



Run Info

Host Name	GXb03422 (localhost)
Position	X1
Experiment Name	ReadUntil_Hydrogenophaga_Assenr_0510221
Sample ID	ReadUntil_Hydrogenophaga_Assenr_0510221
Run ID	42125843-5071-4348-a912-9303de4600a1
Acquisition ID(s)	f3c7598cfa8892eb819f479066c4b6435181394a, 25ab681ad29fa9483a7455684ea7a3dc5c08db17
Flow Cell Id	FAQ86094
Start Time	October 5, 15:13
Run Length	1h 3m

Run Summary

Reads Generated	265.95 k
Passed Bases	383.79 Mb
Failed Bases	34.94 Mb
Estimated Bases	428.1 Mb

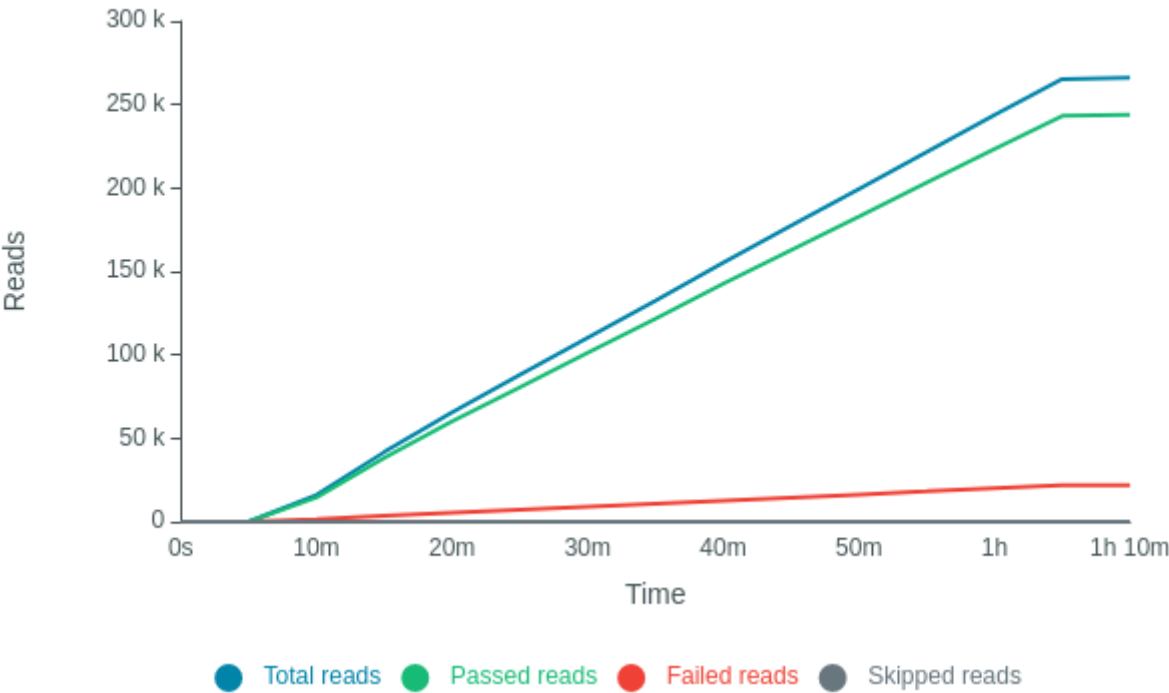
Run Parameters

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/compost_3/Hydrogenophaga_assembly.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/compost_3/Hydrogenophaga_all.fasta"]
Read filtering	min_qscore=9

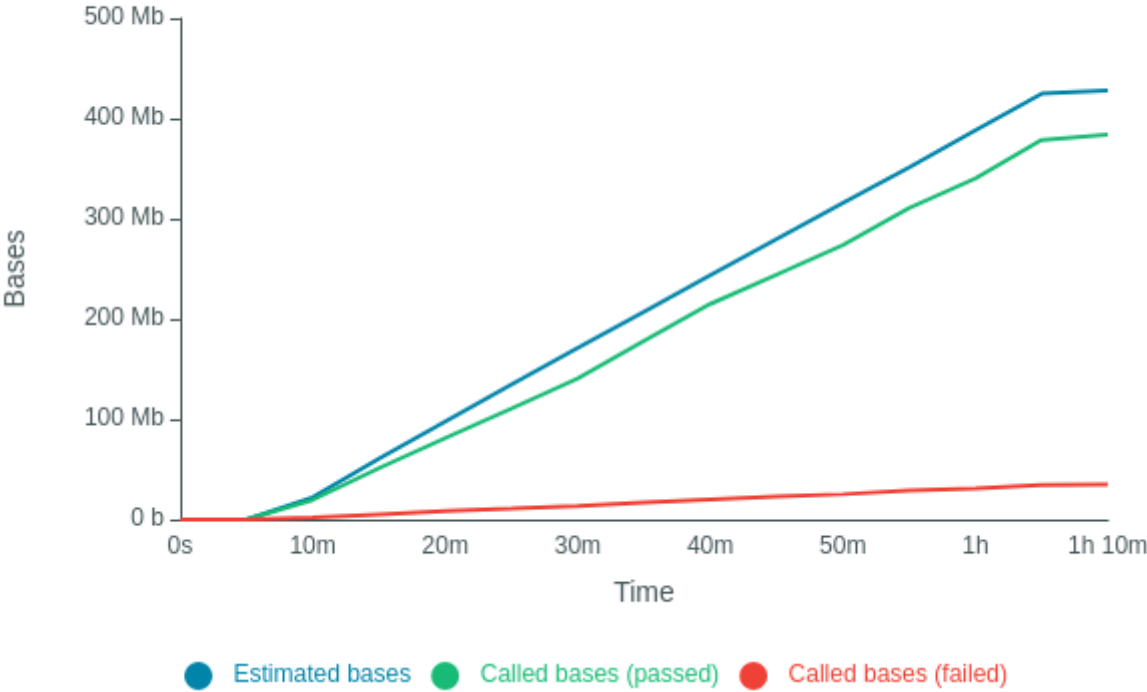
Versions

MinKNOW	21.05.21
MinKNOW Core	4.3.12
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads

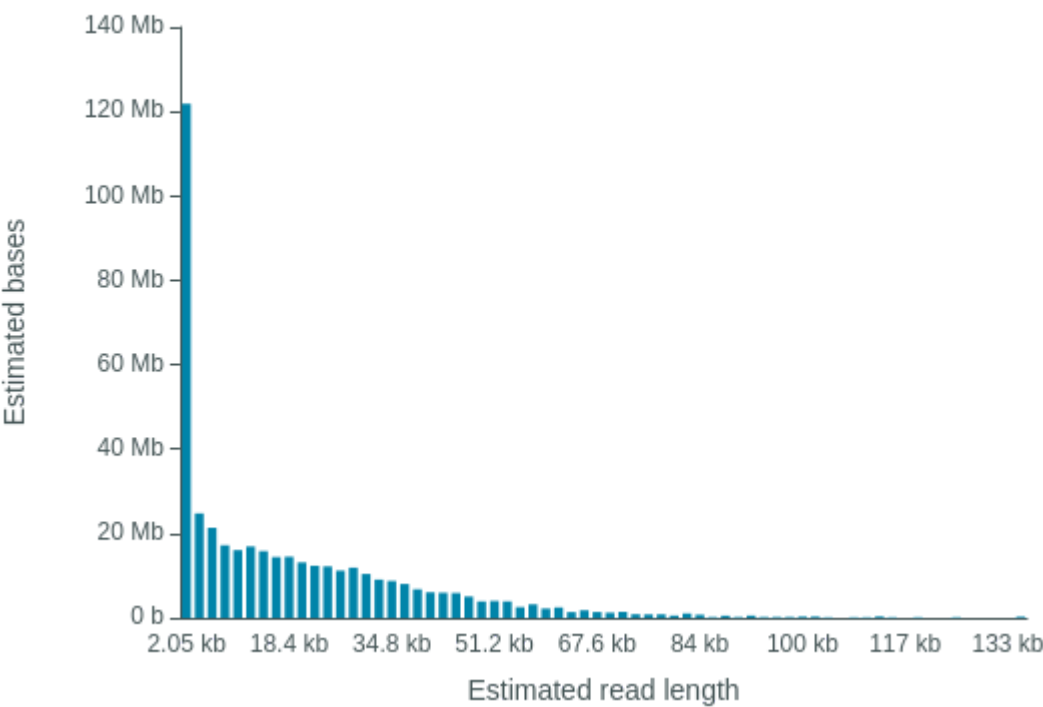


Cumulative Output Bases



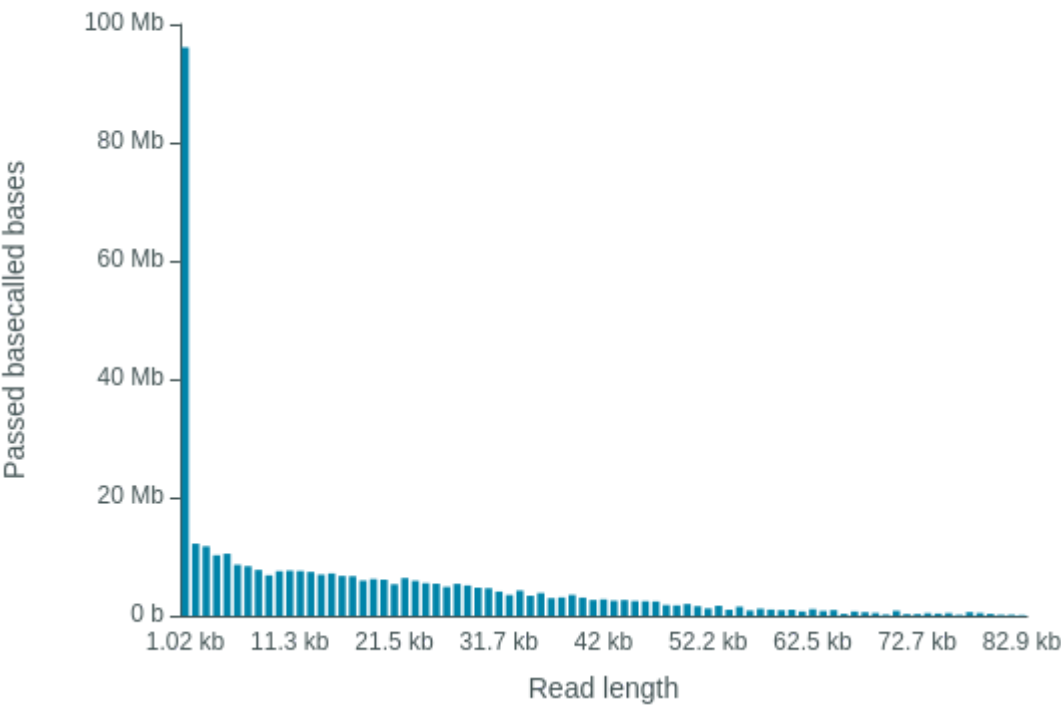
Read Length Histogram Estimated Bases - Outliers Discarded

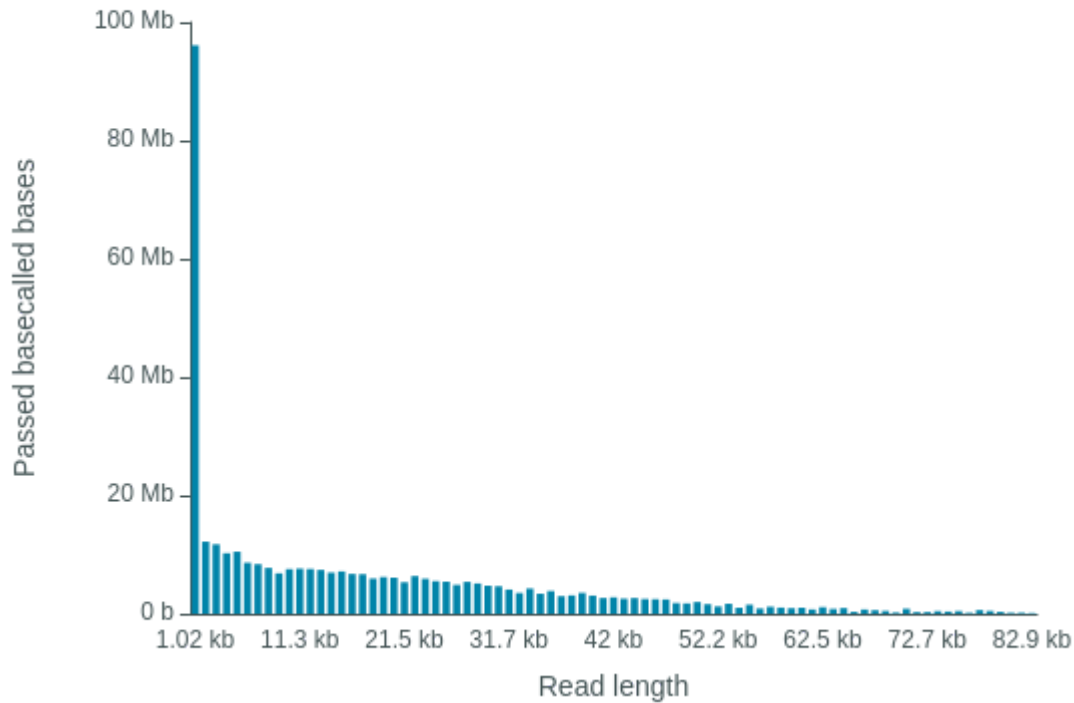
Estimated N50: 11.79 kb



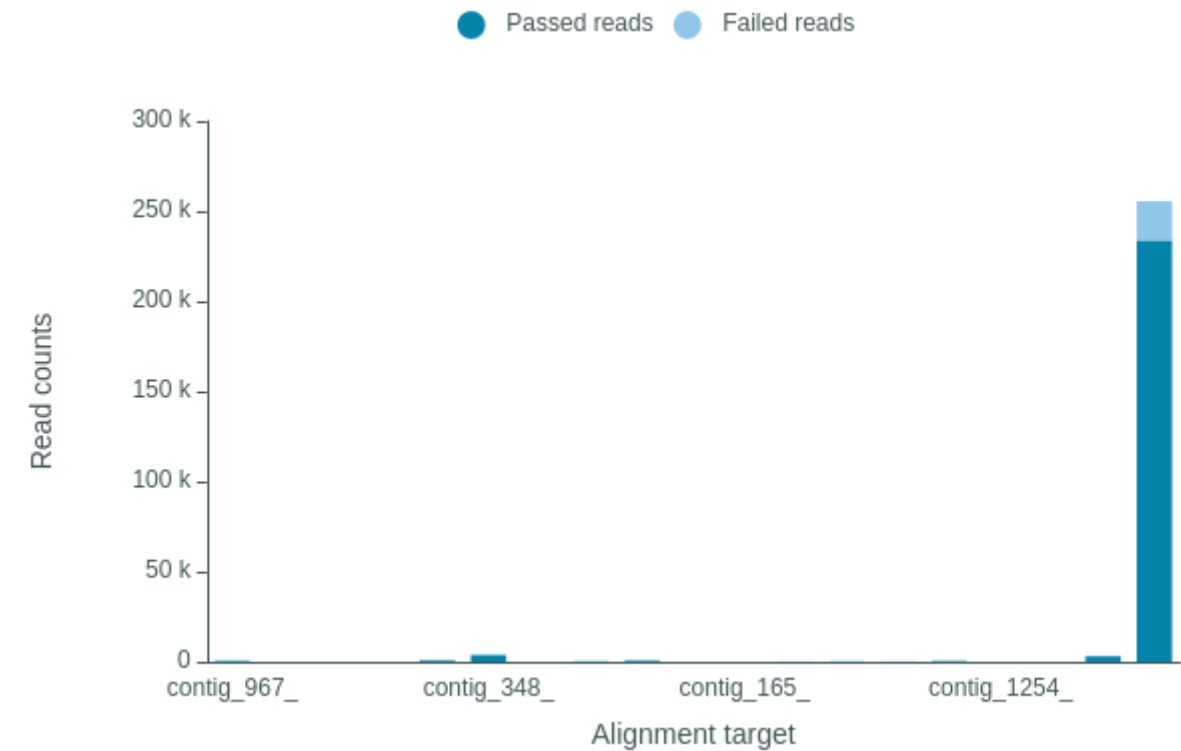
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 11.6 kb

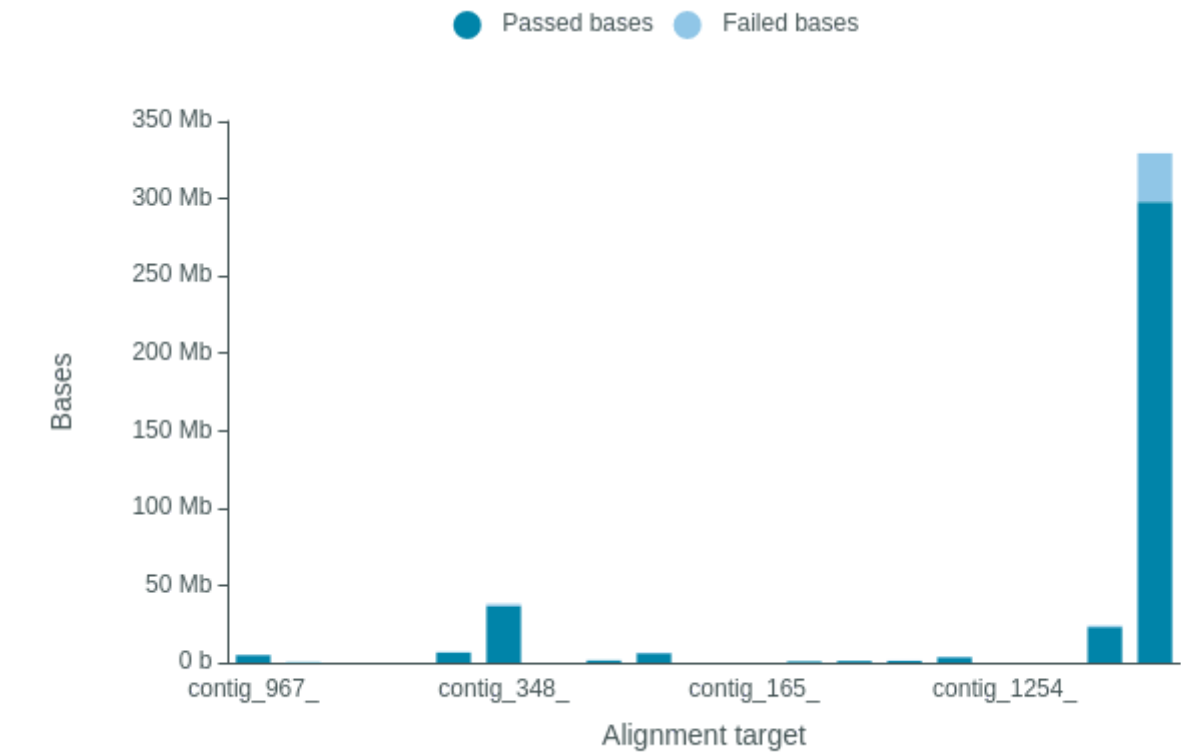




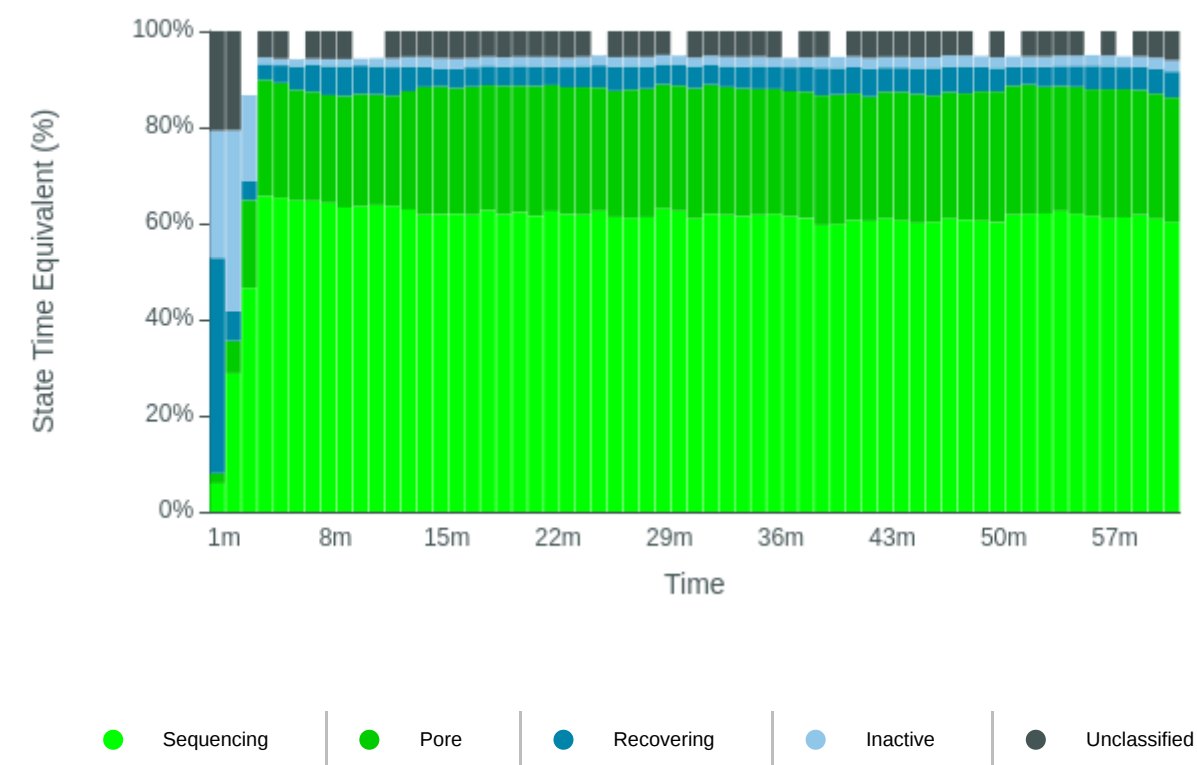
Alignment Target Hits (reads)



Alignment Target Hits (bases)



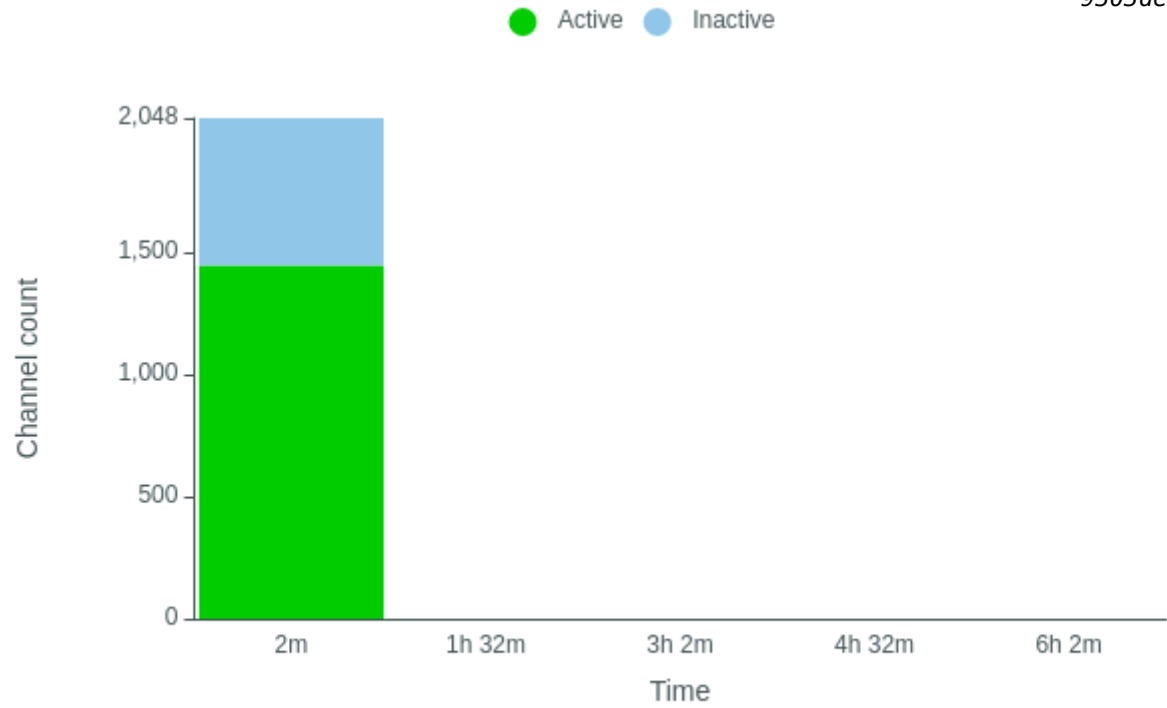
Duty Time Grouped



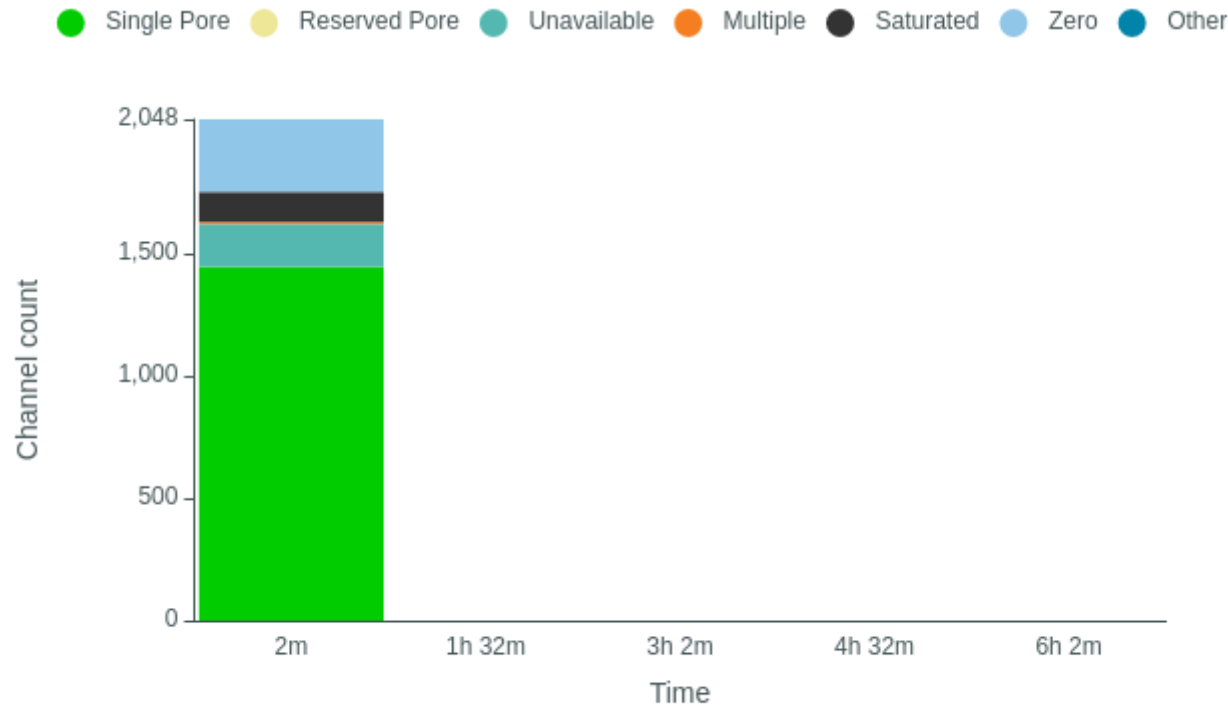
Duty time Categorised



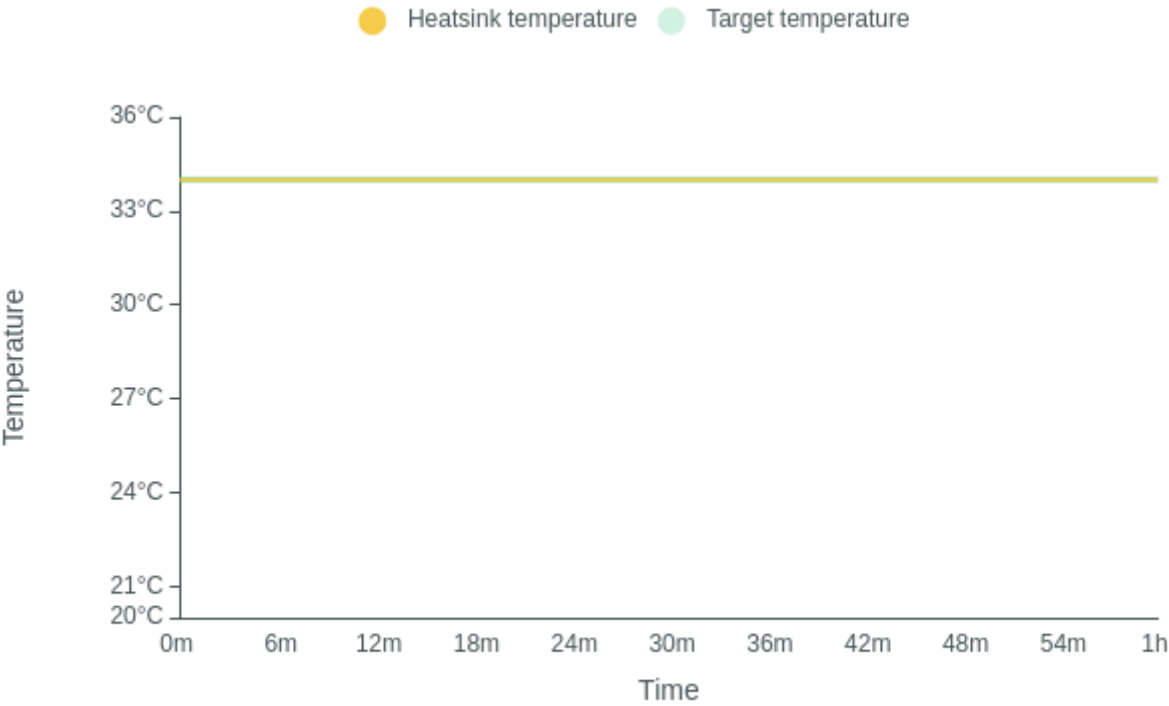
Mux Scan Grouped



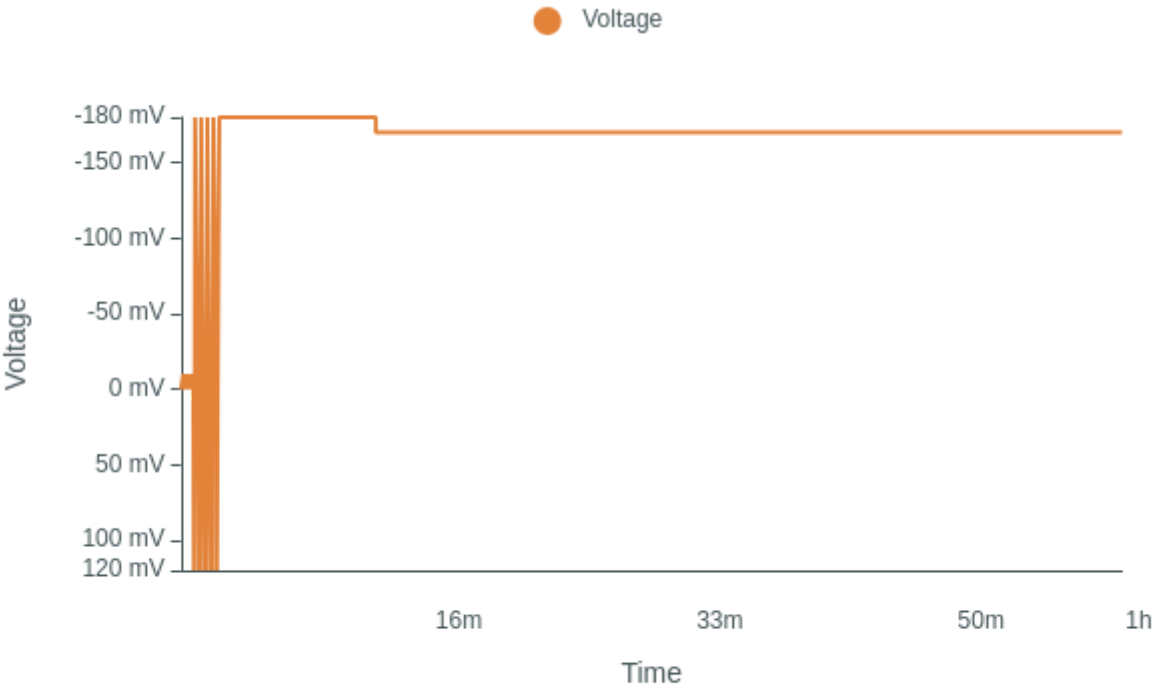
Mux Scan Categorised



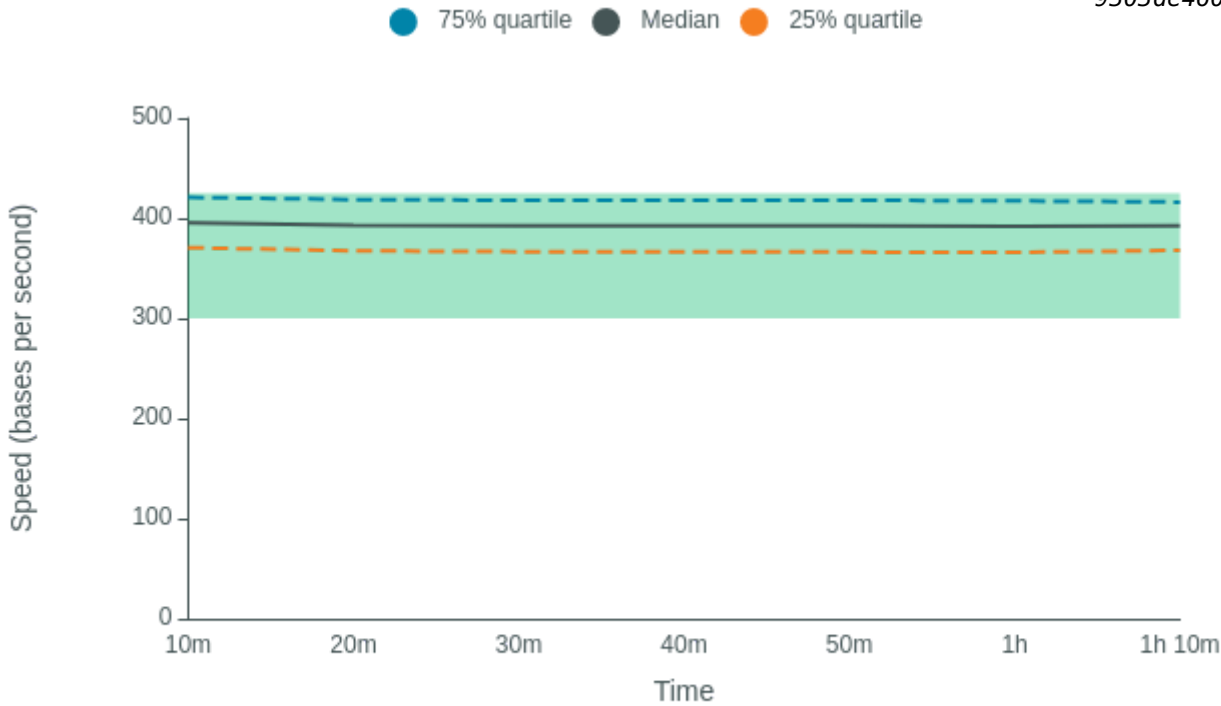
Temperature History



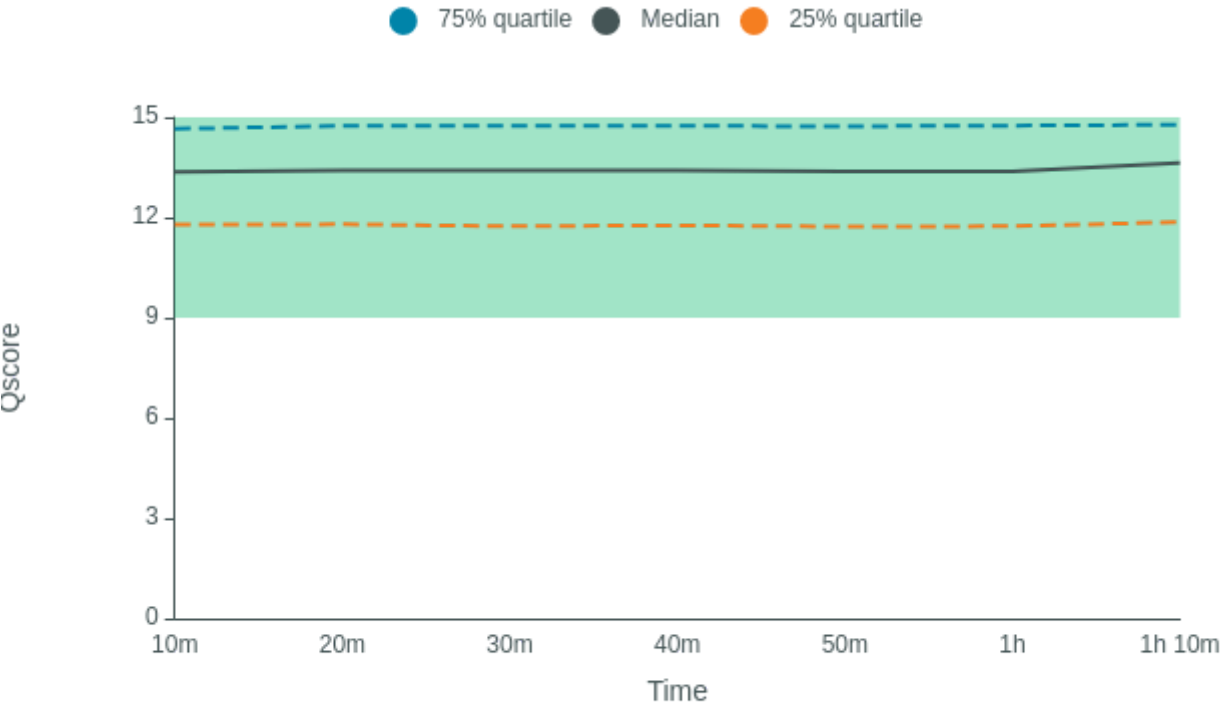
Bias Voltage History



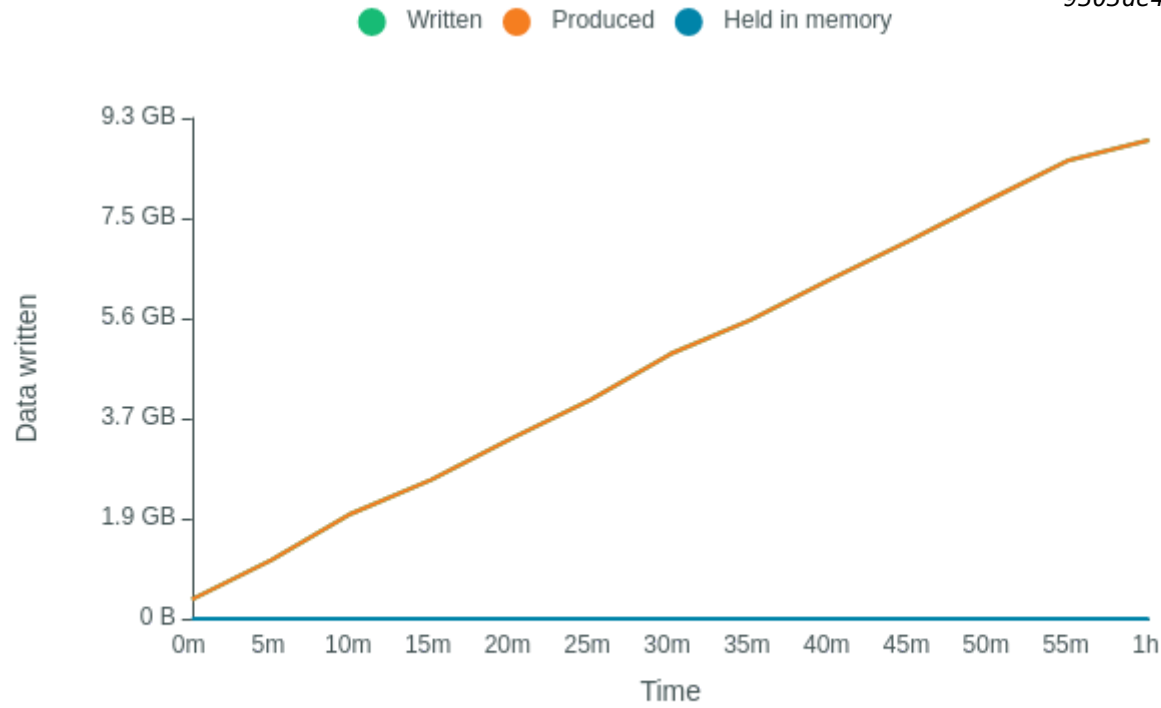
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAQ86094 has found a total of 1445 pores. 505 pores available for immediate sequencing October 5, 15:18
- Performing Mux Scan October 5, 15:16
- Starting sequencing procedure October 5, 15:16
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C October 5, 15:13