Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**ReadUntilMock_15kbSE_MmEnrich_08122020**
Sample ID	**ReadUntilMock_15kbSE_MmEnrich_08122020**
Run ID	**a3a2f40c-83a0-413b-ab2f-fb5a4f0e1a4d**
Flow Cell Id	**FAO52906**
Start Time	**December 8, 12:54**
Run Length	**1h 15m**

Run Summary

Reads Generated	**138.06 K**
Passed Bases	**348.4 Mb**
Failed Bases	**8.66 Mb**
Estimated Bases	**363.46 Mb**

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/references/M_morganii_ref.fasta"],filter_type=enrich,first_channel=1,last_channel=512**
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

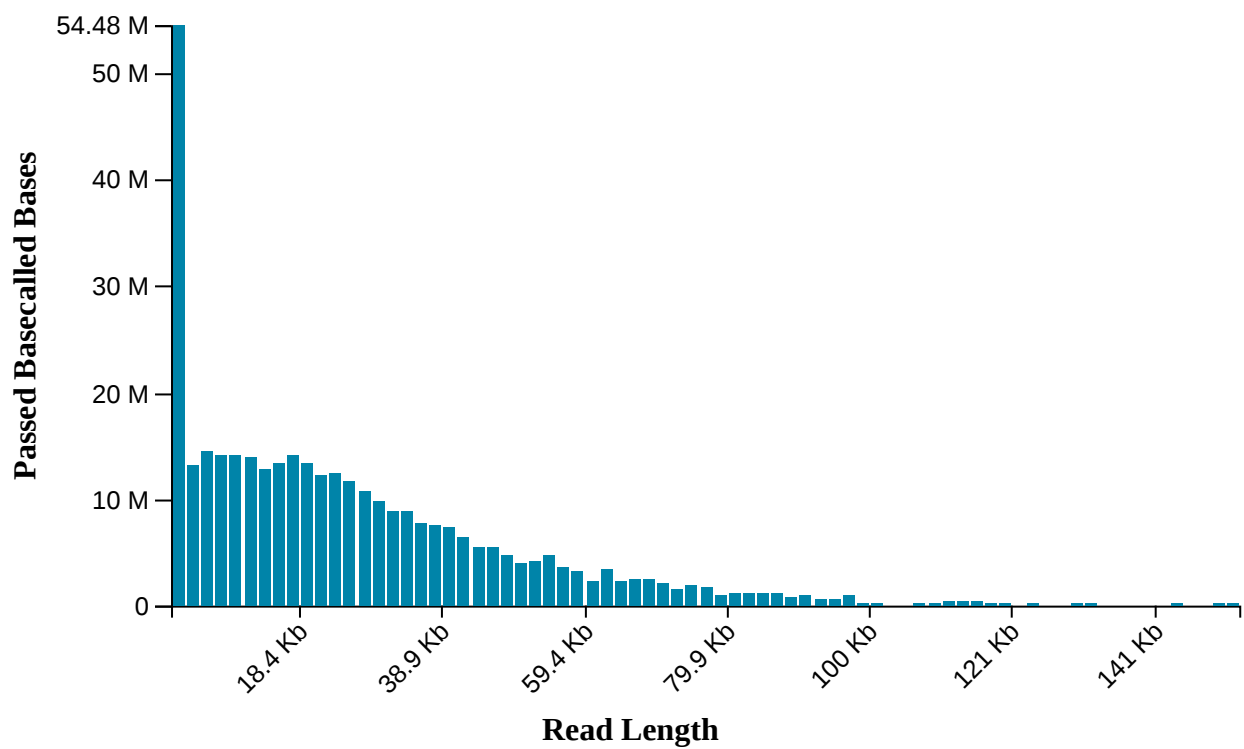|	
MinKNOW	**20.10.6**
MinKNOW Core	**4.1.2**
Bream	**6.1.4**
Guppy	**4.2.3**

Cumulative Output Reads
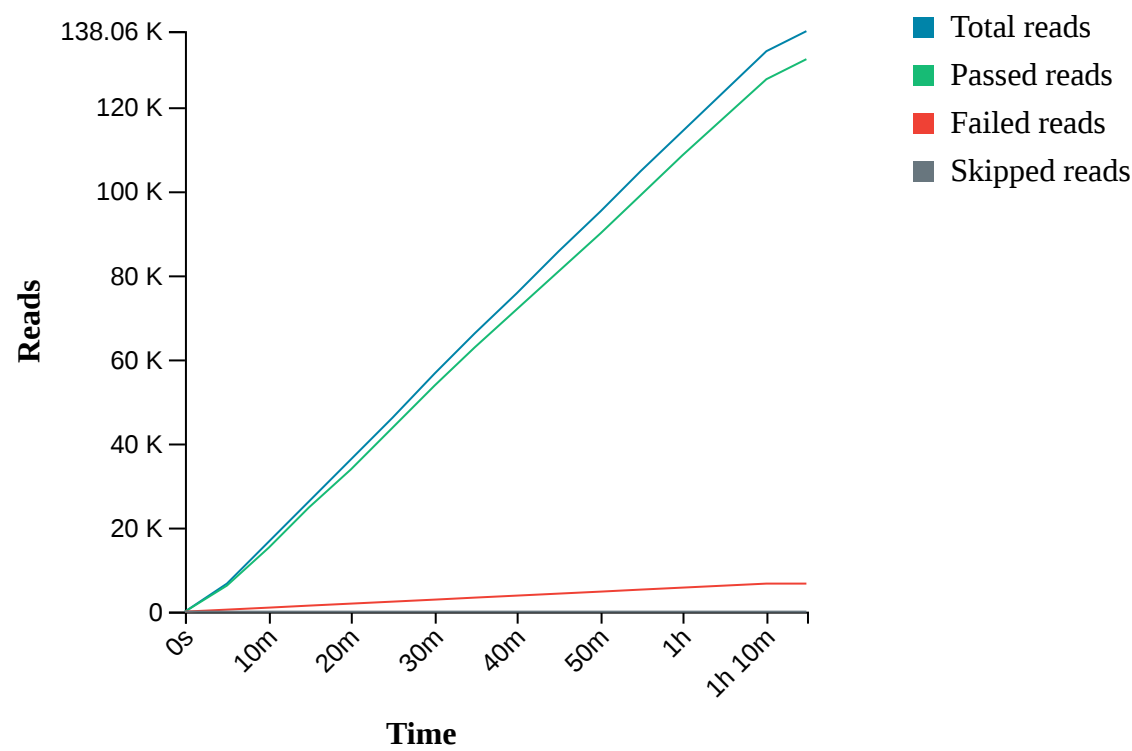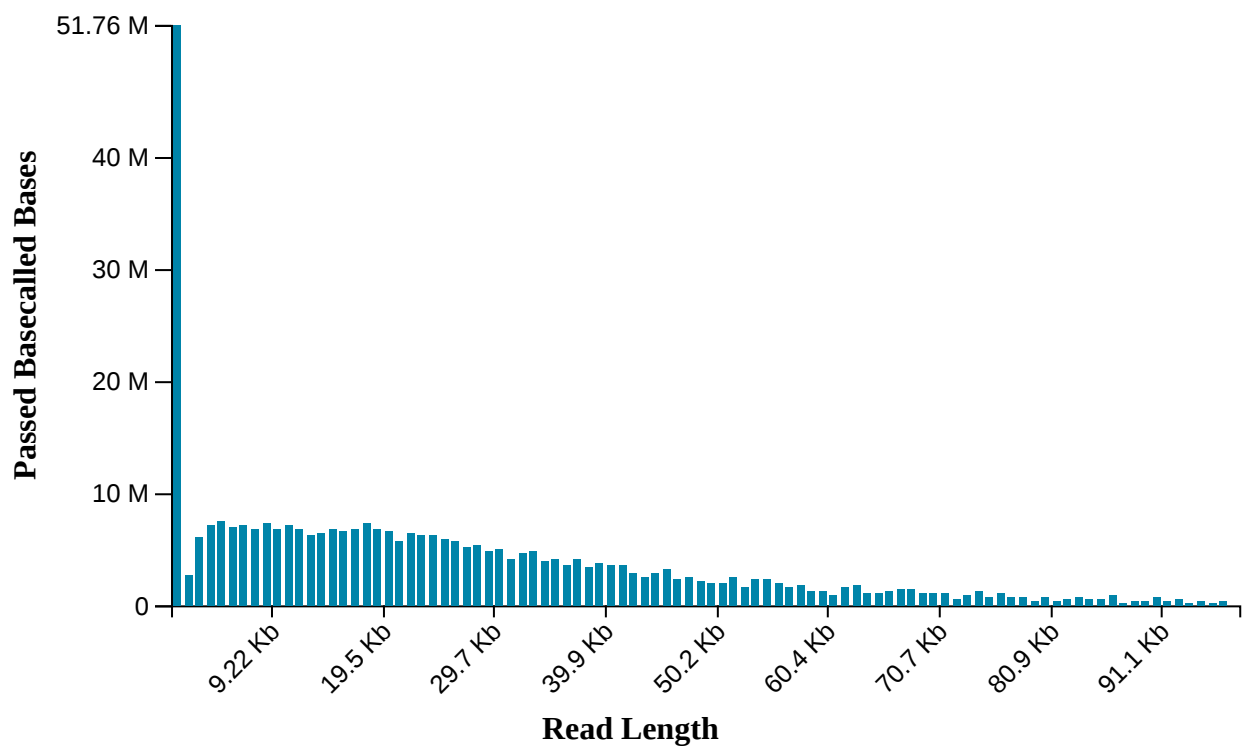

Cumulative Output Bases
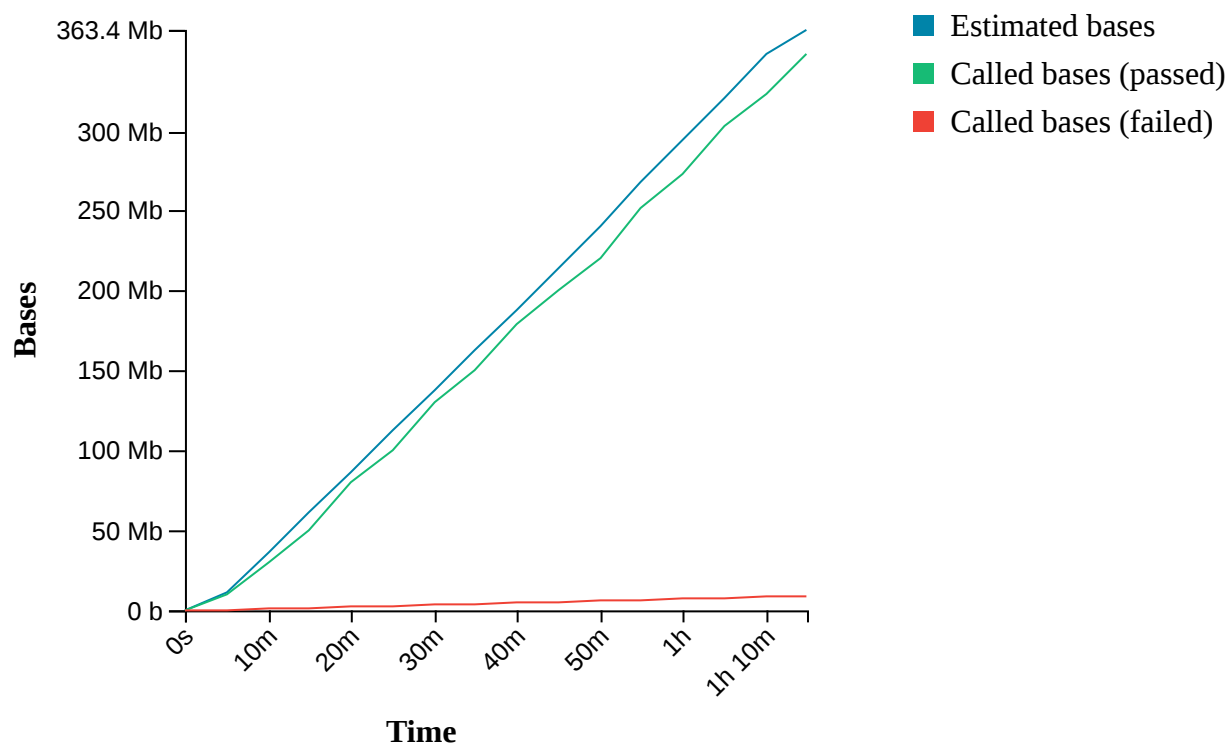
Read Length Histogram Estimated Bases - Outliers Discarded
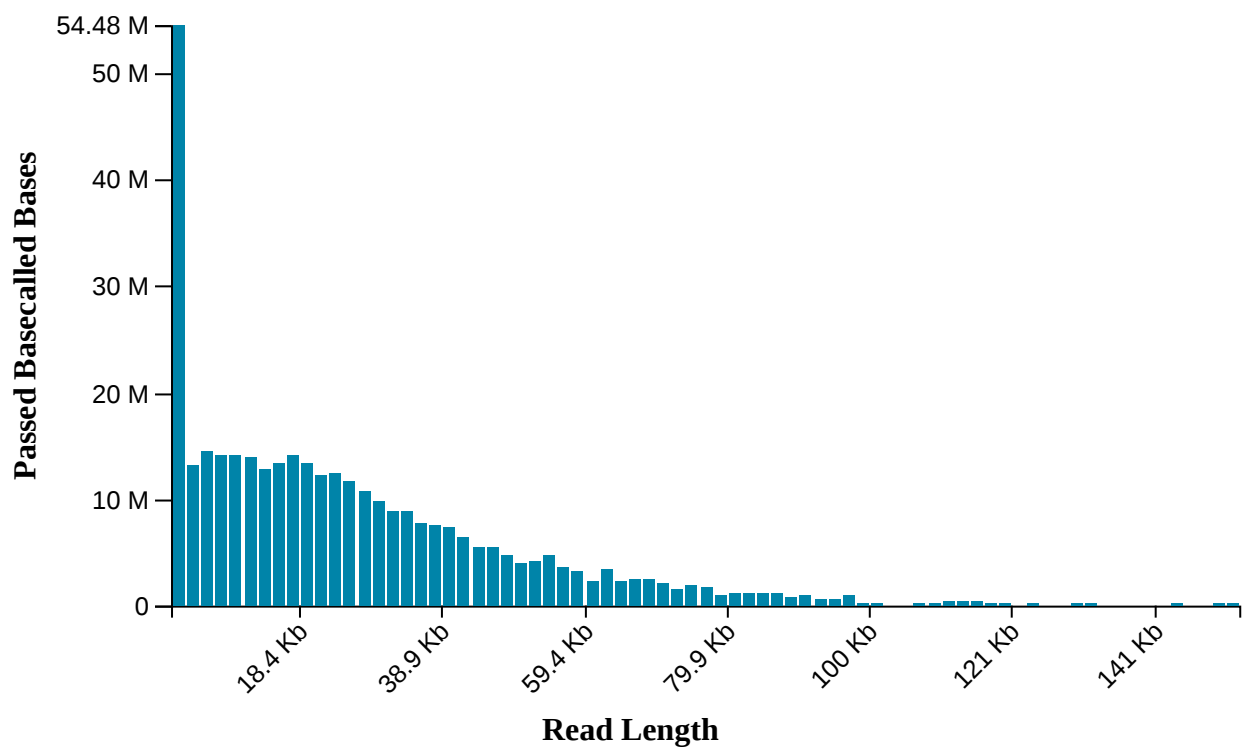
Estimated N50: 19.95 K

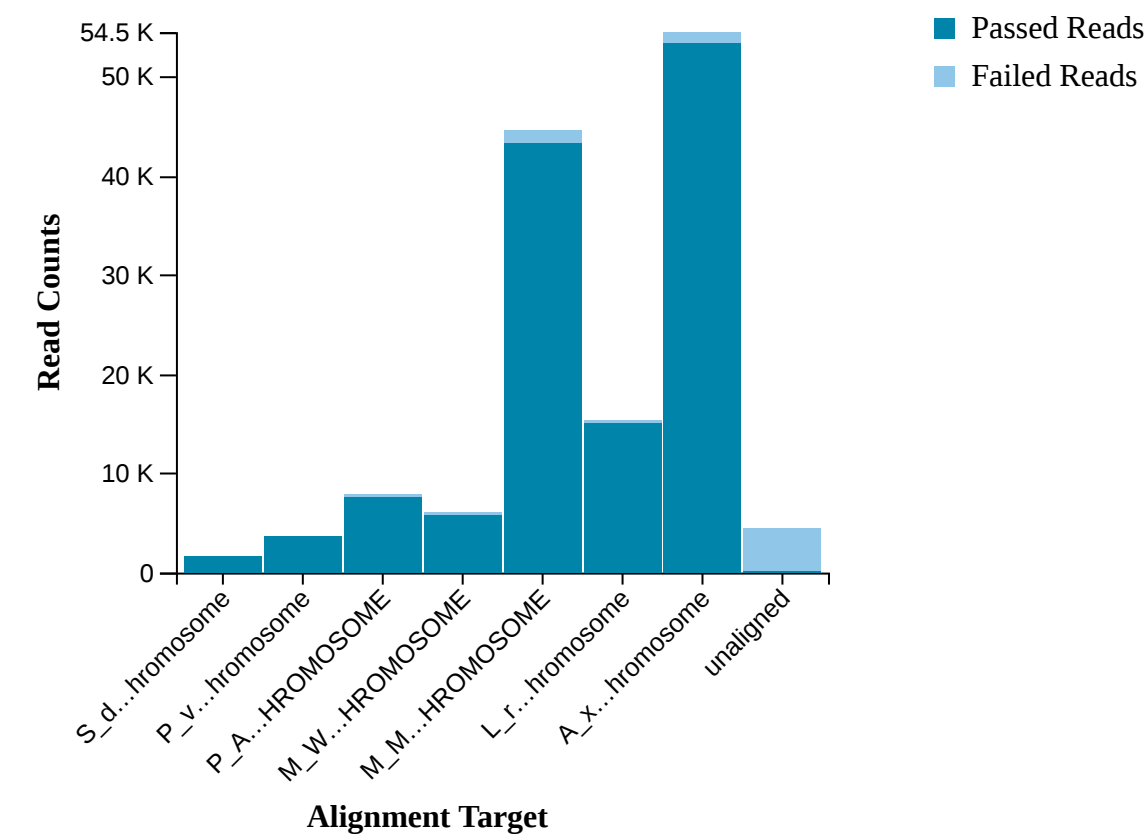## Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 19.66 K
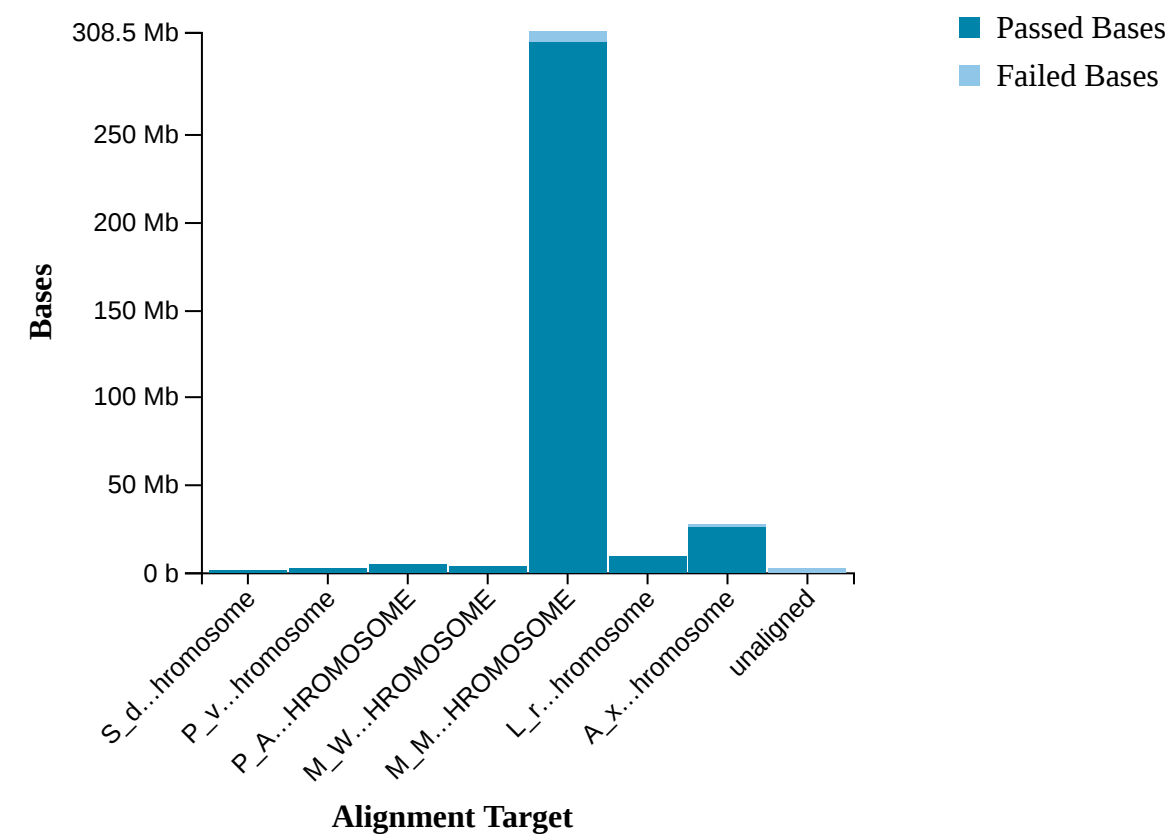
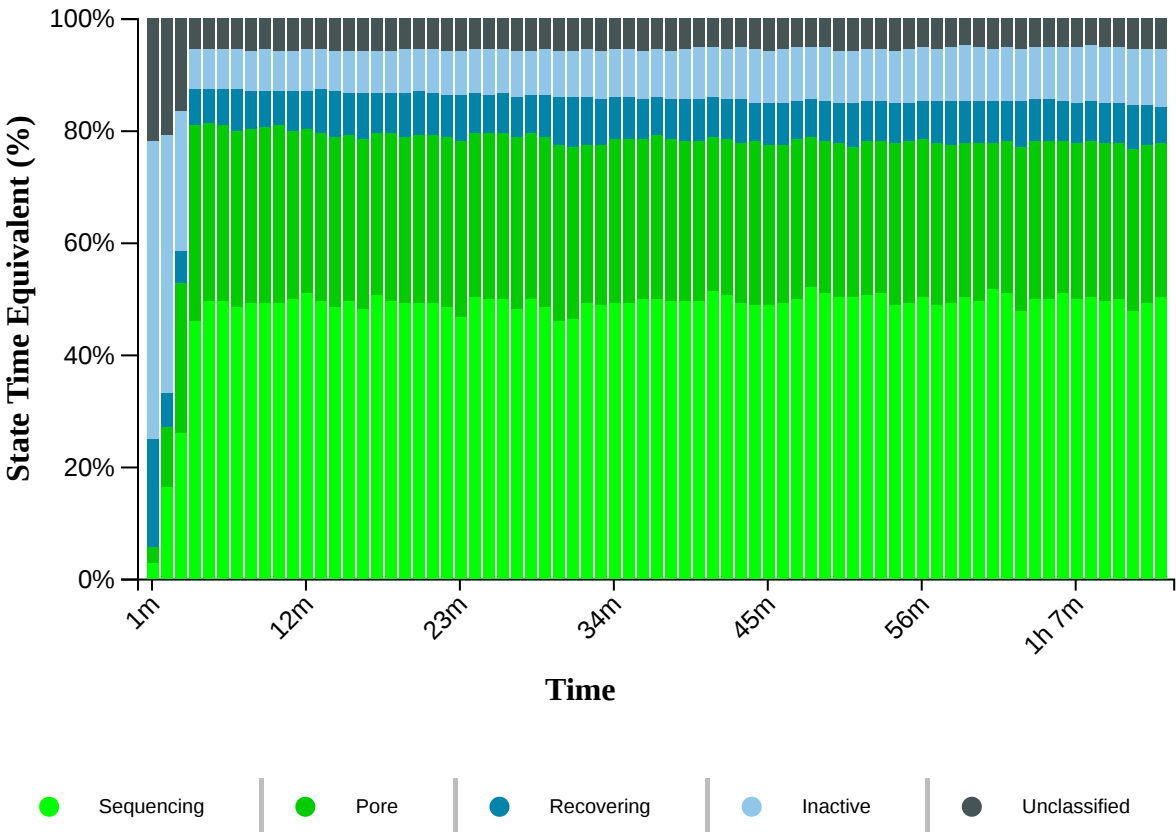## Read Length Histogram Estimated Bases

Estimated N50: 19.95 K

Read Length Histogram Basecalled Bases

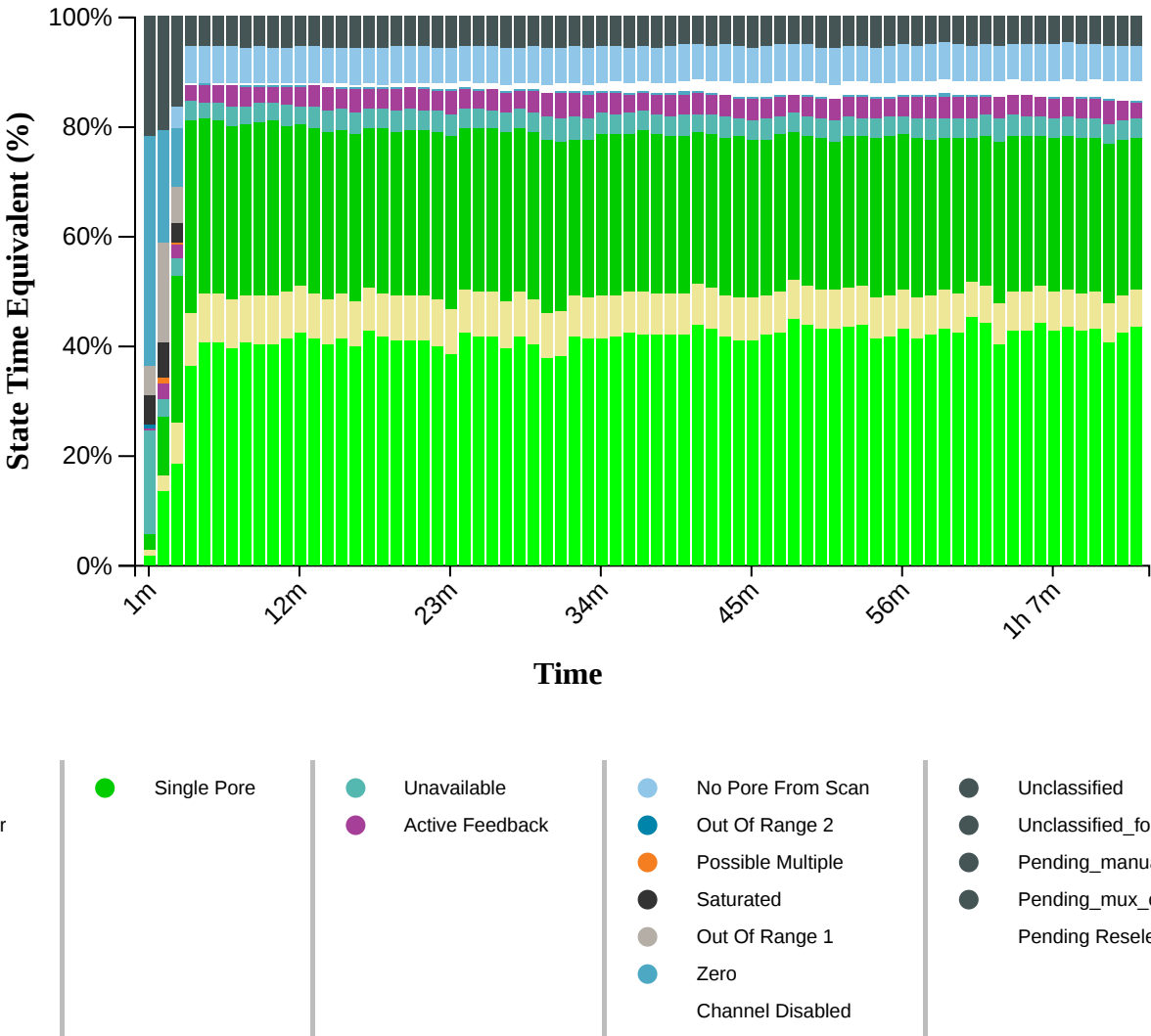Estimated N50: 19.66 K

Alignment Target Hits (reads)
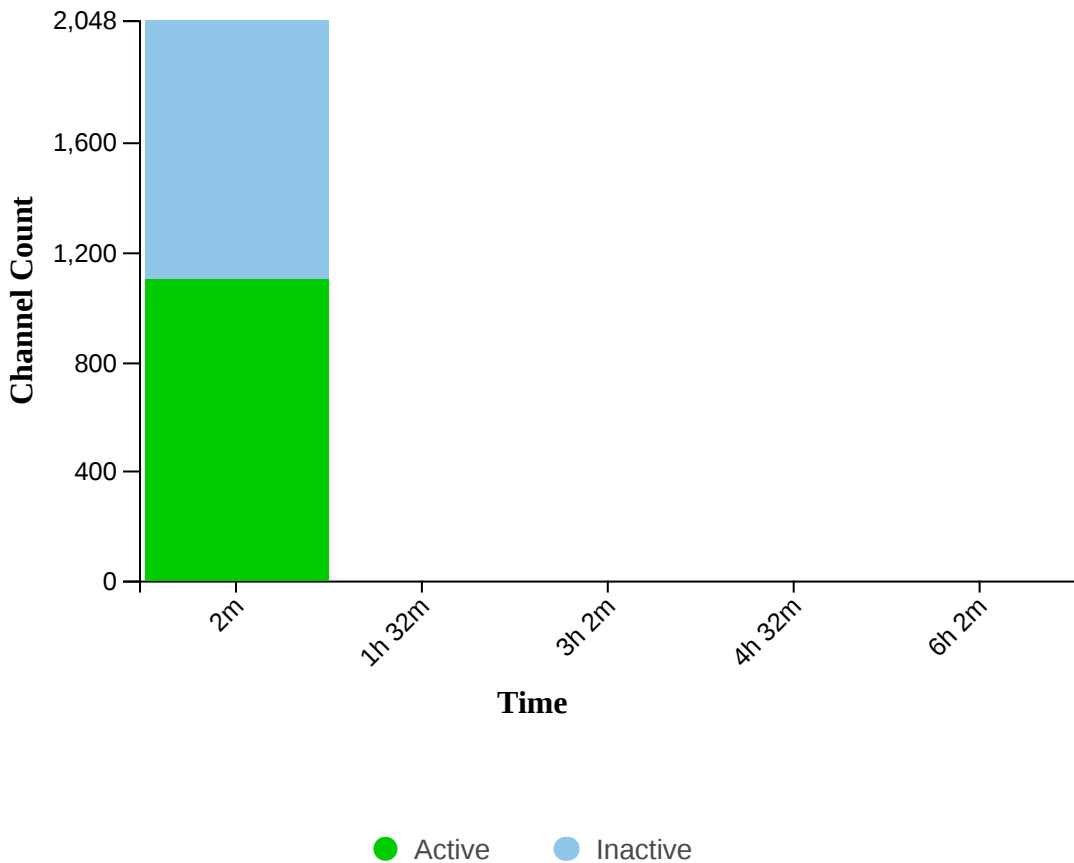

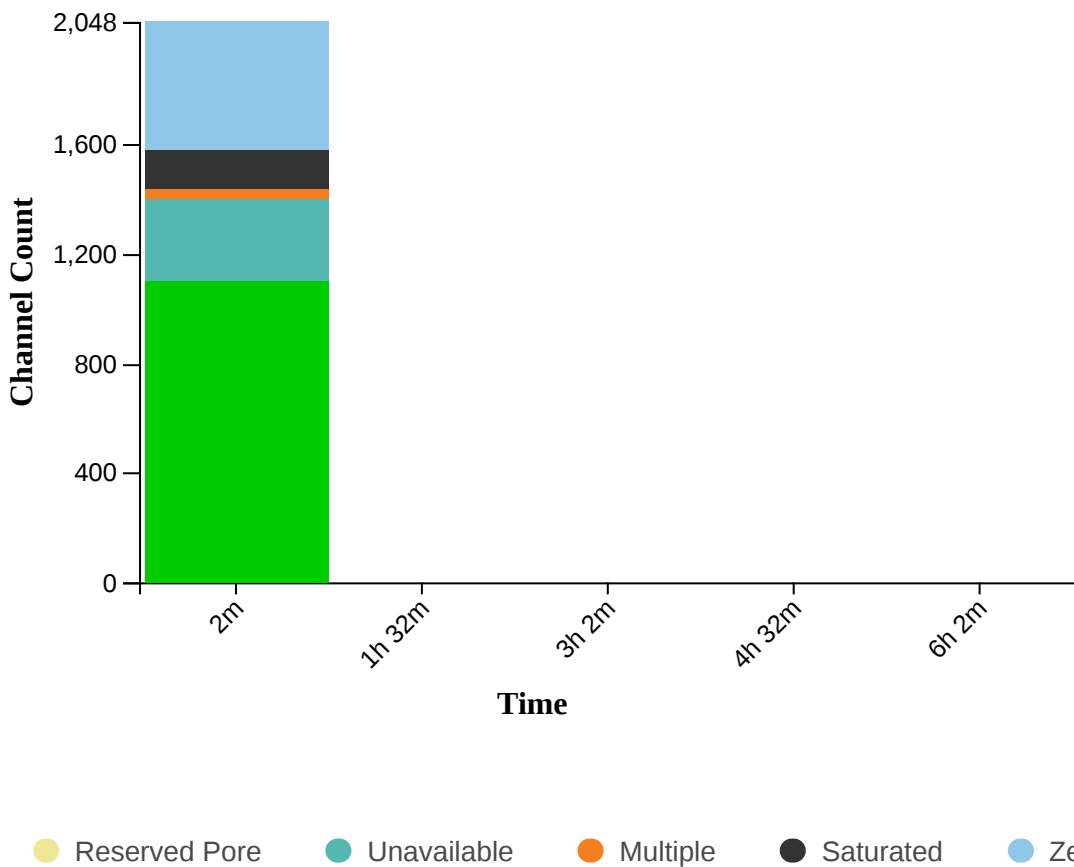## Alignment Target Hits (bases)

Duty Time Grouped

Legend: Sequencing · Pore · Recovering · Inactive · Unclassified

Duty time Categorised

Legend: 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

● Active   ● Inactive

Mux Scan Categorised

● Single Pore   ● Reserved Pore   ● Unavailable   ● Multiple   ● Saturated   ● Zero   ● Other

Temperature History
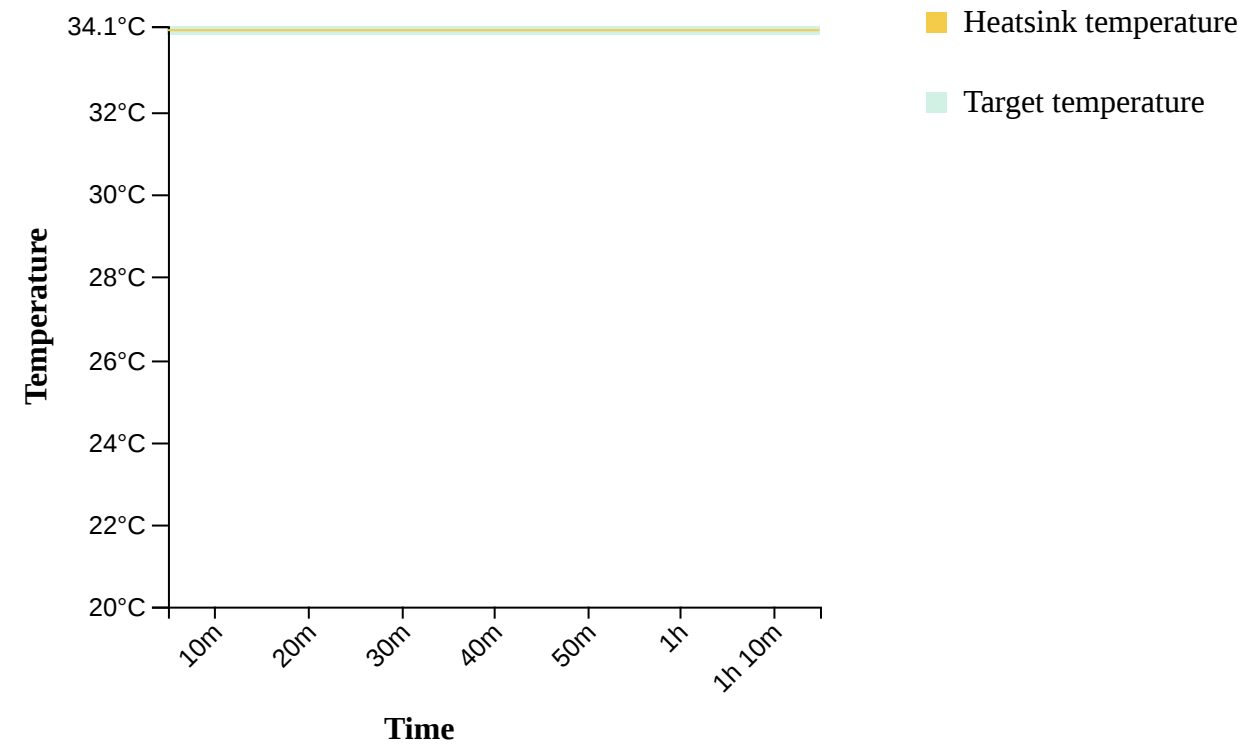
Bias Voltage History
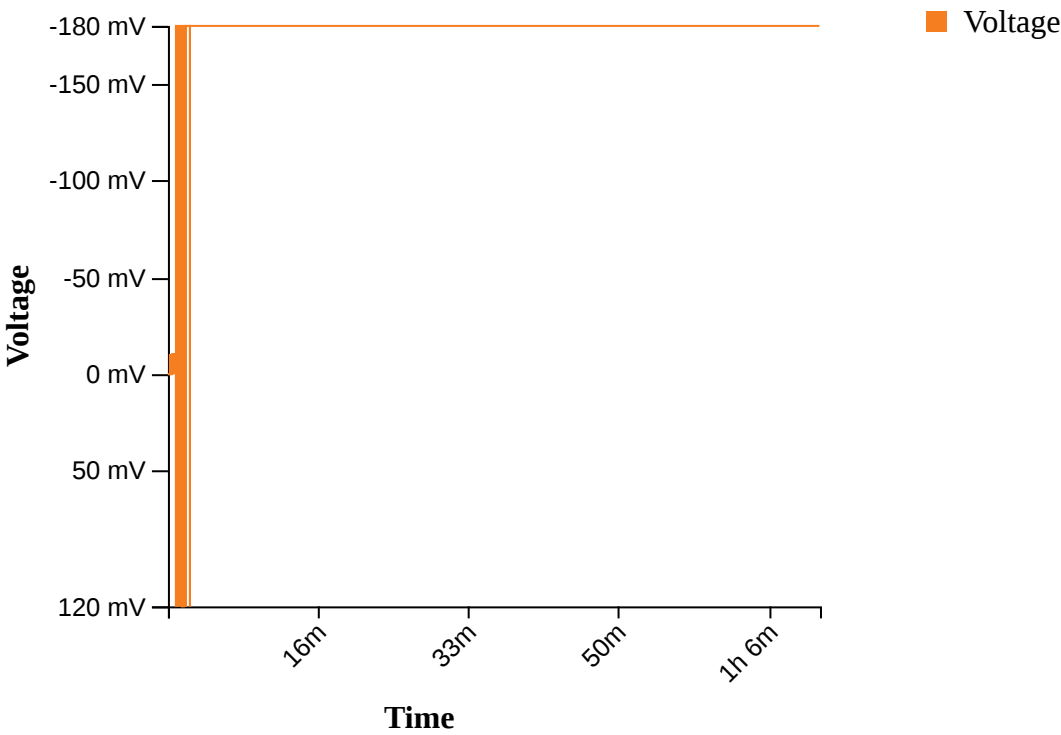
Translocation Speed
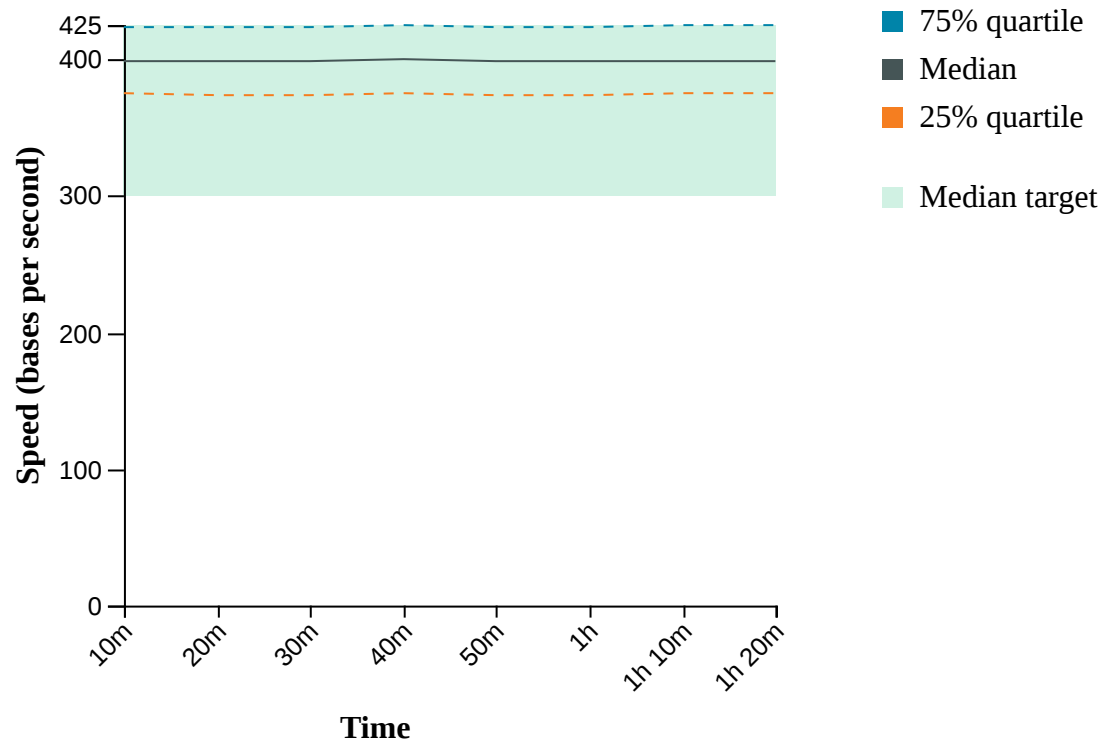
QScore

Disk Write Performance

Legend:
- Produced
- Written
- Held in memory
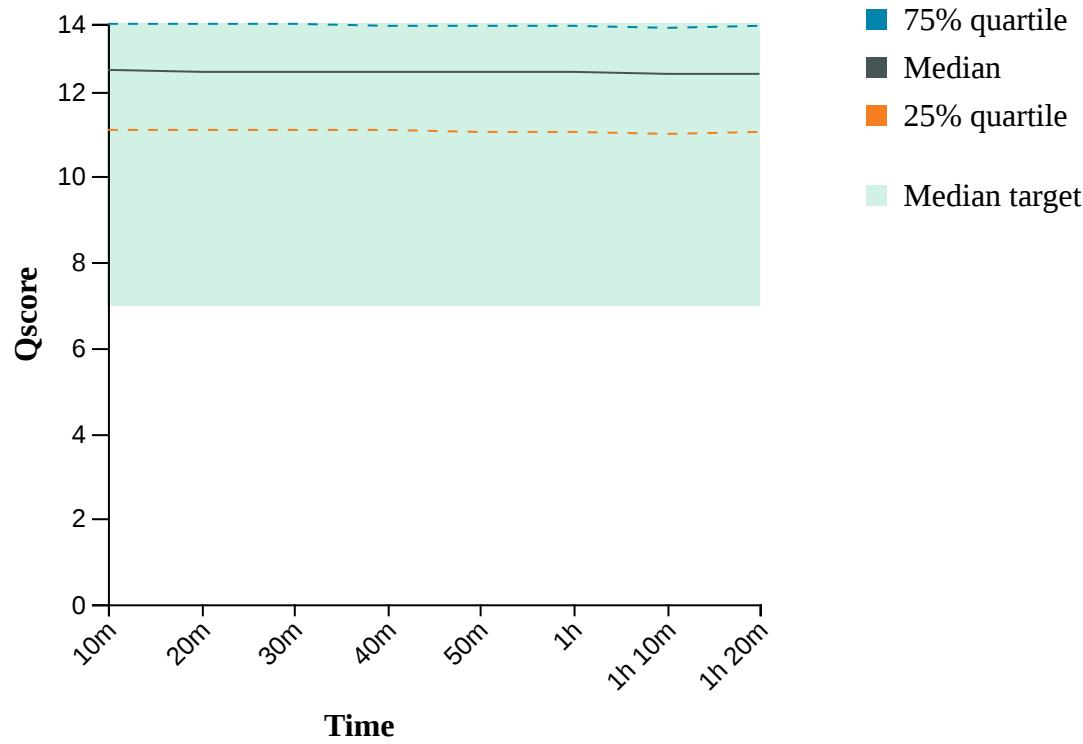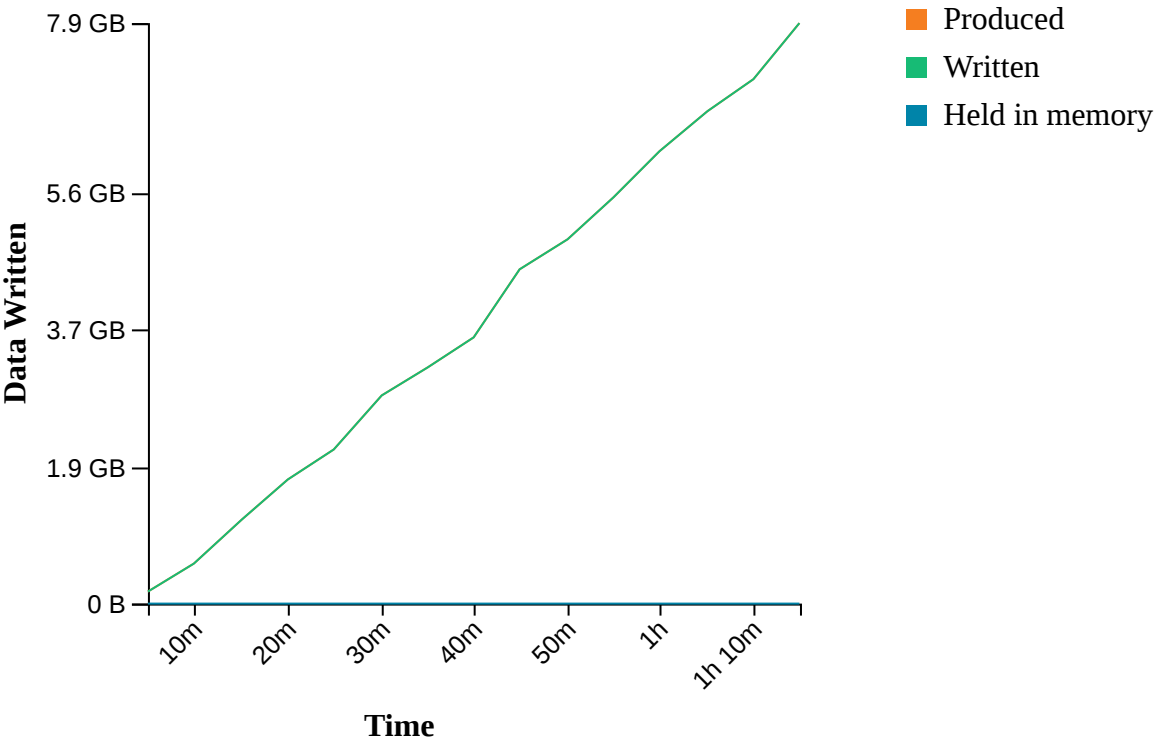
<u>Run Debug Messages</u>

- Mux scan for flow cell FAO52906 has found a total of 1105 pores. 478 pores available for immediate sequencing   December 8, 13:00
- Performing Mux Scan   December 8, 12:58
- Starting sequencing procedure   December 8, 12:58
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   December 8, 12:54