MGI
Microorganism Sequencing Package

High-throughput Metatranscriptome
Sequencing based on DNBSEQ-G50RS* platform

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■ 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 Package 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 package 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, metatranscriptome, library preparation and high-throughput sequencing allows the access of gene sequence information of bacteria, fungi, virus, and other microorganisms in samples, further recognizing whether the sample is infected by single microorganism or multiplex microorganisms, providing references for the diagnosis of suspected samples. Pathogen metatranscriptome sequencing does not depend on known sequences and can acquire the genomic sequence information of unknown microorganisms at the first time. Moreover, this package 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
Microorganism identification	SE50	FCL	20-25	~ 8h
Microbial genome assembly	PE100	FCL	4	~ 24h

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

■ Method

Metatranscriptome Sequencing

Swab fluid of Porcine epidemic diarrhea virus (PEDV, *Alphacoronavirus*, Genome Size: 28033 bp) and Influenza A virus (AIV, *Alphainfluenzavirus*, Genome Size: 13588bp) is used as virus simulation samples (sample No.: AP,A, P. About 10^5 copies of PEDV and AIV in it).

Nucleic acid is extracted from virus simulation samples with MGIEasy Nucleic Acid Extraction Reagent (Item No.: 96 Preps, 1000020471; 1728 Preps, 1000020261). The total RNA library is prepared with rRNA Depletion Kit and MGIEasy Microorganism Rapid RNA Library Prep Set (16 RXN, 940-000107-00; 96 RXN, 940-000108-00). Both of nucleic acid extraction and library preparation are performed on MGISP-100RS Automated Sample Preparation System (900-000206-00). DNB nanoballs are prepared with DNBSEQ Onestep DNB Make Reagent Kit (included in MGIEasy Microorganism Rapid DNA Library Prep Set).

PE100 and SE50 reading sequencing is performed respectively with DNBSEQ-G50RS* High-throughput Sequencing Set*(FCL PE100) (Item No.: 1000019859) and DNBSEQ-G50RS* High-throughput Sequencing Set* (FCS SE100) (Item No.: 1000019860) on DNBSEQ-G50RS* Genetic Sequencer (Item No.: 900-000350-00).

Platform of microorganisms Fast Identification (including PFI, Item No.: 900-000393-00) or Platform of micro-organisms Fast Identification and assembly evolution (including PFI and MGAP, Item No.: 900-000399-00), is either able to support rapid classification, identification and sequence extraction of raw data. The genome assembly is conducted on MGAP.

■ Result

High Sequencing Quality

● Metaranscriptome Sequencing

With Platform of microorganisms Fast Identification (PFI), users can conduct quality control and filtration on raw data from DNBSEQ-G50RS*. The Q30 of SE50 and PE100 sequencing data is over 94%, at an extremely high sequencing quality level. Detailed sequencing data can be found in the Table 2 and 3.

Table 2 DNBSEQ-G50RS* SE50 Sequencing Quality

Total Reads (M)	138.00			
Q30 (%)	94.50			
SplitRate(%)	89.69			
Split CV(%)	10.0			
Sample	AP_RNA	A_RNA	P_RNA	C_RNA
Reads_Length	50	50	50	50
Raw_Reads	38,490,346	35,830,175	34,443,419	29,014,212
Raw_Base	1,924,517,300	1,791,508,750	1,722,170,950	1,450,710,600
Clean_Reads	38,227,623	35,209,656	34,123,248	27,031,312
Clean_Base	1,911,381,150	1,760,482,800	1,706,162,400	1,351,565,600
Clean_Base_Rate	99.32%	98.27%	99.07%	93.17%
Raw_Base_Q20	97.91%	97.88%	97.98%	97.67%
Raw_Base_Q30	94.57%	94.48%	94.78%	94.17%
Clean_Base_Q20	97.91%	97.89%	97.98%	97.61%
Clean_Base_Q30	94.59%	94.53%	94.80%	94.10%

Table 3 DNBSEQ-G50RS* PE100 Sequencing Quality

Total Reads (M)	588.35			
Q30 (%)	96.05			
SplitRate(%)	91.85			
Split CV(%)	6.7			
Sample	AP_RNA	A_RNA	P_RNA	C_RNA
Reads_Length	100	100	100	100
Raw_Reads	309,207,688	287,869,448	264,580,828	314,325,572
Raw_Base	30,920,768,800	28,786,944,800	26,458,082,800	31,432,557,200
Clean_Reads	244,838,770	227,406,214	200,840,354	258,855,376
Clean_Base	24,483,877,000	22,740,621,400	20,084,035,400	25,885,537,600
Clean_Base_Rate	79.18%	79.00%	75.91%	82.35%
Raw_Base_Q20	98.59%	98.66%	98.73%	98.54%
Raw_Base_Q30	95.94%	96.15%	96.30%	95.89%
Clean_Base_Q20	98.52%	98.56%	98.63%	98.45%
Clean_Base_Q30	95.86%	95.99%	96.15%	95.78%

Identify multiple microorganisms one time with high detection sensitivity

Metatranscriptome Microorganisms Identification

With PFI, users can fast complete species identification of RNA microorganisms SE50 and PE100 sequencing data. The platform can detect all known viruses in simulation samples (Table 4).

Table 4   RNA Pathogen Identification

Sample code	Sample type	PFI identification information	SE50		PE100	
			Detected Reads	Relative abundance	Detected Reads	Relative abundance
AP	AIV+PEDV dual mixed simulation sample	*Porcine epidemic diarrhea virus*	201,777	3.322	962,526	2.378
		Influenza A virus	44,075	0.726	244,508	0.604
A	AIV simulation sample	*Influenza A virus*	42,220	0.985	243,516	0.842
P	PEDV simulation sample	*Porcine epidemic diarrhea viru*	226,518	4.110	983,575	2.874

■ **MGAP Assembly**

Through further procedures on MGAP, users can conduct de novo transcriptome assembly on *PEDV*, *AIV*, virus sequences extracted from PE100 sequencing reads. It only takes 3-5min on single virus sample assembly. The whole long genome is available among all. So that our product package is provenly effective and reliable. Detailed assembling results can be found in Table 5.

Table 5 Virus Sequencing Assembly Results

Sample name	Genome Size (bp)	GC (%)	Scaffold num	Gap sizes (bp)	BLAST Comparison Results
PEDV	27937	41.89	1	0	Porcine epidemic diarrhea virus (taxid:28295)
AIV	13586	44.29	8	0	Influenza A virus (A/chicken/Shanghai/10/01(H9N2)) (taxid:329613)

■ Summary

Conducting microorganism metatranscriptome high-throughput sequencing on nucleic acid extracting sample, users can get various microorganism genomic sequencing information from kinds of microorganisms 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 RNA 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 Nucleic Acid Extraction Kit	96 Preps	1000020471
MGIEasy Nucleic Acid Extraction Kit	1728 Preps	1000020261
Library Prep Reagent		
rRNA Depletion Kit	32 RXN	1000005953
MGIEasy Microorganism Rapid RNA Library Prep Set（16 RXN）	16 RXN	940-000107-00
MGIEasy Microorganism Rapid RNA Library Prep Set（96 RXN）	96 RXN	940-000108-00
Sequencing Reagent		
DNBSEQ-G50RS High-throughput Rapid Sequencing Set*	FCS SE100	1000019860
DNBSEQ-G50RS High-throughput Sequencing Set*	FCL SE50	1000019855
DNBSEQ-G50RS High-throughput Sequencing Set*	FCL PE100	1000019859
Data Processing System		
Platform of microorganisms Fast Identification	/	900-000393-00
Platform of microorganisms Fast Identification and assembly evolution	/	900-000399-00

■ Contact Us

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