



Run Info

Host Name	GXB01190 (localhost)
Experiment Name	EIMock_2kbp_MwisconsensusRAD_050121
Sample ID	EIMock_2kbp_MwisconsensusRAD_050121
Run ID	23b833c6-9285-4bf7-b7e4-e37642e39429
Flow Cell Id	FAO53362
Start Time	January 5, 18:04
Run Length	57m

Run Summary

Reads Generated	444.87 K
Passed Bases	190.02 Mb
Failed Bases	21.8 Mb
Estimated Bases	228.6 Mb

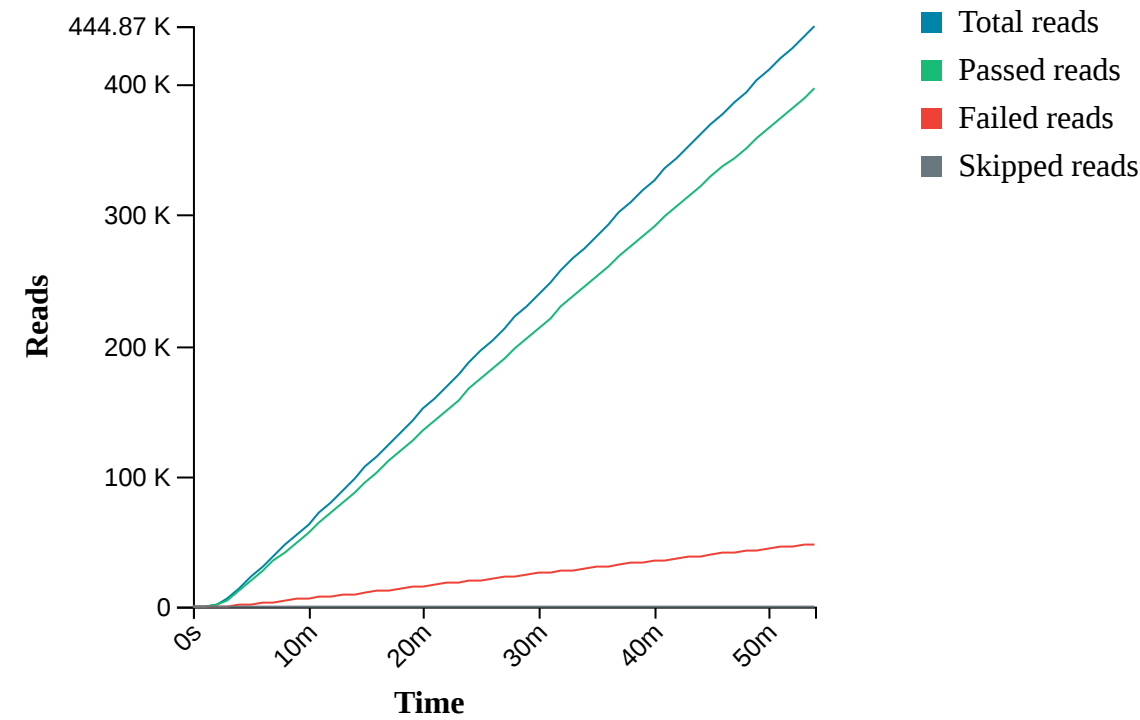
Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-RAD004
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_wisconsensus_ref.fasta"],filter_type=enrich,first_channel=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

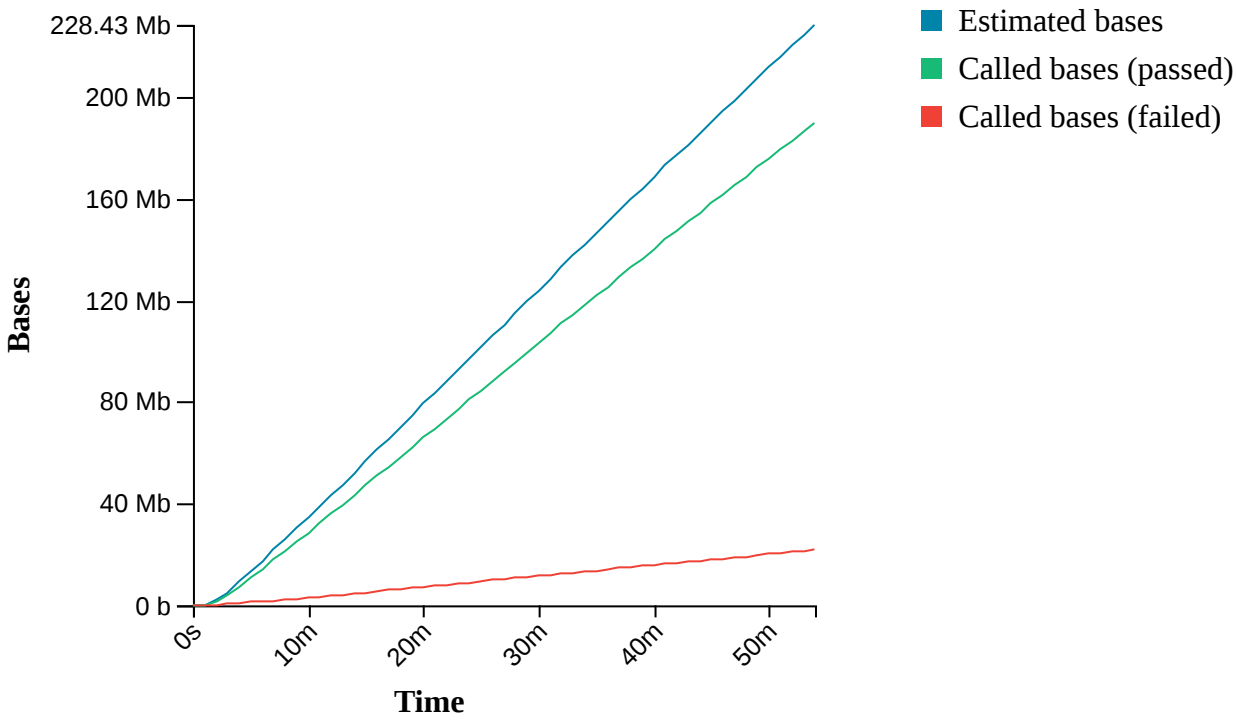
Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

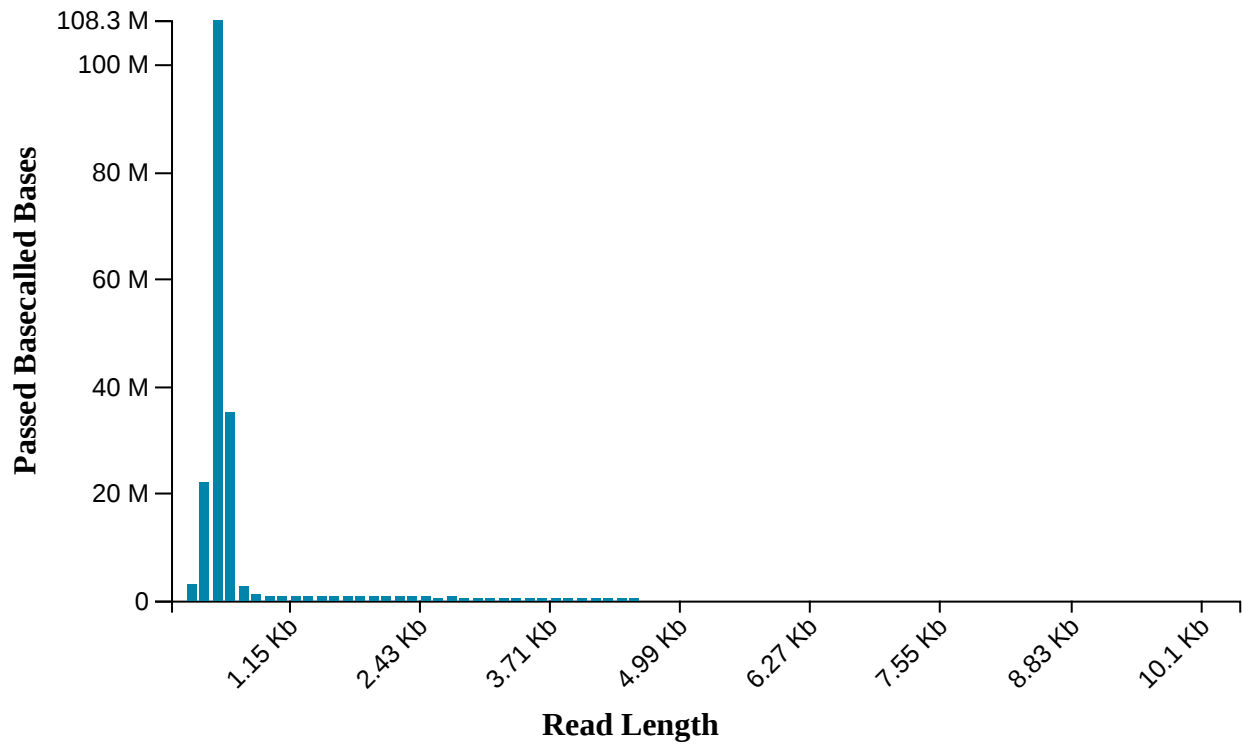


Cumulative Output Bases



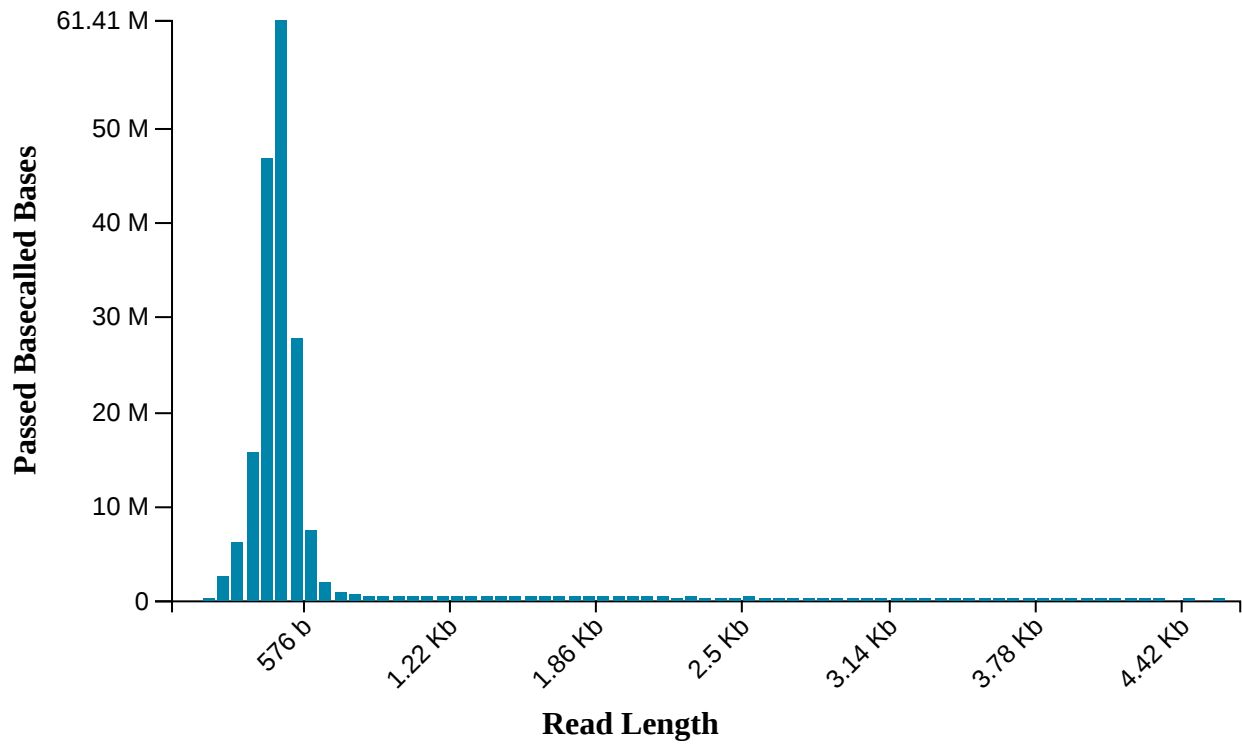
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 470



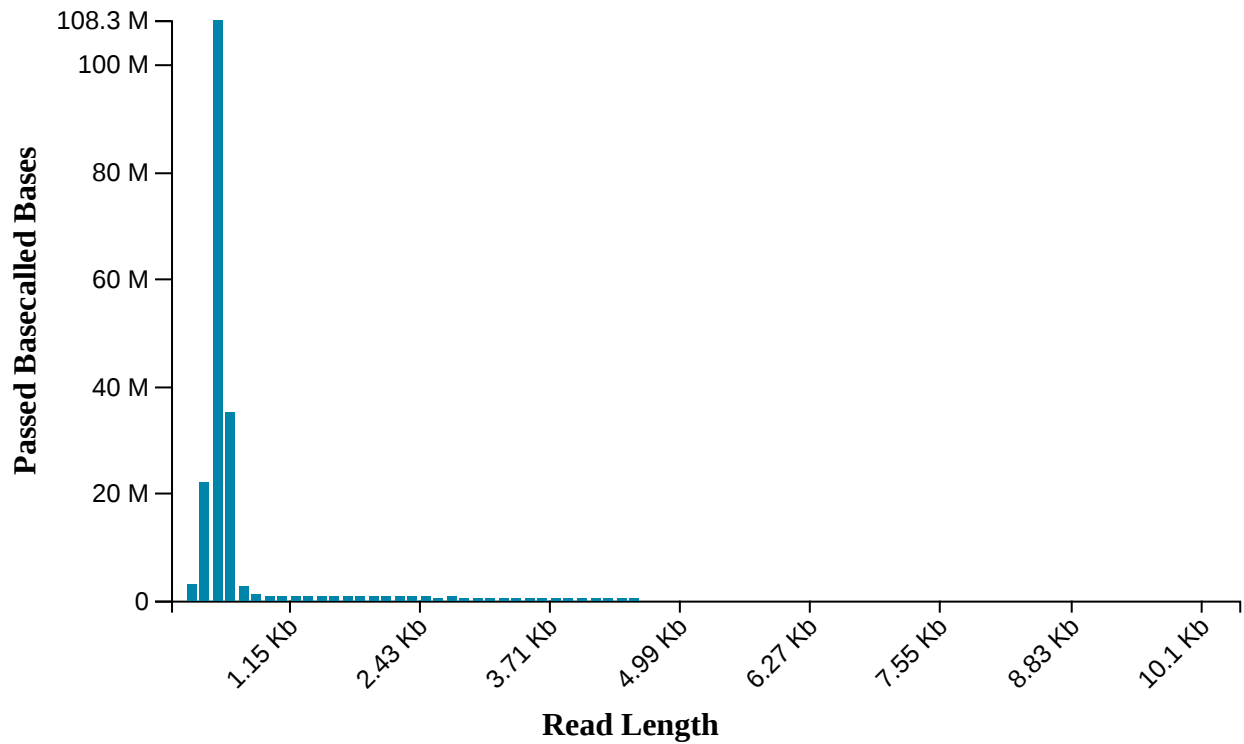
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 469



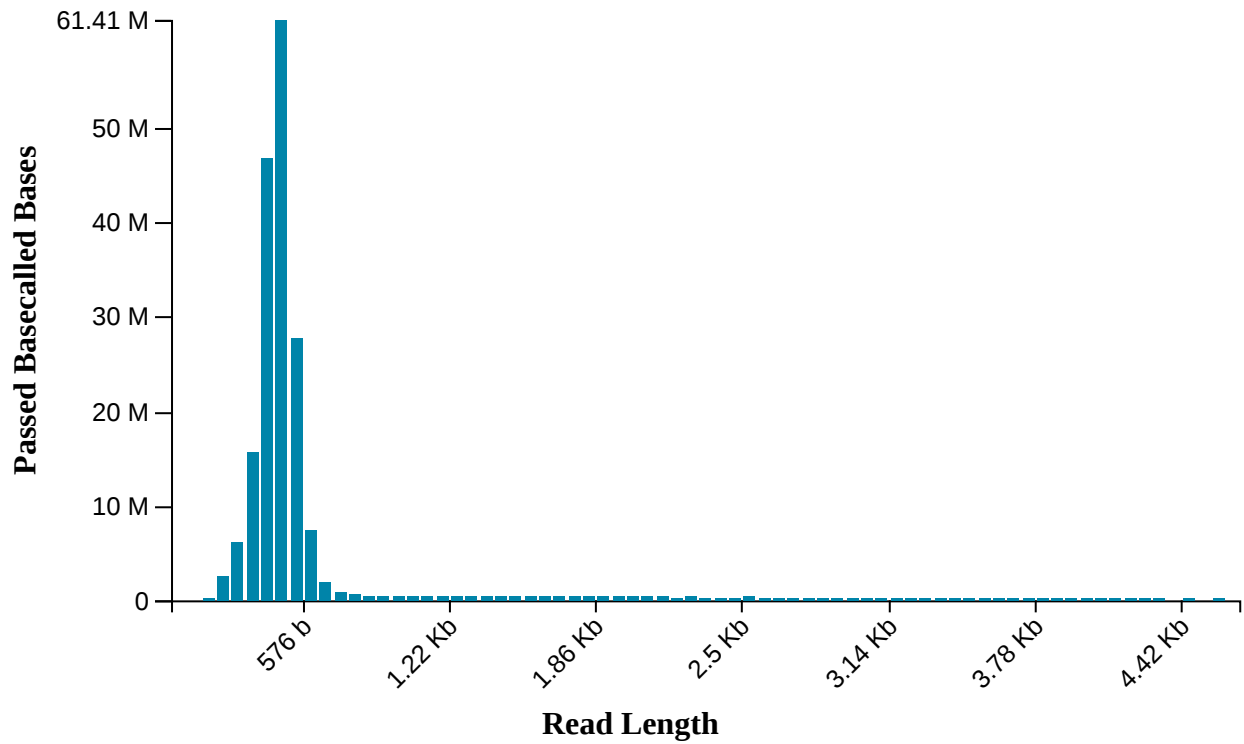
Read Length Histogram Estimated Bases

Estimated N50: 470

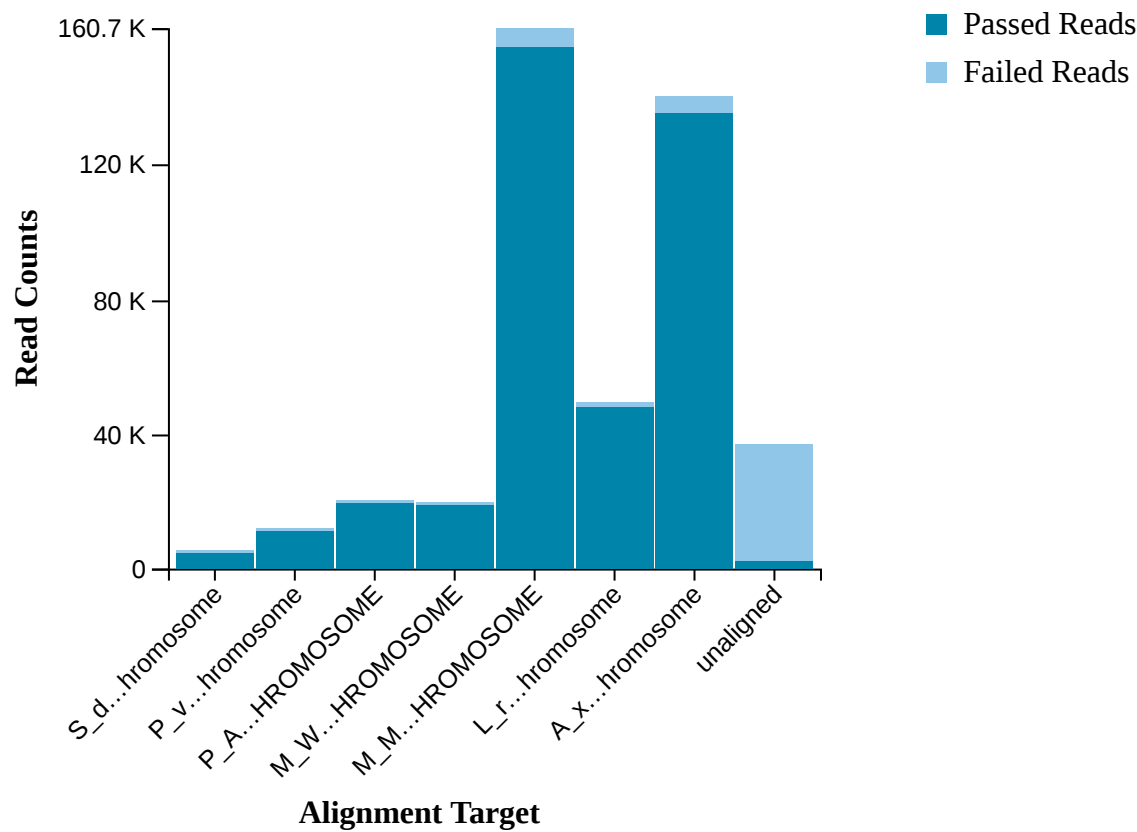


Read Length Histogram Basecalled Bases

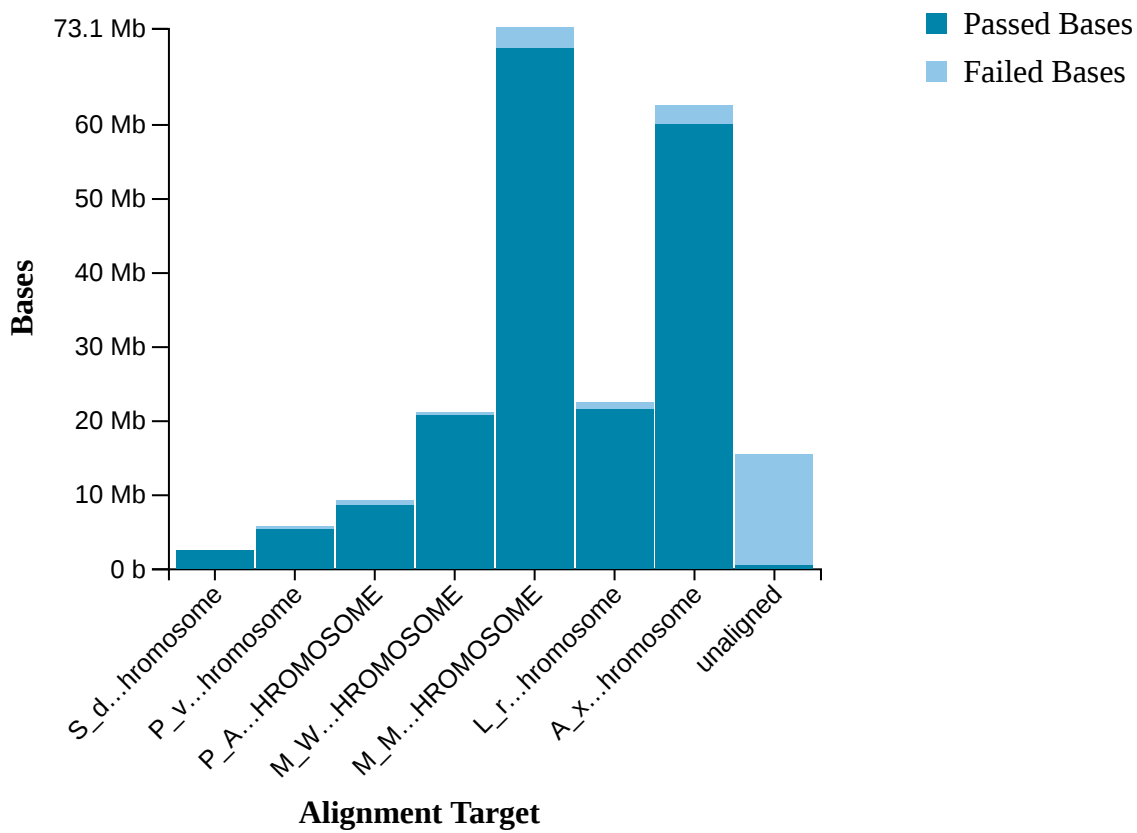
Estimated N50: 469



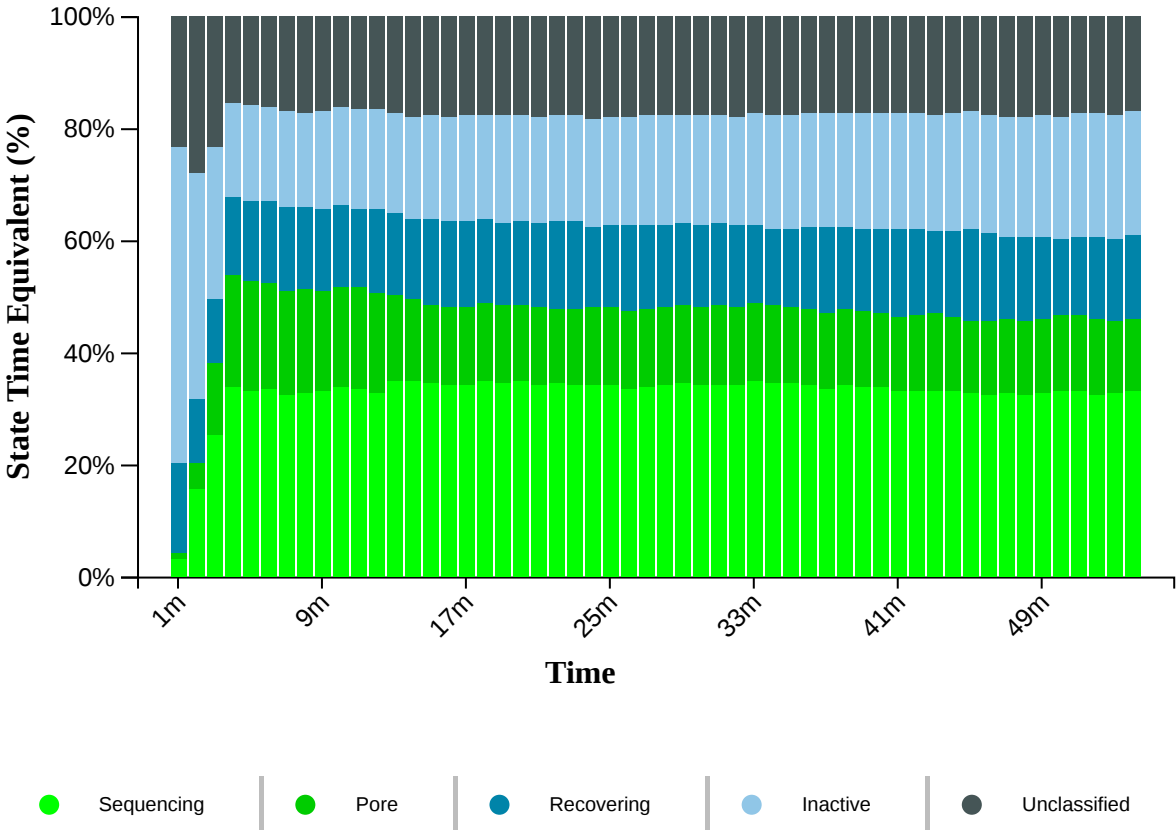
Alignment Target Hits (reads)



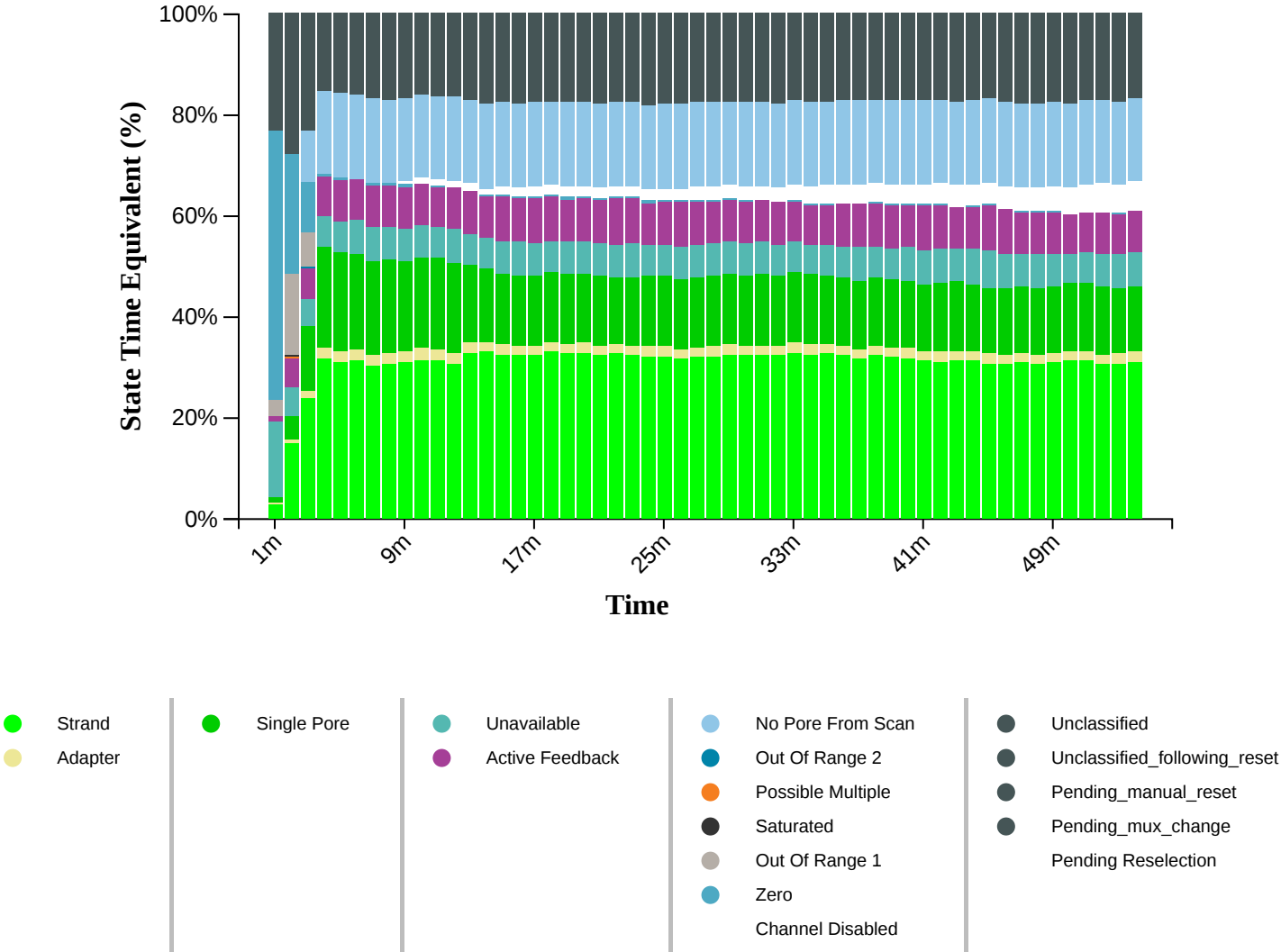
Alignment Target Hits (bases)



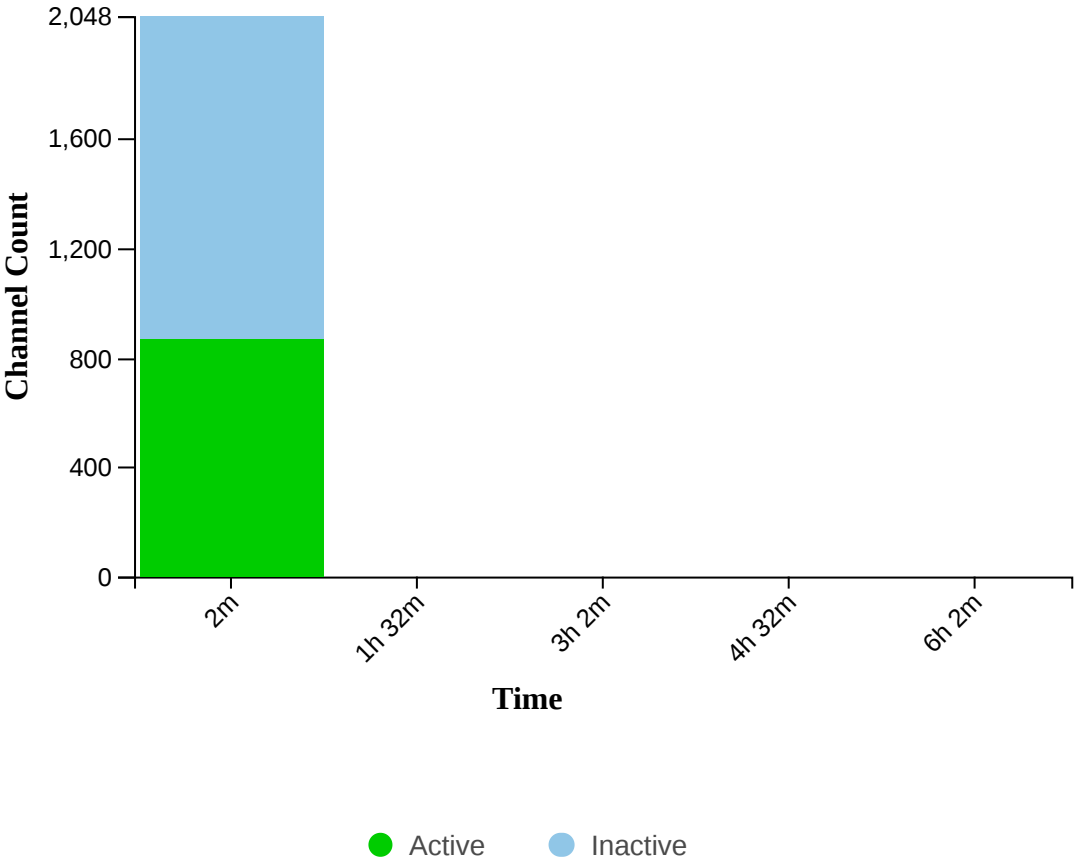
Duty Time Grouped



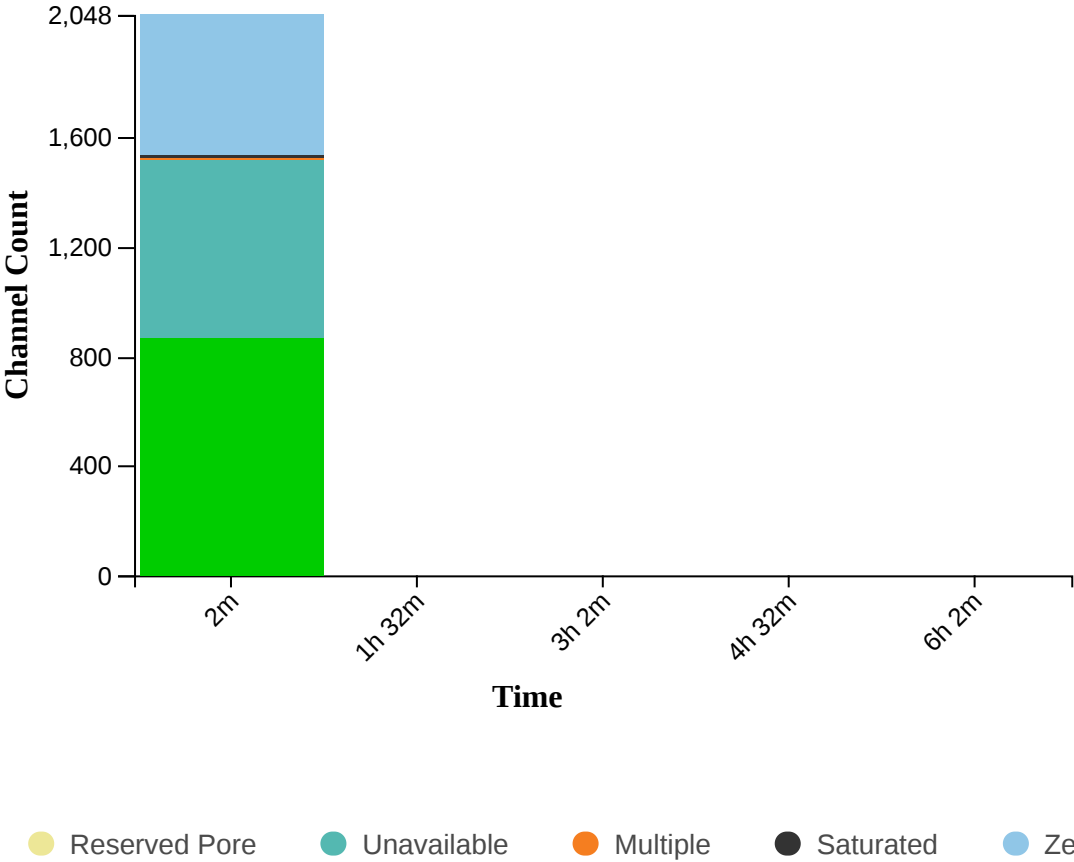
Duty time Categorised



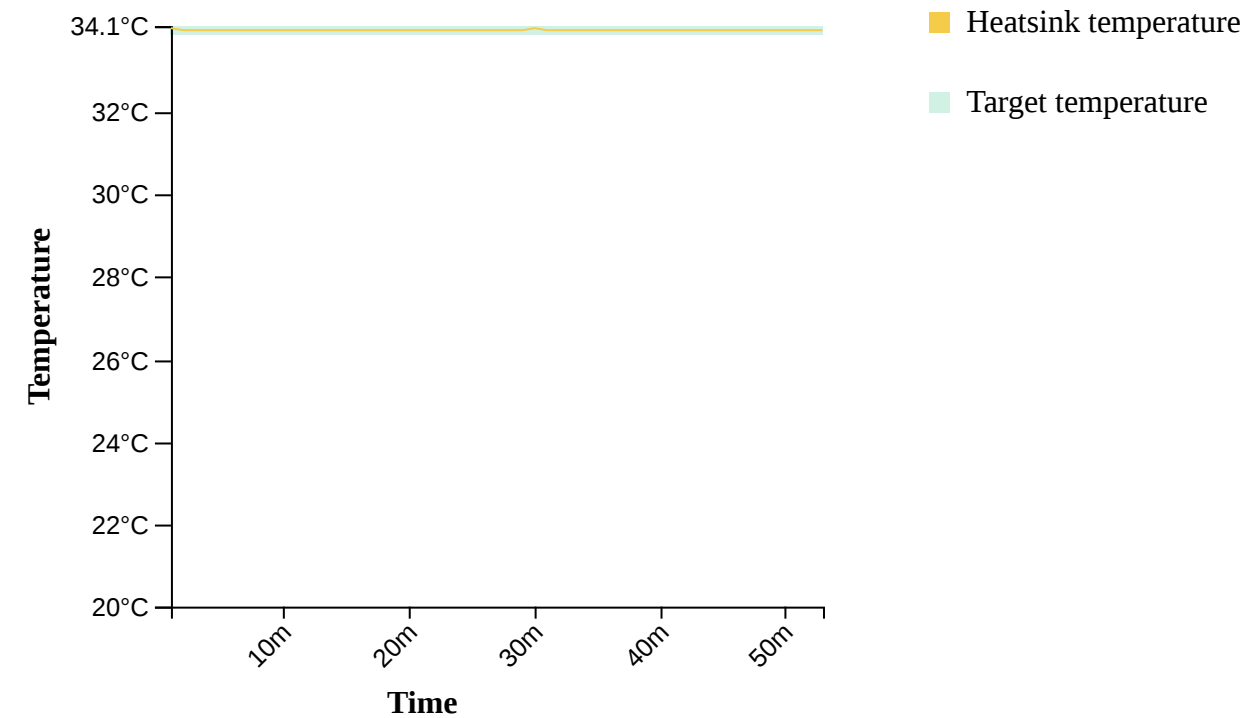
Mux Scan Grouped



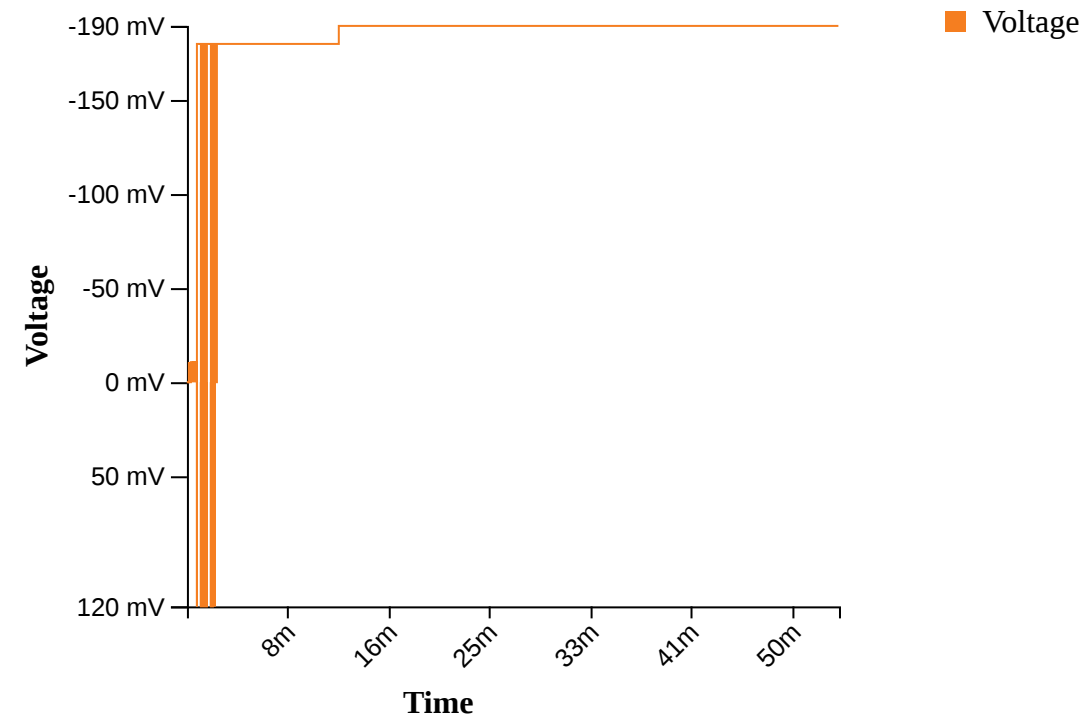
Mux Scan Categorised



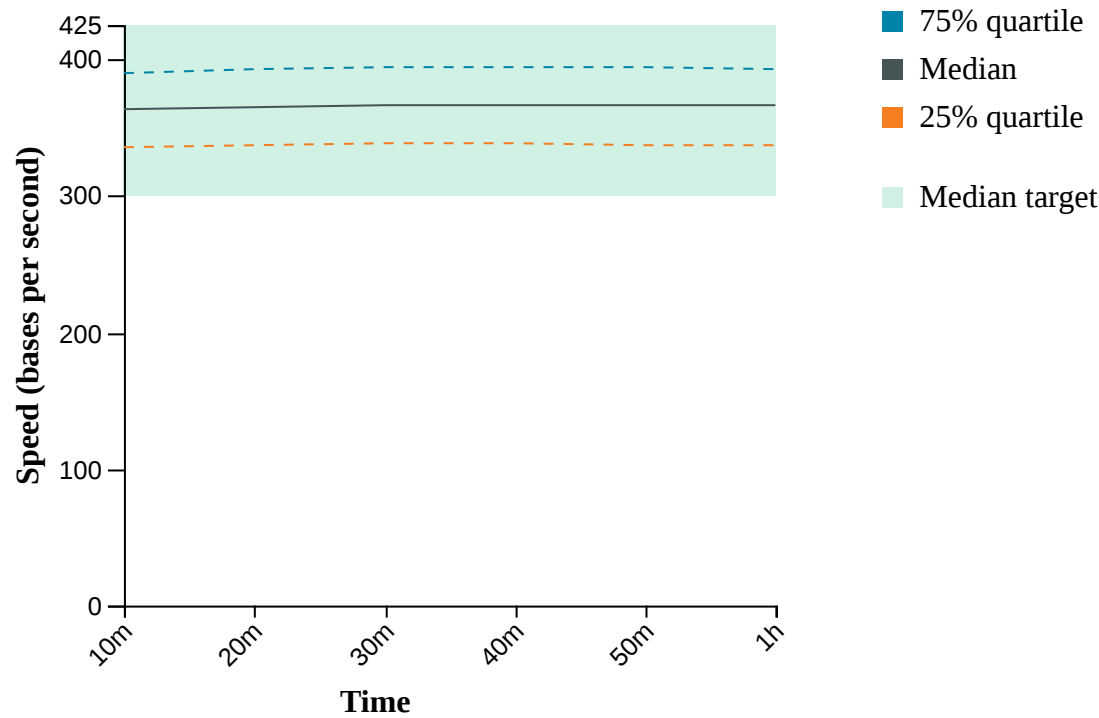
Temperature History.



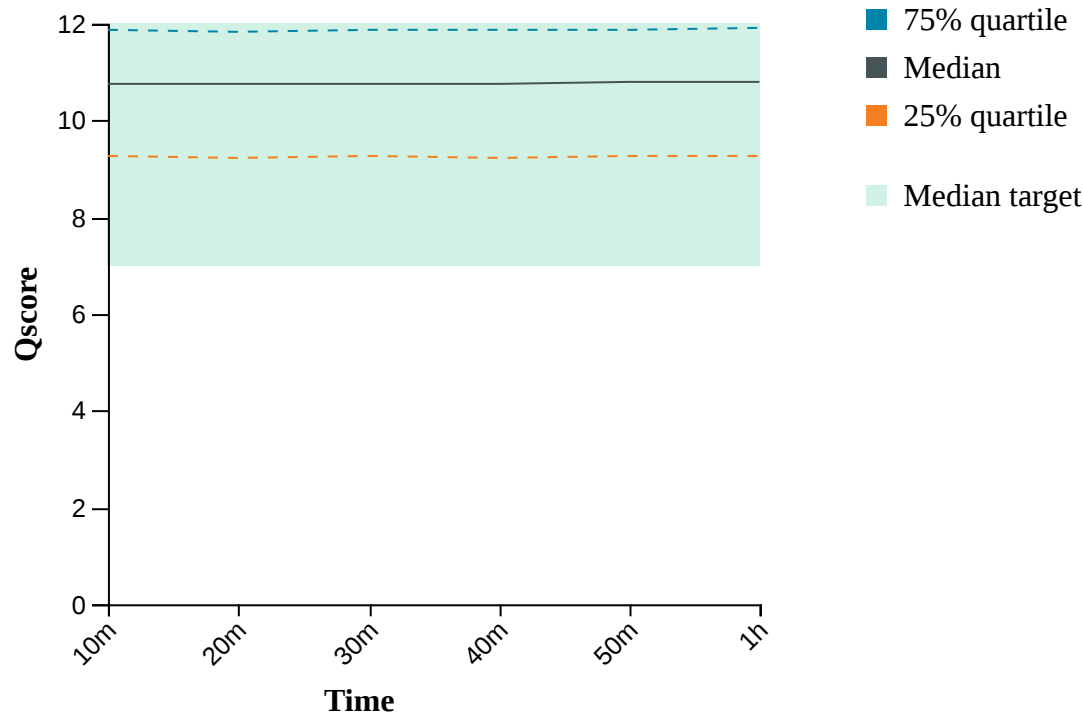
Bias Voltage History.



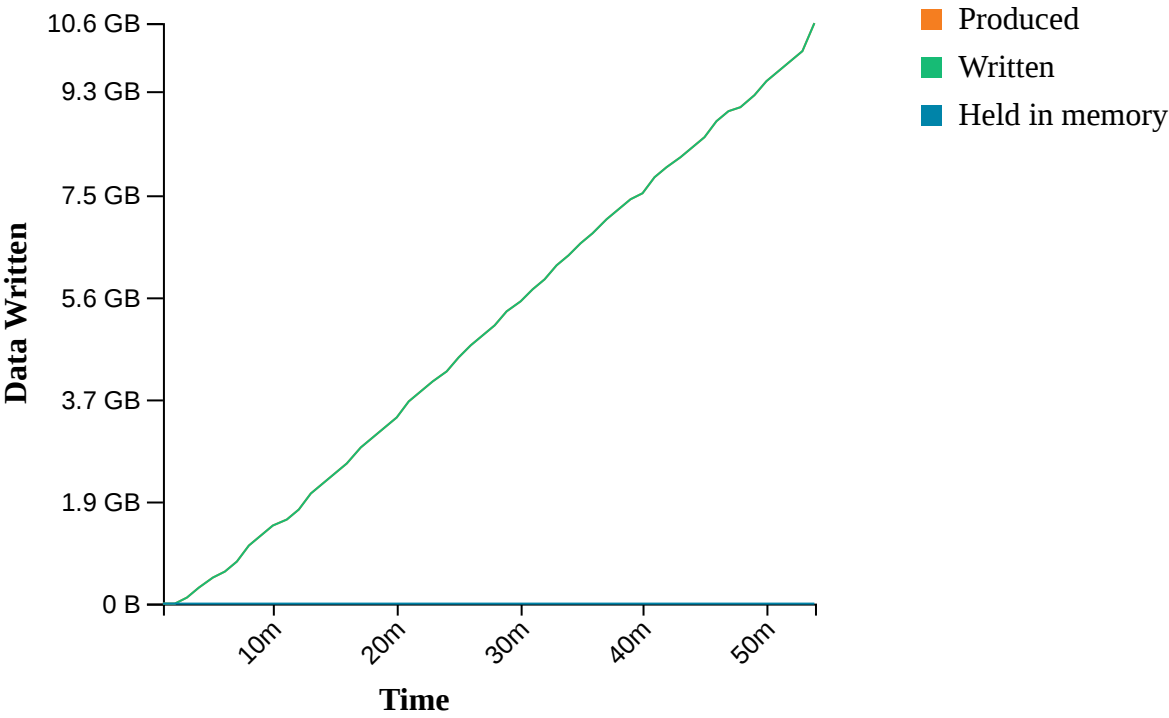
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 872 pores. 427 pores available for immediate sequencing January 5, 18:10
- Performing Mux Scan January 5, 18:07
- Starting sequencing procedure January 5, 18:07
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C January 5, 18:04