Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**EIMock_2kbp_PaeroginosaiRAD_050121**
Sample ID	**EIMock_2kbp_PaeroginosaiRAD_050121**
Run ID	**baecfb80-f232-4537-b708-1da759e35fb5**
Flow Cell Id	**FAO53362**
Start Time	**January 5, 17:02**
Run Length	**59m**

Run Summary

Reads Generated	**480.79 K**
Passed Bases	**209.83 Mb**
Failed Bases	**22.75 Mb**
Estimated Bases	**250.83 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**
Read Until	**reference_files= ["/data/references/P_aeruginosa_ref.fasta"],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**

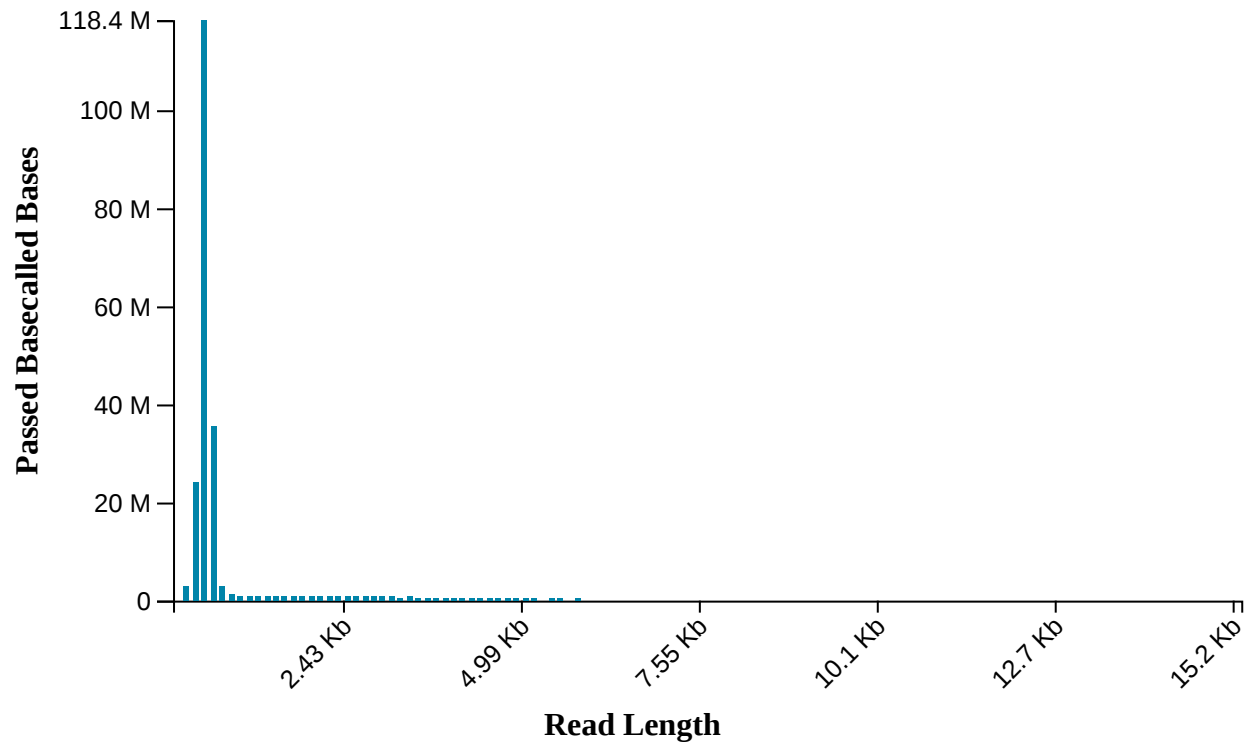## Cumulative Output Reads
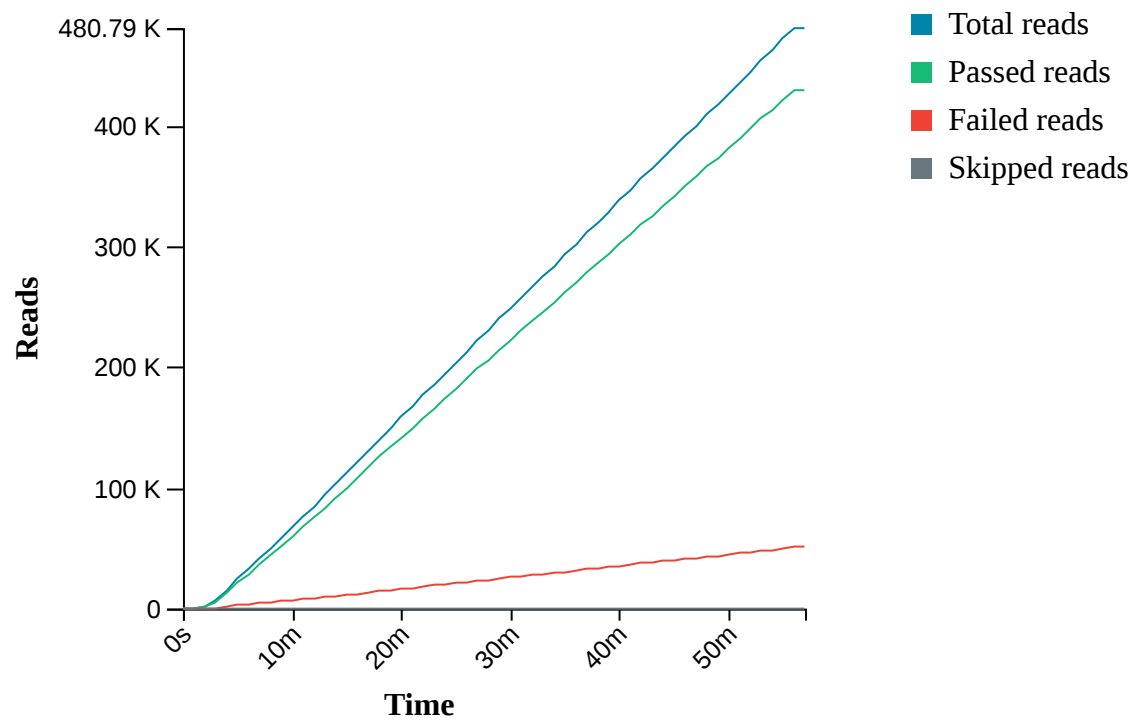
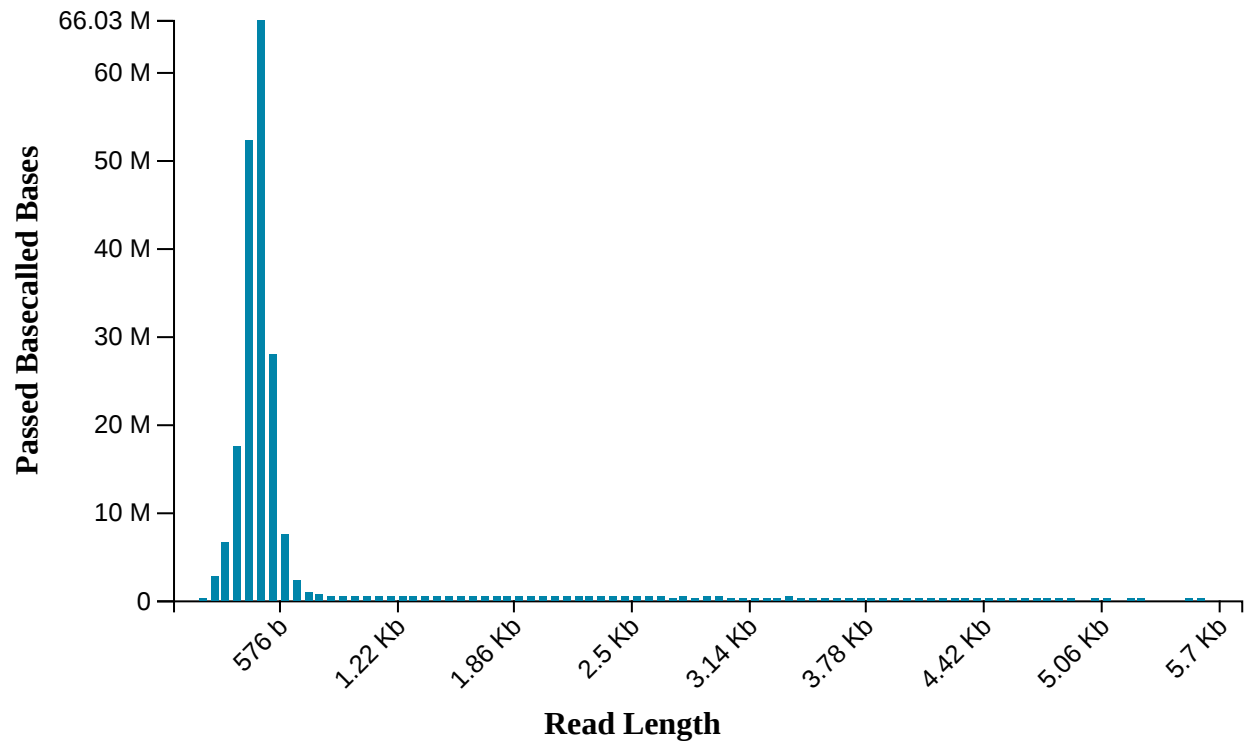## Cumulative Output Bases
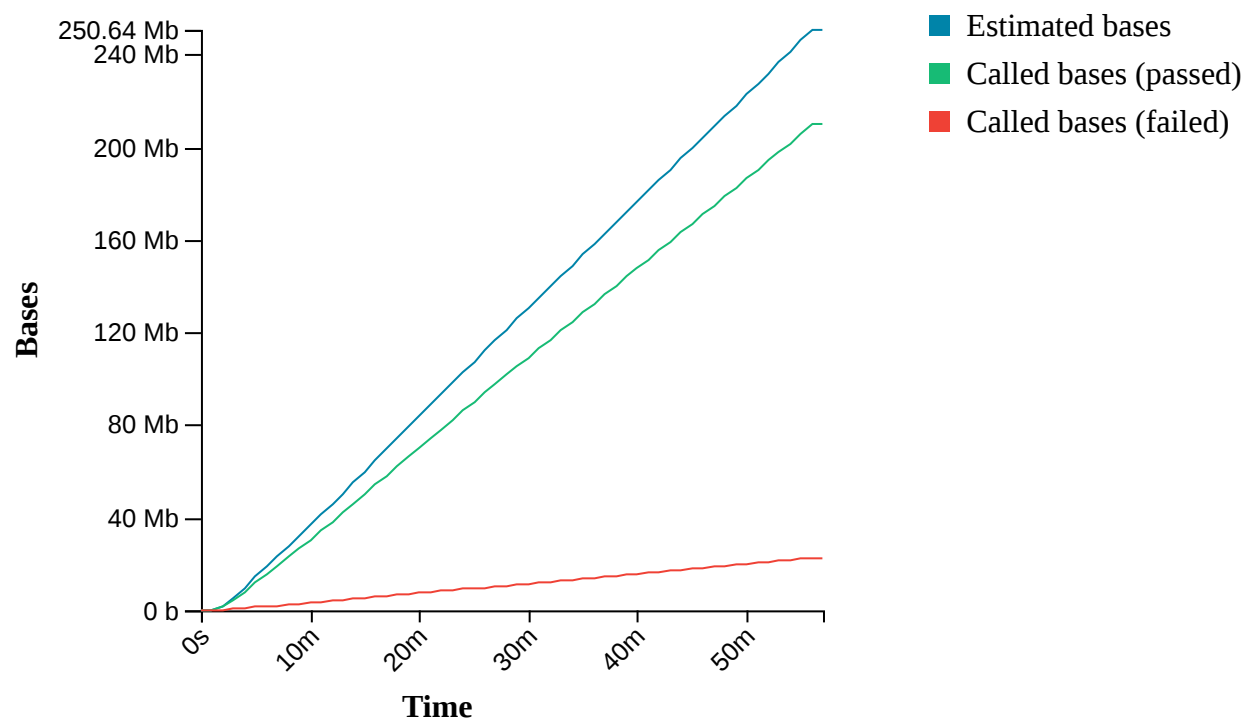
Read Length Histogram Estimated Bases - Outliers Discarded

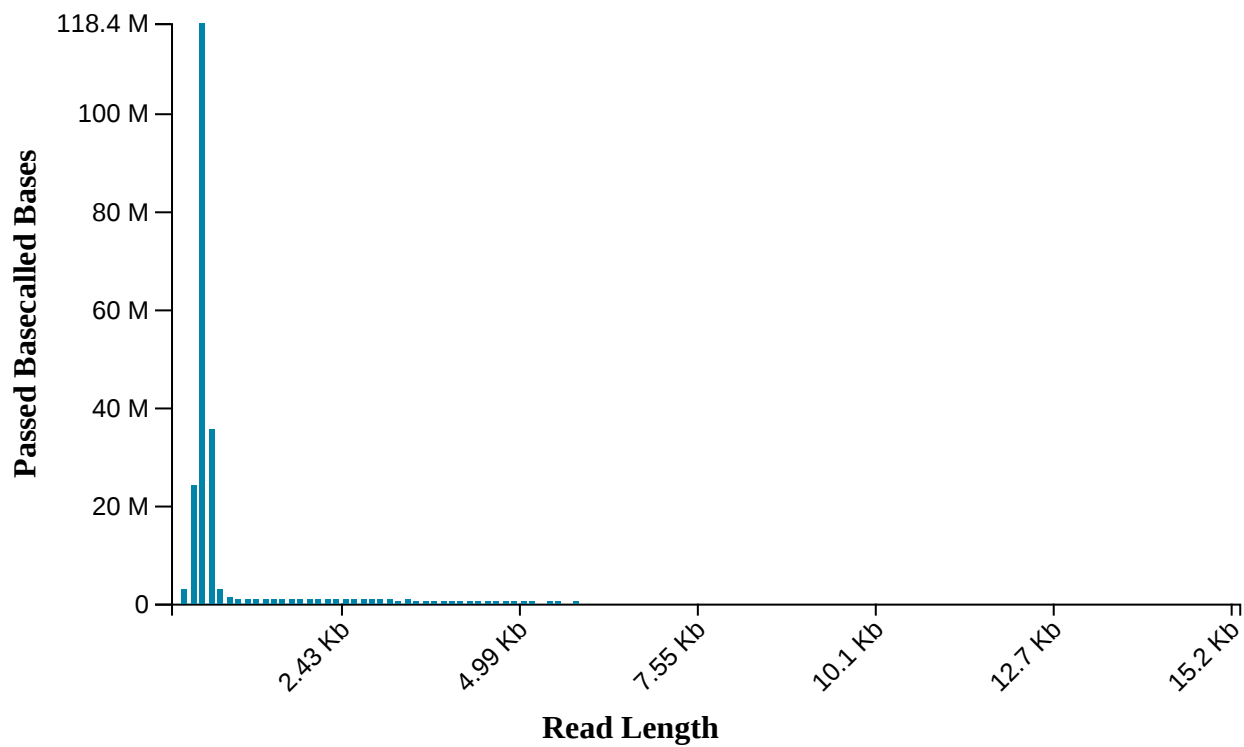Estimated N50: 470

Read Length Histogram Basecalled Bases - Outliers Discarded
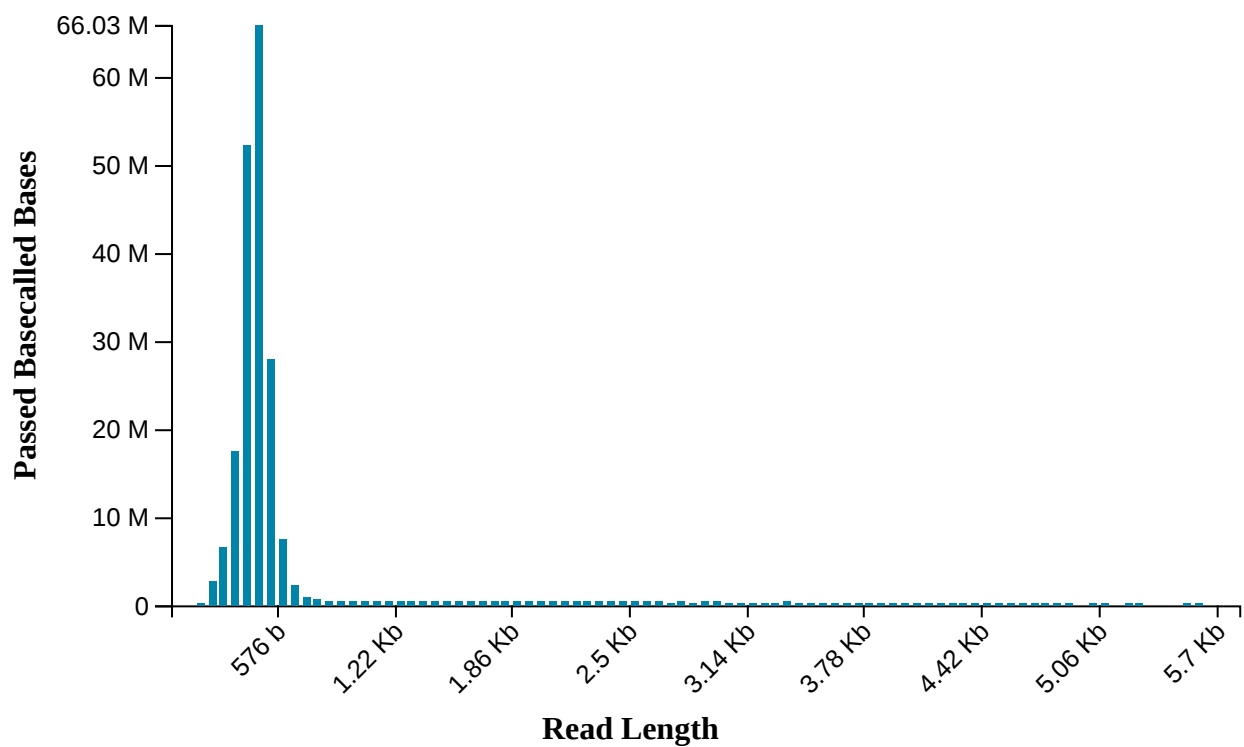
Estimated N50: 469

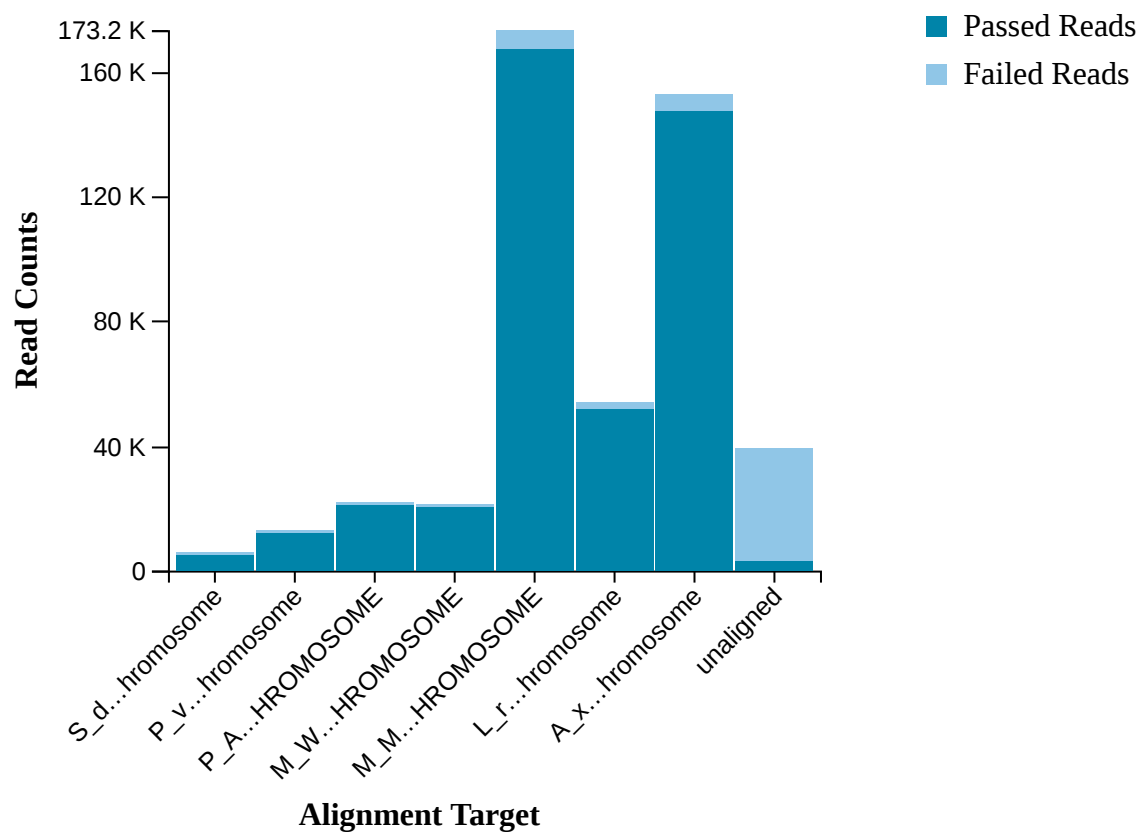## Read Length Histogram Estimated Bases

Estimated N50: 470

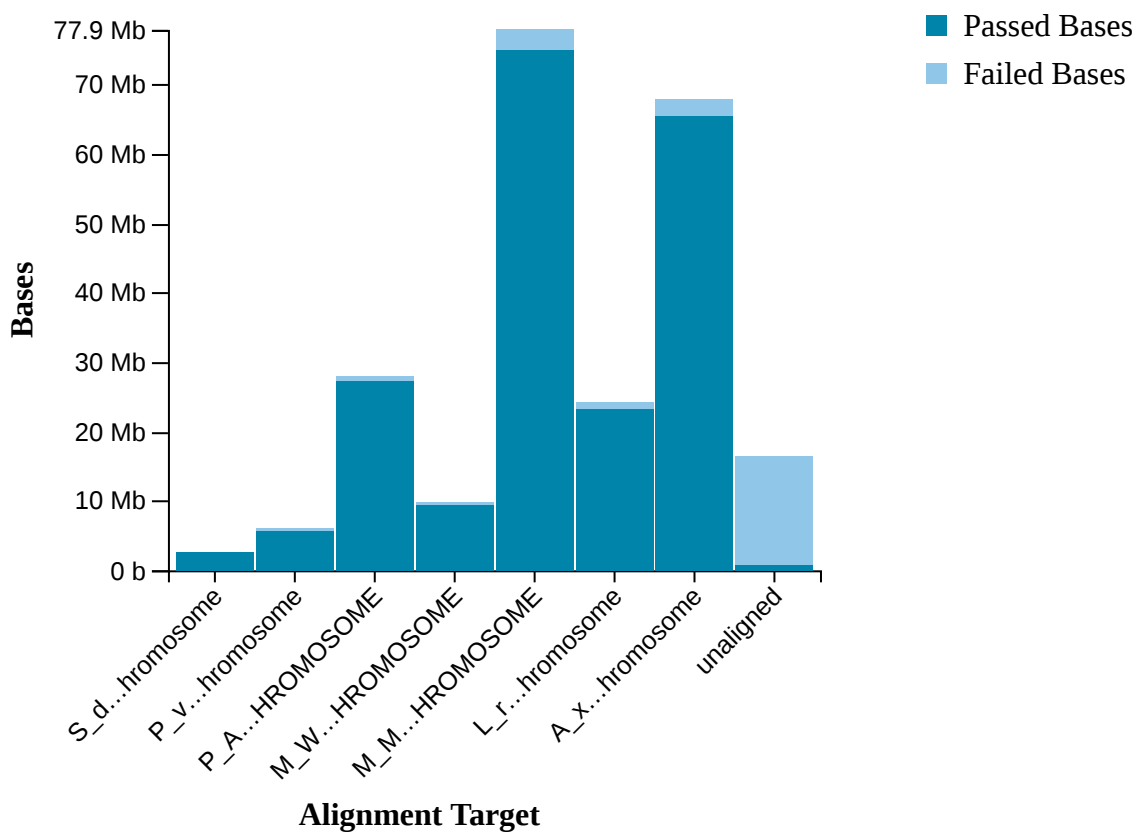

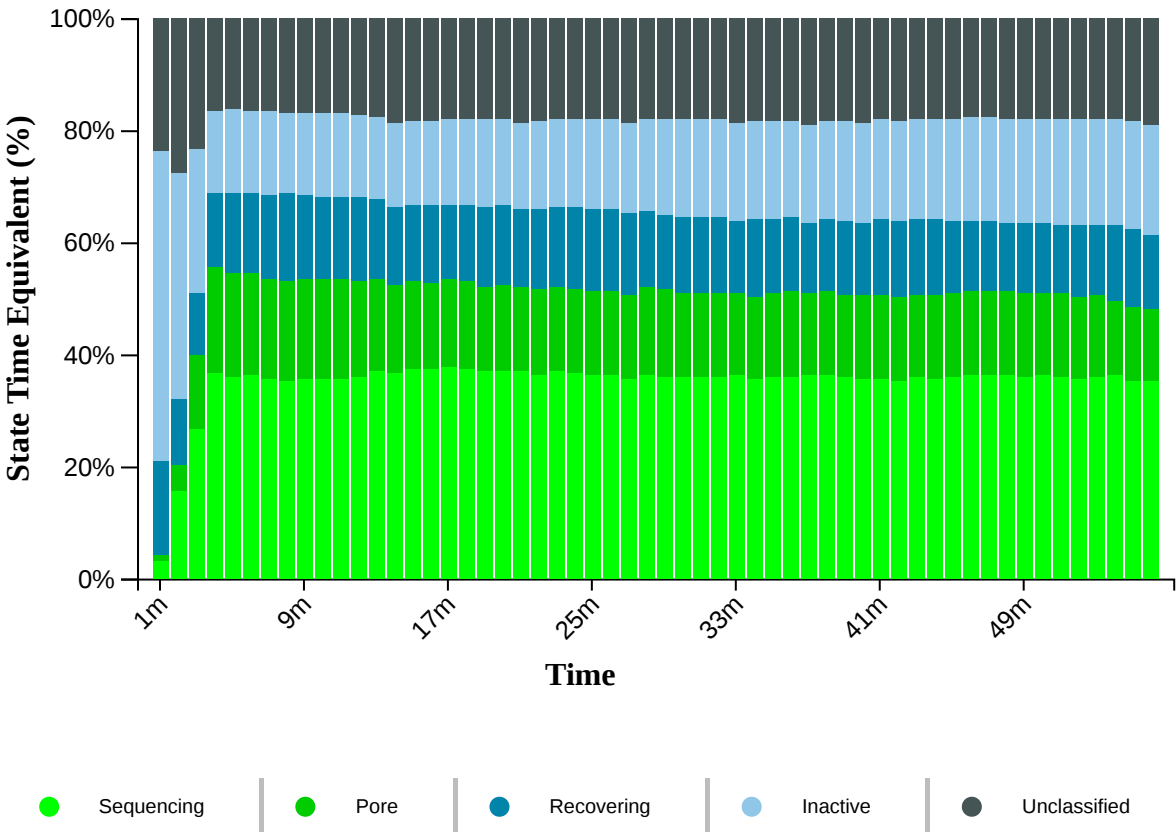## Read Length Histogram Basecalled Bases

Estimated N50: 469

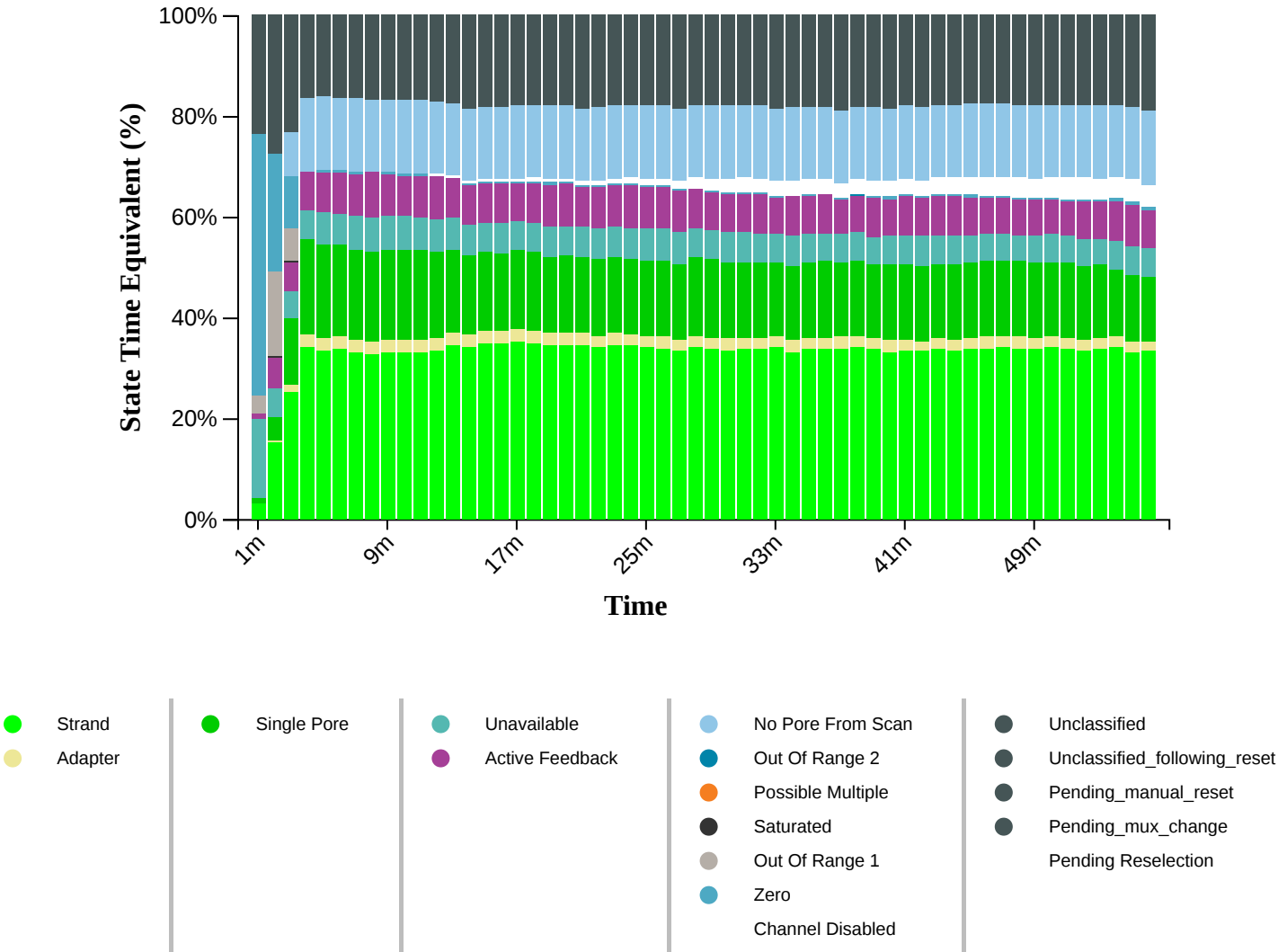## Alignment Target Hits (reads)

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

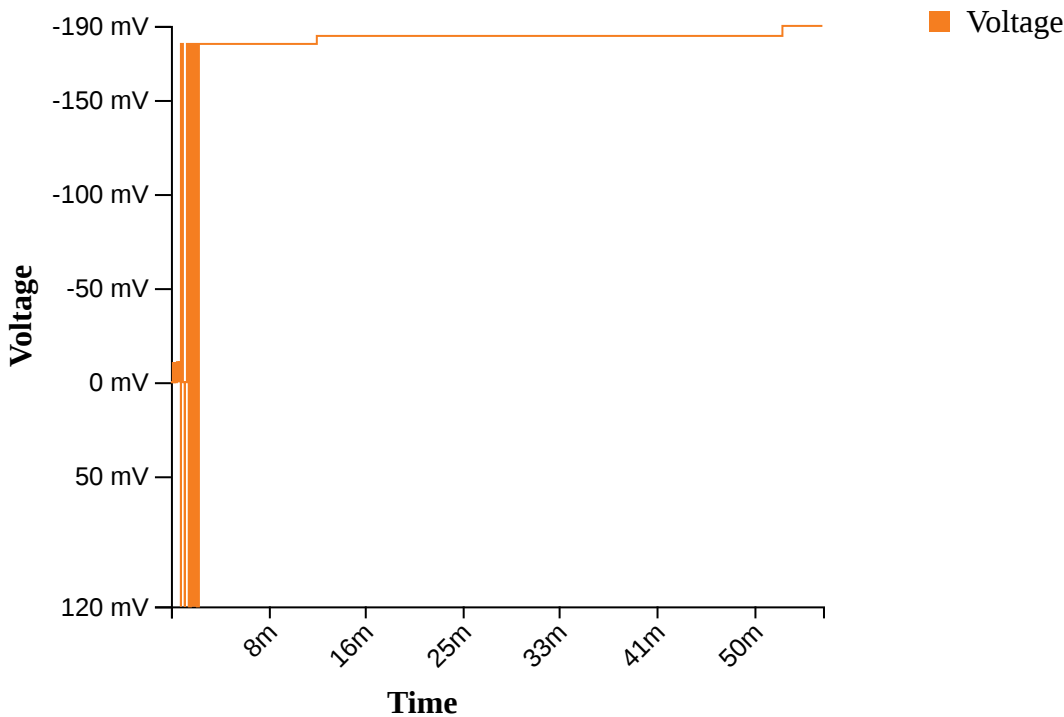Single Pore   Reserved Pore   Unavailable   Multiple   Saturated   Zero   Other
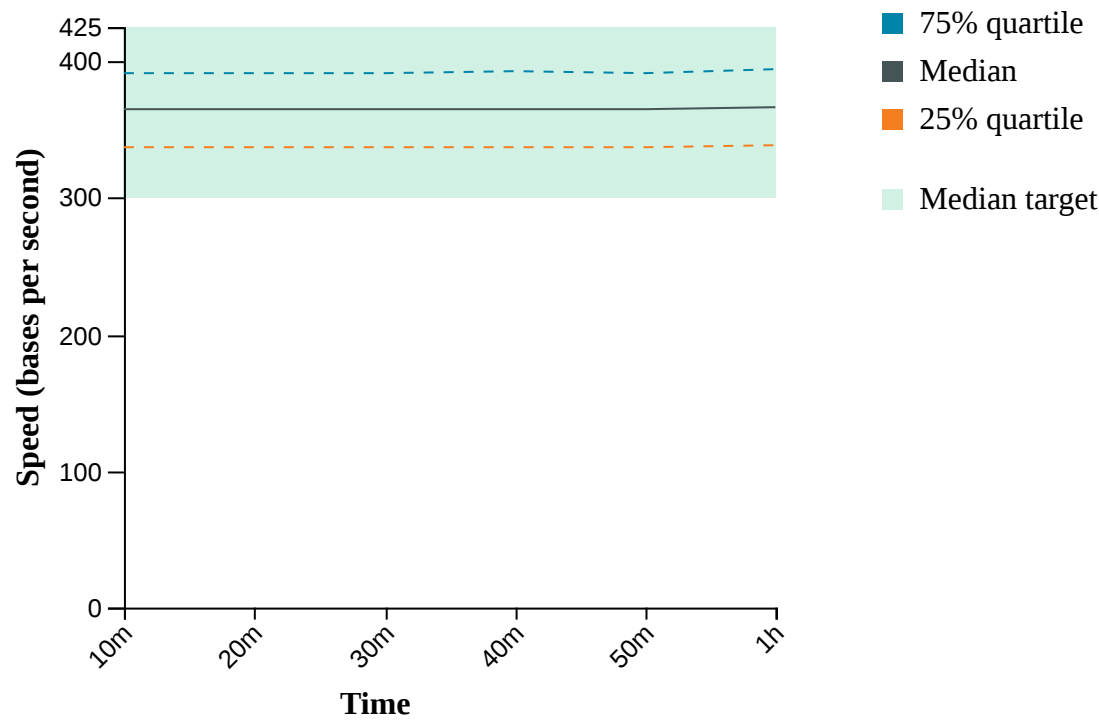
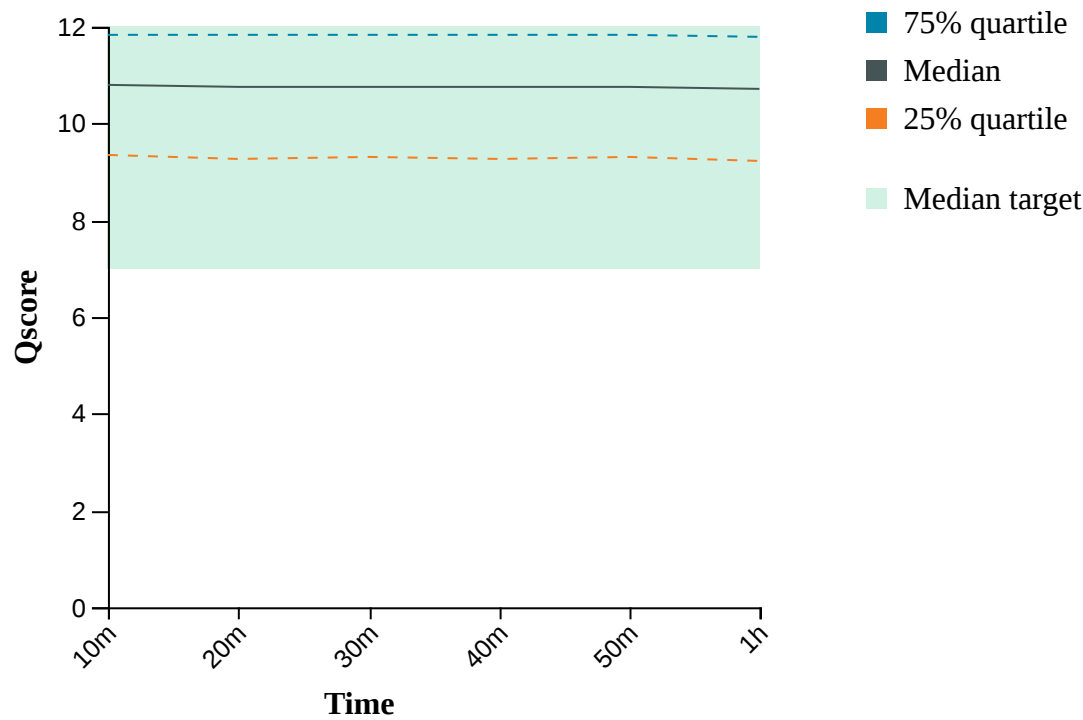## Temperature History
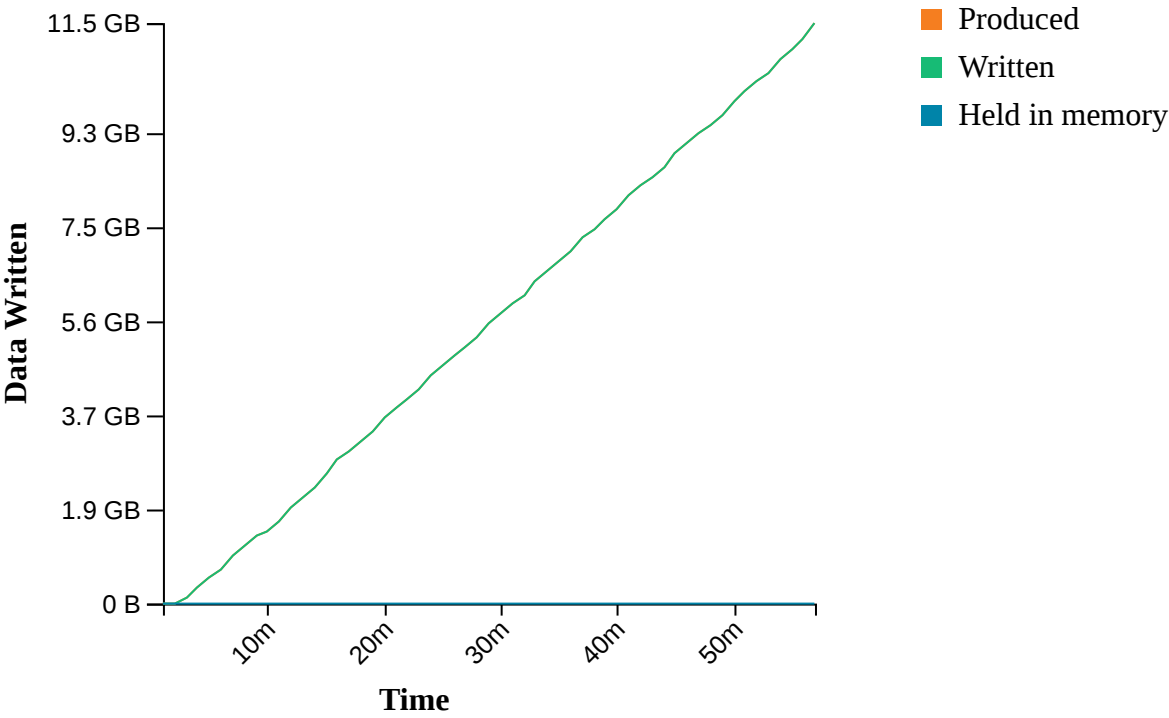

Bias Voltage History

Translocation Speed

QScore

<u>Disk Write Performance</u>

Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 888 pores. 438 pores available for immediate sequencing   January 5, 17:08
- Performing Mux Scan   January 5, 17:06
- Starting sequencing procedure   January 5, 17:06
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   January 5, 17:02