

CoralAmplifi555202009-Cell1

Copy

Analyze...

Export

Delete

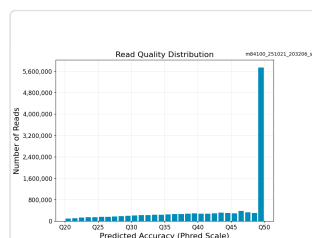
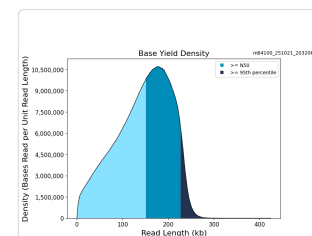
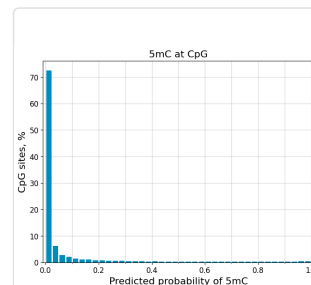
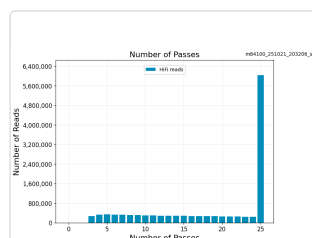
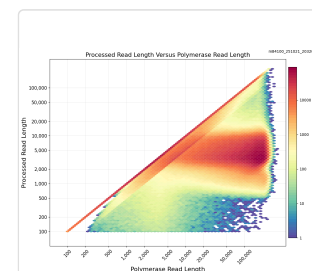
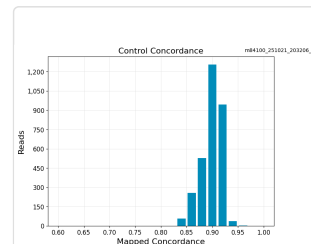
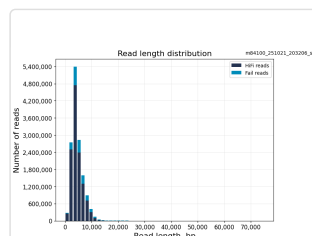
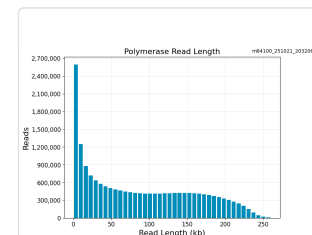
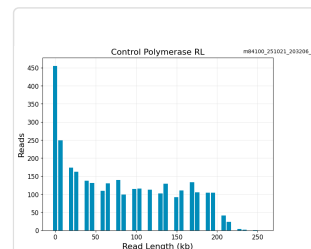
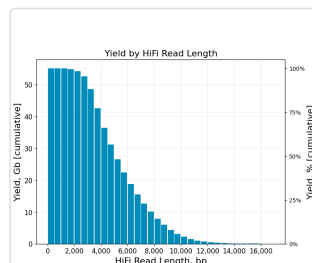
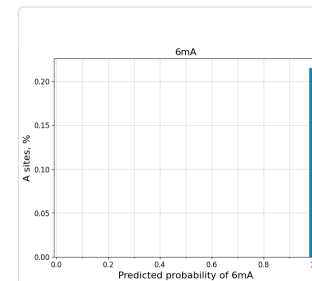
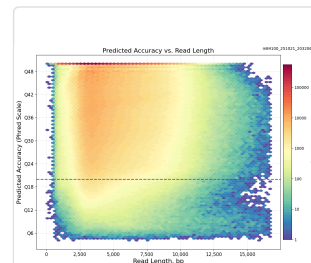
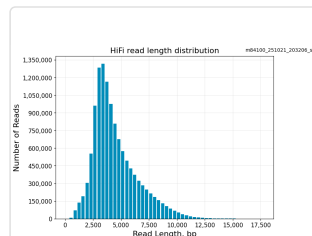
▼Dataset Overview
Status
Thumbnails
Display All
➤Run Preview
➤Run Preview
➤CCS Analysis Report
➤Control Report
➤Loading Report
➤Methylation
➤Raw Data Report
➤Analyses

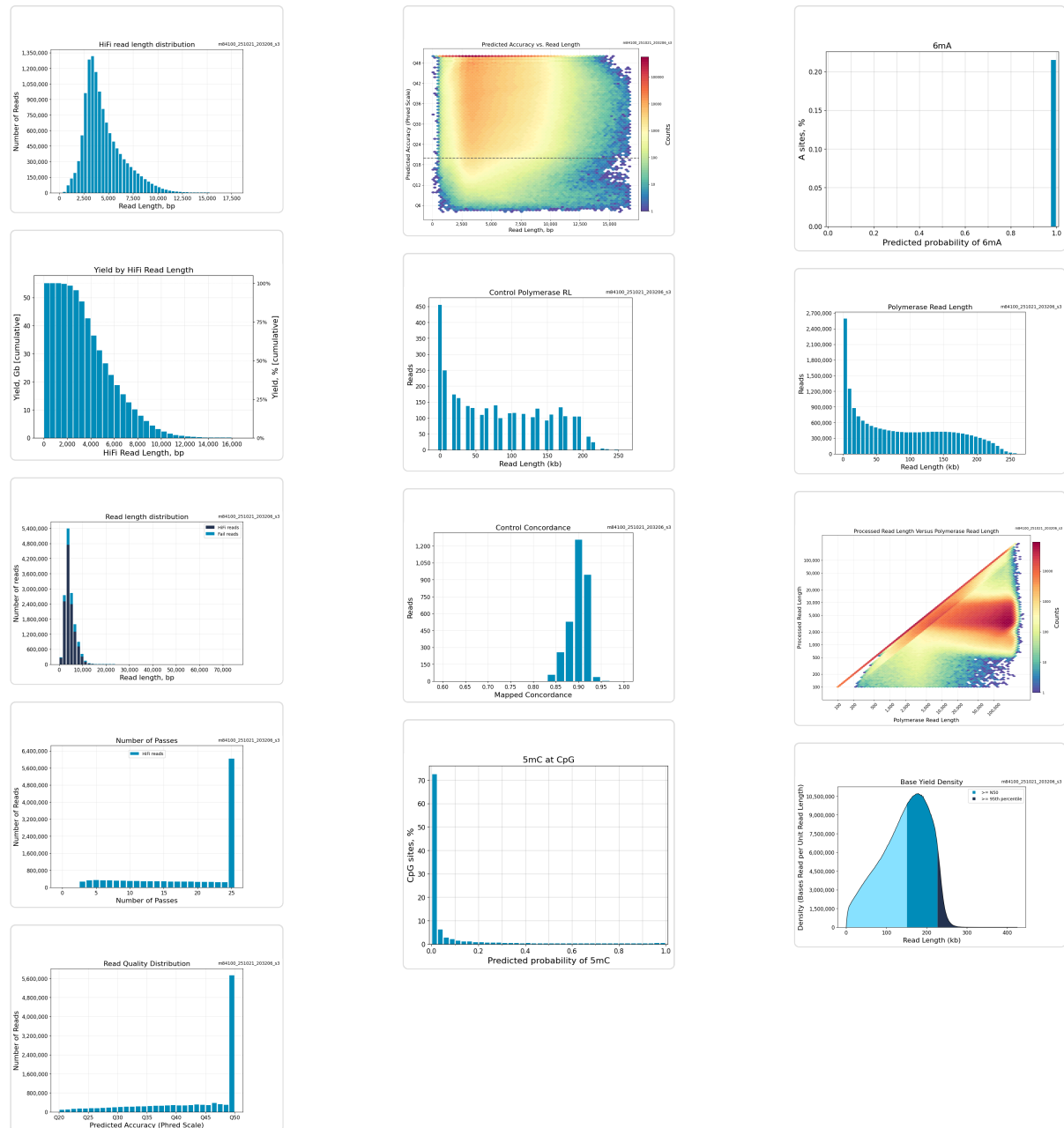
Display All		
Status		
Data Set	CoralAmplifi555202009-Cell1	
Data Set ID	8328	
Data Set UUID	5f149dec-45e5-401e-a96d-271d8f42b0ab	
Well Sample Name	CoralAmplifi555202009	
Biological Sample Name	CoralAmplifi555202009	
Description	Record generated by runqc-reports	
Number of Records	12,313,989	
Total Length	55,141,229,817	
Status	SUCCESSFUL	
Date Created	2025-10-23, 01:49:32 AM	
Date Imported	2025-10-23, 01:49:32 AM	
Date Updated	2025-10-23, 02:40:19 AM	
Job ID	7949	
Data Path	/nobackup/archive/grp/fslg_dnasc/r84100_20251021_202408/1_A01/pb_formats/m8410	
Run name	Run 10.20.2025 12:15	
Cell Index	0	
Cell Id	EA236784	
Instrument Name	84100	
Well Name	A01	
Movie Name	m84100_251021_203206_s3	

Data

Analysis Parameters

Thumbnails





Run Preview

	Value	Analysis Metric
	4288	HiFi read length, mean
	64.9	P1%
	4	Time (Hrs)
	Basic	Workflow
m84100_251021_203206_s3_basic_preview_4hr		Id
m84100_251021_203206_s3		Movie Id

Barcode Preview

Run Preview

	Value	Analysis Metric
	53203538788	Estimated HiFi yield
	47	HiFi read quality, median
	4538	HiFi read length, mean
	23	Time (Hrs)
	Full	Workflow
m84100_251021_203206_s3_full_preview_23hr		Id

Value	Analysis Metric
m84100_251021_203206_s3	Movie Id

Barcode Preview

CCS Analysis Report

Value	Analysis Metric
12.3 M	HiFi reads
54.96 Gb	HiFi reads yield
4.46 kb	HiFi reads length (mean)
3,957	HiFi reads length (median, bp)
4,864	HiFi Read Length N50 (bp)
Q48	HiFi Read Quality (median)
97.77%	Base Quality $\geq$ Q30 (%)
27	HiFi Number of Passes (mean)
2.47%	Missing adapters (%)

HiFi Read Length Summary

Search ...

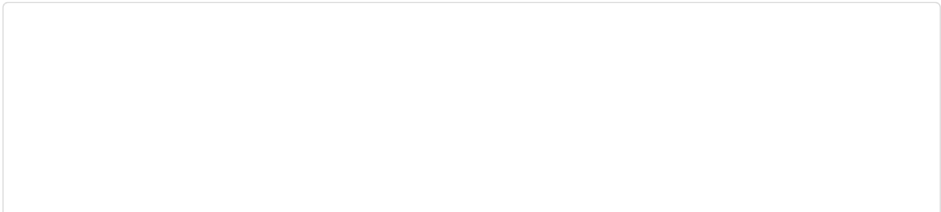
Read Length (kb) ↕	Reads ↕	Reads (%) ↕	Yield (Gb) ↕	Yield (%) ↕
≥ 0	12,313,988	100	54.96 Gb	100
≥ 5,000	3,811,941	31	26.29 Gb	48
≥ 10,000	190,549	2	2.13 Gb	4
≥ 15,000	2,530	0	0.04 Gb	0
≥ 20,000	39	0	0.00 Gb	0
≥ 25,000	0	0	0.00 Gb	0
≥ 30,000	0	0	0.00 Gb	0
≥ 35,000	0	0	0.00 Gb	0
≥ 40,000	0	0	0.00 Gb	0

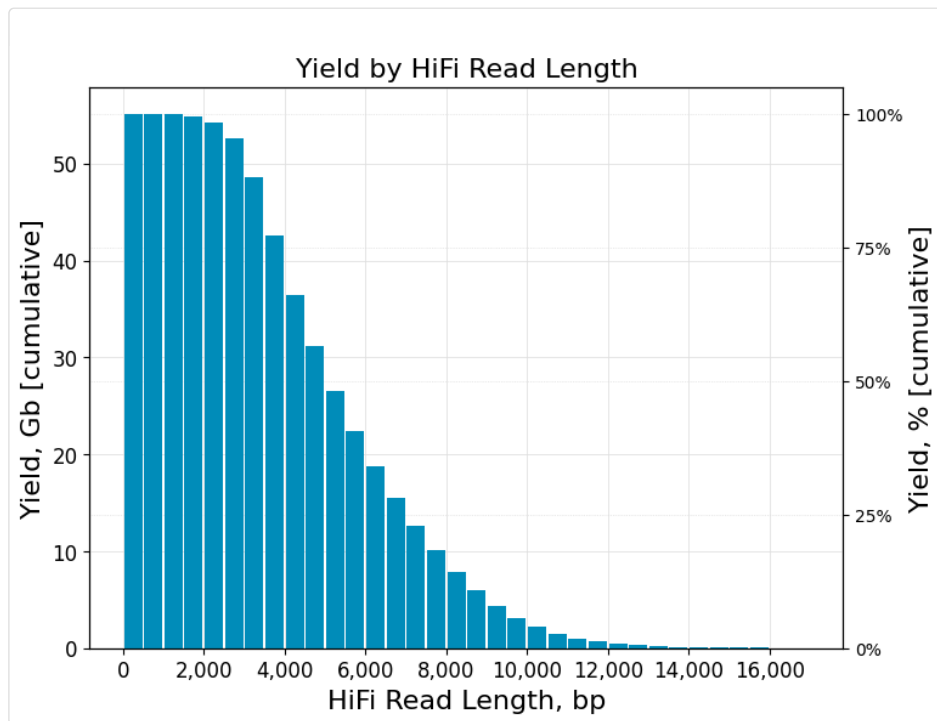
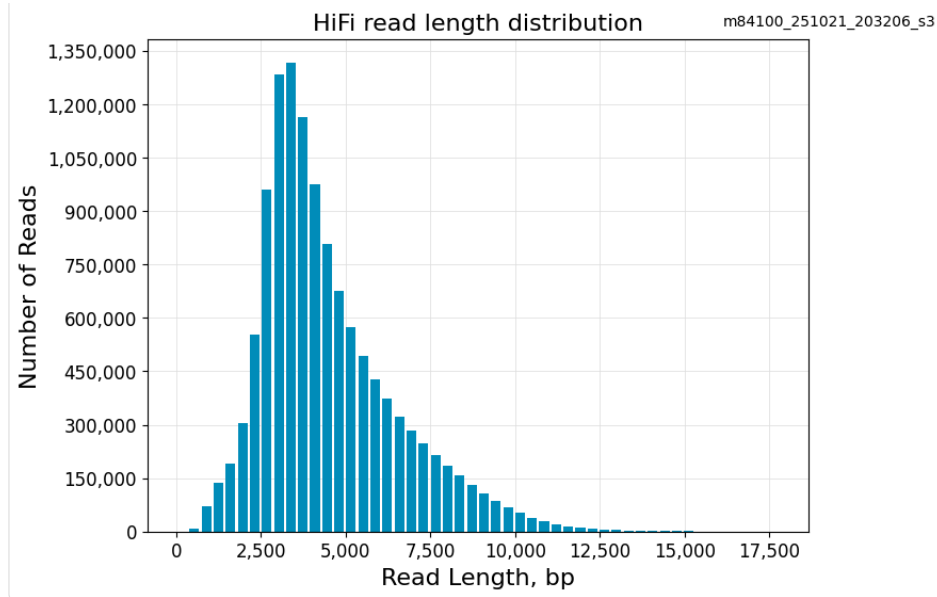
HiFi Read Quality Summary

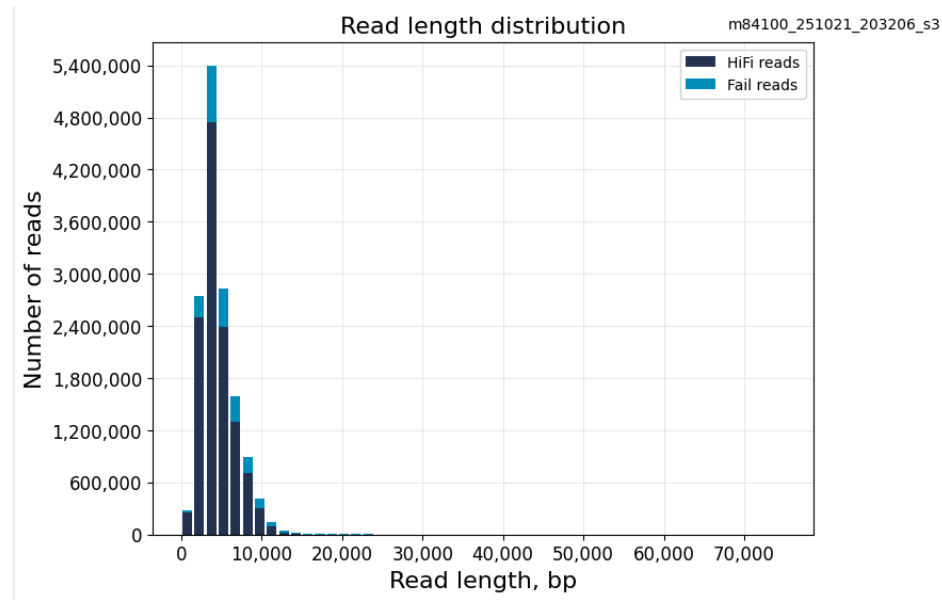
Search ...

Read Quality (Phred) ↕	Reads ↕	Reads (%) ↕	Yield (Gb) ↕	Yield (%) ↕
≥ Q20	12,313,988	100	54.96 Gb	100
≥ Q30	10,875,116	88	47.84 Gb	87
≥ Q40	8,460,303	69	35.91 Gb	65
≥ Q50	5,531,401	45	21.51 Gb	39

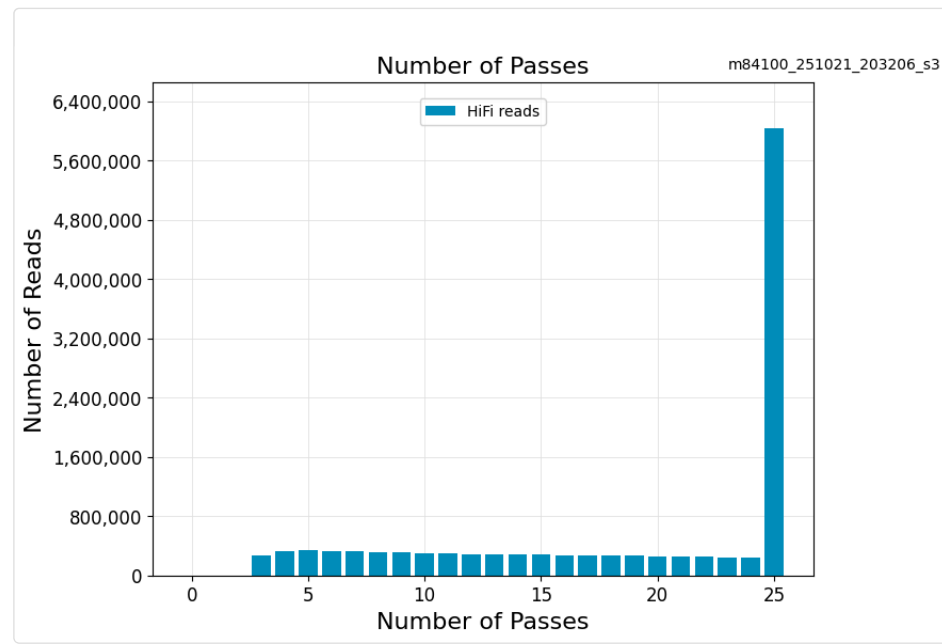
Read Length Distribution



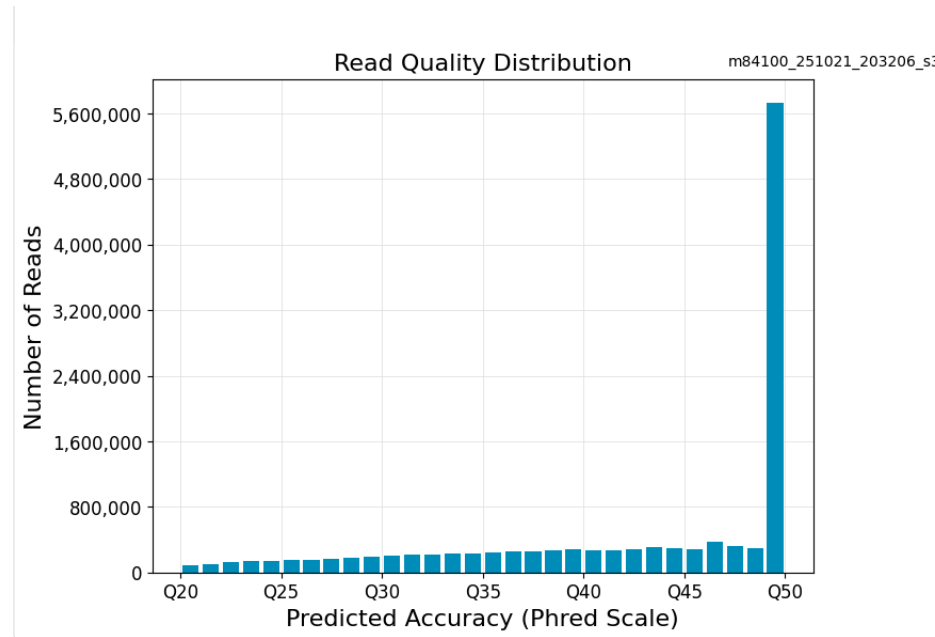




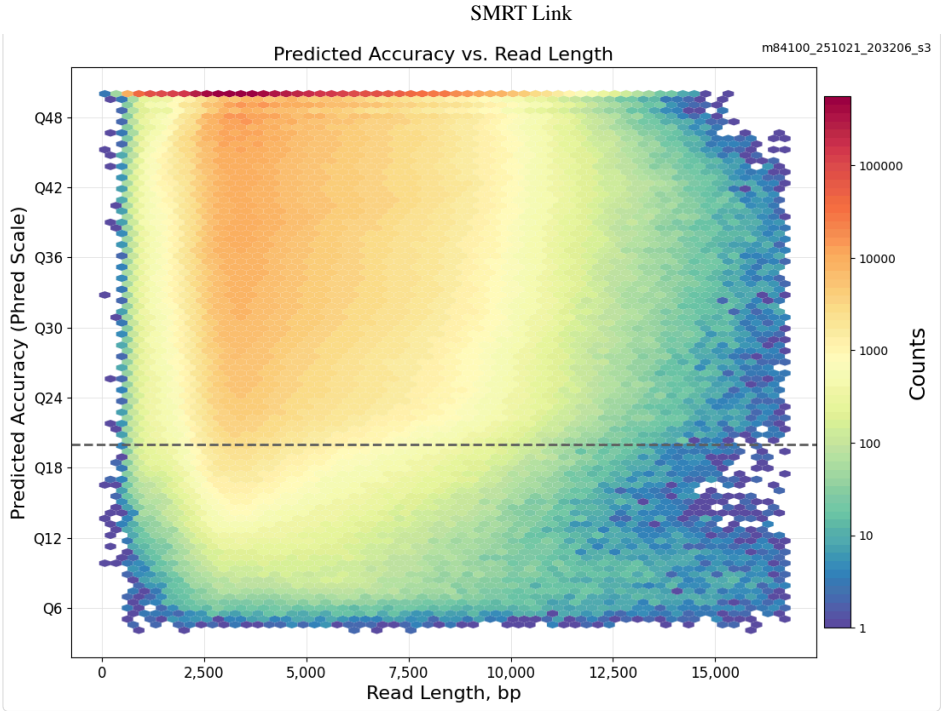
Number of Passes



Read Quality Distribution



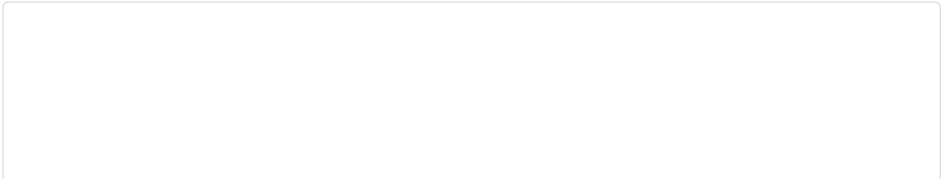
Predicted Accuracy vs. Read Length

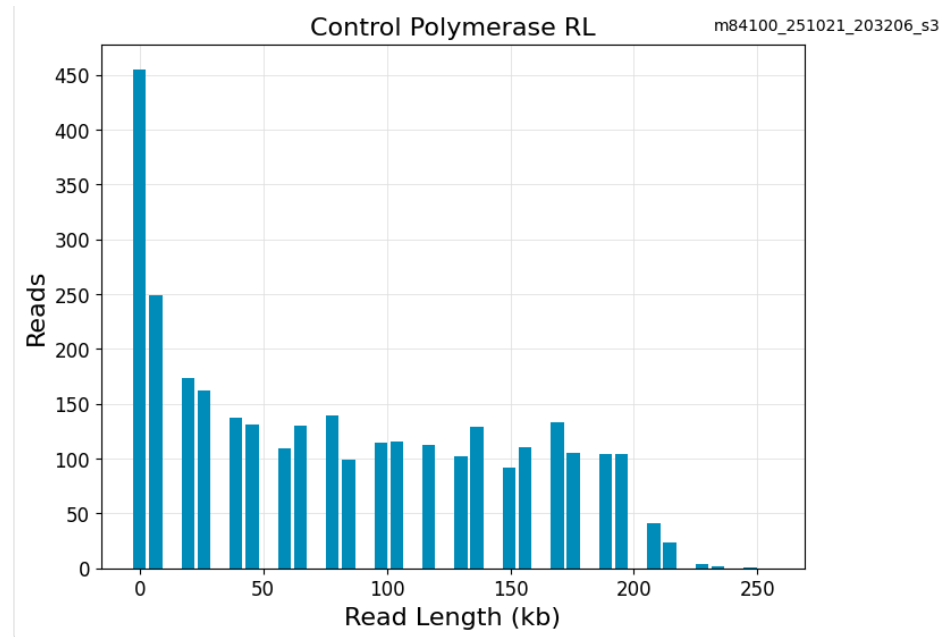


Control Report

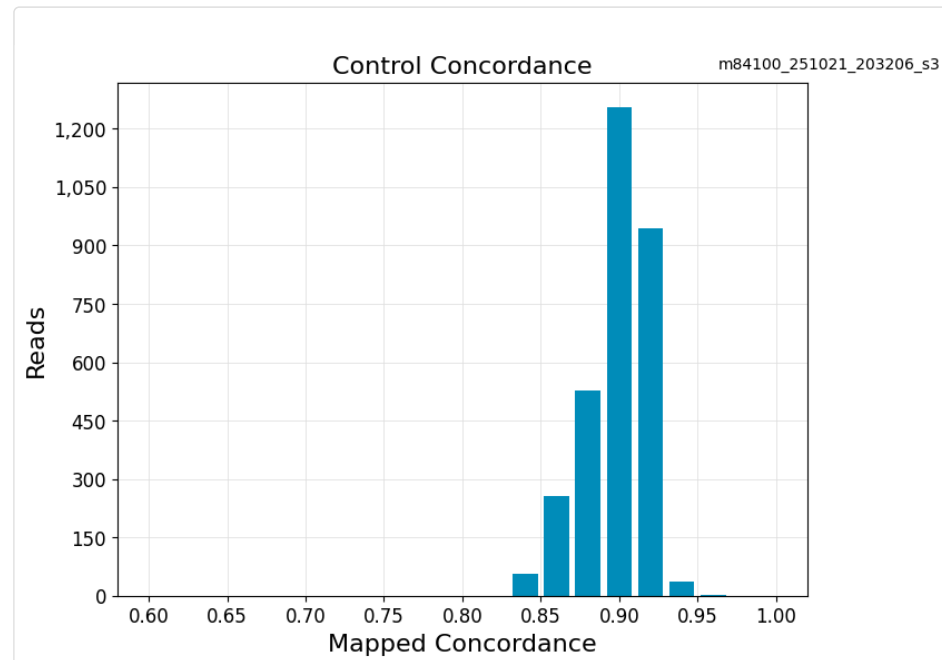
Value	Analysis Metric
3,076	Number of Control Reads
83,691	Control Read Length Mean
0.91	Control Read Concordance Mean
0.91	Control Read Concordance Mode

Control Read Length





Control Read Quality



Loading Report

Value	Analysis Metric
25,165,824	Productive ZMWs
6,485,554	Productivity 0
18,559,716	Productivity 1
120,554	Productivity 2

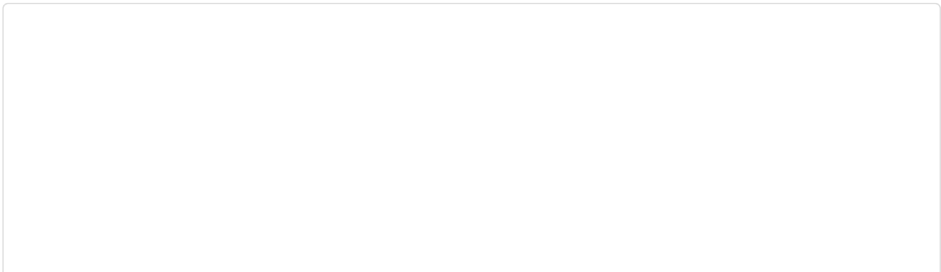
Summary

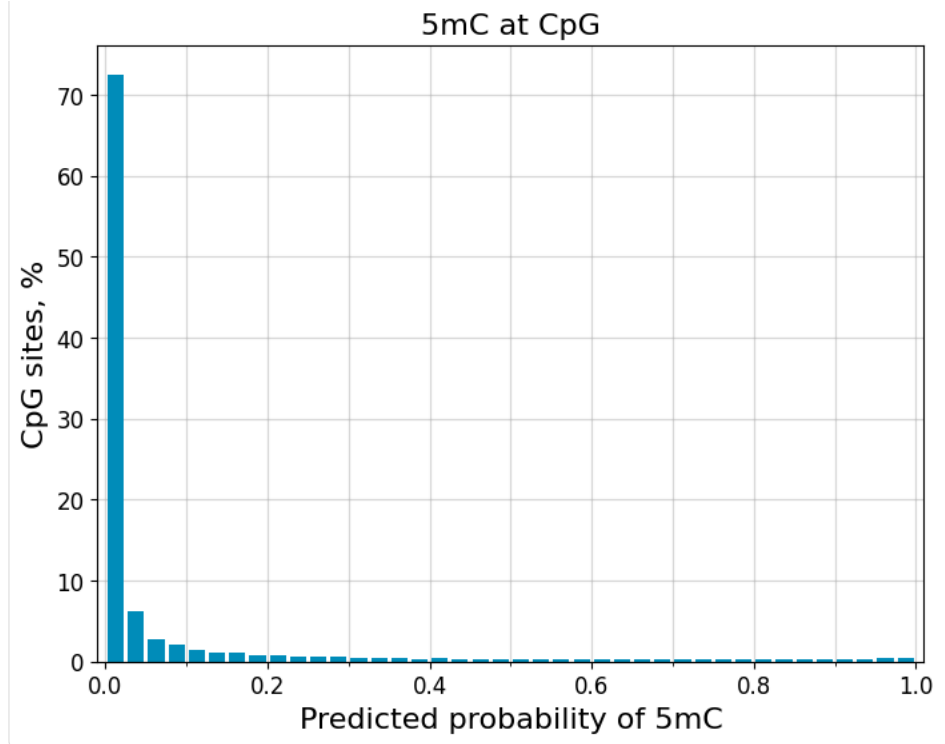
HiFi methylation callers estimate the likelihood of a modification at a specific motif. All models have some false positives and negatives, so consider the known modifications in the sample to avoid mistaking false positives for real modifications. Refer to the [methylation caller assessment](#) for expected performance.

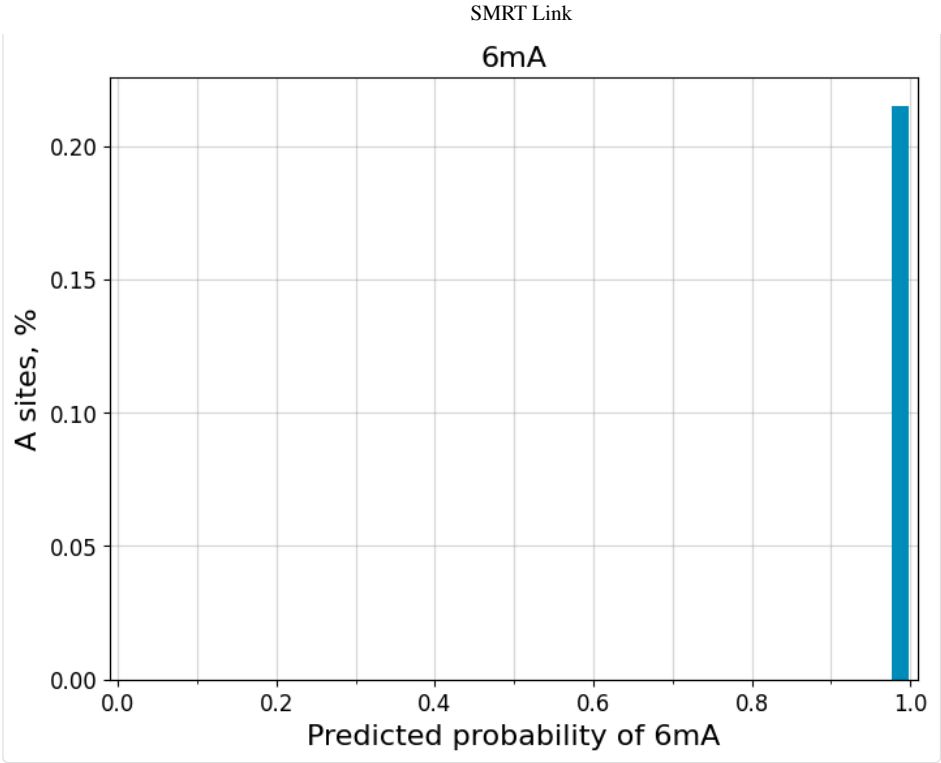
Search ...

Modification ↕	Motif ↕	Scored sites ↕	Modified si
5mC	CpG	99.1%	5.6%
6mA	A	0.2%	0.2%

Score distributions





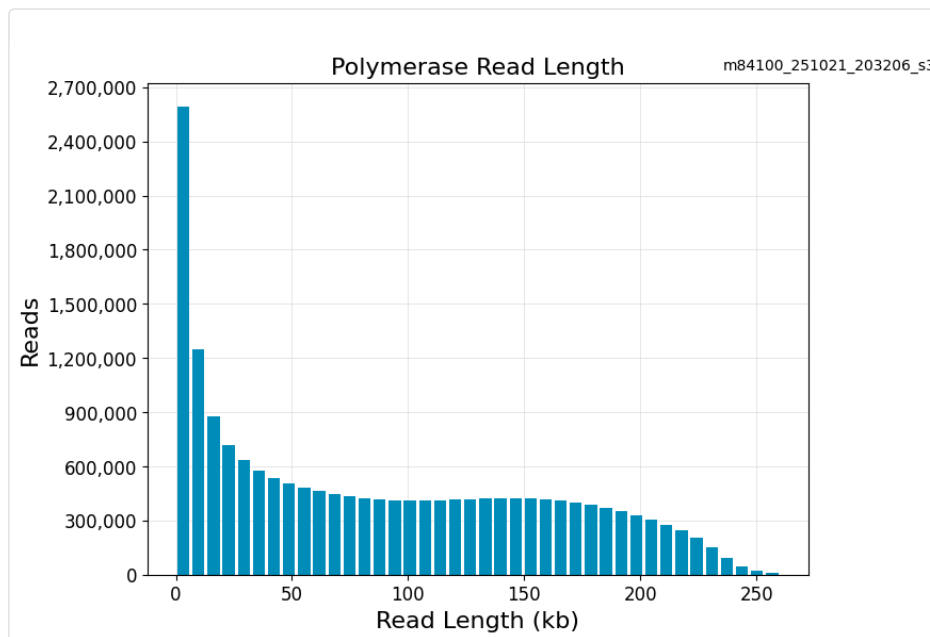


Raw Data Report

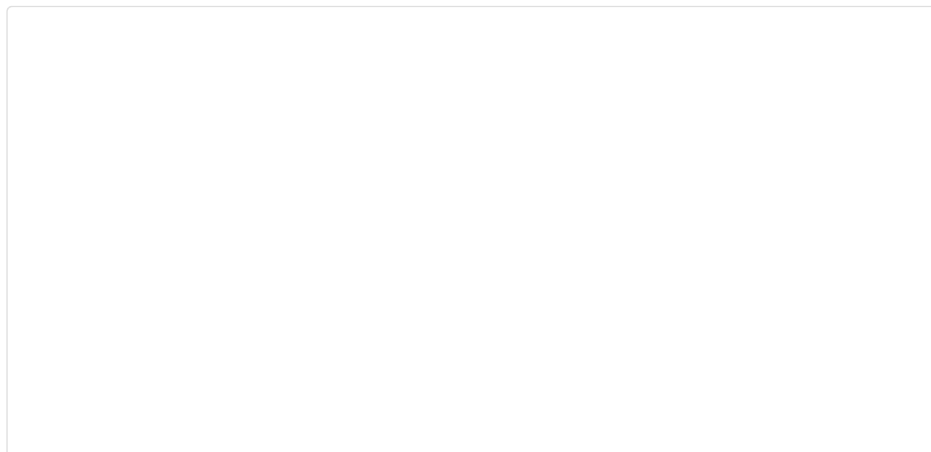
Value	Analysis Metric
1,563,675,269,600	Polymerase Read Bases
18,556,640	Polymerase Reads
84.27 kb	Polymerase Read Length (mean)
152.75 kb	Polymerase read length (N50)
7.83 kb	Polymerase read length longest subread length (mean)
10.25 kb	Polymerase read length longest subread length (N50)
119,765,630,976	Unique Molecular Yield

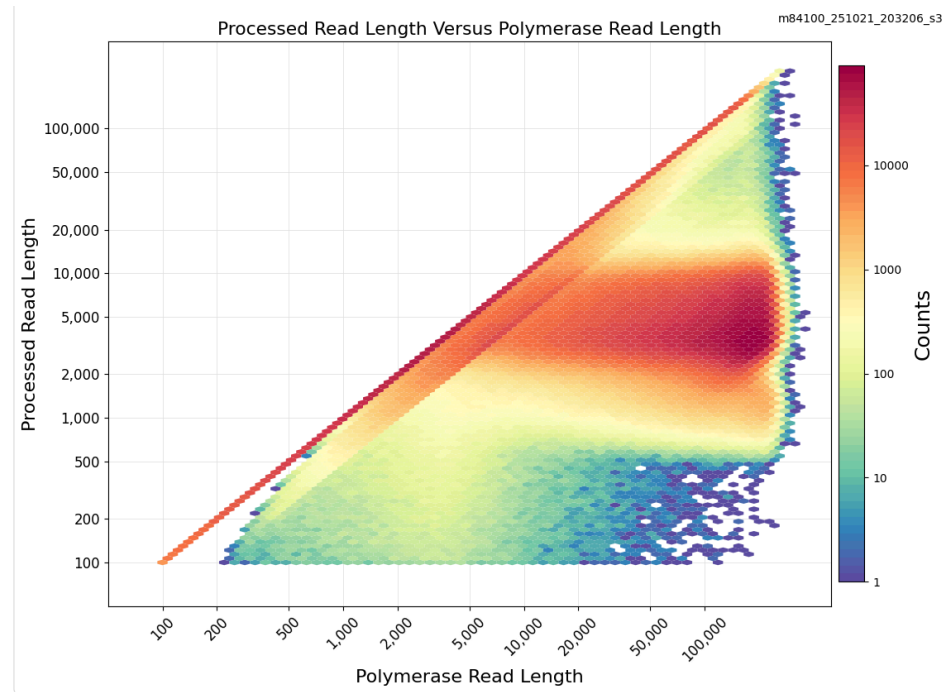
Value	Analysis Metric
2.55	Local Base Rate

Polymerase Read Length

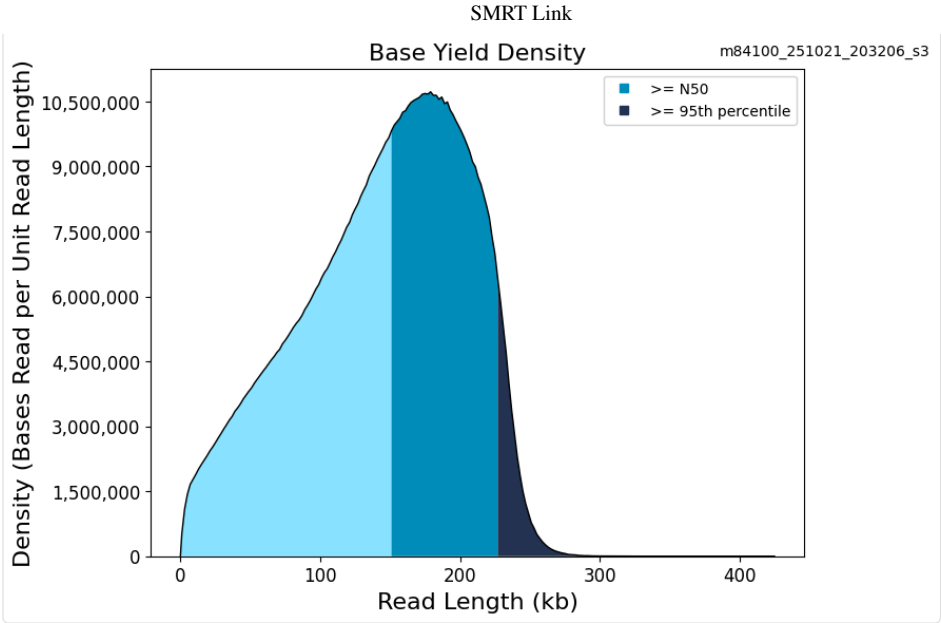


Longest Subread Length Versus Polymerase Read Length





Base Yield Density



Completed Analyses

Name	State	Id	Date Created	Created By	Analysis Application
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File Downloads

Edit Output File Name Prefix

Example:analysis-CoralAmplifi555202009-7949

File ↕	Type ↕	Size	Path
Raw Data Report	JsonReport	4 KB	 /grphome/fslg_dnasc/smrtlink/13.0/userdata/jobs_root/0
Methylation	JsonReport	3 KB	 /grphome/fslg_dnasc/smrtlink/13.0/userdata/jobs_root/0
Loading Report	JsonReport	964 bytes	 /grphome/fslg_dnasc/smrtlink/13.0/userdata/jobs_root/0

SMRT Link			
Control Report	JsonReport	2 KB	 /grphome/fslg_dnasc/smartlink/13.0/userdata/jobs_root/0
CCS Analysis Repc	JsonReport	10 KB	 /grphome/fslg_dnasc/smartlink/13.0/userdata/jobs_root/0
PDF report	pdf	1 MB	 /grphome/fslg_dnasc/smartlink/13.0/userdata/jobs_root/0
SMRT Link Job Log	log	836 bytes	 /grphome/fslg_dnasc/smartlink/13.0/userdata/jobs_root/0

Related Datasets

Data Set 	Type 
No related Data Sets to show	

SMRT Link Log

```
[INFO] [2025-10-23T02:40:17.968-06:00] Initial Setup of resources. Starting to run engine job  
id:7949 type:import-collection  
[INFO] [2025-10-23T02:40:17.968-06:00] Job output directory is  
/grphome/fslg_dnasc/smrtlink/13.0/userdata/jobs_root/0000/0000007/0000007949  
[INFO] [2025-10-23T02:40:19.240-06:00] about to write datastore for job 7949  
[INFO] [2025-10-23T02:40:19.280-06:00] Done writing datastore for job 7949  
[INFO] [2025-10-23T02:40:19.280-06:00] Successfully completed running job 7949  
[INFO] [2025-10-23T02:40:19.483-06:00] Imported 1 files; Linked 5 reports to 5 datasets  
[INFO] [2025-10-23T02:40:19.498-06:00] Updated job 7949 state to SUCCESSFUL  
[INFO] [2025-10-23T02:40:19.510-06:00] Skipping Sending Email for Job 7949 state:SUCCESSFUL.  
type:import-collection userEmail:None, System is not configured for Email sending
```