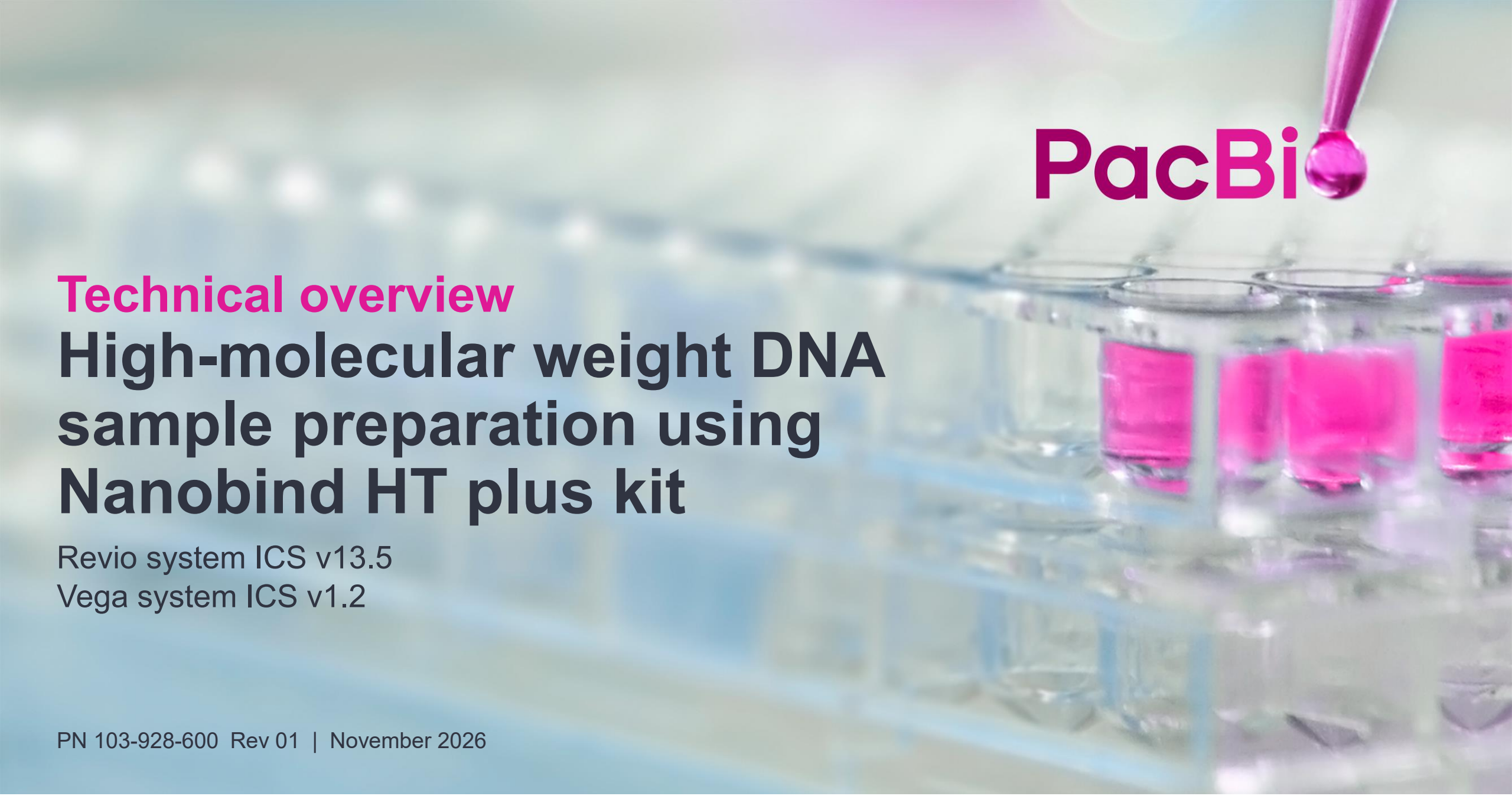


Technical overview

High-molecular weight DNA sample preparation using Nanobind HT plus kit

Revio system ICS v13.5
Vega system ICS v1.2

PN 103-928-600 Rev 01 | November 2026

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Technical overview

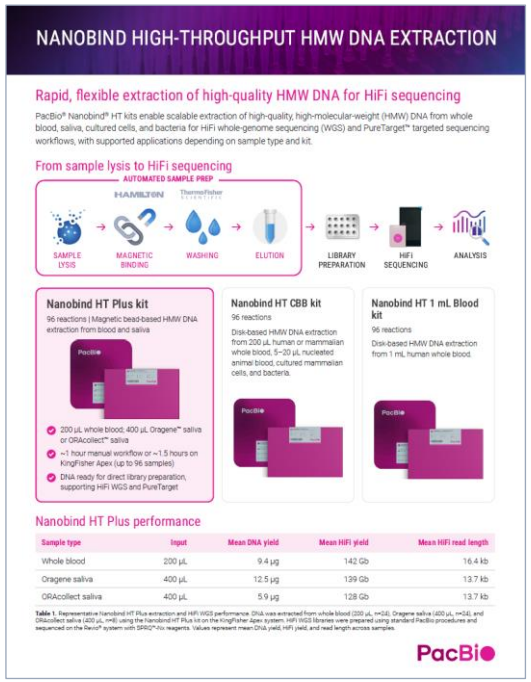
High-molecular weight DNA sample preparation using Nanobind HT plus kit

1. Nanobind HT plus kit configuration and general best practices
2. Nanobind HT plus HMW DNA extraction workflow overview
    i. Nanobind HT plus HMW DNA extraction procedure for human whole blood samples
    ii. Nanobind HT plus HMW DNA extraction procedure for human saliva samples
3. Nanobind HT plus kit example performance
4. Technical documentation & applications support resources

PacBio confidential

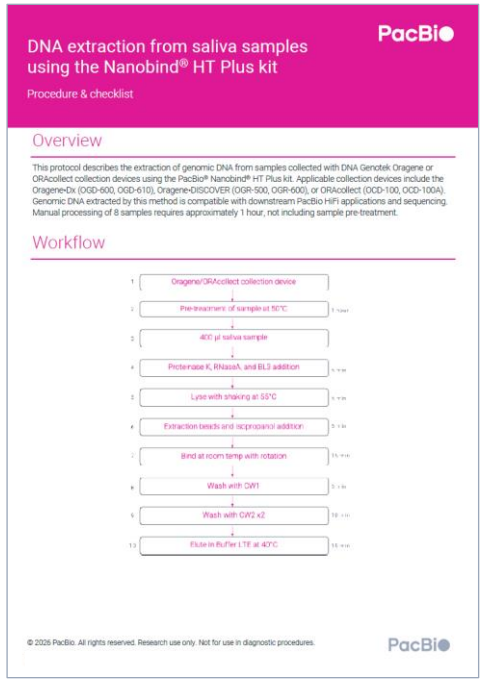
HMW DNA sample preparation using Nanobind HT plus kit: Getting started

Nanobind literature → **Nanobind protocols** → **Nanobind technical overviews** → **DNA sample extraction, library prep & sequencing**



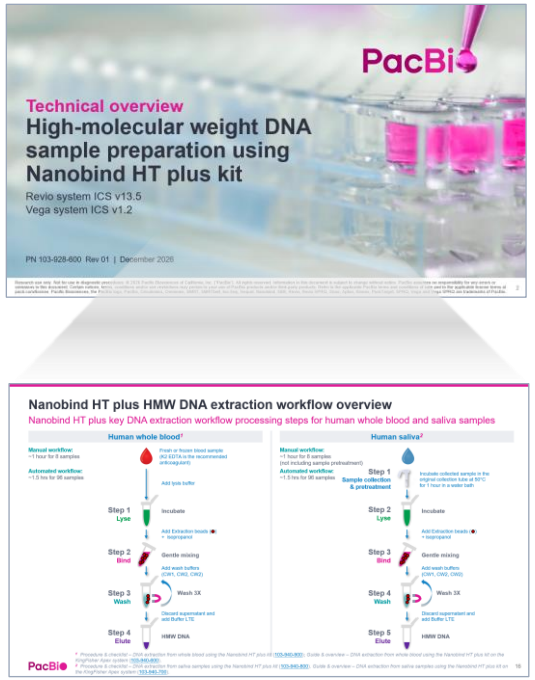
Brochure – Nanobind HT HMW DNA extraction (102-326-565)

Summary overview of Nanobind kits for high-throughput HMW DNA extraction from blood, cultured mammalian cells, and/or bacteria (supported samples types depends on the specific Nanobind HT kit).



Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit (103-940-800)

Refer to PacBio Documentation website for a full list of Nanobind HMW DNA sample preparation protocols.



Technical overview – High-molecular weight DNA sample preparation using Nanobind HT plus kit (103-928-600)

Technical overview presentation describes protocol details for using Nanobind HT plus kit for HMW DNA extraction and also shows example HiFi sequencing performance data.



HMW DNA sample extraction (Nanobind HT plus kit)

Use Nanobind HT plus kit for manual or automated high-quality HMW DNA extraction from human whole blood and saliva samples



SMRTbell library preparation (e.g., SMRTbell prep kit 3.0)

Follow desired Procedure & checklist protocol to construct a SMRTbell library using purified HMW DNA



HiFi sequencing (Revio + Vega systems)

Prepare samples for long-read sequencing by following application-specific sample setup instructions in Procedure & checklist protocol

Nanobind HT plus kit configuration and general best practices

PacBio Nanobind products for HMW genomic DNA extraction

Nanobind kits can be used to extract high-quality, high-molecular weight DNA suitable for HiFi sequencing

Nanobind kit	Binding technology	Reactions per kit	Supported sample types	Supported workflow types	Recommended use
 **Nanobind HT plus kit** (103-898-000)	Extraction beads	96	• Human whole blood (200 µL) • Human saliva (from Oragene devices[1] or ORAcollect devices[2])	• Manual • Automated	• **Default recommendation** for HMW DNA extraction from human whole blood and saliva samples using either manual or automated workflows
 **Nanobind HT CBB kit** (102-762-700)	Nanobind disks	96	• Cultured mammalian cells • Human whole blood (200 µL) • Mammalian animal blood (200 µL) • Non-mammalian (nucleated) animal blood (2.5 – 20 µL) • Cultured bacteria	• Automated (Hamilton NIMBUS Presto, Thermo Fisher KingFisher instruments)	• For high-throughput HMW DNA extraction from cultured mammalian cells, human whole blood, animal blood and cultured bacteria using automated workflows
 **Nanobind HT 1 mL Blood kit** (102-762-800)	Nanobind disks	96	• 1 mL of human whole blood	• Automated (Hamilton NIMBUS Presto, Thermo Fisher KingFisher instruments)	• For high-throughput HMW DNA extraction from 1 mL of whole human blood using automated workflows
 **Nanobind PanDNA kit** (103-260-000)	Nanobind disks	24	• Cultured mammalian cells • Human whole blood (200 µL) • Mammalian animal blood (200 µL) • Non-mammalian (nucleated) animal blood (2.5 – 20 µL) • Cultured bacteria • Animal tissues • Plant nuclei • Insects • RBC lysed human whole blood • Human saliva	• Manual	• **Default recommendation** for HMW DNA extraction from a wide variety of supported sample types using a manual workflow
 **Nanobind CBB kit** (102-762-700)	Nanobind disks	24	• Cultured mammalian cells • Human whole blood (200 µL) • Mammalian animal blood (200 µL) • Non-mammalian (nucleated) animal blood (2.5 – 20 µL) • Cultured bacteria	• Manual	• For HMW DNA extraction from cultured mammalian cells, human whole blood, animal blood and cultured bacteria using a manual workflow

[1] DNA Genotek Oragene saliva collection devices (e.g., 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)) use a liquid spit method for saliva collection where the donor spits into the attached funnel until liquid saliva reaches the fill line on the collection tube (target saliva collection volume is ~2 mL).

[2] DNA Genotek ORAcollect saliva collection devices (e.g., OCR-100 and OCD-100/100A) use an integrated sponge tip to absorb oral/buccal fluid (~200 µL collection volume) rather than requiring a liquid spit or a traditional dry buccal swab. **Note:** DNA extraction from dry buccal swabs and dried blood spots is not supported with the Nanobind HT plus kit.

Nanobind HT plus kit is recommended for high-molecular weight DNA extraction from human blood and saliva samples

Nanobind HT plus kit enables high-quality HMW DNA extraction from human whole blood and saliva samples using flexible manual or automated workflows

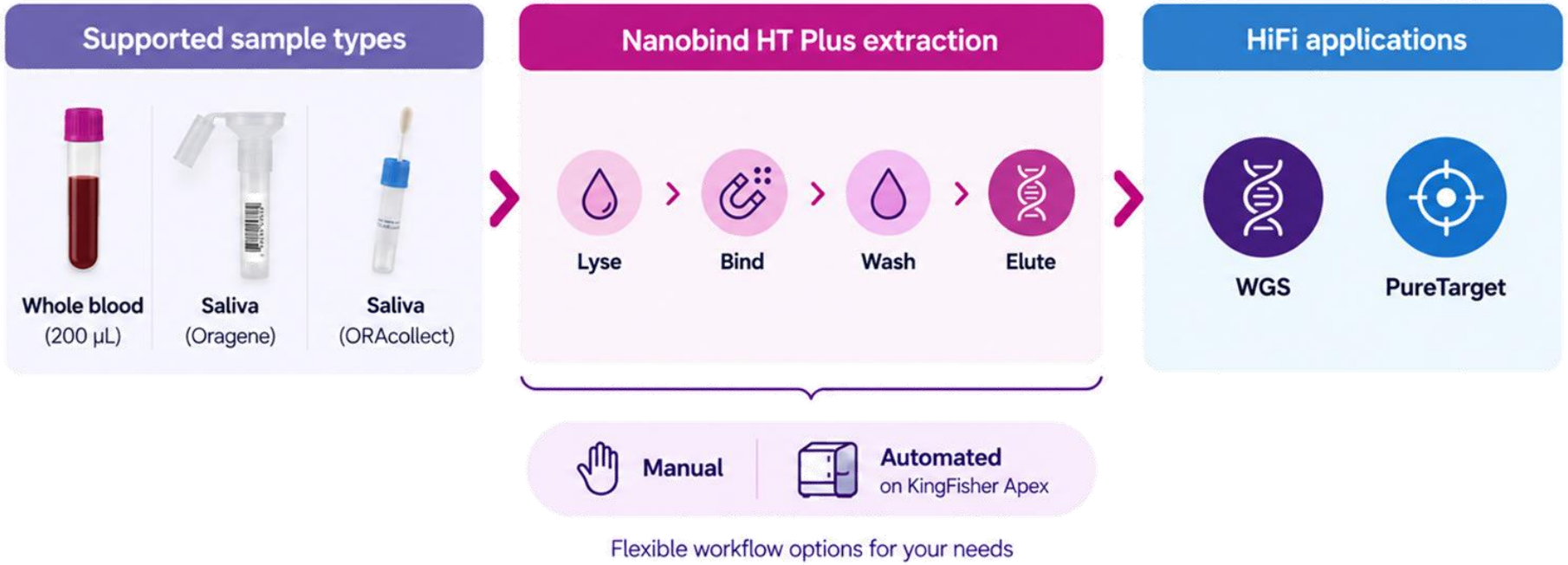


Nanobind HT plus kit (103-898-000)

Supports 96 reactions per kit and includes:

- Nanobind HT plus kit RT (103-872-900)
- Nanobind HT kit 4C (102-763-000)

Nanobind HT plus	Saliva		Blood
Expected performance	From Oragene saliva collection devices[1]	From ORAcollect saliva collection devices[2]	From 200 µL human whole blood
Extracted DNA mass range	2 – 30 µg	1 – 15 µg	3 – 15 µ
Extracted DNA size range	$GQN_{10kb} \approx 6 – 9$	$GQN_{10kb} \approx 3 – 8$	$GQN_{10kb} > 8$ $GQN_{30kb} > 7$



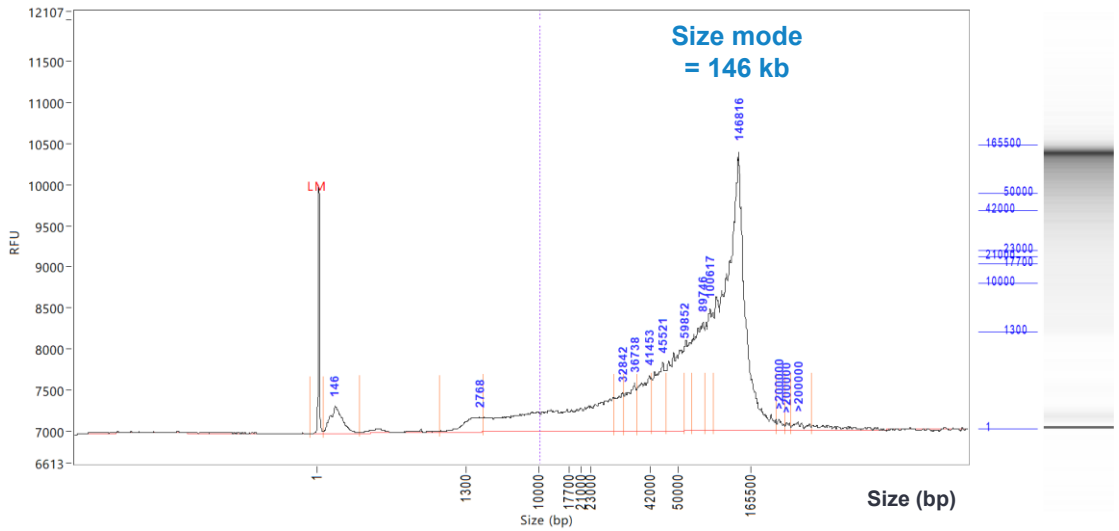
[1] DNA Genotek Oragene saliva collection devices (e.g., Oragene•Dx (OGD-500, OGD-510, OGD-600, OGD-610), Oragene•DISCOVER (OGR-500, OGR-600) and Oragene•DNA (OG-500, OG-510, OG-600, OG-610)) use a liquid spit method for saliva collection where the donor spits into the attached funnel until liquid saliva reaches the fill line on the collection tube (target saliva collection volume is ~2 mL).

[2] DNA Genotek ORAcollect saliva collection devices (e.g., OCR-100 and OCD-100/100A) use an integrated sponge tip to absorb oral/buccal fluid (~200 µL collection volume) rather than requiring a liquid spit or a traditional dry buccal swab. **Note:** DNA extraction from dry buccal swabs and dried blood spots is not supported with the Nanobind HT plus kit.

Nanobind HT plus HMW DNA extraction using Extraction beads – Overview

Extraction beads enable scalable, high-throughput extraction of high-molecular weight DNA from blood and saliva using a simple workflow

Extraction beads are silica-coated magnetic particles that enable high-purity, high-molecular weight DNA isolation using a simple workflow

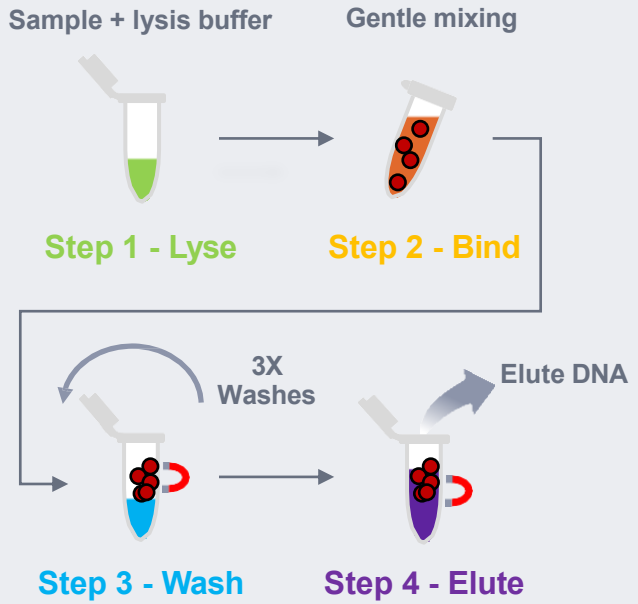


Femto Pulse DNA sizing QC analysis of unsheared genomic DNA isolated from human whole blood using Nanobind extraction bead technology.

Extraction beads can yield HMW DNA **50–300+ kb**

Rapid magnetic purification procedure

- Rapid and simple bind, wash, and elute protocol
- Can perform manual processing using a magnetic separation rack
- Extraction beads are automation compatible[1] for high-throughput applications





Extraction beads
(103-873-000)

[1] See *Brochure – Nanobind HT HMW DNA extraction* (102-326-565).

Nanobind HT plus kit configuration

Nanobind HT plus kit supports HMW DNA extraction for up to 96 samples

Nanobind HT plus kit (96 Rx) (103-898-000)

Nanobind HT kit 4C 102-763-000

4°C kit

#	Component	Part number	Qty	Color	Volume
1	RNase A	102-783-700	1	clear	2.6 mL

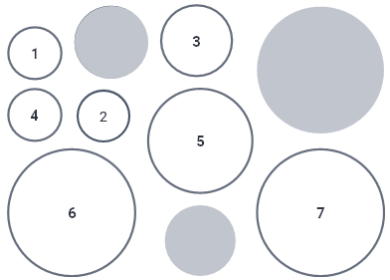


Nanobind HT plus kit RT 103-872-900

RT kit

#	Component	Part number	Qty	Color	Volume
1	Proteinase K	102-783-100	1	clear	2.5 mL
2	EXTRACTION BEADS	103-873-000	1	clear	3 mL
3	Buffer LTE	102-782-800	1	clear	30 mL
4	Buffer CLE3	102-783-200	1	clear	2.5 mL
5	Buffer BL3	102-783-300	1	clear	35 mL
6	Buffer CW1	102-783-400	1	clear	70 mL
7	Buffer CW2	102-783-500	1	clear	70 mL

Note: EXTRACTION BEADS (Cap: Clear; Reagent: Brown/Cloudy)



Component	Purpose
Buffer BL3	DNA binding to Extraction beads
Buffer CLE3	Cell lysis buffer
Buffer CW1	Wash buffer 1
Buffer CW2	Wash buffer 2
Buffer LTE[1]	Resuspension buffer
Extraction beads	For DNA binding during extraction
Proteinase K	For digestion of proteins during cell lysis
RNase A	For removal of RNA



[1] **Note:** LTE resuspension buffer contains a low TE formulation that is slightly different from Low TE Buffer (PN 102-178-400) included in SMRTbell prep kit 3.0.

Nanobind HT plus kit general best practices

Use Protein LoBind tubes

- Eppendorf Protein LoBind tubes are highly recommended for Nanobind extraction procedures to reduce protein contamination
- Protein LoBind tubes are more effective in reducing carryover contamination than DNA LoBind tubes and can result in improved UV purity



Protein LoBind tubes (e.g., Eppendorf PN 022431081 (1.5 mL)) are highly recommended to reduce protein contamination from tube carryover.

Prepare wash buffer working solutions prior to starting

- Nanobind kit wash buffers CW1 and CW2 are supplied as concentrated stocks
- CW1 and CW2 working solution contains 60% final ethanol concentration,
- Prepare working solutions prior to starting DNA extractions by adding the appropriate amount of ethanol (96–100%) to each buffer stock as indicated on bottles



Follow kit storage recommendations

- Store RNase A at 4°C
- Store Extraction beads and all other buffers at room temperature (RT, 18–25°C)





Perform cell lysis steps using a ThermoMixer

- We recommend using a ThermoMixer device for cell lysis incubation steps
- If a ThermoMixer is not available, a heat block or water bath can instead be used with periodic agitation to ensure lysis



A ThermoMixer (Eppendorf PN 5382000023) is recommended for cell lysis incubation steps in Nanobind DNA extraction procedures.

Quality control

- Vortex gDNA prior to quantification with Qubit 1X dsDNA BR/HS assay. If using the Qubit 1X dsDNA HS assay, dilution of the sample may be necessary.
  - **Note:** The extracted DNA mass typically ranges from 3–15 µg and depends on the donor white blood cell count.
- The Agilent Femto Pulse (Genomic DNA 165 kb kit) is recommended for accurately sizing genomic DNA. Dilute the sample to 250 pg/µL according to Agilent SOP.
  - **Note:** GQN10kb of extracted DNA is typically greater than 8; GQN30kb is typically greater than 7.





Nanobind HT plus HMW DNA extraction workflow overview

Nanobind HT plus HMW DNA extraction procedure for human whole blood samples
Nanobind HT plus HMW DNA extraction procedure for human saliva samples

Available Nanobind HT plus HMW DNA extraction protocols

Select the appropriate Nanobind Procedure & checklist to use based on sample type and starting material[1]

Nanobind HT plus manual protocols



Sample type	Starting material	Sample input	Manual workflow time	Procedure & checklist
Blood	Human whole blood	200 µL	~1 hour for 8 samples	*Procedure & checklist – DNA extraction from whole blood using the Nanobind HT plus kit* (103-940-900)[2]
Saliva	Human saliva collected in DNA Genotek Oragene[3] or ORAcollect[4] devices	400 µL	~1 hour for 8 samples	*Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit* (103-940-800)

Nanobind HT plus automation protocols



Sample type	Starting material	Sample input	Automation workflow time	Automation system and robotic script	Procedure & checklist
Blood	Human whole blood	200 µL	~1.5 hours for 96 samples	Thermo Fisher KingFisher Apex Script: `Nanobind HT Plus Blood.kfx2` (103-941-200)	*Guide & overview – DNA extraction from whole blood using the Nanobind HT plus kit on the KingFisher Apex system* (103-940-600)[2]
Saliva	Human saliva collected in DNA Genotek Oragene[3] or ORAcollect[4] devices	400 µL	~1.5 hours For 96 samples	Thermo Fisher KingFisher Apex Script: `Nanobind HT Plus Saliva.kfx2` (103-941-300)	*DNA extraction from saliva samples using the Nanobind HT plus kit on the KingFisher Apex system* (103-940-700)

[1] For a complete list of supported Nanobind HMW DNA extraction procedures, refer to the PacBio Documentation website.
[2] Note that this Nanobind HT plus procedure does not support processing of other types of (non-human) mammalian blood samples that are non-nucleated.
[3] DNA Genotek Oragene saliva collection devices (e.g., 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)) use a liquid spit method for saliva collection where the donor spits into the attached funnel until liquid saliva reaches the fill line on the collection tube (target saliva collection volume is ~2 mL).
[4] DNA Genotek ORAcollect saliva collection devices (e.g., OCR-100 and OCD-100/100A) use an integrated sponge tip to absorb oral/buccal fluid (~200 µL collection volume) rather than requiring a liquid spit or a traditional dry buccal swab. **Note:** DNA extraction from dry buccal swabs and dried blood spots is not supported with the Nanobind HT plus kit.

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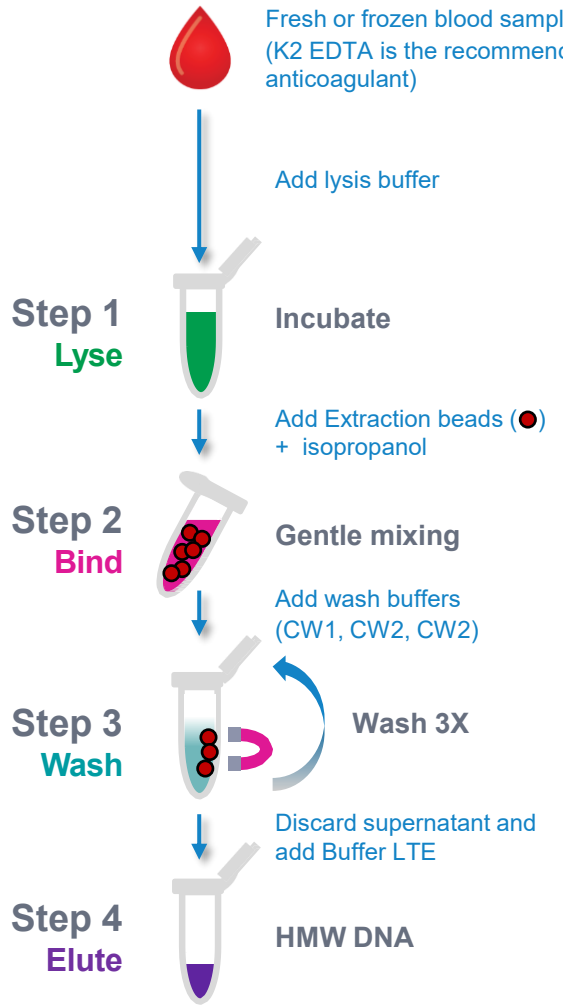
Nanobind HT plus HMW DNA extraction workflow overview

Nanobind HT plus key DNA extraction workflow processing steps for human whole blood and saliva samples

Human whole blood[1]

Manual workflow:
~1 hour for 8 samples

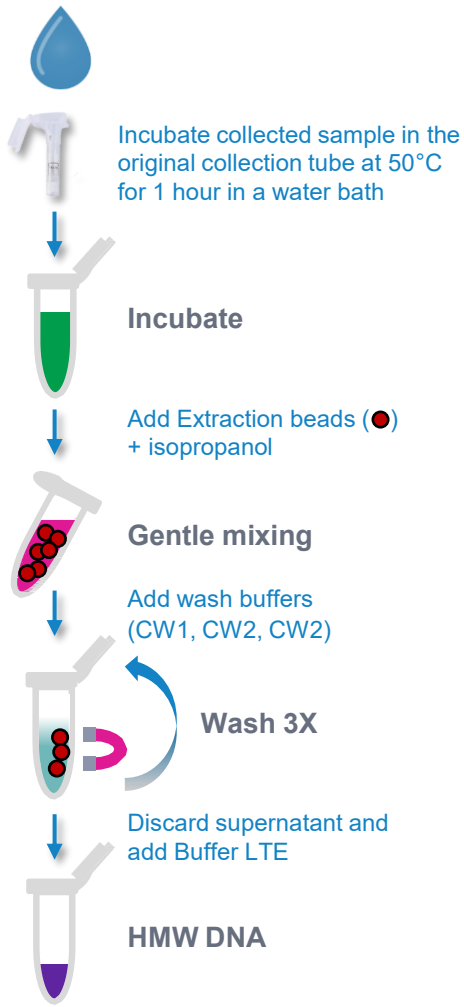
Automated workflow:
~1.5 hrs for 96 samples



Human saliva[2]

Manual workflow:
~1 hour for 8 samples
(not including sample pretreatment)

Automated workflow:
~1.5 hrs for 96 samples



[1] *Procedure & checklist – DNA extraction from whole blood using the Nanobind HT plus kit (103-940-900); Guide & overview – DNA extraction from whole blood using the Nanobind HT plus kit on the KingFisher Apex system (103-940-600).*

[2] *Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit (103-940-800). Guide & overview – DNA extraction from saliva samples using the Nanobind HT plus kit on the KingFisher Apex system (103-940-700).*

How Nanobind HT plus HMW DNA extraction kits work with KingFisher systems

KingFisher sample purification systems employ inverse magnetic particle processing (MPP) technology to enable automated transfer and processing of magnetic Extraction beads in a microplate format.

KingFisher instruments

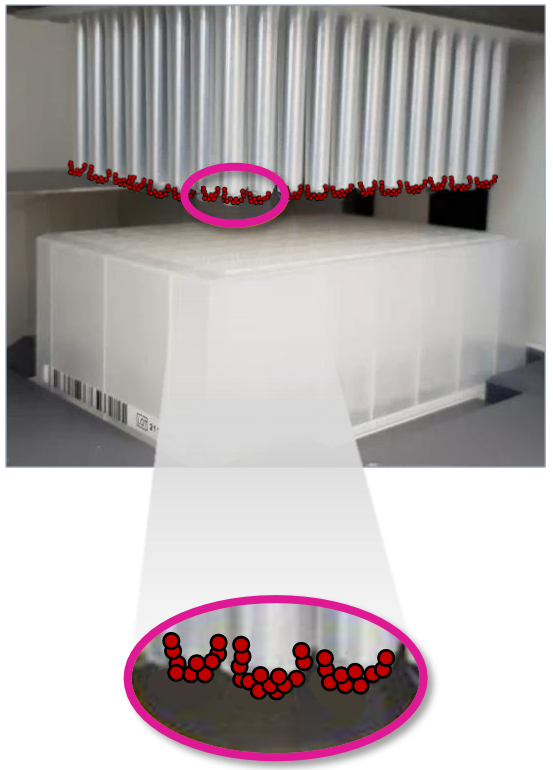


- Automate sample extraction by moving magnetic particles (not liquids)
- Inverse MPP uses magnetic rods covered with a disposable tip comb and PCR or deep-well plates
- Function without any liquid dispensing or aspiration parts or devices
- Enable quicker reaction times and a more efficient wash process



96 deep-well plates (200 – 1,000 µL)

Nanobind HT plus automated HMW DNA extraction protocols[1,2] support KingFisher Apex systems equipped with a 96-deep well magnet head.



Schematic illustration of Extraction beads bound to a KingFisher Apex system 96-deep well magnet head rod array. Note: Extraction beads are not drawn to scale.

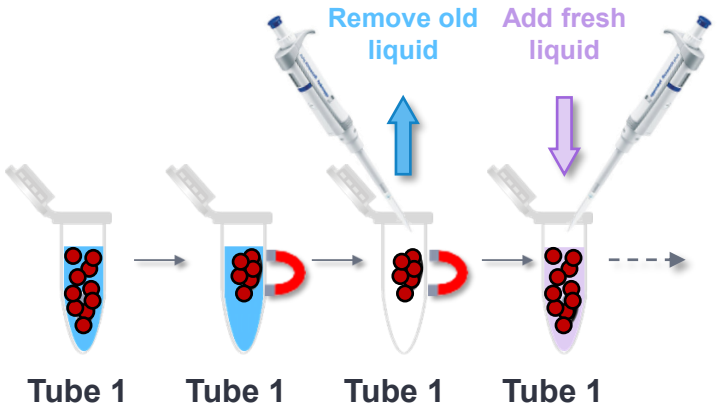
PacBio

[1] *Guide & overview – DNA extraction from whole blood using the Nanobind HT plus kit on the KingFisher Apex system (103-940-600).*
[2] *Guide & overview – DNA extraction from saliva samples using the Nanobind HT plus kit on the KingFisher Apex system (103-940-700).*

How Nanobind HMW DNA extraction kits work with KingFisher systems (cont.)

Standard manual processing with beads

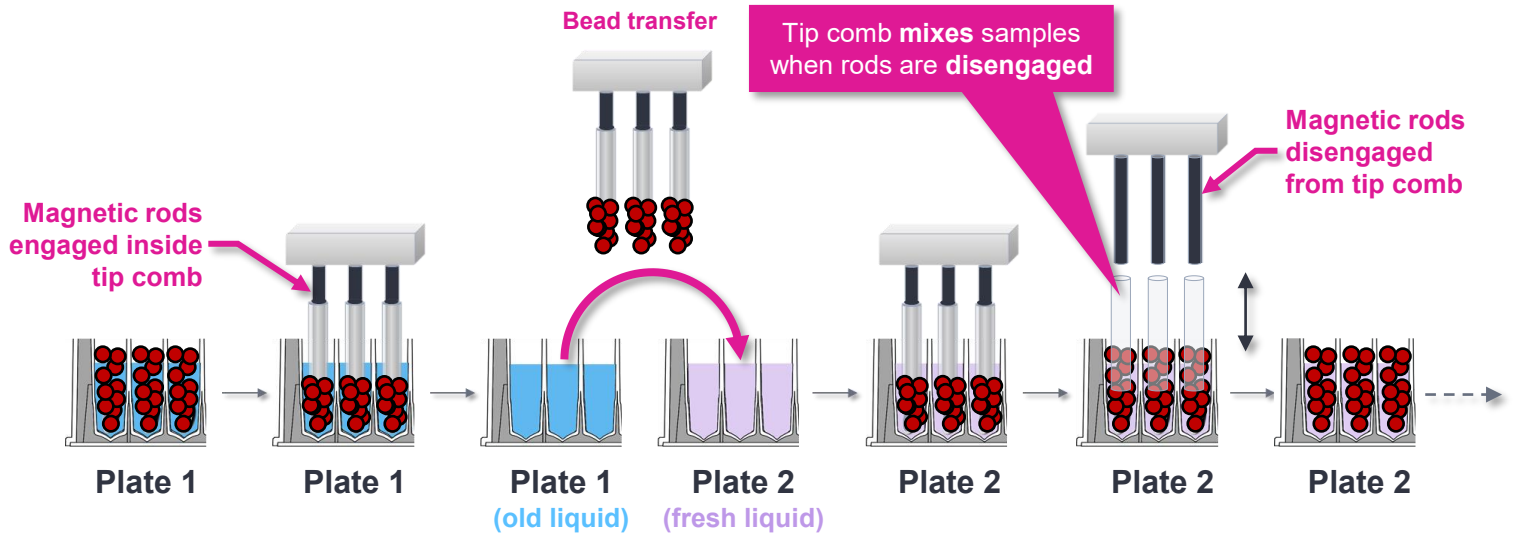
Liquid is moved into and out of a tube using a pipette while magnetic **Extraction beads remain immobilized** inside tube

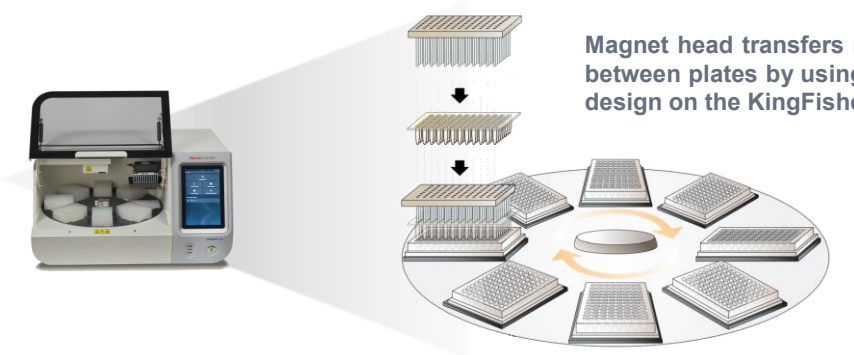




Automated inverse magnetic particle processing (MPP) with beads

Rather than moving liquids, **magnetic Extraction beads are moved** from plate to plate using magnetic rods covered with a disposable plastic tip comb





Magnet head transfers magnetic particles between plates by using a rotary platform design on the KingFisher work deck.

Schematic illustration of KingFisher rotary platform modified *after* Ficarro et al., Anal Chem. 2009 June 1; 81(11): 4566–4575. doi:10.1021/ac9004452.

Nanobind HT plus HMW DNA automated extraction workflow overview

Automation system configuration*

ThermoFisher SCIENTIFIC



KingFisher Apex

Nanobind HT plus automated DNA extraction is currently supported on **KingFisher APEX** system

Verify installation of correct automation script

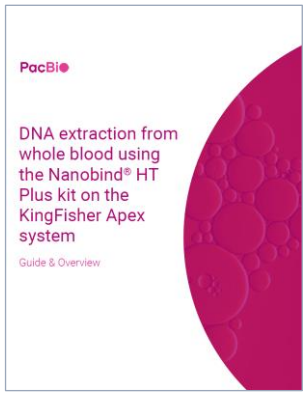


Verify installation of correct magnet head & heat block

Use 96-well magnet head, tips & plate for Nanobind HT plus automated workflows



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Nanobind automation system-specific Procedure & checklist

Nanobind HT plus HMW DNA extraction



PacBio

Nanobind HT plus kit (103-898-000)









Prepare sample, storage & reagent plates

Select appropriate automation script to run

Load prepared plates and other consumables onto work deck

Run Nanobind HT DNA extraction automation program

Store extracted DNA samples and perform QC



Qubit (DNA conc.)



Nanodrop (DNA purity)



Femto Pulse (DNA sizing)

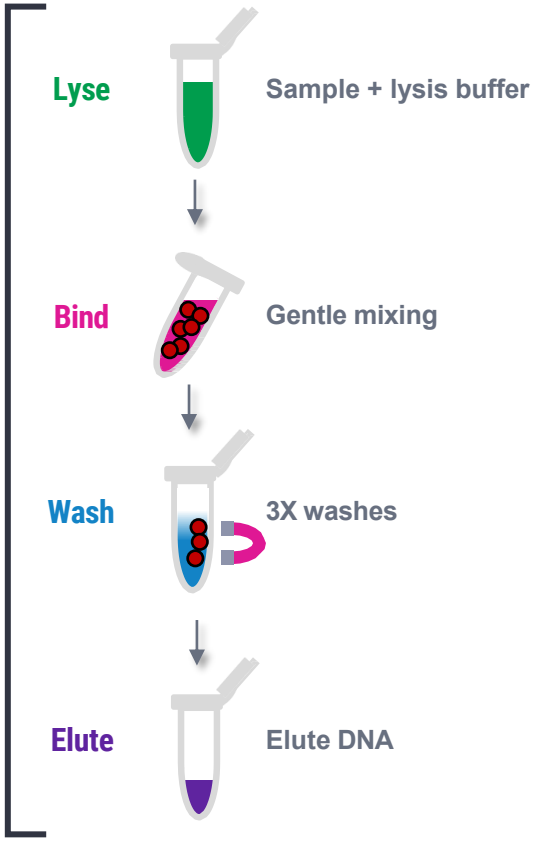
* Refer to appropriate vendor websites to download user guides and other documentation for specific automation systems.

Comparison of Nanobind HT plus HMW DNA extraction using manual workflow *versus* semi-automated workflow on KingFisher APEX system

Nanobind HT plus manual workflow

~1 hour for 8 samples





Nanobind HT plus semi-automated workflow
[KingFisher APEX system]

~1.5 hours [30 min setup + 1 hour instrument runtime] for 96 samples



Prepare deep-well plates containing tip comb & Nanobind HT plus kit reagents

Add samples to lysis / binding DW plate

Load prepared DW plates onto instrument

Upfront manual preparation of DWPs required



Lyse



Add Extraction beads + isopropanol to lysis / binding DW plate

Manual user intervention required to add beads + IPA



Bind

Wash 1 / 2 / 3

Elute



Manual step



Automated step

Nanobind HT plus HMW DNA extraction procedure for human whole blood samples



Nanobind HT plus HMW DNA manual extraction workflow for blood samples

Procedure & checklist – DNA extraction from whole blood using the Nanobind HT plus kit (103-940-900) describes the extraction of genomic DNA from 200 µL of whole blood using the PacBio Nanobind HT plus kit. Genomic DNA extracted by this method is compatible with downstream PacBio HiFi applications and sequencing.

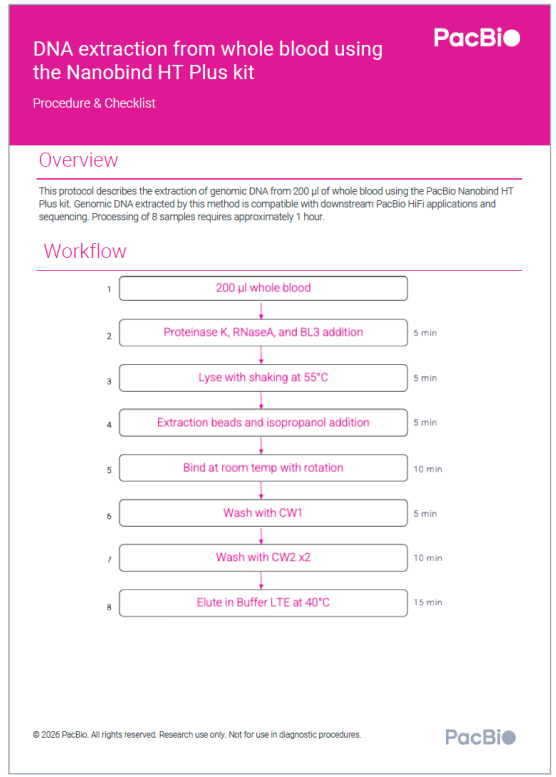
Blood sample input requirements

- Recommended sample input volume: 200 µL of human whole blood
  - Extracted DNA mass typically ranges ~3–15 µg and depends on donor white blood cell count
- K2 EDTA is the recommended anticoagulant[1]
- Blood samples should be aliquoted to avoid repeated freeze-thaws
- Storage at 4°C should be limited to 2 days or less to prevent sample degradation.
- No systematic difference has been observed in DNA QC or sequencing results between fresh and frozen blood samples
- If using frozen blood:
  - Incubate in a water bath or dry block heater at 37°C for 15 minutes to thoroughly thaw the sample.
  - Mix the sample by inverting the tube 15–20 times immediately prior to use.
  - Note: Improperly thawed and insufficiently mixed samples may result in inconsistent DNA yield and purity.



Workflow summary

1	200 µL whole blood	
2	Proteinase K, RNase A and BL3 addition	5 min
3	Lyse with shaking at 55°C	5 min
4	Extraction beads and isopropanol addition	5 min
5	Bind at room temp with rotation	10 min
6	Wash with CW1	5 min
7	Wash with CW2 (x2)	10 min
8	Elute in Buffer LTE at 40°C	15 min



PacBio Documentation (103-940-900)



Manual workflow runtime:
~1 hour for 8 samples

[1] Samples stored in sodium heparin (NaHep) and citrate (NaCit) also performed well in limited testing.

Nanobind HT plus HMW DNA manual extraction workflow for blood samples

Procedural notes

Before you begin:

Set 1.5 mL ThermoMixers to 55°C and 40°C. If only one ThermoMixer is available, set to 55°C and lower to 40°C after step 1.5.

Step	Instructions for extraction from whole blood
1.1	**Important**: The sample and reagents must be added to the tube or well in the order specified below. Add **20 µL of Proteinase K** to a 1.5 mL Protein LoBind tube.
1.2	Add **200 µL of whole blood**. Pulse vortex (1s max speed 10 times) and spin down. **Note:** The addition of blood to Proteinase K rather than vice versa increases lysis efficiency through improved mixing.
1.3	Add **20 µL of RNaseA**. Pulse vortex (1s max speed 10 times) and spin down. Incubate at **room temperature for 3 minutes**.
1.4	Add **200 µL of BL3** slowly against the side of the tube. Pulse vortex (1s max speed 10 times) and spin down. **Note:** Do not add BL3 directly to the sample solution as this may impact extraction performance.
1.5	Incubate on a ThermoMixer at **900 rpm and 55°C for 5 min**. After incubation, pulse vortex (1s max speed 10 times) and spin down.
1.6	Add **25 µL of vortexed Extraction beads** to lysate.
1.7	Add **440 µL of 100% isopropanol** slowly against the side of the tube to lysate containing beads and invert to mix 4 times. **Note:** Do not add isopropanol directly to the sample solution as this may impact extraction performance.
1.8	Mix on a platform rocker at 20 rpm or tube rotator at 9 rpm for **10 min at room temperature**.
1.9	Quick spin the tube and place sample on an appropriate magnet and allow beads to separate fully from the solution. Magnetize for at least 4 minutes. **Note:** The bead pellet will be obscured by blood.

- **Important:** The sample and reagents must be added to the tube or well in the order specified below.
- **Note:** The addition of blood to Proteinase K rather than vice versa increases lysis efficiency through improved mixing
- **Note:** Do not add BL3 directly to the sample solution as this may impact extraction performance.
- **Important:** Incomplete resuspension of beads may lead to low recovery.
- **Note:** Do not add isopropanol directly to the sample solution as this may impact extraction performance.
- **Note:** The bead pellet will be obscured by blood.

1.10	Discard supernatant.
1.11	Add 700 µL of Buffer CW1, remove the tube from the magnet, and invert to mix 4 times. Replace the tube on the magnetic base and discard the supernatant.
1.12	Add 700 µL of Buffer CW2, remove the tube from the magnet, and invert to mix 4 times. Replace the tube on the magnetic base and discard the supernatant.
1.13	Repeat step 1.12 for a total of two CW2 washes.
1.14	Remove residual wash buffer: • Remove samples from the magnet • Quick-spin • Place the tube back on the magnetic separation rack • Remove residual wash buffer and discard.
1.15	Air dry the beads for 1 min. Remove the tube from the magnet.
1.16	Add 50-100 µL of Buffer LTE directly onto the beads.
1.17	Incubate at 40°C for 10 min.
1.18	Pulse vortex until beads are completely resuspended and not adhering to the sides of the walls. Then place sample back at 40°C for 5 min. Important: Incomplete resuspension of beads may lead to low recovery.
1.19	Quick spin the tube and place the sample on an appropriate magnet and allow beads to separate fully from the solution. Transfer the eluate to a new DNA LoBind tube. To avoid bead carryover, aspirate slowly and leave behind 5 µl of eluate.
1.20	Pipette mix and vigorously vortex extracted genomic DNA to ensure it is homogeneous prior to quantification. Measure DNA concentration with a Qubit fluorometer.
	PROTOCOL COMPLETE

No special “Magnetic rack handling procedure” is needed to perform manual HMW DNA extraction using Extraction beads

[1] Visit the PacBio Documentation website to download the latest Procedure & checklist documentation.

Nanobind HT plus HMW DNA automated extraction workflow for blood samples

Guide & overview – DNA extraction from whole blood using the Nanobind HT plus kit on the KingFisher Apex system (103-940-600) describes the extraction of genomic DNA from 200 µL of whole blood using the PacBio Nanobind HT plus kit and the KingFisher Apex system. Genomic DNA extracted by this method is compatible with downstream PacBio HiFi applications and sequencing.

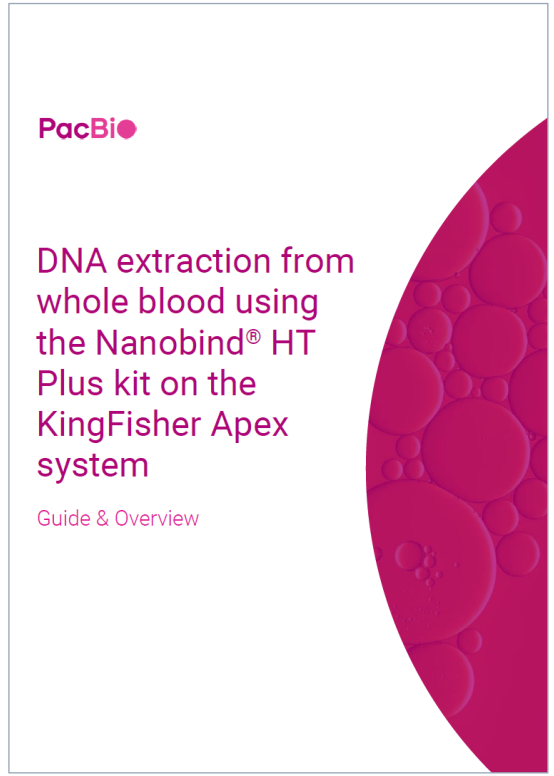
Blood sample input requirements

- Recommended sample input volume: 200 µL of human whole blood
  - Extracted DNA mass typically ranges ~3–15 µg and depends on donor white blood cell count
- K2 EDTA is the recommended anticoagulant[1]
- Blood samples should be aliquoted to avoid repeated freeze-thaws
- Storage at 4°C should be limited to 2 days or less to prevent sample degradation.
- No systematic difference has been observed in DNA QC or sequencing results between fresh and frozen blood samples
- If using frozen blood:
  - Incubate in a water bath or dry block heater at 37°C for 15 minutes to thoroughly thaw the sample.
  - Mix the sample by inverting the tube 15–20 times immediately prior to use.
  - Note: Improperly thawed and insufficiently mixed samples may result in inconsistent DNA yield and purity.



Workflow summary

1	200 µL whole blood	
2	Proteinase K, RNase A and BL3 addition	10 min (manual)
3	Lyse with shaking at 55°C	6 min (automated)
4	Extraction beads and isopropanol addition	10 min (manual)
5	Bind at room temp with rotation	13 min (automated)
6	Wash with CW1	4 min (automated)
7	Wash with CW2 (x2)	7 min (automated)
8	Elute in Buffer LTE at 40°C	17 min (automated)



PacBio Documentation (103-940-600)



Automated workflow runtime:

~1.5 hrs for 96 samples

[30 min setup + 1 hour instrument runtime]

[1] Samples stored in sodium heparin (NaHep) and citrate (NaCit) also performed well in limited testing.

Nanobind HT plus HMW DNA automated extraction workflow for blood samples

Procedural notes

End-to-end overall Nanobind HT plus workflow

Prepare sample, storage & reagent plates

↓

Select appropriate automation script to run

↓

Load prepared plates and other consumables onto work deck

↓

Run selected Nanobind HT DNA extraction protocol

↓

Store extracted DNA samples and perform QC

Before you begin



KingFisher Apex system
(Thermo Fisher)

Prior to beginning Nanobind HT plus automation protocol

☑ Ensure that the proper automation script has been installed

- To obtain **KingFisher automation scripts**, visit PacBio **Third-party automation equipment scripts** or contact **PacBio Technical Support** at support@pacb.com
- Example scripts for Nanobind HT plus automated HMW DNA extraction from blood or saliva samples using KingFisher Apex system:
  - `Nanobind HT Plus Blood.kfx2` (103-941-200) script for Nanobind HT plus 200 µL blood, Apex
  - `Nanobind HT Plus Saliva.kfx2` (103-941-300) script for Nanobind HT plus 400 µL saliva, Apex

☑ Ensure that instrument is set up with the correct magnet head and heating block.[1]

- Example hardware setup for Nanobind HT plus automated HMW DNA extraction from blood or saliva samples using KingFisher Apex system:
  - KingFisher Apex 96 deep-well magnet head (Thermo Fisher Scientific 24079930)
  - KingFisher Apex 96 deep-well heating block (Thermo Fisher Scientific 24075920)

PacBio

[1] KingFisher Apex system supports 24 – 96 samples per run using the KingFisher Apex 96 deep-well magnet head (Thermo Fisher Scientific 24079930) and KingFisher Apex 96 deep-well heating block (Thermo Fisher Scientific 24075920).

Nanobind HT plus HMW DNA automated extraction workflow for blood samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- Run selected Nanobind HT DNA extraction protocol
- Store extracted DNA samples and perform QC

Sample, storage & reagent plate preparations

Manually prepare deep-well plates with required quantities of Nanobind reagents & consumables

Example list of 6 deep-well (DW) plates to be prepared for processing 200 µL of human whole blood using KingFisher Apex.

Apex position	Reagent plate name	Plate purpose	Volume per well and other notes
6	Buffer LTE Plate	Buffer LTE storage	50 – 100 µL[1]
5	Buffer CW2 Plate 2	Buffer CW2 storage	700 µL
4	Buffer CW2 Plate 1	Buffer CW2 storage	700 µL
3	Buffer CW1 Plate	Buffer CW1 storage	700 µL
2	Sample Plate	Sample lysis / binding reactions	Prepare only **after** all other plates have been prepared (see below)
1	Tip Plate	Tip comb storage	KingFisher Apex 96 deep-well tip comb placed in plate

Plate 1 (lysis / binding plate) preparation procedure :

1. Add 20 µL of **Proteinase K**
2. Add 200 µL of **whole blood sample**[2]
3. Add 20 µL of **RNase A**
4. Add 200 µL of **BL3** slowly against the side of the well

Note: Sample and reagents **MUST** be added to each well in the order described in the Procedure



[1] **Note:** For all applications (including PureTarget and WGS), 50 – 100 µL of Buffer LTE may be used when processing 200 µL of human whole blood using KingFisher Apex. 5 – 10 µL volume loss is expected for the final elution step (for all applications).

[2] **Note:** The addition of blood to Proteinase K rather than *vice versa* increases lysis efficiency and purity through improved mixing.

Nanobind HT plus HMW DNA automated extraction workflow for blood samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

Prepare sample, storage & reagent plates

↓

Select appropriate automation script to run

↓

Load prepared plates and other consumables onto work deck

↓

Run selected Nanobind HT DNA extraction protocol

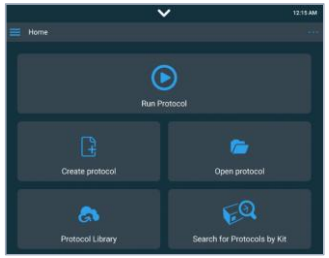
↓

Store extracted DNA samples and perform QC

Automation script selection

Select appropriate Nanobind HT plus protocol script to run based on desired input sample type and volume





Optional (KingFisher Apex):
Enter lot #'s for reagents & plastics, and sample ID



Nanobind HT plus HMW DNA automated extraction workflow for blood samples

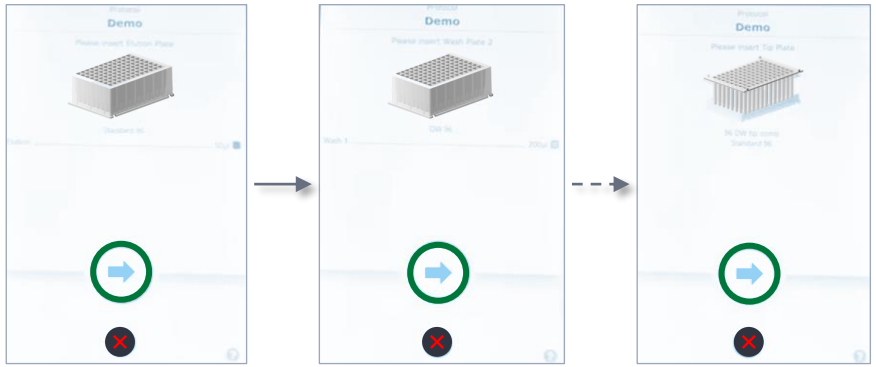
Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- Run selected Nanobind HT DNA extraction protocol
- Store extracted DNA samples and perform QC

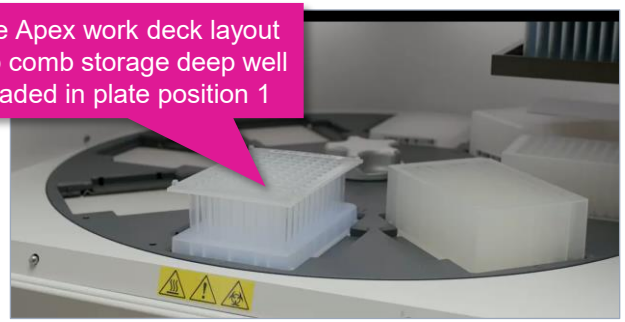
Work deck preparation

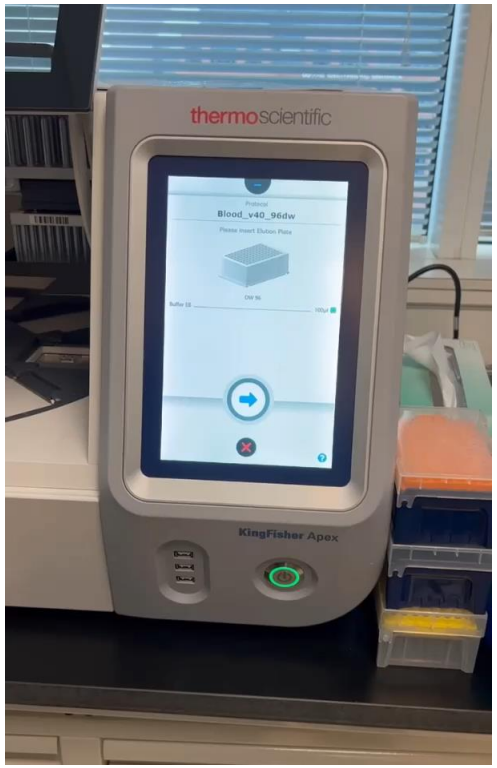
Sequentially load all prepared plates onto instrument work deck[1]



Load 1st plate (Buffer LTE plate) | Load 2nd plate… (Buffer CW2 Plate 2) | Load final plate (Tip plate)

Example Apex work deck layout with a tip comb storage deep well plate loaded in plate position 1





Click here to view example video demonstration of KingFisher Apex work deck loading procedure.

[1] **Note:** If you do not load enough conductive filter tips to complete the run, you will be warned to load additional tips or start the run at your own risk.

Nanobind HT plus HMW DNA automated extraction workflow for blood samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

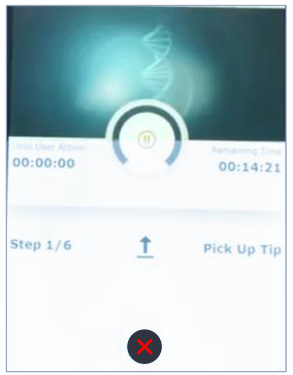
- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- **Run selected Nanobind HT plus DNA extraction protocol**
- Store extracted DNA samples and perform QC

Run selected Nanobind HT plus DNA extraction protocol

The run will start <u>automatically</u> when final plate is loaded and **Next** button is pressed.



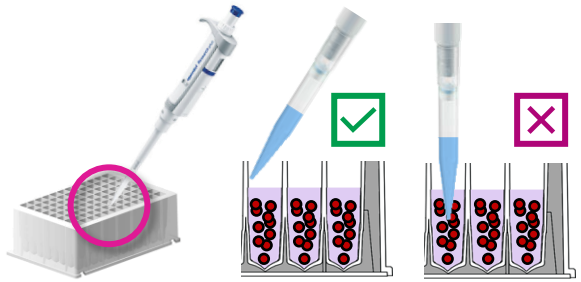
After run starts, screen shows time until user action required, remaining run time, and current protocol step





Click here to view example video demonstration of KingFisher Apex run start procedure.

User action required: When prompted, remove Lysis/Binding plate (**Plate 1**) from instrument and manually add vortexed Extraction beads and IPA to each well. After adding IPA, return plate to instrument and resume program.



Note: Add isopropanol (IPA) gently against the **side** of the well into the Lysis / Binding solution (containing Extraction beads).[1]

[1] Adding IPA directly to the Lysis / Binding solution may affect extraction purity.

Nanobind HT plus HMW DNA automated extraction workflow for blood samples

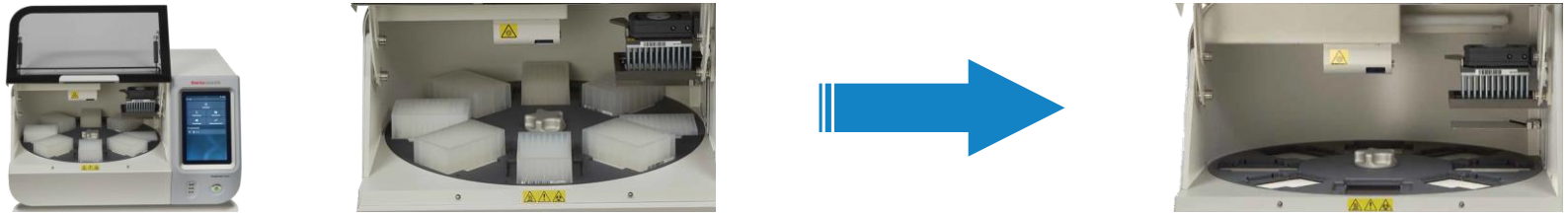
Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

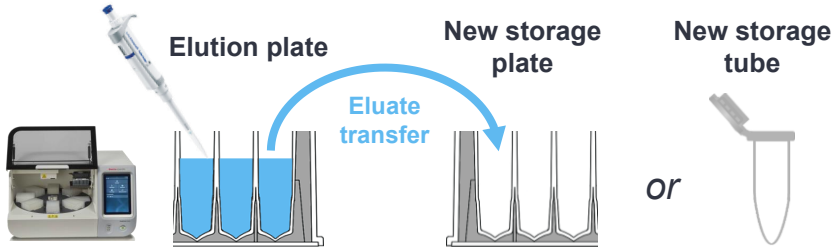
- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- Run selected Nanobind HT DNA extraction protocol
- Store extracted DNA samples and perform QC

Sample storage and QC

When run ends, remove each plate from instrument as prompted.



Manually transfer eluates from Elution Plate to a new storage plate or storage tubes



Pipette mix and vigorously vortex extracted genomic DNA to ensure it is homogeneous prior to quantification.
Measure DNA concentration with a Qubit fluorometer

Vortex gDNA prior to quantification with Qubit 1X dsDNA BR/HS assay. If using the Qubit 1X dsDNA HS assay, dilution of the sample may be necessary.





Agilent Femto Pulse (Genomic DNA 165 kb kit) is recommended for accurately sizing genomic DNA.

Nanobind HT plus HMW DNA extraction procedure for human saliva samples



Nanobind HT plus HMW DNA manual extraction workflow for saliva samples

Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit (103-940-800) describes the extraction of genomic DNA from saliva samples collected with DNA Genotek Oragene or ORAcollect collection devices using the PacBio Nanobind HT plus kit. Genomic DNA extracted by this method is compatible with downstream PacBio HiFi applications and sequencing.

Saliva sample input requirements

- Use 400 µL of input saliva collected and stabilized in a Oragene[1] device or OraCollect[2] device (DNA Genotek)
  - Saliva collected in Oragene devices is stable at RT for up to 5 years[3]
- Perform sample pretreatment (50°C incubation for 1 hour in a water bath) for efficient extraction using Nanobind kits
- Extracted DNA mass from Oragene collection devices typically ranges from 2–30 µg, depending on donor
- Extracted DNA mass from ORAcollect collection devices typically ranges from 1–15 µg, depending on donor



Collect saliva sample using Oragene or ORAcollect device (DNA Genotek)



Pretreat saliva sample by incubating in a water bath at 50°C for 1 hour

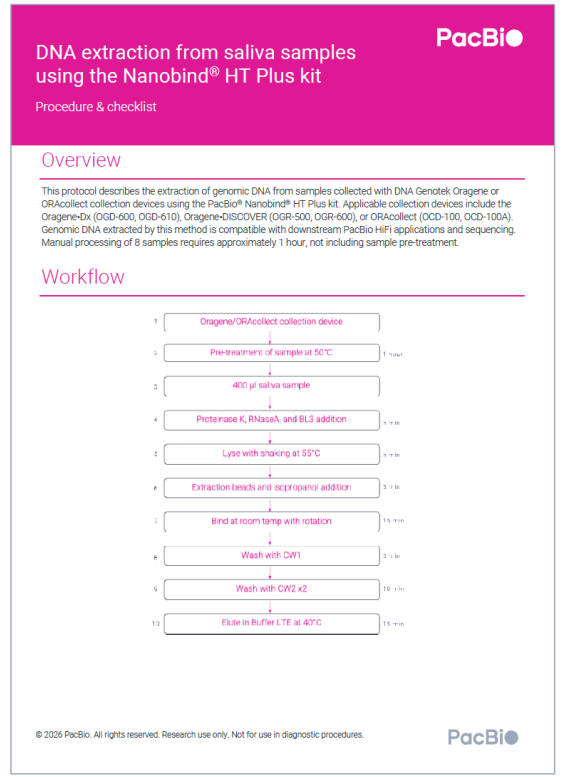
Nanobind HT plus kit (103-898-000)



Perform HMW DNA extraction using 500 µL of saliva sample stabilized in Oragene device buffer

Workflow summary

1	Oragene/ORA collection device	
2	Pre-treatment of sample at 50°C	1 hour
3	400 µL saliva sample	
4	Proteinase K, RNase A and BL3 addition	5 min
5	Lyse with shaking at 55°C	5 min
4	Extraction beads and isopropanol addition	5 min
5	Bind at room temp with rotation	15 min
6	Wash with CW1	5 min
7	Wash with CW2 (x2)	10 min
8	Elute in Buffer LTE at 40°C	15 min



PacBio Documentation (103-940-800)



Manual workflow runtime:
~1 hour for 8 samples

[1] DNA Genotek Oragene saliva collection devices (e.g., 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)) use a liquid spit method for saliva collection where the donor spits into the attached funnel until liquid saliva reaches the fill line on the collection tube (target saliva collection volume is ~2 mL).
[2] DNA Genotek ORAcollect saliva collection devices (e.g., OCR-100 and OCD-100/100A) use an integrated sponge tip to absorb oral/buccal fluid (~200 µL collection volume) rather than requiring a liquid spit or a traditional dry buccal swab. **Note:** DNA extraction from dry buccal swabs and dried blood spots is not supported with the Nanobind HT plus kit.
[3] DNA GenoTek white paper – *Long-term stability of DNA from saliva samples stored in the Oragene® self-collection kit* (PD-WP-005)

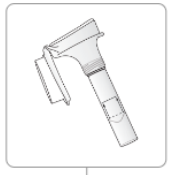
DNA Genotek self-collection saliva kits are recommended for HMW DNA extraction from saliva samples using Nanobind HT plus kit

Oragene saliva collection kit overview

Supported Oragene saliva collection kits for Nanobind HT plus HMW DNA extraction:

- **Oragene • Discover** (OGR-500, OGR-600)
- **Oragene • Dx** (OGD-600, OGD-610)

ORAgene•DISCOVER



5 years stability at RT

ORAgene•Dx



1 year stability at RT

- **Target saliva collection volume: 2 mL**
- **Total sample volume (saliva + stabilizing solution[2]): 4 mL**

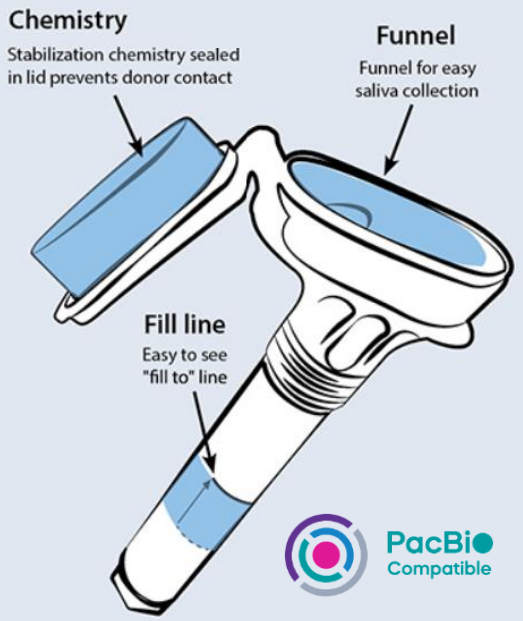


Oragene • Discover series

- Painless + reliable self- or assisted collection
- DNA is stable for years at ambient temp.[1]
- Optimized for both manual sample processing + automated workflows
- Integrated 1D barcode + optional 2D bottom barcode for workflow efficiency

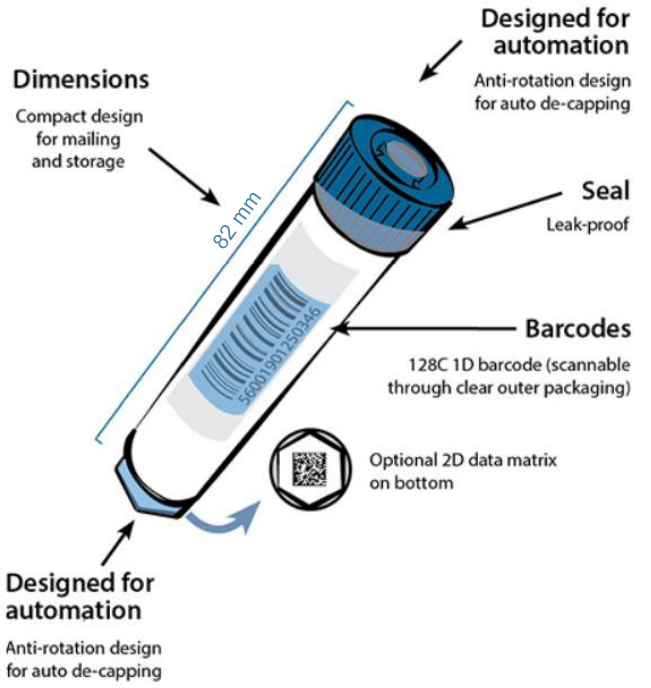
Pre-collection

Intuitive design optimizes donor success



Post-collection

Effective format for transport, storage and processing



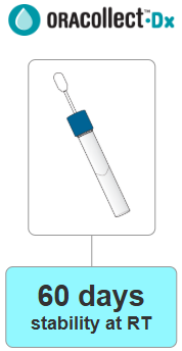
[1] Visit the DNA Genotek website for detailed information about Oragene self-collection saliva kit features and specifications.
[2] Oragene 500 and 600 Series tubes contain 2 mL of stabilizing solution. Oragene Low-volume 610 Series tubes contain 1 mL of stabilizing solution. Warnings and precautions: Wash with water if stabilizing liquid comes in contact with eyes or skin. Do NOT ingest.

DNA Genotek self-collection saliva kits are recommended for HMW DNA extraction from saliva samples using Nanobind HT plus kit (cont.)

ORAcollect saliva collection kit overview

Supported ORAcollect saliva collection kits for Nanobind HT plus HMW DNA extraction:

- **ORAcollect • Dx (OCD-100, OCD-100A)**



- **Saliva collection volume: ~200 µL**
- **Total sample volume (saliva + stabilizing solution[2]): ~1.2 mL**

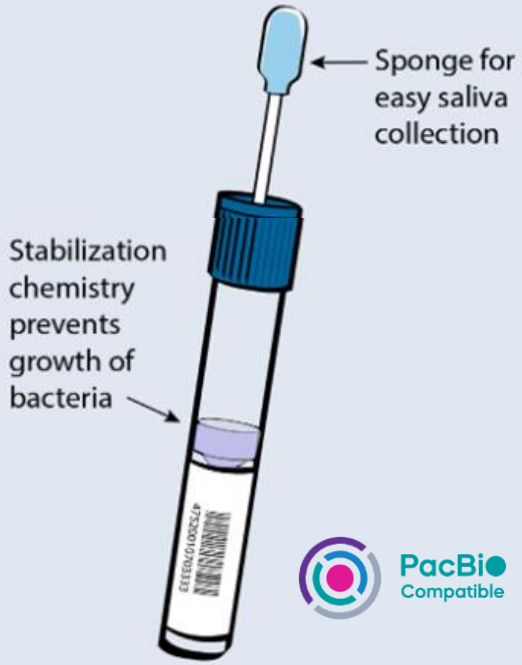


ORAcollect • Dx series

- Painless, non-invasive and easy-to-use DNA collection kit for self-collection or assisted sample collection[1]
- Designed to collect, stabilize and transport DNA samples[3]
- DNA can be used for research or genetic testing applications and clinical diagnostics
- Unlike buccal swabs, collected samples are liquid-based, bacteriostatic and integrate easily in existing lab workflows

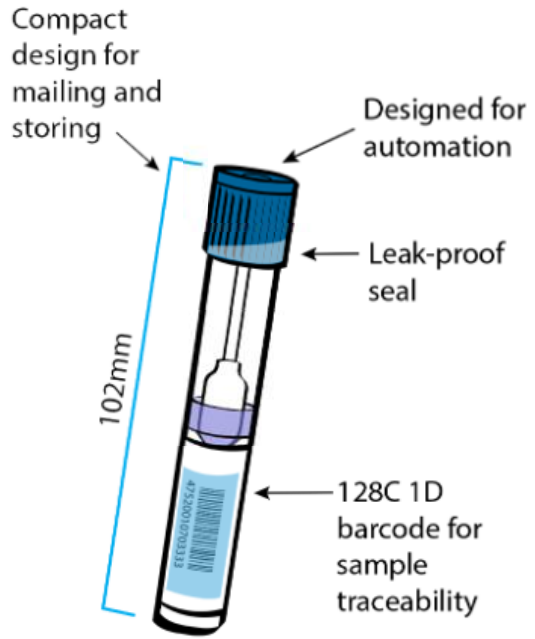
Pre-collection

Intuitive design optimizes donor success



Post-collection

Effective format for transport, storage and processing



[1] Visit the DNA Genotek website for detailed information about ORAcollect self-collection saliva kit features and specifications.
[2] ORAcollect tube contains 1 mL of stabilizing liquid. Warnings and precautions: Wash with water if stabilizing liquid comes in contact with eyes or skin. Do NOT ingest.
[3] DNA collected with DNA Genotek ORAcollect Dx series saliva collection tubes is stable at room temperature for up to 60 days. Visit the DNA Genotek website for detailed information about Oragene self-collection saliva kit features and specifications.

DNA Genotek saliva collection device instructions for use

Procedure for saliva sample collection using Oragene devices

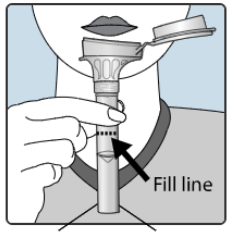
Oragene collection device instructions[1]

Oragene Discover series procedural notes

- **Collection precautions:**
  - Do NOT eat, drink, smoke or chew gum for 30 minutes before giving your saliva sample
  - Do NOT remove the plastic film from the funnel lid[2]
- **Procedure time:** Typically completed within 2 – 5 minutes

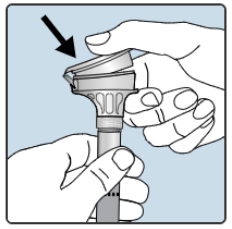


1



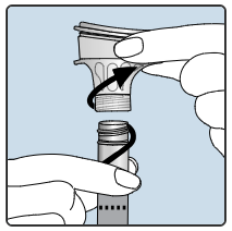
- Spit into funnel until amount of liquid saliva (not in including air bubbles) reaches fill line

2



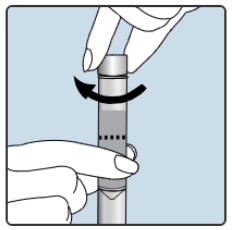
- Hold tube upright with one hand and close funnel lid with other hand by firmly pushing lid until you hear a loud click
- Stabilizing liquid inside lid will be released into tube to mix with the saliva.
- Make sure that lid is closed tightly

3



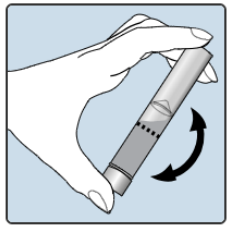
- Hold tube upright and unscrew funnel from the tube

4



- Use the small cap to close the tube tightly.

5



- Shake the capped tube for 5 seconds.
- Discard or recycle the funnel.

See latest Oragene collection instructions from DNA Genotek website.

[1] Visit the DNA Genotek website for more information about collection of human saliva using Oragene self-collection saliva kits and to view saliva collection video demonstrations [YouTube].

[2] Oragene tube contains 2 mL of stabilizing liquid. Warnings and precautions: Wash with water if stabilizing liquid comes in contact with eyes or skin. Do NOT ingest.

DNA Genotek saliva collection device instructions for use (cont.)

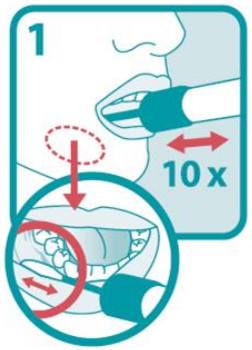
Procedure for saliva sample collection using Oragene ORAcollect devices

ORAcollect collection device instructions[1]

ORAcollect Dx series procedural notes

- **Collection precautions:**
  - Do NOT eat, drink, smoke or chew gum for 30 minutes before giving your saliva sample
  - **Note:** ORAcollect tube contains stabilizing liquid inside[2]
- **Procedure time:** Typically completed within 2 – 5 minutes





- Open package and remove collector without touching sponge tip.
- Place sponge as far back in the mouth as comfortable and rub along the lower gums (see close-up image) in a back and forth motion. Gently rub the gums 10 times.
- If possible, avoid rubbing the teeth.



- Gently repeat rubbing motion on the opposite side of the mouth along the lower gums for an additional 10 times.



- Hold the tube upright to prevent the stabilizing liquid inside the tube from spilling.
- Unscrew the blue cap from the collection tube without touching the sponge.



- Turn the cap upside down, insert the sponge into the tube and close cap tightly.



- Invert the capped tube and shake vigorously 10 times.

See latest ORAcollect collection instructions from DNA Genotek website.

[1] Visit the DNA Genotek website for more information about collection of human saliva using ORAcollect self-collection saliva kits and to view saliva collection video demonstrations [YouTube].

[2] ORAcollect tube contains 1 mL of stabilizing liquid. Warnings and precautions: Wash with water if stabilizing liquid comes in contact with eyes or skin. Do NOT ingest.

DNA Genotek saliva collection device instructions for use (cont.)

General best practices

Considerations when using DNA Genotek kits for collecting saliva samples

Human DNA content

- Saliva DNA is ~80–90% human, compared to dry buccal (cheek) swabs which can be as low as 10%[1]

DNA source

- Most isolated DNA in saliva comes from white blood cells (WBC), not buccal epithelial cells

DNA yield

- Improper collection procedure can result in low DNA yield
  - Recent food or drink intake (within 30 min) can reduce DNA yields and should be avoided (See DNA Genotek website)
  - Mucous saliva collection is less productive than serous saliva which contains more white blood cells
- Incorrect sample collection volume can result in low DNA yield:
  - Too little sample collection will have low white blood cell counts
  - Too much sample volume can dilute the storage solution



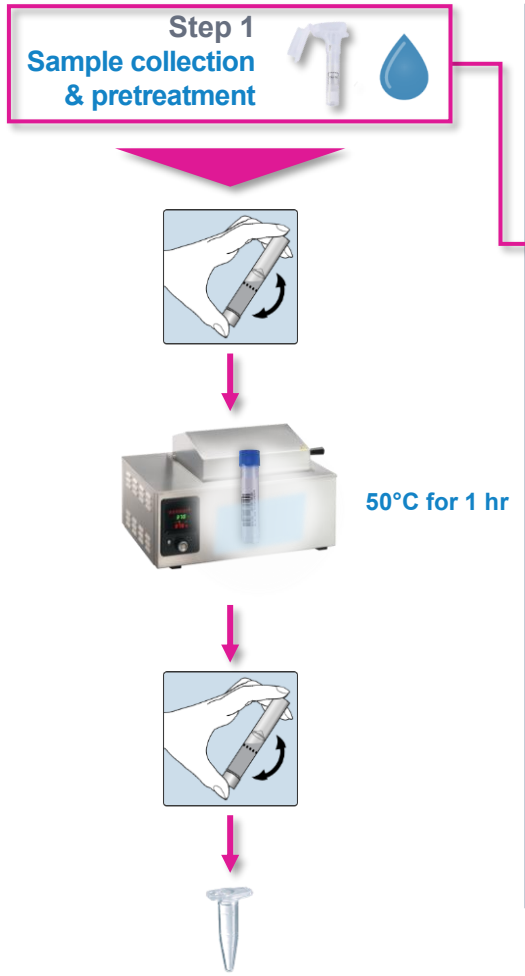
[1] **Note:** ***Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit*** (103-940-800) is intended for use with saliva samples and does **not** support DNA extraction from dry buccal swabs.

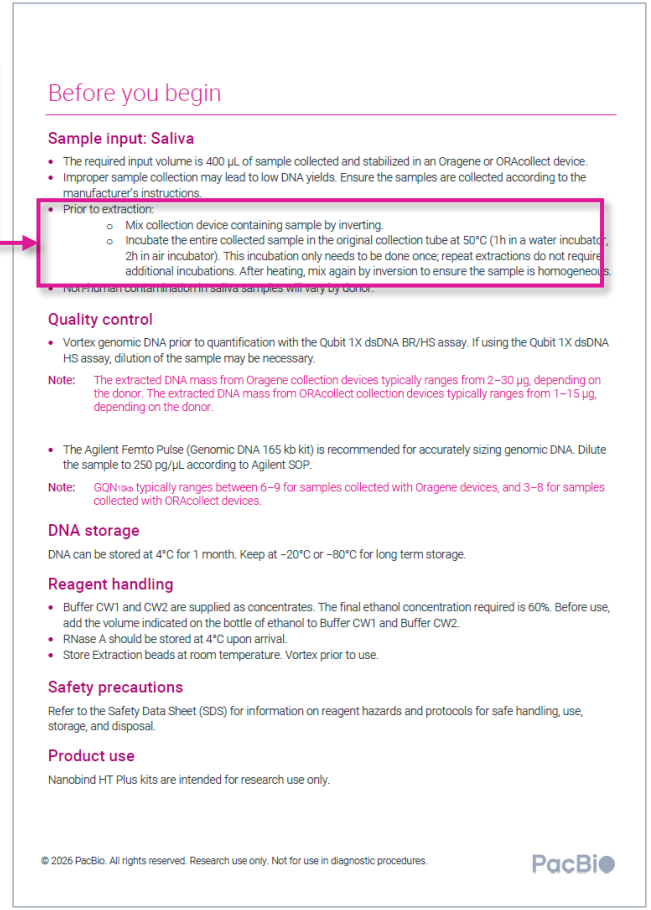
Nanobind HT plus HMW DNA extraction workflow for saliva samples

Procedure notes for ***Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit*** (103-940-800)

Saliva sample collection & pretreatment procedure

- Follow DNA Genotek directions for saliva collection using Oragene kits:
  - ❑ During sample collection, inversion mix thoroughly to ensure saliva and storage solution are completely combined
- **Prior to beginning DNA extraction for first time**, pretreat sample by incubating Oragene or ORAcollect collection tube at 50°C for 1 hr in water incubator or 2 hrs in air incubator
  - ❑ This incubation only needs to be done one time; repeat extractions do not require repeat incubations.
  - ❑ **Note:** If a water bath is used, ensure the sample-containing portion of the tube remains immersed in water.
  - ❑ Following incubation, invert-mix to ensure sample homogeneity.
- Transfer 400 µL of pretreated saliva solution to new 1.5 mL Protein LoBind tube[1]





Before you begin

Sample input: Saliva

- The required input volume is 400 µL of sample collected and stabilized in an Oragene or ORAcollect device.
- Improper sample collection may lead to low DNA yields. Ensure the samples are collected according to the manufacturer's instructions.
- Prior to extraction:
  - Mix collection device containing sample by inverting.
  - Incubate the entire collected sample in the original collection tube at 50°C (1h in a water incubator; 2h in air incubator). This incubation only needs to be done once; repeat extractions do not require additional incubations. After heating, mix again by inversion to ensure the sample is homogeneous.
- Non-human contamination in saliva samples will vary by donor.

Quality control

- Vortex genomic DNA prior to quantification with the Qubit 1X dsDNA BR/HS assay. If using the Qubit 1X dsDNA HS assay, dilution of the sample may be necessary.

Note: The extracted DNA mass from Oragene collection devices typically ranges from 2–30 µg, depending on the donor. The extracted DNA mass from ORAcollect collection devices typically ranges from 1–15 µg, depending on the donor.

- The Agilent Femto Pulse (Genomic DNA 165 kb kit) is recommended for accurately sizing genomic DNA. Dilute the sample to 250 pg/µL according to Agilent SOP.

Note: GQN_{165} typically ranges between 6–9 for samples collected with Oragene devices, and 3–8 for samples collected with ORAcollect devices.

DNA storage

DNA can be stored at 4°C for 1 month. Keep at –20°C or –80°C for long term storage.

Reagent handling

- Buffer CW1 and CW2 are supplied as concentrates. The final ethanol concentration required is 60%. Before use, add the volume indicated on the bottle of ethanol to Buffer CW1 and Buffer CW2.
- RNase A should be stored at 4°C upon arrival.
- Store Extraction beads at room temperature. Vortex prior to use.

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 HT Plus kits are intended for research use only.

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PacBio Documentation (103-940-800)

[1] 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.

Nanobind HT plus HMW DNA manual extraction workflow for saliva samples

Procedure notes for ***Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit*** (103-940-800)

- ***Important:*** Ensure sample has undergone an initial 50°C incubation
- ***Before you begin:*** Set 1.5 mL ThermoMixers to 55°C and 40°C. If only one ThermoMixer is available, set to 55°C and lower to 40°C after step 1.5.

Step	Instructions for extraction from saliva
1.1	**Important:** The sample and reagents must be added to the tube or well in the order specified below. Add **20 µL of Proteinase K** to a 1.5 mL Protein LoBind tube.
1.2	Add **400 µL of stabilized saliva**. Pulse vortex (1s max speed 10 times) and spin down **Note:** The addition of sample to Proteinase K rather than vice versa increases lysis efficiency and purity through improved mixing.
1.3	Add **20 µL of RNaseA**. Pulse vortex (1s max speed 10 times) and spin down. Incubate at **room temperature for 3 minutes**.
1.4	Add **100 µL of BL3** slowly against the side of the tube or well. Pulse vortex and spin down. **Note:** Do not add BL3 directly to the sample solution as this may impact extraction performance.
1.5	Incubate on a ThermoMixer at **900 rpm and 55°C for 5 min**. After incubation, pulse vortex (1s max speed 10 times) and spin down.
1.6	Add **25 µL of vortexed Extraction beads** to lysate.
1.7	Add **540 µL of 100% isopropanol** slowly against the side of the tube to lysate containing beads and invert to mix 4 times. **Note:** Do not add isopropanol directly to the sample solution as this may impact extraction performance.
1.8	Mix on a platform rocker at 20 rpm or tube rotator at 9 rpm for **15 min at room temperature**.
1.9	Quick-spin the tube and place sample on an appropriate magnet and allow beads to separate fully from the solution.
1.10	Discard supernatant.
1.11	Add **700 µL of Buffer CW1**, remove the tube from the magnet, invert to mix 4 times and spin down. Place the tube back on the magnetic base and discard the supernatant.
1.12	Add **700 µL of Buffer CW2**, remove the tube from the magnet, invert to mix 4 times and spin down. Place the tube back on the magnetic base and discard the supernatant.
1.13	Repeat step 1.12 for a total of two CW2 washes.
1.14	Remove residual wash buffer: • Remove samples from the magnet • Quick-spin • Place the tube back on the magnetic separation rack • Remove residual wash buffer and discard
1.15	Air dry the beads for 1 min. Remove the tube from the magnet.
1.16	Add **50–100 µL of Buffer LTE** directly onto the beads and vortex to mix. **Note:** If running the PureTarget application, elution in 50 µl is recommended.
1.17	Incubate at **40°C for 10 min**.
1.18	Pulse vortex until beads are completely resuspended and not adhering to the sides of the walls. Then place sample back at **40°C for 5 min**. **Important**: Incomplete resuspension of beads may lead to low recovery.
1.19	Quick-spin the tube and place sample on an appropriate magnet and allow beads to separate fully from the solution. Transfer the eluate to a new DNA LoBind tube.
1.20	Pipette-mix and vigorously vortex extracted genomic DNA to ensure it is homogeneous prior to quantification. Measure DNA concentration with a Qubit fluorometer.
	PROTOCOL COMPLETE

- **Important:** The sample and reagents must be added to the tube or well in the order specified below.
- **Note:** The addition of blood to Proteinase K rather than vice versa increases lysis efficiency through improved mixing
- **Note:** Do not add BL3 directly to the sample solution as this may impact extraction performance.
- **Important:** Incomplete resuspension of beads may lead to low recovery.
- **Note:** Do not add isopropanol directly to the sample solution as this may impact extraction performance.
- **Note:** running the PureTarget application, elution in 50 µl is recommended

No special “Magnetic rack handling procedure” is needed to perform manual HMW DNA extraction using Extraction beads

[1] Visit the PacBio Documentation website to download the latest Procedure & checklist documentation.

Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

Guide & overview – DNA extraction from saliva samples using the Nanobind HT plus kit on the KingFisher Apex system (103-940-700) describes the extraction of genomic DNA from samples collected with DNA Genotek Oragene or ORAcollect collection devices using the PacBio Nanobind HT plus kit and the KingFisher Apex system. Genomic DNA extracted by this method is compatible with downstream PacBio HiFi applications and sequencing.

Saliva sample input requirements

- Use 400 µL of input saliva collected and stabilized in a Oragene[1] device or OraCollect[2] device (DNA Genotek)
  - Saliva collected in Oragene devices is stable at RT for up to 5 years[3]
- Perform sample pretreatment (50°C incubation for 1 hour in a water bath) for efficient extraction using Nanobind kits
- Extracted DNA mass from Oragene collection devices typically ranges from 2–30 µg, depending on donor
- Extracted DNA mass from ORAcollect collection devices typically ranges from 1–15 µg, depending on donor



Collect saliva sample using Oragene or ORAcollect device (DNA Genotek)



Pretreat saliva sample by incubating in a water bath at 50°C for 1 hour

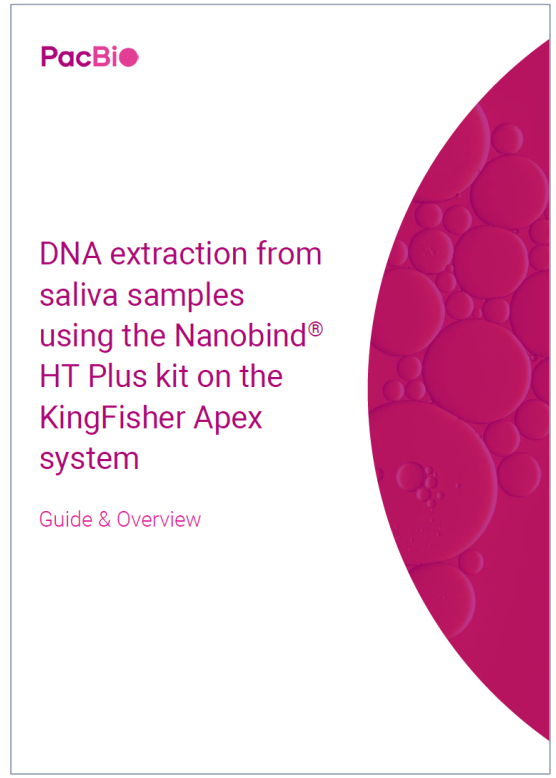
Nanobind HT plus kit (103-898-000)



Perform HMW DNA extraction using 500 µL of saliva sample stabilized in Oragene device buffer

Workflow summary

1	Oragene/ORA collection device	
2	Pre-treatment of sample at 50°C	1 hour (manual)
3	400 µL saliva sample	
4	Proteinase K, RNase A and BL3 addition	10 min (manual)
5	Lyse with shaking at 55°C	6 min (automated)
4	Extraction beads and isopropanol addition	10 min (manual)
5	Bind at room temp with rotation	13 min (automated)
6	Wash with CW1	4 min (automated)
7	Wash with CW2 (x2)	7 min (automated)
8	Elute in Buffer LTE at 40°C	12 min (automated)



PacBio Documentation (103-940-700)



Automated workflow runtime:

~1.5 hrs for 96 samples

[30 min setup + 1 hour instrument runtime]

[1] DNA Genotek Oragene saliva collection devices (e.g., 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)) use a liquid spit method for saliva collection where the donor spits into the attached funnel until liquid saliva reaches the fill line on the collection tube (target saliva collection volume is ~2 mL).

[2] DNA Genotek ORAcollect saliva collection devices (e.g., OCR-100 and OCD-100/100A) use an integrated sponge tip to absorb oral/buccal fluid (~200 µL collection volume) rather than requiring a liquid spit or a traditional dry buccal swab. **Note:** DNA extraction from dry buccal swabs and dried blood spots is not supported with the Nanobind HT plus kit.

[3] DNA GenoTek white paper – *Long-term stability of DNA from saliva samples stored in the Oragene® self-collection kit* (PD-WP-005)

Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

Procedural notes

End-to-end overall Nanobind HT plus workflow

Prepare sample, storage & reagent plates

↓

Select appropriate automation script to run

↓

Load prepared plates and other consumables onto work deck

↓

Run selected Nanobind HT DNA extraction protocol

↓

Store extracted DNA samples and perform QC

Before you begin



KingFisher Apex system
(Thermo Fisher)

Prior to beginning Nanobind HT plus automation protocol

☑ Ensure that the proper automation script has been installed

- To obtain **KingFisher automation scripts**, visit PacBio **Third-party automation equipment scripts** or contact **PacBio Technical Support** at support@pacb.com
- Example scripts for Nanobind HT plus automated HMW DNA extraction from blood or saliva samples using KingFisher Apex system:
  - `Nanobind HT Plus Blood.kfx2` (103-941-200) script for Nanobind HT plus 200 µL blood, Apex
  - `Nanobind HT Plus Saliva.kfx2` (103-941-300) script for Nanobind HT plus 400 µL saliva, Apex

☑ Ensure that instrument is set up with the correct magnet head and heating block.[1]

- Example hardware setup for Nanobind HT plus automated HMW DNA extraction from blood or saliva samples using KingFisher Apex system:
  - KingFisher Apex 96 deep-well magnet head (Thermo Fisher Scientific 24079930)
  - KingFisher Apex 96 deep-well heating block (Thermo Fisher Scientific 24075920)

[1] KingFisher Apex system supports 24 – 96 samples per run using the KingFisher Apex 96 deep-well magnet head (Thermo Fisher Scientific 24079930) and KingFisher Apex 96 deep-well heating block (Thermo Fisher Scientific 24075920).

Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- Run selected Nanobind HT DNA extraction protocol
- Store extracted DNA samples and perform QC

Sample, storage & reagent plate preparations

Manually prepare deep-well plates with required quantities of Nanobind reagents & consumables

Example list of 6 deep-well (DW) plates to be prepared for processing 400 µL of human saliva using KingFisher Apex.

Apex position	Reagent plate name	Plate purpose	Volume per well and other notes
6	Buffer LTE Plate	Buffer LTE storage	50 – 100 µL[1]
5	Buffer CW2 Plate 2	Buffer CW2 storage	700 µL
4	Buffer CW2 Plate 1	Buffer CW2 storage	700 µL
3	Buffer CW1 Plate	Buffer CW1 storage	700 µL
2	Sample Plate	Sample lysis / binding reactions	Prepare only **after** all other plates have been prepared (see below)
1	Tip Plate	Tip comb storage	KingFisher Apex 96 deep-well tip comb placed in plate

Plate 1 (lysis / binding plate) preparation procedure :

1. Add 20 µL of **Proteinase K**
2. Add 200 µL of **whole blood sample**[2]
3. Add 20 µL of **RNase A**
4. Add 200 µL of **BL3** slowly against the side of the well

Note: Sample and reagents **MUST** be added to each well in the order described in the Procedure



[1] **Note:** If running the PureTarget application, **50 µL** is the recommended elution volume when processing 400 µL of human saliva using KingFisher Apex. If running other applications (including WGS), 50 – 100 µL of Buffer LTE may be used. 5 – 10 µL volume loss is expected for the final elution step (for all applications).

[2] **Note:** The addition of blood to Proteinase K rather than *vice versa* increases lysis efficiency and purity through improved mixing.

Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

Prepare sample, storage & reagent plates

↓

Select appropriate automation script to run

↓

Load prepared plates and other consumables onto work deck

↓

Run selected Nanobind HT DNA extraction protocol

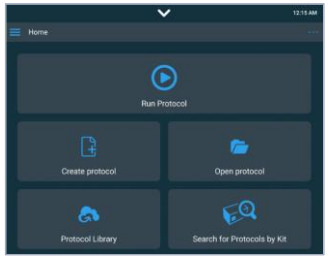
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Store extracted DNA samples and perform QC

Automation script selection

Select appropriate Nanobind HT plus protocol script to run based on desired input sample type and volume





Optional (KingFisher Apex):
Enter lot #'s for reagents & plastics, and sample ID



Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

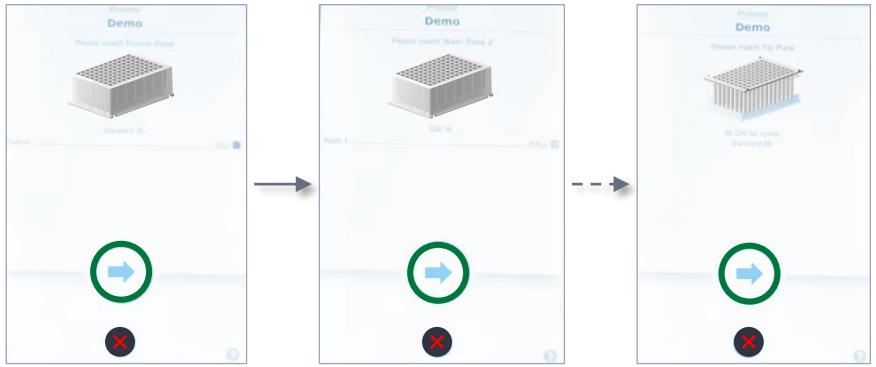
Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

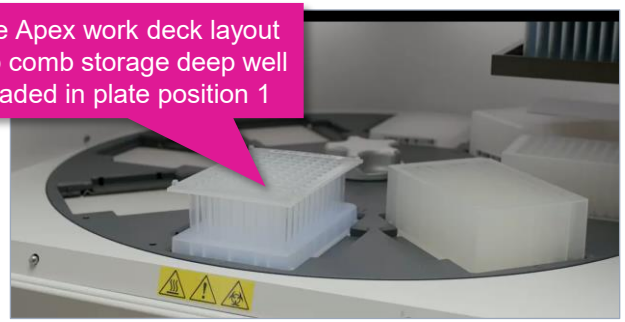
- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- Run selected Nanobind HT DNA extraction protocol
- Store extracted DNA samples and perform QC

Work deck preparation

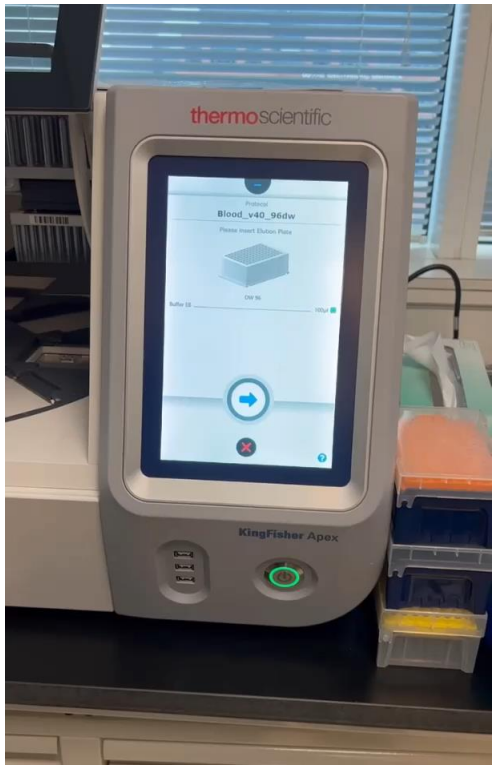
Sequentially load all prepared plates onto instrument work deck[1]



Load 1st plate (Buffer LTE plate) → Load 2nd plate… (Buffer CW2 Plate 2) --→ Load final plate (Tip plate)



Example Apex work deck layout with a tip comb storage deep well plate loaded in plate position 1



[1] **Note:** If you do not load enough conductive filter tips to complete the run, you will be warned to load additional tips or start the run at your own risk.

Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

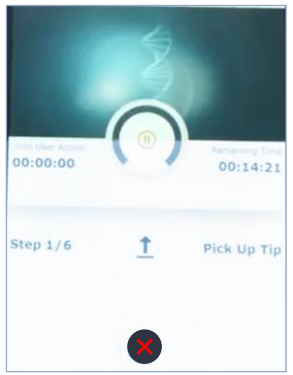
- Prepare sample, storage & reagent plates
- Select appropriate automation script to run
- Load prepared plates and other consumables onto work deck
- **Run selected Nanobind HT plus DNA extraction protocol**
- Store extracted DNA samples and perform QC

Run selected Nanobind HT plus DNA extraction protocol

The run will start <u>automatically</u> when final plate is loaded and **Next** button is pressed.

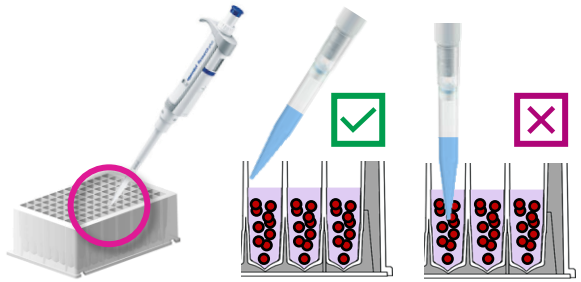


After run starts, screen shows time until user action required, remaining run time, and current protocol step





User action required: When prompted, remove Lysis/Binding plate (**Plate 1**) from instrument and manually add vortexed Extraction beads and IPA to each well. After adding IPA, return plate to instrument and resume program.



Note: Add isopropanol (IPA) gently against the **side** of the well into the Lysis / Binding solution (containing Extraction beads).[1]

[1] Adding IPA directly to the Lysis / Binding solution may affect extraction purity.

Nanobind HT plus HMW DNA automated extraction workflow for saliva samples

Procedural notes (cont.)

End-to-end overall Nanobind HT plus workflow

Prepare sample, storage & reagent plates

↓

Select appropriate automation script to run

↓

Load prepared plates and other consumables onto work deck

↓

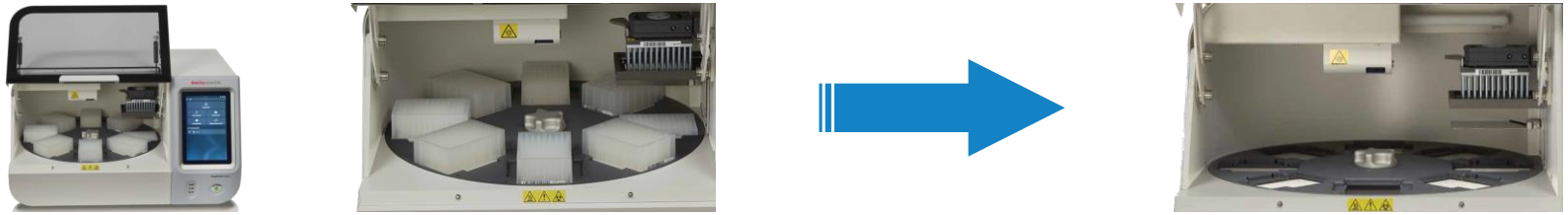
Run selected Nanobind HT DNA extraction protocol

↓

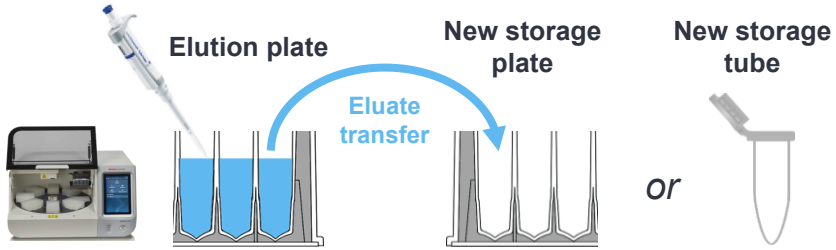
Store extracted DNA samples and perform QC

Sample storage and QC

When run ends, remove each plate from instrument as prompted.



Manually transfer eluates from Elution Plate to a new storage plate or storage tubes



Pipette mix and vigorously vortex extracted genomic DNA to ensure it is homogeneous prior to quantification.
Measure DNA concentration with a Qubit fluorometer

Vortex gDNA prior to quantification with Qubit 1X dsDNA BR/HS assay. If using the Qubit 1X dsDNA HS assay, dilution of the sample may be necessary.





Agilent Femto Pulse (Genomic DNA 165 kb kit) is recommended for accurately sizing genomic DNA.

Nanobind HT plus kit example performance

Expected QC metrics for Nanobind HT plus HMW DNA extracted from supported sample types

Expected Nanobind HT plus DNA extraction QC metrics for human whole blood and saliva samples

Sample type	Input material	Sample Volume	Expected DNA yield	Expected absorbance ratio[1]		Expected DNA size range	Notes
				260/280	260/230		
Blood	Human whole blood	200 µL	~3 – 15 µg	~1.8 – 2.0	~1.9 – 2.3	~50 – 300+ kb	Yield for human whole blood will vary from 3–15 µg based on donor white blood cell (WBC) concentration
Saliva	Human saliva – Oragene	400 µL of sample collected and stabilized in an Oragene device[2]	~2 – 30 µg	~1.4 – 2.0	~1.0 – 1.7	~50 – 300+ kb	DNA Genotek Oragene saliva collection devices use a liquid spit method for saliva collection where the donor spits into the attached funnel until liquid saliva reaches the fill line on the collection tube (target saliva collection volume is ~2 mL)
	Human saliva – ORAcollect	400 µL of sample collected and stabilized in an ORAcollect device[3]	~1 – 15 µg	~1.4 – 2.0	~1.0 – 1.7	~50 – 300+ kb	DNA Genotek ORAcollect saliva collection devices use an integrated sponge tip to absorb oral/buccal fluid (~200 µL collection volume) rather than requiring a liquid spit or a traditional dry buccal swab.

Note: High UV absorbance values are ***not*** always a guarantee of optimal sequencing performance (Not all inhibitors absorb at 230 and 280 nm). Conversely, low UV absorbance values are ***not*** always a guarantee that non-optimal sequencing performance will be obtained → gDNA samples with A260/280 ≥1.7 and A260/230 ratios ≥1.0 can still generate excellent HiFi sequencing performance (see ***PacBio Technical Note: Preparing DNA for PacBio HiFi sequencing – Extraction and quality control*** (102-193-651)).

[1] The expected "typical" range for 260/280 and 260/230 ratios will vary depending on sample type. UV purities outside of these expected ranges may indicate abnormalities in the extraction process.
Note: Some sample types that consistently yield lower UV purities can still sequence well.
[2] For Oragene devices, target saliva collection volume = 2 mL and total sample volume (Saliva + stabilizing solution) = 4 mL.
[3] For ORAcollect devices, saliva collection volume ≈ 200 µL and total sample volume (saliva + stabilizing solution) ≈ 1.2 mL.

Nanobind HT plus kit example WGS sequencing performance

Example Nanobind HT plus DNA extraction QC and HiFi sequencing performance results[1] for human whole blood and saliva samples

Sample type	Input material	Sample volume	DNA yield	DNA mode size	HiFi mean read length	HiFi yield
Blood	Human whole blood	200 µL	8.1 µg	169 kb	16.4 kb	154 Gb
Saliva	Human saliva – Oragene	400 µL of sample collected and stabilized in an Oragene device[2]	12.5 µg	146 kb	13.4 kb	132 Gb
	Human saliva – ORAcollect	400 µL of sample collected and stabilized in an ORAcollect device[3]	8.3 µg	107 kb	14.5 kb	150 Gb

[1] DNA yield and sizing QC data shown in table are for genomic DNA samples extracted manually using Nanobind HT plus kit. HiFi sequencing data are for libraries generated from pooling Nanobind HT plus manual- and automation-extracted genomic DNA samples, performing size selection with Short read eliminator (SRE) kit and shearing to 15–20 kb. HiFi sequencing was performed on the Revio system with SPRQ-Nx chemistry (250 pM loading concentration and *P1* loading ~71–76%).

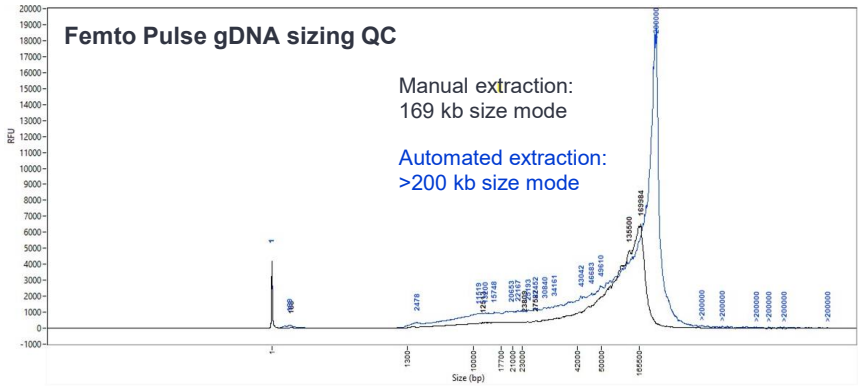
[2] For Oragene devices, target saliva collection volume = 2 mL and total sample volume (Saliva + stabilizing solution) = 4 mL.

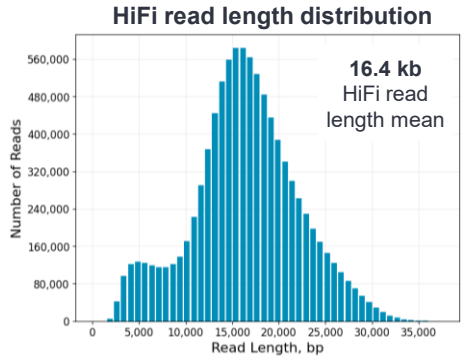
[3] For ORAcollect devices, saliva collection volume ≈ 200 µL and total sample volume (saliva + stabilizing solution) ≈ 1.2 mL.

Nanobind HT plus kit example WGS sequencing performance (cont.)

Human whole blood[1]

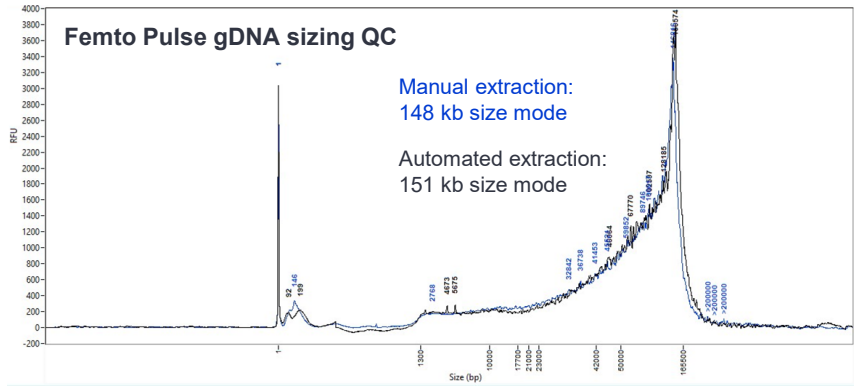
Metric	Value
HiFi Yield	154.5 GB
HiFi Read Length	16.4 kb
GQN 10kb	9.5
GQN 30kb	8.6

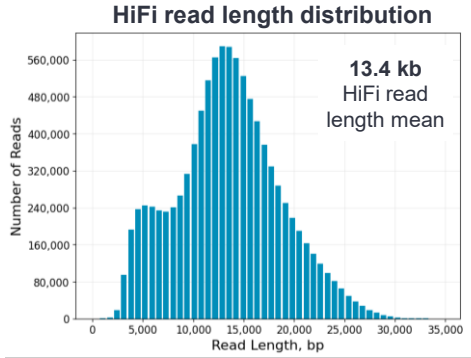




Human saliva – Oragene[1]

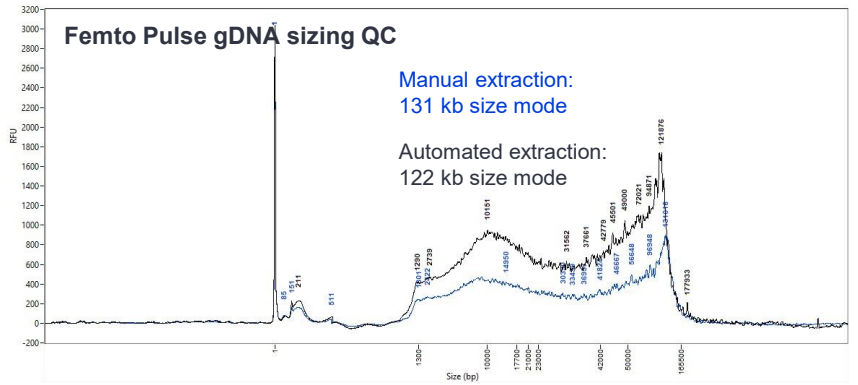
Metric	Value
HiFi Yield	132.5 GB
HiFi Read Length	13.4 kb
GQN 10kb	8.4
GQN 30kb	7.3

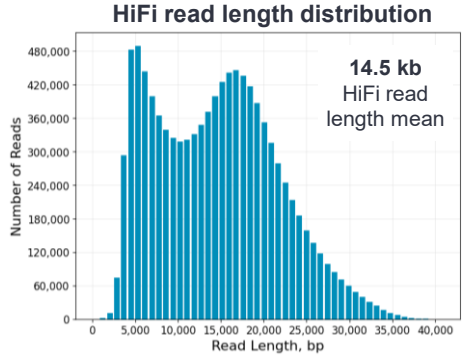




Human saliva – ORAcollect[1]

Metric	Value
HiFi Yield	150.0 GB
HiFi Read Length	14.5 kb
GQN 10kb	6.5
GQN 30kb	4.1

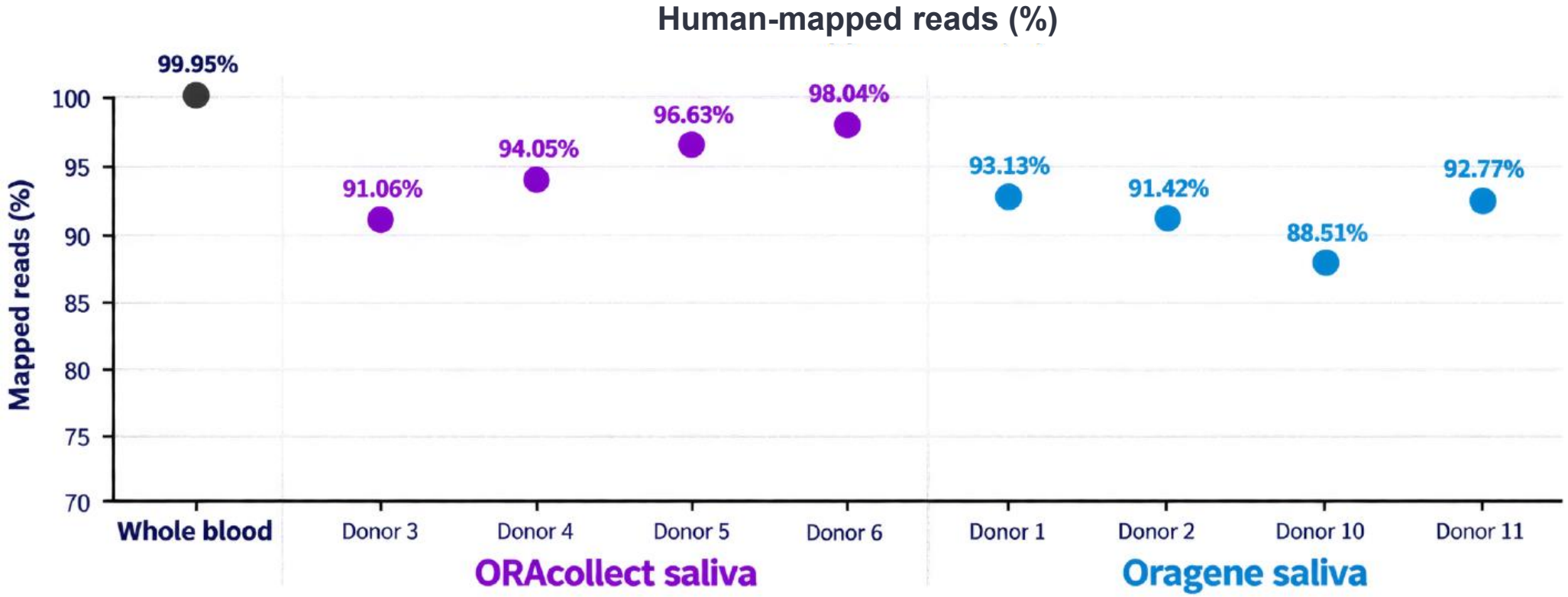




[1] Data shown in tables and HiFi read length plots are for libraries generated from pooling Nanobind HT plus manual- and automation-extracted genomic DNA samples, performing size selection with Short read eliminator (SRE) kit and shearing to 15–20 kb. HiFi sequencing was performed on the Revio system (250 pM loading concentration and *P1* loading ~71–76%).

Nanobind HT plus kit example WGS sequencing performance

Example human read mapping results for human WGS libraries prepared from Oragene and ORAcollect saliva DNA extracted using the Nanobind HT plus kit and sequenced on the Revio system[1]



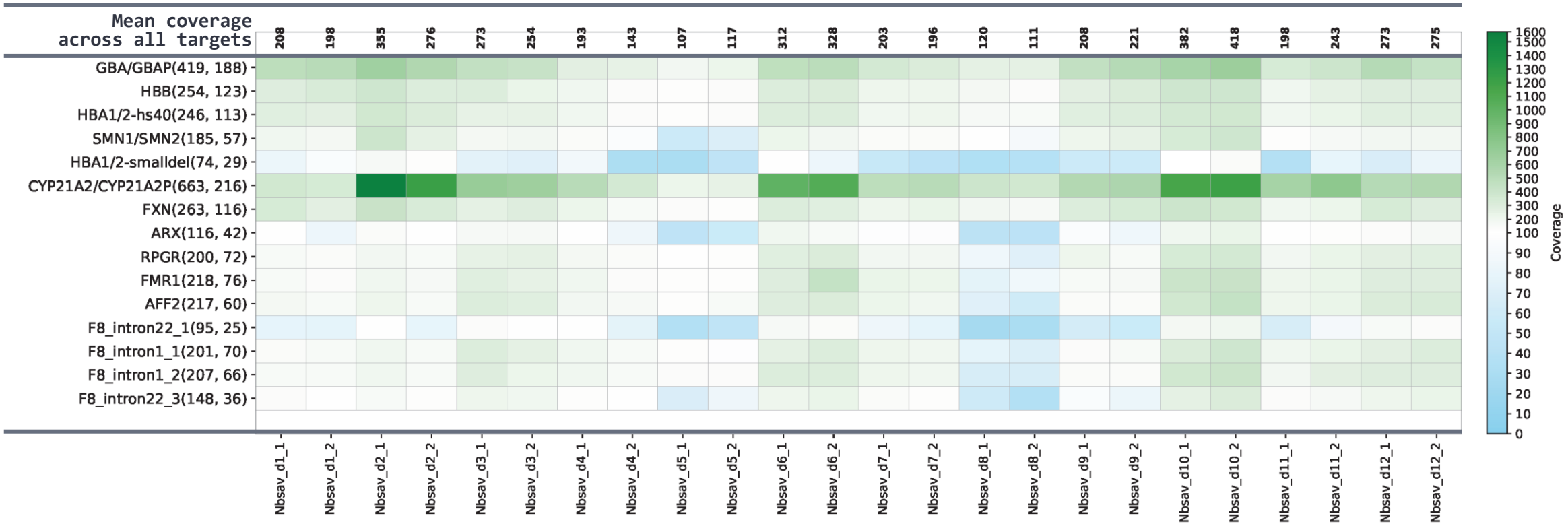
- HiFi reads were mapped to the human reference genome (GRCh38) using SMRT Link to determine the percentage of human-mapped reads
- High human mapping rates (88.5–98.0%) were observed across the analyzed Oragene saliva and ORAcollect saliva samples

[1] Human read mapping across supported sample types. Percentage of HiFi reads mapped to GRCh38 for ORAcollect saliva (n=4 donors) and Oragene saliva (n=4 donors) following automated Nanobind HT plus extraction. Whole blood (99.95%) is shown as a reference. See ***One-hour automated HMW DNA extraction from blood and saliva for HiFi sequencing*** (ASHG 2026 PacBio poster).

Nanobind HT plus kit example PureTarget sequencing performance

Example coverage results for human PureTarget 24 carrier panel libraries prepared from Oragene saliva DNA extracted using the Nanobind HT plus kit and sequenced on the Revio system[1]

PureTarget carrier panel coverage for 12 Oragene saliva donor samples run in duplicate (24 samples)



- 12 donors run in duplicate (24 samples)
- Mean target coverage: 234X (range: ~100X to ~400X)
- All Oragene saliva samples achieved coverage levels greater than the 20X target coverage minimum

[1] PureTarget carrier-panel coverage from Oragene saliva. Twelve donors were analyzed in duplicate following automated Nanobind HT plus extraction. All 24 samples met the required target coverage thresholds. Values in parentheses indicate the mean and minimum coverage for each target across all samples, while values above the heatmap indicate the mean coverage across all targets for each sample. Colors represent target coverage level. See ***One-hour automated HMW DNA extraction from blood and saliva for HiFi sequencing*** (ASHG 2026 PacBio poster).

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Technical documentation & applications support resources

DNA sample extraction documentation[1]

Brochures

- Brochure – Nanobind high-throughput HMW DNA extraction (102-326-565)
- Brochure – Nanobind PanDNA kit (102-326-604)

Technical notes

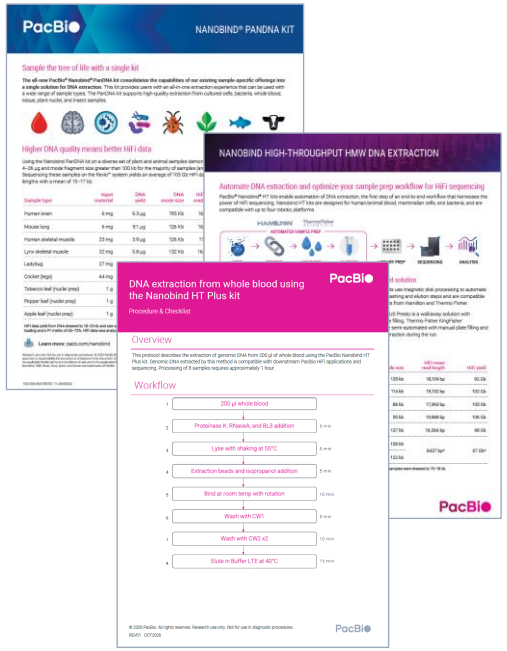
- Technical note – High-throughput DNA extraction (102-326-611)
- Technical note – Insect DNA extraction (102-326-612)
- Technical note – Preparing DNA for PacBio HiFi sequencing – Extraction and quality control (102-193-651)
- Technical note – Sample preparation for PacBio HiFi sequencing from human whole blood (102-326-500)

Nanobind kit protocols and Guides & overviews

- Guide & overview – Nanobind CBB kit (102-572-200)
- Guide & overview – Nanobind PanDNA kit (103-394-800)
- Nanobind Procedures & checklists – see PacBio Documentation
- Overview – Nanobind CBB HMW DNA extraction protocols (103-515-700)
- Overview – Nanobind HT HMW DNA extraction robotic procedures (103-032-000)
- Overview – Nanobind PanDNA HMW DNA extraction protocols (103-510-000)
- Procedure & checklist – DNA extraction from saliva samples using the Nanobind HT plus kit (103-940-800)
- Procedure & checklist – DNA extraction from whole blood using the Nanobind HT plus kit (103-940-900)
- Technical overview – HMW DNA sample preparation for PacBio long-read sequencing using Nanobind PanDNA and SRE kits (103-401-100)
- Technical overview – High-molecular weight DNA sample preparation using Nanobind HT plus kit (103-928-600)

Nanobind high-throughput (HT) automation kit protocols and Guides & overviews

- Guide & overview – DNA extraction from saliva samples using the Nanobind HT plus kit on the KingFisher Apex system (103-940-700)
- Guide & overview – DNA extraction from whole blood using the Nanobind HT plus kit on the KingFisher Apex system (103-940-600)
- Guide & overview – Nanobind HT kits (103-028-100) [For Nanobind HT CBB kit and Nanobind HT 1 ml blood kit]
- Nanobind HT Procedures & checklists – see PacBio Documentation
- Technical overview – Automated high-throughput HMW DNA extraction for PacBio long-read sequencing using Nanobind HT kits (103-401-700)
- Technical overview – High-molecular weight DNA sample preparation using Nanobind HT plus kit (103-928-600)





[1] Refer to PacBio Documentation website for the latest Nanobind HMW DNA extraction procedures.

Nanobind HT plus kit manual + automation protocols

Nanobind HT plus kit HMW DNA extraction procedures for PacBio HiFi sequencing workflows using either manual or robotic automation systems

Sample type	Starting material	Sample input	Automation system protocol and robotic script
			Thermo Fisher KingFisher Apex

Saliva	• Saliva collected with DNA Genotek saliva collection devices, including:[1,2]
	  • Oragene•Dx (OGD-600, OGD-610); or
	  • Oragene•DISCOVER (OGR-500, OGR-600); or
	  • ORAcollect (OCD-100, OCD-100A)
		• 400 µL of sample collected and stabilized in an Oragene or ORAcollect device.	Protocol
			DNA extraction from saliva samples using the Nanobind HT plus kit on the KingFisher Apex system (103-940-700)
			Script
			`Nanobind HT Plus Saliva.kfx2` (103-941-300) script for Nanobind HT plus 400 µL saliva, Apex

Blood	• Human whole blood 200 µL	• 200 µL	Protocol *Guide & overview – DNA extraction from whole blood using the Nanobind HT plus kit on the KingFisher Apex system* (103-940-600) Script `Nanobind HT Plus Blood.kfx2` (103-941-200) script for Nanobind HT plus 200 µL blood, Apex

Full list of available third-party automation equipment scripts for HMW DNA extraction using Nanobind kits can be found on PacBio.com[3]

[1] DNA Genotek Oragene•DISCOVER saliva collection device collects approx. 2 mL of saliva (prior to mixing with the stabilizing liquid). Total sample volume is approx. 4 mL after combining 2 mL saliva plus 2 mL of stabilizing reagent inside the tube.

[2] DNA Genotek ORAcollect saliva collection device collects approx. 200 µL of saliva (prior to mixing with the stabilizing liquid). Total sample volume is approx. 1.2 mL after combining ~0.2 mL saliva plus 1 mL of stabilizing reagent inside the tube.

[3] For a complete list of supported Nanobind HT HMW DNA extraction procedures, refer to the PacBio Documentation website.

Nanobind HT CBB kit and Nanobind HT 1 ml blood kit automation protocols

Nanobind HT kit HMW DNA extraction procedures for PacBio high-throughput HiFi sequencing workflows using robotic automation systems

Sample type	Starting material	Sample input	Automation system protocol and robotic script			
			Hamilton NIMBUS Presto*	Thermo Fisher KingFisher Apex	Thermo Fisher KingFisher Flex	Thermo Fisher KingFisher Duo Prime
Mammalian cultured cells	Cultured cells pellet (approx. 3 Gb genome size)	$1x10^6$ cells	Protocol	Protocol Script PN: 103-416-400	Protocol Script PN: 103-416-600	Protocol Script PN: 103-416-500
Blood	Human whole blood 200 µL	200 µL	Protocol	Protocol Script PN: 103-416-100	Protocol, Script PN: 103-416-300	Protocol Script PN: 103-416-200
	Human whole blood 1 mL**	1 mL	Protocol	Protocol Script PN: 103-415-700	Protocol Script PN: 103-416-000	Protocol Script PN: 103-415-900
	Mammalian whole blood (non human)	200 µL	Protocol	Protocol Script PN: 103-416-800	N/A	N/A
	Nucleated red blood cells (nRBCs)	2.5–20 µL	Protocol	Protocol Script PN: 103-416-700	N/A	N/A
Cultured bacteria	Gram positive and negative bacteria	$5x10^8$ cells	Protocol	Protocol Script PN: 103-416-900	N/A	N/A

* Please contact Hamilton directly for NIMBUS Presto scripts
** All sample types extracted using the Nanobind HT CBB kit (PN 102-762-700) expect 1 mL blood using Nanobind HT 1 mL blood kit (PN 102-762-800)

Available third-party automation equipment scripts for HMW DNA extraction using Nanobind kits can be found here.
For example yield results, see Nanobind HT extraction brochure and further details in the Nanobind HT kit guide & overview.

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[1] *See **Overview – Nanobind HT HMW DNA extraction robotic procedures*** (103-032-000). For a complete list of supported Nanobind HT HMW DNA extraction procedures, refer to the PacBio Documentation website.

Nanobind PanDNA kit manual protocols

Nanobind PanDNA kit HMW DNA extraction procedures for PacBio HiFi sequencing[1]

Sample type	Starting material	Samples input	Workflow time	Protocol
Blood	Human whole blood	200 µL	~1 hr.	Extracting HMW DNA from human whole blood (102-573-500)
	Nucleated red blood cells (nRBCs)	2.5–20 µL	~1 hr.	Extracting HMW DNA from nucleated red blood cells (102-574-000)
	Human whole blood with RBC lysis	400 µL	<1.5 hrs.	Extracting HMW DNA from human whole blood with RBC lysis (103-377-500)
Saliva	Human saliva collected in DNA Genotek™ Oragene™ devices	500 µL	~2 hr.	Extracting HMW DNA from saliva collected in DNA Genotek™ Oragene™ devices (103-544-000)
Animal tissue	Diverse tissue types	2–100 mg	~2.5 hrs.	Extracting HMW DNA from animal tissue (102-574-600)
Insect tissue	Insect whole body or segment	>20 mg	~2.5 hrs.	Extracting HMW DNA extraction from insects (102-377-400)
Plant tissue	Isolated plant nuclei	0.25–5g	~1.5 hrs.[2]	Extracting HMW DNA from plant nuclei (103-378-200)
Mammalian cultured cells	Suspension cell culture	1 x 10^6–5 x 10^6 diploid human cells	~1 hr.	Extracting HMW DNA from cultured suspension cells (103-394-500)
	Adherent cell culture	1 x 10^6–5 x 10^6 diploid human cells	~1 hr.	Extracting HMW DNA from cultured adherent cells (102-573-600)
Cultured bacteria	Gram-negative bacteria	5 x 10^8–5 x 10^9 bacterial cells	~1 hr.	Extracting HMW DNA from Gram-negative bacteria (102-573-800)
	Gram-positive bacteria	5 x 10^8–5 x 10^9 bacterial cells	~1 hr.	Extracting HMW DNA from Gram-positive bacteria (102-573-900)

[2] Upstream plant nuclei prep isolation procedures (e.g., 102-574-900 or 102-574-800) typically take ~3 hours to complete.

[1] *See **Overview – Nanobind PanDNA HMW DNA extraction protocols*** (103-510-000). For a complete list of supported Nanobind HMW DNA extraction procedures, refer to the PacBio Documentation website.

Nanobind CBB kit manual protocols

Nanobind CBB kit HMW DNA extraction procedures for PacBio HiFi sequencing[1]

Sample type	Starting material	Samples input	Workflow time	Protocol
Mammalian cultured cells	Suspension cell culture	1 x 10^6–5 x 10^6 diploid human cells	~1 hr.	Extracting HMW DNA from cultured suspension cells (103-394-500)
	Adherent cell culture	1 x 10^6–5 x 10^6 diploid human cells	~1 hr.	Extracting HMW DNA from cultured adherent cells (102-573-600)
Blood	Human whole blood	200 µL	~1 hr.	Extracting HMW DNA from human whole blood using Nanobind kits (102-573-500)
	Nucleated red blood cells (nRBCs)	2.5–20 µL	~1 hr.	Extracting HMW DNA from nucleated red blood cells (102-574-000)
Saliva	Human saliva collected in DNA Genotek™ Oragene™ devices	500 µL	~2 hr.	Extracting HMW DNA from saliva collected in DNA Genotek™ Oragene™ devices (103-544-000)
Cultured bacteria	Gram-negative bacteria	5 x 10^8–5 x 10^9 bacterial cells	~1 hr.	Extracting HMW DNA from Gram-negative bacteria (102-573-800)
	Gram-positive bacteria	5 x 10^8–5 x 10^9 bacterial cells	~1 hr.	Extracting HMW DNA from Gram-positive bacteria (102-573-900)

[1] *See **Overview – Nanobind CBB HMW DNA extraction protocols*** (103-515-700). For a complete list of supported Nanobind HMW DNA extraction procedures, refer to the PacBio Documentation website.

www.pacb.com

Revision history (description)	Version	Date
Initial release.	01	November 2026

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