Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38kb_MmAxLrDepletion_15042021**
Sample ID	**ReadUntil_38kb_MmAxLrDepletion_15042021**
Run ID	**43533e4d-7255-4e12-bf0b-74bd103465da**
Flow Cell Id	**FAP21642**
Start Time	**April 15, 12:10**
Run Length	**3d 0h 3m**

Run Summary

Reads Generated	**2.69 M**
Passed Bases	**14.05 Gb**
Failed Bases	**1.77 Gb**
Estimated Bases	**16.14 Gb**

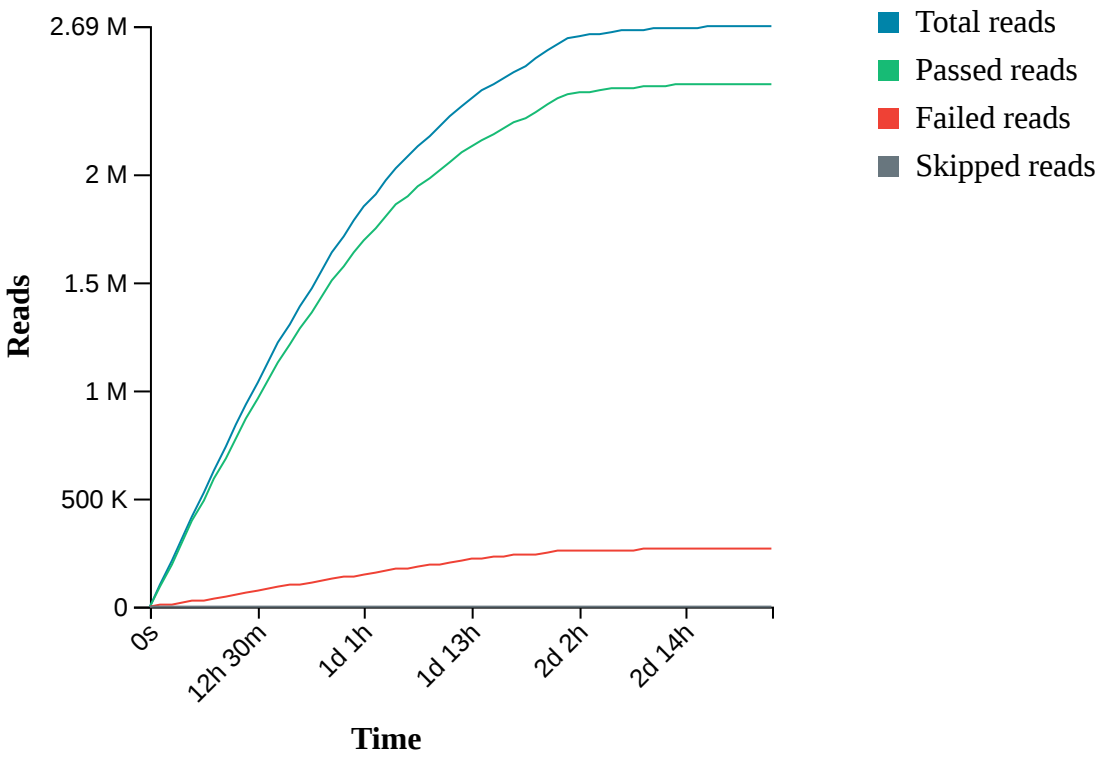
Run Parameters

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/MmAxLr.fa"],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/the7references.fasta"]**
Read Filtering	**min_qscore=7**

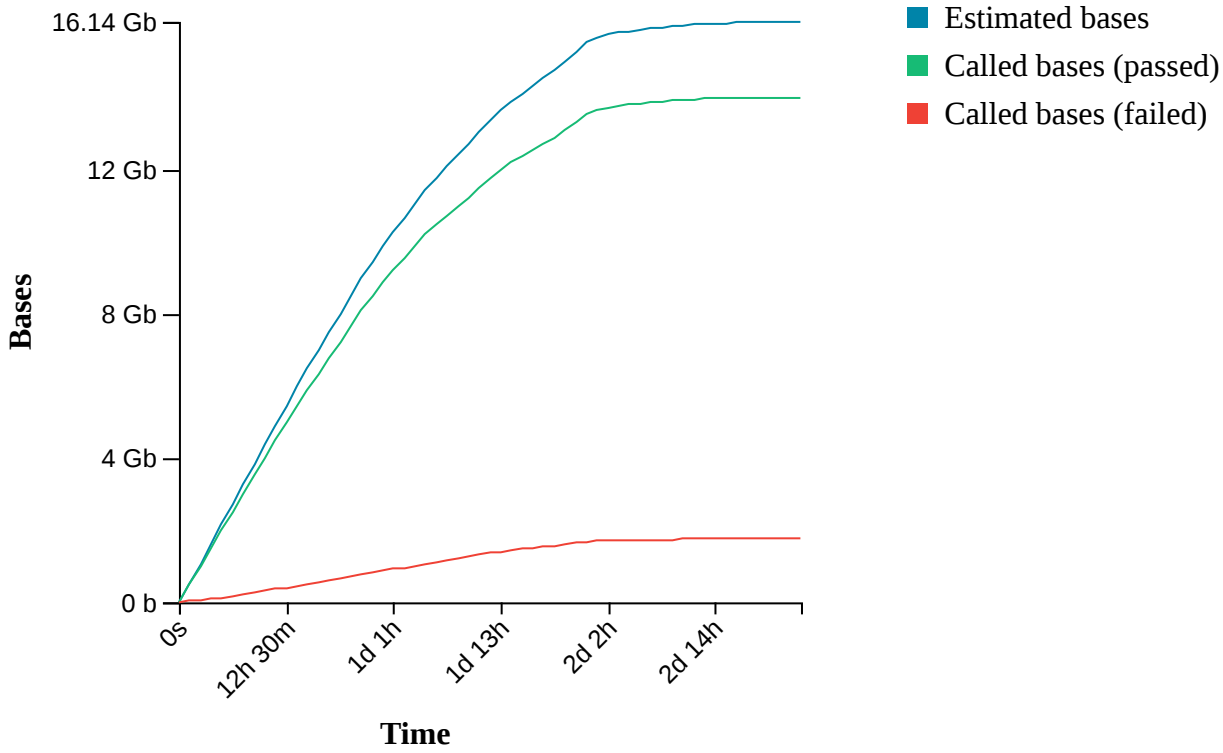
Versions

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

Cumulative Output Reads

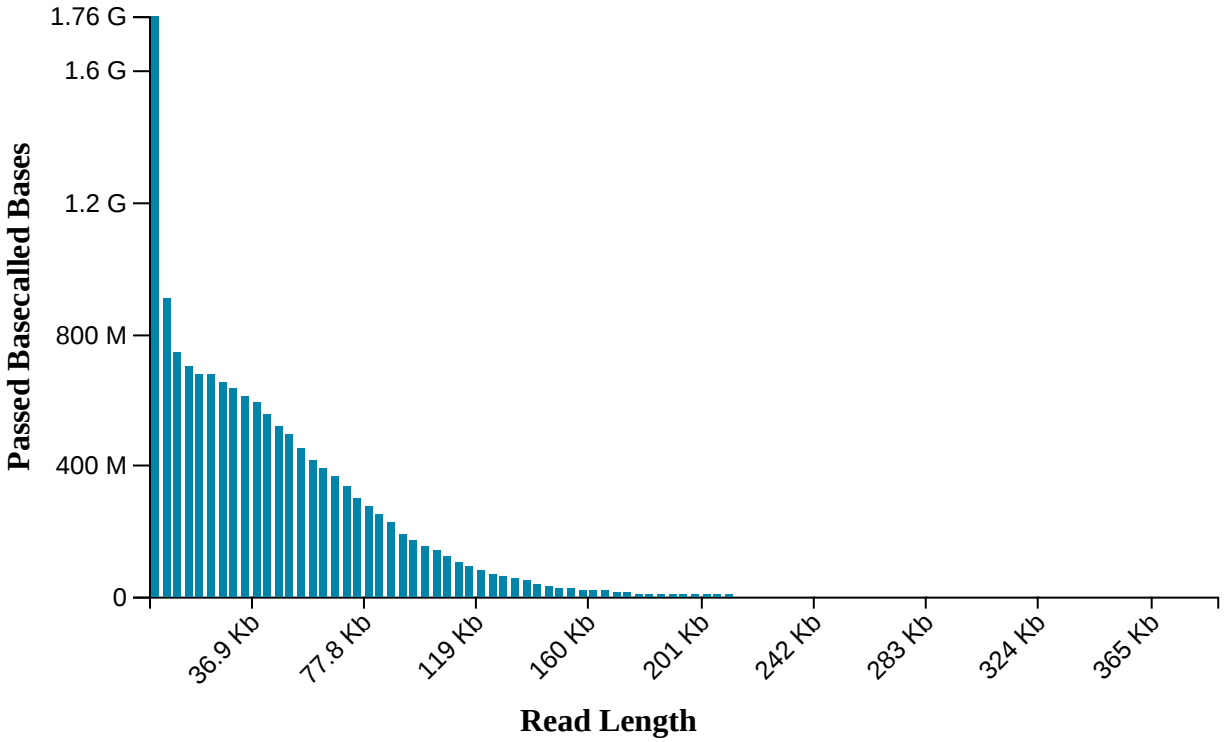


Cumulative Output Bases



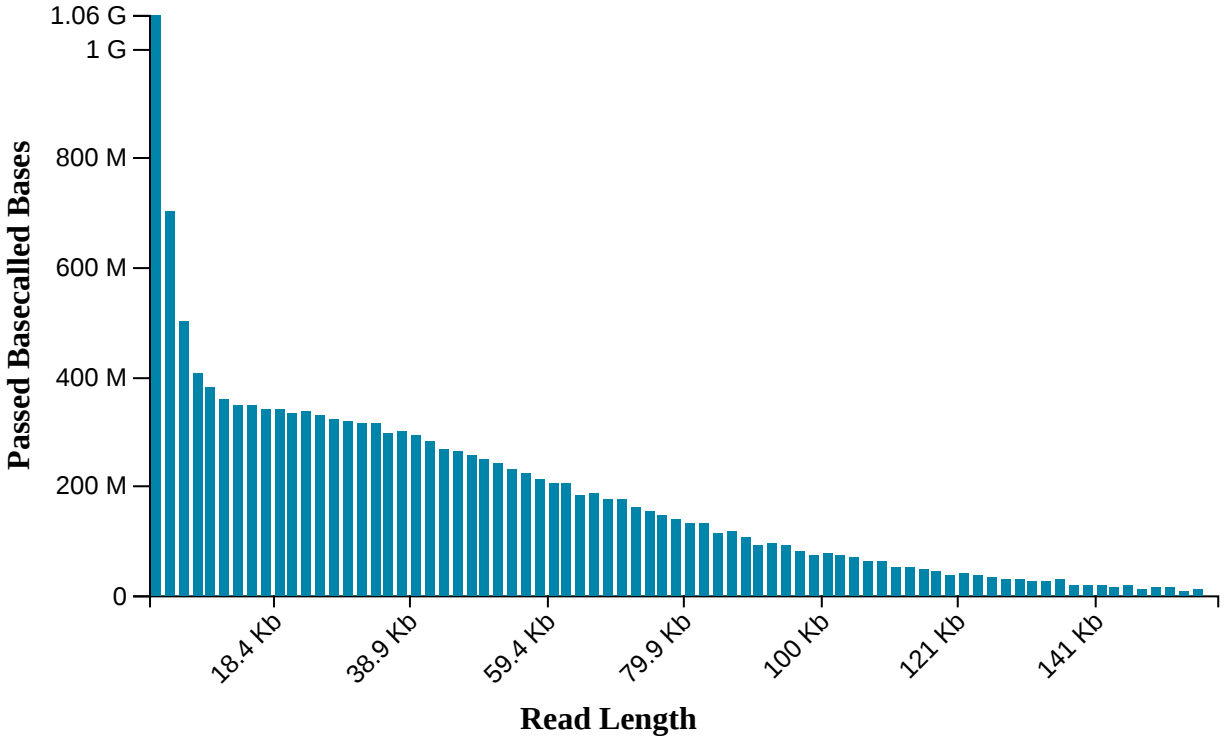
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 34.6 K



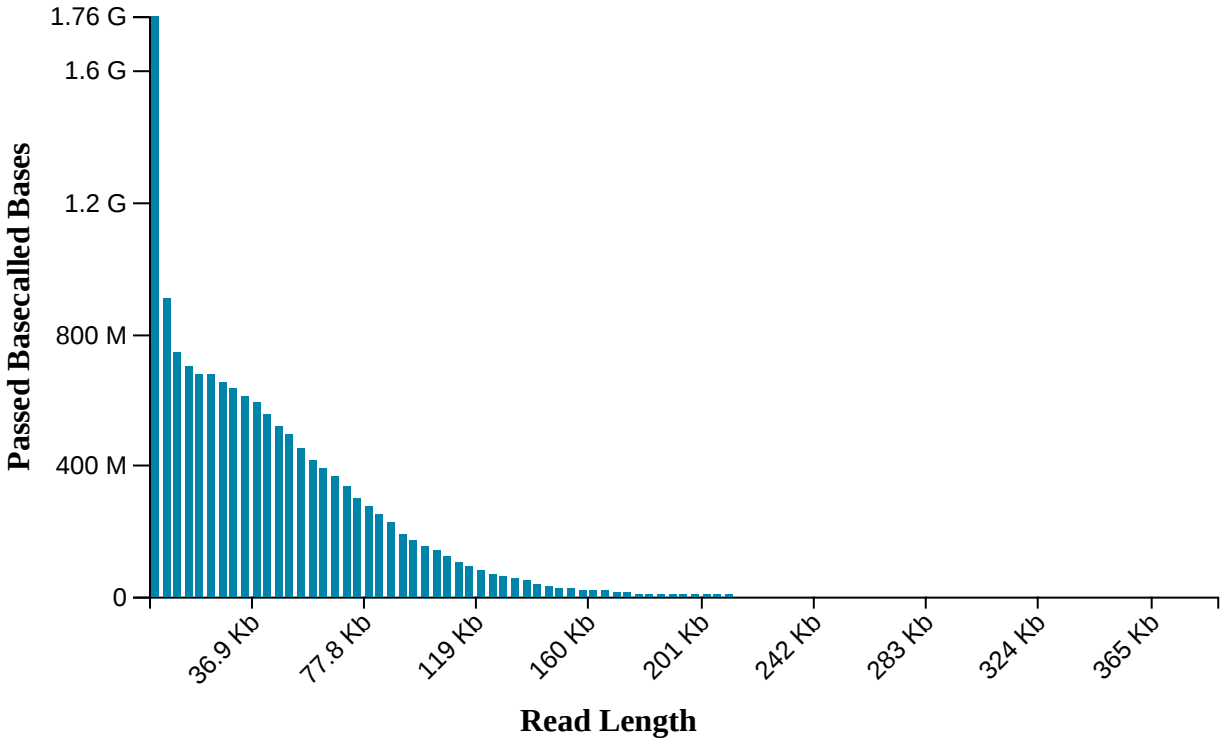
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 34.15 K



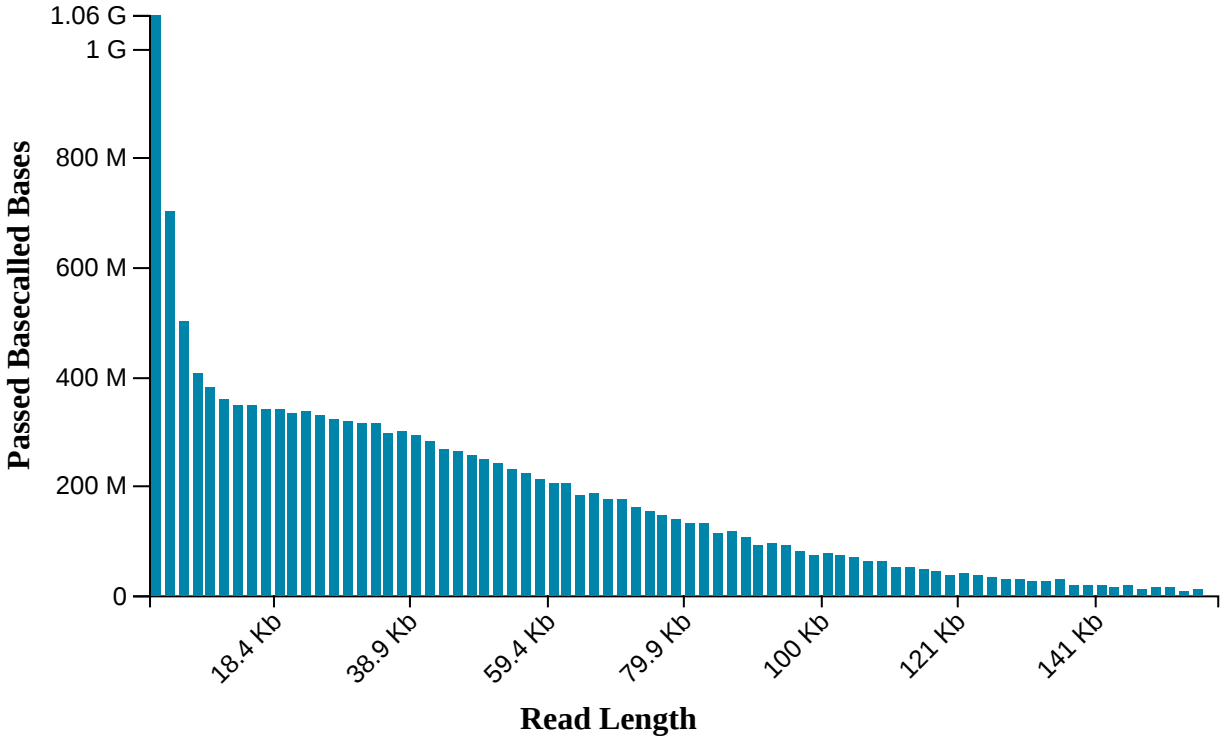
Read Length Histogram Estimated Bases

Estimated N50: 34.6 K

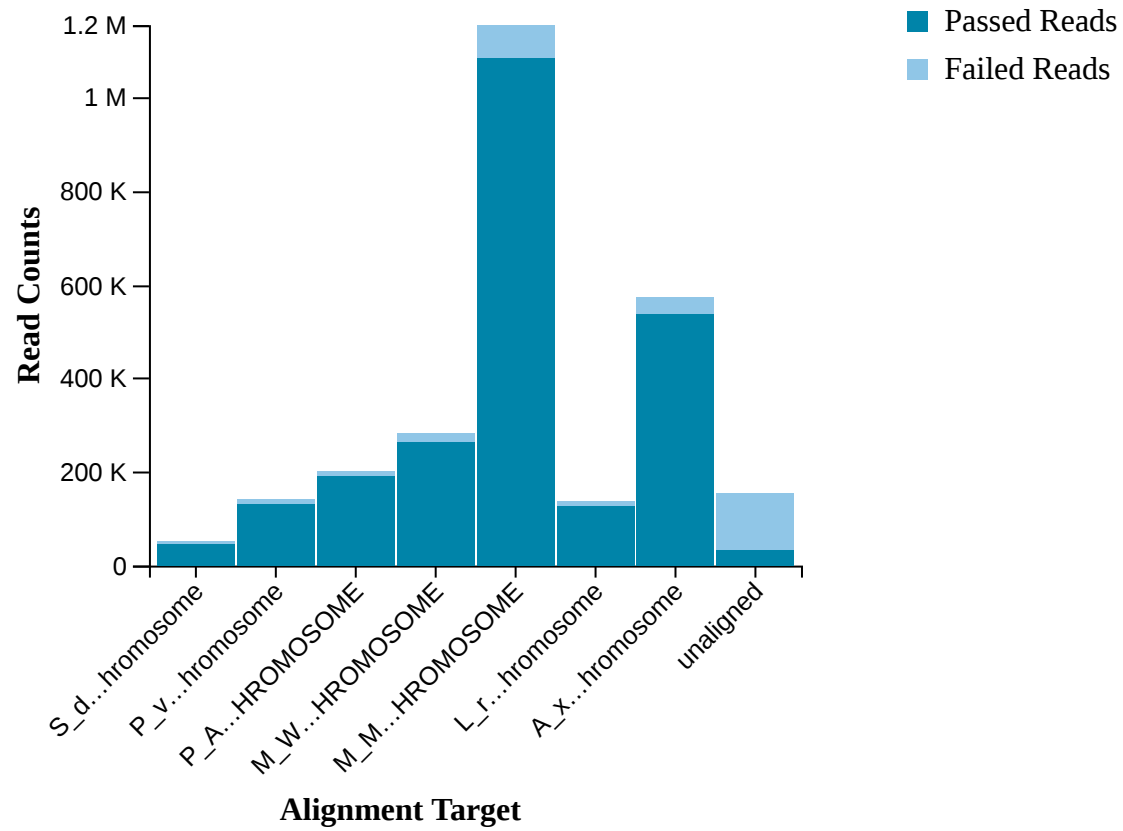


Read Length Histogram Basecalled Bases

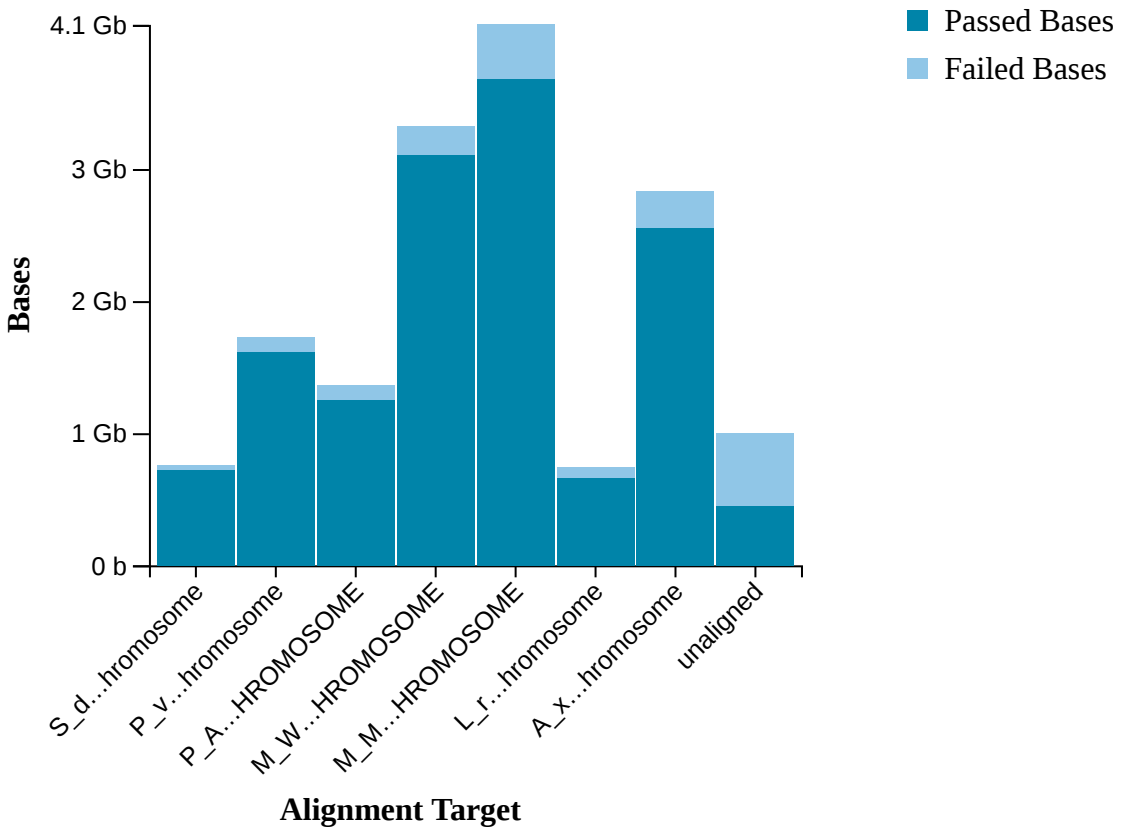
Estimated N50: 34.15 K



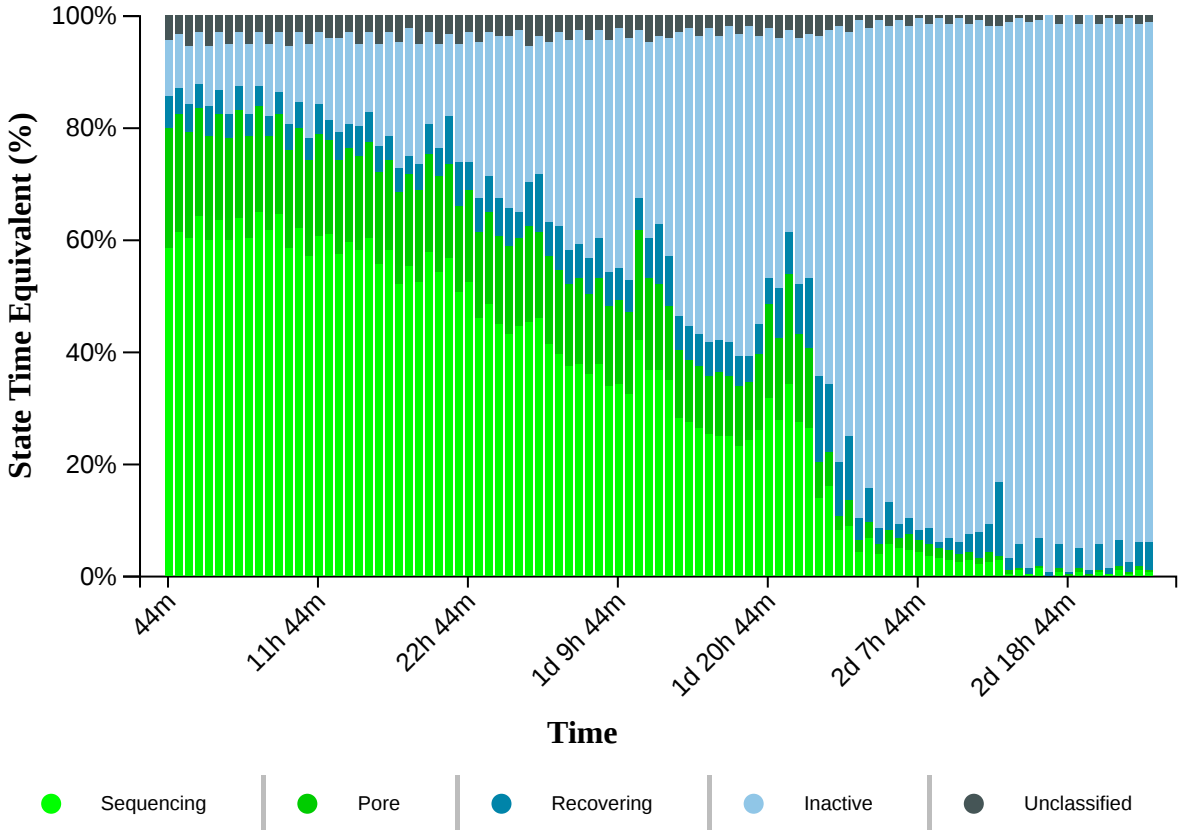
Alignment Target Hits (reads)



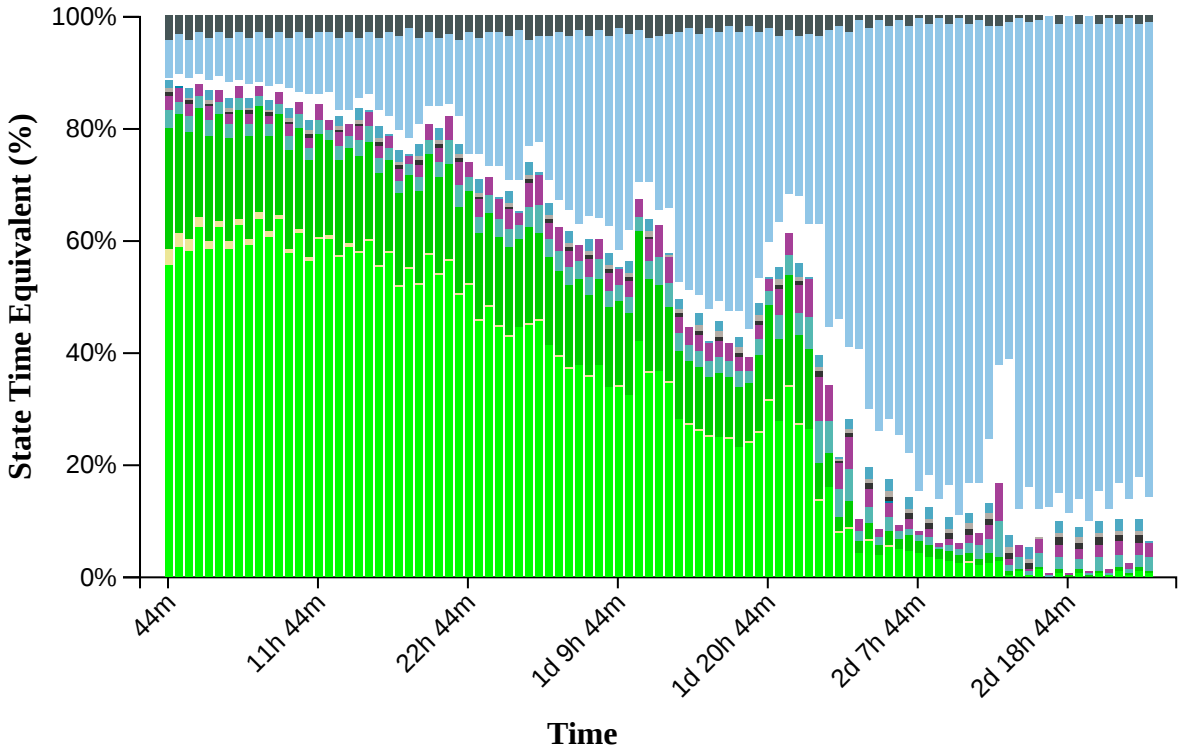
Alignment Target Hits (bases)



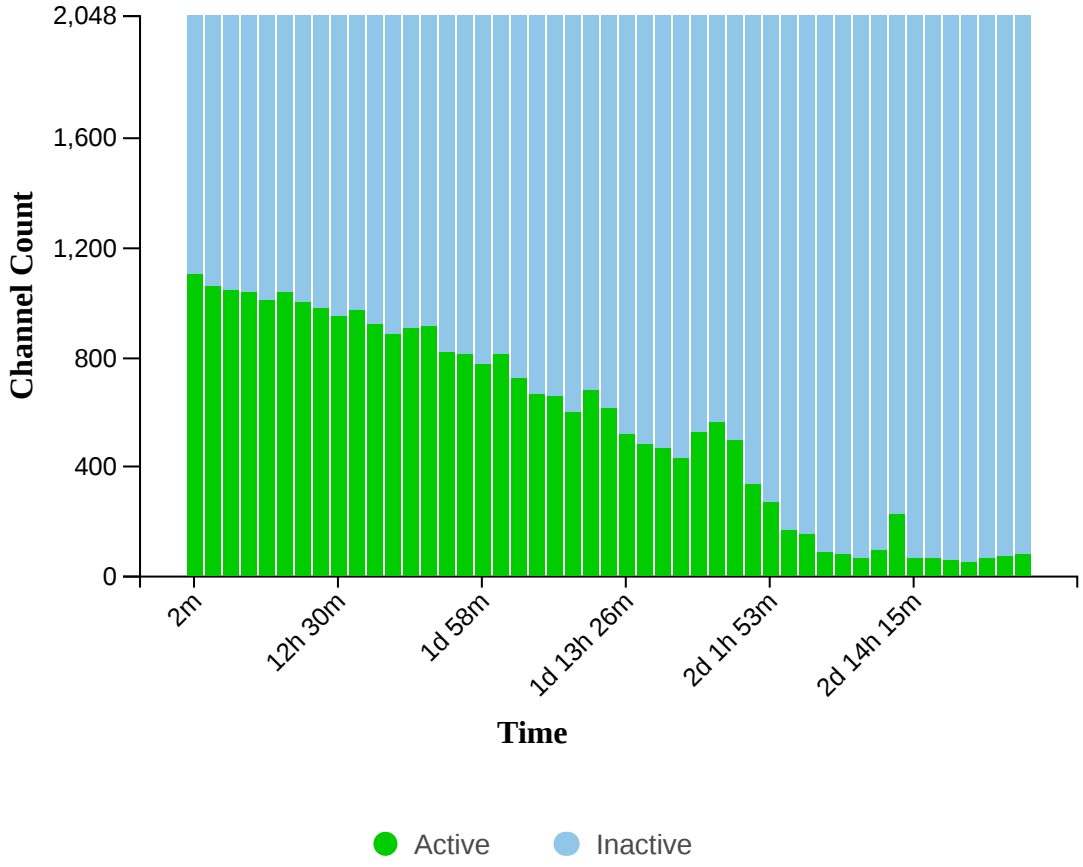
Duty Time Grouped



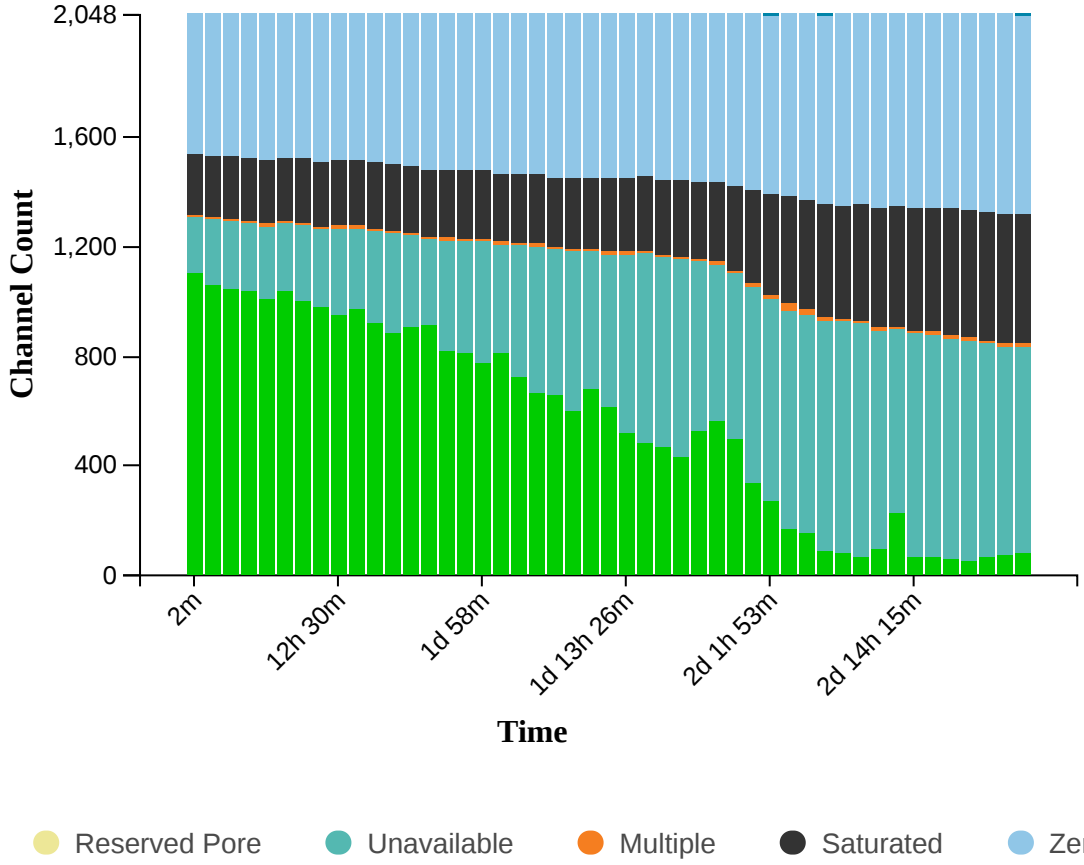
Duty time Categorised



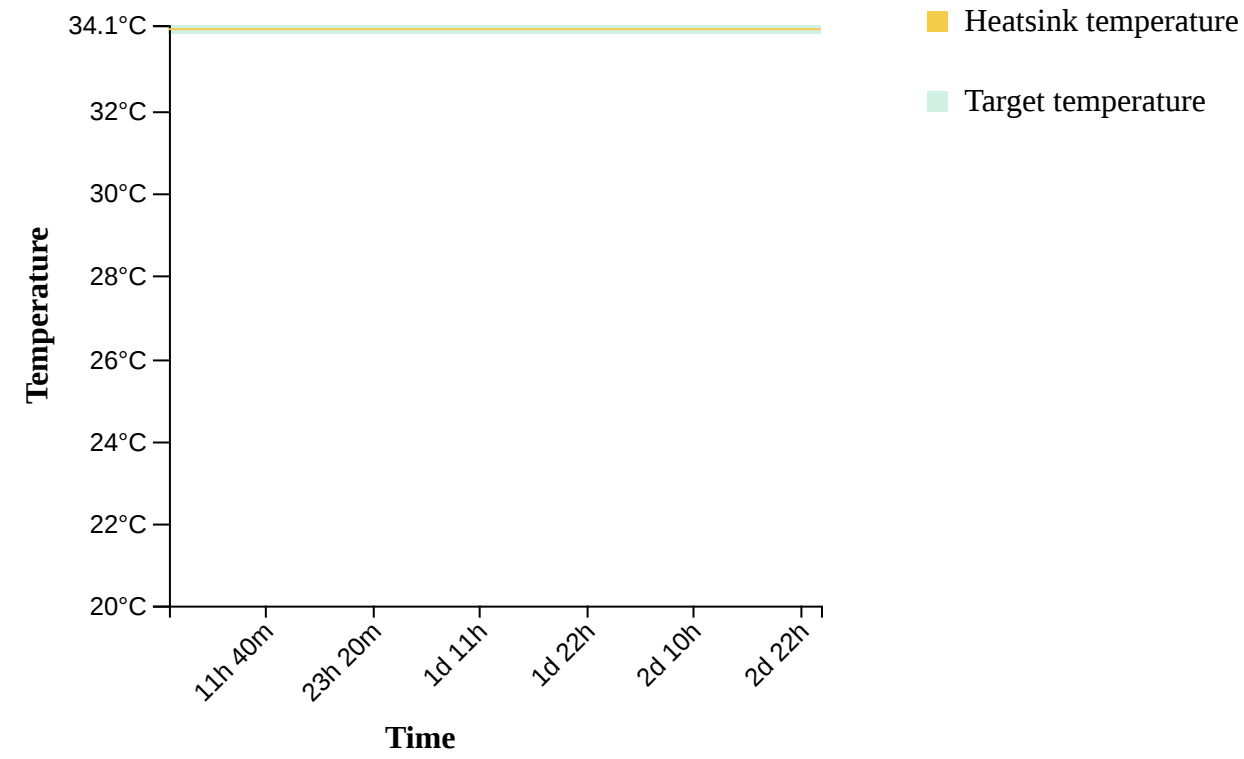
Mux Scan Grouped



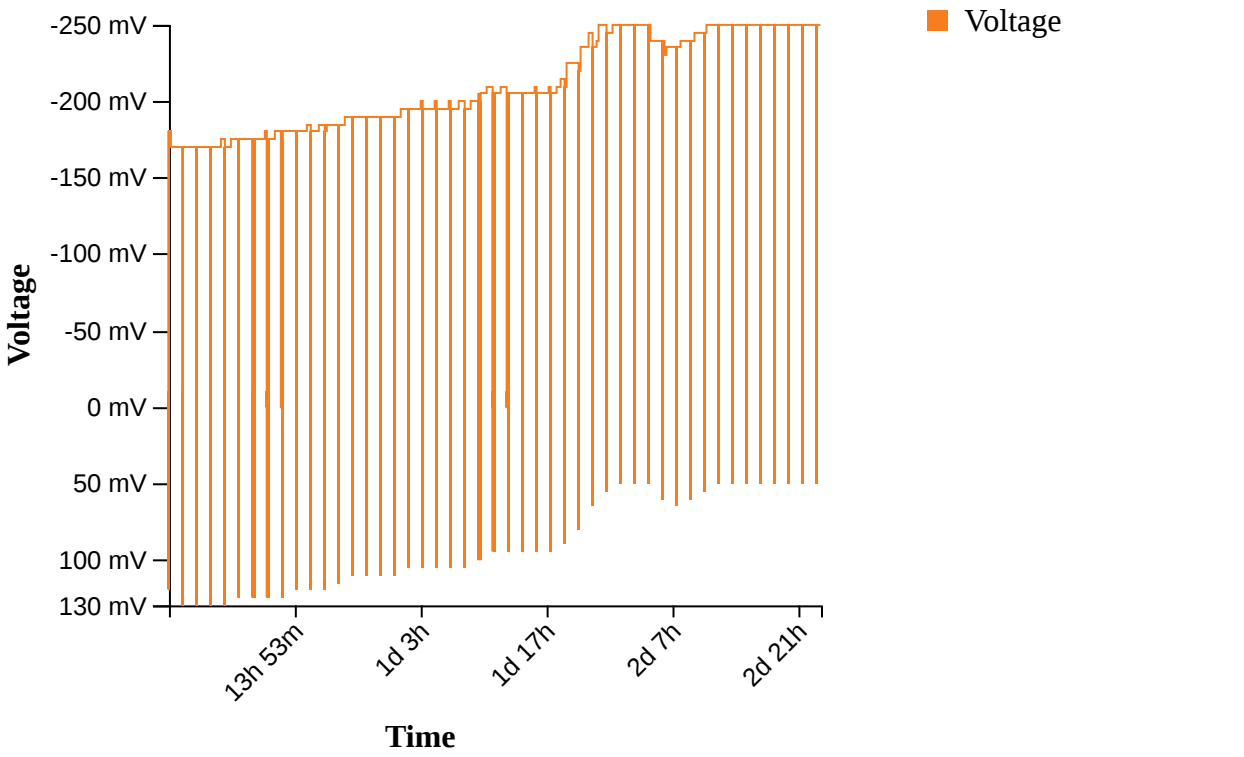
Mux Scan Categorised



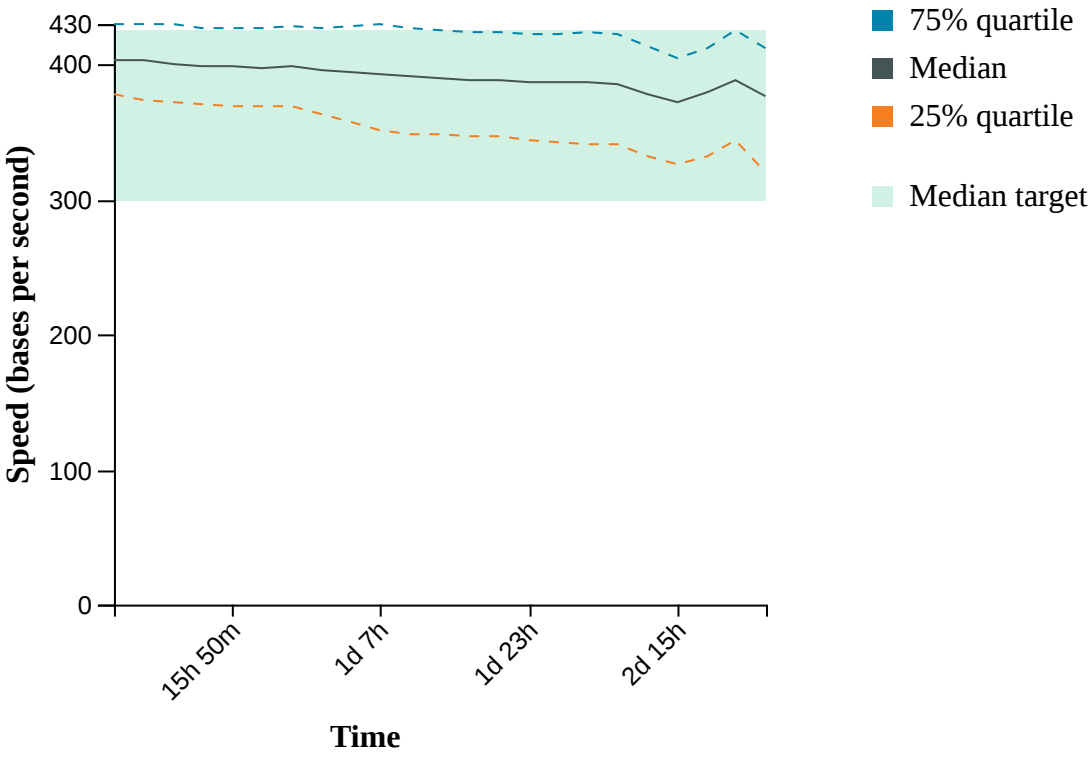
Temperature History



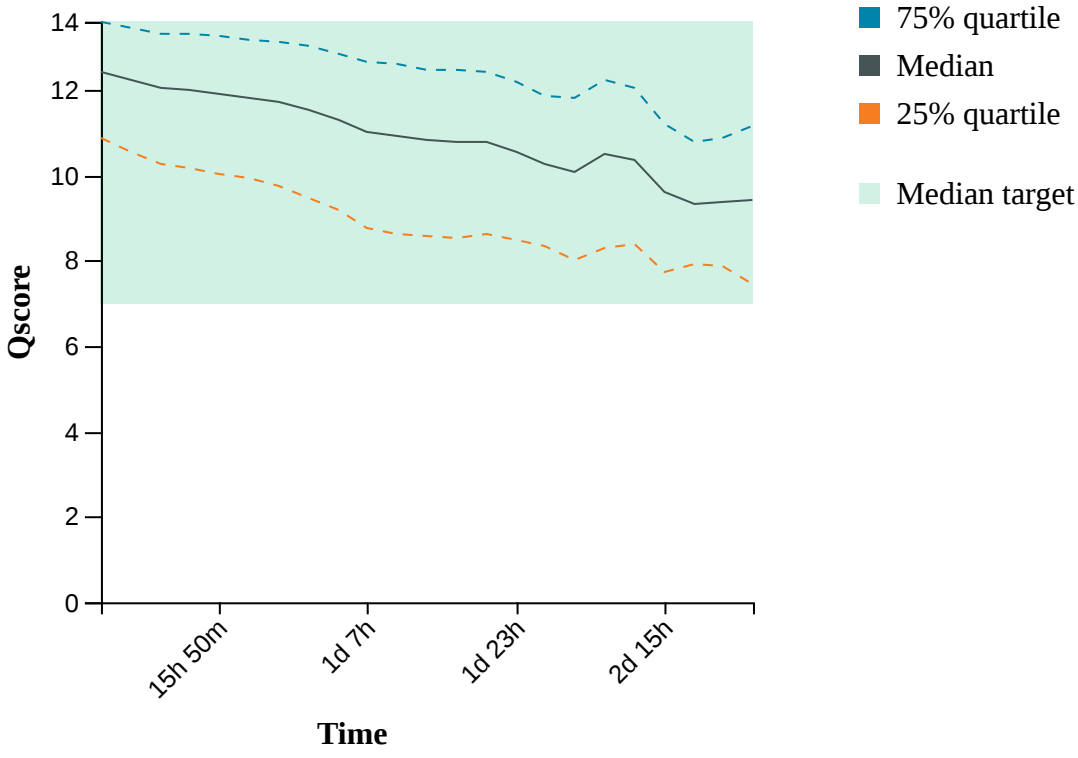
Bias Voltage History



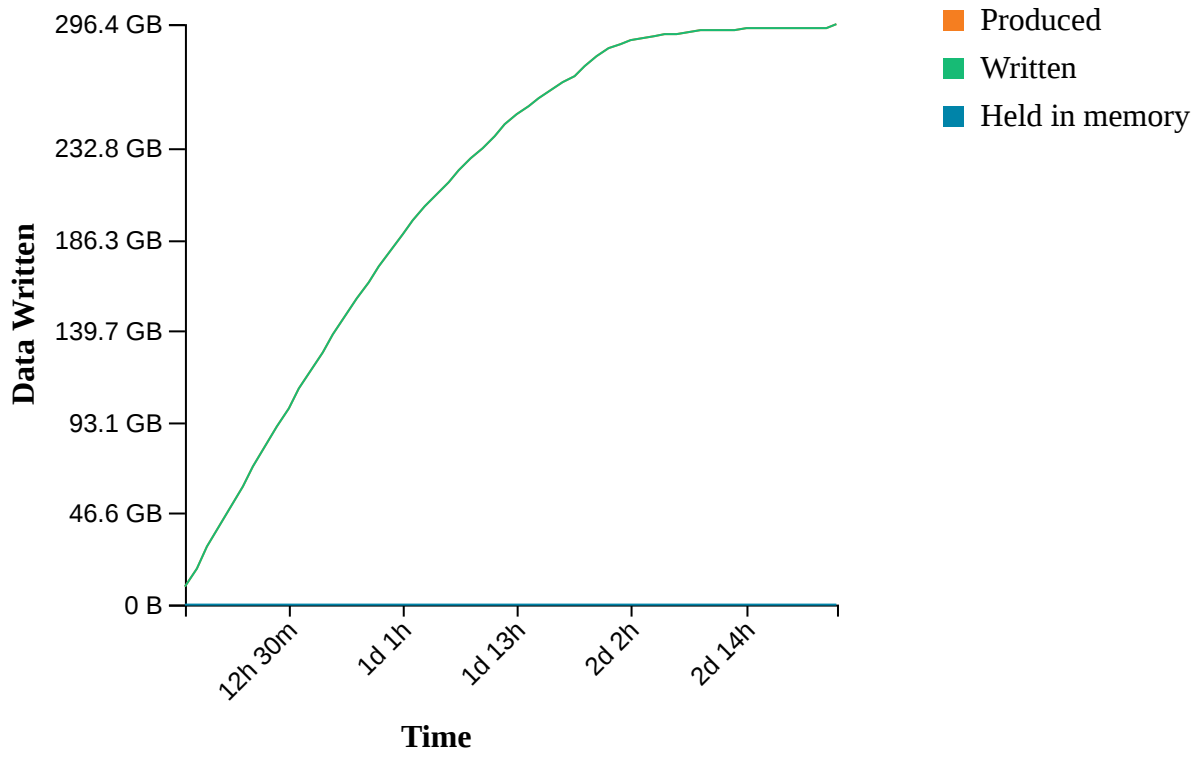
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- The sequencing run has finished, but basecalling may continue April 18, 12:13
- Mux scan for flow cell FAP21642 has found a total of 79 pores. 76 pores available for immediate sequencing April 18, 11:44
- Performing Mux Scan April 18, 11:41
- Mux scan for flow cell FAP21642 has found a total of 74 pores. 73 pores available for immediate sequencing April 18, 10:11
- Performing Mux Scan April 18, 10:09
- Mux scan for flow cell FAP21642 has found a total of 68 pores. 64 pores available for immediate sequencing April 18, 08:39
- Performing Mux Scan April 18, 08:36
- Mux scan for flow cell FAP21642 has found a total of 53 pores. 52 pores available for immediate sequencing April 18, 07:06
- Performing Mux Scan April 18, 07:04
- Mux scan for flow cell FAP21642 has found a total of 62 pores. 59 pores available for immediate sequencing April 18, 05:34
- Performing Mux Scan April 18, 05:31
- Mux scan for flow cell FAP21642 has found a total of 65 pores. 65 pores available for immediate sequencing April 18, 04:01
- Performing Mux Scan April 18, 03:59
- Mux scan for flow cell FAP21642 has found a total of 67 pores. 64 pores available for immediate sequencing April 18, 02:29
- Performing Mux Scan April 18, 02:26
- Mux scan for flow cell FAP21642 has found a total of 228 pores. 202 pores available for immediate sequencing April 18, 00:56
- Performing Mux Scan April 18, 00:54
- Mux scan for flow cell FAP21642 has found a total of 97 pores. 89 pores available for immediate sequencing April 17, 23:24
- Performing Mux Scan April 17, 23:21
- Mux scan for flow cell FAP21642 has found a total of 67 pores. 59 pores available for immediate sequencing April 17, 21:51
- Performing Mux Scan April 17, 21:49
- Mux scan for flow cell FAP21642 has found a total of 80 pores. 73 pores available for immediate sequencing April 17, 20:19
- Performing Mux Scan April 17, 20:16
- Mux scan for flow cell FAP21642 has found a total of 91 pores. 80 pores available for immediate sequencing April 17, 18:46
- Performing Mux Scan April 17, 18:43
- Mux scan for flow cell FAP21642 has found a total of 154 pores. 132 pores available for immediate sequencing April 17, 17:13
- Performing Mux Scan April 17, 17:10
- Mux scan for flow cell FAP21642 has found a total of 166 pores. 136 pores available for immediate sequencing April 17, 15:40
- Performing Mux Scan April 17, 15:38
- Mux scan for flow cell FAP21642 has found a total of 267 pores. 212 pores available for immediate sequencing April 17, 14:07
- Performing Mux Scan April 17, 14:04
- Mux scan for flow cell FAP21642 has found a total of 334 pores. 240 pores available for immediate sequencing April 17, 12:34
- Performing Mux Scan April 17, 12:31

- Mux scan for flow cell FAP21642 has found a total of 498 pores. 338 pores available for immediate sequencing April 17, 11:00
- Performing Mux Scan April 17, 10:58
- Mux scan for flow cell FAP21642 has found a total of 563 pores. 361 pores available for immediate sequencing April 17, 09:27
- Performing Mux Scan April 17, 09:24
- Mux scan for flow cell FAP21642 has found a total of 523 pores. 316 pores available for immediate sequencing April 17, 07:53
- Performing Mux Scan April 17, 07:51
- Mux scan for flow cell FAP21642 has found a total of 433 pores. 236 pores available for immediate sequencing April 17, 06:20
- Performing Mux Scan April 17, 06:17
- Mux scan for flow cell FAP21642 has found a total of 467 pores. 253 pores available for immediate sequencing April 17, 04:46
- Performing Mux Scan April 17, 04:44
- Mux scan for flow cell FAP21642 has found a total of 483 pores. 257 pores available for immediate sequencing April 17, 03:13
- Performing Mux Scan April 17, 03:10
- Mux scan for flow cell FAP21642 has found a total of 516 pores. 272 pores available for immediate sequencing April 17, 01:39
- Performing Mux Scan April 17, 01:37
- Mux scan for flow cell FAP21642 has found a total of 618 pores. 352 pores available for immediate sequencing April 17, 00:06
- Performing Mux Scan April 17, 00:03
- Mux scan for flow cell FAP21642 has found a total of 678 pores. 374 pores available for immediate sequencing April 16, 22:32
- Performing Mux Scan April 16, 22:30
- Mux scan for flow cell FAP21642 has found a total of 602 pores. 309 pores available for immediate sequencing April 16, 20:59
- Performing Mux Scan April 16, 20:56
- Mux scan for flow cell FAP21642 has found a total of 659 pores. 340 pores available for immediate sequencing April 16, 19:25
- Performing Mux Scan April 16, 19:23
- Mux scan for flow cell FAP21642 has found a total of 668 pores. 335 pores available for immediate sequencing April 16, 17:52
- Performing Mux Scan April 16, 17:49
- Mux scan for flow cell FAP21642 has found a total of 721 pores. 358 pores available for immediate sequencing April 16, 16:18
- Performing Mux Scan April 16, 16:16
- Mux scan for flow cell FAP21642 has found a total of 809 pores. 416 pores available for immediate sequencing April 16, 14:45
- Performing Mux Scan April 16, 14:42
- Mux scan for flow cell FAP21642 has found a total of 777 pores. 375 pores available for immediate sequencing April 16, 13:11
- Performing Mux Scan April 16, 13:09
- Mux scan for flow cell FAP21642 has found a total of 812 pores. 389 pores available for immediate sequencing April 16, 11:38
- Performing Mux Scan April 16, 11:35
- Mux scan for flow cell FAP21642 has found a total of 818 pores. 399 pores available for immediate sequencing April 16, 10:04
- Performing Mux Scan April 16, 10:02
- Mux scan for flow cell FAP21642 has found a total of 911 pores. 449 pores available for

immediate sequencing April 16, 08:31

- Performing Mux Scan April 16, 08:28
- Mux scan for flow cell FAP21642 has found a total of 905 pores. 444 pores available for immediate sequencing April 16, 06:57
- Performing Mux Scan April 16, 06:55
- Mux scan for flow cell FAP21642 has found a total of 888 pores. 413 pores available for immediate sequencing April 16, 05:24
- Performing Mux Scan April 16, 05:21
- Mux scan for flow cell FAP21642 has found a total of 923 pores. 435 pores available for immediate sequencing April 16, 03:50
- Performing Mux Scan April 16, 03:48
- Mux scan for flow cell FAP21642 has found a total of 970 pores. 456 pores available for immediate sequencing April 16, 02:17
- Performing Mux Scan April 16, 02:14
- Mux scan for flow cell FAP21642 has found a total of 954 pores. 441 pores available for immediate sequencing April 16, 00:43
- Performing Mux Scan April 16, 00:41
- Mux scan for flow cell FAP21642 has found a total of 981 pores. 457 pores available for immediate sequencing April 15, 23:10
- Performing Mux Scan April 15, 23:07
- Mux scan for flow cell FAP21642 has found a total of 999 pores. 458 pores available for immediate sequencing April 15, 21:36
- Performing Mux Scan April 15, 21:34
- Mux scan for flow cell FAP21642 has found a total of 1036 pores. 465 pores available for immediate sequencing April 15, 20:03
- Performing Mux Scan April 15, 20:00
- Mux scan for flow cell FAP21642 has found a total of 1007 pores. 466 pores available for immediate sequencing April 15, 18:29
- Performing Mux Scan April 15, 18:27
- Mux scan for flow cell FAP21642 has found a total of 1035 pores. 468 pores available for immediate sequencing April 15, 16:56
- Performing Mux Scan April 15, 16:53
- Mux scan for flow cell FAP21642 has found a total of 1047 pores. 473 pores available for immediate sequencing April 15, 15:22
- Performing Mux Scan April 15, 15:20
- Mux scan for flow cell FAP21642 has found a total of 1063 pores. 474 pores available for immediate sequencing April 15, 13:49
- Performing Mux Scan April 15, 13:46
- Mux scan for flow cell FAP21642 has found a total of 1105 pores. 476 pores available for immediate sequencing April 15, 12:15
- Performing Mux Scan April 15, 12:13
- Starting sequencing procedure April 15, 12:13
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 12:10