Run Info

Experiment Name	**ncov_ucdh_env1_run1**
Sample ID	**ncov_ucdh_env1_run1**
Run ID	**25240491-27d6-4219-a825-722520587610**
Flow Cell Id	**FAN33832**
Start Time	**May 23, 00:32**
Run Length	**15h 13m**

Run Summary

Reads Generated	**405.97 K**
Bases Generated	**214.86 Mb**
Estimated Bases	**225.11 Mb**

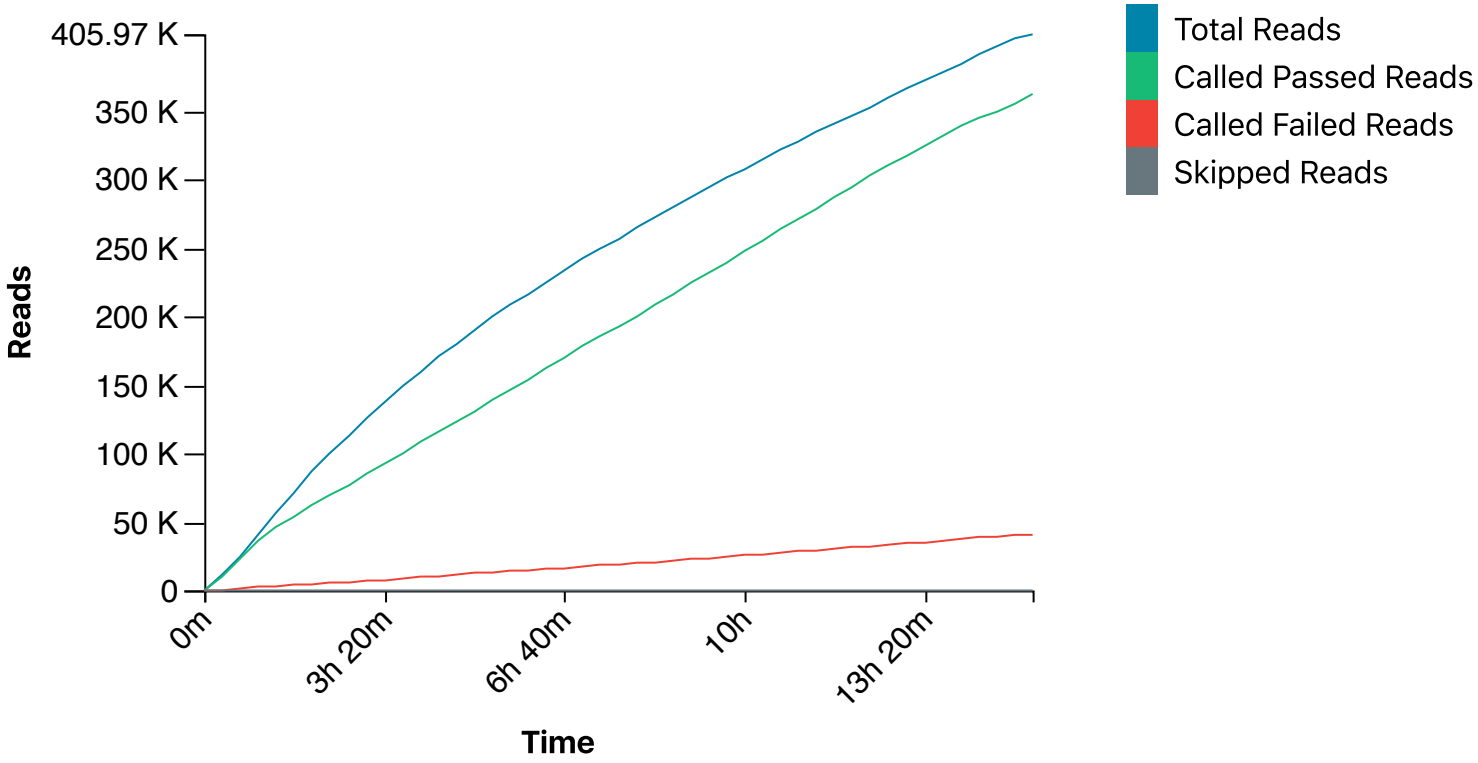
Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-LSK109**
Basecalling	**on**
Specified Run Length	**72 hours**
Initial Bias Voltage	**-180 mV**
FAST5 Output	**Enabled**
FAST5 Output Options	**zlib_compress,fastq,raw**
FAST5 Reads per File	**1000**
FASTQ Output	**Enabled**
FASTQ Reads per File	**1000**
Active Channel Selection	**Enabled**
Mux Scan Period	**1 hour 30 minutes**
Reserved Pores	**0 %**
Basecall Model	**Fast basecalling**

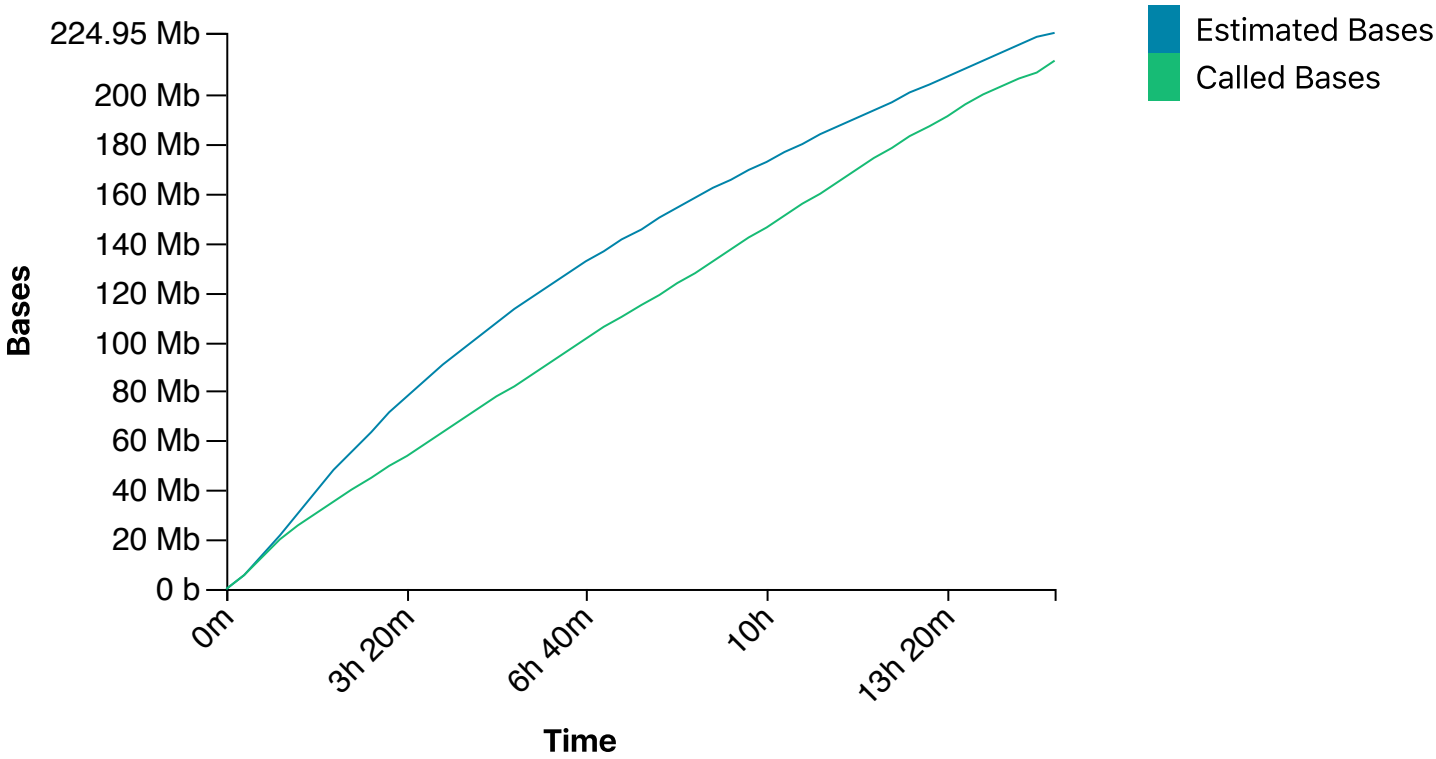
Versions

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

Cumulative Output Reads

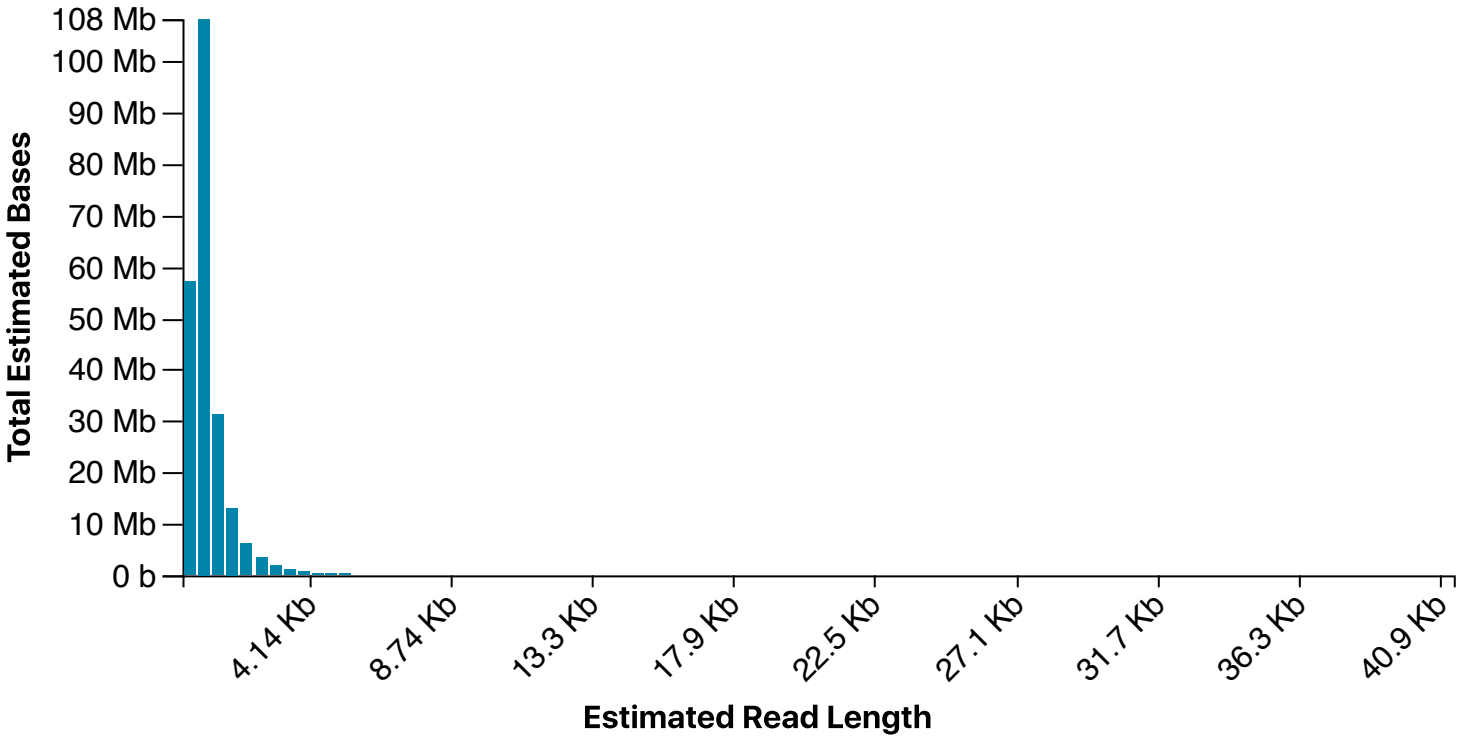


Cumulative Output Bases



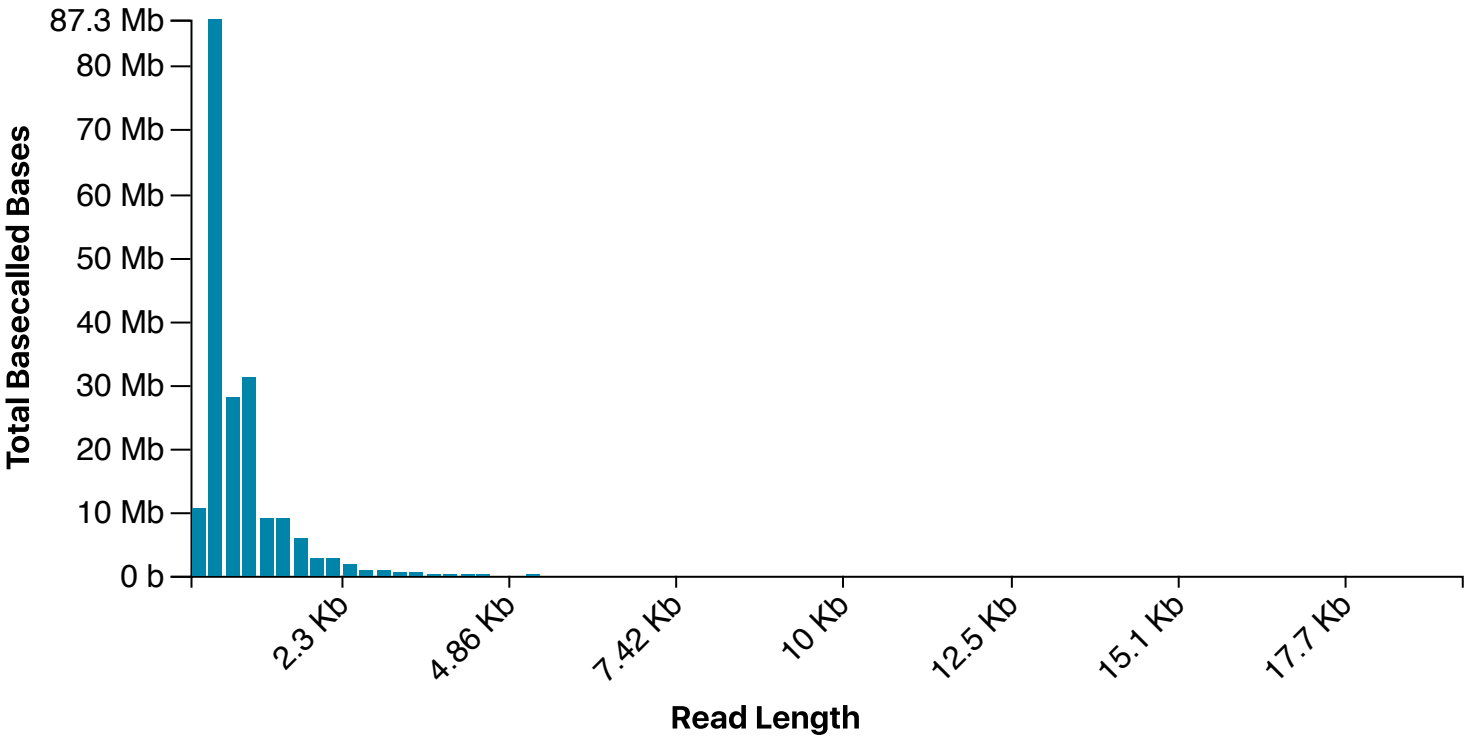
Read Length Histogram Estimated Bases

Estimated N50: 545 b

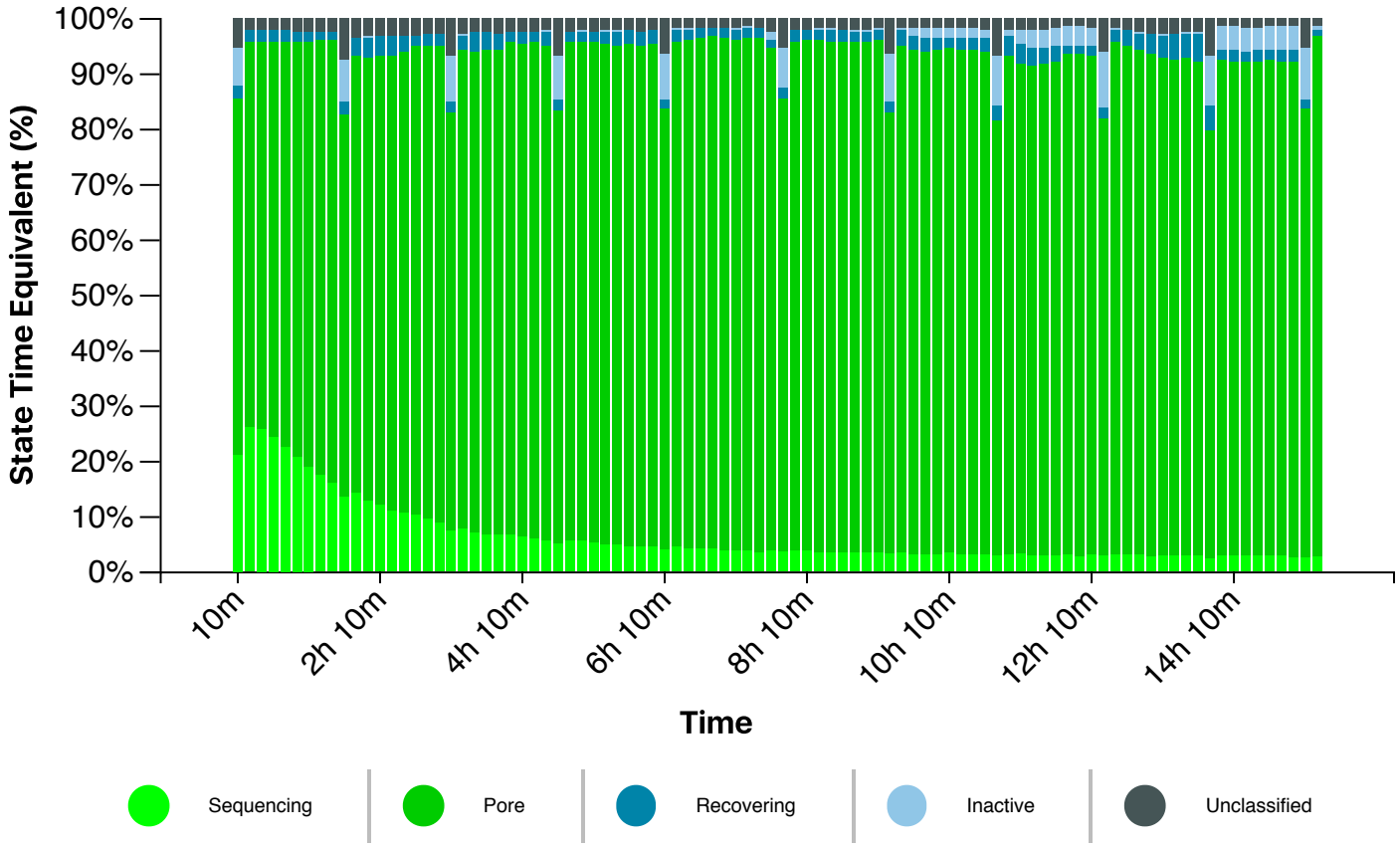


Read Length Histogram Basecalled Bases

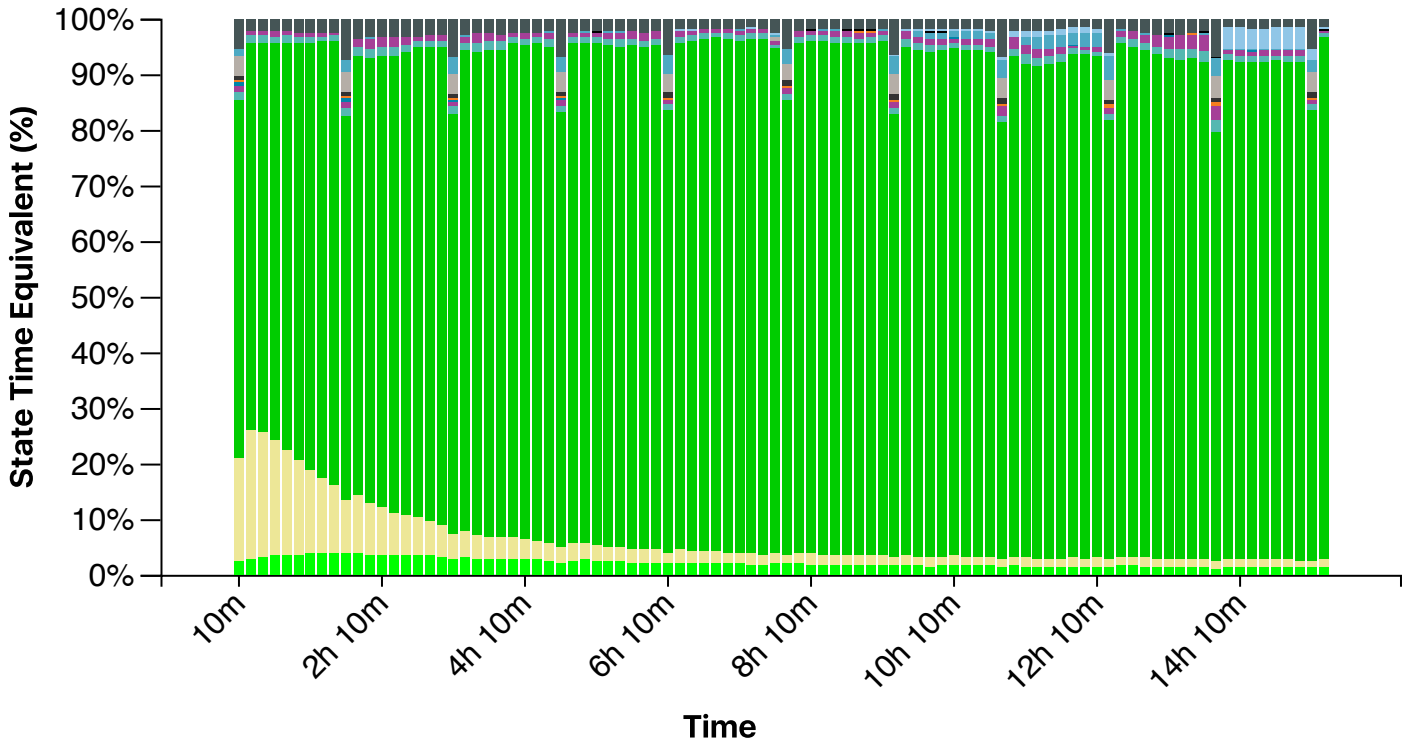
Estimated N50: 510 b



Duty Time Grouped



Duty time Categorised



Strand
Adapter

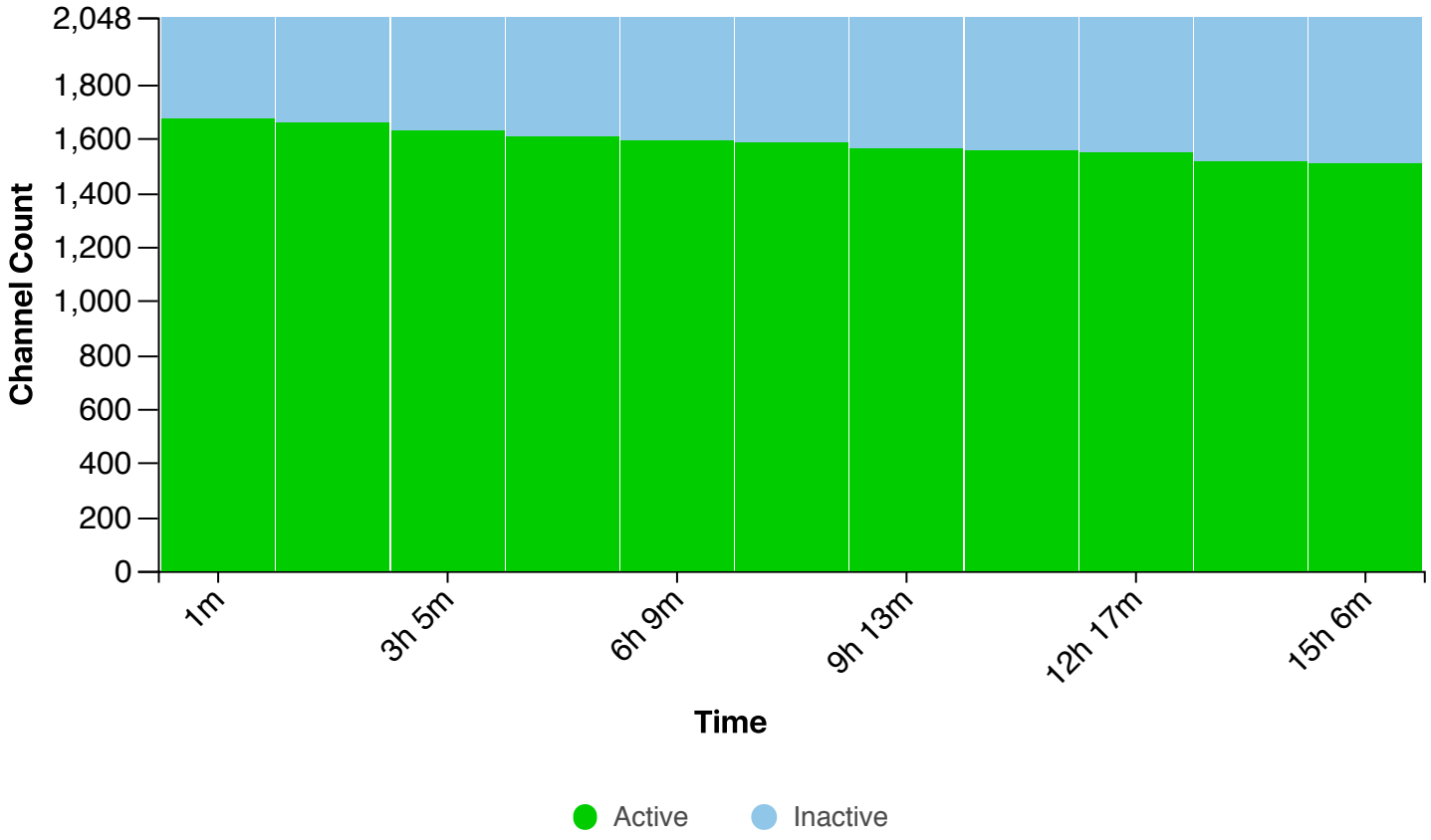
Single Pore

Unavailable
Active Feedback

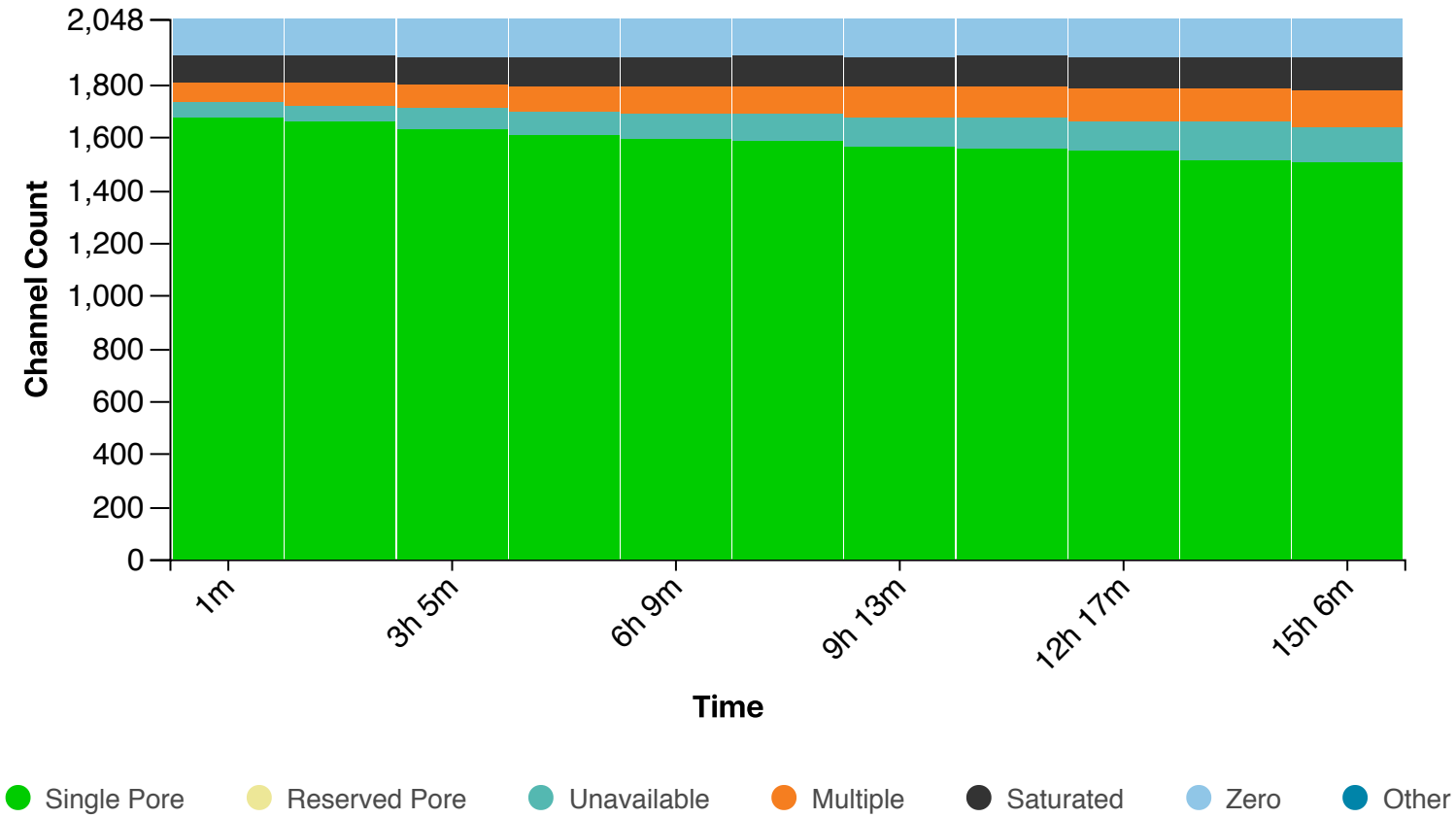
No Pore From Scan
Out Of Range 2
Possible Multiple
Saturated
Out Of Range 1
Zero

Unclassified
Unclassified_following_reset
Pending_manual_reset
Pending_mux_change
Pending Reselection

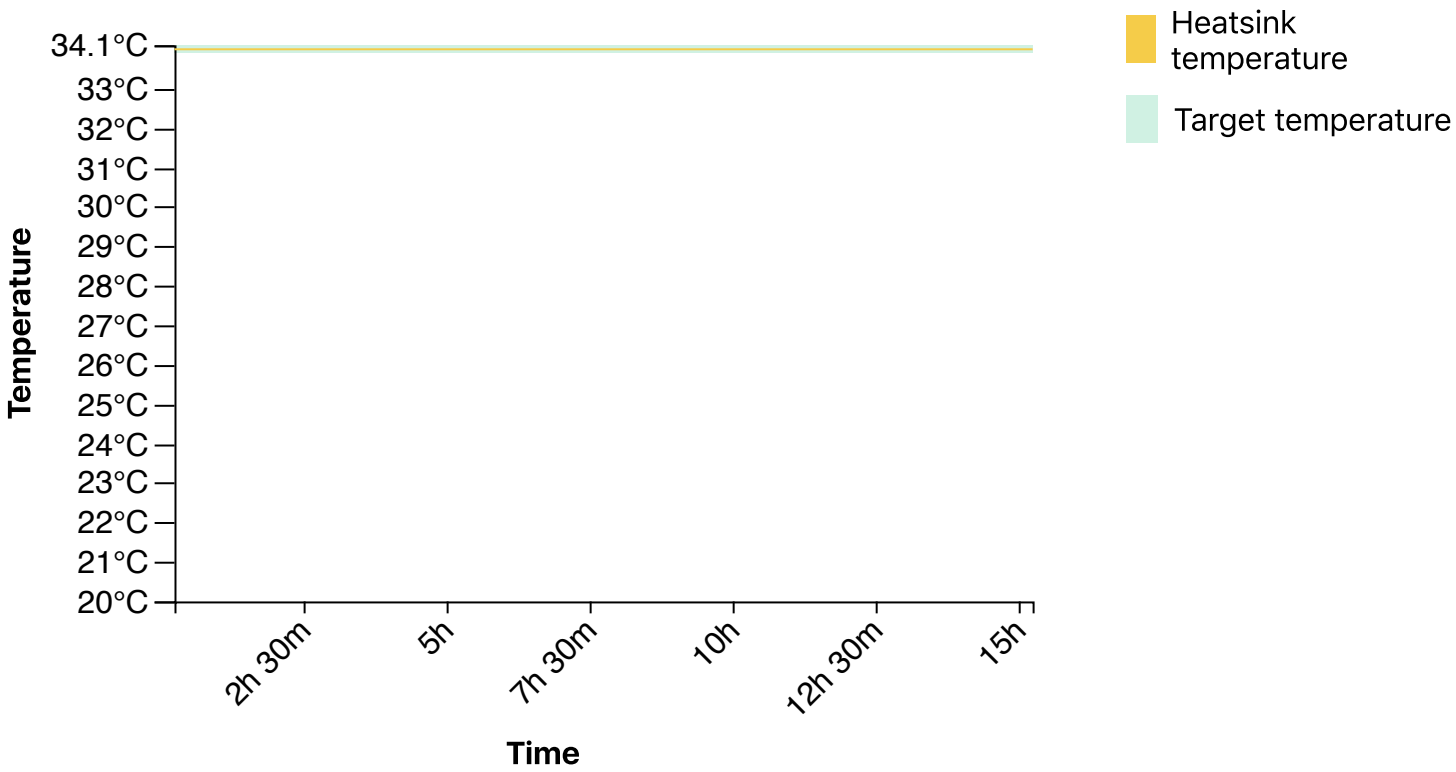
Mux Scan Grouped



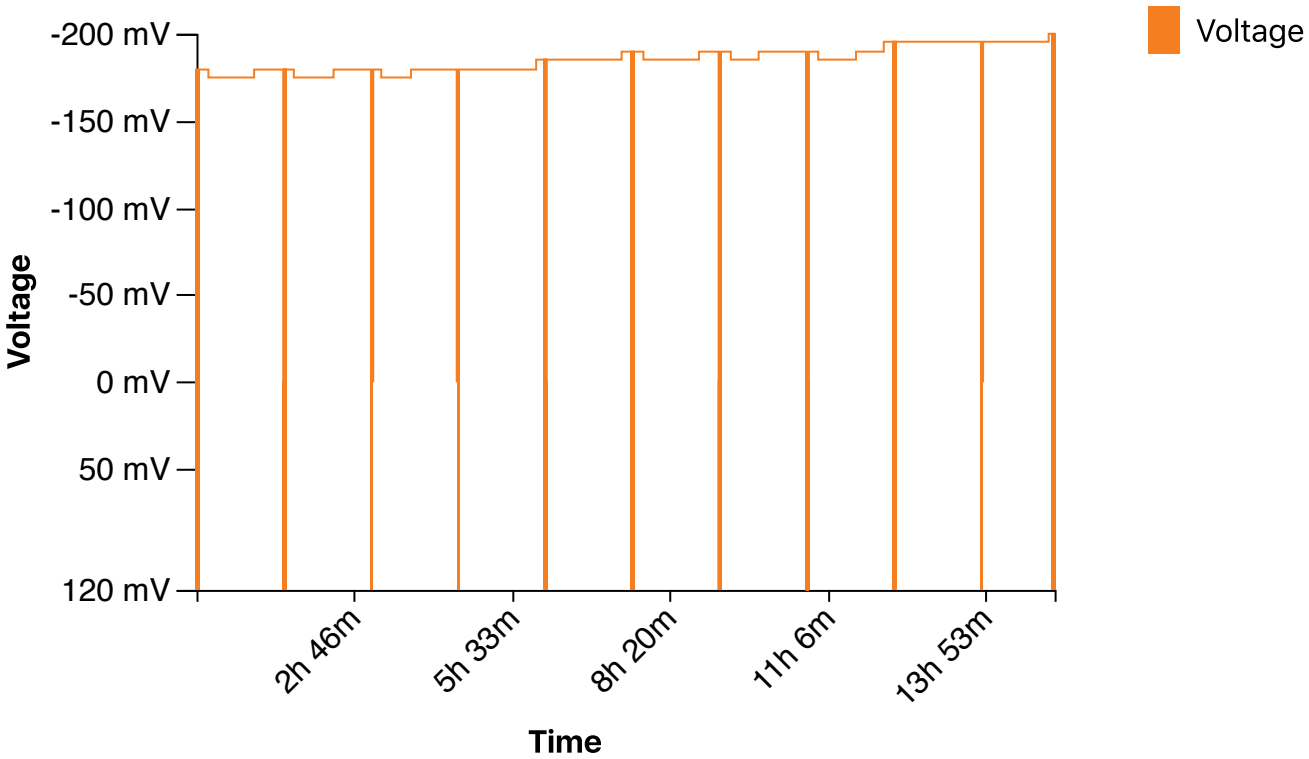
Mux Scan Categorised



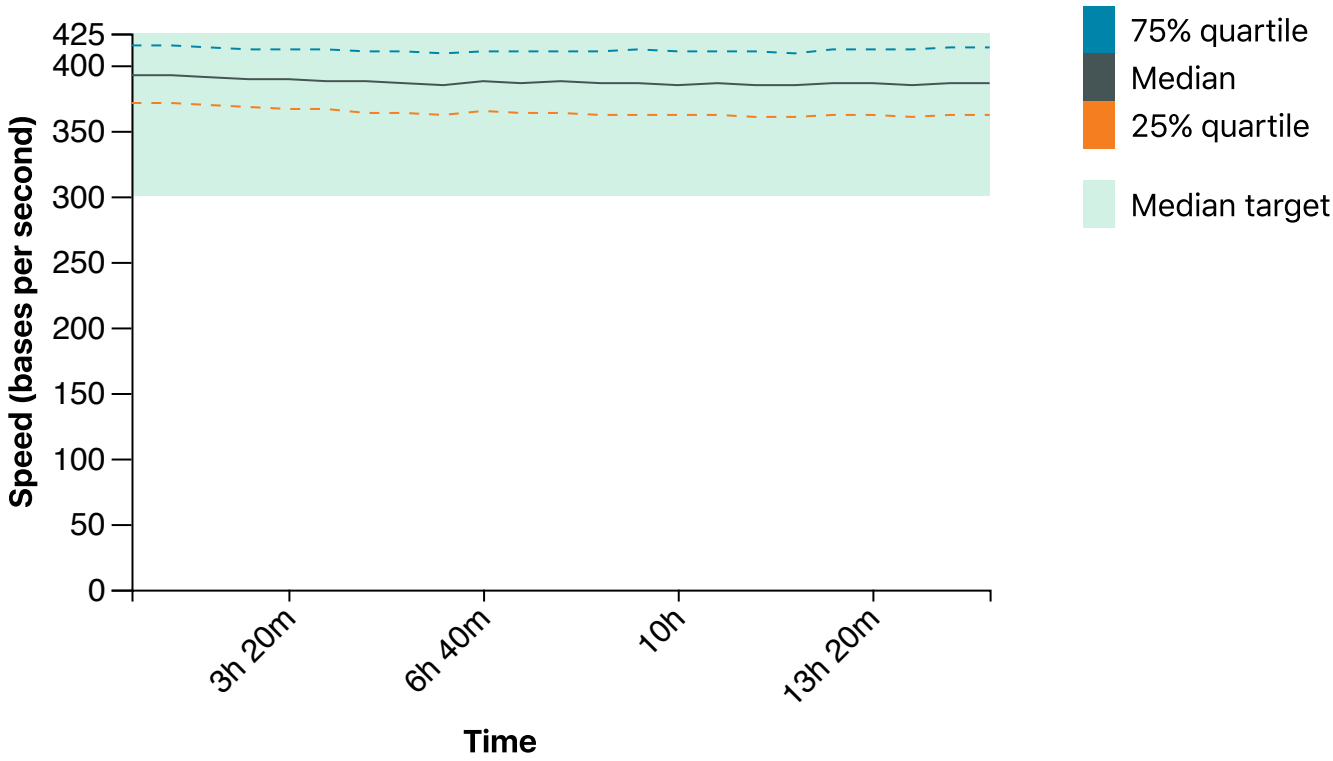
Temperature History



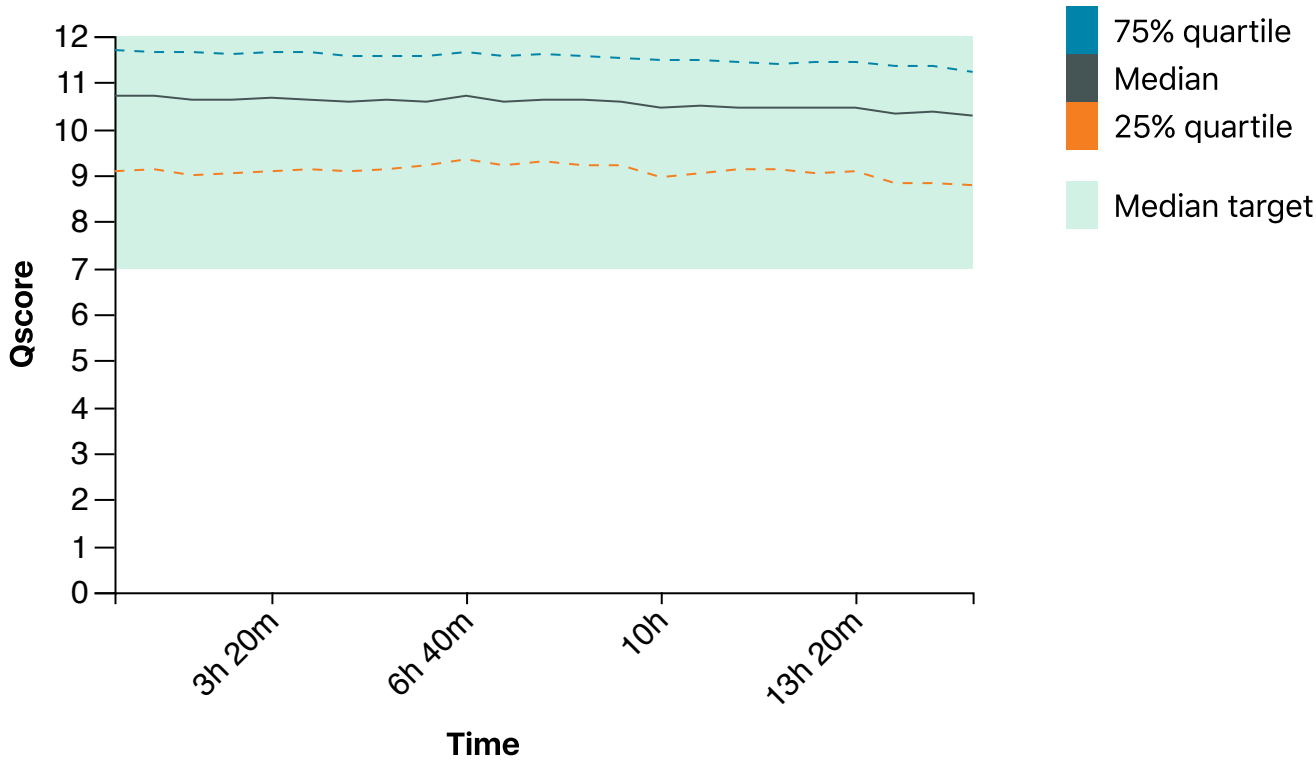
Bias Voltage History



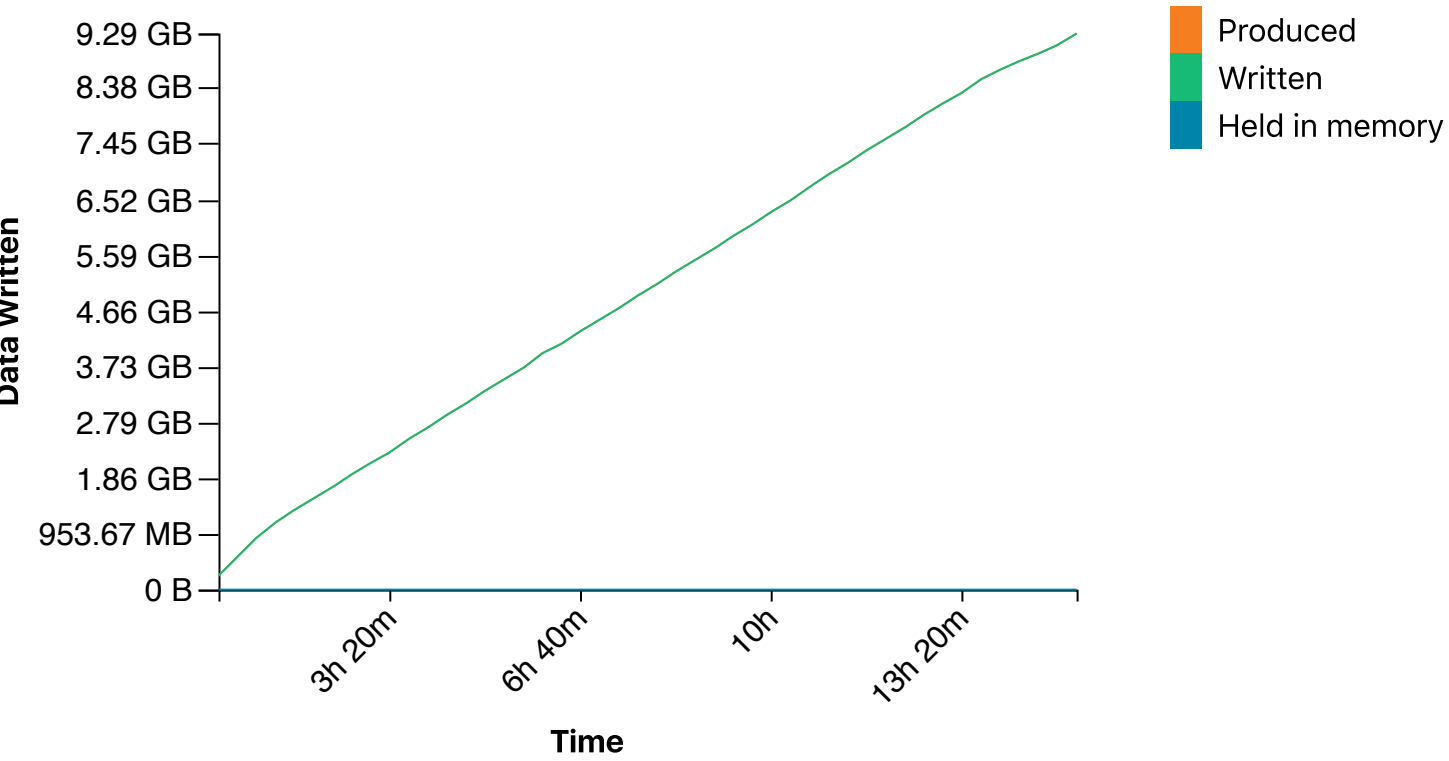
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Flow cell FAN33832 has 1508 pores available for sequencing. Starting sequencing with 510 pores May 23, 15:39
- Performing Mux Scan May 23, 15:37
- Flow cell FAN33832 has 1511 pores available for sequencing. Starting sequencing with 492 pores May 23, 14:23
- Performing Mux Scan May 23, 14:21
- Flow cell FAN33832 has 1550 pores available for sequencing. Starting sequencing with 512 pores May 23, 12:51
- Performing Mux Scan May 23, 12:49
- Flow cell FAN33832 has 1558 pores available for sequencing. Starting sequencing with 507 pores May 23, 11:19
- Performing Mux Scan May 23, 11:17
- Flow cell FAN33832 has 1566 pores available for sequencing. Starting sequencing with 510 pores May 23, 09:47
- Performing Mux Scan May 23, 09:45
- Flow cell FAN33832 has 1587 pores available for sequencing. Starting sequencing with 512 pores May 23, 08:15
- Performing Mux Scan May 23, 08:13
- Flow cell FAN33832 has 1597 pores available for sequencing. Starting sequencing with 511 pores May 23, 06:43
- Performing Mux Scan May 23, 06:41
- Flow cell FAN33832 has 1607 pores available for sequencing. Starting sequencing with 512 pores May 23, 05:11
- Performing Mux Scan May 23, 05:09
- Flow cell FAN33832 has 1632 pores available for sequencing. Starting sequencing with 512 pores May 23, 03:39
- Performing Mux Scan May 23, 03:37
- Flow cell FAN33832 has 1659 pores available for sequencing. Starting sequencing with 512 pores May 23, 02:07
- Performing Mux Scan May 23, 02:05
- Flow cell FAN33832 has 1673 pores available for sequencing. Starting sequencing with 512 pores May 23, 00:35
- Performing Mux Scan May 23, 00:33
- Starting sequencing procedure May 23, 00:33
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C May 23, 00:32
- Disk / has 1881 GB space remaining May 23, 00:32