ACCEL-NGS® METHYL-SEQ DNA LIBRARY KIT

The Accel-NGS Methyl-Seq DNA Library Kit maximizes DNA recovery of bisulfite-converted samples and constructs libraries that accurately represent sample composition. The Accel-NGS Methyl-Seq workflow maximizes DNA recovery through a post-bisulfite library preparation, utilizing a highly efficient adapter attachment that is compatible with single-stranded, bisulfite-converted DNA. Library yields from this kit are up to 100x greater than those from methods that bisulfite convert after library construction. Additionally, the template-independent adapter attachment chemistry of the Accel-NGS Methyl-Seq Kit provides a more complete, less biased library as observed from comprehensive methylome coverage by Whole Genome Bisulfite Sequencing (WGBS).

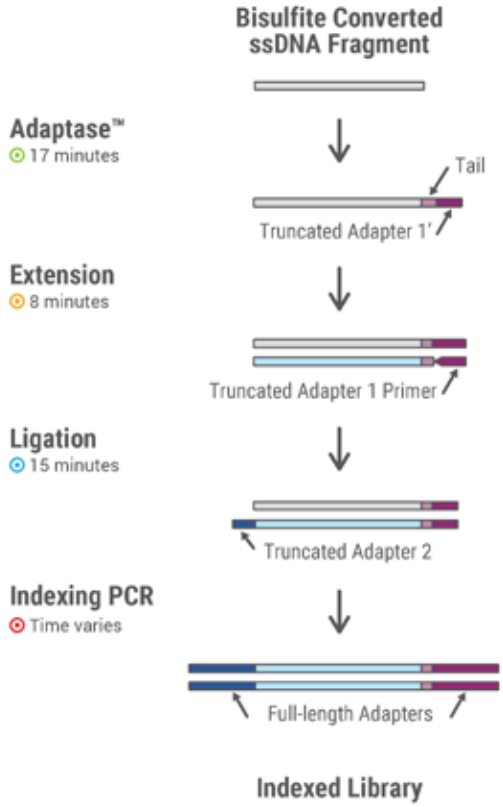
Features

- High recovery of input DNA
- Low bias library preparation
- Simple, 2-hour library prep
- Compatable with Illumina® platforms
- Minimal PCR cycles required
  - 4 cycles for 100 ng
  - 7 cycles for 10 ng
  - 11 cycles for 1 ng
  - 14 cycles for 100 pg

Applications

- WGBS
- Reduced Representation Bisulfite Sequencing (RRBS)
- Detecting genome-wide methylation in 5 ng of cfDNA
- Hybridization capture using NimbleGen™ SeqCap™ Epi Enrichment System
- Bisulfite-converted DNA enriched by MeDIP, ChIP or other methods

Workflow Superior to the Leading Kits



The Accel-NGS Methyl-Seq workflow constructs libraries from single-stranded DNA fragments. The Adaptase step simultaneously performs end repair, tailing of 3' ends, and ligation of the first truncated adapter. The Extension and Ligation steps add the second truncated adapter to the bottom strand only. The Indexing PCR step increases yield and incorporates full length adapters.

Superior Library Complexity and Coverage from 1 ng

To demonstrate the efficient and unbiased performance of the Accel-NGS Methyl-Seq Kit, a titration experiment using 100 ng, 10 ng, or 1 ng of *Arabidopsis* genomic DNA was performed and compared to two alternative methods (random primer and traditional) using these same inputs.

Input	Sample	% Reads Aligned	Genome Coverage	% Duplicate Reads	Estimated Library Size (Millions)	% CpX Missing	% CpX Covered ≥ 10X
100 ng *Arabidopsis*	**Accel-NGS Methyl-Seq**	89.6	22.0X	1.9	714	0.56	92.2
	Traditional	80.2	21.0X	2.7	604	0.57	88.1
	Random Primer	71.4	16.0X	22.1	48	7.70	39.4
10 ng *Arabidopsis*	**Accel-NGS Methyl-Seq**	87.8	22.0X	2.7	406	0.58	90.4
	Traditional	76.7	19.0X	11.9	70	0.57	83.9
	Random Primer	71.9	16.0X	22.2	45	5.20	45.2
1 ng *Arabidopsis*	**Accel-NGS Methyl-Seq**	83.3	18.0X	18.2	38	0.59	77.1
	Traditional	80.7	10.0X	62.3	6	2.00	17.0
	Random Primer	73.4	12.0X	46.1	12	6.60	31.3
10 ng Human	**Accel-NGS Methyl-Seq**	86.4	8.9X	7.9	1,393	N/A	N/A

Each Arabidopsis thaliana *file was normalized to 30.2 million reads and data reported as an average of duplicate bisulfite-converted samples. To assess coverage for the human genome, an Accel-NGS Methyl-Seq library was constructed using HapMap NA12878 DNA and the sequencing data was normalized to 183.5 million reads.*

Nimblegen's SeqCap Epi: CpGiant

The Accel-NGS Methyl-Seq Library Kit was compared to Kapa Biosystems' library prep at 80M reads per sample. The coverage metrics used were evaluated at 1 µg and 100 ng (within input specifications) and at low inputs. An average of two duplicate libraries is shown.

Coverage Metrics

Input	Method	% Aligned	% on Target	% Duplication	Mean Coverage	% Covered ≥ 2X	% Covered ≥ 20X	None Covered
100 ng	**SWIFT**	**90**	**73**	**6.5**	**49x**	**98.6**	**78.6**	**0.8**
1 µg	Kapa	90	80	9.4	51x	98.6	81.1	0.8
10 ng	**SWIFT**	**91**	**77**	**26.0**	**35x**	**98.5**	**71.0**	**0.8**
10 ng	Kapa	87	78	71.0	1x	24.7	0.2	47.7
1 ng	**SWIFT**	**90**	**73**	**62.0**	**8x**	**93.6**	**2.3**	**1.0**

Ordering Information

Product Name	Reactions	Catalog No.
Accel-NGS Methyl-Seq DNA Library Kit	24	30024
Accel-NGS Methyl-Seq DNA Library Kit	96	30096

An Accel-NGS Methyl-Seq Indexing Kit is required for complete functionality of the library kit.

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

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