



Run Info

Host Name	GXB01190 (localhost)
Experiment Name	ReadUntilMock_15kbSE_SdEnrich_08122020
Sample ID	ReadUntilMock_15kbSE_SdEnrich_08122020
Run ID	d46c4b9b-089f-482d-b340-0215111f5d8d
Flow Cell Id	FAO52906
Start Time	December 8, 19:04
Run Length	1h 18m

Run Summary

Reads Generated	249.92 K
Passed Bases	126.37 Mb
Failed Bases	12.01 Mb
Estimated Bases	144.97 Mb

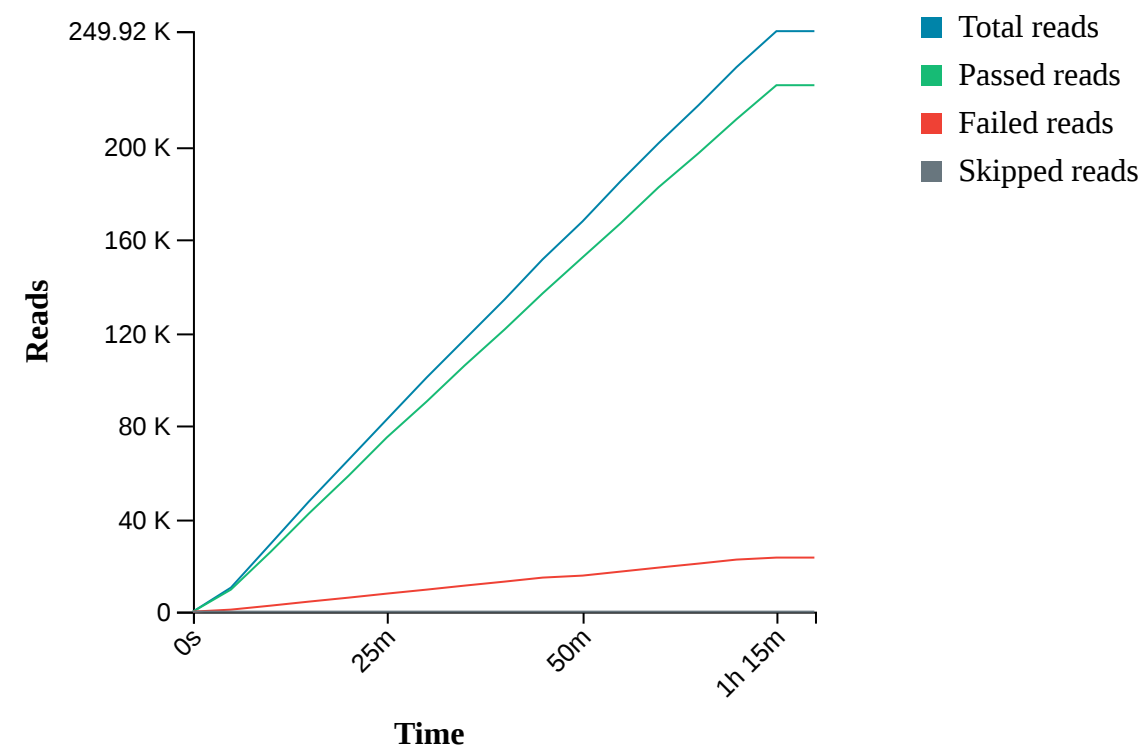
Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-LSK109
Initial Bias Voltage	-185 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/S_dysgalactiae_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

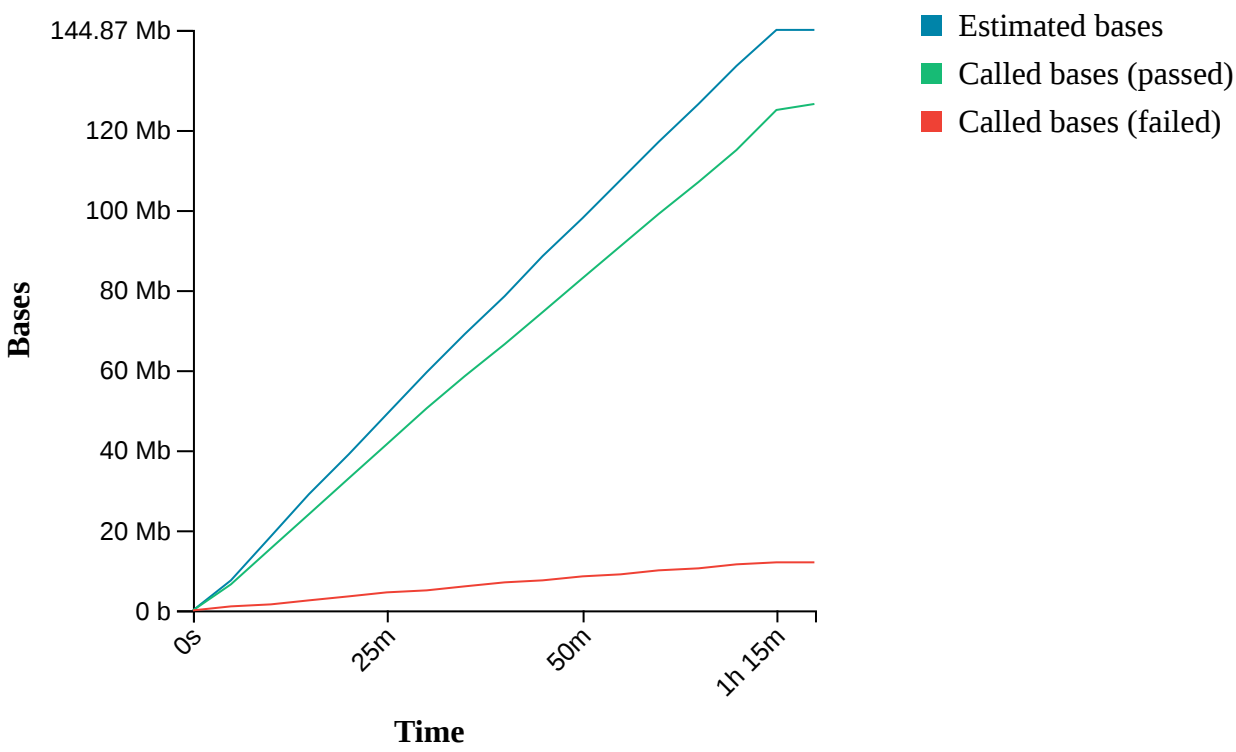
Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

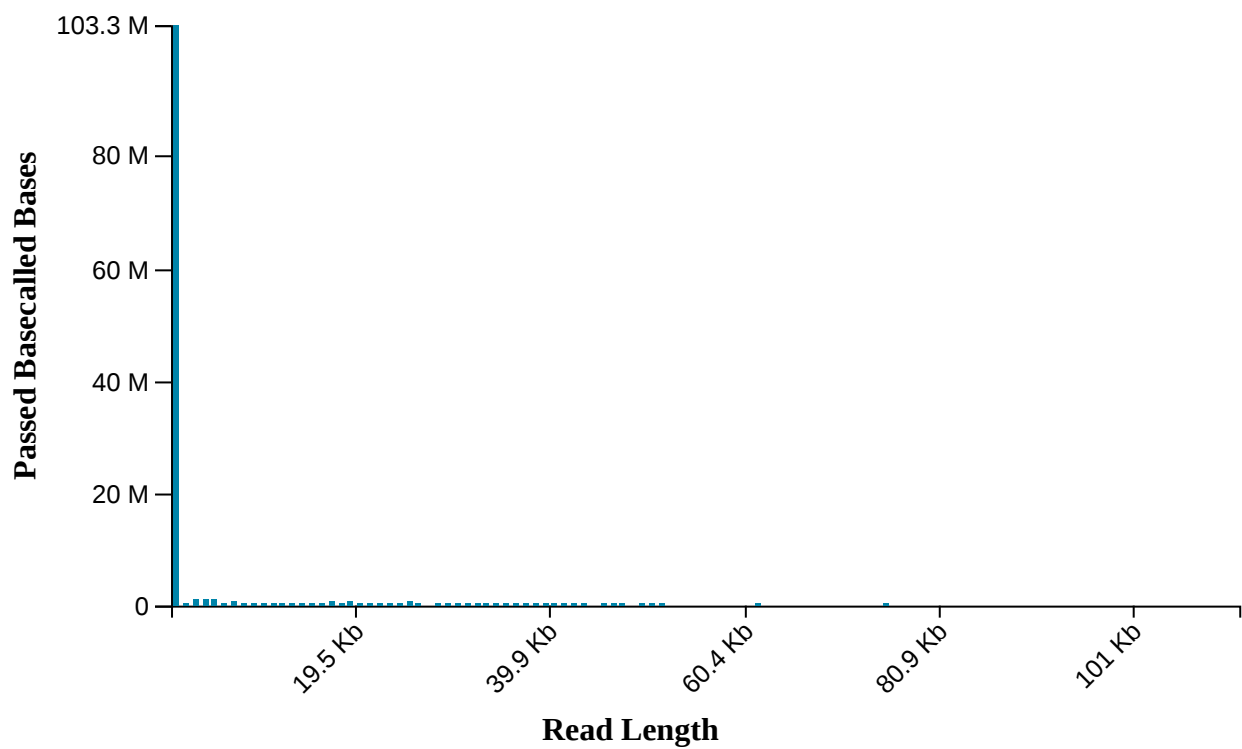


Cumulative Output Bases



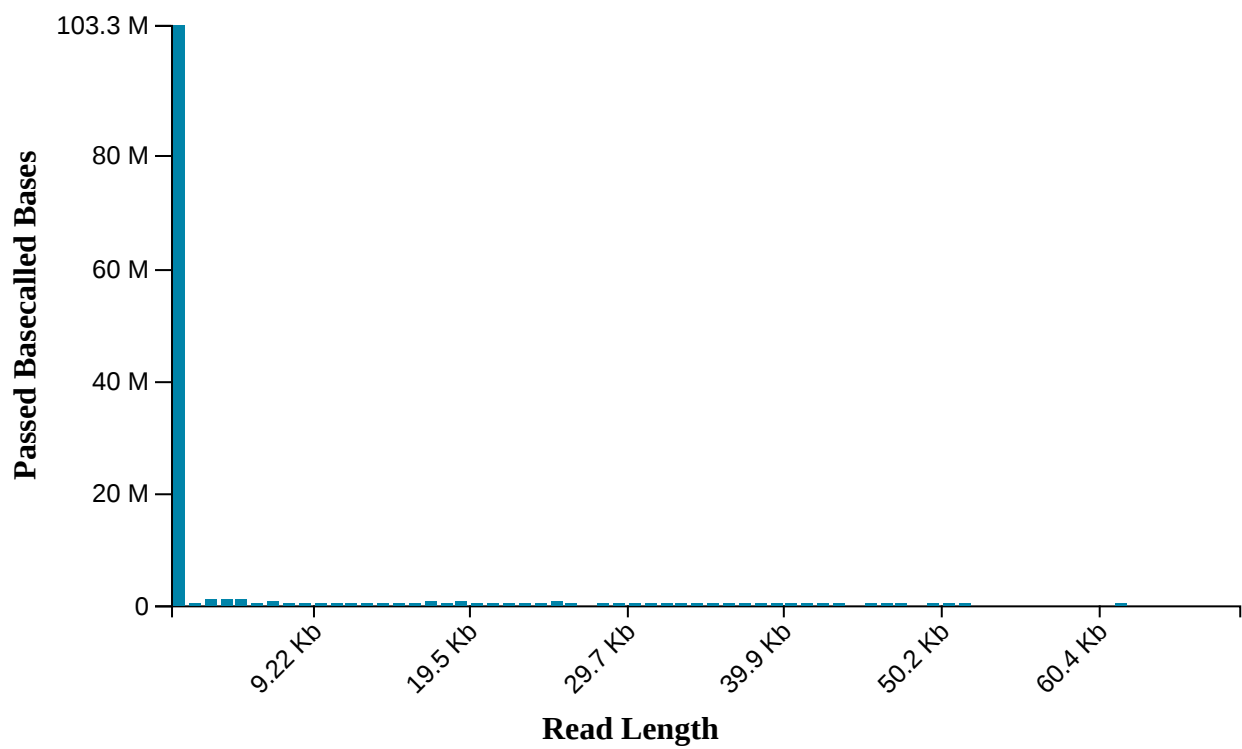
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 492



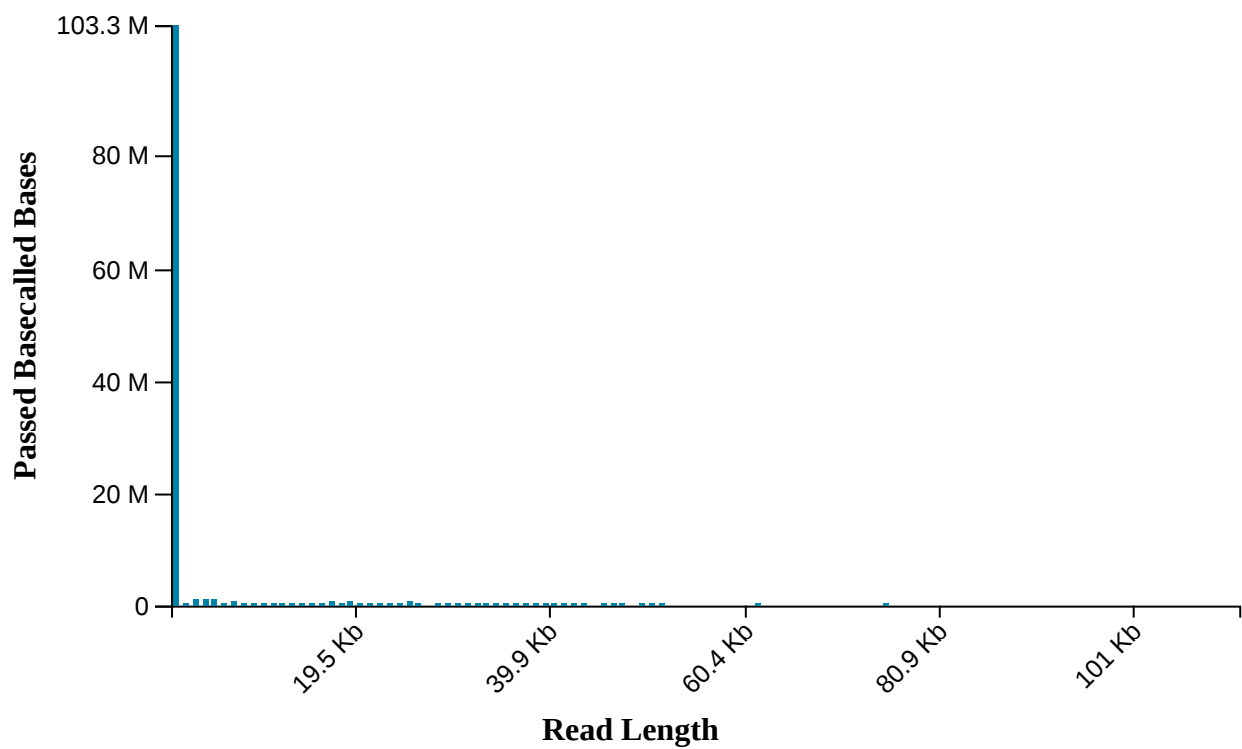
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 490



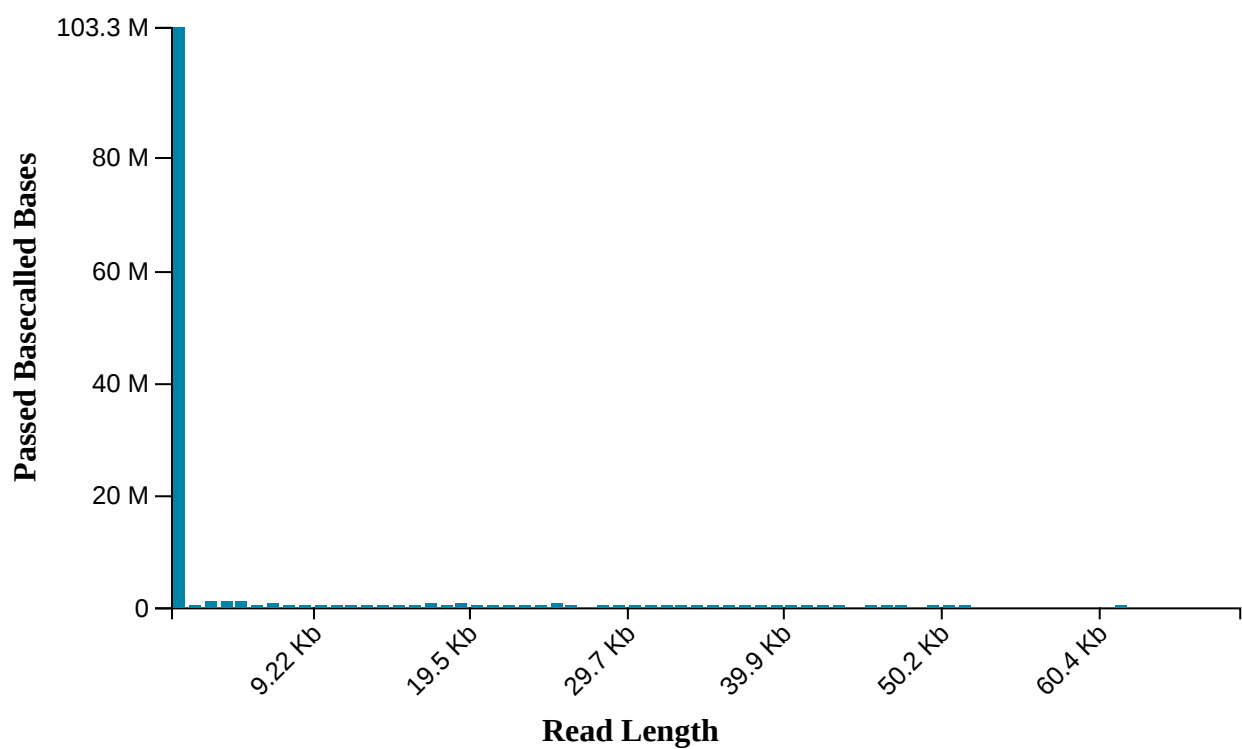
Read Length Histogram Estimated Bases

Estimated N50: 492

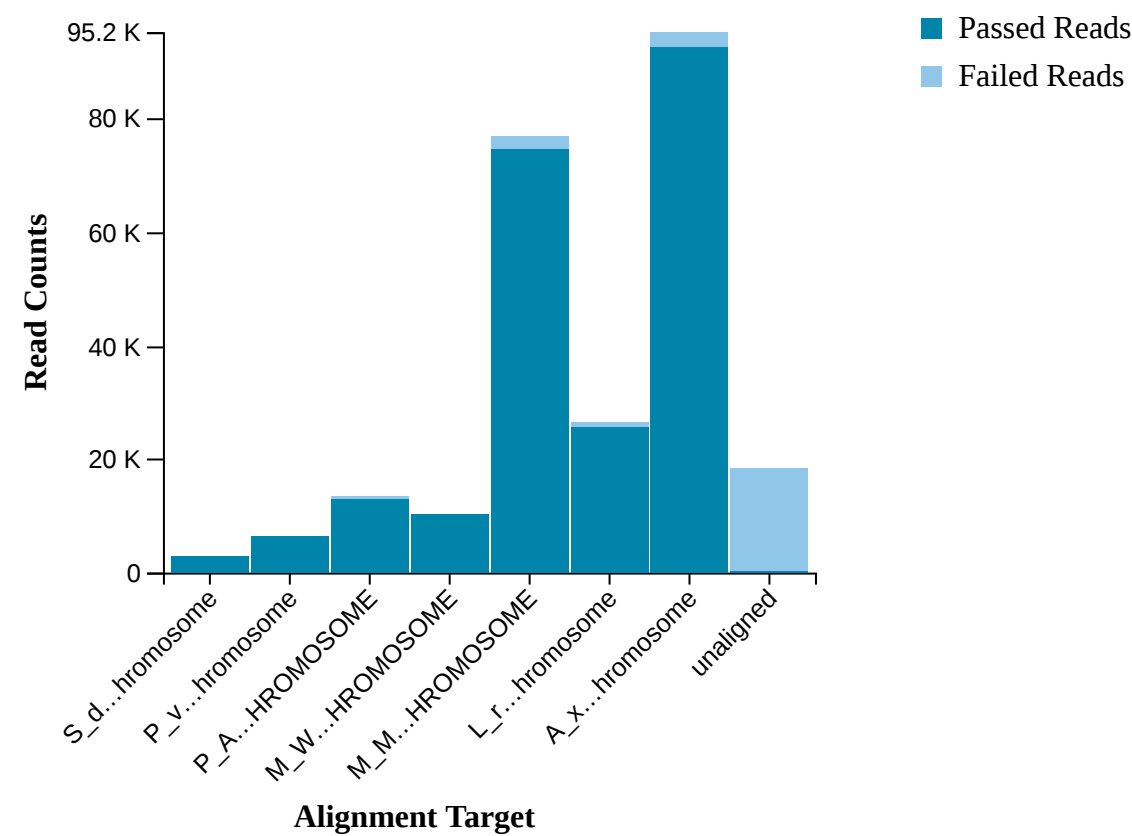


Read Length Histogram Basecalled Bases

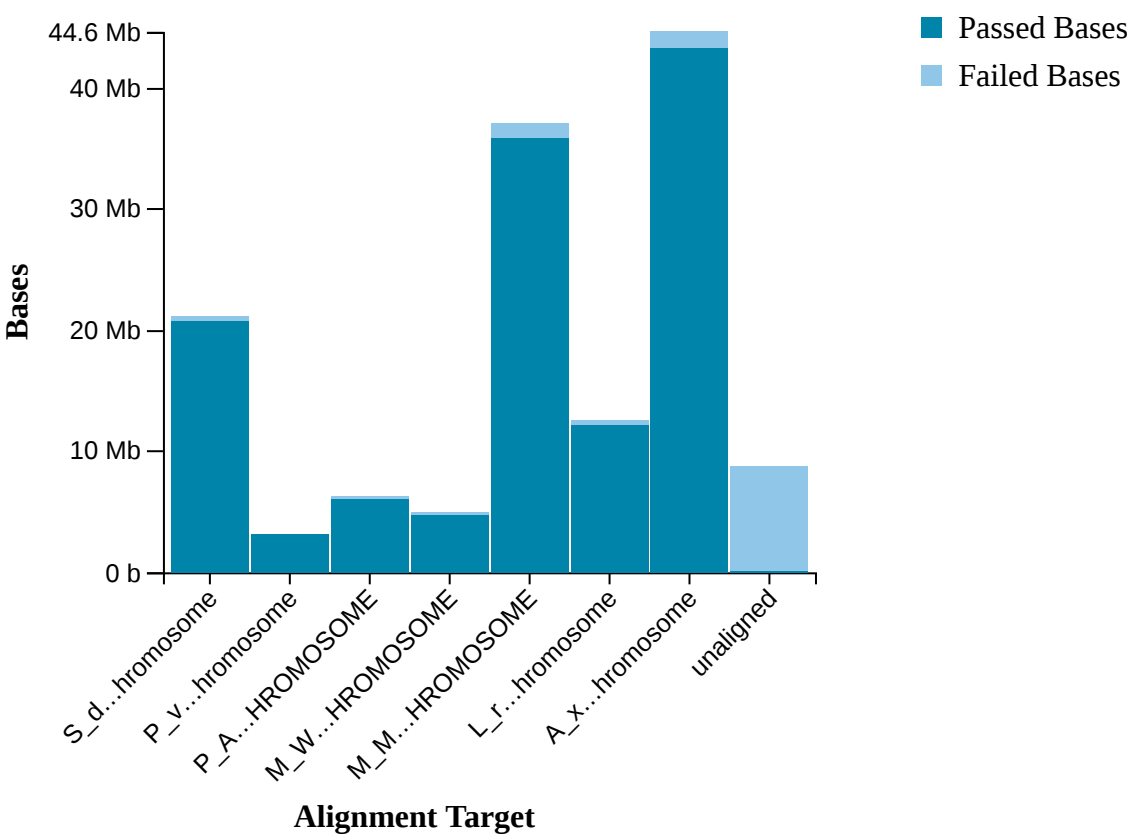
Estimated N50: 490



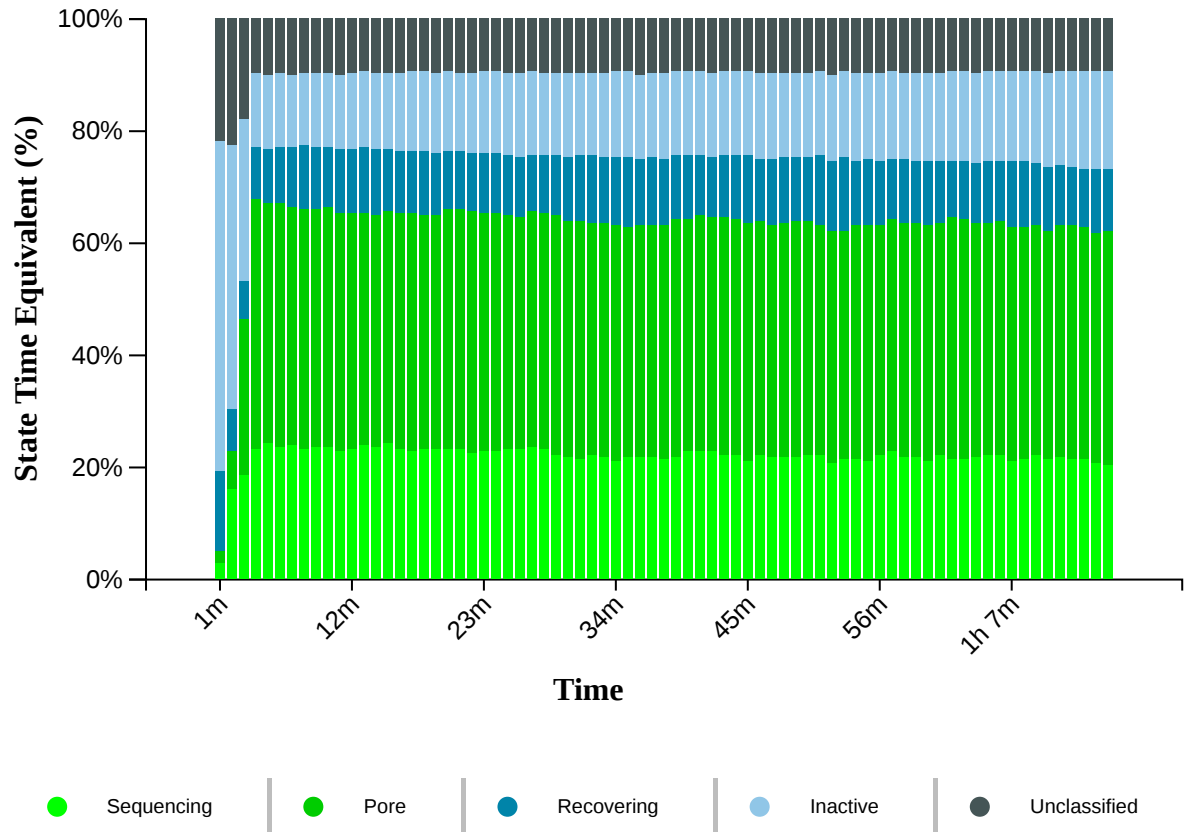
Alignment Target Hits (reads)



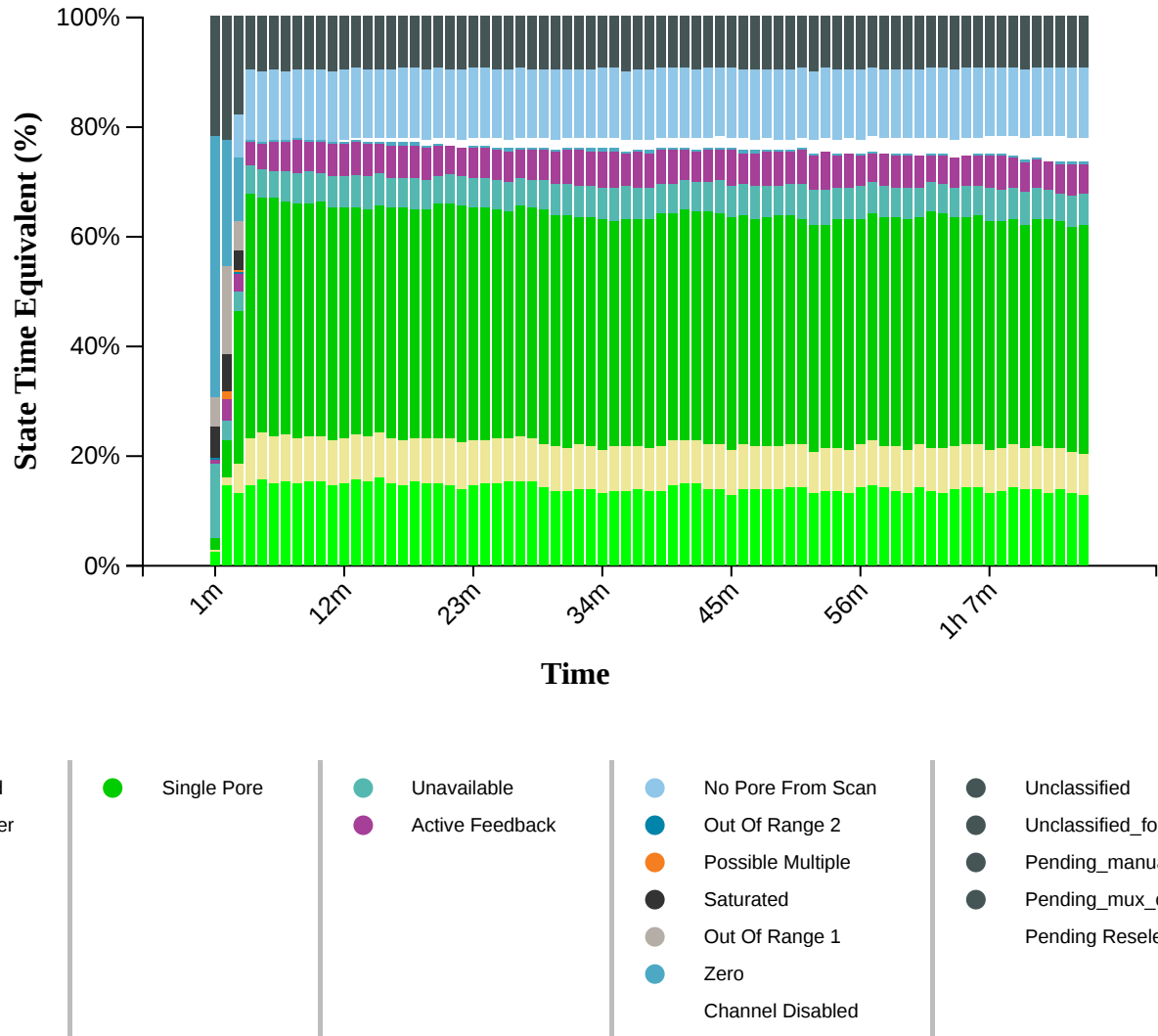
Alignment Target Hits (bases)



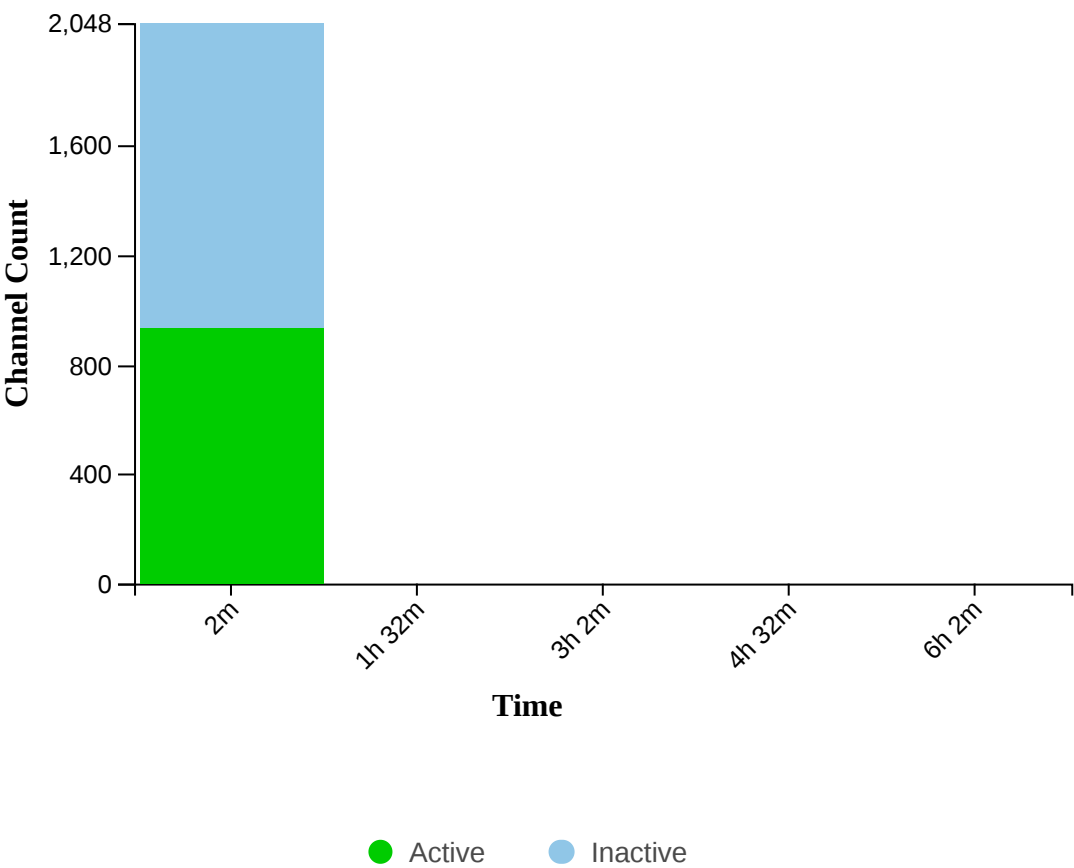
Duty Time Grouped



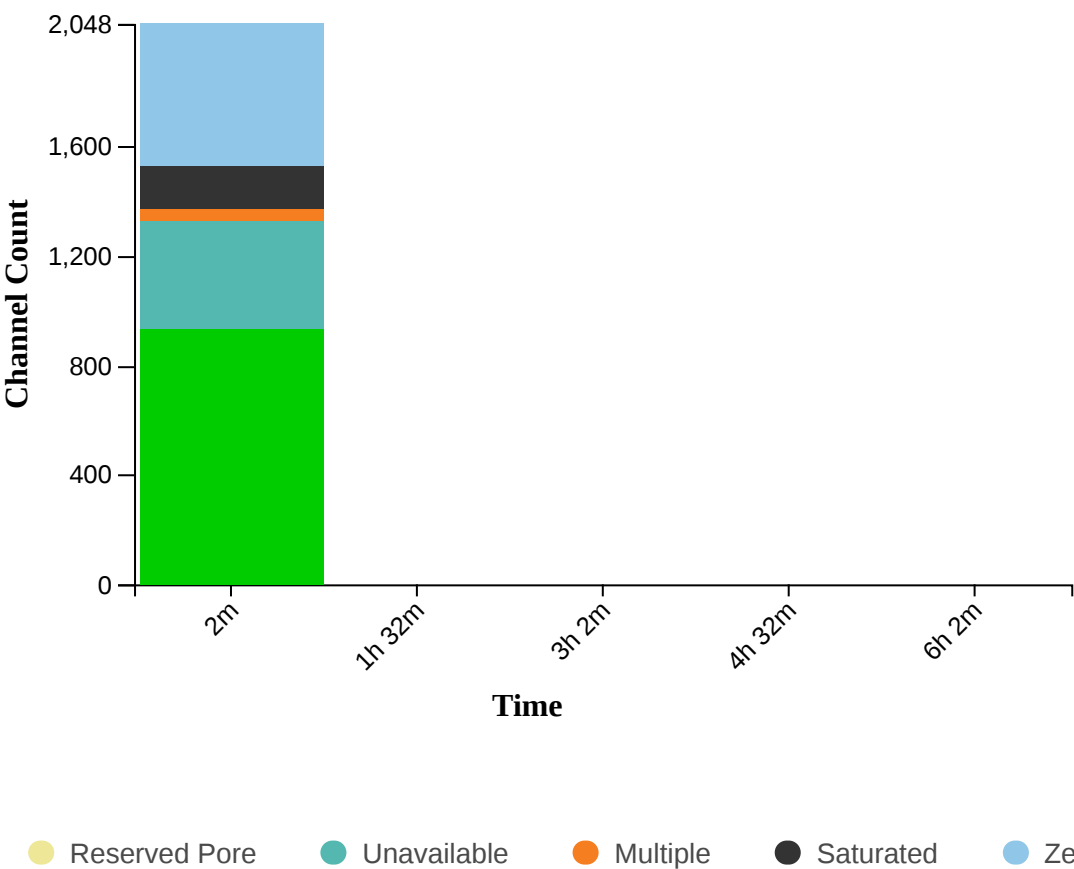
Duty time Categorised



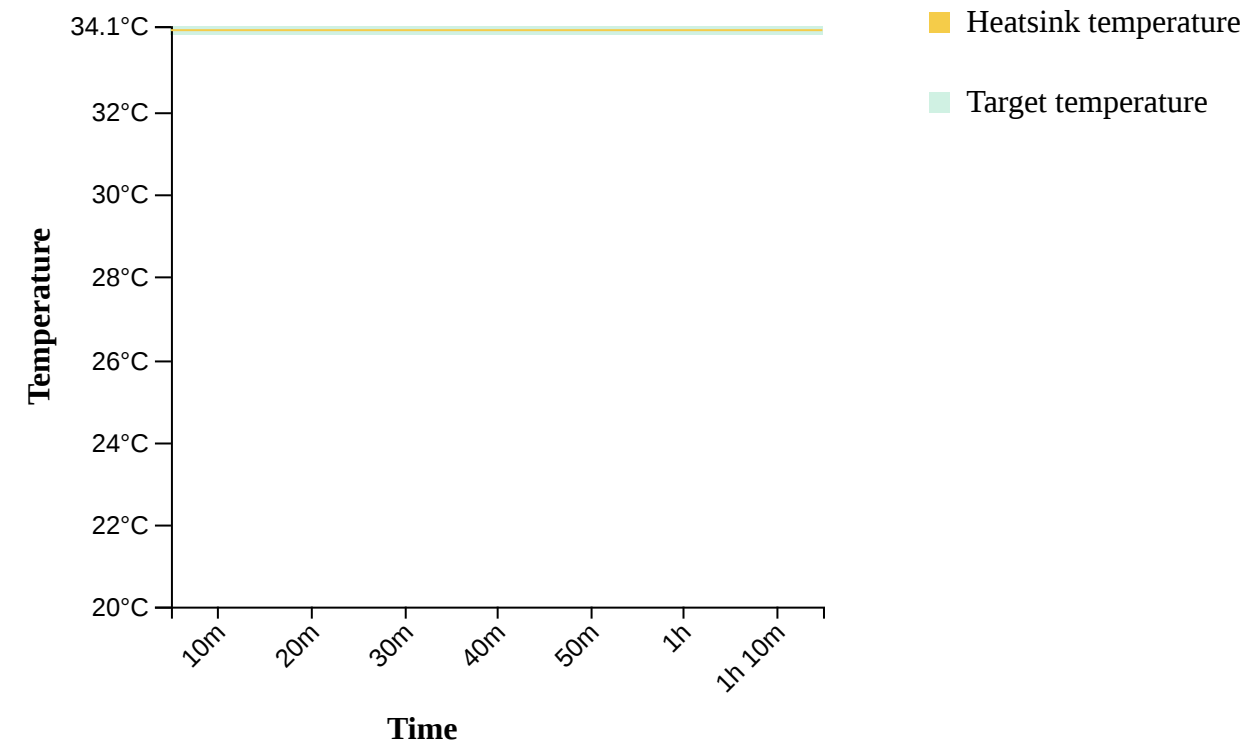
Mux Scan Grouped



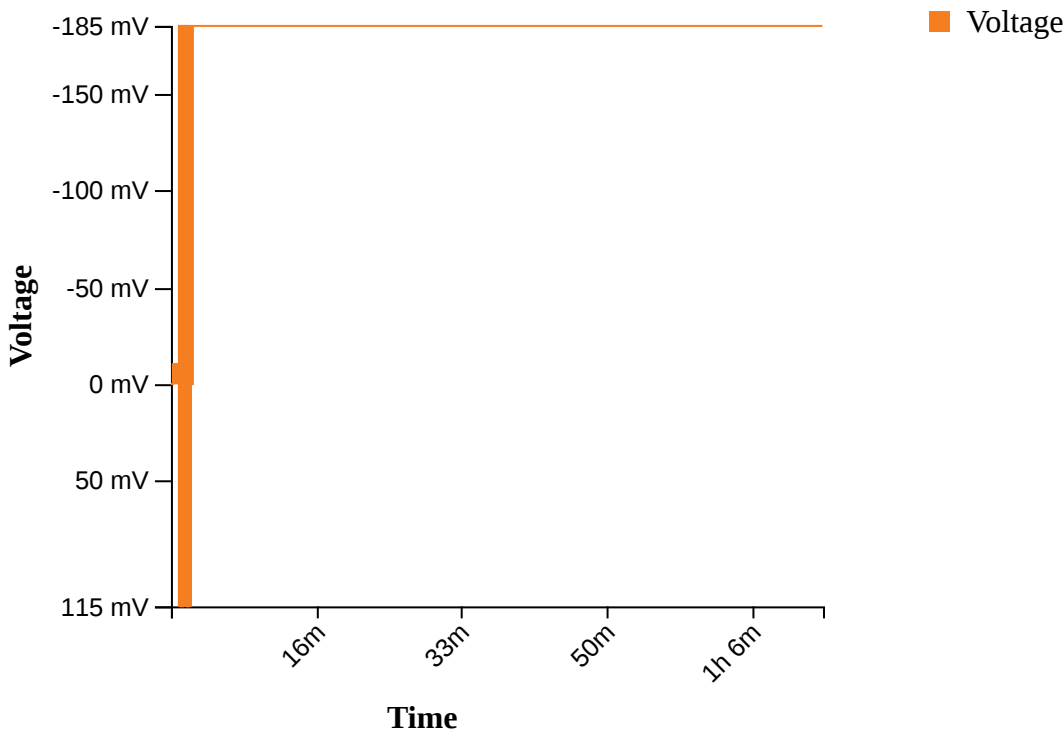
Mux Scan Categorised



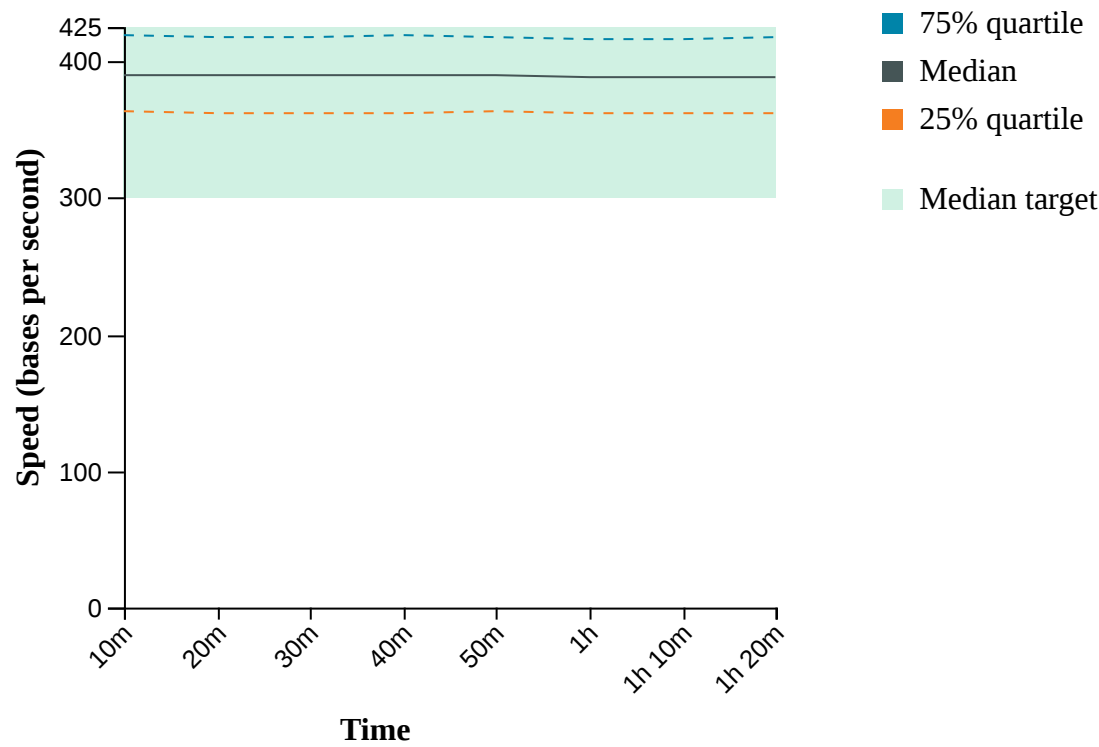
Temperature History.



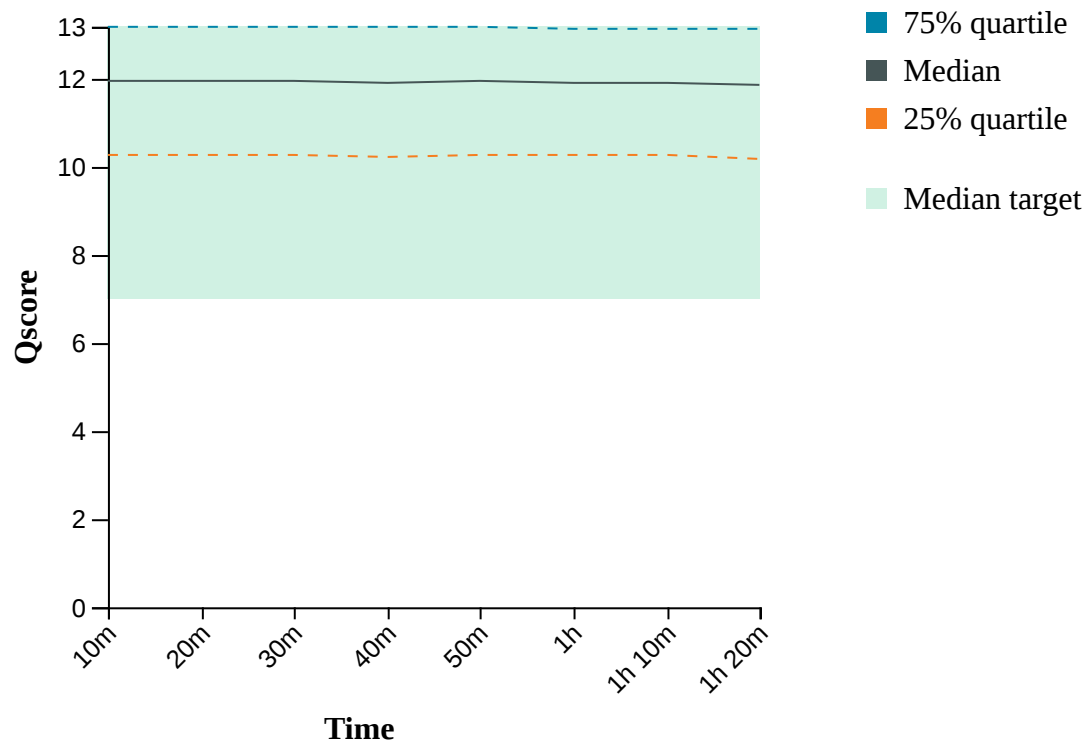
Bias Voltage History.



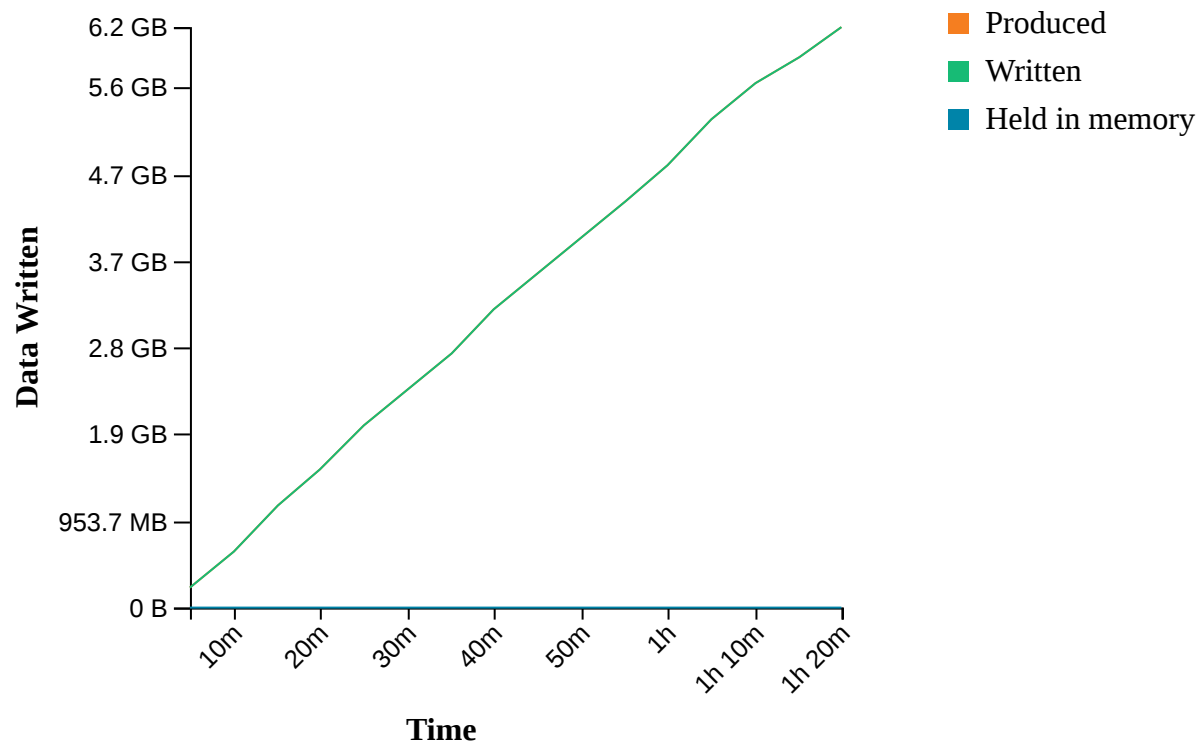
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAO52906 has found a total of 934 pores. 447 pores available for immediate sequencing December 8, 19:10
- Performing Mux Scan December 8, 19:08
- Starting sequencing procedure December 8, 19:08
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C December 8, 19:05