

MGIEasy Universal DNA Library Prep Set

Product Highlights

Low DNA input	Use as low as 0.5 ng fragmented DNA per sample
Wide range of applications	Compatible with different DNA fragmentation methods
Good sample compatibility	gDNA, FFPE, cfDNA, ChIP DNA and other samples with different degrees of degradation are acceptable
Wide range of species	Compatible with many sample types such as human, animal and plant, high and low GC bacteria, fungi and meta sample types
Quick library preparation process	Library preparation can be completed in as little as 4.5 hours

Overview

Whole genome sequencing (WGS), which sequences the genome of different species and individuals and analyzes differences at both individual and population levels, is designed to fully decode the genetic information of individuals and populations. With the increasing number of species with known genomic sequences, WGS is widely used in animal and plant breeding, population evolution, disease research, clinical diagnosis and drug development, and has become one of the most rapid and effective sequencing methods.

With the development of next generation sequencing, researchers have increasing purposes in preparing high-throughput sequencing libraries and therefore need a more general and compatible library preparation method to meet different requirements.

MGIEasy Universal DNA Library Prep Set is designed to meet the demand of various types of fragmented DNA, which is widely used in the whole genome and ChIP DNA sequencing. The requirement of fragmented DNA input is as low as 0.5 ng. The entire process of library preparation can be completed in 4.5 hours, and the resulted single strand circle libraries can be subjected to high-throughput sequencing on MGI high-throughput sequencing platform.

Product Specification

Total time	~4.5 hours
Hands-on time	~30 minutes
Sample input	0.5 ng - 50 ng fragmented DNA
Insert size	100-500 bp
Sample type	gDNA, FFPE, cfDNA, ChIP DNA and etc.
Species Compatibility	human, animals, plants, fungi, bacteria, meta sample and etc.
Application	Whole genome sequencing, ChIP-Seq and etc.
Platform Compatibility	DNBSEQ-G400*, DNBSEQ-G50*, MGISEQ-2000*, MGISEQ-200* and etc.
Sequencing strategy	SE50, PE100, PE150 and etc.

■ Workflow

The MGIEasy universal DNA Library Prep Set operates on extracted genomic DNA. After fragmenting DNA to desired sizes, the MGI adaptors are ligated to both ends and followed by PCR amplification. The purified PCR product is then thermally denatured into single-stranded DNA. Circularization is performed to obtain a sequencing library dedicated to the MGI high-throughput sequencing platform.

■ Product Performance

Good consistency of the library yield

PCR library preparations with the selected samples from five species, including human, mouse, soybeans, E. coli and meta, each with 50 ng of fragmented DNA as the initial amount, result in yields consistently above 400 ng. This indicates that MGIEasy universal DNA library prep set obtains sufficient PCR library yield for subsequent circularization and sequencing for different species and different genome size samples.

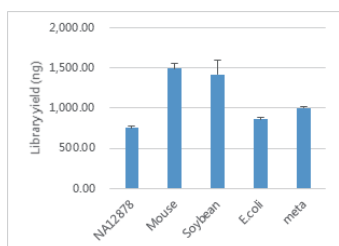


Fig.1a PCR yield of library preparation for different species

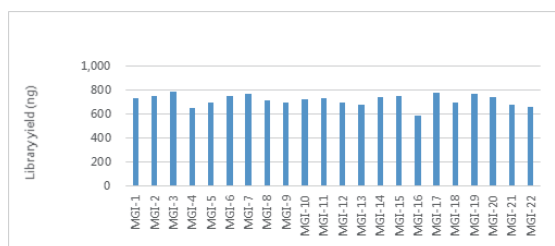


Fig.1b PCR yield of library preparation for NA 12878 standard

22 repetitions of PCR library preparation were performed using NA 12878 standard as a template. The mean library yield was 718.9 ng with a CV value of 6%. This indicates that the MGIEasy Universal DNA Library Prep set is capable of producing stable library yields.

Compatible with different GC content microbial library preparation

Using single bacterial strains with different GC contents as templates, a yield of PCR library above 40 ng can be achieved consistently at various starting amounts of gDNA, which meets the requirements of subsequent circularization and sequencing.

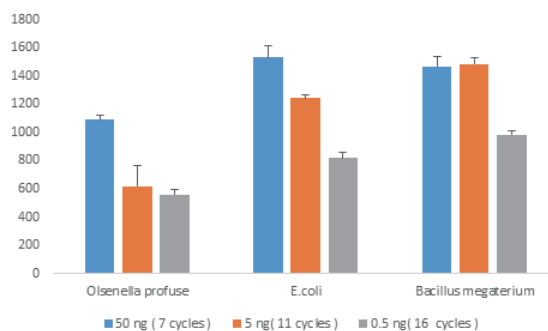


Fig.2 Library preparation of different GC content for single bacterial strains

Using MGIEasy Universal Library Prep Set to construct libraries, GC content of single strains displayed above from left to right is 64%, 50% and 37%, respectively. The gDNA initial amounts used are 50 ng, 5 ng, and 0.5 ng. The PCR reaction is carried out for the corresponding number of amplification cycles.

Good data uniformity

Using NA12878 standard template, MGIEasy Universal DNA Library Prep Set results in better uniformity of data than the competing product from Vendor K, especially in the region that exhibits high GC.

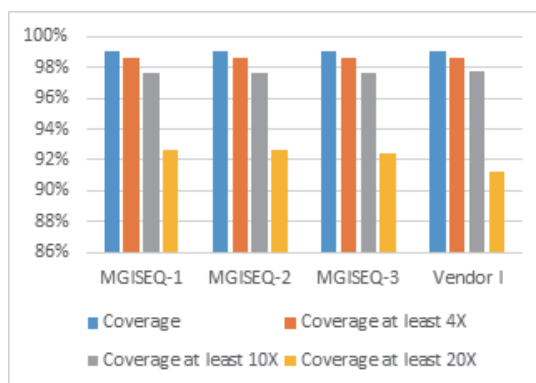


Fig.3 Distribution of GC in NA12878 standard

Library prepared using MGIEasy Universal Library Prep Set is sequenced on the MGISEQ- 2000 platform. The GC distribution is compared to the sequencing data of the brand K library preparation kit on the "N" platform.

Good genome coverage

Using the NA12878 standard as a template, the MGIEasy universal DNA Library Prep Set on the MGISEQ sequencing platform results in consistently better coverage than the competing product from Vendor I (20X coverage: MGI averaged 92.59 % vs Vendor I 91.29 %).

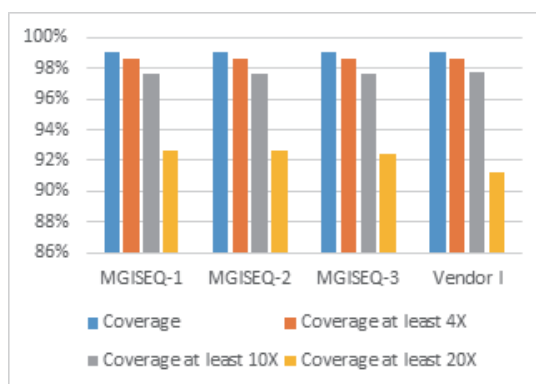


Fig.4 Genomic coverage of NA12878 standard

MGISEQ-1,-2 and -3 represent repeated data results of MGIEasy Universal DNA Library Prep Set on MGISEQ platform. Vendor I corresponds to the data from PE150 sequencing of Vendor A library preparation kit data performed on Vendor I sequencing platform. The analytical data above is extracted from about 30X depth after filtering.

Excellent variation detection performance

Using the NA12878 standard as a template, compared with Vendor I, the MGIEasy Universal DNA Library Prep Set has the same ability to detect SNP, with a consistency rate of 99.2% (Fig.5a). The library of MGI can detect more SNPs, which indicates that the library can preserve more information about the sample and maintain good information fidelity of MGIEasy Universal Library Prep Set. The consistency rate of indel is as high as 85.9% (Fig.5b).

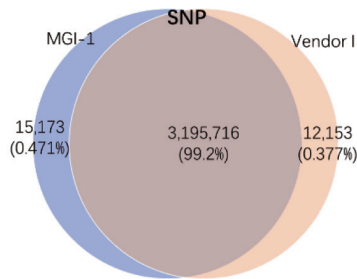


Fig.5a SNP detection performance of NA12878 standard

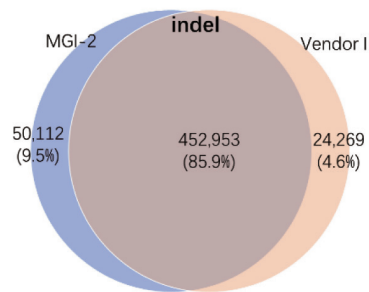


Fig.5b indel detection performance of NA12878 standard

Using MGIEasy Universal DNA Library Prep Set to perform library preparation and sequencing on MGISEQ high throughput sequencing platform, SNP analysis is compared with Vendor I.

Summary

The MGIEasy Universal DNA Library Prep Set is a WGS library preparation reagent kit tailored to the MGI high-throughput sequencing platform. Using this reagent set, genomic DNA can be processed into a single-stranded circular DNA library dedicated to the MGI high-throughput sequencing platform. All reagents provided in the set are subject to stringent quality controls and functional verification to ensure maximal stability and reproducibility of library preparation.

MGIEasy series library preparation products use proprietary MGI library preparation adaptors, a unique joint structure to ensure the best possible conversion of sample sequencing libraries and to avoid loss of sample information. The adaptor ensures the success rate of library preparation and improves the accuracy of detection. The selected corresponding adaptors can support up to 96 samples of mixed library preparation while maintaining the uniformity between the amount of sample data at the same time. The highly efficient enzyme system in the reagent set performs equally well in both high and low GC species and is efficient in library conversion, which supports sample input as low as 0.5 ng.

Ordering information

Product	Specification	Item number
MGIEasy Universal DNA Library Prep Set	16 RXN (with 16RXN Circularization)	1000006985
	96 RXN (with 16RXN Circularization)	1000006986
	96 RXN (with 96RXN Circularization)	1000017571

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