MinION Mk1C (MC-114017) Final report

Oct 31, 23, 10:34 AM UTC+2:00 — Nov 1, 23, 7:58 AM UTC+2:00 · 20231031flonglegyrbuffHiP · no_sample · MC-114017
Protocol run ID: af990f6f-af77-4b14-b66b-90ad1094d168

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Run summary

DATA OUTPUT

Estimated bases	Reads generated
151.53 Mb	**536.75 k**
Estimated N50	Total data produced (pass / fail)
229	**2.48 GB**

BASECALLING

Reads called	Bases called (min Q score: 9)	
100%	**116.87 Mb** Pass	**20.22 Mb** Fail

RUN DURATION

Run time

21 hrs 22 mins / 24 hrs 0 mins (est)

Elapsed time 🟦 Run limit ☐

Run status

STOPPED · *By user*

View unit abbreviations used in this report

Run configuration

RUN SETUP

Flow cell type	FLO-FLG114
Flow cell ID	APK571
Kit type	SQK-NBD114-96
Flongle adapter ID	FA-08678

RUN SETTINGS

Run limit	24 hrs
Active channel selection	On
Pore scan freq.	1.5 hrs
Reserved pores	Off
Minimum read length	20 bp
Read splitting	On
Basecalling	High-accuracy model, 400 bps
Modified basecalling	Off
Trim barcodes	Off
Mid-read barcode filtering	Off

DATA OUTPUT SETTINGS

FAST5 output	Off
FASTQ output	gzip_compress
FASTQ reads per file	1000
BAM output	Off
Bulk file output	Off
Data location	/data/./20231031flonglegyrbuffHiP/no_sample/20231031_0834_MC-114017_APK571_af990f6f

SOFTWARE VERSIONS

MinKNOW	23.07.12
Bream	7.7.6
Configuration	5.7.11
Guppy	7.1.4
MinKNOW Core	5.7.5

Sequence output

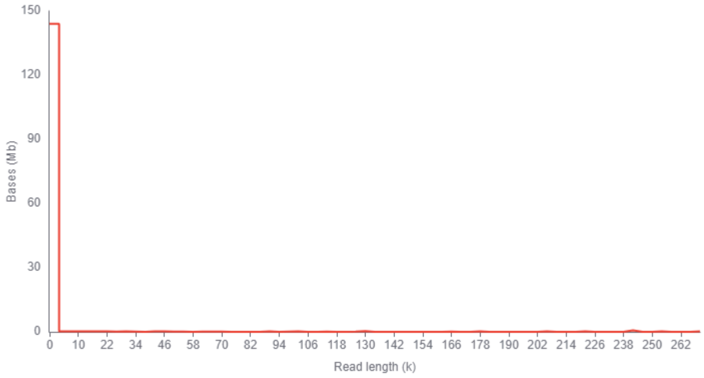
READ LENGTHS · OUTLIERS REMOVED

The read length graph shows the total number of bases vs the read length. The longest 1% of strands are classified as outliers, and excluded to allow focus on the main body of data.

Legend

🟦 Basecalled — Estimated

Estimated N50	% Basecalled
229	**100%**



OUTLIERS

The longest 1% of strands are classified as outliers, and aggregated into groups to show their relative amounts.

Read length (kb)	Aggregated reads (Mb)
1 - 3	1.05
3 - 5	0.08
5 - 7	0.02
7 - 9	0.01
9 - 9.25	0.01

BARCODES

Detected barcodes Bases graph Reads graph

Detected barcodes

The total number of bases and reads for each barcode detected are displayed in table below.
Reads/bases must have a quality score above 9 to pass.

Unclassified data

Reads	Bases
75.98 k (13.3%)	**20.55 Mb** (15%)

Search barcodes

Export CSV

Barcode	Total bases (Mb)	Passed bases (%)	Total reads (k)	Passed reads (%)
barcode01	0.0029	5	0.012	
barcode02	0.0018	24.5	0.008	
barcode03	0.0013	31.7	0.006	3
barcode04	0.0012	15.9	0.006	1
barcode05	0.0013	0	0.006	
barcode06	0.00082	58.6	0.004	
barcode07	0.0012	0	0.006	
barcode08	0.00045	0	0.002	
barcode09	0.00083	22.9	0.004	
barcode10	0.0015	14.4	0.006	1
barcode11	0.00072	63.6	0.003	6

First Prev 1 2 3 4 5 Next Last

CUMULATIVE OUTPUT

The cumulative output shows the total amount of bases or reads sequenced over time by your device.

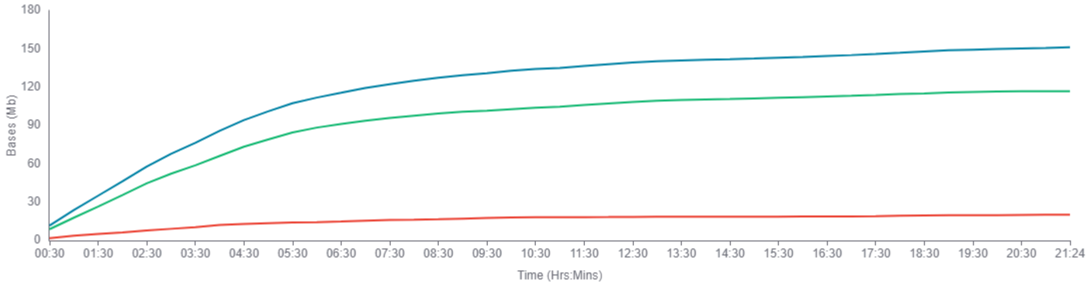
Bases

Legend

— Estimated
Predicted total number of bases, prior to basecalling

— Passed
Bases equal to or above the quality score threshold.

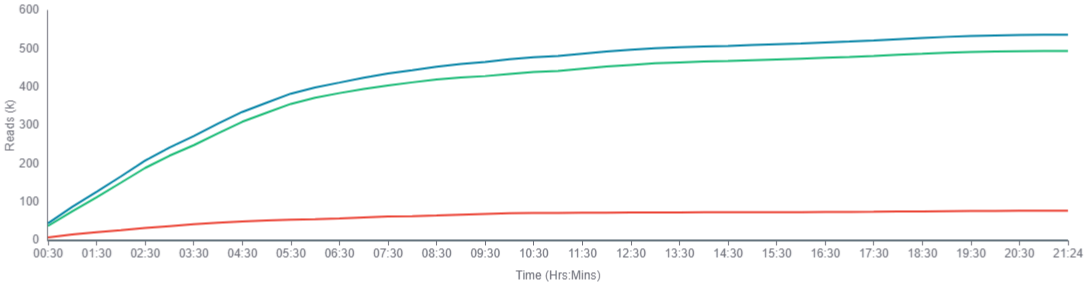
— Failed
Bases below the quality score threshold.



Reads

Legend

Total	Passed	Failed	Skipped
Total number of reads, including passed, failed and skipped.	Reads equal to or above the quality score threshold.	Reads below the quality score threshold.	Reads that will not be basecalled. Post run basecalling is possible.

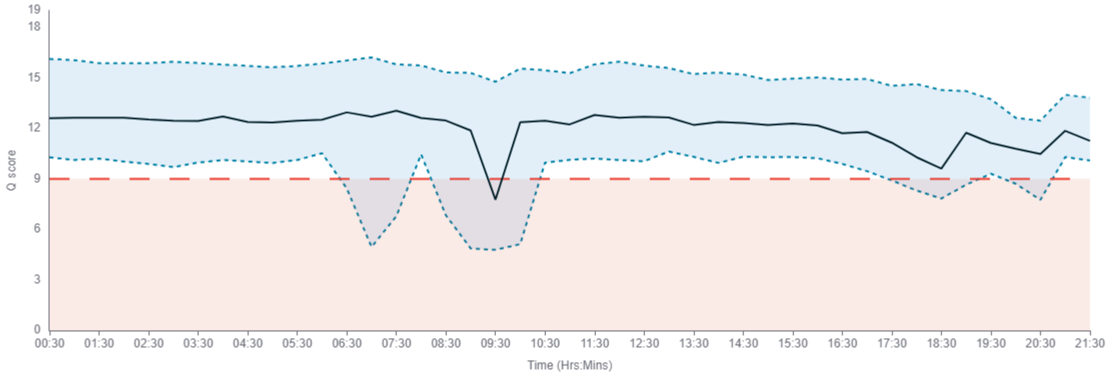


QUALITY SCORE

The quality score is calculated as basecalling is performed on your device. Reads that fall below the minimum value of 9 will be classified as failed reads. You can alter the accepted minimum quality score in MinKNOW.

Legend

— Mode The most frequent quality score of reads in the run.	⬚ Spread The spread of quality scores, found by calculating full width half maximum.	--- Min. quality score Minimum quality score to be accepted as a passed read.



Troubleshooting

Quality score low

This can be due to the translocation speed being out of the accepted range, which can correlate to low quality scores. If you see that the translocation speed is out of the accepted range in the below graph, please see the Flow Cell refuelling page linked here for further troubleshooting.

Run health

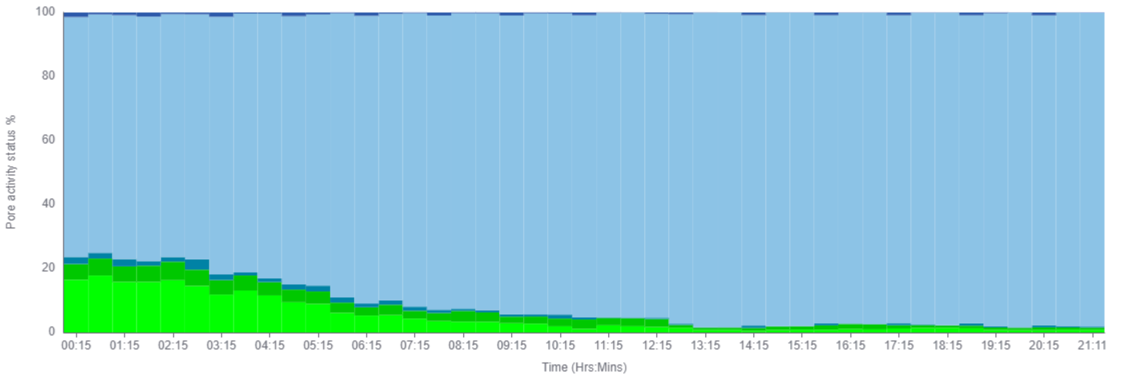
PORE ACTIVITY

The Pore activity graph shows the performance of your sample as it is being sequenced during a run.

☑ Show grouped

Legend

● Sequencing Pore currently sequencing	● Pore available Pore available for sequencing	● Unavailable Pore currently unavailable for sequencing	● Inactive Pore no longer suitable for further sequencing	● Unclassified Pore status unknown



Troubleshooting

General

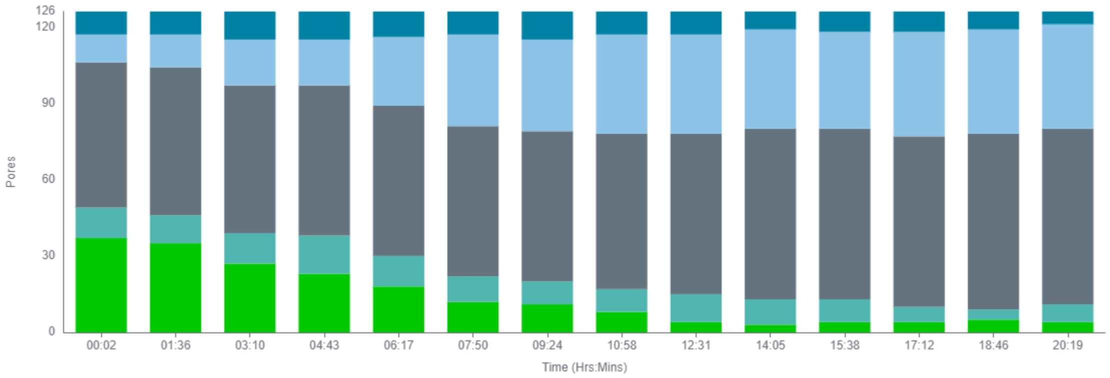
Some commonly seen issues are excess pores classified as Recovering, Open Pore, or Free Adapter. To find out what advice is applicable for your run, visit the user guide.

PORE SCAN

A Pore scan is performed at configurable time intervals to determine the current status of pores within channels on a Flow Cell. For this run a Pore scan is performed every 1.5 hrs.

Legend

● Pore available	● Reserved pore	● Unavailable	● Saturated	● Zero	● Inactive
Pore in channel available for sequencing	Pore in reserve, will return to available when required	Pore inhibited from sequencing	Possible contamination in the sample	No current is passing through this pore, possibly due to bubbles on the membrane	Pore no longer suitable for further sequencing



Troubleshooting

High proportion Unavailable
Possible contaminants in library blocking the pore. Consider using the Flow Cell Wash Kit, and reloading a library.

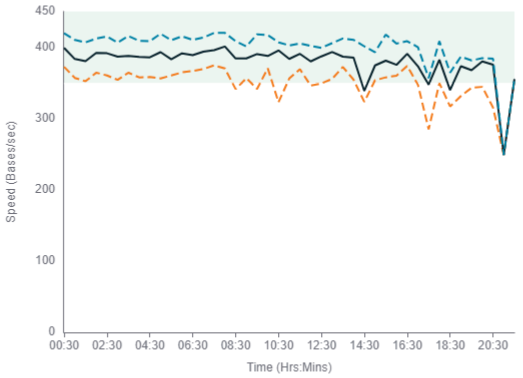
High proportion Inactive
If localised to one area of the Flow Cell, this could indicate that an air bubble has been introduced during the flushing/loading steps. If inactivity is spread across the Flow Cell this could be caused by improper loading of the library, please refer to the user guide for further support.

TRANSLOCATION SPEED

The translocation speed is the rate at which DNA/RNA travels through pores as it is being sequenced.

Legend

— Median --- 75% quartile --- 25% quartile ☐ Accepted range



Troubleshooting

Low speed
Check that the Flow Cell is within the target temperature range.

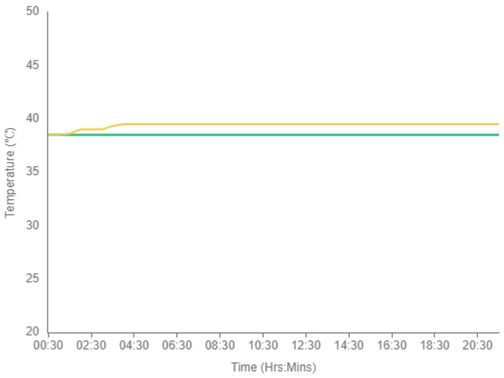
Note
Low-quality and short reads are not included in this graph.

TEMPERATURE

The temperature of the Flow Cell over the run time.

Legend

— Measured — Target



Troubleshooting

Out of range
Check that the Flow Cell is correctly seated and firmly pushed down into the device. Ensure ambient temperature is always within the specified range for your device in the user guide.

Air flow should be good but not excessive. Excessive amounts of cool air blowing on the device could prevent it from reaching target temperature.

Run log

SYSTEM MESSAGES

System messages are a record of the events that occurred in the time covered by this report.

Errors

None

Warnings

None

Events

Disk space · 31 Oct 23, 08:34
Disk /data has 254 GB space remaining

Waiting for temperature · 31 Oct 23, 08:34
Waiting up to 300 seconds for temperature to stabilise at 38.5°C

Starting · 31 Oct 23, 08:35
Starting sequencing procedure

Message · 31 Oct 23, 08:35
Performing Channel Scan

Message · 31 Oct 23, 08:38
Channel scan for flow cell APK571 has found a total of 37 pores. 37 pores available for immediate sequencing

Message · 31 Oct 23, 09:58
Setting temperature to reach 39.1°C

Message · 31 Oct 23, 10:09
Performing Channel Scan

Message · 31 Oct 23, 10:11
Channel scan for flow cell APK571 has found a total of 35 pores. 35 pores available for immediate sequencing

Message · 31 Oct 23, 11:42
Performing Channel Scan

Message · 31 Oct 23, 11:45
Channel scan for flow cell APK571 has found a total of 27 pores. 27 pores available for immediate sequencing

Message · 31 Oct 23, 11:46
Setting temperature to reach 39.5°C

Message · 31 Oct 23, 13:16
Performing Channel Scan

Message · 31 Oct 23, 13:19
Channel scan for flow cell APK571 has found a total of 23 pores. 23 pores available for immediate sequencing

Message · 31 Oct 23, 14:50
Performing Channel Scan

Message · 31 Oct 23, 14:52
Channel scan for flow cell APK571 has found a total of 18 pores. 18 pores available for immediate sequencing

Message · 31 Oct 23, 16:23
Performing Channel Scan

Message · 31 Oct 23, 16:26
Channel scan for flow cell APK571 has found a total of 12 pores. 12 pores available for immediate sequencing

Message · 31 Oct 23, 17:57
Performing Channel Scan

Message · 31 Oct 23, 18:00
Channel scan for flow cell APK571 has found a total of 11 pores. 11 pores available for immediate sequencing

Message · 31 Oct 23, 19:30
Performing Channel Scan

Message · 31 Oct 23, 19:33
Channel scan for flow cell APK571 has found a total of 8 pores. 8 pores available for immediate sequencing

Message · 31 Oct 23, 21:04
Performing Channel Scan

Message · 31 Oct 23, 21:07
Channel scan for flow cell APK571 has found a total of 4 pores. 4 pores available for immediate sequencing

Message · 31 Oct 23, 22:38
Performing Channel Scan

Message · 31 Oct 23, 22:40
Channel scan for flow cell APK571 has found a total of 3 pores. 3 pores available for immediate sequencing

Message · 01 Nov 23, 00:11
Performing Channel Scan

Message · 01 Nov 23, 00:14
Channel scan for flow cell APK571 has found a total of 4 pores. 4 pores available for immediate sequencing

Message · 01 Nov 23, 01:45
Performing Channel Scan

Message · 01 Nov 23, 01:48
Channel scan for flow cell APK571 has found a total of 4 pores. 4 pores available for immediate sequencing

Message · 01 Nov 23, 03:18
Performing Channel Scan

Message · 01 Nov 23, 03:21
Channel scan for flow cell APK571 has found a total of 5 pores. 5 pores available for immediate sequencing

Message · 01 Nov 23, 04:52
Performing Channel Scan

Message · 01 Nov 23, 04:55
Channel scan for flow cell APK571 has found a total of 4 pores. 4 pores available for immediate sequencing

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UNIT ABBREVIATIONS

Byte	B
Kilobyte	KB
Megabyte	MB
Gigabyte	GB
Terabyte	TB

Base	b
Kilobase	kb
Megabase	Mb
Gigabase	Gb
Terabase	Tb

Minutes	mins
Hours	hrs

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