



Run Info

Host Name	GXB03020 (localhost)
Experiment Name	ReadUntil_38kbp_HightoLow_Mm_15042021
Sample ID	ReadUntil_38kbp_HightoLow_Mm_15042021
Run ID	bfece120-d529-4631-ae4-11e2e6535009
Flow Cell Id	FAP21636
Start Time	April 15, 11:27
Run Length	1h 50m

Run Summary

Reads Generated	106.25 K
Passed Bases	670.73 Mb
Failed Bases	24.33 Mb
Estimated Bases	697.53 Mb

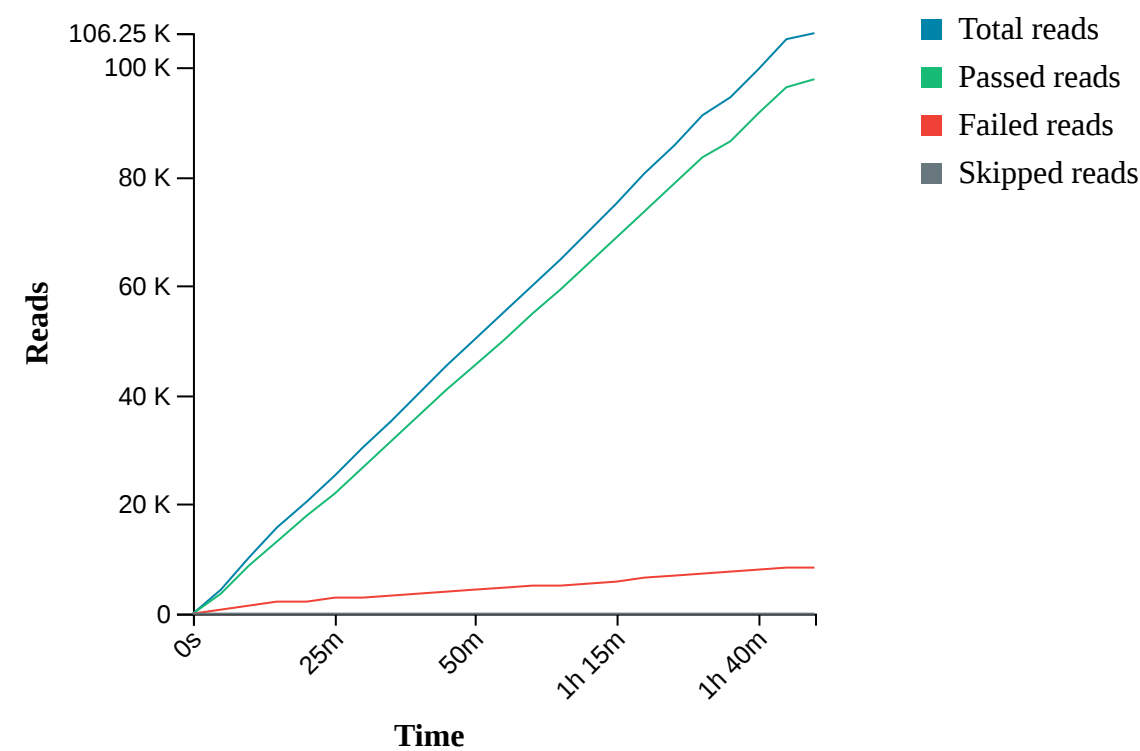
Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-LSK109
Initial Bias Voltage	-180 mV
FAST5 Output	Enabled
FASTQ Output	Enabled
BAM Output	Enabled
Active Channel Selection	Enabled
Basecalling	on
Specified Run Length	72 hours
Read Until	reference_files=[["/data/M_morganii_ref.fasta"],filter_type=enrich,first_channel=1,last_channel=256
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	High-accuracy basecalling
Alignment	reference_files=[["/data/the7references.fasta"]
Read Filtering	min_qscore=7

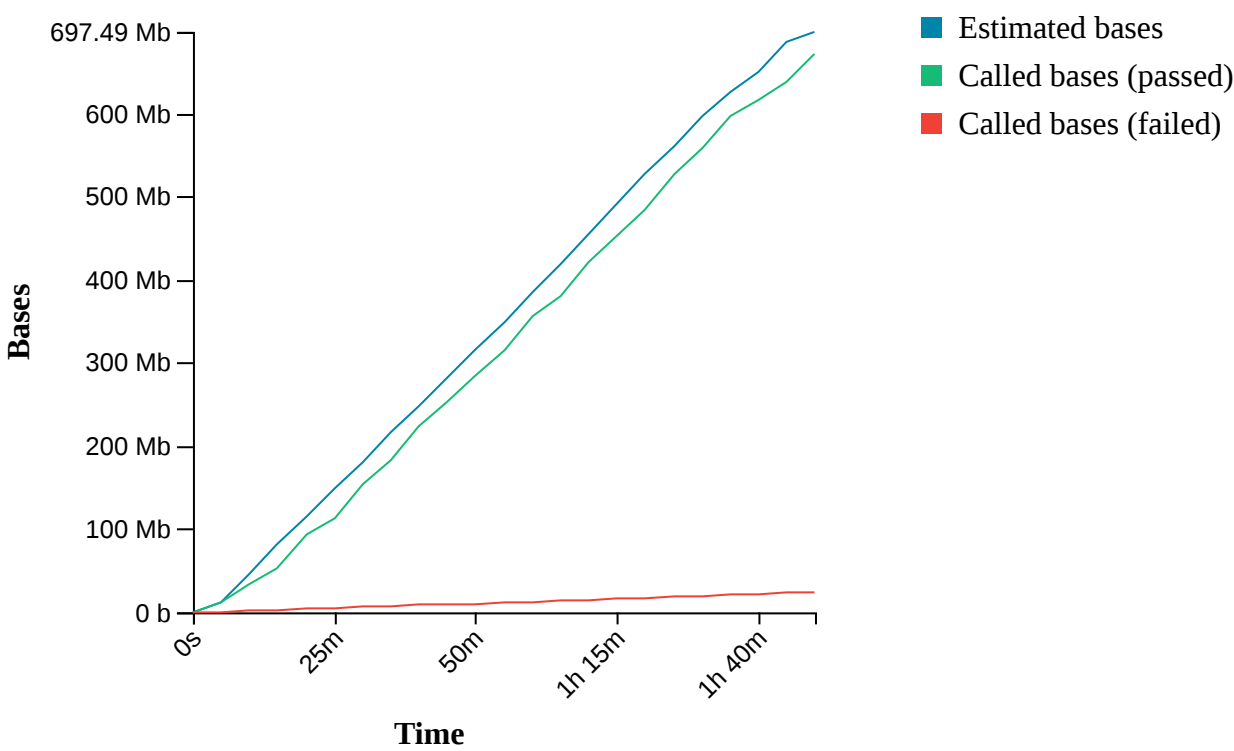
Versions

MinKNOW	21.02.5
MinKNOW Core	4.2.5
Bream	6.1.10
Guppy	4.3.4

Cumulative Output Reads

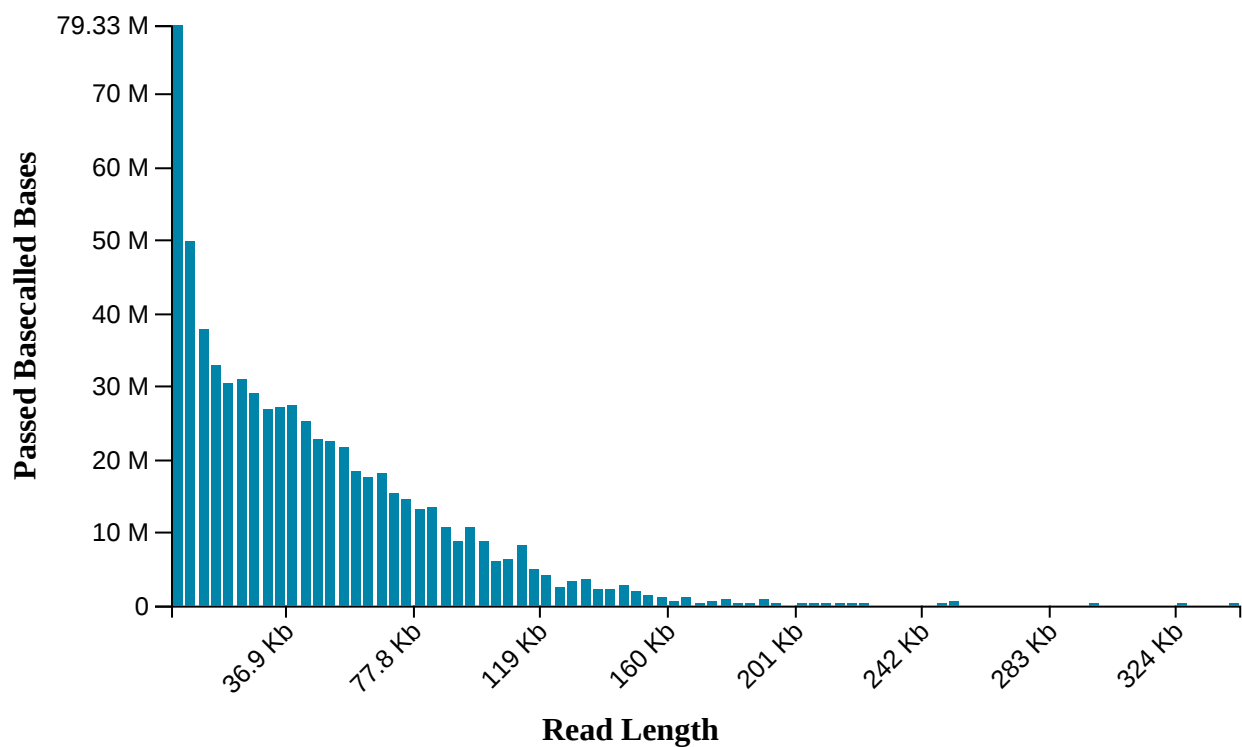


Cumulative Output Bases



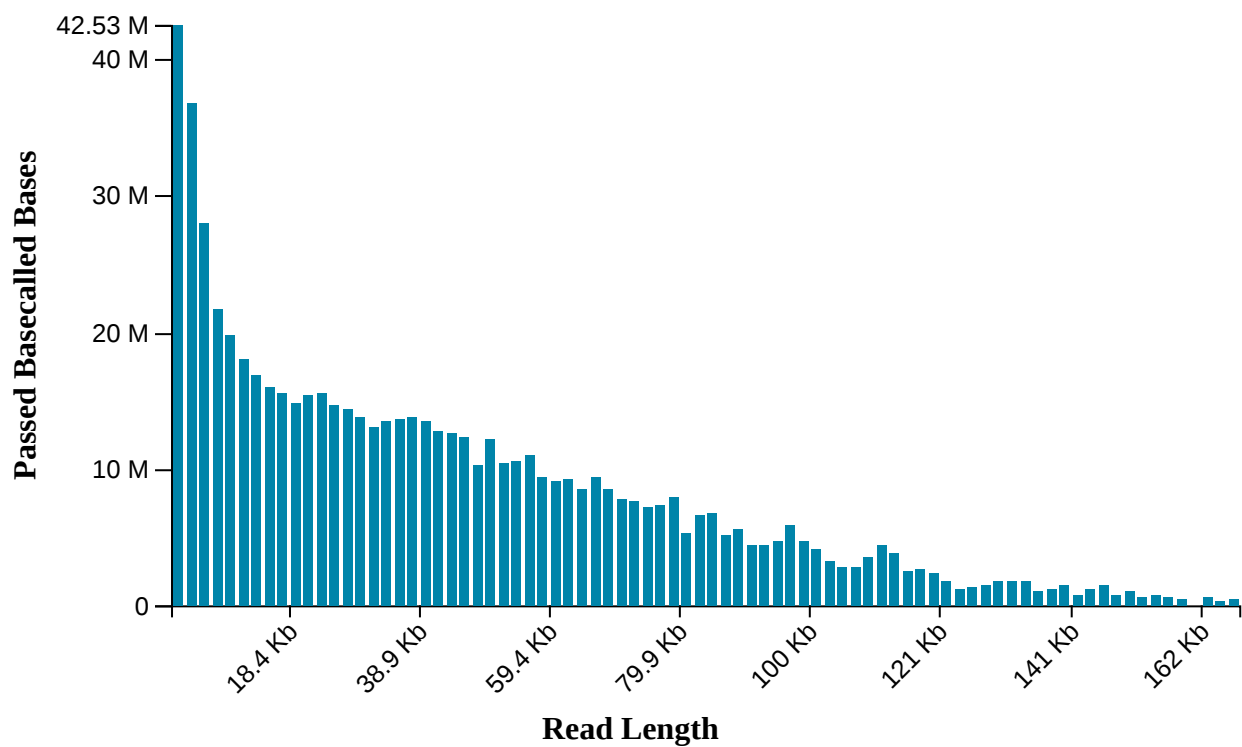
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 35.66 K



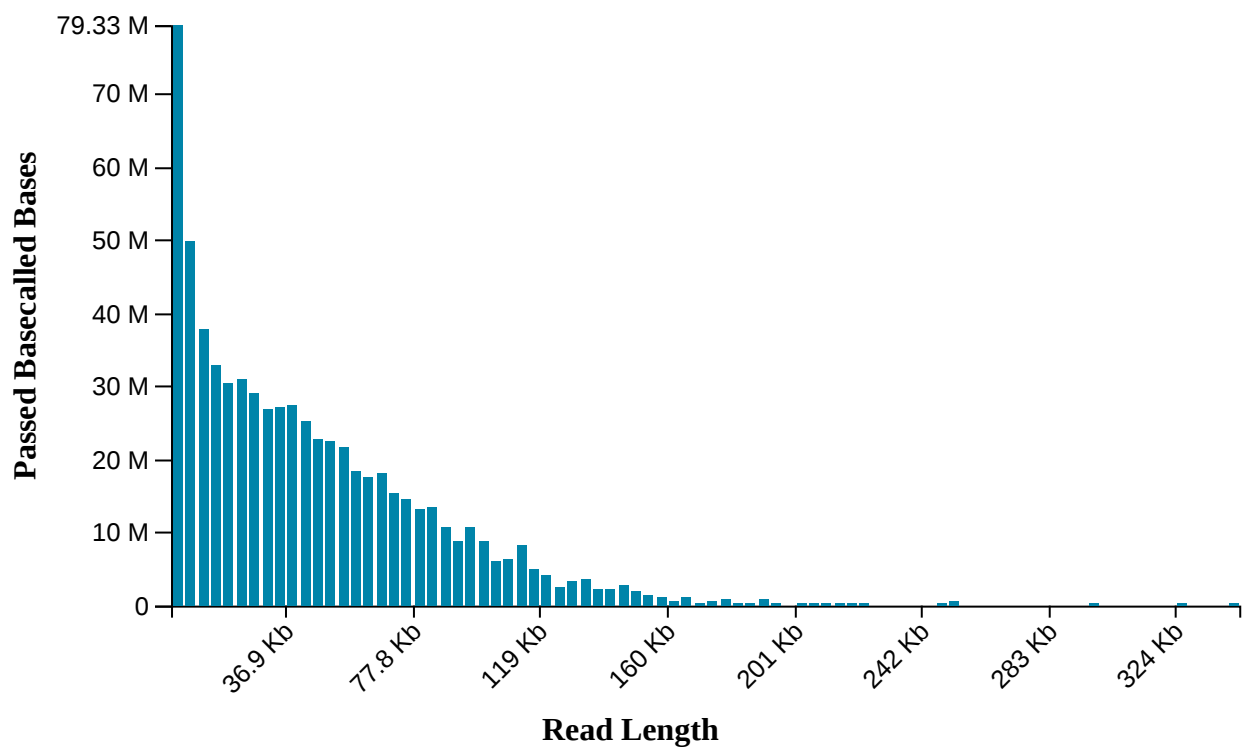
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 35.13 K



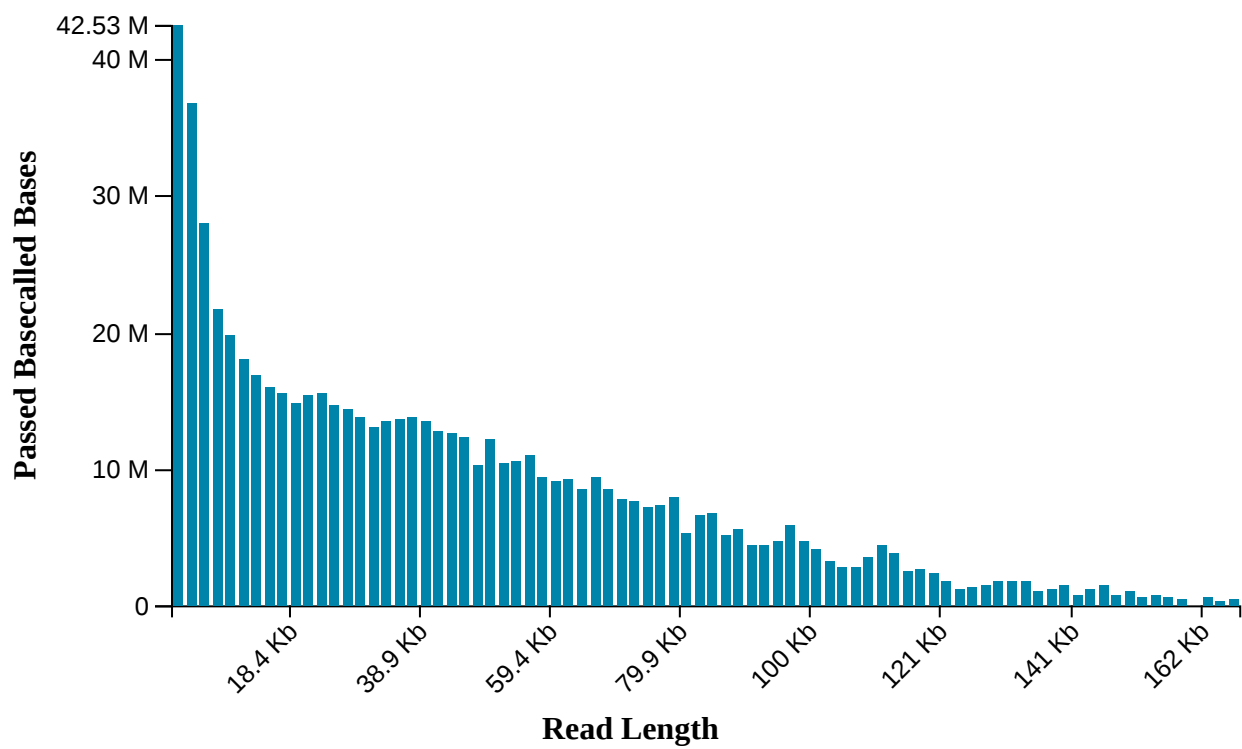
Read Length Histogram Estimated Bases

Estimated N50: 35.66 K

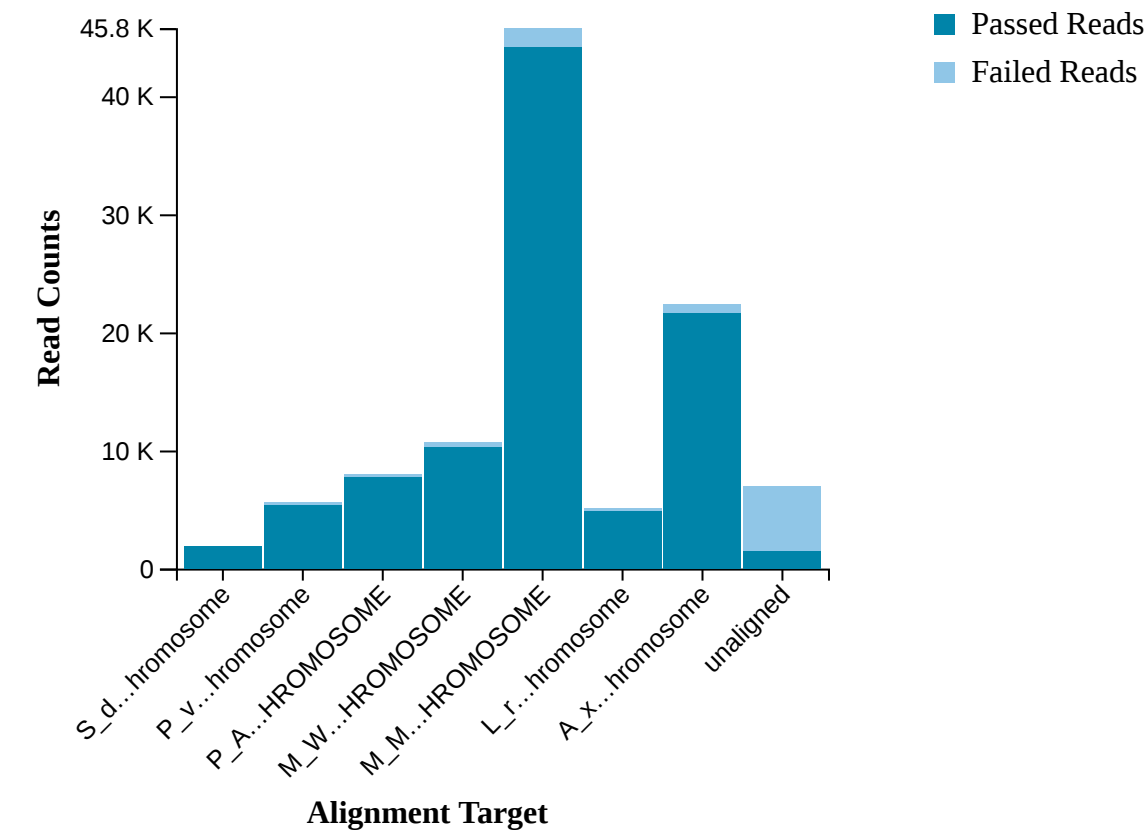


Read Length Histogram Basecalled Bases

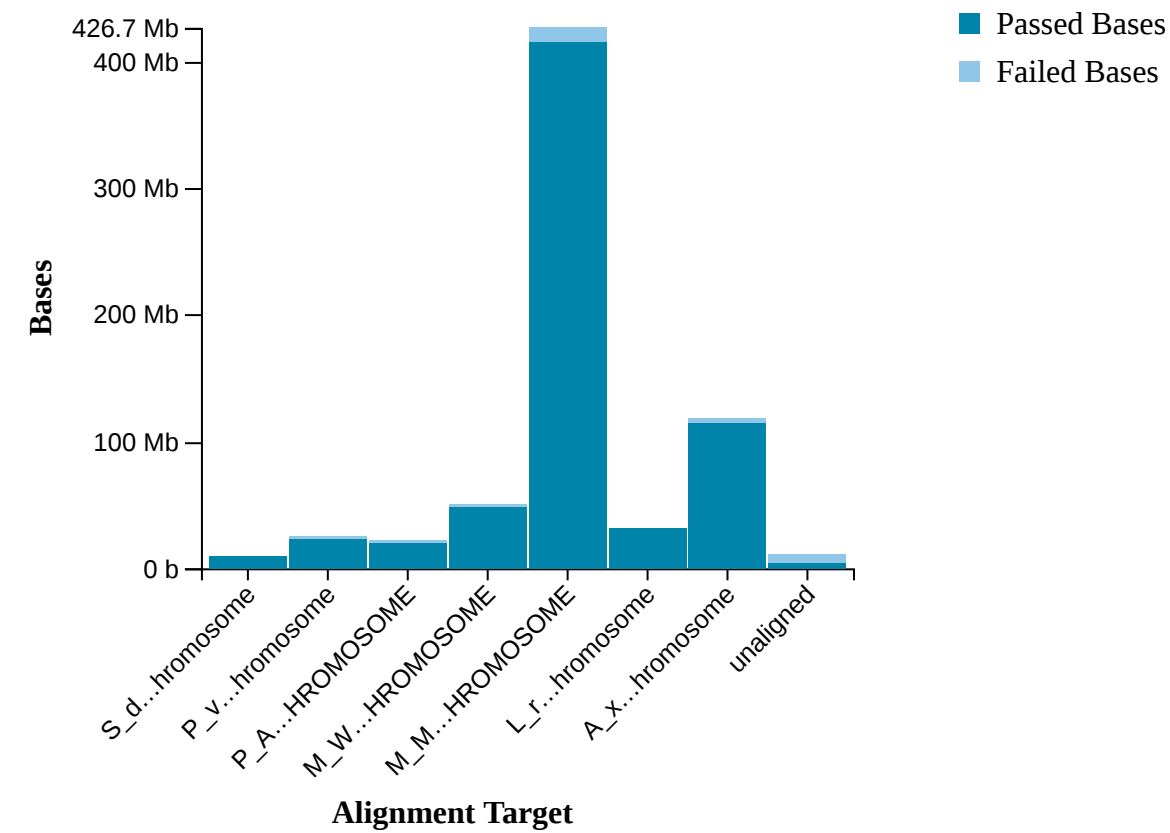
Estimated N50: 35.13 K



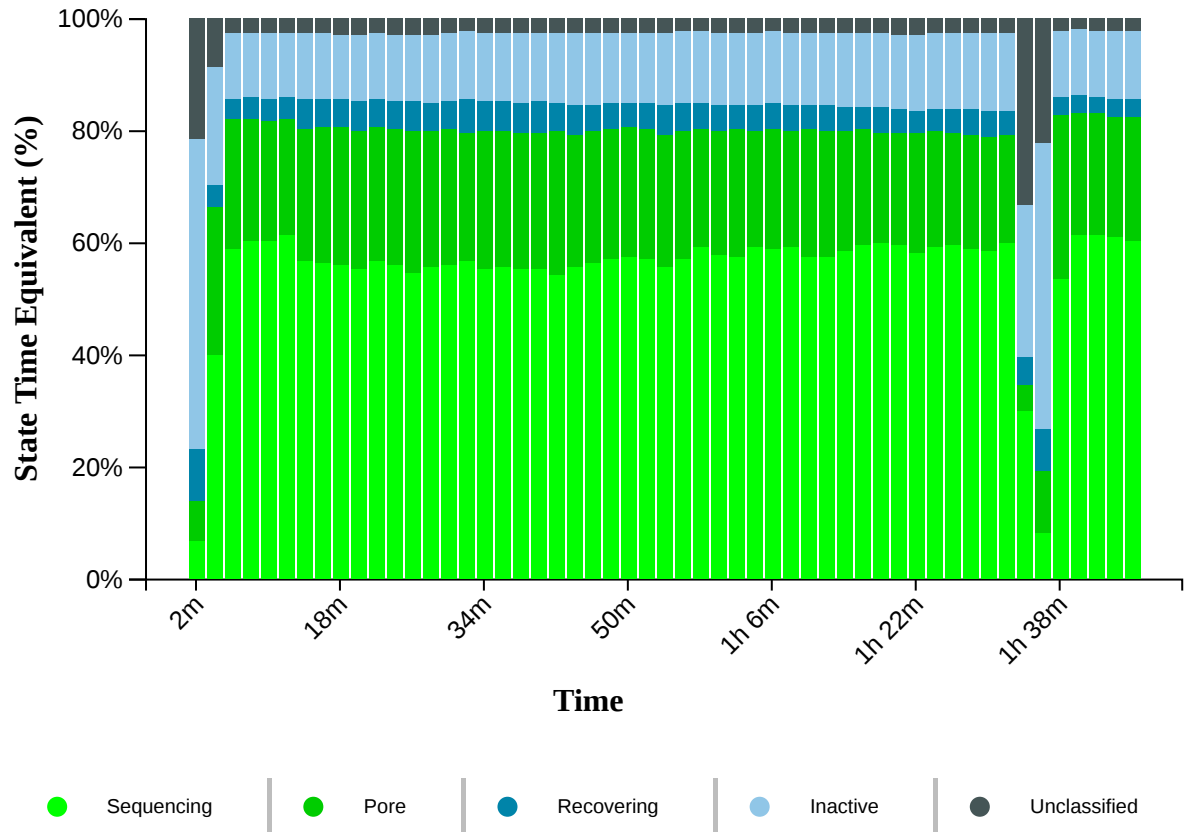
Alignment Target Hits (reads)



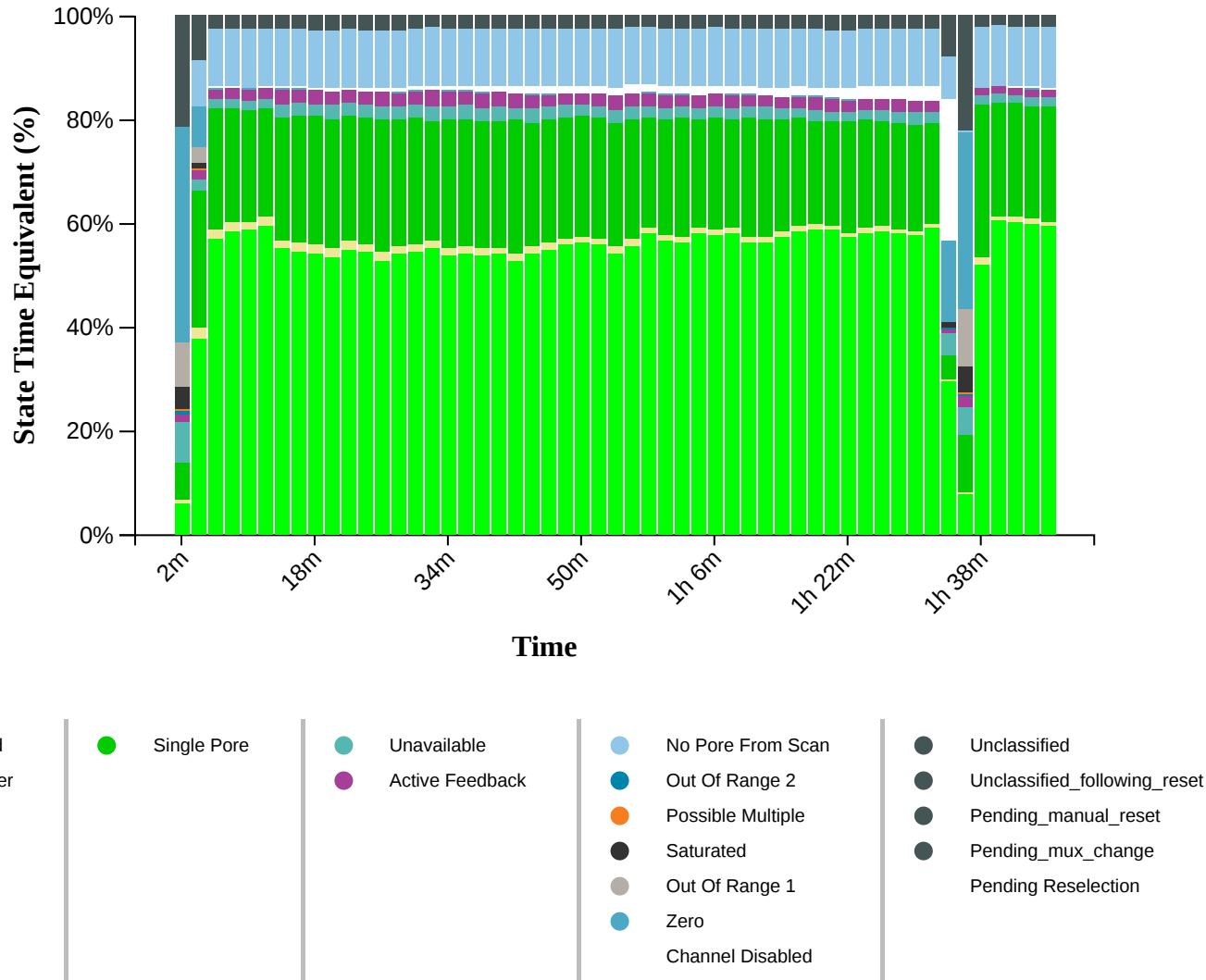
Alignment Target Hits (bases)



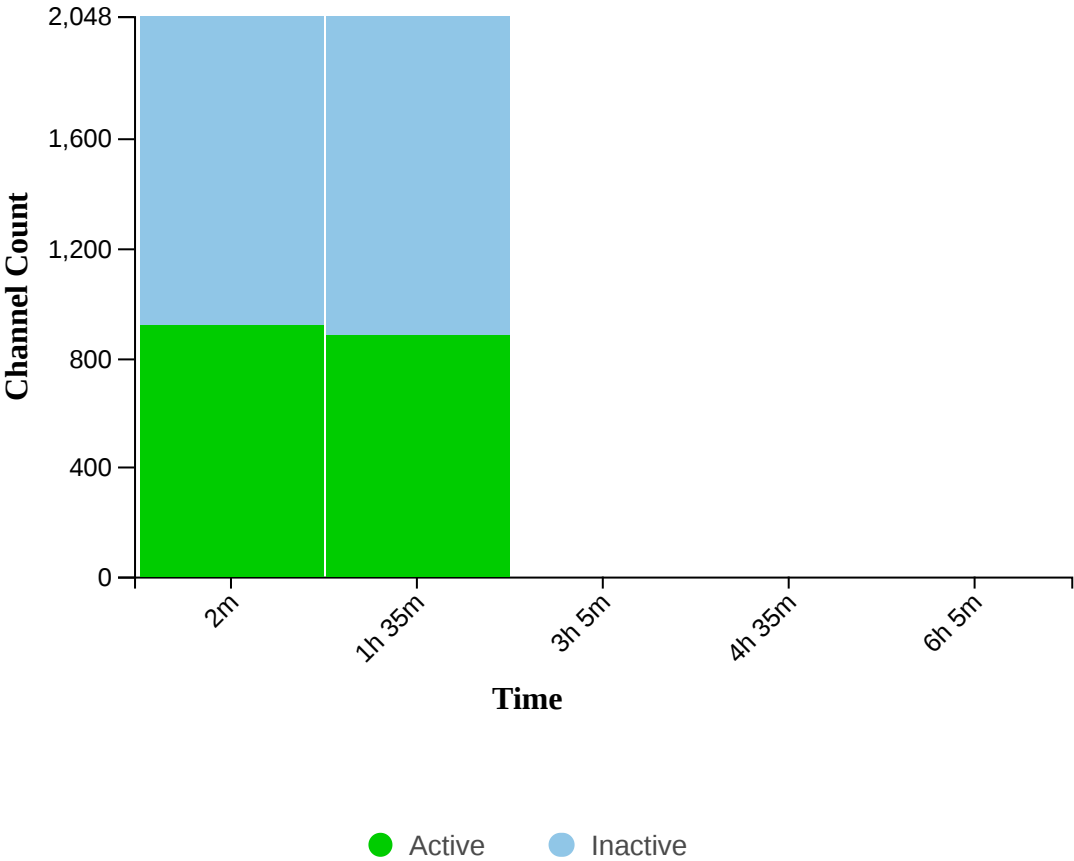
Duty Time Grouped



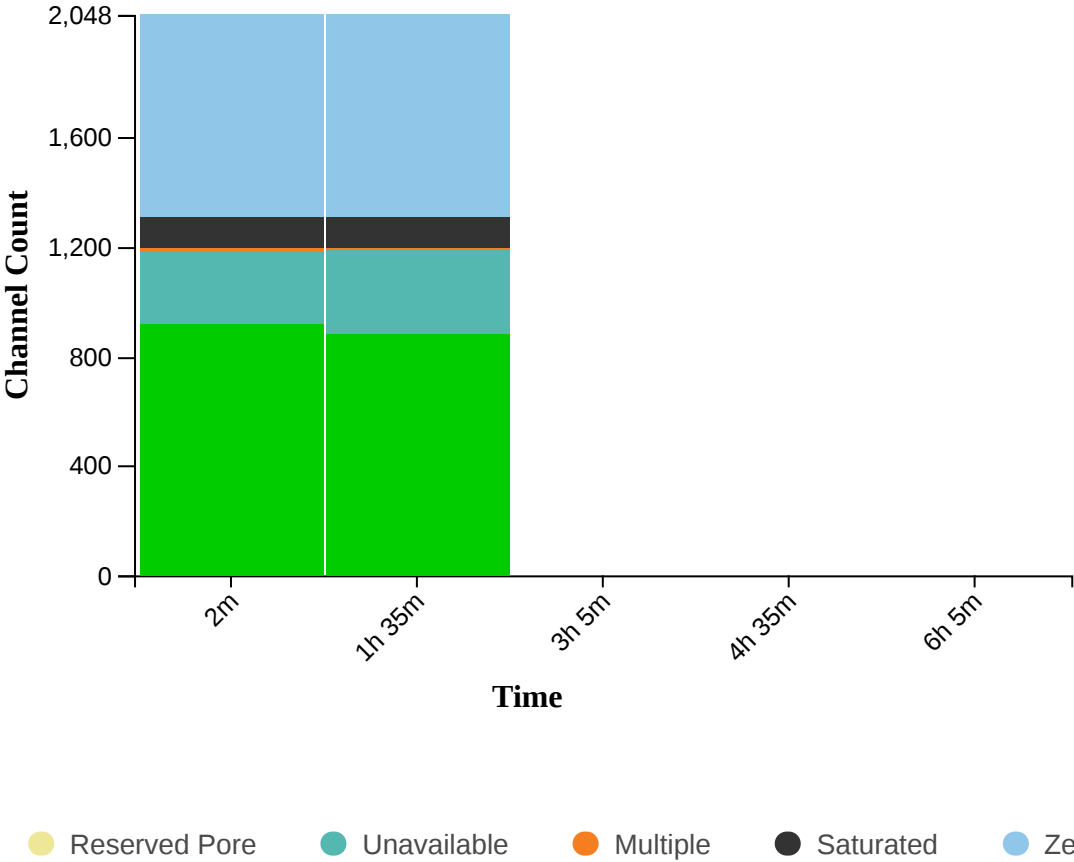
Duty time Categorised



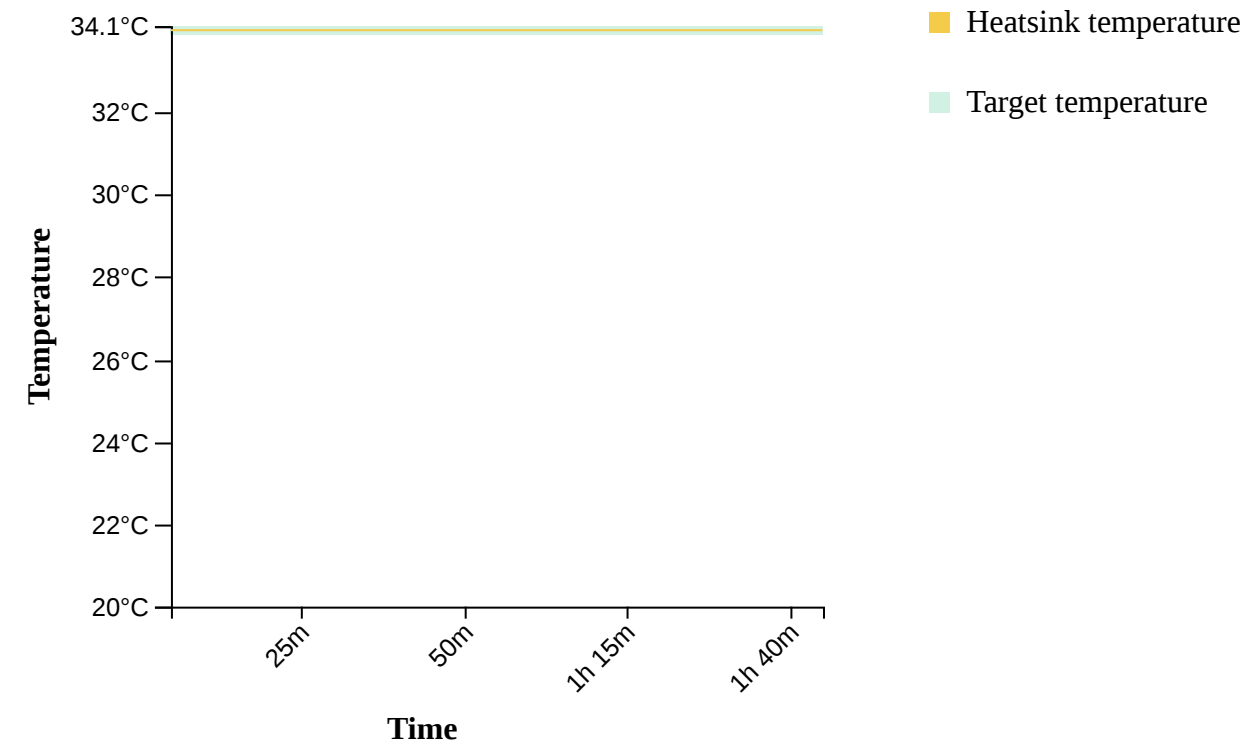
Mux Scan Grouped



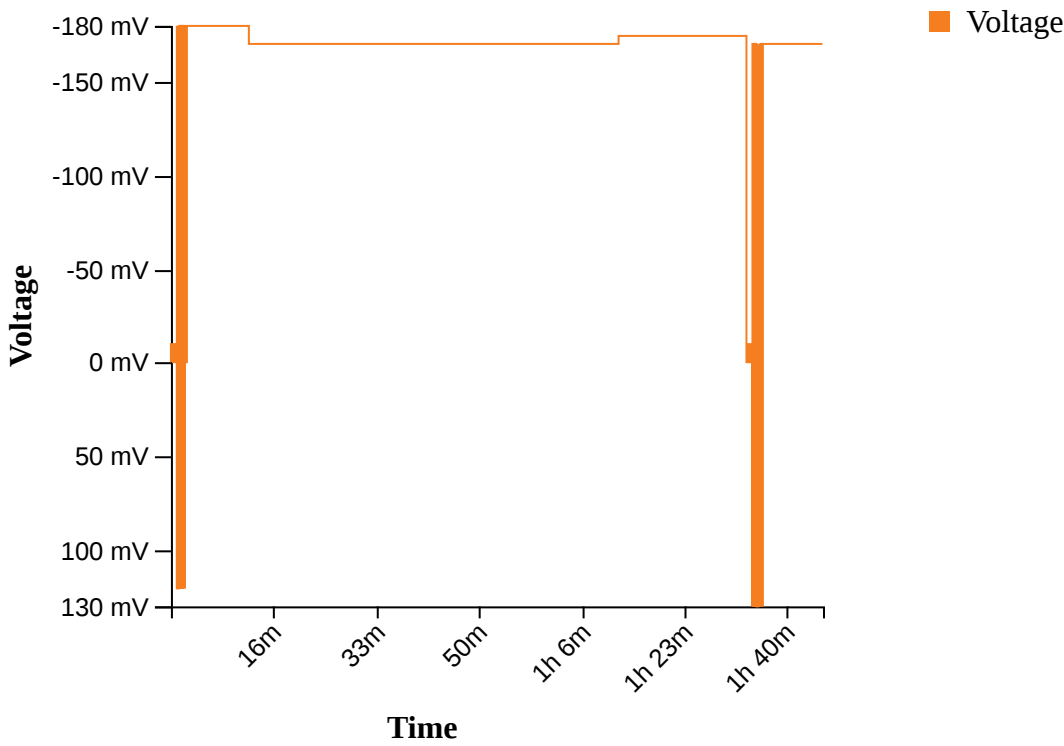
Mux Scan Categorised



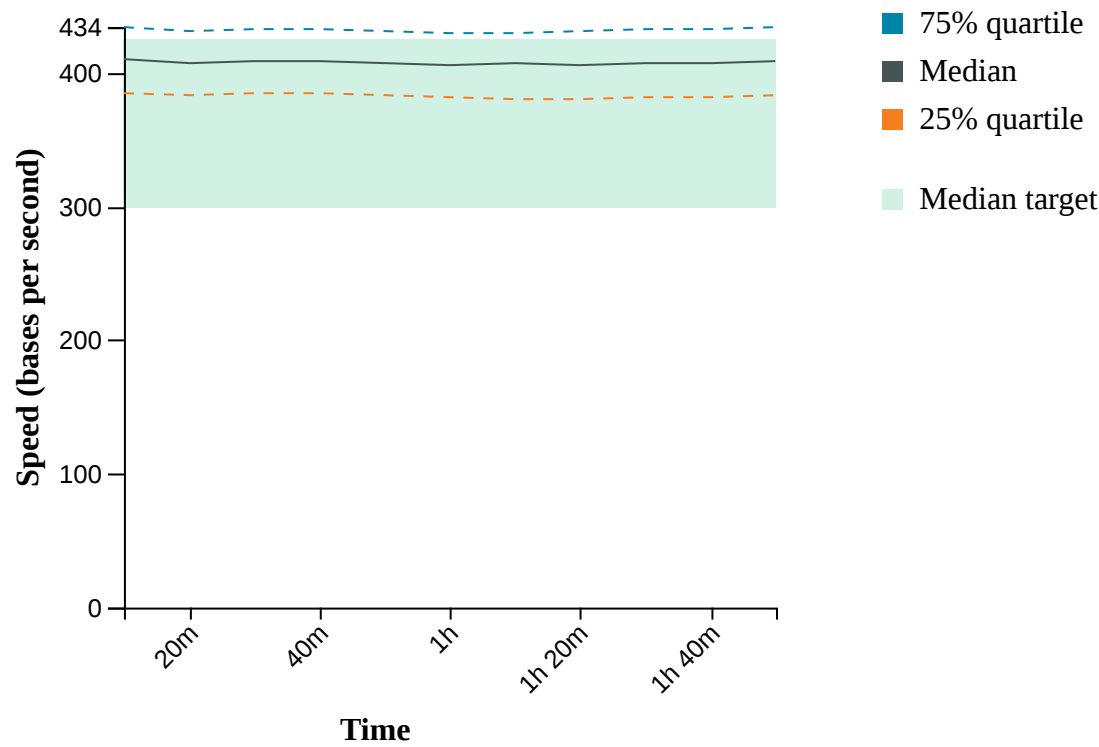
Temperature History.



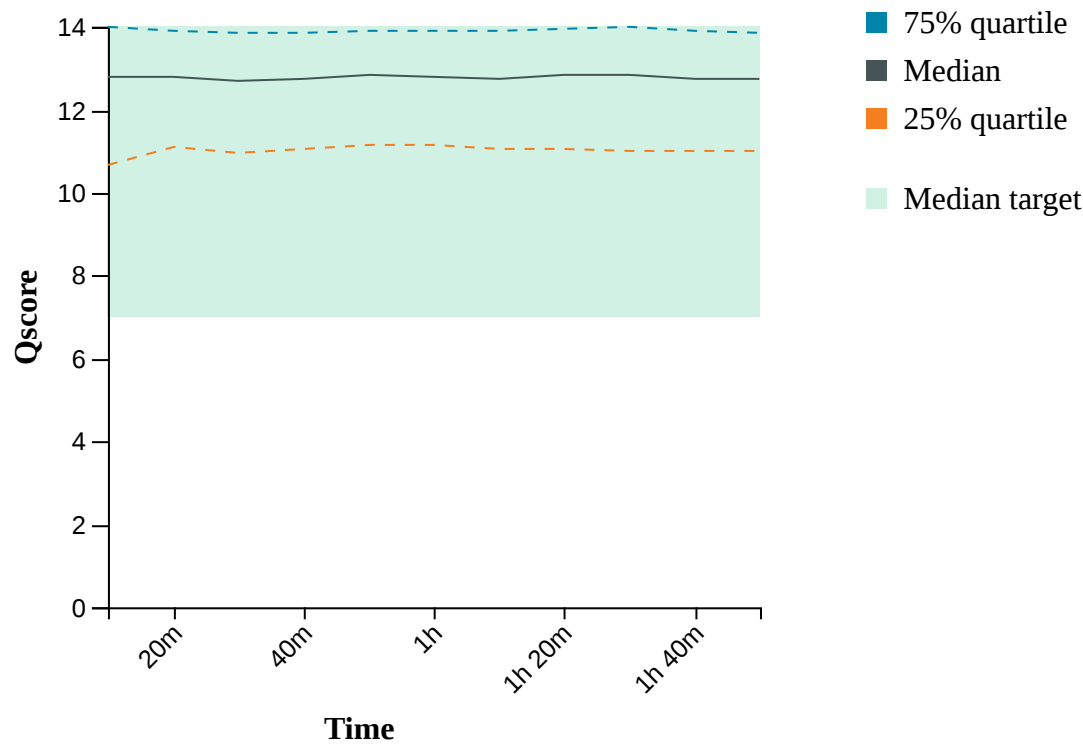
Bias Voltage History.



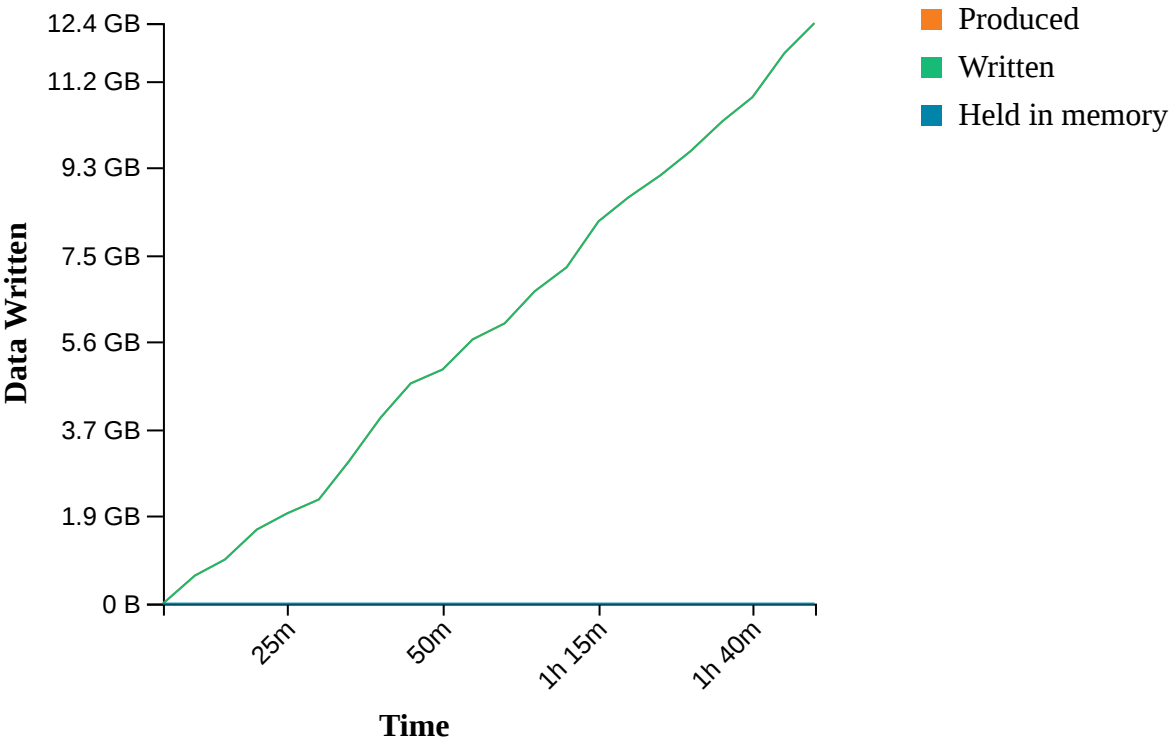
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAP21636 has found a total of 888 pores. 453 pores available for immediate sequencing April 15, 13:08
- Performing Mux Scan April 15, 13:06
- Mux scan for flow cell FAP21636 has found a total of 918 pores. 455 pores available for immediate sequencing April 15, 11:35
- Performing Mux Scan April 15, 11:32
- Starting sequencing procedure April 15, 11:32
- Failed to reach 34.0°C within 300 seconds(with 0.1 tolerance). The experiment will continue anyway. April 15, 11:32
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 11:27