



## Run Info

Host Name	GXB03020 (localhost)
Experiment Name	ReadUntil_38kb_HightoLow_AxEnr_15042021
Sample ID	ReadUntil_38kb_HightoLow_AxEnr_15042021
Run ID	9de83e89-70cb-483f-89be-e9438fcb923a
Flow Cell Id	FAP21636
Start Time	April 15, 13:21
Run Length	1h 0m

## Run Summary

Reads Generated	77.1 K
Passed Bases	375.54 Mb
Failed Bases	18.02 Mb
Estimated Bases	397.57 Mb

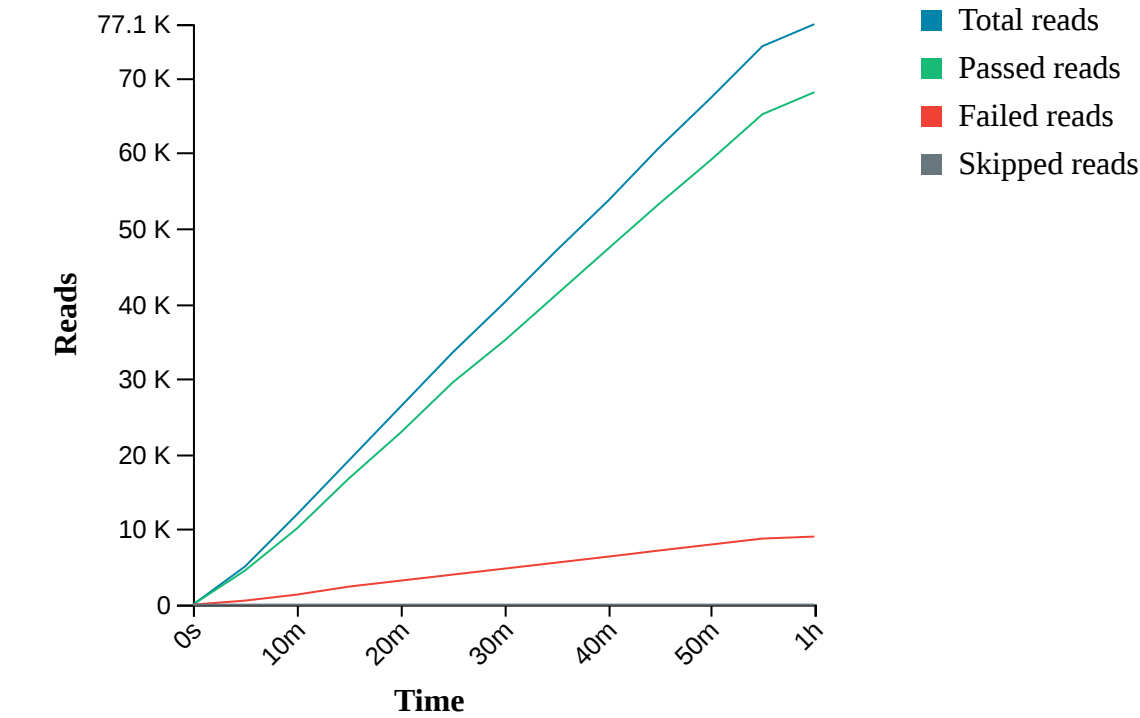
## Run Parameters

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/A_xylooxidans_ref.fa"],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

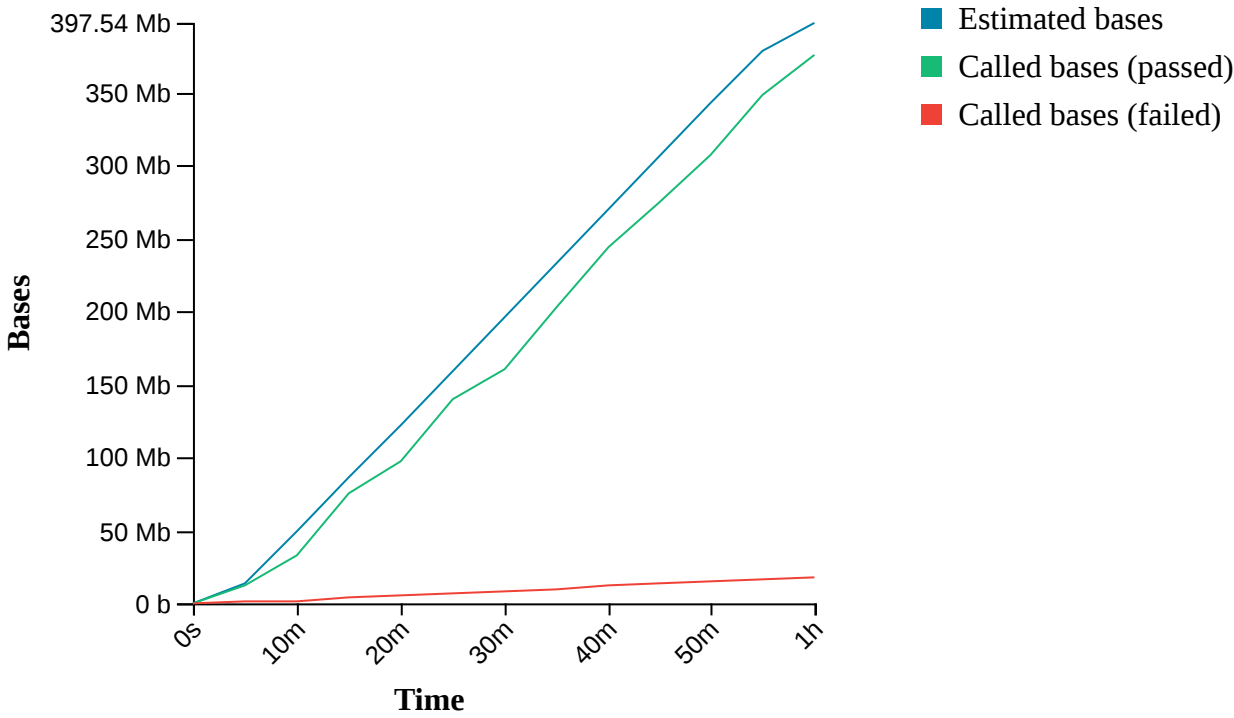
## Versions

MinKNOW	21.02.5
MinKNOW Core	4.2.5
Bream	6.1.10
Guppy	4.3.4

Cumulative Output Reads

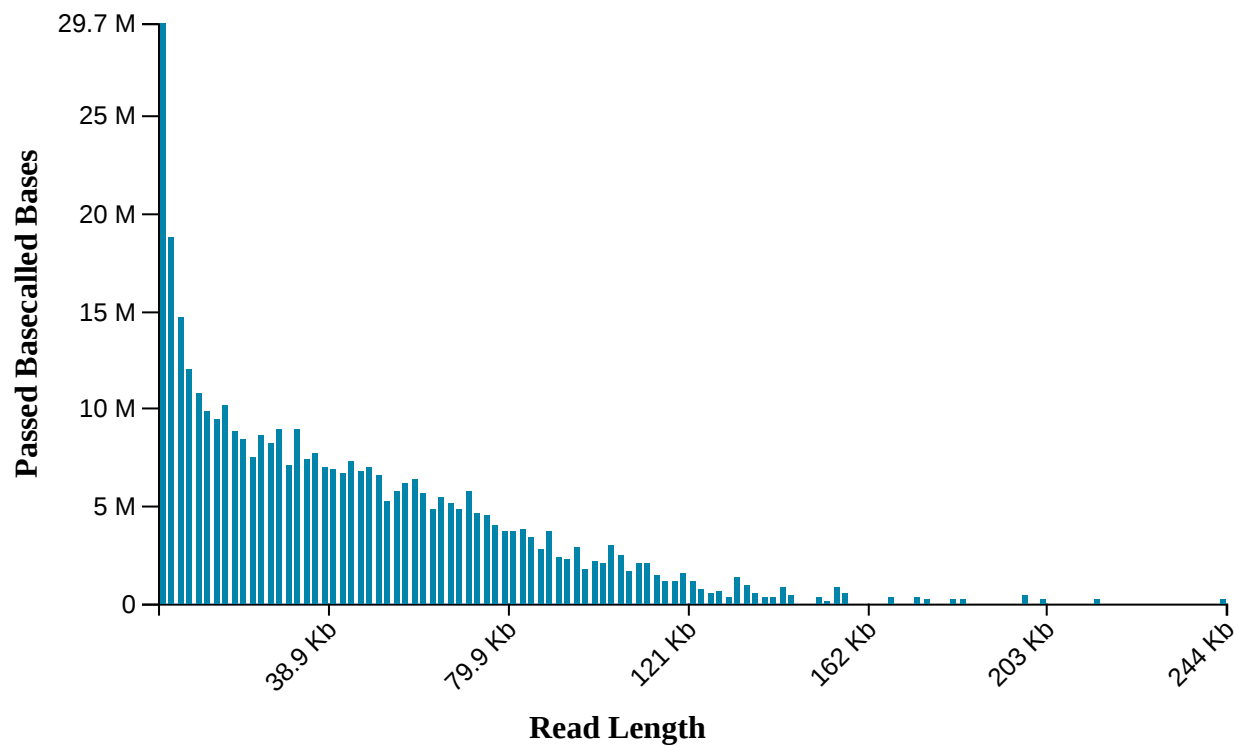


Cumulative Output Bases



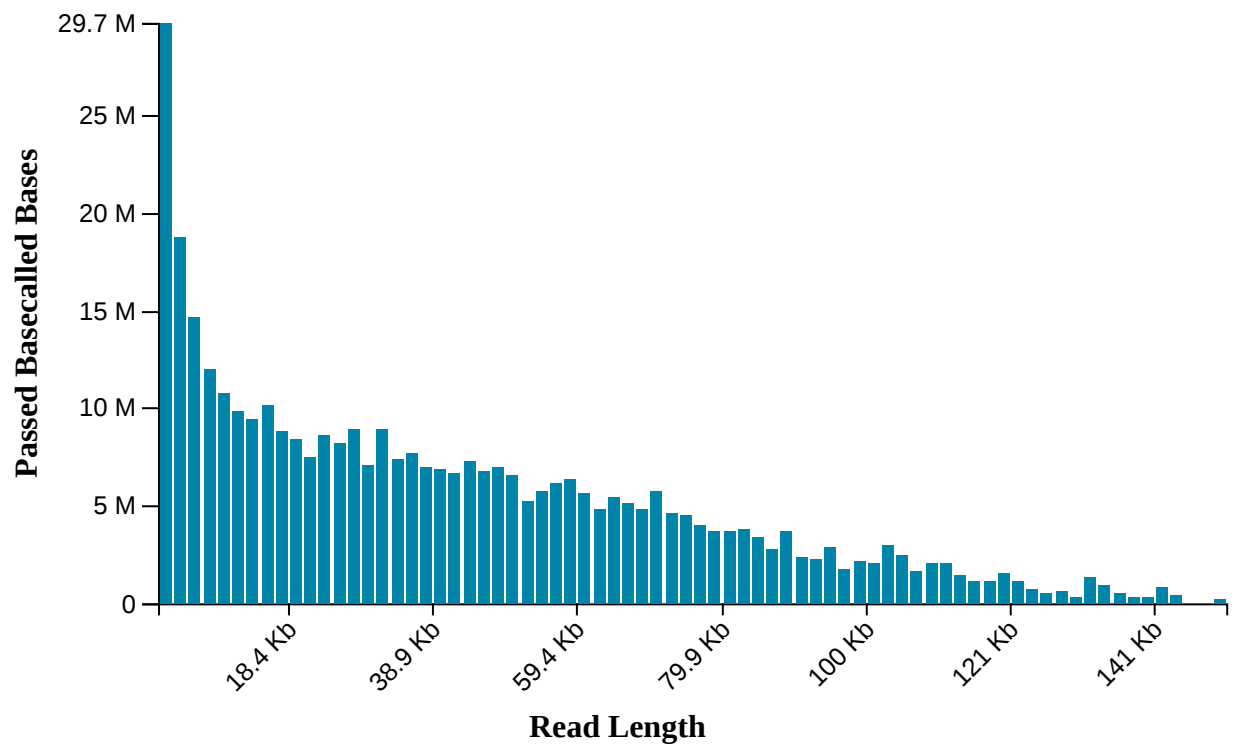
**Read Length Histogram Estimated Bases - Outliers Discarded**

Estimated N50: 34.52 K



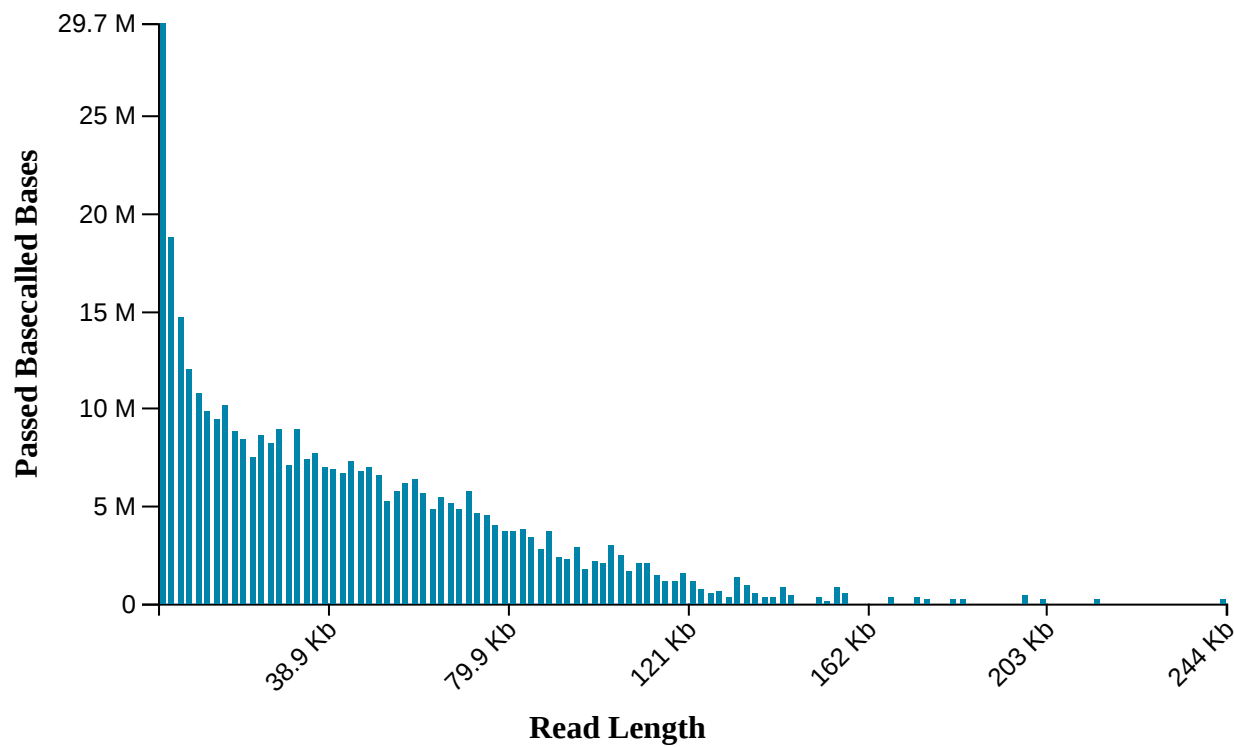
**Read Length Histogram Basecalled Bases - Outliers Discarded**

Estimated N50: 33.98 K



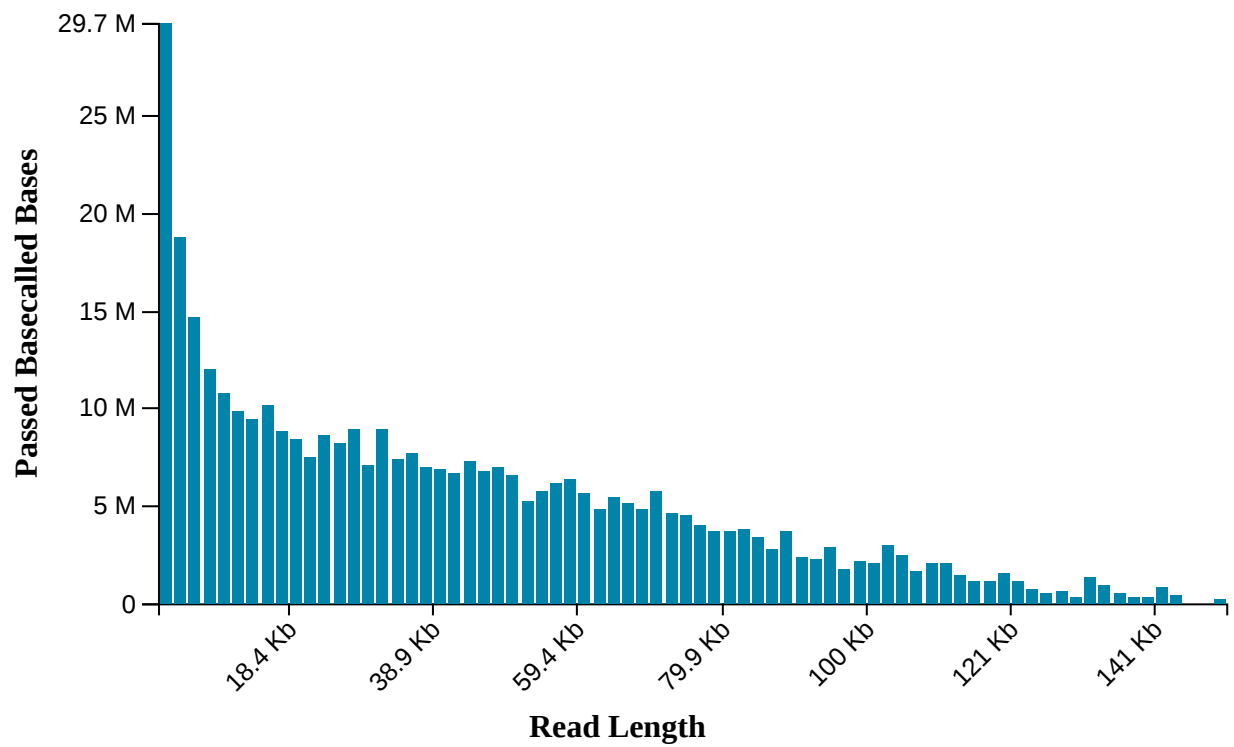
**Read Length Histogram Estimated Bases**

Estimated N50: 34.52 K

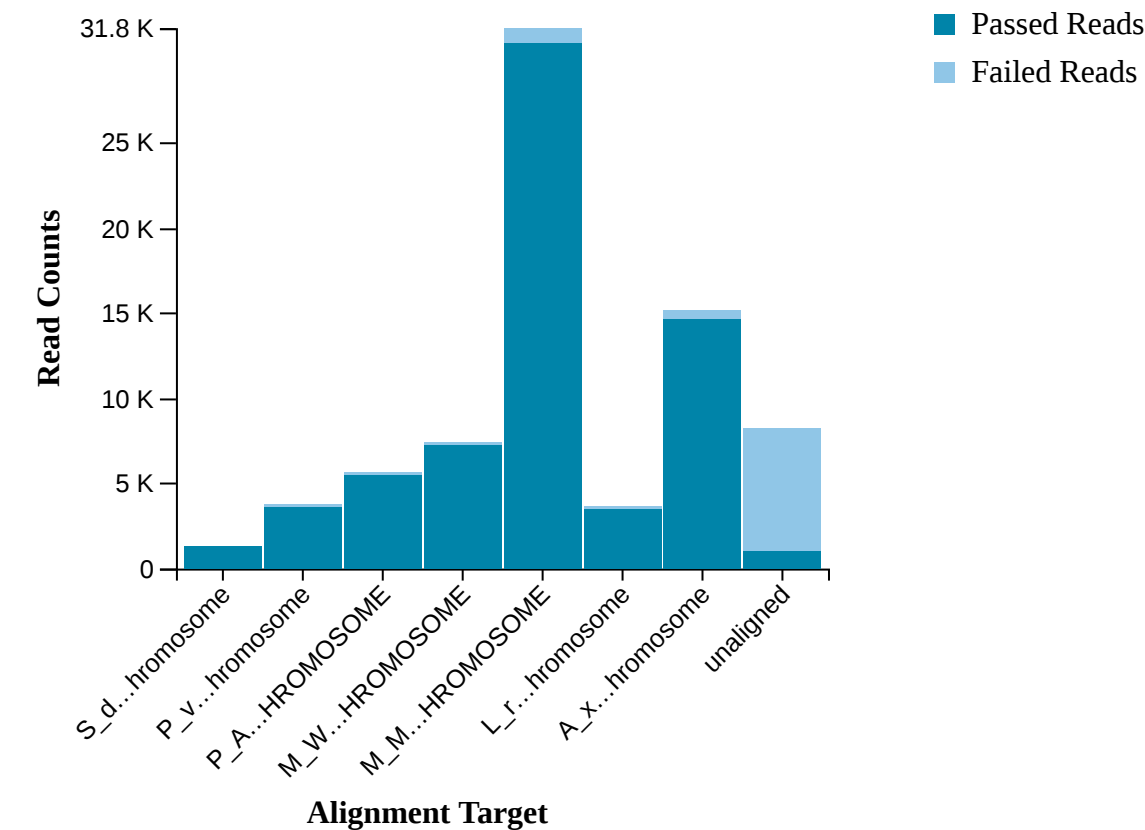


**Read Length Histogram Basecalled Bases**

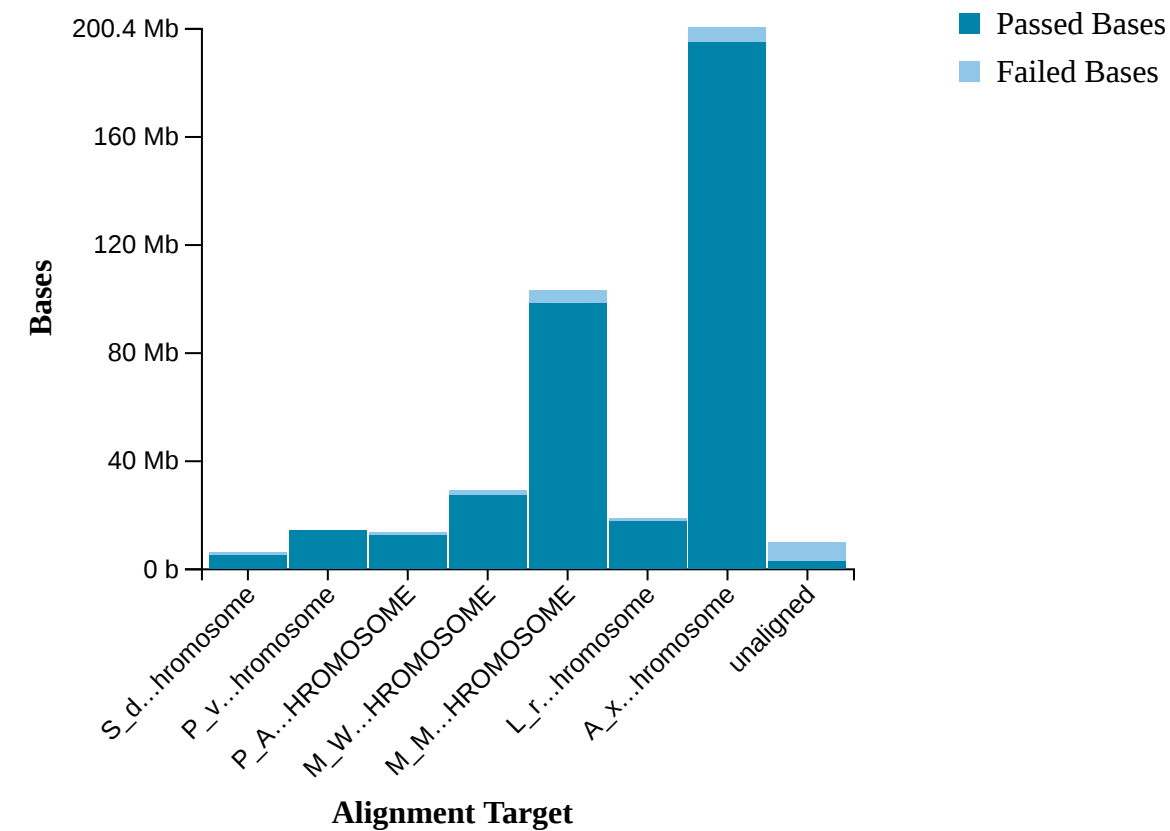
Estimated N50: 33.98 K



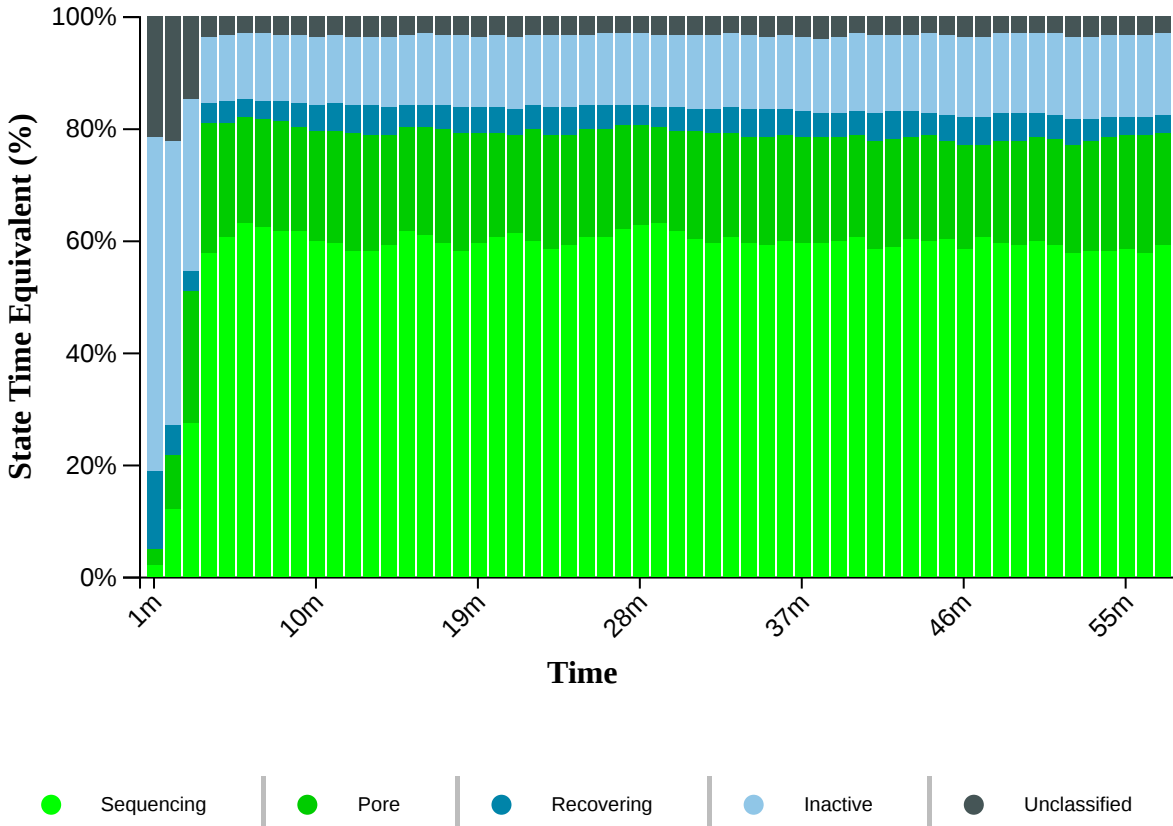
Alignment Target Hits (reads)



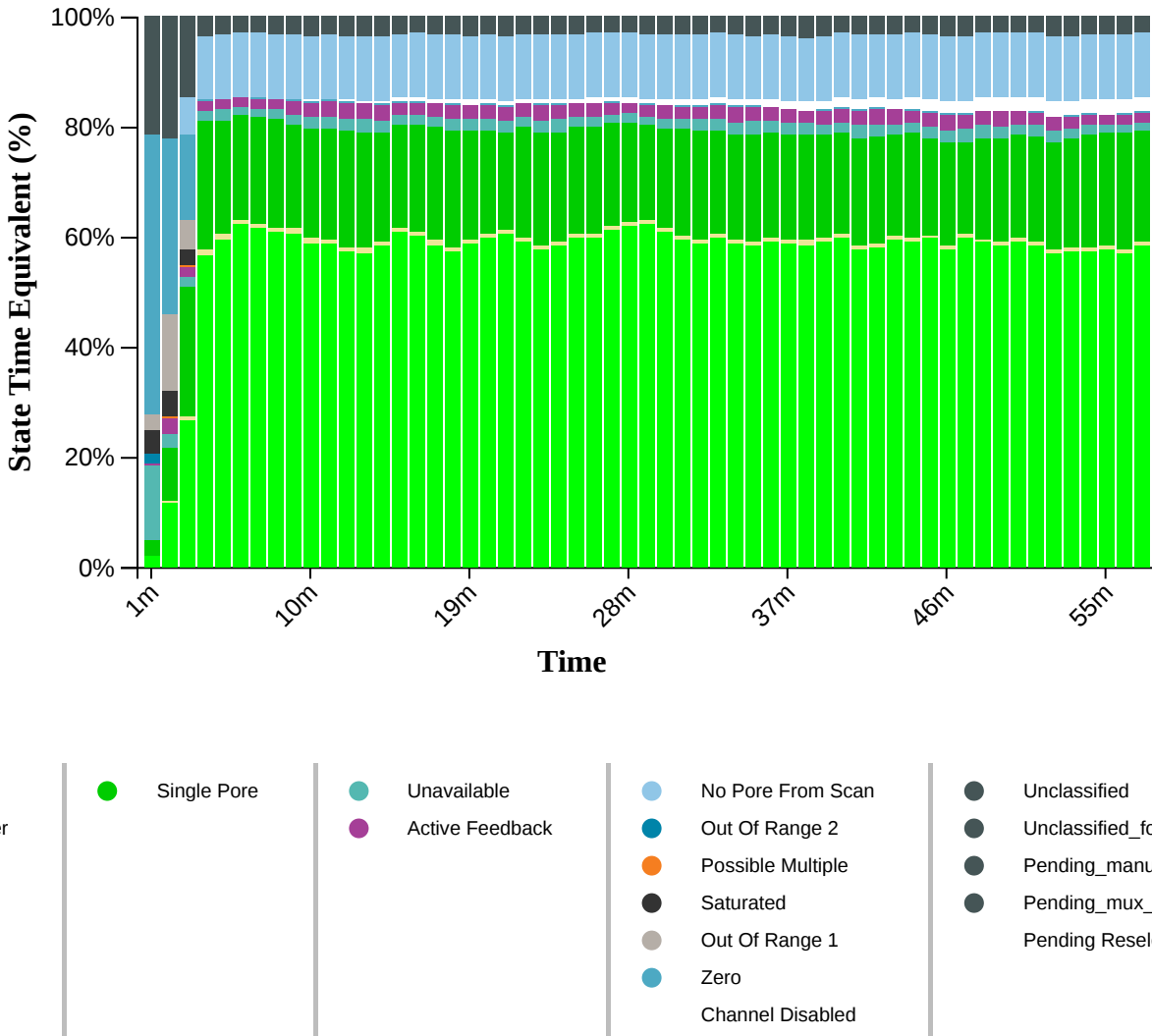
Alignment Target Hits (bases)



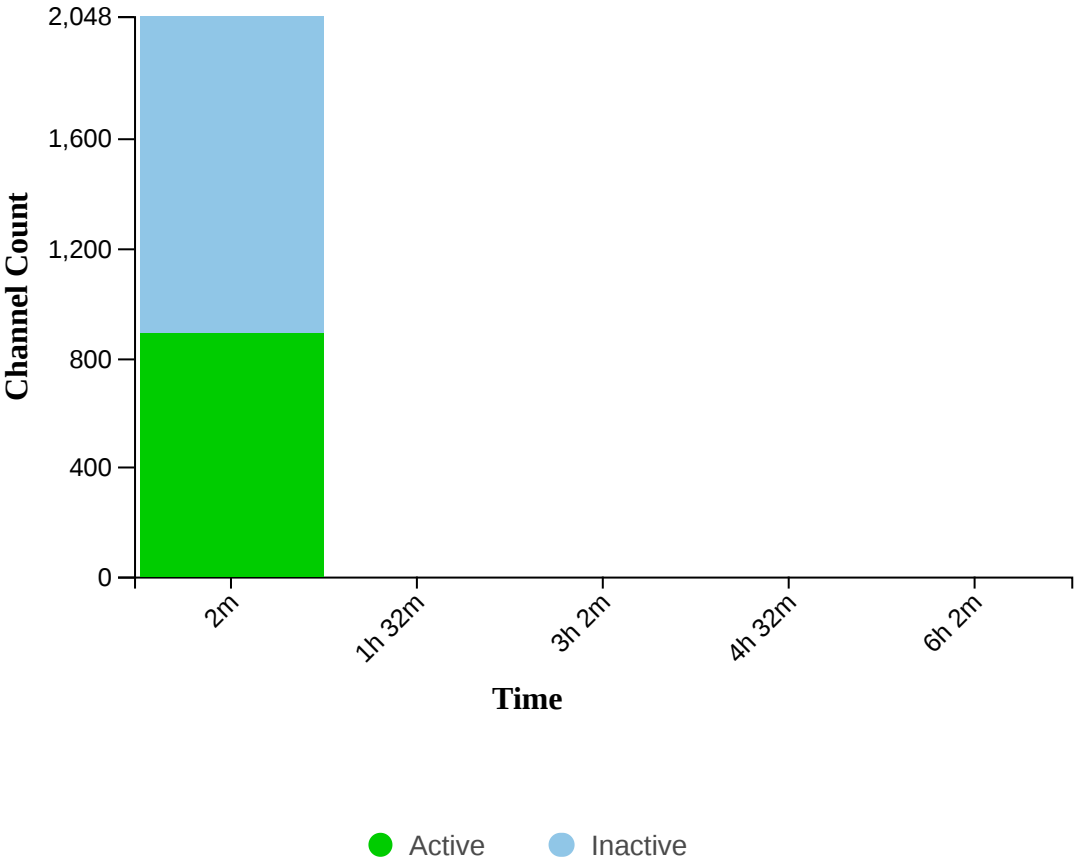
### Duty Time Grouped



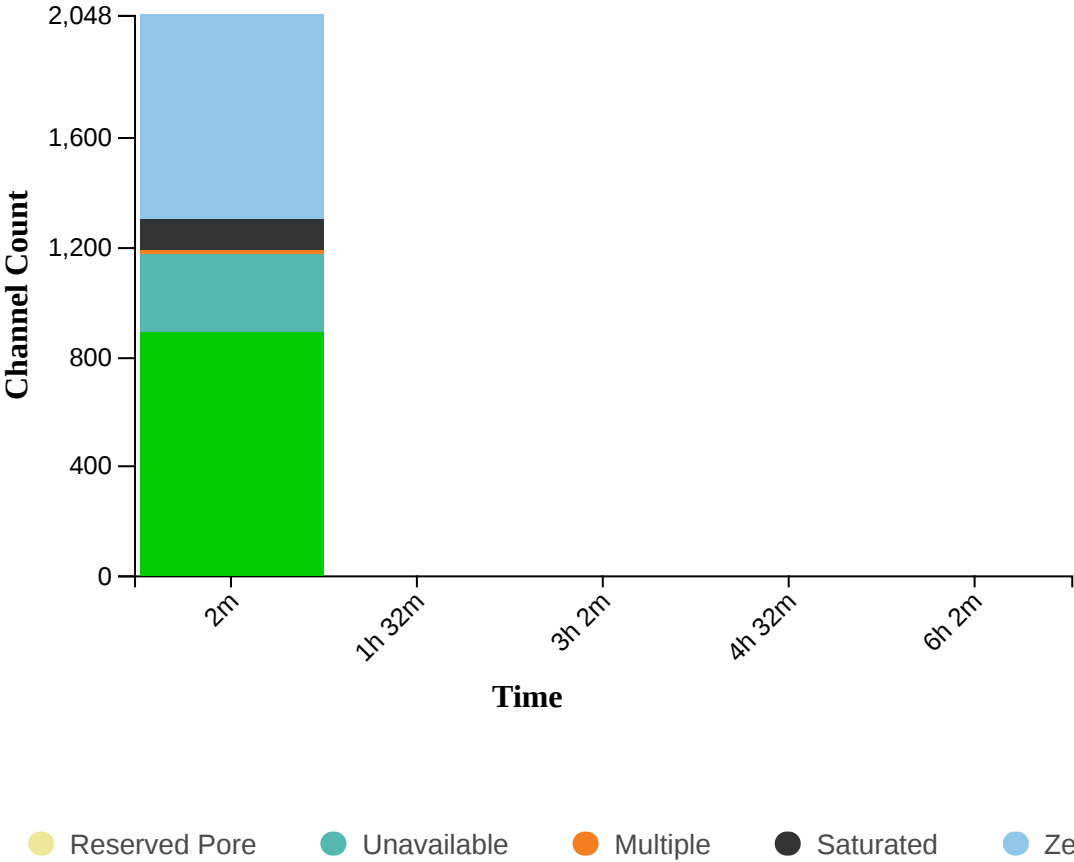
### Duty time Categorised



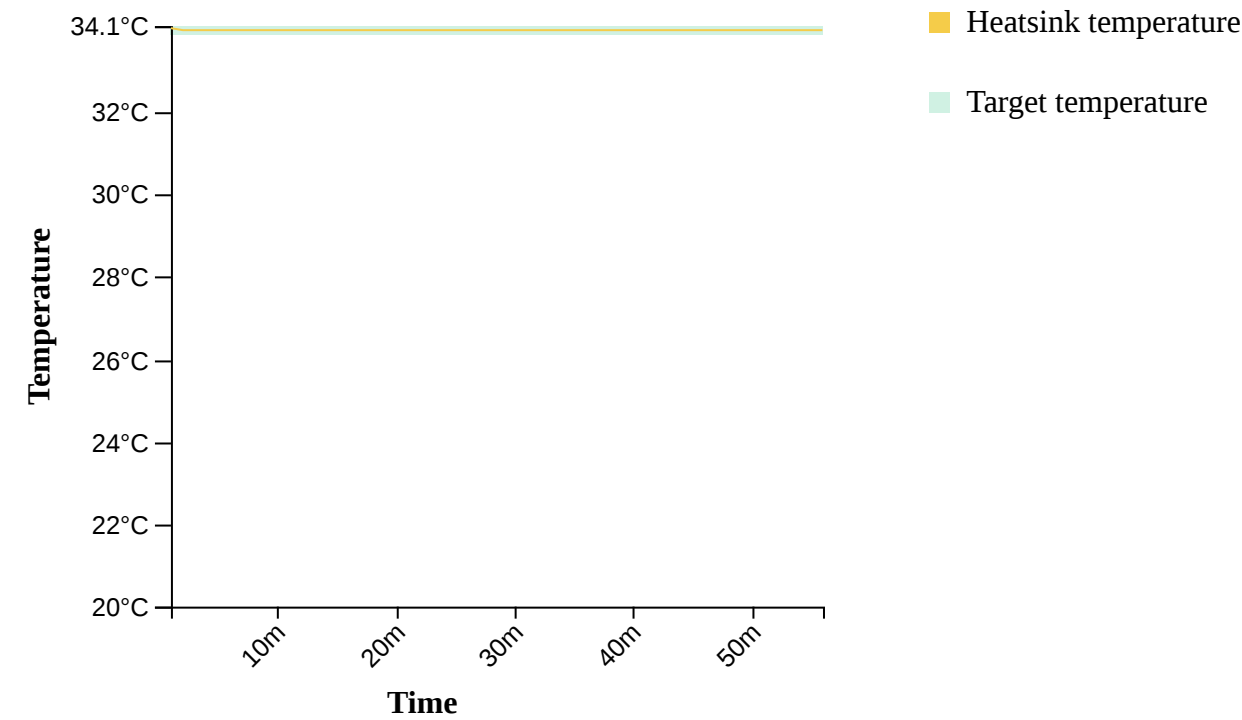
Mux Scan Grouped



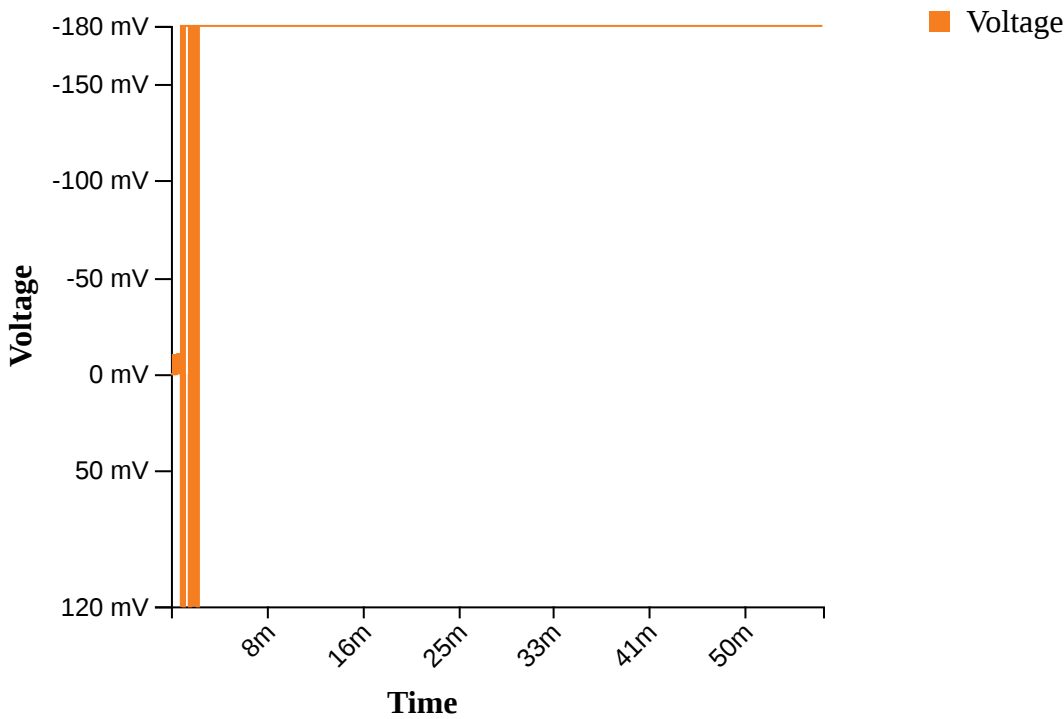
Mux Scan Categorised



Temperature History.

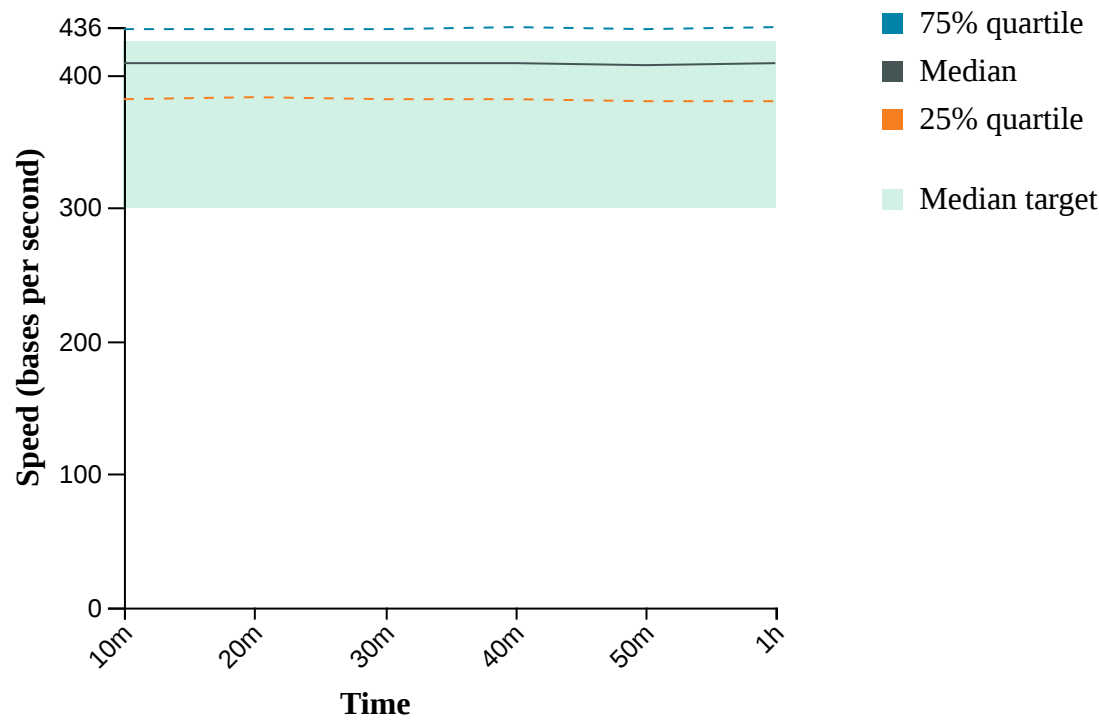


Bias Voltage History.

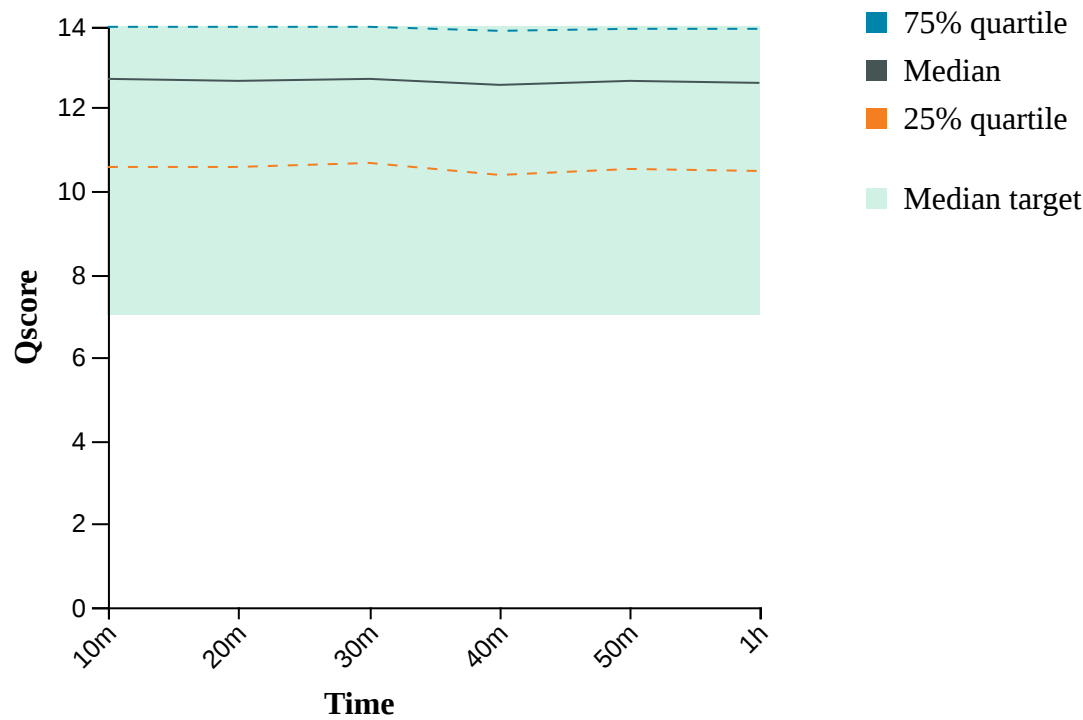




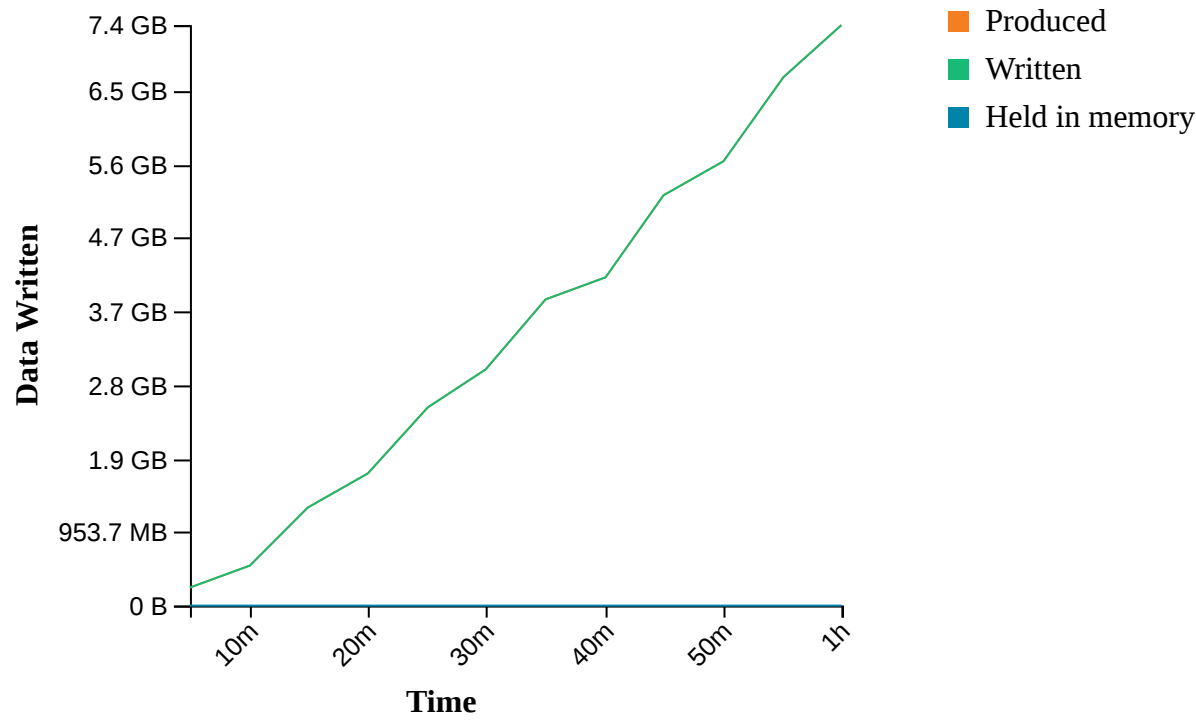
Translocation Speed



QScore



Disk Write Performance



### **Run Debug Messages**

- Mux scan for flow cell FAP21636 has found a total of 894 pores. 452 pores available for immediate sequencing April 15, 13:27
- Performing Mux Scan April 15, 13:25
- Starting sequencing procedure April 15, 13:25
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 13:21