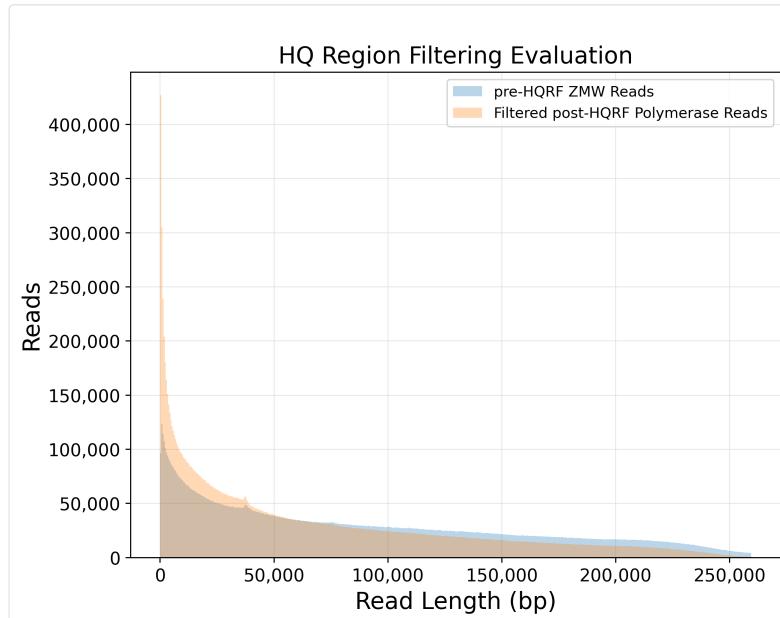


## Loading Statistics

Collection ID	Total ZMW Reads	Produced	(%)	Produced	(%)	Produced
m84036_23...	25,165,824	9,734,813	38.68	15,067,473	59.87	363,531

## HQ Region Filtering Evaluation



## CCS Analysis Report

Value	Analysis Metric
4.7	HiFi Reads
87.35 Gb	HiFi Yield (bp)
18.69 kb	HiFi Read Length (mean, bp)
18,815	HiFi Read Length (median, bp)
18,815	HiFi Read Length N50 (bp)
Q30	HiFi Read Quality (median)
7	HiFi Number of Passes (mean)

## HiFi Read Length Summary

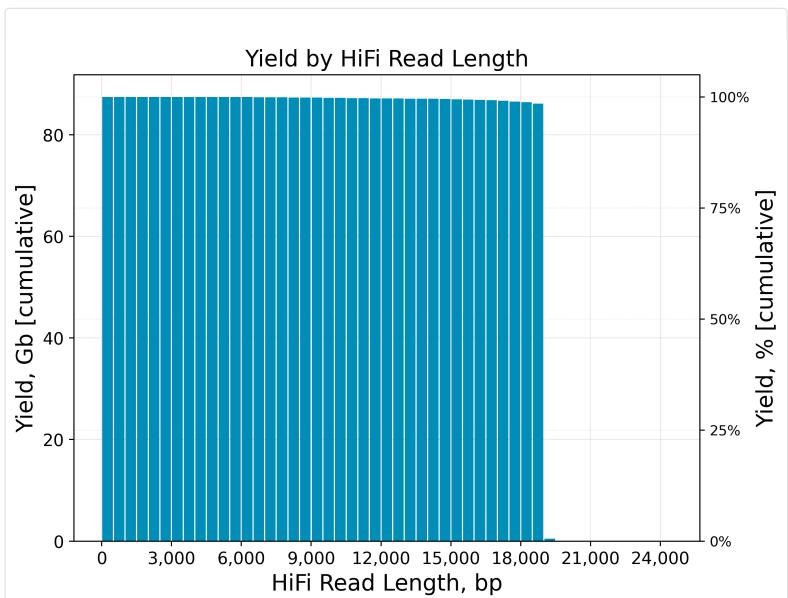
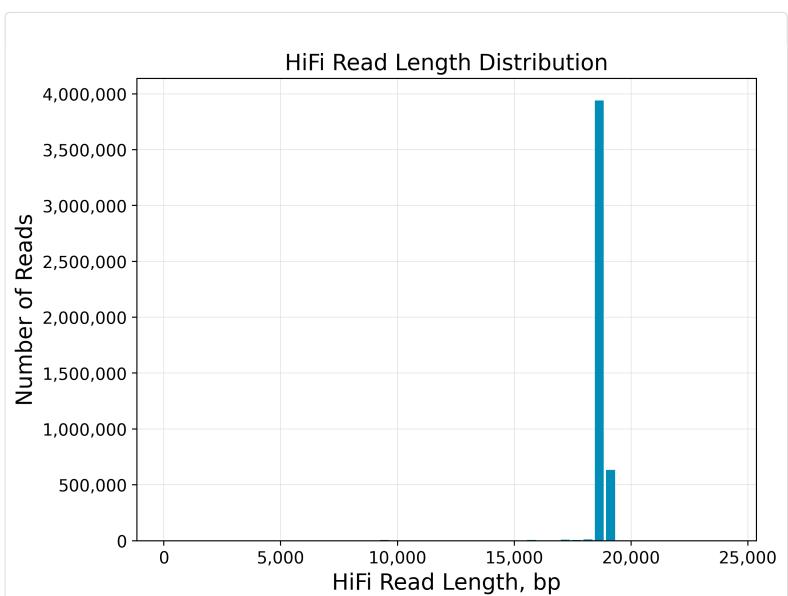
Read Length (bp)	Reads	Reads (%)	Yield (bp)
≥ 0	4,673,096	100	87,347,133,408 Gb
≥ 5,000	4,664,693	100	87,315,018,849 Gb
≤ 10,000	4,630,712	100	87,122,665,508 Gb

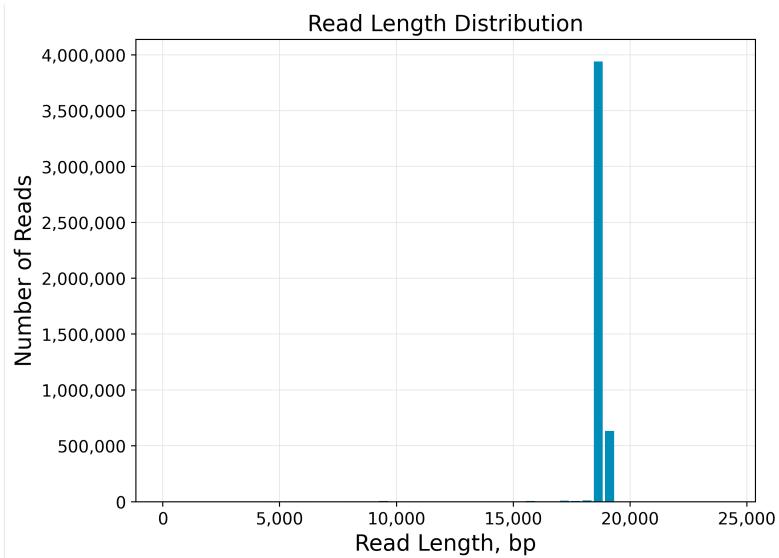
$\leq 10,000$	4,000,000 / 12	0%	87,122,000,000 Gb
$\geq 15,000$	4,620,164	99	86,874,611,357 Gb
$\geq 20,000$	2,357	0	51,505,960 Gb
$\geq 25,000$	193	0	5,309,933 Gb
$\geq 30,000$	30	0	1,027,854 Gb
$\geq 35,000$	11	0	411,919 Gb
$\geq 40,000$	0	0	0 Gb

## HiFi Read Quality Summary

Read Quality (Phred) ↑	Reads ↓	Reads (%) ↓	Yield (Gb) ↓
$\geq Q20$	4,673,096	100	87.35 Gb
$\geq Q30$	2,239,646	48	41.79 Gb
$\geq Q40$	363,099	8	6.64 Gb
$\geq Q50$	5,627	0	0.04 Gb

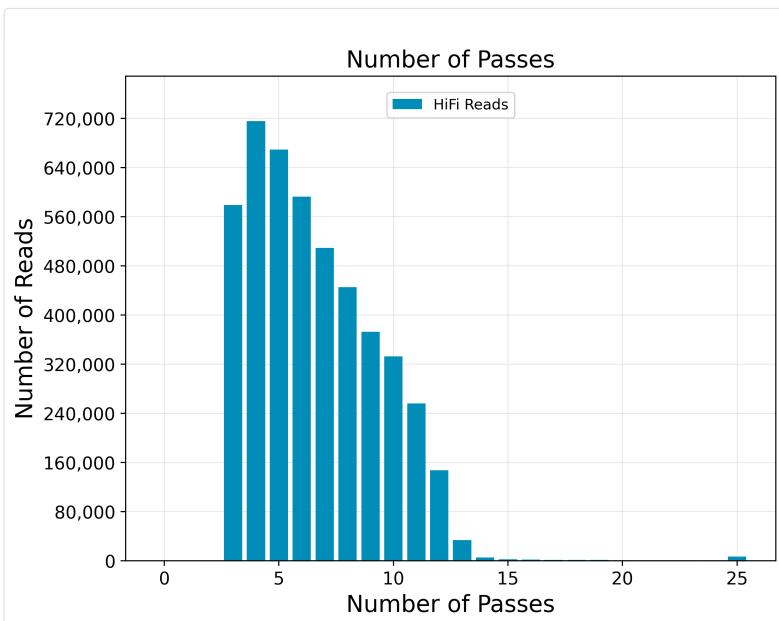
## Read Length Distribution





### Number of Passes

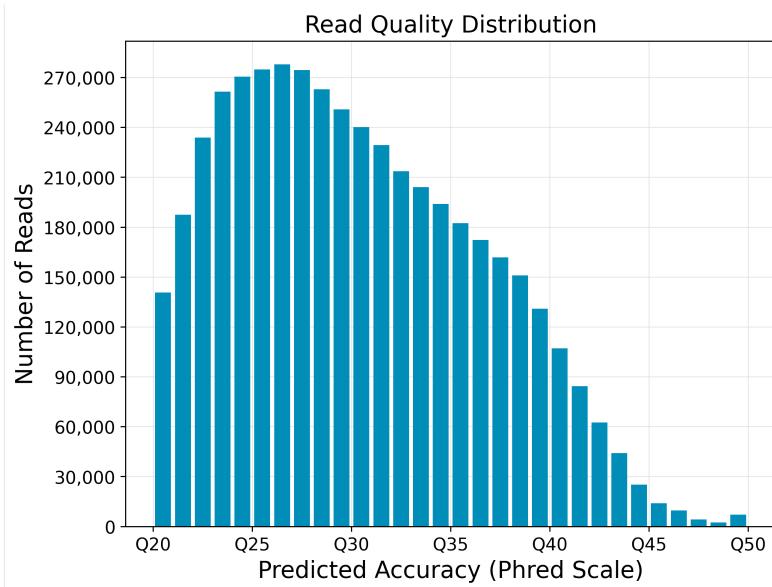
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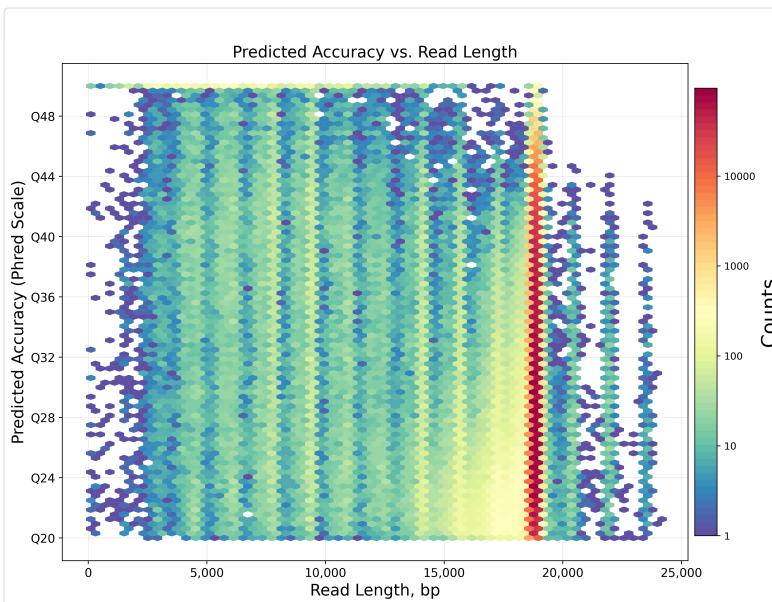
### Read Quality Distribution

---





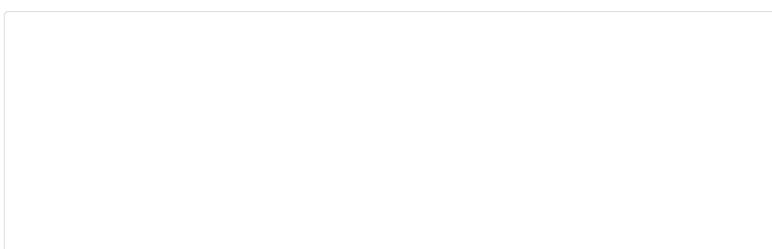
### Predicted Accuracy vs. Read Length



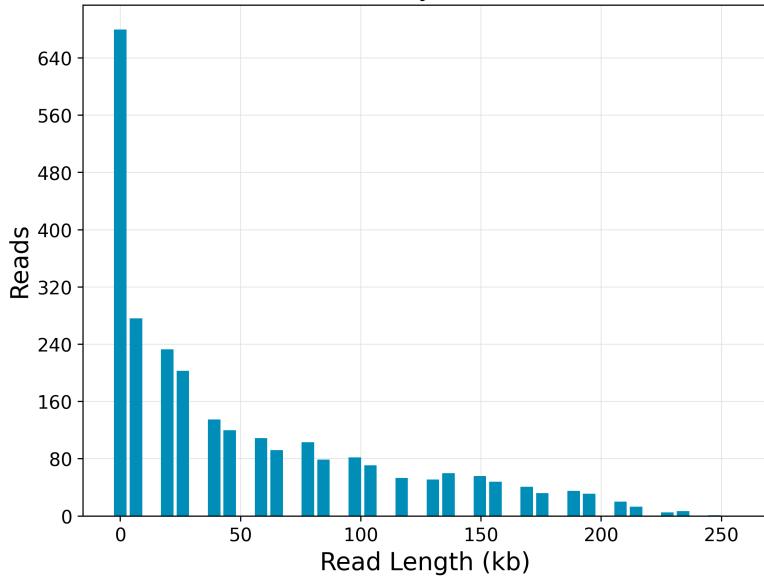
### Control Report

Value	Analysis Metric
2,636	Number of Control Reads
54,424	Control Read Length Mean
0.90	Control Read Concordance Mean
0.91	Control Read Concordance Mode

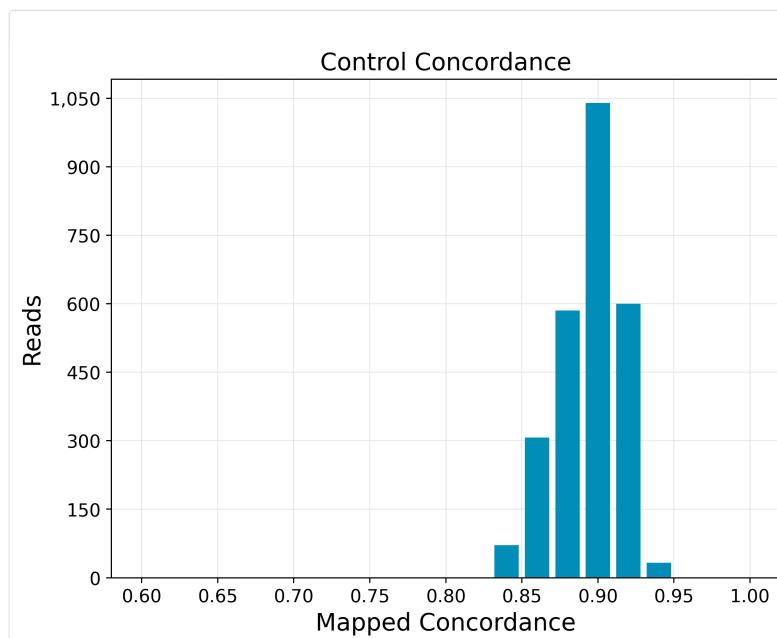
### Control Read Length



### Control Polymerase RL



### Control Read Quality



### Barcodes

Value	Analysis Metric
4	Unique Barcodes
4,654,835	Barcode HiFi Reads
18,261	Unbarcode HiFi Reads
99.60%	Barcode HiFi Reads (%)
87.04 Gb	Barcode HiFi Yield (bp)
0.31 Gb	Unbarcode HiFi Yield (bp)
99.64%	Barcode HiFi Yield (%)
1,163,708	Mean HiFi Reads per Barcode

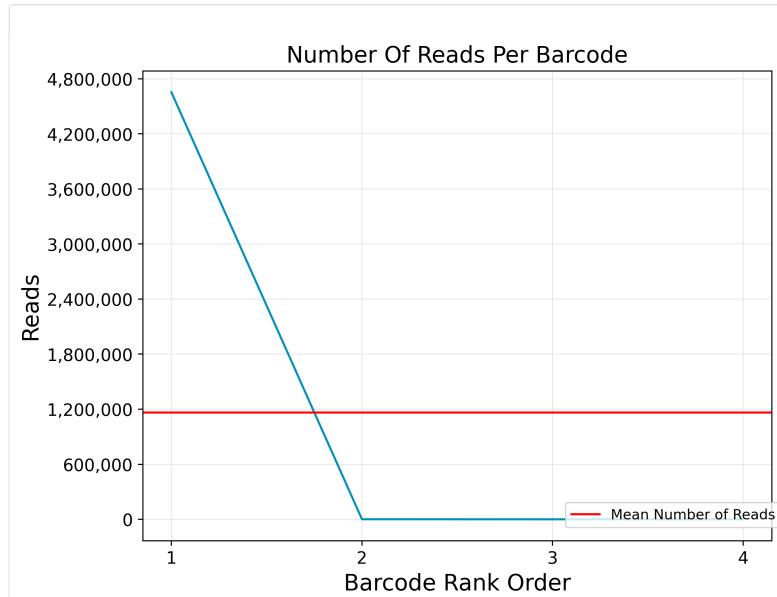
Value	Analysis Metric
4,653,939	Max. HiFi Reads per Barcode
51	Min. HiFi Reads per Barcode
18.70 kb	Barcoded HiFi Read Length (mean, bp)
16.93 kb	Unbarcoded HiFi Read Length (mean, bp)

## Barcode Data

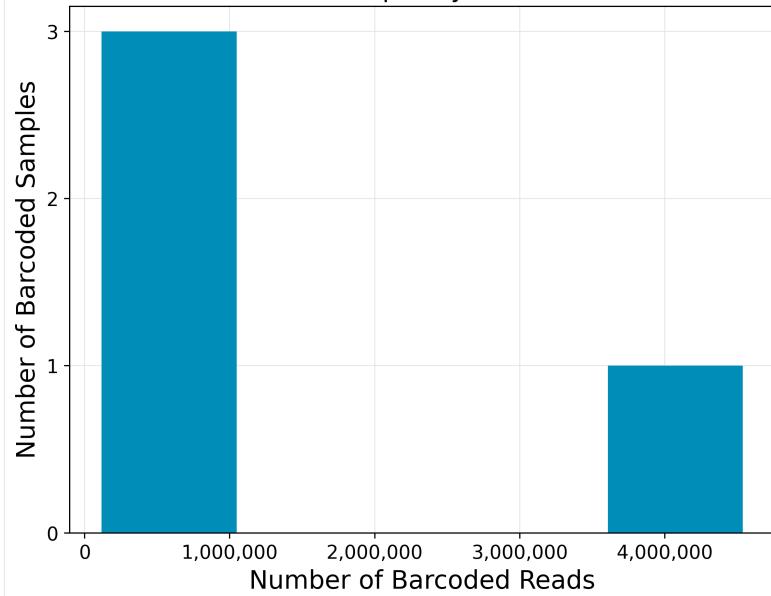
Search ...

Sample Na... ↗	Barcode ↗	Barcode Qu... ↗	HiFi Reads ↗	HiFi Read L... ↗
Bio Sample 1	bcM0001--bcM0001	96.3	4,653,939	18,698
Bio Sample 2	bcM0002--bcM0002	52.8	769	17,514
Bio Sample 3	bcM0003--bcM0003	56.8	76	17,175
Bio Sample 4	bcM0004--bcM0004	54.5	51	17,151
No Name	Not Barcoded	0.0	18,261	16,931

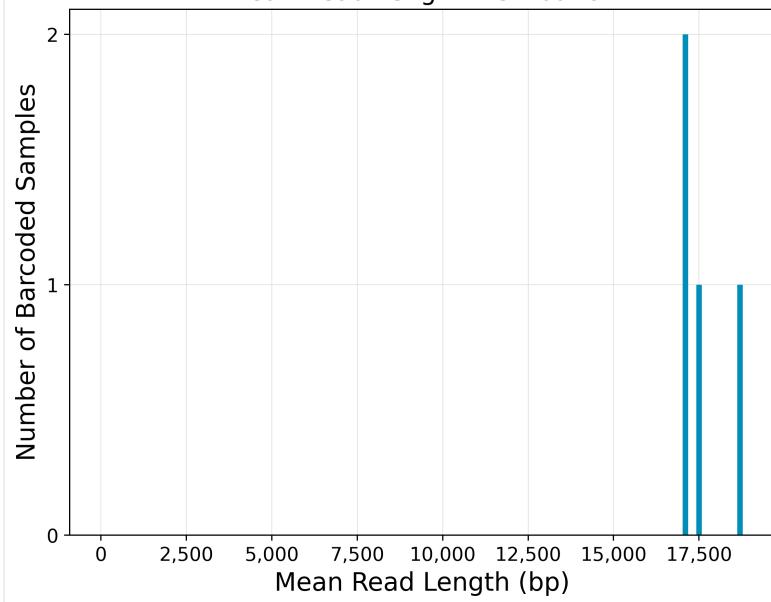
## Barcoded Read Statistics



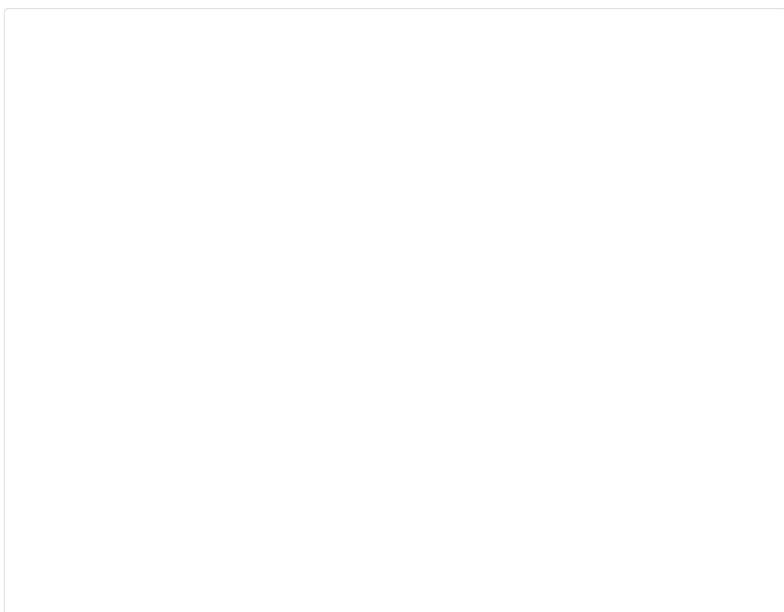
### Barcode Frequency Distribution

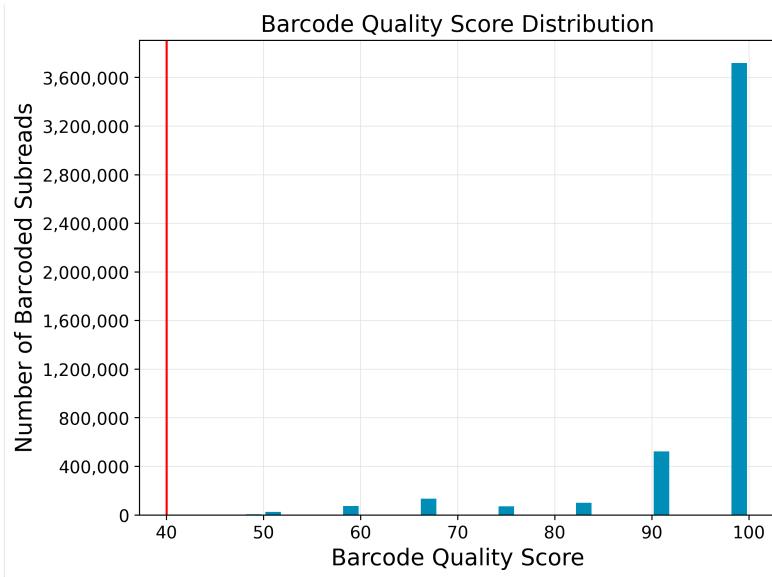


### Mean Read Length Distribution

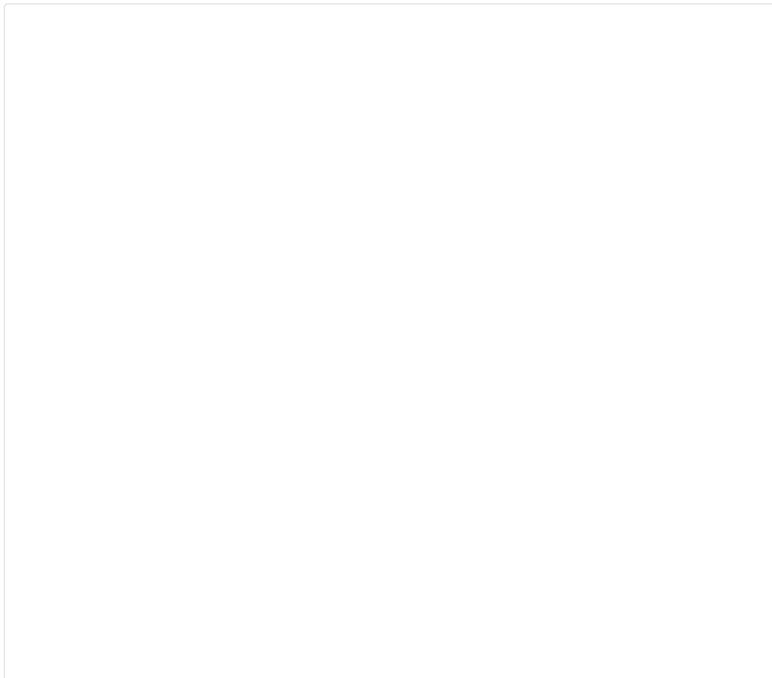
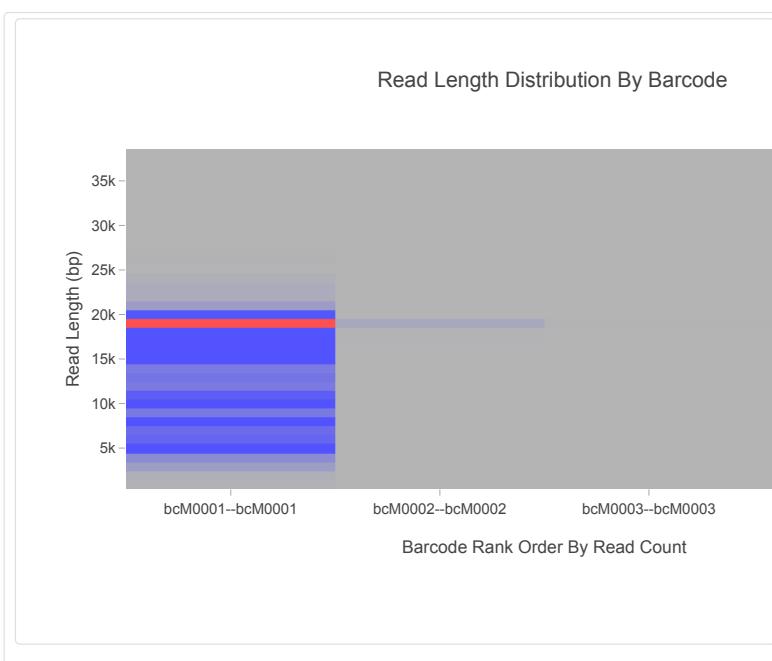


## Barcode Quality Scores





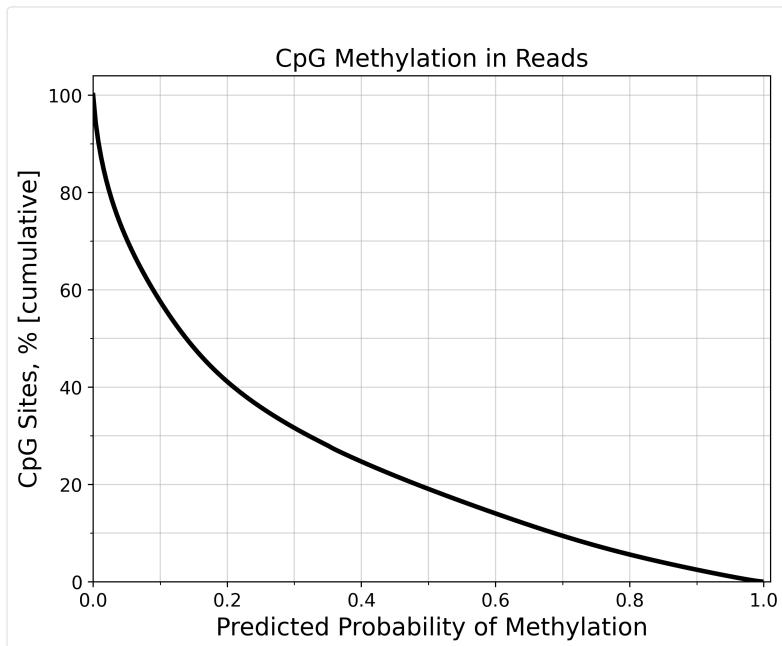
## Barcoded Read Binned Histograms

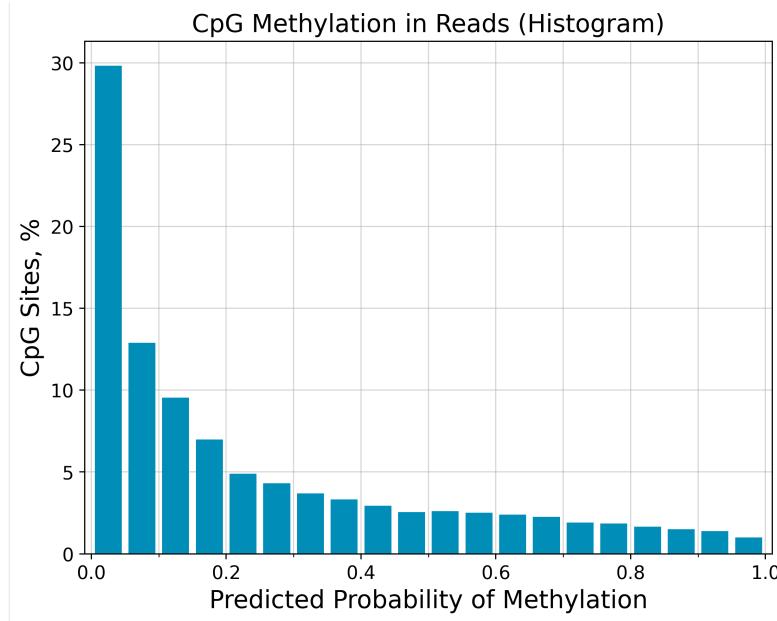


### Barcode Quality Distribution By Barcode



### Methylation Probability





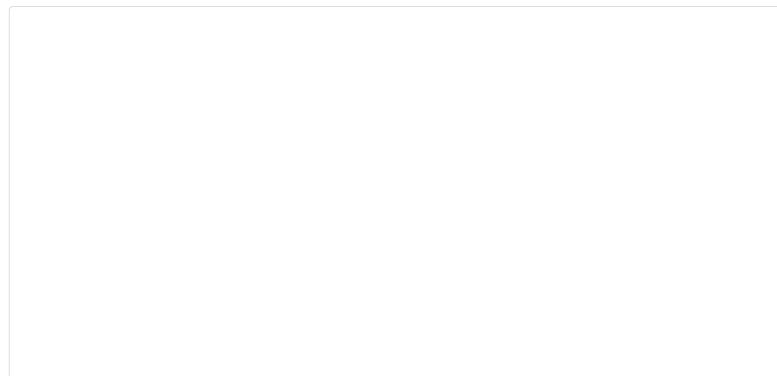
## Adapter Report

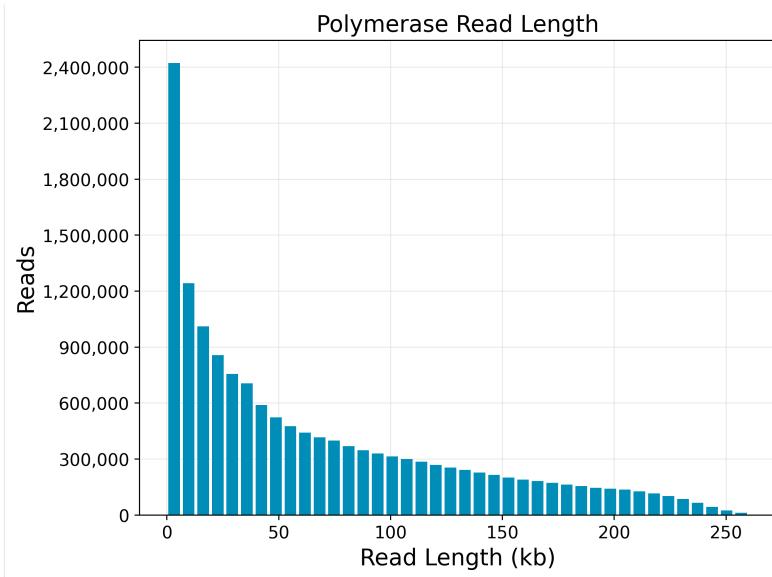
Value	Analysis Metric
0.00 %	Adapter Dimers (0-10bp) %
0.00 %	Short Inserts (11-100bp) %
2.43	Local Base Rate

## Raw Data Report

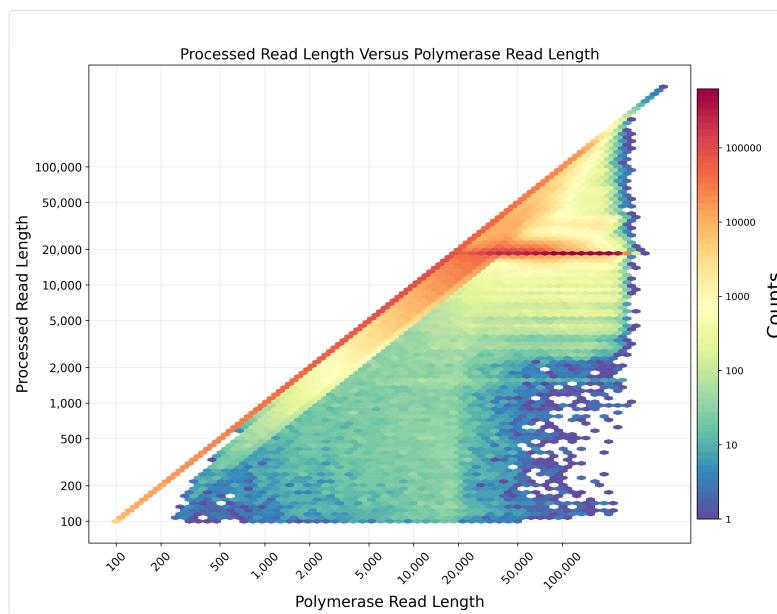
Value	Analysis Metric
983,104,145,913	Polymerase Read Bases
15,064,837	Polymerase Reads
65.26 kb	Polymerase Read Length (mean)
127.25 kb	Polymerase Read N50
18.22 kb	Longest Subread Length (mean)
19.75 kb	Longest Subread N50
258,401,468,416	Unique Molecular Yield

## Polymerase Read Length





### Longest Subread Length Versus Polymerase Read Length



### Base Yield Density

