Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38Kbp_LowtoHigh_MmEnr_15042021**
Sample ID	**ReadUntil_38Kbp_LowtoHigh_MmEnr_15042021**
Run ID	**5a06b53c-cb93-4051-a39a-d7a11d821f83**
Flow Cell Id	**FAP14753**
Start Time	**April 15, 18:38**
Run Length	**3d 0h 3m**

Run Summary

Reads Generated	**1.46 M**
Passed Bases	**8.39 Gb**
Failed Bases	**607.12 Mb**
Estimated Bases	**9.09 Gb**

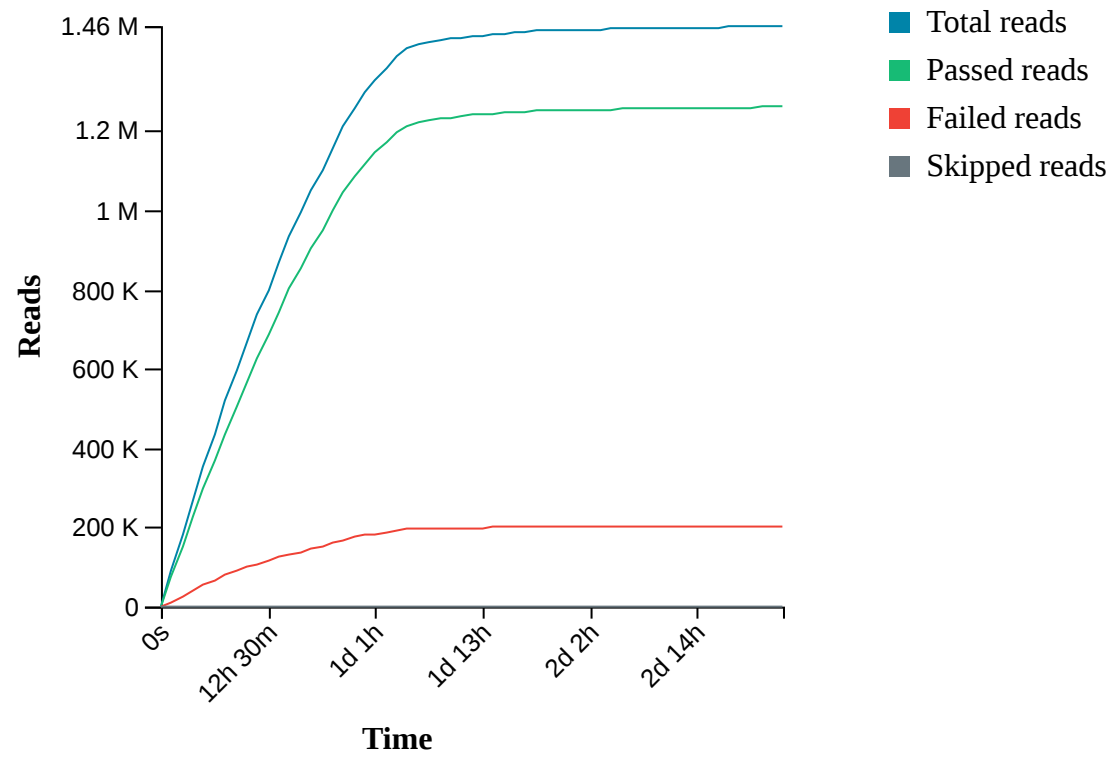
Run Parameters

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/M_morganii_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**

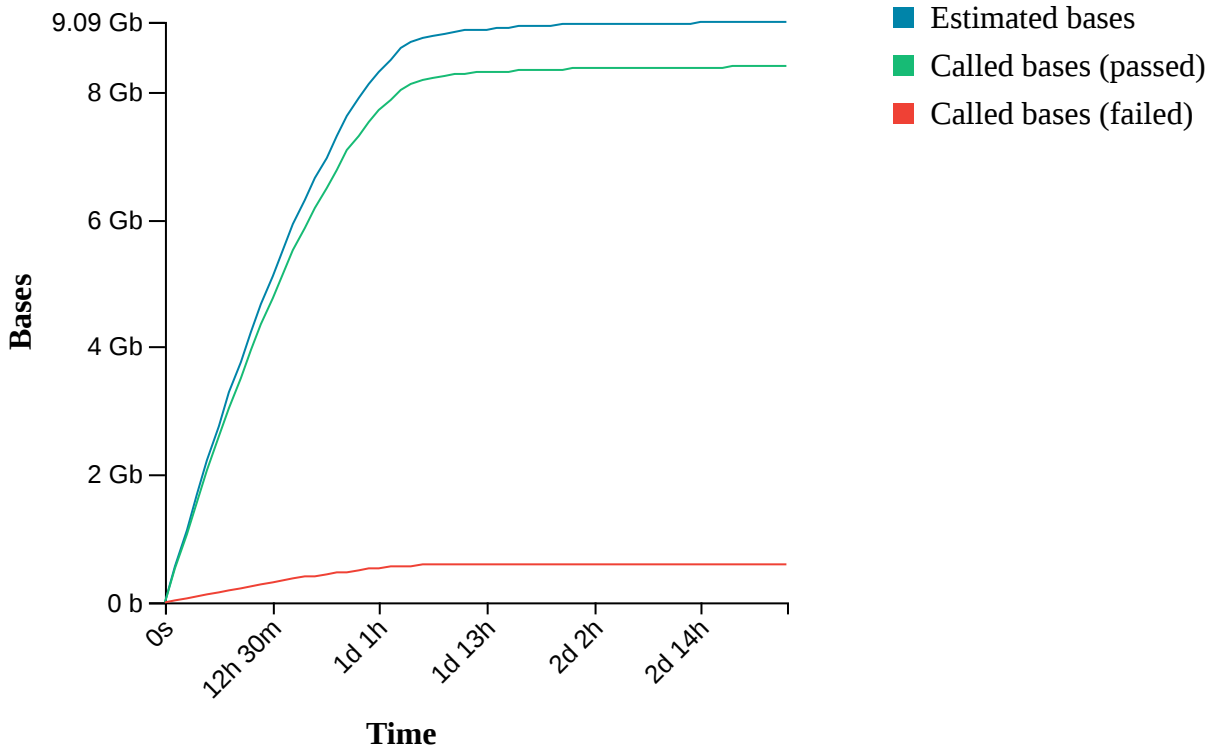
Versions

MinKNOW	**21.02.5**
MinKNOW Core	**4.2.5**
Bream	**6.1.10**
Guppy	**4.3.4**

Cumulative Output Reads

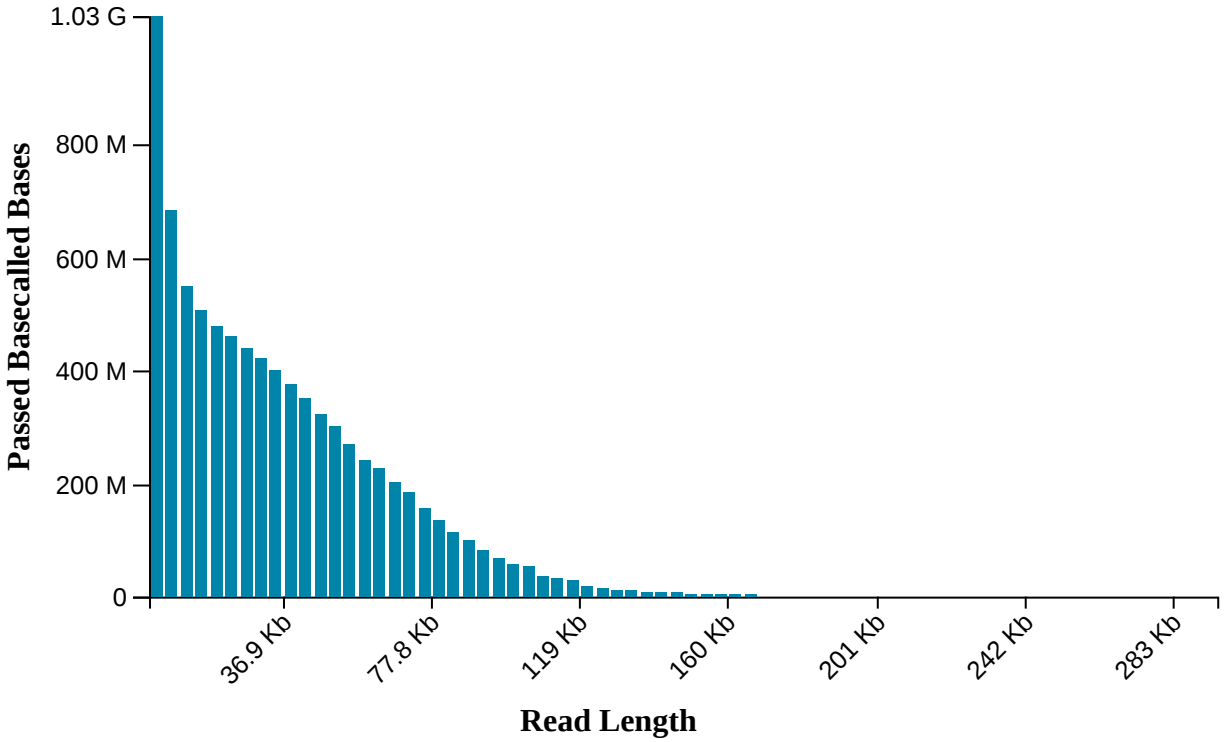


Cumulative Output Bases



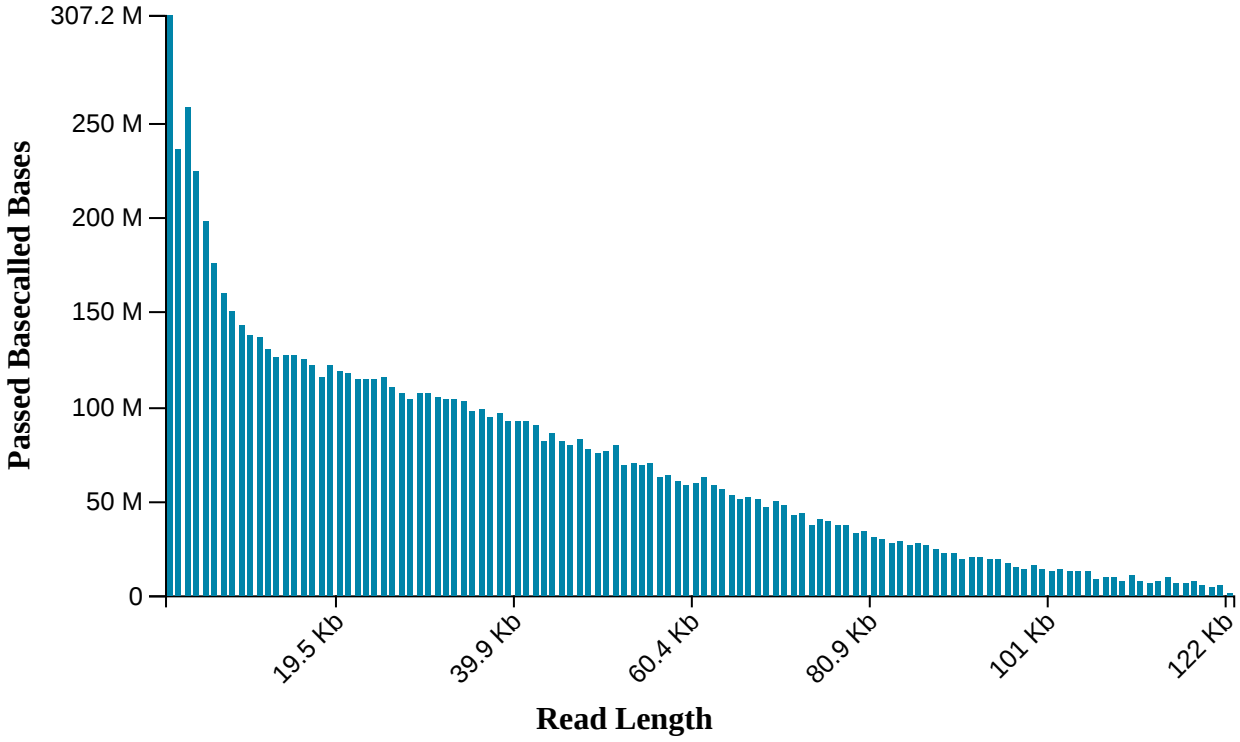
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 29.22 K



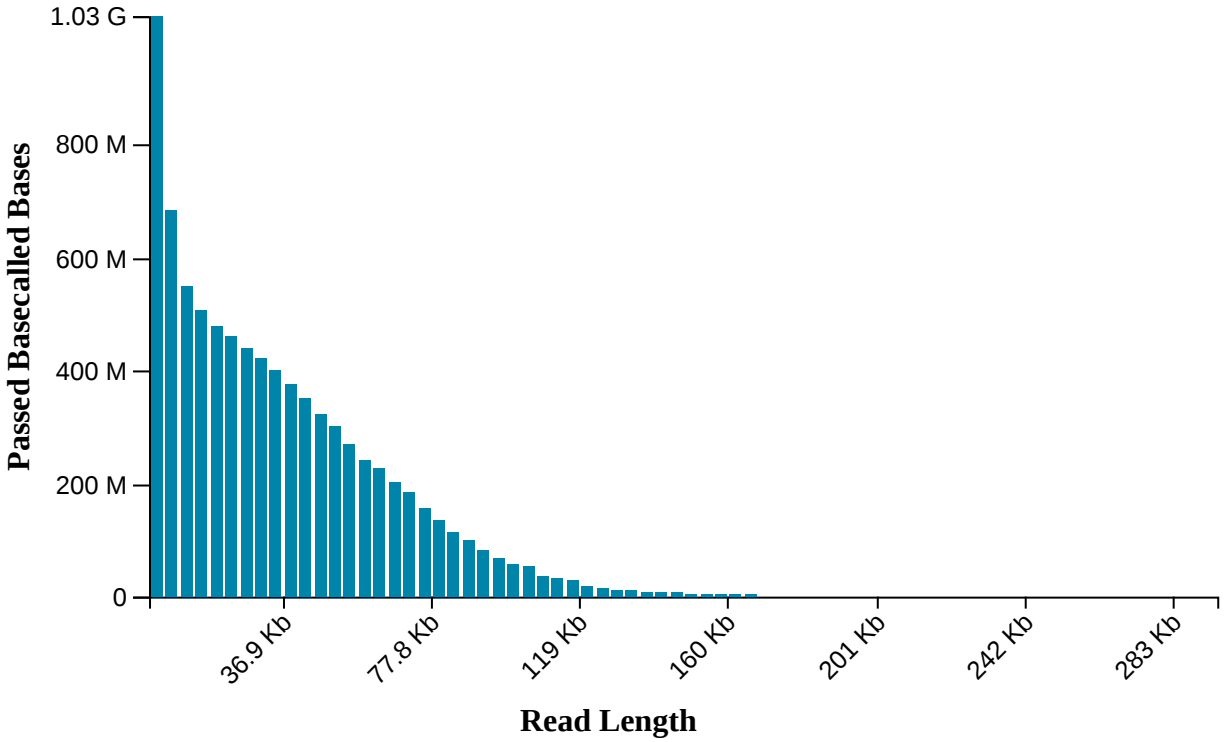
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 28.81 K



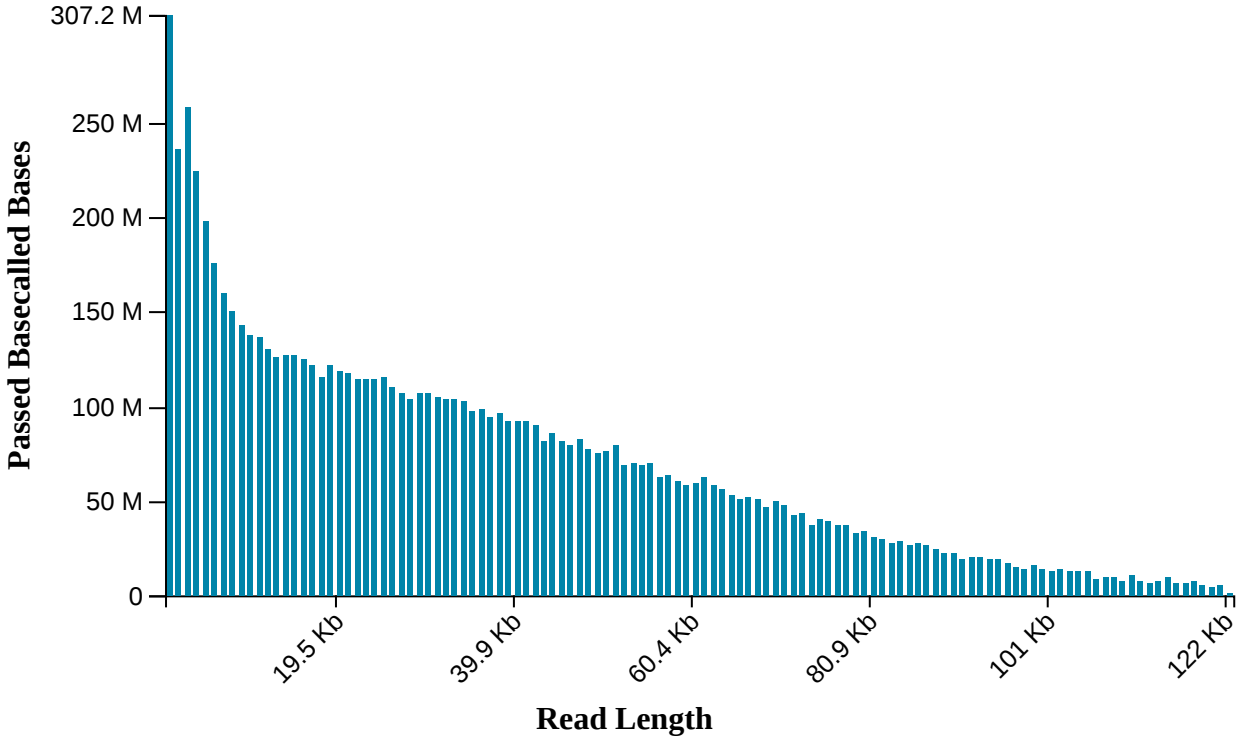
Read Length Histogram Estimated Bases

Estimated N50: 29.22 K

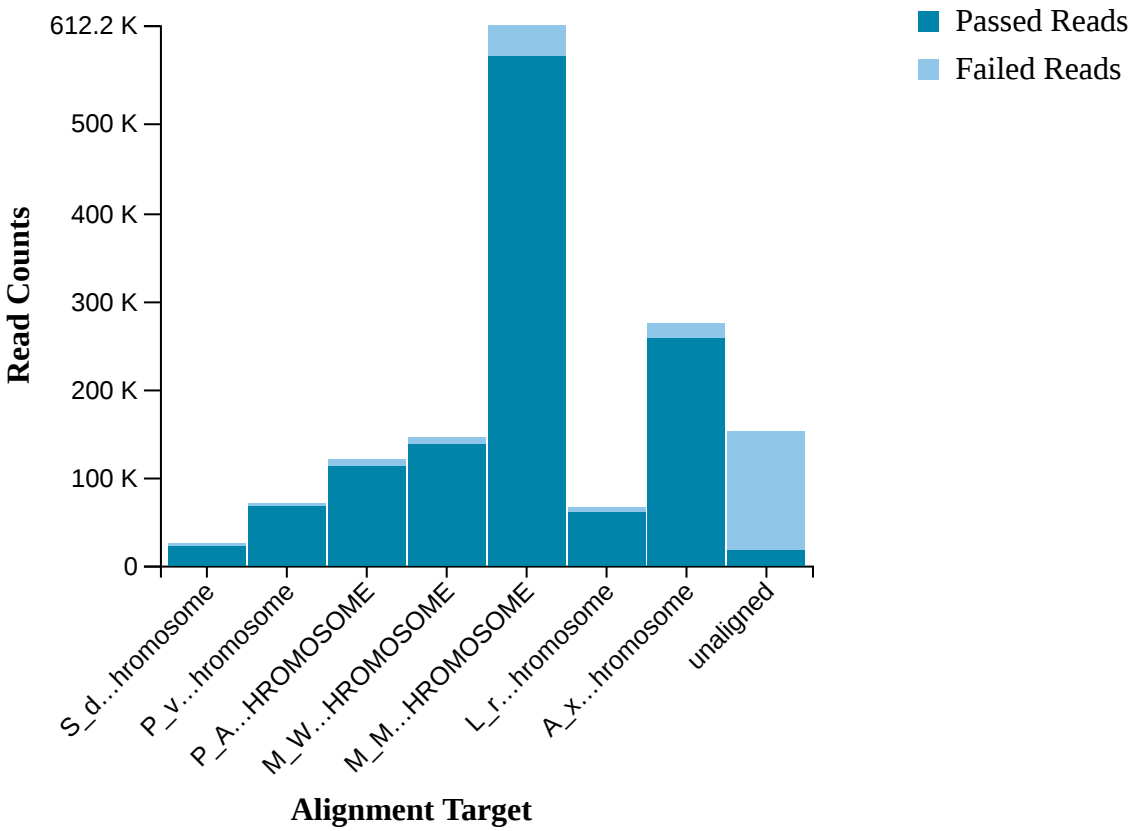


Read Length Histogram Basecalled Bases

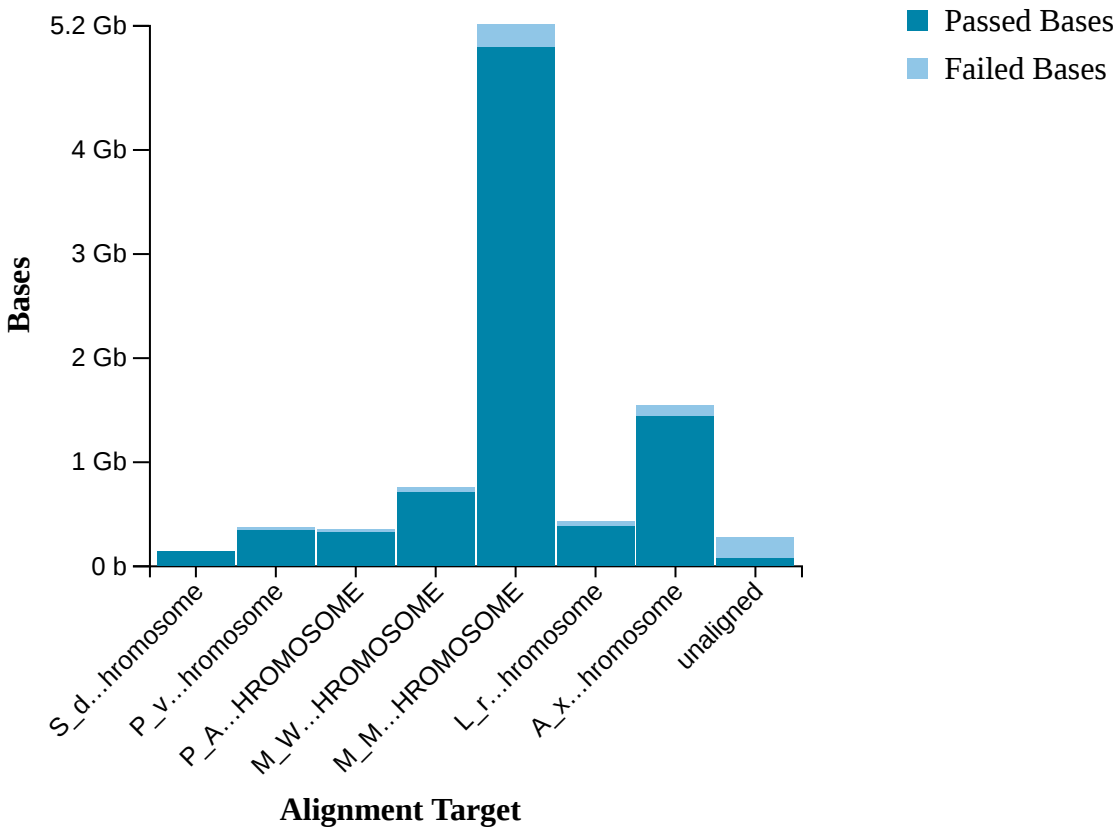
Estimated N50: 28.81 K



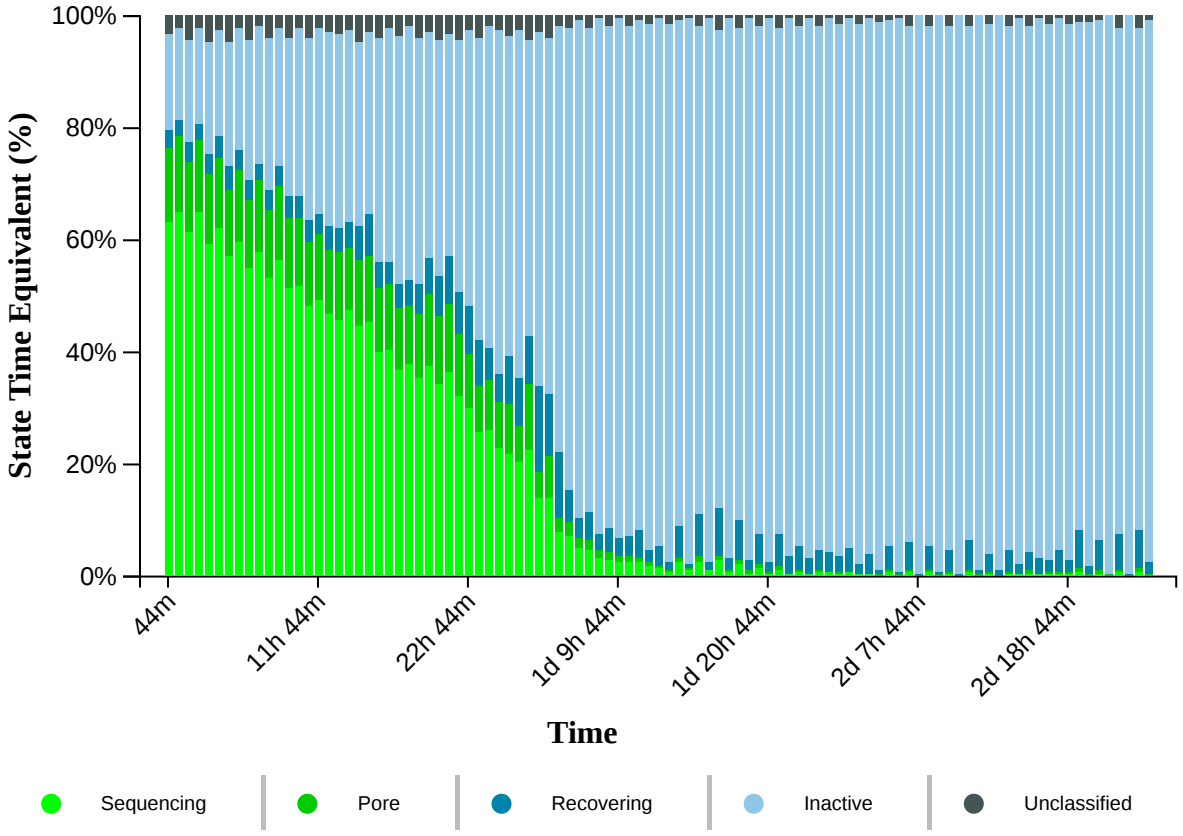
Alignment Target Hits (reads)



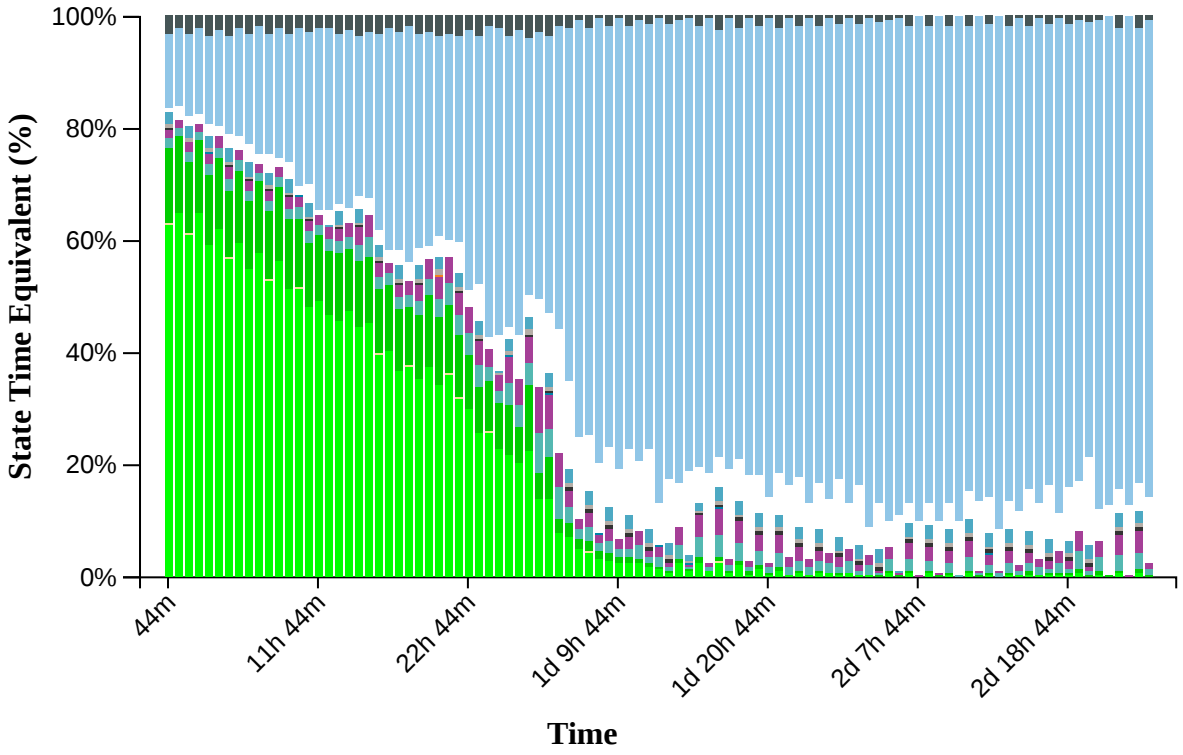
Alignment Target Hits (bases)



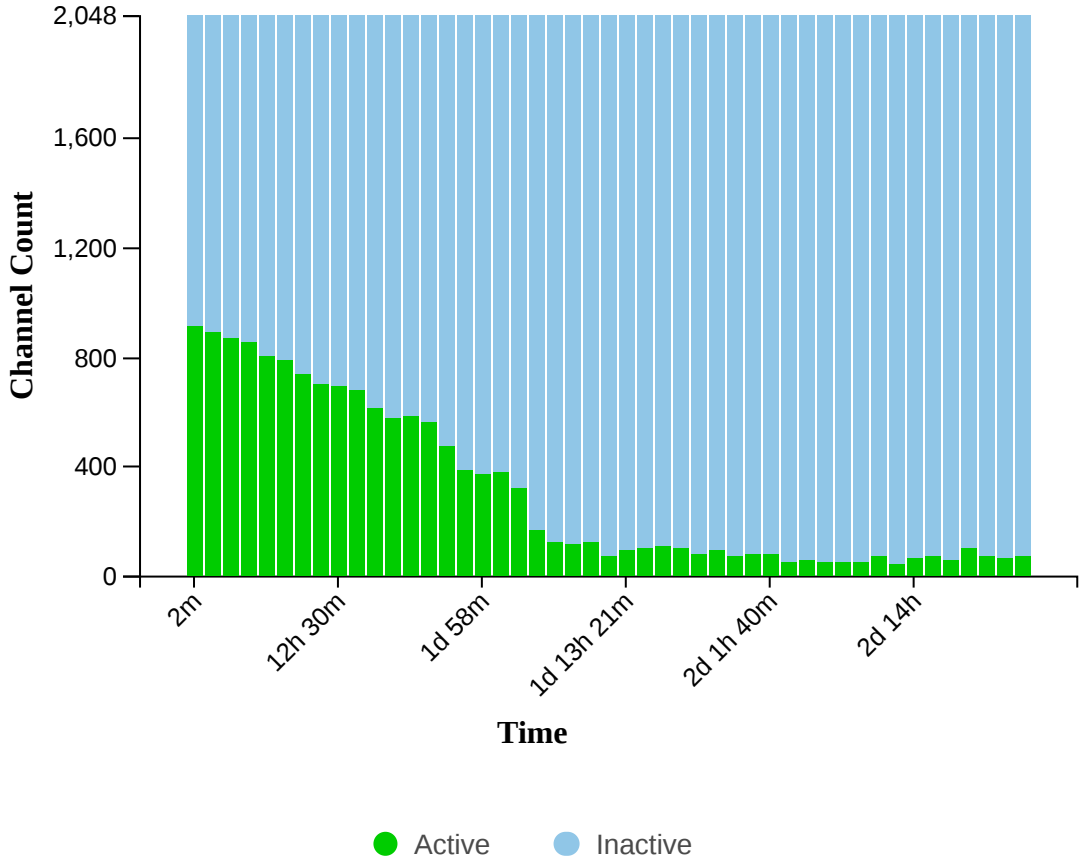
Duty Time Grouped



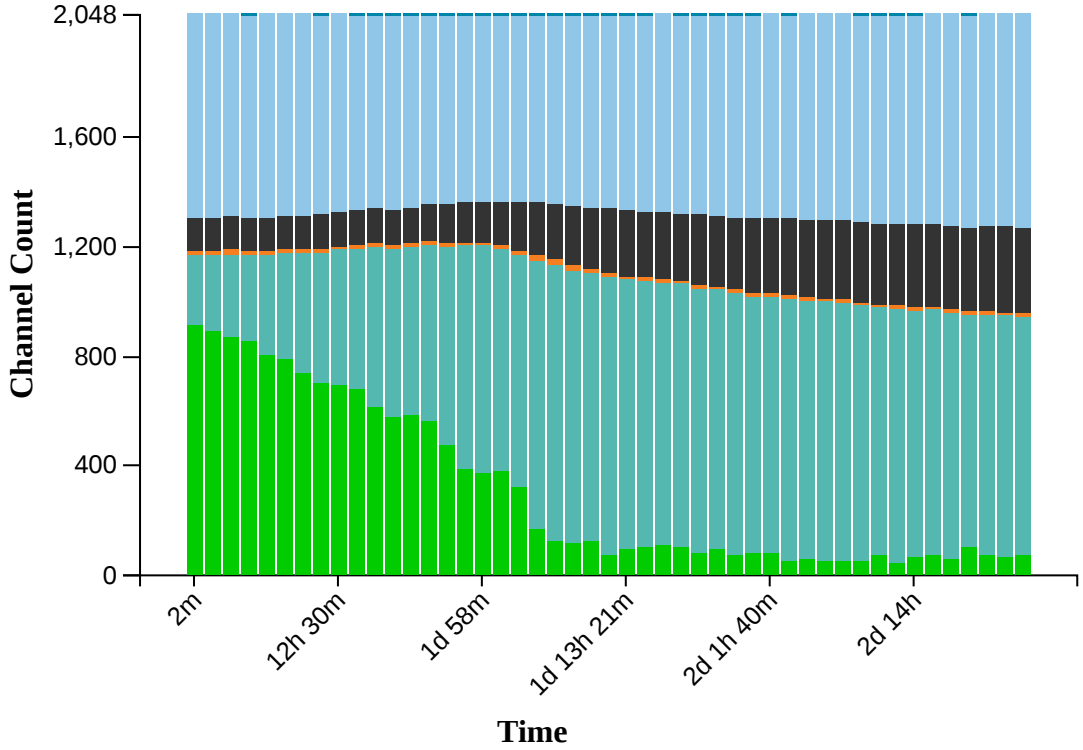
Duty time Categorised



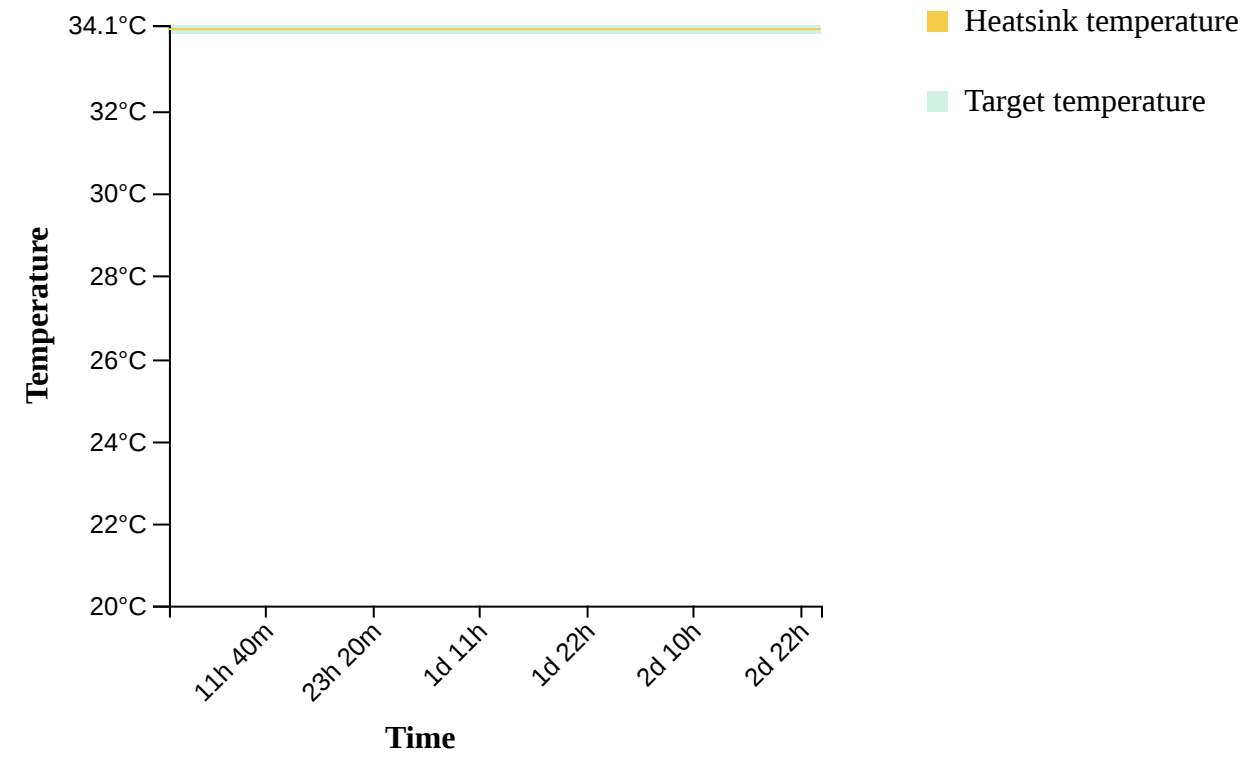
Mux Scan Grouped



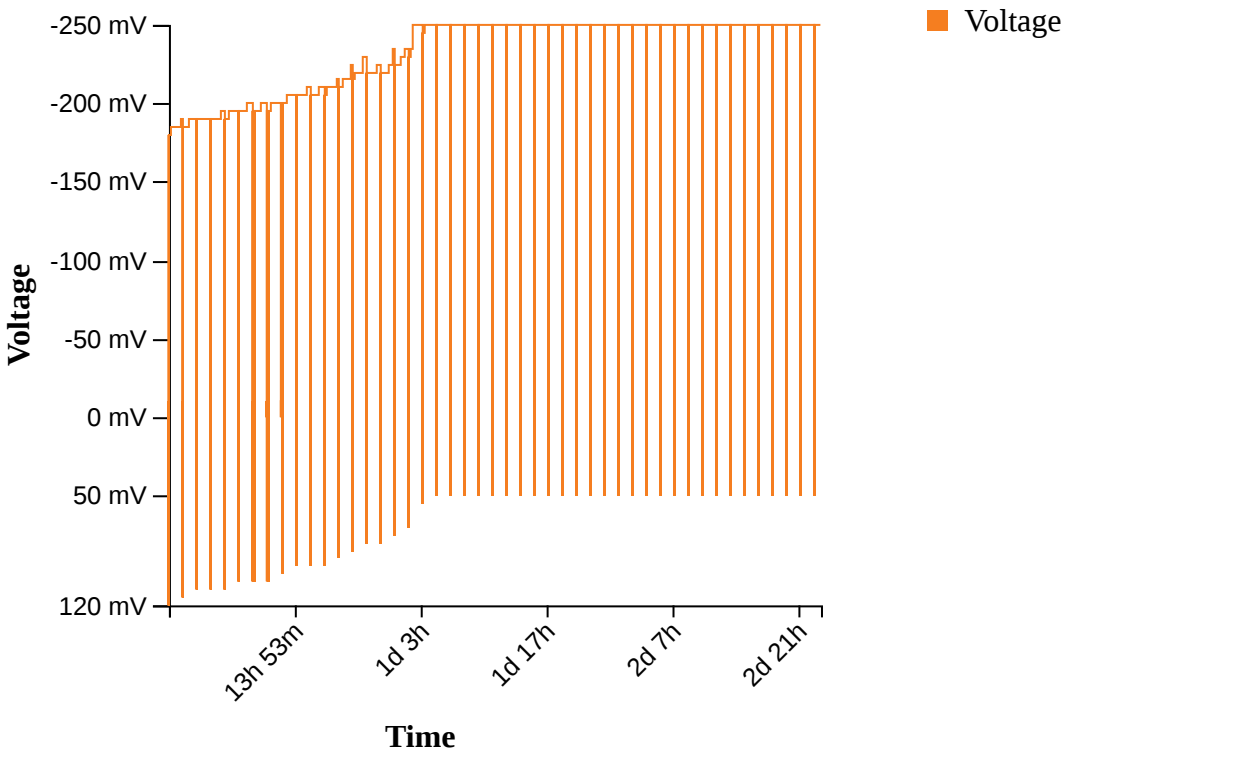
Mux Scan Categorised



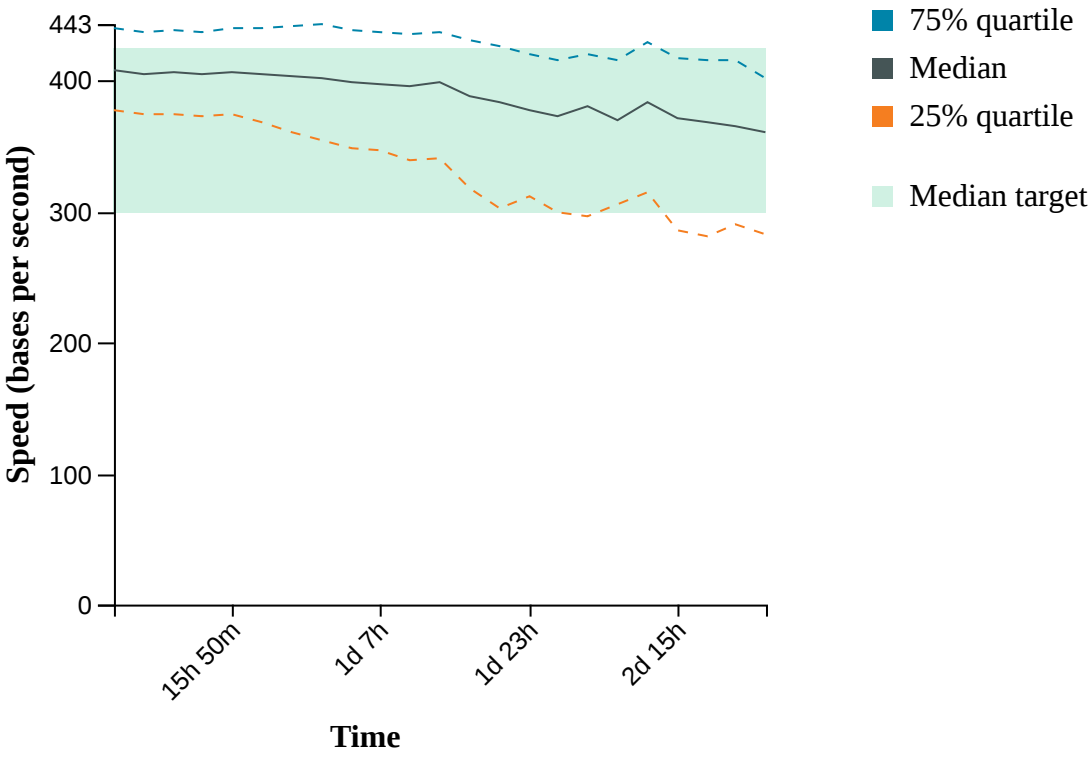
Temperature History



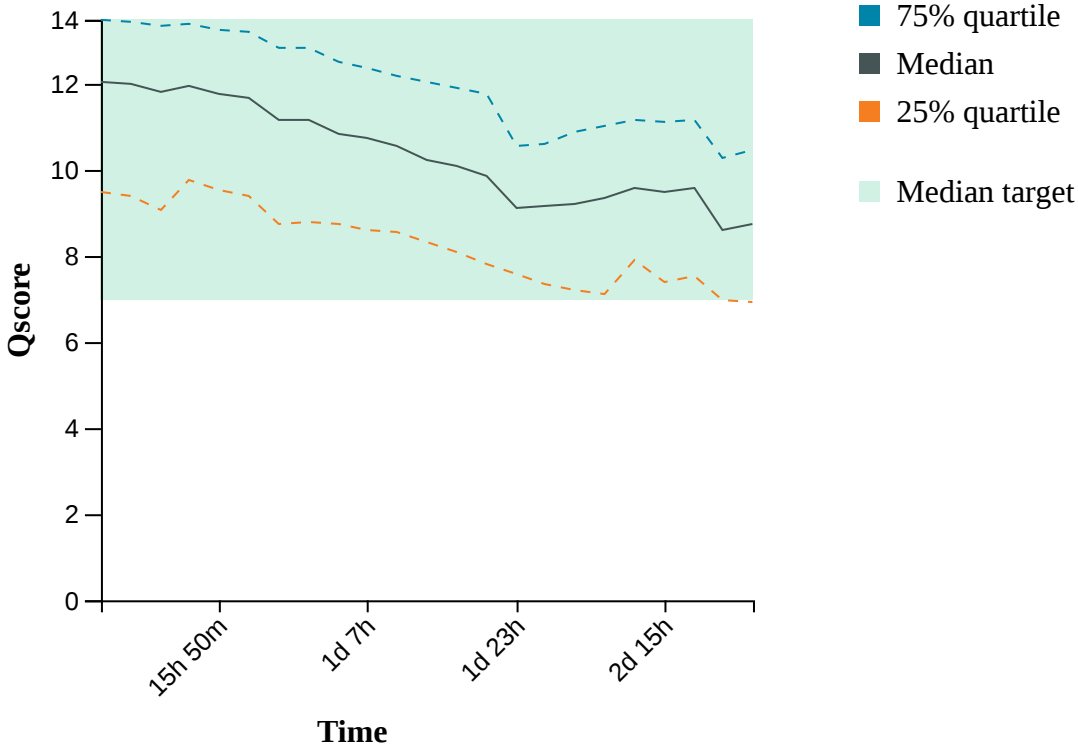
Bias Voltage History



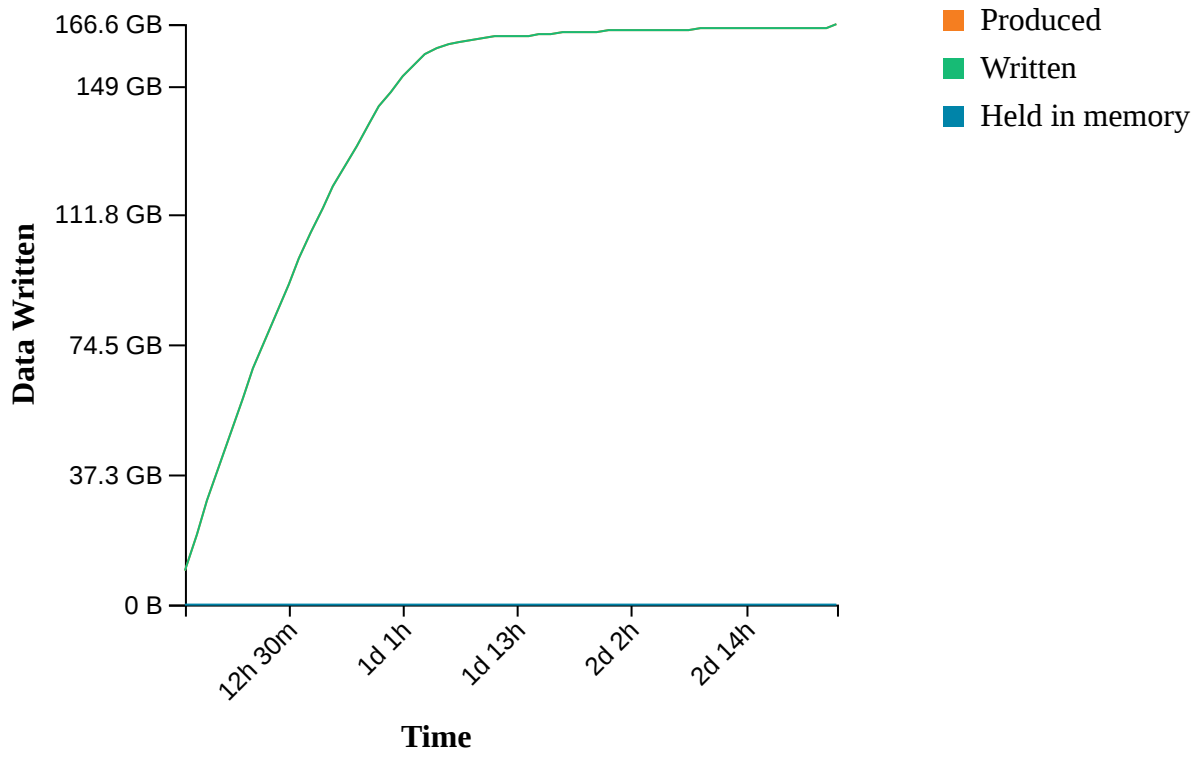
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- The sequencing run has finished, but basecalling may continue April 18, 18:41
- Mux scan for flow cell FAP14753 has found a total of 76 pores. 73 pores available for immediate sequencing April 18, 17:57
- Performing Mux Scan April 18, 17:54
- Mux scan for flow cell FAP14753 has found a total of 69 pores. 66 pores available for immediate sequencing April 18, 16:24
- Performing Mux Scan April 18, 16:22
- Mux scan for flow cell FAP14753 has found a total of 71 pores. 66 pores available for immediate sequencing April 18, 14:52
- Performing Mux Scan April 18, 14:49
- Mux scan for flow cell FAP14753 has found a total of 100 pores. 93 pores available for immediate sequencing April 18, 13:19
- Performing Mux Scan April 18, 13:17
- Mux scan for flow cell FAP14753 has found a total of 62 pores. 61 pores available for immediate sequencing April 18, 11:47
- Performing Mux Scan April 18, 11:45
- Mux scan for flow cell FAP14753 has found a total of 71 pores. 69 pores available for immediate sequencing April 18, 10:14
- Performing Mux Scan April 18, 10:12
- Mux scan for flow cell FAP14753 has found a total of 63 pores. 62 pores available for immediate sequencing April 18, 08:42
- Performing Mux Scan April 18, 08:40
- Mux scan for flow cell FAP14753 has found a total of 46 pores. 45 pores available for immediate sequencing April 18, 07:09
- Performing Mux Scan April 18, 07:07
- Mux scan for flow cell FAP14753 has found a total of 70 pores. 69 pores available for immediate sequencing April 18, 05:37
- Performing Mux Scan April 18, 05:35
- Mux scan for flow cell FAP14753 has found a total of 54 pores. 52 pores available for immediate sequencing April 18, 04:05
- Performing Mux Scan April 18, 04:02
- Mux scan for flow cell FAP14753 has found a total of 53 pores. 51 pores available for immediate sequencing April 18, 02:32
- Performing Mux Scan April 18, 02:30
- Mux scan for flow cell FAP14753 has found a total of 52 pores. 52 pores available for immediate sequencing April 18, 01:00
- Performing Mux Scan April 18, 00:57
- Mux scan for flow cell FAP14753 has found a total of 61 pores. 55 pores available for immediate sequencing April 17, 23:27
- Performing Mux Scan April 17, 23:25
- Mux scan for flow cell FAP14753 has found a total of 48 pores. 47 pores available for immediate sequencing April 17, 21:55
- Performing Mux Scan April 17, 21:52
- Mux scan for flow cell FAP14753 has found a total of 77 pores. 71 pores available for immediate sequencing April 17, 20:22
- Performing Mux Scan April 17, 20:20
- Mux scan for flow cell FAP14753 has found a total of 80 pores. 74 pores available for immediate sequencing April 17, 18:50
- Performing Mux Scan April 17, 18:47

- Mux scan for flow cell FAP14753 has found a total of 74 pores. 69 pores available for immediate sequencing April 17, 17:17
- Performing Mux Scan April 17, 17:15
- Mux scan for flow cell FAP14753 has found a total of 98 pores. 86 pores available for immediate sequencing April 17, 15:45
- Performing Mux Scan April 17, 15:42
- Mux scan for flow cell FAP14753 has found a total of 79 pores. 74 pores available for immediate sequencing April 17, 14:12
- Performing Mux Scan April 17, 14:10
- Mux scan for flow cell FAP14753 has found a total of 100 pores. 94 pores available for immediate sequencing April 17, 12:40
- Performing Mux Scan April 17, 12:37
- Mux scan for flow cell FAP14753 has found a total of 108 pores. 101 pores available for immediate sequencing April 17, 11:07
- Performing Mux Scan April 17, 11:05
- Mux scan for flow cell FAP14753 has found a total of 105 pores. 96 pores available for immediate sequencing April 17, 09:35
- Performing Mux Scan April 17, 09:32
- Mux scan for flow cell FAP14753 has found a total of 94 pores. 90 pores available for immediate sequencing April 17, 08:02
- Performing Mux Scan April 17, 08:00
- Mux scan for flow cell FAP14753 has found a total of 74 pores. 71 pores available for immediate sequencing April 17, 06:30
- Performing Mux Scan April 17, 06:27
- Mux scan for flow cell FAP14753 has found a total of 123 pores. 110 pores available for immediate sequencing April 17, 04:57
- Performing Mux Scan April 17, 04:55
- Mux scan for flow cell FAP14753 has found a total of 119 pores. 102 pores available for immediate sequencing April 17, 03:25
- Performing Mux Scan April 17, 03:22
- Mux scan for flow cell FAP14753 has found a total of 124 pores. 107 pores available for immediate sequencing April 17, 01:52
- Performing Mux Scan April 17, 01:50
- Mux scan for flow cell FAP14753 has found a total of 169 pores. 131 pores available for immediate sequencing April 17, 00:19
- Performing Mux Scan April 17, 00:17
- Mux scan for flow cell FAP14753 has found a total of 322 pores. 236 pores available for immediate sequencing April 16, 22:46
- Performing Mux Scan April 16, 22:44
- Mux scan for flow cell FAP14753 has found a total of 383 pores. 269 pores available for immediate sequencing April 16, 21:13
- Performing Mux Scan April 16, 21:10
- Mux scan for flow cell FAP14753 has found a total of 376 pores. 234 pores available for immediate sequencing April 16, 19:39
- Performing Mux Scan April 16, 19:37
- Mux scan for flow cell FAP14753 has found a total of 387 pores. 229 pores available for immediate sequencing April 16, 18:06
- Performing Mux Scan April 16, 18:03
- Mux scan for flow cell FAP14753 has found a total of 476 pores. 275 pores available for immediate sequencing April 16, 16:32
- Performing Mux Scan April 16, 16:30
- Mux scan for flow cell FAP14753 has found a total of 566 pores. 323 pores available for

immediate sequencing April 16, 14:59

- Performing Mux Scan April 16, 14:56
- Mux scan for flow cell FAP14753 has found a total of 583 pores. 316 pores available for immediate sequencing April 16, 13:25
- Performing Mux Scan April 16, 13:23
- Mux scan for flow cell FAP14753 has found a total of 578 pores. 296 pores available for immediate sequencing April 16, 11:52
- Performing Mux Scan April 16, 11:50
- Mux scan for flow cell FAP14753 has found a total of 618 pores. 309 pores available for immediate sequencing April 16, 10:18
- Performing Mux Scan April 16, 10:16
- Mux scan for flow cell FAP14753 has found a total of 680 pores. 359 pores available for immediate sequencing April 16, 08:45
- Performing Mux Scan April 16, 08:43
- Mux scan for flow cell FAP14753 has found a total of 697 pores. 348 pores available for immediate sequencing April 16, 07:11
- Performing Mux Scan April 16, 07:09
- Mux scan for flow cell FAP14753 has found a total of 704 pores. 345 pores available for immediate sequencing April 16, 05:38
- Performing Mux Scan April 16, 05:36
- Mux scan for flow cell FAP14753 has found a total of 738 pores. 367 pores available for immediate sequencing April 16, 04:05
- Performing Mux Scan April 16, 04:02
- Mux scan for flow cell FAP14753 has found a total of 793 pores. 394 pores available for immediate sequencing April 16, 02:31
- Performing Mux Scan April 16, 02:29
- Mux scan for flow cell FAP14753 has found a total of 807 pores. 395 pores available for immediate sequencing April 16, 00:58
- Performing Mux Scan April 16, 00:55
- Mux scan for flow cell FAP14753 has found a total of 854 pores. 414 pores available for immediate sequencing April 15, 23:24
- Performing Mux Scan April 15, 23:22
- Mux scan for flow cell FAP14753 has found a total of 872 pores. 424 pores available for immediate sequencing April 15, 21:51
- Performing Mux Scan April 15, 21:48
- Mux scan for flow cell FAP14753 has found a total of 889 pores. 433 pores available for immediate sequencing April 15, 20:17
- Performing Mux Scan April 15, 20:15
- Mux scan for flow cell FAP14753 has found a total of 914 pores. 440 pores available for immediate sequencing April 15, 18:44
- Performing Mux Scan April 15, 18:41
- Starting sequencing procedure April 15, 18:41
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 18:38