Version: GDE\_9063\_v109\_revT\_14Aug2019 Last update: 04/03/2020



Oxford NANOPORE Technologies

Before start checklist			
Materials	Consumables	Equipment	
1 μg (or 100-200 fmol) high molecular weight genomic DNA	Agencourt AMPure XP beads	Hula mixer (gentle rotator mixer)	
1.5-3 μg (or 150-300 fmol) high molecular weight genomic DNA if using R10.3 flow cells	NEBNext® Companion Module for Oxford Nanopore Technologies® Ligation Sequencing (cat # E7180S). Alternatively, you can use the three NEBNext® products below:	Magnetic separator, suitable for 1.5 ml     Eppendorf tubes	
OR 100+ ng high molecular weight genomic DNA if performing DNA fragmentation	NEBNext FFPE Repair Mix (M6630)	Microfuge	
Ligation Sequencing Kit (SQK-LSK109)	NEBNext Ultra II End repair/dA-tailing Module (E7546)	☐ Vortex mixer	
Flow Cell Priming Kit (EXP-FLP002)	NEBNext Quick Ligation Module (E6056)	☐ Thermal cycler	
	1.5 ml Eppendorf DNA LoBind tubes	lce bucket with ice	
	0.2 ml thin-walled PCR tubes	Timer	
	Nuclease-free water (e.g. ThermoFisher, cat # AM9937)	Pipettes and pipette tips P2, P10, P20, P100, P200, P1000	
	Freshly prepared 70% ethanol in nuclease- free water		
INSTRUCTIONS		NOTES/OBSERVATIONS	
DNA repair and end-prep			
☐ Thaw DNA CS (DCS) at RT, spin down, mix by	pipetting, and place on ice.	DCS	
Prepare the NEBNext FFPE DNA Repair Mix an in accordance with manufacturer's instructions,	d NEBNext Ultra II End repair / dA-tailing Module reag and place on ice.	gents	
Prepare the DNA in Nuclease-free water			
For R9.4.1 flow cells, transfer 1 μg (or 100-20 tube, or 1.5-3 μg (or 150-300 fmol) genomic	00 fmol) genomic DNA into a 1.5 ml Eppendorf DNA L DNA if using R10.3 flow cells.	oBind	
Adjust the volume to 49 μl with Nuclease-free water			
<ul><li>☐ Mix thoroughly by flicking the tube</li><li>☐ Spin down briefly in a microfuge</li></ul>			

Page 1/5 nanoporetech.com

Version: GDE_9063_v109_revT_14Aug2019 _ast update: 04/03/2020	NANOPORE Technologies
Flow Cell Number:	NOTES/OBSERVATIONS
In a 0.2 ml thin-walled PCR tube, mix the following:  1 µl DNA CS  47 µl DNA  3.5 µl NEBNext FFPE DNA Repair Buffer  2 µl NEBNext FFPE DNA Repair Mix  3.5 µl Ultra II End-prep reaction buffer  3 µl Ultra II End-prep enzyme mix	
☐ 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.	
IMPORTANT  ☐ AMPure XP bead clean-up	
☐ Resuspend the AMPure XP beads by vortexing.	
☐ Transfer the DNA sample to a clean 1.5 ml Eppendorf DNA LoBind tube.	
$\hfill \Box$ Add 60 $\mu I$ 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.	
$\square$ Remove the tube from the magnetic rack and resuspend the pellet in 61 $\mu$ l 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 61 µl of eluate into a clean 1.5 ml Eppendorf DNA LoBind tube.	
Quantify 1 μl of eluted sample using a Qubit fluorometer.	
Take forward the repaired and end-prepped DNA into the adapter ligation step. However, at this point it is also possible to store the sample at 4° C overnight.	
Adapter ligation and clean-up	

Page 2/5 nanoporetech.com

Although the recommended 3rd party ligase is supplied with its own buffer, the ligation efficiency of Adapter Mix (AMX) is higher when using Ligation Buffer supplied within the Ligation Sequencing Kit.

Version: GDE\_9063\_v109\_revT\_14Aug2019 Last update: 04/03/2020



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Technologies

INSTRUCTIONS	NOTES/OBSERVATIONS
Spin down Adapter Mix (AMX) and Quick T4 Ligase, and place on ice.	
☐ Thaw Ligation Buffer (LNB) at RT, spin down and mix by pipetting. Due to viscosity, vortexing this buffer is ineffective. Place on ice immediately after thawing and mixing.	
☐ Thaw the Elution Buffer (EB) at RT, mix by vortexing, spin down 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.	
In a 1.5 ml Eppendorf DNA LoBind tube, mix in the following order:	
60 µl DNA sample from the previous step	
☐ 5 µl Adapter Mix (AMX)	
☐ Mix gently by flicking the tube, and spin down.	
☐ Incubate the reaction for 10 minutes at RT.	
IMPORTANT	
If you have omitted the AMPure purification step after DNA repair and end-prep, do not incubate the reaction for longer than 10 minutes.	
Resuspend the AMPure XP beads by vortexing.	
$\hfill \square$ Add 40 $\mu I$ of resuspended AMPure XP beads to the reaction and mix by flicking the tube.	
☐ Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT.	
Spin down the sample and pellet on a magnet. Keep the tube on the magnet, and pipette off the 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.	

Page 3/5 nanoporetech.com

/ersion: GDE_9063_v109_revT_14Aug2019 .ast update: 04/03/2020	MAITOI	Technologies
Flow Cell Number:		
INSTRUCTIONS	NOTES/OBSERVATIONS	
Remove and retain 15 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.		
The prepared library is used for loading into the flow cell. Store the library on ice until ready to load.		
IMPORTANT		
☐ We recommend loading 5–50 fmol of this final prepared library onto R9.4.1 flow cells or 25-75 fmol onto R10.3 flow cells.		
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 µI):		
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.		

Page 4/5 nanoporetech.com

☐ 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.

Version: GDE\_9063\_v109\_revT\_14Aug2019 Last update: 04/03/2020

Flow Cell Number:	DNA Samples:

Flow Cell Number:	NA Samples:
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 acce	essible.
Load 200 µl of the priming mix into the flow cell via the priming port (not the Spother introduction of air bubbles.	otON sample port), avoiding
$\hfill \square$ 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 fash flows into the port before adding the next.	hion. Ensure each drop
☐ Gently replace the SpotON sample port cover, making sure the bung enters the Spriming port and replace the MinION Mk1B lid.	potON port, close the
Ending the experiment	
After your sequencing experiment is complete, if you would like to reuse the flow of Wash Kit instructions and store the washed flow cell at 2-8°C, OR	cell, please follow the
☐ Follow the returns procedure by washing out the flow cell ready to send back to O	Oxford Nanopore.
IMPORTANT	
If you encounter issues or have questions about your sequencing experiment, pleat Troubleshooting Guide that can be found in the online version of this protocol.	ase refer to the

Page 5/5 nanoporetech.com