abcam

Product datasheet

Bisulfite-Seq High Sensitivity Kit (For Illumina®) ab185907

1 图像

概述

产品名称 Bisulfite-Seq High Sensitivity试剂盒(For Illumina®)

灵敏度 < 0.5 ng

检测时间 8h 00m

产品概述 ab185907 is designed to carry out bisulfite conversion, followed by a "post-bisulfite" library preparation process for Illumina® platform-based bisulfite sequencing, all in one kit. The DNA library is constructed directly from bisulfite-converted DNA generated from a small amount of input DNA (500 pg to 500 ng). Intended applications include whole genome bisulfite sequencing, oxidative bisulfite sequencing, reduced representative bisulfite sequencing, and various other bisulfite-next generation sequencing techniques. The optimized protocol and components of the kit allow the DNA to be bisulfite converted and fragmented simultaneously followed by quick non-barcoded (singleplexed) and barcoded (multiplexed) library construction using sub-nanogram quantities of bisulfite converted DNA.

说明 DNA methylation occurs by the covalent addition of a methyl group (CH_3) at the 5-carbon of the cytosine ring, resulting in 5-methylcytosine (5-mC). DNA methylation is essential in regulating gene expression in nearly all biological processes including development, growth, and differentiation. Alterations in DNA methylation have been demonstrated to cause a change in gene expression. Genome-wide analysis of DNA methylation could provide valuable information for discovering epigenetic markers used for disease diagnosis, and potential targets used for therapeutics. Bisulfite sequencing via next-generation sequencing technologies allow for high volume, lower cost output of DNA sequence data towards a better understanding of DNA methylation.

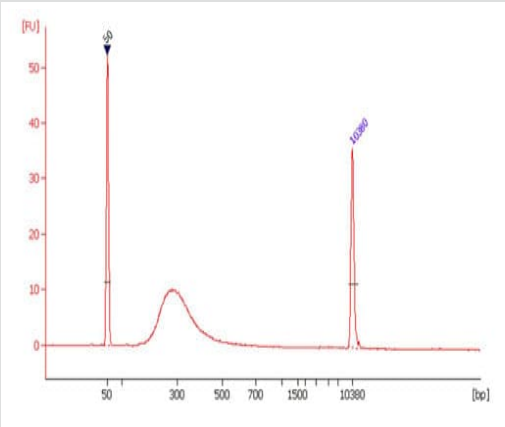
性能

存放说明 Please refer to protocols.

组件	24 tests	12 tests
10X dA-Tailing Buffer	1 x 80µl	1 x 40µl
10X End Repair Buffer	1 x 80µl	1 x 40µl

组件	24 tests	12 tests
2X HiFi PCR Master Mix	1 x 320µl	1 x 160µl
2X Ligation Buffer	1 x 500µl	1 x 250µl
5X Conversion Buffer	1 x 100µl	1 x 50µl
Adaptors (50 µM)	1 x 30µl	1 x 15µl
Conversion Enzyme Mix	1 x 30µl	1 x 15µl
Conversion Primer	1 x 52µl	1 x 26µl
Desulphonation Solution	1 x 140µl	1 x 70µl
DNA Binding Solution	1 x 12ml	1 x 6ml
Elution Buffer	1 x 2ml	1 x 1ml
Elution Solution	1 x 1ml	1 x 0.5ml
End Repair Enzyme Mix	1 x 50µl	1 x 25µl
F-Collection Tube	1 x 30 units	1 x 15 units
F-Spin Column	1 x 30 units	1 x 15 units
Klenow Fragment (3’-5’ exo-)	1 x 30µl	1 x 15µl
Modification Buffer	1 x 6ml	1 x 3ml
Modification Powder	1 x 4 vials	1 x 2 vials
MQ Binding Beads	1 x 3.6ml	1 x 1.8ml
Primer I (10 µM)	1 x 30µl	1 x 15µl
Primer U (10 µM)	1 x 30µl	1 x 15µl
T4 DNA Ligase	1 x 30µl	1 x 15µl

图片



Size distribution of library fragments

Size distribution of library fragments. Post-bisulfite DNA library was prepared from 10 ng of input DNA using ab185907.

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