SWIFT PROTOCOL

Swift Normalase™ Amplicon Panels (SNAP)

Single-tube multiplex PCR NGS library prep with a high-throughput workflow

Protocol for cat. nos.:

Panel specific primers

Oncology (primers only):
562G1-96, 56G Oncology Panel v2
PC8G1-96, 57G Pan-Cancer Profiling Panel
520G1-96, BRCA1 and BRCA2 Panel
570G1-96, BRCA1, BRCA2, and PALB2 Panel
510G1-96, EGFR Pathway Panel
530G1-96, Comprehensive TP53 Panel
LG8G1-96, Lung Cancer Panel
CR8G1-96, Colorectal Cancer Panel
LN8G1-96, Lynch Syndrome Panel
MY8G1-96, Myeloid Panel

Disease susceptibility: (primers only):
550G1-96, CFTR Panel
ACE2G1-96, ACE2 Panel

Sample tracking (primers only):
500G1-96, Sample_ID Panel

SNAP core kits:
Swift Normalase Amplicon Panels (SNAP) Core Kit (96 rxns, no indexing)
Swift Normalase Amplicon Panels (SNAP) Core Kit (4x96 rxns bundle, no indexing)

SNAP indexing primers:
SNAP Set 1A to Set 2B Combinatorial Dual Indexing Primers (96-plex to 384-plex)
SNAP Unique Dual Indexing Primer Plates (96-plex to 1536-plex)

See page 21 for details on product ordering information.

Visit swiftbiosci.com/protocols for updates.

Swift BIOSCIENCES™

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Support

For technical support, please contact Swift at TechSupport@swiftbio.com, or by phone: 734.330.2568
9:00 am – 5:00 pm ET, Monday through Friday.

Product information

SNAP kits offer a robust NGS workflow that provides optimal coverage and NGS data quality on Illumina® sequencing platforms. These kits leverage patented multiplex PCR technology, enabling library construction from a variety of sample types, including formalin-fixed, paraffin-embedded (FFPE) and circulating, cell-free DNA (cfDNA) using tiled, overlapping primer pairs within a single multiplexed pool.

See Appendix A for panel specific information on panel content and size as well as multiplexed sequencing recommendations. See individual panel data sheets for details regarding target design and coverage.

Product feature	Specification
Input material	10-25 ng DNA
Time	2 hours: DNA to library 3 hours: DNA to normalized library pool
Components provided	Included: • Target-specific multiplex primer pool • PCR and library prep reagents Optional: • Combinatorial dual indexed adapters • Swift Normalase Note: Kits do not include RT module or magnetic beads
Multiplexing capability	Up to 384 CDIs or 1536 UDIs
Recommended depth	500X coverage (germline variant detection); 5000X coverage (somatic variant detection down to 1% allele frequency)
Specifications	>90% on target >90% coverage uniformity (at >20% of the mean)

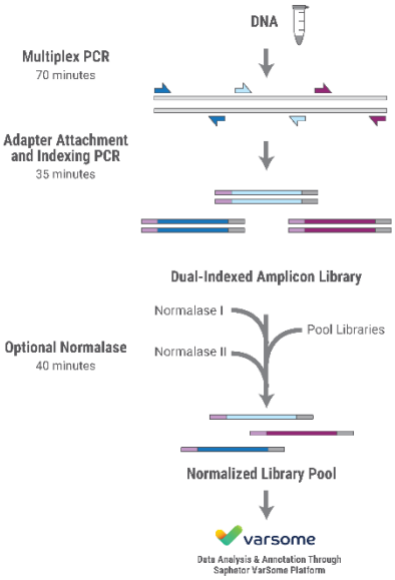
Applications and sample types

Variant discovery research, disease disposition research, oncology research, sample tracking research [sample types: gDNA from fresh frozen samples, FFPE, cell-free DNA (cfDNA), circulating tumor DNA (ctDNA), blood].

SNAP workflow

Swift Normalase Amplicon Panels (SNAP) utilize multiple overlapping amplicons in a single tube, using a rapid, 2-hour workflow to prepare ready-to-sequence libraries. The PCR1+PCR2 workflow generates robust libraries, even from low input quantities. The libraries may be quantified with conventional methods such as Qubit® or Agilent Bioanalyzer and normalized by manual pooling, or normalized enzymatically with the included Swift Normalase reagents.

This protocol includes instructions for a multiplex PCR step to enrich target sequences, an indexing PCR step to amplify and add combinatorial or unique dual indexed adapter sequences, and an optional downstream Normalase step to produce an equal molar library pool.



Kit contents

These kits contain sufficient reagents for the preparation of 96 libraries (10% excess volume provided).

Protocol stage	Component	96 Rxns	Storage
Multiplex PCR (Pre-PCR box)	Reagent G1*	2x 106 µL	-20°C
	Reagent G2	317 µL	
	Enzyme G3	1584 µL	
	Pre-PCR TE	1200 µL	
Indexing PCR (Post-PCR box)	Reagent I1	348 µL	
	Enzyme I2	53 µL	
	Enzyme I3	15 µL	
	Enzyme I4	2640 µL	
	Post-PCR TE	4161 µL	
Indexing box**	SNAP CDI D50X	26 µL each	
	SNAP CDI S7XX	15 µL each	
Indexing plate**	SNAP UDI (pre-mixed pairs)	12 µL per well	
Normalase (Post-PCR box)	Buffer S1	454 µL	
	Reagent S2	21 µL	
	Enzyme S3	53 µL	
	Buffer N1	101 µL	
	Enzyme N2	10 µL	
	Reagent X1	21 µL	
Additional reagents	PEG NaCl	20 mL	Room Temp

*Reagent G1 is included in the Multiplex Primer pool. Additional Pre-PCR and Post-PCR box reagents and PEG NaCl are included in cat. no. SN-5X296.

**Indexing boxes are cat. nos. SN-5S1A96, SN-5S1B96, SN-5S2A96, and SN-5S2B96. Indexing Primer Plates are cat. nos. SN91096-1-PLATE, SN91096-2-PLATE, SN91096-3-PLATE, SN91096-4-PLATE (available as individual plates), and SN91384-PLATES, SN91384-B-PLATES, SN91384-C-PLATES, and SN91384-D-PLATES (available as 4x96 bundle plates).

Storage and usage recommendations

- Upon receipt, store the SNAP Library Kit products at –20°C with the exception of the PEG solution, which is stored at room temperature.
- Separate the multiplex PCR Reagents (keep in pre-PCR area), Indexing and Normalase Reagents (keep in post-PCR area).
- To maximize use of enzyme reagents when ready to use, remove enzyme tubes from –20°C storage and place on ice for 10 minutes prior to pipetting. Attempting to pipette enzymes at –20°C may result in shortage of enzyme reagents.

- After thawing reagents on ice, briefly vortex (except enzymes) to mix well, then pulse spin to collect contents before proceeding. Enzyme G3 is the only enzyme that may be vortexed.
- Always add reagents to the master mix in the specified order as stated throughout the protocol. The indexing primers (SNAP CD and UD Indexes) are the only reagents that are added individually to each sample.

Materials and equipment not included

- SPRIselect beads (Beckman Coulter, cat. nos. B23317/B23318/B23319) or Agencourt AMPure XP beads (Beckman Coulter, cat. nos. A63880/A63881/A63882)
- Permagen Magnetic Separator (Cat. No. MSR812), Agencourt SPRIPlate, or similar magnetic rack for magnetic bead clean-ups
- Qubit®, Nanodrop, or other similar input RNA quantification assay
- qPCR-, electrophoretic-, or fluorometric-based library quantification assay for Illumina® libraries
- Microcentrifuge
- Vortex
- Programmable thermocycler
- 0.2 mL PCR tubes or 96-well plates
- Aerosol-resistant tips and pipettes ranging from 1 to 1,000 µL
- 200 proof (absolute) ethanol and nuclease-free water (both molecular biology grade) for preparation of fresh 80% ethanol
- Pipette tips (e.g., 8-channel or 12-channel), 8-tube strips, an unskirted 96 well plate, or plate puncher for pre-piercing the foil seal if using the single-use UD indexing plates.

Tips and techniques

- Assemble all reagent master mixes and reactions ON ICE and scale volumes as appropriate, using 5% excess volume to compensate for pipetting loss. Calculate the total volume of the master mixes and prepare them in advance to ensure the magnetic beads do not over-dry during size selection steps while awaiting completion of master mix assembly.

- Neglecting to store master mixes and reagents on ice prior to incubations reduces functionality of this product.

- To avoid cross-contamination: physically separate the laboratory space, equipment, and supplies where pre- and post-PCR processes are performed, including appropriate reagent boxes for multiplex PCR and indexing PCR. Clean both the pre-PCR and post-PCR lab areas using 0.5% sodium hypochlorite (10% bleach). Use barrier pipette tips to avoid exposure to potential contaminants. Always change tips between each sample and dispose of pipette tips and other disposables in sealed plastic bags. Move samples to post-PCR area before opening tubes. This workflow, like any amplicon enrichment technology, poses a risk of contamination of surfaces and other samples following the amplification step. Please use caution when opening your sample tubes following the multiplex PCR step.

Input material considerations

The starting material should be quantified with the appropriate assay (qPCR-based for FFPE and cfDNA to determine usable DNA content and sample integrity, Qubit for high quality DNA from whole blood or fresh frozen or cultured cells). Most panels are designed with amplicon size of 140 bp to ensure compatibility with both FFPE and cfDNA samples.

For qPCR-based determination of sample quantity and integrity, Alu primers are available from Swift at www.swiftbiosci.com. Input DNA quantification primers are cat. no. 90396 (see https://swiftbiosci.com/wp-content/uploads/2019/02/17-1480-Input-DNA-Protocol-web.pdf).

The optimal coverage uniformity, sensitivity, and specificity of this technology are achieved with input amounts in the 10–25 ng range. Between 25–100 ng, coverage uniformity may be mildly reduced while sensitivity and specificity are preserved. Using less than 10 ng may reduce specificity of the assay, reduce library yields and reduce sensitivity of variant calling for low frequency alleles. Consider the following example allele frequencies and detection limits. As shown below it is recommended to use at least 10 ng input for 1% allele detection limit to ensure sufficient copy number of the allele of interest. If less than 10 ng is available, expect a lower detection limit. For example, at 1 ng input, a 10% limit of detection is expected. When using damaged samples, ensure that the usable amplifiable input is qualified by a qPCR assay as mentioned above.

Sample quantity	Human genome equivalents	Example allele frequency	Example allele copies	Likelihood of detection
10 ng	3000	10%	300	✓
10 ng	3000	1%	30	✓
1 ng	300	10%	30	✓
1 ng	300	1%	3	X

Prepare SNAP libraries

Multiplex PCR step

1. Load the Multiplex PCR program and allow the block to reach 98°C before loading samples (confirm lid heating is turned ON and is set to reach 105°C).

Pre-program thermocycler

Multiplex PCR thermocycler program	**Lid heating ON**		
	30 sec	98 °C	
	10 sec	98 °C	**4 cycles**
	5 min	* °C	
	1 min	* °C	
	10 sec	98 °C	**18 cycles**
	1 min	64 °C	
	1 min	65 °C	
	Hold	4 °C	

*** NOTE:** Temperature at this step is panel-specific. Please use the following panel-specific annealing temperature specified below:

Panel	Annealing temperature (5 min)	Extension temperature (1 min)
56G Oncology v2 BRCA1 and BRCA2 BRCA1 and BRCA2 and PALB2 CFTR Comprehensive TP53 Sample_ID EGFR Pathway ACE2	63°C	65°C
57G Pan-Cancer Profiling	65°C	65°C
Lung Cancer Myeloid Colorectal Cancer Lynch Syndrome	66°C	66°C

2. Gently nutate Enzyme G3 at room temperature for 5 minutes, or until all solutes appear to be in solution. Place back on ice for remainder of use.
3. Load 10 µl of DNA sample directly into each PCR tube.
4. **Keep all tubes on ice during assembly of the master mix and the reaction until placed in thermocycler.**

Panel-specific multiplex PCR reaction mix

Before mixing, calculate the total volume of the master mix based on the number of reactions required with appropriate overage for pipetting. Vortex components G1 and G2 and pulse-spin tubes to collect contents. Make the multiplex PCR reaction mix. Keep prepared master mix on ice until ready to use.

Component	Volume (1 reaction)
• Reagent G1*	2 µL
• Reagent G2	3 µL
• Enzyme G3	15 µL
Reaction mix	**20 µL**

**Reagent G1 is the panel-specific set of multiplex primers.*

5. Mix the master mix well and then add 20 µL of the multiplex PCR reaction mix to each 10 µL input DNA sample on ice. Mix well, then place in the thermocycler and run the program.

IMPORTANT!
Move samples to post-PCR area before opening tubes.

6. Near the completion of the thermocycler run, prepare the indexing reaction mix (below) in the post-

PCR area. **Assemble this reaction mix on ice and keep cold until adding it to samples in the indexing step**. All components except indexes may be master-mixed when running multiple samples in parallel.

Indexing PCR step

Before mixing, calculate the total volume of the master mix based on the number of reactions of choice, with appropriate overage for pipetting. We recommend preparing at least 10 reactions at any one time to maintain a volume of Enzyme I3 that can be accurately pipetted. Keep prepared master mix on ice.

Component	Volume (1 reaction)
• Reagent I1	3.3 µL
• Enzyme I2	0.5 µL
• Enzyme I3	0.1 µL
• Enzyme I4	25 µL
Reaction mix	**28.9 µL**

Keep prepared master mix on ice during Size selection and clean-up step 1.

Size selection and clean-up step 1

7. Ensure beads and samples are at room temperature. Briefly vortex beads to homogenize before use.
8. Add 30 µL (ratio: 1.0) of magnetic beads to each 30 µL sample. Mix by vortexing. Pulse-spin the samples in a microfuge. Ensure no bead-sample suspension droplets are left on the sides of the tube.
9. Incubate the samples for 5 minutes at room temperature off the magnet.
10. Place the sample tubes on a magnetic rack until the solution clears and a pellet is formed (≈ 5 minutes).
11. While leaving your sample on the magnet, remove and discard the supernatant without disturbing the pellet (approximately 5 µL may be left behind). Leave tubes on the magnet.
12. Add 180 µL of freshly prepared 80% ethanol solution to the pellet while it is still on the magnet. Use care not to disturb the pellet. Incubate for 30 seconds, and then carefully remove the ethanol solution.
13. Repeat for a second wash with the ethanol solution.
14. Pulse-spin the samples in a microfuge, place back onto the magnet and remove any residual ethanol solution from the bottom of the tube with a small volume tip.
15. Resuspend each bead pellet in 17.4 µl Post-PCR TE Buffer. Proceed to the Indexing PCR step. If an off-bead PCR is preferred, place the tubes back on the magnet and transfer the 17.4 uL of eluate to a fresh tube. Then proceed as written.

IMPORTANT!
Continue working in the post-PCR area. Keep samples at room temperature. At no time should "with bead" samples be stored on ice, as this affects binding to magnetic beads.

Indexing PCR Thermocycler Program	**Lid heating ON (105°C)**		
	20 min	37°C	
	30 sec	98°C	
	10 sec	98°C	**5 cycles***
	30 sec	60°C	
	1 min	66°C	
	Hold	4°C	

***The PCR cycle number can be increased for samples that may give low yields.**

16. Load the Indexing PCR program and allow the block to reach 37°C before loading samples (confirm lid heating is turned ON and is set to reach 105°C).

    Add a unique combination of 2 µL SNAP CD Index D50X + 1.7 µL SNAP CD Index S7XX to each sample, OR add 3.7 µL of a pre-mixed SNAP UD indexing primer pair to each sample if using the single use plates (see UDI plate usage guidelines).
17. Add 28.9 µL of the cold Indexing PCR Reaction Mix to each sample and mix thoroughly (total volume 50 µL).
18. Place in the thermocycler and run the program.

Size selection and clean-up step 2

19. Ensure PEG NaCl solution is at room temperature. Briefly vortex the PEG NaCl solution to homogenize before use.
20. Add 42.5 µL (ratio: 0.85) of PEG NaCl solution to each 50 µL sample. Mix by vortexing. Ensure no bead-sample suspension droplets are left on the sides of the tube. If performing an “off bead PCR” use 42.5 µL (ratio: 0.85) of fresh magnetic beads.
21. Incubate the samples for 5 minutes at room temperature off the magnet.
22. Pulse-spin the samples in a microfuge. Place the sample tubes on a magnetic rack until the solution clears and a pellet is formed (≈ 5 minutes).
23. While leaving your sample on the magnet, remove and discard the supernatant without disturbing the pellet (approximately 5 µL may be left behind). Leave tubes on the magnet.
24. Add 180 µL of freshly prepared 80% ethanol solution to the pellet while it is still on the magnet. Use care not to disturb the pellet. Incubate for 30 seconds and then carefully remove the ethanol solution.
25. Repeat, for a second wash with the 80% ethanol solution.
26. Pulse-spin the samples in a microfuge, place back onto the magnet, and remove any residual ethanol solution from the bottom of the tube with a small-volume tip.
27. Proceed immediately to add 20 µL of Post-PCR TE buffer and resuspend the pellet, mixing well by pipetting up and down until homogenous. Incubate at room temperature for 2 minutes off the magnet. Then place the sample back on the magnet and transfer the clean 20 µL library eluate to a fresh tube. Ensure that eluate does not contain magnetic beads (indicated by brown coloration in eluate). If magnetic beads are present, pipette eluate into a new tube, place on magnet, and transfer eluate again.

Library quantification

Accurate library quantification is essential to load the sequencing instrument properly. Libraries can be quantified using fluorometric-, electrophoretic-, or qPCR-based methods and normalized manually. Alternatively, libraries can be enzymatically normalized following the Normalase protocol below. Note, for optimal normalization using Normalase, a minimum of 12 nM yield is needed per sample. If library yields are below 12 nM, increase the number of PCR cycles to pass the 12 nM threshold or switch to the 6 nM threshold Normalase protocol described below.

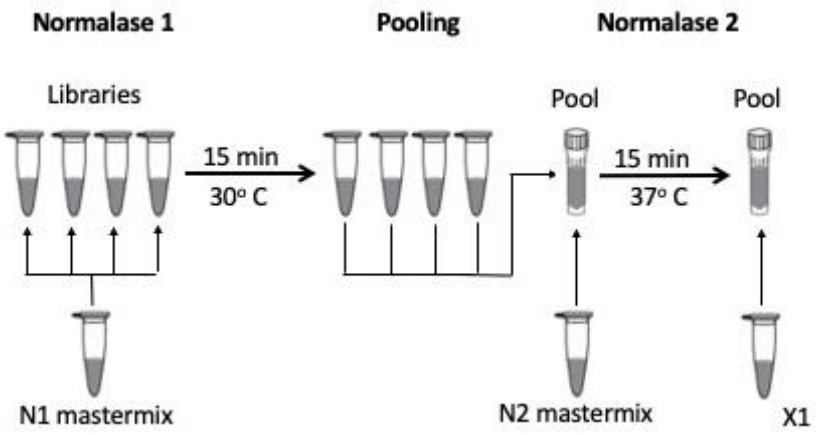
Introduction to Normalase

This guide provides instructions for optional enzymatic normalization of multiplexed SNAP next generation sequencing (NGS) libraries for equimolar pools and balanced sample representation in sequencing. The protocol is designed for SNAP libraries that produce consistent amplified library yields of ≥12 nM following indexing PCR, and it generates an equal molar library pool. Most samples processed with the SNAP protocol produce amplified library yields of 12 nM or greater; however, if there is concern that not all samples will reach 12 nM, adjusting Normalase chemistry to require a minimum of only 6 nM can alternatively be performed.

A simple calculator for converting between ng/µL and nM is available. Please use a finished library size of 285 bp (for use in the Base Pair Length column).

The workflow consists of three steps for libraries amplified to a minimum yield of 12 nM during the adapter attachment and indexing PCR step:

1. **Normalase I** to enzymatically select a 4 nM (or 2 nM if using ≥6 nM option) library fraction
2. **Library pooling** of samples for multiplexed sequencing
3. **Normalase II** to enzymatically generate an equimolar library pool



Workflow schematic: *Normalase I Mastermix is added to samples and incubated at 30ºC for 15 minutes. Sample pooling is then performed, and then the Normalase II Mastermix is added to the pool and incubated at 37ºC for 15 minutes. Reagent X1 inactivates the reaction and a final equal molar pool is produced.*

Notes regarding Normalase specification

The Normalase product specification is defined by cluster density of the Normalase pool when loaded on a MiSeq v2 flow cell at 12 pM to achieve a 1000–1200 K/mm^2 cluster density and CV ≤ 15% within a pool. Across Illumina platforms, library types, and insert sizes, the optimization of loading concentration may be required to achieve the optimal number of reads supported by the flow cell of choice.

Normalase I: enzymatic selection

If you are concerned that the 12 nM threshold has not been met after indexing PCR:

- Spot check library yields using either fluorometric methods (e.g., Qubit) or electrophoretic methods (e.g., Bioanalyzer).
- A Normalase workflow modification can be performed that requires a 6 nM threshold to obtain a 2 nM Normalase pool (see below).

1) Pre-set a thermocycler program as listed below.

Thermocycler program
15 min at 30°C with open lid or lid heating OFF

Prepare the Normalase I master mix as listed in the table below. The mix can be prepared at room temperature and stored on ice until use if prepared in advance. Ensure that it is thoroughly mixed by moderate vortexing followed by a pulse spin to collect contents prior to use. For libraries with lower yields ≥ 6 nM, or for a final pool of 2 nM (instead of 4 nM), please use half of the specified volume of Reagent S2 and add an equal volume of TE, thus reducing concentration by two-fold, then proceed as written.

Reagent	Per library	24 Libraries	96 Libraries
• Buffer S1	4.3 µL	103.2 µL	412.8 µL
• Reagent S2	0.2 µL	4.8 µL	19.2 µL
• Enzyme S3	0.5 µL	12 µL	48 µL
Total volume	**5 µL**	**120 µL**	**480 µL**

IMPORTANT!

The Normalase I Master Mix should be built for a minimum of 10 reactions to ensure pipetting accuracy.

2) Using a calibrated P10 pipette, add 5 µL of Normalase I master mix into each 20 µL library eluate at room temperature and thoroughly mix by moderate vortexing for 5 seconds.

3) Spin down the sample tube in a microfuge. Place in the thermocycler and run the program.

Safe stopping point

Libraries can be stored at –20 °C post-Normalase I.

Equal volume library pooling

Sufficient Normalase II reagents are supplied so this step can be repeated to enable various re-pooling combinations as only 5 µL of post-Normalase I library (out of 25 µL volume) is used for pooling. Also note that stability of normalized pools (after Normalase II) is limited, with a storage time of four weeks, since the resulting normalized pools contain single-stranded DNA. Therefore, if re-sequencing is required after four weeks, for best results re-pool the Normalase I libraries and repeat Normalase II and inactivation.

NOTE: If you are pooling < 5 libraries, contact tech support at TechSupport@swiftbio.com for low-plex pooling recommendations.

NOTE: If pooling 5 µL per sample does not generate a normalized pool of sufficient volume for instrument loading, contact tech support at TechSupport@swiftbio.com for high sample volume pooling recommendations.

IMPORTANT!

Consider your desired number of reads for each sample and only pool those samples together that have the same required depth. For example, samples each requiring 100,000 reads can be pooled together, whereas samples requiring 1 million reads should be combined in a separate pool. Thus, you can adjust your ratio of pools when loading the instrument to achieve the desired sequence depth for each pool.

1. Following the Normalase I incubation, generate a library pool (or pools) by placing 5 µL of each individual library into a 0.2 mL PCR tube if pooling 30 libraries or less (achieves up to a final volume of 186 µL). Alternatively, use a 1.5 mL screw-cap microfuge tube, particularly when pooling greater than 30 libraries, as the volume will exceed the PCR tube maximum volume.

   To ensure even pooling, use of a calibrated P10 pipette will produce the best results.

2. Thoroughly mix, spin the library pools in a microfuge, and proceed to the Normalase II reaction.

Normalase II: enzymatic normalization

1. Pre-set a thermocycler program as listed below. Alternatively, if using a 1.5 mL screw cap microfuge tube, set a heat block at 37 °C.

Thermocycler program	Heat block (1.5 mL screw-cap microfuge tube)
15 min at 37°C with open lid or lid heating OFF	15 min at 37°C

2. Pre-mix Normalase II Master Mix (listed in the table below). The master mix can be stored on ice until use and then added to pools at room temperature.

Reagents*	Per library	24 Libraries	96 Libraries
• Buffer N1	0.96 µL	23.04 µL	92.16 µL
• Enzyme N2	0.04 µL	0.96 µL	3.84 µL
Total volume	**1 µL**	**24 µL**	**96 µL**

*It is recommended to prepare Normalase II master mix for 24 samples even if you are processing less than 24 samples in order to avoid pipetting extremely low volumes; for best results use a calibrated P2 pipet for

adding Enzyme N2. Although sufficient reagents are supplied for up to 5 repeated Normalase II reactions per sample, repeatedly processing a lower number of samples will result in significant loss of Normalase II reagents.

3. Add 1 µL of Normalase II master mix multiplied by the total number of libraries within each prepared pool.
4. Mix well by vortexing for 5 seconds, and spin down the library pools in a microfuge.
5. Place the library pools in the thermocycler and run the program or place the 1.5 mL screw cap microfuge tubes into the 37°C heat block.

Normalase inactivation

1. Following the Normalase II reaction, pre-set a thermocycler program as listed below.

Thermocycler program	Heat block (1.5 mL screw-cap microfuge tube)
Hold at 95ºC 2 min at 95ºC with lid kept at 95ºC Hold at 4ºC	2 min at 95ºC

2. Add 0.2 µL of Reagent X1 multiplied by the total number of libraries within each prepared pool. See examples below:

Reagent	Per library	24-Plex pool	96-Plex pool
• Reagent X1	0.2 µL	4.8 µL	19.2 µL

3. Place the library pools in the thermocycler and advance the program or place the 1.5 mL screw-cap microfuge tubes into the heat block. If using a 1.5 mL screw-cap microfuge tube, set a heat block at 95°C to incubate your library pools, being careful not to incubate the samples longer than 2 minutes.
4. Your final multiplexed library pools are now equimolar. Proceed to qPCR quantification of your Normalase pool and sequencing. It is not necessary to perform an additional purification step.

Quantification and calibration of Normalase pools

To ensure optimal sequencing results, perform a qPCR quantification on your final Normalase pool(s). Final library pools are ssDNA and cannot be quantified by dsDNA-based fluorometric methods or fragment analysis. If you do not have a qPCR assay, validate a commercially available kit by calibrating your qPCR results and sequencer loading concentrations before proceeding (for example, KAPA Library Quantification Kit, cat. no. KK4828).

The Normalase 4 nM formulation may not conform to your qPCR assay quantification due to the lack of precision across different qPCR assays and laboratory practices. Using your validated qPCR assay that reproducibly predicts an optimal number of reads on your sequencing instrument, load your final pool based on your qPCR results. Across other Illumina platforms, library types, and insert sizes, optimization of loading concentration may be required to achieve the optimal number of reads supported by the flow cell of choice. If you have chosen the 6 nM to 2 nM option but require a higher pool concentration for your sequencer, perform a 2.0X SPRI to concentrate pool and then proceed to qPCR quantification and loading.

Sequencing recommendations

SNAP libraries may be sequenced using paired-end sequencing on Illumina instruments. We strongly recommend using 2 x 150 paired-end reads. The depth of coverage required will depend on the application (see page 3). Be sure to use either eight CD or ten UD sequencing cycles for each index read.

See Appendix A for panel specific information on content and size as well as multiplexed sequencing recommendations.

Due to the complexity of the libraries, no PhiX spike-in is required on MiSeq or MiniSeq instruments. The NextSeq550 may be sensitive to low complexity and PhiX, or another suitable high-complexity library spike-in may be required. Contact Illumina technical support for further information regarding sequencing instrument compatibility with low-complexity sequences.

Please refer to the latest version of Illumina Experiment Manager for detailed instructions on how to set up a sample sheet. Be sure to select the appropriate workflow parameters as noted below:

- Read Type: “Paired End”
- Cycle Read 1: “151”,
- Cycles Read 2: “151”

Make sure the “Use Adapter Trimming” and “Use Adapter Trimming Read 2” are selected when setting up the sequencing run. Failure to trim adapter sequences will result in incorrect primer trimming and will lead to inaccurate variant calling. Alternatively, perform adapter trimming by Trimmomatic during data analysis. For more information, see below and consult our Bioinformatics Resources page at swiftbiosci.com/biofx.

Sequencing data analysis

For customers using a SNAP kit who are comfortable with command line tools and want a ready-to-use variant calling analysis workflow they can run on a Linux or MacOS machine, Swift offers a full variant calling workflow with all tools and reference files pre-installed and configured in a Docker image available for download. For customers without command line tools, VarSome Platform may be used for data analysis on selected panels. Please refer to the data sheet for more details.

Features

- One easy install: Docker image file can be downloaded and loaded onto a Linux or MacOS server running the Docker daemon
- Easy-to-run analysis workflow: includes a Bash run script which handles all Docker commands, requiring only the input FASTQ files and the panel master file as arguments

Software minimum requirements

- Linux or MacOS with Docker installed
- At least 8 GB of RAM (≥ 32 GB recommended)

Analysis overview

1. Adapter trimming and filtering out of reads < 30 bases long (Trimmomatic)
2. Alignment (BWA MEM)
3. Primer trimming (Primerclip)
4. On-target and coverage metrics calculation and reporting
5. Variant calling (GATK Haplotype Caller and/or lofreq)

Follow this Download Link for the analysis workflow.
For more detailed information about primer trimming, please review the Primerclip Technical Note.

Indexed adapter sequences

The full-length adapter sequences are below, where the underlined text indicates the location of the index sequences which are 8 b for CDI and 10 b for UDI. These sequences represent the adapter sequences following completion of the indexing PCR step.

Index 1 (i7) adapters:
5’ – GATCGGAAGAGCACACGTCTGAACTCCAGTCACXXXXXXXX(XX)ATCTCGTATGCCGTCTTCTGCTTG – 3’

Index 2 (i5) adapters:
5’ – AATGATACGGCGACCACCGAGATCTACACYYYYYYYY(YY)ACACTCTTTCCCTACACGACGCTCTTCCGATCT – 3’

Please refer to the accompanying Swift Index Master List available at https://swiftbiosci.com/protocols/ for index sequences for preparing your Illumina sequencing sample sheet on your instrument of choice.

Primer sequences

For reference, the primer sequences are below; these primers include full-length Illumina adapter and index sequences.

i7 primer: Replace eight CDI or ten UDI **X’s** with the **REVERSE COMPLEMENT** of the specified i7 index sequence in the Swift Index Master List:
5’ – CAAGCAGAAGACGGCATACGAGAT**XXXXXXXX(XX)**GTGACTGGAGTTCAGACGTGTGCTCTTCCGATCT – 3’

i5 primer: Replace eight CDI or ten UDI **Y’s** with the specified Forward Strand Workflow i5 index sequence in the Swift Index Master List:
5’ – AATGATACGGCGACCACCGAGATCTACAC**YYYYYYYY(YY)**ACACTCTTTCCCTACACGACGCTCTTCCGATCT – 3’

Contact techsupport@swiftbio.com if you would like assistance confirming compatibility of your own primers with the SNAP workflow, or your local sales representative or distributor to inquire about the purchase of custom Swift Normalase Indexing Primers that use your own index sequences.

Appendix A

Multiplex sequencing recommendations table

Panels:	Number of amplicons	Average amplicon size (bp)	Total target size (kb)	Number of multiplexing on MiSeq® v2 standard	
				Germline 500X average depth	Somatic 5000X average depth
Oncology panels					
562G1-96, 56G Oncology Panel v2	263	138	1.5	220	22
PC8G1-96, 57G Pan-Cancer Profiling Panel	285	139	25.9	200	20
520G1-96, BRCA1 and BRCA2 Panel	246	148	22.9	240	24
570G1-96, BRCA1, BRCA2, and PALB2 Panel	302	149	28.9	190	19
510G1-96, EGFR Pathway Panel	17	136	1.5	3520	352
530G1-96, Comprehensive TP53 Panel	21	140	1.8	2850	285
LG8G1-96, Lung Cancer Panel	208	144	18	280	28
CR8G1-96, Colorectal Cancer Panel	186	143	17	320	32
LN8G1-96, Lynch Syndrome Panel	180	140	15	330	33
MY8G1-96, Myeloid Panel	478	142	42	120	12
Disease susceptibility panels					
550G1-96, CFTR Panel	87	143	10.01	384	38
ACE2G1-96, ACE2 Panel	41	150	4.0	1463	146
Sample tracking panel					
500G1-96, Sample_ID Panel	104	145	N/A – SNPs only	90	N/A

Appendix B

Swift 1536 UDIs—plate specifications and dimensions

This product is dispensed in a 96-well plate. Physical specifications are below.

Plate dimension	Low-profile 96-well skirted plates
Length at base plane	127.76 mm
Width at base plane	85.48 mm
Height overall	16.06 mm
Well depth	14.81 mm
Well diameter at opening	5.46 mm
Well diameter at bottom of conical section	2.64 mm
Well volume	200 µl
Well spacing	9.00 mm
Well angle	17.5°
Well offset	
Left edge to well A1	14.38 mm
Top edge to well A1	11.24 mm
Left edge to H12	113.38 mm
Top edge to H12	74.24 mm

Plate usage guidelines

Prior to piercing the foil and pipetting out the necessary indexes, please be sure to thaw the plate at room temperature, vortex briefly, and centrifuge for one minute to spin down the primer reagents to the bottom of the plate wells.

Carefully pre-pierce the foil seal for the intended well(s) prior to pipetting the primer mix out of the plate to add to your reaction(s). Pre-piercing the foil avoids accidental clogging of pipette tips used for liquid pipetting as well as the introduction of foil into the reaction. In addition, pre-piercing the foil reduces the resistance of multi-channel pipettors, which can result in undesired movement of the plate that may cause cross-contamination of reagents. The foil may be pre-pierced with pipette tips (e.g., 8-channel or 12-channel), 8-tube strips, an unskirted 96 well plate, or a plate puncher.

During the **Indexing PCR** step, use 3.7 µL of a unique indexing primer pair (SU001-SU1536 UDIs) to amplify and index each library, where the UDI primer pair must be added individually to each sample.

Libraries made with uniquely indexed adapters may be pooled prior to cluster generation, subjected to Normalase chemistry, and co-sequenced on the same Illumina flow cell.

UDI plates layout

SN91384-PLATES
All four plates (SN91096-1-PLATE, SN91096-2-PLATE, SN91096-3-PLATE, SN91096-4-PLATE) are included in bundle.

SN91096-1-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU001	SU009	SU017	SU025	SU033	SU041	SU049	SU057	SU065	SU073	SU081	SU089
B	SU002	SU010	SU018	SU026	SU034	SU042	SU050	SU058	SU066	SU074	SU082	SU090
C	SU003	SU011	SU019	SU027	SU035	SU043	SU051	SU059	SU067	SU075	SU083	SU091
D	SU004	SU012	SU020	SU028	SU036	SU044	SU052	SU060	SU068	SU076	SU084	SU092
E	SU005	SU013	SU021	SU029	SU037	SU045	SU053	SU061	SU069	SU077	SU085	SU093
F	SU006	SU014	SU022	SU030	SU038	SU046	SU054	SU062	SU070	SU078	SU086	SU094
G	SU007	SU015	SU023	SU031	SU039	SU047	SU055	SU063	SU071	SU079	SU087	SU095
H	SU008	SU016	SU024	SU032	SU040	SU048	SU056	SU064	SU072	SU080	SU088	SU096

SN91096-2-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU097	SU105	SU113	SU121	SU129	SU137	SU145	SU153	SU161	SU169	SU177	SU185
B	SU098	SU106	SU114	SU122	SU130	SU138	SU146	SU154	SU162	SU170	SU178	SU186
C	SU099	SU107	SU115	SU123	SU131	SU139	SU147	SU155	SU163	SU171	SU179	SU187
D	SU100	SU108	SU116	SU124	SU132	SU140	SU148	SU156	SU164	SU172	SU180	SU188
E	SU101	SU109	SU117	SU125	SU133	SU141	SU149	SU157	SU165	SU173	SU181	SU189
F	SU102	SU110	SU118	SU126	SU134	SU142	SU150	SU158	SU166	SU174	SU182	SU190
G	SU103	SU111	SU119	SU127	SU135	SU143	SU151	SU159	SU167	SU175	SU183	SU191
H	SU104	SU112	SU120	SU128	SU136	SU144	SU152	SU160	SU168	SU176	SU184	SU192

SN91096-3-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU193	SU201	SU209	SU217	SU225	SU233	SU241	SU249	SU257	SU265	SU273	SU281
B	SU194	SU202	SU210	SU218	SU226	SU234	SU242	SU250	SU258	SU266	SU274	SU282
C	SU195	SU203	SU211	SU219	SU227	SU235	SU243	SU251	SU259	SU267	SU275	SU283
D	SU196	SU204	SU212	SU220	SU228	SU236	SU244	SU252	SU260	SU268	SU276	SU284
E	SU197	SU205	SU213	SU221	SU229	SU237	SU245	SU253	SU261	SU269	SU277	SU285
F	SU198	SU206	SU214	SU222	SU230	SU238	SU246	SU254	SU262	SU270	SU278	SU286
G	SU199	SU207	SU215	SU223	SU231	SU239	SU247	SU255	SU263	SU271	SU279	SU287
H	SU200	SU208	SU216	SU224	SU232	SU240	SU248	SU256	SU264	SU272	SU280	SU288

SN91096-4-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU289	SU297	SU305	SU313	SU321	SU329	SU337	SU345	SU353	SU361	SU369	SU377
B	SU290	SU298	SU306	SU314	SU322	SU330	SU338	SU346	SU354	SU362	SU370	SU378
C	SU291	SU299	SU307	SU315	SU323	SU331	SU339	SU347	SU355	SU363	SU371	SU379
D	SU292	SU300	SU308	SU316	SU324	SU332	SU340	SU348	SU356	SU364	SU372	SU380
E	SU293	SU301	SU309	SU317	SU325	SU333	SU341	SU349	SU357	SU365	SU373	SU381
F	SU294	SU302	SU310	SU318	SU326	SU334	SU342	SU350	SU358	SU366	SU374	SU382
G	SU295	SU303	SU311	SU319	SU327	SU335	SU343	SU351	SU359	SU367	SU375	SU383
H	SU296	SU304	SU312	SU320	SU328	SU336	SU344	SU352	SU360	SU368	SU376	SU384

SN91384-PLATES-B
All four plates (SN91096-5-PLATE, SN91096-6-PLATE, SN91096-7-PLATE, and SN91096-8-PLATE) are included in bundle.

SN91096-5-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU385	SU393	SU401	SU409	SU417	SU425	SU433	SU441	SU449	SU457	SU465	SU473
B	SU386	SU394	SU402	SU410	SU418	SU426	SU434	SU442	SU450	SU458	SU466	SU474
C	SU387	SU395	SU403	SU411	SU419	SU427	SU435	SU443	SU451	SU459	SU467	SU475
D	SU388	SU396	SU404	SU412	SU420	SU428	SU436	SU444	SU452	SU460	SU468	SU476
E	SU389	SU397	SU405	SU413	SU421	SU429	SU437	SU445	SU453	SU461	SU469	SU477
F	SU390	SU398	SU406	SU414	SU422	SU430	SU438	SU446	SU454	SU462	SU470	SU478
G	SU391	SU399	SU407	SU415	SU423	SU431	SU439	SU447	SU455	SU463	SU471	SU479
H	SU392	SU400	SU408	SU416	SU424	SU432	SU440	SU448	SU456	SU464	SU472	SU480

SN91096-6-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU481	SU489	SU497	SU505	SU513	SU521	SU529	SU537	SU545	SU553	SU561	SU569
B	SU482	SU490	SU498	SU506	SU514	SU522	SU530	SU538	SU546	SU554	SU562	SU570
C	SU483	SU491	SU499	SU507	SU515	SU523	SU531	SU539	SU547	SU555	SU563	SU571
D	SU484	SU492	SU500	SU508	SU516	SU524	SU532	SU540	SU548	SU556	SU564	SU572
E	SU485	SU493	SU501	SU509	SU517	SU525	SU533	SU541	SU549	SU557	SU565	SU573
F	SU486	SU494	SU502	SU510	SU518	SU526	SU534	SU542	SU550	SU558	SU566	SU574
G	SU487	SU495	SU503	SU511	SU519	SU527	SU535	SU543	SU551	SU559	SU567	SU575
H	SU488	SU496	SU504	SU512	SU520	SU528	SU536	SU544	SU552	SU560	SU568	SU576

SN91096-7-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU577	SU585	SU593	SU601	SU609	SU617	SU625	SU633	SU641	SU649	SU657	SU665
B	SU578	SU586	SU594	SU602	SU610	SU618	SU626	SU634	SU642	SU650	SU658	SU666
C	SU579	SU587	SU595	SU603	SU611	SU619	SU627	SU635	SU643	SU651	SU659	SU667
D	SU580	SU588	SU596	SU604	SU612	SU620	SU628	SU636	SU644	SU652	SU660	SU668
E	SU581	SU589	SU597	SU605	SU613	SU621	SU629	SU637	SU645	SU653	SU661	SU669
F	SU582	SU590	SU598	SU606	SU614	SU622	SU630	SU638	SU646	SU654	SU662	SU670
G	SU583	SU591	SU599	SU607	SU615	SU623	SU631	SU639	SU647	SU655	SU663	SU671
H	SU584	SU592	SU600	SU608	SU616	SU624	SU632	SU640	SU648	SU656	SU664	SU672

SN91096-8-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU673	SU681	SU689	SU697	SU705	SU713	SU721	SU729	SU737	SU745	SU753	SU761
B	SU674	SU682	SU690	SU698	SU706	SU714	SU722	SU730	SU738	SU746	SU754	SU762
C	SU675	SU683	SU691	SU699	SU707	SU715	SU723	SU731	SU739	SU747	SU755	SU763
D	SU676	SU684	SU692	SU700	SU708	SU716	SU724	SU732	SU740	SU748	SU756	SU764
E	SU677	SU685	SU693	SU701	SU709	SU717	SU725	SU733	SU741	SU749	SU757	SU765
F	SU678	SU686	SU694	SU702	SU710	SU718	SU726	SU734	SU742	SU750	SU758	SU766
G	SU679	SU687	SU695	SU703	SU711	SU719	SU727	SU735	SU743	SU751	SU759	SU767
H	SU680	SU688	SU696	SU704	SU712	SU720	SU728	SU736	SU744	SU752	SU760	SU768

SN91384-PLATES-C

All four plates (SN91096-9-PLATE, SN91096-10-PLATE, SN91096-11-PLATE, and SN91096-12-PLATE) are included in bundle.

SN91096-9-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU769	SU777	SU785	SU793	SU801	SU809	SU817	SU825	SU833	SU841	SU849	SU857
B	SU770	SU778	SU786	SU794	SU802	SU810	SU818	SU826	SU834	SU842	SU850	SU858
C	SU771	SU779	SU787	SU795	SU803	SU811	SU819	SU827	SU835	SU843	SU851	SU859
D	SU772	SU780	SU788	SU796	SU804	SU812	SU820	SU828	SU836	SU844	SU852	SU860
E	SU773	SU781	SU789	SU797	SU805	SU813	SU821	SU829	SU837	SU845	SU853	SU861
F	SU774	SU782	SU790	SU798	SU806	SU814	SU822	SU830	SU838	SU846	SU854	SU862
G	SU775	SU783	SU791	SU799	SU807	SU815	SU823	SU831	SU839	SU847	SU855	SU863
H	SU776	SU784	SU792	SU800	SU808	SU816	SU824	SU832	SU840	SU848	SU856	SU864

SN91096-10-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU865	SU873	SU881	SU889	SU897	SU905	SU913	SU921	SU929	SU937	SU945	SU953
B	SU866	SU874	SU882	SU890	SU898	SU906	SU914	SU922	SU930	SU938	SU946	SU954
C	SU867	SU875	SU883	SU891	SU899	SU907	SU915	SU923	SU931	SU939	SU947	SU955
D	SU868	SU876	SU884	SU892	SU900	SU908	SU916	SU924	SU932	SU940	SU948	SU956
E	SU869	SU877	SU885	SU893	SU901	SU909	SU917	SU925	SU933	SU941	SU949	SU957
F	SU870	SU878	SU886	SU894	SU902	SU910	SU918	SU926	SU934	SU942	SU950	SU958
G	SU871	SU879	SU887	SU895	SU903	SU911	SU919	SU927	SU935	SU943	SU951	SU959
H	SU872	SU880	SU888	SU896	SU904	SU912	SU920	SU928	SU936	SU944	SU952	SU960

SN91096-11-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU961	SU969	SU977	SU985	SU993	SU1001	SU1009	SU1017	SU1025	SU1033	SU1041	SU1049
B	SU962	SU970	SU978	SU986	SU994	SU1002	SU1010	SU1018	SU1026	SU1034	SU1042	SU1050
C	SU963	SU971	SU979	SU987	SU995	SU1003	SU1011	SU1019	SU1027	SU1035	SU1043	SU1051
D	SU964	SU972	SU980	SU988	SU996	SU1004	SU1012	SU1020	SU1028	SU1036	SU1044	SU1052
E	SU965	SU973	SU981	SU989	SU997	SU1005	SU1013	SU1021	SU1029	SU1037	SU1045	SU1053
F	SU966	SU974	SU982	SU990	SU998	SU1006	SU1014	SU1022	SU1030	SU1038	SU1046	SU1054
G	SU967	SU975	SU983	SU991	SU999	SU1007	SU1015	SU1023	SU1031	SU1039	SU1047	SU1055
H	SU968	SU976	SU984	SU992	SU1000	SU1008	SU1016	SU1024	SU1032	SU1040	SU1048	SU1056

SN91096-12-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU1057	SU1065	SU1073	SU1081	SU1089	SU1097	SU1105	SU1113	SU1121	SU1129	SU1137	SU1145
B	SU1058	SU1066	SU1074	SU1082	SU1090	SU1098	SU1106	SU1114	SU1122	SU1130	SU1138	SU1146
C	SU1059	SU1067	SU1075	SU1083	SU1091	SU1099	SU1107	SU1115	SU1123	SU1131	SU1139	SU1147
D	SU1060	SU1068	SU1076	SU1084	SU1092	SU1100	SU1108	SU1116	SU1124	SU1132	SU1140	SU1148
E	SU1061	SU1069	SU1077	SU1085	SU1093	SU1101	SU1109	SU1117	SU1125	SU1133	SU1141	SU1149
F	SU1062	SU1070	SU1078	SU1086	SU1094	SU1102	SU1110	SU1118	SU1126	SU1134	SU1142	SU1150
G	SU1063	SU1071	SU1079	SU1087	SU1095	SU1103	SU1111	SU1119	SU1127	SU1135	SU1143	SU1151
H	SU1064	SU1072	SU1080	SU1088	SU1096	SU1104	SU1112	SU1120	SU1128	SU1136	SU1144	SU1152

SN91384-PLATES-D

All four plates (SN91096-13-PLATE, SN91096-14-PLATE, SN91096-15-PLATE, and SN91096-16-PLATE) are included in bundle.

SN91096-13-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU1153	SU1161	SU1169	SU1177	SU1185	SU1193	SU1201	SU1209	SU1217	SU1225	SU1233	SU1241
B	SU1154	SU1162	SU1170	SU1178	SU1186	SU1194	SU1202	SU1210	SU1218	SU1226	SU1234	SU1242
C	SU1155	SU1163	SU1171	SU1179	SU1187	SU1195	SU1203	SU1211	SU1219	SU1227	SU1235	SU1243
D	SU1156	SU1164	SU1172	SU1180	SU1188	SU1196	SU1204	SU1212	SU1220	SU1228	SU1236	SU1244
E	SU1157	SU1165	SU1173	SU1181	SU1189	SU1197	SU1205	SU1213	SU1221	SU1229	SU1237	SU1245
F	SU1158	SU1166	SU1174	SU1182	SU1190	SU1198	SU1206	SU1214	SU1222	SU1230	SU1238	SU1246
G	SU1159	SU1167	SU1175	SU1183	SU1191	SU1199	SU1207	SU1215	SU1223	SU1231	SU1239	SU1247
H	SU1160	SU1168	SU1176	SU1184	SU1192	SU1200	SU1208	SU1216	SU1224	SU1232	SU1240	SU1248

SN91096-14-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU1249	SU1257	SU1265	SU1273	SU1281	SU1289	SU1297	SU1305	SU1313	SU1321	SU1329	SU1337
B	SU1250	SU1258	SU1266	SU1274	SU1282	SU1290	SU1298	SU1306	SU1314	SU1322	SU1330	SU1338
C	SU1251	SU1259	SU1267	SU1275	SU1283	SU1291	SU1299	SU1307	SU1315	SU1323	SU1331	SU1339
D	SU1252	SU1260	SU1268	SU1276	SU1284	SU1292	SU1300	SU1308	SU1316	SU1324	SU1332	SU1340
E	SU1253	SU1261	SU1269	SU1277	SU1285	SU1293	SU1301	SU1309	SU1317	SU1325	SU1333	SU1341
F	SU1254	SU1262	SU1270	SU1278	SU1286	SU1294	SU1302	SU1310	SU1318	SU1326	SU1334	SU1342
G	SU1255	SU1263	SU1271	SU1279	SU1287	SU1295	SU1303	SU1311	SU1319	SU1327	SU1335	SU1343
H	SU1256	SU1264	SU1272	SU1280	SU1288	SU1296	SU1304	SU1312	SU1320	SU1328	SU1336	SU1344

SN91096-15-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU1345	SU1353	SU1361	SU1369	SU1377	SU1385	SU1393	SU1401	SU1409	SU1417	SU1425	SU1433
B	SU1346	SU1354	SU1362	SU1370	SU1378	SU1386	SU1394	SU1402	SU1410	SU1418	SU1426	SU1434
C	SU1347	SU1355	SU1363	SU1371	SU1379	SU1387	SU1395	SU1403	SU1411	SU1419	SU1427	SU1435
D	SU1348	SU1356	SU1364	SU1372	SU1380	SU1388	SU1396	SU1404	SU1412	SU1420	SU1428	SU1436
E	SU1349	SU1357	SU1365	SU1373	SU1381	SU1389	SU1397	SU1405	SU1413	SU1421	SU1429	SU1437
F	SU1350	SU1358	SU1366	SU1374	SU1382	SU1390	SU1398	SU1406	SU1414	SU1422	SU1430	SU1438
G	SU1351	SU1359	SU1367	SU1375	SU1383	SU1391	SU1399	SU1407	SU1415	SU1423	SU1431	SU1439
H	SU1352	SU1360	SU1368	SU1376	SU1384	SU1392	SU1400	SU1408	SU1416	SU1424	SU1432	SU1440

SN91096-16-PLATE

	1	2	3	4	5	6	7	8	9	10	11	12
A	SU1441	SU1449	SU1457	SU1465	SU1473	SU1481	SU1489	SU1497	SU1505	SU1513	SU1521	SU1529
B	SU1442	SU1450	SU1458	SU1466	SU1474	SU1482	SU1490	SU1498	SU1506	SU1514	SU1522	SU1530
C	SU1443	SU1451	SU1459	SU1467	SU1475	SU1483	SU1491	SU1499	SU1507	SU1515	SU1523	SU1531
D	SU1444	SU1452	SU1460	SU1468	SU1476	SU1484	SU1492	SU1500	SU1508	SU1516	SU1524	SU1532
E	SU1445	SU1453	SU1461	SU1469	SU1477	SU1485	SU1493	SU1501	SU1509	SU1517	SU1525	SU1533
F	SU1446	SU1454	SU1462	SU1470	SU1478	SU1486	SU1494	SU1502	SU1510	SU1518	SU1526	SU1534
G	SU1447	SU1455	SU1463	SU1471	SU1479	SU1487	SU1495	SU1503	SU1511	SU1519	SU1527	SU1535
H	SU1448	SU1456	SU1464	SU1472	SU1480	SU1488	SU1496	SU1504	SU1512	SU1520	SU1528	SU1536

Product ordering information

Workflow component	Product name	Catalog number
SNAP core kits	Swift Normalase Amplicon Panels (SNAP) Core Kit (96 rxns, no indexing)	SN-5X296
	Swift Normalase Amplicon Panels (SNAP) Core Kit (4x96 rxns Bundle, no indexing)	SN-5X384
Panel-specific primers	Lung Panel (primers only, 96 rxns)	LG8G1-96
	ACE2 Gene Panel (primers only, 96 rxns)	ACE2G1-96
	Colorectal Panel (primers only, 96 rxns)	CR8G1-96
	Lynch Syndrome Panel (primers only, 96 rxns)	LN8G1-96
	Myeloid Panel (primers only, 96 rxns)	MY8G1-96
	57G Pan-Cancer Profiling Panel (primers only, 96 rxns)	PC8G1-96
	56G Oncology Panel v2 (primers only, 96 rxns)	562G1-96
	EGFR Pathway Panel (primers only, 96 rxns)	510G1-96
	BRCA1 and BRCA2 Panel (primers only, 96 rxns)	520G1-96
	BRCA1, BRCA2, and PALB2 Panel (primers only, 96 rxns)	570G1-96
	Comprehensive TP53 Panel (primers only, 96 rxns)	530G1-96
	Sample_ID Panel (primers only, 96 rxns)	500G1-96
	CFTR Panel (primers only, 96 rxns)	550G1-96
SNAP CDI primers	SNAP Set 1A Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S1A96
	SNAP Set 1B Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S1B96
	SNAP Set 2A Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S2A96
	SNAP Set 2B Combinatorial Dual Indexing Primers (96-plex, 96 rxns)	SN-5S2B96
	SNAP Set S1AB-S2AB Combinatorial Dual Indexing Primers (384-plex, 4x96 rxns Bundle)	SN-5S0384
SNAP UDI primer plates	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns, SU001-SU096)	SN91096-1-PLATE
	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns, SU097-SU192)	SN91096-2-PLATE
	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns, SU193-SU288)	SN91096-3-PLATE
	SNAP Unique Dual Indexing Primer Plate (96-plex, 96 rxns, SU289-SU384)	SN91096-4-PLATE
	SNAP Unique Dual Indexing Primer Plates (384-plex, 4x96 rxns Bundle, SU001-SU384)	SN91384-PLATES
	SNAP Unique Dual Indexing Primer Plates (384-plex, 4x96 rxns Bundle, SU385-SU768)	SN91384-B-PLATES
	SNAP Unique Dual Indexing Primer Plates (384-plex, 4x96 rxns Bundle, SU769-SU1152)	SN91384-C-PLATES
	SNAP Unique Dual Indexing Primer Plates (384-plex, 4x96 rxns Bundle, SU1153-SU1536)	SN91384-D-PLATES

Support

For technical support, please contact Swift at TechSupport@swiftbio.com, or by phone: 734.330.2568
9:00 am – 5:00 pm ET, Monday through Friday.

Revision history

Document #	Revision	Date	Description of change
PRT-031	Version 1	08/21/2020	Initial release.
PRT-031	Version 2	10/28/2020	Addition of SNAP 384 UDI plates.
PRT-031	Version 3	05/03/2020	Addition of SNAP 1536 UDI plates.

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