MGIEasy UDB Universal Library Prep Set

Product Highlights

Unique dual barcode to avoid contamination between samples	The cross-contamination rate between samples was less than one in 10,000
Suitable for FFPE samples	For FFPE samples, excellent performance
Good sample compatibility	Humans, animals and plants, high or low GC bacteria and so on
Suitable for different commercial probes	Compatible with the different capture probes, with excellent capture rate

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.In addition, high-throughput sequencers need more barcode marker samples and require higher accuracy of barcode distribution.

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 FFPE DNA sequencing.by using this set,when sample multiplexing is performing for sequencing, the dual barcode adapter design, which helps mitigate barcode contamination and hopping, effectively reduces barcode swapping within samples. In addition,Allowing for the mixing of libraries prior to targeted capture or DNB preparation simplifies sample preparation and reduces the cost of sequencing.

Workflow

The MGIEasy UDB Universal 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 Specifications

Total time	~4.5 hours (30 minutes)
Shelf life	12 month
Sample input	1ng – 1000 ng fragmented DNA
Insert size	200-600 bp
Sample type	gDNA, FFPE, cfDNA, ChIP DNA and etc.
Species Compatibility	human, animals, plants, fungi, bacteria, meta sample and etc.
Application	WGS、de novo WGS、target sequencing (compatible with MGIEasy Dual Barcode Exome Capture Accessory Kit)
Platform Compatibility	DNBSEQ-G400*、DNBSEQ-G50*、DNBSEQ-T7* and etc.
Sequencing strategy	PE100, PE150 and etc.

Product Performance

Unique dual barcode to avoid contamination between samples

The adaptors and incomplete PCR product in the reaction may introduce wrong barcode information and cause inter-sample contamination. Figure 1a shows the effect of dual barcode removal and capture library contamination(16 plex). It can be seen from the figure that cross-contamination data in the 16 sample pooling captured library data are real (red area). the dual barcode,which helps mitigate barcode contamination and hopping.

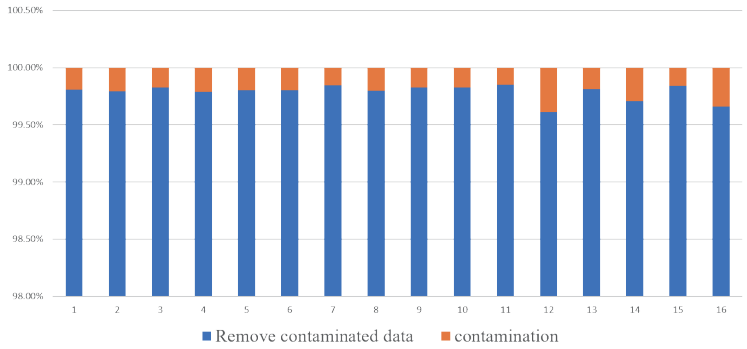

Figure 1a Dual barcode remove capture library contamination (16 plex)

If there is a strong positive sample in the same lane and weak positive samples mixed with a large number of contaminated samples, it is impossible to detect the weak positivie samples because of the contamination between samples. The dual barcode technology could reduce contamination, which will improve the sensitivity and accuracy of weak positive sample detection.

Figure 1b When there are strong positive samples (reach to 100,000-200,000 reads) in the same lane, combined with dual barcode, the contamination rate can be reduced, so as to avoid the contamination of negative samples as far as possible. It can be seen from the figure that, even if mixed sequencing is performed with strong positive samples, the contaminated sequence of negative samples will be reduced to below ten reads.

Figure 1c shows low contamination rate can effectively improve the discrimination of target bacteria/background bacteria. When the contamination rate is 0.001%, the weak positive samples can be distinguished from background bacteria even if the read number less than 10. Thus the sensitivity and accuracy of the detection of weak positive samples are significantly improved.

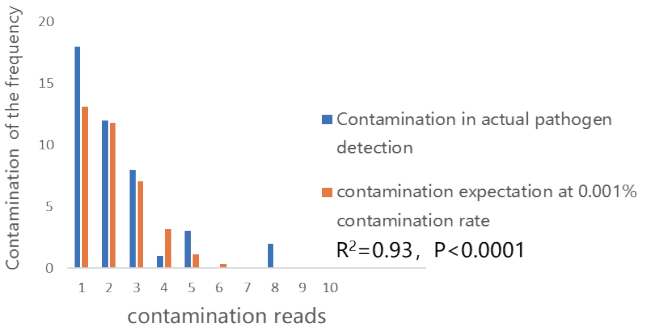

Figure 1b Actual and simulated distribution of contamination between samples

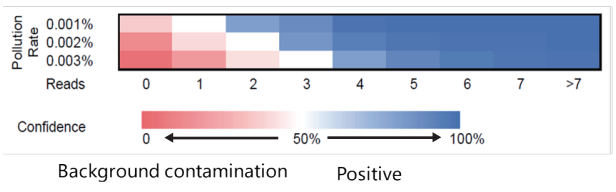

Figure 1c Positive bacteria determination confidence simulation (when strongly positive samples are less than 200,000 reads)

Suitable for FFPE samples

For FFPE samples, comparing the other kits on the market, the MGIEasy UDB Universal Library Prep Set has the best performance. (Figure 2).

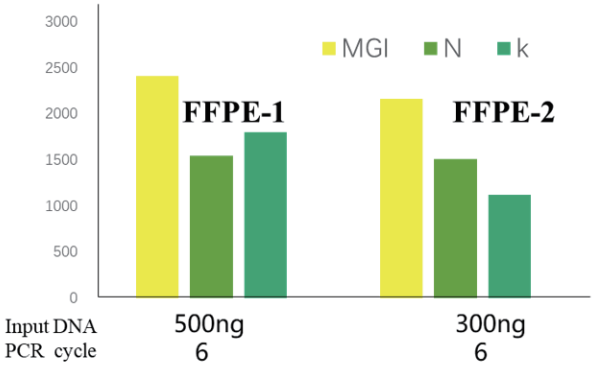

Figure2 Different vendor Kit PCR Yield Comparison (FFPE Sample)

Good sample compatibility

Library construction was made with different input amounts DNA from human, rice, nude mice, yeast, meta, E. coli, and Arabidopsis thaliana, the yield of PCR library are all above 400ng, as shown in Figure 3a.
It shows that the MGIEasy UDB Universal Library Prep Set can obtain enough PCR yield for samples of different species and different genome sizes, and the stability of library construction is good. As to ctDNA samples,the output was stable and efficient with different input amount (Figure 3b).

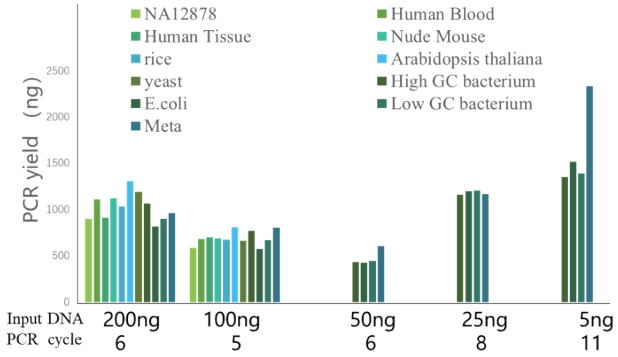

Figure3a The results of different input quantity libraries for multiple species

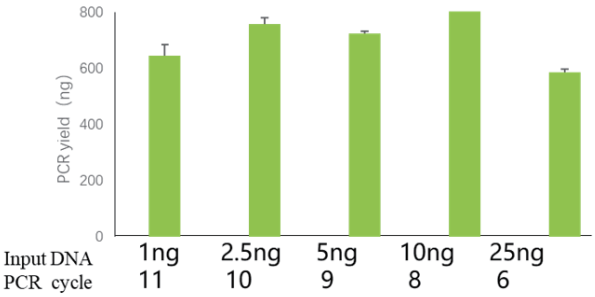

Figure3b PCR yield of different input ctDNA samples

Compatible with the different capture probes, with excellent capture rate

The MGIEasy UDB Universal Library Prep Set is compatible with the different probes to achieve exome capture and sequencing. The tissue sample were respectively tested by the MGIeasy exome capture V4 probe reagent kit (1000007745) and the tumor panel (500K). Figure 4 shows the good capture rate and uniformity on different capture probes.

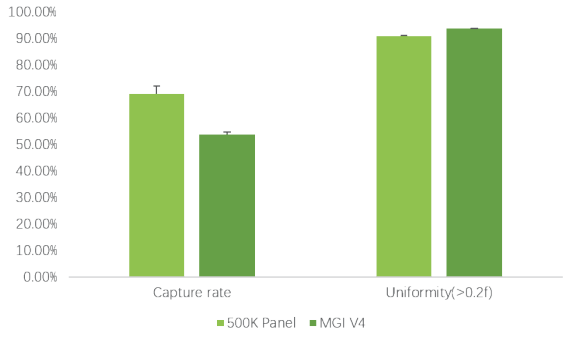

Figure4 Different probe capture efficiency

Summary

The MGIEasy UDB Universal Library Prep Set is specifically designed for constructing libraries for MGI sequencing platform. This library prep set is optimized to convert 1–1000 ng of fragmented DNA into a customized library and is compatible with various commercial probes for capture based on MGI sequencing platform. This set incorporates improved adapter ligation technology and high-fidelity PCR enzymes, which significantly increase library yield and conversion rate. Specifically, when sample multiplexing is performing for sequencing, the dual barcode adapter design, which helps mitigate barcode contamination and hopping, effectively reduces barcode swapping within samples. All reagents provided within this set have passed stringent quality control and functional verification procedures, ensuring performance stability and reproducibility.

Ordering Information

Product	Specification	Item number
MGIEasy UDB Universal Library Prep Set	16 RXN (with 16RXN Circularization)	1000022803
	96 RXN (with 16RXN Circularization)	1000022804
	192 RXN (with 32RXN Circularization)	1000022805

Contact Us

MGI Tech Co.,Ltd
Address: Building 11,Beishan Industrial Zone, Yantian District, Shenzhen, CHINA 518083
Email: MGI-service@mgi-tech.com, MGI_ATOPlex@mgi-tech.com
Website: en.mgi-tech.com
Tel: 4000-966-988
Version: October 2021 | MGPD111810200-02

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