MGI Microorganism Sequencing Product Portfolio

——High-throughput Metagenome Sequencing based on DNBSEQ-G50RS platform

Highlight

Short run-time

Run more samples in a short time, speed up the progress of your study.

Fully-automated workflow

Fully-automated sequencing workflow and bioinformatic processing make walkaway operation available, greatly reducing the reliance on manpower.

Excellent Data Quality

DNB and cPAS technologies ensure the accuracy and efficiency of sequencing and provide high-quality sequencing data.

Flexible operation modes to support diverse applications

Multiple read lengths are supported with accessible diverse applications, from microorganisms identification to genome assembly.

Flexible throughput configurations to meet different sample needs

Various flow cells are configured to meet the different sequencing throughput requirements.

Overview

MGI's Microorganism Sequencing Product Portfolio is based on the data generated by independent high-throughput sequencing platform, automated sample preparation system, self-developed compatible reagents, and self-developed rapid identification system for microorganisms, which could realize the full automation in the entire sequencing workflow of microorganism nucleic acid sequencing experiment and data processing from sample to report. This Product Portfolio allows fast, accurate and comprehensive high-throughput sequencing for unknown microorganisms, providing references for microorganism identification. Users can flexibly choose the appropriate hardware devices, compatible reagent kits and data processing system according to their own needs.

Nucleic acid extraction, metagenome, library preparation and high-throughput sequencing allows the access of gene sequence information of bacteria, fungi, virus, and other microorgan isms in samples, further recognizing whether the sample is infected by single microorganism or multiplex microorganisms, providing references for the diagnosis of suspected samples. Pathogen metagenomics/me tatranscriptome sequencing does not depend on known sequences and can acquire the genomic sequence information of unknown microorganisms at the first time. Moreover, this Product Portfolio can realize virus genome assembly, comparative genome processing, phylogenetic processing and so on.

DNBSEQ-G50RS is a compact and flexible benchtop genetic sequencer. With the design of two different Flow Cells, it empowers flexibility and creates an ideal balance between speed and affordability. FCS (Flow Cell Small) allows short turnaround time(STAT) samples and FCL (Flow Cell Large) enables higher throughput. Users can flexibly choose the sequencing strategy according to the actual situations to complete the whole sequencing task within a reasonable time. The whole workflow is streamlined, and can meet users' different requirements for time cost and throughput in different application scenarios (Table 1).

Table 1 DNBSEQ-G50RS Recommended Sample Throughput

Application	Read length recommended	Flow Cell recommended	Sample throughput/Run recommended	Sequencing time
Microorganism identification	SE50	FCS	4	~ 6h
Microbial genome assembly	PE100	FCL	4	~ 24h

- Based on testing data from DNBSEQ-G50RS Genetic Sequencer (Config 2)

Method

Metagenomic Sequencing

Clinical samples with known microorganism information (sample types: alveolar lavage fluid, sputum; Sample No: C2, C3, C15) and NA12878 (sample No: SH) supplemented with 1% mircrobial community Meta DNA standard products are used as samples.

DNA is extracted from clinical samples with MGIEasy Microorganisms DNA Extraction Kit (Item No.: 1000027955). Library is prepared automatically on MGISP-100RS Automated Sample Prep System (Cat.No.:900-000206-00) with MGIEasy Fast FS DNA Library Prep Set (Cat.No.:940-000029-00). DNB nanoballs are made with DNBSEQ Onestep DNB Make Reagent Kit (Cat. No: 1000026466).

SE50 read length sequencing is conducted with DNBSEQ-G50RS Sequencer .

Platform of microorganisms Fast Identification and assembly evolution (Item No.: 900-000399-00) including Platform of microorganisms Fast Identification (PFI, Item No.: 900-000393-00) and Microbial Genome Data Processing Software (MGAP), or only PFI, is able to support fast classification, identification, and sequencing extraction.

Result

High Sequencing Quality

Metagenomic Sequencing

With PFI software, users can conduct quality control and filtration on raw data from DNBSEQ-G50RS. The Q30 of metagenome SE50 sequencing data is over 93%, at a high sequencing quality level, with 99% being utilizable clean data (no host). Details can be found in Table 2.

Table 2 DNBSEQ-G50RS SE50 Metagenomic Sequencing Quality

Total Reads (M)	149.97
Q30 (%)	94.50
SplitRate(%)	96.52
Split CV(%)	14.9

Sample	C2_DNA	C3_DNA	C15_DNA	SH_DNA
Reads_Length	50	50	50	50
Raw_Reads	44,925,953	38,606,855	36,949,240	29,239,574
Raw_Base	2,246,297,650	1,930,342,750	1,847,462,000	1,461,978,700
Clean_Reads	44,896,683	38,590,339	36,927,370	29,235,442
Clean_Base	2,244,834,150	1,929,516,950	1,846,368,500	1,461,772,100
Clean_Base_Rate	99.93%	99.96%	99.94%	99.99%
Raw_Base_Q20	98.2%	98.16%	98.22%	97.67%
Raw_Base_Q30	94.79%	94.68%	94.88%	93.46%
Clean_Base_Q20	98.20%	98.16%	98.22%	97.67%
Clean_Base_Q30	94.79%	94.69%	94.88%	93.47%

Identify multiple microorganisms one time with high detection sensitivity

Metagenomic Microorganism Identification

Users can identify the species of microorganisms according to the reads from sequencing metagenome SE50 with PFI software and detect all known microorganisms including bacteria and fungi (Table 3) in samples. 10 microorganisms species (8 bacteria and 2 fungi) in the standard sample were ranked in top 10 during this identification (Table 4), which shows the reliability of identification results.

Table 3 Metagenome SE50 Microorganisms Identification Results

Sample code	Sample type	Sample original pathogen information	Metagenome SE50 Sequencing	
			Detected Reads	Relative abundance
C2	Alveolar lavage fluid	*Legionella pneumophila*	485	8.930
		Acinetobacter baumannii	18	0.331
		Prevotella melaninogenica	6	0.110
C3	Alveolar lavage fluid	*Stenotrophomonas maltophilia*	9953	66.531
		Klebsiella pneumoniae	459	3.068
		Klebsiella variicola	401	2.747
		Pseudomonas aeruginosa	411	2.680
		Haemophilus parainfluenzae	62	0.414
		Acinetobacter baumannii	9	0.060
		Human betaherpesvirus 5	50	0.334
C15	sputum	*Streptococcus pneumoniae*	381	9.568
SH	Meta standard product + human tissue	*Lactobacillus fermentum*	35977	11.986
		Bacillus subtilis	24372	8.240
		Salmonella enterica	26543	8.813
		Listeria monocytogenes	25890	8.625
		Enterococcus faecalis	29122	9.702
		Staphylococcus aureus	22729	7.572
		Escherichia coli	3114	1.037
		Pseudomonas aeruginosa	3273	1.090
		Cryptococcus neoformans	6936	2.311
		Saccharomyces cerevisiae	4224	1.407

Table 4 Top 10 of Metagenome SE50 Sequencing Standard Product Sample Bacteria and Funga Identification Results

No.	Species	Reads	Relative abundance
1	*Limosilactobacillus fermentum*	35,977	11.986
2	*Enterococcus faecalis*	29,122	9.702
3	*Salmonella enterica*	26,453	8.813
4	*Listeria monocytogenes*	25,890	8.625
5	*Bacillus subtilis*	24,732	8.24
6	*Staphylococcus aureus*	22,729	7.572
7	*Pseudomonas aeruginosa*	3,273	1.09
8	*Escherichia coli*	3,114	1.037
9	*Ralstonia solanacearum*	192	0.064
10	*Chondromyces crocatus*	54	0.018

Top 10 of SH Bacterial Identification Results

No.	Species	Reads	Relative abundance
1	*Cryptococcus neoformans*	6,936	2.311
2	*Saccharomyces cerevisiae*	4,224	1.407
3	*Saccharomyces paradoxus*	33	0.011
4	*Lachnellula hyalina*	13	0.004
5	*Cryptococcus gattii VGI*	10	0.003
6	*Botrytis cinerea*	7	0.002
7	*Amorphotheca resinae*	6	2.00E-03
8	*Aspergillus sclerotioniger*	4	1.00E-03
9	*Marssonina brunnea*	4	1.00E-03
10	*Parastagonospora nodorum*	4	1.00E-03

Top 10 of SH Fungal Bacteria Identification Results

Summary

Conducting microorganism metagenomic high-throughput sequencing on nucleic acid extracting sample, users can get various microorganism genomic sequencing information from kinds of micro organisms including bacteria, fungi, virus, parasites and so on in the sample, detect multiple pathogens and identify mixed infection, thereby recognizing potential single or multiple microorganisms in sample, providing references for diagnosing suspected samples. Based on MGI's self-developed reagents, MGISP-100RS Automation Sample Prep System and DNBSEQ-G50RS High-throughput Sequencing Platform, equipped with MGI's self-developed Platform of microorganisms Fast Identification and assembly evolution, MGI microorganism sequencing packages can provide high-quality and fast automated microorganism identification. MGI sequencing package is your ideal choice for microorganism identification, mutation detection and virus evolution, helping you complete your research objects fast and conveniently.

MGI Microorganism DNA Sequencing Package

Product	Specification	Item No.
Sequencer and Automated Sample Prep System		
Genetic Sequencer DNBSEQ-G50RS	Configuration 2	900-000354-00
MGISP-100RS Automated Sample Prep System	Standard configuration	900-000206-00
Sample Treatment Reagent		
MGIEasy Microorganism DNA Extraction Kit	96 Preps	1000027955
Library Prep Reagent		
MGIEasy Fast FS DNA Library Prep Set	16 RXN	940-000029-00
MGIEasy Fast FS DNA Library Prep Set	96 RXN	940-000027-00
DNBSEQ OneStep DNB Make Reagent Kit (OS-DB)	4 RXN	1000026466
Sequencing Reagent		
DNBSEQ-G50RS High-throughput Sequencing Set	FCL SE50	1000019855
DNBSEQ-G50RS High-throughput Sequencing Set	FCL PE100	1000019859
Data analysis system		
Platform of microorganisms Fast Identification	/	900-000393-00

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