

Genomic DNA by ligation (SQK-LSK109-XL)

Version: GD_X_9095_v109_revB_24Jan2020
 Last update: 28/01/2020



Flow Cell Number:

DNA Samples:

Before start checklist		
Materials	Consumables	Equipment
<input type="checkbox"/> 1 µg (or 100-200 fmol) high molecular weight genomic DNA	<input type="checkbox"/> Agencourt AMPure XP beads	<input type="checkbox"/> Magnetic separator suitable for 96-well PCR plates, e.g. DynaMag™-96 Side Skirted Magnet (Thermo Fisher, # 12027)
<input type="checkbox"/> 1.5-3 µg (or 150-300 fmol) high molecular weight genomic DNA if using R10.3 flow cells	<input type="checkbox"/> NEBNext® Companion Module for Oxford Nanopore Technologies® Ligation Sequencing (cat # E7180S). Alternatively, you can use the three NEBNext® products below:	<input type="checkbox"/> OR magnetic separator suitable for 0.2 ml PCR tube strips, e.g. DynaMag™-PCR Magnet (Thermo Fisher, #492025) or DynaMag™-96 Side Magnet (Thermo Fisher, #12331D)
<input type="checkbox"/> OR 100+ ng high molecular weight genomic DNA if performing DNA fragmentation	<input type="checkbox"/> NEBNext FFPE Repair Mix (M6630)	<input type="checkbox"/> Microfuge
<input type="checkbox"/> Ligation Sequencing Kit XL (SQK-LSK109-XL)	<input type="checkbox"/> NEBNext Ultra II End repair/dA-tailing Module (E7546)	<input type="checkbox"/> Microplate centrifuge, e.g. Fisherbrand™ Mini Plate Spinner Centrifuge (Fisher Scientific, #11766427)
<input type="checkbox"/> Flow Cell Priming Kit XL (EXP-FLP002-XL)	<input type="checkbox"/> NEBNext Quick Ligation Module (E6056)	<input type="checkbox"/> Vortex mixer
	<input type="checkbox"/> Nuclease-free water (e.g. ThermoFisher, cat # AM9937)	<input type="checkbox"/> Thermal cycler
	<input type="checkbox"/> Freshly prepared 70% ethanol in nuclease-free water	<input type="checkbox"/> Multichannel pipettes suitable for dispensing 2–20 µl and 20–200 µl, and tips
	<input type="checkbox"/> 1.5 ml Eppendorf DNA LoBind tubes	<input type="checkbox"/> Ice bucket with ice
	<input type="checkbox"/> Eppendorf twin.tec® PCR plate 96 LoBind, semi-skirted (Cat # 0030129504) with heat seals	<input type="checkbox"/> Timer
	<input type="checkbox"/> OR 0.2 ml thin-walled PCR tubes	<input type="checkbox"/> Pipetting troughs
	<input type="checkbox"/> 15 or 50 ml Falcon tubes	<input type="checkbox"/> Pipettes and pipette tips P2, P10, P20, P100, P200, P1000

INSTRUCTIONS	NOTES/OBSERVATIONS
<p>DNA repair and end-prep</p> <p><input type="checkbox"/> 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.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> It is important that the NEBNext FFPE DNA Repair Buffer and NEBNext Ultra II End Prep Reaction Buffer are mixed well by vortexing.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> Do not vortex the NEBNext FFPE DNA Repair Mix or NEBNext Ultra II End Prep Enzyme Mix.</p>	

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<p>Prepare the DNA in Nuclease-free water</p> <ul style="list-style-type: none"> <input type="checkbox"/> For each sample, transfer 1 µg (or 100-200 fmol) genomic DNA into a separate well of a 96-well PCR plate, or a 0.2 ml PCR tube within a PCR tube strip. Start with 1.5-3 µg (or 150-300 fmol) if using R10.3 flow cells <input type="checkbox"/> Adjust the volume to 47 µl with Nuclease-free water <input type="checkbox"/> Mix thoroughly by pipetting up and down, or by flicking the tube <input type="checkbox"/> If necessary, seal and spin down briefly in an appropriate centrifuge <p>To each sample, add the following:</p> <ul style="list-style-type: none"> <input type="checkbox"/> 1 µl DNA CS <input type="checkbox"/> 3.5 µl NEBNext FFPE DNA Repair Buffer <input type="checkbox"/> 2 µl NEBNext FFPE DNA Repair Mix <input type="checkbox"/> 3.5 µl Ultra II End-prep reaction buffer <input type="checkbox"/> 3 µl Ultra II End-prep enzyme mix <ul style="list-style-type: none"> <input type="checkbox"/> Mix well by gently pipetting the entire volume within each well/tube up and down 10 times, or by flicking the tubes, and spin down. <input type="checkbox"/> Seal the plate, or close the tube lids. <input type="checkbox"/> Using a thermal cycler, incubate the samples at 20°C for 5 minutes and 65°C for 5 mins. <p>AMPure XP bead clean-up</p> <ul style="list-style-type: none"> <input type="checkbox"/> Resuspend the AMPure XP beads by vortexing and transfer to a pipetting trough. Ensure that the volume transferred is enough for 60 µl to be added to each DNA sample, with an excess to allow for dead volume within the pipetting trough. 	
<p>IMPORTANT</p> <ul style="list-style-type: none"> <input type="checkbox"/> Resuspend and transfer the beads to the pipetting trough immediately before use to ensure beads do not settle. 	
<ul style="list-style-type: none"> <input type="checkbox"/> Keep the DNA samples in their original wells/PCR tubes. Add 60 µl of resuspended AMPure XP beads to each sample and mix by pipetting at least 100 µl up and down ten times. Retain any unused beads. <input type="checkbox"/> Incubate for 5 minutes at RT. <input type="checkbox"/> Prepare fresh 70% ethanol in Nuclease-free water and pour into a pipetting trough. Allow enough for 500 µl per sample, with an excess to allow for dead volume within the pipetting trough. After the bead washing steps, discard any unused ethanol. <input type="checkbox"/> Pellet the beads on a magnet for at least 2 min, or until the supernatant is clear. Keep the plate/tube strip on the magnet and pipette off the supernatant. <input type="checkbox"/> Keeping the plate/tube strip on the magnet, wash each pellet of beads with 200 µl of the freshly-prepared 70% ethanol without disturbing the pellets. Remove the 70% ethanol using a pipette and discard. <input type="checkbox"/> Repeat the previous step. <input type="checkbox"/> Seal the plate, or close the tube lids. Spin down and place the plate/tube strip back on the magnet. Pipette off any residual ethanol. 	

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<ul style="list-style-type: none"> <input type="checkbox"/> Pour Nuclease-free water into a pipetting trough. Allow enough for 61 µl per sample, with an excess to allow for dead volume within the pipetting trough. <input type="checkbox"/> Remove the plate/tube strip from the magnetic rack and resuspend each pellet in 61 µl Nuclease-free water from the pipetting trough. Pipette the entire volume up and down ten times). <input type="checkbox"/> Seal the plate or close the tube lids, and incubate for 10 min at 37°C. <input type="checkbox"/> Pellet the beads on a magnet until the eluate is clear and colourless, for at least 1 min. <input type="checkbox"/> Remove and retain 61 µl of each eluate in a separate, clean well/tube within a 96-well PCR plate or PCR tube strip. Dispose of the pelleted beads. 	
<p>Quantify 1 µl of each eluted sample using a Qubit fluorometer.</p>	
<p>Take forward the repaired and end-prepped DNA into the adapter ligation step. However, at this point it is also possible to store the samples at 4° C overnight.</p>	
<p>Adapter ligation and clean-up</p>	
<p>IMPORTANT</p> <ul style="list-style-type: none"> <input type="checkbox"/> 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 SQK-LSK109-XL. 	
<ul style="list-style-type: none"> <input type="checkbox"/> Spin down the Adapter Mix (AMX) and Quick T4 Ligase, and place on ice. <input type="checkbox"/> 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. <input type="checkbox"/> Thaw the Elution Buffer (EB) at RT, mix by vortexing, and place on ice. 	
<p>IMPORTANT</p> <ul style="list-style-type: none"> <input type="checkbox"/> 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. 	
<ul style="list-style-type: none"> <input type="checkbox"/> To enrich for DNA fragments of 3 kb or longer, thaw one bottle of L Fragment Buffer (LFB) at RT, mix by vortexing, and place on ice. <input type="checkbox"/> To retain DNA fragments of all sizes, thaw one bottle of S Fragment Buffer (SFB) at RT, mix by vortexing, and place on ice. <p>To each repaired/end-prepped DNA sample (60 µl), add the following:</p> <ul style="list-style-type: none"> <input type="checkbox"/> 25 µl Ligation Buffer (LNB) <input type="checkbox"/> 10 µl NEBNext Quick T4 DNA Ligase <input type="checkbox"/> 5 µl Adapter Mix (AMX) <ul style="list-style-type: none"> <input type="checkbox"/> Mix well by gently pipetting the entire volume within each well/tube up and down 10 times. <input type="checkbox"/> Incubate the reaction for 10 minutes at RT. 	

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<p>IMPORTANT</p> <p><input type="checkbox"/> If you have omitted the AMPure purification step after DNA repair and end-prep, do not incubate the reaction for longer than 10 minutes.</p>	
<p><input type="checkbox"/> Resuspend the AMPure XP beads by vortexing and transfer to a pipetting trough. Ensure that the volume transferred is enough for 40 µl to be added to each DNA sample, with an excess to allow for dead volume within the pipetting trough.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> Resuspend and transfer the beads to the pipetting trough immediately before use to ensure beads do not settle.</p> <p><input type="checkbox"/> Add 40 µl of resuspended AMPure XP beads to each sample and mix by pipetting the entire combined volume up and down 10 times.</p> <p><input type="checkbox"/> Incubate for 5 minutes at RT.</p> <p><input type="checkbox"/> Add sufficient LFB or SFB to a pipetting trough. Allow enough for 400 µl per sample, with an excess to allow for dead volume within the pipetting trough. Retain any unused reagent after the wash steps.</p> <p><input type="checkbox"/> Pellet the beads on a magnet for at least 2 min, or until the supernatant is clear. Keep the plate/tube strip on the magnet and pipette off the supernatant.</p> <p><input type="checkbox"/> Remove the plate/tube strip from the magnetic rack and wash each pellet of beads by adding either 200 µl L Fragment Buffer (LFB) or 200 µl S Fragment Buffer (SFB). Resuspend each pellet thoroughly by pipetting the entire volume of buffer up and down ten times. Fully resuspending the beads at this step ensures optimal kit performance. Return the plate/tube strip to the magnetic rack and allow the beads to pellet until the supernatant is clear. Remove the supernatant using a pipette and discard.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> It is essential that beads are resuspended fully and not simply moved around the tubes through use of the magnet.</p>	
<p><input type="checkbox"/> Repeat the previous step.</p> <p><input type="checkbox"/> Seal the plate, or close the tube lids. Spin down and place the plate/tube strip back on the magnet. Pipette off any residual supernatant.</p> <p><input type="checkbox"/> Add sufficient EB to a pipetting trough. Allow enough for 15 µl per sample, with an excess to allow for dead volume within the pipetting trough. Retain any unused EB after the elution step.</p> <p><input type="checkbox"/> Remove the plate/tube strip from the magnetic rack and resuspend each pellet in 15 µl Elution Buffer (EB) from the pipetting trough, pipetting the entire volume up and down 10 times.</p> <p><input type="checkbox"/> Seal the plate (or close the tube lids), and incubate for 10 min at 37°C in a thermal cycler. Any heated lid used should be limited to 50°C.</p> <p><input type="checkbox"/> Pellet the beads on a magnet until the eluate is clear and colourless.</p> <p><input type="checkbox"/> Remove and retain 15 µl of each eluate in a separate, clean well/tube within a 96-well PCR plate or PCR tube strip. Dispose of the pelleted beads.</p>	
<p>Quantify 1 µl of each eluted sample using a Qubit fluorometer.</p>	

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<p>The prepared libraries are used for loading into the flow cells. Store the libraries on ice until ready to load.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> We recommend loading 5–50 fmol of these final prepared libraries onto R9.4.1 flow cells, or 25-75 fmol onto R10.3 flow cells.</p>	
<p>Priming and loading the SpotON flow cell</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> 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.</p>	
<p><input type="checkbox"/> Thaw the Sequencing Buffer (SQB), Loading Beads (LB), Flush Tether (FLT) and Flush Buffer (FB) at RT.</p> <p><input type="checkbox"/> Mix the Sequencing Buffer (SQB), Flush Buffer (FB) and Flush Tether (FLT) tubes by vortexing and spin down at RT.</p> <p><input type="checkbox"/> Open the MinION Mk1B lid and slide the flow cell under the clip.</p> <p><input type="checkbox"/> Slide the priming port cover clockwise to open the priming port.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> 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.</p>	
<p>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):</p> <ul style="list-style-type: none"> <input type="checkbox"/> Set a P1000 pipette to 200 μl <input type="checkbox"/> Insert the tip into the priming port <input type="checkbox"/> Turn the wheel until the dial shows 220-230 μl, or until you can see a small volume of buffer entering the pipette tip <p><input type="checkbox"/> Prepare the flow cell priming mix: in a suitable vial, prepare a mix of Flush Buffer (FB) and Flush Tether (FLT) for priming all flow cells to be loaded. Allow 30 μl of Flush Tether (FLT) and 1.17 ml of Flush Buffer (FB) for every flow cell; no excess is required. Once combined, mix well by briefly vortexing.</p> <p><input type="checkbox"/> 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.</p> <p><input type="checkbox"/> Meanwhile, thoroughly mix the contents of the thawed Loading Beads (LB) tube(s) by vortexing.</p>	
<p>IMPORTANT</p> <p><input type="checkbox"/> 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.</p>	

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<p>In a separate 0.2 ml PCR tube for each library, prepare for loading by adding the following reagents:</p> <ul style="list-style-type: none"> <input type="checkbox"/> 37.5 µl Sequencing Buffer (SQB) <input type="checkbox"/> 25.5 µl Loading Beads (LB), mixed immediately before use <input type="checkbox"/> 12 µl DNA library <p>Complete the flow cell priming:</p> <ul style="list-style-type: none"> <input type="checkbox"/> Gently lift the SpotON sample port cover to make the SpotON sample port accessible. <input type="checkbox"/> 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. <input type="checkbox"/> Mix the prepared libraries gently by pipetting up and down just prior to loading. <input type="checkbox"/> 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. <input type="checkbox"/> 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. 	
<p>Ending the experiment</p>	
<ul style="list-style-type: none"> <input type="checkbox"/> 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 <input type="checkbox"/> Follow the returns procedure by washing out the flow cell ready to send back to Oxford Nanopore. 	
<p>IMPORTANT</p> <ul style="list-style-type: none"> <input type="checkbox"/> 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. 	