



Run Info

Host Name	GXb03422 (localhost)
Position	X1
Experiment Name	ReadUntil_Hydrogenophaga_Allenrich_05102
Sample ID	ReadUntil_Hydrogenophaga_Allenrich_05102
Run ID	d98d2371-0dd3-4f2b-9012-48056d44fd54
Acquisition ID(s)	d628a149d39b7eaea410a522e55a751327bdecf3,8fc445ff6e2374ff8b34234ffe77af9594db1af9
Flow Cell Id	FAQ86094
Start Time	October 5, 14:06
Run Length	1h 3m

Run Summary

Reads Generated	258.49 k
Passed Bases	383.74 Mb
Failed Bases	36.3 Mb
Estimated Bases	426.74 Mb

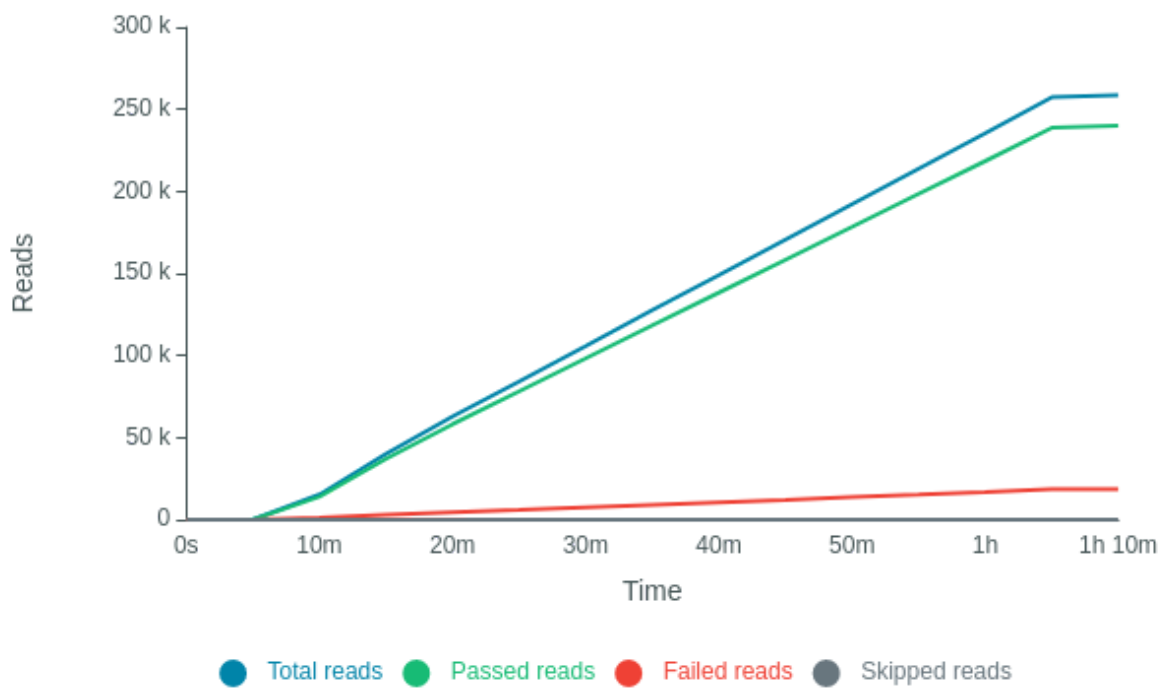
Run Parameters

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_all.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

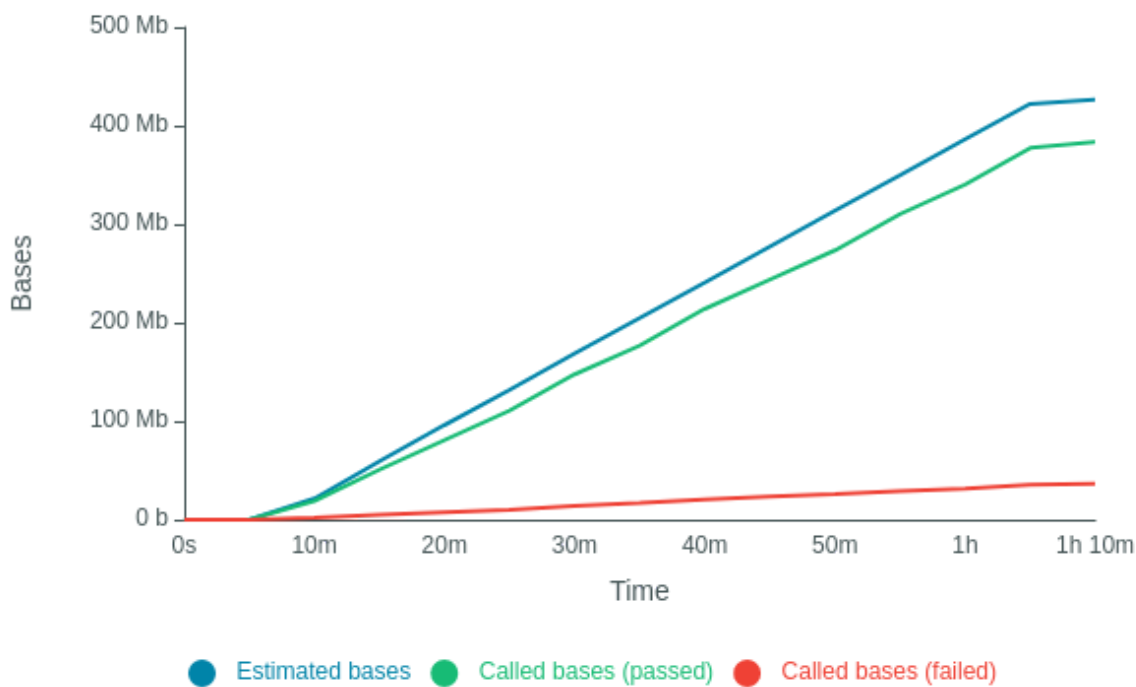
Versions

MinKNOW	21.05.21
MinKNOW Core	4.3.12
Bream	6.2.6
Guppy	5.0.13

Cumulative Output Reads

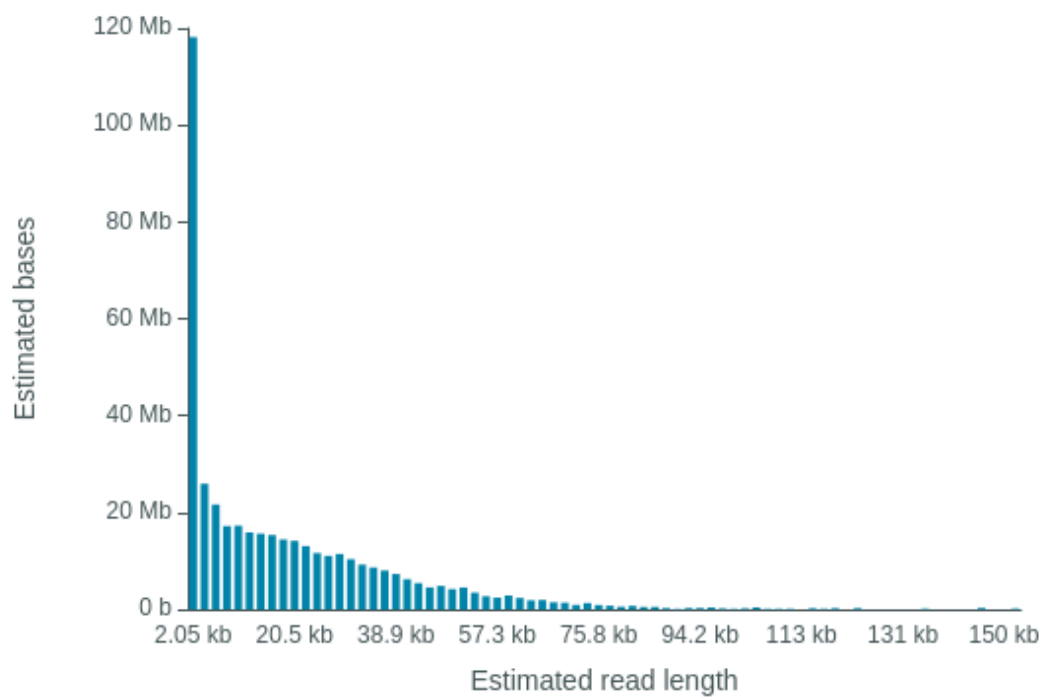


Cumulative Output Bases



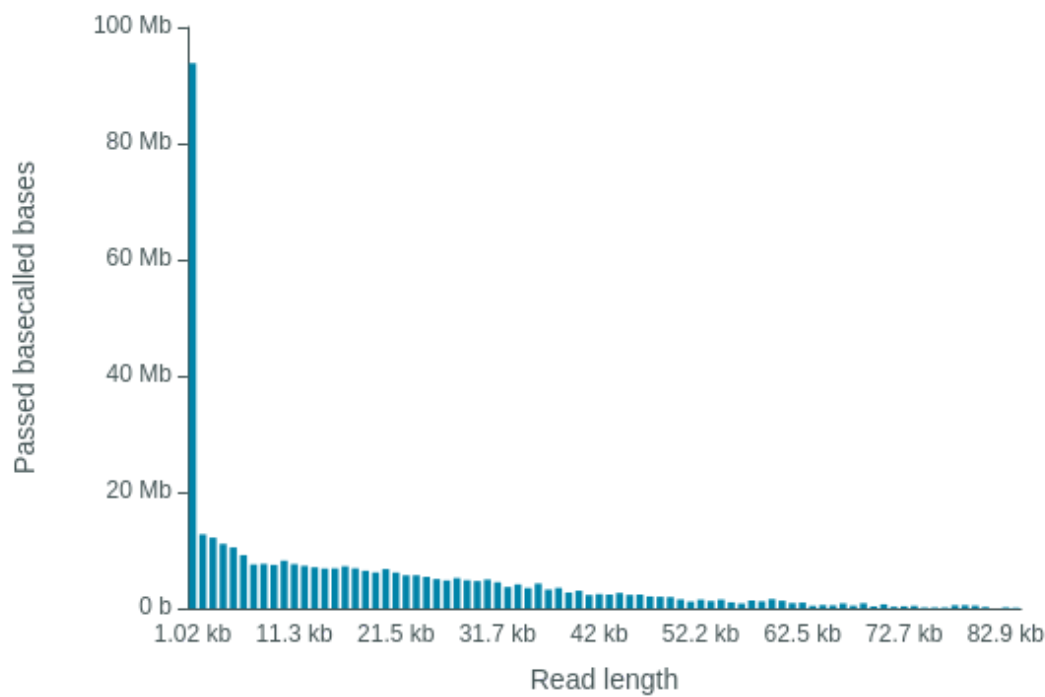
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 11.9 kb



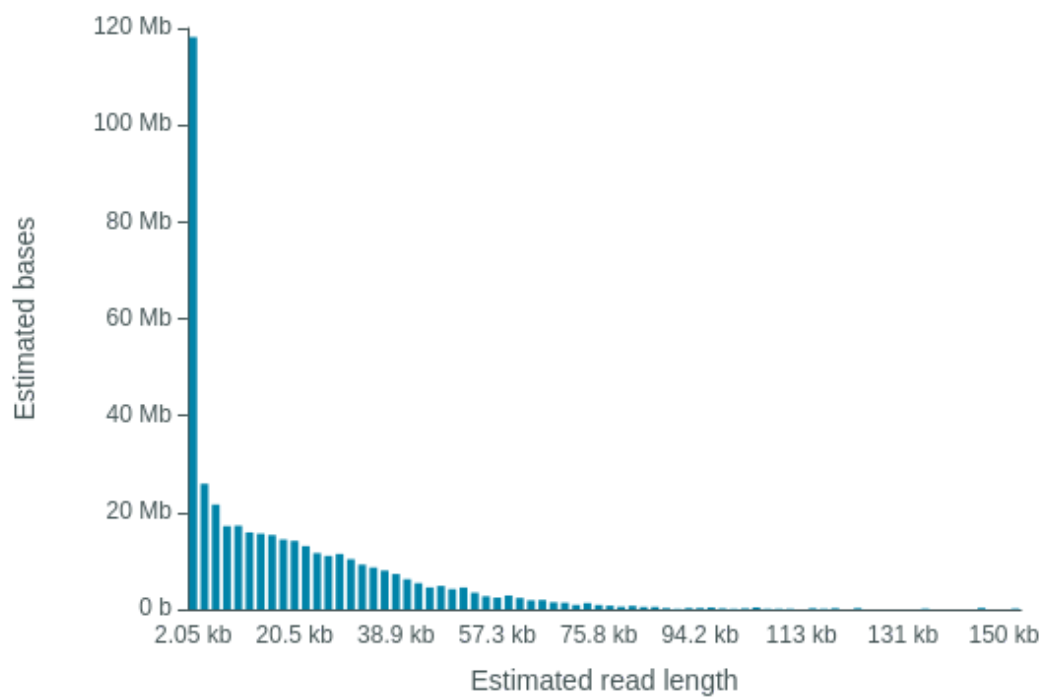
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 11.53 kb



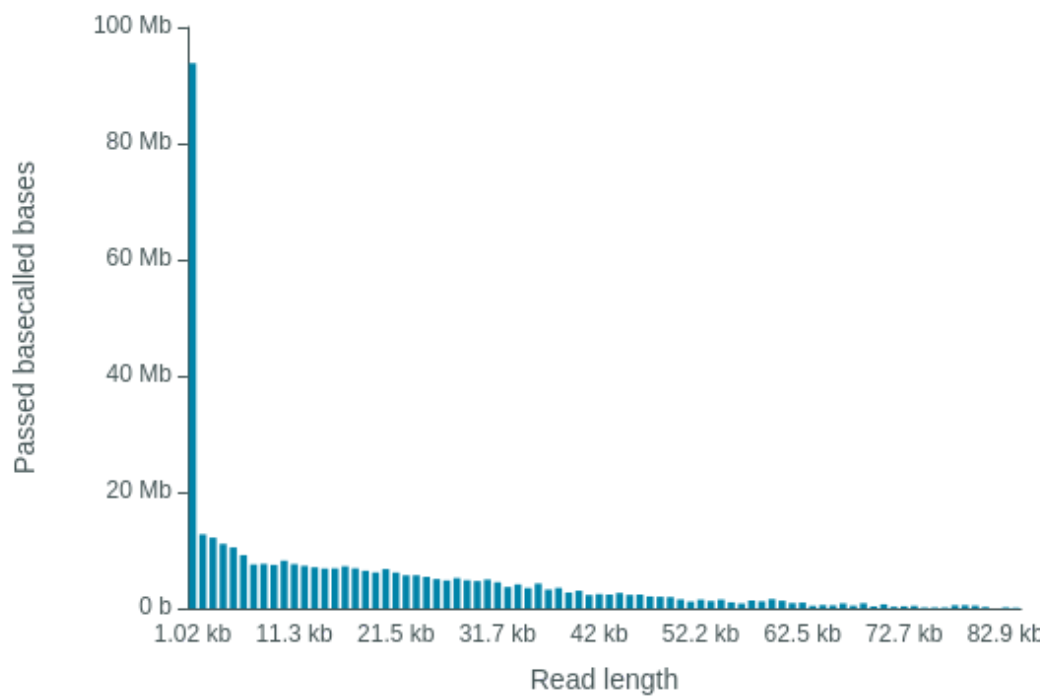
Read Length Histogram Estimated Bases

Estimated N50: 11.9 kb

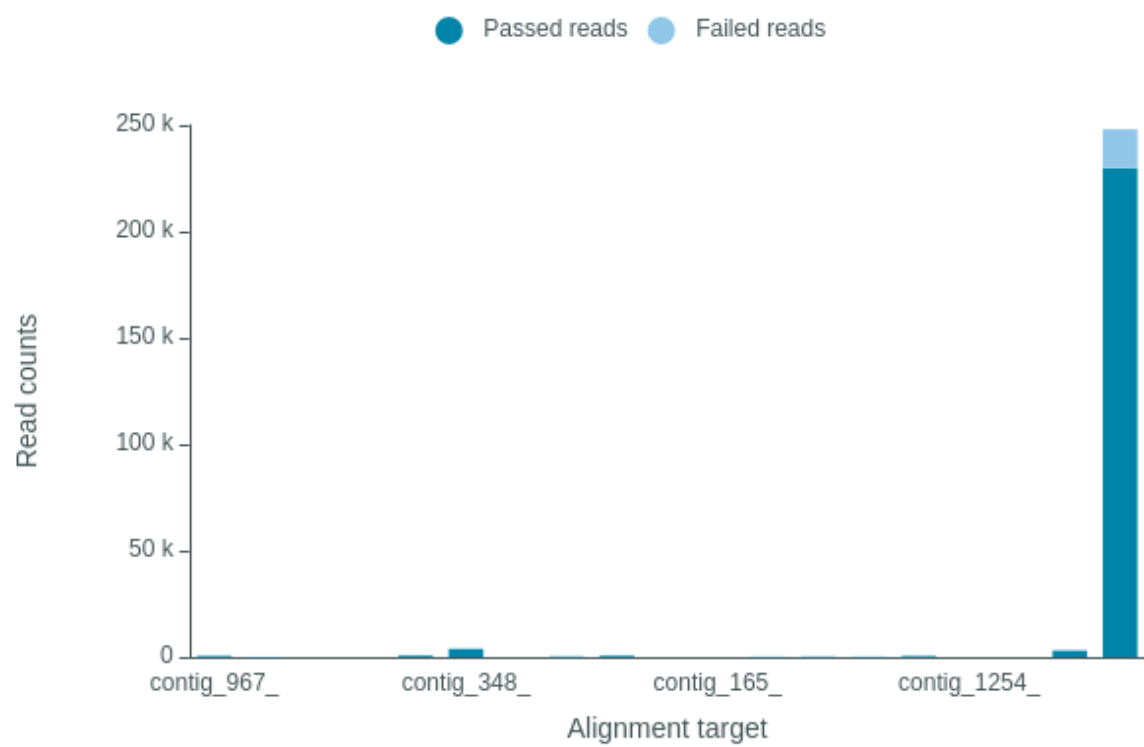


Read Length Histogram Basecalled Bases

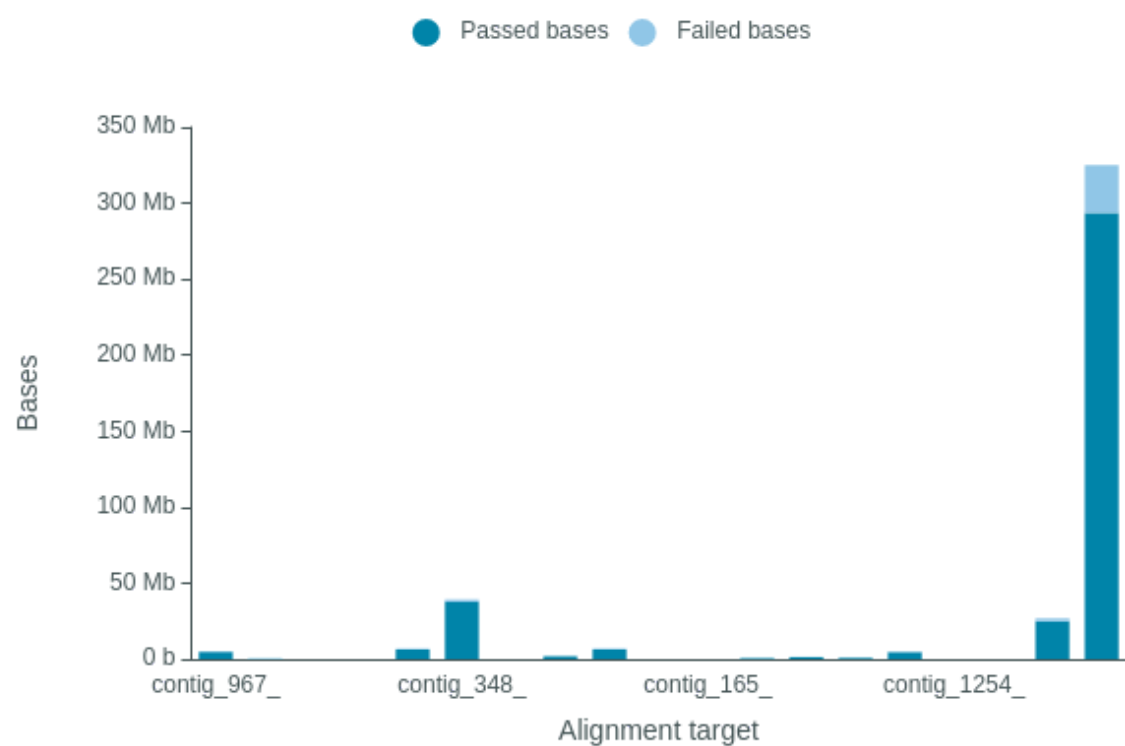
Estimated N50: 11.53 kb



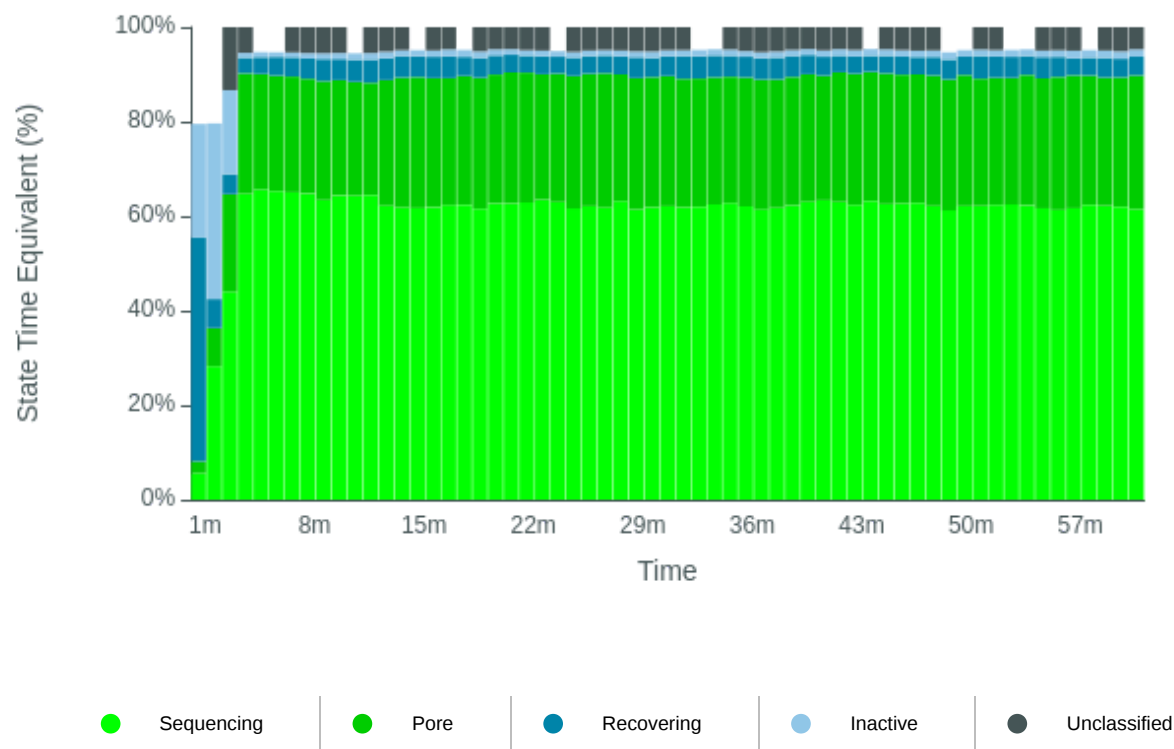
Alignment Target Hits (reads)



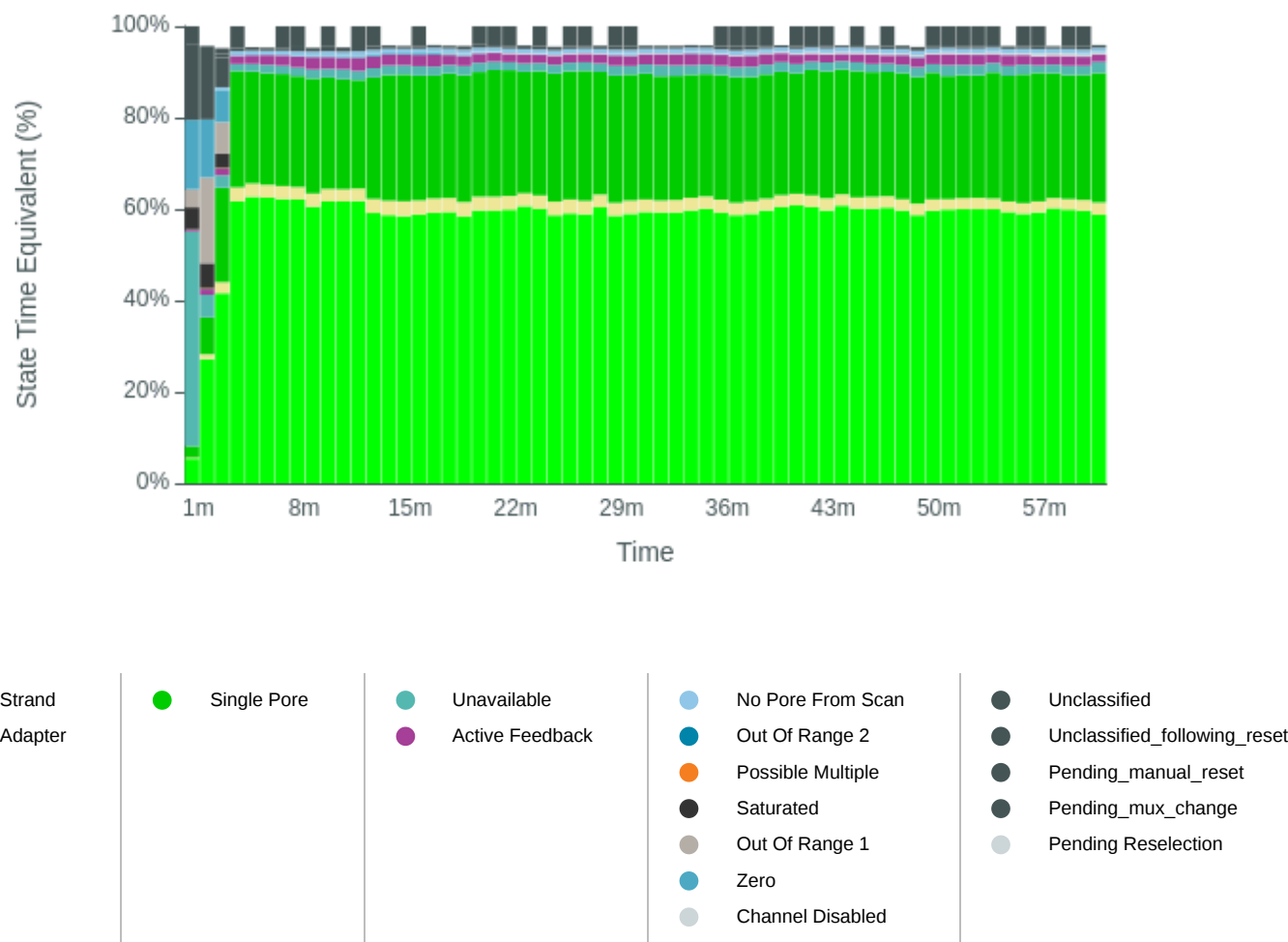
Alignment Target Hits (bases)



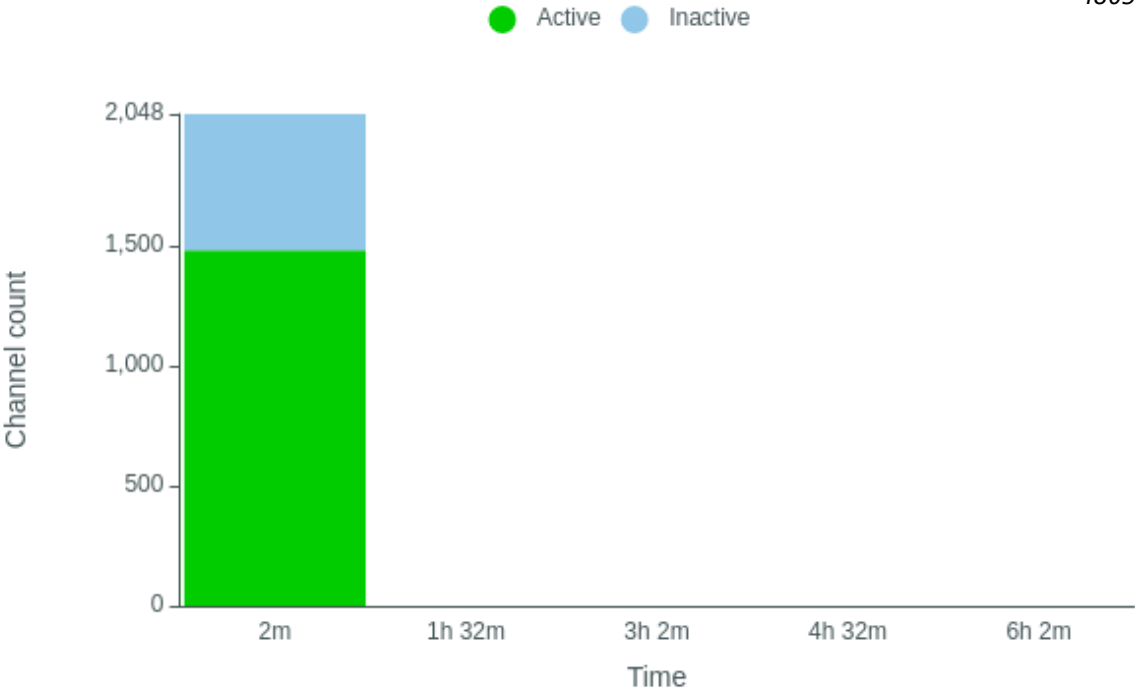
Duty Time Grouped



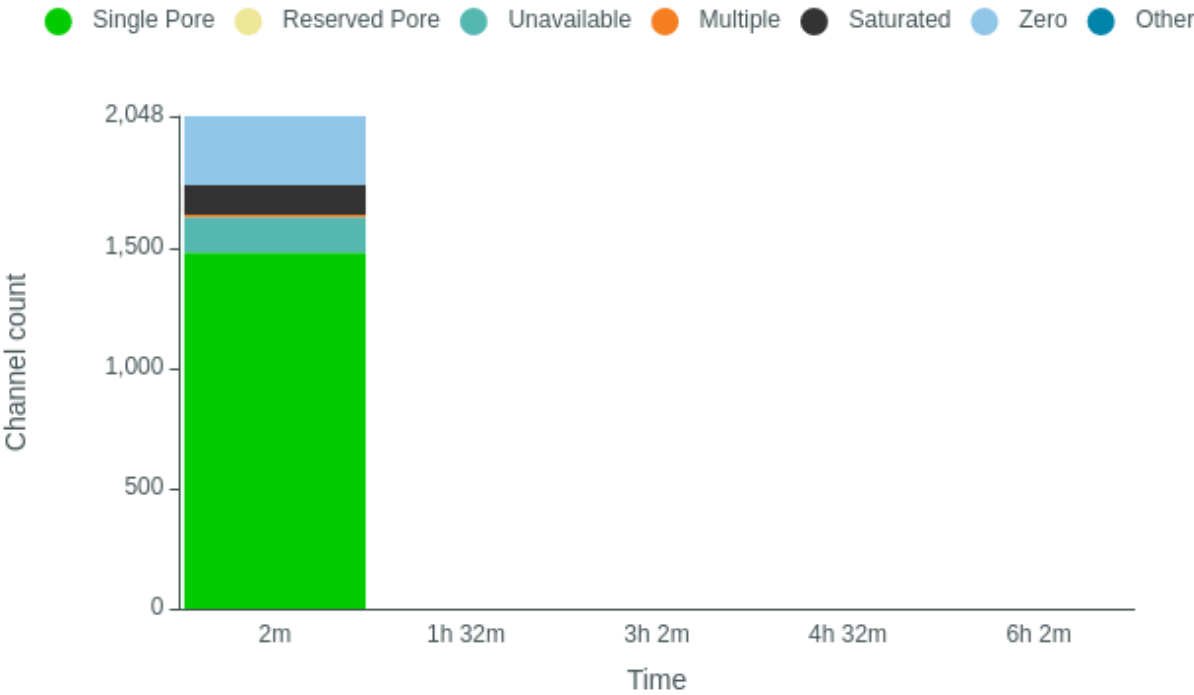
Duty time Categorised



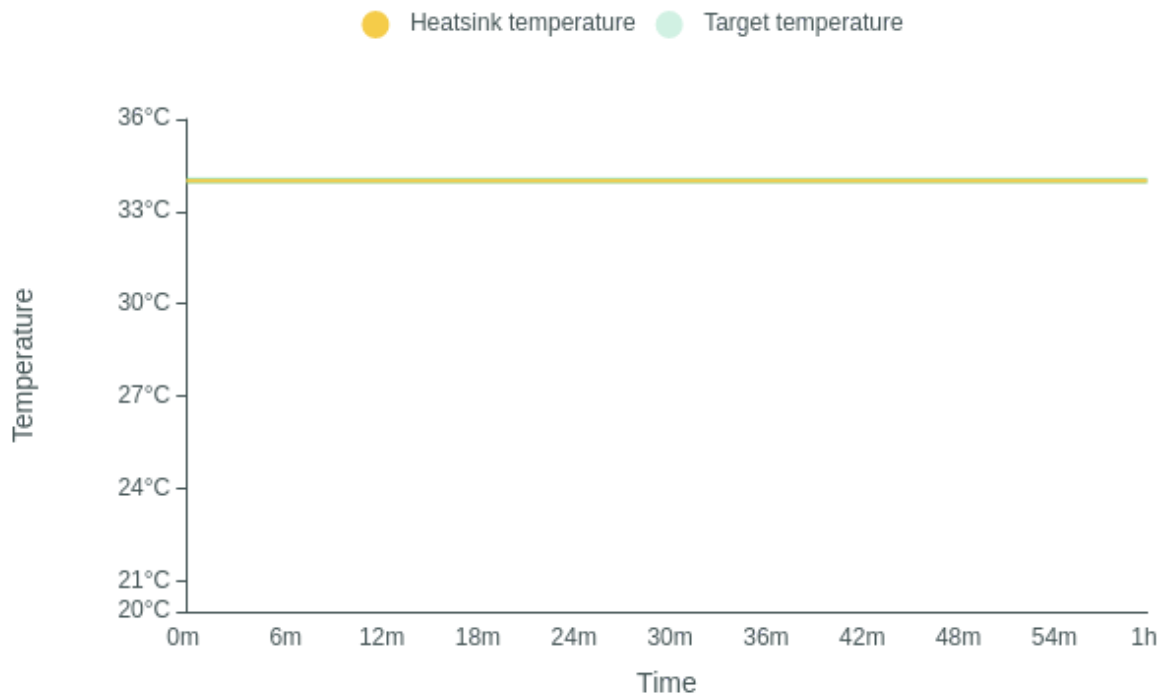
Mux Scan Grouped



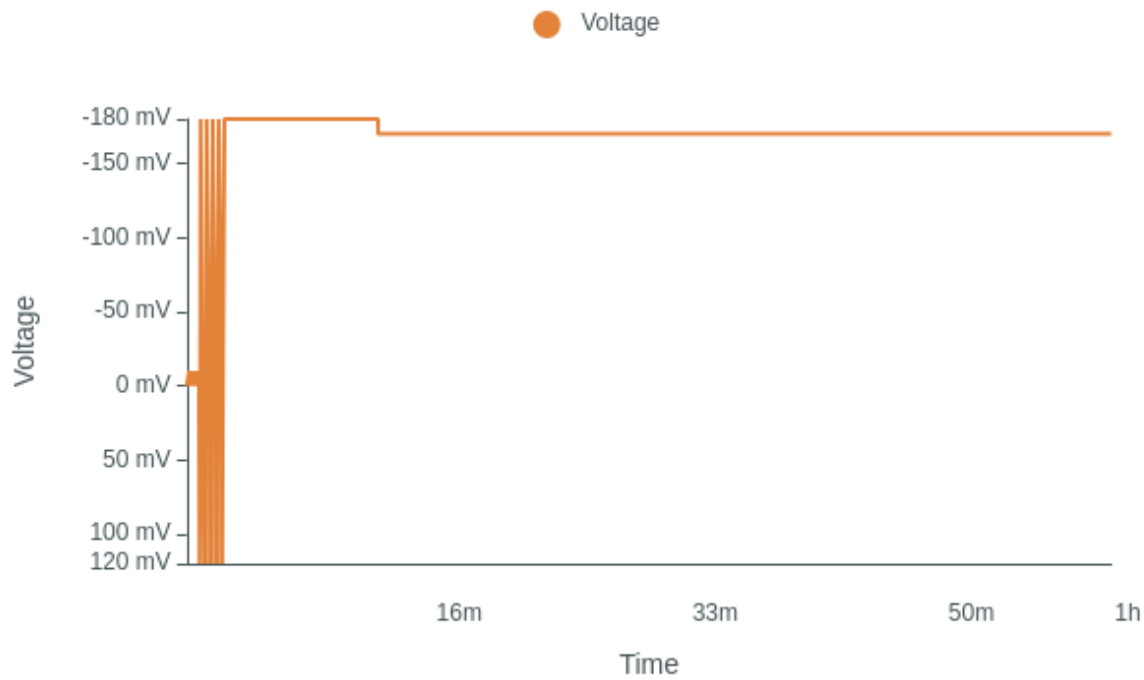
Mux Scan Categorised



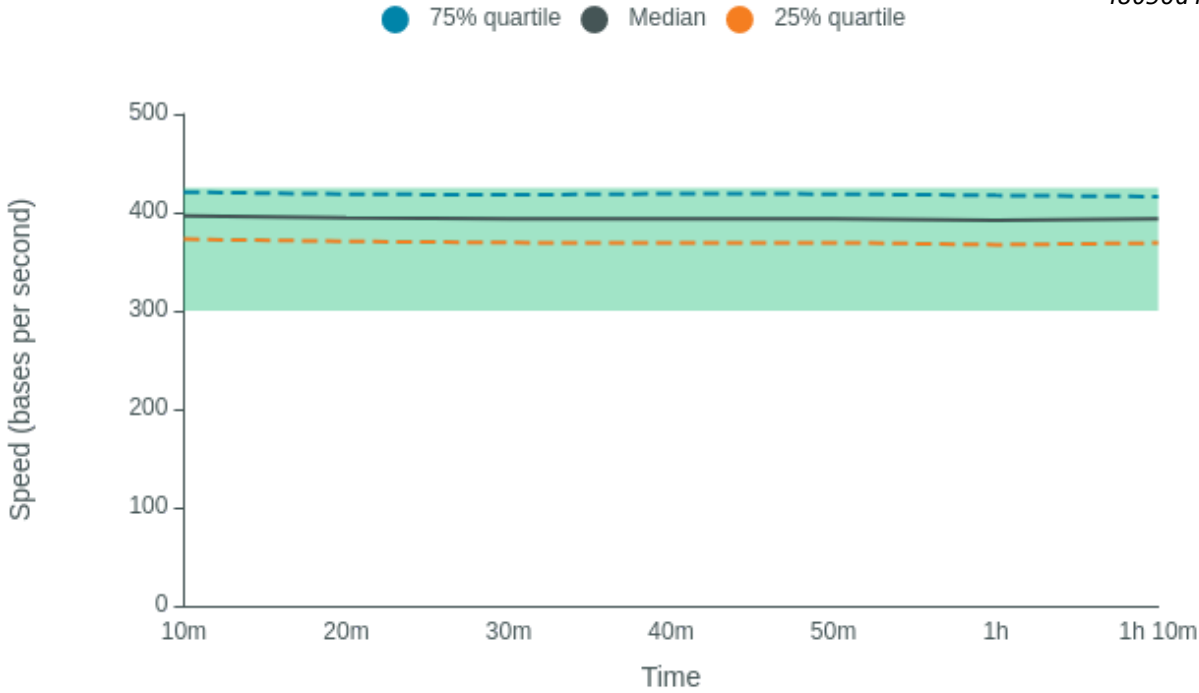
Temperature History



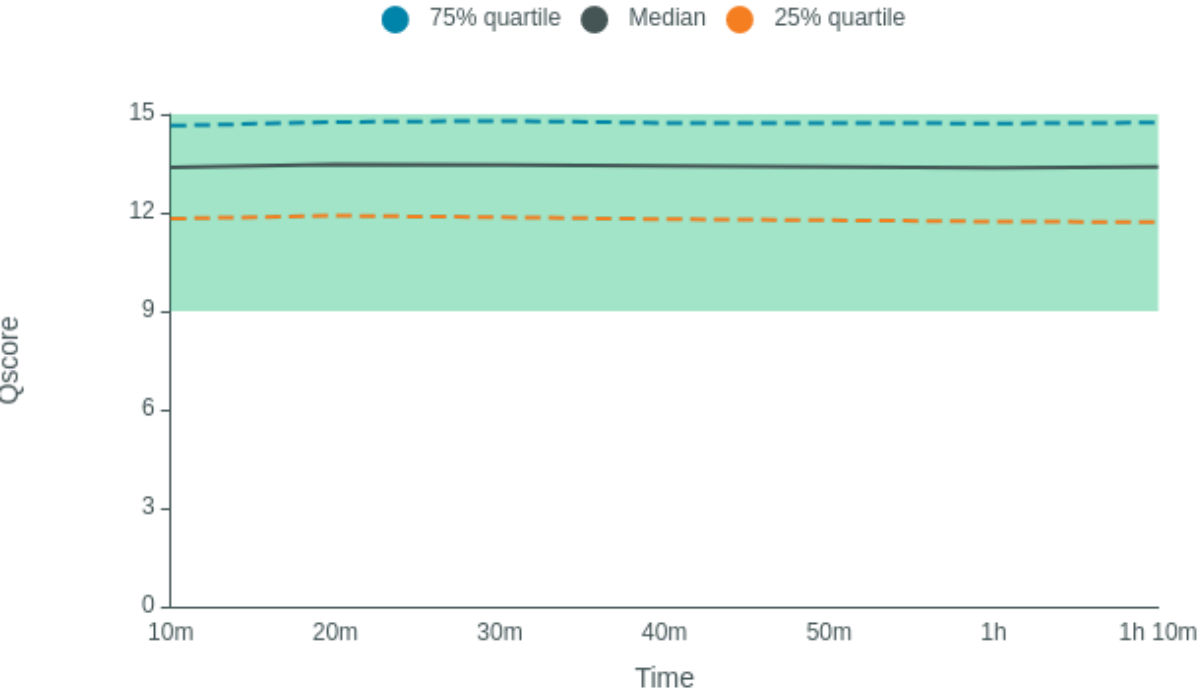
Bias Voltage History



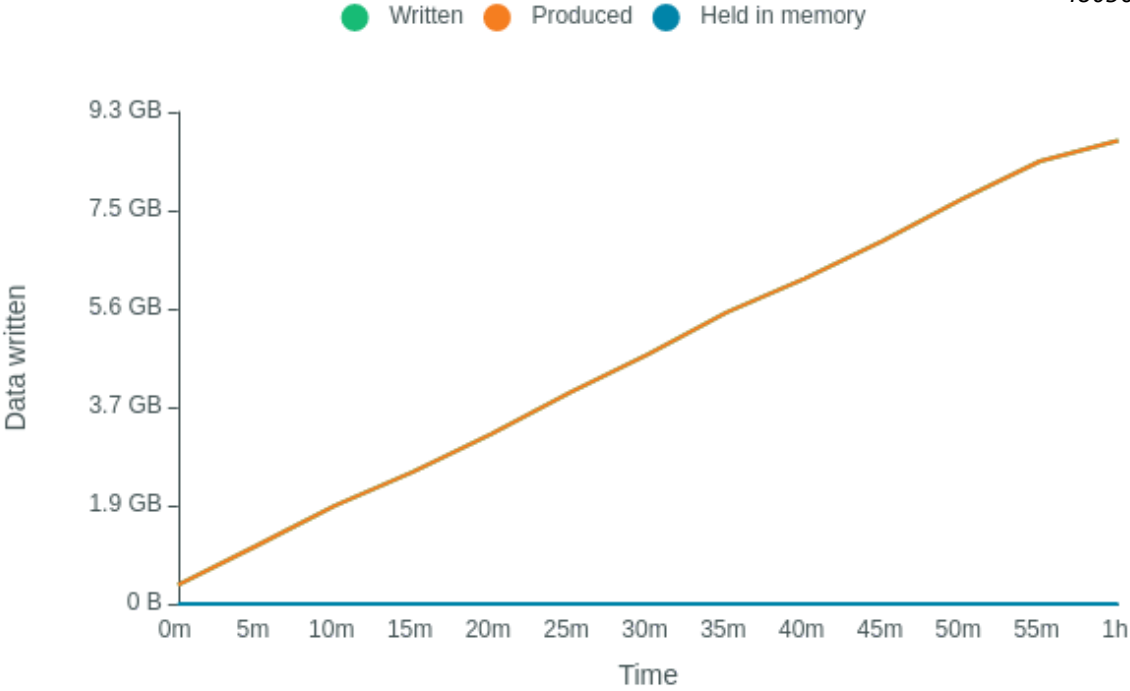
Translocation Speed



QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAQ86094 has found a total of 1480 pores. 507 pores available for immediate sequencing October 5, 14:12
- Performing Mux Scan October 5, 14:09
- Starting sequencing procedure October 5, 14:09
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C October 5, 14:06