MinION Mk1B (MN19362) Final report

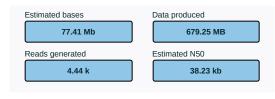


16 Jun 23, 17:24 — 16 Jun 23, 17:49 · RU_test · no_sample · MN19362 Protocol run ID: cf0b707b-477e-454b-82c2-f532dae16fc5

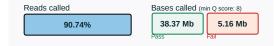
Run summary | Run configuration | Sequence output | Run health | Run log

Run summary

DATA OUTPUT



BASECALLING



RUN DURATION



View unit abbreviations used in this report

Run configuration

RUN SETUP

Flow cell type FLO-MIN106

Flow cell ID sim

Kit type SQK-LSK109

RUN SETTINGS

Run limit 72h
Active channel selection On
Pore scan freq. 1.5 hrs
Reserved pores On
Minimum read length 200 bp
Read splitting Off

Basecalling Fast model, 450 bps

Modified basecalling 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 /var/lib/minknow/data/./RU_

test/no_sample/20230616_ 1324_MN19362_sim_cf0b7

07b

SOFTWARE VERSIONS

 MinKNOW
 23.04.5

 Bream
 7.5.9

 Configuration
 5.5.13

 Guppy
 6.5.7

 MinKNOW Core
 5.5.3

% Basecalled

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.

Estimated N50

Legend 38.23 kb 90.74% Basecalled — Estimated

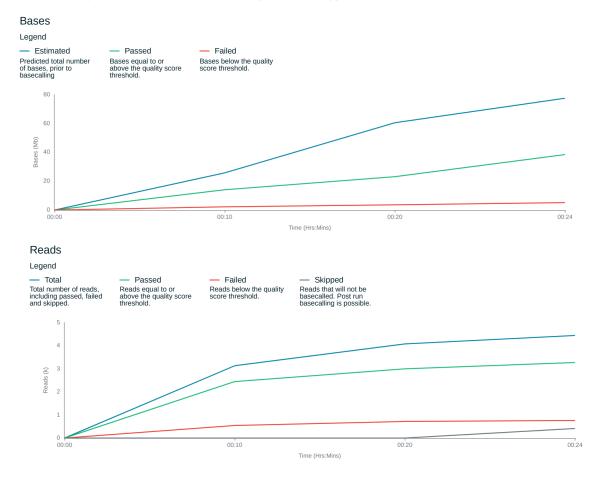
OUTLIERS

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

Read Aggregated reads (kb) length (kb) 392 - 396 383.7

CUMULATIVE OUTPUT

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



QUALITY SCORE

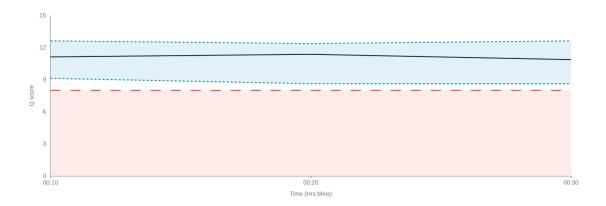
The quality score is calculated as basecalling is performed on your device. Reads that fall below the minimum value of 8 will be classified as failed reads. You can alter the accepted minimum quality score in MinKNOW.

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

Run health

PORE ACTIVITY

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

Legend

Sequencing Pore currently sequencing

Current is positive but unavailable for

sequencing Unclassified Pore status unknown

Adapter Pore currently sequencing adapter Out of range-high

Out of range-low Multiple Current is negative but unavailable for sequencing Multiple pores detected. Unavailable for sequencing.

Pore available Pore available for sequencing

Saturated The channel has switched off as current levels exceed hardware limitations

Unavailable

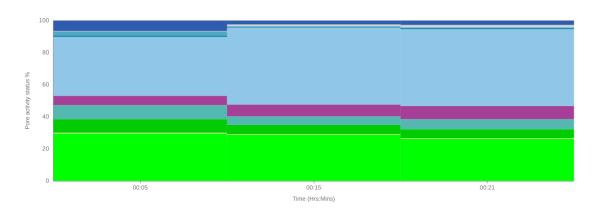
Pore unavailable for sequencing

 Active feedback Channel ejecting analyte

Zero Pore currently unavailable for sequencing

No pore No pore detected in channel

Channel disabled Channel is disabled and awaiting another pore



Troubleshooting

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

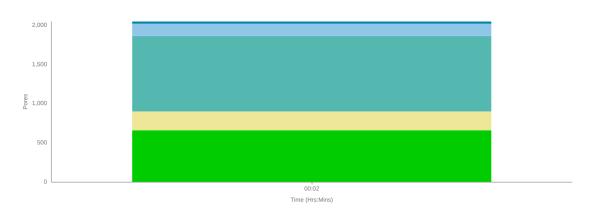
 Reserved pore Pore in reserve, will return to available when required

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.

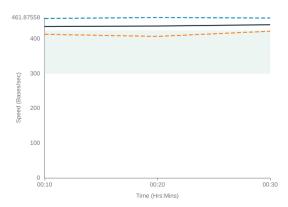
High proportion Inactive
If localised to one area of the Flow Cell, this could indicate that an air bubble has been introduced during the flushing/loading steps. If inactivity is spread across the Flow Cell this could be caused by improper loading of the library, please refer to the user guide for further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

TRANSLOCATION SPEED

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

Legend



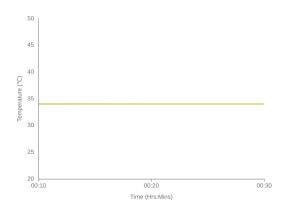


TEMPERATURE

The temperature of the Flow Cell over the run time.

Legend





Troubleshooting

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

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

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 <u>user guide.</u>

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.

Please view the original run report, which would have been generated at the end of the run, to see the system messages.

UNIT ABBREVIATIONS

Byte	В	
Kilobyte	KB	
Megabyte	MB	
Gigabyte	GB	
Terabyte	TB	

Base	b
Kilobase	kb
Megabase	Mb
Gigabase	Gb
Terabase	Tb

Minutes mins Hours hrs

Generated using Run Report Template v.5.5.6