



Run Info

Host Name	GXb03422 (localhost)
Position	X2
Experiment Name	ReadUntil_ZGM_EcoliEnrich_JM109_23092021
Sample ID	ReadUntil_ZGM_EcoliEnrich_JM109_23092021
Run ID	478c45ab-e792-4fc0-bbfc-c498b44d13bf
Acquisition ID(s)	8772ee6f173c9d1a96ebffd722c708d4072b8ff5, f0351f0871b8d7cf6d5586c400fcca53782757ed
Flow Cell Id	FAR13458
Start Time	September 23, 16:19
Run Length	1h 3m

Run Summary

Reads Generated	236.86 k
Passed Bases	458.03 Mb
Failed Bases	34.99 Mb
Estimated Bases	519.6 Mb

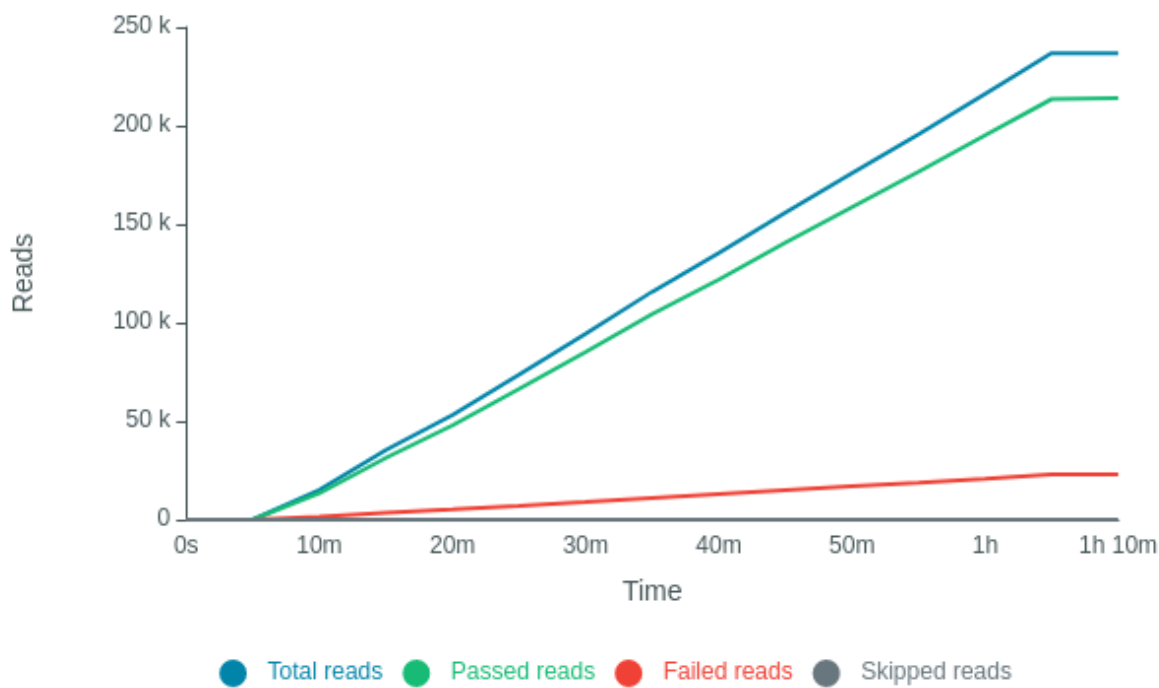
Run Parameters

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_JM109.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

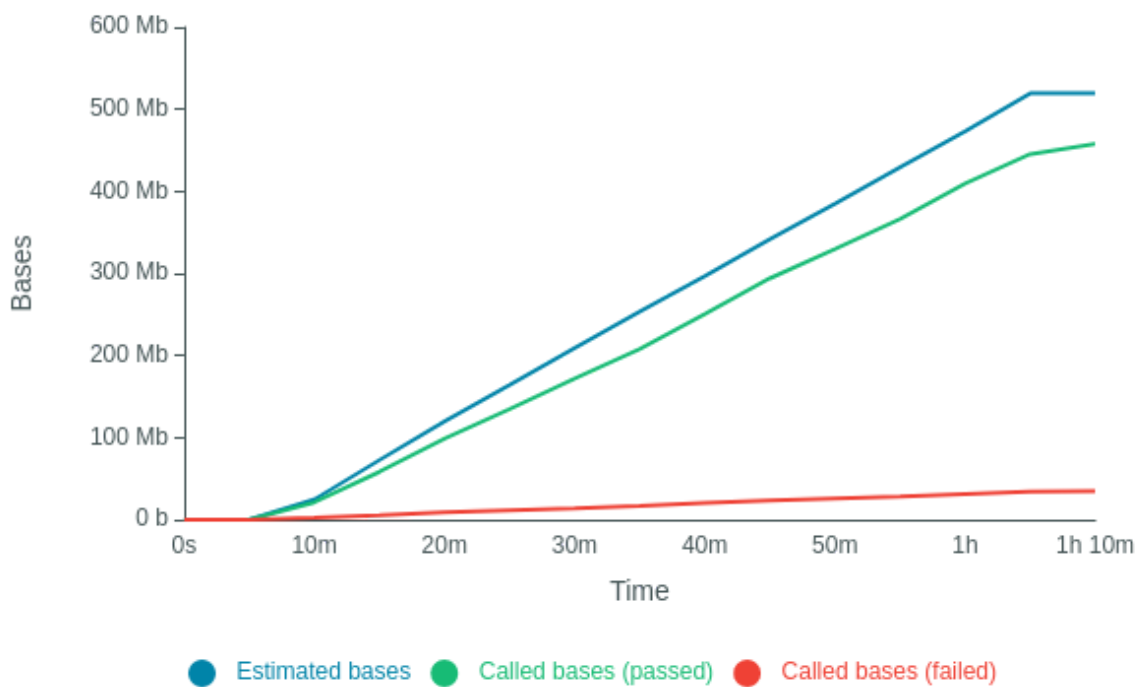
Versions

MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads

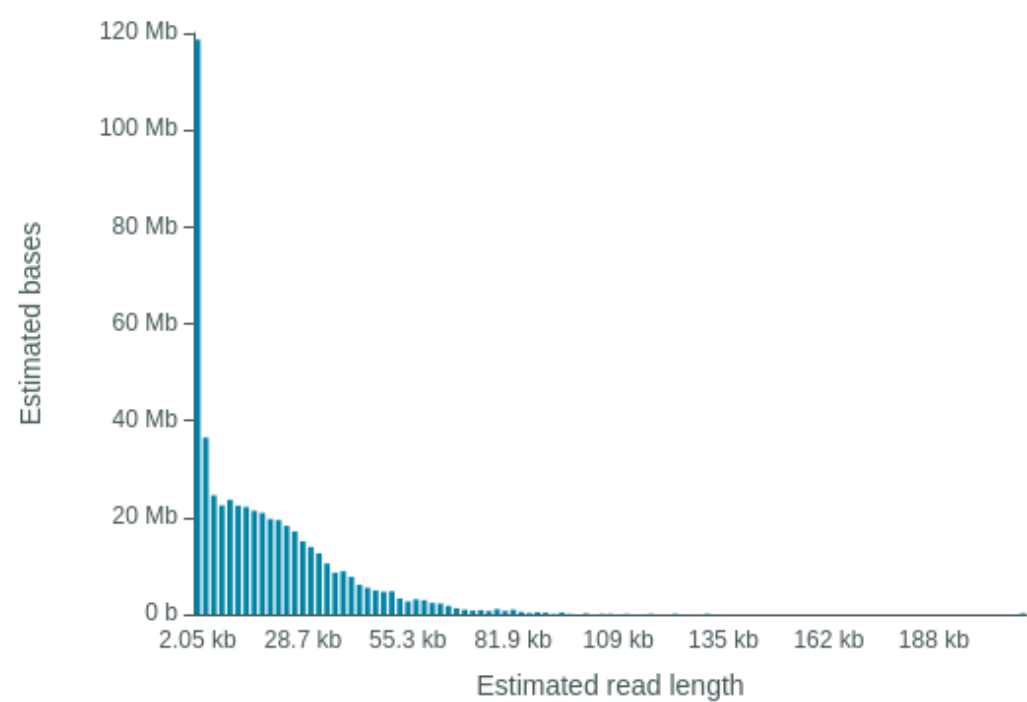


Cumulative Output Bases



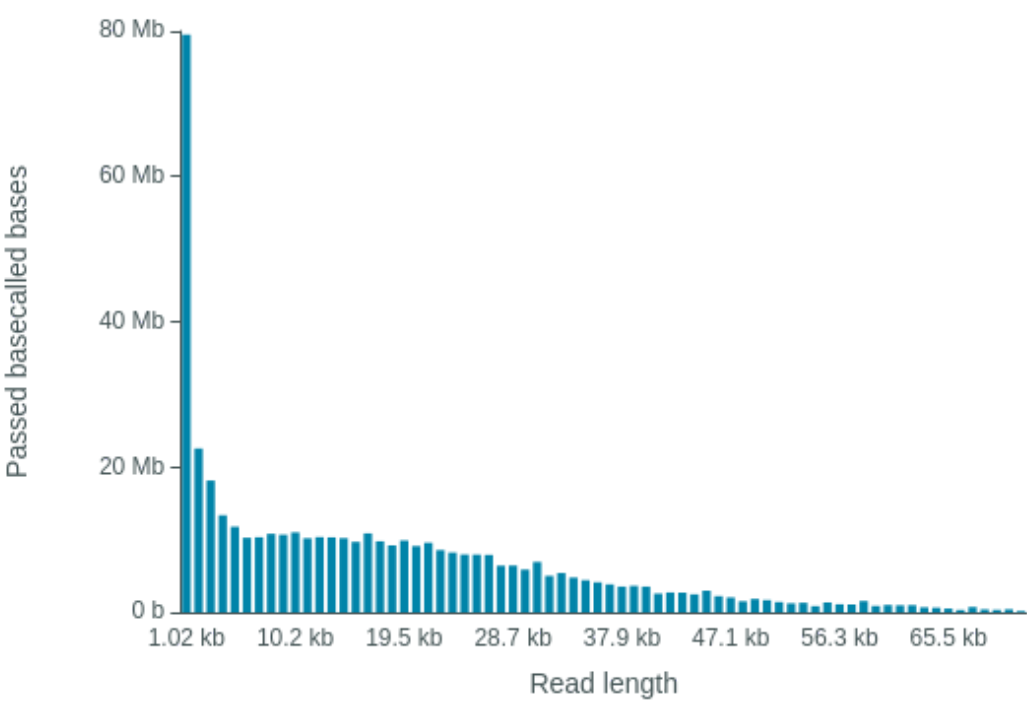
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 13.35 kb



Read Length Histogram Basecalled Bases - Outliers Discarded

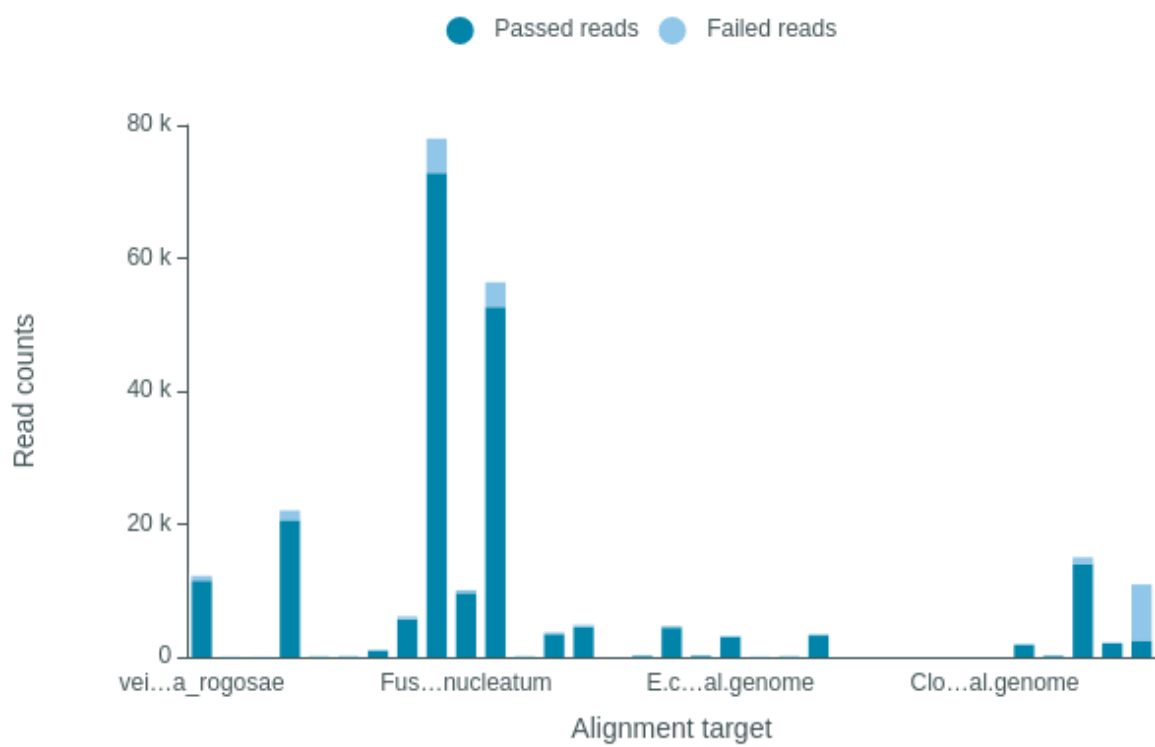
Estimated N50: 13.04 kb



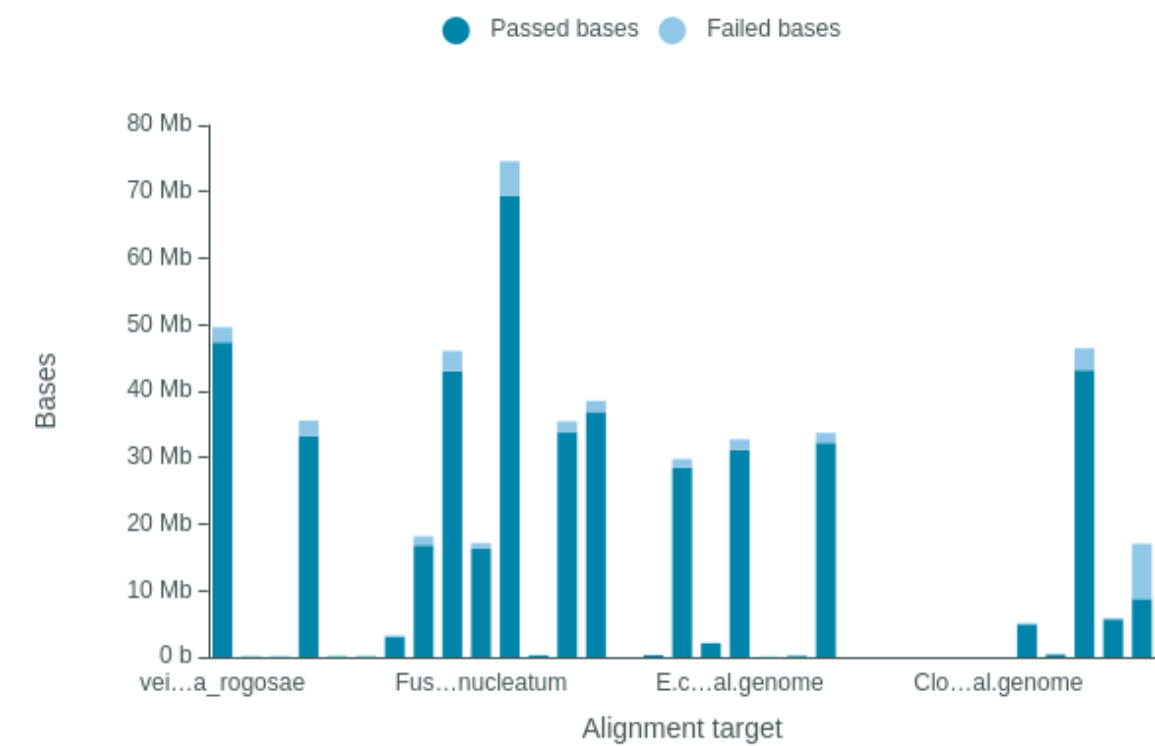
Estimated N50: 13.35 kb

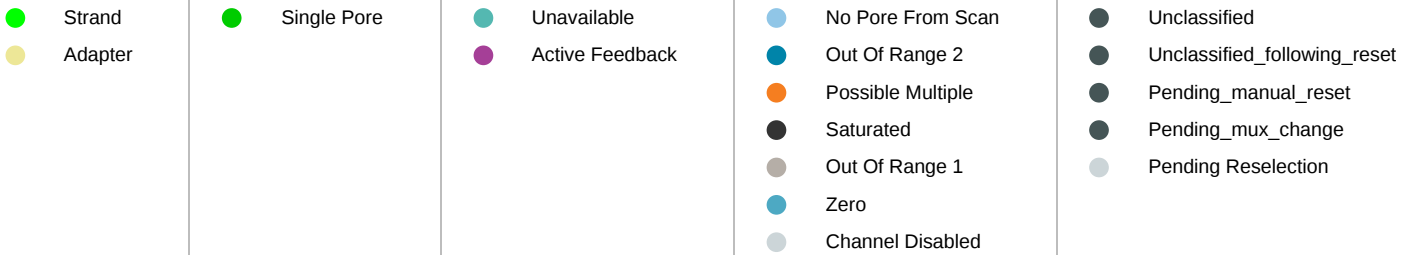
[illegible]

Alignment Target Hits (reads)

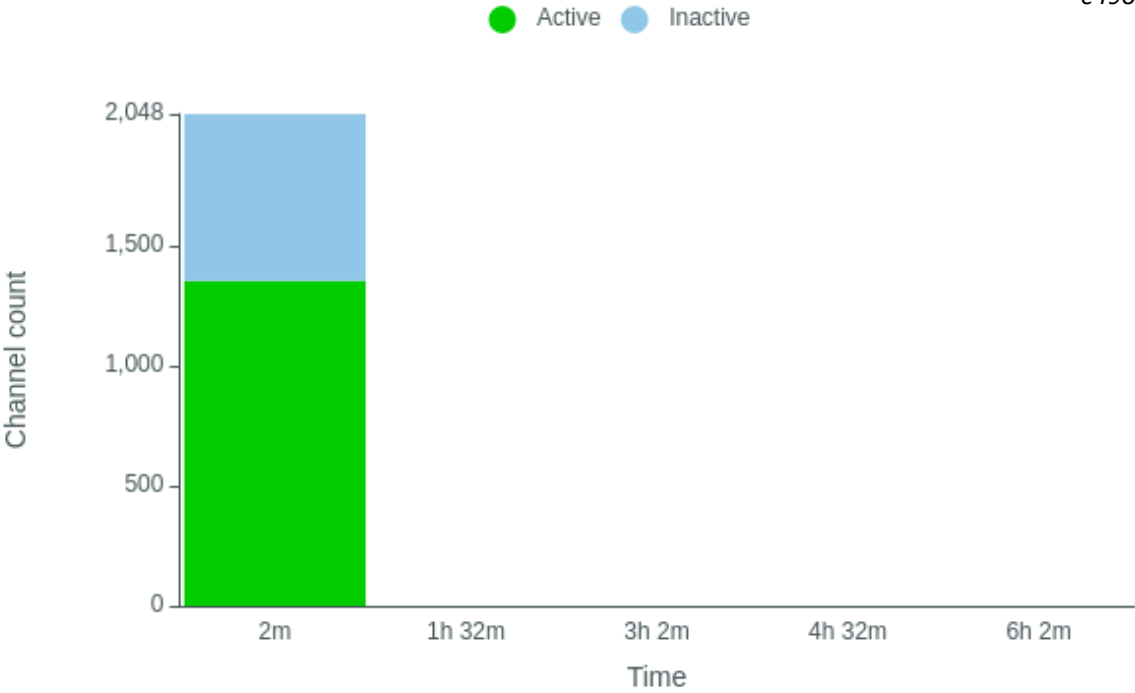


Alignment Target Hits (bases)

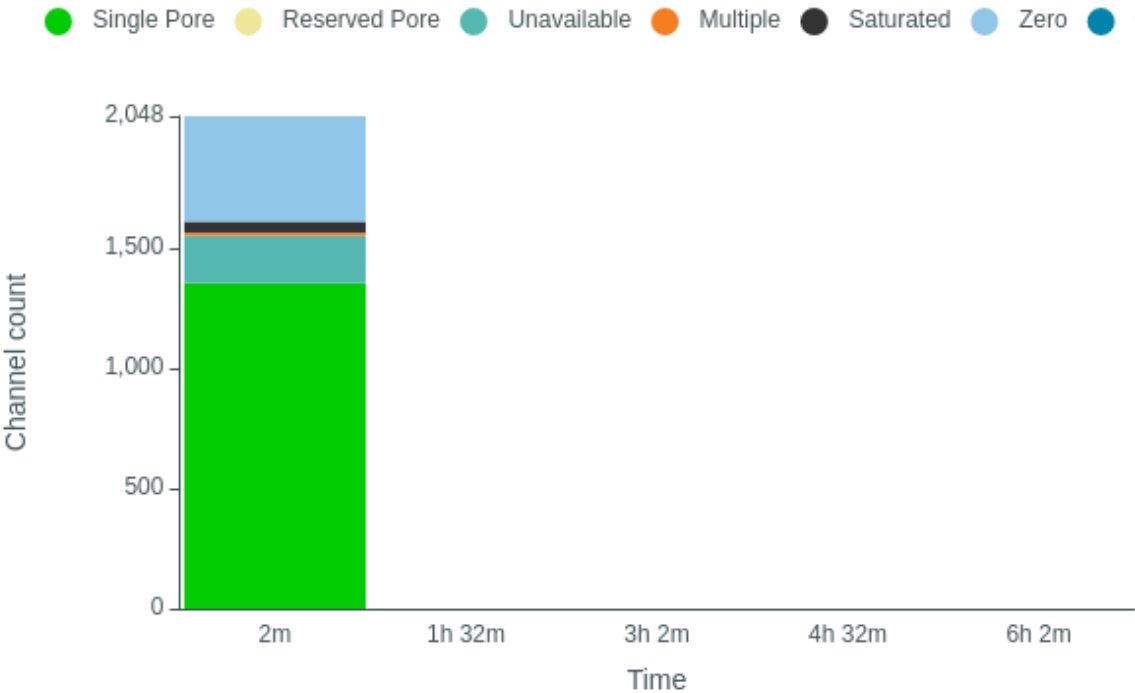




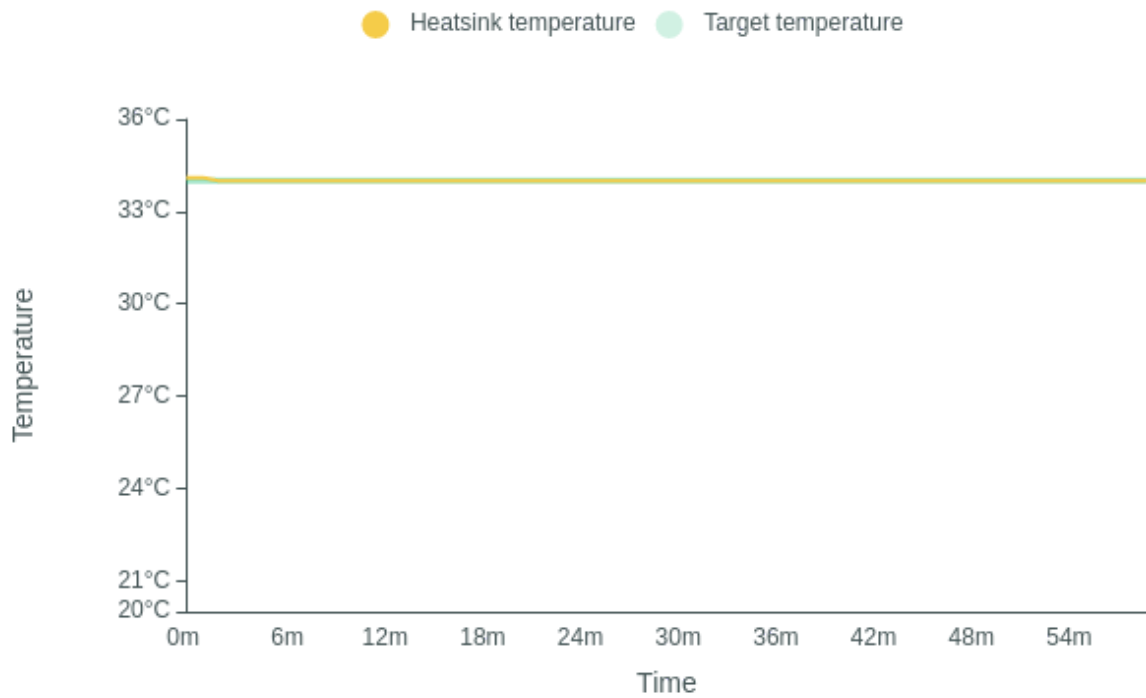
Mux Scan Grouped



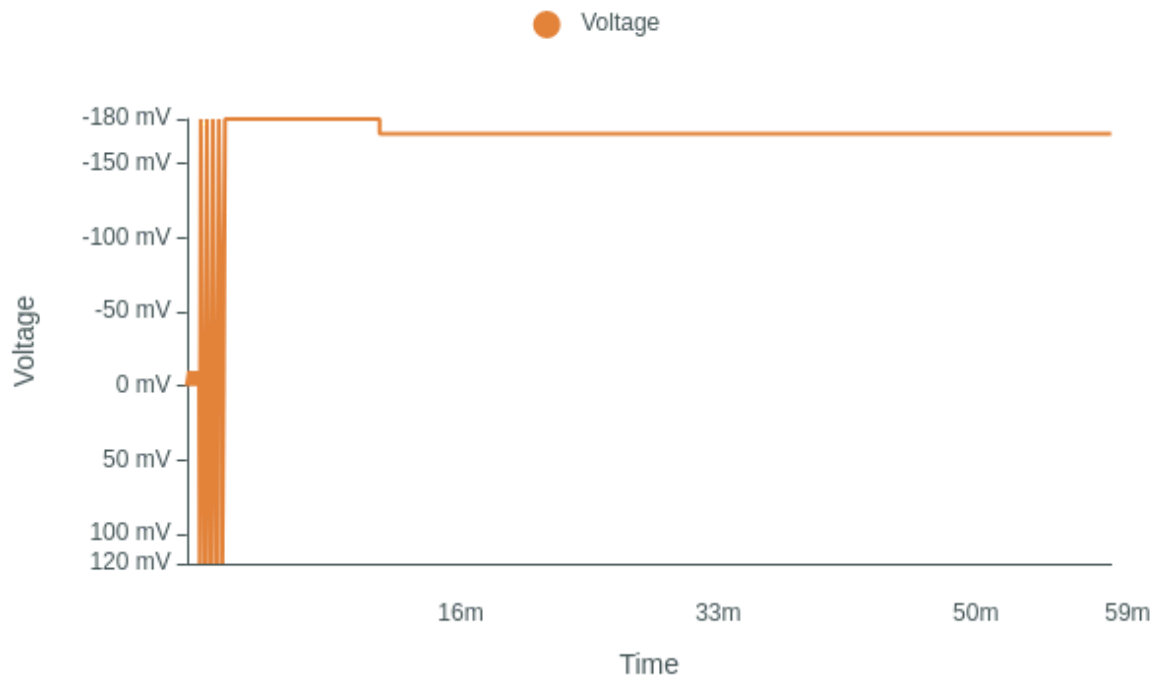
Mux Scan Categorised



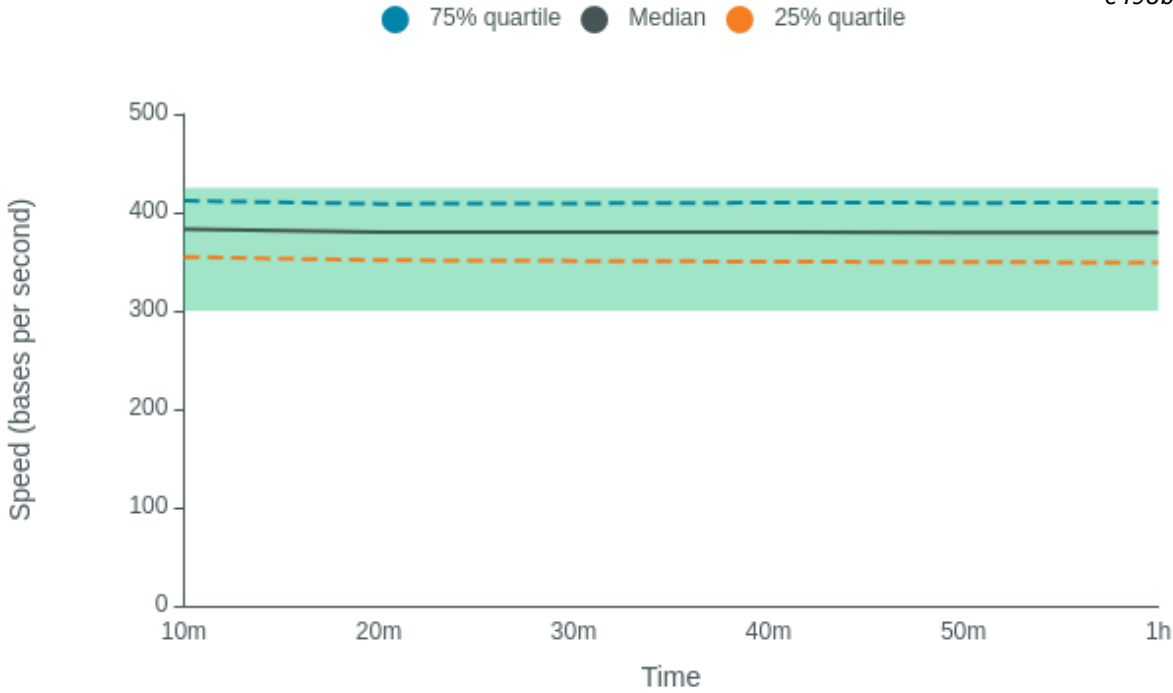
Temperature History



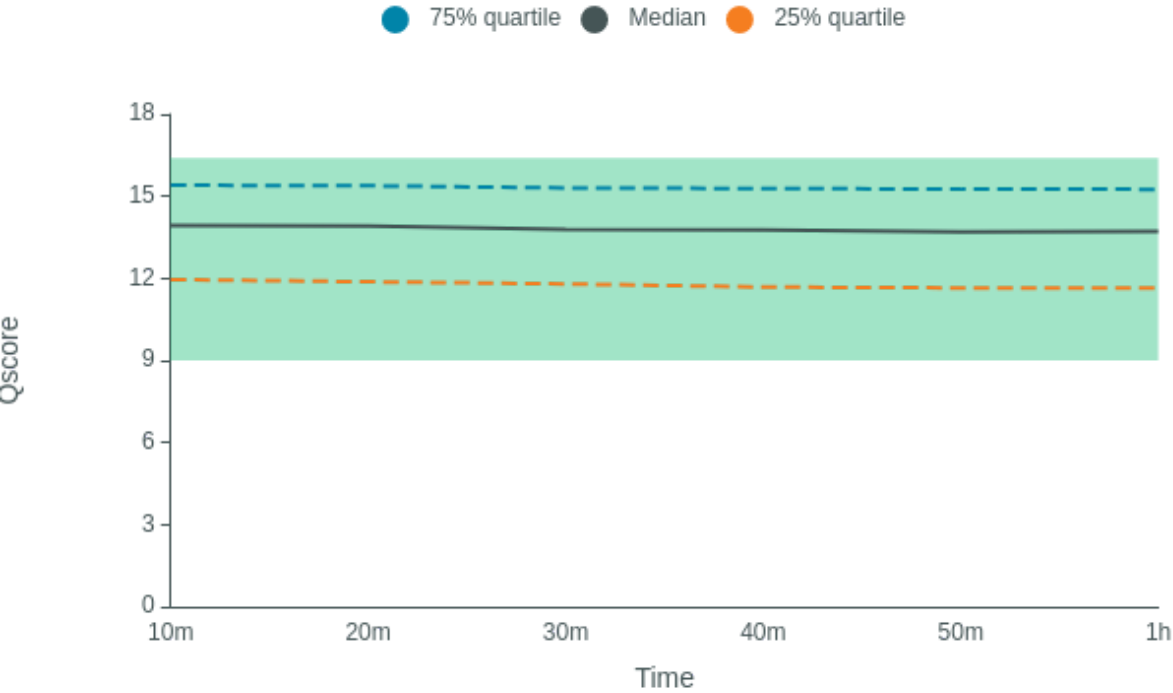
Bias Voltage History



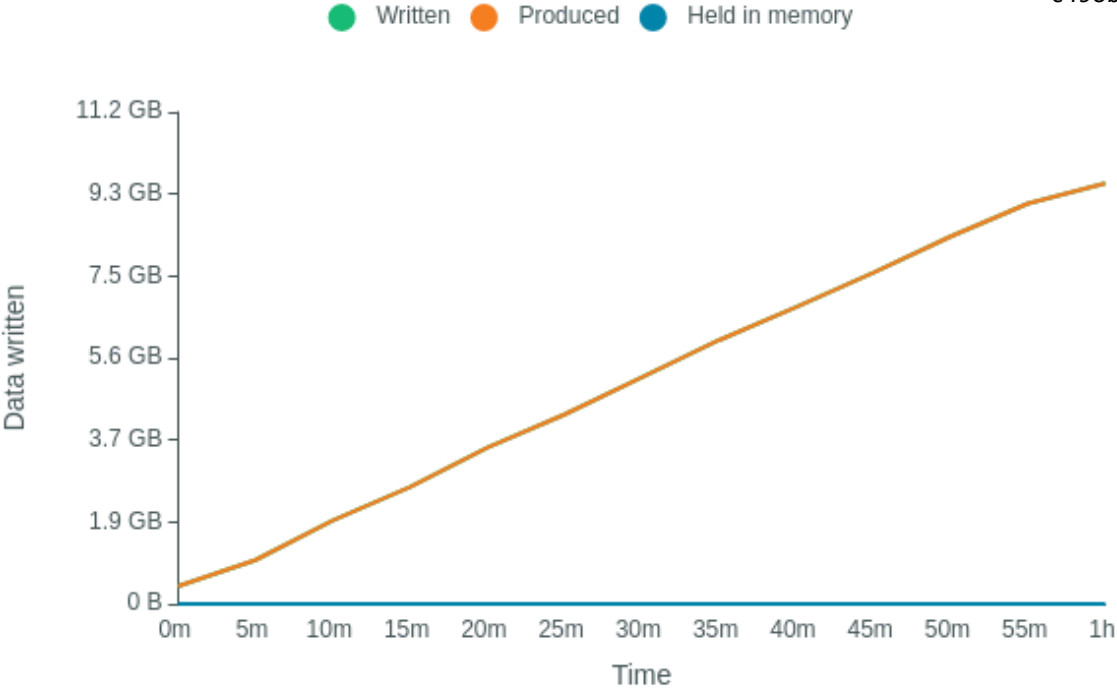
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13458 has found a total of 1354 pores. 497 pores available for immediate sequencing September 23, 16:25
- Performing Mux Scan September 23, 16:23
- Starting sequencing procedure September 23, 16:23
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 16:19