Run Info

Host Name	**GXb03422 (localhost)**
Position	**X2**
Experiment Name	**ReadUntil_ZGM_EcoliEnrich_B3008_23092021**
Sample ID	**ReadUntil_ZGM_EcoliEnrich_B3008_23092021**
Run ID	**21702a70-ed26-4d24-8473-a5eb92b1e81d**
Acquisition ID(s)	**9da1bb9b29669d3d50de0da732b688907e141af0, c5174fb226efa52d87bf22b8b152025c6ce88739**
Flow Cell Id	**FAR13458**
Start Time	**September 23, 13:05**
Run Length	**1h 3m**

Run Summary

Reads Generated	**251.52 k**
Passed Bases	**472.5 Mb**
Failed Bases	**28.56 Mb**
Estimated Bases	**522.29 Mb**

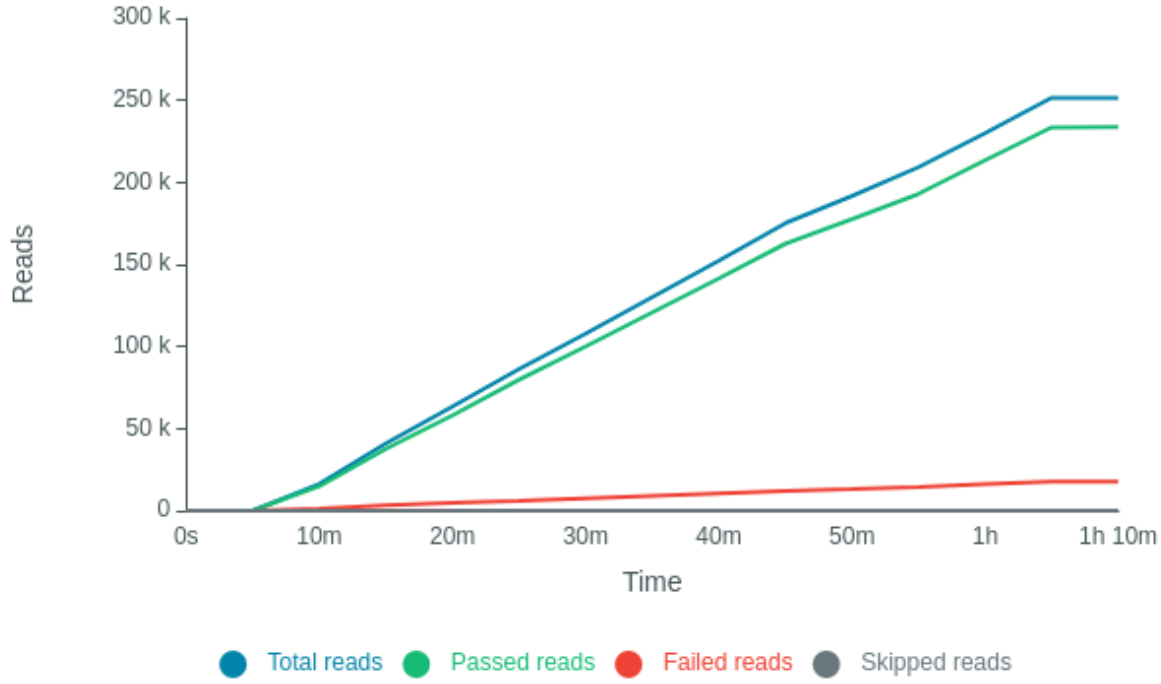
Run Parameters

Flow Cell Type	**FLO-MIN106**
Kit	**SQK-LSK109**
Initial bias voltage	**-180 mV**
FAST5 output	**Enabled**
FASTQ output	**Enabled**
BAM output	**Enabled**
Bulk file output	**Disabled**
Active channel selection	**Enabled**
Basecalling	**Enabled**
Specified run length	**72 hours**
Adaptive sampling	**reference_files= ["/data/references/zymo_gut_mock/Escherichia_coli_B3008.fasta"],filter_type=enrich,first_channel=1,last_channel=256**
FAST5 reads per file	**4000**
FAST5 output options	**vbz_compress,fastq,raw**
FASTQ reads per file	**4000**
FASTQ output options	**compress**
Mux scan period	**1 hour 30 minutes**
Reserved pores	**0 %**
Basecall model	**High-accuracy basecalling**
Alignment	**reference_files= ["/data/references/zymo_gut_mock/zymo_minus_two.fasta"]**
Read filtering	**min_qscore=9**

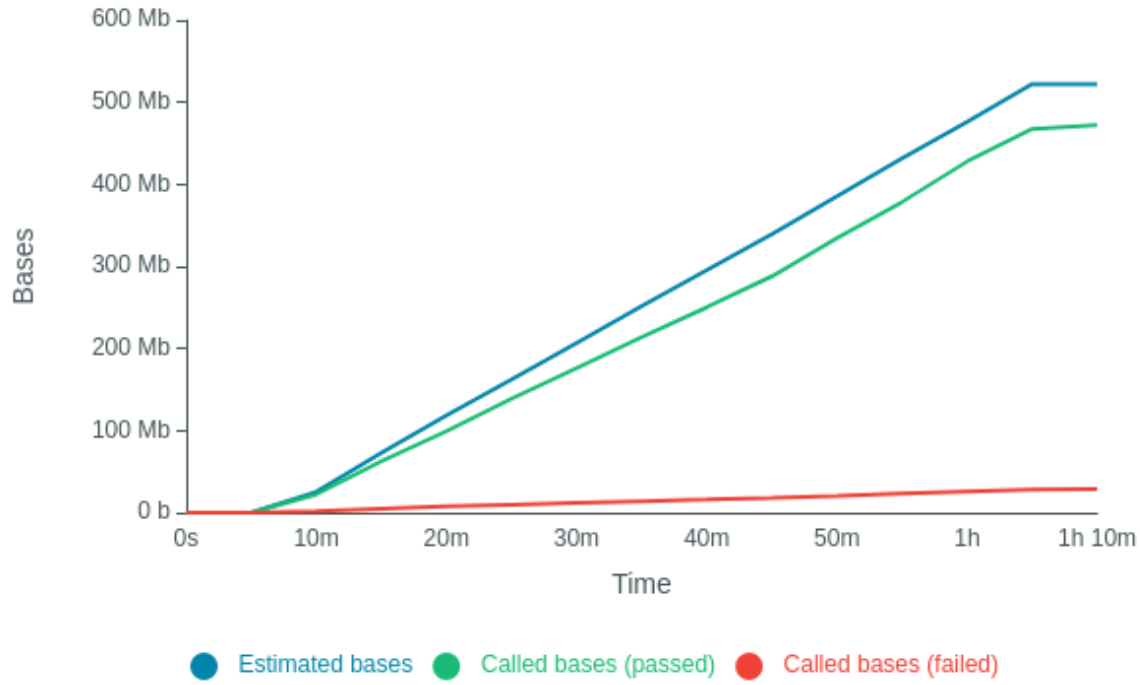
Versions

MinKNOW	**21.05.20**
MinKNOW Core	**4.3.11**
Bream	**6.2.6**
Guppy	**5.0.13**

Cumulative Output Reads

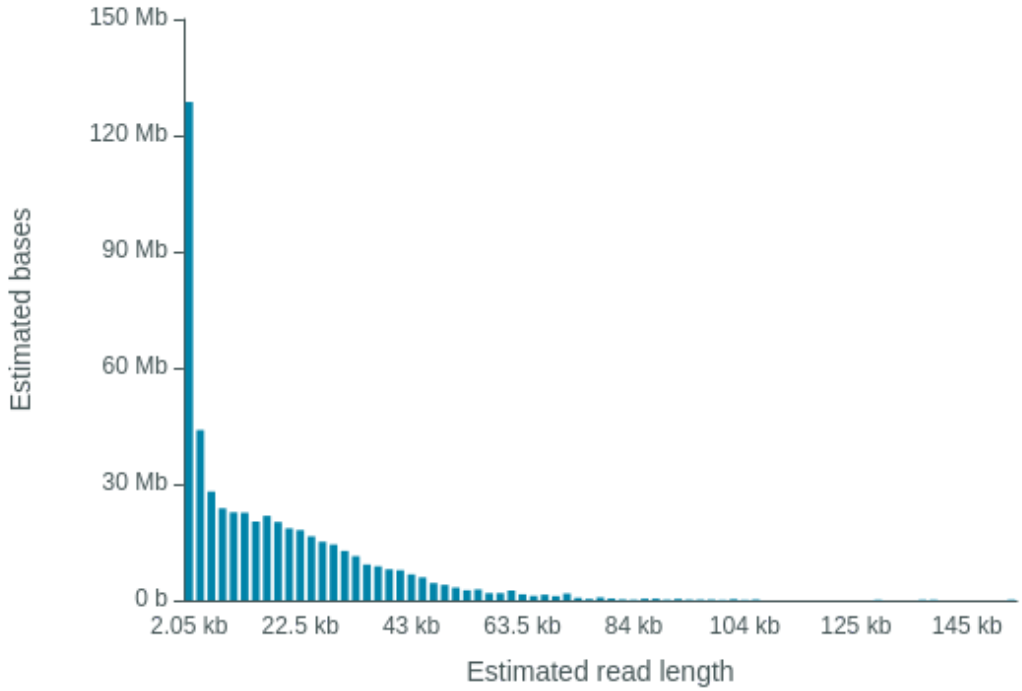


Cumulative Output Bases



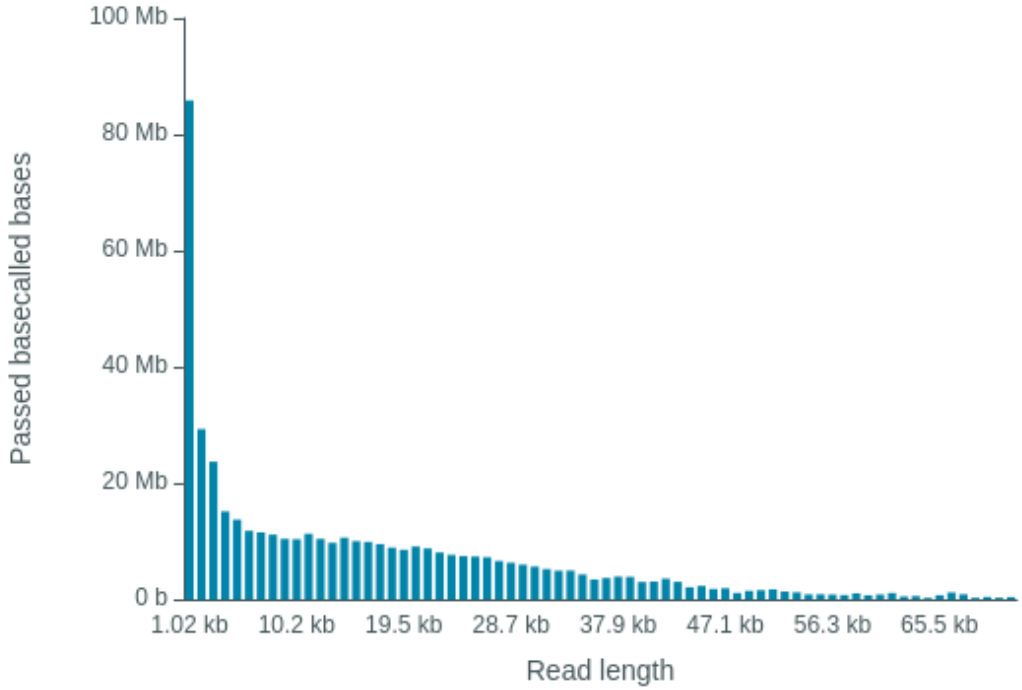
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 11.54 kb



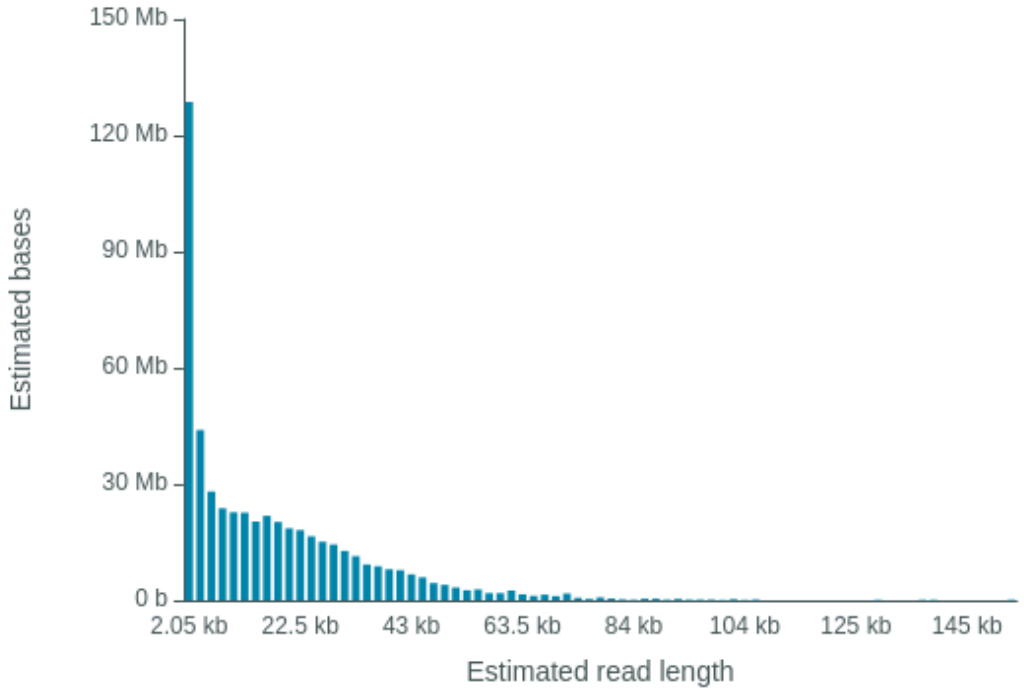
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 11.24 kb



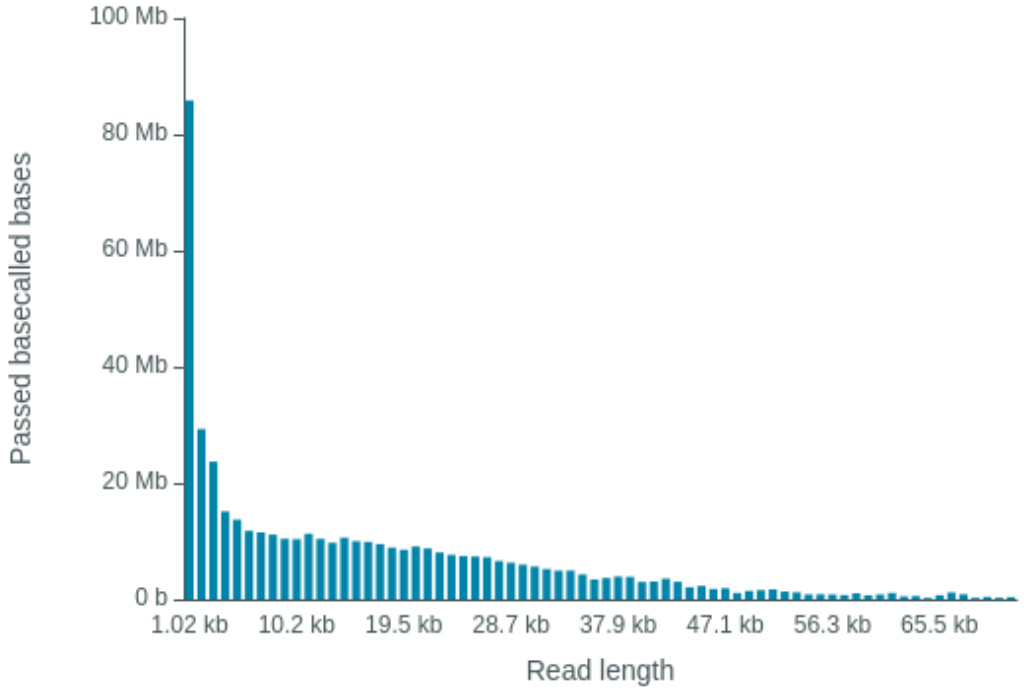
Read Length Histogram Estimated Bases

Estimated N50: 11.54 kb

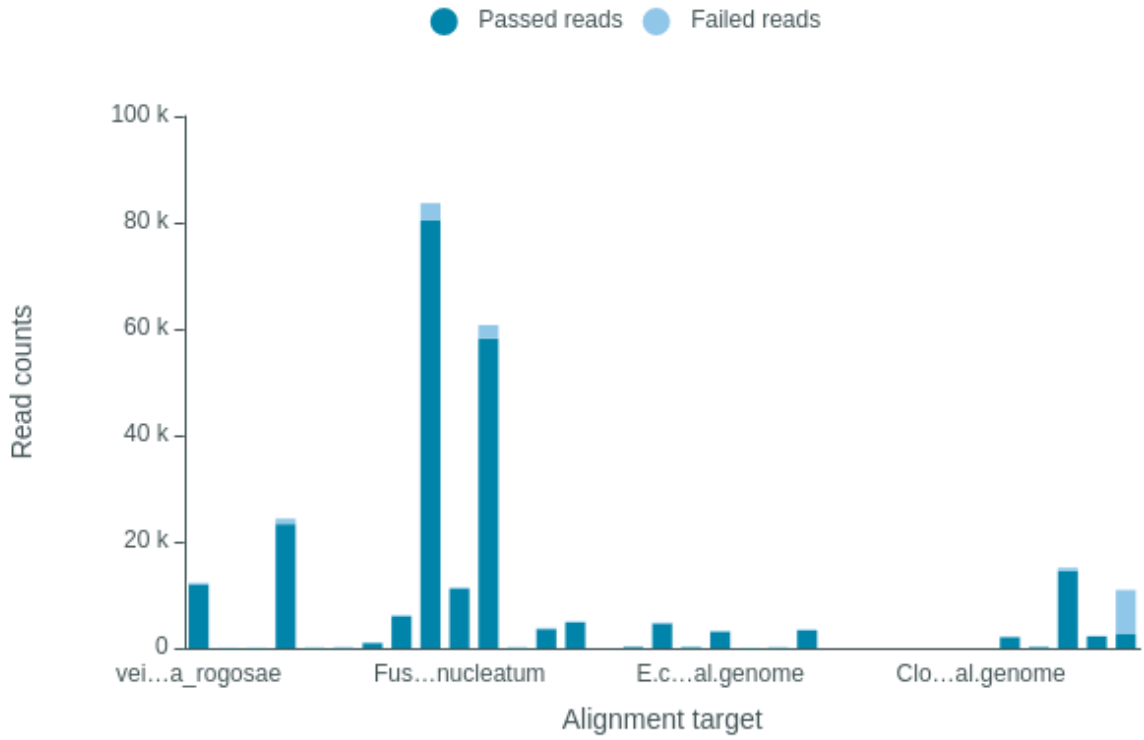


Read Length Histogram Basecalled Bases

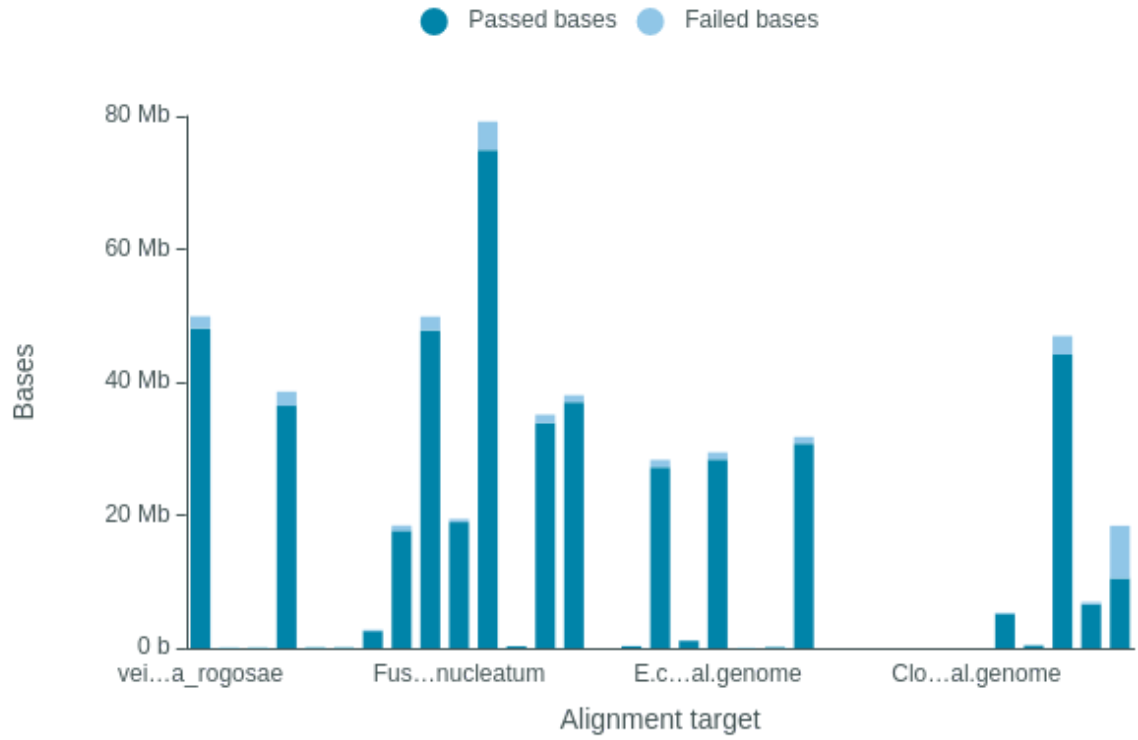
Estimated N50: 11.24 kb



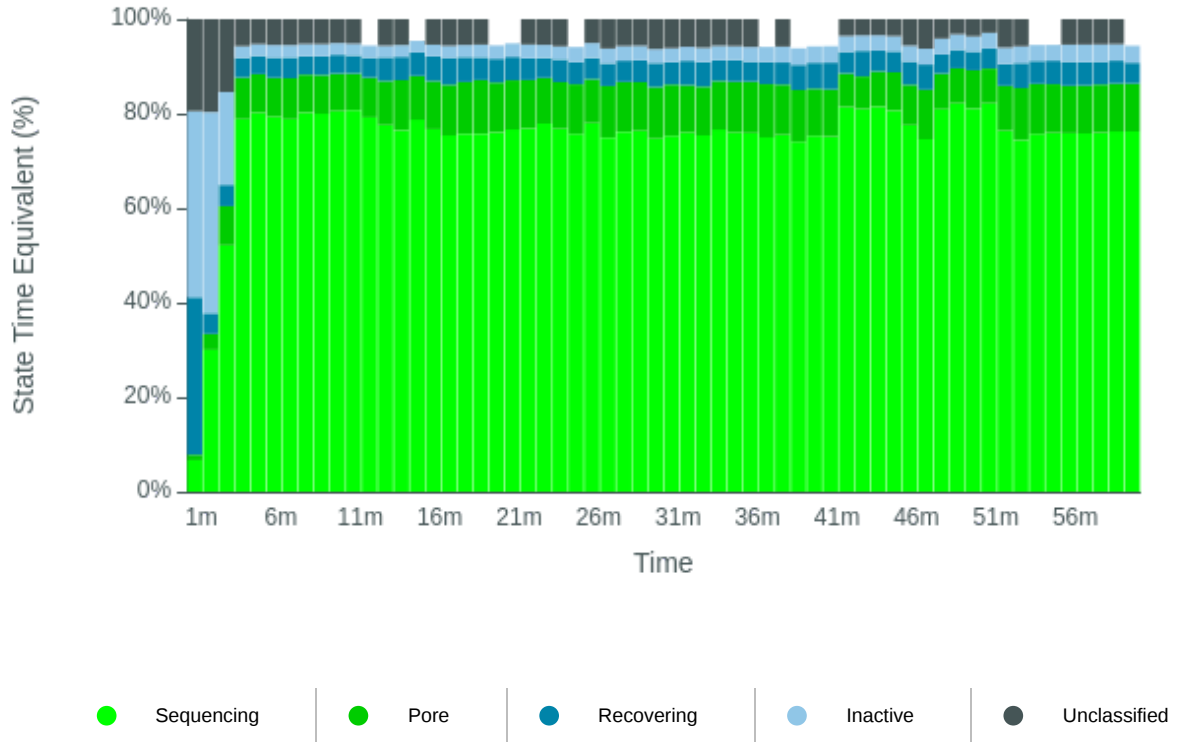
Alignment Target Hits (reads)



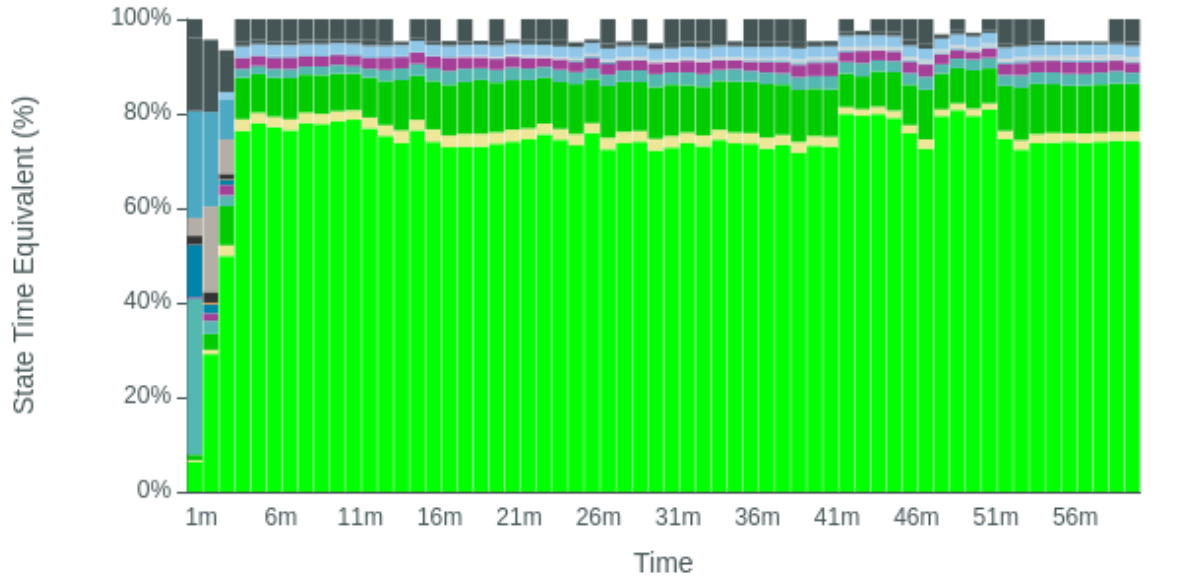
Alignment Target Hits (bases)



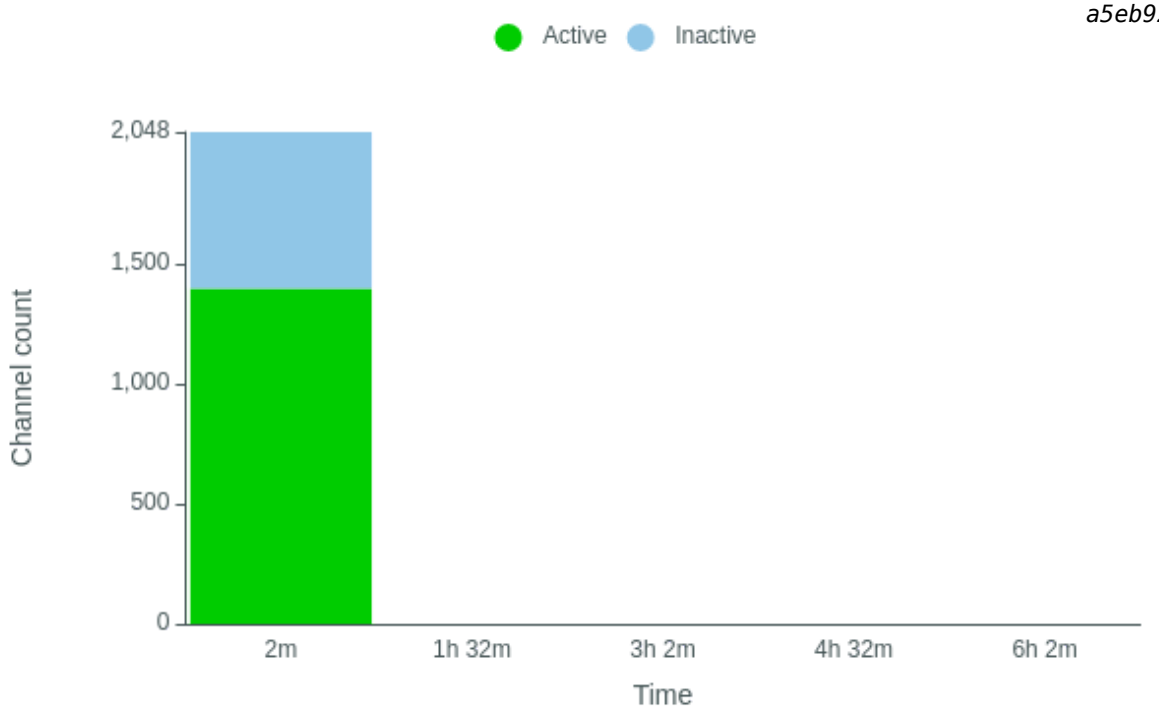
Duty Time Grouped



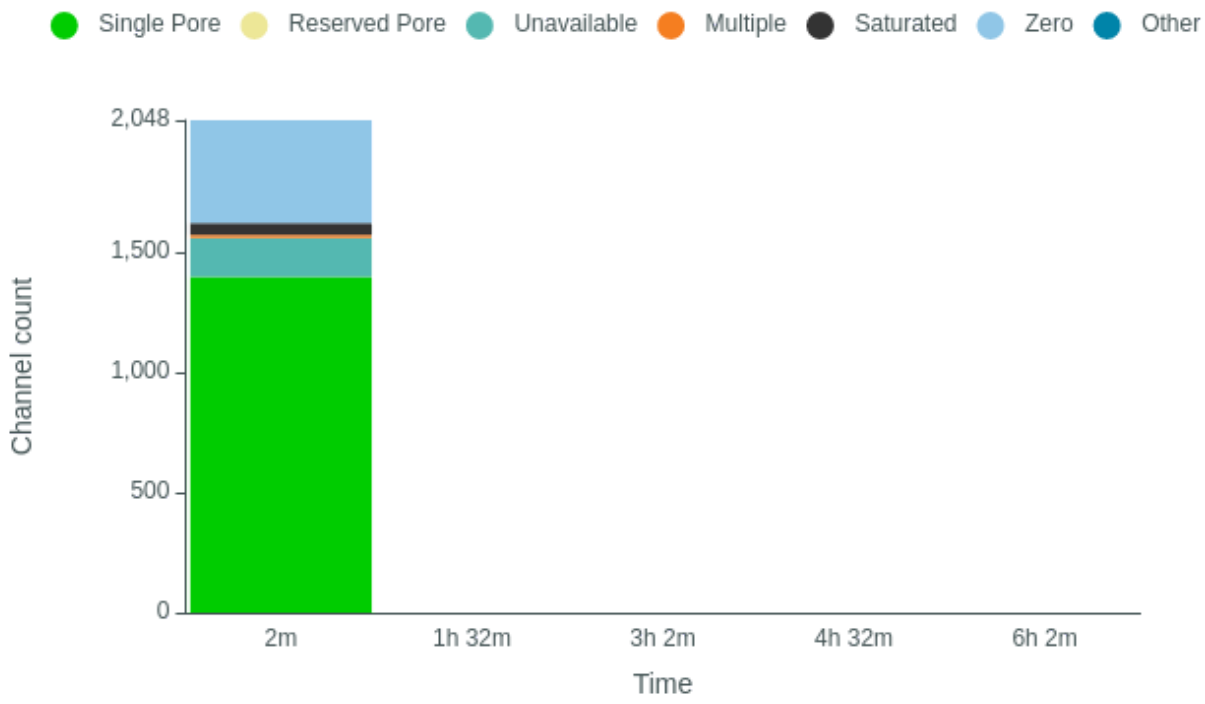
Duty time Categorised



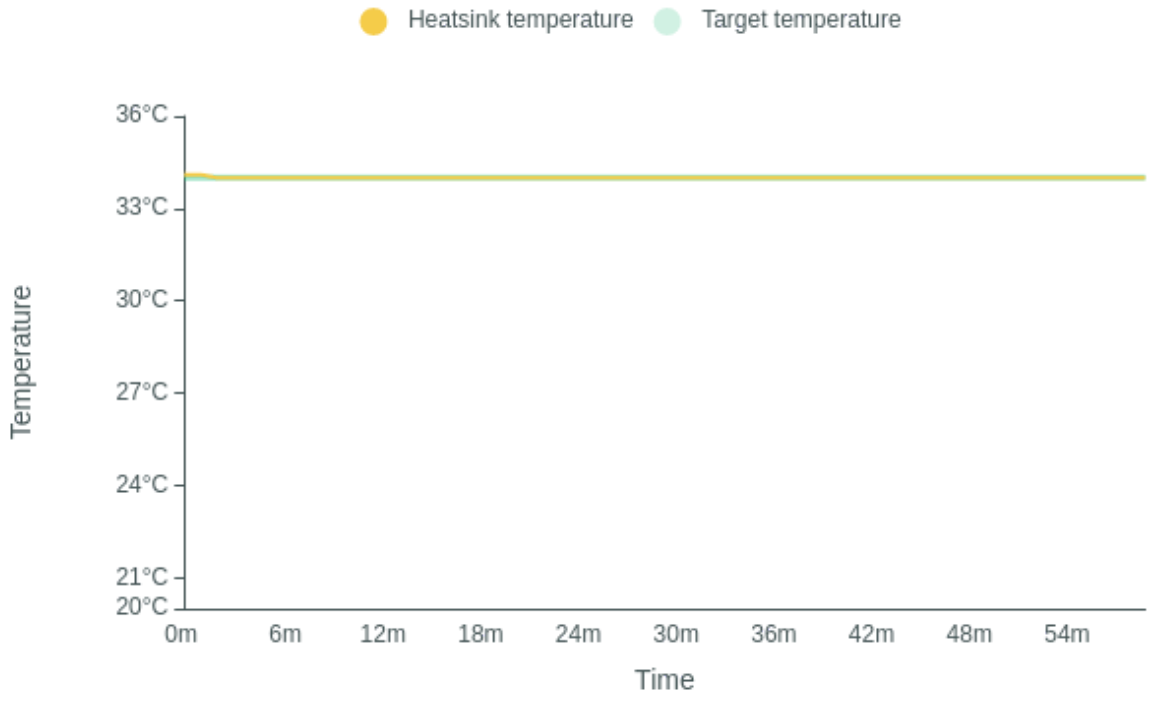
Mux Scan Grouped



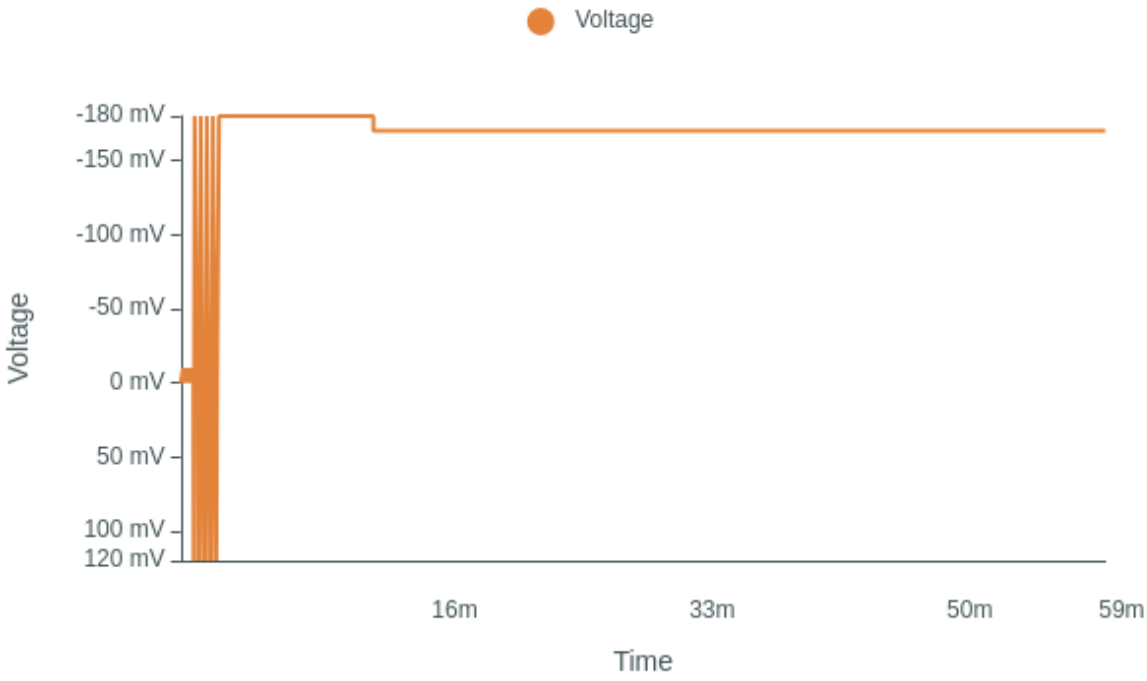
Mux Scan Categorised



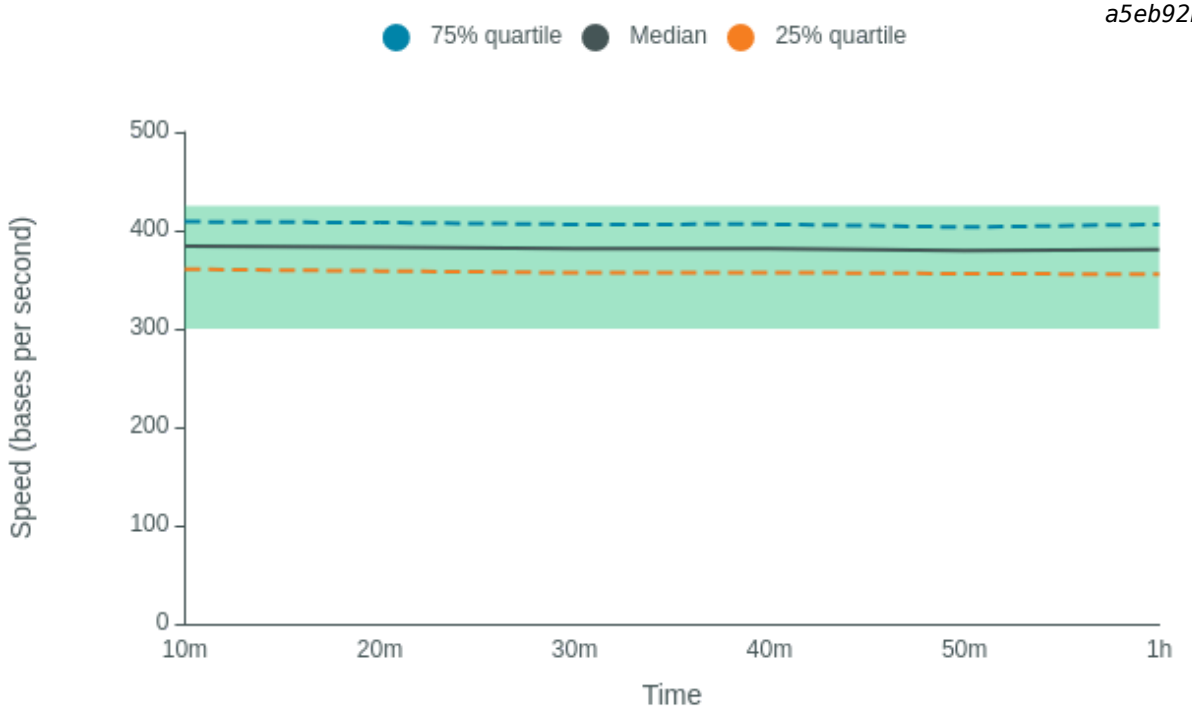
Temperature History



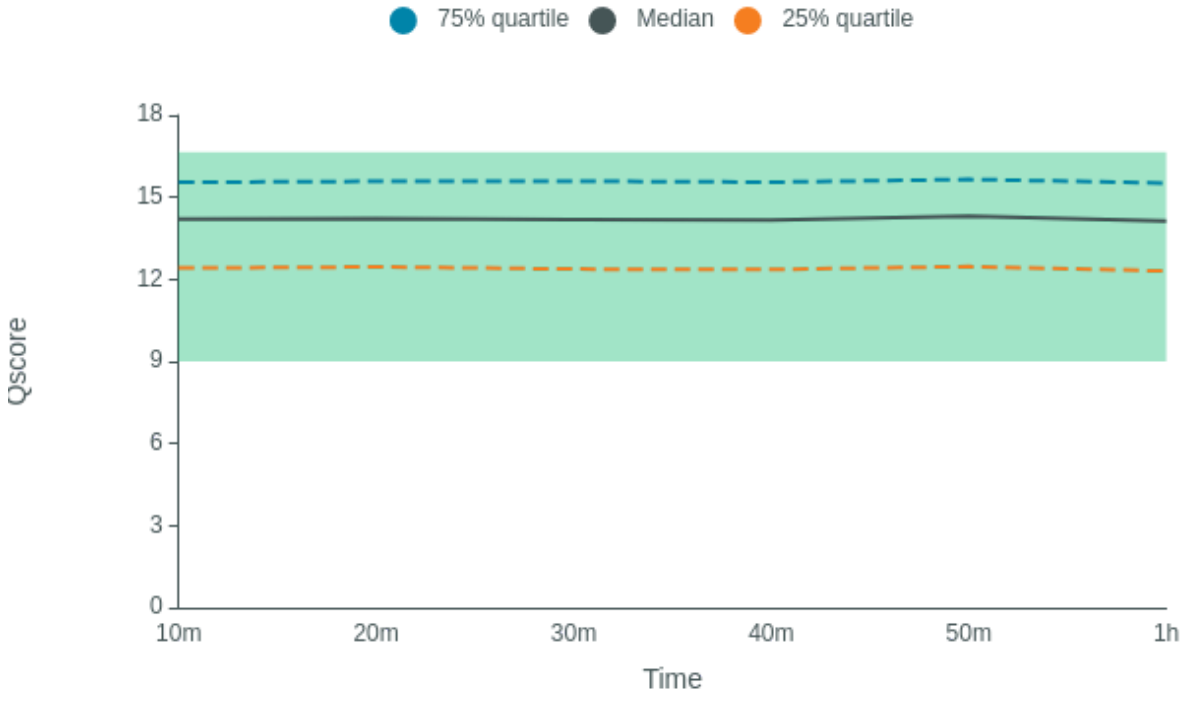
Bias Voltage History



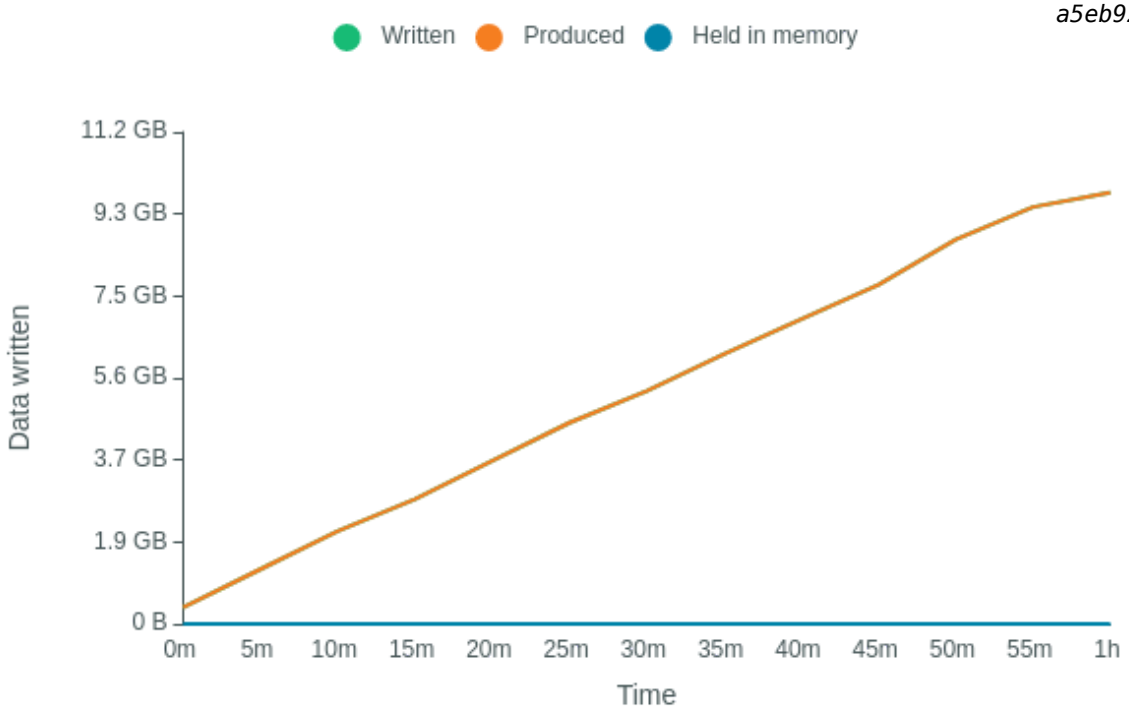
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13458 has found a total of 1396 pores. 500 pores available for immediate sequencing September 23, 13:11
- Performing Mux Scan September 23, 13:09
- Starting sequencing procedure September 23, 13:09
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 13:05