



Run Info

Host Name	GXB01190 (localhost)
Experiment Name	EIMock_2kbp_NoEnrich2RAD_050121
Sample ID	EIMock_2kbp_NoEnrich2RAD_050121
Run ID	80e6515c-8b94-4f2a-b393-8489880919f2
Flow Cell Id	FAO53362
Start Time	January 5, 21:11
Run Length	16h 21m

Run Summary

Reads Generated	2.01 M
Passed Bases	2.84 Gb
Failed Bases	479.86 Mb
Estimated Bases	3.66 Gb

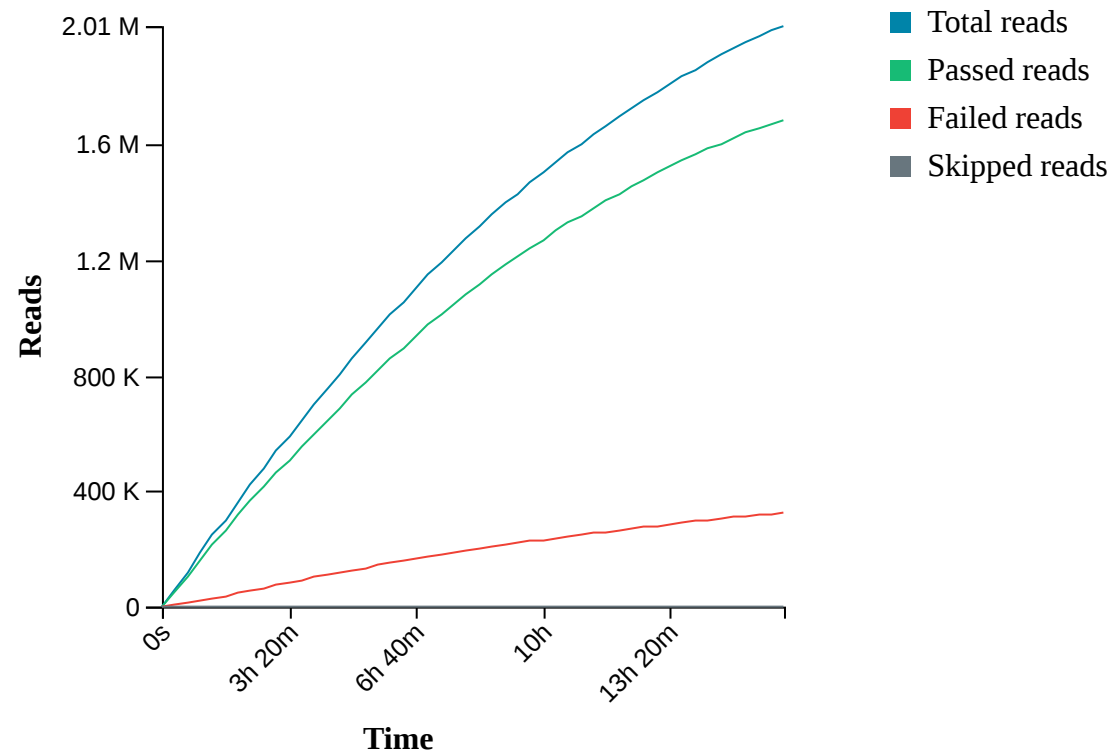
Run Parameters

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
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

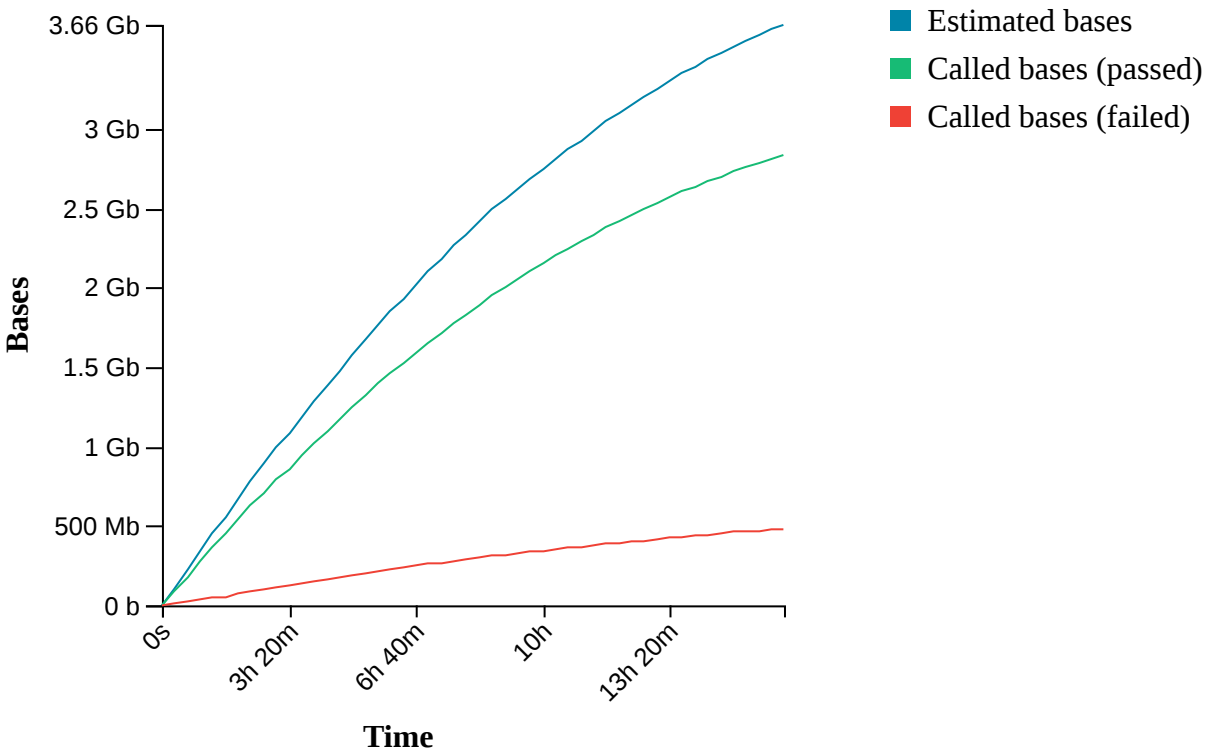
Versions

MinKNOW	20.10.6
MinKNOW Core	4.1.2
Bream	6.1.4
Guppy	4.2.3

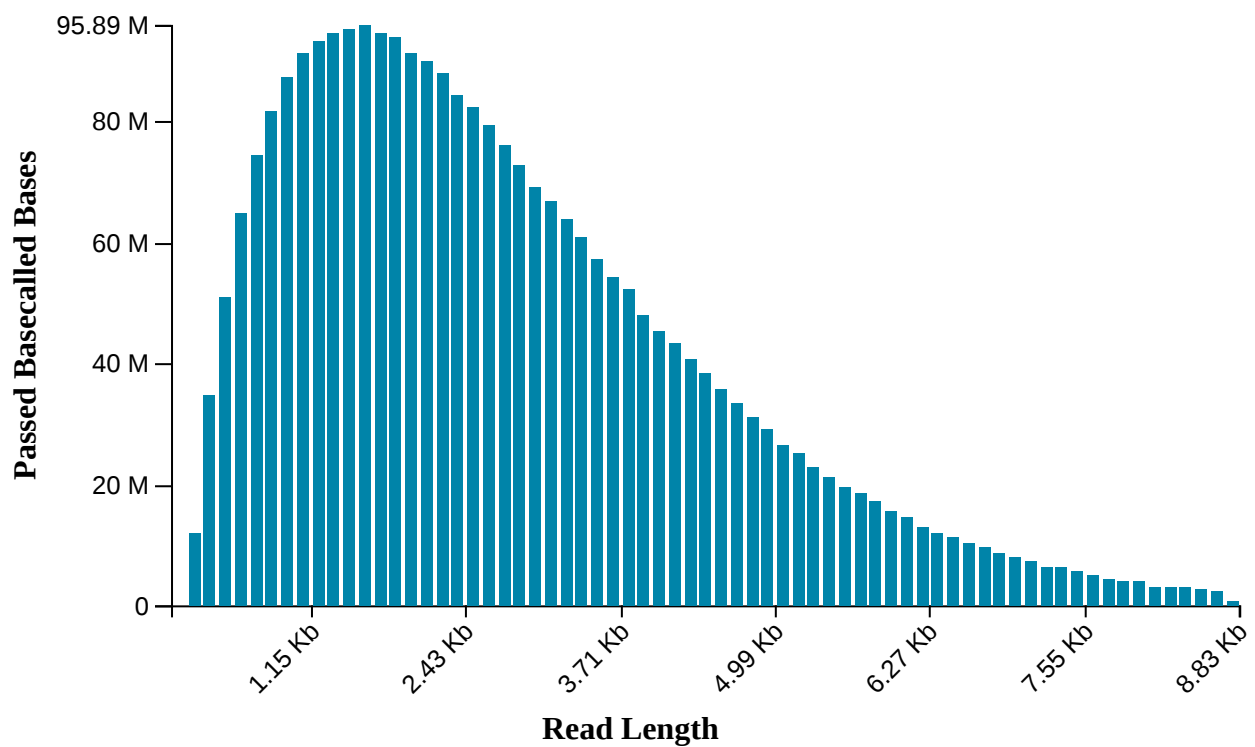
Cumulative Output Reads



Cumulative Output Bases

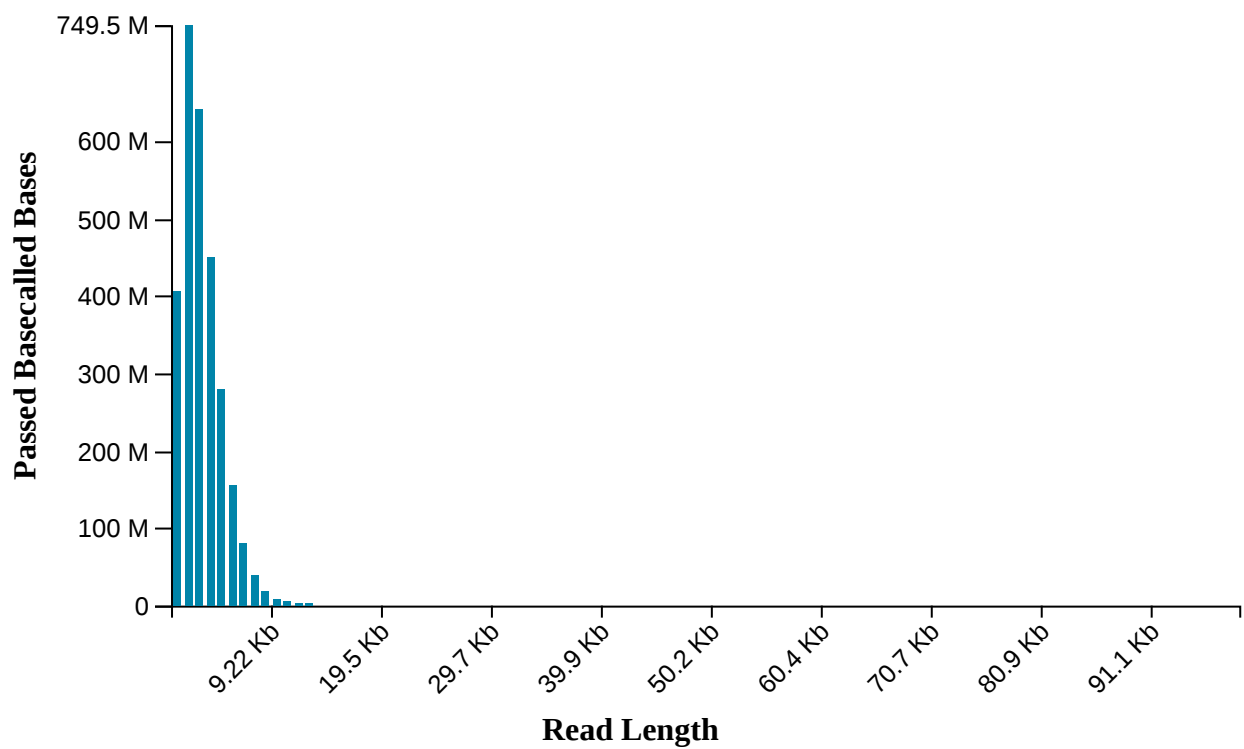


Estimated N50: 2.43 K



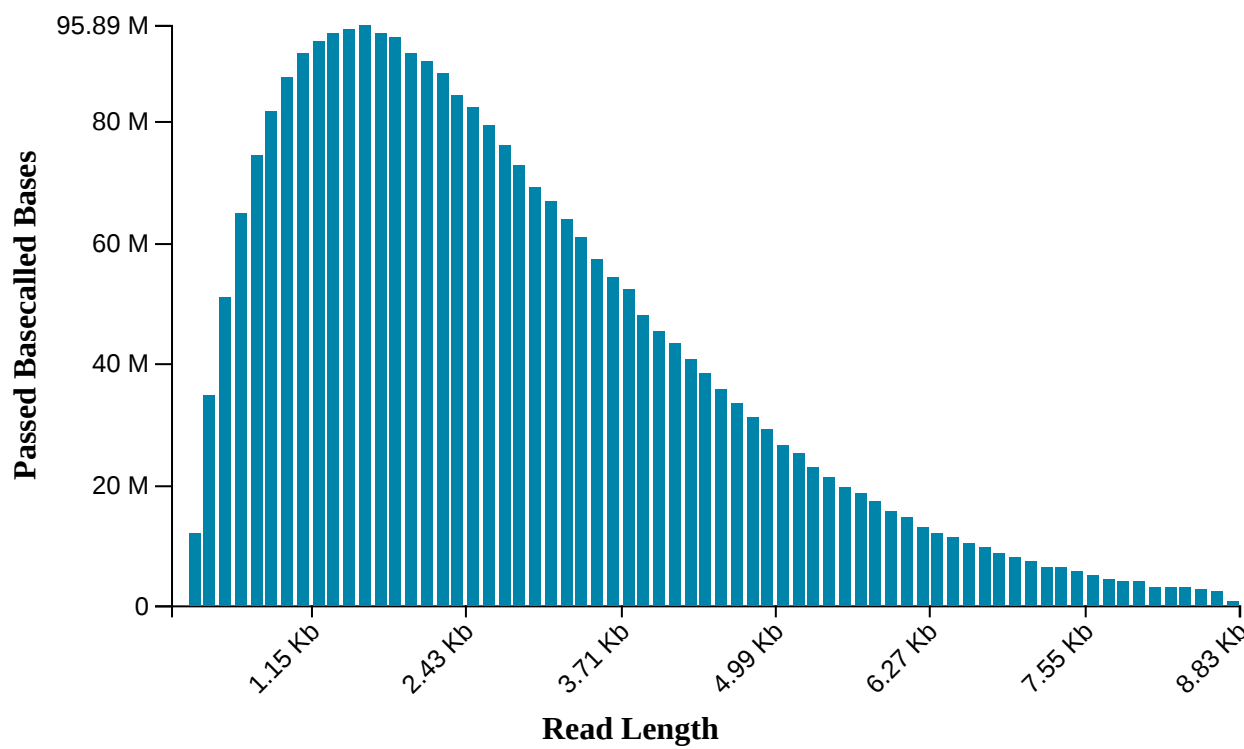
Read Length Histogram Estimated Bases

Estimated N50: 2.43 K

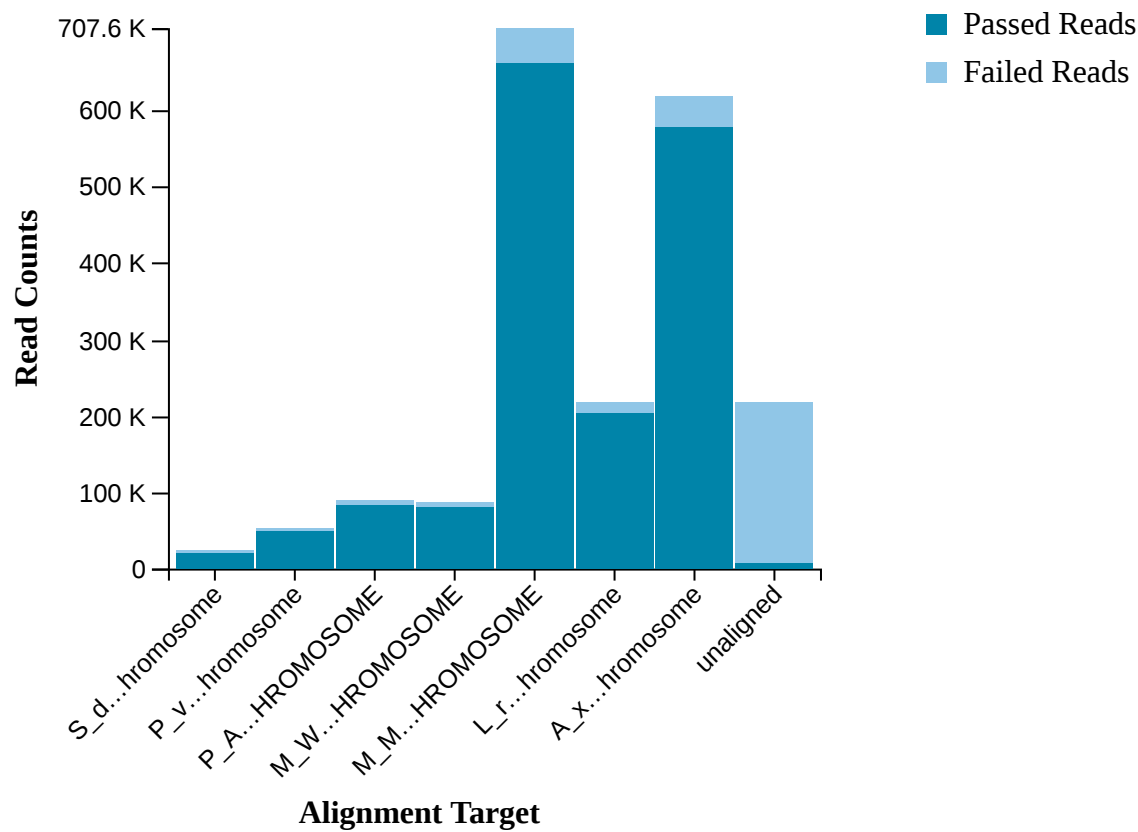


Read Length Histogram Basecalled Bases

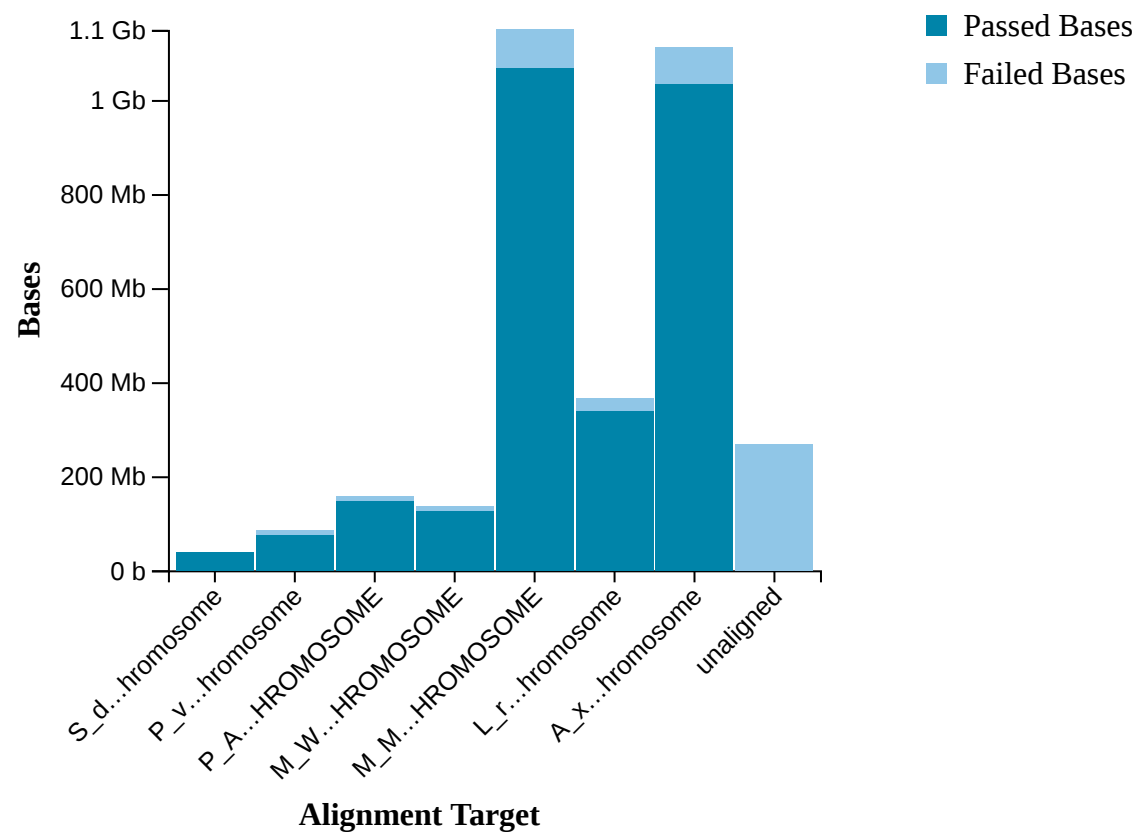
Estimated N50: 2.41 K



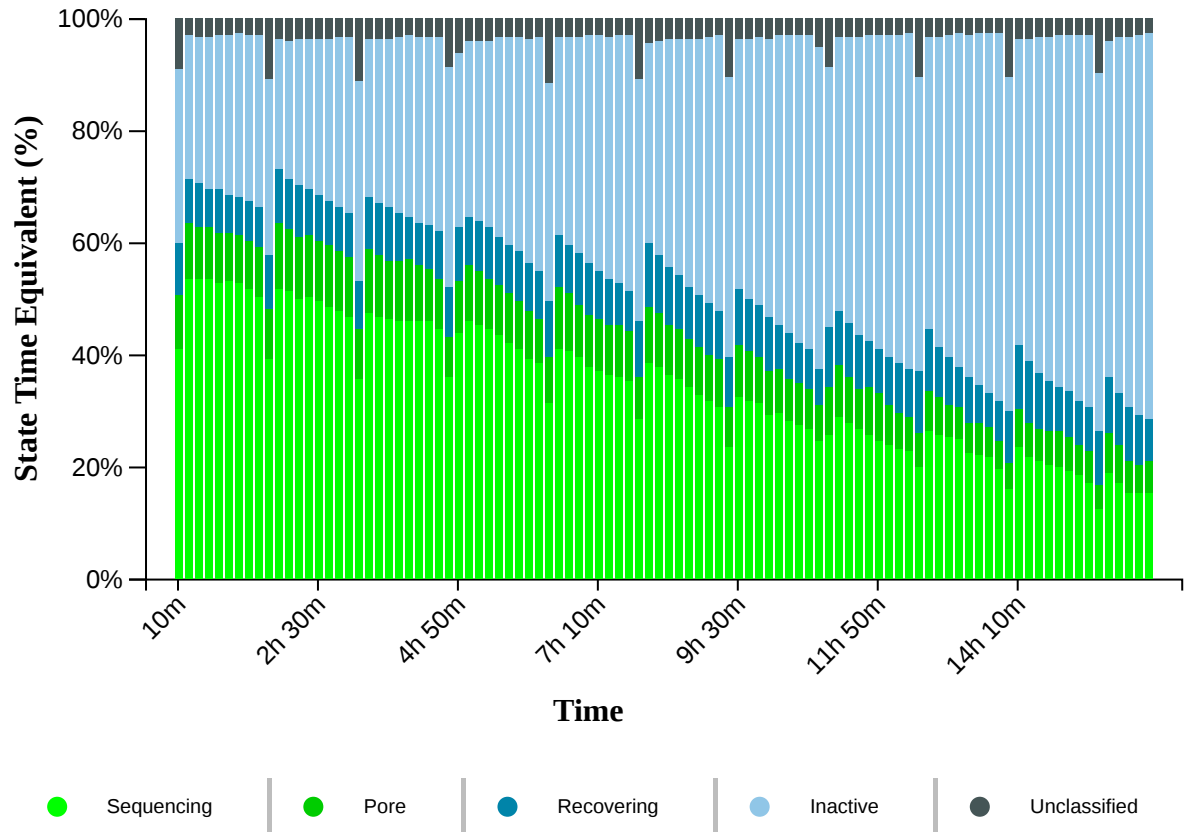
Alignment Target Hits (reads)



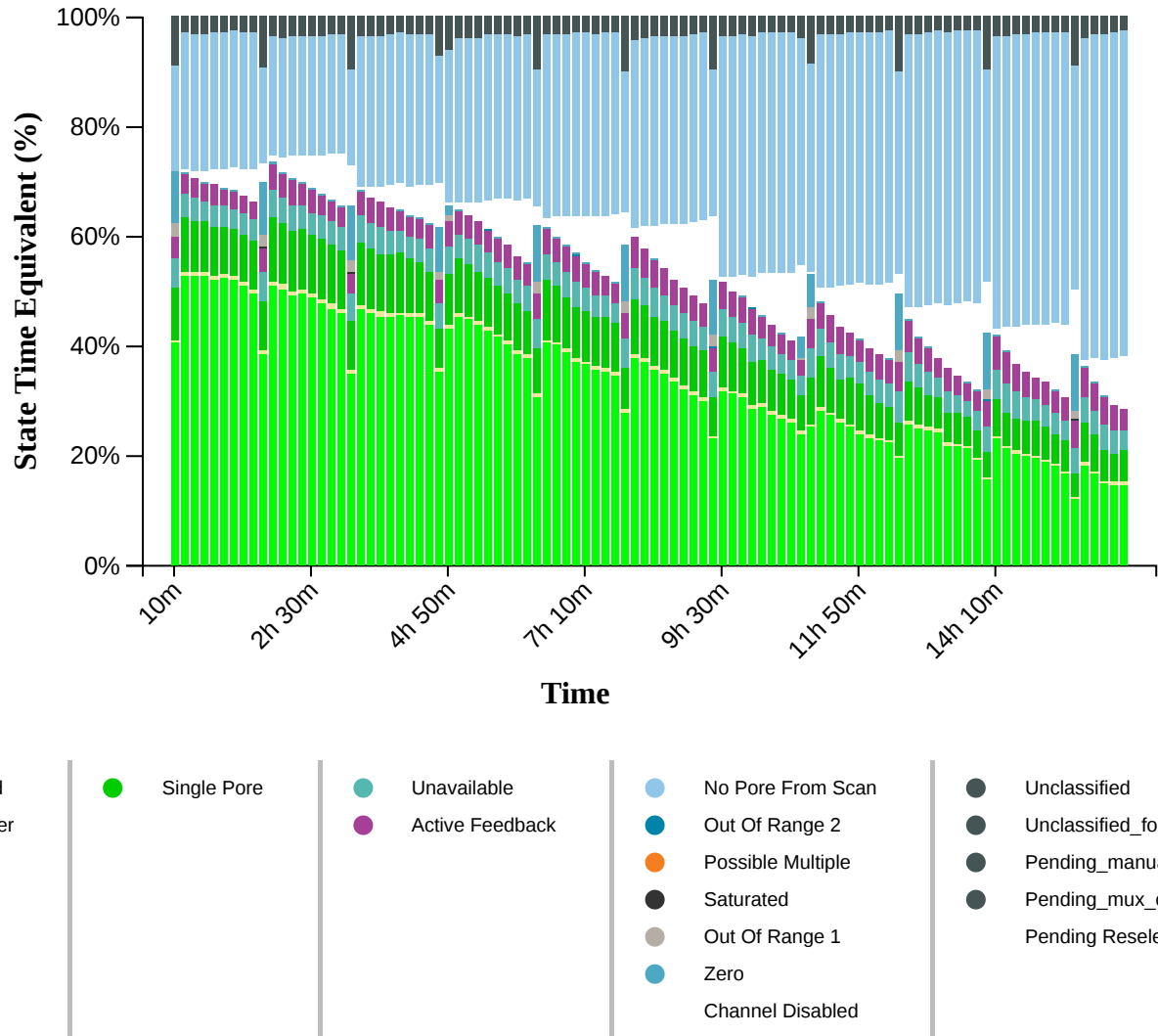
Alignment Target Hits (bases)



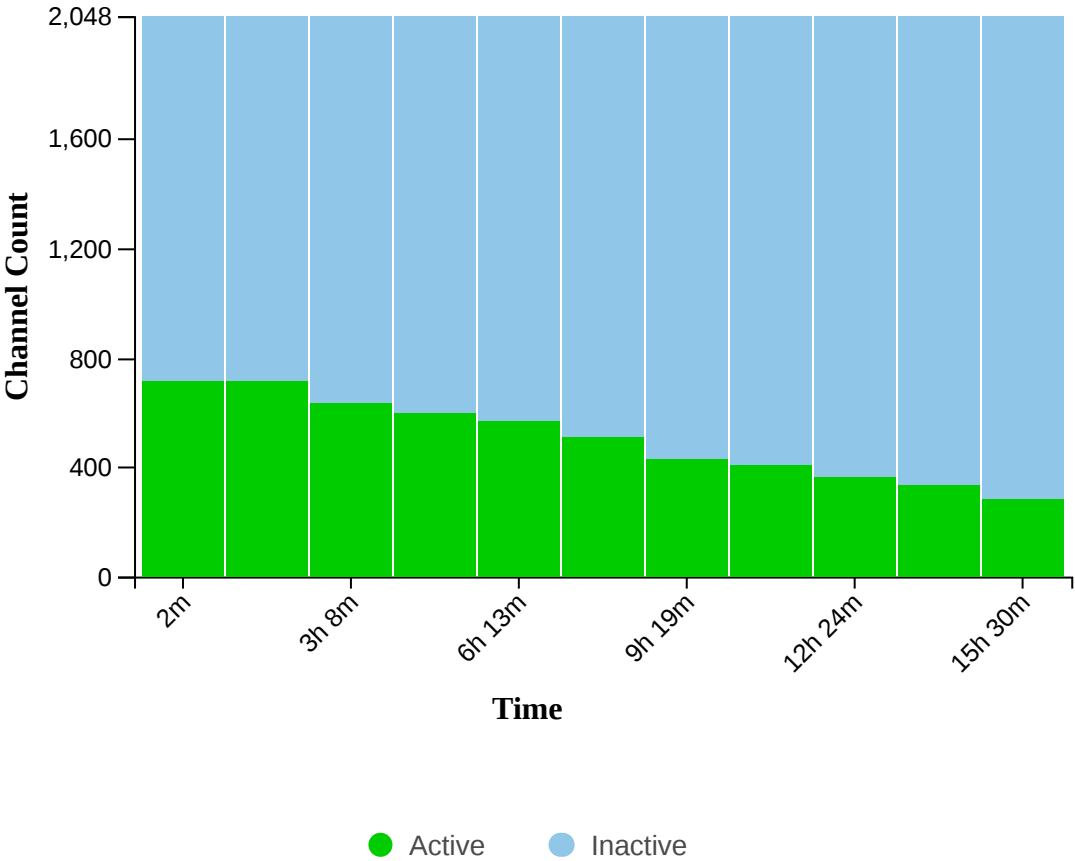
Duty Time Grouped



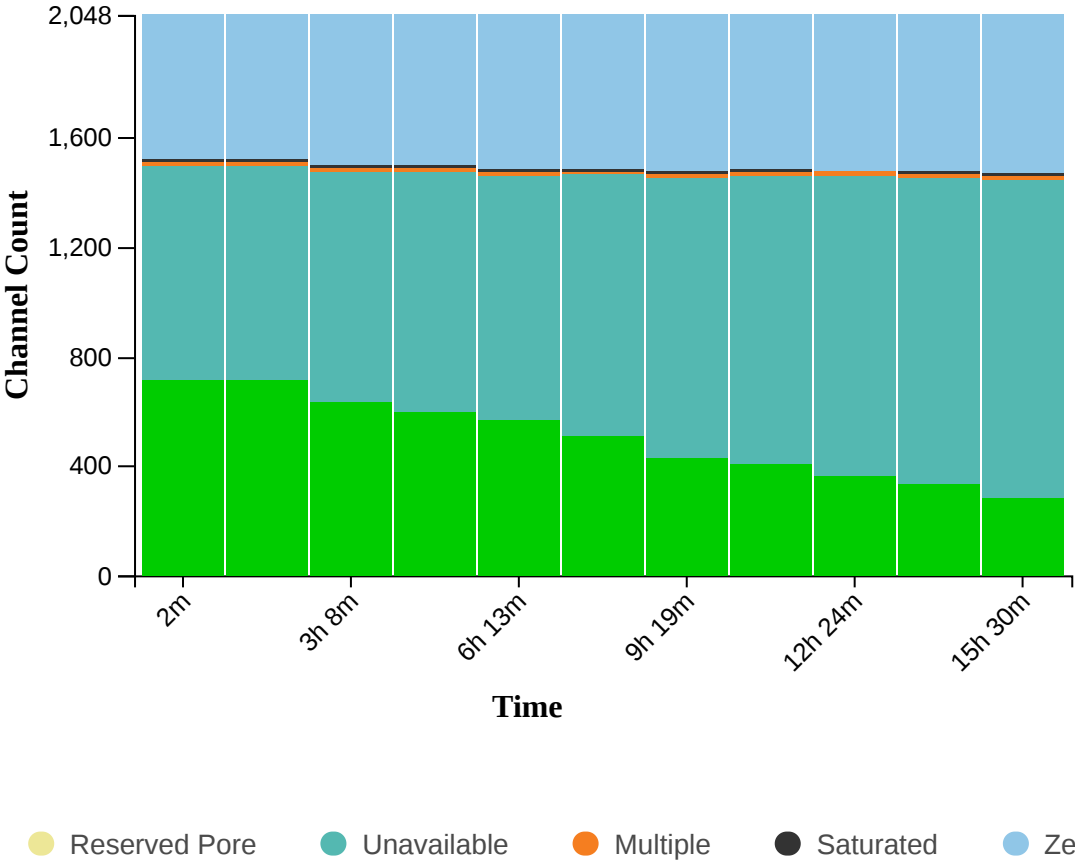
Duty time Categorised



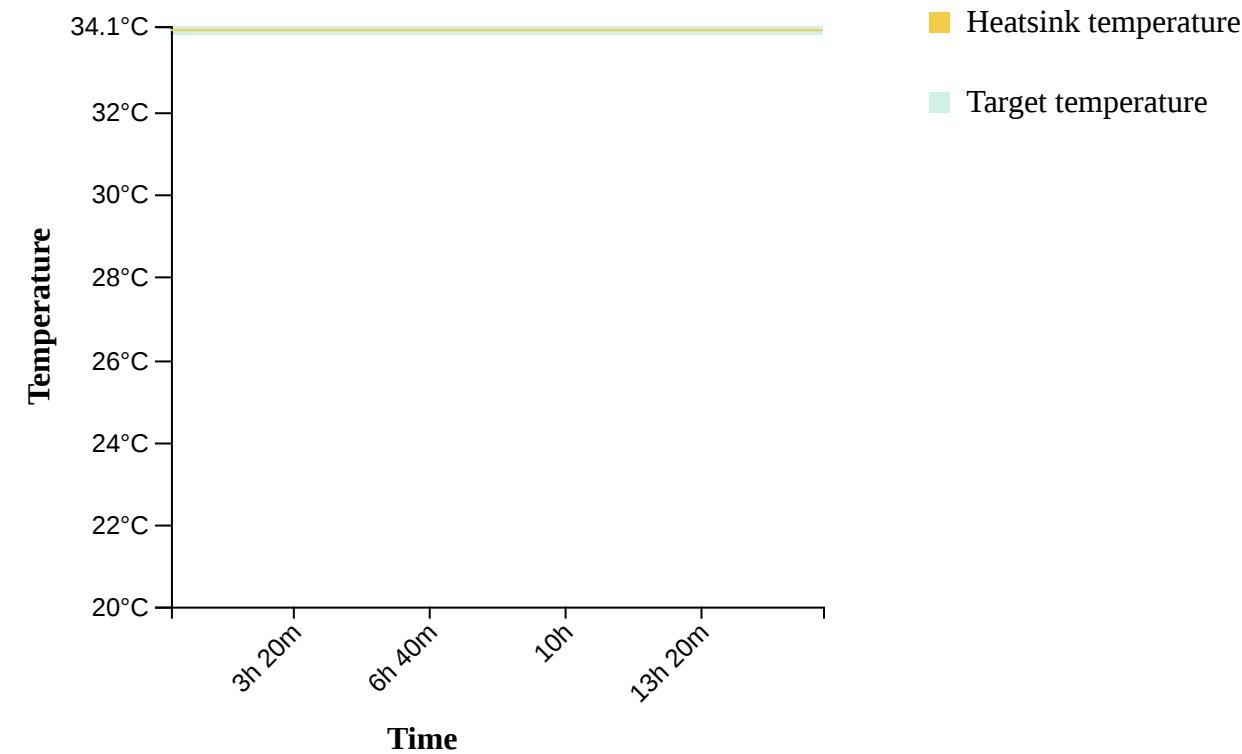
Mux Scan Grouped



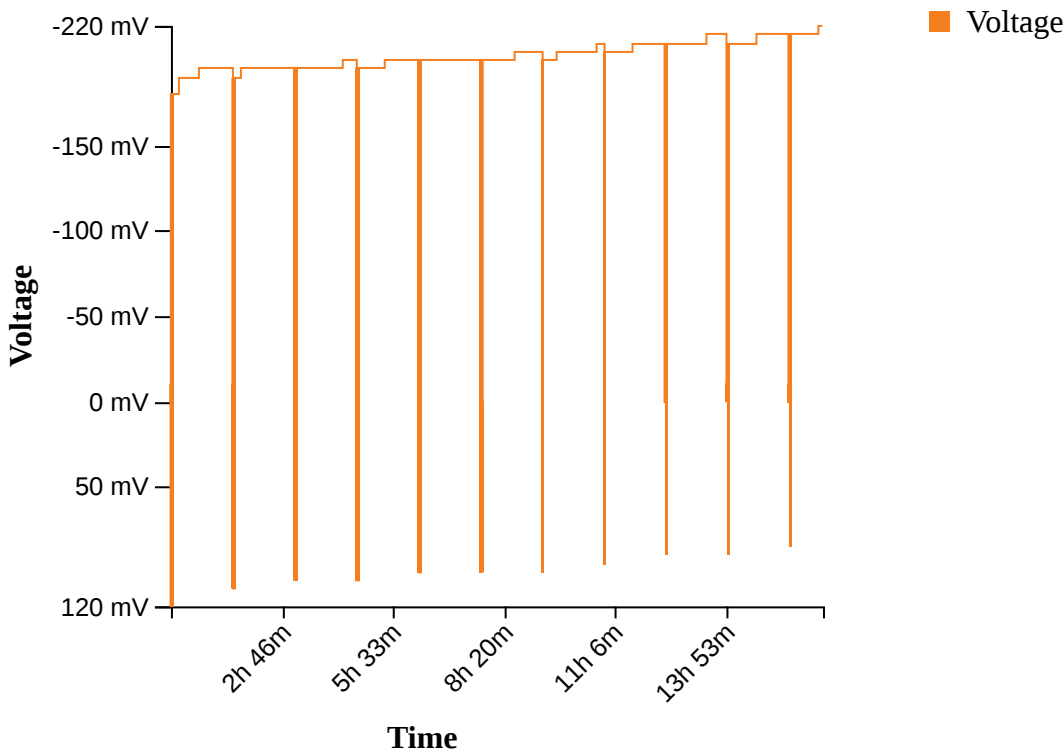
Mux Scan Categorised



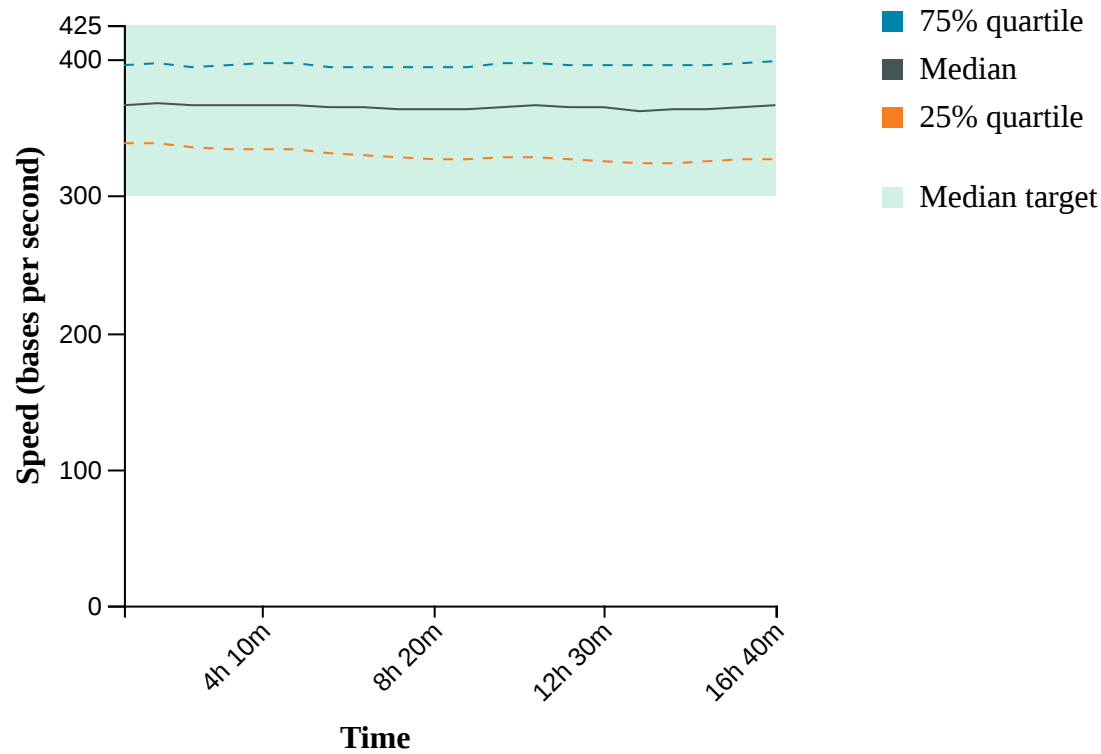
Temperature History.



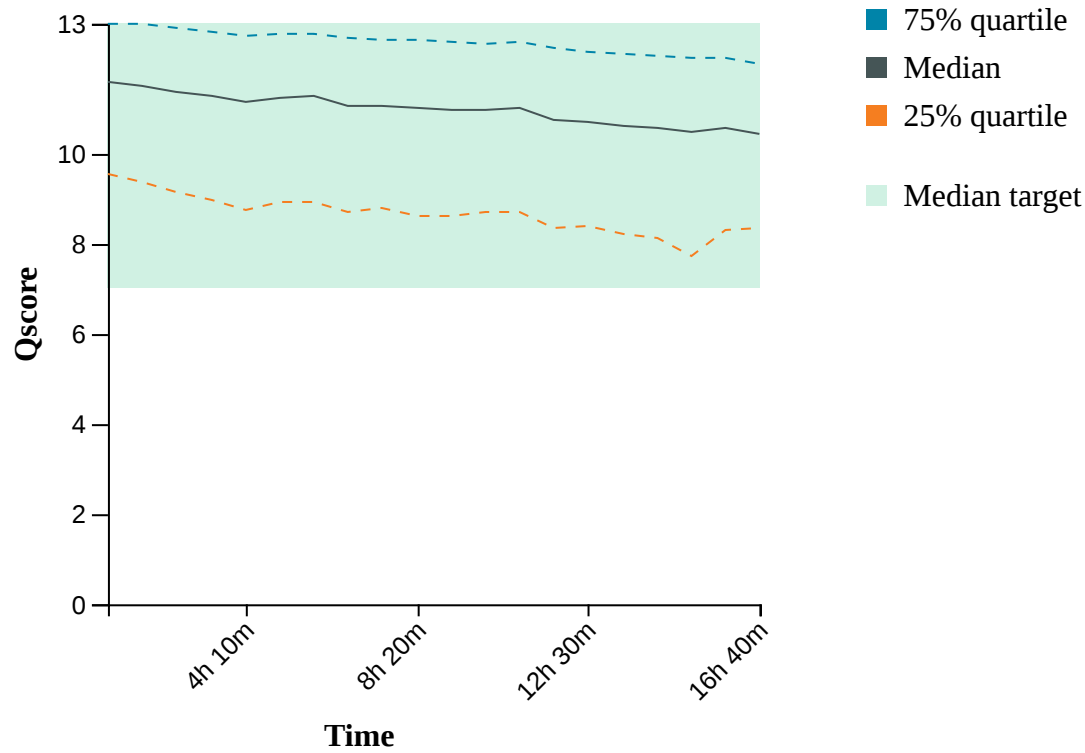
Bias Voltage History.



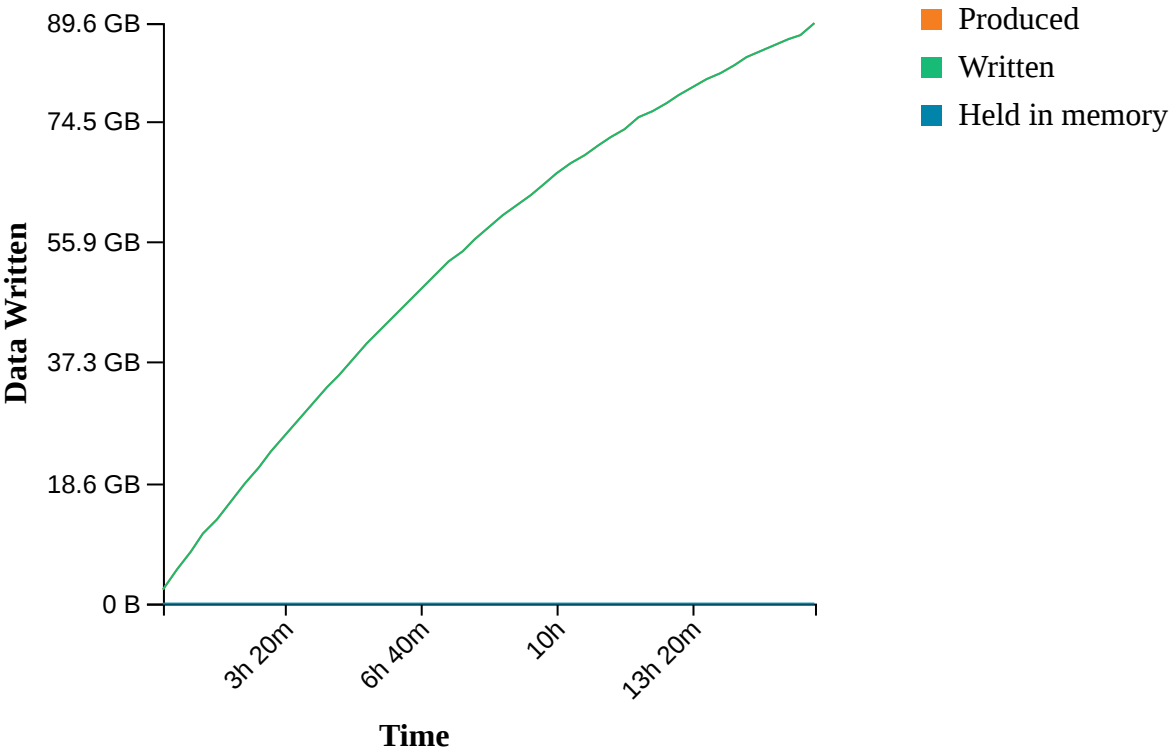
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 282 pores. 209 pores available for immediate sequencing January 6, 12:44
- Performing Mux Scan January 6, 12:42
- Mux scan for flow cell FAO53362 has found a total of 333 pores. 240 pores available for immediate sequencing January 6, 11:11
- Performing Mux Scan January 6, 11:09
- Mux scan for flow cell FAO53362 has found a total of 366 pores. 258 pores available for immediate sequencing January 6, 09:38
- Performing Mux Scan January 6, 09:36
- Mux scan for flow cell FAO53362 has found a total of 407 pores. 277 pores available for immediate sequencing January 6, 08:06
- Performing Mux Scan January 6, 08:03
- Mux scan for flow cell FAO53362 has found a total of 435 pores. 287 pores available for immediate sequencing January 6, 06:33
- Performing Mux Scan January 6, 06:31
- Mux scan for flow cell FAO53362 has found a total of 512 pores. 336 pores available for immediate sequencing January 6, 05:00
- Performing Mux Scan January 6, 04:58
- Mux scan for flow cell FAO53362 has found a total of 567 pores. 341 pores available for immediate sequencing January 6, 03:28
- Performing Mux Scan January 6, 03:25
- Mux scan for flow cell FAO53362 has found a total of 603 pores. 358 pores available for immediate sequencing January 6, 01:55
- Performing Mux Scan January 6, 01:52
- Mux scan for flow cell FAO53362 has found a total of 638 pores. 371 pores available for immediate sequencing January 6, 00:22
- Performing Mux Scan January 6, 00:20
- Mux scan for flow cell FAO53362 has found a total of 717 pores. 400 pores available for immediate sequencing January 5, 22:49
- Performing Mux Scan January 5, 22:47
- Mux scan for flow cell FAO53362 has found a total of 714 pores. 384 pores available for immediate sequencing January 5, 21:16
- Performing Mux Scan January 5, 21:14
- Starting sequencing procedure January 5, 21:14
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C January 5, 21:11