





Apr 19, 2022

## © DNA extraction and Nanopore library prep from single wild-caught drosophilids V.1

P DNA extraction and Nanopore library prep from 15-30 whole flies

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dx. doi. org/10.17504/protocols. io. dm6gpbdn8lzp/v1

Bernard Kim Petrov Lab, Stanford University

We have been assembling the genomes of many *Drosophila* species. This protocol fork allows for the sequencing of single wild-caught flies using Nanopore MinION sequencers, in contrast to our previous protocol that originally used gDNA extracted from tens or hundreds of flies from an inbred line.

While read lengths are not nearly close to what we were seeing before, libraries range from 2-10kb read N50 and typically produce genome assemblies with contig N50 > 1 Mbp.

The protocol for ultra-long read sequencing from large pools of flies can be found here: dx.doi.org/10.17504/protocols.io.bdfqi3mw

Please cite the associated paper if you use this protocol: https://doi.org/10.7554/eLife.66405

An update to the original paper that includes many single wild-caught fly genomes is in progress.

DO

dx. doi. org/10.17504/protocols. io. dm6gpbdn8lzp/v1

Bernard Y Kim 2022. DNA extraction and Nanopore library prep from single wild-caught drosophilids. **protocols.io** 

https://dx.doi.org/10.17504/protocols.io.dm6gpbdn8lzp/v1

protocol

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Kim, B. Y., Wang, J. R., Miller, D. E., Barmina, O., Delaney, E., Thompson, A., ... & Petrov, D. A. (2021). Highly contiguous assemblies of 101 drosophilid genomes. Elife, 10, e66405. https://doi.org/10.7554/eLife.66405

DNA extraction and Nanopore library prep from 15-30 whole flies, Bernard Kim

Drosophila, nanopore, ligation, HMW, single fly
protocol ,

Apr 18, 2022

Apr 19, 2022

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Flies were collected from the wild and stored in 95% ethanol at -20C. We have successfully assembled genomes from samples ranging from 4 months to 15 years old. Younger samples perform better, of course. Ideally the samples are no older than 5 years and stored properly (e.g. alcohol has not evaporated).

Apart from the gDNA extraction steps, this protocol mostly follows the standard LSK110 protocol. Slight modifications were made to improve library recovery and pore occupancy.

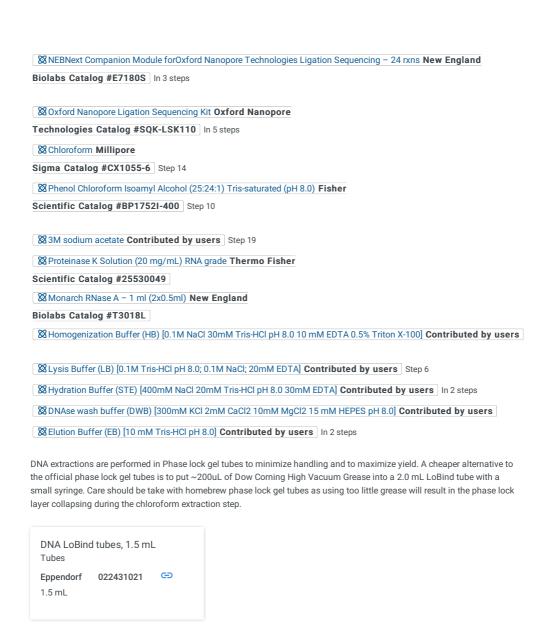
**MATERIALS** 

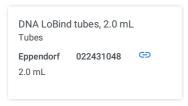
**⊠** 10% SDS solution **Contributed by users** 



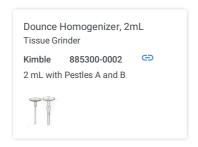
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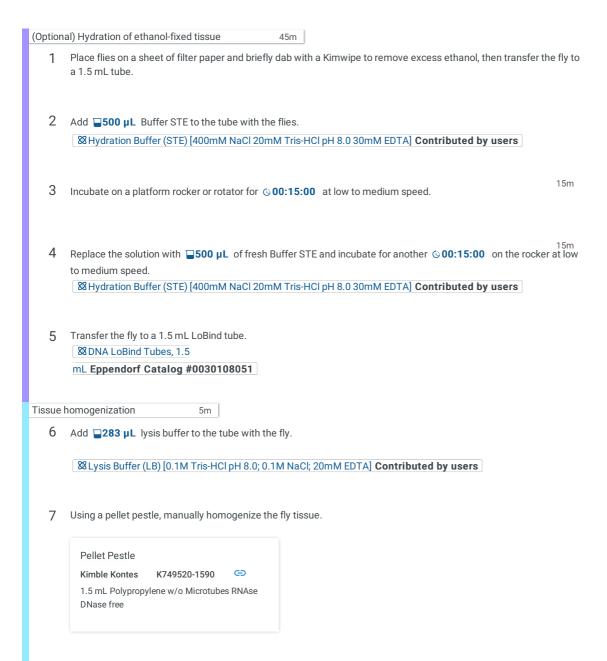




Large-orifice pipet tips, 200uL
Pipette tips
Fisher 02-707-134 © 200 uL



5PRIME Phase Lock Gel tube, light, 2mL Quantabio 2302830 (=) Light





3

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TIP: Make sure fly bits aren't stuck on the pestle before discarding. Every bit of tissue counts!

Phenol chloroform extraction

1h

8 Spin down 1 phase lock gel tube per sample at  $@15000 \times g$  for @00:00:30.

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 minimal 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/



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

5PRIME Phase Lock Gel tube, light, 2mL

Quantabio 2302830 

Light

- 9 Briefly spin down the homogenate/lysis solution, then transfer to the phase lock gel tube by decanting or pipetting with a wide-bore tip.
- 10 Add an equal volume (about 350 μL) of Tris-saturated phenol chloroform isoamyl alcohol (PCI) to the phase lock tube.



This should be performed inside the fume hood.

⊠Phenol Chloroform Isoamyl Alcohol (25:24:1) Tris-saturated (pH 8.0) Fisher

Scientific Catalog #BP1752I-400

11 Mix by placing tubes on a rocker at medium speed for **© 00:08:00** .

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.

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4

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- 12 Centrifuge the phase lock tube at **316000** x g for **00:08:00**. Phase lock layer should now separate aqueous and organic layers.
- 13 Perform one more PCI extraction: go to step #10 .

Use the same tube for the entire extraction, i.e. just add another 350uL of PCI/CHCl3 to the tube and proceed. The phase lock layer should hold through the extraction steps.

Decant aqueous (top) layer into the phase lock tube. Add an equal volume (usually 350 μL) of chloroform to the tube.

We find decanting more effective than pipetting. If the pipette tip touches the phase lock gel, it makes a huge mass



This should be performed inside the fume hood.

 Chloroform Millipore

Sigma Catalog #CX1055-6

- 15~ Mix by placing tubes on a rocker at medium speed for  $\,\odot\,00:08:00~$  .
- 16 Centrifuge the phase lock tube at @16000 x g for @00:08:00. Phase lock layer should now separate aqueous and organic layers.
- 17 Quickly decant the aqueous (top) layer into a fresh 1.5 mL LoBind tube.

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 chloroform 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 to 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.

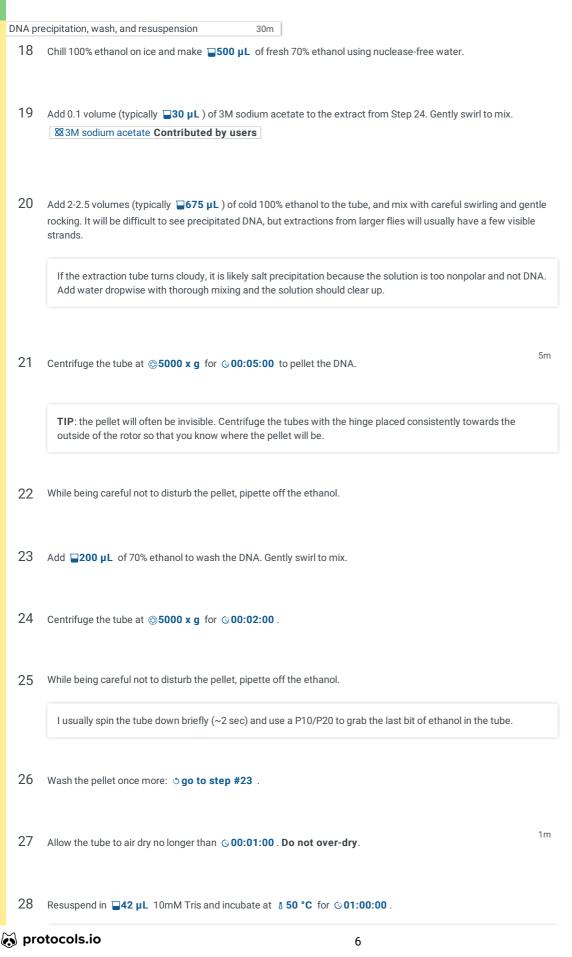


This should be performed inside the fume hood.

DNA LoBind tubes, 1.5 mL Tubes Eppendorf 022431021 © 1.5 mL



5



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https://dx.doi.org/10.17504/protocols.io.dm6qpbdn8lzp/v1

Carefully pipette the Tris up and down the back of the tube to ensure you've resuspended all the DNA. Sometimes it will be spread out rather than pelleted cleanly on the bottom.

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

29 Briefly spin down tube to gather any condensation and store at  $\, \delta \, 4 \, ^{\circ} \text{C} \, .$ 

DNA resuspension

15m

- 30 Pipette mix slowly 5X with a P200 tip to ensure proper resuspension.

Ideally, you'll have recovered >250ng DNA and absorbance ratios 260/280 > 1.8 and 260/230 > 2.0. We have successfully prepared Nanopore libraries with as little as 208ng of gDNA at this point.

Reserve DNA for short-read sequencing

15m

32 Reserve at least **20 ng** gDNA in **6 μL** Tris for Illumina library prep. Store at 8 -20 °C until ready for library prep.

This is a conservative amount. As of April 2022, we use the Illumina kit with 1/5 reaction volumes to prepare libraries. We have in the past successfully prepared Illumina libraries with as little as 4-6 ng of gDNA depending on the kit and protocol. Your mileage may vary.

Although Illumina sequencing may no longer be necessary for genome assembly with the release of new flow cell chemistries, a short-read library will be useful for variant calling so this is recommended irrespective of flow cell/kit chemistry.

## DNA repair and end-prep

33 Thaw NEBNext repair and dA-tailing mixes and buffers from the Nanopore Companion Module. Mix buffers by vortexing and mixes by flicking. Spin down tubes and keep chilled on ice.

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

Add all non-reserved DNA (typically  $\blacksquare 40~\mu L$ ) to a PCR tube. Dilute the HMW DNA with water to a final volume of  $\blacksquare 48.5~\mu L$ . Add  $\blacksquare 3.5~\mu L$  of FFPE DNA repair buffer,  $\blacksquare 3.5~\mu L$  of end-prep reaction buffer,  $\blacksquare 2~\mu L$  of FFPE DNA repair mix, and  $\blacksquare 3~\mu L$  of end-prep reaction mix to the tube. Mix tube with gentle flicking (or very gentle pipetting with a cut-off P200 tip).

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



7

⊠ Nuclease-free water or water filtered using a Milli-Q filtering system Ambion Catalog #AM9932 35 In a thermal cycler, incubate at § 20 °C for © 01:00:00 then § 65 °C for © 00:30:00 . After this, sample can be held at § 4 °C temporarily until ready to proceed. Using a cut-off P200 tip (a wide bore will be too small to fit in the PCR tube), gently transfer sample to a 1.5 mL DNA 36 LoBind tube. Add  $\Box 60~\mu L$  AMPure beads. Using a wide-bore P200 tip, quickly but gently mix the tube. ■ DNA LoBind Tubes, 1.5 mL Eppendorf Catalog #0030108051 ⊠Large-Orifice Pipet Tips 200µL Fisher Scientific Catalog #02-707-134 Coulter Catalog #A63880 Allow the sample to sit at least  $\odot$  00:05:00 at 8 Room temperature to allow the beads to bind the DNA. Meanwhile, prepare 

500 μL fresh 70% ethanol with nuclease-free water. 38 Pellet the beads by placing the tube onto a magnetic tube rack for © 00:05:00 or until sample has completely cleared. Magnetic 1.5 mL tube rack NA Pipette off the supernatant, taking care not to disturb the bead pellet. 40 Add  $\blacksquare$  175  $\mu$ L of 70% ethanol. Pipette slowly, with the tip touching the front wall of the tube, so that the pellet is not disturbed Pipette off the supernatant, taking care not to disturb the DNA pellet. Make sure all the supernatant is removed and 41 only the pellet remains. Wash the pellet once more with 70% ethanol ∴ go to step #40 Briefly spin the sample tube down and place back onto the magnet. Remove any remaining drops on the bottom of the tube with a P10.



8

Magnetic 1.5 mL tube rack Any 44 30m 45 Incubate the tube on the heat block at § 50 °C for © 00:30:00 . Every 5 minutes, gently flick the tube to encourage any settled beads to resuspend. Briefly spin down the tube to collect condensation then place tube back on the magnetic rack. Allow tube to sit for 46 © 00:05:00 or until sample has completely cleared. 47 With a cut-off P200 tip, transfer  $\blacksquare$ 31  $\mu$ L eluate to a fresh 1.5 mL LoBind tube. DNA LoBind tubes, 1.5 mL Tubes Eppendorf 022431021 👄 1.5 mL Check for recovery with Qubit using 🔲 1 µL of sample. Recovery should be at least 🖫 150 ng DNA at this point. Adapter ligation Thaw AMXII, T4 ligase, LNB, and LFB from the NEBNext Nanopore Companion Module and the Nanopore LSK110  $kit.\ Mix\ AMXII,\ T4\ ligase,\ and\ LFB\ by\ flicking.\ Mix\ LNB\ by\ pipetting.\ Briefly\ spin\ the\ tubes\ down\ and\ keep\ chilled\ on$ ⊗NEBNext Companion Module for Oxford Nanopore Technologies Ligation Sequencing – 24 rxns New England **Biolabs Catalog #E7180S** Technologies Catalog #SQK-LSK110 Add 30 µL prepared DNA sample, 2.5 µL AMX, and 5 µL T4 ligase to a fresh 1.5 mL DNA LoBind tube. Gently flick the tube to mix. These are 1/2 the standard prep volumes, hence elution in 31uL in Step 47. **⊠DNA LoBind Tubes, 1.5** mL Eppendorf Catalog #0030108051 SNEBNext Companion Module for Oxford Nanopore Technologies Ligation Sequencing − 24 rxns New England Biolabs Catalog #E7180S

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9

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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.

∅ Oxford Nanopore Ligation Sequencing Kit Oxford Nanopore

Technologies Catalog #SQK-LSK110

□ Large-Orifice Pipet Tips 200µL Fisher

Scientific Catalog #02-707-134

52 Incubate the reaction mixture at  $\ 8$  Room temperature for  $\ \odot$  00:30:00.

30m

53 Add 20 μL AMPure beads and mix gently by flicking until uniform in color. Let sample sit for at least 0.00:05:00 so the DNA can bind to the beads.

5m

Coulter Catalog #A63880

Pellet the beads by placing the tube onto a magnetic tube rack for **© 00:05:00** or until sample has completely cleared

ъm

Magnetic 1.5 mL tube rack

Any NA

- 55 Pipette off the supernatant, being careful not to disturb the bead pellet.
- Remove tube from magnetic rack and add  $\blacksquare 100 \ \mu L$  of LFB to the tube, flicking to mix.

⊗ Oxford Nanopore Ligation Sequencing Kit **Oxford Nanopore** 

Technologies Catalog #SQK-LSK110



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

Pellet the beads by replacing the tube onto the magnetic tube rack for © 00:05:00 or until sample has completely cleared.

Magnetic 1.5 mL tube rack Any NA Being careful not to disturb the pellet, pipette off all the supernatant. Remove the tube from the magnet and briefly spin down. Replace tube onto magnet and remove any remaining 59 drops of supernatant with a P10. Wash the pellet with LFB one more time. 5 go to step #56 Resuspend beads in 26 µL EB. ⊠ Elution Buffer (EB) [10 mM Tris-HCl pH 8.0] Contributed by users Incubate beads on the heat block at 8 37 °C for  $\odot$  00:15:00 . Briefly spin down the tube to collect condensation. 5m Place sample tube onto magnetic rack for at least © 00:05:00 or until sample has cleared. Magnetic 1.5 mL tube rack Using a cut-off P200 tip, transfer **□26** µL eluate into a fresh 1.5 mL LoBind tube. DNA LoBind tubes, 1.5 mL Tubes 022431021 Eppendorf 1.5 mL Quantify library concentration with Qubit using  $\Box 1 \mu L$  of the prepared library. Tips for sequencing the library Thaw 1 tube sequencing buffer SBII (SQK-LSK110), 1 tube loading solution LS (SQK-LSK110), 1 tube flush buffer FB (EXP-FLP002), and 1 tube flush tether FLT (EXP-FLP002). Mix SBII, LS, and FB by flicking. Mix FLT with a pipette. Spin down and keep reagents on ice until ready to sequence.

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11

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Make sure the right versions of reagents from the ligation and/or auxiliary/expansion kits are being used.

Technologies Catalog #SQK-LSK110

With a cut off P200 tip, transfer at least **100 ng** of prepared library to a fresh 1.5mL LoBind tube. This should not exceed **25 μL** in volume (i.e. the volume of the eluate from Step 64).

**⊠ DNA LoBind Tubes, 1.5** 

mL Eppendorf Catalog #0030108051

These libraries tend to be pretty fragmented, with read N50s ranging from 2-10kbp. More than 100 ng library is needed for longer N50 libraries, but it often helps to have 2 library loads so that a flush & reload can be used to improve throughput. So this part is a bit of a guessing game that depends on library yield and sample quality.

68 Add the volume of LS that will result in a total volume of **25** μL in the LoBind tube. For example, if **15** μL of prepared library was initially added to the tube, add **10** μL of LS for a total **25** μL library + LS.

Technologies Catalog #SQK-LSK110

69 Add  $\mathbf{25} \, \mu L$  SBII to the tube for a total volume of  $\mathbf{50} \, \mu L$ .

50 uL is significantly lower than the standard preparation of 75 uL library+SQB+LS/LBII. We use this amount because 50 uL is enough to barely cover the flow cell membrane; this is more visibly apparent if using LBII instead of LS. This allows us to improve the concentration of library for very low yield samples.

THIS VOLUME HAS NOT BEEN TESTED ON PROMETHION FLOW CELLS. Validation is needed.

70 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 Fisher

Scientific Catalog #02-707-134

71 Over the course of a sequencing run, pores will get clogged and become inactive. If you have enough library, we recommend to flush the flow cell at 10-14 hour intervals to make these pores available again.

⊠ Flowcell Wash Kit Oxford Nanopore

Technologies Catalog #EXP-WSH003

