



Run Info

Host Name	MT-111233 (localhost)
Experiment Name	KIDH_01
Sample ID	C2020
Run ID	378c00ac-c642-4a1f-a167-524c471186dd
Flow Cell Id	FAP48412
Start Time	March 10, 21:48
Run Length	10h 21m

Run Summary

Reads Generated	2.74 M
Passed Bases	959.3 Mb
Failed Bases	250.63 Mb
Estimated Bases	1 Gb

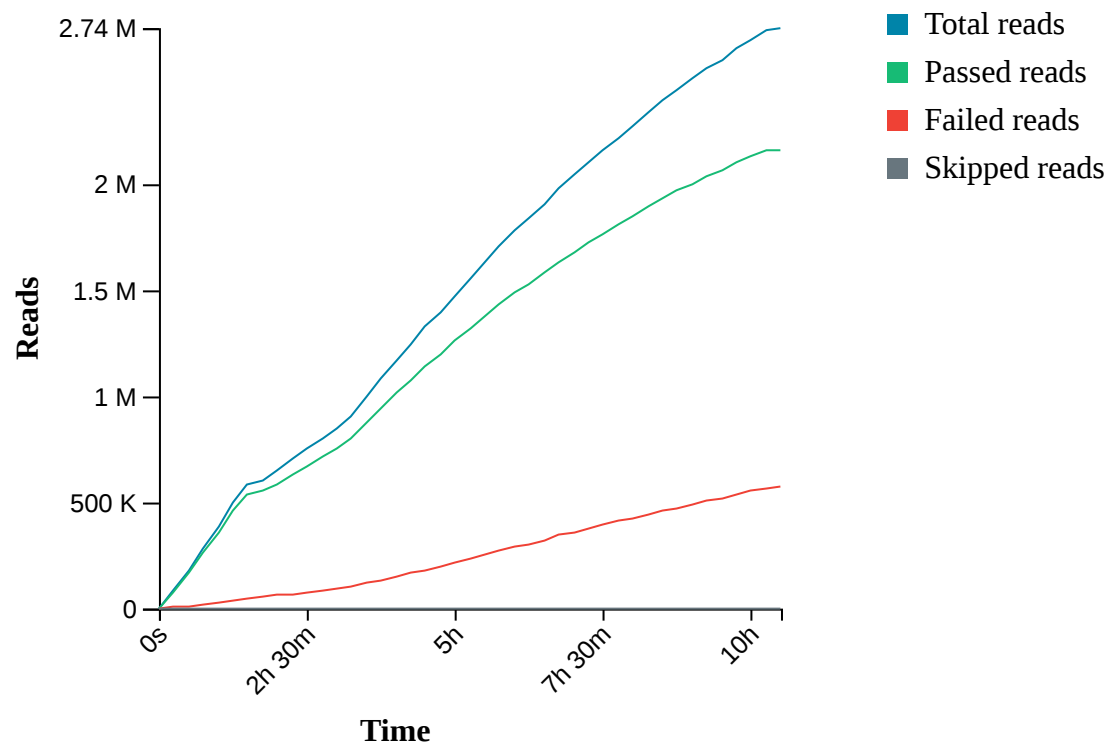
Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-LSK109
Initial Bias Voltage	-180 mV
FAST5 Output	Enabled
FASTQ Output	Enabled
BAM Output	Disabled
Active Channel Selection	Enabled
Basecalling	on
Specified Run Length	72 hours
FAST5 Reads per File	4000
FAST5 Output Options	zlib_compress,fastq,raw
FASTQ Reads per File	4000
Mux Scan Period	1 hour 30 minutes
Reserved Pores	0 %
Basecall Model	Fast basecalling
Read Filtering	min_qscore=7

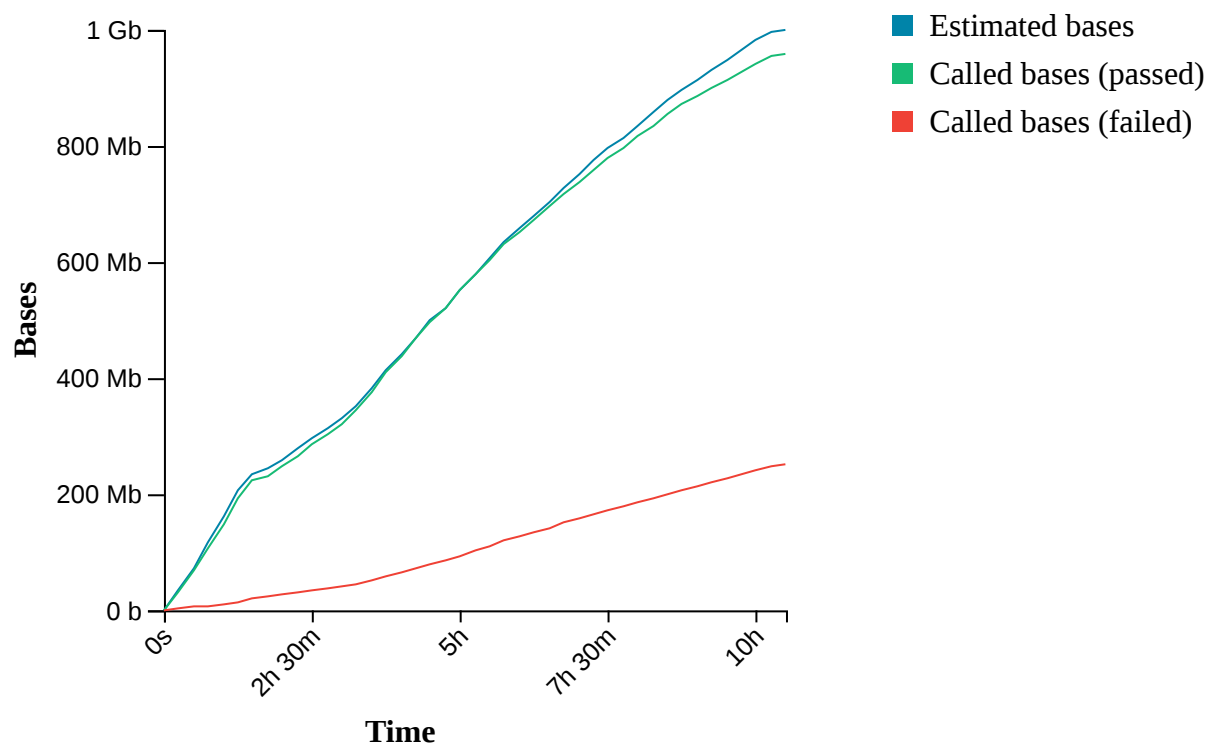
Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

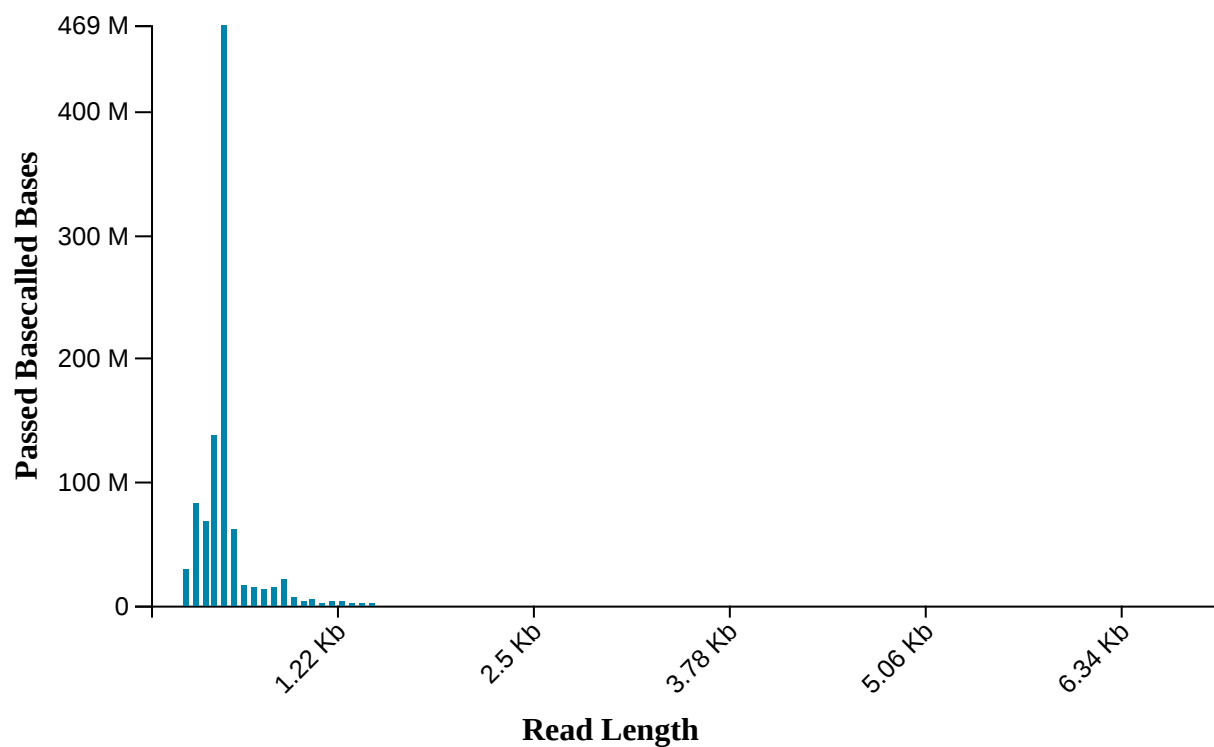


Cumulative Output Bases

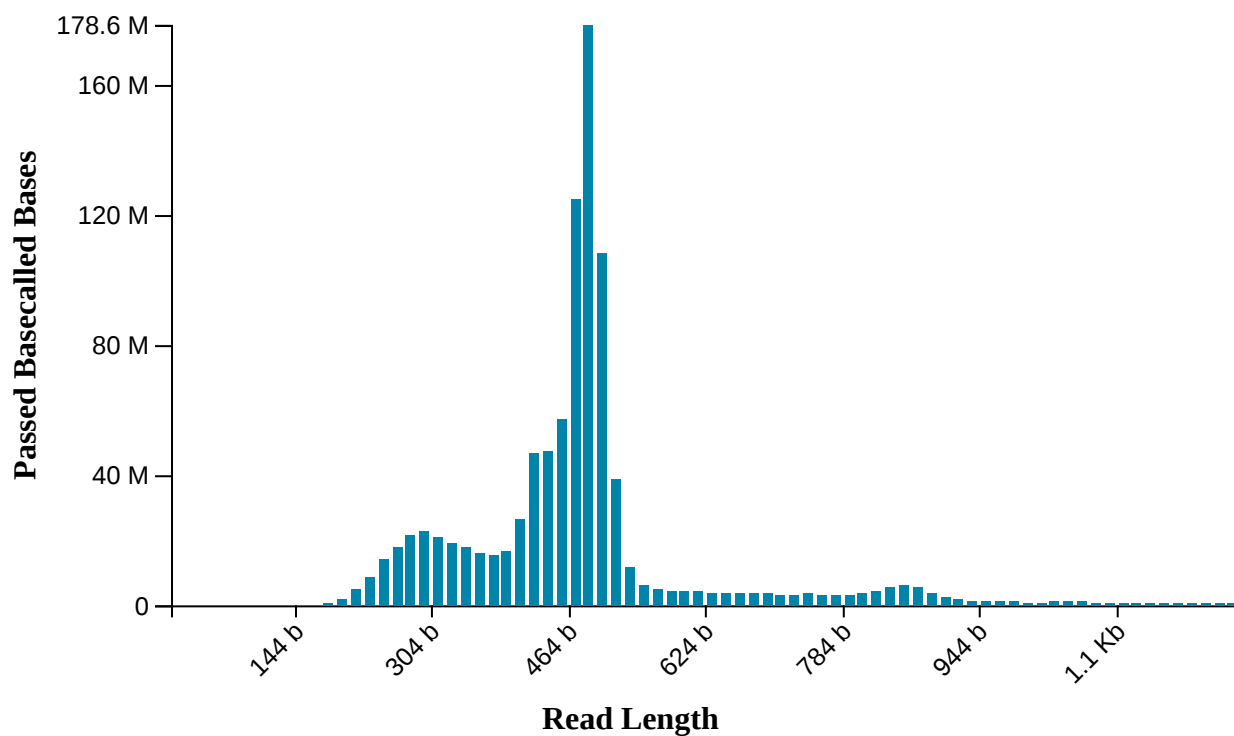


Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 477

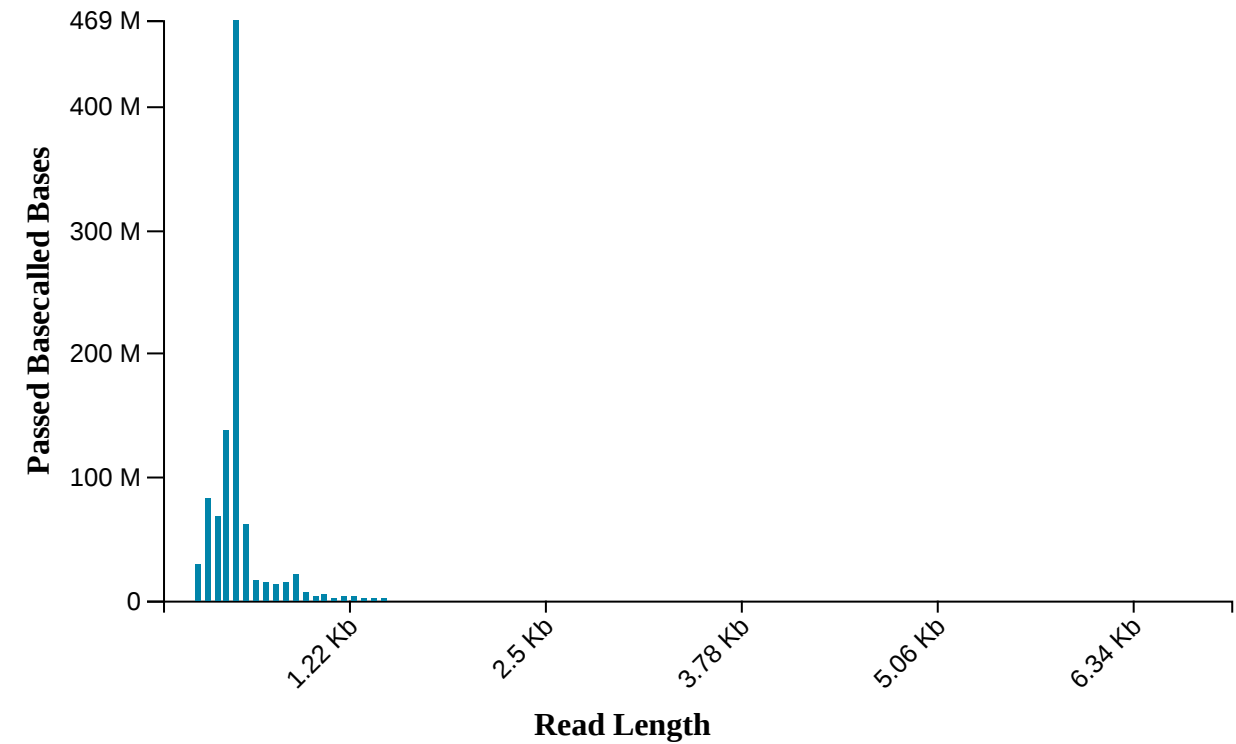
**Read Length Histogram Basecalled Bases - Outliers Discarded**

Estimated N50: 477



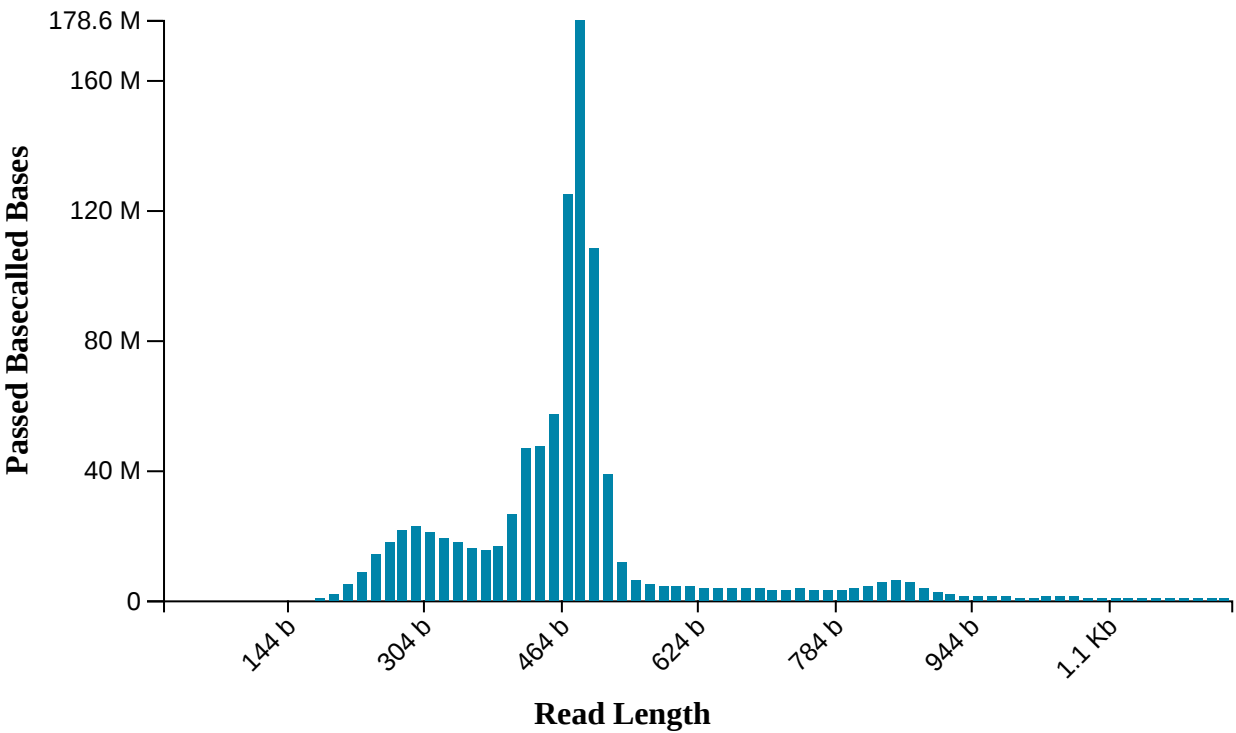
Read Length Histogram Estimated Bases

Estimated N50: 477

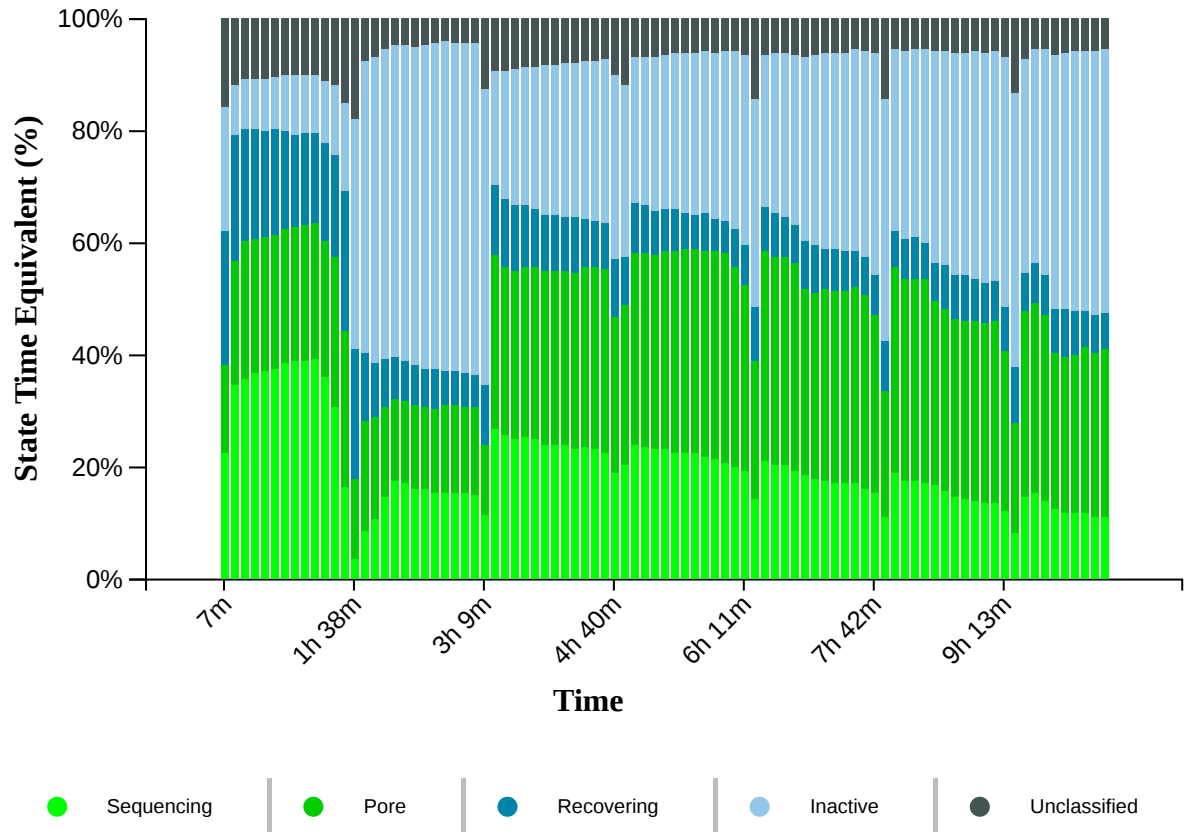


Read Length Histogram Basecalled Bases

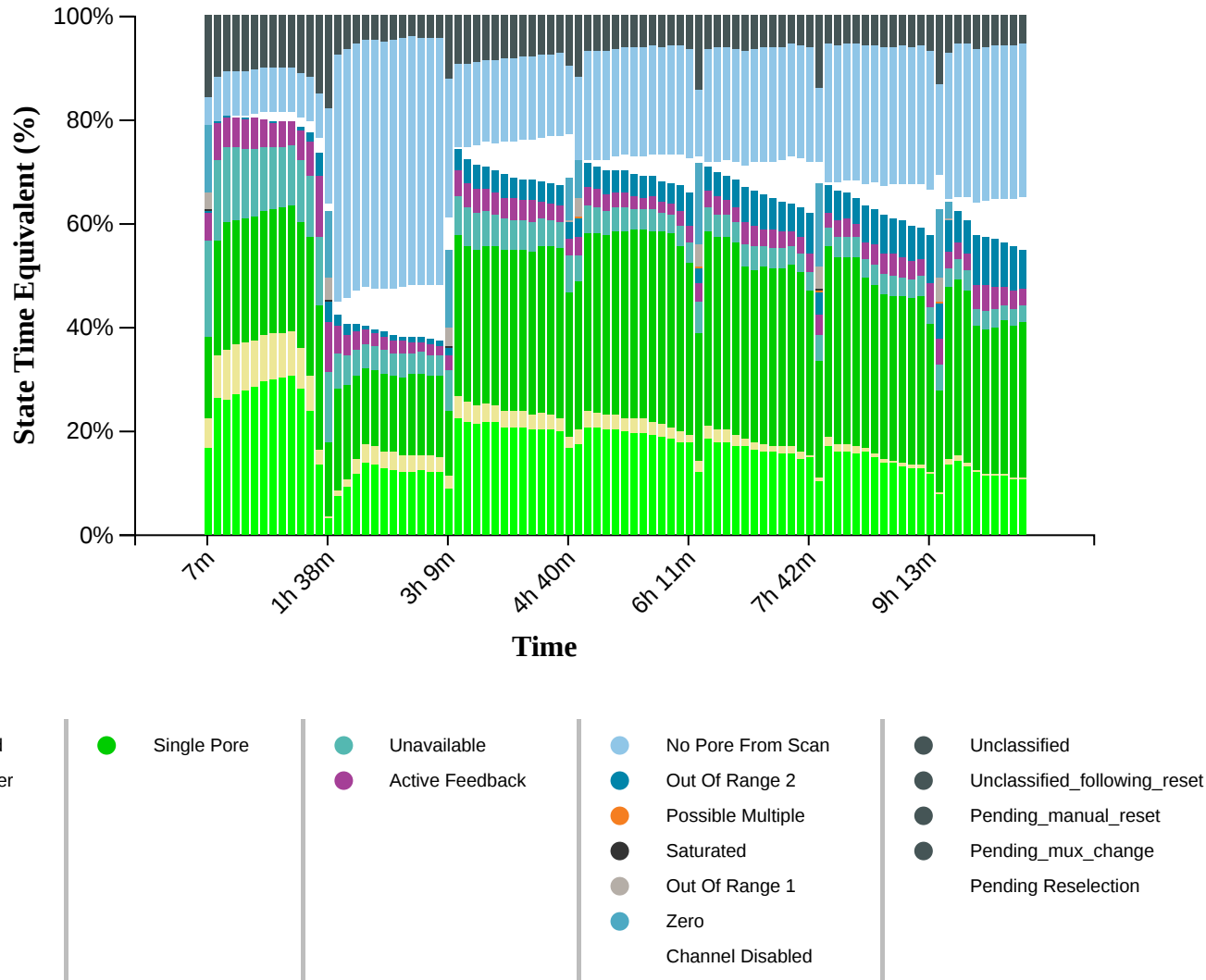
Estimated N50: 477



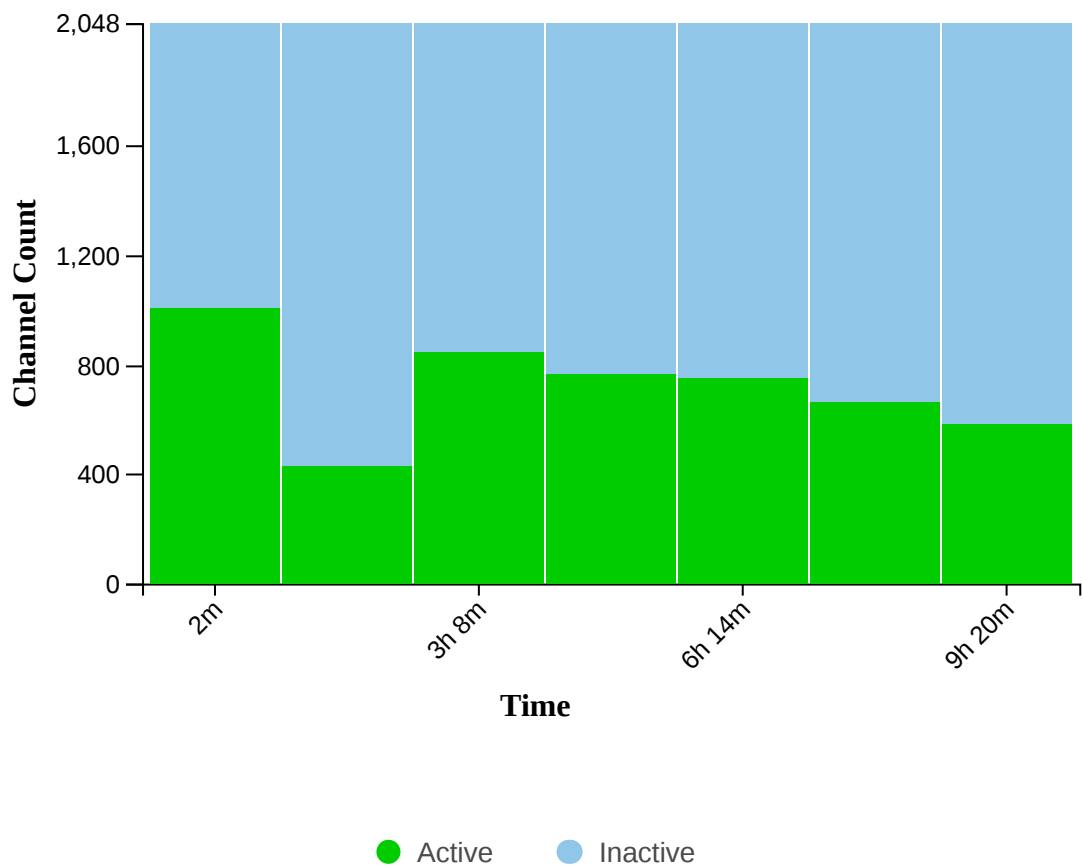
Duty Time Grouped



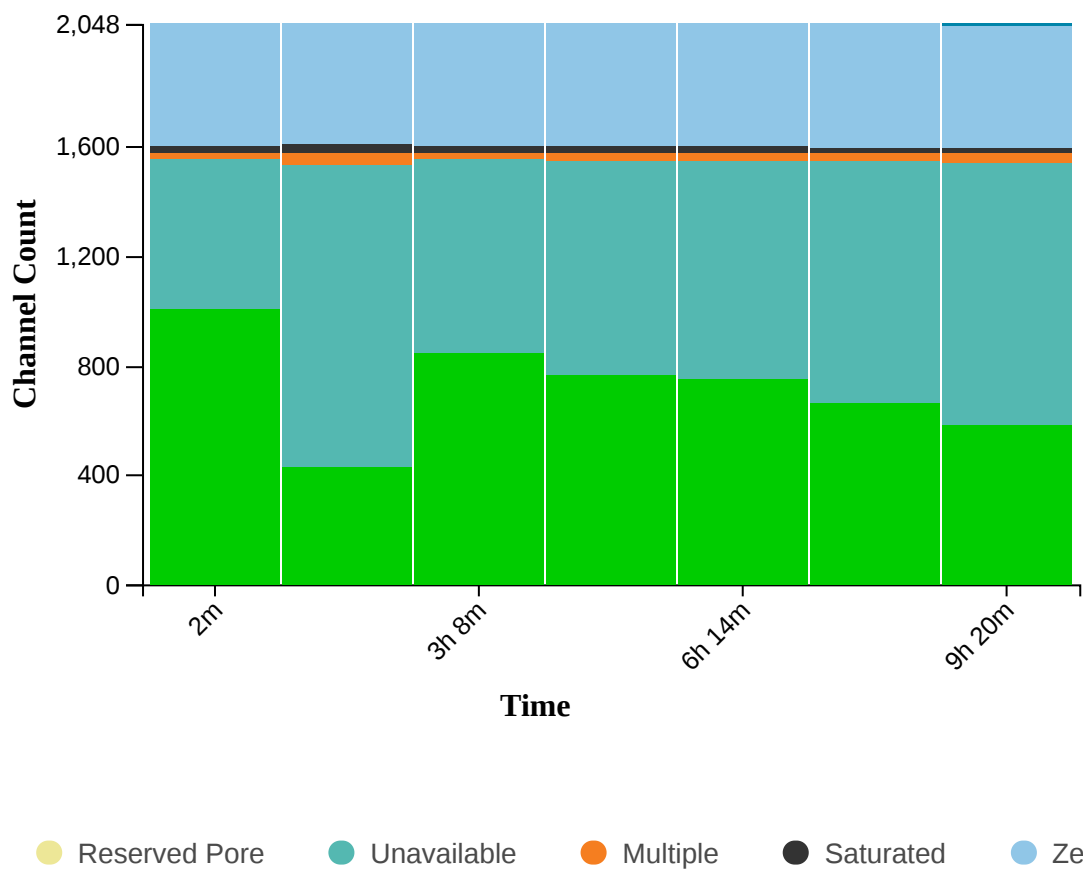
Duty time Categorised



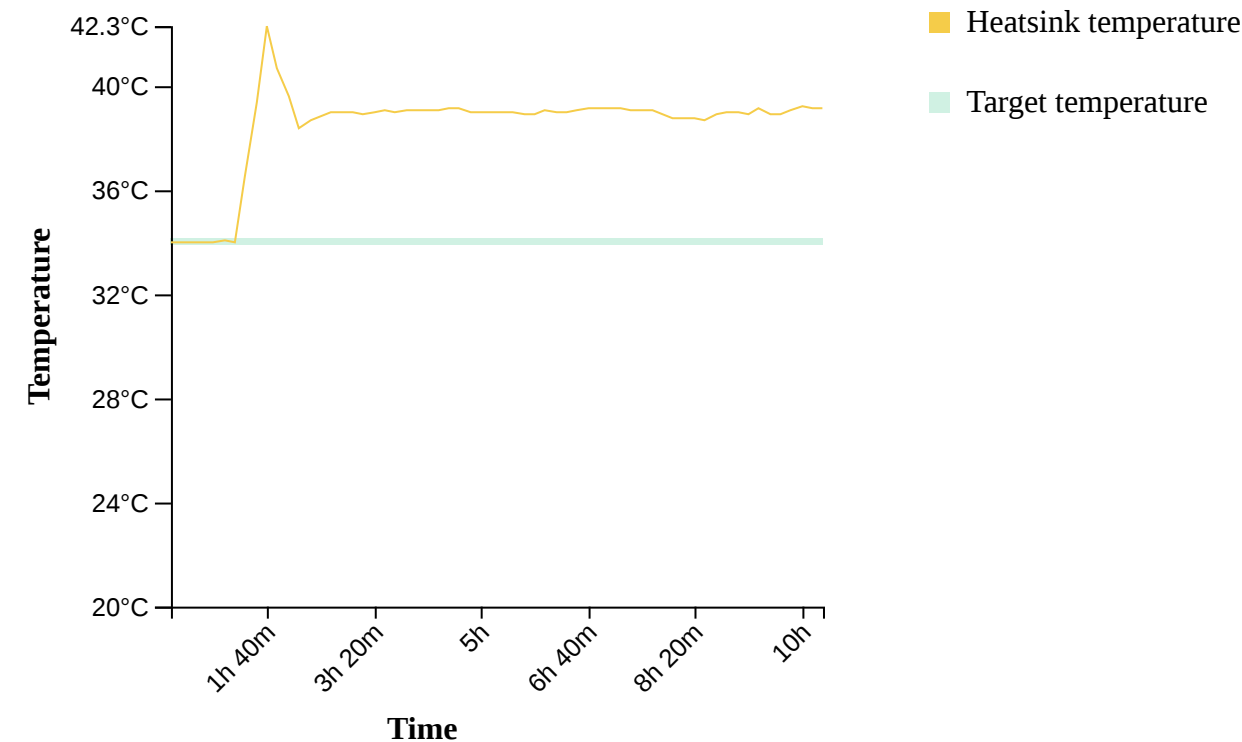
Mux Scan Grouped



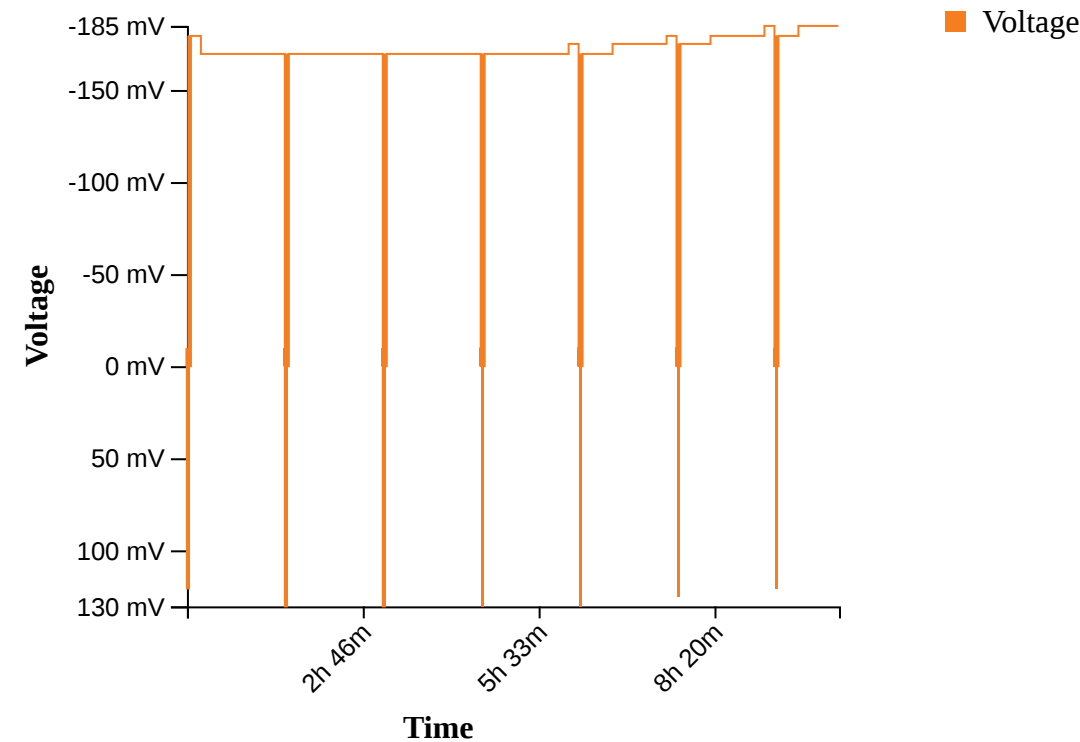
Mux Scan Categorised



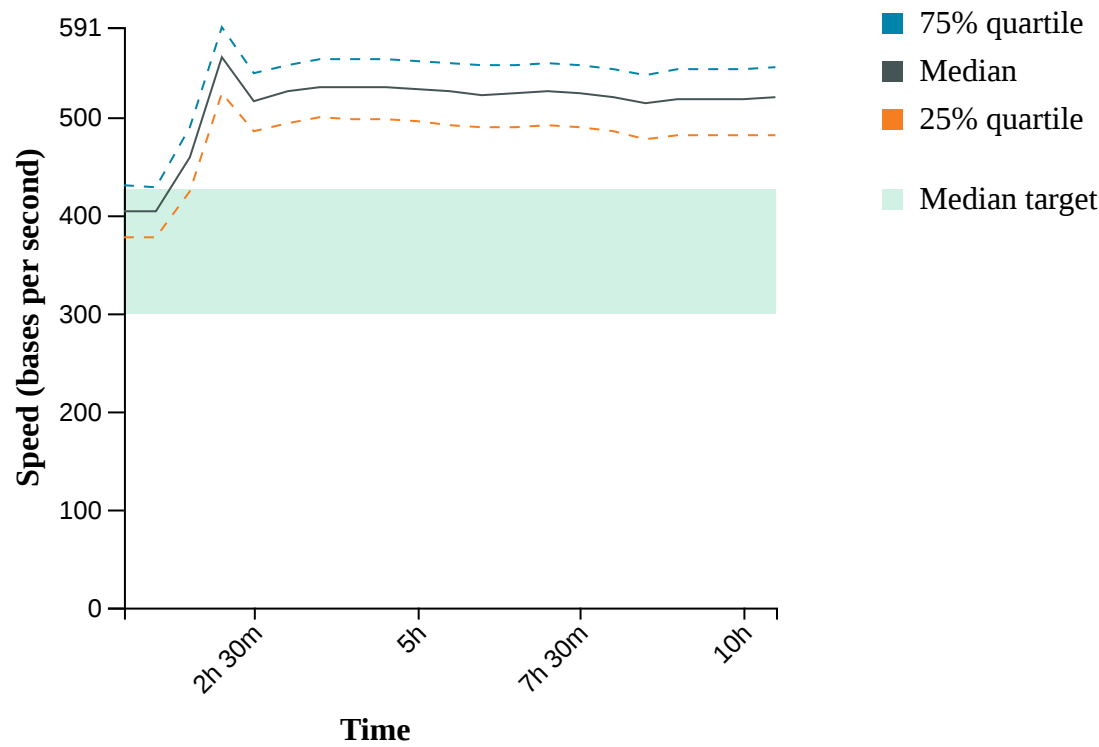
Temperature History.



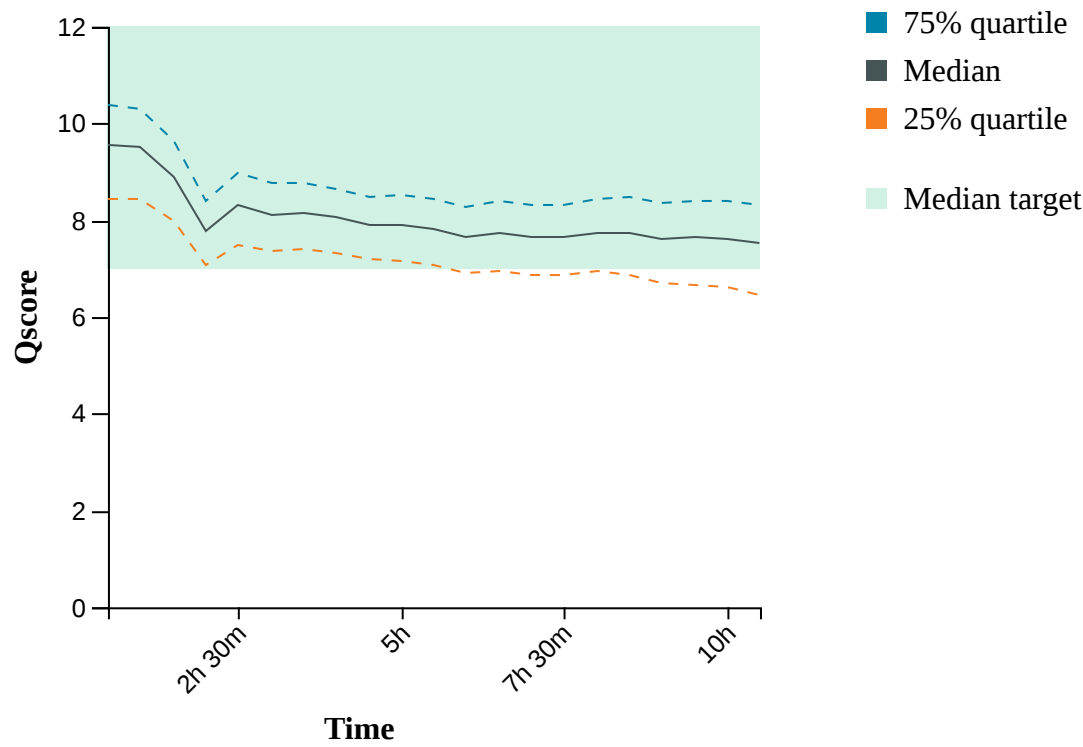
Bias Voltage History.



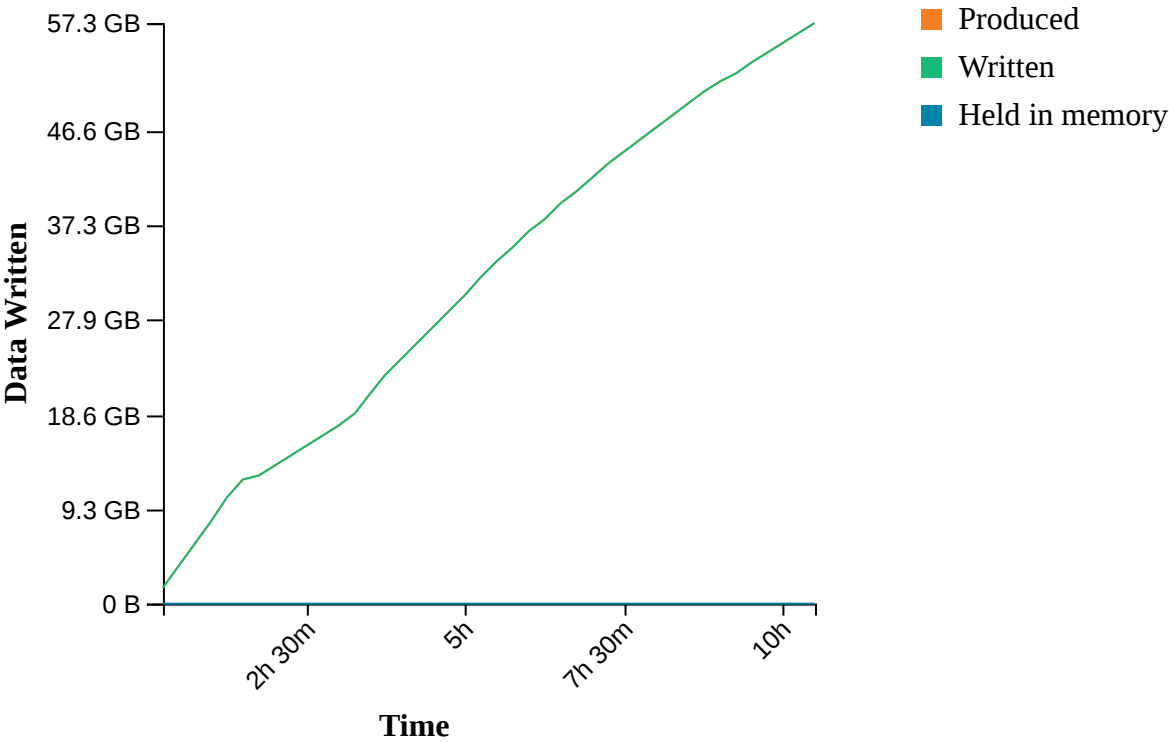
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAP48412 has found a total of 582 pores. 360 pores available for immediate sequencing March 11, 07:11
- Performing Mux Scan March 11, 07:08
- Mux scan for flow cell FAP48412 has found a total of 664 pores. 376 pores available for immediate sequencing March 11, 05:38
- Performing Mux Scan March 11, 05:36
- Mux scan for flow cell FAP48412 has found a total of 750 pores. 400 pores available for immediate sequencing March 11, 04:05
- Performing Mux Scan March 11, 04:03
- Mux scan for flow cell FAP48412 has found a total of 770 pores. 405 pores available for immediate sequencing March 11, 02:32
- Performing Mux Scan March 11, 02:30
- Mux scan for flow cell FAP48412 has found a total of 848 pores. 430 pores available for immediate sequencing March 11, 01:00
- Performing Mux Scan March 11, 00:57
- Mux scan for flow cell FAP48412 has found a total of 434 pores. 268 pores available for immediate sequencing March 10, 23:27
- Performing Mux Scan March 10, 23:24
- Mux scan for flow cell FAP48412 has found a total of 1010 pores. 468 pores available for immediate sequencing March 10, 21:54
- Performing Mux Scan March 10, 21:51
- Starting sequencing procedure March 10, 21:51
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C March 10, 21:48