



## Run Info

Host Name	GXB03020 (localhost)
Experiment Name	ReadUntil_38Kbp_HightoLow_SdEnr_15042021
Sample ID	ReadUntil_38Kbp_HightoLow_SdEnr_15042021
Run ID	aaa9ece6-a2d7-4220-b95f-8121e74a693e
Flow Cell Id	FAP21636
Start Time	April 15, 18:37
Run Length	3d 0h 4m

## Run Summary

Reads Generated	1.97 M
Passed Bases	5.96 Gb
Failed Bases	544.51 Mb
Estimated Bases	6.69 Gb

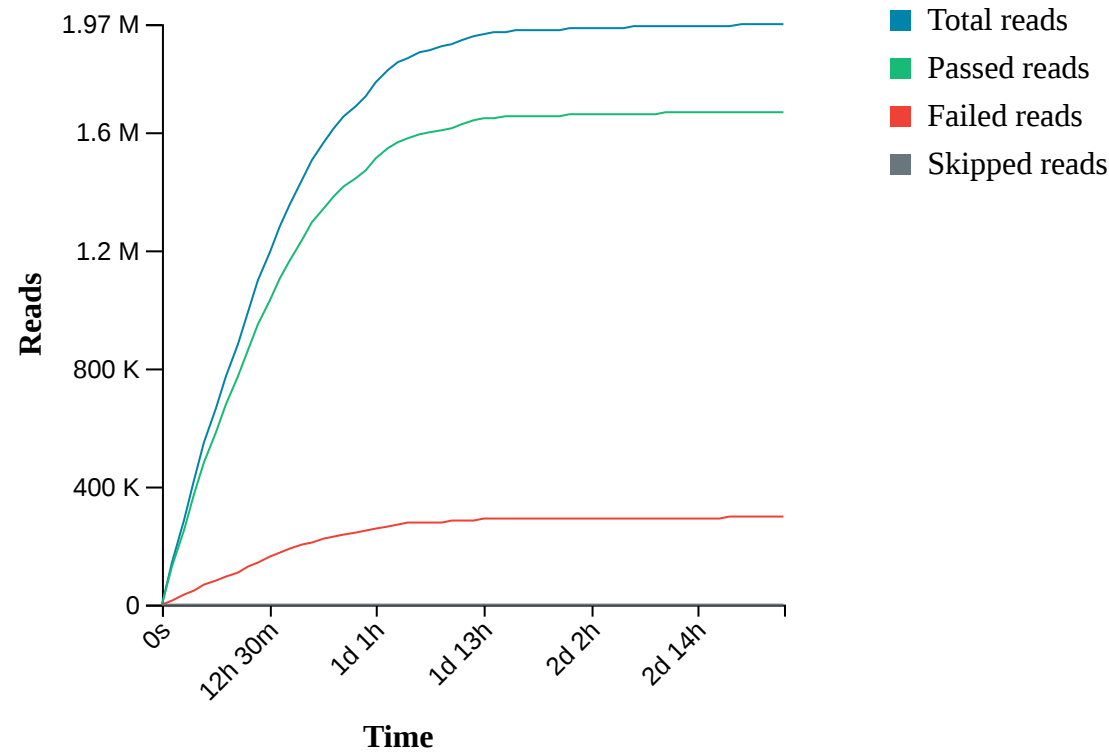
## Run Parameters

Flow Cell Type	FLO-MIN106
Kit	SQK-LSK109
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/S_dysgalactiae_ref.fasta"],filter_type=enrich,first_channel=1 ,last_channel=256
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/the7references.fasta"]
Read Filtering	min_qscore=7

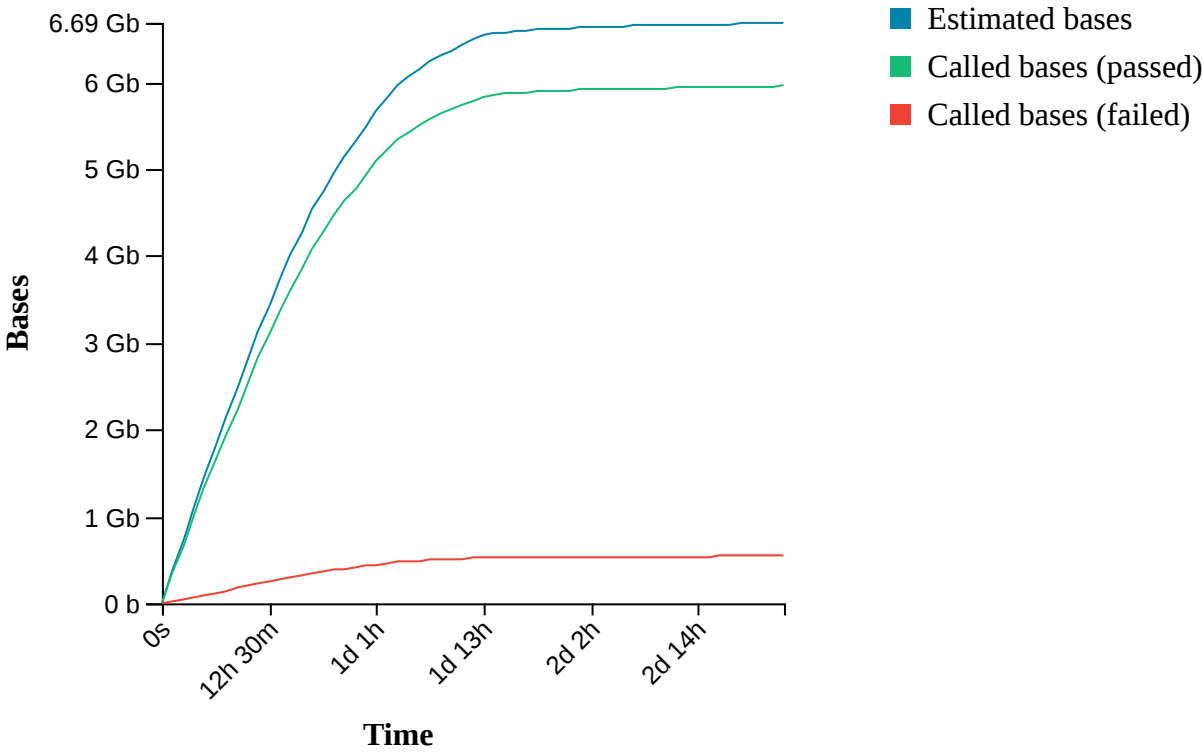
## Versions

MinKNOW	21.02.5
MinKNOW Core	4.2.5
Bream	6.1.10
Guppy	4.3.4

Cumulative Output Reads

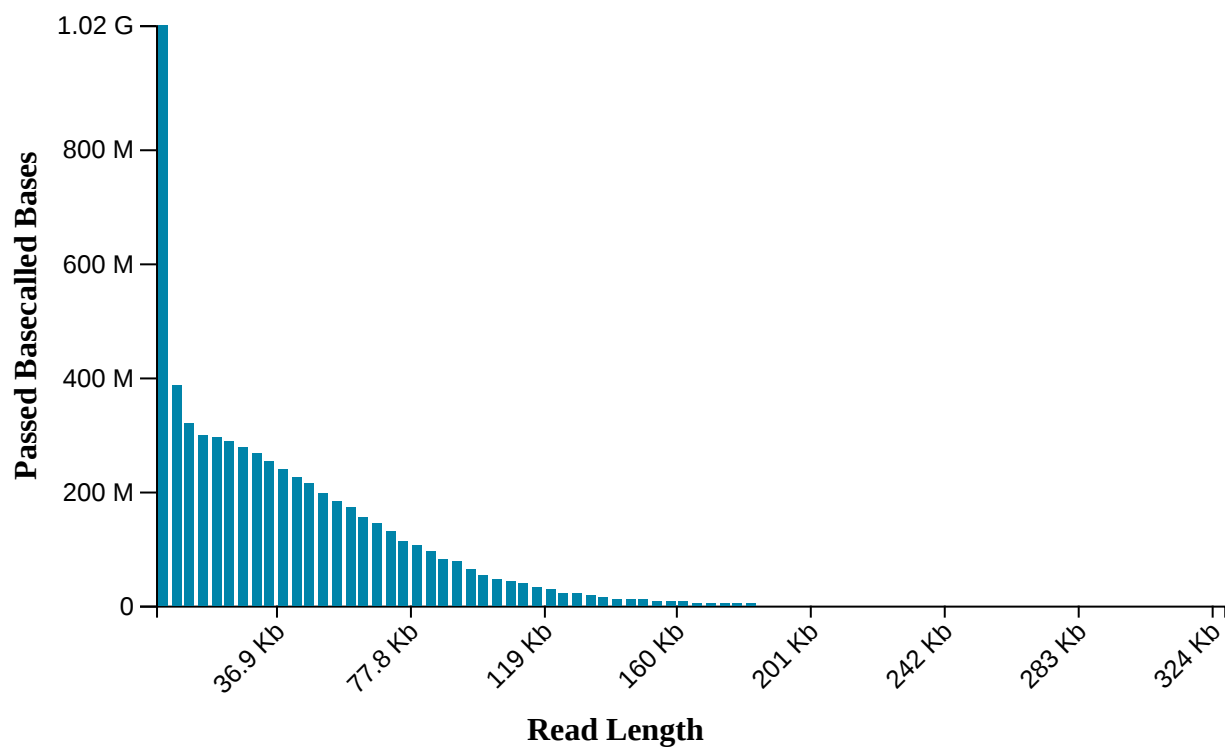


Cumulative Output Bases



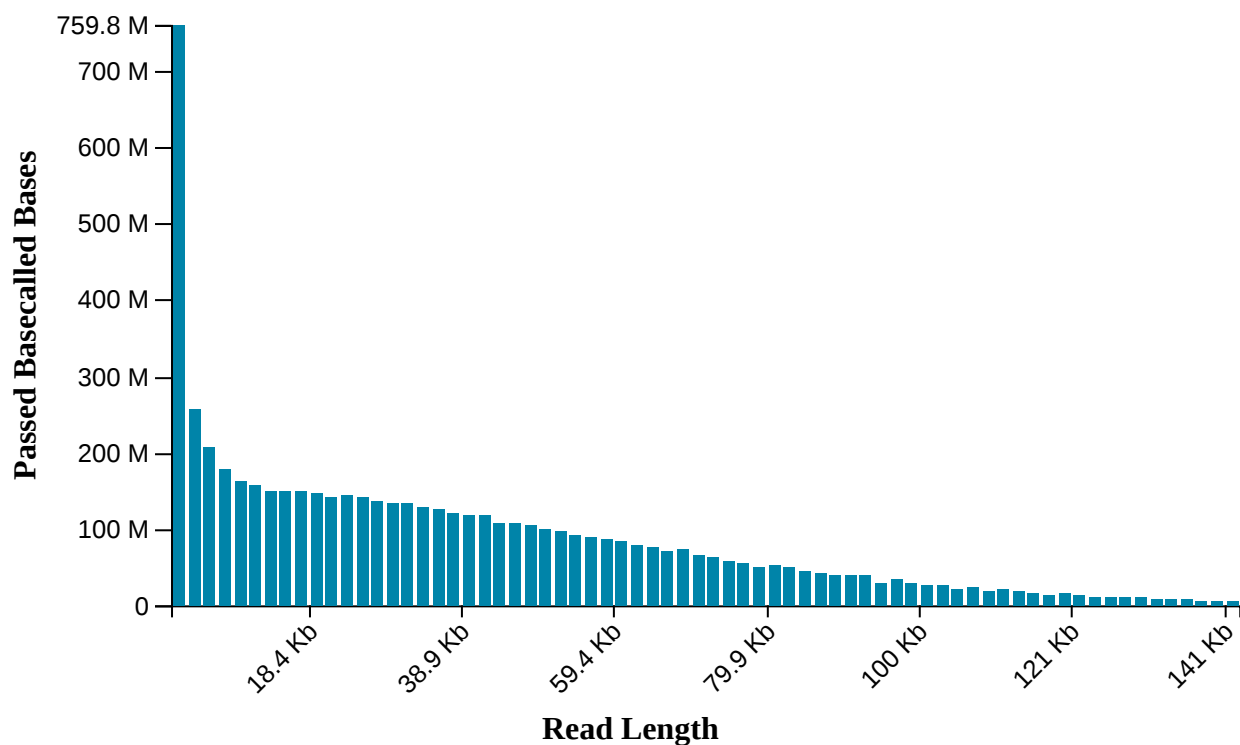
### Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 30.26 K



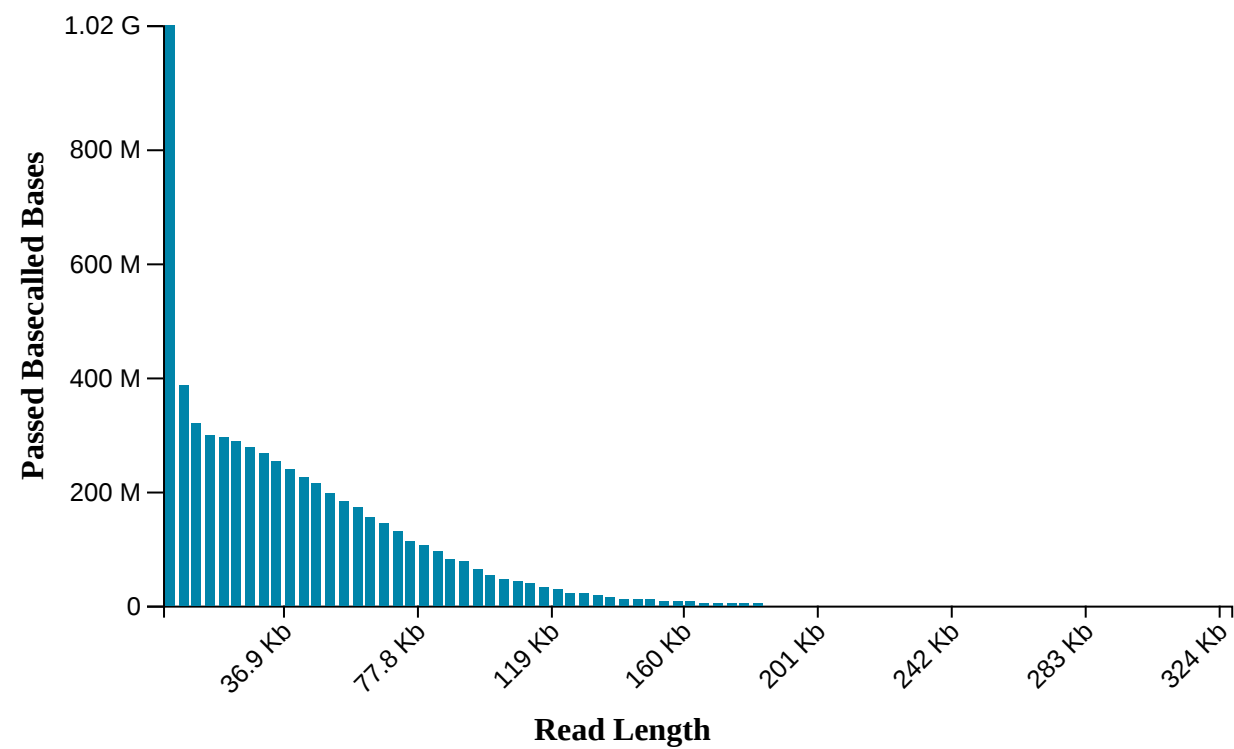
### Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 29.8 K



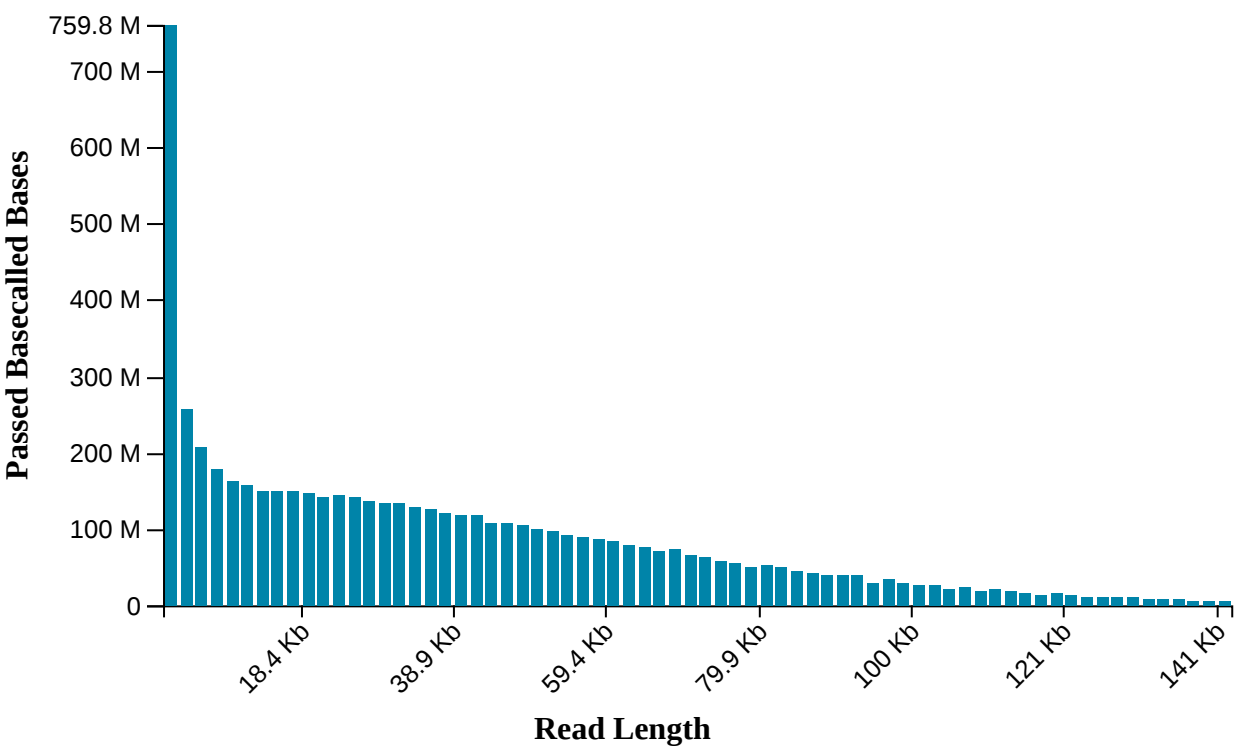
**Read Length Histogram Estimated Bases**

Estimated N50: 30.26 K

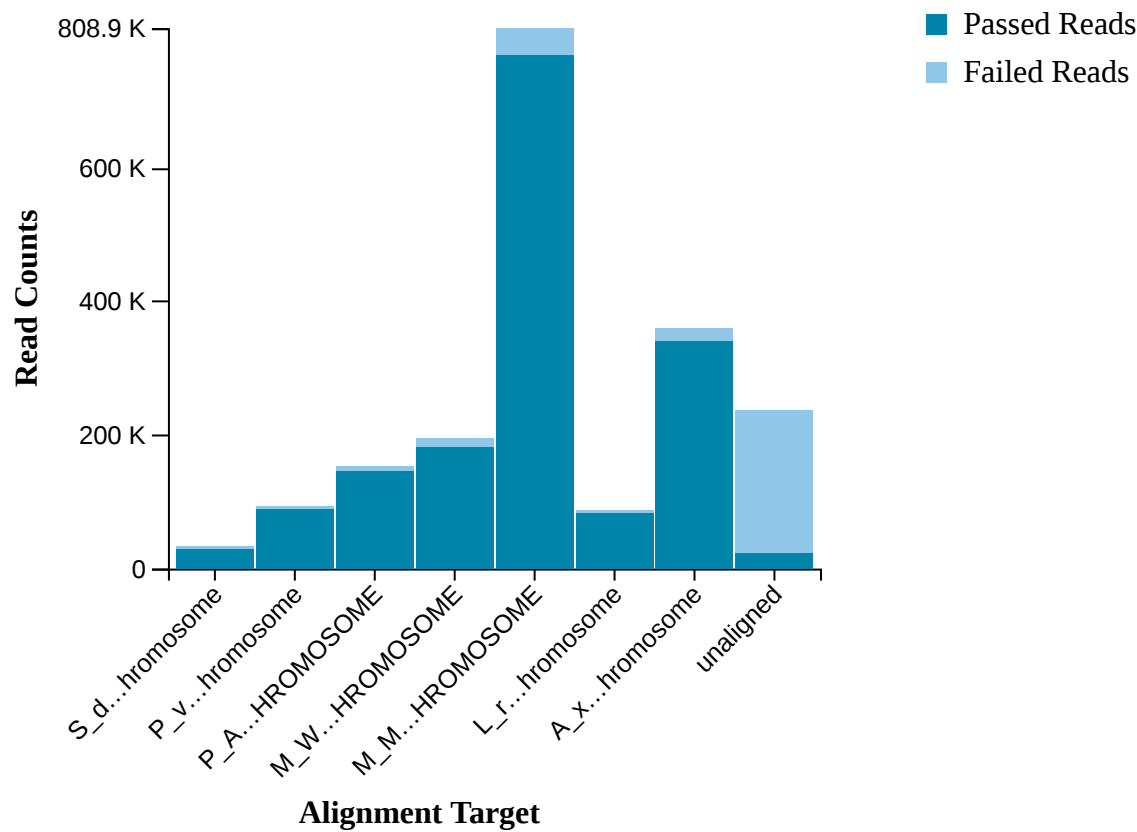


**Read Length Histogram Basecalled Bases**

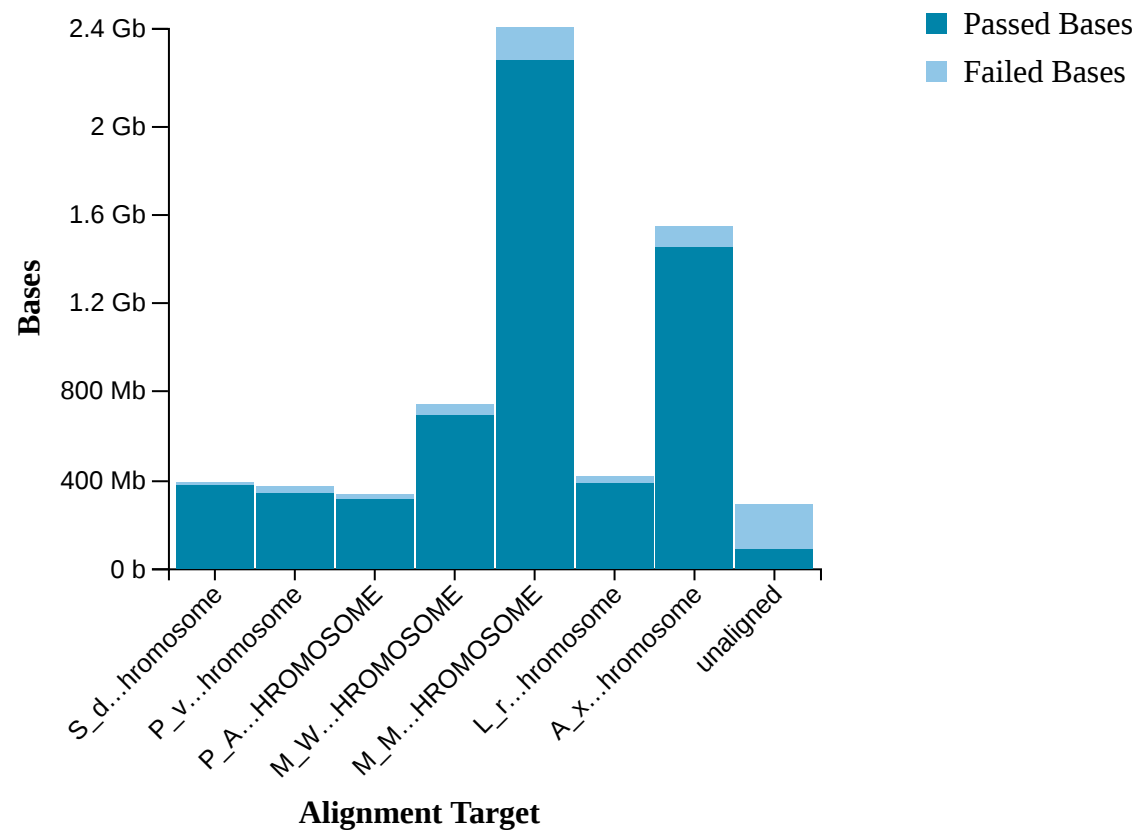
Estimated N50: 29.8 K



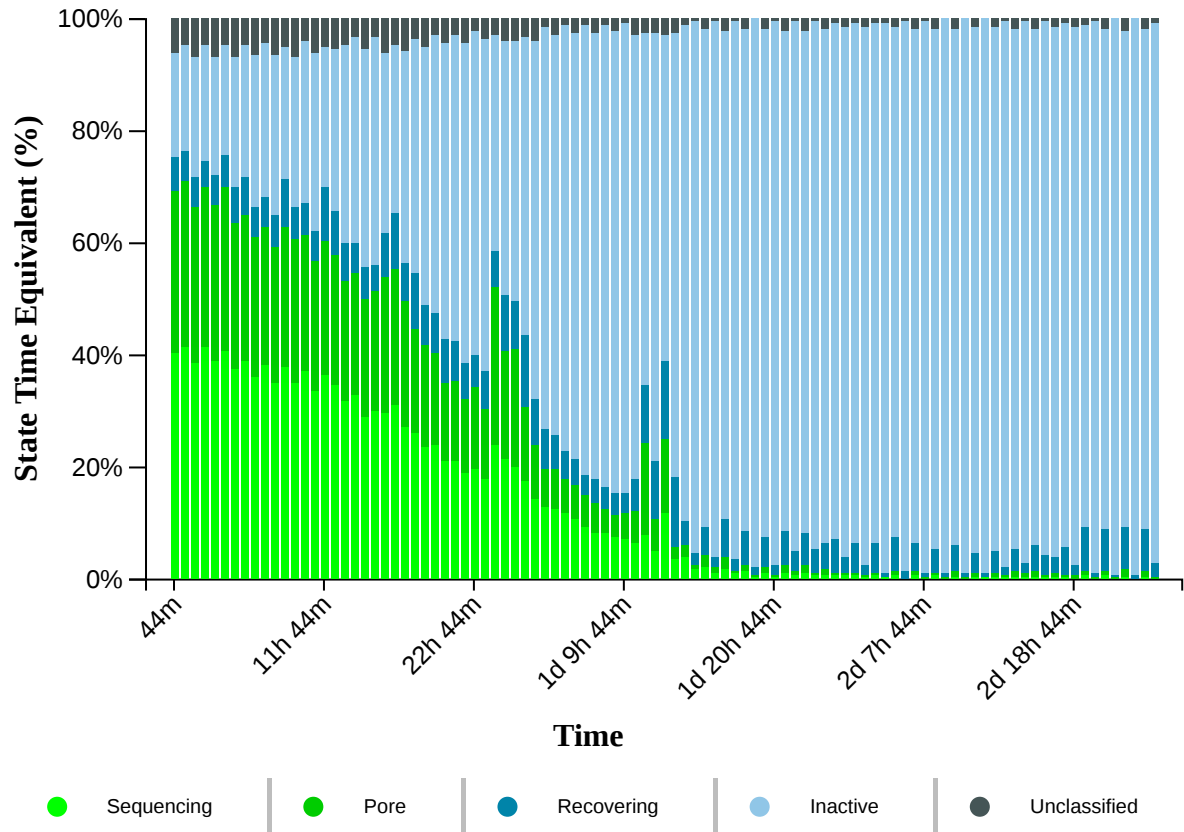
Alignment Target Hits (reads)



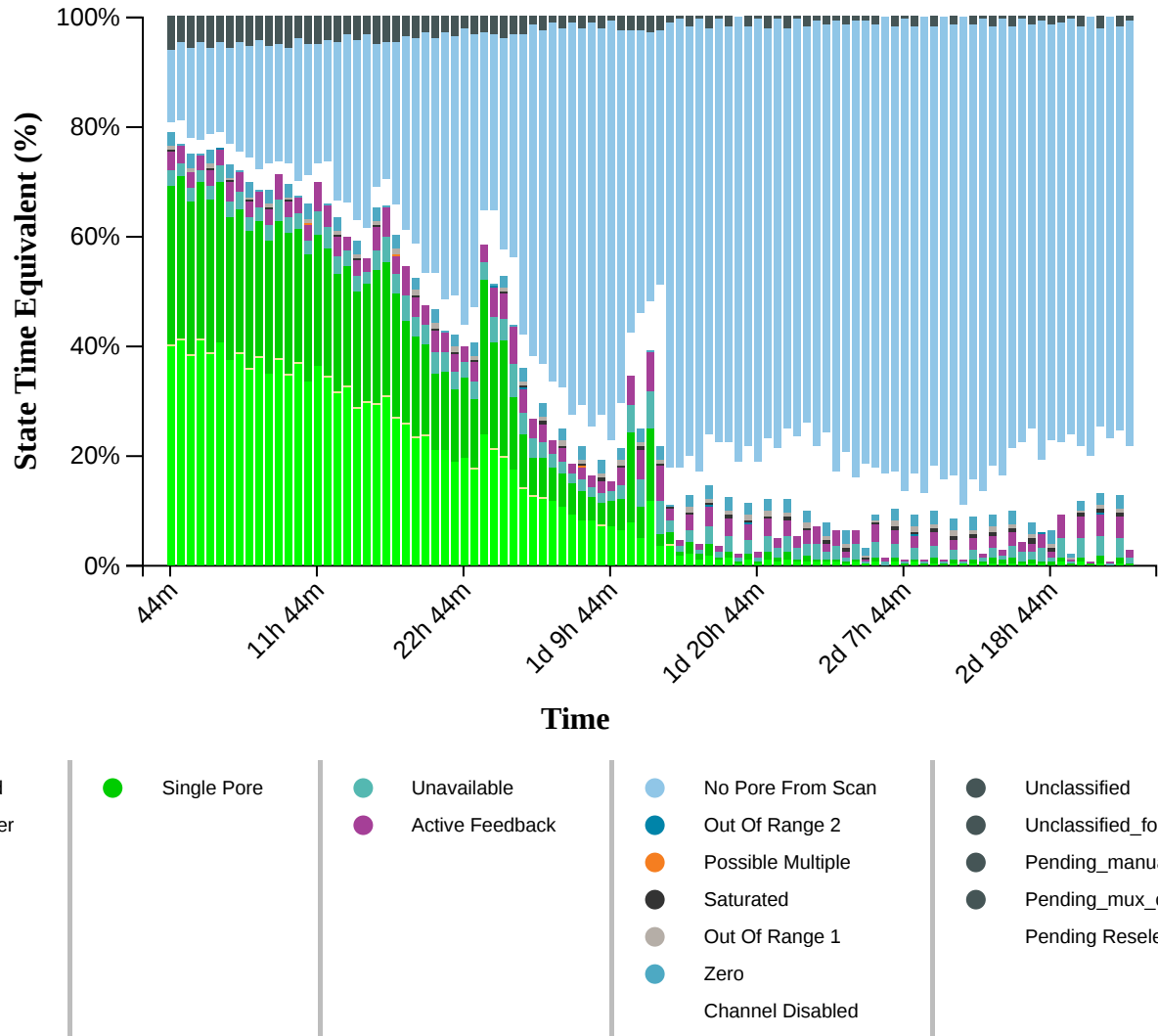
Alignment Target Hits (bases)



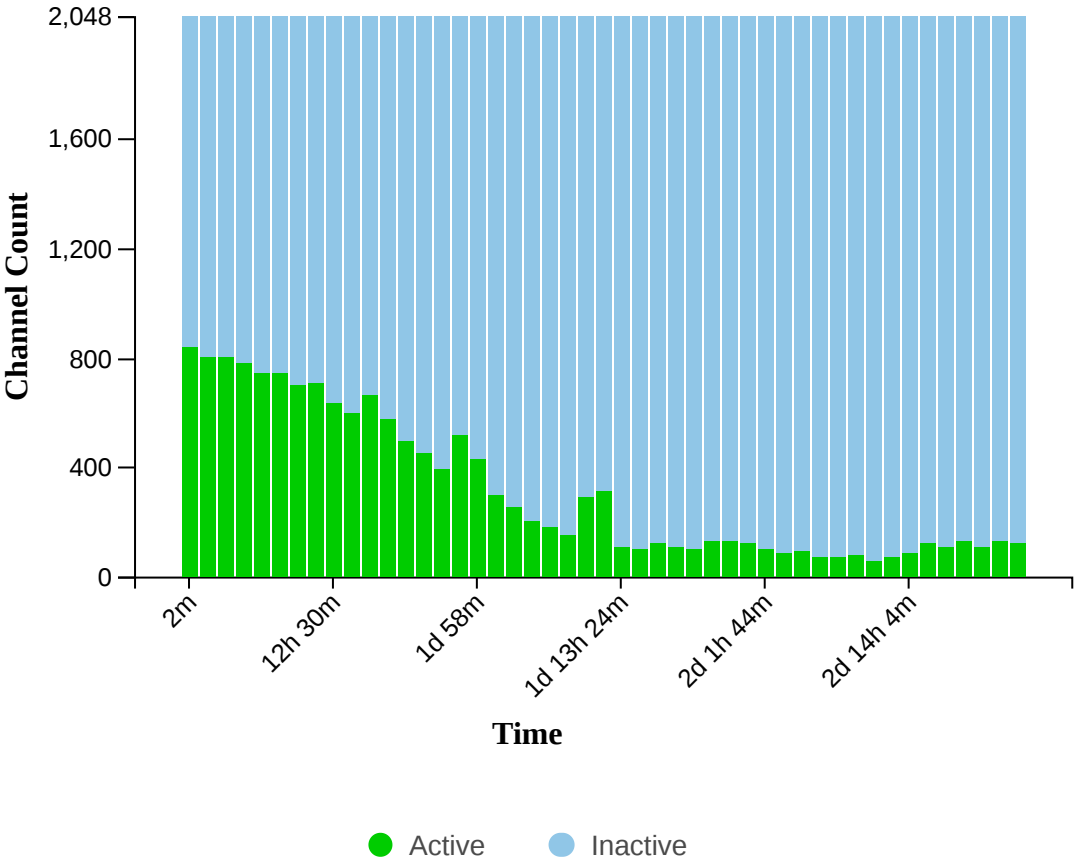
Duty Time Grouped



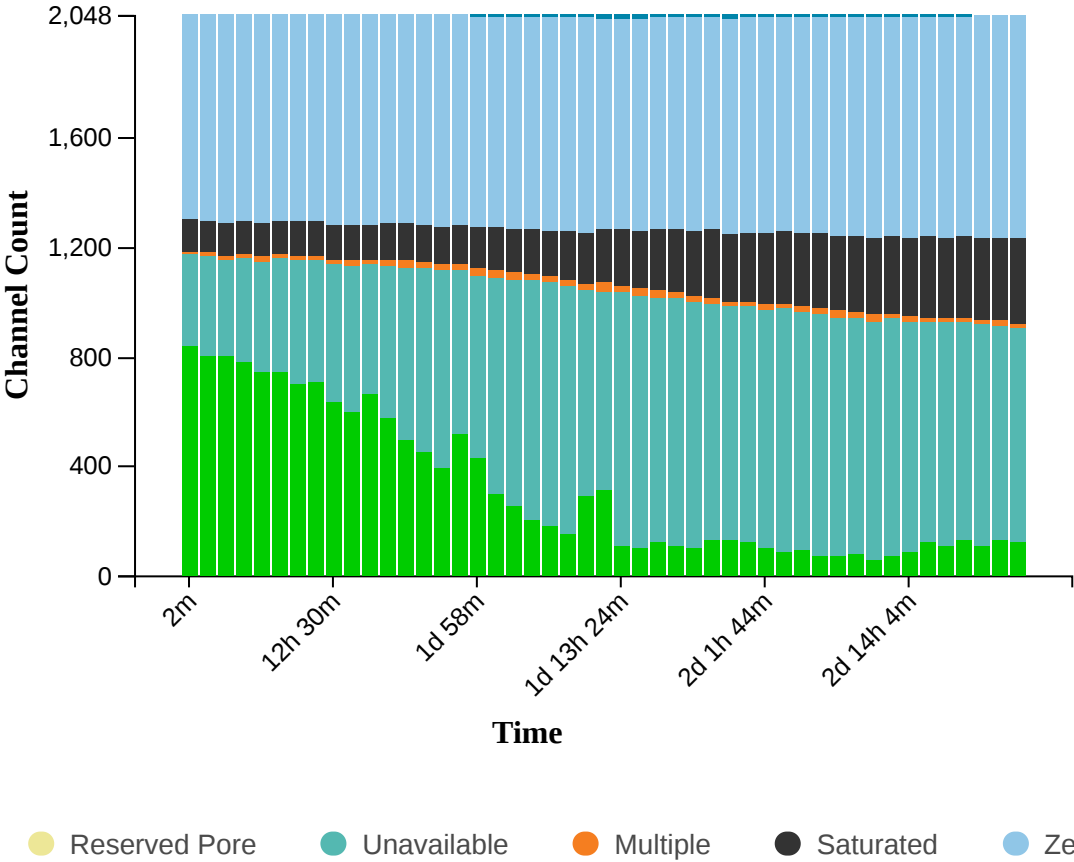
Duty time Categorised



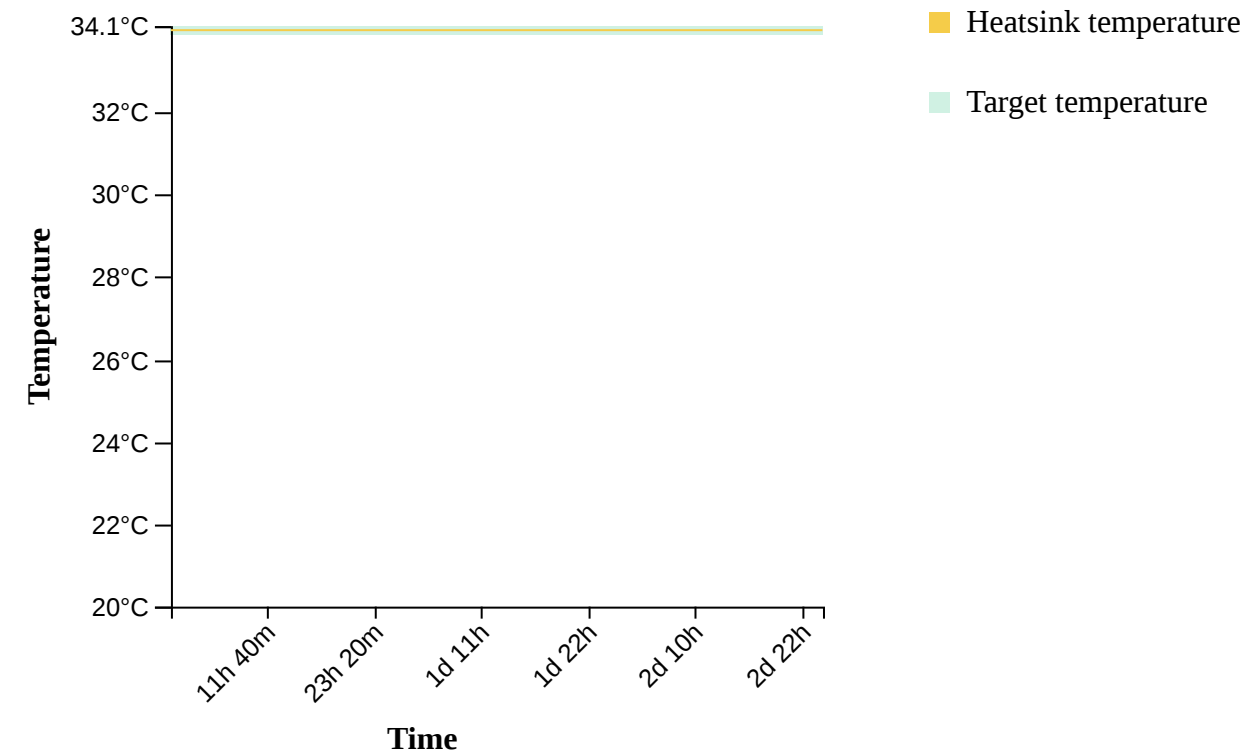
Mux Scan Grouped



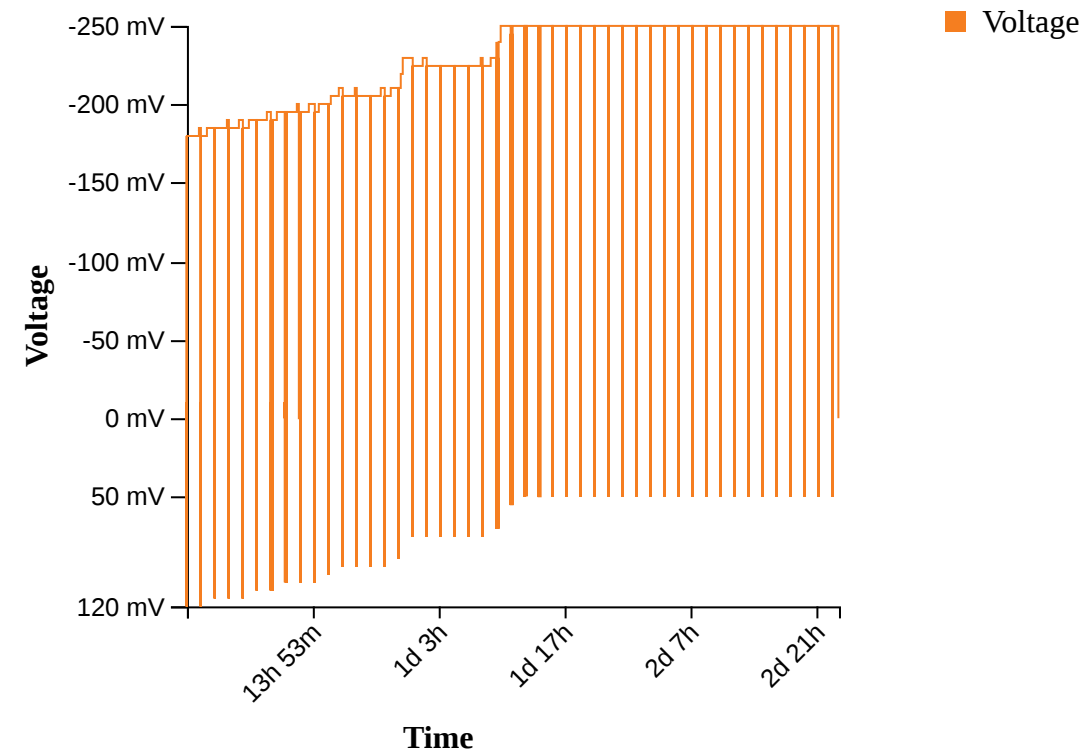
Mux Scan Categorised



Temperature History.

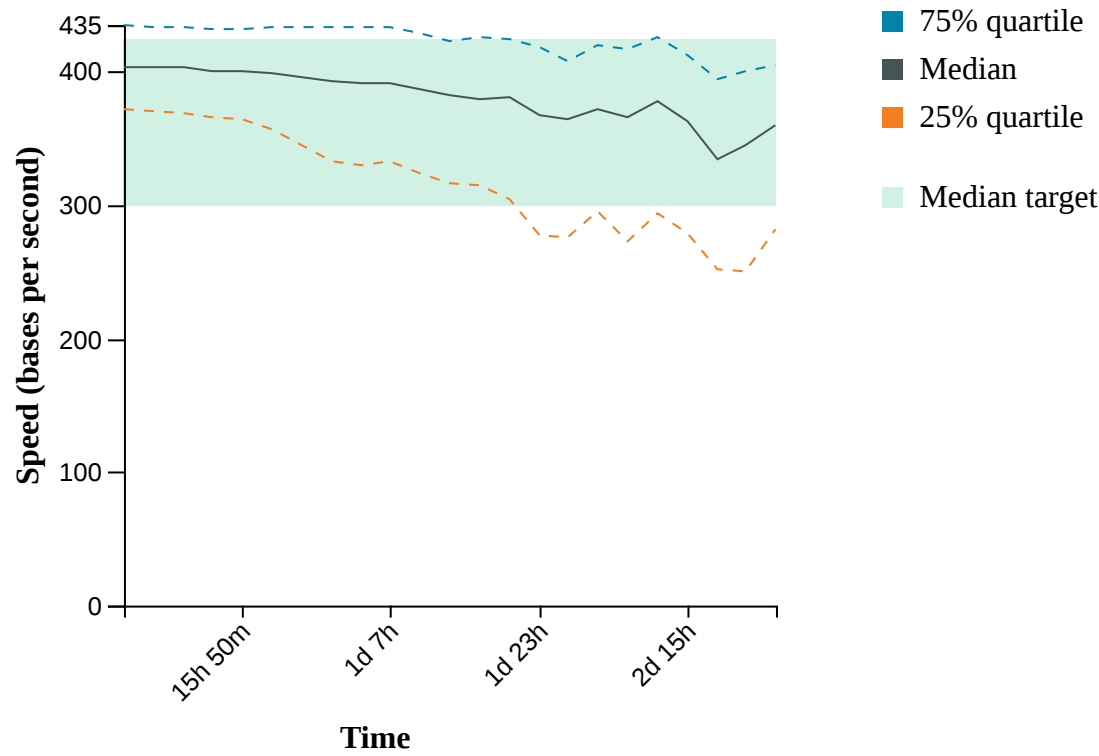


Bias Voltage History.

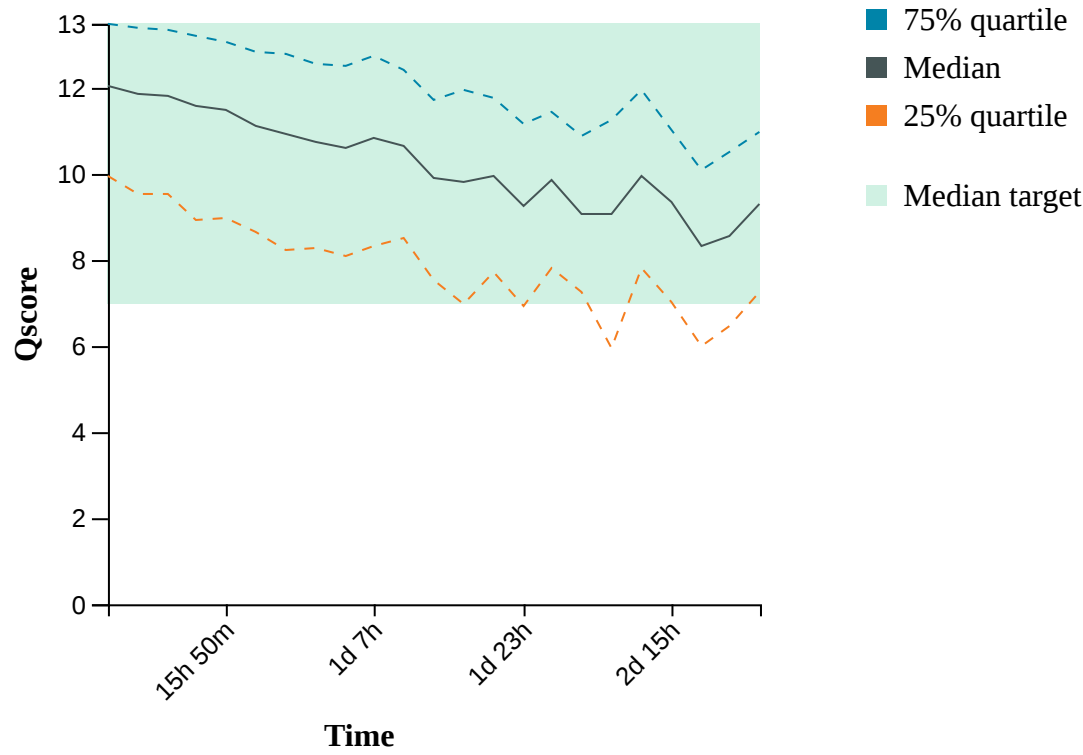




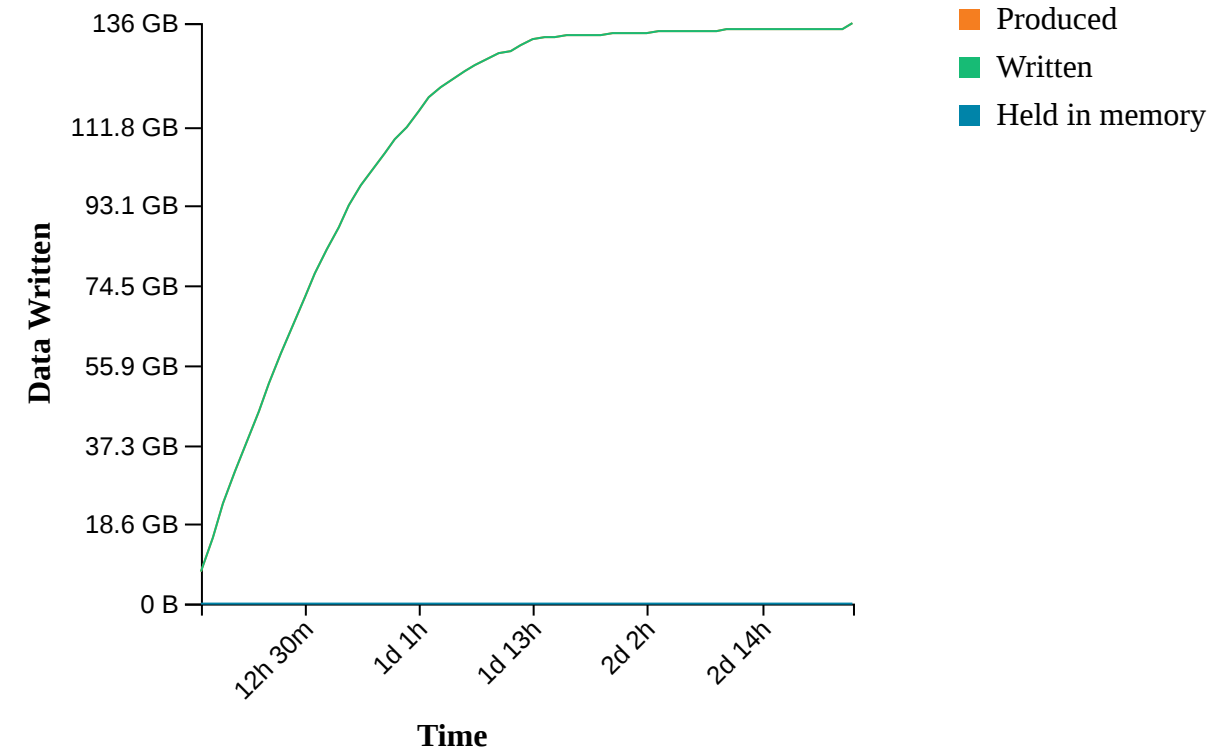
Translocation Speed



QScore



Disk Write Performance



## **Run Debug Messages**

- The sequencing run has finished, but basecalling may continue April 18, 18:40
- Mux scan for flow cell FAP21636 has found a total of 122 pores. 113 pores available for immediate sequencing April 18, 17:59
- Performing Mux Scan April 18, 17:57
- Mux scan for flow cell FAP21636 has found a total of 129 pores. 120 pores available for immediate sequencing April 18, 16:27
- Performing Mux Scan April 18, 16:24
- Mux scan for flow cell FAP21636 has found a total of 109 pores. 102 pores available for immediate sequencing April 18, 14:54
- Performing Mux Scan April 18, 14:52
- Mux scan for flow cell FAP21636 has found a total of 135 pores. 120 pores available for immediate sequencing April 18, 13:22
- Performing Mux Scan April 18, 13:19
- Mux scan for flow cell FAP21636 has found a total of 112 pores. 101 pores available for immediate sequencing April 18, 11:49
- Performing Mux Scan April 18, 11:47
- Mux scan for flow cell FAP21636 has found a total of 123 pores. 117 pores available for immediate sequencing April 18, 10:17
- Performing Mux Scan April 18, 10:14
- Mux scan for flow cell FAP21636 has found a total of 87 pores. 86 pores available for immediate sequencing April 18, 08:44
- Performing Mux Scan April 18, 08:42
- Mux scan for flow cell FAP21636 has found a total of 74 pores. 71 pores available for immediate sequencing April 18, 07:12
- Performing Mux Scan April 18, 07:09
- Mux scan for flow cell FAP21636 has found a total of 61 pores. 58 pores available for immediate sequencing April 18, 05:39
- Performing Mux Scan April 18, 05:37
- Mux scan for flow cell FAP21636 has found a total of 82 pores. 81 pores available for immediate sequencing April 18, 04:07
- Performing Mux Scan April 18, 04:05
- Mux scan for flow cell FAP21636 has found a total of 76 pores. 69 pores available for immediate sequencing April 18, 02:34
- Performing Mux Scan April 18, 02:32
- Mux scan for flow cell FAP21636 has found a total of 75 pores. 71 pores available for immediate sequencing April 18, 01:02
- Performing Mux Scan April 18, 01:00
- Mux scan for flow cell FAP21636 has found a total of 93 pores. 87 pores available for immediate sequencing April 17, 23:29
- Performing Mux Scan April 17, 23:27
- Mux scan for flow cell FAP21636 has found a total of 90 pores. 85 pores available for immediate sequencing April 17, 21:57
- Performing Mux Scan April 17, 21:55
- Mux scan for flow cell FAP21636 has found a total of 99 pores. 91 pores available for immediate sequencing April 17, 20:25
- Performing Mux Scan April 17, 20:22
- Mux scan for flow cell FAP21636 has found a total of 123 pores. 114 pores available for immediate sequencing April 17, 18:52
- Performing Mux Scan April 17, 18:50

- Mux scan for flow cell FAP21636 has found a total of 129 pores. 123 pores available for immediate sequencing April 17, 17:20
- Performing Mux Scan April 17, 17:17
- Mux scan for flow cell FAP21636 has found a total of 130 pores. 113 pores available for immediate sequencing April 17, 15:47
- Performing Mux Scan April 17, 15:45
- Mux scan for flow cell FAP21636 has found a total of 105 pores. 98 pores available for immediate sequencing April 17, 14:15
- Performing Mux Scan April 17, 14:12
- Mux scan for flow cell FAP21636 has found a total of 110 pores. 98 pores available for immediate sequencing April 17, 12:42
- Performing Mux Scan April 17, 12:40
- Mux scan for flow cell FAP21636 has found a total of 127 pores. 116 pores available for immediate sequencing April 17, 11:10
- Performing Mux Scan April 17, 11:07
- Mux scan for flow cell FAP21636 has found a total of 102 pores. 89 pores available for immediate sequencing April 17, 09:37
- Performing Mux Scan April 17, 09:35
- Mux scan for flow cell FAP21636 has found a total of 109 pores. 93 pores available for immediate sequencing April 17, 08:05
- Performing Mux Scan April 17, 08:02
- Mux scan for flow cell FAP21636 has found a total of 313 pores. 261 pores available for immediate sequencing April 17, 06:32
- Performing Mux Scan April 17, 06:30
- Mux scan for flow cell FAP21636 has found a total of 293 pores. 230 pores available for immediate sequencing April 17, 04:59
- Performing Mux Scan April 17, 04:57
- Mux scan for flow cell FAP21636 has found a total of 155 pores. 121 pores available for immediate sequencing April 17, 03:26
- Performing Mux Scan April 17, 03:23
- Mux scan for flow cell FAP21636 has found a total of 181 pores. 134 pores available for immediate sequencing April 17, 01:52
- Performing Mux Scan April 17, 01:50
- Mux scan for flow cell FAP21636 has found a total of 204 pores. 146 pores available for immediate sequencing April 17, 00:19
- Performing Mux Scan April 17, 00:17
- Mux scan for flow cell FAP21636 has found a total of 253 pores. 177 pores available for immediate sequencing April 16, 22:45
- Performing Mux Scan April 16, 22:43
- Mux scan for flow cell FAP21636 has found a total of 299 pores. 203 pores available for immediate sequencing April 16, 21:12
- Performing Mux Scan April 16, 21:10
- Mux scan for flow cell FAP21636 has found a total of 434 pores. 304 pores available for immediate sequencing April 16, 19:38
- Performing Mux Scan April 16, 19:36
- Mux scan for flow cell FAP21636 has found a total of 519 pores. 346 pores available for immediate sequencing April 16, 18:05
- Performing Mux Scan April 16, 18:03
- Mux scan for flow cell FAP21636 has found a total of 394 pores. 235 pores available for immediate sequencing April 16, 16:31
- Performing Mux Scan April 16, 16:29
- Mux scan for flow cell FAP21636 has found a total of 453 pores. 263 pores available for

- immediate sequencing April 16, 14:58
- Performing Mux Scan April 16, 14:56
- Mux scan for flow cell FAP21636 has found a total of 497 pores. 286 pores available for immediate sequencing April 16, 13:25
- Performing Mux Scan April 16, 13:22
- Mux scan for flow cell FAP21636 has found a total of 579 pores. 331 pores available for immediate sequencing April 16, 11:51
- Performing Mux Scan April 16, 11:49
- Mux scan for flow cell FAP21636 has found a total of 666 pores. 385 pores available for immediate sequencing April 16, 10:18
- Performing Mux Scan April 16, 10:15
- Mux scan for flow cell FAP21636 has found a total of 602 pores. 331 pores available for immediate sequencing April 16, 08:44
- Performing Mux Scan April 16, 08:42
- Mux scan for flow cell FAP21636 has found a total of 639 pores. 355 pores available for immediate sequencing April 16, 07:11
- Performing Mux Scan April 16, 07:08
- Mux scan for flow cell FAP21636 has found a total of 709 pores. 399 pores available for immediate sequencing April 16, 05:37
- Performing Mux Scan April 16, 05:35
- Mux scan for flow cell FAP21636 has found a total of 705 pores. 380 pores available for immediate sequencing April 16, 04:04
- Performing Mux Scan April 16, 04:01
- Mux scan for flow cell FAP21636 has found a total of 747 pores. 402 pores available for immediate sequencing April 16, 02:30
- Performing Mux Scan April 16, 02:28
- Mux scan for flow cell FAP21636 has found a total of 746 pores. 392 pores available for immediate sequencing April 16, 00:57
- Performing Mux Scan April 16, 00:54
- Mux scan for flow cell FAP21636 has found a total of 781 pores. 409 pores available for immediate sequencing April 15, 23:23
- Performing Mux Scan April 15, 23:21
- Mux scan for flow cell FAP21636 has found a total of 808 pores. 429 pores available for immediate sequencing April 15, 21:50
- Performing Mux Scan April 15, 21:47
- Mux scan for flow cell FAP21636 has found a total of 808 pores. 420 pores available for immediate sequencing April 15, 20:16
- Performing Mux Scan April 15, 20:14
- Mux scan for flow cell FAP21636 has found a total of 842 pores. 440 pores available for immediate sequencing April 15, 18:43
- Performing Mux Scan April 15, 18:40
- Starting sequencing procedure April 15, 18:40
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 18:37