Run Info

Host Name	**GXB01190 (localhost)**
Experiment Name	**EIMock_2kbp_SdysgalactiaeRAD_050121**
Sample ID	**EIMock_2kbp_SdysgalactiaeRAD_050121**
Run ID	**cc90cc4b-49e9-43bd-8d9f-7af6314f7bd4**
Flow Cell Id	**FAO53362**
Start Time	**January 5, 20:07**
Run Length	**59m**

Run Summary

Reads Generated	**432.83 K**
Passed Bases	**171.02 Mb**
Failed Bases	**24.81 Mb**
Estimated Bases	**211.92 Mb**

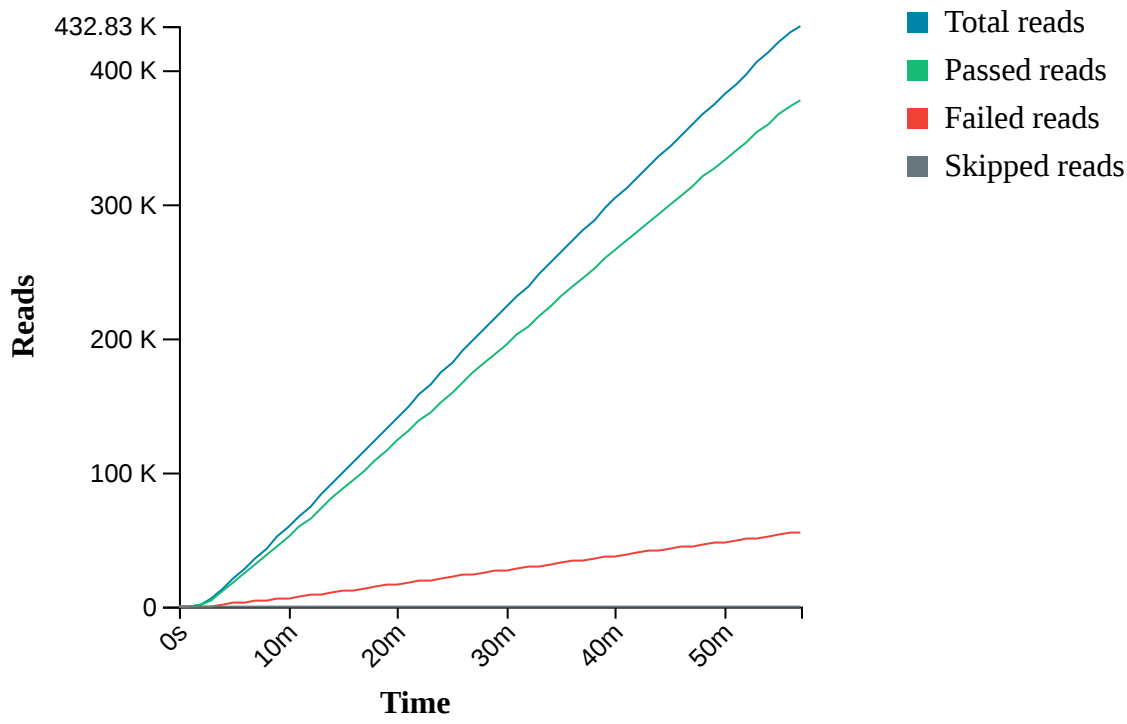
Run Parameters

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/S_dysgalactiae_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**

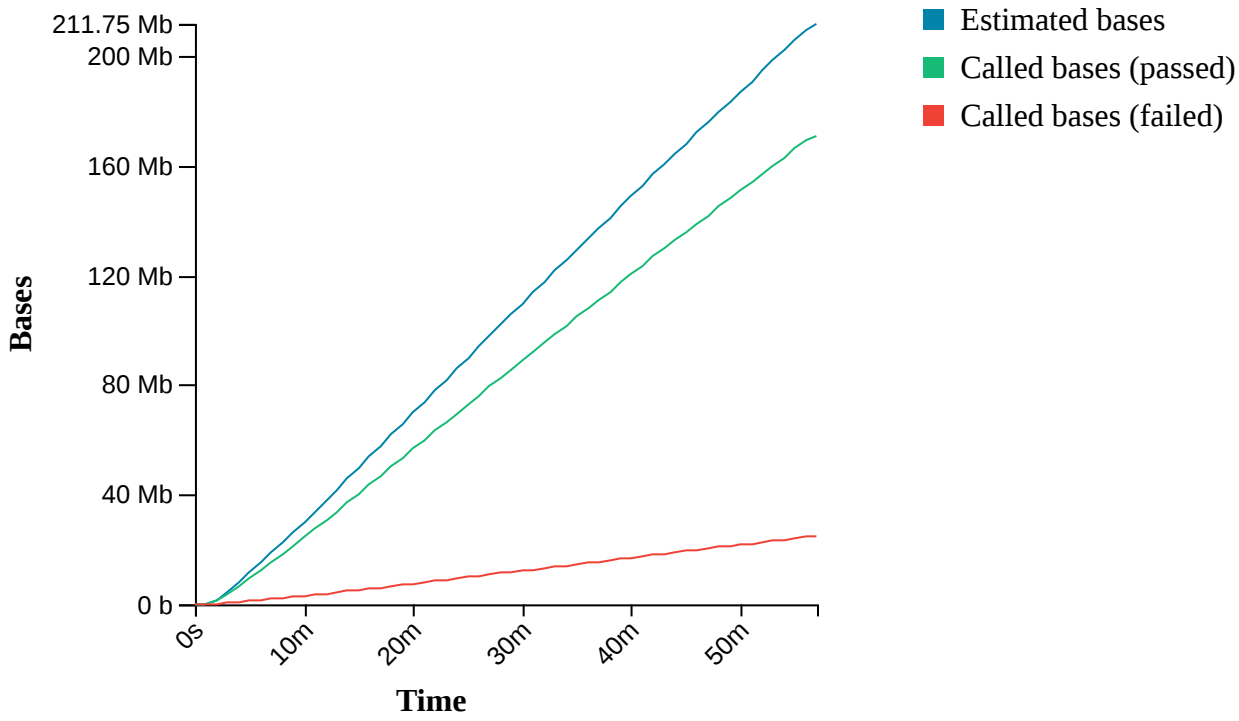
Versions

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

Cumulative Output Reads

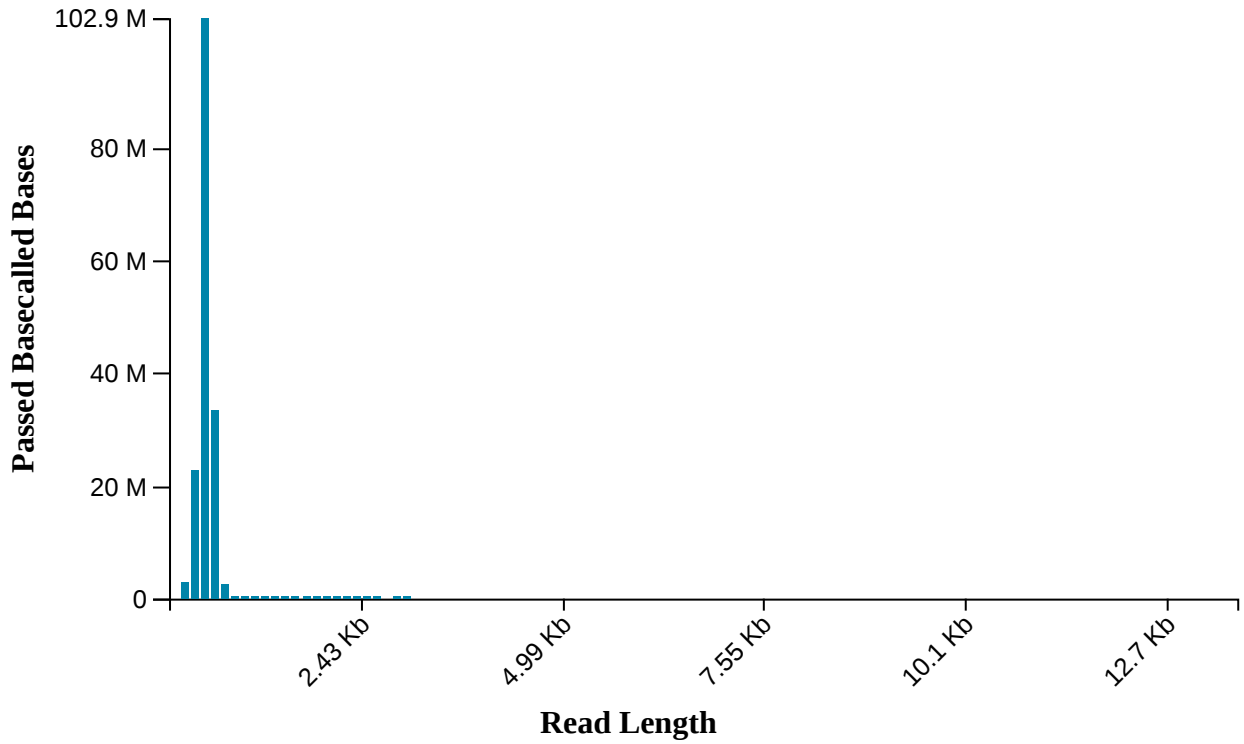


Cumulative Output Bases



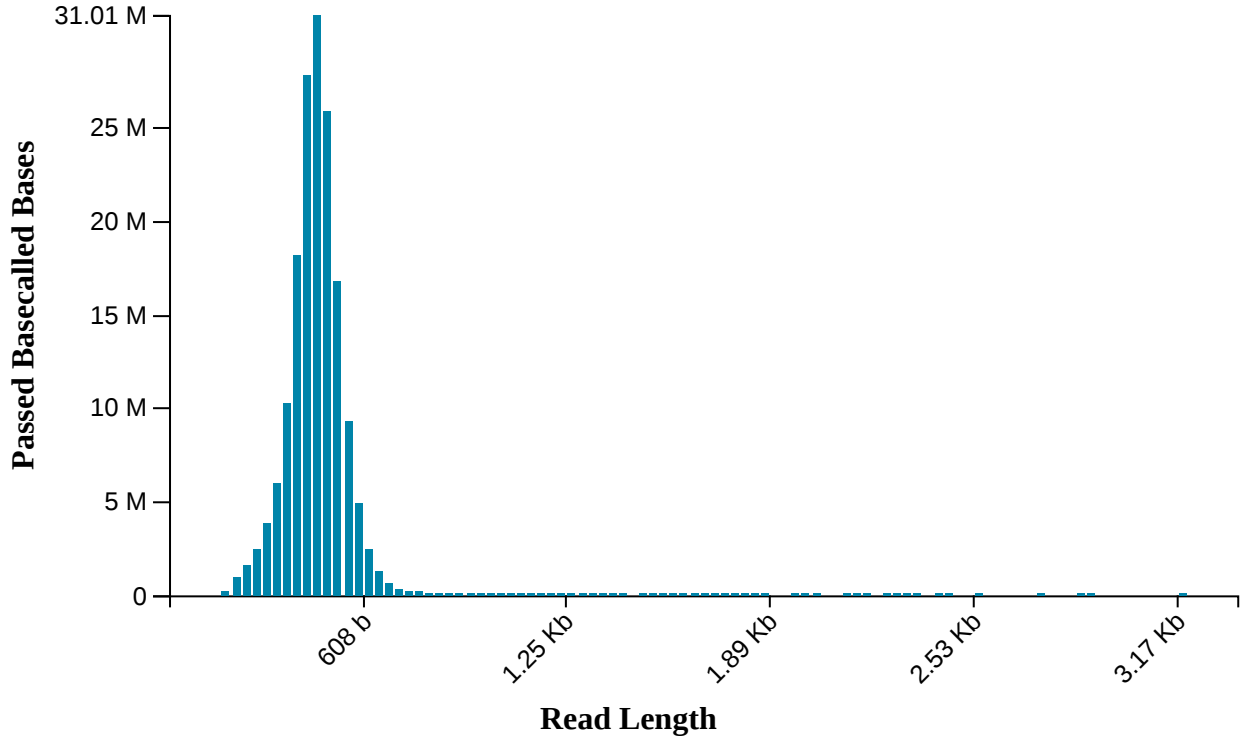
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 462



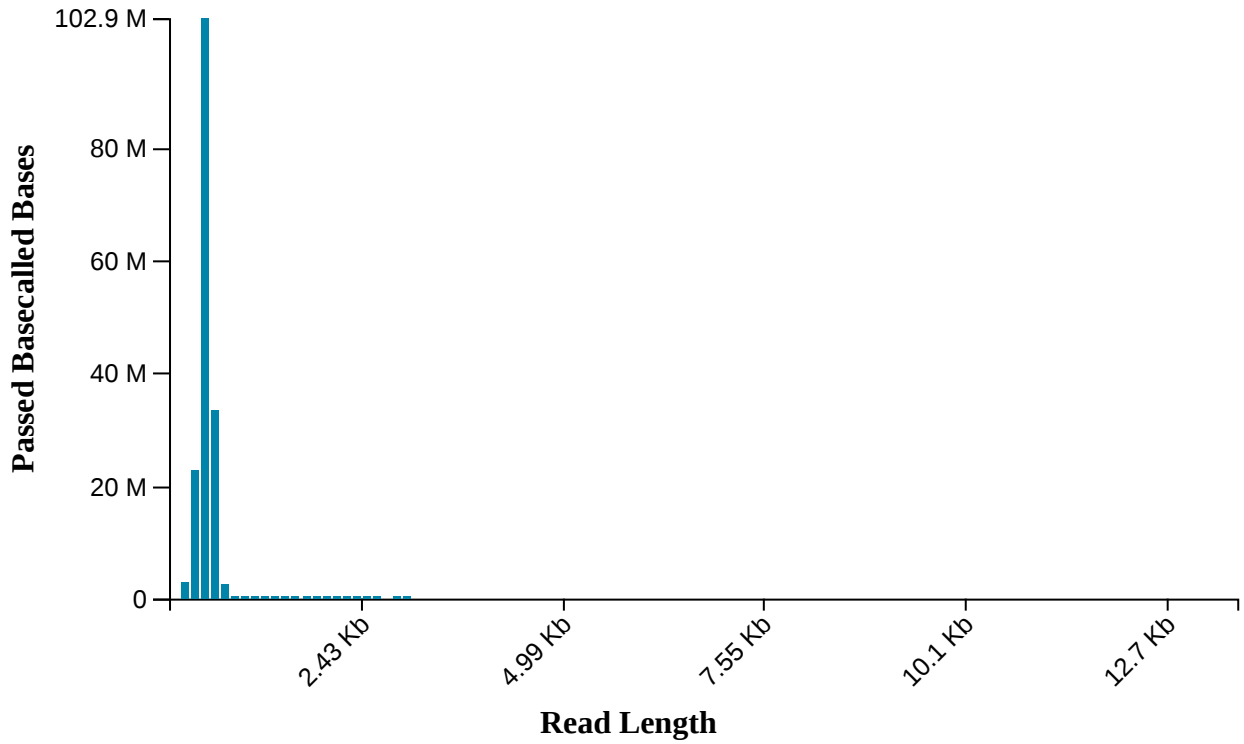
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 461



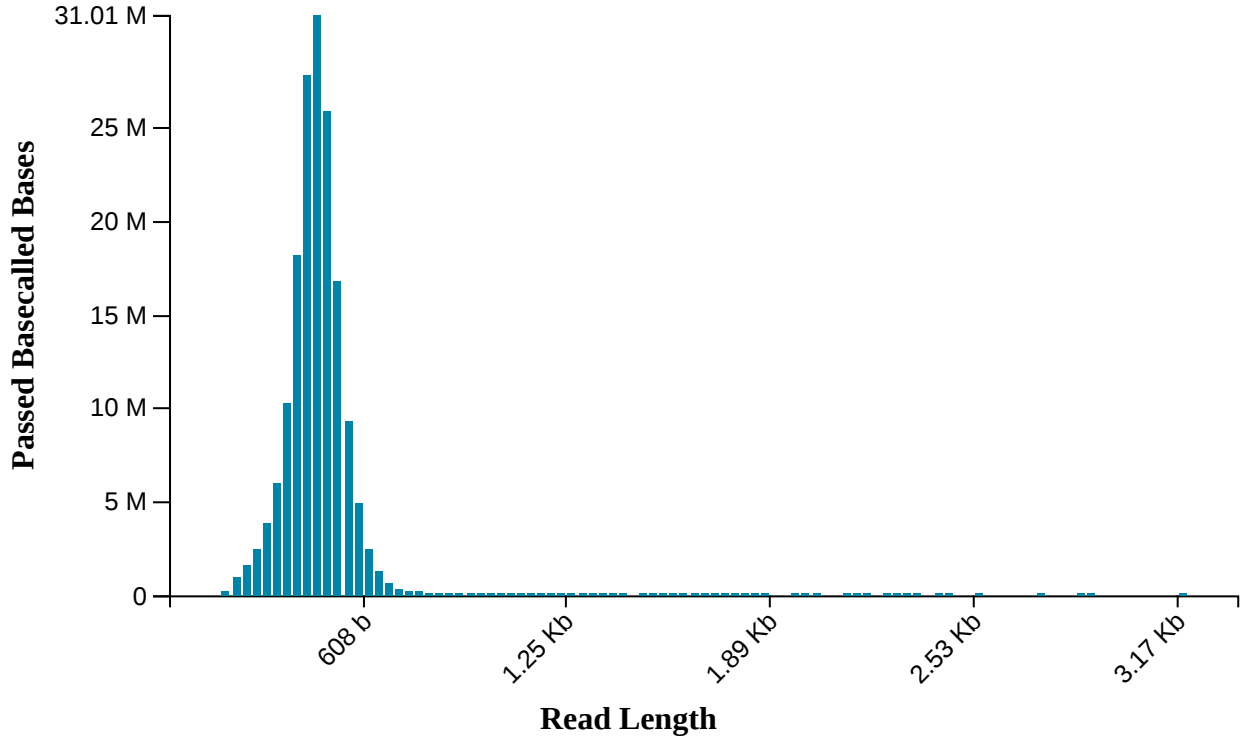
Read Length Histogram Estimated Bases

Estimated N50: 462

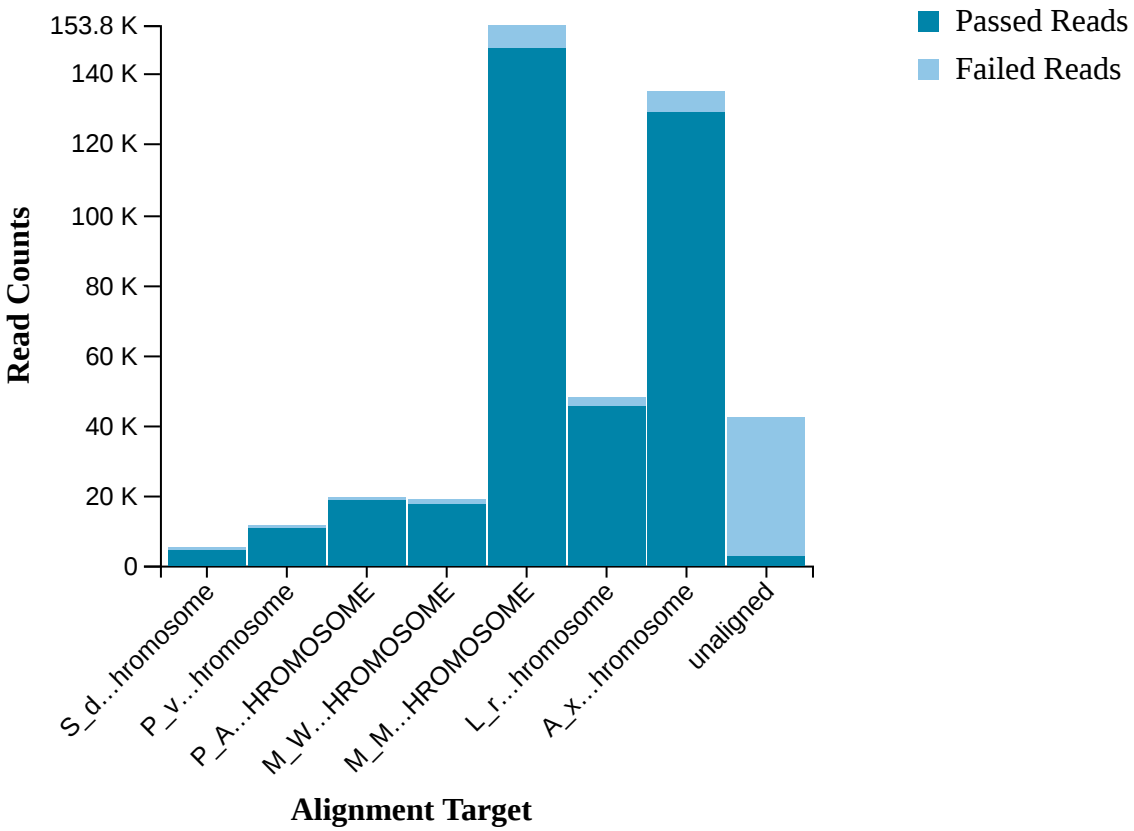


Read Length Histogram Basecalled Bases

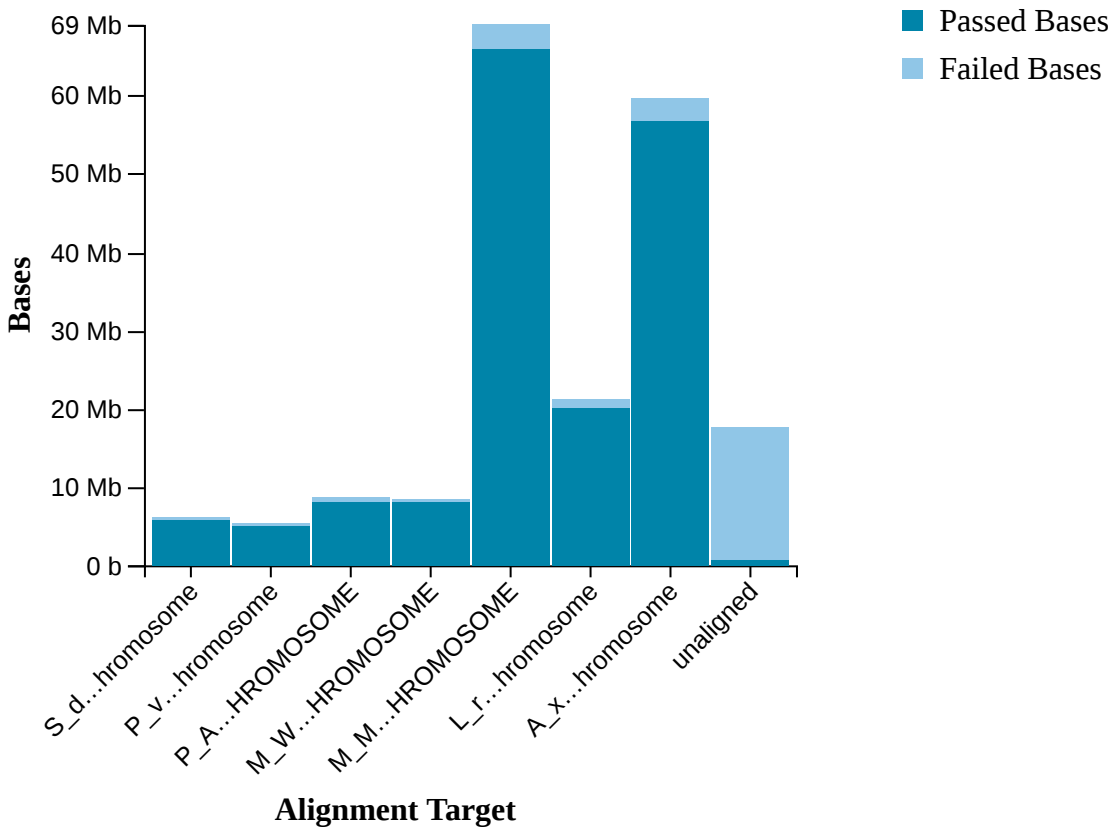
Estimated N50: 461



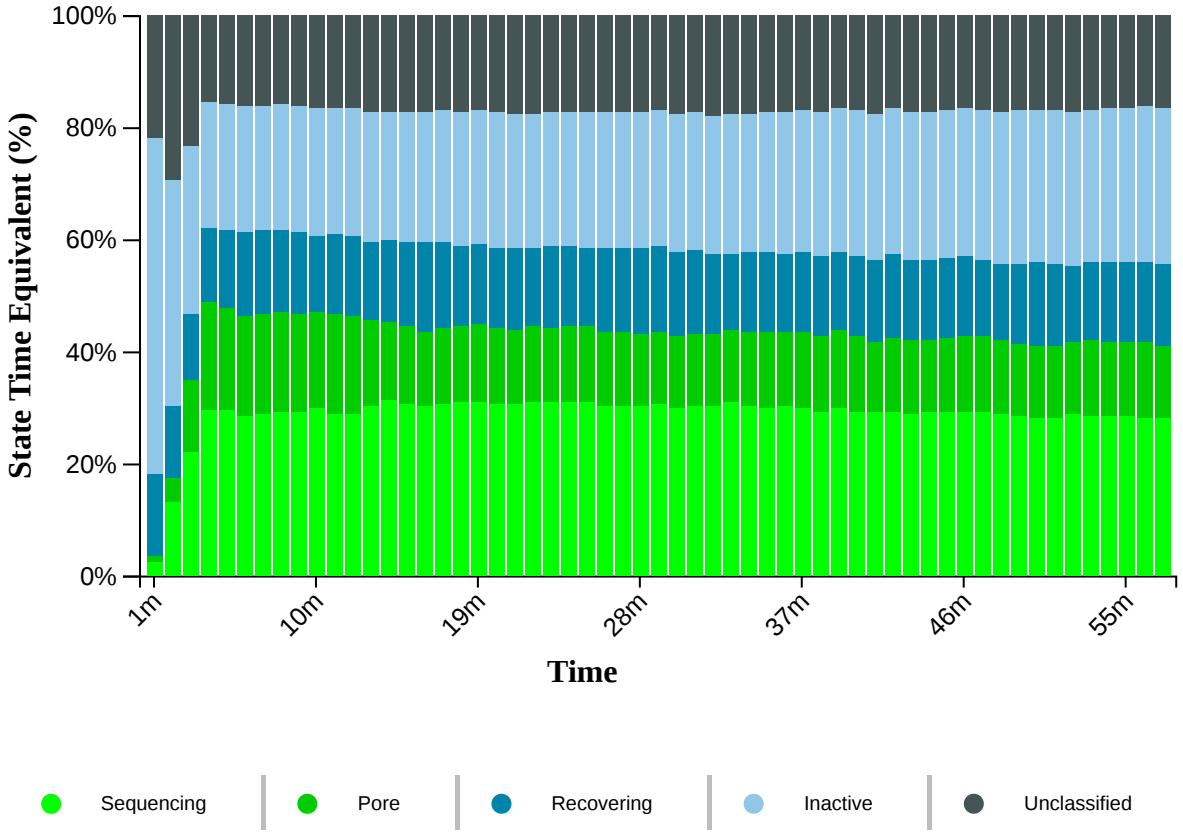
Alignment Target Hits (reads)



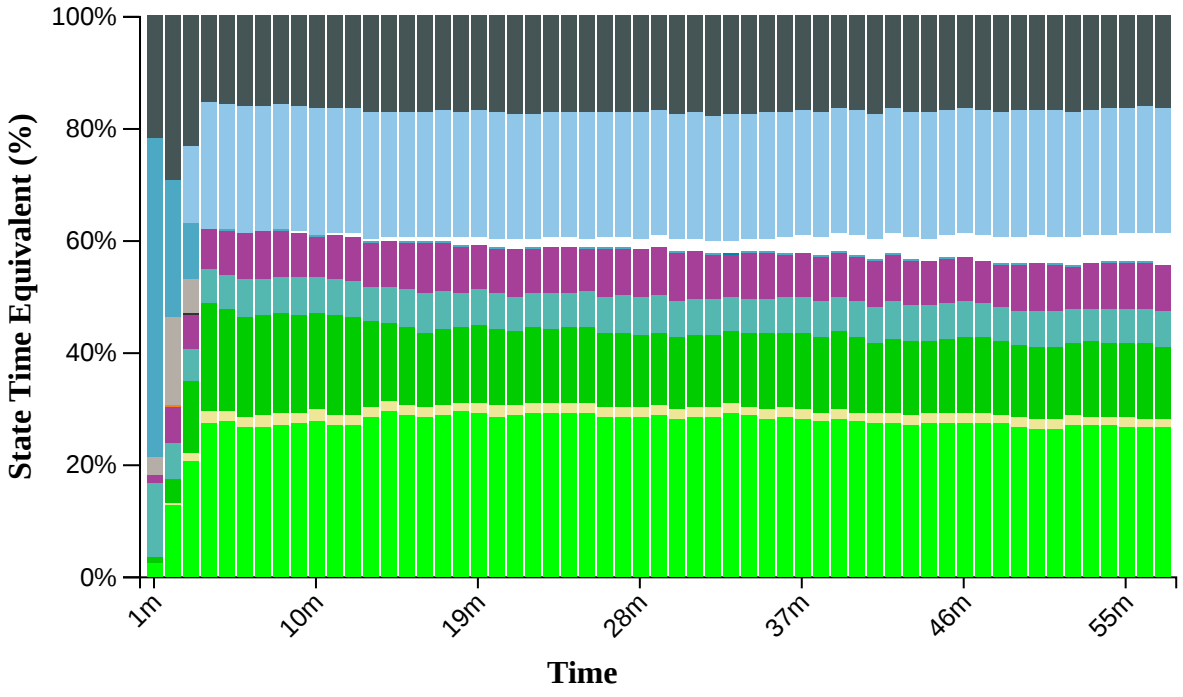
Alignment Target Hits (bases)



Duty Time Grouped



Duty time Categorised



Strand
Adapter

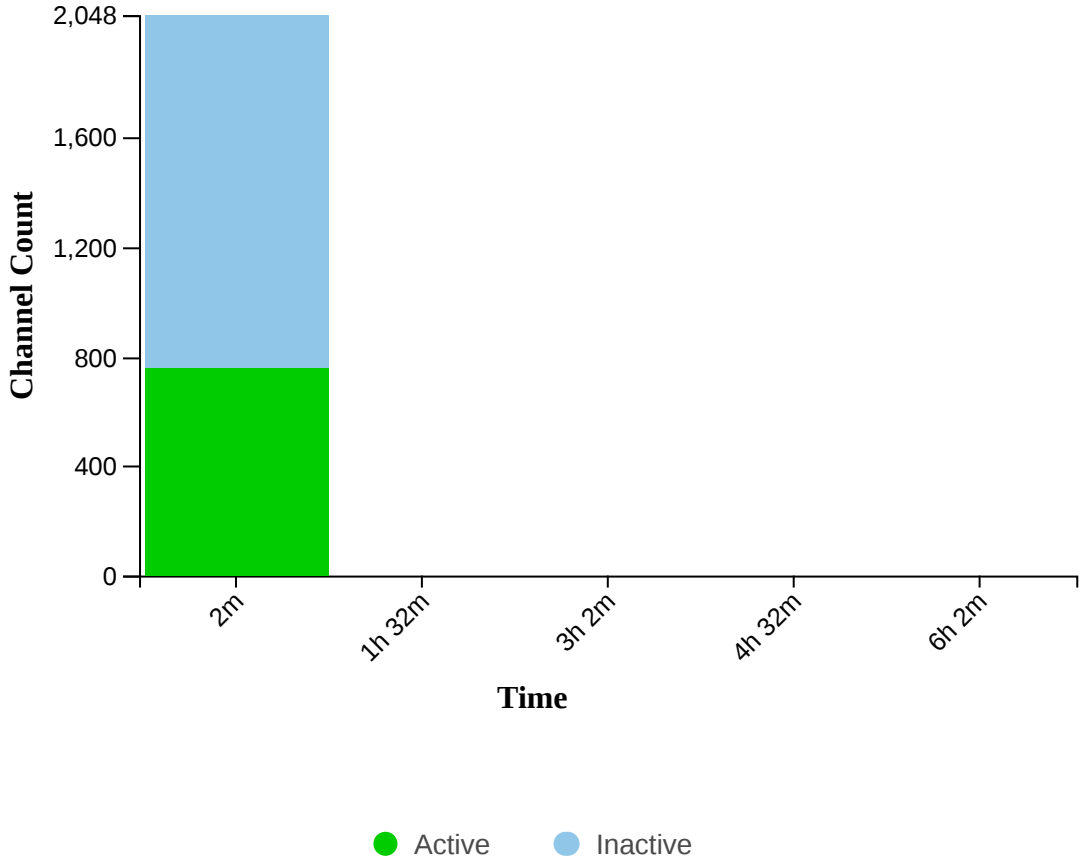
Single Pore

Unavailable
Active Feedback

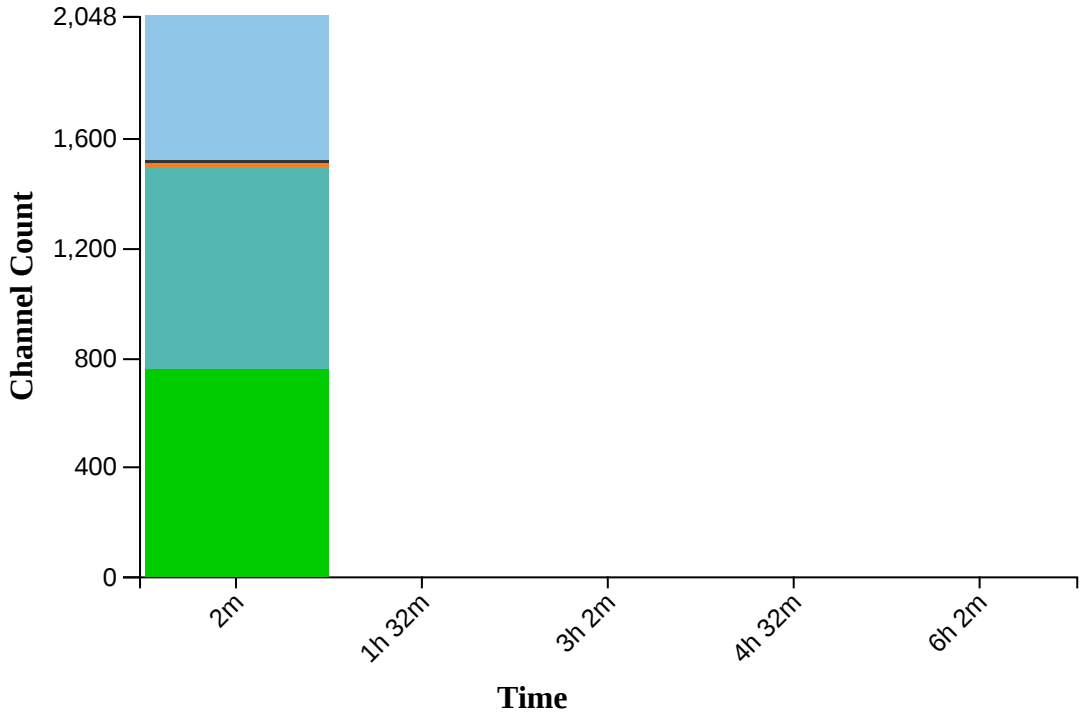
No Pore From Scan
Out Of Range 2
Possible Multiple
Saturated
Out Of Range 1
Zero
Channel Disabled

Unclassified
Unclassified_following_reset
Pending_manual_reset
Pending_mux_change
Pending Reselection

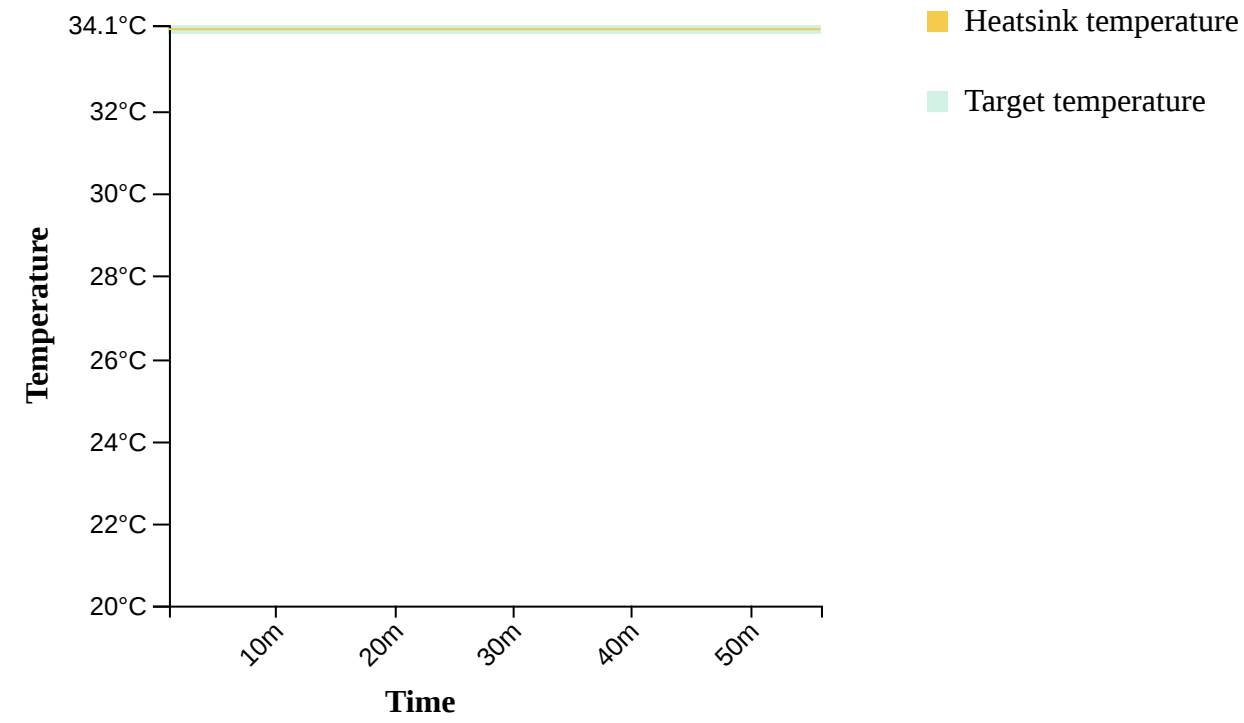
Mux Scan Grouped



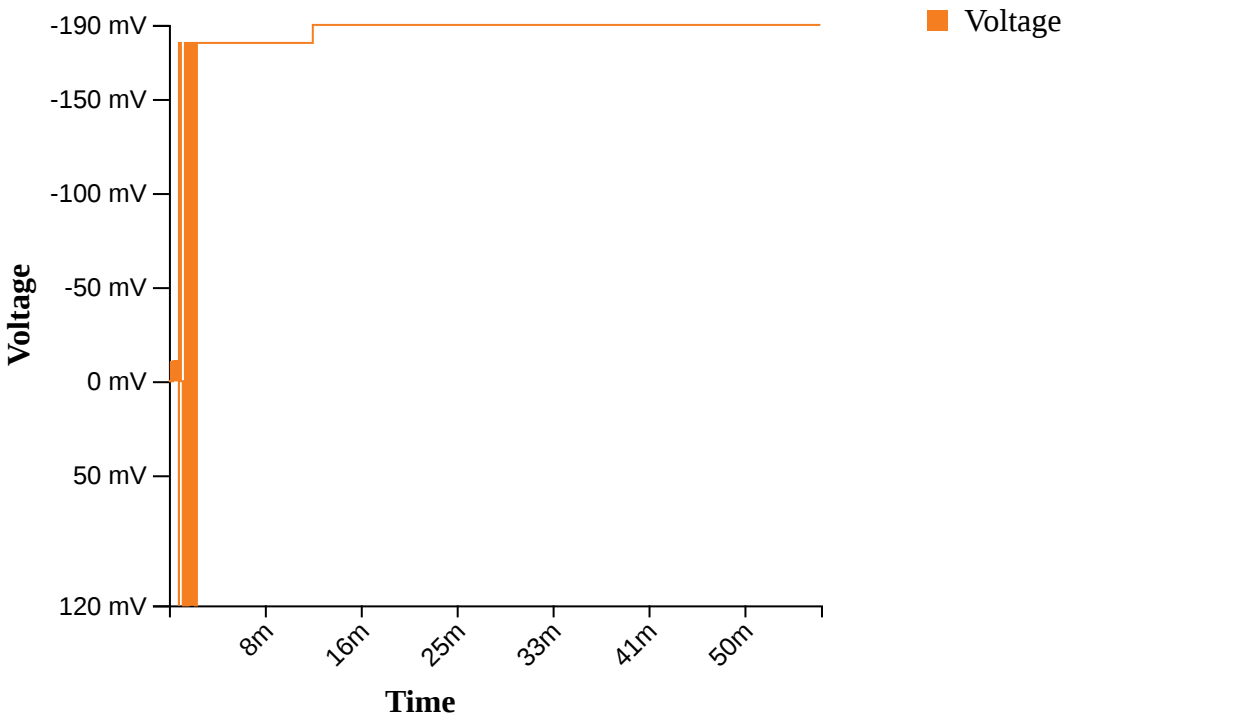
Mux Scan Categorised



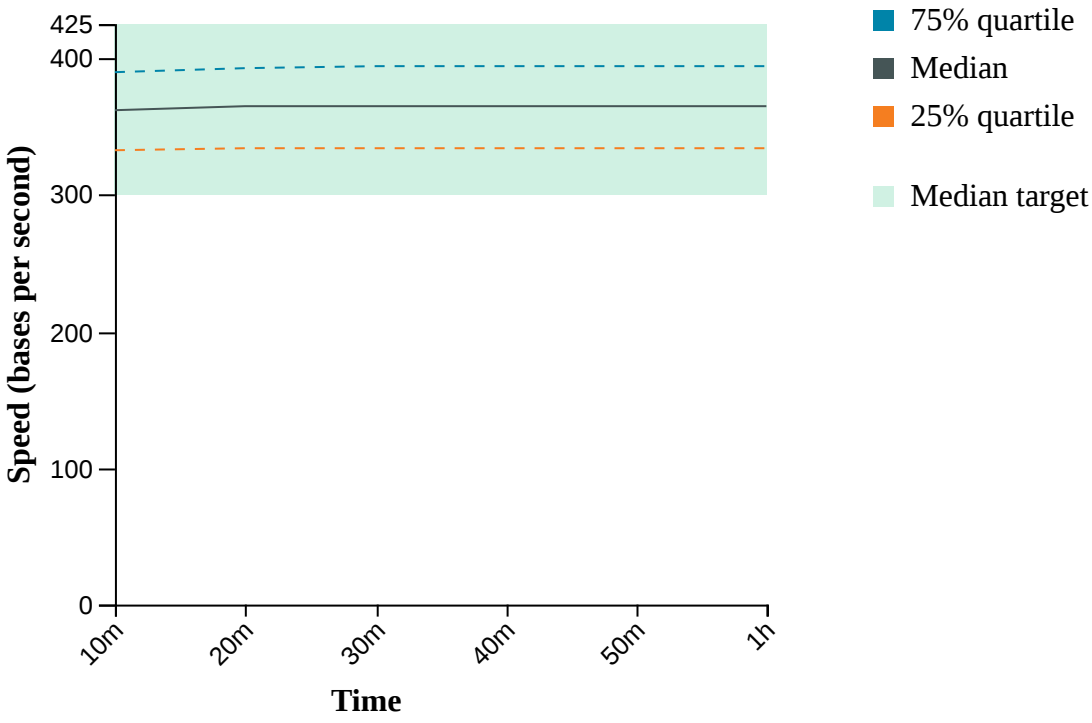
Temperature History



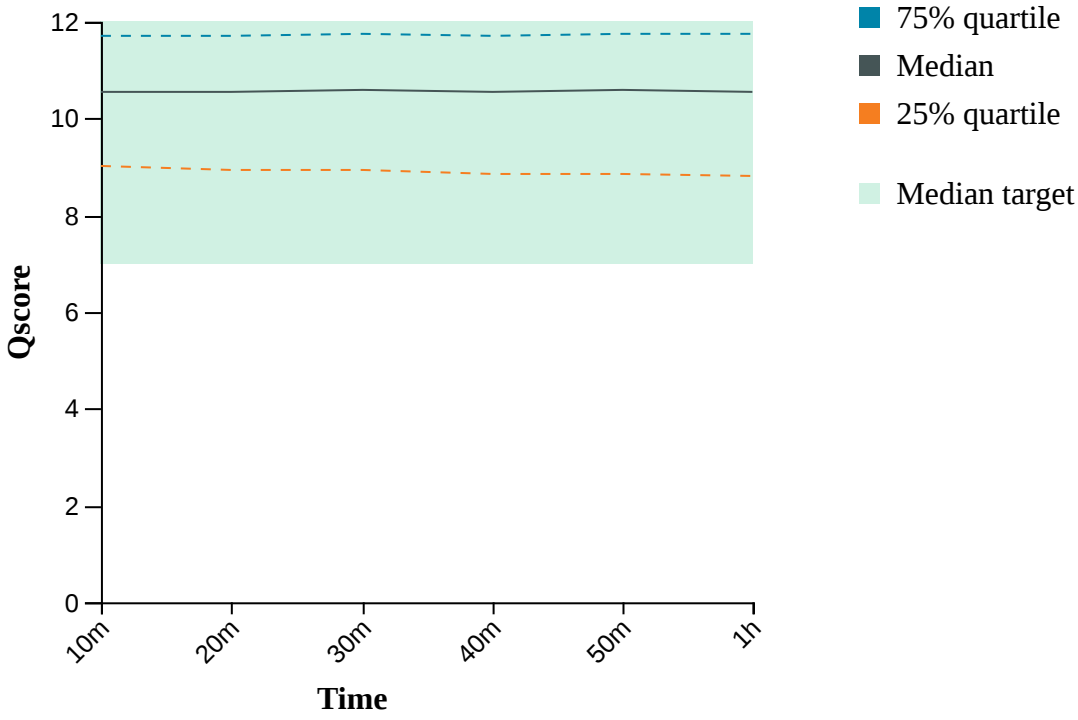
Bias Voltage History



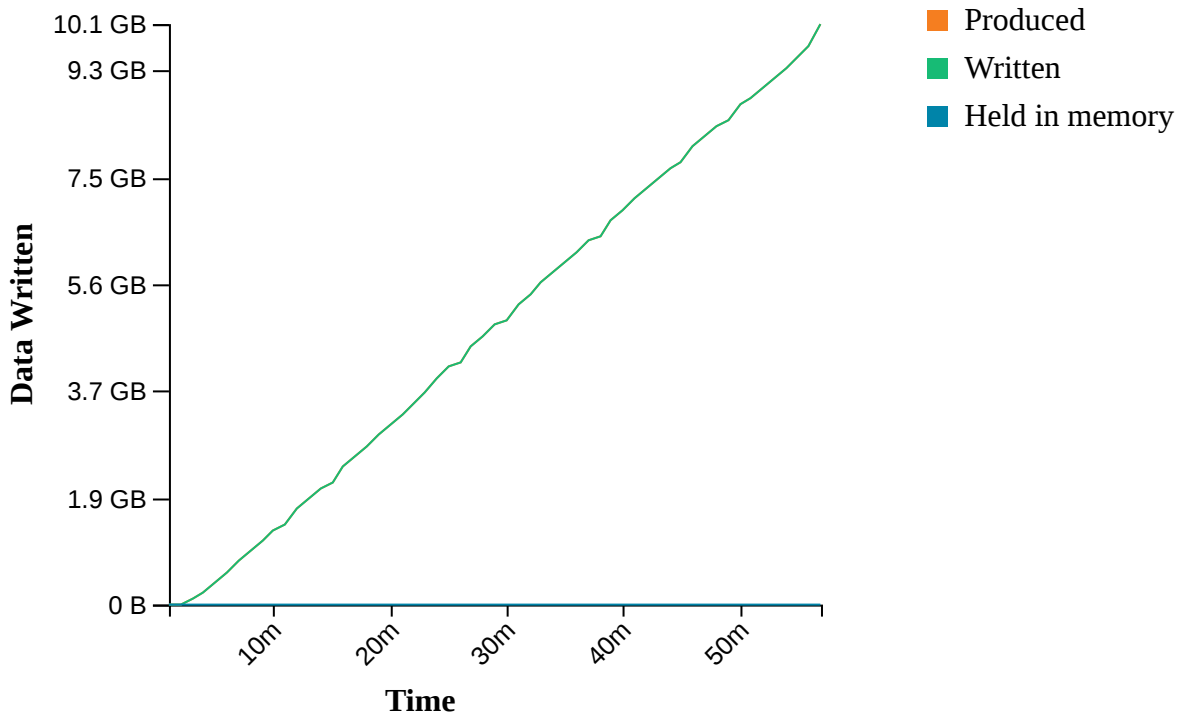
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAO53362 has found a total of 758 pores. 398 pores available for immediate sequencing January 5, 20:12
- Performing Mux Scan January 5, 20:10
- Starting sequencing procedure January 5, 20:10
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C January 5, 20:07