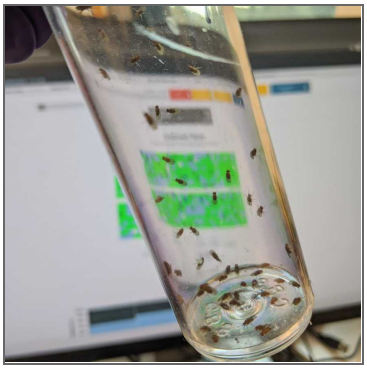

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MANUSCRIPT CITATION:

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

DNA extraction and Nanopore library prep from single flies

Forked from DNA extraction and Nanopore library prep from 15-30 whole flies- V.3.2

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ABSTRACT

This protocol is optimized for rapid and cost-effective (about $150) genome assembly of Drosophila species from single flies using ONT PromethION sequencers. Following this protocol, a typical Drosophila Nanopore sequencing run should have read N50 of 5-20kbp. Sequencing is halted at about 40-60X depth of coverage (10-14 Gbp on MinKNOW for most species, assuming ~20% of data is removed by a quality filter).

GUIDELINES

This protocol is used to prepare 10-1000 ng of Nanopore library from a single reaction. The amount loaded onto the flow cell depends on the quality of the library. Larger amounts of longer libraries should be loaded to keep the molar concentration of adapted ends consistent. However, longer libraries tend to clog the flow cell more quickly, necessitating frequent DNase flushing and reloading and reducing throughput. Two libraries with the same N50 but where one has a larger number of >100kb fragments will sequence differently.

Ballpark estimates of R10.4.1 library loads maintaining good pore occupancy are:
Read N50 1kb: 10-15 ng library
Read N50 5kb: 25 ng library
Read N50 10kb: 50 ng library
Read N50 20kb: 100 ng library
Read N50 30kb: 200 ng library
Read N50 40kb+: 300 ng library

To maximize read lengths, one should not wait until all active pores have been depleted to flush and reload. A DNase flush should take place as soon as sequencing throughput starts to decrease, or about every 8 hours. A flow cell with loaded library can be stored at 4C overnight with no ill effects.

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PROTOCOL integer ID: 87469

Keywords: Drosophila, nanopore, ligation, bead-free, HMW, ultra-long, single insect, single fly

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MATERIALS

MATERIALS

- 10% SDS solution **Contributed by users**
- NEBNext Companion Module forOxford Nanopore Technologies Ligation Sequencing – 24 rxns **New England Biolabs Catalog #E7180S**
- Ligation sequencing kit 1D **Oxford Nanopore Technologies Catalog #SQK-LSK109**
- Chloroform **Millipore Sigma Catalog #CX1055-6**
- Phenol Chloroform Isoamyl Alcohol (25:24:1) Tris-saturated (pH 8.0) **Fisher Scientific Catalog #BP1752I-400**
- 3M sodium acetate **Contributed by users**
- Proteinase K Solution (20 mg/mL) RNA grade **Thermo Fisher Scientific Catalog #25530049**
- RNase A solution **Millipore Sigma Catalog #R6148**
- Tris-EDTA (TE) buffer pH 8.0 1X **Contributed by users**
- Homogenization Buffer (HB) [0.1M NaCl 30mM Tris-HCl pH 8.0 10 mM EDTA 0.5 Triton X-100] **Contributed by users**
- Lysis Buffer (LB) [0.1M Tris-HCl pH 8.0; 0.1M NaCl; 20mM EDTA] **Contributed by users**
- Hydration Buffer (STE) [400mM NaCl 20mM Tris-HCl pH 8.0 30mM EDTA] **Contributed by users**
- DNAse wash buffer (DWB) [300mM KCl 2mM CaCl2 10mM MgCl2 15 mM HEPES pH 8.0] **Contributed by users**
- Elution Buffer (EB) [10 mM Tris-HCl pH 8.0] **Contributed by users**
- Short Read Eliminator (SRE) **Circulomics Catalog #SS-100-101-01**

DNA extractions are performed in Phase lock gel tubes to minimize handling and to maximize yield. A cheaper alternative to the official phase lock gel tubes is to put ~200uL of Dow Corning High Vacuum Grease into a 2.0 mL LoBind tube with a small syringe. Care should be take with homebrew phase lock gel tubes as using too little grease will result in the phase lock layer collapsing during the chloroform extraction step.

Although less effective, a solution of [0.8M NaCl, 9% w/v PEG8000, 10mM Tris-Cl pH 8.0] can be substituted for the Short Read Eliminator. See John Tyson's "Rocky

Mountain" protocol for more details (https://www.protocols.io/view/rocky-mountain-adventures-in-genomic-dna-sample-pr-7euhjew). The SRE XS or XL versions can be used if DNA is short or sufficiently long. This may require a bit of trial and error to figure out.

Equipment

DNA LoBind tubes, 1.5 mL	NAME
Tubes	TYPE
Eppendorf	BRAND
022431021	SKU
https://online-shop.eppendorf.us/US-en/Laboratory-Consumables-44512/Tubes-44515/DNA-LoBind-Tubes-PF-56252.html	LINK
1.5 mL	SPECIFICATIONS

Equipment

DNA LoBind tubes, 2.0 mL	NAME
Tubes	TYPE
Eppendorf	BRAND
022431048	SKU
https://online-shop.eppendorf.us/US-en/Laboratory-Consumables-44512/Tubes-44515/DNA-LoBind-Tubes-PF-56252.html	LINK
2.0 mL	SPECIFICATIONS

Equipment

Large-orifice pipet tips, 200uL

NAME

Pipette tips

TYPE

Fisher

BRAND

02-707-134

SKU

https://www.fishersci.com/shop/products/fisherbrand-large-orifice-pipet-tips-1-200-l-packaging-hrs-10-x-96/02707134

LINK

200 uL

SPECIFICATIONS

Equipment

Dounce Homogenizer, 2mL

NAME

Tissue Grinder

TYPE

Kimble

BRAND

885300-0002

SKU

https://www.kimble-chase.com/advancedwebpage.aspx?cg=886&cd=4&SKUTYPE=202&SKUFLD=SKU&DM=1250&WEBID=6856

LINK

2 mL with Pestles A and B

SPECIFICATIONS

Equipment	
5PRIME Phase Lock Gel tube, light, 2mL	NAME
Quantabio	BRAND
2302830	SKU
https://www.quantabio.com/phase-lock-gel	LINK
Light	SPECIFICATIONS

PROTOCOL MATERIALS

Tris-EDTA (TE) buffer pH 8.0 1X **Contributed by users** — Materials

Lysis Buffer (LB) [0.1M Tris-HCl pH 8.0; 0.1M NaCl; 20mM EDTA] **Contributed by users**

Materials

DNA Precipitation Buffer (PB) [0.8 M NaCl 9% w/v PEG 8000 10mM Tris-HCl pH 8.0] **Contributed by users**

Step 83

Agencourt AmPure XP beads **Contributed by users Catalog #A63880** — Step 51

DNAse wash buffer (DWB) [300mM KCl 2mM CaCl2 10mM MgCl2 15 mM HEPES pH 8.0] **Contributed by users**

Materials

Phenol Chloroform Isoamyl Alcohol (25:24:1) Tris-saturated (pH 8.0) **Fisher Scientific Catalog #BP1752I-400**

Materials, Step 12

Homogenization Buffer (HB) [0.1M NaCl 30mM Tris-HCl pH 8.0 10 mM EDTA 0.5 Triton X-100] **Contributed by users**

Materials

Proteinase K Solution (20 mg/mL) RNA grade **Thermo Fisher Scientific Catalog #25530049**

Materials

Ligation sequencing kit 1D **Oxford Nanopore Technologies Catalog #SQK-LSK109**

In Materials and 6 steps

10% SDS solution **Contributed by users** Materials

NEBNext Companion Module forOxford Nanopore Technologies Ligation Sequencing – 24 rxns **New England Biolabs Catalog #E7180S**

In Materials and 3 steps

DNA LoBind Tubes, 1.5 mL **Eppendorf Catalog #0030108051** In 3 steps

Chloroform **Merck MilliporeSigma (Sigma-Aldrich) Catalog #CX1055-6**

Materials, Step 16

Flow Cell Priming Kit (EXP-FLP002) **Oxford Nanopore Technologies Catalog #EXP-FLP002**

Step 92

3M Sodium Acetate **Contributed by users** In 3 steps

3M sodium acetate **Contributed by users** Materials

Lysis Master Mix (LMM) **Contributed by users** In 2 steps

Proteinase K Solution (20 mg/ml) RNA grade **Thermo Fisher Scientific Catalog #25530-049**

Step 4.4

Nuclease-free water or water filtered using a Milli-Q filtering system **Ambion Catalog #AM9932**

Step 47

RNase A solution **Merck MilliporeSigma (Sigma-Aldrich) Catalog #R6148**

Materials, Step 7

Hydration Buffer (STE) [400mM NaCl 20mM Tris-HCl pH 8.0 30mM EDTA] **Contributed by users**

Materials, Step 2

Large-Orifice Pipet Tips 200µL **Fisher Scientific Catalog #02-707-134** In 4 steps

Lysis Buffer **Contributed by users** In 2 steps

10 mM Tris-HCL pH 8.0 **Contributed by users** Step 32

Elution Buffer (EB) [10 mM Tris-HCl pH 8.0] **Contributed by users**

In Materials and 3 steps

Short Read Eliminator (SRE) **Circulomics Catalog #SS-100-101-01**

In Materials and 2 steps

Flowcell Wash Kit **Oxford Nanopore Technologies Catalog #EXP-WSH003**

In 2 steps

10% SDS **Contributed by users**

In 2 steps

PCR Tubes, 0.2mL, flat cap, natural, PCR Tube; 0.2mL; Natural; w/flat cap; 1000/Pk. **Thermo Fisher Catalog #3412**

Step 47

BEFORE START INSTRUCTIONS

This protocol is for DNA extraction from whole Drosophila. Before starting the protocol, individual flies are collected into 95% ethanol or other nucleic acid preservation liquid. We have sequenced flies shipped through the postal service (7 days in transit) without any major issues. Flies should ideally be preserved less than 6 months ago but the protocol has worked for 20 year old samples.

(Optional) Hydration of ethanol-fixed tissue

1h

1 Place flies on a sheet of filter paper and briefly dab with a Kimwipe to remove excess ethanol, then transfer the flies to a 1.5 mL tube.

2 Add 300 µL Buffer STE to the tube with the flies.

Hydration Buffer (STE) [400mM NaCl 20mM Tris-HCl pH 8.0 30mM EDTA] **Sigma Aldrich**

3 Incubate at room temperature for at least 00:15:00. 15m

Tissue homogenization

15m

4 Prepare Lysis Buffer **Sigma Aldrich**, 10% SDS **Sigma Aldrich**, 3M Sodium Acetate **Sigma Aldrich**, and Lysis Master Mix (LMM) **Sigma Aldrich**

4.1 For Lysis Buffer **Sigma Aldrich**:

- 5 mL [M] 0 Molarity (M) Tris-HCl pH 8.0
- 2 mL [M] 0.5 Molarity (M) EDTA
- 0.292 g NaCl
- 43 mL DI H20

4.2 For 10% SDS **Sigma Aldrich**:

5 g SDS
50 mL Distilled H20

4.3 For 3M Sodium Acetate **Sigma Aldrich**:

- 2.461 g NaOAc
- 10 mL DI H20

4.4 Per 1 fly, prepare Lysis Master Mix (LMM) **Sigma Aldrich**:

- 250 µL Lysis Buffer
- 3.13 µL of [M] 20 mg/mL Proteinase K Solution (20 mg/ml) RNA grade **Sigma Aldrich Catalog #25530-049** (final concentration of 561 µg/mL)
- 5 µL of [M] 2 mg/mL final concentration of 0.28% SDS)

5 Add 1 fly to a LoBind tube

Equipment	
DNA LoBind tubes, 1.5 mL	NAME
Tubes	TYPE
Eppendorf	BRAND
022431021	SKU
https://online-shop.eppendorf.us/US-en/Laboratory-Consumables-44512/Tubes-44515/DNA-LoBind-Tubes-PF-56252.html	LINK
1.5 mL	SPECIFICATIONS

6 Homogenize flies with NEB pestle, working quickly to avoid endogenous nuclease digestion of DNA. Add 200 µL LMM to the LoBind tube and mix thoroughly using the pestle.

Equipment	
Monarch Pestle Set	NAME
New England BioLabs	BRAND
T3000L	SKU
https://www.neb.com/products/t3000-monarch-pestle-set#Product%20Information	LINK

7 4 µL of [M] 20 mg/mL RNase A solution **Sigma Aldrich Catalog #R6148** (final concentration of 186 µg/mL)

Lysis

4h

8 Incubate lysis tube at 50 °C for 03:00:00. Mix the tube with gentle rocking and 3h 30m

inversion, until solution appears relatively homogeneous, at 00:30:00 intervals.

9

Phenol chloroform extraction

1h

10 Spin down 1 phase lock gel tube per sample at 15000 x g for 00:00:30 .

Note

Although not essental, phase lock gel tubes help minimize shearing and loss of yield caused by repeated pipetting. Dow Corning High Vacuum Grease is compositionally identical to the light phase lock gel material. We buy the 5.3oz tube from Amazon and squeeze some into a 10mL BD syringe for dispensing. This size of tube/syringe fits well for minimial mess and hassle. Avoid overfilling and air bubbles. Autoclave but be warned this may cause a mess, so wrap the syringe in foil beforehand.

About 250 µL of grease is placed into a 2mL LoBind tube to make the homebrew phase lock gel tube.

IMPORTANT: If an insufficient amount of grease is applied, the phase lock layer will collapse during the chloroform extraction.

Reference: https://bitesizebio.com/18944/diy-phase-separating-gel-clean-and-cheap/

Safety information

WARNING: If you are using normal tubes in lieu of LoBinds, do not use polystyrene tubes for the phenol-chloroform extraction. They will melt and burst in the centrifuge. Polypropylene tubes do not melt.

Equipment

5PRIME Phase Lock Gel tube, light, 2mL	NAME
Quantabio	BRAND
2302830	SKU
https://www.quantabio.com/phase-lock-gel	LINK
Light	SPECIFICATIONS

11 Transfer the homogenate/lysis solution to the phase lock gel tube by pipetting with a wide-bore tip.

12 Add an equal volume (about 200 µL) of Tris-saturated phenol chloroform isoamyl alcohol (PCI) to the phase lock tube.

Safety information

This should be performed inside the fume hood.

Phenol Chloroform Isoamyl Alcohol (25:24:1) Tris-saturated (pH 8.0) **Sigma Aldrich Catalog #BP1752I-400**

13 Mix by placing tubes on a rocker at medium speed for 00:08:00 . 8m

Note

Before placing on the rocker, invert by hand until you see the phenol-chloroform and sample as well mixed in the tube.

Note

We use a rocking platform, so the tubes are placed on their sides horizontally to maximize the surface area. When solution is well mixed, aqueous (top) layer will be a cloudy milky color.

14 Centrifuge the phase lock tube at 10000 x g for 00:08:00. Phase lock layer should now separate aqueous and organic layers. 8m

15 Repeat Phenol-Chloroform extraction: go to step #12

16 Add an equal volume (usually 200 µL) of chloroform to the tube.

Safety information

This step should be performed inside the fume hood.

Chloroform **Merck MilliporeSigma (Sigma-Aldrich) Catalog #CX1055-6**

17 Mix by placing tubes on a rocker at medium speed for 00:08:00. 8m

18 Centrifuge the phase lock tube at 15000 x g for 00:08:00. Phase lock layer should now separate aqueous and organic layers. 8m

19 Quickly decant the aqueous (top) layer into a fresh 1.5 mL LoBind tube.

Note

Try to perform the decanting step in a few seconds, and don't tap/shake the phase lock tube to get the last drops out. Care must be taken as the chloform significantly weakens the phase lock gel layer. If the phase lock tube is inverted for too long during decanting, the layer will collapse and everything will pour out. It's best to leave a couple of drops behind but avoid the hassle of cleaning this up.

IMPORTANT: It is highly recommended to use LoBind tubes in this and subsequent steps. The coating will prevent DNA sticking to the tube. This is helpful for maximizing yield and minimizing shearing.

Safety information

This step should be performed inside the fume hood.

Equipment

DNA LoBind tubes, 1.5 mL	NAME
Tubes	TYPE
Eppendorf	BRAND
022431048	SKU
https://online-shop.eppendorf.us/US-en/Laboratory-Consumables-44512/Tubes-44515/DNA-LoBind-Tubes-PF-56252.html	LINK
1.5 mL	SPECIFICATIONS

DNA precipitation, wash, and resuspension

1h 30m

20 Chill 100% ethanol on ice and make 500 µL per sample of fresh 70% ethanol using nuclease-free water.

21 Add 0.1x volume (typically 20 µL) of 3M sodium acetate to the extract from Step 19. Gently tap to mix.

3M Sodium Acetate **Contributed by users**

22 Add 2-2.5x volumes (typically 440 µL) of cold 100% ethanol to the tube, and mix with careful swirling and gentle rocking.

Expected result

DNA should slowly precipitate into a single white stringy clump, and un-precipitated DNA should be visible as shimmering strands at the bottom of the tube that are attached to the white clump. Depending on the size of the fly, DNA precipitation may not be visible.

Note

If the extraction tube turns cloudy, it is likely salt precipitation because the solution is too nonpolar and not DNA. Add water dropwise with thorough mixing and the solution should clear up.

23 Centrifuge the tube at 10000 x g for 00:10:00. 10m

24 While being careful not to disturb the pellet, pipette off the ethanol.

Note

We recommend leaving ~10-15uL of supernatant at the bottom of the tube, especially in cases where the DNA pellet may be invisible.

25 Add 175 µL of 70% ethanol.

26 Spin at 12500 x g for 00:05:00. 5m

27 Being careful not to disturb the DNA pellet, remove the ethanol.

28 Wash the pellet once more: go to step #25 and increase to 200uL 70% ethanol.

29 Spin at 12500 rcf for 00:01:00. 1m

30 Using a 10uL pipette, remove any excess ethanol.

31 Allow the DNA to air dry right until the moment it becomes translucent (usually 00:02:00). 2m
Do not over-dry the pellet.

> **Note**
>
> Oftentimes the whole DNA pellet will not become translucent but the edges of the pellet will. It is essential to not let the pellet dry out. Especially when working with "invisible pellets," shorten drying time.

32 Resuspend in 30uL of 10 mM Tris-HCL pH 8.0 **Sigma Aldrich** and incubate at 50 °C for at least 01:00:00. 1h

Note

We recommend 30uL of Tris for resuspension for R10.4.1 sequencing

33 Briefly spin down tube to gather any condensation and store at 4 °C.

DNA resuspension

1w

34 Keep the DNA at 4C for at least, one night depending on previous pellet size. It could be left to resuspend for even 1 week to obtain proper resuspension if need be.

Note

Due to sample limitations of working with single flies, there are no shearing steps in this protocol (different from the previous protocol). Instead, take all precautions to protect DNA from shearing.

35 Check sample concentration and quality of 1 µL aliquots using Qubit and Nanodrop.

Note

Ideally, this should Qubit at >75 ng/uL and have Nanodrop ratios of 260/280 >1.8 and 260/230 >2.0. If sample is above 150 ng/uL consider diluting with more 10mM tris.

Short Read Elimination 1

36 If sample concentration is greater than 40ng/uL, add equal volume (usually around 30 µL) SRE XL buffer. Using a wide-bore P200 tip, quickly but gently mix the tube. The precipitation buffer described here can be used in place of the SRE buffer but is not as effective at removing small DNA fragments as SRE.

Short Read Eliminator (SRE) **Circulomics Catalog #SS-100-101-01**

DNA LoBind Tubes, 1.5 mL **Eppendorf Catalog #0030108051**

Large-Orifice Pipet Tips 200µL **Sigma Aldrich Catalog #02-707-134**

37 Centrifuge the sample at 10000 x g for 00:30:00 or until DNA has pelleted and solution is no longer viscous. Meanwhile, prepare 500 µL fresh 70% ethanol with nuclease-free water.

38 Pipette off the supernatant, taking care not to disturb the DNA pellet.

> **Note**
>
> We have increased our yield by leaving 10-15 uL of supernatant in the bottom of the tube going into the first wash. This is particularly important if the pellet is invisible.

39 Add 150 µL of 70% ethanol. Pipette slowly, with the tip touching the front wall of the tube, so that the pellet is not disturbed.

40 Centrifuge at 10000 x g for 00:02:00.

41 Pipette off the supernatant, taking care not to disturb the DNA pellet. Make sure all the supernatant is removed and only the pellet remains.

42 Repeat wash: go to step #39

> **Note**
>
> The second centrifuge (step 43) can be shorter, ~1 minute.

43 Briefly spin sample and use a P10 to remove any remaining ethanol.

44 Resuspend pellet in 25 µL EB.

Elution Buffer (EB) [10 mM Tris-HCl pH 8.0] **Sigma Aldrich**

45 Incubate the tube on the heat block at 50 °C for at least 01:00:00. Briefly spin down the tube to collect condensation. Incubate for at least 48:00:00 at 4 °C.

> **Note**
>
> Before proceeding to the next stage, we recommend 1 µL Qubit to ensure there is still DNA.

DNA repair and end-prep

46 Thaw NEBNext repair and DNA-tailing mixes and buffers from the Nanopore Companion Module. Vortex buffers and flick mixes after thawing. Spin down tubes and keep chilled on ice.

NEBNext Companion Module forOxford Nanopore Technologies Ligation Sequencing – 24 rxns **New England Biolabs Catalog #E7180S**

47 Add 1.75 µL of FFPE DNA Repair Buffer, 1.75 µL of End-Prep Reaction Buffer, 1 µL of FFPE DNA Repair Mix, and 1.5 µL of End-Prep Reaction Mix to a PCR tube. Add remaining 24 µL of DNA sample to the PCR tube using a cut-off P200 tip. Mix tube with gentle flicking (or very gentle pipetting with the cut-off P200 tip), and then briefly spin down.

Note

To increase efficiency and decrease amount of pipette tips needed, prep PCR tubes with buffers and mixes and add the HMW DNA sample last. We have found no change in yield by halving the standard protocol, even with use of more than one fly.

PCR Tubes, 0.2mL, flat cap, natural, PCR Tube; 0.2mL; Natural; w/flat cap; 1000/Pk.**Thermo Fisher Catalog #3412**

Nuclease-free water or water filtered using a Milli-Q filtering system **Ambion Catalog #AM9932**

48 In a thermal cycler, incubate at 20 °C for 01:00:00 then 65 °C for 00:30:00. 1h 30m After this, sample can be held at 4 °C temporarily until ready to proceed.

Bead Clean Up

49 Prepare 250 µL of 80% ethanol per sample.

50 Transfer sample from PCR tube to a LoBind tube using a cut-off P200 tip.

51 Add equal volume of AmPure XP beads (normally 30 µL) to the sample. Immediately use a P200 wide bore tip to mix 5x.

Note

This step must be performed quickly; otherwise, DNA will precipitate onto pipette tip and will result in sample loss.

Note

If needed, briefly spin down to ensure there are no bubbles or any sample on the wall of the LoBind tube.

Agencourt AmPure XP beads **Contributed by users** **Catalog #A63880**

52 Incubate at room temperature for 00:20:00. 20m

53 Place the LoBind tube on a magnetic rack and wait until solution is clear and the beads are pelleted.

54 Remove the supernatant by placing pipette tip on the wall of the LoBind tube opposite of the beads. Pipette very slowly to ensure no DNA is pulled off.

Note

If DNA is pulled off, add supernatant back to tube and wait for solution to clear. Then try again.

55 Wash by adding 100 µL of 80% ethanol (enough to cover the beads on the wall of the LoBind tube).

Note

Work quickly to add the 80% ethanol at this step to avoid the beads drying out.

56 Remove and discard ethanol.

57 Wash again by adding 115 µL of 70% ethanol.

58 Remove and discard ethanol.

Note

Briefly spin and use a P10 pipette to remove any remaining excess of ethanol.

59 Resuspend sample in 32 µL of nuclease-free water.

60 Place tube on heat block at 50 °C until the pellet has dissolved.

Note

This step can take a long time. If there is concern about the DNA not resuspending off the beads, the tube can be stored at 4 °C overnight and then the sample removed from the beads the following morning.

61 Place LoBind tube on magnet rack until solution is clear.

62 Using a cut off P200 tip, remove the supernatant containing the aqueous DNA.

Note

Qubit 1 µL of sample to ensure DNA concentration before proceeding to next step.

Note

This is a safe stopping point. Sample can be stored at 4 °C .

Adapter ligation

63 Thaw AMXF, Quick T4 ligase, LNB, and LFB from the NEBNext Nanopore Companion Module and the Nanopore LSK110 kit. Mix AMXF, Quick T4 ligase, and LFB by flicking. Mix LNB by pipetting. Briefly spin the tubes down and keep chilled on ice.

NEBNext Companion Module forOxford Nanopore Technologies Ligation Sequencing – 24 rxns **New England Biolabs Catalog #E7180S**

Ligation sequencing kit 1D **Sigma Aldrich Catalog #SQK-LSK109**

64 Add 30 µL prepared DNA sample (the extra 1 µL can be used to Qubit), 2.5 µL AMXF, and 5 µL Quick T4 ligase to a fresh 1.5 mL DNA LoBind tube. Gently flick the tube to mix.

DNA LoBind Tubes, 1.5 mL **Eppendorf Catalog #0030108051**

NEBNext Companion Module forOxford Nanopore Technologies Ligation Sequencing – 24 rxns **New England Biolabs Catalog #E7180S**

Ligation sequencing kit 1D **Sigma Aldrich Catalog #SQK-LSK109**

65 Add 12.5 µL LNB to the sample. Working quickly, mix by gentle pipetting with a wide-bore tip. DNA precipitation is normal, but if the DNA precipitates before you finish mixing it will stick to your pipette tip and you will lose a significant amount of library.

Ligation sequencing kit 1D **Sigma Aldrich Catalog #SQK-LSK109**

Large-Orifice Pipet Tips 200µL **Sigma Aldrich Catalog #02-707-134**

66 Incubate the reaction mixture at room temperature for 00:20:00. 20m

67 Add 20 µL of AmPure XP beads and mix quickly with wide-bore tip.

68 Incubate at room temperature for 00:20:00. 20m

69 Place tubes on magnetic and wait for solution to clear.

70 On the magnet, use a cut-off P200 tip to pull the supernatant off the beads very slowly, then dispense the supernatant back onto the bead pellet slowly. Let the sample sit on the magnet for a few minutes.

71 Pipette off supernatant with a normal pipette tip, pipetting from the front of the tube away from the pellet.

72 Add 95 µL of LFB to the tube. SFB or a 1:1 dilution of PB can be used here.

Ligation sequencing kit 1D **Sigma Aldrich Catalog #SQK-LSK109**

Note

DO NOT USE ETHANOL TO WASH PREPARED LIBRARY. It will denature the motor protein.

Lightly tap the tube to encourage adapter on the beads to come off, but not necessarily for beads to resuspend.

73 Being careful not to disturb the pellet, pipette off all the supernatant.

74 Wash again using 105 µL of LFB. Pipette LFB on to the beads more quickly to get the pellet off the side of the tube. Lightly tap the tube to mix but not fully resuspend.

75 While on magnet remove LFB. Briefly spin and use a P10 pipette to remove any remaining excess of LFB.

76 Resuspend pellet in 21 µL EB for R9.4.1 sequencing or in 30 µL for R10.4.1 sequencing.

Elution Buffer (EB) [10 mM Tris-HCl pH 8.0] **Contributed by users**

77 Incubate library on the heat block at 34 °C for 01:00:00. Briefly spin down the tube to collect condensation then incubate for at least 48:00:00 before the next step. 2d 1h

78 Place sample on magnet wait until solution is clear. Use a cut off P200 tip to remove sample from beads and place in a new 1.5mL Lo Bind tube.

(Optional) Library size selection with SRE buffer

79 Quantify library concentration using 1 µL of the prepared library with Qubit. This step should not be performed unless library concentration is greater than 40 ng/uL. If the concentration is greater than 100ng/uL the library should be diluted to improve size selection performance.

80 Add an equal volume (20 µL) of SRE XL buffer to the library and gently pipette mix using a wide-bore tip.

Short Read Eliminator (SRE) **Circulomics Catalog #SS-100-101-01**

Large-Orifice Pipet Tips 200µL **Fisher Scientific Catalog #02-707-134**

81 Centrifuge at 10000 x g, 00:30:00 .

82 Pipette off the supernatant, being careful not to disturb the DNA pellet at the bottom of the tube.

Note

Similar to previous SRE step, leave 10-15uL of supernatant in the bottom of the tube for the first wash.

83 Add 100 uL of LFB, SFB, or 1:1 diluted PB (similar to step 46) to wash the pellet. It does not really matter which one is used.

Note

DO NOT USE ETHANOL TO WASH PREPARED LIBRARY. It will denature the motor protein.

Ligation sequencing kit 1D **Sigma Aldrich Catalog #SQK-LSK109**

DNA Precipitation Buffer (PB) [0.8 M NaCl 9% w/v PEG 8000 10mM Tris-HCl pH 8.0] **Contributed by users**

84 Centrifuge tube at 10000 x g, Room temperature for 00:02:00 .

85 Being careful not to disturb the pellet, pipette off all the supernatant.

86 Repeat wash:

87 Resuspend pellet in 21 µL EB for R9.4.1 sequencing or in 30 µL for R10.4.1 sequencing.

Elution Buffer (EB) [10 mM Tris-HCl pH 8.0] **Contributed by users**

88 Incubate the tube on the heat block at 37 °C for 01:00:00 . Briefly spin down the tube to collect condensation, and incubate at least 48:00:00 at 4 °C before sequencing.

Tips for sequencing the library- R9.4.1

89 Thaw 1 tube SQB (SQK-LSK109), 2 tubes FB (EXP-FLP002), and 1 tube FLT (EXP-FLP002). Mix SQB and FB by flicking. Mix FLT with a pipette. Keep reagents on ice until ready to sequence.

Note

We recommend marking one tube of FB to use as dilution buffer for subsequent runs. Only one tube should be used to prepare the priming mix.

Safety information

The FB must be from the EXP-FLP002 kit. This will not work with version 1 of the kit.

90 Quantify the concentration of 1 µL library with Qubit. We usually end up with 1000 ng - 2000 ng of total library at this stage.

91 With a cut off P200 tip, transfer about 350 ng of prepared library to a fresh 1.5mL LoBind tube. This should not exceed 35 µL in volume.

DNA LoBind Tubes, 1.5 mL **Sigma Aldrich Catalog #0030108051**

Note

To maximize throughput and read length, it is critical to load enough library that flow cell pores will be occupied but not so much that they are oversaturated. The molar concentration of the library is a function of the fragment lengths so it is difficult to say exactly how much library to load. The average library prepared in this manner usually sequences well when 300 ng to 500 ng of DNA is loaded. Note that flow cells need to be flushed and reloaded so we usually aim to have at least 3 library loads.

92 Add an equal volume of SQB to the tube. Then, add FB from the marked tube (the one that we are not going to prepare the priming mix with) to a final volume of 70 µL.

For example, if 10 µL of [M] 35 Mass Percent library was transferred in step 77, add 10 µL of SQB and 50 µL FB to the tube.

Ligation sequencing kit 1D **Sigma Aldrich Catalog #SQK-LSK109**

Flow Cell Priming Kit (EXP-FLP002) **Sigma Aldrich Catalog #EXP-FLP002**

93 Follow the official instructions to prime the flow cell, then add the prepared library to the flow cell. When loading the library, be sure to use a wide-bore pipette tip. Gently pipette mix the library before loading to ensure even distribution of the library across the flow cell membrane.

Large-Orifice Pipet Tips 200µL **Sigma Aldrich Catalog #02-707-134**

94 Over the course of a sequencing run, pores will get clogged and become inactive. It is essential to flush the flow cell at 10-14 hour intervals to make these pores available again. We recommend Nanopore's Flow Cell Wash Kit (EXP-WSH003).

Flowcell Wash Kit **Sigma Aldrich Catalog #EXP-WSH003**

Tips for sequencing the library-R10.4.1

30m

95 Thaw 1 tube SB (LSK110), 1 tube LIS, 1 tube of FCF per sample, and 1 tube FCT. Mix SQB and FB by flicking.

96 Warm the FCF at 37 °C for 00:30:00

30m

97 Add 30 µL FCT to FCF and pipette 10x to ensure thorough mixing

Note

We recommend marking the top of the FCF tube after FCT has been added.

98 Follow the official instructions to prime the flow cell.

99 While the flow cell is priming, prepare the library by adding 70uL of LIS, 30uL library (LIS and library should total to 100uL), and 100uL SB. Lightly tap to mix until swirls disappear but wait to

pipette mix until just before loading.

100 Pipette mix prepared library 2x times and then following official instructions to load the flow cell.

101 Over the course of a sequencing run, pores will get clogged and become inactive. It is essential to flush the flow cell at 10-14 hour intervals to make these pores available again. We recommend Nanopore's Flow Cell Wash Kit (EXP-WSH00).

Flowcell Wash Kit **Sigma Aldrich Catalog #EXP-WSH003**