Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**EIMock_2kbp_AxylosoxidansRAD_050121**
Sample ID	**EIMock_2kbp_AxylosoxidansRAD_050121**
Run ID	**01eca510-2c36-43a3-8feb-1d5f61ce17b3**
Flow Cell Id	**FAO53362**
Start Time	**January 5, 13:56**
Run Length	**1h 0m**

Run Summary

Reads Generated	**421.72 K**
Passed Bases	**297.18 Mb**
Failed Bases	**18.14 Mb**
Estimated Bases	**339.11 Mb**

Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-RAD004**
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/A_xylosoxidans_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

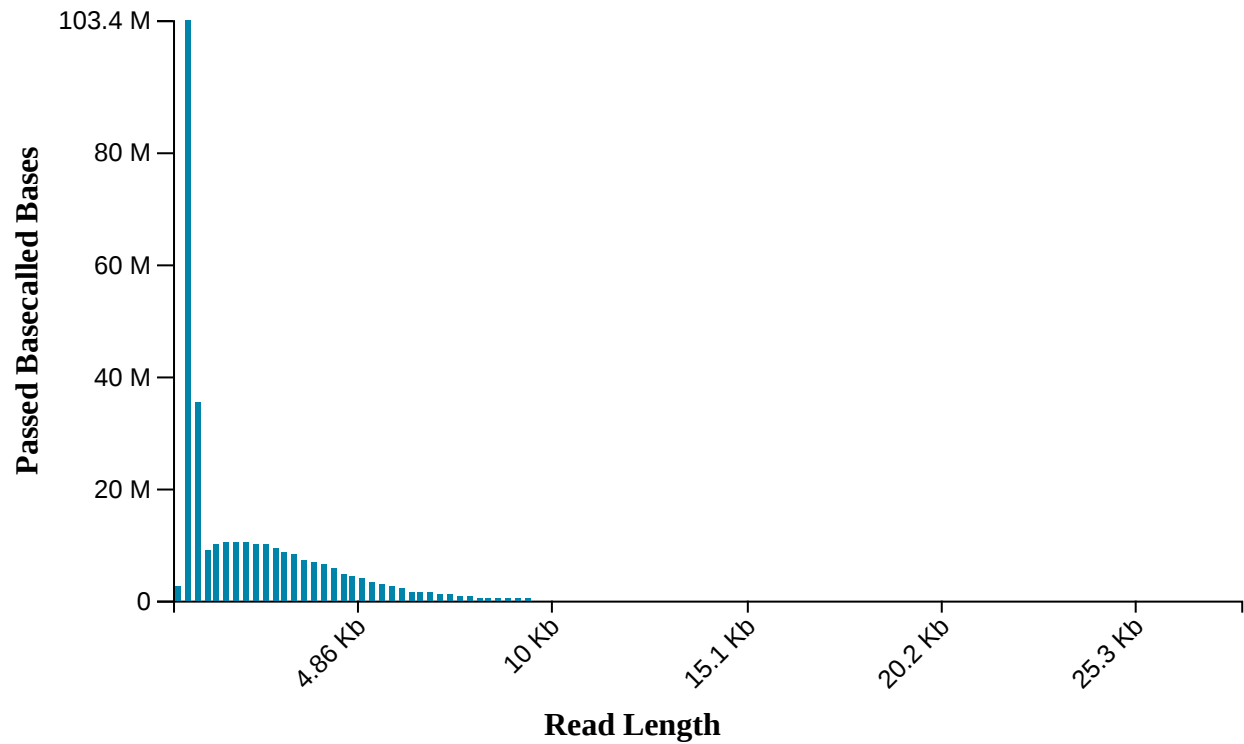|	
MinKNOW	**20.10.6**
MinKNOW Core	**4.1.2**
Bream	**6.1.4**
Guppy	**4.2.3**

Cumulative Output Reads
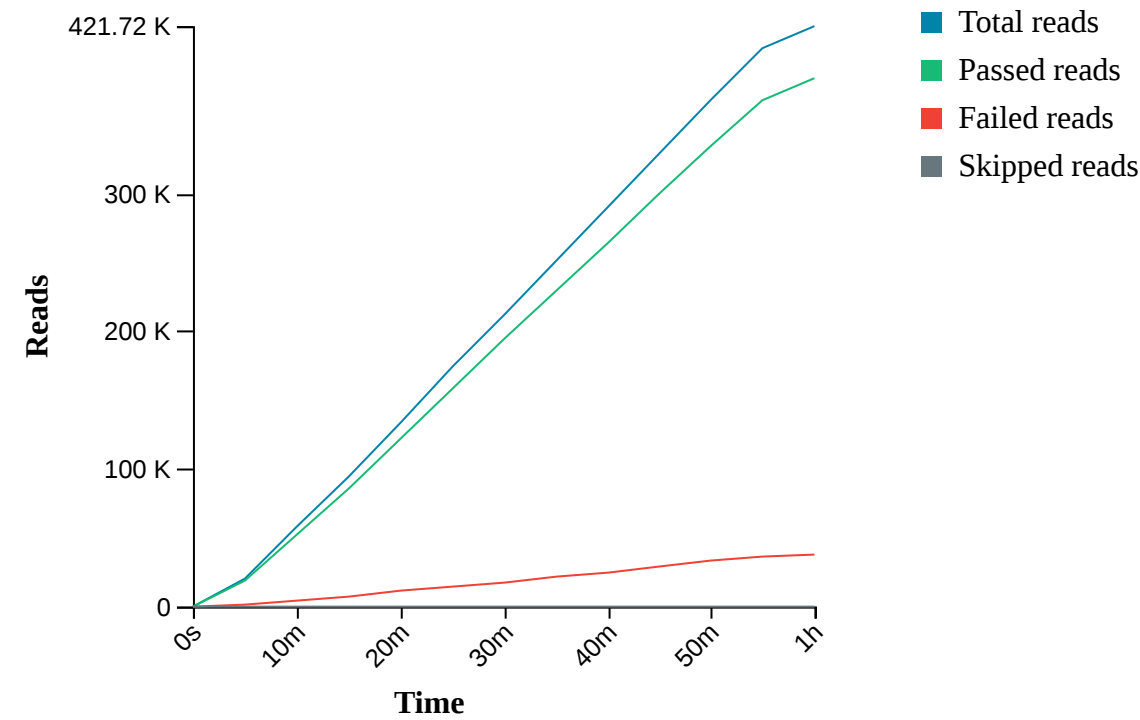
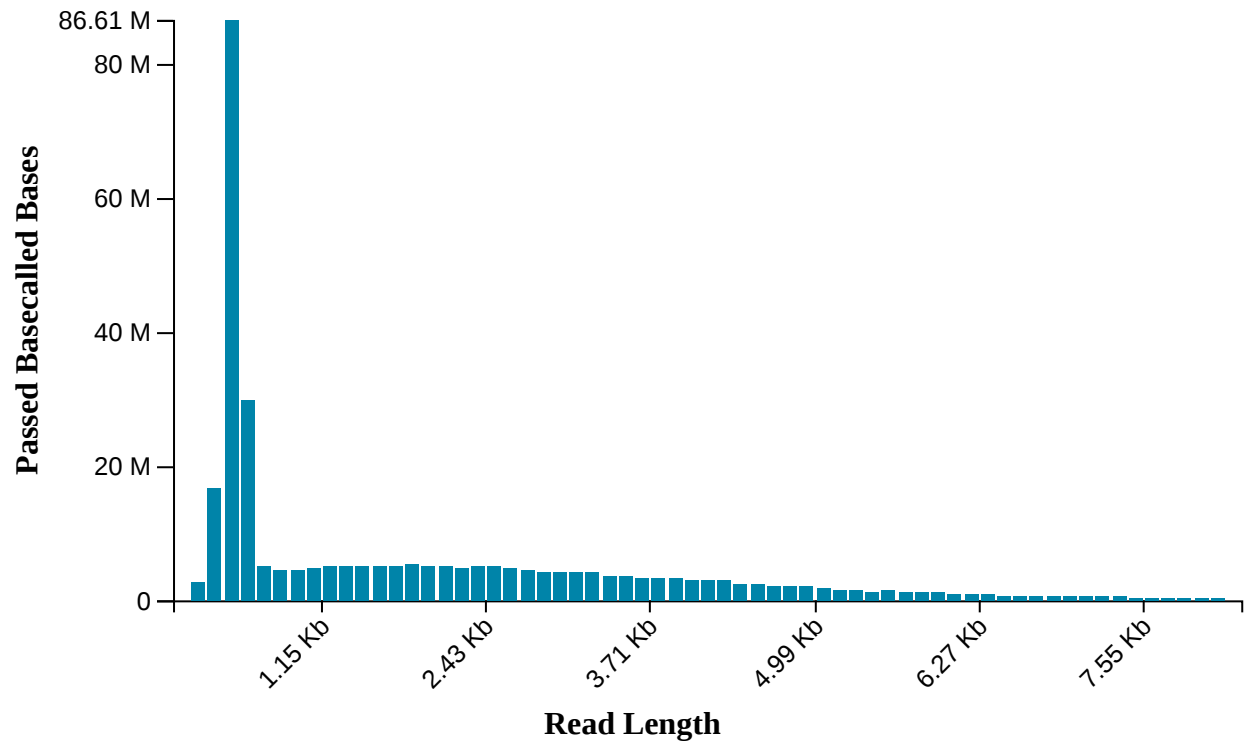

Cumulative Output Bases
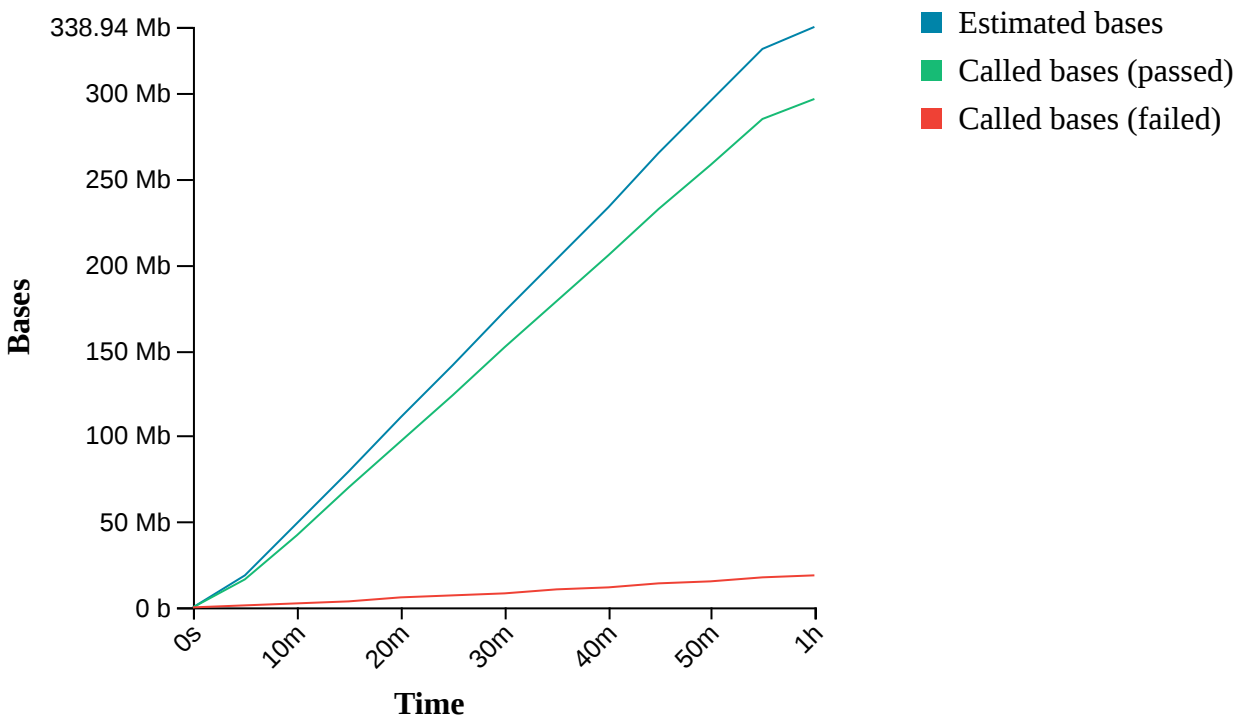
Read Length Histogram Estimated Bases - Outliers Discarded
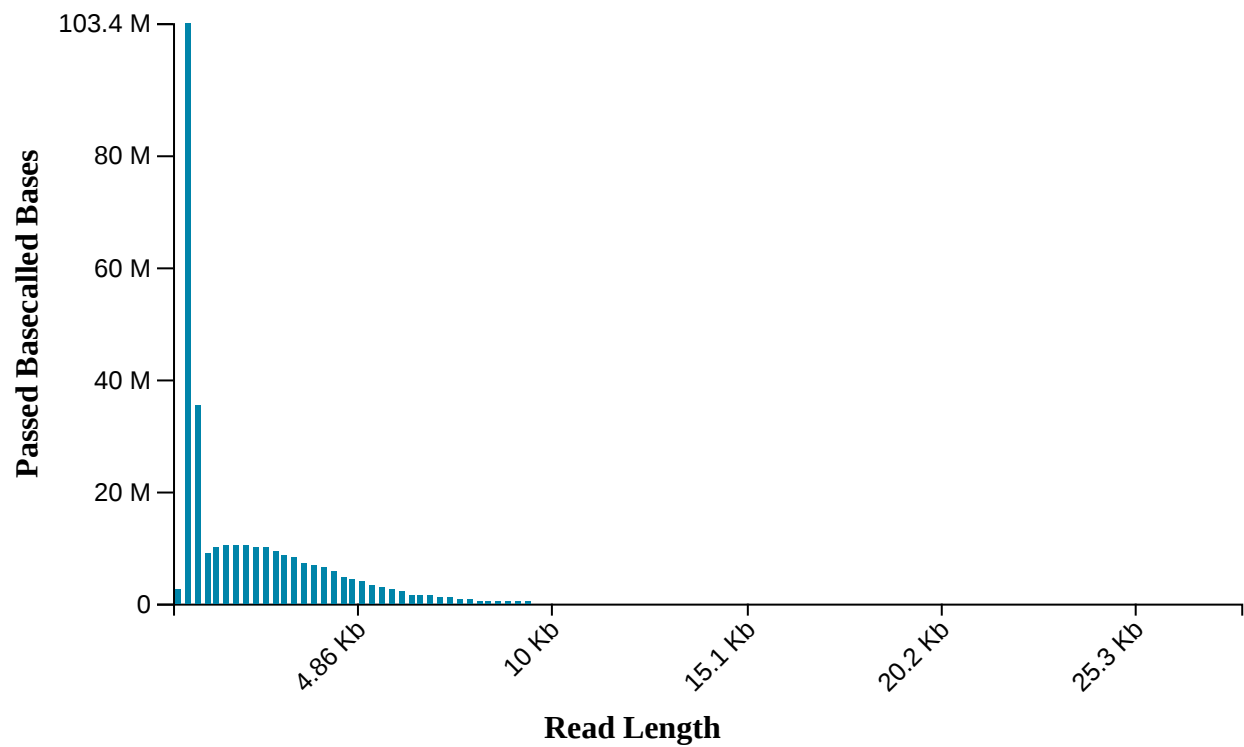
Estimated N50: 985

Read Length Histogram Basecalled Bases - Outliers Discarded
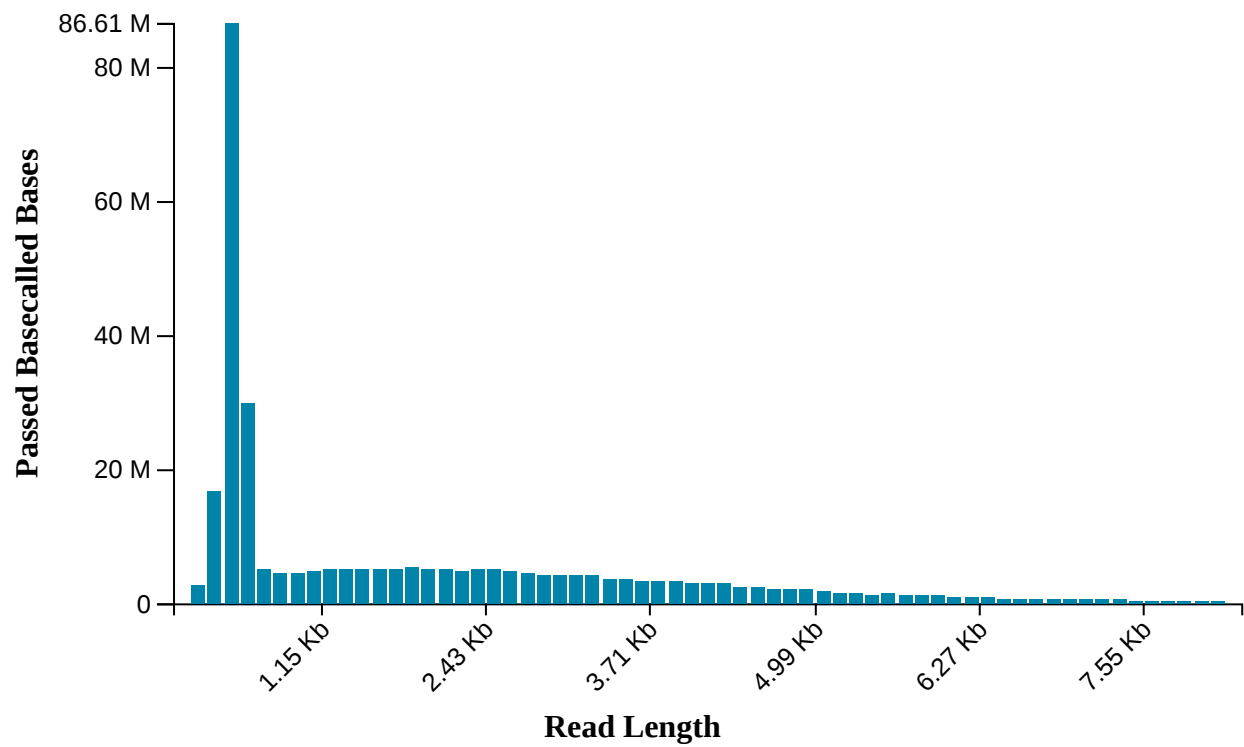
Estimated N50: 945

Read Length Histogram Estimated Bases

Estimated N50: 985

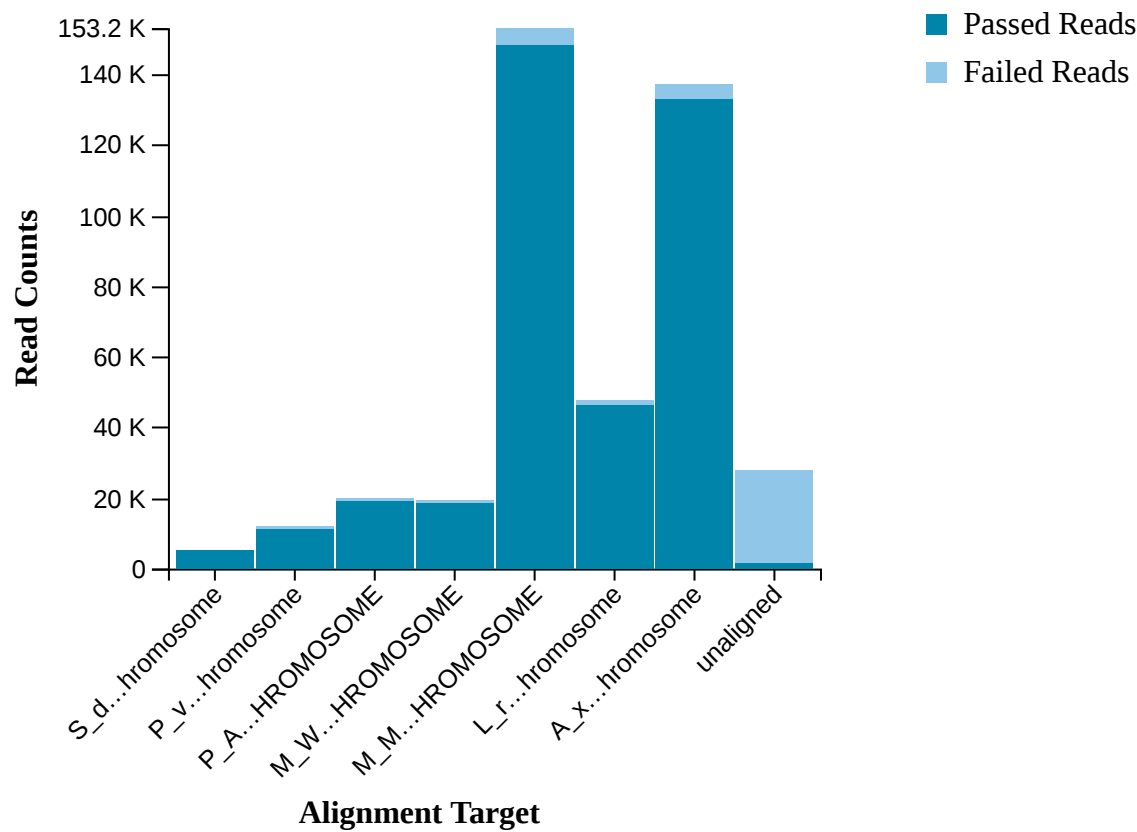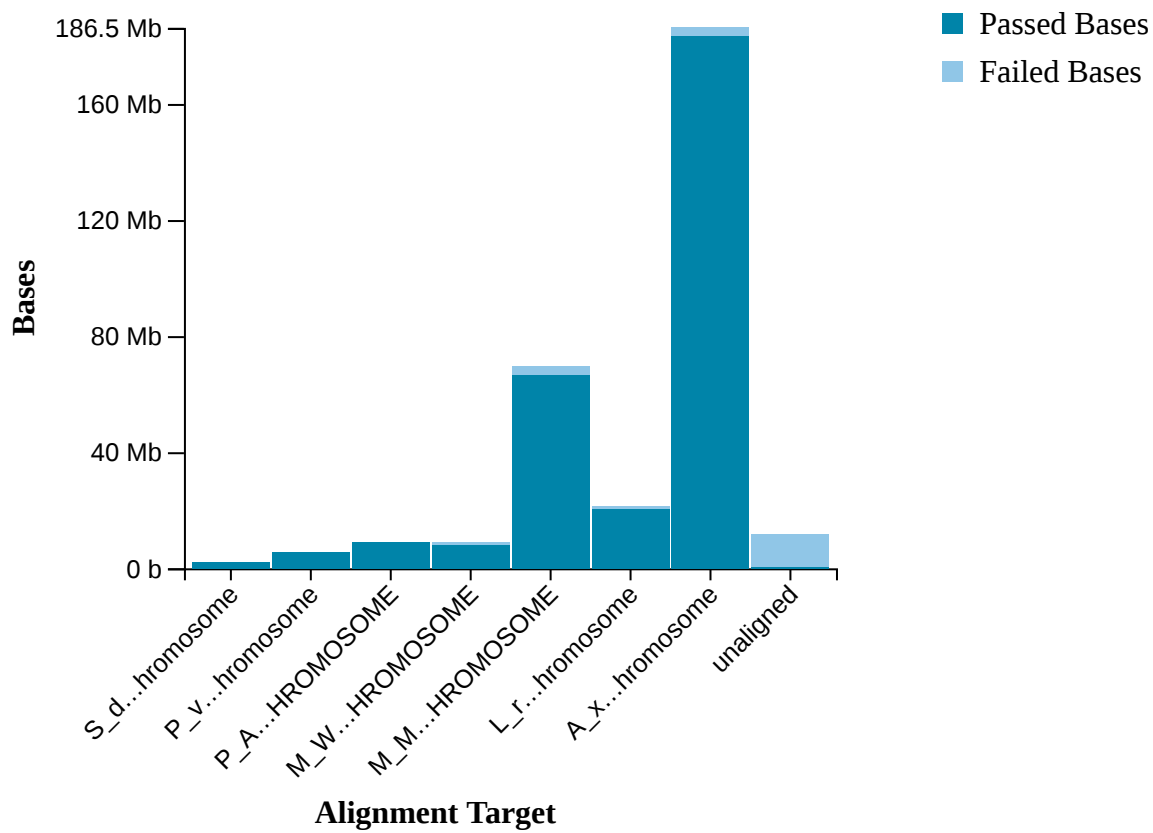## Read Length Histogram Basecalled Bases
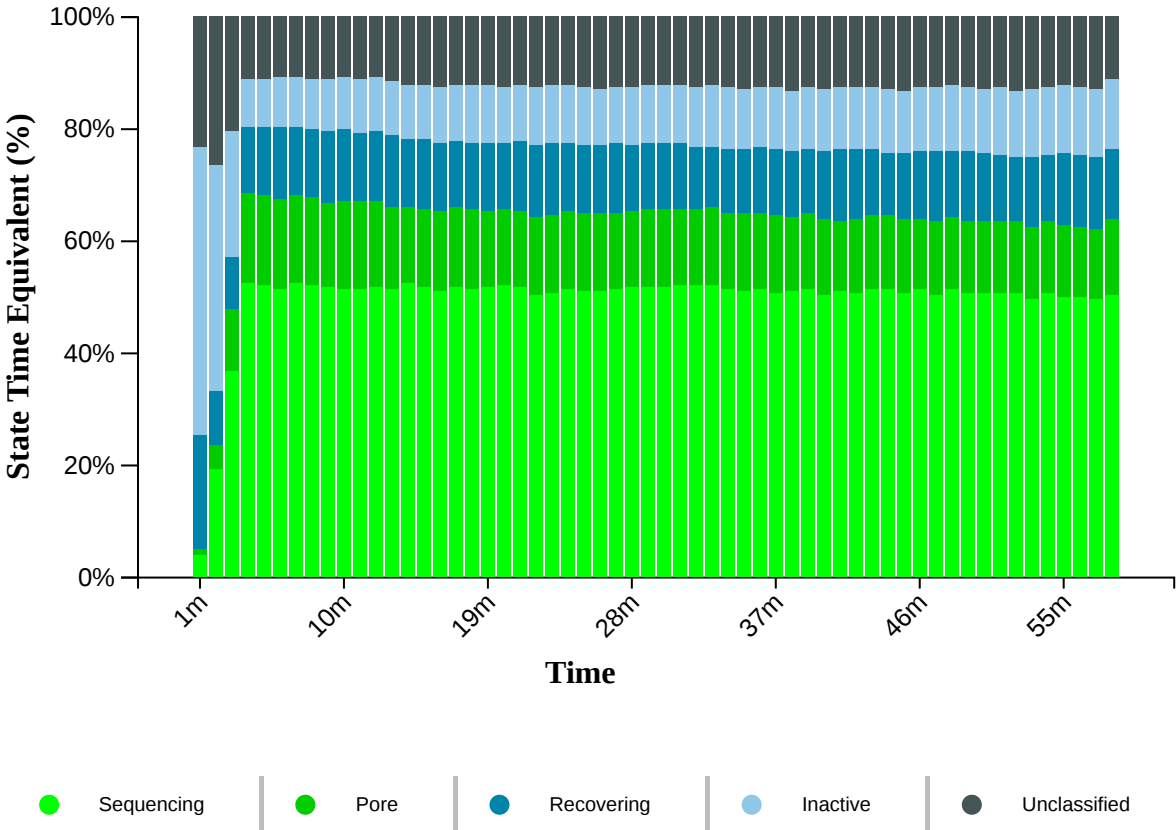
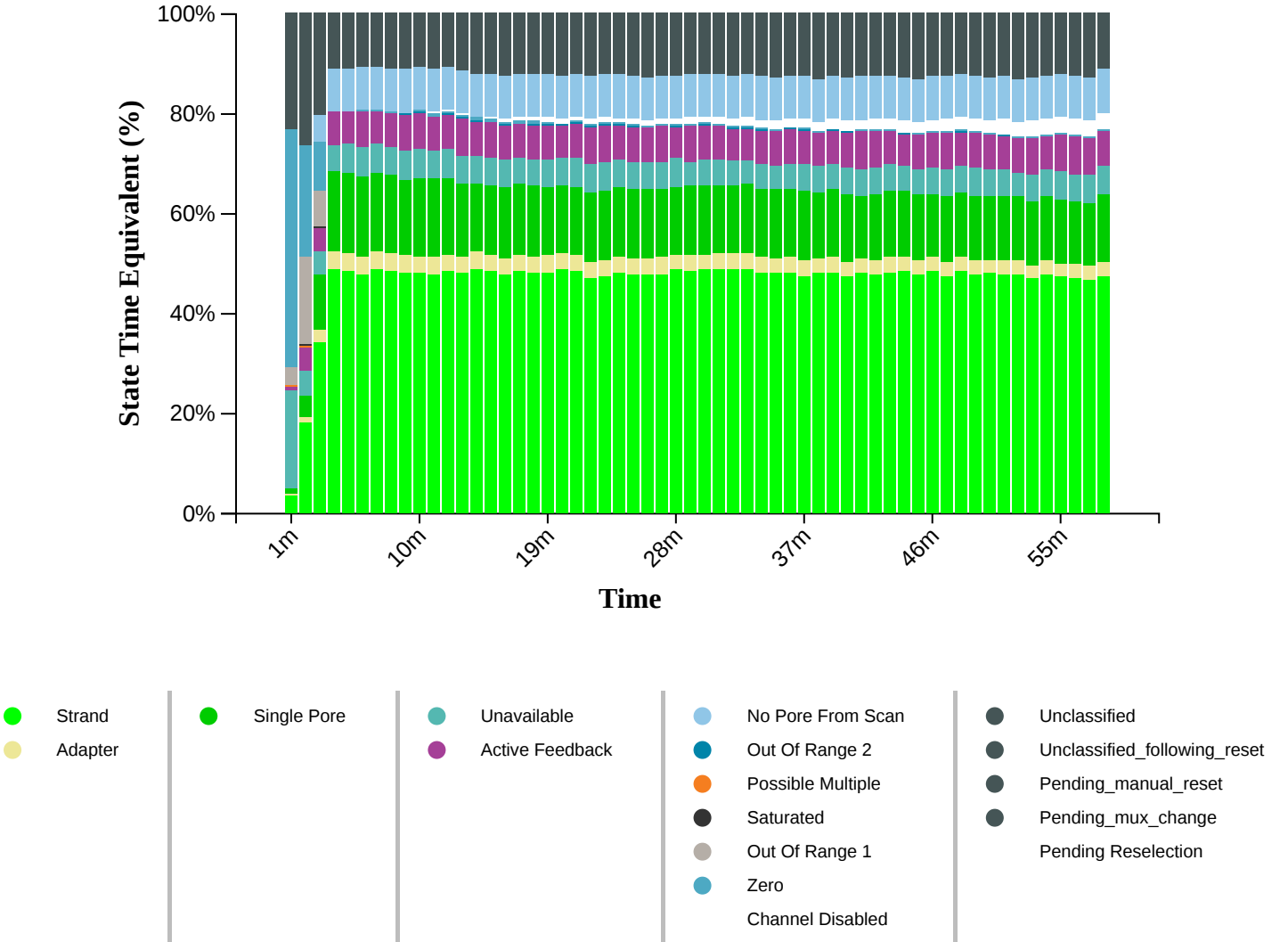Estimated N50: 945

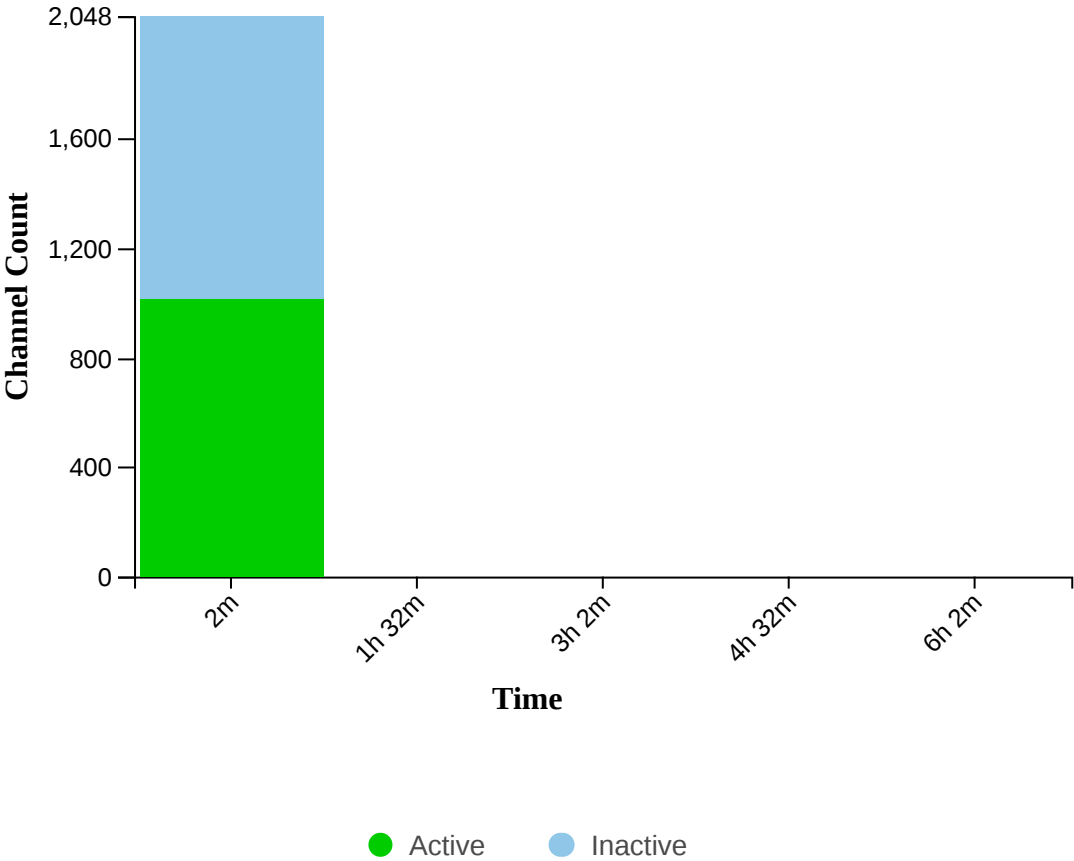## Alignment Target Hits (reads)

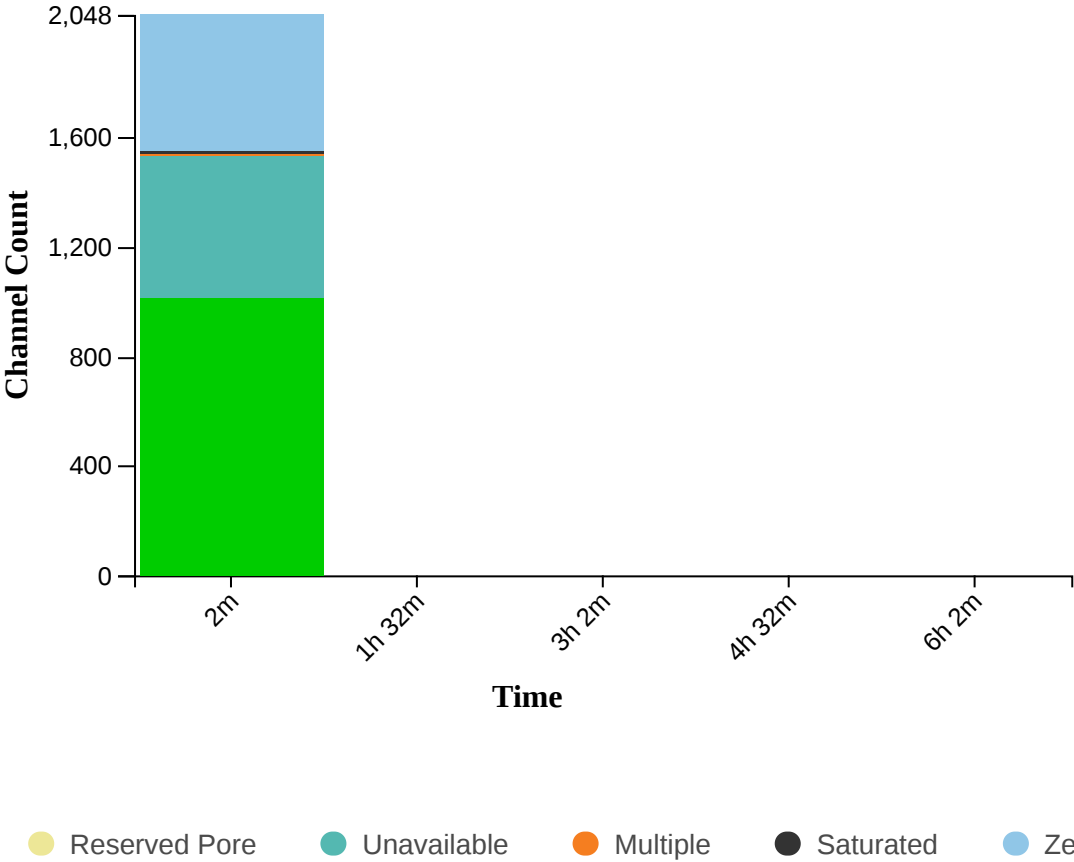## Alignment Target Hits (bases)
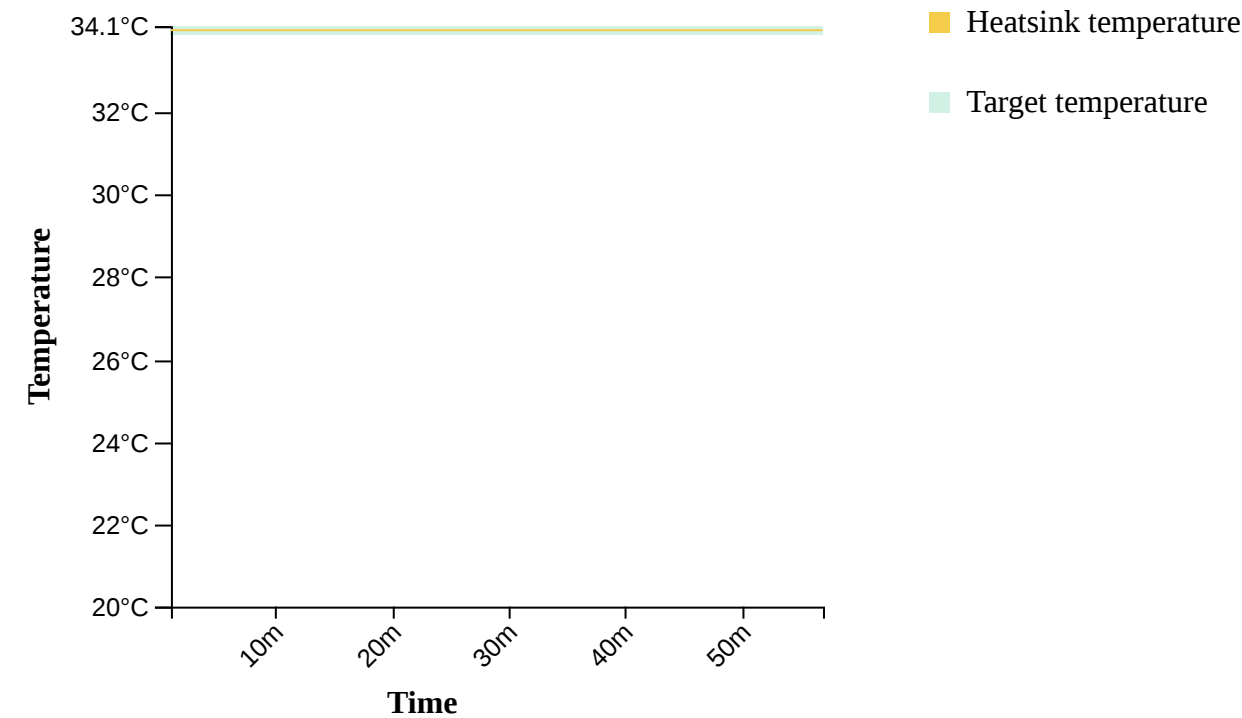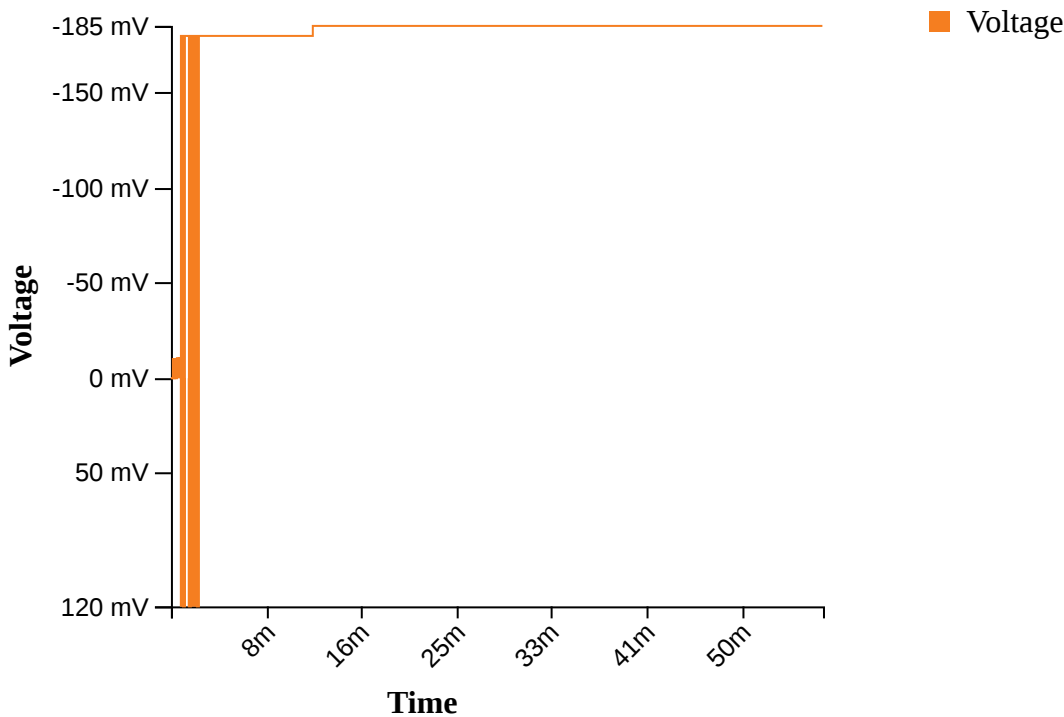
Duty Time Grouped

Duty time Categorised

Mux Scan Grouped

● Active   ● Inactive

Mux Scan Categorised

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

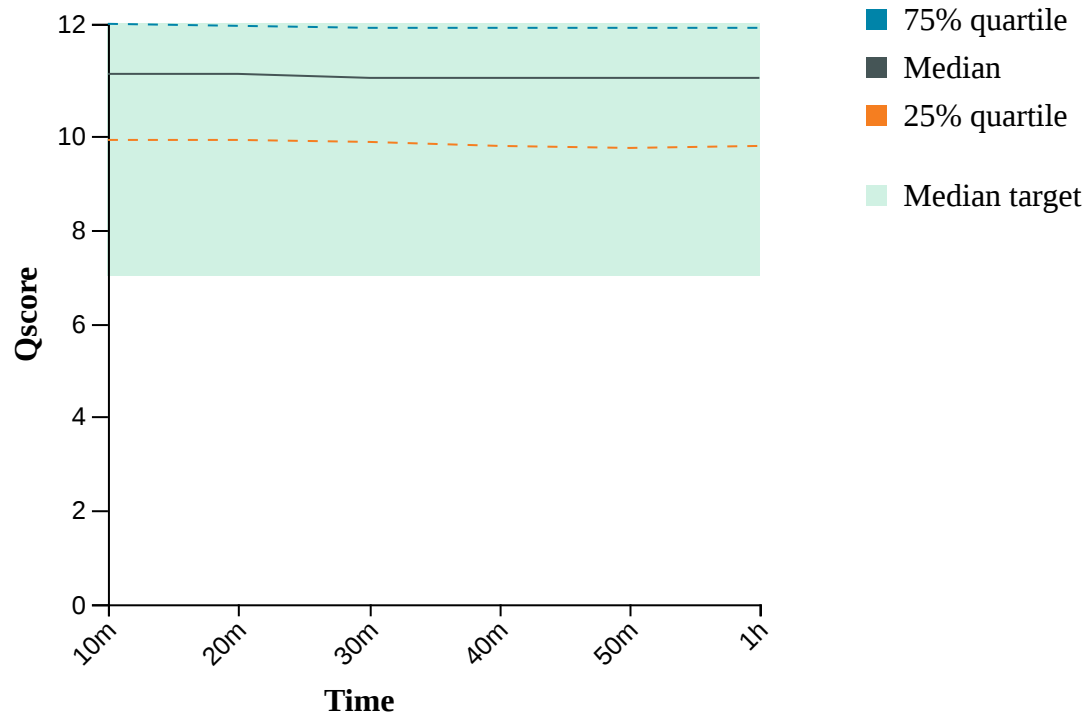## Temperature History

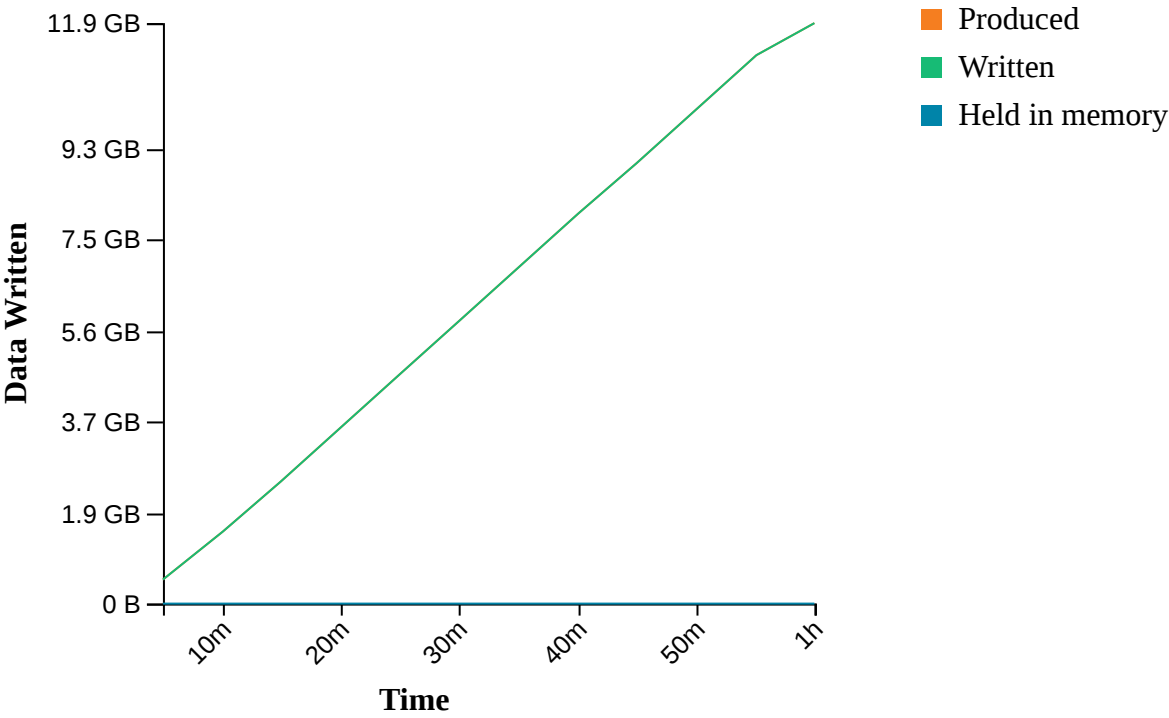## Bias Voltage History

Translocation Speed
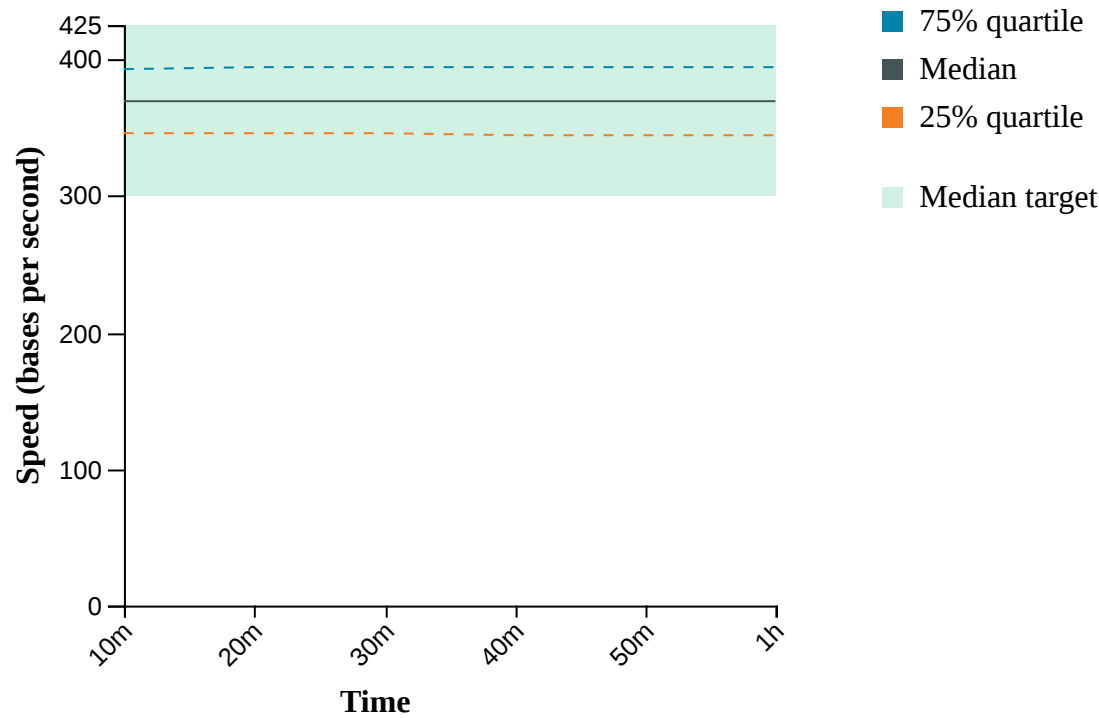
QScore

<u>Disk Write Performance</u>

Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 1015 pores. 468 pores available for immediate sequencing   January 5, 14:01
- Performing Mux Scan   January 5, 13:59
- Starting sequencing procedure   January 5, 13:59
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   January 5, 13:56

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