



UNLEASH YOUR ULTIMATE SEQUENCING SPEED

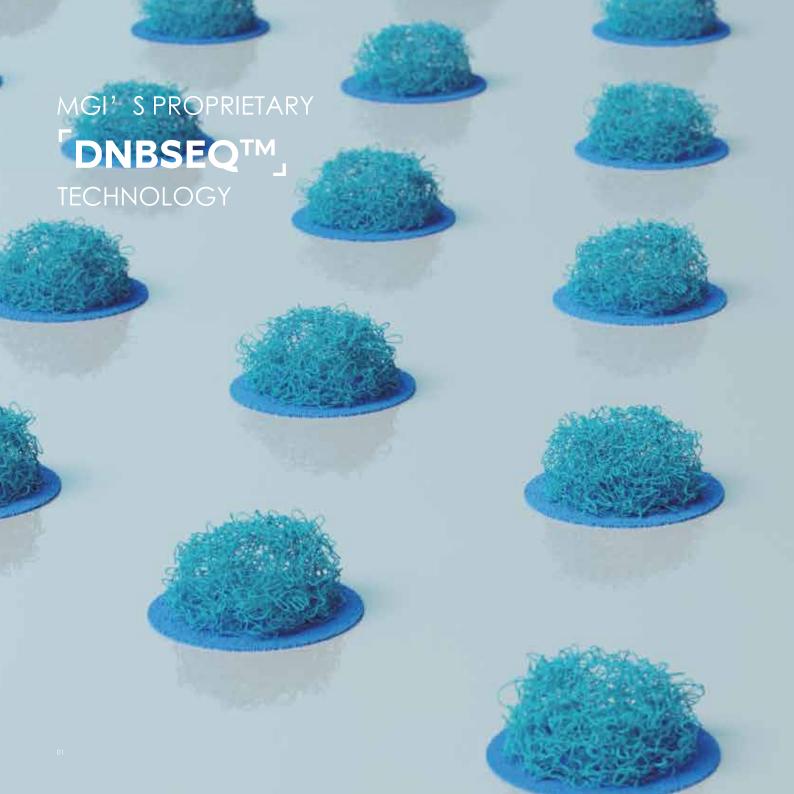
Benchtop Genetic Sequencer

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 sinale machine.





Genetic Sequencer

DNBSEQ-G99

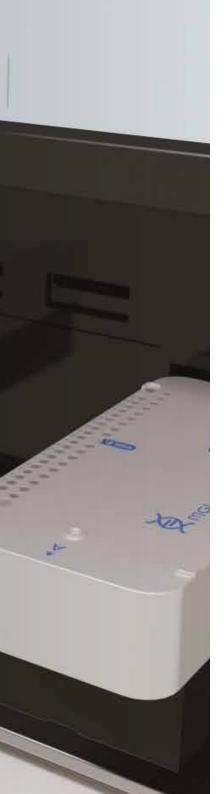


DNBSEQ-G99 is developed based on MGI¹ s core DNBSEQ™ sequencing technology, Enabled by innovations in biochemistry, optics, fluidics, temperature control, and other core systems, DNBSEQ-G99 boasts the fastest speed amongst all medium-to-low throughput sequencers globally. DNBSEQ-G99 is especially applicable 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.



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

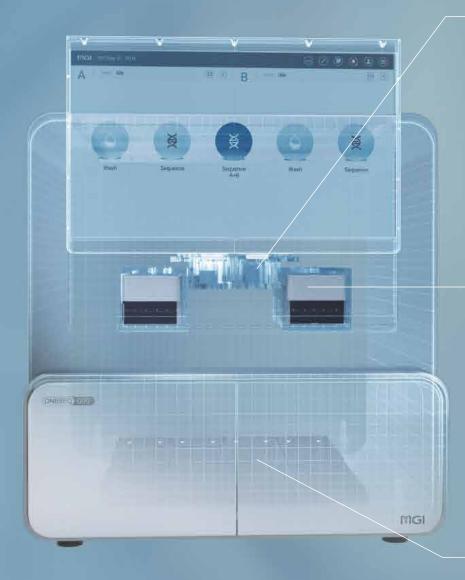


Data Security

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

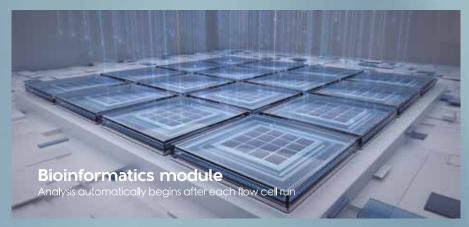
Flexible Customize your run

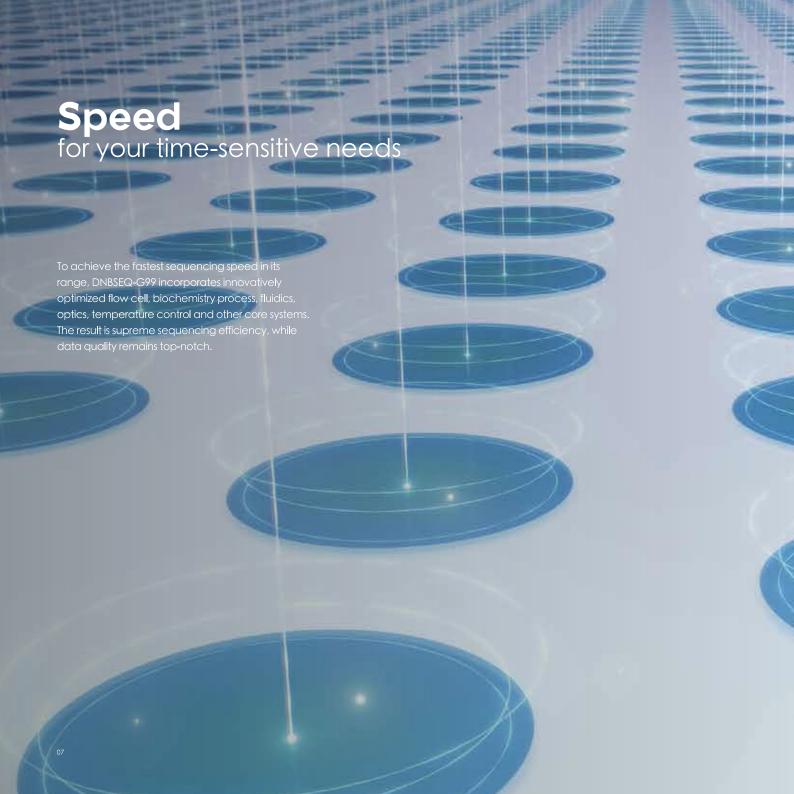
DNBSEQ-G99 is the only medium-to-low throughput sequencer with a dual flow cell loading configuration, providing ultimate flexibility in sequencing throughput. The dual flow cells can be operated with different read lengths independently or concurrently. Three flow cell loading modes are supported on 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.



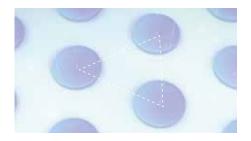












High Density Flow Cell

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



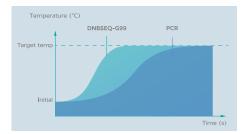
Super Fast Biochemistry

- 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
	Oncology panel	PE100,PE150	Sma l panel: ~1 Gb/sample	24/FC, 48/RUN
▼ Targeted	Hereditary disease sma ll 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
Capture/ Multiplex PCR	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
	Metagenomics for pathogen detection	SE50, SE100	Meta: 20 M reads/sample	4/FC, 8/RUN
Small Genome Sequencing	Microbial WG\$	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 who l e-genome	NIPT	SE50	NIPT/PGS: ~10 M reads/sample	8/FC. 16/RUN
sequencing	PGS	SE50	THE THE GOLD TO MICE GOLD STATE OF THE COLUMN TO THE COLUM	6/1 6/10/NOT
RNA sequencing	Expression profi l ing 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.

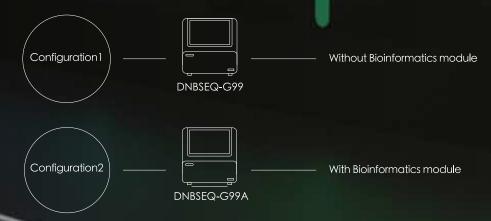
² Recommend method

Performance Parameters

Maximum number of Flow cells	Lanes/ Flow cell	Minimum Effective Reads*/ Flow Cell	Supported Reads Lengths+	Data Output	Q30**	Run Time		
	- 13		SE100/PE50	8~16 G	>90%	5 h		
	- 11		PE150	24~48 G	>85%	12 h		
2	1	20.1	90.44	80 M	APP-C SE100	8-16 G	>90%	5 h
2		50 M	APP-C PE150	24~48 G	>85%	12 h		
			PE300	48~96 G	>85%	30 h		
- 1			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.

Available Models



^{**} 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.

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

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

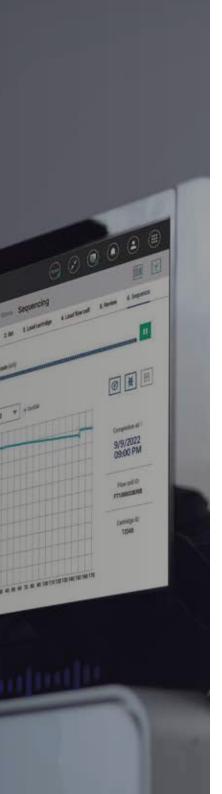
Sequencing Summary

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 %).

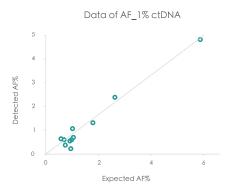


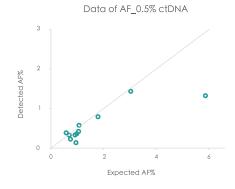


• Sequencing Result

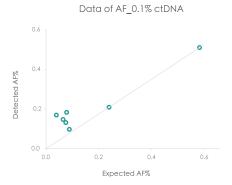
	Total reads (M)	Q30	EstErr(%)	Time (h)
Mean value	126.22	94.00	0.22	9.15
Standard deviation	7.41	0.52	0.02	0.11

• Analysis Result











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

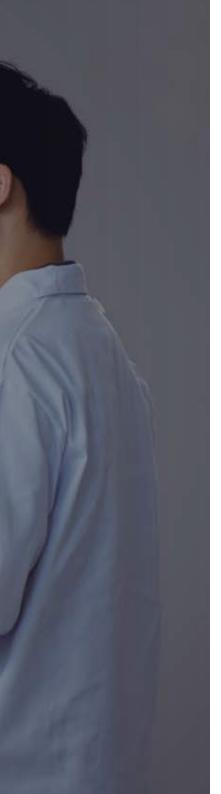
libraries, and data uniformity for targeted methylation regions.

Sequencing Summary

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

Analysis Summary

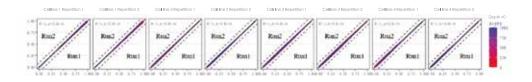
- Highly concordant average methylation fractions (AMF) measured between both runs for all tested samples.
- For results of the same samples on different instruments: AMF of the samples is highly consistent.

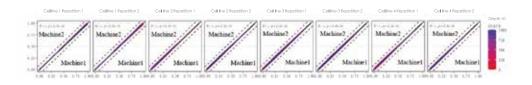


• Sequencing Results

	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







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

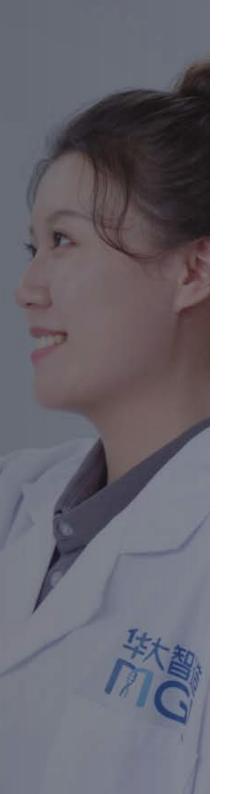
Test Purpose: Assess DNBSEQ-G99 capability for assembling whole bacteriophage genome

Sequencing Summary

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

Analysis Summary

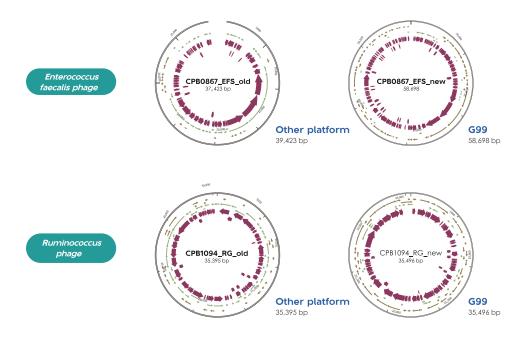
- Conserved protein genes for phage capsid, portal, and terminase were successfully detected in the DNBSEQ-G99 assemblies.
- DNBSEQ-G99 outperforms other platform for bacteriophage whole genome assembly, achieving higher assembly integrity.



• Sequencing Results

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

Analysis Results



Small Genome Sequencing 16s Sequencing

mai

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 R² > 0.99 between parallel sequencing libraries, which showed high consistency of test results.



• 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%.



• Sequencing result

Total	Total reads (M)		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 100 V-240 V Rated frequency 50/60 Hz Rated Power 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	IPXO			
Operating Environment Requirements	Temperature Relative Humidity Atmospheric Pressure Maximum Altitude (above sea level)	19-30°C 20-80 %RH 70 kPa-106 kPa 3000 m		
Computer Configurations	CPU Internal Storage HDD Operating System	Intel 19-10900e 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

^{*} 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-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



DNBSEO-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



DNBSEQ-G400*

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: 35-40 B Number of sides: 6 Data output: 42-72 Tb



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