Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38kbp_SdEnrich_Sd_15042021**
Sample ID	**ReadUntil_38kbp_SdEnrich_Sd_15042021**
Run ID	**d30e4e7e-3158-4318-9147-dcf334c205d4**
Flow Cell Id	**FAP14669**
Start Time	**April 15, 11:50**
Run Length	**3d 0h 3m**

Run Summary

Reads Generated	**5.47 M**
Passed Bases	**14.13 Gb**
Failed Bases	**1.45 Gb**
Estimated Bases	**15.88 Gb**

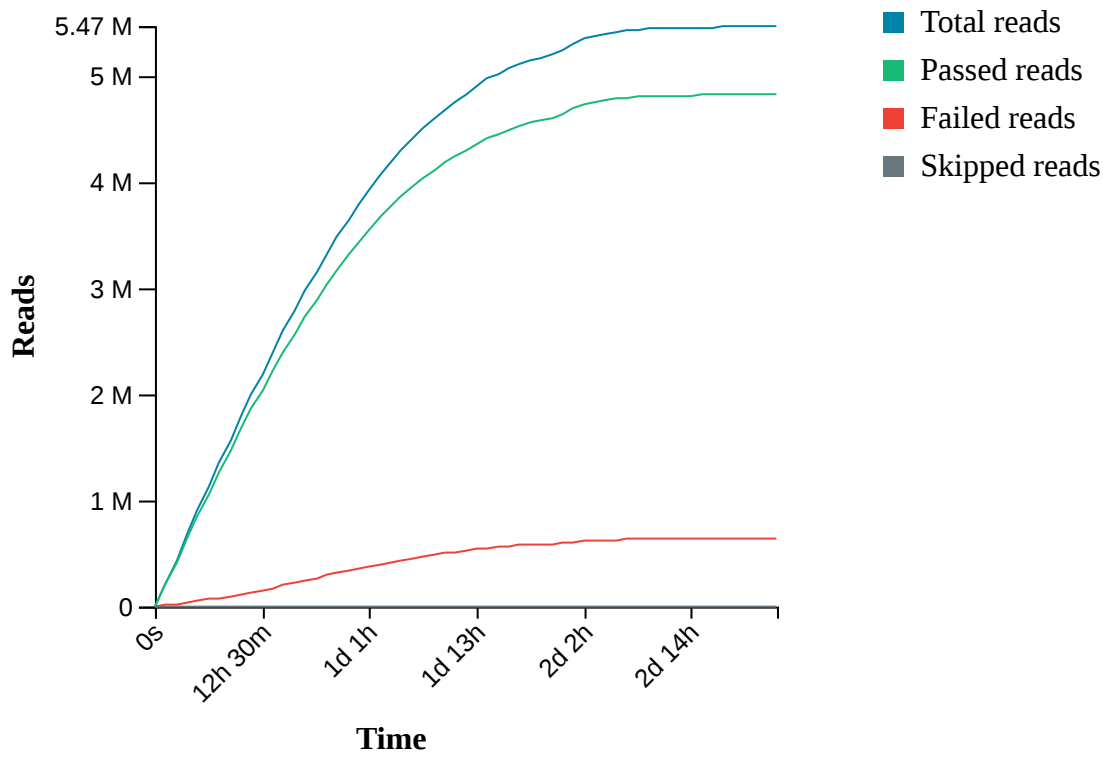
Run Parameters

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**

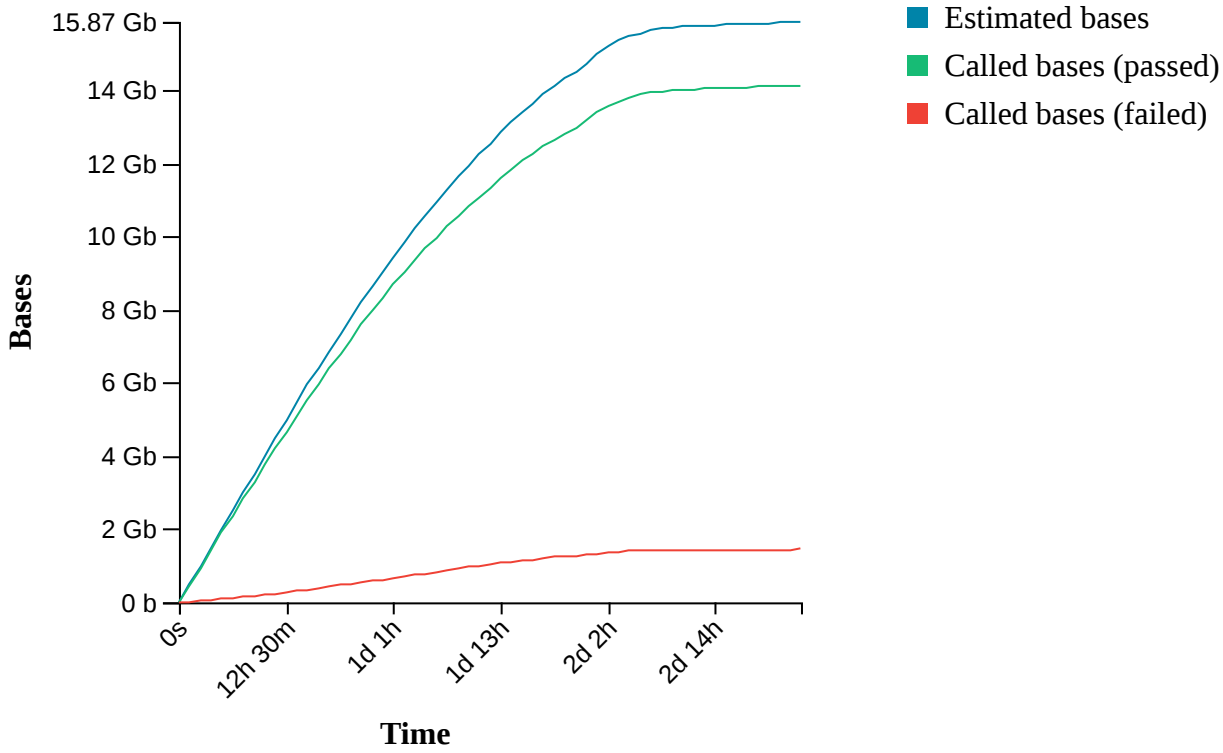
Versions

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

Cumulative Output Reads

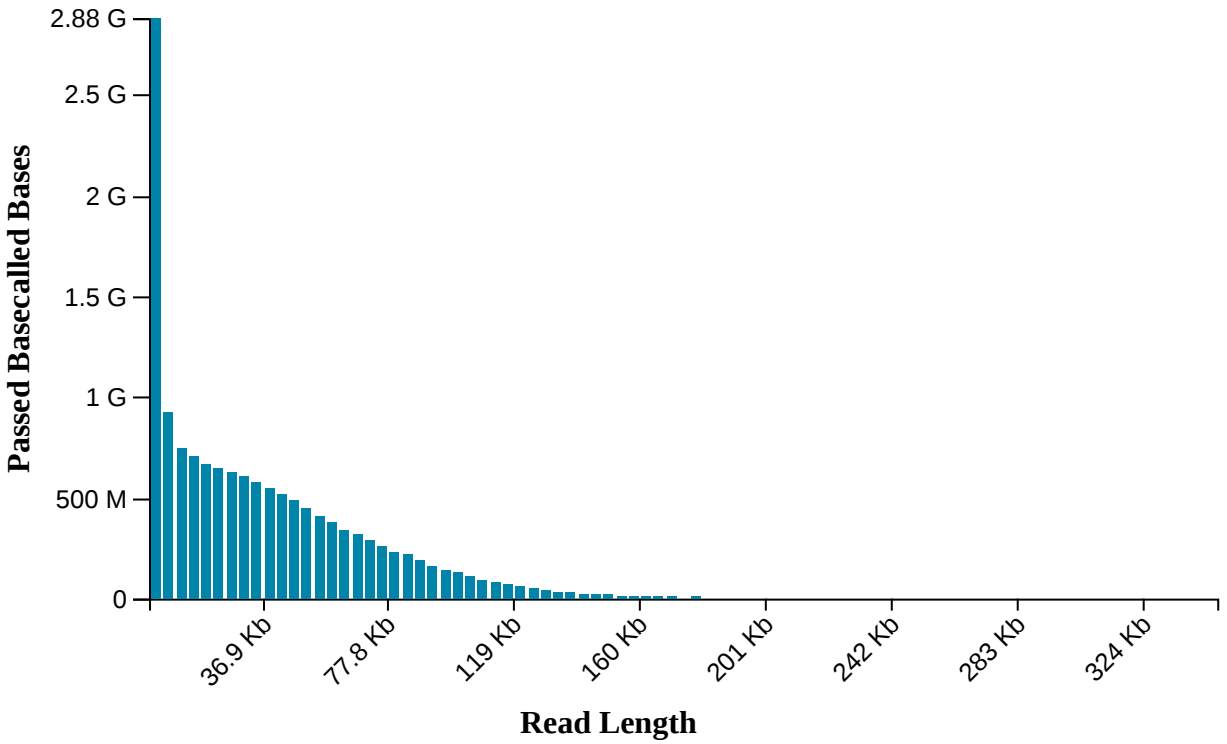


Cumulative Output Bases



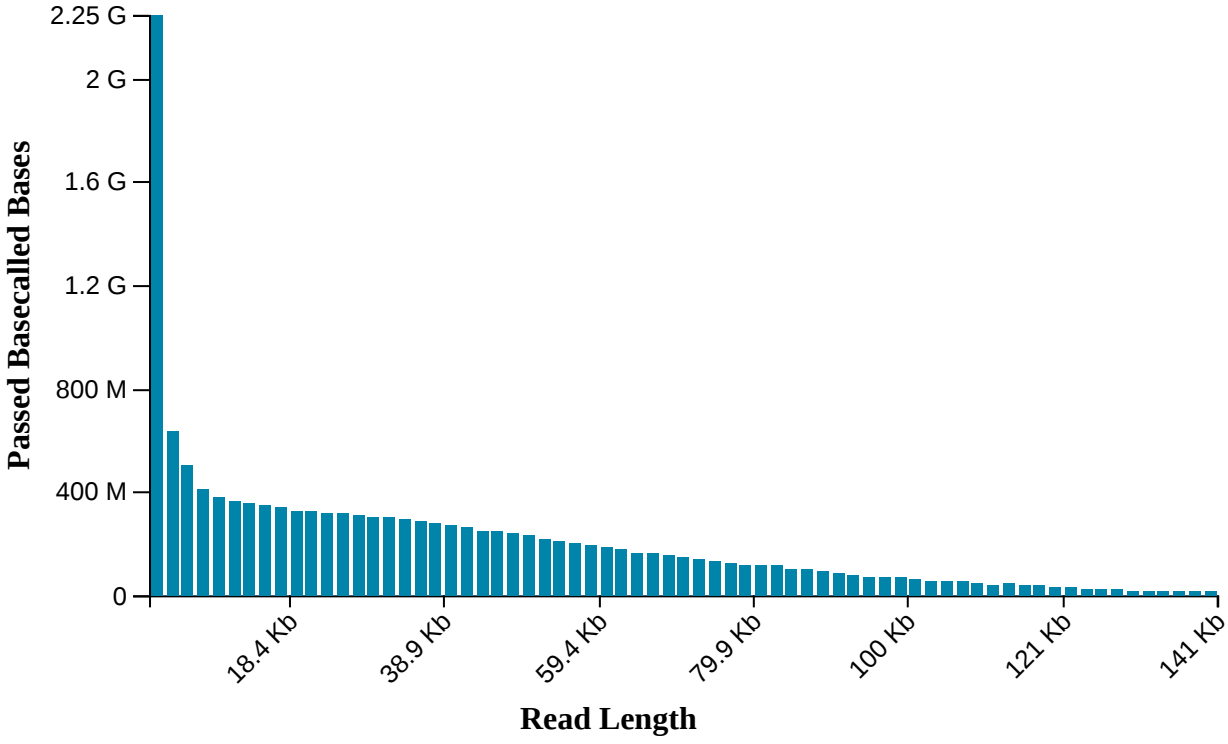
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 27.92 K



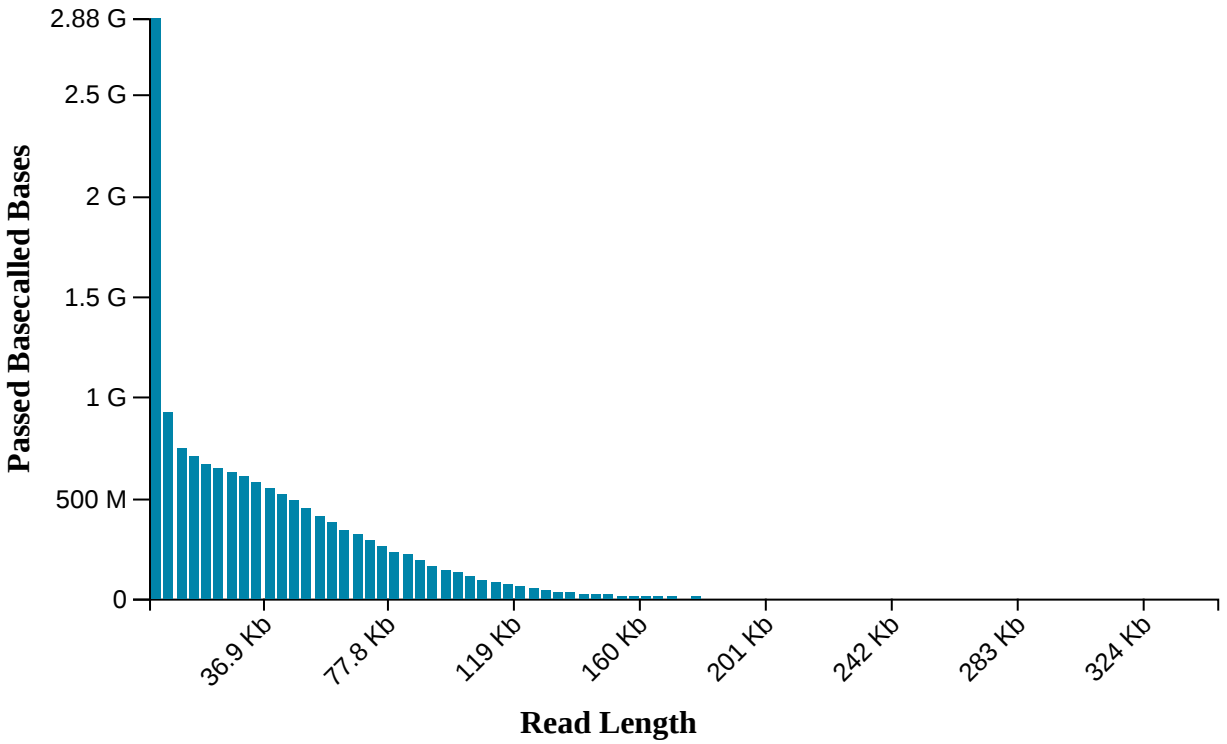
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 27.46 K



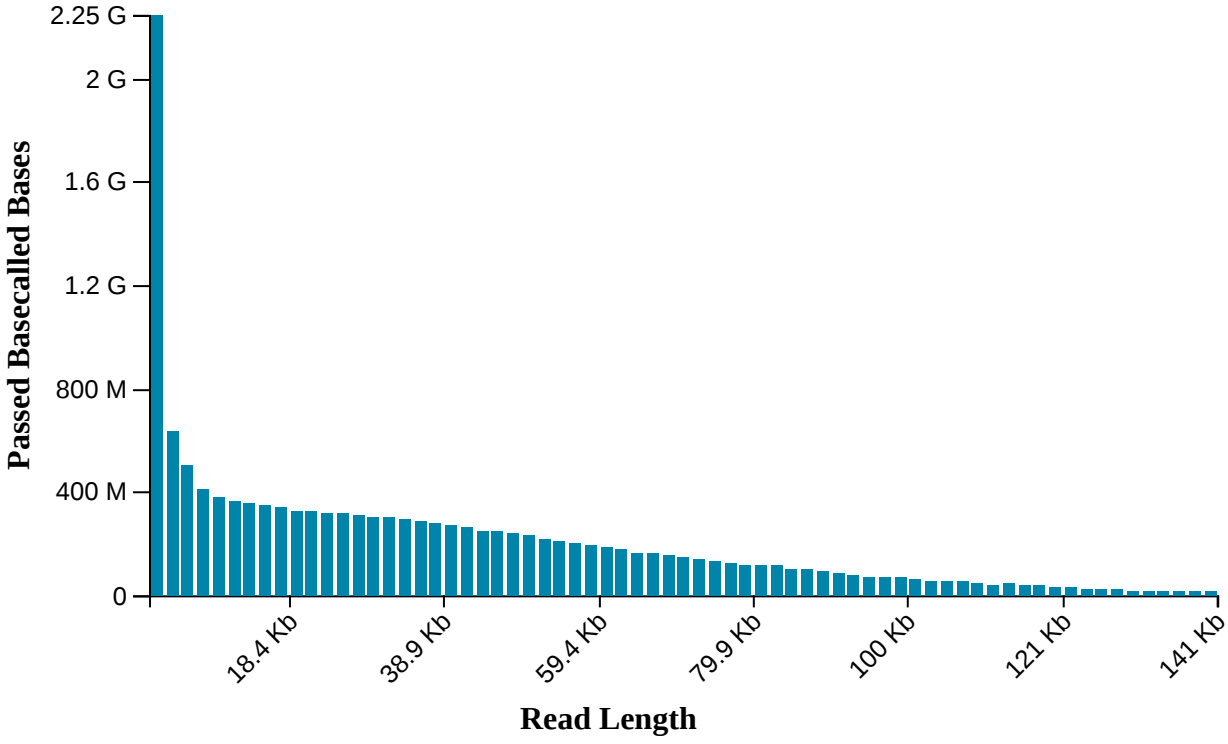
Read Length Histogram Estimated Bases

Estimated N50: 27.92 K

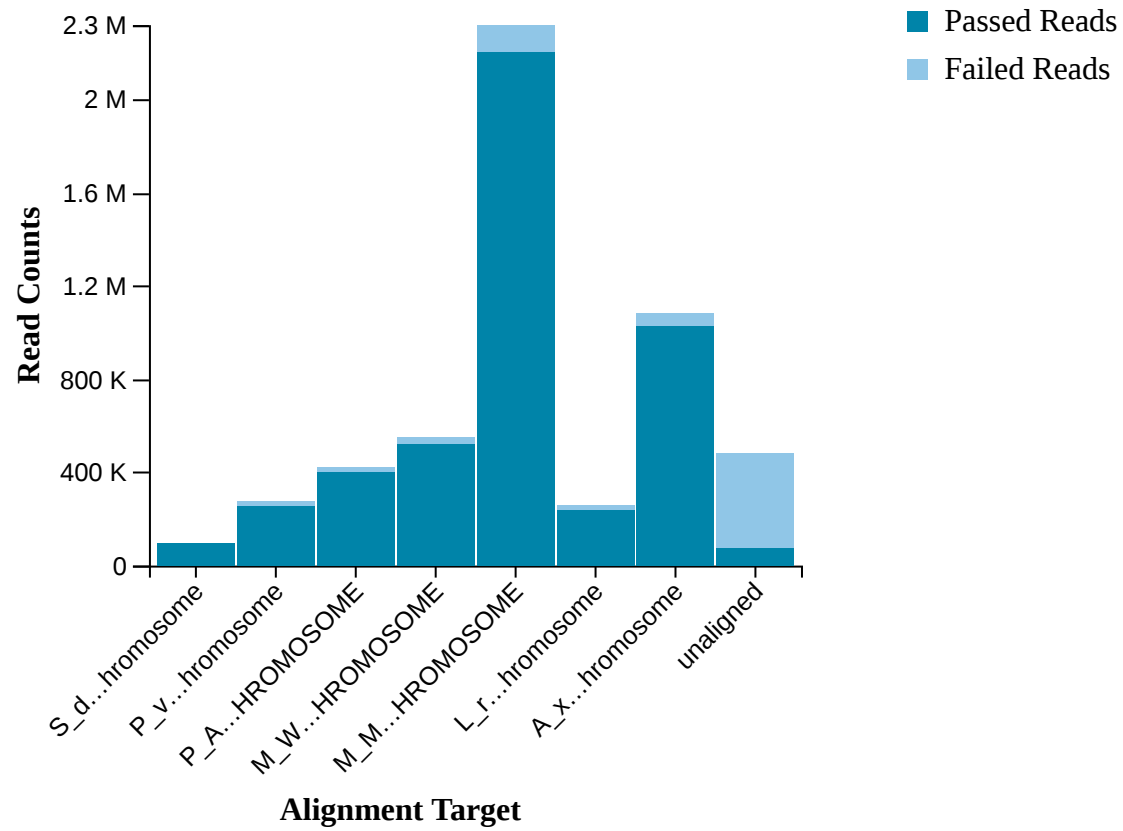


Read Length Histogram Basecalled Bases

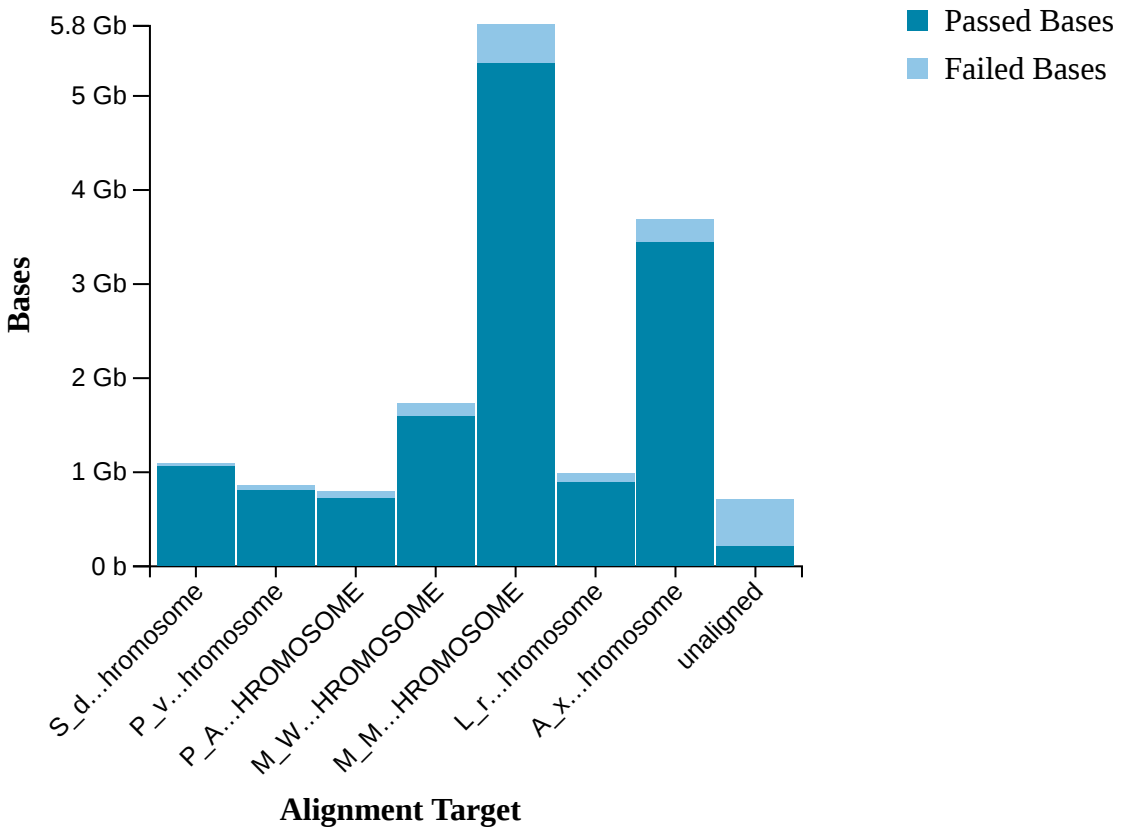
Estimated N50: 27.46 K



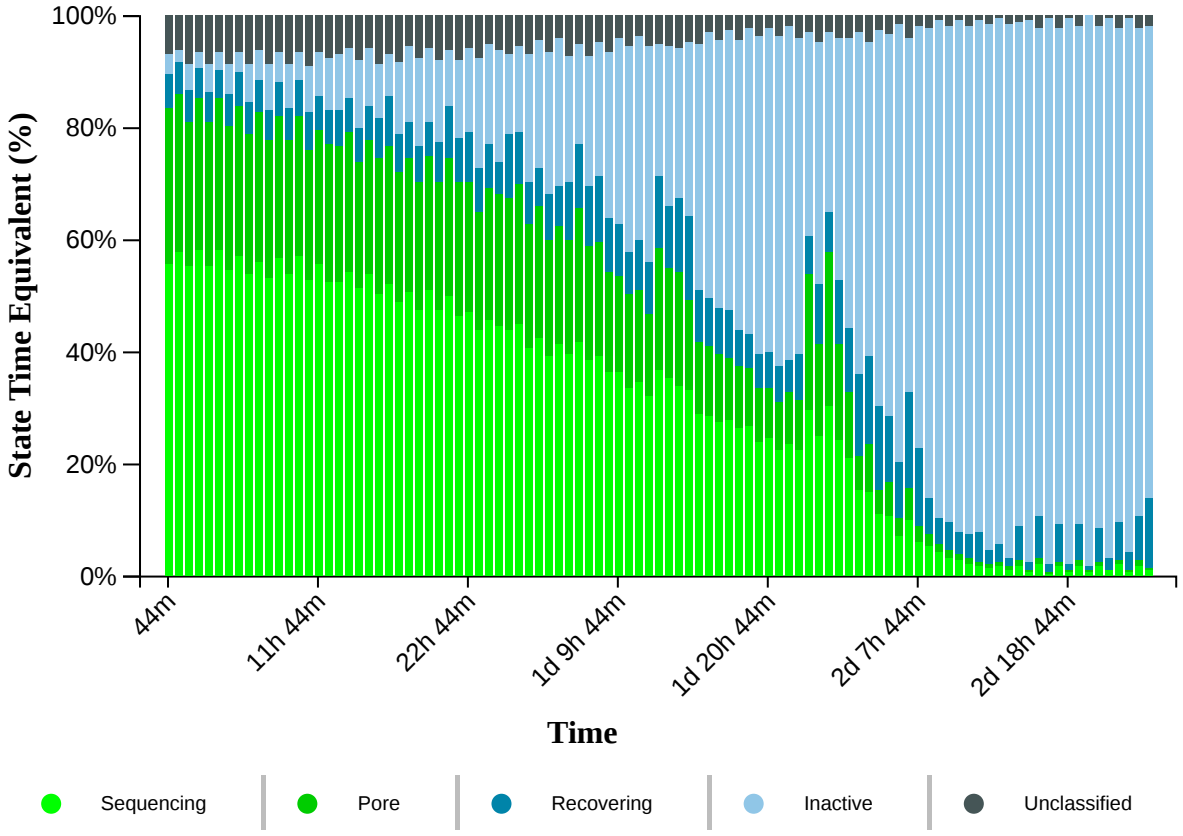
Alignment Target Hits (reads)



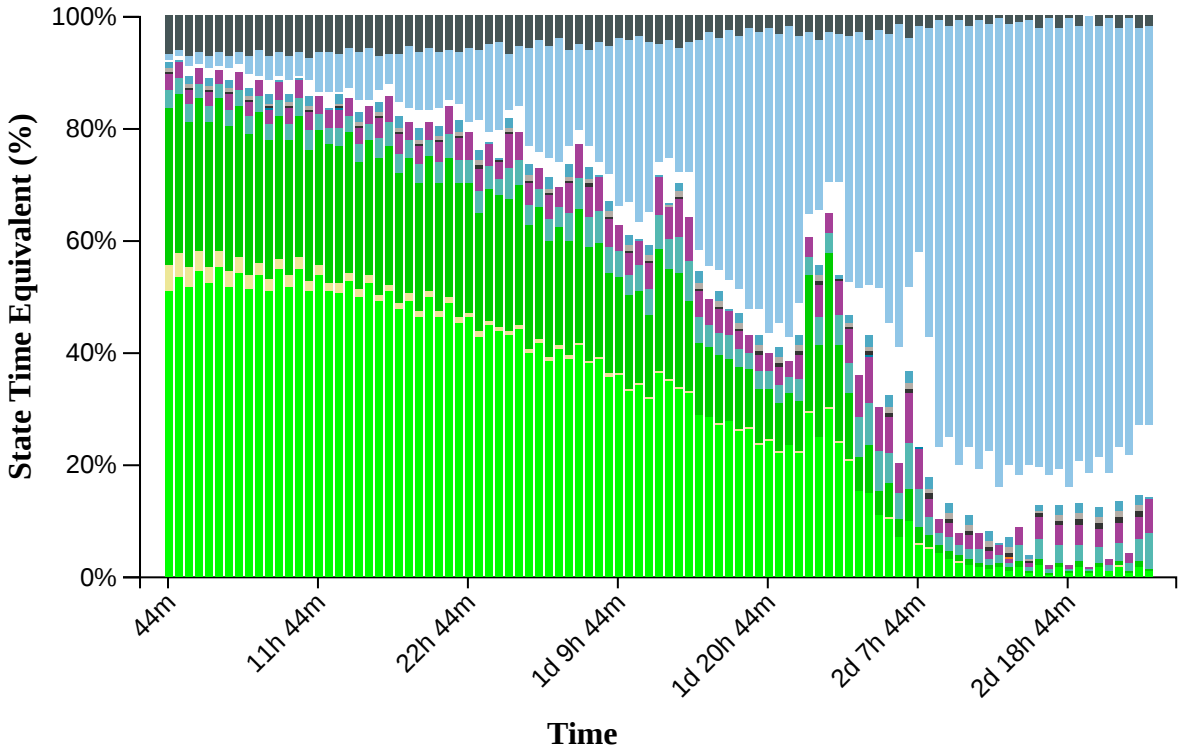
Alignment Target Hits (bases)



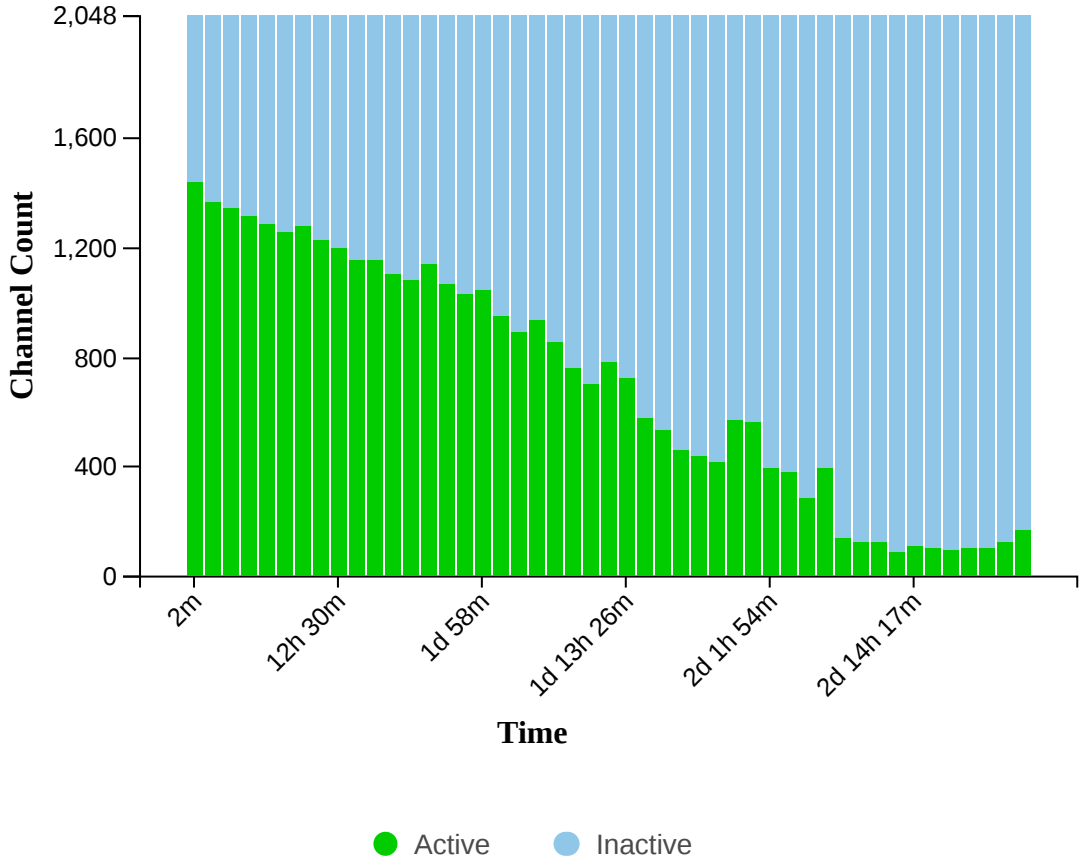
Duty Time Grouped



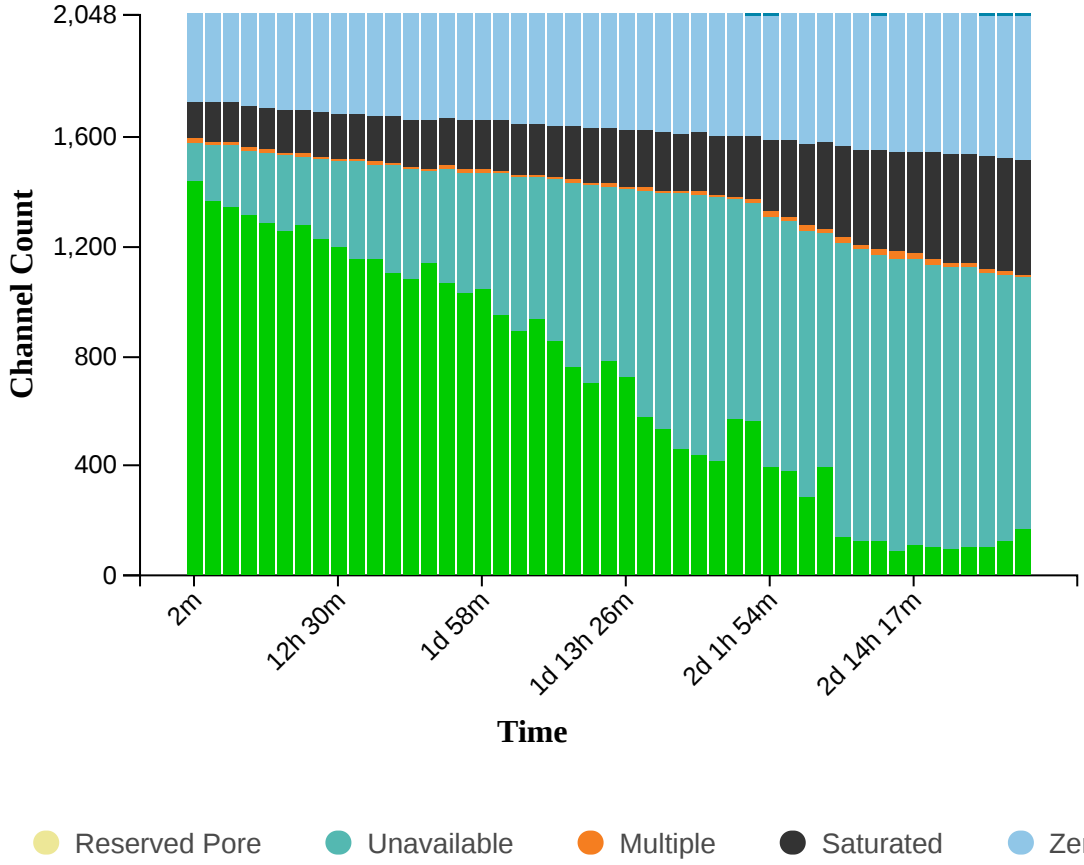
Duty time Categorised



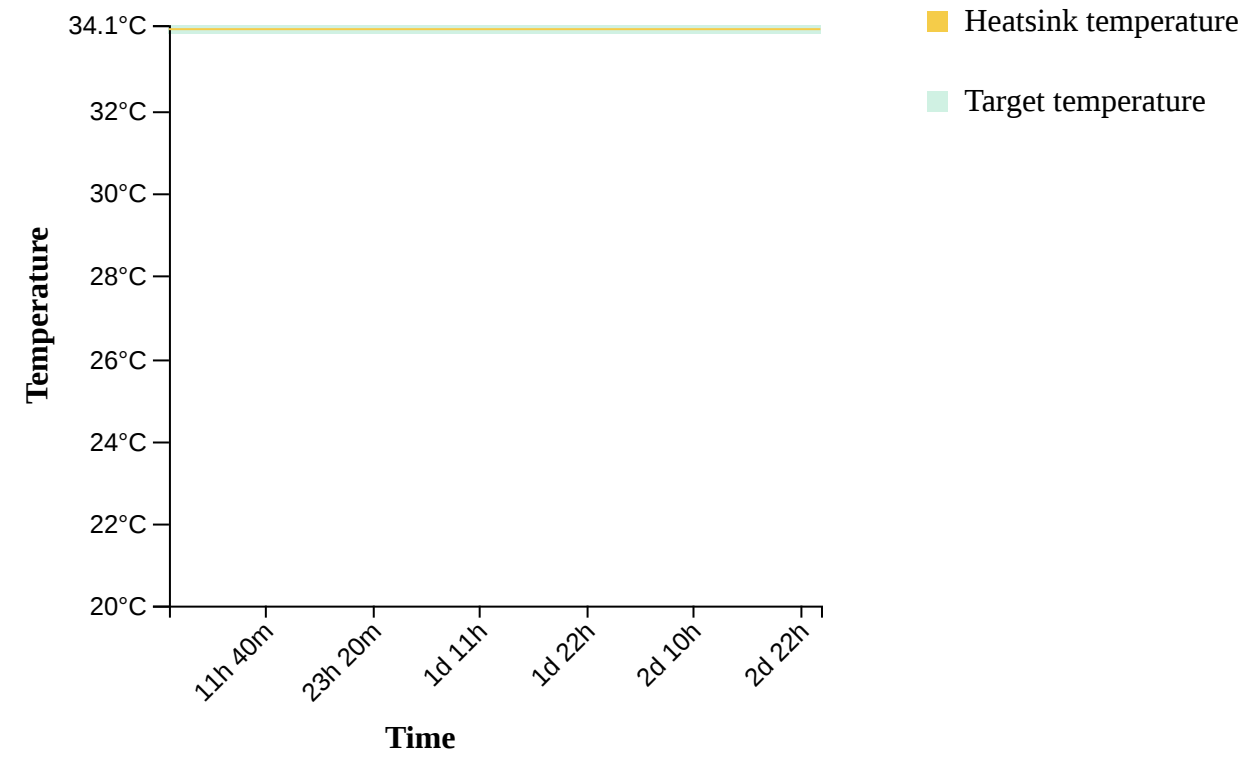
Mux Scan Grouped



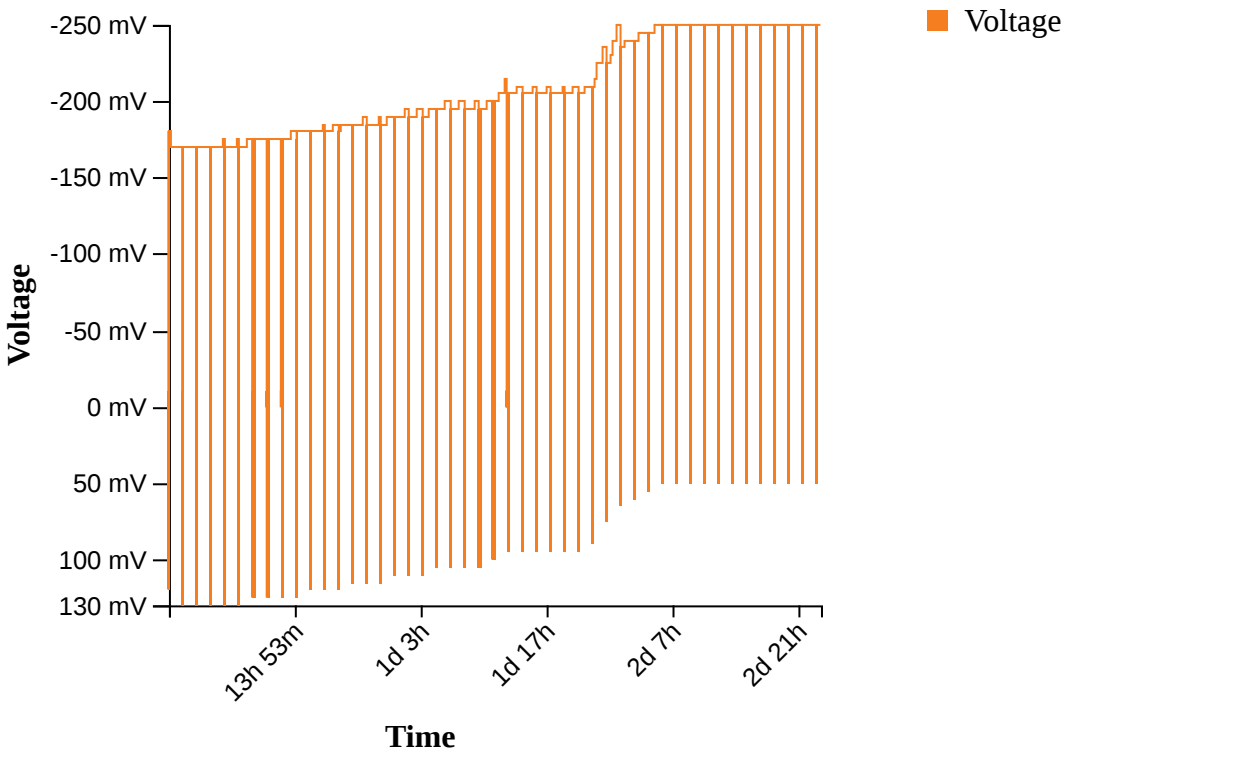
Mux Scan Categorised



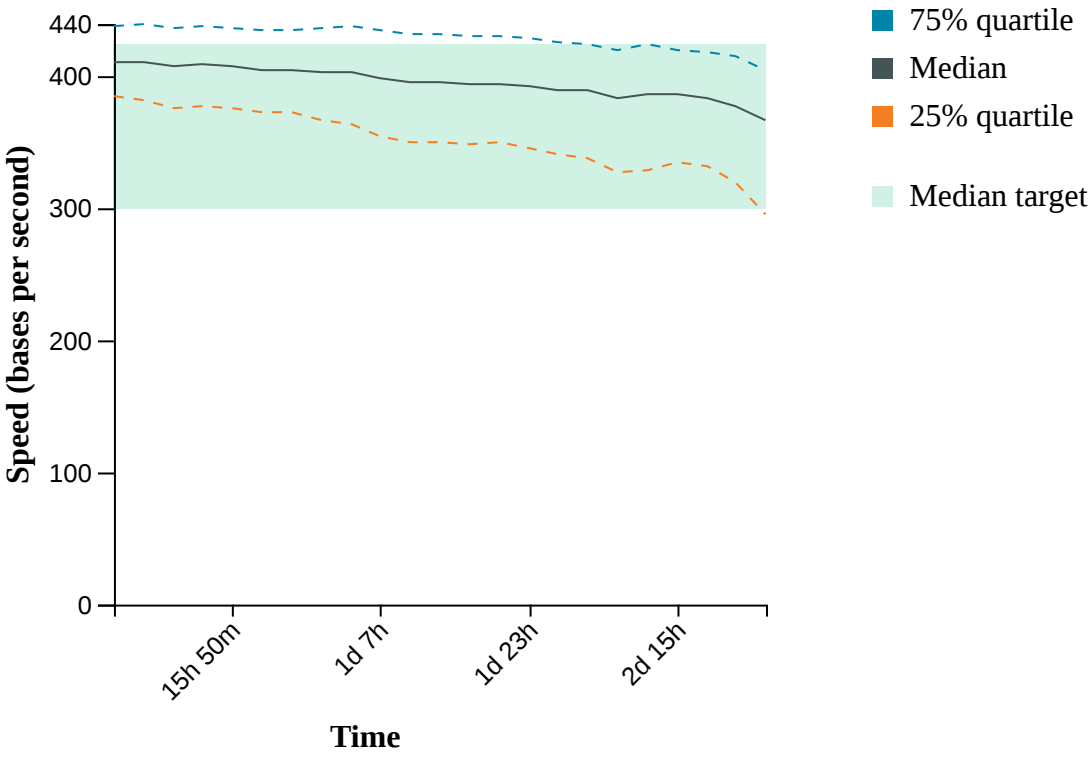
Temperature History



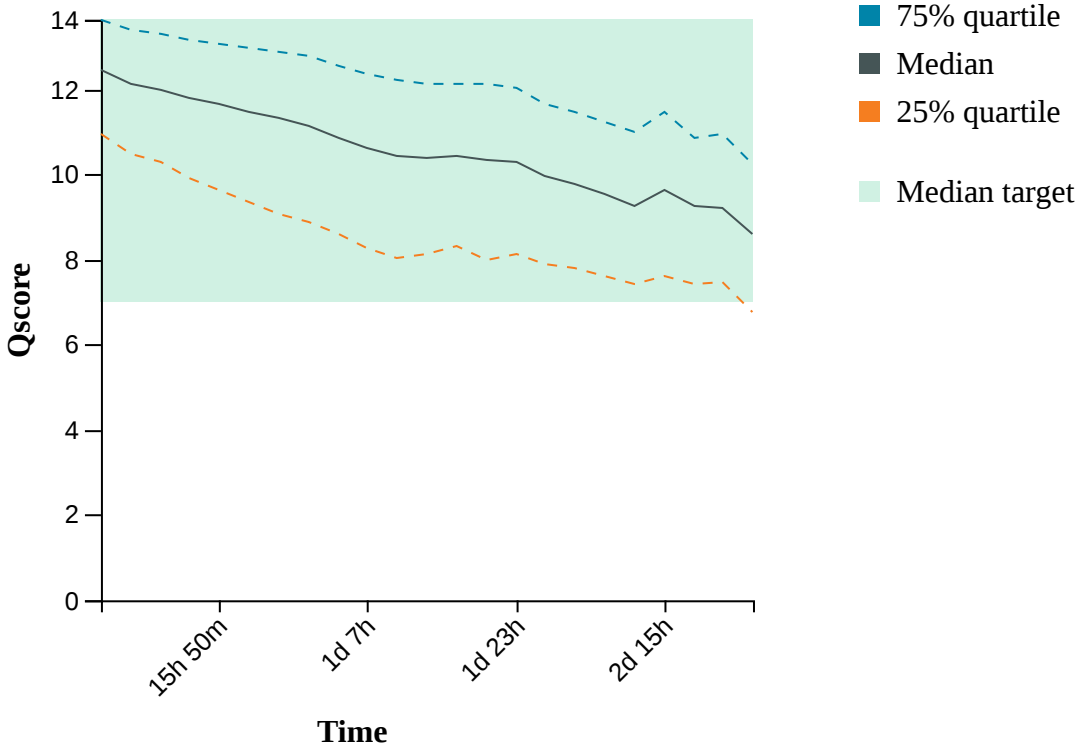
Bias Voltage History



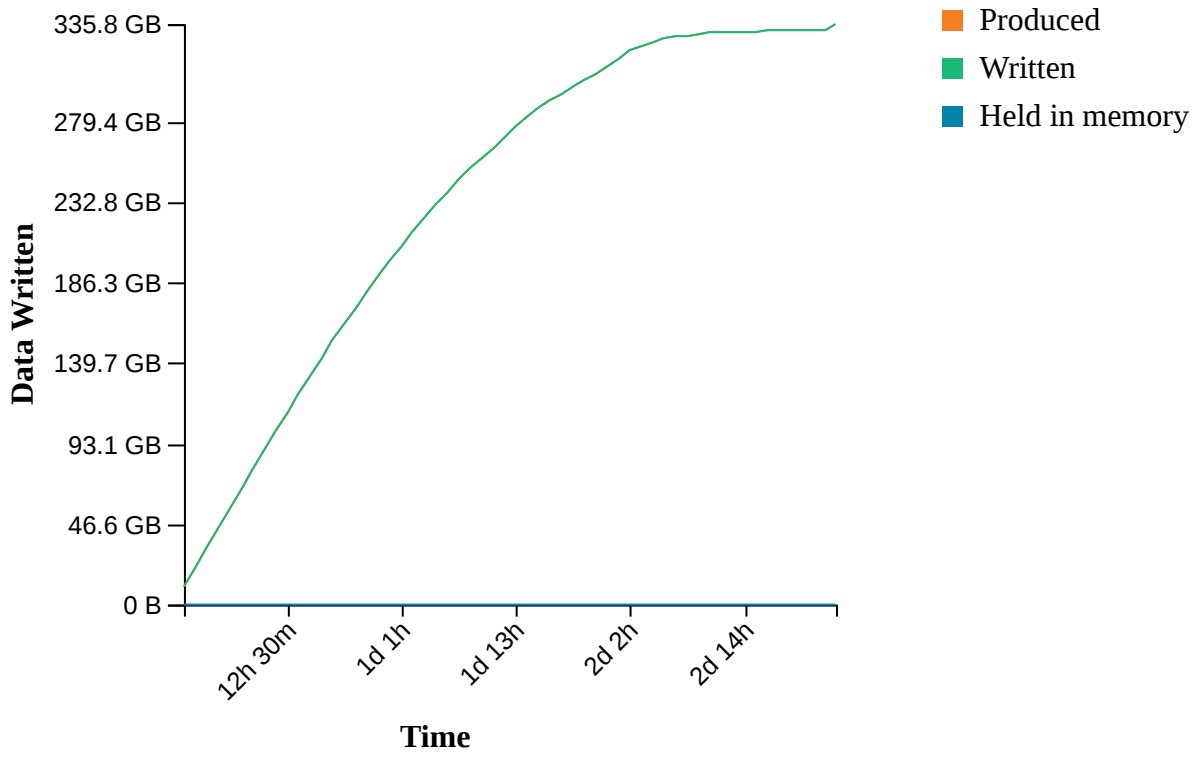
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- The sequencing run has finished, but basecalling may continue April 18, 11:53
- Mux scan for flow cell FAP14669 has found a total of 167 pores. 147 pores available for immediate sequencing April 18, 11:26
- Performing Mux Scan April 18, 11:23
- Mux scan for flow cell FAP14669 has found a total of 124 pores. 113 pores available for immediate sequencing April 18, 09:53
- Performing Mux Scan April 18, 09:51
- Mux scan for flow cell FAP14669 has found a total of 103 pores. 96 pores available for immediate sequencing April 18, 08:21
- Performing Mux Scan April 18, 08:18
- Mux scan for flow cell FAP14669 has found a total of 103 pores. 95 pores available for immediate sequencing April 18, 06:48
- Performing Mux Scan April 18, 06:46
- Mux scan for flow cell FAP14669 has found a total of 94 pores. 84 pores available for immediate sequencing April 18, 05:16
- Performing Mux Scan April 18, 05:13
- Mux scan for flow cell FAP14669 has found a total of 101 pores. 95 pores available for immediate sequencing April 18, 03:43
- Performing Mux Scan April 18, 03:41
- Mux scan for flow cell FAP14669 has found a total of 110 pores. 98 pores available for immediate sequencing April 18, 02:11
- Performing Mux Scan April 18, 02:08
- Mux scan for flow cell FAP14669 has found a total of 89 pores. 84 pores available for immediate sequencing April 18, 00:38
- Performing Mux Scan April 18, 00:36
- Mux scan for flow cell FAP14669 has found a total of 121 pores. 103 pores available for immediate sequencing April 17, 23:06
- Performing Mux Scan April 17, 23:03
- Mux scan for flow cell FAP14669 has found a total of 123 pores. 106 pores available for immediate sequencing April 17, 21:33
- Performing Mux Scan April 17, 21:31
- Mux scan for flow cell FAP14669 has found a total of 137 pores. 122 pores available for immediate sequencing April 17, 20:01
- Performing Mux Scan April 17, 19:58
- Mux scan for flow cell FAP14669 has found a total of 393 pores. 306 pores available for immediate sequencing April 17, 18:28
- Performing Mux Scan April 17, 18:25
- Mux scan for flow cell FAP14669 has found a total of 285 pores. 218 pores available for immediate sequencing April 17, 16:54
- Performing Mux Scan April 17, 16:52
- Mux scan for flow cell FAP14669 has found a total of 380 pores. 276 pores available for immediate sequencing April 17, 15:21
- Performing Mux Scan April 17, 15:18
- Mux scan for flow cell FAP14669 has found a total of 393 pores. 278 pores available for immediate sequencing April 17, 13:47
- Performing Mux Scan April 17, 13:45
- Mux scan for flow cell FAP14669 has found a total of 563 pores. 375 pores available for immediate sequencing April 17, 12:14
- Performing Mux Scan April 17, 12:11

- Mux scan for flow cell FAP14669 has found a total of 571 pores. 345 pores available for immediate sequencing April 17, 10:40
- Performing Mux Scan April 17, 10:38
- Mux scan for flow cell FAP14669 has found a total of 419 pores. 229 pores available for immediate sequencing April 17, 09:07
- Performing Mux Scan April 17, 09:05
- Mux scan for flow cell FAP14669 has found a total of 439 pores. 234 pores available for immediate sequencing April 17, 07:33
- Performing Mux Scan April 17, 07:31
- Mux scan for flow cell FAP14669 has found a total of 464 pores. 256 pores available for immediate sequencing April 17, 06:00
- Performing Mux Scan April 17, 05:58
- Mux scan for flow cell FAP14669 has found a total of 537 pores. 284 pores available for immediate sequencing April 17, 04:26
- Performing Mux Scan April 17, 04:24
- Mux scan for flow cell FAP14669 has found a total of 576 pores. 297 pores available for immediate sequencing April 17, 02:53
- Performing Mux Scan April 17, 02:51
- Mux scan for flow cell FAP14669 has found a total of 723 pores. 393 pores available for immediate sequencing April 17, 01:20
- Performing Mux Scan April 17, 01:17
- Mux scan for flow cell FAP14669 has found a total of 780 pores. 403 pores available for immediate sequencing April 16, 23:46
- Performing Mux Scan April 16, 23:44
- Mux scan for flow cell FAP14669 has found a total of 703 pores. 342 pores available for immediate sequencing April 16, 22:13
- Performing Mux Scan April 16, 22:10
- Mux scan for flow cell FAP14669 has found a total of 763 pores. 358 pores available for immediate sequencing April 16, 20:39
- Performing Mux Scan April 16, 20:37
- Mux scan for flow cell FAP14669 has found a total of 857 pores. 403 pores available for immediate sequencing April 16, 19:06
- Performing Mux Scan April 16, 19:03
- Mux scan for flow cell FAP14669 has found a total of 938 pores. 434 pores available for immediate sequencing April 16, 17:32
- Performing Mux Scan April 16, 17:30
- Mux scan for flow cell FAP14669 has found a total of 893 pores. 399 pores available for immediate sequencing April 16, 15:59
- Performing Mux Scan April 16, 15:56
- Mux scan for flow cell FAP14669 has found a total of 951 pores. 410 pores available for immediate sequencing April 16, 14:25
- Performing Mux Scan April 16, 14:23
- Mux scan for flow cell FAP14669 has found a total of 1044 pores. 458 pores available for immediate sequencing April 16, 12:52
- Performing Mux Scan April 16, 12:49
- Mux scan for flow cell FAP14669 has found a total of 1034 pores. 431 pores available for immediate sequencing April 16, 11:18
- Performing Mux Scan April 16, 11:16
- Mux scan for flow cell FAP14669 has found a total of 1071 pores. 446 pores available for immediate sequencing April 16, 09:45
- Performing Mux Scan April 16, 09:42
- Mux scan for flow cell FAP14669 has found a total of 1144 pores. 467 pores available for

immediate sequencing April 16, 08:11

- Performing Mux Scan April 16, 08:09
- Mux scan for flow cell FAP14669 has found a total of 1079 pores. 454 pores available for immediate sequencing April 16, 06:38
- Performing Mux Scan April 16, 06:35
- Mux scan for flow cell FAP14669 has found a total of 1107 pores. 456 pores available for immediate sequencing April 16, 05:04
- Performing Mux Scan April 16, 05:02
- Mux scan for flow cell FAP14669 has found a total of 1158 pores. 483 pores available for immediate sequencing April 16, 03:31
- Performing Mux Scan April 16, 03:28
- Mux scan for flow cell FAP14669 has found a total of 1159 pores. 465 pores available for immediate sequencing April 16, 01:57
- Performing Mux Scan April 16, 01:55
- Mux scan for flow cell FAP14669 has found a total of 1197 pores. 476 pores available for immediate sequencing April 16, 00:24
- Performing Mux Scan April 16, 00:21
- Mux scan for flow cell FAP14669 has found a total of 1227 pores. 475 pores available for immediate sequencing April 15, 22:50
- Performing Mux Scan April 15, 22:48
- Mux scan for flow cell FAP14669 has found a total of 1278 pores. 491 pores available for immediate sequencing April 15, 21:17
- Performing Mux Scan April 15, 21:14
- Mux scan for flow cell FAP14669 has found a total of 1258 pores. 489 pores available for immediate sequencing April 15, 19:43
- Performing Mux Scan April 15, 19:41
- Mux scan for flow cell FAP14669 has found a total of 1286 pores. 489 pores available for immediate sequencing April 15, 18:10
- Performing Mux Scan April 15, 18:07
- Mux scan for flow cell FAP14669 has found a total of 1313 pores. 500 pores available for immediate sequencing April 15, 16:36
- Performing Mux Scan April 15, 16:34
- Mux scan for flow cell FAP14669 has found a total of 1348 pores. 500 pores available for immediate sequencing April 15, 15:03
- Performing Mux Scan April 15, 15:00
- Mux scan for flow cell FAP14669 has found a total of 1365 pores. 501 pores available for immediate sequencing April 15, 13:29
- Performing Mux Scan April 15, 13:27
- Mux scan for flow cell FAP14669 has found a total of 1438 pores. 506 pores available for immediate sequencing April 15, 11:56
- Performing Mux Scan April 15, 11:53
- Starting sequencing procedure April 15, 11:53
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 11:50