Native barcoding genomic DNA (with EXP-NBD104, EXP-NBD114, and SQK-LSK109)

Version: NBE_9065_v109_revV_14Aug2019
Last update: 21/02/2020

Flow Cell Number: ..... DNA Samples: .....

Before start checklist

Materials

- [ ] 1 µg (or 100-200 fmol) high molecular weight genomic DNA for every sample to be barcoded
- [ ] 1.5-3 µg (or 150-300 fmol) high molecular weight genomic DNA for every sample to be barcoded, if using R10.3 flow cells
- [ ] OR 100+ ng high molecular weight genomic DNA if performing DNA fragmentation
- [ ] Native Barcoding Expansion 1-12 (EXP-NBD104) and 13-24 (EXP-NBD114) if multiplexing more than 12 samples
- [ ] Ligation Sequencing Kit (SQK-LSK109)
- [ ] Flow Cell Priming Kit (EXP-FLP002)

Consumables

- [ ] NEB Blunt/TA Ligase Master Mix (M0367)
- [ ] NEBNext® Quick Ligation Reaction Buffer (NEB B6058)
- [ ] NEBNext® Companion Module for Oxford Nanopore Technologies® Ligation Sequencing (cat # E7180S)
- [ ] Alternatively to the NEBNext® Companion Module and the NEBNext® Quick Ligation Reaction Buffer, you can use the three NEBNext® products below:
- [ ] NEBNext FFPE Repair Mix (M6630)
- [ ] NEBNext Ultra II End repair/dA-tailing Module (E7546)
- [ ] NEBNext Quick Ligation Module (E6056)
- [ ] Agencourt AMPure XP beads
- [ ] 1.5 ml Eppendorf DNA LoBind tubes
- [ ] 0.2 ml thin-walled PCR tubes
- [ ] Nuclease-free water (e.g. ThermoFisher, cat # AM9937)
- [ ] Freshly prepared 70% ethanol in nuclease-free water

Equipment

- [ ] Hula mixer (gentle rotator mixer)
- [ ] Magnetic separator, suitable for 1.5 ml Eppendorf tubes
- [ ] Microfuge
- [ ] Vortex mixer
- [ ] Thermal cycler
- [ ] Ice bucket with ice
- [ ] Timer
- [ ] Pipettes and pipette tips P2, P10, P20, P100, P200, P1000

INSTRUCTIONS	NOTES/OBSERVATIONS
DNA repair and end-prep	
- [ ] Prepare the NEBNext FFPE DNA Repair Mix and NEBNext Ultra II End repair / dA-tailing Module reagents in accordance with manufacturer's instructions, and place on ice. Prepare the DNA in Nuclease-free water. - [ ] For R9.4.1 flow cells, transfer 1 µg (or 100-200 fmol) genomic DNA into a 1.5 ml Eppendorf DNA LoBind tube, or 1.5-3 µg (or 150-300 fmol) genomic DNA if using R10.3 flow cells. - [ ] Adjust the volume to 47 µl with Nuclease-free water - [ ] Mix thoroughly by flicking the tube - [ ] Spin down briefly in a microfuge	

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INSTRUCTIONS	NOTES/OBSERVATIONS
In a 0.2 ml thin-walled PCR tube, mix the following: ☐ 48 µl DNA ☐ 3.5 µl NEBNext FFPE DNA Repair Buffer ☐ 3.5 µl Ultra II End-prep reaction buffer ☐ 3 µl Ultra II End-prep enzyme mix ☐ 2 µl NEBNext FFPE DNA Repair Mix ☐ Mix well by pipetting using wide-bore pipette tips. Alternatively, if you are concerned about preserving the integrity of very long DNA fragments, mix gently by flicking the tube, and spin down. ☐ Using a thermal cycler, incubate at 20°C for 5 mins and 65°C for 5 mins. ☐ Transfer the DNA sample to a clean 1.5 ml Eppendorf DNA LoBind tube. ☐ Resuspend the AMPure XP beads by vortexing. ☐ Add 60 µl of resuspended AMPure XP beads to the end-prep reaction and mix by flicking the tube. ☐ Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT. ☐ Prepare 500 µl of fresh 70% ethanol in Nuclease-free water. ☐ Spin down the sample and pellet on a magnet until eluate is clear and colourless. Keep the tube on the magnet, and pipette off the supernatant. ☐ Keep the tube on the magnet and wash the beads with 200 µl of freshly prepared 70% ethanol without disturbing the pellet. Remove the ethanol using a pipette and discard. ☐ Repeat the previous step. ☐ Spin down and place the tube back on the magnet. Pipette off any residual ethanol. Allow to dry for ~30 seconds, but do not dry the pellet to the point of cracking. ☐ Remove the tube from the magnetic rack and resuspend the pellet in 25 µl Nuclease-free water. Spin down and incubate for 2 minutes at RT. ☐ Pellet the beads on a magnet until the eluate is clear and colourless. ☐ Remove and retain 25 µl of eluate into a clean 1.5 ml Eppendorf DNA LoBind tube. ☐ Quantify 1 µl of end-prepped DNA using a Qubit fluorometer - recovery aim > 700 ng.	
Take forward the repaired and end-prepped DNA into the native barcode ligation step.	
Native barcode ligation	
☐ Thaw the native barcodes at RT, enough for one barcode per sample. Individually mix the barcodes by pipetting, and place them on ice. ☐ Select a unique barcode for every sample to be run together on the same flow cell, from the provided 24 barcodes. Up to 24 samples can be barcoded and combined in one experiment.	

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INSTRUCTIONS	NOTES/OBSERVATIONS
☐ Dilute 500 ng (750 ng if sequencing on R10.3 flow cells) of each end-prepped sample to be barcoded to 22.5 µl in Nuclease-free water. Add the reagents in the order given below, mixing by flicking the tube between each sequential addition: ☐ 22.5 µl 500 ng end-prepped DNA (750 ng if using R10.3 flow cells) ☐ 2.5 µl Native Barcode ☐ 25 µl Blunt/TA Ligase Master Mix ☐ Mix well by pipetting using wide-bore pipette tips. Alternatively, if you are concerned about preserving the integrity of very long DNA fragments, mix gently by flicking the tube, and spin down. ☐ Incubate the reaction for 10 minutes at RT. ☐ Resuspend the AMPure XP beads by vortexing. ☐ Add 50 µl of resuspended AMPure XP beads to the reaction and mix by pipetting. ☐ Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT. ☐ Prepare 500 µl of fresh 70% ethanol in Nuclease-free water. ☐ Spin down the sample and pellet on a magnet. Keep the tube on the magnet, and pipette off the supernatant. ☐ Keep the tube on the magnet and wash the beads with 200 µl of freshly prepared 70% ethanol without disturbing the pellet. Remove the ethanol using a pipette and discard. ☐ Repeat the previous step. ☐ Spin down and place the tube back on the magnet. Pipette off any residual ethanol. Allow to dry for ~30 seconds, but do not dry the pellet to the point of cracking. ☐ Remove the tube from the magnetic rack and resuspend pellet in 26 µl Nuclease-free water. Incubate for 2 minutes at RT. ☐ Pellet the beads on a magnet until the eluate is clear and colourless. ☐ Remove and retain 26 µl of eluate containing the DNA library into a clean 1.5 ml Eppendorf DNA LoBind tube. ☐ Quantify 1 µl of eluted sample using a Qubit fluorometer. ☐ Pool equimolar amounts of each barcoded sample into a 1.5 ml Eppendorf DNA LoBind tube, ensuring that sufficient sample is combined to produce a pooled sample of 700 ng total (1050 ng if sequencing on R10.3 flow cells). ☐ Quantify 1 µl of pooled and barcoded DNA using a Qubit fluorometer. ☐ Dilute 700 ng (1050 ng for R10.3 flow cells) pooled sample to 65 µl in Nuclease-free water.	

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INSTRUCTIONS	NOTES/OBSERVATIONS
Adapter ligation and clean-up	
☐ Thaw the Elution Buffer (EB) and NEBNext Quick Ligation Reaction Buffer (5x) at RT, mix by vortexing, spin down and place on ice. Check the contents of each tube are clear of any precipitate. ☐ Spin down the T4 Ligase and the Adapter Mix II (AMII), and place on ice.	
IMPORTANT ☐ Depending on the wash buffer (LFB or SFB) used, the clean-up step after adapter ligation is designed to either enrich for DNA fragments of >3 kb, or purify all fragments equally.	
☐ To enrich for DNA fragments of 3 kb or longer, thaw one tube of Long Fragment Buffer (LFB) at RT, mix by vortexing, spin down and place on ice. ☐ To retain DNA fragments of all sizes, thaw one tube of Short Fragment Buffer (SFB) at RT, mix by vortexing, spin down and place on ice. Taking the pooled and barcoded DNA, perform adapter ligation as follows, mixing by flicking the tube between each sequential addition. ☐ 65 µl 700 ng (1050 ng if using R10.3 flow cells) pooled barcoded sample ☐ 5 µl Adapter Mix II (AMII) ☐ 20 µl NEBNext Quick Ligation Reaction Buffer (5X) ☐ 10 µl Quick T4 DNA Ligase ☐ Mix gently by flicking the tube, and spin down. ☐ Incubate the reaction for 10 minutes at RT. ☐ Resuspend the AMPure XP beads by vortexing. ☐ Add 50 µl of resuspended AMPure XP beads to the reaction and mix by pipetting. ☐ Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT. ☐ Place on magnetic rack, allow beads to pellet and pipette off supernatant. ☐ Wash the beads by adding either 250 µl Long Fragment Buffer (LFB) or 250 µl Short Fragment Buffer (SFB). Flick the beads to resuspend, spin down, then return the tube to the magnetic rack and allow the beads to pellet. Remove the supernatant using a pipette and discard. ☐ Repeat the previous step. ☐ Spin down and place the tube back on the magnet. Pipette off any residual supernatant. Allow to dry for ~30 seconds, but do not dry the pellet to the point of cracking. ☐ Remove the tube from the magnetic rack and resuspend the pellet in 15 µl Elution Buffer (EB). Spin down and incubate for 10 minutes at RT. For high molecular weight DNA, incubating at 37° C can improve the recovery of long fragments. ☐ Pellet the beads on a magnet until the eluate is clear and colourless. ☐ Remove and retain 15 µl of eluate containing the DNA library into a clean 1.5 ml Eppendorf DNA LoBind tube.	

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INSTRUCTIONS	NOTES/OBSERVATIONS
☐ Quantify 1 µl of adapter ligated and barcoded DNA using a Qubit fluorometer - recovery aim ~430 ng.	
IMPORTANT ☐ We recommend loading 5–50 fmol (25-75 fmol for R10.3 flow cells) of this final prepared library onto the flow cell. Loading more than 50 fmol can have a detrimental effect on throughput. Dilute the library in EB if required. If you are using the Flongle for sample prep development, we recommend loading 3–20 fmol instead.	
The prepared library is used for loading onto the MinION Mk1B flow cell. Store the library on ice until ready to load.	
Priming and loading the SpotON flow cell	
IMPORTANT ☐ Please note that the Sequencing Tether (SQT) tube will NOT be used in this protocol. It is provided in the kit for potential future product compatibility.	
☐ 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), Flush Buffer (FB) and Flush Tether (FLT) tubes by vortexing, spin down then return to ice. ☐ Open the MinION Mk1B lid and slide the flow cell under the clip. ☐ Slide the priming port cover clockwise to open the priming port.	
IMPORTANT ☐ Take care when drawing back buffer from the flow cell. Do not remove more than 20-30 µl, and make sure that the array of pores are covered by buffer at all times. Introducing air bubbles into the array can irreversibly damage pores.	
After opening the priming port, check for a small air bubble under the cover. Draw back a small volume to remove any bubbles (a few µl): ☐ Set a P1000 pipette to 200 µl ☐ 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 ☐ To prepare the flow cell priming mix, add 30 µl of thawed and mixed Flush Tether (FLT) directly to the tube of thawed and mixed Flush Buffer (FB), and mix by vortexing. ☐ 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. During this time, prepare the library for loading by following the steps below. ☐ Thoroughly mix the contents of the Loading Beads (LB) by pipetting.	
IMPORTANT ☐ 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.	

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INSTRUCTIONS	NOTES/OBSERVATIONS
In a new tube, prepare the library for loading as follows: ☐ 37.5 µl Sequencing Buffer (SQB) ☐ 25.5 µl Loading Beads (LB), mixed immediately before use ☐ 12 µl DNA library 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. ☐ Mix the prepared library gently by pipetting up and down just prior to loading. ☐ Add 75 µl 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 Mk1B lid.	
Ending the experiment	
☐ After your sequencing experiment is complete, if you would like to reuse the flow cell, please follow the Wash Kit instructions and store the washed flow cell at 2-8°C, OR ☐ Follow the returns procedure by washing out the flow cell ready to send back to Oxford Nanopore.	
IMPORTANT ☐ If you encounter issues or have questions about your sequencing experiment, please refer to the Troubleshooting Guide that can be found in the online version of this protocol.	