



Run Info

Host Name	GXb03422 (localhost)
Position	X2
Experiment Name	ReadUntil_ZGM_Control_23092021
Sample ID	ReadUntil_ZGM_Control_23092021
Run ID	33a5d215-32fe-4e12-986c-4cf143de364b
Acquisition ID(s)	290b98f064e60a766e4acb1e52490a7650c43744, 670c17c0e6b2f627d223a9e90ec552e5ff8140c0
Flow Cell Id	FAR13458
Start Time	September 23, 10:55
Run Length	1h 2m

Run Summary

Reads Generated	113.73 k
Passed Bases	460.67 Mb
Failed Bases	28.24 Mb
Estimated Bases	500.66 Mb

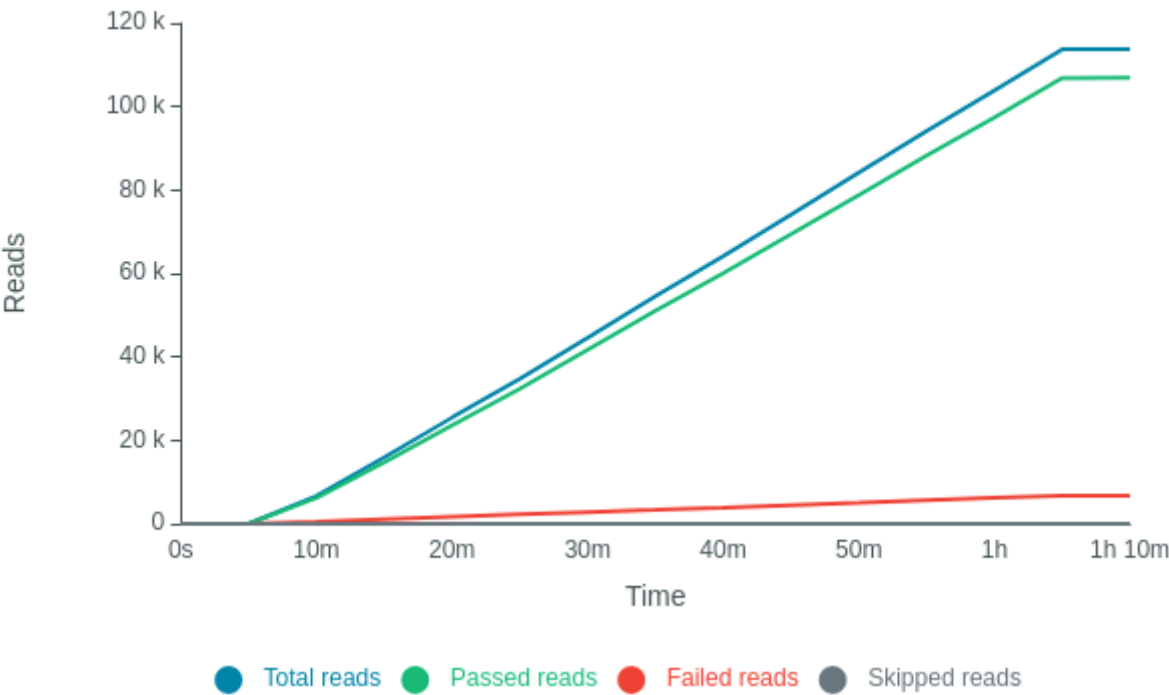
Run Parameters

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
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

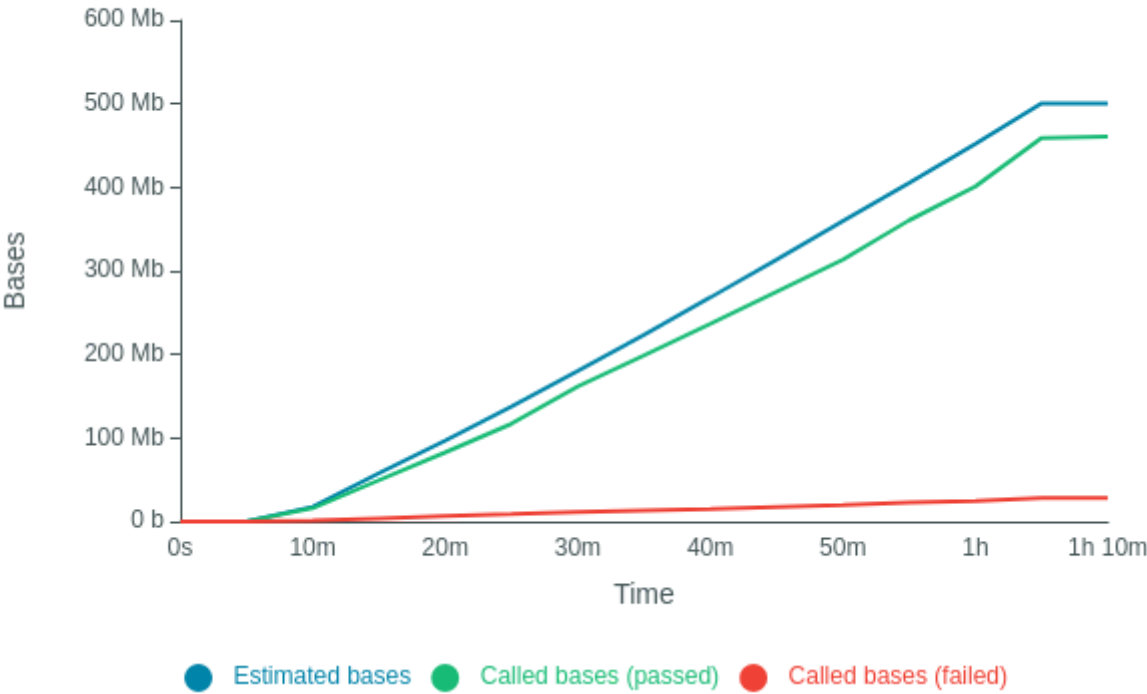
Versions

MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads

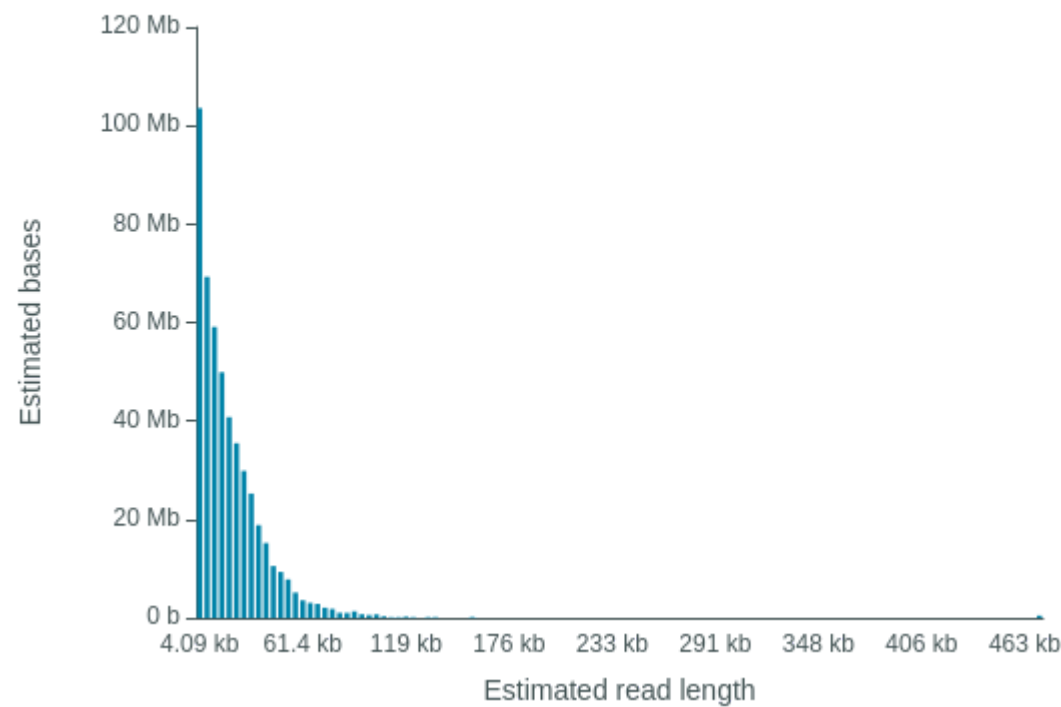


Cumulative Output Bases



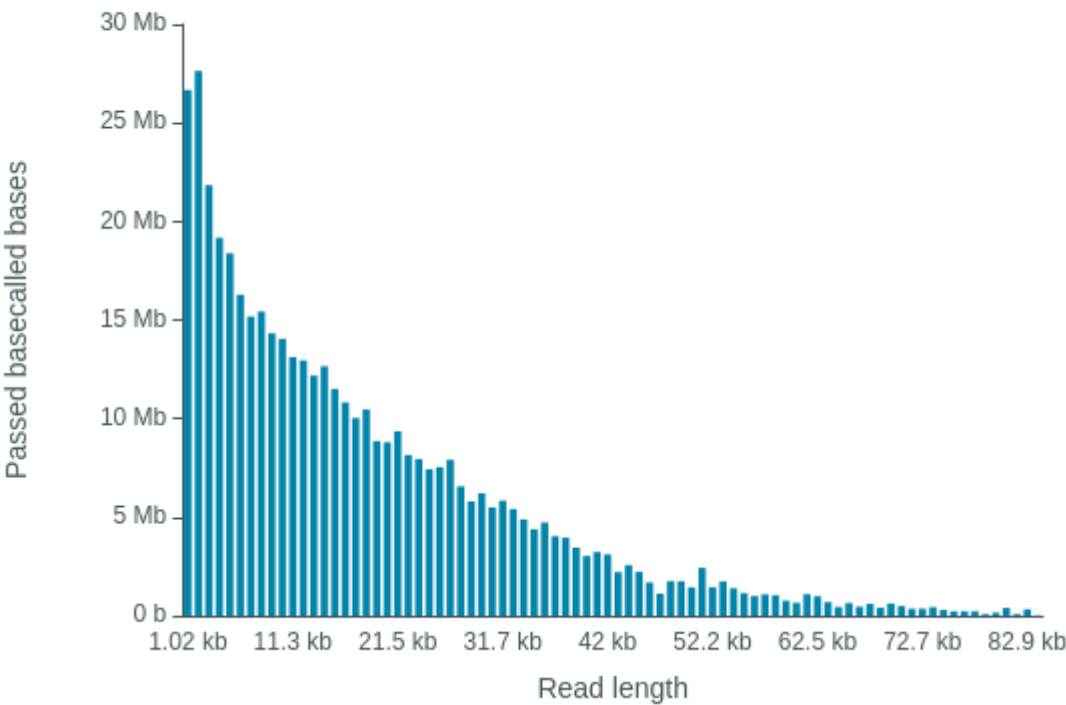
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 13.73 kb



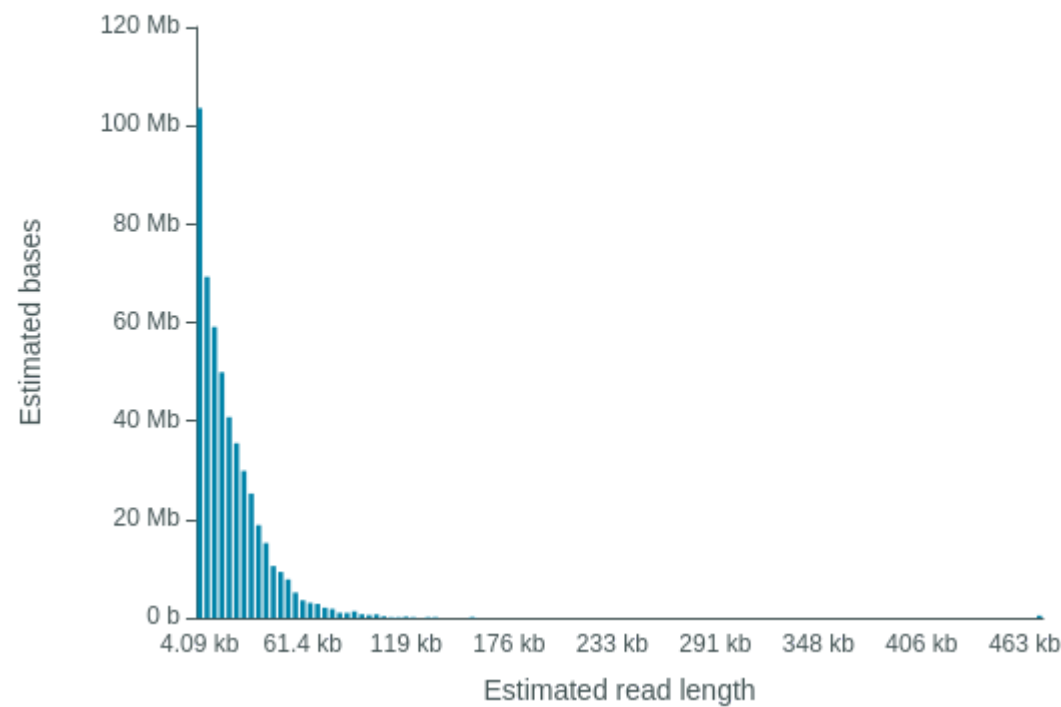
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 13.38 kb



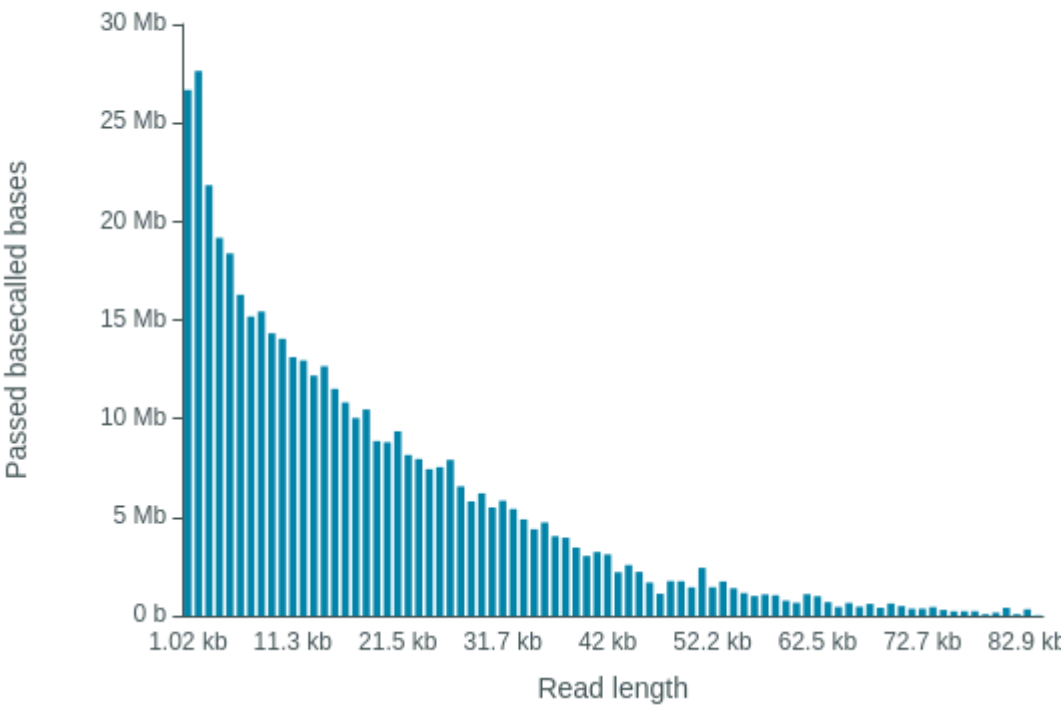
Read Length Histogram Estimated Bases

Estimated N50: 13.73 kb

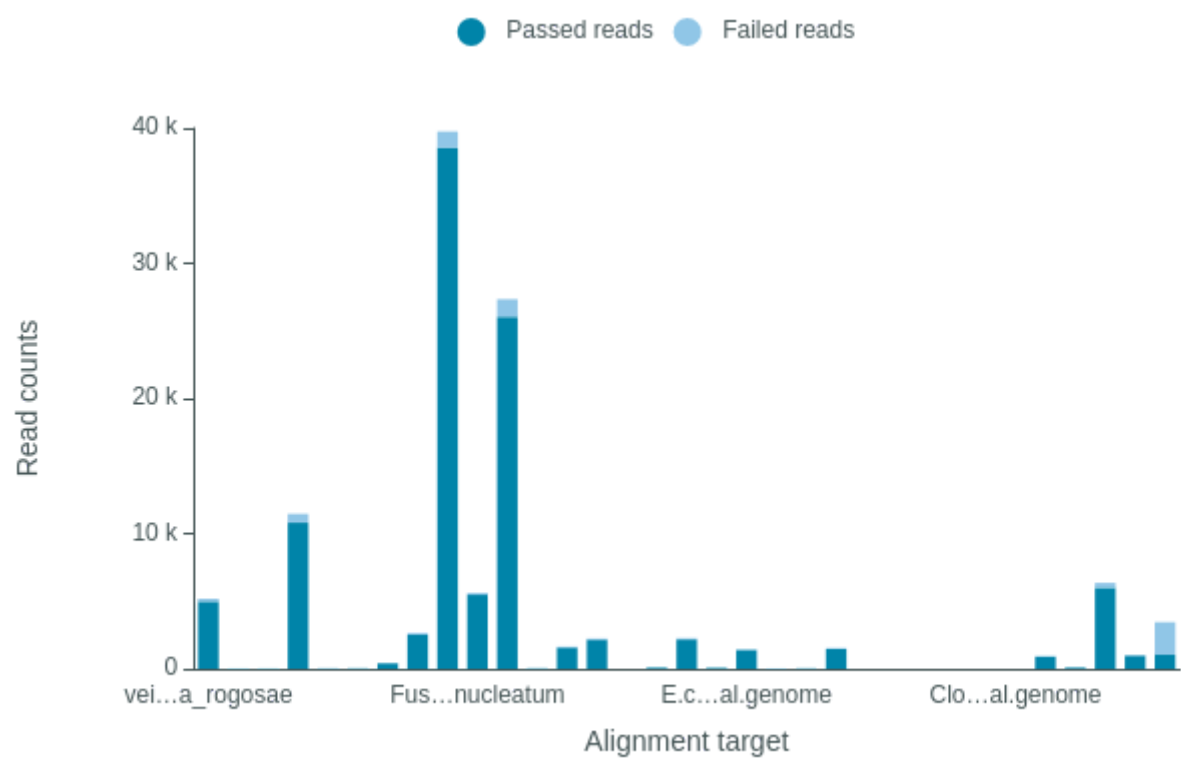


Read Length Histogram Basecalled Bases

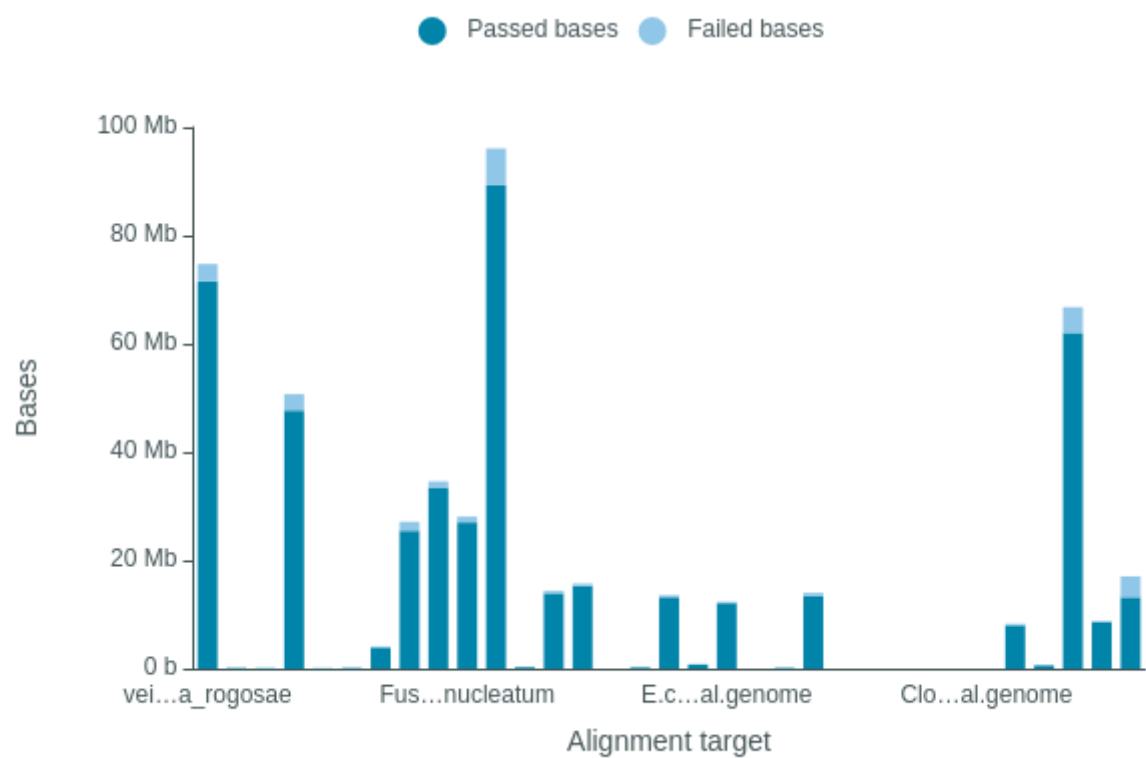
Estimated N50: 13.38 kb



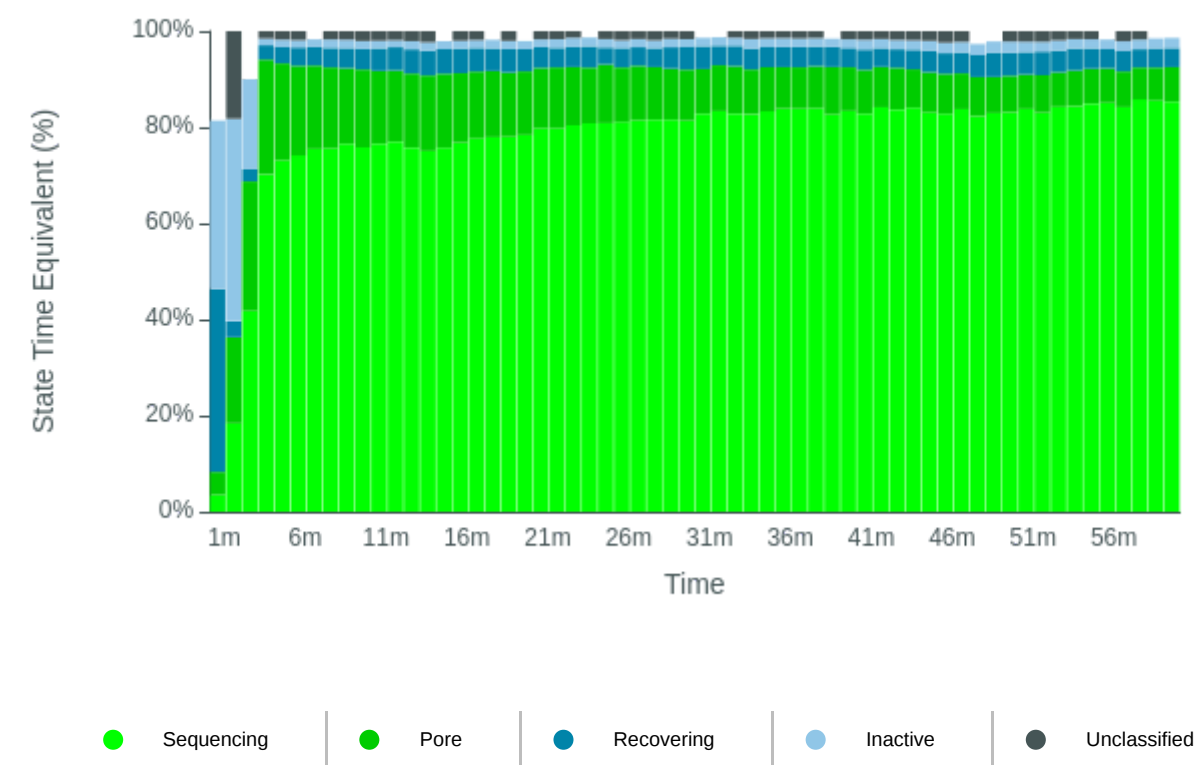
Alignment Target Hits (reads)



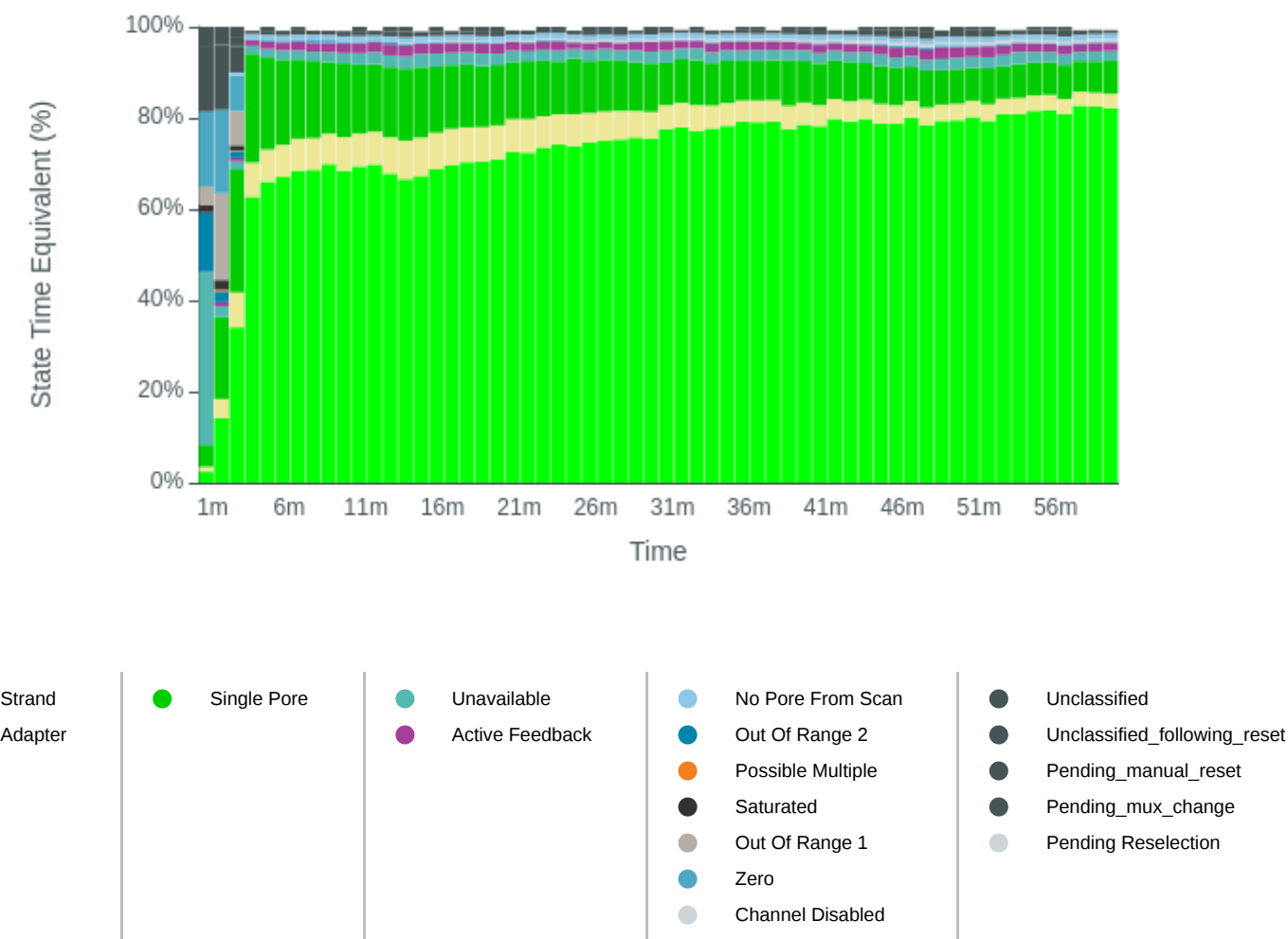
Alignment Target Hits (bases)



Duty Time Grouped

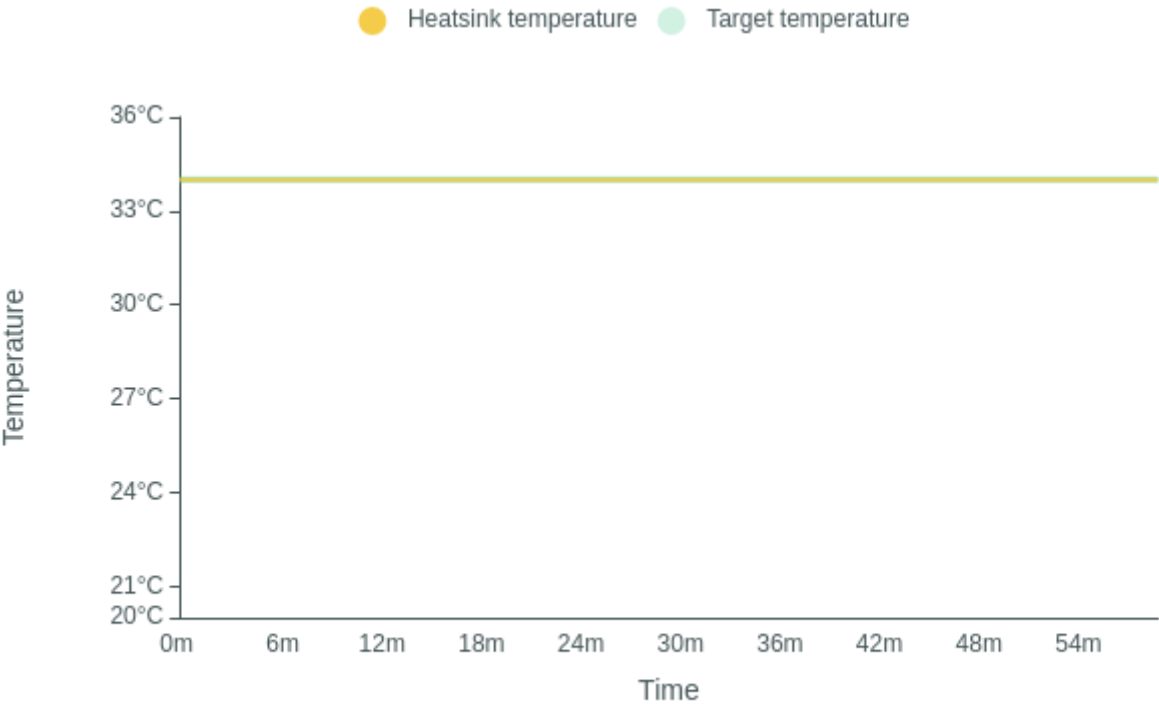


Duty time Categorised

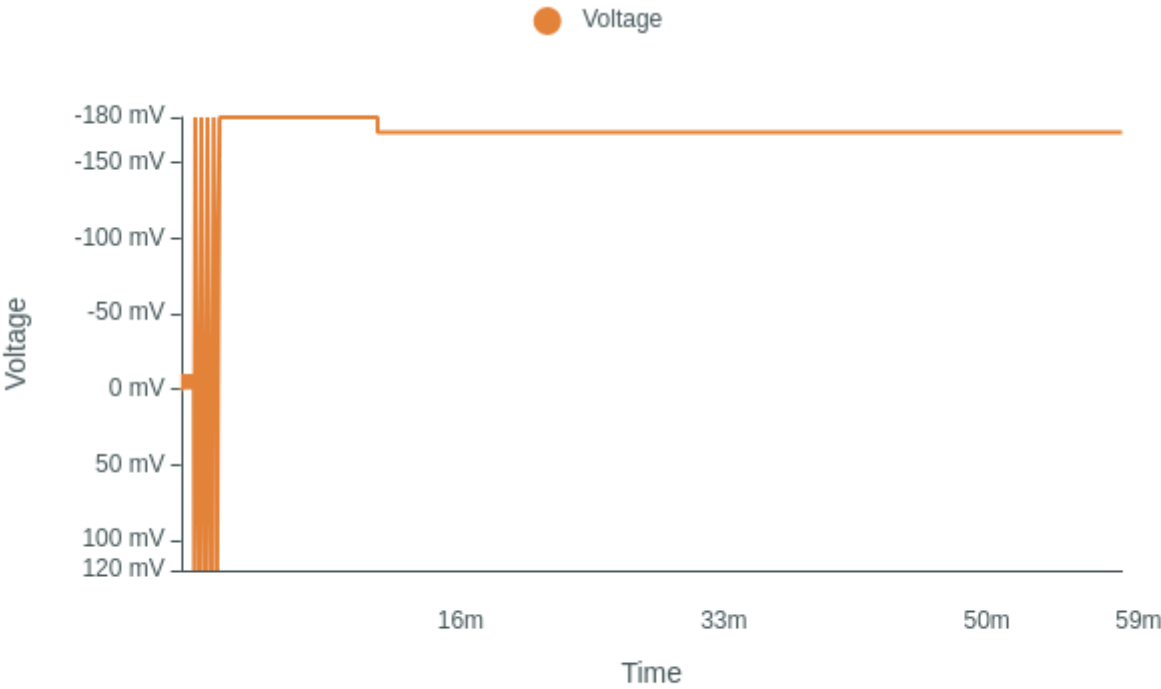


Activity	Time (minutes)
Green	1,500
Blue	100
Orange	50
Black	50
Light Blue	400

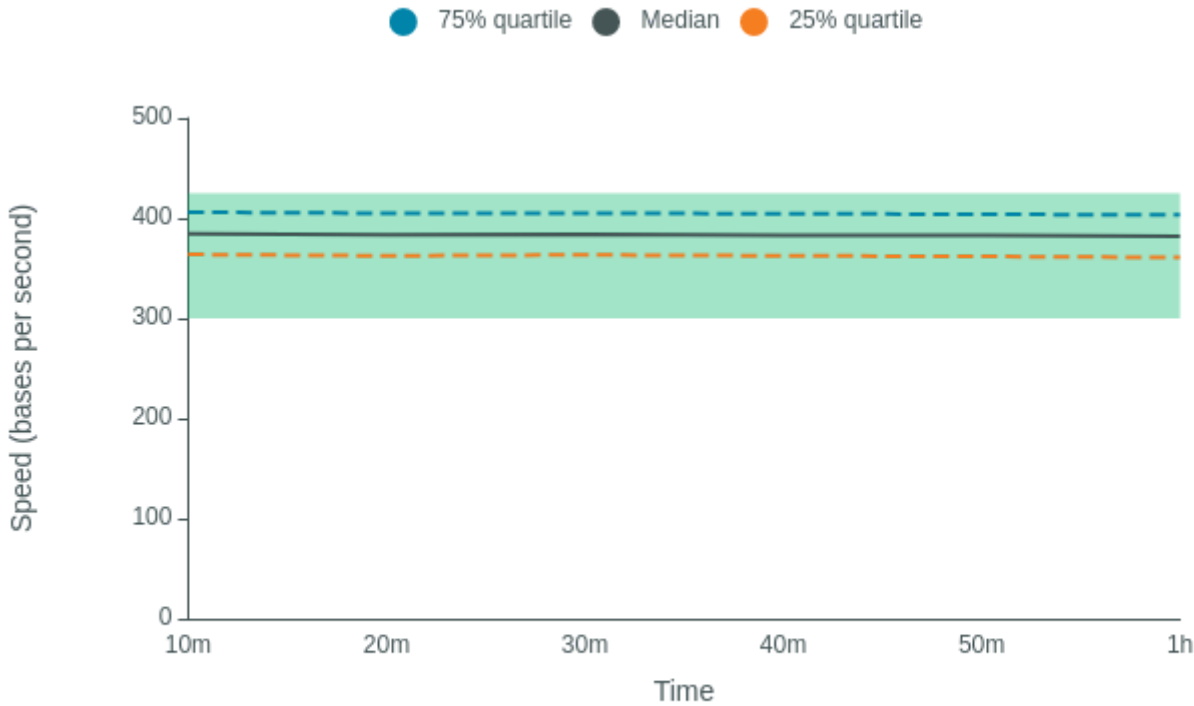
Temperature History



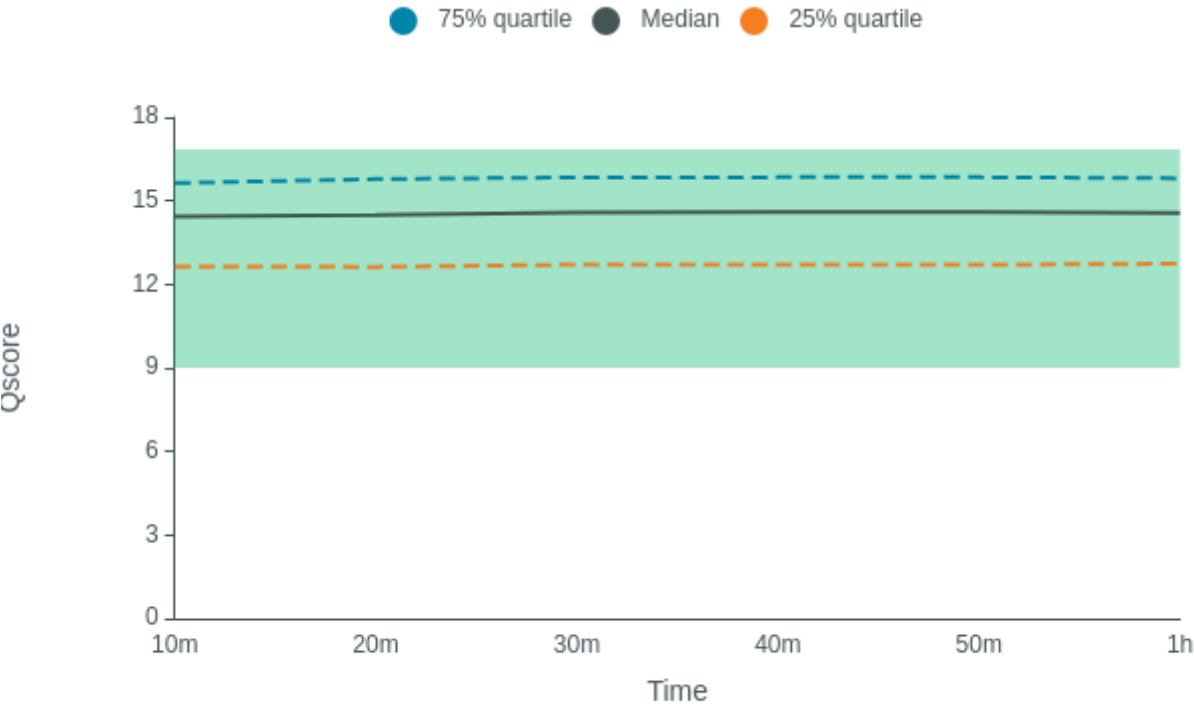
Bias Voltage History



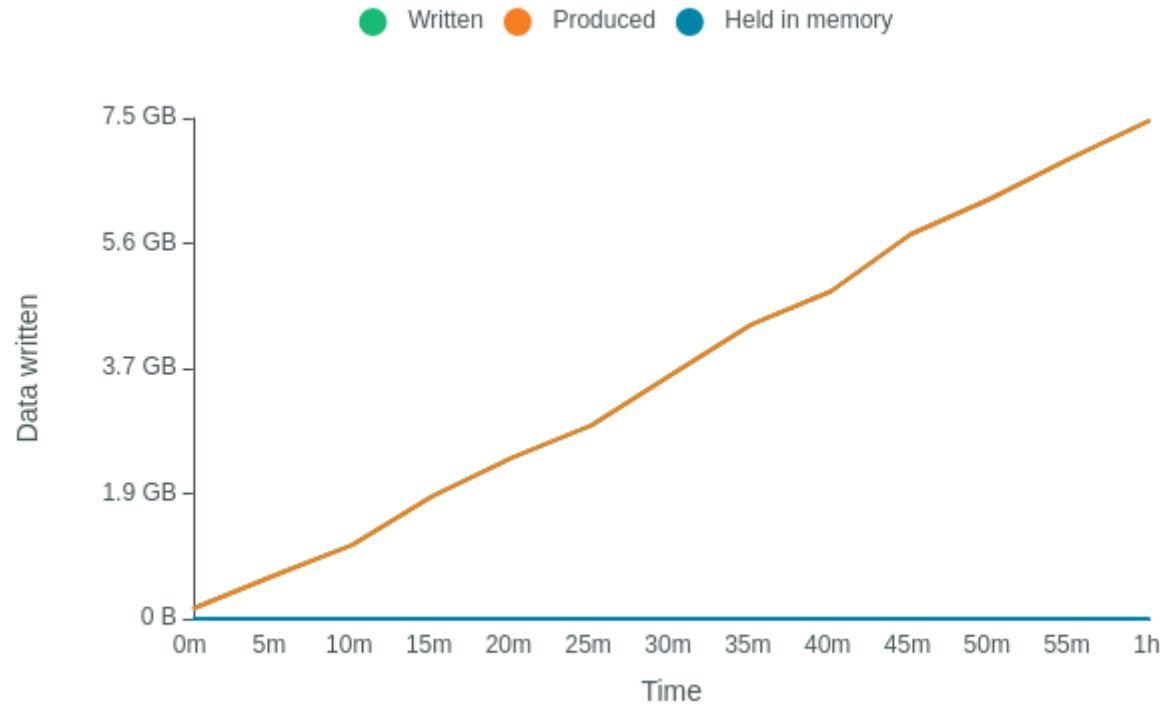
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13458 has found a total of 1519 pores. 506 pores available for immediate sequencing September 23, 11:01
- Performing Mux Scan September 23, 10:58
- Starting sequencing procedure September 23, 10:58
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 10:55