Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**ReadUntilMock_15kbSE_LrEnrich_08122020**
Sample ID	**ReadUntilMock_15kbSE_LrEnrich_08122020**
Run ID	**05552138-3657-44c3-8b70-792ea64e1ecc**
Flow Cell Id	**FAO52906**
Start Time	**December 8, 14:12**
Run Length	**1h 7m**

Run Summary

Reads Generated	**161.86 K**
Passed Bases	**221.3 Mb**
Failed Bases	**7.07 Mb**
Estimated Bases	**233.89 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/L_richardii_ref.fa"],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

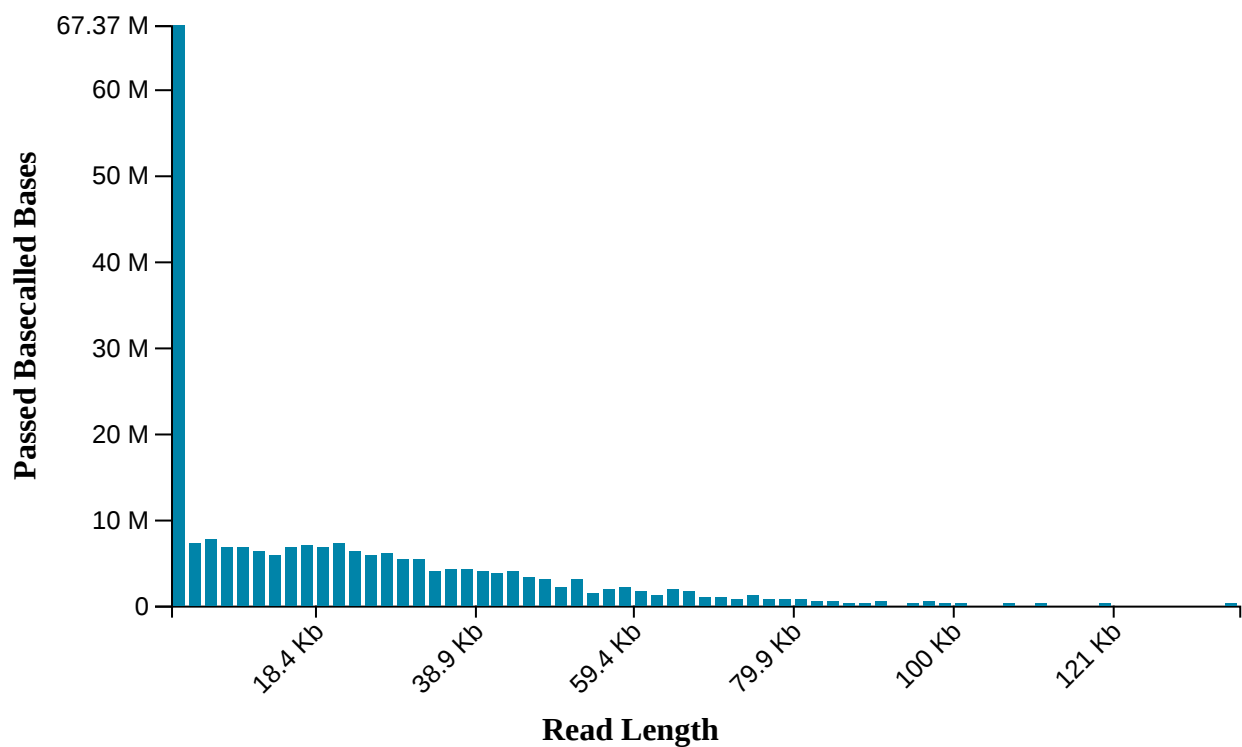|	
MinKNOW	**20.10.6**
MinKNOW Core	**4.1.2**
Bream	**6.1.4**
Guppy	**4.2.3**

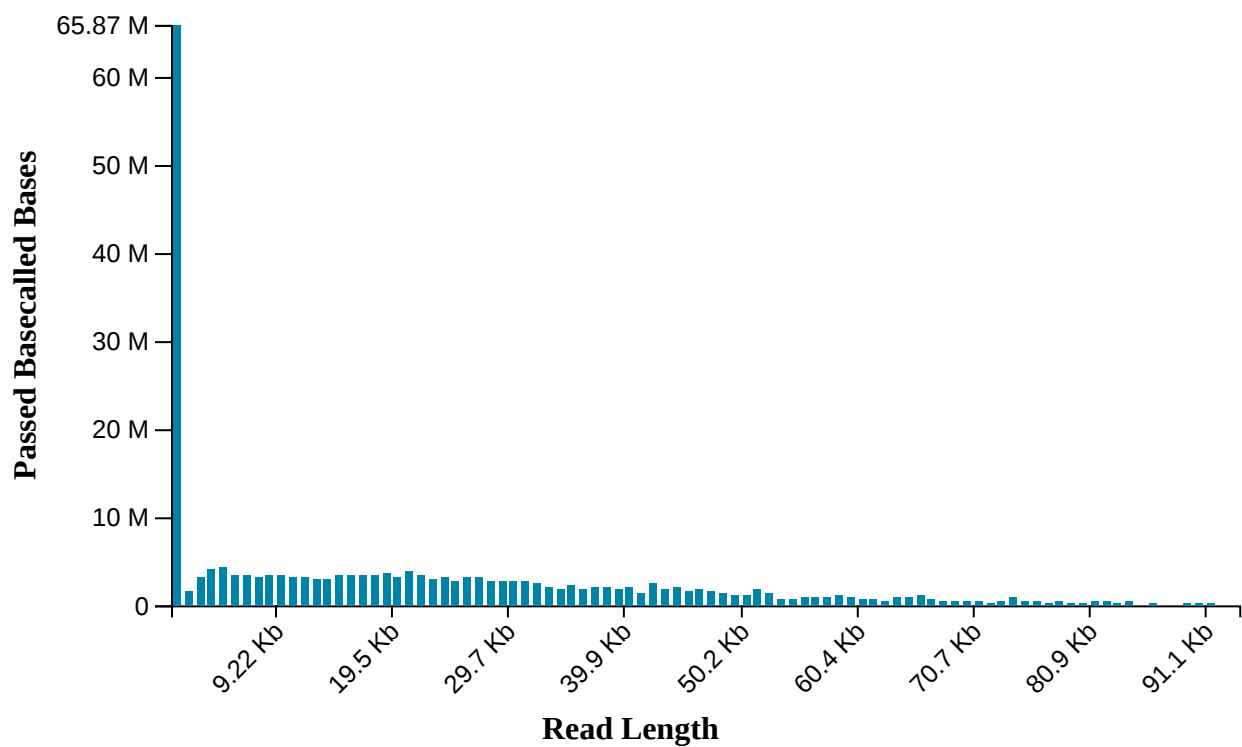## Cumulative Output Reads
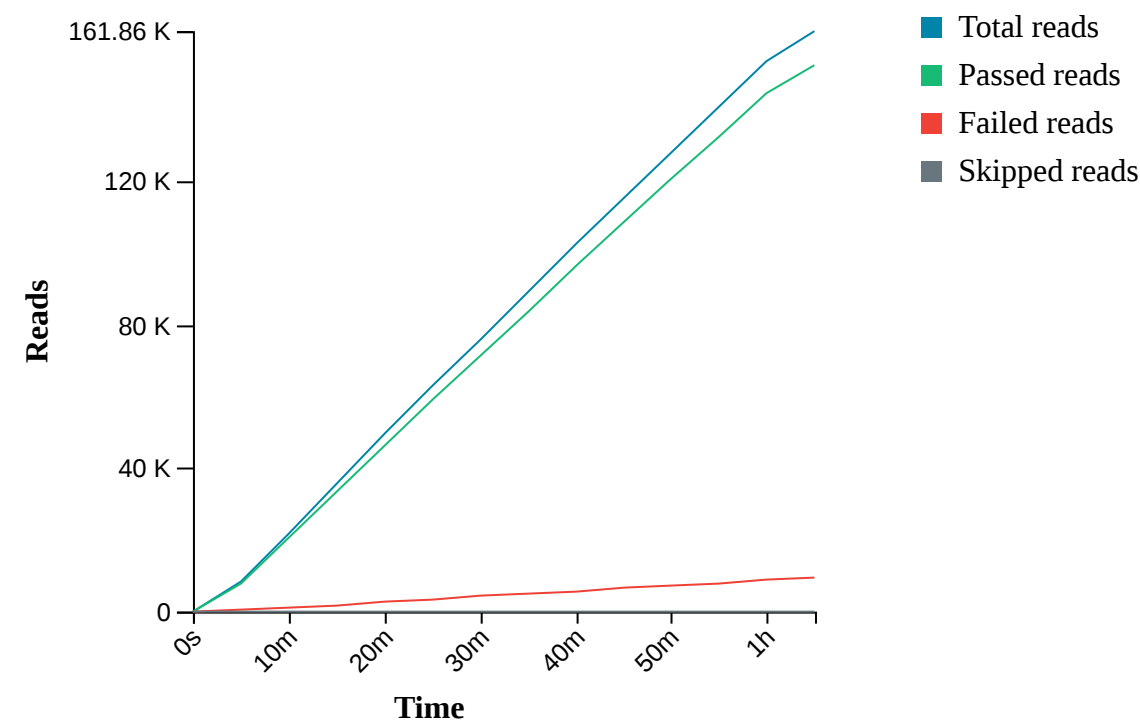
Cumulative Output Bases
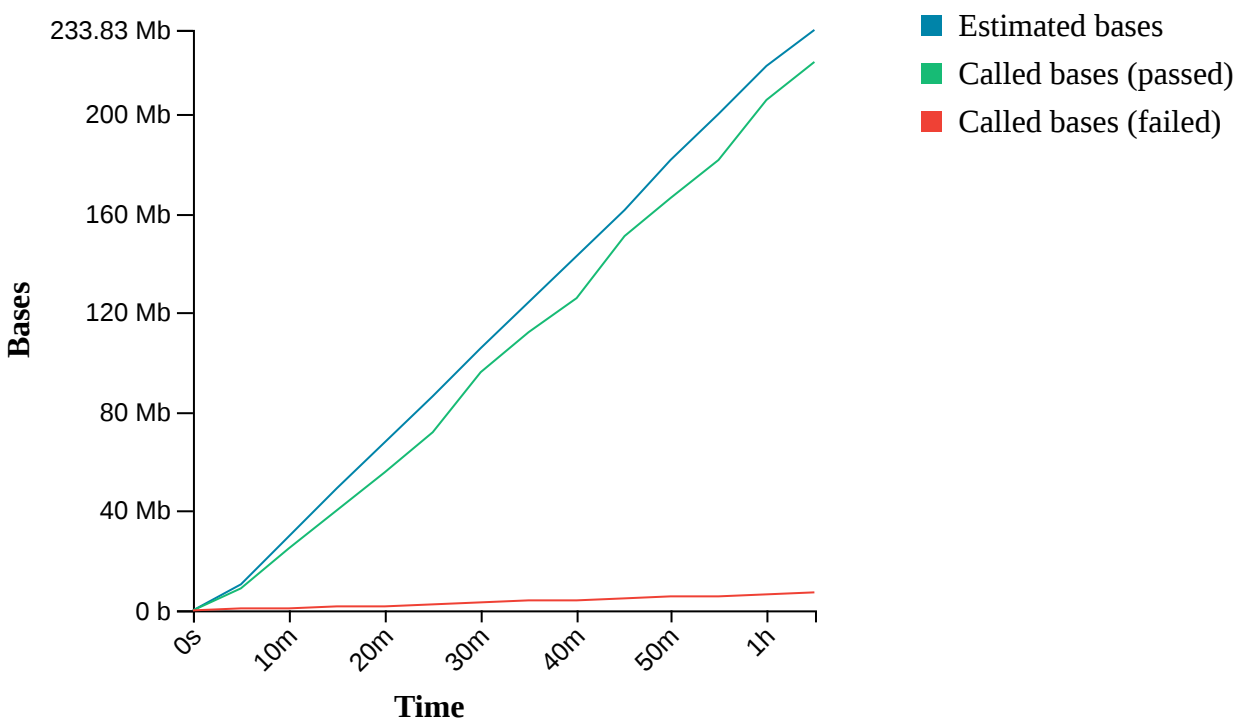
Read Length Histogram Estimated Bases - Outliers Discarded
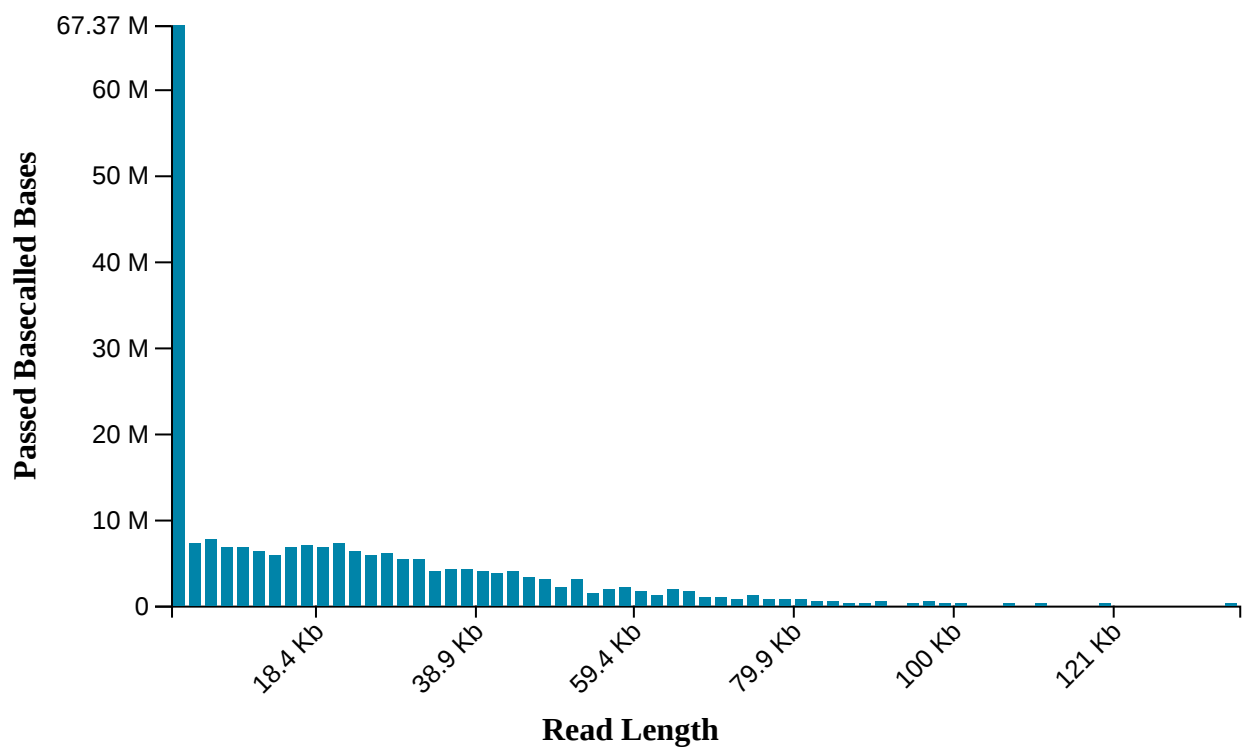
Estimated N50: 15.15 K

Read Length Histogram Basecalled Bases - Outliers Discarded
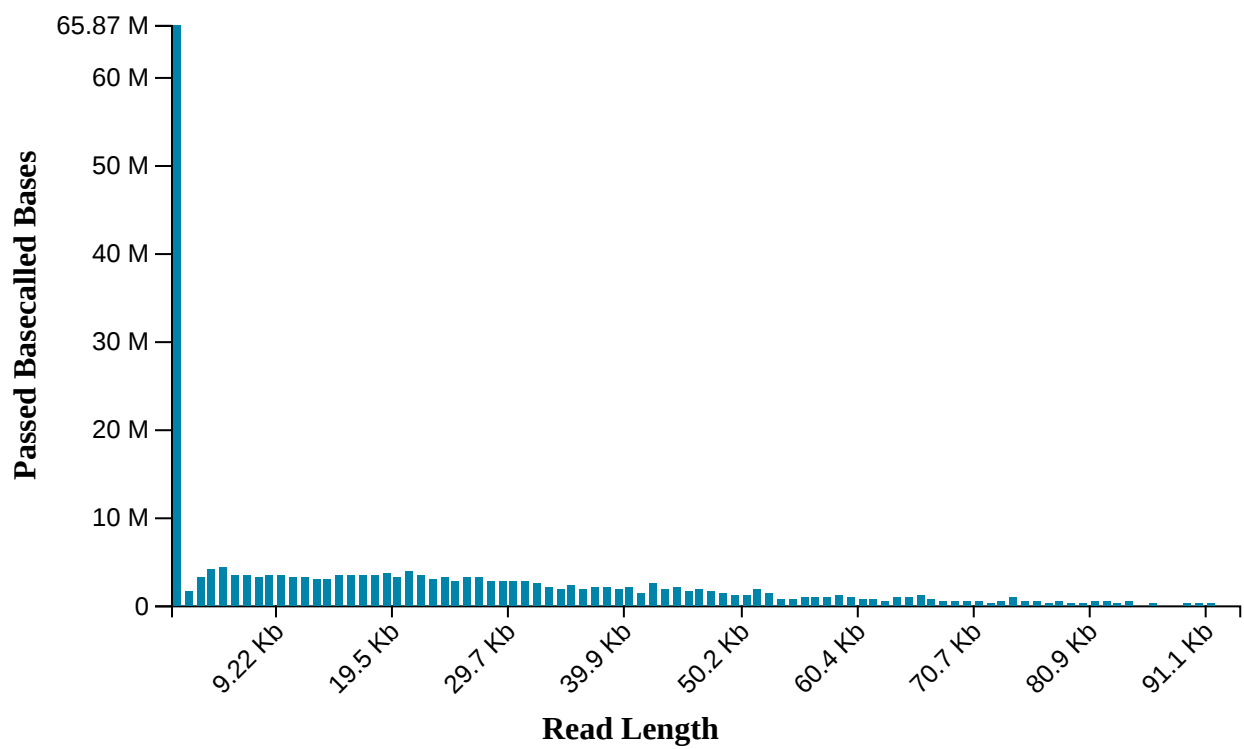
Estimated N50: 14.8 K

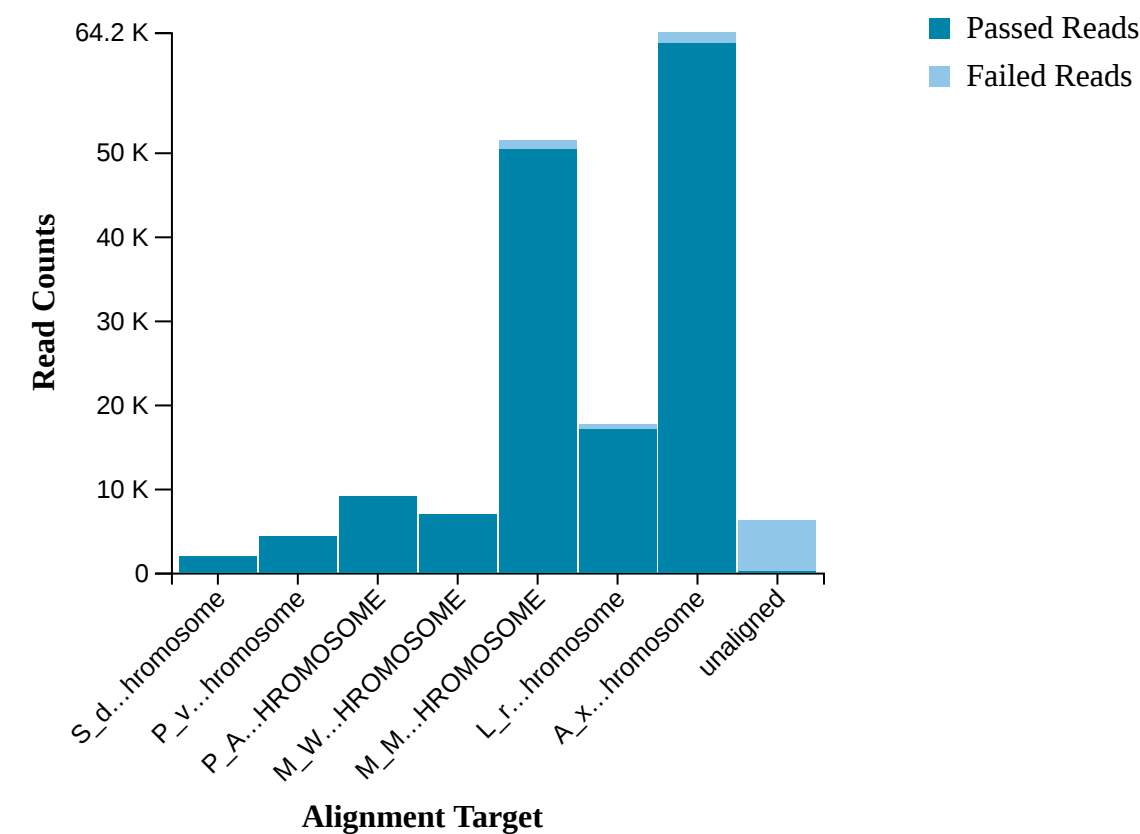## **Read Length Histogram Estimated Bases**

Estimated N50: 15.15 K
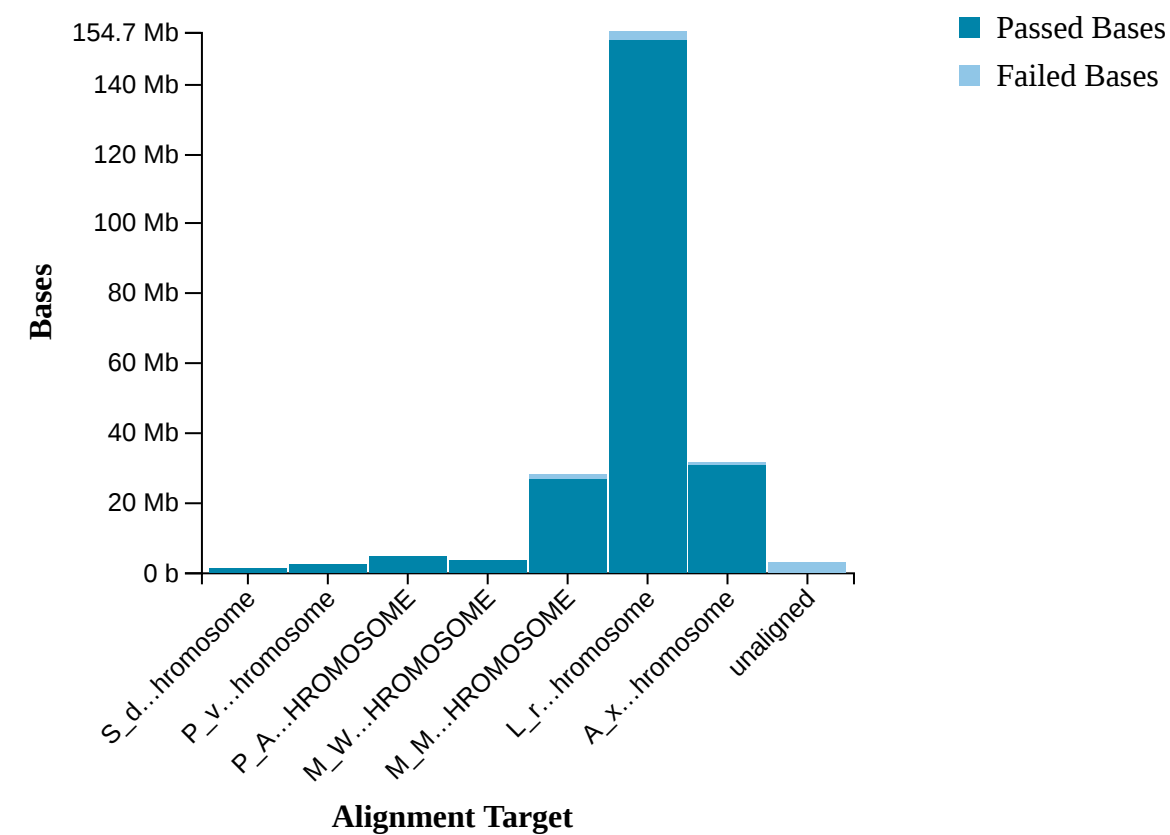

Read Length Histogram Basecalled Bases

Estimated N50: 14.8 K

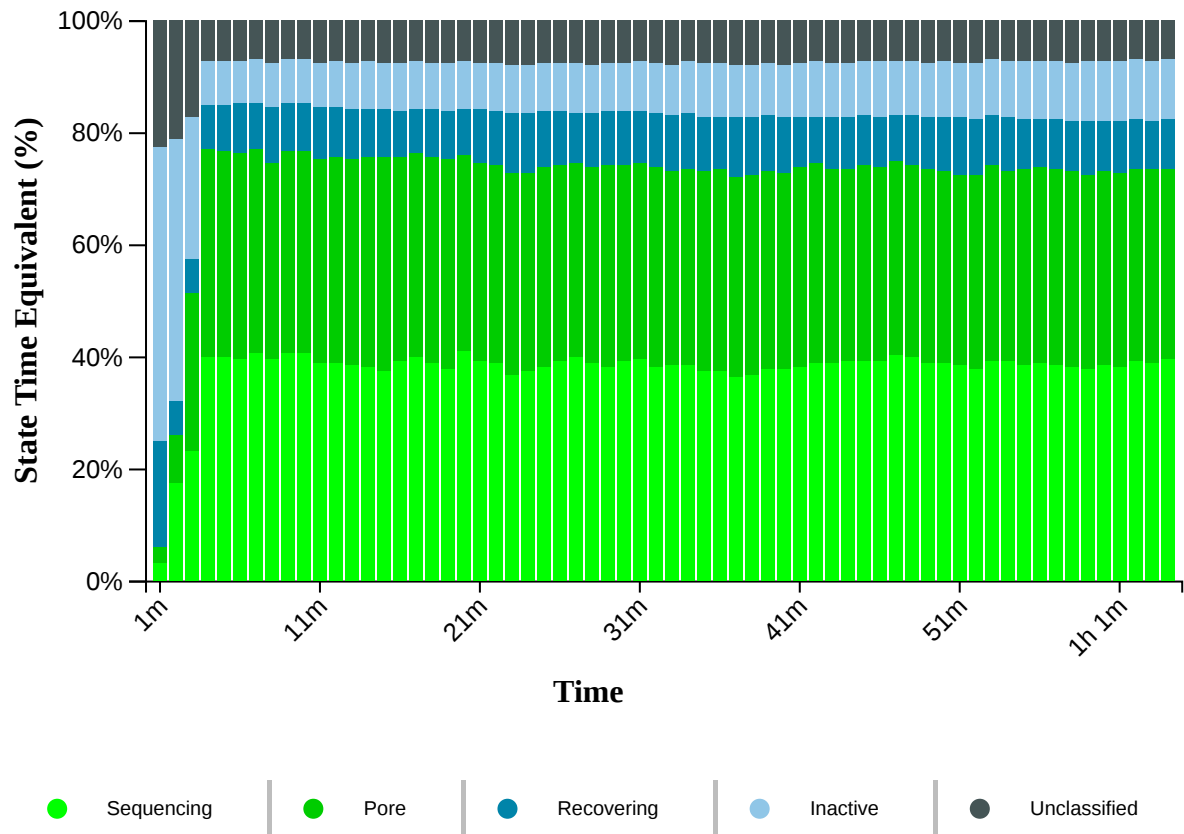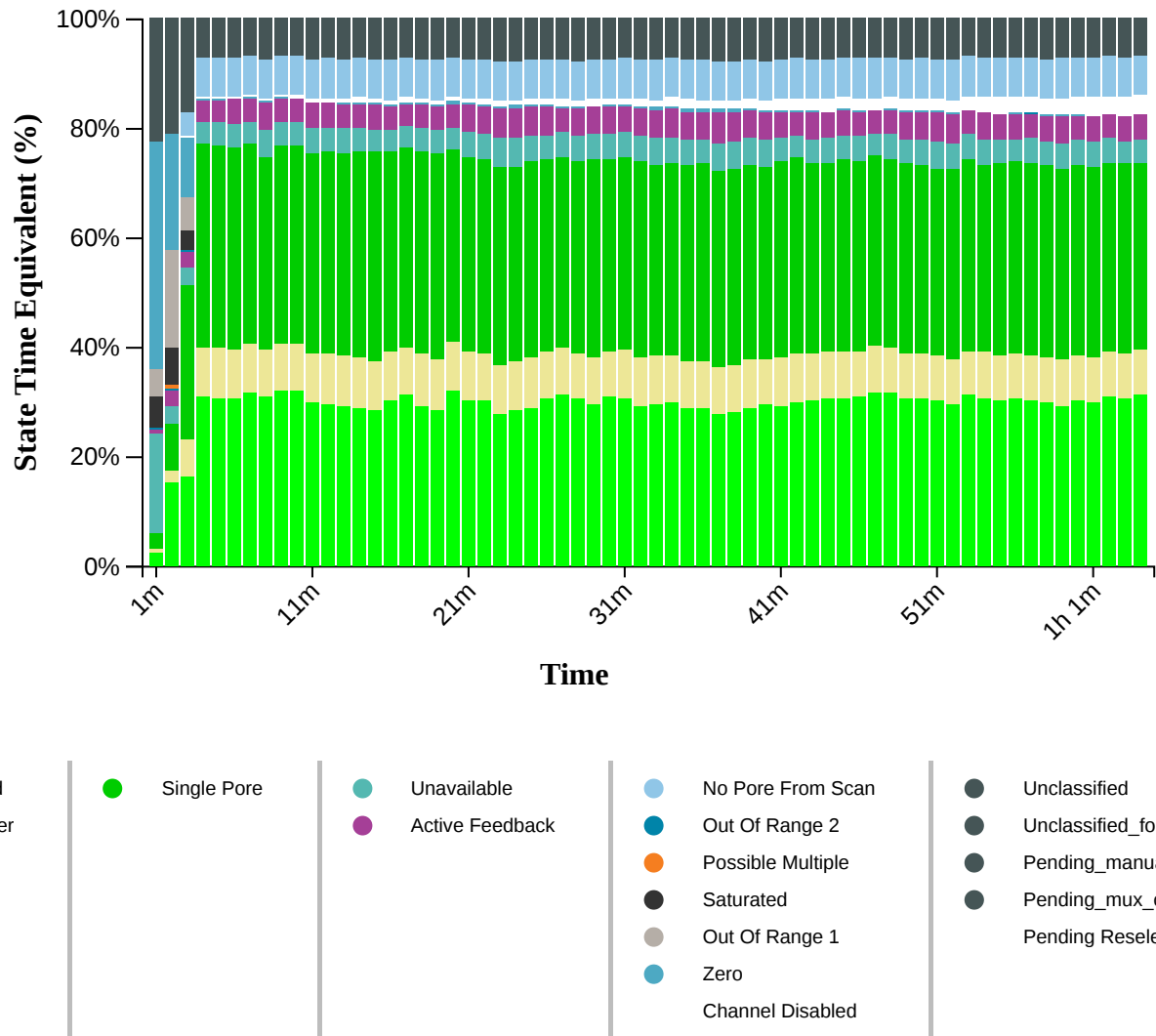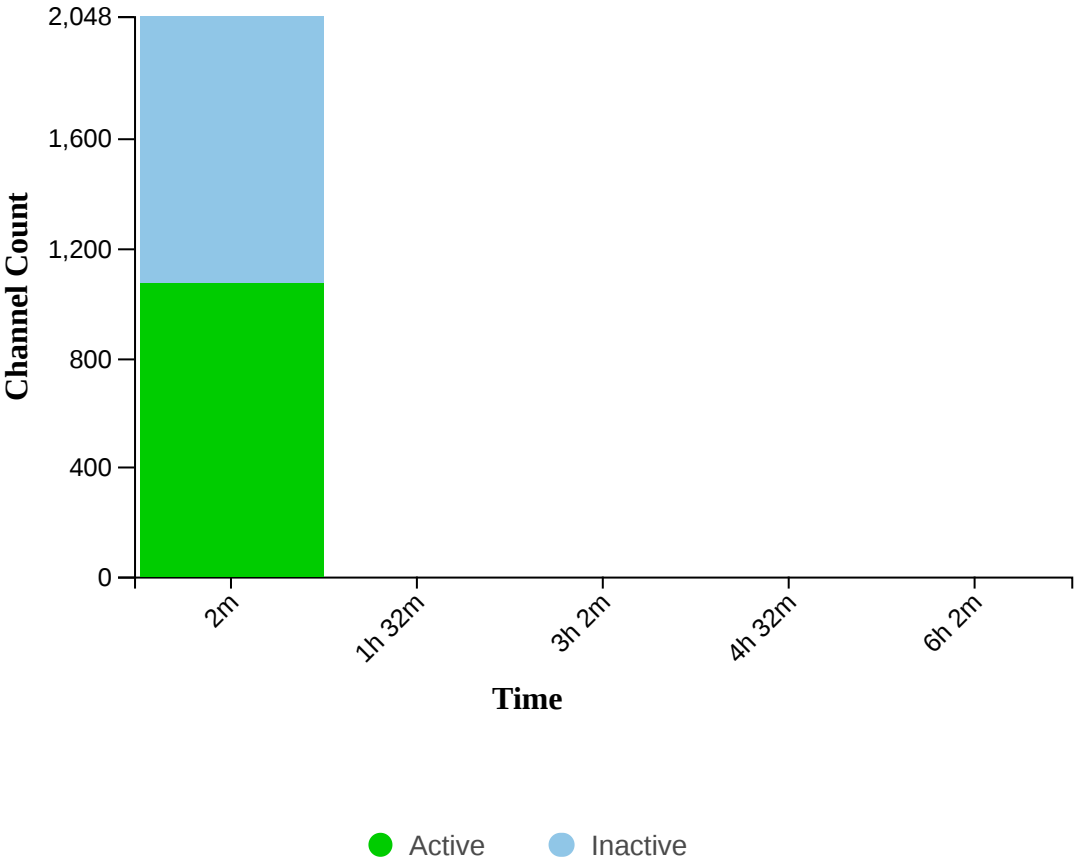## Alignment Target Hits (reads)
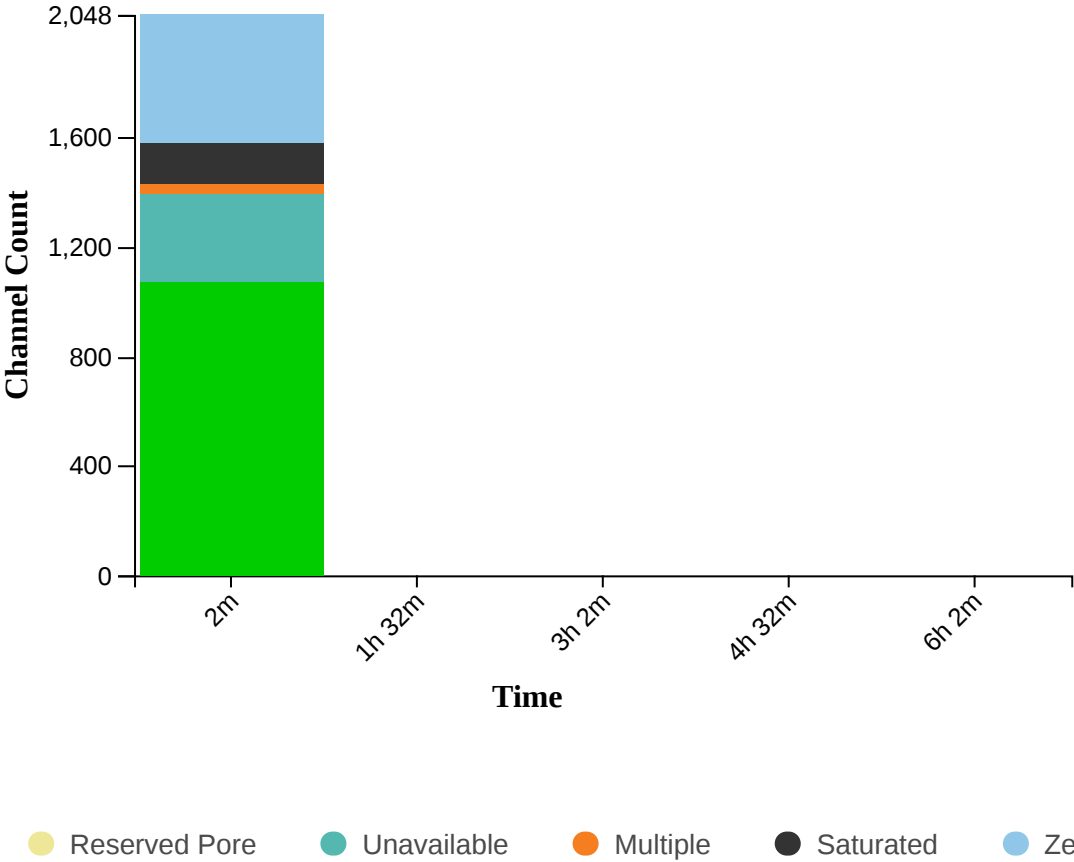

Alignment Target Hits (bases)
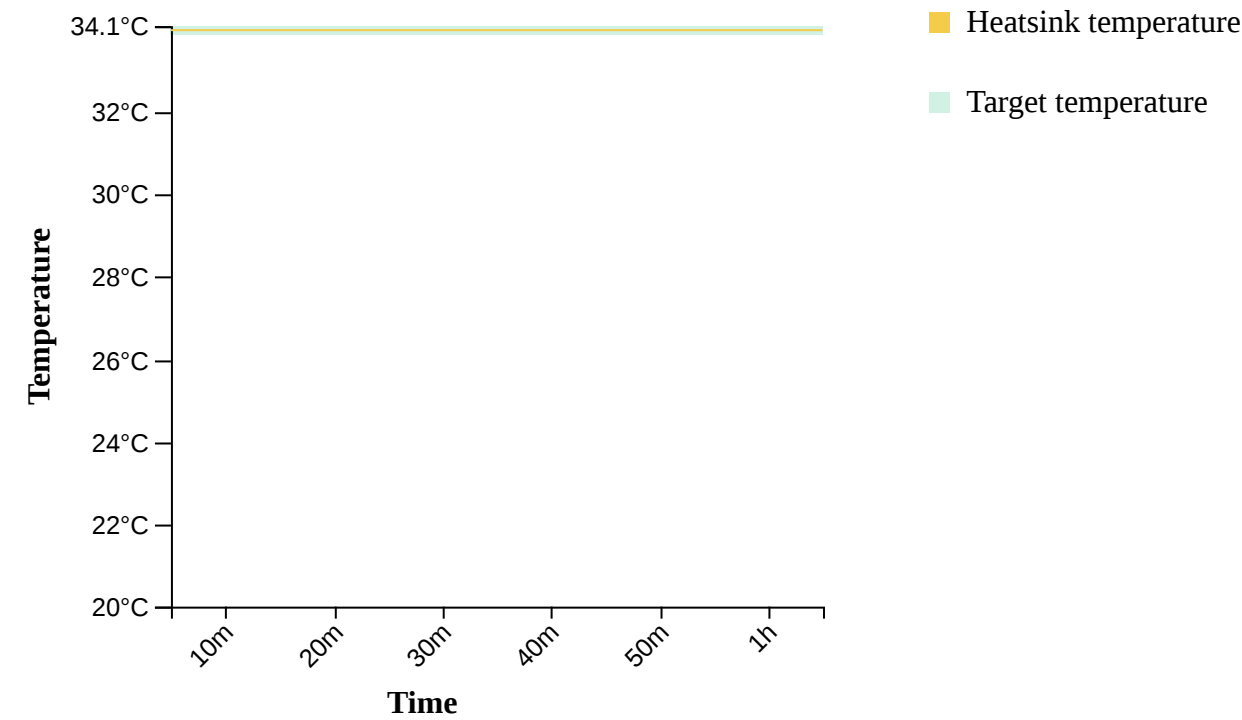
Duty Time Grouped

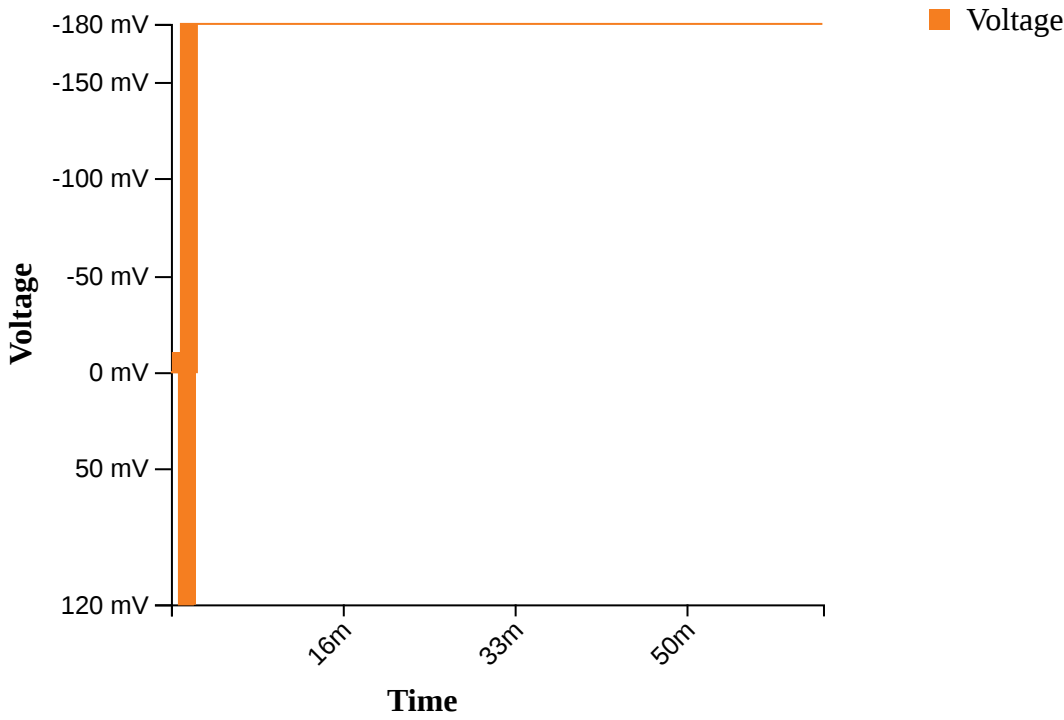## Duty time Categorised

Mux Scan Grouped

Active   Inactive

Mux Scan Categorised

Single Pore   Reserved Pore   Unavailable   Multiple   Saturated   Zero   Other

Temperature History

Bias Voltage History

Translocation Speed
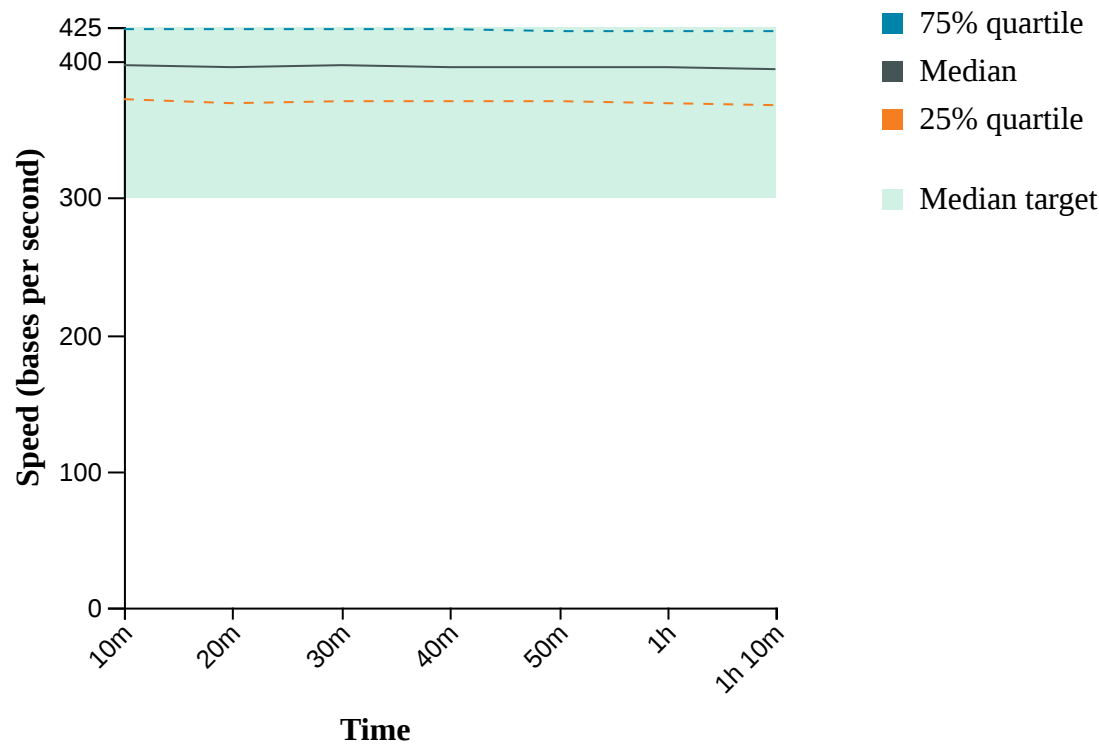
QScore

Disk Write Performance

- Produced
- Written
- Held in memory
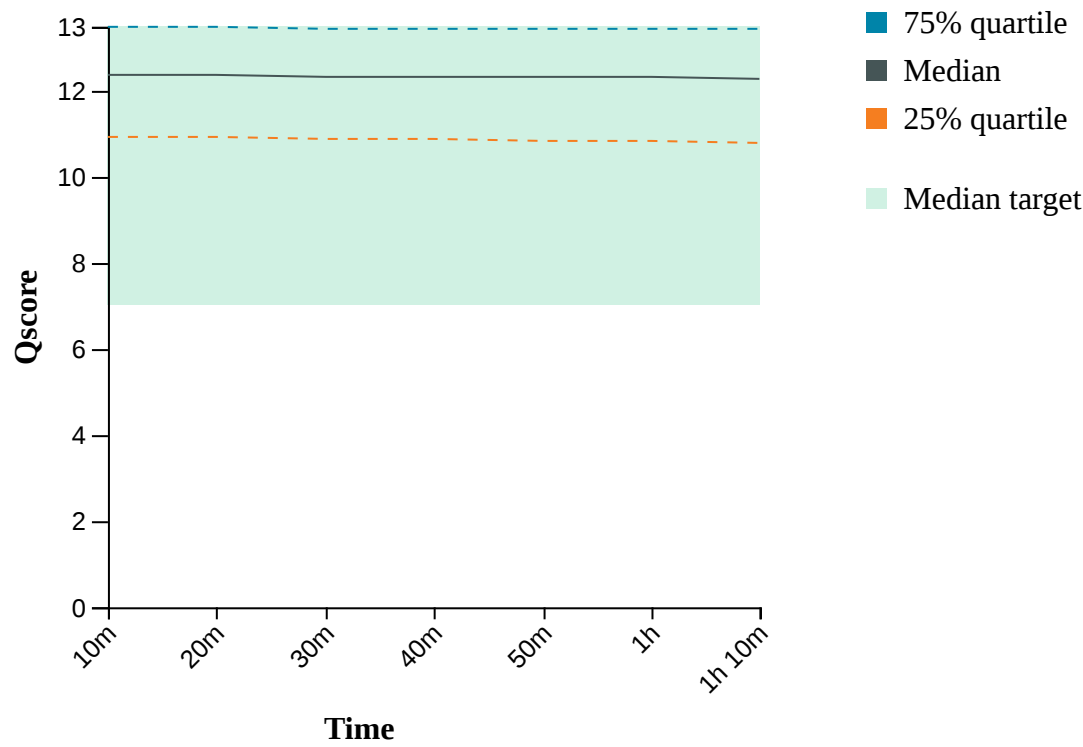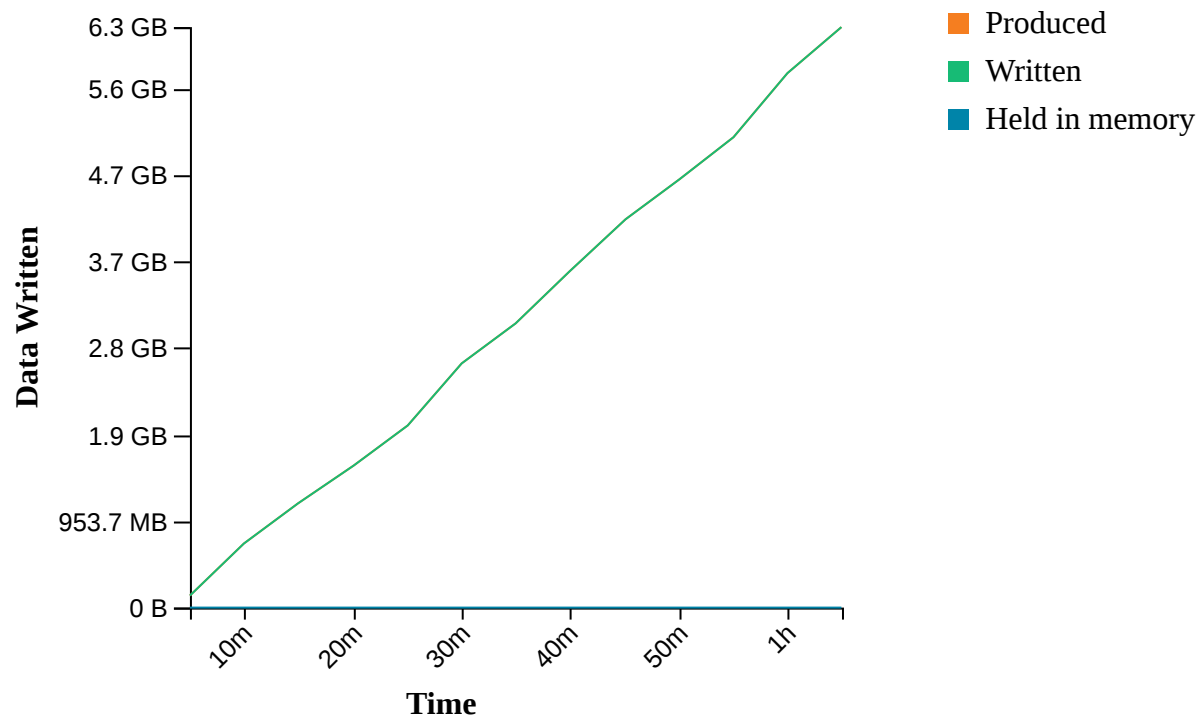
Run Debug Messages

- Mux scan for flow cell FAO52906 has found a total of 1076 pores. 475 pores available for immediate sequencing   December 8, 14:18
- Performing Mux Scan   December 8, 14:16
- Starting sequencing procedure   December 8, 14:16
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   December 8, 14:12