MGIEasy Whole Genome Bisulfite Sequencing Library Prep Kit

Features

- Use 10–100 ng DNA fragment as input
- Suitable for common animals, plants, fungus etc
- 9 hours to finish the library preparation
- Lower duplication rate. Highly reliable methylation results.

Introduction

DNA methylation is one of the important epigenetic mechanisms. Single-base cytosine methylation mapping in the whole genome is essential to understanding temporal and spatial gene expression and chromatin remodeling in epigenetic study. MGIEasy Whole Genome Bisulfite Sequencing Library Prep Kit is optimized to convert 10–100ng fragmented DNA into a sequencing library for MGI High-throughput sequencing platforms.

Product Specification

Assay Time	~9 hours
Input Quantity	10–100 ng of DNA fragment
Sample Types	Tissues, plasma and FFPE sample
Species	Human, animals, plants and fungi
DNA Treatment	Ultrasonic (no need for cell free DNA)
Insert Size	100–500 bp
Platform	DNBSEQ-G400*、DNBSEQ-T7*
Read Length	PE100、PE150
Sequencing Data	30X Clean data

Data Performance

Low input

This kit is compatible with a variety of sample types including human, animals, plants, fungi and FFPE samples. When starting with 10 ng or 100 ng DNA fragment from different species, the PCR yield are all above 350 ng which is enough for sequencing.

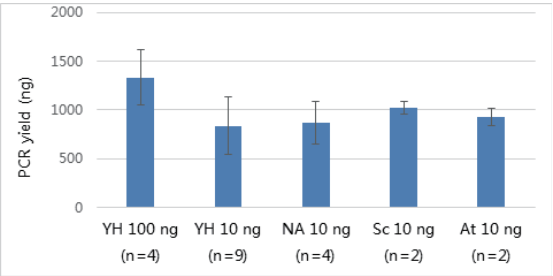

Fig.1 Library yield

PCR yield of different samples (YH, NA12878, Arabidopsis and yeast) and different fragment DNA input (10 ng and 100 ng).

High mapping and coverage rate

The same NA12878 sample is sequenced on N platform and DNBSEQ-G400* respectively to achieve 110GB data for analysis. Compared to N_NA data, MGI_NA data shows a higher mapping rate and lower duplication rate, resulting in a greater sequencing depth at the same clean data amount (Table 1).

Table 1 Comparation on mapping and coverage

Library ID	N_NA	MGI_NA
NA12878 DNA input (ng)	100	20
Clean data amount (Gb)	110	110
Read length	PE150	PE100
Mapping rate (%)	82.09	91.1
Unique mapping rate (%)	79.26	86.82
Duplication rate (%)	16.82	15.23
Average depth (X)	25.08	28.12
Genome Coverage (%)	98.4	98.01
Fraction covered with at least 10x (%)	91.702	94.322
Fraction covered with at least 20x (%)	61.768	80.649

Coverage analysis

MGI_NA shows very high data coverage in whole-genome analysis of CG sites with above 95% coverage. For methylation analysis, the global methylation level distribution of CG site in MGI_NA and N_NA is highly consistent, and equivalent CG site methylation level in Element methylation analysis (Fig 2a, b).

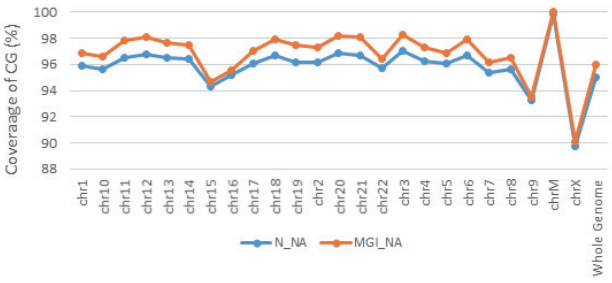

Fig 2a Chromosome coverage of CG site

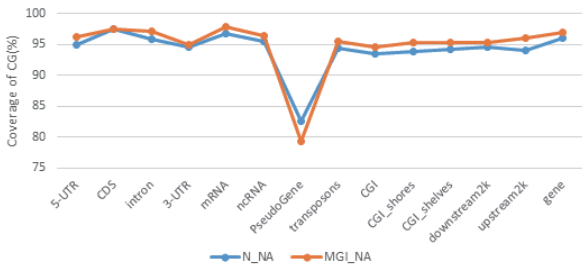

Fig 2b CG coverage of different elements

The same NA12878 sample was also analyzed by the Infinium Methylation EPIC BeadChip chip, which detects 858,900 CpG sites (Table 2a). We analyzed the Concordance CG rate and Unique CG rate among MGI_NA, N_NA and Infinium Methylation EPIC BeadChip results and statistically analyzed the detection sensitivity of MGI_NA and N_NA. The MGI_NA shows a highly concordant performance with Infinium Methylation EPIC BeadChip chip at 4X and 10X sequencing depth(Table 2b).

Table 2a Infinium MethylationEPIC BeadChip info

CG number covered by chip	Genome CG number	CG site covered rate of 850K chip
858,900	56,434,896	1.50%

Table 2b Concordance CG rate and Unique CG rate

Sample	Sequencing depth	Concordance CG rate* (%)	Unique CG rate** (%)	Sensitivity*** (%)
MGI_NA	≥4X	85%	8%	93%
N_NA	≥4X		3%	88%
MGI_NA	≥10X	33%	20%	54%
N_NA	≥10X		17%	51%

*The concordance CG rate of all three platforms in all CG sites detected by microarray
**The percentage of CG sites detected by microarray and only one of the NGS platforms in all CG sites by microarray
***The percentage of CG sites in microarray being covered by DNBSEQ or N Platform

Methylation analysis

MGI_NA, which prepared and sequenced by the MGIEasy Whole Genome Methylation Library Preparation Kit and DNBSEQ-G400* Sequencing platform, demonstrated an accurate methylation level detection. The methylation level between MGI_NA and N_NA is consistent (Fig 3a, b, c).

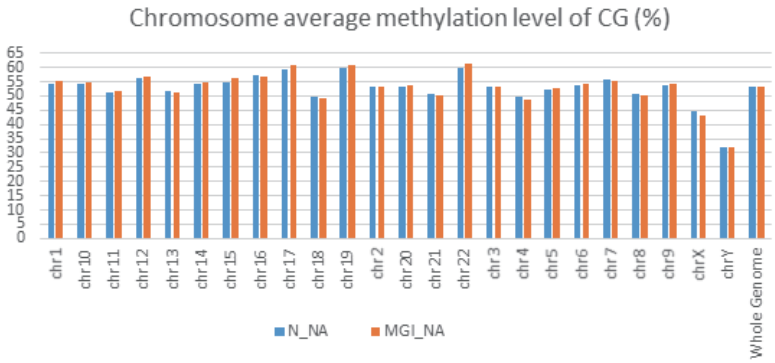

Fig.3b Methylation rate of CH pattern

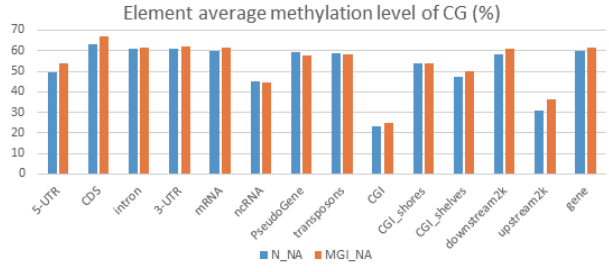

Fig.3a Methylation rate of CG pattern

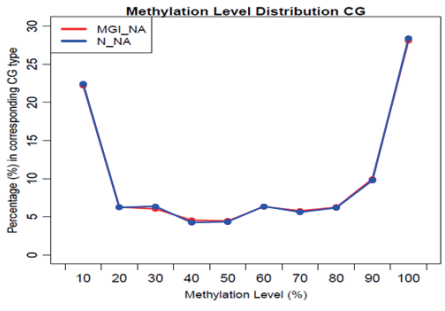

Fig.3b Methylation rate of CH pattern

We also analyzed the correlation of methylation rates of co-coverage sites among MGI_NA, N_NA, and Infinium Methylation EPIC BeadChip. The results show that the average P-value of methylation level correlation between any two results is above 0.9; Correlation increases as sequencing depth increases. The methylation level of the coverage sites is highly consistent among different result at 20X sequencing depth (Figure 4).

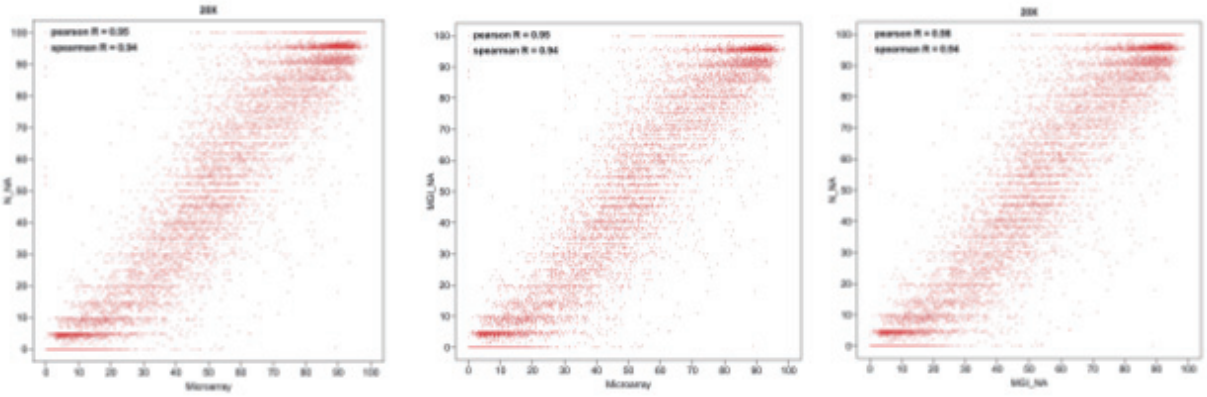

Fig 4 Consistency between MGI_NA, N_NA and Infinium Methylation EPIC BeadChip

Summary

The MGIEasy Whole Genome Bisulfite Sequencing Library Prep Kit provides an efficient workflow for library construction, enabling excellent mapping and coverage quality, high accuracy on methylation level, and stability using different inputs amounts and qualities of DNA, from a wide range of samples.

Product Information

Product	Configuration	Catalog No.
MGIEasy Whole Genome Bisulfite Sequencing Library Prep Kit	16 RXN	1000005251

Reference

[1] Lister, R. et al. Human DNA methylomes at base resolution show widespread epigenomic differences. Nature (2009). doi: 10.1038/nature08514
[2] Su, Z., Han, L. & Zhao, Z. Conservation and divergence of DNA methylation in eukaryotes. Epigenetics (2011). doi: 10.4161/epi.6.2.13875
[3] He, Y. & Ecker, J. R. Non-CG Methylation in the Human Genome. Annu. Rev. Genomics Hum. Genet. (2015). doi: 10.1146/annurev-genom-090413-025437

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