Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**EIMock_6kbp_control2_050121**
Sample ID	**EIMock_6kbp_control2_050121**
Run ID	**0cce89f2-889b-44cb-978f-1922dab681b3**
Flow Cell Id	**FAO54786**
Start Time	**January 5, 00:09**
Run Length	**9h 35m**

Run Summary

Reads Generated	**336.62 K**
Passed Bases	**1.43 Gb**
Failed Bases	**207.75 Mb**
Estimated Bases	**1.68 Gb**

Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-LSK109**
Initial Bias Voltage	**-195 mV**
FAST5 Output	**Enabled**
FASTQ Output	**Enabled**
BAM Output	**Enabled**
Active Channel Selection	**Enabled**
Basecalling	**on**
Specified Run Length	**72 hours**
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

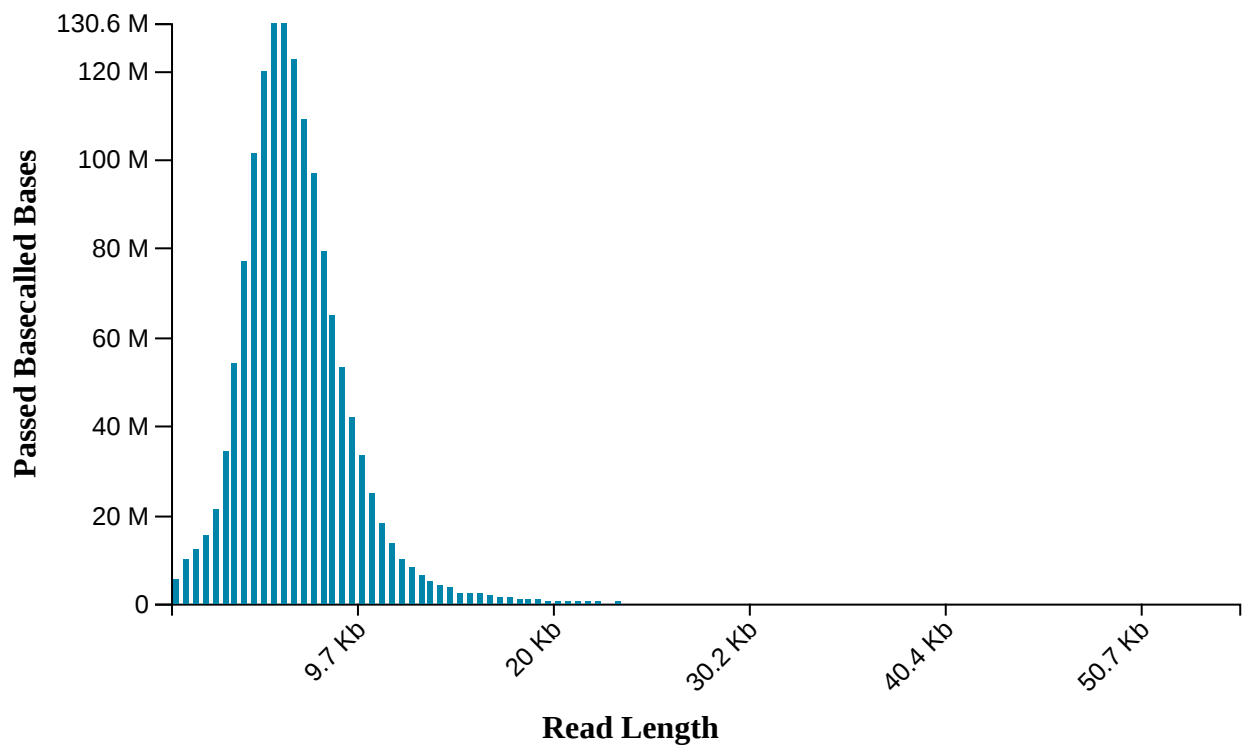|	
MinKNOW	**20.10.6**
MinKNOW Core	**4.1.2**
Bream	**6.1.4**
Guppy	**4.2.3**

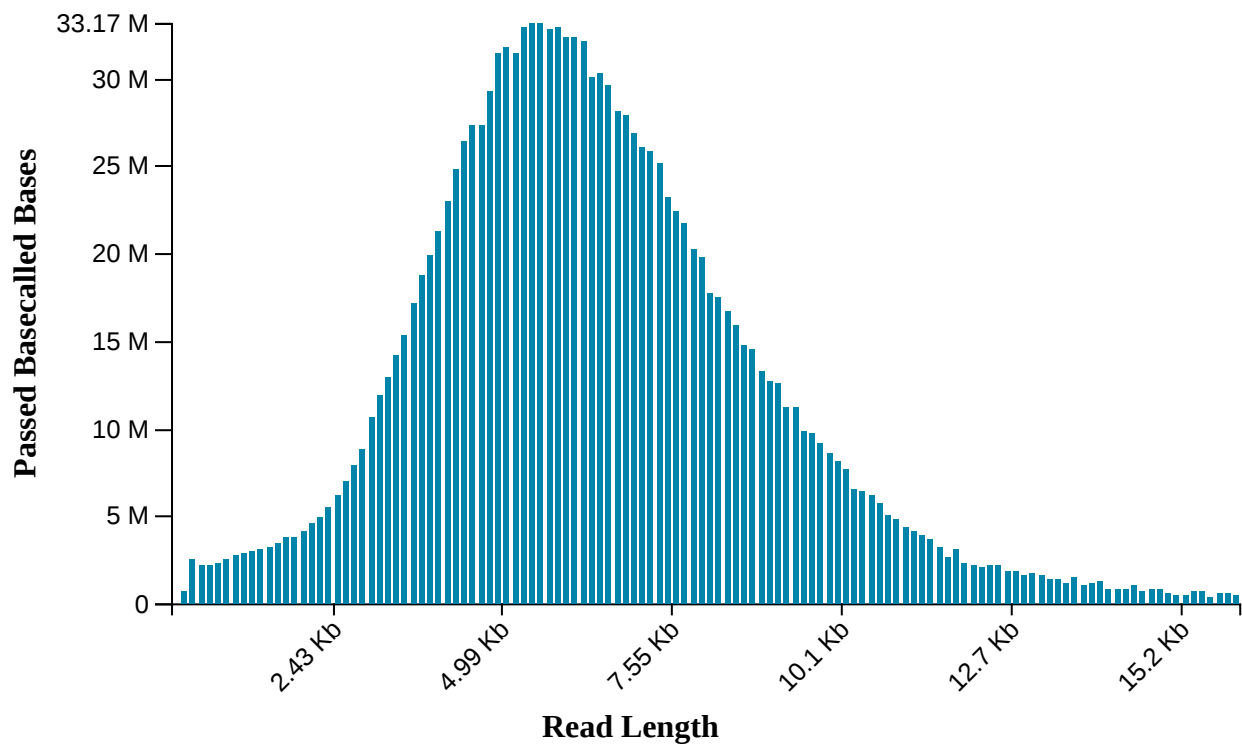## **Cumulative Output Reads**
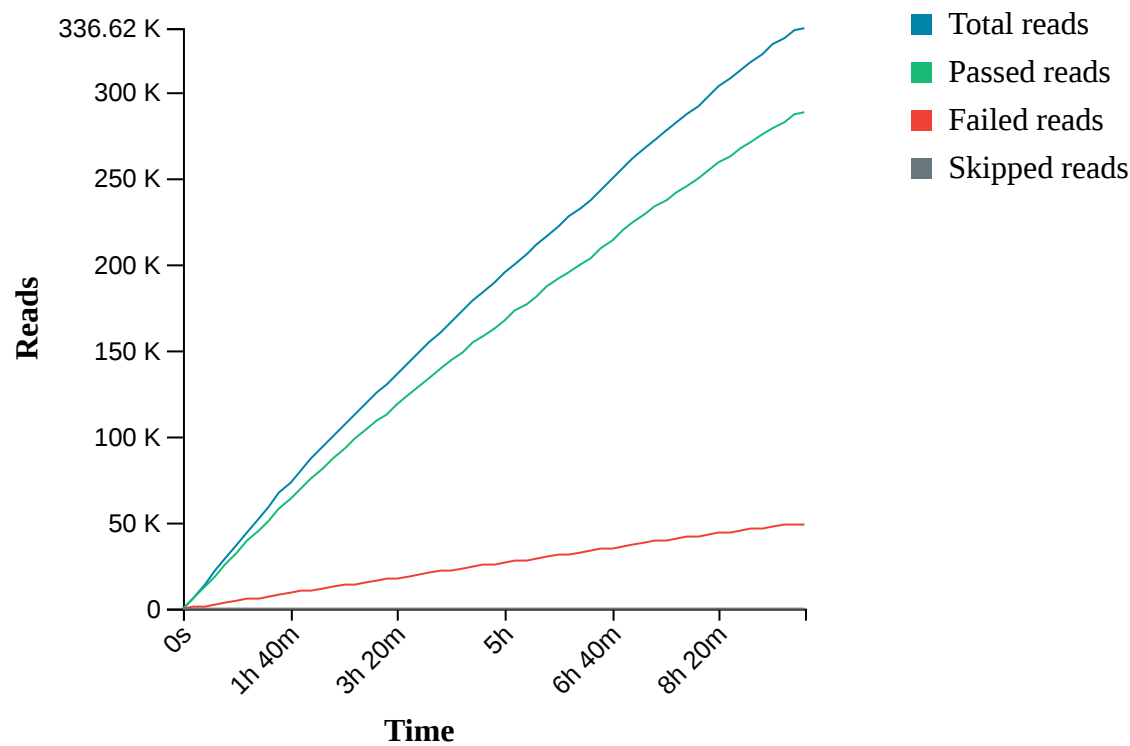
Cumulative Output Bases
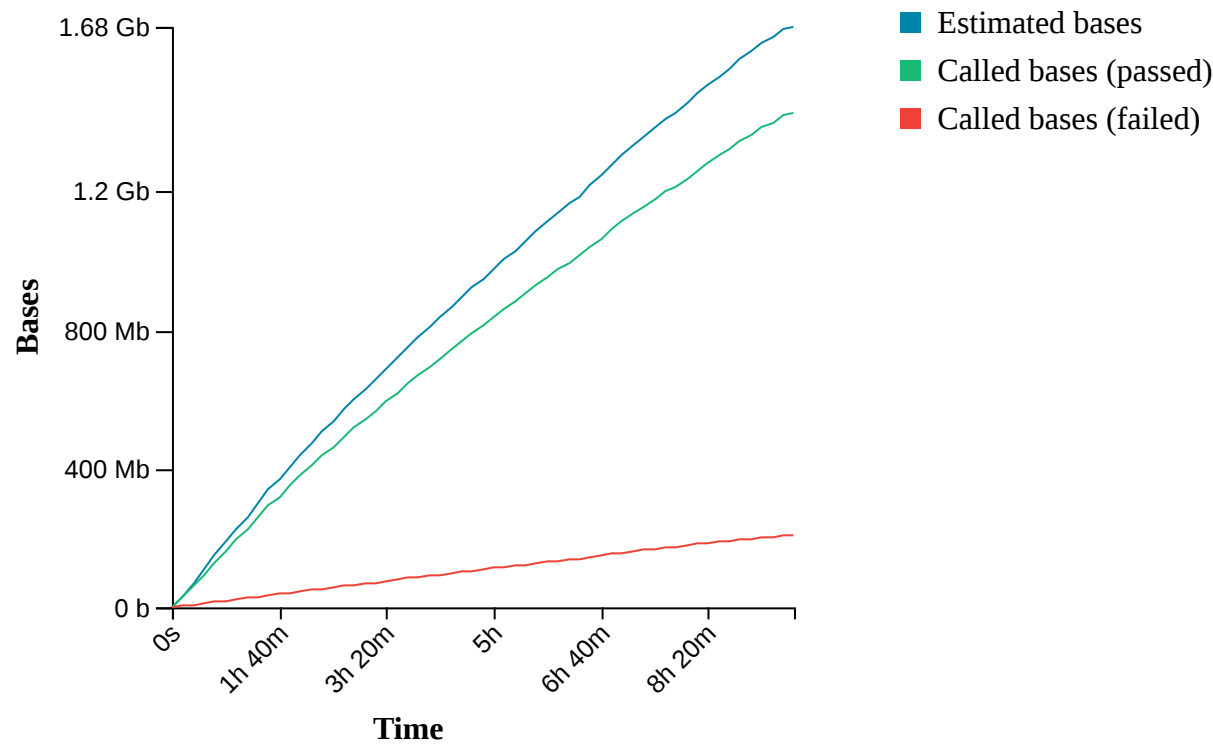
Read Length Histogram Estimated Bases - Outliers Discarded
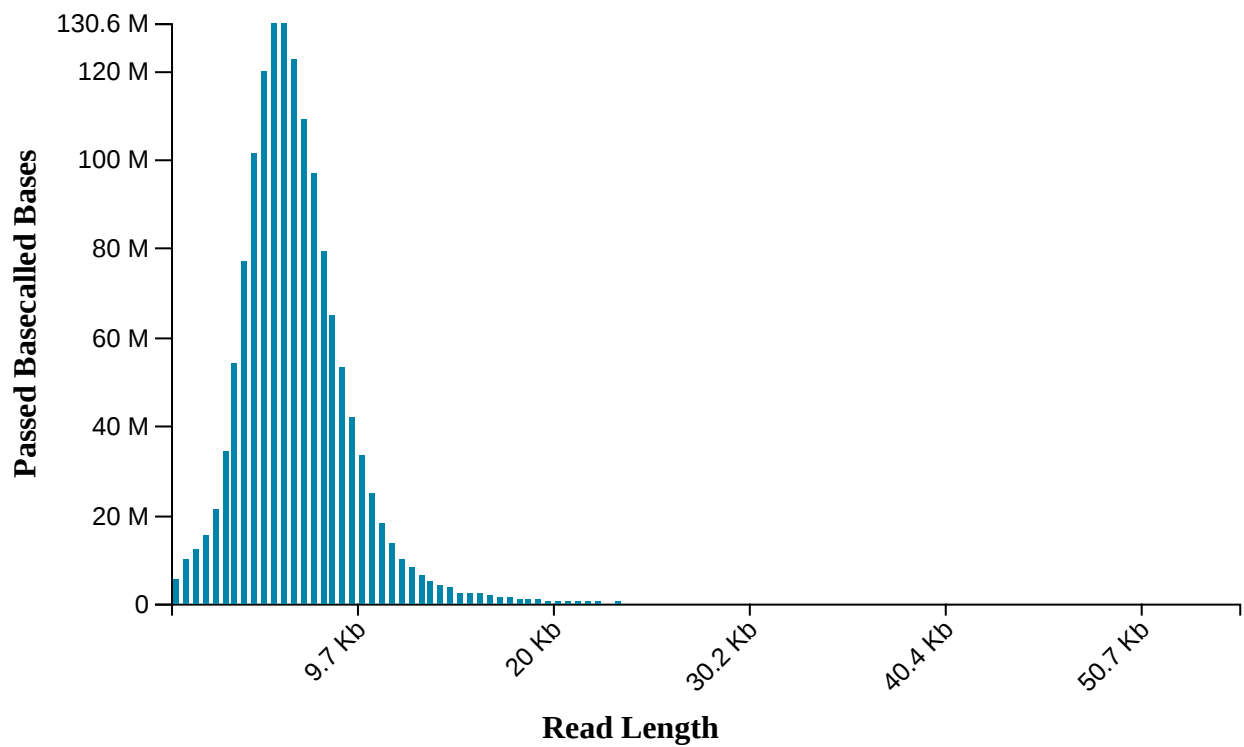
Estimated N50: 6.15 K

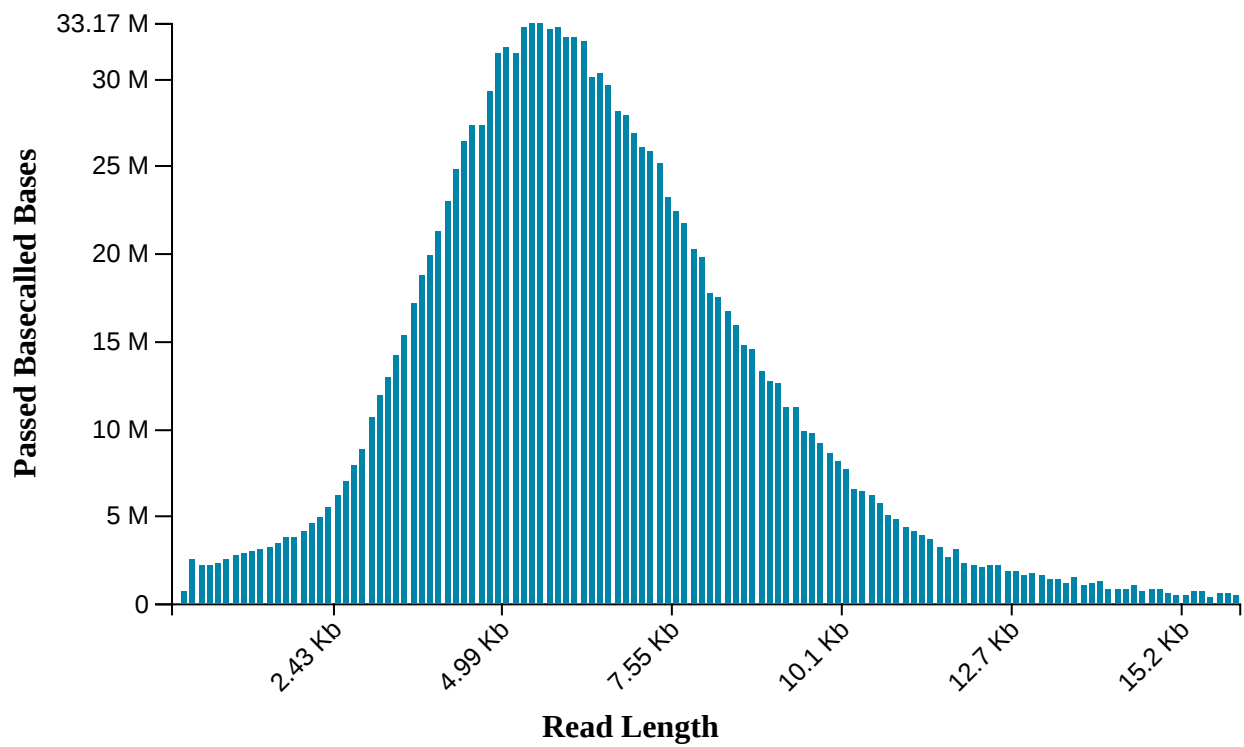## **Read Length Histogram Basecalled Bases - Outliers Discarded**

Estimated N50: 6.12 K

Read Length Histogram Estimated Bases

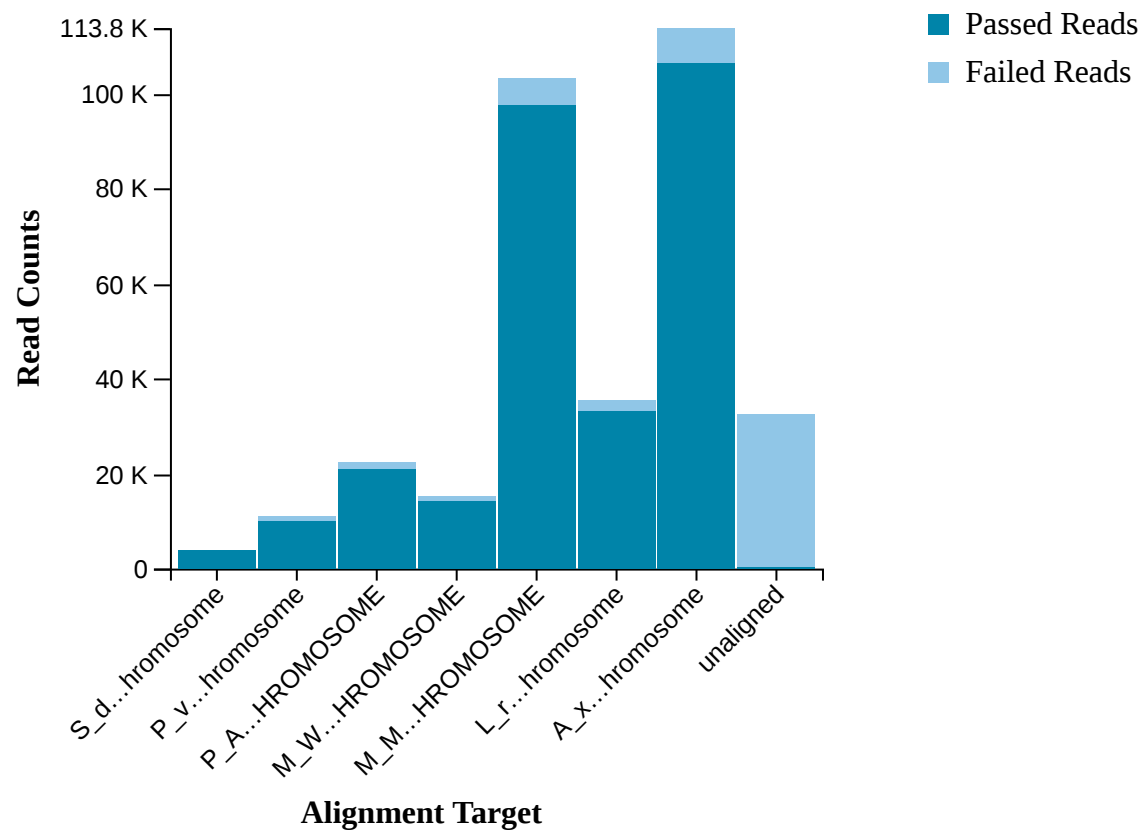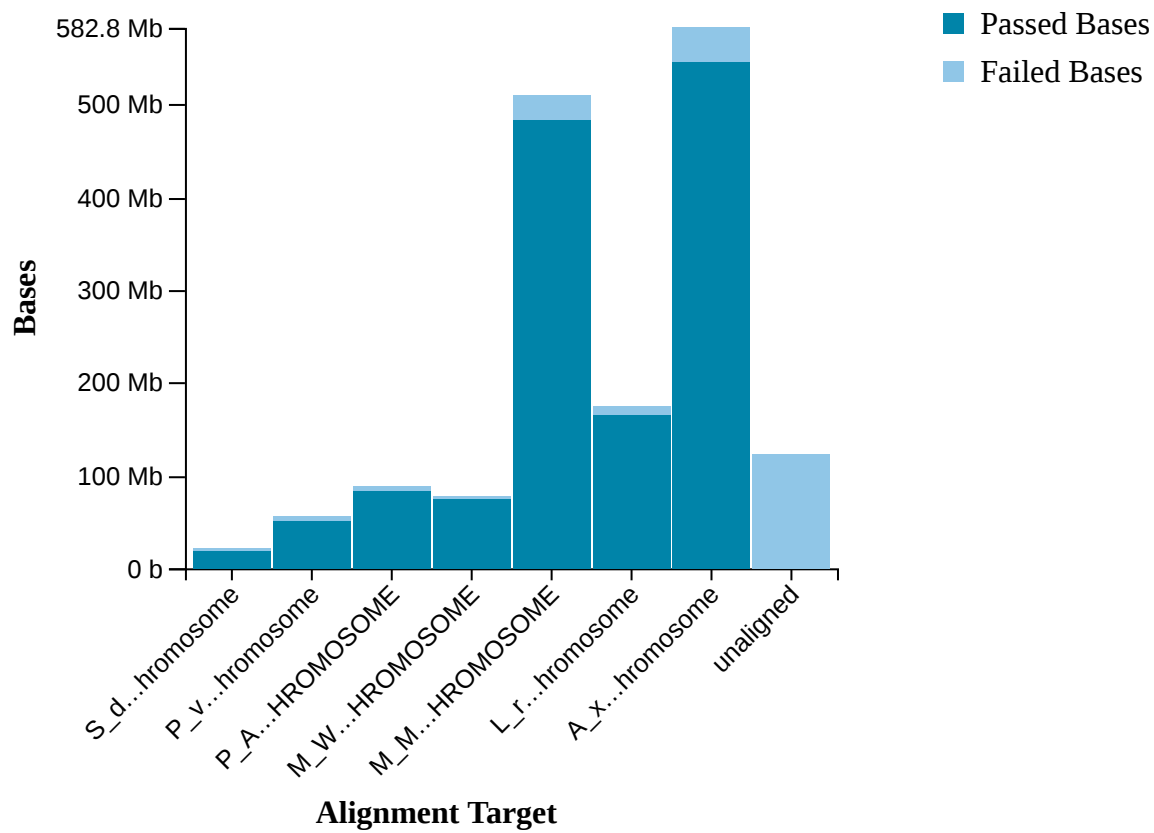Estimated N50: 6.15 K

Read Length Histogram Basecalled Bases
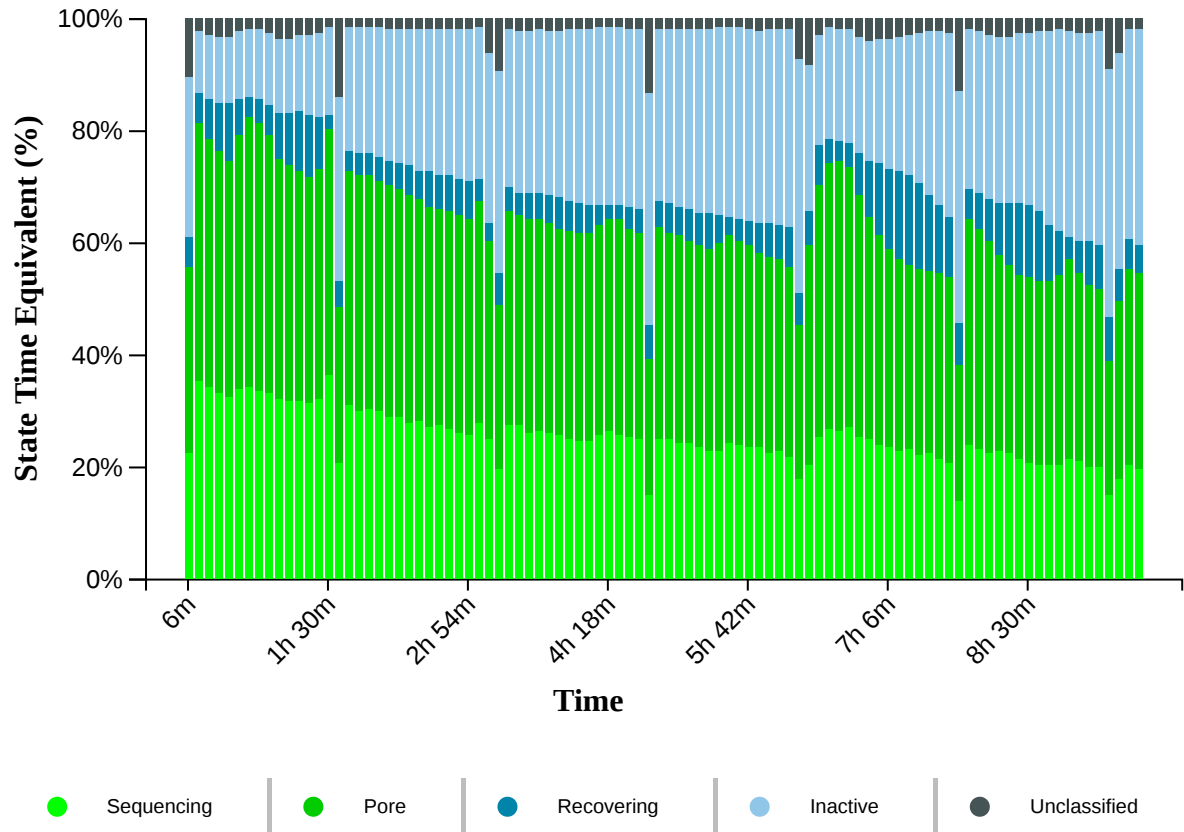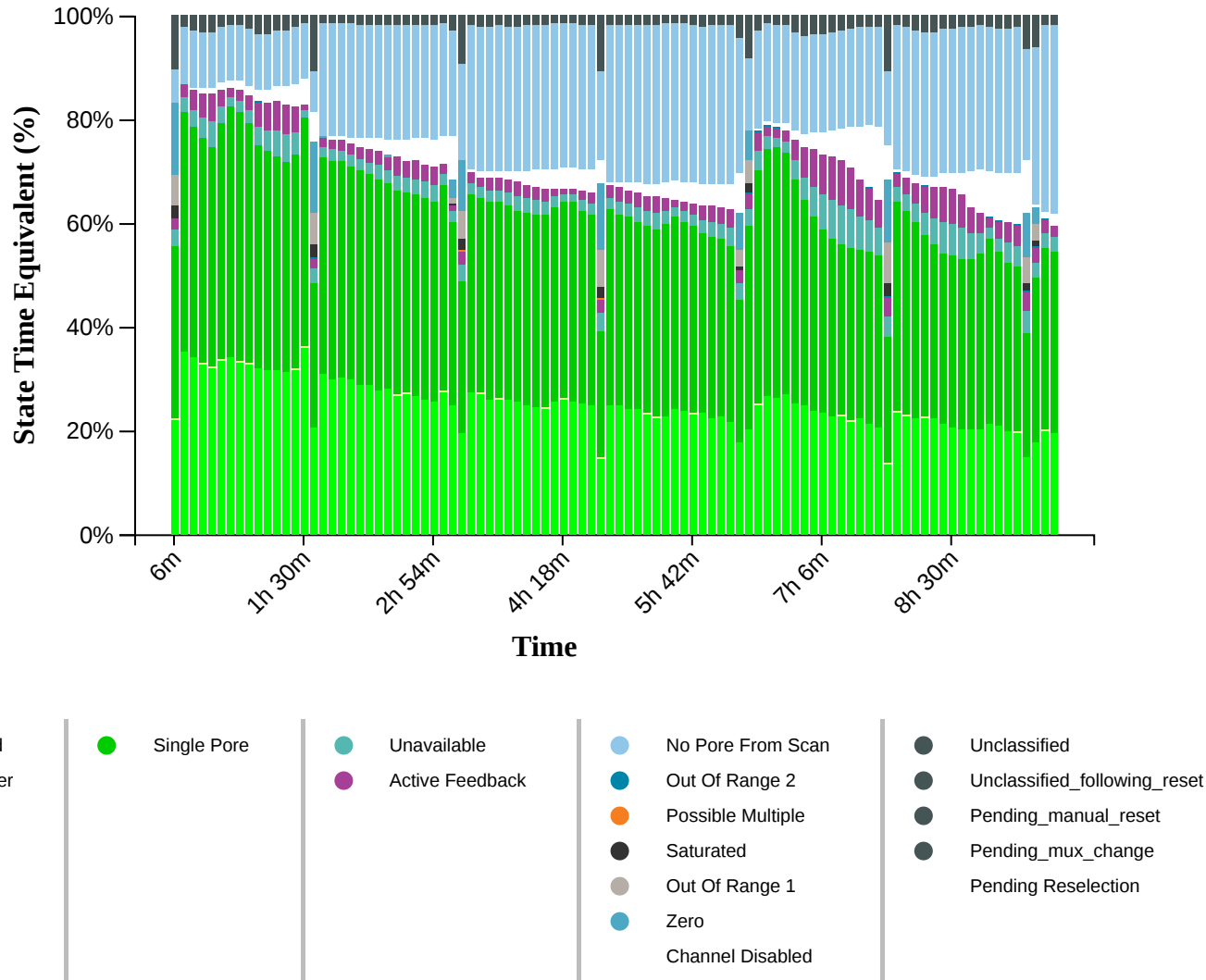
Estimated N50: 6.12 K

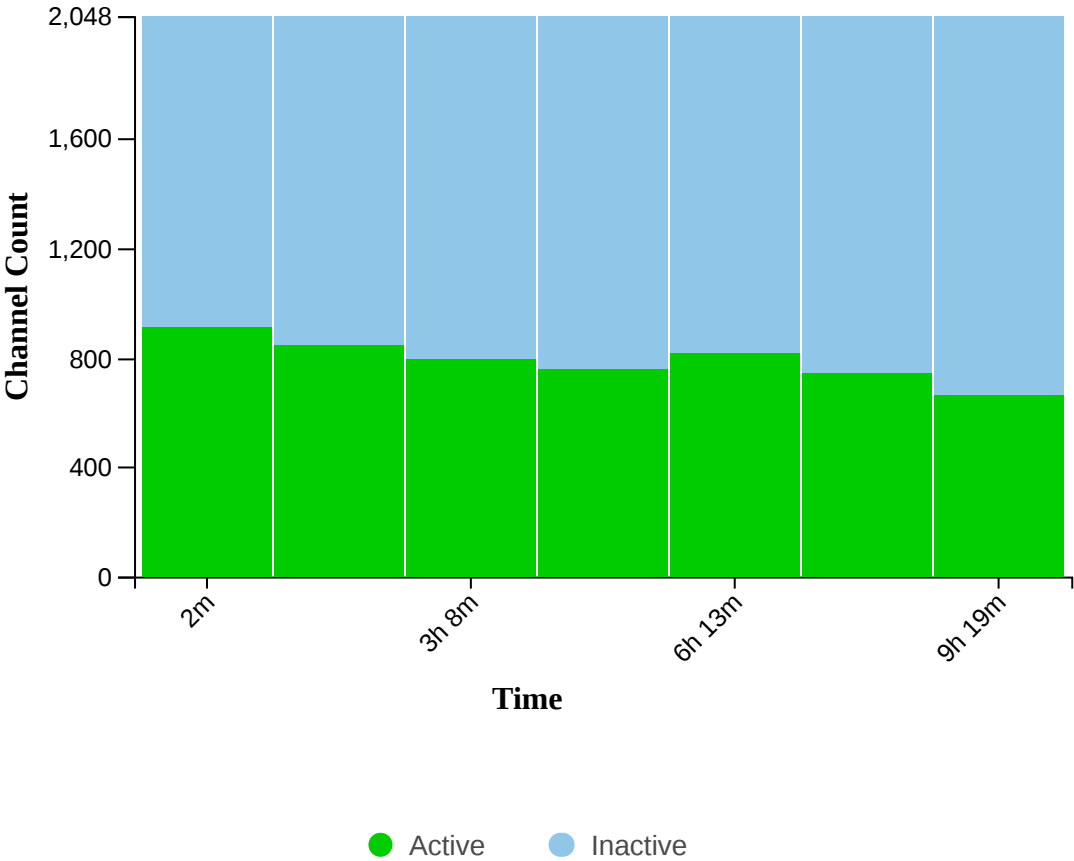## Alignment Target Hits (reads)

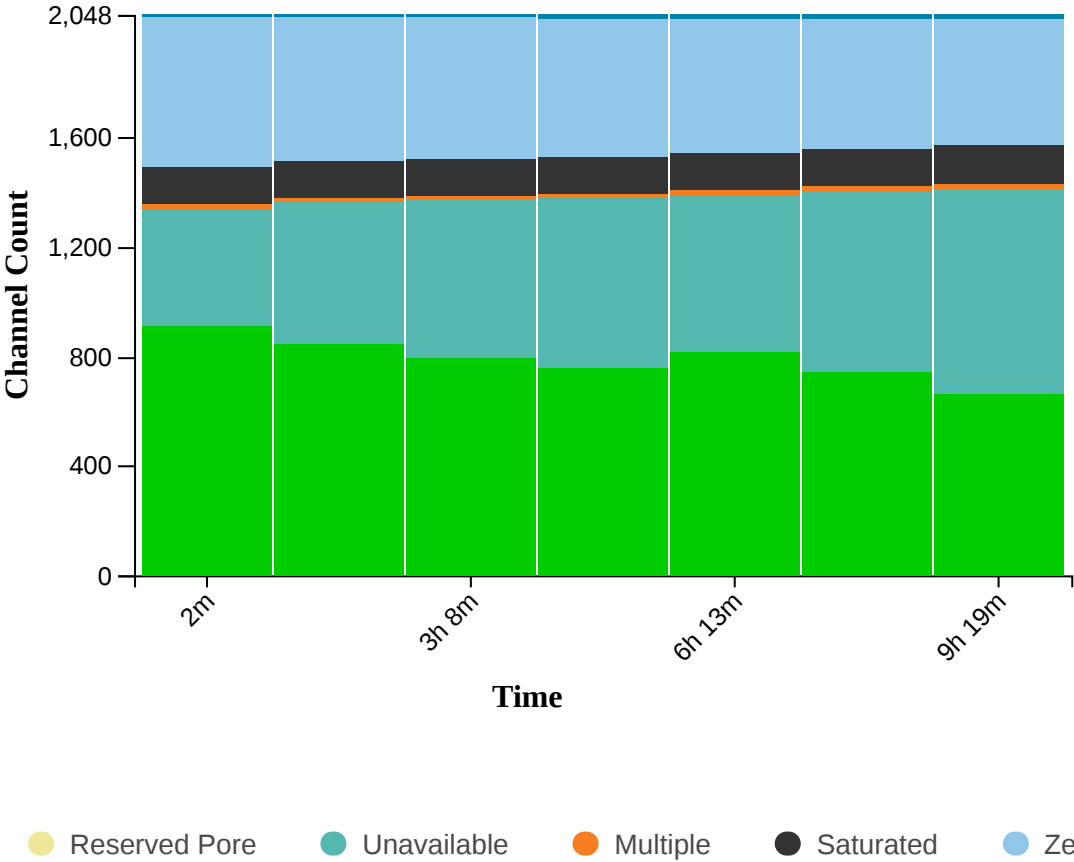## Alignment Target Hits (bases)

Duty Time Grouped

Sequencing | Pore | Recovering | Inactive | Unclassified

Duty time Categorised

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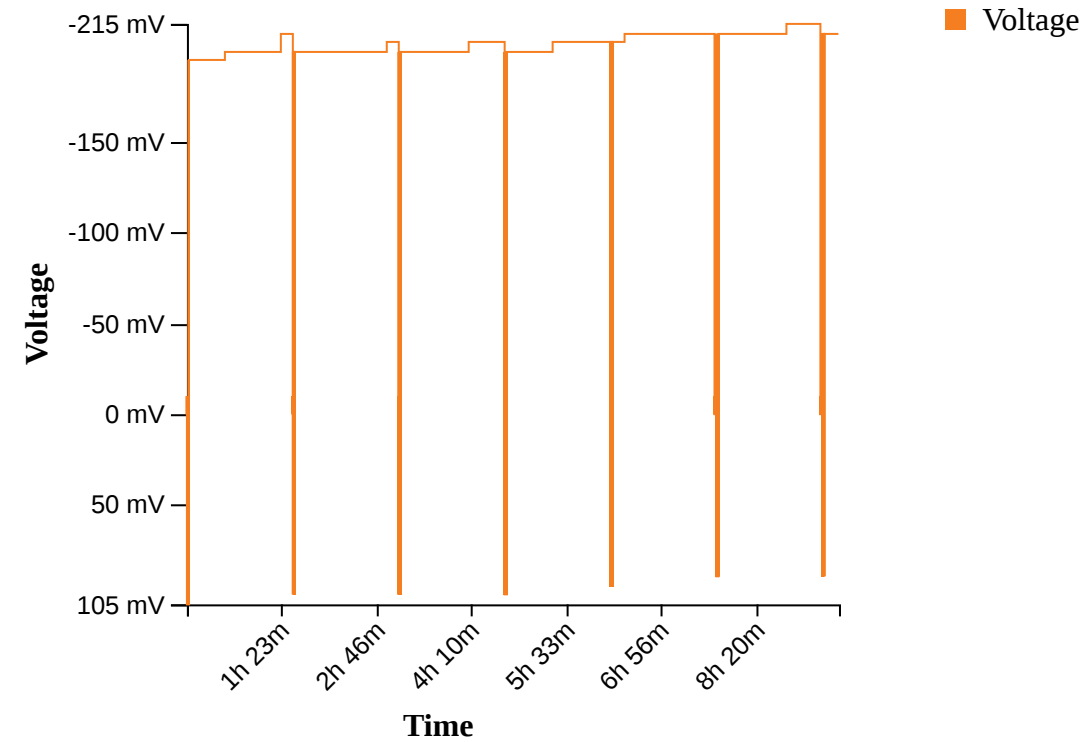| | | Channel Disabled

Mux Scan Grouped
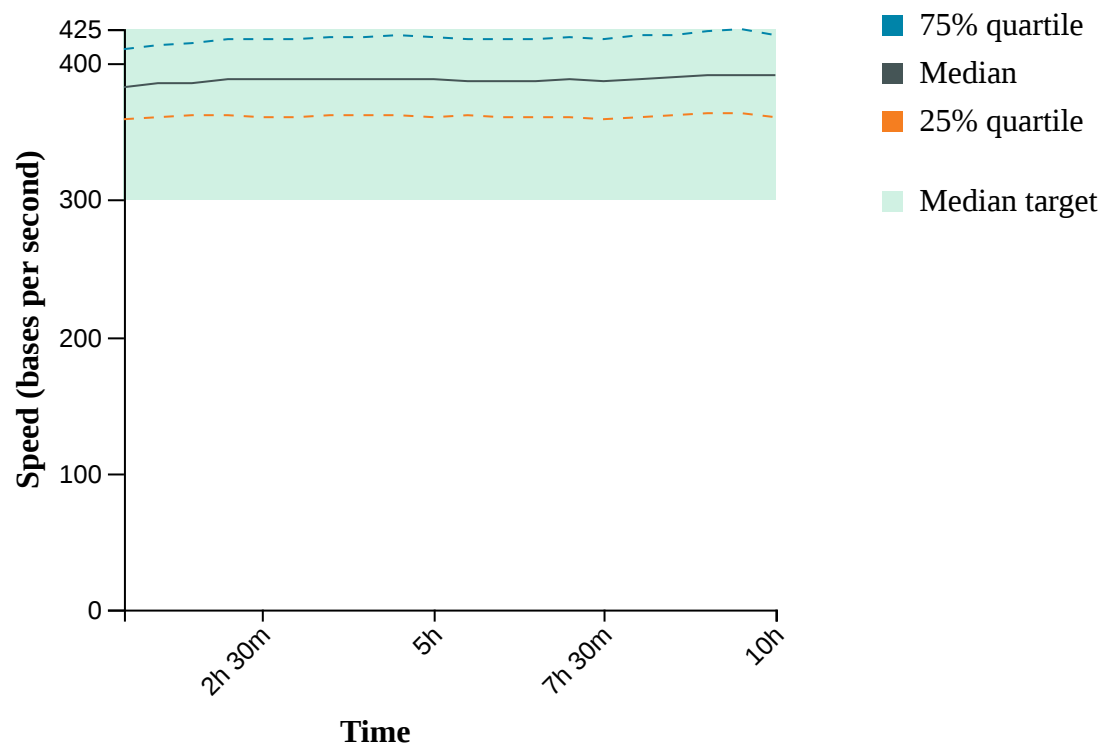

Mux Scan Categorised
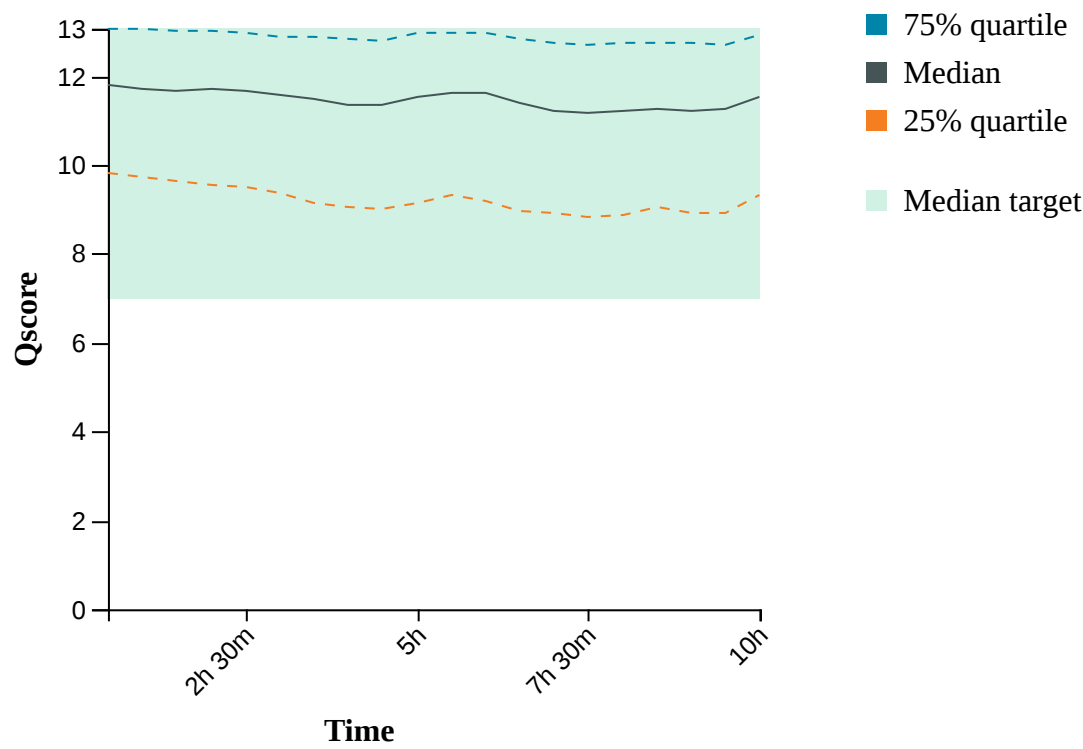
Temperature History
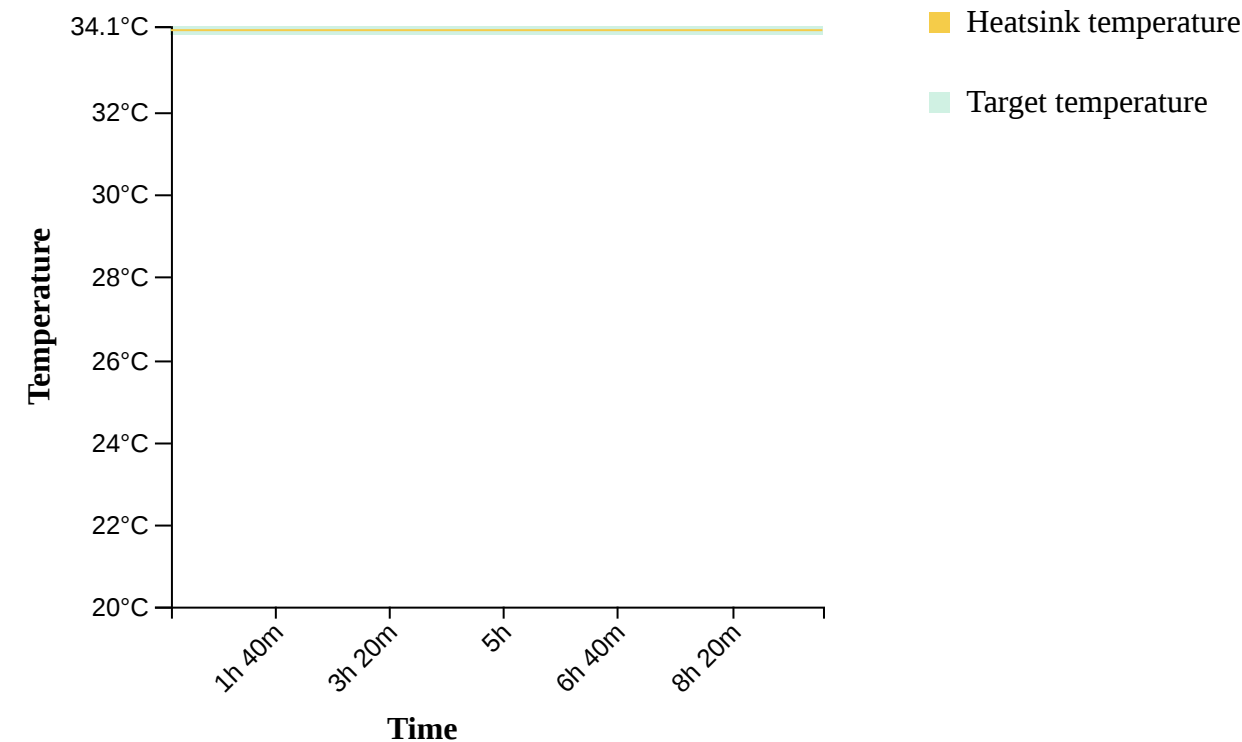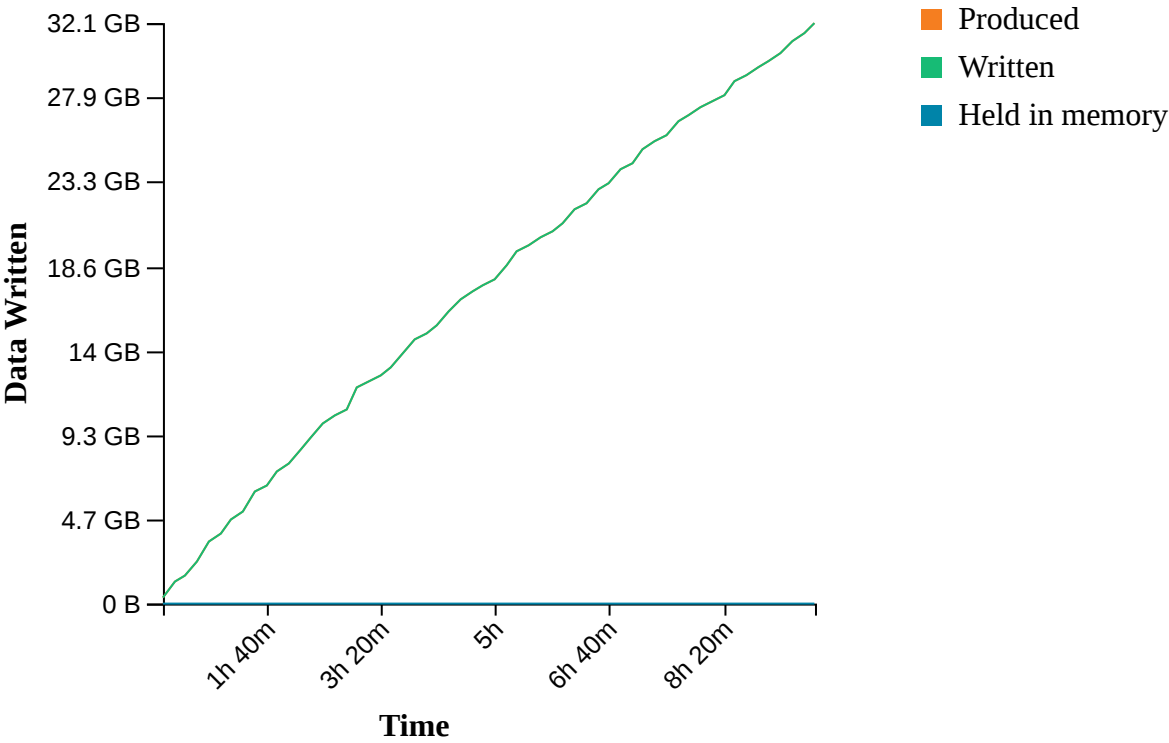

Bias Voltage History

Translocation Speed

QScore

Disk Write Performance

Run Debug Messages

- Mux scan for flow cell FAO54786 has found a total of 667 pores. 326 pores available for immediate sequencing   January 5, 09:31
- Performing Mux Scan   January 5, 09:29
- Mux scan for flow cell FAO54786 has found a total of 743 pores. 369 pores available for immediate sequencing   January 5, 07:59
- Performing Mux Scan   January 5, 07:56
- Mux scan for flow cell FAO54786 has found a total of 818 pores. 415 pores available for immediate sequencing   January 5, 06:26
- Performing Mux Scan   January 5, 06:24
- Mux scan for flow cell FAO54786 has found a total of 761 pores. 356 pores available for immediate sequencing   January 5, 04:53
- Performing Mux Scan   January 5, 04:51
- Mux scan for flow cell FAO54786 has found a total of 798 pores. 369 pores available for immediate sequencing   January 5, 03:20
- Performing Mux Scan   January 5, 03:18
- Mux scan for flow cell FAO54786 has found a total of 846 pores. 400 pores available for immediate sequencing   January 5, 01:48
- Performing Mux Scan   January 5, 01:45
- Mux scan for flow cell FAO54786 has found a total of 913 pores. 457 pores available for immediate sequencing   January 5, 00:15
- Performing Mux Scan   January 5, 00:12
- Starting sequencing procedure   January 5, 00:12
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   January 5, 00:09