Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38kbp_Sdenrich_con_15042021**
Sample ID	**ReadUntil_38kbp_Sdenrich_con_15042021**
Run ID	**241f161d-ea8e-4d8e-8c35-1f9f754533f0**
Flow Cell Id	**FAP14669**
Start Time	**April 15, 10:47**
Run Length	**1h 0m**

Run Summary

Reads Generated	**53.65 K**
Passed Bases	**446.93 Mb**
Failed Bases	**26.68 Mb**
Estimated Bases	**469.01 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**
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

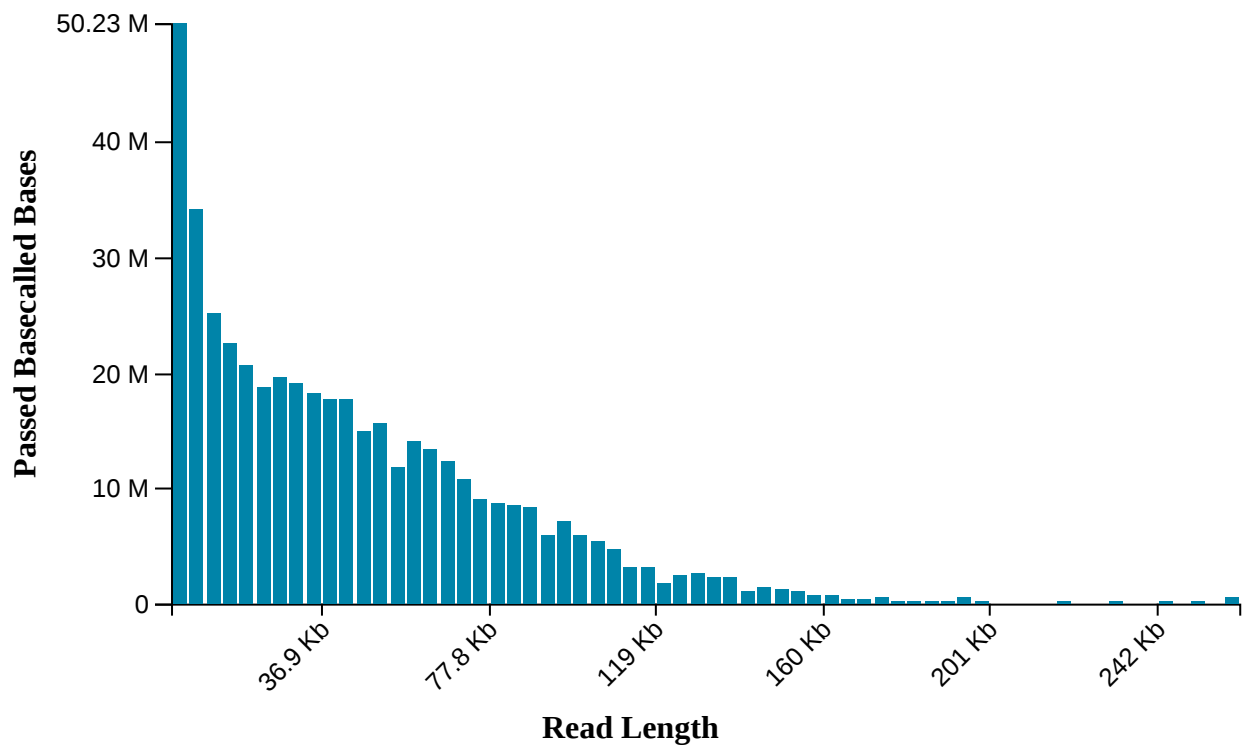|	
MinKNOW	**21.02.5**
MinKNOW Core	**4.2.5**
Bream	**6.1.10**
Guppy	**4.3.4**

Cumulative Output Reads
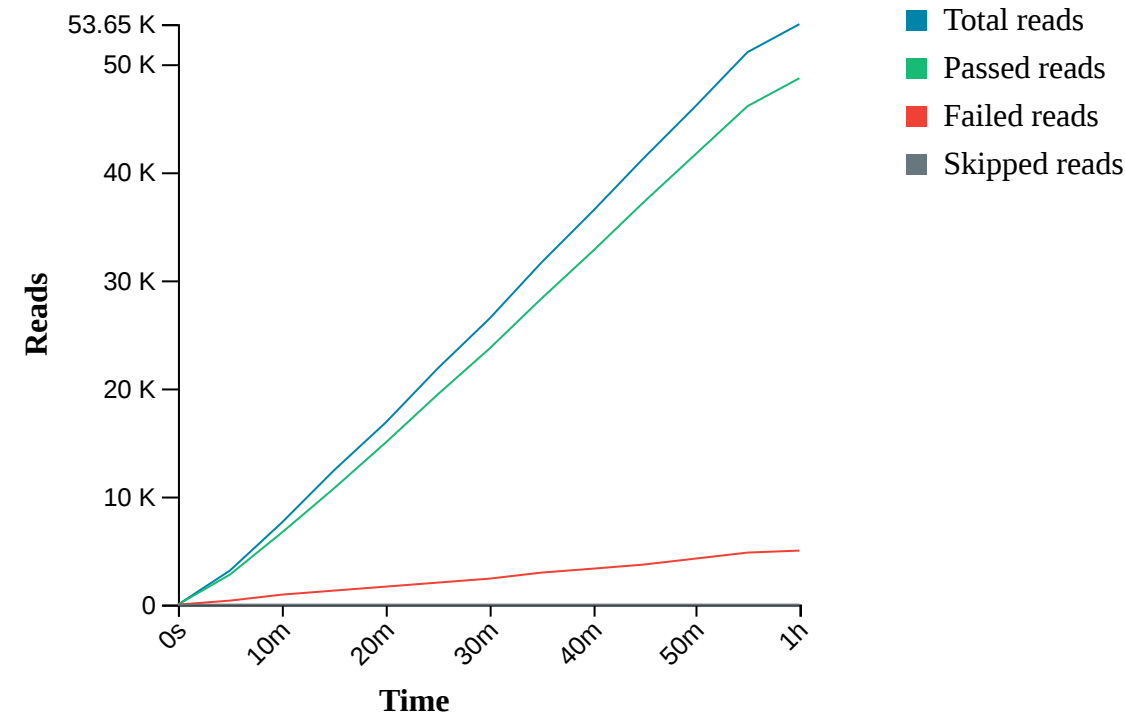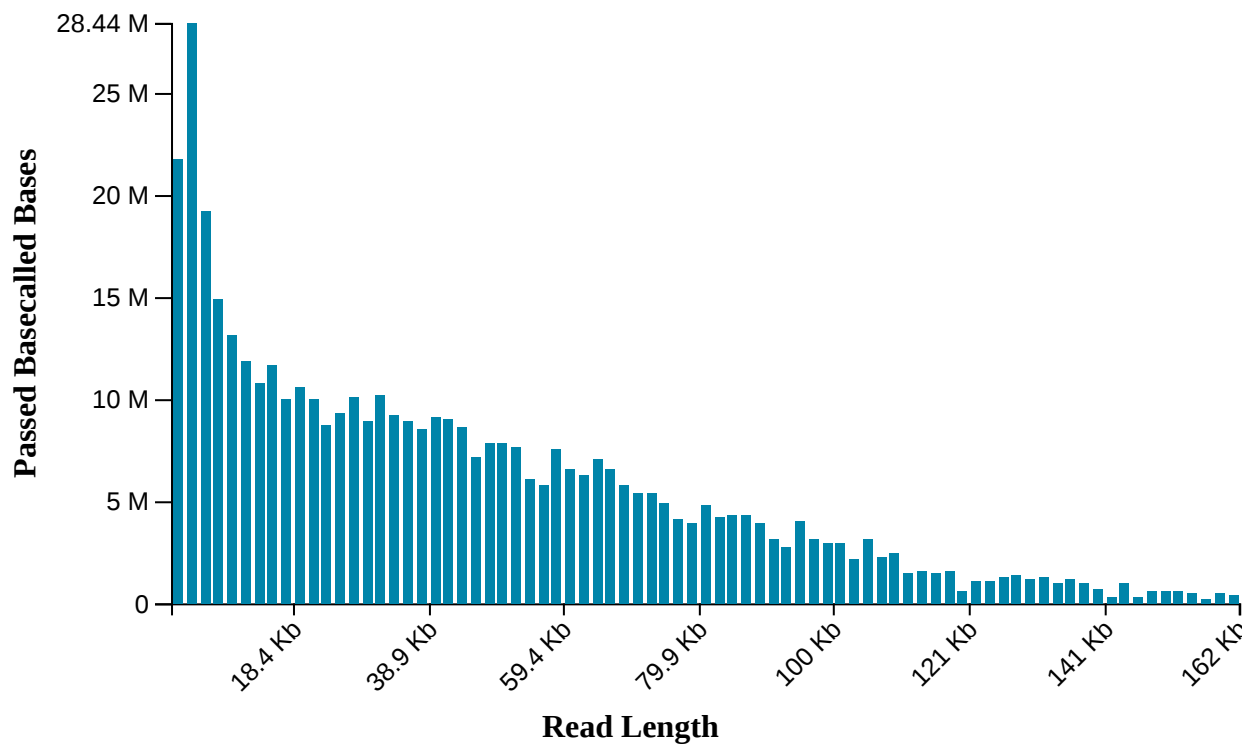

Cumulative Output Bases
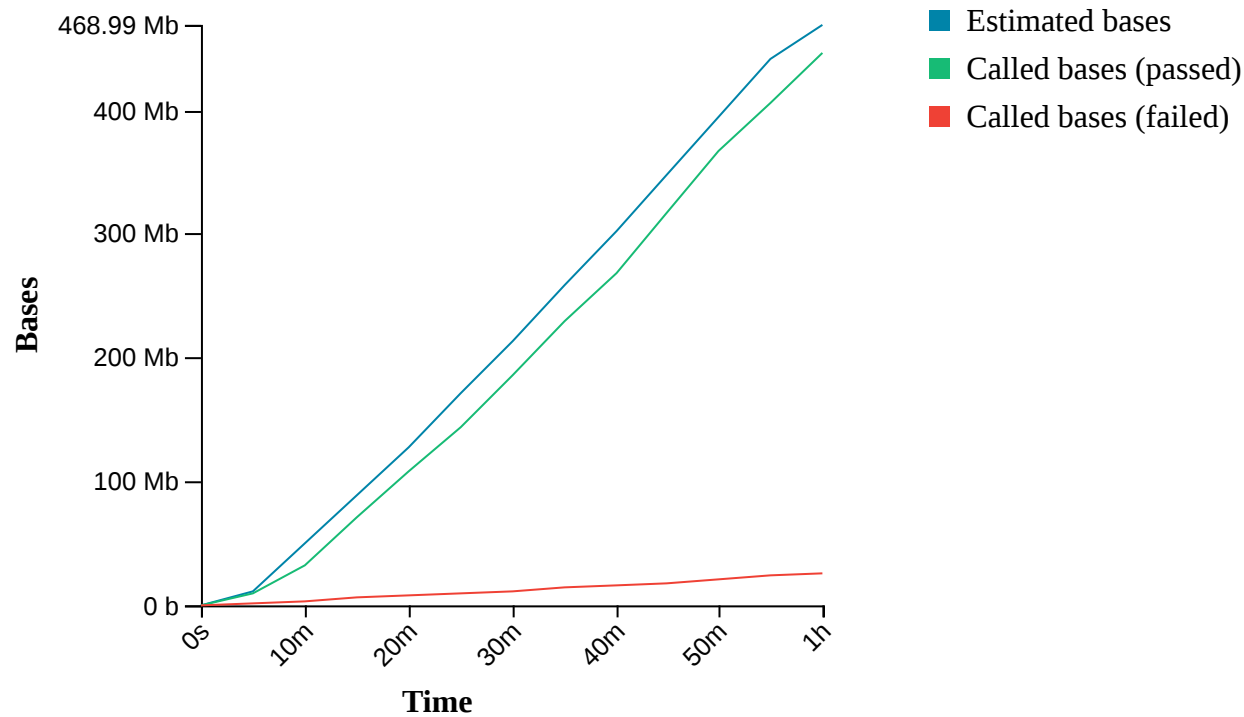
Read Length Histogram Estimated Bases - Outliers Discarded
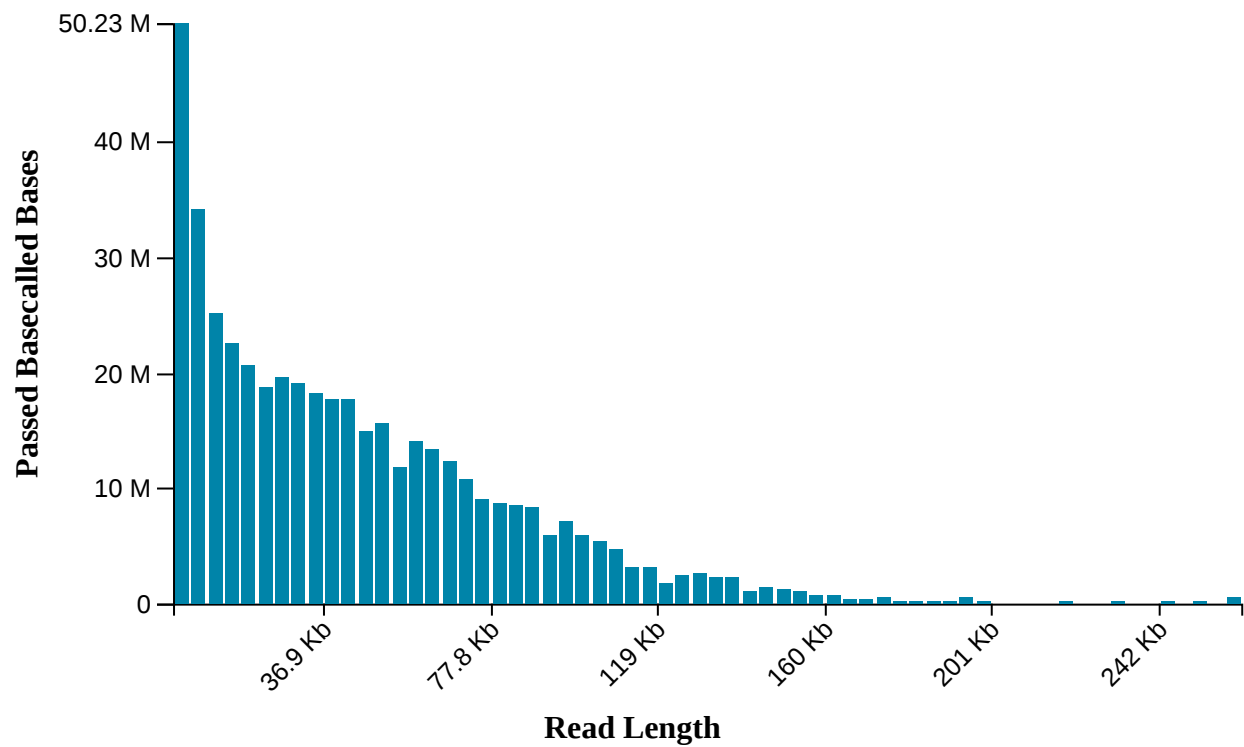
Estimated N50: 35.88 K

Read Length Histogram Basecalled Bases - Outliers Discarded
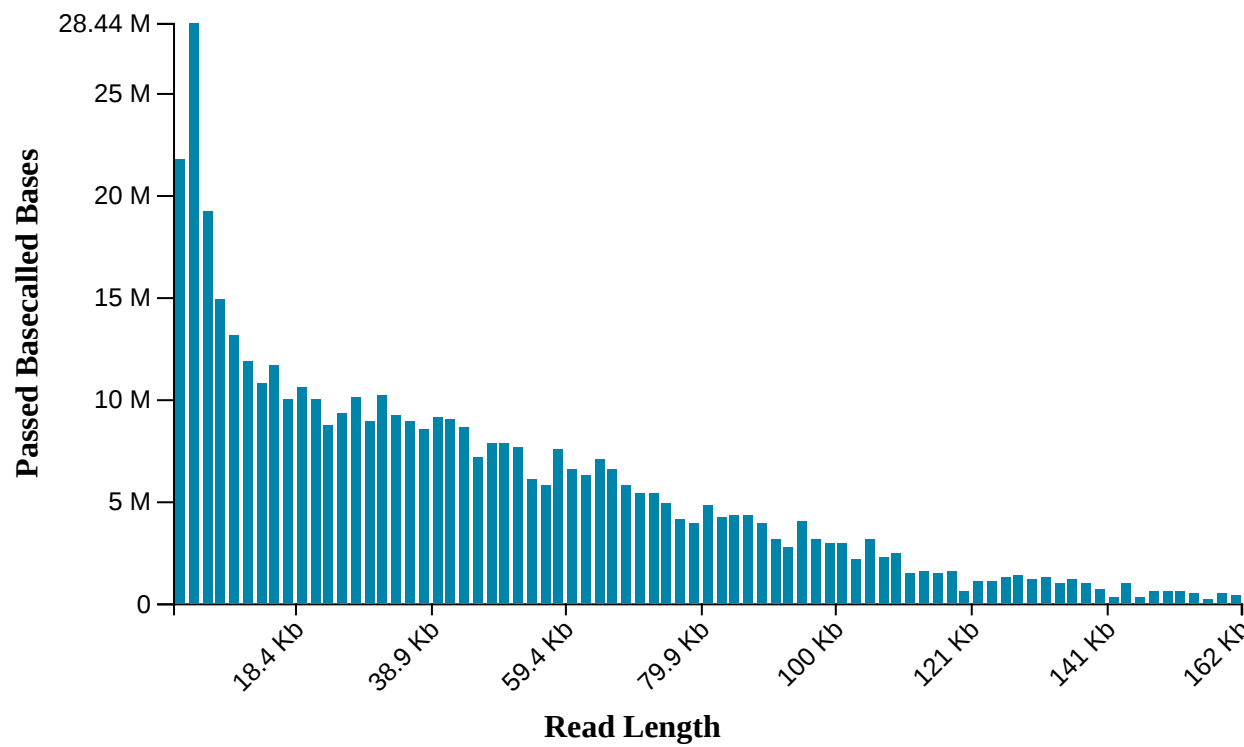
Estimated N50: 35.37 K

__Read Length Histogram Estimated Bases__
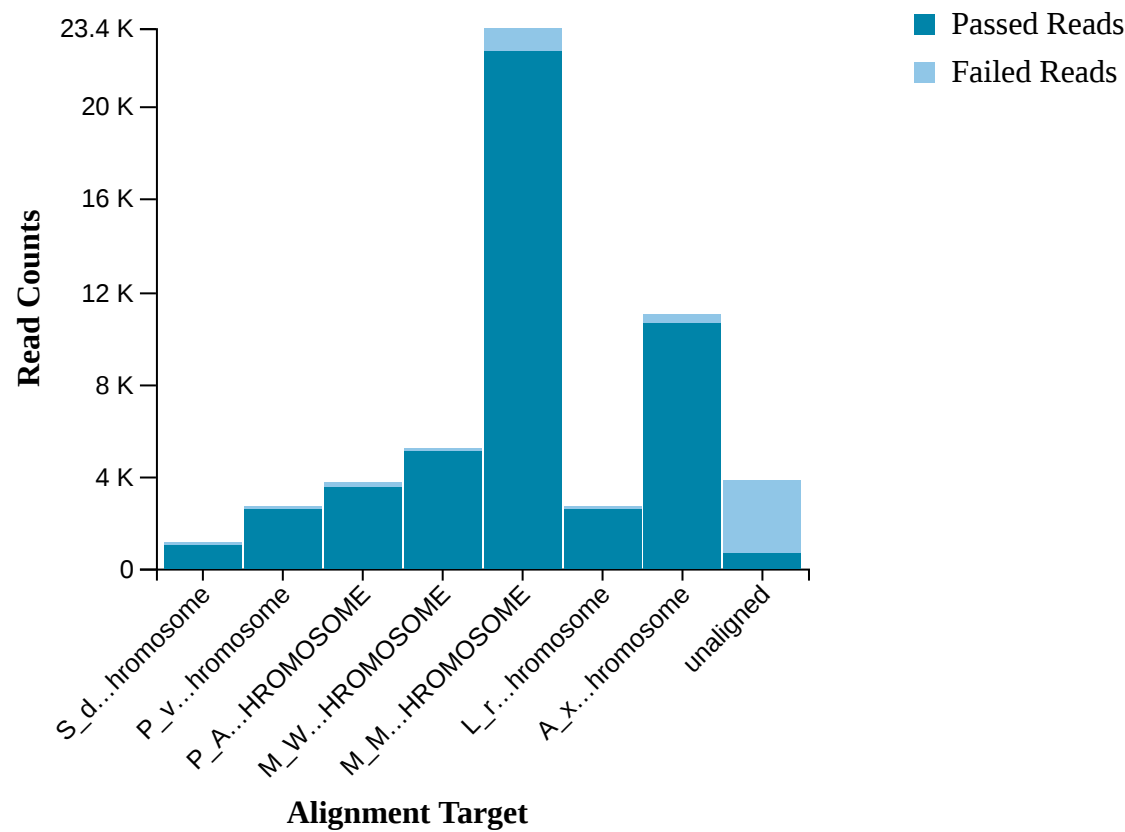
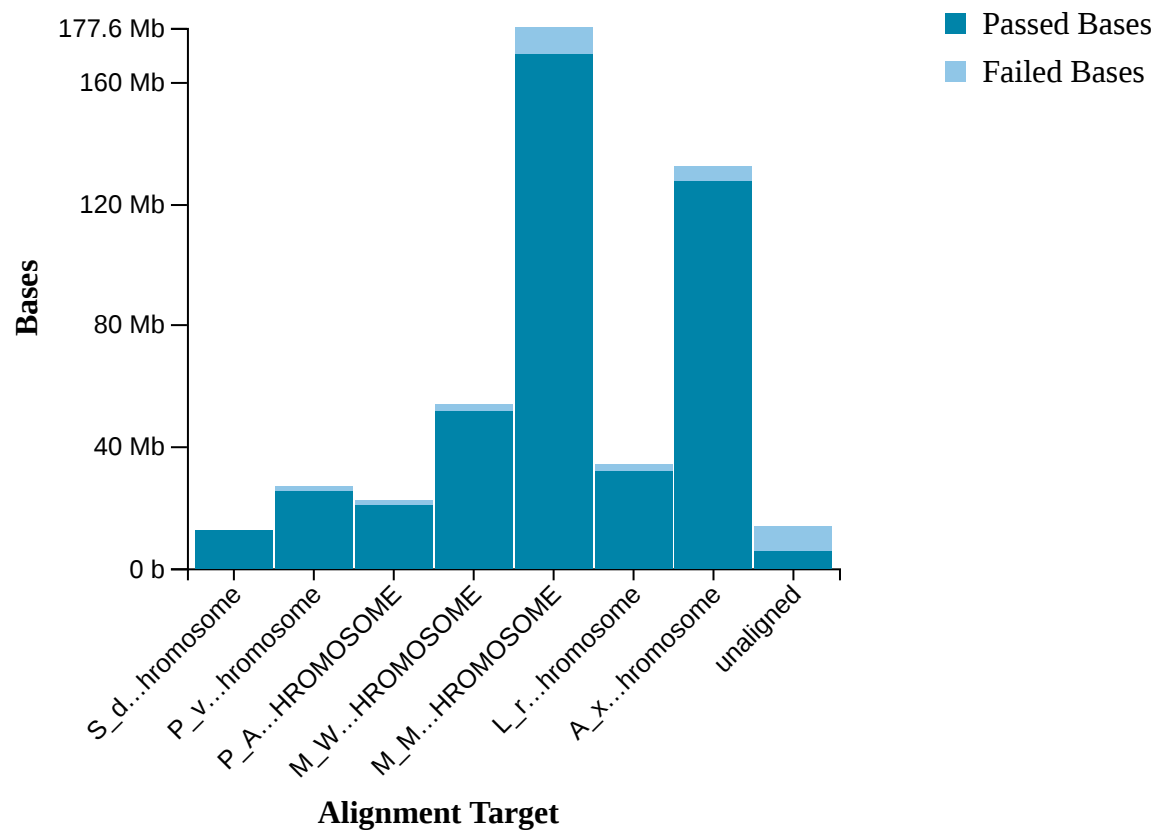Estimated N50: 35.88 K

__Read Length Histogram Basecalled Bases__
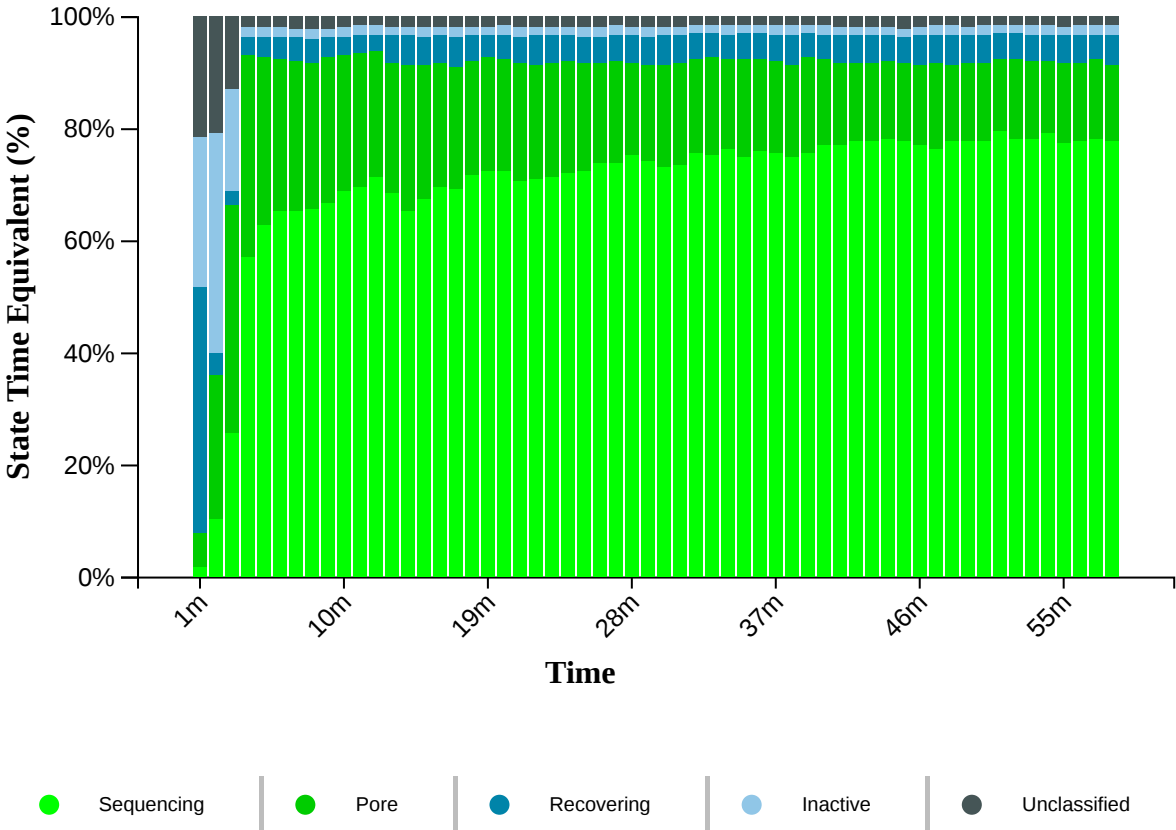
Estimated N50: 35.37 K

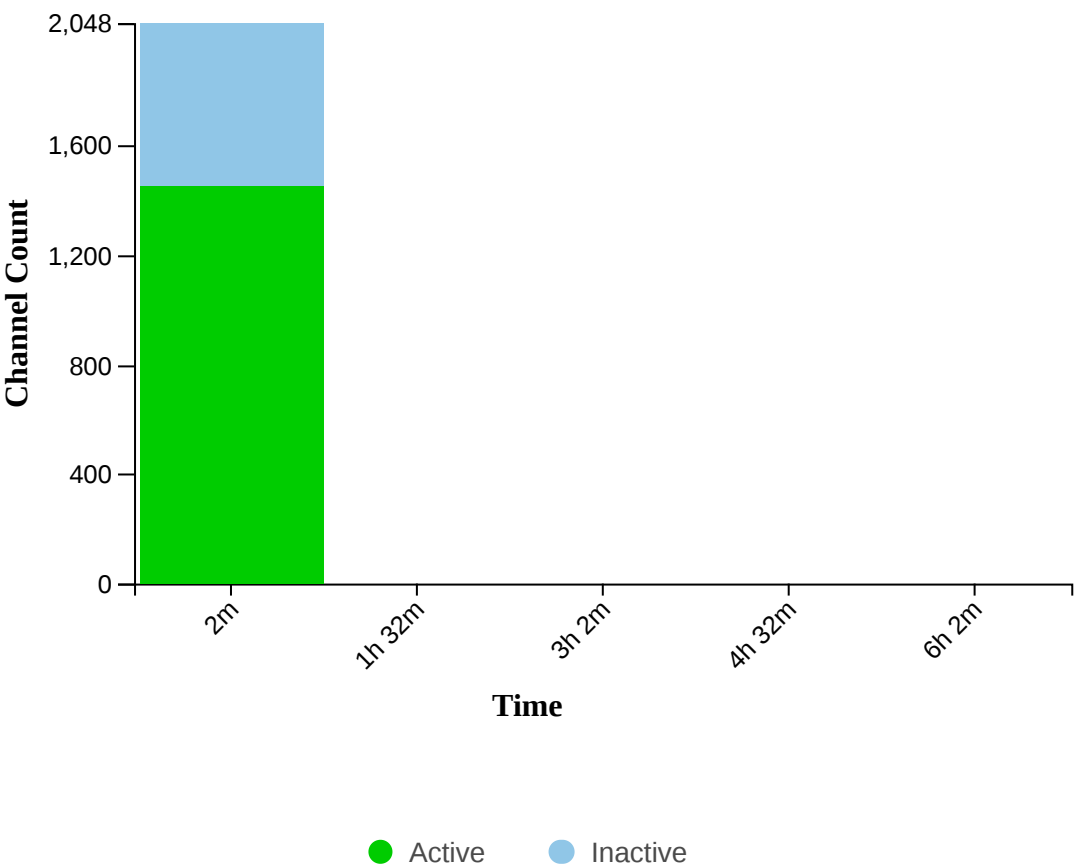## Alignment Target Hits (reads)

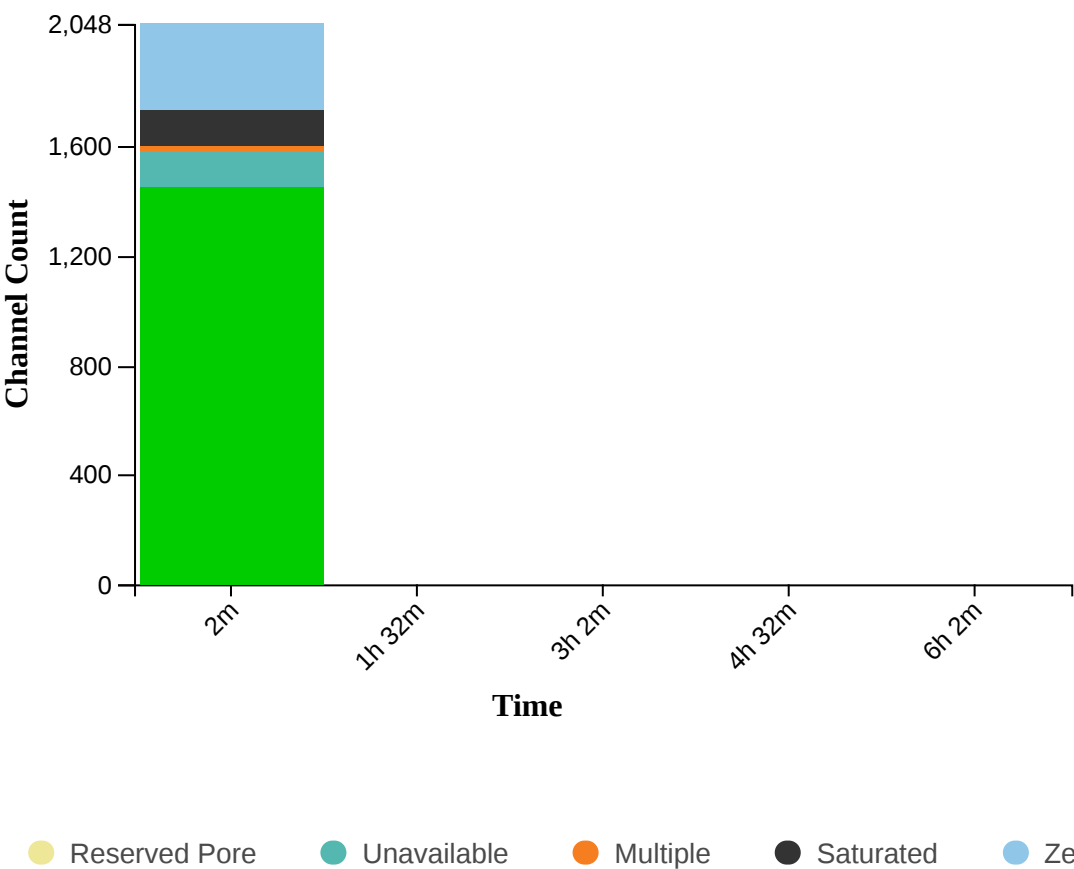## Alignment Target Hits (bases)

Duty Time Grouped

Legend:
- Sequencing
- Pore
- Recovering
- Inactive
- Unclassified

Duty time Categorised

Legend:
- Strand
- Adapter
- Single Pore
- Unavailable
- Active Feedback
- No Pore From Scan
- Out Of Range 2
- Possible Multiple
- Saturated
- Out Of Range 1
- Zero
- Channel Disabled
- Unclassified
- Unclassified_following_reset
- Pending_manual_reset
- Pending_mux_change
- Pending Reselection

Mux Scan Grouped

● Active   ● Inactive

Mux Scan Categorised

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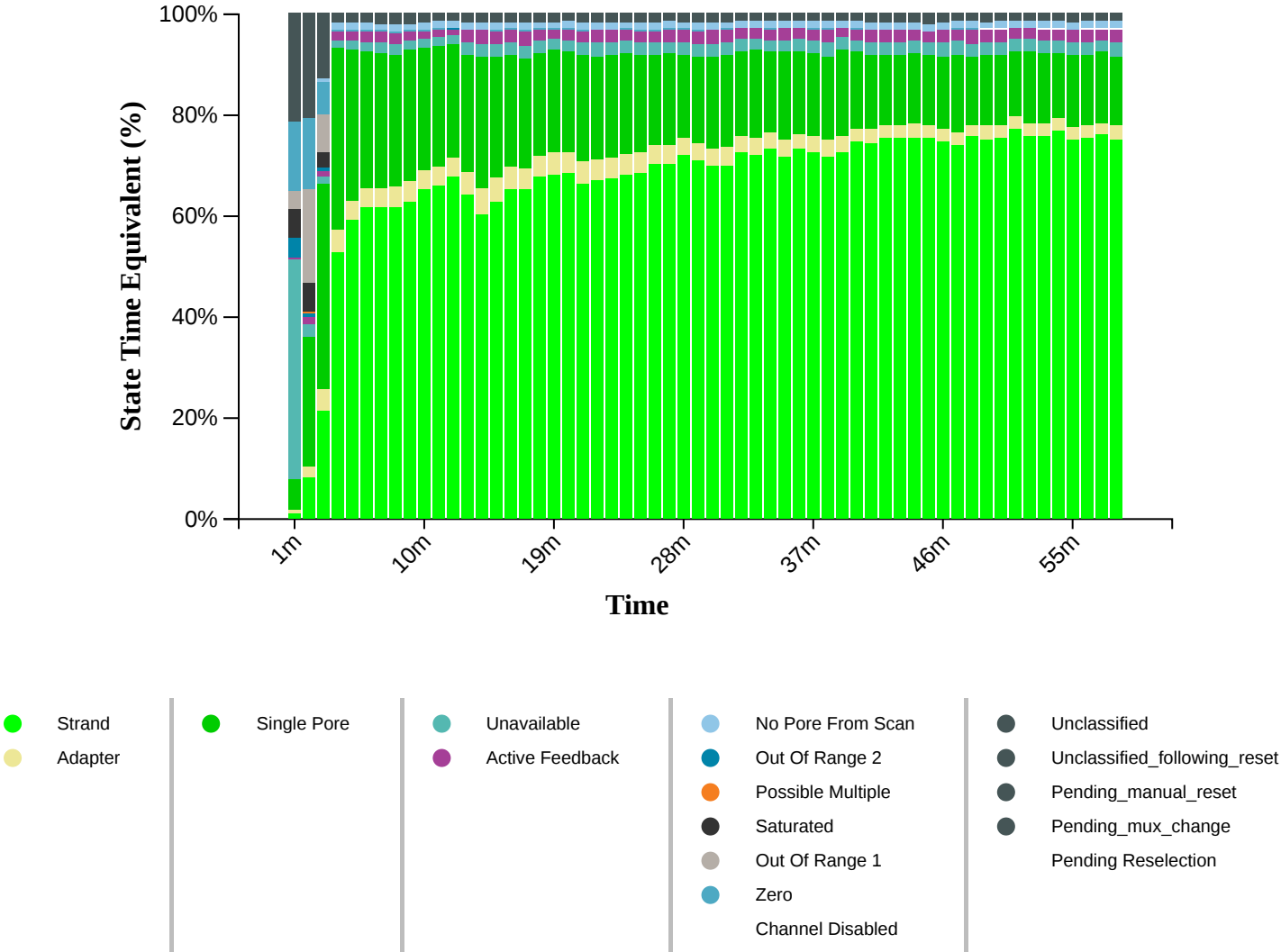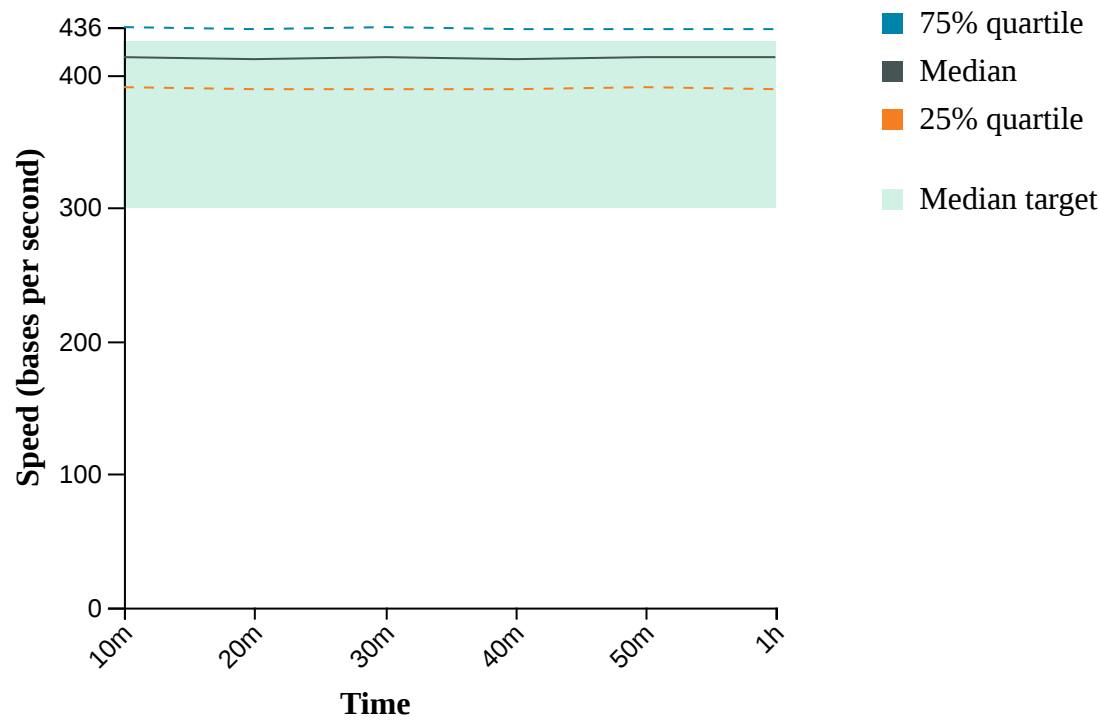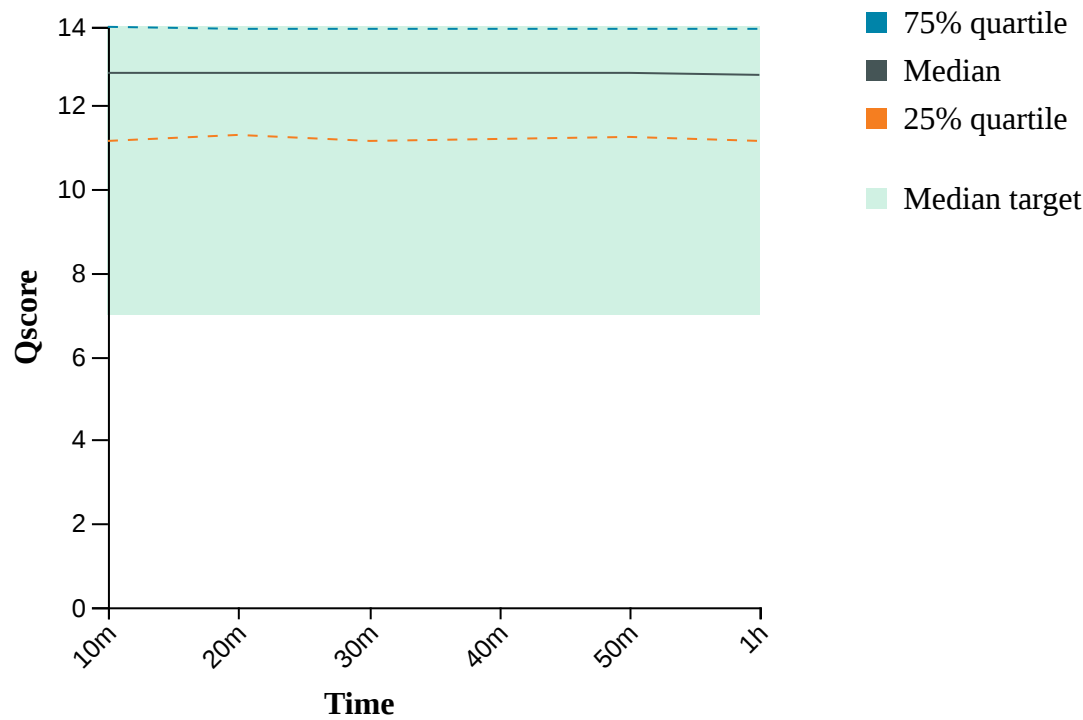
Temperature History
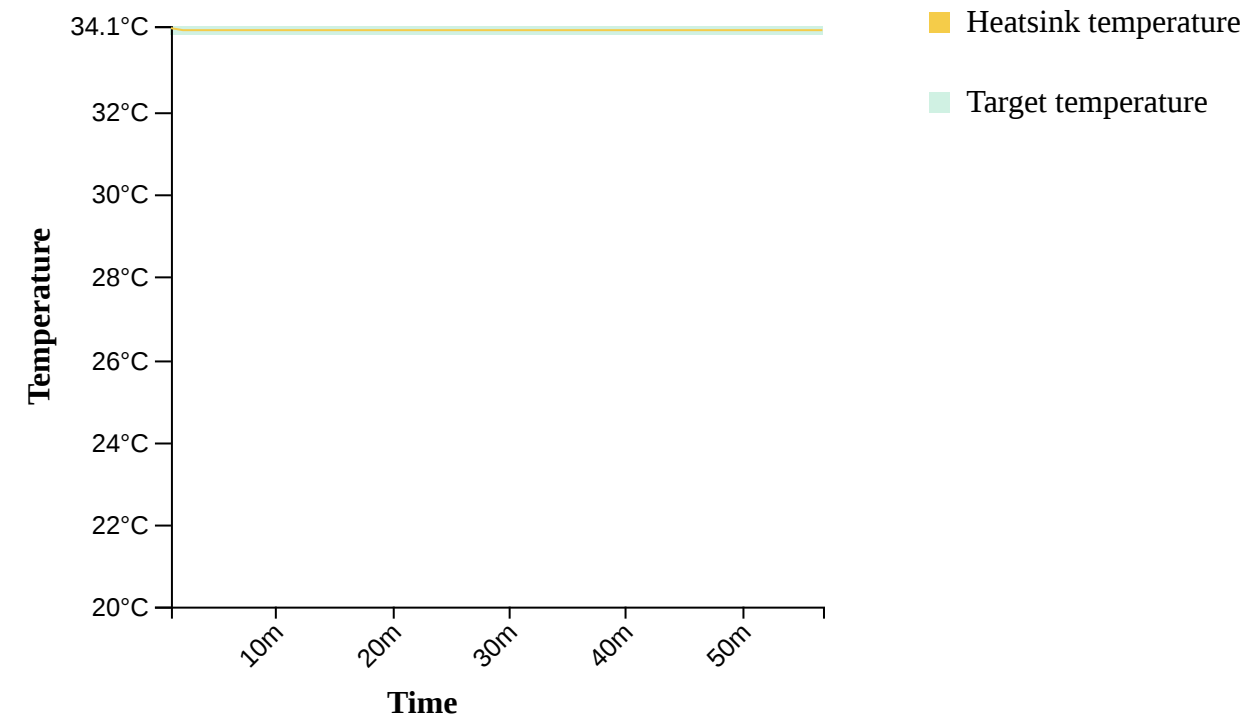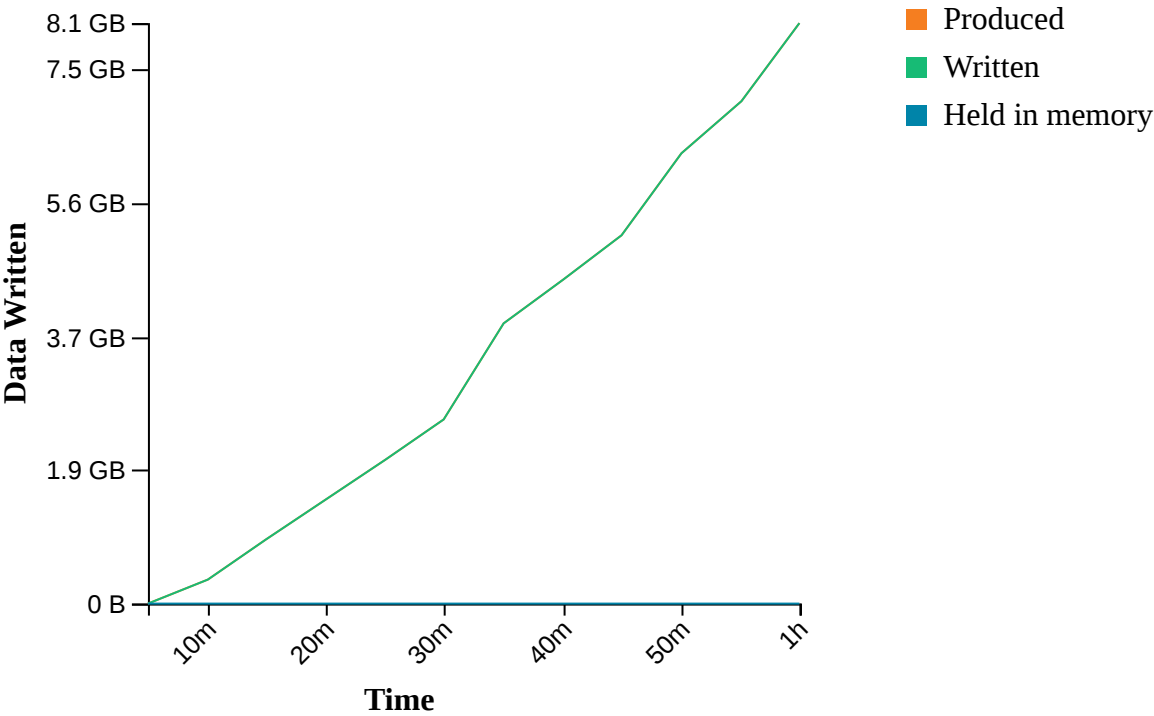

Bias Voltage History
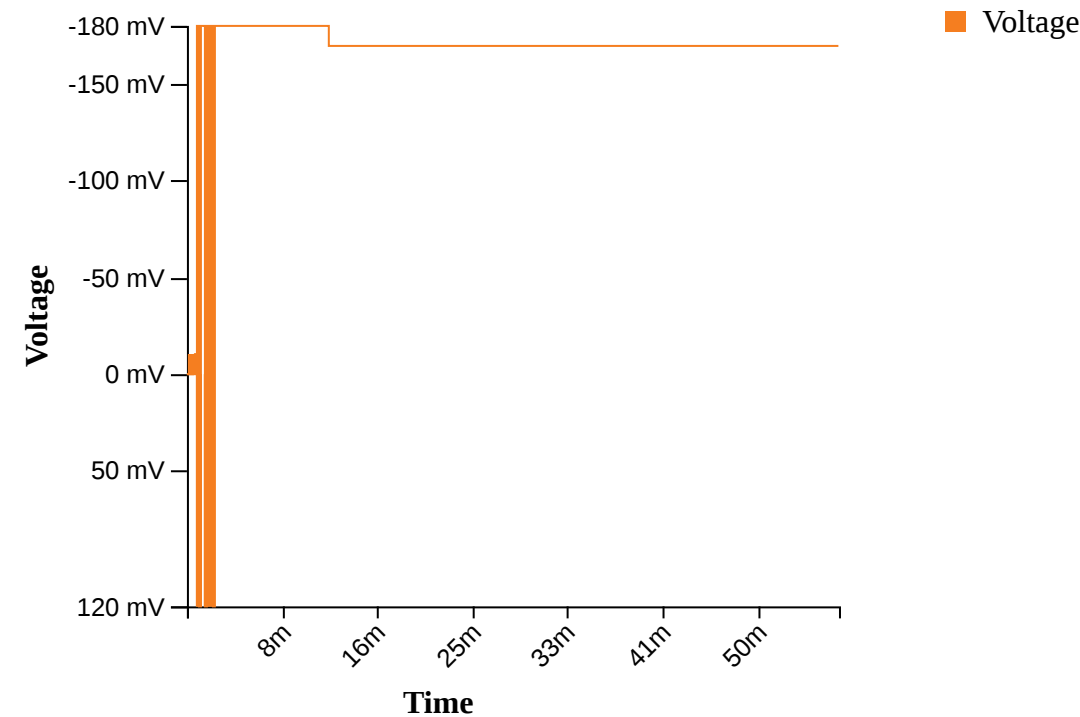
Translocation Speed

QScore

Disk Write Performance

Run Debug Messages

- Mux scan for flow cell FAP14669 has found a total of 1455 pores. 505 pores available for immediate sequencing   April 15, 10:53
- Performing Mux Scan   April 15, 10:50
- Starting sequencing procedure   April 15, 10:50
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   April 15, 10:47