

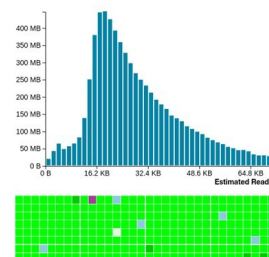
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Version 2

Nuclear DNA purification from recalcitrant plant species for long-read sequencing V.2

DOI

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High molecular weight D...

Team Schwessinger



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Verified across multiple genera.

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Abstract

Evolution has driven genetic diversity of life on Earth, but also created highly complex genomes that are difficult to sequence. Current draft genomes can have thousands to hundreds of thousands of contigs rather than chromosomes, containing incorrect assemblies, gaps and errors. With rapid advances in long-read technologies, it is becoming possible to resolve complex genomes, including repetitive, polyploid plant genomes. Despite the technology being available, a challenge persists: the extraction of pure high molecular weight DNA suitable for long-read sequencing. This is particularly true of recalcitrant native Australian trees such as Eucalypts and Acacias. To resolve this, firstly we optimised a density gradient and detergent based nuclei extraction to limit reads from high copy count plastid genomes. Secondly, we optimised a gentle high molecular weight DNA extraction free of columns and high centrifugation, to limit DNA fragmentation. Finally, the DNA was purified and size selected by gel electrophoresis. For sequencing, we adopted the portable MinION sequencer from Oxford Nanopore Technologies. Using these approaches, we have been obtaining >9 gigabases of sequencing from a single MinION flow cell, including reads over 100 kb in length. Such ultra-long reads assist the assembly of high quality genomes, from telomere to telomere.



Guidelines

This protocol is a modified and optimised combination of the following two publications. When citing, please also note the original publications below.

Bolger *et al.* (2014). The genome of the stress-tolerant wild tomato species *Solanum pennellii*. *Nature Genetics* **46**, 1034.

Mayjonade *et al.* (2016). Extraction of high-molecular-weight genomic DNA for long-read sequencing of single molecules. *BioTechniques* **61**, 203-205.

This research builds on the work of Benjamin Schwessinger and Miriam Schalamun; a warm thanks for their contributions.

Eucalyptus and Acacia tissue used in this protocol was kindly provided by the Australian National Botanic Gardens, Canberra, Australia.

Troubleshooting



Before start

This protocol is designed for two sample nuclei isolations and DNA extractions, although upscaling is possible. Prepare the following for two samples:

- Autoclave x2 500 mL Nalgene bottles, x10 1 L Schott bottles, x2 beakers and x2 funnels.
- Collect a branch of Eucalyptus leaves, harvest and wash leaves with tap water.
- Weigh 50 g of leaves into 50 g takeaway containers.
- Pre-chill the blender in 4°C cold room.
- For two sample extractions, on the day prepare 1 L nuclei isolation buffer and 1 L of nuclei wash buffer, and cool both down to 4°C.
- Prepare lysis buffer fresh on the day of use.
- Prepare all other solutions as listed below, storing at room temperature until use.

Nuclei isolation buffer (1 L for two samples)

- Adjust to pH 6 (add HCl; estimate listed below).
- Cool down to 4°C

	Com pon ent	MW	Stoc k	Qua ntity (1 L)
	1 M Hex ylen e gylc ol (2- Met hyl- 2,4- pent aned iol)	118.1 7	7.51 M (ship ped liqui d)	133 mL
	10 mM PIPE S	302. 4	0.5 M	20 mL
	10 mM MgC l ₂	203. 3	1 M	10 mL
	10 mM Sodi um meta	190.1 1	10% = 0.53 M	20 mL

	bisulfite			
	6 mM Ethylene glycol tetraacetic acid (EGTA) pH 7	380.4	0.5 M	12 mL
	pH 6 equilibration with HCl	36.46	5 M	4 mL
	0.5 % (w/v) Sodium diethyldithiocarbamate	171.26	10%	50 mL
	4% (w/v) PVP-10	10,000	powder	20 g
	200 mM L-lysine	146.19	powder	36.53 g
	1 mM Dithiothreitol (DTT)	154.25	powder	0.154 g

Nuclei wash buffer (1 L for two samples)

- Adjust to pH 7 (add NaOH; estimate listed below).
- Cool down to 4°C

	Com pon ent	MW	Stoc k	Qua ntity (1 L)
	0.5 M Hex ylen e glyc ol (2- Met hyl- 2,4- pent aned iol)	118.1 7	7.51 M (ship ped liqui d)	66.6 6 mL
	10 mM PIPE S	302. 4	0.5 M	20 mL
	10 mM MgC l ₂	203. 3	1 M	10 mL
	10 mM Sodi um meta bisul fite	190.1 1	10% = 0.53 M	20 mL
	6 mM Ethyl ene glyc ol tetra aceti c acid (EGT A) pH 7	380. 4	0.5 M	12 mL
	pH 7 equil ibrat ion with	40.0 0	5 M	3 mL



	NaO H			
	0.5 % (v/v) Trito n X- 100	647	10%	50 mL
	200 mM L- lysin e	182. 65	pow der	36.5 3
	1 mM Dithi othr eitol (DTT)	154. 25	pow der	0.15 4 g

Lysis buffer (10 mL per sample)

- Prepare a fresh solution for optimal results. The solution should be clear before use.

	Com pon ent	MW	Stoc k	Qua ntity (10 mL)
	1% Poly vinyl pyrr olido ne 40 (PVP -40)	40,0 00	10%	1 mL
	1% Sodi um meta bisul fite	190.1 1	10%	1 mL
	0.5 M NaCl	58.4 4	5 M	1 mL
	100 mM TRIS	121.1 4	1 M	1 mL



-HCl pH 8.0			
5 mM EDT A pH 8.0	292. 24	0.5 M	1 mL
3% Sodi um dod ecyl sulfa te (SD S)	288. 37	20%	1.5 mL
Wat er	-	-	3.5 mL

2% Sera-Mag beads solution (10 mL stock)

- Sera-Mag SpeedBead magnetic carboxylate modified particles (Thermo Scientific 65152105050250).
- Store at 4°C for up to 6 months.
- First prepare buffer without the beads. Let the Sera-Mag beads come to room temperature.

Com pon ent	MW	Stoc k	Qua ntity (10 mL)
18% Poly ethyl ene glyc ol (PEG) 8,00 0	8,00 0	25%	7,20 0 μ L
1 M NaCl	58.4 4	5 M	2,00 0 μ L
10 mM TRIS -HCl pH 8.0	121.1 4	1 M	100 μ L

1 mM EDT A pH 8.0	292.24	0.5 M	20 μ L
0.05 % Tween 20	1,227.54	10%	50 μ L
Water	-	-	430 μ L

- Homogenise Sera-Mag beads thoroughly by shaking and swirling.
- Prepare 2% Sera-Mag beads (200 μ L for 10 mL buffer) by washing 4 times with water to remove sodium azide. Magnetise, remove supernatant, add ~500 μ L H₂O, flick tube, magnetise etc.
- Resuspend the clean Sera-Mag beads in the buffer prepared.
- Note: Agencourt AMPure XP (Beckman Coulter) can be used but they must be washed 4 times with water and resuspended in their initial buffer.

Binding buffer solution (10 mL per sample)

- 2 g of PEG 8,000 (or 8 mL of 25% stock) [final = 20%]
- 75 g of sodium chloride [final = 3 M]
- Adjust to 10 mL with molecular biology grade water (approx 2 mL).

Mix until the solution becomes clear. If PEG8000 is not dissolved, it can lead to a poor yield as PEG 8000 makes gDNA to bind to the beads.

Other solutions

- Triton X-100 (ideally 10% solution)
- Ethanol (100% and 70%)
- RNase A (e.g. 20 mg/mL Invitrogen PureLink)
- 5 M Potassium acetate

Special equipment (for two samples)

- 500 mL Nalgene bottles (x2)
- 1 L Schott bottles (x10)
- Beakers (x2)



- Funnel (preferably glass) (x2)
- Large fine hair paint brushes (x2) (e.g. J.Burrows Mop Goat Hair 24 #9341694325125)
- etic rMack (for Falcon and Eppendorf tubes)
- 15 mL Falcon tubes
- 50 mL Falcon tubes
- DNA LoBind Eppendorf tubes (e.g. 022431021)
- Sieve or mesh, 300 μm (e.g. Kartell disk membrane; ART 844)
- Miracloth or stretcher sheets (e.g Drager 334201)
- 200 μL wide-bore pipette tips (e.g. Vertex 4290-00)



BLENDER LYSIS (4°C cold room)

- 1 Place 50 g of leaves into a blender with enough nuclei isolation buffer to cover the blades (approximately 150 mL).

Note

Optimised for Eucalyptus, a diploid ~500 Mb genome. Larger genomes or polyploid plants can have less input accordingly.

BLENDER LYSIS (4°C cold room)

- 2 Homogenise the tissue on max speed. Transfer to a beaker, repeatedly washing out blender with nuclei isolation buffer (500 mL buffer is allocated per extraction).
- 3 Clean the blender with tap water, 70% ethanol and then MQW; process the other sample (repeating steps 1 and 2).

FILTRATION (ideally 4°C cold room)

- 4 Filter homogenate using a sieve (or disk membrane mesh placed in a funnel) into a 1 L Schott bottle. Forcibly squeeze out as much residual homogenate from the leaf debris as possible, maximising nuclei capture.

FILTRATION (ideally 4°C cold room)

- 5 Filter homogenate through 1 layer of Miracloth using a funnel and 1 L Schott bottle. Gently squeeze residual homogenate through the Miracloth.

Note

May need to change the layer half way through (very dirty and clogged).

FILTRATION (ideally 4°C cold room)

- 6 Repeat Filtration through 2 layers of Miracloth then 4 layers (using new Schott bottles).

FILTRATION (ideally 4°C cold room)



- 7 Finally, gravity filter through 8 layers of Miracloth (no squeezing) into a 500 mL Nalgene bottle. Repeat steps 4-6 for the second sample.

NUCLEI ISOLATION

- 8 Add 2.5 mL of 100% Triton X-100, or 25 mL of 10% (final concentration 0.5%).

NUCLEI ISOLATION

- 9 Incubate mixture on an ice bath with gentle rocking for 30 min.

Note

Use this time to clean the mess made with the blender and filtering

NUCLEI ISOLATION

- 10 Weigh the Nalgene bottles with contents and lids to ensure they are equal for balancing purposes. Also ensure the Nalgene bottle has an intact o-ring to avoid leakage during centrifugation.

NUCLEI ISOLATION

- 11 Centrifuge at 600 rcf and 4 °C for 20 minutes.

Note

4,600 rpm on a Sorvall RC5C using rotor SLA-3000 (00).

NUCLEI ISOLATION

- 12 Discard the supernatant and add 200 mL of nuclei wash buffer.

NUCLEI ISOLATION

- 13 Gently resuspend the pellet using a large fine hair paint brush, soaked in freshly made pre-chilled nuclei wash buffer.

**Note**

Ensure the bottles are balanced and have an o-ring as previously described.

NUCLEI ISOLATION

- 14 Centrifuge at 600 rcf and 4°C for 20 minutes.

NUCLEI ISOLATION

- 15 Discard supernatant and repeat with another 200 mL of nuclei wash buffer. The pellet should become grey-white with no traces of green. If not, make more nuclei wash buffer and repeat the resuspending and washing steps.

Note

1 L of nuclei wash buffer is suitable for x2 samples to be washed x2 times with 200 mL each, then a final resuspension with 100 mL each.

NUCLEI ISOLATION

- 16 After the final spin down, discard the supernatant and resuspend the pellet with 50 mL of nuclei wash buffer. Transfer evenly across two 50 mL Falcon tubes. Repeat the resuspension with another 50 mL of buffer and add to the two Falcon tubes.

NUCLEI ISOLATION

- 17 Centrifuge at 600 rcf and 4°C for 30 minutes.

NUCLEI ISOLATION

- 18 Discard the supernatant. The nuclei pellets can now be stored -80°C.

DNA EXTRACTION FROM NUCLEI

- 19 Prepare 10 mL of fresh lysis buffer per sample. Ideally, pre-heat at 50-65°C.

**Note**

The solution should be clear before use.

DNA EXTRACTION FROM NUCLEI

- 20 To a 3-5 mL nuclei pellet, add 10 mL of lysis buffer.

Note

Therefore, the SDS will be approximately 2% final concentration. Usually just one of the two Falcon tubes of a nuclei prep per sample are used.

DNA EXTRACTION FROM NUCLEI

- 21 Add 200 μ L of RNase A to each sample (20 mg/mL Invitrogen PureLink).

DNA EXTRACTION FROM NUCLEI

- 22 Incubate the samples at 50-60°C for 1 h, shaking at 400 - 900 rpm if possible.

Note

Higher temperatures and longer incubations lead to DNA damage.

DNA EXTRACTION FROM NUCLEI

- 23 Add 1/3 volume of 5 M Potassium Acetate and mix by inverting to precipitate the proteins and the polysaccharides that will complex with SDS.

DNA EXTRACTION FROM NUCLEI

- 24 Incubate on ice (4°C) for 10 min (don't rotate, DNA vulnerable).

DNA EXTRACTION FROM NUCLEI

- 25 Centrifuge at 5,000 rcf for 5 min at 4°C.



DNA EXTRACTION FROM NUCLEI

- 26 Transfer supernatant to a new tube, centrifuge again at 5,000 rcf for 10 min at 4°C.

DNA EXTRACTION FROM NUCLEI

- 27 Transfer to a new tube and add 1.2x binding buffer. Ideally, split across x2 15 mL Falcon tubes.

DNA EXTRACTION FROM NUCLEI

- 28 Add 1 mL of 2% Sera-Mag beads (500 µL per Falcon tube if split).

Note

Beads are in excess and could be reduced.

DNA EXTRACTION FROM NUCLEI

- 29 Mix by inverting the tube 20 times. Incubate with gentle agitation using a rotator or a rocker platform for 15 min at room temperature.

DNA EXTRACTION FROM NUCLEI

- 30 Place the tube in a magnetic rack for 30 min or more (until the solution becomes clear, can be over an hour).

DNA EXTRACTION FROM NUCLEI

- 31 Remove the supernatant without disturbing the beads.

DNA EXTRACTION FROM NUCLEI

- 32 Wash the beads by filling the tube with 70% ethanol, let beads settle if disturbed, and pour out ethanol.



DNA EXTRACTION FROM NUCLEI

- 33 Repeat the ethanol wash another 3-5 times, until satisfied the beads are clean.

Note

If the beads are very dirty, remove the tube from the magnetic rack, resuspend beads by flicking the tube, magnetise until clear, remove supernatant, repeat washing.

DNA EXTRACTION FROM NUCLEI

- 34 Transfer the beads to an Eppendorf tube. This can be done in a series of small volume ethanol washes that resuspend the beads, transfer to Eppendorf tube, then place on the magnetic rack, remove supernatant and repeat into the same tube.

DNA EXTRACTION FROM NUCLEI

- 35 Remove all traces of ethanol, and let the beads air dry for 1-4 min. Do not let the beads dry completely, they will crack and significantly reduce DNA recovery.

DNA EXTRACTION FROM NUCLEI

- 36 Using a wide-bore pipette tip, add 220 μ L of ultra-pure H₂O to the beads, gently resuspending. Gently tapping the tube is also suitable.

Note

Larger volume based on PippinHT input across x1 whole cassette.

DNA EXTRACTION FROM NUCLEI

- 37 Place the tubes in the magnetic rack for ~30 min. Let the solution become clear.

Note

Highly concentrated DNA will take a long time. The tube can be left on the magnetic rack overnight, or add more water.

DNA EXTRACTION FROM NUCLEI

- 38 Transfer 200 μL of supernatant (contains DNA) to a new tube, avoiding any carry-over of beads.

GEL PURIFICATION: PIPPIN PREP

- 39 For some species, the DNA may be pure enough for sequencing at this point. However, for most recalcitrant plants, the DNA will still have impurities and DNA fragmentation is inevitable. Gel purification is an ideal solution to both problems.
- 40 Using a PippinHT (Sage Science) or similar automated electrophoresis product, gel purify approximately 30 μg , following the manufacturer's instructions. A 15 kb high pass separation is recommended, however if DNA is plentiful, 20 kb high pass is more suitable. The PippinHT has 12 lanes, however a lane pair needs be dedicated to an external ladder, leaving 10 lanes for samples. 20 μL of DNA goes into each lane (therefore 200 μL elution in previous section). The manufacturer recommends a maximum 1.5 μg per lane (15 μg total per cassette), however, can be successfully overloaded to 3 μg per lane (perhaps more). The size selection will not be as precise, but is of no concern here.

Note

Alternatively, a chloroform: isoamyl alcohol 24:1 clean-up can be performed to remove residual phenols and proteins. Other possibilities (untested), are digestion with proteinase K and another bead clean up. Also would be interesting to experiment with adding PVP to the binding buffer to further reduce polyphenols.

- 41 After separation, wait at least 45 min (hours or overnight is suitable), to aid elution and recovery.
- 42 Collect the contents of all elution wells into a DNA LoBind Eppendorf tube (approx. 300 μL).
- 43 Add 30 μL of 0.1% tween solution to each elution well (provided in kit). Wait at least 10 min and then transfer the contents to the same DNA LoBind Eppendorf tube (another 300 μL , tube total is approx. 600 μL).
- 44 Add 1.2x binding buffer (approx. 720 μL), and 100 μL of 2% Sera-Mag beads to the DNA LoBind Eppendorf tube. Incubate, magnetise and ethanol wash as previously described in 'DNA extraction from nuclei'.
- 45 After drying the beads elute with 65 μL of ultra-pure water. Incubate, magnetise and transfer to a new DNA LoBind Eppendorf tube using a wide-bore pipette tip. Expect 20-30% recovery relative to total input (~6-9 μg).

SEQUENCING LIBRARY PREPARATION

- 46 For sequencing, we adopted the portable MinION sequencer from Oxford Nanopore Technologies. There are two native genomic DNA library preparations available; a rapid transposase based method (SQK-RAD004) and ligation based method (SQK-LSK108/109). Following the manufacturer's instructions, prepare a library. Note that Oxford Nanopore recommends a mass of DNA optimised for 0.2 pmol (193 fmol). However, this is based on an average length of 8 kb. Therefore, the amount of input DNA needs to be adjusted. The following is recommended based on PippinHT size selection:

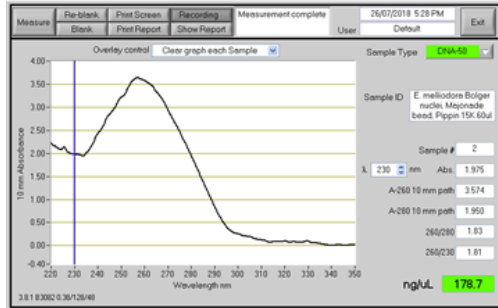
Fragment sizes	Rapid SQK - RAD004	Ligation SQK - LSK108/109
No size selection, ~8 kb	800 ng	4,000 ng
15 kb high pass	1,000 ng	4,000 ng
20 kb high pass	1,200 ng	4,000 ng

- 47 Load the MinION and perform sequencing according to Oxford Nanopore's instructions. Ensure no bubbles are introduced into the array.

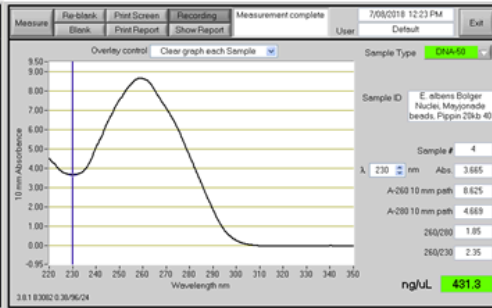
Expected result

Using the protocol described, we have been obtaining clean high molecular weight DNA (Figure 1, Table 1). DNA fragment size has been predominantly 20-140 kb in length (Figure 2). During sequencing, we have been obtaining >9 gigabases from a single MinION flow cell for recalcitrant *Eucalyptus* and *Acacia* species, including reads over 100 kb in length (Table 2, Figure 3). N50 values depend on library preparation method, but can reproducibly obtain N50 values >20 kb using ligation kits. A troubleshooting guide is presented in Figure 4, illustrating the most common problems researchers have.

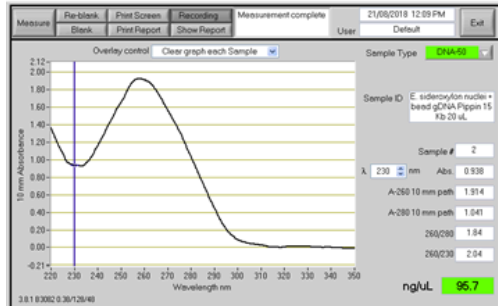
(A) *Eucalyptus melliodora*



(B) *Eucalyptus albens*



(C) *Eucalyptus sideroxylon*



(D) *Acacia acuminata*

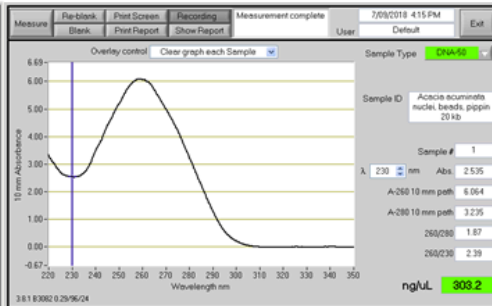


Figure 1: Spectrophotometer results of a nuclear DNA purification performed on recalcitrant *Eucalyptus* and *Acacia* species. Readings taken using 1 μ L on a Thermo Scientific Nanodrop 1000.

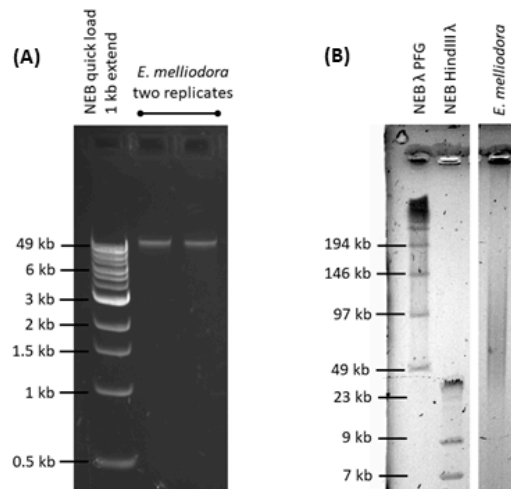


Figure 2: Gel electrophoresis analysis of DNA quality. *Eucalyptus melliodora* is shown as a representative example. (A) 50 ng of DNA separated on a 1% agarose gel. (B) 300 ng of DNA separated by pulsed field gel electrophoresis.

Table 1: DNA quantification and pippin prep. One of two nuclei pellets processed.

Sample	Approx DNA μ g	Pippin input	Pippin setting	Qubit ng/ μ L	Nano ng/ μ L	260/280	260/230	Recovery μ g
<i>E. melliodora</i>	36	18	15 kb	134	178.7	1.83	1.81	8.0 (44%)
<i>E. marginata</i>	29	29	20 kb	139	170.0	1.88	2.37	8.6 (30%)
<i>E. albens</i>	32	32	20 kb	259	431.3	1.85	2.35	8.8 (28%)
<i>E. sideroxylon</i>	7.6	7.6	15 kb	95.6	95.7	1.84	2.04	1.9 (25%)
<i>A. acuminata</i>	98	39	20 kb	312	303	1.87	2.39	19 (19%)

Table 2: Sequencing results with a MinION flow cell per sample (FLO-MIN 106 R9.4.1 revC), except for the first entry, which shows the results of a PromethION flow cell performed at a sequencing facility. For library input with ligation kits, first number is the initial input, second number is the recovery after all cleans.

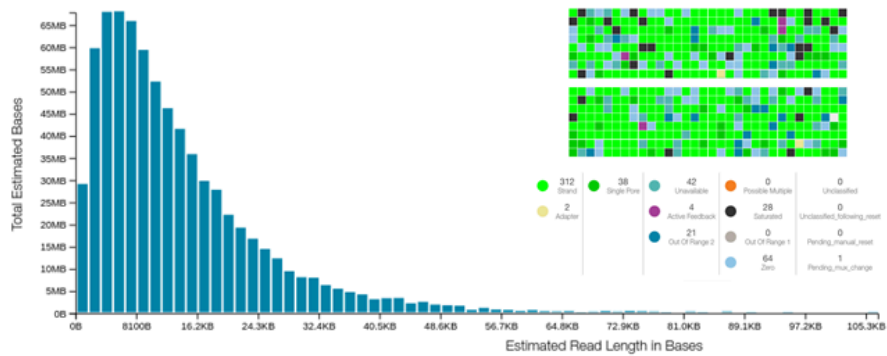
Sample	Pippin prep \geq	Library input μ g	Library preparation	Pores	Output Gb	Base call Gb	N50 kb
<i>E. melliodora</i> ¹	20 kb	1/?	PromethION LSK109	2,270	?	34.33	33.01
<i>E. melliodora</i>	15 kb	0.8	Rapid SQK-RAD004	1,313	10.20	9.37	8.05
<i>E. melliodora</i>	15 kb	4/1.1	Ligation SQK-LSK109	1,289	9.39	7.99	22.05
<i>E. marginata</i>	20 kb	1	Rapid SQK-RAD004	1,384	10.10	9.33	11.24
<i>E. marginata</i>	20 kb	4/0.9	Ligation SQK-LSK109	1,325	11.05	9.25	25.86
<i>E. albens</i> ²	20 kb	1	Rapid SQK-RAD004	1,208	9.26	7.74	9.02
<i>E. albens</i>	20 kb	4/1.1	Ligation SQK-LSK109	1,279	12.50	9.82	24.00
<i>E. sideroxylon</i>	15 kb	1	Rapid SQK-RAD004	1,584	13.15	11.26	7.66
<i>E. sideroxylon</i> ³	15 kb	0.6	Rapid SQK-RAD004	1,443	6.71	5.95	7.75
<i>A. acuminata</i>	20 kb	4/1.4	Ligation SQK-LSK109	1,229	14.72	10.68	12.23
<i>A. acuminata</i>	20 kb	4/1.4	Ligation SQK-LSK109	1,239	15.85	12.50	13.05

¹Using 4 μ g is recommended (this run was performed externally by sequencing facility staff).

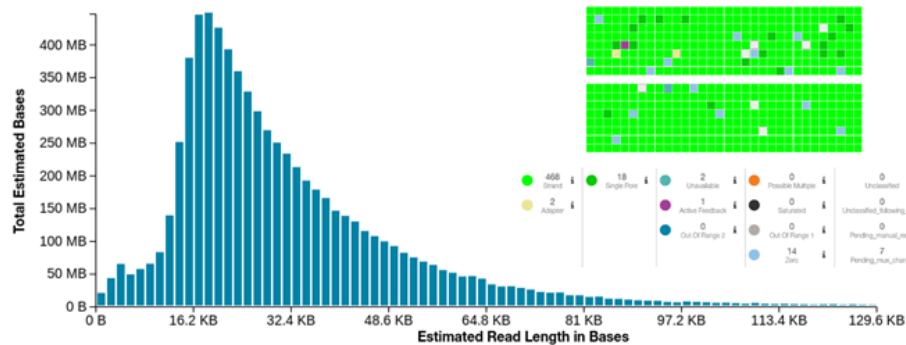
²Device disconnected for several hours due to IT issues (lost reads).

³Not enough DNA (depleted) but required more coverage. Resulted in lower sequencing yield.

(A) *Eucalyptus melliodora*; rapid transposase library prep (SQK-RAD004). Output: 10.20 Gb.



(B) *Eucalyptus melliodora*; end ligation library prep (SQK-LSK109). Output: 9.39 Gb.



(C) *Eucalyptus albens*; end ligation library prep (SQK-LSK109). Output: 12.50 Gb.

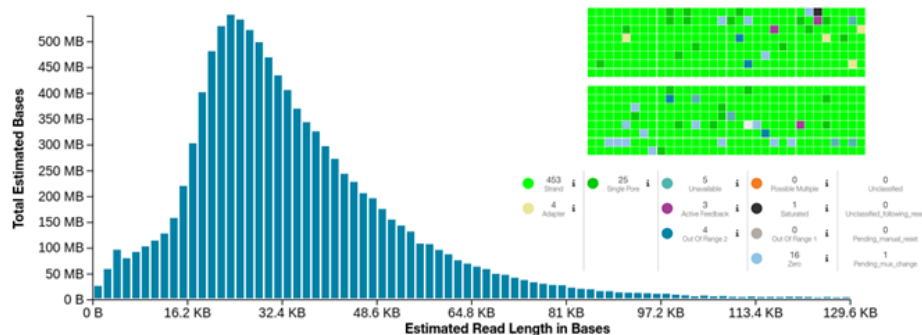
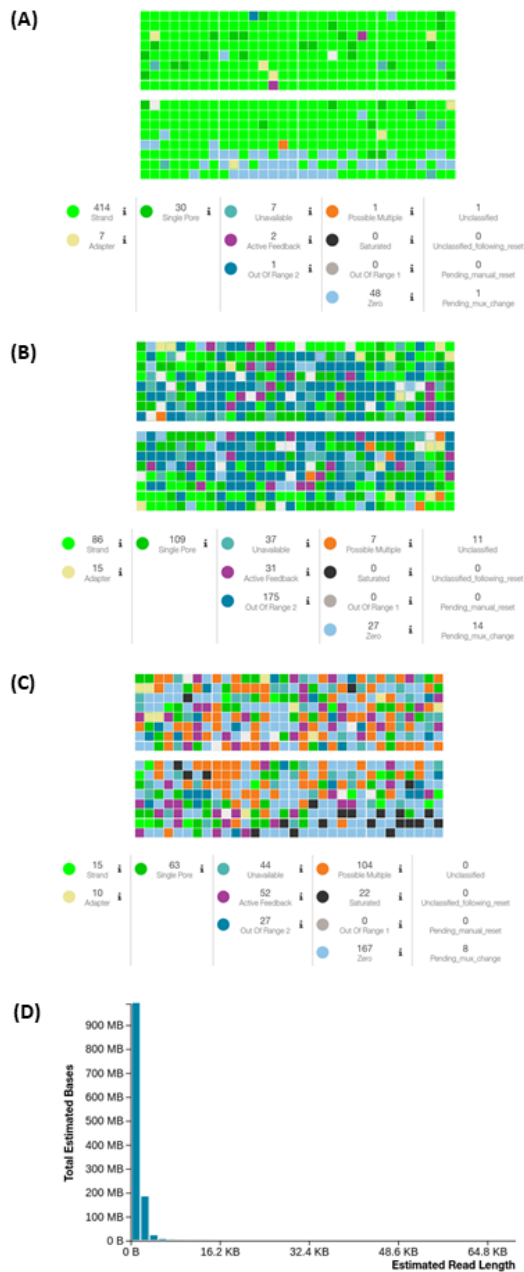


Figure 3: Expected read length histogram on MinKNOW 2.0. An *E. melliodora* DNA prep was processed with rapid transposase (A) and end ligation (B) library preps. (C) *E. albens* processed by ligation library prep. Inserts show pore usage.



Air bubble introduced into array during MinION loading. Pipetting all FLB buffer into the priming port is not necessary; ensure no air is introduced. Pull pipette away while dispensing. Gently load SpotON port drop-wise, keeping the pipette tip away from the port.

Expected output: 6-9 Gb.

More inactive pores (single) than actively sequencing (strand). Check molarity; high number of DNA fragments are necessary to collide with a nanopore. Active feedback and out of range indicates contamination, which may have inhibited the ligation of adapters.

Expected output: 3-6 Gb.

High amount of contamination, pores are being destroyed. Likely high levels of endogenous phenols and secondary metabolites from plant cells. Check 260/230 value on Nanodrop; should be 2 or higher. Clean DNA further by gel purification or chloroform phase separation.

Expected output: < 1 Gb.

DNA highly sheared and/or degraded during DNA extraction. All reads < 10 kb. Avoid column-based DNA extractions, vortexing, high concentrations of acids and high temperatures. Beware of contamination with exogenous DNases. There may not be enough adapter to ligate onto too many DNA fragments. Degraded DNA will ligate poorly.

Figure 4: Troubleshooting guide for poorly performing MinION runs. MinION performance is largely dependent on DNA quality, which can inhibit sequencing through the nanopore. Technical issues include air bubbles and undesirable DNA shearing. MinKNOW 2.0 screenshots shown from anonymous colleagues with permission.