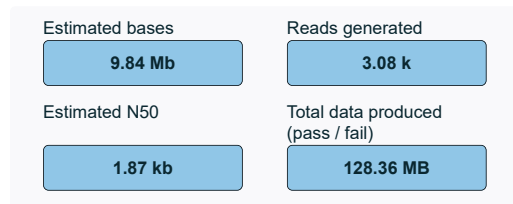## MinION Mk1B (MN27167) Final report

Apr 15, 24, 3:22 PM UTC-7:00 — Apr 15, 24, 6:31 PM UTC-7:00 ·
KLH_PRACTICE_RUN1 · no_sample · MN27167
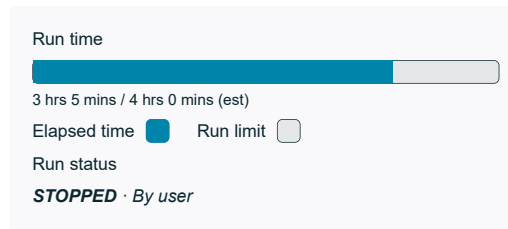Protocol run ID: e79adb5a-7827-4b2b-8d8d-547308dfc836

Run summary | Run configuration | Sequence output | Run health | Run log
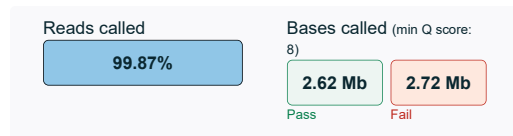
Run summary

DATA OUTPUT

Estimated bases	Reads generated
9.84 Mb	**3.08 k**

Estimated N50	Total data produced (pass / fail)
1.87 kb	**128.36 MB**

BASECALLING

Reads called	Bases called (min Q score: 8)	
99.87%	**2.62 Mb**	**2.72 Mb**
	Pass	Fail

RUN DURATION

Run time

3 hrs 5 mins / 4 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-MIN114
Flow cell type alias	FLO-MIN114
Flow cell ID	FAX68352
Kit type	SQK-LSK114-XL
Expansion kit	EXP-PBC096

RUN SETTINGS

Run limit	4 hrs
Active channel selection	On
Pore scan freq.	1.5 hrs
Reserved pores	On
Minimum read length	200 bp
Read splitting	On
Basecalling	Fast model, 400 bps
Modified basecalling	Off
Trim barcodes	Off
Mid-read barcode filtering	Off

DATA OUTPUT SETTINGS

FAST5 output	vbz_compress
FAST5 reads per file	4000
FASTQ output	gzip_compress
FASTQ reads per file	4000
BAM output	Off
Bulk file output	Off
Data location	E:\MinKnow_Data\. \KLH_PRACTICE_RUN 1/no_sample/ 20240415_1522_MN27 167_FAX68352_e79ad b5a

SOFTWARE VERSIONS

MinKNOW	23.07.8
Bream	7.7.6
Configuration	5.7.8
Guppy	7.0.8
MinKNOW Core	5.7.2

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.
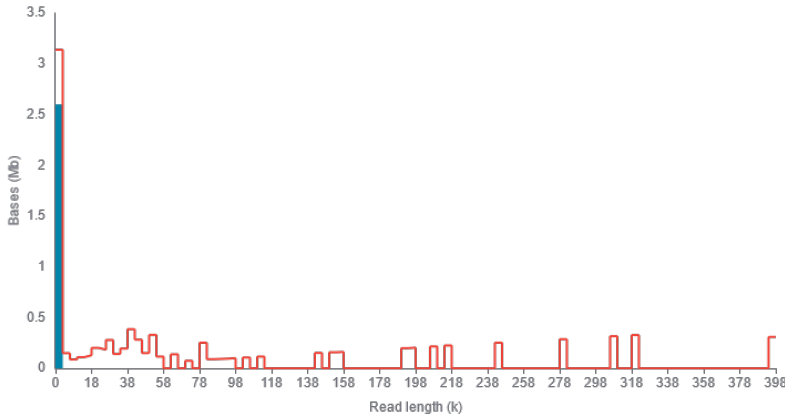
Legend

■ Basecalled   — Estimated

Estimated N50	% Basecalled
1.87 kb	**99.87%**

OUTLIERS

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

Read length (kb)	Aggregated reads (kb)
4.875 - 5.875	9.61
5.875 - 6.875	6.86
6.875 - 7.875	*None*
7.875 - 8.875	*None*
8.875 - 9.5	9.71

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

3.07 k (99.8%)	**5.33 Mb** (99.9%)
Reads	Bases

🔍 Search barcodes   Export CSV ⬆

Barcode	Total bases (Mb)	Passed bases (%)	Total reads (k)	Passed reads
barcode01	0	0	0	0
barcode02	0	0	0	0
barcode03	0	0	0	0
barcode04	0	0	0	0
barcode05	0	0	0	0
barcode06	0	0	0	0
barcode07	0	0	0	0
barcode08	0	0	0	0
barcode09	0	0	0	0
barcode10	0	0	0	0
barcode11	0	0	0	0
barcode12	0	0	0	0

First   Prev   **1**   2   3   4   5   Next   Last
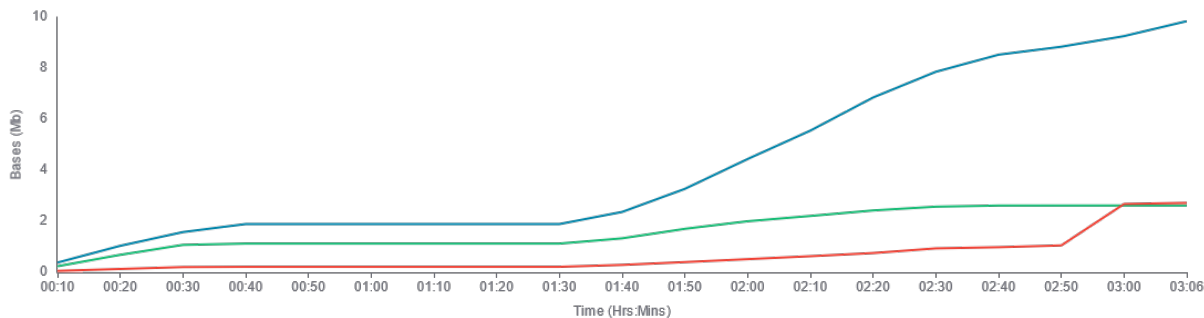
CUMULATIVE OUTPUT

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

### Bases

Legend

— Estimated   — Passed   — Failed

Predicted total number of bases, prior to basecalling

Bases equal to or above the quality score threshold.

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.
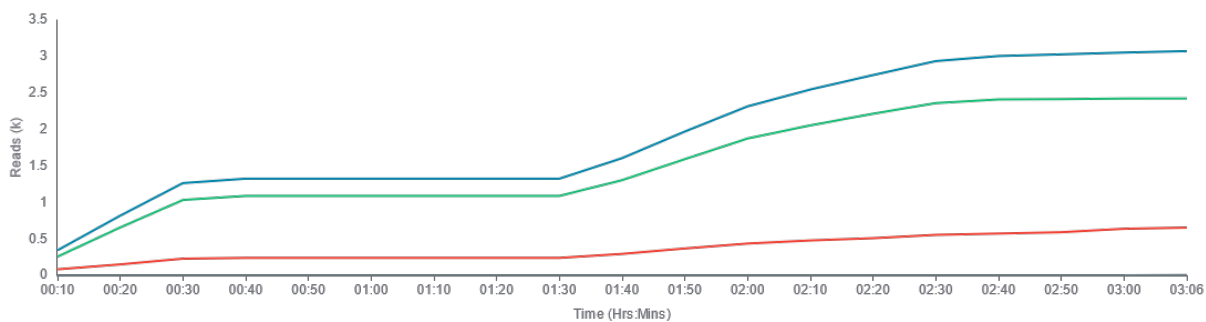
QUALITY SCORE

The quality score is calculated as basecalling is performed on your device. Reads that fall below the minimum value of 8 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.
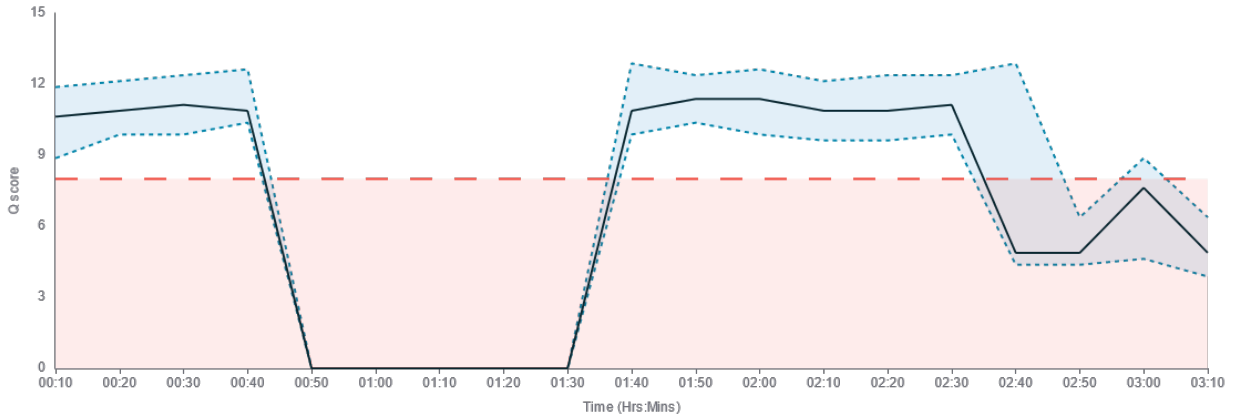
Troubleshooting

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
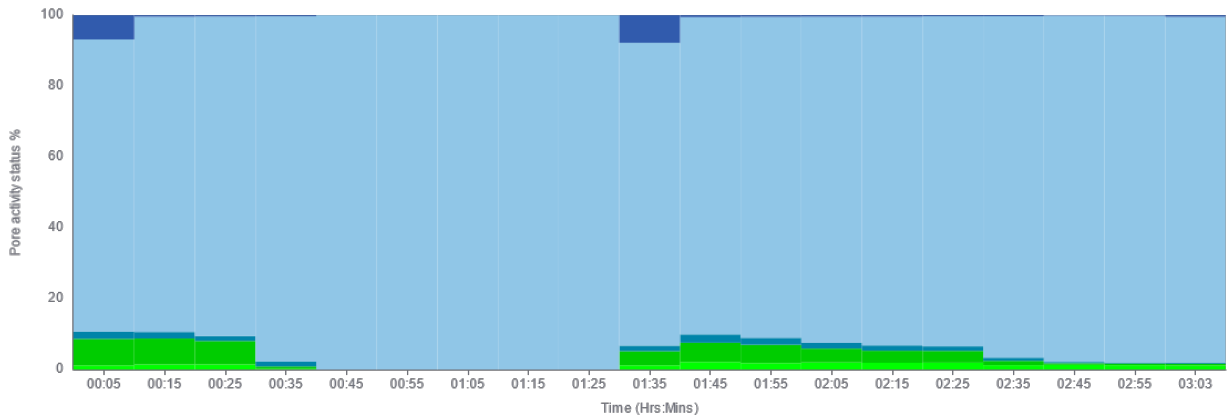
Troubleshooting

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**
Pore in channel available for sequencing

🟡 **Reserved pore**
Pore in reserve, will return to available when required

🟢 **Unavailable**
Pore inhibited from sequencing

⚫ **Saturated**
Possible contamination in the sample

🔵 **Zero**
No current is passing through this pore, possibly due to bubbles on the membrane

🔵 **Inactive**
Pore no longer suitable for further sequencing
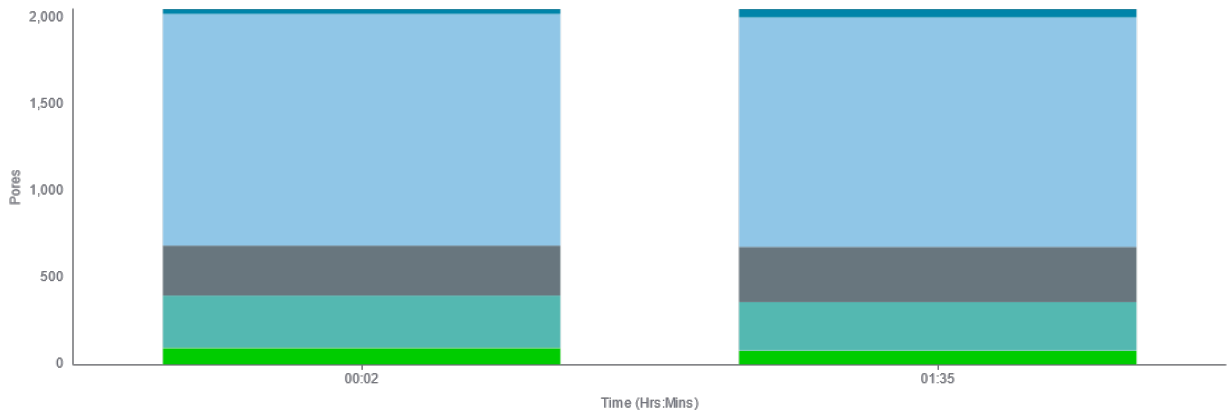
Troubleshooting

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
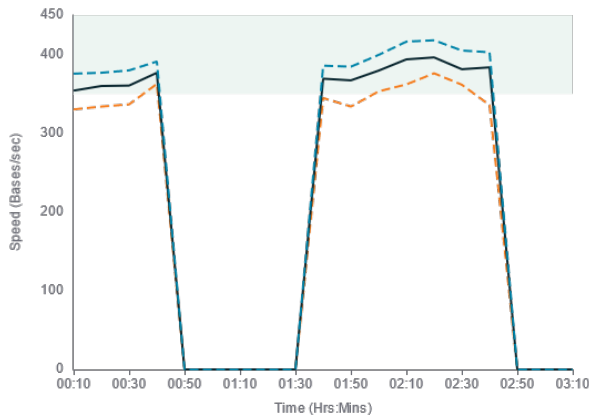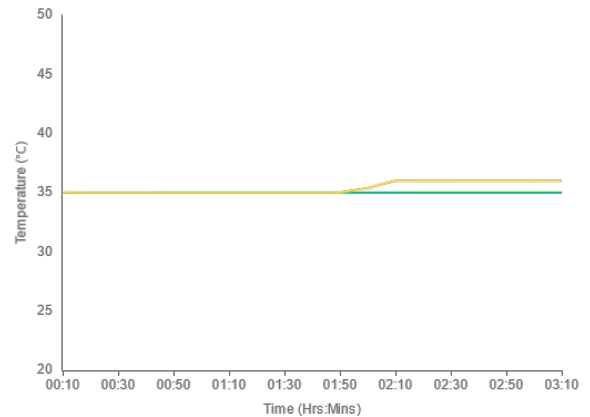

Troubleshooting

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

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.

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

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

ℹ️ Events

Disk space · 15 Apr 24, 22:22
Disk E:\ has 3710 GB space remaining

Waiting for temperature · 15 Apr 24, 22:22
Waiting up to 300 seconds for temperature to stabilise at 35.0°C

Starting · 15 Apr 24, 22:26
Starting sequencing procedure

Pore scan starting · 15 Apr 24, 22:26
Performing Pore Scan

Pore scan result · 15 Apr 24, 22:29
Pore scan for flow cell FAX68352 has found a total of 94 pores. 73 pores available for immediate sequencing

Pore scan starting · 15 Apr 24, 23:59
Performing Pore Scan

Pore scan result · 16 Apr 24, 00:01
Pore scan for flow cell FAX68352 has found a total of 79 pores. 66 pores available for immediate sequencing

Message · 16 Apr 24, 00:21
Setting temperature to reach 36.0°C

Pore scan starting · 16 Apr 24, 01:31
Performing Pore Scan

UNIT ABBREVIATIONS

Byte	B		Base	b		Minutes	mins
Kilobyte	KB		Kilobase	kb		Hours	hrs
Megabyte	MB		Megabase	Mb			
Gigabyte	GB		Gigabase	Gb			
Terabyte	TB		Terabase	Tb			