



Version 3 ▼

Mar 15, 2021

NEBNext® ARTIC SARS-CoV-2 Companion Kit (Oxford Nanopore Technologies®) E7660 V.3

New England Biolabs¹¹New England Biolabs

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Works for me

dx.doi.org/10.17504/protocols.io.btcentite

Coronavirus Method Development Community

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SUBMIT TO PLOS ONE

ABSTRACT

This protocol details methods for the NEBNext® ARTIC SARS-CoV-2 Companion Kit (Oxford Nanopore Technologies®), NEB #E7660S/L 24/96 reactions.

EXTERNAL LINK

<https://www.neb.com/-/media/nebus/files/manuals/manuale7660.pdf?rev=48c42313dcb64b0dbb16c4bfd1563a27>

DOI

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EXTERNAL LINK

<https://www.neb.com/-/media/nebus/files/manuals/manuale7660.pdf?rev=48c42313dcb64b0dbb16c4bfd1563a27>

PROTOCOL CITATION

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KEYWORDS

NEBNext, NEB, ARTIC, SARS-CoV-2, Oxford, Nanopore

LICENSE

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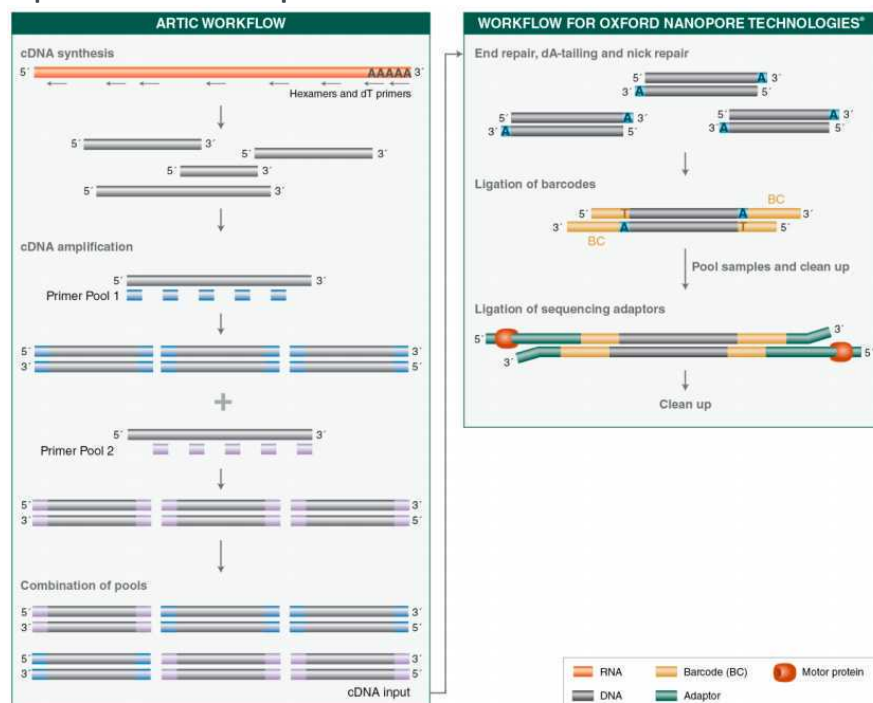
Overview

The NEBNext ARTIC SARS-CoV-2 Companion Library Prep Kit (Oxford Nanopore Technologies) contains the enzymes, buffers, beads and oligos required to convert a broad range of total RNA input amounts into targeted, high quality libraries for next-generation sequencing on the Oxford Nanopore platform. Primers targeting the human EDF1 and NEDD8 genes are supplied as optional internal controls. The fast, user-friendly workflow also has minimal hands-on time.

Each kit component must pass rigorous quality control standards, and for each new lot the entire set of reagents is functionally validated together by construction and sequencing of an indexed library on the Oxford Nanopore sequencing platform.

For larger volume requirements, customized and bulk packaging is available by purchasing through the OEM/Bulks department at NEB. Please contact OEM@neb.com for further information.

Figure 1. Workflow demonstrating the use of NEBNext ARTIC SARS-CoV-2 Companion Library Prep Kit for Oxford Nanopore.



MATERIALS TEXT

The Library Kit Includes

The volumes provided are sufficient for preparation of up to 24 barcoding reactions (NEB #E7660S, minimum 6 barcoding samples per run for total 4 runs) and 96 barcoding reactions (NEB #E7660L, minimum 24 barcoding samples per run for total 4 runs). If one plans to follow a different protocol, additional reagents can be purchased separately.

Package 1: Store at -20°C.

- (lilac) LunaScript® RT SuperMix (5X)
- (lilac) Q5® Hot Start High-Fidelity 2X Master Mix
- (green) NEBNext Ultra II End Prep Enzyme Mix
- (green) NEBNext Ultra II End Prep Reaction Buffer
- (red) Blunt/TA Ligase Master Mix
- (red) NEBNext Quick T4 Ligase
- (red) NEBNext Quick Ligation Reaction Buffer

(lilac) NEBNext ARTIC SARS-CoV-2 Primer Mix 1
 (lilac) NEBNext ARTIC SARS-CoV-2 Primer Mix 2
 (lilac) NEBNext ARTIC Human Control Primer Pairs 1
 (lilac) NEBNext ARTIC Human Control Primer Pairs 2
 (white) Nuclease-free water

Package 2: Store at room temperature. Do not freeze.

NEBNext Sample Purification Beads

Required Materials Not Included

- 80% Ethanol (freshly prepared)
- DNA LoBind Tubes (Eppendorf® #022431021)
- Oxford Nanopore Technologies Native Barcoding Expansion kits 1-12 (EXP-NBD104) and 13-24 (EXP-NBD114)
- Oxford Nanopore Technologies Ligation Sequencing Kit (SQK-LSK109)
- Oxford Nanopore Technologies SFB Expansion Kit (EXP-SFB001)
- Qubit® dsDNA HS Assay Kit (Thermo Fisher Scientific, Inc.® Q32851)
- Magnetic rack/stand (NEB #S1515, Alpaqua®, cat. #A001322 or equivalent)
- Thermal cycler
- Vortex Mixer
- Microcentrifuge
- Agilent® Bioanalyzer® or similar fragment analyzer and associated consumables (#4150 or #4200 TapeStation System)
- DNase RNase free PCR strip tubes (USA Scientific 1402-1708)
- 1.5 ml tube magnet stand (NEB #S1506)

Kit Components

NEB #E7660S Table of Components

A	B	C
NEB #	PRODUCT	VOLUME
E7651A	LunaScript RT SuperMix (5X)	0.048 ml
E7652A	Q5 Hot Start High-Fidelity 2X Master Mix	0.30 ml
E7661A	NEBNext Ultra II End Prep Enzyme Mix	0.018 ml
E7662A	NEBNext Ultra II End Prep Reaction Buffer	0.042 ml
E7663A	Blunt/TA Ligase Master Mix	0.24 ml
E7664A	NEBNext Quick T4 DNA Ligase	0.020 ml
E7665A	NEBNext Quick Ligation Reaction Buffer	0.040 ml
E7725A	NEBNext ARTIC SARS-CoV-2 Primer Mix 1	0.042 ml
E7726A	NEBNext ARTIC SARS-CoV-2 Primer Mix 2	0.042 ml
E7727A	NEBNext ARTIC Human Control Primer Pairs 1	0.007 ml
E7728A	NEBNext ARTIC Human Control Primer Pairs 2	0.007 ml
E7667A	Nuclease free-Water	1.50 ml
E7666S	NEBNext Sample Purification Beads	0.872 ml

NEB #E7660L Table of Components

A	B	C
NEB #	PRODUCT	VOLUME
E7651AA	LunaScript RT SuperMix (5X)	0.192 ml
E7652AA	Q5 Hot Start High-Fidelity 2X Master Mix	1.2 ml
E7661AA	NEBNext Ultra II End Prep Enzyme Mix	0.072 ml
E7662AA	NEBNext Ultra II End Prep Reaction Buffer	0.168 ml
E7663AA	Blunt/TA Ligase Master Mix	0.96 ml
E7664A	NEBNext Quick T4 DNA Ligase	0.020 ml
E7665A	NEBNext Quick Ligation Reaction Buffer	0.040 ml
E7725AA	NEBNext ARTIC SARS-CoV-2 Primer Mix 1	0.168 ml
E7726AA	NEBNext ARTIC SARS-CoV-2 Primer Mix 2	0.168 ml
E7727A	NEBNext ARTIC Human Control Primer Pairs 1	0.007 ml
E7728A	NEBNext ARTIC Human Control Primer Pairs 2	0.007 ml
E7667AA	Nuclease free-Water	4.7 ml
E7666L	NEBNext Sample Purification Beads	2.90 ml

NEBNext ARTIC Human Primers

A	B	C	D
PRIMER MIX	GENE	POSITION	PRIMERS
NEBNext ARTIC Human Control Primer Mix 1	EDF1	113 bp – 501 bp	GGCCAAATCCAAGCAGGCTA GTGTTTCATTTCCGCCTAGGC
NEBNext ARTIC Human Control Primer Mix 2	NEDD8	110 bp – 489 bp	AAAGTGAAGACGCTGACCGG GGGATCCTCACAGTCTCCCA

Detailed information for the ARTIC Human control primers can be found at: <https://doi.org/10.5281/zenodo.4495958>

NEBNext ARTIC SARS-CoV-2 Primers

NEBNext ARTIC SARS-CoV-2 Primers for SARS-CoV-2 genome amplification are based on hCoV-2019/nCoV-2019 Version 3 (v3) sequences with balanced primer concentrations. Sequence information can be found at:

https://github.com/joshquick/artic-ncov2019/blob/master/primer_schemes/nCoV-2019/V3/nCoV-2019.tsv

SAFETY WARNINGS

Please refer to Safety Data Sheets (SDS) for health and environmental hazards.

This product is intended for research purposes only. This product is not intended to be used for therapeutic or diagnostic purposes in humans or animals.

BEFORE STARTING

Note: The amount of RNA required for detection depends on the abundance of the RNA of interest. In general, we recommend, using > 10 copies of the (SARS-CoV-2) viral genome as input. In addition, we recommend setting up a no template control reaction and **all reactions are set-up in a hood**.

The presence of carry-over products can interfere with sequencing accuracy, particularly for low copy targets. Therefore, it is important to carry out the appropriate no template control (NTC) reactions to demonstrate that positive reactions are meaningful.

cDNA Synthesis

1 

Gently mix 10 times by pipetting and spin down the LunaScript RT SuperMix reagents (contains primers). Prepare the cDNA synthesis reaction as described below:

A	B
COMPONENT	VOLUME
RNA Sample*	8 µl
(lilac) LunaScript RT SuperMix	2 µl
<i>Total Volume</i>	10 µl

*Up to 0.5 µg total RNA can be used in a 10 µl reaction.



Flick the tube or pipet up and down to mix followed by a quick spin.



For no template controls, mix the following components:

A	B
COMPONENT	VOLUME
(white) Nuclease-free Water	8 µl
(lilac) LunaScript RT SuperMix	2 µl
<i>Total Volume</i>	10 µl



Flick the tube or pipet up and down to mix followed by a quick spin.



Incubate reactions in a thermocycler with lid temperature at 105°C with the following steps:

A	B	C	D
CYCLE STEP	TEMP	TIME	CYCLE
Primer Annealing	25°C	2 minutes	1
cDNA Synthesis	55°C	20 minutes	
Heat Inactivation	95°C	1 minute	
Hold	4°C	∞	

*Set heated lid to 105°C

Samples can be stored at -20 °C if they are not used immediately.

Targeted cDNA Amplification

6

4.5 µl cDNA input is recommended. If using less than 4.5 µl of cDNA, add nuclease-free water to a final volume of 4.5 µl. We recommend setting up the cDNA synthesis and cDNA amplification

reactions in different rooms to minimize cross-contamination of future reactions.

Use of the NEBNext ARTIC Human Control Primer Pairs 1 and 2 are optional. If used, the appropriate NEBNext ARTIC Human Control Primer Pairs and NEBNext ARTIC SARS-CoV-2 Primer Mix should be combined prior to use. More specifically, NEBNext ARTIC Human Control Primer Pairs 1 should be combined with NEBNext ARTIC SARS-CoV-2 Primer Mix 1 and NEBNext ARTIC Human Control Primer Pairs 2 with NEBNext ARTIC SARS-CoV-2 Primer Mix 2. Mixing directions are listed below.



Gently mix Q5 Hot Start High Fidelity 2X MM 10 times by pipetting and spin down reagents. Prepare the split pool amplification reactions as described below:

For Pool Set A:

If using the NEBNext ARTIC Human Primer Pairs and a 24 reaction kit, combine

▢ 0.7 µl NEBNext ARTIC Human Control Primer Pairs 1 with

▢ 42 µl NEBNext ARTIC SARS-CoV-2 Primer Mix 1, vortex and spin down reagents. If using a 96 reaction kit, combine ▢ 2.8 µl NEBNext ARTIC Human Control Primer Pairs 1 with

▢ 168 µl NEBNext ARTIC SARS-CoV-2 Primer Mix 1, vortex and spin down reagents. Use

▢ 1.75 µl combined mix for each Pool Set A reaction.

A	B
COMPONENT	VOLUME
cDNA (Step 5)	4.5 µl
(lilac) Q5 Hot Start High-Fidelity 2X MM	6.25 µl
NEBNext ARTIC SARS-CoV-2 Primer Mix 1*	1.75 µl
Total Volume	12.5 µl

** If using NEBNext ARTIC Human Control Primer Pairs 1, add 1.75 µl of the combined NEBNext ARTIC SARS-CoV-2 Primer Mix 1 and NEBNext ARTIC Human Control Primer Pairs 1

For Pool Set B:

If using the NEBNext ARTIC Human Control Primer Pairs and a 24 reaction kit, combine

▢ 0.7 µl NEBNext ARTIC Human Control Primer Pairs 2 with

▢ 42 µl NEBNext ARTIC SARS-CoV-2 Primer Mix 2, vortex and spin down reagents. If using 96 reaction kit, combine ▢ 2.8 µl NEBNext ARTIC Human Control Primer Pairs 2 with

▢ 168 µl NEBNext ARTIC SARS-CoV-2 Primer Mix 2. Use ▢ 1.75 µl combined mix for each Pool Set B reaction.

A	B
COMPONENT	VOLUME
cDNA (Step 5)	4.5 µl
(lilac) Q5 Hot Start High-Fidelity 2X MM	6.25 µl
NEBNext ARTIC SARS-CoV-2 Primer Mix 2*	1.75 µl
Total Volume	12.5 µl

* If using NEBNext Human Control Primer Pairs 2, add 1.75 µl of the combined NEBNext ARTIC SARS-CoV-2 Primer Mix 2 and NEBNext ARTIC Human Control Primer Pairs 2.

8 Flick the tube or pipet up and down to mix followed by a quick spin.

9  

Incubate reactions in a thermocycler* with the following steps:


A	B	C	D
CYCLE STEP	TEMP	TIME	CYCLES
Initial Denaturation	98°C	30 seconds	1
Denature	95°C	15 seconds	35
Annealing/Extension	63°C	5 minutes	
Hold	4°C	∞	1

* Set heated lid to 105°C.

Samples can be stored at  -20 °C if they are not used immediately.


Cleanup of cDNA Amplicons

- 10 If you prefer to omit the cleanup step, please follow the newer version of nCoV-2019 sequencing protocol v3 (LoCost) by following the link provided below, otherwise continue to Cleanup of cDNA Amplicons (step 10). <https://www.protocols.io/view/ncov-2019-sequencing-protocol-v3-locost-bh42j8ye/abstract>

SPRIselect or AMPure® XP Beads can be used as well. If using AMPure XP Beads, allow the beads to warm to  Room temperature for at least 30 minutes before use. These bead volumes may not work properly for a cleanup at a different step in the workflow. For cleanups of samples contained in different buffer conditions, the volumes may need to be experimentally determined.

- 11 For each sample, combine pool A and pool B PCR Reactions.
- 12 Vortex SPRIselect or NEBNext Sample Purification Beads to resuspend.


13 

Add  20 µl (0.8X) resuspended beads to the combined PCR reaction. Mix well by flicking the tube or pipetting up and down to mix and a very short 2-3 seconds quick centrifugation. Be sure to stop the centrifugation before the beads start to settle out.

14 




10m

Incubate samples at  **Room temperature** for  **00:10:00** .

- 15 Place the tubes on an appropriate magnetic stand to separate the beads from the supernatant. If necessary, quickly^{3s} spin the sample  **00:00:03** to collect the liquid from the sides of the tube before placing on the magnetic stand.
- 16 After 2 minutes (or when the solution is clear), carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.




Caution: do not discard the beads.


- 17  30s


Add  **200 µl 80% freshly prepared ethanol** to the tube while in the magnetic stand. Incubate at  **Room temperature** for  **00:00:30** , and then carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.

- 18  33s

Repeat previous step once for a total of two washes:


Add  **200 µl 80% freshly prepared ethanol** to the tube while in the magnetic stand. Incubate at  **Room temperature** for  **00:00:30** , and then carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.

Be sure to remove all visible liquid after the second wash. If necessary, briefly spin the tube for  00:00:03 , place back on the magnetic stand and remove traces of ethanol with a p10 pipette tip.



- 19 Air dry the beads for  **00:00:30** while the tube is on the magnetic stand with the lid open. 30s

Caution: Do not over-dry the beads. This may result in lower recovery of DNA. Elute the samples when the beads are still dark brown and glossy looking. When the beads turn lighter brown and start to crack, they are too dry.

- 20 


Remove the tube from the magnetic stand. Elute the DNA target from the beads by adding  **21 µl Nuclease-free water** .

- 21  10m

Mix well by flicking the tube or pipetting up and down to mix and followed by a very short centrifugation. Incubate for  **00:10:00** at  **Room temperature** . If necessary, quickly spin the sample to collect the liquid from the sides of

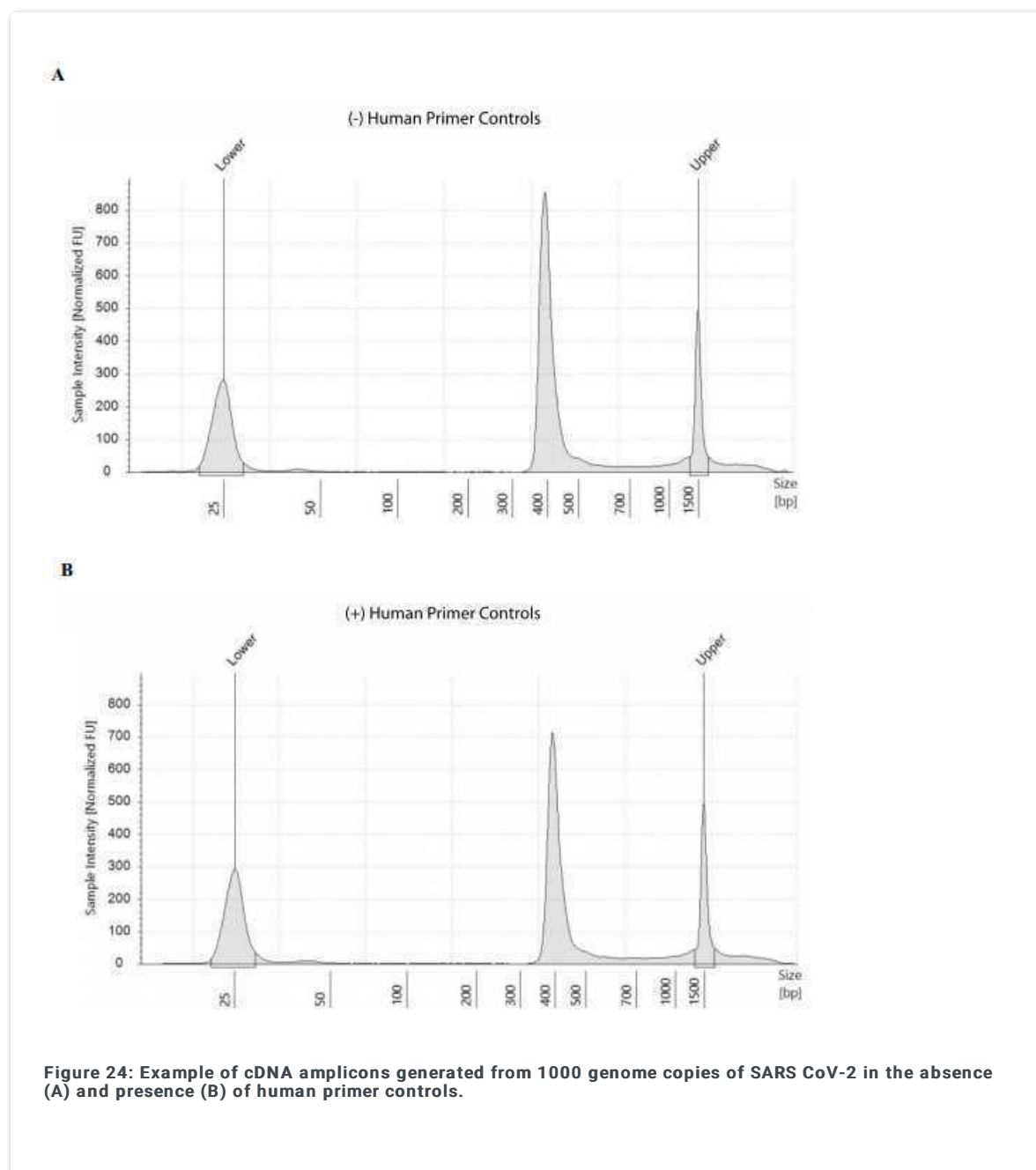
the tube or plate wells before placing back on the magnetic stand.

22 

Place the tube on the magnetic stand. After 2 minutes (or when the solution is clear), transfer  20 µl to PCR tubes.

23  

We recommend assessing cDNA concentrations with a Qubit fluorometer. Amplicons may also be run on a Bioanalyzer® or a TapeStation to confirm 400 bp size of amplicons.



Samples can be stored at  -20 °C if they are not used immediately

Samples can be stored at -20°C if they are not used immediately.

NEBNext End Prep

24 

Dilute each amplicon sample (Step 22) into 50 ng / $12.5\text{ }\mu\text{l}$ concentration using Nuclease-free water. Add the following components to a PCR tube (End Prep Reaction and Buffer can be pre-mixed and stable On ice for 4 hours):

A	B
COMPONENT	VOLUME
Targeted cDNA Amplicons (Step 22)	$12.5\text{ }\mu\text{l}$
(green) NEBNext Ultra II End Prep Reaction Buffer	$1.75\text{ }\mu\text{l}$
(green) NEBNext Ultra II End Prep Enzyme Mix	$0.75\text{ }\mu\text{l}$
Total Volume	$15\text{ }\mu\text{l}$

25 

Flick the tube or pipet up and down to mix the solution. Perform a quick spin to collect all liquid from the sides of the tube.

It is important to mix well. The presence of a small amount of bubbles will not interfere with performance.

26 

20m

Place in a thermocycler, with the heated lid set to $\geq 75^{\circ}\text{C}$, and run the following program:

$00:10:00$ @ 20°C

$00:10:00$ @ 65°C

Hold at 4°C

If necessary, samples can be stored at -20°C for a few days; however, a slight loss in yield (~20%) may be observed. We recommend continuing with barcode ligation before stopping.

Barcode Ligation

27 

Add the following components directly to a sterile nuclease-free PCR tube:

A	B
COMPONENT	VOLUME
(white) Nuclease-free water	6 µl
End-prepped DNA (Previous Step)	1.5 µl
Native Barcode*	2.5 µl
(red) Blunt/TA Ligase Master Mix**	10 µl
<i>Total Volume</i>	20 µl

* Native Barcodes are provided in Oxford Nanopore Technologies Native Barcoding Expansion 1-12 (EXP-NBD104) and 13-24 (EXP-NBD114)

** Mix the Blunt/TA Ligase Master Mix by pipetting up and down several times prior to adding to the reaction

28 

Flick the tube or pipet up and down to mix solution. Perform a quick spin to collect all liquid from the sides of the tube.

Caution: The Blunt/TA Ligase Master Mix is very viscous. Care should be taken to ensure adequate mixing of the ligation reaction, as incomplete mixing will result in reduced ligation efficiency. The presence of a small amount of bubbles will not interfere with performance.

29 

31m

Incubate at  **Room temperature** for  **00:20:00**

Incubate at  **65 °C** for  **00:10:00**.

Place  **On ice** for  **00:01:00**.

30 Pool all barcoded samples into one 1.5 ml DNA LoBind Tube.

Cleanup of Barcoded cDNA


31 The following section is for cleanup of the ligation reaction.


The volumes of SPRIselect or NEBNext Sample Purification Beads provided here are for use with the sample contained in the exact buffer at this step. AMPure XP Beads can be used as well. If using AMPure XP Beads, allow the beads to warm to  **Room temperature** for at least 30 minutes before use.

32 Vortex NEBNext Sample Purification Beads to resuspend.

33 

3s

Add 0.4X resuspended beads to pooled barcode samples (Step 30) (for example,  **192 µl of resuspended beads**

should be added to a pool of 24 barcoded samples where the sample volume is 480 µl). Mix well by flicking the tube. Perform a quick spin for  **00:00:03** to collect all liquid from the sides of the tube.

34



10m

Incubate samples on bench top for  **00:10:00** at  **Room temperature**.

35

Place the tube on a 1.5 ml magnetic stand (such as NEB S1506) to separate the beads from the supernatant. If necessary, quickly spin the sample to collect the liquid from the sides of the tube or plate wells before placing on the magnetic stand.

36



After 2 minutes (or when the solution is clear), carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.

Caution: do not discard the beads.

37



3s

Wash the beads by adding  **250 µl Short Fragment buffer (SFB)**. Flick the tube or pipet up and down to mix to resuspend pellet. If necessary, quickly spin the sample for  **00:00:03** to collect the liquid from the sides of the tube or plate wells before placing back on the magnetic stand.

38



Place the tube on an appropriate magnetic stand for 2 minutes (or until the solution is clear) to separate the beads from the supernatant. Remove the supernatant.

39



3s




Repeat previous 2 steps once for a total of two washes:

Wash the beads by adding  **250 µl Short Fragment buffer (SFB)**. Flick the tube or pipet up and down to mix to resuspend pellet. If necessary, quickly spin the sample for  **00:00:03** to collect the liquid from the sides of the tube or plate wells before placing back on the magnetic stand.

Place the tube on an appropriate magnetic stand for 2 minutes (or when the solution is clear) to separate the beads from the supernatant. Remove the supernatant.

Be sure to remove all visible liquid after the second wash. If necessary, briefly spin the tube, place back on the magnetic stand and remove traces of SFB with a p10 pipette tip


40

Add  **200 µl 80% freshly prepared ethanol** to the tube while on the magnetic stand. Incubate at  **Room temperature** for  **00:00:30**, and then carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.


30s


41

A quick spin and place the sample tube on the magnetic stand, remove any residual ethanol.



42 Air dry the beads for  **00:00:30** while the tube is on the magnetic stand with the lid open.


Caution: Do not over-dry the beads. This may result in lower recovery of DNA target. Elute the samples when the beads are still dark brown and glossy looking, but when all visible liquid has evaporated. When the beads turn lighter brown and start to crack, they are too dry.


43 

Remove the tube from the magnetic stand. Elute the DNA target from the beads by adding  **33 µl Nuclease-free water**.

44 

Resuspend the pellet by flicking the tube or pipetting up and down to mix. Incubate for at least 2 minutes at  **Room temperature**. If necessary, quickly spin the sample for  **00:00:03** to collect the liquid from the sides of the tube before placing back on the magnetic stand.

45 


Place the tube on the magnetic stand. After 2 minutes (or when the solution is clear), transfer  **32 µl** to a new 1.5 ml Eppendorf DNA LoBind Tube or PCR tube.

46  

We recommend assessing cDNA concentrations with a Qubit fluorometer. Use 1 µl for the Qubit fluorometer.

Samples can be stored at  -20 °C if they are not used immediately.

Adapter Ligation

47 

Add the following components into a 1.5 ml Eppendorf DNA LoBind Tube:


A	B
COMPONENT	VOLUME
Native barcoded and purified DNA (45)	30 µl
Adapter Mix II (AMII)**	5 µl
(red) NEBNext Quick Ligation Reaction Buffer	10 µl
(red) NEBNext Quick T4 Ligase	5 µl
<i>Total Volume</i>	50 µl

* Mix the NEBNext Quick Ligation Reaction Buffer by pipetting up and down several times prior to adding to the reaction.

** Adapter Mix II is provided by Oxford Nanopore Technologies Native Barcoding Expansion 1-12 (EXP-NBD104), 13-24 (EXP-NBD114) and 1-96 (EXP-NBD-196) kits.

48  

3s

Flick the tube or pipet up and down to mix solution. Perform a quick spin for  **00:00:03** to collect all liquid from the sides of the tube.

Caution: The NEBNext Quick Ligation Buffer is viscous. Care should be taken to ensure adequate mixing of the ligation reaction, as incomplete mixing will result in reduced ligation efficiency. The presence of a small amount of bubbles will not interfere with performance.

49 


20m

Incubate at  **25 °C** or at  **Room temperature** for  **00:20:00**.


50 Proceed to Cleanup of Adapter-ligated cDNA in the next section.

Cleanup of Adapter Ligated DNA 20m 3s



51

The volumes of SPRIselect or NEBNext Sample Purification Beads provided here are for use with the sample contained in the exact buffer at this step. AMPure XP beads can be used as well. If using AMPure XP beads, allow the beads to warm to  **Room temperature for at least 30 minutes before use. These volumes may not work properly for a cleanup at a different step in the workflow.**

52 Vortex NEBNext Sample Purification Beads to resuspend.

53  

3s

Add  **50 µl (1X) resuspended beads** to the ligation mix. Mix well by flicking the tube or pipetting up and down to mix followed by a quick spin for  **00:00:03**.

54 

10m


Incubate samples for  **00:10:00** at  **Room temperature**.

55 Place the tube on an appropriate magnetic stand to separate the beads from the supernatant. If necessary, quickly spin the sample to collect the liquid from the sides of the tube or plate wells before placing on the magnetic stand.

- 56 After 2 minutes (or when the solution is clear), carefully remove and discard the supernatant. Be careful not to disturb the beads that contain DNA targets.

Caution: do not discard the beads.


- 57 

Wash the beads by adding  **250 µl Short Fragment Buffer (SFB)** . Flick the tube or pipet up and down to mix to resuspend pellet. If necessary, quickly spin the sample to collect the liquid from the sides of the tube or plate wells before placing back on the magnetic stand. Place the tube on an appropriate magnetic stand.

- 58 Wait for 2 minutes (or until the solution is clear) to separate the beads from the supernatant. Remove the supernatant.

- 59 

Repeat previous 2 steps once for a total of two washes:


Wash the beads by adding  **250 µl Short Fragment Buffer (SFB)** . Flick the tube or pipet up and down to mix to resuspend pellet. If necessary, quickly spin the sample to collect the liquid from the sides of the tube or plate wells before placing back on the magnetic stand. Place the tube on an appropriate magnetic stand.

Wait for 2 minutes (or when the solution is clear) to separate the beads from the supernatant. Remove the supernatant.

Be sure to remove all visible liquid after the second wash. If necessary, briefly spin the tube/plate, place back on the magnet and remove traces of SFB with a p10 pipette tip.



- 60 

Remove the tube from the magnetic stand. Elute the DNA target from the beads by adding


 **15 µl Elution Buffer (EB)** provided in SQK-LSK109 kit from Oxford Nanopore.

- 61 


10m

Resuspend the pellet well in EB buffer by flicking the tube or pipetting up and down to mix. Incubate for  **00:10:00** at  **Room temperature** . If necessary, quickly spin the sample to collect the liquid from the sides of the tube or plate wells before placing back on the magnetic stand.

- 62 

Place the tube/plate on the magnetic stand. After 2 minutes (or when the solution is clear), transfer  **15 µl** to a new DNA LoBind tube.

- 63 

Use Qubit to quantify  **1 µl DNA sample** . Follow Oxford Nanopore Protocol SQK-LSK109 to prepare MinION® flow cell and DNA library sequencing mix using up to 15 ng adapter-ligated cDNA sample (previous step).

