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ARTIC SARS-CoV-2 sequencing protocol v4 (LSK114) V.4

Version 1 is forked from Ebola virus sequencing protocol

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We use this protocol and it's working

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Abstract

Amplicon sequencing protocol for SARS-CoV-2 v4 (LSK114)

We thank the ARTIC network, Oxford Nanopore Technologies, New England Biolabs, BCCDC, COG-UK, CanCOGen and protocols.io commenters for their assistance developing this protocol.

Changes in this version:

-Up to 95 samples per run with EXP-NBD196 native barcode kit
-Substitution of SuperScript IV for LunaScript RT SuperMix and reaction volume reduced to 10 uL.
-Substitution of Ultra II Ligation Module for Blunt/TA Ligase Master Mix and reaction volume reduced to 10 µL.
-Native barcode ligation reaction volume reduced to 10 uL.
-SFB wash volume reduced.

Materials

	Component	Supplier	Part number
	ARTIC nCoV-2019 V3 panel (100uM)	IDT	See links below
	LunaScript RT SuperMix Kit	NEB	E3010
	Q5 Hot Start HF Polymerase or	NEB	M0493
	Q5 Hot Start High-Fidelity 2X Master Mix	NEB	M0494
	dNTP Solution Mix (10 mM ea.)	NEB	N0447
	Nuclease-free water (100 mL)	NEB	B1500
	NEBNext Ultra II End Repair/dA-tailing module	NEB	E7546
	Blunt/TA Ligase Master Mix	NEB	M0367
	Native Barcoding Expansion Kit 1-12 and/or	ONT	EXP-NBD104
	Native Barcoding Expansion Kit 13-24 or	ONT	EXP-NBD114
	Native Barcoding Expansion Kit 96	ONT	EXP-NBD196
	AMPure XP beads	Beckman	A63881
	NEBNext Quick Ligation Module	NEB	E6056S
	Sequencing Auxiliary Vials	ONT	EXP-AUX001
	Short Fragment Buffer Expansion Kit	ONT	EXP-SFB001
	Qubit dsDNA HS Assay Kit	Thermo	Q32854
	Flow Cell Priming Kit	ONT	EXP-FLP002
	Flow Cell Wash Kit (optional)	ONT	EXP-WSH003

	R9.4.1 flow cells	ONT	FLO-MIN106

IDT premixed **ARTIC nCoV-2019 V3 panel** or order oligos **individually**.

Before start

Prepare between 11 and 95 RNA samples plus 1 negative control using this protocol.

cDNA preparation

30m

1 Prepare between 11 and 95 RNA samples plus 1 negative control of nuclease-free water per library. If previously frozen, mix by briefly vortexing and pulse spin to collect liquid. Keep samples on ice at all times.

Note

At least 11 samples are required to have sufficient material to load on the sequencer at the end. If you process >23 you will need the EXP-NBD196 expansion kit.
N.B. If you are processing <11 samples, the quantities of DNA used downstream can be increased to compensate (see Section 11, Native Barcoding).

Note

A positive control can also be included which may be a synthetic RNA constructs or high-titre clinical sample which can be diluted. This can help monitor run performance.

2 Mix the following components in a PCR strip-tubes/plate. Gently mix by pipetting and pulse spin the tube to collect liquid.

	Component	Volume
	LunaScript RT SuperMix (5X)	2 µL
	Template RNA	8 µL
	Total	10 µL

Note

Viral RNA input from a clinical sample should be between Ct 18-35. If Ct is between 12-15, then dilute the sample 100-fold in water, if between 15-18 then dilute 10-fold in water. This will reduce the likelihood of PCR-inhibition.

Note

To prevent pre-PCR contamination the mastermix should be added to the PCR strip-tubes/plate in the **mastermix** cabinet which should should be cleaned with decontamination wipes and UV sterilised before and after use.

RNA samples should be added in the **extraction/sample addition** cabinet which should should be cleaned with decontamination wipes and UV sterilised before and after use.

3 Incubate the reaction as follows:

25 °C for 00:02:00
55 °C for 00:10:00
95 °C for 00:01:00
Hold at 4 °C

Primer pool preparation (optional) 2h

4 If making up primer pools from individual oligos fully resuspend lyophilised oligos in 1xTE to a concentration of [M] 100 micromolar (µM) , vortex thoroughly and spin down.

Note

If using IDT ARTIC nCoV-2019 V5.3.2 Panel ([M] 100 micromolar (µM)) skip to step 6.

5 Sort all odd regions primers into one or more tube racks. Add 5 µL of each odd region primer to a 1.5 mL Eppendorf tube labelled "Pool 1 ([M] 100 micromolar (µM))". Repeat the process for all even region primers for Pool 2. These are your [M] 100 micromolar (µM) stocks of each primer pool.

Note

Primers should be diluted and pooled in the **mastermix** cabinet which should be cleaned with decontamination wipes and UV sterilised before and after use.

Note

For more information see Figure 2 in;

Quick, J. et al. Multiplex PCR method for MinION and Illumina sequencing of Zika and other virus genomes directly from clinical samples. Nat Protoc 12, 1261–1276 (2017). https://doi.org/10.1038/nprot.2017.066

6 Dilute [M] 100 micromolar (µM) pools 1:10 in molecular grade water, to generate [M] 10 micromolar (µM) primer stocks.

Note

Primers are used at a final concentration of [M] 15 nanomolar (nM) per primer. In this case V3 pools have 110 primers in pool 1 and 108 primers in pool 2. so the requirement is ~ 4 µL primer pool ([M] 10 micromolar (µM)) per 25 µL reaction.

Note

Make up multiple 100 µL aliquots of [M] 10 micromolar (µM) primer dilutions and freeze them in case of degradation or contamination.

Multiplex PCR

4h

7 Set up the two PCR reactions per sample as follows in strip-tubes or plates. Gently mix by pipetting and pulse spin the tube to collect liquid at the bottom of the tube.

	Component	Reaction 1	Reaction 2
	5X Q5 Reaction Buffer	5 µL	5 µL
	10 mM dNTPs	0.5 µL	0.5 µL
	Q5 Hot Start DNA Polymerase	0.25 µL	0.25 µL
	V3 Pool 1 (10µM)	4 µL	0 µL
	V3 Pool 2 (10µM)	0 µL	4 µL

	Nuclease-free water	12.75 µL	12.75 µL
	Total	22.5 µL	22.5 µL

For M0493

or

	Component	Reaction 1	Reaction 2
	Q5 Hot Start High-Fidelity 2X Master Mix	12.5 µL	12.5 µL
	V3 Pool 1 (10µM)	4 µL	0 µL
	V3 Pool 2 (10µM)	0 µL	4 µL
	Nuclease-free water	6 µL	6 µL
	Total	22.5 µL	22.5 µL

For M0494

Note

Q5 Hot Start High-Fidelity 2X Master Mix can also be used instead of the component kit. Half-scale PCR reactions can also be used to save costs as you will only require 2.5 µL for downstream steps.

Note

To prevent pre-PCR contamination the mastermix for each pool should be made up in the **mastermix** cabinet which should should be cleaned with decontamination wipes and UV sterilised before and after use and aliquoted into PCR strip-tubes/plate

8 Add 2.5 µL cDNA to each of the PCR reactions, gently mix by pipetting and pulse spin the tube to collect liquid at the bottom of the tube.

Note

Up to 5 µL cDNA can be added to each PCR reaction (in place of nuclease-free water) to improve amplification of low titre samples. Using 5 µL cDNA will require a 20 µL cDNA reaction and may be more likely to cause inhibition so use cautiously.

Note

cDNA should be added in the **extraction and sample addition** cabinet which should should be cleaned with decontamination wipes and UV sterilised before and after use.

9 0 µL Set-up the following program on the thermal cycler:

Step	Temperature	Time	Cycles
Heat Activation	98 °C	00:00:30	1
Denaturation	98 °C	00:00:15	25-35
Annealing	65 °C	00:05:00	25-35
Hold	4 °C	Indefinite	1

Note

Cycle number should be 25 for Ct 18-21 up to a maximum of 35 cycles for Ct 35.

Note

Thermocycler calibration can vary instrument to instrument. If you see amplicon 64 dropout then decrease the annealing/extension temperature to 63 °C. Denaturation temperature of 95 °C can also be used and may slightly increase PCR yields.

9.1 **Optional step**: If you wish you can check the DNA concentration of your reactions before proceeding, to determine successful amplification (or failure in the case of the negative control). If you are processing many samples, to save time, you can check the concentration of a few samples to check amplification success. In our experience, reactions are typically around 80-100ng/μL. If your samples are <50ng/μL you can double the amount used in the next step. We recommend quantifying DNA with a fluorometer, such as a Qubit or Quantus.

PCR dilution

10m

10 Label strip-tubes/plate and combine the following volumes of each PCR reaction for 10 μL each sample:

	Component	Volume
	Pool 1 PCR reaction	2.5 μL
	Pool 2 PCR reaction	2.5 μL
	Nuclease-free water	45 μL
	Total	50 μL

Note

The PCR post-clean up concentration is typically around [M] 100 ng/μL. This means we can pool them without quantification/normalisation to make a significant time saving. If you require very even barcode representation perform clean-up and normalise to [M] 10 ng/μL then continue.

Note

Amplicons should be added in the **post-PCR** cabinet which should should be cleaned with decontamination wipes and UV sterilised before and after use.

Native barocoding

2h

11 Barcode the amplicon pools using the one-pot native barcoding approach.

Protocol

NAME

One-pot native barcoding of amplicons v3 (LoCost)

CREATED BY

Josh Quick

PREVIEW

11.1 In a new PCR strip-tube/plate set up the following reaction for each sample:

	Component	Volume
	PCR dilution from previous step	3.3 µL
	Ultra II End Prep Reaction Buffer	1.2 µL
	Ultra II End Prep Enzyme Mix	0.5 µL
	Nuclease-free water	5 µL
	Total	10 µL

Note

Make a master mix of end-preparation reagents and nuclease-free water and aliquot into strip-tube/plate to improve reproducability.

11.2 Incubate at room temperature for 00:15:00

Incubate at 65 °C for 00:15:00

Incubate on ice for 00:01:00

11.3 In a new PCR strip-tube/plate set up the following reaction for each sample:

	Component	Volume
	End-preparation reaction mixture	0.75 µL
	NBXX barcode	1.25 µL

	Blunt/TA Ligase Master Mix	5 µL
	Nuclease-free water	3 µL
	Total	10 µL

Note

Use one native barcode from the EXP-NBD104 (1-12), EXP-NBD114 (13-24) or EXP-NBD196 per sample. Use 12 or more barcodes per library or there will be insufficient total material to achieve good yields.

11.4 Incubate at room temperature for 00:20:00

Incubate at 65 °C for 00:10:00

Incubate on ice for 00:01:00

Note

The 65°C incubation is to inactivate the DNA ligase to prevent barcode cross-ligation when reactions are pooled in the next step.

11.5 In a new 1.5 mL Eppendorf tube pool all one-pot barcoding reactions together.

Note

If processing 12-24 samples pool all 10 µL from each native barcoding reaction.
if processing 48 samples pool 5 µL from each native barcoding reaction.
If processing 96 samples pool 2.5 µL from each native barcoding reaction so as not to exceed a pool volume of 240 µL which would make the clean-up volume too large.

11.6 Add 0.4x volume of SPRI beads to the sample tube and mix gently by either flicking or pipetting. For example add 96 µL SPRI beads to 240 µL pooled one-pot barcoding reactions.

Note

0.4x volume of SPRI is sufficient to bind 400 bp amplicons in the presence of ligation buffer, do not use 1x as this will result in an excessive large bead pellet.

11.7 Mix by vortexing and pulse centrifuge to collect all liquid at the bottom of the tube. Incubate for 00:05:00 at room temperature.

11.8 Place on magnetic rack and incubate for 00:02:00 or until the beads have pelleted and the supernatant is completely clear. Carefully remove and discard the supernatant, being careful not to touch the bead pellet.

11.9 Add 250 µL SFB and resuspend beads completely by pipette mixing. Pulse centrifuge to collect all liquid at the bottom of the tube and place on the magnet. Remove supernatant and discard.

Note

SFB will remove excess adapter without damaging the adapter-protein complexes. Do not use 70% ethanol as in early clean-ups.

11.10 Repeat steps 11.9 to perform a second SFB wash. Pulse centrifuge and remove any residual SFB.

Note

You do not need to allow to air dry with SFB washes.

11.11 Add 200 µL of room-temperature [M] 70 % volume ethanol to bathe the pellet. Carefully remove and discard ethanol, being careful not to touch the bead pellet.

Note

Only perform 1x 70% ethanol wash

11.12 Pulse centrifuge to collect all liquid at the bottom of the tube and carefully remove as much residual ethanol as possible using a P10 pipette.

11.13 With the tube lid open incubate for 00:01:00 or until the pellet loses it's shine (if the pellet dries completely it will crack and become difficult to resuspend).

11.14 Resuspend pellet in 30 µL [M] 10 millimolar (mM) Tris pH 8.0, mix gently by either flicking or pipetting and incubate for 00:02:00 .

11.15 Place on magnet and transfer sample to a clean 1.5 mL Eppendorf tube ensuring no beads are transferred into this tube.

12 Quantify the barcoded amplicons using a fluorometer such as a Qubit or Quatus. Concentration will vary depending on number and Ct of samples and but you need about 30 ng total at this stage to achieve maximum run yield.

13 Set up the following Native Adapter (NA) ligation and clean-up with SFB.

14 Quantify the barcoded amplicons using a fluorometer such as a Qubit or Quatus. Concentration will vary depending on number and Ct of samples but 15 ng final library is usually required to acheive maximum run yield.

Note

Final library can be now be stored in [M] 10 millimolar (mM) Tris pH 8 at 4 °C for up to a week if needed otherwise proceed directly to MinION sequencing.

MinION sequencing

1d

15 Prime the flowcell and load 15 ng sequencing library onto the flowcell.

Note

From experience we know 15 ng is optimum loading input for short amplicons. Speed drop during the run indicates excessive library was loaded. Low run yield <20M reads indicates insufficient library.

16 Start the sequencing run using MinKNOW.

Protocol

NAME

Starting a MinION sequencing run using MinKNOW

CREATED BY

Josh Quick

PREVIEW

Note

If using Live basecalling ensure to turn on double-ended barcoding in the basecalling settings.

16.1 If required plug the MinION into the computer and wait for the MinION and flowcell to ben detected.

16.2 Choose flow cell 'FLO-MIN106' from the drop-down menu.

16.3 Then select the flowcell so a tick appears.

16.4 Click the 'New Experiment' button in the bottom left of the screen.

16.5 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: Selection: Select LSK109 as there is no option for native barcoding (NBD104).

Run Options: Set the run length to 6 hours (you can stop the run once sufficient data has been collected as determined using RAMPART).

Basecalling: Leave basecalling turned but select 'fast basecalling'.

Output: The number of files that MinKNOW will write to a single folder. By default this is set to 4000 but can be reduced to make RAMPART update more frequently.

Click 'Start run'.

16.6 Monitor the progress of the run using the MinKNOW interface.