Compact & flexible

Enhancing your daily sequencing capability

Genetic Sequencer

DNBSEQ-G50*

- Low-pass whole genome sequencing
  Flexible throughput of 100M/500M
- Low-frequency variant detection
  Down to 0.5%
- Small genome assembly
  PE100 in 26 hours

Leading Life Science Innovation

About
MGI Tech Co., Ltd.

MGI Tech Co., Ltd. (referred to as MGI) is committed to building core tools and technology to lead life science through intelligent innovation. MGI focuses on R&D, production and sales of DNA sequencing instruments, reagents, and related products to support life science research, agriculture, precision medicine and healthcare. MGI is a leading producer of clinical high-throughput gene sequencers, and its multi-omics platforms include genetic sequencing, mass spectrometry, medical imaging, and laboratory automation.

Founded in 2016, MGI has more than 1000 employees, nearly half of whom are R&D personnel. MGI operates in 39 countries and regions and has established multiple research and production bases around the world. Providing real-time, comprehensive, life-long solutions, its vision is to enable effective and affordable healthcare packages for all.

About DNBSEQ-G50*

01 Product Introduction

Techonolgy

Specifications

Applications

Total packages

02 Customer Stories

Low-pass whole genome sequencing

Low-frequency mutation detection

Full-length assembly of small genome

Transcriptome sequencing

CRISPR gene editing

Pathogen evolution analysis

Whole exome sequencing

Genomics education

03 Appendix

System specifications

MGI global presence

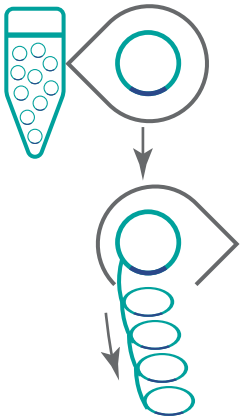
References

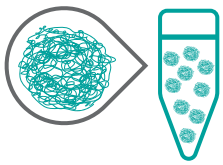
◎ PRODUCT INTRODUCTION

DNBSEQ-G50* is a compact and flexible benchtop genetic sequencer. With the design of two different flow cells, it empowers flexibility and creates a perfect balance between speed and affordability. FCS (Flow Cell Small) allows short turnaround time for short turnaround time (STAT) samples and FCL (Flow Cell Large) enables lower cost per sample.

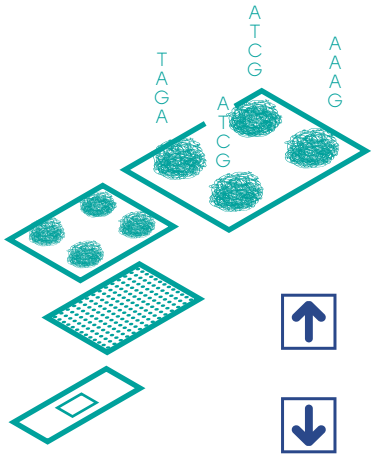
DNBSEQ-G50* offers 3-4 read length options for both FCS and FCL, which support a wide range of research and clinical applications such as low-pass whole genome sequencing, targeted sequencing, small whole genome sequencing, RNA sequencing and whole exome sequencing, etc.

MGI'S PROPRIETARY 「DNBSEQ™」 TECHNOLOGY





DNA Nanoballs (DNB)



Patterned Array

- INCREASED ACCURACY
- DECREASED DUPLICATES
- REDUCED INDEX HOPPING

Flow cell specifications

Flow cell type	Reads*	Read length	Data output	Run time**	Q30**
FCS	100M	SE100	~10G	~10 hrs	>80%
	100M	PE100	~20G	~20 hrs	>85%
	75~100M	PE150	23~30G	~28 hrs	>80%
FCL	500M	SE50	~25G	~9 hrs	>85%
	500M	SE100	~50G	~13 hrs	>85%
	500M	PE100	~100G	~26 hrs	>85%
	500M	PE150	~150G	~40 hrs	>80%

*The maximum number of effective reads are based on the sequencing of an internal standard library. Actual output may vary depending on the sample type and library preparation method.

** The percentage of base above Q30 is the average of an internal standard library over the entire run. The actual performance may vary depending the sample type, library quality and insert fragment length.

Key Applications

FCS
100M reads
SE100, PE100, PE150

FCL
500M reads
SE50, SE100, PE100, PE150

Applications	FCS	FCL
Low-pass Whole Genome Sequencing (e.g. Preimplantation genetic screening, copy number variation detection, etc.)	▲	▲
Hybridization capture-/multiplex PCR- based Targeted Sequencing (e.g. oncology panels, inherited diseases panel, etc.)	▲	▲
Small Whole Genome Sequencing (eg. microbial metagenomics, isolated bacteria, etc.)	▲	▲
RNA Sequencing (e.g. RNA expression profiling, transcriptome sequencing, etc.)	▲	▲
Whole Exome Sequencing	▲	▲
Human Whole Genome Sequencing		▲

* Compatible applications ▲
** Key applications ▲

Total Package

Based on DNBSEQ-G50*, MGI offers automated total packages to cover the entire sequencing workflow from automated library preparation, sequencing, to bioinformatic analysis. The total packages are developed based on the same set of hardware compatible with different applications, providing an ease-to-use one-stop workflow for end users.

The total packages support a wide range of applications to improve your daily sequencing capabilities, including low-pass whole genome sequencing, hybridization capture- and multiplex PCR-based targeted sequencing, small whole genome sequencing, RNA sequencing and whole exome sequencing, human whole genome sequencing, etc.

Library preparation	Sequencing	Data analysis
		
MGISP-100 Automated sample preparation system	**DNBSEQ-G50*** Benchtop genetic sequencer	**MegaBOLT** Bioinformatics analysis accelerator

Highly automated

The sample extraction and library preparation processes are highly automated driven by MGISP-100. With downstream sequencing data automatically transferred to bioinformatic workstation for data analysis and reporting, the entire sequencing workflow are simplified with less hands-on time and less dependent on manpower. This allows end users without a technical background to pick up high throughput sequencing packages easily.

High accuracy

The library preparation process is highly automated to avoid risks of manual error or variability; The sequencing process is guaranteed with a high level of accuracy and reduced index hopping by DNBSEQ™ technology; The data analysis process is empowered by MegaBOLT, providing a perfect balance between speed and accuracy.

High compatibility

The total package is an open system, which supports mainstream third-party library preparation kits and bioinformatic software.

◎ CUSTOMER STORIES

Enhancing your daily sequencing capability

Case 1

Low-pass Whole Genome Sequencing

Background

DNBSEQ-G50* is used for pre-implantation genetic screening (PGS) in one clinical services laboratory to detect chromosome aneuploidy in embryos. The test assesses all 23 pairs of chromosomes, including the two sex chromosomes (X and Y). Only healthy embryos are selected for subsequent implantation to increase In Vitro Fertilization (IVF) pregnancy success rate.

Result

DNBSEQ-G50* shows excellent reproducibility with low CV (coefficient of variation) values in copy number ratio in validation studies involving large number of national standards and clinical samples. This allows the laboratory to detect microduplication and microdeletion as small as 4Mb.

Conclusion

DNBSEQ-G50* generates highly consistent and reproducible data which enables the accurate detection of subchromosomal copy number variations.

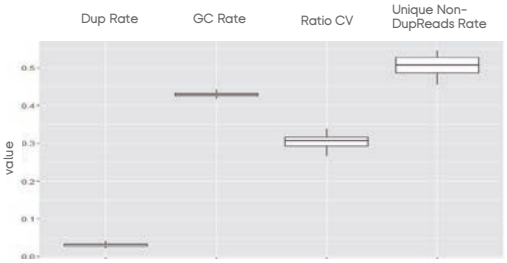


Fig.1-1 Consistency on key data parameters

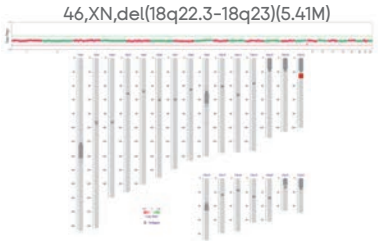


Fig.1-2 Example report with small-size aneuploidy

Case 2

Low-Frequency Variant Detection (capture-based panels)

Background

A clinical services laboratory developed a pan-cancer panel based on DNBSEQ-G50* platform. The hybridization capture-based panel covers single nucleotide variant (SNV), insertion and deletion (Indel), and structural variant (SV) in one analysis.

Result

DNBSEQ-G50* generates an average of 579M reads and Q30 of 90% with PE100 sequencing. Using dual barcodes with UMI, the detection rate on low-frequency variants ranging from 0.5%-1% reaches 100%.

Conclusion

Using dual barcodes with UMI, DNBSEQ-G50* can be used for detection of low-frequency tumor variants down to 0.5%.

Fig.2-1 Major variants covered in the panel

Mutation type	Gene	Mutation site
Indel	EGFR	p.Δ E746-A750
Indel	EGFR	p.V769_D770insASV
SNV	AKT1	p.E17K
SNV	PIK3CA	p.E545K
SV	EML4-ALK	p.COSF734 (EML4-ALK)
SV	ROS1	p.CD74-ROS1 fusion

Fig.2-2 Key data parameters

Item	Total Reads (M)	Q30 (%)
Run1	582	90.2
Run2	579	90
Run3	577	90
AVG	579	90
STD	2.9	0.1
CV	0.50%	0.10%

Case 3

Low-Frequency Variant Detection (multiplex PCR-based panels)

Background

A clinical services laboratory used DNBSEQ-G50* to detect two pan-cancers panel (~500x amplicons) in one run. Test samples include FFPE and blood samples.

Results

Results show that the coverage, uniformity and Q30 of the two panels are similar to expectations, and the detection result is 100% consistent with expectation.

Conclusion

DNBSEQ-G50* is able to provide high-quality data for low diversity library sequencing.

Tab.3-1 Coverage and uniformity of different panels

Coverage	Panel 1	Panel 2 germline	Panel 2 somatic
Expectation	99.98%	100.00%	100.00%
DNBSEQ-G50* Run1	100.00%	100.00%	100.00%
DNBSEQ-G50* Run2	100.00%	100.00%	100.00%

Uniformity	Panel 1	Panel 2 germline	Panel 2 somatic
Expectation	97.33%	100.00%	100.00%
DNBSEQ-G50* Run1	97.14%	100.00%	100.00%
DNBSEQ-G50* Run2	97.23%	100.00%	100.00%

Tab.3-2 Detection consistency of different panels

Consistent rate	Panel 1	Panel 2 germline	Panel 2 somatic
DNBSEQ-G50* Run1	100%	100%	100%
DNBSEQ-G50* Run2	100%	100%	100%

Case 4

Low-Frequency Variant Detection (pooled libraries)

Background

A clinical service laboratory launched several pan-cancer panels with both capture-based and multiplex PCR-based detection. Mutation type includes SNV, Indel and Fusion. When sequencing is carried out in hospitals, pooling different detection panels in the same run is inevitable.

Results

In this case, a mix of three different panels was run on a FCL PE150. Result shows total reads as high as 770-780M with a Q30 of 92%. The mutation frequency of the tested samples ranges from 1% to 45%. All positive samples were successfully detected, and the mutation frequency was consistent with expectation.

Conclusion

DNBSEQ-G50 helps users to perform accurate mutation detection even with pooled libraries.

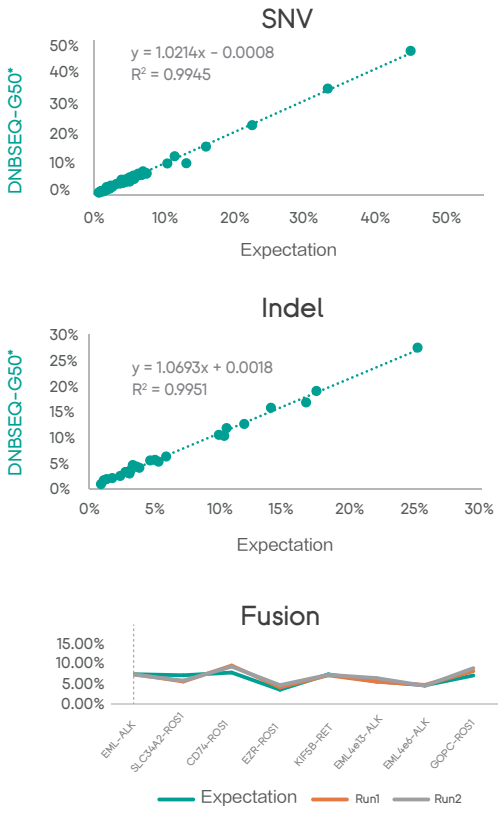


Fig.4 Comparison of variation results with expectation

Case 5

Small Whole Genome Assembly

Background

Center for Disease Control and Prevention (CDC) in East China used DNBSEQ-G50* to confirm and study the first coronavirus case found in the region.

Result

Respiratory sample from the first local case of coronavirus was deep-sequenced on DNBSEQ-G50* with SE100. Data output is 32Gb with total reads of 318M. 2,337,442 SARS-Cov-2 reads were identified and assembled with highly-efficient IDBA method by compatible software. As a result, the full-length SARS-Cov-2 whole genome (29.9Kbp) was obtained.

Conclusion

DNBSEQ-G50* enables end users to identify unknown pathogens and obtain whole genome information in a short period of time.

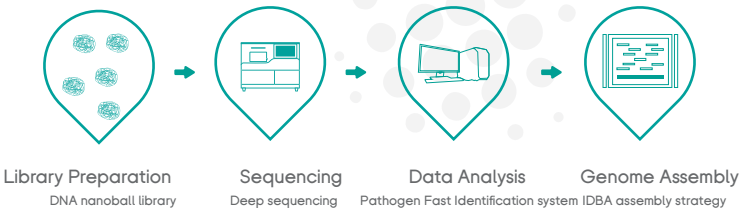


Fig.5-1 Virus identification and genome assembly workflow

Tab.5-1 Pathogen Fast Identification Report

#	Species	Reads	Relative abundance
1	2019-nCoV	2,337,442	60.685
2	Proteus phage VB PmiS-Isfahan	3,344	0.087
3	Parvovirus NIH-CQV	203	0.005
4	Severe acute respiratory syndrome-related coronavirus	140	0.004
5	uncultured crAssphage	64	0.002
6	Bat coronavirus BM48-31/BGR/2008	43	0.001
7	Staphylococcus virus IPLA5	42	0.001
8	Rhodoferax phage P26218	41	0.001
9	Acanthamoeba polyphaga moumouvirus	34	8.827e-04
10	Megavirus chilensis	22	5.712e-04

Case 6

Transcriptome Sequencing

Background

The RNA Research Center of Korea Institute of Basic Science and Korea Center for Disease Control and Prevention used DNBSEQ-G50* combined with single-molecule sequencing technology to analyze the transcriptome and epitranscriptome of SARS-CoV-2.

Results

RNA of Vero cells from a COVID-19 patient was extracted and sequenced with PE100. Results show data output exceeds 60Gb with a high accuracy and deep coverage of whole genome (Fig.6-1). This helps researchers to study transcriptome on a fine level and enables discoveries on classic TRS-mediated mechanism to produce most sgRNAs and non-classic recombination events different from TRS-medicated recombination (Fig. 6-2).

Conclusion

The high accuracy of DNBSEQ-G50* allows researchers to confirm and examine the genome on an unprecedented scale.

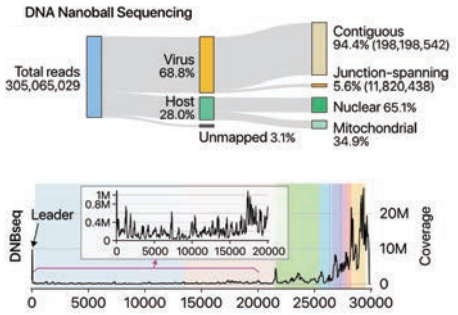


Fig.6-1 Read counts and genome coverage from DNBSEQ-G50* sequencing

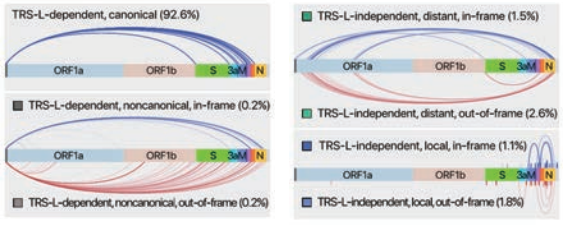


Fig.6-2 Classical and non-classical recombination sites of SARS-CoV-2 analyzed by sequencing data

Case 7

CRISPR Gene Editing

Background

The Institute of Neuroscience of Peking University used CRISPR-SaCas9 technology to edit function-specific gene in the brain of rats. In order to measure the effect of gene editing, researchers used multiplex PCR-based method to amplify the on-target and off-target loci, and the libraries were subject to sequencing on DNBSEQ-G50* subsequently.

Results

Sequencing results verify that SaCas9 is highly resistant to off-target effect. It also revealed that most of the off-target sites exhibited indel generation at least two magnitudes lower than that of corresponding on-targets. At the same time, sequencing also confirmed indel formation in the targeted cbp locus at the single-cell level (Fig. 7-1).

Conclusion

DNBSEQ-G50* provides high-precision and reliable deep sequencing for gene editing technology research.

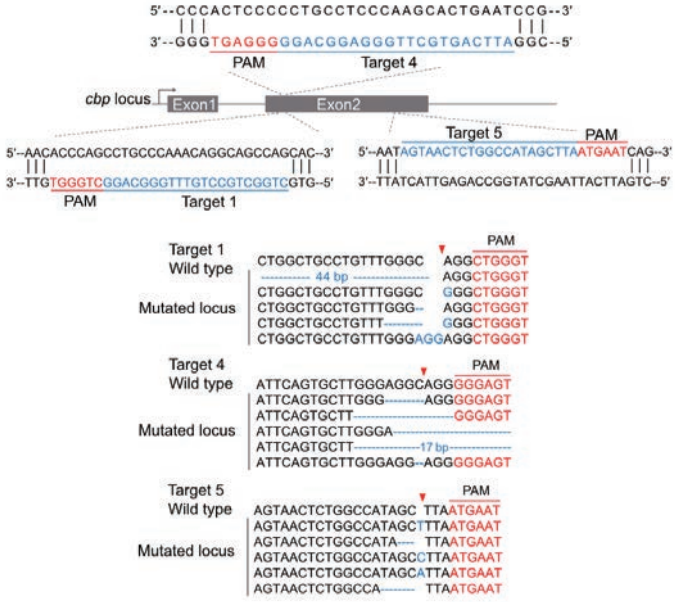


Fig.7 Gene editing target sequence and sequencing results after gene editing

Case 8

Pathogen Evolution Analysis

Background

In this case, a female patient developed cholera symptoms. The local center for disease control and prevention used DNBSEQ-G50* to sequence the whole genome of the patient sample to determine the characteristics and source of the virus.

Results

The whole genome of the fecal isolate 2018HL24 was sequenced. Sequencing reads were assembled with SPAdes into a genome of 4,108,238 bp, which contains 129 scaffolds. By analyzing and comparing with the existing virus genome, the virus source and characteristics were determined (Fig. 8). Combined with epidemiological data and phylogenetic analysis, it is speculated that the patient may be infected in Nepal-India.

Conclusion

Combining DNBSEQ-G50* sequencing with epidemiological investigation, the ability of pathogen identification was greatly improved, which helps controlling the spread of infectious diseases.

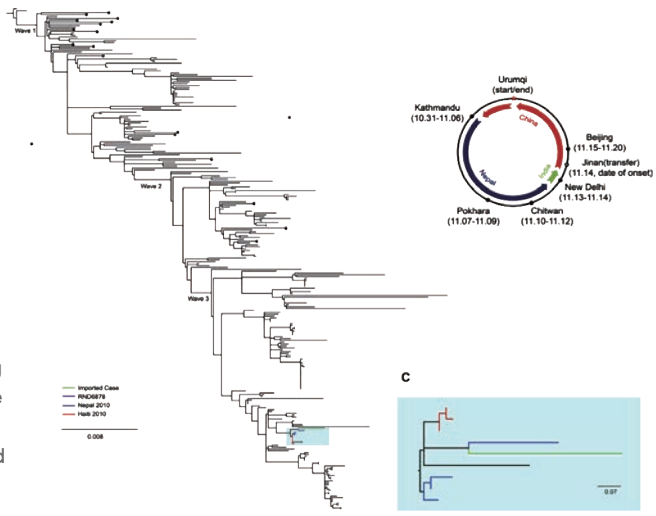


Fig.8 Cholera virus phylogenetic tree

Case 9

Whole Exome Sequencing

Background

The genetic pathogenesis of SCAD (spontaneous coronary artery dissection) is still unclear. Researchers from the First Affiliated Hospital of Shenzhen University used DNBSEQ-G50* platform to explore the genetic pathogenesis of SCAD.

Results

The whole exome sequencing (WES) was performed using DNA extracted from the peripheral blood of the patient with DNBSEQ-G50* sequencer. Result achieved an average coverage ≥ 100X on target and 95% of bases covered ≥20X. The sequencing data revealed a novel heterozygous missense variant. This variant is confirmed by Sanger sequencing, and is identified as a potential predisposing factor for artery fragility.

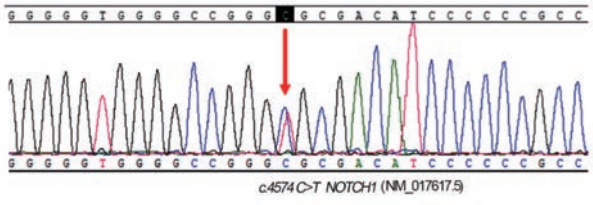


Fig.9 Novel mutation in NOTCH1 verified by Sanger sequencing

Conclusion

Using DNBSEQ-G50* to sequence the whole exome of patients with rare diseases, the potential pathogenic variation can be found accurately and efficiently, which helps exploring rare disease genetic pathogenesis.

Case 10

Genomics Education

Background

A High-tech Laboratory has been put into use for teaching recently in High School Affiliated to Renmin University of China, Shenzhen. As the core teaching tool, DNBSEQ-G50* is used for genomics education.

Results

This training program allows students to use saliva samples and extract DNA on their own. The prepared libraries were sequenced on DNBSEQ-G50* with FCS SE50 and the data was analyzed using a connected server. Output report includes phenotypic prediction results such as hair color, pupil color, wet and dry earwax, lactose tolerance, alcohol flush reaction, sports explosive power and endurance and other interesting information.

Conclusion

With its compact and flexible features, DNBSEQ-G50* is a perfect fit for genomic education in schools and universities.

◎ APPENDIX

System specifications

	Model*	Intended Use
Model*	DNBSEQ-G50*	IVD (In Vitro Diagnostics)
	DNBSEQ-G50RS*	RUO (Research Use Only)
Dimensions	654 × 489 × 545 mm	
Power	Voltage	100 V ~ 240 V
	Frequency	50/60 Hz
	Rated power	900 VA
Touch Screen	LCD touch screen	
	Touch screen size	10 inches
	Touch screen resolution	1280 × 800 (60 Hz)
Maximum Sound Pressure	70 dB	
Shell Protection Grade	IPX0	
Operating Environment Requirements**	Temperature	19℃~25℃
	Humidity	20% RH ~ 80% RH，non-condensing
	Air pressure	70 kPa ~ 106 kPa
	Altitude	3000 m
Control Computer Configurations***	CPU	8th Gen Core i7
	RAM	32GB
	Hard disk	≥4TB
	Operating system	Windows 10

- The model no. is model classification for internal references. Performances are the same across all the models.
- ** For indoor use only; The flow cells can be stored and transported at 2-8℃. No liquid is needed.
- *** Supporting computer configurations and system updates.

MGI Global Presence

Technical Support Globally

The technical support team has a complete global coverage including technical services centers and multiple locations in major international regions to maximize customer satisfaction.

Multiple local technical support centers around the world provide timely and effective technical support and training

Spare part centers in Shenzhen, Wuhan, Qingdao, Tianjin, Hong Kong (China); Brisbane (Australia); and Riga (Latvia), to ensure sufficient supply of parts for machine maintenance;

Online technical support accessible worldwide, with a fully functioning call center (Toll-Free Hotline: 4000-688-114) (9:00AM-12:00PM,13:00PM-18:00PM, Beijing time, workday) and multi-language online training courses coming soon

Comprehensive Instrument Service and Warranty Plans Globally

Warehouses in Shenzhen, Wuhan, Qingdao, Tianjin, Hong Kong, Taipei, Bangkok (Asia-Pacific); Brisbane (Australia, Oceania); Riga (Latvia, Europe); and San Jose (the USA, Americas) are established to ensure sufficient supply of maintenance parts for major regions.

Free installation and system verification services (including the QC reagents and consumables) are provided to turn your investment into production quickly.

MGI is responsible for any manufacturing defects or faults on the system within the warranty. Warranty covers labor, parts and travel charges.

One Free instrument preventive maintenance provided with warranty, along with a variety of available extended warranty support plans.

References

[1] Kim D, Lee J Y, Yang J S, et al. The architecture of SARS-CoV-2 transcriptome[J]. Cell, 2020.

[2] Sun H, Fu S, Cui S, et al. Development of a CRISPR-SaCas9 system for projection-and function-specific gene editing in the rat brain[J]. Science Advances, 2020, 6(12): eaay6687.

[3] Piper A M, Batovska J, Cogan N O I, et al. Prospects and challenges of implementing DNA metabarcoding for high-throughput insect surveillance[J]. GigaScience, 2019, 8(8): giz092.

[4] Zhang Y, Lu G, Zhang H, et al. Enhancement of nitrogen and phosphorus removal, sludge reduction and microbial community structure in an anaerobic/anoxic/oxic process coupled with composite ferrate solution disintegration[J]. Environmental Research, 2020, 190: 110006.

[5] Li F, Pang B, Yan H, et al. Investigation of an imported cholera case in China with whole genome sequencing[J]. Infection, Genetics and Evolution, 2020: 104362.

[6] Bai B, Zhang M, Zhuang Y, et al. The pregnancy-associated spontaneous coronary artery dissection in a young woman with a novel missense mutation in NOTCH1: a case report[J]. BMC Medical Genetics, 2020, 21: 1-8.

*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, Portugal, Austria and Romania.

Sequencer Portfolio

Full range of high-throughput sequencers

DNBSEQ-G50 *

Compact and flexible sequencers for small whole genome and targeted sequencing offered as part of total packages.

DNBSEQ-G400 *

Stable and flexible sequencer, for medium to large genome sequencing projects.

DNBSEQ-T7 *

Fast and flexible ultra-high-throughput sequencer, for large genome sequencing projects and population studies.

MGI Tech Co.,Ltd

Building 11, Beishan Industrial Zone,
Yantian District, Shenzhen.CHINA
518083

en.mgi-tech.com MGI-service@mgi-tech.com

4000-688-114

Version: February 2023 | MGPA0103002