



Run Info

Host Name	GXb03422 (localhost)
Position	X4
Experiment Name	ReadUntil_ZGM_Enrich_Senterica_23092021
Sample ID	ReadUntil_ZGM_Enrich_Senterica_23092021
Run ID	b0c60f33-7d99-4984-a24b-353584d1e30c
Acquisition ID(s)	2860b122fff2f7552692409ed8239a4a0e75451f, ef22430d84c15582c242b0d38bf94339fe79258b
Flow Cell Id	FAR13419
Start Time	September 23, 14:46
Run Length	1h 3m

Run Summary

Reads Generated	330.81 k
Passed Bases	418.92 Mb
Failed Bases	28.96 Mb
Estimated Bases	465.27 Mb

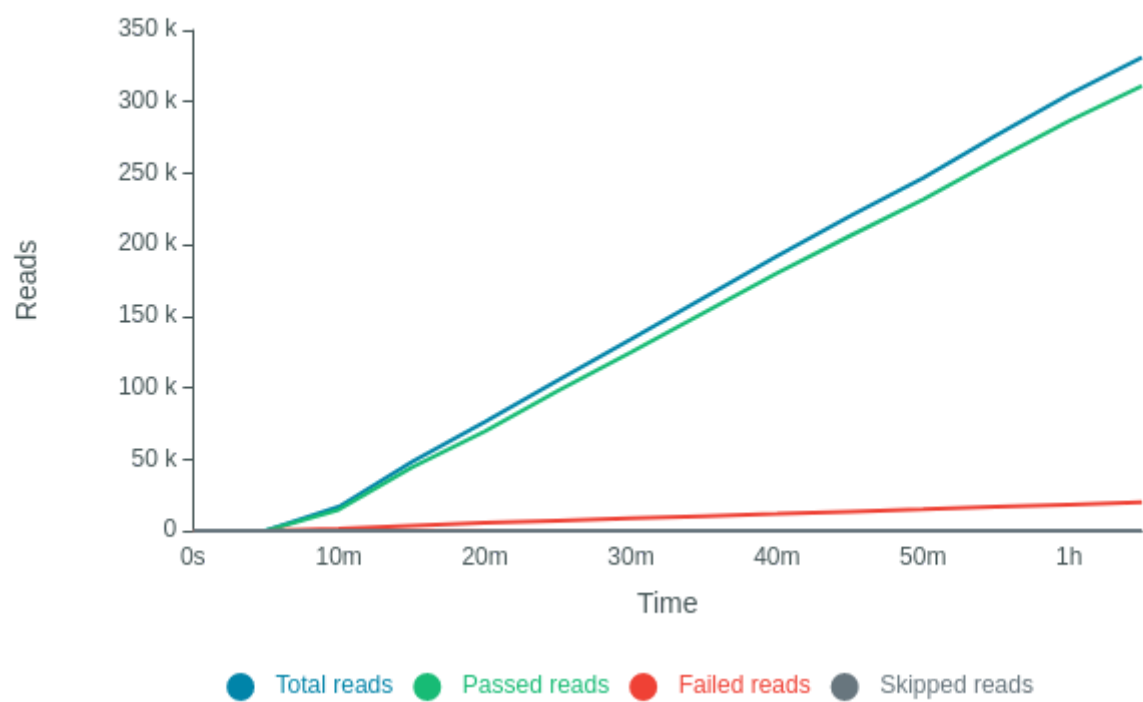
Run Parameters

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/Salmonella_enterica.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

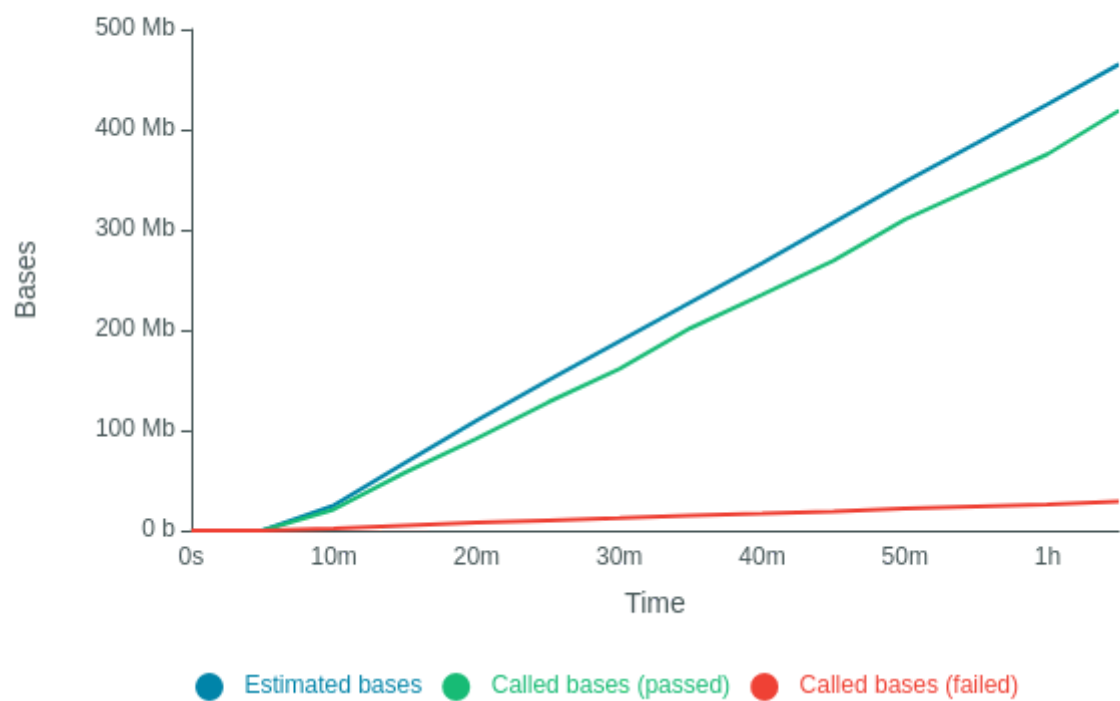
Versions

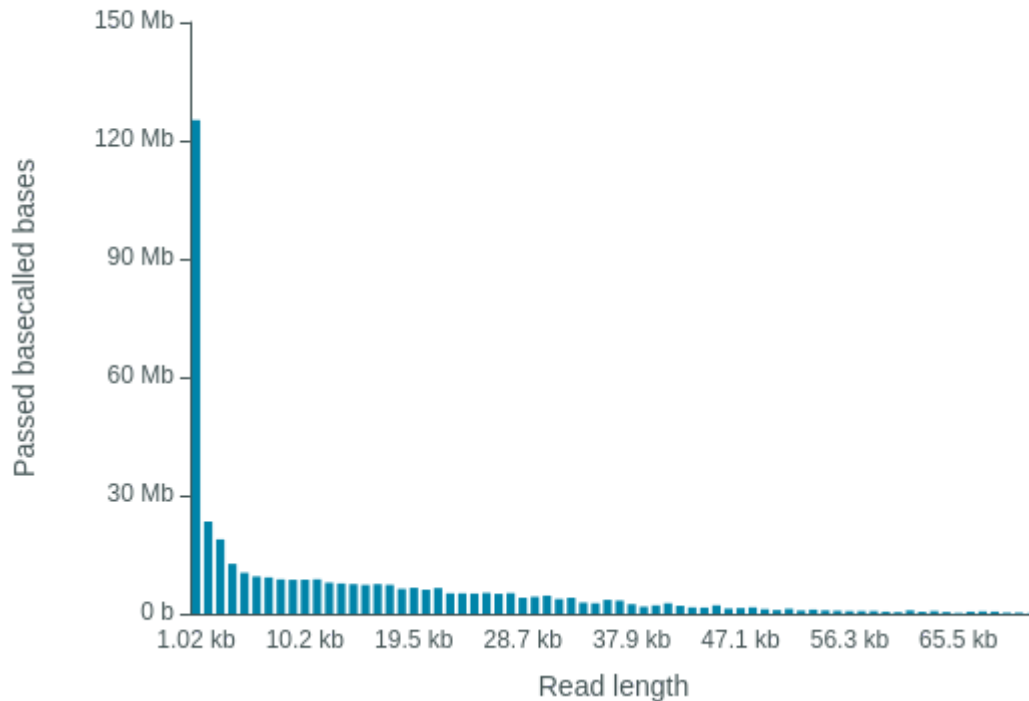
MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads



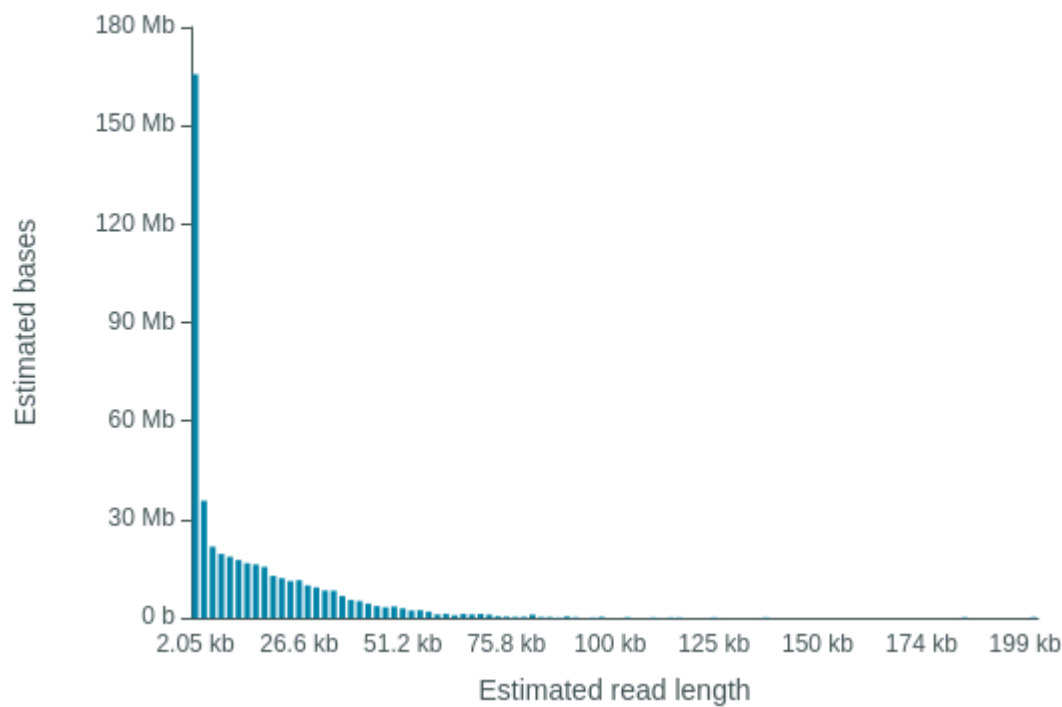
Cumulative Output Bases





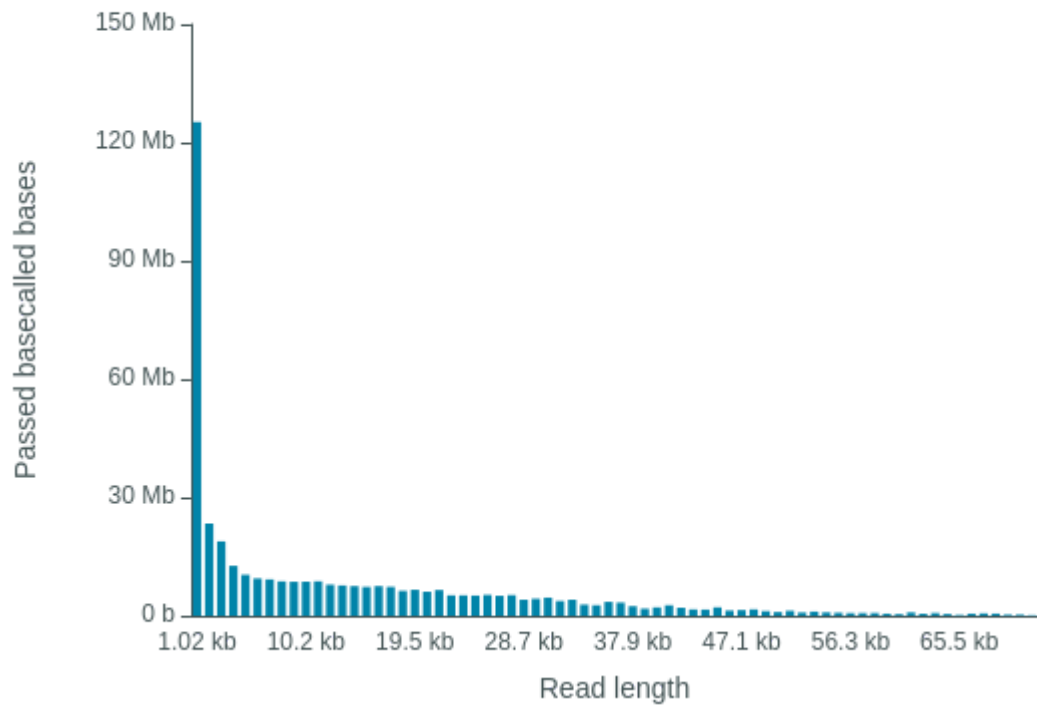
Read Length Histogram Estimated Bases

Estimated N50: 7.12 kb

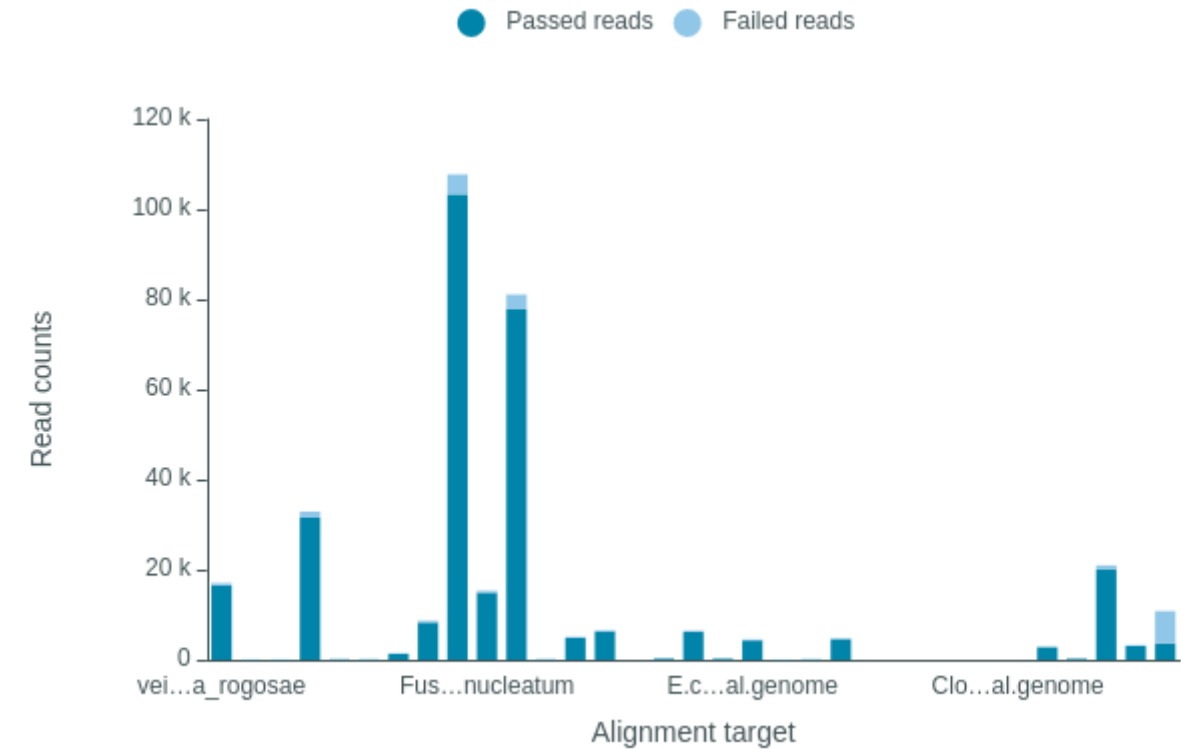


Read Length Histogram Basecalled Bases

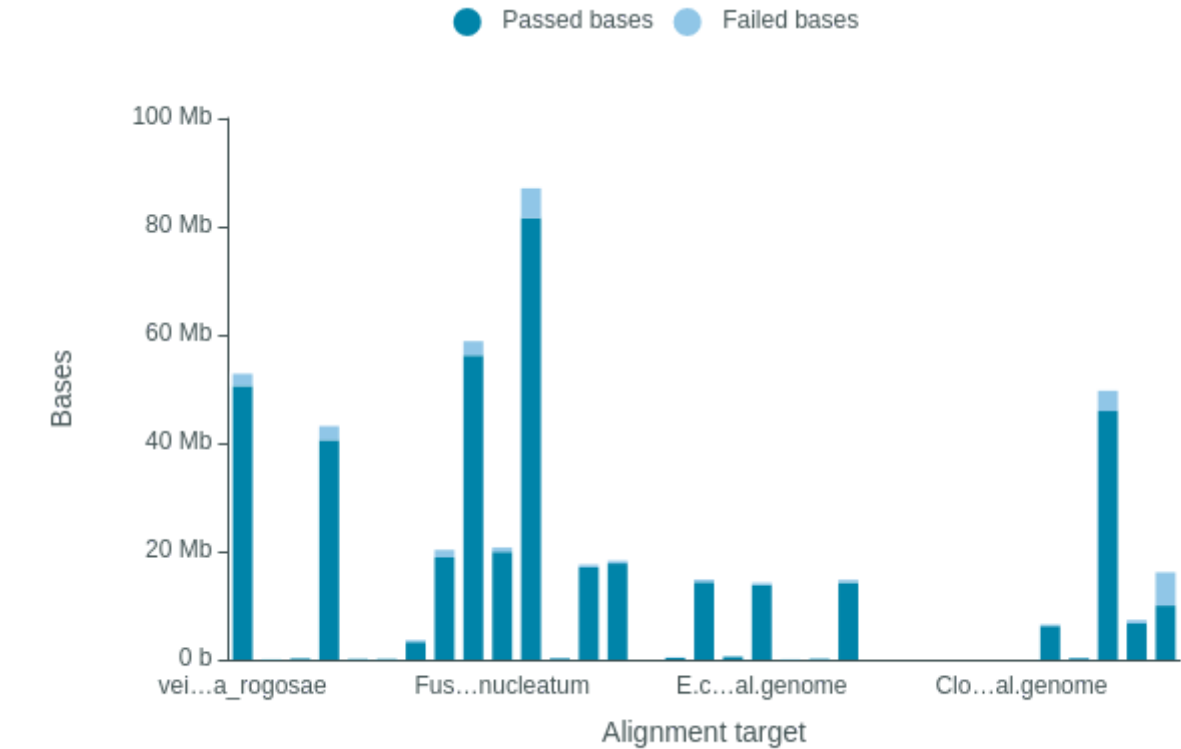
Estimated N50: 6.96 kb



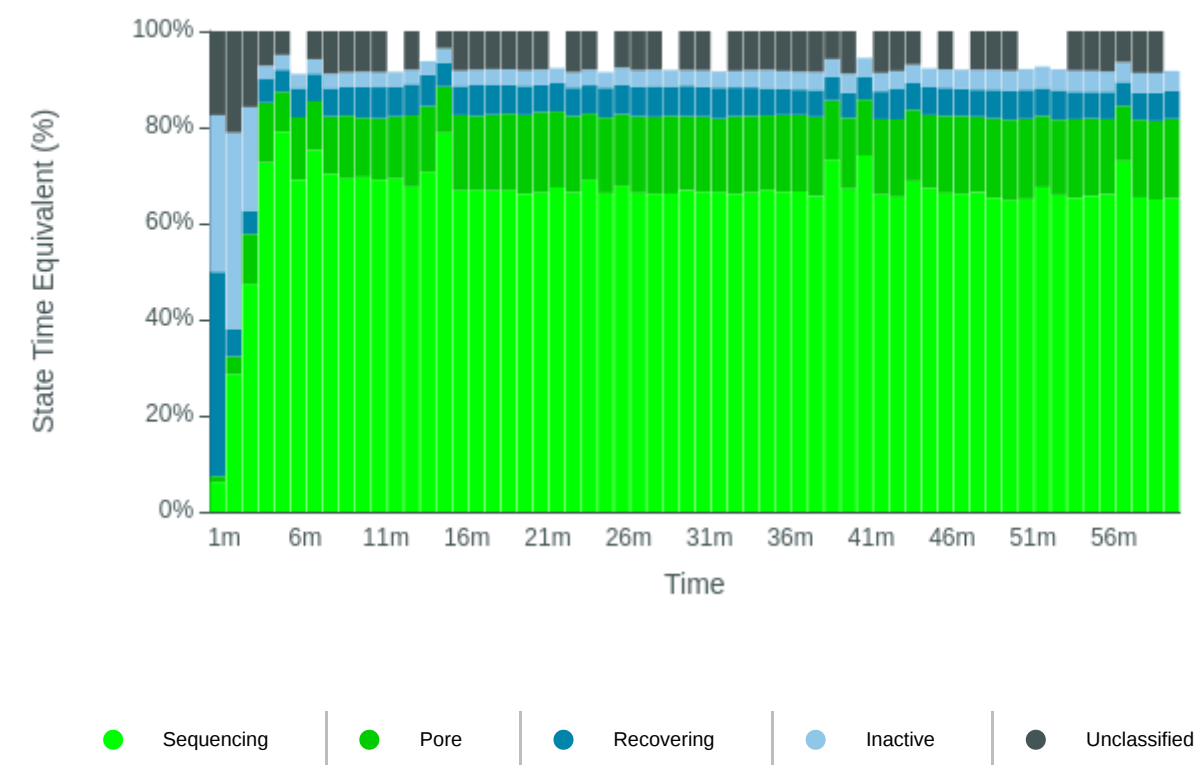
Alignment Target Hits (reads)



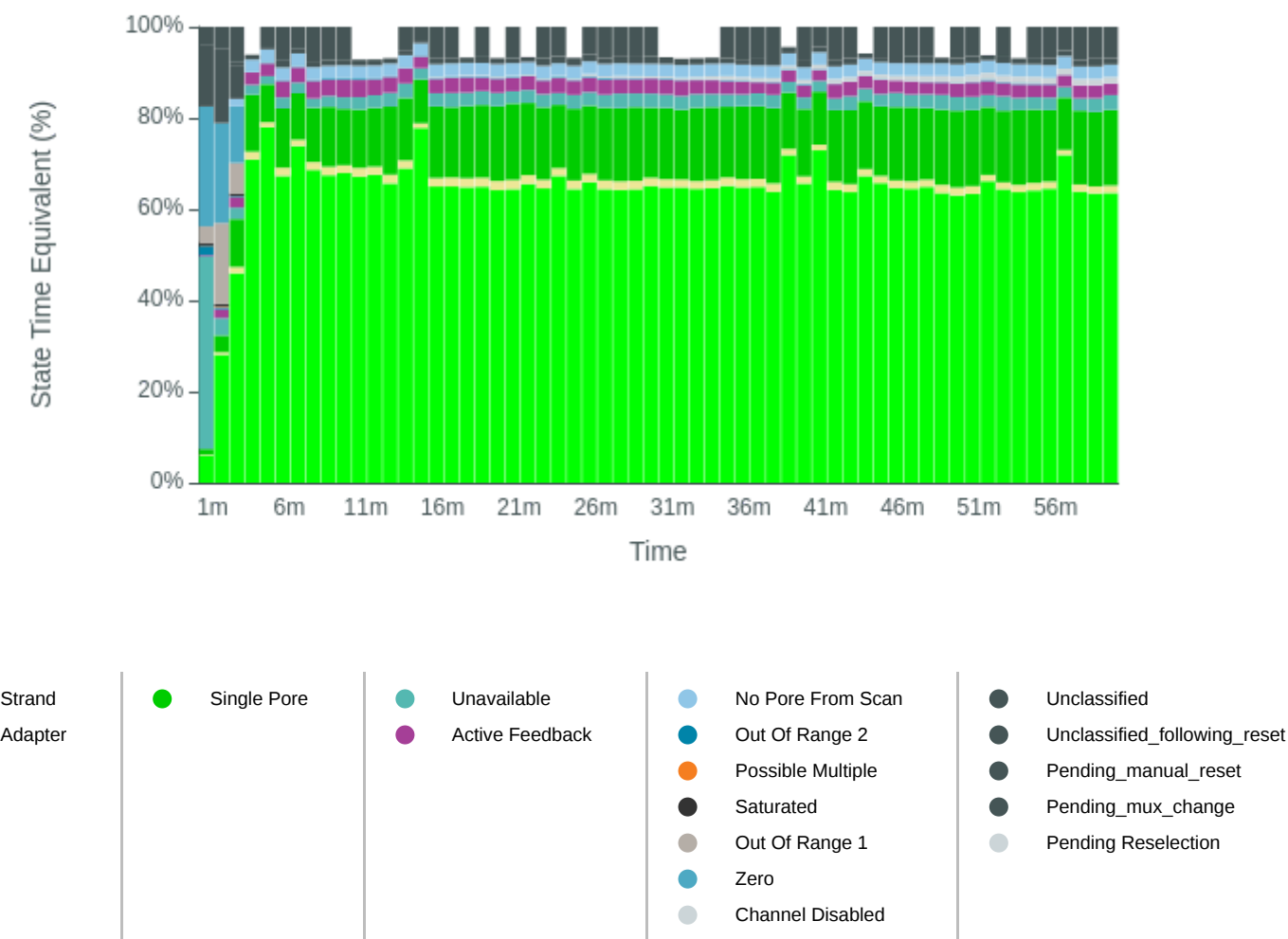
Alignment Target Hits (bases)



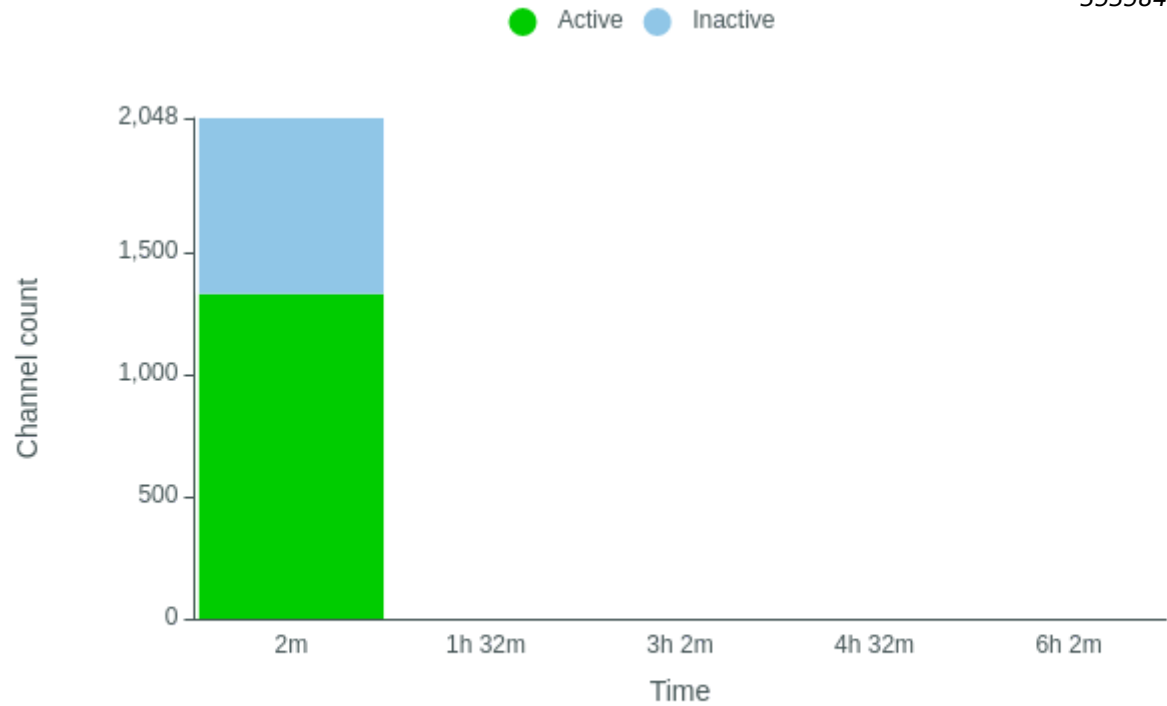
Duty Time Grouped



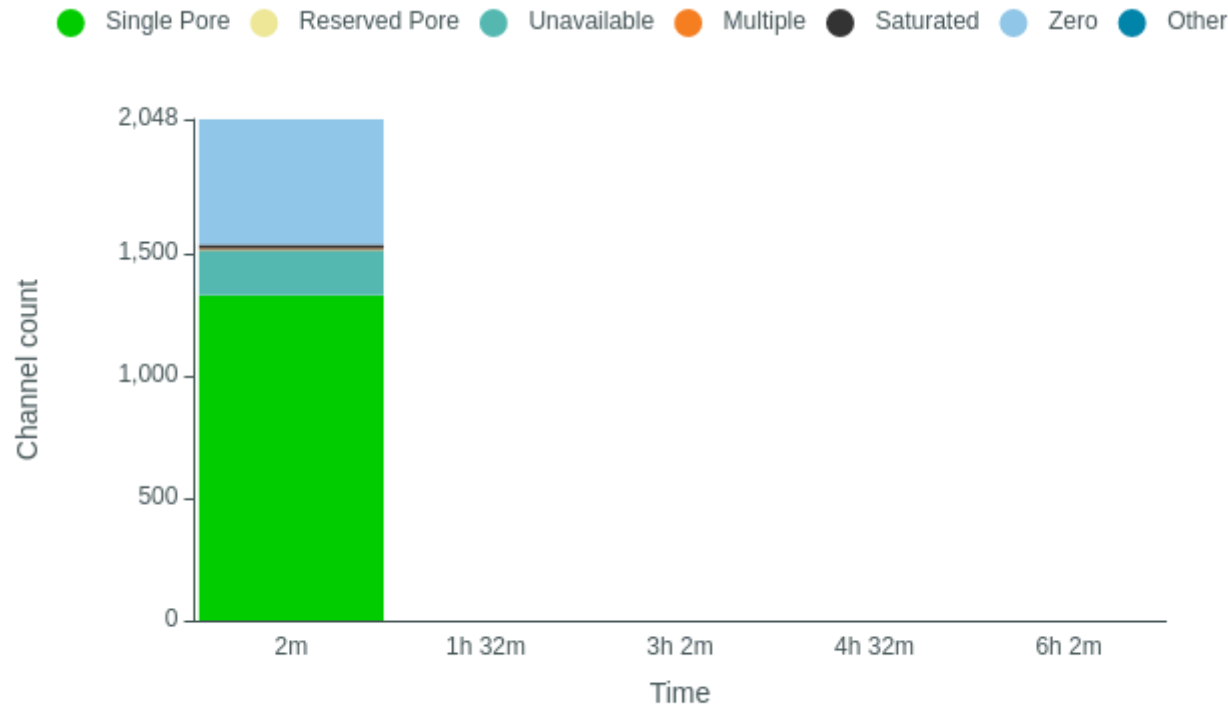
Duty time Categorised



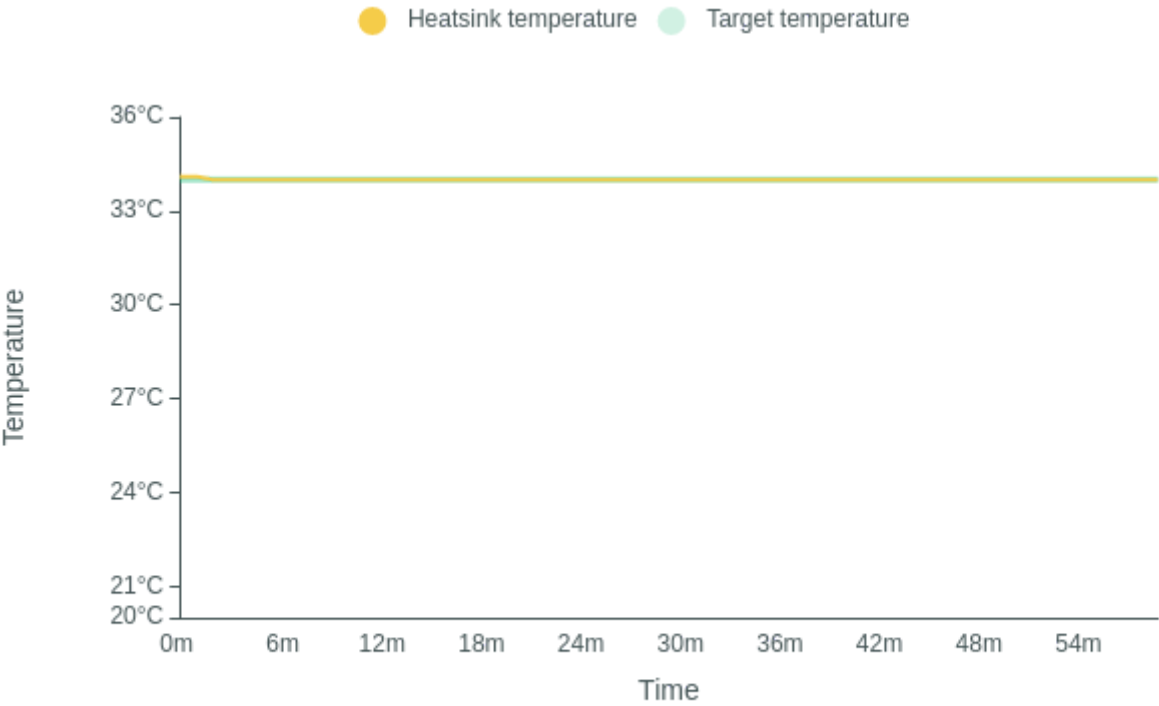
Mux Scan Grouped



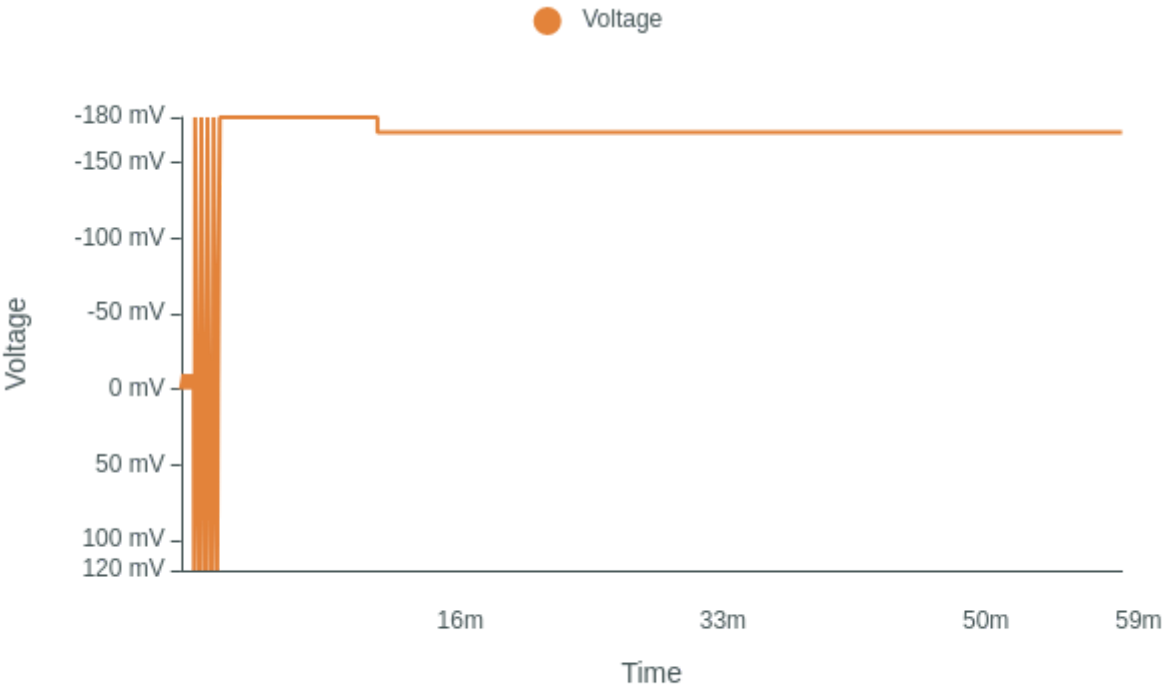
Mux Scan Categorised



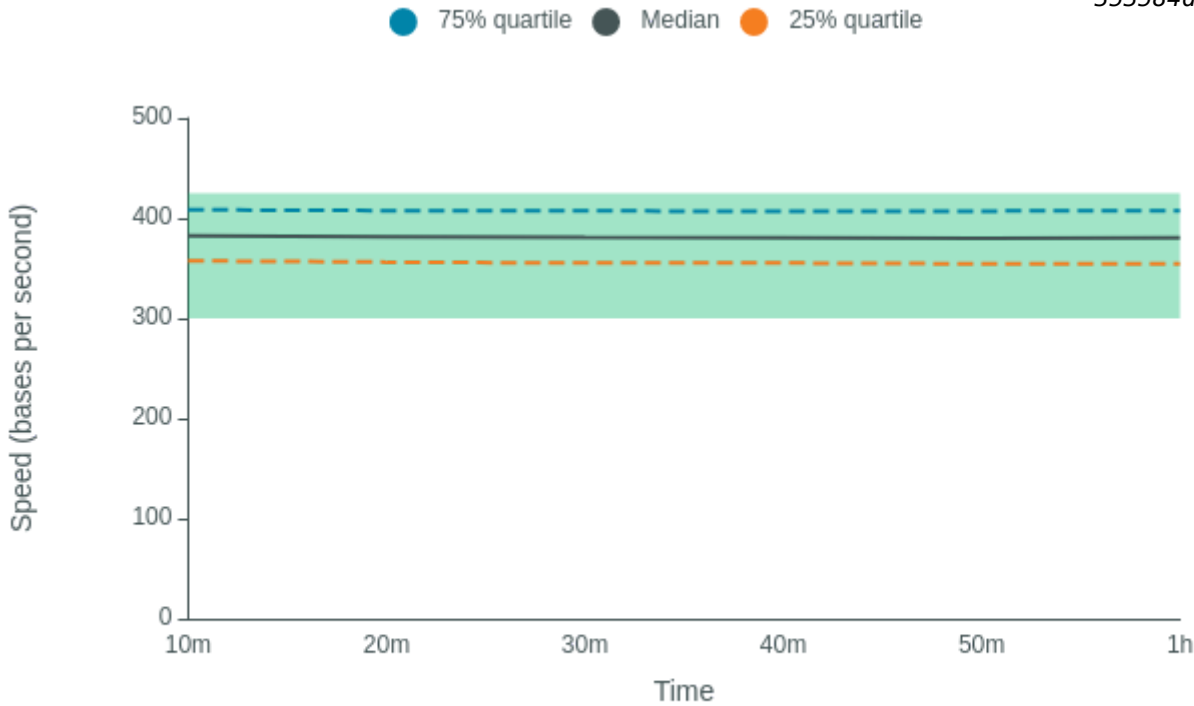
Temperature History



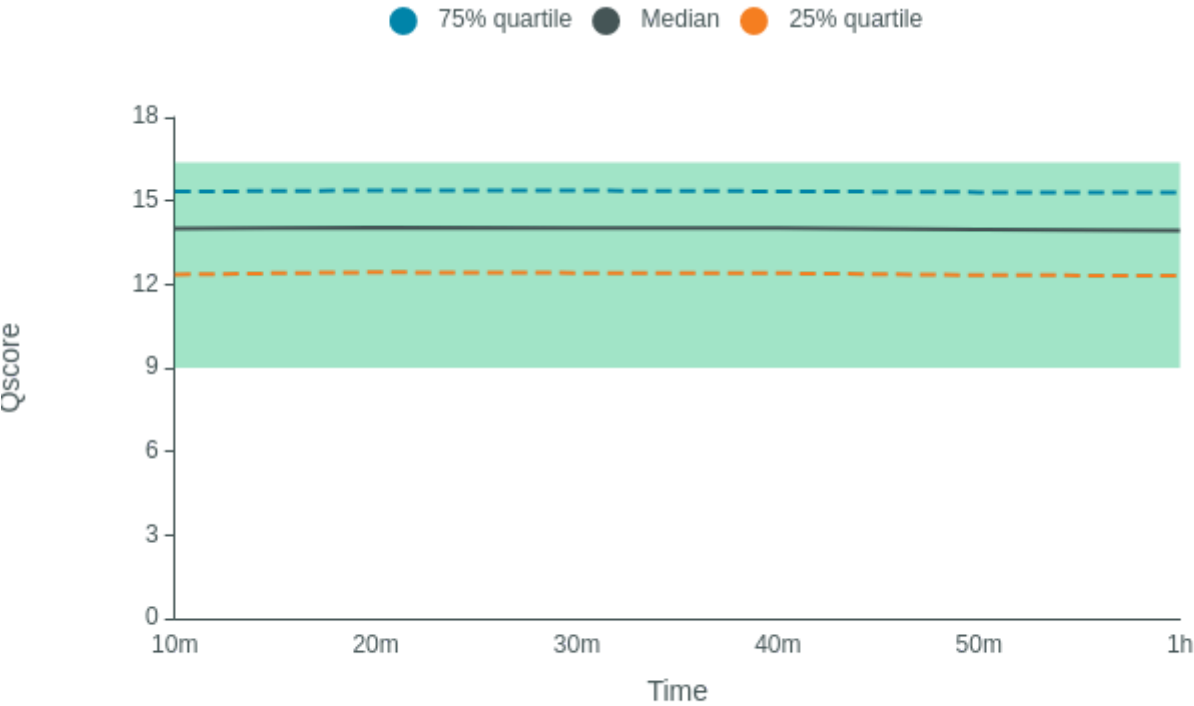
Bias Voltage History



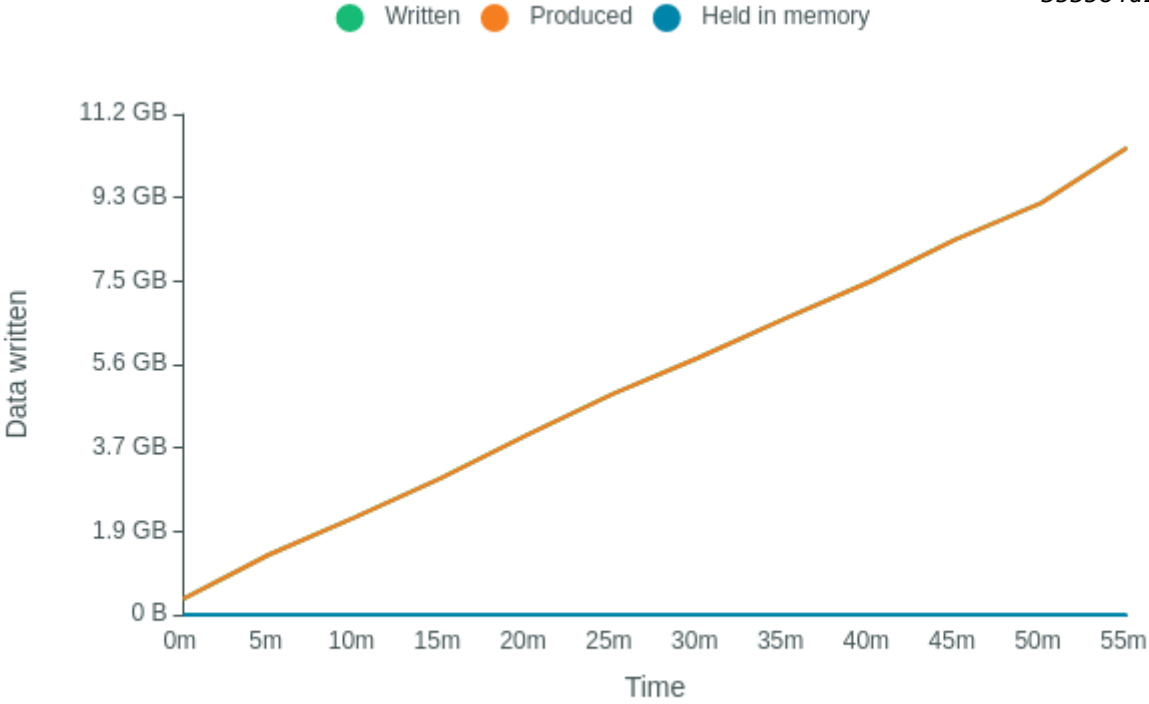
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13419 has found a total of 1329 pores. 498 pores available for immediate sequencing September 23, 14:52
- Performing Mux Scan September 23, 14:50
- Starting sequencing procedure September 23, 14:50
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 14:46