Summary

MGICare Single Cell Chromosomal Copy Number Variation Detection Kit can be used to amplify whole genome and construct the library of human single cell or multiple cells simply and quickly. This kit has good uniformity of whole genome amplification, stable library yield, good data performance and high detection accuracy. This kit is the best option to facilitate your research on detection of single cell chromosomal copy number variation.

Order Information

Product	Specification	Item number
MGICare Single cell Chromosome Copy Number Variation Detection Kit	48 RXN	1000005291

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：2019.4

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

https://twitter.com/MGI_BGI

MGICare Single Cell Chromosomal Copy Number Variation Detection Kit

Features

Low input amounts	As low as single cell or multiple cells (1~10 cells)
The experiment process is simple and fast	The entire workflow from whole genome amplification to library construction can be completed within 6.4 hours, the library construction step can be automated.
High stability of library construction	Stable library yields among different batches of kit.
High uniformity of whole genome amplification	Can evenly amplify single cell whole genome, which is conducive to the detection of chromosomal copy number variations.
Excellent data performance	Applicable for detection of chromosomal copy number variations larger than 4Mb

Introduction

Copy Number Variant (CNV) analysis has been widely applied for scientific research and clinical uses such as evolutionary research, regulation of gene expression, and reproductive genetics. Take preimplantation genetic screening (PGS) as an example. PGS is the genetic test to identify genetic defects within embryos before implantation. It helps select the best embryo for transplant to the uterus and improve the chances of successful pregnancy. However, the amount of DNA from a few cells obtained by embryo biopsy is too limited to perform this molecular analysis. Hence, PGS requires gene amplification methods to amplify scarce genomic DNA from single cell.

This kit offer solutions for single-cell DNA sequencing. It incorporates the whole genomic application (WGA) technology and next-generation sequencing (NGS) technology to analyze chromosomal abnormalities in a single cell accurately.

Product performance data

High stability of library construction

DNA libraries were prepared independently 3 batches of MGICare Single Cell Chromosomal Copy Number Variation Detection Kit. Twenty libraries were constructed by each batch of kits using single human lymphocyte. The average library yield of each batch of kit was above 700 ng. There is no significant difference in library yield between different batches of kit, and the library yield in each batch is stable.

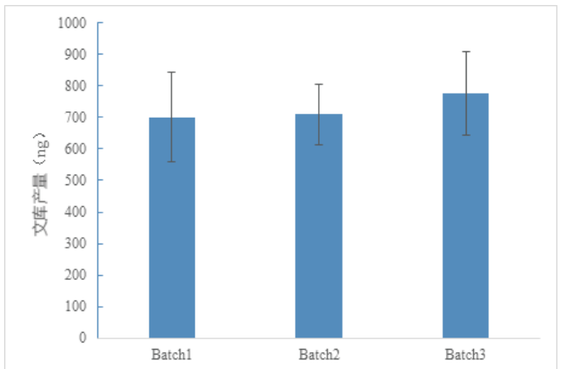

Fig.1 The yield of libraries prepared from 3 batches of kit.

High uniformity of Whole genome amplification

MGICare Single Cell Chromosomal Copy Number Variation Detection Kit can amplify single cell whole genome evenly. MGICare Single Cell Chromosomal Copy Number Variation Detection Kit and other brands of the same type of kits were used to perform whole genome amplification and library construction of single human lymphocyte. The libraries were sequenced by MGI high-throughput sequencing platform. Evaluated the uniformity of single cell whole genome amplification using the same amount of sequencing data (The CV of copy ratio can be used to reflect the uniformity of amplification. The lower the Copy Ratio CV value, the better the uniformity of amplification, and the higher the value, the worse.). The results showed that the uniformity of MGICare Single Cell Chromosomal Copy Number Variation Detection Kit was higher than that of other brands of the same type of kits.

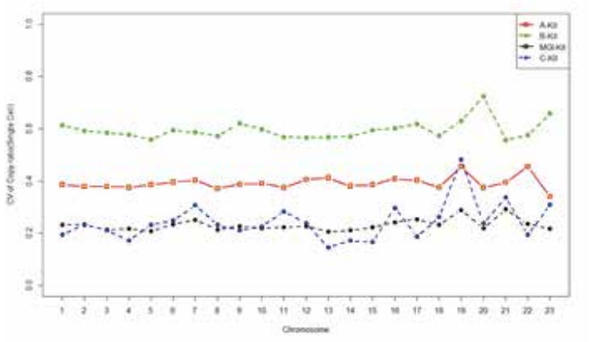

Fig. 2 Comparison of amplification uniformity of single cell whole genome amplification by different kits

Sequencing data is performing well

The library constructed by the MGICare Single Cell Chromosomal Copy Number Variation Detection Kit has good sequencing data that obtained by sequencing with the MGI high-throughput platform. It can detect copy number variations more than 4Mb in single cell. The copy ratio of each chromosome of a normal single cell fluctuates around 1 (Fig. 3). Single cell with copy number variation will show significant chromosomal copy ratio fluctuations in the corresponding regions. (Fig. 4)

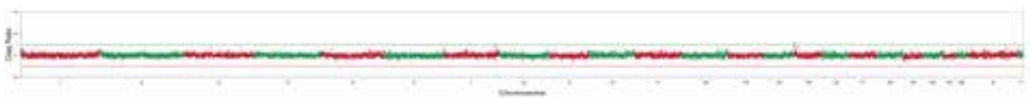

Fig. 3 Chromosome copy ratio of normal samples

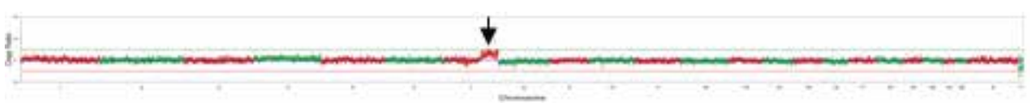

Fig. 4 Chromosome copy ratio of samples with copy number variation

Application

MGICare Single Cell Chromosomal Copy Number Variation Detection Kit can be applied to preimplantation genetic screening to detect chromosome copy number variations.

184 embryos were detected by using MGICare Single Cell Chromosomal Copy Number Variation Detection Kit. Chromosomal abnormalities were detected in 125 embryos (44 embryos were aneuploid and 81 embryos have copy number variation over 4Mb), 59 embryos are normal. Compared with the results of aCGH, the sensitivity and specificity are both 100%.

		MGI Kit Results	aCGH Results	Sensitivity	Specificity
Normal		59	59	–	100.00%
Chromosomal abnormalities	**Chromosome aneuploidy**	44	44	100.00%	–
	CNVs（>4M）	81	81	100.00%	–
Total		184	184	100.00%	100.00%

Case 1

A couple chose to undergo preimplantation genetic screening because the wife carries a chromosomal balance translocation. Three embryos were obtained after ovulation induction and in vitro fertilization. Three embryos were detected for chromosomal copy number variation, 2 of the 3 embryos have detected chromosomal abnormalities, and 1 embryos did not detect copy number variations. (Fig. 5)

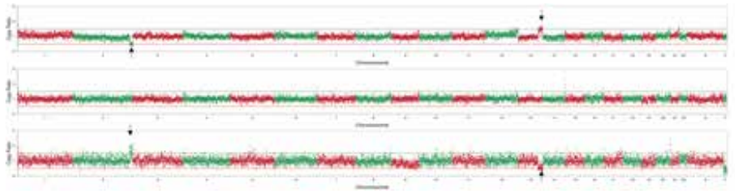

Fig. 5 Chromosome copy ratio of 3 embryo embryos

Product specification

Assay Time	~6.5 h
Hands-On Time	~1 h
Input Quantity	1 cell~10 cells
Sample types	Human cell
Applications	Chromosomal copy number variation detection
Platform Compatibility	BGISEQ-500、BGISEQ-50、MGISEQ-2000、MGISEQ-200 and so on
Recommended Read Length	SE35
Recommended software	Preimplantation aneuploidy detection software
Recommended sequencing data	10 M raw reads（SE35）

For Research Use Only. Not for use in diagnostic procedures.