

INSTRUCTIONS FOR USE

16, 32, 48 and 96 Samples

SOPHiA DDM™

Myeloid Solution



Using the SOPHiA GENETICS™
DNA Library Prep Kit I





SUMMARY INFORMATION

Product Name	SOPHiA DDM™ Myeloid Solution
Product Type	Bundle Solution
Product Family	Molecular kit + analytics
Algorithm ID	ILL1XG1S9_CNV_1 and ILL1XG1S4_CNV_NextSeq
Gene Panel ID	MYS_v1
Product Version	v1.0
Release Version	Not Applicable
Sample Type	Somatic DNA isolated from peripheral blood and bone marrow
Sequencer	Illumina® NextSeq® 500/550 and Illumina® MiSeq®
Document ID	SG-00241
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This Instructions For Use is applicable to all SOPHiA DDM™ versions.

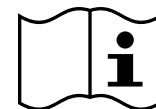
Please read the Instructions For Use thoroughly before using this product.



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BS0103ILLRSMY01-048;
BS0103ILLRSMY01-096





PRODUCT CODES

	FULL PRODUCT CODE	BOX 1	BOX 2	LIBRARY PREPARATION KIT
REF	BS0103ILLRSMY01-016	B1.E1.0003.R-16	B2.0000.R-16	700232
	BS0103ILLRSMY01-032	B1.E1.0003.R-32	B2.0000.R-32	700232
	BS0103ILLRSMY01-048	B1.E1.0003.R-48	B2.0000.R-48	700234
	BS0103ILLRSMY01-096	B1.E1.0003.R-96	B2.0000.R-48	700234



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REVISION HISTORY

DOCUMENT ID / VERSION	DATE	DESCRIPTION OF CHANGE
SG-00241 – v4.0	Aug 2023	<ul style="list-style-type: none"> • Added new sections <i>Product Codes</i> and <i>Product Introduction</i> • Removed mention of third-party provider's intellectual property from sections 2.2.1 <i>Kit Content</i>, 2.3.1 <i>Library Pooling for Hybridization and Capture</i>, and 2.4.1 <i>Hybridization</i>. • Update of trademark symbols and product names • Cosmetic text and formatting changes and minor document restructuring • Specified "NextSeq®" sequencer as "NextSeq® 500/550" • Renaming of the following reagents: <ul style="list-style-type: none"> • "FX" to "Fragmentation" • "DNA Ligase" to "Ligation Enzyme" • "DNA Ligase Buffer" to "Ligation Buffer" • Increased incubation time on the magnetic rack during Post-Ligation Clean Up (step 11), Post-Amplification Clean Up (step 11), and Post-Capture Amplification Clean Up (step 11) from 3 min to 5 min.
SG-00241 – v3.0	Aug 2022	<ul style="list-style-type: none"> • PCR Master Mix volume updated. • Product Name Updated with Trademark symbol. • Library preparation kit name changed to SOPHiA DDM™. • Blocking Oligo name updated. • Company address updated to Rolle.



DOCUMENT ID / VERSION	DATE	DESCRIPTION OF CHANGE
SG-00241 – v2.0	Jun 2022	<ul style="list-style-type: none"> • Product Name Updated • Pipeline ID Updated • Document ID Updated
ID-60101-59 – v1.0	09 Aug 2021	<ul style="list-style-type: none"> • Title page, Company logo, Header, Footer, Last page. • Combined four kit size "User guides" together to include different sample numbers. Included tables and made appropriate changes as and when necessary for this purpose. • Following Kit "User guide" documents were combined: <ul style="list-style-type: none"> • PM_RUO_B.2.1.2.115_r1en • PM_RUO_B.2.1.2.114_r1en • PM_RUO_B.2.1.2.113_r1en • Minor changes for clarity in the following sections: <ul style="list-style-type: none"> • Section 3.1 Library Pooling • Section 3.5 Wash Streptavidin Beads to Remove Unbound DNA



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1 PRODUCT INTRODUCTION

The SOPHiA DDM™ Myeloid Solution is a bundle solution including library preparation and capture kit, as well as a fully integrated FASTQ-to-report bioinformatic workflow for the analysis, interpretation, and reporting of sequencing data obtained on Illumina® NextSeq® 500/550 and Illumina® MiSeq® instrument(s). The performance of the workflow has been optimized for the analysis and interpretation of sequencing data for the detection of somatic variants in genes known to be associated with myelodysplastic syndromes, myeloproliferative neoplasms, and leukemia.

The workflow consists of a secondary analysis pipeline and tertiary analytical tools and resources. The secondary analysis pipeline detects Single Nucleotide Variants (SNVs), Insertions/Deletions (INDELs), and Copy Number Variants (CNVs), as well as FLT3 internal tandem duplications.



2 PROTOCOL

2.1 Materials

2.1.1 Initial Considerations

Upon receipt, please ensure that all tubes are physically intact and stored at recommended temperatures for optimum kit performance. Inappropriate handling and storage of the kit components under other conditions may adversely affect the kit's performance.

2.1.2 Kit Content (16, 32, 48 And 96 Samples)



Always briefly spin the tubes before use to collect all liquid.

Depending on the kit format, the following components are provided:

COMPONENT	NUMBER OF ITEMS DEPENDING ON KIT FORMAT			
	16 SAMPLE KIT	32 SAMPLE KIT	48 SAMPLE KIT	96 SAMPLE KIT
Box 1	1	1	1	2 (48 samples each)
Illumina®-compatible Dual Index Adapters (in 96-well plate format included in Box 1)	16	32	48	96 (Plate contained in one of the two Box 1)
Box 2	1	1	1	2 (48 samples each)
SOPHiA GENETICS™ DNA Library Prep Kit I	1	2 (16 samples each)	1	2 (48 samples each)

Box 1 (Store At -25°C To -15°C)

- Universal Blockers - TS Mix (12 µl)
- Human Cot DNA (25 µl)
- Myeloid Solution Probes by SOPHiA GENETICS (20 µl)
- 2x Hybridization Buffer (50 µl)



- Hybridization Buffer Enhancer (20 µl)
- 2x Bead Wash Buffer (1250 µl)
- 10x Stringent Wash Buffer (200 µl)
- 10x Wash Buffer I (160 µl)
- 10x Wash Buffer II (110 µl)
- 10x Wash Buffer III (110 µl)
- Depending on the kit format: 16, 32, 48 or 96 Illumina®-compatible Dual Index Adapters in 96-well plate format (7 µl adapter per well). See Appendix I for adapter display and sequences.
- Post-Capture Illumina® Primers Mix (20 µl)
- Post-Capture PCR Enhancer (20 µl)
- Post-Capture PCR Master Mix (122 µl)

Box 2 (Store At +2°C To +8°C)

- Dynabeads® M-270 Streptavidin (440 µl)
- Agencourt® AMPure® XP (3 x 1.5 ml for 16 samples, 8.7 ml for 32 samples and 11.6 ml for 48 samples, see Note below for 96 samples)
- IDTE Low TE Buffer (10 ml)
- Nuclease-free water (20 ml)

Note: For 96 samples, two times Box 2 of 48 samples are provided (see table on previous page).

2.1.3 SOPHiA GENETICS™ DNA Library Prep Kit I* (Store At -25°C To -15°C)*

REAGENT	KIT FORMAT	
	16 SAMPLES	48 SAMPLES
HiFi PCR Master Mix 2x (µl)	500	1560
Primer Mix Illumina® Library Amp (µl)	30	95
Fragmentation Enzyme Mix (µl)	200	625
Fragmentation Buffer 10x (µl)	100	315
Fragmentation Enhancer (µl)	100	315
Ligation Enzyme (µl)	200	625
Ligation Buffer 5x (µl)	400	1250

* SOPHiA GENETICS is the exclusive distributor of this Library Prep kit.



* For 32 samples, two 16-sample kits are provided.

* For 96 samples, two 48-sample kits are provided.





Refer to Warnings and Precautions below for additional details.



2.1.4 Warnings and Precautions

PRODUCT NAME	GHS PICTOGRAM	H&P STATEMENTS	SIGNAL WORD	HAZARDOUS COMPONENT
2x Hybridization Buffer	 	<ul style="list-style-type: none"> • H300 Fatal if swallowed. • H311 Toxic in contact with skin. • H315 Causes skin irritation. • H370 Causes damage to organs. • H370 Causes damage to organs (Central nervous system). • H411 Toxic to aquatic life with long-lasting effects. • P260 Do not breathe vapor/ spray. • P264 Wash contaminated skin thoroughly after handling. • P270 Do not eat, drink or smoke when using this product. • P273 Avoid release to the environment. • P280 Wear protective gloves/ protective clothing/ eye protection/face protection. • P301+P310 If swallowed: Immediately call a poison center/doctor. • P302+P352 If on skin: Wash with plenty of water. • P308+P311 If exposed or concerned: Call a poison center or doctor. • P321 Specific treatment (see medical advice on this label). • P330 Rinse mouth. • P332+P313 If skin irritation occurs: Get medical advice/ attention. • P362+P364 Take off contaminated clothing and wash it before reuse. • P391 Collect spillage. • P405 Store locked up. • P501 Dispose of contents/ container in accordance with national regulations. 	Danger	Tetramethyl- ammonium chloride
Hybridization Buffer Enhancer		<ul style="list-style-type: none"> • H351 Suspected of causing cancer. • H360 May damage fertility or the unborn child. • H373 May cause damage to 	Danger	Formamide



PRODUCT NAME	GHS PICTOGRAM	H&P STATEMENTS	SIGNAL WORD	HAZARDOUS COMPONENT
		<p>organs through prolonged or repeated exposure.</p> <ul style="list-style-type: none"> • P201 Obtain special instructions before use. • P202 Do not handle until all safety precautions have been read and understood. • P260 Do not breathe vapour/ spray. • P280 Wear protective gloves/ protective clothing/ eye protection/ face protection. • P308+P313 IF exposed or concerned: Get medical advice/ attention. • P314 Get medical advice/ attention if you feel unwell. • P405 Store locked up. • P501 Dispose of contents/ container in accordance with national regulations. 		
10x Stringent Wash Buffer		<ul style="list-style-type: none"> • H302 Harmful if swallowed. • H315 Causes skin irritation. • H319 Causes serious eye irritation 	Danger	Ethylenediaminetetraacetic acid disodium salt
10x Wash Buffer I		<ul style="list-style-type: none"> • H228 Flammable solid. • H302 Harmful if swallowed. • H315 Causes skin irritation. • H318 Causes serious eye damage. • H332 Harmful if inhaled. • H401 Toxic to aquatic life. • H402 Harmful to aquatic life. • H412 Harmful to aquatic life with long lasting effects. • P273 Avoid release to the environment. • P280 Wear protective gloves/ protective clothing/ eye protection/ face protection. • P305+P351+P338 If in eyes: Rinse cautiously with water for several minutes. Remove contact lenses, if present and easy to do. Continue rinsing. • P310 Immediately call a poison 	Danger	Sodium dodecyl sulfate



PRODUCT NAME	GHS PICTOGRAM	H&P STATEMENTS	SIGNAL WORD	HAZARDOUS COMPONENT
		center/ doctor. • P501 Dispose of contents/ container in accordance with national regulations.		



Please use

and



as personal protective equipment.

2.1.5 Materials Required (Not Provided)

User-Supplied Materials (To Be Purchased Separately)

Lab-related plasticware

- DNA low binding 1.5 ml tubes
- 50 ml conical tubes
- Filter tips
- 1.5 ml tubes
- RNase/DNase-free 0.2 ml 8-tube strips

Reagents

- Ethanol (molecular biology grade)

Other

- Ice to ensure reagents and pre-mixes are kept at 4 °C
- Illumina® sequencing reagents

Laboratory Equipment

To avoid sample contamination, separate the workspace into:

- *Pre-PCR zone*
 - Fluorometric quantitation equipment and reagents
 - Magnetic separation rack (96-well type)
 - Multichannel pipettes (P10 or P20; P100; P200)
 - Tabletop microcentrifuge (8-tube strips compatible)



- Thermal cycler (programmable heated lid)
- Vortex mixer
- *Post-PCR zone*
 - Capillary electrophoresis system
 - DNA vacuum concentrator
 - Fluorometric quantitation equipment and reagents
 - Magnetic separation rack (1.5 ml tube compatible)
 - Magnetic separation rack (96-well type)
 - Multichannel pipettes (P10 or P20; P100; P200)
 - Tabletop microcentrifuge (8-tube strips compatible)
 - Thermal cycler (programmable heated lid)
 - Thermoblock or water bath (1.5 ml tube compatible)
 - Vortex mixer



2.2 Library Preparation

2.2.1 Input Material Preparation

Materials

- Double-stranded high quality genomic DNA (gDNA)
- Fragmentation Enhancer
- IDTE
- RNase/DNase-free 0.2 ml 8-tube strips

Input Recommendations

DNA integrity, concentration, and purity are critical during this step. The purity of the DNA can be assessed using a UV spectrophotometer. Recommended absorbance ratios are between 1.8–2.0 for the 260/280 nm ratio and within 1.6–2.4 for 260/230 nm. We recommend confirmation of the sample integrity by capillary electrophoresis or an equivalent technique.

To avoid mistakes with DNA input, an initial dilution to obtain a concentration in the 50–100 ng/μl range is recommended. The DNA concentration should be confirmed by a fluorometric quantification method (e.g., Qubit®, Thermo Fisher), and the obtained value should be used to calculate the final dilution.

Preparation

Remove the Fragmentation Enhancer from -20°C storage and thaw at room temperature. After thawing, mix the reagent by gently inverting the tube 5 times and briefly spin in a microcentrifuge.

Depending on the kit format, the number of DNA samples to be pooled per capture reaction will vary according to the following table. This must be taken into consideration before starting.

KIT FORMAT	16 SAMPLE KIT	32 SAMPLE KIT	48 SAMPLE KIT	96 SAMPLE KIT*
Number of individual libraries per capture	4	8	12	12

*For 96 samples, two 48 sample kits are provided which include 8 capture reactions.

Procedure

1. Prepare the following PCR strips according to the number of reactions:


NUMBER OF REACTIONS	4	8	12	16	24	32	48
PCR strip	4-tube	4-tube	4-tube	8-tube	8-tube	8-tube	8-tube
Number of strips	1	2	3	2	3	4	6

2. Prepare a dilution for each extracted DNA sample into the appropriate number of PCR strips, in the following manner:



DNA DILUTION	
DNA	200 ng
IDTE	Complete to 30 μ l

- Mix briefly by gently pipetting up and down 5 times followed by a brief spin in a microcentrifuge to collect all liquid.

 Safe stopping point overnight at 4 °C.

- Depending on the number of samples, proceed as follows:

- If processing **4 samples**, add 5 μ l of Fragmentation Enhancer to each tube of the 4-tube strip containing 30 μ l of DNA samples (total of 35 μ l in each tube of the 4-tube strip).
- If processing **8 or more samples**, proceed as follows:
 - To facilitate pipetting, create a reservoir of Fragmentation Enhancer by adding the following volumes to a new set of 4 or 8-tube strips, according to the following scheme:

NUMBER OF REACTIONS	8	12	16	24	32	48
PCR Strip (1 strip)	4-tube	4-tube	8-tube	8-tube	8-tube	8-tube
Fragmentation Enhancer (μ l)	11.5	17.5	11.5	17.5	24	36

- Using a multichannel pipette, add 5 μ l of Fragmentation Enhancer from the above tubes to 30 μ l of DNA samples (total of 35 μ l in each tube of the 4 or 8-tube strips).
- Using a multichannel pipette set to 20 μ l, mix gently by pipetting up and down 5 times and briefly spin in a microcentrifuge.
- Keep on ice until Enzymatic Fragmentation reaction set-up.

2.2.2 Pre-Mixes and Reagents Preparation

Components And Reagents

- Fragmentation Enzyme Mix
- Fragmentation Buffer 10x
- DNA Ligase
- DNA Ligase Buffer 5x
- HiFi PCR Master Mix 2x
- Primer Mix Illumina® Library Amp
- Nuclease-free water



- AMPure® XP beads
- Ethanol

Preparation

1. Remove the SOPHiA GENETICS™ DNA Library Prep Kit I components from -20 °C storage and thaw on ice.
2. Remove the Dual Index Adapters Plate from -20°C storage and put it into 4°C refrigerator for later use.
3. Remove the AMPure® XP beads from 2–8 °C storage and let them equilibrate at room temperature for at least 30 minutes. Vortex the AMPure® XP beads thoroughly, to ensure proper resuspension of the beads, prior to use in all subsequent steps.
4. Prepare fresh 80% Ethanol (volume according to the following scheme based on number of reactions):

80% ETHANOL VOLUMES							
Number of Reactions	4	8	12	16	24	32	48
80% Ethanol (ml)	10	20	30	30	40	50	70

5. Once the SOPHiA GENETICS™ DNA Library Prep Kit I components are thawed, mix the reagents by inverting the tube 5–10 times to ensure that there is no remaining precipitate and briefly spin in a microcentrifuge. Place on ice.

Pre-Mixes

1. Prepare the **Fragmentation pre-mix** as follows:

FRAGMENTATION PRE-MIX							
Number of Reactions	4	8	12	16	24	32	48
Fragmentation Buffer 10x (µl)	23.6	47.1	75	95	150	190	300
Fragmentation Enzyme (µl)	47.1	94.2	150	190	300	380	600

- Mix thoroughly by pipetting up and down 10 times and spin briefly.
- Keep on ice.

2. Prepare the **Ligation pre-mix** as follows:

LIGATION PRE-MIX							
Number of Reactions	4	8	12	16	24	32	48
Ligation Buffer 5x (µl)	95	190	300	380	600	760	1200
Ligation Enzyme (µl)	47.5	95	150	190	300	380	600
Nuclease-free water (µl)	71.3	142.5	225	285	450	570	900

- Mix thoroughly by pipetting up and down 10 times and spin briefly.
- Keep on ice.



The Ligation Buffer 5x is highly viscous, pipette gently and make sure to obtain a homogeneous Ligation pre-mix.

3. Prepare the **PCR pre-mix** as follows:

PCR PRE-MIX							
Number of Reactions	4	8	12	16	24	32	48
HiFi PCR Master Mix 2x (µl)	115	230	345	460	690	920	1380
Primer Mix Illumina® Library Amp (µl)	6.9	13.8	20.7	27.6	41.4	55.2	82.8
Nuclease-free water (µl)	16.1	32.2	48.3	64.4	96.6	128.2	193.2

- Mix thoroughly by pipetting up and down 10 times and spin briefly.
- Keep on ice.

2.2.3 Enzymatic Fragmentation, End Repair and A-Tailing

Materials

- Diluted and conditioned double stranded gDNA in 35 µl
- Fragmentation pre-mix
- RNase/DNase-free 0.2 ml 8-tube strips

Preparation

1. Program the thermal cycler for Fragmentation with the following settings:

	TEMPERATURE (°C)	TIME (MINUTES)
Lid	70	-
Step 1	4	1
Step 2	32	5
Step 3	65	30
Hold	4	∞

2. Start the Fragmentation program. When the block reaches Step 1 (4 °C), pause the program.

Procedure



Always keep the samples and pre-mix on ice before and after the incubation to block the enzymatic reaction.



- Depending on the number of samples, proceed as follows:
 - If processing **4 samples**, proceed to step 2.
 - If processing **8 or more samples**, to facilitate pipetting, create a reservoir of Fragmentation pre-mix by adding the following volumes to a new set of 4 or 8-tube strips according to the following scheme:

NUMBER OF REACTIONS	8	12	16	24	32	48
PCR strip (1 strip)	4-tube	4-tube	8-tube	8-tube	8-tube	8-tube
Fragmentation pre-mix (µl)	33	52.5	33	52.5	66	105

- Assemble the reaction as follows:
 - Using a multichannel pipette, if processing 8 or more samples, add 15 µl of Fragmentation pre-mix to each of the 35 µl of DNA samples (total of 50 µl in 4 or 8-tube strips).
 - Using a multichannel pipette set to 40 µl, mix thoroughly by pipetting up and down 5 times and briefly spin in a microcentrifuge.
- Place in the thermal cycler and continue the Fragmentation program.

Proceed immediately to Ligation.

2.2.4 Ligation

Materials

- Fragmentation reaction products in 50 µl each
- Ligation pre-mix
- Dual Index Adapters
- RNase/DNase-free 0.2 ml 8-tube strips

Preparation

- Remove the Dual Index Adapters plate from 4 °C (transferred from -20 °C to 4 °C earlier) and briefly spin the plate to collect all the liquid. Refer to Appendix I for the respective plate format.
- During the Fragmentation, prepare new PCR strips with 5 µl of different Dual Index Adapters per tube according to the following scheme:

NUMBER OF REACTIONS	4	8	12	16	24	32	48
PCR strip (1 strip)	4-tube	4-tube	4-tube	8-tube	8-tube	8-tube	8-tube
Number of strips	1	2	3	2	3	4	6

- Set up the thermal cycler at 20 °C (open lid).



Procedure



Always keep the samples and pre-mix on ice before and after the incubation to block the enzymatic reaction.

- Depending on the number of samples, proceed as follows:
 - If processing **4 samples**, proceed to step 2.
 - If processing **8 or more samples**, to facilitate pipetting, create a reservoir of Ligation pre-mix by adding the following volumes to a new set of 4 or 8-tube strips according to the following scheme:

NUMBER OF REACTIONS	8	12	16	24	32	48
PCR strip (1 strip)	4-tube	4-tube	8-tube	8-tube	8-tube	8-tube
Ligation pre-mix (µl)	100	160	100	160	200	320

- Using a multichannel pipette, transfer the 50 µl of each Fragmentation reaction product to the 4 or 8-tube strips containing 5 µl of Dual Index Adapters.
- Mix thoroughly by pipetting up and down 10 times and spin briefly.
- Using a multichannel pipette, add 45 µl of Ligation pre-mix to each Fragmentation reaction product (55 µl in each tube of the 4 or 8-tube strip).
- Mix thoroughly by pipetting up and down 10 times and spin briefly.
- Incubate in the thermal cycler at 20 °C for 15 minutes (open lid).

Proceed to Post-Ligation Clean Up.



Do not place the strip(s) on ice at the end of the ligation as it might decrease the binding of the DNA to the beads.

2.2.5 Post-Ligation Clean Up

Materials

- Ligation reaction products in 100 µl each
- AMPure® XP beads equilibrated at room temperature
- Freshly prepared ethanol 80%
- Nuclease-free water
- RNase/DNase-free 0.2 ml 8-tube strips



Procedure

1. Using a multichannel pipette, add 80 µl of AMPure® XP beads to each of the 100 µl ligation reaction products. Mix thoroughly by pipetting up and down 10 times.
2. Incubate at room temperature for 5 minutes and spin briefly if required.
3. Place the 4 or 8-tube strip on a 96-well plate format magnetic rack for 5 minutes or until the liquid becomes clear.
4. Carefully discard 170 µl of supernatant using a multichannel pipette.

Keep the tubes on the magnetic rack for the following steps.

5. Using a multichannel pipette, add 170 µl of 80% ethanol to the beads. Incubate for 30 seconds to 1 minute.
6. Carefully discard the ethanol using a multichannel pipette.
7. Repeat steps 5 and 6 once.
8. Remove the residual ethanol using a P10 or P20 multichannel pipette.
9. Air-dry the beads at room temperature for 5 minutes. Do not over-dry the beads because this could decrease the amount of recovered DNA.

Remove the tubes from the magnetic rack.

10. Using a multichannel pipette, add 105 µl of nuclease-free water to the beads and wait for a few seconds. Mix thoroughly by pipetting up and down 10 times.
11. Incubate at room temperature for 5 minutes and spin briefly if required.
12. Place the 4 or 8-tube strip on a 96-well plate format magnetic rack for 5 minutes or until the liquid becomes clear.
13. Using a multichannel pipette, carefully transfer 100 µl of the supernatant to new, labelled 4 or 8-tube strip.

Proceed to Dual Size Selection.

2.2.6 Dual Size Selection

Materials

- Ligation reaction products in 100 µl each
- AMPure® XP beads equilibrated at room temperature
- Freshly prepared ethanol 80%
- IDTE
- RNase/DNase-free 0.2 ml 8-tube strips

Procedure

1. Using a multichannel pipette, add 60 µl of AMPure® XP beads to each of the 100 µl ligation reaction products. Mix thoroughly by pipetting up and down 10 times.
2. Incubate at room temperature for 5 minutes and spin briefly if required to collect all liquid.
3. Place the 4 or 8-tube strip on a 96-well plate format magnetic rack for 5 minutes or until the liquid becomes clear.



4. Using a multichannel pipette, carefully transfer 140 μ l of the supernatant to a new, labelled 4 or 8-tube strip containing 20 μ l of AMPure[®] XP beads. Mix thoroughly by pipetting up and down 10 times.
5. Incubate at room temperature for 5 minutes and spin briefly if required to collect all liquid.
6. Place the 4 or 8-tube strip on a 96-well plate format magnetic rack for 5 minutes or until the liquid becomes clear.
7. Carefully discard 150 μ l of supernatant using a multichannel pipette.

Keep the tubes on the magnetic rack for the following steps.

8. Using a multichannel pipette, add 170 μ l of 80% ethanol to the beads. Incubate for 30 seconds to 1 minute.
9. Carefully discard the ethanol using a multichannel pipette.
10. Repeat steps 8 and 9 once.
11. Remove the residual ethanol using a P10 or P20 multichannel pipette.
12. Air-dry the beads at room temperature for 4 minutes. Do not over-dry the beads because this could decrease the amount of recovered DNA.

Remove the tubes from the magnetic rack.

13. Using a multichannel pipette, add 20 μ l of IDTE to the beads. Mix thoroughly by pipetting up and down 10 times and spin briefly.

Proceed to Library Amplification.

2.2.7 Library Amplification

Materials

- Dual size selected Ligation reaction products and beads resuspended in 20 μ l IDTE each
- PCR pre-mix

Preparation

1. Program the thermal cycler for Library Amplification with the following settings:


	TEMPERATURE (°C)	TIME (SECONDS)	
Lid	99	-	8 cycles
Step 1: Initial Denaturation	98	120	
Step 2: Denaturation	98	20	
Step 3: Annealing	60	30	
Step 4: Extension	72	30	
Step 5: Final Extension	72	60	
Hold	10	∞	



Procedure

- Depending on the number of samples, proceed as follows:
 - If processing **4 samples**, proceed to step 2.
 - If processing **8 or more samples**, to facilitate pipetting, create a reservoir of PCR pre-mix by adding the following volumes to a new set of 4 or 8-tube strips according to the following scheme:

NUMBER OF REACTIONS	8	12	16	24	32	48
PCR strip (1 strip)	4-tube	4-tube	8-tube	8-tube	8-tube	8-tube
PCR pre-mix (µl)	65	100	65	100	130	200

- Assemble the reaction as follows:
 - Using a multichannel pipette, add 30 µl of PCR pre-mix to the dual size selected ligation products and beads (50 µl in 4 or 8-tube strips).
 - Mix thoroughly by pipetting up and down 10 times and spin briefly.
 - Place the tubes in the thermal cycler and run the Library Amplification program.
-  Safe stopping point overnight at 4 °C.

2.2.8 Post-Amplification Clean Up

Materials

- PCR reaction products in 50 µl each
- AMPure® XP beads equilibrated at room temperature
- Freshly prepared ethanol 80%
- Nuclease-free water
- DNA low-binding tubes for the storage of libraries

Procedure

- Using a multichannel pipette, add 50 µl of AMPure® XP beads to each 50 µl of the PCR product. Mix thoroughly by pipetting up and down 10 times.
- Incubate at room temperature for 5 minutes and spin briefly if required.
- Place the 4 or 8-tube strips on a 96-well plate format magnetic rack for 5 minutes or until the liquid becomes clear.
- Carefully discard 90 µl supernatant using a multichannel pipette.

Keep the tubes on the magnetic rack for the following steps.



5. Using a multichannel pipette, add 170 μ l of 80% ethanol to the beads. Let the tubes stand for 30 seconds to 1 minute.
6. Carefully discard the ethanol using a multichannel pipette.
7. Repeat steps 5 and 6 once.
8. Remove the residual ethanol using a P10 or P20 multichannel pipette.
9. Air-dry the beads at room temperature for 5 minutes. Do not over-dry the beads because this could decrease the amount of recovered DNA.

Remove the tubes from the magnetic rack.

10. Using a multichannel pipette, add 20 μ l of nuclease-free water to the beads. Mix thoroughly by pipetting up and down 10 times. Incubate at room temperature for 5 minutes and spin briefly if required.
11. Place the 4 or 8-tube strip on a 96-well plate format magnetic rack for 5 minutes or until liquid becomes clear.
12. Carefully transfer 18 μ l (transferring two times 9 μ l is recommended at this step) of the supernatant to a new and labeled library storage tube.



Safe stopping point overnight at 4 °C or -20 °C for longer storage.

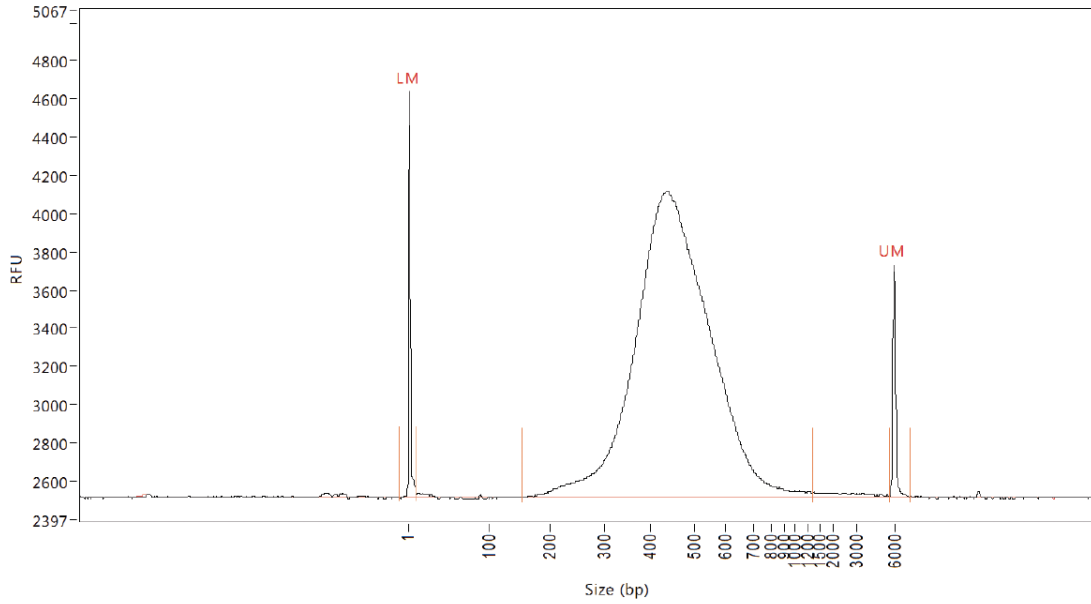
2.2.9 Individual Library Quantification and Quality Control

Materials

- Fluorometric quantitation equipment and reagents
- Capillary electrophoresis system
- Nuclease-free water
- RNase/DNase-free 0.2 ml 8-tube strips

Procedure

1. Prepare a 4-time dilution of each library with nuclease-free water (e.g., 2 μ l of library in 6 μ l nuclease-free water).
2. Quantify the libraries with a fluorometric method (e.g., Qubit HS quantification using 2 μ l of the 4x library dilution prepared previously).
3. Quality control the libraries by analyzing their profile via capillary electrophoresis. Library DNA fragments should have a size distribution between 300 bp and 700 bp.



Example of a DNA library distribution obtained with the Agilent Fragment Analyzer™ capillary electrophoresis system. LM: Lower Marker, UM: Upper Marker.



2.3 Library Pooling

2.3.1 Library Pooling for Hybridization and Capture

Materials

- Individual sequencing libraries
- Human Cot DNA
- Universal Blockers – TS Mix
- DNA low-binding 1.5 ml tubes

Procedure


1. Prepare a library Capture pre-mix of the following in a DNA low-binding tube:

CAPTURE PRE-MIX				
Number of captures	1	2	3	4
Human Cot DNA (µl)	5	11	16.5	22
Universal Blockers – TS Mix (µl)	2	4.4	6.6	8.8

2. Prepare one DNA low-binding 1.5 ml tube per capture.
3. Pipette 7 µl of the above Capture pre-mix into individual DNA low-binding tubes for each capture.
4. To the individual tubes containing the above Capture pre-mix, add a pool of individual libraries according to the kit format:

KIT FORMAT	16 SAMPLES KIT	32 SAMPLES KIT	48 SAMPLES KIT	96 SAMPLES KIT
Number of individual libraries per capture	4	8	12	12
Amount of each library per capture	300 ng	200 ng	150 ng	150 ng
Total amount of libraries per capture	1200 ng	1600 ng	1800 ng	1800 ng

5. Mix thoroughly by pipetting up and down 10 times and spin briefly.
6. Dry each mix using a vacuum DNA concentrator until mix is completely lyophilized. Use mild heating (45–50 °C) to speed up the lyophilization.

 Safe stopping point overnight at -20 °C.



2.4 Capture

2.4.1 Hybridization

Materials

- Lyophilized libraries
- 2x Hybridization Buffer
- Hybridization Buffer Enhancer
- Myeloid Solution Probes
- Nuclease-free water
- RNase/DNase-free 0.2 ml 8-tube strips
- 1.5 ml Tubes
- 10x Wash Buffer I
- 10x Wash Buffer II
- 10x Wash Buffer III
- 10x Stringent Wash Buffer
- 2x Beads Wash Buffer

Preparation

1. Pre-warm the thermal cycler to 95 °C (set lid to 99 °C).
2. After the 10-minute denaturation, switch directly to 65 °C (set lid to 75 °C).



We recommend the use of different thermal cyclers for 95 °C and 65 °C incubations, if available.



Procedure

1. Prepare a Hybridization pre-mix according to the number of capture reactions:

HYBRIDIZATION PRE-MIX				
Number of captures	1	2	3	4
2x Hybridization Buffer (μl)	8.5	18.7	28.05	37.4
Hybridization Buffer Enhancer (μl)	3.4	7.48	11.22	14.96
Nuclease-free Water (μl)	1.1	2.42	3.63	4.84

2. Resuspend the lyophilized pellet in 13 μl of the Hybridization pre-mix.
3. Transfer the resuspended pellet to a PCR tube (one tube per capture reaction).
4. Incubate in the thermal cycler at 95 °C for 10 minutes.



Do not let the tube temperature drop below 65 °C from step 4 to 6 as this can lead to incorrect probe annealing.

5. Move the PCR tube from the 95 °C to 65 °C thermal cycler, then add 4 μl of probes to the mix. Using a pipette set to 13 μl, mix thoroughly by pipetting up and down 5 times.
6. Incubate in the thermal cycler at 65 °C for 4 hours.
7. Prepare the 1x working solutions of different wash buffers in advance as described in the following sections to allow them to reach equilibrium during the hybridization reaction.

Wash Buffer Preparation For 1 Reaction

BUFFER	STOCK BUFFER (μl)	WATER (μl)	FINAL VOLUME 1X (μl)
10x Wash Buffer I	33	297	330
10x Wash Buffer II	22	198	220
10x Wash Buffer III	22	198	220
10x Stringent Wash Buffer	44	396	440
2x Bead Wash Buffer	275	275	550



Pre-warm 1x Stringent Buffer and an aliquot of 110 μl of 1x Wash Buffer I at 65 °C in a thermoblock or water bath for at least 2 hours. Keep the remaining Wash Buffer I at room temperature.

Wash Buffer Preparation For 2 Reactions

BUFFER	STOCK BUFFER (μl)	WATER (μl)	FINAL VOLUME 1X (μl)
10x Wash Buffer I	66	594	660
10x Wash Buffer II	44	396	440



BUFFER	STOCK BUFFER (μl)	WATER (μl)	FINAL VOLUME 1X (μl)
10x Wash Buffer III	44	396	440
10x Stringent Wash Buffer	88	792	880
2x Bead Wash Buffer	550	550	1100



Pre-warm 1x Stringent Buffer and an aliquot of 220 μl of 1x Wash Buffer I at 65 °C in a thermoblock or water bath for at least 2 hours. Keep the remaining Wash Buffer I at room temperature.

Wash Buffer Preparation For 3 Reactions

BUFFER	STOCK BUFFER (μl)	WATER (μl)	FINAL VOLUME 1X (μl)
10x Wash Buffer I	99	891	990
10x Wash Buffer II	66	594	660
10x Wash Buffer III	66	594	660
10x Stringent Wash Buffer	132	1188	1320
2x Bead Wash Buffer	825	825	1650



Pre-warm 1x Stringent Buffer and an aliquot of 330 μl of 1x Wash Buffer I at 65 °C in a thermoblock or water bath for at least 2 hours. Keep the remaining Wash Buffer I at room temperature.

Wash Buffer Preparation For 4 Reactions

BUFFER	STOCK BUFFER (μl)	WATER (μl)	FINAL VOLUME 1X (μl)
10x Wash Buffer I	132	1188	1320
10x Wash Buffer II	88	792	880
10x Wash Buffer III	88	792	880
10x Stringent Wash Buffer	176	1584	1760
2x Bead Wash Buffer	1100	1100	2200



Pre-warm 1x Stringent Buffer and an aliquot of 440 μl of 1x Wash Buffer I at 65 °C in a thermoblock or water bath for at least 2 hours. Keep the remaining Wash Buffer I at room temperature.

2.4.2 Streptavidin Beads Preparation

Materials

- Streptavidin beads equilibrated at room temperature
- 1x Bead Wash Buffer



- 1.5 ml tubes
- RNase/DNase-free 0.2 ml 8-tube strips

Procedure

Perform these steps just before the end of the hybridization incubation.

1. Mix the beads by vortexing them for 15 seconds.
2. Transfer 100 μ l of beads per capture (200 μ l for 2 reactions, 300 μ l for 3 reactions, 400 μ l for 4 reactions) to a single 1.5 ml tube.
3. Place the tube on a magnetic rack and let it stand until the solution becomes clear. Carefully remove and discard the supernatant.
4. Add 200 μ l of 1x Bead Wash Buffer per capture (400 μ l for 2 reactions, 600 μ l for 3 reactions, 800 μ l for 4 reactions) to the tube. Vortex for 10 seconds.
5. Place the tube on a magnetic rack and let it stand until the solution becomes clear. Carefully remove and discard the supernatant.
6. Repeat steps 4 and 5 once.
7. Add 100 μ l of 1x Bead Wash Buffer per capture (200 μ l for 2 reactions, 300 μ l for 3 reactions, 400 μ l for 4 reactions) to the tube. Vortex for 10 seconds.
8. Transfer 100 μ l of cleaned beads to a new PCR tube (one tube per capture reaction).
9. Place tube(s) on a 96-well plate format magnetic rack and let it/them stand until the solution becomes clear. Carefully remove and discard the supernatant.



Do not allow the beads to dry.

Proceed immediately to Binding of Hybridized Targets to the Beads.

2.4.3 Binding of Hybridized Targets to the Beads

Materials

- Cleaned Streptavidin beads in PCR tube(s)
- Hybridization reaction(s)

Procedure



Work quickly to ensure that the temperature of the sample(s) remains close to 65 °C.

1. Remove the hybridization reaction(s) from the thermal cycler and briefly spin down the tube(s) and place them back on the thermocycler.



2. Place the washed Streptavidin bead tubes in the thermocycler (no more than two tubes at a time to avoid drying of beads).
3. For each hybridization reaction, transfer 17 μ l of the hybridization reaction solution to one PCR tube containing cleaned beads. Resuspend the beads by pipetting up and down until the solution is homogeneous.
4. Bind the DNA to the beads by placing the tube(s) into a thermal cycler set at 65 °C (lid at 75 °C). Incubate for 45 minutes.
5. During the incubation, gently pipette up and down the tube(s) every 15 minutes to ensure that the beads remain in suspension.

Proceed immediately to Wash Streptavidin Beads to Remove Unbound DNA.

2.4.4 Wash Streptavidin Beads to Remove Unbound DNA

Materials

- Hybridized targets on beads
- RNase/DNase-free 0.2 ml 8-tube strips
- DNA low-binding 1.5 ml tubes
- 1x Wash Buffer I ($\frac{1}{3}$ at 65 °C and $\frac{2}{3}$ at room temperature)
- 1x Wash Buffer II
- 1x Wash Buffer III
- 1x Stringent Wash Buffer (at 65 °C)
- Nuclease-free water
- IDTE

Procedure



Ensure that the temperature remains close to 65 °C for steps 1 to 7.

Note: If working with 2 or more capture tubes, work in a staggered manner from steps 2 to step 8, including the following:

1. When placing the first tube in thermoblock at 65 °C for the first incubation of 5 min (step 5), start a timer.
2. Begin processing the second tube.
3. When placing the second tube at 65 °C, note the time separating the tubes and ensure to respect this time gap along step 2 to step 8 to ensure each tube incubates exactly 5 min at 65 °C with the stringent wash.



1. Add 100 µl of 1x Wash Buffer I (at 65 °C) to each of the hybridized target/streptavidin beads tubes.
2. Working with one tube at a time, resuspend and transfer the mix one by one to a new DNA low-binding 1.5 ml tube. If working with two or more capture tubes, work in a staggered manner as indicated above.
3. Place tube on a magnetic rack and let it stand until the solution becomes clear. Carefully remove and discard the supernatant.
4. Add 200 µl of 1x Stringent Wash Buffer (at 65 °C) to the tube. Gently resuspend the beads by pipetting up and down.



Strong mixing of beads with the stringent wash buffer could decrease the quality of the capture.

5. Incubate at 65 °C for 5 minutes.
6. Place the tube on a magnetic rack and let it stand until the solution becomes clear. Carefully remove and discard the supernatant.
7. Repeat steps 4 to 6 once.

Work at room temperature.

8. Add 200 µl of 1x Wash Buffer I (at room temperature) to your tube. Gently resuspend the beads by pipetting up and down.

If working with 2 or more capture tubes; from this step on, process all the tubes at the same time.

9. Vortex for 2 minutes.
10. Place tube(s) on a magnetic rack and let it/them stand until the solution becomes clear. Carefully remove and discard the supernatant.
11. Add 200 µl of 1x Wash Buffer II to each tube(s). Vortex for 1 minute.
12. Place tube(s) on a magnetic rack and let it/them stand until the solution becomes clear. Carefully remove and discard the supernatant.
13. Add 200 µl of 1x Wash Buffer III to each tube(s). Vortex for 30 seconds. Spin briefly to collect all the liquid.
14. Place tube(s) on a magnetic rack and let them stand until the solution becomes clear. Carefully remove and discard the supernatant.
15. Add 200 µl of 1x IDTE to each tube(s). Resuspend the beads. Spin briefly to collect all the liquid.
16. Place tube(s) on a magnetic rack and let it/them stand until the solution becomes clear. Carefully remove and discard the supernatant.
17. Remove all the remaining liquid by using a P10 or P20 pipette.
18. Add 20 µl of nuclease-free water to each tube(s), resuspend and transfer the beads/water mix to a new PCR tube.

2.4.5 Post-Capture Amplification

Materials

- Streptavidin beads/nuclease-free water suspension (20 µl)
- Post-Capture PCR Master Mix 2x



- Post-Capture Illumina® Primers Mix
- Post-Capture PCR Enhancer
- Nuclease-free water

Preparation

1. Program the thermal cycler for Post-Capture Amplification using the following settings:


	TEMPERATURE (°C)	TIME (SECONDS)	
Lid	99	-	15 cycles
Step 1: Initial Denaturation	98	120	
Step 2: Denaturation	98	20	
Step 3: Annealing	60	30	
Step 4: Extension	72	30	
Step 5: Final Extension	72	60	
Hold	10	∞	

Procedure

1. Prepare the PCR pre-mix as follows:

PCR PRE-MIX				
Number of Reaction(s)	1	2	3	4
Post-Capture PCR Master Mix 2x (μl)	25	55	82.5	110
Post-Capture Illumina® Primers Mix (μl)	2.5	5.5	8.25	11
Post-Capture PCR Enhancer (μl)	2.5	5.5	8.25	11

2. Add 30 μl of PCR pre-mix to each bead suspension. Mix thoroughly by pipetting up and down 10 times and spin briefly.
3. Place the tube(s) in the thermal cycler and run the Post-Capture Amplification program.

 Safe stopping point overnight at 4 °C or -20 °C for longer storage.

2.4.6 Post-Capture Amplification Clean Up

Materials

- PCR reaction products in 50 μl each
- AMPure® XP beads equilibrated at room temperature



- Freshly prepared ethanol 80%
- IDTE
- DNA low-binding tubes for library storage

Procedure

1. Add 50 μ l of AMPure[®] XP beads to each of the 50 μ l PCR reaction products. Mix thoroughly by pipetting up and down 10 times.
2. Incubate at room temperature for 5 minutes and spin briefly if required to remove the liquid from the tube walls.
3. Place tube(s) on a magnetic rack for 5 minutes or until the liquid becomes clear.
4. Carefully discard 90 μ l supernatant using a multichannel pipette.

Keep the tube(s) on the magnetic rack for the following steps.

5. Using a multichannel pipette, add 170 μ l of 80% ethanol to the beads. Let the tube(s) stand for 30 seconds to 1 minute.
6. Carefully discard the ethanol.
7. Repeat steps 5 and 6 once.
8. Remove the residual ethanol using a P10 or P20 pipette.
9. Air-dry the beads at room temperature for 5 minutes. Do not over-dry the beads because this could decrease the amount of recovered DNA.

Remove the tube(s) from the magnetic rack.

10. Add 20 μ l of IDTE to the beads. Mix thoroughly by pipetting up and down 10 times. Incubate at room temperature for 5 minutes and spin briefly if required to remove the liquid from the tube walls.
11. Place tube(s) on a magnetic rack for 5 minutes or until liquid becomes clear.
12. Carefully transfer 18 μ l of the supernatant (transferring two times 9 μ l is recommended at this step) to a new, labeled library storage tube.



Safe stopping point overnight at 4 °C or -20 °C for longer storage.

2.4.7 Final Library Quantification and Quality Control

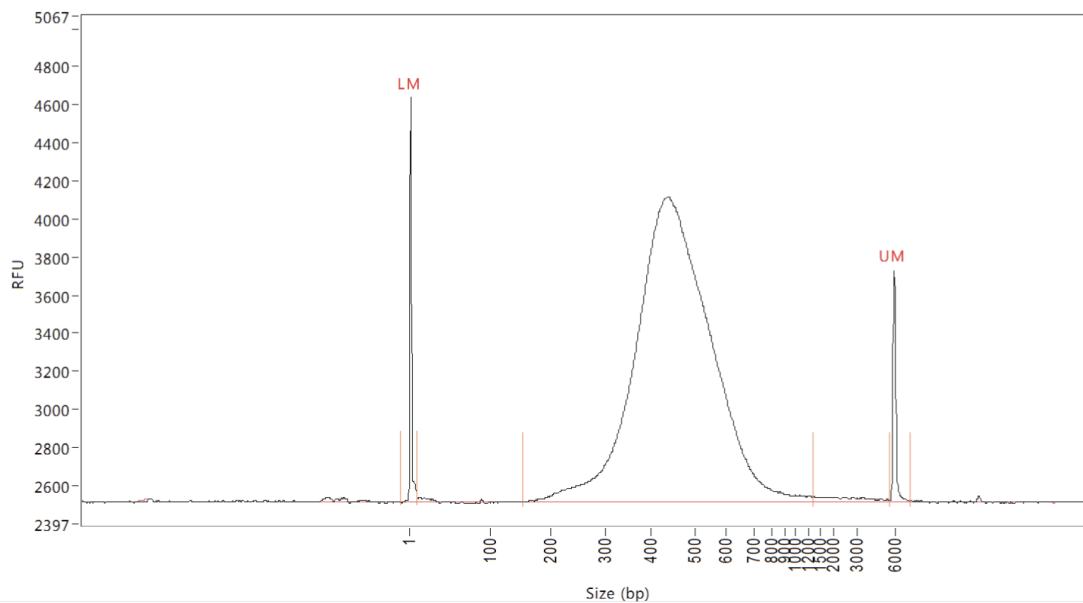
Materials

- Fluorometric quantitation equipment and reagents
- Capillary electrophoresis system



Procedure

1. Quantify each captured library pool with a fluorometric method (e.g., Qubit® HS quantification using 2 µl of the library).
2. Control the quality of the captured pools of libraries by analyzing their profile via capillary electrophoresis. Library DNA fragments should have a size distribution between 300 bp and 700 bp.



Example of post-capture library pool size distribution obtained with the Agilent Fragment Analyzer™ capillary electrophoresis system. LM: Lower Marker, UM: Upper Marker.



2.5 Sequencing

2.5.1 Sequencing Preparations

Materials

- Illumina® MiSeq® or NextSeq® 500/550 Sequencing Kits
- Final captured libraries
- EBT Buffer or similar

Procedure

1. Determine the molarity of each captured pool with the average size of the library (peak size in base pairs) and concentration (ng/μl) obtained during step 2.4.7 *Final Library Quantification and Quality Control* as follows:

$$\text{Library molarity (nM)} = \frac{\text{Library concentration (ng/}\mu\text{l)}}{\text{Average size in base pairs} \times 649.5} \times 10^6$$

2. Dilute each captured pool to 4 nM.
3. If processing multiple sequencing pools, mix them in equal amounts (e.g., 5 μl of each) and use this dilution according to Illumina® standard denaturation recommendations.
4. For loading dilution, see the table below:

SEQUENCING INSTRUMENT	LOADING DILUTION
MiSeq®	10 pM
NextSeq® 500/550 (Mid-Output)	1.3 pM
NextSeq® 500/550 (High-Output)	1.4 pM
	[Adjust the dilution (1.1 pM to 1.5 pM range) according to the number of clusters obtained in the first run]

The loading dilutions below are the guidelines recommended by the manufacturers. Adjust them according to the number of clusters you observe for your individual machine. Sample multiplexing must be adjusted depending on the instrument used. Please note that the following sequencers are not covered by this particular pipeline and would require testing via an additional setup program:










- For HiSeq®, load a 10 pM dilution.
- For MiniSeq™, load a 1.8 pM dilution.

5. For recommended reads per sample, see the table below:

READ LENGTH (BP)	RECOMMENDED TOTAL READS PER SAMPLE
150	2.7 million
≥ 200	2 million



3 SYMBOLS

SYMBOL	TITLE
	Consult instructions for use
	Catalog number
	Manufacturer
	Research Use Only
	Refer to Warnings and Precautions section.
	Refer to Warnings and Precautions section.
	Refer to Warnings and Precautions section.
	Refer to Warnings and Precautions section.
	Refer to Warnings and Precautions section.



4 SUPPORT

In case of difficulty using the SOPHiA DDM™ Desktop App, please consult the troubleshooting section of the "General information about usage of SOPHiA DDM™" document or contact our support line by telephone at +41 21 694 10 60 or e-mail support@sophiagenetics.com. Please visit www.sophiagenetics.com for further details.

Any serious incident occurring in relation to the device should be promptly reported to SOPHiA GENETICS and the competent authorities of the member state where the user is established.

Do not use components that are damaged. Contact support@sophiagenetics.com if there are any concerns with the kits.



5 APPENDICES

5.1 Appendix I: Dual Index Adapter Plates

5.1.1 16 Illumina®-compatible Dual Index Adapters In 96-well Plate Format (7 µl Each)

	1	2	3	4	5	6	7	...	12
A	701-501	701-502	701-503	701-504					
B	702-501	702-502	702-503	702-504					
C	703-501	703-502	703-503	703-504					
D	704-501	704-502	704-503	704-504					
E									
F									
G									
H									

5.1.2 32 Illumina®-compatible Dual Index Adapters In 96-well Plate Format (7 µl Each)

	1	2	3	4	5	6	7	...	12
A	701-501	701-502	701-503	701-504					
B	702-501	702-502	702-503	702-504					
C	703-501	703-502	703-503	703-504					
D	704-501	704-502	704-503	704-504					
E	705-501	705-502	705-503	705-504					
F	706-501	706-502	706-503	706-504					
G	707-501	707-502	707-503	707-504					
H	708-501	708-502	708-503	708-504					



5.1.3 48 Illumina®-compatible Dual Index Adapters In 96-well Plate Format (7 µl Each)

	1	2	3	4	5	6	7	...	12
A	701-501	703-502	705-503	707-501	709-502	711-503			
B	702-501	704-502	706-503	708-501	710-502	712-503			
C	703-501	705-502	701-504	709-501	711-502	707-504			
D	704-501	706-502	702-504	710-501	712-502	708-504			
E	705-501	701-503	703-504	711-501	707-503	709-504			
F	706-501	702-503	704-504	712-501	708-503	710-504			
G	701-502	703-503	705-504	707-502	709-503	711-504			
H	702-502	704-503	706-504	708-502	710-503	712-504			

5.1.4 96 Illumina®-compatible Dual Index Adapters In 96-well Plate Format (7 µl Each)

	1	2	3	4	5	6	7	8	9	10	11	12
A	701-501	702-501	703-501	704-501	705-501	706-501	707-501	708-501	709-501	710-501	711-501	712-501
B	701-502	702-502	703-502	704-502	705-502	706-502	707-502	708-502	709-502	710-502	711-502	712-502
C	701-503	702-503	703-503	704-503	705-503	706-503	707-503	708-503	709-503	710-503	711-503	712-503
D	701-504	702-504	703-504	704-504	705-504	706-504	707-504	708-504	709-504	710-504	711-504	712-504
E	701-505	702-505	703-505	704-505	705-505	706-505	707-505	708-505	709-505	710-505	711-505	712-505
F	701-506	702-506	703-506	704-506	705-506	706-506	707-506	708-506	709-506	710-506	711-506	712-506
G	701-507	702-507	703-507	704-507	705-507	706-507	707-507	708-507	709-507	710-507	711-507	712-507
H	701-508	702-508	703-508	704-508	705-508	706-508	707-508	708-508	709-508	710-508	711-508	712-508



5.1.5 Index Sequences For The Illumina®-compatible Dual Index Adapters

i5	I5 SEQUENCES FOR SAMPLE SHEET MiSeq®, HiSeq® 2000/2500, NextSeq® 1000/2000 (sample sheet v2), NovaSeq™ 6000 (v1.0 reagent kits)	I5 SEQUENCES FOR SAMPLE SHEET NextSeq® 500/550, HiSeq® 3000/4000/X, NextSeq® 1000/2000 (sample sheet v1), NovaSeq™ 6000 (v1.5 reagent kits), MiniSeq™
D501	TATAGCCT	AGGCTATA
D502	ATAGAGGC	GCCTCTAT
D503	CCTATCCT	AGGATAGG
D504	GGCTCTGA	TCAGAGCC
D505	AGGCGAAG	CTTCGCCT
D506	TAATCTTA	TAAGATTA
D507	CAGGACGT	ACGTCCTG
D508	GTACTGAC	GTCAGTAC

i7	i7 SEQUENCE
D701	ATTACTCG
D702	TCCGAGGA
D703	CGCTCATT
D704	GAGATTCC
D705	ATTCAGAA
D706	GAATTCGT
D707	CTGAAGCT
D708	TAATGCGC
D709	CGGCTATG
D710	TCCGCGAA
D711	TCTCGCGC
D712	AGCGATAG



5.2 Appendix II: Laboratory Equipment Used in SOPHiA GENETICS Laboratory

USER-SUPPLIED MATERIALS	SUPPLIER	PRODUCT NAME	CATALOG N°
RNase/DNase-free 8-tube strips (0.2 ml)	Thermo Fisher Scientific	EasyStrip Snap Tubes	AB-2000
DNA low binding tubes (1.5 ml)	Axygen	MaxyClear Microcentrifuges Tubes	MCT-175-C
Tubes (1.5 ml)	Eppendorf	Eppendorf Tubes	3810X
Conical tubes (15 ml and 50 ml)	Falcon	15 ml & 50 ml Conical Centrifuge Tubes	352096 & 352070
Filter tips	Starlab	TipOne RPT	S1180-3710, S1183-1740, S1180-8710, S1180-9710, S1182-1730
Ethanol (molecular biology grade)	Merck	Ethanol Absolute	1.00983.1000

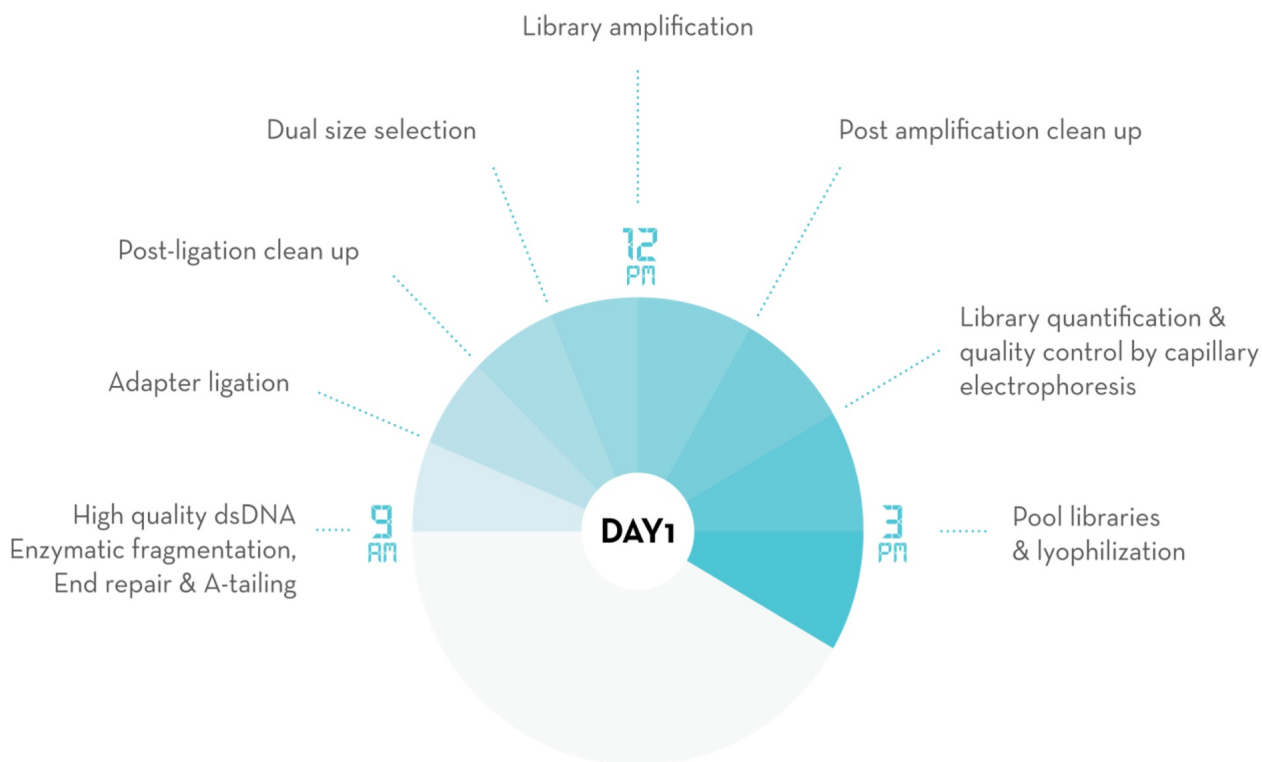
PRE-PCR ZONE	SUPPLIER	PRODUCT NAME	CATALOG N°
Vortex mixer	Scientific Industries	Vortex Genie 2	SI-0236
Table top microcentrifuge (8-tube strips compatible)	Starlab	Mini Centrifuge	N2631-0007
Magnetic separation rack 96-well type	Alpaqua	96S Super Magnet Plate	A001322
Magnetic separation rack 96-well type	Thermo Fisher Scientific	DynaMag-96 Side Magnet	12331D
Multichannel pipettes (P10; P100; P300)	StarLab	ErgoOne	S7108-0510, S7108-1100, S7108-3300
Thermal cycler with programmable heated lid	Biometra	TAdvanced 96	
Fluorometric quantitation equipment and reagents	Thermo Fisher Scientific	Qubit 3.0 Fluorometer & Qubit dsDNA HS Assay kit	Q33216 & Q32854
Single channel pipettes (P10; P100; P200; P1000)	StarLab	ErgoOne	S7100-0510, S7100-1100, S7100-2200, S7100-1000



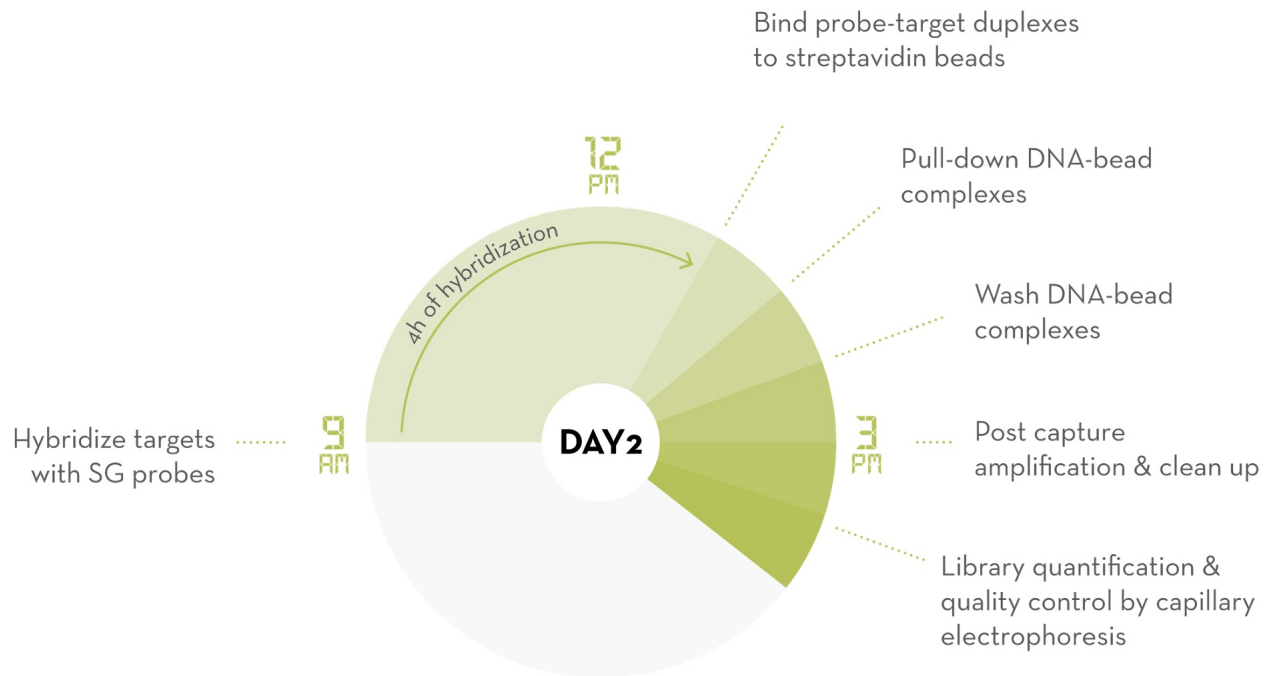
POST-PCR ZONE	SUPPLIER	PRODUCT NAME	CATALOG N°
Thermal cycler with programmable heated lid	Biometra	TAdvanced 96	
Capillary electrophoresis system	Advanced Analytical	Agilent Fragment Analyzer	
Vacuum concentrator (SpeedVac™ or similar)	Thermo Fisher Scientific	Savant DNA120-230	
Dry block heater or water bath(1.5 ml tube compatible)	Techne	Dri-Block DB-1	
Magnetic separation rack (1.5 ml tube compatible)	Thermo Fisher Scientific	MagJET Separation Rack, 12 x 1.5 mL tube	MR02
Magnetic separation rack (96-well type)	Alpaqua	96S Super Magnet Plate	A001322
Magnetic separation rack 96-well type	Thermo Fisher Scientific	DynaMag-96 Side Magnet	12331D
Vortex mixer	Grant instrument	Multi-tube Vortex Mixer, V32	
Vortex mixer	Scientific Industries	Vortex Genie 2	SI-0236
Table top microcentrifuge (8- tube strips compatible)	StarLab	Mini Centrifuge	N2631-0007
Multichannel pipettes (P10; P100; P300)	StarLab	ErgoOne	S7108-0510, S7108- 1100, S7108-3300
Fluorometric quantitation equipment and reagent	Thermo Fisher Scientific	Qubit 3.0 Fluorometer & Qubit dsDNA HS Assay kit	Q33216 & Q32854
Single channel pipettes (P10; P100; P200; P1000)	StarLab	ErgoOne	S7100-0510, S7100- 1100, S7100-2200, S7100-1000



5.3 Appendix III: General Workflow SOPHiA DDM™ Capture Solution



Library Preparation with SOPHiA GENETICS™ DNA Library Prep Kit I



CAPTURE

EASY WORKFLOW

- ONLY 1-4 TUBES TO HANDLE (MULTIPLEX POOLED LIBRARIES)
- ONLY 3 HOURS HANDS-ON TIME



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Document Approvals

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Approval Verdict: Approve	Martin Fritzsche, (mfritzsche@sophiagenetics.com) Technical Approval 11-Aug-2023 09:41:02 GMT+0000
Approval Verdict: Approve	Nahimi Amara Bekele, (namarebekele@sophiagenetics.com) Regulatory Approval 15-Aug-2023 08:49:35 GMT+0000
QA Approval Verdict: Approve	Brian Acon, (bacon@sophiagenetics.com) Quality Assurance Approval 16-Aug-2023 07:54:17 GMT+0000