Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**EIMock_2kbp_NoEnrichRAD_050121**
Sample ID	**EIMock_2kbp_NoEnrichRAD_050121**
Run ID	**7f4a7183-0cc2-4ba5-847e-a067f8b22fa5**
Flow Cell Id	**FAO53362**
Start Time	**January 5, 12:56**
Run Length	**56m**

Run Summary

Reads Generated	**229.07 K**
Passed Bases	**361.42 Mb**
Failed Bases	**23.1 Mb**
Estimated Bases	**414.79 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**
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

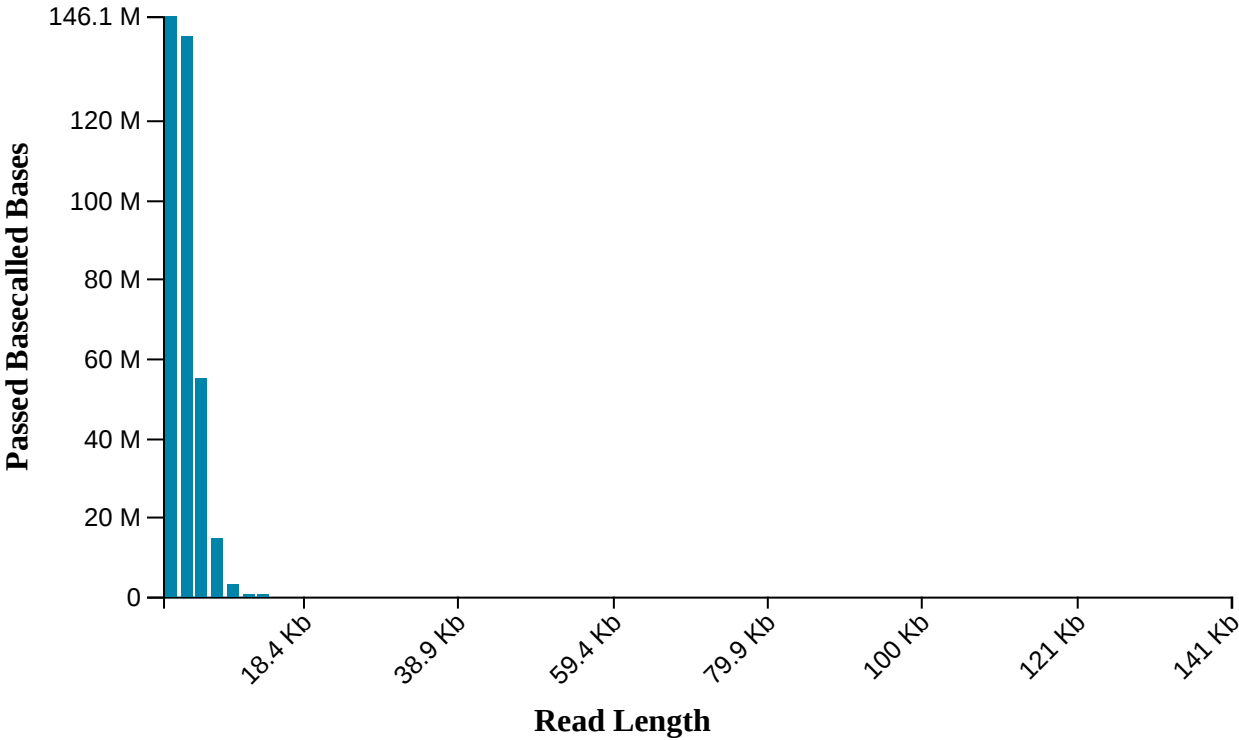|	
MinKNOW	**20.10.6**
MinKNOW Core	**4.1.2**
Bream	**6.1.4**
Guppy	**4.2.3**

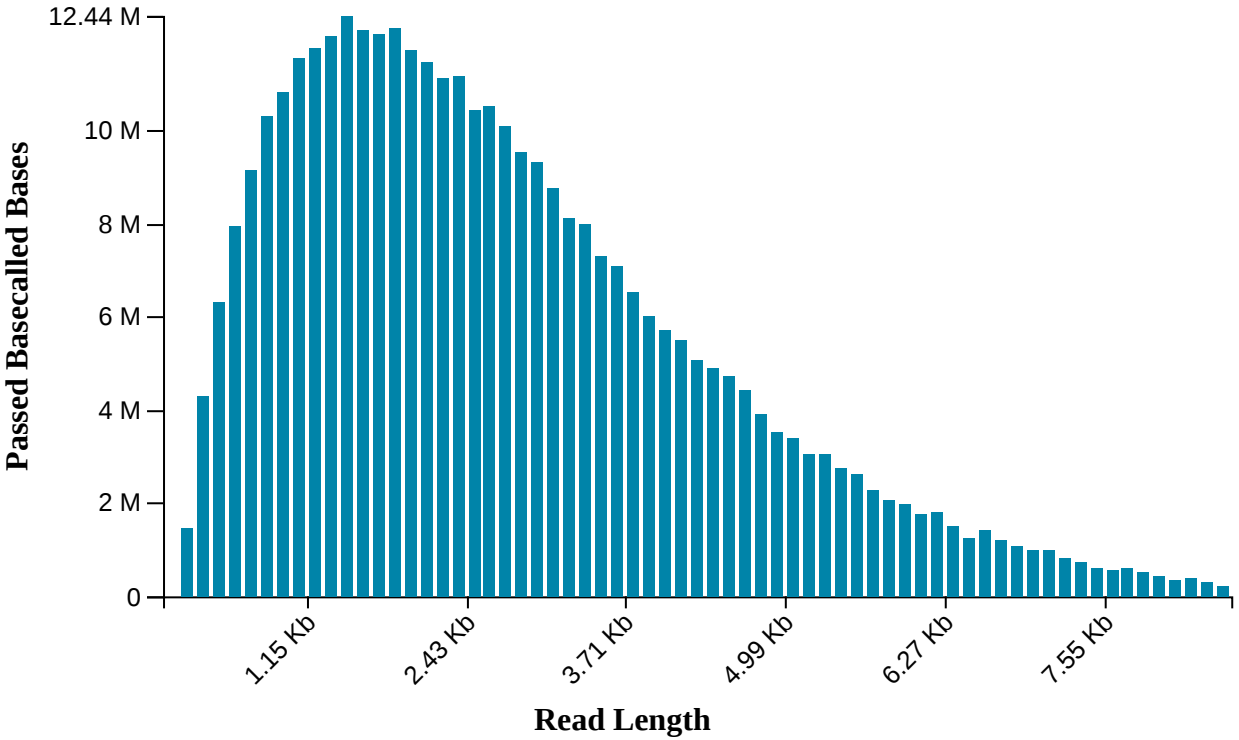## Cumulative Output Reads
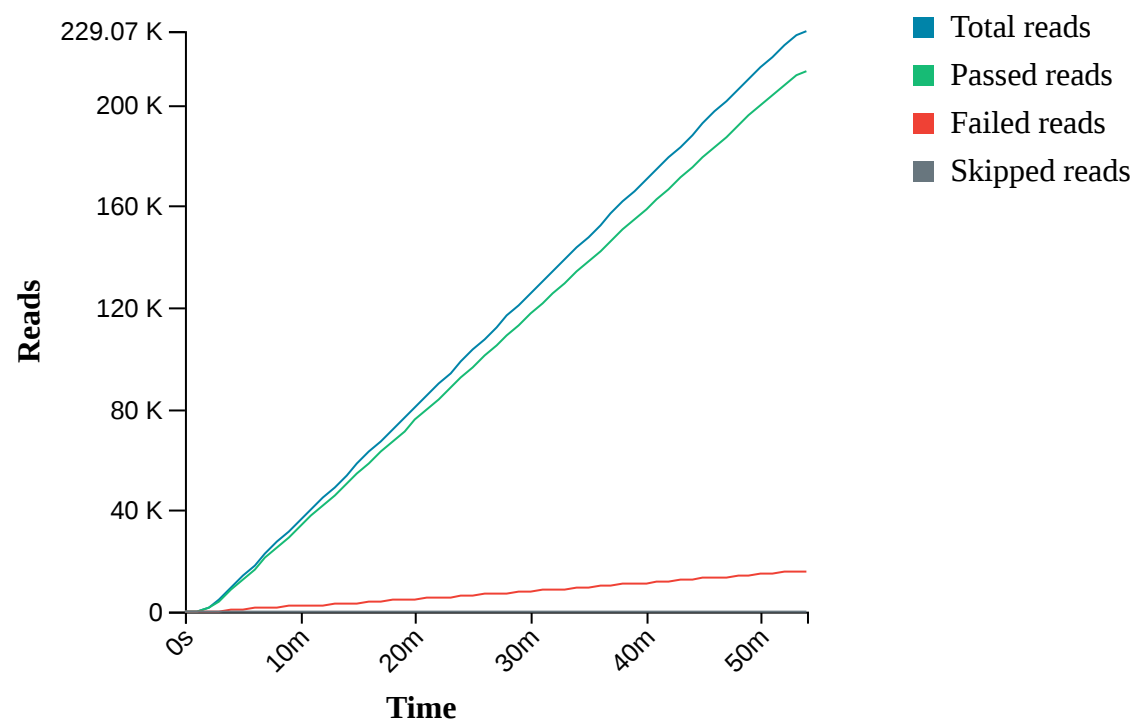
Cumulative Output Bases
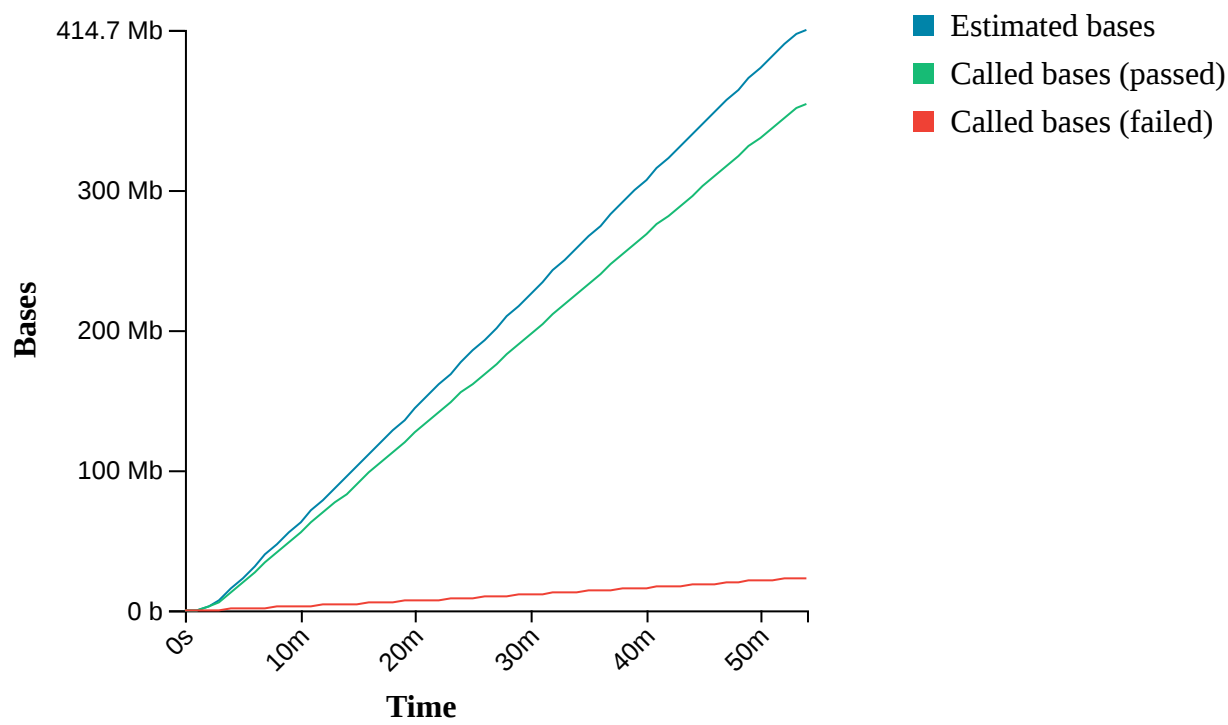
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 2.44 K

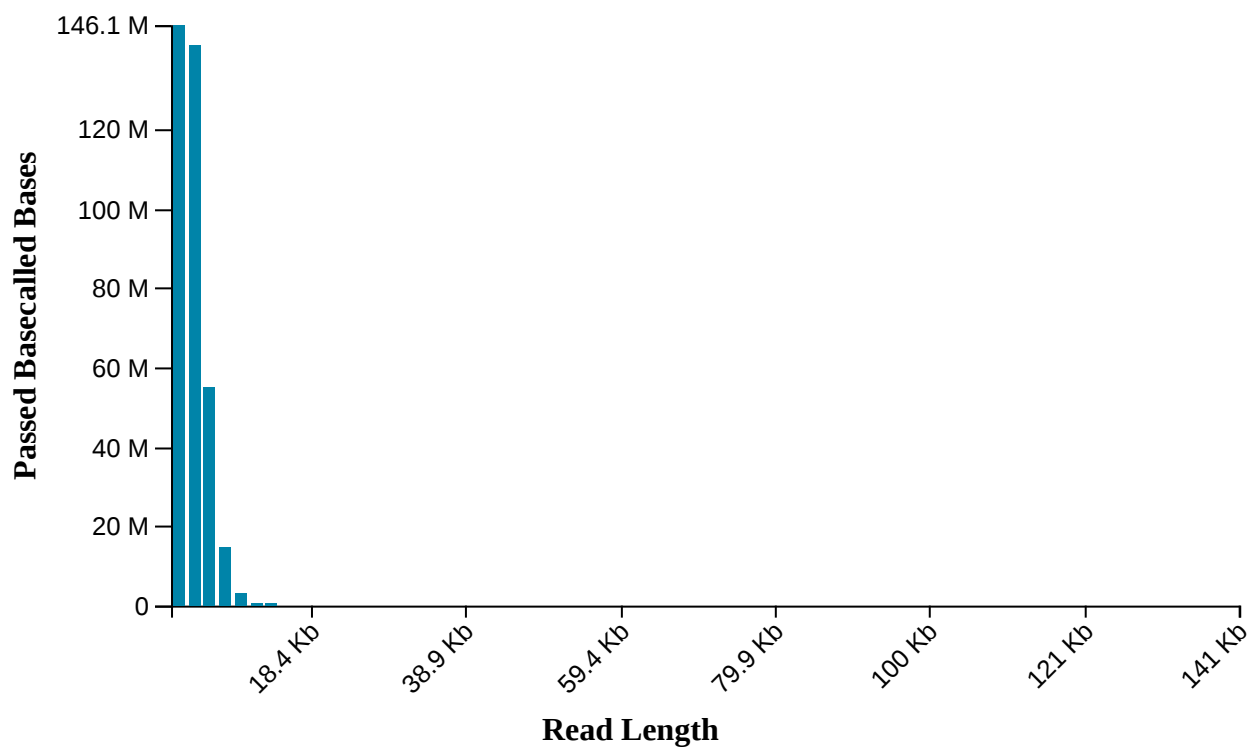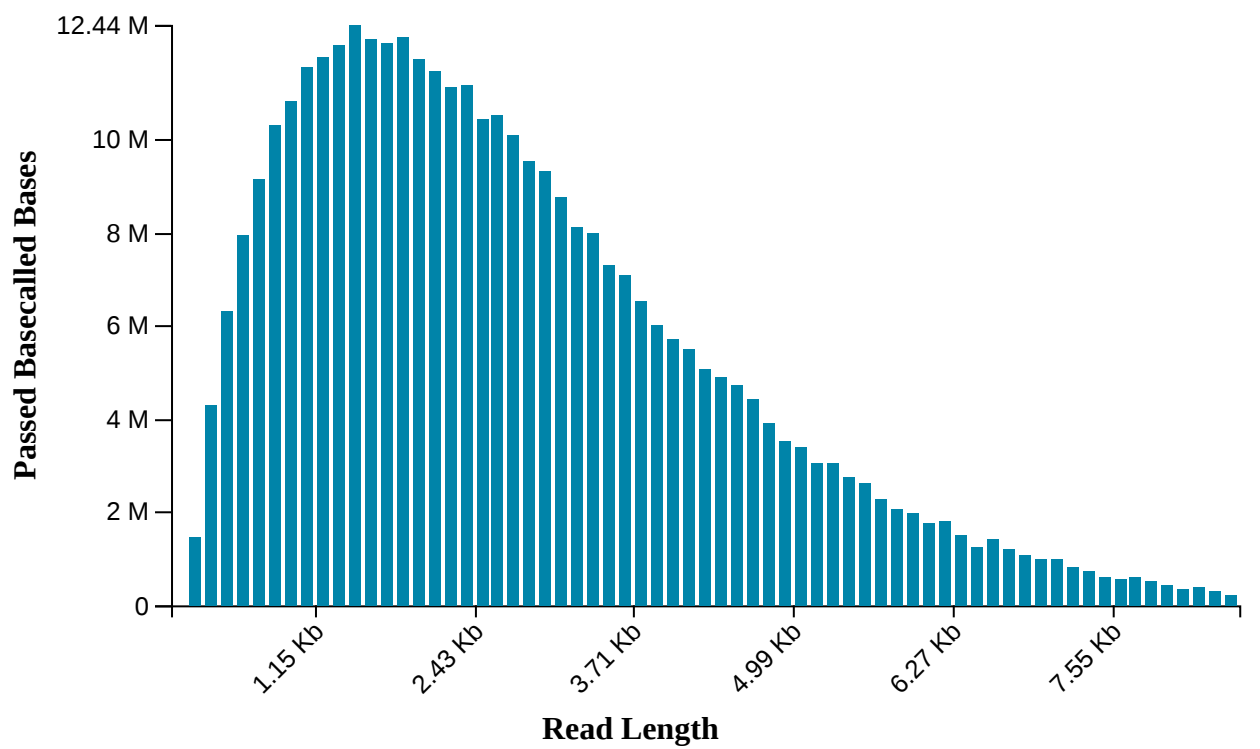## Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 2.42 K

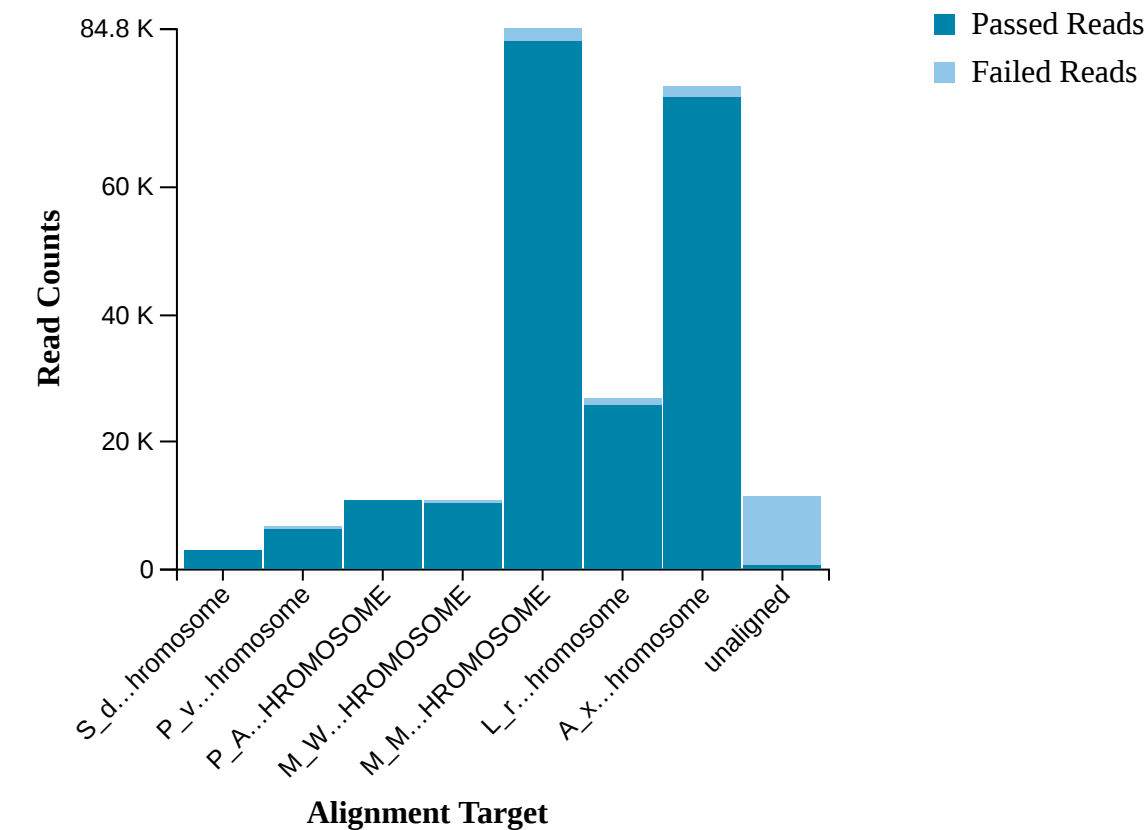## Read Length Histogram Estimated Bases

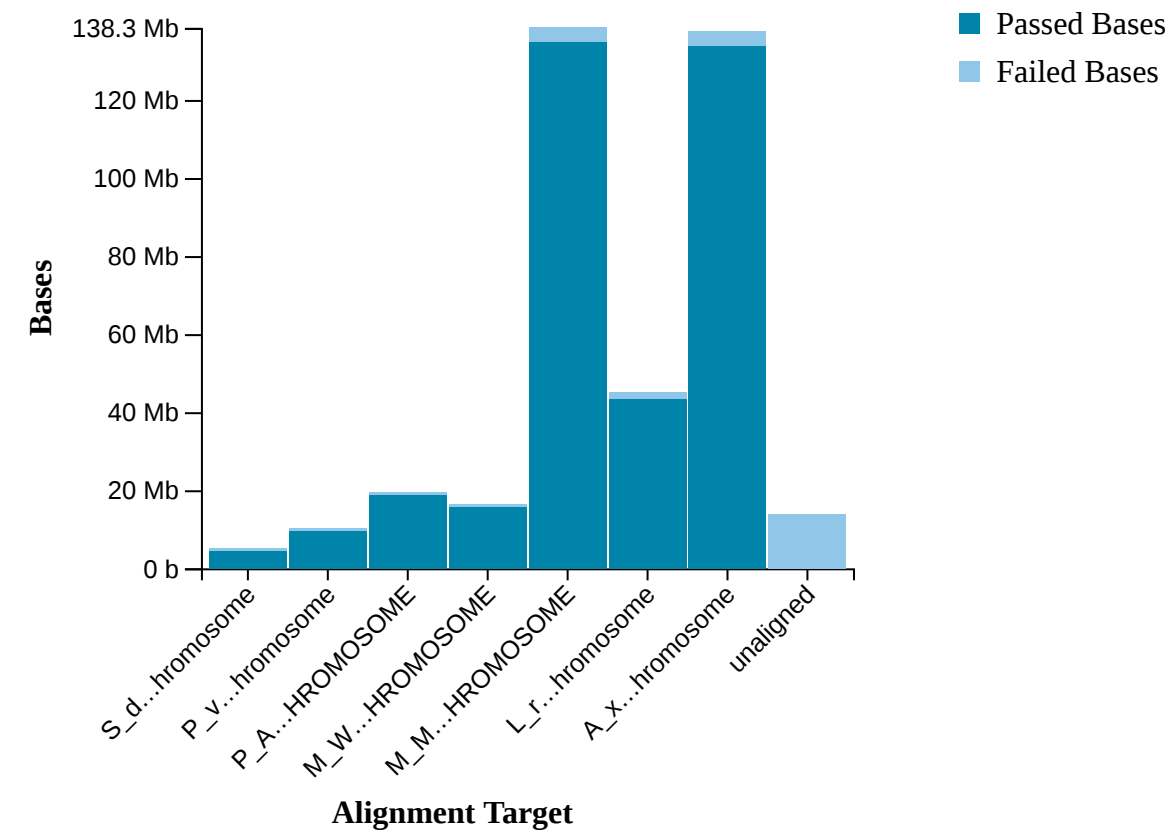Estimated N50: 2.44 K

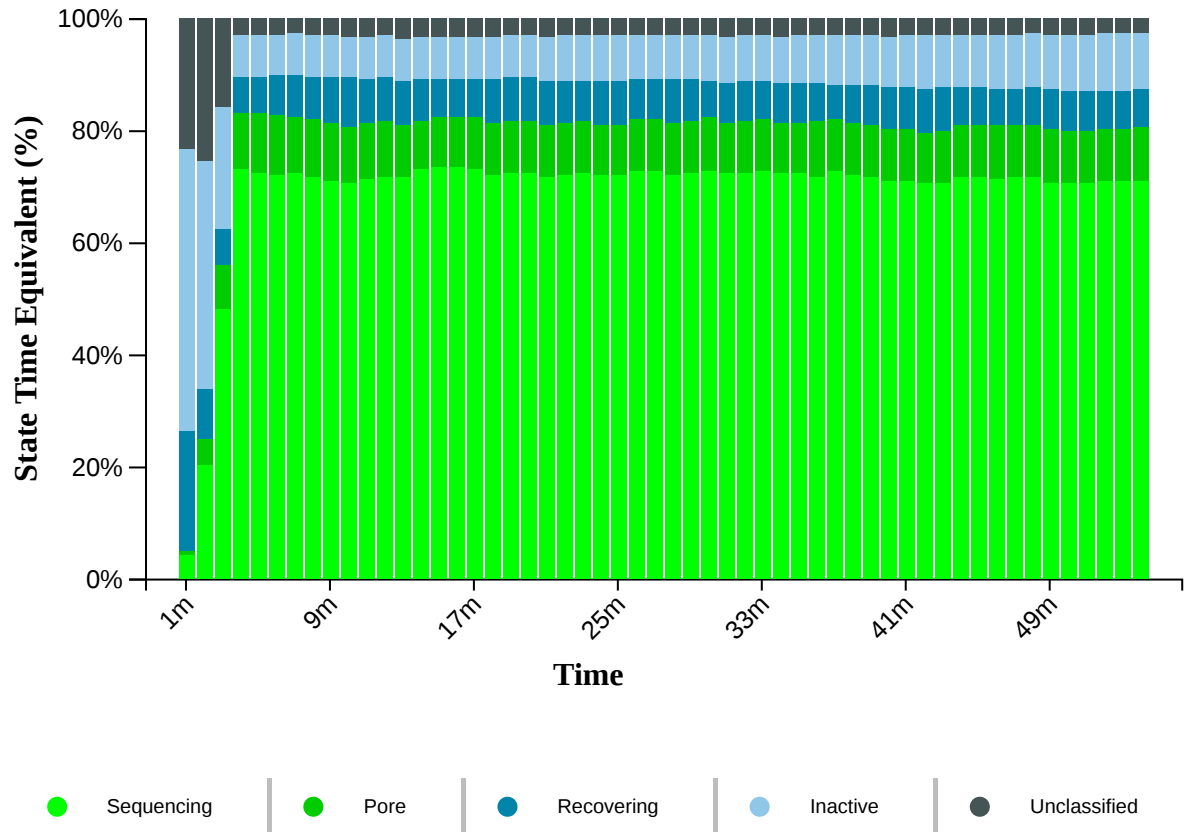## Read Length Histogram Basecalled Bases

Estimated N50: 2.42 K

Alignment Target Hits (reads)

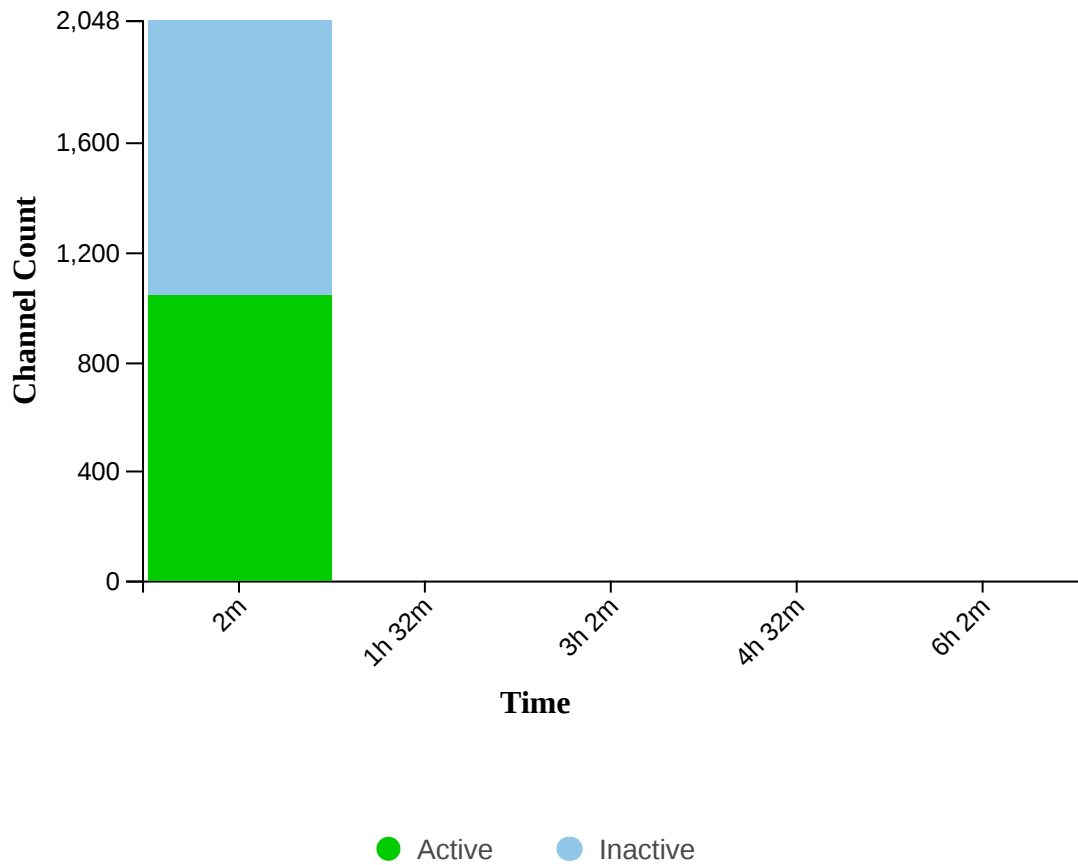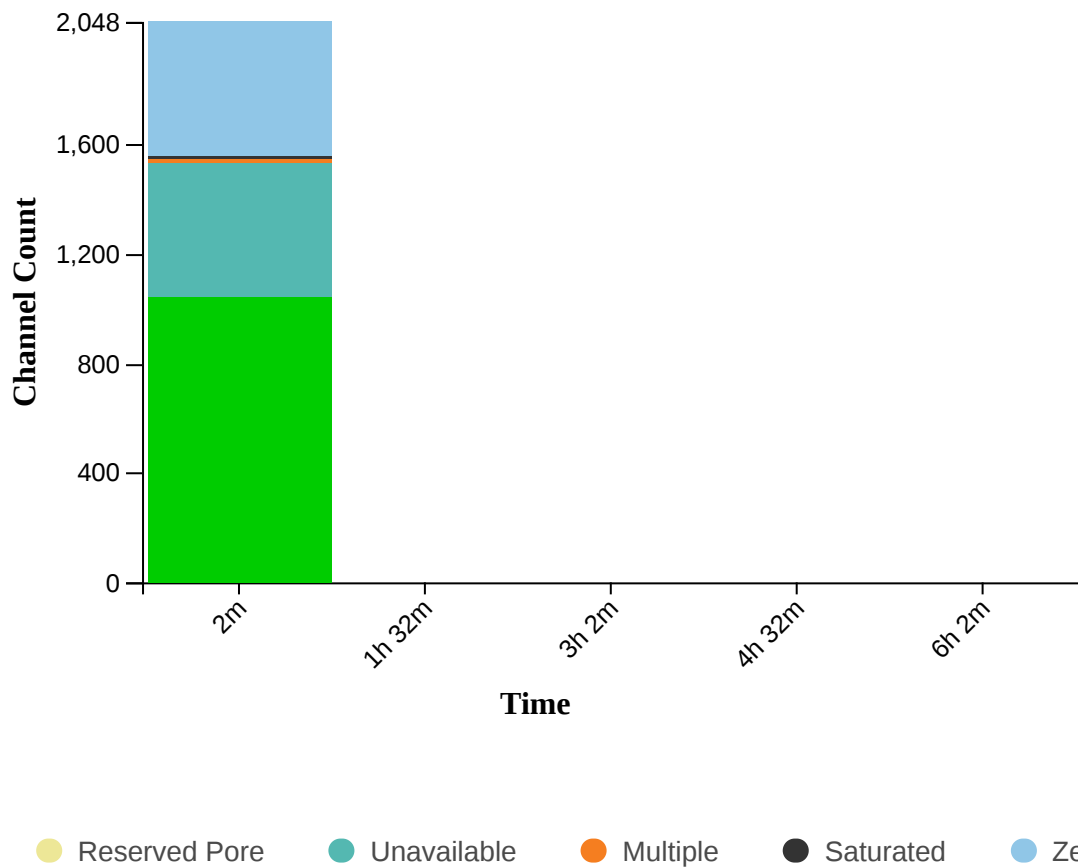## Alignment Target Hits (bases)

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

Legend: ● Active   ● Inactive

Mux Scan Categorised

Legend: ● Single Pore   ● Reserved Pore   ● Unavailable   ● Multiple   ● Saturated   ● Zero   ● Other
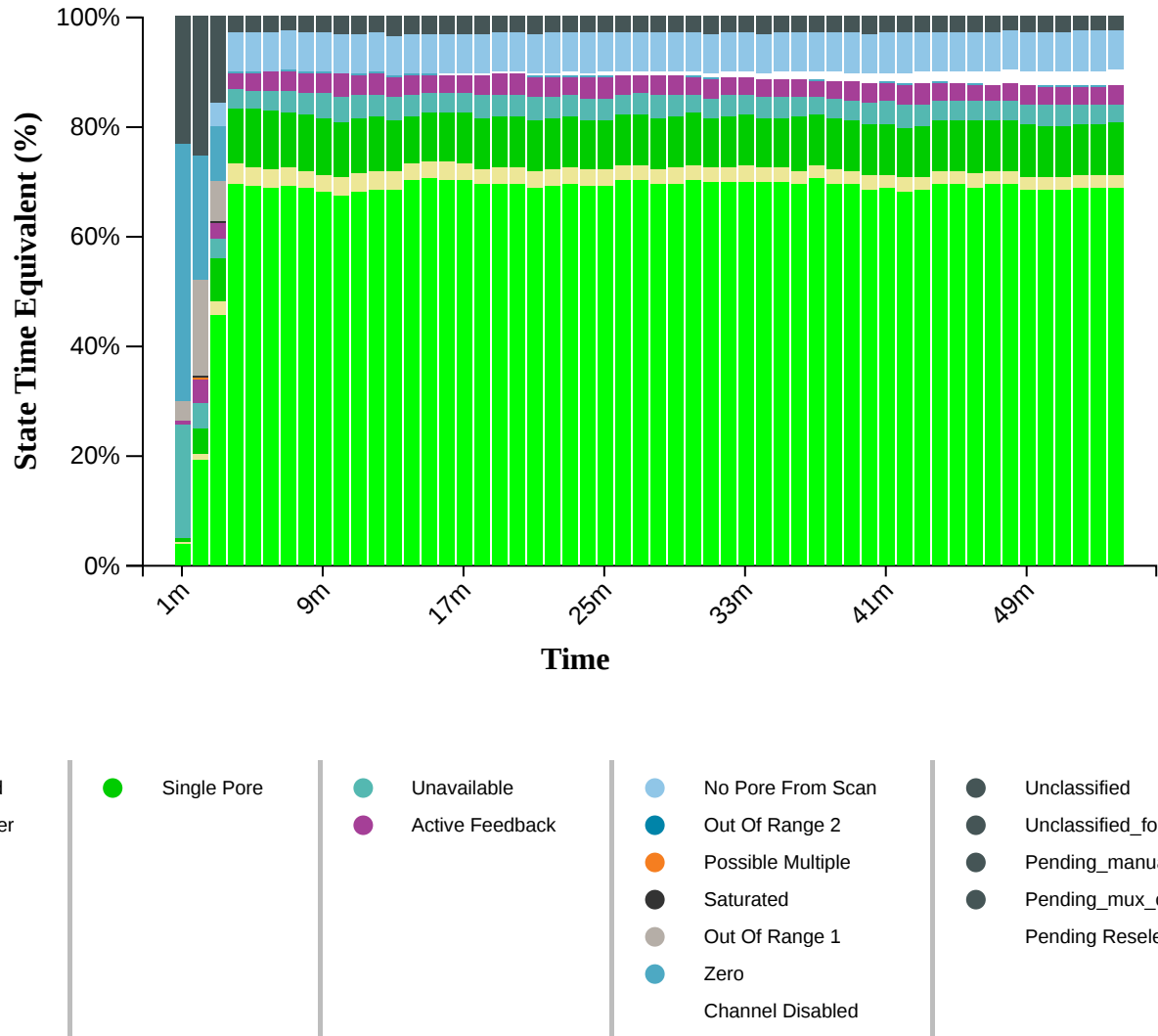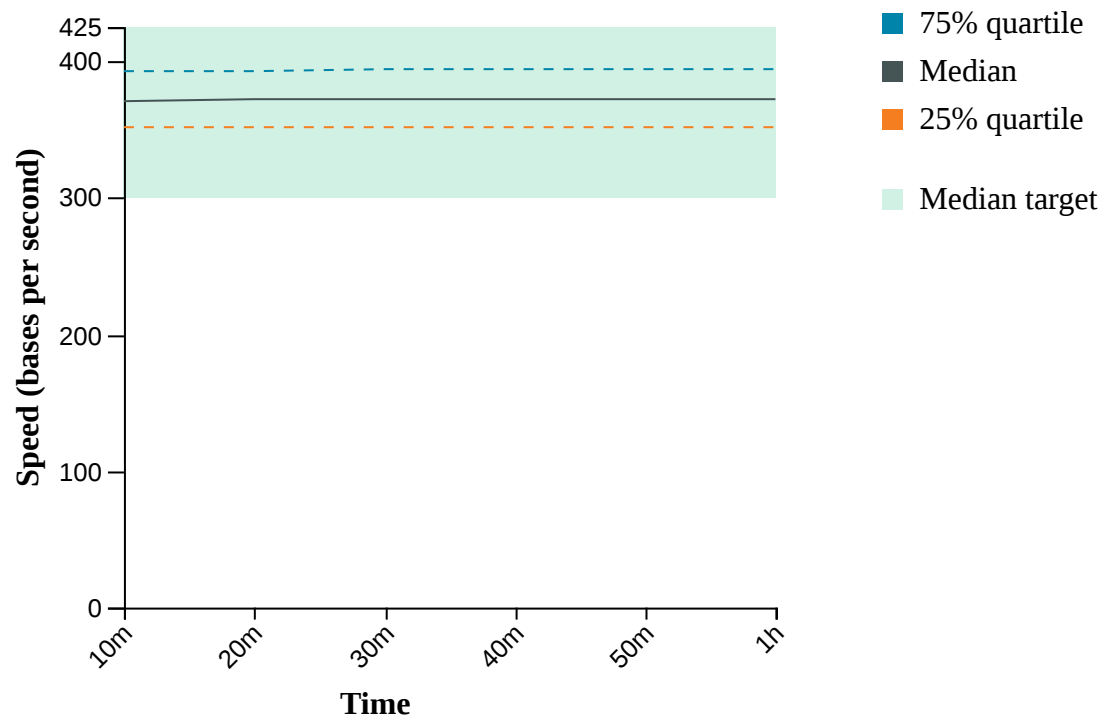
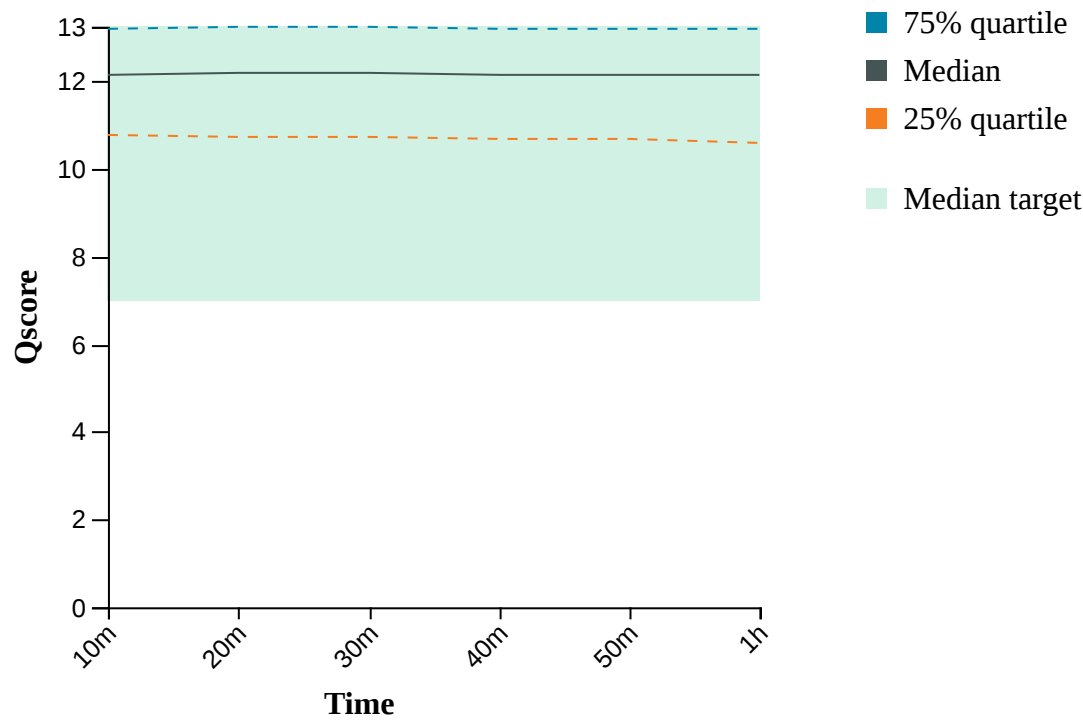## Temperature History
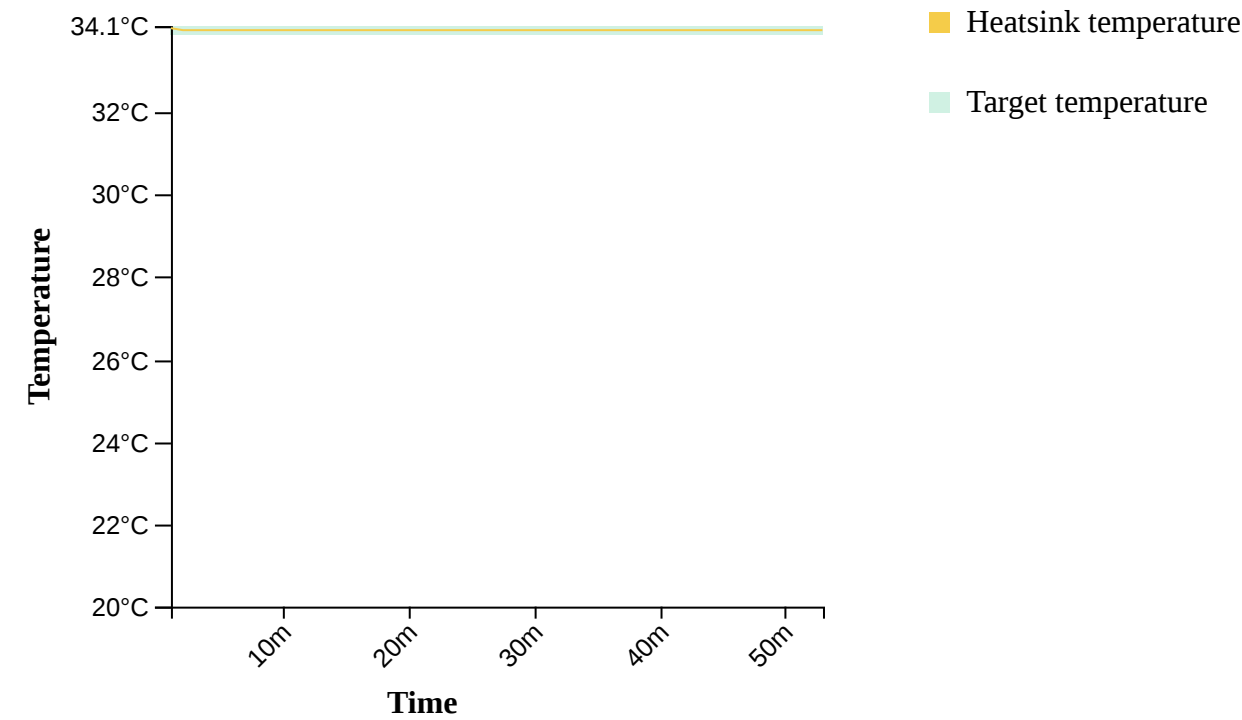
Bias Voltage History
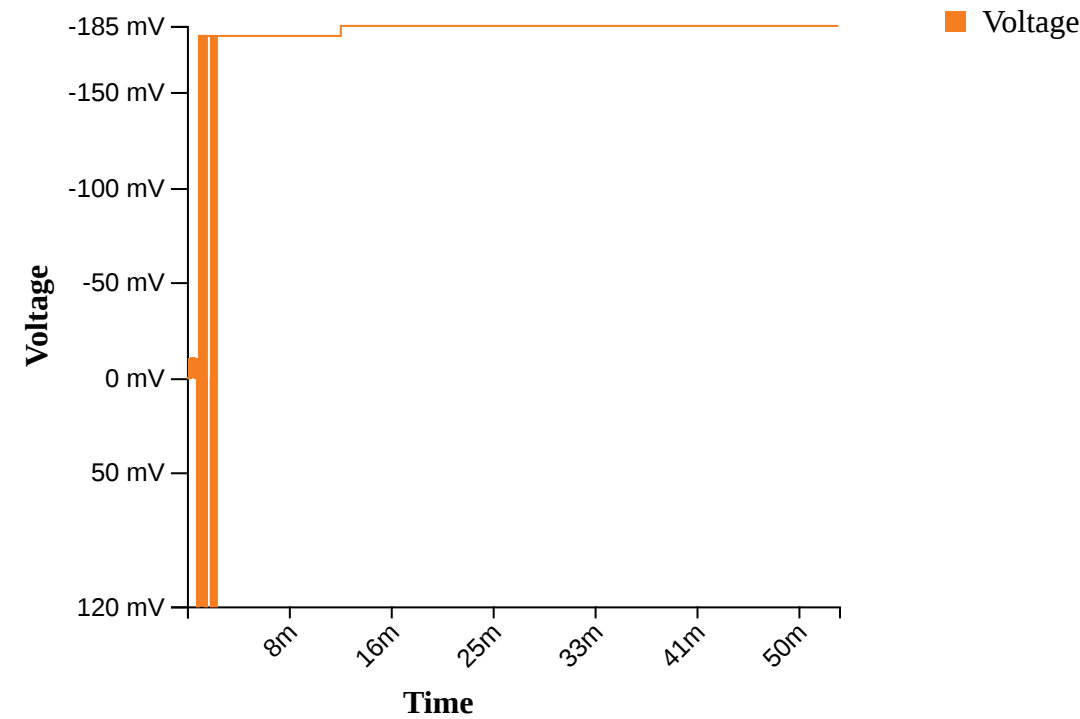
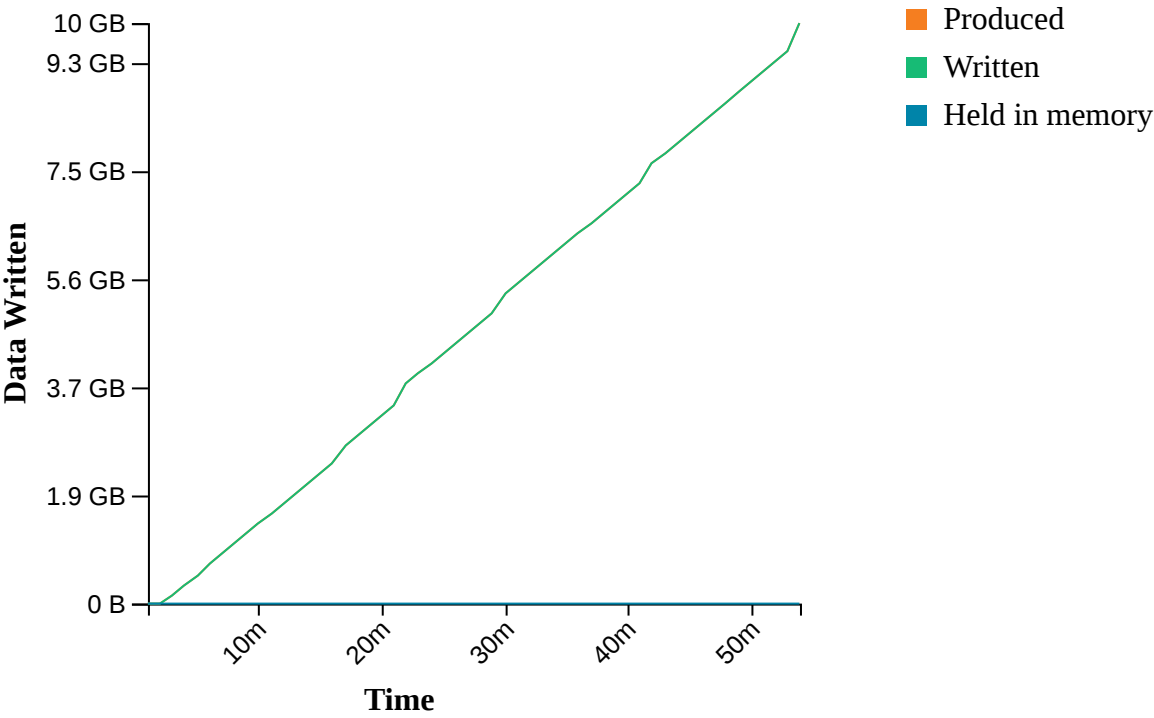## Translocation Speed

QScore

<u>Disk Write Performance</u>

Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 1048 pores. 475 pores available for immediate sequencing   January 5, 13:02
- Performing Mux Scan   January 5, 13:00
- Starting sequencing procedure   January 5, 13:00
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   January 5, 12:56