TruSeq® DNA Methylation Kit

Whole-genome bisulfite sequencing libraries from only 50 ng DNA.

Highlights

- **Sequence limited amounts of sample**
  Only 50 ng of DNA is required to create a TruSeq DNA Methylation Kit library
- **Maximize sample usage**
  Postbisulfite conversion method ensures all ssDNA fragments are captured
- **Obtain comprehensive whole-genome data**
  Discover methylation patterns of all CpG, CHH, and CHG regions

Sequence the Entire Sample

The process of bisulfite treatment denatures genomic DNA into single-stranded DNA (ssDNA). The TruSeq DNA Methylation Kit converts bisulfite-treated, ssDNA into an Illumina sequencing library. All ssDNA fragments are captured during the procedure, eliminating sample loss associated with other methods.

Workflow

With the TruSeq DNA Methylation Kit, bisulfite-treated ssDNA is randomly primed using a polymerase able to read uracil nucleotides to synthesize DNA strands containing a specific sequence tag (Figure 1). The 3′ ends of the newly synthesized DNA strands are then selectively tagged with a second specific sequence tag, using a patented procedure.

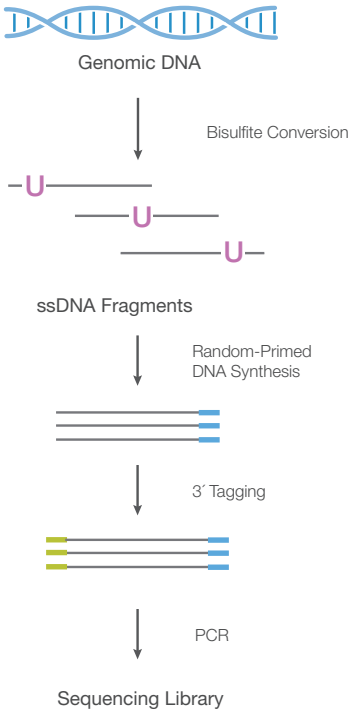

Figure 1: Workflow for the TruSeq DNA Methylation Kit. The kit uses a postbisulfite conversion method to greatly reduce loss of DNA fragments and can generate WGBS libraries from as little as 50 ng of input DNA.

This process generates di-tagged DNA molecules with known sequence tags at their 5′ and 3′ ends. The di-tagged DNA is enriched in PCR, resulting in double-stranded DNA (dsDNA) with the appropriate Illumina sequences for use on any Illumina platform.

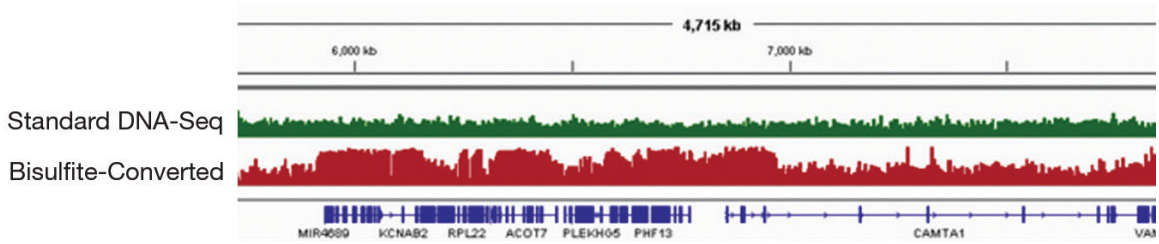

Figure 2: CpG Methylation Patterns. Example of methylation across a region of chromosome 1 indicates high CpG methylation (red) compared to coverage patterns from nonbisulfite-treated DNA (green). The TruSeq DNA Methylation Kit library was prepared from 50 ng input GM12878 lymphoblastoid genomic DNA after bisulfite treatment. Data analysis was done using Bismark software (v0.7.2) and a custom analysis pipeline.

Deep Coverage of Critical Regions

Depth of coverage is enhanced in genomic areas with biological utility (Figure 2). The TruSeq DNA Methylation Kit captures full sample diversity of critical areas, including:

- Coding region start and end sites for genes known to be involved in cancer, taken from SOMA and CRUK panels as well as literature-derived cancer genes
- Genes defined by the American College of Medical Genetics as being medically relevant (ACMG_genes)
- Exonic coding regions from Ensemble 70 (exons_ensemble70)
- List of 100 promoters defined by the Broad Institute as being of high interest and difficult to sequence (fosmid_promoters)

The increased throughput of the HiSeq® systems enables complete methylation information to be captured from a growing number of samples.

Ordering Information

Product	Size	Catalog No.
TruSeq DNA Methylation Kit	12 rxn	EGMK81312
	24 rxn	EGMK91324
	96 rxn	EGMK91396
Index PCR Primers	12 indexes × 10 rxn	EGIDX81312
FailSafe™ PCR Enzyme Mix The FailSafe PCR Enzyme Mix is required for the TruSeq DNA Methylation Kit	100 units	FSE51100

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