



Run Info

| | |
|-----------------|--|
| Host Name | GXB03020 (localhost) |
| Experiment Name | ReadUntil_38Kbp_HightoLow_PvEnr_15042021 |
| Sample ID | ReadUntil_38Kbp_HightoLow_PvEnr_15042021 |
| Run ID | 9db77db9-e765-4dcc-9146-06e40d2c77bc |
| Flow Cell Id | FAP21636 |
| Start Time | April 15, 17:34 |
| Run Length | 1h 0m |

Run Summary

| | |
|-----------------|-----------|
| Reads Generated | 100.17 K |
| Passed Bases | 298.76 Mb |
| Failed Bases | 16.72 Mb |
| Estimated Bases | 318.42 Mb |

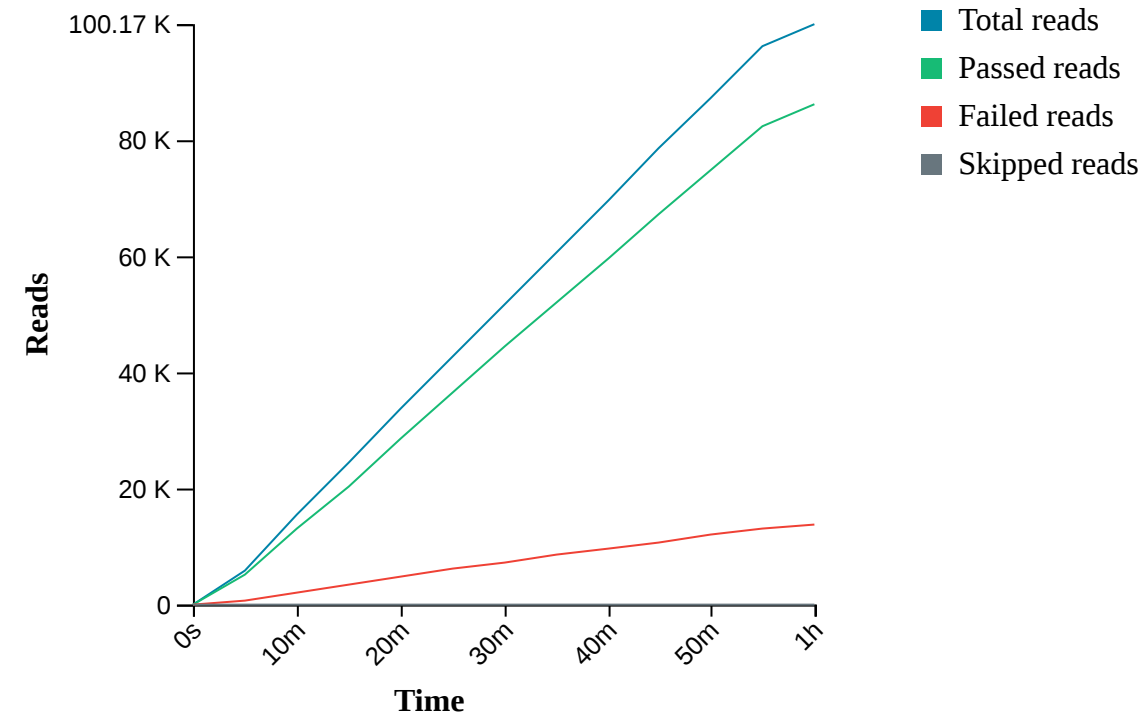
Run Parameters

| | |
|--------------------------|--|
| 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/P_vulgaris_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 |

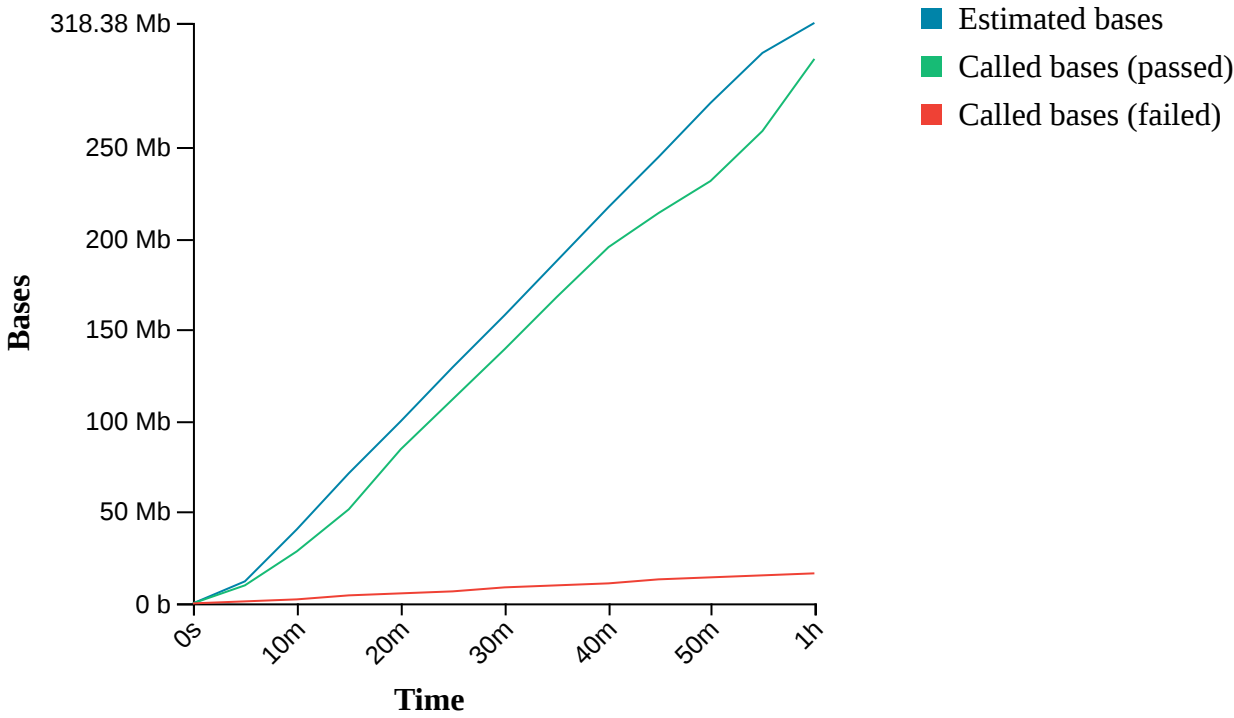
Versions

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

Cumulative Output Reads

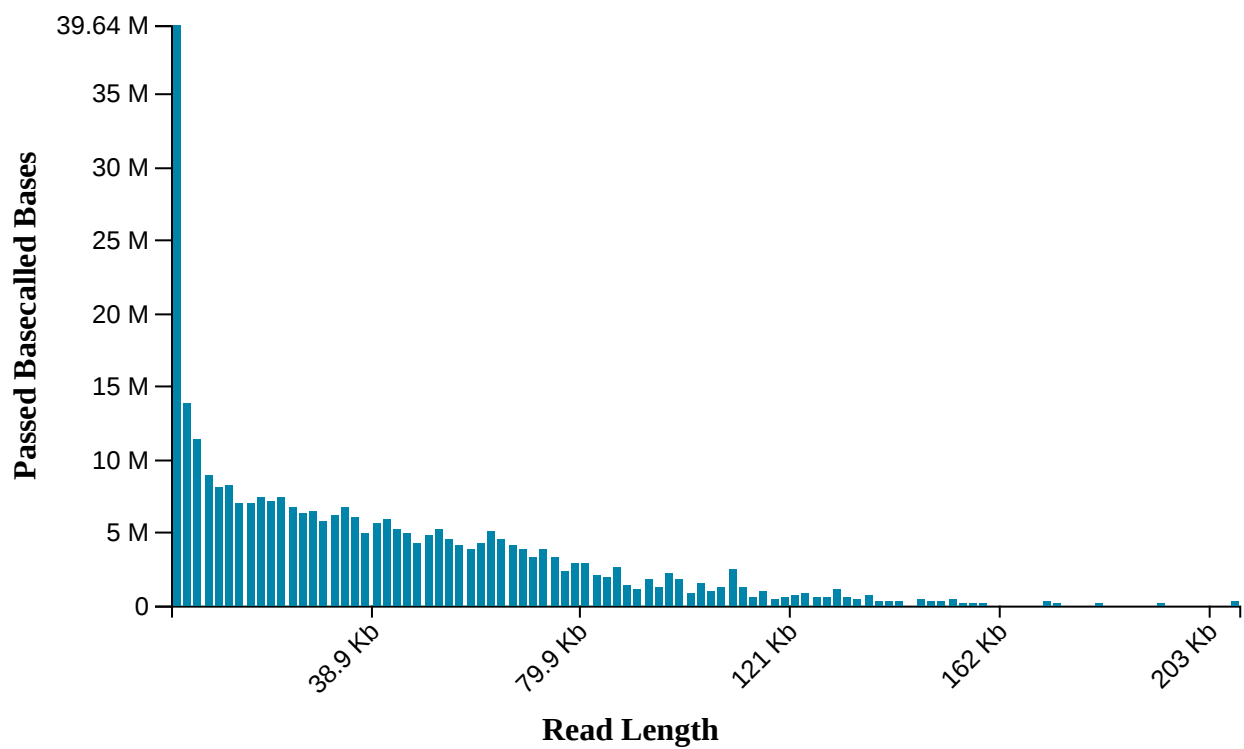


Cumulative Output Bases



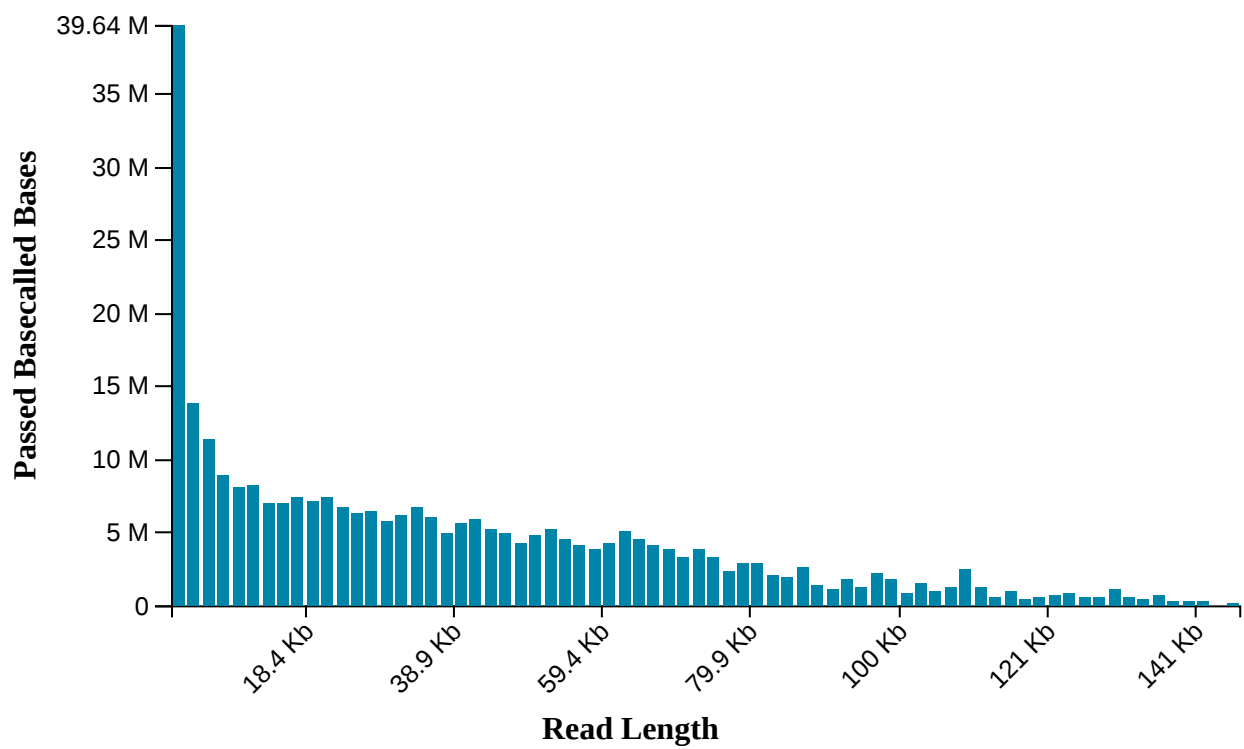
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 30.17 K



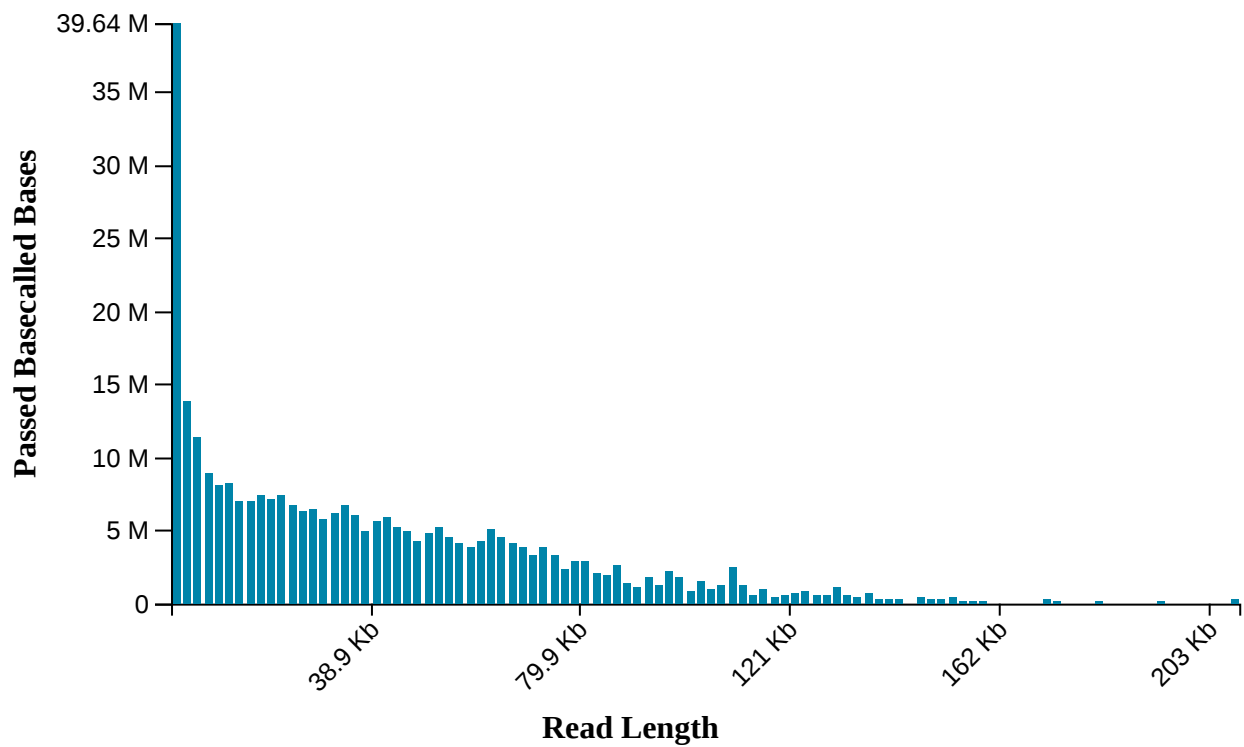
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 29.64 K



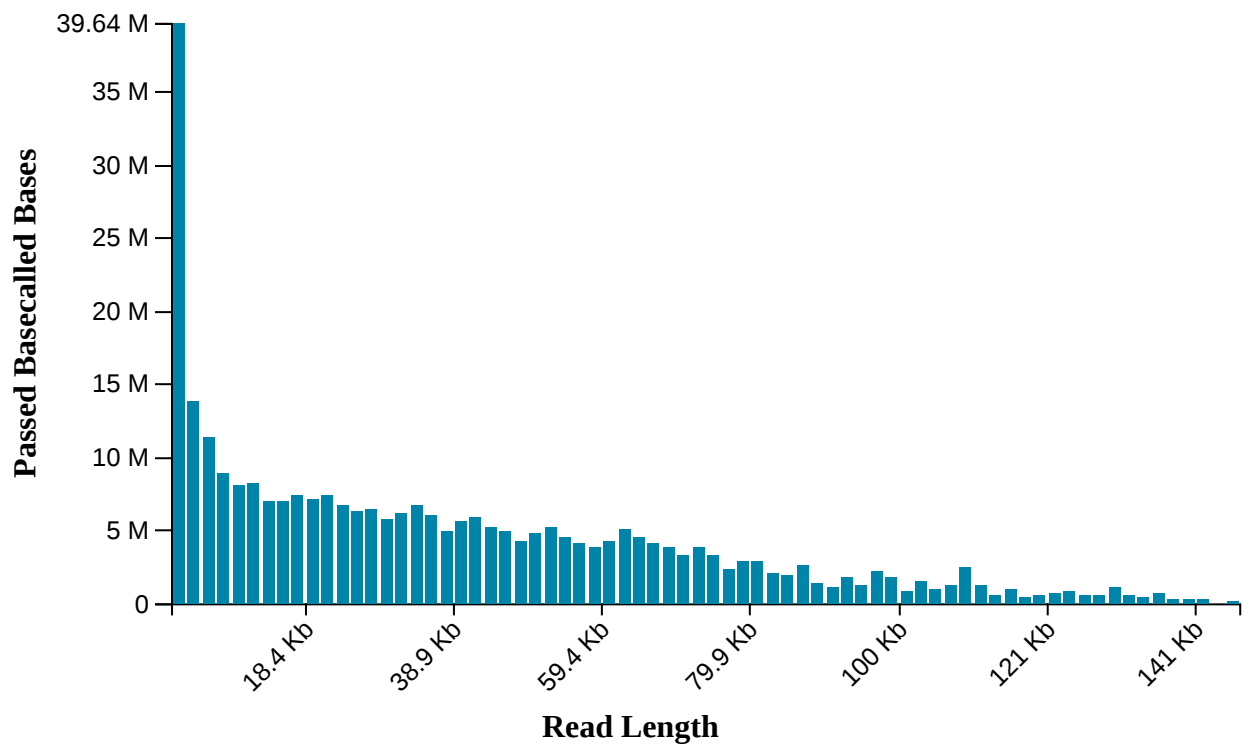
Read Length Histogram Estimated Bases

Estimated N50: 30.17 K

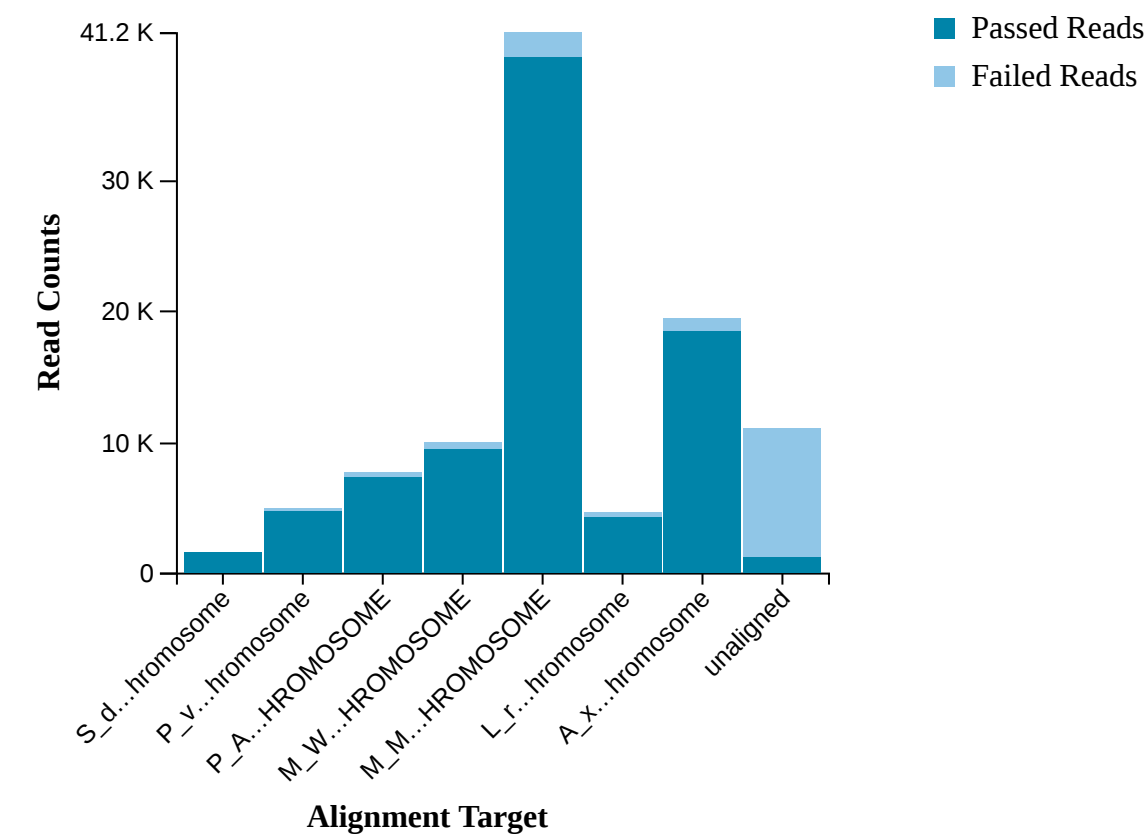


Read Length Histogram Basecalled Bases

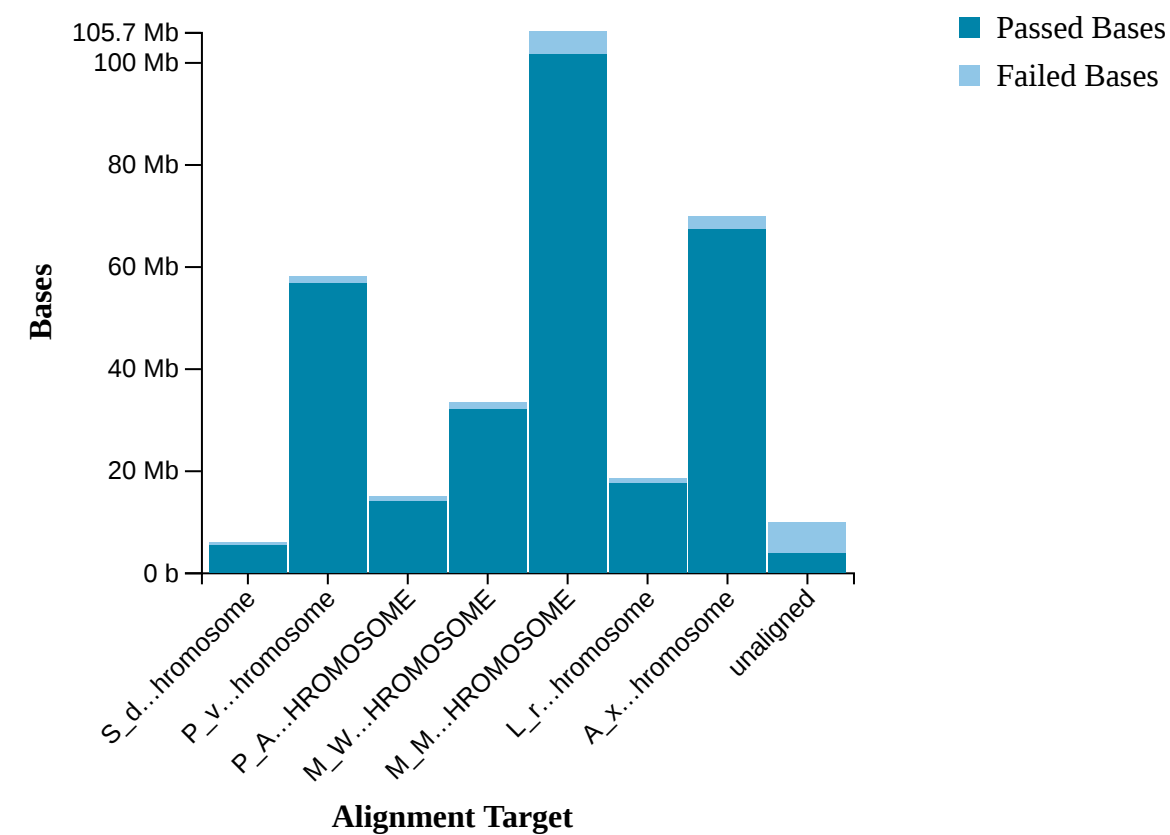
Estimated N50: 29.64 K



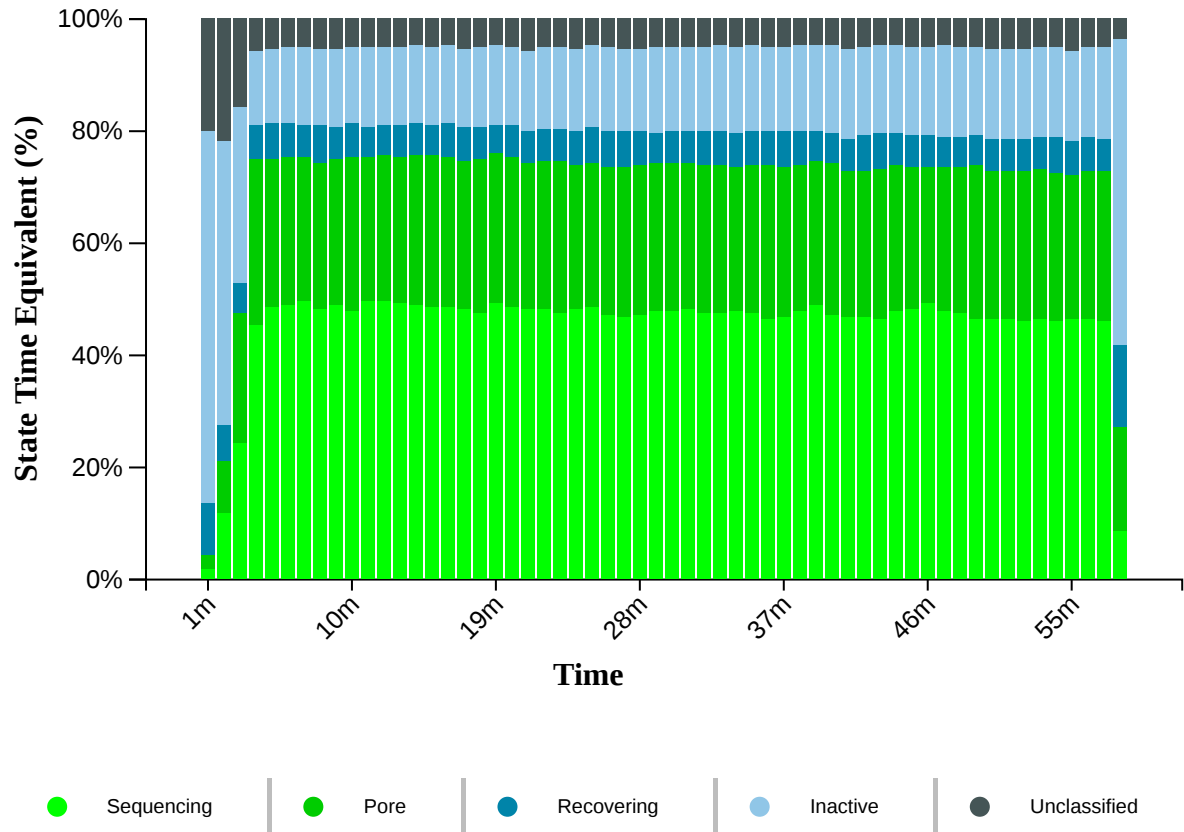
Alignment Target Hits (reads)



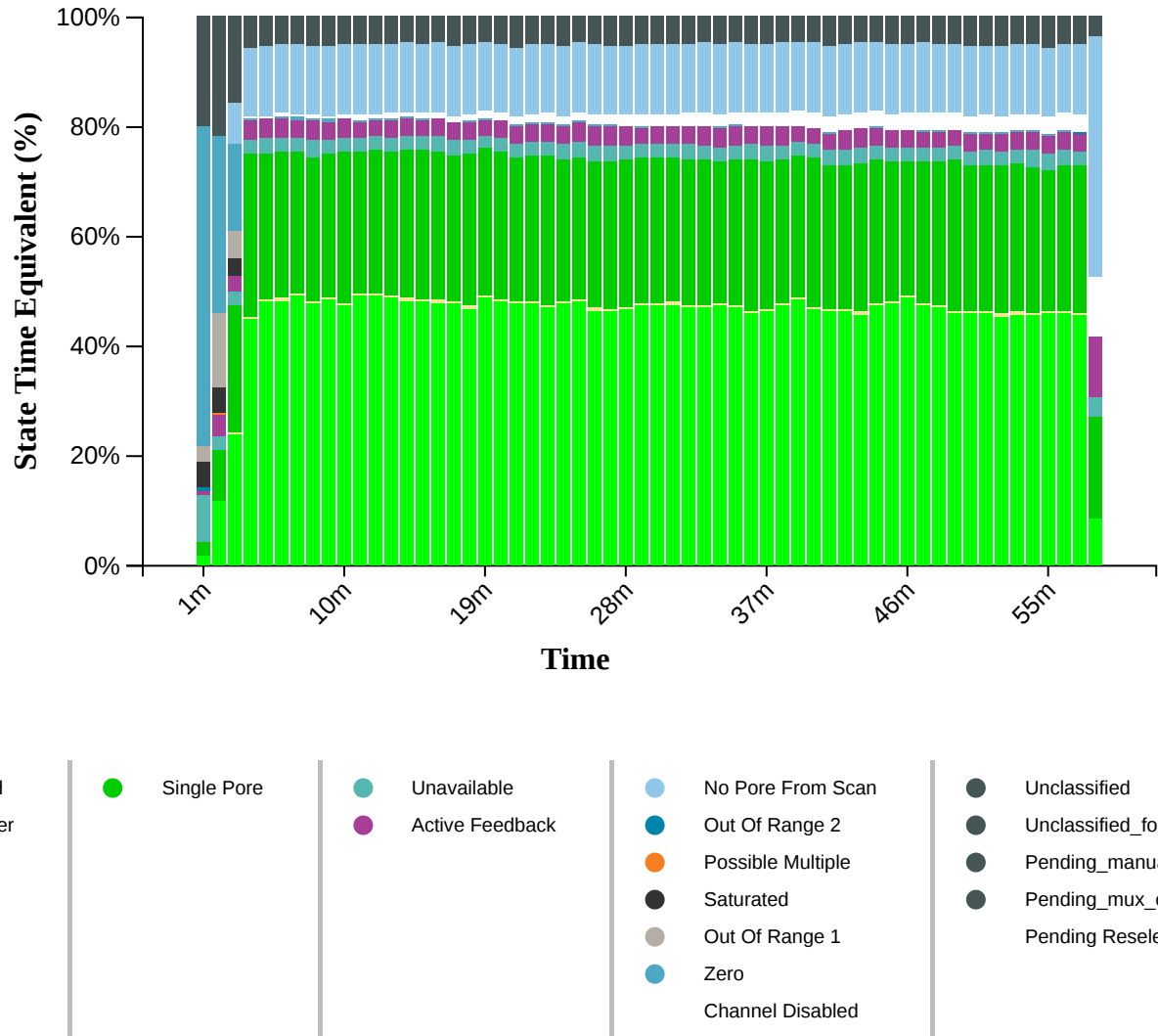
Alignment Target Hits (bases)



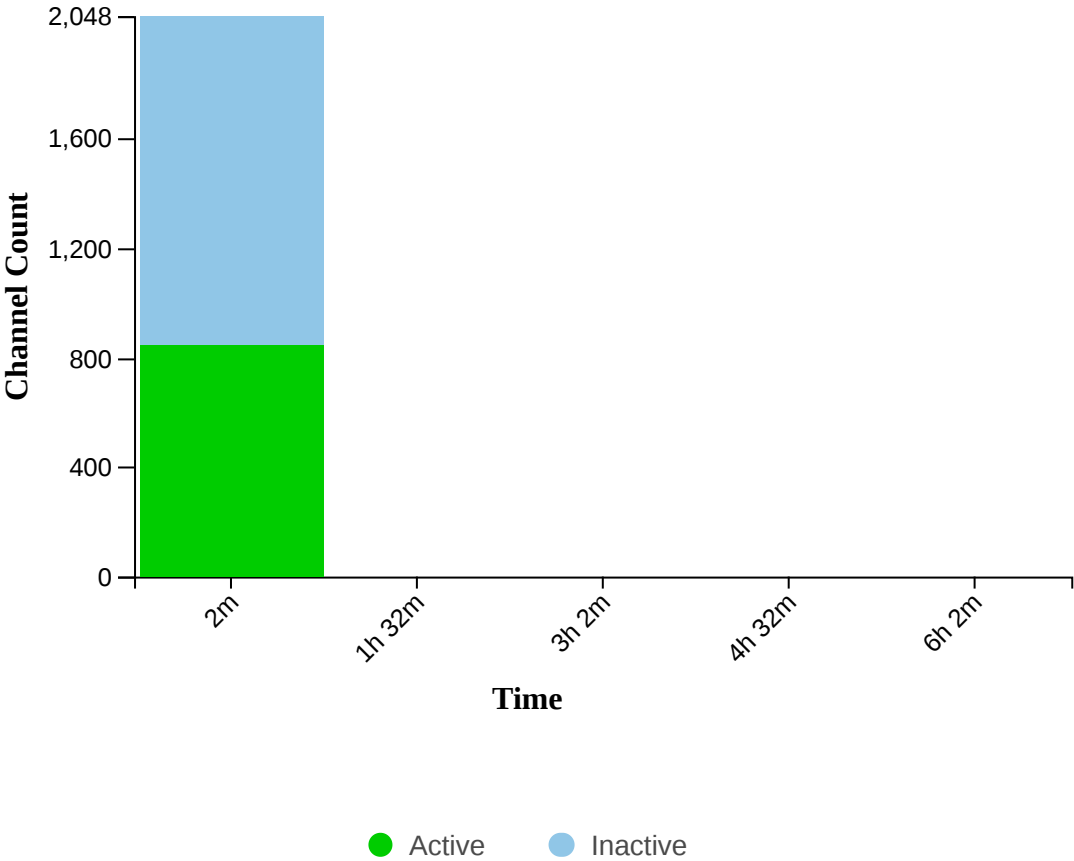
Duty Time Grouped



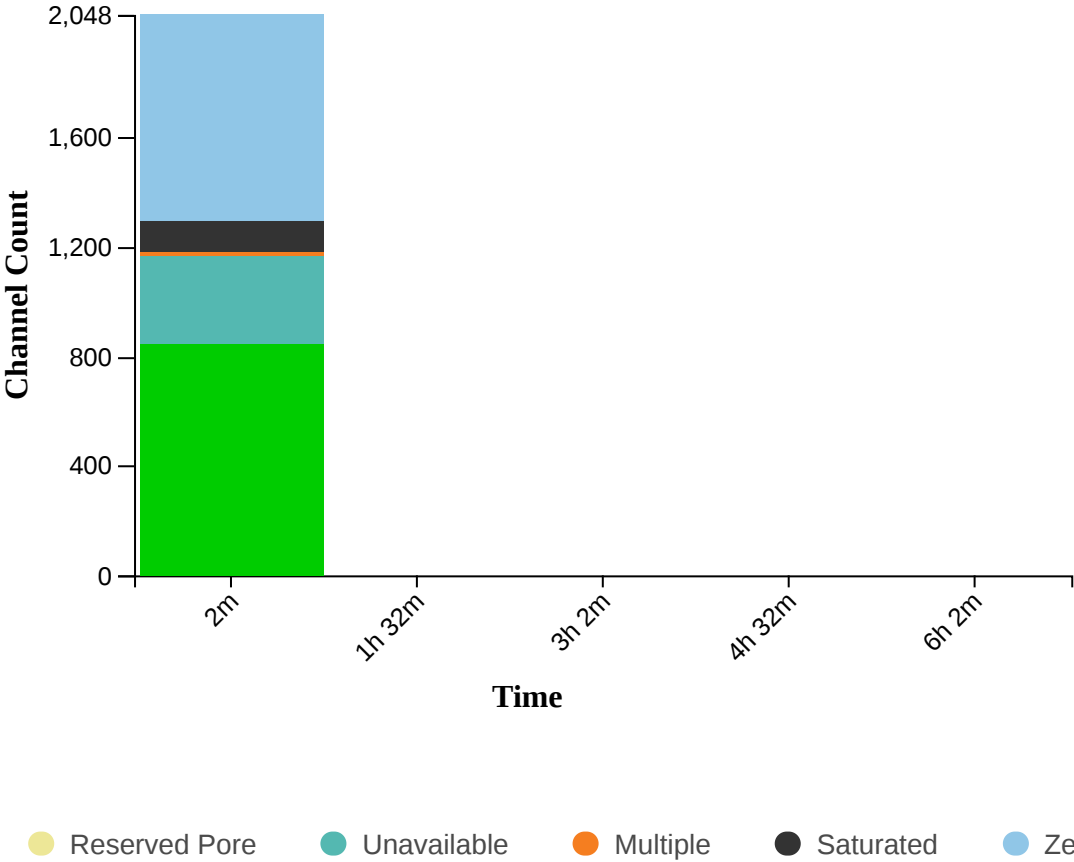
Duty time Categorised



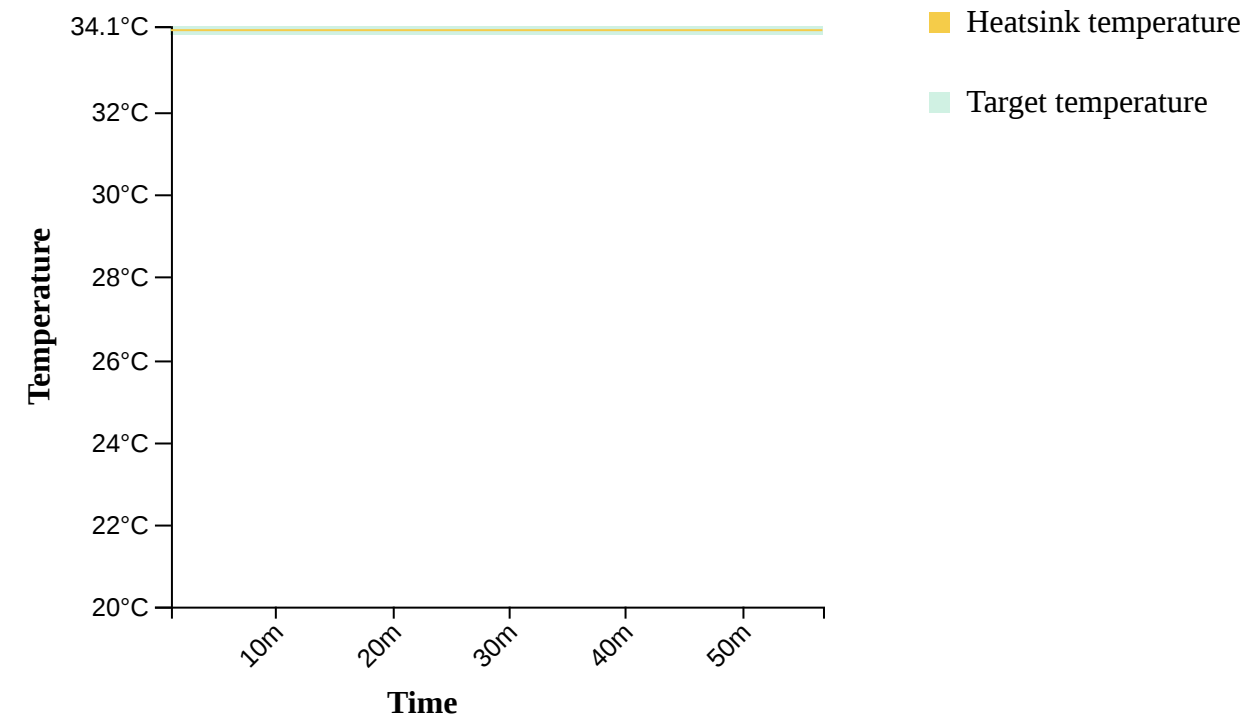
Mux Scan Grouped



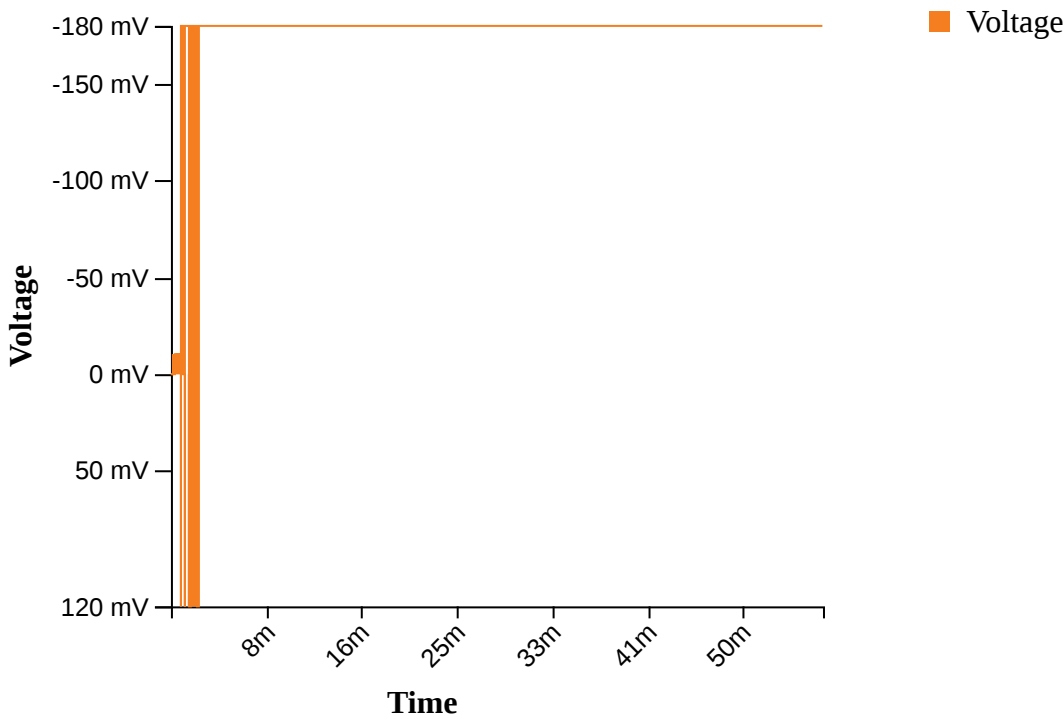
Mux Scan Categorised



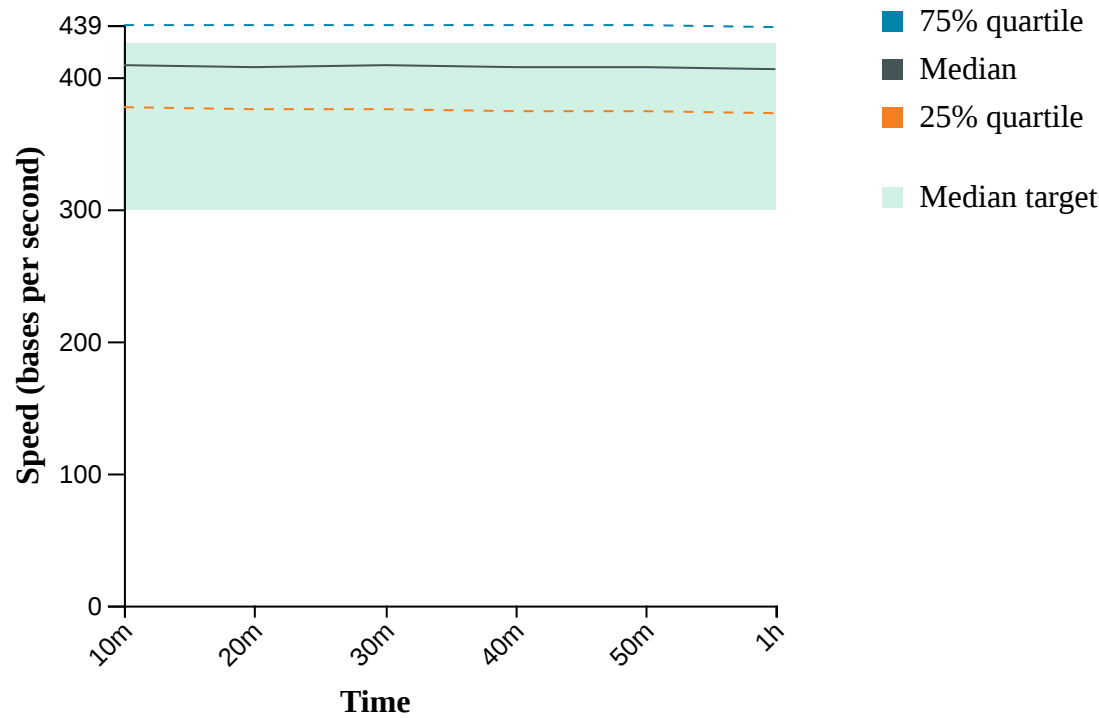
Temperature History.



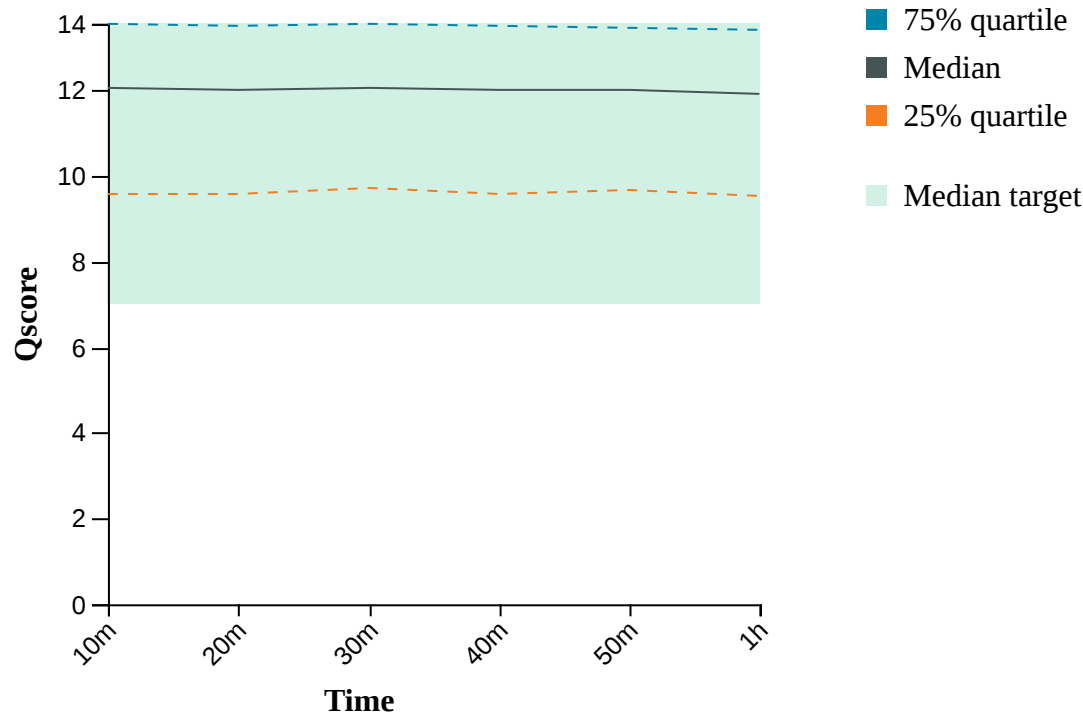
Bias Voltage History.



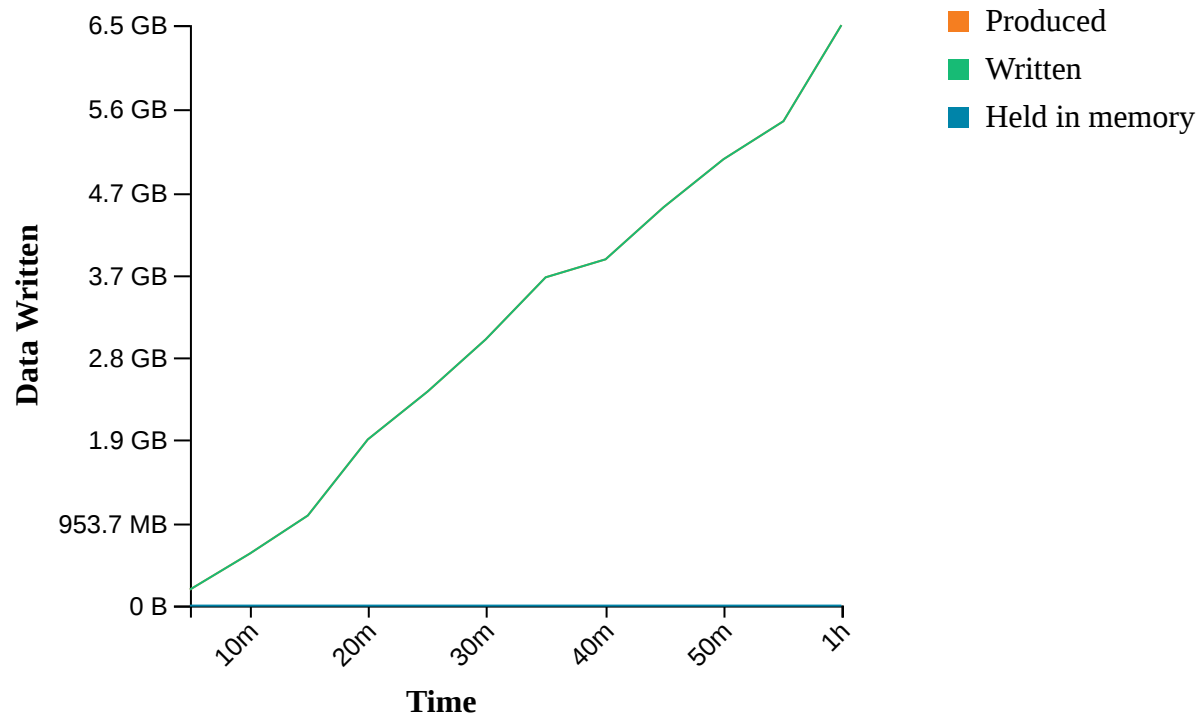
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAP21636 has found a total of 849 pores. 447 pores available for immediate sequencing April 15, 17:40
- Performing Mux Scan April 15, 17:38
- Starting sequencing procedure April 15, 17:38
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 17:34