



Feb 09, 2021

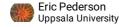
RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing

Eric RA Pederson¹

¹Uppsala University

1 Works for me dx.doi.org/10.17504/protocols.io.bj7tkrnn

methods



SUBMIT TO PLOS ONE

ABSTRACT

RNA extraction of extraction using the Qiagen Allprep RNA extraction kit followed by nanopore sequencing on the MinION.

DOI

dx.doi.org/10.17504/protocols.io.bj7tkrnn

PROTOCOL CITATION

Eric RA Pederson 2021. RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing . **protocols.io**

https://dx.doi.org/10.17504/protocols.io.bj7tkrnn

LICENSE

This is an open access protocol distributed under the terms of the Creative Commons Attribution License, which permits unrestricted use, distribution, and reproduction in any medium, provided the original author and source are credited

CREATED

Aug 23, 2020

LAST MODIFIED

Feb 09, 2021

PROTOCOL INTEGER ID

40915

MATERIALS TEXT

MATERIALS

⊗ b-mercaptoethanol **Sigma-**

aldrich Catalog #M3148-25ML Step 5

users Catalog #ZROB20-RNA

Step 3

- Forceps

- Scientific Catalog #AM9780

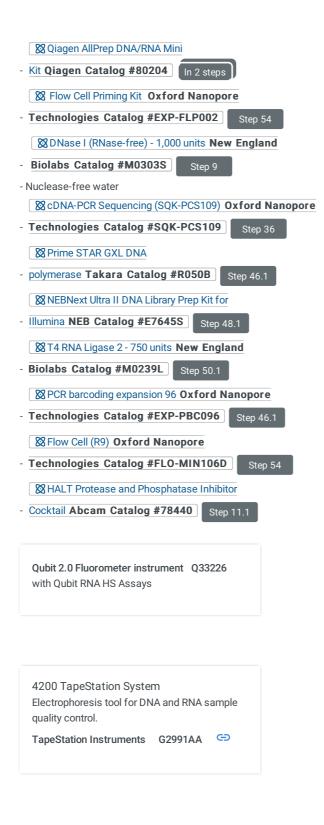
In 2 steps



02/09/2021

6

 $\textbf{Citation:} \ \ \text{Eric RA Pederson (02/09/2021). RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing . \\ \underline{\text{https://dx.doi.org/10.17504/protocols.io.bj7tkrnn}}$



SAFETY WARNINGS

<u>b-mercaptoethanol</u> is dangerous to work with Always use gloves and a flow hood

BEFORE STARTING

See pre-experiment steps

protocols.io

02/09/2021

Pre-experiment Book RNA extraction room 2 Spray with ETOH and then Scientific Catalog #AM9780 in the fume hood Prepare labelled 2 ml low bind tubes with 4 Zirconium Oxide Beads 2.0 mm RNase Free 4 mL beads in each 3 ⊠ Zirconium Oxide Beads 2.0 mm RNase Free 4 mL Contributed by users Catalog #ZROB20-RNA Make 3 1.5 ml eppendorf tubes for each sample; 1 with sterile water, 1 with 99% ETOH and 1 with Scientific Catalog #AM9780 5 From the Kit Qiagen Catalog #80204 Add 1 ml buffer RLT to 10 ul b-mercaptoethanol Each sample requires 600 ul of buffer RLT + b-mercaptoethanol So for example for 6 samples one would need 3.6 ml of the buffer RLT + b-mercaptoethanol mix. Thus, one would need to prepare 4 ml buffer RLT + 40 ul b-mercaptoethanol. aldrich Catalog #M3148-25ML 6 Buffer AW1 is supplied as a concentrate. Ensure that ethanol is added to Buffer AW1 before use Buffer AW2 is supplied as a concentrate. Ensure that ethanol is added to Buffer AW2 before use Label all the spin columns and the collection tubes properly Turn on centrfuge to 4°. 9 **⊠** DNase I (RNase-free) - 1,000 units **New England** From the **Biolabs Catalog #M0303S** Make DNase solution.

- 9.1 Prepare DNase I stock solution before using the RNase-Free DNase Set for the first time. Dissolve the solid DNase I (1500 Kunitz units) in 550 µl of the RNase-free water provided. To avoid loss of DNase I, do not open the vial. Inject RNase-free water into the vial using an RNase-free needle and syringe. Mix gently by inverting the vial. Do not vortex.
- 9.2 For long-term storage of DNase I, remove the stock solution from the glass vial, divide it into single-use aliquots, and store at -20oC for up to 9 months. Thawed aliquots can be stored at 2-8oC for up to 6 weeks. Do not refreeze the aliquots after thawing.

Tissue destruction

- Add to the 2.0 ml eppidendorf tube that already has the beads (<u>Zirconium Oxide Beads 2.0 mm RNase Free 4 mL</u>) with 600 ul RLT buffer and <u>b-mercaptoethanol</u> mixture.
- 11 Get tissue from the -80 freezer and place on dry ice
 - 11.1 Materials to take to the basement -80° freezer;
 - gloves
 - white warm gloves
 - dry ice
 - blades
 - wipes
 - forceps
 - ethanol spray
 - petri-dishes (tissue type written on the lid)
 - marker
 - paper tape
 - normal ice
 - tubes with Beads, PBS and

X HALT Protease and Phosphatase Inhibitor

Cocktail Abcam Catalog #78440

on ice

In the most sterile way possible, cut a small piece of tissue, half a pea size or so, and put it into one of the labelled 2ml tubes with Beads and the RLT mixture on ice

Make sure to use the ethanol to clean everything and not to cut yourself.

Use the forceps to grab the tissue that flies away.

- 13 Use the bullet blender to destroy the tissue (Tape on lids)
 - 3 minutes
 - speed setting 8
- 14 Centrifuge the lysate for 3 min at maximum speed.

 $\textbf{Citation:} \ \ \text{Eric RA Pederson (02/09/2021). RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing.} \\ \underline{\text{https://dx.doi.org/10.17504/protocols.io.bj7tkrnn}}$

15 SQiagen AllPrep DNA/RNA Mini

From the Kit Qiagen Catalog #80204

Carefully remove the supernatant by pipetting, and transfer it to the AllPrep DNA spin column placed in a 2 ml collection tube (supplied). Close the lid gently, and centrifuge for 30 s at \geq 8000 x g (\geq 10,000 rpm).

Place the AllPrep DNA spin column in a new 2 ml collection tube (supplied), and store at room temperature (15–25oC) or at 4oC for later DNA purification in steps 14–17. Use the flow-through for RNA purification in the following steps

RNA extraction

- 17 Add 1 volume (usually 600 μ l) of 70% ethanol to the flow-through from step 5, and mix well by pipetting. Do not centrifuge.
- Transfer up to 700 μ l of the sample, including any precipitate that may have formed, to an RNeasy spin column placed in a 2 ml collection tube (supplied). Close the lid gently, and centrifuge for 15 s at \geq 8000 x g (\geq 10,000 rpm). Discard the flowthrough.
- 19 Add 350 μl Buffer RW1 to the RNeasy spin column, and centrifuge for 15 s at ≥8000 x g (≥10,000 rpm) to wash the spin column membrane. Discard the flow-through.* Reuse the collection tube in step E4.
- 20 Add 10 µl DNase I stock solution (see above) to 70 µl Buffer RDD. Mix by gently inverting the tube, and centrifuge briefly to collect residual liquid from the sides of the tube.

Buffer RDD is supplied with the RNase-Free DNase Set.

Note: DNase I is especially sensitive to physical denaturation. Mixing should only be carried out by gently inverting the tube. Do not vortex

21 Add the DNase I incubation mix (80 μ I) directly to the RNeasy spin column membrane, and incubate at room temperature (20–30oC) for 15 min.

Note: Be sure to add the DNase I incubation mix directly to the RNeasy spin column membrane. DNase digestion will be incomplete if part of the mix sticks to the walls or the O-ring of the spin column.

22 Add 350 µl Buffer RW1 to the RNeasy spin column, and centrifuge for 15 s at ≥8000 x g (≥10,000 rpm). Discard the flow-through.

Continue with step 9 (22) of the protocol on page 26 (i.e., the first wash with Buffer RPE).

Reuse the collection tube in step 9 (22).

 $\textbf{Citation:} \ \ \text{Eric RA Pederson (02/09/2021). RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing . \\ \underline{\text{https://dx.doi.org/10.17504/protocols.io.bj7tkrnn}}$

23	Add 500 μ l Buffer RPE to the RNeasy spin column. Close the lid gently, and centrifuge for 15 s at \geq 8000 x g (\geq 10,000 rpm) to wash the spin column membrane. Discard the flow-through.			
24	Add 500 μ l Buffer RPE to the RNeasy spin column. Close the lid gently, and centrifuge for 2 min at \geq 8000 x g (\geq 10,000 rpm) to wash the spin column membrane			
25	Place the RNeasy spin column in a new 2 ml collection tube (supplied), and discard the old collection tube with the flow-through. Centrifuge at full speed for 1 min.			
26	Place the RNeasy spin column in a new 1.5 ml collection tube (supplied). Add 30 μ l RNase-free water directly to the spin column membrane. Close the lid gently, and centrifuge for 1 min at \geq 8000 x g (\geq 10,000 rpm) to elute the RNA.			
27	If the expected RNA yield is > 30 μ g, repeat the previous step using another 30 μ l of RNase-free water, or using the eluate from step 12 (if high RNA concentration is required). Reuse the collection tube from the previous step.			
28	Run the tapestation and the nanodrop on the RNA.			
29	Store the RNA in the -80 freezer for long term storage, or leave on ice until after the DNA extractions to preform the cDNA synthesis			
DNA extraction				
30	Add 500 μ l Buffer AW1 to the AllPrep DNA spin column from before the RNA extraction. Close the lid gently, and centrifuge for 15 s at \geq 8000 x g (10,000 rpm). Discard the flow-through.			

ு protocols.io 6 02/09/2021 6 02/09/2021 € 02/09/2021

Add 500 µl Buffer AW2 to the AllPrep DNA spin column. Close the lid gently, and centrifuge for 2 min at full speed to 31 wash the spin column membrane. Place the AllPrep DNA spin column in a new 1.5 ml collection tube (supplied). Add 100 μl Buffer EB directly to the spin 32 column membrane and close the lid. Incubate at room temperature (15-25oC) for 1 min, and then centrifuge for 1 min at \geq 8000 x g (10,000 rpm) to elute the DNA. Repeat previous step to elute further DNA. 33 Run the tapestation (genomic) and the Qubit on the DNA. 34 Store the DNA in the -20° or -80° freezer for long term storage. 35 cDNA synthesis 36 From the **Technologies Catalog #SQK-PCS109** Prepare the following reaction in a 0.2 ml PCR tube (X ul) 1 ng PolyA+ RNA (or ~50 ng total RNA) 36.1 (1 ul) VN primers (VNP), at 2 uM (1 ul) 10 mM dNTPs (9-X ul) RNase-free water Total volume of 11 ul Mix gently by flicking the tube and spin down 37 Incubate at 65° for 5 minutes and then snap cool on a pre-chilled freezer block 38 In a separate 0.2 ml PCR tube, mix the following reaction 39

- 39.1 (4 ul) 5x RT buffer
 - (1 ul) RNase Out
 - (1 ul) Nuclease-free water
 - (2 ul) Strand-Switching Primer (SSP, at 10 uM)

Total vollume of 8 ul

- 40 Mix gently by flicking the tube and spin down
- 41 Add the strand-switching buffer to the snap-cooled, annealed mRNA and mix by flicking the tube and spin down
- 42 Incubate at 42° for 2 minutes
- 43 Add 1 ul of Maxima H minus Reverse Transciptase.

The total volume should now be 20 ul

- 44 Mix by flicking the tube and spin down
- 45 Incubate using the following protocol

45.1

Cycle step	Temp	Time	# of
			cycles
Reverse Transcription and strand-switching	42°	90 minutes	1
Heat inactivation	85°	5 minutes	1
Hold	4°	∞	-

Adapator extension

46 Add adaptors to the cDNA using PCR

46.1 SPrime STAR GXL DNA

From the polymerase Takara Catalog #R050B

And

⊠ PCR barcoding expansion 96 **Oxford Nanopore**

Technologies Catalog #EXP-PBC096

Reaction mix;

(10 ul) 5x Prime STAR GXL buffer

(1 ul) 10 mM KAPA dNTP mix

(1 ul) Prime STAR GXL DNA polymerase

(5 ul) cDNA

(1 ul) primer (Barcode mix from nanopore

46.2 PCR program

1 cycle

98° - 30 seconds

10 cycles

98° - 10 seconds

64° - 15 seconds

68° - 10 seconds

1 cycle

68° - 5 minutes

4° - ∞

47 Serapure/Ampure purification

47.1 Bead extraction:

- Add 1.8X beads to samples
- flick to mix
- incubate for 10 minutes at room temperature
- use the magnet to collect the DNA-beads
- discard supernatant
- wash with 70% ethanol
- dry at 37° for 3 minutes
- elute with 20 ul TE buffer
- incubate for 5 minutes at room temperature
- use the magnet to collect the DNA-beads
- collect supernatant into a new tube

Ligation reaction

48 First step

48.1 Significant William Willi

From the Illumina NEB Catalog #E7645S

(7 ul) Ultra II End prep reaction buffer (NEB, E7647AA) (3 ul) Ultra I End prep Enzyme mix (NEB, E7646AA)

(50 ul) cDNA with adapters

Total volume of 60 ul

 $\textbf{Citation:} \ \ \text{Eric RA Pederson (02/09/2021)}. \ \ \text{RNA and DNA extraction (Qiagen) of frozen tissue to nanopore sequencing} \ \ .$

48.2 PCR program

20° for 5 minutes 65° for 5 minutes

49 Serapure/Ampure purification using a 1:1 mix ration (60:60)

49.1 Bead extraction:

- Add 1.8X beads to samples
- flick to mix
- incubate for 10 minutes at room temperature
- use the magnet to collect the DNA-beads
- discard supernatant
- wash with 70% ethanol
- dry at 37° for 3 minutes
- elute with 20 ul TE buffer
- incubate for 5 minutes at room temperature
- use the magnet to collect the DNA-beads
- collect supernatant into a new tube

50 Ligation reaction

From the Biolabs Catalog #M0239L

(60 ul) purified DNA (25 ul) Ligation buffer (10 ul) Ligase (5 ul) adaptor mix

- 51 Incubate for 10 minutes at room temperature
- 52 /

Modified Serapure/Ampure bead purification

- 52.1 Add 1.8X beads to samples
 - flick to mix
 - incubate for 10 minutes at room temperature
 - use the magnet to collect the DNA-beads
 - discard supernatant
 - wash with SFB (250 ul)
 - dry at 37° for 3 minutes
 - elute with 15 ul TE buffer
 - incubate for 5 minutes at room temperature
 - use the magnet to collect the DNA-beads

53 Run Qubit

Loading Nanopore flow cell

54 ⊠ Flow Cell Priming Kit Oxford Nanopore

From the **Technologies Catalog #EXP-FLP002**

⊠ Flow Cell (R9) **Oxford Nanopore**

And using a **Technologies Catalog #FLO-MIN106D**

DNA library - 12 ul (of the 14 ul) Sequencing buffer (SQB) - 37.5 ul Loading Beads - 25.5 ul

Total volume of 75 ul

- Thaw the Sequencing Buffer (SQB), Loading Beads (LB), Flush Tether (FLT) and one tube of Flush Buffer (FB) at RT before placing the tubes on ice as soon as thawing is complete
- Mix the Sequencing Buffer (SQB) and Flush Buffer (FB) tubes by vortexing, spin down and return to ice.
- 57 Spin down the Flush Tether (FLT) tube, mix by pipetting, and return to ice.
- Open the lid of the nanopore sequencing device and slide the flow cell's priming port cover clockwise so that the priming port is visible.
- After opening the priming port, check for small bubbles under the cover. Draw back a small volume to remove any bubble (a few μ I) as follows:
 - **59.1** Set a P1000 pipette to 200 μl
 - 59.2 Insert the tip into the priming port
 - Turn the wheel until the dial shows 220-230 μl, or until you can see a small volume of buffer entering the pipette tip
 Care must be taken when drawing back buffer from the flow cell. The array of pores must be covered by buffer at all times. Removing more than 20-30 μl risks a loss of sequencing channels.
 - 59.4 Care must be taken when drawing back buffer from the flow cell. The array of pores must be covered

by buffer at all times. Removing more than 20-30 µl risks a loss of sequencing channels.

60	Prepare the flow	cell priming	mix as follows:
----	------------------	--------------	-----------------

- Add 30 µl of thawed and mixed Flush Tether (FLT) directly to the tube of thawed and mixed Flush Buffer (FB), and mix by pipetting up and down.
- 61 Load 800 μl of the priming mix into the flow cell via the priming port, avoiding the introduction of air bubbles. Wait for 5 minutes.
- Thoroughly mix the contents of the Loading Beads (LB) by pipetting. Note that The Loading Beads (LB) tube contains a suspension of beads.

These beads settle very quickly. It is vital that they are mixed immediately before use.

- 63 In a new tube, prepare the library for loading as follows:
 - 63.1 37.5 μl Sequencing Buffer (SQB)
 - 25.5 µl Loading Beads (LB), mixed immediately before use
 - 12 µl cDNA library prepared as described in SOP ID:0005 75 ul Total
- 64 Complete the flow cell priming:
 - Gently lift the SpotON sample port cover to make the SpotON sample port accessible.
 - 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.
- 65 Mix the prepared library gently by pipetting up and down just prior to loading.
- Add 75 μ I 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.
- Gently replace the SpotON sample port cover, making sure the bung enters the SpotON port, close the priming port and replace the MinION lid.