MGIEasy FS DNA Library Prep Set

Product Highlights

Low sample input	5 ng - 400 ng of genomic DNA (gDNA) samples can be processed
Good sample compatibility	gDNA , FFPE and samples with different degrees of degradation
Wide range of species	Humans, animals and plants, high or low GC bacteria, fungi, and low input of meta sample types
Quick library preparation process	Library preparation can be completed in 5.5 hours without mechanical interruption
Repeatable library yield	Good consistency of the library yield
Achieve full automated process	Compatible with automated sample preparation system MGISP-100/MGISP-960

Overview

With the rapidly decreasing sequencing cost, whole genome sequencing(WGS) has found more widespread use in studies of human, plants, animals and microorganisms. Rapid screening of genetic variation and structural variability within the genome has been applied to human genetics, population chemistry, molecular breeding, rapid identification of microorganisms, and pathogenicity of pathogens.

The MGIEasy FS DNA Library Prep Set produces whole-genome libraries of each sample type in a simple and efficient way, especially for difficult-to-enrich microbial samples. No additional fragmentation equipment is necessary, and the amount of input DNA can be as low as 5 ng. This kit can be run on the MGISP-100/MGISP-960 automated sample preparation system, which can greatly streamline the library preparation process.

Product Specifications

Total time	~5.5 hours
Hands on time	~40 minutes
Sample input	5 ng - 400 ng gDNA
Insert size	200-500 bp
Sample type	gDNA, FFPE and etc.
Species source	human, animals, plants, fungi, bacteria, meta sample and etc.
Application	whole genome sequencing of various species
Sequencing platform	DNBSEQ-G400*, DNBSEQ-G50*, MGISEQ-2000*, MGISEQ-200* and etc.
Sequencing strategy	SE50, PE100, PE150 and etc.
Adaptation automation platform	MGISP-100/ MGISP-960 automated sample preparation system

Workflow

The MGIEasy FS DNA Library Prep Set is applied on gDNA by firstly randomly fragmenting with enzyme. Then MGI adaptor is ligated to both ends of the fragmented DNA. Following PCR amplification, the purified PCR product is thermally denatured, resulting in single-stranded DNA, which can then be circularized to obtain a sequencing library dedicated to the MGI high-throughput sequencing platform.

Product Performance

Meeting the needs of different inserts

Using NA12878 standard as a template, by controlling the enzyme digestion time of the fragmentation step and the magnetic bead selecting step, PCR products with different sizes can be consistently obtained, satisfying the needs of various inserts and sequencing read lengths.

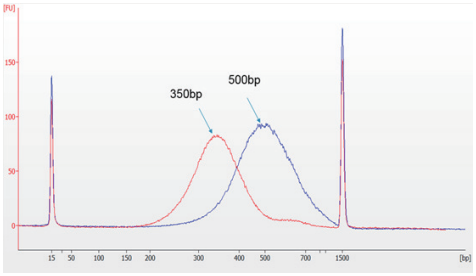

Fig.1 Library quality control graph of different inserts

According to the MGIEasy FS DNA Library Prep Set, when the sample DNA is fragmented for 8 min and select the DNA fragment by 0.8 + 0.2X beads may consistently obtain the 250 bp DNA fragment from the main band; when fragmented for 5 min and select the DNA fragment by 0.6 + 0.2X beads may consistently obtain the the 350 bp DNA from the main band.For the specific fragment selected conditions, please refer to the instruction manual.

Compatible with microbial library preparation of different GC content

Microbial samples with different GC content were used as templates to achieve a stable range of 600 ng within the recommended amount of gDNA. The yield of the PCR library above meets the requirements for subsequent circularization and sequencing. The coverage plots of high GC bacteria and low GC bacteria are similar to middle GC bacteria, and close to the expected normalized coverage of 1.0. This indicates the FS DNA Library Prep Set has uniform GC coverage over a broad range of GC content .

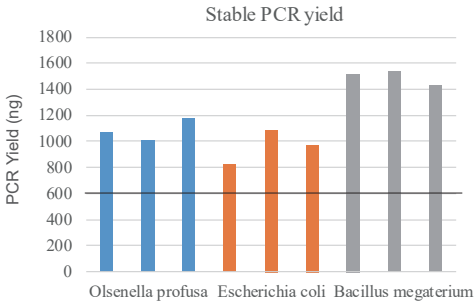

Fig.2a PCR yield of microbial samples with a range of GC content

The library was constructed using the MGIEasy FS DNA Library Prep Set. The GC content of each microbial species in Fig.2a was 62%, 50%, and 38% from left to right. each microbial have three library preparation repeats，the library yield can be stable to more than 600 ng.

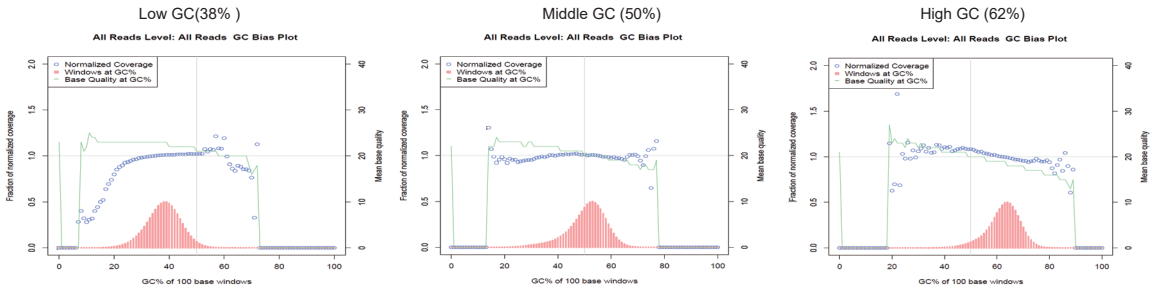

Fig.2b GC bias plot of bacteria with different genome GC content (Bacillus megaterium, 38% GC; E.Coli. , 50% GC and Olsenella, 62% GC).

Libraries were prepared with MGIEasy FS DNA Library Prep Set .The plots were assessed by calculating the GC content of the reference in 100 bp bins. The expected normalized coverage of 1.0 is indicated by the horizontal grey line, and the blue dotted lines represent the normalized coverage for each library. The closer the blue dot lines near to 1.0, the better the coverage uniformity.

High library conversion rate

Using NA12878 standard as a template with an initial amount of gDNA of 300 ng, and the conversion rate of the library was over 90%. When the initial amount of genomic DNA was 100 ng, the conversion rate of the library was above 60%. For the lower initial amounts (5ng and 10ng), the library conversion rate was about 40%. This demonstrates that the MGIEasy FS DNA Library Prep Set has a good library conversion efficiency.

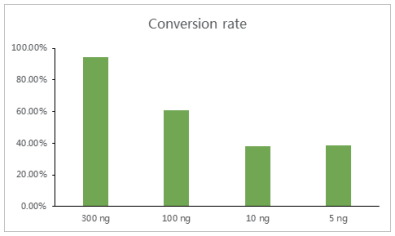

Fig.3 Library conversion rate

Using the MGIEasy FS DNA Library Prep Set to prepare library for different sample inputs, adaptor conversion rate was calculated using qPCR for quantification method by DNA with adaptors/DNA inputs.

Low duplicate rate, high genome coverage, high detection rate

Using NA12878 standard as a template, the duplicate rate was only about 2% for the MGIEasy FS DNA Library Prep Set on the MGI sequencing platform, which was much lower than the duplicate rate of 12% on “N” sequencing platform of brand A. At 30X sequencing depth, coverage is much higher than “N” platform (Especially at 20X, average coverage is 93.16% for the MGI platform and 90.16% for “N”platform).

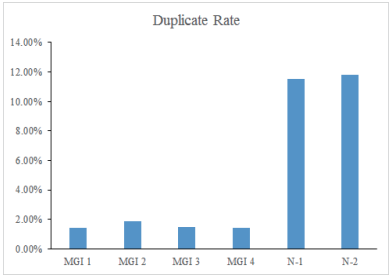

Fig.4a Duplication of 30X sequencing depth

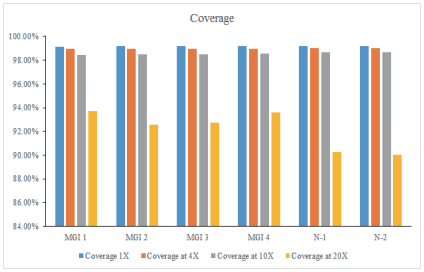

Fig.4b Coverage of genome

MGI 1, 2,3, 4 represents the data of library prepared using the MGIEasy kit repeated four times on the MGISEQ PE150 sequencing platform, N represents the PE150 data performance of brand A library preparation kit sequenced on “N” sequencing platform. The above data was analysed after normalize to 30X sequencing depth.

Benchmark analysis of the MGIEasy FS DNA Library Prep Set showed that the SNP Precision was slightly better than that of brand A library preparation kit on “N” sequencing platform , while the sensitivity on the indel was significantly better than that of the “N” sequencing platform.

	MGI 1	MGI 2	MGI 3	MGI 4	N-1	N-2
SNP_TP	3181769	3186188	3186485	3187661	3190584	3190065
SNP_FP	4422	3377	2891	2704	3483	3466
SNP_FN	28488	24069	23772	22596	19673	20192
SNP_Precision	99.86%	99.89%	99.91%	99.92%	99.89%	99.89%
SNP_Sensitivity	99.11%	99.25%	99.26%	99.30%	99.39%	99.37%
indel_TP	445314	448379	449973	452351	442687	441102
indel_FP	28497	25362	23071	21957	30603	31881
indel_FN	35950	32886	31292	28913	38582	40164
indel_Precision	93.99%	94.65%	95.12%	95.37%	93.53%	93.26%
indel_Sensitivity	92.53%	93.17%	93.50%	93.99%	91.98%	91.65%

MGI 1,2,3,4 represent the results of PE150 sequencing on the MGISEQ platform using the MGIEasy FS DNA Library Prep Set, and N represents the PE150 sequencing on the N sequencing platform using the brand A library preparation kit. The above data were normalized to about 30X sequencing depth for analysis.

Good reproducibility of the set performance

Use NA12878 standard as a template , the kit data were compared for repeatability. The results of the variation test showed that the data consistency produced by different batches of library preparation set reached 99.2% in the high confidence interval, indicating high repeatability for the MGIEasy FS DNA Library Prep Set data .

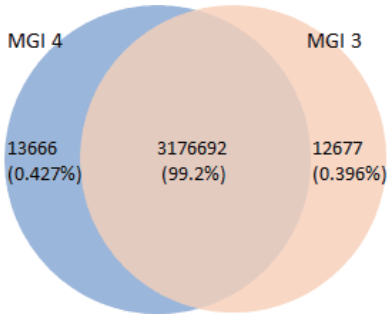

Fig.5 Consistency of SNPs in high confidence intervals

Different batches of the MGIEasy FS DNA Library Prep Set were used to prepare libraries on the MGISEQ-2000 platform with read length at PE150,the data was normalized to about 30X sequencing depth for analysis. SNP sites in the high confidence interval were used for consistency comparison.

Summary

The MGIEasy FS DNA Library Prep Set is a WGS library preparation reagent kit tailored for the MGI high-throughput sequencing platforms. This reagent kit can quickly prepare 5-400 ng of genomic DNA into a library optimized for the MGI high-throughput sequencing platform. The kit consists of high-quality enzymology, improved linker and high-fidelity enzymes with strong amplification efficiency, significantly improving library conversion and amplification efficiency. All reagents provided in the kit undergo rigorous quality control and functional verification to ensure maximal stability and reproducibility of library preparation.

Ordering information

Product	Specification	Item number
MGIEasy FS DNA Library Prep Set	16 RXN (with 16RXN Circularization)	1000006987
	96 RXN (with 16RXN Circularization)	1000006988
	96 RXN (with 96RXN Circularization)	1000017572

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