



Run Info

Host Name	GXB01190 (localhost)
Experiment Name	EIMock_6kbp_MmorganiiEnrich_04012021
Sample ID	EIMock_6kbp_MmorganiiEnrich_04012021
Run ID	669926d9-6173-43f1-80b3-df108d4bba21
Flow Cell Id	FAO54786
Start Time	January 4, 13:00
Run Length	1h 0m

Run Summary

Reads Generated	97.27 K
Passed Bases	133.72 Mb
Failed Bases	5.59 Mb
Estimated Bases	142.9 Mb

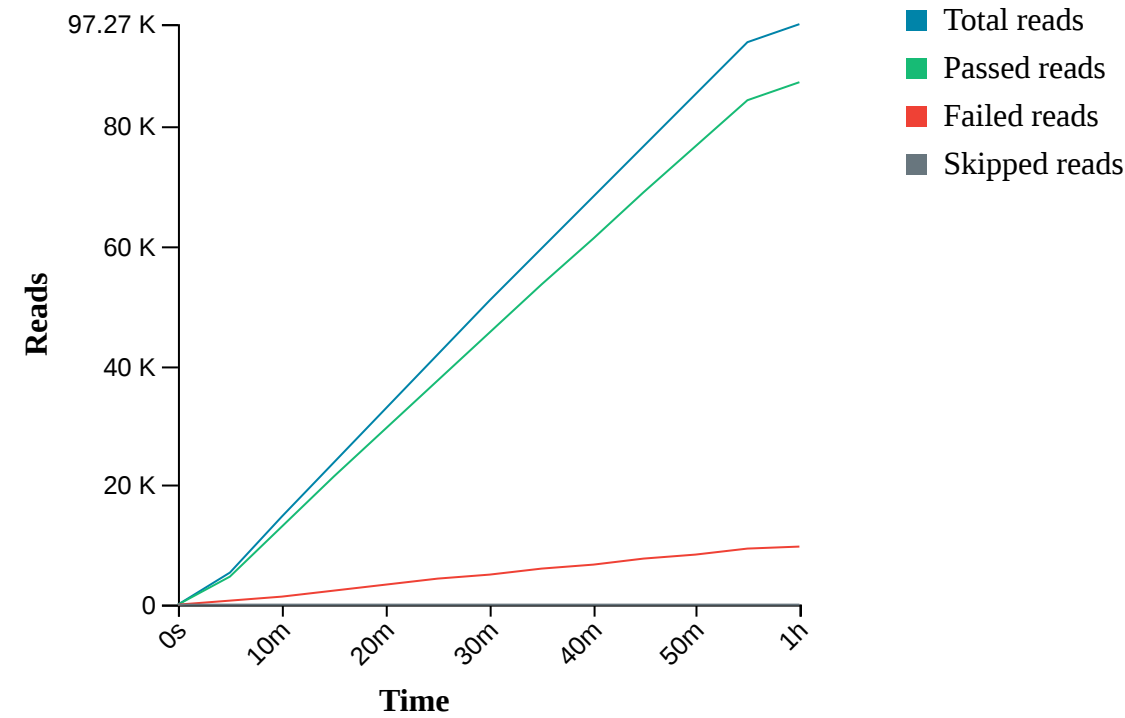
Run Parameters

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/references/M_morganii_ref.fasta"],filter_type=enrich,first_c hannel=1,last_channel=512
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/references/the7references.fasta"]
Read Filtering	min_qscore=7

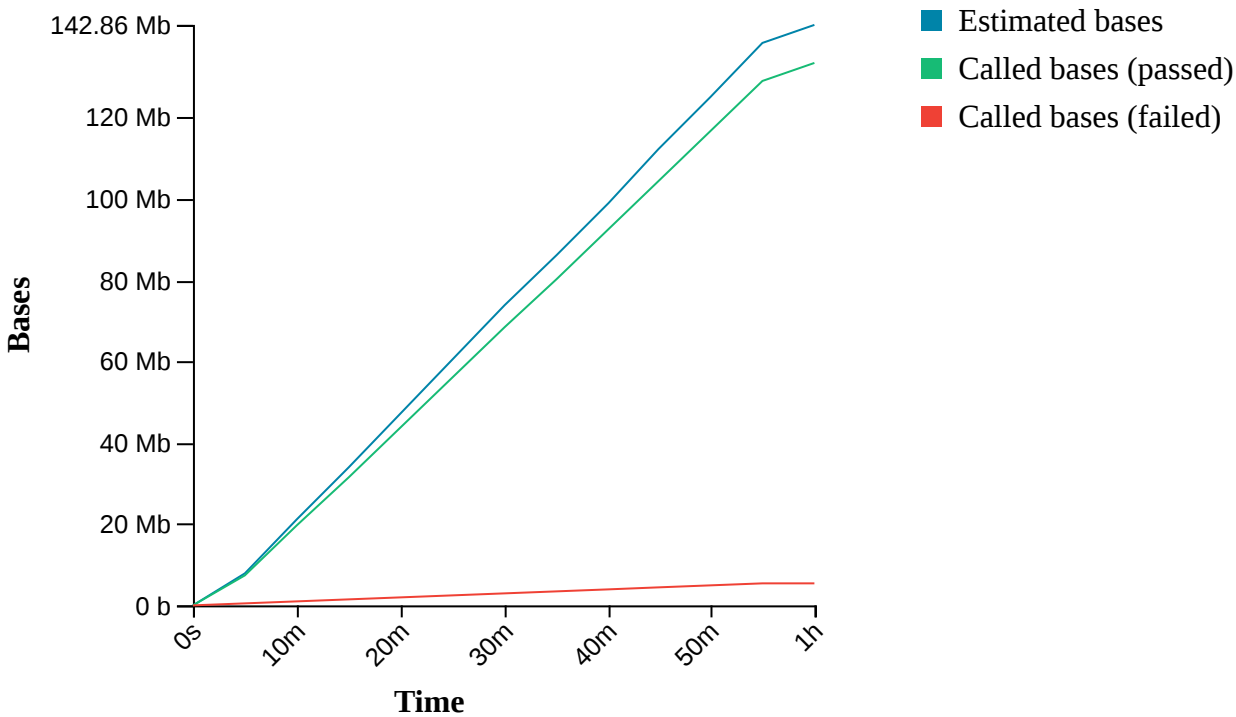
Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

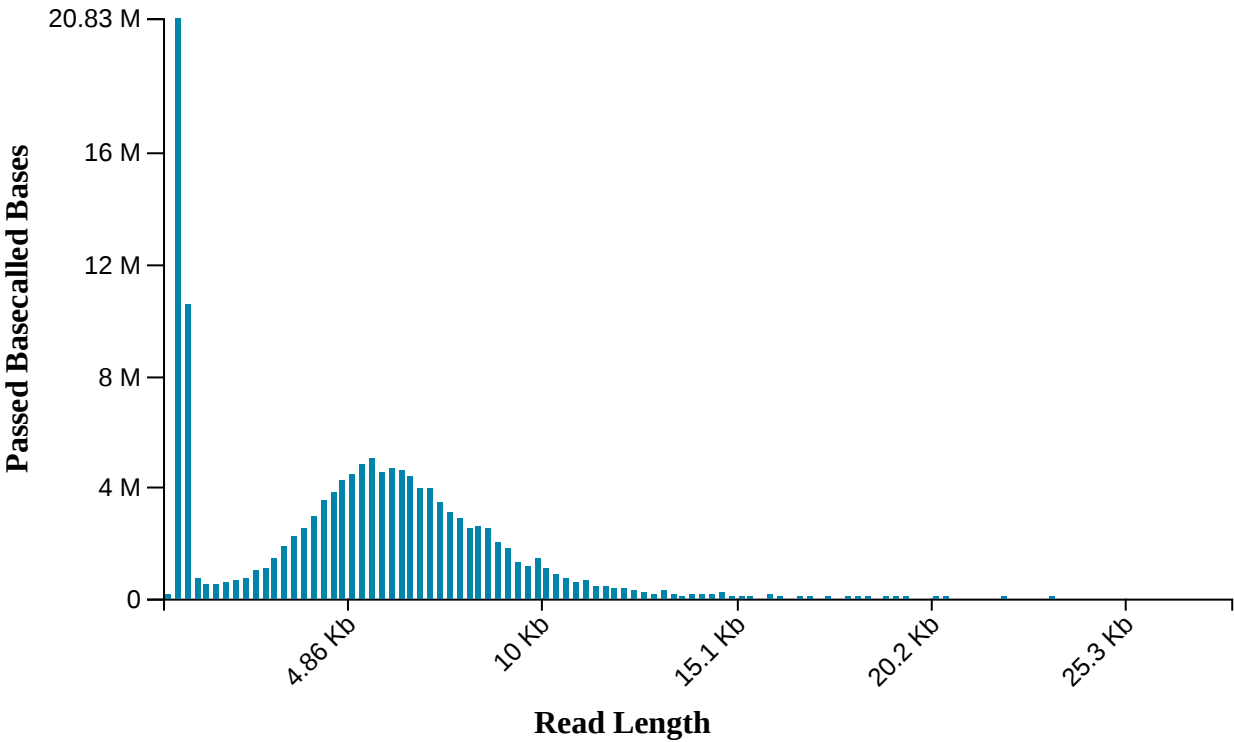


Cumulative Output Bases



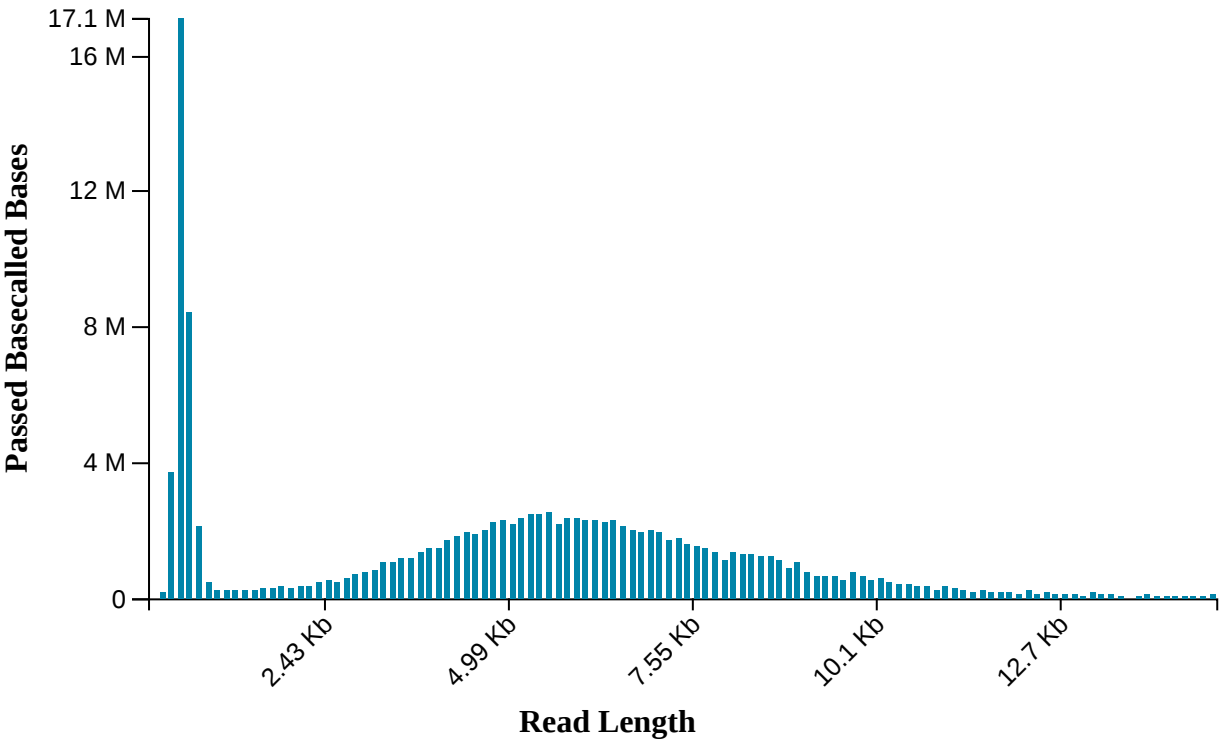
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 5.25 K



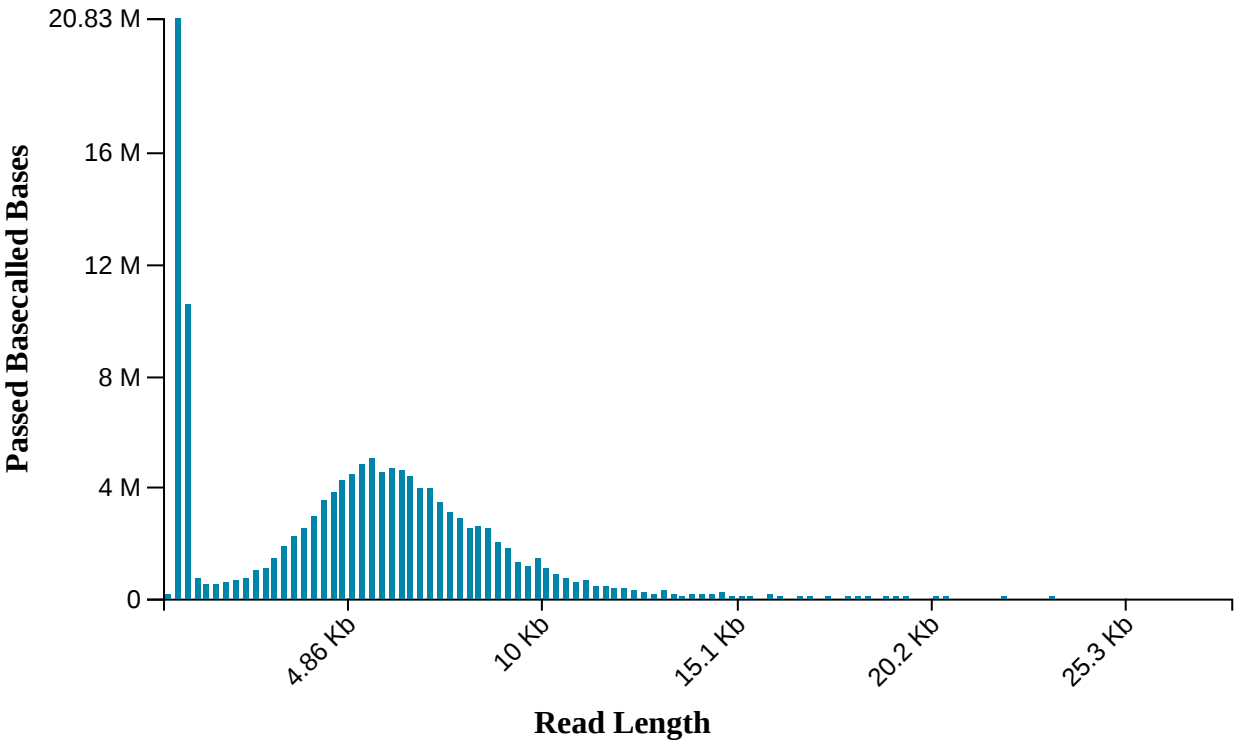
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 5.22 K



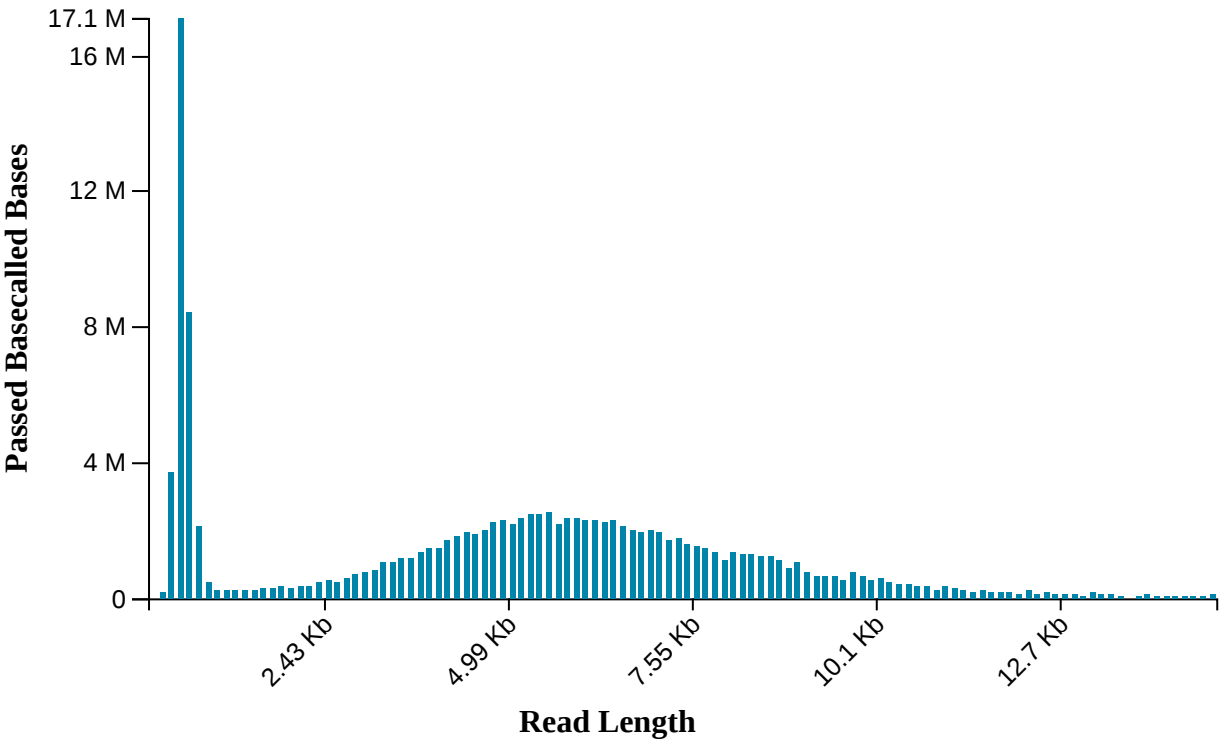
Read Length Histogram Estimated Bases

Estimated N50: 5.25 K

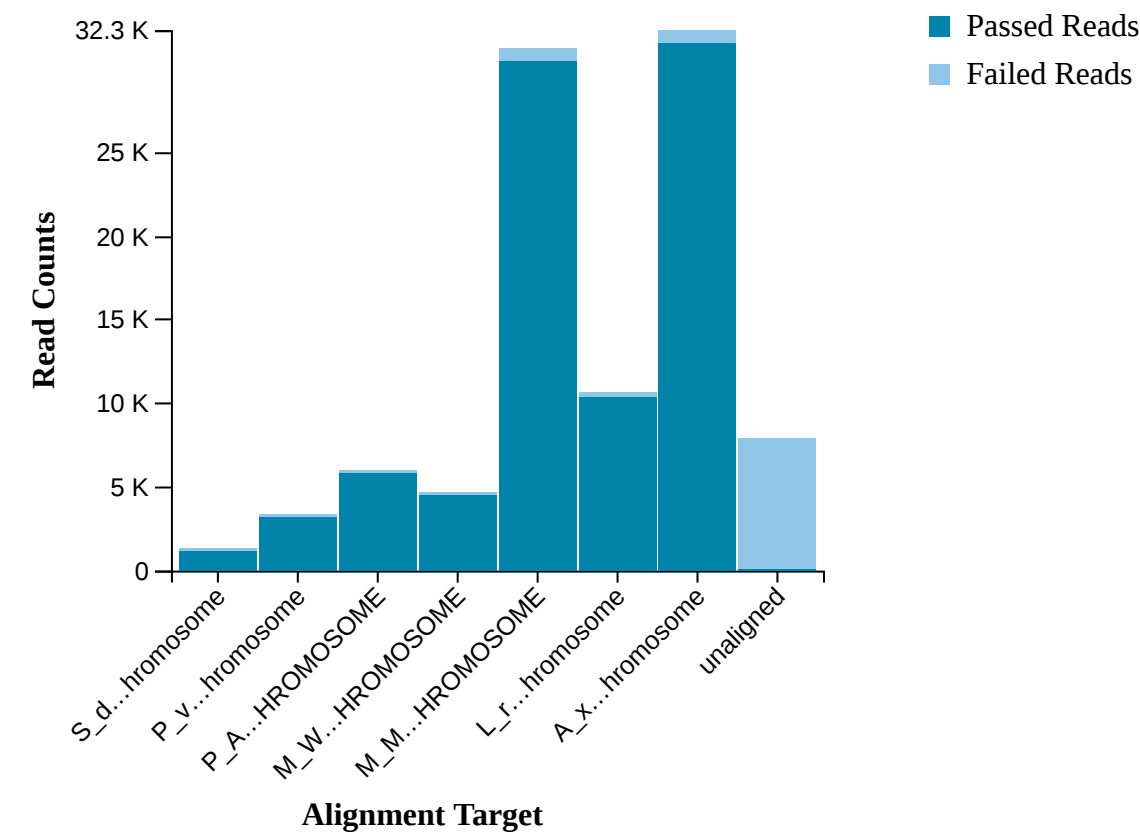


Read Length Histogram Basecalled Bases

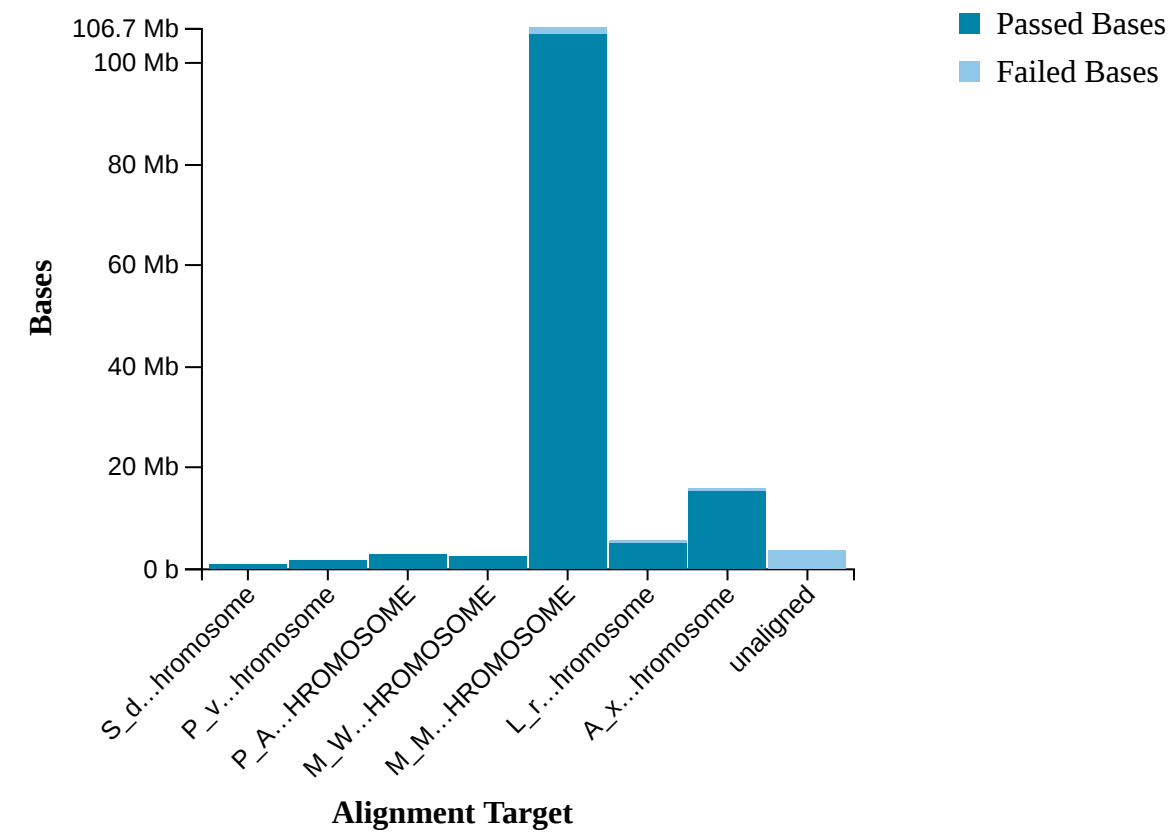
Estimated N50: 5.22 K



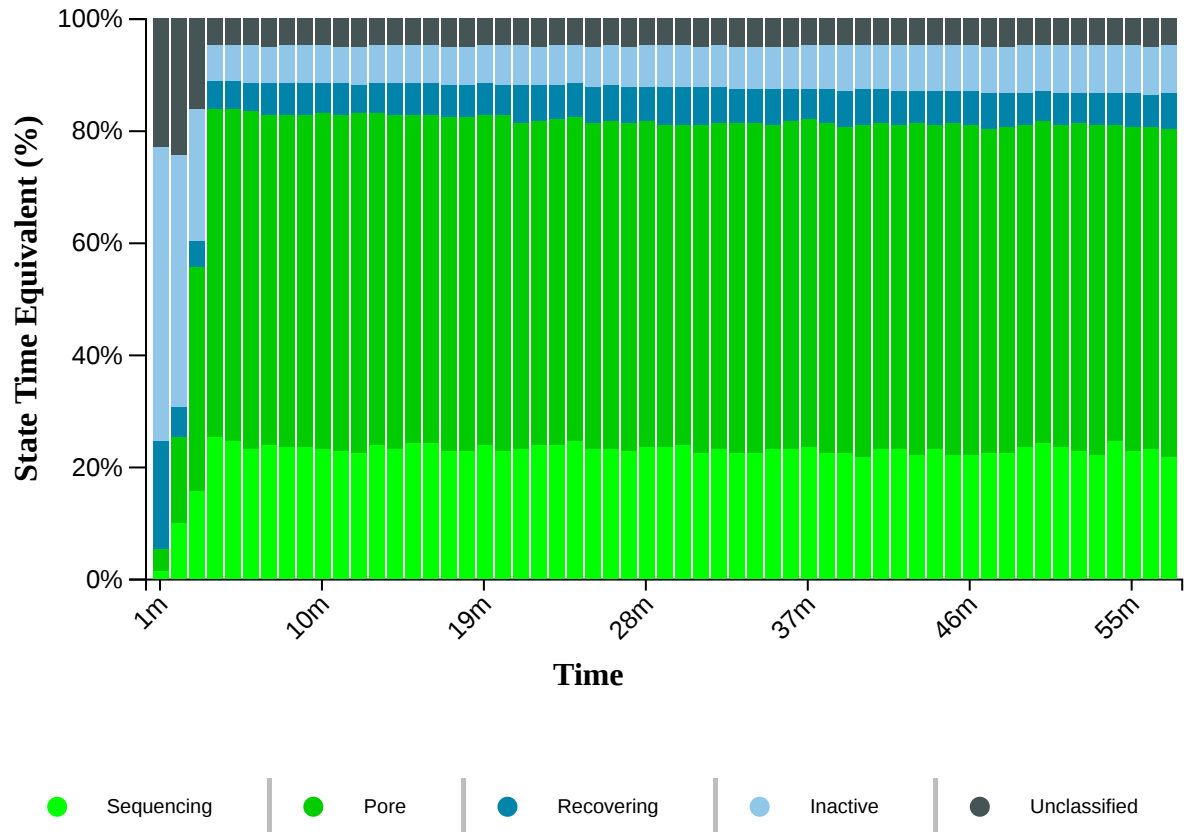
Alignment Target Hits (reads)



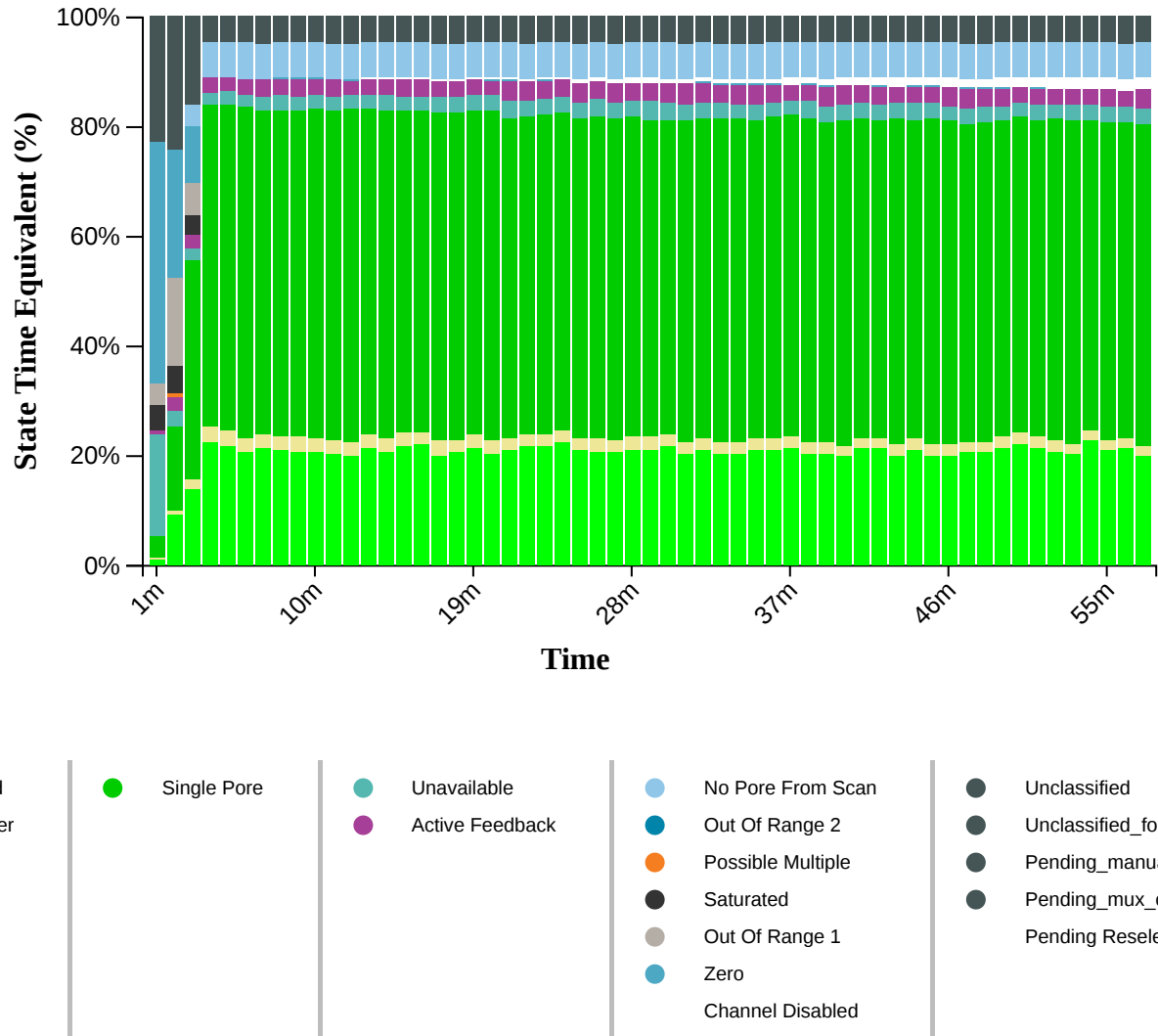
Alignment Target Hits (bases)



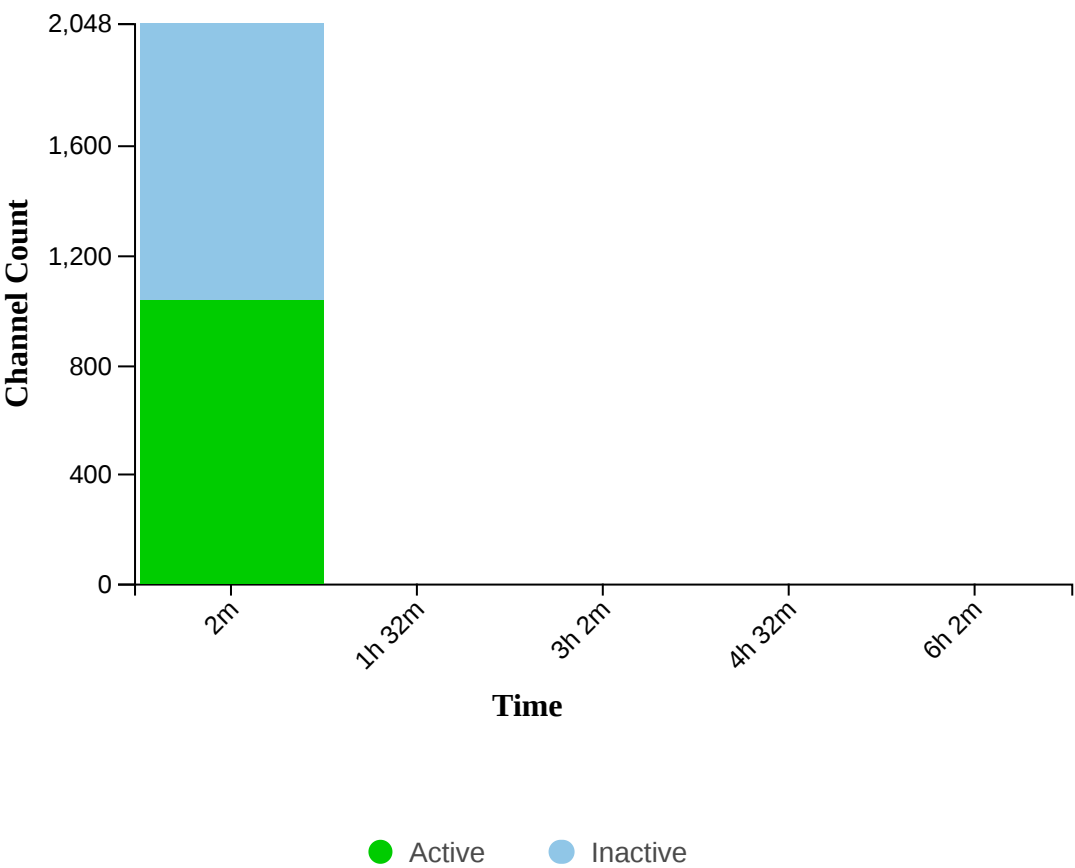
Duty Time Grouped



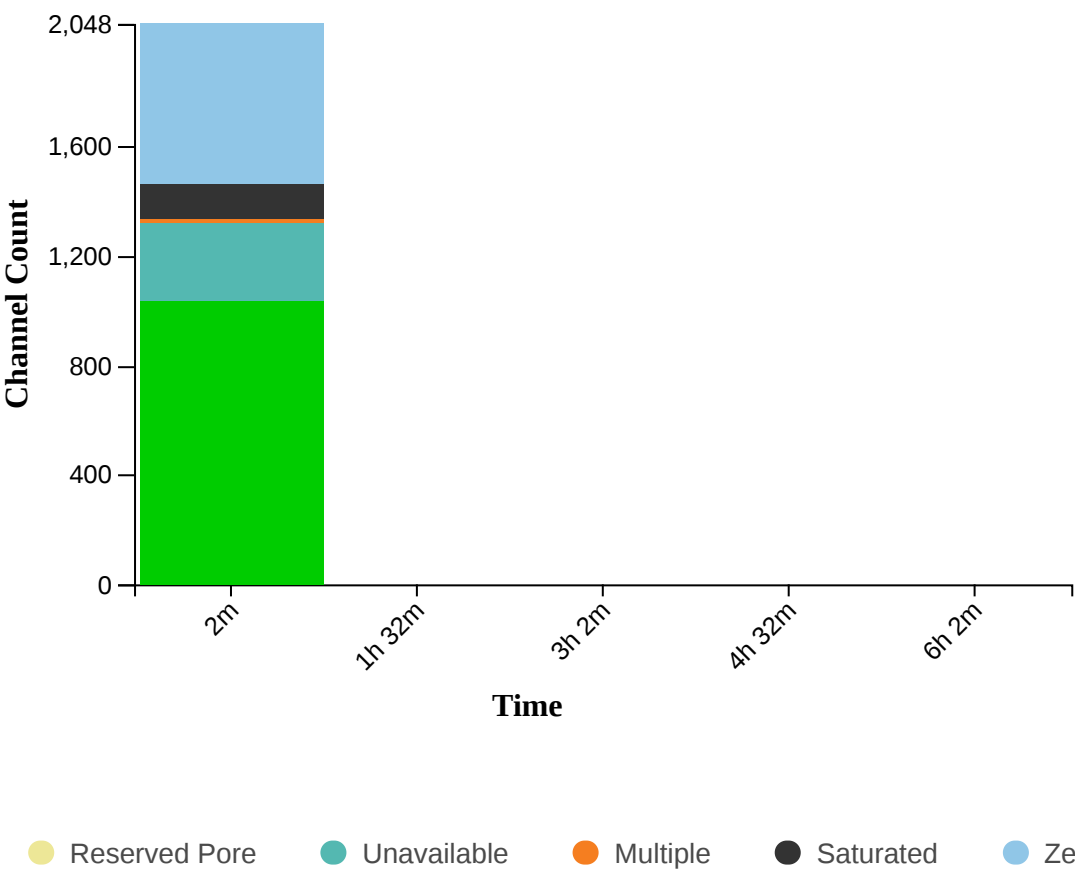
Duty time Categorised



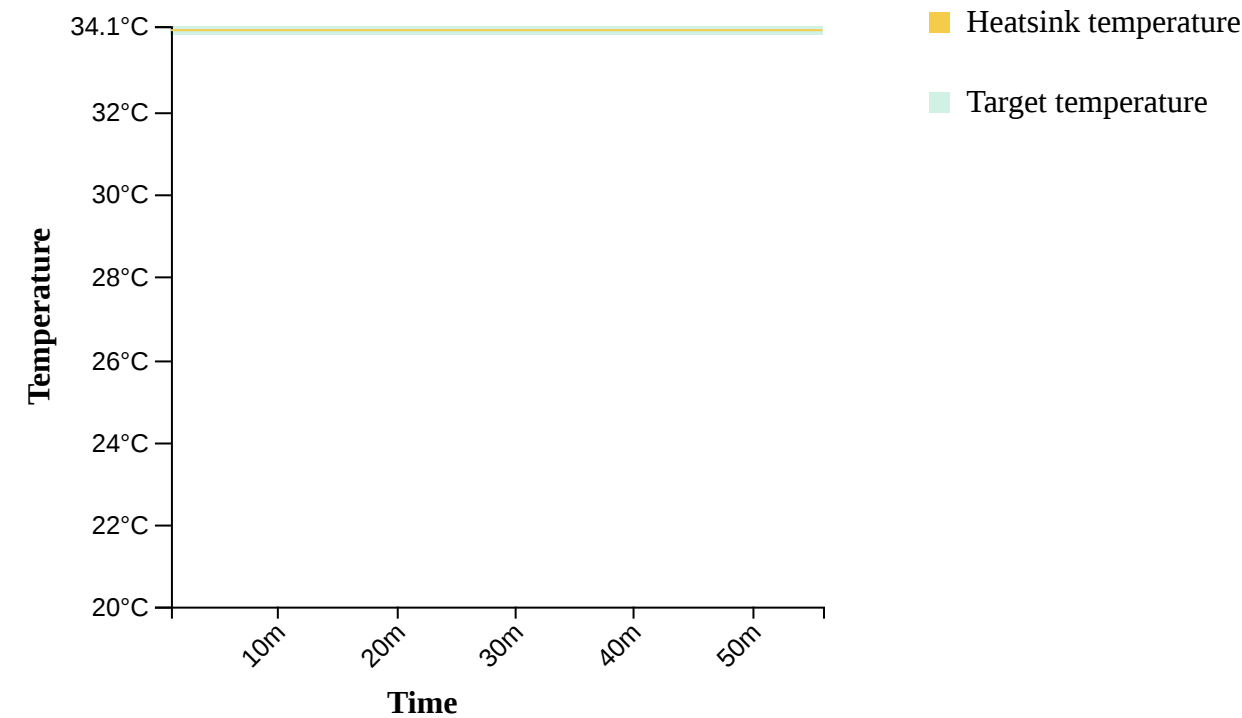
Mux Scan Grouped



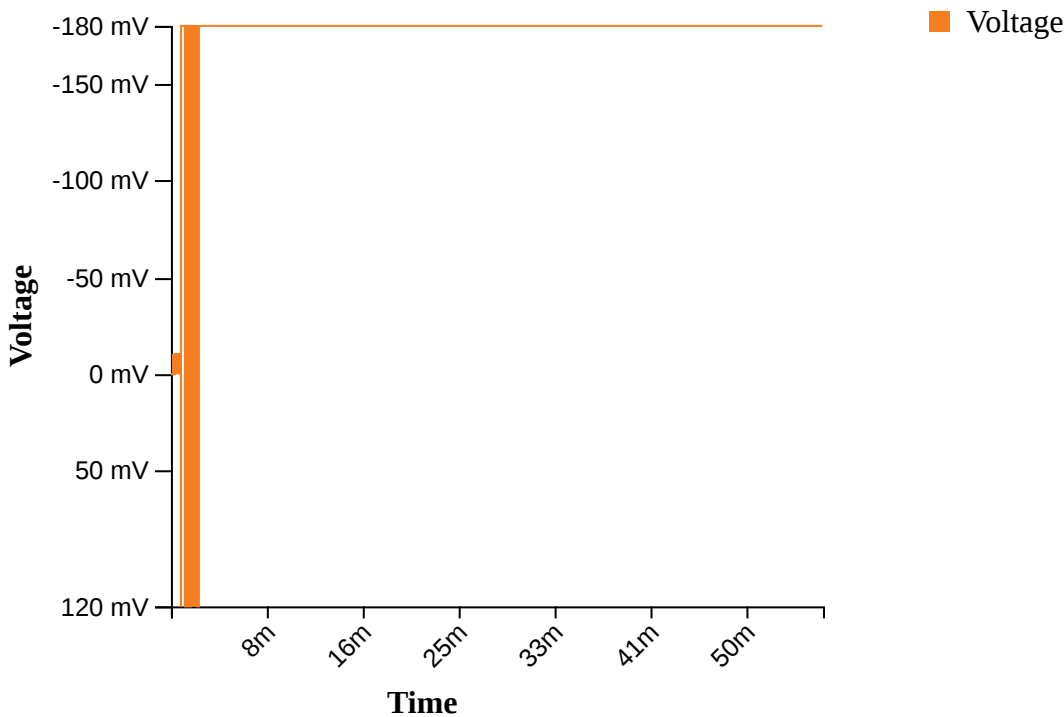
Mux Scan Categorised



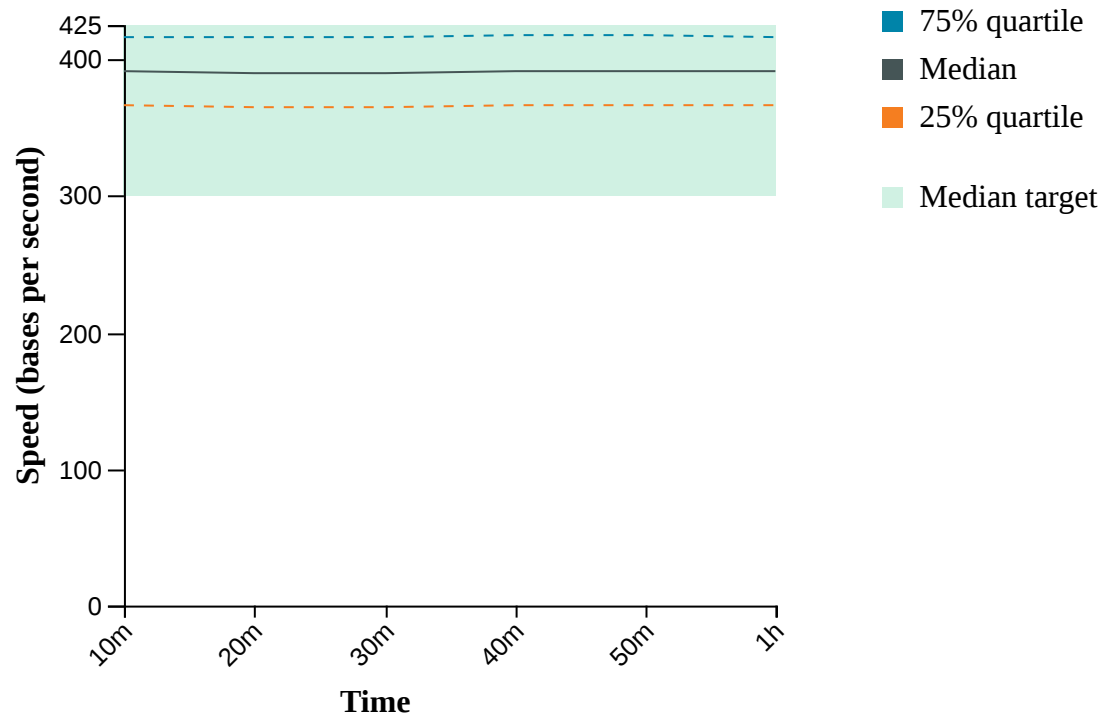
Temperature History.



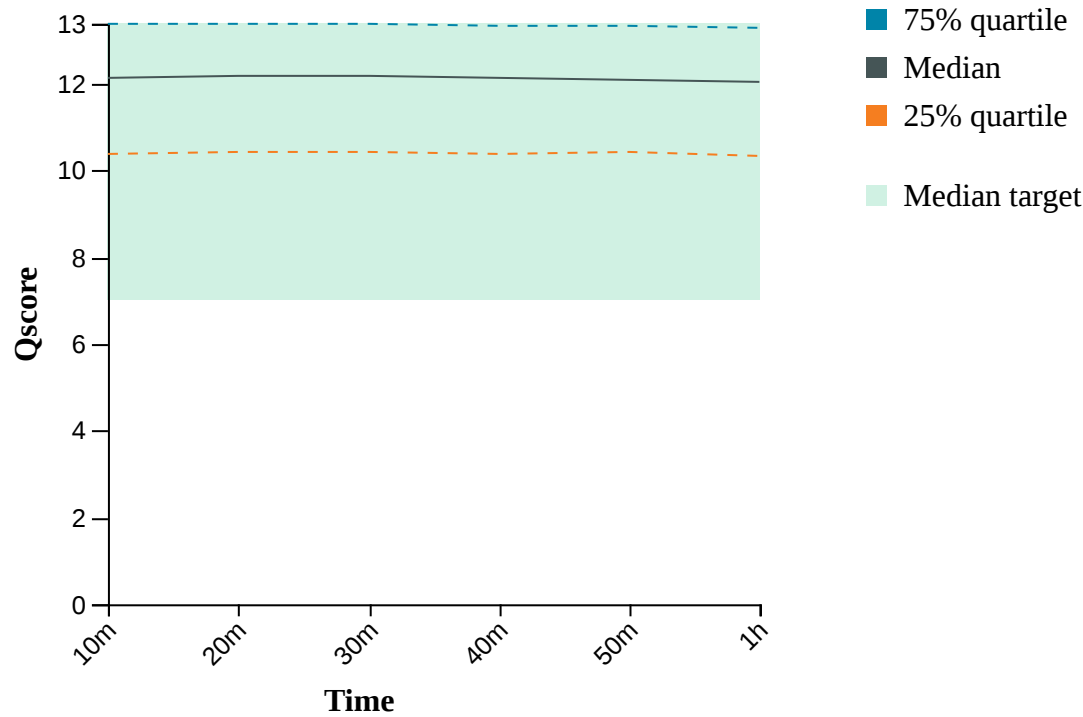
Bias Voltage History.



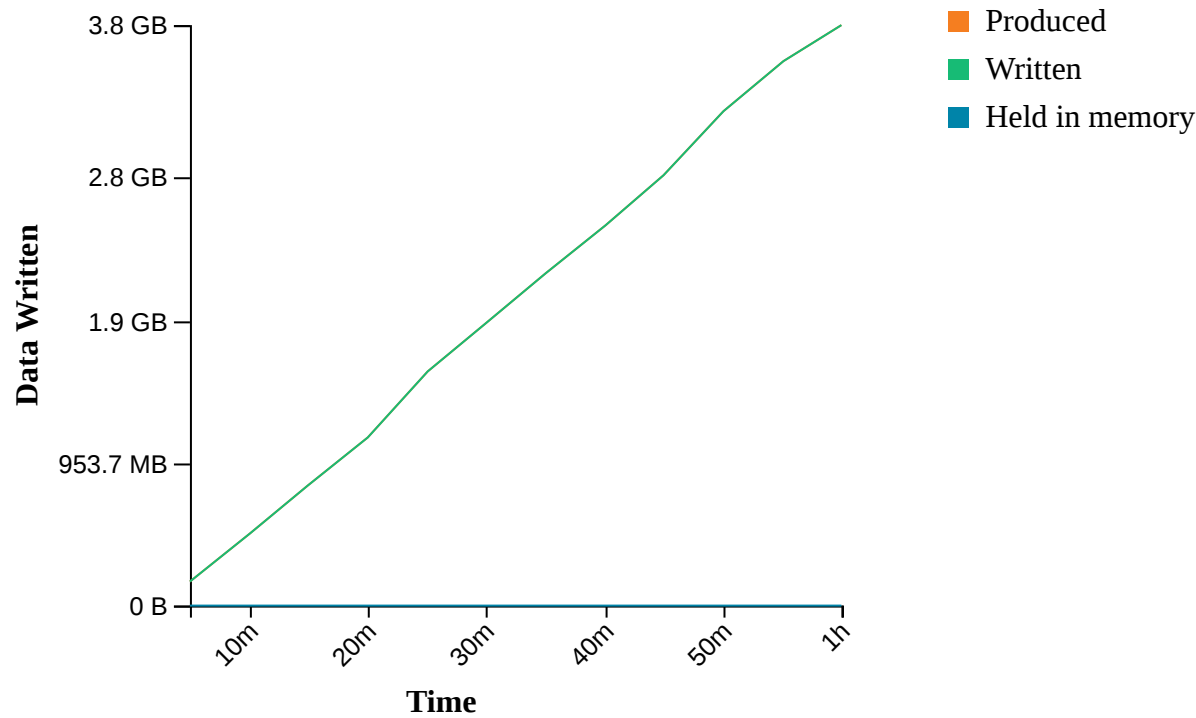
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAO54786 has found a total of 1038 pores. 479 pores available for immediate sequencing January 4, 13:06
- Performing Mux Scan January 4, 13:04
- Starting sequencing procedure January 4, 13:04
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C January 4, 13:00