MGIEasy rRNA Depletion Kit V1.1

■ Features

Low RNA input	Use as low as 10 ng total RNA per sample
Compatible with various sample types	Including low-quality RNA, FFPE RNA
Efficient elimination of rRNA	High efficiency on 99% rRNA depletion and keep mRNA and non-coding RNA
Easy to Use	The entire depletion workflow can be completed within 2 hours
Flexible solutions	Provide flexible solutions for compatible with various RNA sequencing library preparation kits

■ Introduction

Ribosomal RNA (rRNA) has the highest abundance in total RNA, accounting for more than 80% of total RNA. These rRNAs contain little transcriptome information, resulting in the waste of valuable sequencing resources in RNA sequencing, which makes the detection of specific types of RNA difficult.

MGIEasy rRNA Depletion Kit can efficiently remove rRNA from total RNA and keep mRNA and non-coding RNA to increase the proportion of useful data. It depletes rRNA from human, mouse and rat total RNA with an input of total RNA ranging from 10 ng-1 μg. It is compatible with both intact and degraded RNA (e.g. FFPE RNA).

Product Specification

Assay Time	~2 hours
Hands-On Time	~12 min
Input Quantity	10 ng - 1 μg of total RNA
Sample types	tissues and FFPE sample
Species Compatibility	Human, mouse, rat
Applications	RNA-Seq, Transcriptome Sequencing, total RNA sequencing, lncRNA Sequencing
Platform Compatibility	BGISEQ-500, MGISEQ-2000, DNBSEQ-G400
Recommended Read Length	SE50/PE100/PE150
Recommended sequencing data per sample	25 M raw reads（SE50）/8 Gb raw data（PE100/PE150）
Removed rRNA types	cytoplasmic 5S rRNA, 5.8S rRNA, 18S rRNA, 28S rRNA, mitochodrial ribosomal RNA 12S rRNA and 45S pre-ribosomal RNA, 16S rRNA

■ Data Performance

Efficient elimination of rRNA

Compared with other depletion kits, MGIEasy rRNA Depletion Kit has a better depletion efficiency, the percent of remaining rRNA is lower than 1%.
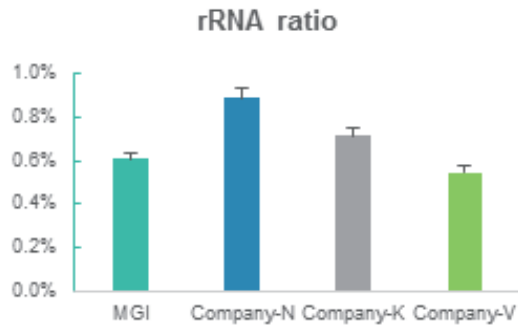

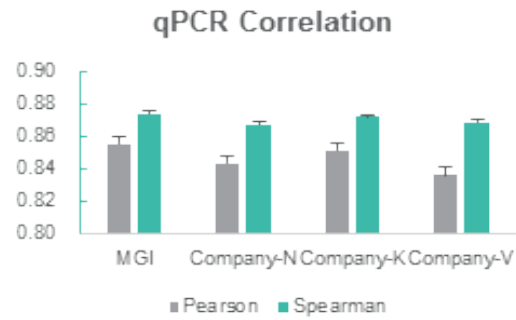Fig.1a Depletion efficiency of different depletion kits

Fig.1b qPCR correlation of different depletion kits

Fig.1 Ribosomal RNA of 200 ng Universal Human Reference RNA (UHRR) was depleted with different rRNA depletion kits. The resulting rRNA-depleted RNA were prepared libraries using the MGIEasy RNA Directional Library Prep Set (MGI, Cat. No.1000006385/1000006386) and sequenced on BGISEQ-500 at PE100 read-length. After data filtering, approximately 8 Gb of data was used per library for analysis.

Flexible total RNA input

MGIEasy RNA Depletion Kit is compatible with a range of 10 ng -1 μg input total RNA. The libraries prepared from MGIEasy RNA Depletion Kit exhibit excellent quality on sequencing data and transcript annotation, even the input total RNA be as low as 10 ng. With different amount of total RNA inputs，the rRNA depletion efficiency is more than 99%. The numbers of genes detected are more than 20000.
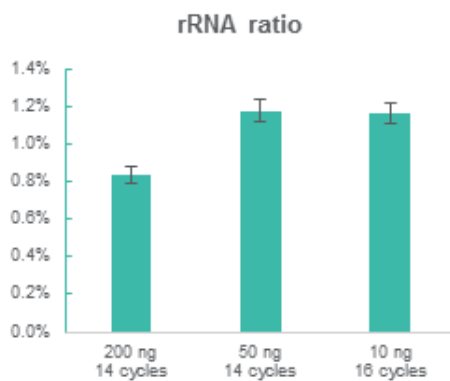

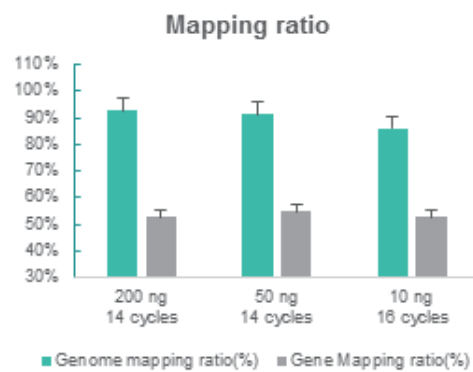Fig.2a The rRNA residual ratio of different amount of input RNA

Fig.2b The ratios of alignment in different input amounts of total RNA

gene number

qPCR Correlation
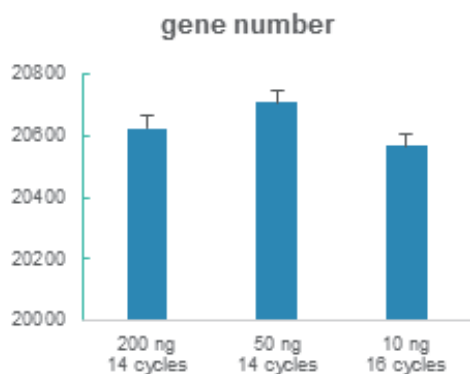

■ Spearman ■ Pearson

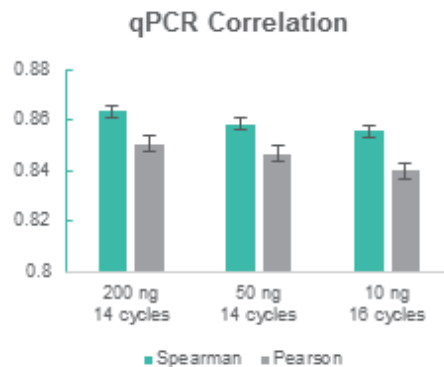Fig.2c The number of genes detected in different input amounts of total RNA

Fig.2d The qPCR correlation in different input amounts of total RNA

Fig.2 Libraries were prepared from 200ng, 50ng, 10ng input total RNA of Universal Human Reference RNA according to the MGIEasy rRNA Depletion Kit and the MGIEasy RNA Library Prep Set (MGI, Cat. No. 1000006383/1000006384), and sequenced on BGISEQ-500.

Efficient Removal of rRNA from Degraded RNA (FFPE)

Lung Cancer FFPE RNA samples with different RNA Integrity Numbers (RIN) ranges (FFPE-1= 5, FFPE-2= 3 and FFPE-3 <3) were used to prepare libraries with the MGIEasy rRNA Depletion Kit and the MGIEasy RNA Library Prep Set (MGI, Cat. No. 1000006383/1000006384). The sequencing result of these libraries indicates that the rRNA depletion efficiency is more than 96%, and the numbers of genes detected are more than 19000 (Fig. 3).
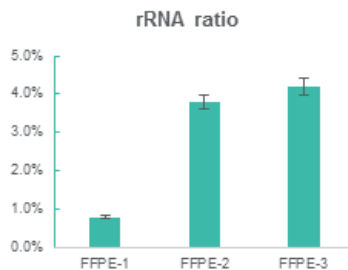
rRNA ratio

Fig.3a The rRNA residual ratio in different FFPE RNA Samples

Mapping ratio

■Genome mapping ratio ■ Gene mapping ratio
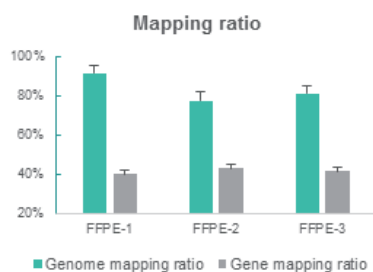
gene number

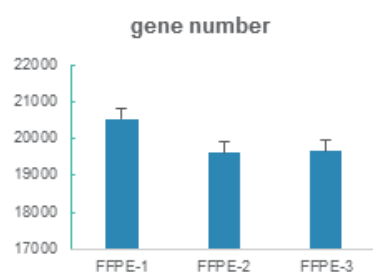Fig.3b The ratios of alignment in different FFPE RNA Samples

Fig.3c The numbers of genes detected in different FFPE RNA Samples

Fig.3 Libraries were prepared from different Lung Cancer FFPE RNA using the MGIEasy rRNA Depletion Kit and the MGIEasy RNA Library Prep Set (MGI, Cat. No. 1000006383/1000006384), and sequenced on BGISEQ-500.

Flexible Solutions

The library prepared by using this kit with RNA Library Prep Kit (e.g. MGIEasy RNA Library Prep Set or MGIEasy RNA Directional Library Prep Set) is suitable for RNA quantitation, transcriptome or non-coding RNA research applications.

Table 1 Corresponding use options for different sample types

Library preparation	Sequencing	Applications
rRNA depletion kit with mRNA library preparation kit	SE50/PE100/PE150	mRNA quantification and transcriptome analysis
rRNA depletion kit with RNA directional library preparation kit	SE50/PE100/PE150	RNA quantification and transcriptome/non-coding RNA analysis

■ Summary

MGIEasy rRNA Depletion Kit provides an efficient solution for removing rRNA from total RNA of human, mouse and rat, enabling efficient elimination of rRNA and keep both mRNA and non-coding RNA. MGIEasy rRNA Depletion Kit provide flexible solutions compatible with various RNA library preparation kit and a wide range of sample types, including FFPE.

Ordering information

Product	Configuration	Catalog No.
MGIEasy rRNA Depetion Kit	32 RXN	1000005953

■ Reference

【1】 Zhenqiang Su, *et al*. A comprehensive assessment of RNA-seq accuracy, reproducibility and information content by the Sequencing Quality Control Consortium. Nature Biotechnology, 2014, 32: 903-914.e Biotechnology, 2014, 32: 888–895.

■ Contact Us

MGI Tech Co., Ltd
Add.: Building11, Beishan Industrial Zone,
     Yantian District, Shenzhen, CHINA 518083
Email: MGI-service@genomics.cn
Website: www.mgitech.cn
Tel: 4000-966-988
Revision：2018.09

https://www.linkedin.com/company/mgi-bgi

https://twitter.com/MGI_BGI