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*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*

CB CE EAC NMPA

- Rapid sequencing
  Only 12 hrs for FCL 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.

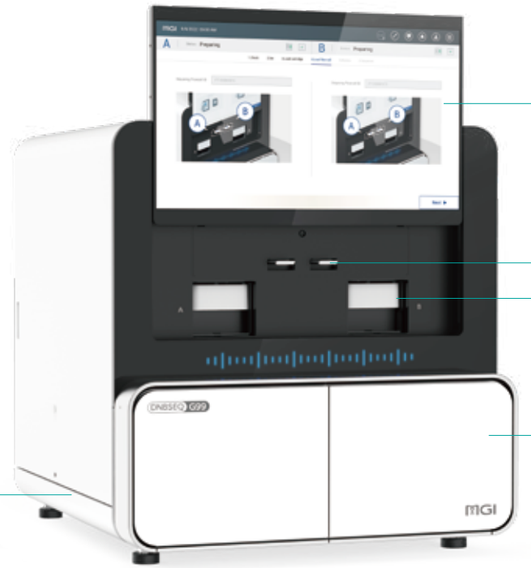
MGI'S PROPRIETARY

DNBSEQ™

TECHNOLOGY

Genetic Sequencer

DNBSEQ-G99



DNBSEQ-G99 is developed based on MGI's core DNBSEQTM 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*. Different types of flow cells can be selected for sequencing according to the sample quantity.

By adopting the DNBSEQ™ technology with the innovative StandardMPS 2.0 sequencing reagents, this upgrade delivers an impressive proportion of 85%* or higher for base quality scores reaching or exceeding Q40 during the sequencing process. Also, powered by 4-color sequencing technology, DNBSEQ-G99 has an optional built-in bioinformatics module, allowing 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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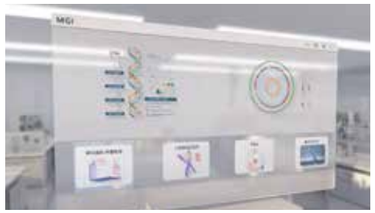
Designed for **Simplicity**

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

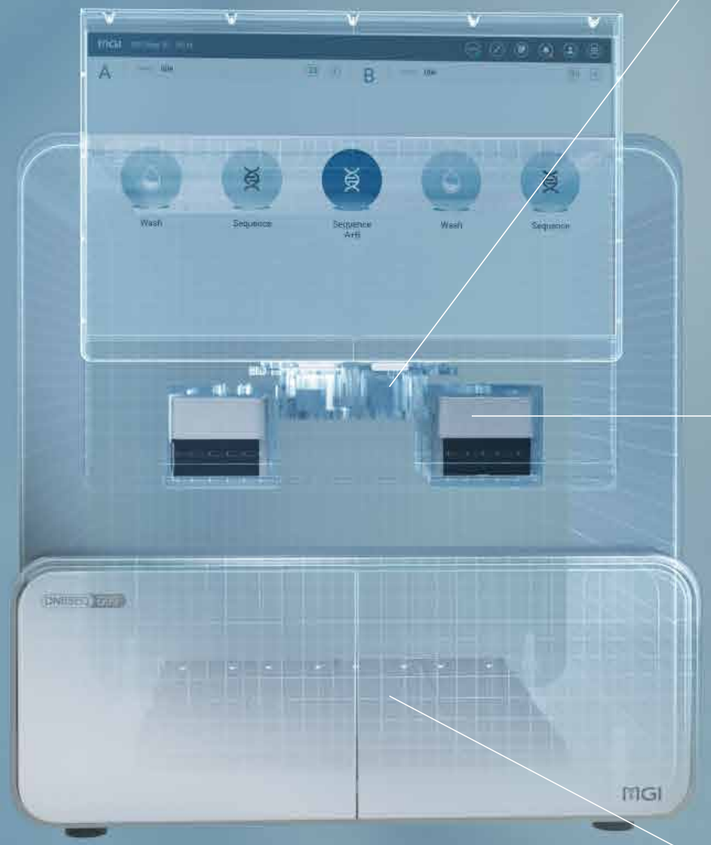
- Advanced analysis begins automatically after run, and supports Bioanalysis by Sequencing (BBS) mode
- ZLIMS-compatible, achieve efficient workflow management and local data output

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.



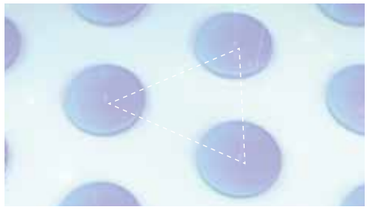
Dual flow cells
Plug-and-play as needed

Reagent cartridge
Two independent cartridges for two flow cells

Bioinformatics module
Analysis automatically begins after each flow cell run

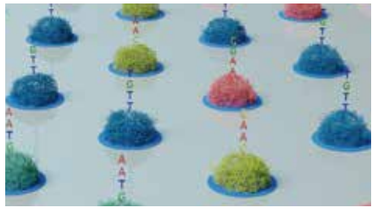
Speed
for your time-sensitive needs

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.



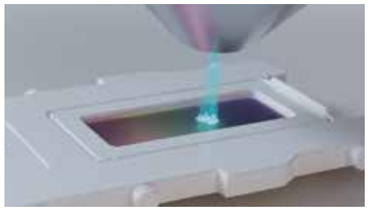
High Density Flow Cell

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



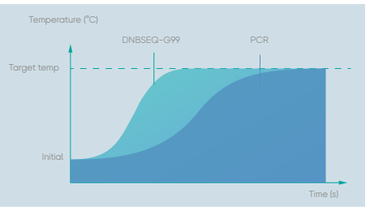
Super Fast Biochemistry

- 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	Recommended data size	FCS Recommended sample /RUN	FCL Recommended sample /RUN	FCU Recommended sample /RUN
⚑ Target capture/ multiplex PCR	Onco panel	Small panel: ~1Gb/sample	Small panel: ~1Gb/sample	12/FC，24/RUN	24/FC，48/RUN	48/FC，96/RUN
	Genetic disease diagnosis small panel(Thalassemia, deafness, etc.)	PE150	Deafness: ~5Gb/sample	2/FC，4/RUN	4/FC，8/RUN	9/FC，18/RUN
			Thalassemia: ~0.2M reads/ sample	200/FC, 400/RUN	400/FC, 800/RUN	800/FC, 1600/RUN
	ATOPlex panel(Respiratory, COVID-19, etc.)	PE100/PE150	Respiratory panel: 5M reads/ sampleCOVID-19 panel: 5M reads/sample	8/FC，16/RUN	16/FC，32/RUN	32/FC，64/RUN
	WES	PE150	15Gb/sample	/	1-2/FC，2-4/RUN	3/FC，6/RUN
⚑ Methylation	Onco targeted methylation panel	PE150	~5Gb/sample	2/FC，4/RUN	4/FC，8/RUN	9/FC，18/RUN
⚑ Small genome sequencing	Metagenomics for pathogen detection	SE50/SE100	Meta: 20M reads/sample	/	4/FC，8/RUN	8/FC，16/RUN
	Microbial WGS sequencing	PE100/PE150	Single bacterium: ~1Gb/sample	12/FC，24/RUN	24/FC，48/RUN	48/FC，96/RUN
	16S sequencing	PE300	~0.1 M reads/sample	/	640/FC, 1280/RUN	1280/FC, 2560/RUN
Low-pass WGS sequencing	NIPT	SE50	NIPT/PGS: ~10M reads/sample	/	8/FC，16/RUN	16/FC，32/RUN 6/FC，12/RUN
	PGS	SE50				
Transcriptome sequencing	RNA-Seq	SE50/PE150	Expression profiling: ~25M/ sample	/	3/FC，6/RUN	8/FC，16/RUN
			Transcriptome: ~6Gb/sample	/	4/FC，8/RUN	/
Forensics	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

Performance Parameters

Maximum number of Flow Cells	Lanes/Flow Cell	Flow Cell Type	reads/Flow Cell*	Supported Read Lengths	Data Output	Q30**	Q40**	Run Time***
2	1	FCS	40M	App-D PE150	12-24 Gb	>90%	>85%	11h
		FCL	80M	SE100/PE50	8-16 Gb	>90%	>85%	5h
				PE150	24-48 Gb	>90%	>85%	12h
				App-D SE100	8-16 Gb	>90%	>85%	5h
				App-D PE150	24-48 Gb	>85%	>85%	12h
				App-D PE300	48-96 Gb	>85%	>80%	30h
				SE400	32-64 Gb	>75%	>70%	20h
		FCU	160M	App-D SE100	16-32 Gb	>90%	>85%	7h
				App-D PE150	48-96 Gb	>85%	>85%	16h
				App-D PE300	96-192 Gb	>85%	>80%	35h

* Effective reads is determined using a standard library. Actual output may vary depending on sample type and library preparation method.

** The percentage of bases above Q30 and run time is the average of an internal standard library over the entire run. The actual performance is affected by factors such as sample type, library quality, and insert fragment length. Only StandardMPS 2.0(SM 2.0) reagents support the generation of Q40 data.

*** The sequencing time is the statistical duration for single flow cell sequencing and dual flow cell simultaneous sequencing.

★ The instrument is equipped with SE50 and PE100 sequencing modes, and the existing reagent kits support SE50 and PE100 read length sequencing.

Note: APP-D has built-in Illumina's Truseq, Nextera adapters, and MGI adapter, which supporting mixed testing of Illumina's Truseq, Nextera adapters, and MGI adapter libraries.

Available Models

Oncology Application
Low Frequency Variants Detection

Experiment Scheme

Sample: GeneWell FFPE and gDNA standards
Library Prep: Multiplex amplification library preparation kit from third party company
Sequencing strategy: PE100 single barcode sequencing
Objective: To evaluate the mutation detection capability of the platform and establish a 24-hour fully automated oncology application solution based on the DNBSEQ-G99 platform

Sequencing Summary

Without balancing the library, the output was 136.66M reads, with Q30 reaching 97.88% and Q40 reaching 94.35%. Eight samples were pooled and sequenced together, achieving an overall split rate of 99%. The deviation in split rate for each sample was 0.9%, demonstrating excellent uniformity in sample splitting, and the data volume for each sample met the analysis standards.

Analysis Summary

- Quality control metrics: high mapping rate, on-target rate, and uniformity (0.2x coverage).
- Comparing the mutation detection frequency of the DNBSEQ-G99 platform at different mutation sites with the theoretical mutation frequency, the detection frequency for FFPE. samples was close to the theoretical frequency. The DNBSEQ-G99 platform can detect mutation frequencies of 5% and 1% with 100% accuracy.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
Results	136.66	97.88	94.35	99%

Total Process Time: The entire process from sample extraction to the output of the analysis report takes 25.5 hours for FFPE samples and 21.5 hours for blood samples.

Analysis Result

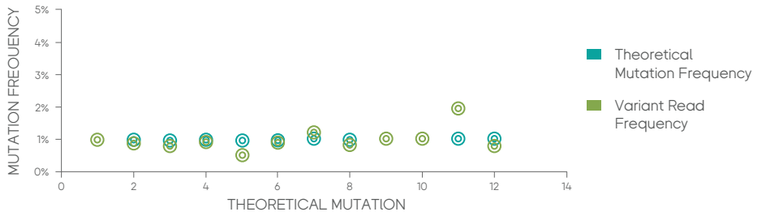


Fig. 1-1 Comparison of Actual and Theoretical Mutation Frequencies (1%) in FFPE Samples

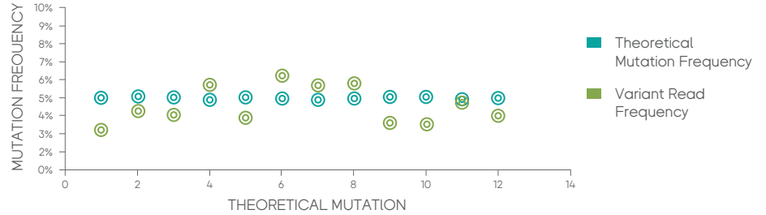


Fig. 1-2 Comparison of Actual and Theoretical Mutation Frequencies (5%) in FFPE Samples

Small Genome Sequencing
Pathogen Detection

Experiment Scheme

Sample: Zymo Research D6305 Microbial Community DNA Standard
Library Prep: NadPrep® Rapid DNA Enzyme Library Preparation Kit v2
Sequencing strategy: SE100 dual barcode sequencing
Objective: To evaluate the platform's ability to identify unknown pathogens

Sequencing Summary

Generated 125M reads, Q30 reached 96%, Q40 exceeded 90%. Results from SM2.0 with OS 4.0 were consistent with universal circularization results.

Analysis Summary

- Comparison of two circularization methods showed similar species detection abundance.
- Pathogen identification results using Microbial Rapid Identification (PFI) were consistent with the species in the standard sample.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
SM2.0+OS4.0	129.49	96.17	90.85	93.72
SM2.0	127.37	95.62	90.17	93.72

Analysis Result

Fig. 2-1 Species detection abundance for different circularization methods

Whole Exome Sequencing

Experiment Scheme

Sample: NA12878
Library Prep: SureSelect XT HS2 DNA Starter Kit, MGIEasy FS DNA Library Prep Kit
Sequencing strategy: PE150 dual barcode sequencing
Objective: To evaluate the platform's ability to detect whole exomes.

Sequencing Summary

Generated 130M reads, Q30 reached 96%, Q40 exceeded 91%.

Analysis Summary

- The metrics for mapping rate, duplication rate, and mismatch rate were better with SM2.0 compared to SM reagents.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
SM 2.0	130.96	96.64	91.94	97.46

Analysis Result

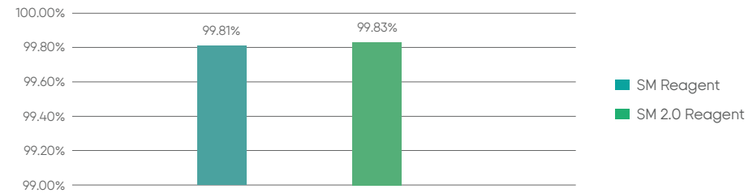


Fig. 3-1 Maping Rate comparasion

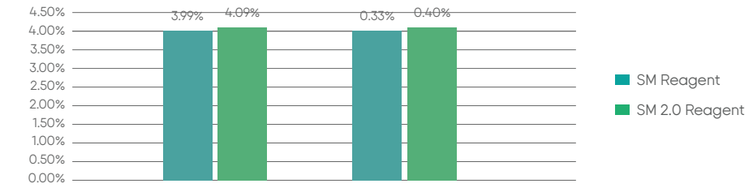


Fig. 3-2 Maping Rate comparasion

Small Genome Sequencing
16s Sequencing

Experiment Scheme

Sample: Zymobiomics D6305 Standard
Library Prep: ATOPlex 16S & 18S rDNA Library Preparation Kit
Test Strategy: App-D PE300 Dual Barcode Sequencing
Test Purpose: To evaluate the platform's detection capability for the 16S amplicon library.

Sequencing Summary

Generated 131M reads, with Q30 reaching 97% and Q40 exceeding 94%; Compared to other platforms, the G99 platform shows a more stable curve and higher quality.

Analysis Summary

- Metrics such as Filtered Rate, Merge Rate Filtered, and Feature Rate Filtered are superior to those of other manufacturers.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
SM2.0 App-D PE300	129.49	129.49	90.85	93.72

Q Value Result

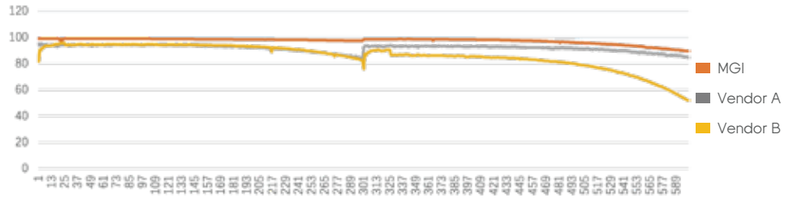


Fig. 4-1 Mean Q per cycle

Analysis Result

	Filtered Rate	MergeRate Filtered	FeatureRate Filtered
DNBSEQ-G99	90.20%	99.77%	89.86%
Vendor A	81.57%	94.29%	74.10%
Vendor B	89.35%	99.85%	89.18%

Forensic Application
DNA Signature Identification

Experiment Scheme

Sample: MGI Signature Identification DNA library
Library Prep: MGIEasy Signature Identification Library Prep Kit
Sequencing strategy: SE10+10+400
Objective: To evaluate the detection rate and consistency rate of SM2.0 reagent for individual identification libraries

Sequencing Summary

- The average total reads for 6 runs is as high as 126M, and the average Q30 for the first 100 cycles is as high as 97%.
- TAT from library prep to analysis is less than 30 hours.

Analysis Summary

- Statistical analysis of key indicators was conducted for 6 runs, and the detection rate and consistency rate of STR sites were better than the standard.

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

- Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	First 100 Cycle Q30(%)
Run 1	125.78	67.18	62.52	97.92
Run 2	127.74	66.45	61.09	97.31
Run 3	127.46	64.97	59.27	96.74
Run 4	119.63	64.07	57.30	95.70
Run 5	130.29	66.51	61.14	97.44
Run 6	130.36	65.38	59.99	97.09
Average	126.88	65.76	60.22	97.03

- Analysis Result

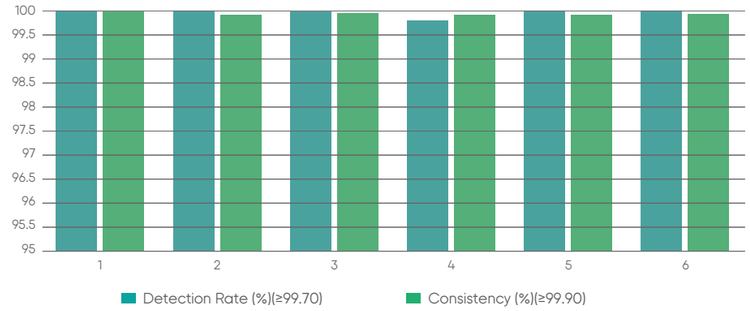


Fig. 5-1 Comparison betwwen Detection Rate(%) and Consistency(%)

Hardware Specifications

Model	DNBSEQ-G99 DNBSEQ-G99A	Outputs FASTQ files Equipped with bioinformatics module for advanced analysis
Dimension (W*D*H)/Net Weight	607x689x657 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)	15-30℃ 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
Sequencer	900-000607-00	DNBSEQ-G99RS
	900-000609-00	DNBSEQ-G99ARS
FCS	940-002649-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCS PE150）
FCL	940-001268-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 FCL SE100/PE50）
	940-001269-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 FCL PE150）
	940-001267-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCL SE100）
	940-001274-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCL PE150）
	940-001716-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCL PE300）
	940-001757-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 FCL SE400）
FCU	940-002776-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCU SE100）
	940-002775-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCU PE150）
	940-002773-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCU PE300）
	940-000624-00	DNBSEQ-G99RS Cleaning Reagent Kit（G99 SM FCL）

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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-D FCL PE150)
940-000525-00	Universal Sequencing Reaction Kit (G99 SM App-D 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 E Series Sequencer

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

DNBSEQ G Series Sequencer

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

DNBSEQ-T1+
Reads per flow cell: 500-2000M
Number of flow cells: 2
Data output: 25 Gb-1.2 Tb

DNBSEQ T Series Sequencer

About

MGI Tech Co., Ltd.

2,670+
Employees

32.16%
R&D Personnel

3,000+
Customers

100+
Countries & Regions

MGI Tech Co., Ltd. (or its subsidiaries, together referred to MGI), is committed to building core tools and technologies that drive innovation in life science. Our focus lies in research & development, manufacturing, and sales of instruments, reagents, and related products in the field of life science and biotechnology. We provide real-time, multi-omics, and full spectrum of digital equipment and systems for precision medicine, agriculture, healthcare and various other industries.

Founded in 2016, MGI has grown into a leader in life science, serving customers across six continents and have established research, manufacturing, training, and after-sales service facilities globally. MGI stands out as one of the few companies capable of independently developing and mass-producing clinical-grade gene sequencers with varying throughput capacities, ranging from Gb to Tb levels. With unparalleled expertise, cutting-edge products, and a commitment to global impact, MGI continues to shape the trajectory of life sciences into the future.

As of June 30, 2024, MGI has a team over 2,670 employees, with research and development personnel accounting for approximately 32.16%. Our business spans over 100 countries and regions worldwide, serving more than 3,000 users.

Vision

Leading Life Science Innovation

Mission

To Develop and Promote Advanced Life Science Tools for Future Healthcare

UNLEASH YOUR ULTIMATE SEQUENCING SPEED

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DNBSEQ-G99*

Q40

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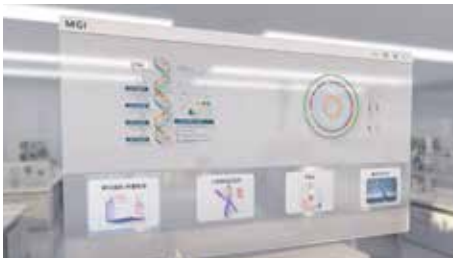

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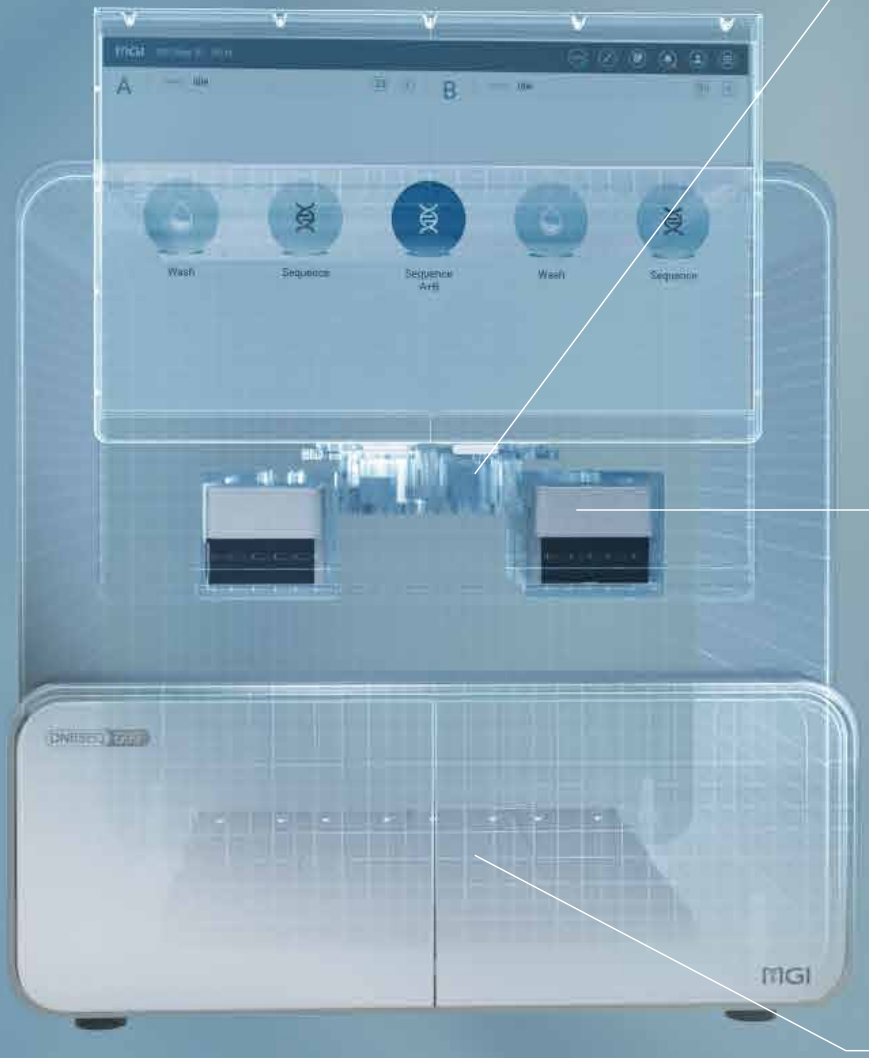
- Advanced analysis begins automatically after run, and supports Bioanalysis by Sequencing (BBS) mode
- ZLIMS-compatible, achieve efficient workflow management and local data output

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

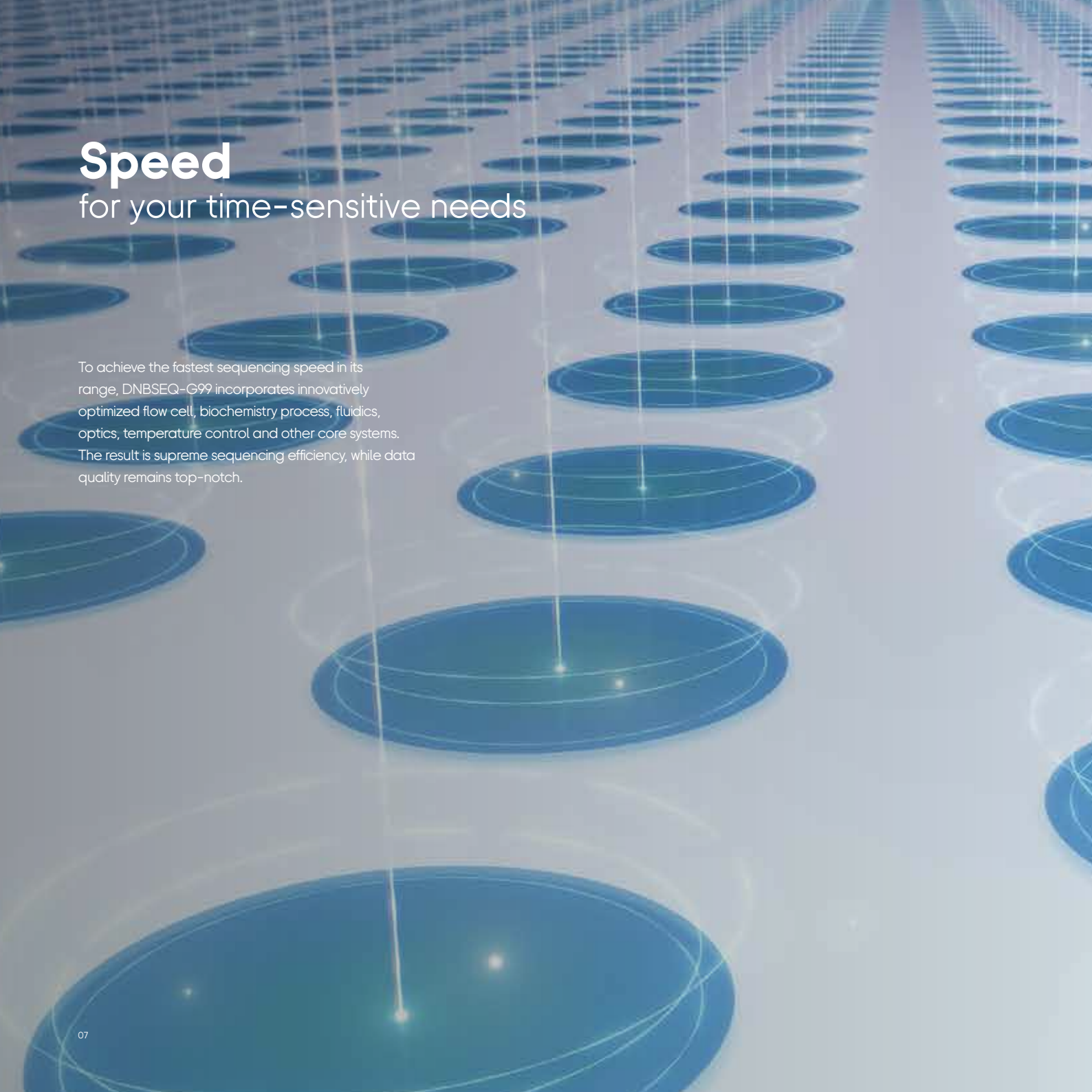
Plug-and-play as needed

Reagent cartridge

Two independent cartridges for two flow cells

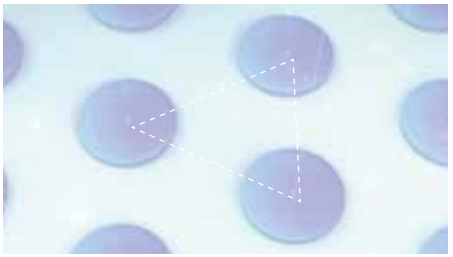
Bioinformatics module

Analysis automatically begins after each flow cell run



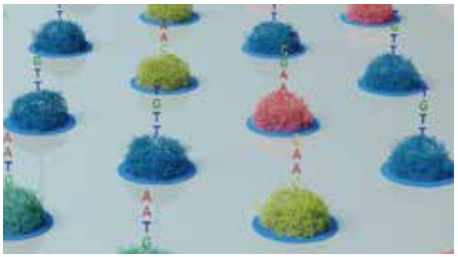
Speed
for your time-sensitive needs

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.



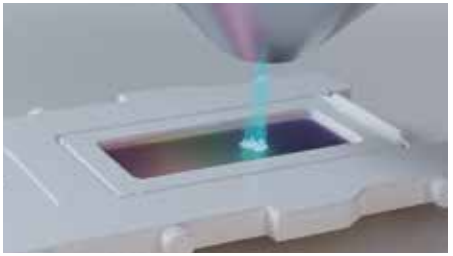
High Density Flow Cell

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



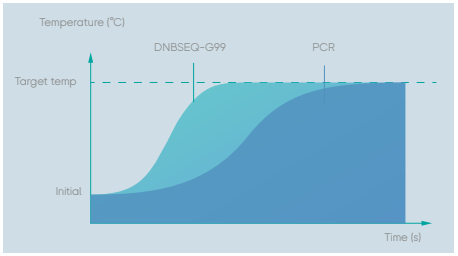
Super Fast Biochemistry

- 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	Recommended data size	FCS Recommended sample /RUN	FCL Recommended sample /RUN	FCU Recommended sample /RUN
⚑ Target capture/ multiplex PCR	Onco panel	Small panel: ~1Gb/sample	Small panel: ~1Gb/sample	12/FC，24/RUN	24/FC，48/RUN	48/FC，96/RUN
	Genetic disease diagnosis small panel(Thalassemia, deafness, etc.)	PE150	Deafness: ~5Gb/sample	2/FC，4/RUN	4/FC，8/RUN	9/FC，18/RUN
			Thalassemia: ~0.2M reads/ sample	200/FC, 400/RUN	400/FC, 800/RUN	800/FC, 1600/RUN
	ATOPlex panel(Respiratory, COVID-19, etc.)	PE100/PE150	Respiratory panel: 5M reads/ sampleCOVID-19 panel: 5M reads/sample	8/FC，16/RUN	16/FC，32/RUN	32/FC，64/RUN
	WES	PE150	15Gb/sample	/	1-2/FC，2-4/RUN	3/FC，6/RUN
⚑ Methylation	Onco targeted methylation panel	PE150	~5Gb/sample	2/FC，4/RUN	4/FC，8/RUN	9/FC，18/RUN
⚑ Small genome sequencing	Metagenomics for pathogen detection	SE50/SE100	Meta: 20M reads/sample	/	4/FC，8/RUN	8/FC，16/RUN
	Microbial WGS sequencing	PE100/PE150	Single bacterium: ~1Gb/sample	12/FC，24/RUN	24/FC，48/RUN	48/FC，96/RUN
	16S sequencing	PE300	~0.1 M reads/sample	/	640/FC, 1280/RUN	1280/FC, 2560/RUN
Low-pass WGS sequencing	NIPT	SE50	NIPT/PGS: ~10M reads/sample	/	8/FC，16/RUN	16/FC，32/RUN 6/FC，12/RUN
	PGS	SE50				
Transcriptome sequencing	RNA-Seq	SE50/PE150	Expression profiling: ~25M/ sample	/	3/FC，6/RUN	8/FC，16/RUN
			Transcriptome: ~6Gb/sample	/	4/FC，8/RUN	/
Forensics	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

Performance Parameters

Maximum number of Flow Cells	Lanes/Flow Cell	Flow Cell Type	reads/Flow Cell*	Supported Read Lengths	Data Output	Q30**	Q40**	Run Time***
2	1	FCS	40M	App-D PE150	12-24 Gb	>90%	>85%	11h
		FCL	80M	SE100/PE50	8-16 Gb	>90%	>85%	5h
				PE150	24-48 Gb	>90%	>85%	12h
				App-D SE100	8-16 Gb	>90%	>85%	5h
				App-D PE150	24-48 Gb	>85%	>85%	12h
				App-D PE300	48-96 Gb	>85%	>80%	30h
				SE400	32-64 Gb	>75%	>70%	20h
		FCU	160M	App-D SE100	16-32 Gb	>90%	>85%	7h
				App-D PE150	48-96 Gb	>85%	>85%	16h
				App-D PE300	96-192 Gb	>85%	>80%	35h

* Effective reads is determined using a standard library. Actual output may vary depending on sample type and library preparation method.

** The percentage of bases above Q30 and run time is the average of an internal standard library over the entire run. The actual performance is affected by factors such as sample type, library quality, and insert fragment length. Only StandardMPS 2.0(SM 2.0) reagents support the generation of Q40 data.

*** The sequencing time is the statistical duration for single flow cell sequencing and dual flow cell simultaneous sequencing.

★ The instrument is equipped with SE50 and PE100 sequencing modes, and the existing reagent kits support SE50 and PE100 read length sequencing.

Note: APP-D has built-in Illumina's Truseq, Nextera adapters, and MGI adapter, which supporting mixed testing of Illumina's Truseq, Nextera adapters, and MGI adapter libraries.

Available Models

Configuration1 — DNBSEQ-G99 — Without Bioinformatics module

Configuration2 — DNBSEQ-G99A — With Bioinformatics module

Oncology Application
Low Frequency Variants Detection

Experiment Scheme

Sample: GeneWell FFPE and gDNA standards
Library Prep: Multiplex amplification library preparation kit from third party company
Sequencing strategy: PE100 single barcode sequencing
Objective: To evaluate the mutation detection capability of the platform and establish a 24-hour fully automated oncology application solution based on the DNBSEQ-G99 platform

Sequencing Summary

Without balancing the library, the output was 136.66M reads, with Q30 reaching 97.88% and Q40 reaching 94.35%. Eight samples were pooled and sequenced together, achieving an overall split rate of 99%. The deviation in split rate for each sample was 0.9%, demonstrating excellent uniformity in sample splitting, and the data volume for each sample met the analysis standards.

Analysis Summary

- Quality control metrics: high mapping rate, on-target rate, and uniformity (0.2x coverage).
- Comparing the mutation detection frequency of the DNBSEQ-G99 platform at different mutation sites with the theoretical mutation frequency, the detection frequency for FFPE. samples was close to the theoretical frequency. The DNBSEQ-G99 platform can detect mutation frequencies of 5% and 1% with 100% accuracy.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
Results	136.66	97.88	94.35	99%

Total Process Time: The entire process from sample extraction to the output of the analysis report takes 25.5 hours for FFPE samples and 21.5 hours for blood samples.

Analysis Result

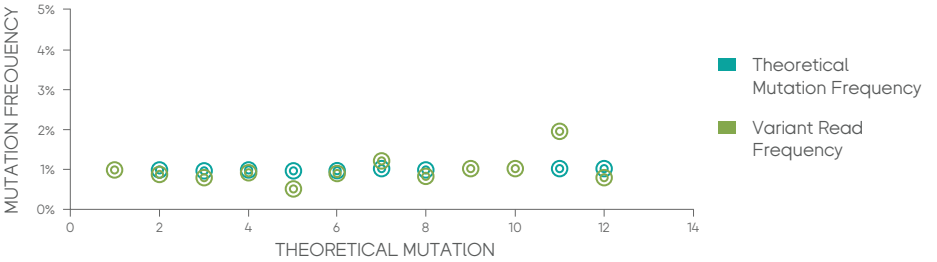


Fig. 1-1 Comparison of Actual and Theoretical Mutation Frequencies (1%) in FFPE Samples

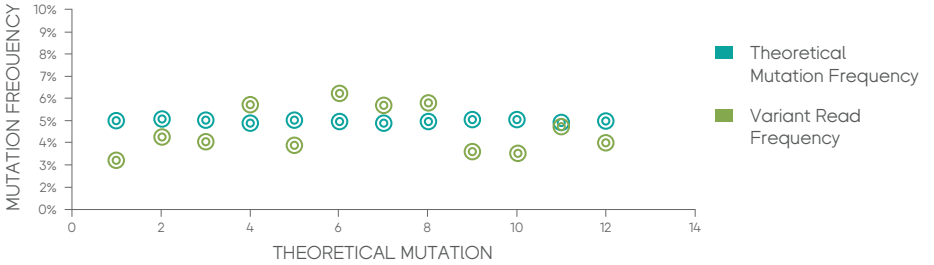


Fig. 1-2 Comparison of Actual and Theoretical Mutation Frequencies (5%) in FFPE Samples

Small Genome Sequencing
Pathogen Detection

Experiment Scheme

Sample: Zymo Research D6305 Microbial Community DNA Standard
Library Prep: NadPrep® Rapid DNA Enzyme Library Preparation Kit v2
Sequencing strategy: SE100 dual barcode sequencing
Objective: To evaluate the platform's ability to identify unknown pathogens

Sequencing Summary

Generated 125M reads, Q30 reached 96%, Q40 exceeded 90%. Results from SM2.0 with OS 4.0 were consistent with universal circularization results.

Analysis Summary

- Comparison of two circularization methods showed similar species detection abundance.
- Pathogen identification results using Microbial Rapid Identification (PFI) were consistent with the species in the standard sample.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
SM2.0+OS4.0	129.49	96.17	90.85	93.72
SM2.0	127.37	95.62	90.17	93.72

Analysis Result

Fig. 2-1 Species detection abundance for different circularization methods

Whole Exome Sequencing

Experiment Scheme

Sample: NA12878
Library Prep: SureSelect XT HS2 DNA Starter Kit, MGIEasy FS DNA Library Prep Kit
Sequencing strategy: PE150 dual barcode sequencing
Objective: To evaluate the platform's ability to detect whole exomes.

Sequencing Summary

Generated 130M reads, Q30 reached 96%, Q40 exceeded 91%.

Analysis Summary

- The metrics for mapping rate, duplication rate, and mismatch rate were better with SM2.0 compared to SM reagents.

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
SM 2.0	130.96	96.64	91.94	97.46

Analysis Result

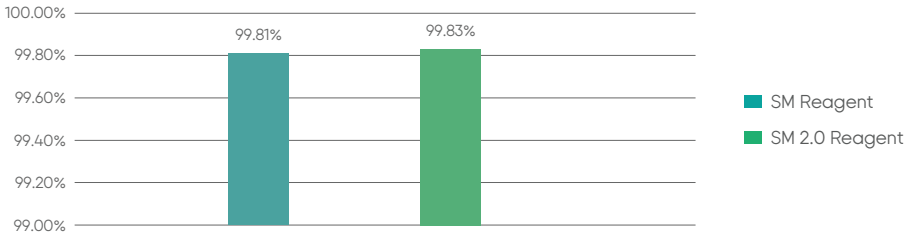


Fig. 3-1 Maping Rate comparasion

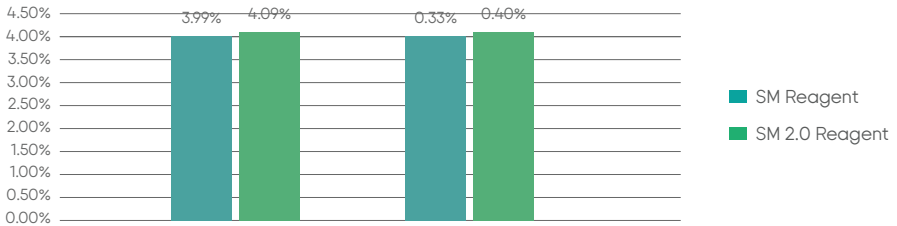


Fig. 3-2 Maping Rate comparasion

Small Genome Sequencing
16s Sequencing

Experiment Scheme

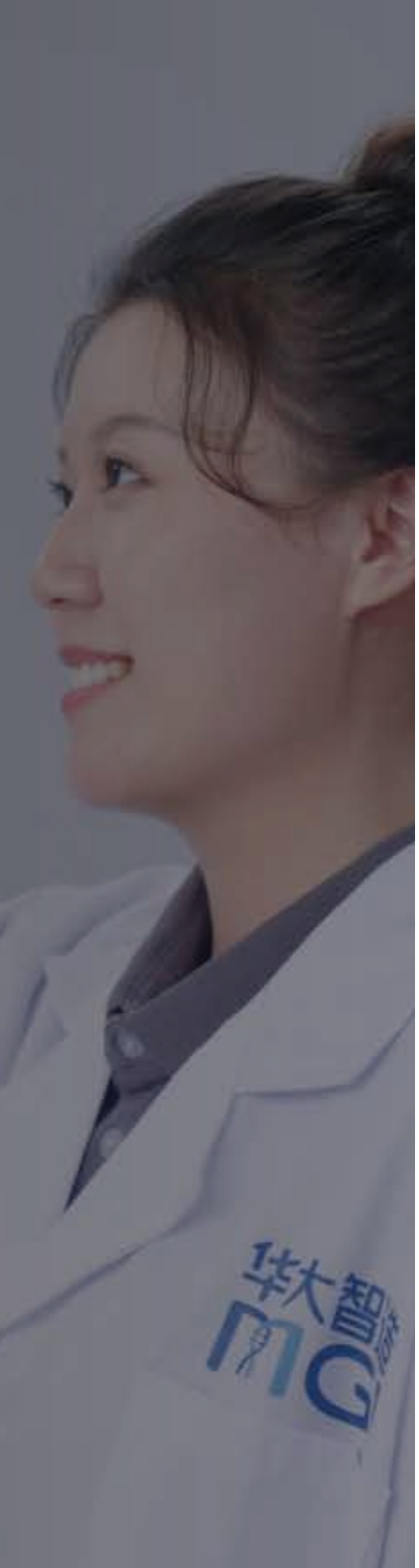
Sample: Zymobiomics D6305 Standard
Library Prep: ATOPlex 16S & 18S rDNA Library Preparation Kit
Test Strategy: App-D PE300 Dual Barcode Sequencing
Test Purpose: To evaluate the platform's detection capability for the 16S amplicon library.

Sequencing Summary

Generated 131M reads, with Q30 reaching 97% and Q40 exceeding 94%; Compared to other platforms, the G99 platform shows a more stable curve and higher quality.

Analysis Summary

- Metrics such as Filtered Rate, Merge Rate Filtered, and Feature Rate Filtered are superior to those of other manufacturers.



Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	SplitRate (%)
SM2.0 App-D PE300	129.49	129.49	90.85	93.72

Q Value Result

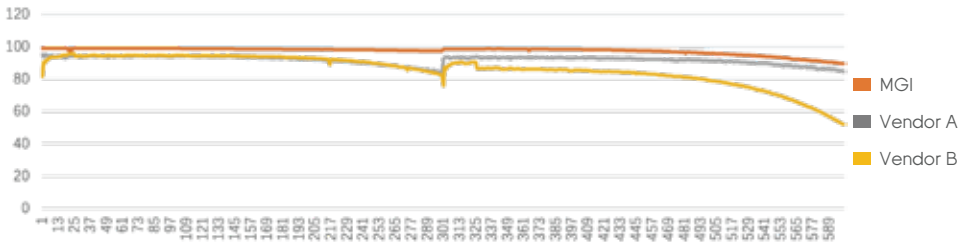


Fig. 4-1 Mean Q per cycle

Analysis Result

	Filtered Rate	MergeRate Filtered	FeatureRate Filtered
DNBSEQ-G99	90.20%	99.77%	89.86%
Vendor A	81.57%	94.29%	74.10%
Vendor B	89.35%	99.85%	89.18%

Forensic Application
DNA Signature Identification

Experiment Scheme

Sample: MGI Signature Identification DNA library
Library Prep: MGIEasy Signature Identification Library Prep Kit
Sequencing strategy: SE10+10+400
Objective: To evaluate the detection rate and consistency rate of SM2.0 reagent for individual identification libraries

Sequencing Summary

- The average total reads for 6 runs is as high as 126M, and the average Q30 for the first 100 cycles is as high as 97%.
- TAT from library prep to analysis is less than 30 hours.

Analysis Summary

- Statistical analysis of key indicators was conducted for 6 runs, and the detection rate and consistency rate of STR sites were better than the standard.

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

Sequencing Result

	Total reads (M)	Q30 (%)	Q40 (%)	First 100 Cycle Q30(%)
Run 1	125.78	67.18	62.52	97.92
Run 2	127.74	66.45	61.09	97.31
Run 3	127.46	64.97	59.27	96.74
Run 4	119.63	64.07	57.30	95.70
Run 5	130.29	66.51	61.14	97.44
Run 6	130.36	65.38	59.99	97.09
Average	126.88	65.76	60.22	97.03

Analysis Result

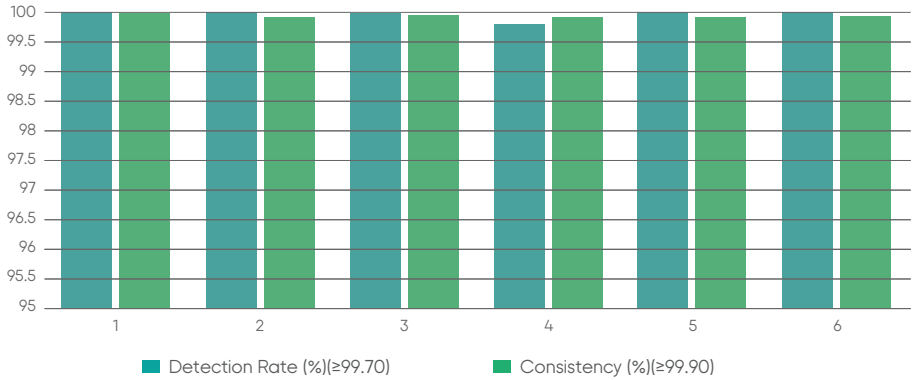


Fig. 5-1 Comparison betwwen Detection Rate(%) and Consistency(%)

Hardware Specifications

Model	DNBSEQ-G99 DNBSEQ-G99A	Outputs FASTQ files Equipped with bioinformatics module for advanced analysis
Dimension (W*D*H)/Net Weight	607x689x657 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)	15-30℃ 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
Sequencer	900-000607-00	DNBSEQ-G99RS
	900-000609-00	DNBSEQ-G99ARS
FCS	940-002649-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCS PE150）
FCL	940-001268-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 FCL SE100/PE50）
	940-001269-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 FCL PE150）
	940-001267-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCL SE100）
	940-001274-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCL PE150）
	940-001716-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCL PE300）
	940-001757-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 FCL SE400）
FCU	940-002776-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCU SE100）
	940-002775-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCU PE150）
	940-002773-00	DNBSEQ-G99 High-throughput Sequencing Set（G99 App-D FCU PE300）
	940-000624-00	DNBSEQ-G99RS Cleaning Reagent Kit（G99 SM FCL）

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

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-D FCL PE150)
940-000525-00	Universal Sequencing Reaction Kit (G99 SM App-D 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 E Series Sequencer

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

DNBSEQ G Series Sequencer

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

DNBSEQ-T1+
Reads per flow cell: 500-2000M
Number of flow cells: 2
Data output: 25 Gb-1.2 Tb

DNBSEQ T Series Sequencer

MGI Tech Co., Ltd.

Building 11, Beishan Industrial Zone,
Yantian District, Shenzhen.CHINA
518083

Version: March 2025 I MGPA0603002-03

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MGI-service@mgi-tech.com

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