PacBio

Nanobind® CBB kit

Guide & overview

For extraction of HMW (50–300+ kb) genomic DNA from cultured cells, cultured bacteria, and blood.

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Prior to starting

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

Kit storage

The Nanobind CBB kit 4C (102-207-700) should be stored at 4°C upon arrival.

The Nanobind CBB kit RT (102-207-600) should be stored at room temperature (15–30°C).

Safety precautions

Refer to the Safety Data Sheet (SDS) for information on reagent hazards and protocols for safe handling, use, storage, and disposal.

Product use

Nanobind CBB kits are intended for research use only.

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Equipment and reagent list

Equipment/reagent	Manufacturer (part number)
Nanobind CBB kit	PacBio® (102-301-900)
Magnetic tube rack	Thermo Fisher Scientific DynaMag-2 (12321D)
Mini-tube rotator	Fisher Scientific Mini Tube Rotator (05-450-127)
Heat block (or water bath)	Fisher Scientific Isotemp dry bath incubator (11-715-125DQ)
Mini-centrifuge	Ohaus (FC5306)
Micro-centrifuge	Eppendorf (5404000413)
ThermoMixer	Eppendorf (5382000023)
1.5 mL Protein LoBind microcentrifuge tubes	Eppendorf (022431081)
Ethanol (96–100%)	Any major lab supplier (MLS)
Isopropanol (100%)	Any MLS
1X PBS	Any MLS
UV/Vis	Thermo Fisher Scientific NanoDrop 2000
Fluorescent DNA quantification	Invitrogen Qubit 3.0, dsDNA BR and RNA BR assay kits
Tris-HCl, 1 M, pH 8.0	Invitrogen (15568025)
Ethylenediaminetetraacetic acid (EDTA), 0.5 M, pH 8.0	Thermo Fisher Scientific (15575020)
Sucrose	Fisher Scientific (BP220)
Triton X-100	Sigma-Aldrich (X100)
Lysozyme	MP Biomedicals (100831)
Lysostaphin	Sigma-Aldrich (L7386)
26G blunt end needle	SAI Infusion (B26150)
1 mL syringe	Fisher Scientific (14-823-30)

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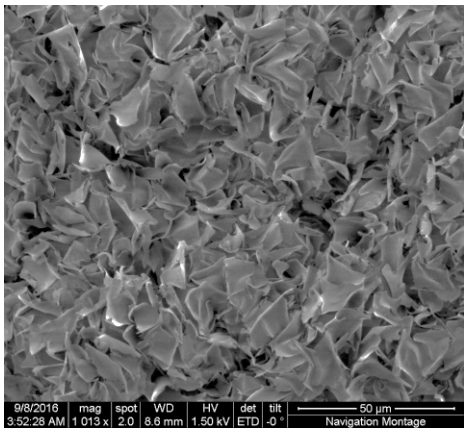
Introduction

Nanobind is a novel magnetic disk covered with a high density of micro- and nanostructured silica that can be used for rapid extraction and purification of high-quality DNA and RNA. The high surface area and unique binding mechanism give it an extraordinary binding capacity, allowing isolation of high purity, high molecular weight (HMW) DNA in a microcentrifuge tube format. It uses a standard lyse, bind, wash, and elute procedure that is common for silica DNA extraction technologies. A single disk is used in each tube. However, unlike magnetic beads and silica spin columns which shear large DNA, Nanobind disks bind and release DNA without fragmentation, to yield DNA up to megabases in length.



SEM image of Nanobind's silica surface structure.

Kit overview

The Nanobind CBB kit is used for the extraction of HMW (50–300+ kb) DNA from cultured cells, cultured bacteria, blood, and saliva. It has been used for both mammalian and non-mammalian cell culture samples, a diverse array of Gram-negative and Gram-positive bacteria, mammalian blood from a variety of species, and nucleated blood from birds, fish, and reptiles. The extracted DNA is suitable for HiFi sequencing on PacBio systems. Process time is approximately 45–120 minutes.

The **Sample information** section provides example extraction and sequencing results from a wide variety of sample types.

Protocols listed in the

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HMW (50–300+ kb) DNA extraction protocols section are updated frequently so please check the PacBio Documentation page for the most up-to-date list and for the current versions of the protocols. These protocols are recommended for PacBio HiFi sequencing.

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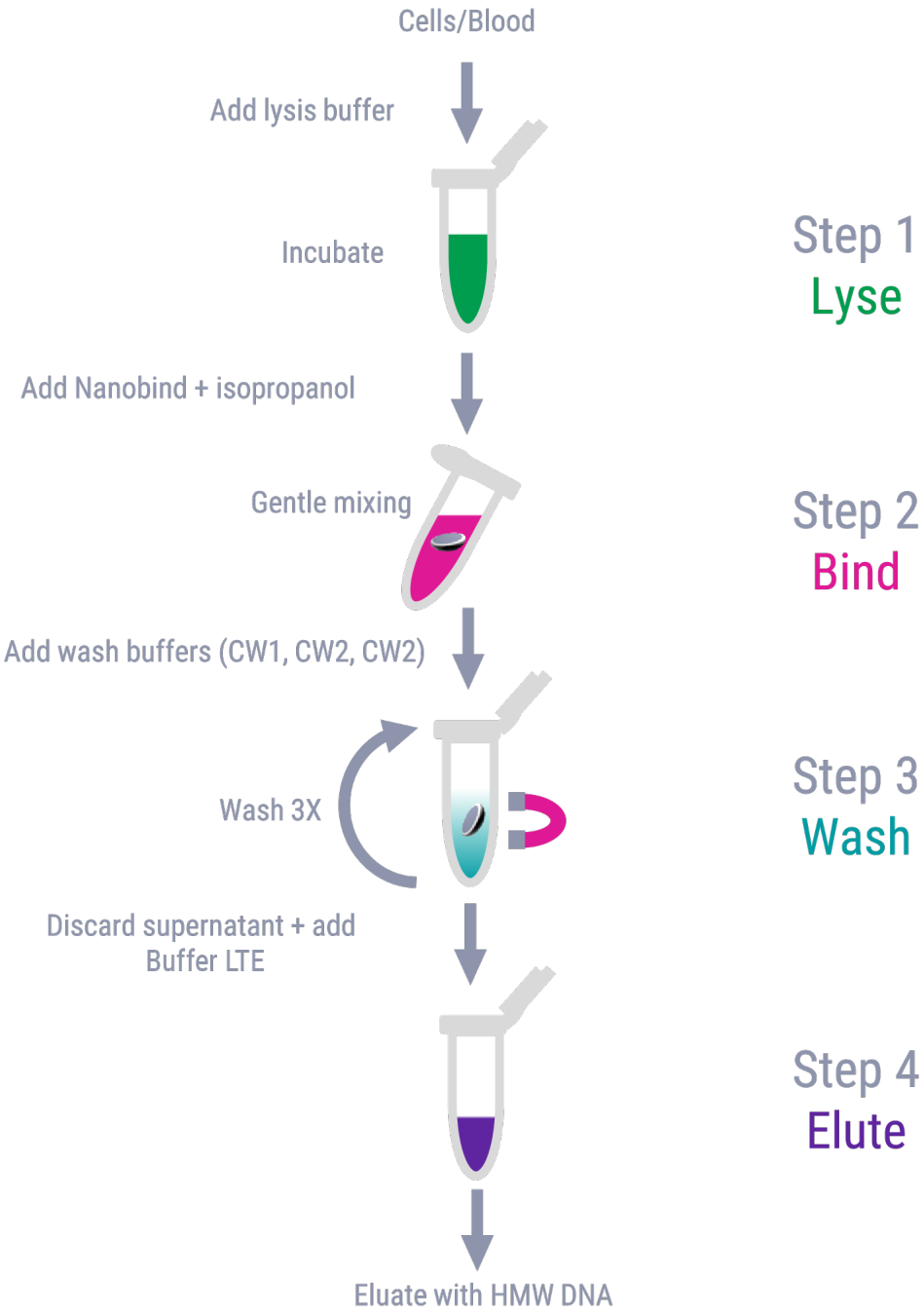
Workflow



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Sample information

Yields of HMW genomic DNA will vary depending on the sample being processed. The following table provides suggested input ranges and expected yields for the validated sample types. Each sample has been validated by long-read sequencing.

Expected yields

Sample	Suggested input[1]	Example input	Example 260/280	Example 260/230	ExampleYield (µg)
MCF-7 cells (tetraploid)	$0.5x10^6$–$10x10^6$ cells	$1x10^6$ cells	1.9	2.0	13.5
MDA-MB-231 (tetraploid)	$0.5x10^6$–$10x10^6$ cells	$1x10^6$ cells	1.9	2.0	14.9
MCF-10A cells (diploid)	$0.5x10^6$–$10x10^6$ cells	$2x10^6$ cells	1.9	2.0	12.3
GM12878 cells (diploid)	$0.5x10^6$–$10x10^6$ cells	$5x10^6$ cells	1.9	2.2	37.2
Escherichia coli[2]	$5x10^8$–$5x10^9$ cells	1 mL	1.8	1.4	18.3
Shigella sonnei[2]	$5x10^8$–$5x10^9$ cells	0.25 mL	1.8	1.4	27.7
Salmonella enterica[2]	$5x10^8$–$5x10^9$ cells	0.25 mL	1.8	1.5	23.4
Listeria monocytogenes[2]	$5x10^8$–$5x10^9$ cells	1 mL	1.8	1.9	21.7
Human whole blood	200 µL	200 µL	1.9	1.9	5.6
Human saliva collected in DNA Genotek™ Oragene™ devices	500 µL	500 µL	1.8	1.6	9.0

[1]Higher input levels can be used with appropriate optimization of buffer volumes and enzyme levels.

[2]Input based on cell pellet from stated volume of overnight culture.

Blood anticoagulant validation

Sample	260/280	260/230	DNA yield (µg)
Whole blood – K2 EDTA	1.9	2.0	5.5
Whole blood – Sodium citrate	1.9	2.0	5.0
Whole blood – Heparin	1.9	1.9	5.1
Whole blood – ACD	1.9	1.8	4.4

Nanobind was used to extract HMW DNA (up to 300 kb) from 200 µL of fresh human whole blood (n=3). All four samples showed similar yields and UV purity. HiFi sequencing performance was best for samples stored in potassium EDTA (K2 EDTA). Samples stored in Heparin and sodium citrate also performed well in limited testing.

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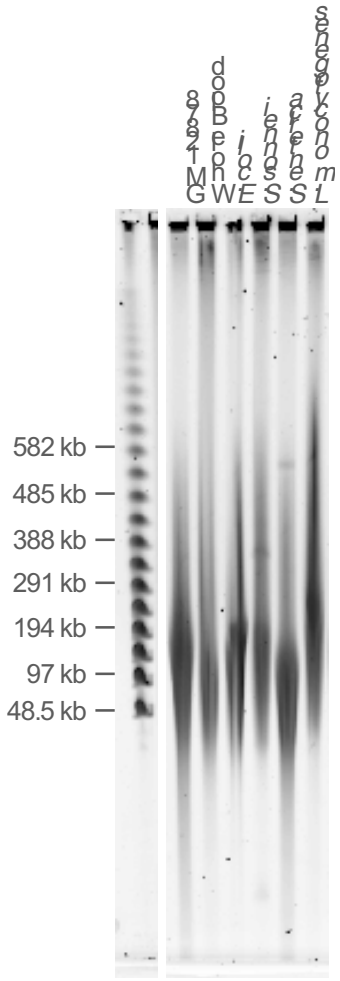
DNA size

The HMW DNA Extraction Protocols typically yield DNA in the 50–300+ kb size range. The exact size will vary depending on sample type, the quality of the starting material, and processing parameters. For most long-read sequencing applications, superior sequencing performance will be obtained using the HMW DNA Extraction Protocols.



Pulsed Field Gel Electrophoresis (PFGE) of DNA extracted using the HMW DNA Extraction Protocol from various sample types. The HMW protocols typically result in DNA from 50–300+ kb.

Preservation methods

High quality samples are the key to obtaining high quality DNA. Either fresh or frozen samples can be used equivalently. However, care should be taken to minimize freeze-thaws and to minimize the time samples spend at ambient or at 4°C.

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Fresh vs. frozen cells

No systematic difference has been seen in either DNA QC or sequencing results between fresh and frozen cell pellets. Cell pellets should be frozen in minimal liquid after harvesting. No cryoprotectant is necessary. When using frozen cell pellets, it is important to fully resuspend the cell pellets before processing.

Fresh vs. frozen blood

No systematic difference has been seen in either DNA QC or sequencing results between fresh and frozen blood samples. Blood samples should be frozen as quickly as possible after being drawn. Storage at 4°C should be limited to 2 days from collection to extraction to prevent sample degradation. Blood samples should be aliquoted to avoid repeated freeze-thaws. For frozen blood, we recommend thawing at 37°C for 10–15 min.

Blood Anti-coagulant

K2 EDTA is the preferred anti-coagulant. Samples stored in sodium heparin (NaHep) and citrate (NaCit) also performed well in very limited testing.

Ethanol-preserved nucleated blood

Nucleated-blood preserved in ethanol (e.g.,1:10 blood to ethanol) can be used by first centrifuging the blood at 10,000 x *g* for 2 minutes to pellet the cells and then following the nucleated blood protocols.

Saliva

Saliva collected in Oragene devices is stable at RT up to 5 years as described in this white paper from DNA Genotek.

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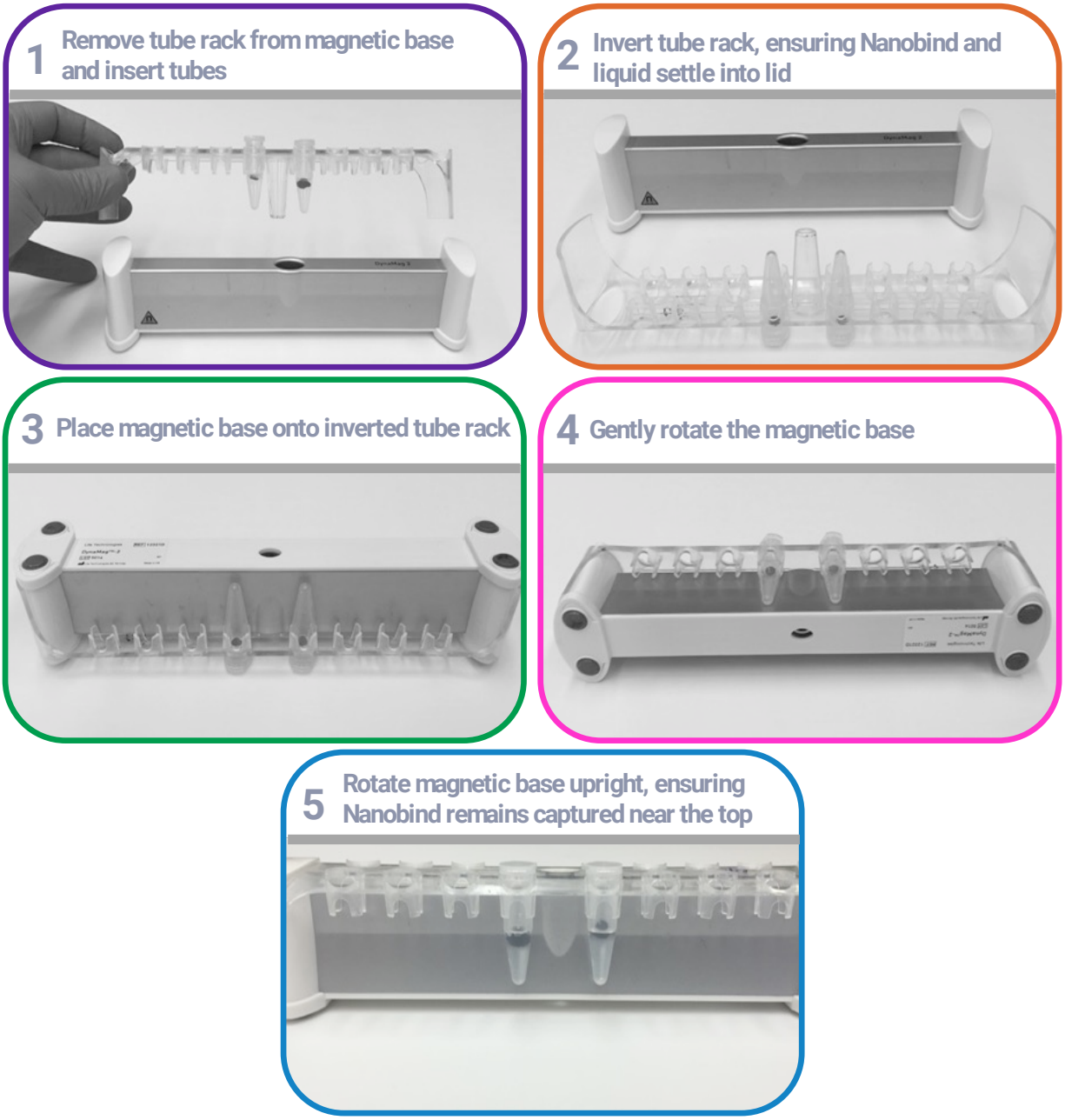
Processing tips

Magnetic rack handling procedure

To capture the Nanobind disk and enable simple processing, the microcentrifuge tubes are placed in a tube rack that is used with a magnetic base. Although DNA is bound quite robustly, proper pipetting and handling will ensure thorough washing and minimize disturbance of the bound DNA. For best results, the Nanobind disk should be captured near the top of the tube so that fluid can be easily removed from the bottom of the tube. The following procedure is recommended.



Recommended procedure for capturing Nanobind disk on a tube rack and magnetic base. This procedure ensures that the Nanobind disk is captured near the top of the liquid interface, minimizing disturbance of the bound DNA and facilitating processing.

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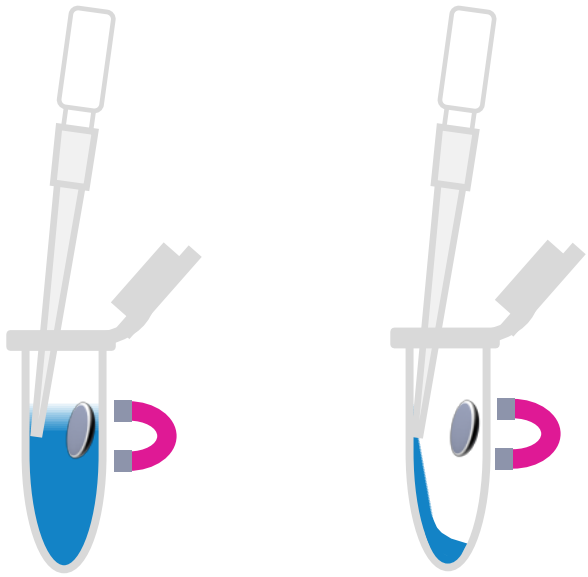
Pipetting

When removing liquid from the microcentrifuge tube, the Nanobind disk should not be disturbed. Carefully insert the pipette tip against the wall opposite the Nanobind disk and remove liquid by pipetting from the liquid surface. This will minimize the chances of accidentally pipetting bound DNA. Likewise, when adding liquid, dispense against the wall opposite the Nanobind disk.



Pipetting procedure for removal (left) and addition (right) of liquid during wash steps. Avoid disrupting the Nanobind disk and bound nucleic acids.

Heterogeneity and viscosity

The extracted HMW DNA can be highly viscous and heterogeneous. This is normal and is one of the challenges of working with HMW DNA. The heterogeneity and viscosity of the DNA eluate will vary depending on sample type, DNA size, sample input, and processing parameters. More gentle processing will yield larger DNA size but will also result in higher heterogeneity and larger amounts of highly viscous, unsolubilized "jellies." Processing that is too gentle can dramatically reduce DNA purity and yield. To minimize the challenges of heterogeneity and viscosity, we recommend that new users err on the side of being overly aggressive. Listed below are tips for working with HMW DNA.

Following elution of the HMW DNA

Pipette mix the extracted DNA 5–10X with a standard P200 pipette. Pipette mixing will help to loosen and coax the viscous DNA into solution. Moderate amounts of pipette mixing will not significantly impact DNA length. Pipette mixing is a standard part of our DNA elution process. For greater accuracy, the pipette mixed DNA should be left overnight at RT before quantifying the concentration.

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Heterogeneous DNA and large amounts of unsolubilized “jellies”

The most common reason for high sample heterogeneity and low purity is insufficient mixing during lysis. More aggressive mixing will result in samples with improved purity due to more efficient lysis and digestion. Improved sample purity will lead to improved DNA homogeneity and reduced “jellies.” Aggressive mixing during lysis will not significantly impact DNA length.

Accurate HMW DNA quantification

Pipette mix the DNA 5X with a standard P200 pipette again. Perform triplicate Nanodrop readings by sampling the top, middle, and bottom of the eluate. If the concentration %CV > 30, perform an additional 5X pipette mixing using a standard P200 pipette. Let the DNA rest for at least 1 hr and repeat the Nanodrop measurements.

To accurately determine the concentration of dsDNA, we recommend making triplicate measurements using the Qubit dsDNA BR Assay.

For immediate quantification following extraction

The extracted DNA can be sheared 5X using a 26G blunt end stainless-steel needle and 1 mL syringe. Moderate amounts of needle shearing will not significantly impact DNA length. This will decrease heterogeneity, improving quantification accuracy. Needle shearing may also facilitate shearing of concentrated, HMW DNA with Corvaris g-TUBE or Diagenode Megauptor 3.

Shearing HMW DNA

Concentrated, HMW DNA can be difficult to shear with either the Corvaris g-TUBE or Diagenode Megauptor 3 Hydropore - long. In some cases, the viscous DNA could clog the shearing consumables. For these samples, we recommend trying the following:

1. Pre-shear the HMW DNA 5X using a 26G blunt end stainless-steel needle and 1 mL syringe.
2. Pre-shear using the Megaruptor 3 DNAFluid+ Kit. We recommend 100 µL of sample, concentrations <500 ng/µL, and a speed setting of 59.

Both of these options will help to decrease the sample viscosity without negatively affecting sequencing performance.

Follow the shearing guidelines outlined in the appropriate library prep Procedure & checklist.

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HMW (50–300+ kb) DNA extraction protocols

As of the document release date, the following Procedures & checklists are available for HMW (50–300+ kb) DNA extraction. They are recommended for most long-read sequencing applications. This includes PacBio HiFi sequencing.

Extracting HMW DNA from cultured suspension cells using Nanobind kits (103-394-500)

This protocol describes the extraction of HMW DNA from cultured suspension cells. This protocol has been validated on cell lines including HG001 and HG002. This protocol requires the Nanobind CBB kit (102-301-900) or the Nanobind PanDNA kit (103-260-000).

Extracting HMW DNA from cultured adherent cells using Nanobind kits (102-573-600)

This protocol describes the extraction of HMW DNA from cultured cells. This protocol has been validated on several cell types including GM12878 and MCF-7. This protocol requires the Nanobind CBB kit (102-301-900) or Nanobind tissue kit (102-302-100).

Extracting HMW DNA from Gram-negative bacteria using Nanobind kits (102-573-800)

This protocol describes the extraction of HMW DNA from Gram-negative bacteria. This protocol has been validated on several Gram-negative bacterial species including *E. coli, S. sonnei,* and *S. enterica*. This protocol requires the Nanobind CBB kit (102-301-900) or Nanobind tissue kit (102-302-100).

Extracting HMW DNA from Gram-positive bacteria using Nanobind kits (102-573-900)

This protocol describes the extraction of HMW DNA from Gram-positive bacteria. This protocol has been validated on several Gram-positive bacterial species including *L. monocytogenes*, *S. aureus*, and *E. faecalis*. This protocol requires the Nanobind CBB kit (102-301-900) or Nanobind tissue kit (102-302-100)).

Extracting HMW DNA from human whole blood using Nanobind kits (102-573-500)

This protocol describes the extraction of HMW DNA from 200 µL of mammalian whole blood. It has been validated using fresh and frozen whole blood. Other volumes can also be used with modification to the protocol. This protocol requires the Nanobind CBB kit (102-301-900) or Nanobind tissue kit (102-302-100).

Extracting HMW DNA from nucleated red blood cells using Nanobind kits (102-574-000)

This protocol describes the extraction of HMW DNA from 5–30 µL of nucleated blood. It has been validated on fish, bird, and lizard blood including fresh, frozen, and ethanol preserved blood samples. This protocol requires the Nanobind CBB kit (102-301-900) or Nanobind tissue kit (102-302-100).

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Extracting HMW DNA from saliva collected in DNA Genotek™ Oragene™ devices using Nanobind kits (103-544-000)

This protocol describes the extraction of HMW DNA (50–300+ kb) from saliva collected with a DNA Genotek Oragene•DNA saliva collection device using Nanobind kits. Applicable collection devices are the Oragene•Dx (OGD-500, OGD-510, OGD-600, OGD-610), Oragene•DISCOVER (OGR-500, OGR-600) and Oragene•DNA (OG-500, OG-510, OG-600, OG-610). This protocol is recommended for PacBio HiFi sequencing and requires the Nanobind CBB kit (102-301-900) or the Nanobind PanDNA kit (103-260-000).

QC procedures

Accurate quantification of HMW can be challenging due to sample inhomogeneity, often leading to concentration measurements with high concentration CVs. We recommend performing replicate Nanodrop UV/Vis, replicate Qubit BR DNA Assay measurements, and a single, optional Qubit BR RNA Assay measurement.

See individual HMW DNA extraction protocols for detailed guidance.

Storage of DNA

DNA can be stored in Nanobind kit Buffer LTE (formerly 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.

Troubleshooting FAQ

See individual DNA extraction protocols for details.

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Revision history (description)	Version	Date
Initial release	01	July 2022
Minor updates	02	July 2022
Minor updates, deleted old PacBio sequencing-related results	03	December 2022
Minor updates, deleted UHMW DNA information	04	May 2023
Updated to align with PanDNA kit and to change buffer name from Buffer EB to Buffer LTE	05	August 2024
Updated to include saliva protocol	06	October 2024

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