Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**EIMock_6kbp_AxylosoxidansEnrich_04012021**
Sample ID	**EIMock_6kbp_AxylosoxidansEnrich_04012021**
Run ID	**4b65cf3f-f670-4d1e-872e-812f3d3d59fb**
Flow Cell Id	**FAO54786**
Start Time	**January 4, 11:58**
Run Length	**1h 0m**

Run Summary

Reads Generated	**91.63 K**
Passed Bases	**135.11 Mb**
Failed Bases	**4.35 Mb**
Estimated Bases	**144.41 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/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

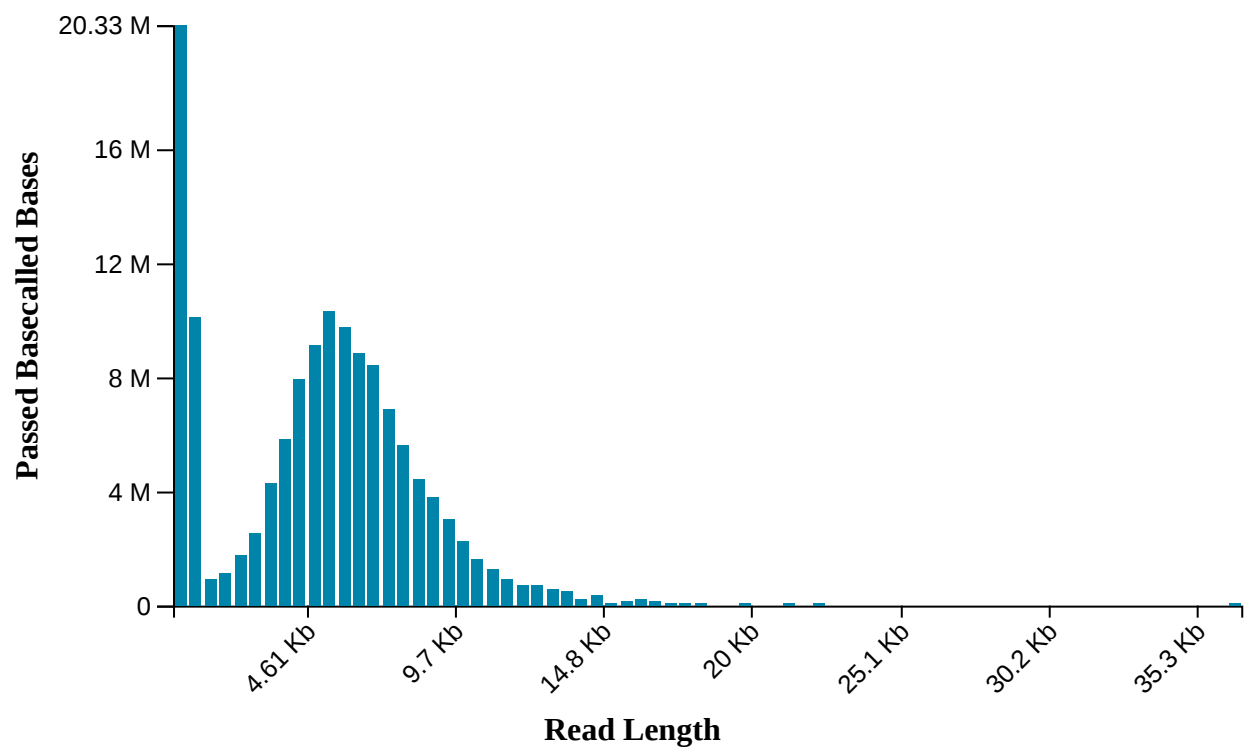|	
MinKNOW	**20.10.6**
MinKNOW Core	**4.1.2**
Bream	**6.1.4**
Guppy	**4.2.3**

Cumulative Output Reads
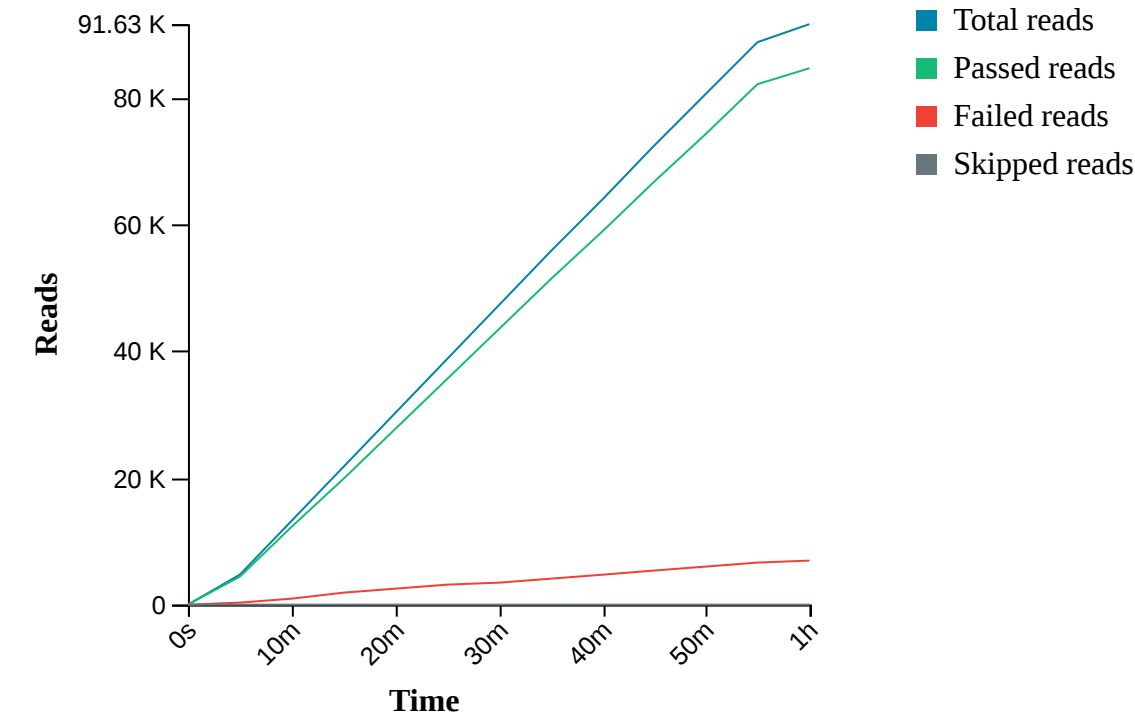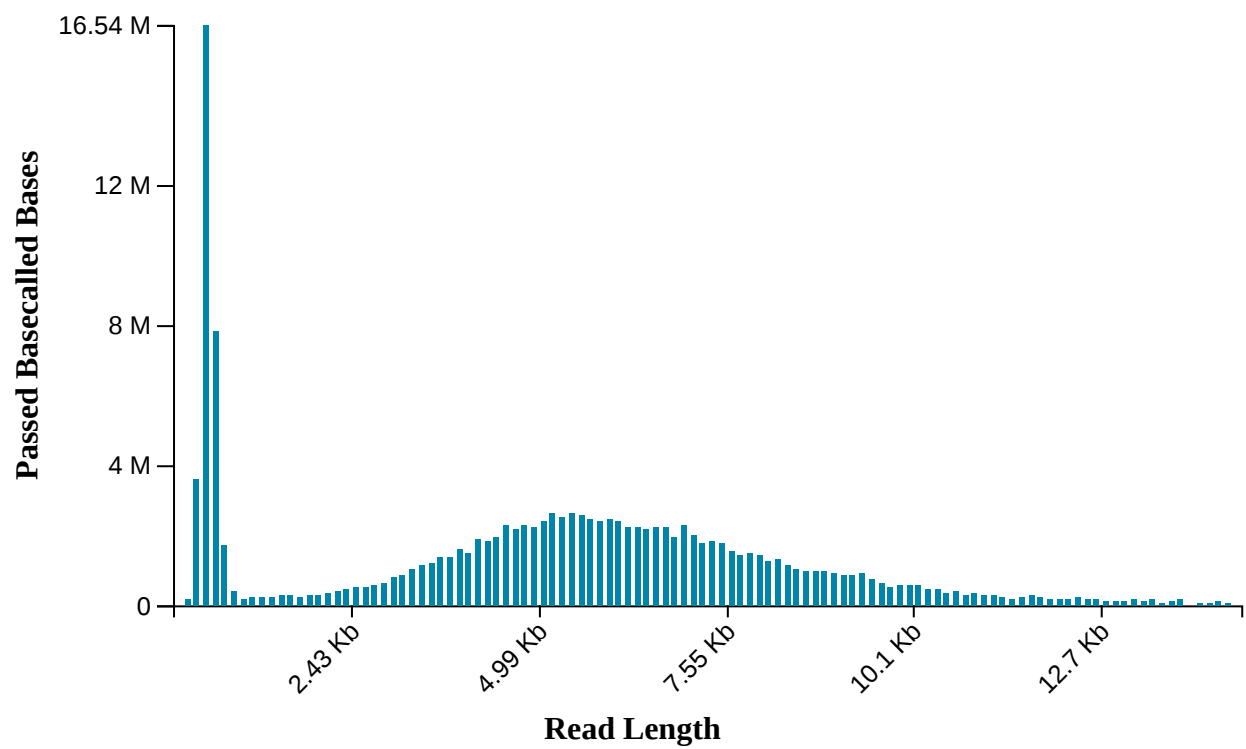

Cumulative Output Bases
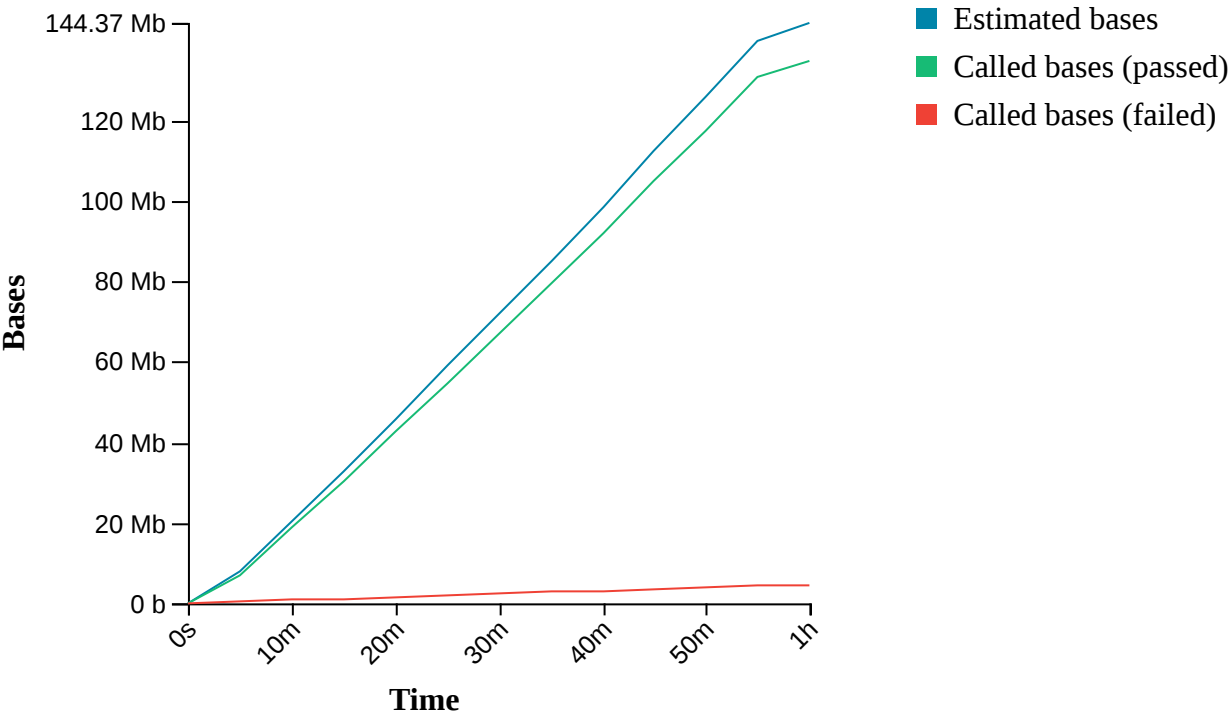
Read Length Histogram Estimated Bases - Outliers Discarded
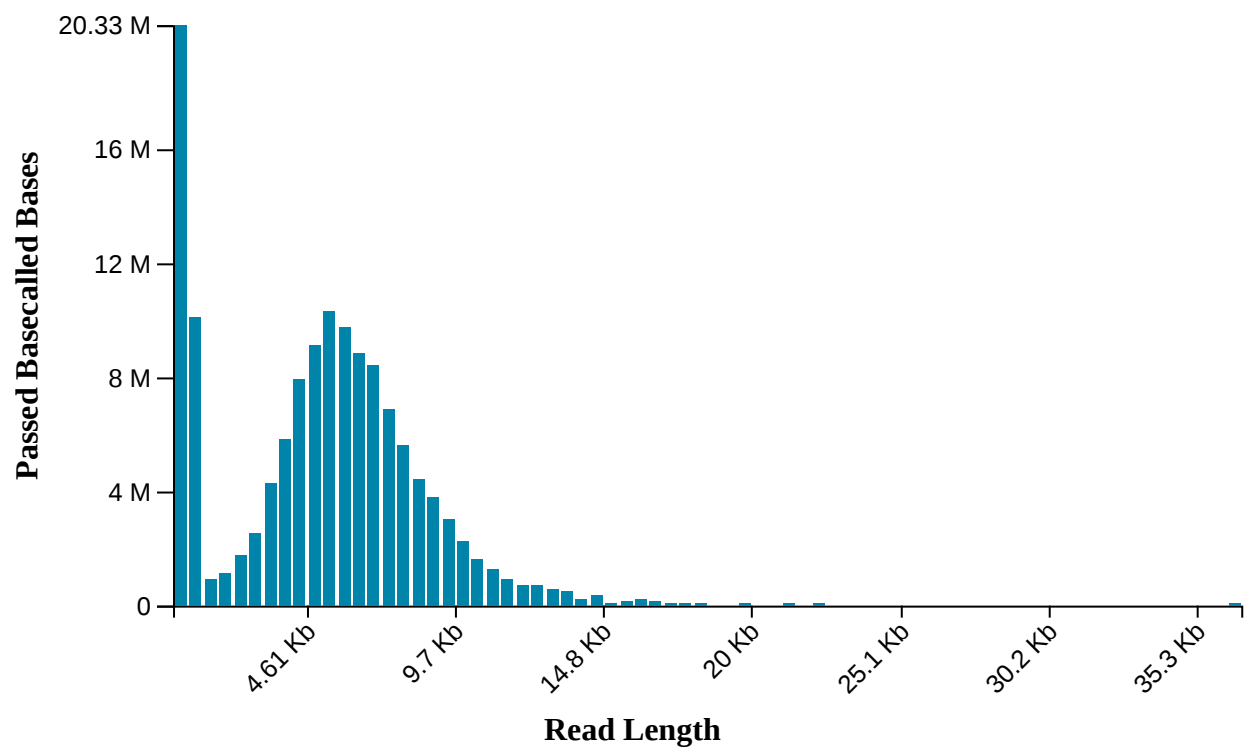
Estimated N50: 5.3 K

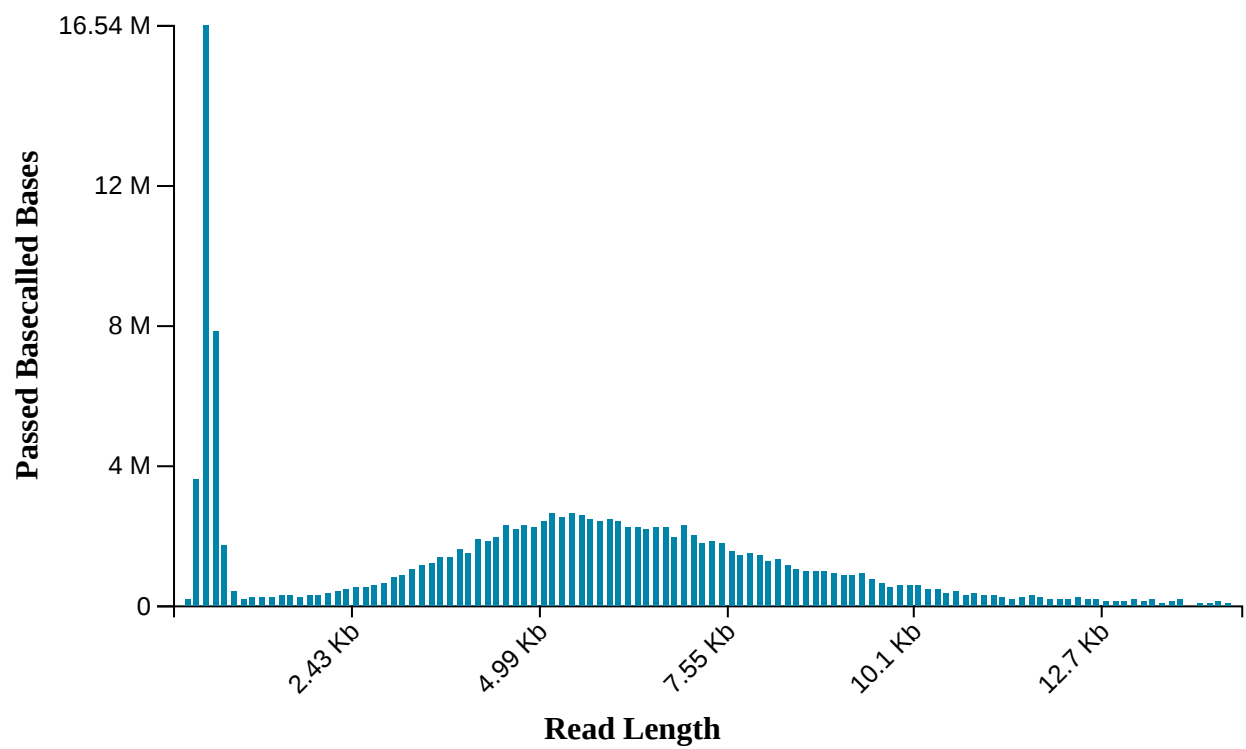## Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 5.26 K

Read Length Histogram Estimated Bases
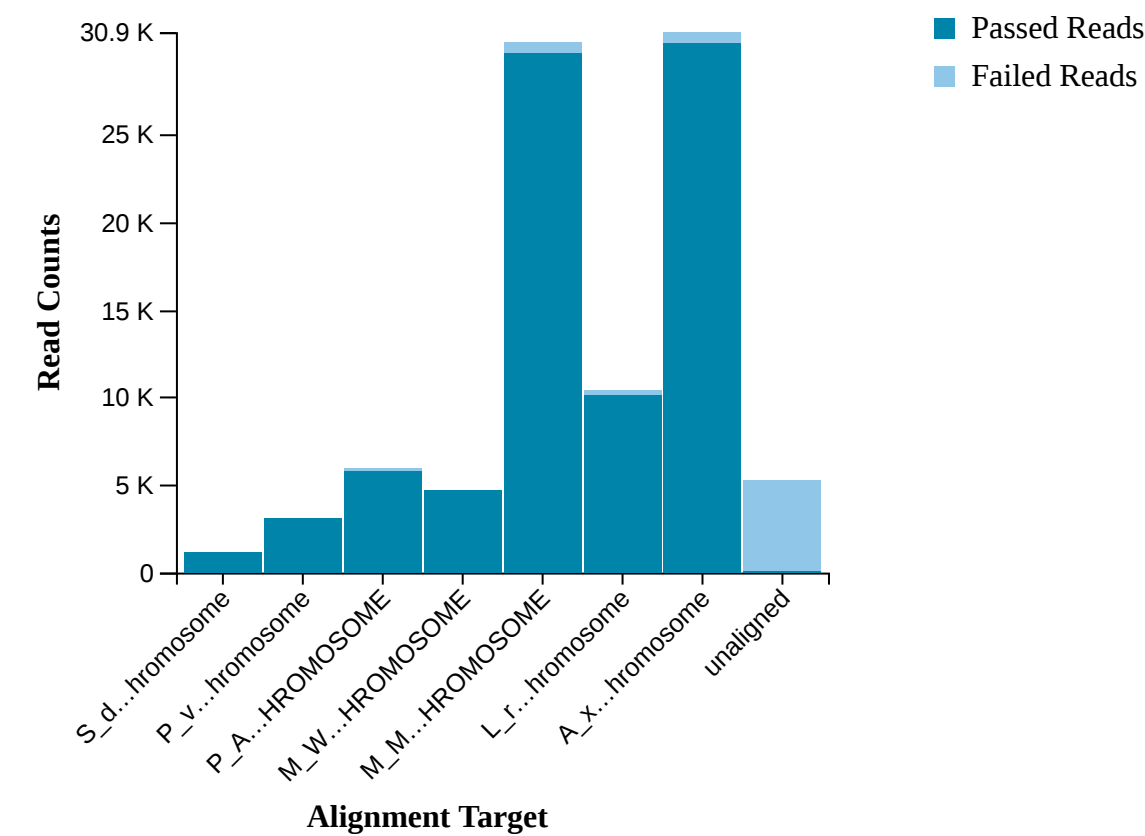
Estimated N50: 5.3 K
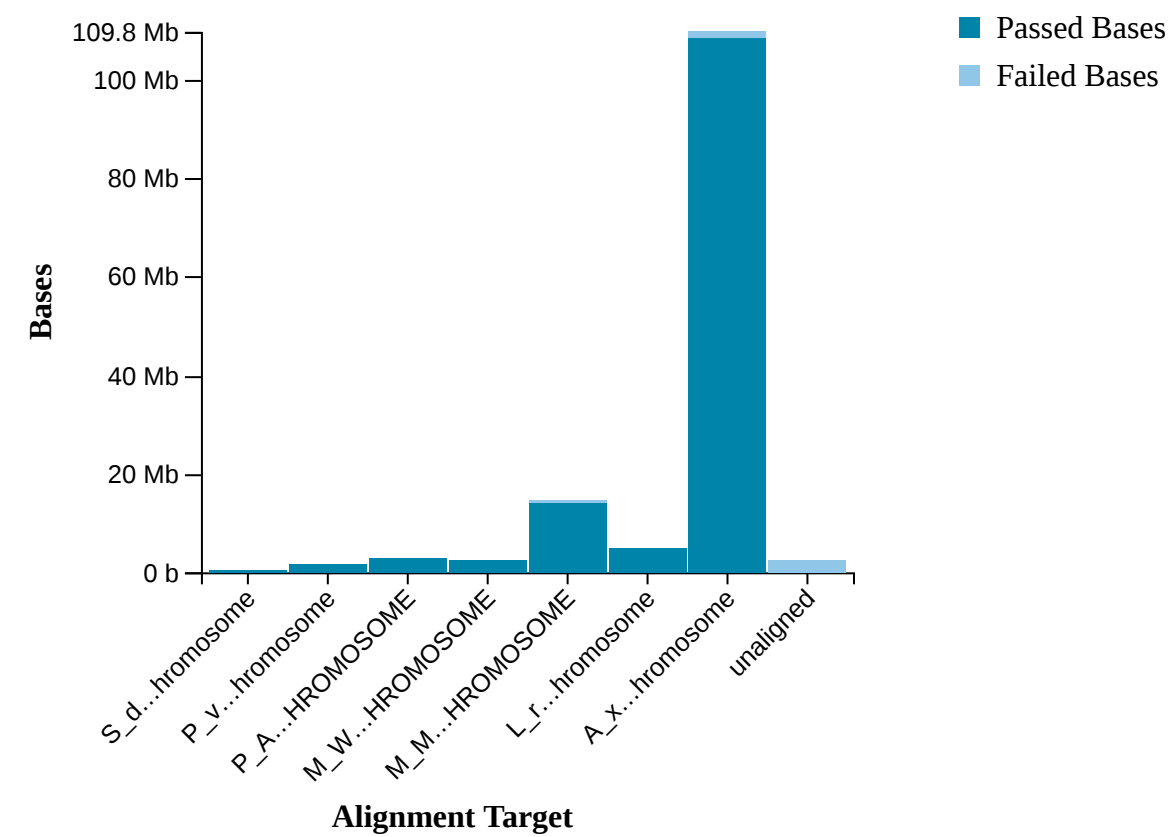

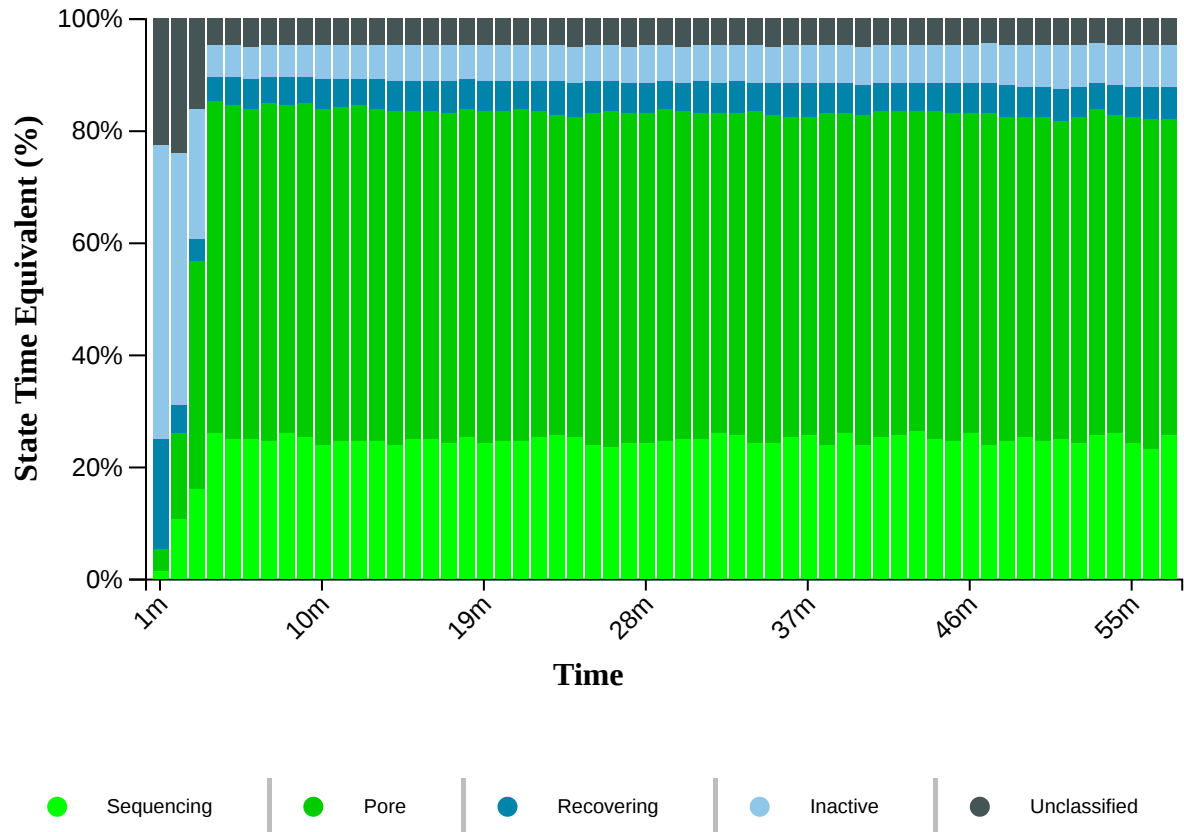## Read Length Histogram Basecalled Bases

Estimated N50: 5.26 K
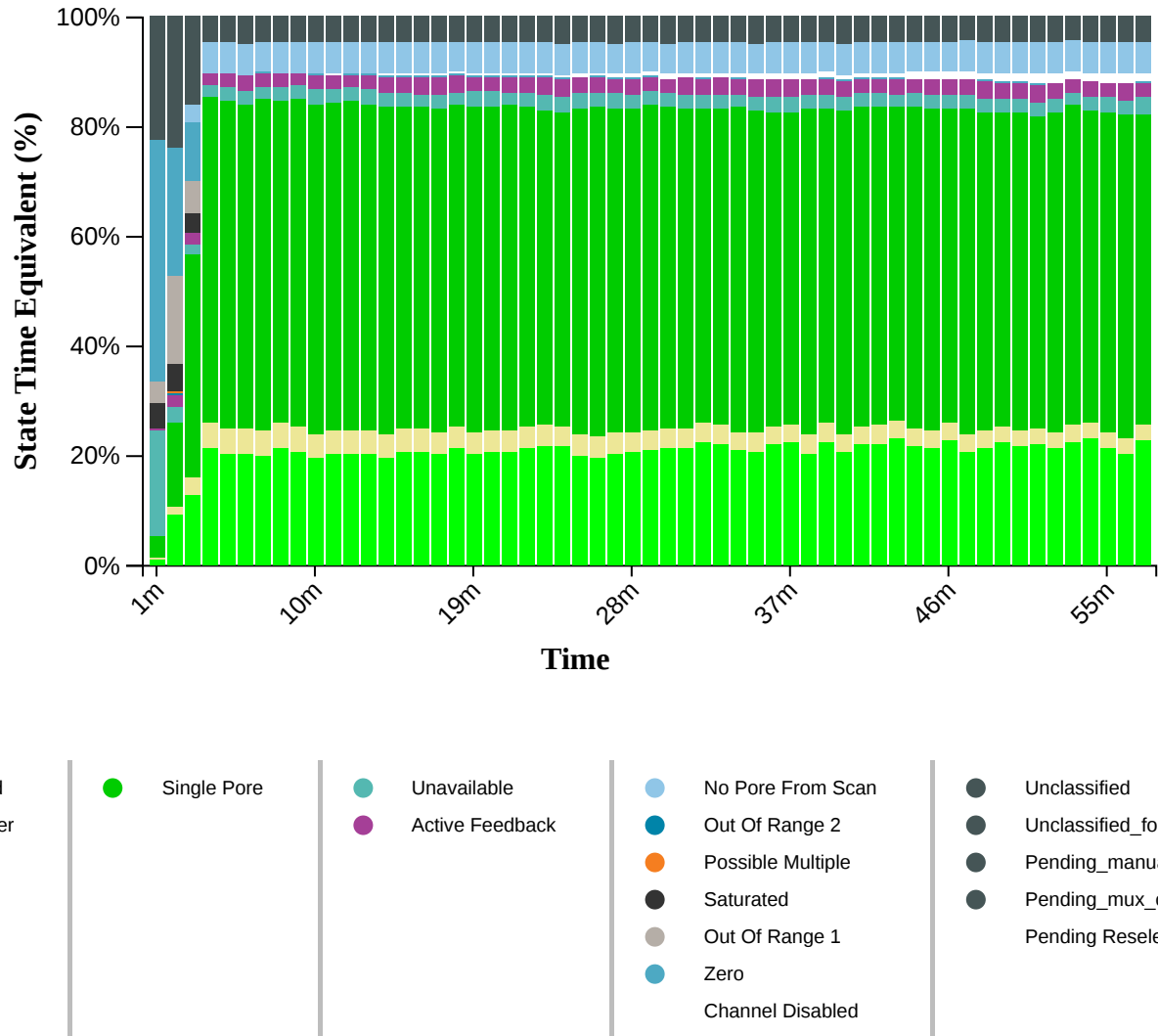
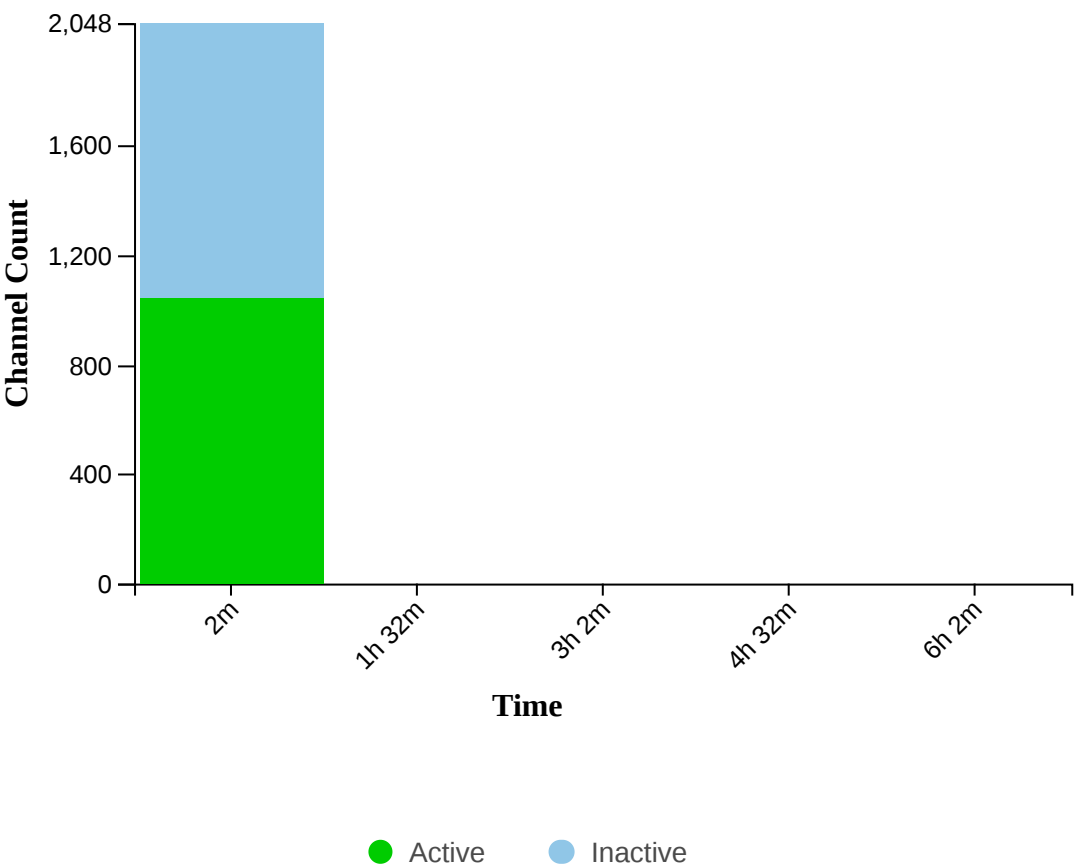## Alignment Target Hits (reads)

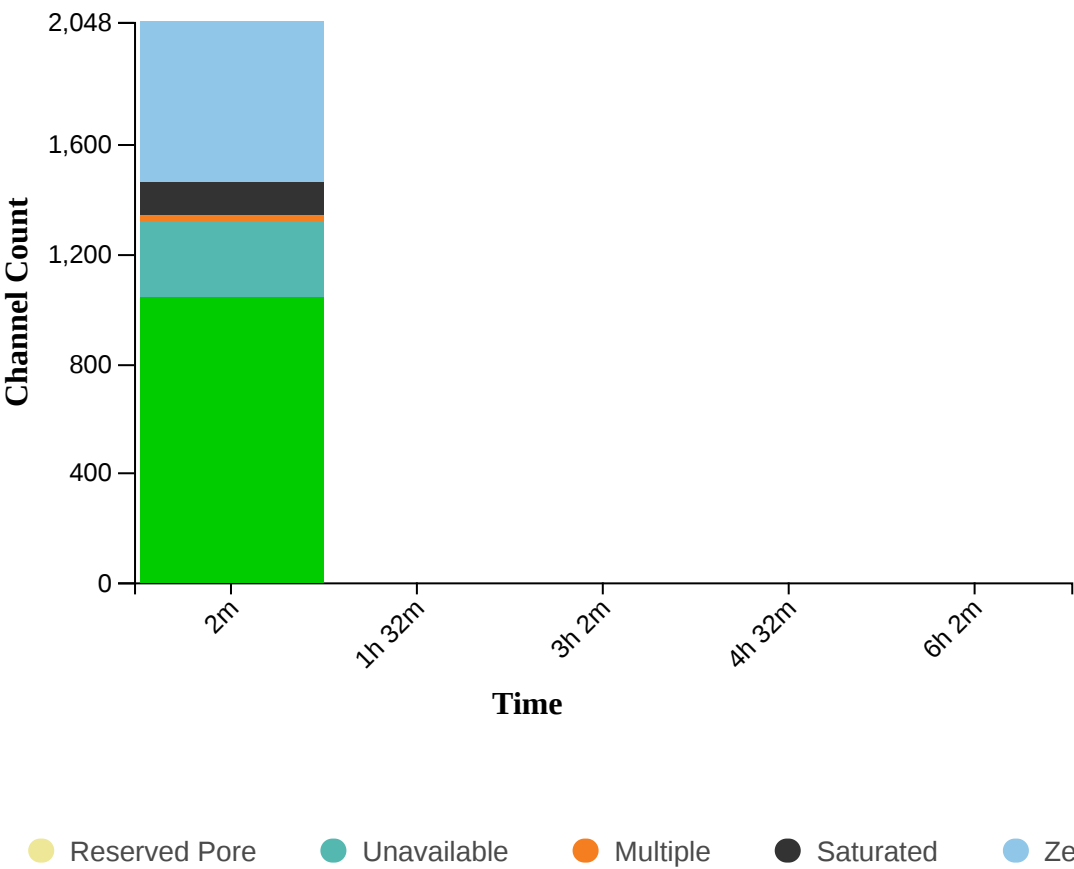## Alignment Target Hits (bases)

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

Active   Inactive

Mux Scan Categorised

Single Pore   Reserved Pore   Unavailable   Multiple   Saturated   Zero   Other

Temperature History
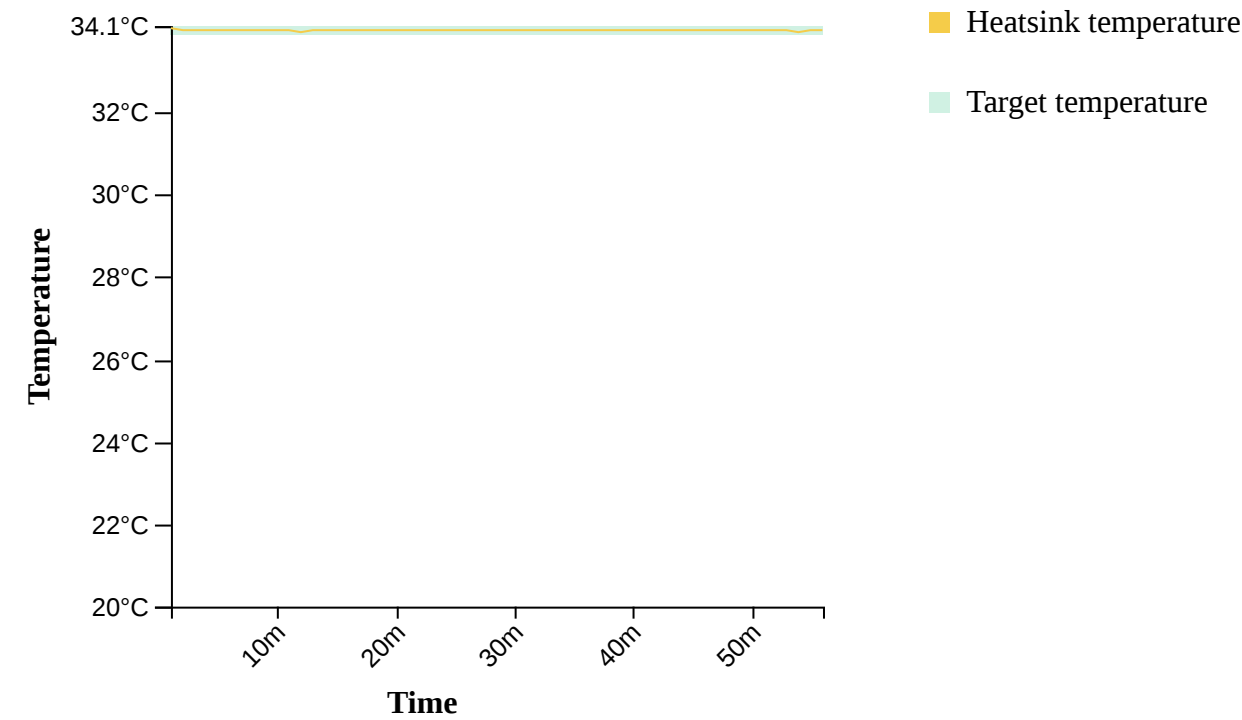
Bias Voltage History
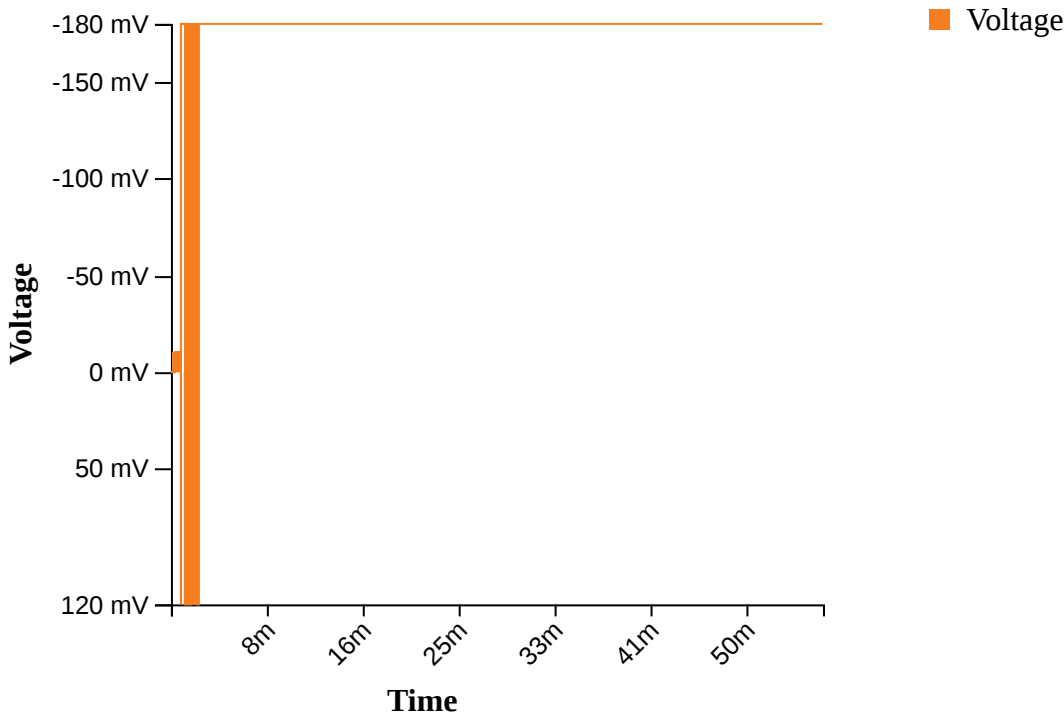
Translocation Speed
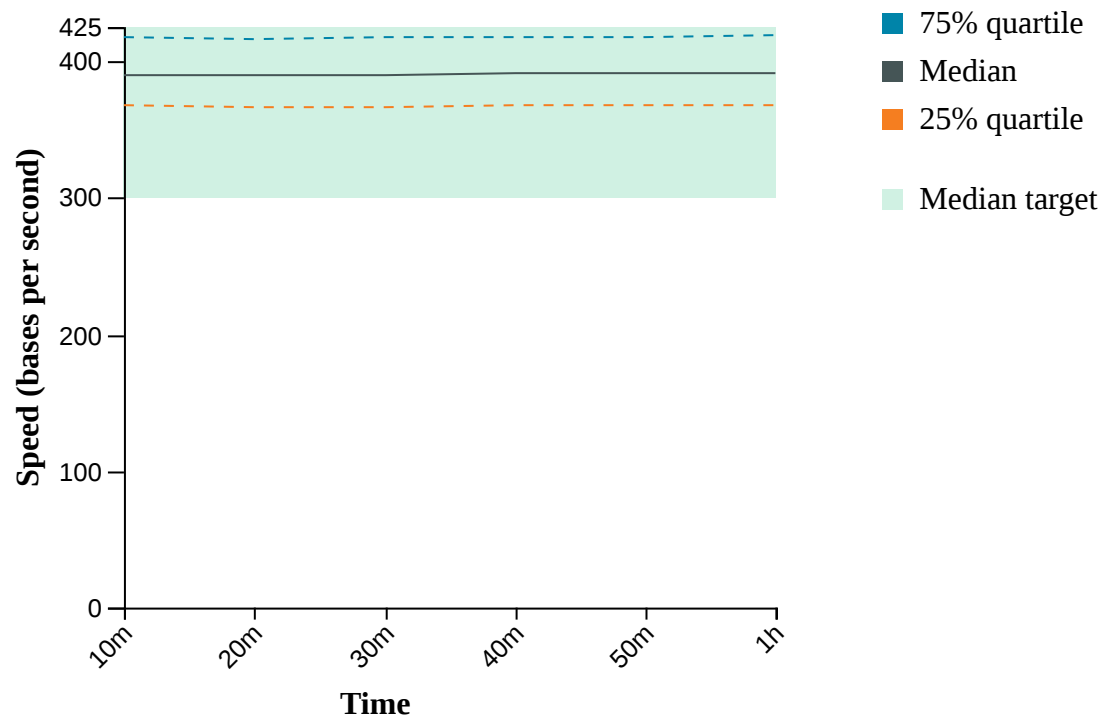
QScore

Disk Write Performance

Legend:
- Produced
- Written
- Held in memory

Y-axis: **Data Written** (0 B, 476.8 MB, 953.7 MB, 1.4 GB, 1.9 GB, 2.3 GB, 2.8 GB, 3.3 GB, 3.7 GB)

X-axis: **Time** (10m, 20m, 30m, 40m, 50m, 1h)
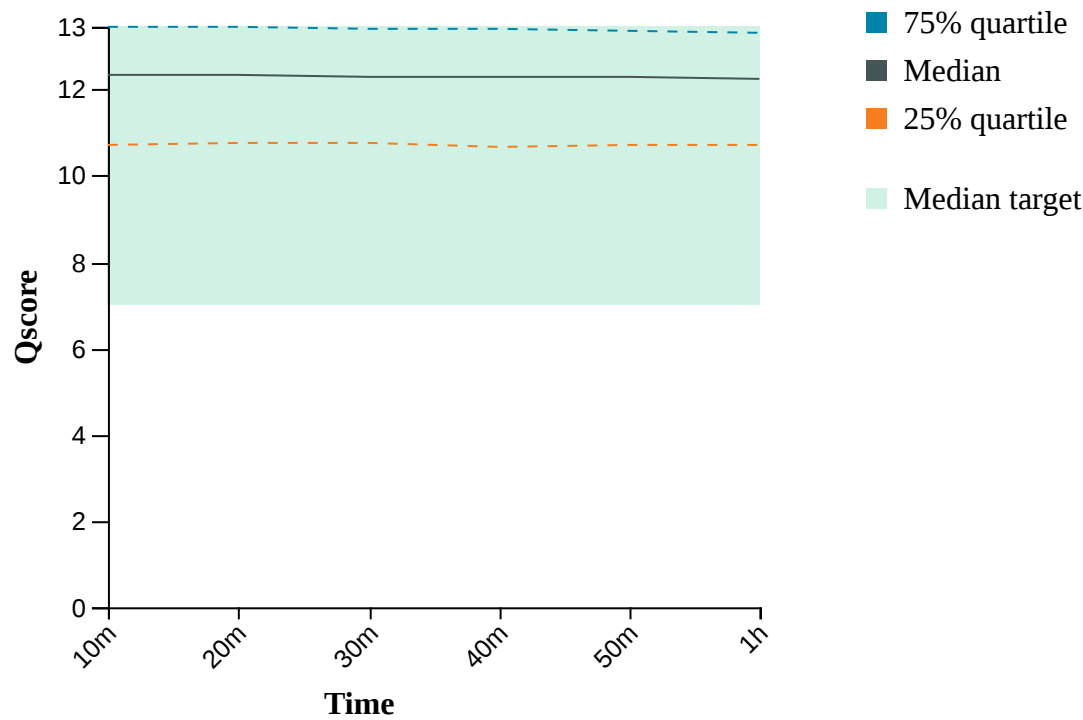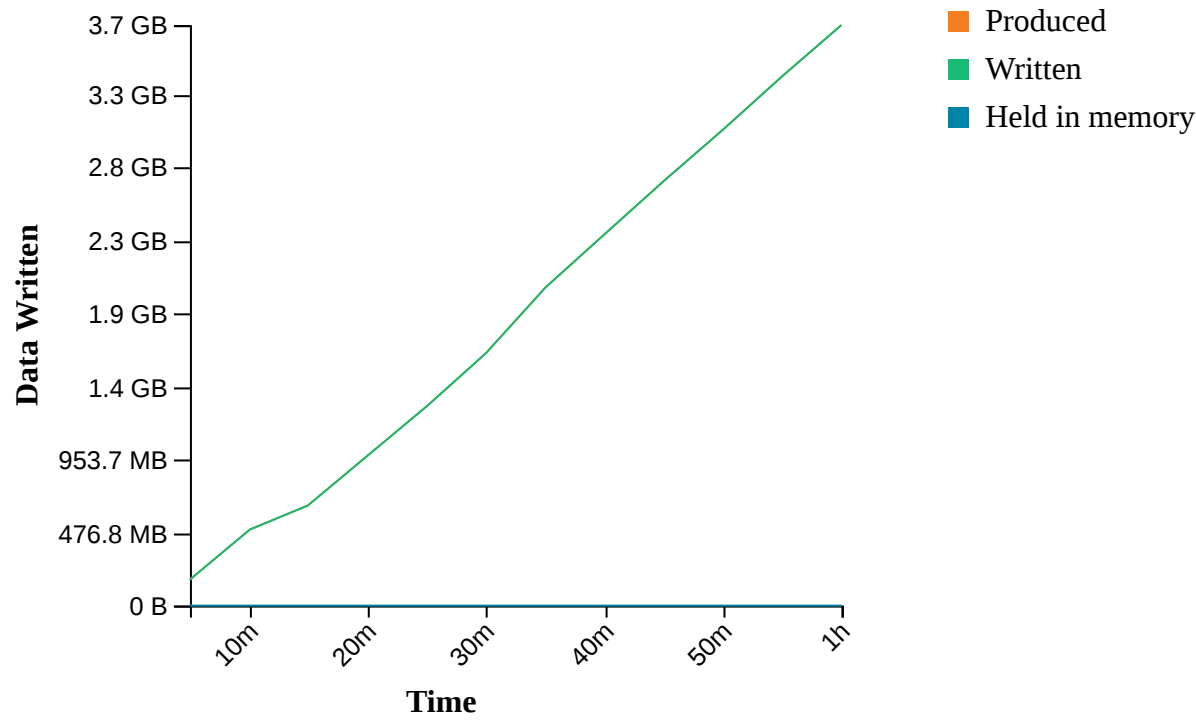
Run Debug Messages

- Mux scan for flow cell FAO54786 has found a total of 1046 pores. 483 pores available for immediate sequencing   January 4, 12:05
- Performing Mux Scan   January 4, 12:02
- Starting sequencing procedure   January 4, 12:02
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   January 4, 11:59