BACK TO LAB

Cultek
Your partner in Life Sciences

SOLUCIONES PARA NGS

Purifique fragmentos de ADN del tamaño que necesite para la preparación de librerías

Descripción	Referencia
NucleoSpin® Gel and PCR Clean-up	22740609.50
NucleoMag NGS and Size Select	22744970.50

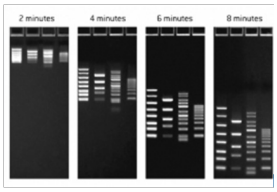
Kits de preparación de librerías para plataformas de Illumina

- Aplicaciones: epigenética, genotipado, oncología, metagenómica y transcriptómica
- Paneles de amplicones pre-diseñados
- Paneles de amplicones personalizados
- Kits de preparación de librerías
- Kits de secuenciación del ARN
- Kits de captura por hibridación
- Kits de secuenciación del metiloma
- Kits de normalización
- Varios tipos de muestra: Biopsia líquida, FFPE, ADN dañado o degradado de una sola hebra, muestras ambientales, de patógenos, etc.

Flash Gel System

- Rápida electroforesis de fragmentos de ADN, para el análisis de hasta 32 muestras
- Separación y recuperación de bandas en 5 minutos

Descripción	Referencia
FlashGel Starter Pack kit	H357026



Pippin Prep

- Selección de fragmentos de ADN para NGS (100 pb – 1.5 Kb)
- Más rápido y fácil en comparación al método tradicional, que usa geles de agarosa
- Aplicaciones: secuenciación pair-end, emPCR, RNA-Seq y CHIP-Seq

BACK TO LAB

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Kits de qPCR para cuantificar librerías y estándares de ADN

Contiene todos los componentes necesarios para la cuantificación precisa de librerías de secuenciación masiva, preparadas para plataformas de Illumina.

Descripción	Referencia
NGSBIO Kit de cuantificación de librerías para Illumina con qPCRBIO SyGreen Lo-ROX (100 rxns)	K7PB71.11-01
NGSBIO Kit de cuantificación de librerías para Illumina con qPCRBIO SyGreen Hi-ROX (100 rxns)	K7PB71.12-01
NGSBIO Kit de cuantificación de librerías para Illumina con qPCRBIO SyGreen con ROX separado (100 rxns)	K7PB71.14-01
NGSBIO Kit de cuantificación de librerías Blue para Illumina con qPCRBIO SyGreen Lo-ROX (100 rxns)	K7PB71.15-01
NGSBIO Kit de cuantificación de librerías Blue para Illumina con qPCRBIO SyGreen Hi-ROX (100 rxns)	K7PB71.16-01
NGSBIO Kit de cuantificación de librerías Blue para Illumina con qPCRBIO SyGreen con ROX separado (100 rxns)	K7PB71.17-01
NGSBIO estándares de ADN para Illumina, 85ul cada uno	K7PB71.22-05

*También disponible en formato de 500 reacciones

Estándar de referencia OncoSpan

- Permite validar protocolos con paneles de genes y exomas en oncología
- Estándar de referencia derivado de una línea celular, que contiene los datos específicos de secuenciación de 385 variantes de 152 genes clave

Descripción	Referencia
OncoSpan gDNA	K9HD827
OncoSpan cfDNA	K9HD833
OncoSpan FFPE	K9HD832

Condiciones

• Transporte gratuito para pedidos superiores a 200 € (sin IVA).
• Gastos de transporte: 20 € (+IVA).
• En el caso de envíos que incluyan productos que requieran hielo seco, tendrán así mismo un cargo adicional por este concepto.

Cultek S.L.U.
Your partner in life sciences

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SWIFT 2S® TURBO DNA LIBRARY KITS

The Easiest NGS Workflow for Routine Sequencing

Highlights

- **Simple, fast, and reliable**
  Minimal steps and hands-on time with consistent fragmentation regardless of DNA input amount.
- **For many genomes**
  Compatible with diverse genome types of low or high complexity.
- **More applications, one workflow**
  One universal approach for whole genome, exome, metagenomics, and large gene studies.

Introduction

The Swift 2S Turbo DNA Library Kits offer a versatile solution that streamlines NGS sample preparation of double-stranded DNA on Illumina® sequencing platforms. This technology leverages rapid and highly reproducible fragmentation and library construction, enabling manual and fully automatable workflow compatible with Normalase® technology.

Supported Applications

Swift 2S Turbo DNA Library Kits are available in two configurations to support variety of sample inputs and applications. Swift 2S Turbo is an “all in one” kit for quick implementation of core applications. The Swift 2S Turbo Flexible workflow supports an expanded menu of applications and is compatible with your choice of adapters & indices.

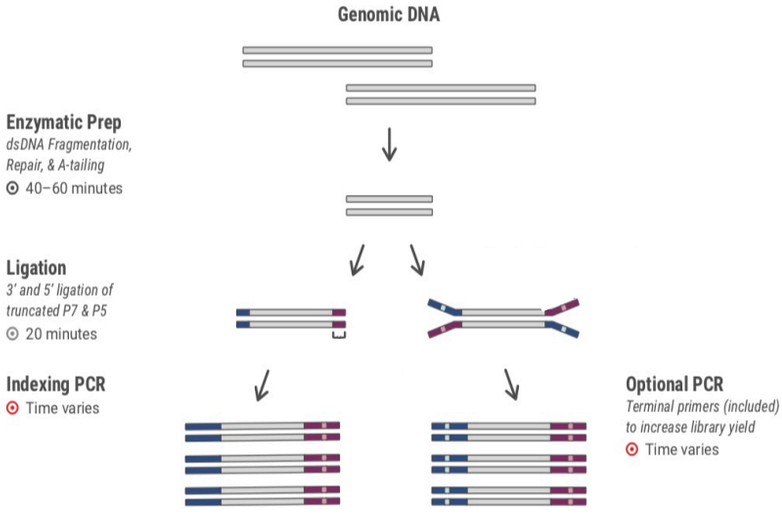

Fig1. Turbo workflow with Swift 2S Turbo workflow on the left and Swift 2S Turbo Flexible on the right.

Application	Swift 2S Turbo	Swift 2S Turbo Flexible
Whole Genome Sequencing	√	√
Whole Exome Sequencing	√	√
Variant Detection	Germline	Germline + Somatic
Genotyping	√	√
CNV Detection	√	√
PCR Free	—	√
Low Input	—	√

Fastest, Easiest Workflow

The Swift 2S Turbo leverages a fast and efficient workflow consisting of two enzymatic incubations spanning 80 minutes and a bead-based purification step, thereby reducing sample handling and overall library preparation time to less than two hours. Following ligation and the optional PCR step, depending on the intended application, a bead-based purification is used to remove oligonucleotides and small fragments.

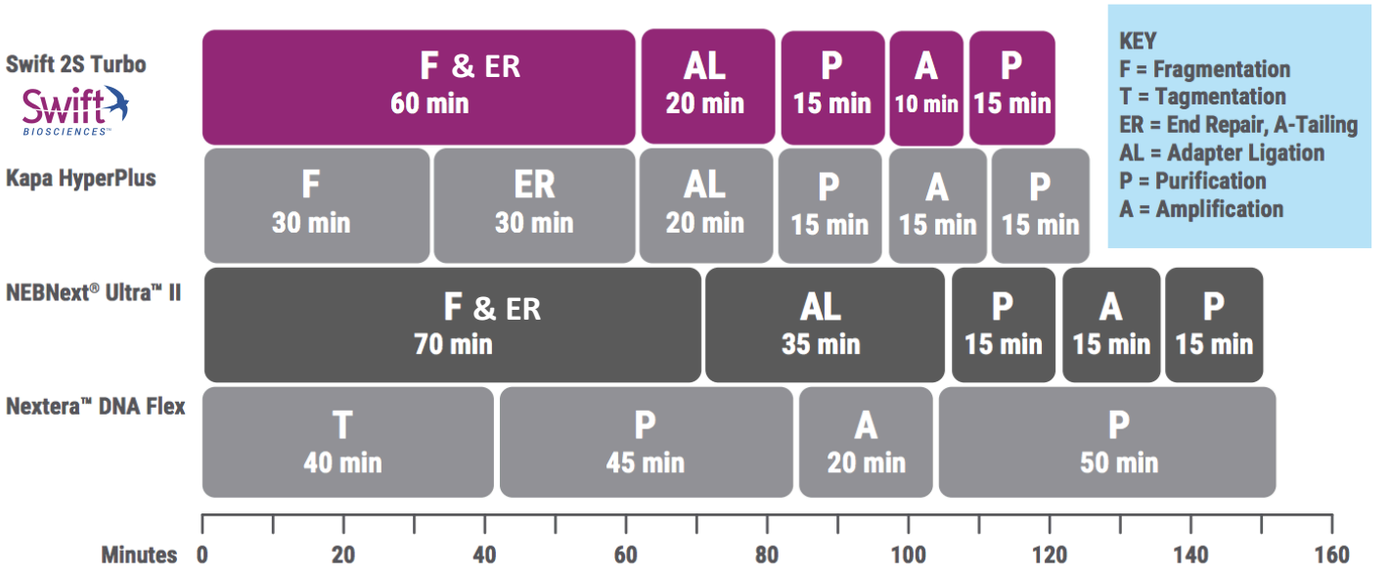

Fig 2. This diagram shows Swift's workflow with two enzymatic steps as compared to the Kapa Hyper Plus workflows, and less overall time compared to Nextera™ DNA Flex Library Kit and NEBNext® Ultra™ II. Time comparisons assumes 100 ng DNA input going into the library preparation and fragmenting to an insert size of ~ 200 bp.

High Quality Data

Swift 2S Turbo offers reproducible and consistent aligned insert sizes across a broad range of input GC content, genome size, or DNA input amounts. Consistent fragmentation and a lot specific certificate of analysis with recommended fragmentation times for 200 and 350 bp inserts provides high quality data without optimization for obtaining desired library sizes. The example below shows low variation in insert size resulting in superior representation of bacteria in a mock community regardless of input amount (Fig 3). Evenness of coverage across distinct GC compositions is further demonstrated with PCR-free libraries performed on cell-line gDNA with 100 to 1000 ng input (Fig4).

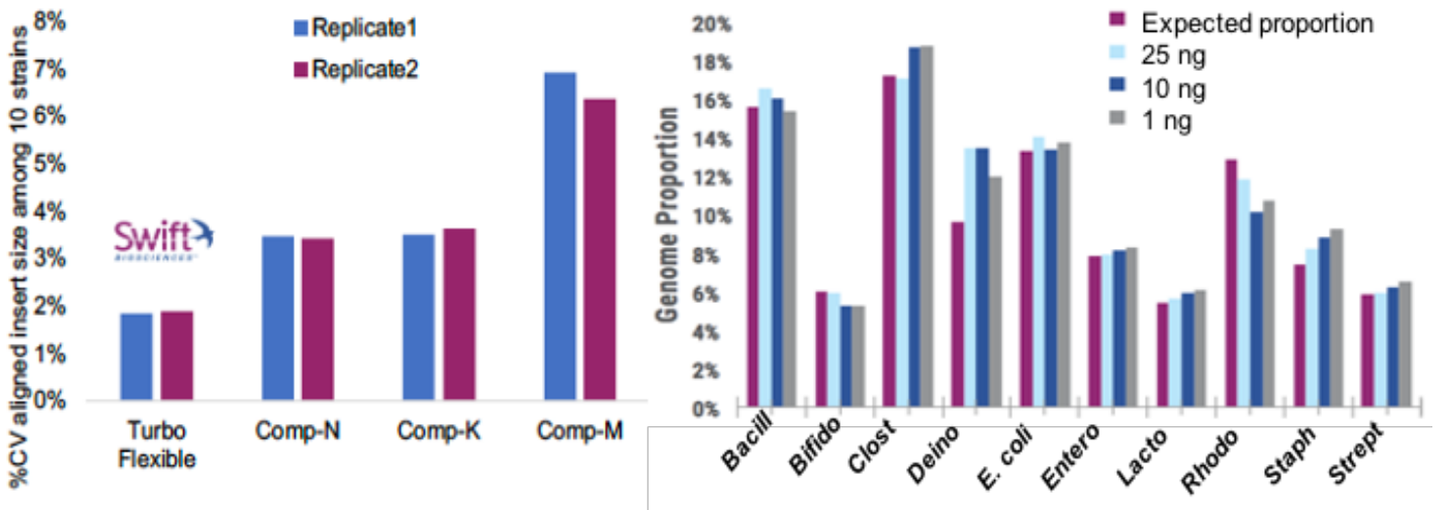

Fig 3. NGS libraries were constructed from: Left panel: five nanograms of high-quality genomic DNA (ATCC MSA-1000), using a fragmentation time required to achieve library mode sizes of ~ 350 bp (plus ~ 125 bp, the length of the adapters) via Turbo and competitor kits. The libraries were co-sequenced on Illumina NovaSeq Instrument. The library modes and the median sequence insert sizes (% aligned insert) demonstrate reproducibility in fragmentation across a range of DNA inputs. Right panel: Despite significant variation in GC composition, Swift 2S Turbo's workflow enabled detection of each strain's genome sequences at the accurate frequency with minimal bias. Run on a MiSeq, the results demonstrate that variability in GC composition, size of the genomes, and input amounts do not influence the performance level of Swift 2S Turbo. B. cereus (GC% = 35.5), B. adolescentis (GC% = 59.4), C. beijerinckii (GC% = 29.9), D. radiodurans (GC% = 66.7), E. faecalis (GC% = 37.8), E. coli (GC% = 50.8), L. gasseri (GC% = 35.3), R. sphaeroides (GC% = 68.9), S. epidermidis (GC% = 32.0), S. mutans (GC% = 36.8).

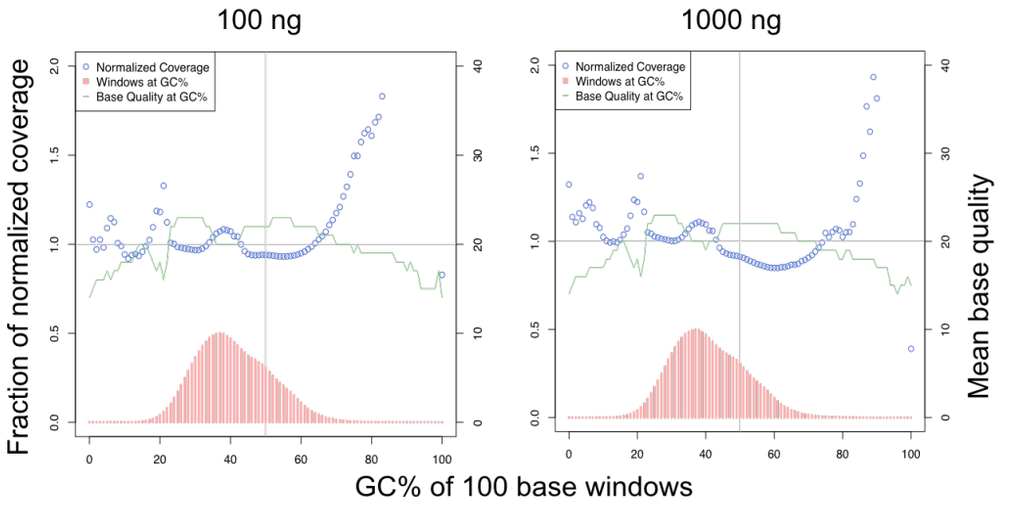

Fig 4. 2S Turbo was used for PCR-free NGS libraries constructed from high quality genomic DNA (NA12878) for whole genome sequencing with 100, 250, 500, and 1000 ng input. The libraries were co-sequenced on Illumina HiSeq 4000 instrument. The Picard diagram demonstrates evenness of coverage across distinct GC compositions. The table shows high coverage uniformity of libraries, with number of reads normalized to $3x10^8$ for all libraries.

Sample	Mean Cov	%Cov 1X	%Cov 5X	%Cov 10X	%Cov 15X	%Cov 20X
100 ng	22.3	98.4	97.9	97.2	92.5	70.6
250 ng	22.8	98.4	97.9	97.3	93.3	73.8
500 ng	24.2	98.4	97.9	97.4	94.7	80.2
1000 ng	24.5	98.4	97.9	97.3	94.7	81.0

Swift 2S Turbo was evaluated for enrichment with Swift's Exome and Pan-Cancer panels (Table 4); in which comprehensive target coverage and high complexity was observed with multiple sample types, input quantities, and platforms MiSeq® (non-patterned flow cells) and HiSeq® 4000 (patterned flow-cell). Numbers listed for Exome and Pan-Cancer captures represent mean of duplicate or single libraries, respectively. Coverage uniformity and complexity was higher with low input Turbo libraries compared to competitors. Outstanding coverage uniformity was also obtained from low integrity FFPE samples.

Prep	Capture	Input (ng)	%Dup	Mean Cov	%Cov 20x	%Cov 50x	%Cov 100x	%On Target
Turbo	Exome	100	18	154	97.9	87.7	53.0	93.6
Comp-N	Exome	100	25	155	97.7	88.1	47.9	94.2
Comp-K	Exome	100	15	155	92.3	73.0	47.0	94.4
Turbo	Exome	10	19	149	98.0	87.5	51.5	94.2
Comp-N	Exome	10	19	149	97.0	84.0	50.0	94.3
Comp-K	Exome	10	21	148	92.3	70.2	44.3	94.4
Turbo	Exome	1	48	151	97.2	74.3	14.1	94.3
Comp-N	Exome	1	79	155	74.1	1.01	0.03	93.9
Comp-K	Exome	1	73	147	66.1	21.0	0.05	94.3
Turbo	PanCan	25	6	142	99.7	98.6	91.9	73.0
Turbo	PanCan	24*FFPE	4	163	99.1	98.1	89.7	70.3
Turbo	PanCan	79*HD200	6	151	99.4	98.5	90.2	69.6

*Table 4. The Swift 2S Turbo and competitor library preparation kits were evaluated with the Swift Exome and Pan-Cancer enrichment panels using high quality cell line gDNA and *FFPE sample inputs. Exome captured libraries were sequenced on a HiSeq 4000 with 150 bp PE reads. All samples run on the HiSeq 4000 were normalized to the same number of reads. PanCan captured libraries were sequenced on a MiSeq run with 100 bp PE reads. The FFPE sample integrity was assessed based on the Alu 247/115 repeat fragment ratios, which was 0.34. The fragmentation times were adjusted (10-15 min) for damaged/degraded FFPE targeting library insert size of ~ 200 bp; however, the sequence metrics achieved are comparable to the metrics observed for high quality DNA.*

Specifications

Feature	Swift 2S Turbo	Swift 2S Turbo Flexible
Sample Type	Fresh frozen tissue, genomic DNA, PCR amplicons, high quality FFPE*	
Input Range	50-250 ng (human), 1-250 (microbial)	1-250 ng (human or microbial)
Indexing Compatibility	Combinatorial Dual Indexing up to 768-Plex Unique Dual Indexing up to 96-Plex	Third party supplier for full length adapters Swift indexing primers for custom truncated adapters
System Compatibility and Multiplexing Format	All Illumina sequencing instruments	
Workflow Capability	Manual & Automated (For list of liquid handling robots and scripts, please inquire!)	
Kit Size	24 or 96 reactions, for > 96 reactions, please inquire!	

** Optimization of the enzymatic fragmentation step may be required*

Ordering Information

Product Name	Reactions	Catalog No.
Swift 2S Turbo DNA Library Kit	24	44024
	96	44096
Swift 2S Turbo Flexible DNA Library Kit	24	45024
	96	45096
Swift 2S Turbo Single Indexing Primer Kit	24, Set A	46024
Swift 2S Turbo Combinatorial Dual Indexing Primer Kit	96	48096
Swift 2S Turbo Set S1-S4 Combinatorial Dual Indexing Primer Kits	24 x 8	485192 - 488192
	96 x 8	489768
Swift 2S Turbo Unique Dual Indexing Primer Kit	96	49096
	384	490384
Swift 2S Turbo SureSelect Compatibility Module	24	46424
	96	4649
Swift Deceleration Reagent*	96	90596

**Swift Deceleration Reagent enables even more control and flexibility with your Swift 2S Turbo DNA Library Kits. The Reagent DE included in the module:*

- *Produces Swift 2S Turbo DNA libraries with a 550 bp insert size*
- *Controls fragmentation time on automation platforms*

***Please inquire for custom index primer compatibility (UDIs, etc.).*

*Visit **www.swiftbiosci.com** for easy ordering*

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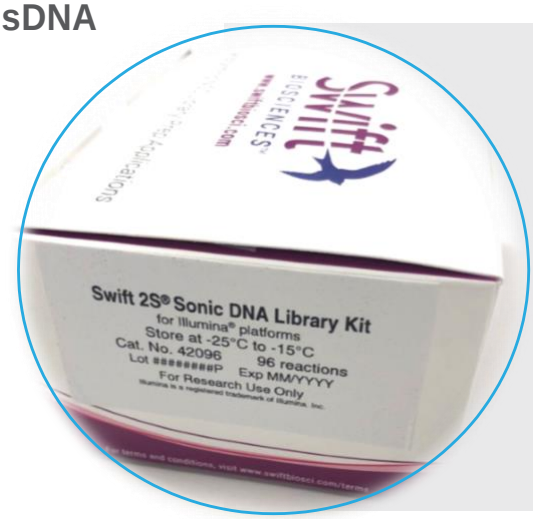
SWIFT 2S® SONIC DNA LIBRARY KITS

High Throughput Library Prep for Fragmented dsDNA



Highlights

- Compatible with Covaris® sheared DNA
- PCR-free libraries from 50 ng input
- Streamlined 2 step workflow with optional PCR
- Data quality equal to leading supplier kits
- Readily automated and compatible with Swift Normalase®
- Economical pricing to support high throughput laboratories
- Up to 768 combinatorial dual and 384 unique dual indexing

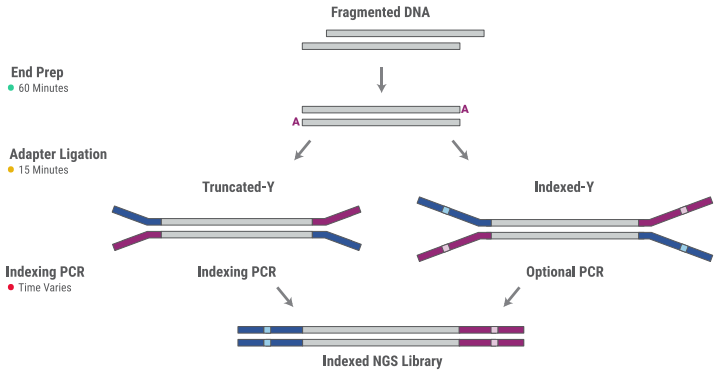
Introduction

The Swift 2S Sonic DNA Library Kits offer a versatile solution that streamlines NGS sample preparation for dsDNA on Illumina® sequencing platforms. This workflow processes fragmented DNA for rapid and highly efficient end repair, adenylation, and adapter ligation with an optional library amplification step, enabling manual and automated workflows. These kits can be used for targeted hybridization capture, where the Swift HiFi Polymerase Master Mix supplied in the kit is suitable for pre-hyb PCR to produce yields of 500 ng or greater from as low as 1 ng DNA input.
These kits are also compatible with Swift Hybridization Capture Panels, IDT xGen® Lockdown Panels and Twist Bioscience Panels.

Rapid Flexible Workflow

The Swift 2S Sonic protocol contains two enzymatic incubations, an optional PCR and bead-purification steps, thereby minimizing sample handling and overall library preparation time to two hours with PCR.

The Swift 2S Sonic DNA Library Kits are available in two configurations to support two indexing workflows. The incubation steps consist of end repair, polishing of dsDNA, and A-tailing, all performed in a single End Prep reaction followed by ligation of either the Swift truncated Y adapter (Swift 2S Sonic, left) or full-length indexed Y adapters (Swift 2S Sonic Flexible, right). Following adapter ligation, the Swift 2S Sonic workflow incorporates an indexing PCR step to complete the adapter sequences whereas for the Flexible kit, PCR is an optional step. 2S Sonic Flexible is compatible with your choice of full-length indexed Y adapters (not supplied by Swift).

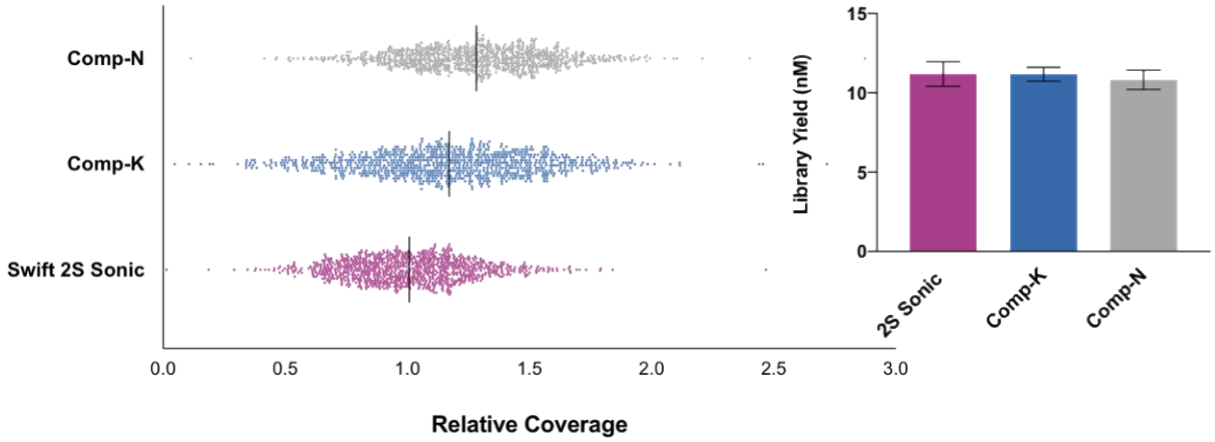


The Swift 2S Sonic workflow is comparable to leading kit suppliers N and K, where a 60-minute end repair/A-tailing step (ER/A) is followed by a 15-minute adapter ligation step (L), a bead-based purification (B), an optional library amplification step (PCR) and a second bead-base purification (B).

Specifications

Feature	Swift 2S Sonic DNA Library Kits
Sample Types	Genomic DNA extracted from tissue, blood, microbial isolates and environmental samples
Input Material	1 ng – 1 μg input DNA in 50 μl volume
Fragmentation	Covaris shearing or other method
Time	2 Hours with PCR
Multiplexing Capability	Up to 768 CDI and 384 UDI Compatible with full-length indexed Y Adapters (not supplied by Swift)
Supported Applications	Whole genome sequencing (WGS) Hybridization capture of targeted genomic regions (exome) Metagenomic sequencing Detection of germline inherited SNVs and Indels Low frequency somatic variant detection of SNVs and Indels Detection of copy number variation (CNV)

PCR-free Sequencing Produces Balanced Genome Coverage



PCR-free libraries were constructed using Swift 2S Sonic Flexible and Competitor kits, K and N with 100 ng Covaris-sheared Coriell NA12878 DNA at 350 bp, in duplicate. All libraries were constructed using IDT for Illumina TruSeq® UD DNA Indexes (Cat. No. 20020590) at supplier-specified concentration. A consistent bead ratio was used to generate equivalent insert sizes across supplier kits for direct comparison. Libraries were quantified by qPCR and sequenced on a NovaSeq® and data normalized to 270M reads per sample. Right Panel: PCR-free library yields were comparable across all three kits. Left Panel: Swift 2S Sonic demonstrated more balanced coverage of 971 high GC regions relative to the mean coverage than Kits K and N that both represented the high GC regions greater than the mean coverage. A deviation from a relative coverage of 1 represents a reduction in coverage uniformity (GC rich bed file from Ross et al, Characterizing and Measuring Bias in Sequence Data; Genome Biol. 2013).

Robust Performance with Swift Exome and Pan-Cancer Panels

Swift 2S Sonic and competitor kits K and N were evaluated with the Swift Pan-Cancer and Exome enrichment panels using duplicate samples of Coriell NA12878 genomic DNA at 10 ng (Pan-Cancer) or 100 ng (Exome) Covaris-sheared to 200 bp. For Pan-Cancer, Swift 2S Sonic and competitor libraries were prepared with truncated Y adapters at supplier-specified concentration and a Swift Combinatorial Dual Indexing Primer kit. The Exome libraries were prepared with the Swift 2S Sonic Flexible and competitor kits using IDT for Illumina TruSeq UD DNA Indexes (Cat. No. 20020590) at supplier-specified concentration. For both panels, a consistent bead ratio was used to generate equivalent insert sizes across supplier kits for direct comparison.

Prep	Capture Run	Input (ng)	Pre-Hyb Yield (ng/ul)	Total Reads	Mean Insert (bp)	Mean Cov	% Dup	ELS	Fold 80 Base Penalty	%Cov @50X	%Cov @100X	%OT
Sonic	PanCan MiSeq®	10	97.2	1.5 M	201	205X	9.4	10 X10^6	0	99.1	99	80.3
			110		201	206X	8.8	11 X10^6		99.1	98.9	80.3
Comp-K			101		201	203X	9.6	10 X10^6		99.2	99	80.2
			96		201	200X	10.6	9 X10^6		99.2	99	80
Comp-N			99.6		196	203X	10.1	9 X10^6		99.1	99	80.3
			105		196	203X	9.9	9 X10^6		99.1	98.9	80.2
Sonic	Exome NovaSeq®	100	100	80 M	212	146X	9.1	N/A	1.53	85.6	77	89.1
			110		211	146X	8.2		1.48	85.9	78	88.6
Comp-K			96.5		211	143X	9.1		1.58	85.6	76	88.7
			101		213	141X	9		1.54	85.8	76	88.2
Comp-N			96		201	145X	8.2		1.57	85.6	76	89.1
			98.4		207	141X	9		1.55	85.8	76	88.7

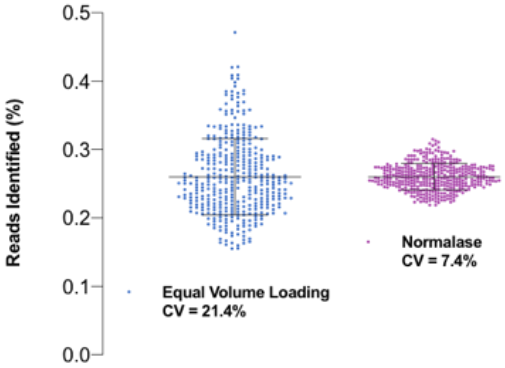
Upper panel: Pan-Cancer captured libraries were sequenced on a MiSeq® with PE100 and normalized to 1.5M reads. Sonic library yields using the Swift HiFi Master Mix were equivalent to competitor kit yields using Kapa HiFi Hot Start Ready Mix, demonstrating robust library amplification for pre-hyb PCR. Due to MiSeq chemistry, PCR duplicates directly reflect library complexity, where all three kits demonstrated similar target coverage, estimated library size and uniformity of target coverage.

Lower panel: Exome capture libraries were sequenced on a NovaSeq with PE150 and normalized to 80M reads. Sonic library yields using the Swift HiFi Master Mix were equivalent to competitor kit yields using Kapa HiFi Hot Start Ready Mix, demonstrating robust library amplification for pre-hyb PCR. Due to NovaSeq chemistry, PCR duplicates include cluster duplicates and do not directly reflect library complexity (cannot estimate library size). However, all three kits demonstrated similar target coverage and uniformity of target coverage.

Abbreviations: % Dup= % Duplicates, ELS= Estimated Library Size (Picard), %Cov= % Coverage, %OT= % On Target; Fold 80 Base Penalty is the fold over-coverage necessary to raise 80% of bases in "non-zero-cvg" targets to the mean coverage.

Swift 2S Sonic Leverages Normalase Technology

384 Swift 2S Sonic Libraries were generated with 1 ng Coriell NA12878 gDNA and each uniquely indexed with Swift Normalase Unique Dual Indexing primers during library amplification. Libraries were pooled using equal volume following PCR and the pool was quantified by Qubit and loaded on a MiSeq to obtain percent Reads Identified from each index. The equal volume pools CV was 21% demonstrating robust and reproducible amplification using the Normalase indexing primers. The same libraries were then enzymatically normalized using Swift Normalase to generate an equimolar library pool of 4 nM then loaded on a MiSeq. The Normalase pool CV was reduced to 7.4% demonstrating robust normalization of multiplexed libraries using Swift Normalase. Lines represent the median and 95% confidence interval.



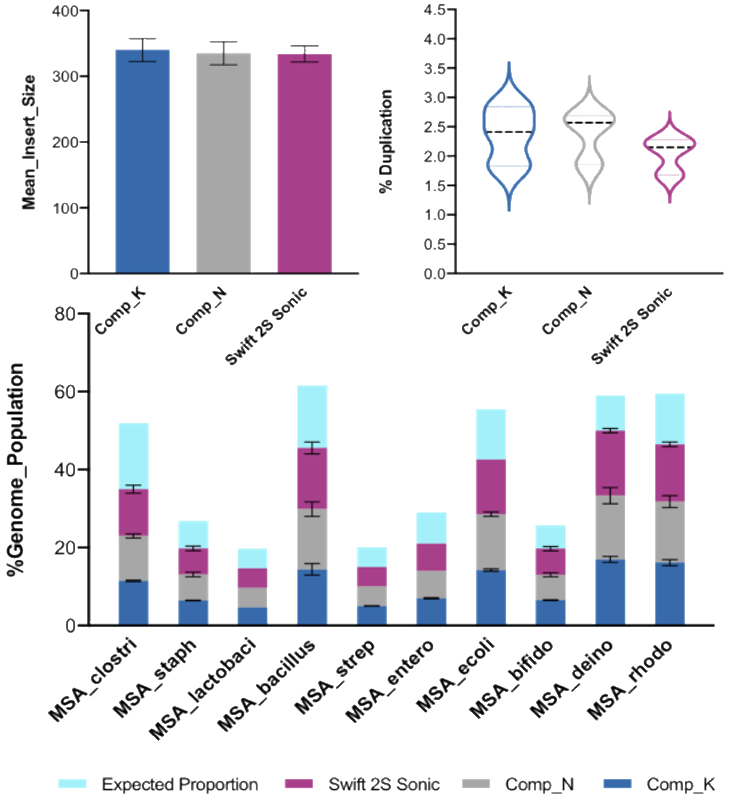
Comprehensive Metagenomics Sequencing

NGS libraries were constructed using Swift 2S Sonic Flexible and competitor kits K and N from 1 ng of mock metagenome DNA (ATCC MSA-1000) Covaris-sheared to 350 bp in duplicate. Libraries were prepared using IDT for Illumina TruSeq UD DNA Indexes (Cat. No. 20020590) at supplier-specified adapter concentration and amplified with the Polymerase supplied in each kit. Libraries were quantified by Qubit and Agilent Bioanalyzer 2100, and sequenced on a MiSeq with PE150 reads. Data for each library was normalized to 1M reads and achieved a metagenome mean coverage of 20X.

Top Panel: Size selecting libraries using the same SPRI ratio resulted in an unbiased comparison of the sequencing results. Comparable mean insert sizes and duplication rates were obtained with Swift 2S Sonic compared to competitor kits K and N.

Bottom Panel: Despite significant variation in base composition, the Swift 2S Sonic and competitor kits K and N enabled detection of each strain's genome at the expected frequency with minimal bias. These results demonstrate that variability in GC composition and size of the genomes does not influence the performance of Swift 2S Sonic. Genome base composition was as follows:

B. cereus (GC% = 35.5), B. adolescentis (GC% = 59.4), C. beijerinckii (GC% = 29.9), D. radiodurans (GC% = 66.7), E. faecalis (GC% = 37.8), E. coli (GC% = 50.8), L. gasseri (GC% = 35.3), R. sphaeroides (GC% = 68.9), S. epidermidis (GC% = 32.0), S. mutants (GC% = 36.8).



Ordering Information

Workflow Component	Product Name	Catalog Number
Library Kits	Swift 2S® Sonic DNA Library Kit (24 reactions)	42024
	Swift 2S® Sonic DNA Library Kit (96 reactions)	42096
	Swift 2S® Sonic Flexible DNA Library Kit (24 reactions)	43024
	Swift 2S® Sonic Flexible DNA Library Kit (96 reactions)	43096
UDI Primers	Swift Unique Dual Indexing Primer Kit (24-plex, 96 reactions)	X9096
	Swift Unique Dual Indexing Primer Kit (96-plex, 384 reactions)	X90384
	Swift Unique Dual Indexing Primer Plate (96-plex, 96 reactions, single-use plate)	X9096-PLATE
	Swift Normalase® Unique Dual Indexing Primer Plates (384-pex, 4x96 reactions)	X91384-PLATE
	Swift Normalase® Unique Dual Indexing Primer Plate, 96-plex, 96 reactions (SU001-SU096)	X91096-1-PLATE
	Swift Normalase® Unique Dual Indexing Primer Plate, 96-plex, 96 reactions (SU097-SU192)	X91096-2-PLATE
	Swift Normalase® Unique Dual Indexing Primer Plate, 96-plex, 96 reactions (SU193-SU288)	X91096-3-PLATE
	Swift Normalase® Unique Dual Indexing Primer Plate, 96-plex, 96 reactions (SU289-SU384)	X91096-4-PLATE
SI Primers	Swift Single Indexing Primer Kit, Set A (12-plex, 24 reactions)	X6024
CDI Primers	Combinatorial Dual Indexing Primer Kit (96 combinations, 1 reaction ea.)	X8096
	Set S1 Combinatorial Dual Indexing Primer Kit (192 indices, 192 reactions)	X85192
	Set S2 Combinatorial Dual Indexing Primer Kit (192 indices, 192 reactions)	X86192
	Set S3 Combinatorial Dual Indexing Primer Kit (192 indices, 192 reactions)	X87192
	Set S4 Combinatorial Dual Indexing Primer Kit (192 indices, 192 reactions)	X88192
	Set S1-S4 Combinatorial Dual Indexing Primer Kit (768 indices, 768 reactions)	X89768

Visit **www.swiftbiosci.com** for easy ordering.

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