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.

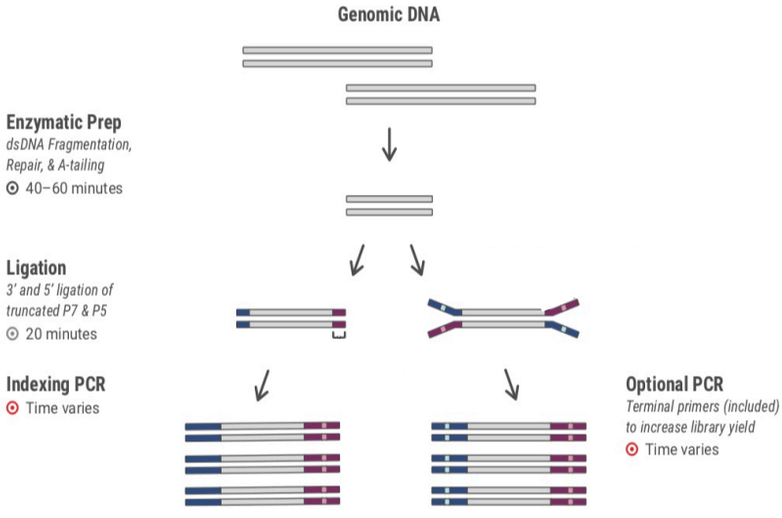

Fig1. Turbo workflow with Swift 2S Turbo workflow on the left and Swift 2S Turbo Flexible on the right.

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.

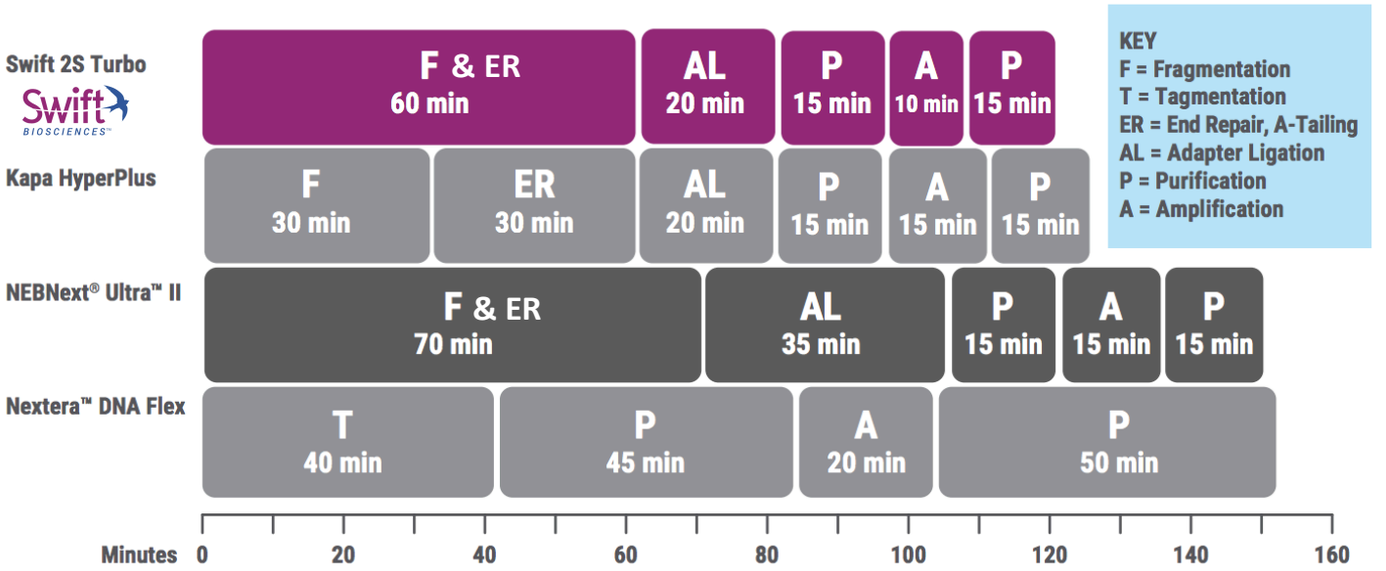

Fig 2. This diagram shows Swift's workflow with two enzymatic steps as compared to the Kapa Hyper Plus workflows, and less overall time compared to Nextera™ DNA Flex Library Kit and NEBNext® Ultra™ II. Time comparisons assumes 100 ng DNA input going into the library preparation and fragmenting to an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

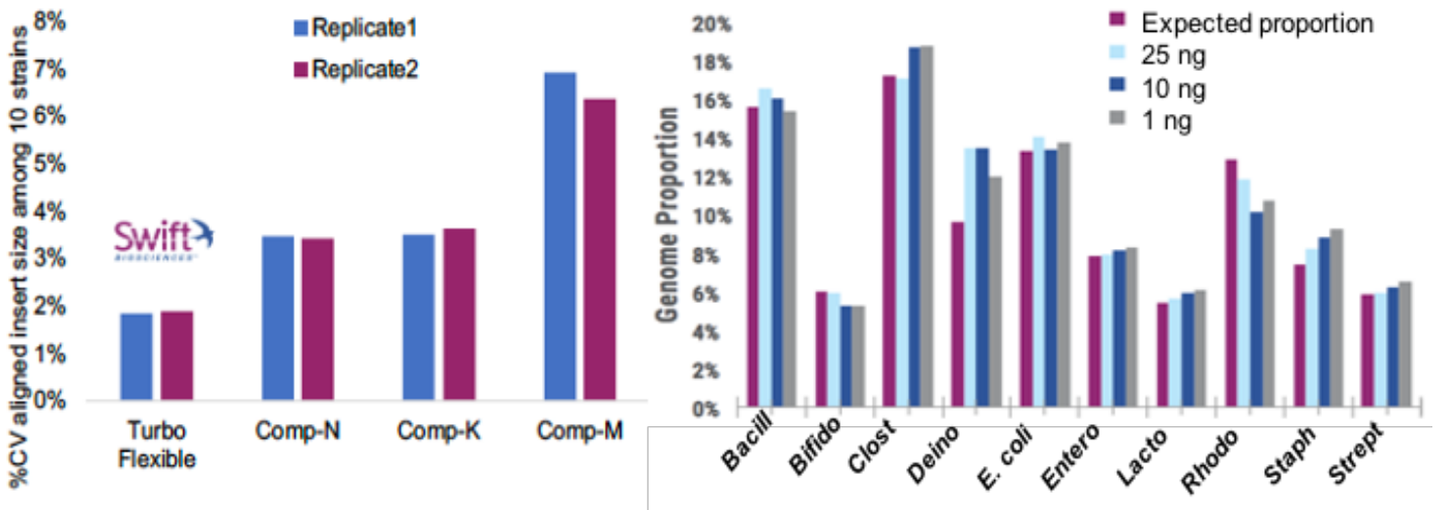

Fig 3. NGS libraries were constructed from: Left panel: five nanograms of high-quality genomic DNA (ATCC MSA-1000), using a fragmentation time required to achieve library mode sizes of ~ 350 bp (plus ~ 125 bp, the length of the adapters) via Turbo and competitor kits. The libraries were co-sequenced 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).

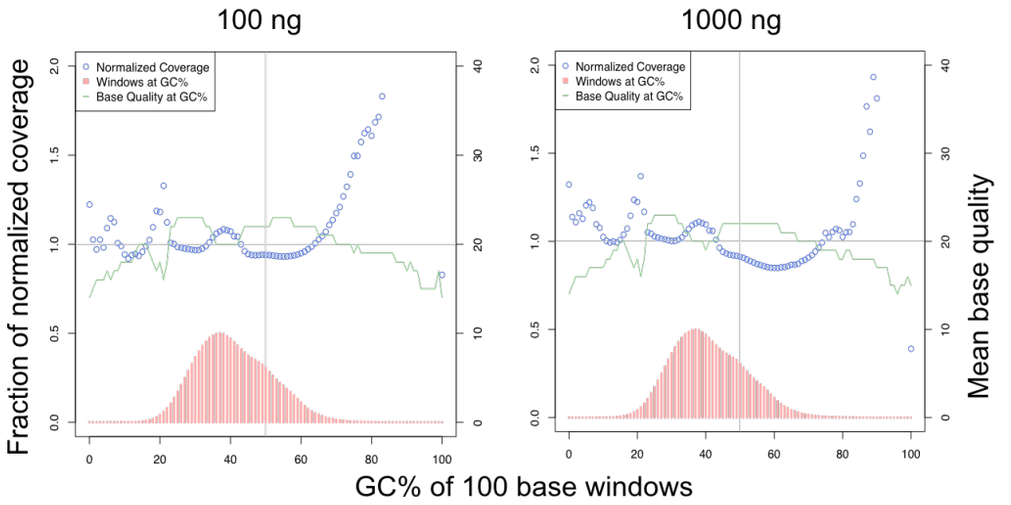

Fig 4. 2S Turbo was used for PCR-free NGS libraries constructed from high quality genomic DNA (NA12878) for whole genome sequencing with 100, 250, 500, and 1000 ng input. The libraries were co-sequenced on Illumina HiSeq 4000 instrument. The Picard diagram demonstrates evenness of coverage across distinct 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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