



Run Info

Host Name	GXb03422 (localhost)
Position	X4
Experiment Name	ReadUntil_ZGM_Enrich_Amuciniphila_230920
Sample ID	ReadUntil_ZGM_Enrich_Amuciniphila_230920
Run ID	014e4f39-967e-480a-bb6d-828dcaecc48f
Acquisition ID(s)	c5b198cc5ac5cba429272f5fee3ddd3c7cdf306a, e6f4367731bc587697ac48b5d7ca5c52e8e5bc8b
Flow Cell Id	FAR13419
Start Time	September 23, 13:42
Run Length	1h 2m

Run Summary

Reads Generated	299.24 k
Passed Bases	412.11 Mb
Failed Bases	28.45 Mb
Estimated Bases	457.58 Mb

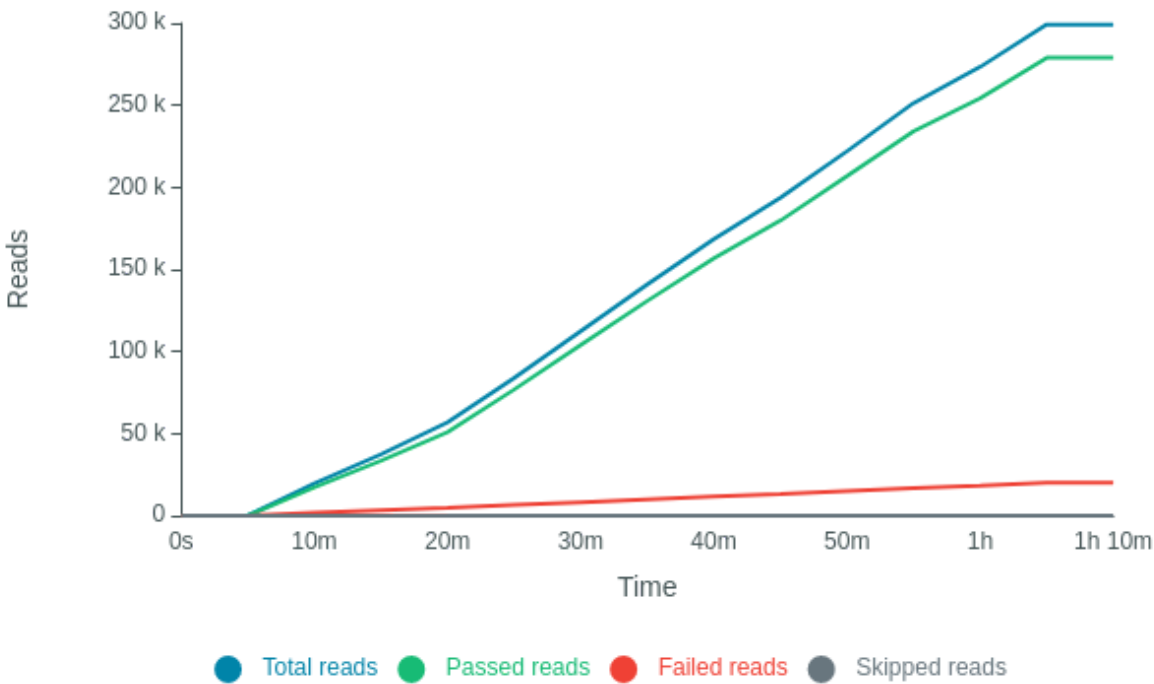
Run Parameters

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/Akkermansia_muciniphila.fasta"],f ilter_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

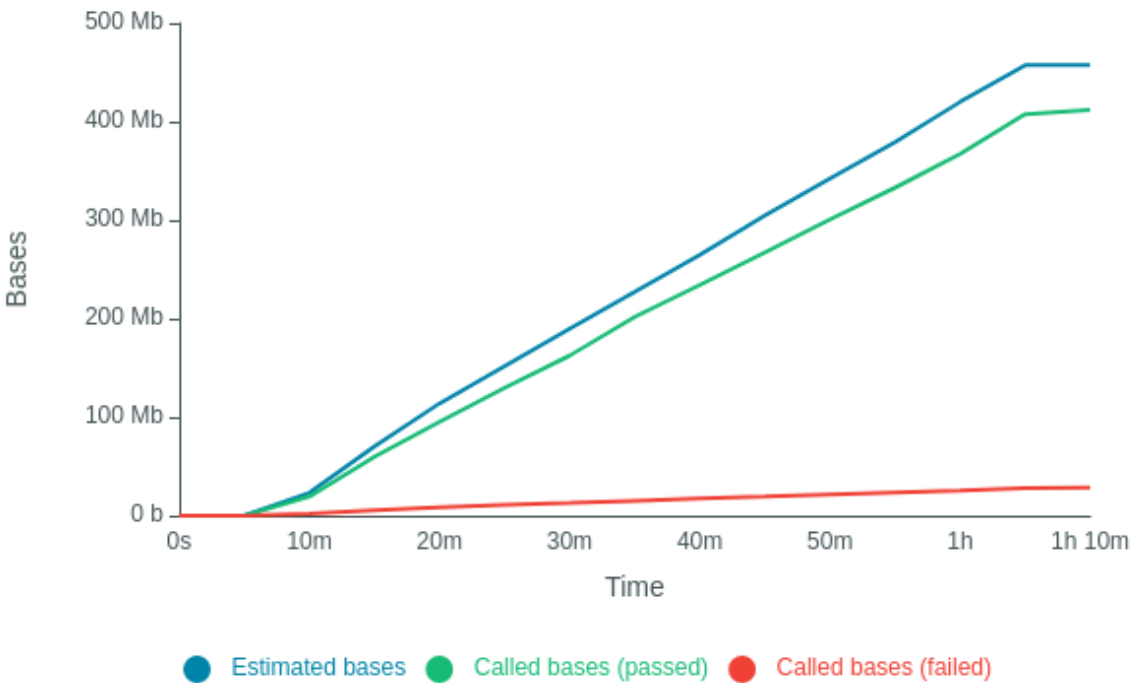
Versions

MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads



Cumulative Output Bases



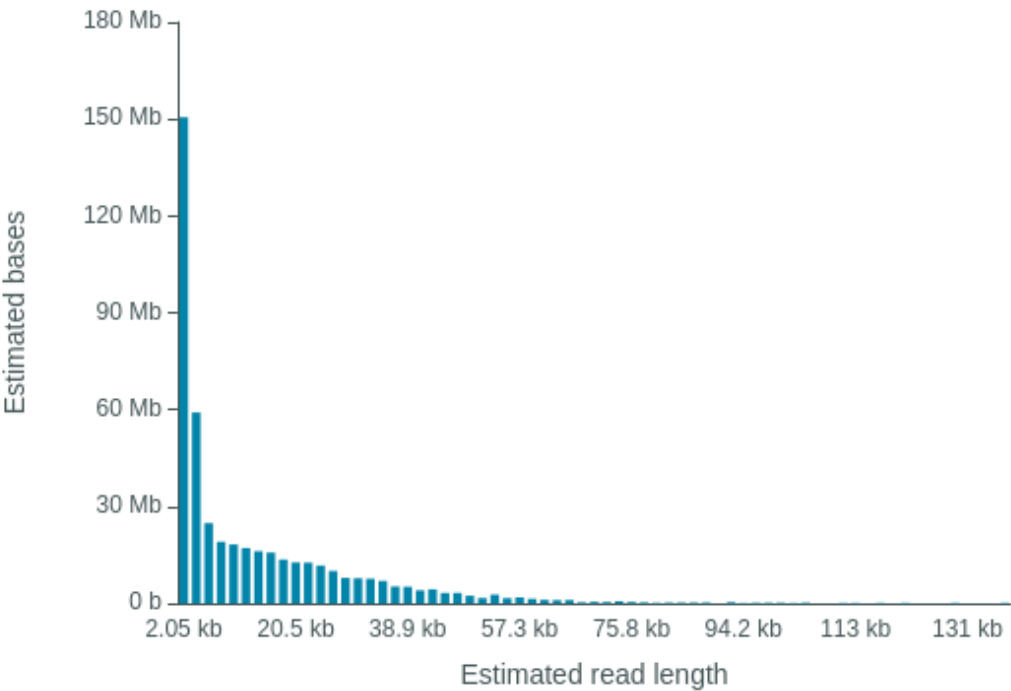
Estimated N50: 5.58 kb



The bar chart displays the distribution of read lengths. The y-axis, labeled 'Passed basecalled bases', ranges from 0 to 120 Mb in increments of 20 Mb. The x-axis, labeled 'Read length', ranges from 0 to 65.5 kb with major ticks at 1.02 kb, 10.2 kb, 19.5 kb, 28.7 kb, 37.9 kb, 47.1 kb, 56.3 kb, and 65.5 kb. The distribution is highly skewed towards shorter read lengths, with a peak around 1.02 kb reaching approximately 105 Mb. The number of bases decreases rapidly as read length increases, with most reads being shorter than 10 kb.

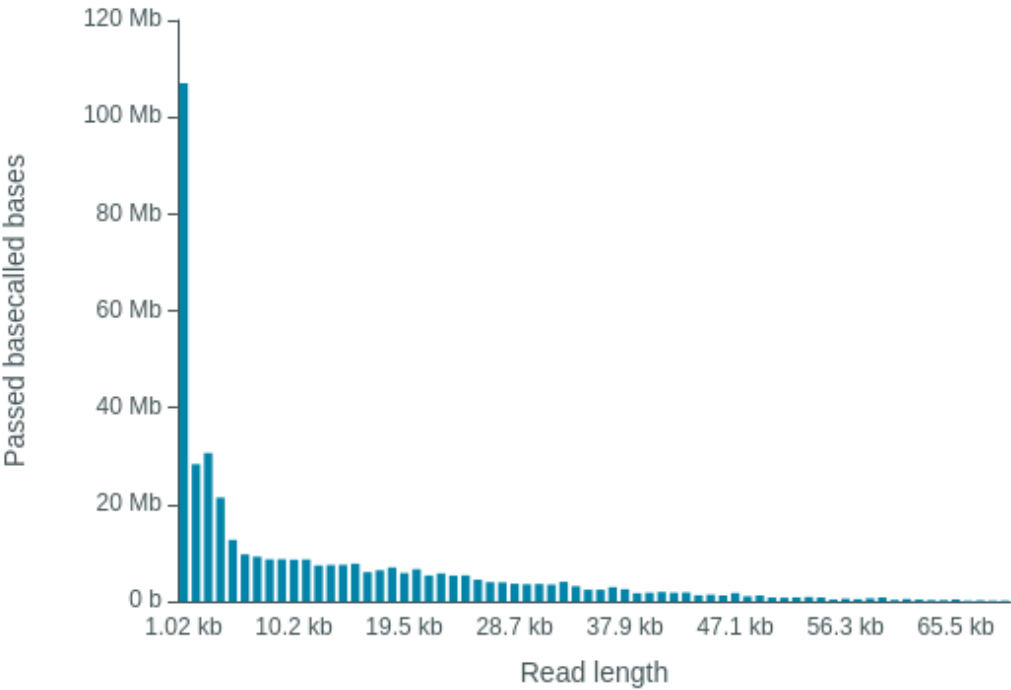
Read Length Histogram Estimated Bases

Estimated N50: 5.58 kb

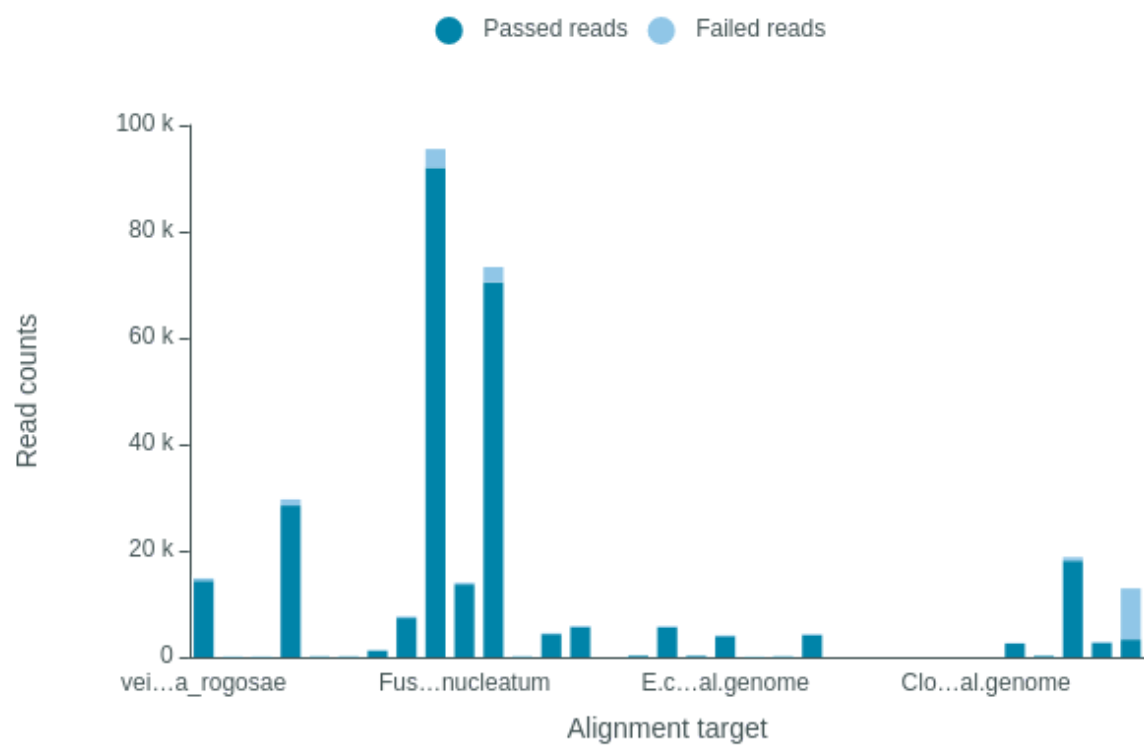


Read Length Histogram Basecalled Bases

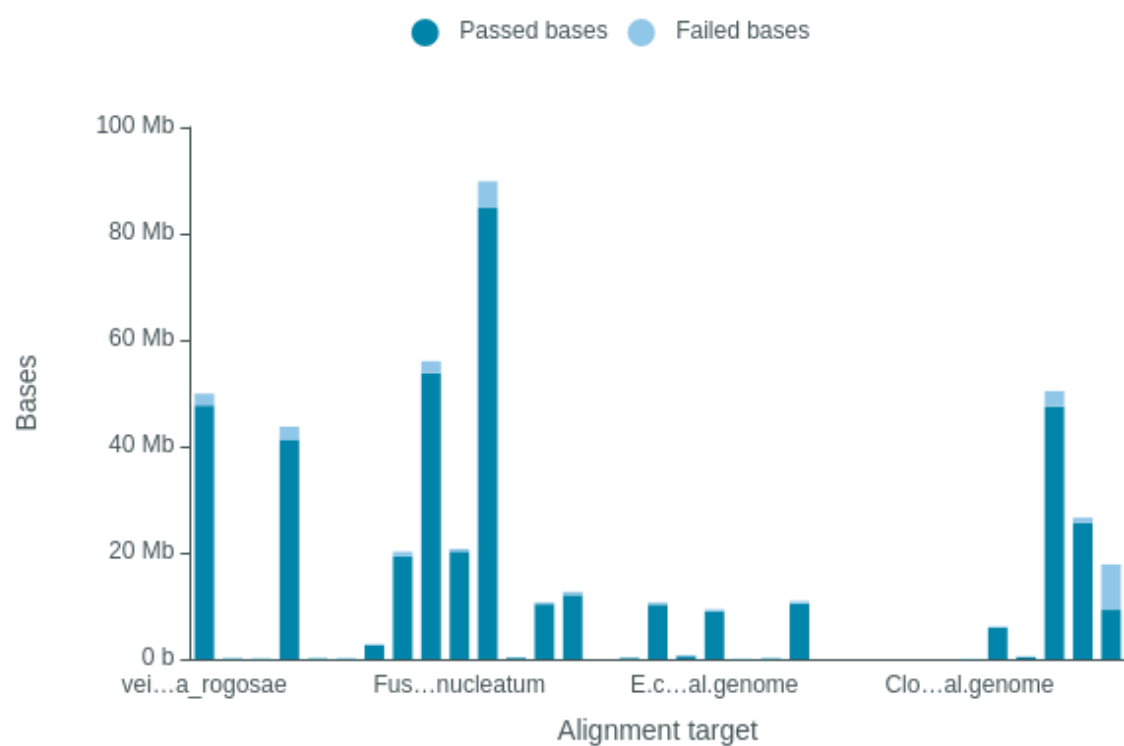
Estimated N50: 5.51 kb

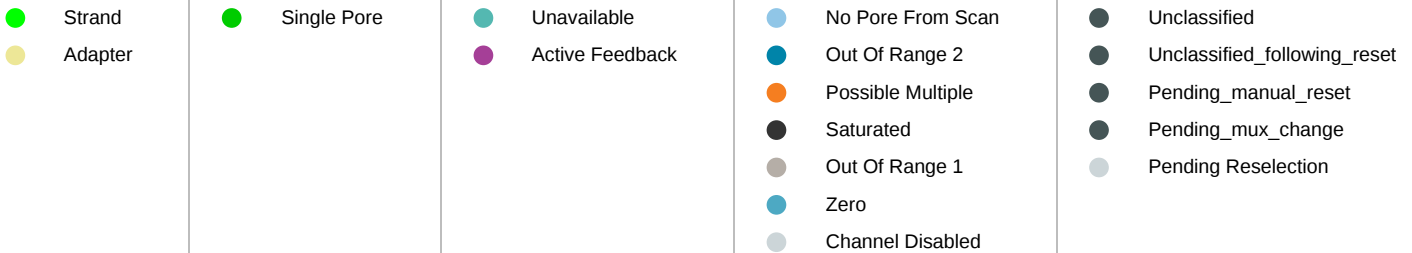


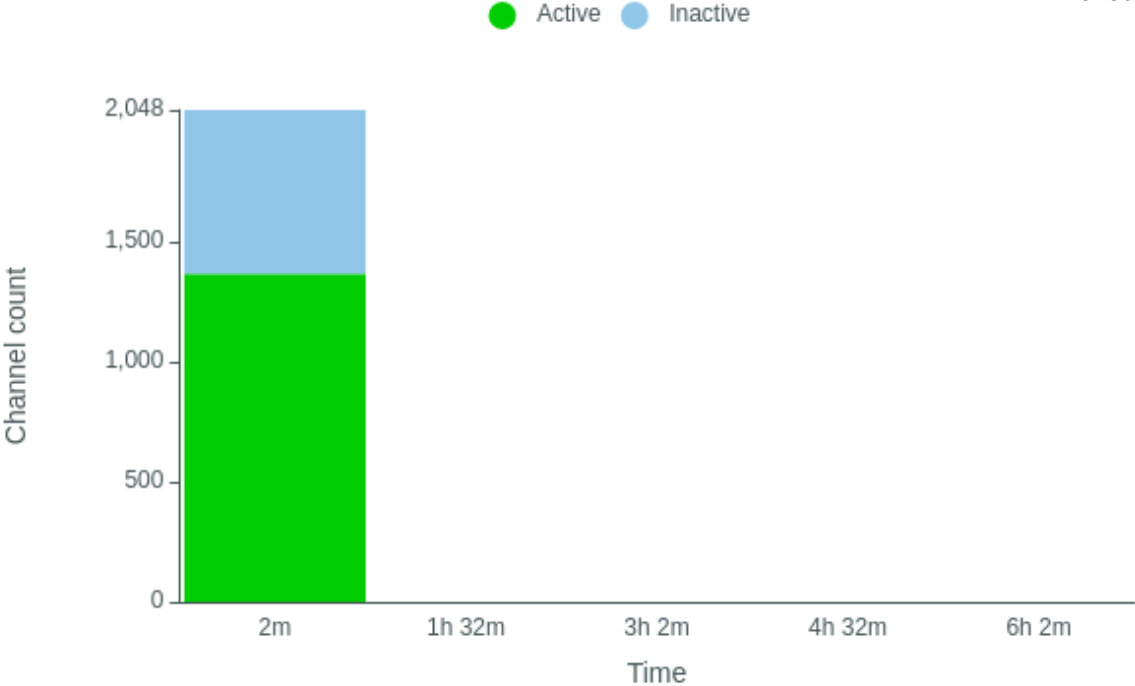
Alignment Target Hits (reads)



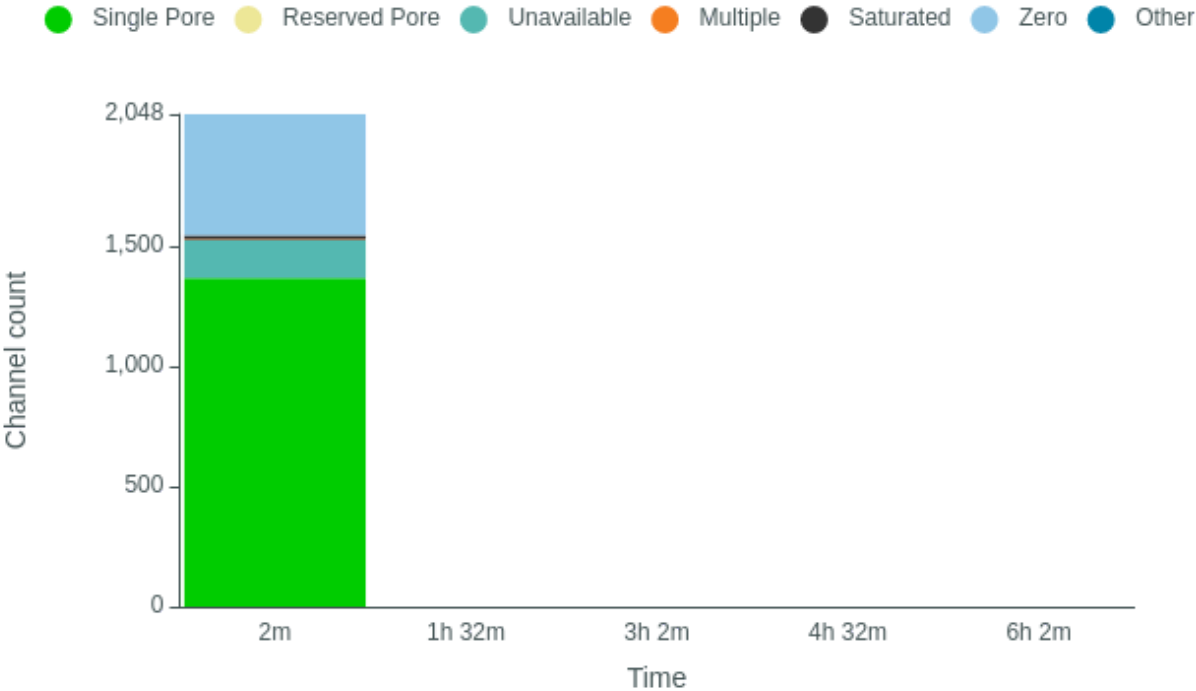
Alignment Target Hits (bases)



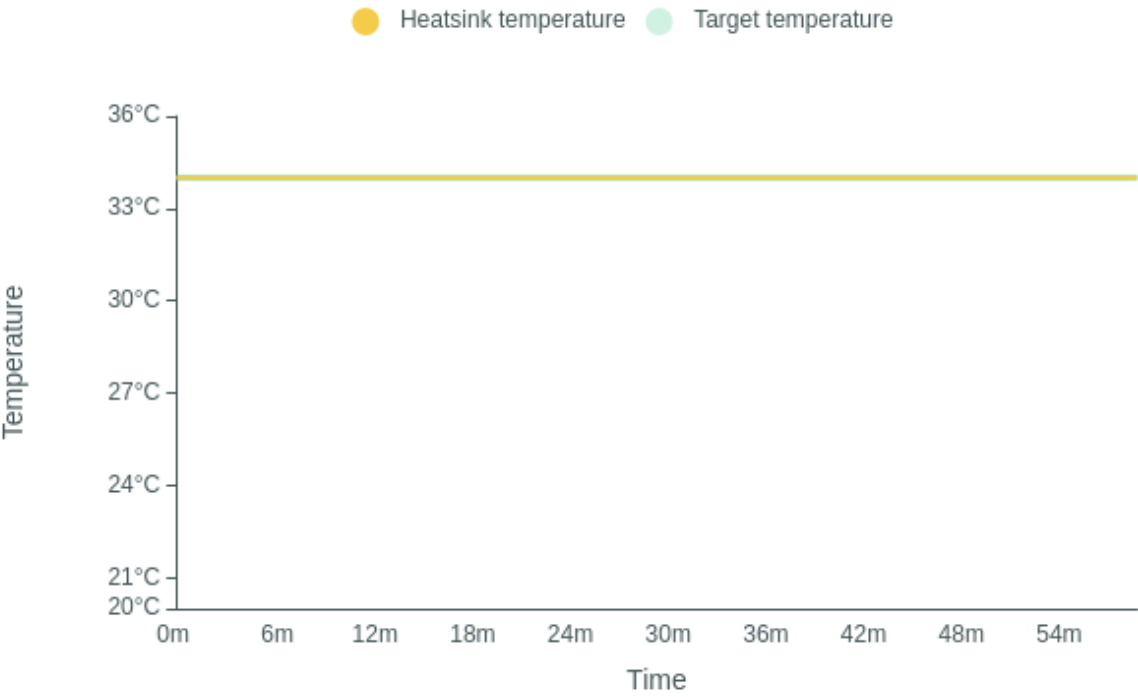




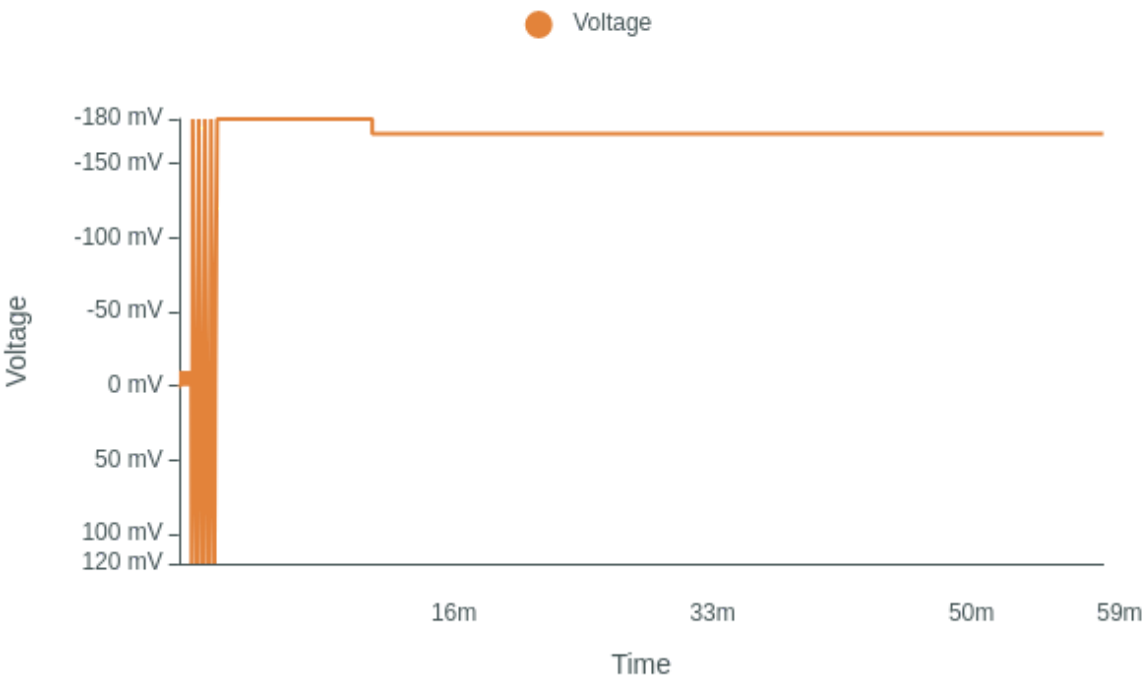
Mux Scan Categorised



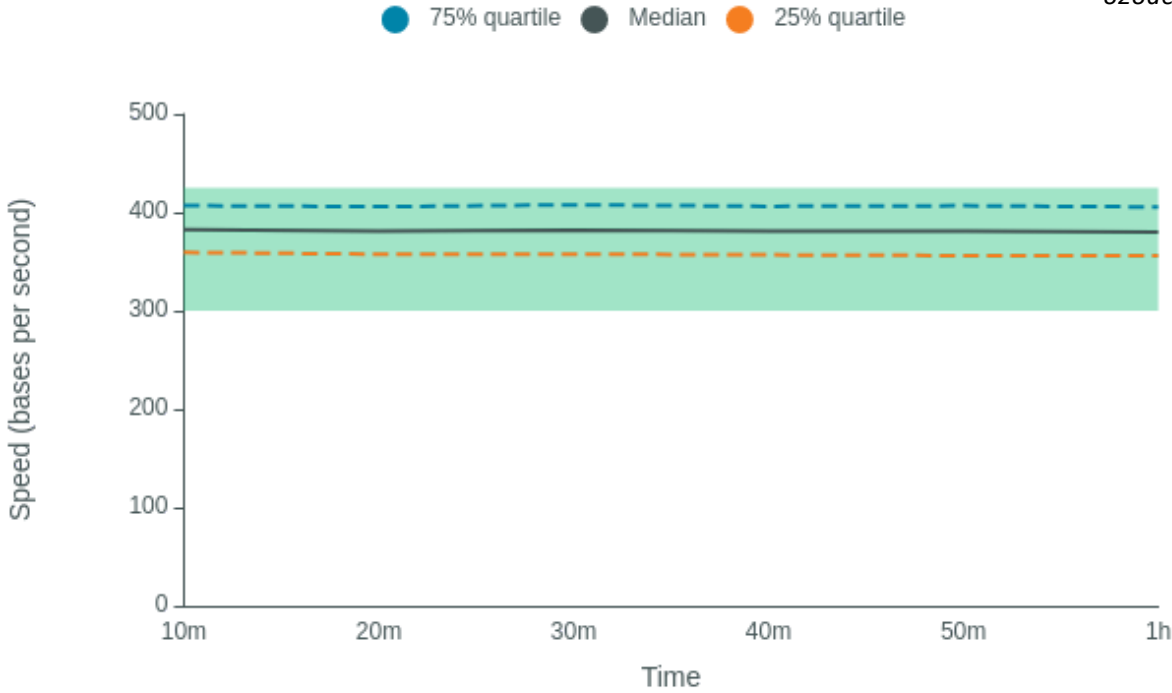
Temperature History



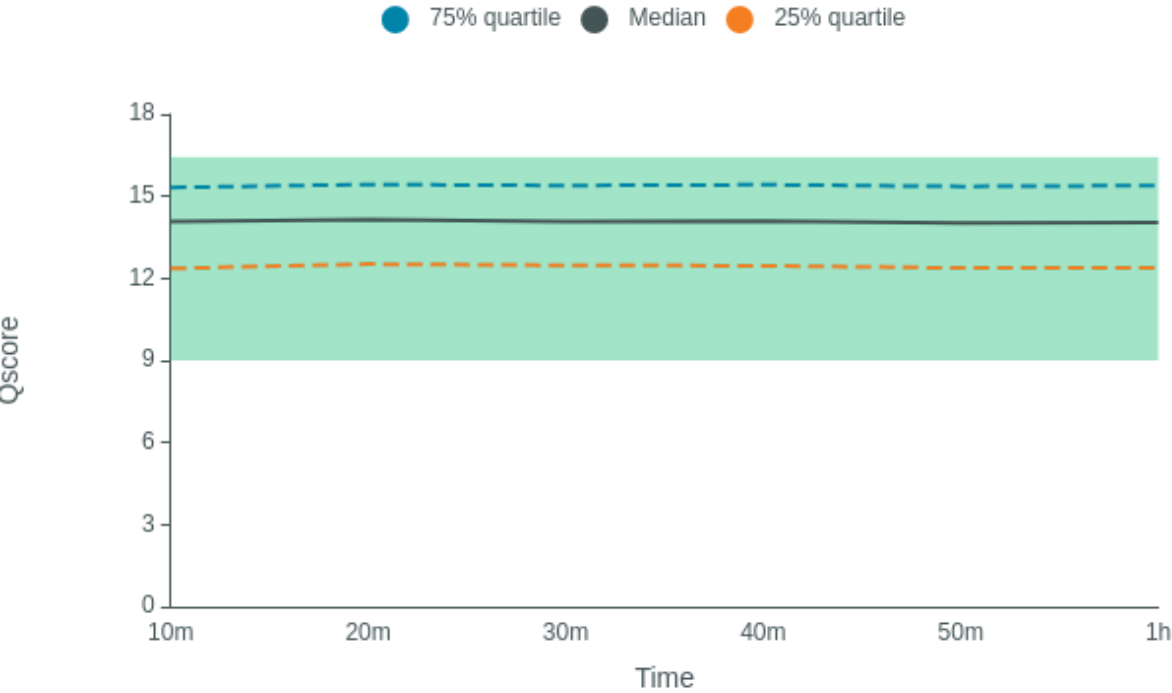
Bias Voltage History



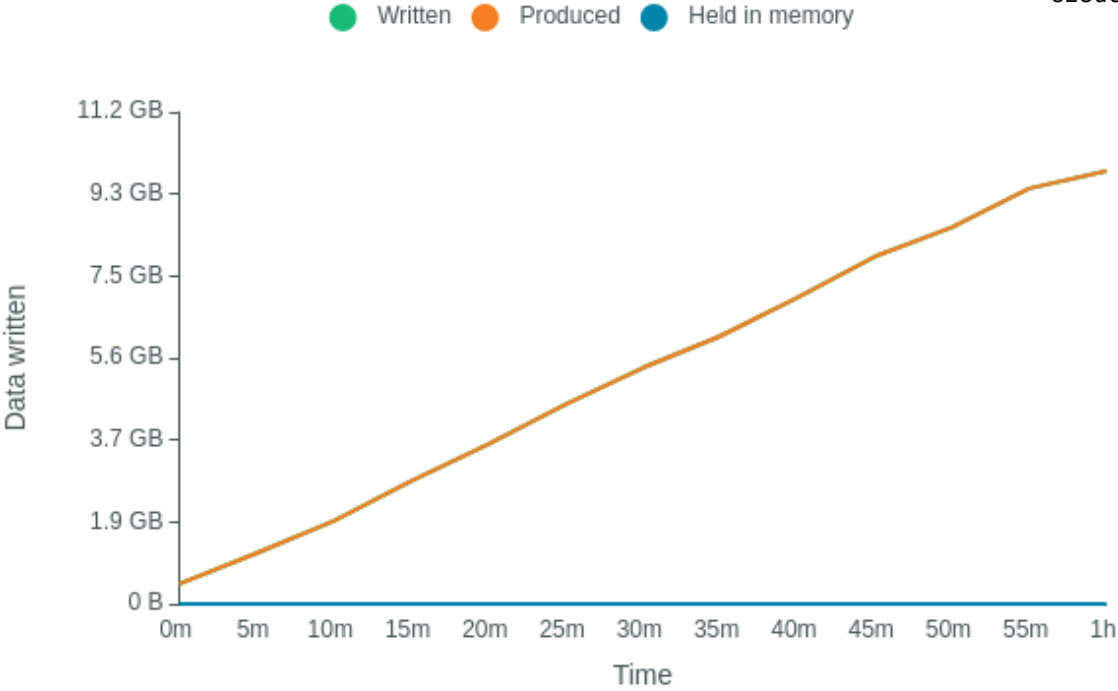
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13419 has found a total of 1367 pores. 499 pores available for immediate sequencing September 23, 13:47
- Performing Mux Scan September 23, 13:45
- Starting sequencing procedure September 23, 13:45
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 13:42