



## Run Info

Host Name	GXb03422 (localhost)
Position	X2
Experiment Name	ReadUntil_ZGM_EcoliEnrich_B766_23092021
Sample ID	ReadUntil_ZGM_EcoliEnrich_B766_23092021
Run ID	fa2da362-750b-4676-8f63-2d636174ec4b
Acquisition ID(s)	a198339ff6dcca153211db0f4faaad8bb3ec5ea5,9ac77fa0aa98d57f49e81050f63b52c29cdcabd6
Flow Cell Id	FAR13458
Start Time	September 23, 12:00
Run Length	1h 3m

## Run Summary

Reads Generated	249.99 k
Passed Bases	443.68 Mb
Failed Bases	25.06 Mb
Estimated Bases	486.64 Mb

## Run Parameters

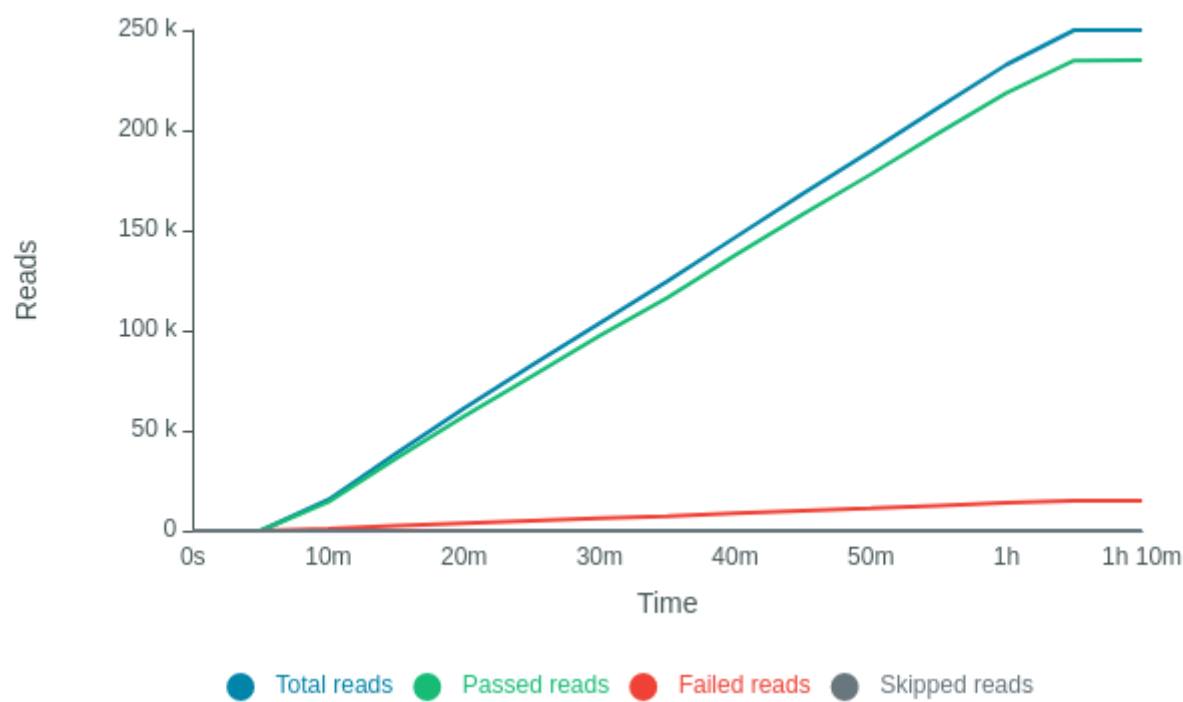
Flow Cell Type	FLO-MIN106
Kit	SQK-LSK109
Initial bias voltage	-180 mV
FAST5 output	Enabled
FASTQ output	Enabled
BAM output	Enabled
Bulk file output	Disabled
Active channel selection	Enabled
Basecalling	Enabled
Specified run length	72 hours
Adaptive sampling	reference_files=["/data/references/zymo_gut_mock/Escherichia_coli_B766.fasta"],filter_type=enrich,first_channel=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

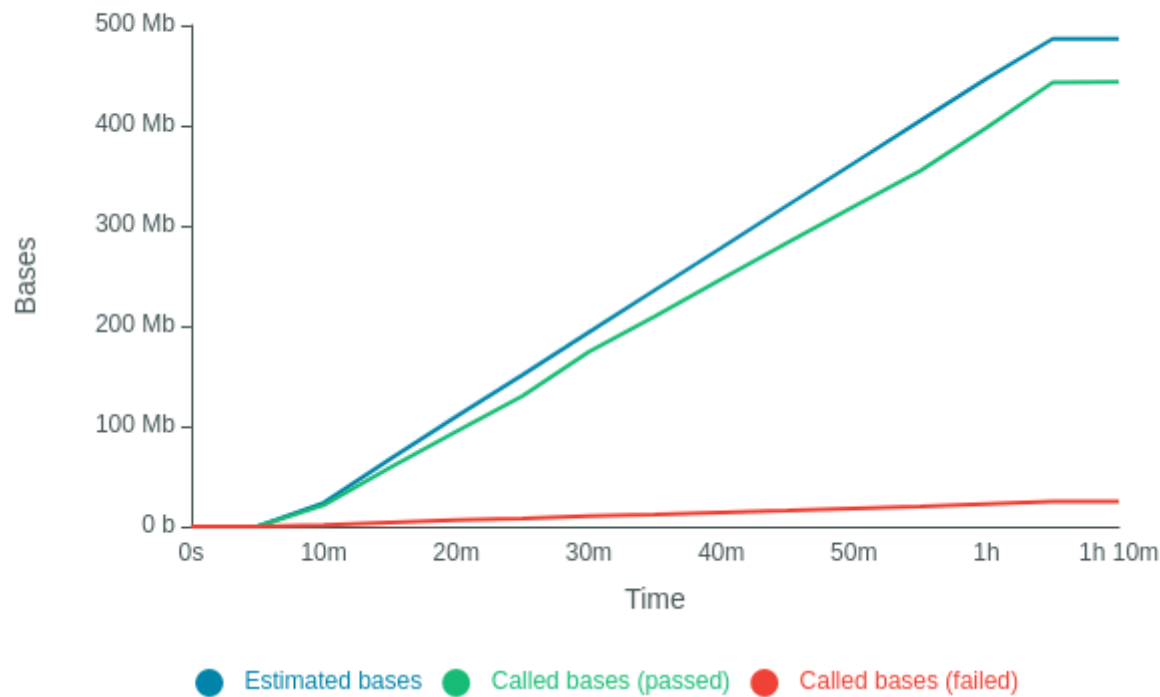
MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13



Cumulative Output Reads

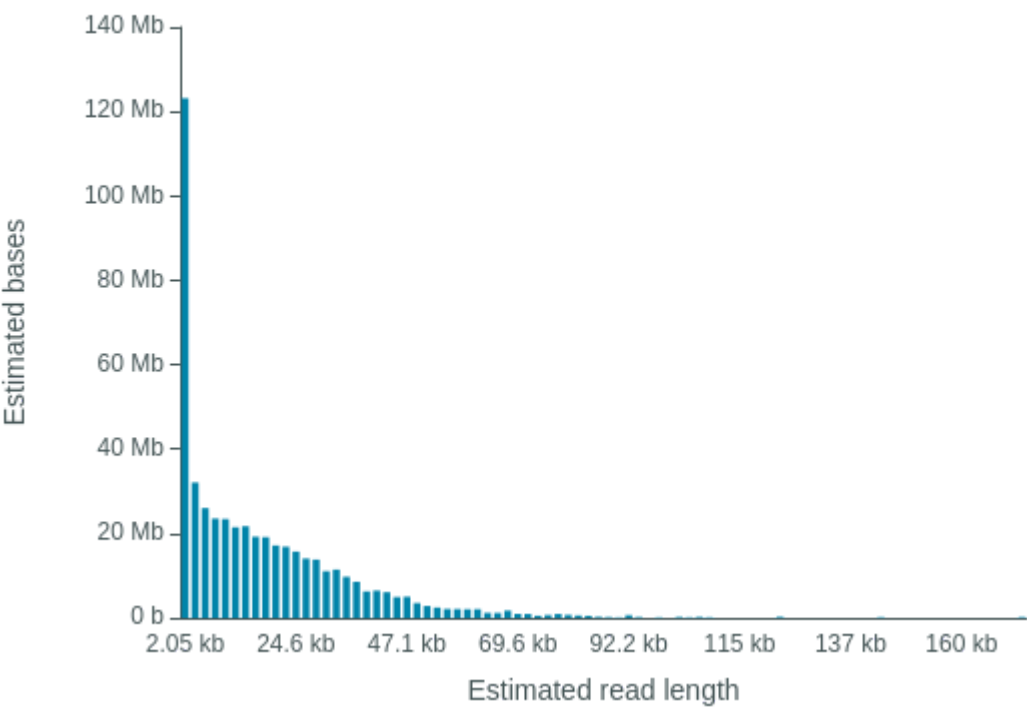


Cumulative Output Bases



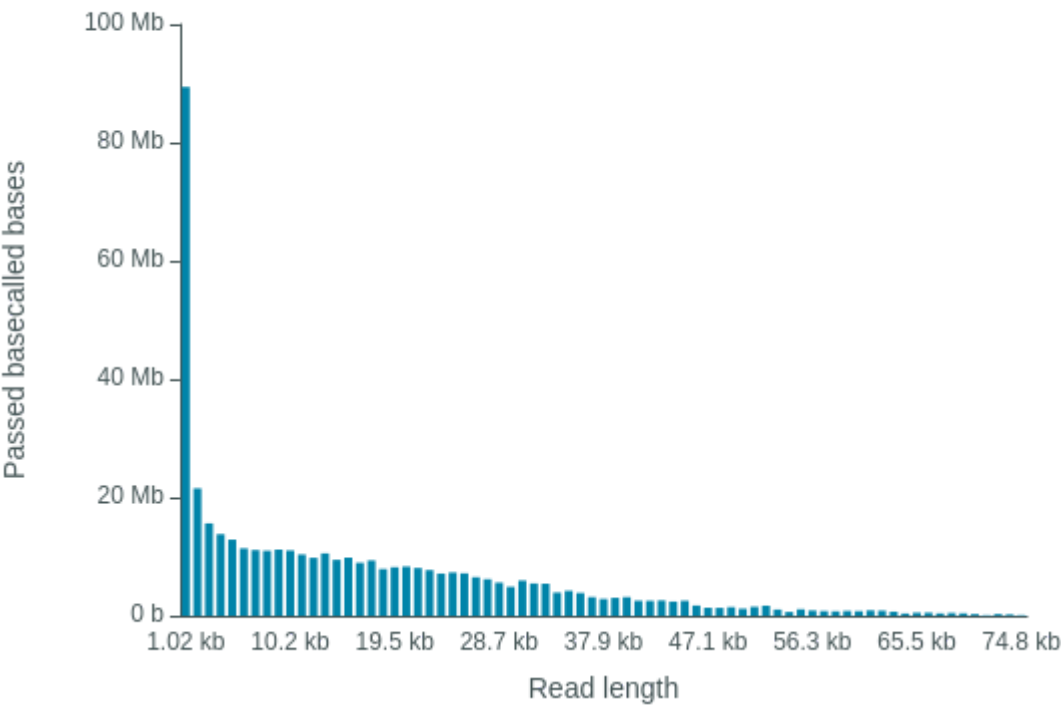
**Read Length Histogram Estimated Bases - Outliers Discarded**

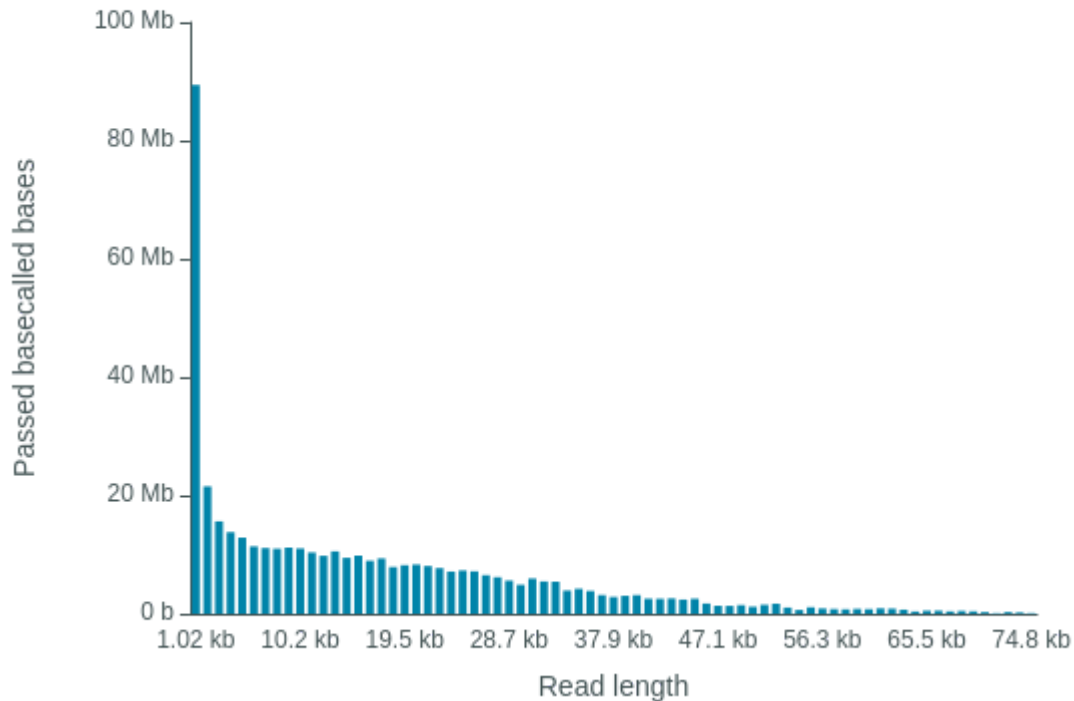
Estimated N50: 11.66 kb

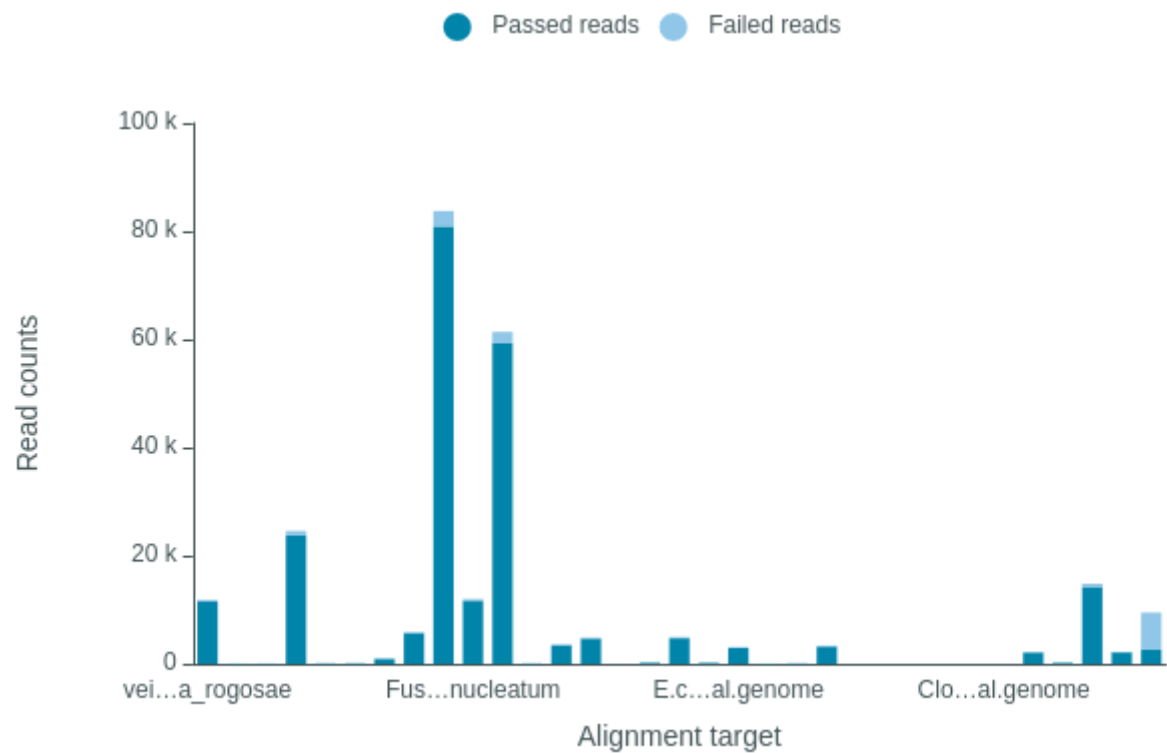


**Read Length Histogram Basecalled Bases - Outliers Discarded**

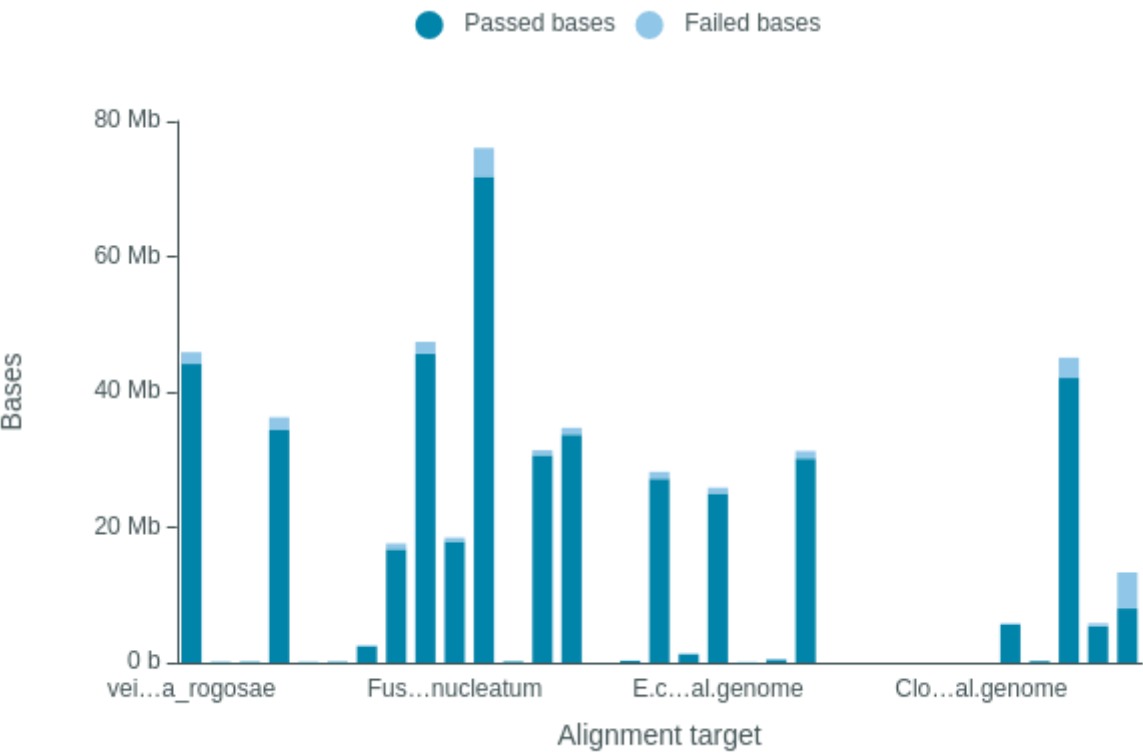
Estimated N50: 11.29 kb



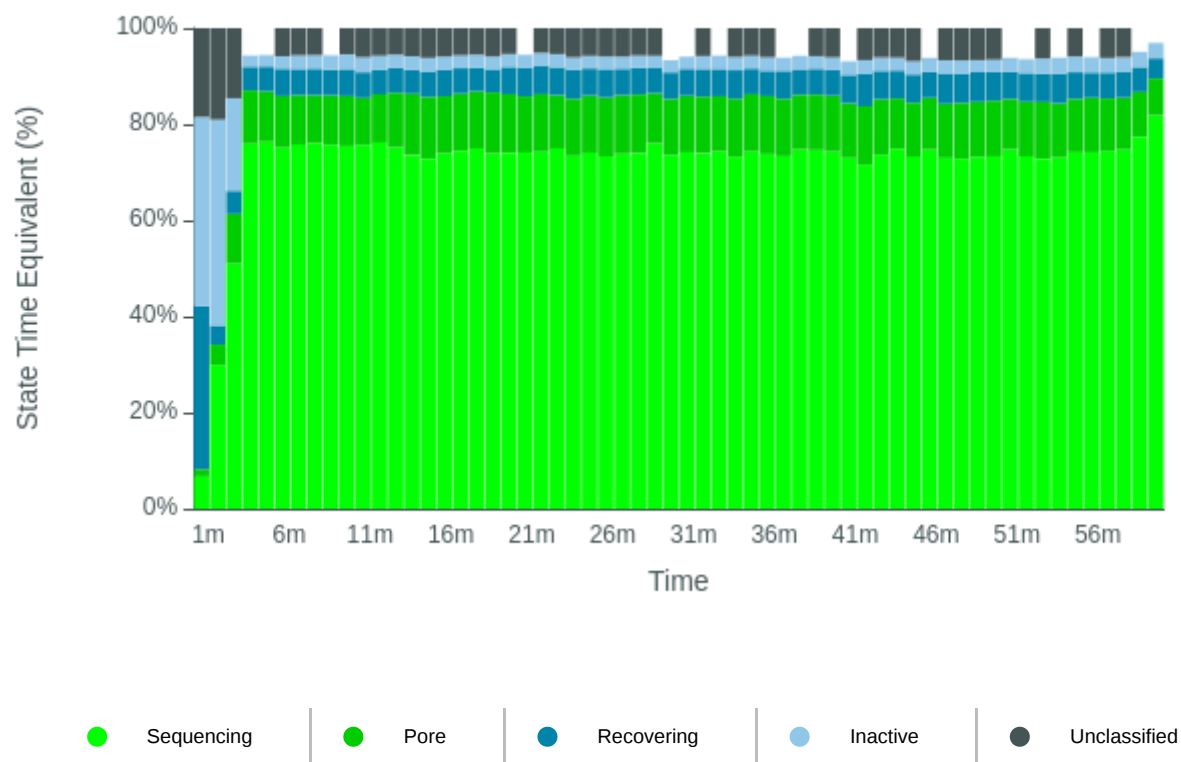




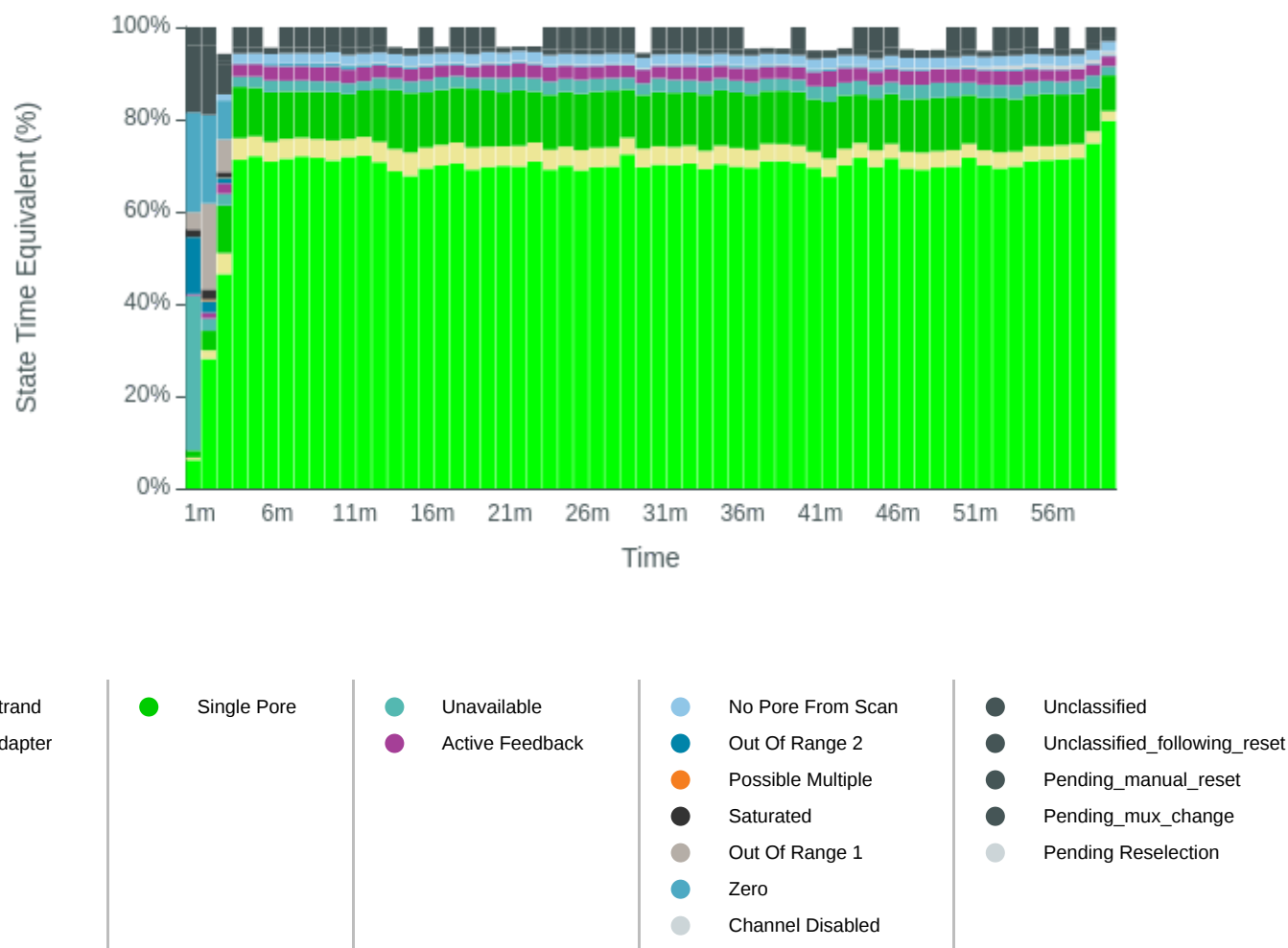
**Alignment Target Hits (bases)**



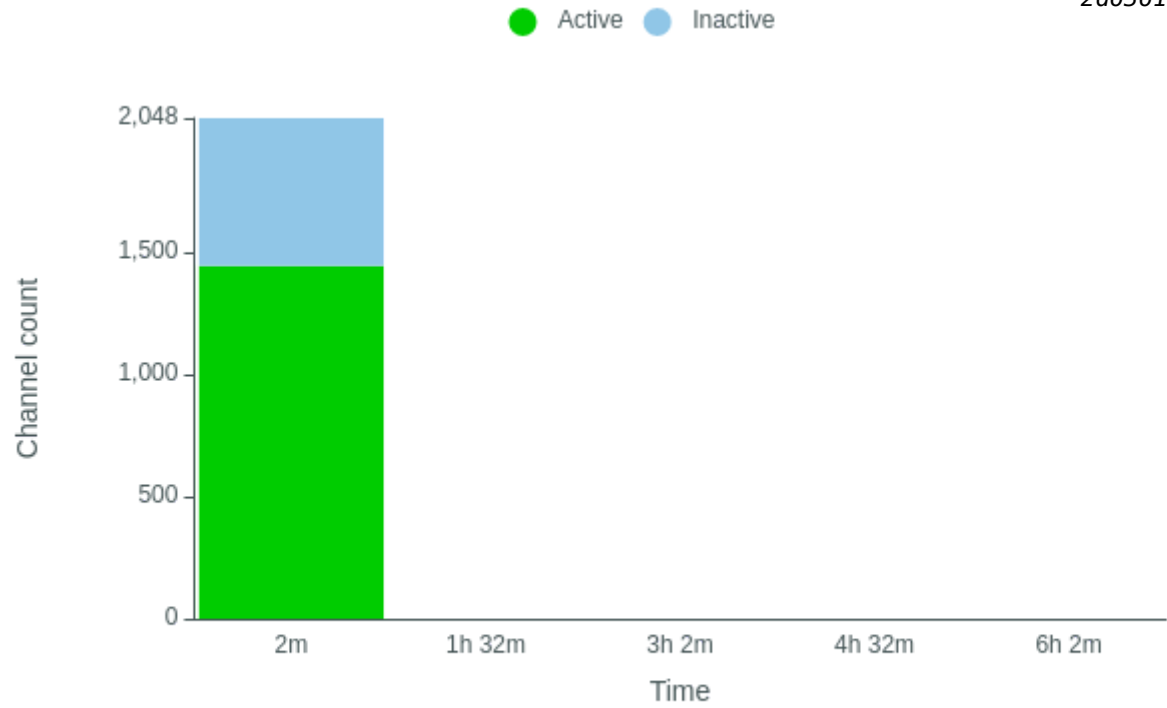
Duty Time Grouped



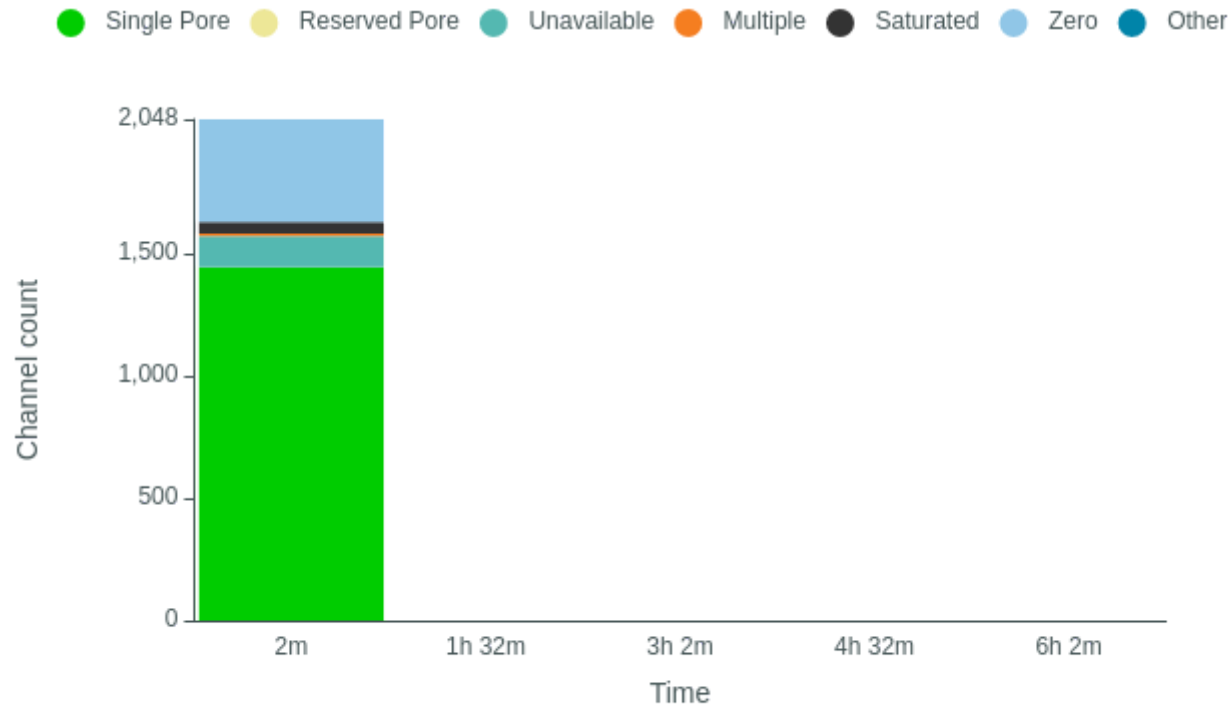
Duty time Categorised



Mux Scan Grouped

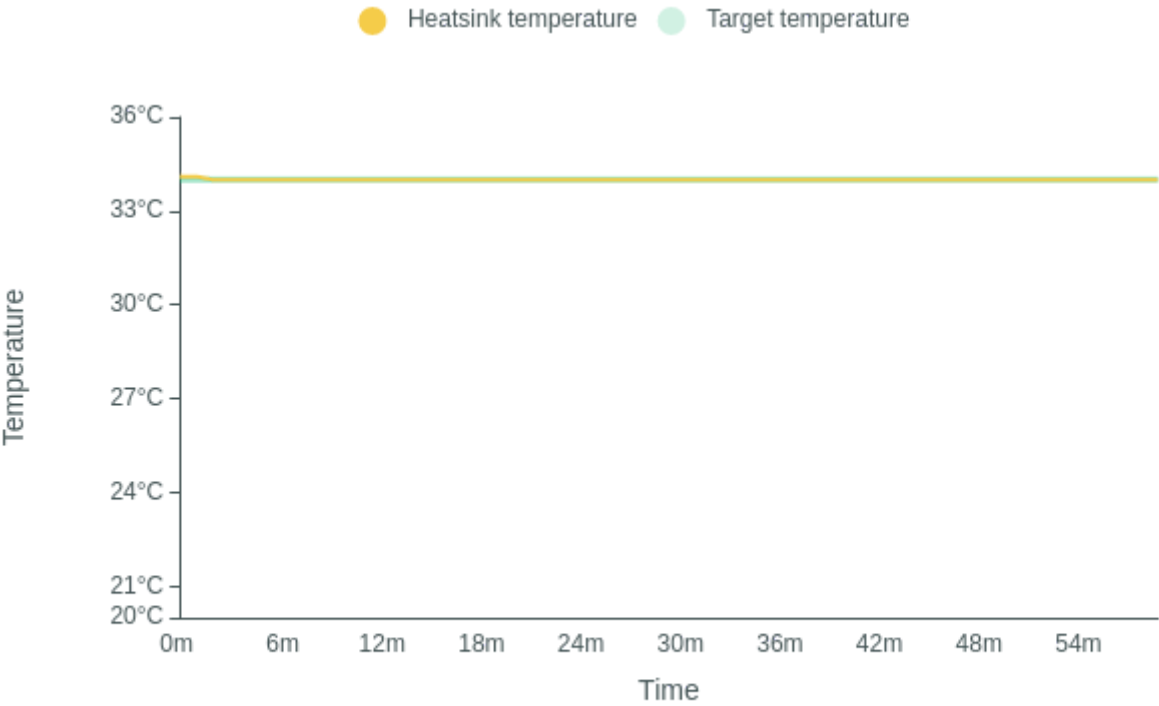


Mux Scan Categorised

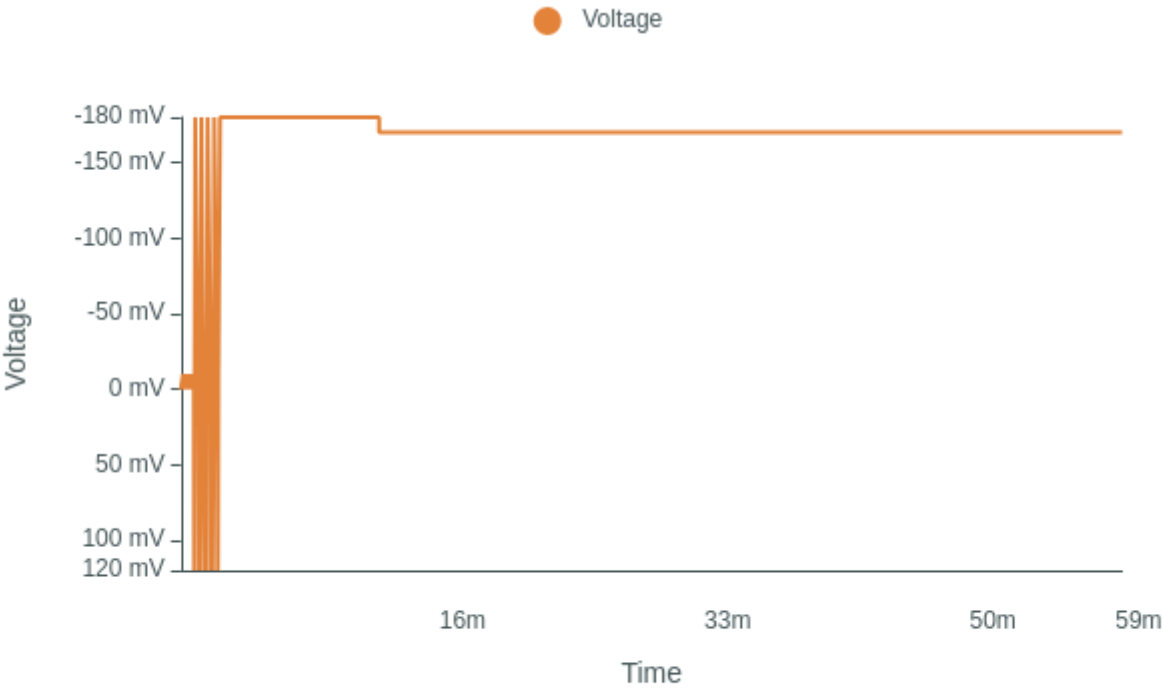




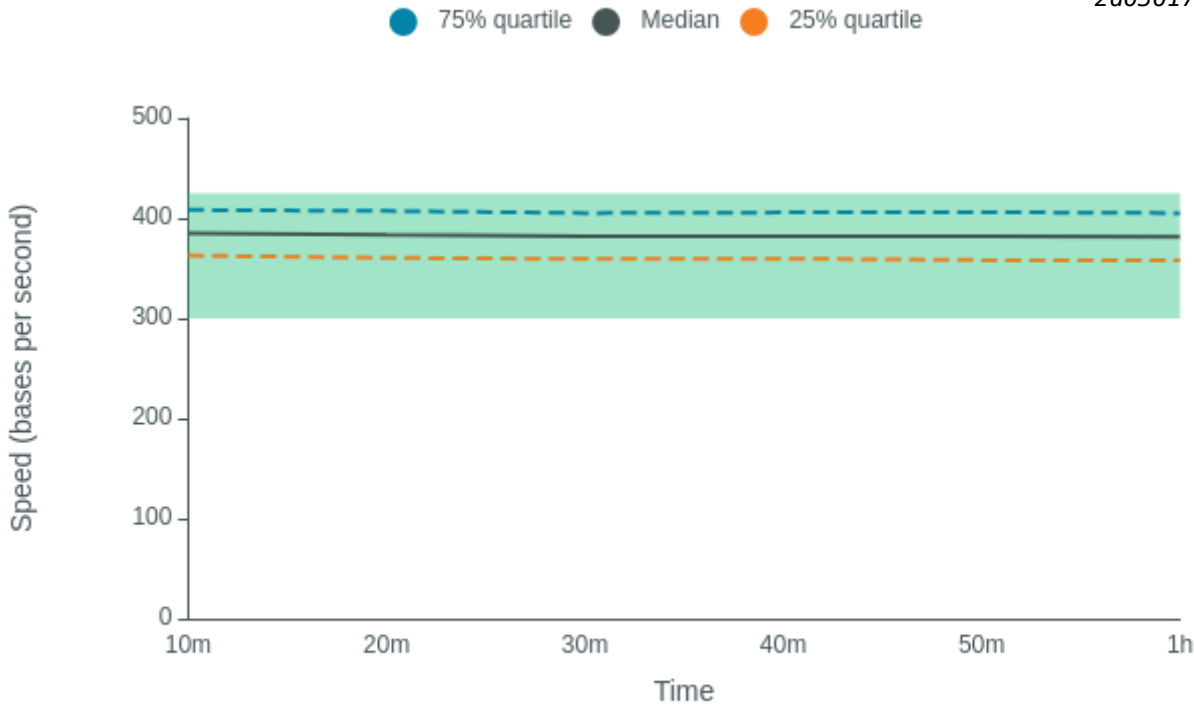
Temperature History



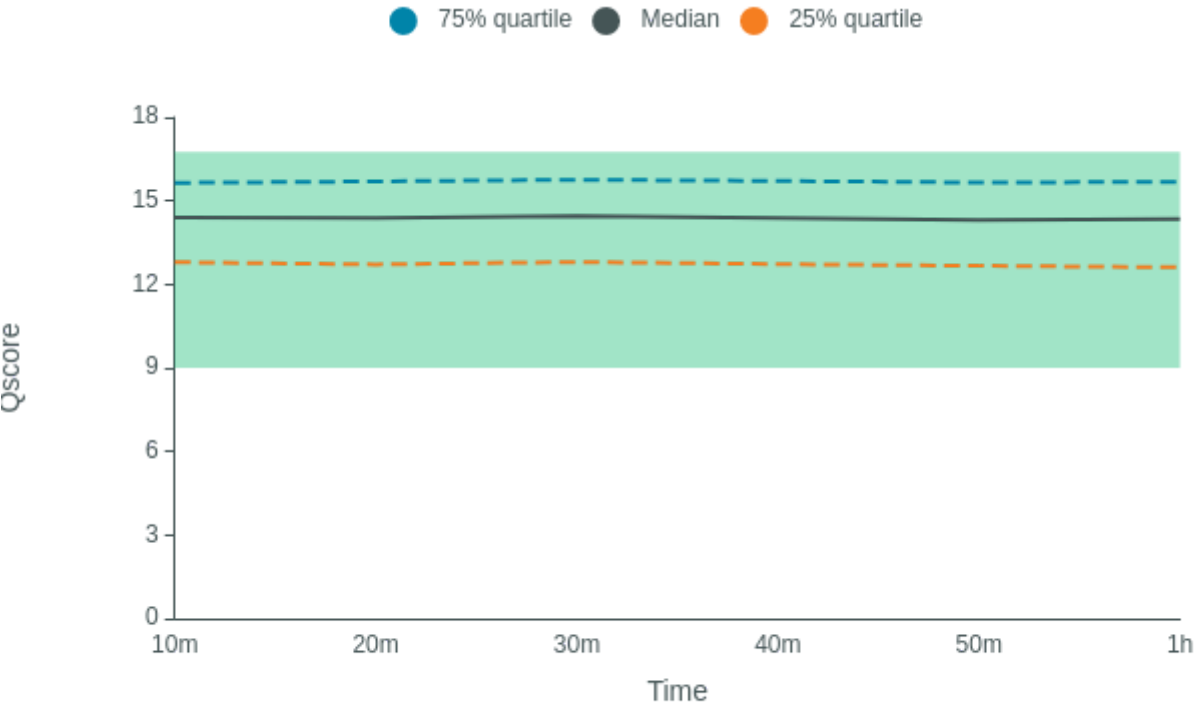
Bias Voltage History



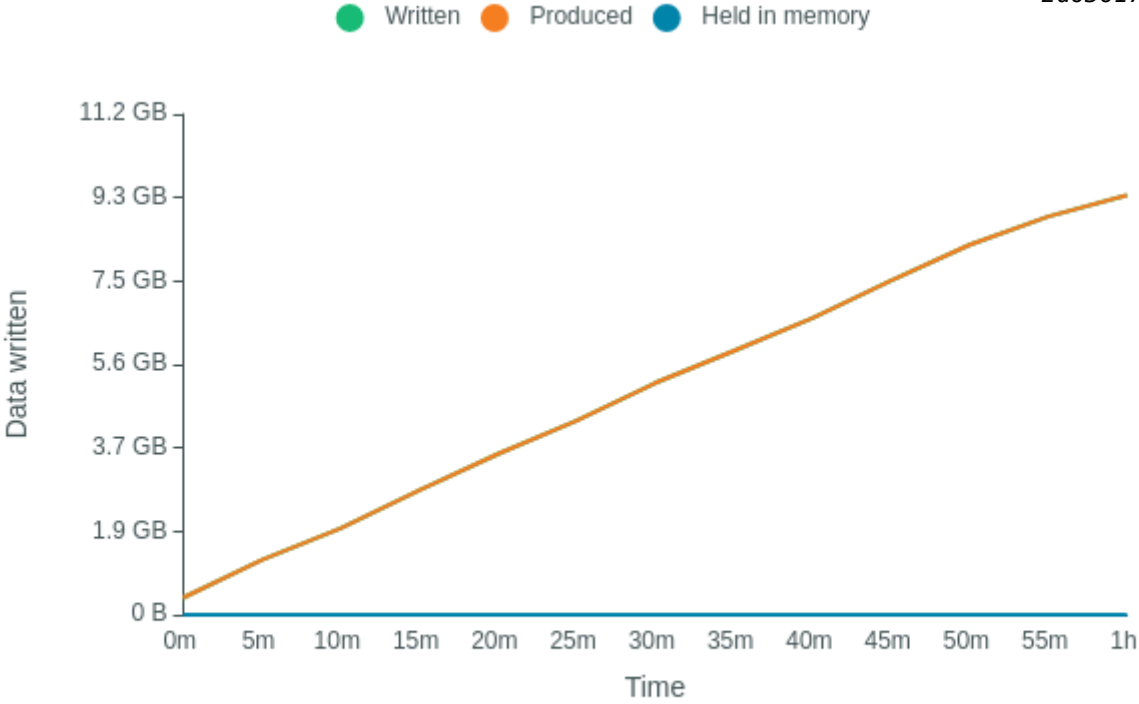
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13458 has found a total of 1444 pores. 501 pores available for immediate sequencing   September 23, 12:06
- Performing Mux Scan   September 23, 12:04
- Starting sequencing procedure   September 23, 12:04
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C   September 23, 12:00