Run Info

Experiment Name	**Lmin010720**
Sample ID	**Lmin**
Run ID	**634663b8-21af-45fc-a2ec-9ec6f01975fd**
Flow Cell Id	**FAO01594**
Start Time	**July 1, 18:21**
Run Length	**14h 39m**

Run Summary

Reads Generated	**1.43 M**
Bases Generated	**3.19 Gb**
Estimated Bases	**3.13 Gb**
Percentage Basecalled	**94%**

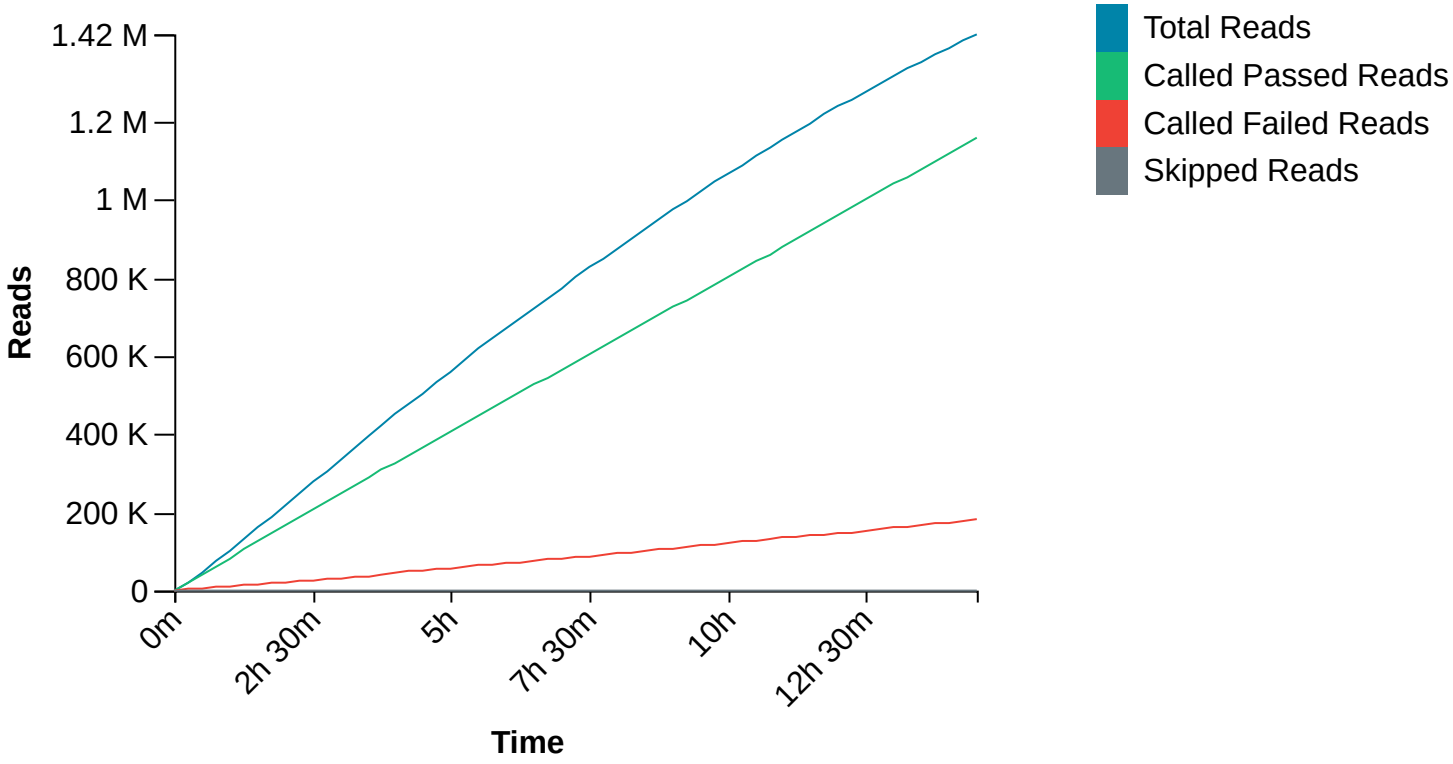
Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-LSK109**
Basecalling	**on**
Specified Run Length	**72 hours**
Initial Bias Voltage	**-185 mV**
FAST5 Output	**Enabled**
FAST5 Output Options	**zlib_compress,fastq,raw**
FAST5 Reads per File	**4000**
FASTQ Output	**Enabled**
FASTQ Reads per File	**4000**
Active Channel Selection	**Enabled**
Mux Scan Period	**1 hour 30 minutes**
Reserved Pores	**0 %**
Basecall Model	**Fast basecalling**

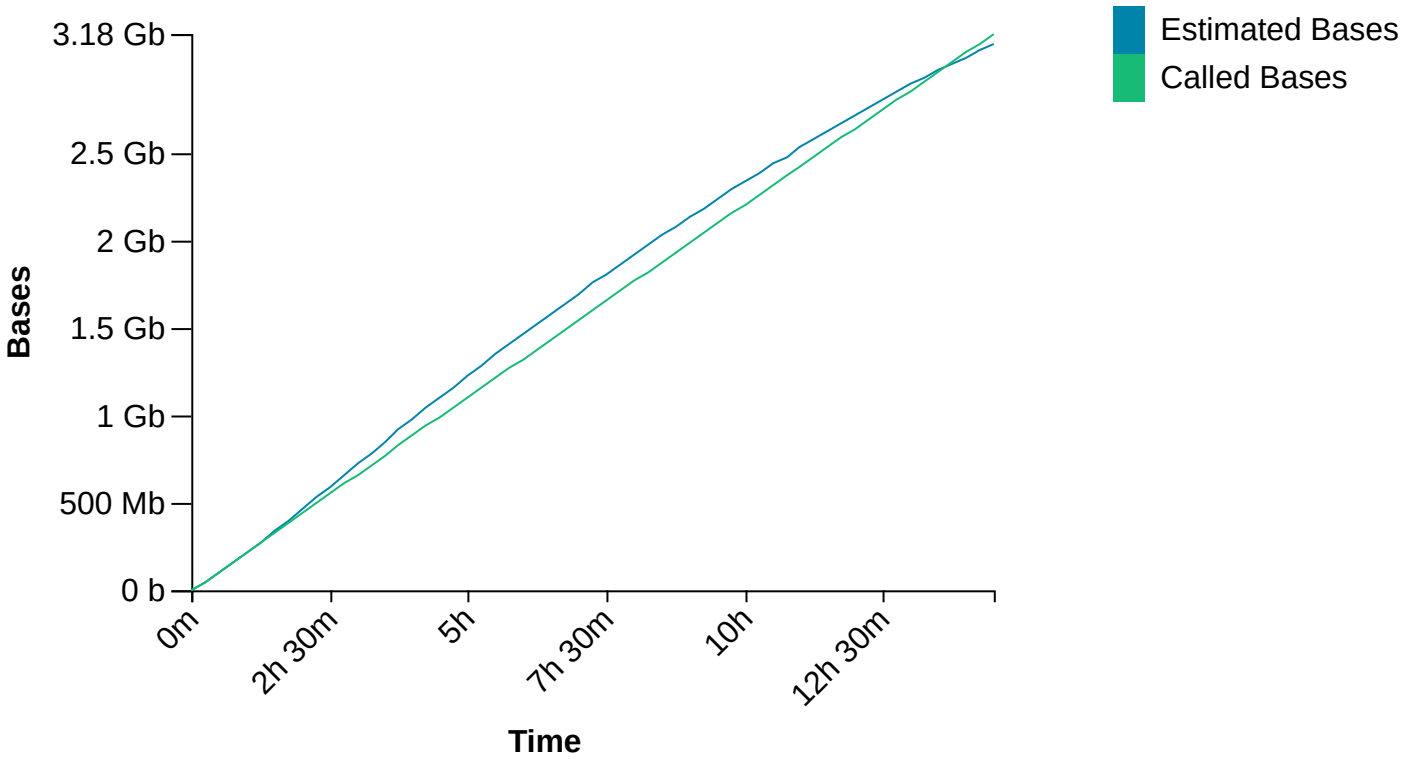
Versions

MinKNOW Core	**3.6.5**
Bream	**4.3.16**
Guppy	**3.2.10**

Cumulative Output Reads

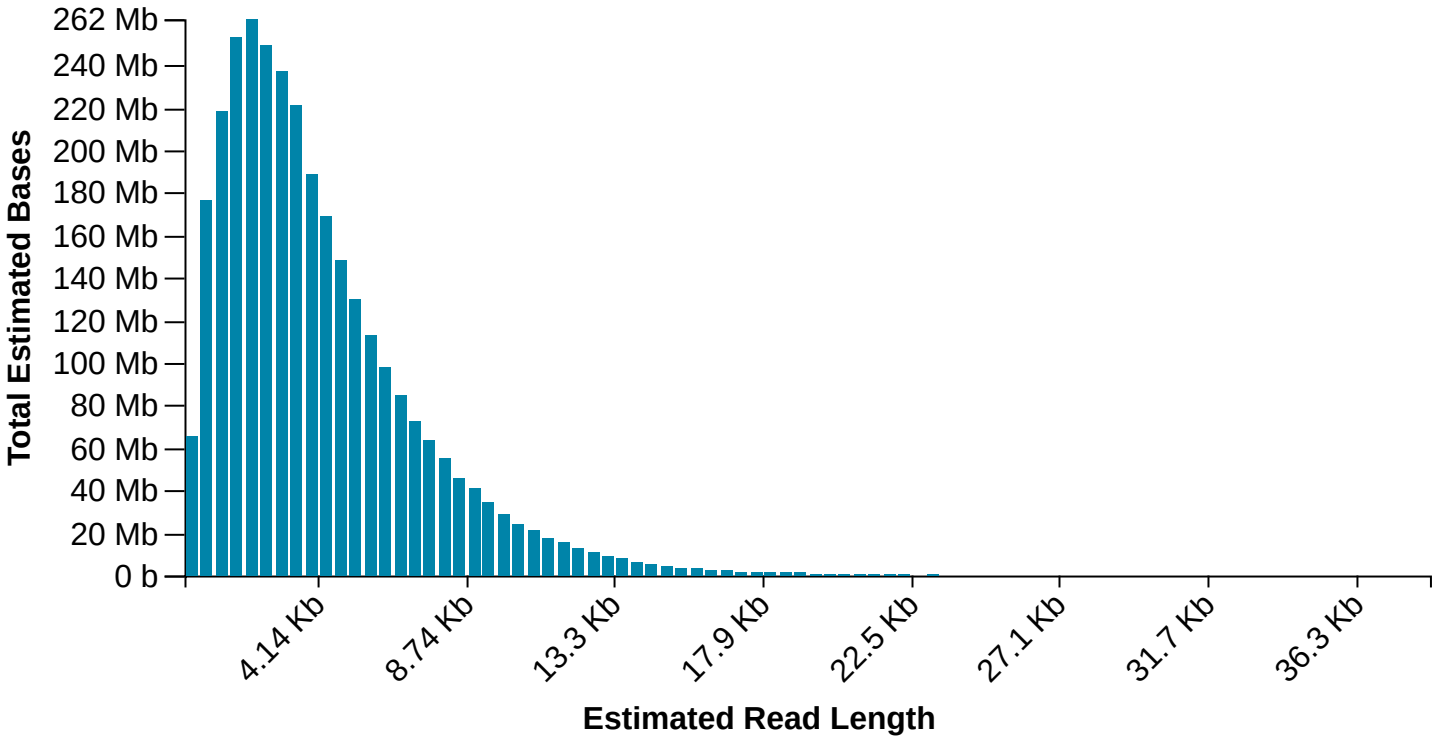


Cumulative Output Bases



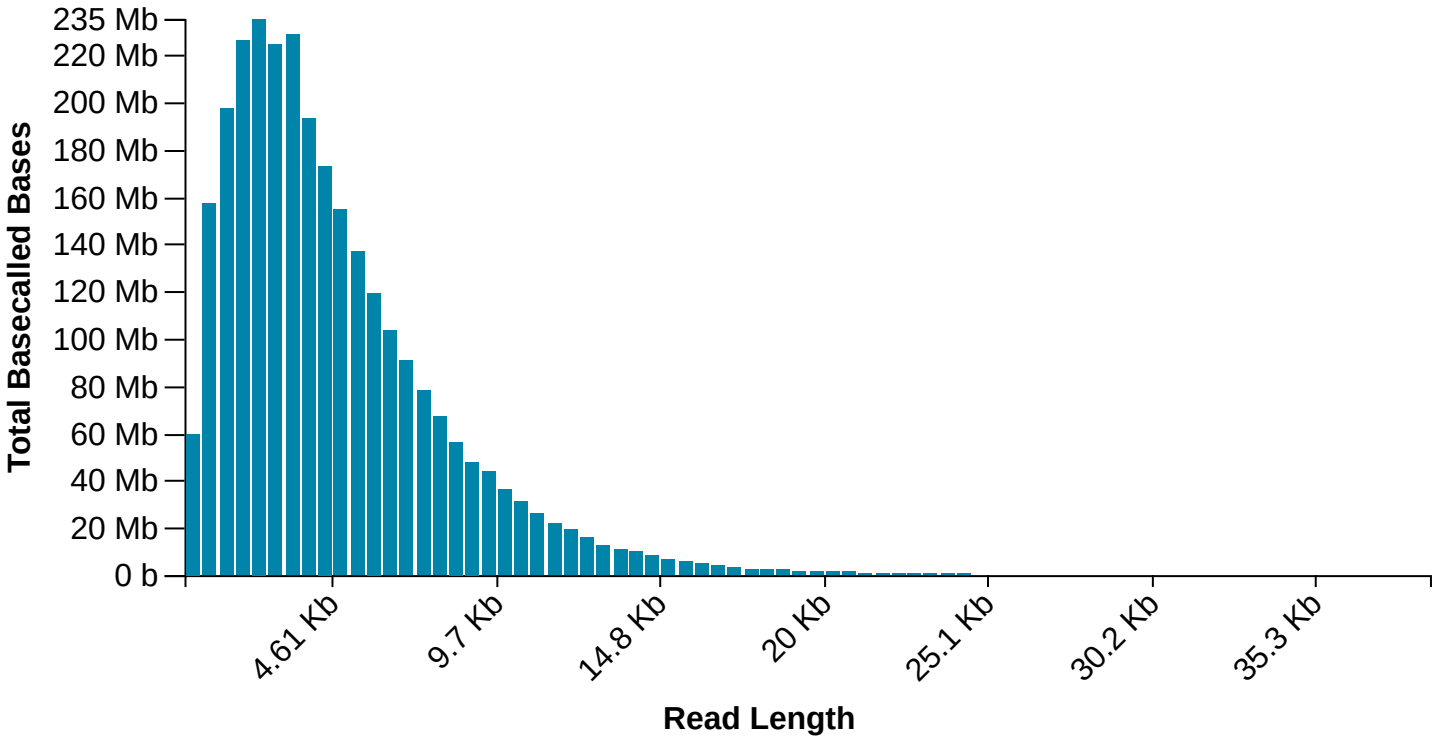
Read Length Histogram Estimated Bases

Estimated N50: 3.42 Kb

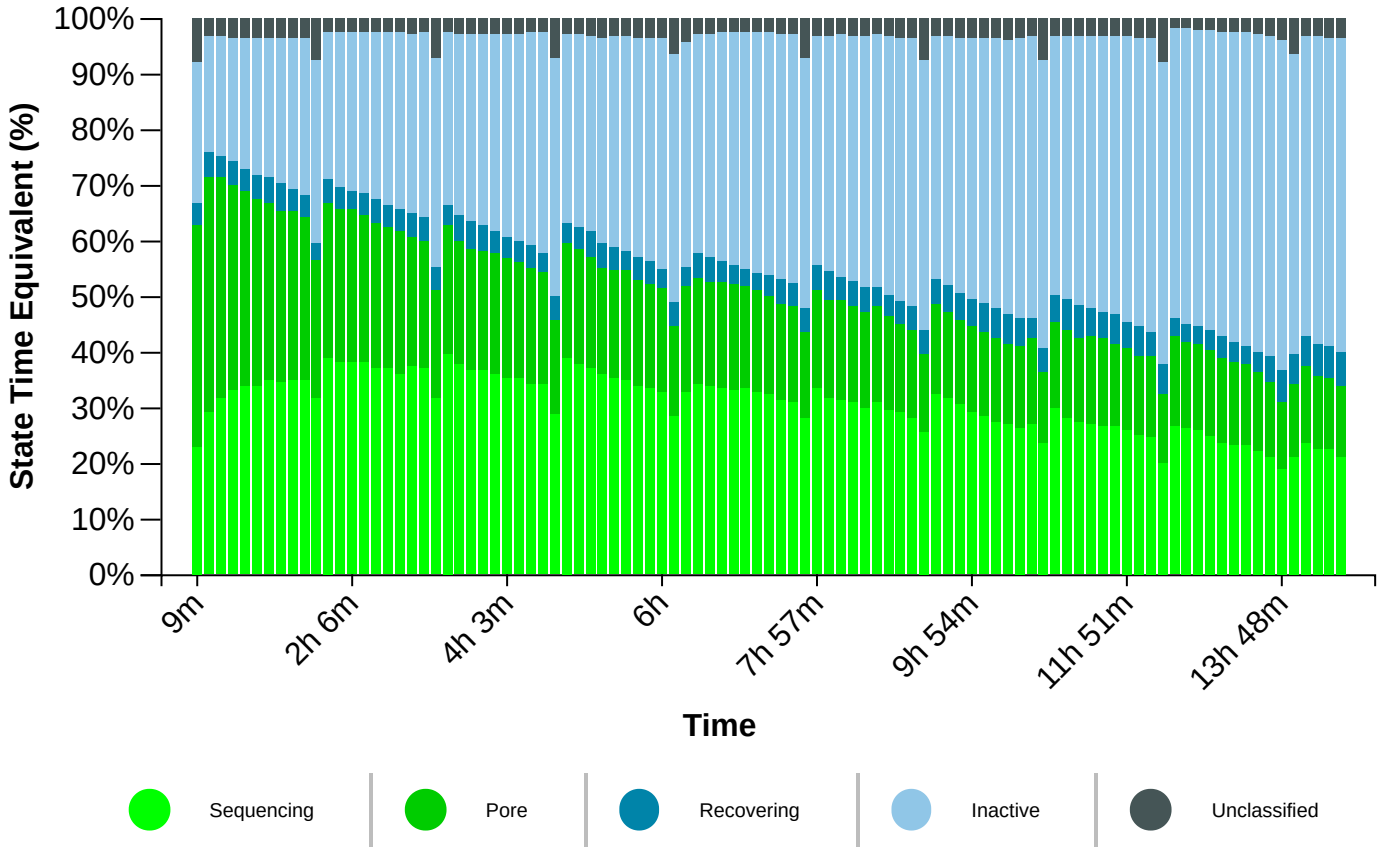


Read Length Histogram Basecalled Bases

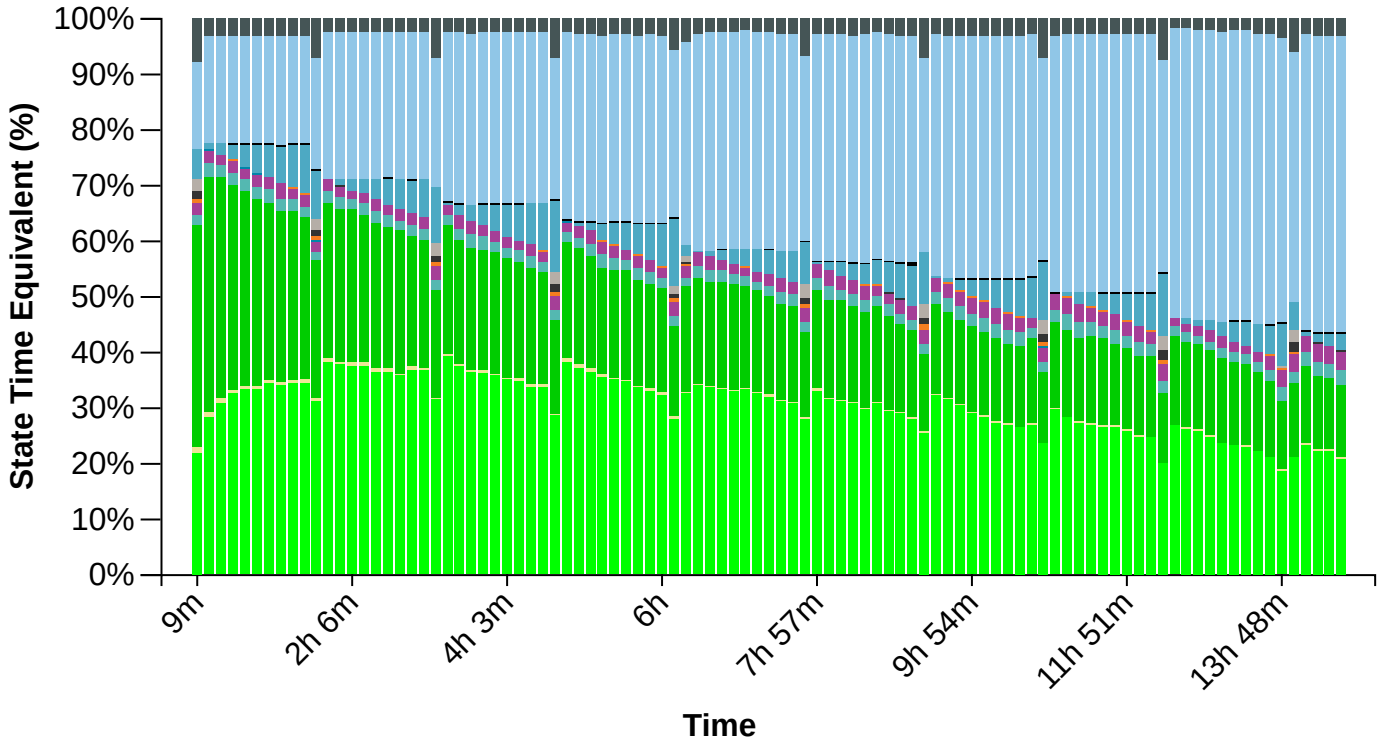
Estimated N50: 3.81 Kb



Duty Time Grouped

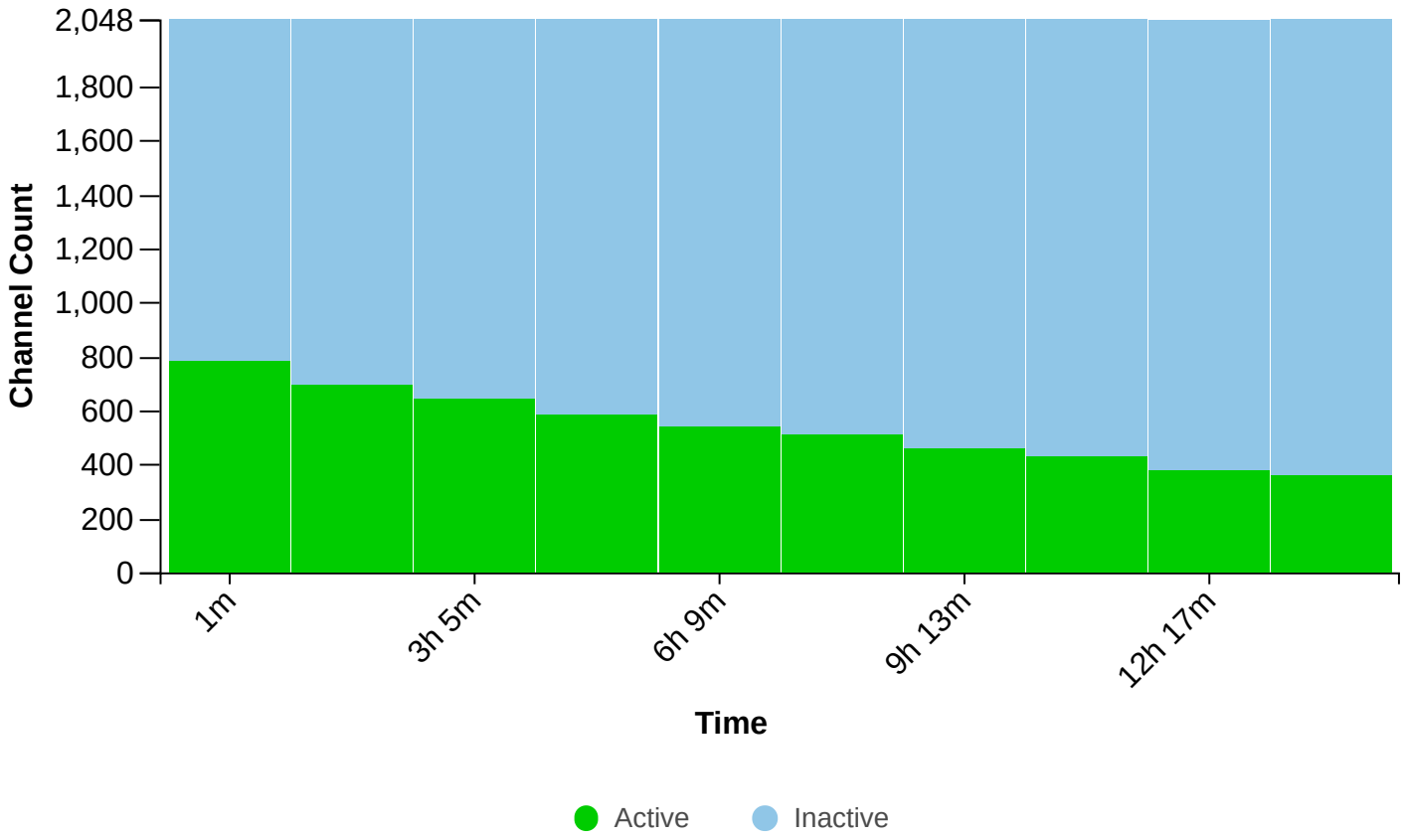


Duty time Categorised

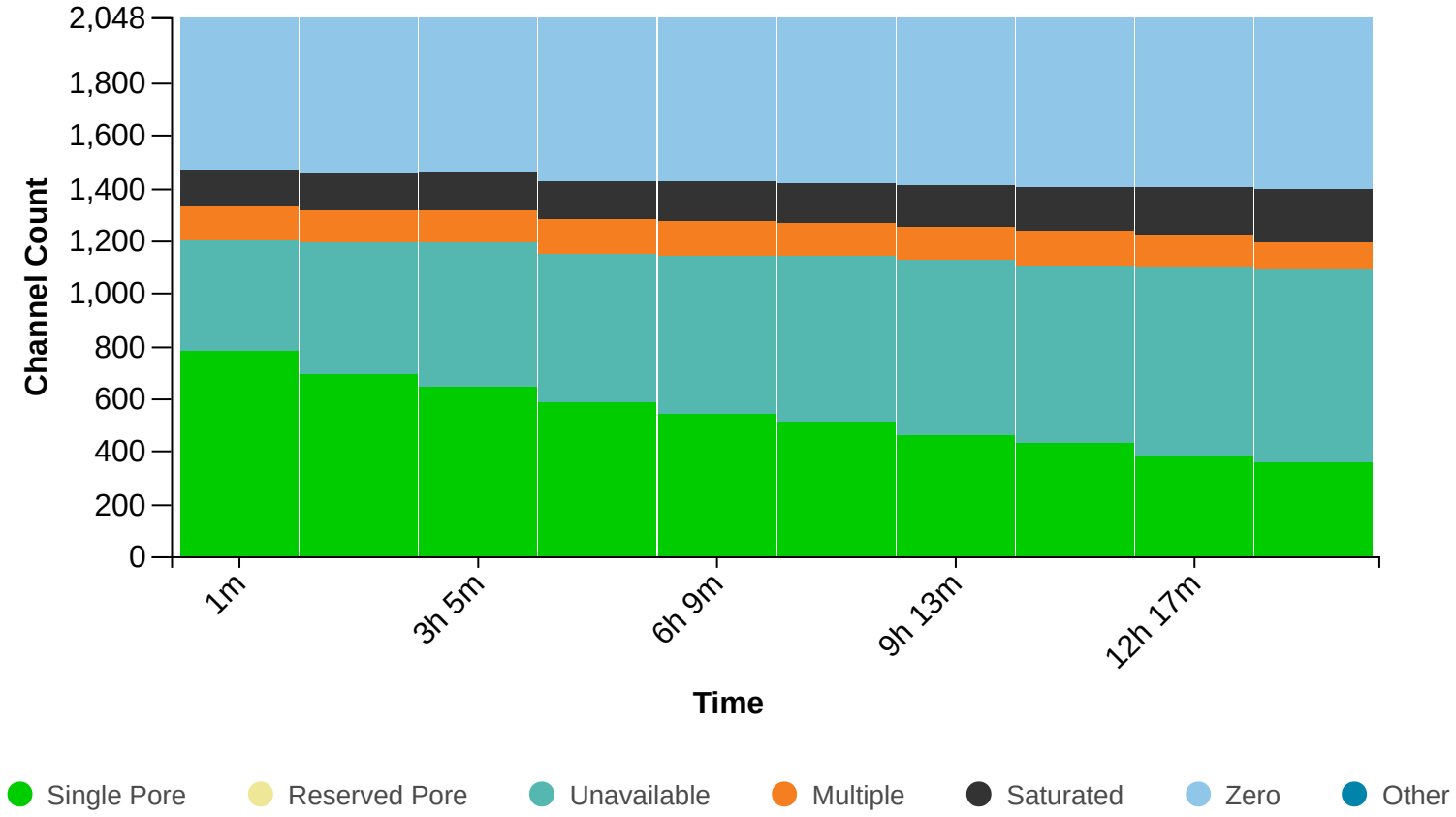


Strand
Adapter
Single Pore
Unavailable
Active Feedback
No Pore From Scan
Out Of Range 2
Possible Multiple
Saturated
Out Of Range 1
Zero
Unclassified
Unclassified_following_reset
Pending_manual_reset
Pending_mux_change
Pending Reselection

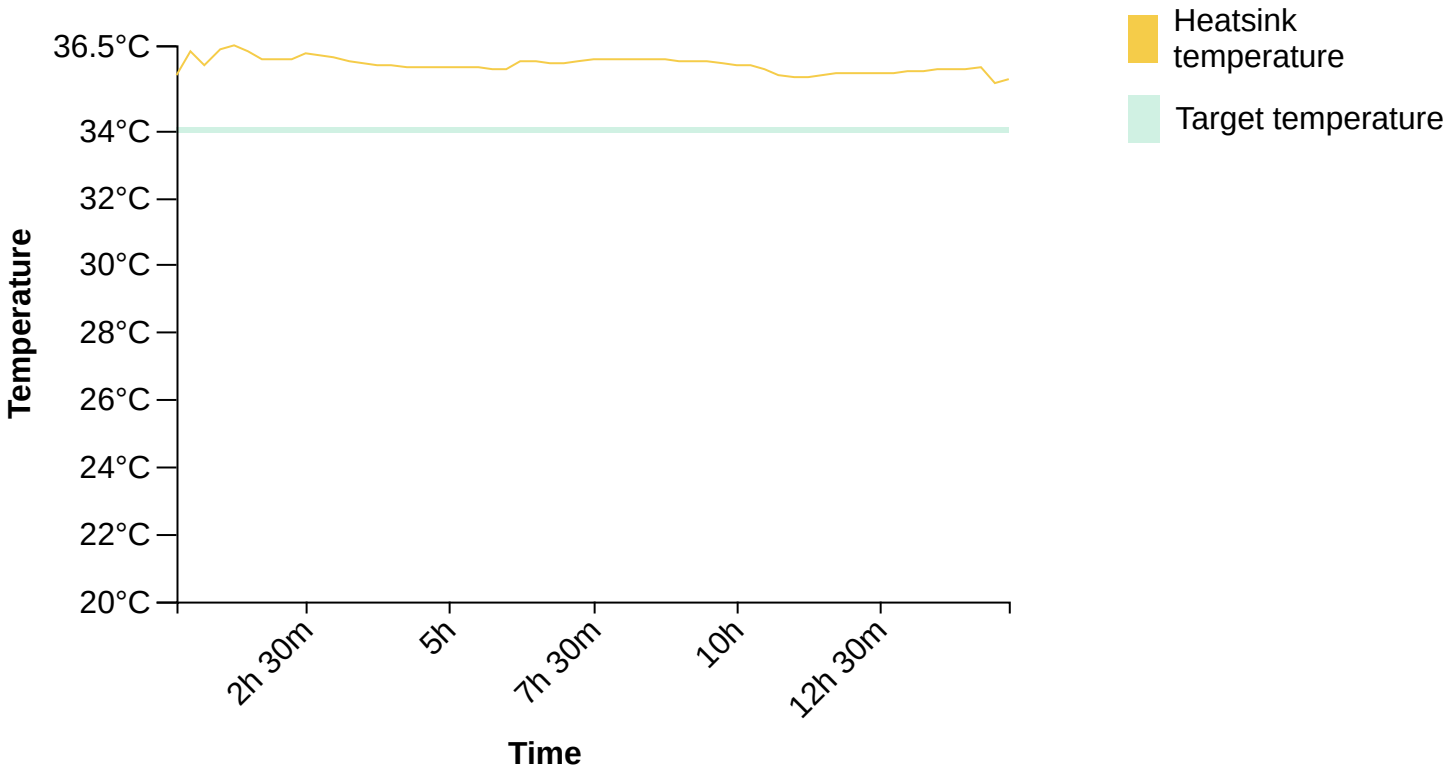
Mux Scan Grouped



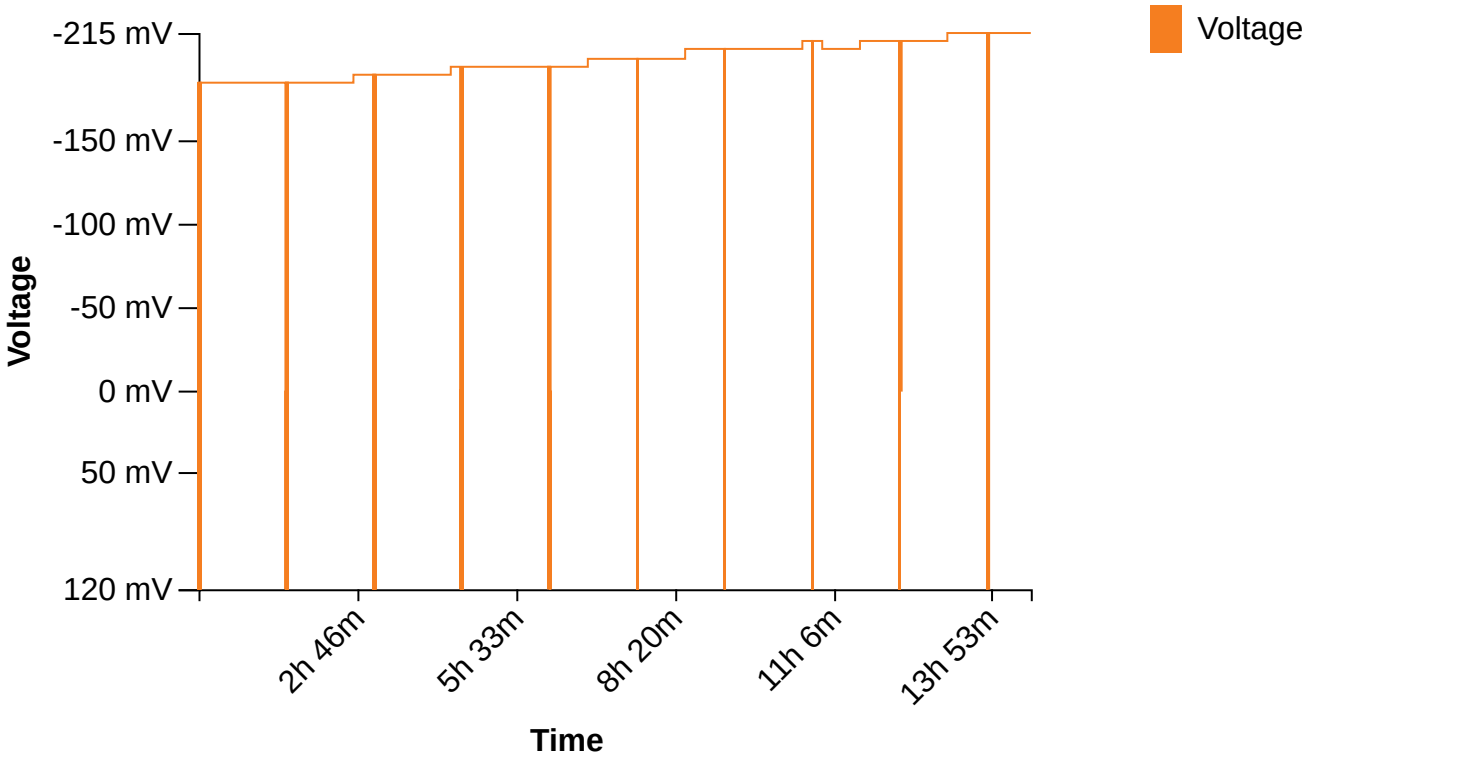
Mux Scan Categorised



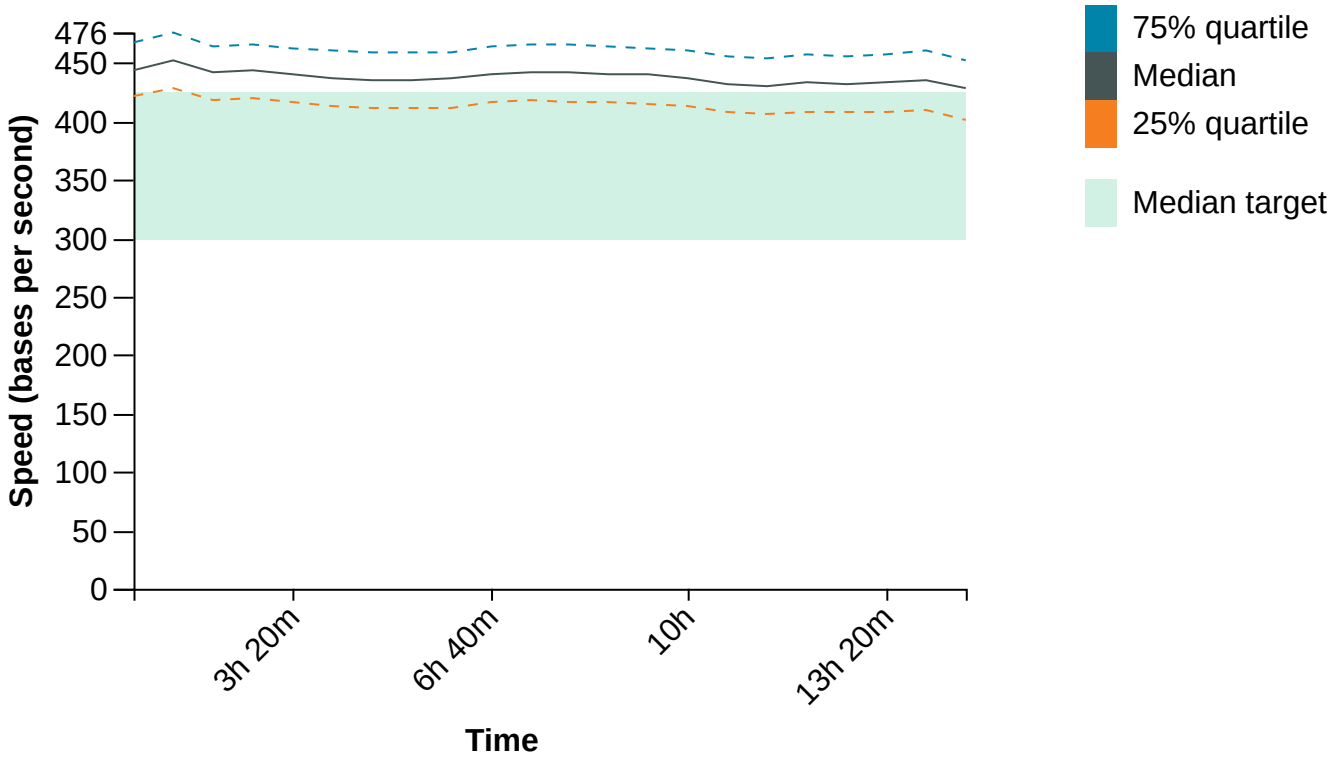
Temperature History



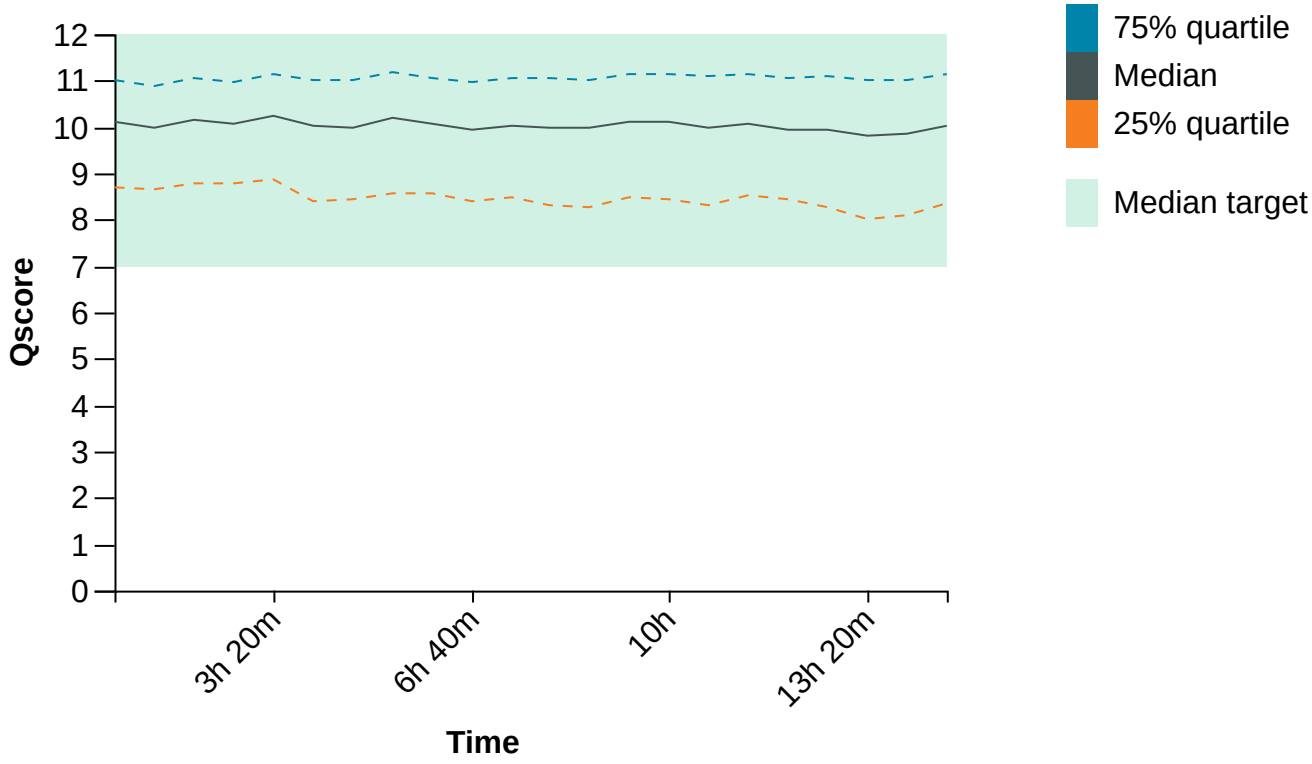
Bias Voltage History



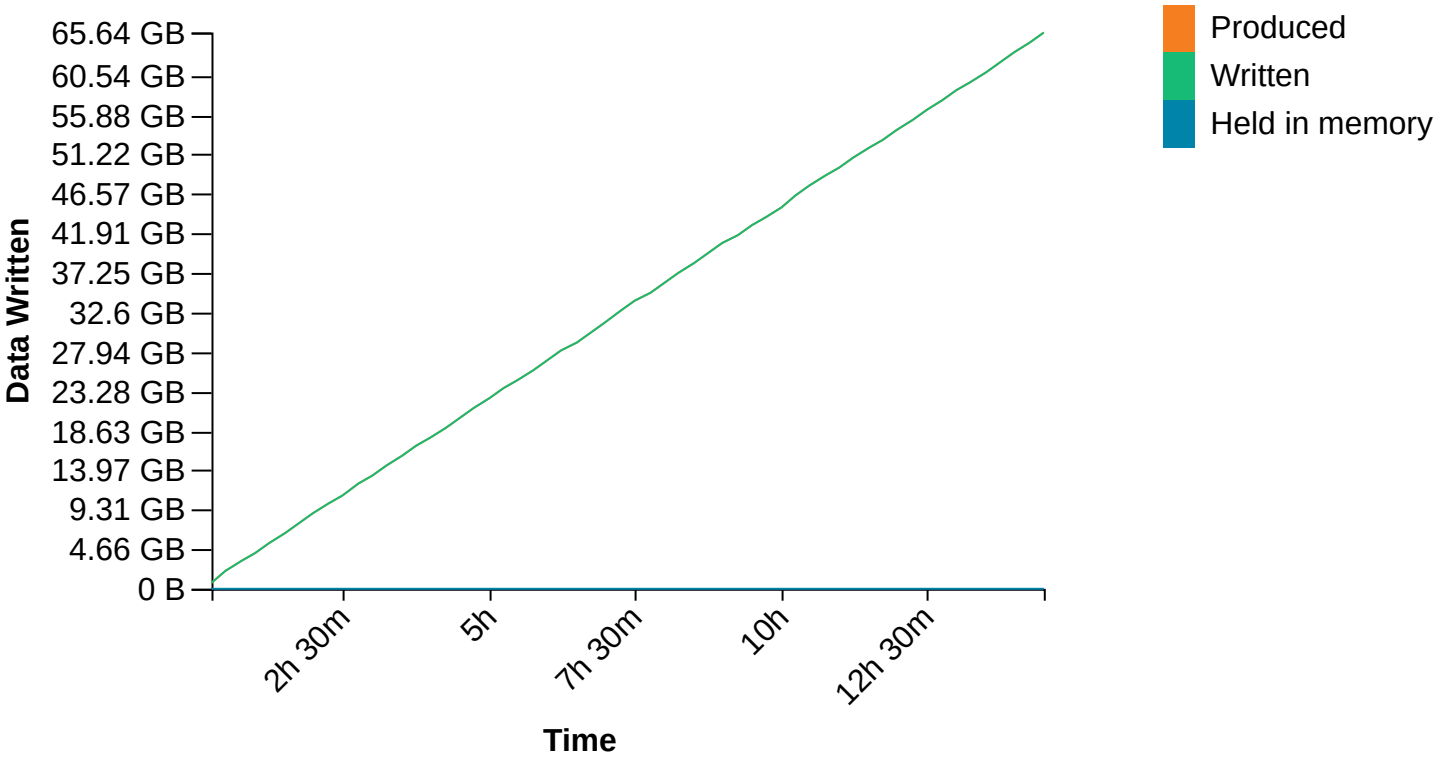
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Flow cell FAO01594 has 358 pores available for sequencing. Starting sequencing with 239 pores July 2, 08:15
- Performing Mux Scan July 2, 08:14
- Flow cell FAO01594 has 384 pores available for sequencing. Starting sequencing with 245 pores July 2, 06:44
- Performing Mux Scan July 2, 06:42
- Flow cell FAO01594 has 435 pores available for sequencing. Starting sequencing with 275 pores July 2, 05:12
- Performing Mux Scan July 2, 05:10
- Flow cell FAO01594 has 461 pores available for sequencing. Starting sequencing with 289 pores July 2, 03:40
- Performing Mux Scan July 2, 03:38
- Flow cell FAO01594 has 514 pores available for sequencing. Starting sequencing with 303 pores July 2, 02:08
- Performing Mux Scan July 2, 02:06
- Flow cell FAO01594 has 540 pores available for sequencing. Starting sequencing with 312 pores July 2, 00:36
- Performing Mux Scan July 2, 00:34
- Flow cell FAO01594 has 582 pores available for sequencing. Starting sequencing with 340 pores July 1, 23:04
- Performing Mux Scan July 1, 23:02
- Flow cell FAO01594 has 641 pores available for sequencing. Starting sequencing with 355 pores July 1, 21:32
- Performing Mux Scan July 1, 21:30
- Flow cell FAO01594 has 697 pores available for sequencing. Starting sequencing with 377 pores July 1, 20:00
- Performing Mux Scan July 1, 19:58
- Disk usage alert – you only have 392 GB of space free, which is insufficient for the run. Please free up some space, otherwise your run will stop in approximately 1d 21h 11m. July 1, 18:39
- Flow cell FAO01594 has 780 pores available for sequencing. Starting sequencing with 413 pores July 1, 18:28
- Performing Mux Scan July 1, 18:26
- Starting sequencing procedure July 1, 18:26
- Failed to reach 34.0°C within 300 seconds(with 0.1 tolerance). The experiment will continue anyway. July 1, 18:26
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C July 1, 18:21
- Disk / has 394 GB space remaining July 1, 18:21