



Run Info

Host Name	GXB01190 (localhost)
Experiment Name	EIMock_2kbp_LrichardiiRAD_050121
Sample ID	EIMock_2kbp_LrichardiiRAD_050121
Run ID	66a5d21f-d510-4007-86f5-829b37b81f75
Flow Cell Id	FAO53362
Start Time	January 5, 16:00
Run Length	59m

Run Summary

Reads Generated	471.35 K
Passed Bases	228.96 Mb
Failed Bases	22.21 Mb
Estimated Bases	269.52 Mb

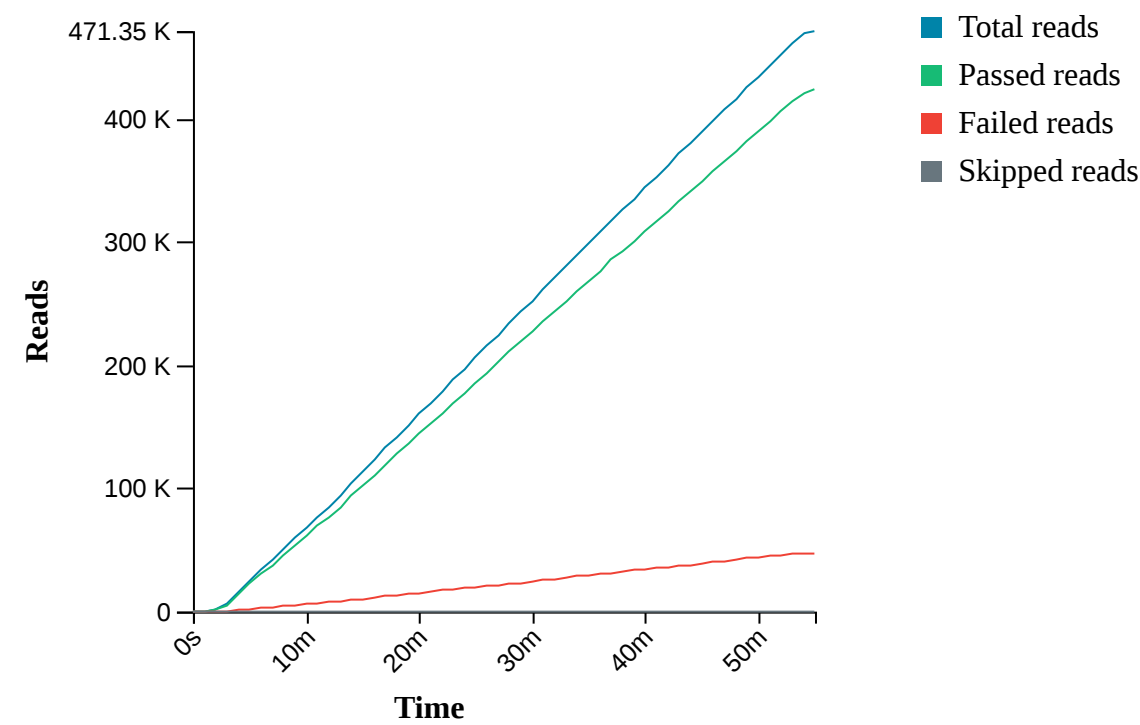
Run Parameters

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/L_richardii_ref.fa"],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

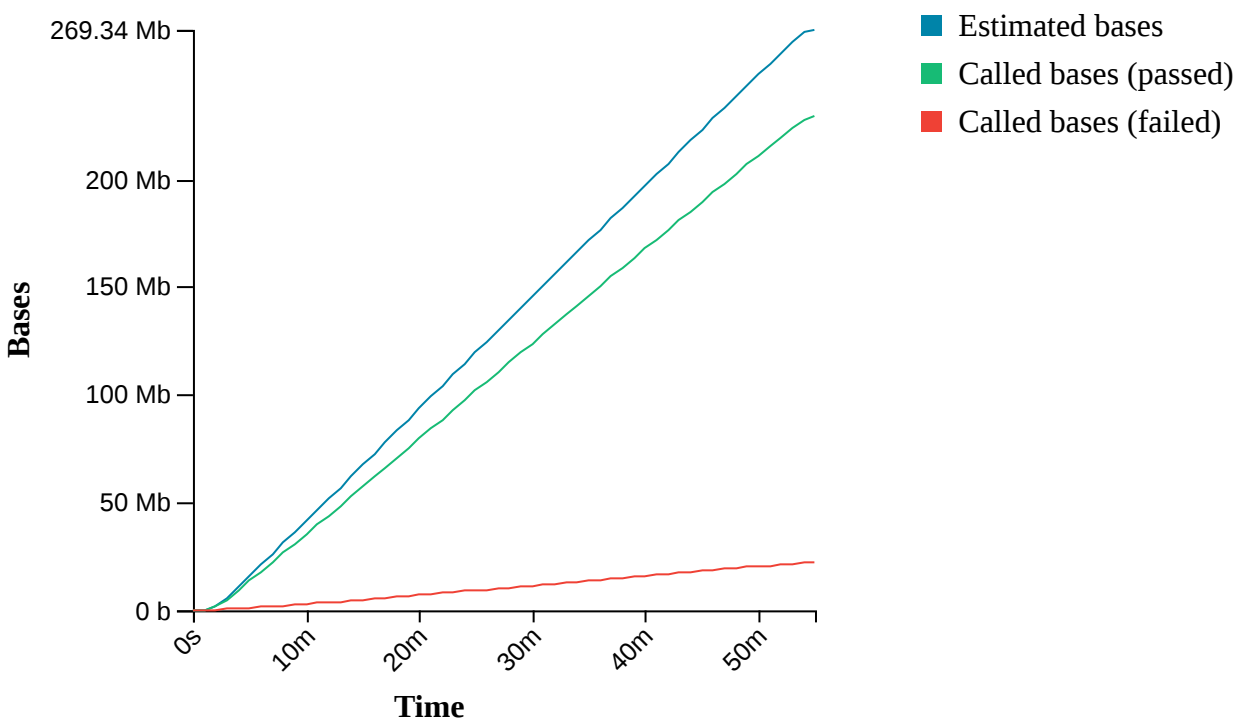
Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

Cumulative Output Reads

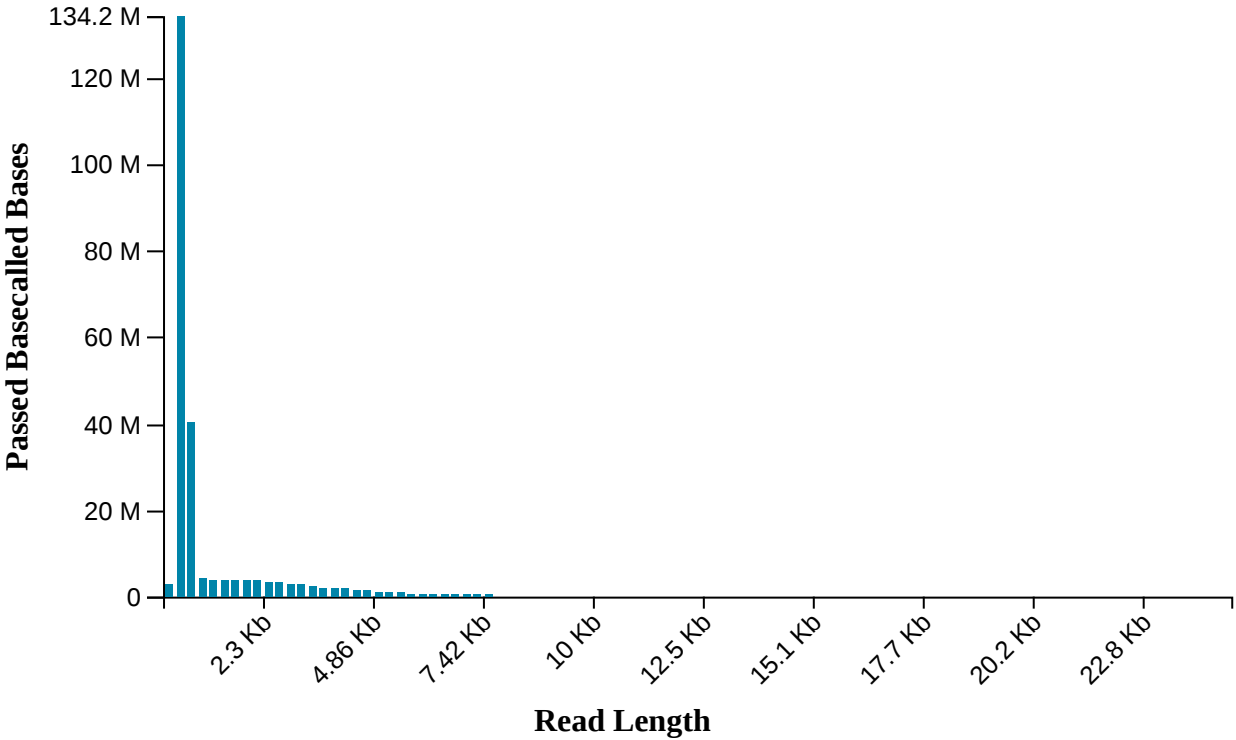


Cumulative Output Bases



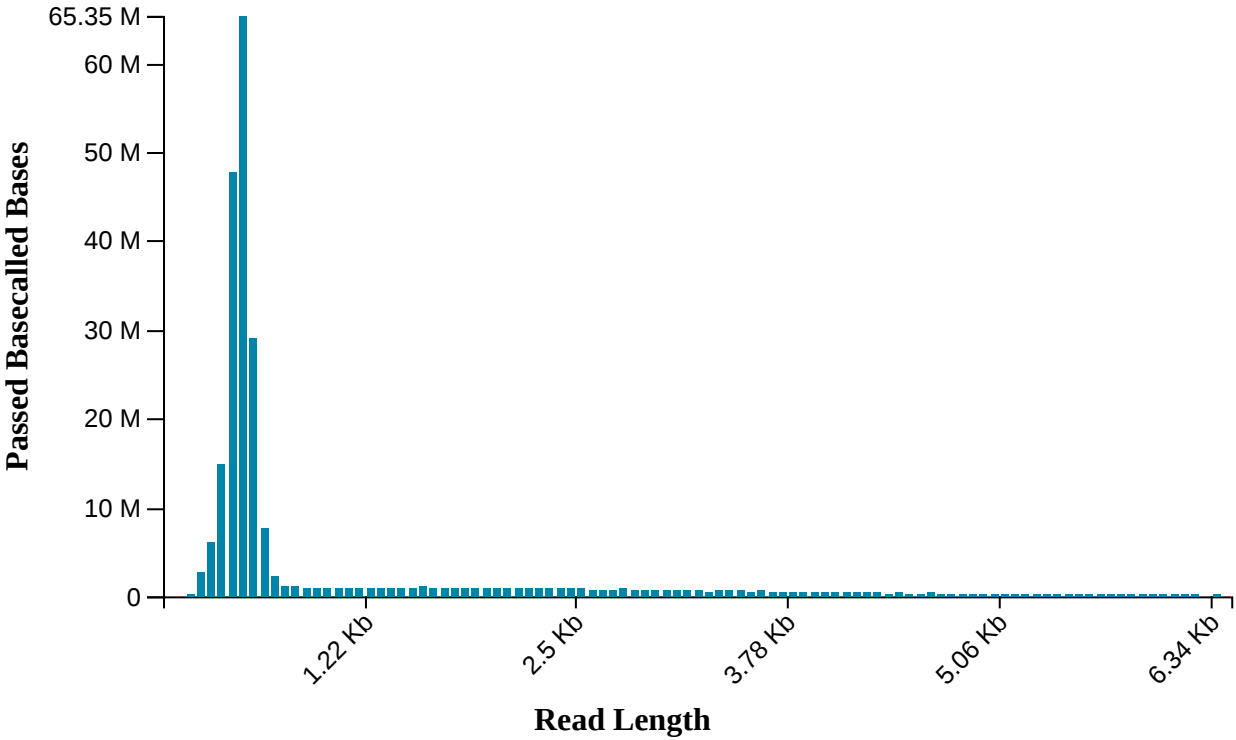
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 486



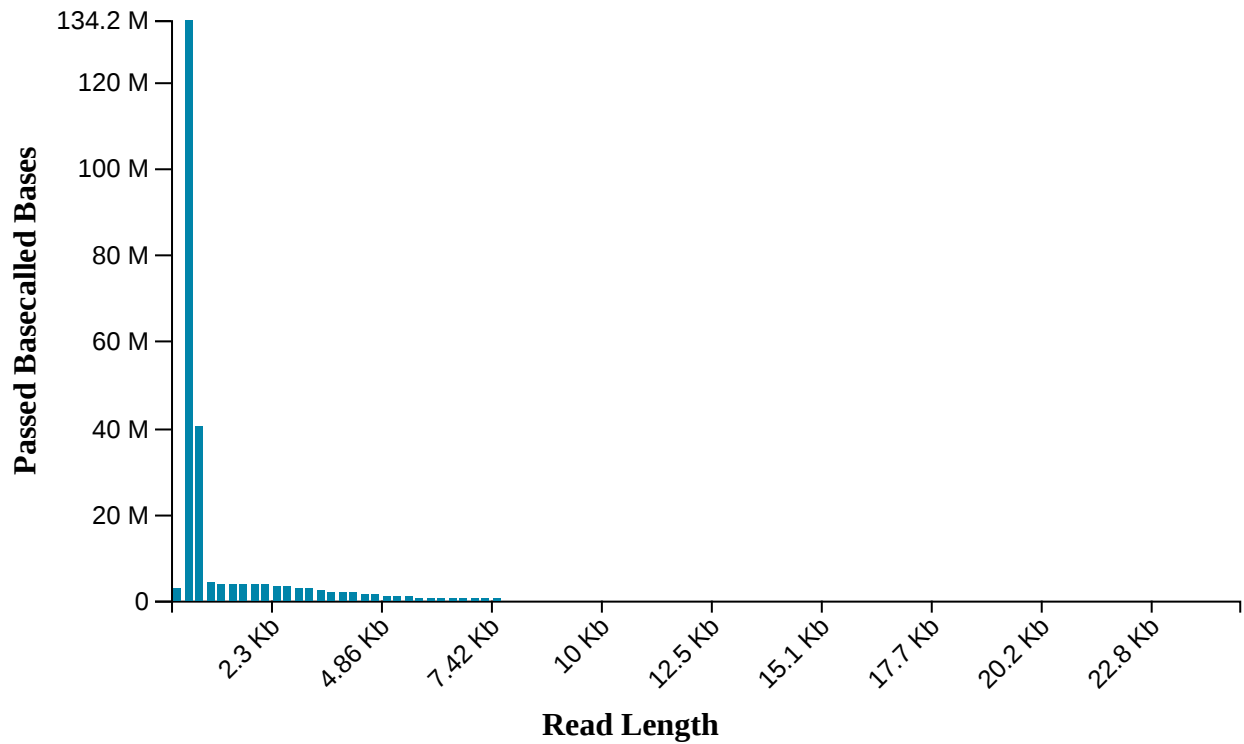
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 485



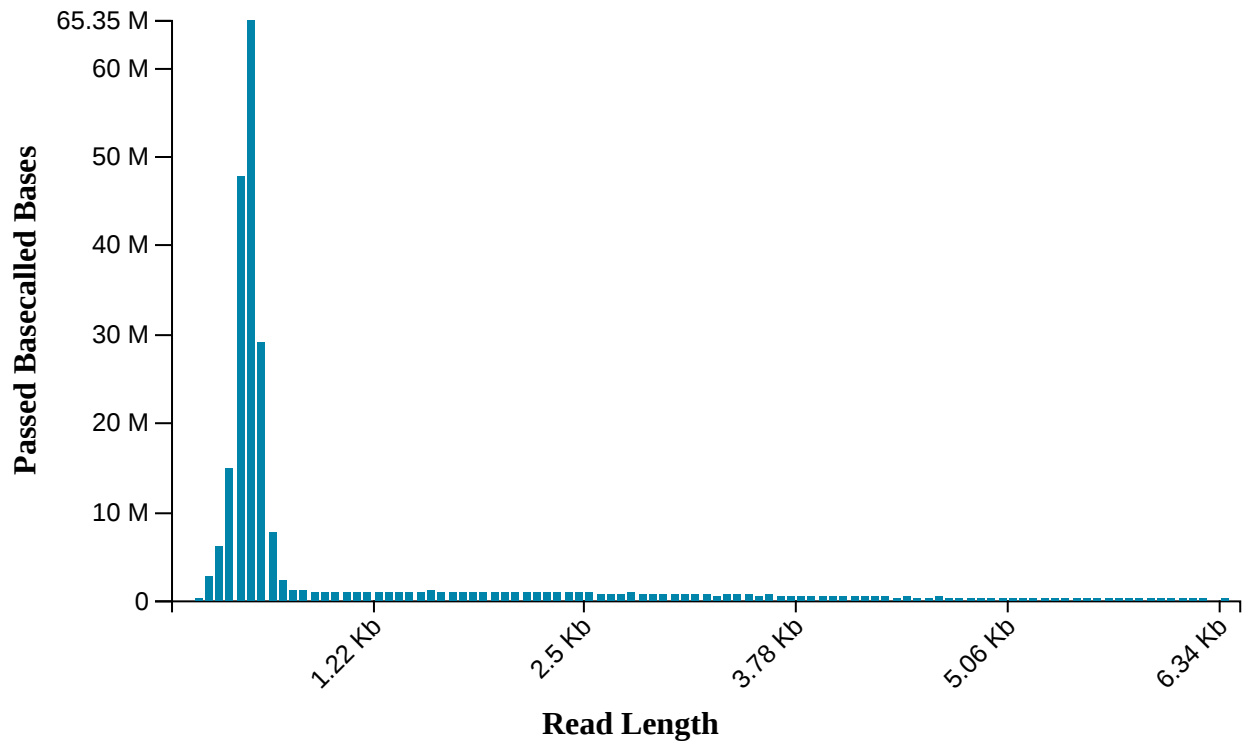
Read Length Histogram Estimated Bases

Estimated N50: 486

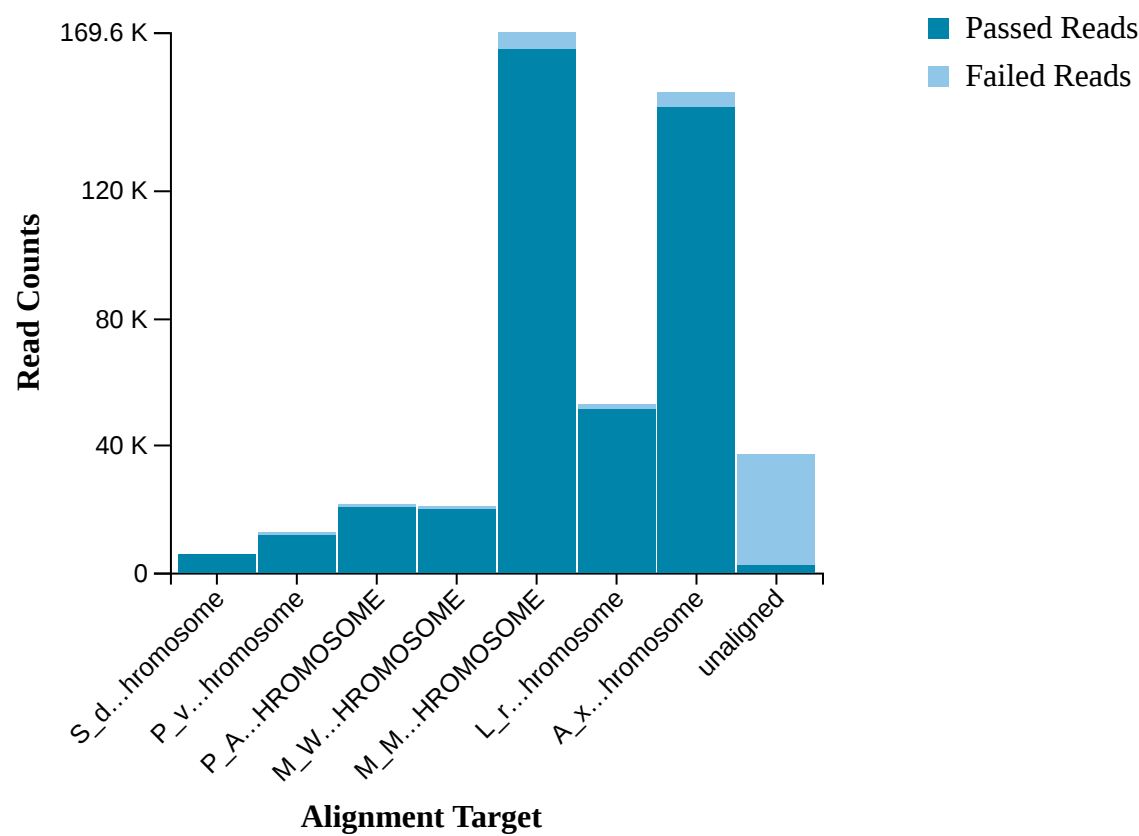


Read Length Histogram Basecalled Bases

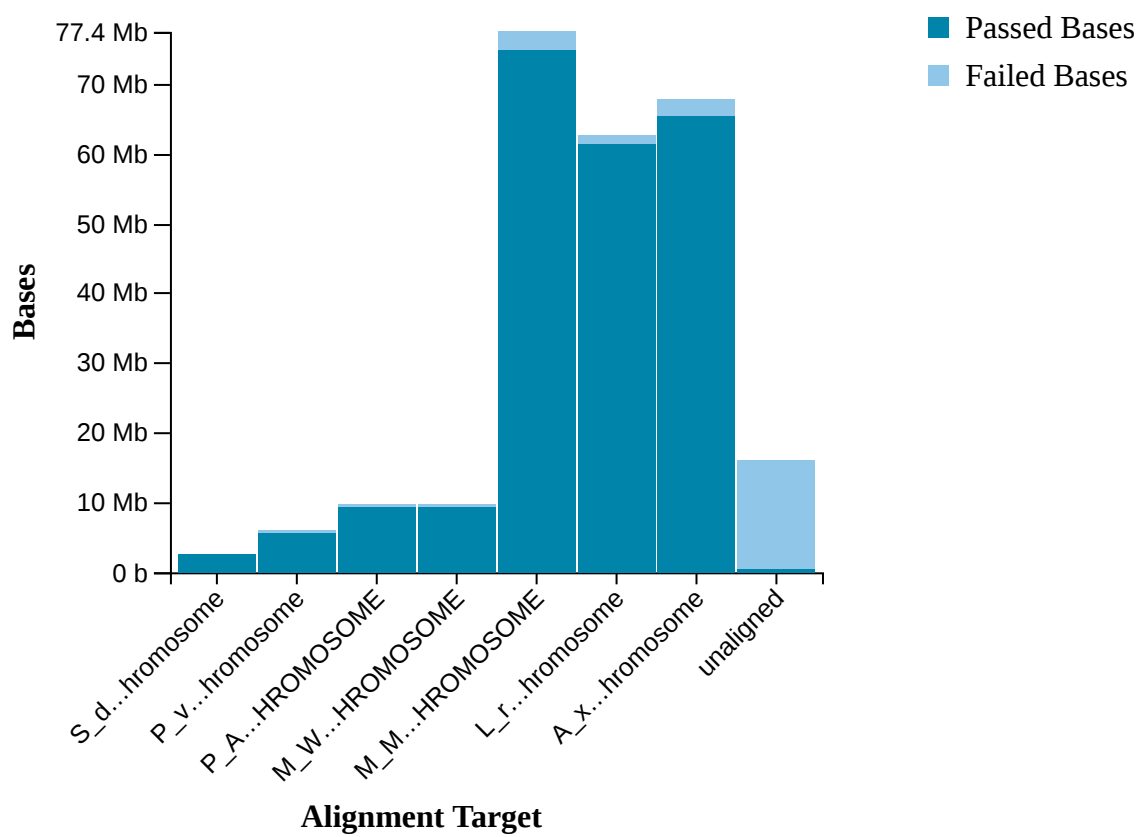
Estimated N50: 485

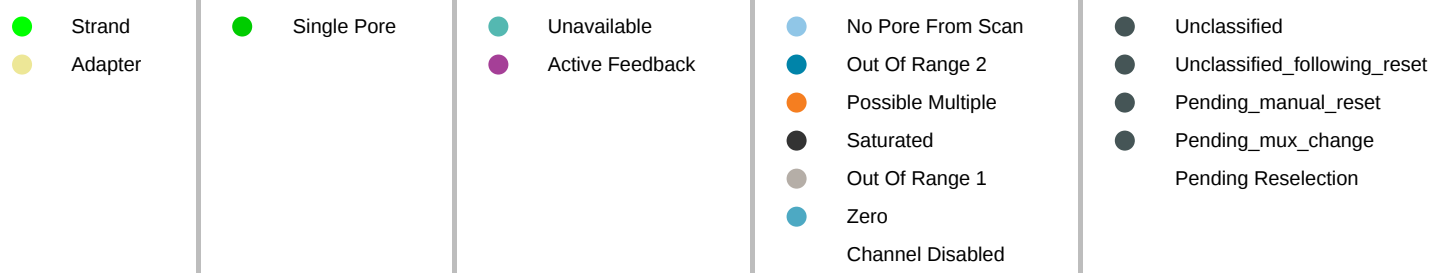
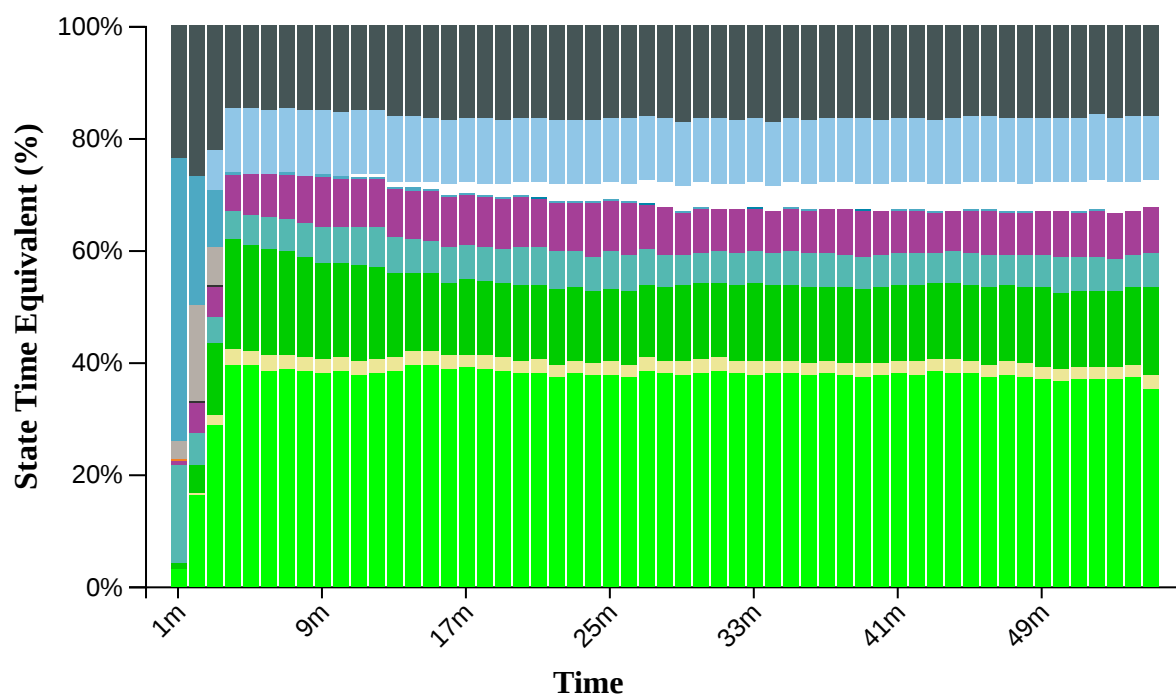


Alignment Target Hits (reads)

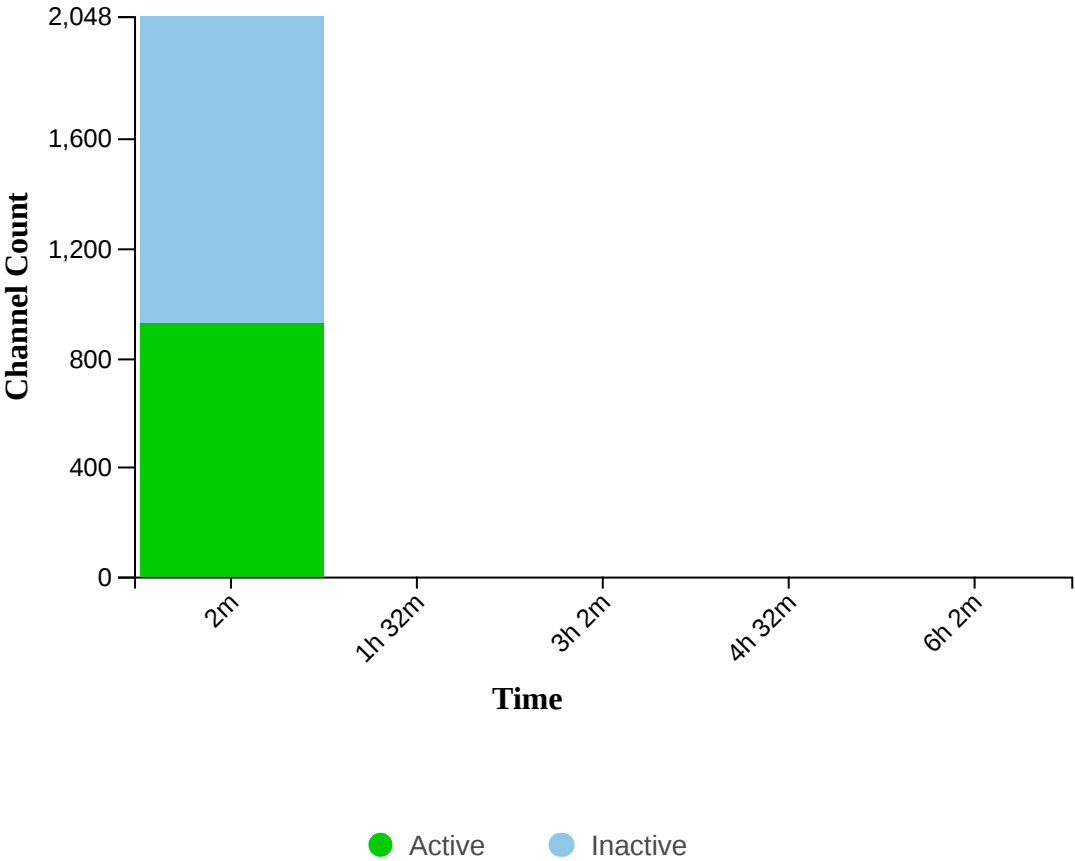


Alignment Target Hits (bases)

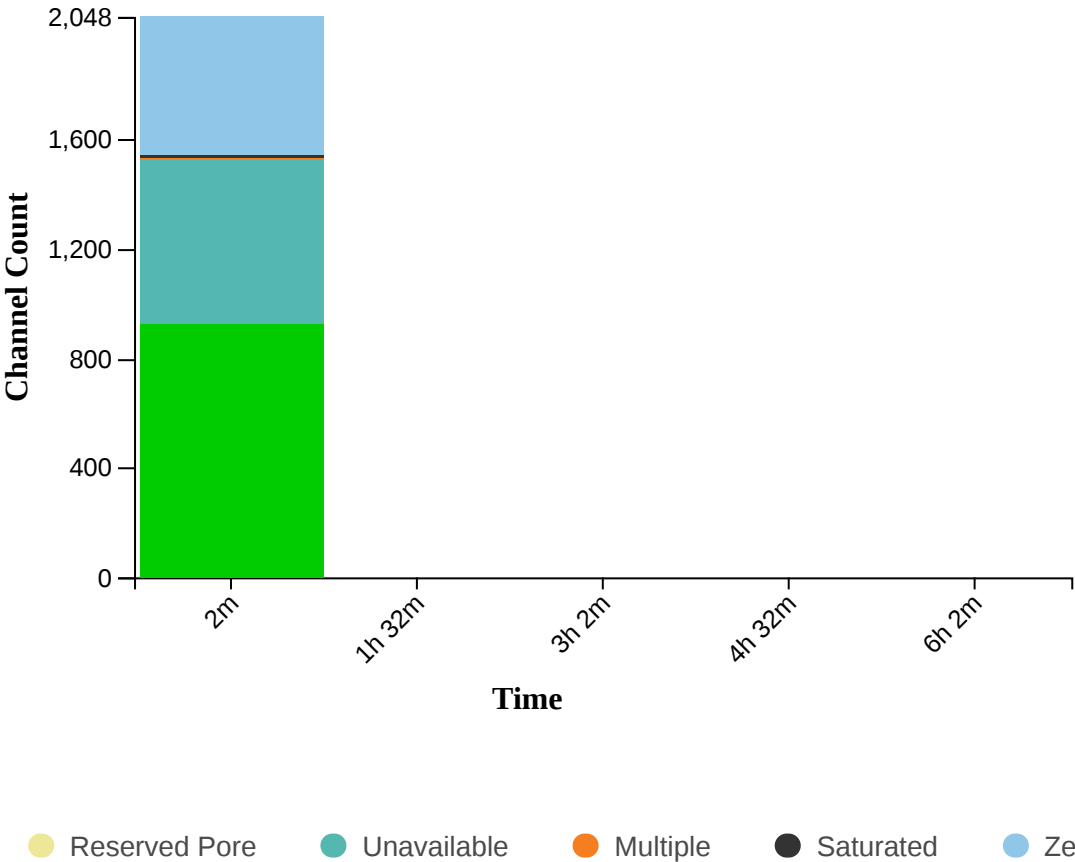


[illegible]

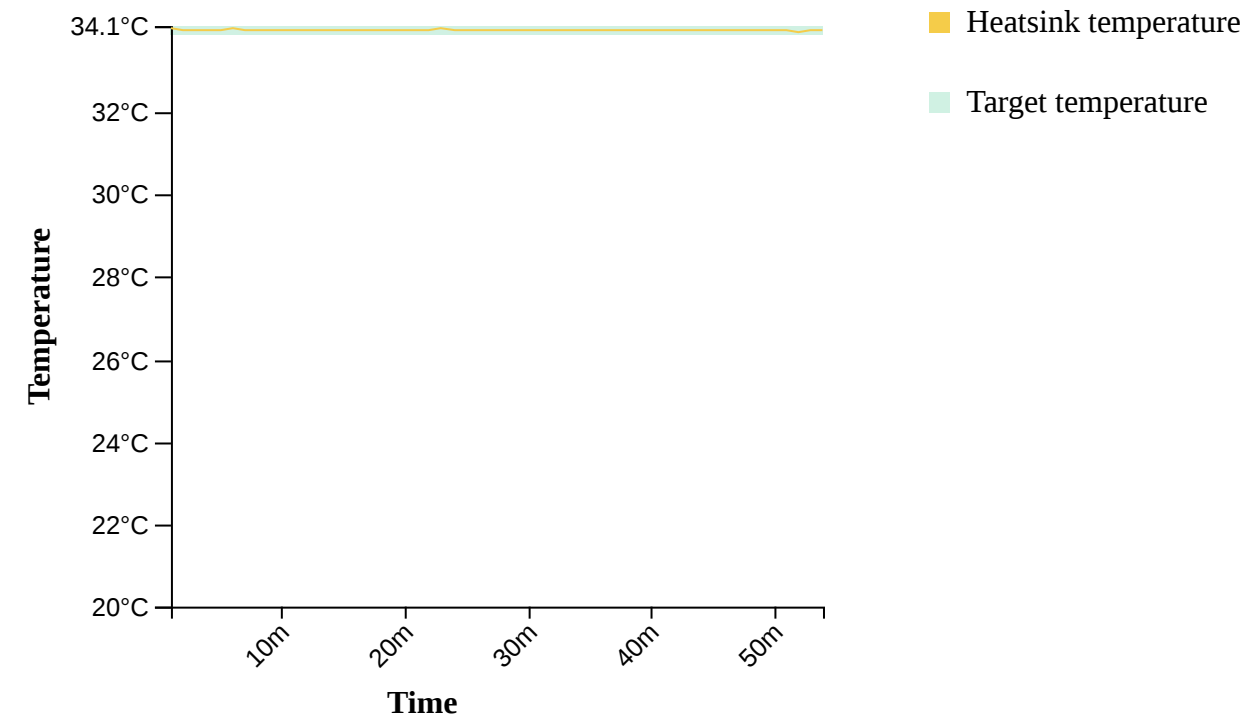
Mux Scan Grouped



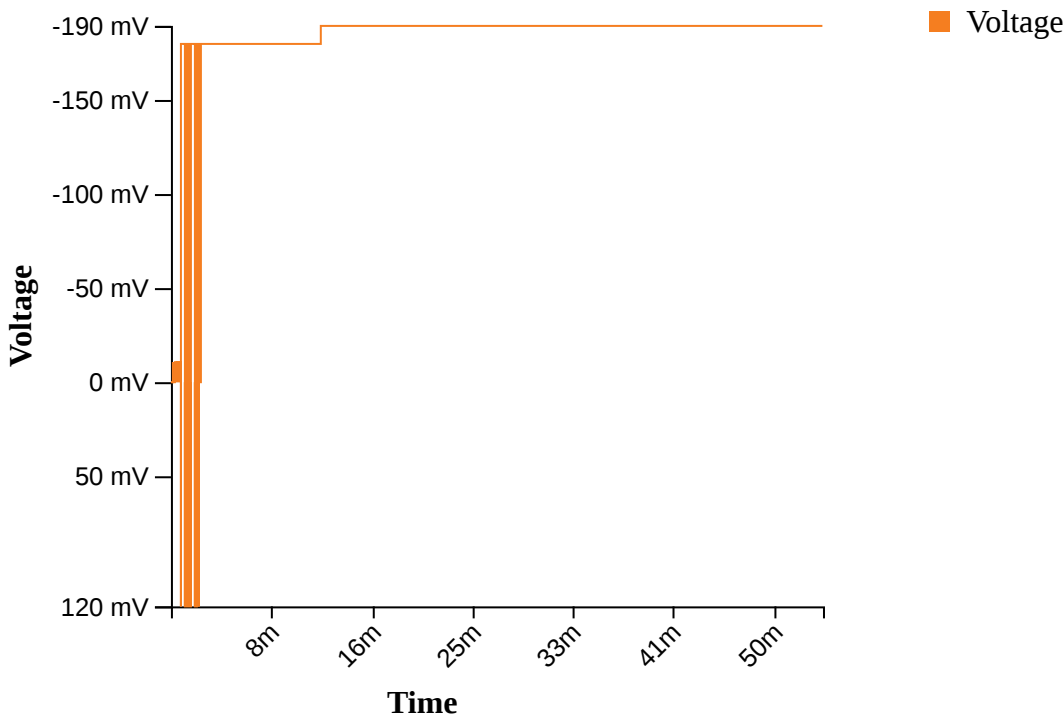
Mux Scan Categorised



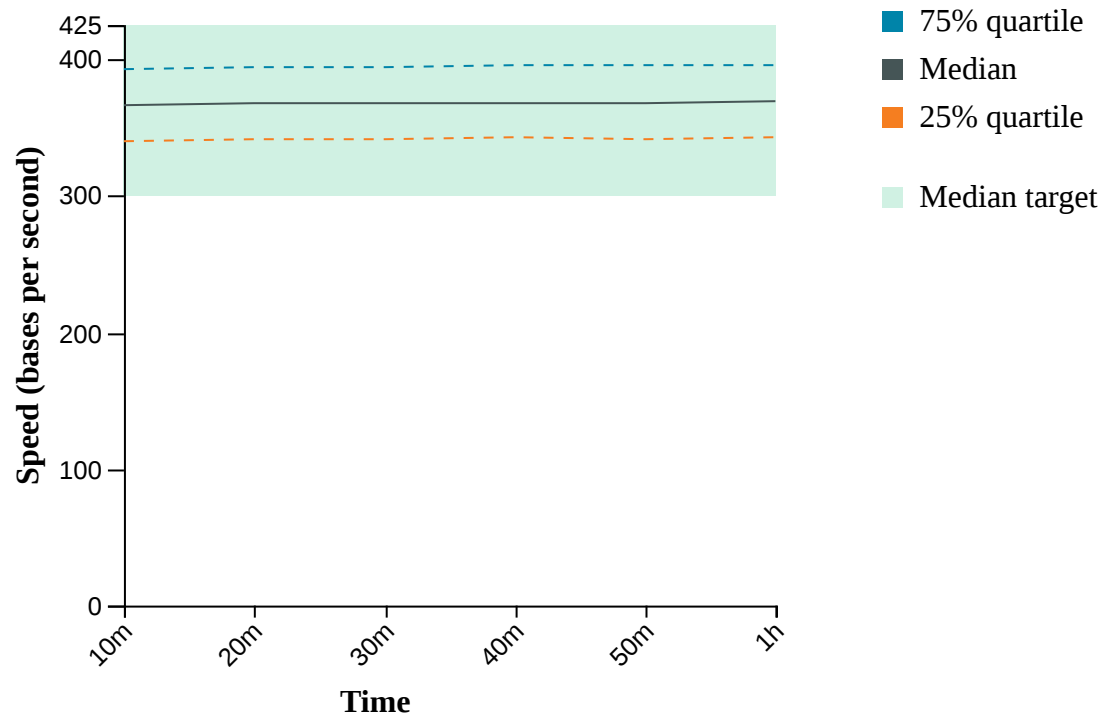
Temperature History.



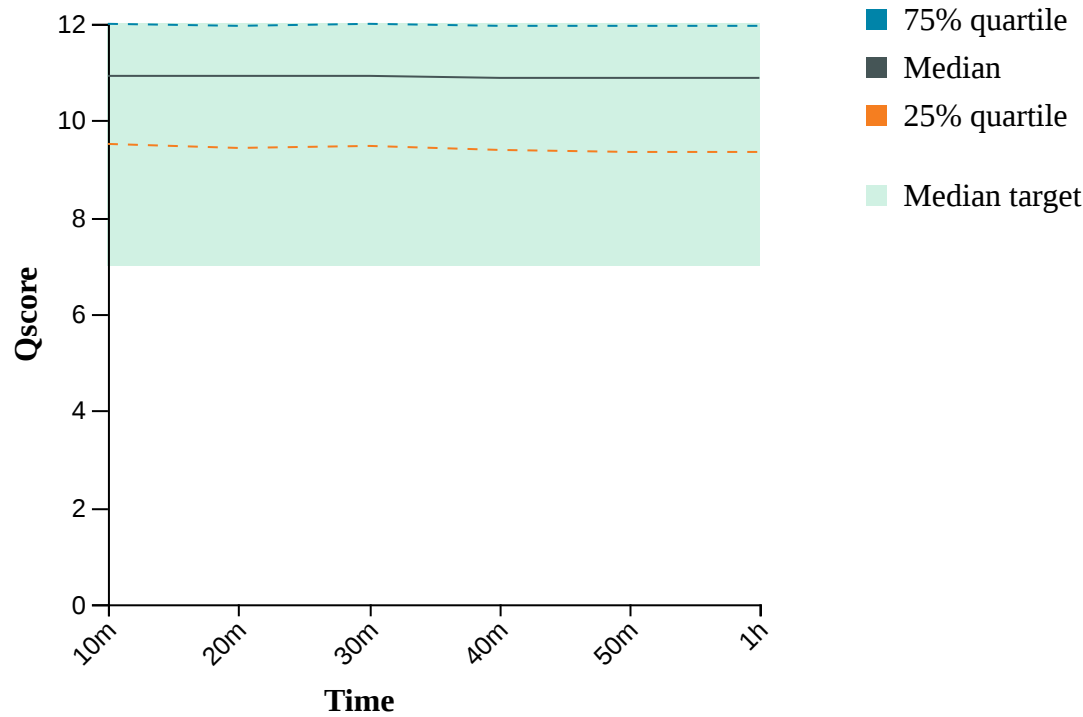
Bias Voltage History.



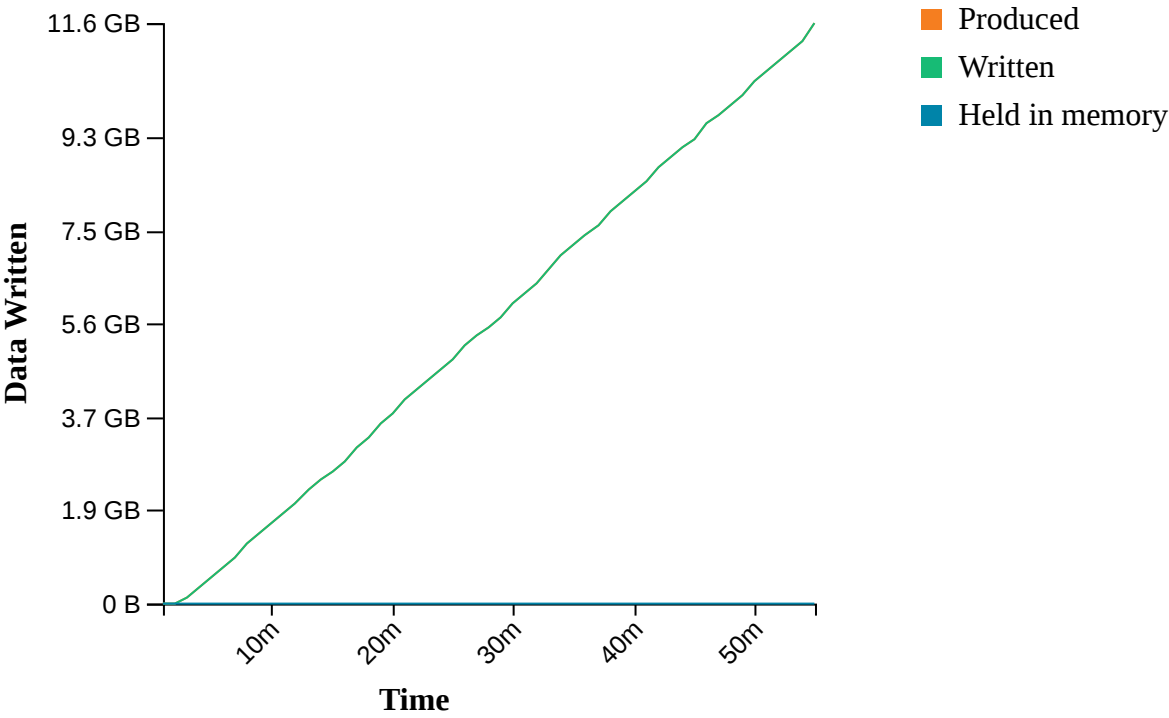
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 927 pores. 453 pores available for immediate sequencing January 5, 16:07
- Performing Mux Scan January 5, 16:05
- Starting sequencing procedure January 5, 16:05
- Failed to reach 34.0°C within 300 seconds(with 0.1 tolerance). The experiment will continue anyway. January 5, 16:05
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C January 5, 16:00