

Flow Cell Number: .....

DNA Samples: H3+G2 .....

**Before start checklist**

**Materials**

- 50 ng PolyA+ RNA
- cDNA-PCR Sequencing Kit (SQK-PCS108)
- PCR Barcoding Kit (SQK-PBK004)

**Consumables**

- 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
- 10 mM dNTP solution (e.g. NEB N0447)
- LongAmp Taq 2X Master Mix (e.g. NEB M0287)
- SuperScript IV reverse transcriptase, 5x RT buffer and 100 mM DTT (ThermoFisher Scientific, 18090050)
- RNaseOUT™, 40 U/μl (Life Technologies, 10777019)
- Exonuclease I (NEB, M0293)
- Pipette tips P2, P10, P20, P100, P200, P1000

**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
- Pre-chilled freezer block at -20° C for 200 μl tubes (e.g. Eppendorf 022510509)
- Qubit fluorometer (or equivalent for QC check)
- Pipettes P2, P10, P20, P100, P200, P1000

**INSTRUCTIONS**

**NOTES/OBSERVATIONS**

**Preparing input RNA**

- Prepare the RNA in Nuclease-free water.
- Transfer 50 ng RNA into a DNA LoBind tube
  - Adjust the volume to up to 9 μl with Nuclease-free water
  - Mix by flicking the tube to avoid unwanted shearing
  - Spin down briefly in a microfuge
  - Record the quality, quantity and size of the input RNA.

*H3 = 9ng @ 4.4 ng/ul  
 G2 = 9ng @ ? 2 ng/ul*

*24.475M READS  
 MORE THAN HIK*

Flow Cell Number: ..... *52121* .....

DNA Samples: .....

INSTRUCTIONS	NOTES/OBSERVATIONS
<p><b>IMPORTANT</b></p> <p>Criteria for input RNA</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Average fragment size: ~2 kb</li> <li><input type="checkbox"/> Input mass, as measured by Qubit RNA HS assay: 50 ng</li> <li><input type="checkbox"/> A 260:280 ratio of ~2.0</li> <li><input type="checkbox"/> A 260:230 ratio of 2.0-2.2</li> <li><input type="checkbox"/> No detergents or surfactants in the buffer</li> </ul>	
<p><b>Check your flow cell</b></p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Set up the MinION, flow cell and host computer</li> </ul> <p>Once successfully plugged in, you will see a light and hear the fan.</p> <p>Open the MinKNOW GUI from the desktop icon and establish a local or remote connection.</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> If running a MinION on the same host computer, plug the MinION into the computer.</li> <li><input type="checkbox"/> If running a MinION on a remote computer, first enter the name or IP address of the remote host under Connect to a remote computer (if running from the Connection page), or Connections (if running from the homepage) and click Connect.</li> <li><input type="checkbox"/> Choose the flow cell type from the selector box. Then mark the flow cell as "Selected":</li> </ul> <p>Click "Check flow cells" at the bottom of the screen.</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> R9.4.1 FLO-MIN106</li> <li><input type="checkbox"/> R9.5.1 FLO-MIN107</li> </ul> <ul style="list-style-type: none"> <li><input type="checkbox"/> Click "Start test".</li> <li><input type="checkbox"/> Check the number of active pores available for the experiment, reported in the System History panel when the check is complete.</li> </ul>	
<p>Flow cell check complete.</p>	
<p><b>Reverse transcription and strand-switching</b></p> <p>Prepare the following reaction in a 0.2 ml PCR tube:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> x µl poly A+ RNA, 50 ng</li> <li><input type="checkbox"/> 1 µl VNP</li> <li><input type="checkbox"/> 1 µl 10 mM dNTPs</li> <li><input type="checkbox"/> 9-x µl RNase-free water</li> </ul> <ul style="list-style-type: none"> <li><input type="checkbox"/> Mix gently by flicking the tube, and spin down.</li> <li><input type="checkbox"/> Incubate at 65° C for 5 minutes and then snap cool on a pre-chilled freezer block.</li> </ul> <p>In a separate tube, mix together the following:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> 4 µl Superscript IV buffer</li> <li><input type="checkbox"/> 1 µl RNaseOUT</li> <li><input type="checkbox"/> 1 µl 100 mM DTT</li> <li><input type="checkbox"/> 2 µl Strand-Switching Primer (SSP)</li> </ul>	

cDNA-PCR Barcoding (SQK-PCS108 with SQK-PBK004)

Version: PCB\_9037\_v108\_revK\_30Jun2017  
 Last update: 03/09/2018



Flow Cell Number: .....

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INSTRUCTIONS	NOTES/OBSERVATIONS
<p><input type="checkbox"/> Mix gently by flicking the tube, and spin down.</p> <p><input type="checkbox"/> Add the strand-switching buffer to the snap-cooled, annealed mRNA, mix by flicking the tube and spin down.</p> <p><input type="checkbox"/> Incubate at 42° C for 2 minutes.</p> <p><input type="checkbox"/> Add 1 µl of 200 U / µl SuperScript IV Reverse Transcriptase. The total volume is now 20 µl.</p> <p><input type="checkbox"/> Mix gently by flicking the tube, and spin down.</p> <p>Incubate using the following protocol:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Reverse transcription 10 mins @ 50° C (1 cycle)</li> <li><input type="checkbox"/> Strand switching 10 mins @ 42° C (1 cycle)</li> <li><input type="checkbox"/> Heat inactivation 10 mins @ 80° C (1 cycle)</li> <li><input type="checkbox"/> Hold @ 4° C</li> </ul>	
<p><b>Selecting for full-length transcripts by PCR and barcoding samples</b></p>	
<p>The PCR step outlined below adds barcodes to each cDNA sample. The barcoded primers are provided in the PCR Barcoding Kit (SQK-PBK004), and can be used to multiplex up to 12 individual samples on a single flow cell.</p>	
<p><b>IMPORTANT</b></p> <p><input type="checkbox"/> Each PCR reaction uses 5 µl of reverse-transcribed RNA (out of a 20 µl reaction). Therefore, sufficient material is available to perform four PCR reactions per reverse transcription reaction. Do NOT use all 20 µl of the reverse transcription reaction in a single PCR reaction.</p>	
<p>In order to generate sufficient PCR product to make best use of the capacity of the flow cell, it is recommended that at least four PCR reactions (each of 50 µl) are performed. If four, or more, samples are being prepared for barcoded sequencing, it is recommended that one 50 µl PCR reaction is performed per sample. If two samples are being prepared, the recommendation is to perform two 50 µl PCR reactions per sample.</p> <p>It is recommended that any remaining reverse transcription reaction is retained to allow for further PCR reactions if greater yield is required.</p> <p>For each sample (up to 12), prepare the following reaction at RT:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> 25 µl 2x LongAmp Taq Master Mix</li> <li><input type="checkbox"/> 1.5 µl LWB 01-12</li> <li><input type="checkbox"/> 18.5 µl Nuclease-free water</li> <li><input type="checkbox"/> 5 µl Reverse-transcribed RNA sample</li> </ul> <p>Amplify using the following cycling conditions:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Initial denaturation 30 secs @ 95 °C (1 cycle)</li> <li><input type="checkbox"/> Denaturation 15 secs @ 95 °C (11-18* cycles)</li> <li><input type="checkbox"/> Annealing 15 secs @ 62 °C (11-18* cycles)</li> <li><input type="checkbox"/> Extension 50 secs per kb @ 65 °C (11-18* cycles)</li> <li><input type="checkbox"/> Final extension 6 mins @ 65 °C (1 cycle)</li> <li><input type="checkbox"/> Hold @ 4 °C</li> </ul> <p style="text-align: right; color: blue; font-family: cursive;">A3=LWB01 G2=LWB02</p>	

cDNA-PCR Barcoding (SQK-PCS108 with SQK-PBK004)

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INSTRUCTIONS	NOTES/OBSERVATIONS
<ul style="list-style-type: none"> <li><input type="checkbox"/> Add 1 µl of NEB Exonuclease 1 (20 units) directly to each PCR tube.</li> <li><input type="checkbox"/> Incubate the reaction at 37° C for 15 min, followed by 80° C for 15 min.</li> <li><input type="checkbox"/> Pool the four PCR reactions (total 204 µl) in a clean 1.5 ml Eppendorf DNA LoBind tube.</li> <li><input type="checkbox"/> Prepare the AMPure XP beads for use; resuspend by vortexing.</li> <li><input type="checkbox"/> Add 160 µl of resuspended AMPure XP beads to the reaction and mix by pipetting.</li> <li><input type="checkbox"/> Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT.</li> <li><input type="checkbox"/> Prepare 500 µl of fresh 70% ethanol in Nuclease-free water.</li> <li><input type="checkbox"/> Spin down the sample and pellet on a magnet. Keep the tube on the magnet, and pipette off the supernatant.</li> <li><input type="checkbox"/> Keep on magnet, wash beads with 200 µl of freshly prepared 70% ethanol without disturbing the pellet. Remove the 70% ethanol using a pipette and discard.</li> <li><input type="checkbox"/> Repeat the previous step.</li> <li><input type="checkbox"/> Spin down and place the tube back on the magnet. Pipette off any residual 70% ethanol. Briefly allow to dry.</li> <li><input type="checkbox"/> Remove the tube from the magnetic rack and resuspend pellet in 21 µl of Rapid Annealing Buffer (RAB).</li> <li><input type="checkbox"/> Incubate on a Hula mixer (rotator mixer) for 10 minutes at RT.</li> <li><input type="checkbox"/> Pellet beads on magnet until the eluate is clear and colourless.</li> <li><input type="checkbox"/> Remove and retain 21 µl of eluate into a clean 1.5 ml Eppendorf DNA LoBind tube.</li> <li><input type="checkbox"/> Analyse 1 µl of the amplified DNA for size, quantity and quality. <span style="color: blue; font-family: cursive;">4.8 ng/µl</span></li> </ul>	
<p><b>IMPORTANT</b></p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Sometimes a high-molecular weight product is visible in the wells of the gel when the PCR products are run, instead of the expected smear. These libraries are typically associated with poor sequencing performance. We have found that repeating the PCR with fewer cycles can remedy this.</li> </ul>	
<p>In a 1.5 ml Eppendorf DNA LoBind tube, pool together a total of 350-600 fmol of the amplified cDNA barcoded samples to a final volume of 23 µl in RAB. <span style="color: blue; font-family: cursive;">350-600</span></p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Please check the Mass to Molarity table in the protocol</li> </ul>	
<p><b>Adapter addition</b></p>	
<ul style="list-style-type: none"> <li><input type="checkbox"/> Add 2 µl of cDNA Adapter Mix (cAMX) to the amplified cDNA library.</li> <li><input type="checkbox"/> Mix gently by flicking the tube, and spin down.</li> <li><input type="checkbox"/> Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT.</li> <li><input type="checkbox"/> Spin down briefly.</li> </ul>	

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INSTRUCTIONS	NOTES/OBSERVATIONS						
<p><b>AMPure XP bead binding</b></p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Prepare the AMPure XP beads for use; resuspend by vortexing.</li> <li><input type="checkbox"/> Add 20 µl of resuspended AMPure XP beads to the reaction and mix by flicking the tube.</li> <li><input type="checkbox"/> Incubate on a Hula mixer (rotator mixer) for 5 minutes at RT.</li> <li><input type="checkbox"/> Place on magnetic rack, allow beads to pellet and pipette off supernatant.</li> <li><input type="checkbox"/> Add 140 µl of ABB Buffer (ABB) to the beads. Close the tube lid, and resuspend the beads by flicking the tube. Return the tube to the magnetic rack, allow beads to pellet and pipette off the supernatant.</li> <li><input type="checkbox"/> Repeat the previous step.</li> <li><input type="checkbox"/> Remove the tube from the magnetic rack and resuspend pellet in 13 µl Elution Buffer (ELB).</li> <li><input type="checkbox"/> Incubate on a Hula mixer (rotator mixer) for 10 minutes at RT.</li> <li><input type="checkbox"/> Pellet the beads on a magnet until the eluate is clear and colourless.</li> </ul> <p>Remove and retain 13 µl of eluate into a clean 1.5 ml Eppendorf DNA LoBind tube.</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Remove and retain the eluate which contains the cDNA library in a clean 1.5 ml Eppendorf DNA LoBind tube</li> <li><input type="checkbox"/> Dispose of the pelleted beads</li> </ul>							
<p>Quantify 1 µl of eluted sample using a Qubit fluorometer.</p>	<p>4.18 ng / µl = 150 ng</p>						
<p>The prepared library is used for loading into the MinION flow cell. Store the library on ice until ready to load.</p>							
<p><b>Before sequencing checklist</b></p> <table border="0" style="width: 100%;"> <tr> <td><input type="checkbox"/> Prepared library on ice</td> <td><input type="checkbox"/> Computer set up to run MinKNOW</td> <td><input type="checkbox"/> Hardware check complete</td> </tr> <tr> <td><input type="checkbox"/> Sequencing device connected to computer with SpotON Flow Cell inserted</td> <td><input type="checkbox"/> Desktop Agent set up (if applicable)</td> <td><input type="checkbox"/> Flow cell check complete</td> </tr> </table>		<input type="checkbox"/> Prepared library on ice	<input type="checkbox"/> Computer set up to run MinKNOW	<input type="checkbox"/> Hardware check complete	<input type="checkbox"/> Sequencing device connected to computer with SpotON Flow Cell inserted	<input type="checkbox"/> Desktop Agent set up (if applicable)	<input type="checkbox"/> Flow cell check complete
<input type="checkbox"/> Prepared library on ice	<input type="checkbox"/> Computer set up to run MinKNOW	<input type="checkbox"/> Hardware check complete					
<input type="checkbox"/> Sequencing device connected to computer with SpotON Flow Cell inserted	<input type="checkbox"/> Desktop Agent set up (if applicable)	<input type="checkbox"/> Flow cell check complete					
<p><b>Priming and loading the SpotON flow cell</b></p>							
<p>IMPORTANT</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Thoroughly mix the contents of the RBF tube by vortexing or pipetting, and spin down briefly.</li> </ul>							
<ul style="list-style-type: none"> <li><input type="checkbox"/> Flip back the MinION lid and slide the priming port cover clockwise so that the priming port is visible.</li> </ul>							
<p>IMPORTANT</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Care must be taken when drawing back buffer from the flow cell. The array of pores must be covered by buffer at all times. Removing more than 20-30 µl risks damaging the pores in the array.</li> </ul>							

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<p>After opening the priming port, check for small bubble under the cover. Draw back a small volume to remove any bubble (a few µls):</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Set a P1000 pipette to 200 µl</li> <li><input type="checkbox"/> Insert the tip into the priming port</li> <li><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</li> </ul> <p>Prepare the flow cell priming mix in a clean 1.5 ml Eppendorf DNA LoBind tube.</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> 576 µl RBF</li> <li><input type="checkbox"/> 624 µl Nuclease-free water</li> </ul> <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.</p> <p><input type="checkbox"/> Thoroughly mix the contents of the RBF and LLB tubes by pipetting.</p> <p>Prepare the library for loading as follows:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> 35.0 µl RBF</li> <li><input type="checkbox"/> 25.5 µl LLB</li> <li><input type="checkbox"/> 2.5 µl Nuclease-free water</li> <li><input type="checkbox"/> 12 µl DNA library</li> </ul> <p>Complete the flow cell priming:</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Gently lift the SpotON sample port cover to make the SpotON sample port accessible.</li> <li><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.</li> </ul> <p><input type="checkbox"/> Mix the prepared library gently by pipetting up and down just prior to loading.</p> <p><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.</p> <p><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 lid.</p>	
<p><b>Starting a sequencing run</b></p>	
<ul style="list-style-type: none"> <li><input type="checkbox"/> Double-click the MinKNOW icon located on the desktop to open the MinKNOW GUI.</li> <li><input type="checkbox"/> If your MinION was disconnected from the computer, plug it back in.</li> <li><input type="checkbox"/> Choose the flow cell type from the selector box. Then mark the flow cell as "Selected".</li> <li><input type="checkbox"/> Click the "New Experiment" button at the bottom left of the GUI.</li> </ul> <p>On the New experiment popup screen, select the running parameters for your experiment from the individual tabs.</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Output settings - FASTQ: The number of basecalls that MinKNOW will write in a single file. By default this is set to 4000</li> <li><input type="checkbox"/> Output settings - FAST5: The number of files that MinKNOW will write to a single folder. By default this is set to 4000</li> </ul>	

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<p><input type="checkbox"/> Click "Start run".</p> <p>Allow the script to run to completion.</p> <p><input type="checkbox"/> The MinKNOW Experiment page will indicate the progression of the script; this can be accessed through the "Experiment" tab that will appear at the top right of the screen</p> <p><input type="checkbox"/> Monitor messages in the Message panel in the MinKNOW GUI</p> <p>The basecalled read files are stored in :\\data\\reads</p>	
<p><b>Progression of MinKNOW protocol script</b></p>	
<p>The running experiment screen</p> <p>Experiment summary information</p> <p>Check the number of active pores reported in the MUX scan are similar (within 10-15%) to those reported at the end of the Flow Cell Check</p> <p><input type="checkbox"/> If there is a significant reduction in the numbers, restart MinKNOW.</p> <p><input type="checkbox"/> If the numbers are still significantly different, close down the host computer and reboot.</p> <p><input type="checkbox"/> When the numbers are similar to those reported at the end of the Flow Cell Check, restart the experiment on the Connection page. There is no need to load any additional library after restart.</p> <p><input type="checkbox"/> Stopping the experiment is achieved by clicking "Stop run" button at the top of the screen.</p> <p>Data acquisition will stop, but the software will continue basecalling unless the user clicks the "Stop basecalling" button.</p> <p><input type="checkbox"/> Check that the temperature has reached 34° C.</p> <p>Check pore occupancy in the channel panel at the top of the experimental view.</p> <p><input type="checkbox"/> A good library will be indicated by a higher proportion of light green channels in Sequencing than are in Pore. The combination of Sequencing and Pore indicates the number of active pores at any point in time. A low proportion of Sequencing channels will reduce the throughput of the run.</p> <p><input type="checkbox"/> Recovering indicates channels that may become available for sequencing again. A high proportion of this may indicate additional clean up steps are required during your library preparation.</p> <p><input type="checkbox"/> Inactive indicates channels that are no longer available for sequencing. A high proportion of these as soon as the run begins may indicate an osmotic imbalance.</p> <p><input type="checkbox"/> Unclassified are channels that have not yet been assigned one of the above classifications</p> <p><input type="checkbox"/> Monitor the pore occupancy</p> <p>Duty time plots</p> <p><input type="checkbox"/> Monitor the development of the read length histogram.</p> <p>Cumulative throughput</p> <p><input type="checkbox"/> the number of reads that have been sequenced and basecalled; and whether the reads have passed of failed the quality filters</p> <p>Trace viewer</p>	

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INSTRUCTIONS	NOTES/OBSERVATIONS
<p><b>Onward analysis of MinKNOW basecalled data</b></p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Open the Desktop Agent using the desktop shortcut.</li> <li><input type="checkbox"/> Click on the New Workflow tab in the Desktop Agent and select the FASTQ barcoding workflow.</li> <li><input type="checkbox"/> Check the correct settings are selected in the Desktop Agent.</li> <li><input type="checkbox"/> Click "Start Run" to start data analysis.</li> <li><input type="checkbox"/> Follow the progression of upload and download of read files in the Desktop Agent.</li> </ul> <p>Click on VIEW REPORT.</p> <ul style="list-style-type: none"> <li><input type="checkbox"/> Click on VIEW REPORT to navigate to the Metrichor website, this can be done at any point during data exchange</li> <li><input type="checkbox"/> Return to the Desktop Agent to see progression of the exchange</li> </ul>	
<p><b>Close down MinKNOW and the Desktop Agent</b></p>	
<ul style="list-style-type: none"> <li><input type="checkbox"/> Quit Desktop Agent using the close x.</li> <li><input type="checkbox"/> Quit MinKNOW by closing down the web GUI.</li> <li><input type="checkbox"/> Disconnect the MinION.</li> </ul>	
<p><b>Prepare the flow cell for re-use or return to Oxford Nanopore.</b></p>	
<ul style="list-style-type: none"> <li><input type="checkbox"/> If you would like to reuse the flow cell, follow the Wash Kit instructions and store the washed flow cell at 2-8 °C, OR</li> <li><input type="checkbox"/> Follow the returns procedure by washing out the MinION Flow Cell ready to send back to Oxford Nanopore.</li> </ul>	