



## Run Info

Host Name	GXB01190 (localhost)
Experiment Name	EIMock_2kbp_PvulgarisRAD_050121
Sample ID	EIMock_2kbp_PvulgarisRAD_050121
Run ID	0a3681a3-d561-4b8d-8b52-5ce26a97e1b7
Flow Cell Id	FAO53362
Start Time	January 5, 19:05
Run Length	58m

## Run Summary

Reads Generated	423.19 K
Passed Bases	177.82 Mb
Failed Bases	19.68 Mb
Estimated Bases	213.1 Mb

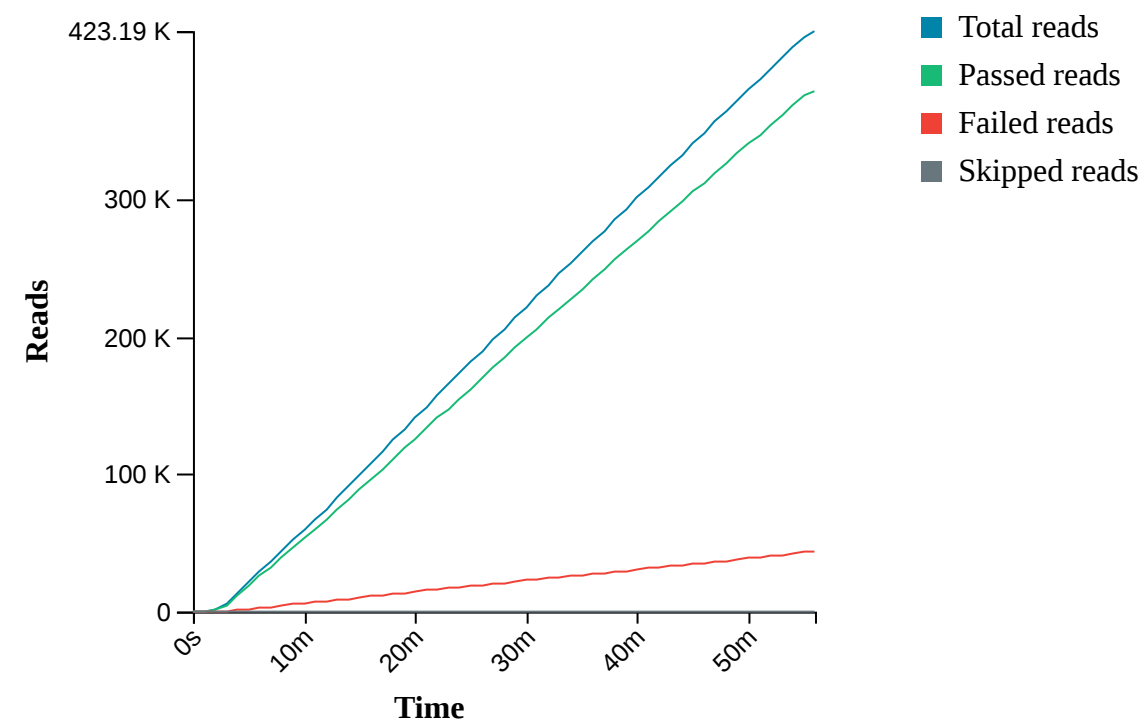
## Run Parameters

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/P_vulgaris_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

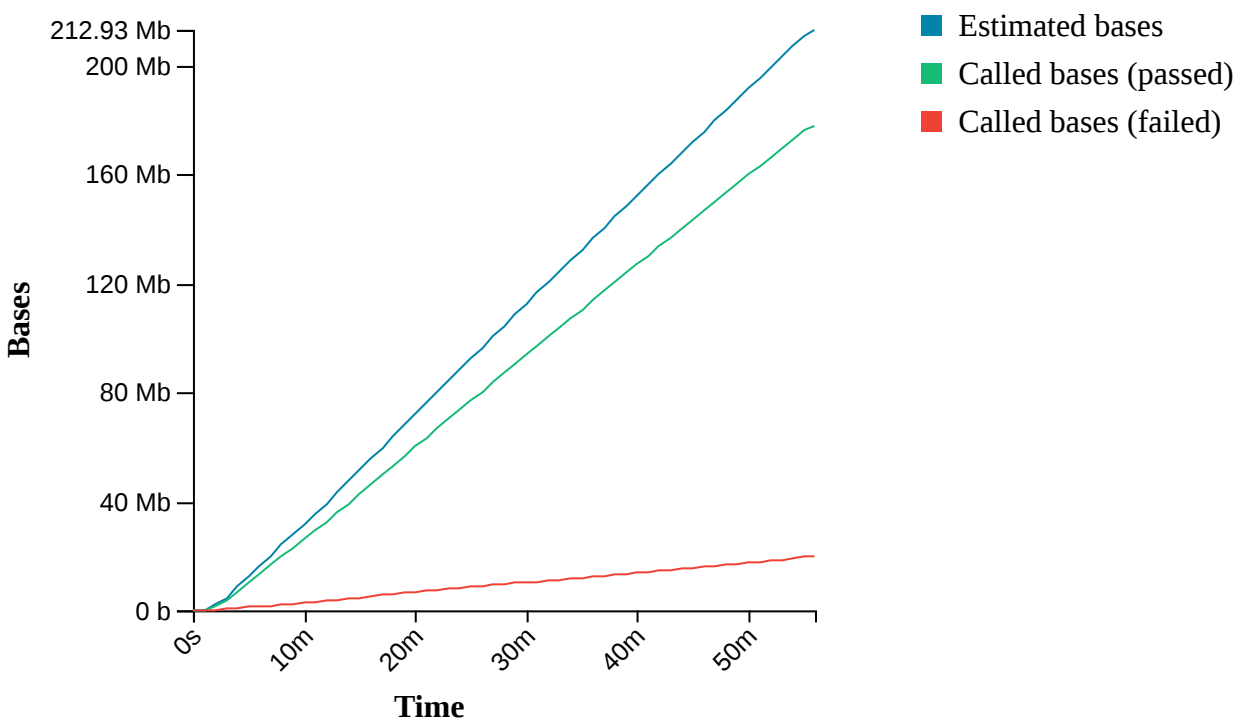
## Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

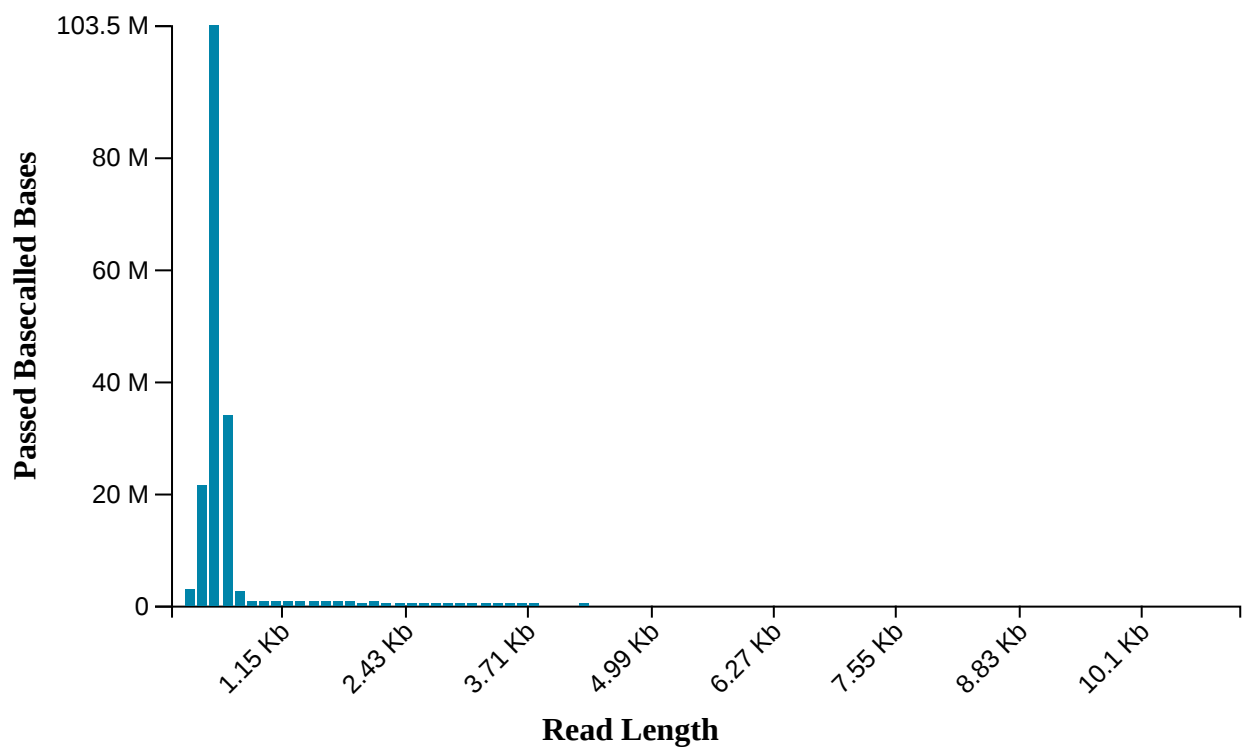


Cumulative Output Bases



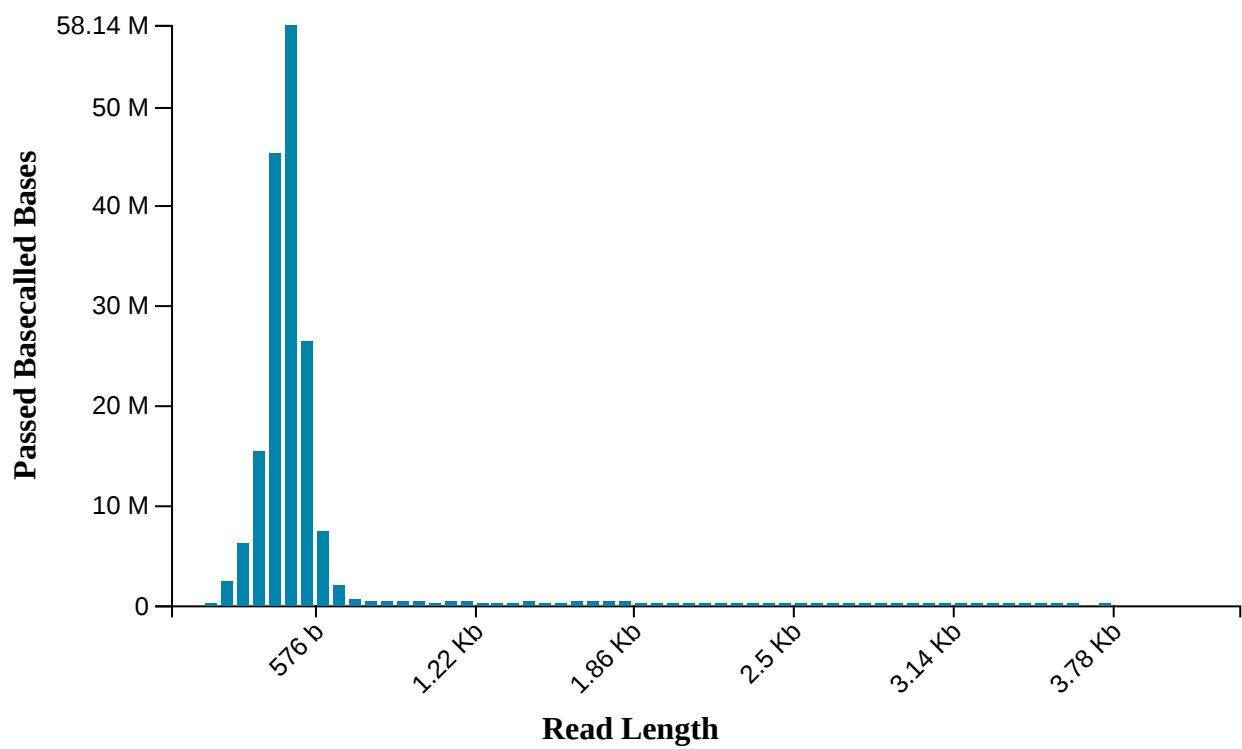
**Read Length Histogram Estimated Bases - Outliers Discarded**

Estimated N50: 467



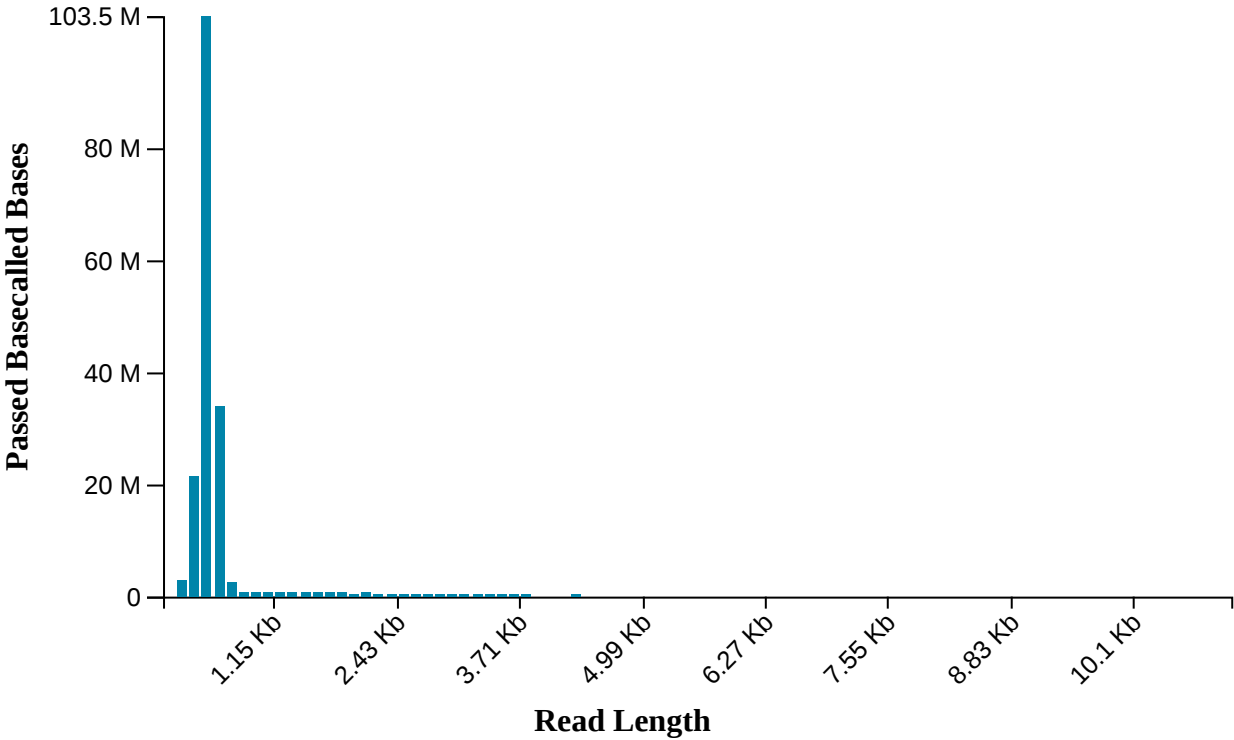
**Read Length Histogram Basecalled Bases - Outliers Discarded**

Estimated N50: 466



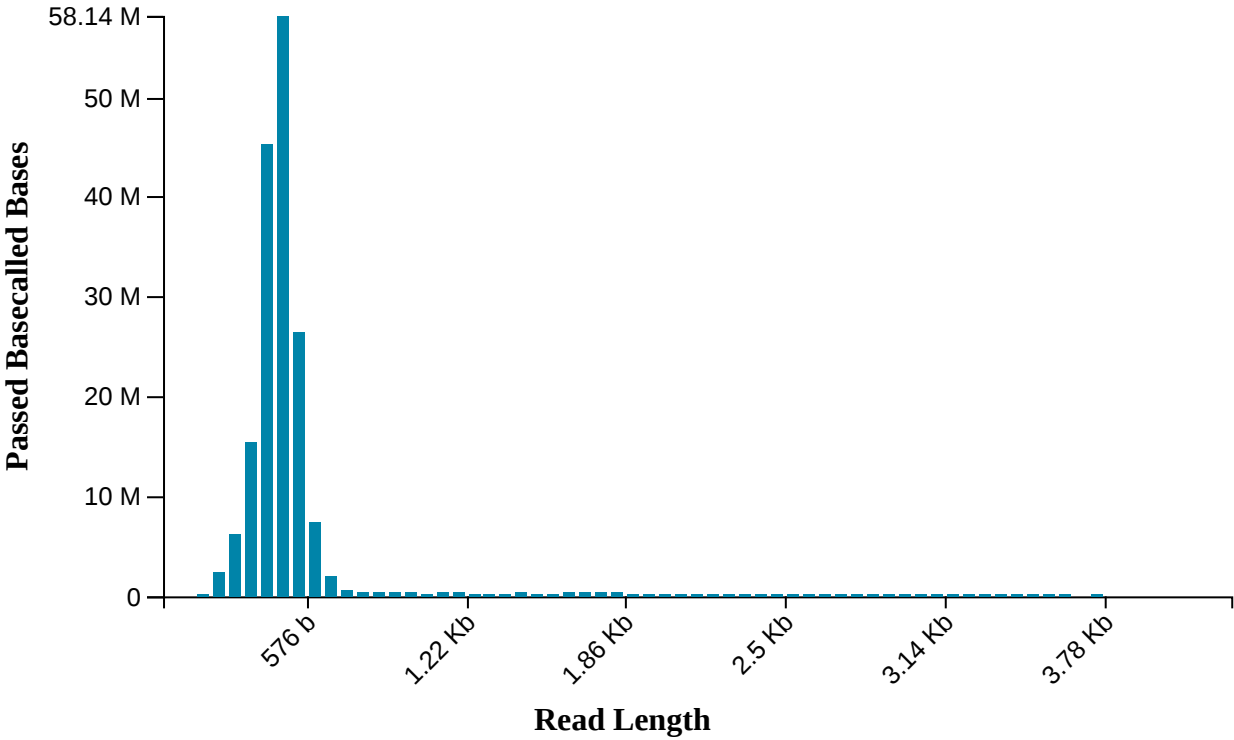
**Read Length Histogram Estimated Bases**

Estimated N50: 467

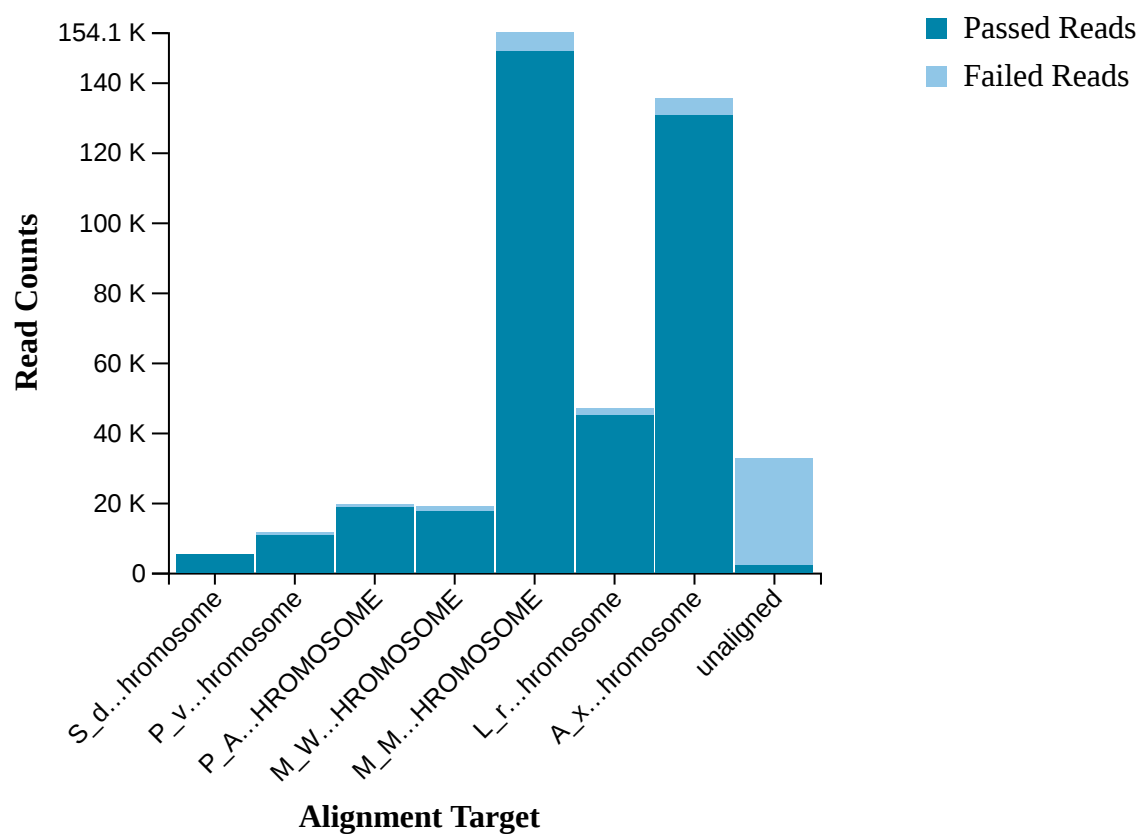


**Read Length Histogram Basecalled Bases**

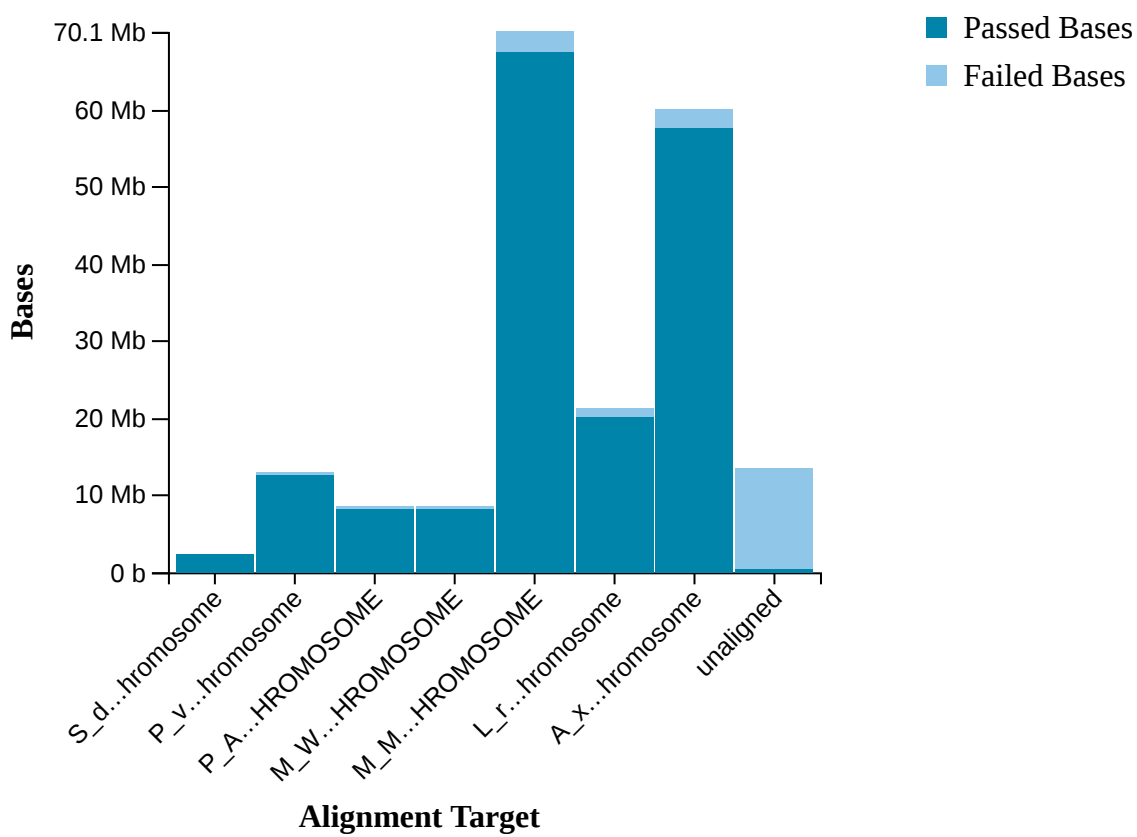
Estimated N50: 466



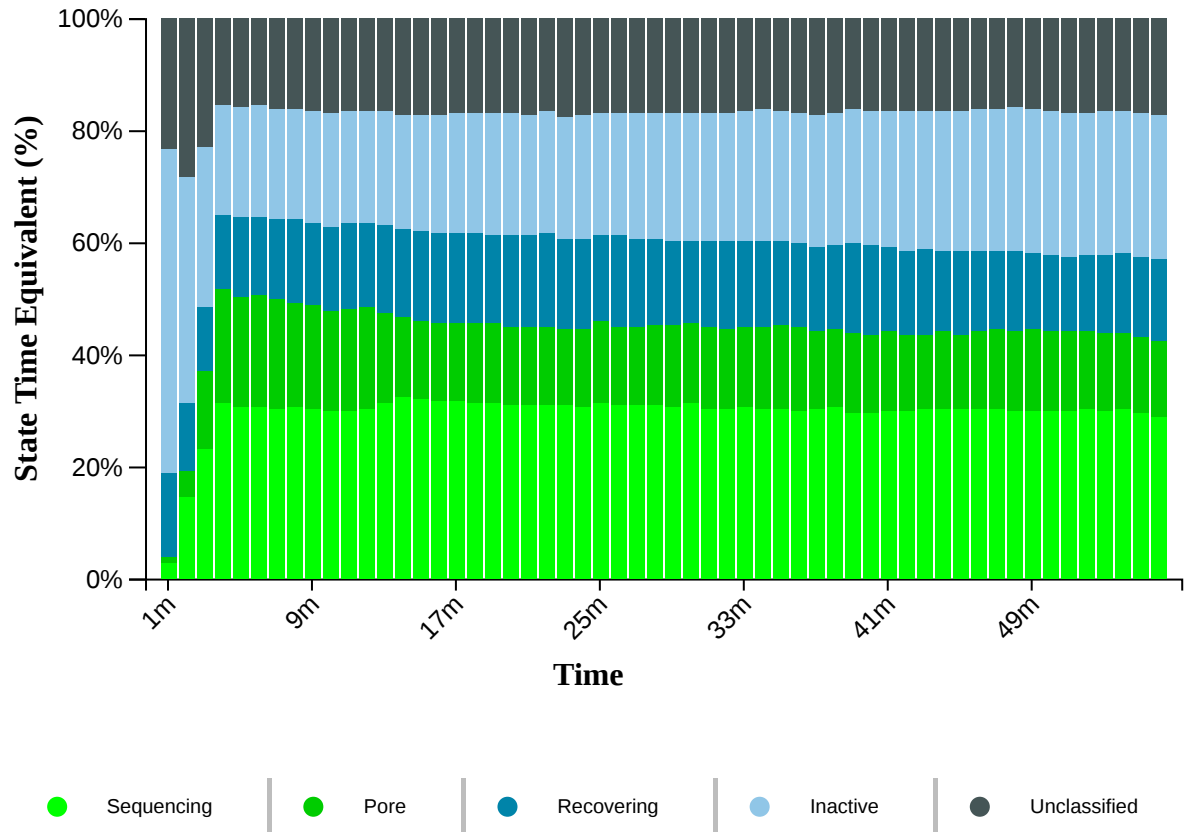
Alignment Target Hits (reads)



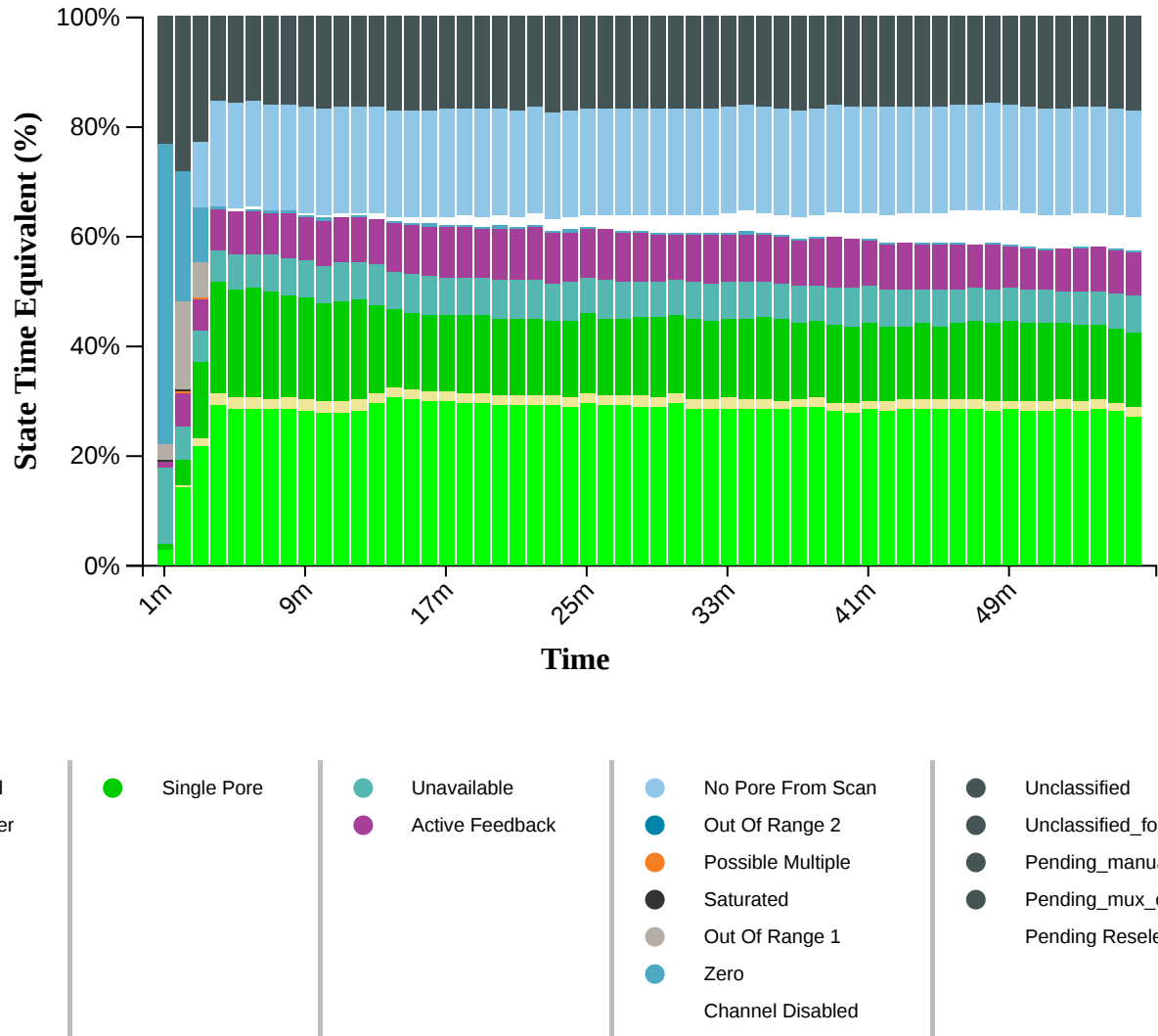
Alignment Target Hits (bases)



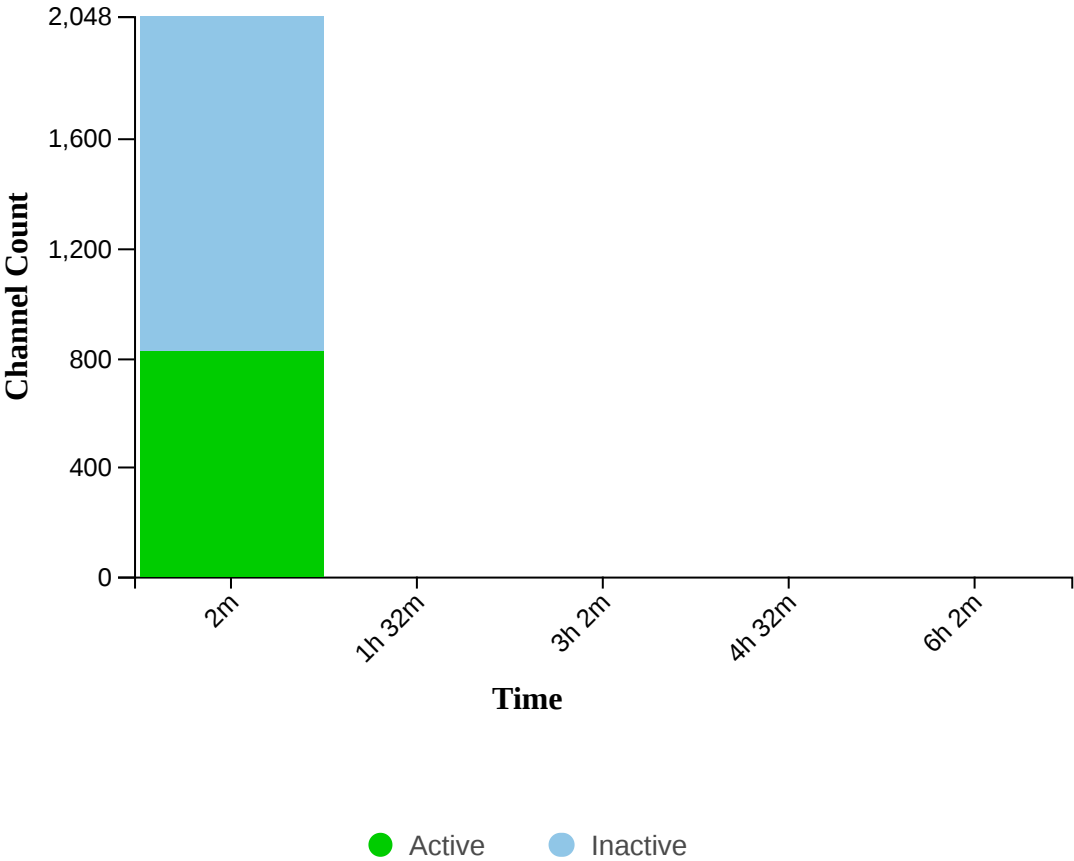
Duty Time Grouped



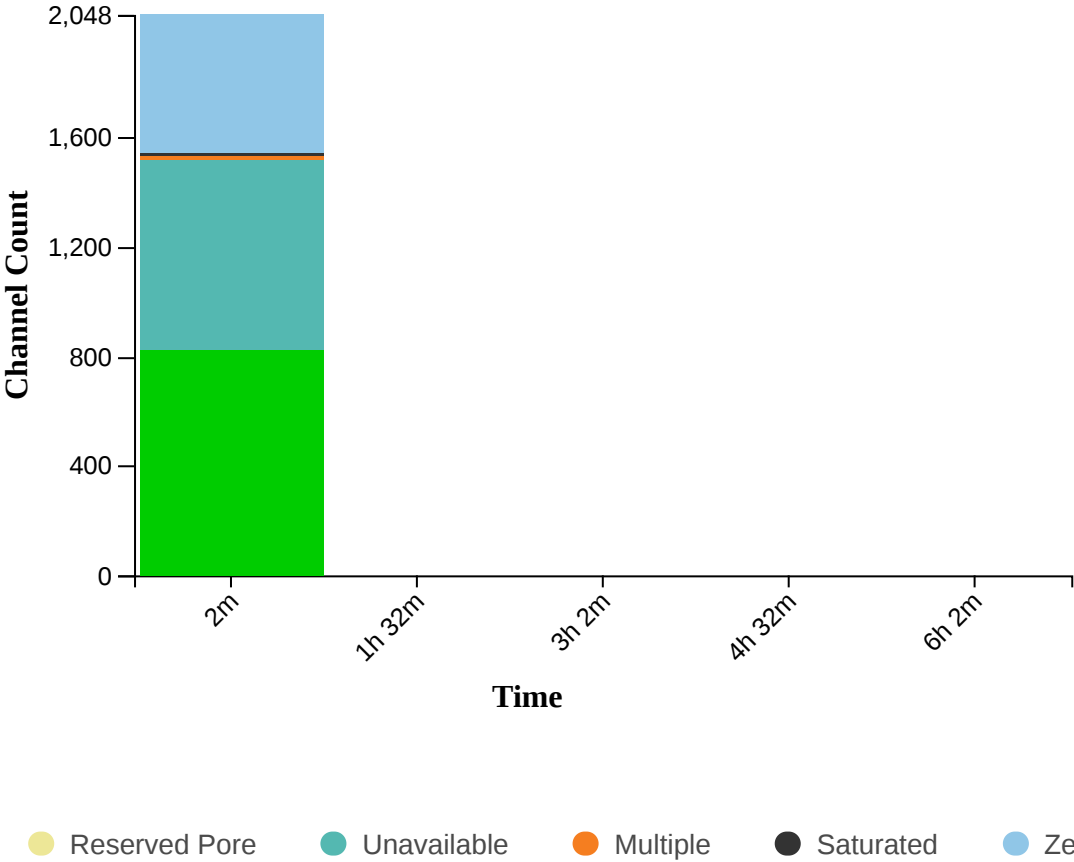
Duty time Categorised



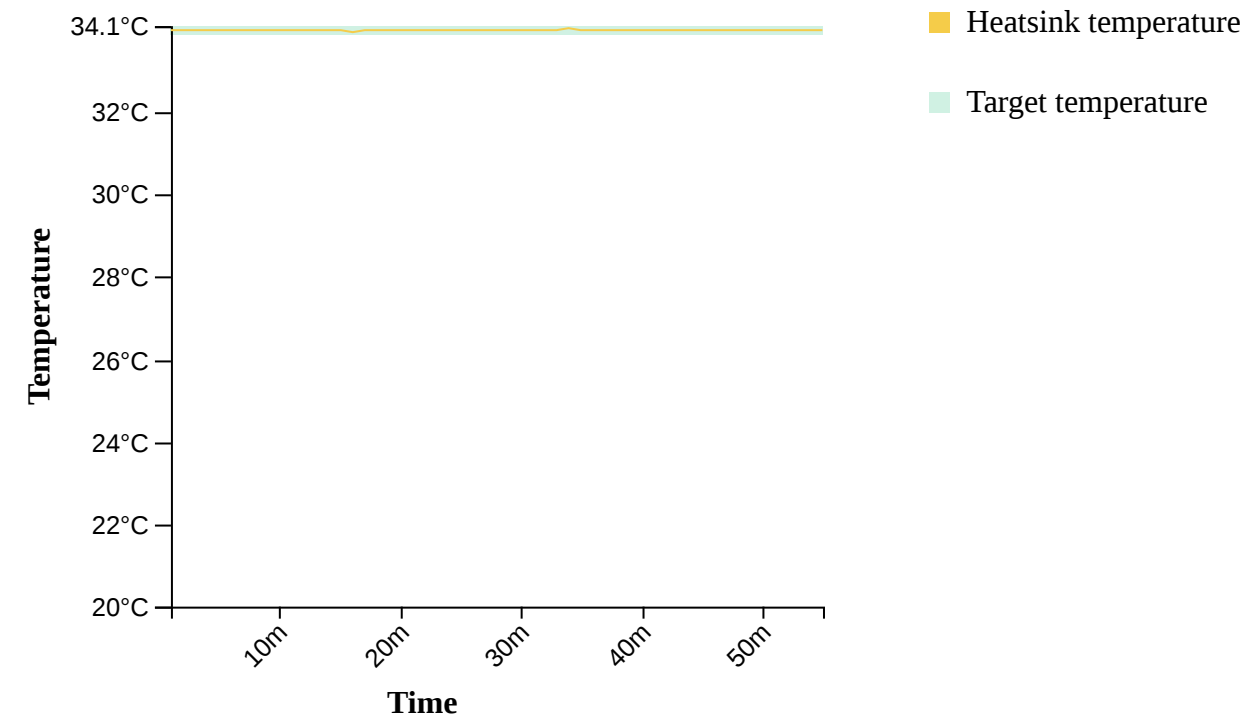
Mux Scan Grouped



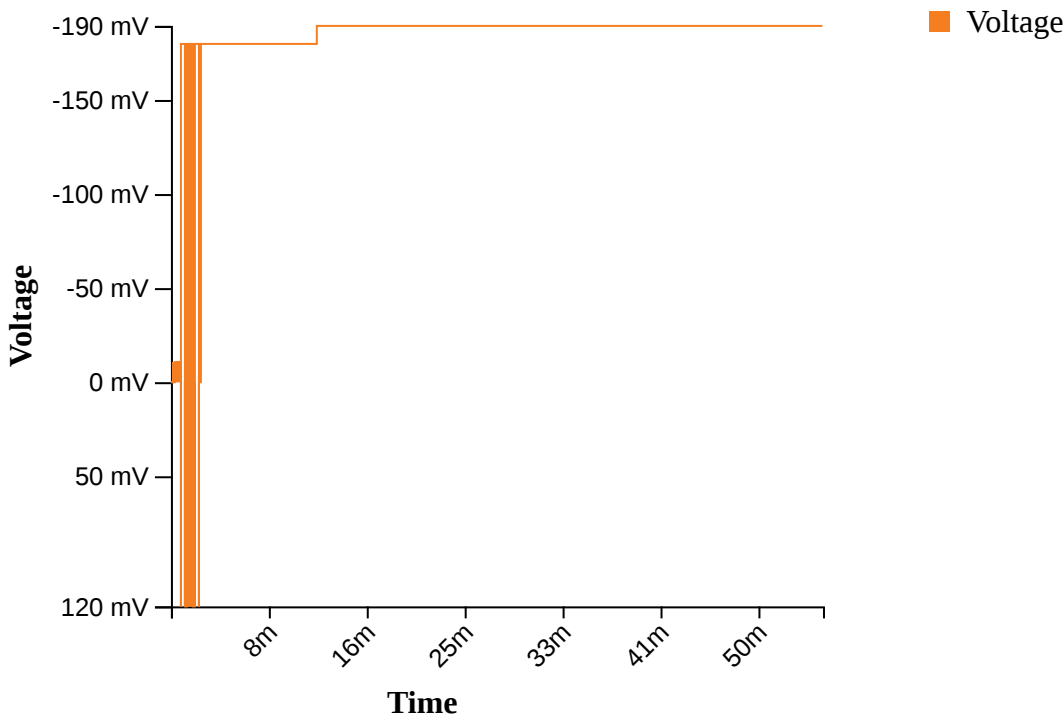
Mux Scan Categorised



Temperature History.

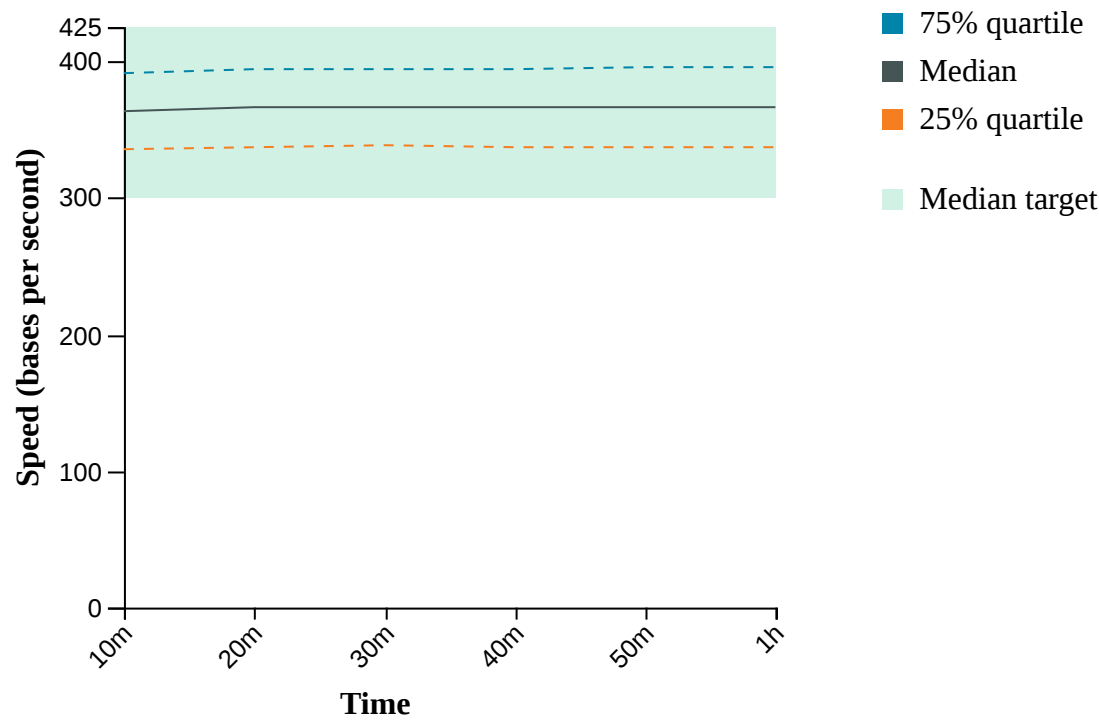


Bias Voltage History.

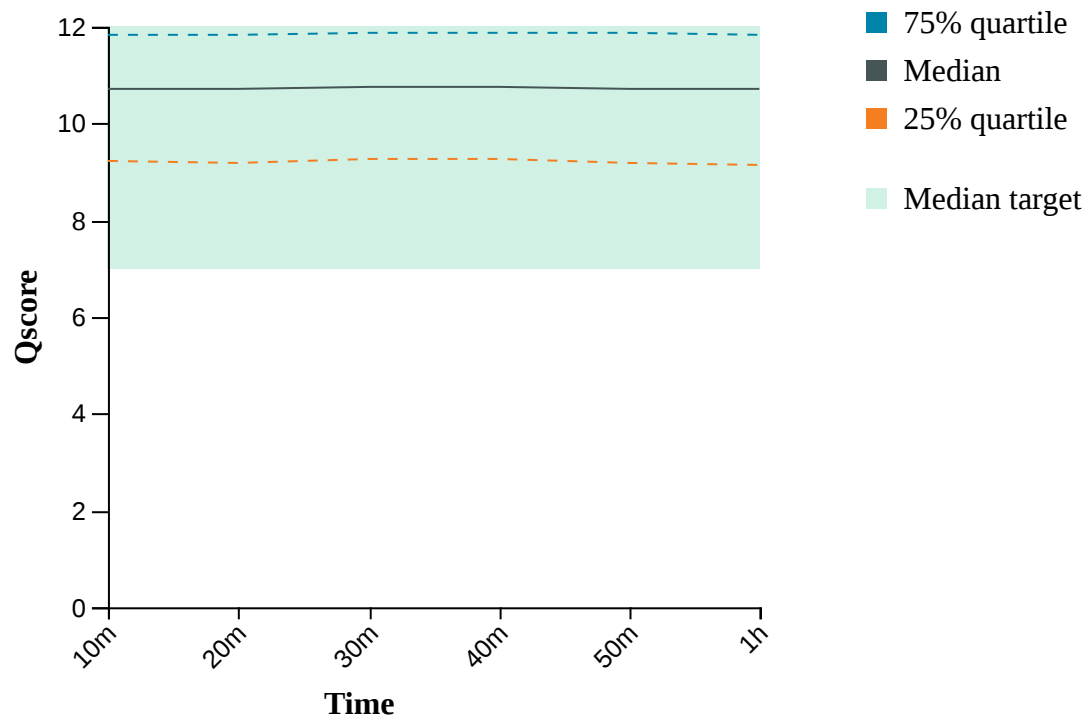




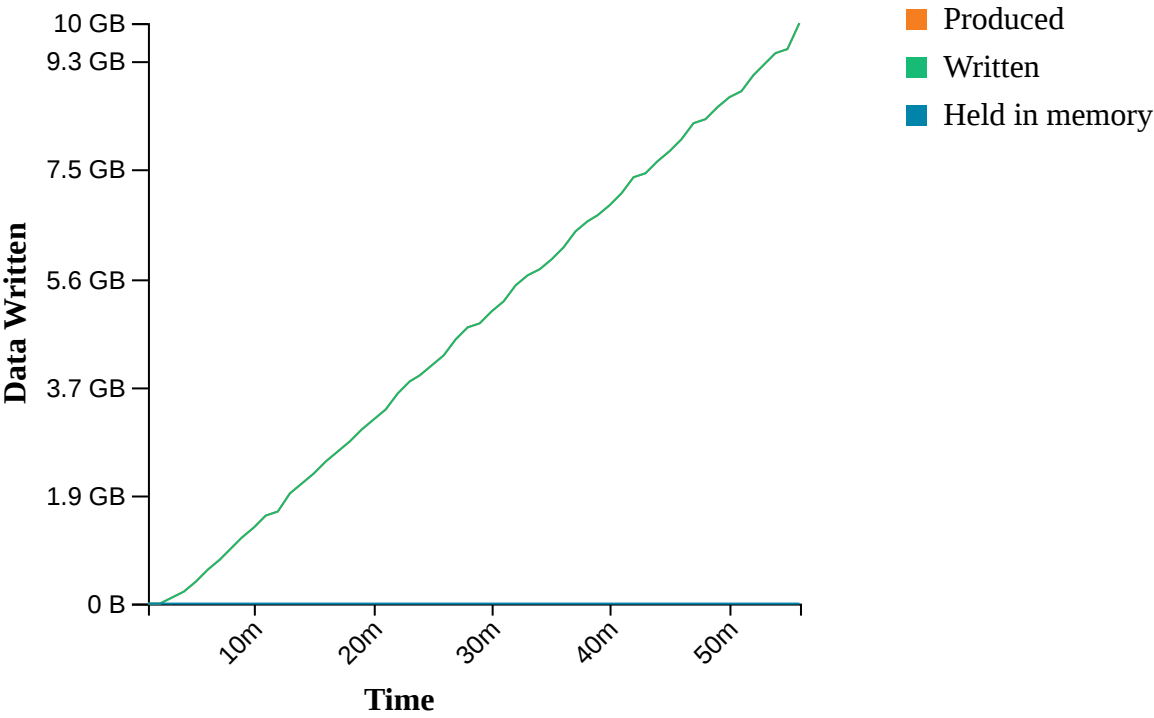
Translocation Speed



QScore



**Disk Write Performance**



### **Run Debug Messages**

- Mux scan for flow cell FAO53362 has found a total of 829 pores. 413 pores available for immediate sequencing January 5, 19:10
- Performing Mux Scan January 5, 19:08
- Starting sequencing procedure January 5, 19:08
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C January 5, 19:05