Report for m84137_260129_065824_s1

Dataset details

Name: Curebound_RRN_Pool1-Cell3 (all samples)

Path: /yeolab5/seqdata/smrt_scrm/NLRS_OpenbiomePool12_Curebound_RRNPool12/r84137_20260129_024328/2_C01/pb_formats/m84137_260129_065824_s1.hifi_reads.consensusreadset.xml

Unique ID: ca340511-69c9-4622-9470-b6d5630d9d9e

Created at: 2026-01-30T17:27:17.612Z

HiFi sequences: 11,677,312

HiFi bases: 38,745,998,556

Bio sample name: [multiple]

Well sample name: Curebound_RRN_Pool1

Run name: NLRS_OpenbiomePool12_Curebound_RRNPool12

Movie name: m84137_260129_065824_s1

Instrument name: 84137

ICS version: 13.3.0.253824

Number of child datasets: 29

Number of HiFi BAM files: 29

CCS Analysis Report

Summary Metrics

HiFi reads	11.8 M
HiFi reads yield	39.21 Gb
HiFi reads length (mean)	3.32 kb
HiFi reads length (median, bp)	3,076
HiFi Read Length N50 (bp)	3,683
HiFi Read Quality (median)	Q41
HiFi Read Quality (median)	41
Base Quality ≥Q30 (%)	97.68%
HiFi Number of Passes (mean)	27
Missing adapters (%)	24.36%

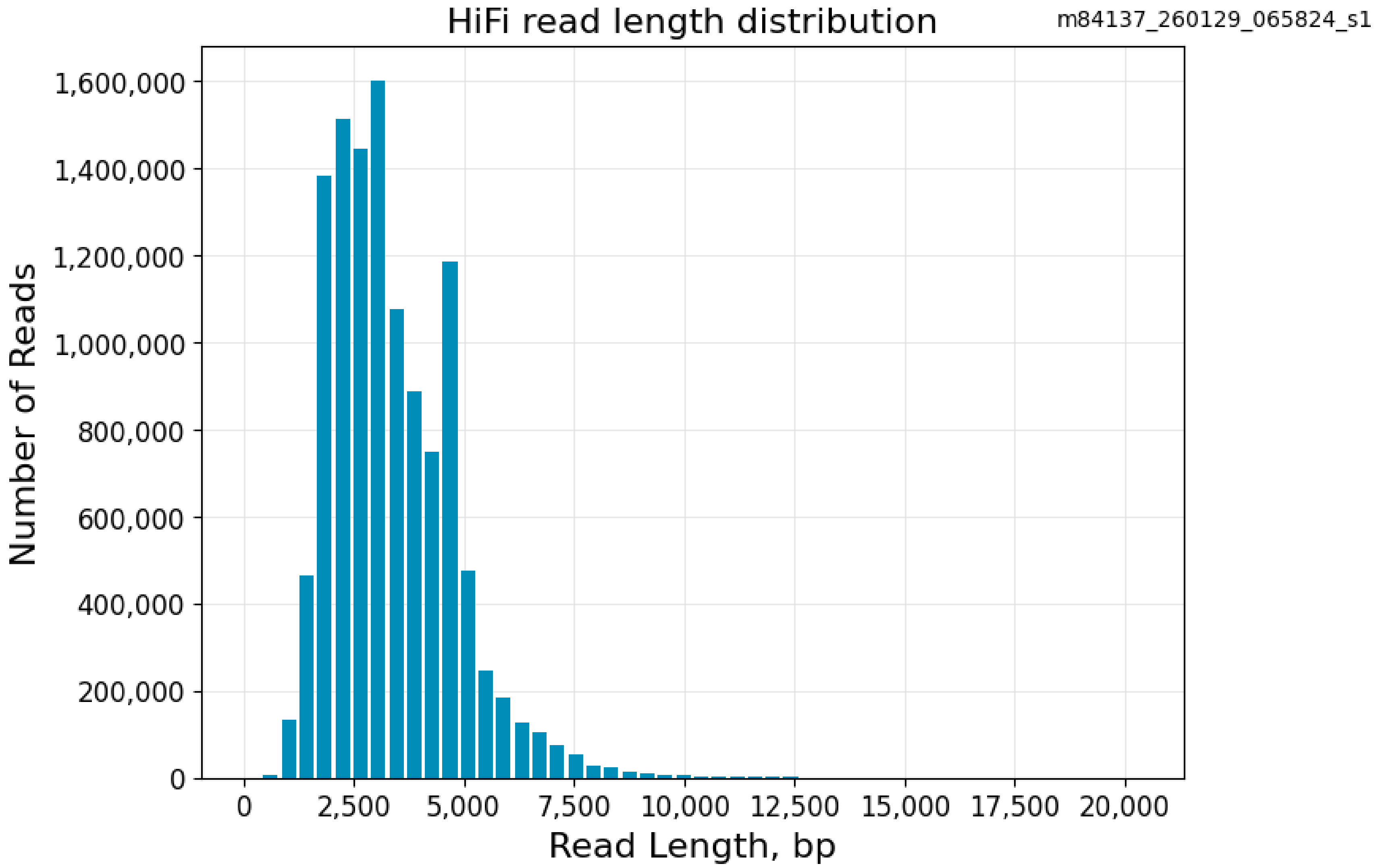
HiFi Read Length Summary

Read Length (kb)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ 0	11,814,160	100	39.21 Gb	100
≥ 5,000	1,202,258	10	7.37 Gb	19
≥ 10,000	19,340	0	0.23 Gb	1
≥ 15,000	1,558	0	0.03 Gb	0
≥ 20,000	277	0	0.01 Gb	0
≥ 25,000	66	0	0.00 Gb	0
≥ 30,000	13	0	0.00 Gb	0
≥ 35,000	4	0	0.00 Gb	0
≥ 40,000	1	0	0.00 Gb	0

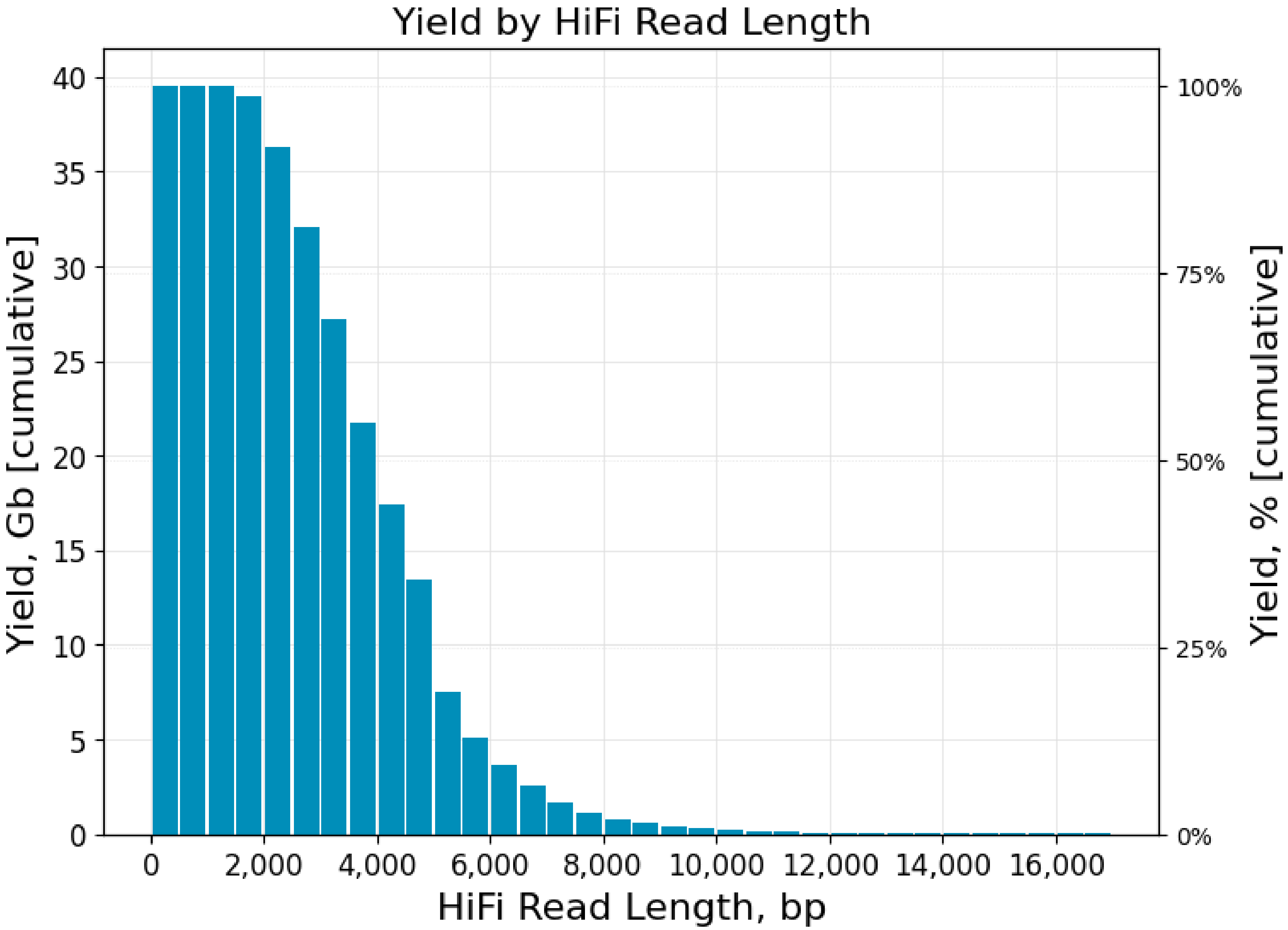
HiFi Read Quality Summary

Read Quality (Phred)	Reads	Reads (%)	Yield (Gb)	Yield (%)
≥ Q20	11,814,160	100	39.21 Gb	100
≥ Q30	9,022,311	76	29.37 Gb	75
≥ Q40	6,134,127	52	18.97 Gb	48
≥ Q50	3,743,220	32	10.80 Gb	28

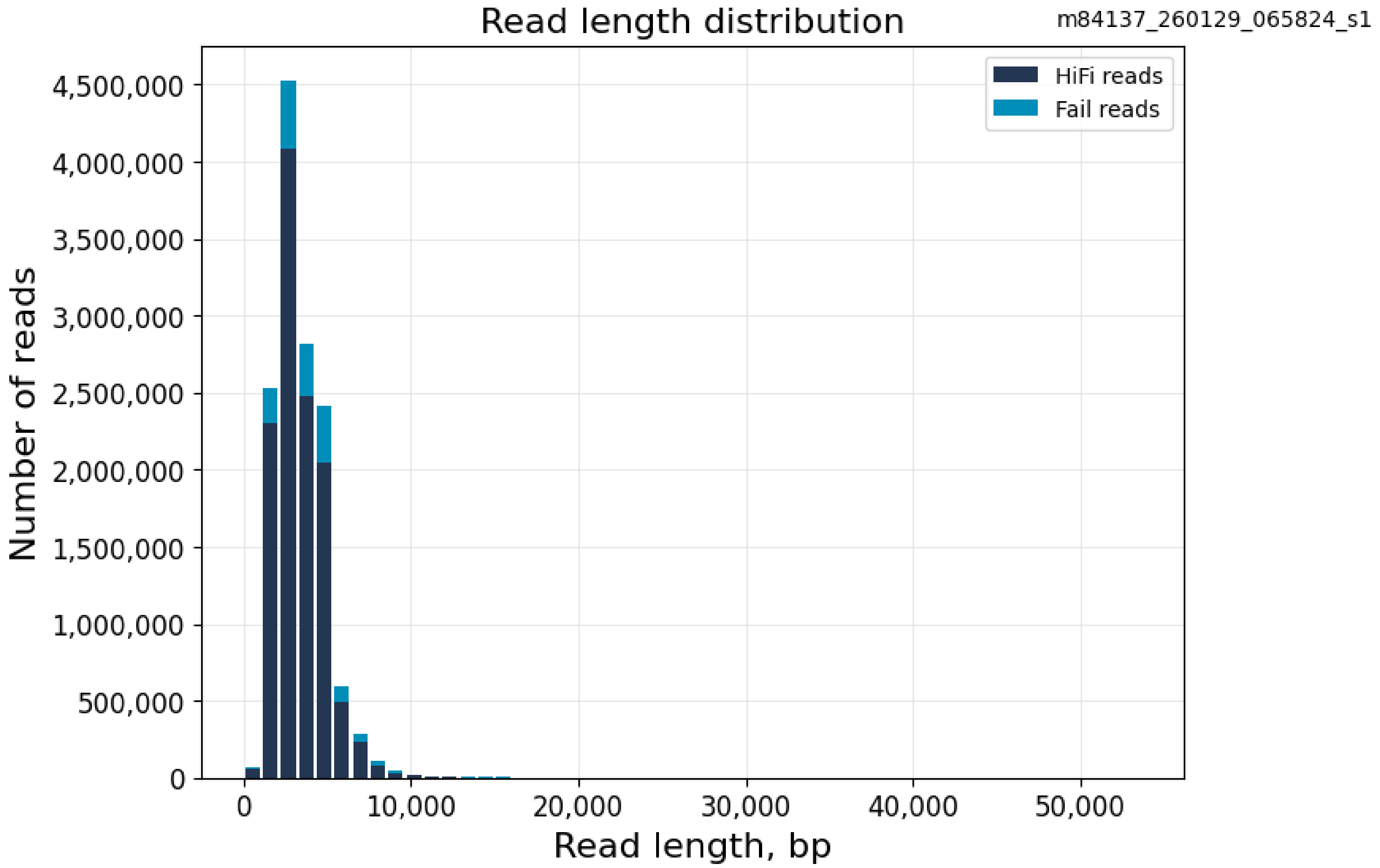
Read Length Distribution: HiFi read length distribution



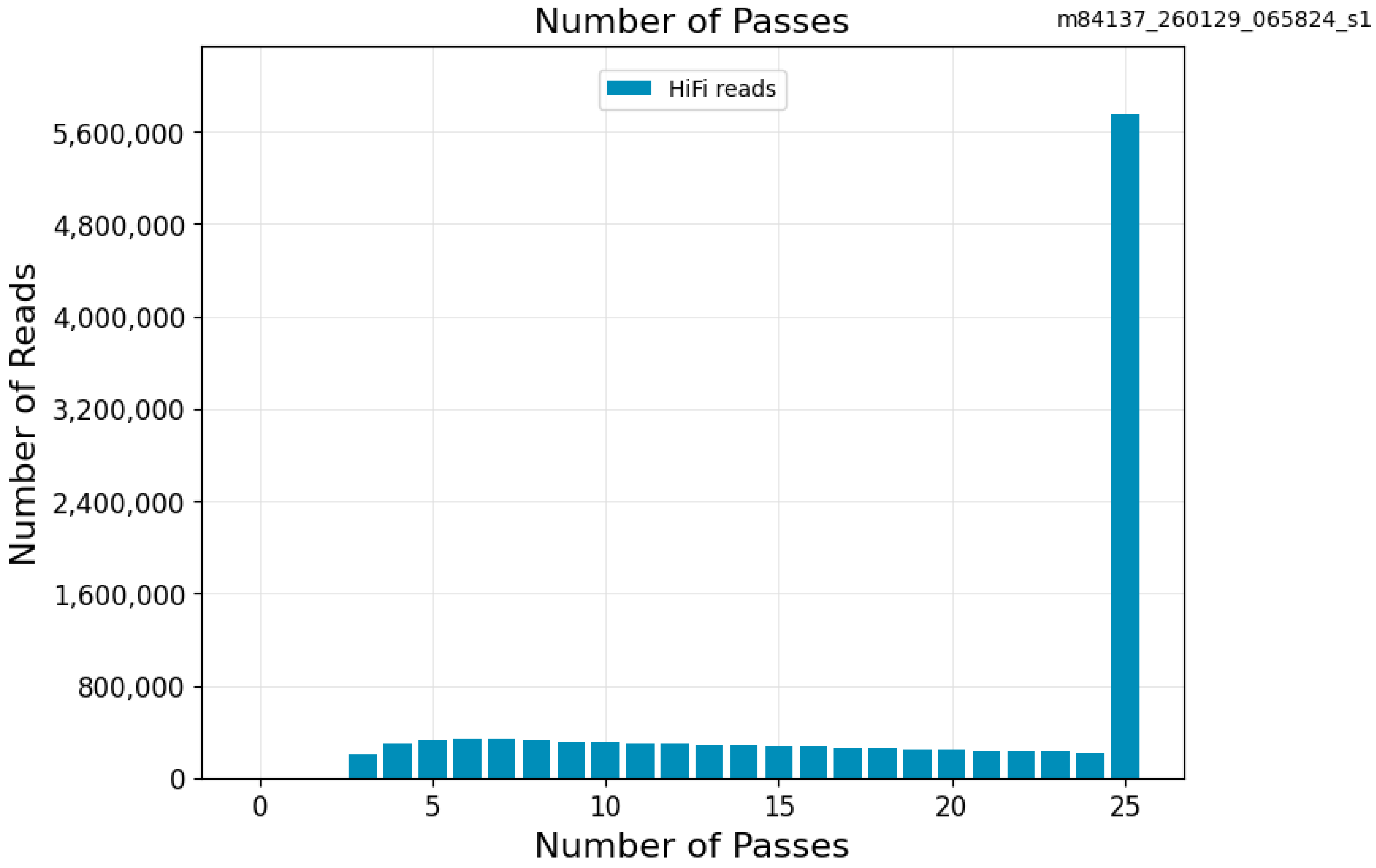
Read Length Distribution: Yield by HiFi Read Length



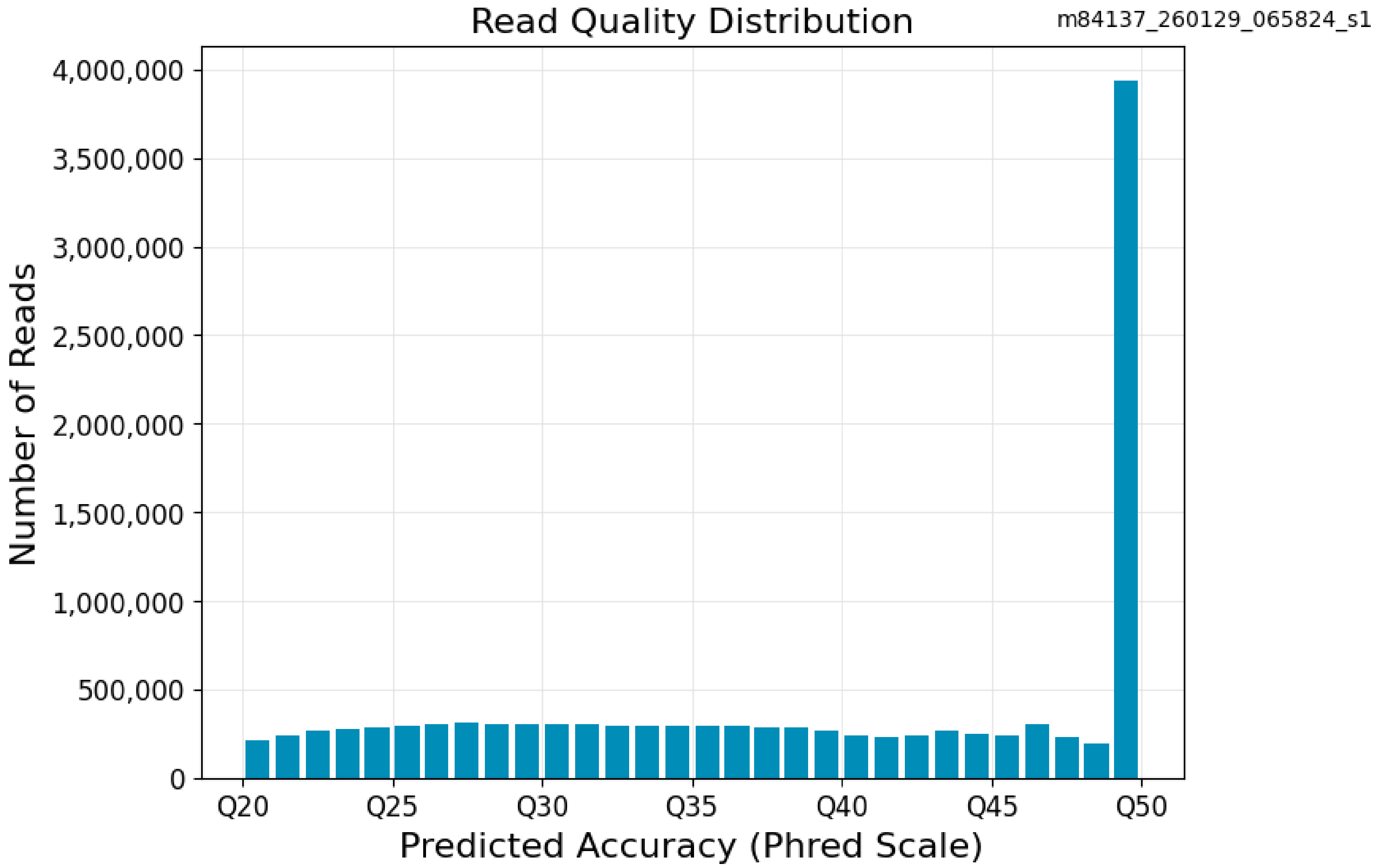
Read Length Distribution: Read length distribution



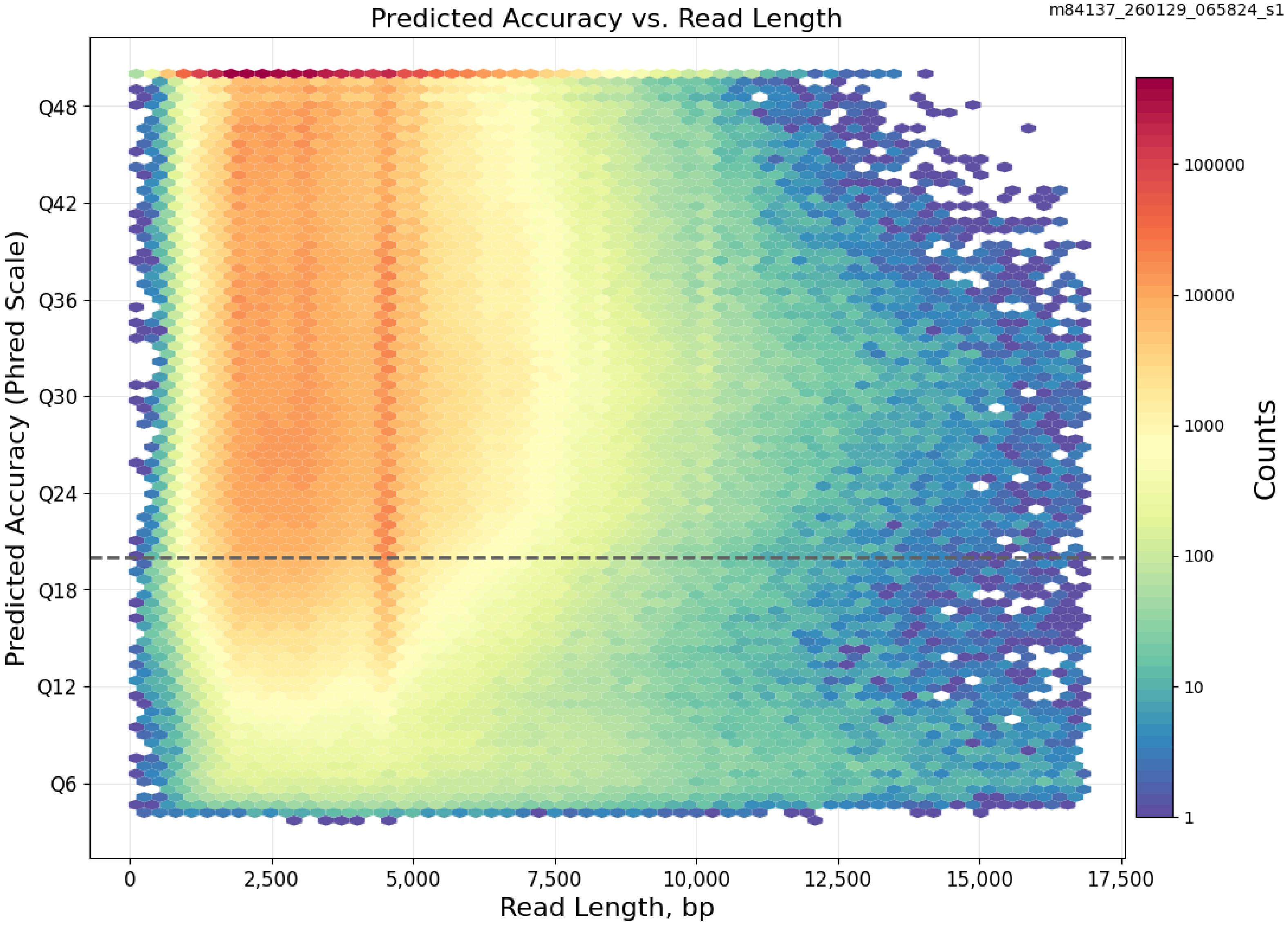
Number of Passes



Read Quality Distribution



Predicted Accuracy vs. Read Length

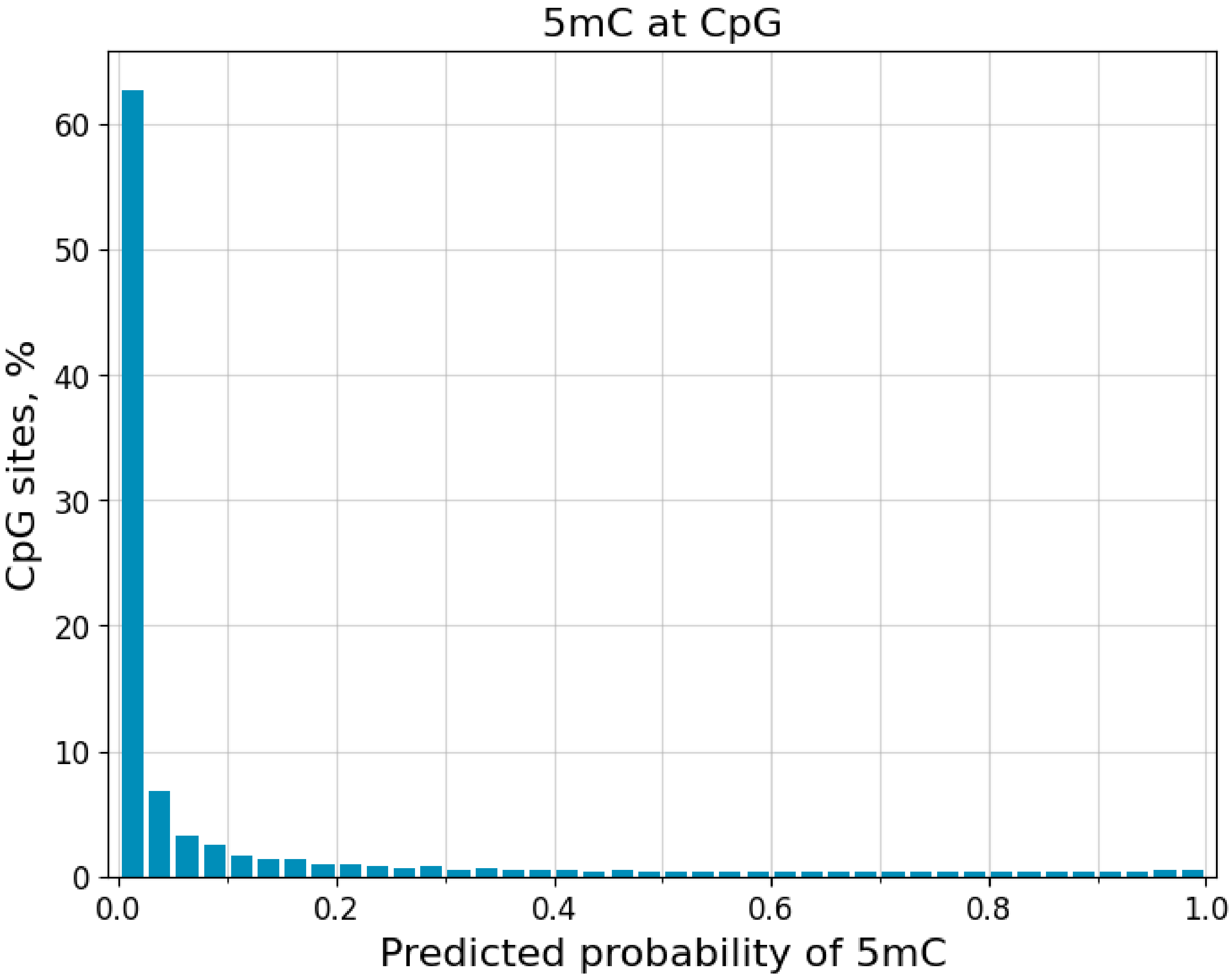


Methylation

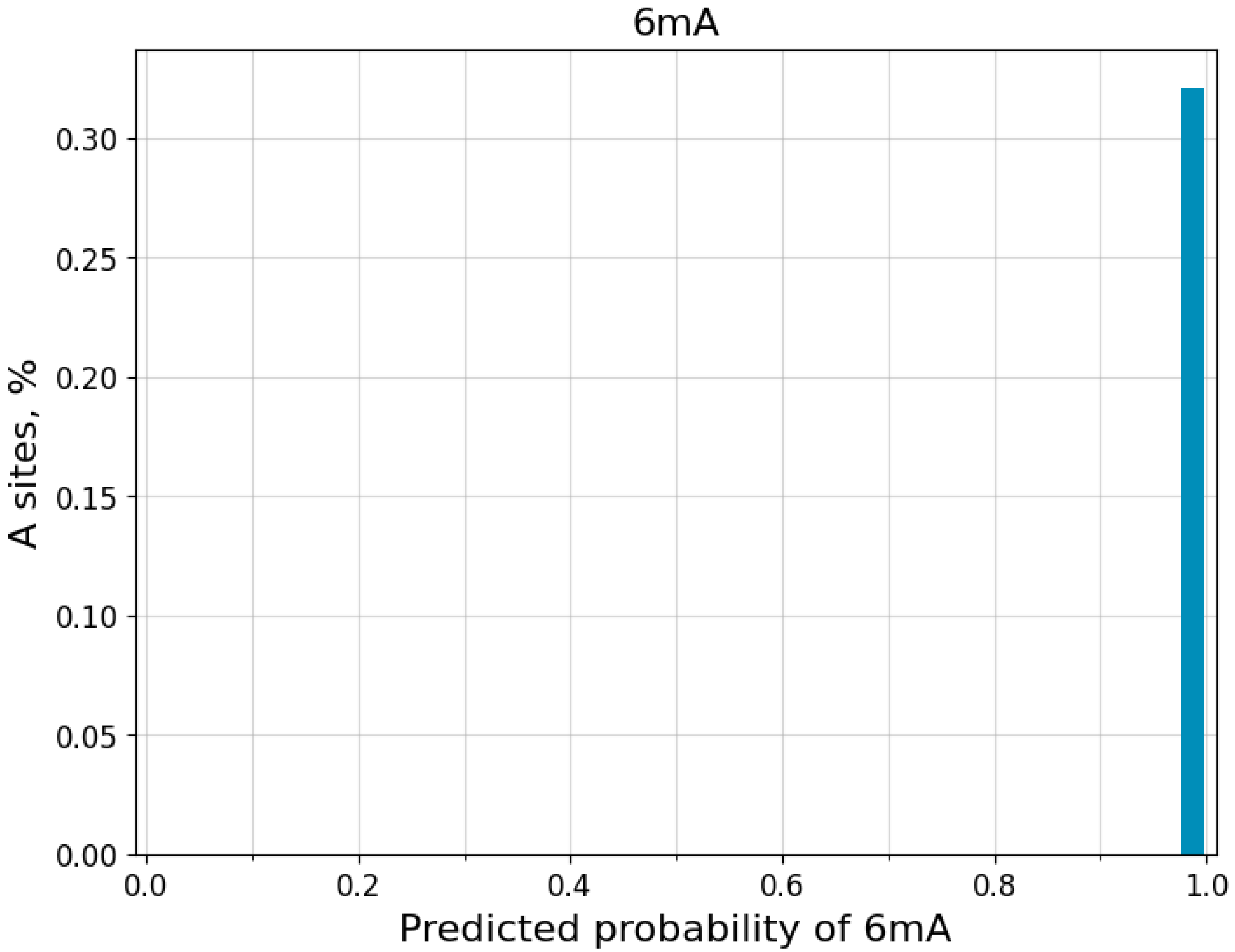
Summary

Modification	Motif	Scored sites	Modified sites (Pr > 0.5)
5mC	CpG	95.7%	7.7%
6mA	A	0.3%	0.3%

Score distributions: 5mC at CpG



Score distributions: 6mA



Barcodes

Summary Metrics

Unique Barcodes	28
Barcoded HiFi Reads	11,677,312
Unbarcoded HiFi Reads	136,848
Barcoded HiFi Reads (%)	98.84 %
Barcoded HiFi yield (Gb)	38.75 Gb
Unbarcoded HiFi yield (Gb)	0.46 Gb
Barcoded HiFi Yield (%)	98.82 %
Mean HiFi Reads per Barcode	417,046
Max. HiFi Reads per Barcode	698,930
Min. HiFi Reads per Barcode	1
Barcoded HiFi read length (mean, kb)	3.32 kb
Unbarcoded HiFi read length (mean, kb)	3.37 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)
MCCT_1257frozen	bc2001--bc2001	98.0	557,918	3,331	Q41	1,858,965,175	95,387
MCCT_1258frozen	bc2002--bc2002	96.2	624,695	3,001	Q42	1,874,924,678	93,873
MCCT_1259frozen	bc2003--bc2003	98.0	182,638	2,290	Q38	418,258,033	92,081
MCCT_12510frozen	bc2004--bc2004	96.5	690,598	3,483	Q43	2,405,738,869	95,781
MCCT_12511frozen	bc2005--bc2005	96.7	616,164	3,296	Q43	2,031,100,940	95,065
MCCT_12512frozen	bc2006--bc2006	97.9	522,896	3,249	Q40	1,699,373,549	95,390
MCCT_12513frozen	bc2007--bc2007	97.7	698,930	3,296	Q42	2,303,963,858	95,327
MCCT_12514frozen	bc2008--bc2008	97.6	494,966	3,227	Q39	1,597,414,156	95,402
MCCT_12515frozen	bc2009--bc2009	97.9	515,017	3,189	Q41	1,642,670,466	94,639
MCCT_12516frozen	bc2010--bc2010	97.5	434,958	3,233	Q40	1,406,371,941	95,855
MCCT_12518frozen	bc2011--bc2011	97.2	577,867	3,287	Q43	1,899,502,734	95,201
PBS_control_frozenCB	bc2012--bc2012	90.1	10	2,652	Q55	26,521	93,930
DNA_shield_control_frozenCB	bc2013--bc2013	97.1	4,429	2,730	Q47	12,092,655	90,042
MCCT_12536frozen	bc2014--bc2014	97.6	536,799	3,181	Q42	1,708,045,022	95,085
MCCT_12540frozen	bc2015--bc2015	97.4	548,169	3,196	Q42	1,752,399,846	94,614
MCCT_12542frozen	bc2016--bc2016	97.4	573,617	3,249	Q42	1,863,919,287	95,302
MCCT_12550frozen	bc2017--bc2017	97.7	467,296	3,338	Q39	1,559,853,460	96,504
MCCT_12555frozen	bc2018--bc2018	97.8	508,795	3,227	Q40	1,642,008,878	95,355
PBS_control_frozenGW	bc2019--bc2019	97.4	359	4,119	Q43	1,478,759	97,638
extraction_blank_frozenGW	bc2020--bc2020	85.0	3	1,445	Q53	4,337	96,189
101mousetumor	bc2083--bc2083	97.8	656,592	3,323	Q43	2,182,253,844	94,603
103-Lmousetumor	bc2084--bc2084	97.2	476,990	3,642	Q39	1,737,656,535	97,264

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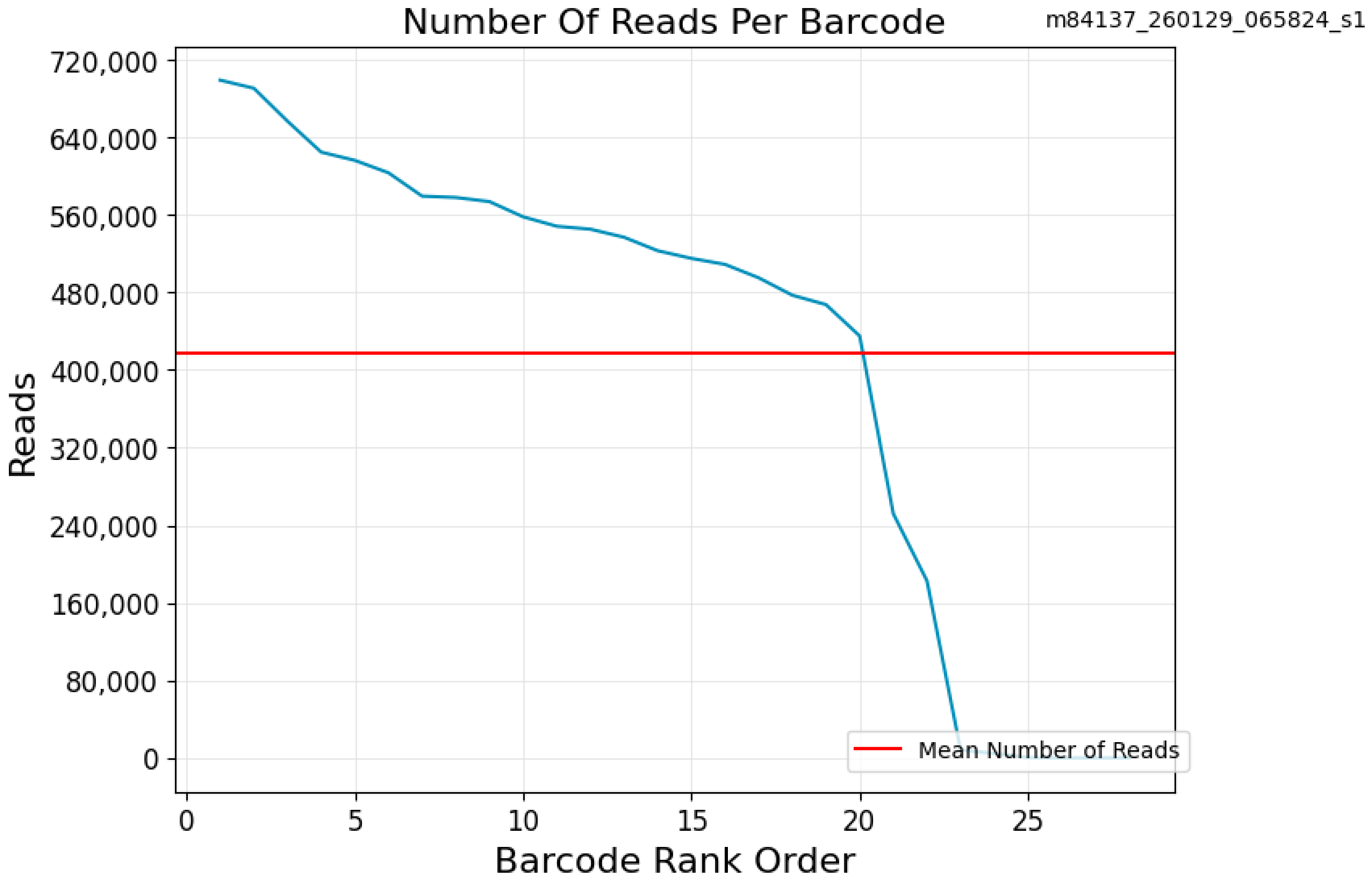
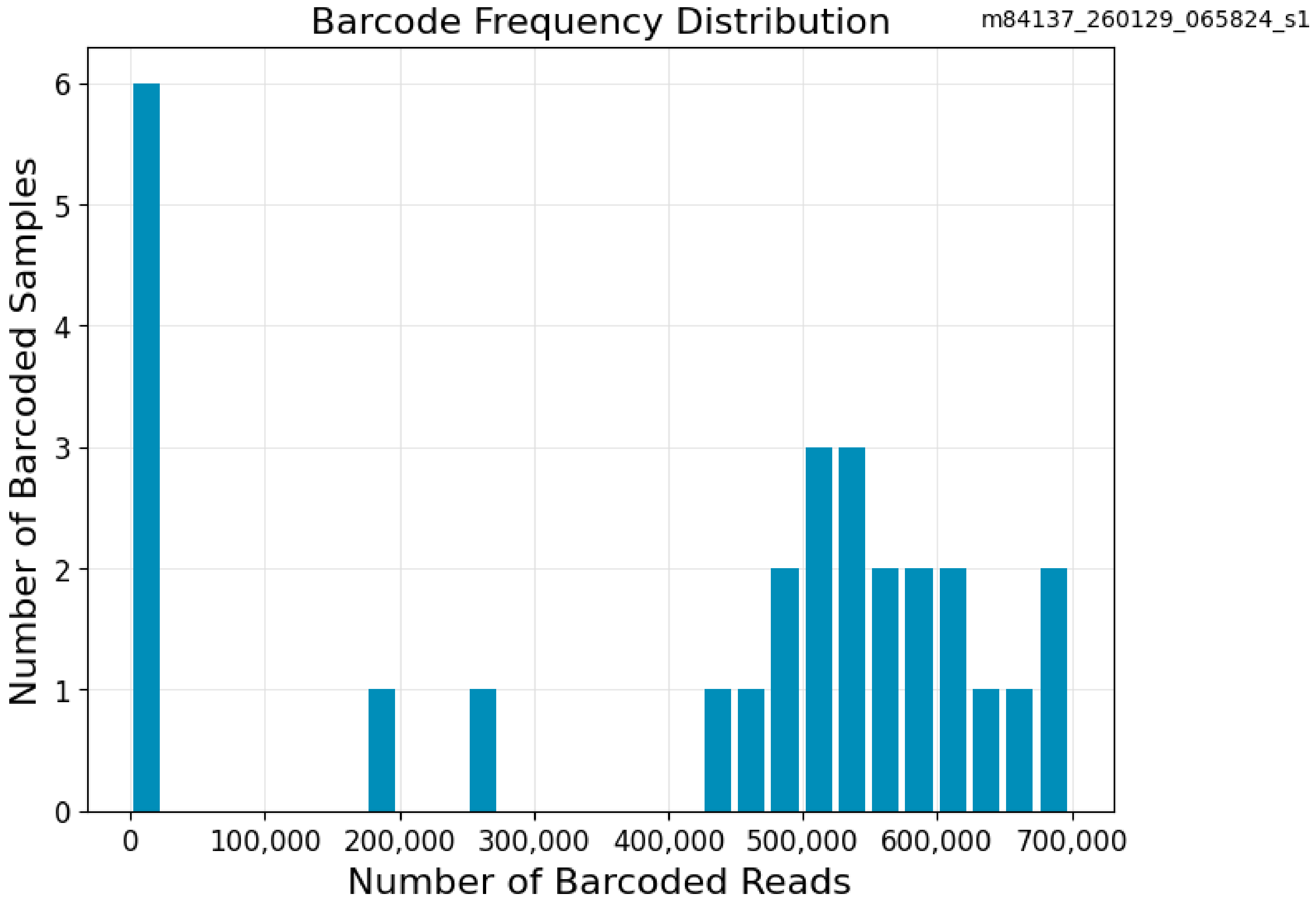
Sample Name	Barcode	Barcode Quality	HiFi Reads	HiFi Read Length (mean, bp)	HiFi Read Quality (median, QV)	HiFi Yield (bp)	Polymerase Read Length (mean, bp)
108mousetumor	bc2085--bc2085	97.1	579,234	3,674	Q40	2,128,468,162	97,197
113-Rmousetumor	bc2086--bc2086	97.2	545,126	3,484	Q42	1,899,527,638	95,626
122-Lmousetumor	bc2087--bc2087	97.4	603,351	3,428	Q41	2,068,390,273	95,873
mousetumorextractionblank	bc2088--bc2088	97.1	7,980	3,973	Q42	31,706,067	96,456
DonorActrl	bc2089--bc2089	97.7	251,914	4,048	Q33	1,019,882,102	100,207
PCR1NTC	bc2090--bc2090	100.0	1	771	Q60	771	82,197
No Name	Not Barcoded	0.0	136,848	3,374	Q29	461,856,340	91,706

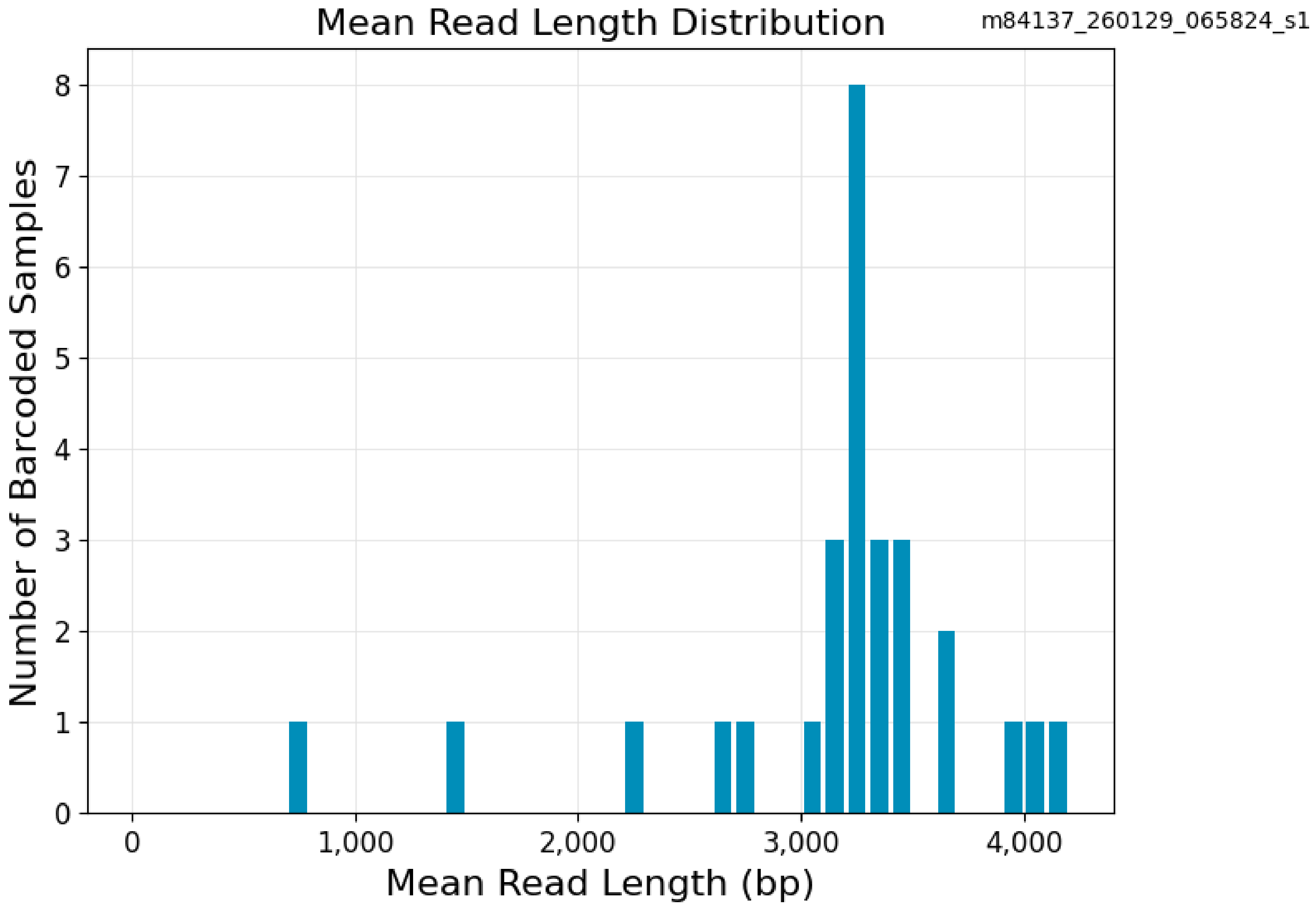
Barcoded Read Statistics: Number Of Reads Per Barcode



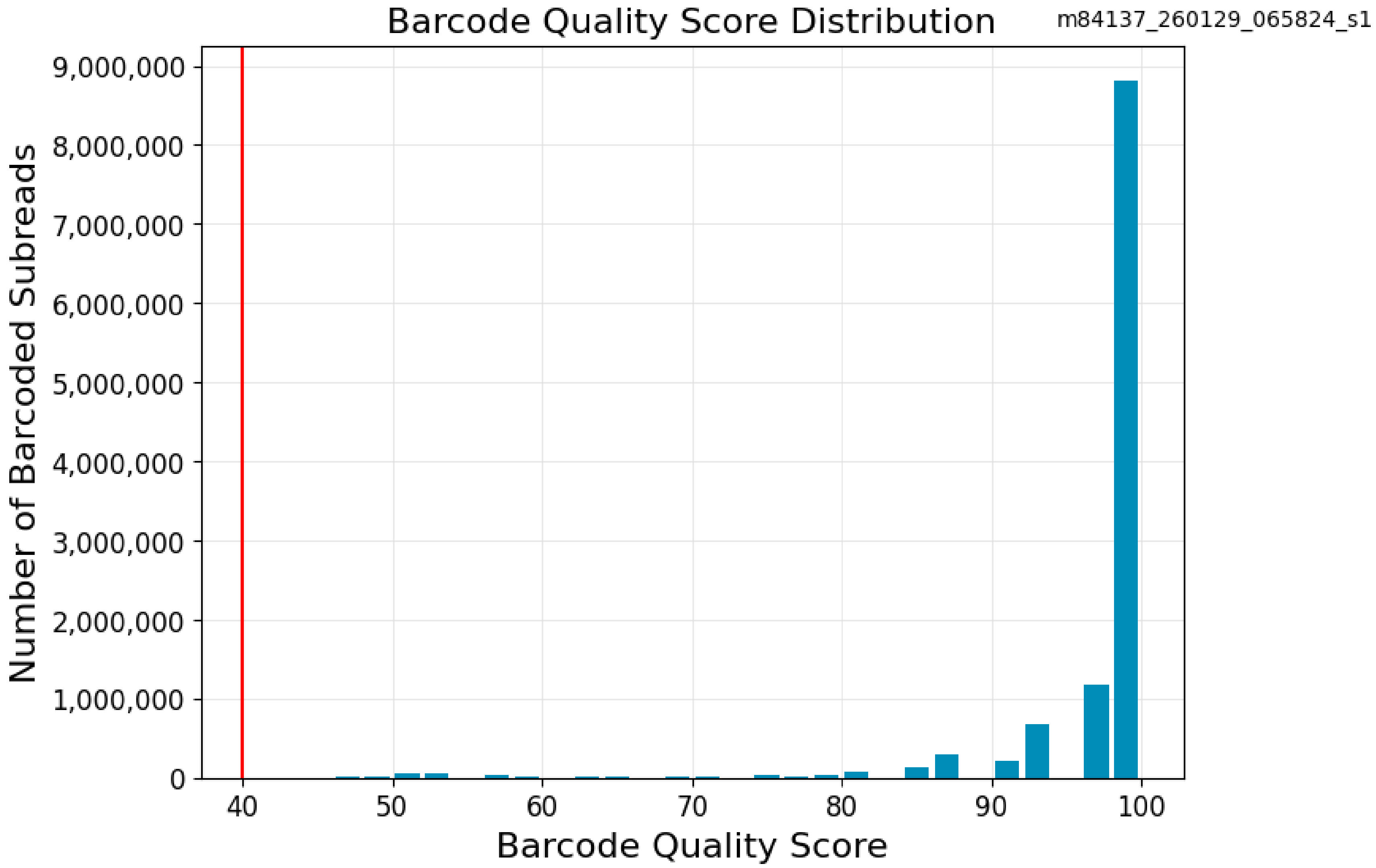
Barcoded Read Statistics: Barcode Frequency Distribution



Barcoded Read Statistics: Mean Read Length Distribution



Barcode Quality Scores: Barcode Quality Score Distribution



Loading Report

Summary Metrics

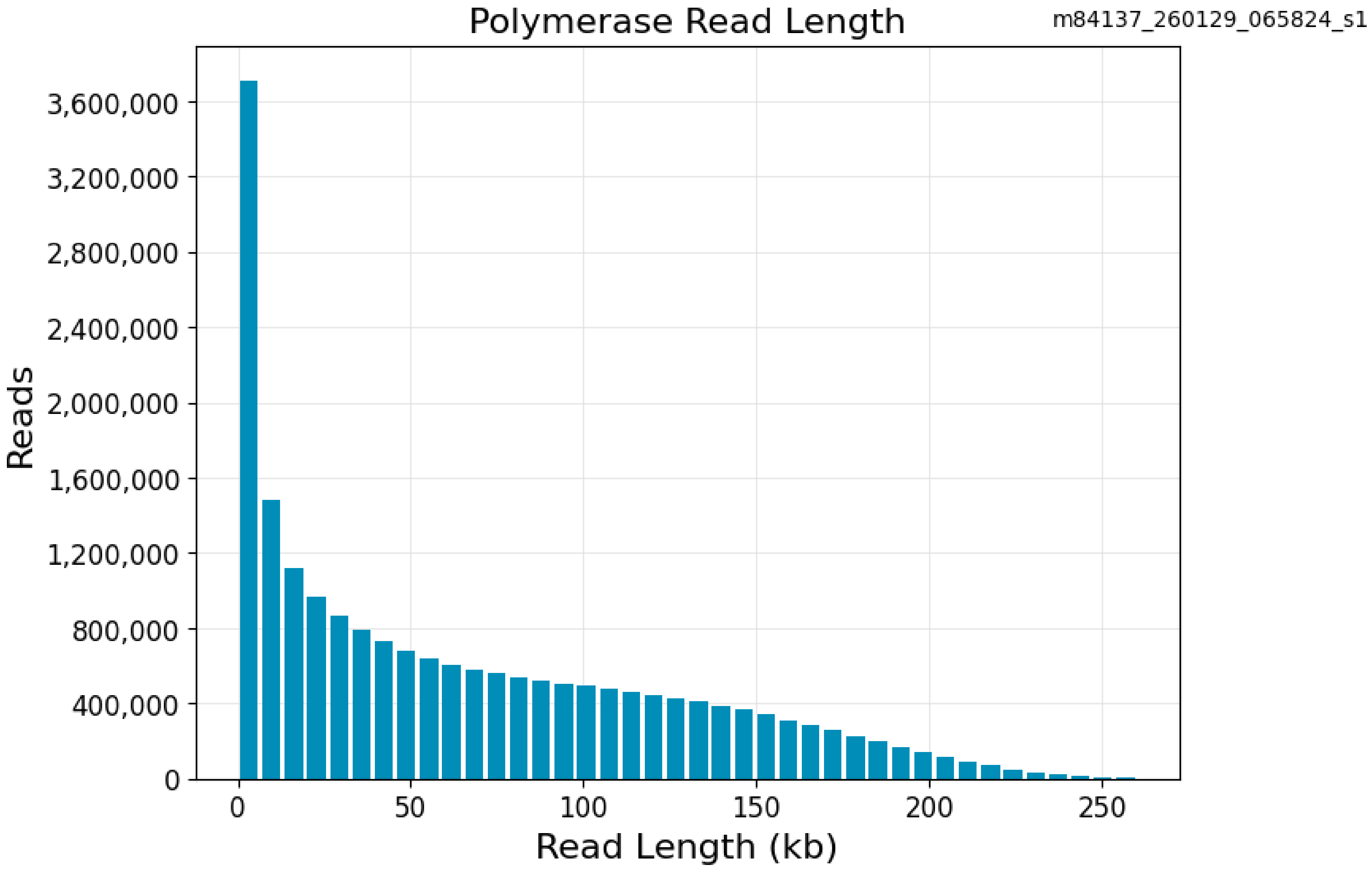
Productive ZMWs	25,165,824
Productivity 0	4,873,415
Productivity 1	20,127,513
Productivity 2	164,896

Raw Data Report

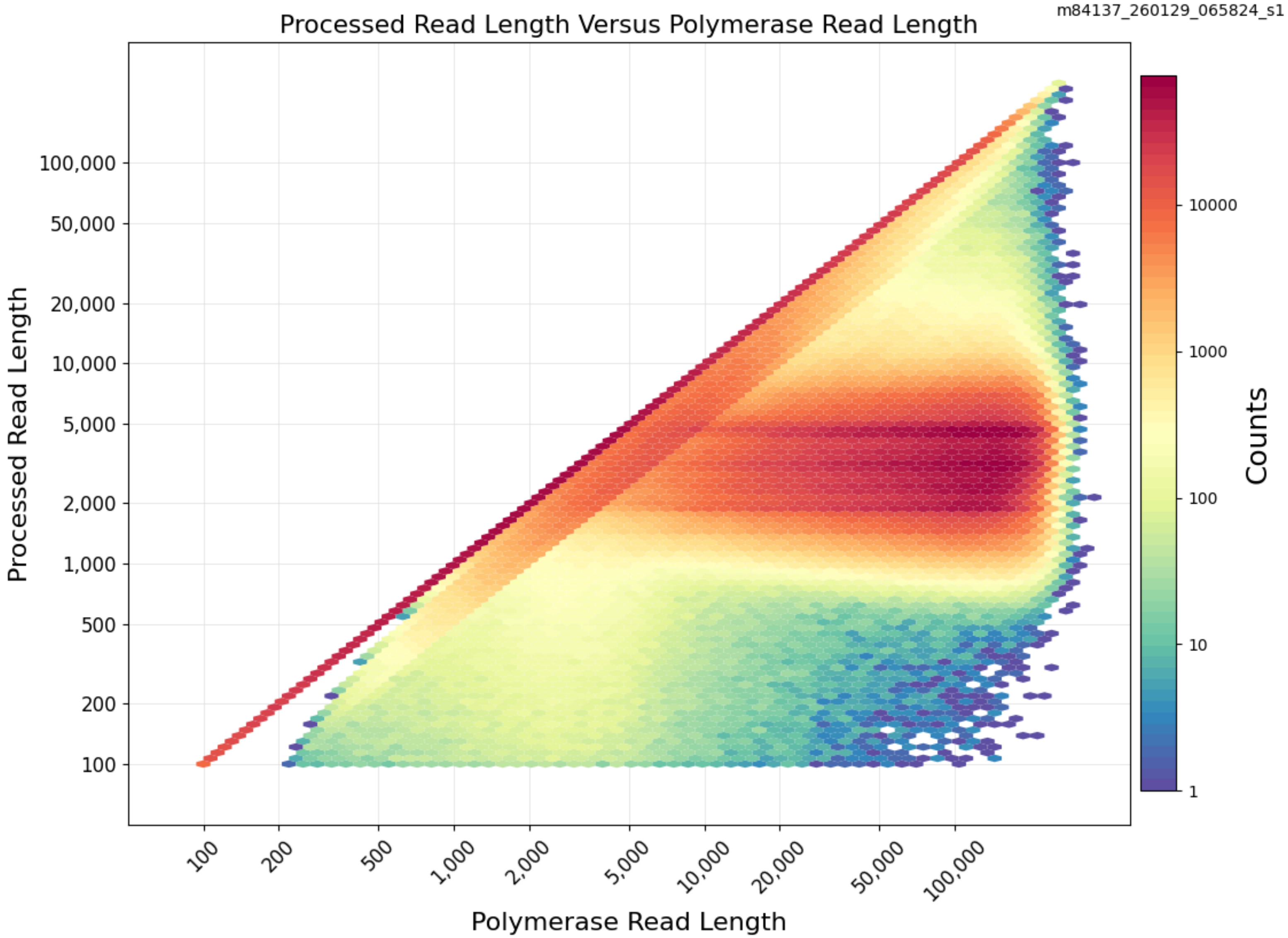
Summary Metrics

Polymerase Read Bases	1,274,705,718,983
Polymerase Reads	20,121,669
Polymerase Read Length (mean)	63.35 kb
Polymerase read length (N50)	120.75 kb
Polymerase read length longest subread length (mean)	7.12 kb
Polymerase read length longest subread length (N50)	12.75 kb
Unique Molecular Yield	108,942,761,984
Local Base Rate	2.21

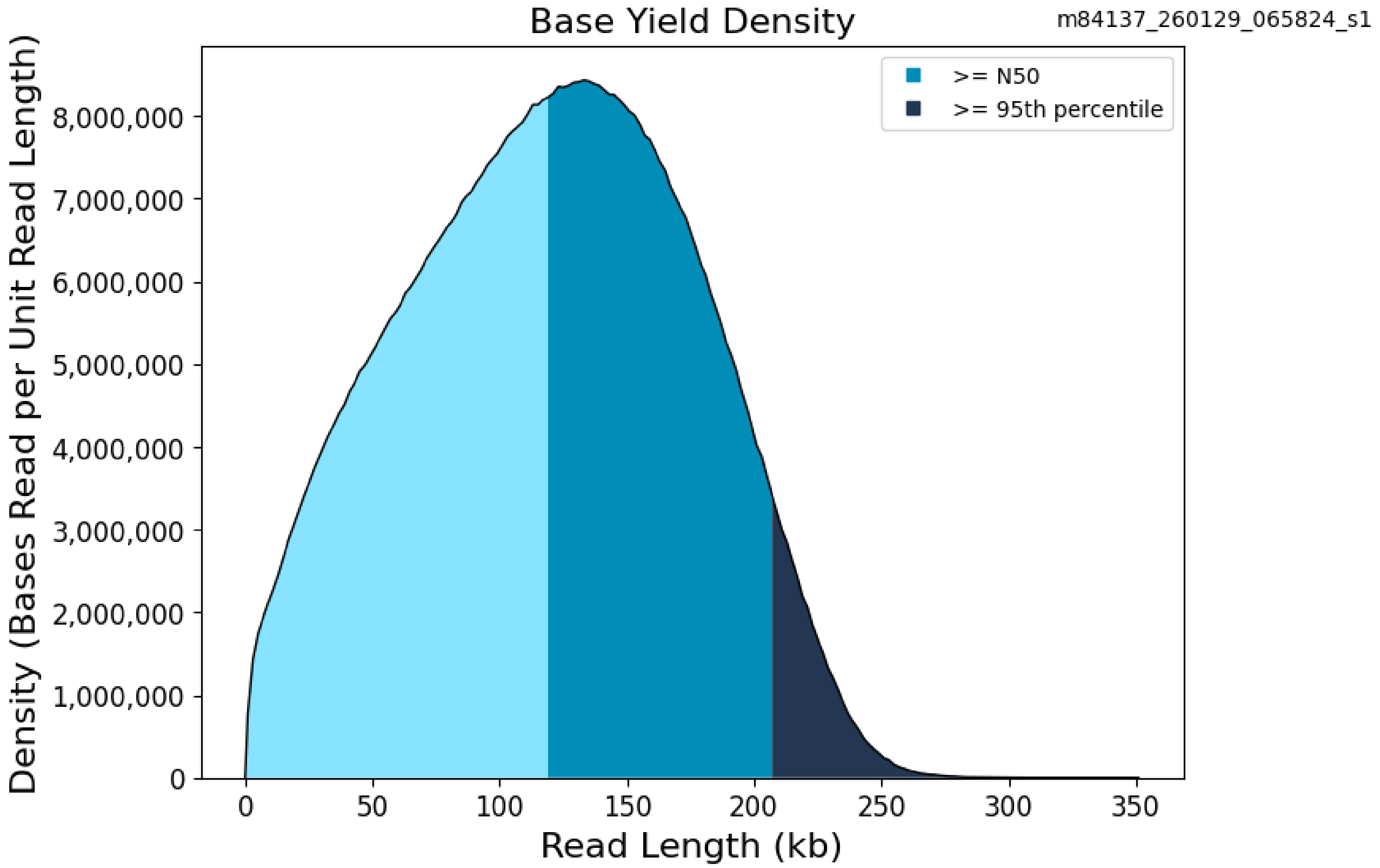
Polymerase Read Length



Longest Subread Length Versus Polymerase Read Length



Base Yield Density

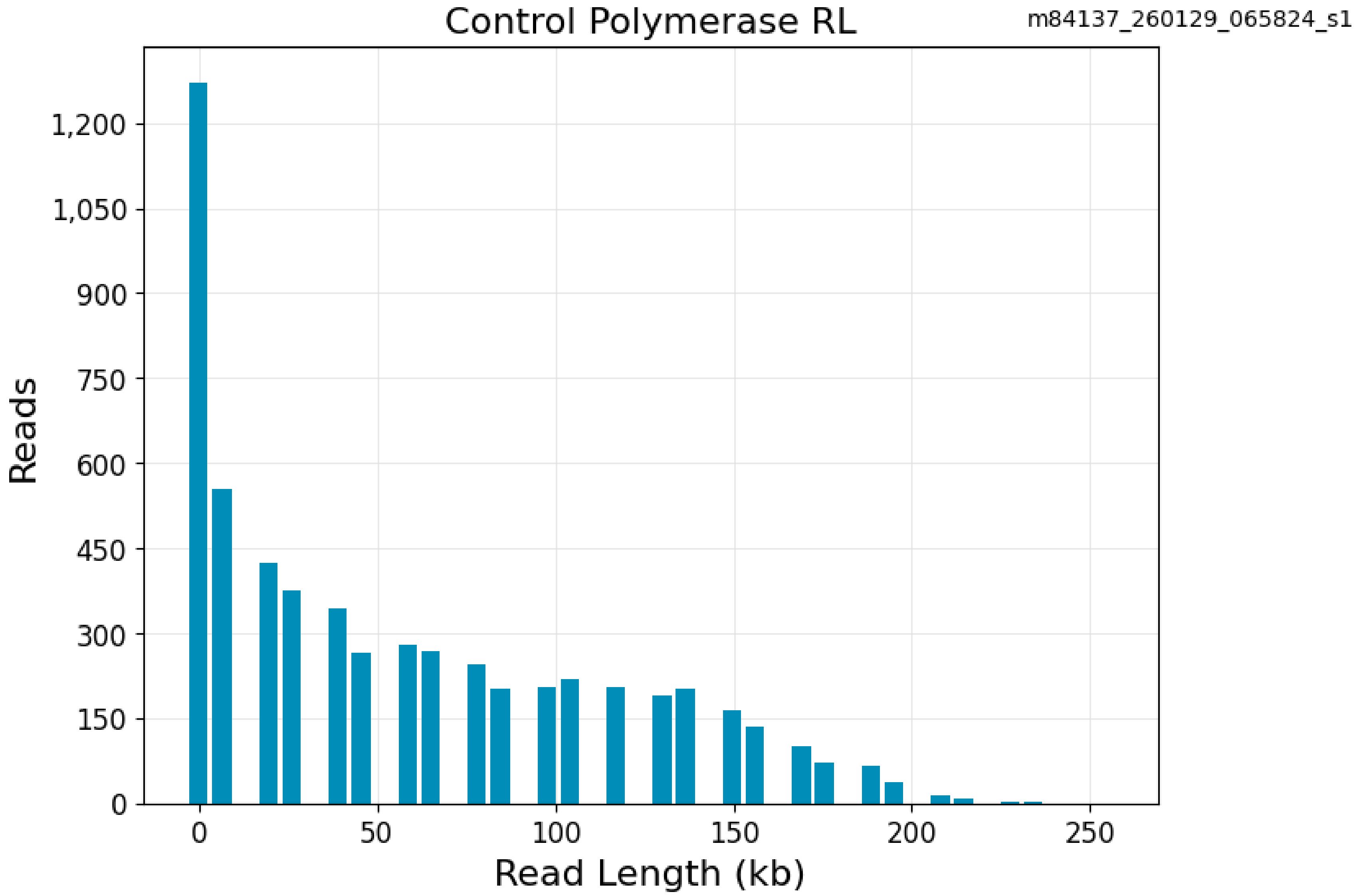


Control Report

Summary Metrics

Number of Control Reads	5,844
Control Read Length Mean	60,109
Control Read Concordance Mean	0.91
Control Read Concordance Mode	0.91

Control Read Length: Control Polymerase RL



Control Read Quality: Control Concordance