



## Run Info

Host Name	GXB01190 (localhost)
Experiment Name	ReadUntilMock_15kbSE_MwEnrich_08122020
Sample ID	ReadUntilMock_15kbSE_MwEnrich_08122020
Run ID	8fd337af-bae6-48c4-8bd6-0f7ad84e9ffe
Flow Cell Id	FAO52906
Start Time	December 8, 17:48
Run Length	1h 13m

## Run Summary

Reads Generated	226.2 K
Passed Bases	159.57 Mb
Failed Bases	9.94 Mb
Estimated Bases	176.83 Mb

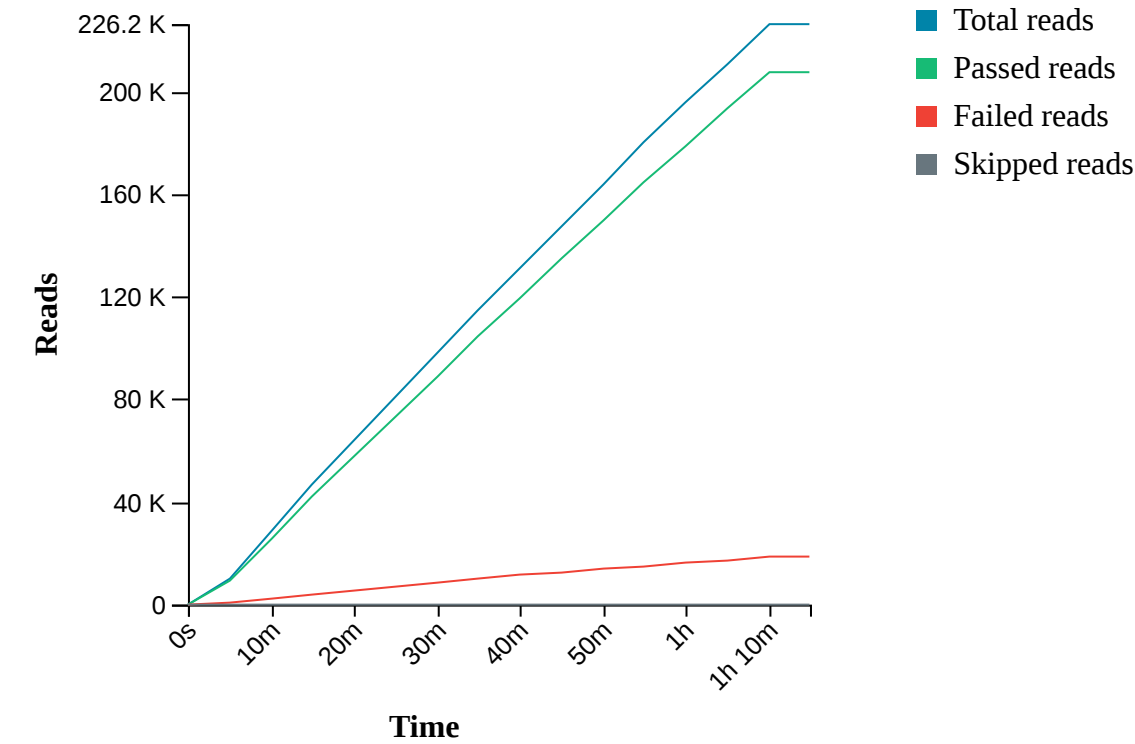
## Run Parameters

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/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

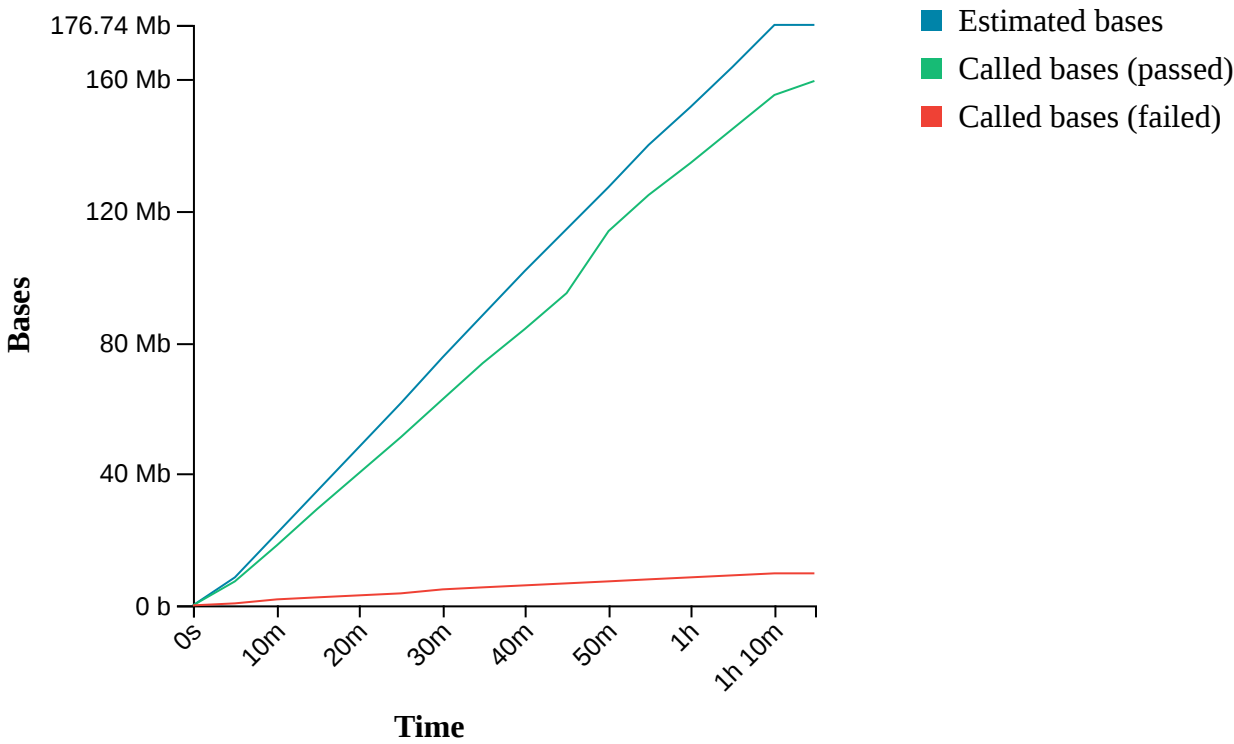
## Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

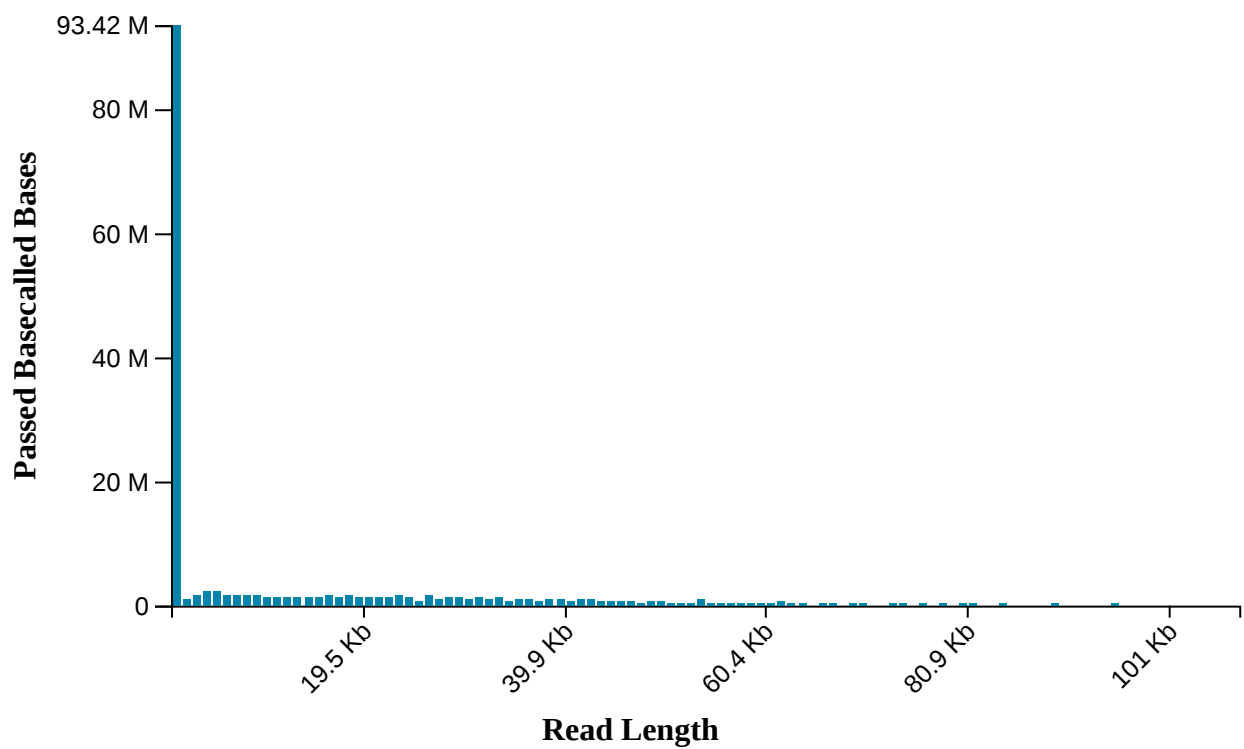


Cumulative Output Bases



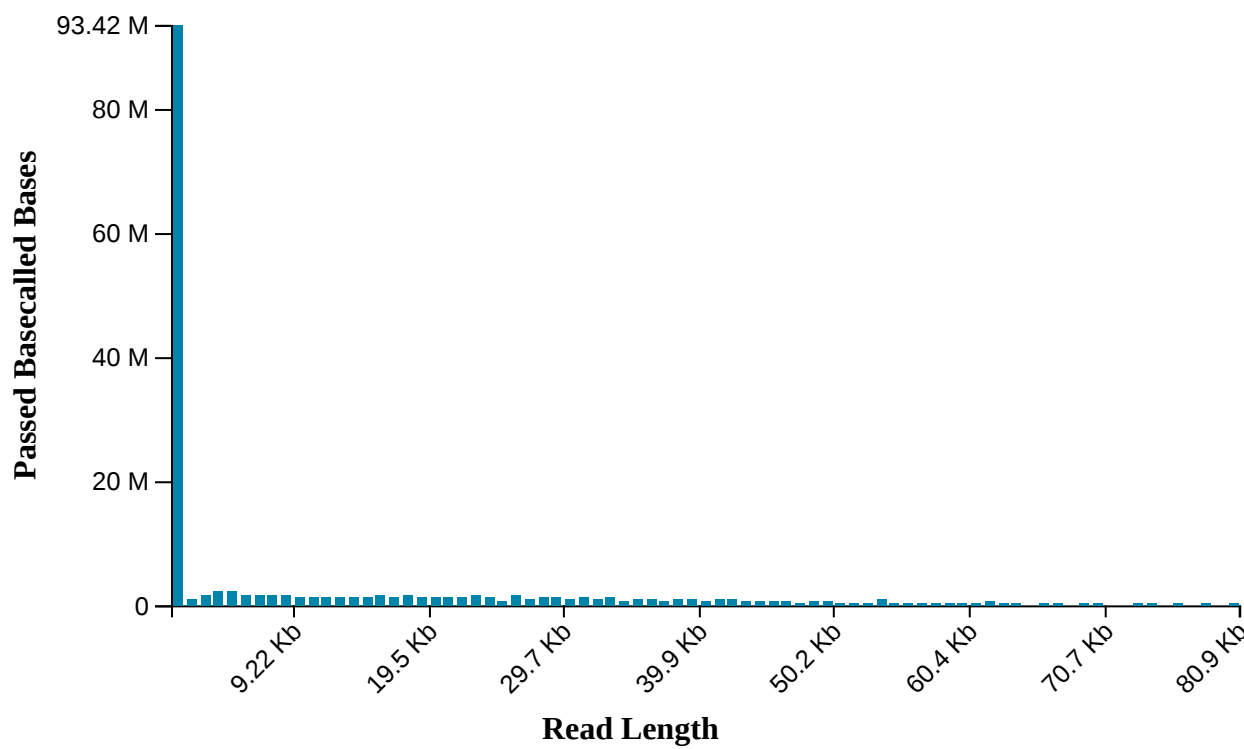
**Read Length Histogram Estimated Bases - Outliers Discarded**

Estimated N50: 558



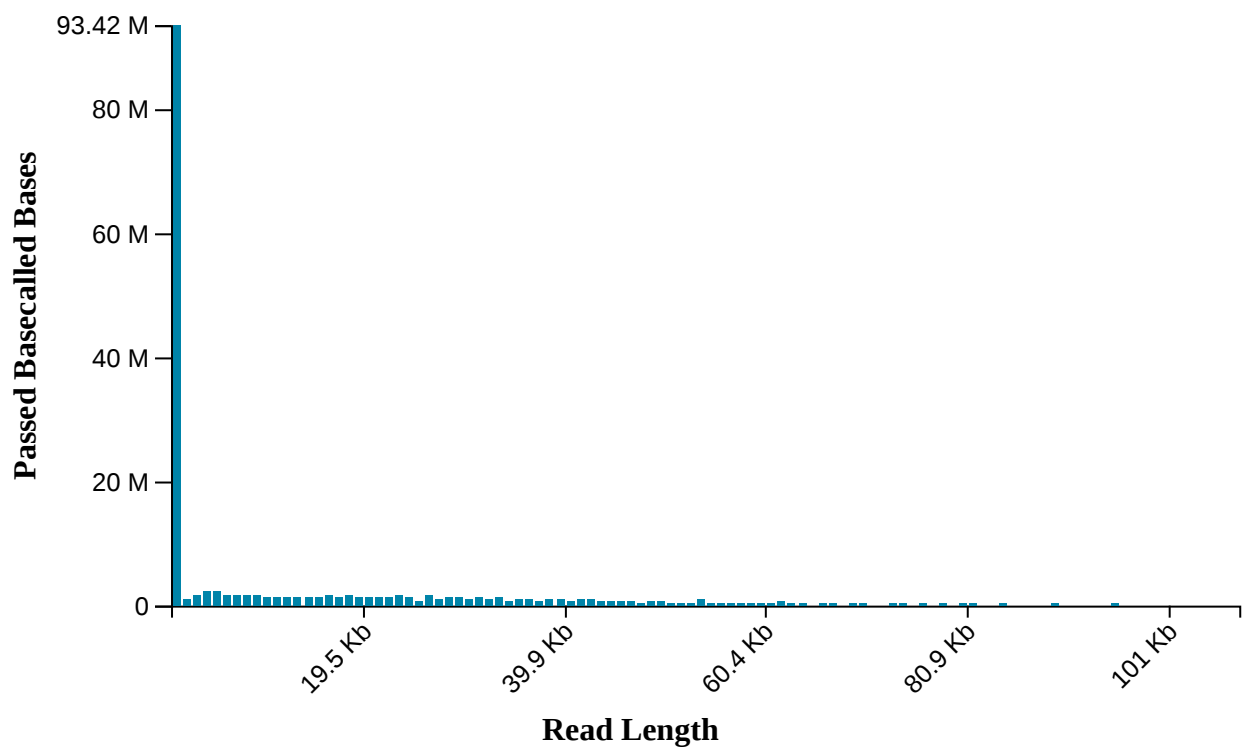
**Read Length Histogram Basecalled Bases - Outliers Discarded**

Estimated N50: 555



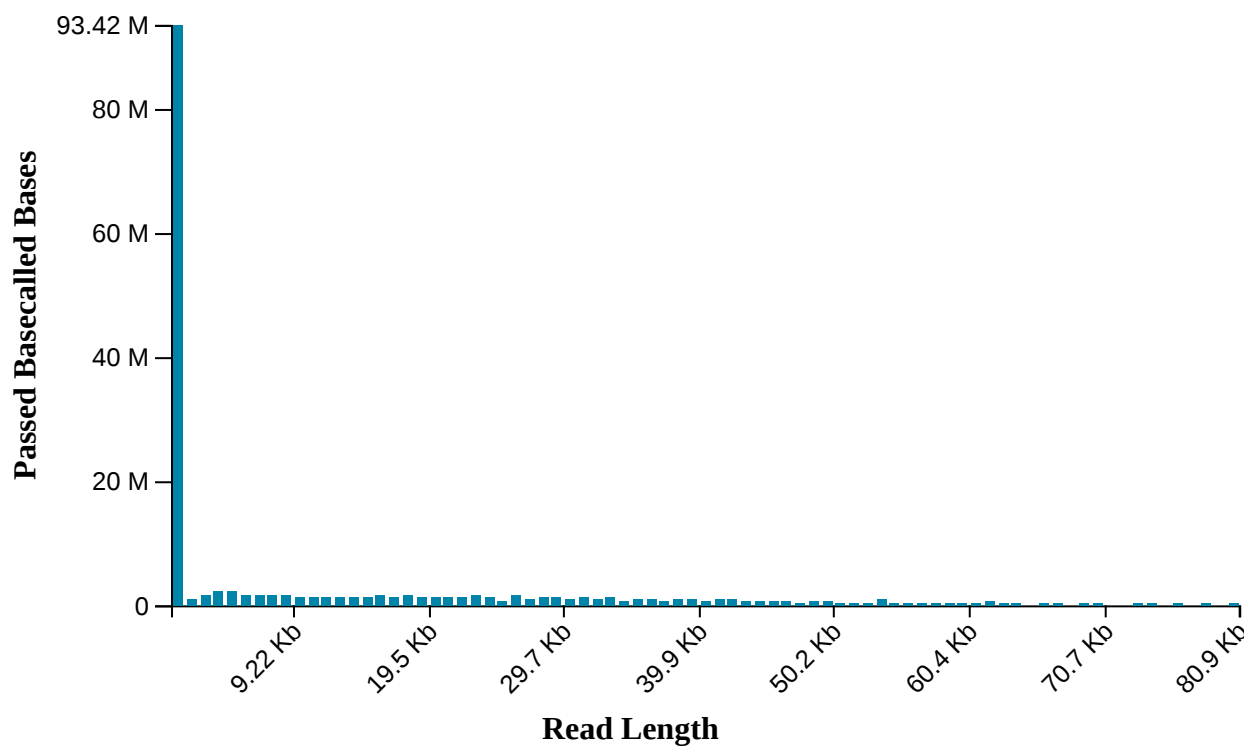
**Read Length Histogram Estimated Bases**

Estimated N50: 558

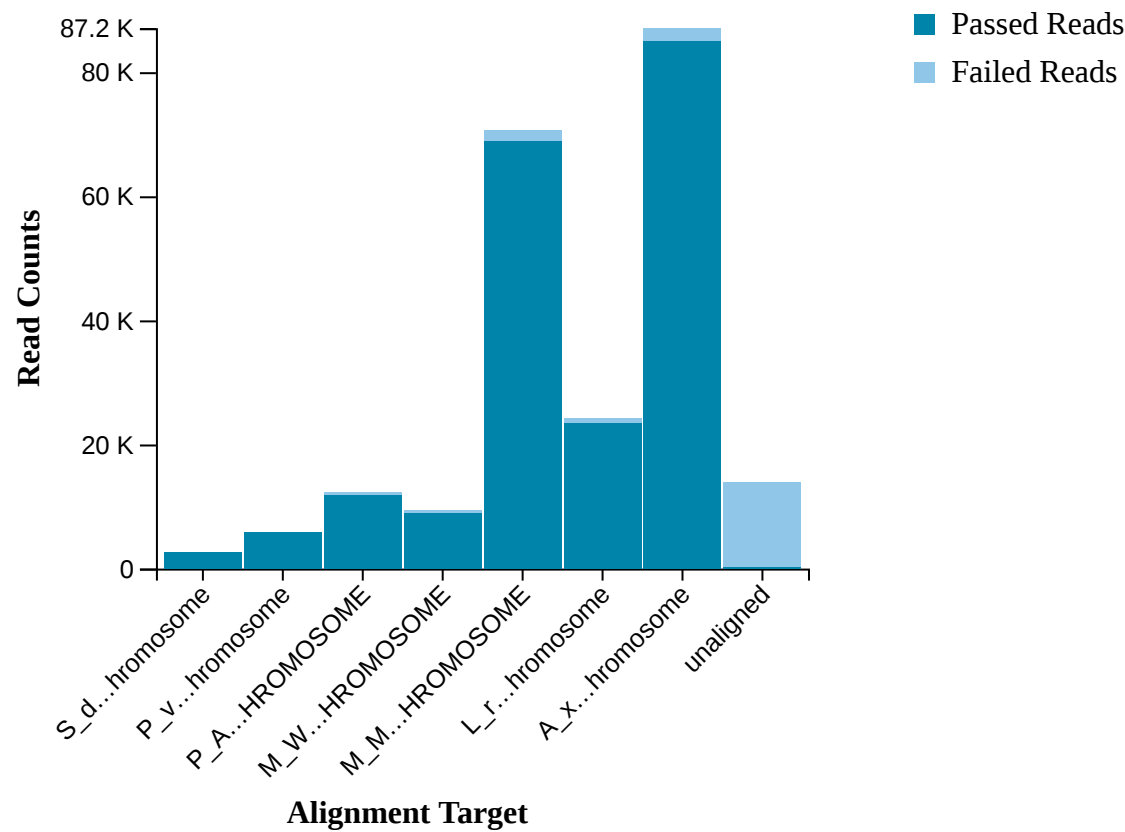


**Read Length Histogram Basecalled Bases**

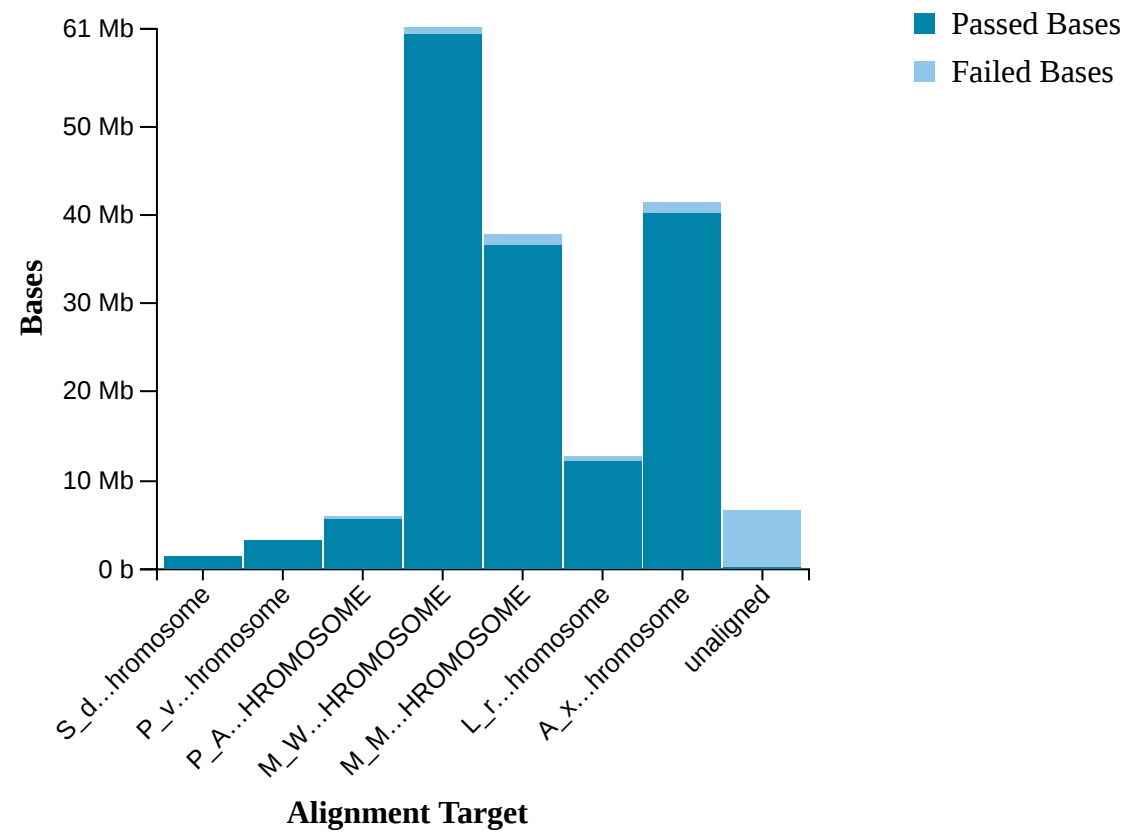
Estimated N50: 555



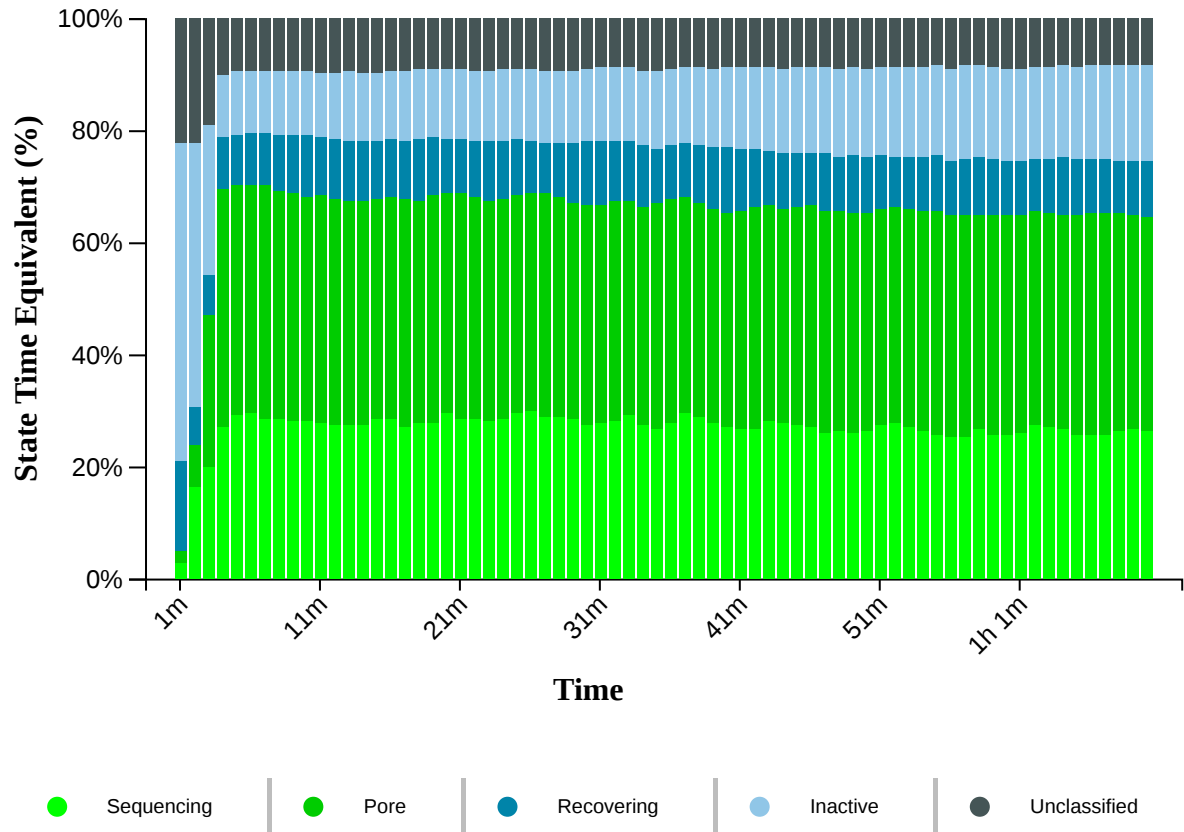
**Alignment Target Hits (reads)**



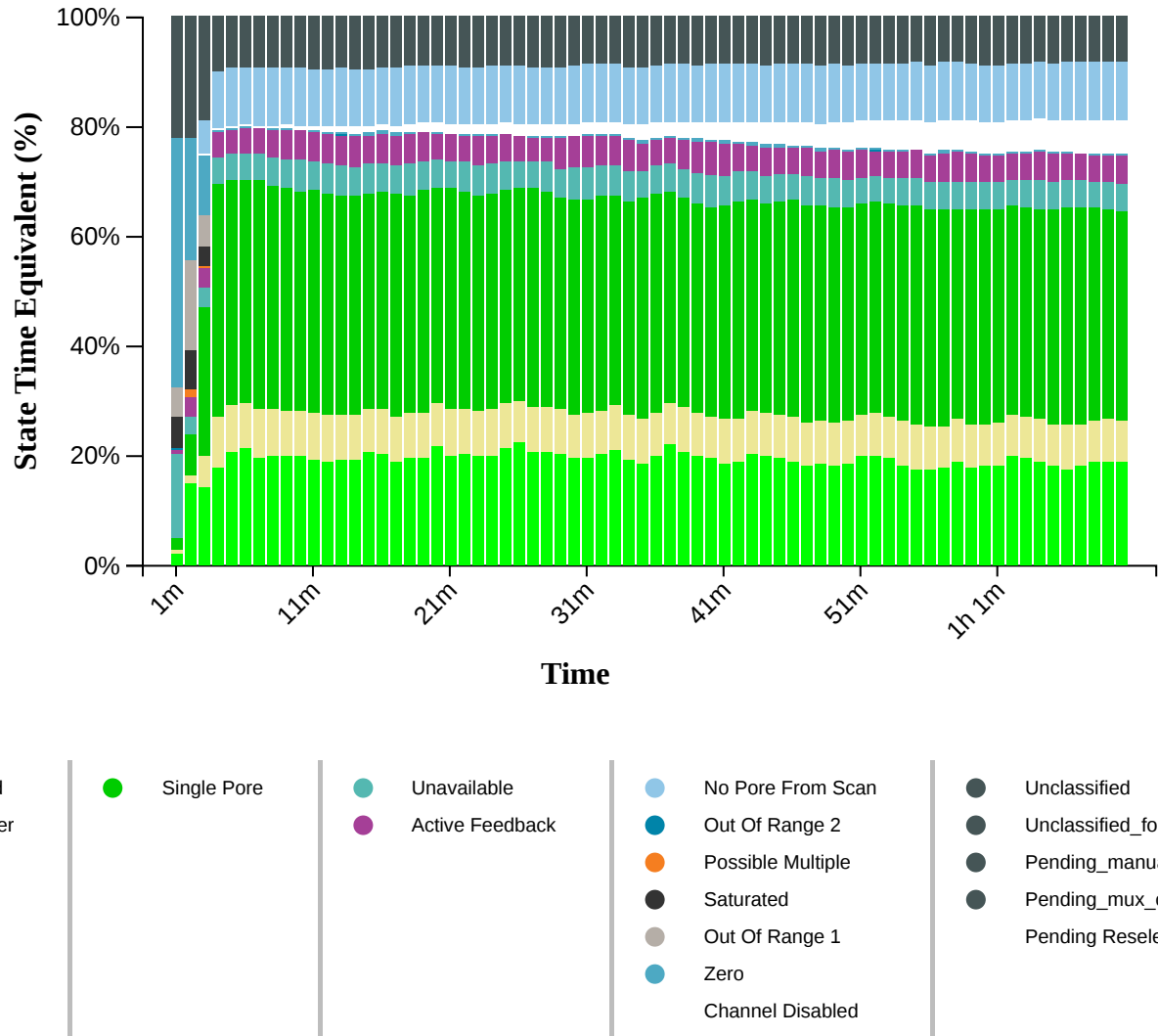
**Alignment Target Hits (bases)**



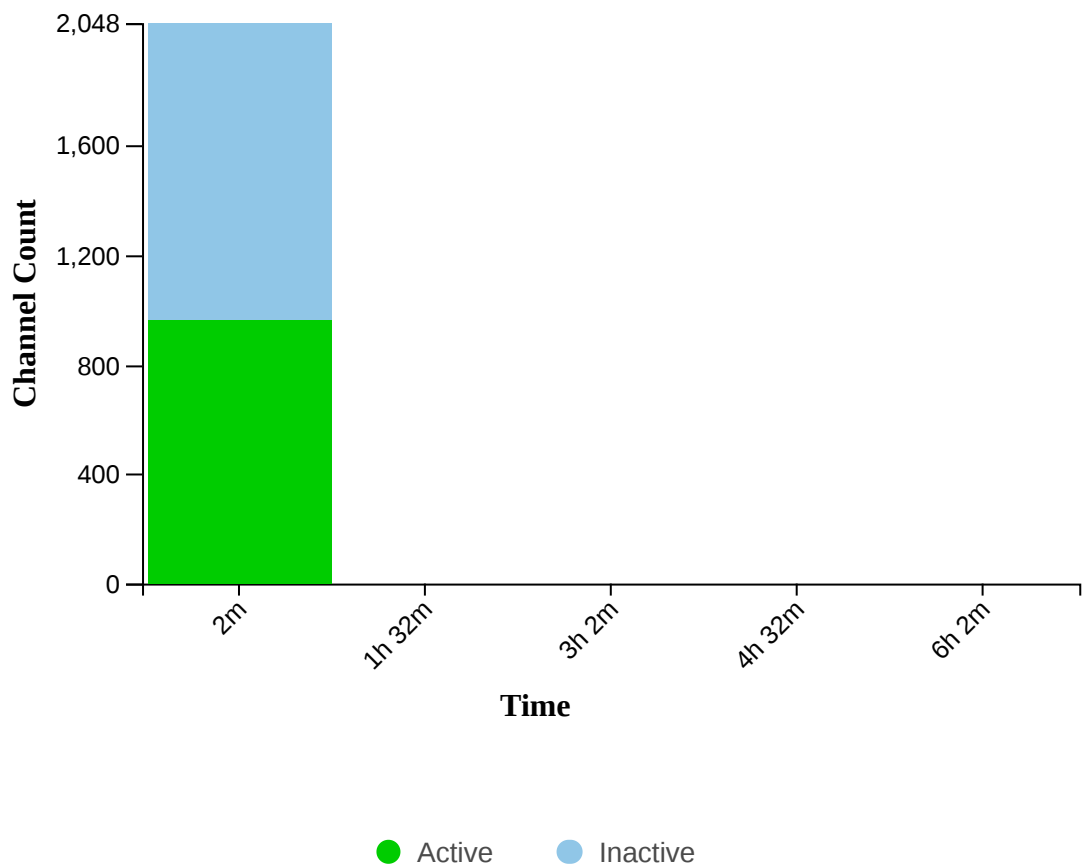
**Duty Time Grouped**



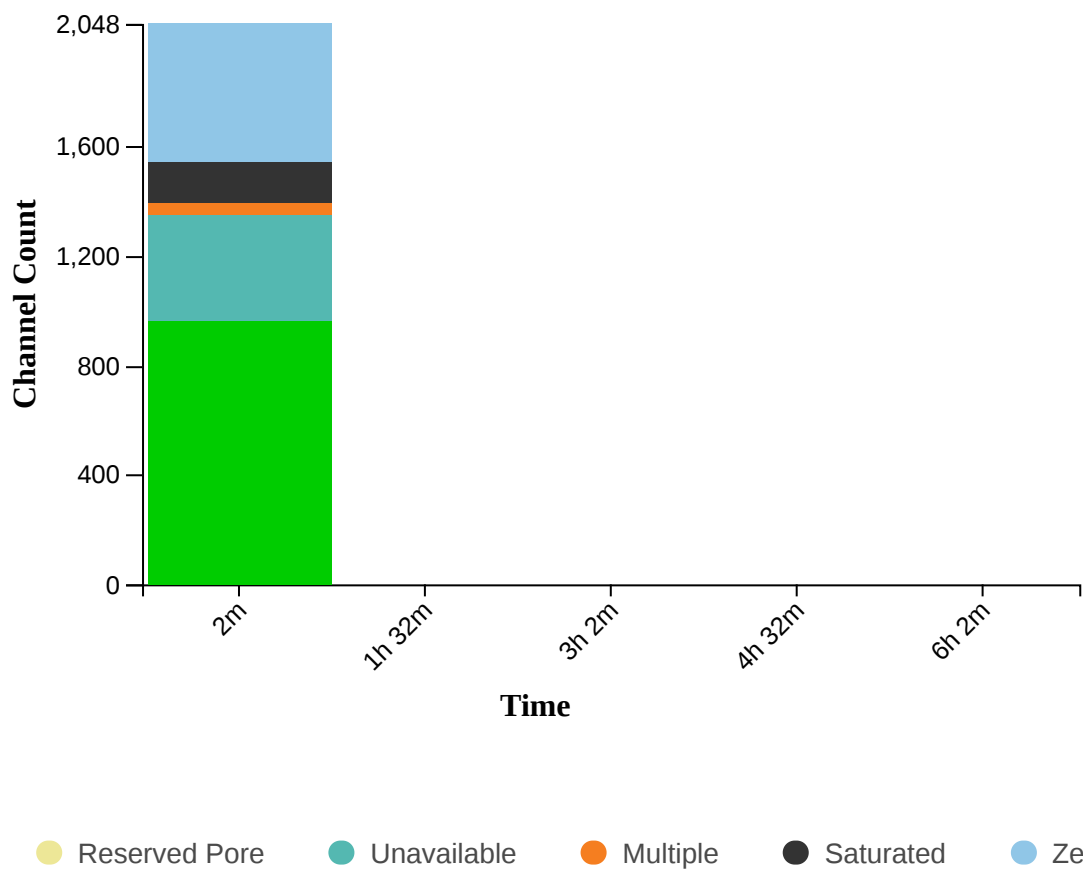
**Duty time Categorised**



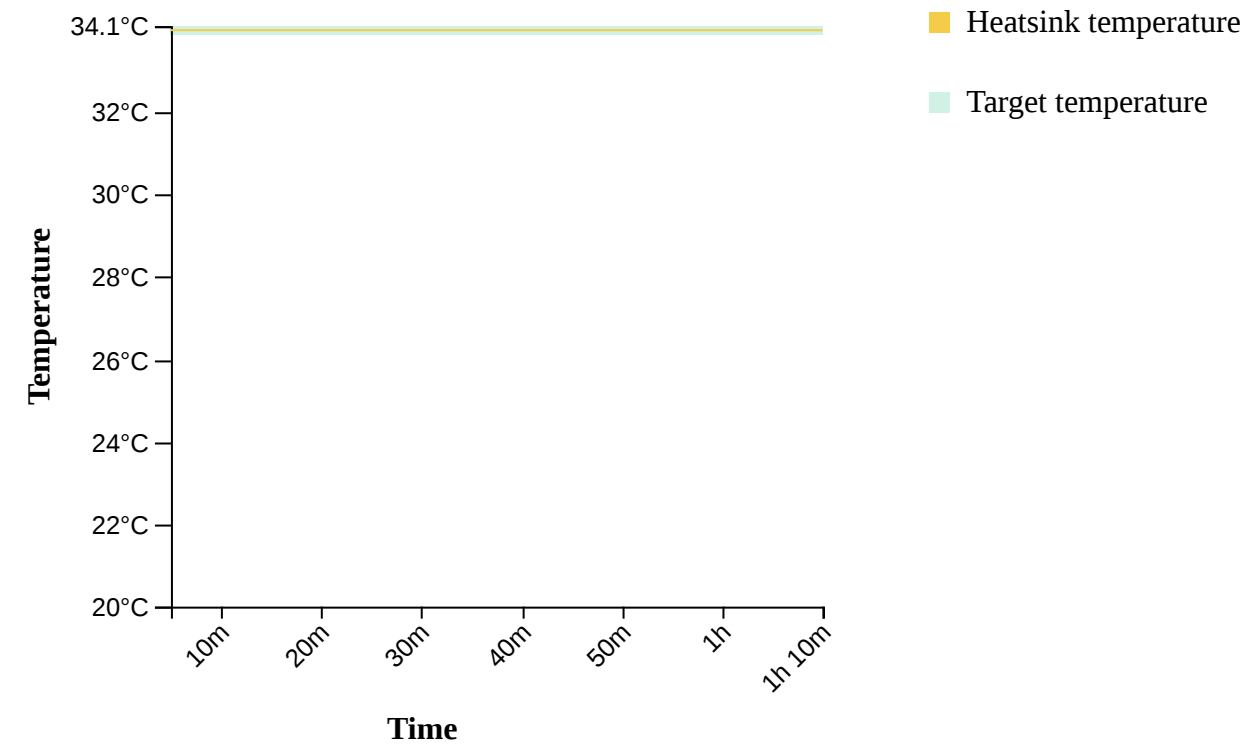
Mux Scan Grouped



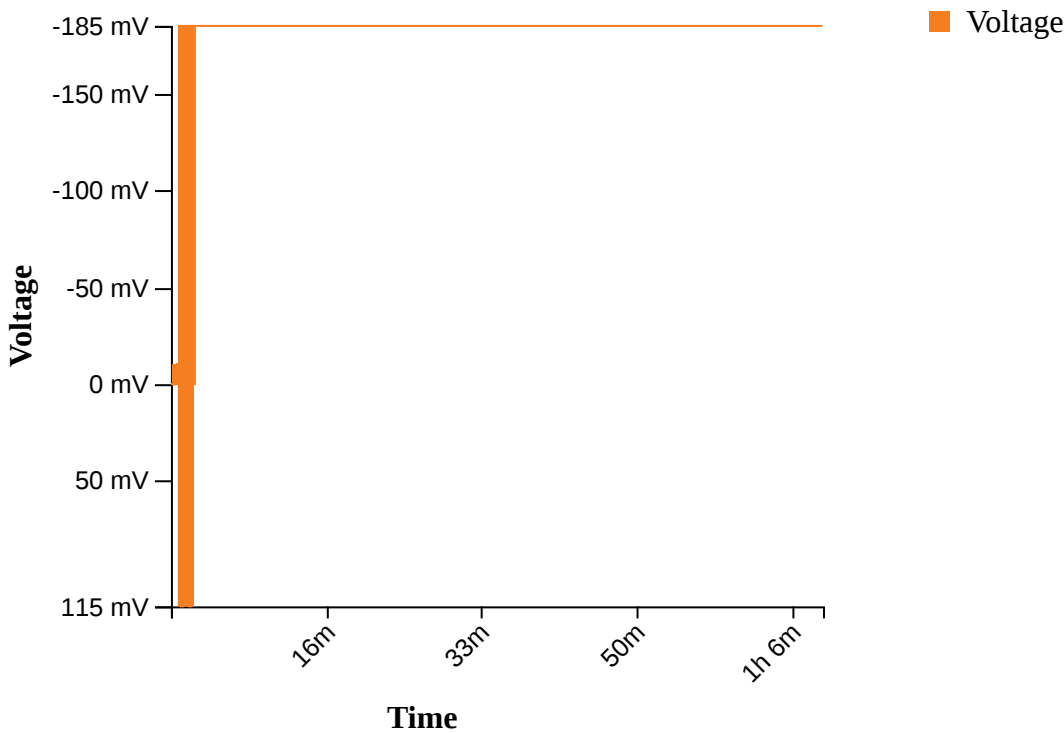
Mux Scan Categorised



**Temperature History.**

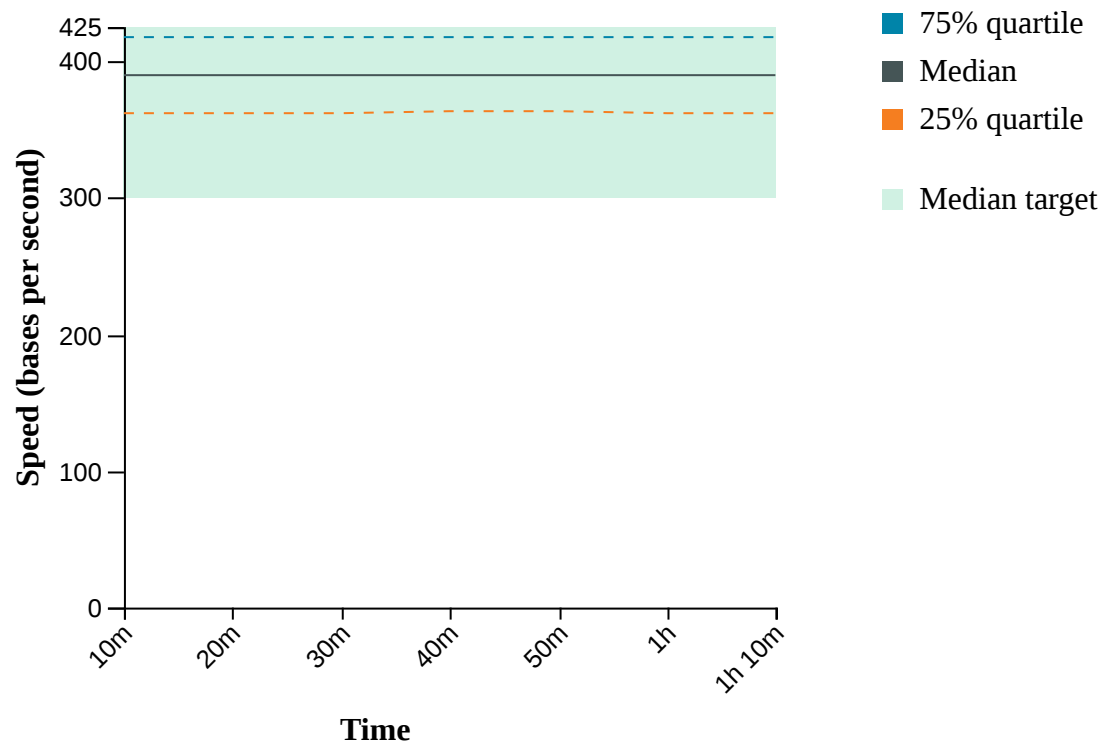


**Bias Voltage History.**

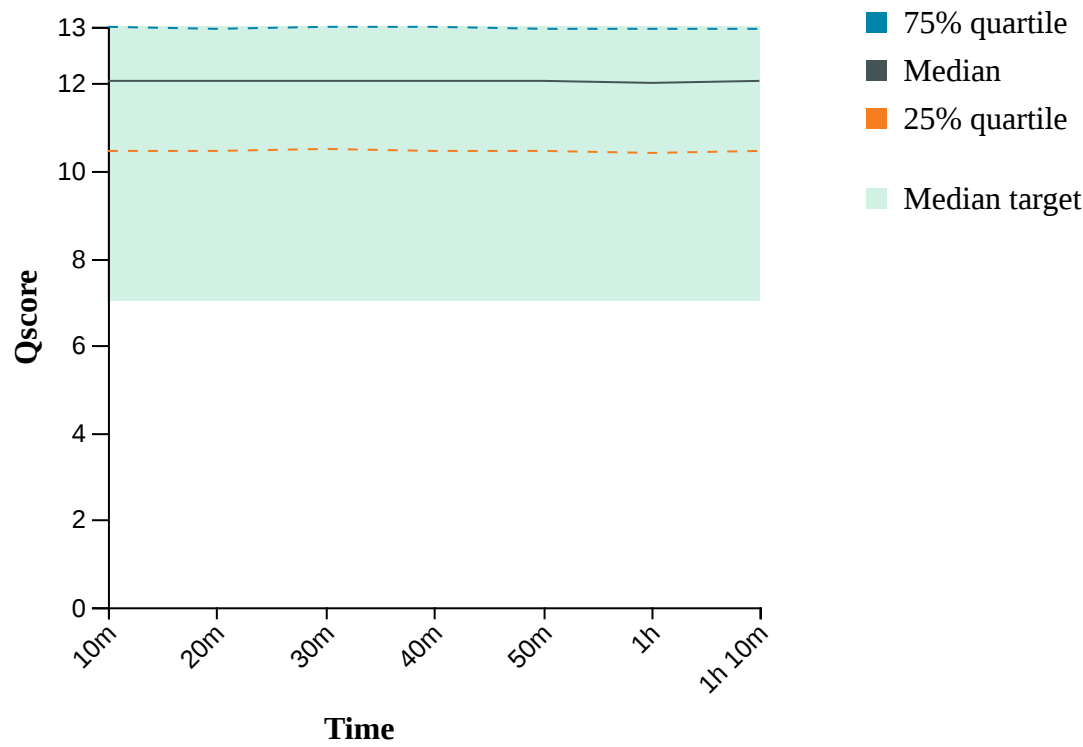




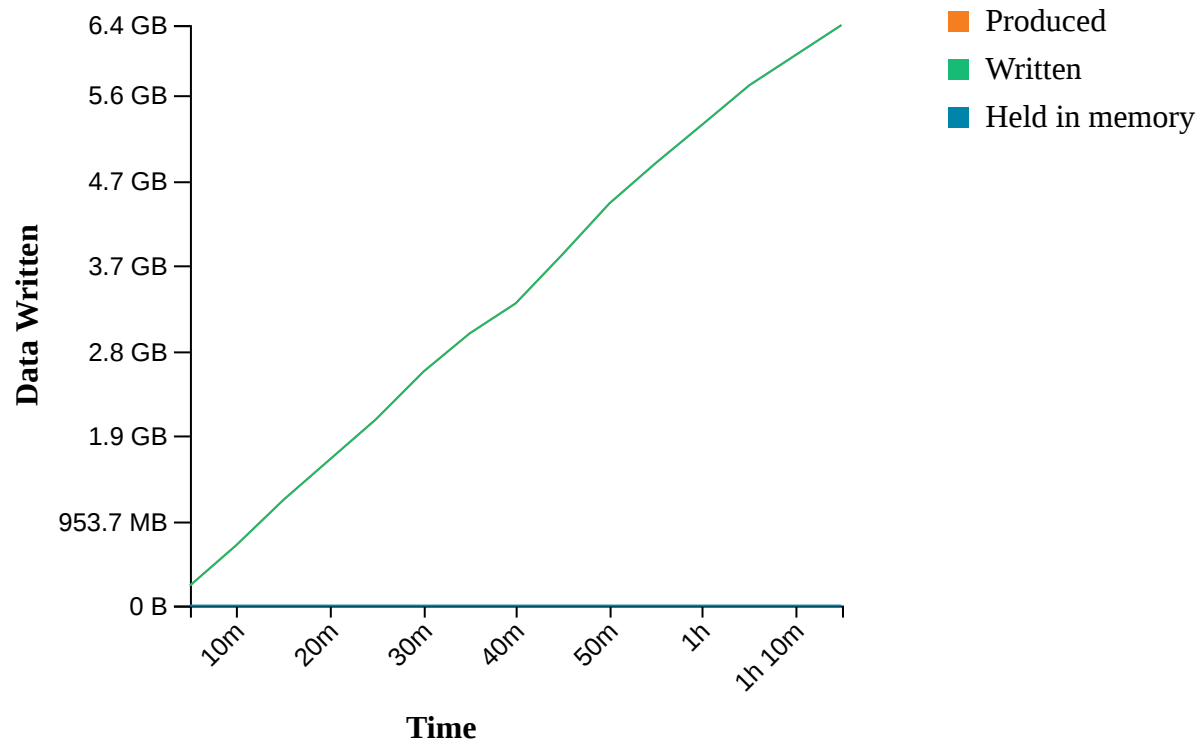
**Translocation Speed**



**QScore**



Disk Write Performance



### **Run Debug Messages**

- Mux scan for flow cell FAO52906 has found a total of 965 pores. 458 pores available for immediate sequencing December 8, 17:54
- Performing Mux Scan December 8, 17:52
- Starting sequencing procedure December 8, 17:52
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C December 8, 17:48