Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**ReadUntil_38kb_MmDepletion_15042021**
Sample ID	**ReadUntil_38kb_MmDepletion_15042021**
Run ID	**637aed78-b222-4a41-b25f-8375a71d5c14**
Flow Cell Id	**FAP14879**
Start Time	**April 15, 10:53**
Run Length	**3d 0h 3m**

Run Summary

Reads Generated	**1.9 M**
Passed Bases	**15.85 Gb**
Failed Bases	**1.49 Gb**
Estimated Bases	**17.51 Gb**

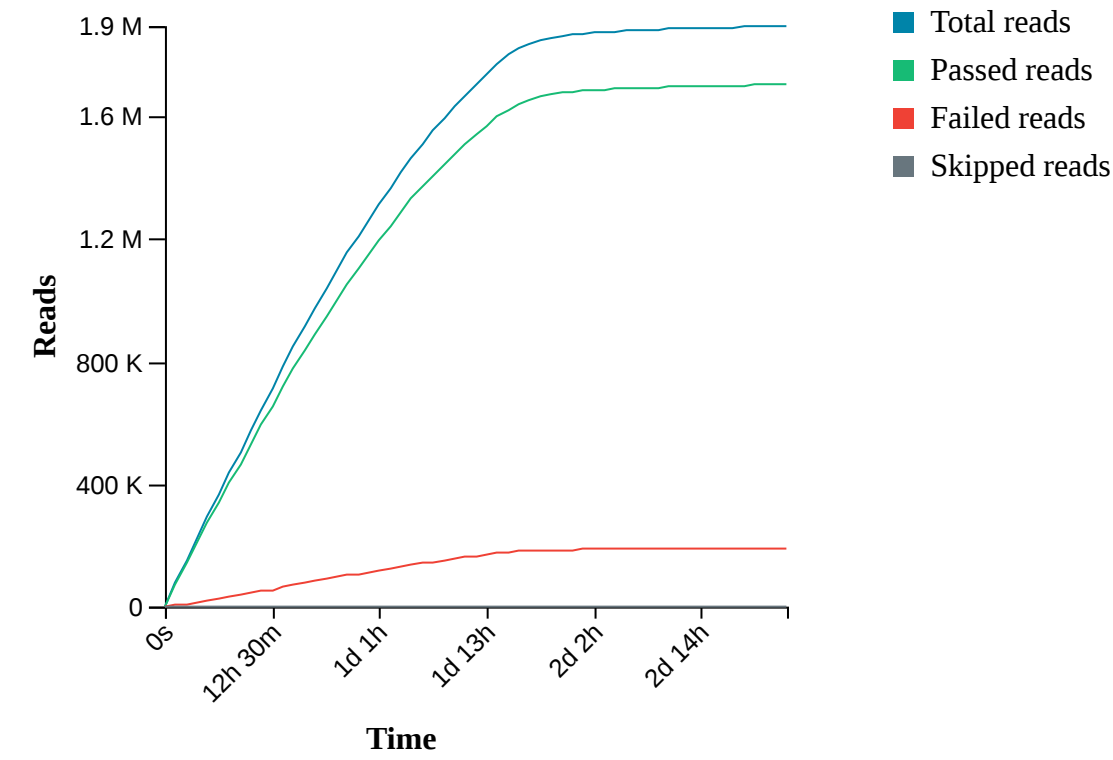
Run Parameters

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/references/M_morganii_ref.fasta"],filter_type=deplete,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/references/the7references.fasta"]**
Read Filtering	**min_qscore=7**

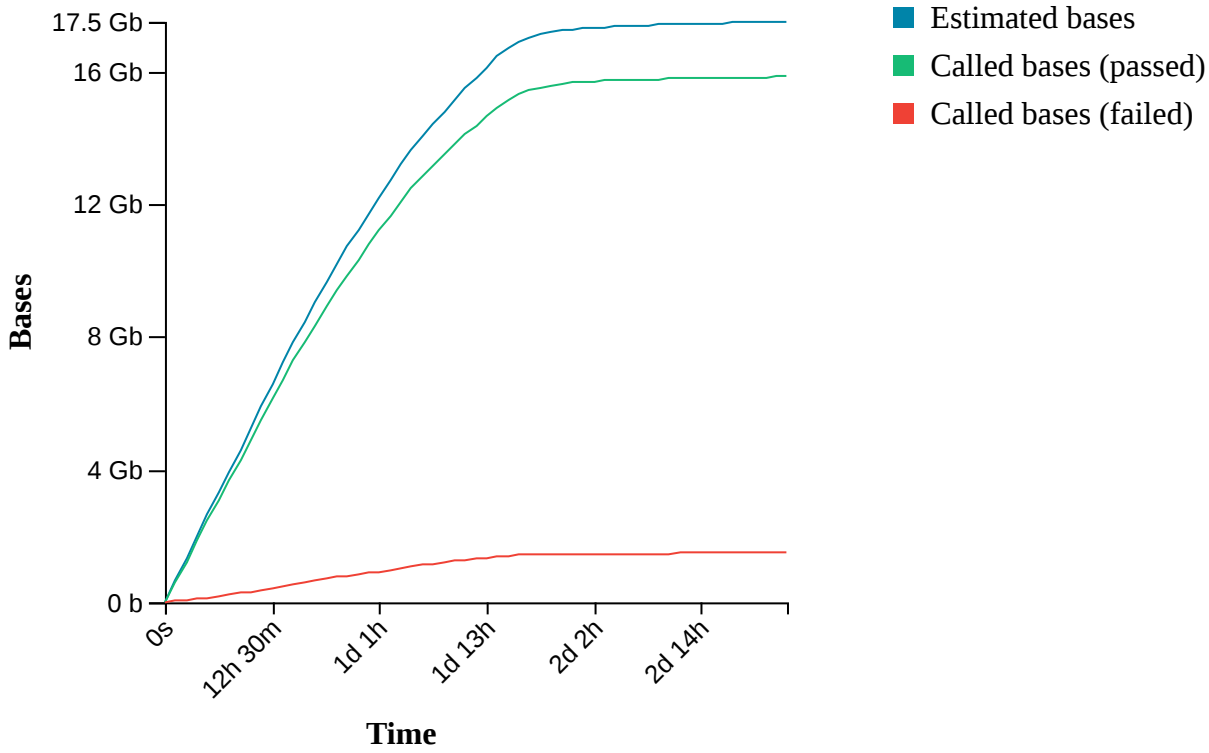
Versions

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

Cumulative Output Reads

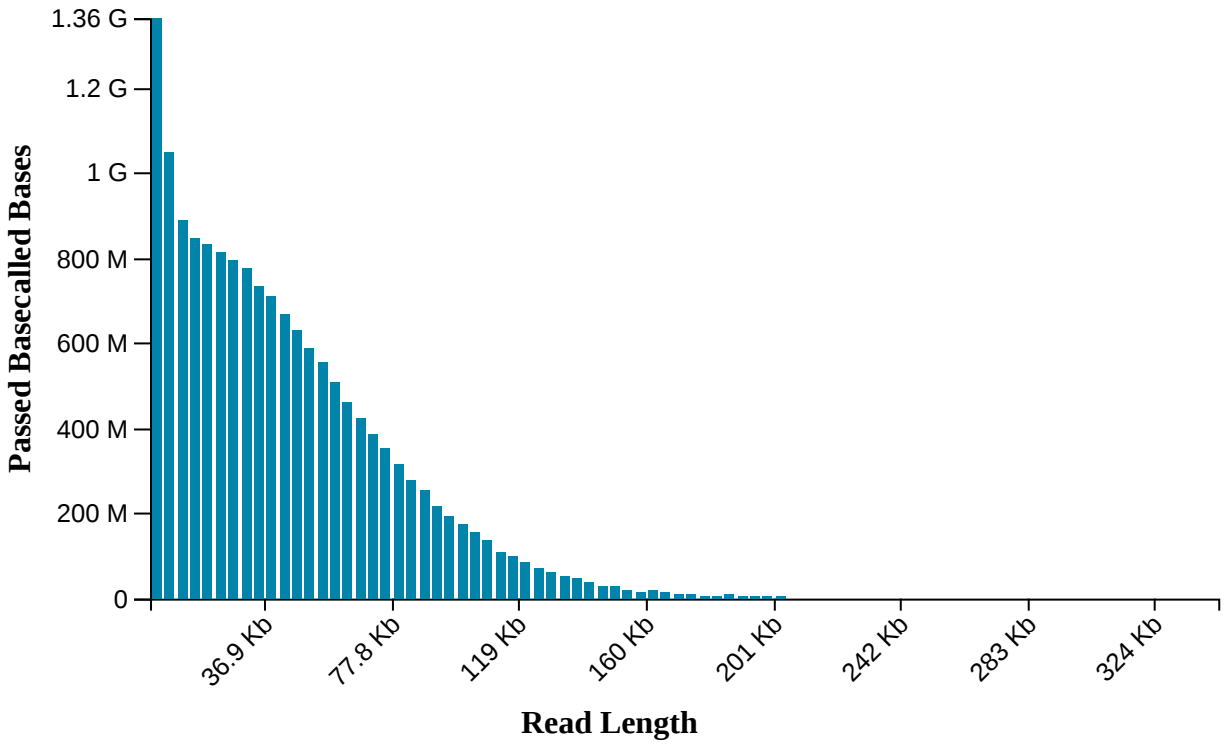


Cumulative Output Bases



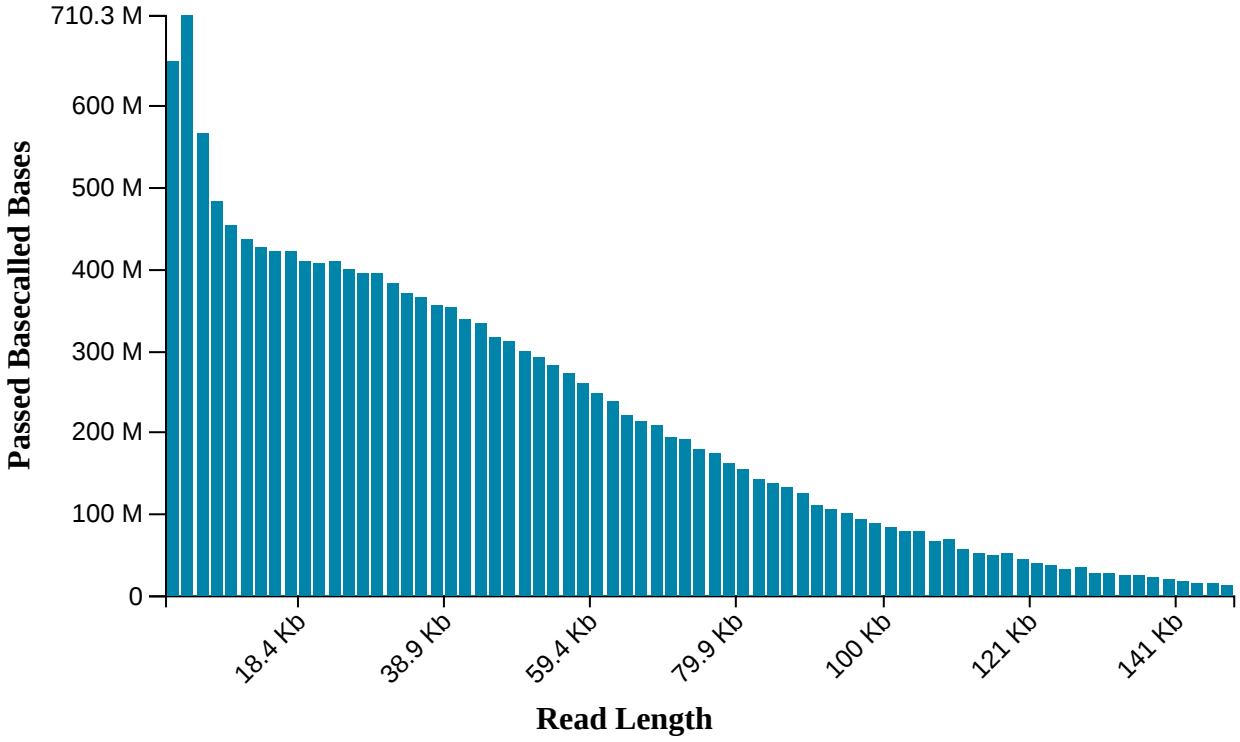
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 35.89 K



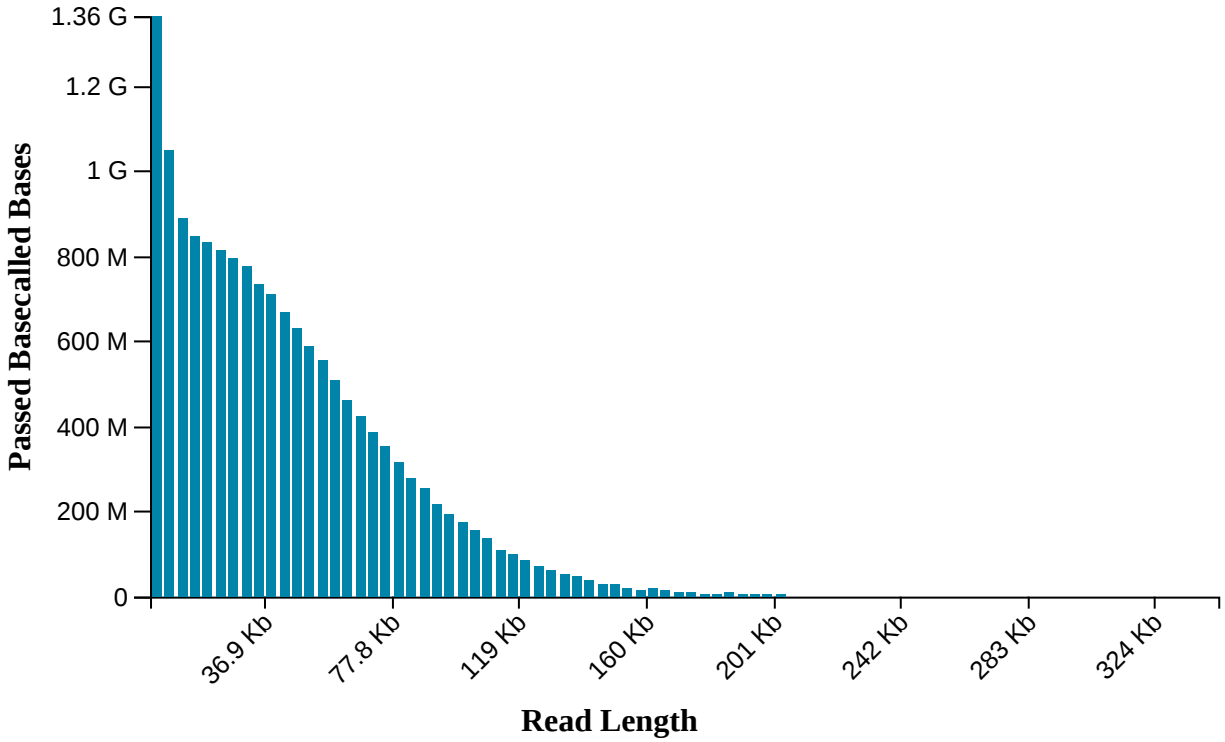
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 35.46 K



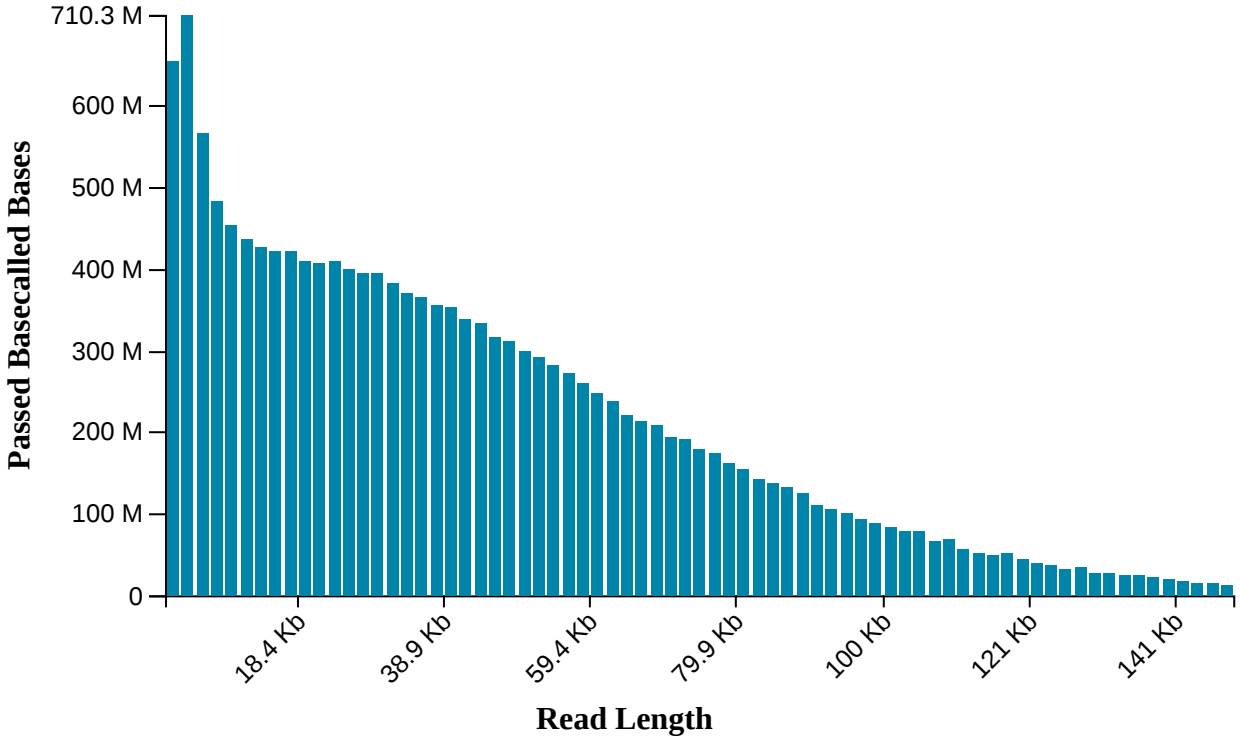
Read Length Histogram Estimated Bases

Estimated N50: 35.89 K

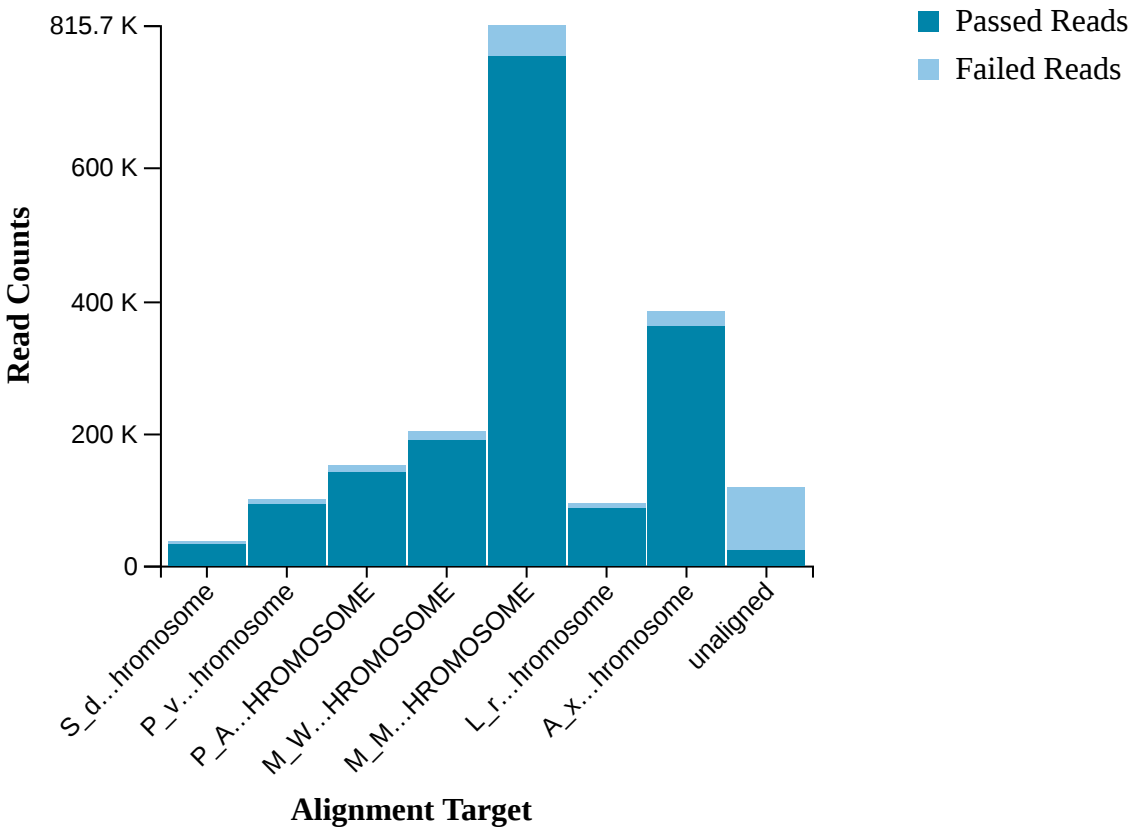


Read Length Histogram Basecalled Bases

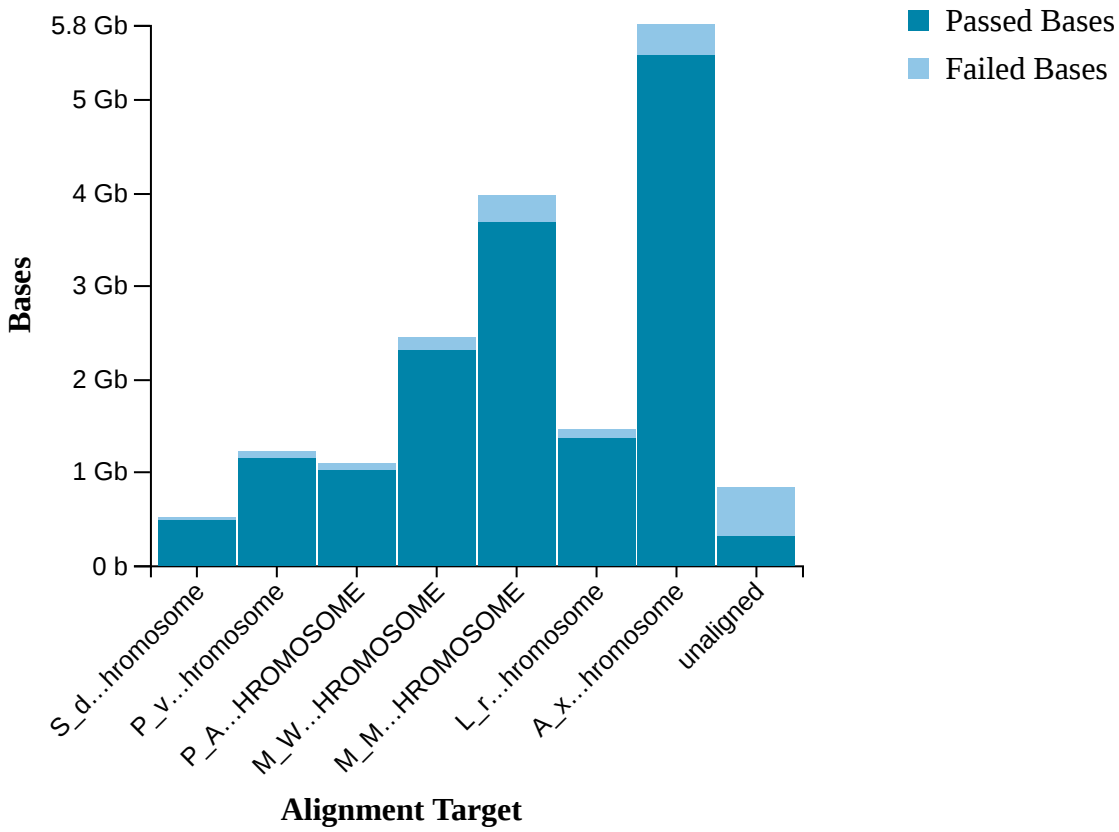
Estimated N50: 35.46 K



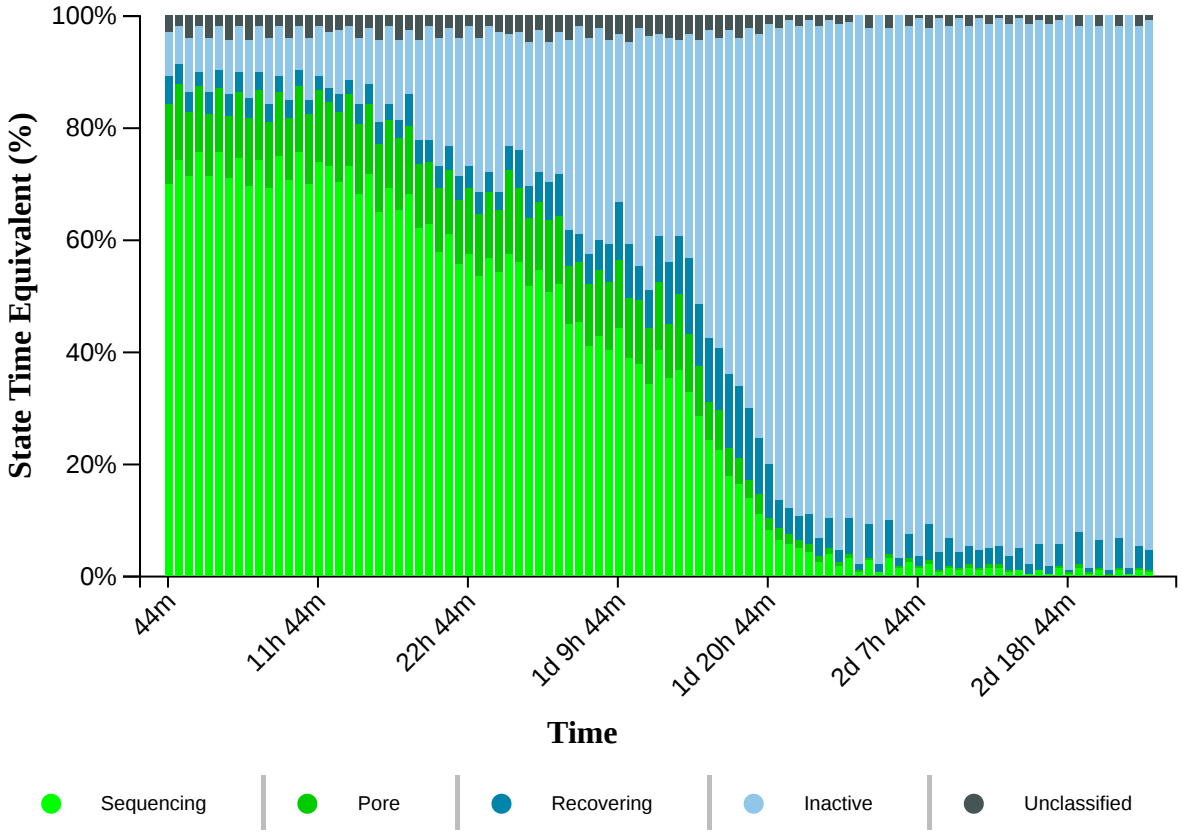
Alignment Target Hits (reads)



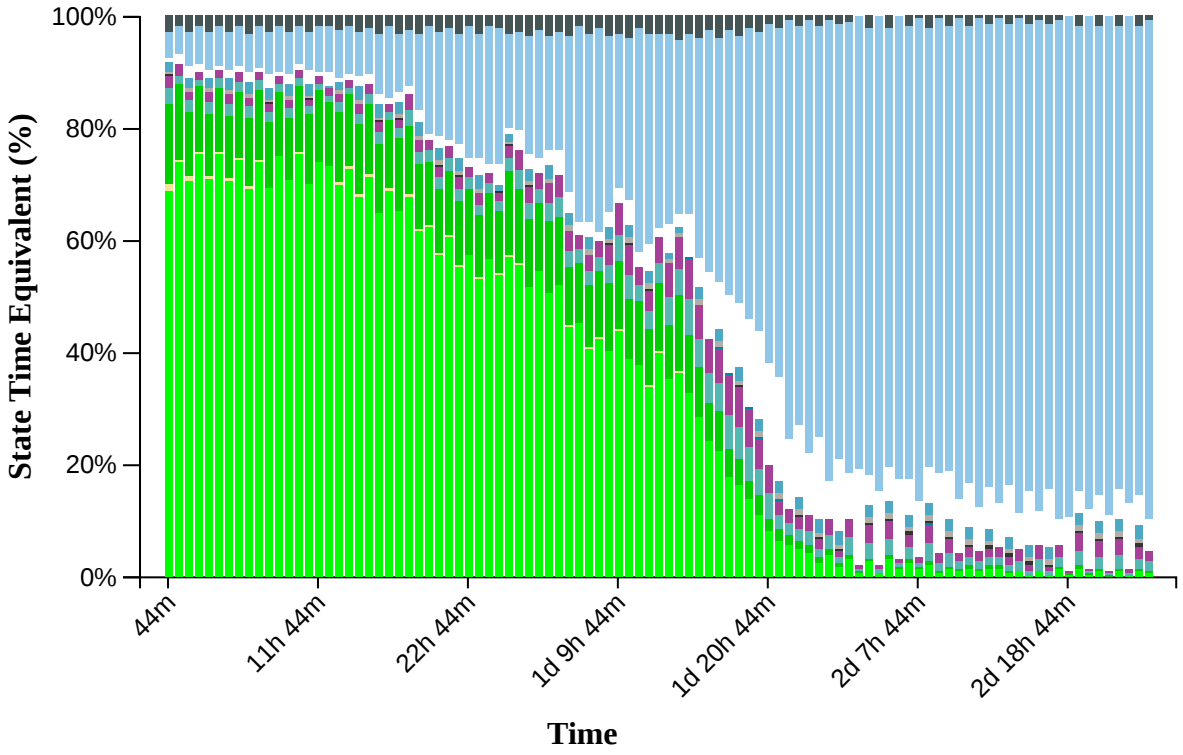
Alignment Target Hits (bases)



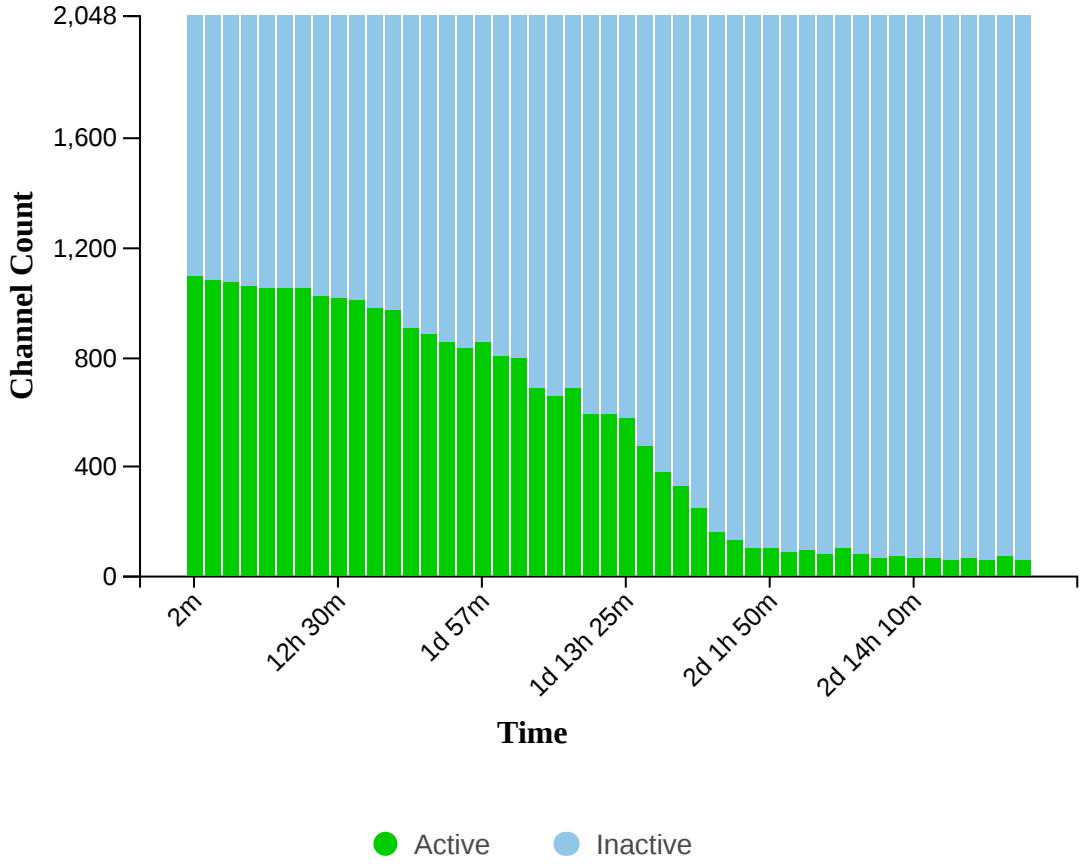
Duty Time Grouped



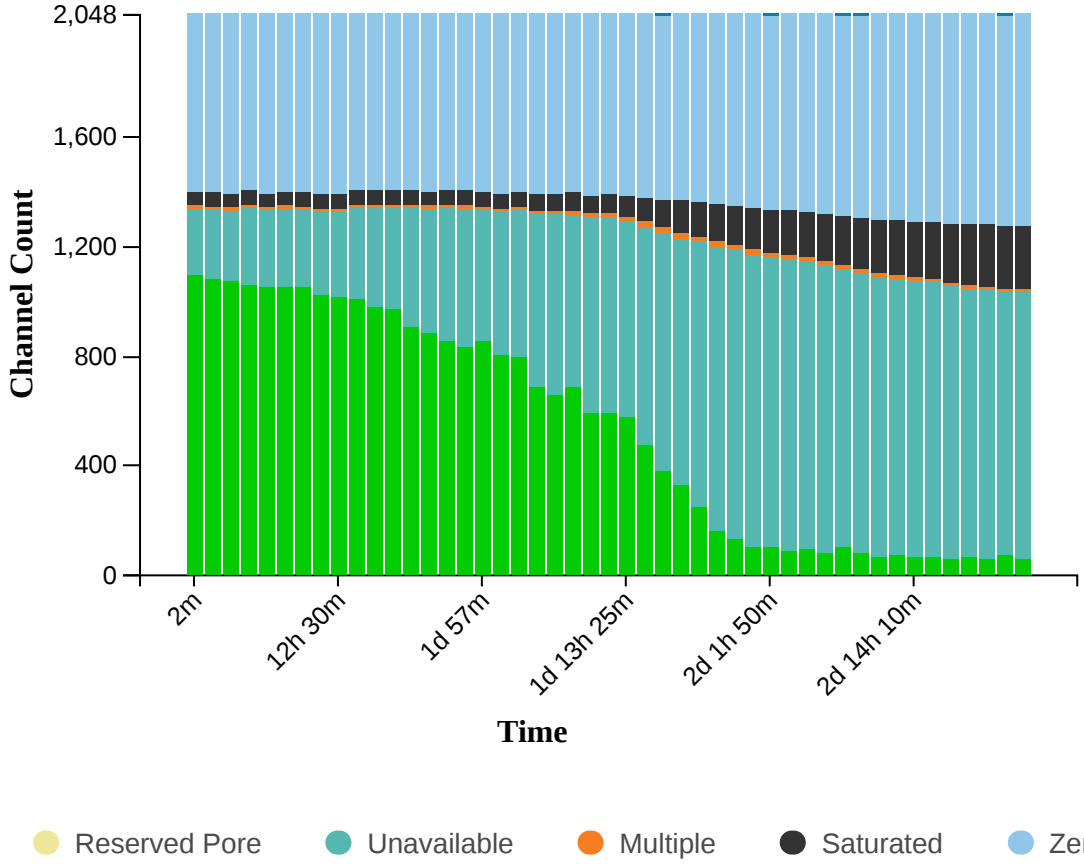
Duty time Categorised



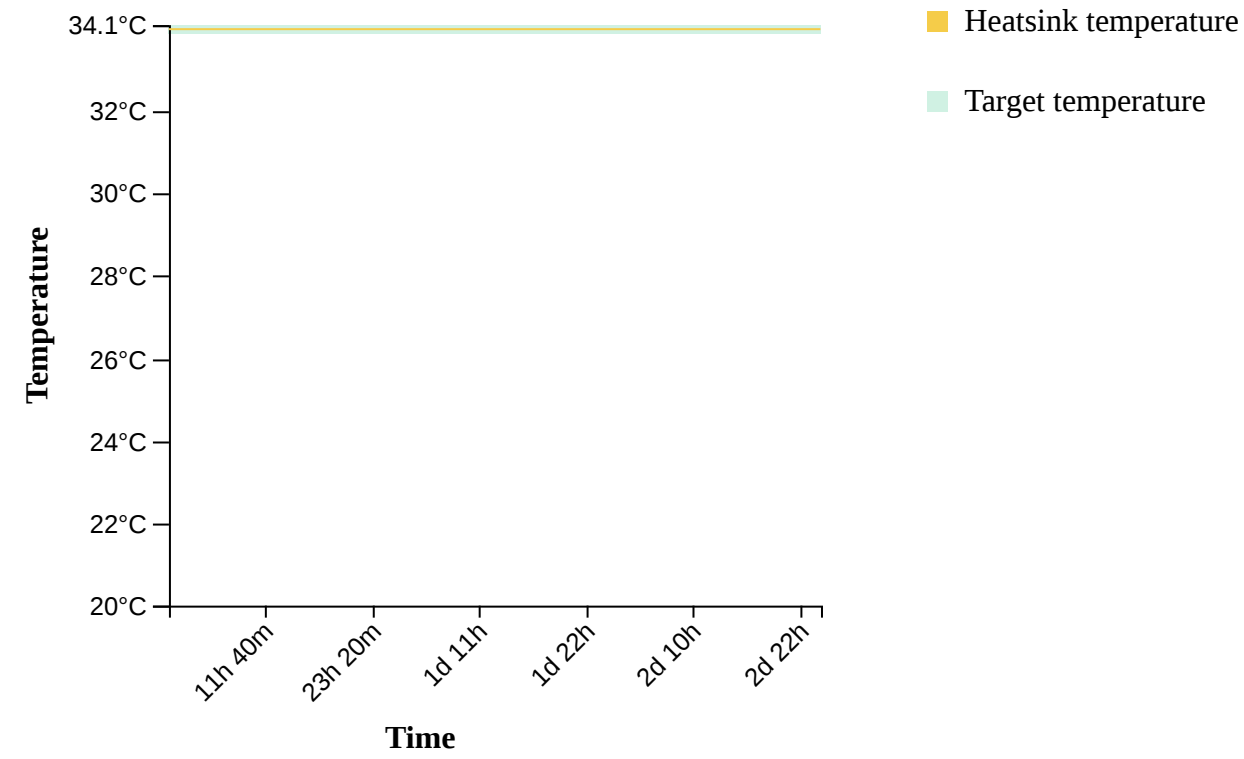
Mux Scan Grouped



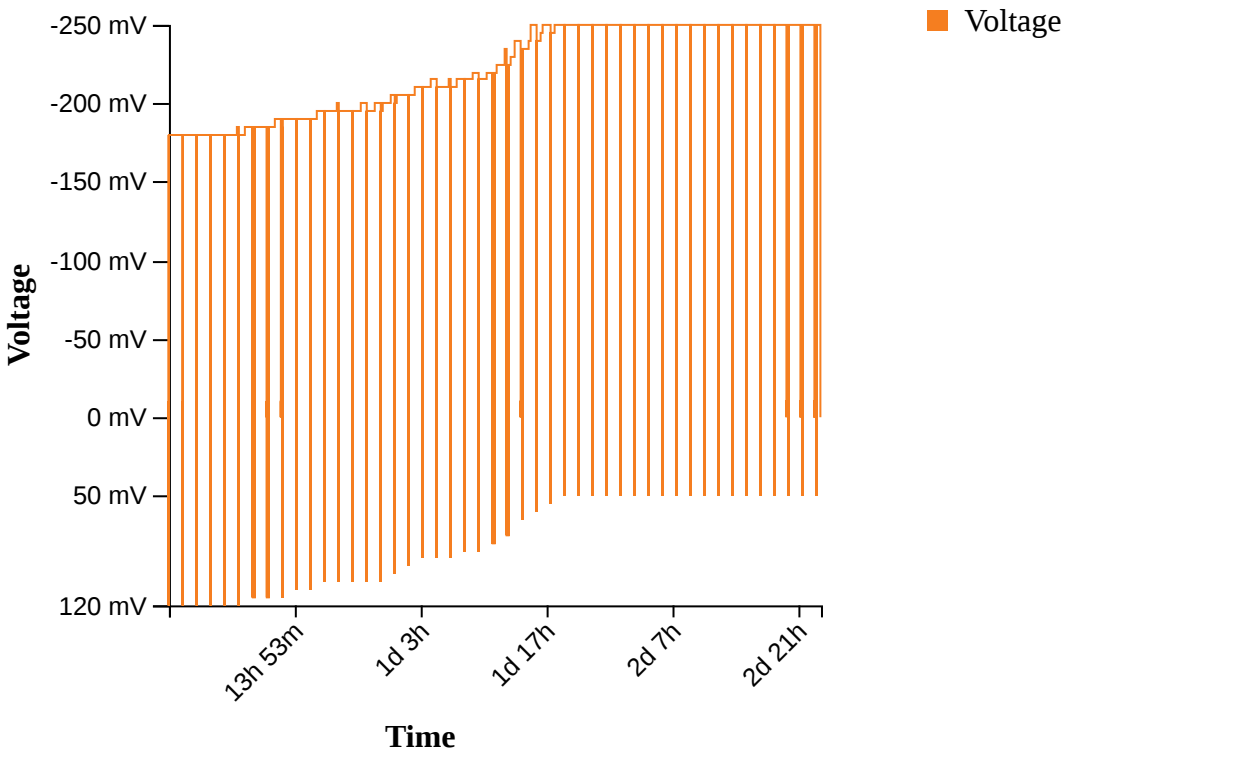
Mux Scan Categorised



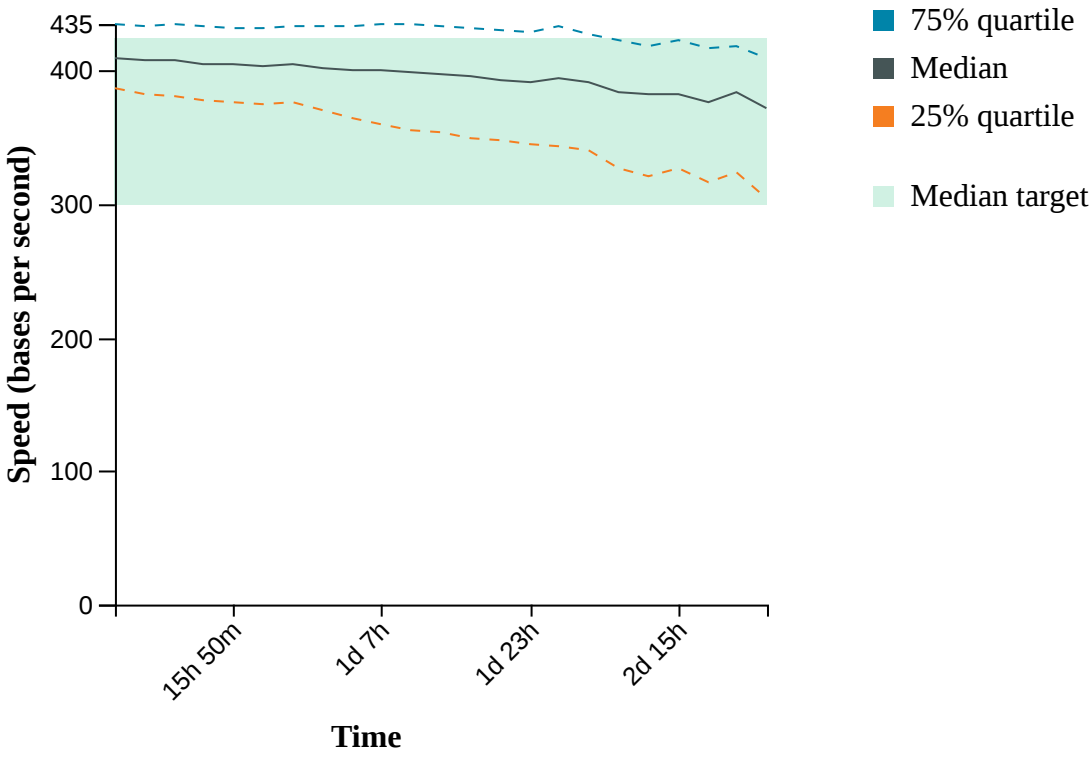
Temperature History



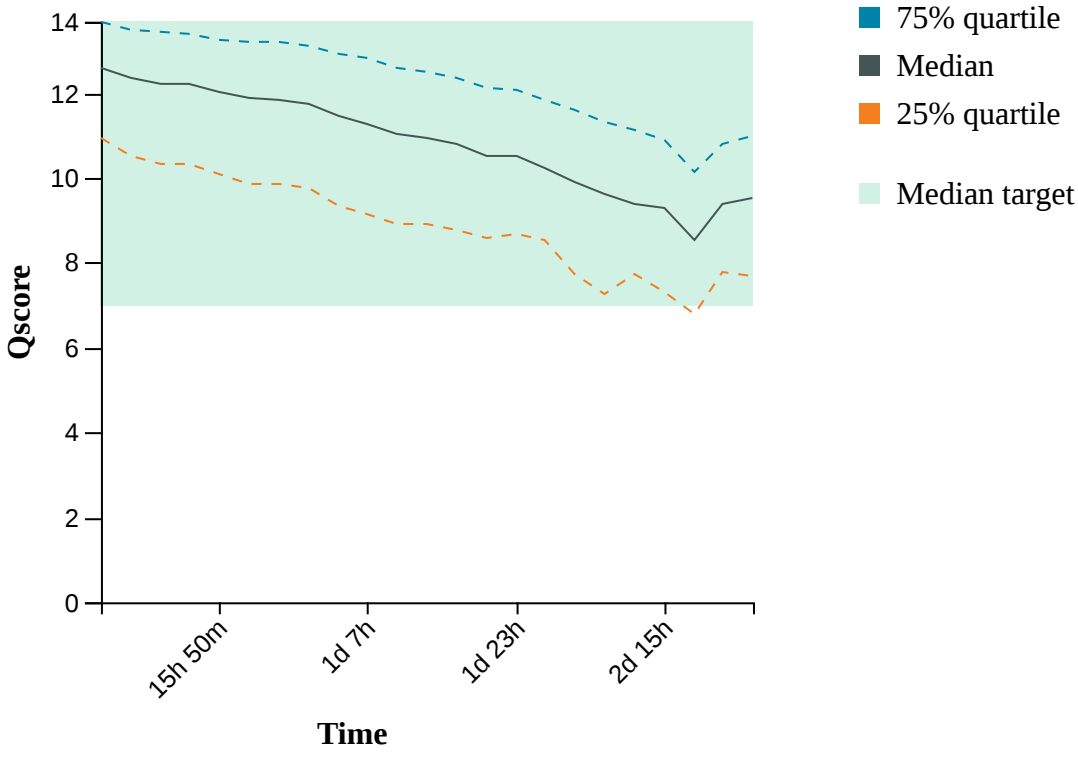
Bias Voltage History



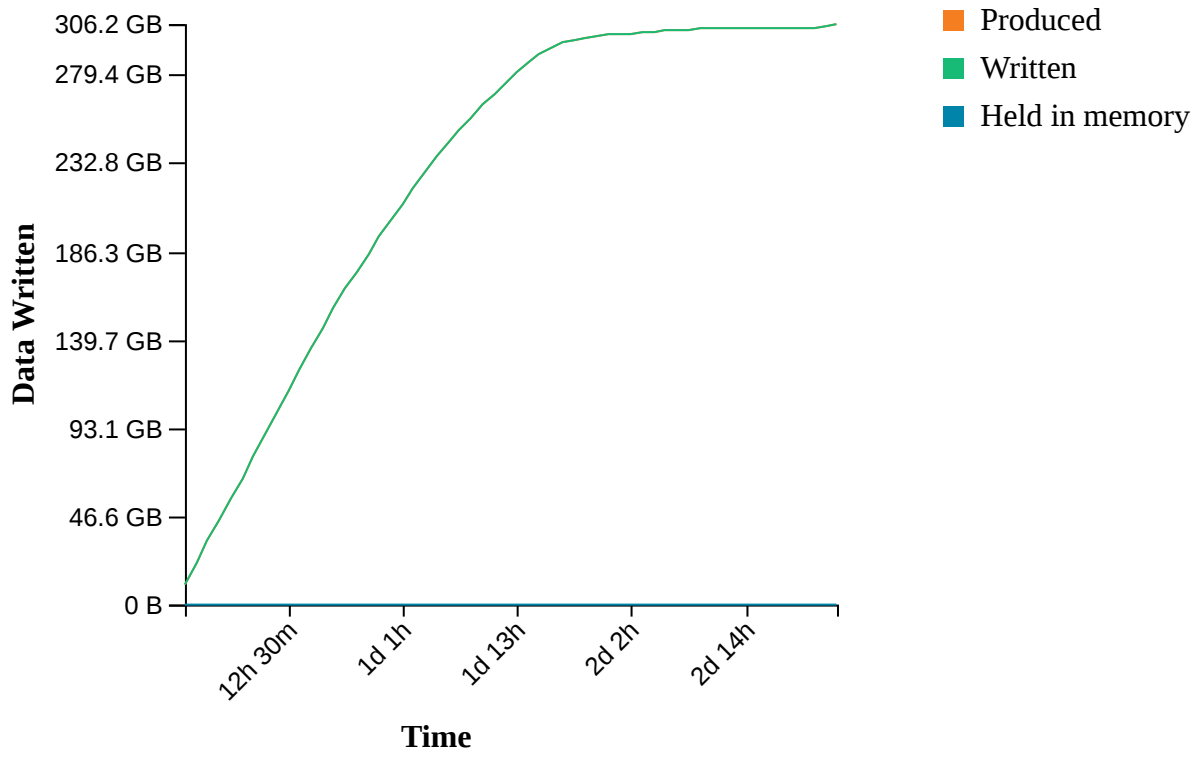
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- The sequencing run has finished, but basecalling may continue April 18, 10:56
- Mux scan for flow cell FAP14879 has found a total of 57 pores. 55 pores available for immediate sequencing April 18, 10:21
- Performing Mux Scan April 18, 10:19
- Mux scan for flow cell FAP14879 has found a total of 70 pores. 68 pores available for immediate sequencing April 18, 08:49
- Performing Mux Scan April 18, 08:46
- Mux scan for flow cell FAP14879 has found a total of 61 pores. 58 pores available for immediate sequencing April 18, 07:16
- Performing Mux Scan April 18, 07:14
- Mux scan for flow cell FAP14879 has found a total of 65 pores. 63 pores available for immediate sequencing April 18, 05:44
- Performing Mux Scan April 18, 05:41
- Mux scan for flow cell FAP14879 has found a total of 61 pores. 56 pores available for immediate sequencing April 18, 04:11
- Performing Mux Scan April 18, 04:09
- Mux scan for flow cell FAP14879 has found a total of 67 pores. 63 pores available for immediate sequencing April 18, 02:39
- Performing Mux Scan April 18, 02:36
- Mux scan for flow cell FAP14879 has found a total of 63 pores. 61 pores available for immediate sequencing April 18, 01:06
- Performing Mux Scan April 18, 01:04
- Mux scan for flow cell FAP14879 has found a total of 75 pores. 70 pores available for immediate sequencing April 17, 23:34
- Performing Mux Scan April 17, 23:32
- Mux scan for flow cell FAP14879 has found a total of 67 pores. 65 pores available for immediate sequencing April 17, 22:02
- Performing Mux Scan April 17, 21:59
- Mux scan for flow cell FAP14879 has found a total of 78 pores. 73 pores available for immediate sequencing April 17, 20:29
- Performing Mux Scan April 17, 20:27
- Mux scan for flow cell FAP14879 has found a total of 101 pores. 97 pores available for immediate sequencing April 17, 18:57
- Performing Mux Scan April 17, 18:54
- Mux scan for flow cell FAP14879 has found a total of 78 pores. 71 pores available for immediate sequencing April 17, 17:24
- Performing Mux Scan April 17, 17:22
- Mux scan for flow cell FAP14879 has found a total of 93 pores. 90 pores available for immediate sequencing April 17, 15:52
- Performing Mux Scan April 17, 15:49
- Mux scan for flow cell FAP14879 has found a total of 85 pores. 79 pores available for immediate sequencing April 17, 14:19
- Performing Mux Scan April 17, 14:17
- Mux scan for flow cell FAP14879 has found a total of 103 pores. 99 pores available for immediate sequencing April 17, 12:47
- Performing Mux Scan April 17, 12:44
- Mux scan for flow cell FAP14879 has found a total of 100 pores. 92 pores available for immediate sequencing April 17, 11:14
- Performing Mux Scan April 17, 11:12

- Mux scan for flow cell FAP14879 has found a total of 130 pores. 118 pores available for immediate sequencing April 17, 09:42
- Performing Mux Scan April 17, 09:40
- Mux scan for flow cell FAP14879 has found a total of 160 pores. 131 pores available for immediate sequencing April 17, 08:09
- Performing Mux Scan April 17, 08:06
- Mux scan for flow cell FAP14879 has found a total of 251 pores. 202 pores available for immediate sequencing April 17, 06:36
- Performing Mux Scan April 17, 06:33
- Mux scan for flow cell FAP14879 has found a total of 328 pores. 246 pores available for immediate sequencing April 17, 05:02
- Performing Mux Scan April 17, 05:00
- Mux scan for flow cell FAP14879 has found a total of 381 pores. 271 pores available for immediate sequencing April 17, 03:29
- Performing Mux Scan April 17, 03:26
- Mux scan for flow cell FAP14879 has found a total of 472 pores. 292 pores available for immediate sequencing April 17, 01:55
- Performing Mux Scan April 17, 01:53
- Mux scan for flow cell FAP14879 has found a total of 581 pores. 348 pores available for immediate sequencing April 17, 00:22
- Performing Mux Scan April 17, 00:19
- Mux scan for flow cell FAP14879 has found a total of 596 pores. 334 pores available for immediate sequencing April 16, 22:48
- Performing Mux Scan April 16, 22:46
- Mux scan for flow cell FAP14879 has found a total of 592 pores. 306 pores available for immediate sequencing April 16, 21:15
- Performing Mux Scan April 16, 21:12
- Mux scan for flow cell FAP14879 has found a total of 691 pores. 372 pores available for immediate sequencing April 16, 19:41
- Performing Mux Scan April 16, 19:39
- Mux scan for flow cell FAP14879 has found a total of 658 pores. 326 pores available for immediate sequencing April 16, 18:08
- Performing Mux Scan April 16, 18:05
- Mux scan for flow cell FAP14879 has found a total of 688 pores. 333 pores available for immediate sequencing April 16, 16:34
- Performing Mux Scan April 16, 16:32
- Mux scan for flow cell FAP14879 has found a total of 794 pores. 404 pores available for immediate sequencing April 16, 15:01
- Performing Mux Scan April 16, 14:59
- Mux scan for flow cell FAP14879 has found a total of 806 pores. 394 pores available for immediate sequencing April 16, 13:28
- Performing Mux Scan April 16, 13:25
- Mux scan for flow cell FAP14879 has found a total of 856 pores. 422 pores available for immediate sequencing April 16, 11:54
- Performing Mux Scan April 16, 11:52
- Mux scan for flow cell FAP14879 has found a total of 835 pores. 386 pores available for immediate sequencing April 16, 10:21
- Performing Mux Scan April 16, 10:18
- Mux scan for flow cell FAP14879 has found a total of 854 pores. 391 pores available for immediate sequencing April 16, 08:47
- Performing Mux Scan April 16, 08:45
- Mux scan for flow cell FAP14879 has found a total of 888 pores. 410 pores available for

immediate sequencing April 16, 07:14

- Performing Mux Scan April 16, 07:11
- Mux scan for flow cell FAP14879 has found a total of 910 pores. 414 pores available for immediate sequencing April 16, 05:40
- Performing Mux Scan April 16, 05:38
- Mux scan for flow cell FAP14879 has found a total of 976 pores. 460 pores available for immediate sequencing April 16, 04:07
- Performing Mux Scan April 16, 04:04
- Mux scan for flow cell FAP14879 has found a total of 980 pores. 447 pores available for immediate sequencing April 16, 02:33
- Performing Mux Scan April 16, 02:31
- Mux scan for flow cell FAP14879 has found a total of 1013 pores. 470 pores available for immediate sequencing April 16, 01:00
- Performing Mux Scan April 16, 00:57
- Mux scan for flow cell FAP14879 has found a total of 1019 pores. 467 pores available for immediate sequencing April 15, 23:26
- Performing Mux Scan April 15, 23:24
- Mux scan for flow cell FAP14879 has found a total of 1021 pores. 470 pores available for immediate sequencing April 15, 21:53
- Performing Mux Scan April 15, 21:51
- Mux scan for flow cell FAP14879 has found a total of 1054 pores. 476 pores available for immediate sequencing April 15, 20:19
- Performing Mux Scan April 15, 20:17
- Mux scan for flow cell FAP14879 has found a total of 1050 pores. 470 pores available for immediate sequencing April 15, 18:46
- Performing Mux Scan April 15, 18:44
- Mux scan for flow cell FAP14879 has found a total of 1051 pores. 473 pores available for immediate sequencing April 15, 17:13
- Performing Mux Scan April 15, 17:10
- Mux scan for flow cell FAP14879 has found a total of 1060 pores. 476 pores available for immediate sequencing April 15, 15:39
- Performing Mux Scan April 15, 15:37
- Mux scan for flow cell FAP14879 has found a total of 1078 pores. 476 pores available for immediate sequencing April 15, 14:06
- Performing Mux Scan April 15, 14:03
- Mux scan for flow cell FAP14879 has found a total of 1081 pores. 477 pores available for immediate sequencing April 15, 12:32
- Performing Mux Scan April 15, 12:30
- Mux scan for flow cell FAP14879 has found a total of 1100 pores. 487 pores available for immediate sequencing April 15, 10:59
- Performing Mux Scan April 15, 10:56
- Starting sequencing procedure April 15, 10:56
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 10:53