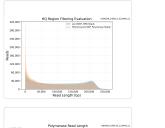
# 12plex\_UHRR\_Brain\_Kinnex\_IDTcaptured-Cel l1 (all samples)

🔓 Сору		🖹 Analyze		🛃 Export		🛍 Delete
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✓Dataset Overview	Display All		
◆Dataset Overview	Status		
Status	Data Set	12plex_UHRR_Brain_Kinnex_IDTcaptured	I-Cell1 (all samples)
Thumbnails	Data Set ID Data Set UUID	8343 bcc8e533-e25c-4a85-91d6-8e2ec82de	419
	Well Sample Name	12plex_UHRR_Brain_Kinnex_IDTcaptured	
Display All	<b>Biological Sample</b>	Bio Sample 1	
Run Preview	Name		
Run Preview			
CCS Analysis Report			
▶5mC CpG Report			
>Adapter Report			
Loading Report			
Raw Data Report			
Control Report			
Barcodes			
➤Analyses	Thumbnails	Read Ouglity Distribution were years around	CpG Methylation in Reads
<b>&gt;</b> Data	94.000 95 60.000 130.000 130.000 1	HADD HADD HADD HADD HADD HADD HADD HADD	Coo Stee, % (combined a a b a a a a a a a a a a a a a
	Read length distribution mean_rean_parent	Predicted focusity vs. Baid (seigh)	0 02 04 05 10 Predicted Probability of Methylation
	222000 21500 2		CpG Methylation in Reads (Histogram)
	Number of Passas		and a first of the second seco

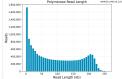


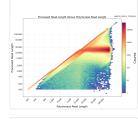
1,900,000 7,900,000 7,900,000 7,900,000 7,900,000 7,900,000 7,900,000 7,900,000 7,900,000

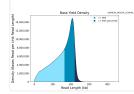
Number of Ba

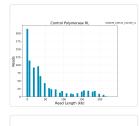
Barcode Fr

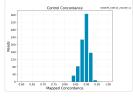
ency Distribution

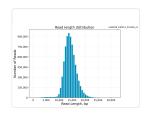


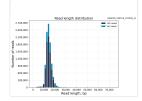


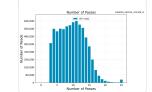


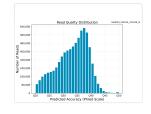


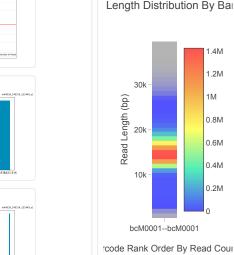


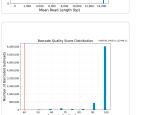




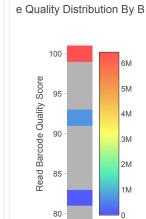






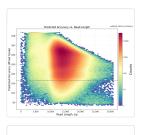


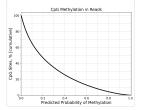
60 Barr



bcM0001--bcM0001 arcode Rank Order By Read Cou







Length Distribution By Bai

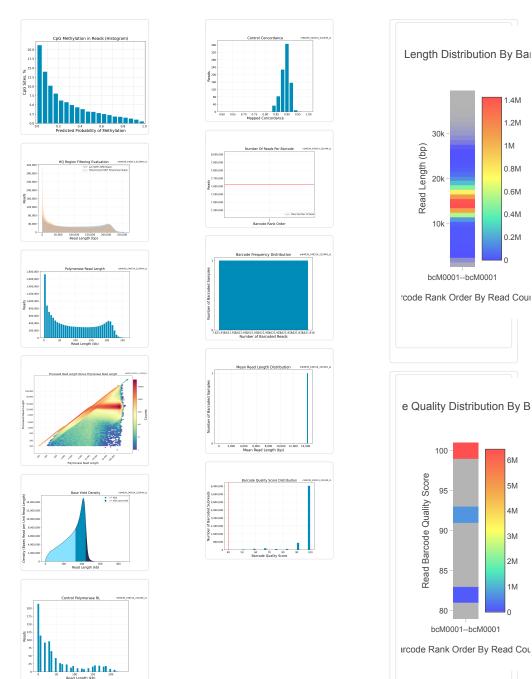
1.4M 1.2M

1M

0.8M

0.6M 0.4M

0.2M 0



1.4M

1.2M

1M

0.8M

0.6M 0.4M

0.2M

0

6M

5M

4M

ЗM

2M

1M

0



17.5 215.0 % 12.5 10.0 7.5

5.0 2.5

120.000 290.000 200.000 120.000 120.000 120.000 0 0 0

8,000.00

4,000.00

200 -115 -150 -50 -50 -25 -25 -0 -

Value	Analysis Metric
undefined	Estimated HiFi yield
undefined	HiFi read quality, median
13483	HiFi read length, mean
55.7	P1%
4	Time (Hrs)
Basic	Workflow
m84039_240514_222449_s1_basic_preview_4hr	Id

Value	Analysis Metric
m84039_240514_222449_s1	Movie Id

## Barcode preview

		Search
Barcode ↓î	HiFi reads ↓î	HiFi read length (mean
bcM0001bcM0001	94.4%	13493
Other	0.6%	11419
Not Barcoded	5.1%	13258

#### **Run Preview**

Value	Analysis Metric
100358369325	Estimated HiFi yield
33	HiFi read quality, median
14173	HiFi read length, mean
undefined	P1%
23	Time (Hrs)
Full	Workflow
m84039_240514_222449_s1_full_preview_23hr	ld
m84039_240514_222449_s1	Movie Id

# Barcode preview

		Search
Barcode ↓	HiFi reads ↓î	HiFi read length (mean
bcM0001bcM0001	98.9%	14179
Other	0.2%	2010
Not Barcoded	1.0%	14357

# CCS Analysis Report

Value	Analysis Metric
7.6 M	HiFi reads
109.17 Gb	HiFi reads yield
14.30 kb	HiFi reads length (mean)

Value	Analysis Metric
14,130	HiFi reads length (median, bp)
14,461	HiFi Read Length N50 (bp)
Q34	HiFi Read Quality (median)
95.44%	Base Quality ≥Q30 (%)
10	HiFi Number of Passes (mean)

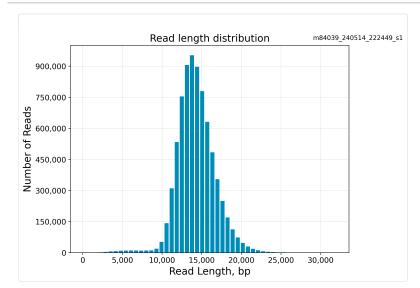
# HiFi Read Length Summary

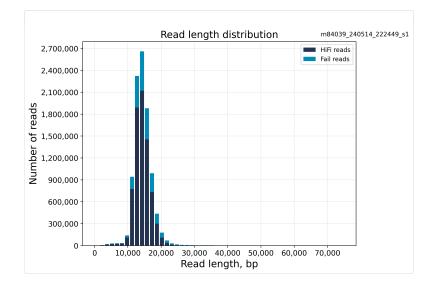
			Search	
Read Length (kb) 🔱	Reads ↓î	Reads (%) ↓î	Yield (Gb) ↓î	Yield
≥ 0	7,634,506	100	109.17 Gb	100
≥ 5,000	7,608,611	100	109.07 Gb	100
≥ 10,000	7,501,793	98	108.20 Gb	99
≥ 15,000	2,635,919	35	44.14 Gb	40
≥ 20,000	113,695	1	2.44 Gb	2
≥ 25,000	5,121	0	0.14 Gb	0
≥ 30,000	565	0	0.02 Gb	0
≥ 35,000	22	0	0.00 Gb	0
≥ 40,000	0	0	0.00 Gb	0

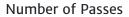
# HiFi Read Quality Summary

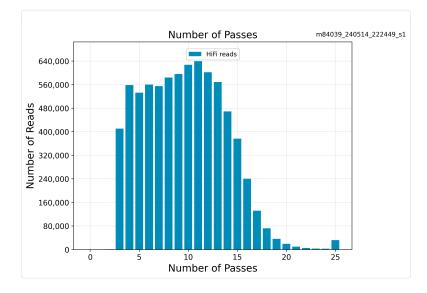
			Search	
Read Quality (Phree	d)	Reads (%) ↓î	Yield (Gb) ↓î	Yield
≥ Q20	7,634,506	100	109.17 Gb	100
≥ Q30	5,573,208	73	79.32 Gb	73
≥ Q40	645,204	8	8.21 Gb	8
≥ Q50	8,381	0	0.04 Gb	0

# Read Length Distribution

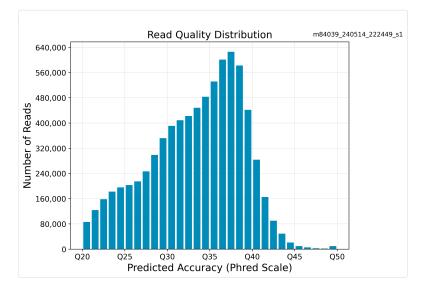




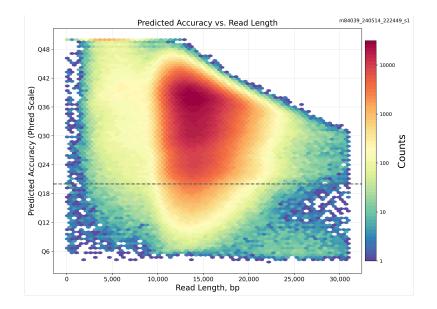




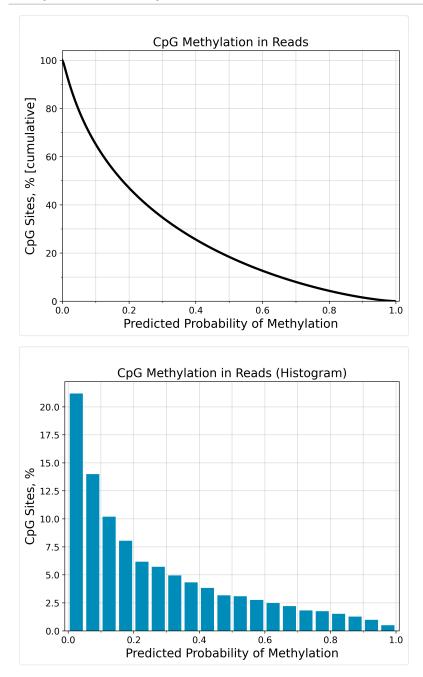
## Read Quality Distribution



Predicted Accuracy vs. Read Length



## Methylation Probability



## Adapter Report

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

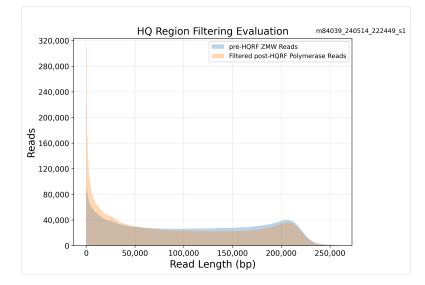
#### Loading Report

Value	Analysis Metric
25,165,824	Productive ZMWs
10,311,312	Productivity 0
14,739,409	Productivity 1
115,103	Productivity 2

#### Loading Statistics

				Search			
Collecti 🕸	Total ZM ↓	Producti ↓	P0 (%) 🇯	Producti ↓	P1 (%) ↓î	Producti	Ĵ P2 (%)
m84039	25,165,824	10,311,312	40.97	14,739,409	58.57	115,103	0.46

#### HQ Region Filtering Evaluation

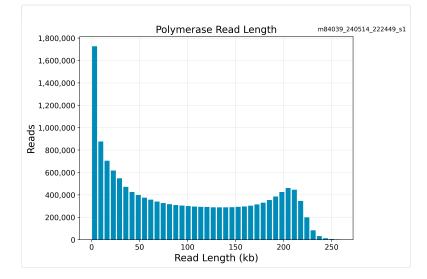


## Raw Data Report

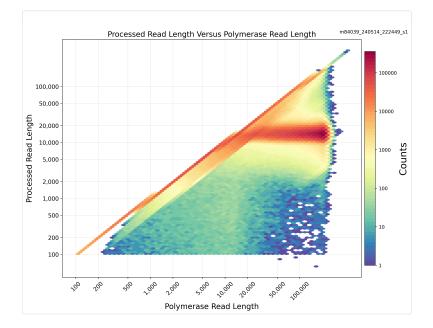
Value	Analysis Metric
1,356,910,594,042	Polymerase Read Bases

Value	Analysis Metric
14,738,535	Polymerase Reads
92.07 kb	Polymerase Read Length (mean)
166.75 kb	Polymerase read length (N50)
17.41 kb	Polymerase read length longest subread length (mean)
16.75 kb	Polymerase read length longest subread length (N50)
239,372,468,224	Unique Molecular Yield

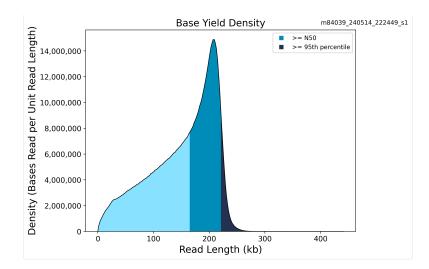
#### Polymerase Read Length



#### Longest Subread Length Versus Polymerase Read Length



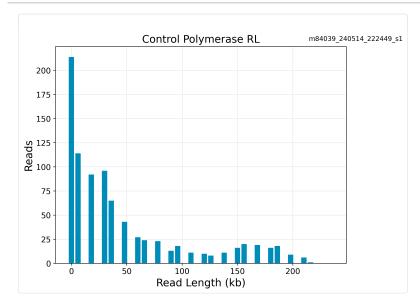
#### Base Yield Density



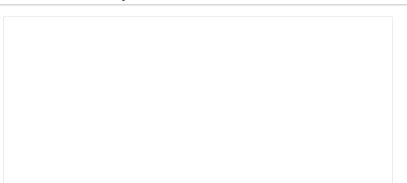
#### **Control Report**

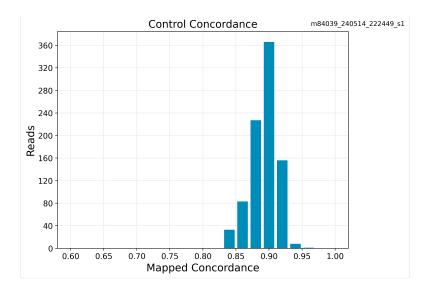
Value	Analysis Metric
874	Number of Control Reads
48,582	Control Read Length Mean
0.90	Control Read Concordance Mean
0.91	Control Read Concordance Mode

# Control Read Length



#### **Control Read Quality**





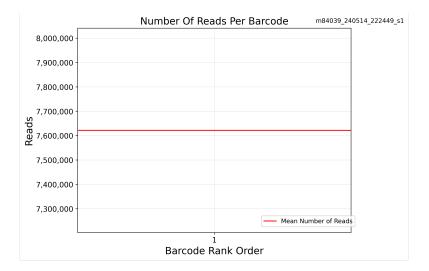
#### Barcodes

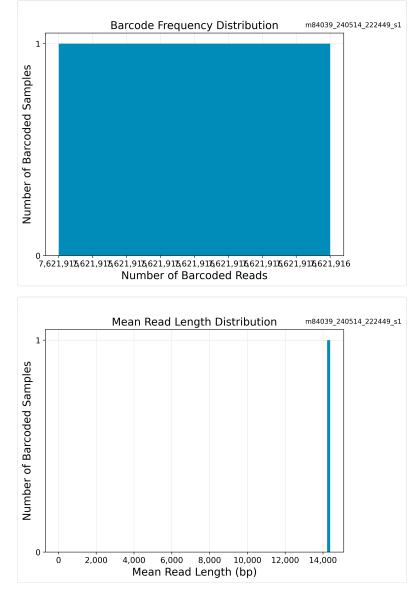
Value	Analysis Metric
1	Unique Barcodes
7,621,916	Barcoded HiFi Reads
12,590	Unbarcoded HiFi Reads
99.83%	Barcoded HiFi Reads (%)
109.00 Gb	Barcoded HiFi yield (Gb)
0.16 Gb	Unbarcoded HiFi yield (Gb)
99.84%	Barcoded HiFi Yield (%)
7,621,916	Mean HiFi Reads per Barcode
7,621,916	Max. HiFi Reads per Barcode
7,621,916	Min. HiFi Reads per Barcode
14.30 kb	Barcoded HiFi read length (mean, kb)
13.04 kb	Unbarcoded HiFi read length (mean, kb)

#### Barcode Data

				Search	
rcode ∬	Barcode Q		HiFi Read	↓ HiFi Read	∬ HiFi Yield (.
cM0001	97.1	7,621,916	14,301	Q34	109,002,86
lot Barcod	0.0	12,590	13,044	Q26	164,225,24
	сМ0001	cM0001 97.1	cM0001 97.1 7,621,916	cM0001 97.1 7,621,916 14,301	cM0001 97.1 7,621,916 14,301 Q34

## **Barcoded Read Statistics**





#### Barcode Quality Scores

