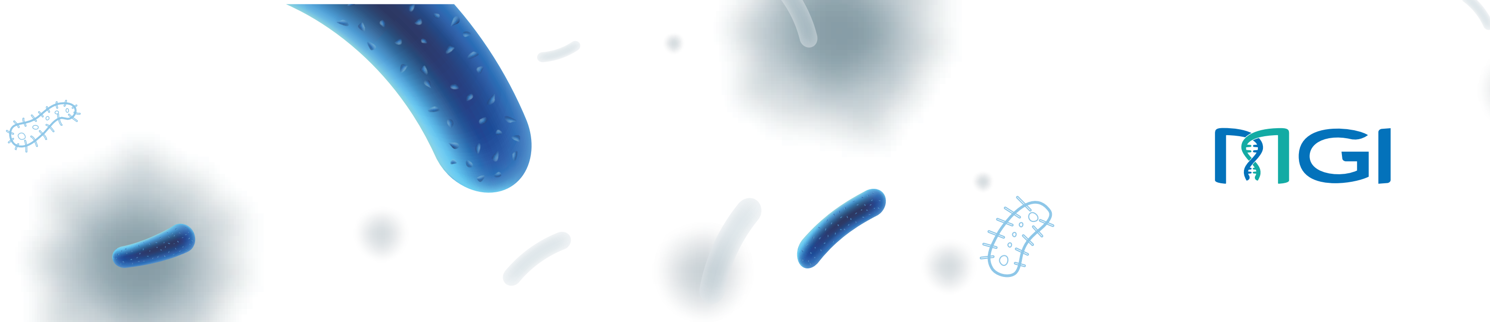

MGI pathogens metagenomic sequencing products package based on DNBSEQ-G99

A fast and accurate sequencing solution that provides a powerful tool for the identification of unknown pathogens and epidemiological research.

Highlights

- **Short TAT**
  With the DNBSEQ-G99ARS sequencer, PE100 sequencing can be completed in 9 hours.

- **Excellent data quality**
  The unique DNBSEQ sequencing technology provides high-quality sequencing data for downstream analysis.

- **Automation friendly**
  With the MGISP-100 automated library preparation system and data analysis software, automated library preparation and data analysis can be achieved, reducing manual labor.

- **Comprehensive analysis functions**
  The self-developed software meets the needs of identification, genome assembly, variation detection and traceability.

Introduction

Based on MGI's reagents, automated sample preparation systems, high-throughput sequencing platforms and data processing systems, the entire process from sample to result is covered. This enables fast and accurate high-throughput sequencing of samples, allowing for pathogenic microbiome typing, genome assembly, prediction of virulence and drug resistance genes, and systematic evolutionary analysis, provides tool for the precise identification, monitoring, early warning, tracing of epidemics.

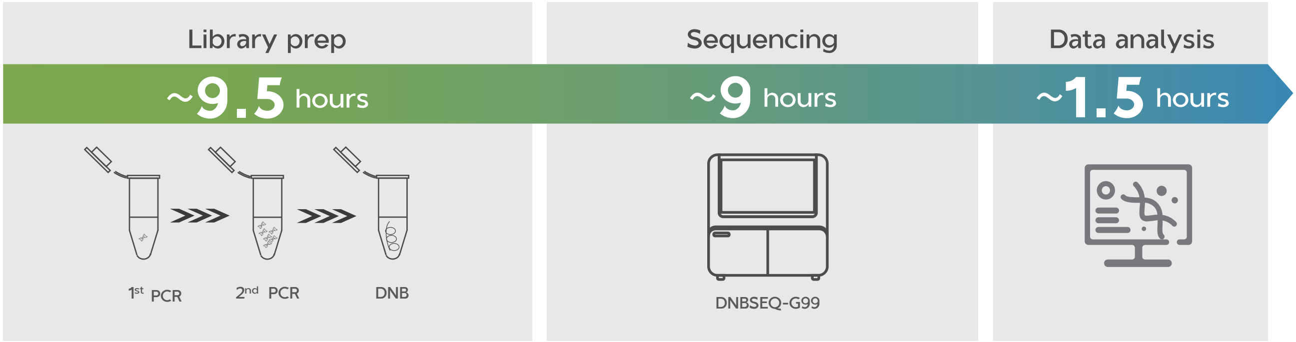

Fig 1. Flowchart

DNBSEQ-G99ARS is one of the fastest models among global mid-sized sequencer, capable of completing PE150 sequencing in 12 hours. It provides efficient and high-quality data output. With built-in computational modules, it achieves integration of sequencing and bioinformatics analysis. It can be used with the BBS (Bioanalysis By Sequencing) to perform data analysis in SE40, SE100, and PE100 formats, enabling rapid identification of pathogens.

Table 1. Parameters

Intended use	Reads length	Reads number	Samples/FC
RNA pathogens sequencing	Identification：SE50	Identification：20M	Identification：4 samples/FC
	Genome assemble：PE100	Genome assemble：80M	Genome assemble：1 samples/FC

The MGAP is based on MPS and genomics technology, which enables the assembly of genomes, systematic evolutionary analysis, and automatic calculation of variation detection results from sequencing data. It also allows flexible selection of analysis modules according to specific needs. The Pathogen Fast Identification software (PFI) is a microbial rapid identification system developed based on the DNBSEQ sequencing platform. It enables fast and accurate identification of microorganisms in the original specimens, automatically generating analysis results, and providing reference for the study of infectious diseases.

Performance

A simulated sample containing swine transmissible gastroenteritis virus (TGEV) RNA was prepared, sequenced, and analyzed. The sample consisted of 1% virus RNA and 99% Universal Human Reference RNA. The total number of reads obtained was 121 million reads, with a Q30 score of 96%. The splitting rate was above 92%, meeting the requirements for downstream analysis.

Table 2. Data QC

Total reads (M)	Q30（%）	SplitRate（%）
121.1	96.69	92.3

Based on software analysis, the sample was identified at the genus level as Alphacoronavirus 1 and at the subgenus level as Transmissible gastroenteritis virus, as shown in Table 3 and Table 4. The analysis results are consistent with expectations.

Table 3. species identification results

Type	Scientific Name	Real Reads	Estimated Reads	Relative Abundance
Viruses	*Alphacoronavirus 1*	110,118	110,118	80.90%
Viruses	*Porcine epidemic diarrhea virus*	13,147	13,147	9.66%
Bacteria	*Pseudomonas putida*	344	5,057	3.72%
Viruses	*Alphapapillomavirus 7*	2,996	2,996	2.20%
Bacteria	*Pseudomonas stutzeri*	257	2,147	1.58%
Bacteria	*Ralstonia mannitolilytica*	159	1,546	1.14%
Bacteria	*Pseudomonas fluorescens*	74	991	0.73%
Bacteria	*Thermus aquaticus*	97	116	0.08%

Table 4. subspecies identification results

Type	Scientific Name	Real Reads	Estimated Reads	Relative Abundance
Viruses	*Transmissible gastroenteritis virus*	46,717	154,587	100.00%

The results of the reference-based assembly show a mapping rate of 100% and a coverage of over 99%. The assembly quality is excellent.

Table 5. sAssembly result

Mapped reads	Mapping rate	Mean depth	Median depth	Coverage（%）	4×Coverage（%）	10×Coverage（%）	30×Coverage（%）	100×Coverage（%）
220225	100.00	769	707	100.00	99.92	99.86	99.86	99.63

The PFI software analyzed virulence genes and antibiotic resistance genes based on the public databases "VFDB" and "MEGARes". The annotation results are provided in Table 6 and Table 7.

Table 6. virulence genes analysis result

Virulence Factor	Microorganism	Virulence Protein	Coverage	Depth
Z1307	*Escherichia coli O157:H7 str. EDL933*	VFG043544(gi:15800816)	98.37	16.92
ECS88_3547	*Escherichia coli O45:K1:H7 str. S88*	VFG043545(gi:218560235)	76.58	7.24
rpoS) sigma S (sigma 38	*Salmonella enterica subsp. enterica serovar Typhimurium str. LT2*	VFG000477(gi:16766230)	96.67	5.23
fimA) major type 1 subunit fimbrin (pilin	*Escherichia coli O111:H- str. 11128*	VFG033211(gi:260871034)	68.80	1.26
fimC	*Salmonella enterica subsp. enterica serovar Choleraesuis str. SC-B67*	VFG004079(gi:3333009)	58.70	1.07
flgG	*Pseudomonas putida GB-1*	VFG015654(gi:167034941)	63.69	0.89
Z2200	*Escherichia coli O157:H7 str. EDL933*	VFG042713(gi:15801631)	39.61	0.71
mucA	*Pseudomonas fluorescens SBW25*	VFG019912(gi:229588995)	53.66	0.68
flgH	*Pseudomonas putida GB-1*	VFG015656(gi:167034940)	56.69	0.58
flgF	*Pseudomonas putida GB-1*	VFG015652(gi:167034942)	48.24	0.54

Table 7. Resistance genes analysis results

Group	Gene	Class	Mechanism	Type	Coverage	Depth
SODB	MEG_6545	Peroxide resistance	peroxide resistance protein	Biocides	100.00	15.08
YCHH	MEG_7813	Biocide and metal resistance	Biocide and metal resistance protein	Multi-compound	91.01	11.32
RPOS	MEG_6141	Multi-biocide resistance	Multi-biocide resistance regulator	Biocides	98.93	8.17
YGIW	MEG_7831	Biocide and metal resistance	Biocide and metal resistance protein	Multi-compound	98.47	6.61
GADA	MEG_3076	Acid resistance	Acid resistance protein	Biocides	75.57	3.07
SOXS	MEG_6551	Drug and biocide and metal resistance	Drug and biocide and metal resistance regulator	Multi-compound	98.76	2.48
CUEO	MEG_2440	Copper resistance	Copper resistance protein	Metals	93.03	2.32
TOLC	MEG_7263	Multi-biocide resistance	Multi-biocide RND efflux pump	Biocides	94.08	2.29
COPA	MEG_2020	Copper resistance	Copper resistance protein	Metals	52.96	2.23
COPA	MEG_2019	Copper resistance	Copper resistance protein	Metals	67.89	2.08

Ordering information

Products	Specifications	Item No.
Instrument		
DNA Sequencing Library Preparation System MGISP-100RS	Standard	900-000206-00
DNBSEQ-G99ARS	With server	900-000609-00
Reagent		
MGIEasy rRNA Depletion Kit	32 RXN	1000005953
MGIEasy RNA Library Prep Set	16 RXN	1000006383
MGIEasy RNA Library Prep Set	96 RXN	1000006384
DNBSEQ OneStep DNB Make Reagent Kit	4 RXN	1000026466
High-throughput Sequencing Set (G99 SM FCL PE150)	1 Test / Kit	940-000410-00
Software		
Platform of microorganisms Fast Identification software	——	970-000208-00
MGI MGAP	——	970-000109-00

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