Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38Kbp_HightoLow_MwEnr_15042021**
Sample ID	**ReadUntil_38Kbp_HightoLow_MwEnr_15042021**
Run ID	**4d696280-7145-499c-a342-3391ccdae81f**
Flow Cell Id	**FAP21636**
Start Time	**April 15, 16:32**
Run Length	**1h 0m**

Run Summary

Reads Generated	**94.89 K**
Passed Bases	**323.5 Mb**
Failed Bases	**22.14 Mb**
Estimated Bases	**349.95 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/M_wisconsensis_ref.fasta"],filter_type=enrich,first_channel= 1,last_channel=256**
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/the7references.fasta"]**
Read Filtering	**min_qscore=7**

Versions

MinKNOW	**21.02.5**
MinKNOW Core	**4.2.5**
Bream	**6.1.10**
Guppy	**4.3.4**

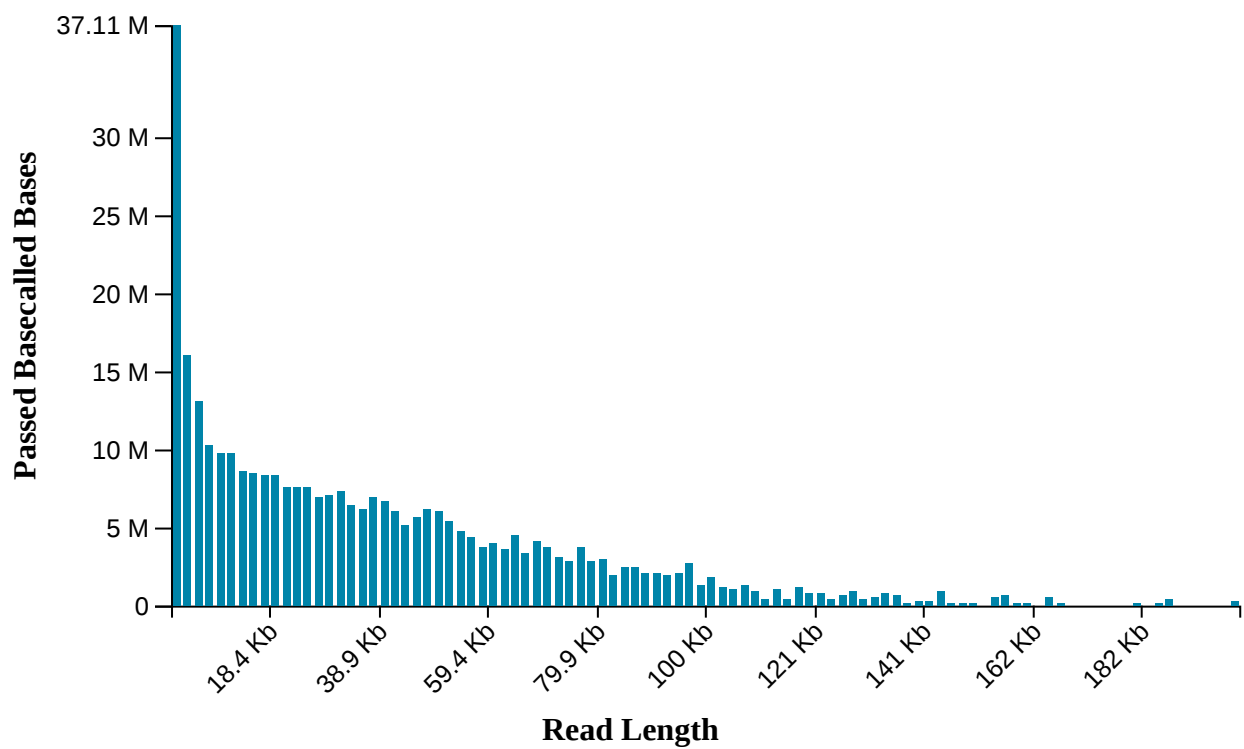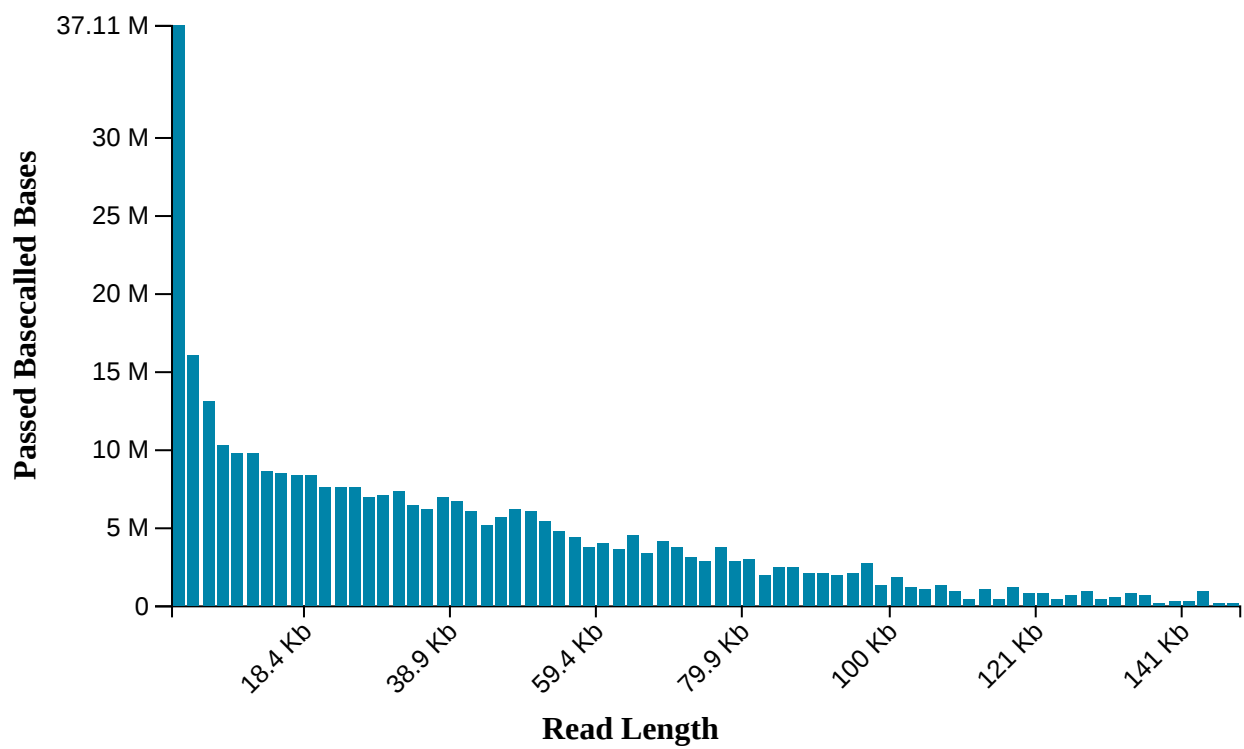## Cumulative Output Reads
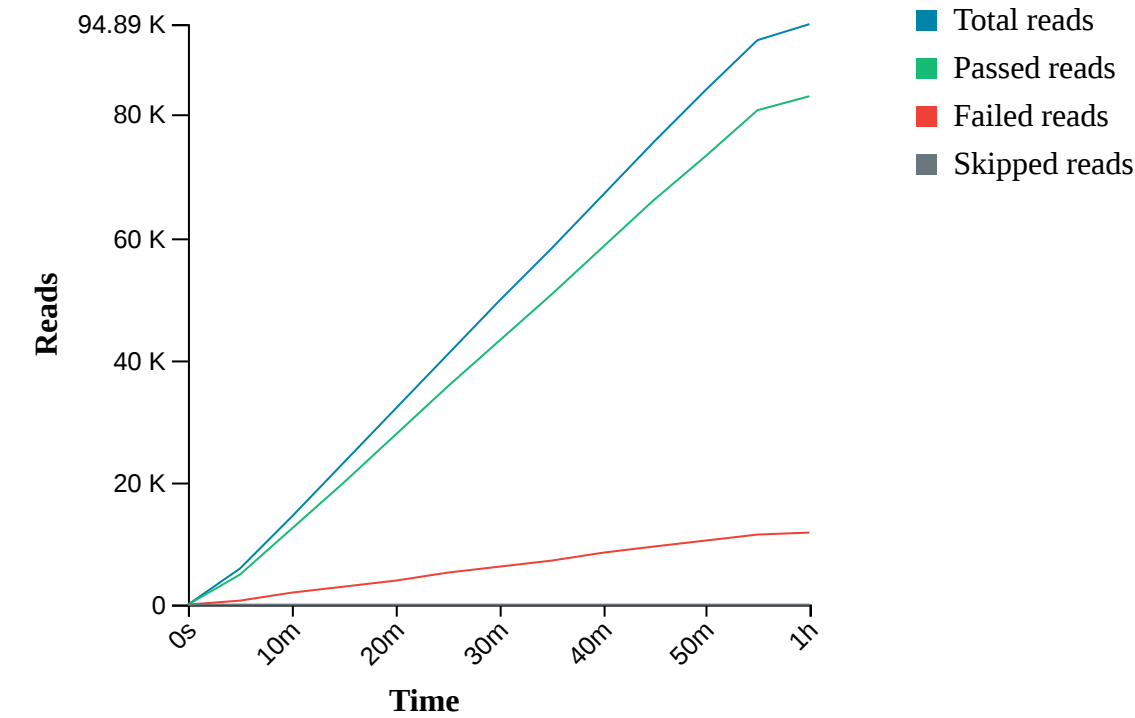
Cumulative Output Bases
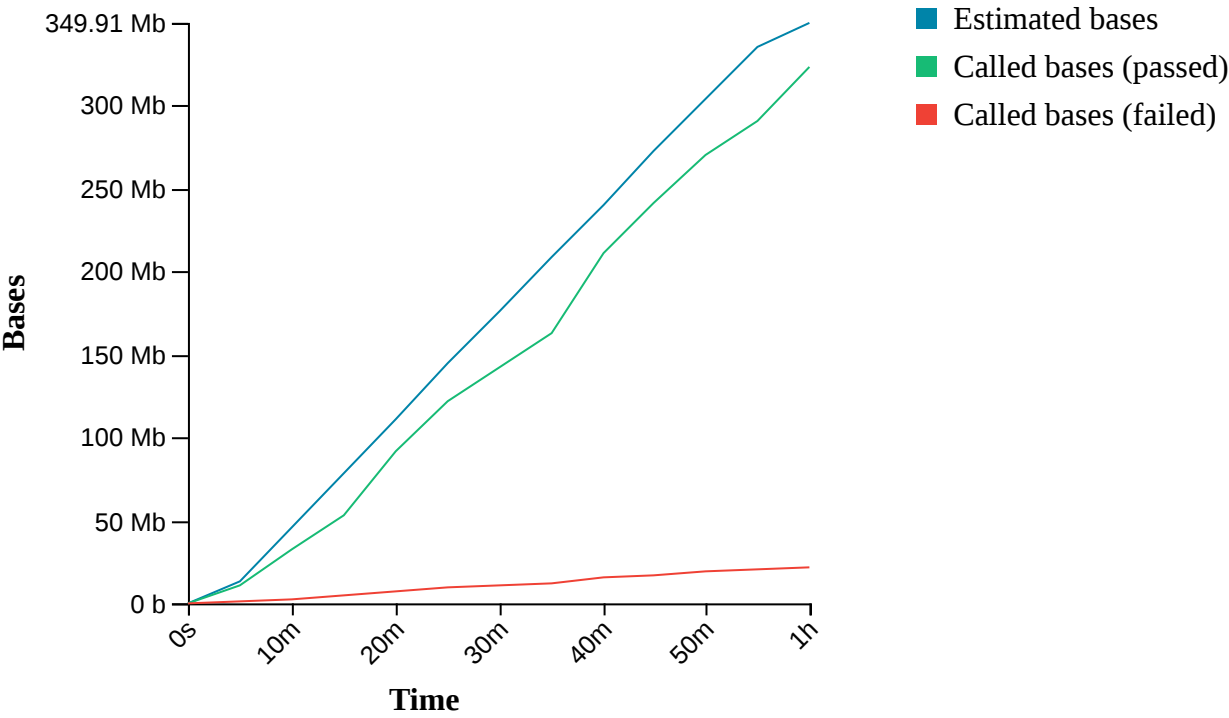
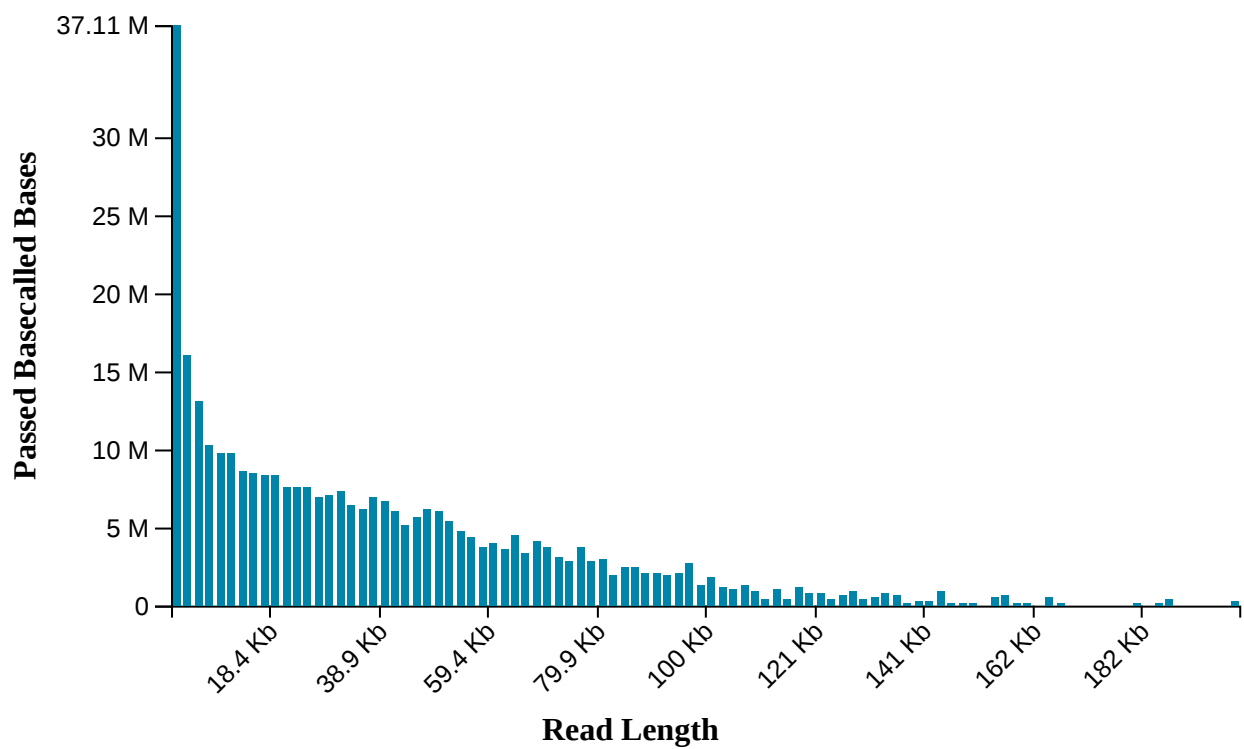## Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 29.44 K

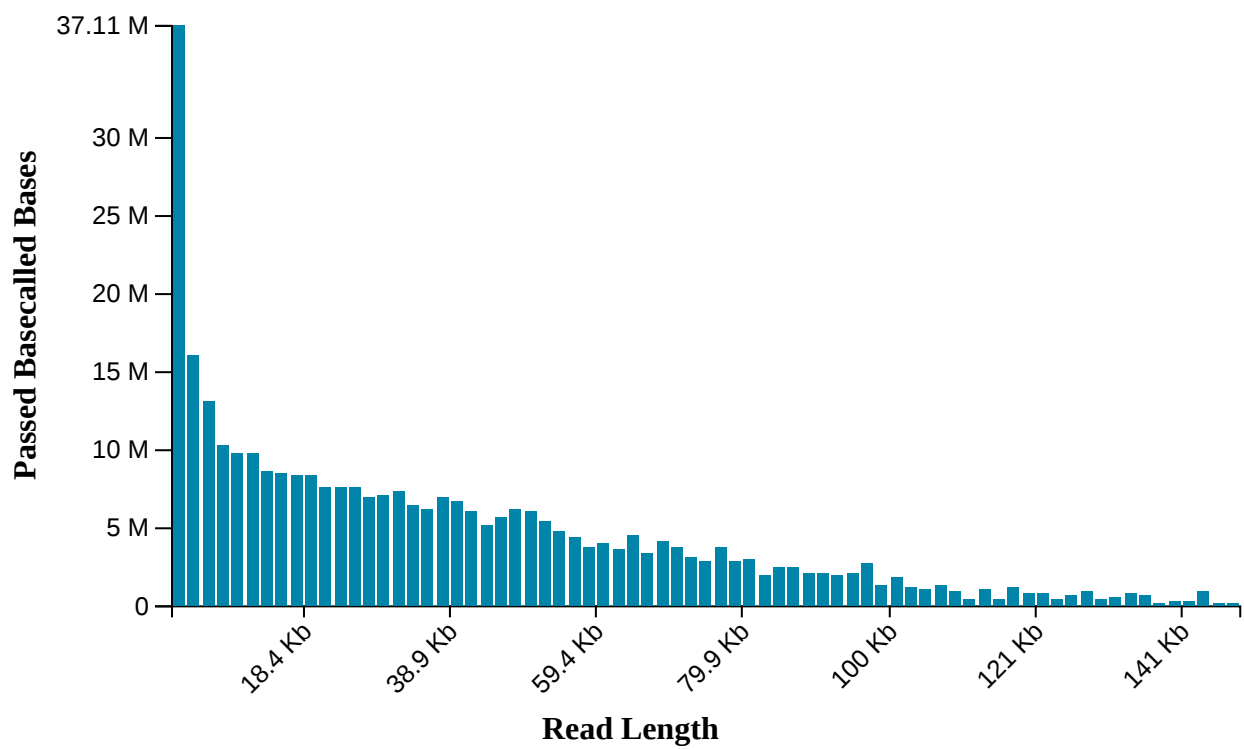## Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 29.02 K

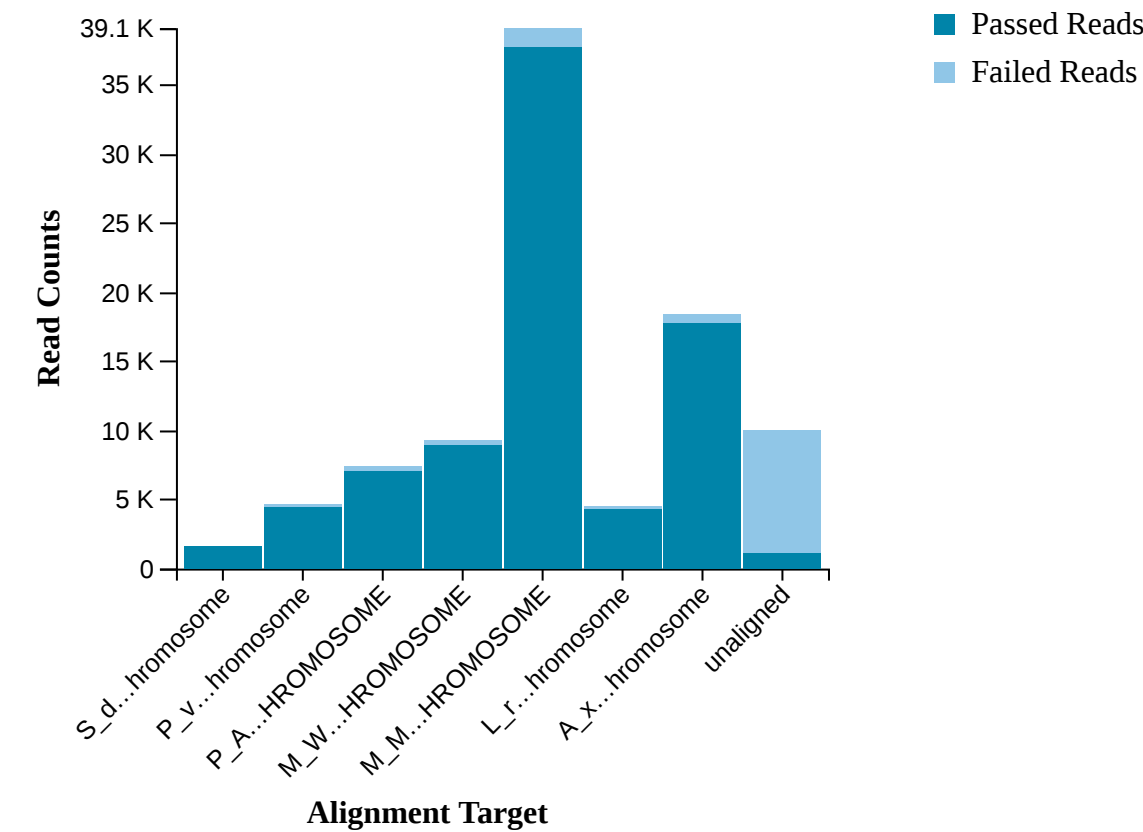## Read Length Histogram Estimated Bases

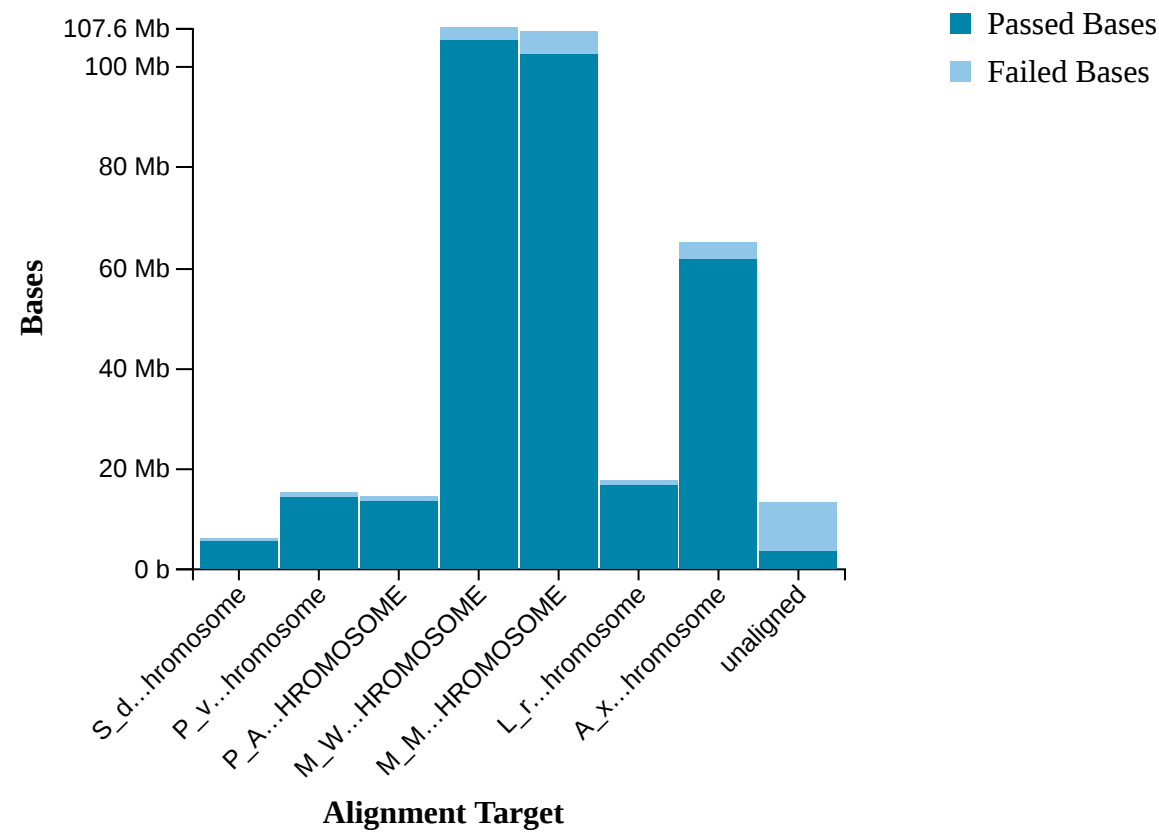Estimated N50: 29.44 K

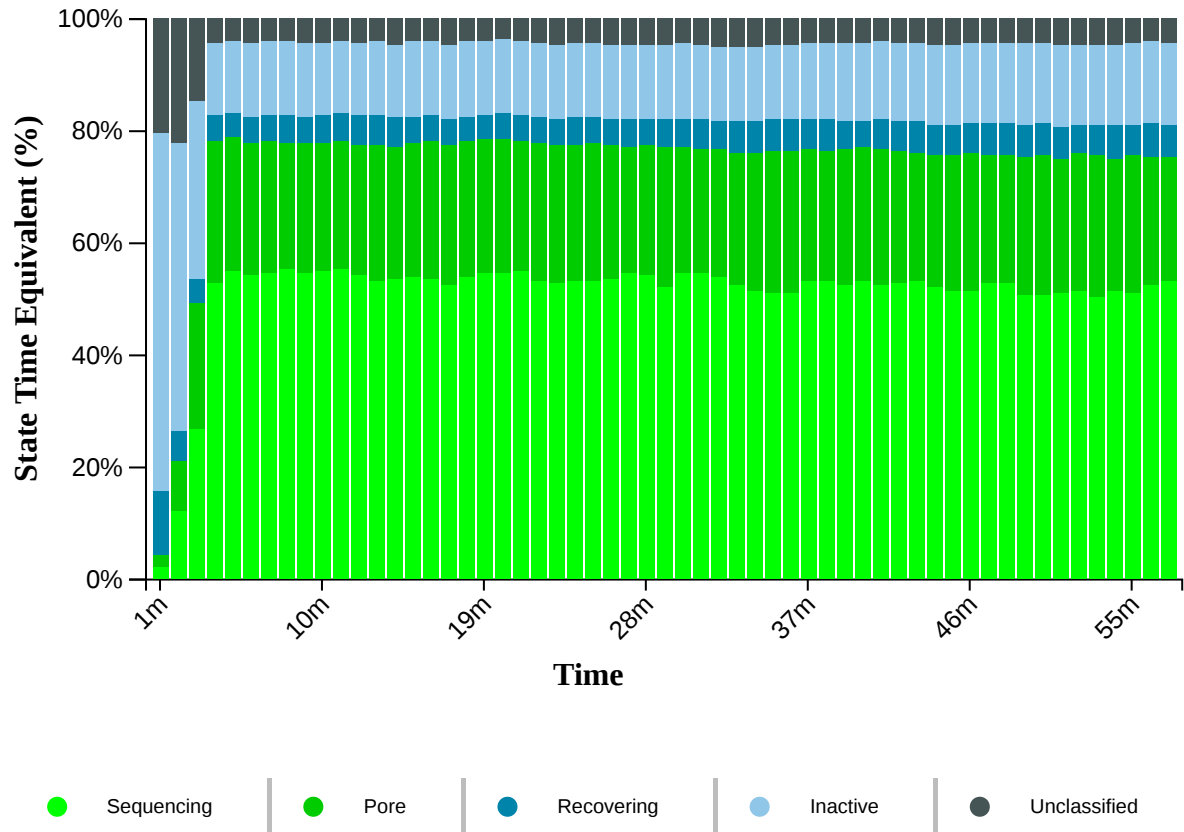## Read Length Histogram Basecalled Bases

Estimated N50: 29.02 K

Alignment Target Hits (reads)

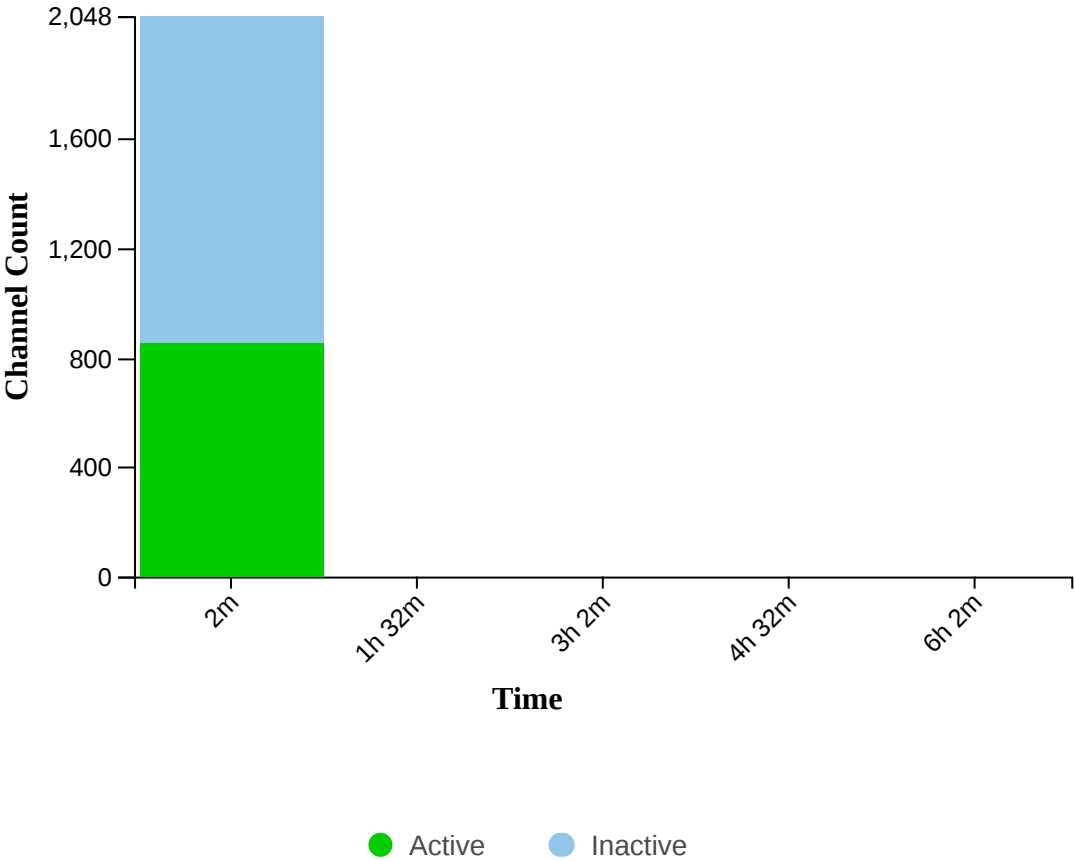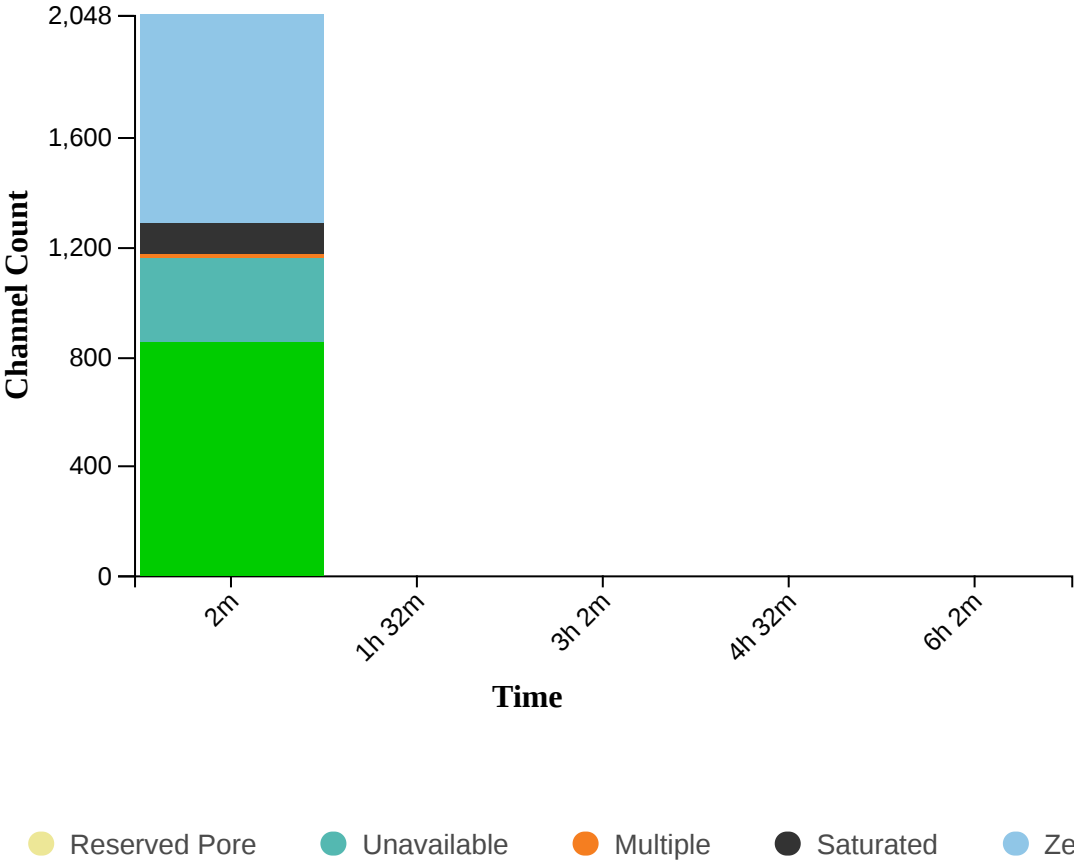## Alignment Target Hits (bases)

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
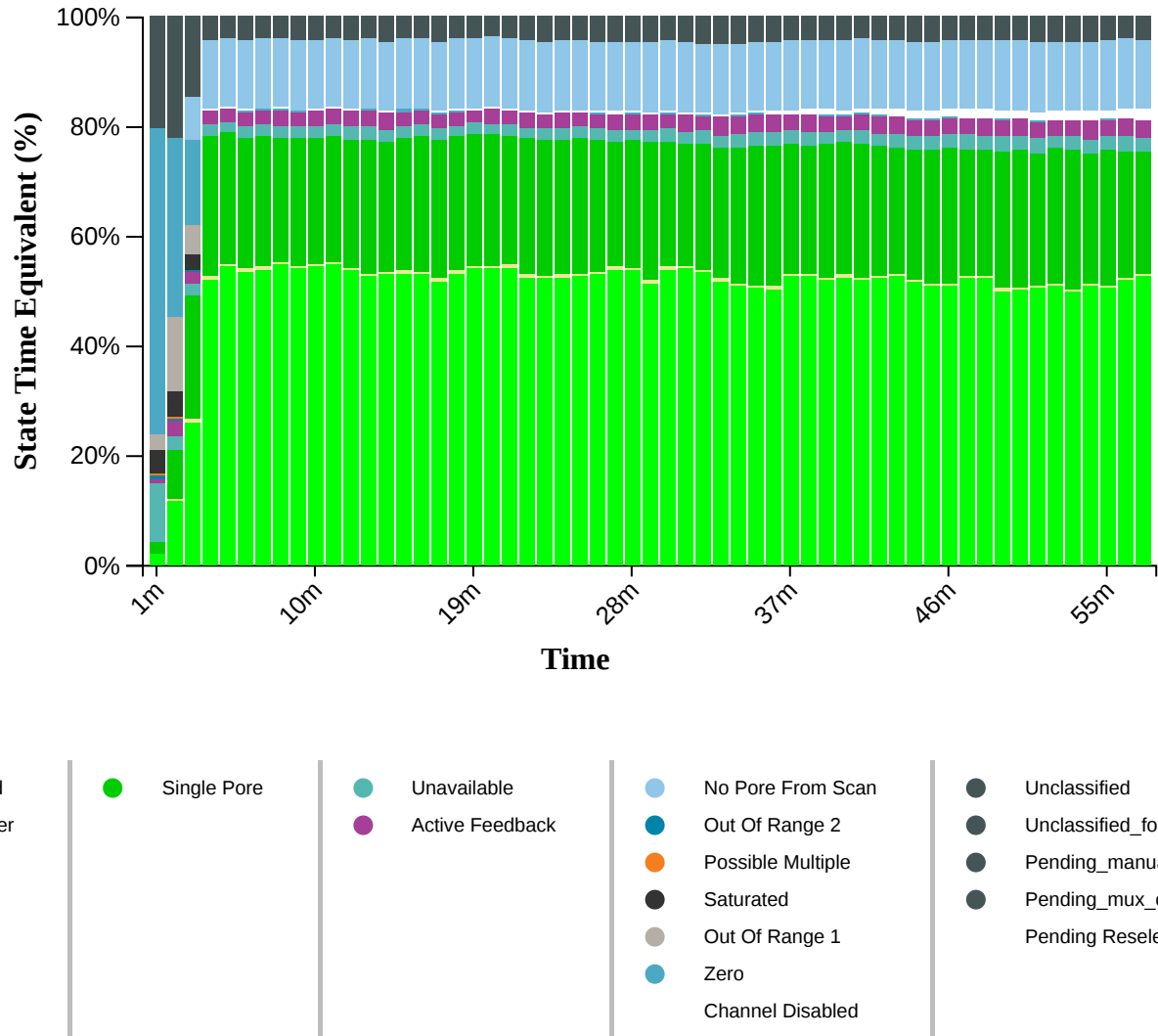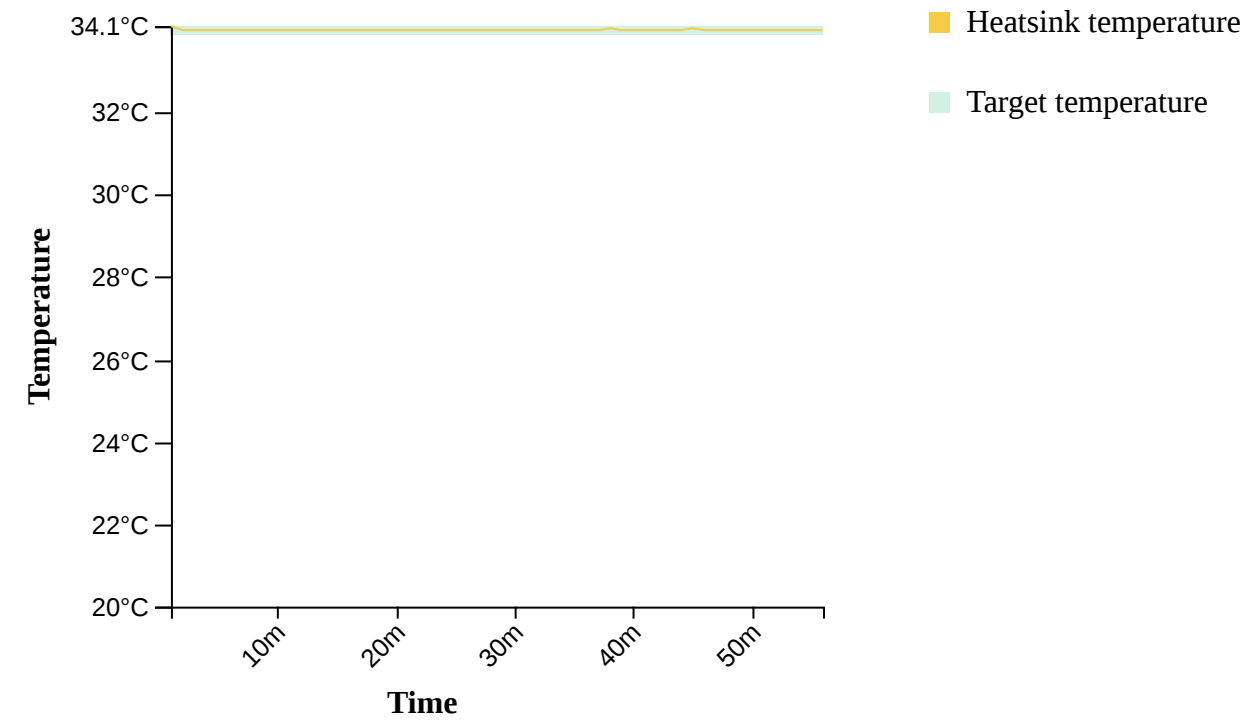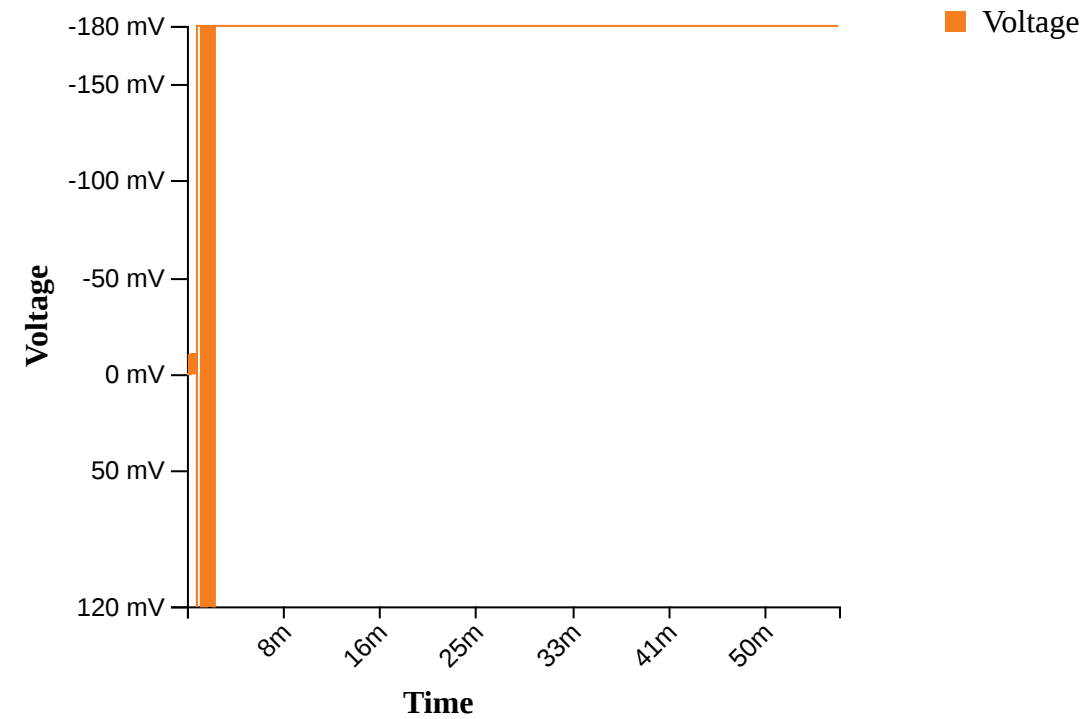
Mux Scan Grouped

Mux Scan Categorised

Temperature History

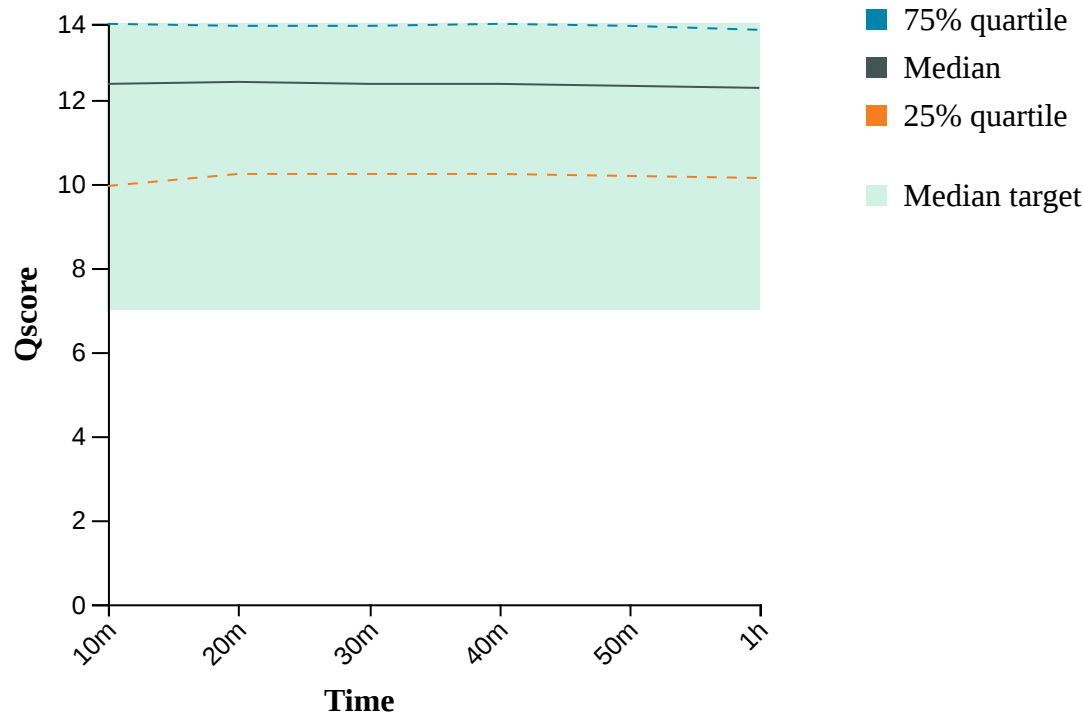## Bias Voltage History
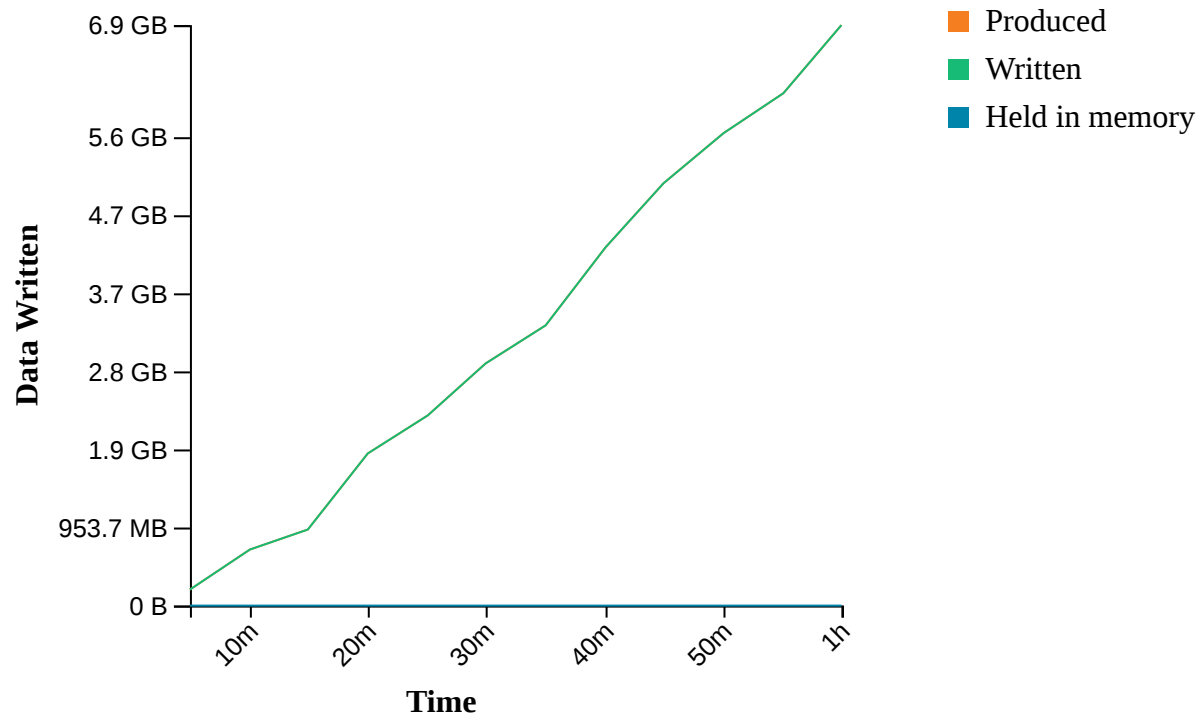
Translocation Speed
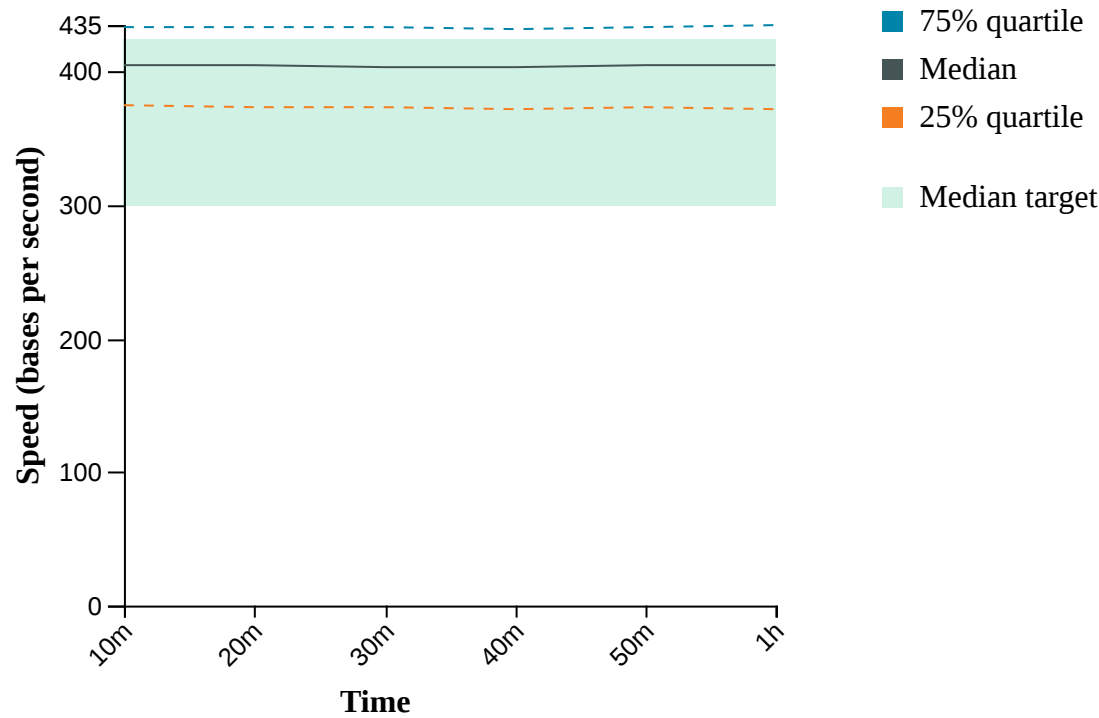
QScore

Disk Write Performance

Legend:
- Produced
- Written
- Held in memory

Run Debug Messages

- Mux scan for flow cell FAP21636 has found a total of 855 pores. 447 pores available for immediate sequencing   April 15, 16:38
- Performing Mux Scan   April 15, 16:35
- Starting sequencing procedure   April 15, 16:35
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   April 15, 16:32