

Run Info

Host Name GXB01190 (localhost)

Experiment Name ReadUntil_38kbp_MmDeplete_Con_15042021 ReadUntil_38kbp_MmDeplete_Con_15042021 Sample ID Run ID 5ff605ea-1717-49d7-8a45-0125ac3b65ab

Flow Cell Id FAP14879 Start Time April 15, 09:50

Run Length 1h 0m

Run Summary

41.73 K Reads Generated 424.87 Mb Passed Bases Failed Bases 24.59 Mb **Estimated Bases** 444.12 Mb

Run Parameters

Flow Cell Type FLO-MIN106 Kit SQK-LSK109 -180 mV Initial Bias Voltage FAST5 Output **Enabled FASTQ Output Enabled BAM Output Enabled** Active Channel Selection **Enabled** Basecalling on Specified Run Length 72 hours FAST5 Reads per File 4000

FAST5 Output Options zlib_compress,fastq,raw

4000 FASTQ Reads per File

Mux Scan Period 1 hour 30 minutes

Reserved Pores 0 %

Basecall Model **High-accuracy basecalling**

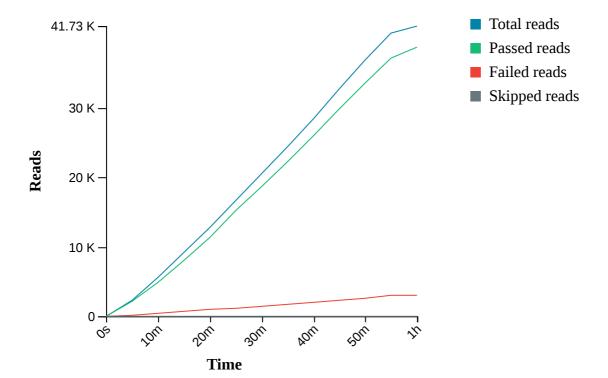
Alignment reference_files=["/data/references/the7references.fasta"]

Read Filtering min_qscore=7

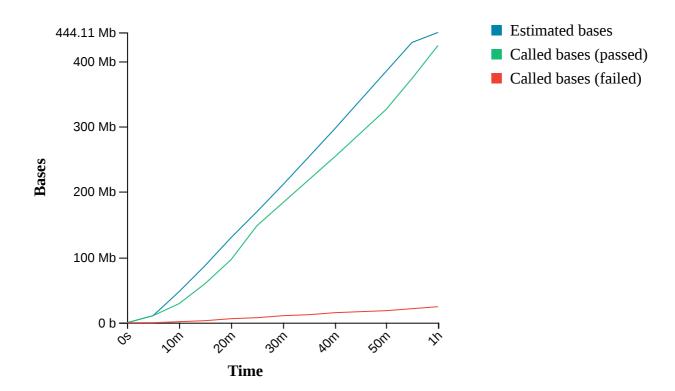
Versions

MinKNOW 21.02.5 MinKNOW Core 4.2.5 Bream 6.1.10 Guppy 4.3.4

Cumulative Output Reads

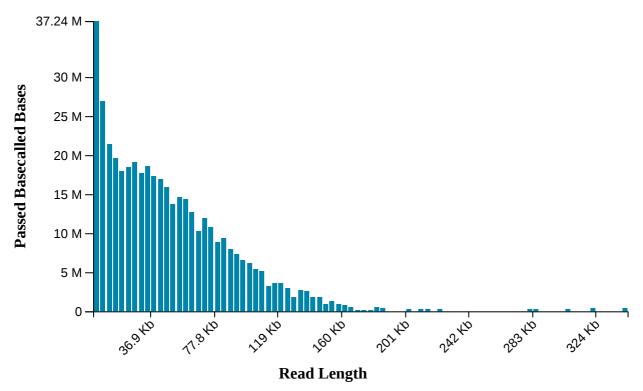


Cumulative Output Bases



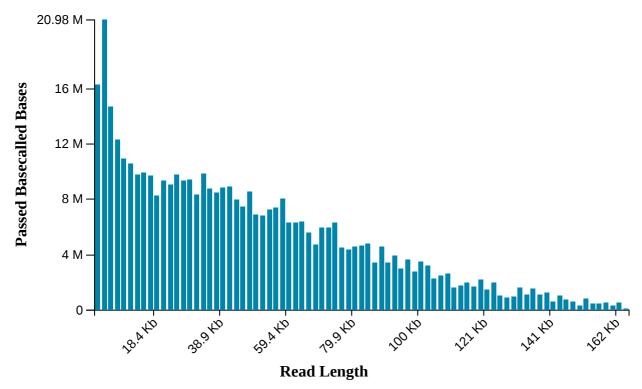
Read Length Histogram Estimated Bases - Outliers Discarded

Estimated N50: 40.56 K



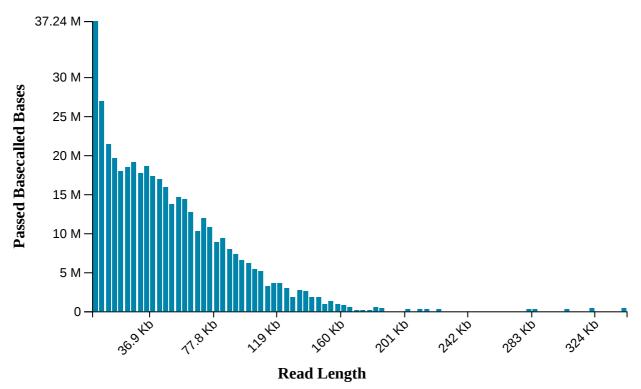
Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 40.1 K



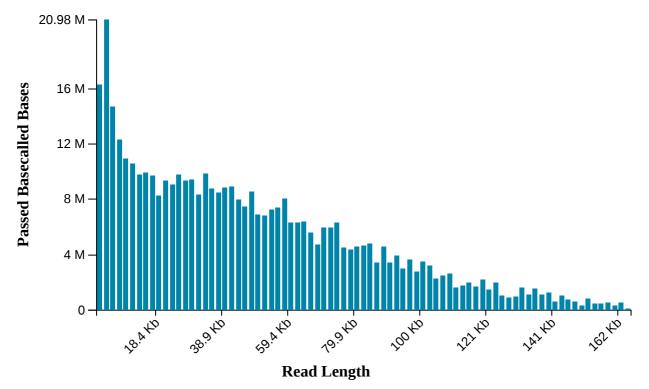
Read Length Histogram Estimated Bases

Estimated N50: 40.56 K

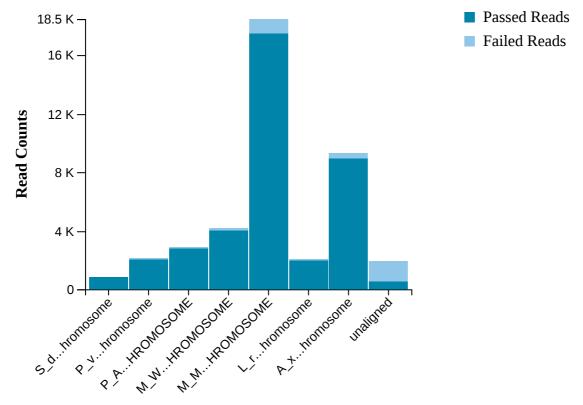


Read Length Histogram Basecalled Bases

Estimated N50: 40.1 K

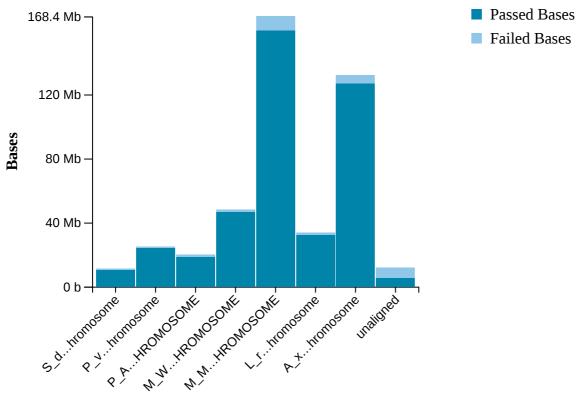


Alignment Target Hits (reads)

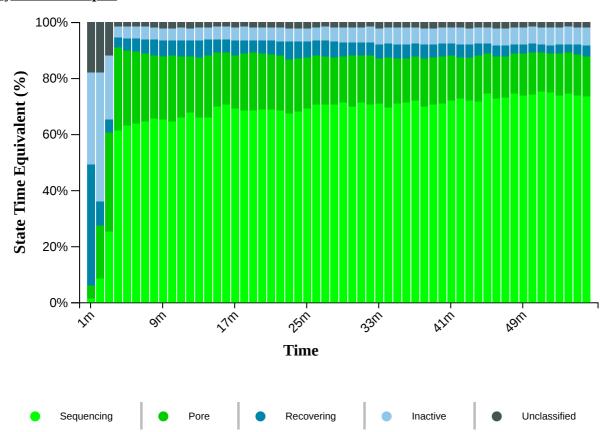


Alignment Target

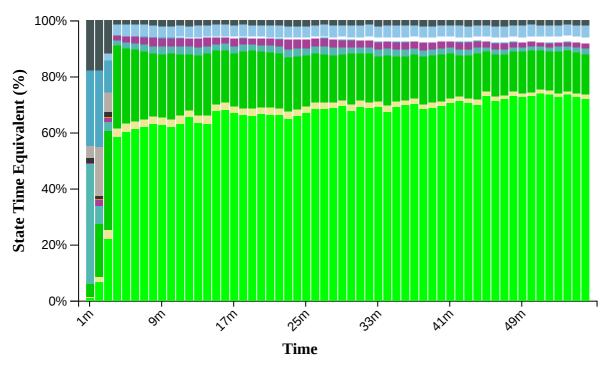
Alignment Target Hits (bases)



Alignment Target

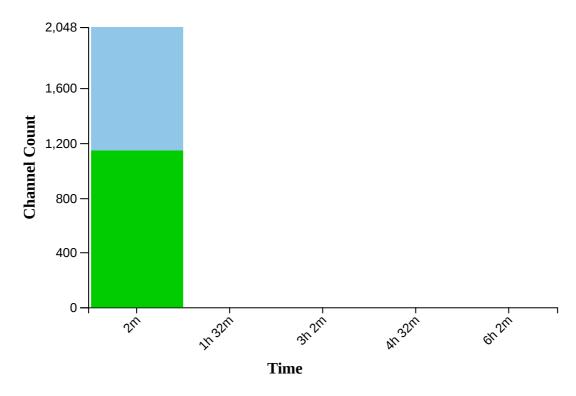


Duty time Categorised

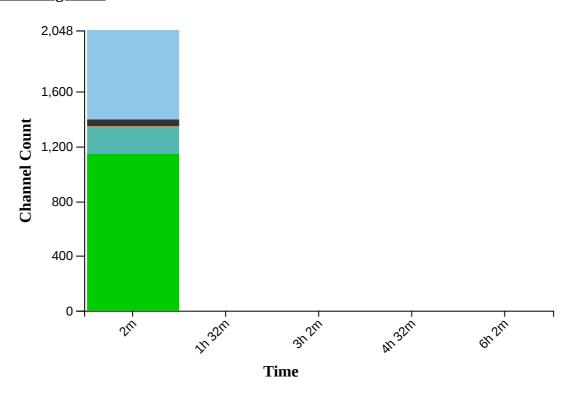




Mux Scan Grouped



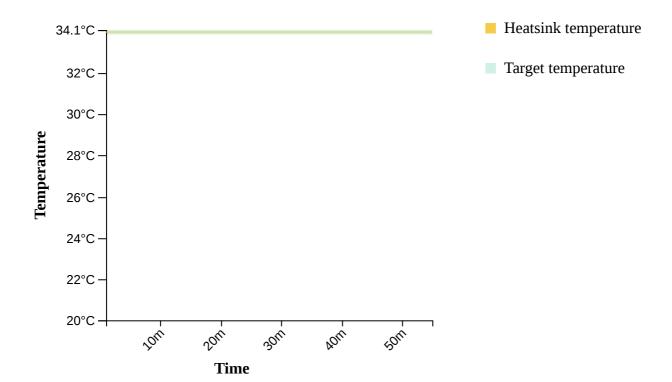
Mux Scan Categorised



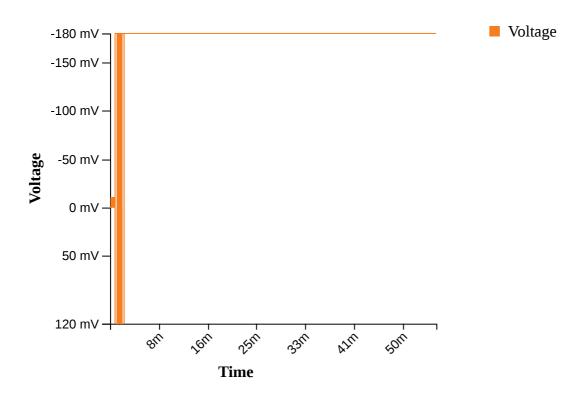
Inactive

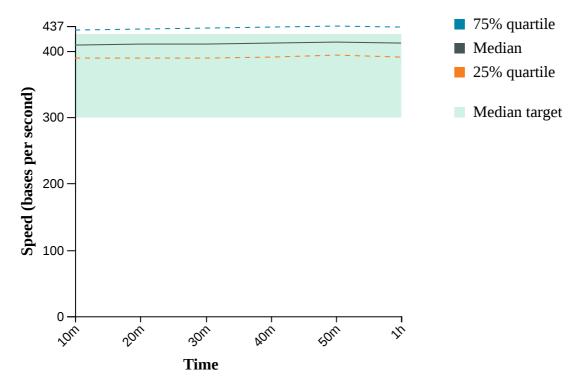
Active

Single Pore
Reserved Pore
Unavailable
Multiple
Saturated
Zero
Other

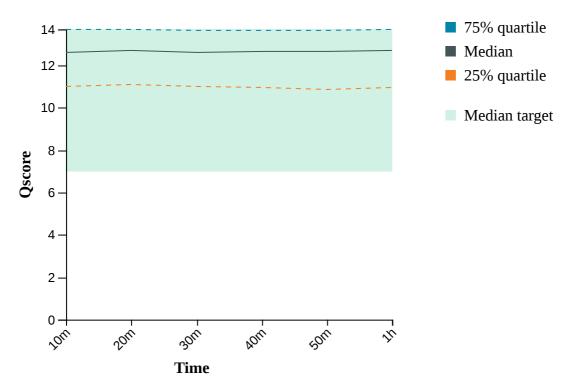


Bias Voltage History

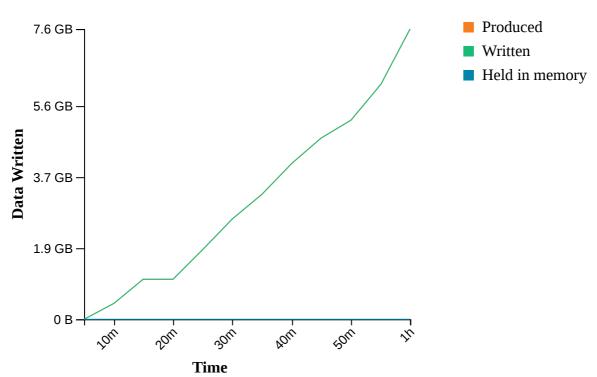




QScore



Disk Write Performance



Run Debug Messages

- Mux scan for flow cell FAP14879 has found a total of 1147 pores. 491 pores available for immediate sequencing April 15, 09:57
- Performing Mux Scan April 15, 09:54
- Starting sequencing procedure April 15, 09:54
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 15, 09:50