Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38Kbp_HightoLow_PaEnr_15042021**
Sample ID	**ReadUntil_38Kbp_HightoLow_PaEnr_15042021**
Run ID	**5a413f7a-1577-40ef-9eae-2d33ba4a245a**
Flow Cell Id	**FAP21636**
Start Time	**April 15, 15:28**
Run Length	**1h 2m**

Run Summary

Reads Generated	**115.21 K**
Passed Bases	**314.76 Mb**
Failed Bases	**16.78 Mb**
Estimated Bases	**336.31 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/P_aeruginosa_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

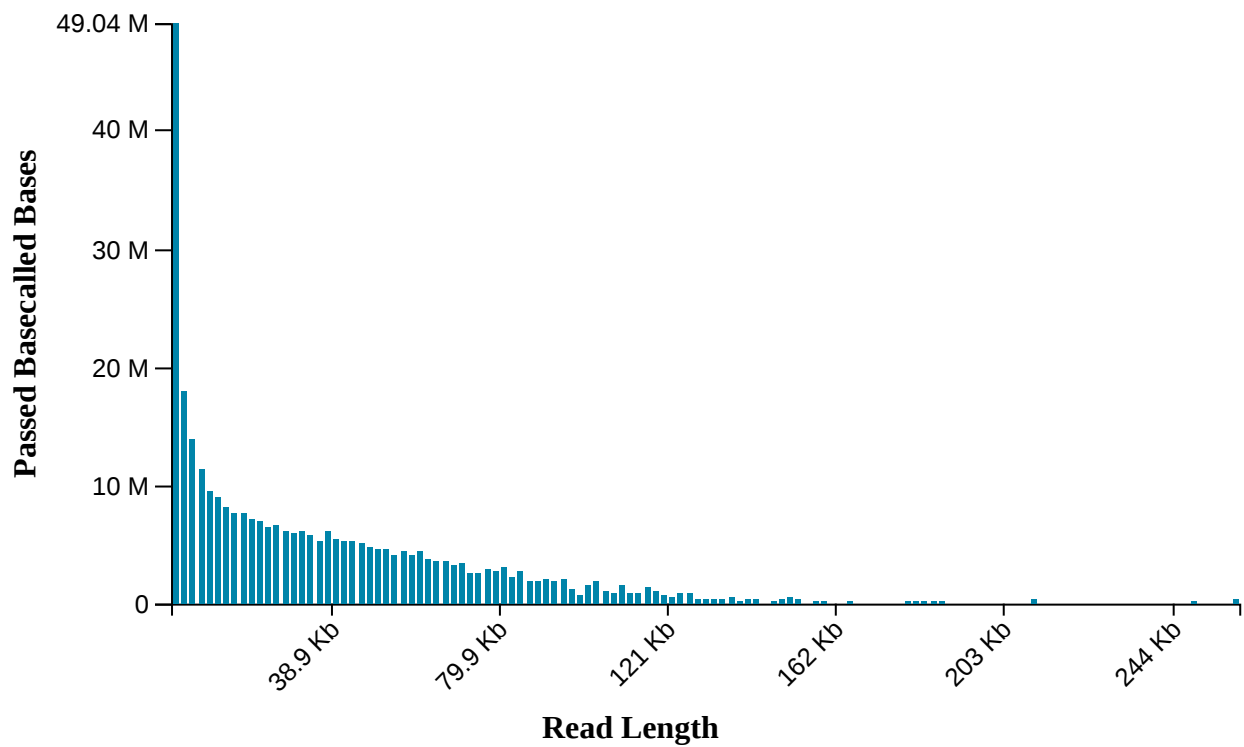|	
MinKNOW	**21.02.5**
MinKNOW Core	**4.2.5**
Bream	**6.1.10**
Guppy	**4.3.4**

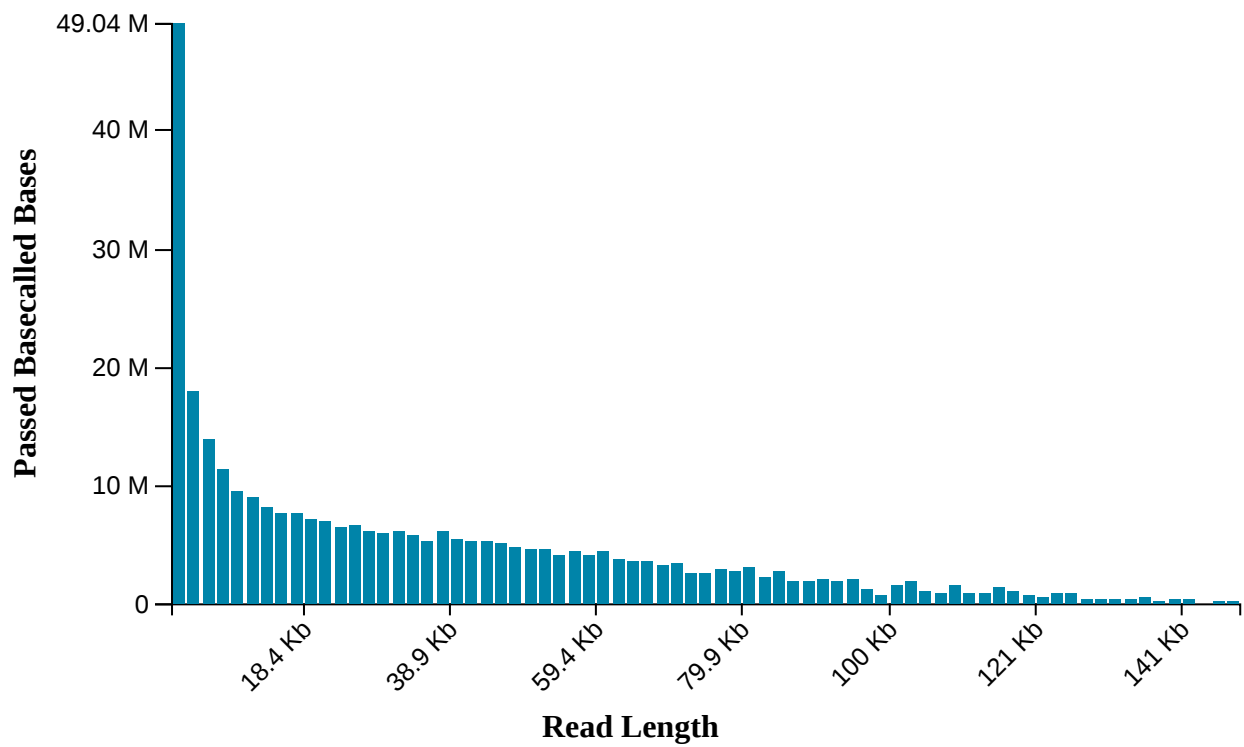## Cumulative Output Reads
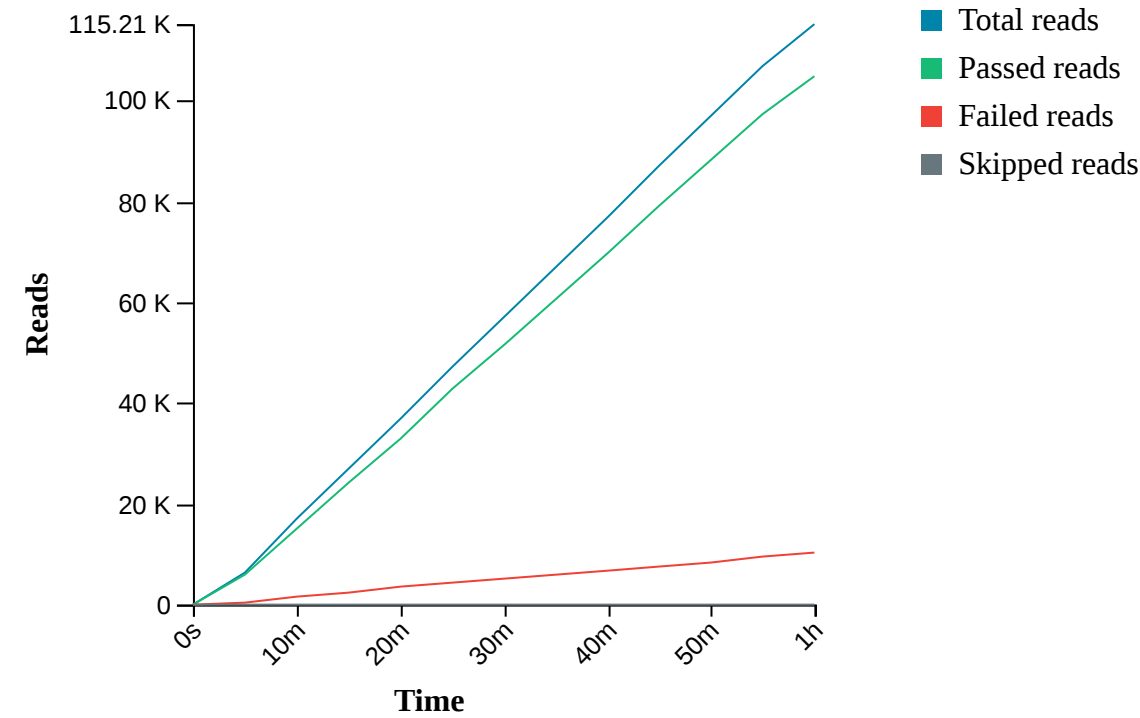
Cumulative Output Bases
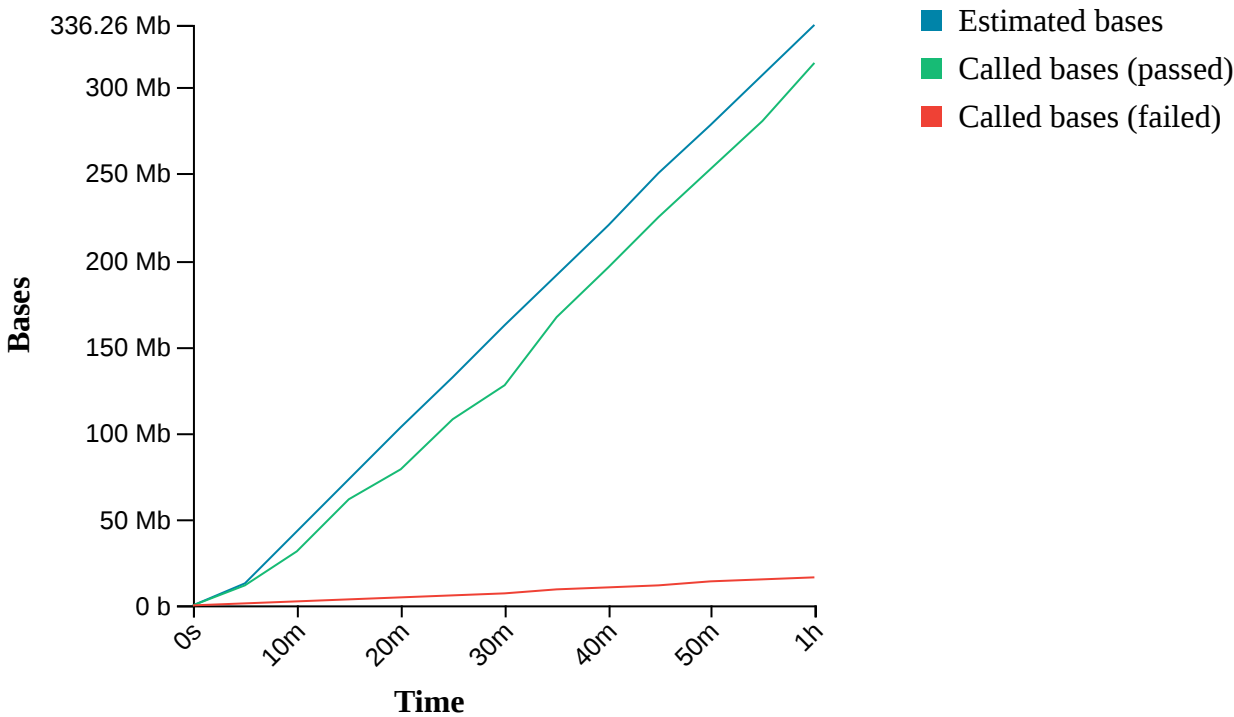
Read Length Histogram Estimated Bases - Outliers Discarded
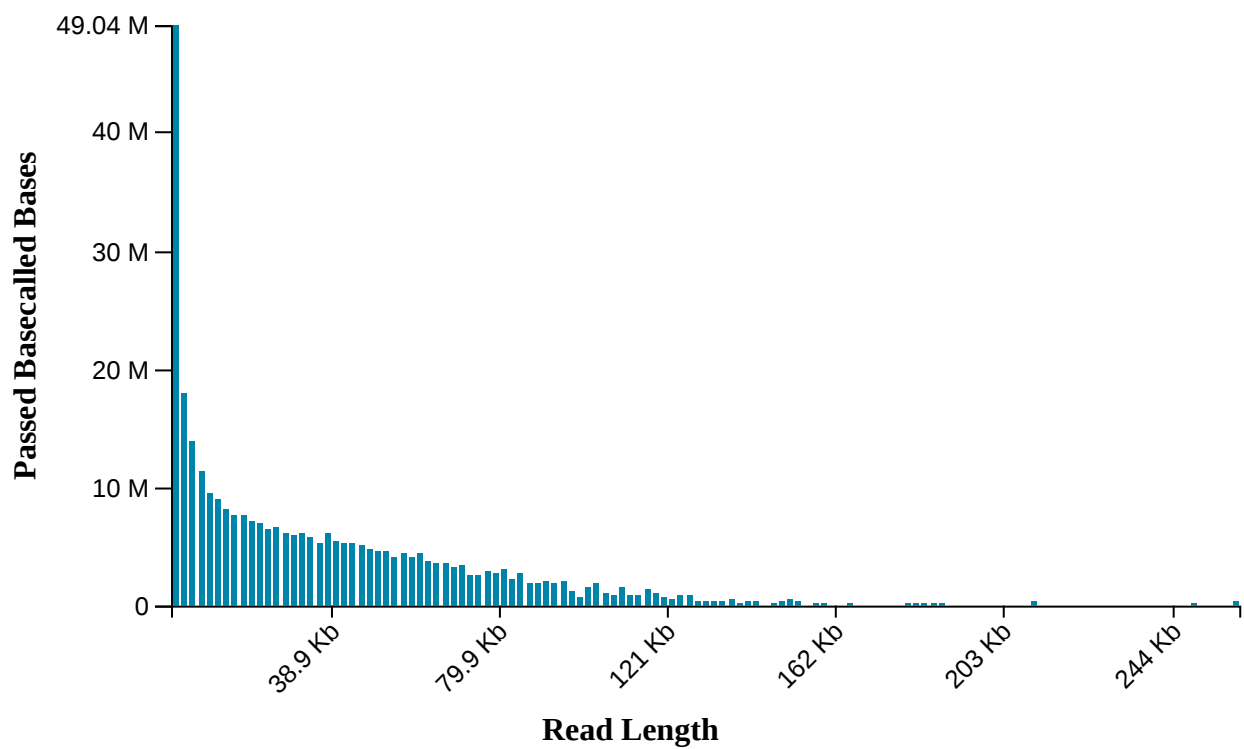
Estimated N50: 25.48 K

Read Length Histogram Basecalled Bases - Outliers Discarded
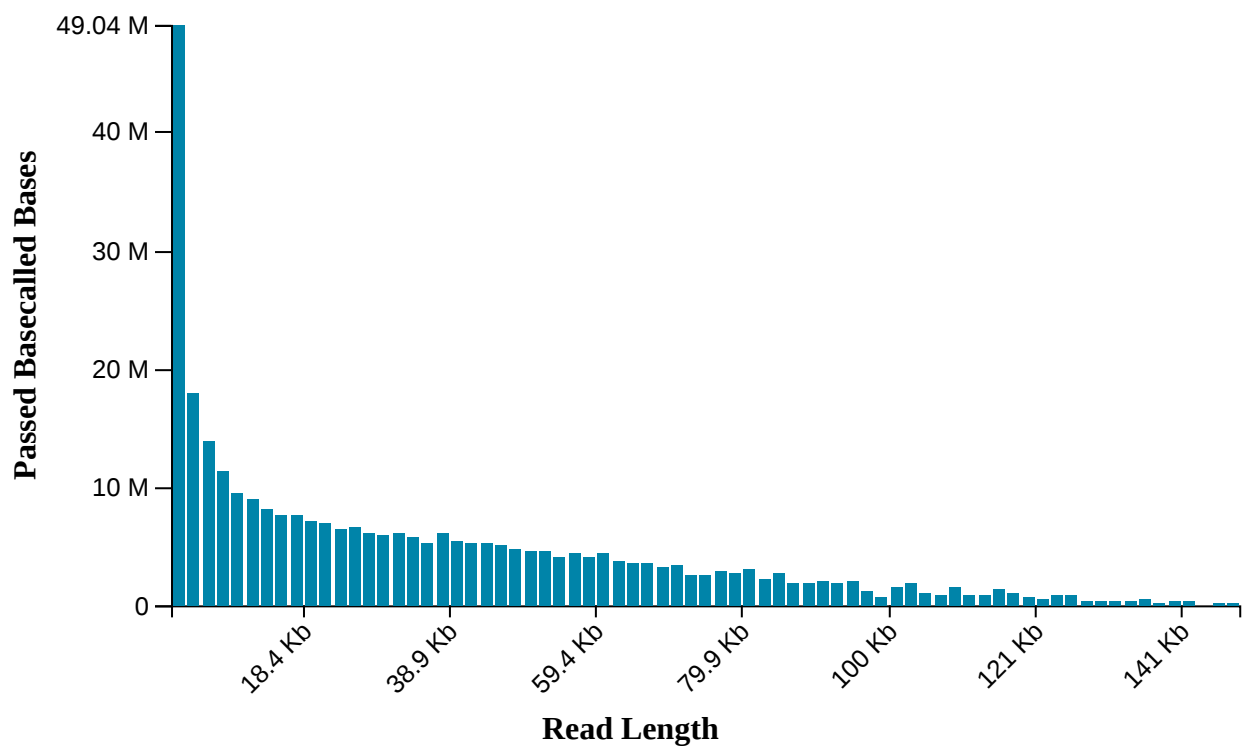
Estimated N50: 25 K

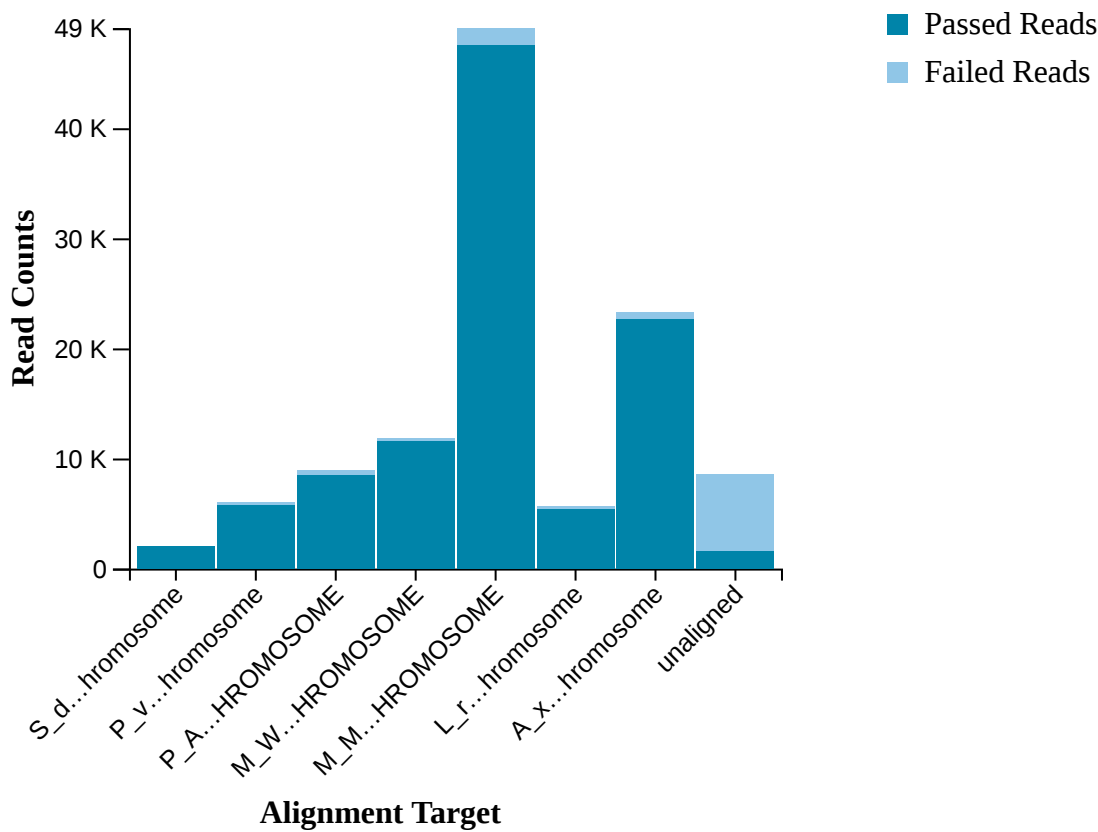## Read Length Histogram Estimated Bases

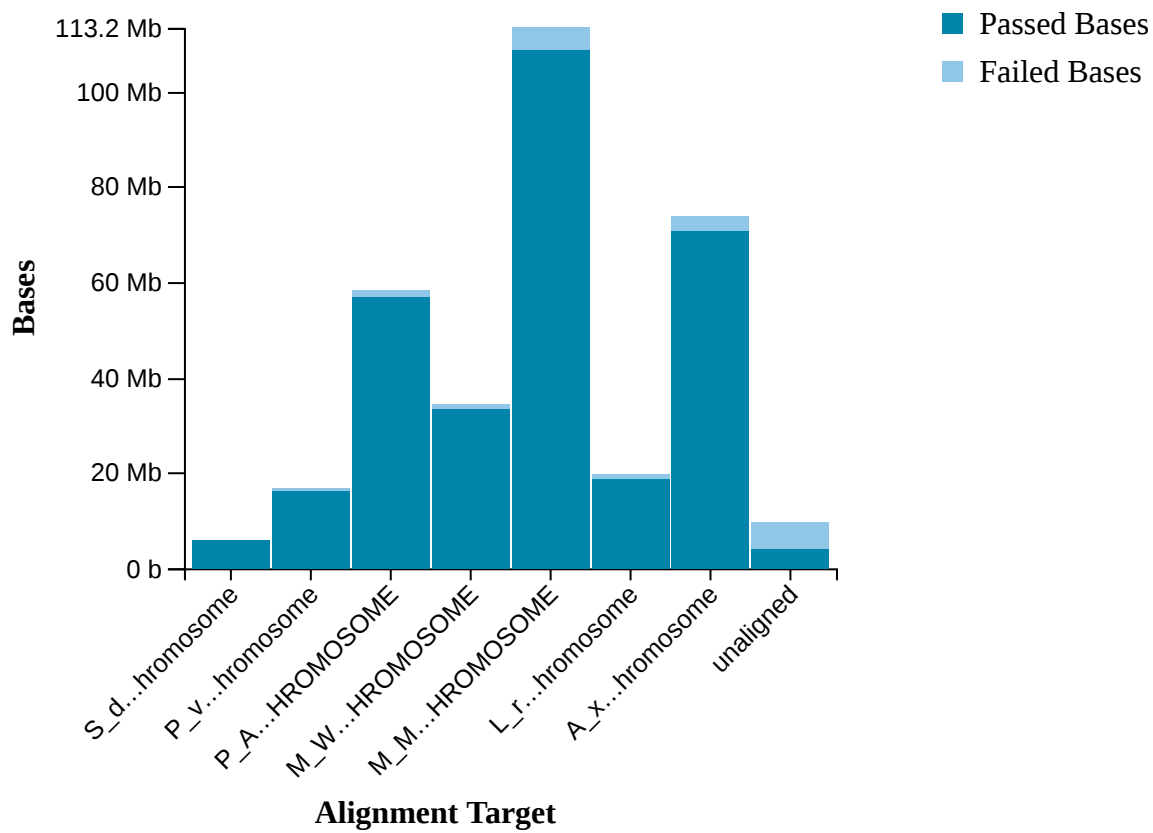Estimated N50: 25.48 K

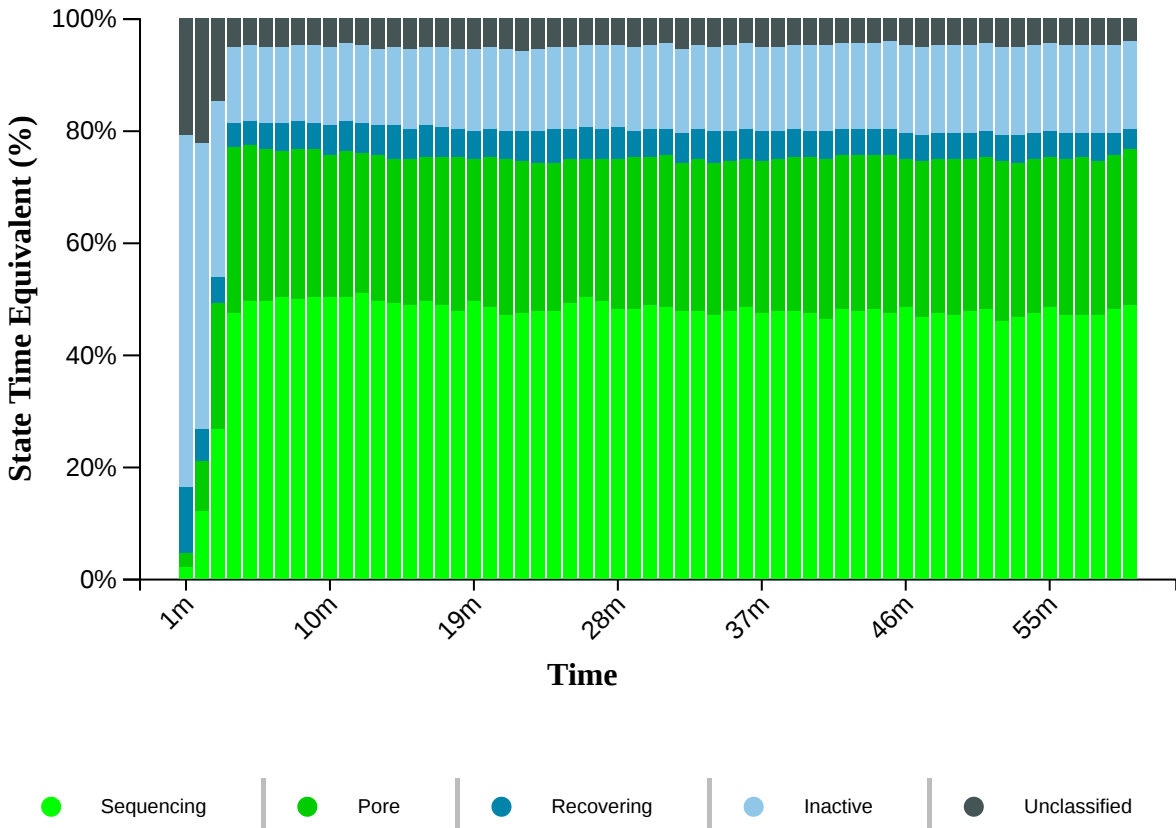## Read Length Histogram Basecalled Bases

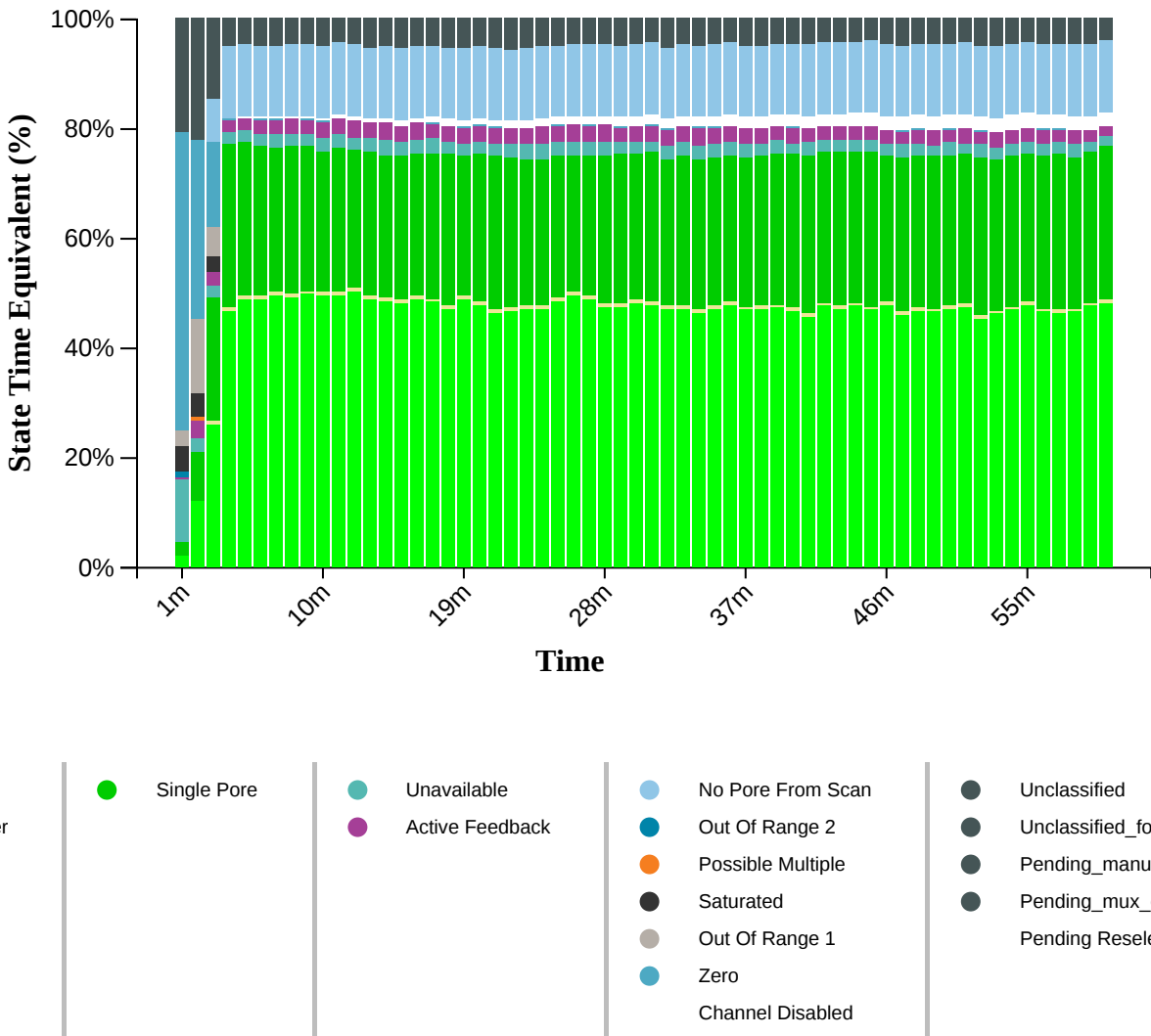Estimated N50: 25 K

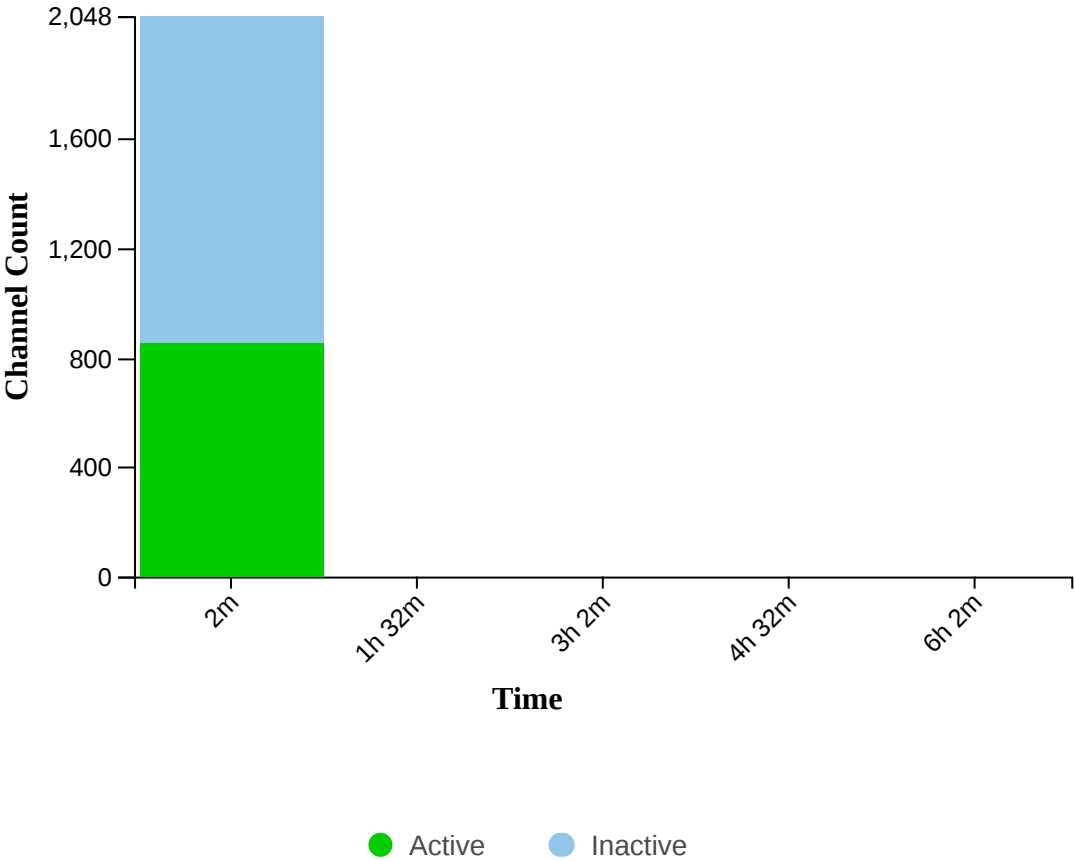## Alignment Target Hits (reads)
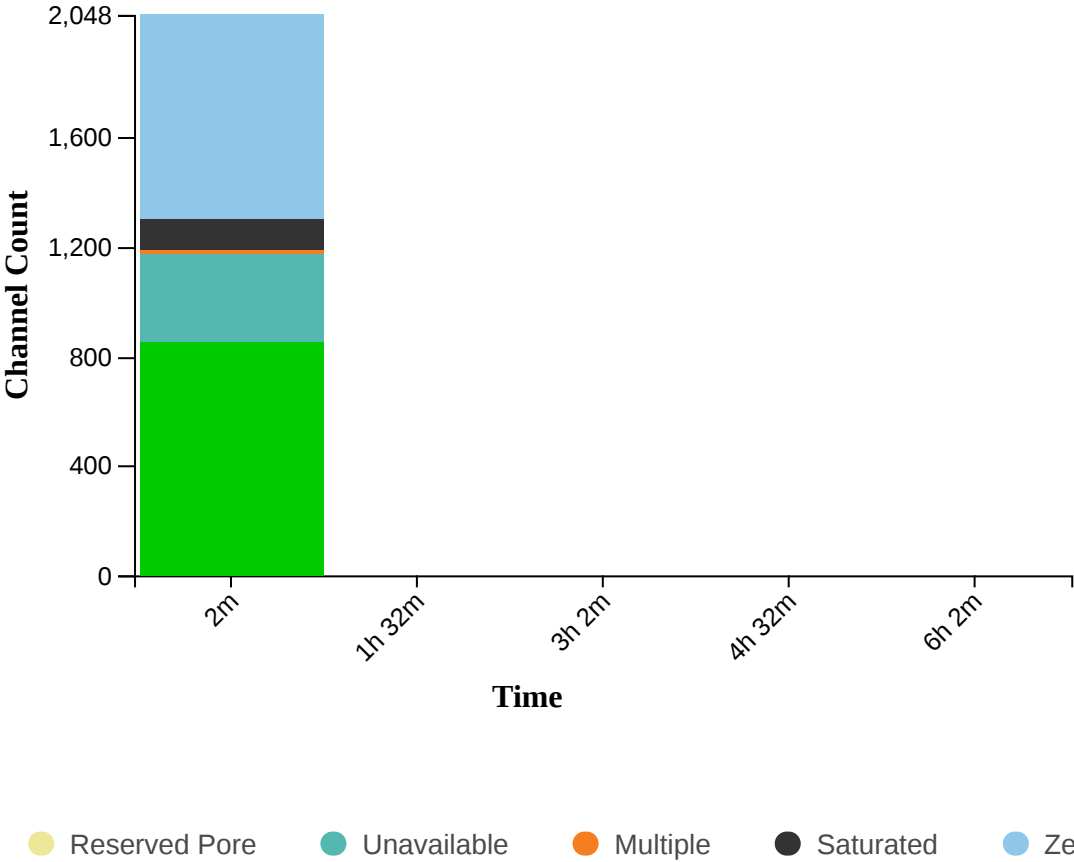

Alignment Target Hits (bases)
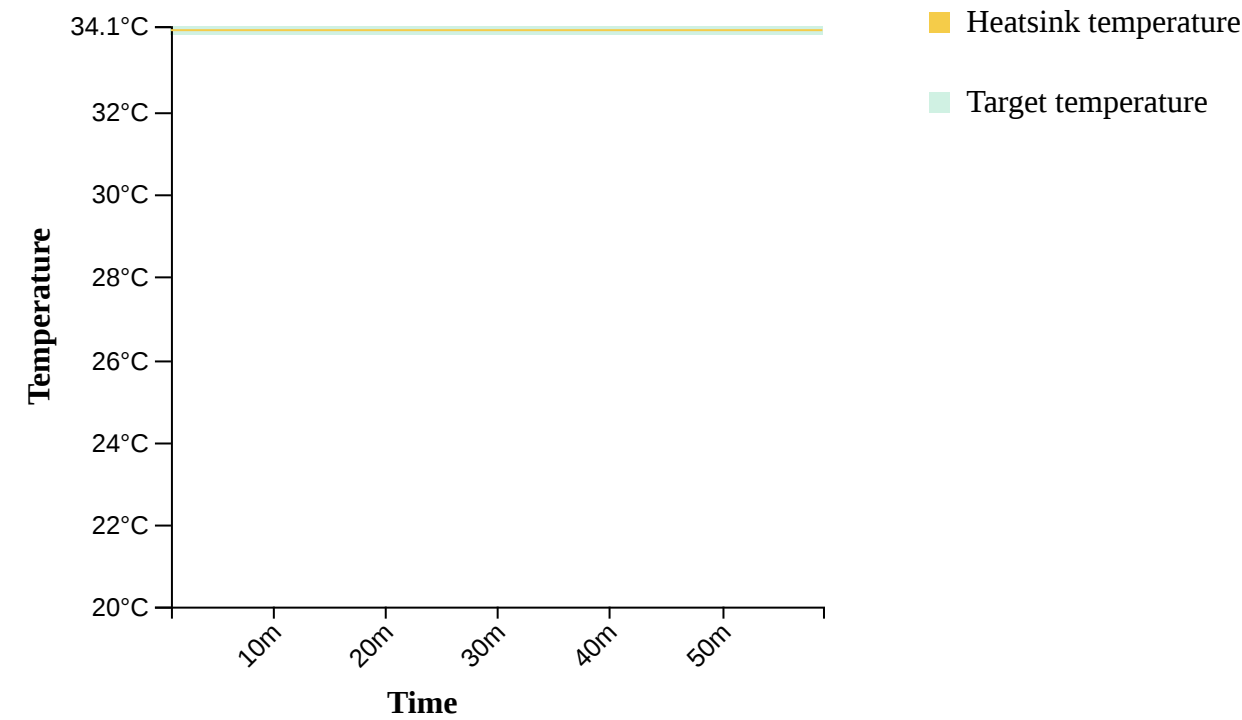
Duty Time Grouped

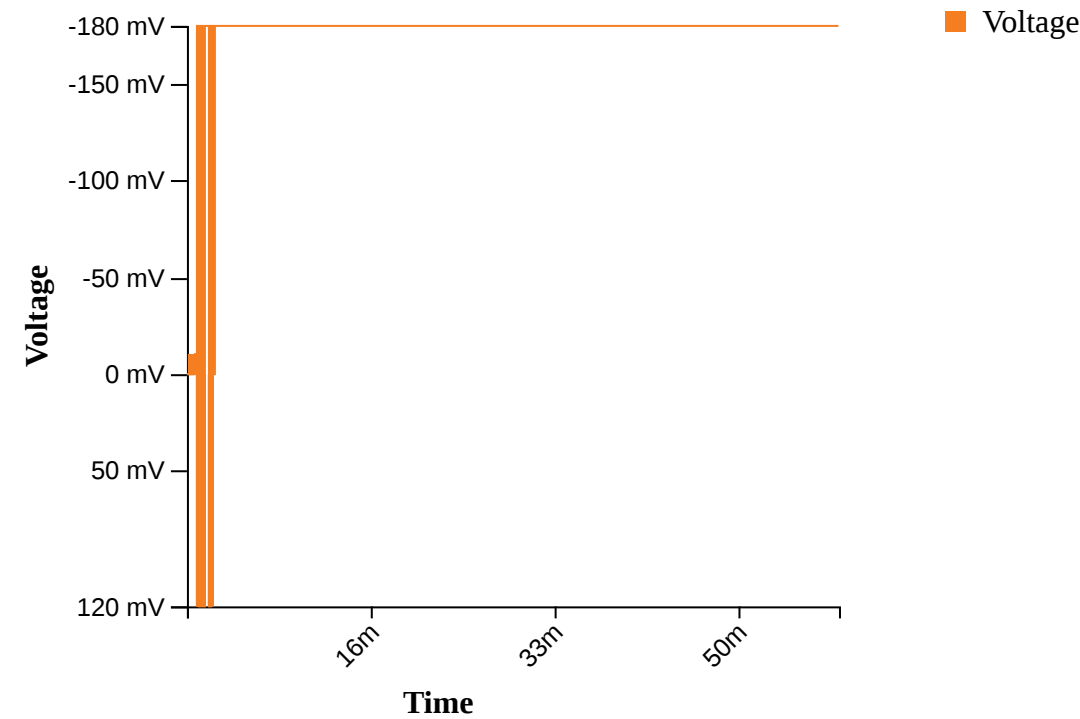## Duty time Categorised

Mux Scan Grouped

Active   Inactive

Mux Scan Categorised

Single Pore   Reserved Pore   Unavailable   Multiple   Saturated   Zero   Other
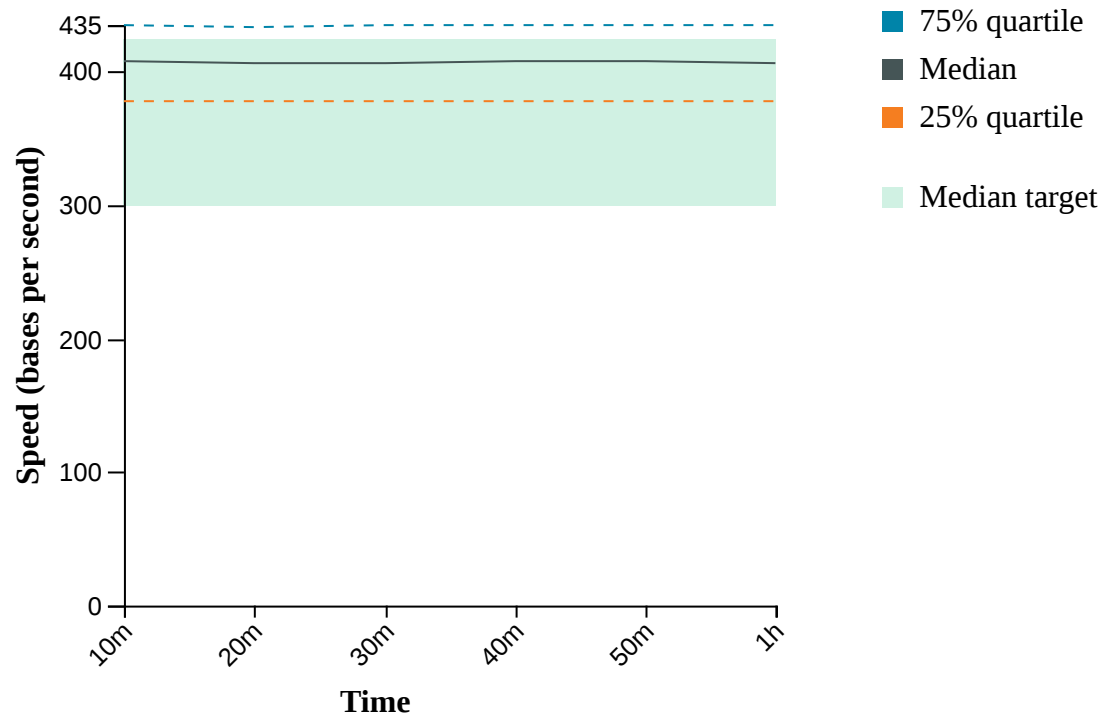
Temperature History
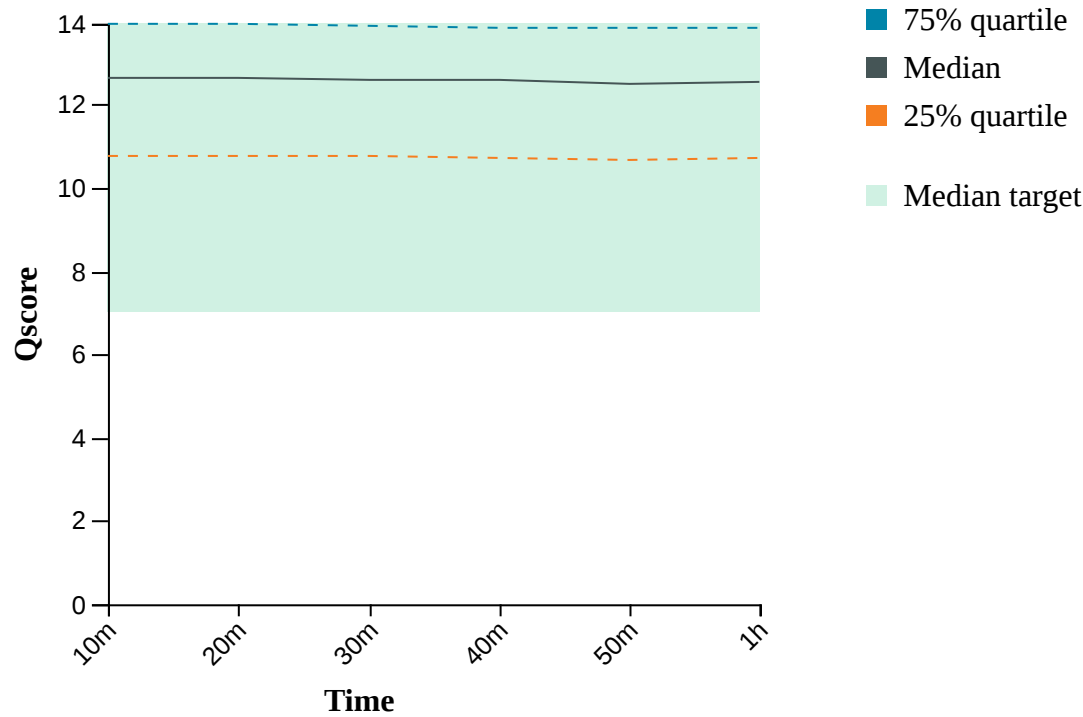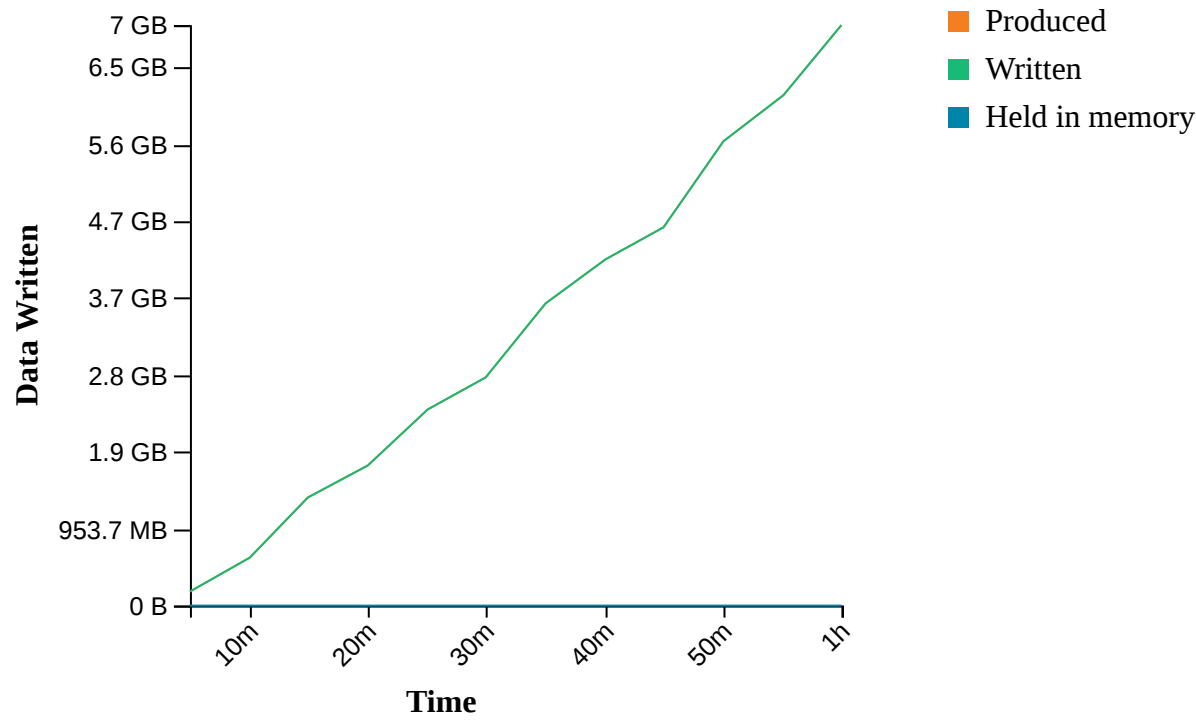

Bias Voltage History

Translocation Speed

QScore

Disk Write Performance

Run Debug Messages

- Mux scan for flow cell FAP21636 has found a total of 854 pores. 445 pores available for immediate sequencing   April 15, 15:33
- Performing Mux Scan   April 15, 15:31
- Starting sequencing procedure   April 15, 15:31
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   April 15, 15:28