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GALEAS™ Hereditary^{Plus} kit

DNA target enrichment for next generation sequencing

Protocol guide V1.2

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Revision history

Revision	Date	Revision description
1.0	August 2023	First iteration
1.1	November 2023	Updates to section 3.C Prepared captured library for Illumina sequencing
1.2	September 2026	Update in line with the new branding guidelines

Intended use

The GALEAS Hereditary^{Plus} kit is an advanced solution for Next-Generation Sequencing (NGS) library preparation and targeted enrichment. This kit is designed to facilitate the analysis and profiling of 146 genes associated with a predisposition for hereditary cancers, such as breast, prostate, Lynch syndrome, and Wilms tumor.

The curated gene content allows to profile diagnostically meaningful SNVs, INDELs, and a wide range of CNVs across the targeted regions. GALEAS Hereditary^{Plus} is specifically optimized to work with genomic DNA (gDNA) derived from either blood or saliva samples, allowing flexibility in sample collection methods, and has been optimised for 10–100 ng input range.

The kit is available in 2 different pack sizes (NGS_GAL_HCP_FR_16 and NGS_GAL_HCP_FR_96), each containing the necessary components for processing 16 or 96 samples.

This protocol explains how to use the GALEAS Hereditary^{Plus} kit to perform DNA library preparation and target enrichment for NGS on various sequencing platforms, using gDNA extracted from saliva or blood as input material.

For Research Use Only (RUO). Not for use in diagnostic procedures.

Key features

- Optimised for greater than or equal to 10 ng of gDNA input
- Single tube solution for library preparation reduces the number of bead clean-up steps, maximises yield and facilitates automation
- Protocol supports library preparation with enzymatic fragmentation reagents for library preparation of gDNA, which avoids the need to physically shear gDNA by sonication
- Adapters containing Unique Dual Indexes (UDI) to identify and avoid sample index skipping
- Unique Molecular Identifiers (UMI) 9 bp long for PCR/sequencing error removal and single molecule counting in bioinformatic analysis. Please note, the use of UMIs is not required for GALEAS Hereditary^{Plus} bioinformatic analysis but are available if required
- Pooling of libraries prior to hybridization and capture limits the number of capture reactions and amount of panel required

Workflow overview

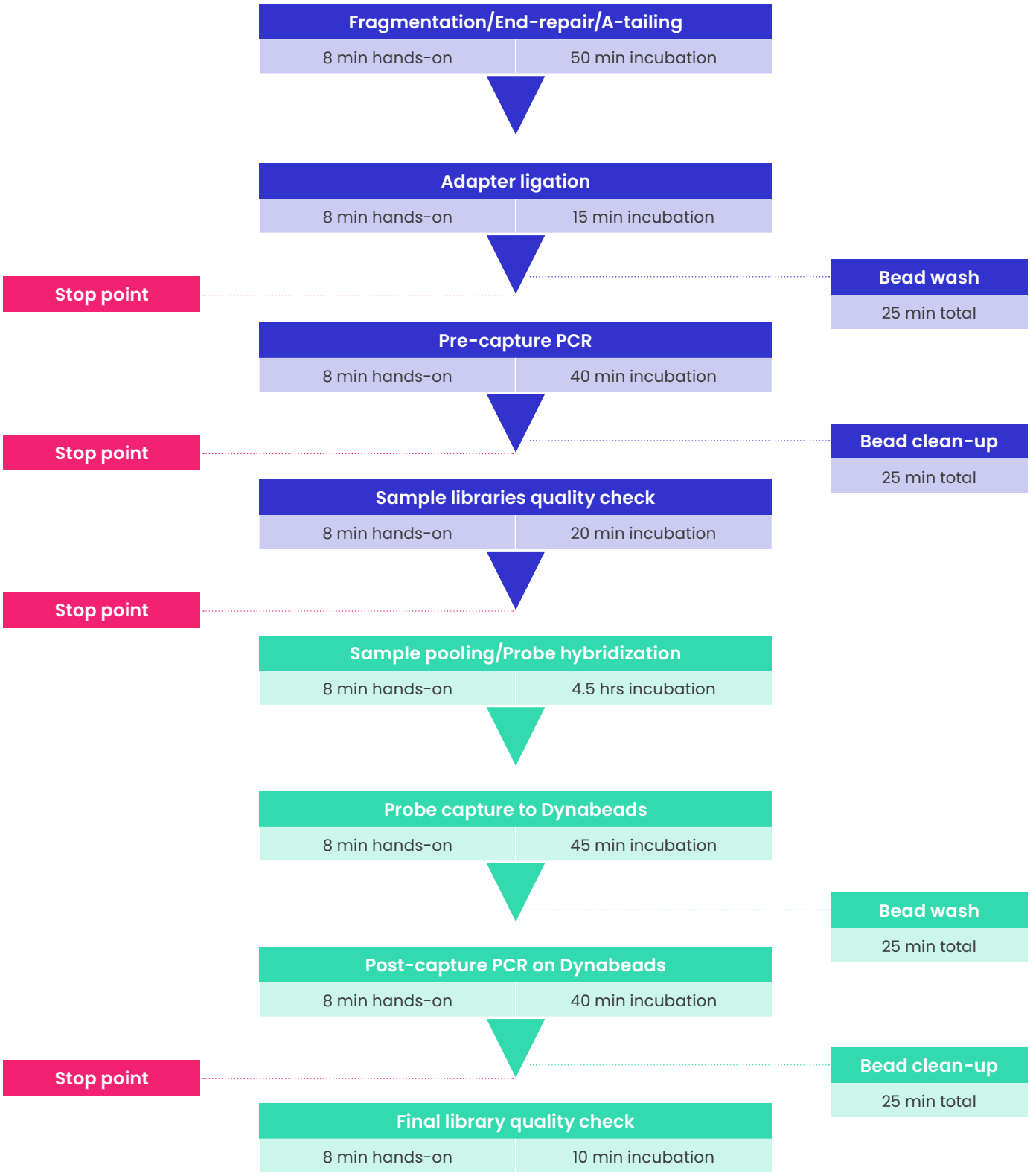

Figure 1. Flow chart outlining the main steps of the GALEAS Hereditary^Plus kit workflow. Blue boxes refer to library preparation steps (3.5 hours); while green boxes refer to probe hybridization/capture and target enrichment steps (8 hours).

Kit contents

Library preparation kit V2 (b)

Reagent	Reagent volume and product codes				Storage (°C)	Reagent tube colour code
	16 samples NGS_ACC_LV2_FR_16		96 samples NGS_ACC_LV2_FR_96			
Fragmentation enzyme	96 µl	C3TV2-FGE16	2 × 288 µl	C3TV2-FGE48	-20	Red
Fragmentation buffer	64 µl	C3TV2-FGB16	2 × 192 µl	C3TV2-FGB48	-20	Red
Ligation mix	320 µl	C3TV2-LIG16	2 × 960 µl	C3TV2-LIG48	-20	Blue
PreCap amplification mix	400 µl	C3TV2-PAM16	2 × 1.2 ml	C3TV2-PAM48	-20	Green
PreCap primer mix	80 µl	C3TV2-PPM16	2 × 240 µl	C3TV2-PPM48	-20	Black
UMIRC_AD* (Adapter plate)	01–16	NGS_ACC_ ADP_1-16	A–196 B 9–7192 C 193–288 D 289–384	NGS_ACC_ ADP_A/B/C/D	-20	-

*NOTE: NGS_GAL_TCP_FR_96_A includes adapter plate A (1-96 indexes), NGS_GAL_TCP_FR_96_B includes adapter plate B (97-192 indexes), NGS_GAL_TCP_FR_96_C includes adapter plate C (193-288 indexes), NGS_GAL_TCP_FR_96_C includes adapter plate D (289-384 indexes) and NGS_GAL_TCP_FR_16 (1-16 indexes).

GALEAS Hereditary^{Plus} panel

Product code	Reaction size	Volume (µl)	Storage (°C)	No. of samples recommended for pre-capture pooling
NGS_GAL_HCP_16	16	9	-20	8–16 samples
NGS_GAL_HCP_96	96	54	-20	8–16 samples

NOTE: See section 2.A Library pooling and probe hybridization, for more information.

Hybridization and capture enrichment kit V2

Reagent	Reagent volume and product codes				Storage (°C)	Reagent tube colour code
	4 rxns* NGS_ACC_HV2_4		12 rxns NGSACC_HV2_12			
Hybridization buffer (2×)	76 µl	C3TV2-THB04	228 µl	C3TV2-THB12	-20	Blue
Hybridization enhancer	24 µl	C3TV2-THE04	72 µl	C3TV2-THE12	-20	Brown
Stringent wash buffer (10×)	160 µl	C3TV2-TSB04	480 µl	C3TV2-TSB12	-20	White (S)
Wash buffer 1 (10×)	120 µl	C3TV2-TW104	360 µl	C3TV2-TW112	-20	White (1)
Wash buffer 2 (10×)	80 µl	C3TV2-TW204	240 µl	C3TV2-TW212	-20	White (2)
Wash buffer 3 (10×)	80 µl	C3TV2-TW304	240 µl	C3TV2-TW312	-20	White (3)
Bead wash buffer (2×)	1 ml	C3TV2-TWB04	2 × 1.5 ml	C3TV2-TWB12	-20	White (B)
Universal blockers	8 µl	C3TV2-TUB04	24 µl	C3TV2-TUB12	-20	Orange
COT-1 human DNA	30 µl	C3TV2-TCO04	90 µl	C3TV2-TCO12	-20	Red
PostCap amplification mix	100 µl	C3TV2-PCM04	300 µl	C3TV2-PCM12	-20	Green
PostCap primer mix*	10 µl	C3TV2-TPO04	30 µl	C3TV2-TPO12	-20	Black

NOTE: The 4 rxn Hybridization and capture enrichment kit V2 is suitable for use with the 16 rxn GALEAS Hereditary^{Plus} Panel.

GALEAS Hereditary^{Plus} total covered region size (Mb)

Design ID	Genome	Total target size (bp)	Total covered region size (bp)	Total covered region size (Mb)
GALEAS Hereditary^{Plus}	GRCh38	425286	809521	0.81

Required laboratory reagents and consumables not supplied

Item	Recommended source
Elution Buffer (EB)	Qiagen, Cat # 19086 (or equivalent: 10 mM Tris-HCl, pH 8.0)
Digital electrophoresis system consumables	**Agilent Technologies:** D1000 reagents, Cat # 5067-5583; D1000 ScreenTape, Cat # 5067-5582 High sensitivity D1000 reagents, Cat # 5067-5585 High sensitivity D1000 ScreenTape, Cat # 5067-5584 gDNA ScreenTape, Cat # 5067-5365 gDNA reagents, Cat # 5067-5366 (Recommended: If not available, see Appendix IV)
DNA low binding tubes, 1.5 ml PCR-clean	DNA LoBind 1.5 ml, Eppendorf, Cat # 022431021
Dynabeads™ M-270 Streptavidin IMPORTANT: We have validated our protocol with Dynabeads. Other beads are NOT recommended for use with the GALEAS Hereditary^{Plus} kit protocol	Life technologies, Cat # 65305
Ethanol (absolute, 100%)	Various sources available
Fluorometer consumables	**Invitrogen:** Qubit assay tubes, Cat # Q32856 Qubit dsDNA BR assay kit, Cat # Q32853 Qubit dsDNA HS assay kit, Cat # Q32854)
Quantitative/Real-Time PCR library quantification kit	KAPA Library Quantification kit–Illumina/Universal kit, Roche (optional)
Nuclease-free, molecular biology grade water	Various sources available
PCR-clean 0.2 ml PCR tubes/8-well tube strips with caps/ 96-well plates with caps/seals	Various sources available
PCR-clean 1.5–2 ml microcentrifuge tubes	Various sources available
Target Pure™ NGS Clean-up Beads	Nonacus, Cat # NGS_ACC_CUB_10

Required equipment

Item	Source
Digital electrophoresis system	Agilent 4200 TapeStation, Agilent Technologies, Cat # G2965AA (Recommended: If not available, see Appendix IV)
Fluorometer for DNA fluorometric quantitation	Qubit™ 3.0 Fluorometer, Invitrogen, Cat # Q33216 Qubit 4 Fluorometer, Invitrogen, Cat # Q33238
Magnetic separation rack capable of accommodating 0.2 ml tubes/8-well tube strips/96-well plates	DynaMag™-96 Side Magnet, Invitrogen, Cat # 12331D (Recommended: If not available, see Appendix II)
Magnetic separation rack capable of accommodating 1.5–2 ml tubes	DynaMag-2 Magnet, Invitrogen, Cat # 12321D (Optional, if a 96-well magnetic separation rack is not available)
Micro-centrifuge capable of accommodating 1.5–2 ml tubes	Various sources available
Mini-centrifuge capable of accommodating 0.2 ml PCR tubes/8-well tube strips	Various sources available
Multichannel pipettes (10, 100, 200 µl capacity)	Various sources available
Plate centrifuge capable of accommodating 0.2 ml 96-well plates	Various sources available
Single channel pipettes (10, 100, 200, 1000 µl capacity)	Various sources available
Thermocycler with heated lid capable of accommodating 96-well plates	Various sources available
Vacuum concentrator	Concentrator Plus, Eppendorf, Cat #5305000304 or vacuum lyophiliser/freeze-dryer (such as the ScanVac CoolSafe, Labogene) (Recommended: If not available, see Appendix III)
Vortex mixer	Various sources available

Storage and handling

- All kit components should be stored as indicated in the component list for each kit, as stated above
- The enzyme mixes and adapters in the Library Preparation kit V2 (b); the PostCap Amplification Mix and PostCap Primer Mix in the Hybridization and Capture Enrichment kit V2; and the probe set in the GALEAS Hereditary^{Plus} Panel should be thawed on ice and kept on ice during the relevant procedures
- Briefly vortex mix all components after thawing and prior to use, with the exception of the Fragmentation Enzyme, the Ligation Mix, PreCap Amplification Mix and PostCap Amplification Mix components, all of which should be mixed by light flicking the tube or pipette mixing
- All components should be briefly spun down after mixing

Chapter 1: Library preparation

Input DNA requirements

- Only high-purity DNA samples which are free of residual salts, proteins, detergents, or other contaminants should be used as input material. Library preparation can be conducted using 1–1000 ng of gDNA extracted from blood or saliva. However, for optimal results using the GALEAS Hereditary^{Plus} panel, it is recommended to use an input between 10 and 100 ng of gDNA
- Fluorometric methods (such as the Qubit assay, Invitrogen) are recommended to accurately determine DNA concentration, especially when using less than 100 ng of DNA as input

IMPORTANT: We would advise against the use of a Nanodrop or similar spectrophotometry-based methods for DNA quantitation as these cannot accurately distinguish between DNA and RNA and have reduced sensitivity for less than 100 ng/µl concentrations.

- Resuspend extracted DNA in molecular biology grade water, a low EDTA concentration Tris-HCl buffer (such as 0.1 mM EDTA TE buffer) or a 10 mM TrisHCl pH 8.0 saline buffer (such as QIAGEN Buffer EB)
- If DNA samples are kept in a high EDTA concentration buffer (such as 1× TE), DNA needs to be purified using a commercially available kit or DNA Purification Beads (such as Target Pure™ NGS clean-up beads) and resuspended in one of the above-mentioned buffers

1.A Enzymatic fragmentation and End-repair/A-tailing for intact gDNA samples

In this step, gDNA is sheared to a size of 180–250 bp by enzymatic fragmentation and the resulting fragments undergo end-repair and dA-tailing in a single reaction. This converts high molecular weight DNA into short 5'-phosphorylated and 3'-dA-tailed DNA fragments, enabling direct ligation of adapters.

Before you start

- Thaw the Fragmentation Buffer (red cap) from the Library Preparation kit V2 (b) at room temperature and briefly vortex mix
- Mix the Fragmentation Enzyme (red cap) and the Ligation Mix (blue cap) from the Library Preparation kit V2 (b) kit by lightly flicking the tube or pipette mix
- Briefly centrifuge all three reagents to collect the liquid to the bottom of the tubes and keep on ice

IMPORTANT: All library preparation reaction setup procedures should be conducted on ice, unless stated otherwise.

Procedure

1. Set up the following thermocycler program.

Step	Temperature (˚C)	Time
1	4	Hold
2	37	20 min
3	65	30 min
4	4	Hold

NOTE: Set the thermocycler heated lid to 105˚C, the sample volume is 50 µl.

2. Prepare the DNA sample in a total volume of 40 µl (according to the input amount), use nuclease free water to dilute the DNA, if required. **Make sure to keep the reaction on ice during the whole procedure.**

3. Prepare the following reaction mix for each DNA sample as indicated in the table below. Vortex thoroughly to ensure appropriate mixing is achieved without the formation of bubbles.

Components	Volume for 1 reaction (µl)
Fragmentation buffer	4
Fragmentation enzyme	6
DNA sample	X
Nuclease-free water	(40–X)
Total	50

NOTE: The Fragmentation Buffer and Fragmentation Enzyme can be combined as a master mix when processing multiple samples. Include a 10% overage to allow accurate pipetting of 10 µl into 40 µl DNA sample. Vortex the master mix at moderate speed for 5 seconds to ensure thorough mixing without generating bubbles.

4. Add 10 µl of prepared End-repaird/A-tailed reaction mix to each reaction for a total volume of 50 µl. Mix thoroughly by vortex mixing and briefly centrifuge to collect liquid at the bottom of the tube.

5. Immediately transfer sample to the pre-chilled thermocycler (4˚C) and “skip” to the next step in the program.

6. When the program finishes, and the thermocycler has returned to 4˚C, remove the samples from the cycling block and place on ice. **Immediately proceed to the ligation step (1.B).**

1.B Ligation of adapters

During the ligation step, adapters are ligated on both ends of the 5'-phosphorylated/3'-dA-tailed DNA fragments. A clean-up step is performed immediately after adapter ligation using Target Pure™ NGS clean-up beads to purify the DNA library and remove residual non-ligated adapters, enzymes, and buffers.

Before you start

- Equilibrate the Target Pure NGS clean-up beads to room temperature for 20–30 minutes ready for use in step 8
- Remove the adapter-containing 96-well plate from the freezer and thaw on ice
- Centrifuge the plate collect the liquid at the bottom of the tubes

Refer to Appendix VI, Table 2 for the location of each adapter within the supplied Illumina UMI Adapter 96-well plate, (one adapter per sample library) containing wells with 96 adapters.

Procedure

1. Set up the following thermocycler program.

Step	Temperature (˚C)	Time
1	4	Hold
2	20	15 min

Note: Set the lid to **"not heated"** (or leave the lid open), the sample volume is 75 µl.

Adapters are provided at a concentration of 15 µM. Depending on the input, the required adapter concentration needs to be adjusted. Refer to the guidelines on the appropriate adapter concentration below.

- When using a DNA input quantity of less than 10 ng, prepare a 1:5 dilution for the adapters using molecular grade water, ready for use in the ligation step (ie, a final concentration of 3 µM)
- When using a DNA input quantity of more than 10 ng of input DNA, use the adapters directly from the tube undiluted, at 15 µM

2. While keeping the end-repaired/A-tailed DNA samples on ice, add 5 µl of the selected adapter (either the 15 µM or the 3 µM concentration depending on the initial input, as explained in the guidelines above) to each sample and mix gently by pipette mixing or briefly vortex mixing.

IMPORTANT: Use only one adapter-containing well from the 96-well plate at a time by piercing the aluminium seal to access the adapter. Adapters are single use only; diluted adapters cannot be stored for further use as they will degrade.

3. Add 20 µl of Ligation Mix (blue cap) into each reaction for a total final volume of 75 µl. **Keep on ice.**

4. Mix well by pipetting up and down 10–15 times or briefly vortex (2–3 seconds). Briefly centrifuge to collect all the liquid at the bottom of the tubes.

5. Immediately transfer adapter ligated sample to the pre-chilled thermocycler (4˚C) and "skip" to the next step in the program.

6. After the program finishes, proceed immediately to the clean-up step using Target Pure™ NGS clean-up beads.

Clean-up of adapter ligated library

7. Thoroughly vortex the room temperature equilibrated Target Pure NGS clean-up beads.

8. Add 67.5 µl of Target Pure NGS clean-up beads to a new 0.2 ml PCR tube/8-well tube strip/96-well plate for each sample.

NOTE: DNA clean-up with Target Pure NGS clean-up beads can also be performed in 1.5 ml tubes, as explained in Appendix II.

9. Transfer the whole 75 µl of adapter ligation reaction to the 67.5 µl of Target Pure NGS clean-up beads and mix well by pipetting up and down 15–20 times, taking care to avoid the formation of bubbles.

10. Incubate the mixture for 5 minutes at room temperature.

11. Prepare a solution of 80% ethanol (400 µl per sample is required for each clean-up step). For two washes and including an overage, 1000 µl per sample should be prepared for the entire library preparation procedure.

12. Place the sample on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tubes/wells.

13. Keeping the sample on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

14. Add 200 µl of 80% ethanol to the sample and incubate at room temperature for 30 seconds.

15. Repeat steps 13–14 for a total of two 80% ethanol washes.

16. Keeping the sample on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

17. Remove any residual liquid from the tubes/wells using a pipette.

18. Keeping the sample on the magnetic stand, incubate at room temperature with open lids for 3–5 minutes or until the beads are dry.

IMPORTANT: Avoid over-drying of beads, as this can result in a significant loss of DNA recovered. When dry, beads will appear matt in appearance, but should not be cracked.

19. Remove the sample from the magnetic stand and resuspend the dried beads in 22 µl of Buffer EB or equivalent buffer saline solution (10 mM Tris-HCl, ph 8.0) by pipette mixing up and down 10–15 times, taking care to avoid the formation of bubbles.

NOTE: If proceeding immediately to pre-capture library amplification (chapter 1.C), molecular biology grade water can also be used to elute the library DNA from beads.

20. Incubate the sample for 2 minutes at room temperature.

21. Place the sample on the magnetic stand for 2 minutes at room temperature to pellet the beads on the side of the tubes/wells.

22. Carefully recover 20 µl of supernatant and transfer it to a new 1.5 ml low-bind tube.

STOPPING POINT: At this point, adapter ligated libraries can be stored at -20˚C, if not proceeding immediately to the library amplification step.

1.C Library amplification

A high-fidelity amplification step is performed to ensure that sufficient library yield is available for the following targeted enrichment procedure. This is conducted using primers that bind to the adapter ligated DNA fragments at the start of the standard P5 and P7 sequences, which are present in all adapters.

Before you start

- Thaw the PreCap Amplification Mix (green cap) and the PreCap Primer Mix (**black** cap) from the Library Preparation kit V2 (b) on ice
- Once thawed, lightly flick the tube or pipette mix containing the PreCap Amplification Mix to ensure adequate mixing of the reagent **(do not vortex)**
- Briefly vortex mix the PreCap Primer Mix
- Centrifuge all reagents to collect the liquid at the bottom of the tubes. Keep both tubes on ice for the whole procedure
- Equilibrate the Target Pure™ NGS clean-up beads to room temperature for 20–30 minutes for use in step 6 and prepare 80% ethanol (500 µl per sample to allow for overage), if not done so already in section 1.B, step 11

Procedure

1. Set up the following thermocycler program.

Step	Temperature (˚C)	Time	Cycles
1	98	Hold	1
2	98	45 sec	1
3	98	15 sec	3–12*
4	60	30 sec	
5	72	30 sec	
6	72	1 min	1
7	4	Hold	1

NOTE: Set the thermocycler heated lid to 105˚C, the sample volume is 50 µl.

*IMPORTANT: Recommended number of amplification cycles.

Starting DNA input (ng)	Recommended number of amplification cycles
	High quality DNA
1	12–13
5	9–10
10	8–9
50	5–6
100	4–5
200	3–4

For further guidance, please contact us at **support@nonacus.com**.

2. Prepare the following PCR master mix on ice in a separate 1.5 ml tube as indicated in the following table.

3. Mix well by pipette mixing up and down 10 times or briefly vortex mix for 4 seconds. Centrifuge to collect the liquid at the bottom of the tube.

NOTE: For multiple samples, prepare PCR master mix in a 1.5 ml tube by multiplying the volume of each reagent by the number of samples, add extra volumes (overage) to compensate for volume loss due to pipetting. Aliquot 30 µl of the prepared mix in a new 0.2 ml PCR tube/8-well tube strip/96-well plate for each sample.

IMPORTANT: Do not store the PCR master mix for periods of time exceeding 2 hours.

Components	Volume for 1 reaction (µl)
PreCap amplification mix	25
PreCap primer mix	5
Total	30

4. Transfer 20 µl of adapter-ligated and purified sample library to the 30 µl of PCR reaction master mix from step 2 and mix well by pipette mixing up and down 10 times or briefly vortex mixing for 4 seconds. Centrifuge to collect liquid at the bottom of the tube.

5. Transfer the sample to the pre-heated thermocycler (98˚C) and skip to the next step in the program.

6. When the program finishes, and the thermocycler has returned to 4˚C, remove the samples from the cycling block and proceed immediately to library clean-up using Target Pure™ NGS clean-up beads.

Clean-up of amplified library

7. Thoroughly vortex the room temperature equilibrated Target Pure NGS clean-up beads.

8. Add 50 µl of Target Pure NGS clean-up beads to a new 0.2ml PCR tube/8-well tube strip/96-well plate for each sample.

NOTE: DNA clean-up with Target Pure NGS clean-up beads can also be performed in 1.5 ml tubes, as explained in Appendix II.

9. Transfer the entire 50 µl volume of PCR amplified library to the 50 µl of Target Pure NGS clean-up beads and mix well by pipette mixing up and down 15–20 times, taking care to avoid the formation of bubbles.

10. Incubate the mixture for 5 minutes at room temperature.

11. Place the sample on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tubes/wells.

12. Keeping the sample on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

13. Add 200 µl of 80% ethanol to the tube/well and incubate at room temperature for 30 seconds.

14. Repeat steps 12–13 for a total of two 80% ethanol washes.

15. Keeping the sample on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

16. Remove any residual liquid from the tubes/wells using a pipette.

17. Keeping the sample on the magnetic stand, incubate at room temperature with open lids for 3–5 minutes or until the beads are dry.

IMPORTANT: Avoid over-drying of beads, as this can result in a significant loss of DNA recovered. When dry, beads will appear matt in appearance, but should not be cracked.

18. Remove the sample from the magnetic stand and resuspend the dried beads in 32.5 µl of nuclease-free water by pipette mixing up and down 10–15 times, taking care to avoid the formation of bubbles.

19. Incubate the sample for 2 minutes at room temperature.

20. Place the sample on the magnetic stand for 2 minutes at room temperature to pellet the beads on the side of the tubes/wells.

21. Carefully recover 30 µl of supernatant and transfer it to a new 1.5 ml low-bind tube.

STOPPING POINT: At this point, amplified libraries can be stored at 4˚C overnight or at -20˚C for long term storage, if not proceeding immediately to the library quality check step.

1.D Library quality check

Libraries are assessed by determining:

- DNA **quantity** in terms of concentration (ng/µl) and total yield (ng)
- DNA **quality** in terms of expected fragment size distribution and absence of additional lower or higher molecular weight peaks (recommended)

Library DNA quantity

- Libraries prepared from high-purity DNA usually generate more than 500 ng of total DNA yield (ie, more than 16 ng/µl in a volume of 30 µl)
- Use of fluorometric assays for dsDNA (such as the Qubit dsDNA BR assay kit, Invitrogen) is recommended for accurate determination of DNA concentration. If library yield is below the expected parameters, refer to the troubleshooting guide

Library DNA quality

- By ligating dual indexed adapters containing UMIs to DNA fragments, the library preparation procedure adds 144 bp to the fragment length. This can be assessed by analysing libraries with digital electrophoresis systems (such as the Agilent 4200 TapeStation with D1000 reagents and screentape, Agilent Technologies) and determining the peak size within the fragment distribution
- Library yield can also be assessed using a digital electrophoresis system, but the measurement is not as accurate as that obtained with fluorometric assays (such as the Qubit), as it tends to underestimate DNA quantity. However, if the discrepancy between the measurement taken with a fluorometric assay and a digital electrophoresis assay is higher than 50%, then this might indicate PCR over-amplification of the library (refer to the troubleshooting guide to learn about this issue and how to fix it)
- Presence of carried-over adapters, adapter-dimers and primer-dimers can also be observed in the 60–160 bp range (refer to the troubleshooting guide). Note that adapter-dimers are generally removed during probe hybridization and therefore do not affect the targeted enrichment procedure. While this quality control procedure is recommended, it is not mandatory and correct fragment size can be obtained by performing size selection, as explained in Appendix IV. See example below for reference on how to check library quality

The Library Preparation kit V2 (b) enables the preparation of libraries using high molecular weight gDNA. The enzymatic fragmentation procedure included in the kit fragments the DNA to the required fragment length. Libraries successfully prepared using this kit show a single peak in the fragment size distribution graph (see Figure 2, on the next page). Libraries which have not been completely fragmented show a tail of variable size in the long fragment range (see Figure 3). In these cases, refer to the Troubleshooting Guide for further assistance.

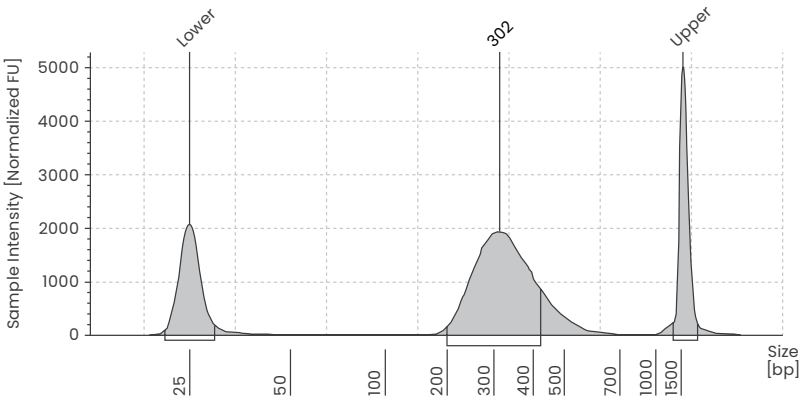

Figure 2. Fragment size distribution of library prepared with 100 ng of input high molecular weight gDNA.

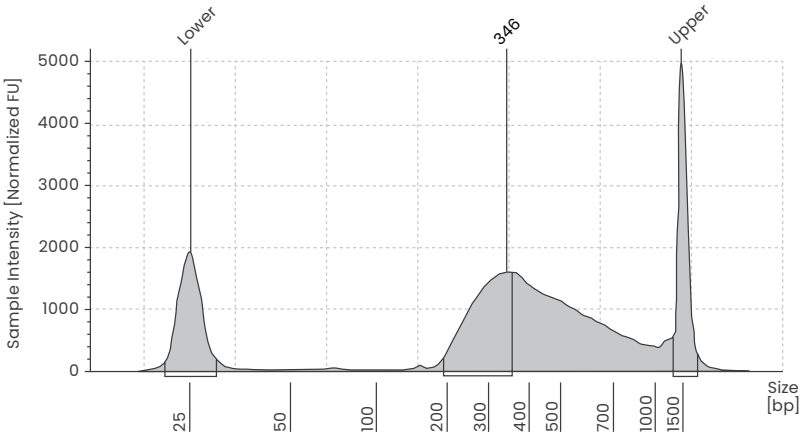

Figure 3. Fragment size distribution of unsuccessful library prepared with 100 ng of input high molecular weight gDNA.

The presence of a tail in the long fragment size range suggests that the sample was not entirely sheared during enzymatic fragmentation.

STOPPING POINT: At this point, amplified libraries can be stored at 4˚C overnight or at -20˚C for long term storage, if not proceeding immediately to hybridization and capture.

Chapter 2: Probe hybridization and capture enrichment

The Hybridization and Capture Enrichment kit V2 enables probe hybridization-based targeted enrichment of sequencing libraries (ie, containing adapters) prepared from gDNA as input material in combination with the GALEAS Hereditary^{Plus} Panel.

2.A Library pooling and probe hybridization

In this step, individual libraries prepared with the Library Preparation kit V2 (b) are pooled together in equal amounts and hybridized with DNA biotin-labelled probes, to enrich for the targeted region of interest.

IMPORTANT: We recommend pooling 8–16 samples per hybridization and capture reaction.
Further considerations are noted below:

- Enough reagents to perform a minimum of 8 libraries per capture are provided. If pooling less than 8 libraries per capture, not all the reactions in the kit will be utilised
- If pooling less than 4 libraries per capture and sequencing the final captured library on a single run (less than 4 libraries in the sequencing run overall), there will be issues with lack of complexity in the indices on Illumina sequencers, resulting in low quality data

For further support, please email us at **support@nonacus.com**.

Before you start

- Switch on a vacuum concentrator and set the temperature to 70˚C or lower. Alternatively, switch on a vacuum lyophiliser/freeze dryer. If this equipment is not available, pooled libraries can be concentrated using Target Pure™ NGS clean-up beads as described in Appendix III
- Thaw the Hybridization Buffer (2×) (blue cap), the Hybridization Enhancer (brown cap), the Universal Blockers (orange cap) and the COT-1 Human DNA (red cap) from the Hybridization and Capture Enrichment kit V2 at room temperature
- Thaw the GALEAS Hereditary^{Plus} Panel capture reactions on ice
- Mix each component vigorously by vortex mixing, then centrifuge to collect the liquid at the bottom of the tube

NOTE: Inspect the Hybridization Buffer (2×) (blue cap) for crystallization of salts. If crystals are present, heat the tube at 65˚C in a heat block and vortex every few minutes until the buffer is completely homogenised (this may require heating for 30–60 minutes).

Procedure

1. Set up the following thermocycler program.

Step	Temperature (˚C)	Time	Cycles
1	95	Hold	1
2	95	30 sec	1
3	65	4–16 hours	1
4	65	Hold	1

NOTE: Set the thermocycler heated lid to 100˚C, the sample volume is 17 µl.

2. If individual sample libraries were frozen, ensure that they are completely thawed and briefly vortex mixed.

3. Pool equal concentrations (in ng) of individual sample libraries into a new 1.5 ml low-bind tube to reach a total combined quantity of 1000 ng.

4. Add 5 µl (equivalent to 5 µg) of COT-1 Human DNA and 2 µl of Universal Blockers to the library pool. Briefly vortex mix and centrifuge to collect the liquid at the bottom of the tube.

5. Place the tube with the lid open in the vacuum concentrator or vacuum lyophiliser/freeze dryer and press start.

NOTE: Depending on the amount of liquid present in the tube, the drying procedure may take from 10 to 60 minutes in a vacuum concentrator; and from 30 to 90 minutes in a vacuum lyophiliser/freeze dryer. Ensure that all liquid has evaporated from the tube before proceeding to the next step.

NOTE: If a vacuum concentrator or vacuum lyophiliser/freeze dryer are not available, pooled libraries can be concentrated using Target Pure™ NGS clean-up beads as described in Appendix III.

STOPPING POINT: At this point, the dried down library pool/COT-1 Human DNA/Universal Blockers can be stored overnight at 4˚C, if not proceeding immediately to probe hybridization and capture enrichment.

6. Prepare the hybridization reaction mix by adding the components in the table below to the 1.5 ml low-bind tube containing the dried-up library pool/COT-1 Human DNA/Universal Blockers.

Components	Volume for 1 reaction (µl)
Hybridization buffer (2×)	8.5
Hybridization enhancer	2.7
GALEAS Hereditary^{Plus} panel	4
Nuclease-free water	1.8
Total	17

7. Gently pipette mix up and down 10 times, then briefly centrifuge to ensure the liquid is collected at the bottom of the tube and incubate at room temperature for 10 minutes.

8. Transfer the whole volume of hybridization reaction mix to a 0.2 ml PCR tube and briefly centrifuge to ensure that the liquid is collected at the bottom of the tube.

9. Place the 0.2 ml PCR tube containing the hybridization reaction mix in the pre-heated thermocycler (95˚C) and skip to the next step in the program.

10. Leave the hybridization reaction mix at 65˚C on the thermocycler to incubate for 4 hours.

NOTE: Alternatively, and if it aids the efficiency of the workflow, the hybridization reaction can be incubated for 16 hours or overnight. This may improve performance for GC-rich or small panels (less than 100 kb in size).

2.B Probe capture on Streptavidin beads and washes

Biotin-labelled probes hybridized to their DNA targets are captured on streptavidin-coated beads. The beads are then washed multiple times to remove non-targeted DNA.

Before you start

- Equilibrate the Dynabeads™ M-270 Streptavidin to room temperature for 30 minutes for use in step 6
- Thaw the Stringent Wash Buffer (10×) (white cap, S), the Wash Buffer 1 (10×) (white cap, 1), the Wash Buffer 2 (10×) (white cap, 2), the Wash Buffer 3 (10×) (white cap, 3) and the Bead Wash Buffer (2×) (white cap, B) from the Hybridization and Capture Enrichment kit V2 at room temperature
- Thoroughly vortex mix and centrifuge in a microcentrifuge to collect the liquid at the bottom of the tube
- Set a thermocycler to 65˚C on hold with the heated lid set at 70˚C in advance to prepare for steps 18 onwards

NOTE: If necessary, heat the Wash Buffer 1 (10×) at 65˚C in a heat block to completely resuspend precipitated particles.

NOTE: Dynabeads M-270 Streptavidin washes can also be performed in a 1.5 ml tube using a magnetic stand capable of accommodating 1.5–2 ml tubes, as outlined in Appendix II. In this case, turn on a heat block and set to 65˚C.

Preparation of wash buffers

1. Dilute the following components for each capture reaction to prepare a 1× working solution in 1.5 ml tubes, as indicated in the table below. For multiple samples, prepare the buffers by multiplying the volume of each reagent by the number of samples, add extra volume (overage) to compensate for pipetting loss.

Components	Stock solution (µl)	Nuclease-free water (µl)	Total (µl)
Stringent wash buffer (10×)	40	360	400
Wash buffer 1 (10×)	30	270	300
Wash buffer 2 (10×)	20	180	200
Wash buffer 3 (10×)	20	180	200
Bead wash buffer (2×)	250	250	500

2. Mix each diluted component thoroughly by vortex mixing and centrifuge to collect liquid at the bottom of the tube.

3. Transfer 100 µl of 1× Wash Buffer 1 into a fresh 0.2 ml PCR tube and pre-heat it in a thermocycler at 65˚C for at least 15 minutes before use.

4. Split the 1× Stringent Wash Buffer into two 0.2 ml PCR tubes, transferring 200 µl in each tube, and pre-heat both aliquots in a thermocycler at 65˚C for at least 15 minutes.

NOTE: Both the 100 µl aliquot of 1× Wash Buffer 1 and the two 200 µl aliquots of 1× Stringent Wash Buffer can be pre-heated on the same thermocycler where the hybridization reaction is taking place.

5. Store the 200 µl of 1× Wash Buffer 1 and the remaining 1× wash buffers at room temperature until needed.

Preparation of Dynabeads™ M-270 Streptavidin

6. After equilibration at room temperature, mix the Dynabeads M-270 Streptavidin thoroughly by vortex mixing for 15 seconds.

7. Aliquot 50 µl of Dynabeads M-270 Streptavidin per capture reaction into a fresh 1.5 ml tube.

NOTE: If preparing more than one capture reaction, up to 300 µl of Dynabeads M-270 Streptavidin can be aliquoted into a single 1.5 ml tube for bead preparation.

8. Place the 1.5 ml tube in a magnetic stand and incubate 20–30 seconds until all beads have separated from the supernatant and have pelleted on the side of the tube.

9. Carefully remove and discard the supernatant, taking care not to disturb the bead pellet.

10. Add 200 µl of 1× Bead Wash Buffer per capture reaction, remove the tube from the magnetic stand and vortex for 10 seconds.

11. Repeat steps 8–10 once more for a total of two washes.

12. Place the 1.5 ml tube in a magnetic stand and incubate 20–30 seconds until all beads have separated from the supernatant and have pelleted on the side of the tube.

13. Carefully remove and discard the supernatant, taking care not to disturb the bead pellet.

14. Add 100 µl of 1× Bead Wash Buffer per capture reaction, remove the tube from the magnetic stand and vortex briefly.

15. Transfer 100 µl of resuspended beads into a new 0.2 ml PCR tube/8-well tube strip for each capture reaction.

NOTE: At this stage, Dynabeads M-270 Streptavidin resuspended in 100 µl of Bead Wash Buffer can be transferred to a 1.5 ml tube to conduct bead capture and washes on a magnetic stand capable of accommodating 1.5–2 ml tubes, as explained in Appendix II.

NOTE: Washed Dynabeads M-270 Streptavidin can be kept in solution at room temperature. Proceed to the next step only when the hybridization (section 2.A, step 10) incubation ends.

Procedure

16. Set a thermocycler at 65˚C on hold with the heated lid set at 70˚C (If not already completed at the start of the procedure).

IMPORTANT: It is important that the heated lid is set to 70˚C during the washes of Dynabeads M-270 Streptavidin post-capture. Ensure that the hybridization reaction is kept at 65˚C throughout the hybridization, capture and washes with 1× Stringent Wash Buffer steps to avoid unspecific binding of non-target DNA to the probes.

17. Place the tube on a magnetic stand and incubate for 1–2 minutes until all beads have separated from the supernatant and have pelleted on the side of the tube/well.

18. Carefully remove and discard the supernatant, taking care not to disturb the bead pellet, and proceed immediately to the next step.

NOTE: Small amounts of residual 1× Bead Wash Buffer will not interfere with downstream binding of the biotin-labelled probes to the Dynabeads™ M-270 Streptavidin.

19. Transfer the 0.2 ml PCR tube/8-well tube strip containing pelleted Dynabeads M-270 Streptavidin adjacent to the thermocycler set to 65˚C (with the heated lid set to 70˚C).

20. Immediately transfer the whole amount of hybridization reaction mix on the thermocycler (from section 2.A, step 10) to the 0.2 ml PCR tube/8-well tube strip containing the pelleted Dynabeads M-270 Streptavidin. Pipette mix the Dynabeads and hybridization reaction mix up and down 10 times on the thermocycler.

21. Incubate the hybridization reaction mix with the Dynabeads M-270 Streptavidin on the thermocycler for 45 minutes.

NOTE: At this stage, if bead capture and washes are conducted in 1.5–2 ml tubes, incubate the Dynabeads M-270 Streptavidin mixed with the hybridization reaction mix in a heat block set at 65˚C, as explained in Appendix II.

22. Every 12 minutes during the 45 minute incubation at 65˚C, carefully pipette mix whilst on the thermocycler. If it's not possible to pipette mix on the thermocycler, briefly vortex mix on a low speed to avoid splashing, for 3 seconds, to ensure the beads remain suspended in solution and then place back on the thermocycler.

23. Remove the reaction from the thermocycler and add 100 µl of pre-heated 1× Wash Buffer 1 (from step 3).

24. Pipette mix up and down 10 times and place the reaction on a magnetic stand for to allow the beads to separate from the supernatant and pellet on the side of the tube/well, this should happen within 2–5 seconds.

25. Once the liquid is clear, immediately remove the supernatant, taking care not to disturb the bead pellet. Remove the reaction from the magnetic stand and add 200 µl of pre-heated 1× Stringent Wash Buffer (from step 4).

26. Mix well by pipette mixing up and down 10 times, taking care to avoid the formation of bubbles.

27. Transfer the reaction to a thermocycler set to 65˚C (with the heated lid set to 70˚C) and incubate for 5 minutes.

28. After incubation, remove the reaction from the thermocycler and place on a magnetic stand to allow beads to separate from supernatant and pellet on the side of the tube/well. As soon as the liquid is clear, remove the supernatant, this should happen within 2–5 seconds from placing samples on the magnet.

29. Repeat steps 25–28 for a total of two washes with pre-heated 1× Stringent Wash Buffer.

30. As soon as steps 25–29 are complete, immediately remove the supernatant, taking care not to disturb the bead pellet.

31. Remove the reaction from the magnetic stand and add 200 µl of room temperature 1× Wash Buffer 1.

32. Vortex mix thoroughly for 2 minutes and briefly centrifuge to collect the liquid at the bottom of the tube.

33. Place the reaction on a magnetic stand for 20–30 seconds to allow the beads to separate from the supernatant and pellet on the side of the tube/well.

34. Carefully remove the supernatant, taking care not to disturb the bead pellet.

35. Remove the reaction from the magnetic stand and add 200 µl of room temperature 1× Wash Buffer 2.

36. Vortex mix thoroughly for 1 minute and briefly centrifuge to collect the liquid at the bottom of the tube.

37. Place the reaction on a magnetic stand for 20–30 seconds to allow the beads to separate from the supernatant and pellet on the side of the tube/well.

38. Carefully remove the supernatant, taking care not to disturb the bead pellet.

39. Remove the reaction from the magnetic stand and add 200 µl of room temperature 1× Wash Buffer 3.

40. Vortex mix thoroughly for 30 seconds and briefly centrifuge to collect the liquid at the bottom of the tube.

41. Place the reaction on a magnetic stand for 1–2 minutes to allow the beads to separate from the supernatant and pellet on the side of the tube/well.

42. Carefully remove the supernatant, taking care not to disturb the bead pellet.

43. Remove the reaction from the magnetic stand and resuspend the bead pellet in 24 µl of nuclease-free water by pipette mixing up and down 10–15 times.

2.C Captured library amplification and clean-up

Targeted library DNA sequences hybridized to the biotin-labelled probes and captured on Dynabeads™ M-270 Streptavidin are amplified by PCR using primers that specifically bind to the P5-P7 sequences on Illumina adapters. Target Pure™ NGS clean-up beads are then used to clean-up the amplified captured library.

Before you start

- Thaw the PostCap Amplification Mix (green cap) and the PostCap Primer Mix (**black** cap) from the Hybridization and Capture Enrichment kit V2 on ice
- Once thawed, lightly flick the containing the PostCap Amplification Mix to ensure adequate mixing of the reagent **(do not vortex)**
- Briefly vortex mix the PostCap Primer Mix
- Centrifuge to collect the liquid at the bottom of the tubes. Keep both tubes on ice for the whole procedure
- Equilibrate the Target Pure NGS clean-up beads to room temperature for 20–30 minutes (for use in step 6) and prepare a solution of 80% Ethanol (500 µl required per capture reaction including overage, for use in step 11)

Procedure

1. Set up the following thermocycler program.

Step	Temperature (˚C)	Time	Cycles
1	98	Hold	1
2	98	45 sec	1
3	98	15 sec	12
4	60	30 sec	
5	72	30 sec	
6	72	1 min	1
7	4	Hold	1

NOTE: Set the thermocycler heated lid to 105˚C, the sample volume is 50 µl.

2. Prepare the PCR reaction mix in a new 1.5 ml tube on ice. For each capture reaction, prepare one PCR reaction mix in a 0.2 ml PCR tubes/8-well tube strip as indicated in the table below.

3. Mix thoroughly by pipetting up and down 10 times or briefly vortex, then centrifuge to collect liquid at the bottom of the tube.

NOTE: For multiple samples, prepare the PCR master mix in a 1.5 ml tube by multiplying the volume of each reagent by the number of capture reactions, add extra volume (overage) to compensate for pipetting loss.

Components	Volume for 1 reaction (µl)
PostCap amplification mix	25
PostCap primer mix	2.5
Total	27.5

IMPORTANT: Do not store the PCR master mix for periods of time exceeding 2 hours.

4. Transfer 22.5 µl of resuspended Dynabeads™ M-270 Streptavidin with captured library DNA (from section 2.B, step 42) to the 27.5 µl of PCR reaction master mix from step 2 and mix well by pipette mixing up and down 10–15 times.

5. Transfer the reaction to the pre-heated thermocycler (98˚C) and skip to the next step in the program.

6. When the program finishes, and the thermocycler has returned to 4˚C, remove the samples from the cycling block and proceed immediately to library clean-up using Target Pure™ NGS clean-up beads.

Clean-up of amplified captured library

7. Thoroughly vortex the room temperature equilibrated Target Pure NGS clean-up beads.

8. Add 75 µl of thoroughly vortexed room-temperature equilibrated Target Pure NGS clean-up beads to a new 0.2 ml PCR tube/8-well tube strip for each captured library.

NOTE: DNA clean-up with Target Pure NGS clean-up beads can also be performed in 1.5 ml tubes, as explained in Appendix II.

9. Transfer the entire 50 µl of PCR product for each captured library to the 75 µl of Target Pure NGS clean-up beads and mix well by pipette mixing up and down 15–20 times, taking care to avoid the formation of bubbles.

10. Incubate the mixture for 5 minutes at room temperature.

11. Place the reaction on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tubes/wells.

12. Keeping the reaction on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

13. Add 200 µl of 80% ethanol to the tube/well and incubate at room temperature for 30 seconds.

14. Repeat steps 12–13 for a total of two 80% ethanol washes.

15. Keeping the reaction on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

16. Remove any residual liquid from the tubes/wells using a pipette.

17. Keeping the reaction on the magnetic stand, incubate at room temperature with open lids for 3–5 minutes or until the beads are dry.

IMPORTANT: Avoid over-drying of beads, as this can result in a significant loss of DNA recovered. When dry, beads will appear matt in appearance, but should not be cracked.

18. Remove the reaction from the magnetic stand and resuspend the dried beads in 32.5 µl of Buffer EB or equivalent buffer saline solution (10 mM Tris-HCl, ph8.0) by pipette mixing up and down 10–15 times, taking care to avoid the formation of bubbles.

19. Incubate the reaction for 2 minutes at room temperature.

20. Place the reaction on the magnetic stand for 2 minutes at room temperature to pellet the beads on the side of the tube/well.

21. Carefully recover 30 µl of supernatant and transfer it to a fresh 1.5 ml low-bind tube.

STOPPING POINT: At this point, the captured DNA library can be stored at -20˚C, if not proceeding immediately to the library quality check step.

2.D Captured library quality check

Libraries are assessed by determining:

- DNA **quantity** in terms of concentration (ng/µl) and total yield (ng)
- DNA **quality** in terms of expected fragment size distribution and absence of additional lower or higher molecular weight peaks

Captured library DNA quantity

- Captured libraries should yield 60–300 ng of total DNA. Use of high sensitivity fluorometric assays for dsDNA (such as the Qubit dsDNA HS assay kit, Invitrogen) is recommended for accurate determination of DNA concentration. If libraries yield less than 60 ng or greater than 300 ng in total, refer to the troubleshooting guide

Captured library DNA quantification by quantitative PCR (Optional)

- Quantitative PCR (qPCR) is widely regarded as the most accurate way of measuring library concentration
- This assumption is based on the principle that only DNA fragments correctly ligated with the Illumina P5 and P7 adapters will amplify in the qPCR reaction and will therefore be quantified. Therefore, the calculated DNA concentration is relevant only to the fraction of properly adapted DNA fragments which can be sequenced
- Library quantification kits by qPCR are commercially available, such as the KAPA Library Quantification – Illumina/Universal kit (Roche). To ensure an accurate measurement of library DNA concentration when using these kits, follow the manufacturer's guidelines and use a 1:10,000–1:40,000 dilution of the captured library as input material

Captured library DNA quality

- A high sensitivity digital electrophoresis system (such as the Agilent 4200 TapeStation with High Sensitivity D1000 reagents and screentape, Agilent Technologies) should be used to determine the peak size within the fragment distribution and the average fragment size. The latter is required to calculate the molar concentration of the captured library, which is essential for final library dilution and preparation for sequencing. See examples of captured libraries below for reference

Library obtained after targeted enrichment with the GALEAS Hereditary^{Plus} Panel and Hybridization and Capture Enrichment kit V2.

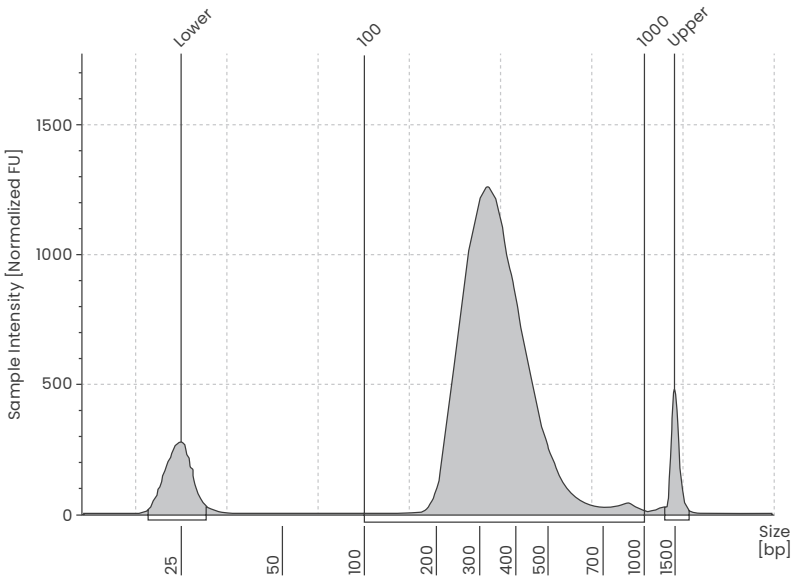

Figure 4. Fragment size distribution showing the range of 100–1000 bp within which the average fragment size is calculated. Average fragment size: 355 bp.

Chapter 3: Sequencing of captured libraries

Libraries enriched by targeted capture using GALEAS Hereditary^{Plus} kit Target technology are ready for sequencing on Illumina platforms (such as NextSeq, HiSeq and NovaSeq instruments).

3.A Calculate captured library molar concentration

An accurate molar concentration can be calculated in the following ways:

- In combination with fluorometric assay reading: use the following formula to calculate molarity

$$\text{concentration in nM} = \frac{\text{concentration in ng/ul}}{\left(660 \frac{9}{\text{mol}} \times \text{average library size in bp}\right)} \times 10^6$$

- In combination with the KAPA Library Quantification–Illumina/Universal kit or equivalent: insert the average fragment size in bp into the required field of the KAPA Library Quantification Data Analysis worksheet (or equivalent from other supplier) to determine library molar concentration

3.B Choice of Illumina sequencing platform and kit size

- GALEAS Hereditary^{Plus} kit Target technology is compatible with a range of Illumina sequencers, including MiSeq, MiniSeq, and larger Illumina platforms. The recommended cycling parameters for libraries are, 2 × 100 or 2 × 150 given that the average fragment length is 180–300 bp. Irrespective of the cycling parameters chosen, the GALEAS Hereditary^{Plus} kit Target technology requires paired end sequencing with dual indexing to be performed. The latter is necessary for sample de-multiplexing and requires 16 sequencing cycles (8 for i7 index/barcode sequencing + 8 for i5 index sequencing)
- The use of UMIs is **not** required for GALEAS Hereditary^{Plus} bioinformatics analysis. However, should UMIs be required for alternative types of analysis, then 25 sequencing cycles will be needed (17 for i7 index/barcode sequencing + 8 for i5 index sequencing)
- In every Illumina sequencing kit, a certain quantity of reagent excess is provided to allow for sequencing of indexes. However, the amount of excess reagents vary between kit sizes, so it is important to be aware of the maximum number of sequencing cycles which can be performed for the selected sequencing kit
- Appendix V, Table 1, outlines available kit sizes for each compatible Illumina platform; the excess number of cycles included, and the maximum sequencing read length which can be selected when using GALEAS technology in combination with the Illumina UMI Adapters–96 reactions format

3.C Prepare captured library for Illumina sequencing

- To obtain optimal results and call germline alterations robustly at 100× average depth of coverage, it is recommended that each sample be sequenced to achieve 0.2 Gb of data, or 1 million reads using 2 × 100 bp paired end sequencing. To obtain optimal CNV alteration calling we would recommend each sample be sequenced to achieve 0.4 Gb of data, or 2 million reads using 2 × 100 bp paired end sequencing. On this basis, select the Illumina platform and flow cell that will enable desired throughput at these conditions
- Following Illumina guidelines for the chosen sequencing platform, denature and dilute the captured library to the recommended concentration and load onto the cartridge. Primers for sequencing are included in Illumina sequencing reagents and no additional custom sequencing primers are required

Troubleshooting guide

The following guide is meant to address the most common issues which might arise during library preparation and targeted capture enrichment. For further guidance, please contact us at **support@nonacus.com**.

A) Individual sample library yield less than 500 ng

- Library preparation reaction setup should be conducted on ice, in order to ensure that enzymatic activity does not start before all components have been added to the reaction mix
- After thawing, all components should be thoroughly vortex mixed or tubes tapped for enzyme mixes, (as indicated in the protocol) to ensure that salts and/or enzymes are homogenously mixed and in solution
- Prior to incubation, all reaction mixes should be thoroughly vortex mixed or pipette mixed (as indicated in the protocol) to ensure maximum enzymatic activity
- The number of cycles in the pre-capture PCR amplification step may need to be optimized. Repeat the library preparation procedure increasing the number of cycles by 1 or 2
- Ensure that Target Pure™ NGS clean-up beads have been equilibrated at room temperature for 20–30 minutes prior to use, as the beads DNA binding capacity is reduced at low temperatures
- During bead clean-up steps, 80% ethanol solution should be prepared fresh on the same day, as evaporation of ethanol over time can increase the water fraction and cause elution of DNA from the Target Pure NGS clean-up beads during washes
- Over-drying of bead pellet during bead clean-up can significantly reduce DNA recovery in eluate. After drying beads at room temperature for 5 minutes, inspect the bead pellet frequently to ensure it does not over-dry. Bead pellets that show signs of cracking have been dried for too long, beads should matt in appearance

B) Larger than expected fragment size in individual sample library from gDNA input

- Optimize fragmentation time. Find the optimal fragmentation parameters by increasing the fragmentation time by intervals of 5 minutes
- If the DNA sample is kept in buffer containing more than 0.1 mM EDTA, use a bead or column clean-up procedure and elute the DNA sample in nuclease-free water or a 10 mM Tris-HCl, pH 8.0 solution (such as Buffer EB, Qiagen), then repeat the library preparation procedure

C) Discrepancy between Qubit and Tapestation measured sample library yield

- The sample library may have been over-amplified
- When a considerable discrepancy between Qubit and digital electrophoresis measurement of sample library yield is observed, this may be due to an excess in PCR cycles post-ligation. This causes the formation of a secondary population of fragments of around 800–900 bp in length which is often difficult to notice on a Tapestation D1000 screentape electropherogram or a Bioanalyser 7500 assay but becomes apparent on a genomic DNA screentape electropherogram or a Bioanalyser High Sensitivity assay
- Sample library over-amplification does not have a negative impact on the yield of viable DNA fragments used in the hybridization and capture stage, as the secondary peak is caused by fragments containing different insert sequences which hybridize at the adapter sequences, thus creating a “bubble” in the fragment which causes it to migrate slower during electrophoresis. However, this causes under-estimation of the sample library yield by Qubit and digital electrophoresis methods, which will impact on the amount of sample library pooled in the hybridization reaction. Reducing the number of PCR cycles post-ligation will solve the issue

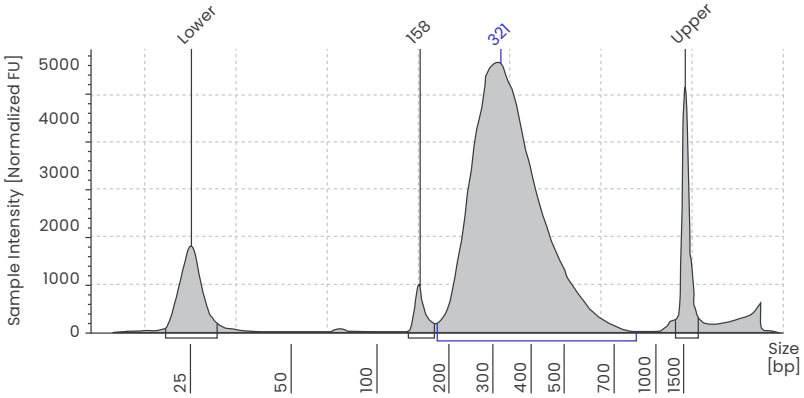

Figure 5. D1000 screentape electropherogram of a sample library prepared from 10 ng input gDNA and amplified for 8 cycles in the post-ligation PCR.

D) Low molecular weight peaks present in individual sample library

- A low molecular weight peak of 150–160 bp in size indicates the presence of adapter-dimers carried over from the adapter ligation reaction. Adapter-dimers are generally lost during the targeted capture enrichment procedure and therefore will not affect downstream processes. If individual sample libraries are used for whole genome sequencing, large quantities of adapter-dimers may affect sequencing yield by sequestering space on the flow cell. Perform a size selection clean-up using SPRI-purification to remove adapter-dimers. Small quantities of adapter-dimers do not significantly affect downstream sequencing
- Make sure that the right quantity of adapters is used according to DNA input quantity. Excess amount of adapters increases the formation of adapter-dimers. Refer to the adapter concentration adjustment based on DNA input guidelines in section 1.B
- Make sure that the correct amount of Target Pure™ NGS clean-up beads is used in the clean-up of amplified library step (see section 1.C). Use of a higher bead to sample volume ratio leads to the additional purification of smaller DNA fragments, such as adapters and adapter-dimers from the ligation reaction step (see section 1.B); and primer-dimers from the library amplification step (see section 1.C)

E) Captured library yield is lower than expected

- PCR cycle number in post-capture amplification may require optimization. Increase the cycle number by 1 or 2 cycles
- Ensure that individual sample libraries are eluted in nuclease-free water and not in saline solutions, such as Buffer EB or TE, during the clean-up of amplified library step (section 1.C). Use of saline buffers to elute library DNA at this stage may interfere with probe hybridization (see section 2.A)
- Follow protocol recommendations when capturing hybridized probes to Dynabeads™ M-270 Streptavidin and target DNA to Target Pure NGS clean-up beads. Make sure that Dynabeads M-270 Streptavidin are equilibrated to room temperature for 20–30 minutes prior to use, as the biotin binding capacity is reduced at low temperatures. Ensure that target DNA clean-up using Target Pure NGS clean-up beads is conducted as recommended in the protocol (see relevant tips for DNA clean-up outlined in section A of the troubleshooting guide)

F) Low molecular weight peaks present in the captured library

- A low molecular weight peak of 150–160 bp in size indicates the presence of adapter-dimers, which are formed during the ligation reaction step in the library preparation procedure (see section 1.B). Adapter dimers should not hybridize to the probes and therefore are usually removed during the probe capture step (see section 2.B). Make sure 1× Wash Buffer 1 and 1× Stringent Wash Buffer are pre-heated at 65˚C prior to use in steps 21–28 in section 2.B; and that these steps are performed as quickly as possible to ensure that the capture reaction does not considerably cool down below 65˚C. This is to ensure the removal of non-hybridized DNA fragments, including adapter-dimers
- Make sure that the correct amount of Target Pure™ NGS clean-up beads is used in the clean-up of amplified captured library step (see section 2.C), as explained in section D of the troubleshooting guide

Appendix

The following information is intended to help users with the technical procedures described in this guide. For further support, please email us at **support@nonacus.com**.

I. Fragmentation protocol to achieve alternative size of the inserts

Enzymatic DNA fragmentation is influenced by reaction time, temperature and quantity of input DNA. In order to obtain alternative length of the insert, the fragmentation temperature and time can be altered. Fragmentation may be performed at 30˚C or 37˚C. Additionally, the time of the fragmentation can be adjusted based on the required insert length. We highly recommend optimizing the reaction time by using the same DNA sample or very similar samples and to start with multiple timepoints. Choose the initial fragmentation time and temperature appropriate for required length using the below tables as a guideline.

Fragment size				
250 bp	**300 bp**	**350 bp**	**400 bp**	**550 bp**
15	10	5	4	3
Fragmentation time at 30˚C (min)				

Fragment size			
300 bp	**250 bp**	**200 bp**	**150 bp**
5	10	20	30
Fragmentation time at 37˚C (min)			

NOTE: The table above should only be used as a guideline for optimization of fragmentation time in order to achieve the required insert size.

1. Set up the following thermocycler program.

Step	Temperature (˚C)	Time
1	4	Hold
2	30 or 37*	3–30 min*
3	65	30 min
4	4	Hold

*Fragmentation time and temperature as determined above.

NOTE: Set the thermocycler heated lid to 105˚C, the sample volume is 50 µl.

2. Prepare the DNA sample in a total volume of 40 µl (according to the input amount). Use nuclease-free water to dilute the DNA, if required. Make sure to keep the reaction on ice during the whole procedure.

3. Prepare the following reaction mix for each DNA sample indicated in the following table. Vortex thoroughly to ensure appropriate mixing is achieved without formation of bubbles and briefly centrifuge.

Components	Volume for 1 reaction (µl)
Fragmentation buffer	4
Fragmentation enzyme mix	6
DNA sample	X
Nuclease-free water	(40–X)
Total	50

NOTE: When processing multiple samples, combine Fragmentation Buffer and Enzyme into a master mix with 10% overage for consistent 10 µl additions to 40 µl DNA. Vortex 5 seconds at moderate speed to mix without bubbles.

4. Add 10 µl of prepared End-repair/A-tailing reaction mix to each reaction for a total final volume of 50 µl. Mix thoroughly by vortex mixing and briefly centrifuge to collect the liquid at the bottom of the tube.

5. Immediately transfer the sample to the pre-chilled thermocycler (4˚C) and "skip" to the next step in the program.

6. When the program finishes, and the thermocycler has returned to 4˚C, remove the samples from the cycling block and place on ice. Immediately proceed to the ligation step (1.C).

II. Alternative procedure for magnetic bead clean-up steps

- All handling of magnetic beads described in this protocol (ie, Dynabeads™ M-270 Streptavidin and Target Pure™ NGS clean-up beads) requires the use of a magnetic rack capable of accommodating 0.2 ml PCR tubes, 8-well tube strips or 96-well plates
- Alternatively, all clean-up steps performed with Target Pure NGS clean-up beads (see sections 1.B, 1.C and 2.C) and Dynabeads M-270 Streptavidin capture and bead washes (see section 2.B) can be performed in 1.5 ml tubes on a magnetic rack capable of accommodating 1.5–2 ml tubes
- For Dynabeads M-270 Streptavidin capture and washes at 65˚C, set a heat block at 65˚C and incubate for 45 minutes for capture (see section 2.B, step 21); and for 5 minutes for washes (see section 2.B, step 28). Centrifuge the 1.5–2 ml tube containing the Dynabeads M-270 Streptavidin before vortex mixing during capture (see section 2.B, 22) to ensure that any condensation present on the cap is recovered at the bottom of the tube. After each 5-minute incubation of the Dynabeads M-270 Streptavidin during washes with Stringent Wash Buffer (see section 2.B, 26), centrifuge the 1.5–2ml tube to ensure that any condensation present on the cap is recovered at the bottom of the tube

III. Alternative procedure for concentrating pooled sample libraries prior to hybridization using Target Pure™ NGS clean-up beads

If a vacuum concentrator or vacuum lyophiliser/freeze dryer are not available for use, pooled sample libraries can be concentrated using Target Pure NGS clean-up beads. However, please note that this procedure does introduce a minor GC bias.

Before you start

- Equilibrate the Target Pure NGS clean-up beads to room temperature for 20–30 minutes (for use in step 4) and prepare a solution of 80% Ethanol (400 µl required per capture reaction, for use in step 8)

Proceeding from section 2.A, step 2:

1. Prepare the hybridization reaction mix (for use in step 13 below) in a new 1.5 ml tube as indicated in the table below.

Components	Volume for 1 reaction (µl)
Hybridization buffer (2×)	9.5
Hybridization enhancer	3
Universal blockers	2
GALEAS Hereditary^{Plus} Panel	4.5
Total	19

2. Pool equal concentrations (in ng) of individual sample libraries into a fresh 1.5 ml low-bind tube to reach a total combined quantity of 1000 ng.

3. Add 7.5 µl (equivalent to 7.5 µg) of COT-1 Human DNA to the library pool. Briefly vortex mix and centrifuge in a microcentrifuge to collect the liquid at the bottom of the tube.

4. Add 1.8× volume of Target Pure NGS clean-up beads and mix thoroughly by pipette mixing 15–20 times, taking care to avoid the formation of bubbles.

5. Incubate the mixture for 10 minutes at room temperature.

6. Place the tube on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tube.

7. Keeping the tube on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

8. Add enough volume of ethanol to ensure the bead pellet is fully submerged, then incubate at room temperature for 30 seconds.

9. Repeat steps 7–8 for a total of two 80% ethanol washes.

10. Keeping the tube on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

11. Remove any residual liquid from the tubes/wells using a pipette.

12. Keeping the reaction on the magnetic stand, incubate at room temperature with open lids for 5 minutes or until the beads are dry.

IMPORTANT: Avoid over-drying of beads, as this can result in a significant loss of DNA recovered. When dry, beads will appear matt in appearance, but should not be cracked.

13. Remove the reaction from the magnetic stand and resuspend the dried beads in 19 µl of hybridization reaction mix.

14. Incubate the reaction for 5 minutes at room temperature.

15. Place the reaction on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tubes/wells.

16. Carefully recover 17 µl of supernatant and transfer it to a fresh 0.2 ml PCR tube/8-well tube strip/96-well plate.

NOTE: Make sure to avoid bead carryover during the transfer process.

17. Place the 0.2 ml PCR tube/8-well tube strip/96-well plate containing the hybridization mix into the pre-heated (95˚C) thermocycler and skip to the next step on the program.

18. Incubate for 4 hours until the thermocycler program reaches the hold step.

NOTE: For GC-rich or small panels (less than 100 kb in size), longer hybridization times (up to 16 hours) may improve performance.

19. Proceed to section 2.B in the protocol.

IV. Size selection protocol

- If the fragment length in sample libraries is not assessed by digital electrophoresis (see chapter 1.D) after library amplification, then a size selection step should be performed instead of a standard clean-up (in chapter 1.C) to ensure that libraries only contain fragments within the required length range
- Depending on the selected fragment length chosen during library preparation of genomic DNA (independently on whether this is achieved through mechanical shearing or the use of the Library Preparation kit V2 (b), the fragment length range may vary
- The following protocol explains how to perform size selection and lists the amount of beads needed to obtain determined ranges of fragment lengths

1. Depending on the selected library size, use the following bead-to-sample ratios:
   - 250–450 bp library fragment length: use a 0.6×–0.9× bead ratio
   - 300–750 bp library fragment length: use a 0.5×–0.8× bead ratio
2. After library amplification (chapter 1.C, step 5), perform the first size cut by adding the following quantity of Target Pure NGS clean-up beads to a fresh 0.2 ml PCR tube/8-well tube strip/96-well plate for each sample:
   - When using the 0.6×–0.9× bead ratio, add 30 µl of beads
   - When using the 0.5×–0.8× bead ratio, add 25 µl of beads
3. Transfer the whole 50 µl of PCR amplified library to the 25–30 µl of Target Pure™ NGS clean-up beads and mix well by pipetting up and down 15–20 times, taking care to avoid the formation of bubbles.
4. Incubate the mixture for 5 minutes at room temperature.
5. Place the reaction on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tubes/wells.
6. Keeping the reaction on the magnetic stand, slowly recover the supernatan (taking care not to disturb the pelleted beads) and transfer it to a fresh 0.2 ml tube/8-well tube strip/96-well plate.
7. Discard the 0.2 ml PCR tube/8-well tube strip/96-well plate containing the beads to which the larger library fragments are bound.
8. Perform the second size cut by adding 15 µl of Target Pure NGS clean-up beads to the recovered supernatant of each sample and mix well by pipette mixing up and down 15–20 times, taking care to avoid the formation of bubbles.
9. Incubate the mixture for 5 minutes at room temperature.
10. Place the reaction on the magnetic stand for 5 minutes at room temperature to pellet the beads on the side of the tubes/wells.
11. Keeping the reaction on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

12. Add 200 µl of 80% ethanol to the tube/well and incubate at room temperature for 30 seconds.

13. Repeat steps 11–12 for a total of two 80% ethanol washes.

14. Keeping the reaction on the magnetic stand, slowly remove and discard the supernatant, taking care not to disturb the pelleted beads.

15. Remove any residual liquid from the tubes/wells using a pipette.

16. Keeping the reaction on the magnetic stand, incubate at room temperature with open lids for 3–5 minutes or until the beads are dry.

IMPORTANT: Avoid over-drying of beads, as this can result in a significant loss of DNA recovered. When dry, beads will appear matt in appearance, but should not be cracked.

17. Remove the reaction from the magnetic stand and resuspend the dried beads in 32.5 µl of nuclease-free water by pipetting up and down 10–15 times, taking care to avoid the formation of bubbles.

18. Incubate the reaction for 2 minutes at room temperature.

19. Place the reaction on the magnetic stand for 2 minutes at room temperature to pellet the beads on the side of the tubes/wells.

20. Carefully recover 30 µl of supernatant and transfer it to a fresh 1.5 ml low-bind tube.

V. Illumina sequencing platforms and kit sizes

Table 1. Breakdown of kit sizes, excess cycles provided and maximum number of cycles usable for Illumina sequencing platforms when using GALEAS Target technology in combination with the Illumina UMI Adapters.

Reagent type	Kit size	Excess cycles provided	Max number of cycles	GALEAS Target dual indexing cycles	Max usable sequencing cycles
MiniSeq	100	28	128	25	2 × 51
	75	17	92	25	2 × 33
	150	18	168	25	2 × 71
	300	18	318	25	2 × 146
MiSeq V2	50	29	79	25	2 × 27
	300	29	329	25	2 × 152
	500	29	529	25	2 × 252
MiSeq V3	150	29	179	25	2 × 77
	600	29	629	25	2 × 302
NextSeq 500/550 V2	75	17	92	25	2 × 33
	150	18	168	25	2 × 71
	300	18	318	25	2 × 146
HiSeq TruSeq SBS V3	50	8	58	25	2 × 16
	200	9	209	25	2 × 92
HiSeq TruSeq SBS V4	50	29	79	25	2 × 27
	250	29	279	25	2 × 127
HiSeq Rapid SBS V2	50	29	79	25	2 × 27
	200	29	229	25	2 × 102
	500	29	529	25	2 × 252
HiSeq 3000/4000 SBS	50	29	79	25	2 × 27
	150	29	179	25	2 × 77
	300	29	329	25	2 × 152
NextSeq 1000/2000 P1	100	38	138	25	2 × 56
	300	38	338	25	2 × 156
	600	38	638	25	2 × 306
NextSeq 1000/2000 P2	100	38	138	25	2 × 56
	200	38	238	25	2 × 106
	300	38	338	25	2 × 156
NextSeq 1000/2000 P3	50	38	88	25	2 × 31
	100	38	138	25	2 × 56
	200	38	238	25	2 × 106
	300	27	327	25	2 × 151
NovaSeq 6000 S1 and S2	100	38	138	25	2 × 56
	200	38	238	25	2 × 106
	300	38	338	25	2 × 156

Reagent type	Kit size	Excess cycles provided	Max number of cycles	GALEAS Target dual indexing cycles	Max usable sequencing cycles
NovaSeq 6000 S4	35	37	72	25	2 × 47
	200	38	238	25	2 × 106
	300	38	338	25	2 × 156
NovaSeq 6000 SP	100	38	138	25	2 × 56
	200	38	238	25	2 × 106
	300	38	338	25	2 × 156
	500	38	538	25	2 × 256
NovaSeq X/ NovaSeq X Plus B10	100	38	138	25	2 × 56
	200	38	238	25	2 × 106
	300	38	338	25	2 × 156

VI. Index sequences of Illumina UMI adapters

Table 2. List of adapters contained in the Library Preparation kit V2 (b). i7 index and i5 index sequences are listed for each adapter. The reverse and complement sequence of the i5 index is also shown for the relevant Illumina platforms. Sequences are unique in the i5 and i7 position to detect sample index skipping. The 9 bp "NNNNNNNNN" sequence stands for the Unique Molecular Identifier (UMI), which is sequenced on the same read as the i7 index and allows PCR/sequencing error removal and single molecule counting.

IMPORTANT:

- If demultiplexing with bcl2fastq2 or bcl-convert, do not include the 'NNNNNNNNN' sequence in the i7 index
- If using bcl2fastq to demultiplex, use a V1 Sample Sheet. If using Dragen or bcl-convert to demultiplex, then use a V2 Sample Sheet

Well position	Adapter ID	i7 index	i5 index forward HiSeq 2000/2500 MiSeq (all systems) NovaSeq 6000 (V1 reagent kit)	i5 index reverse HiSeq 3000/4000, HiSeq X NextSeq (all systems) NovaSeq 6000 (V1.5 reagent kits) iSeq 100
A1	UMIRC_AN01	CTGATCGTNNNNNNNNN	ATATGCGC	GCGCATAT
B1	UMIRC_AN02	ACTCTCGANNNNNNNNN	TGGTACAG	CTGTACCA
C1	UMIRC_AN03	TGAGCTAGNNNNNNNNN	AACCGTTC	GAACGGTT
D1	UMIRC_AN04	GAGACGATNNNNNNNNN	TAACCGGT	ACCGGTTA
E1	UMIRC_AN05	CTTGTCGANNNNNNNNN	GAACATCG	CGATGTTC
F1	UMIRC_AN06	TTCCAAGGNNNNNNNNN	CCTTGTAG	CTACAAGG
G1	UMIRC_AN07	CGCATGATNNNNNNNNN	TCAGGCTT	AAGCCTGA
H1	UMIRC_AN08	ACGGAACANNNNNNNNN	GTTCTCGT	ACGAGAAC
A2	UMIRC_AN09	CGGCTAATNNNNNNNNN	AGAACGAG	CTCGTTCT
B2	UMIRC_AN10	ATCGATCGNNNNNNNNN	TGCTTCCA	TGGAAGCA
C2	UMIRC_AN11	GCAAGATCNNNNNNNNN	CTTCGACT	AGTCGAAG
D2	UMIRC_AN12	GCTATCCTNNNNNNNNN	CACCTGTT	AACAGGTG
E2	UMIRC_AN13	TACGCTACNNNNNNNNN	ATCACACG	CGTGTGAT
F2	UMIRC_AN14	TGGACTCTNNNNNNNNN	CCGTAAGA	TCTTACGG
G2	UMIRC_AN15	AGAGTAGCNNNNNNNNN	TACGCCTT	AAGGCGTA
H2	UMIRC_AN16	ATCCAGAGNNNNNNNNN	CGACGTTA	TAACGTCG
A3	UMIRC_AN17	GACGATCTNNNNNNNNN	ATGCACGA	TCGTGCAT
B3	UMIRC_AN18	AACTGAGCNNNNNNNNN	CCTGATTG	CAATCAGG
C3	UMIRC_AN19	CTTAGGACNNNNNNNNN	GTAGGAGT	ACTCCTAC
D3	UMIRC_AN20	GTGCCATANNNNNNNNN	ACTAGGAG	CTCCTAGT
E3	UMIRC_AN21	GAATCCGANNNNNNNNN	CACTAGCT	AGCTAGTG
F3	UMIRC_AN22	TCGCTGTTNNNNNNNNN	ACGACTTG	CAAGTCGT
G3	UMIRC_AN23	TTCGTTGGNNNNNNNNN	CGTGTGTA	TACACACG
H3	UMIRC_AN24	AAGCACTGNNNNNNNNN	GTTGACCT	AGGTCAAC
A4	UMIRC_AN25	CCTTGATCNNNNNNNNN	ACTCCATC	GATGGAGT
B4	UMIRC_AN26	GTCGAAGANNNNNNNNN	CAATGTGG	CCACATTG
C4	UMIRC_AN27	ACCACGATNNNNNNNNN	TTGCAGAC	GTCTGCAA

Well position	Adapter ID	i7 index	i5 index forward HiSeq 2000/2500 MiSeq (all systems) NovaSeq 6000 (V1 reagent kit)	i5 index reverse HiSeq 3000/4000, HiSeq X NextSeq (all systems) NovaSeq 6000 (V1.5 reagent kits) iSeq 100
D4	UMIRC_AN28	GATTACCGNNNNNNNNN	CAGTCCAA	TTGGACTG
E4	UMIRC_AN29	GCACAACTNNNNNNNNN	ACGTTCAG	CTGAACGT
F4	UMIRC_AN30	GCGTCATTNNNNNNNNN	AACGTCTG	CAGACGTT
G4	UMIRC_AN31	ATCCGGTANNNNNNNNN	TATCGGTC	GACCGATA
H4	UMIRC_AN32	CGTTGCAANNNNNNNNN	CGCTCTAT	ATAGAGCG
A5	UMIRC_AN33	GTGAAGTGNNNNNNNNN	GATTGCTC	GAGCAATC
B5	UMIRC_AN34	CATGGCTANNNNNNNNN	GATGTGTG	CACACATC
C5	UMIRC_AN35	ATGCCTGTNNNNNNNNN	CGCAATCT	AGATTGCG
D5	UMIRC_AN36	CAACACCTNNNNNNNNN	TGGTAGCT	AGCTACCA
E5	UMIRC_AN37	TGTGACTGNNNNNNNNN	GATAGGCT	AGCCTATC
F5	UMIRC_AN38	GTCATCGANNNNNNNNN	AGTGGATC	GATCCACT
G5	UMIRC_AN39	AGCACTTCNNNNNNNNN	TTGGACGT	ACGTCCAA
H5	UMIRC_AN40	GAAGGAAGNNNNNNNNN	ATGACGTC	GACGTCAT
A6	UMIRC_AN41	GTTGTTCGNNNNNNNNN	GAAGTTGG	CCAACTTC
B6	UMIRC_AN42	CGGTTGTTNNNNNNNNN	CATACCAC	GTGGTATG
C6	UMIRC_AN43	ACTGAGGTNNNNNNNNN	CTGTTGAC	GTCAACAG
D6	UMIRC_AN44	TGAAGACGNNNNNNNNN	TGGCATGT	ACATGCCA
E6	UMIRC_AN45	GTTACGCANNNNNNNNN	ATCGCCAT	ATGGCGAT
F6	UMIRC_AN46	AGCGTGTTNNNNNNNNN	TTGCGAAG	CTTCGCAA
G6	UMIRC_AN47	GATCGAGTNNNNNNNNN	AGTTCGTC	GACGAACT
H6	UMIRC_AN48	ACAGCTCANNNNNNNNN	GAGCAGTA	TACTGCTC
A7	UMIRC_AN49	GAGCAGTANNNNNNNNN	ACAGCTCA	TGAGCTGT
B7	UMIRC_AN50	AGTTCGTCNNNNNNNNN	GATCGAGT	ACTCGATC
C7	UMIRC_AN51	TTGCGAAGNNNNNNNNN	AGCGTGTT	AACACGCT
D7	UMIRC_AN52	ATCGCCATNNNNNNNNN	GTTACGCA	TGCGTAAC
E7	UMIRC_AN53	TGGCATGTNNNNNNNNN	TGAAGACG	CGTCTTCA
F7	UMIRC_AN54	CTGTTGACNNNNNNNNN	ACTGAGGT	ACCTCAGT
G7	UMIRC_AN55	CATACCACNNNNNNNNN	CGGTTGTT	AACAACCG
H7	UMIRC_AN56	GAAGTTGGNNNNNNNNN	GTTGTTCG	CGAACAAC
A8	UMIRC_AN57	ATGACGTCNNNNNNNNN	GAAGGAAG	CTTCCTTC
B8	UMIRC_AN58	TTGGACGTNNNNNNNNN	AGCACTTC	GAAGTGCT
C8	UMIRC_AN59	AGTGGATCNNNNNNNNN	GTCATCGA	TCGATGAC
D8	UMIRC_AN60	GATAGGCTNNNNNNNNN	TGTGACTG	CAGTCACA
E8	UMIRC_AN61	TGGTAGCTNNNNNNNNN	CAACACCT	AGGTGTTG
F8	UMIRC_AN62	CGCAATCTNNNNNNNNN	ATGCCTGT	ACAGGCAT
G8	UMIRC_AN63	GATGTGTGNNNNNNNNN	CATGGCTA	TAGCCATG
H8	UMIRC_AN64	GATTGCTCNNNNNNNNN	GTGAAGTG	CACTTCAC
A9	UMIRC_AN65	CGCTCTATNNNNNNNNN	CGTTGCAA	TTGCAACG

Well position	Adapter ID	i7 index	i5 index forward HiSeq 2000/2500 MiSeq (all systems) NovaSeq 6000 (V1 reagent kit)	i5 index reverse HiSeq 3000/4000, HiSeq X NextSeq (all systems) NovaSeq 6000 (V1.5 reagent kits) iSeq 100
B9	UMIRC_AN66	TATCGGTCNNNNNNNNN	ATCCGGTA	TACCGGAT
C9	UMIRC_AN67	AACGTCTGNNNNNNNNN	GCGTCATT	AATGACGC
D9	UMIRC_AN68	ACGTTCAGNNNNNNNNN	GCACAACT	AGTTGTGC
E9	UMIRC_AN69	CAGTCCAANNNNNNNNN	GATTACCG	CGGTAATC
F9	UMIRC_AN70	TTGCAGACNNNNNNNNN	ACCACGAT	ATCGTGGT
G9	UMIRC_AN71	CAATGTGGNNNNNNNNN	GTCGAAGA	TCTTCGAC
H9	UMIRC_AN72	ACTCCATCNNNNNNNNN	CCTTGATC	GATCAAGG
A10	UMIRC_AN73	GTTGACCTNNNNNNNNN	AAGCACTG	CAGTGCTT
B10	UMIRC_AN74	CGTGTGTANNNNNNNNN	TTCGTTGG	CCAACGAA
C10	UMIRC_AN75	ACGACTTGNNNNNNNNN	TCGCTGTT	AACAGCGA
D10	UMIRC_AN76	CACTAGCTNNNNNNNNN	GAATCCGA	TCGGATTC
E10	UMIRC_AN77	ACTAGGAGNNNNNNNNN	GTGCCATA	TATGGCAC
F10	UMIRC_AN78	GTAGGAGTNNNNNNNNN	CTTAGGAC	GTCCTAAG
G10	UMIRC_AN79	CCTGATTGNNNNNNNNN	AACTGAGC	GCTCAGTT
H10	UMIRC_AN80	ATGCACGANNNNNNNNN	GACGATCT	AGATCGTC
A11	UMIRC_AN81	CGACGTTANNNNNNNNN	ATCCAGAG	CTCTGGAT
B11	UMIRC_AN82	TACGCCTTNNNNNNNNN	AGAGTAGC	GCTACTCT
C11	UMIRC_AN83	CCGTAAGANNNNNNNNN	TGGACTCT	AGAGTCCA
D11	UMIRC_AN84	ATCACACGNNNNNNNNN	TACGCTAC	GTAGCGTA
E11	UMIRC_AN85	CACCTGTTNNNNNNNNN	GCTATCCT	AGGATAGC
F11	UMIRC_AN86	CTTCGACTNNNNNNNNN	GCAAGATC	GATCTTGC
G11	UMIRC_AN87	TGCTTCCANNNNNNNNN	ATCGATCG	CGATCGAT
H11	UMIRC_AN88	AGAACGAGNNNNNNNNN	CGGCTAAT	ATTAGCCG
A12	UMIRC_AN89	GTTCTCGTNNNNNNNNN	ACGGAACA	TGTTCCGT
B12	UMIRC_AN90	TCAGGCTTNNNNNNNNN	CGCATGAT	ATCATGCG
C12	UMIRC_AN91	CCTTGTAGNNNNNNNNN	TTCCAAGG	CCTTGGAA
D12	UMIRC_AN92	GAACATCGNNNNNNNNN	CTTGTCGA	TCGACAAG
E12	UMIRC_AN93	TAACCGGTNNNNNNNNN	GAGACGAT	ATCGTCTC
F12	UMIRC_AN94	AACCGTTCNNNNNNNNN	TGAGCTAG	CTAGCTCA
G12	UMIRC_AN95	TGGTACAGNNNNNNNNN	ACTCTCGA	TCGAGAGT
H12	UMIRC_AN96	ATATGCGCNNNNNNNNN	CTGATCGT	ACGATCAG

NOTE: To view the list of all 384 adapters indexes available with Library Preparation kit V2 (b), please refer to the Nonacus 1-384 UMI adapter plate format which can be downloaded from **nonacus.com**.

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