

Mar 22, 2023

Version 4

Extraction and ONT MinION Library Preparation of uHMW gDNA V.4

DOI

<https://dx.doi.org/10.17504/protocols.io.j8nlkww11l5r/v4>

Kaylee S. Herzog¹, jfauver¹

¹University of Nebraska Medical Center



Kaylee S. Herzog

UNMC

Create & collaborate more with a free account

Edit and publish protocols, collaborate in communities, share insights through comments, and track progress with run records.

Create free account

OPEN  ACCESS



DOI: <https://dx.doi.org/10.17504/protocols.io.j8nlkww11l5r/v4>

Protocol Citation: Kaylee S. Herzog, jfauver 2023. Extraction and ONT MinION Library Preparation of uHMW gDNA. protocols.io <https://dx.doi.org/10.17504/protocols.io.j8nlkww11l5r/v4> Version created by **Kaylee S. Herzog**

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

Protocol status: Working

We use this protocol and it's working

Created: March 22, 2023



Last Modified: March 22, 2023

Protocol Integer ID: 79273

Keywords: extraction, gDNA, MinION, nematode, library preparation, uHMW gDNA, ONT, ont minion library preparation of uhmw gdna, uhmw gdna, parasitic nematode, ont minion library preparation, oxford nanopore technology, minion library preparation, genomic dna, dnatm magbead, single adult hookworm, dna

Abstract

This custom protocol optimizes extraction, purification, and Oxford Nanopore Technologies (ONT) MinION library preparation for ultra-high molecular weight genomic DNA (uHMW gDNA) from parasitic nematodes. It can be used effectively with both low-input samples (e.g., a single adult hookworm) and high-input samples (e.g., a chunk of tissue from an *Ascaris* sp. adult).

Protocols on which this workflow is based:

- [Zymo® Quick-DNA™ Magbead Plus Kit protocol](#)
- [Oxford Nanopore Technologies® SQK-LSK-109 gDNA Ligation Sequencing.protocol](#)
- [Zymo® DNA Clean & Concentrator™ Magbead Kit](#)



Protocol materials

- ☒ Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-1**
- ☒ Zymo Biofluid & Solid Tissue Buffer **Zymo Research Catalog #D4081-3-25**
- ☒ Zymo Proteinase K **Zymo Research Catalog #D3001-2-20**
- ☒ NEB Monarch Pestle **NEB Catalog #T3002-1**
- ☒ Zymo Quick-DNA™ MagBinding Buffer **Zymo Research Catalog #D4077-1-150**
- ☒ Zymo MagBinding Beads **Zymo Research Catalog #D4100-2-6**
- ☒ Zymo DNA Pre-Wash Buffer **Zymo Research Catalog #D3004-5-250**
- ☒ Zymo g-DNA Wash Buffer **Zymo Research Catalog #D3004-2-200**
- ☒ Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-50**
- ☒ Nuclease-free Water
- ☒ NEBNext Ultra II End Prep Reaction Buffer **New England Biolabs Catalog #E7647**
- ☒ NEBNext Ultra II End Prep Enzyme Mix **New England Biolabs Catalog #E7646**
- ☒ NEBNext® FFPE DNA Repair Buffer **New England Biolabs Catalog #E7180S**
- ☒ NEBNext FFPE DNA Repair Mix - 96 rxns **New England Biolabs Catalog #M6630L**
- ☒ Zymo DNA MagBinding Buffer **Zymo Research Catalog #D4012-1-50**
- ☒ Zymo MagBinding Beads **Zymo Research Catalog #D4100-5-2**
- ☒ Zymo DNA Wash Buffer **Zymo Research Catalog #D4003-2-24**
- ☒ Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-10**
- ☒ AMPure XP Beads **Beckman Coulter Catalog #A63880**
- ☒ ONT Adaptor Mix (AMX) **Oxford Nanopore Technologies**
- ☒ Quick T4 DNA Ligase **New England Biolabs Catalog #E7180S**
- ☒ ONT Ligation Buffer (LNB) **Oxford Nanopore Technologies**
- ☒ Elution Buffer (EB) **Oxford Nanopore Technologies**
- ☒ Short Fragment Buffer (SFB) **Oxford Nanopore Technologies**
- ☒ Long Fragment Buffer (LFB) **Oxford Nanopore Technologies**
- ☒ Short Fragment Buffer (SFB) **Oxford Nanopore Technologies**
- ☒ Elution Buffer (EB) **Oxford Nanopore Technologies**



Before start

For new kits, add 1,040 μ L Zymo Proteinase K Storage Buffer to each tube of Zymo Proteinase K (20 mg) prior to use. The final concentration of Proteinase K is ~20 mg/ml. Store resuspended Proteinase K at -20°C after mixing.



Part 1: Ultra-HWM gDNA extraction | Zymo Quick-DNA HWM MagBead Plus Kit | ~3 hr

- 1 Set dry bath to  55 °C
- 2 For each sample, add the following to a clean 1.5 mL microcentrifuge tube to create a master mix:

 95 µL Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-1** 95 µL Zymo Biofluid & Solid Tissue Buffer **Zymo Research Catalog #D4081-3-25** 10 µL Zymo Proteinase K **Zymo Research Catalog #D3001-2-20**

- 2.1 Vortex the master mix gently to mix, then spin down and keep on ice

- 3 Using a new pipette tip or sterilized forceps, add one whole worm (or a piece of tissue) directly from tissue preservative to the bottom of a clean 1.5 mL microcentrifuge tube

Note

Transfer as little tissue preservative liquid as possible to the new tube during this process

- 4 Use a new  NEB Monarch Pestle **NEB Catalog #T3002-1** to grind and crush the tissue in the tube. Keep the pestle in the tube
- 5 Add  200 µL master mix (prepared in Part 1 Step 2) to each tube containing tissue and pestle
- 6 Continue using the pestle to grind the tissue within the master mix until fully homogenized. Remove the pestle, being careful to keep any tissue in the tube by wiping the pestle on the tube edges as it is removed
- 7 Close the tube and mix by inverting and flicking gently, then spin down briefly to recollect tissue and liquids



- 8 Incubate sample in dry bath at 55°C for 02:30:00 or until tissue solubilizes. During incubation, flick tube every 00:20:00 to agitate tissues, then briefly spin down to recollect liquids and replace tube in dry bath

2h 50m

**Note**

If a very large amount of input tissue was used: It is likely there will still be visible tissue even after hours of lysis. If so, centrifuge the sample for 00:01:00 at

10000 x g or greater to pellet debris, then pipette all liquids into a new clean 1.5 μL microcentrifuge tube. (The majority of gDNA will be contained in the layer of liquid just above the pellet, so pipette carefully to get as much liquid as possible without disturbing the debris.) Discard the tube contain the pelleted debris and use the retained supernatant for Part 2.

Part 2: Ultra-HWM gDNA purification | Zymo Quick-DNA HWM MagBead Plus Kit | ~4 hr + overnight incubation

2h 20m

- 9 Set dry bath to 37°C
- 10 Add 400 μL Zymo Quick-DNA™ MagBinding Buffer Zymo Research Catalog #D4077-1-150 to each sample
- 11 Flick tubes to mix, then spin down briefly to recollect liquids
- 12 Add 33 μL Zymo MagBinding Beads Zymo Research Catalog #D4100-2-6 to each sample

Note

MagBinding Beads settle quickly, so ensure beads are kept in suspension while dispensing by vortexing the beads each time before they are added to a sample



- 13 To ensure DNA binds to beads, mix on a rotator mixer at a low speed for  01:30:00 at  Room temperature . Spin down briefly before proceeding with the next step

1h 30m



- 14 Set sample tubes on a magnetic stand until beads have separated from solution, then remove and discard the supernatant. Remove sample tubes from the magnetic stand.

Note

Some beads may adhere to the sides of the tube. When removing supernatant, aspirate slowly to allow these beads to be pulled to the magnet as the liquid level is lowered.

- 15 Add  500 μ L  Zymo Quick-DNA™ MagBinding Buffer **Zymo Research Catalog #D4077-1-150** to each sample

- 16 Flick to mix initially, then mix on a rotator mixer at a low speed for  00:20:00 at  Room temperature . Spin down briefly before proceeding with the next step

20m



- 17 Set sample tubes on a magnetic stand until beads have separated from the solution, then remove and discard the supernatant. Remove sample tubes from the magnetic stand

Note

Some beads may adhere to the sides of the tube. When removing supernatant, aspirate slowly to allow these beads to be pulled to the magnet as the liquid level is lowered.

- 18 Add  500 μ L  Zymo DNA Pre-Wash Buffer **Zymo Research Catalog #D3004-5-250** to each sample

- 19 Flick to mix, then spin down briefly

- 20 Set sample tubes on a magnetic stand until beads have separated from solution, then remove and discard the supernatant. Remove sample tubes from the magnetic stand

**Note**

Some beads may adhere to the sides of the tube. When removing supernatant, aspirate slowly to allow these beads to be pulled to the magnet as the liquid level is lowered.

- 21 Add  900 μ L
 Zymo g-DNA Wash Buffer **Zymo Research Catalog #D3004-2-200** to each sample

- 22 Flick to mix, then spin down briefly

- 23 Transfer the entire sample (all liquid and beads) to a new clean 1.5 mL microcentrifuge tube

**Note**

Transfer to a new tube ensures that any salts that are stuck to the lid of the tube do not get carried over

- 24 Set samples (now in new tubes) on a magnetic stand until beads have separated from the solution, then remove and discard the supernatant. Remove sample tubes from the magnetic stand

Note

Some beads may adhere to the sides of the tube. When removing supernatant, aspirate slowly to allow these beads to be pulled to the magnet as the liquid level is lowered

- 25 Add  900 μ L
 Zymo g-DNA Wash Buffer **Zymo Research Catalog #D3004-2-200** to each sample

- 26 Flick to mix, then spin down briefly

- 27 Transfer the entire sample (all liquid and beads) to a new clean 1.5 mL microcentrifuge tube



**Note**

Transfer to a new tube ensures that any salts that are stuck to the lid of the tube do not get carried over

- 28 Set samples (now in new tubes) on a magnetic stand until beads have separated from the solution, then remove and discard the supernatant. Leave sample tubes on the magnetic stand

Note

Some beads may adhere to the sides of the tube. When removing supernatant, aspirate slowly to allow these beads to be pulled to the magnet as the liquid level is lowered

- 28.1 Use a P10 pipette to remove any residual liquid from the bottom of the tube

- 29 Air dry the beads for up to  00:20:00 and proceed to next step once beads are dry, but not over-dry

20m

Note

It may take less time for the beads to dry, so check them often during this process. Beads will change in appearance from glossy black when still wet to a matte black/brown when fully dry. Over drying the beads may result in lower gDNA recovery.

- 30 Add  50 μ L  Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-50** to each sample and flick gently several times to mix. Spin down briefly

Note

If you plan to Qubit and TapeStation the extraction, it is a good idea to elute in 52 μ L (rather than 50 μ L) to have 1 μ L easily available for each quality control analysis



31 Incubate in dry bath at 37°C for 02:00:00 . During incubation, flick tube every 00:20:00 to agitate tissues, then briefly spin down to recollect liquids and replace tube in dry bath

2h 20m



32 Incubate on bench top at Room temperature overnight.



33 After overnight incubation, set tubes on a magnetic stand until beads have separated from solution, then move the supernatant (now containing eluted gDNA) to a new clean 1.5 mL microcentrifuge tube

Note

The eluted DNA can be used immediately or stored at 4°C or -20°C for future use

33.1 Re-suspend beads in $20\ \mu\text{L}$ of Nuclease-free Water in case there is no (or not enough) gDNA in final elution

34 Use $1\ \mu\text{L}$ of final elution to quantify extraction via Qubit analysis

35 Use $1\ \mu\text{L}$ of final elution to assess fragment size distribution via TapeStation



Part 3: DNA repair and end-prep | Zymo Clean & Concentrator, ONT Ligation Sequencing, & NEBNext Companion Kits | ~1.5 hr

1h

36 Set dry bath to 65°C

37 Defrost the needed NEB DNA and End Repair reagents on ice (see Part 3 Step 38)

38 For each sample, add the following to a clean 0.2 mL PCR tube to create a master mix, pipetting 10–20 times between each addition to mix:



🧪 3.5 µL

⊗ NEBNext® FFPE DNA Repair Buffer **New England Biolabs Catalog #E7180S**

🧪 2 µL

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

🧪 3.5 µL

⊗ NEBNext Ultra II End Prep Reaction Buffer **New England Biolabs Catalog #E7647**

🧪 3 µL

⊗ NEBNext Ultra II End Prep Enzyme Mix **New England Biolabs Catalog #E7646**

38.1 Keep master mix on ice

39 Add 🧪 12 µL of master mix (prepared in Part 3 Step 38) from the PCR tube directly into each 1.5 mL microcentrifuge tube containing extracted & purified uHWM gDNA (from Part 2). Mix all components by gently flicking, and spin tubes down to recollect liquids

40 Incubate samples at 🌡 Room temperature for ⌚ 00:10:00

10m



41 Incubate samples in dry bath at 🌡 65 °C for ⌚ 00:10:00

10m



42 Add 4 volumes of
⊗ Zymo DNA MagBinding Buffer **Zymo Research Catalog #D4012-1-50** to each sample and mix well by flicking and inverting

Note

Example for calculating 4 volumes: If input is 50 µL gDNA, add 200 µL DNA MagBinding Buffer

43 Spin samples down briefly and add 🧪 20 µL

⊗ Zymo MagBinding Beads **Zymo Research Catalog #D4100-5-2**

**Note**

MagBinding Beads settle quickly, so ensure beads are kept in suspension while dispensing by vortexing beads each time before they are added to a sample

44 Mix samples on rotating mixer at a low speed at Room temperature for

01:30:00

1h 30m



45 Briefly spin down samples and pellet on a magnetic stand (1–2 min) until the supernatant is clear and colorless. With the tubes still on the magnet, pipette off and discard the supernatant

46 Add 500 µL Zymo DNA Wash Buffer **Zymo Research Catalog #D4003-2-24** and then remove from magnetic stand, and mix well by flicking and inverting

47 Briefly spin samples down briefly and transfer to magnetic stand to allow beads to pellet until solution is clear (1–2 min). With the tubes still on the magnet, pipette off and discard the supernatant

48 Add 500 µL Zymo DNA Wash Buffer **Zymo Research Catalog #D4003-2-24** and then remove from magnetic stand, and mix well by flicking and inverting

49 Briefly spin samples down briefly and transfer to magnetic stand to allow beads to pellet until solution is clear (1–2 min). With the tubes still on the magnet, pipette off and discard the supernatant

50 Air dry the beads for 00:10:00

10m

Note

MagBinding Beads utilize a different chemistry than SPRI beads (e.g., AMPure XP beads) so there is not the same risk of over-drying. It is important for optimal elution that the residual buffer is completely removed/evaporated from the beads

51 Add 51 µL Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-10**



- 52 Manually agitate samples for 00:10:00 by gently flicking/inverting (and occasionally spinning down to recollect liquids)

10m

**Note**

This volume is too small to be able to use most rotator mixers effectively, so manual agitation is necessary

- 53 Briefly spin samples down and pellet the beads on a magnet until the eluate is clear and colorless (1–2 min)
- 54 Remove and retain the 51 μL of eluate (containing repaired & end-prepped DNA) to a new clean 1.5 mL microcentrifuge tube
- 55 Use 1 μL of final elution to quantify via Qubit assay

Part 4: Adaptor ligation and clean up | ONT Ligation Sequencing & NEBNext Companion Kits | ~3 hr + overnight incubation

1h

- 56 Set dry bath to 37 °C
- 57 Remove AMPure XP Beads **Beckman Coulter Catalog #A63880** from storage at 4 °C and allow them to come to Room temperature
- 58 Spin down ONT Adaptor Mix (AMX) **Oxford Nanopore Technologies** and Quick T4 DNA Ligase **New England Biolabs Catalog #E7180S** and place on ice
- 59 Thaw ONT Ligation Buffer (LNB) **Oxford Nanopore Technologies** at Room temperature, spin down, and mix by pipetting. Place on ice immediately after thawing and mixing
- 60 Thaw Elution Buffer (EB) **Oxford Nanopore Technologies** at Room temperature, vortex to mix, spin down, and place on ice



61 Thaw one tube each of

 Short Fragment Buffer (SFB) **Oxford Nanopore Technologies** and

 Long Fragment Buffer (LFB) **Oxford Nanopore Technologies** at

 Room temperature , vortex to mix, spin down, and place on ice

62 For each sample, add the following, in order, to a new clean 1.5 mL microcentrifuge tube, pipetting 10–20 times between each addition to mix:

 25 μL  **ONT Ligation Buffer (LNB) Oxford Nanopore Technologies**

 10 μL  **Quick T4 DNA Ligase New England Biolabs Catalog #E7180S**

 5 μL  **ONT Adaptor Mix (AMX) Oxford Nanopore Technologies**

62.1 Keep master mix on ice after mixing

63 For each sample, prepare 1:3 SFB:LFB titrated wash mix by adding the following to a new clean 1.5 mL microcentrifuge tube, and then vortex to mix:

 125 μL  **Short Fragment Buffer (SFB) Oxford Nanopore Technologies**

 375 μL  **Long Fragment Buffer (LFB) Oxford Nanopore Technologies**

Note

For samples of sufficiently high input concentration where read length can be prioritized over gDNA retention, you may wish to instead use 1:5 SFB:LFB (i.e., 16.66 μL SFB: 88.34 μL LFB) or LFB, only

63.1 Keep titrated wash mix on ice after vortexing

64 Pipette  40 μL of master mix (prepared in Part 4 Step 62) directly into entire volume of repaired and end-prepped gDNA from Part 3. Mix all components by gently flicking and spin tube down to recollect liquids

65 Incubate the reaction  00:15:00 at  Room temperature

15m



**Note**

If you have omitted the bead-based purification steps from the second half of Part 3, do not incubate the reaction for longer than ⌚ 00:10:00

- 66 Resuspend  AMPure XP Beads **Beckman Coulter Catalog #A63880** by vortexing and add 0.4X volume resuspended beads to each sample, then flick to mix

Note

AMPure XP Beads settle quickly, so ensure beads are kept in suspension while dispensing by vortexing beads each time before they are added to a sample

Note

Example for calculating 0.4X volume: If input is 89 μL (after adding master mix), add 35.6 μL AMPure XP Beads

- 67 Mix on a rotator mixer at a low speed for ⌚ 01:00:00 at 🌡 Room temperature 1h
- 68 Spin down the sample and pellet on a magnetic stand. Keeping the tube on the stand, pipette off and discard the supernatant
- 69 Wash the beads by adding  250 μL 1:3 SFB:LFB titrated wash mix (prepared in Part 4 Step 63). Flick the beads to resuspend, spin down, then return to the magnetic rack and allow the beads to pellet. Remove the supernatant using a pipette and discard
- 70 Wash the beads by adding  250 μL 1:3 SFB:LFB titrated wash mix (prepared in Part 4 Step 63). Flick the beads to resuspend, spin down, then return to the magnetic rack and allow the beads to pellet. Remove the supernatant using a pipette and discard
- 71 Spin down the beads and place them back on the magnetic rack. Use a P10 pipette to pipette off any residual liquid and allow beads to air-dry for ⌚ 00:00:30 to 2m 30s



00:02:00

Note

Do not allow the pellet of beads to dry to the point of cracking! Over-drying beads will result in reduced yields

72 Remove the tube from the magnetic stand and resuspend the beads in 15 μL

Elution Buffer (EB) **Oxford Nanopore Technologies**

73 Briefly spin down and incubate in dry bath at 37 °C for 02:00:00 . During incubation, flick tube every 00:20:00 to agitate tissues, then briefly spin down to recollect liquids and replace tube in dry bath

2h 20m

**Note**

For HMW & uHMW gDNA, incubation at 37 °C for longer times can improve the recovery of long fragments

74 Incubate on the bench top at Room temperature overnight



75 After overnight incubation, pellet the beads on a magnet until the eluate is clear and colorless (at least 1 min)

76 Remove and retain the 15 μL of eluate (containing the prepared library) to a new clean 1.5 mL microcentrifuge tube

77 Use 1 μL of final elution to quantify library via Qubit analysis



Note

Note: For same-day or near-future sequencing, store the prepared library on ice or at

🌡️ 4 °C

until ready to be loaded onto a flow cell. Otherwise, store libraries at

🌡️ -20 °C

78 Use 🧴 1 µL of final elution to assess fragment size distribution via TapeStation

