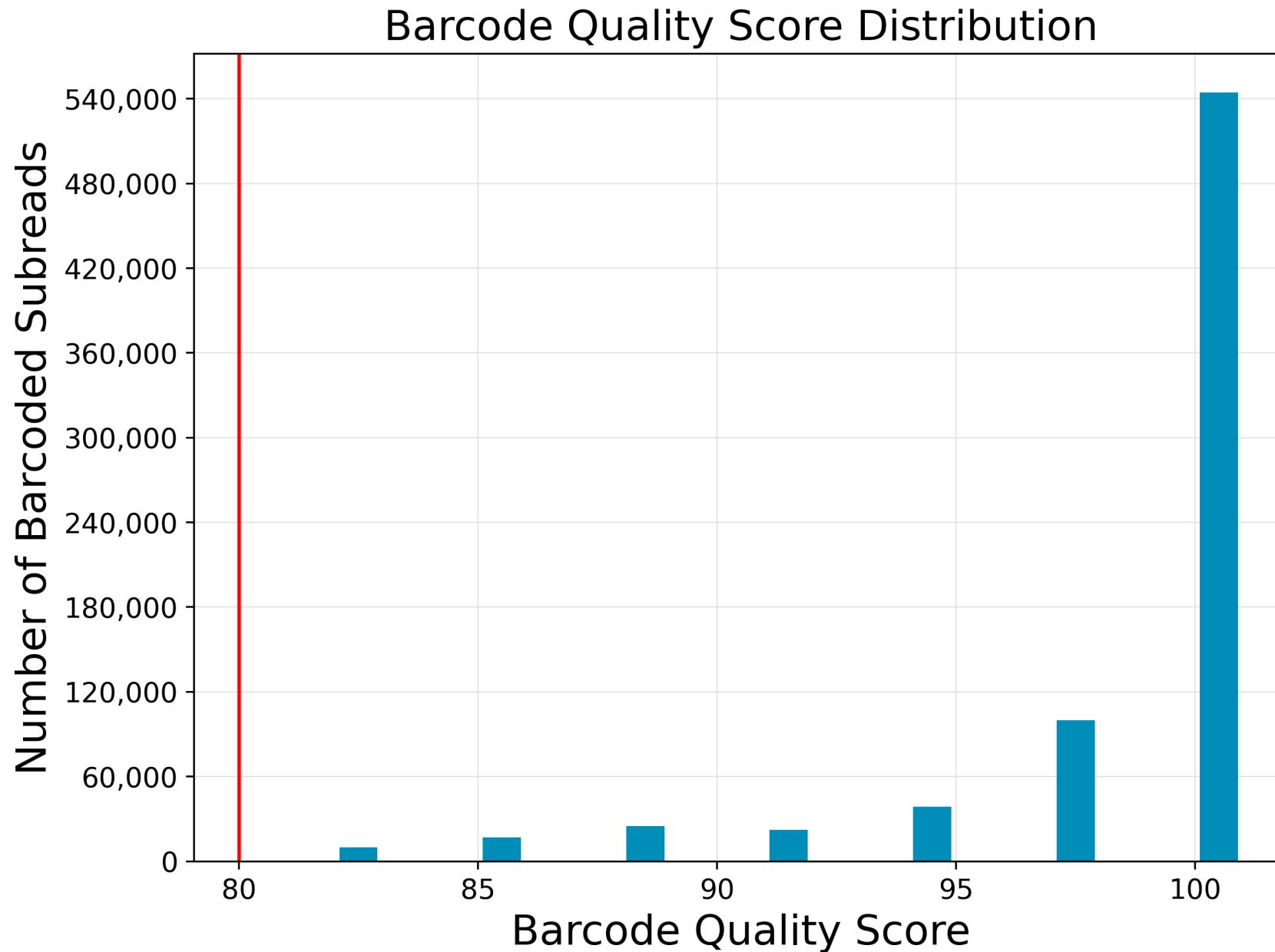
## Barcode Frequency Distribution



## Mean Read Length Distribution



## Barcode Quality Score Distribution

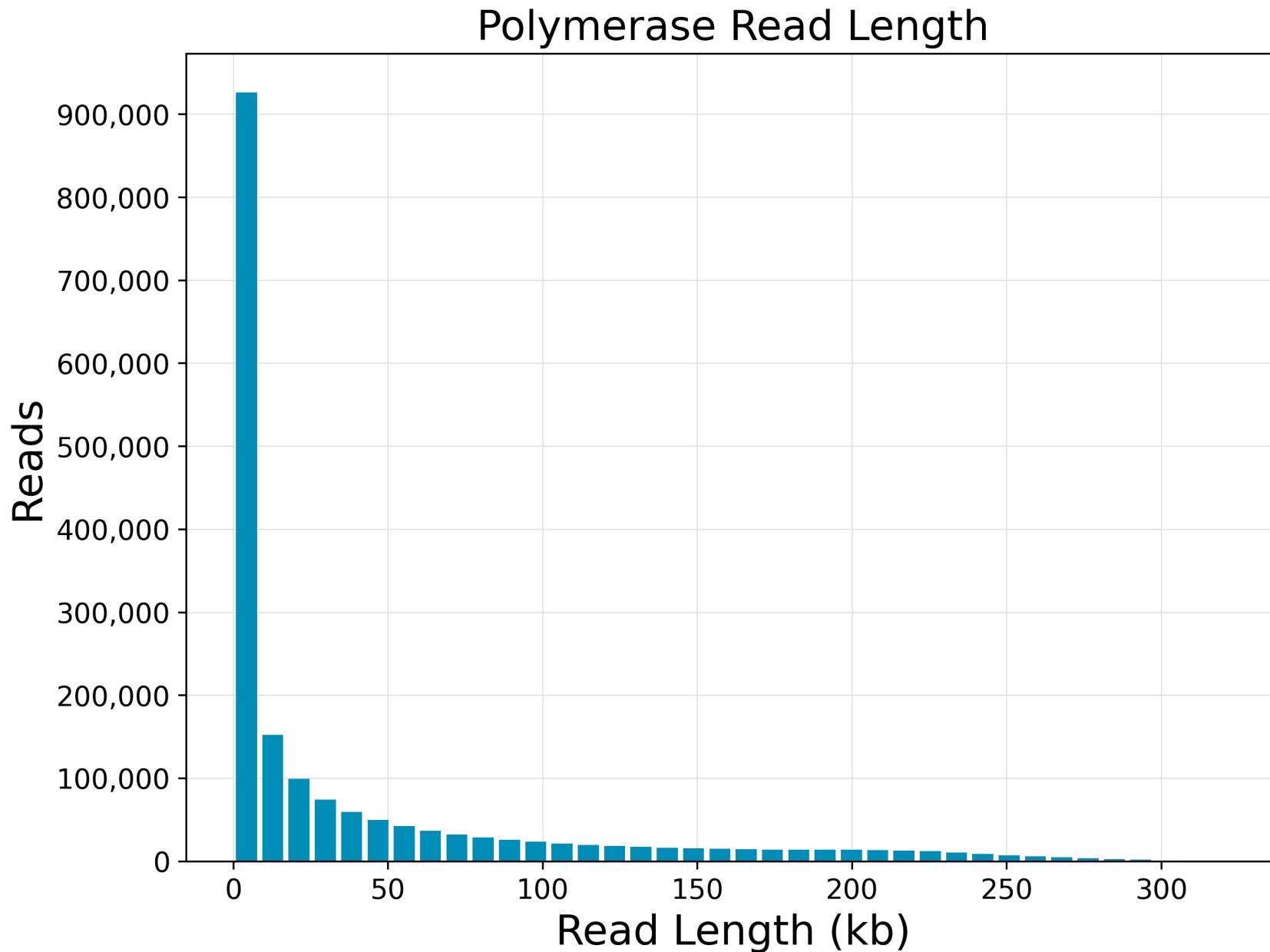


# Raw Data Report

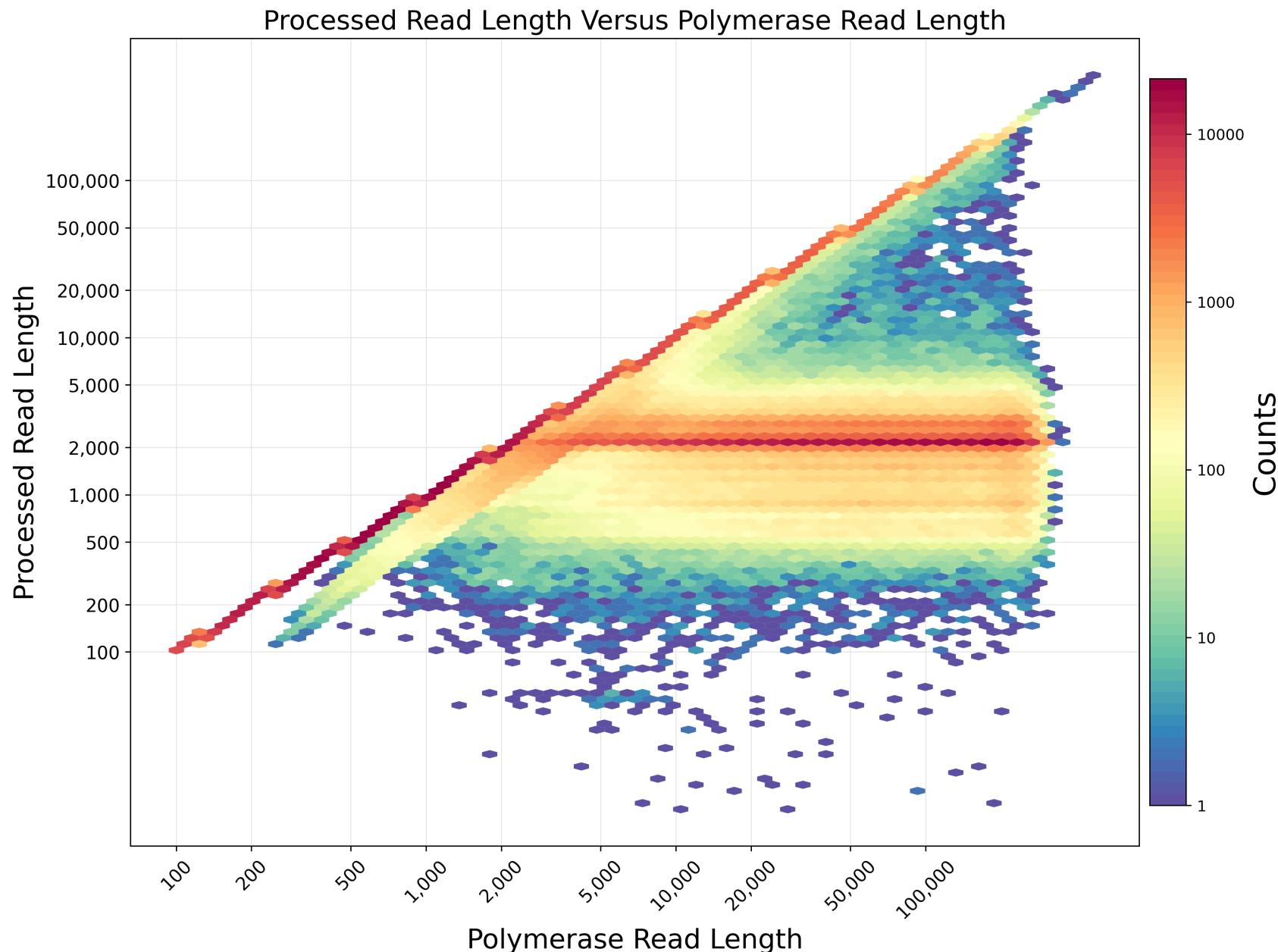
## Summary

|                               |                |
|-------------------------------|----------------|
| Polymerase Read Bases         | 75,272,989,526 |
| Polymerase Reads              | 1,831,072      |
| Polymerase Read Length (mean) | 41,109         |
| Polymerase Read N50           | 144,750        |
| Longest Subread Length (mean) | 5,505          |
| Longest Subread N50           | 29,750         |
| Unique Molecular Yield        | 8,055,613,952  |

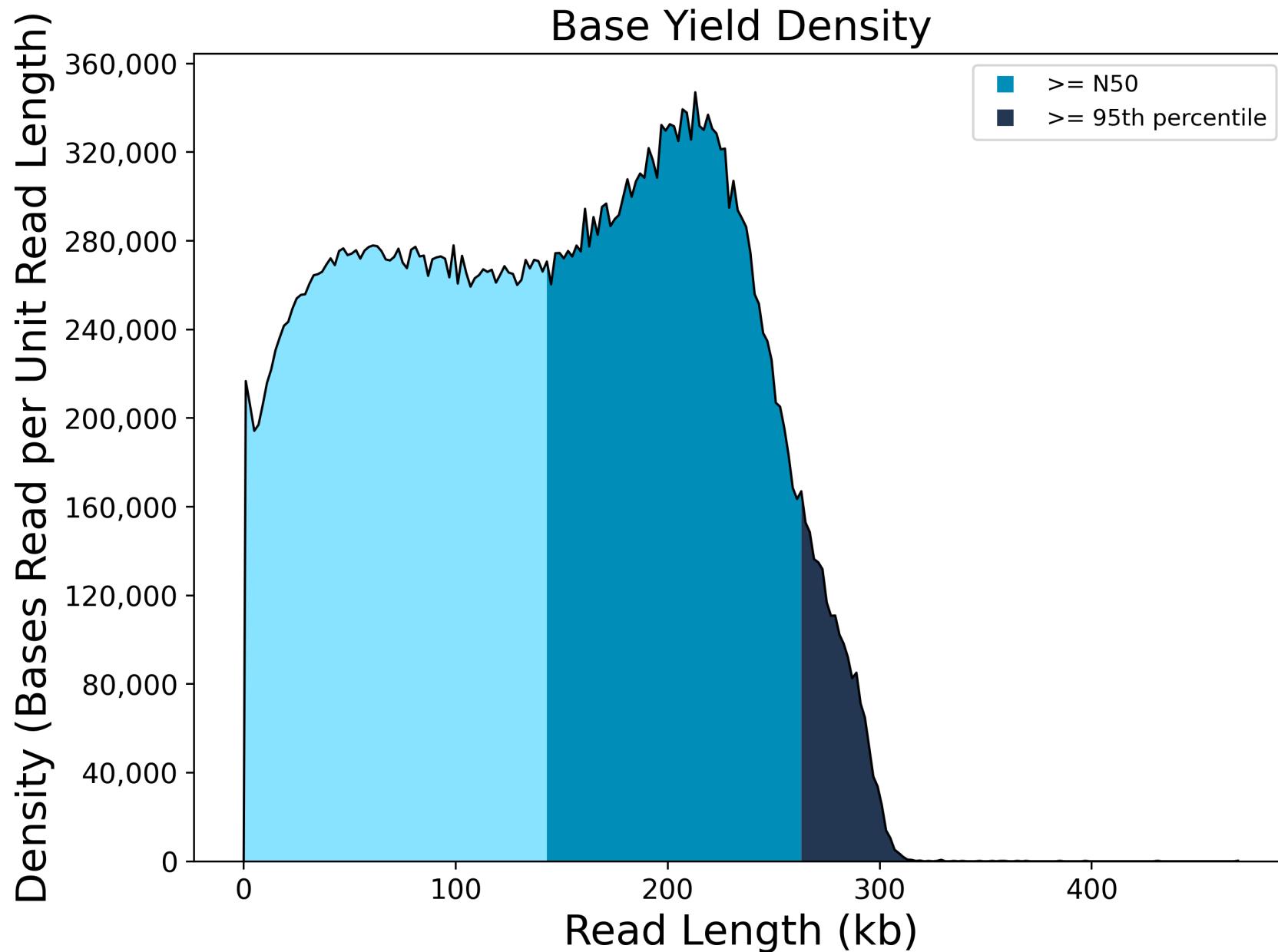
## Polymerase Read Length



## Longest Subread Length Versus Polymerase Read Length



## Base Yield Density



# CCS Processing

## Summary

|                          |           |
|--------------------------|-----------|
| ZMWs input               | 1,797,917 |
| ZMWs pass filters        | 776,214   |
| ZMWs fail filters        | 58,551    |
| ZMWs shortcut filters    | 963,152   |
| ZMWs with tandem repeats | 1,664     |
| Below SNR threshold      | 17,303    |
| Median length filter     | 0         |
| Lacking full passes      | 0         |
| Heteroduplex insertions  | 9,890     |
| Coverage drops           | 732       |
| Insufficient draft cov   | 14,344    |
| Draft too different      | 0         |
| Draft generation error   | 16,124    |
| Draft above --max-length | 0         |
| Draft below --min-length | 26        |
| Reads failed polishing   | 0         |
| Empty coverage windows   | 15        |
| CCS did not converge     | 117       |
| CCS below minimum RQ     | 0         |
| Unknown error            | 0         |
| ZMWs missing adapters    | 18,665    |

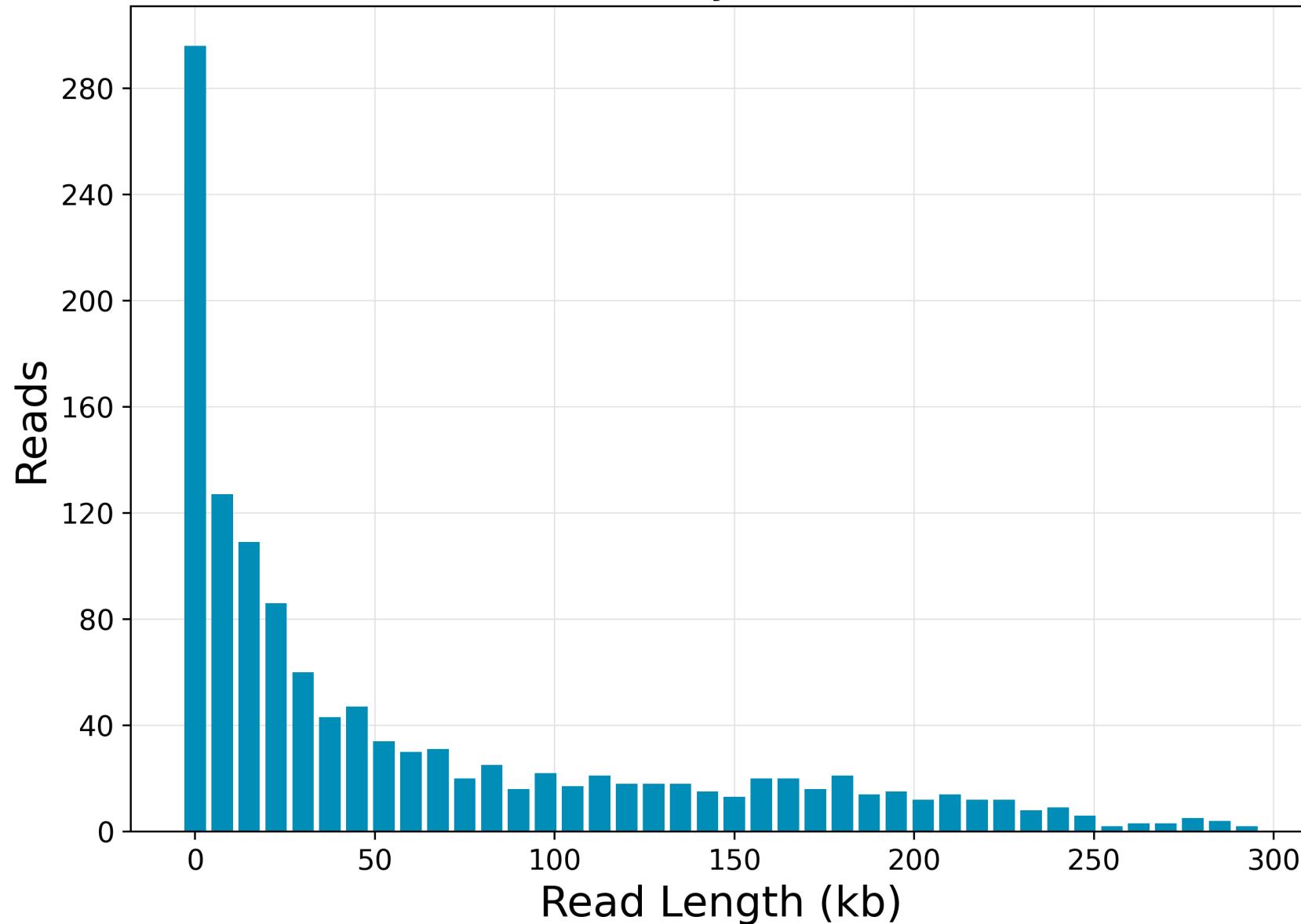
# **Control Report**

## **Summary**

|                                      |        |
|--------------------------------------|--------|
| <b>Number of Control Reads</b>       | 1,264  |
| <b>Control Read Length Mean</b>      | 65,279 |
| <b>Control Read Concordance Mean</b> | 0.86   |
| <b>Control Read Concordance Mode</b> | 0.89   |

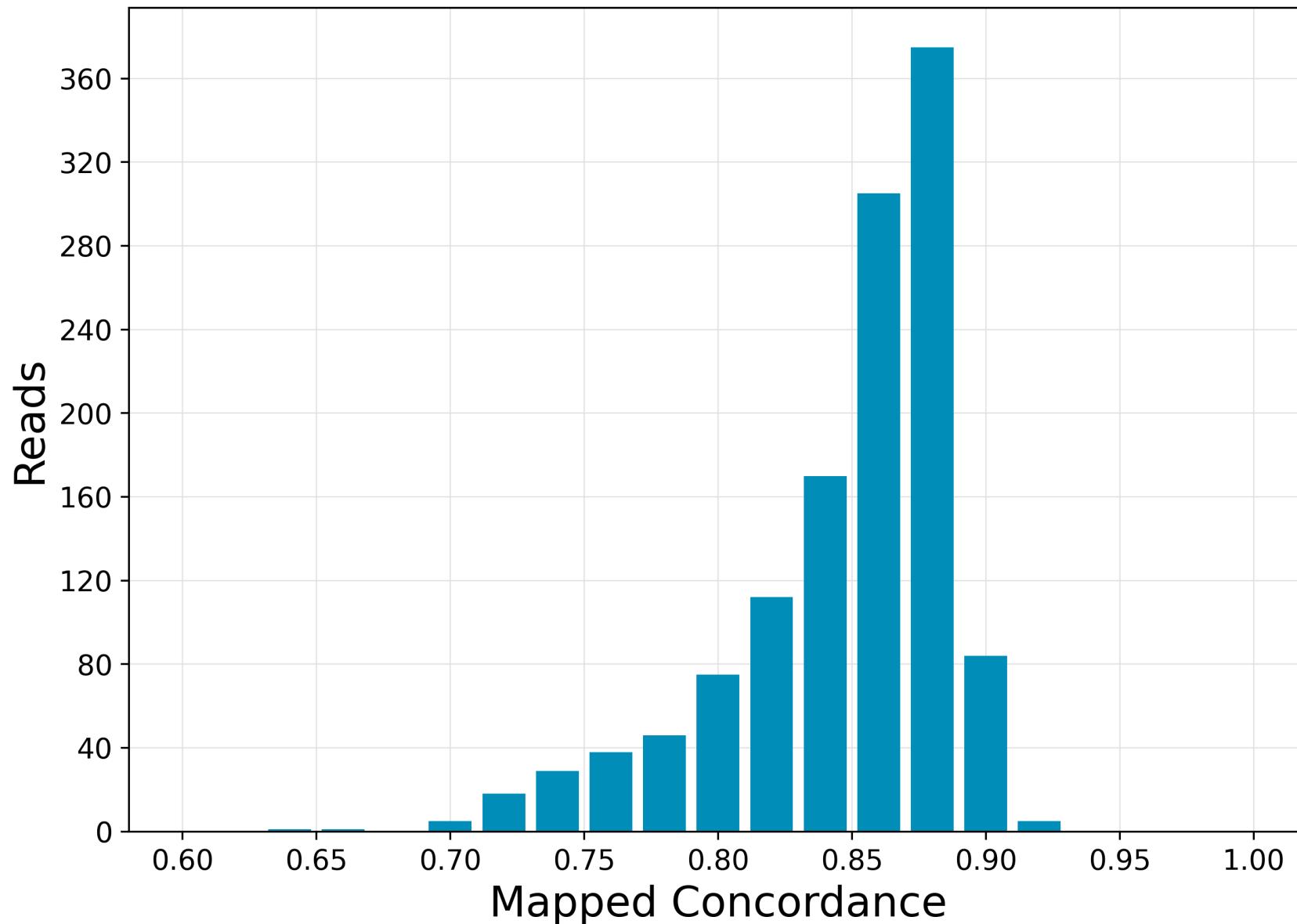
**Control Polymerase RL**

Control Polymerase RL



**Control Concordance**

## Control Concordance



# Loading Report

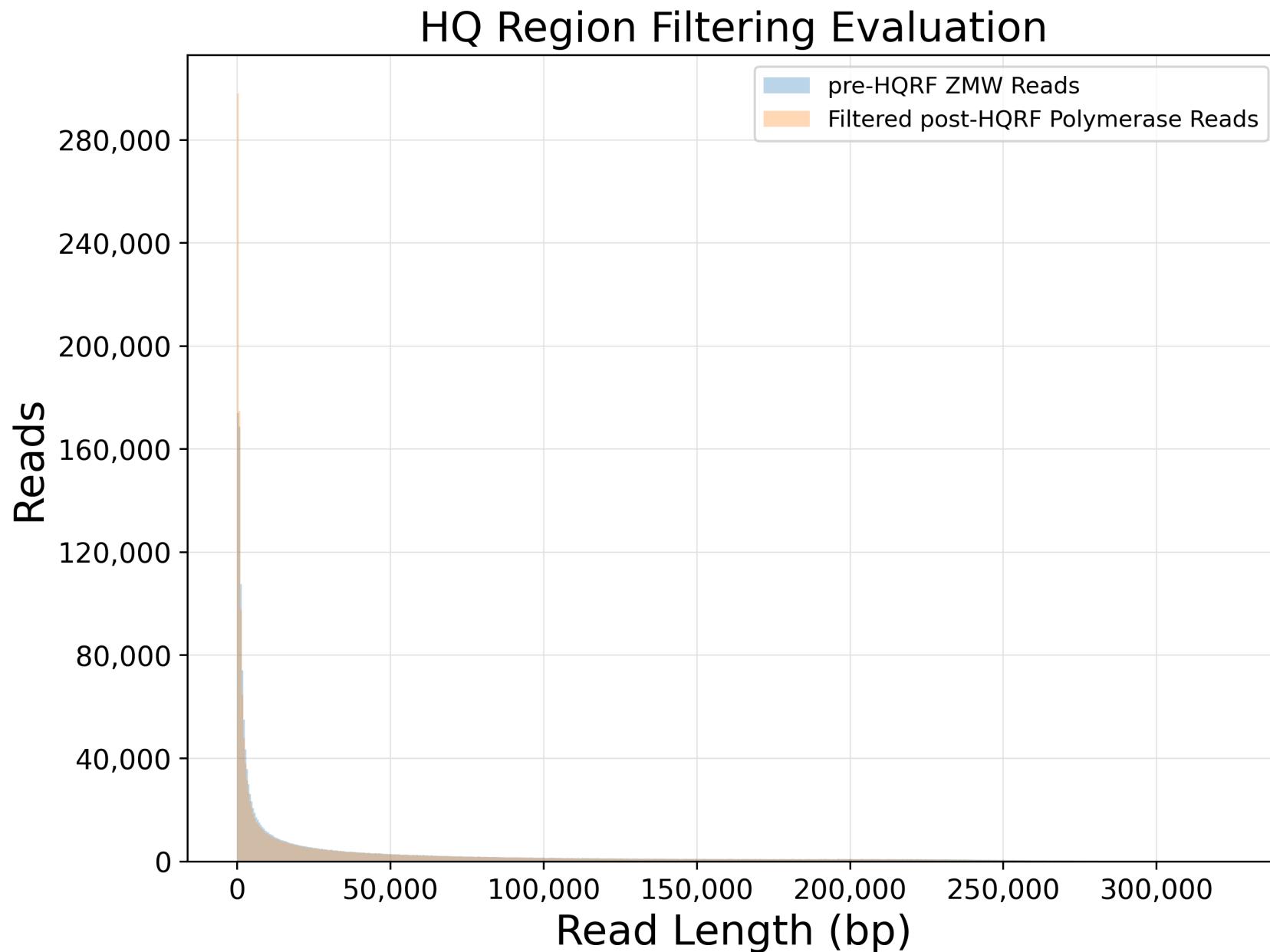
## Summary

|                 |           |
|-----------------|-----------|
| Productive ZMWs | 8,013,407 |
| Productivity 0  | 6,061,044 |
| Productivity 1  | 1,832,336 |
| Productivity 2  | 121,291   |

## Loading Statistics

| Collection Context    | Productive ZMWs | Productivity 0 | (%)   | Productivity 1 | (%)   | Productivity 2 | (%)  | Loading type |
|-----------------------|-----------------|----------------|-------|----------------|-------|----------------|------|--------------|
| m64219e_220701_164756 | 8013407         | 6061044        | 75.62 | 1832336        | 22.86 | 121291         | 1.51 | Diffusion    |

## HQ Region Filtering Evaluation



**No Sample Setup found**

## Instrument run(s)

### Run d7408cf3-45a5-46a5-bd5c-9b60e722496d

#### Summary

|                          |                               |
|--------------------------|-------------------------------|
| Name                     | SQ64219e-NS2778-NS2800-NS2801 |
| Status                   | COMPLETE                      |
| Created                  | 2022-07-01 14:00:25.664       |
| Started                  | 2022-07-01 16:38:01.711       |
| Completed                | 2022-07-05 16:28:16.433       |
| Context                  | r64219e_20220701_163641       |
| Instrument Name          | 64219e                        |
| Instrument Serial Number | 64219e                        |
| ICS Version              | 11.0.0.144466                 |
| Primary Analysis Version | 11.0.0.144466                 |
| Chemistry Version        | 11.0.0.143406                 |

## Parent jobs (1)

### Job 413

#### Summary

|                          |   |
|--------------------------|---|
| <b>Job Type</b>          | import-dataset                            |
| <b>Pipeline</b>          | cromwell.workflows.sl_dataset_reports     |
| <b>Name</b>              | import-dataset                            |
| <b>Comments</b>          | Description for job Import PacBio DataSet |
| <b>Created At</b>        | 2022-07-03 10:40:48.997                   |
| <b>SMRT Link Version</b> | 11.0.0.146107                             |

# Job 413: Barcoding Inferred Barcodes Report

## Inferred Barcodes

| Barcode Name   | #ZMWs   | Mean Barcode Score |
|----------------|---------|--------------------|
| bc1001--bc1001 | 16139.0 | 97.0               |
| bc1002--bc1002 | 15483.0 | 97.0               |
| bc1003--bc1003 | 4811.0  | 98.0               |
| bc1008--bc1008 | 1776.0  | 98.0               |
| bc1009--bc1009 | 3282.0  | 98.0               |

**No child jobs found**