



# **7- Oxford Nanopore Technologies Additional Details & Troubleshooting**

**DARRELL L. DINWIDDIE, PHD**

**DARYL B. DOMMAN, PHD**

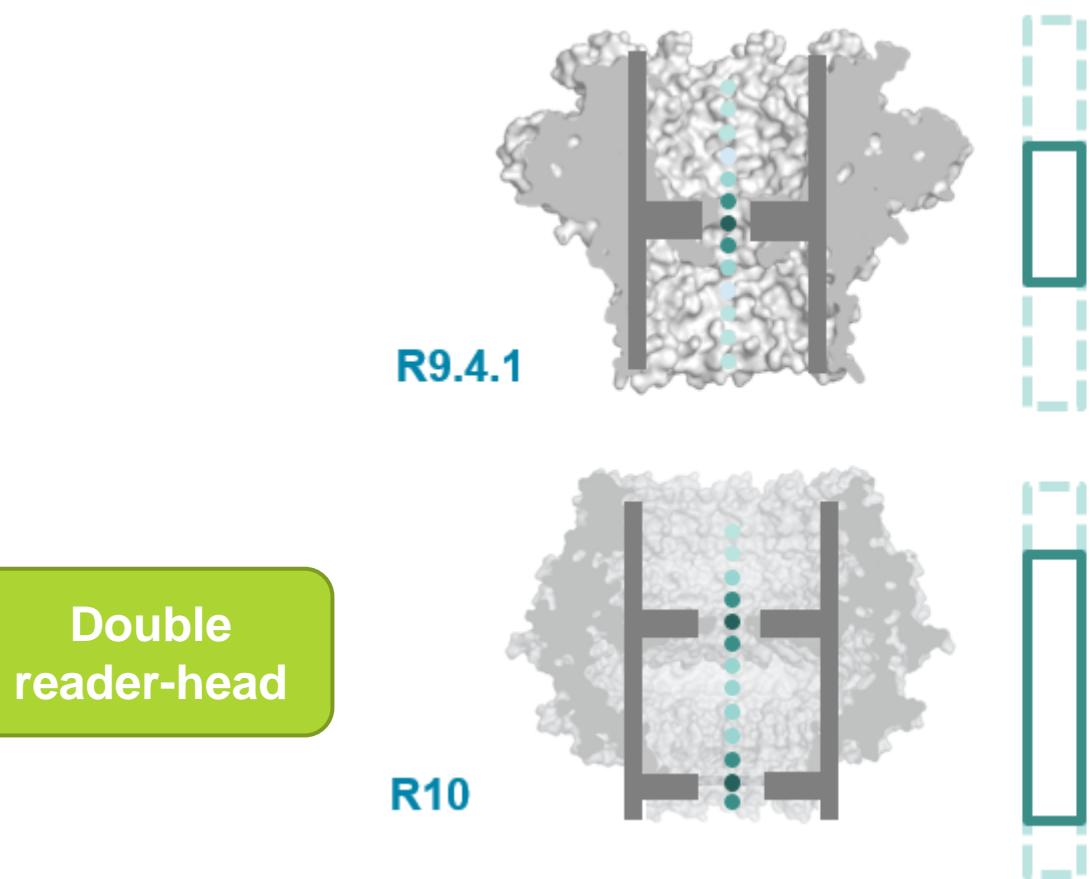
# ONT Flowcell Update



# R9.4 vs R10.4 Flowcells

- ▶ R10 is our nanopore chemistry designed to deliver highest consensus accuracy. Paired with the Kit 12 (also referred to as Q20+) chemistry, R10.4 generates data at a modal accuracy above 99%.
- ▶ It contains the proprietary sensor array, Application-Specific Integrated Circuit (ASIC), and R10 nanopores. The R10 series of nanopores contains a double reader-head, and is suitable for experiments where high consensus accuracy is required.
- ▶ **Note: R10.4 flow cells currently require Kit 12 chemistry.**
- ▶ **Currently only available as an Early Access product**

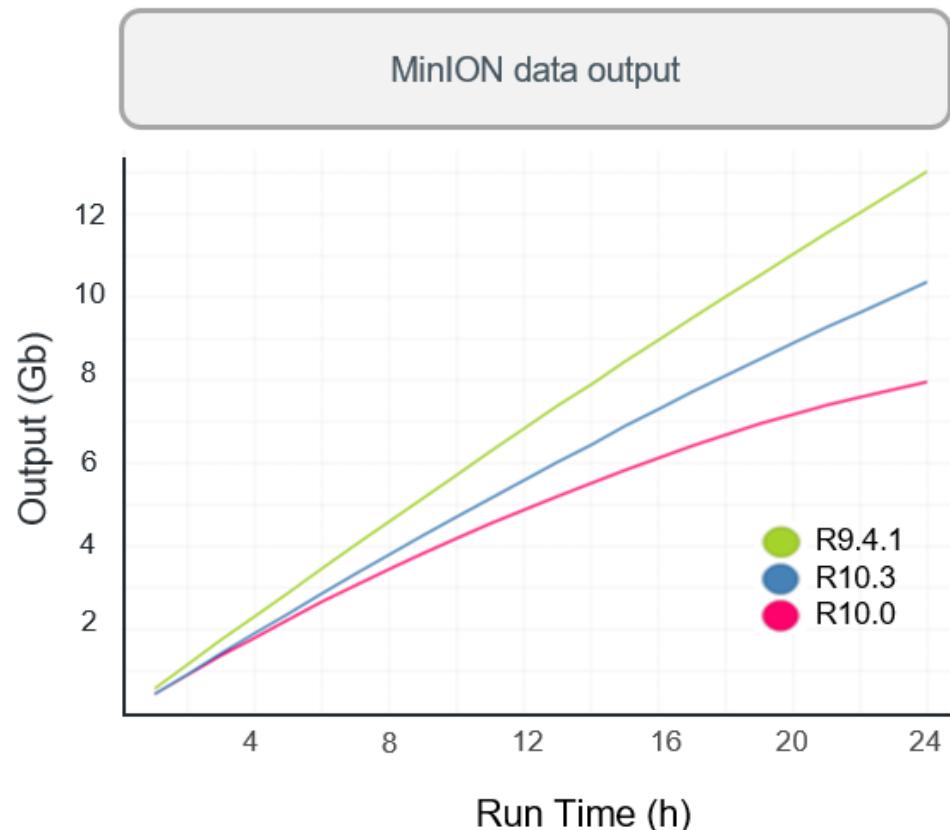
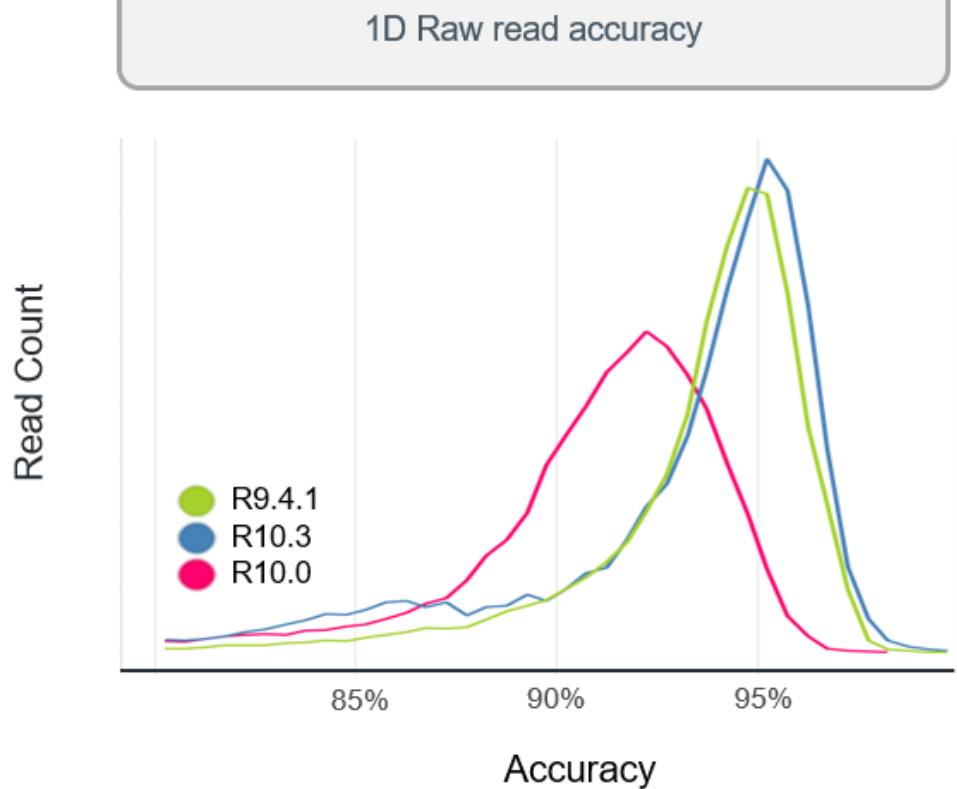
# ONT Flowcells



ATCGGAAAAAAATCACGCCACGTCCAAA



# ONT R10 Flowcell



Input Requirements:

R9.4.1	R10.3	R10.0
5 – 50 fmol	25 – 75 fmol	50 – 100 fmol

# ONT MinKNOW



Component	Recommended specification: GPU high-accuracy basecalling	Minimal specification: data acquisition/CPU basecalling  <b>(note: CPU basecalling performance is limited - a GPU is recommended)</b>
Operating system	Windows – 10 Linux – Ubuntu 18.04	Windows – 10 OSX – Mojave, Catalina Linux – Ubuntu 18.04
Memory/RAM	16 GB RAM	16 GB RAM
CPU	Intel i7†, i9, Xeon, or better  Ryzen 5, 7, or better, with at least 4 cores/8 threads	Intel i7†, i9, Xeon, or better  Ryzen 5, 7, or better, with at least 4 cores/8 threads
GPU	<p>NVIDIA GPU RTX 2060 or better, with at least 8 GB of GPU memory. Theoretical performance is only a guide, but more is better. Technical information can be found on various websites, for example <a href="https://www.techpowerup.com/gpu-specs/">https://www.techpowerup.com/gpu-specs/</a>.</p> <p>Widely-available examples include the RTX 2060, RTX 2070, RTX 3060, RTX 3070.</p> <p>If you are working with a different type of GPU than the models listed above, please ensure that it has a CUDA Compute Capability &gt;6.1 (for more information about CUDA-enabled GPUs, see the <a href="#">NVIDIA website</a>).</p>	-
Storage	1 TB internal SSD	1 TB internal SSD
Ports	USB3.0‡	USB3.0‡

† Users need to verify that their i7 is a four-core model or better

‡ The MinION device is CE marked using USB3.0. If a user wished to use USBC, they may, but this invalidates the CE marking

# Storage Requirements

Typically, 1 Gbase of sequence data takes up approximately 11 Gbytes of storage. This typically comprises 90% .fast5 files, 9% FASTQ files and 1% sequence summary file.

Example file sizes below are based on different outputs from a flow cell, with a run saving both .fast5 and FASTQ files with a read N50 of 25 kb.

<b>Output (Gbases)</b>	<b>.fast5 storage (Gbytes)</b>	<b>FASTQ storage (Gbytes)</b>	<b>.fast5 + FASTQ storage (Gbytes)</b>
10	100	10	110
15	150	15	165
30	300	30	330

As an experiment progresses, .fast5 files are produced for all reads. If basecalling is chosen, these reads are utilised by the onboard software (more information below) to generate sequence data which is then stored in FASTQ files and as a FASTQ record within the .fast5 file.



MinION



MinION Mk1C

# MinKNOW

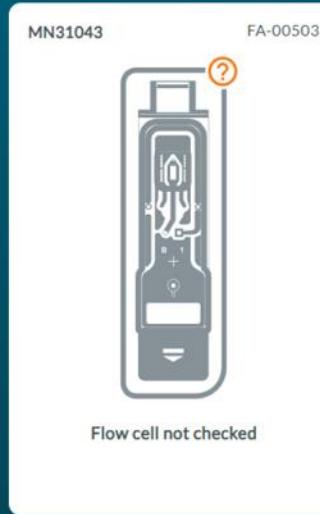
[Log in with your Nanopore account](#) ?

[Log in with your Nanopore account](#)

[Continue as guest](#)



- Start
- Sequencing overview
- Experiments
- System messages
- Host settings >



MinION  
Detected

GXBO3497  
My device

Start

Sequencing overview

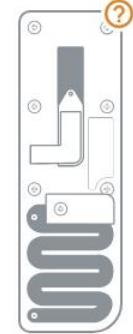
Experiments

System messages

Host settings &gt;

X1

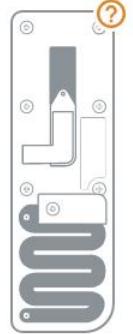
FAH80885



Flow cell not checked

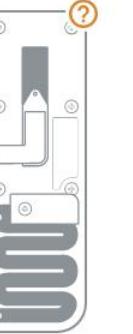
X2

FAP50597



Flow cell not checked

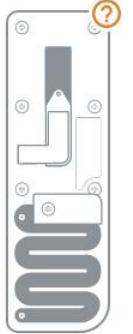
X3



Flow cell not checked

X4

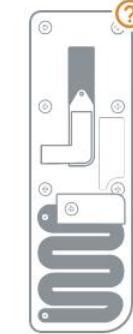
FAL14709



Flow cell not checked

X5

FAO29860



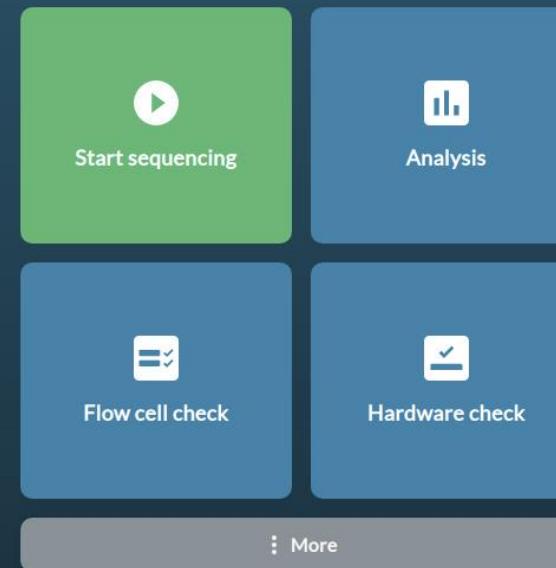
Flow cell not checked

GridION  
5 Flowcells

Connection manager



Start Screen



Hardware  
Check



## Hardware check

[Select all available](#)

5 of 5 positions selected

✓ Ready to start

CONFIGURATION  
TEST CELL

Please ensure that the configuration test cell has been inserted correctly.

Checking  
Hardware  
Use Test Cell

[Back to start](#)[Start](#)



≡

DD

X1 FAH80885

CONFIGURATION TEST CELL



Checking hardware

X2 FAP50597

CONFIGURATION TEST CELL



Checking hardware

X3

CONFIGURATION TEST CELL



Checking hardware

X4 FAL14709

CONFIGURATION TEST CELL



Checking hardware

X5 FAO29860

CONFIGURATION TEST CELL

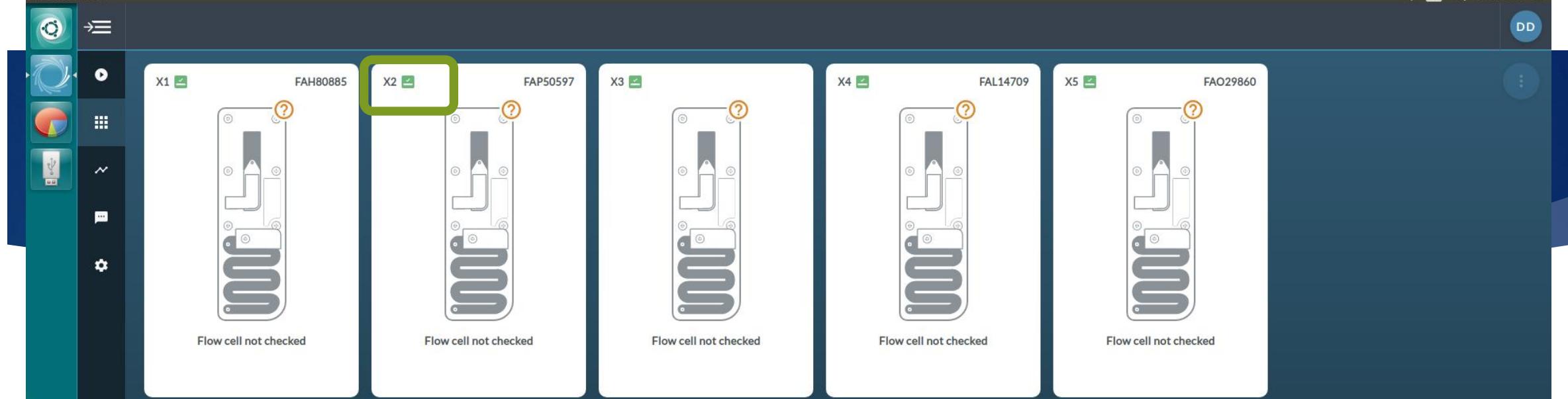


Checking hardware

...

Checking  
Hardware  
Use Test Cell





Green  
check if  
hardware is  
working

GXBO3497  
My device

Start

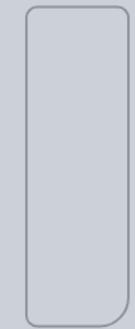
Sequencing overview

Experiments

System messages

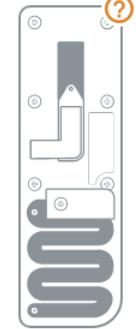
Host settings &gt;

X1



No flow cell detected

X2



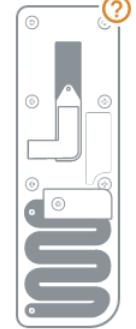
Flow cell not checked

X3



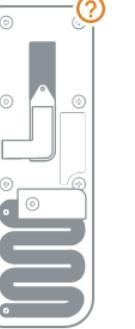
Flow cell not checked

X4

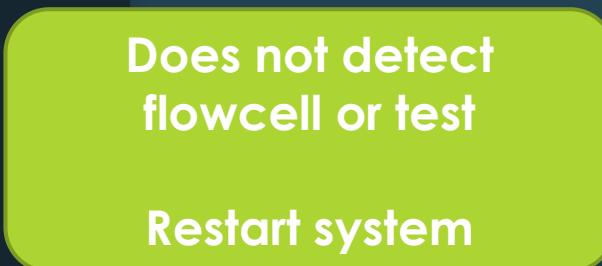


Flow cell not checked

X5



Flow cell not checked

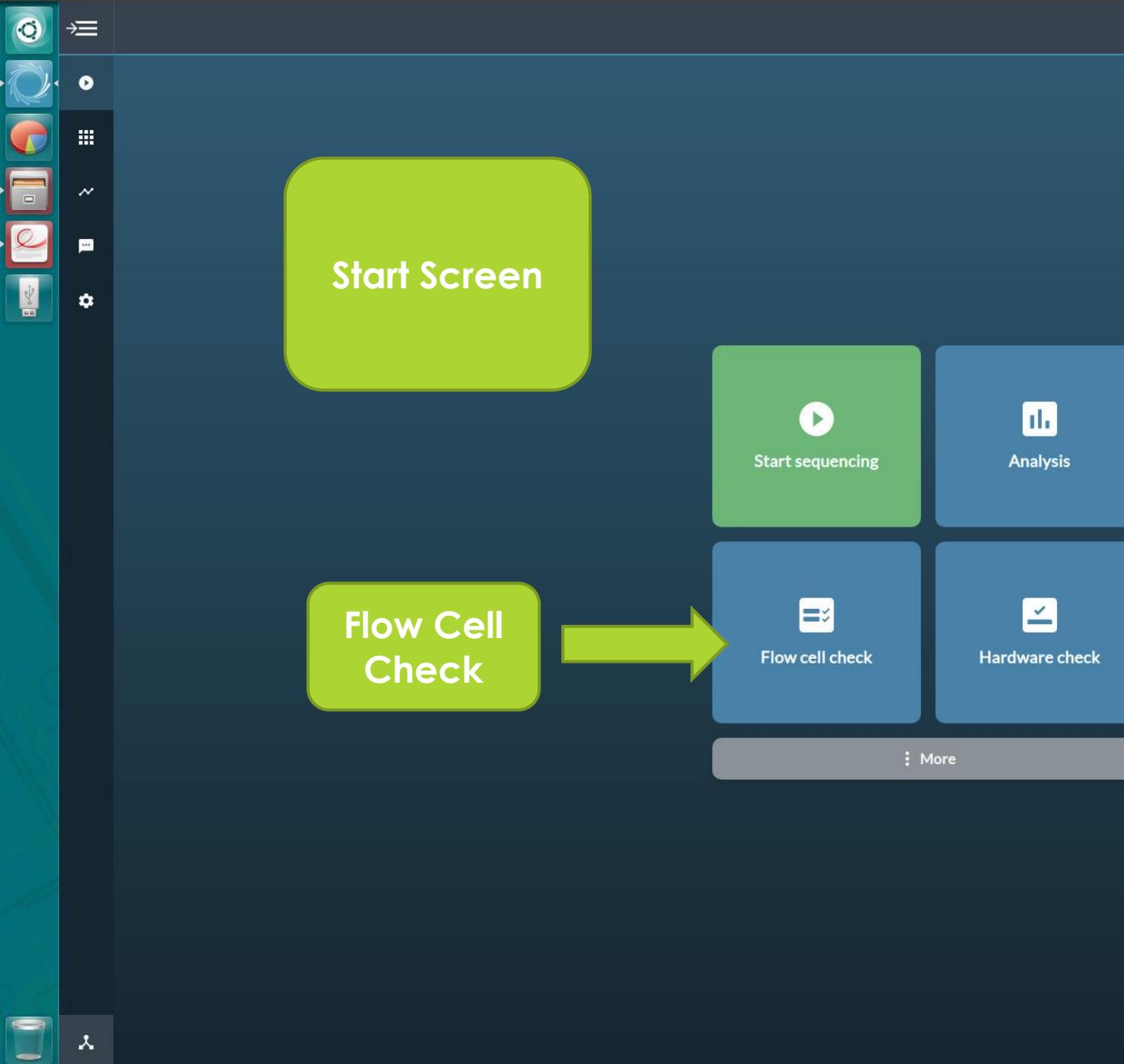


Does not detect  
flowcell or test

Restart system



Connection manager



GXBO3497  
My device

Start

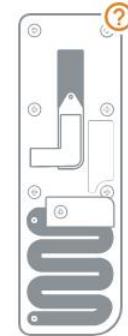
Sequencing overview

Experiments

System messages

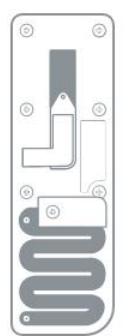
Host settings &gt;

X1 FAH80885



Flow cell not checked

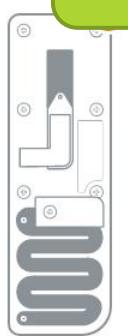
X2 FAR55844



Checking flow cell

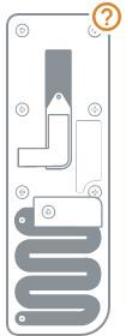
Flowcell ID

FAL14709



Flow cell not checked

X5 FAO29860



Flow cell not checked

Warms to 37C  
Checks for Pores  
~20 minutes

Connection manager

GXBO3497  
My device

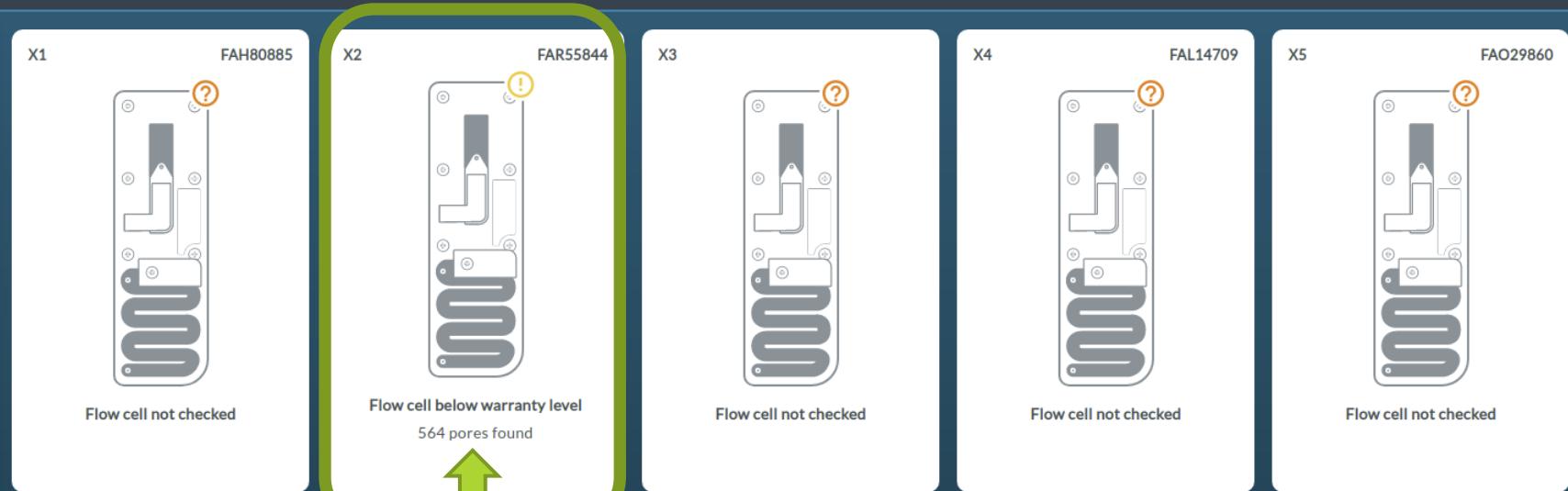
Start

Sequencing overview

Experiments

System messages

Host settings &gt;



Pores Found

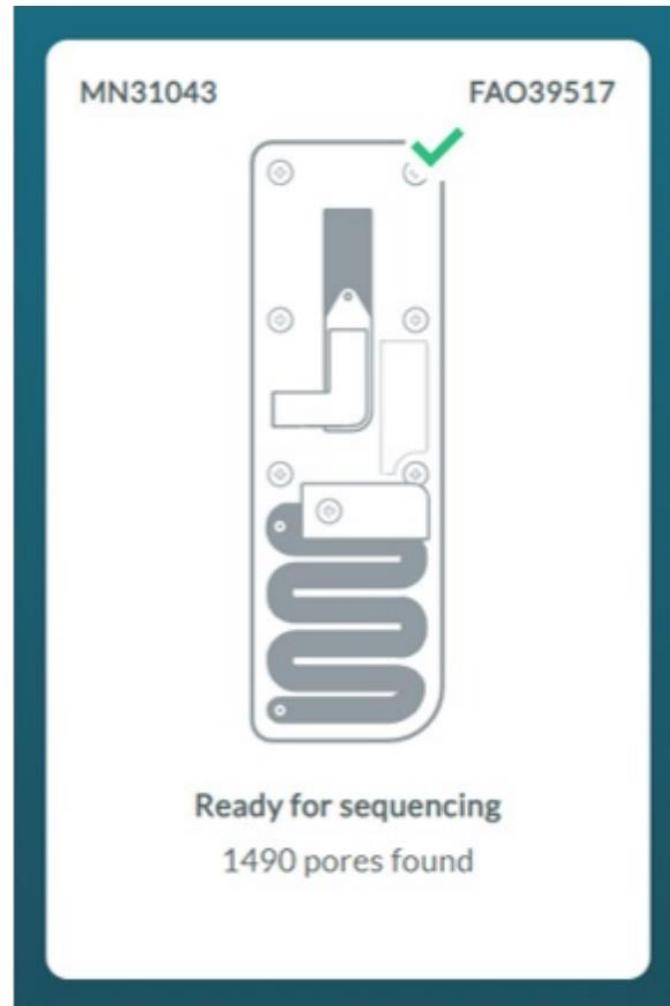
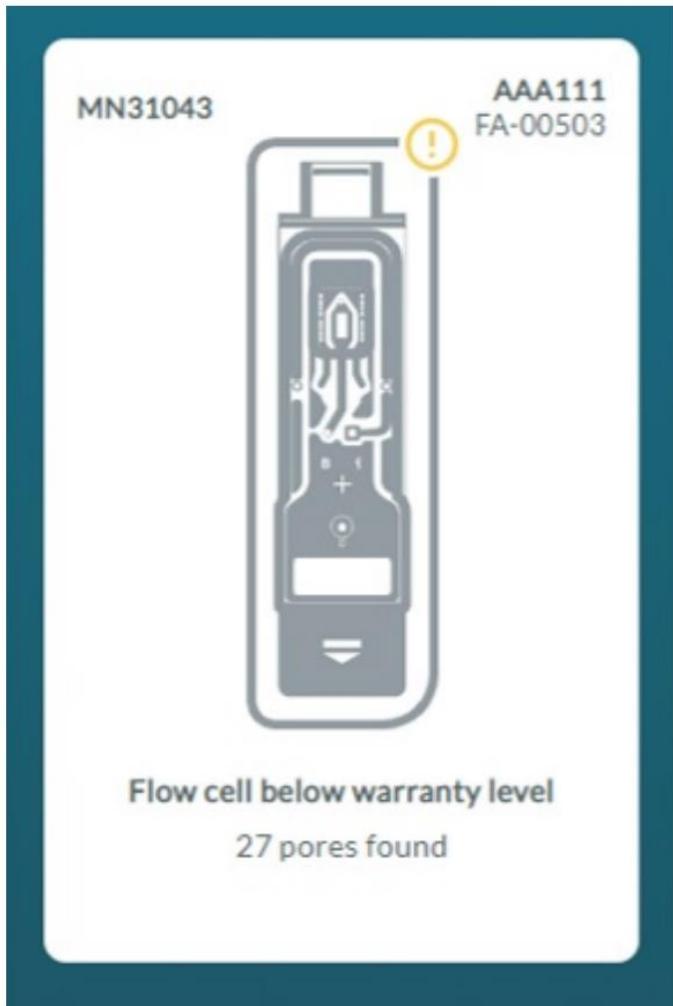
12/4/2022: Flowcell used  
12/6/2022: Washed, 948 pores  
Stored at 4C  
5/16/2022: 564 pores

~60% of pores still  
active after 6  
months of  
storage



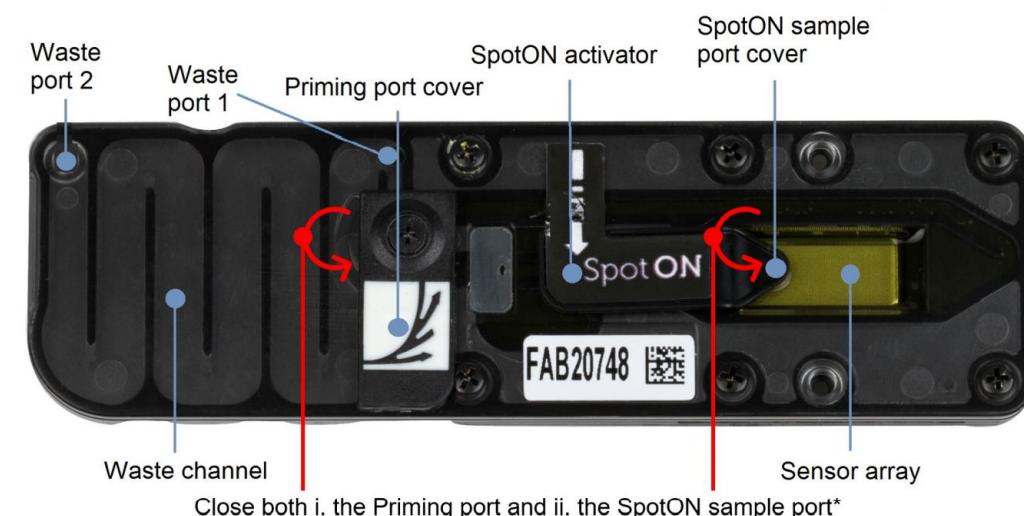
Connection manager

## Failed Flowcell Check

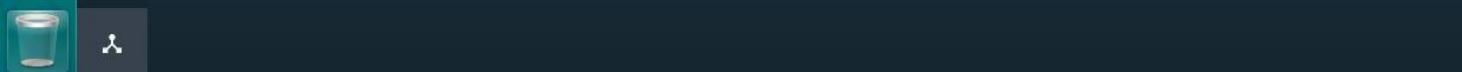
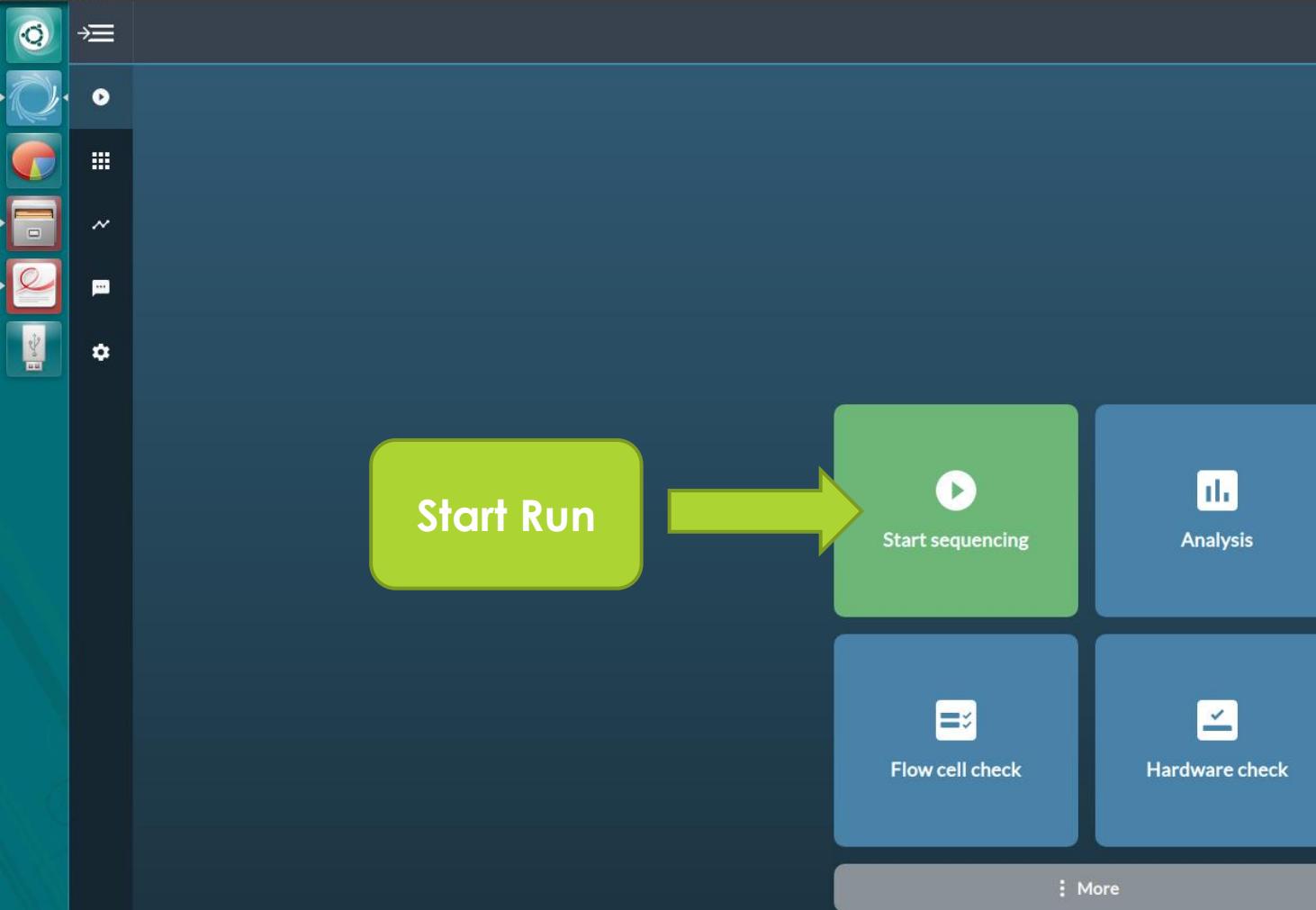


# Flow Cell Pores

Flow cell	Minimum number of active pores covered by warranty
Flongle Flow Cell	50
MinION/GridION Flow Cell	800
PromethION Flow Cell	5000



\*Both ports are shown in a closed position



GXBO3497  
My device

Start

Sequencing overview

Experiments

System messages

Host settings

Select Position

1. Positions

## Name Run

## Select positions

Ensure the experiment name does not contain any personally-identifiable information.

Test-1

Join existing

Load settings from template

⋮



Select all available

Position	Flow cell ID	Flow cell type	Sample ID
X2	FAR55844	FLO-MIN106	Sample ID

Optional Sample ID

&lt; Back to start

Continue to kit selection &gt;

Skip to final review &gt;



Connection manager



Start

- Sequencing overview
- Experiments
- System messages

Host settings



## Select Kit & Workflow

1. Positions

2. Kit

3. Run options

4. Basecalling

5. Output

6. Review

### Kit selection

Sample type

 DNA     RNA

PCR-free

 PCR     PCR-free

Multiplexing

 Yes     No Control

Reset filters

Ligation Sequencing Kit SQK-LSK109	Rapid Barcoding Kit SQK-RBK004	<input checked="" type="checkbox"/> Rapid Sequencing Kit SQK-RAD004	Direct RNA Sequencing Kit SQK-RNA002
PCR Barcoding Kit SQK-PBK004	16S Barcoding Kit (BC1-24) SQK-16S024	CAS109 Sequencing Protocol SQK-CAS109	CAS109 Sequencing Kit SQK-CS9109
Direct cDNA Sequencing Kit SQK-DCS109	Field Sequencing Kit SQK-LRK001	Ligation Sequencing Kit (48 reactions) SQK-LSK109-XL	Ligation Sequencing Kit SQK-LSK110
Ligation Sequencing Kit XL SQK-LSK110-XL	Ligation Sequencing Kit SQK-LSK112	Ligation Sequencing Kit XL SQK-LSK112-XL	Multiplex Ligation Sequencing Kit XL SQK-MLK110-96-XL
Multiplex Ligation Sequencing Kit XL SQK-MLK111-96-XL	Native Barcoding Sequencing Kit 24 SQK-NBD110-24	Native Barcoding Sequencing Kit 96 SQK-NBD110-96	Native Barcoding Sequencing Kit 24 SQK-NBD112-24
Native Barcoding Sequencing Kit 96 SQK-NBD112-96	PCR cDNA Barcoding Kits SQK-PCB109	PCR-cDNA Barcoding Kit 24 SQK-PCB110-24	PCR cDNA Barcoding Kit - 24 SQK-PCB111-24
PCR-cDNA Sequencing Kit SQK-PCS109	PCR cDNA Sequencing Kit SQK-PCS110	PCR cDNA Sequencing Kit SQK-PCS111	Pore-C Sequencing Protocol SQK-PRC109
PCR Sequencing Kit SQK-PSK004	Q20 Early Access Kit SQK-Q20EA	Rapid Sequencing Kit SQK-RAD112	Rapid Barcoding Kit 96 SQK-RBK110-96
Rapid PCR Barcoding Kit SQK-RPB004	Ultra-Long DNA Sequencing Kit SQK-ULK001	VolTRAX PCR Tiling 1-12 COVID-19 VSK-PTC001	VolTRAX Multiplex Sequencing Kit VSK-VMK002
VolTRAX Multiplex Sequencing Kit VSK-VMK003	VolTRAX Sequencing Kit VSK-VSK002	VolTRAX Sequencing Kit VSK-VSK003	16S Barcoding Kit SQK-RAB204

[◀ Back to position selection](#)[Continue to run options ➞](#)[Skip to final review ➞](#)

Connection manager



# SARS-CoV-2 Midnight Primers Rapid Barcoding

## My device

art

 Sequencing overview

↗ Experiments

 System messages

## Kit selection

Sample type	PCR-free	Multiplexing	<input type="checkbox"/> Control
DNA	PCR	Yes	
RNA	PCR-free	No	

[Reset](#)

[Reset filters](#)

Ligation Sequencing Kit SQK-LSK109	Rapid Barcoding Kit SQK-RBK004	Rapid Sequencing Kit SQK-RAD004	Direct RNA Sequencing Kit SQK-RNA002
PCR Barcoding Kit SQK-PBK004	16S Barcoding Kit (BC1-24) SQK-16S024	CAS109 Sequencing Protocol SQK-CAS109	CAS109 Sequencing Kit SQK-CS9109
Direct cDNA Sequencing Kit SQK-DCS109	Field Sequencing Kit SQK-LRK001	Ligation Sequencing Kit (48 reactions) SQK-LSK109-XL	Ligation Sequencing Kit SQK-LSK110
Ligation Sequencing Kit XL SQK-LSK110-XL	Ligation Sequencing Kit SQK-LSK112	Ligation Sequencing Kit XL SQK-LSK112-XL	Multiplex Ligation Sequencing Kit XL SQK-MLK110-96-XL
Multiplex Ligation Sequencing Kit XL SQK-MLK111-96-XL	Native Barcoding Sequencing Kit 24 SQK-NBD110-24	Native Barcoding Sequencing Kit 96 SQK-NBD110-96	Native Barcoding Sequencing Kit 24 SQK-NBD112-24
Native Barcoding Sequencing Kit 96 SQK-NBD112-96	PCR cDNA Barcoding Kits SQK-PCB109	PCR-cDNA Barcoding Kit 24 SQK-PCB110-24	PCR cDNA Barcoding Kit - 24 SQK-PCB111-24
PCR-cDNA Sequencing Kit SQK-PCS109	PCR cDNA Sequencing Kit SQK-PCS110	PCR cDNA Sequencing Kit SQK-PCS111	Pore-C Sequencing Protocol SQK-PRC109
PCR Sequencing Kit SQK-PSK004	Q20 Early Access Kit SQK-Q20EA	Rapid Sequencing Kit SQK-RAD112	Rapid Barcoding Kit 96 SQK-RBK110-96 <input checked="" type="checkbox"/>
Rapid PCR Barcoding Kit SQK-RPB004	Ultra-Long DNA Sequencing Kit SQK-ULK004	VolTRAX PCR Tiling 1-12 COVID-19 SQK-DTC004	VolTRAX Multiplex Sequencing Kit SQK-MXK002

#### Select expansion pack

Midnight RT PCR Expansion  
EXP-MRT001

Spike Seq RT PCR Expansion  
EXP-SRT001

[Back to position selection](#)

**Continue to run options >**

[Skip to final review >>](#)



## Connection manager



Start

1. Positions

2. Kit

3. Run options

4. Basecalling

5. Output

6. Review

Sequencing overview

Experiments

System messages

Host settings &gt;

## Run options

Run length ?

72 hours

Bias voltage ?

-180 mV

 Adaptive sampling ?

Disabled

Options

&gt; Show advanced user options

Adjust Run Time  
Normally 24-36 hrs  
max



Connection manager

&lt; Back to kit selection

Continue to basecalling &gt;

Skip to final review &gt;

GXBO3497  
My device

Start

Sequencing overview

Experiments

System messages

Host settings &gt;

Only use high accuracy basecalling if running on GPU

1. Positions

2. Kit

3. Run options

4. Basecalling

5. Output

6. Review

## Basecalling

 Basecalling ?

Config: High-accuracy basecalling

⚙ Options

 Barcoding ?

Enabled

⚙ Options

 Alignment ?

Disabled

⚙ Options

Poor Performance  
Using High Accuracy  
Basecalling on Mk1C



Connection manager

&lt; Back to run options

Continue to output &gt;

Skip to final review &gt;



Start

Sequencing overview

Experiments

System messages

Host settings &gt;

1. Positions

2. Kit

3. Run options

4. Basecalling

5. Output

6. Review

## Output

Output location ?

/data/.

Output format ? FAST5 ? FASTQ ? BAM Filtering ?

Qscore: 9 | Readlength: Unfiltered | Read splitting: Disabled

? Options

&gt; Show advanced user options

Normally run with  
default (both fast5 &  
fastq) selected

&lt; Back to basecalling

Continue to final review &gt;



Connection manager



Start

Sequencing overview

Experiments

System messages

Host settings

1. Positions

2. Kit

3. Run options

4. Basecalling

5. Output

6. Review

## Test-1

## Selected positions

## Kit

Selected kit: SQK-RBK110-96  
Expansion packs: EXP-MRT001

Edit

## Run options

Run length: 72 hours  
Bias voltage: -180 mV  
Adaptive sampling: Off

Edit

&gt; Advanced run options

## Basecalling

Basecalling: On (High-accuracy basecalling)  
Barcode: On  
Alignment: Off

Edit

## Output

Location: /data/.  
FAST5: On (Raw, FASTQ record, VBZ, 4000 reads per ...  
FASTQ: On (GZip, 4000 reads per file)  
Read filtering: Qscore: 9 | Readlength: Unfiltered | Read split...

Edit

&gt; Advanced run options

Normally run with  
default (both fast5 &  
fastq) selected

&lt; Back to output

Save settings as template

Start



Connection manager

# Pore Channels Panel



GXB03153 REMOTE  
gxb03153

Start

Sequencing overview

Experiments

System messages

Host settings >

X1 FAQ16580 X2 FAQ13638 X3 X4 X5

Sequencing Sequencing No flow cell detected No flow cell detected No flow cell detected

Overview of flowcells sequencing

The screenshot shows the NextSeq 500 software interface for run GXB02294. The left sidebar includes options for Start, Sequencing overview, Experiments (which is selected), System messages, and Host settings. The main panel displays experiment details: Experiments last 7 days, search bar for experiments, and tabs for RR\_Ladder, OP\_TEST, Workflow 1, and RR\_Midnight\_22\_03. Control buttons include Resume, Pause, Stop, Start pore scan, and Export run report. A table lists flowcell positions X4 and X5 with their respective details: FAO29273 and FAS02937, no sample, health status (green for X4, yellow for X5), run time (15 h / 72 h), active state, 5.32 M and 4.27 M reads, 1.3 Gb and 1.05 Gb basecalled, and 1.46 Gb and 1.17 Gb estimated bases. A progress bar indicates sequencing completion at 100% for both flowcells.

Position	Flow cell ID	Sample ID	Health	Run time	Run state	Reads	Bases	Basecalled %
X4	FAO29273	no_sample	<div style="width: 100%; background-color: green; height: 10px;"></div>	15 h / 72 h	Active	5.32 M	1.3 Gb basecalled 1.46 Gb estimated	100%
X5	FAS02937	no_sample	<div style="width: 20%; background-color: yellow; height: 10px;"></div>	15 h / 72 h	Active	4.27 M	1.05 Gb basecalled 1.17 Gb estimated	100%

Overview of  
flowcells  
sequencing

Note: Poor  
sequencing  
on X4

GXB03153 REMOTE  
gxb03153 Guest

Start Sequencing overview Experiments System messages Host settings >

Filters 4\_3\_basecalling\_test

Reads: 236.22 k Estimated bases: 1.07 Gb Basecalled bases: 1.11 Gb Active runs: 2 Total runs: 4

Resume Pause Stop Start pore scan Export run report Experiment group

Position	Flow cell ID	Sample ID	Health	Run time	Run state	Reads	Bases	Basecalled %
X1	FAQ16580	fast_basecalling	<div style="width: 70%; background-color: green;"></div>	16 m / 72 h	Active	19.65 k	86.77 Mb basecalled 84.64 Mb estimated	100%
X2	FAQ13638	fast_basecalling	<div style="width: 70%; background-color: green;"></div>	16 m / 72 h	Active	20.96 k	97.4 Mb basecalled 94.12 Mb estimated	100%
X1	FAQ16580	no_sample	—	1 h 1 m	Complete	89.91 k	413.74 Mb basecalled 399.62 Mb estimated	100%
X2	FAQ13638	no_sample	—	1 h 1 m	Complete	105.7 k	510.42 Mb basecalled 487.38 Mb estimated	100%

GXB03214 REMOTE  
Host settings

Back to main menu

Device settings

Software

File manager

System

Help

## Device settings

### System

GXB03214

Shut down

### Date and time

Wed 2022-03-23 13:27:01 Europe/London (time.oxfordnanolabs.local)

Change date and time

Change time zone

### Disk management

Add network drive

Internal drive

System storage

40.8 GB used - 18.4 GB free

/data

2.1 TB used - 1.2 TB free

Share

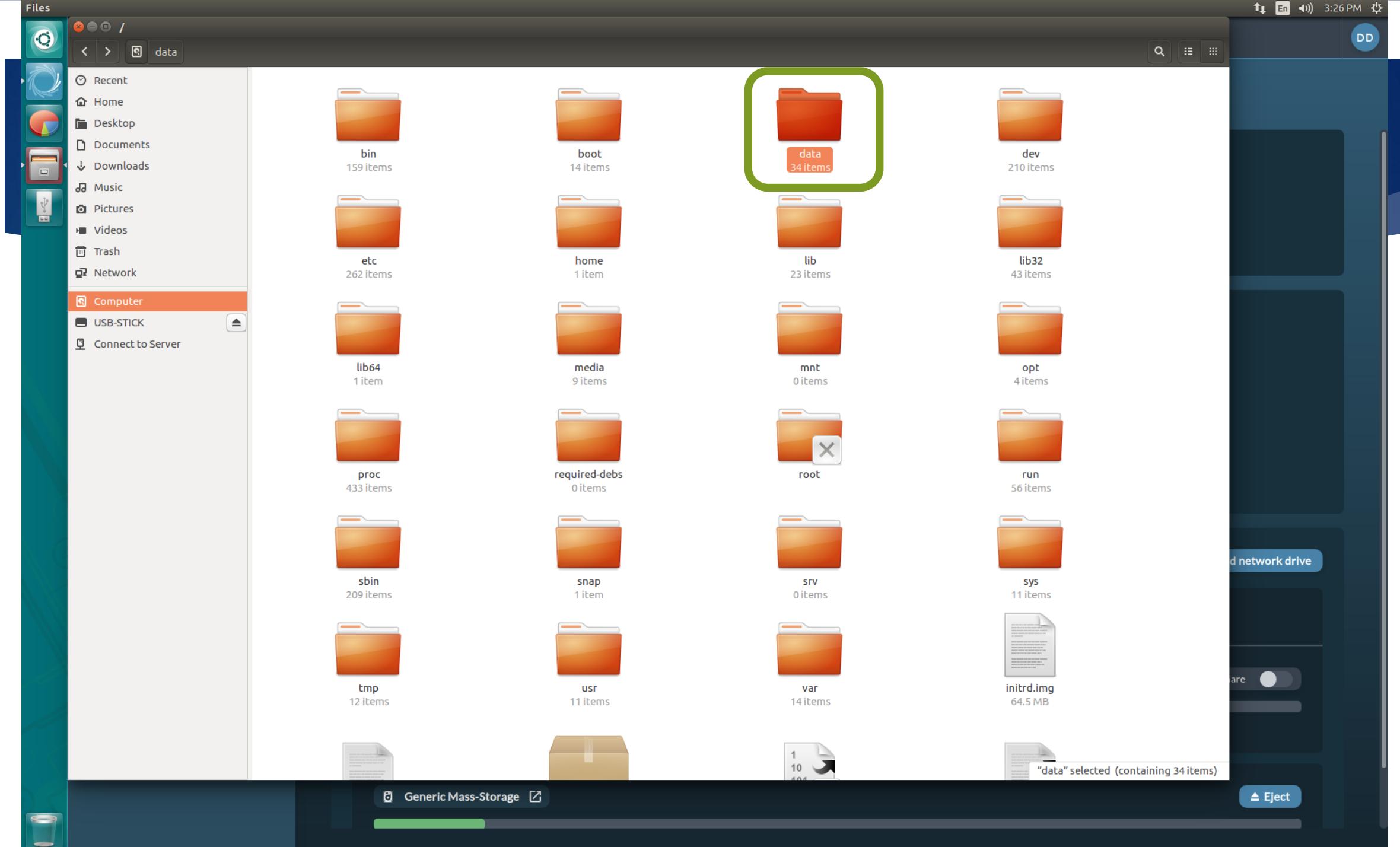
Check for hard  
drive space  
before starting run

The screenshot shows the MinKNOW software interface. At the top, there's a header with 'GXB03214' and a 'REMOTE' button. Below the header, the title 'Host settings' is displayed. On the left side, there's a sidebar with the following options: 'Back to main menu', 'Device settings', 'Software' (which is highlighted with a yellow border), 'File manager', 'System', and 'Help'. The main content area is titled 'Software' and contains two sections: 'MinKNOW' and 'System'. The 'MinKNOW' section shows the 'Installed version: 22.a.33 (xenial)' and the 'Available version: 22.a.35 (xenial)'. A green button labeled 'Install update' is visible. The 'System' section displays 'Total packages: 121' and 'Security packages: 75'. A note states: 'If you see some system packages remain after a system update, please update MinKNOW and the number should return to zero.' A green button labeled 'Install packages' is also present.

Check for  
software updates  
before starting run

# ONT Data Output







GXB03497  
My device

Start Sequencing overview Experiments System messages Host settings

NMCurative289\_384

Resume Pause Stop Start MUX scan Export PDF Experiment group

Position	Flow cell ID	Sample ID	Health	Run time	Run state	Reads	Bases	Basecalled %
X2	FAS69901	NMCurative289_384	-	1 d 6 h	Complete	8.39 M	5.34 Gb basecalled 5.49 Gb estimated	100%

report\_FAS76468\_20220427\_1401\_f062b3b3.pdf

1 of 13 87.82% Thumbnails X2 TRLIF193\_200\_3F1\_88 TRLIF193\_200\_3F1\_88 f062b3b3-fa62-4dc3-927c-2b979ce3d513

20220421\_1041\_X2\_FAS69938\_0c6a18ad

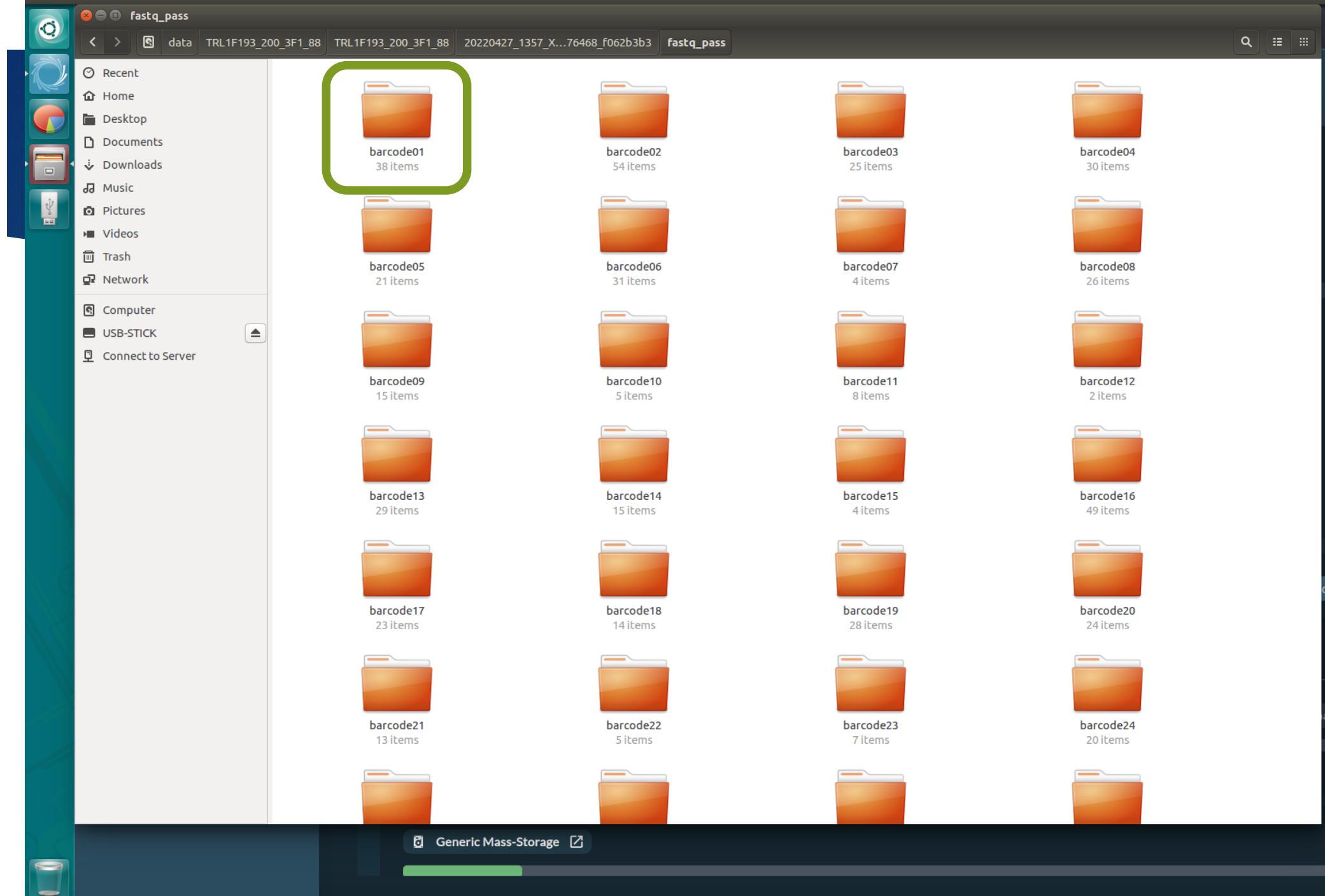
data TRL\_1F\_001\_096 TRL\_1F\_001\_096 20220421\_1041...9938\_0c6a18ad

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fast5\_fail fast5\_pass fast5\_fail fastq\_pass other\_reports barcode\_alignment\_FAS69938\_294a03dc... duty\_time\_FAS69938\_294a03dc.csv final\_summary\_FAS69938\_294a03dc.txt

report\_FAS69938\_20220421\_1046\_0c6a18ad.md report\_FAS69938\_20220421\_1046\_0c6a18ad.pdf sequencing\_summary\_FAS69938\_294a03dc.txt throughput\_FAS69938\_294a03dc.csv

"report\_FAS69938\_20220421\_1046\_0c6a18ad.pdf" selected (567.2 kB)



barcode01

data TRL1F193\_200\_3F1\_88 TRL1F193\_200\_3F1\_88 20220427\_1357\_X...76468\_f062b3b3 fastq\_pass barcode01

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FAS76468\_pass\_barcode01\_4db4895e\_1.fastq.gz 3.8 MB FAS76468\_pass\_barcode01\_4db4895e\_2.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_3.fastq.gz 3.9 MB

FAS76468\_pass\_barcode01\_4db4895e\_4.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_5.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_6.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_7.fastq.gz 3.9 MB

FAS76468\_pass\_barcode01\_4db4895e\_8.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_9.fastq.gz 3.8 MB FAS76468\_pass\_barcode01\_4db4895e\_10.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_11.fastq.gz 3.9 MB

FAS76468\_pass\_barcode01\_4db4895e\_12.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_13.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_14.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_15.fastq.gz 3.9 MB

FAS76468\_pass\_barcode01\_4db4895e\_16.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_17.fastq.gz 3.9 MB FAS76468\_pass\_barcode01\_4db4895e\_18.fastq.gz 3.8 MB FAS76468\_pass\_barcode01\_4db4895e\_19.fastq.gz 3.9 MB

Generic Mass-Storage

Eject

GXB03497  
My device

Start Sequencing overview Experiments System messages Host settings

NMCurative289\_384

Position — Flow cell ID — Sample ID — Health Run time — Run state — Reads — Bases — Basecalled %

X2 FAS69901 NMCurative289\_384 — 1 d 6 h Complete 8.39 M 5.34 Gb basecalled 5.49 Gb estimated 100%

Export PDF Experiment group

report\_FAS76468\_20220427\_1401\_f062b3b3.pdf

1 of 13 87.82% X2 TRLIF193\_200\_3F1\_88 TRLIF193\_200\_3F1\_88 f062b3b3-fa62-4dc3-927c-2b979ce3d513

20220421\_1041\_X2\_FAS69938\_0c6a18ad

data TRL\_1F\_001\_096 TRL\_1F\_001\_096 20220421\_1041...9938\_0c6a18ad

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fast5\_fail fast5\_pass fast5\_fail fastq\_pass other\_reports barcode\_alignment\_FAS69938\_294a03dc... duty\_time\_FAS69938\_294a03dc.csv final\_summary\_FAS69938\_294a03dc.txt

report\_FAS69938\_20220421\_1046\_0c6a18ad.pdf

sequencing\_summary\_FAS69938\_294a03dc.txt throughput\_FAS69938\_294a03dc.csv

"report\_FAS69938\_20220421\_1046\_0c6a18ad.pdf" selected (567.2 kB)



## Run Info

Host Name	<b>GXB03497 (localhost)</b>
Position	<b>X3</b>
Experiment Name	<b>TRL3F89_184</b>
Sample ID	<b>TRL3F89_184</b>
Run ID	<b>9c1a2212-3f3d-428b-825f-391a2b6e6492</b>
Acquisition ID(s)	<b>4231a08ef8776a4c19649916575b02b94bd339f2, d67886505f5121d758cdfa3eed9385fb0c40c34</b>
Flow Cell Id	<b>FAS76433</b>
Start Time	<b>April 27, 13:58</b>
Run Length	<b>1d 6h 5m</b>

**Summary of Run**

## Run Summary

Reads Generated	<b>12.2 M</b>
Passed Bases	<b>5.77 Gb</b>
Failed Bases	<b>1.59 Gb</b>
Estimated Bases	<b>7.76 Gb</b>

# Run Parameters

Flow Cell Type	<b>FLO-MIN106</b>
Kit	<b>SQK-RBK110-96</b>
Initial bias voltage	<b>-180 mV</b>
FAST5 output	<b>Enabled</b>
FASTQ output	<b>Enabled</b>
BAM output	<b>Disabled</b>
Bulk file output	<b>Disabled</b>
Active channel selection	<b>Enabled</b>
Basecalling	<b>Enabled</b>
Specified run length	<b>30 hours</b>
FAST5 reads per file	<b>4000</b>
FAST5 output options	<b>vbz_compress,fastq,raw</b>
FASTQ reads per file	<b>4000</b>
FASTQ output options	<b>compress</b>
Mux scan period	<b>1 hour 30 minutes</b>
Reserved pores	<b>0 %</b>
Basecall model	<b>High-accuracy basecalling</b>
Barcoding	<b>barcoding_kits=["SQK-RBK110-96"],trim_barcodes="off",require_barcodes_both_ends="off",detect_mid_strand_barcodes="off"</b>
Read filtering	<b>min_qscore=9</b>
Read splitting	<b>enable=off</b>

**Summary of Run Parameters**

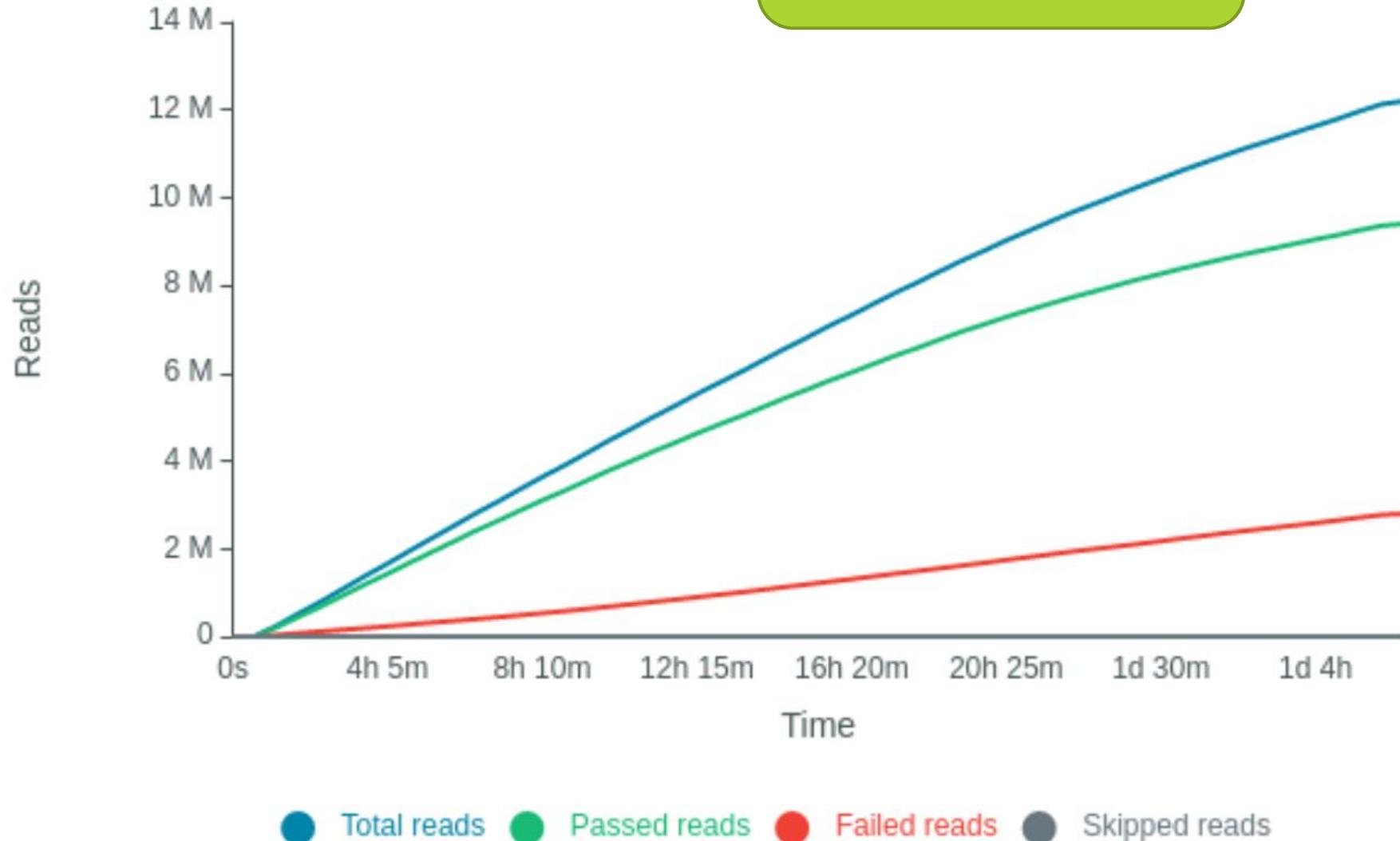
# Program Versions

Check for latest  
software

## Versions

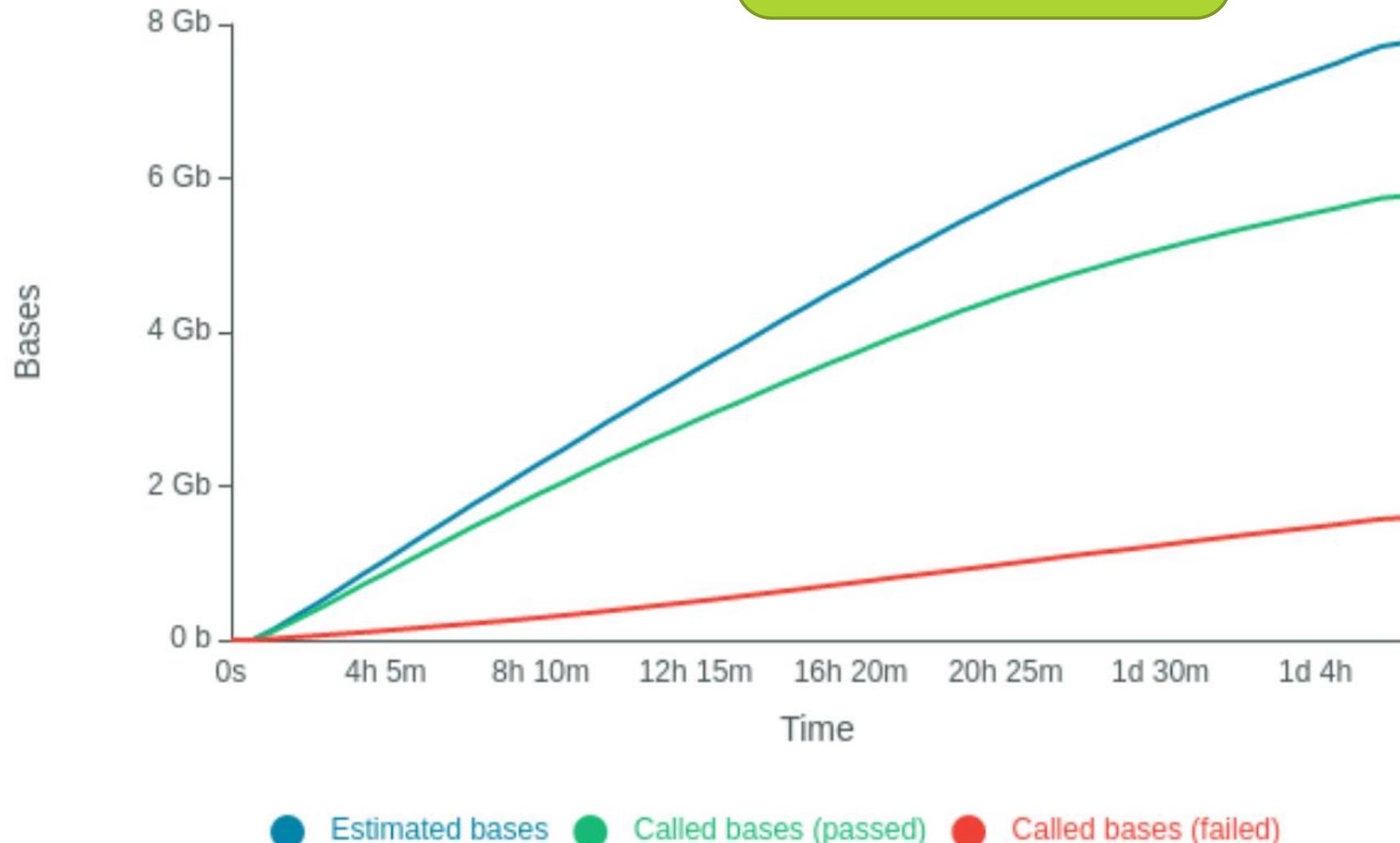
MinKNOW	<b>21.11.7</b>
MinKNOW Core	<b>4.5.4</b>
Bream	<b>6.3.5</b>
Guppy	<b>5.1.13</b>

## Cumulative Output Reads



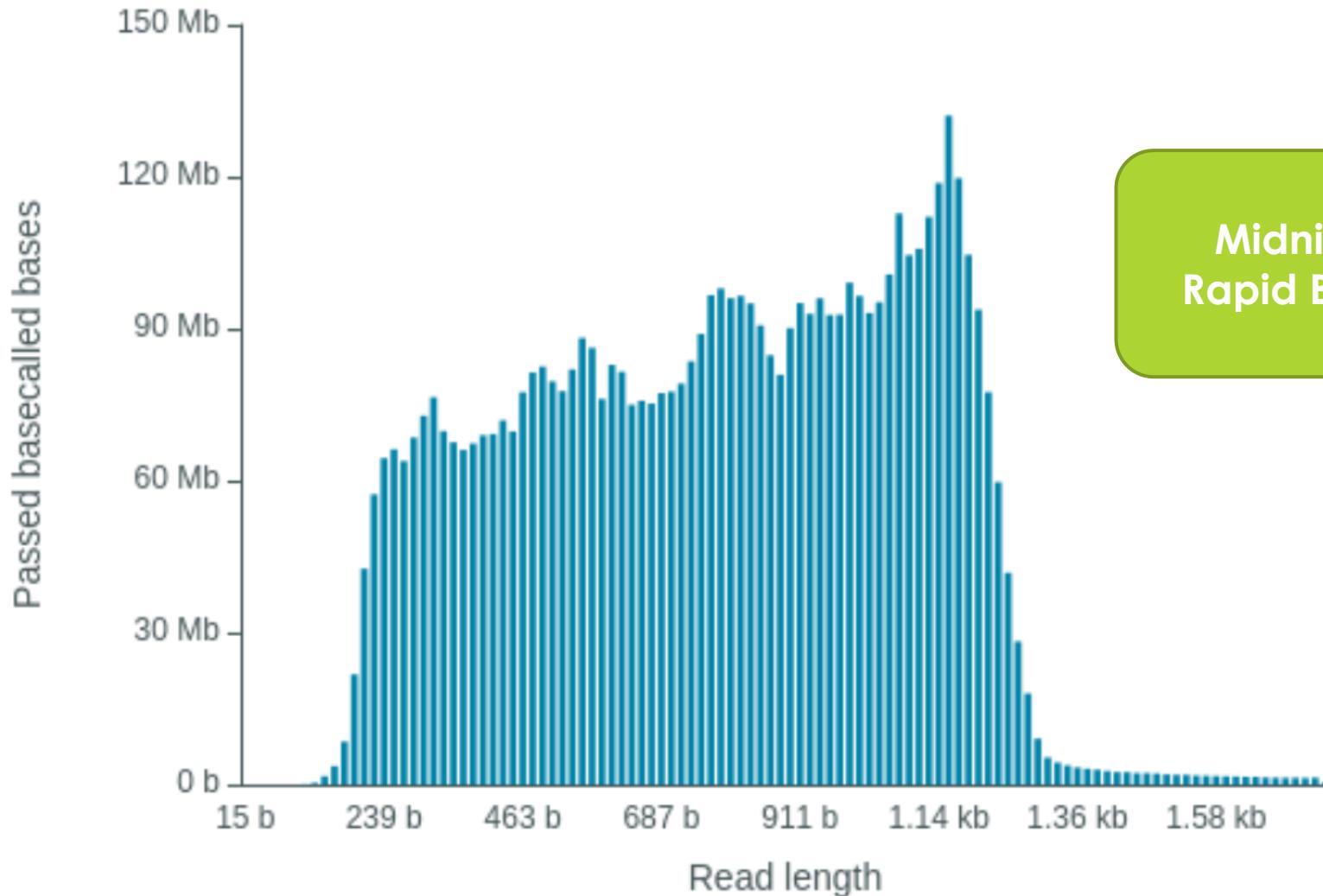
## Cumulative Output Bases

Base Output matches  
Read Output



## Read Length Histogram Basecalled Bases - Outliers Discarded

Estimated N50: 789 b

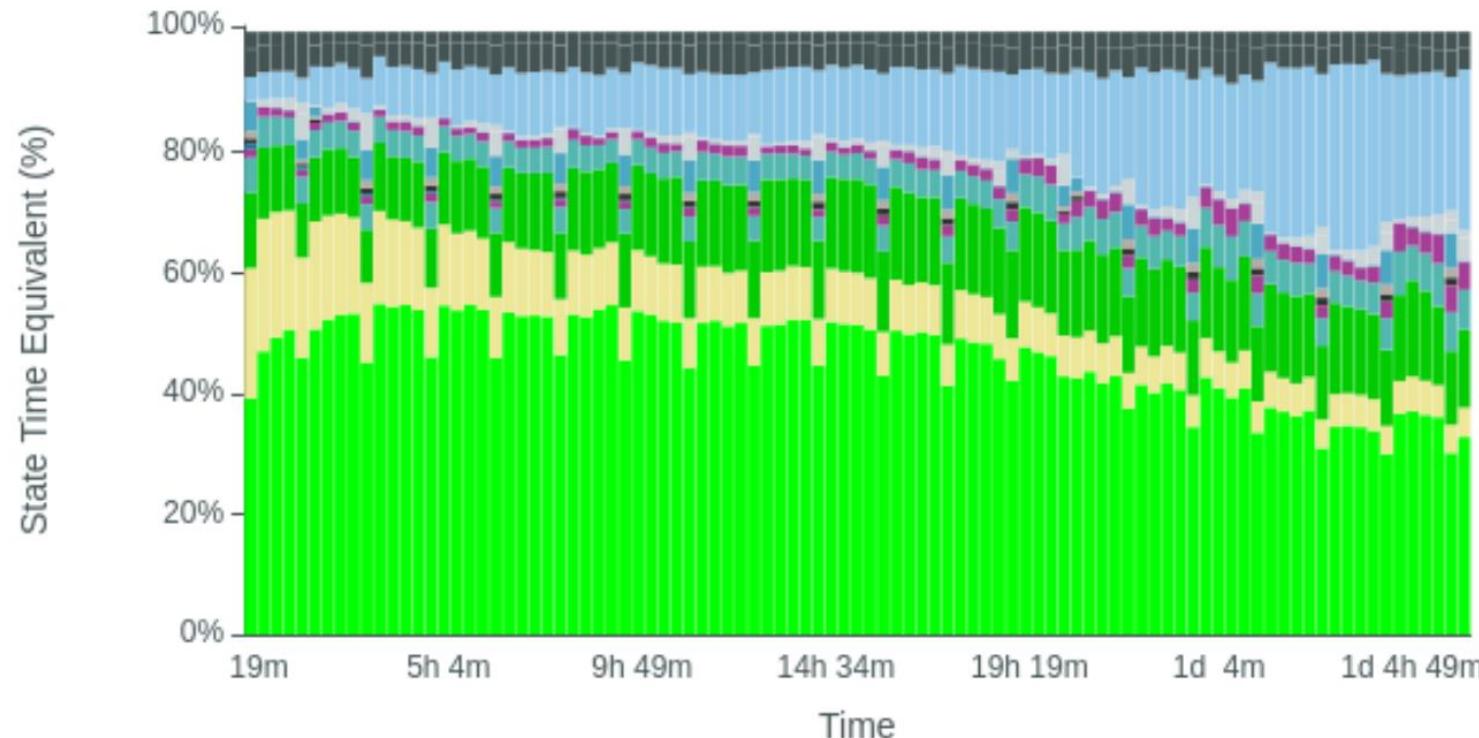


Midnight Primers  
Rapid Barcoding Kit

## Duty Time Grouped



## Duty time Categorised



Great Graph for Troubleshooting

Strand  
Adapter

Single Pore

Unavailable  
Active Feedback

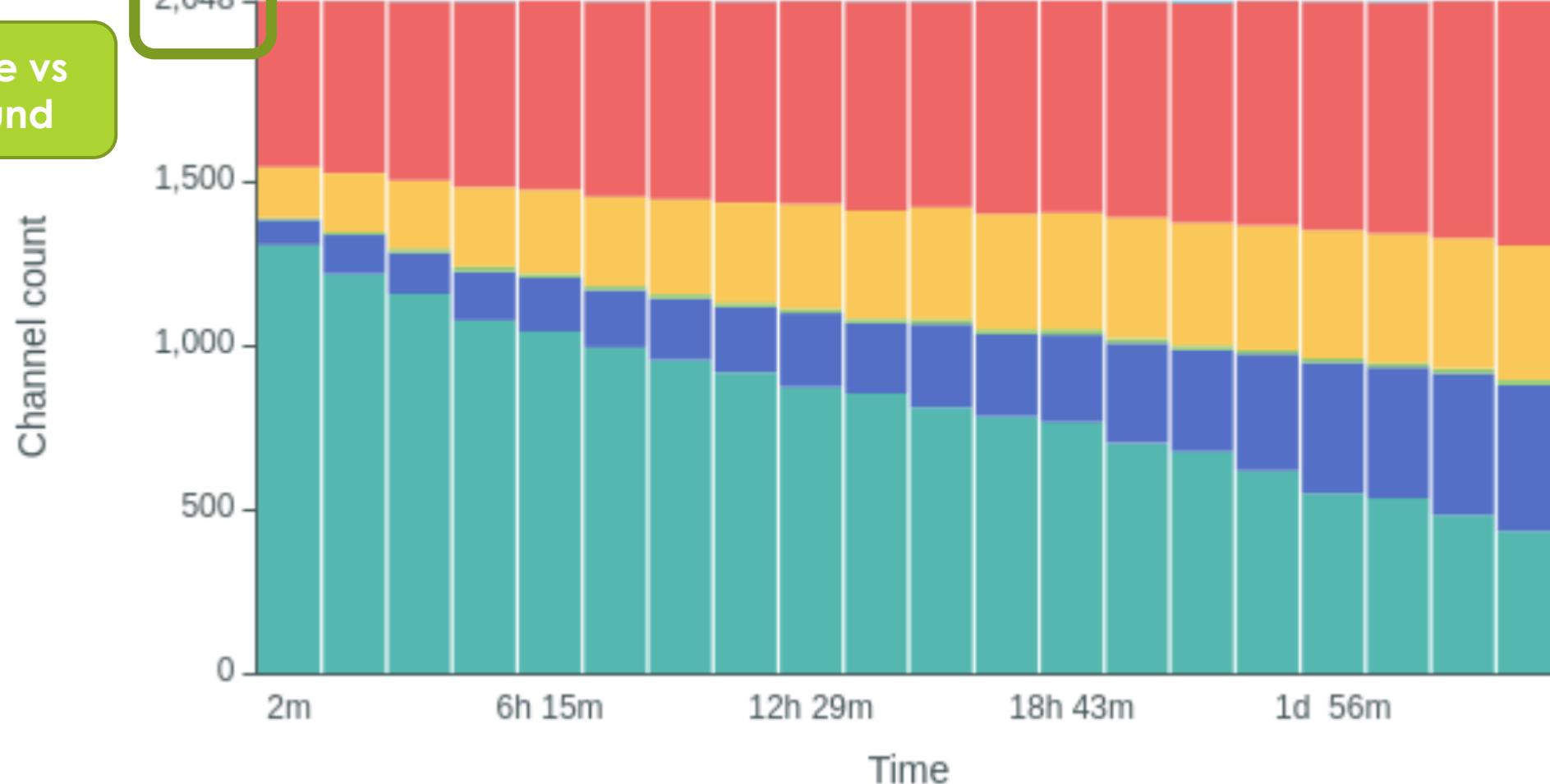
No Pore From Scan  
Out Of Range 2  
Possible Multiple  
Saturated  
Out Of Range 1  
Zero  
Channel Disabled

Unclassified  
Unclassified\_following\_reset  
Pending\_manual\_reset  
Pending\_mux\_change  
Pending Reselection

## Mux Scan Categorised

● Single Pore ● Reserved Pore ● Unavailable ● Multiple ● Saturated ● Zero ● Other

Note Scale vs  
Pores Found



Messages Displayed in  
Reverse Order (Last First)

## Run Debug Messages

- The sequencing run has finished, but basecalling may continue April 28, 20:04
- Mux scan for flow cell FAS76433 has found a total of 681 pores. 375 pores available for immediate sequencing April 28, 19:40
- Performing Mux Scan April 28, 19:38
- Mux scan for flow cell FAS76433 has found a total of 721 pores. 390 pores available for immediate sequencing April 28, 18:07
- Performing Mux Scan April 28, 18:05
- Mux scan for flow cell FAS76433 has found a total of 717 pores. 354 pores available for immediate sequencing April 28, 16:34
- Performing Mux Scan April 28, 16:31
- Mux scan for flow cell FAS76433 has found a total of 748 pores. 368 pores available for immediate sequencing April 28, 15:00

- Performing Mux Scan April 27, 18:43
- Mux scan for flow cell FAS76433 has found a total of 1088 pores. 470 pores available for immediate sequencing April 27, 17:12
- Performing Mux Scan April 27, 17:10
- Mux scan for flow cell FAS76433 has found a total of 1114 pores. 478 pores available for immediate sequencing April 27, 15:38
- Performing Mux Scan April 27, 15:36
- Mux scan for flow cell FAS76433 has found a total of 1199 pores 489 pores available for immediate sequencing April 27, 14:05
- Performing Mux Scan April 27, 14:03
- Starting sequencing procedure April 27, 14:03
- Waiting up to 300 seconds for temperature to stabilise at 34.0°C April 27, 13:58

Pores Found

Questions?

