



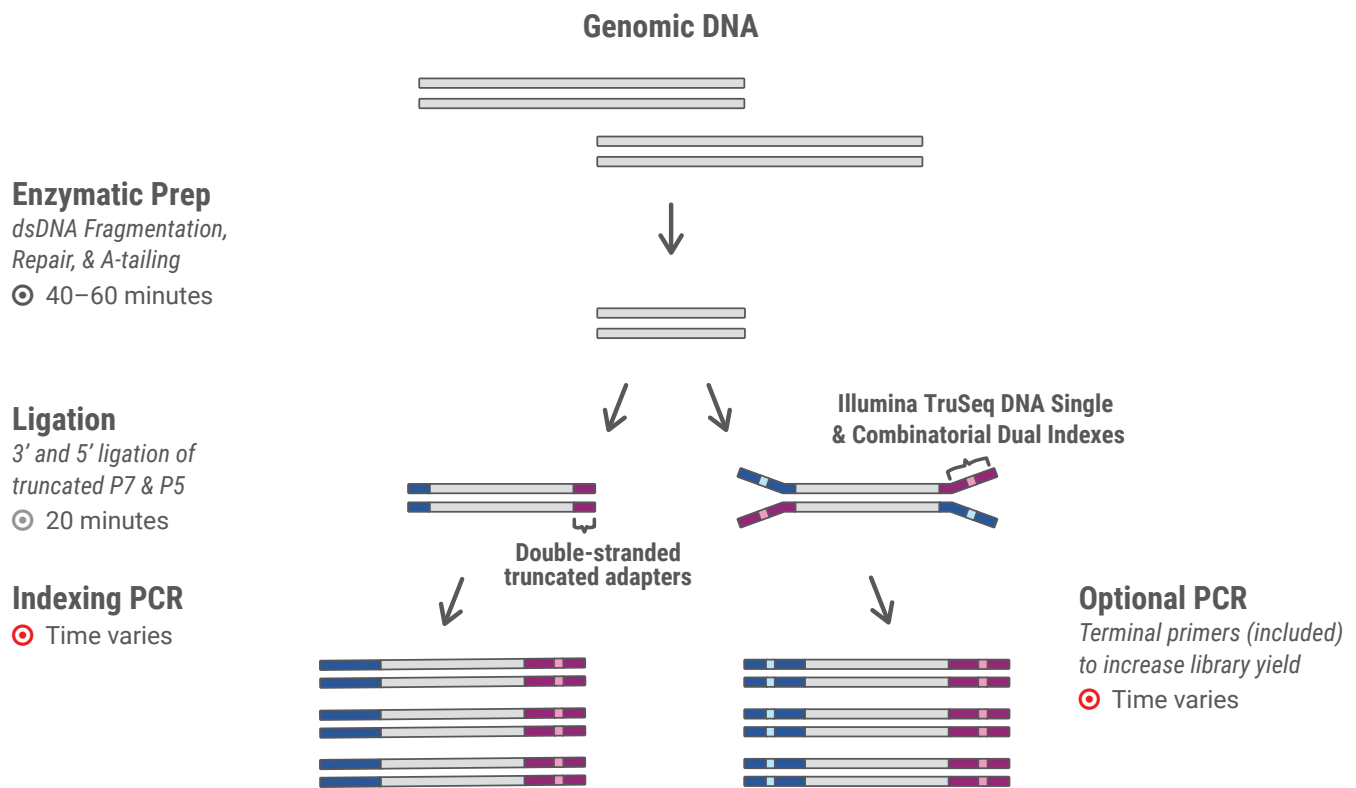
SWIFT 2S TURBO DNA LIBRARY KITS

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, and large gene studies.

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 workflows.



Supported Applications

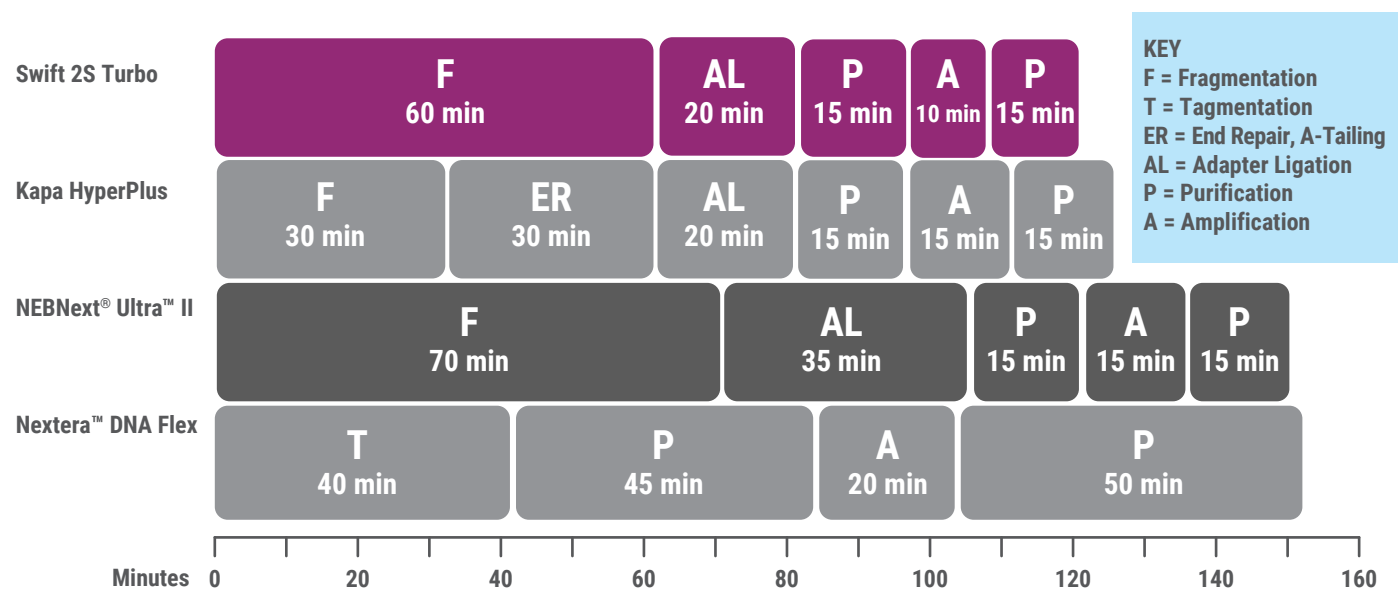
Swift 2S Turbo DNA Library Kits are available in two configurations to support variety of sample inputs and applications. Swift 2S Turbo is an “all in one” kit for quick implementation of core applications. The Swift 2S Turbo Flexible workflow supports an expanded menu of applications and is compatible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

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

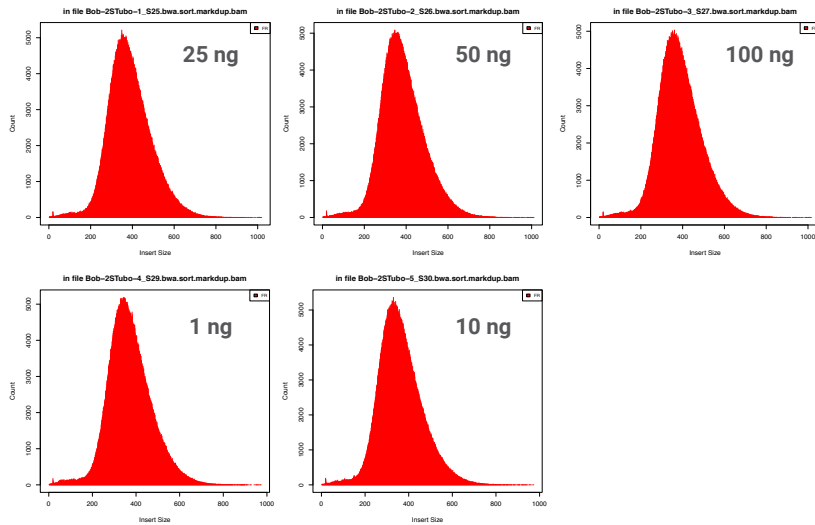
The Swift 2S Turbo leverages a fast, efficient workflow consisting of two enzymatic incubations spanning 80 minutes and two bead-based purification steps, thereby reducing sample handling and overall library preparation time to two hours. Following ligation and the optional PCR step, depending on the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

This diagram shows Swift’s workflow with two enzymatic steps as compared to the Nextera™ DNA Flex Library Kit, NEBNext® Ultra™ II, and Kapa Hyper Plus workflows. The comparisons were done assuming 100 ng DNA inputs going into the library preparation kits targeting insert sizes of ~ 200 bp.

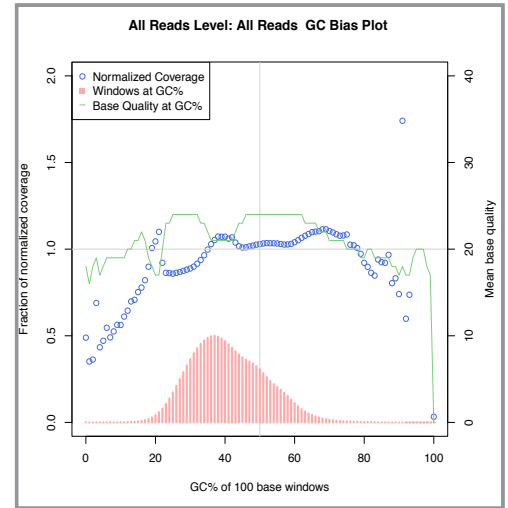


High Quality Data

Swift 2S Turbo offers reproducible and consistent aligned insert sizes across a broad range DNA input amounts.



NA12878 Input (ng)	Bioanalyser Library Mode (bp)	Median Sequence Insert (bp)
1	562	363
10	550	353
25	580	379
50	574	373
100	587	378

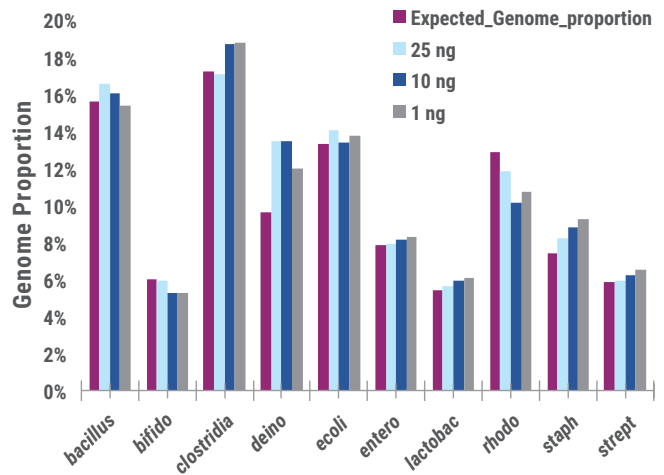


NGS libraries were constructed from high quality genomic DNA (NA12878) for whole genome sequencing. The fragmentation times required to achieve library mode sizes of ~ 350 bp (plus ~ 125 bp, the length of the adapters) were 8- and 10-minutes for DNA ≥ 25 ng and DNA < 25 ng, respectively. The libraries were co-sequenced on Illumina NovaSeq instrument. Left panel: The library modes and the median sequence insert sizes (% aligned insert) demonstrate reproducibility in fragmentation across a range of DNA inputs. Right panel: the Picard diagram demonstrates evenness of coverage across distinct GC compositions.

Swift 2S Turbo provides superior representation of an artificial microbial community of 10 strains.

The artificial microbial community was comprised of *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).

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. 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.



Swift 2S Turbo enables reproducible library preparation from FFPE samples of distinct integrity to achieve outstanding coverage uniformity for somatic mutation detection.

Sample Integrity	Input (ng)	% Duplicates	Mean Bait Coverage	% Covered ≥ 20X	% Covered ≥ 50X	% Covered ≥ 100X	% Bases On-Target
0.24	25	6	176X	99.5	98.3	90.7	73.8
0.26	25	8	173X	99.6	98.5	94.6	74.9
0.34	24	4	163X	99.1	98.1	89.7	70.3
0.34	79	6	151X	99.4	98.5	90.2	69.6

The Swift 2S Turbo was evaluated with the IDT xGen Pan-Cancer probes and DNA inputs from FFPE of different quality. Libraries were sequenced on a MiSeq run with 100 bp PE reads. The integrity of FFPE inputs were qualified via qPCR of Swift Alu 115 repeats. The sample integrity was assessed based on the Alu 247/115 repeat fragment ratios. 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 with comparable % bases on-target within the range of 68-75%.

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	<ul style="list-style-type: none"> • Swift 2S Turbo Single Indexing Primer Kit Set A • Swift 2S Turbo Combinatorial Dual Indexing Primer Kit • Swift 2S Turbo Unique Dual Indexing Primer Kit • >96 indexing, please inquire! 	<ul style="list-style-type: none"> • Third party supplier for full length adapters • Swift indexing primers for custom truncated adapters
System Compatibility and Multiplexing Format	2- and 4-channel 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 Set A	24	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	46496

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