



Run Info

Host Name	GXb03422 (localhost)
Position	X4
Experiment Name	ReadUntil_ZGM_Enrich_Pcorporis_23092021
Sample ID	ReadUntil_ZGM_Enrich_Pcorporis_23092021
Run ID	1feff835-19c8-4cba-ae75-02f35e70f00b
Acquisition ID(s)	7b6c145927882b63ec48365b15002d0e780d3552, 65df353245e81327572e8ea390554e095364f8ae
Flow Cell Id	FAR13419
Start Time	September 23, 12:37
Run Length	1h 2m

Run Summary

Reads Generated	268.81 k
Passed Bases	414.05 Mb
Failed Bases	28.22 Mb
Estimated Bases	456.19 Mb

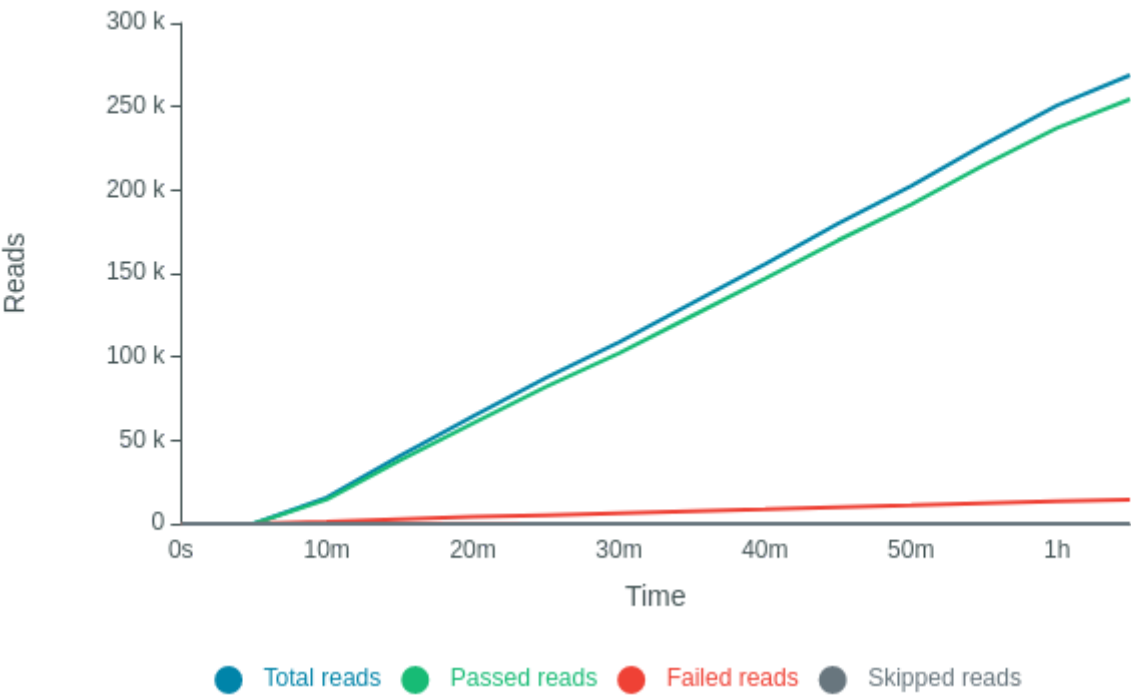
Run Parameters

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/Prevotella_corporis.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

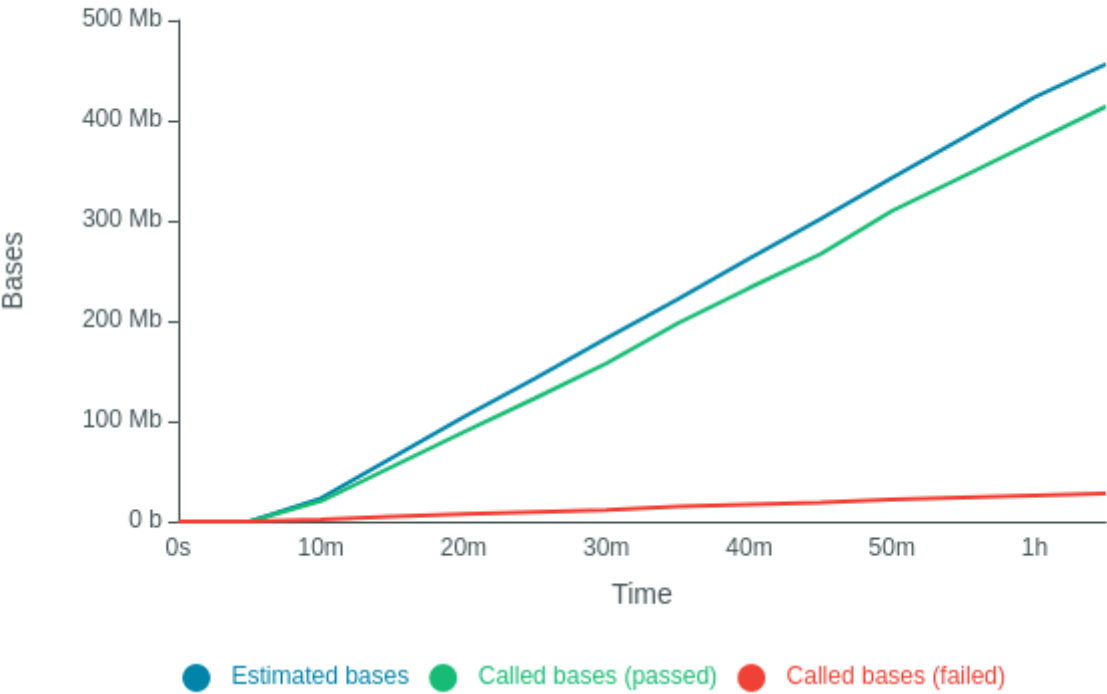
Versions

MinKNOW	21.05.20
MinKNOW Core	4.3.11
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads



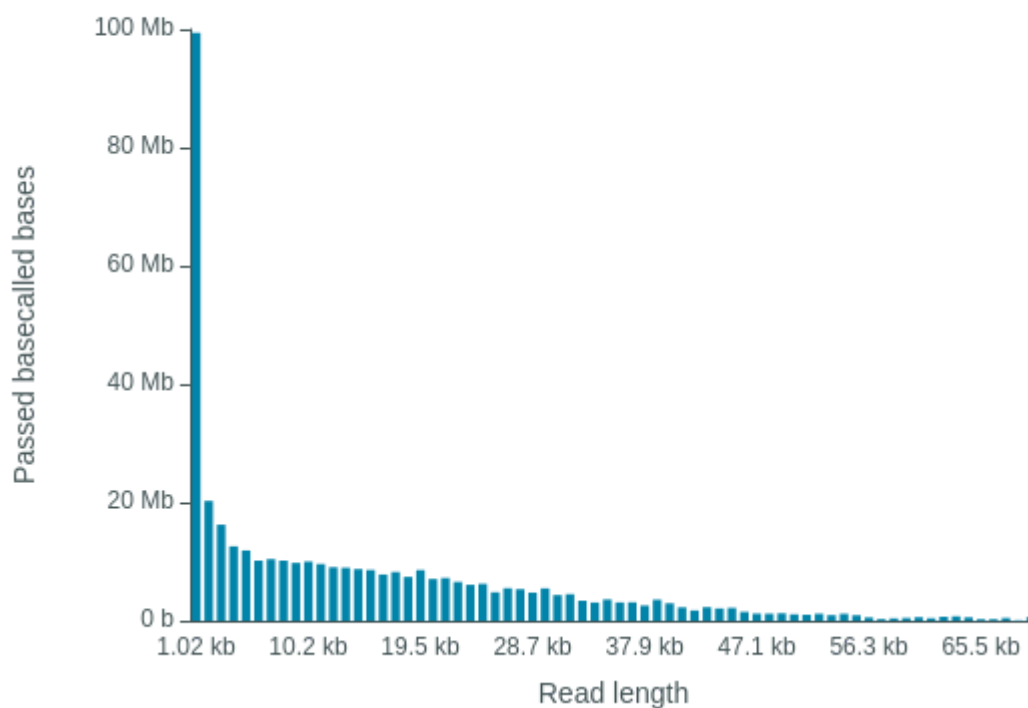
Cumulative Output Bases



Estimated N50: 9.85 kb



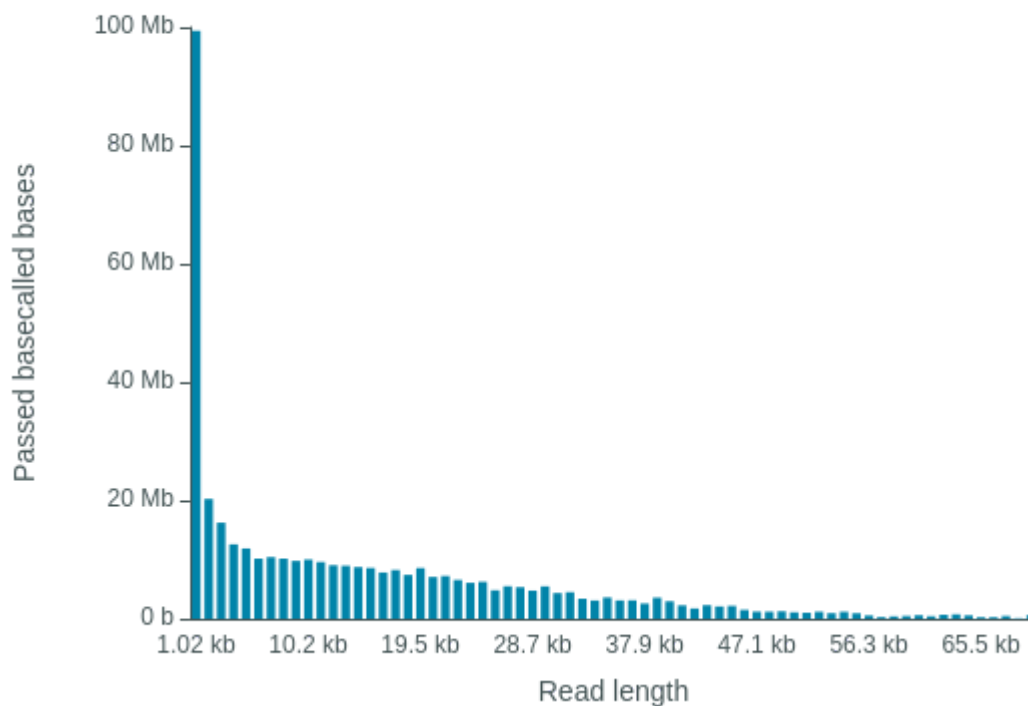
Estimated N50: 9.63 kb



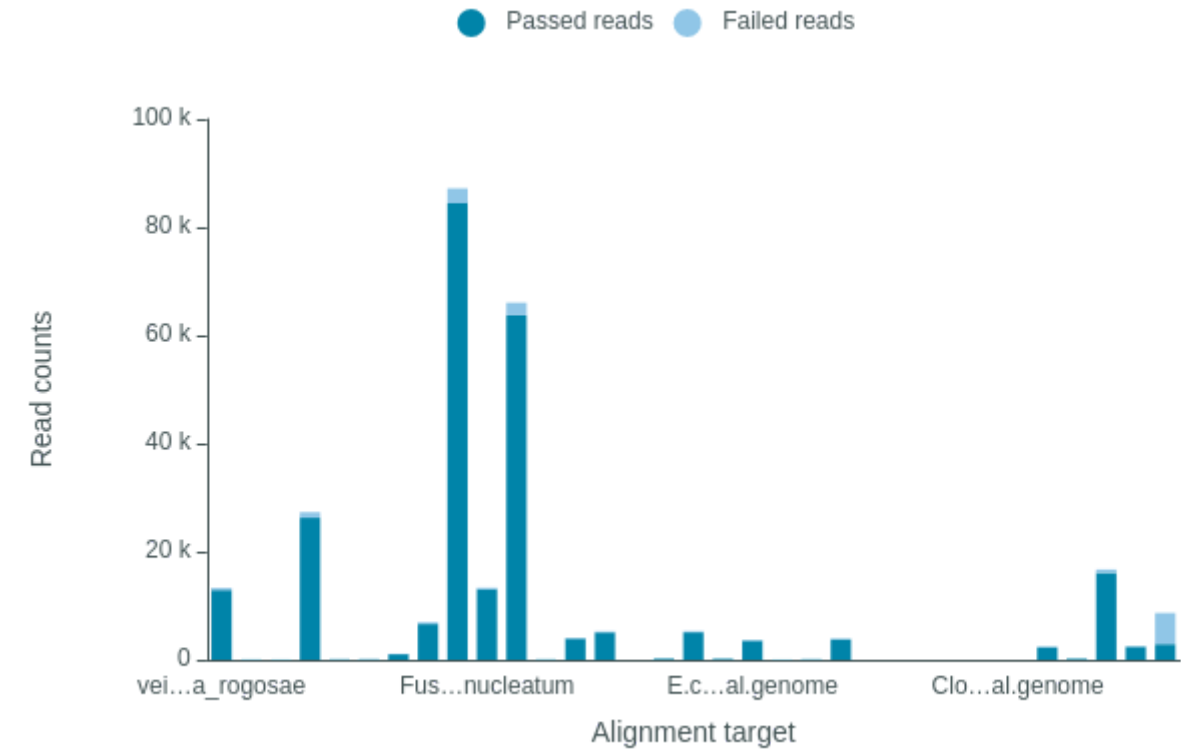
Estimated N50: 9.85 kb



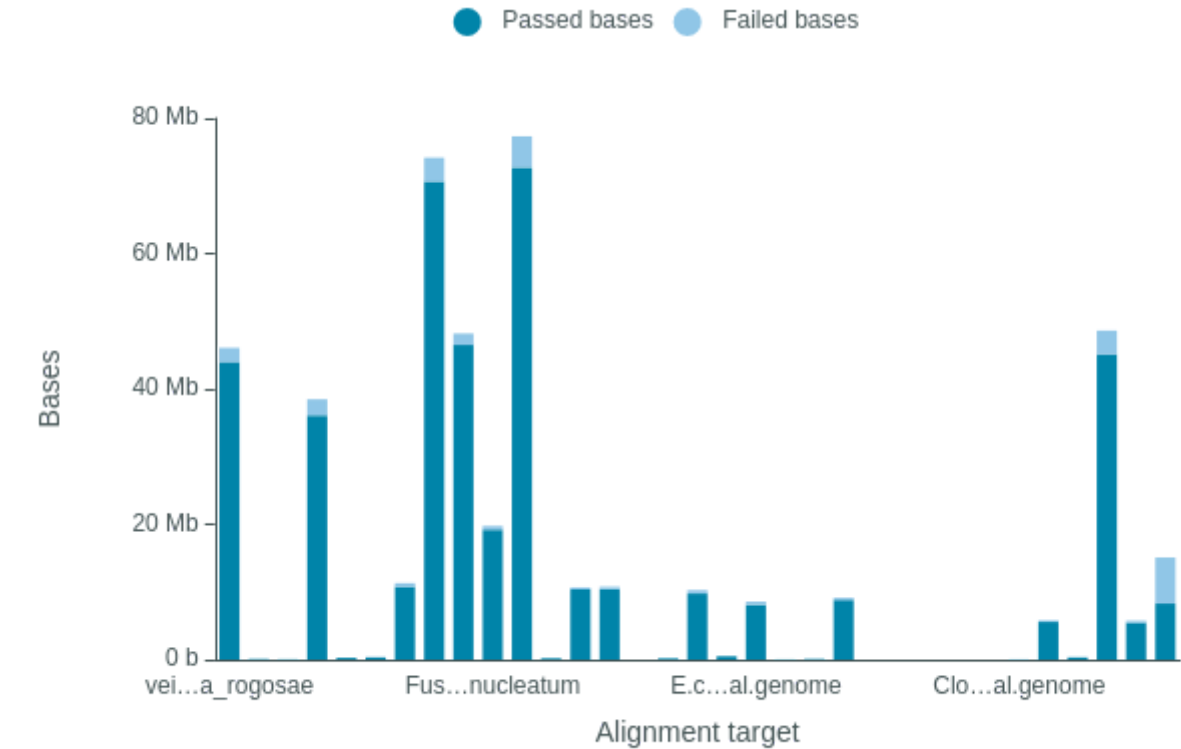
Estimated N50: 9.63 kb



Alignment Target Hits (reads)



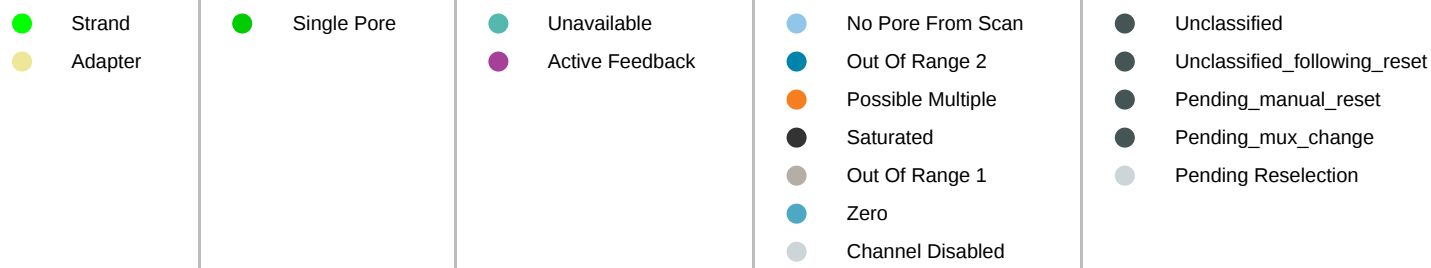
Alignment Target Hits (bases)



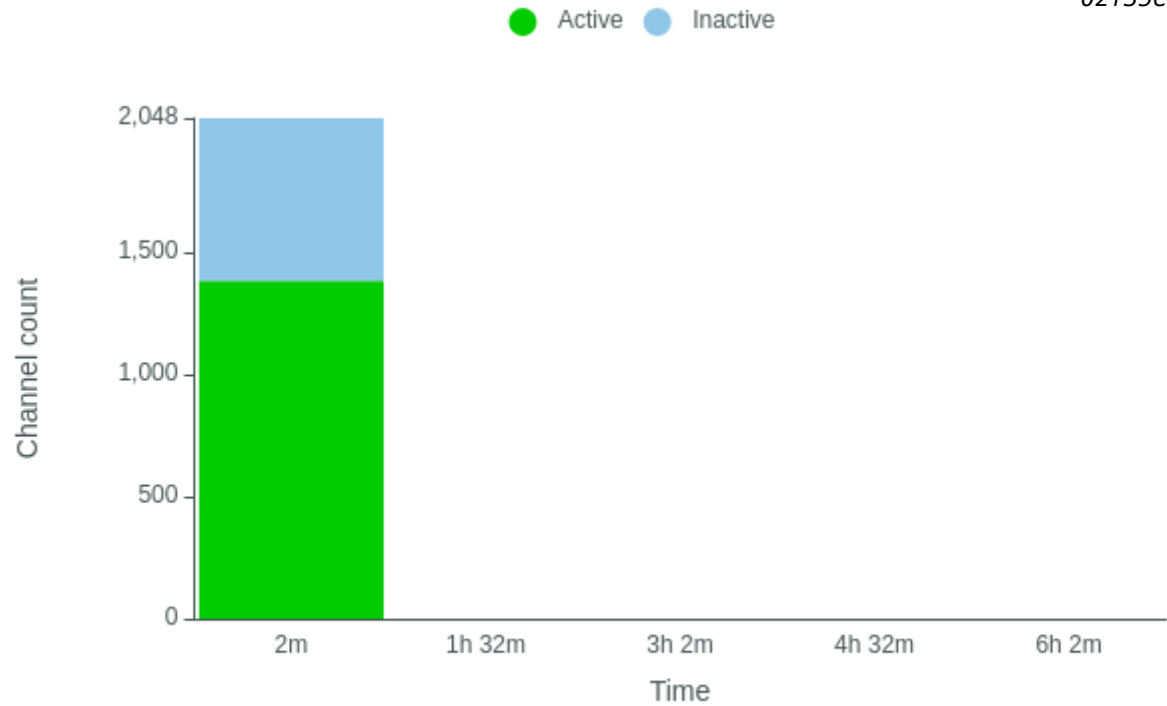
1feff835-
19c8-4cba-
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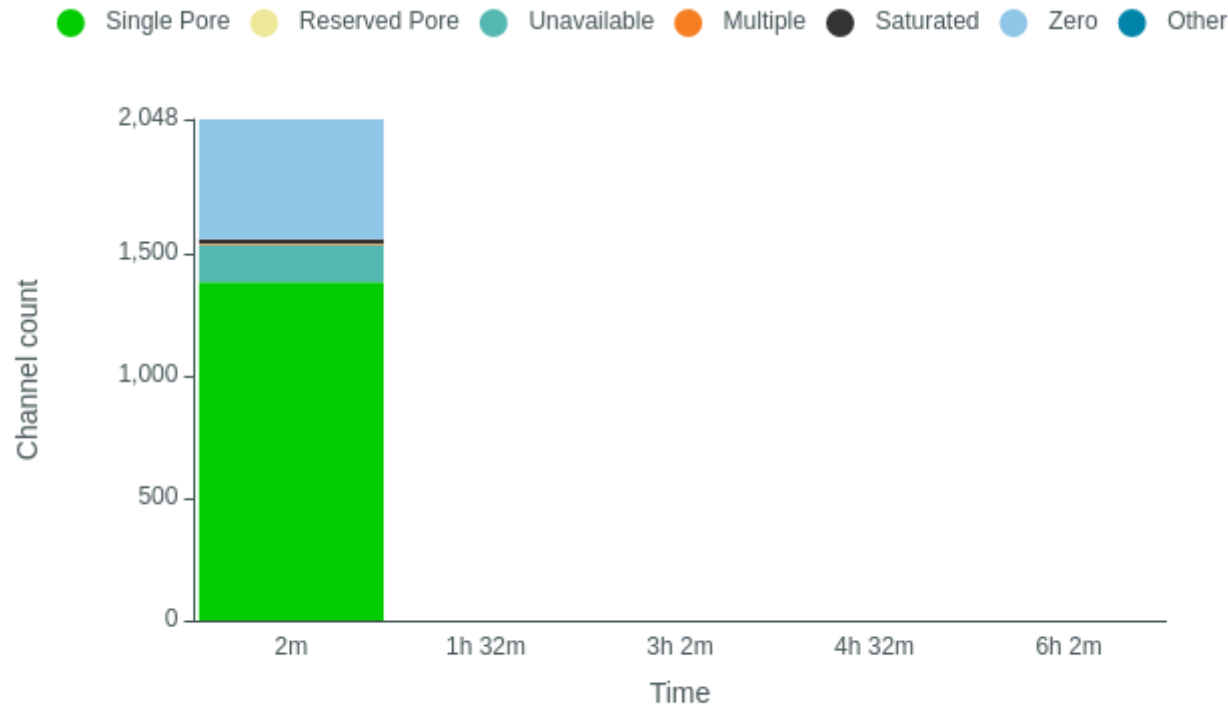
1feff835-
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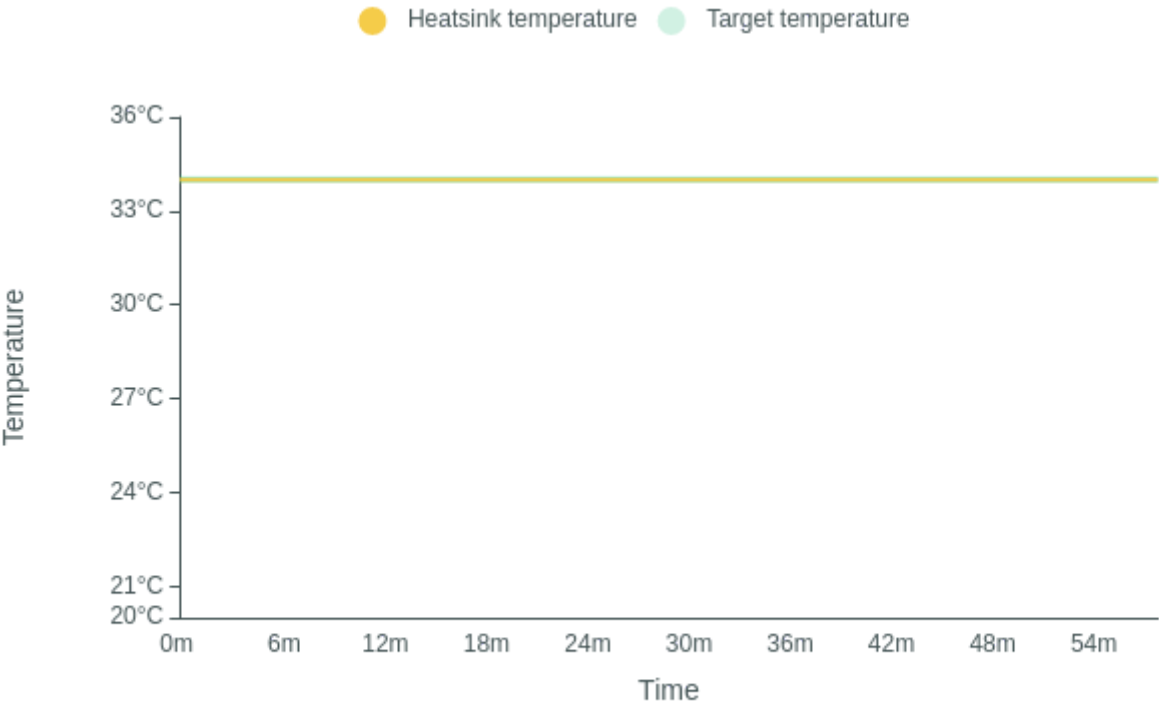
Mux Scan Grouped



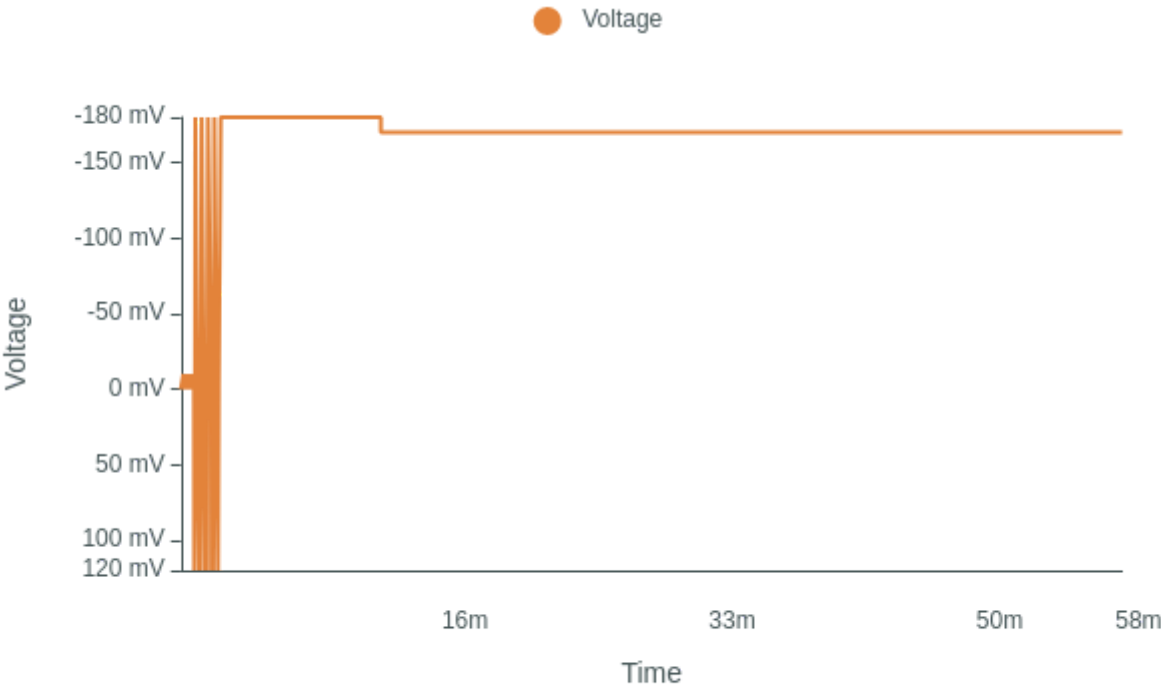
Mux Scan Categorised



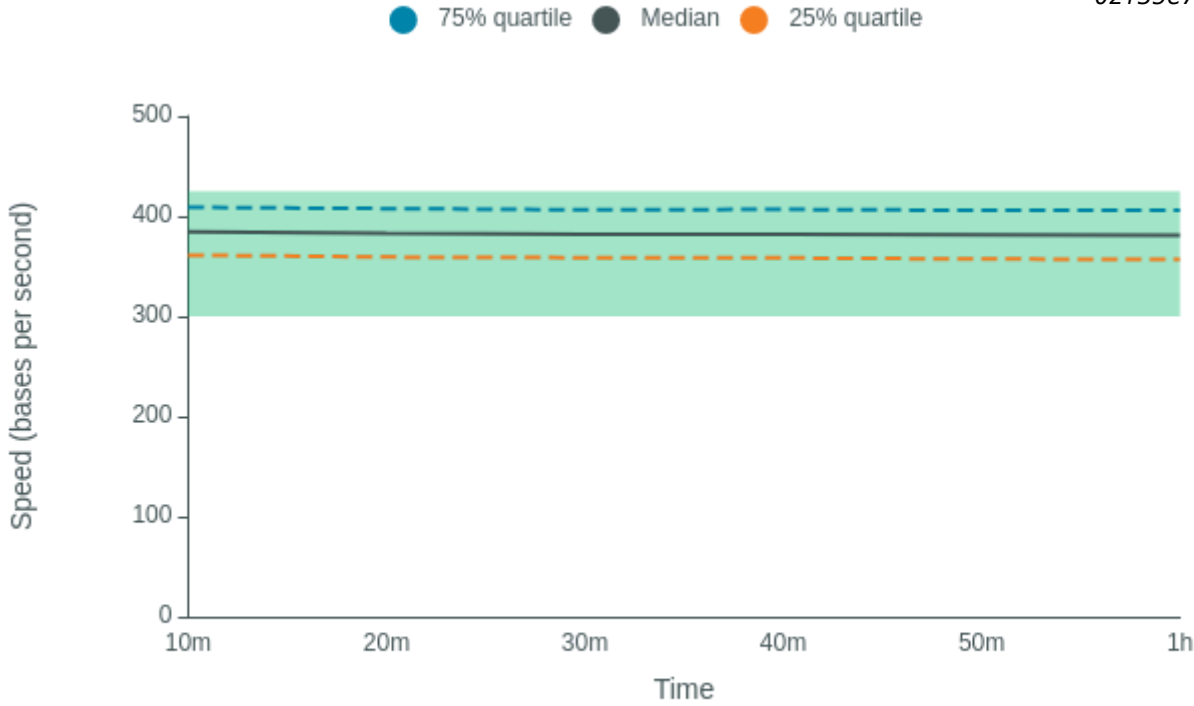
Temperature History



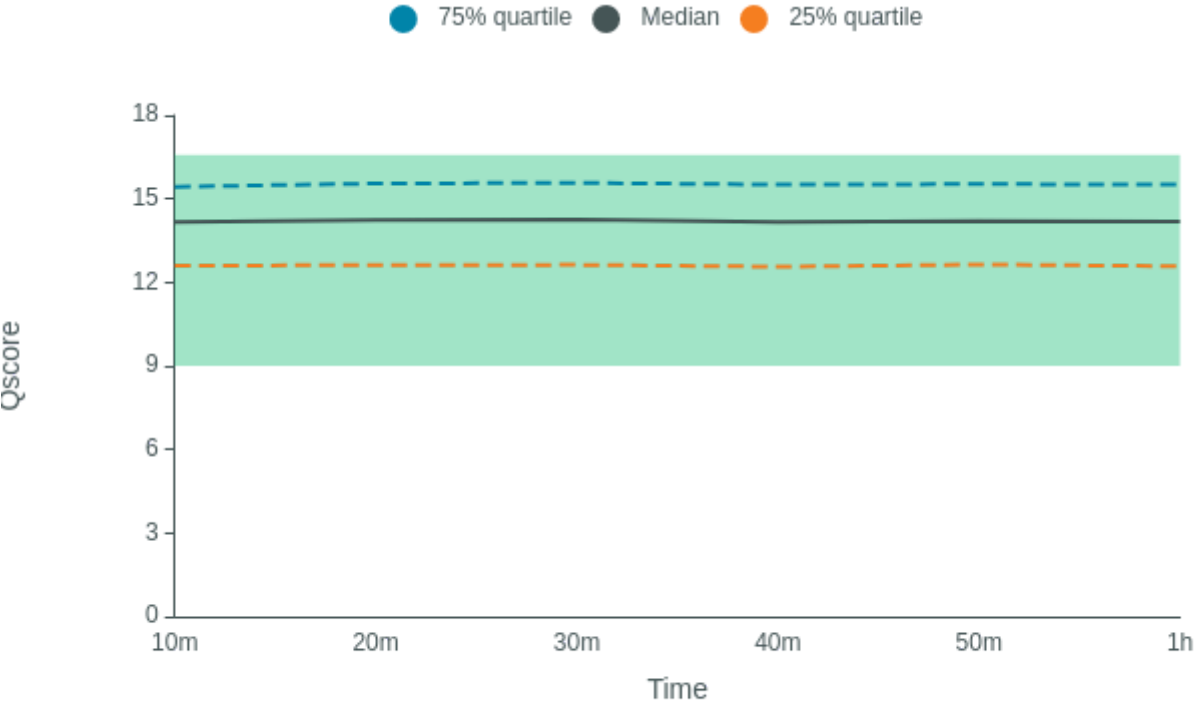
Bias Voltage History



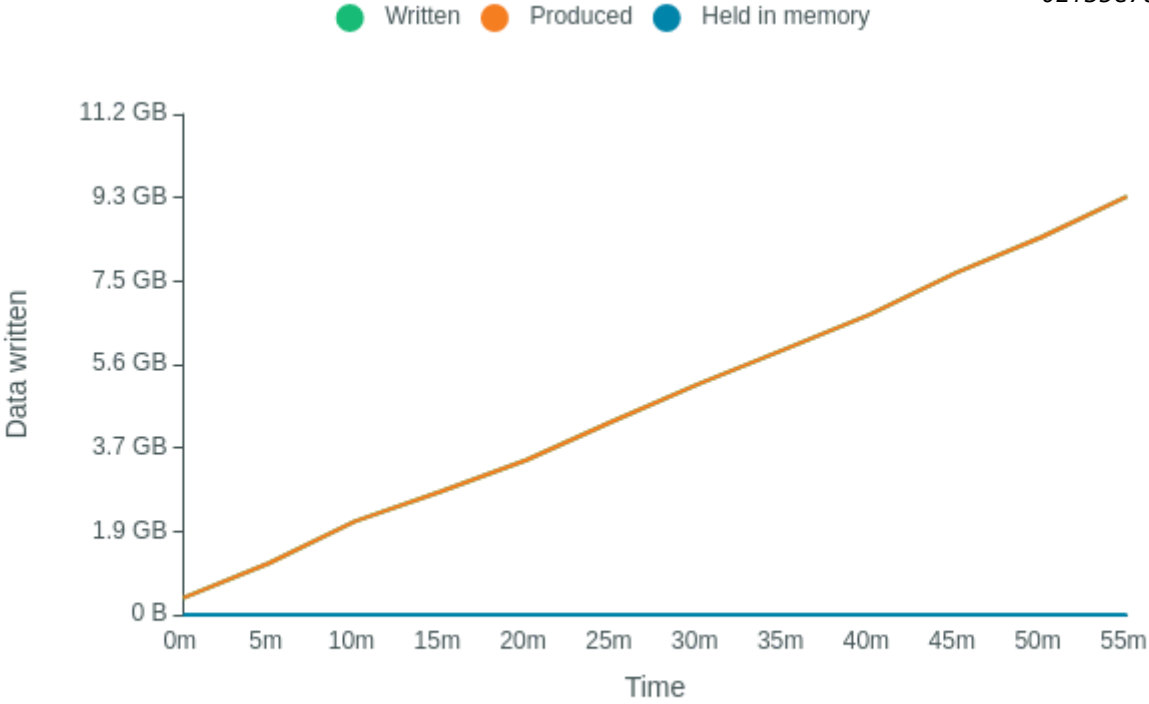
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAR13419 has found a total of 1382 pores. 503 pores available for immediate sequencing September 23, 12:44
- Performing Mux Scan September 23, 12:41
- Starting sequencing procedure September 23, 12:41
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C September 23, 12:37