MGI Tech Co., Ltd.
Building 11, Beishan Industrial Zone,
Yantian District, Shenzhen.CHINA
518083

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

*Unless otherwise informed, this StandardMPS sequencing reagent is not available in Germany, UK, Sweden, and Switzerland.

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.

For research use only. Not for use in diagnostic procedures.

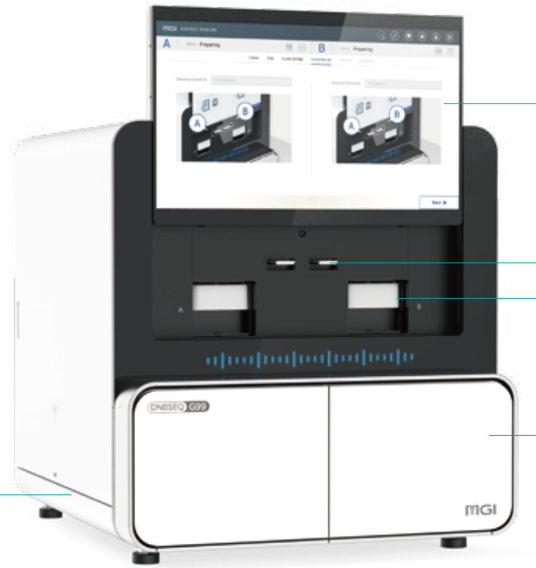
MGI' S PROPRIETARY

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*, 16s metagenomics sequencing*, small panel sequencing of 24-28 samples, or whole-exome sequencing of 1-4 samples.

Powered by 4-color sequencing technology, 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.

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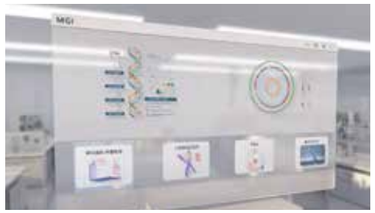
Designed for **Simplicity**

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
- Intuitive animations are included to guide flow cell loading, minimizing operational errors

Built-in Bioinformatics Module

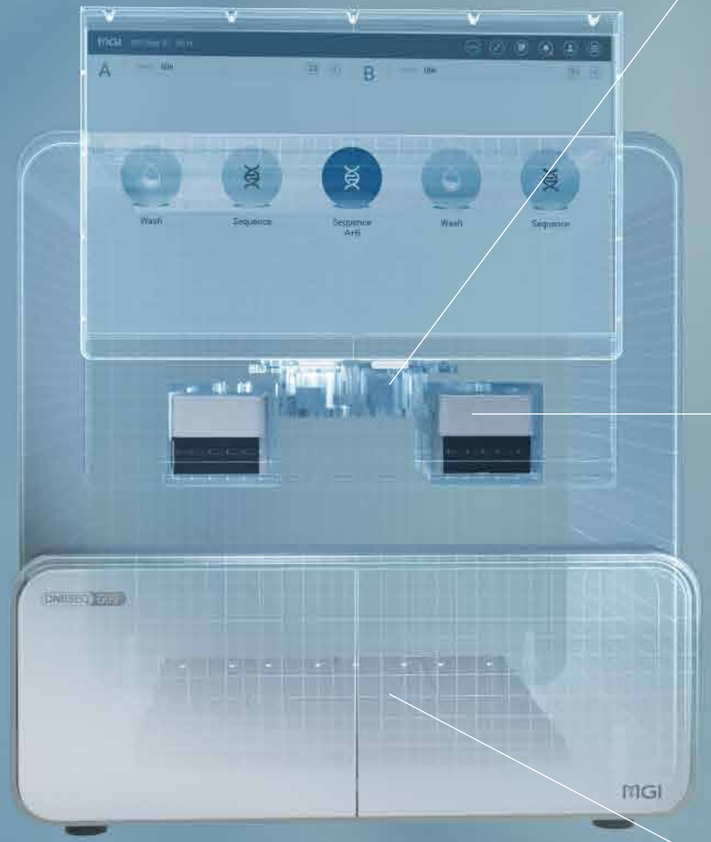
- Advanced analysis begins automatically after run, and supports Bioanalysis by Sequencing (BBS) mode
- ZLIMS-compatible, achieve efficient workflow management and local data output

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.



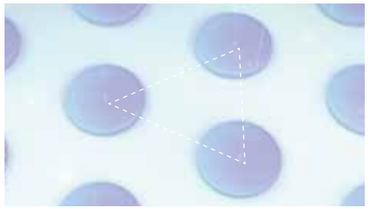
Dual flow cells
Plug-and-play as needed

Reagent cartridge
Two independent cartridges for two flow cells

Bioinformatics module
Analysis automatically begins after each flow cell run

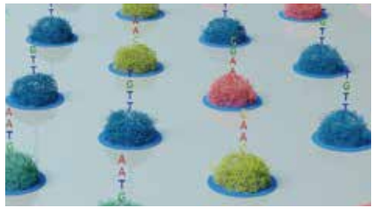
Speed
for your time-sensitive needs

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.



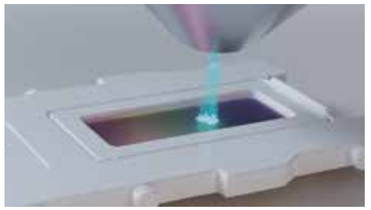
High Density Flow Cell

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



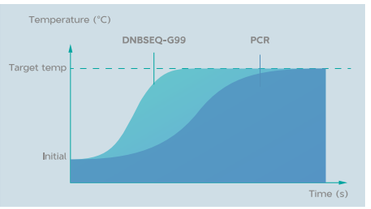
Super Fast Biochemistry

- 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 sequencing, etc.

In addition, DNBSEQ-G99A 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 per Sample	Samples per Run
⚑ Targeted Capture/ Multiplex PCR	Oncology panel	PE100,PE150	Small panel: ~1 Gb/sample	24/FC, 48/RUN
	Hereditary disease small panel (Thalassemia, deafness, etc.)	PE150	Deafness：~5 Gb/sample Thalassemia：~0.2 M reads/sample	Deafness: 4/FC, 8/RUN Thalassemia: 400/FC, 800/RUN
	ATOPlex panel (respiratory disease, SARS-CoV-2, etc.)	PE100,PE150	Respiratory tract panel: 5 M reads/sample COVID-19 panel: 5 M reads/sample	16/FC, 32/RUN
	WES	PE150	~15 Gb/sample	1-2/FC, 2-4/RUN
⚑ Methylation Analysis	Oncology targeted methylation panel	PE150	~5 Gb/sample	4/FC, 8/RUN
⚑ Small Genome Sequencing	Metagenomics for pathogen detection	SE50, SE100	Meta: 20 M reads/sample	4/FC, 8/RUN
	Microbial WGS	PE100, PE150	Isolated bacteria: ~1 Gb/sample	16-24/FC, 32-48/RUN
	16s V3-V4 sequencing	PE300*	≥0.1 M reads/sample	576/FC, 1152/RUN
Low pass whole-genome sequencing	NIPT	SE50	NIPT/PGS: ~10 M reads/sample	8/FC, 16/RUN
	PGS	SE50		
RNA sequencing	Expression profiling Transcriptome	SE50 PE150	Expression profiling: ~25 M reads/sample Transcriptome: ~6 Gb/sample	Expression profiling: 3/FC, 6/RUN Transcriptome: 4/FC, 8/RUN
Forensic	DNA Signature Identification	SE400*	0.8M reads/sample	96/FC, 192/RUN

① Recommended data output and sample numbers are only for reference, actual application will require optimisation adjustments.
② ⚑ Recommend method
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Performance Parameters

Maximum number of Flow cells	Lanes/ Flow cell	Minimum Effective Reads*/ Flow Cell	Supported Reads Lengths+	Data Output	Q30**	Run Time
2	1	80 M	SE100/PE50	8~16 G	>90%	5 h
			PE150	24~48 G	>85%	12 h
			APP-C SE100	8~16 G	>90%	5 h
			APP-C PE150	24~48 G	>85%	12 h
			PE300*	48~96 G	>85%	30 h
			SE400*	32-64 G	>75%	20 h

* 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.
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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 126 M reads on average, Q30 >93%, with excellent uniformity observed.

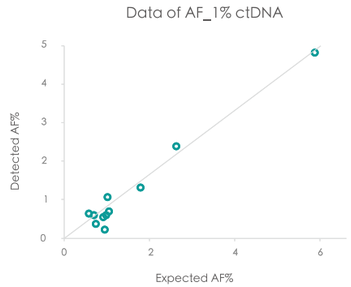
Analysis Summary

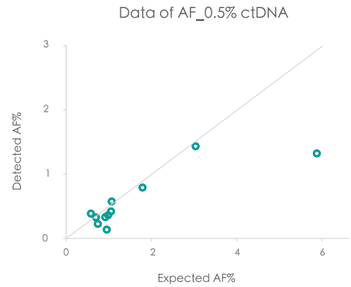
- 100% detection of SNV mutation sites in the samples (1 %, 0.5 %, 0.2 %, 0.1 %).

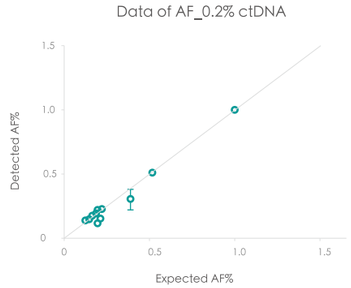
Sequencing Result

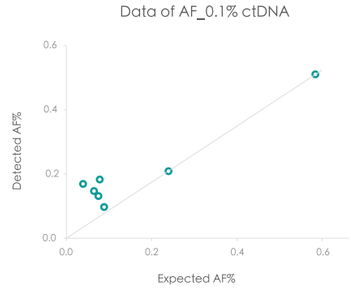
	Total reads (M)	Q30	EstErr(%)	Time (h)
Mean value	126.22	94.00	0.22	9.15
Standard deviation	7.41	0.52	0.02	0.11

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 101 M reads, with Q30 >86 %, showing good compatibility with the low diversity libraries.

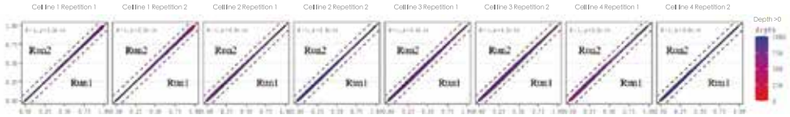
Analysis Summary

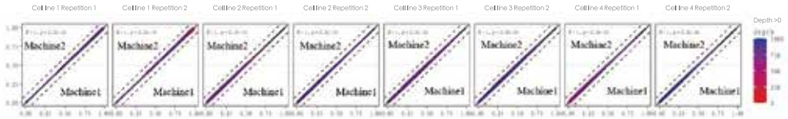
- Highly concordant average methylation fractions (AMF) measured between both runs for all tested samples.
- For results of the same samples on different instruments: AMF of the samples is highly consistent.

Sequencing Results

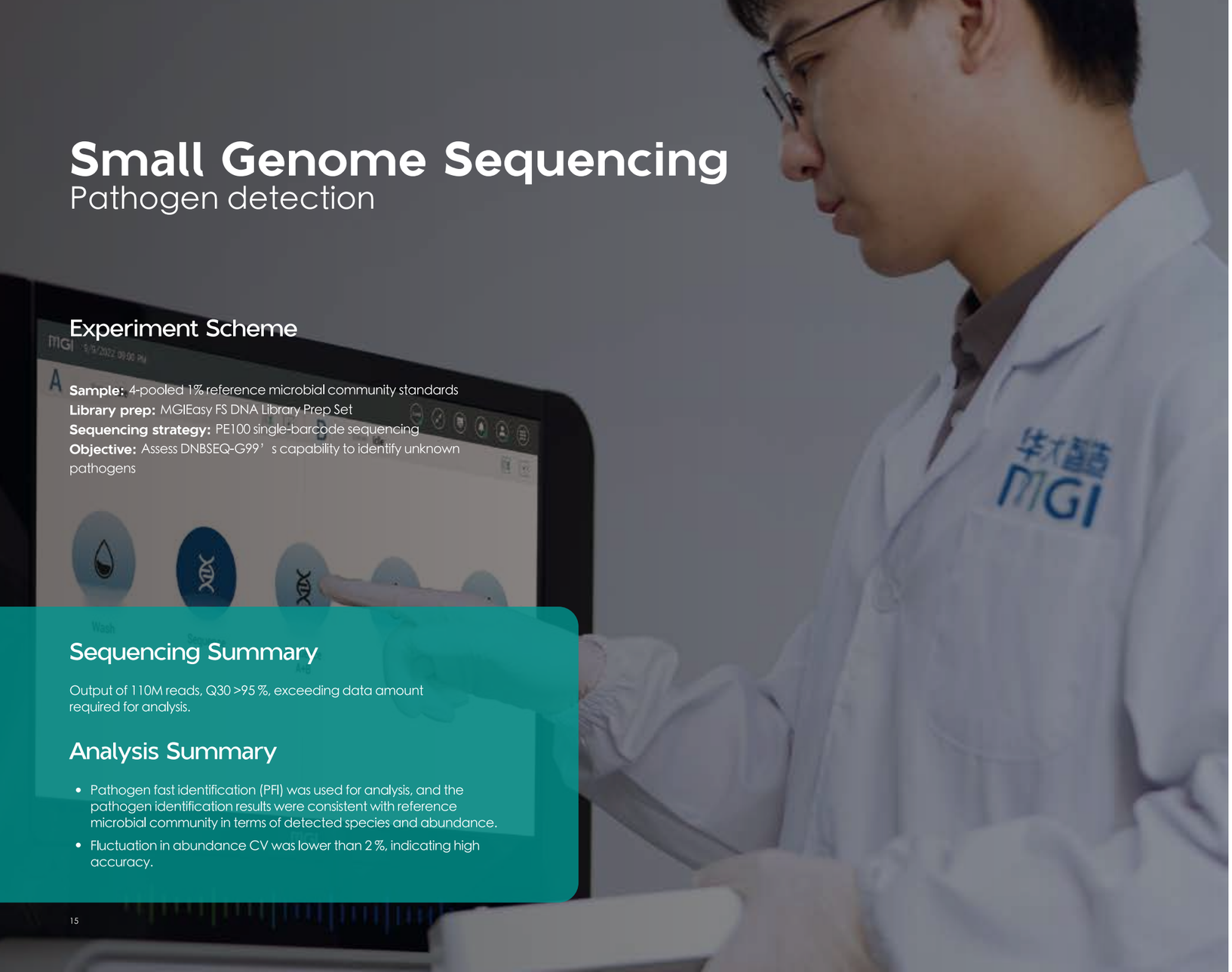
	Total reads (M)	Q30 (%)	SplitRate (%)	Time (h)
Run 1	103.12	86.42	98.36	9.20
Run 2	99.08	90.57	98.02	9.15

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	110.17	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%	0.82%
Pseudomonas aeruginosa	14.12%	14.00%	13.83%	14.12%	12.00%	14.02%	0.14%	1.00%
Bacillus subtilis	13.30%	13.14%	13.46%	13.30%	12.00%	13.30%	0.13%	0.98%
Escherichia coli	11.75%	12.32%	11.90%	11.75%	12.00%	11.93%	0.27%	2.26%
	11.13%	11.30%	11.24%	11.13%	12.00%	11.20%	0.08%	0.71%
Listeria monocytogenes	11.12%	11.02%	11.12%	11.12%	12.00%	11.10%	0.05%	0.45%
Staphylococcus aureus	10.18%	10.23%	10.30%	10.18%	12.00%	10.22%	0.06%	0.59%
Limosilactobacillus fermentum	9.52%	9.48%	9.46%	9.52%	12.00%	9.50%	0.03%	0.32%
Cryptococcus neoformans	1.49%	1.49%	1.52%	1.49%	2.00%	1.50%	0.02%	1.33%
Saccharomyces cerevisiae	1.47%	1.42%	1.45%	1.47%	2.00%	1.45%	0.02%	1.38%

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

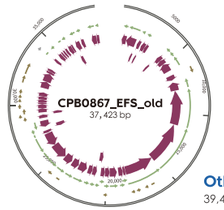
- Conserved protein genes for phage capsid, portal, and terminase were successfully detected in the DNBSEQ-G99 assemblies.
- DNBSEQ-G99 outperforms other platform for bacteriophage whole genome assembly, achieving higher assembly integrity.

Sequencing Results

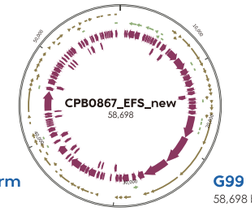
	Total reads (M)	Q30 (%)	SplitRate (%)	Time (h)
Output	106.99	92.32	97.97	12

Analysis Results

Enterococcus faecalis phage

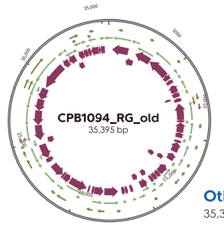


Other platform
39,423 bp

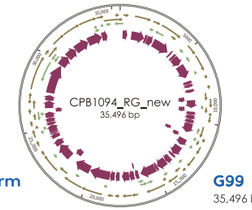


G99
58,698 bp

Ruminococcus phage



Other platform
35,395 bp



G99
35,496 bp

Small Genome Sequencing
16s Sequencing*

Experiment Scheme

Sample: Zymobiomics D6305 reference standard samples
Library prep: ATOPlex 16S V3 V4 rDNA Library Preparation Set
Sequencing strategy: PE300 dual barcode sequencing
Objective: To evaluate the data quality of DNBSEQ-G99 for 16s samples

Sequencing Summary

4 runs had an average output of 93.45 M, with Q30>90 %, which can meet the demand of bioinformatics analysis.

Analysis Summary

- The OUT results showed that the abundence at the genus level was highly consistent with the expected results.
- For the same sample in different runs, the correlation coefficient $R^2 > 0.99$ between parallel sequencing libraries, which showed high consistency of test results.

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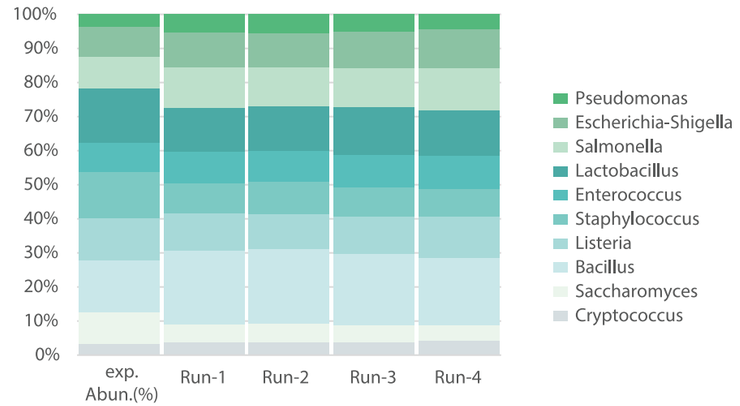
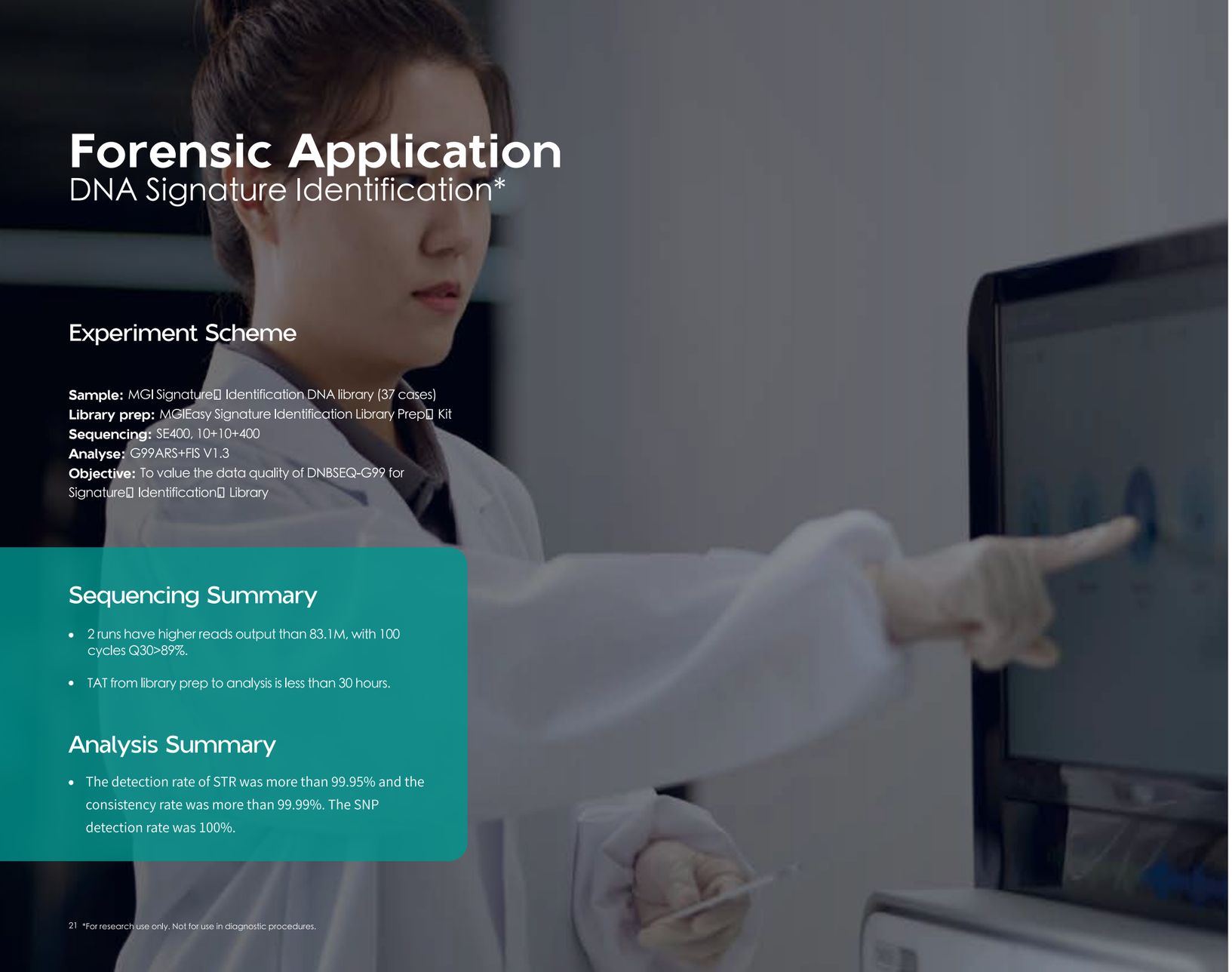
Sequencing Result

Total reads (M)		Q30 (%)	SplitRate (%)
Run-1	89.89	89.93	96.28
Run-2	94.97	90.21	96.65
Run-3	99.68	90.2	96.8
Run-4	89.25	89.82	95.34
Average	93.45	90.04	96.27

Analysis Result



Forensic Application
DNA Signature Identification*



Experiment Scheme

Sample: MGI Signature® Identification DNA library (37 cases)
Library prep: MGIEasy Signature Identification Library Prep® Kit
Sequencing: SE400, 10+10+400
Analyse: G99ARS+FIS V1.3
Objective: To value the data quality of DNBSEQ-G99 for Signature® Identification® Library

Sequencing Summary

- 2 runs have higher reads output than 83.1M, with 100 cycles Q30>89%.
- TAT from library prep to analysis is less than 30 hours.

Analysis Summary

- The detection rate of STR was more than 99.95% and the consistency rate was more than 99.99%. The SNP detection rate was 100%.

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Sequencing result

Total reads (M)		First100Cycle Q30(%)	Q30
Run-1	117.81	94.07	68.6
Run-2	83.1	89.02	62.95

Analysis result

The detection rate of STR	The consistency rate of STR	The detection rate of SNP
100.00%	100.00%	100.00%
100.00%	100.00%	100.00%

Sequencing time

Time of preparation	Sequencing time of dual barcodes
<5min	20h
<5min	19h51min

Hardware Specifications

Model	DNBSEQ-G99 DNBSEQ-G99A	Outputs FASTQ files Equipped with bioinformatics module for advanced analysis
Dimensions/Net Weight	607*680*640 mm/~140 kg	
Power	Rated Voltage Rated frequency Rated Power	100 V-240 V 50/60 Hz 1000 VA, [working current]: ⩾10 A
Touch Screen	LCD touch screen	
	Touch screen size Touch screen resolution	21.5 inch 1920×1080
Maximum Sound Pressure	75 dB(A)	
Shell Protection Grade	IPX0	
Operating Environment Requirements	Temperature Relative Humidity Atmospheric Pressure Maximum Altitude (above sea level)	19-30 ℃ 20-80 %RH 70 kPa-106 kPa 3000 m
Computer Configurations	CPU Internal Storage HDD Operating System	Intel I9-10900e 2.80 GHz 64 GB 6 TB Windows 10
Bioinformatis Module Configuretions	CPU Memory System Disk Cache Disk Storage Disk Ethernet	Intel Xeon 5220S 18C/36T 2.7GHz * 2 256 GB 960 GB 960 GB 32 TB Gigabit Ethernet RJ45 * 2

* The maximum sound pressure is measured and calculated at any position with the maximum sound pressure level 1m away from the housing during normal use
** For indoor use only
*** Support computer configuration and system version upgrade

Ordering Information

RUO*

Cat. No	Product Name
900-000607-00	DNBSEQ-G99RS
900-000609-00	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)
940-000415-00	High-throughput Sequencing Set (G99 SM FCL PE300)
940-000413-00	High-throughput Sequencing Set (G99 SM FCL APP-C PE150)
940-000520-00	High-throughput Sequencing Set (G99 SM App-C FCL SE100)
940-000417-00	High-throughput Sequencing Set (G99 SM FCL SE400)
940-000624-00	DNBSEQ-G99 Cleaning Reagent Kit
Selected as needed	UPS

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IVD

Cat. No	Product Name
900-000612-00	DNBSEQ-G99
900-000628-00	DNBSEQ-G99A
940-000428-00	Universal Sequencing Reaction Kit (G99 SM FCL SE100/PE50)
940-000431-00	Universal Sequencing Reaction Kit (G99 SM FCL PE150)
940-000434-00	Universal Sequencing Reaction Kit (G99 SM App-C FCL PE150)
940-000525-00	Universal Sequencing Reaction Kit (G99 SM App-C FCL SE100)

Technical Support Available Globally

Local technical support and Customer Experience Centers (CECs) have been established in multiple countries and regions worldwide to ensure timely and effective technical support and training.

Local warehouses and spare part centers have been established in multiple countries and regions worldwide to ensure the continuous availability of machine parts for maintenance.

Online technical support is available globally with a fully functional call center (Toll-Free Hotline 4000-688-114) accessible during workdays from 9:00 AM-12:00 PM and 13:00 PM-18:00 PM (Beijing time, GMT+8).

Providing installation services and system verification services as needed to ensure smooth implementation and operation. The value-added services are available for personalized services such as secondary relocation.

Responsible for any failure caused by non-human factors and non-force majeure factors within the warranty.

Providing instrument preventive maintenance services within the warranty period, along with a host of available extended warranty support plans to ensure optimal performance and reliability.

MGI Genetic Sequencers

DNBSEQ-E25*
Reads per flow cell: 25 M
Number of flow cells: 1
Data output: 2.5-7.5 Gb

DNBSEQ-G99*
Reads per flow cell: 80 M
Number of flow cells: 2
Data output: 8-96 Gb

DNBSEQ-G50*
Reads per flow cell: 100-500 M
Number of flow cells: 1
Data output: 10-150 Gb

DNBSEQ-G400*
Reads per flow cell: 300-1800 M
Number of flow cells: 2
Data output: 55-1440 Gb

DNBSEQ-T7*
Reads per flow cell: 5800 M
Number of flow cells: 4
Data output: 1-7 Tb

DNBSEQ-T20×2*
Reads: 40 B
Number of sides: 6
Data output: 42-72 Tb