



Run Info

Host Name	GXb03422 (localhost)
Position	X2
Experiment Name	ReadUntil_ZGM_EcoliEnrich_B1109_23092021
Sample ID	ReadUntil_ZGM_EcoliEnrich_B1109_23092021
Run ID	75c72f93-1bea-4b4b-8fd7-19dd02c203f2
Acquisition ID(s)	92ebef7047051051e553a12918c87082a98b95d1, fae7e284df614cbc1e03316e0c892ee60f3621d5
Flow Cell Id	FAR13458
Start Time	September 23, 15:15
Run Length	1h 2m

Run Summary

Reads Generated	238.08 k
Passed Bases	450.89 Mb
Failed Bases	34.54 Mb
Estimated Bases	509.79 Mb

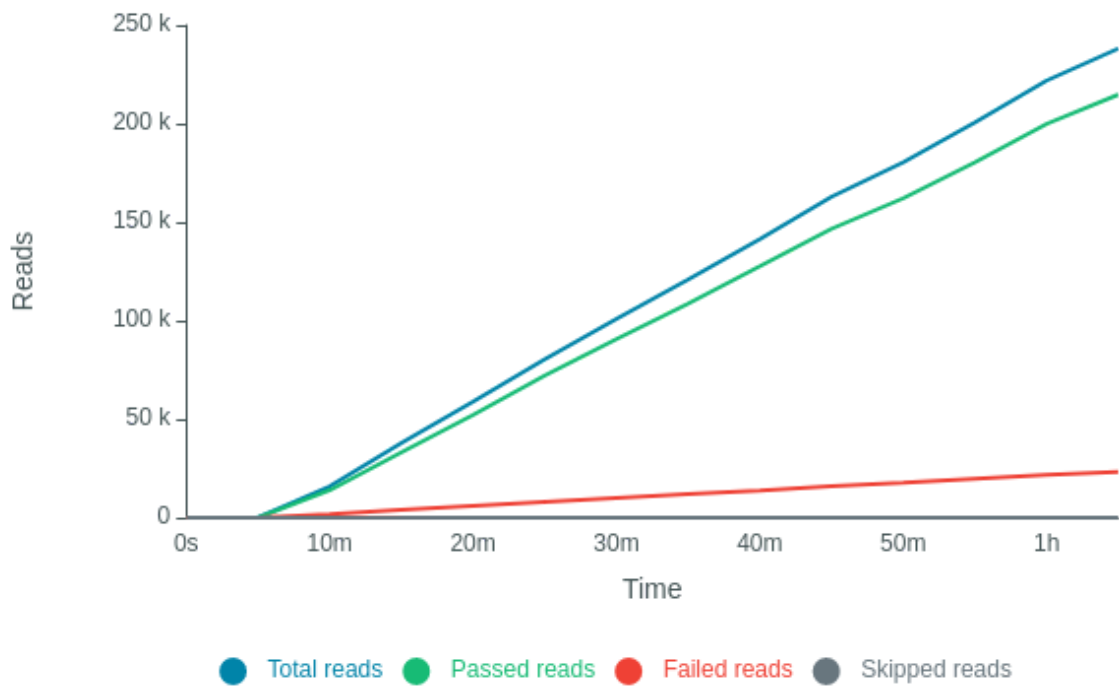
Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-LSK109
Initial bias voltage	-180 mV
FAST5 output	Enabled
FASTQ output	Enabled
BAM output	Enabled
Bulk file output	Disabled
Active channel selection	Enabled
Basecalling	Enabled
Specified run length	72 hours
Adaptive sampling	reference_files= ["/data/references/zyzo_gut_mock/Escherichia_coli_B1109.fasta"],filter_type=enrich,first_channel=1,last_channel=256
FAST5 reads per file	4000
FAST5 output options	vbz_compress,fastq,raw
FASTQ reads per file	4000
FASTQ output options	compress
Mux scan period	1 hour 30 minutes
Reserved pores	0 %
Basecall model	High-accuracy basecalling
Alignment	reference_files= ["/data/references/zyzo_gut_mock/zyzo_minus_two.fasta"]
Read filtering	min_qscore=9

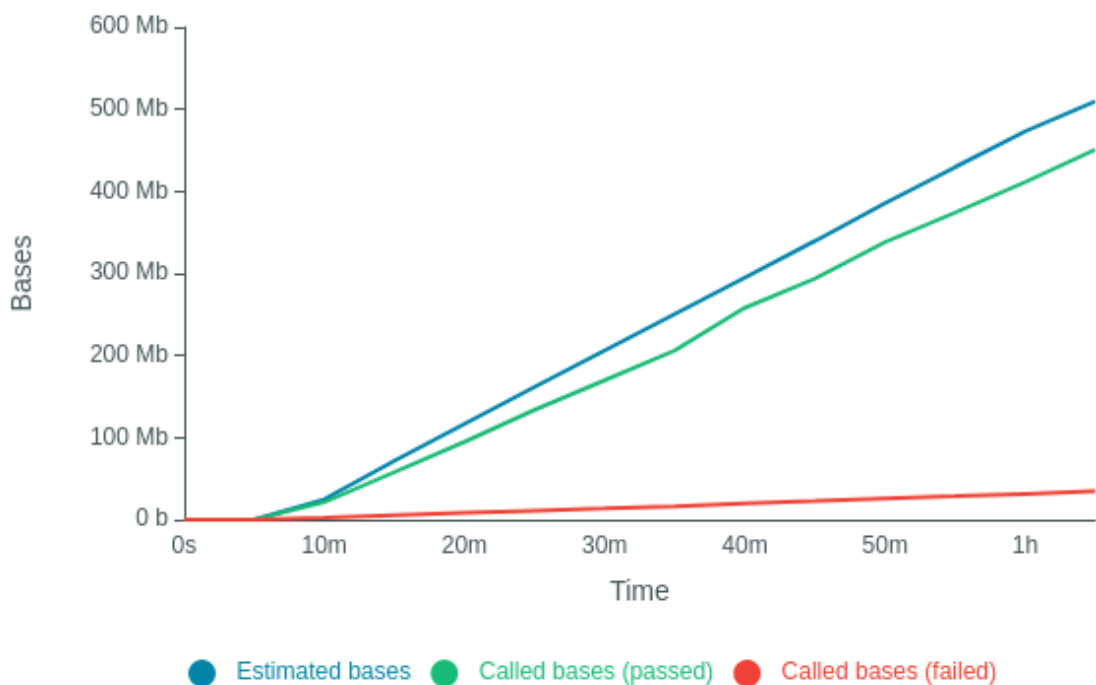
Versions

MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads



Cumulative Output Bases



Estimated N50: 12.92 kb

[illegible]

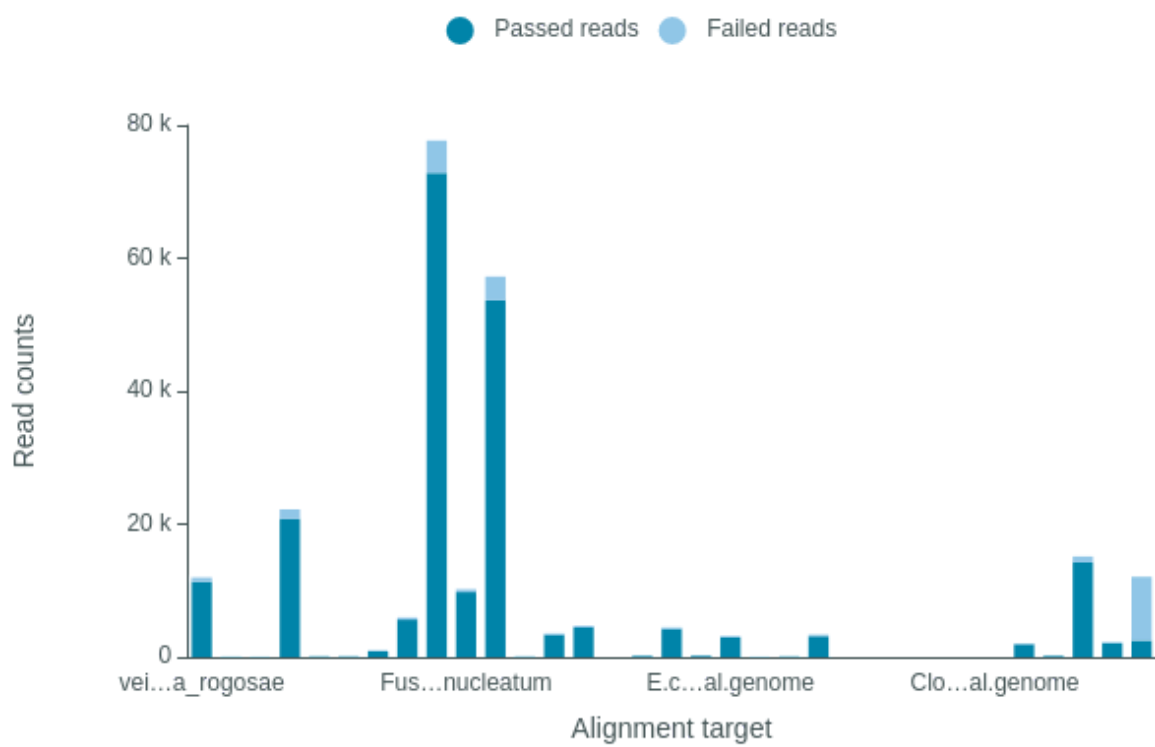
Estimated N50: 12.92 kb



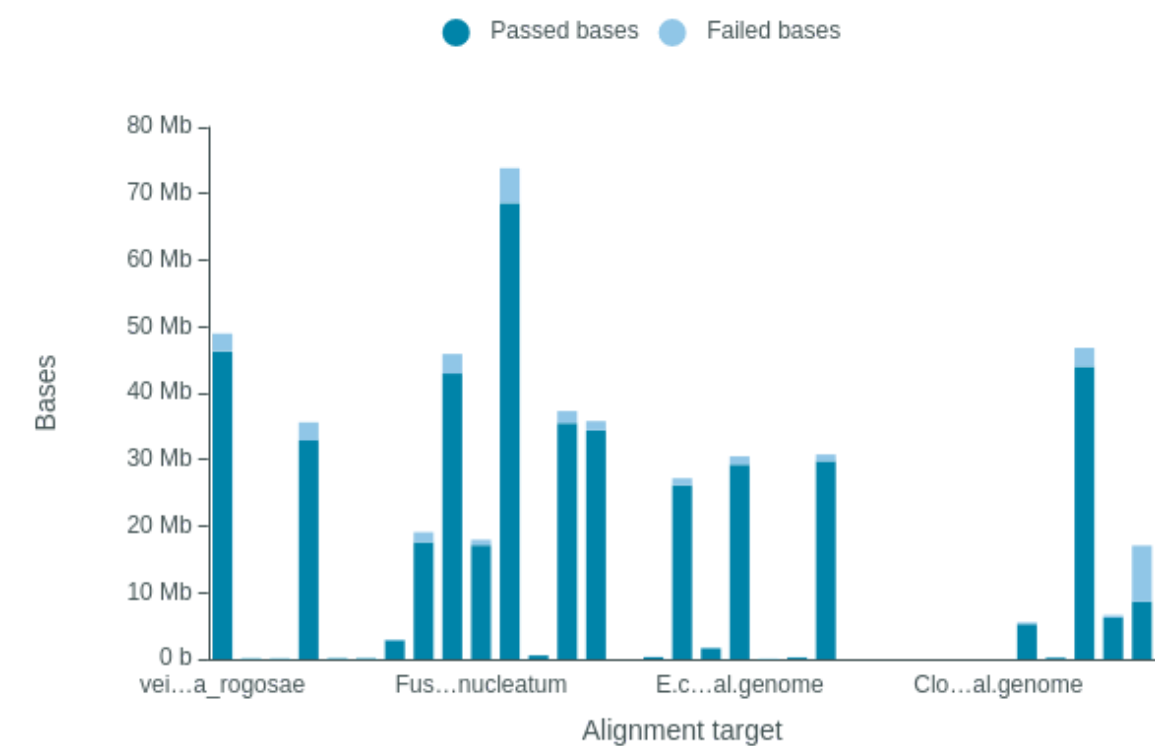
The bar chart displays the distribution of read lengths. The y-axis, labeled 'Passed basecalled bases', ranges from 0 to 80 Mb. The x-axis, labeled 'Read length', shows various intervals from 1.02 kb to 65.5 kb. The distribution is highly skewed, with the highest frequency of reads occurring at the shortest length (1.02 kb), which exceeds the 80 Mb mark on the y-axis. The frequency decreases rapidly as read length increases, with most reads falling below 10 kb.

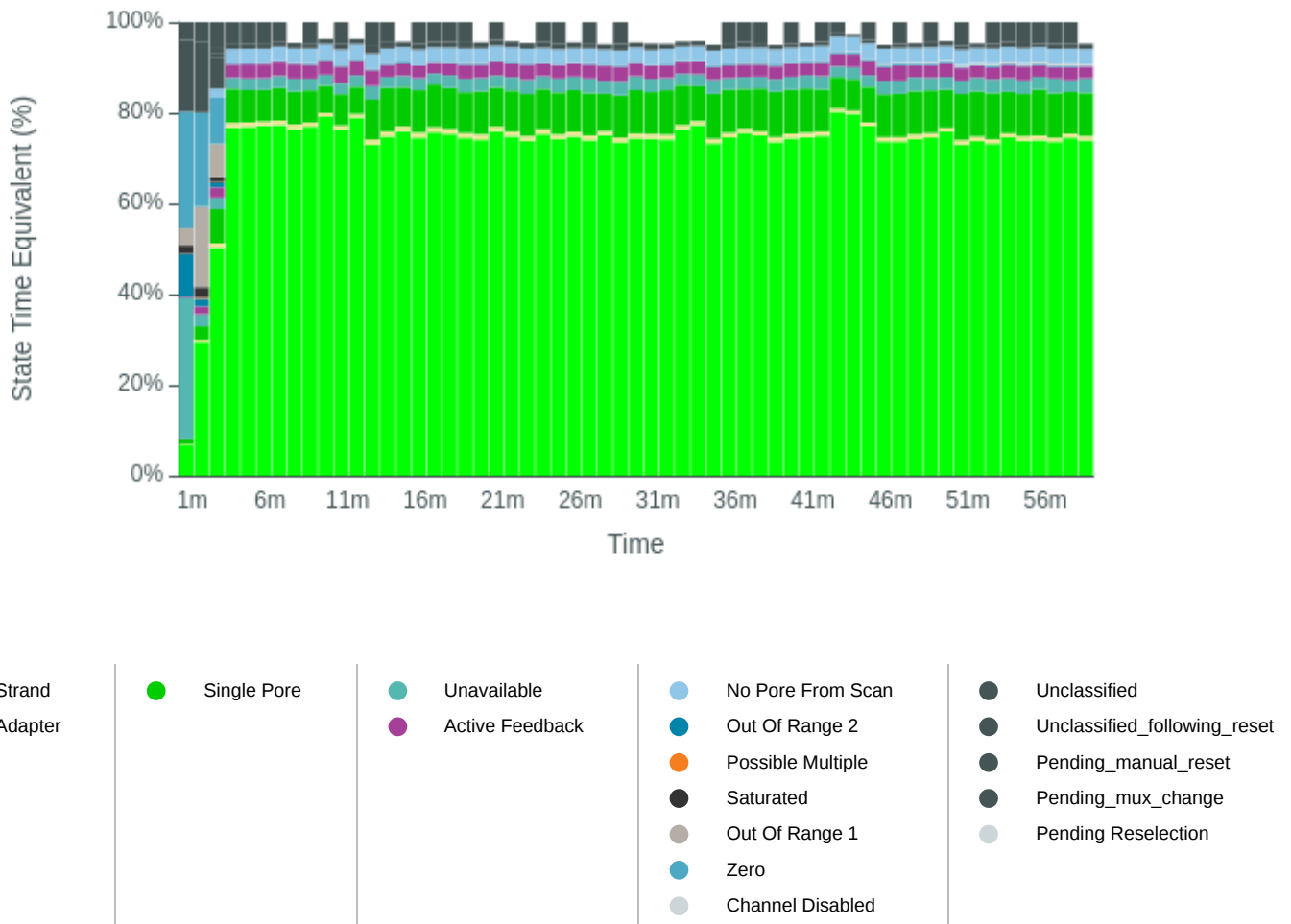
Read length (kb)	Passed basecalled bases (Mb)
1.02	> 80
2.04	~24
3.06	~17
4.08	~12
5.10	~11
6.12	~10
7.14	~10
8.16	~10
9.18	~10
10.20	~10
11.22	~9
12.24	~9
13.26	~9
14.28	~9
15.30	~9
16.32	~9
17.34	~9
18.36	~9
19.38	~9
20.40	~9
21.42	~9
22.44	~9
23.46	~9
24.48	~9
25.50	~9
26.52	~9
27.54	~9
28.56	~9
29.58	~9
30.60	~9
31.62	~9
32.64	~9
33.66	~9
34.68	~9
35.70	~9
36.72	~9
37.74	~9
38.76	~9
39.78	~9
40.80	~9
41.82	~9
42.84	~9
43.86	~9
44.88	~9
45.90	~9
46.92	~9
47.94	~9
48.96	~9
49.98	~9
50.00	~9
51.02	~9
52.04	~9
53.06	~9
54.08	~9
55.10	~9
56.12	~9
57.14	~9
58.16	~9
59.18	~9
60.20	~9
61.22	~9
62.24	~9
63.26	~9
64.28	~9
65.30	~9

Alignment Target Hits (reads)

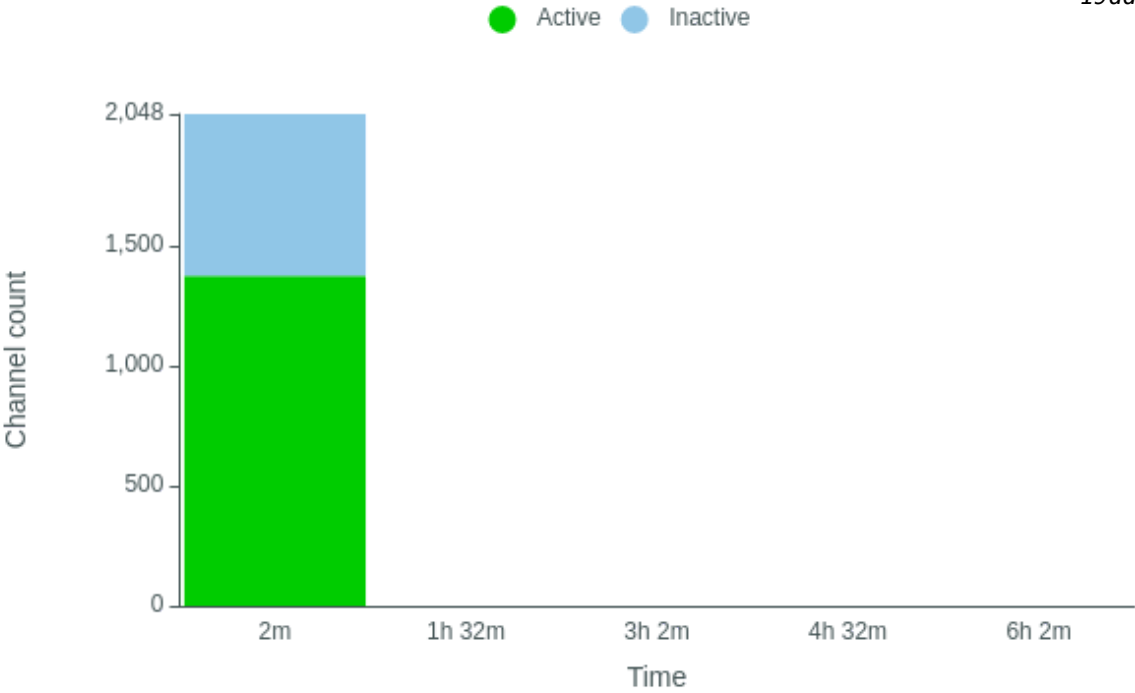


Alignment Target Hits (bases)

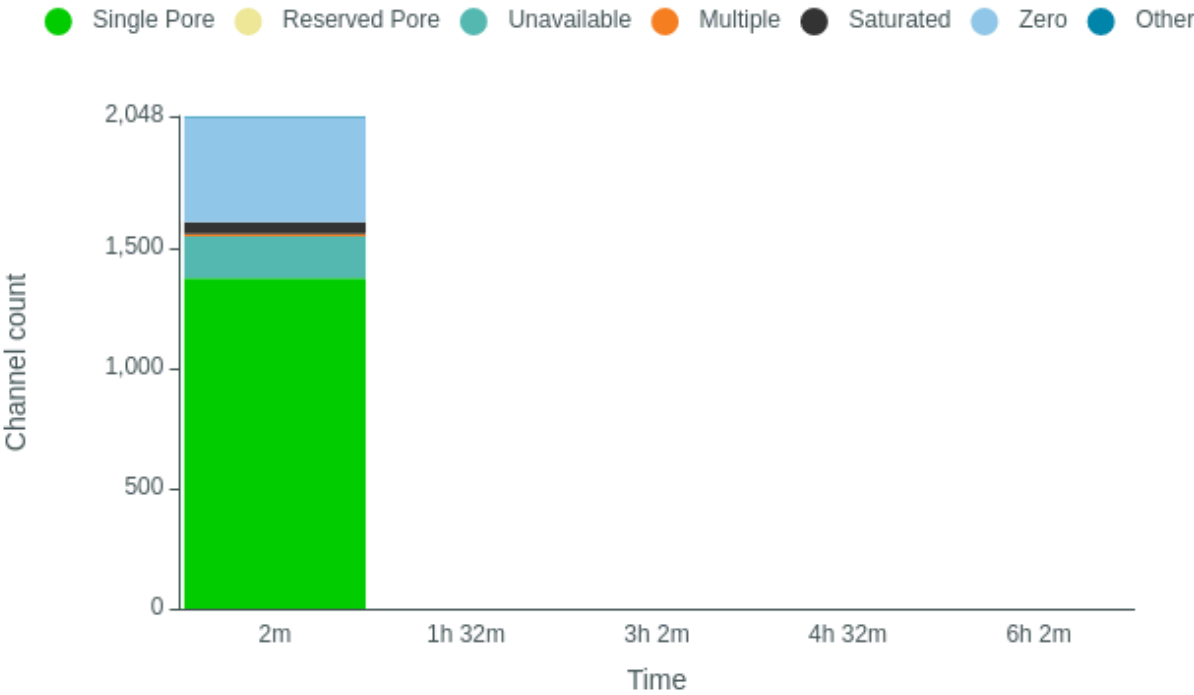




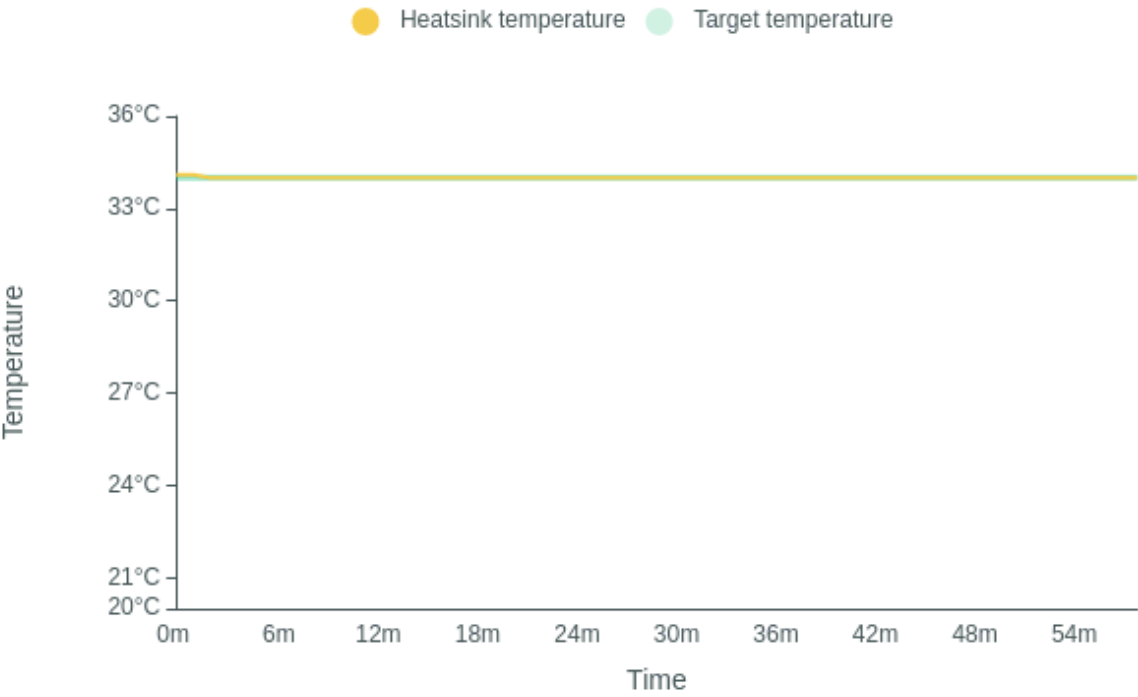
Mux Scan Grouped



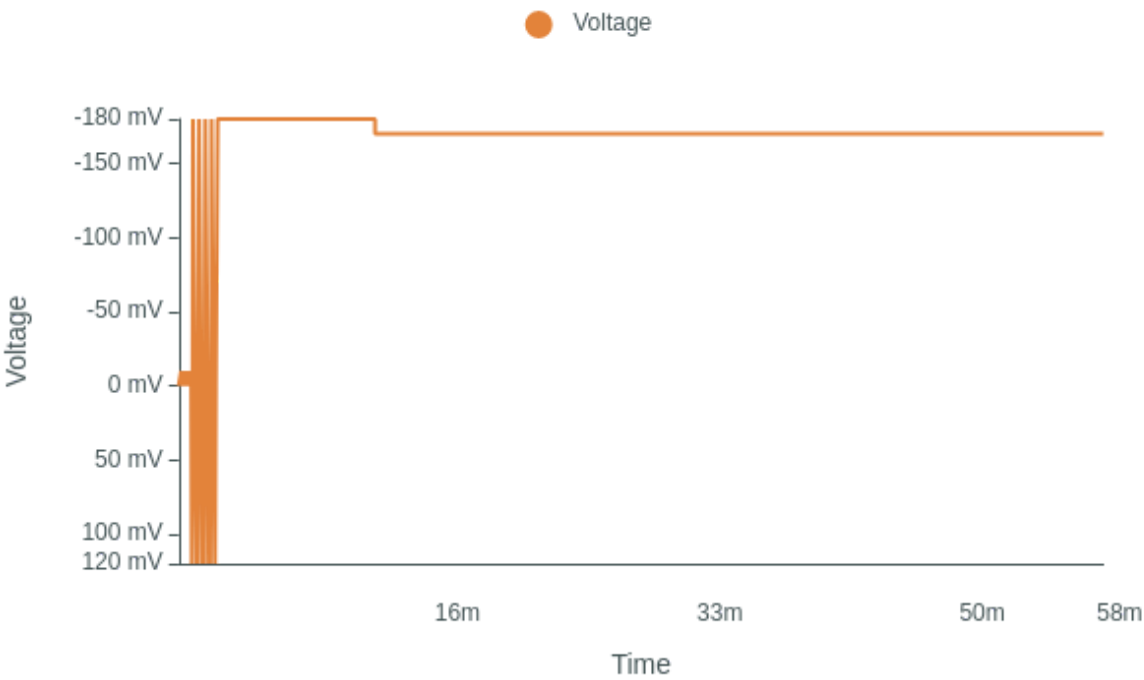
Mux Scan Categorised



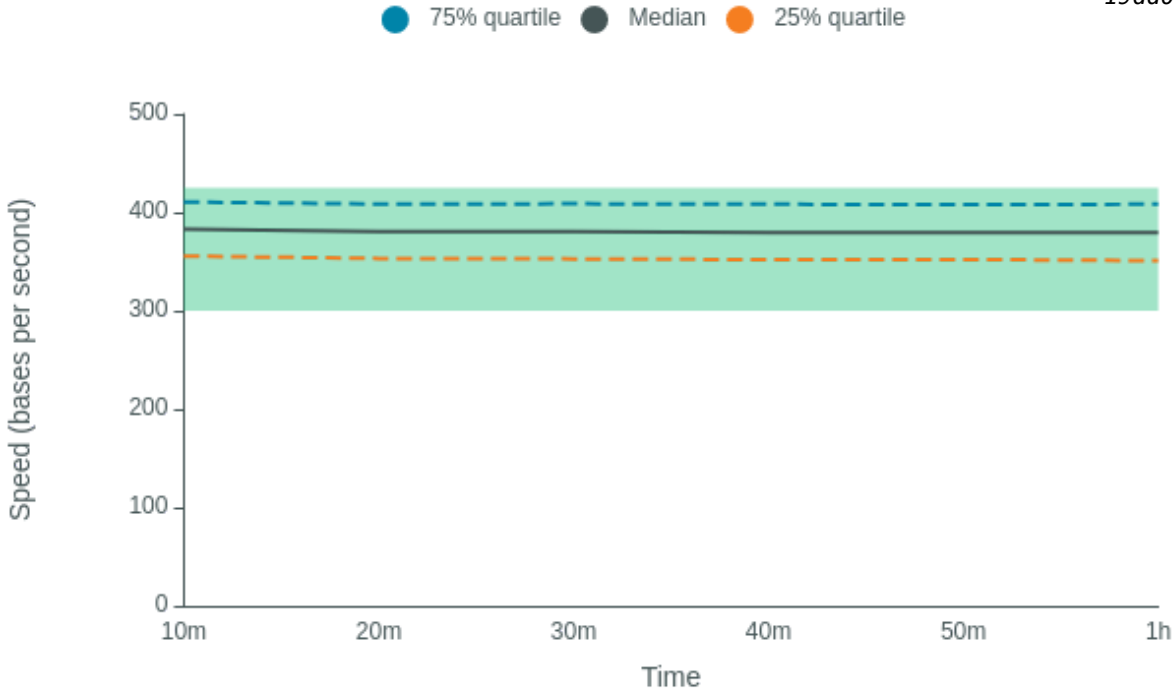
Temperature History



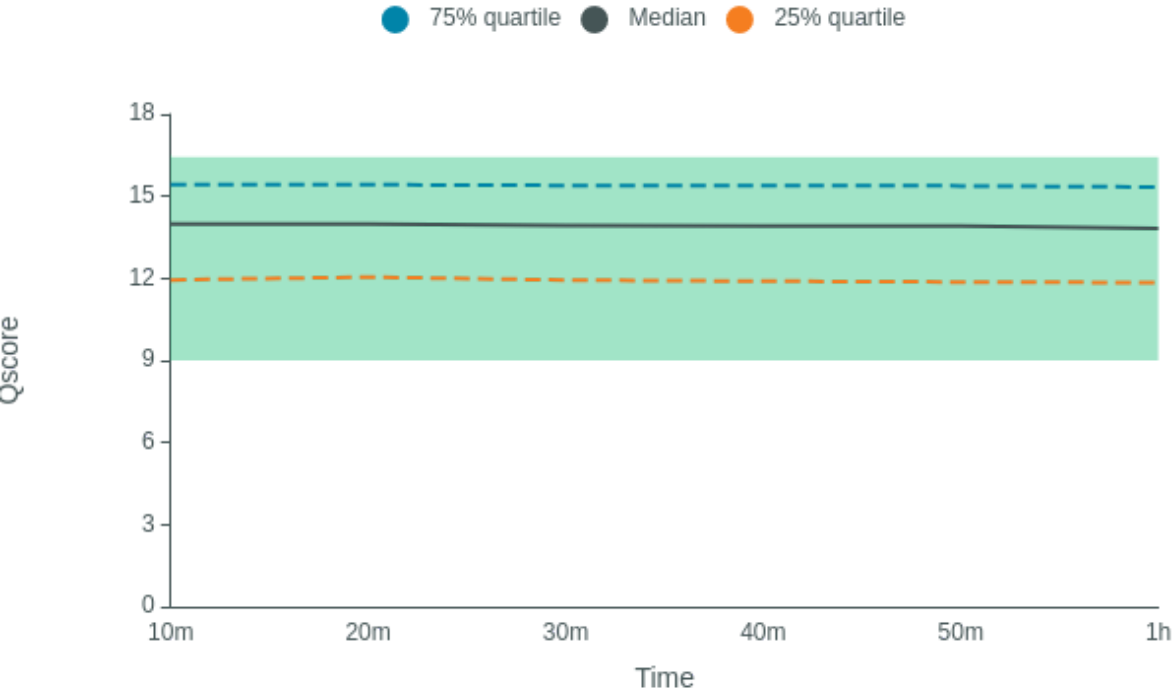
Bias Voltage History



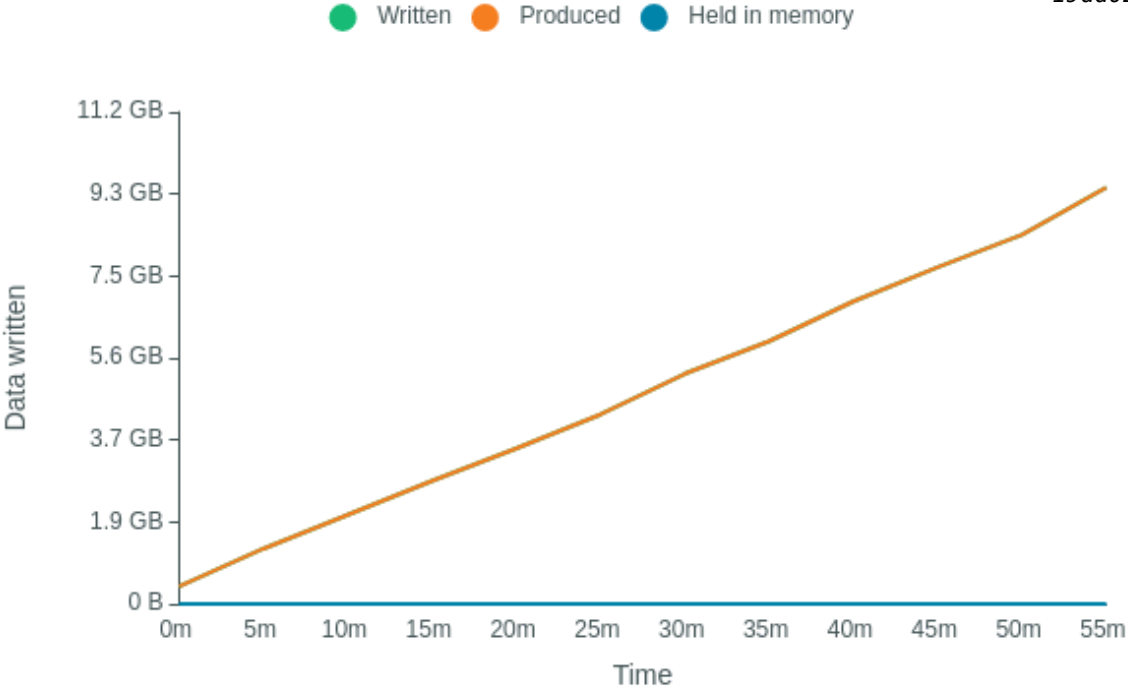
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13458 has found a total of 1374 pores. 495 pores available for immediate sequencing September 23, 15:21
- Performing Mux Scan September 23, 15:19
- Starting sequencing procedure September 23, 15:19
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 15:15