UNLEASH YOUR ULTIMATE SEQUENCING SPEED

Benchtop Genetic Sequencer

DNBSEQ-G99

- **Rapid sequencing**
  Only 12 hrs for PE150 (from loading to FASTQ).
- **Flexible throughput**
  Independent loading and running of dual flow cells.
- **Bioinformatics integrated**
  Option to include built-in bioinformatics module to support sequencing and advanced analysis in a single machine.

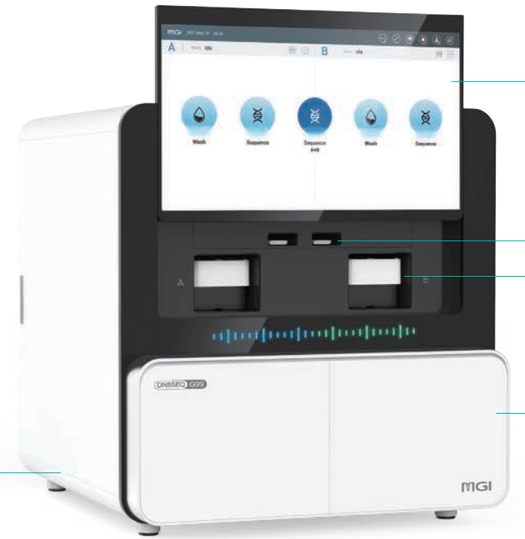
MGI'S PROPRIETARY

「DNBSEQ™」

TECHNOLOGY

Genetic Sequencer

DNBSEQ-G99



DNBSEQ-G99 is developed based on MGI's core DNBSEQ™ sequencing technology. Enabled by innovations in biochemistry, optics, fluidics, temperature control, and other core systems, DNBSEQ-G99 boasts the fastest speed amongst all medium-to-low throughput sequencers globally. DNBSEQ-G99 is especially applicable for targeted oncology panel sequencing, infectious disease sequencing, oncology methylation sequencing, small whole-genome sequencing, low-depth whole genome sequencing, individual identification, small panel sequencing of 24-28 samples, or whole-exome sequencing of 1-4 samples.

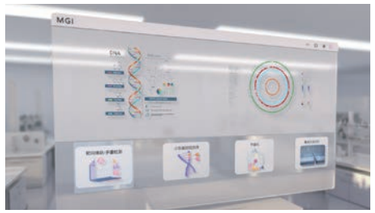
DNBSEQ-G99 also comes with an optional build-in bioinformatics module, which allows advanced analysis to begin automatically after the sequencing run. This facilitates a tremendously efficient and simple workflow, thus accelerating the application of omics technology to advance global life sciences and clinical research.

Designed for **Simplicity**

Newly designed flow cell, reagent cartridge, and user interface are introduced in DNBSEQ-G99, providing laboratory personnel with unparalleled ease and peace of mind in the entire sequencing workflow. A built-in bioinformatics module can also be included, achieving from sample to report all in one equipment.

Novel Reagent Cartridge Design

- Pre-loaded reagents within cartridge, one-step operation: simply press to load
- Sequencing and cleaning cartridges combined 2-in-1, cleaning initiates automatically after run.



Intelligent Interaction

- Visualize the entire sequencing process in real-time
- Animations are included to guide flow cell loading, minimizing operational errors

Built-in Bioinformatics Module

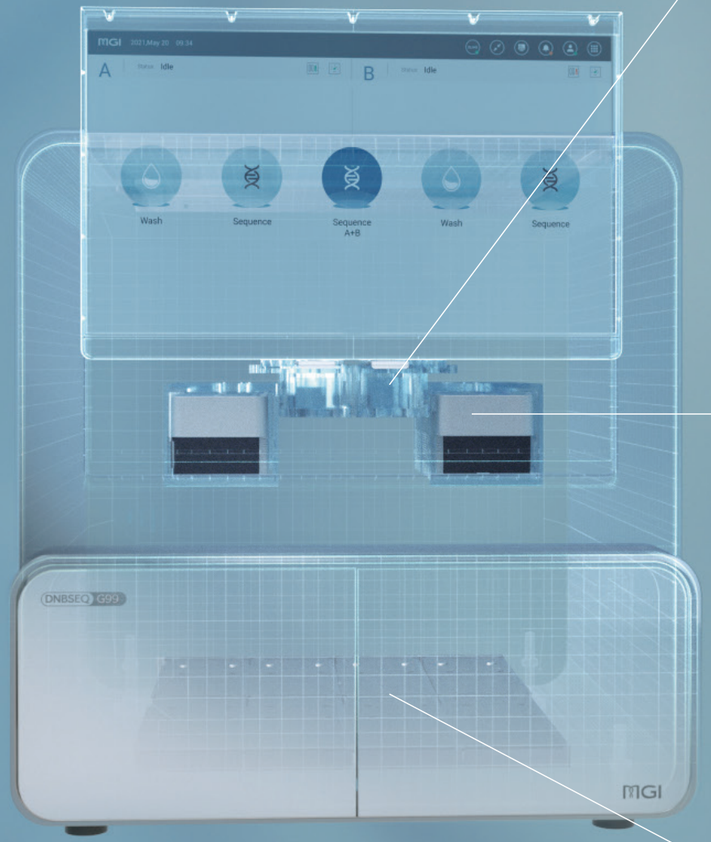
- advanced analysis begins automatically after run, and supports Bioanalysis by Sequencing (BBS) mode
- ZLIMS-compatible, achieve efficient workflow management and local data output

Data Security

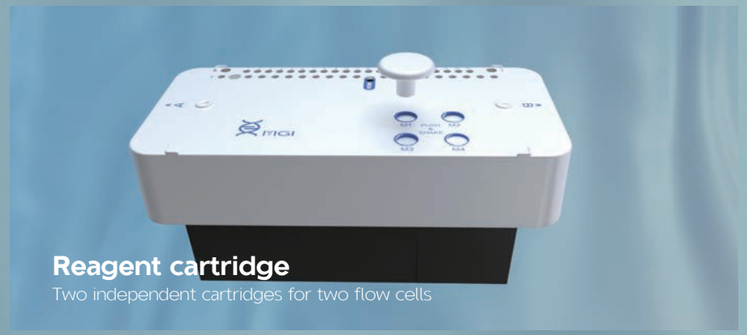
- Designed based on GDPR privacy protection requirement
- Secure storage to safeguard your sensitive data

Flexible
Customize your run

DNBSEQ-G99 is the only medium-to-low throughput sequencer with a dual flow cell loading configuration, providing ultimate flexibility in sequencing throughput. The dual flow cells can be operated with different read lengths independently or concurrently. Three flow cell loading modes are supported on DNBSEQ-G99: Single, Dual concurrent, or Dual independent. Laboratory technicians can decide number of flow cells to operate in accordance with the sample size and requirements.



Dual flow cells
Plug-and-play as needed

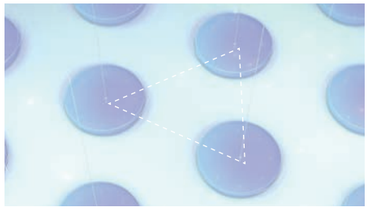


Reagent cartridge
Two independent cartridges for two flow cells

Bioinformatics module
Analysis automatically begins after each flow cell run

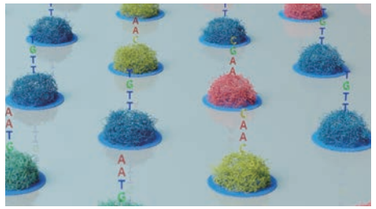
Speed
for your time-sensitive needs

To achieve the fastest sequencing speed in its range, DNBSEQ-G99 incorporates innovatively optimized flow cell, biochemistry process, fluidics, optics, temperature control and other core systems.
The result is supreme sequencing efficiency, while data quality remains top-notch.



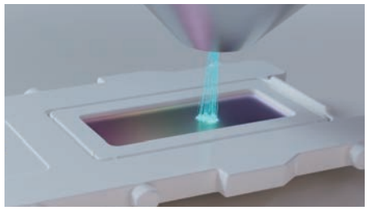
High Density Flow Cell

- 600nm pitch high density patterning
- 68% more DNB loading per unit area
- Novel triangular configuration



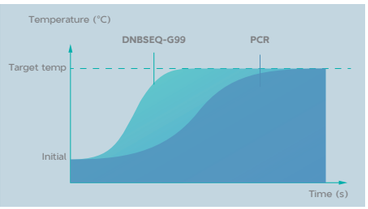
Super Fast Biochemistry

- 10s rapid fluorescence reaction
- Biochemistry incubation reaction sped up from minutes-range to seconds-range



Surpassing the Optical Diffraction Limit

- In-house developed ultra-high quality objective lens
- Improvement of signal capture efficiency by decreasing scan area



Rapid Temperature Control

- ~7 °C/s for heating and cooling
- Doubles the heating and cooling speed of conventional PCR instrument

Superior Performance

DNBSEQ-G99 delivers uncompromised high data quality. A multitude of applications can be executed on DNBSEQ-G99, such as targeted sequencing, small genome and Low pass WGS WGS sequencing, etc.

In addition, DNBSEQ-G99ARS supports the retrieval of data at intermediate time points under the Bioanalysis by Sequencing (BBS) mode. Users can obtain the first batch of summary report as quick as 2.5 hrs from the start of sequencing run (read length: SE40).

Method	Application	Recommended read length	Data size	Samples per Run	
				1 flow cell	2 flow cells
				80M	160M
⚑ Targeted Capture/ Multiplex PCR	Oncology panel	PE150	Small panel: ~1GB/Sample	24	48
	Genetic disease diagnosis (small panel)	PE150	Thalassemia:~0.2M/Sample Deafness:~5G/Sample	4	8
	ATOPlex panel	PE100/PE150	Respiratory tract panel: 5M/Sample COVID-19 panel:5M/Sample	16	32
	WES	PE150	15GB/Sample	1-2	2-4
⚑ Methylation	Oncology targeted methylation panel	PE150	~5Gb/Sample	4	8
⚑ Small Genome Sequencing	Metagenomics for pathogen detection	SE50, SE100	Meta:20M reads/Sample	4	8
	Microbial WGS	PE100, PE150	Single bacterium:~1GB/Sample	16-24	32-48
Low pass whole-genome sequencing	NIPT	SE35	NIPT/PGS:~10M reads/Sample	8	16
	PGS	SE35			
Transcriptome sequencing	RNA-Seq	SE50/PE100/PE150	Expression profiling:~1GB/ Transcriptome:~8GB/Sample	2-4	4-8

① The data volume recommendation and sample number are only for reference. The specific data volume and sample number need to be adjusted according to the actual situation.

② The longer read lengths will be released in 2023.

③ ⚑ recommend method

Performance Parameters

Maximum number of Flow cells	Lanes/ Flow cell	Effective Reads*/ Flow Cell	Supported Reads Lengths+	Data Output/ Flow Cell	Q30**	Run Time
2	1	80M	SE100/PE50	8~16G	>90%	5h
			PE150	24~48G	>85%	12h
			APP-C SE100***	8~16G	>90%	5h
			APP-C PE150	24~48G	>85%	12h

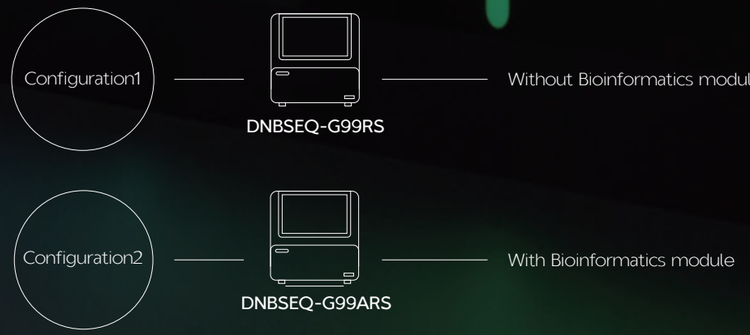
* The effective reads are based on the sequencing of an internal standard library. Actual output may vary depending on sample type and library preparation method.

** The percentage of bases above Q30 is the average of an internal standard library over the entire run. Actual performance is affected by factors such as sample type, library quality, and insert fragment length.

*** Estimated release in 2023 Q1

\+ DNBSEQ-G99 also supports SE50 and PE100 sequencing, and the existing kits can support SE50, PE100 read length sequencing.

Available Models



Oncology Application
Low Frequency Variants Detection

Experiment Scheme

Sample: Lung cancer ctDNA standards, diluted to 1%, 0.5%, 0.2%, and 0.1% variant ctDNA samples
Library prep: Targeted capture kit from third party
Sequencing strategy: PE100 dual-barcode sequencing, 4 repeated runs were tested
Objective: To test DNBSEQ-G99 variant detection capability

Sequencing Summary

The 4 runs generated 126M reads on average, Q30 >93%, with excellent uniformity observed.

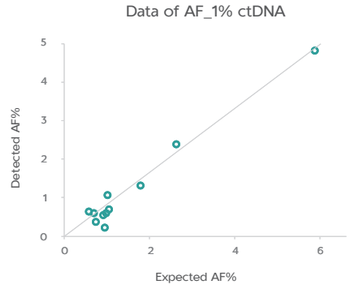
Analysis Summary

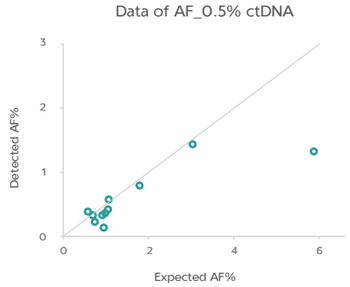
- 100% detection of SNV mutation sites in the samples (1%,0.5%,0.2%, 0.1%).

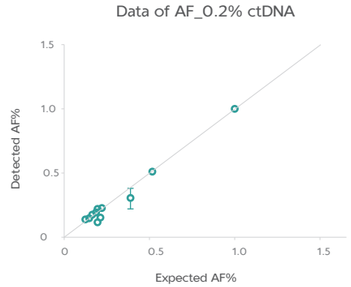
Sequencing Result

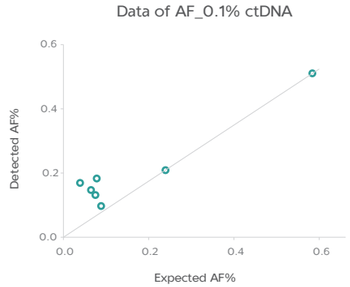
	Total reads (M)	Q30	EstErr(%)	Time (h)
Mean value	126.22	94.00	0.22	9.15
Standard deviation	7.41	0.52	0.02	0.11

Analysis Result









Oncology Application
Methylation Sequencing (Targeted Capture)

Experiment Scheme

Sample: Fragmented DNA from 4 cell lines
Library prep: Targeted capture double stranded library kit from third party
Sequencing strategy: PE100 dual-barcode sequencing, 2 repeated runs were tested
Objective: To evaluate DNBSEQ-G99's compatability with low-diversity libraries, and data uniformity for targeted methylation regions.

Sequencing Summary

Without addition of a spike-in balanced library, 2 runs had an averafe output of 101M reads, with Q30 >86%, showing good compatibility with the low diversity libraries.

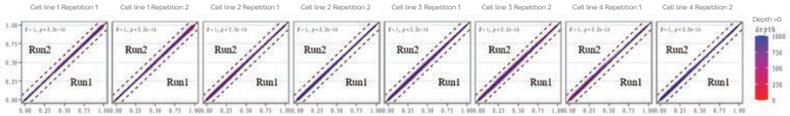
Analysis Summary

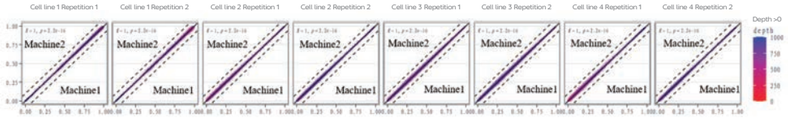
- Highly concordant average methylation fractions (AMF) measured between both runs for all tested samples.
- For results of the same samples on different instruments: average methylation level of the samples is highly consistent.

Sequencing Results

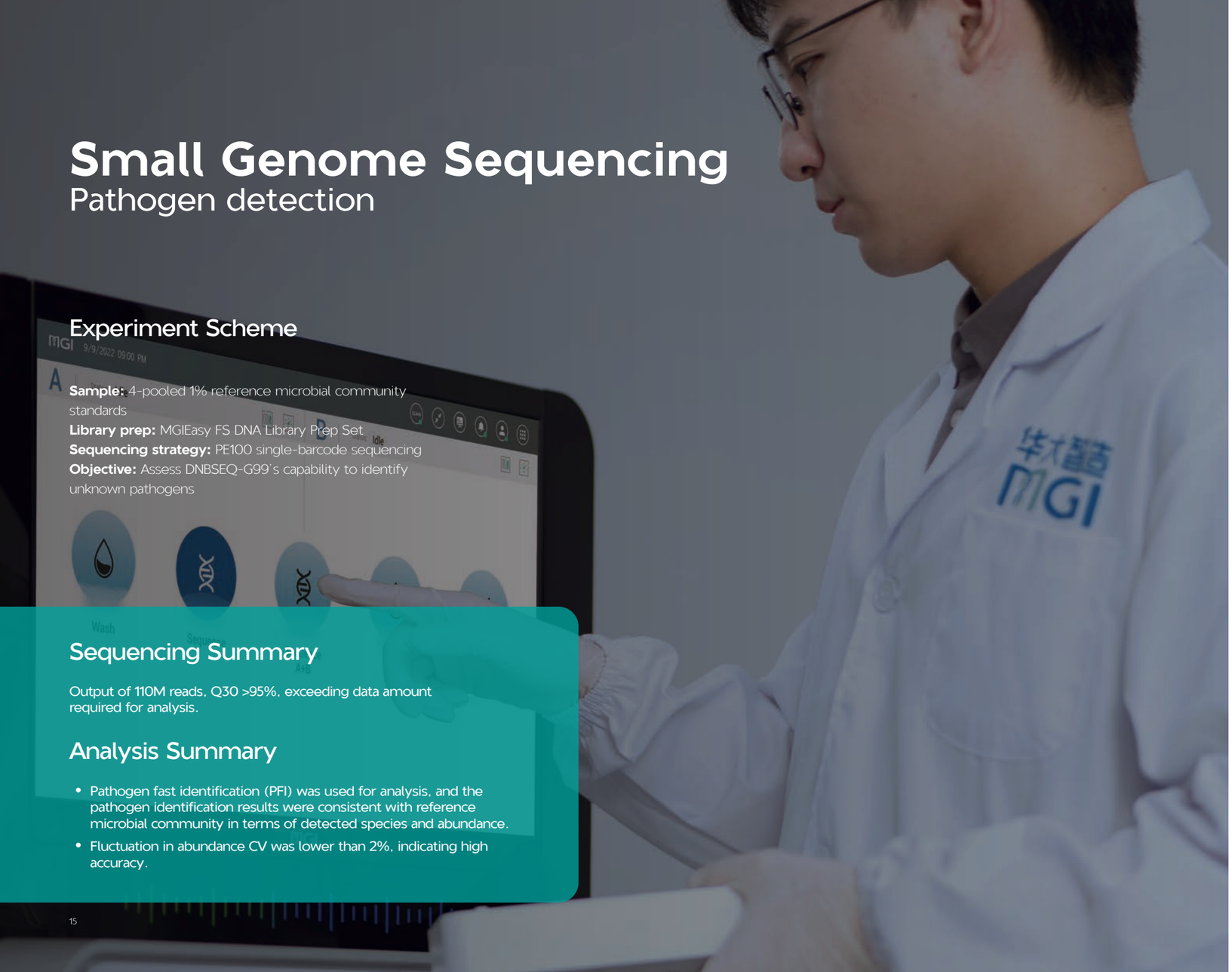
	Total reads (M)	Q30 (%)	SplitRate (%)	Time (h)
Run 1	103.12	86.42	98.36	9.20
Run 2	99.08	90.57	98.02	9.15

Analysis Results





Small Genome Sequencing
Pathogen detection



Experiment Scheme

Sample: 4-pooled 1% reference microbial community standards
Library prep: MGIEasy FS DNA Library Prep Set
Sequencing strategy: PE100 single-barcode sequencing
Objective: Assess DNBSEQ-G99's capability to identify unknown pathogens

Sequencing Summary

Output of 110M reads, Q30 >95%, exceeding data amount required for analysis.

Analysis Summary

- Pathogen fast identification (PFI) was used for analysis, and the pathogen identification results were consistent with reference microbial community in terms of detected species and abundance.
- Fluctuation in abundance CV was lower than 2%, indicating high accuracy.

Sequencing Results

	Total reads (M)	Q30(%)	SplitRate(%)	Time(h)
Output	110.17M	95.22	96.95	9

Analysis Results

Species	Sample 1	Sample 2	Sample 3	Sample 4	Standard abundance	mean	SD	CV
Salmonella enterica	15.87%	15.60%	15.72%	15.87%	12.00%	15.77%	0.13%	0.008
Pseudomonas aeruginosa	14.12%	14.00%	13.83%	14.12%	12.00%	14.02%	0.14%	0.010
Bacillus subtilis	13.30%	13.14%	13.46%	13.30%	12.00%	13.30%	0.13%	0.010
Escherichia coli	11.75%	12.32%	11.90%	11.75%	12.00%	11.93%	0.27%	0.023
Enterococcus faecalis	11.13%	11.30%	11.24%	11.13%	12.00%	11.20%	0.08%	0.008
Listeria monocytogenes	11.12%	11.02%	11.12%	11.12%	12.00%	11.10%	0.05%	0.005
Staphylococcus aureus	10.18%	10.23%	10.30%	10.18%	12.00%	10.22%	0.06%	0.006
Limosilactobacillus fermentum	9.52%	9.48%	9.46%	9.52%	12.00%	9.50%	0.03%	0.003
Cryptococcus neoformans	1.49%	1.49%	1.52%	1.49%	2.00%	1.50%	0.02%	0.010
Saccharomyces cerevisiae	1.47%	1.42%	1.45%	1.47%	2.00%	1.45%	0.02%	0.016

Small Genome Sequencing
Phage Assembly

Experiment Scheme

Sample: 16 pure bacteriophage cultures
Library prep: MGIEasy universal DNA library prep set
Test Strategy: PE150 dual-barcode
Test Purpose: Assess DNBSEQ-G99 capability for assembling whole bacteriophage genome

Sequencing Summary

Output of 106M reads, Q30 >92%, exceeding data amount required for analysis.

Analysis Summary

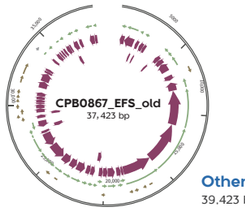
- Conserved protein genes for phage capsid, portal, and terminase were successfully detected in the G99 assemblies.
- G99 outperforms other platform for bacteriophage whole genome assembly, achieving higher assembly integrity.

Sequencing Results

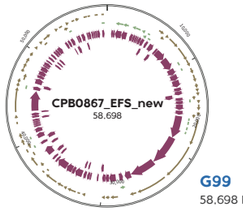
	Total reads (M)	Q30 (%)	SplitRate (%)	Time (h)
Output	106.99M	92.32	97.97	12

Analysis Results

Enterococcus faecalis phage

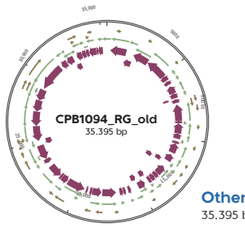


Other
39,423 bp

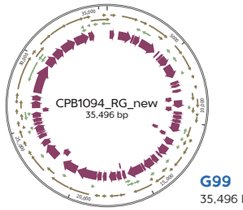


G99
58,698 bp

Ruminococcus phage



Other
35,395 bp



G99
35,496 bp

Hardware Specifications

Model	DNBSEQ-G99RS	Outputs FASTQ files
	DNBSEQ-G99ARS	Equipped with bioinformatics module for advanced analysis
Dimensions	607*680*640 mm	
Power	Rated Voltage	100V-240V
	Rated frequency	50/60Hz
	Rated Power	11000 VA. [working current]: ⩾10A
Touch Screen	LCD touch screen	
	Touch screen size	1.5inch
	Touch screen resolution	1920×1080
Maximum Sound Pressure	75 dB(A)	
Shell Protection Grade	IPX0	
Operating Environment Requirements	Temperature	19-30 ℃
	Relative Humidity	20-80 %RH
	Atmospheric Pressure	70 kPa-106 kPa
	Maximum Altitude (above sea level)	3000 m
Computer Configurations	CPU	Intel I9-10900e 2.80 GHz
	Internal Storage	64 GB
	HDD	6 TB
	Operating System	Windows 10

Ordering Information

Cat. No	Product Name
900-000561-00	DNBSEQ-G99RS
900-000560-00	DNBSEQ-G99ARS
940-000409-00	High-throughput Sequencing Set (G99 SM FCL SE100/PE50)
940-000410-00	High-throughput Sequencing Set (G99 SM FCL PE150)
940-000413-00	High-throughput Sequencing Set (G99 SM FCL APP-C PE150)
940-000624-00	DNBSEQ-G99RS Cleaning Reagent Kit
Selected as needed	UPS

*Unless otherwise informed, StandardMPS and CoolMPS sequencing reagents, and sequencers for use with such reagents are not available in Germany, Spain, UK, Hong Kong, Sweden, Belgium, Italy, Finland, Czech Republic, Switzerland, Portugal, Austria and Romania. No purchase orders for StandardMPS products will be accepted in the USA until after January 1, 2023.

MGI Global Presence

Technical Support Available Globally

The MGI technical support team has a complete global coverage, including technical service centers in major international regions and multiple locations 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 4000-966-988) (9:00AM-12:00PM,13:00PM-18:00PM, Beijing time (GMT+8), workday). Multi-language online training courses coming soon.

Comprehensive Instrument Service and Warranty Plans Globally

Warehouses in Shenzhen, Wuhan, Qingdao, Tianjin, Hong Kong, Taipei, Singapore(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 (inclusive of necessary reagents and consumables) to quickly turn your investment into production.

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 is provided with warranty, along with a variety of available extended warranty support plans.

MGI Genetic Sequencers

DNBSEQ-E5/25
Reads: 5-25Million
Data output: 0.5-7.5GB

DNBSEQ-G99
Reads: 80Million
Data output: 8-48GB

DNBSEQ-G50
Reads: 100-500Million
Data output: 10-150GB

DNBSEQ-G400
Reads: 300-1800Million
Data output: 55-14400GB

DNBSEQ-T7
Reads: 6000Million
Data output: 250-6000GB

DNBSEQ-T10x4
Reads: 27.5-45Billion
Data output: 66-72TB

@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 1800 employees, nearly half of whom are R&D personnel. MGI operates in more than 80 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.

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Version: September 2022

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