

MGIEasy Fast FS DNA Library Prep Set

Introduction

The MGIEasy Fast FS DNA Library Prep Set is specifically designed for WGS library construction for MGI high-throughput sequencing platforms. This library prep set is optimized to convert 1-200 ng genomic DNA into a customized library and uses high-quality fast frag enzymes to simplify the operation process and significantly shorten the DNA library construction time. This library prep set is applicable for microbial genomic DNA extracted from saliva, oral swabs, sputum and other samples.

The MGIEasy Fast FS DNA Library Prep Set adapts to automatic library preparation system MGISP-960 and MGISP-100 and can complete 96 libraries preparation in 2.5 hours on MGISP-960. This library prep set series produce highly uniform and consistent insert sizes and high uniform genomic coverage across a wide DNA input range (1-200 ng) and microbes with varying GC content, which enable to support flexible sample types including precious samples with low starting amount.

Highlights

Fast library prep workflow

Combine the DNA fragmentation, end-repair and add A into one step and short the library preparation time in less than 2.5 hours.

Flexible Throughput Options

Up to 192 selected barcodes enable flexible throughput for 8~192 samples multiplexing.

Flexible Workflow with 1-200ng DNA Input Range

Compatible with 1ng -200ng DNA input, supports flexible sample types, including precious samples with low starting amount

Uniform coverage across genomes with varying GC content

Provide high uniform genomic coverage across the microbial genome of varying GC content

Wide range of microbial genome sequencing applications

Applicable to wide range of microbial genome sequencing for Bacteria, viruses and other Microbes with varying GC contents and metagenome sequencing for meta samples.

Efficient automatable workflow

Adapt to MGISP-100 and MGISP-960

Specification

Version	V1.0
Assay Time	~2-2.3 hours
Hands-On Time	~60 min
Barcode	~192 barcodes
Input Quantity	1 ng - 200 ng gDNA
Insert size	200 bp - 600 bp
Sample types	gDNA from microbial culture, saliva, oral swab sample, sputum
Species Compatibility	Bacteria, viruses and other Microbes with varying GC contents, Meta sample
Applications	Microbial whole genome sequencing, Metagenome sequencing
Platform Compatibility	DNBSEQ-G400*, DNBSEQ-G50*, DNBSEQ-T7*
Recommended Read Length	SE50/PE100/PE150
Adaptation automation platform	MGISP-100 (16RXN) , MGISP-960 (96RXN、192RXN)

Product performance

Fast and Flexible workflow

The MGIEasy Fast PCR-FREE FS Library Prep Set uses high-quality fast fragmentase to combine the fragmentation, end-repair and add A into one step, and significantly shorten the library preparation time in less than 2.5 hours (from gDNA to PCR library).

The	Library preparation < 2.5 hours (from gDNA to PCR library)						
preparation process	DNA Fragmentation & End-repair and A-tailing	Purification	Adapter ligation	Purification	PCR	Purification	
time (min)	28-32	15	10	25	12-24	30	

Table 1 The library preparation process of the MGIEasy Fast FS DNA Library Prep Set

Adapt to two circularization sequencing methods

The prepared library adapts to two circularization methods, MGI universal circularization or MGI one-step DNB. MGI universal circularization method: the cyclization of the prepared library by using the MGI circularization kit (MGI Cat No.1000020570) to obtain single-stranded circular DNA (ssCirDNA). The process from gDNA to ssCirDNA takes 3.3 hours.

MGI one-step DNB method: using the MGI one-step DNB kit (MGI Cat No.1000026466) to complete the library cyclization and DNB making in one step to obtain DNB directly, which simplifies the preparation process from the library to DNB and shortens the DNB preparation time. The whole process from gDNA to DNB can be shortened to less than 3 hours by using the MGIEasy Fast FS DNA Library Prep Set combined with the MGI one-step DNB kit.

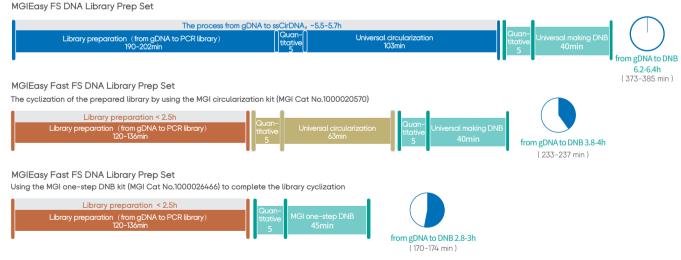


Figure 1The whole process from gDNA to DNB under different library preparation methods and circularization methods

Calculations made assuming 4 samples were processed at a time by manual. The MGIEasy Fast FS DNA Library Prep Set adapts to two circularization methods: 1) MGI universal circularization method, it takes 3.3 hours to complete the process from gDNA to ssCirDNA. Adding universal making DNB step, the whole process from gDNA to DNB is in 3.8~4 hours. 2) MGI one-step DNB method, it only takes 2.8~3 hours to complete the process from gDNA to DNB. The universal making DNB step: using the make DNB reagent in the MGI sequencing reagent set to make DNB.



Uniform and consistent insert sizes

The MGIEasy Fast FS DNA Library Prep Set adopts high-quality to provide stable DNA fragmentation. It produces highly uniform and consistent insert sizes across a wide DNA input range and microbial genome of varying GC content under the same fragmentation conditions.

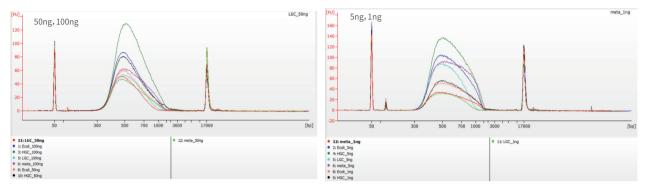


Figure 2 The uniform and consistent insert sizes across microbial genome with a wide DNA input range and varying GC content under the same fragmentation conditions.

Libraries were prepared from the gDNA from three different bacterial species with a range of low (27%), medium (50%), and high (64%) GC content and the Meta Standard sample, with starting amount of 1 ng, 5 ng, 50 ng and 100 ng, by using the MGIEasy Fast FS DNA Library Prep Set.

Uniform coverage across genomes of varying GC content

The MGIEasy Fast FS DNA Library Prep Set is compatible with microbial genome of varying GC content and provides high uniform genomic coverage. The libraries prepared from bacterial species with a range of low, medium, and high GC content using the MGIEasy Fast FS DNA Library Prep Set were used to assess coverage performance. The sequencing data showed that under different DNA input amounts (1ng-100ng), the MGIEasy Fast FS DNA Library Prep Set provided consistent coverage across bacterial species with a range of low (27%), medium (50%), and high (64%) GC content.

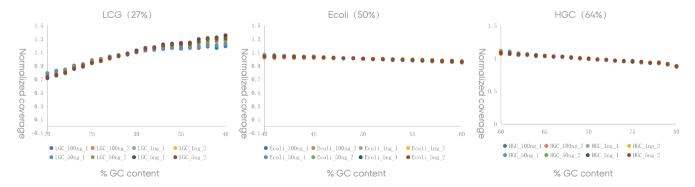
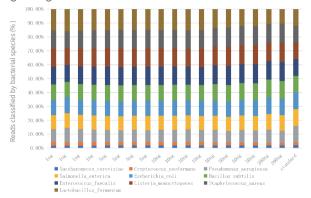


Figure 3 Normalized coverage of three different bacterial species with varying GC content, HGC (64%), LGC (27%), Ecoli (50%)

Libraries were prepared from the gDNA from three different bacterial species with a range of low (27%), medium (50%), and high (64%) GC content, with starting amount of 1 ng, 5 ng, 50 ng and 100 ng, by using the MGIEasy Fast FS DNA Library Prep Set combined with the MGI circularization kit (1000020570). Sequencing was performed on DNBSEQ-G400* at PE100.

Highly concordant bacterial species identification and distribution

To assess the performance of bacterial species identification and distribution under different DNA input amount using the meta standard. The MGIEasy Fast FS DNA Library Prep Set performs highly concordant bacterial species identification and distribution across a wide DNA input range (1-200 ng). Even the DNA input amount is as low as 1ng, the MGIEasy Fast FS DNA Library Prep Set still had good performance and the bacterial species relative abundance change range was<15%.



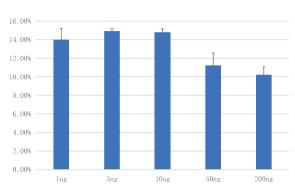


Figure 4a Highly concordant bacterial species identification and distribution under different DNA input amounts

Figure 4b The change range of bacterial species relative abundance under a wide DNA input range (1-200 ng)

Figure 4 The performance of libraries prepared using the MGIEasy Fast FS DNA Library Prep Set in metagenomic profiling

Libraries were prepared from the gDNA from meta standard (ZymoBIOMICS Microbial Community DNA Standard, D6305) ranging from 1-200ng using the MGIEasy Fast FS DNA Library Prep Set combined with the MGI circularization kit (1000020570). Sequencing was performed on DNBSEQ-G400* at PE100, average 10G/library. MGI PFI software was used for the bacterial species identification and distribution evaluation. Evaluation criteria: bacterial species relative abundance change range <30%.

Summary

The MGIEasy Fast FS DNA Library Prep Set provides the fast, flexible and automatable library preparation workflow that enables to complete libraries preparation in less than 2.5 hours. This library prep set series produce highly uniform and consistent insert sizes and high uniform genomic coverage across a DNA input range of 1-200 ng and microbial genome of varying GC content. And it performs highly concordant bacterial species identification and distribution across a DNA input range of 1-200 ng in metagenome sequencing. The MGIEasy Fast FS DNA Library Prep Set is applicable for microbial genomic DNA from saliva, oral swabs, sputum and other samples and applicable to wide range of microbial genome sequencing.

Ordering Information

Product	Configuration	Cat No.
	16 RXN	940-000029-00
MGIEasy Fast FS DNA Library Prep Set	96 RXN	940-000027-00
	192 RXN	940-000030-00

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^{*}Unless otherwise informed, StandardMPS and CoolMPS sequencing reagents, and sequencers for use with such reagents are not available in Germany, USA, Spain, UK, Hong Kong, Sweden, Belgium, Italy, Finland, Czech Republic, Switzerland and Portugal.