

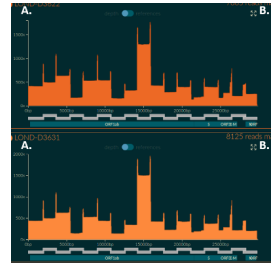


Version 2

Long reads nanopore sequencing to recover SARS-CoV-2 whole genome V.2

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Abstract

This protocol describes step-by-step instructions for building long (~2kb) amplicon libraries to recover SARS-CoV-2 genomes using the nanopore sequencing.

It can be applied for sequencing on the MinION device or GridION.

This protocol was developed in collaboration with the Laboratory of Respiratory Viruses and Measles, Oswaldo Cruz Institute, FIOCRUZ, Brazil, and the two sequencing facilities at Pathogen Genomic Unit (PGU) and UCL Genomics, University College London (UCL), United Kingdom.

This document describes the manual steps to perform the protocol, but for further information about the automation of the protocol, please, contact Pathogen Genomics Unit (PGU) - UCL.

Manager: Rachel Williams

<https://www.ucl.ac.uk/infection-immunity/pathogen-genomics-unit>

This protocol is based on the amplicon tiling strategy described previously by Quick J et al 2017. However, we have applied this strategy to recover long reads (2kb), then some adjustments were performed in the protocol.

Citation

Quick J, Grubaugh ND, Pullan ST, Claro IM, Smith AD, Gangavarapu K, Oliveira G, Robles-Sikisaka R, Rogers TF, Beutler NA, Burton DR, Lewis-Ximenez LL, de Jesus JG, Giovanetti M, Hill SC, Black A, Bedford T, Carroll MW, Nunes M, Alcantara LC Jr, Sabino EC, Baylis SA, Faria NR, Loose M, Simpson JT, Pybus OG, Andersen KG, Loman NJ (2017)

. Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples.

Nature protocols.

<https://doi.org/10.1038/nprot.2017.066>

LINK

If you have doubts, we are happy to help you to test or implement the protocol.



Materials

MATERIALS

☒ NEBNext Ultra II End Repair/dA-Tailing Module - 96 rxns **New England Biolabs Catalog #E7546L**

☒ NEBNext Ultra II Ligation Module - 96 rxns **New England Biolabs Catalog #E7595L**

☒ Qubit® dsDNA HS Assay kit **Thermo Fisher Scientific Catalog #Q32854**

☒ NEB Blunt/TA Ligase Master Mix **Catalog #M0367**

☒ Agencourt AMPure XP beads **Beckman Coulter Catalog #A63881**

☒ Ethanol **Merck Millipore (EMD Millipore) Catalog #100983**

☒ SuperScript® IV First-Strand Synthesis System **Thermo Fisher Catalog #18091200**

☒ ONT MinION Flow Cell R9.4.1 **Oxford Nanopore Technologies Catalog #FLO-MIN106D**

☒ Ligation sequencing kit 1D **Oxford Nanopore Technologies Catalog #SQK-LSK109**

☒ Flowcell Wash Kit **Oxford Nanopore Technologies Catalog #EXP-WSH003**

☒ NEB Q5® Hot Start High-Fidelity 2X Master Mix **New England Biolabs Catalog #M0494L**

☒ Native Barcoding Expansion 1-12 (PCR-free) **Oxford Nanopore Technologies Catalog #EXP-NBD104**

☒ Native Barcoding Expansion 13-24 (PCR-free) **Oxford Nanopore Technologies Catalog #EXP-NBD114**

☒ Primer set SARS-CoV-2_v1

RT (Optional)

- SuperScript™ IV First-Strand Synthesis System. (200 reactions) Cat: 18091200 Invitrogen

PCR (Optional)

- Q5® Hot Start High-Fidelity 2X Master Mix Cat: M0494
- Primer set SARS-CoV-2_v1 Pool 1 and Pool 2 (2kb) Paola Resende

Clean-up and QC

- Qubit ds DNA HS kit. Cat: Q32854 Thermofisher
- Ampure XP. Cat: A63881 Beckman Coulter

End-Prep, Barcoding, Adapter Ligation and Sequencing

- NEBNext® Ultra™ II Ligation Module. Cat: E7595L NEB
- NEBNext® Ultra™ II End Repair/dA-Tailing Module. Cat: E7546L NEB
- NEB Blunt/TA Ligase Master Mix. Cat: M0287L NEB
- Ligation Sequencing Kit. Cat: SQK-LSK109 ONT
- Native Barcoding Expansion 1-12 (PCR-free). Cat: EXP-NBD104 ONT
- Native Barcoding Expansion 13-24 (PCR-free). Cat: EXP-NBD114 ONT
- Flow Cell (R9.4.1) ONT

Flow cell wash

- Flow Cell Wash Kit. Cat: EXP-WSH003 ONT

Real-time data analysis



- Computer operational system LINUX
- MinKnow
- RAMPART (<https://github.com/artic-network/rampart>)

Primers dilution

1 Instructions for Primer Scheme dilution:

Note

The primer scheme dilution should be prepared in **Master Mix Hood** or **Clean Room**. To avoid cross-contamination make sure that your original stock reagents have no contact with RNA or any amplified DNA material.

If lyophilised each primer should be resuspended to **100 micromolar (μM)** **(Stock dilution 1)**

The primers from **Primer Scheme 2kb_v1 Pool 1** and **Primer Scheme 2kb_v1 Pool 2** are:

Primer Scheme 2kb_v1 Pool 1: F1, R1, F3, R3, F5, R5, F7, R7, F9, R9, F11, R11, F13, R13, F15, R15, F17, R17
(9 primers pairs)

Primer Scheme 2kb_v1 Pool 2: F2, R2, F4, R4, F6, R6, F8, R8, F10, R10, F12, R12, F14, R14, F16, R16
(8 primers pairs)

	Primer Scheme 2kb_v1 Pool 1		Primer Scheme 2kb_v1 Pool 2
Oligo name	Oligo sequence (5' to 3')	Oligo name	Oligo sequence (5' to 3')
hCoV_F1_2kb	ACCAACCAACTTTTCGATCTCT TGT	hCoV_F2_2kb	CTGCTCAA AATTCTGT GCGTGT
hCoV_R1_2kb	ACACCACCTGTAATGTAGGCC A	hCoV_R2_2kb	GGTCAGCA CCAAAAAT ACCAGCT
hCoV_F3_2kb	AGCGGACACAATCTTGCTAAA CA	hCoV_F4_2kb	TTGTGCAC TTATCTTAG CCTACTGT
hCoV_R3_2kb	GGTTGTCTGCTGTTGTCCACA A	hCoV_R4_2kb	TGCCAAAA ACCACTCT GCAACT



hCoV_F5 _2kb	CACTATTGCAACCTACTGTACT GGT	hCoV_F6 _2kb	GTACACTG ACTTTGCA ACATCAGC
hCoV_R5 _2kb	CGTGTGTCAGGGCGTAACTT T	hCoV_R6 _2kb	AACGGCAA TTCCAGTT TGAGCA
hCoV_F7 _2kb	TGTACGCTGCTGTTATAAATGG AGA	hCoV_F8 _2kb	TGGTACAA CATTACT TATGCATC AGC
hCoV_R7 _2kb	TTTGACAGCAGAATTGGCCCT T	hCoV_R8 _2kb	TGGGTGGT ATGTCTGA TCCCAA
hCoV_F9 _2kb	CCTTGACCAGGGCTTTAACTG C	hCoV_F1 0_2kb	AGCAAAAT GTTGGACT GAGACTGA
hCoV_R9 _2kb	ATCATCTACAAAACAGCCGGC C	hCoV_R1 0_2kb	CCAAGCAG GGTTACGT GTAAGG
hCoV_F1 1_2kb	GCTGAAATTGTTGACACTGTG AGT	hCoV_F1 2_2kb	TGCATTCC ACACACCA GCTTTT
hCoV_R1 1_2kb	AGCACCACCTAAATTGCAACG T	hCoV_R1 2_2kb	TAACAAAG GCTGTCCA CCATGC
hCoV_F1 3_2kb	ACAAAAGAAAATGACTCTAAA GAGGGTTT	hCoV_F1 4_2kb	CAGGCTGC GTTATAGC TTGGAA
hCoV_R1 3_2kb	TGTGCTACCGGCCTGATAGAT T	hCoV_R1 4_2kb	CATGACAA ATGGCAGG AGCAGT
hCoV_F1 5_2kb	TCAGAGTGTGTACTTGGACAA TCAA	hCoV_F1 6_2kb	ACGTGAGT CTTGTA ACCTTCTT TTT
hCoV_R1 5_2kb	GTACCGTTGGAATCTGCCATG G	hCoV_R1 6_2kb	ACTGCCAG TTGAATCT GAGGGT
hCoV_F1 7_2kb	GGAATCATCACAACCTGTAGCT GCA		
hCoV_R1 7_2kb	TAGGCAGCTCTCCCTAGCATT G		

Primer scheme to recover 2 kilobases amplicon of SARS-CoV-2 genome.



1.1 Prepare the **Primer Scheme 2kb_v1 Pool 1 and Pool 2** [M] 100 micromolar (μM) (stock dilution 2)

Add  20 μL of each primer [M] 100 micromolar (μM) (stock dilution 1) to a 1.5mL tube labelled as **Primer Scheme 2kb_v1 Pool 1**. The final volume will be  360 μL

Add  20 μL of each primer [M] 100 micromolar (μM) (stock dilution 1) to a 1.5mL tube labelled as **Primer Scheme 2kb_v1 Pool 2**. The final volume will be  320 μL

1.2 Prepare the **Primer Scheme 2kb_v1 Pool 1 and Pool 2** [M] 10 micromolar (μM) (concentration to be used)

Add  20 μL of each primer [M] 100 micromolar (μM) of **Primer Scheme 2kb_v1 Pool 1** (stock dilution 2) to a 1.5mL tube labelled as **Primer Scheme 2kb_v1 Pool 1**
[M] 10 micromolar (μM)

Add  180 μL of water nuclease-free. The final volume will be  200 μL

Add  20 μL of each primer [M] 100 micromolar (μM) of **Primer Scheme 2kb_v1 Pool 2** (stock dilution 2) to a 1.5mL tube labelled as **Primer Scheme 2kb_v1 Pool 2**
[M] 10 micromolar (μM)

Add  180 μL of water nuclease-free. The final volume will be  200 μL

Master Mix for cDNA and PCR steps

30m

2 Instructions to prepare the Master Mix for cDNA and PCR steps

Note

You can save time if you prepare both Master Mix cDNA and PCR to be used on the same day.

Note

The master mix for cDNA and PCR step should be prepared in **Master Mix Hood** or **Clean Room**. To avoid cross-contamination make sure that your original stock reagents have no contact with RNA or any amplified DNA material.

**Note**

A **Negative Control** (H₂O nuclease free) should be included from cDNA step until the end.

Note

Keep the enzymes on ice and thaw the other reagents at room temperature before placing on ice.

2.1 Master Mix RT_1:

Prepare the following components in a 0.2mL 8-strip tube for the number of samples that will be tested (positive samples + a negative control)

VOLUME COMPONENT

 1 µL	50µM random hexamers
 1 µL	10mM dNTPs mix (10mM each)

2.2 Master Mix RT_2:

Prepare the following components in a 1.5mL tube and keep the Master Mix2-RT on ice. (7uL per sample)

VOLUME COMPONENT

 4 µL	5x SSIV Buffer
 1 µL	100mM DTT
 1 µL	RNaseOUT RNase Inhibitor
 1 µL	SSIV Reverse transcriptase

2.3 Master Mix PCR Pool 1 and Pool 2:

Prepare the following components in two 1.5mL tubes and keep the Master Mix PCR Pool 1 and Pool 2 on ice

VOLUME Pool1	VOLUME Pool 2	COMPONENT
 5 µL	 5 µL	5X Q5 Reaction Buffer

 10 μL 10 μL

10 mM dNTPs

 0.25 μL 0.25 μL

Q5 Hot Start DNA Polymerase

 3.0 μL 3.0 μL Primer Pool 1 or 2 (10 micromolar (μM)) 4.25 μL 4.25 μL H_2O Nuclease free

Mix the master mix by inversion several times, briefly spin to collect the contents at the bottom of the tube.

Dispense 22.5 μL per tube 0.2mL 8-strip PCR tubes Pool 1 and Pool 2

Note

Label the side of the tubes, not the lids as the marker may be removed by the heat in the PCR machine.

cDNA

1h 30m

3 Instructions for the cDNA step:

Note

This step should be conducted in the pre PCR area.

Note

Keep all the Master Mix (cDNA_2 and PCR) in the fridge.

3.1 Set up the thermocycler for the following condition:

 65 $^{\circ}\text{C}$

3.2 Spin down the **Master Mix RT_1**;

3.3 Add 11 μL RNA to each 0.2 mL tube containing the **Master Mix RT_1**;



3.4 Mix by pipetting; and pulse centrifuge the tubes to collect the contents at the bottom of the tube.

3.5 Incubate the reaction for 65 °C 00:05:00

5m

3.6 Once this step is completed add 7 µL of **Master Mix RT_2** in each tube

3.7 Mix by pipetting and pulse centrifuge the tubes to collect the contents at the bottom of the tube.

3.8 Incubate the reaction in the thermocycler for:

42 °C 00:50:00

70 °C 00:10:00

4 °C hold

1h

Note

The cDNA can be stored in -20 °C . If needed, it is a safe stop point.

Note

The remaining RNA should be stored in -80 °C

PCR

4 Instructions for the PCR step:

Note

This step should be conducted in the pre PCR area.

4.1 Set up the thermocycler for the following conditions:



1 cycle



98 °C



00:02:00

Heat Activation

35 cycles



98 °C



00:00:10

Denaturation



65 °C



00:05:00

Annealing

1 cycle



4 °C

Hold

- 4.2 Add  2.5 µL cDNA of each sample to each 0.2mL 8-strip PCR tube containing the **Master Mix PCR Pool 1** and **Master Mix PCR Pool 2**
- 4.3 Mix by pipetting and pulse centrifuge the tubes to collect the contents at the bottom of the tube.
- 4.4 Incubate in the thermocycler following the conditions described in **substep 4.1**

Clean-up

5 Instructions for the DNA purification using magnetic beads AMPURE

Note

This step should be conducted in the PCR room

Note

Keep the Ampure beads and Qubit standards in room temperature  00:15:00 before start.

Note

Prepare FRESH  80 % (v/v) ethanol. Do not use  80 % (v/v) Ethanol prepared in the previous day.



- 6 After the RT-PCR, Pool 1 and Pool 2 can be mixed (final volume  50 μL)
- 7 Add an equal volume of AmpureXP PCR Clean-up beads ( 50 μL) to the tube (ratio of 1:1 of Ampure beads).
- 8 Mix gently by either flicking or pipetting 8-10 times.

Note

If long reads (2 Kb) avoid the vortex
- 9 Incubate for  00:05:00 at room temperature.
- 10 Pulse centrifuge the tubes to remove any beads or solution from the lid or side of the tube.
- 11 Place on a magnetic rack and incubate for  00:02:00 or until the beads have pelleted against the magnet and the solution is completely clear.
- 12 Carefully remove and discard the solution, being careful not to displace the bead pellet.
- 13 Add  200 μL of fresh room-temperature  80 % (v/v) Ethanol to the pellet.
- 14 Incubate for  00:01:00 .
- 15 Carefully remove and discard Ethanol, being careful not to displace the bead pellet.
- 16 Repeat Ethanol wash steps 13-15 to wash the pellet again and continue from step 17.
- 17 Briefly pulse centrifuge the pellet and carefully remove as much ethanol as possible using a  10 μL tip.



- 18 Allow the pellet to dry for 00:02:00 , being careful not to over-dry (if the pellet is cracking, then it is too dry). Pellet should appear opaque and slightly shiny.
- 19 Resuspend the pellet thoroughly in 32 μL of water, and incubate for 00:02:00
- 20 Pulse centrifuge to remove content in the lid.
- 21 Place on magnet and CAREFULLY remove water and transfer 32 μL to a clean 1.5mL Eppendorf tube.

Note

MAKE SURE that no beads are transferred into this tube. In some cases, a pulse centrifugation can be used to pellet residual beads.

Quality Control (QC)

22 Instructions to measure the amount of DNA

Note

Quantify 2 μL of the amplicon library using the Qubit fluorometer following the dsDNA protocol.

Note

To avoid any cross-contamination, we recommend that you remove the total amount of working solution required for your samples and standards from the working solution bottle and then add the required volume to the appropriate tubes instead of pipetting directly from the bottle to each tube.

- 23 Set up the required number of 0.5mL tubes for standards and samples. The Qubit™ 1X dsDNA HS Assay requires 2 standards.



- 24 Label the tube lids. Do not label the side of the tube as this could interfere with the sample read. Label the lid of each standard tube correctly. Calibration of the Qubit™ Fluorometer requires the standards to be inserted into the instrument in the right order.
- 25 Add the Qubit™ 1X dsDNA 1X buffer to each tube standard tube ( 190 µL) and each sample tube ( 198 µL)
- 26 Add  10 µL of each Qubit™ standards 1 and 2 to the appropriate tube.
- 27 Add  2 µL of each sample to the appropriate tube
- 28 Vortex all tubes and incubate at room temperature for  00:02:00 , then proceed to “Read standards and samples”.
- 29 Carefully record all results to perform the DNA normalisation to prepare the library.

Normalisation

30m

30 Instructions to normalise the DNA to prepare the library

For the barcoding step is needed  12.5 µL of DNA in a concentration of 60ng (long reads) per sample.

Note

For an efficient barcoding step, we observe that DNA in the barcoding step should range of 25 to 50 fmol (2kb). Then, we are using 60ng per sample.

Note

This is a safe stop point.

End-prep and barcoding Master Mix

31 Instructions to prepare the End-prep and barcoding Master Mix

**Note**

The **End-prep and barcoding Master Mix** should be prepared in **Master Mix Hood** or **Clean Room**. To avoid cross-contamination make sure that your original stock reagents have no contact with RNA or any amplified DNA material.

31.1 Master Mix End-prep:

Prepare the following components in a 1.5mL tube and keep the Master Mix PCR on ice.

VOLUME COMPONENT

 1.75 µL Ultra II End Prep Reaction Buffer

 0.75 µL Ultra II End Prep Enzyme Mix

31.2 Master Mix barcoding:

Prepare the following components in a 1.5mL tube and keep the Master Mix PCR on ice.

VOLUME COMPONENT

 17.5 µL Ultra II Ligation Master Mix

 0.5 µL Ligation Enhancer

End-prep**32 Instructions to End-prep reaction****Note**

This is a 'one-pot ligation' protocol for native barcoded ligation libraries.

Note

This step should be conducted in the PCR room

33 Add  2.5 µL of **Master Mix End-prep** to each tube containing  12.5 µL of pre-normalised DNA (~ 60ng for 2 kb) and mix well by pipetting.



34 Incubate in a thermocycler at 20°C for 00:10:00 then 65°C for 00:05:00

35 Place on ice for 00:00:30

Barcoding

25m

36

Instructions to Barcoding reaction

Note

Use a SINGLE native barcode (NBXX) per biological sample.

Note

This step should be conducted in the PCR room

37 Add $2.5\ \mu\text{L}$ NBXX barcode to each tube containing $15\ \mu\text{L}$ DNA end-prepped.

38 Add $18\ \mu\text{L}$ of the barcoding mix to each tube and mix well by pipetting. The total volume will be $35.5\ \mu\text{L}$.

39 Incubate:

 20°C 00:15:00 70°C 00:10:00

Then place on ice.

Note

The 70°C incubation is to inactivate the DNA ligase to prevent barcode cross-ligation when reactions are pooled in the next step

25m



Pooling and clean-up

25m

40 Instructions to pool all samples and perform a clean-up

Pool all barcoded samples together into a clean 1.5 ml Eppendorf tube.  35 μL per sample

Note

If the number of samples processed is more than 20 samples this pooling needs to be done in a 2.0mL Eppendorf tube.

41 Add a proportion 1:1 of AMPURE beads in the barcoded DNA pooled.
If necessary measure the volume of the above reaction and add the same volume of AMPURE beads, to get a 1:1 solution.

42 Incubate for  00:05:00 in the HulaMixer.

43 Spin down the liquid and place on a magnet rack for  00:03:00 or until clear.

44 Remove all the solutions without touch in the pellet

45 Add  500 μL of [M] 80 % (v/v) ethanol to the tube still on the magnetic rack to wash.

46 Remove the tube from the magnet rack and remove and turn 180° and place the tube again in the magnetic rack.

47 Remove and discard [M] 80 % (v/v) ethanol without disturbing the pellet.

48 Repeat steps 45 and 47 and after continue from step 49.



49 Spin down and remove residual [M] 80 % (v/v) ethanol and air dry for ⌚ 00:02:00 .

2m

50 Resuspend in 🧴 32 µL EB.

51 Incubate off the magnetic rack for ⌚ 00:02:00 and after spin down.

2m

52 Replace the magnetic rack for ⌚ 00:02:00

53 Wait until clear, then carefully remove the solution and transfer to a clean 1.5 mL Eppendorf tube labeled such as the name of your processing file.

QC

25m

54 Remove 🧴 2 µL and assess concentration by Qubit as described in the previous section. Keep the records in your processing file.

Normalisation

25m

55 Dilute 100-200 fmol (~ 150ng for 2kb) pooled sample to 🧴 30 µL in Elution Buffer (EB).

Adapter ligation

25m

56 Set up the following adapter ligation reaction in a 1.5mL tube:

VOLUME	COMPONENT
--------	-----------

🧴 30 µL	Cleaned-up barcoded amplicon pools (100-200 fmol)
---------	---

🧴 10 µL	NEBNext Quick Ligation Reaction Buffer (5X)
---------	---

🧴 5 µL	AMII Adapter mix II
--------	---------------------

🧴 5 µL	Quick T4 DNA Ligase
--------	---------------------

57 Incubate at RT for ⌚ 00:30:00



Note

Remove the **SFB** from the freezer and let equilibrate to room temperature to be used in the next step

Clean-up

25m

58

Clean-up

After 00:30:00 incubation add 50 μL Ampure beads (1x the volume of the total reaction volume)

59

30 μL Incubate for 00:05:00

60

Spin down.

61

Place on a magnetic rack until clear.

62

Remove supernatant.

63

Add 200 μL **SFB**. Remove and turn the tube in the magnetic rack.

Safety information

CAUTION: **DO NOT USE** 80 % (v/v) ETHANOL

64

Place on a magnetic rack until clear.

65

Remove supernatant.



66 Repeat **SFB** wash

67 Spin down and remove residual SFB .

Note

SFB is used for short fragments < 3kb.
LFB is used just for long fragments > 3Kb.

68 Add  14 μL EB and resuspend by flicking.

69 Incubate at RT for  00:02:00

70 Place on a magnetic rack.

71 Carefully transfer the solution to a clean 1.5 mL Eppendorf tube.

QC

25m

72 Remove  2 μL and assess concentration by Qubit fluorometer- recovery aim 50-100 fmol, 61.80 - 123.6 ng for 2Kb amplicons

Note

The library can be now stored at 4°C overnight if required, but for best results, proceed immediately to sequencing.

Testing the flow cell

25m

73



Note

During this testing to save time you can thaw the following reagents at room temperature before placing on ice: Sequencing buffer (SQB); Loading beads (LB); Flush buffer (FB); and Flush tether (FLT). They will be used in the next step

Note

Choose a flow cell, record the name of the flow cell on your working sheet

- 74 Insert the flow cell in the MinION device or GridION.
- 75 Test the flow cell using the MinKnow software to observe the number of active pores, keep this record on your working sheet.
- 76 Select the flowcell ticking the box
- 77 Click "check flowcell"
- 78 Click "start test".

Loading the flow cell

25m

- 79 For this step please follow the protocol described by Josh Quick below:

Citation

Josh Quick (2026). Priming and loading a MinION flowcell.

dx.doi.org/10.17504/protocols.io.7q5hmy6

LINK



MinKnow software

25m

- 80 Double-click the MinKNOW icon located on the desktop to open the MinKNOW software.
- 81 If your MinION was disconnected from the computer, plug it back in.
- 82 Choose the following flow cell type from the selector box: FLO-MIN106 : R9.4.1 flow cell
- 83 Then mark the flow cell as Selected.
- 84 Click the New Experiment button at the bottom left of the screen.
- 85 On the new experiment popup screen select the running parameters for your experiment from the individual tabs:

Experiment

On the New experiment popup screen, select the running parameters for your experiment from the individual tabs

Experiment: Name the run in the experiment field, leave the sample field blank.

Kit: Select LSK109. Do not select barcoding kits.

Run Options: Set the run length to 12 hours (you can stop the run once sufficient data has been collected as determined using RAMPART software).

Basecalling: Leave base calling turned but select 'high accuracy basecalling'.

Click 'Start run'.

Wash a flow cell

40m

- 86 **Washing the flow cell:**

Note

This step should be performed to reuse the flow cell after a previous run.



Note

The flow cell should be washed on the same day or on the following day of the run. Do not wait too much time to wash the Flow Cell.

For this step please follow the protocol described by Kirstyn Brunker bellow:

Citation

Kirstyn Brunker (2026). Washing a MinION flowcell.

[dx.doi.org/10.17504/protocols.io.bddzi276](https://doi.org/10.17504/protocols.io.bddzi276)

LINK

Citations

Quick J, Grubaugh ND, Pullan ST, Claro IM, Smith AD, Gangavarapu K, Oliveira G, Robles-Sikisaka R, Rogers TF, Beutler NA, Burton DR, Lewis-Ximenez LL, de Jesus JG, Giovanetti M, Hill SC, Black A, Bedford T, Carroll MW, Nunes M, Alcantara LC Jr, Sabino EC, Baylis SA, Faria NR, Loose M, Simpson JT, Pybus OG, Andersen KG, Loman NJ. Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples.

<https://doi.org/10.1038/nprot.2017.066>

Step 79

Josh Quick. Priming and loading a MinION flowcell

[dx.doi.org/10.17504/protocols.io.7q5hmy6](https://doi.org/10.17504/protocols.io.7q5hmy6)

Step 86

Kirstyn Brunker. Washing a MinION flowcell

[dx.doi.org/10.17504/protocols.io.bddzi276](https://doi.org/10.17504/protocols.io.bddzi276)