



JAN 09, 2024

T-4 TICK TESTING

REDI-NET
Consortium¹

¹REDI-NET Consortium



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University of Notre Dame, Naval Medical Research Center, Wal...

DISCLAIMER

OPEN ACCESS



DOI:
dx.doi.org/10.17504/protocols.io.kxygx3ozzg8j/v1

Protocol Citation: REDI-NET Consortium 2024. T-4 TICK TESTING. **protocols.io** <https://dx.doi.org/10.17504/protocols.io.kxygx3ozzg8j/v1>

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Protocol status: Working
We use this protocol and it's working

Created: Oct 26, 2023

Last Modified: Jan 09, 2024

This work is supported by the US Army Medical Research and Development Command under Contract No.W81XWH-21-C-0001, W81XWH-22-C-0093 and HT9425-23-C-0059. The views, opinions and/or findings contained in this report are those of the author(s) and should not be construed as an official Department of the Army or Navy position, policy or decision unless so designated by other documentation.

ABSTRACT

This protocol details standard operating procedure for tick testing.

GUIDELINES

OBJECTIVE

To outline the procedures for properly using the Oxford Nanopore Sequencing platforms (GridION or MinION Mk1C) to sequence gDNA and TNA extracted from collected tick samples.

SUMMARY/SCOPE

This SOP provides guidance on procedures of Oxford Nanopore sequencing to generate sequencing reads for downstream data analysis and pathogen detection.

RESPONSIBLE PERSON

Principal Investigator, Study Coordinator, Entomology Component Lead, Managers

PROTOCOL integer ID:
89956

Keywords: SEQUENCING
LIBRARY PREPARATION, ONT
Native Barcoding Kit v14,
Total nucleic acid
sequencing, gDNA
sequencing, cDNA
sequencing, Whole genome
shotgun sequencing

Funders

Acknowledgement:

USAMRAA
Grant ID: W81XWH-21-C-
0001,

USAMRAA
Grant ID: W81XWH-22-C-
0093

USAMRAA
Grant ID: HT9425-23-C-0059

Note

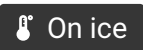
NOTE: All study procedures must be conducted in compliance with national and local policies for the prevention and control of COVID-19 infection.

MAINTENANCE OF EQUIPMENT

CAUTION ON RNA HANDLING:

1. RNases are very stable and difficult to inactivate and only minute amounts are sufficient to destroy RNA.
2. Care should be taken to avoid inadvertently introducing RNases into the samples during or after the purification procedure.
3. Clean the work surfaces with RNA Zap to remove nucleases, then wipe the surfaces with 70% to 100% molecular biology grade ethanol to remove additional contaminants.

HANDLING ENZYMATIC REACTIONS

Reagents containing enzymes should be handled  before mixed and transferred to the assigned activation temperature.

REFERENCES

REDI-NET Overview Summary

Double-stranded cDNA synthesis (NEB first and second strand cDNA synthesis protocols):

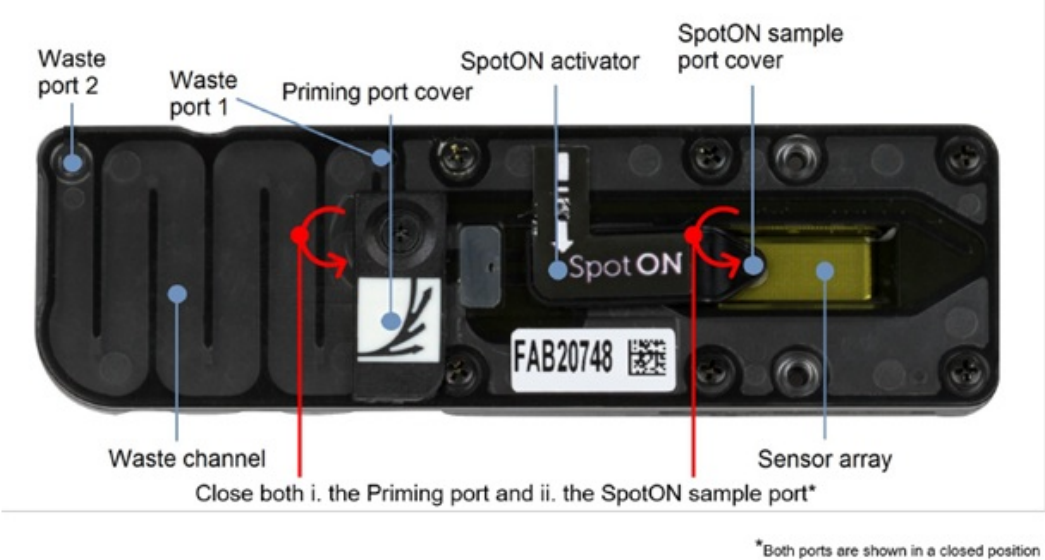
- NEBNext Ultra II RNA First Strand synthesis manual E7771
- NEBNext Ultra II Non-directional RNA Second Strand synthesis manual E6111
- ezdnase_PI

Oxford Nanopore Manufacturer's protocols:

- Ligation sequencing gDNA - Native Barcoding Kit 96 V14 (SQK-NBD114.96)-minion.
- ligation-sequencing-gdna-native-barcoding-v14-sqk-nbd114-96-NBE_9171_v114_revG_15Sep2022-minion
- ligation-sequencing-gdna-native-barcoding-v14-sqk-nbd114-96-NBE_9171_v114_revG_15Sep2022-gridion

APPENDICES

APPENDIX 1. FLOW CELL

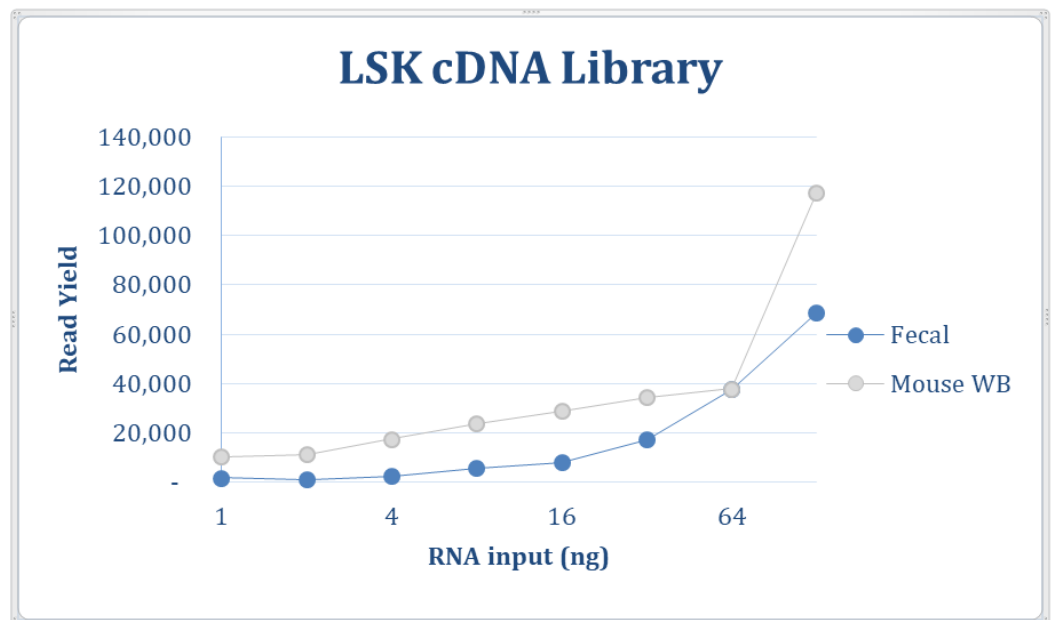
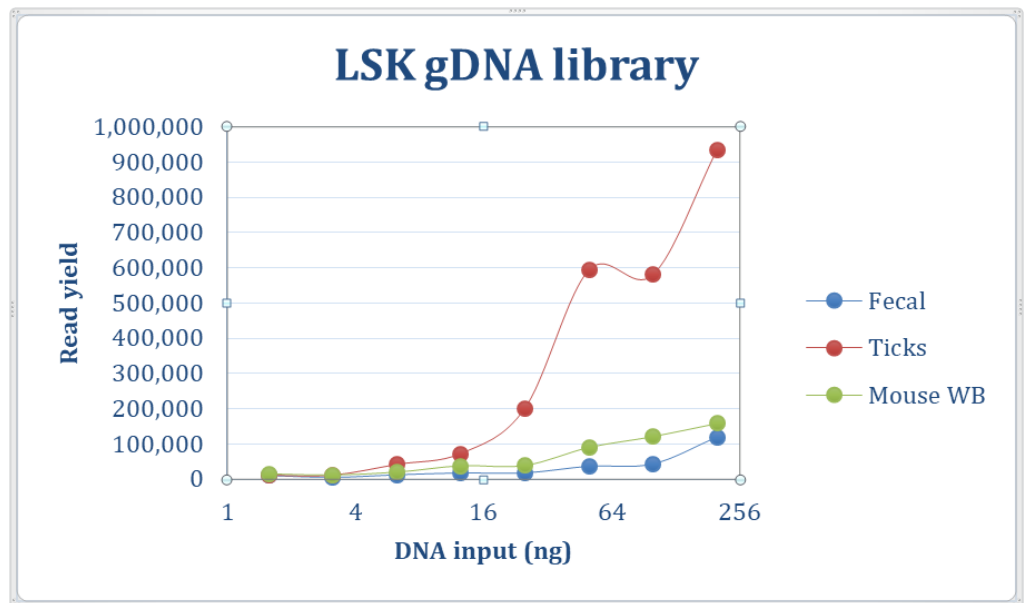


APPENDIX 2. cDNA END-PREP MASTER MIX PREPARATION

A	B	C
Component	Volume for 1 reaction	Volume for n+1 reactions
cDNA sample	20 µl	20 µl
Nuclease-free water	30 µl	... µl
Ultra II End-prep reaction buffer	7 µl	... µl
Ultra II End-prep enzyme mix	3 µl	... µl
Final total volume	60 µl	... µl

APPENDIX 3. EXPECTED OUTCOMES

The DNA or RNA inputs vs the sequencing read yields.



MATERIALS

EQUIPMENT AND MATERIALS

Note

NOTE: If product number is listed, please ensure use of this or equivalent product.

A	B
Equipment	Mfg / Product #
Oxford Nanopore GridION or MinION Mk1C device	Oxford Nanopore Technologies, GRD-CapEx or Oxford Nanopore Technologies, M1CCapEx
Computer monitor (with HDMI port or Display port), mouse and keyboard	Locally sourced
MinkNOW - software equipped already in the GridION and MinION Mk1C device	Oxford Nanopore Technologies
Ice bucket with ice	Locally sourced
Qubit fluorometer	ThermoFisher, Q33238 or equivalent
DynaMag-2 magnet	Invitrogen, 12321D or equivalent
DynaMag-96 Side Magnet	Invitrogen, 12331D or equivalent
Hula sample mixer	ThermoFisher, 15920D
Microplate centrifuge	Locally sourced
Timer	Locally sourced
Thermal cycler	Locally sourced
96-well PCR plate holder	Locally sourced
P1000 pipette and tips	Locally sourced
P200 pipette and tips	Locally sourced
P20 pipette and tips	Locally sourced
P10 pipette and tips	Locally sourced
P10 8-channel pipette	Locally sourced
P300 8-channel pipette	Locally sourced

A	B	C
Material	Description	Mfg / Product #
200 ng DNA from a sample	Per sample from SOP B-2 (gDNA Preparation)	REDI-NET DNA sample
20 ul eluents from negative control extraction	From SOP B-2 (gDNA Preparation)	REDI-NET negative control

A	B	C
100 ng DNA from positive control extraction	From SOP B-2 (gDNA Preparation)	REDI-NET positive control
160 ng RNA from a sample	Per sample from SOP B-2 (TNA preparation)	REDI-NET RNA sample
40 ng RNA from positive control extraction	from SOP B-2 (TNA preparation)	REDI-NET negative control
8 µl total nucleic acid negative control extraction	From SOP B-2 (TNA preparation)	REDI-NET positive control
10 µl total nucleic acid	Per sample from SOP B-2 (TNA Preparation)	REDI-NET TNA sample
10 µl total nucleic acid from negative control extraction	From SOP B-2 (TNA Preparation)	REDI-NET negative control
10 µl total nucleic acid from positive control extraction	from SOP B-2 (TNA Preparation)	REDI-NET positive control
Native Barcoding Kit 96 V14	(Sequencing Library Preparation)	Oxford Nanopore, SQK-NBD114.96
ezDNase	(cDNA synthesis)	ThermoFisher, Invitrogen 11766051
NEBNext Ultra II RNA First Strand Synthesis Module	(cDNA synthesis)	New England Biolabs, E7771L
NEBNext Ultra II Non-Directional RNA Second Strand Synthesis Module	(cDNA synthesis)	New England Biolabs, E6111L
Random primer mix (Random hexamer and poly-T mixture)	(cDNA synthesis)	New England Biolabs, S1330
USB Dithiothreitol (DTT), 0.1M Solution	(cDNA synthesis)	ThermoFisher, 707265ML
Agencourt AMPure XP beads	(Sequencing Library Preparation)	Beckman Coulter, A63881
NEBNext End repair / dA-tailing Module	(Sequencing Library Preparation)	New England Biolabs, E7546L
NEBNext FFPE Repair Mix	(Sequencing Library Preparation)	New England Biolabs, M6630L
NEB Blunt/TA Ligase Master Mix	(Sequencing Library Preparation)	New England Biolabs, M0367L
NEBNext Quick Ligation Module	(Sequencing Library Preparation)	New England Biolabs, E6056L
R10.4.1 flow cells	Flow cells for sequencing experiment (<i>consumable</i>)	Oxford Nanopore, FLO-MIN114
low DNA binding tubes	1.5 mL (<i>consumable</i>)	Eppendorf, 022131021 or equivalent
low DNA binding tubes	2.0 mL (<i>consumable</i>)	Eppendorf, 022431048 or equivalent

A	B	C
PCR tubes	0.2 mL thin-walled (<i>consumable</i>)	Eppendorf, 951010006 or equivalent
PCR plate	96 well, low DNA binding, semi-skirted with heat seals (<i>consumable</i>)	Eppendorf, 0030129504 or equivalent
BRAND Self-adhesive Plate Sealing Film	Aluminum (<i>consumable</i>)	Fisher Scientific, 13-882- 329
Clear Adhesive Film	For PCR plate sealing	ThermoFisher, 4306311
Qubit Assay Tubes	For Qubit DNA/RNA measurement (<i>consumable</i>)	Thermo Fisher, Q32856
Qubit 1X dsDNA HS Assay Kit	(<i>consumable</i>)	ThermoFisher, Q33230
Qubit RNA HS Assay Kit	(<i>consumable</i>)	ThermoFisher, Q32852
Nuclease-free water	To prepare ethanol dilutions (<i>consumable</i>)	Locally sourced
Freshly prepared 80% ethanol in nuclease-free water	Prepared from 100% molecular biology grade ethanol (<i>consumable</i>)	Locally sourced
Freshly prepared 70% ethanol in nuclease free water	Prepared from 100% molecular biology grade ethanol (<i>consumable</i>)	Locally sourced
Data sheets	REDI-NET DCS B-4 Testing	REDI-NET Data Portal

Equipment

Qubit Fluorometer

NAME

Fluorometer

TYPE

Invitrogen

BRAND

Q33238




SKU


<https://www.thermofisher.com/order/catalog/product/Q33238#/Q33238>


LINK


Equipment	
DynaMag™-2 Magnet	NAME
Magnet	TYPE
DynaMag™	BRAND
12321D	SKU
https://www.thermofisher.com/order/catalog/product/12321D	LINK


Equipment	
Hula mixer	NAME
Mixer	TYPE
Invitrogen	BRAND
15920D	SKU
Any rotator mixer	SPECIFICATIONS


-  Native Barcoding Kit 96 V14 Oxford Nanopore Technologies Catalog #SQK-NBD114.96
-  ezDNase™ Enzyme Thermo Fisher Catalog #11766051
-  NEBNext Ultra II RNA First Strand Synthesis Module - 96 rxnsNew England Biolabs Catalog #E7771L
-  NEBNext Ultra II Non-Directional RNA Second Strand Synthesis Module - 100 rxns New England Biolabs Catalog #E6111L
-  Random primer mix New England Biolabs Catalog #S1330S
-  USB Dithiothreitol (DTT) 0.1M Solution Thermo Fisher Scientific Catalog #707265ML


 Agencourt AMPure XP beads Beckman
Coulter Catalog #A63881


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

 NEBNext FFPE DNA Repair Mix - 96 rxns New England
Biolabs Catalog #M6630L


 Blunt/TA Ligase Master Mix - 250 rxns New England
Biolabs Catalog #M0367L


 NEBNext Quick Ligation Module - 100 rxns New England
Biolabs Catalog #E6056L


 Nanopore Flow Cell R10.4.1 Oxford Nanopore
Technologies Catalog #FLO-MIN114


 DNA LoBind Tubes 2.0
ml Eppendorf Catalog #022431048

 Eppendorf PCR
Tubes Eppendorf Catalog #951010006

 96 well LoBind PCR plates Semi-
skirted Eppendorf Catalog #0030129504

 NEBNext Microbiome DNA Enrichment Kit - 6 rxns New England
Biolabs Catalog #E2612S

 RNaseOUT™ Recombinant Ribonuclease Inhibitor Thermo Fisher
Scientific Catalog #10777019

 BRAND™ Self-adhesive Plate Sealing Film Fisher
Scientific Catalog #13-882-329

 MicroAmp™ Clear Adhesive Film Thermo Fisher
Scientific Catalog #4306311

 Qubit assay tubes Thermo Fisher Scientific Catalog #Q32856



Qubit 1X dsDNA High Sensitivity Assay Kit Thermo Fisher
Scientific Catalog #Q33230



Qubit RNA HS (High Sensitivity) assay Thermo Fisher
Scientific Catalog #Q32852

SAFETY WARNINGS



RISKS AND PERSONAL PROTECTION

Gloves should be worn all the time when handling samples.

BEFORE START INSTRUCTIONS

BEFORE START

1. Check the DNA and RNA concentrations in each sample of total nucleic acid (TNA) extraction.
2. If the concentrations are detectable, choose the sequencing approach following the table below.
3. If DNA or RNA concentration is not detectable, prepare the library for the detectable one.
4. Use sections **gDNA PREPARATION** and **TNA PREPARATION** for gDNA and TNA preparation, respectively, then subject the prepared gDNA and TNA to Section **SEQUENCING LIBRARY PREPARATION**.

A	B	C	D	E
		DNA concentration (ng/ul)		
		< 1 ng/ul	1-10 ng/ul	> 10 ng/ul
RNA concentration (ng/ul)	< 4 ng/ul	TNA	DNA	DNA
	4-20 ng/ul	TNA	TNA	TNA
	>20 ng/ul	TNA	TNA	TNA

gDNA PREPARATION

1



When the RNA concentration of the sample is lower than the detectable range of the Qubit High Sensitivity Assay ($< 0.01 \text{ ng/ul}$), the sample is subjected to gDNA sequencing. The cDNA synthesis can be skipped.

2

When the DNA concentration $> 10 \text{ ng/ul}$, calculate the required volume of 200 ng DNA, then transfer the volume to a new $200\mu\text{l}$ PCR tube or a well of a 96-well PCR plate. Adjust the volume with nuclease-free water to a final volume of $20 \mu\text{L}$.

3

Prepare 100 ng gDNA from positive control extraction in $20 \mu\text{L}$ nuclease-free water in a new $200\mu\text{l}$ PCR tube or a well of a 96-well PCR plate.

4

Transfer $20 \mu\text{L}$ negative control extraction to a new tube or a well of a 96-well PCR plate.

5

All samples are subjected to section SEQUENCING LIBRARY PREPARATION.

TNA PREPARATION

6

To prepare TNA for sequencing both cDNA and gDNA, cDNA needs to be prepared separately and then mixed with TNA from the original sample.


7

Prepare cDNA following section cDNA SYNTHESIS (positive control and negative control included) until step 40.

8






















Transfer $10 \mu\text{L}$ double-stranded cDNA of section cDNA SYNTHESIS step 40 to a new $200 \mu\text{l}$ PCR tube or a well of a 96-well PCR plate. Add $10 \mu\text{L}$ of TNA from the original sample to make the final volume $20 \mu\text{L}$.

- 9 Subject the  20 μL double-stranded cDNA/TNA mixture to section SEQUENCING LIBRARY PREPARATION.

Note



NOTE: Twenty-four samples must be pooled in one sequencing run to make the most out of a sequencing flow cell. For collecting 24 samples, the samples from gDNA and TNA preparations can be placed in the same 96-well plate for End-prep and Barcode Ligation before pooling, then pooled for the subsequent steps of library preparation.

cDNA SYNTHESIS: DNase treatment

- 10 If RNA concentration >  20 ng/ μL , calculate the required volume of  160 ng RNA, then transfer the volume to a new 200 μL PCR tube or a well of a 96-well PCR plate. Adjust the volume with nuclease-free water to a final volume of  8 μL . If the concentration of the RNA <  20 ng/ μL , directly transfer  8 μL of RNA to a new 200 μL PCR tube or a well of a 96-well PCR plate. Keep the tube or plate  On ice.
- 11 Prepare  40 ng RNA from positive control extraction and adjust the volume to final  8 μL with nuclease-free water in a new 200 μL PCR tube or a well of a 96-well PCR plate.
- 12 Transfer  8 μL negative control extraction to a new tube or a well of a 96-well PCR plate.
- 13 **Remove contaminated DNA (~ 15 mins):** Thaw total nucleic acid, 10x ezDNase Buffer, and DTT on  7m 5s ice at  Room temperature. Vortex 10x ezDNase Buffer and DTT briefly, spin down by centrifugation for  00:00:05, and place  On ice. ezDNase is not frozen and should be placed  On ice before use. Set up thermal cycler programs:  37 $^{\circ}\text{C}$,  00:02:00, and  55 $^{\circ}\text{C}$,  00:05:00.
- 13.1  Mix the following components in an RNase-free tube or plate. For processing multiple samples, make a master mix for 10x ezDNase buffer and ezDNase with 10% overage. Aliquot the master mix into the wells of a 96-well plate, then add TNAs.

A	B
Component	Volume
10× ezDNase Buffer	1 µl
ezDNase	1 µl
RNA from step 6	8 µl
Total volume	10 µl

13.2 Gently mix the samples then centrifuge the tube (Include a reaction for extraction positive control and negative control of each batch nucleic acid extraction).

13.3 Incubate the sample for  00:02:00 at  37 °C .

2m






13.4 Add  1 µL 100mM DTT into the reaction tube.







13.5 Incubate the sample at  55 °C for  00:05:00 to inactivate the enzyme.




5m



13.6 Chill the tube  On ice to bring the sample to  Room temperature , then spin down and place the tube  On ice .

cDNA SYNTHESIS: First strand cDNA Synthesis (~ 1hr)

14 **BEFORE START:** Thaw 60 µM stock Random Primer Mix (NEB, S1330S) at  Room temperature . DO  5s **NOT USE** the Random Primer provided by the NEBNext First Strand Synthesis Module. Thaw Random Primer Mix solution, NEBNext First Strand Reaction Buffer, NEBNext Second Strand Reaction Buffer at  Room temperature then place  On ice . Vortex the vials briefly, spin done by centrifugation for

 00:00:05 , and place  On ice . First and Second Strand Enzyme Mix are not frozen, should be briefly centrifuged and placed  On ice before use.

15



Add the following reagents into the ezDNase-treated RNA from step 13.6. For processing multiple samples, make a master mix for the 60 μ M Random Primer Mix and nuclease-free water with 10% overage.

A	B
Component	Volume
ezDNase treated RNA	10 μ l
60 μ M Random Primer	1 μ l
Nuclease free water	3 μ l
Total volume	14 μ l

16



Mix gently, spin down and incubate at  65 °C for  00:05:00 . Chill  On ice , spin down again  5m and place  On ice .

17

Add the following components in the indicated order, if multiple reactions will be processed at the same time, make a master mix with a 10% overage:

A	B
Component	Volume
NEBNext First Strand Synthesis Reaction Buffer	4 μ l
NEBNext First Strand Synthesis Enzyme Mix	2 μ l
Total volume	20 μ l

18

Mix gently and spin down.

19 Incubate the tube for  00:10:00 at  25 °C followed by  00:15:00 at  42 °C . 25m





20 Terminate the reaction by heating at  70 °C for  00:15:00 . 15m



21 Place the tube  On ice or pre-chilled freezer block.

22 Continue immediately with the second strand synthesis reaction as described below.

cDNA SYNTHESIS: Second strand cDNA Synthesis (~ 1hr)

23 Pipette the following components directly into the first strand reaction tube (with  20 µL mixture)  On ice in the indicated order, if multiple reactions will be processed at the same time, make a master mix with a 10% overage:

A	B
Component	Volume
5x NEBNext Second Strand Synthesis Reaction Buffer	5 µl
NEBNext Second Strand Synthesis Enzyme Mix	2.5 µl
Nuclease-free water	22.5 µl
Final total volume	50 µl

24 Mix gently and centrifuge briefly.



25 Incubate at 16 °C for 01:00:00 (heated lid set at ≤ 40 °C).

1h



26 Proceed with cDNA purification or store the reaction mixture at -20 °C before the subsequent cDNA purification (the double-stranded cDNA is ready to be shipped to Gold Labs if necessary).

cDNA SYNTHESIS: Purification of double-stranded cDNA (~ 15...

27

Note

NOTE: Before starting, prepare fresh 70% ethanol in nuclease-free water sufficient for your samples. (500 µl per sample).

Resuspend the AMPure XP beads by vortexing.

28 Transfer the sample (50 µL) to a clean 1.5ml low DNA binding tube.

29 Add 40 µL of resuspended AMPure XP beads to the reaction and mix by flicking the tube.






30 Incubate on a Hula mixer (rotator mixer) for 00:05:00 at Room temperature .

5m



31 Spin down the sample and pellet on the magnet. Keep the tube on the magnet, and using a pipette, discard the supernatant.

- 32**  Keep the tube on the magnet and wash the beads with **200 μ L** of freshly prepared 70% ethanol without disturbing the pellet. Remove the ethanol using a pipette and discard.
- 33** Repeat the previous step X1.
- 34** Spin down and place the tube back on the magnet. Using a pipette, remove any residual ethanol. Allow **30s** dry for ~ **00:00:30**, but do not dry the pellet to the point of cracking.
- 35** Remove the tube from the magnetic rack and resuspend the pellet in **13 μ L** nuclease-free water.
- 36**  Incubate on a Hula mixer (rotator mixer) for **00:10:00** at **Room temperature**. **10m**
- 37** Spin down and pellet beads on magnet until the eluate is clear and colorless.
- 38** Remove and retain **11 μ L** of eluate into a clean 1.5ml low DNA binding tube.
- 39**  **Optional:** Analyze **1 μ L** of the purified double-stranded cDNA for quantity using Qubit fluorometer and Qubit 1X dsDNA HS Assay Kit.

40

Subject

🧪 10 µL

purified double-stranded cDNA for section

SEQUENCING LIBRARY PREPARATION.

II

Note

STOP POINT: The synthesized double-stranded cDNA can be stored at 🧊 -20 °C before sequencing.

SEQUENCING LIBRARY PREPARATION

41

Before starting, prepare fresh 70% ethanol in nuclease-free water sufficient for your samples (🧪 1 mL per sample). Program the thermal cycler or use a heat block for 96 well plate: 🧊 20 °C for ⌚ 00:05:00 and 🧊 65 °C for ⌚ 00:05:00 . Thaw Ultra II End-prep reaction buffer, NEBNext FFPE DNA Repair Buffer, Barcode Plate(from SQK-NBD114.96 Kit),and Blunt/TA Ligase Master Mix 🧊 On ice . After fully thaw, mix by vortex, spin down briefly, and place 🧊 On ice . Check that there is no precipitate present (the Blunt/TA Master Mix can sometimes form a precipitate). Spin down Ultra II End-prep enzyme mix and place 🧊 On ice .

10m

SEQUENCING LIBRARY PREPARATION: End-prep (~ 50 minutes)

42

Mix the following reagents in a 0.2ml PCR tube. To process 24 samples, prepare a master mix by multiplying gradients except for cDNA by 24 with a 10% overage. Aliquot the master mix into a 96-well plate, then add cDNA or TNA (see Appendix 2 for master mix preparation):

🔧

A	B
Component	Volume
DNA/TNA sample	20 µl
Nuclease-free water	4 µl
Ultra II End-prep reaction buffer	1.75 µl
Ultra II End-prep enzyme mix	1.5 µl
NEBNext FFPE DNA Repair Buffer	1.75 µl
NEBNext FFPE DNA Repair Mix	1 µl
Final total volume	30 µl


43 Mix gently by pipetting and spin down.





44 Using a thermal cycler, incubate at  20 °C for  00:05:00 and  65 °C for  00:05:00 . 10m



45 Resuspend the AMPure XP beads by vortexing.

46 Add  50 µL of resuspended AMPure XP beads to the end-prep reaction and mix by pipetting (use an 8-channel pipette for reagent transfer of multiple samples).




47 Incubate on a Hula mixer (rotator mixer) for  00:05:00 at  Room temperature . 5m



48 Spin down the sample and pellet on a magnet (DynaMag-2 for 1.5ml tube and DynaMag-96 for PCR plate). Keep the tube on the magnet, and using a pipette, discard the supernatant.



49 Keep the tube on the magnet and wash the beads with  200 µL of freshly prepared 70% ethanol without disturbing the pellet. Remove the ethanol using a pipette and discard.




50 Repeat the previous step X1.

51 Spin down and place the tube back on the magnet. Using a pipette, remove any residual ethanol. Allow 30s





dry for ~  00:00:30, but do not dry the pellet to the point of cracking.

52

Remove the tube from the magnetic rack and resuspend the pellet in  12 μL nuclease-free water. 2m




Incubate for  00:02:00 at  Room temperature.

53

Pellet the beads on a magnet until the eluate is clear and colorless.

54

Remove and retain  11 μL of eluate into a clean 1.5ml low DNA binding tube.

SEQUENCING LIBRARY PREPARATION: Barcode ligation (~ 25 m.

55

Add the reagents in the order given below, mixing by flicking the tube between each sequential addition:



Note

NOTE: When working on 24 End-prepped gDNA/TNA, set up the reactions in a low DNA binding 96-well plate. The Native barcodes can be transferred by an 8-channel pipette directly punching through the sealing foil with tips of the barcode plate. Please reseal the used wells with trimmed adhesive foil. Each well provides sufficient volume for two barcoding ligations.

A	B
Component	Volume
End-prepped DNA	10 μl
Native Barcode (pick one form Native Barcoding Expansion 1-96)	2 μl
Blunt/TA Ligase Master Mix	12 μl
Final total volume	24 μl


56

Mix gently by flicking the tube and spin down.



57 Incubate the reaction for  00:20:00 at  Room temperature . 20m





58 Add  3 μL of EDTA to each well and mix thoroughly by pipetting and spin down briefly.




Note

At this point, samples should be individually barcoded and ready to be subjected to pooling.

SEQUENCING LIBRARY PREPARATION: Library pooling for mult...

59 Pool every 24 barcoded samples  12 μL from each sample, (total  288 μL /pool) in a new 1.5ml low DNA binding tube.


60 Resuspend the AMPure XP beads by vortexing.


61 Add  518 μL (1.8x volume of the pooled library) of resuspended AMPure XP beads to the pooled library and mix by pipetting.



62 Incubate on a Hula mixer (rotator mixer) for  00:10:00 at  Room temperature . 10m



63 Spin down the sample and pellet on a magnet. Keep the tube on the magnet for  00:05:00 , and use 5m a pipette, discard the supernatant.

- 64  Keep the tube on the magnet and wash the beads with **700 µL** of freshly prepared 80% ethanol without disturbing the pellet. Remove the ethanol using a pipette and discard.
- 65 Repeat the previous step X1.
- 66 Spin down and place the tube back on the magnet. Using a pipette, remove any residual ethanol. Allow **30s** dry for ~ **00:00:30**, but do not dry the pellet to the point of cracking.
- 67  Remove the tube from the magnetic rack and resuspend the pellet in **35 µL** nuclease-free water **10m**. Incubate for **00:10:00** at **37 °C** temperature.
- 68 Spin down and pellet the beads on a magnet until the eluate is clear and colorless.
- 69 Remove and retain **35 µL** of eluate into a clean 1.5ml low DNA binding tube.

SEQUENCING LIBRARY PREPARATION: Adapter ligation (~ 45 m.)

- 70 **BEFORE STARTING:** Thaw Short Fragment Buffer (SFB), Elution Buffer (EB), and NEBNext Quick Ligation Reaction Buffer (5×) at **Room temperature**, mix by vortexing, spin down, and place **On ice**. Check that the contents of each tube are clear of any precipitate. Spin down the T4 Ligase and the Native Adapter (NA), and place **On ice**.
- 71 Taking the pooled and barcoded DNA, perform adapter ligation as follows, mixing by flicking the tube between each sequential addition.

A	B
Pooled barcoded sample	30 μ l
Native Adapter (NA)	5 μ l
NEBNext Quick Ligation Reaction Buffer (5 \times)	10 μ l
Quick T4 DNA Ligase	5 μ l
Final total volume	50 μ l


72 Mix gently by flicking the tube, and spin down.

73 Incubate the reaction for  00:20:00 at  Room temperature .



20m



74 Resuspend the AMPure XP beads by vortexing.

75 Add  90 μ L of resuspended AMPure XP beads to the reaction and mix by pipetting.




76 Incubate on a Hula mixer (rotator mixer) for  00:10:00 at  Room temperature .












10m





77 Place on the magnetic rack, allow beads to pellet and using a pipette, discard the supernatant.

78 Add  125 μ L of the Short Fragment Buffer (SFB) to the beads. Close the tube lid and resuspend the



-  beads by flicking the tube. Return the tube to the magnetic rack, allow beads to pellet and using a pipette, discard the supernatant.
- 79 Repeat the previous step X1.
- 80 Spin down and place the tube back on the magnet. Using a pipette, remove any residual supernatant.
- 81 Remove the tube from the magnetic rack and resuspend the pellet in  13 μL of Elution Buffer (EB).
- 82 Incubate on at  37 °C for  00:10:00 at  Room temperature, agitate the sample for 10s e  10m
 2 min.
- 83 Pellet beads on magnet until the eluate is clear and colorless.
- 84 Remove and retain  13 μL of eluate into a clean 1.5ml low DNA binding tube.
- 85 Quantify  1 μL of eluted sample using a Qubit fluorometer and Qubit 1X dsDNA HS Assay Kit (recovery aim ~  430 ng in total).
- 86 Make up the library to  12 μL at 10-20 fmol.

- 87 Put the library  On ice until ready to load or store the library at  -20 °C for future sequencing.

Priming and loading the SpotON Flow Cell


- 88 Check the number of pores in your flow cell.

Note

NOTE: before starting the flow cell pore checking, check the hardware following the manufacturer's guidance.

- 88.1 Turn on GridION (or MinION Mk1C) device. Make sure all the connections for the display, mouse, keyboard, and internet are ready.
- 88.2 Depending on the number of pooled samples, get one to four new flow cells from the fridge and check the expiration date.
- 88.3 Double-click the MinkNOW icon shown on the desktop to initiate the program.
- 88.4 Use Oxford Nanopore Community username and password to login.
- 88.5 Select the device shown on the screen.
- 88.6 Open the lid of GridION (or MinION Mk1C) and insert the flow cells under the clips, press down the



flow cell to ensure good thermal and electrical contact.


- 88.7** The Sequencing Overview tab should show the **flow cell not checked** in each position in use.
- 88.8** Navigate to the Start tab and select **Flow Cell Check**.
- 88.9** Select the flow cells to assign the flow cell type FLO-MIN114 from the dropdown menu.
- 88.10** Click **Start** to begin the flow cell check.
- 88.11** Record the port number and date of checking on the original package of the flow cell. The flow cell with less than 800 pores should not be used for the sequencing. If the flow cell is not expired, contact Oxford Nanopore Company for customer service.
- 88.12** If the flow cell is going to be used immediately, keep it on the GridION or MinION Mk1C sequencer for priming. Otherwise put the flow cell back to the original pouch, store at  4 °C for next day use. The opened flow cell should be used within one week.

Priming and loading the SpotON Flow Cell: Flow cell priming



89

BEFORE STARTING:

Thaw the Sequencing Buffer (SB), Library Beads (LIB), Flow Cell Tether (FCT) and one tube of Flow Cell Flush (FCF) at  Room temperature . Mix SB by tapping or pipetting (DO NOT Vortex) and vortex the other tubes. Spin down tubes at  Room temperature .

- 90
- Check the air bubble of priming pore.
- 91
- Slide open the GridION lid (or MinION Mk1C) and insert flow cell with minimum 800 pores.
- 92
- Slide the priming port cover clockwise to open the priming port.
- Note
- NOTE:** Please see **Appendix 1** for the positions of the flow cell ports.
- 93
- After opening the priming port, check for a small air bubble under the cover. Draw back a small volume (20-30 µl) to remove any bubbles:
- 93.1
- Set a P1000 pipette to 200 µl. Insert the tip into the priming port. Turn the volume adjustment wheel counter-clockwise until the dial shows 220-230 µl, or until you can see a small buffer volume entering the pipette tip.
- Note
- IMPORTANT:** Take care when drawing back the buffer from the flow cell. Do not remove more than  20-30 µL, and make sure that the array of pores is always covered by the buffer. Introducing air bubbles into the array can irreversibly damage pores.
- 94
- Prepare the flow cell priming mix and prime flow cells.
- 94.1
- Using a 2.0 mL low DNA binding tube, prepare flow cell priming mix with components as follows, mix by inverting the tube and pipetting.
- | | |
|---|---|
| A | B |
|---|---|

A	B
Component	Volume
Bovine Serum Albumin (BSA) (50 mg/ml)	5 µl
Flow Cell Tether (FCT)	30 µl
Flow Cell Flush (FCF)	1170 µl
Final total volume	1205 µl

94.2 Load  800 µL of the priming mix into each flow cell via the priming port, avoiding the introduction of air bubbles. Wait for  00:05:00.

95 Prepare the library for loading.

Note




IMPORTANT: The Library Beads (LIB) tube contains a suspension of beads. These beads settle very quickly. It is vital that they are mixed immediately before use.

95.1 Thoroughly mix the contents of the Library Beads (LIB) by pipetting.

95.2 In a new tube, prepare each library for loading as follows:

A	B
Component	Volume
Sequencing Buffer (SB)	37.5 µl
Library Beads (LIB)	25.5 µl
DNA library	12 µl
Final total volume	75 µl


96 Complete the flow cell priming.

- 96.1** Gently lift the SpotON sample port cover to make the SpotON sample port accessible.
- 96.2** Load  200 µL of the priming mix into the flow cell via the priming port (not the SpotON sample port), avoiding the introduction of air bubbles.
- 97** Loading samples.
- 97.1** Mix the prepared library gently by pipetting up and down just prior to loading.
- 97.2** Add  75 µL of sample to the flow cell via the SpotON sample port in a dropwise fashion. Ensure each drop flows into the port before adding the next drop.
- 
- 97.3** Gently replace the SpotON sample port cover, making sure the bung enters the SpotON port, close the priming port and replace the GridION lid.

Priming and loading the SpotON Flow Cell: Data acquisition a... ^{2d}

- 98** Double-click the MinKNOW icon displayed on the desktop to initiate the program.
- 99** Use Oxford Nanopore Community username and password to login or continue as Guest.

- 00 Select the device shown on the screen.
- 01 Go to the Start tab, and click the Start Sequencing option to choose the running parameters.
- 101.1 Type in the **Experiment Name** using the scheme, [YYYY_MM_DD_Approach(gDNA or TNA)_Sample type (soil, water,... etc.)]
- 101.2 Type in **Sample ID** (same as experiment name)
- 101.3 Choose flow cell FLO-MIN114 from the drop-down menu
- 02 Click **Continue to Kit Selection** to move to the next page.
- 102.1 Click the kit **SQK-NBD114-96** from the Kit Selection menu.
- 03 Click **Continue to Run Options** to choose run parameters.

- 103.1** Set run length to  48:00:00 and minimum read length 200 bp. Let adaptive sampling be unchecked. 2d
- 04** Click **Continue to Analysis** to choose basecalling and Barcoding parameters.
- 104.1** In the Basecalling options, checkup the basecalling with configuration: High accuracy basecalling.
- 104.2** In the Barcoding options, turn on the Trim barcodes and Mid-read barcoding filtering.
- 104.3** Do not turn on the Alignment option.
- 05** Click **Continue to output** to the next page.
- 105.1** Select the output data location, format, and filtering options. Check up the box for Raw reads in POD5 format and Basecalled reads in FASTQ format. Keep the filter score as the system default.
- 06** Click **Continue to final review** to proceed.
- 07** Review the settings listed in the Run Setup page. Correct any errors. Select **Start** to run the experiment.

08 The system will automatically navigate the Sequencing Overview when sequencing starts.

09 48 hrs later, check the sequencing data. Use 1 mL pipette to remove 1 mL waste solution in the waste channel via waste port 1 (see Appendix 1 under Guidelines & Warnings tab). Remove the flow cells on the device, put it back in the original package, and turn off the device.