

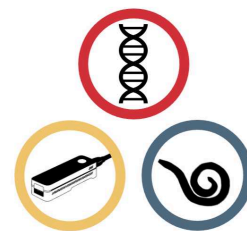
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Version 5

# Extraction and ONT MinION Library Preparation of uHMW gDNA V.5

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Kaylee S. Herzog<sup>1</sup>, jfauver<sup>1</sup>

<sup>1</sup>University of Nebraska Medical Center



Kaylee S. Herzog

UNMC

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**Protocol status:** Working

**We use this protocol and it's working**

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## 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-114 gDNA Ligation Sequencing protocol](#)
- [Zymo® DNA Clean & Concentrator™ Magbead Kit](#)

## Materials

- Oxford Nanopore Technologies Ligation Sequencing Kit V14 (SQK-LSK-114)
- Zymo Quick-DNA Magbead Plus Kit (D4081)
- Zymo DNA Clean & Concentrator Magbead Kit (D4012)
- NEBNext Companion Module for Oxford Nanopore Technologies Ligation Sequencing (E7180S)
- NEB Monarch Pestle (one per specimen; T3000L)
- AMPure XP streptavidin beads (A63880)
- Minicentrifuge
- Micropipettors & tips (wide-bore tips STRONGLY recommended for pipetting up gDNA or libraries)
- Dry bath
- Rotator mixer (e.g., PR1MA Roto-Mini Mixer)
- Magnetic separation rack (e.g., MagJET Separation Rack)
- 1.5 mL microcentrifuge tubes (DNase-free, DNA low bind STRONGLY recommended)
- 0.2 mL PCR tubes
- Microcentrifuge (only if processing large [i.e., >2 cm] specimens)



## 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® FFPE DNA Repair Buffer **New England Biolabs Catalog #E7180S**
- ✕ NEBNext FFPE DNA Repair Mix - 96 rxns **New England Biolabs Catalog #M6630L**
- ✕ NEBNext Ultra II End Prep Reaction Buffer **New England Biolabs Catalog #E7647**
- ✕ NEBNext Ultra II End Prep Enzyme Mix **New England Biolabs Catalog #E7646**
- ✕ 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**
- ✕ Ligation Adaptor (LA) **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  $\mu$ 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 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  $55^{\circ}\text{C}$  for 02:30:00 to Overnight 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

3h 10m

**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  $\mu\text{L}$  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  $37^{\circ}\text{C}$
- 10 Add 400  $\mu\text{L}$  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  $\mu\text{L}$  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  02:00:00 at  Room temperature . Spin down briefly before proceeding with the next step

2h



- 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  $\mu$ 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  $\mu$ 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  $\mu\text{L}$

 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  $\mu\text{L}$

 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  $\mu$ 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  $\mu$ L (rather than 50  $\mu$ L) to have 1  $\mu$ 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 µL of Nuclease-free Water in case there is no (or not enough) gDNA in final elution

34 Use 1 µL of final elution to quantify extraction via Qubit analysis

35 Use 1 µL 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  $\mu$ L 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  $\mu$ L 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 52  $\mu$ L Zymo DNA Elution Buffer **Zymo Research Catalog #D3004-4-10**



- 52 Manually agitate samples for 00:10:00 to 00:20:00 by gently flicking/inverting (and occasionally spinning down to recollect liquids)

30m

**Note**

This volume is too small to be able to use most rotator mixers effectively, so manually 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 52  $\mu\text{L}$  of eluate (containing repaired & end-prepped DNA) to a new clean 1.5 mL microcentrifuge tube

- 55 Use 1  $\mu\text{L}$  of final elution to quantify via Qubit assay

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

\*

**Note**

The sequencing adaptors ligated in the next section will affect the validity of TapeStation runs, so assessing the fragment distribution at this stage (i.e., after DNA repair and end preparation) is crucial for being able to estimate the molarity of your final library

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

1h

- 57 Set dry bath to 37 °C

- 58 Remove AMPure XP Beads **Beckman Coulter Catalog #A63880** from storage at 4 °C and allow them to come to Room temperature



- 59 Spin down Ligation Adaptor (LA) **Oxford Nanopore Technologies** and Quick T4 DNA Ligase **New England Biolabs Catalog #E7180S** and place on ice
- 60 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
- 61 Thaw Elution Buffer (EB) **Oxford Nanopore Technologies** at Room temperature , vortex to mix, spin down, and place on ice
- 62 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
- 63 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 Ligation Adaptor (LA) **Oxford Nanopore Technologies**
  - 10 µL Quick T4 DNA Ligase **New England Biolabs Catalog #E7180S**
  - 5 µL Ligation Adaptor (LA) **Oxford Nanopore Technologies**
- 63.1 Keep master mix on ice after mixing
- 64 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 untitrated LFB, only



64.1 Keep titrated wash mix on ice after vortexing

65 Pipette  40  $\mu\text{L}$  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

66 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



67 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  $\mu\text{L}$  (after adding master mix), add 35.6  $\mu\text{L}$  AMPure XP Beads

68 Mix on a rotator mixer at a low speed for  01:00:00 at  Room temperature

1h

69 Spin down the sample and pellet on a magnetic stand. Keeping the tube on the stand, pipette off and discard the supernatant

70 Wash the beads by adding  250  $\mu\text{L}$  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 Wash the beads by adding  250  $\mu\text{L}$  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

- 72 Spin down the beads and place them back on the magnetic rack. Use a P10 pipette to pipette of 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

- 73 Remove the tube from the magnetic stand and resuspend the beads in  15  $\mu\text{L}$

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

- 74 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

- 75 Incubate on the bench top at  Room temperature overnight



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





- 77 Remove and retain the  15  $\mu\text{L}$  of eluate (containing the prepared library) to a new clean 1.5 mL microcentrifuge tube
- 78 Use  1  $\mu\text{L}$  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