Nanobind HMW DNA Extraction – Cultured Cells Protocol

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For HMW (50 kb – 300+ kb) DNA extraction from cultured cells for standard long-read sequencing applications

circulomics

Equipment and Reagent List

Equipment/Reagent	Manufacturer (Part Number)
Nanobind CBB Big DNA Kit or Nanobind Tissue Big DNA Kit	Circulomics (NB-900-001-01 or NB-900-701-001)
Magnetic Tube Rack	Thermo Fisher DynaMag-2 (12321D)
Mini-Tube Rotator	Fisher Scientific (05-450-127)
Mini-centrifuge	Ohaus (FC5306)
Micro-centrifuge	Eppendorf (5404000413)
ThermoMixer	Eppendorf (5382000023)
1.5 mL Protein LoBind Microcentrifuge Tubes	Eppendorf (022431081)
Ethanol (96–100%)	
Isopropanol (100%)	
1X PBS	
UV/Vis	Thermo Fisher Scientific NanoDrop 2000
Fluorescent DNA Quantification	Thermo Qubit 3.0, dsDNA BR and RNA BR Assay Kits
26g Blunt End Needle	SAI Infusion (B26150)
1 mL Syringe	Fisher Scientific (14-823-30)

For All Protocols

Eppendorf Protein LoBind tubes (Eppendorf #022431081) are highly recommended for all extractions to reduce protein contamination from tube carryover. Protein LoBind tubes are more effective in reducing carryover contamination than DNA LoBind tubes or other tubes and will result in improved UV purity.

Prior to Starting

Buffer CW1 and CW2 are supplied as concentrates. This kit uses CW1 with a 60% final ethanol concentration. This kit uses CW2 with a 60% final ethanol concentration. Before using, add the appropriate amount of ethanol (96–100%) to Buffer CW1 and Buffer CW2 as indicated on the bottles.

Kit Storage

RNase A and Buffer CT (Nanobind Tissue Big DNA kit, NB-900-701-001, only) should be stored at 4 °C upon arrival.

Nanobind disks and all other buffers should be stored at room temperature (18–25 °C).

Safety Precautions

Buffer BL3 and Buffer CW1 contain guanidine hydrochloride. Warning! Guanidine hydrochloride is harmful if swallowed or inhaled and causes skin and eye irritation. DO NOT mix with bleach or acidic solutions.

Product Use

Nanobind Big DNA Kits are intended for research use only.

HMW (50 kb – 300+ Mb) DNA Extraction Protocol

This protocol describes the extraction of HMW DNA from cultured cells. It is recommended for most long-read sequencing applications. This includes PacBio CLR and HiFi sequencing and nanopore sequencing using Oxford Nanopore Ligation and Rapid Sequencing Kits. For standard long-read sequencing applications this HMW DNA extraction protocol will result in superior sequencing performance than the UHMW DNA extraction protocol**.** This protocol requires the Nanobind CBB Big DNA Kit (NB-900-001-01) or the Nanobind Tissue Big DNA Kit (NB-900-701-01).

Please refer to the Circulomics Support Page (https://www.circulomics.com/support-nanobind) for the latest version of this protocol and the appropriate Nanobind Kit Handbook for additional experimental details.

Cell Input Requirements

Amount: $1x10^6$ – $5x10^6$ diploid human cells or equivalent

- Cell counts should be accurately determined using a hemocytometer or cell counter.
- For non-diploid or non-human cells, the cell input should be scaled appropriately to contain 5–30 µg of DNA.
- Up to $25x10^6$ cells can be processed by scaling the buffer volumes. Contact Circulomics for more information.
- This protocol has been validated on cell lines including GM12878, MCF-7, and MCF-10A.
- No systematic difference has been seen in either DNA QC or sequencing results between fresh and frozen cell samples.
- Cell pellets should be frozen dry with as much liquid removed as possible. No cryoprotectant is needed.

HMW DNA Extraction – Cultured Cells

1. **Harvest cells and centrifuge at 500 x *g* for 3–5 min at 4 °C to pellet cells in a 1.5 mL Protein LoBind tube; remove the supernatant.**
    - Frozen cell pellets may also be substituted here.
2. **Add 20 µL of 1x PBS and pipette mix 10X with a standard P200 pipette to resuspend cells.**
    - Mix until cell pellet is fully resuspended without visible lumps. Sticky cell types may require additional pipette mixing or vortexing.
    - Aggressive mixing at this step will not affect DNA size. However, incomplete resuspension will result in inefficient lysis and digestion which will lead to low yield, low purity, and high heterogeneity.
3. **Add 20 µL of Proteinase K.**
4. **Add 20 µL of Buffer CLE3 and pulse vortex for 1 s x 10 times (max setting).**
5. **Incubate on a ThermoMixer at 55 °C and 900 rpm for 10 min.**
    - If a ThermoMixer is not available, a heat block or water bath can instead be used with periodic agitation to ensure lysis.
6. **Optional for removal of RNA: add 20 µL of RNase A, pulse vortex for 1 s x 5 times (max setting), and incubate at RT (18–25 °C) for 3 min.**
7. **Add 200 µL of Buffer BL3 and pulse vortex for 1 s x 10 times (max setting).**
    - A white precipitate may form after addition of BL3. This is completely normal and usually disappears during the step 8 incubation.

VORTEXING IS YOUR FRIEND

Quick Tip

Complete resuspension of the cell pellet is critical for ensuring efficient lysis.

Quick Tip

Do not skip vortexing steps. Mix aggressively. Even with aggressive vortexing, the DNA will be hundreds of kilobases in length.

- Insufficient mixing in step 2, step 4, and step 7 will result in very large DNA but also low purity, low yield, high heterogeneity, and difficult elution.

8. **Incubate on a ThermoMixer at 55 °C and 900 rpm for 10 min.**
    - Cell inputs greater than $5x10^6$ may require longer incubation times to ensure complete lysis. If cellular aggregates are visible, extend lysis time by 10 min (up to 30 min).
9. **Add Nanobind disk to cell lysate and add 300 µL of isopropanol. Inversion mix 5X.**
    - The Nanobind disk must be added before isopropanol.
10. **Mix on tube rotator at 9 rpm at RT for 10 min.**
    - Some white precipitate may be seen attached to the DNA as it binds to the disk. This is normal.
11. **Place tubes on the magnetic tube rack.**
    - Use the method described in the **Kit Handbook Magnetic Rack Handling Procedure** section.
12. **Discard the supernatant with a pipette, taking care to avoid pipetting the DNA or contacting the Nanobind disk.**
    - Refer to the **Kit Handbook Pipetting** section for details.
13. **Add 700 µL of Buffer CW1, remove tube rack from magnetic base, inversion mix 4X, replace tube rack on the magnetic base, and discard the supernatant.**
    - Remove excess liquid from the tube cap to minimize carryover contamination.
14. **Add 500 µL of Buffer CW2, remove tube rack from magnetic base, inversion mix 4X, replace tube rack on the magnetic base, and discard the supernatant.**
    - Remove excess liquid from the tube cap to minimize carryover contamination.
15. **Repeat step 14.**
16. **Spin the tube on a mini-centrifuge for 2 s. With the tube rack already on the magnetic base and right-side-up, place tube on tube rack and remove residual liquid.**
    - If the Nanobind disk is blocking the bottom of the tube, gently push it aside with the tip of the pipette. At this stage, DNA is tightly bound to the disk and gently manipulating the disk with a pipette tip should not cause any damage.
17. **Repeat step 16.**
18. **Add 75–200 µL of Buffer EB and incubate at RT for 10 min.**
19. **Collect DNA by transferring eluate to a new 1.5 mL microcentrifuge tube with a standard P200 pipette. Repeat until all eluate is transferred.**
20. **Spin the tube containing the Nanobind disk on a micro-centrifuge at 10,000 x *g* for 15 s and combine any additional liquid that comes off the disk with the previous eluate. Repeat if visible DNA remains on the disk.**
    - A small amount of liquid or gel like material may remain on the Nanobind disk after transferring the eluate in step 19. **This clear gel is DNA!** The spin in step 20 will allow DNA to slide off the Nanobind disk into the bottom of the tube, after which it can be pipetted out and combined with the previously transferred eluate.
    - This should not require any more than 1–2 spins.

Quick Tip

Pipette from the liquid interface rather than the bottom of the tube to avoid pipetting any dangling DNA

Quick Tip

This 15 s spin is **CRITICAL** for recovering the DNA. We do not recommend a 2nd elution.

21. **Pipette mix the sample 10X with a standard P200 pipette to homogenize and disrupt any unsolubilized "jellies" that may be present.**
    - Take care to disrupt any regions that feel more viscous than other regions.
    - Limited pipette mixing will not noticeably reduce DNA size or sequencing read lengths but is important for accurate quantitation and consistent sequencing performance.
22. **Let sample rest at RT for overnight to allow DNA to solubilize.**
    - Visible "jellies" should disperse after resting.
23. **Following overnight rest, pipette mix 10X with a standard P200 pipette and analyze the recovery and purity as described in QC Procedure.**
    - If the concentration %CV exceeds 30% or if perceptible "jellies" remain, pipette mix 10X with a standard P200 pipette or needle shear 5X with a 26g needle and allow DNA to rest at RT for 2 hours. Take care to disrupt any regions that feel more viscous than other regions. Remeasure with NanoDrop.
    - Heterogeneity can result from insufficient vortexing in step 4 and step 7. Use aggressive mixing until familiar with the protocol.

Quick Tip

The DNA will solubilize after resting at RT or by coaxing it into solution using gentle mixing. For samples that need to be used immediately, we recommend pipette mixing or needle shearing.

QC Procedures

It is recommended that QC is performed after the DNA has been allowed to rest at RT overnight and appears homogeneous under visual examination and when pipetting.

1. **Perform triplicate NanoDrop UV/VIS measurements from top, middle, and bottom of tube to determine total nucleic acid concentration as well as purity (A260/A280, A260/230).**
    - HMW DNA is inherently difficult to work with as viscosity and inhomogeneity are often issues. We recommend taking at least three measurements, sampling from the top, middle, and bottom of the tube, to get an accurate concentration reading. We typically see concentration %CV values of <20%. However, if the DNA is very large, the %CV can exceed 30–40%.
    - If the DNA is very heterogeneous or contains large amounts of unsolubilized "jellies, refer to the **Kit Handbook Heterogeneity and Viscosity** and **Troubleshooting FAQ** sections.
2. **Perform triplicate Qubit dsDNA BR Assay measurements from top, middle, and bottom of tube to determine DNA concentration.**
    - We recommend taking the average of multiple measurements to ensure an accurate DNA concentration reading.
    - We recommend the Qubit 3.0 (Thermo Fisher Scientific) with the dsDNA BR Assay kit. We do not recommend the dsDNA HS Assay kit as we have found the concentration measurements to be unreliable.
3. **Perform a single Qubit RNA BR Assay measurement to determine RNA concentration (optional).**
    - We recommend taking a single measurement to get an approximate RNA concentration reading.
    - We recommend the Qubit 3.0 (Thermo Fisher Scientific) with the RNA BR Assay kit.
4. **Run pulsed field gel electrophoresis to determine size.**
    - The size of the extracted genomic DNA can be determined using pulsed field gel electrophoresis (PFGE). We recommend loading 200 ng of DNA per well. For analysis of 50 kb – 1+ Mb DNA, we recommend the following PFGE conditions:
        - Instrument: Bio-Rad CHEF-DR III Variable Angle System or CHEF Mapper XA System
        - Agarose: 1.0% Certified Megabase Agarose (Bio-Rad #1613109)
        - 30-well comb (Bio-Rad #1704344)
        - Buffer: 0.5X TBE
        - Lambda DNA Ladder: Bio-Rad #1703635, Lonza #50401, or NEB #N0341S
        - 6X gel loading dye (NEB #B7021S)
        - Temperature: 14 °C
        - Initial Switch Time: 35 seconds
        - Final Switch Time: 90 seconds
        - Run Time: 22 hours
        - Angle: 120°
        - Voltage Gradient: 5.5 V/cm
    - Stain for 1 hr using SYBR Gold and image immediately.
    - Agilent Femto Pulse results should be interpreted cautiously as large HMW DNA can generate inconsistent sizing results.

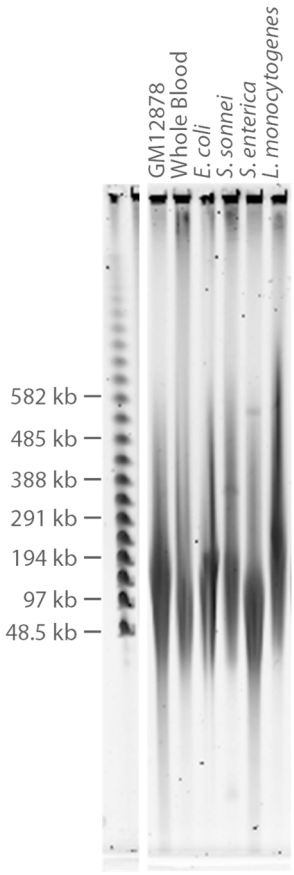
Storage of DNA

DNA can be stored in Buffer EB at 4 °C for several months. Long term storage at -20 °C or -80 °C can be used if necessary. Avoid freeze/thaw cycles since this can degrade high molecular weight DNA.

Results

- DNA was extracted from MCF-7, MDA-MB-231, MCF-10A, and GM12878 cells.
- 260/280 ratios should consistently be in 1.8–2 range.
- 260/230 ratio can vary from 1.7–2.2.
- Samples with UV purities within the expected range should sequence well. UV purities outside of these ranges may indicate abnormalities in the extraction process.
- Higher input levels can be used with appropriate optimization of buffer volumes and enzyme levels.

Sample	Input Amount	260/280	260/230	Nanodrop Top (ng/µL)	Nanodrop Middle (ng/µL)	Nanodrop Bottom (ng/µL)	Nanodrop Avg (ng/µL)	Qubit DNA Yield (µg)
MCF-7 (tetraploid)	$1x10^6$ cells	1.9	2.0	185.7	185.9	186.1	186.0	13.5
MDA-MB-231 (tetraploid)	$1x10^6$ cells	1.9	2.0	240.1	207.3	205.6	217.7	14.9
MCF-10A (diploid)	$2x10^6$ cells	1.9	2.0	149.1	147.5	153.0	149.9	12.3
GM12878 (diploid)	$5x10^6$ cells	1.9	2.2	578.9	485.4	480.3	514.9	37.2



22 hour Pulsed Field Gel Electrophoresis (PFGE) image of HMW DNA extracted from cultured human cells (GM12878)

Troubleshooting FAQ

1. What do I do if the DNA is heterogenous and/or contains visible insoluble "jellies"?

- HMW DNA is inherently difficult to work with. The bigger it is, the more heterogeneous it tends to be.
- Homogeneity can be improved by mixing 5–10X with a standard P200 pipette. Take care to disrupt any particularly viscous regions. Overnight incubation at RT will then allow the HMW DNA to relax back into solution.
- High heterogeneity can be caused by insufficient mixing during the lysis steps. Many users will tend to be too gentle during the mixing steps. The resulting DNA will be bigger but will be difficult to handle and will tend to have lower purity. It is important to follow the vortexing steps outlined in the protocols. We recommend erring on the side of being overly aggressive. Even with all the vortexing, the DNA will still be 50-300 kb in length.
- We recommend doing triplicate NanoDrop ensure accurate concentration readings and triplicate Qubit dsDNA BR assay measurements to ensure accurate DNA concentration readings.

2. I transferred the eluate, but there is still liquid or a gel-like material on the Nanobind disk. What do I do?

- This is perfectly normal. The remaining DNA can be recovered by spinning the tube containing the Nanobind disk on a micro-centrifuge at 10,000 x g for 15 s. The disk will be wedged in the taper of the 1.5 mL tube, and the DNA will spin off the disk to the bottom of the tube. You may repeat this step until all the DNA is spun off. Typically, this spin step only needs to be performed 1–2 times.
- We do not recommend a second elution. This is usually unnecessary and will result in a diluted, less-concentrated DNA sample.

3. Why is my DNA yield lower than expected?

- Make sure that all the DNA is recovered from the Nanobind disk by centrifuging the tube containing the Nanobind disk at 10,000 x g for 15 s.
- If the sample is heterogeneous, you may be sampling from an area of the eluate that is a lot less concentrated. Take measurements from the top, middle, and bottom of the eluate to get an average concentration.
- Your input could be too low. For cultured human cells, we recommend $1x10^6$ – $5x10^6$ cells. For example, $5x10^6$ GM12878 cells should recover >30 µg of DNA.
- The lysis could be inefficient due to improper resuspension of the cell pellet. Make sure the cell pellet is completely resuspended in step 2 and that no visible cell clumps remain. We recommend being overly aggressive at this step.

4. Why are the purities lower than expected? Is this this a problem?

- We do NOT see a correlation between UV purity and sequencing performance and do not pay particular attention to the UV purity as long as it is within the expected range for that particular sample type. Generally, cultured human cells give UV purities of 260/230 >1.7 and 260/280 >1.8. Samples with UV purity slightly outside of this range will likely still sequence well. Samples with UV purity far outside this range should be treated with caution.
- The purity could be lower due to insufficient lysis resulting from too high of a cell input. We recommend $1x10^6$ – $5x10^6$ cells. Inputs greater than this can overwhelm the lysis chemistry, resulting in lower recoveries and lower purity.
- Lower purity can also be caused by insufficient mixing during the lysis steps. Many users will tend to be too gentle during the mixing steps. The resulting DNA will be bigger but will be difficult to handle and will tend to have lower purity. It is important to follow the vortexing steps outlined in the protocols. We recommend erring on the side of being overly aggressive. Even with all the vortexing, the DNA will still be 50–300 kb in length.