



Run Info

Host Name	meqneuropat17 (localhost)
Experiment Name	B1992_24268_20211126_BC12
Sample ID	B1992_24268_20211126_BC12
Run ID	b1e50e6a-ec99-4990-af6d-7ff34492d20d
Flow Cell Id	FAQ51001
Start Time	November 26, 10:30
Run Length	2h 5m

Run Summary

Reads Generated	198.16 K
Passed Bases	133.69 Mb
Failed Bases	25.04 Mb
Estimated Bases	150.13 Mb

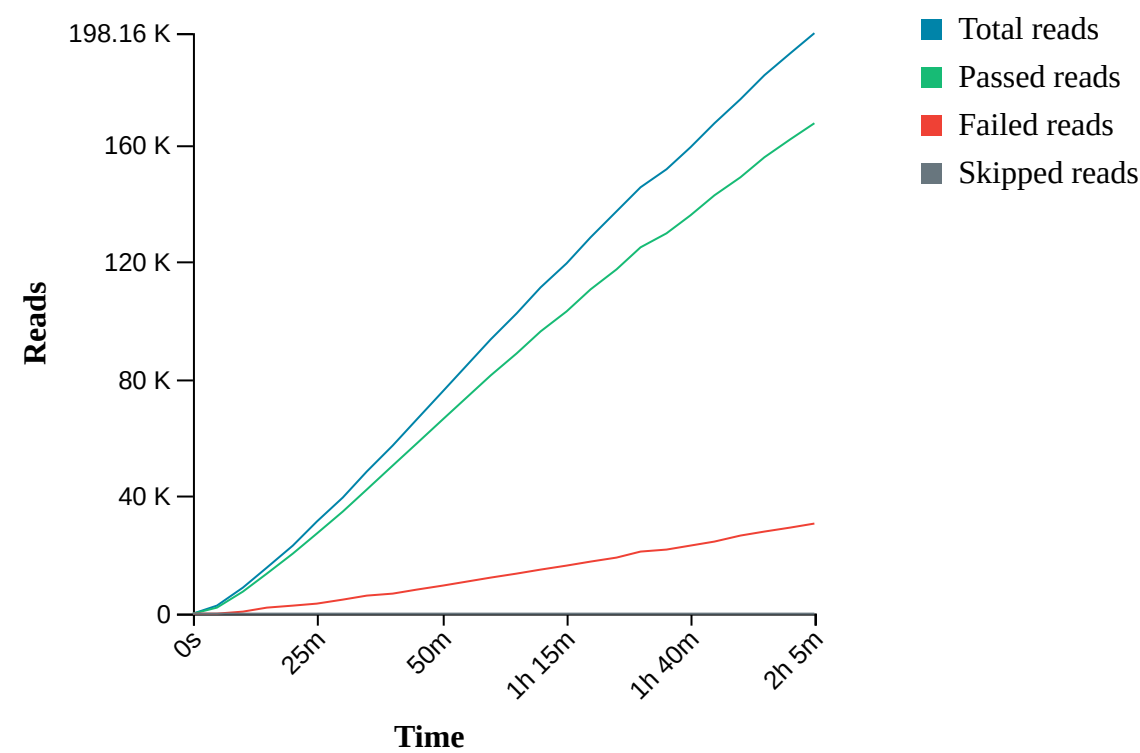
Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-RBK004
Basecalling	on
Barcoding	barcoding_kits=['SQK-RBK004',]
Specified Run Length	72 hours
FAST5 Output	Enabled
FAST5 Output Options	zlib_compress,fastq,raw
FAST5 Reads per File	400
FASTQ Output	Enabled
FASTQ Reads per File	400
BAM Output	Disabled
Active Channel Selection	Enabled
Mux Scan Period	1 hour 30 minutes
Bulk File Output	Enabled
Bulk Output Options	raw=[[1,512]],events=[[1,512]],read_table=[[1,512]]
Initial Bias Voltage	-180 mV

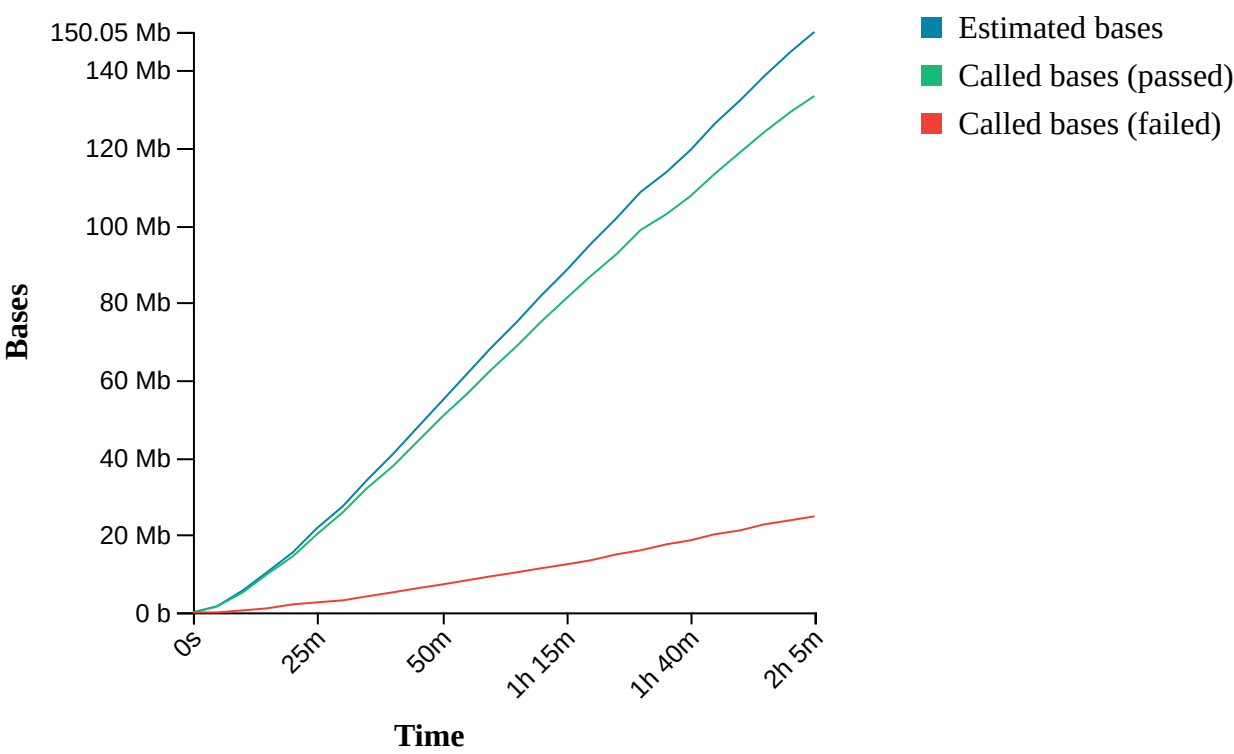
Versions

MinKNOW	unknown
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.2

Cumulative Output Reads

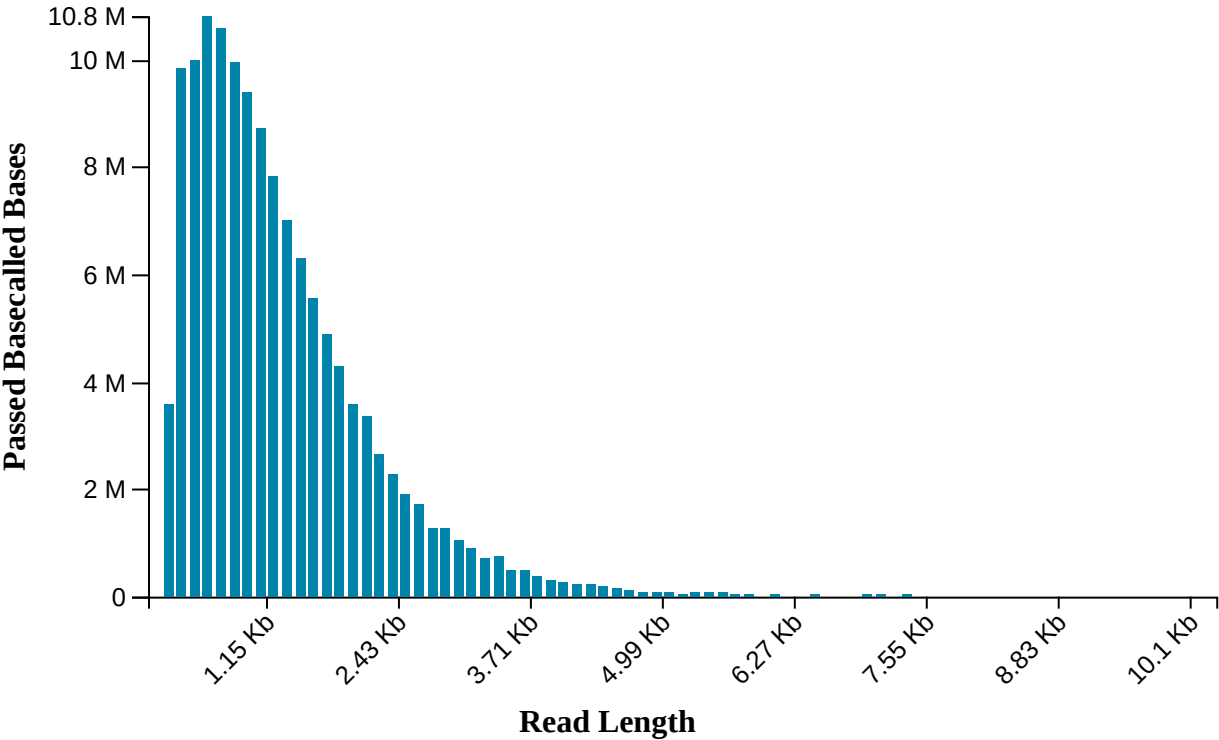


Cumulative Output Bases



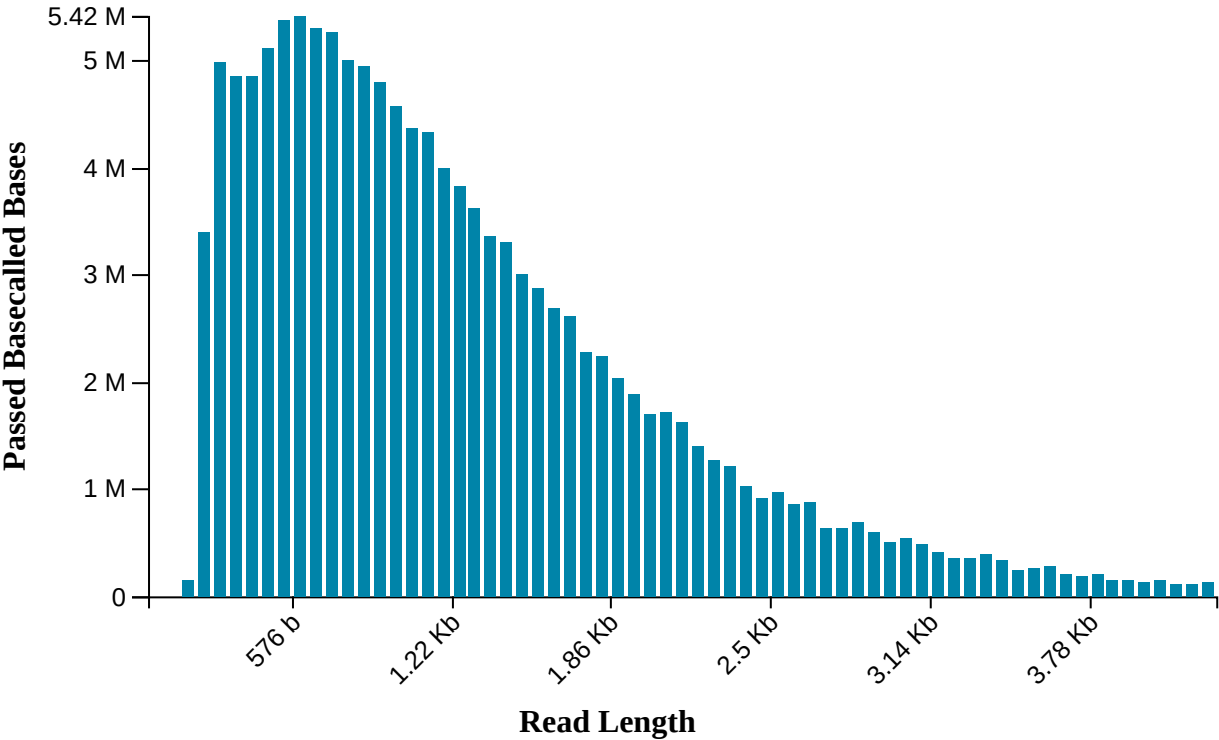
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 1.06 K



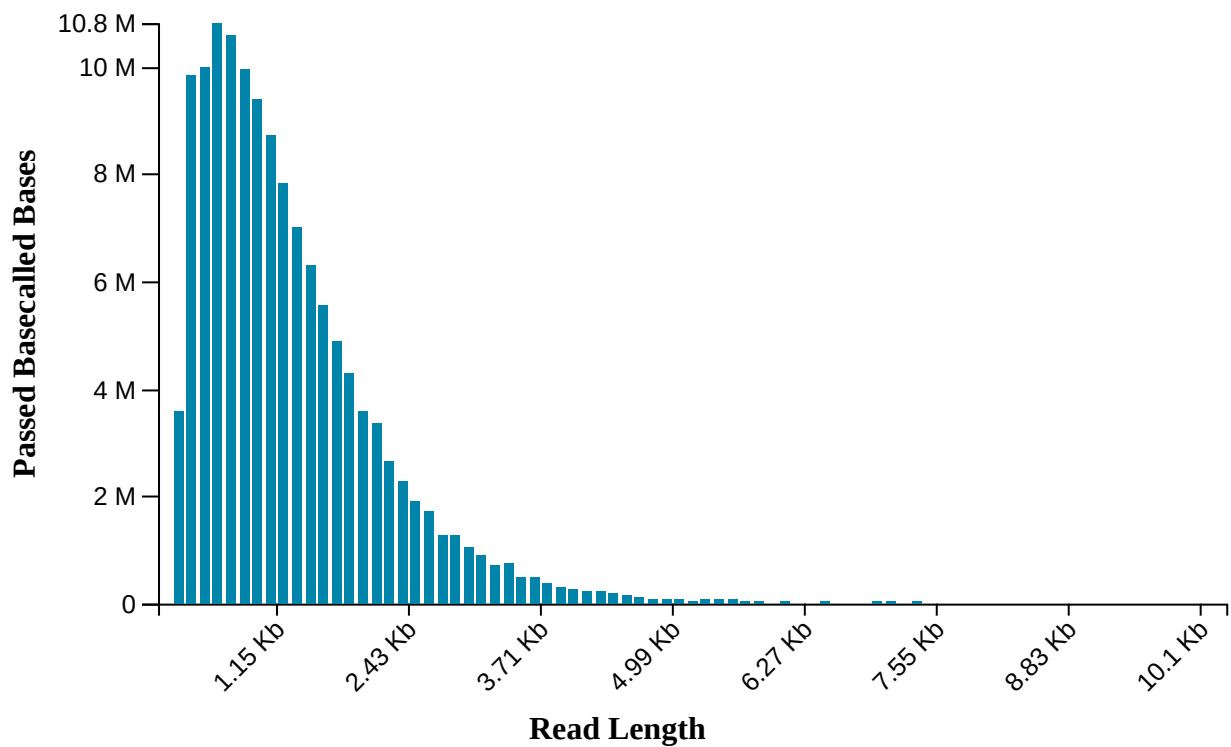
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 1.05 K



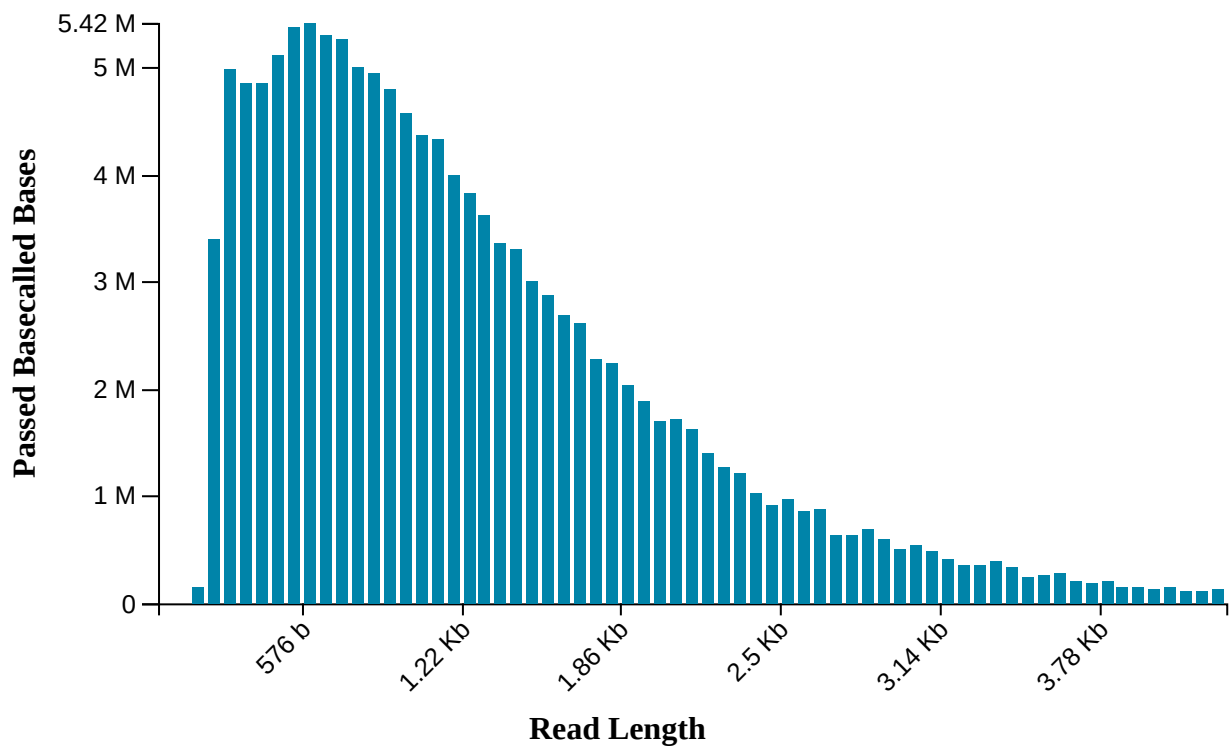
Read Length Histogram Estimated Bases

Estimated N50: 1.06 K

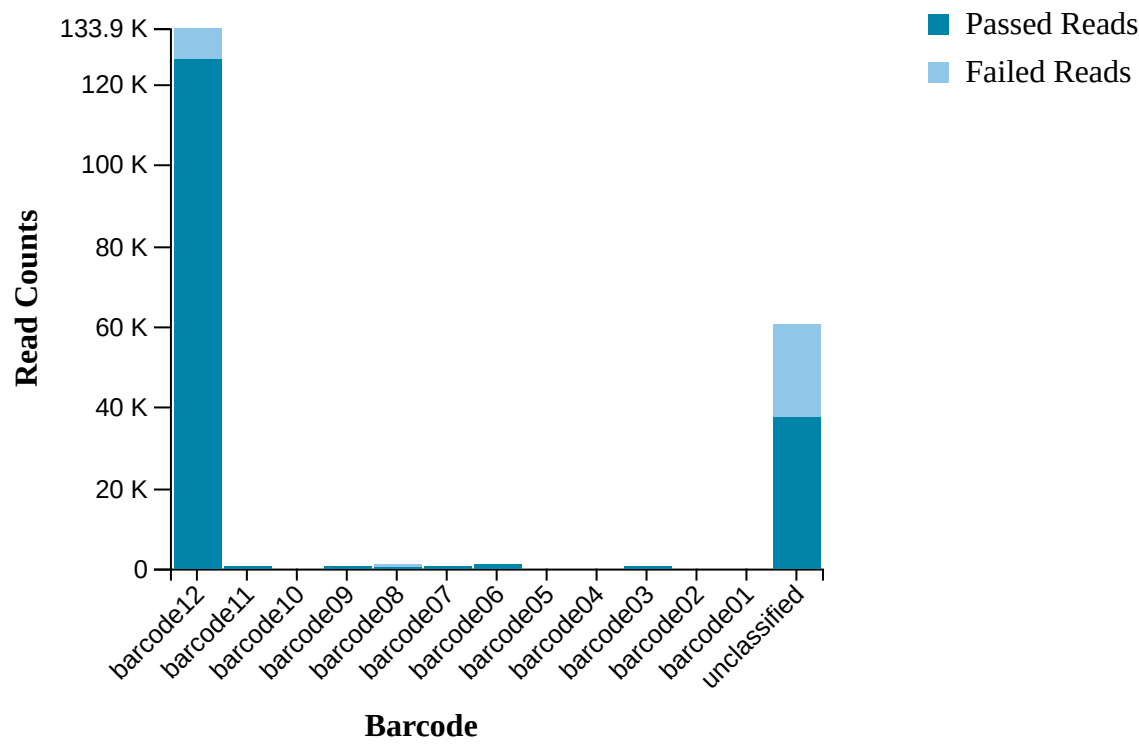


Read Length Histogram Basecalled Bases

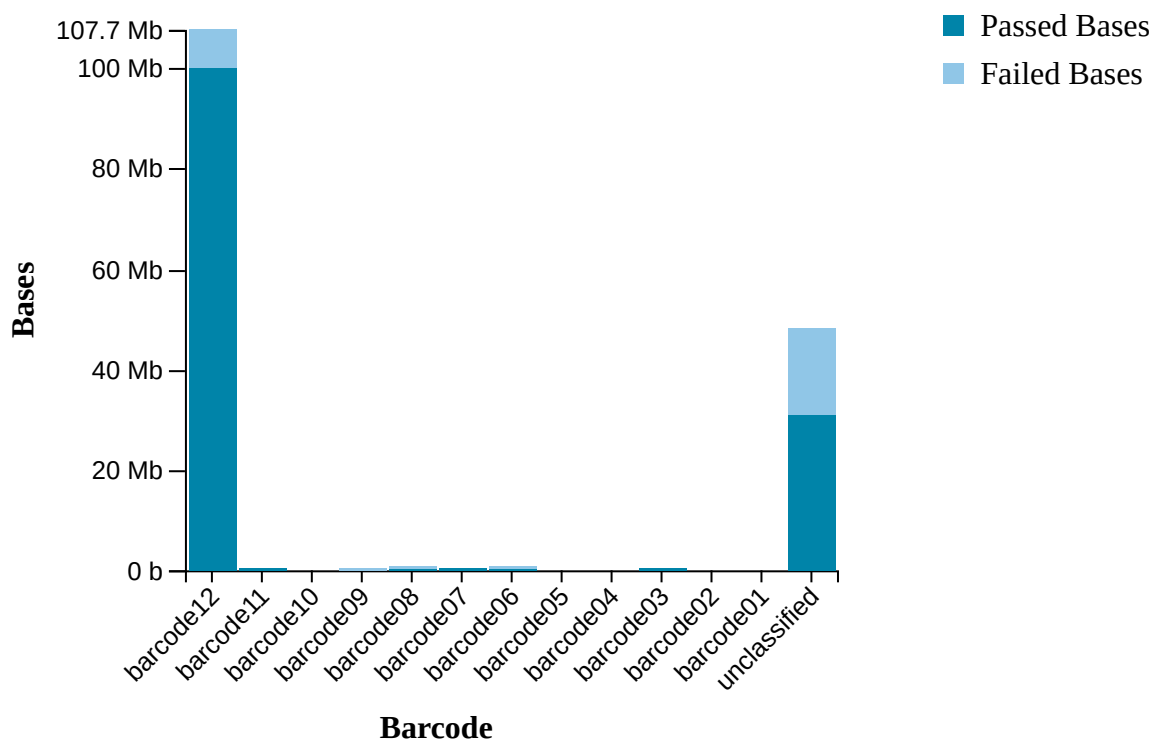
Estimated N50: 1.05 K



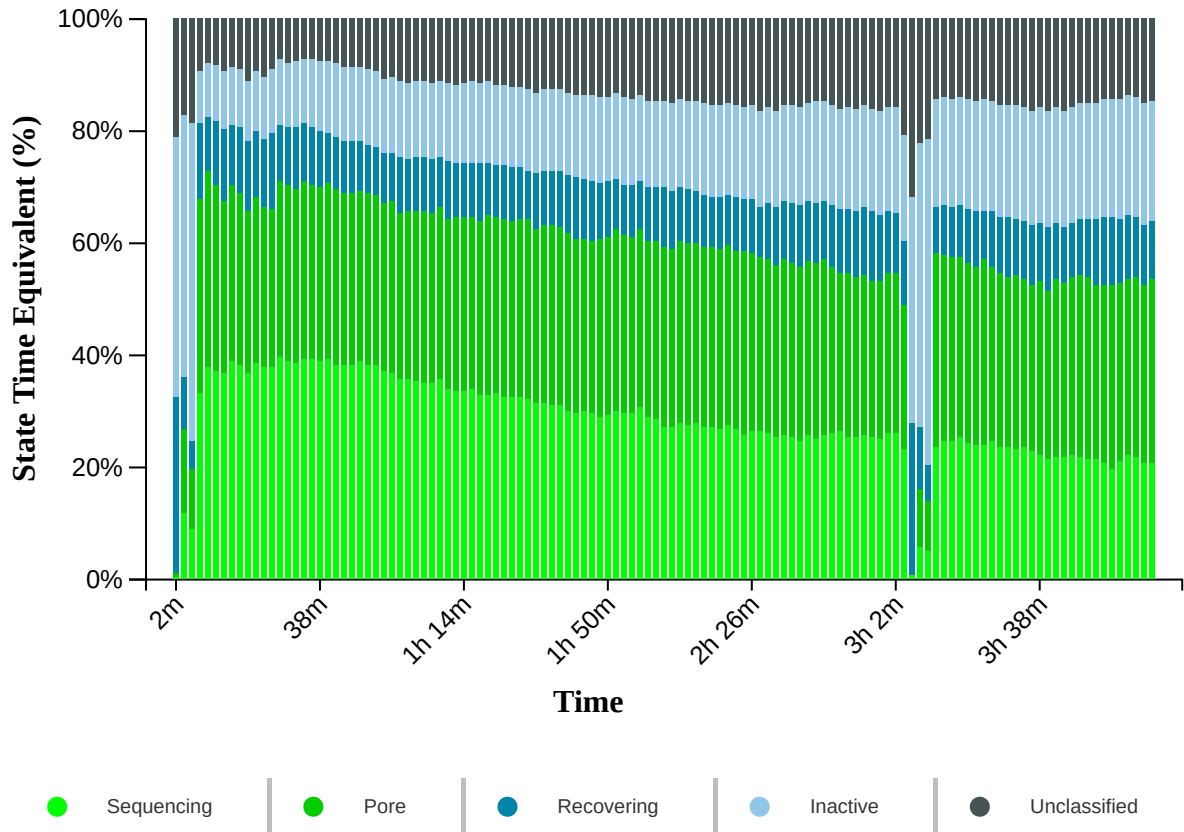
Barcode Read Counts



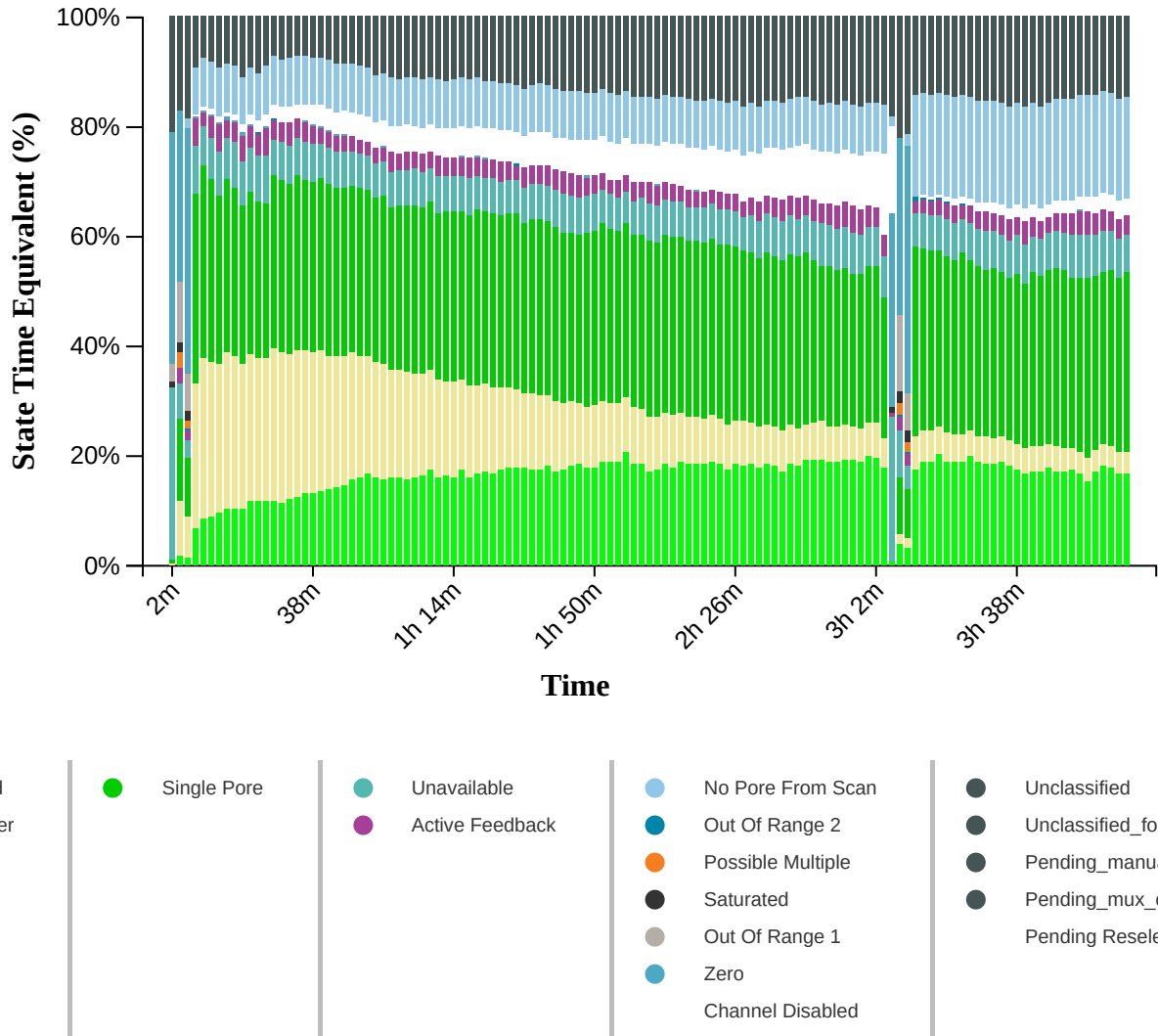
Barcode Read Counts



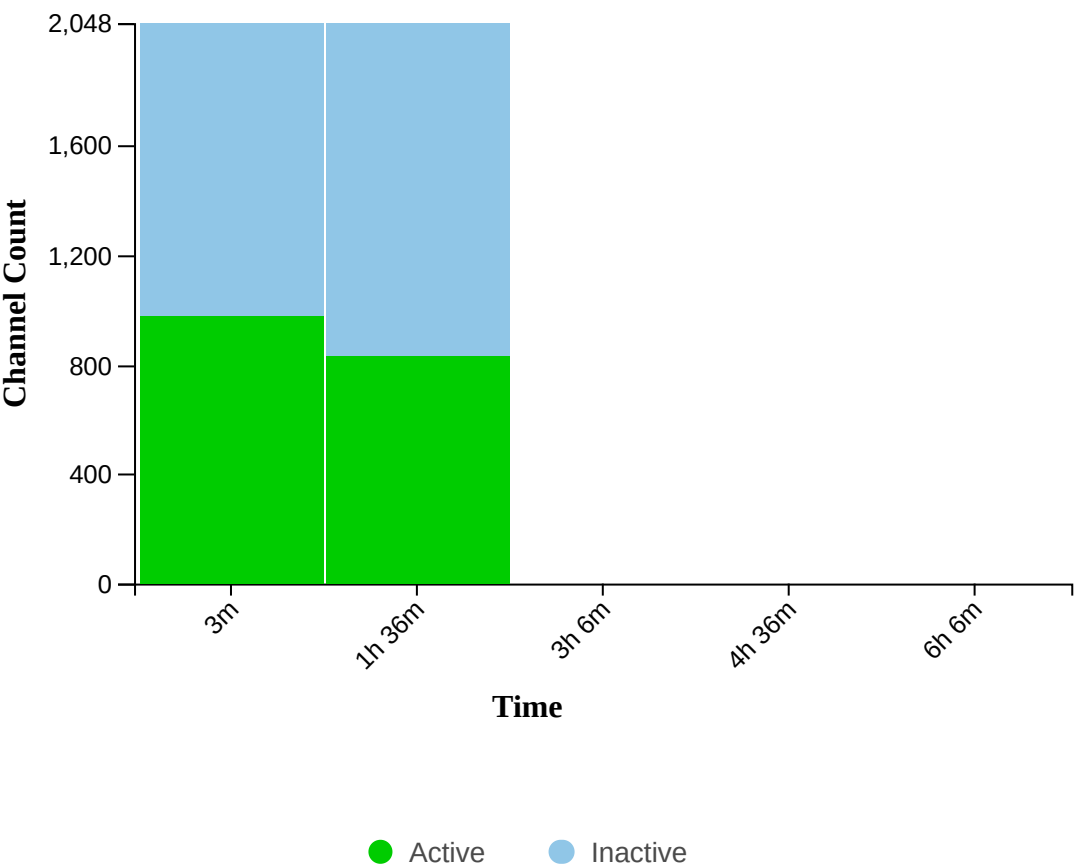
Duty Time Grouped



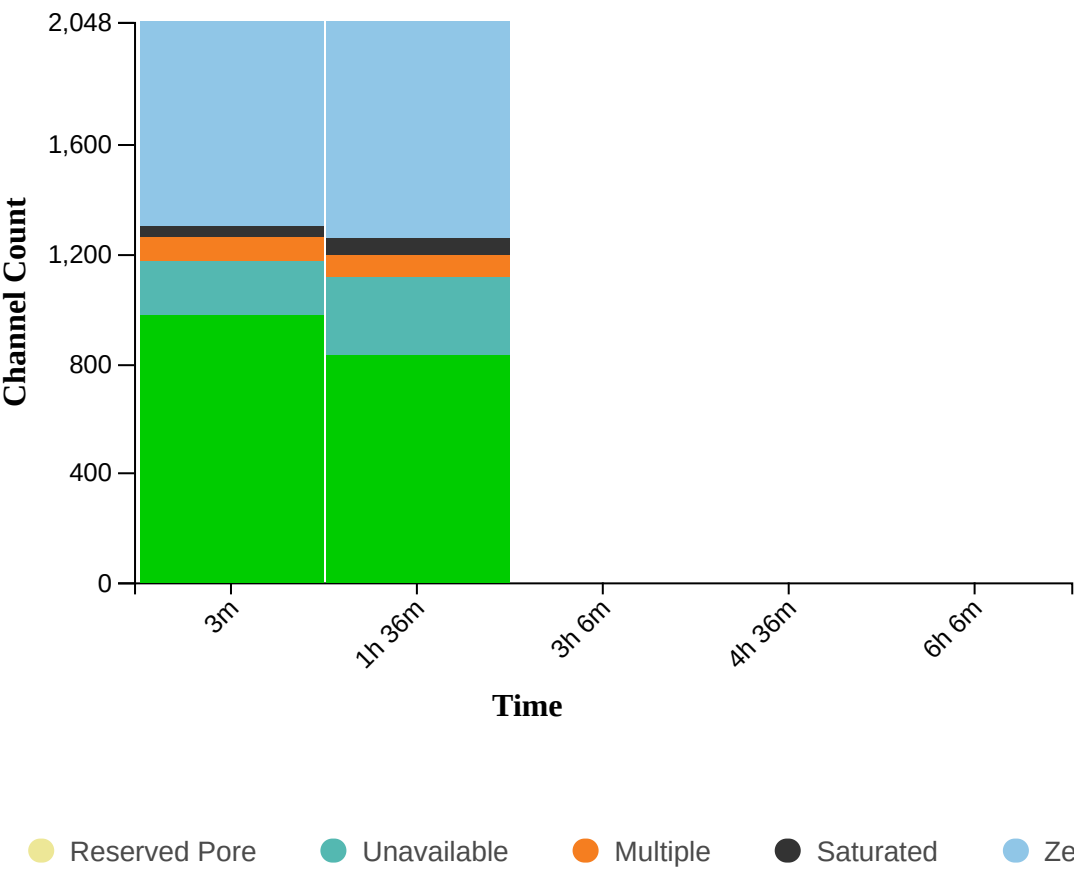
Duty time Categorized



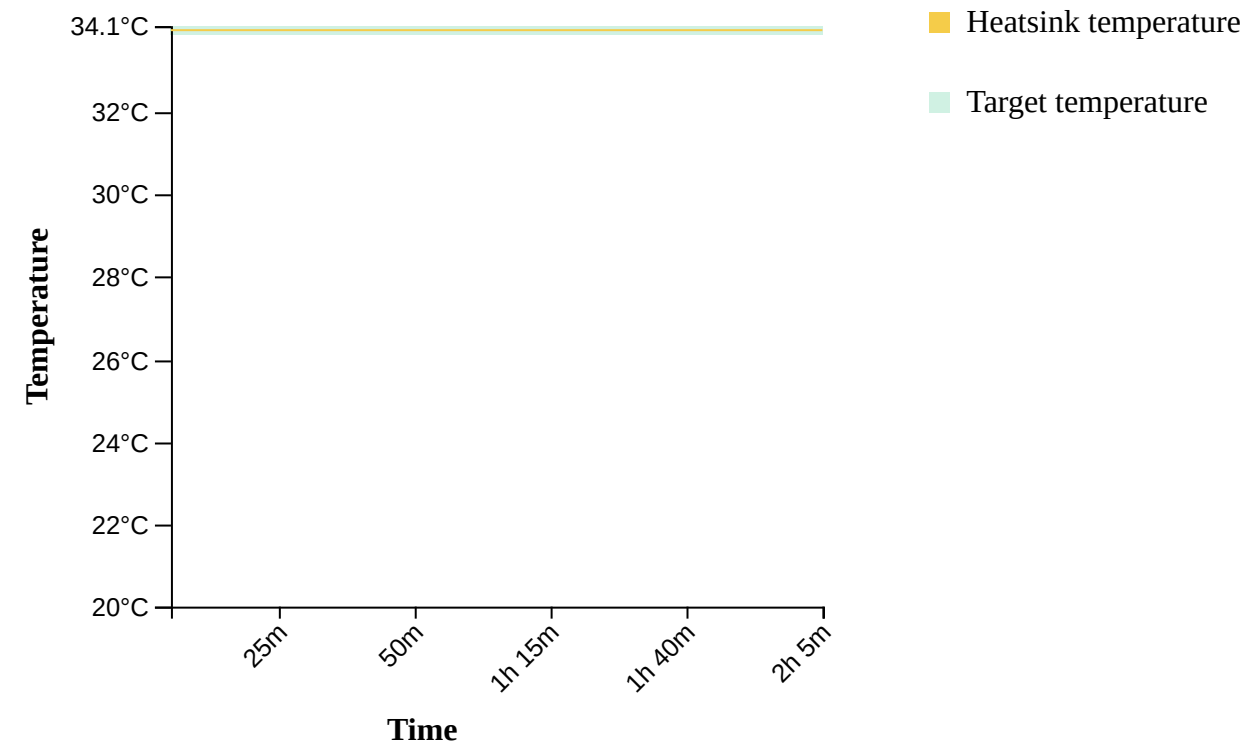
Mux Scan Grouped



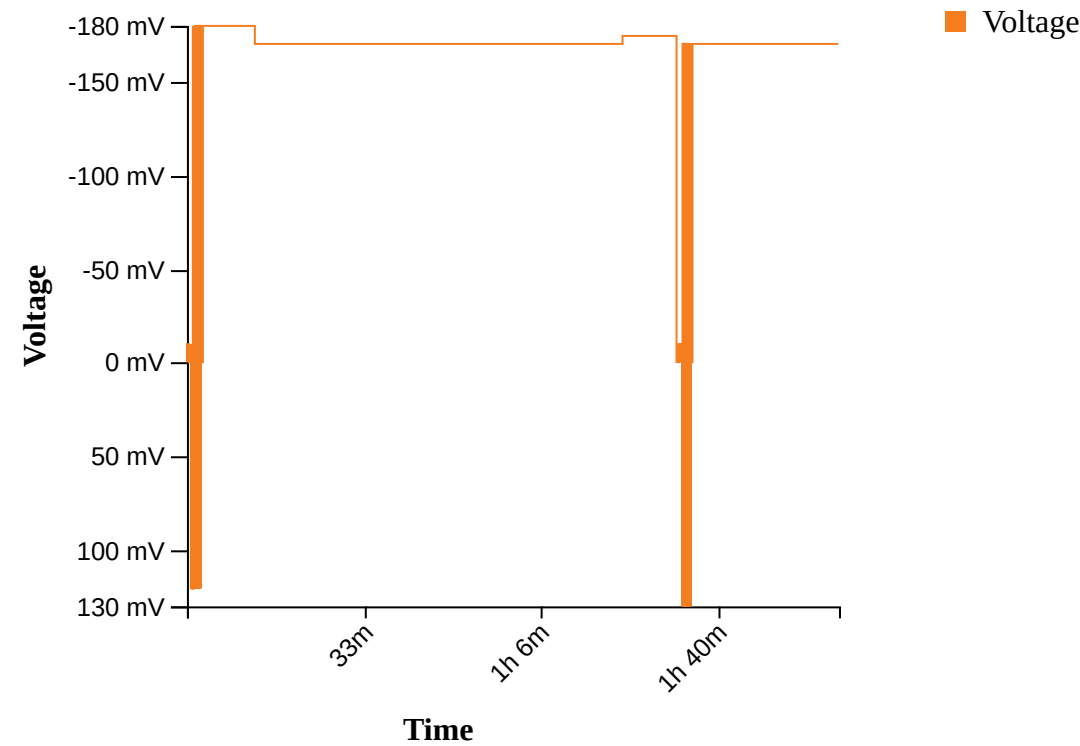
Mux Scan Categorised



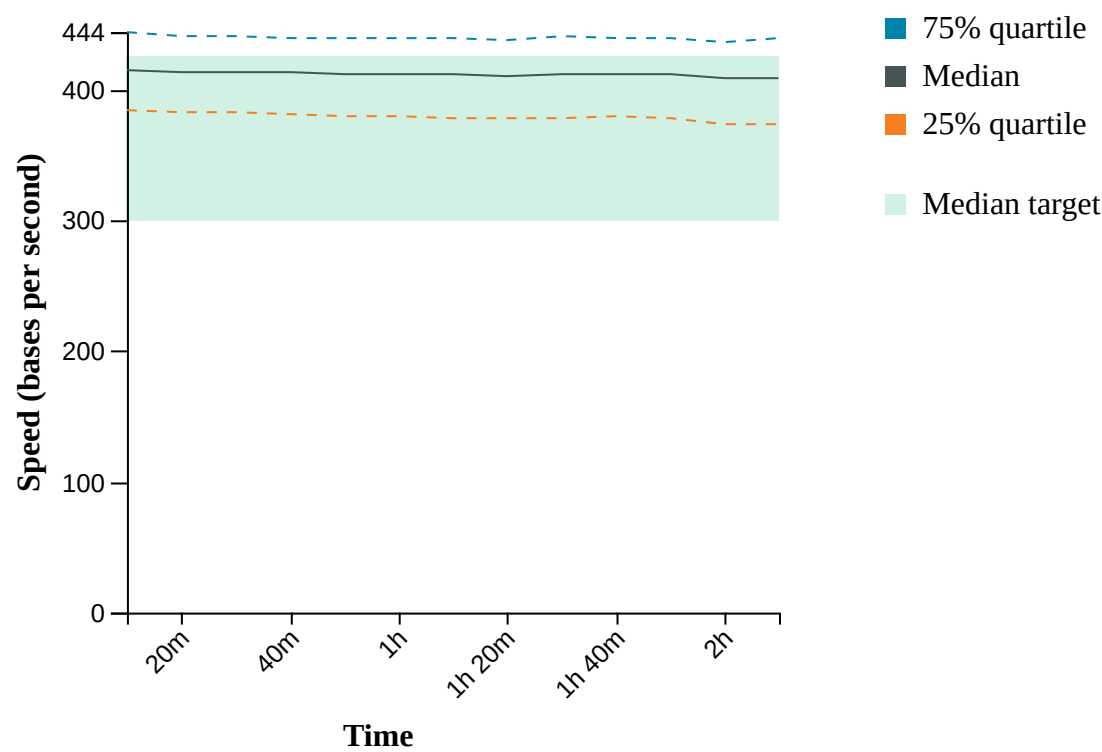
Temperature History.



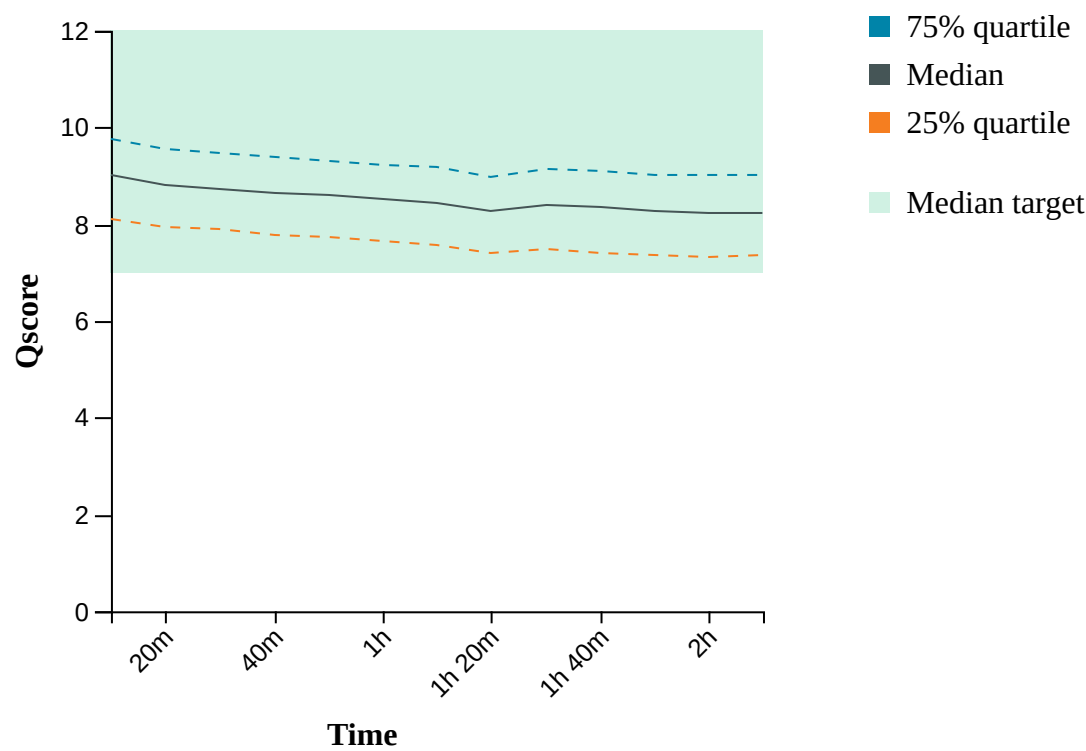
Bias Voltage History.



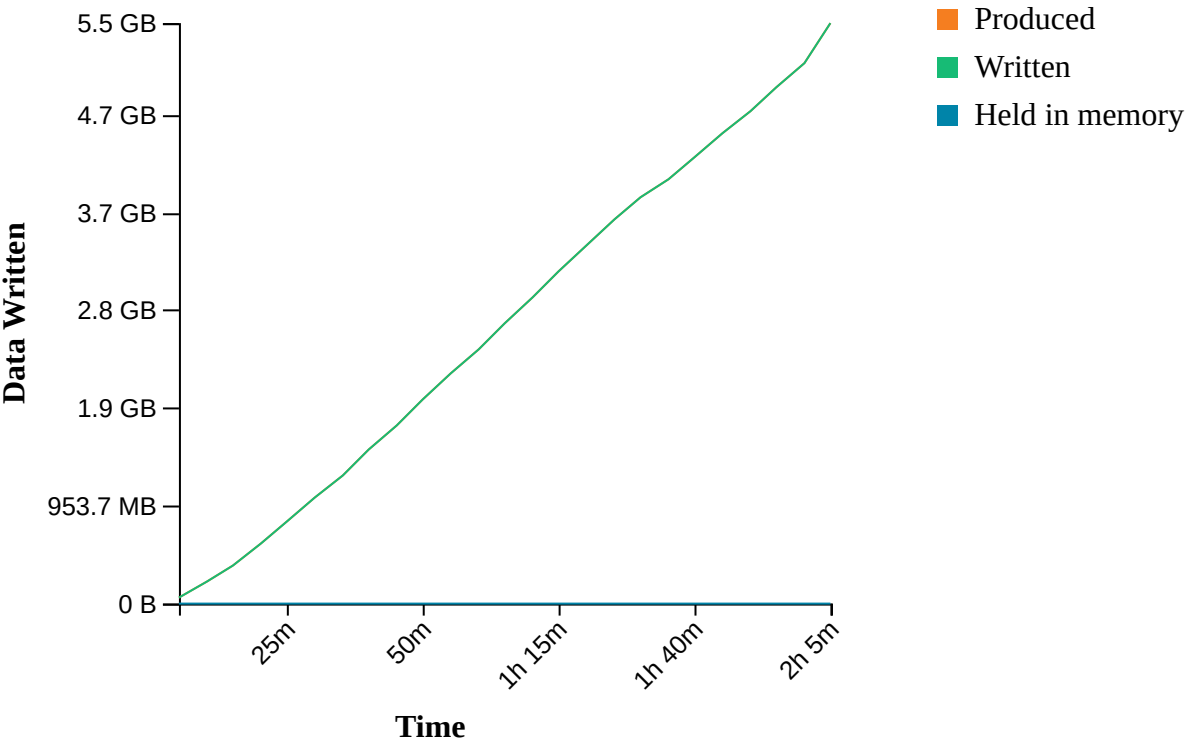
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAQ51001 has found a total of 835 pores. 417 pores available for immediate sequencing November 26, 12:08
- Performing Mux Scan November 26, 12:05
- Mux scan for flow cell FAQ51001 has found a total of 977 pores. 467 pores available for immediate sequencing November 26, 10:35
- Performing Mux Scan November 26, 10:32
- Starting sequencing procedure November 26, 10:32
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C November 26, 10:31