Run Info

Host Name	**GXB03020 (localhost)**
Experiment Name	**ReadUntil_38kbp_LowtoHigh_Sd_15042021**
Sample ID	**ReadUntil_38kbp_LowtoHigh_Sd_15042021**
Run ID	**92bb4292-6ee3-429c-8661-e5a166b68fa5**
Flow Cell Id	**FAP14753**
Start Time	**April 15, 11:28**
Run Length	**1h 50m**

Run Summary

Reads Generated	**252.05 K**
Passed Bases	**604.18 Mb**
Failed Bases	**29.36 Mb**
Estimated Bases	**629.13 Mb**

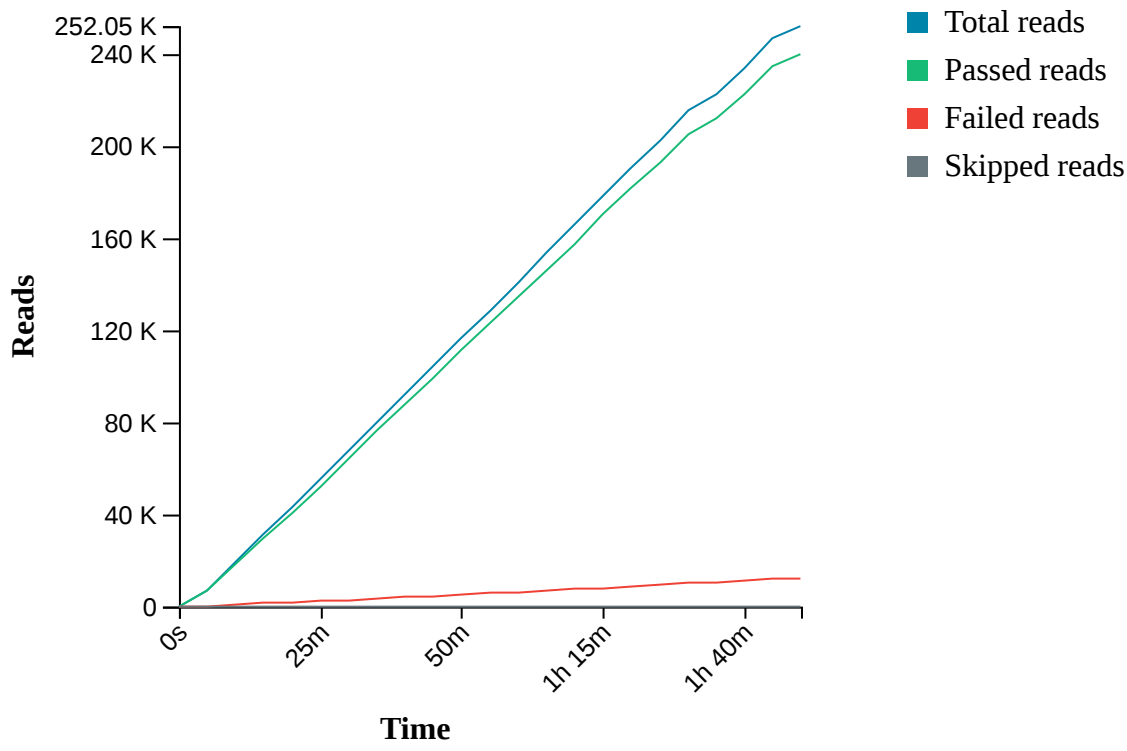
Run Parameters

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/S_dysgalactiae_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**

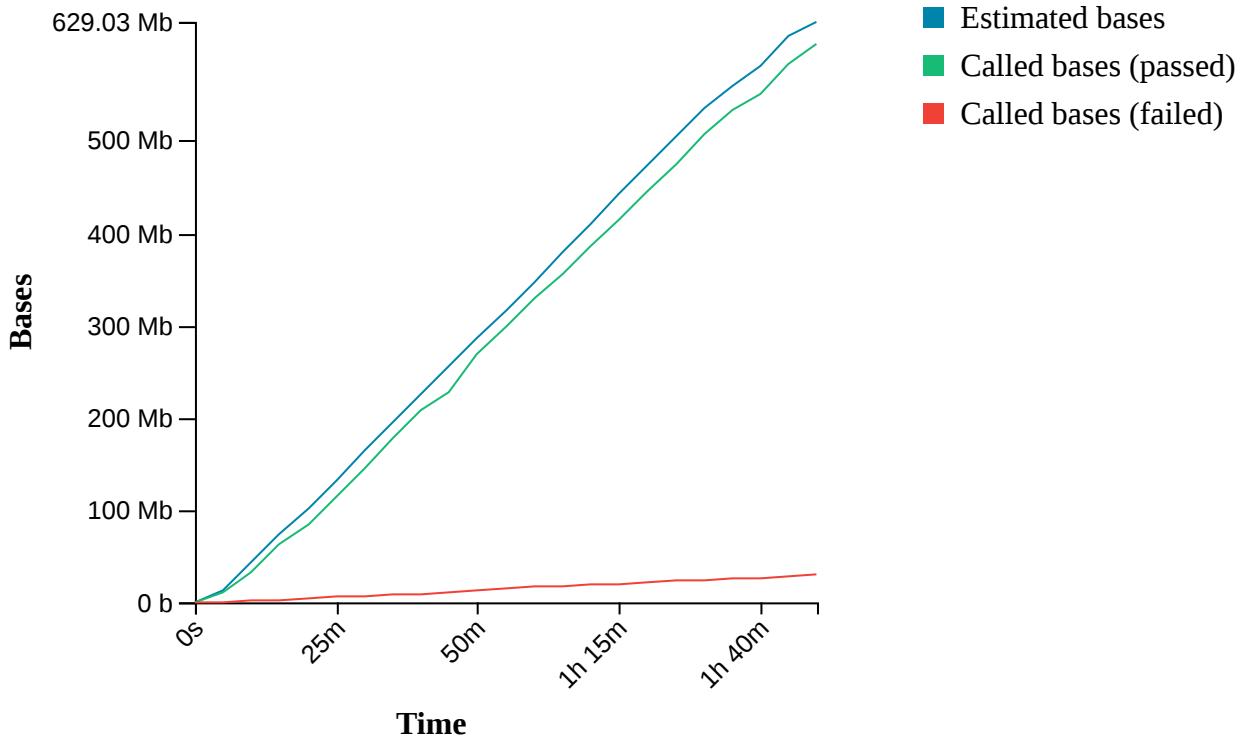
Versions

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

Cumulative Output Reads

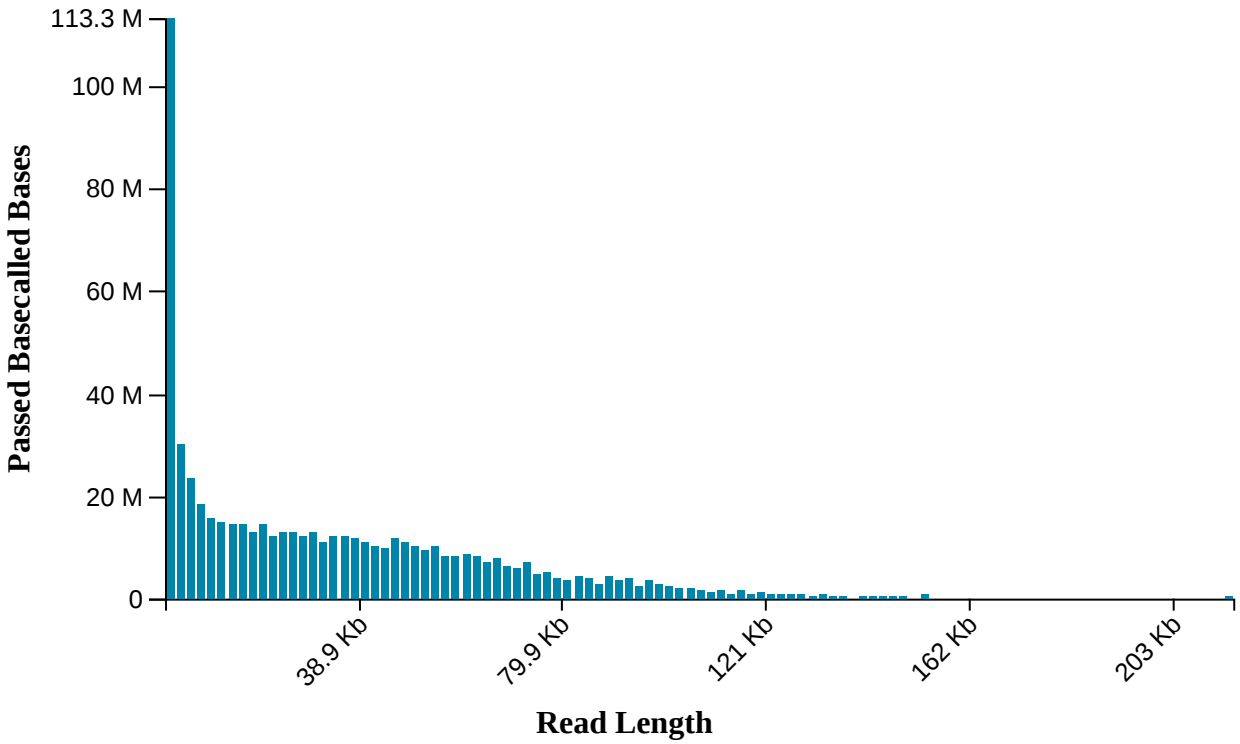


Cumulative Output Bases



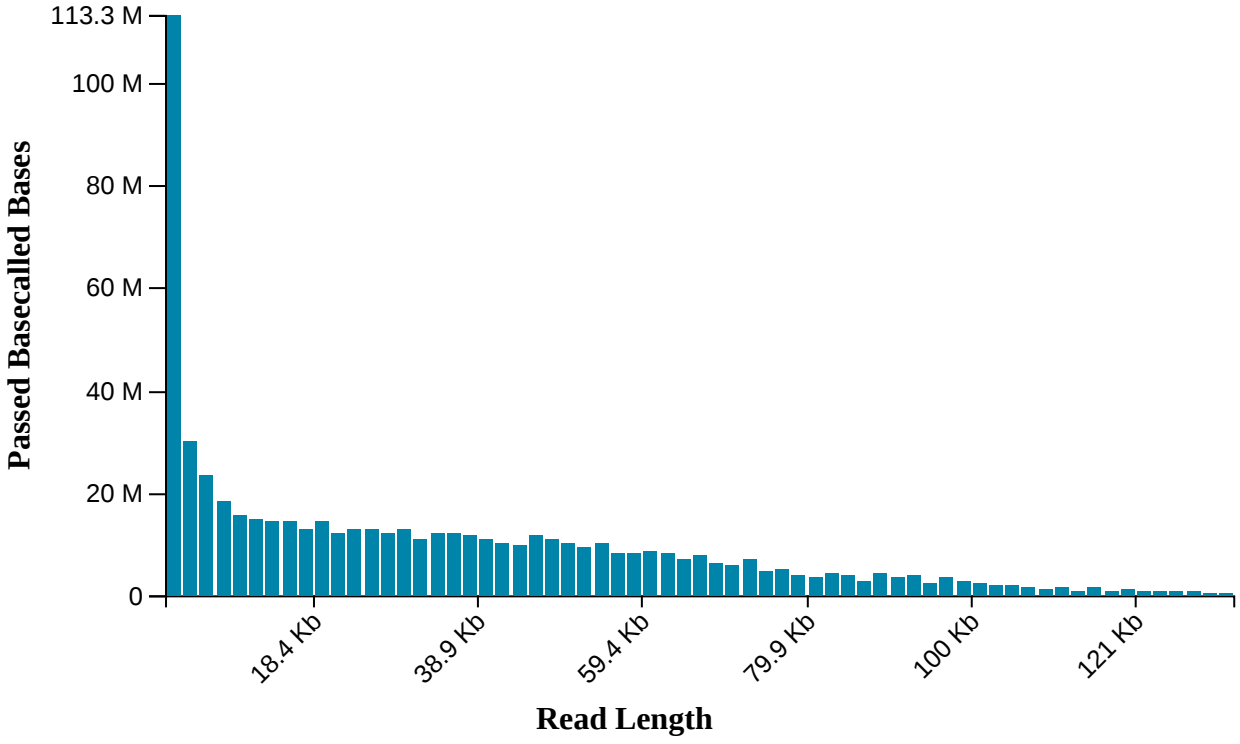
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 25.46 K



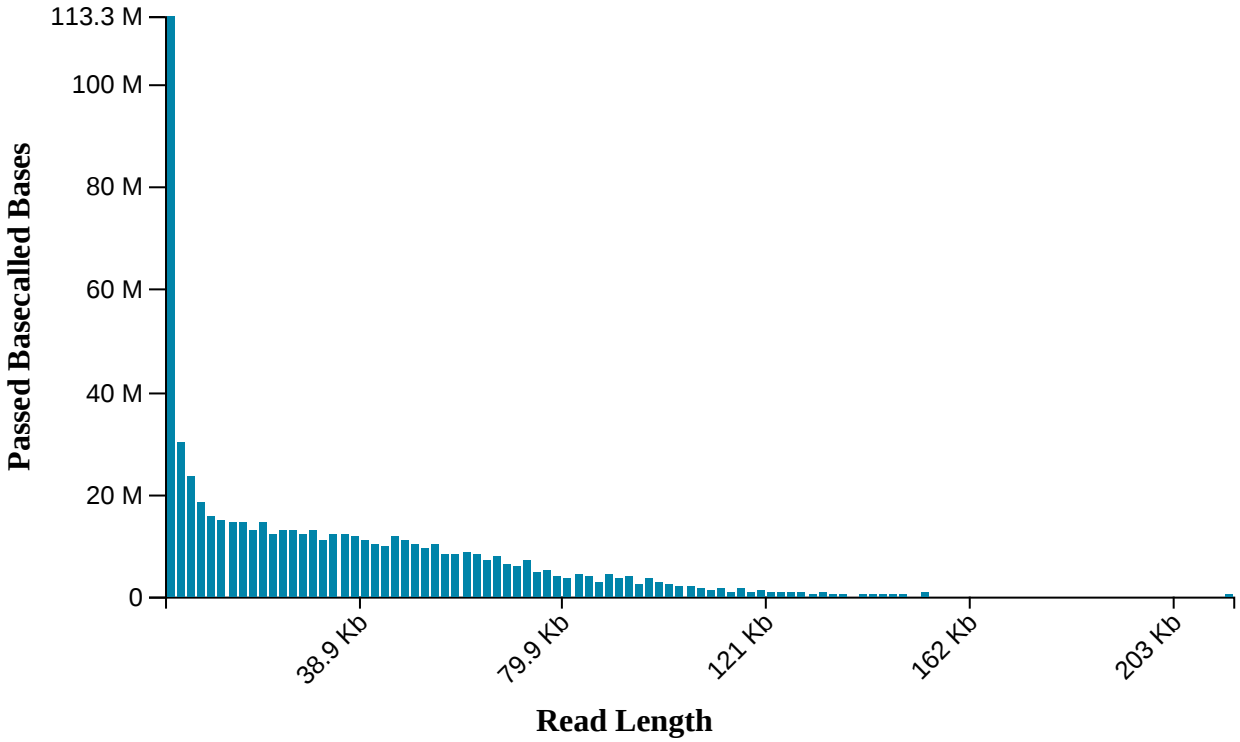
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 24.89 K



Read Length Histogram Estimated Bases

Estimated N50: 25.46 K



Read Length Histogram Basecalled Bases

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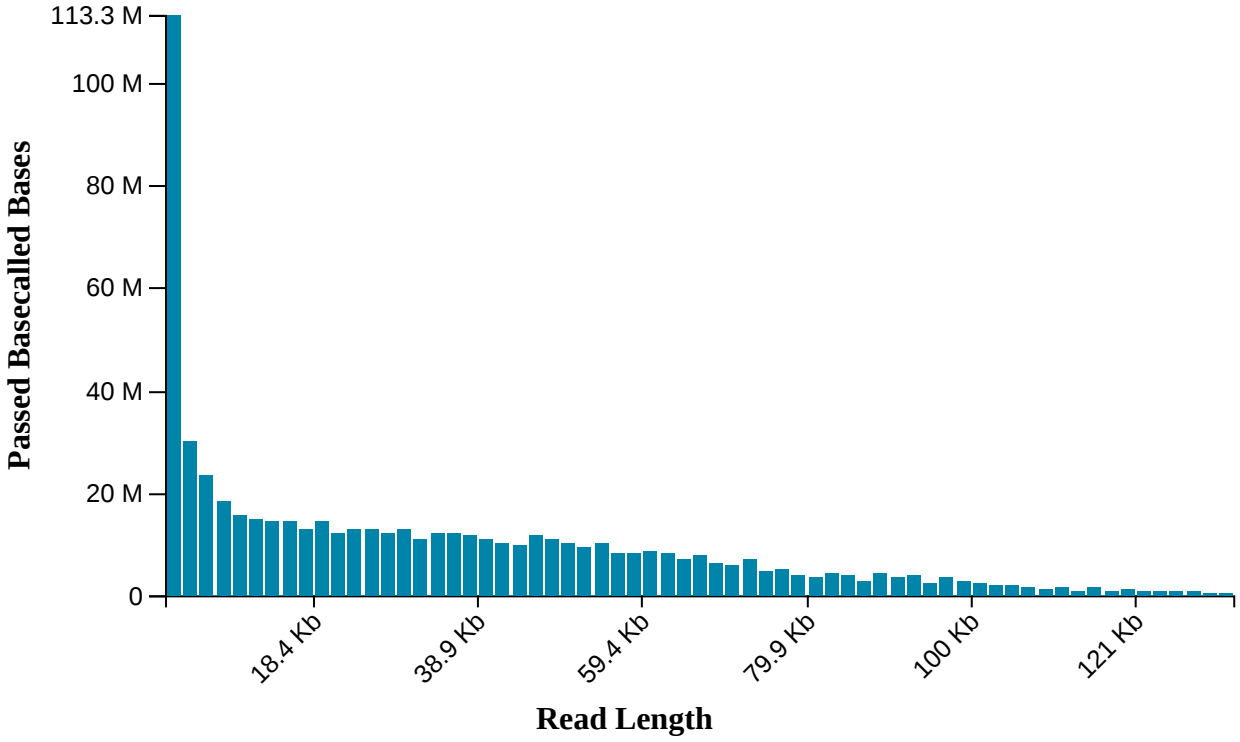
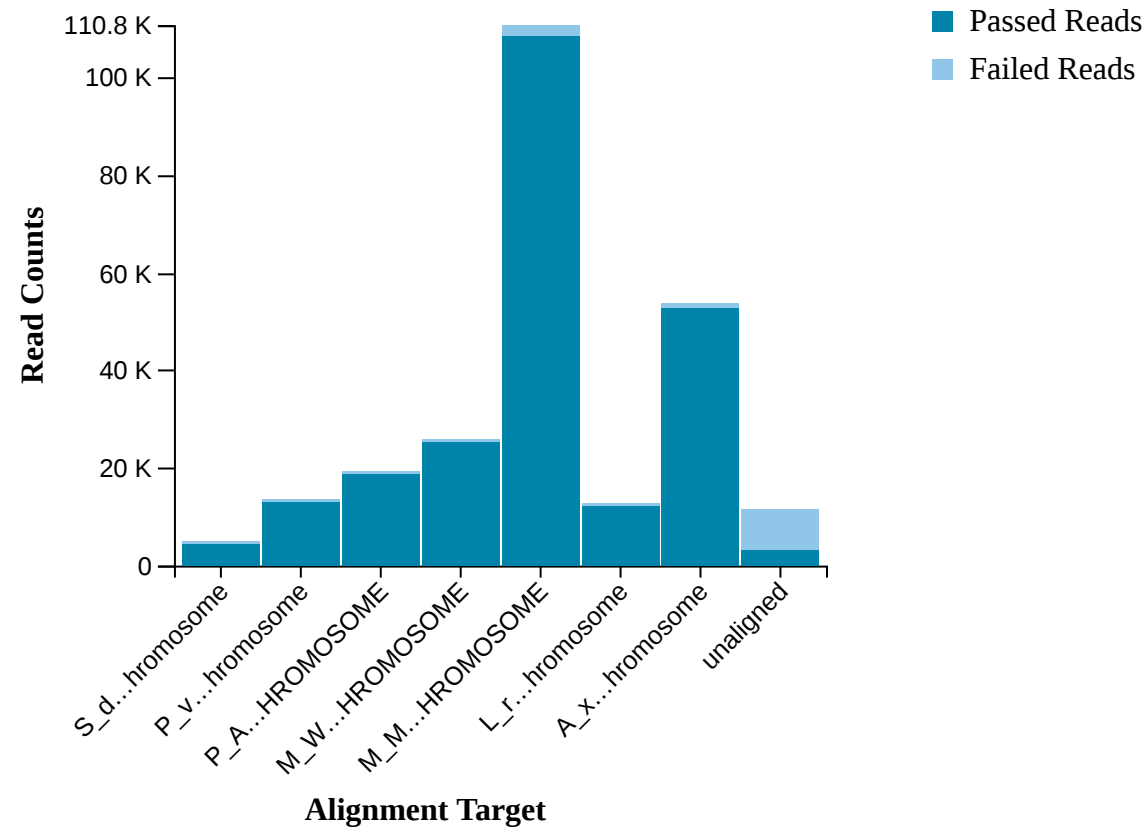
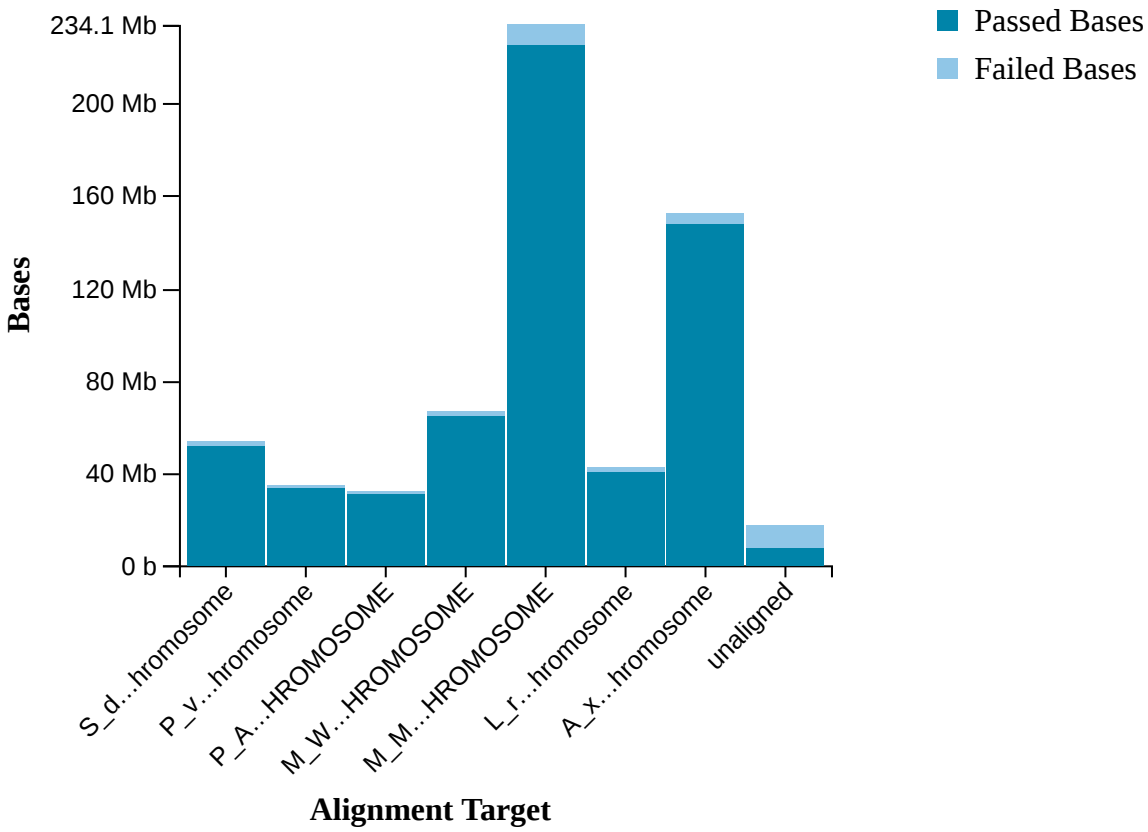


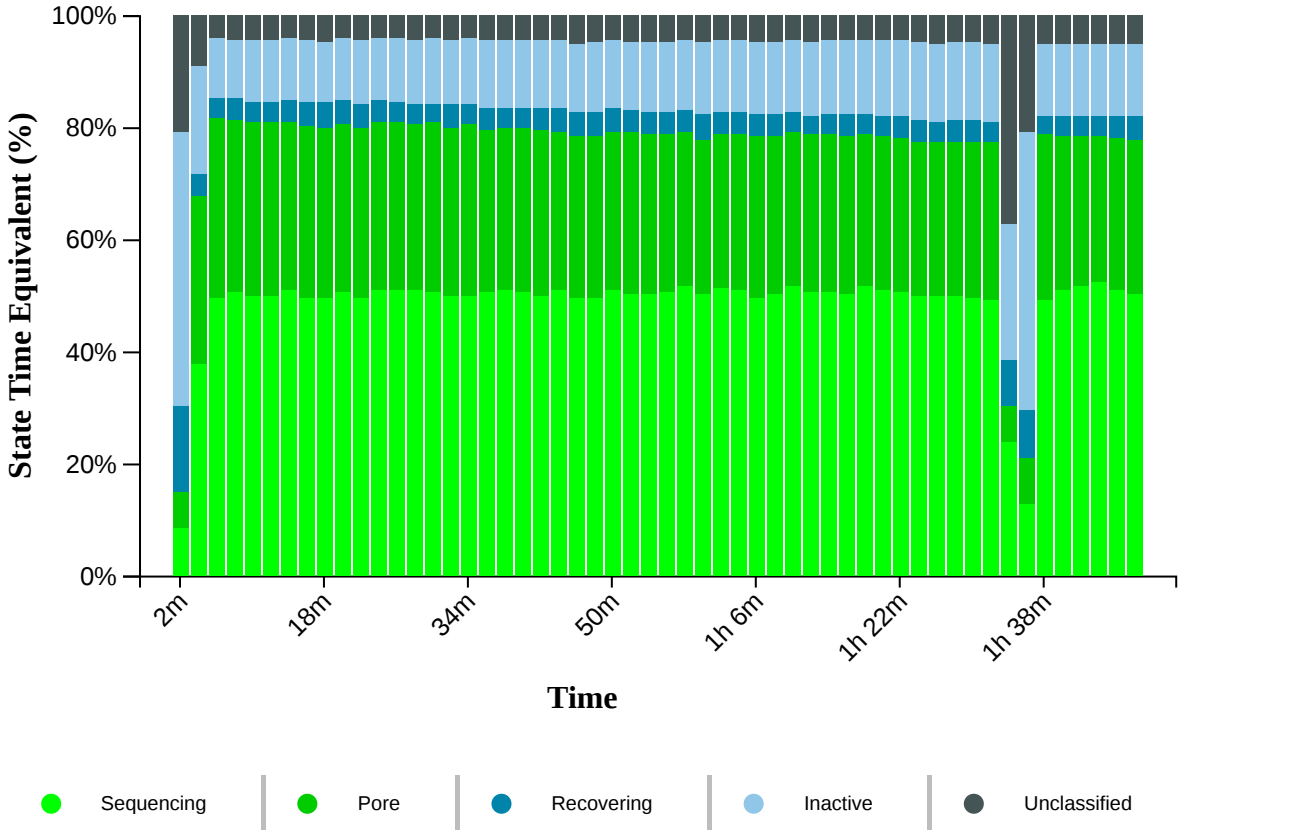
Alignment Target Hits (reads)



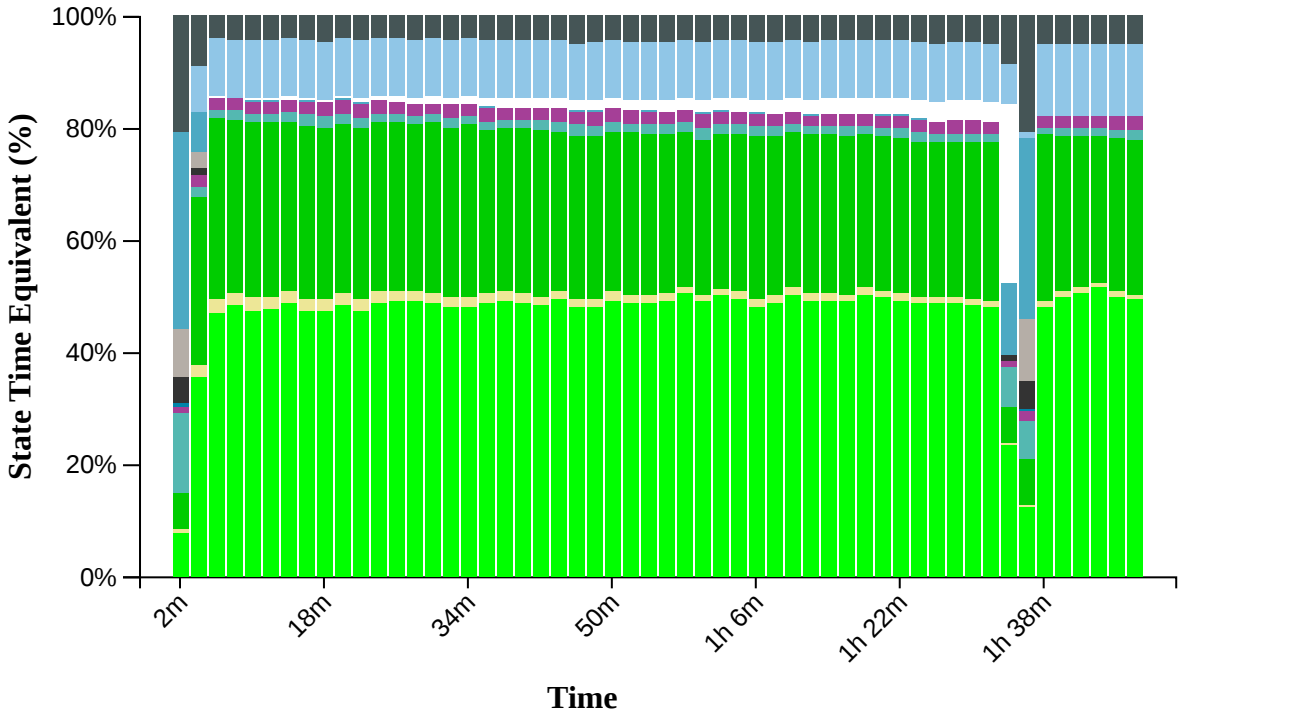
Alignment Target Hits (bases)



Duty Time Grouped



Duty time Categorised



Strand
Adapter

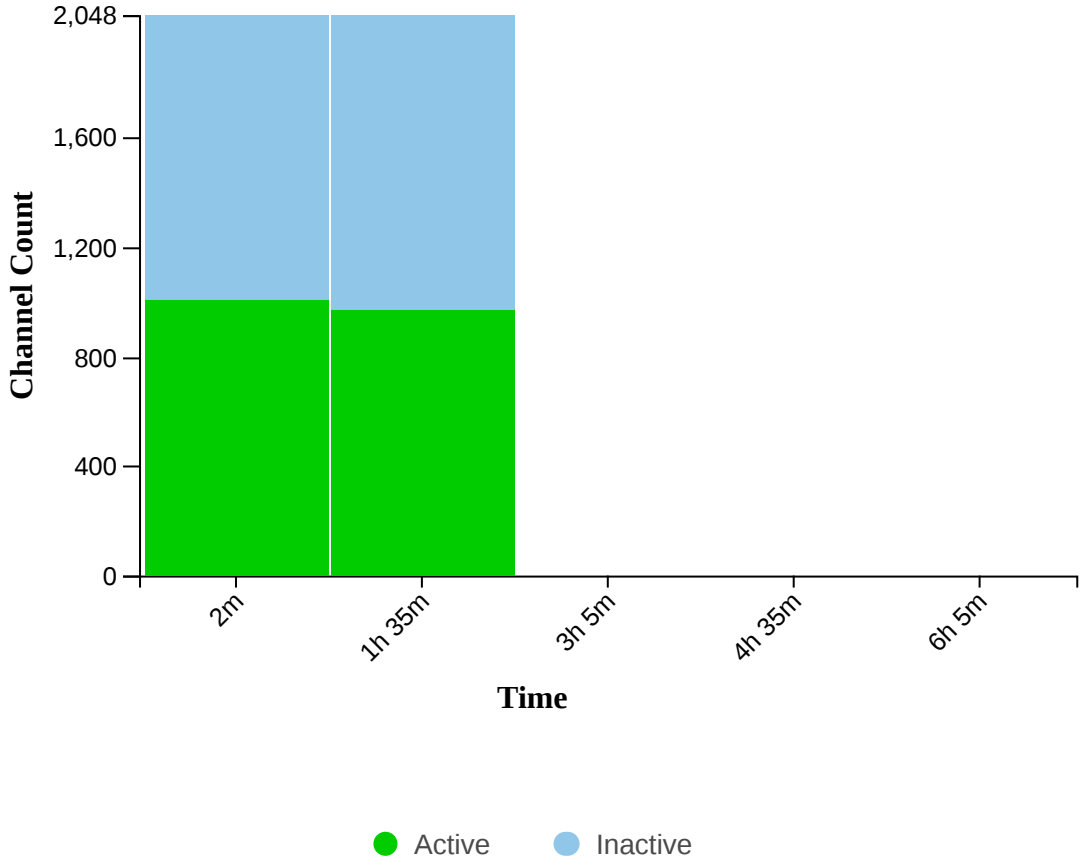
Single Pore

Unavailable
Active Feedback

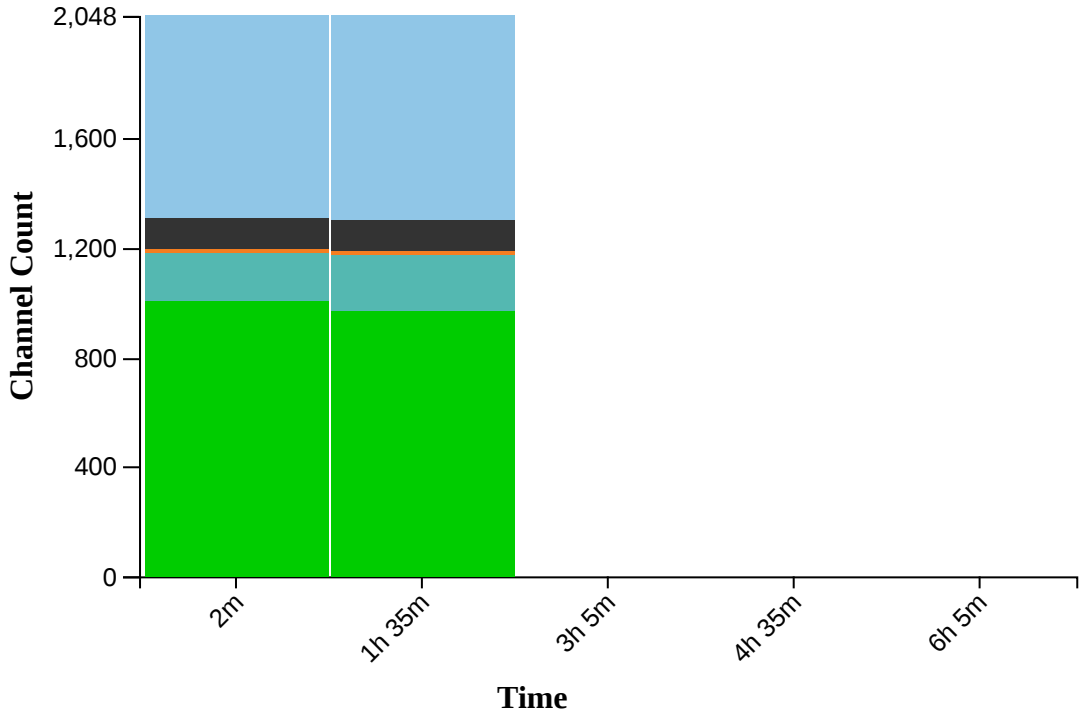
No Pore From Scan
Out Of Range 2
Possible Multiple
Saturated
Out Of Range 1
Zero
Channel Disabled

Unclassified
Unclassified_following_reset
Pending_manual_reset
Pending_mux_change
Pending Reselection

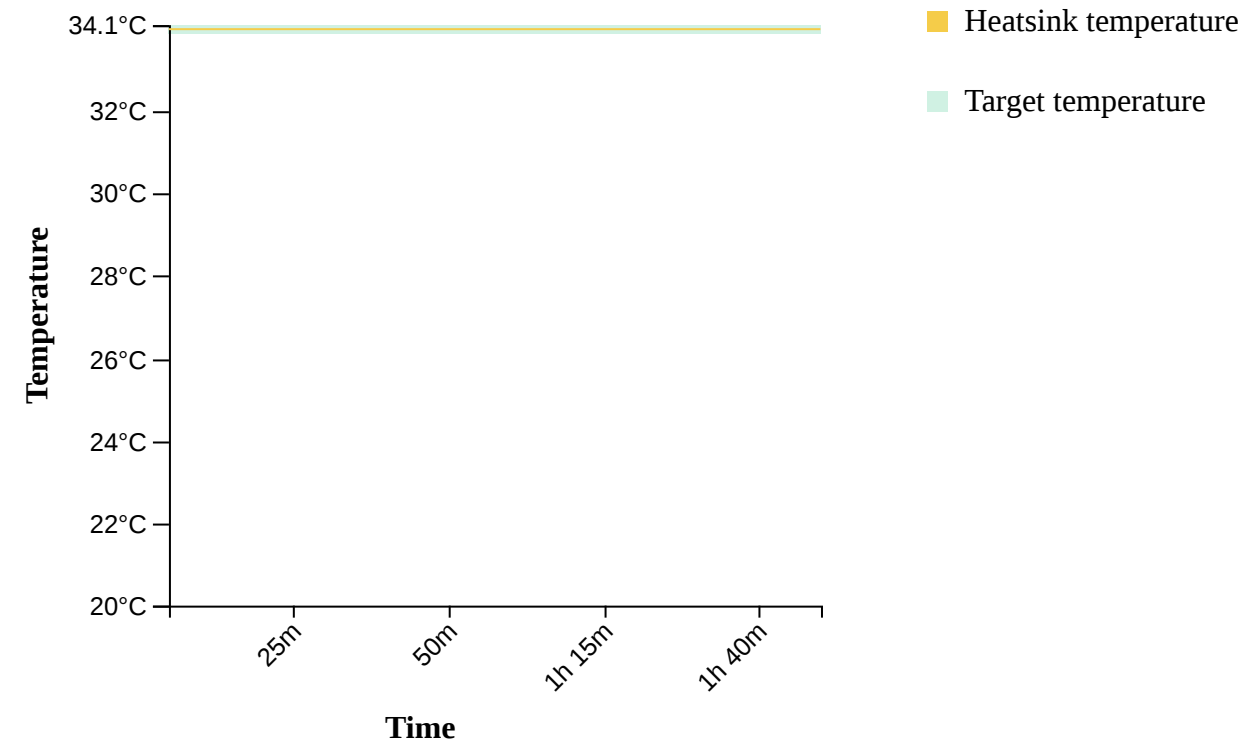
Mux Scan Grouped



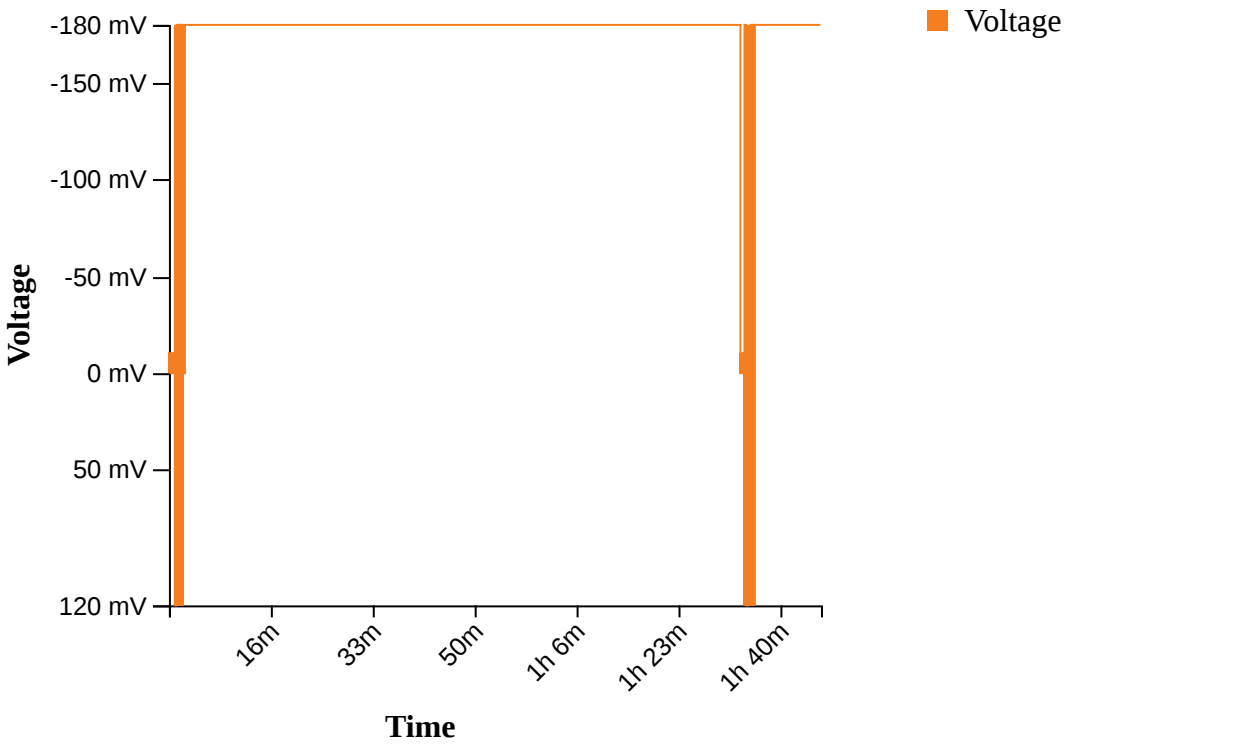
Mux Scan Categorised



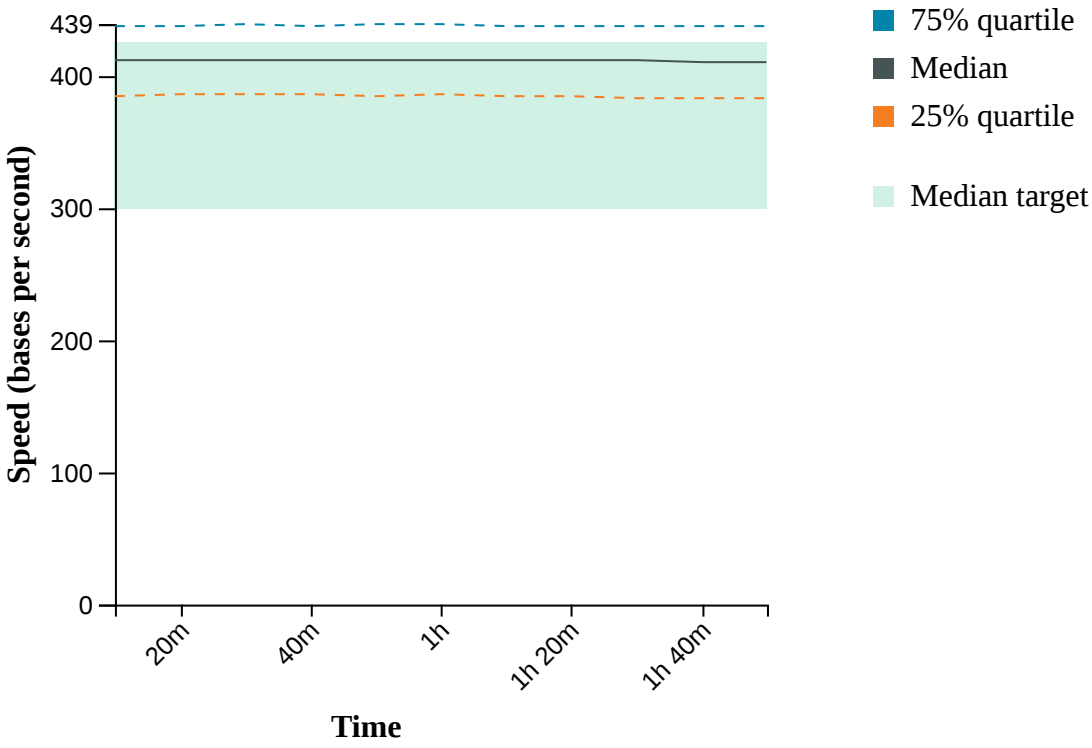
Temperature History



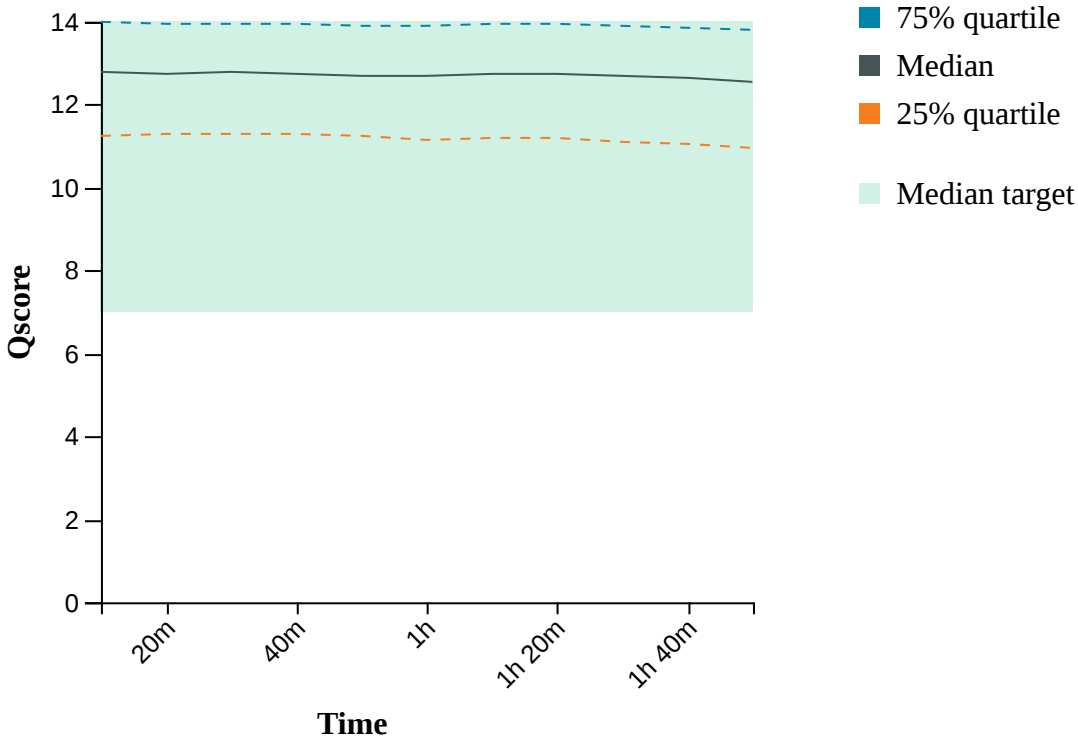
Bias Voltage History



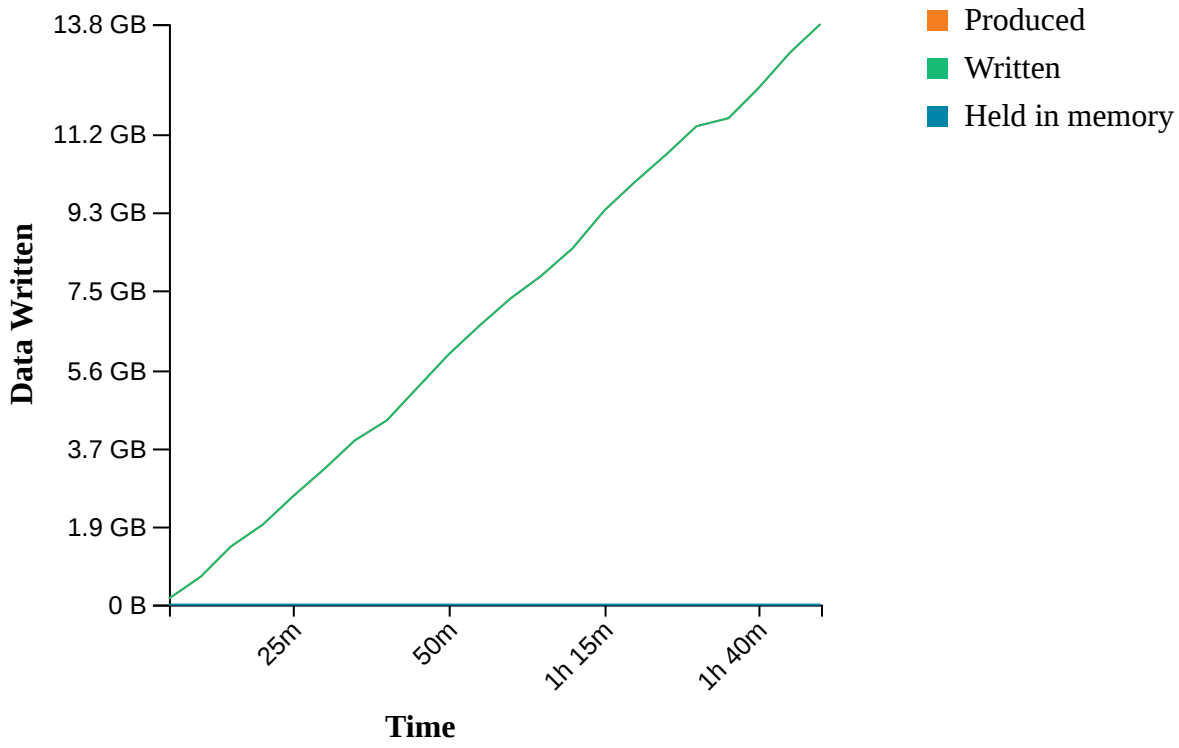
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAP14753 has found a total of 973 pores. 446 pores available for immediate sequencing April 15, 13:07
- Performing Mux Scan April 15, 13:05
- Mux scan for flow cell FAP14753 has found a total of 1007 pores. 459 pores available for immediate sequencing April 15, 11:34
- Performing Mux Scan April 15, 11:31
- Starting sequencing procedure April 15, 11:31
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 11:28