



## Run Info

Host Name	GXB03020 (localhost)
Experiment Name	ReadUntil_38Kbp_LowtoHigh_MwEnr_15042021
Sample ID	ReadUntil_38Kbp_LowtoHigh_MwEnr_15042021
Run ID	7a2587c6-fcc6-4ea1-ab8b-b5fdea5ae965
Flow Cell Id	FAP14753
Start Time	April 15, 14:26
Run Length	1h 0m

## Run Summary

Reads Generated	103.57 K
Passed Bases	377.53 Mb
Failed Bases	17.11 Mb
Estimated Bases	391.73 Mb

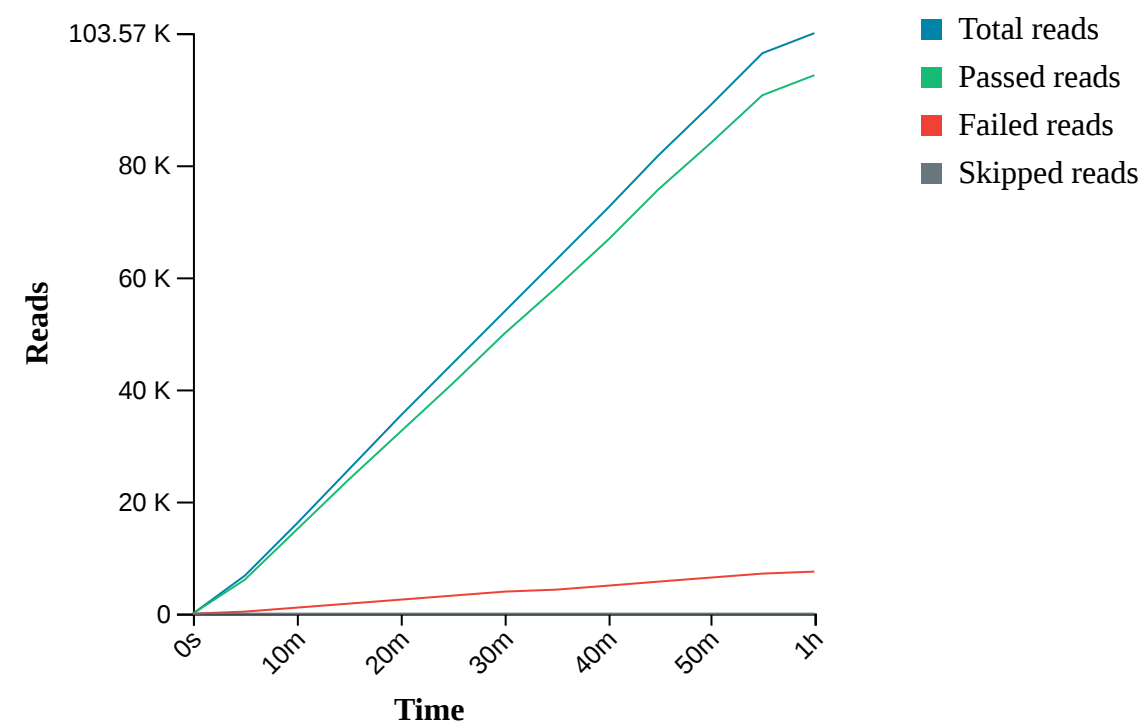
## Run Parameters

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_wisconsensus_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

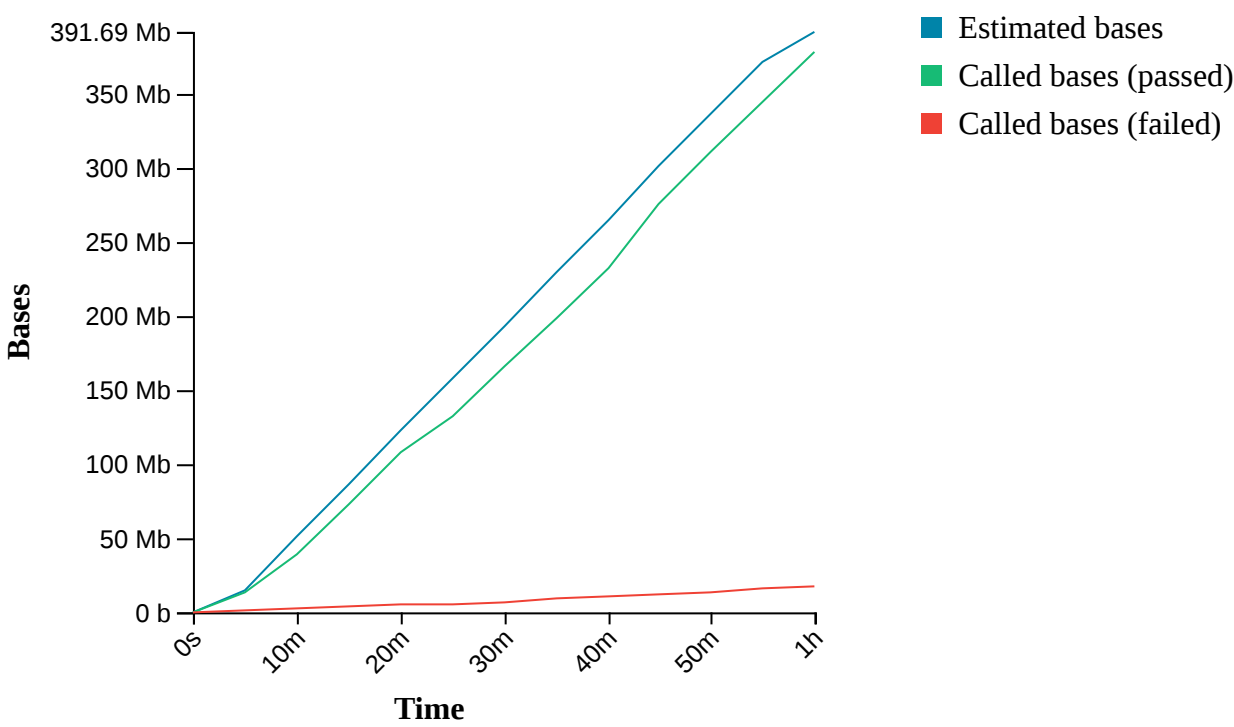
## Versions

MinKNOW	21.02.5
MinKNOW Core	4.2.5
Bream	6.1.10
Guppy	4.3.4

Cumulative Output Reads

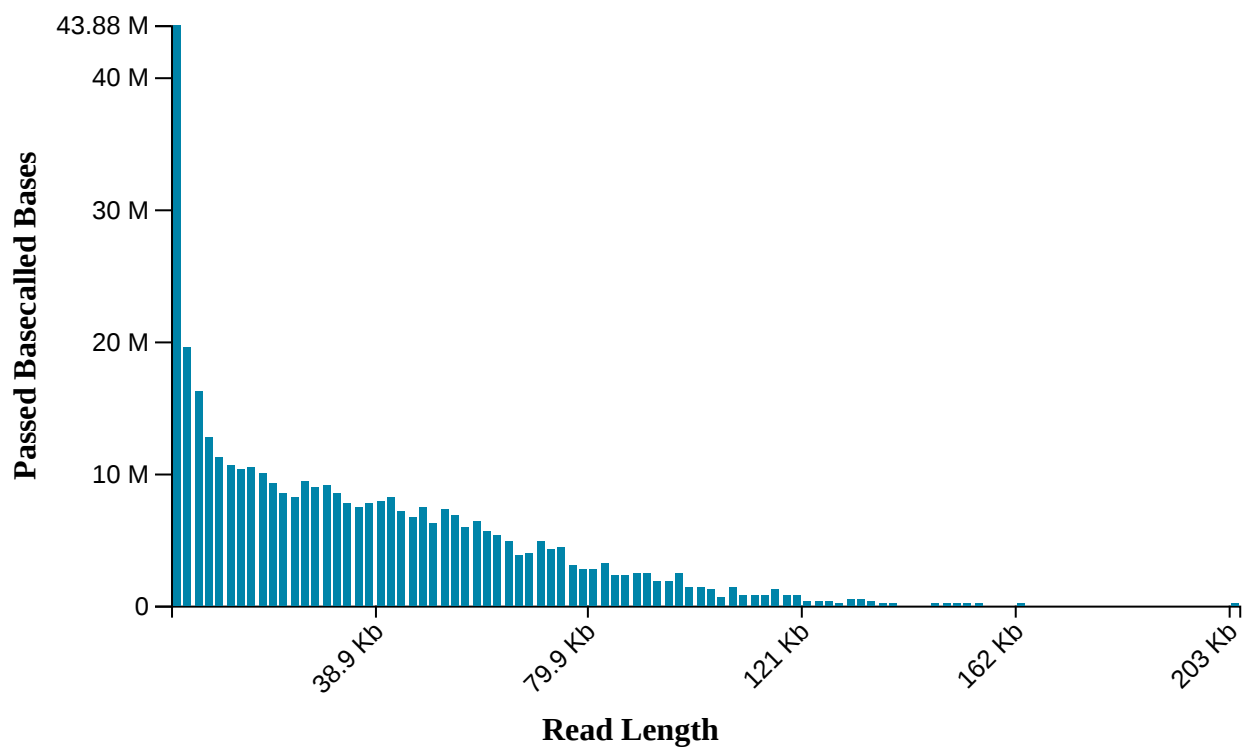


Cumulative Output Bases



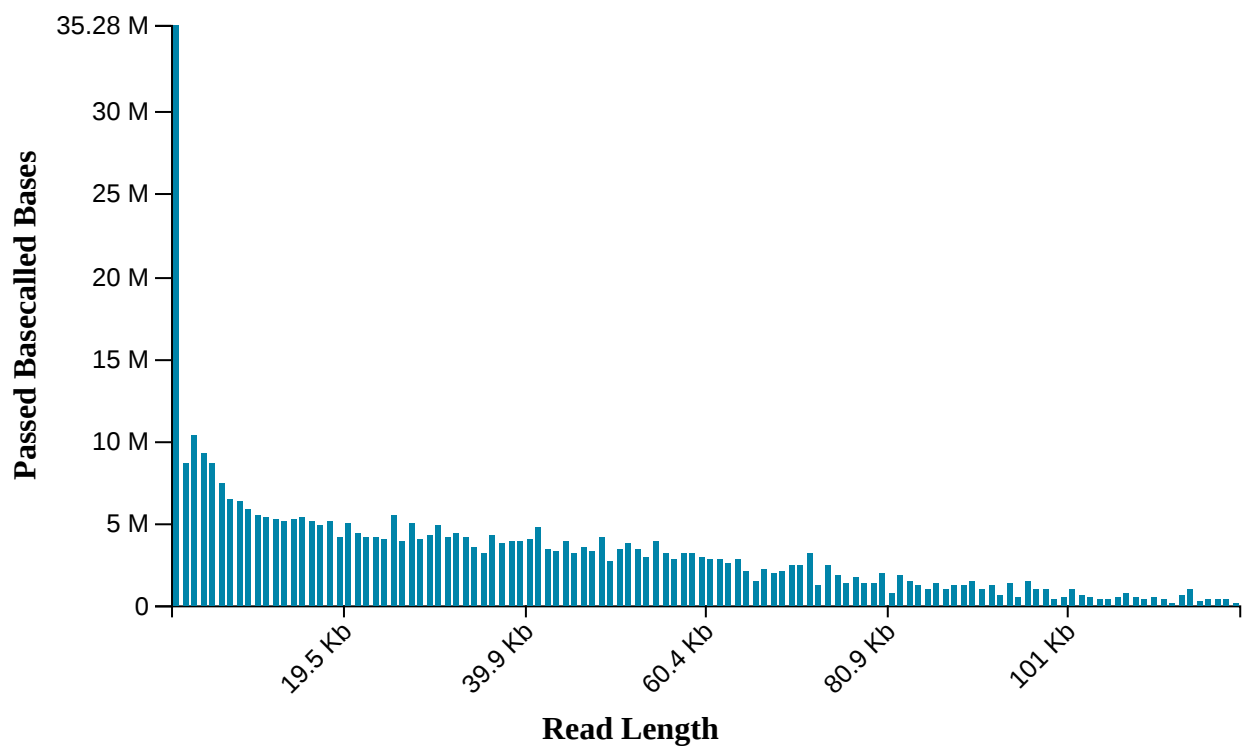
**Read Length Histogram Estimated Bases - Outliers Discarded**

Estimated N50: 28.61 K



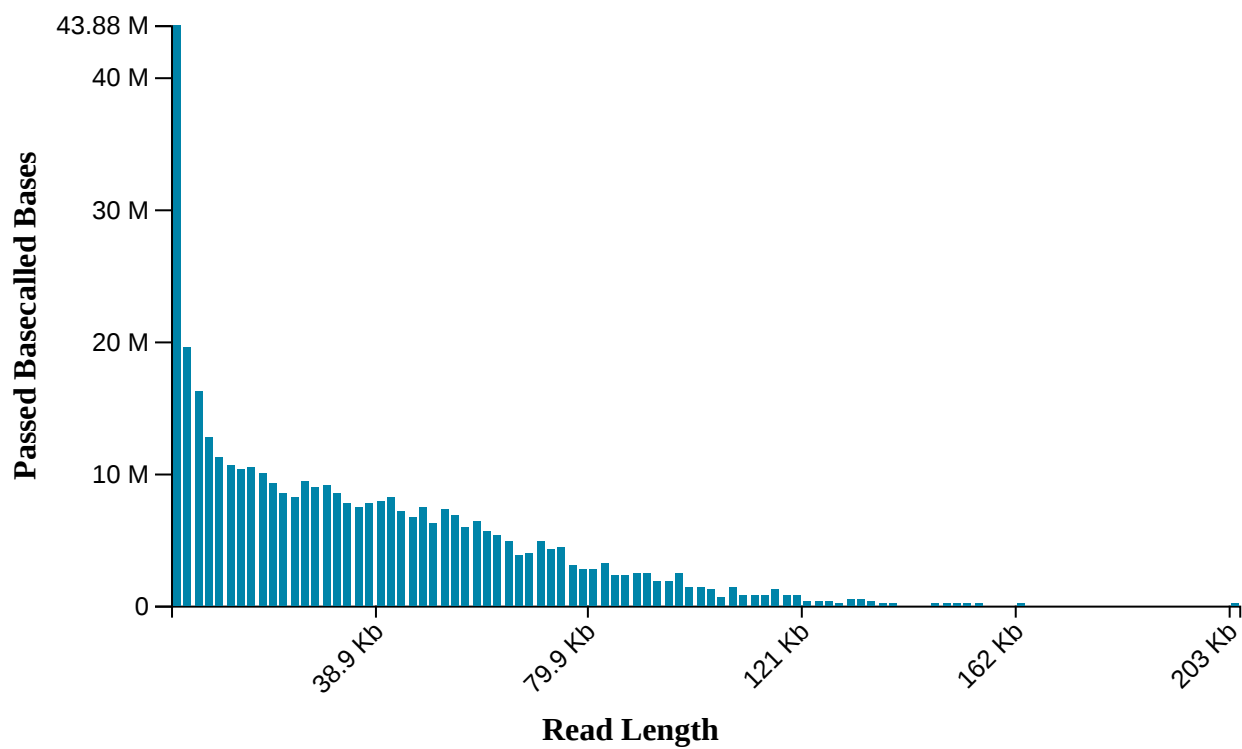
**Read Length Histogram Basecalled Bases - Outliers Discarded**

Estimated N50: 28.12 K



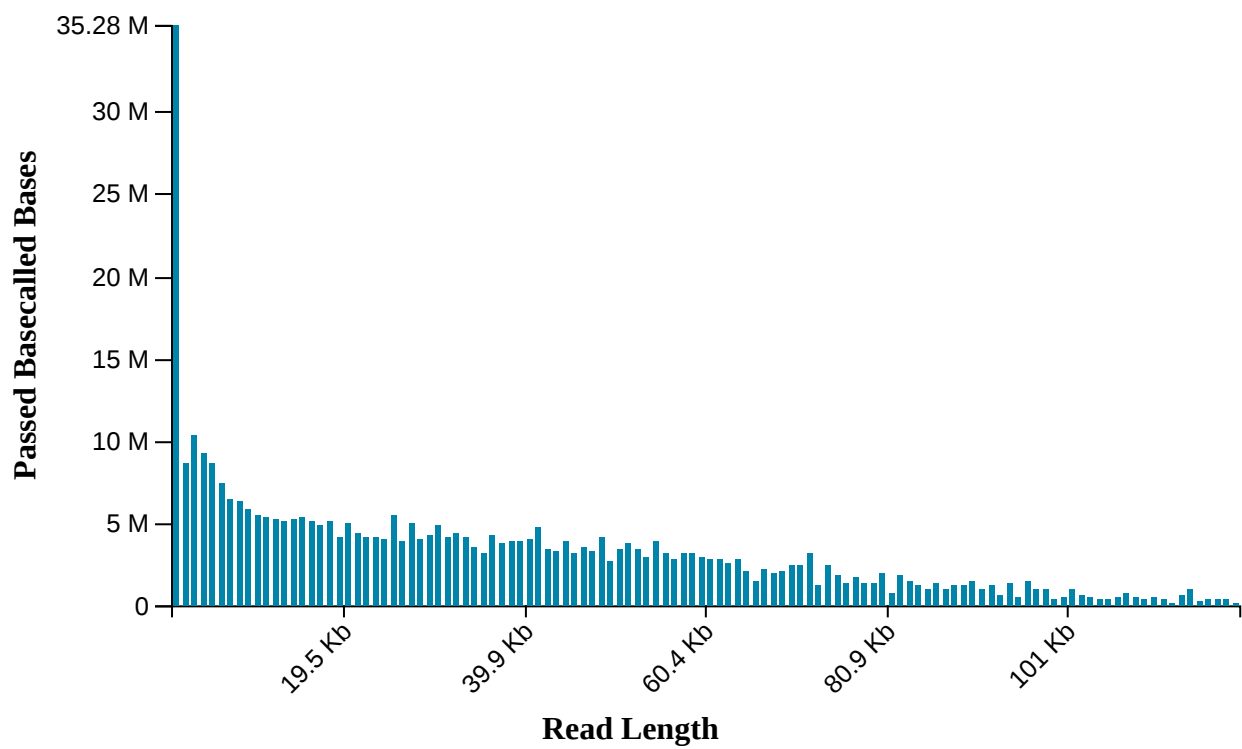
**Read Length Histogram Estimated Bases**

Estimated N50: 28.61 K

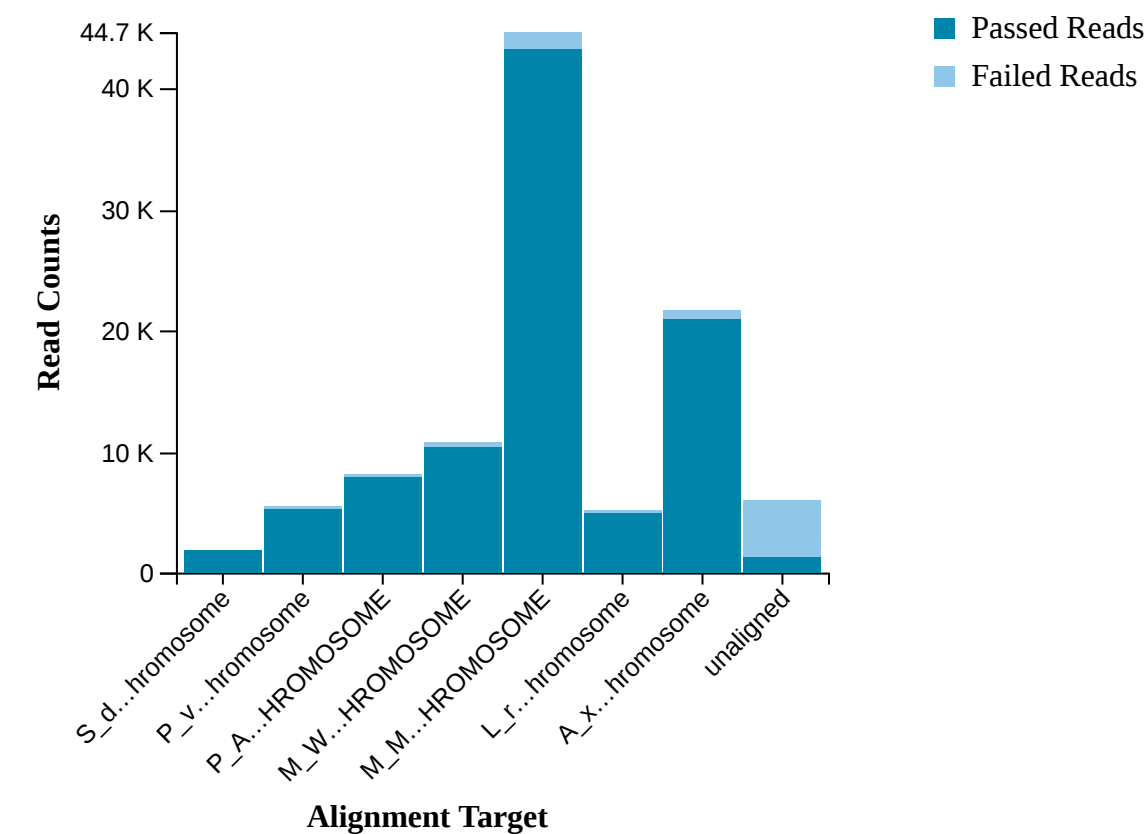


**Read Length Histogram Basecalled Bases**

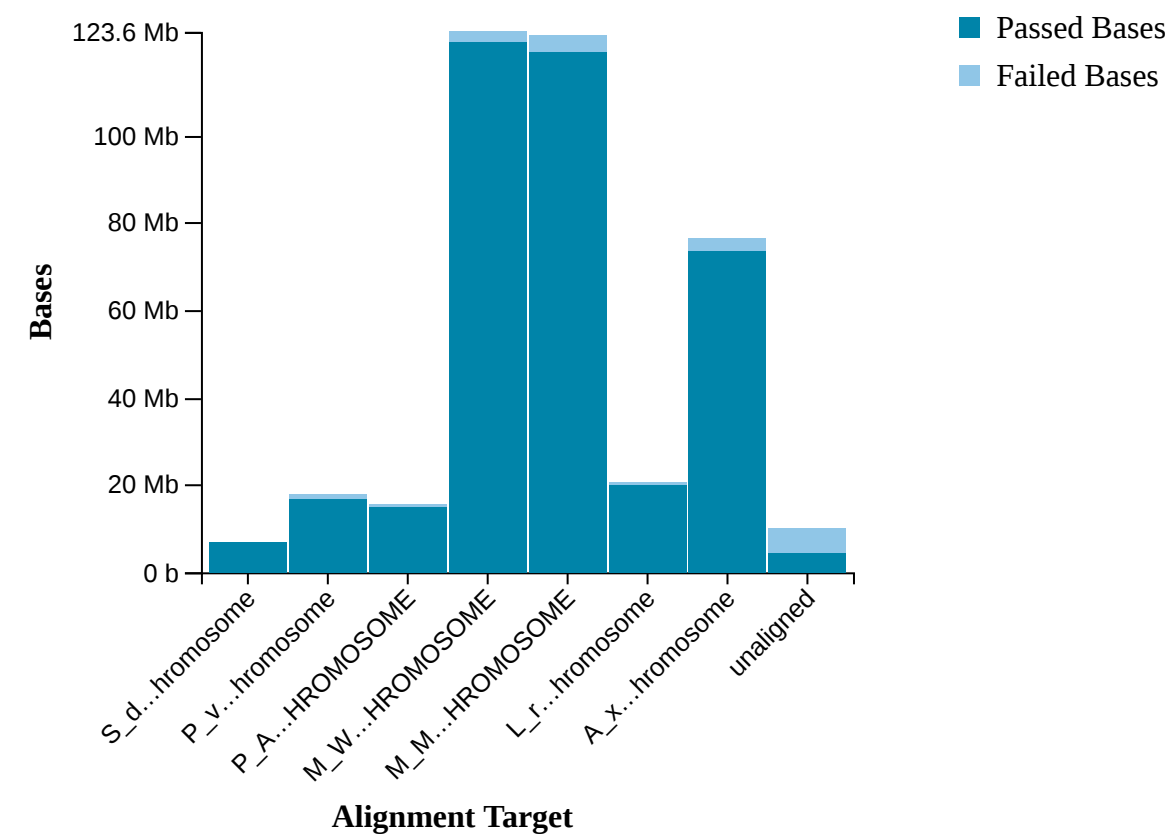
Estimated N50: 28.12 K



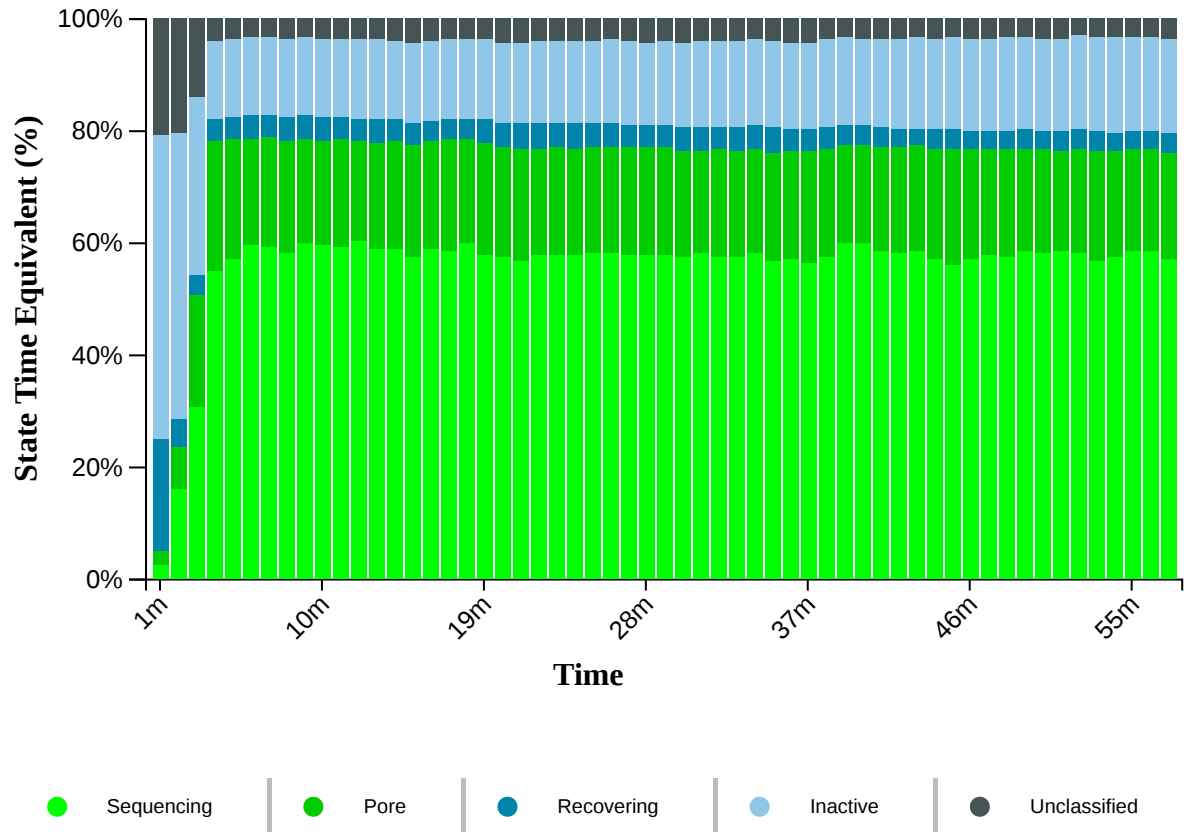
Alignment Target Hits (reads)



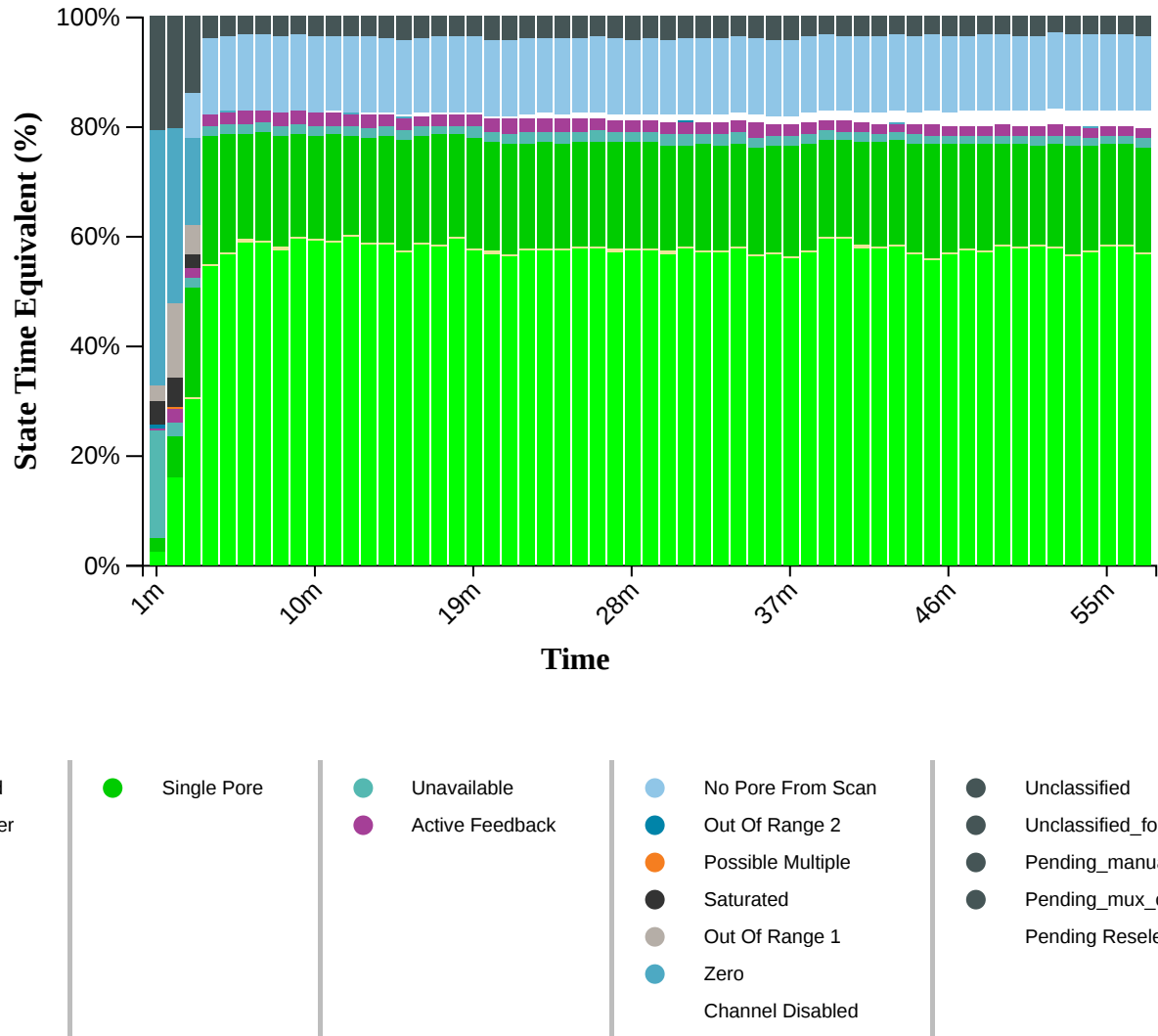
Alignment Target Hits (bases)



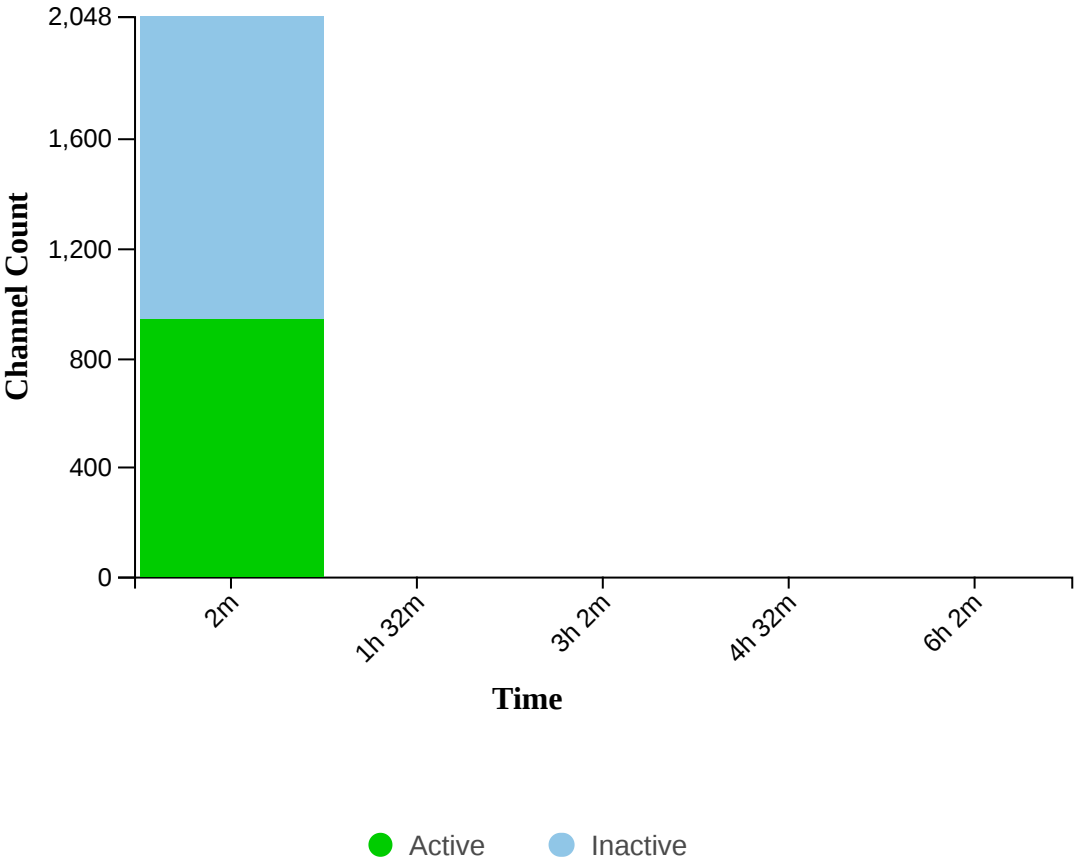
Duty Time Grouped



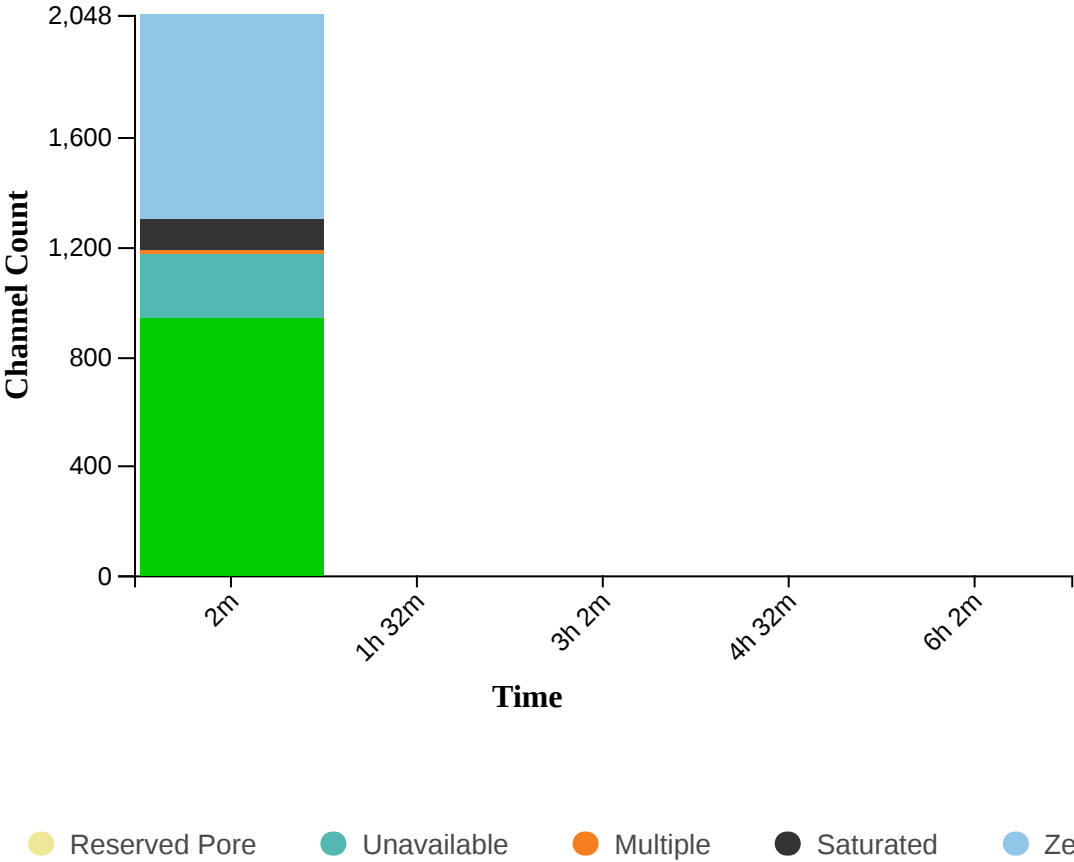
Duty time Categorised



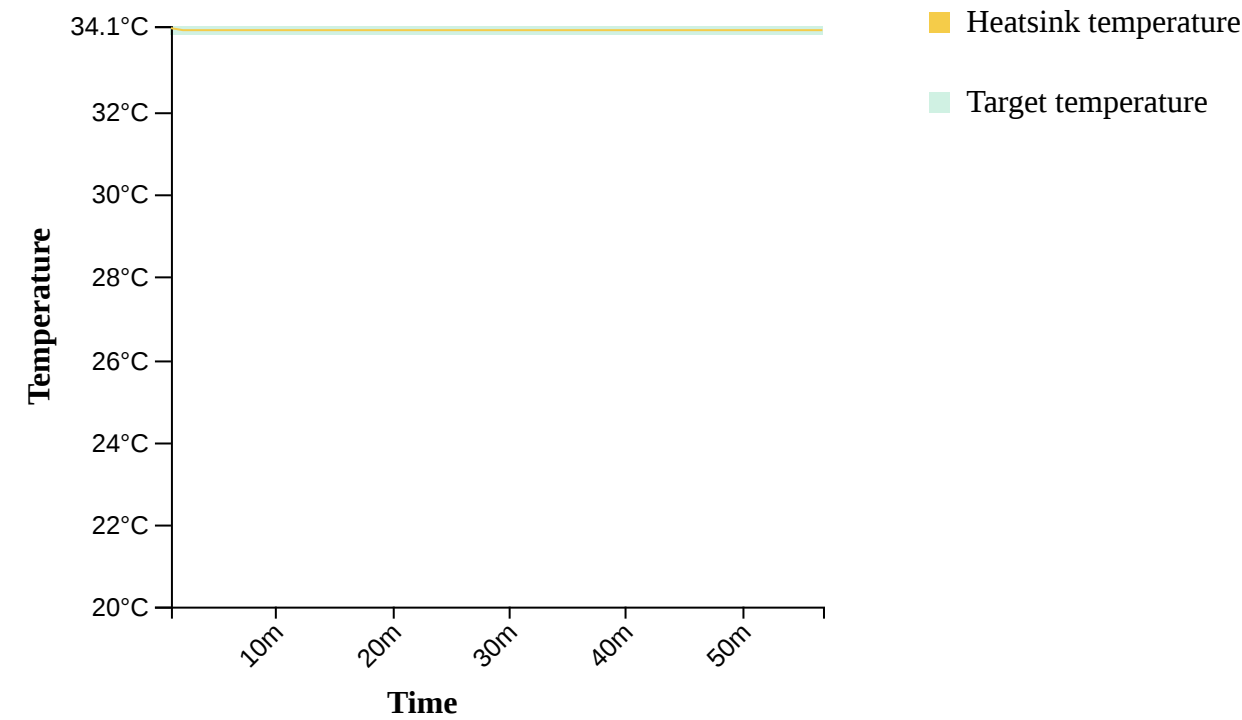
Mux Scan Grouped



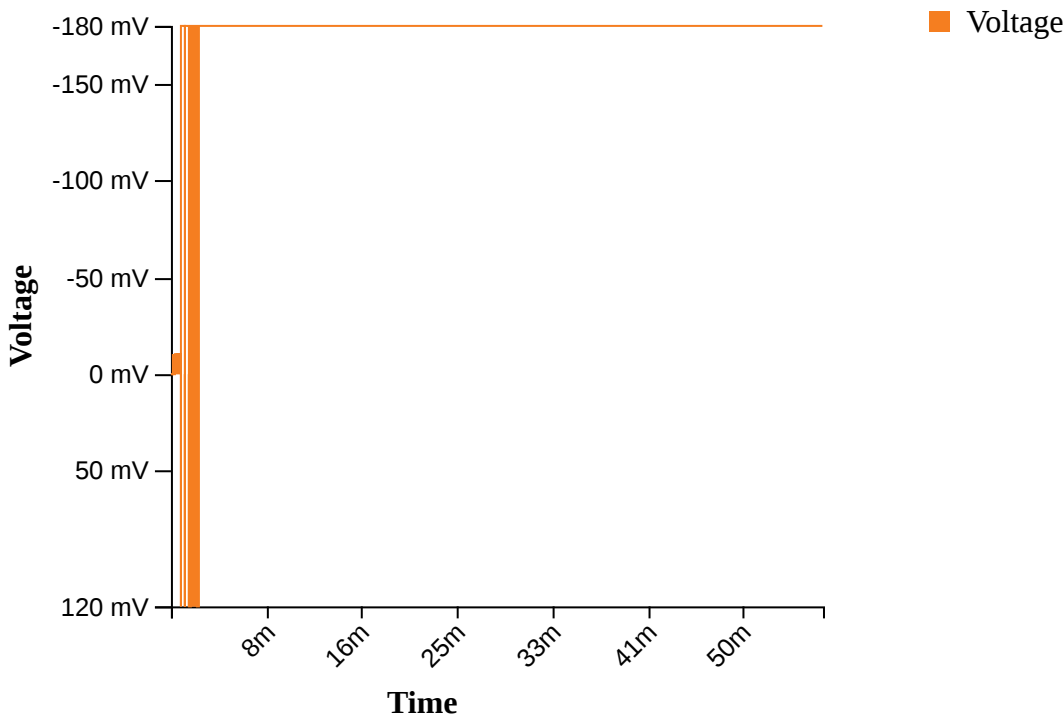
Mux Scan Categorised



Temperature History.

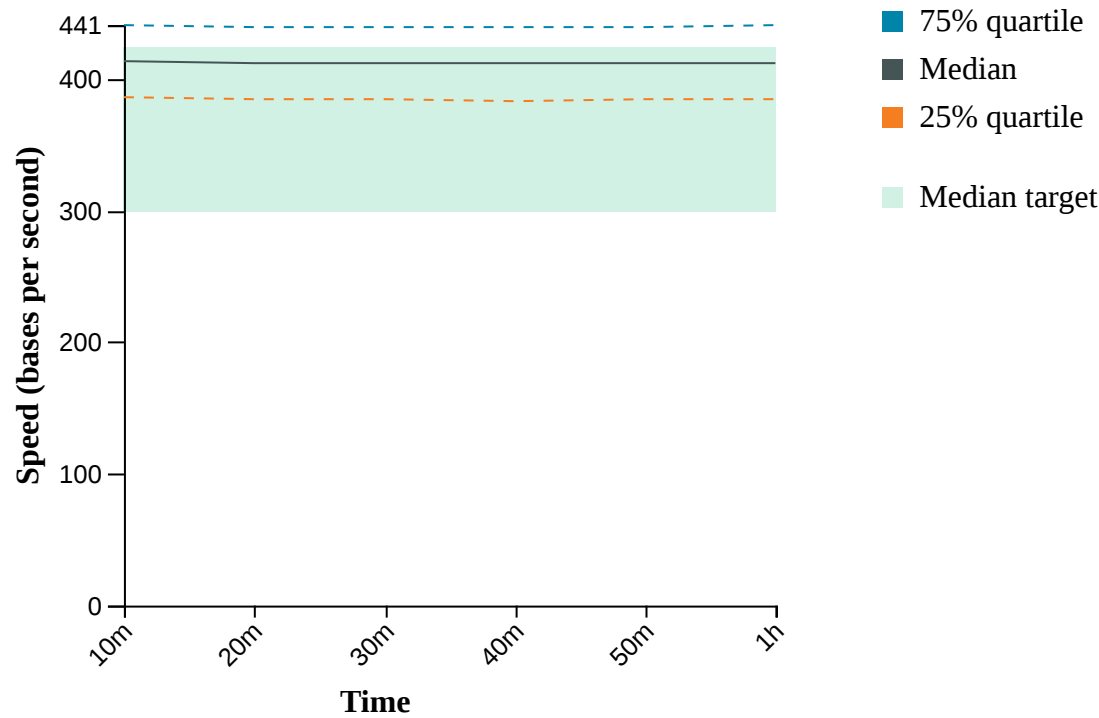


Bias Voltage History.

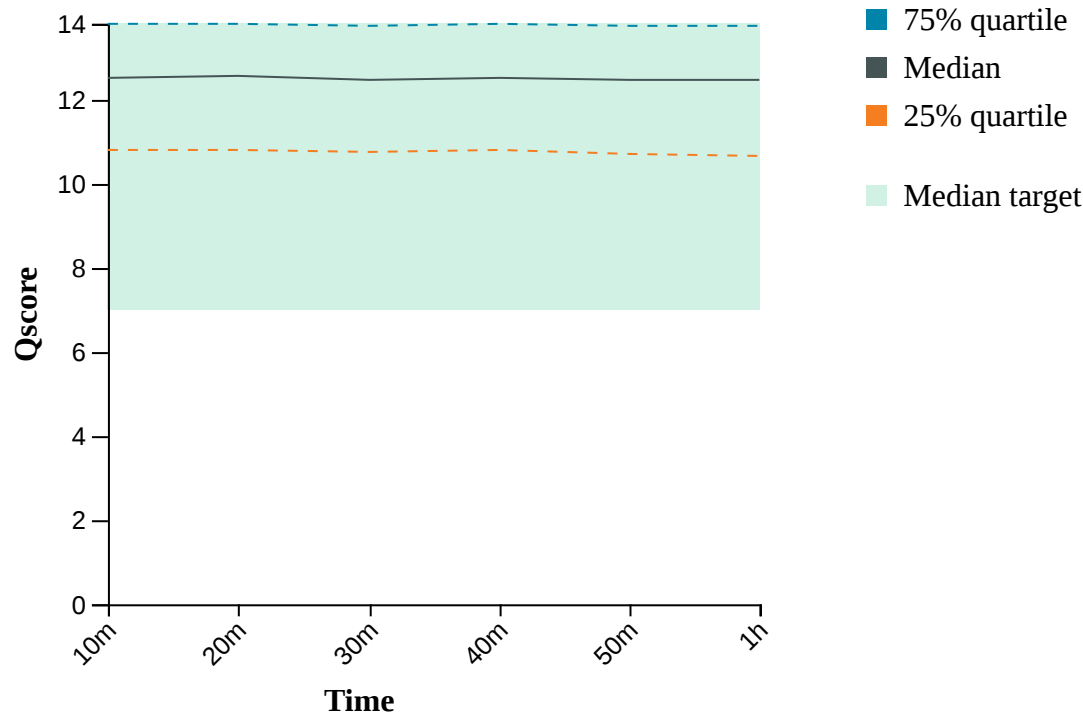




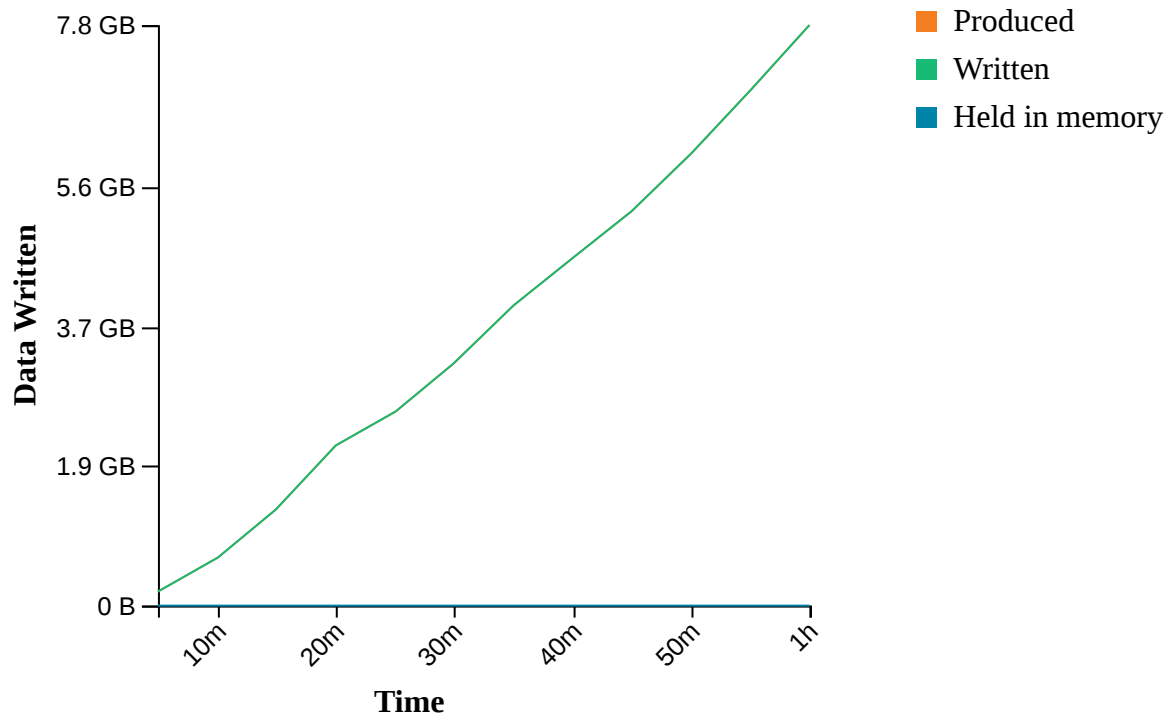
Translocation Speed



QScore



Disk Write Performance



### **Run Debug Messages**

- Mux scan for flow cell FAP14753 has found a total of 947 pores. 441 pores available for immediate sequencing April 15, 14:31
- Performing Mux Scan April 15, 14:29
- Starting sequencing procedure April 15, 14:29
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 14:26