

Genetic Sequencer

DNBSEQ-G400*



Strengthen your daily sequencing capability



**Flexible, stable, and well-qualified,
offering more choices**

- 2** Flow Cell Types
- 5** Sequencing Modes
- 7** Sequencing Lengths

© About MGI

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. As of December 31, 2022, MGI has more than 2,800 employees, and 36% of whom are R&D personnel. Founded in 2016, MGI operates in more than 90 countries and regions, serving more than 2,000 customers. It has established scientific research and production bases, global training and service network in many countries and regions around the world. MGI is one of the two companies in the world that can independently develop and mass-produce clinical gene sequencers of low, medium and high-throughput from Gb to Tb. Providing real-time, comprehensive, life course solutions, its vision is to lead life science innovation.

© About

DNBSEQ-G400*

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Flexible, high quality
Activate your daily sequencing capability

Product Introduction

DNBSEQ-G400* is a versatile benchtop sequencer providing users with comprehensive, flexible and efficient sequencing options. The high-throughput sequencing reagents (StandardMPS), provide more choices for users in pursuing higher sequencing quality. With stable high-intensity signals and random low sequencing error rate, exhibit excellent performance in scientific and clinical applications.

DNBSEQ-G400* sequencer supports a wide range of applications including scientific research, clinical research, disease prevention, environment studies and agriculture, etc., increasing the popularity of high-throughput sequencing systems in medical and scientific research fields.

Multiple choices

- **Two flow cell types**

FCL 1800M reads, FCS 550M reads

- **Dual flow cell system**

One or two flow cells covering 550M~3600M reads/run

High quality

- **Advantages of DNBSEQ™ technology**

Extremely low PCR amplification error accumulation, low amplification bias, low index hopping

High speed

- **Short sequencing time**

FCS SE100 from DNB to FASTQ takes only 13 hours

Various applications

- **Wide range of application fields**

Satisfy both scientific research and clinical test

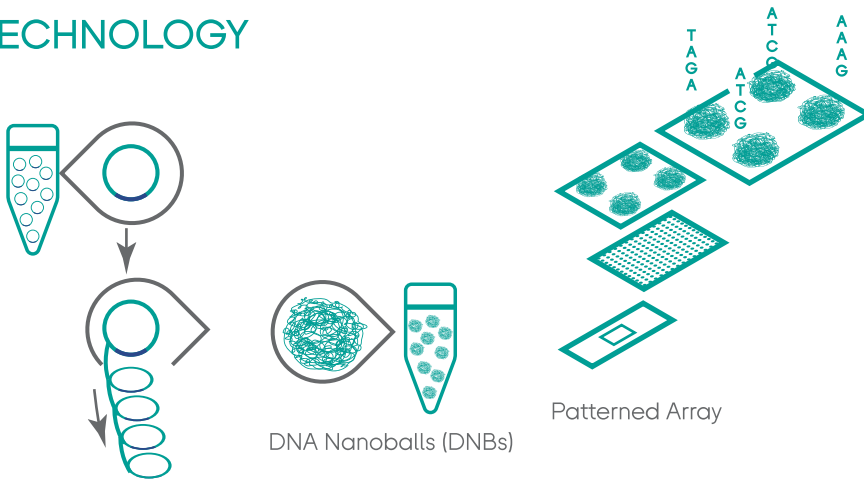
DNBSEQ-G400* is built with a dual flow cell system that can perform different types of flow cell individually in a single run, giving users a more flexible and streamlined sequencing experience.



Sequencer	Reagent type	FCS	FCL
DNBSEQ-G400RS*	StandardMPS	●	●
DNBSEQ-G400*	StandardMPS	●	●

© Technical principle

MGI'S PROPRIETARY 「DNBSEQ™」 TECHNOLOGY

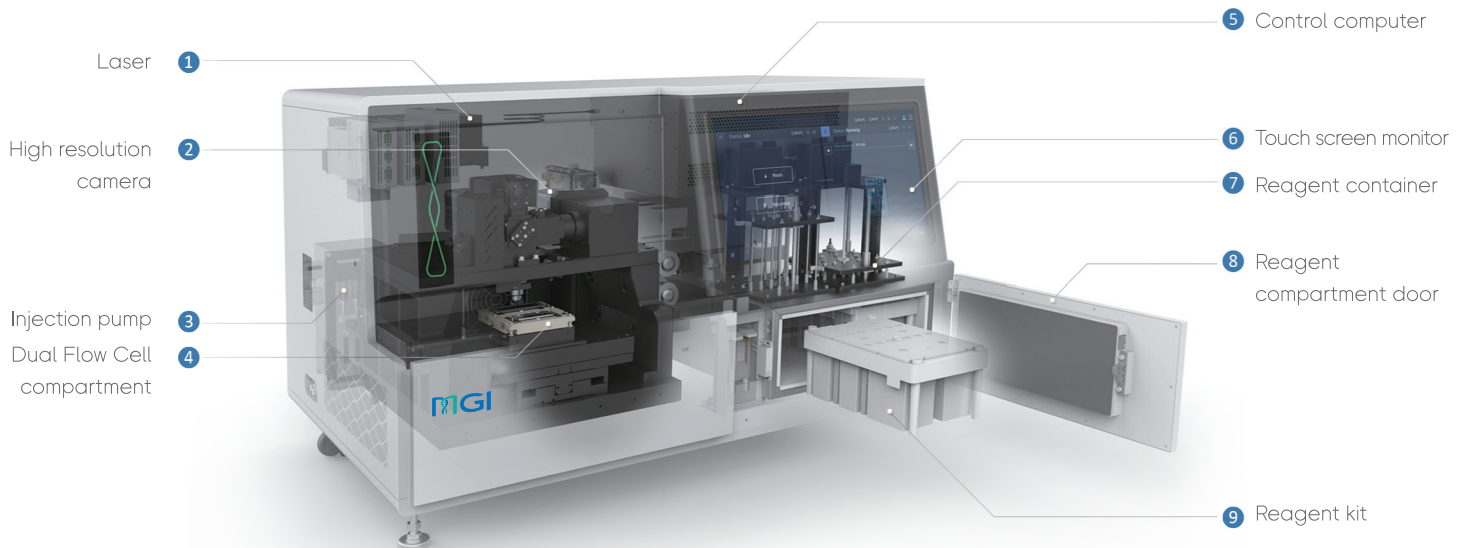


- ↑ INCREASED ACCURACY
- ↓ DECREASED DUPLICATES
- ↓ REDUCED INDEX HOPPING

DNA Nanoball sequencing technology – No accumulation of amplification errors

© Hardware Platform

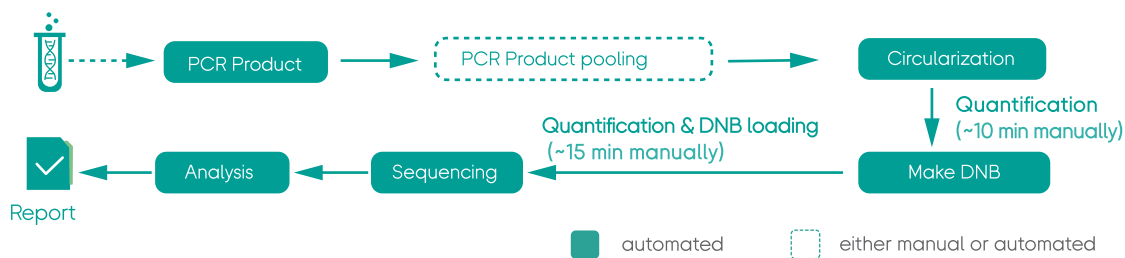
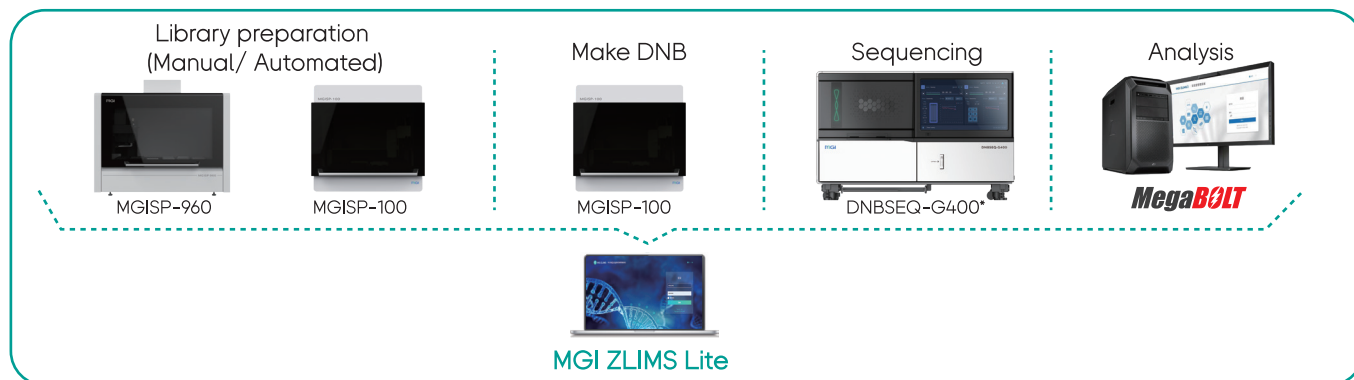
DNBSEQ-G400* sequencer utilizes an innovative flow cell system which can support various sequencing modes and an optimized optical and biochemical system that enables the whole sequencing process to be completed within a short period of time, offering the user a simplified and streamlined sequencing experience.



Packages

Versatile Library Prep, Sequencing & Analysis Package

Genetic Sequencer DNBSEQ-G400RS* 2006A fully automated workflow & all scenarios applicable



⊙ Performance Parameters

Reagent Type	Flow Cell Type	Effective Reads /Flow Cell*	Read Lengths	Data Output /Flow Cell	Run Time**	Q30***
Standard MPS	FCS	550M	SE100	55G	13H	>85%
			PE100	110G	26H	>85%
			PE150	165G	37H	>85%
	FCL	1500-1800M	PE300	180G	98H	>80%
			SE50	75-90G	14H	>90%
			SE100	150-180G	25H	>90%
			PE50*	150-180G	25.2H	>90%
			PE100	300-360G	38H	>85%
			PE150	450-540G	56H	>85%
			SE400	600-720G	109H	>70%
PE200	600-720G	107H	>75%			

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

** Run time was calculated based on dual flow cell mode, and includes sample loading, sequencing, base calling and data processing

*** The percentage of base above Q30 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.

*This read length is for IVD use only.

© Adapted Applications

Application Type	Recommended Read Length	Recommended sample numbers for a single run on DNBSEQ-G400*				
		1*FCS 550M reads	2*FCS 1100M reads	1*FCL 1800M reads	1*FCL+1*FCS 2350M reads	2*FCL 3600M reads
NIPT 10 M reads/sample	SE50/SE100	44 Samples	88 Samples	144 Samples	188 Samples	288 Samples
Small RNA 25 M reads/sample	SE50	/	/	58 Samples	/	116 Samples
RNA-Seq 25 M reads/sample	SE50	/	/	58 Samples	/	116 Samples
Metagenomics for Pathogen Detection 20 M reads/sample	SE50/SE100	22 Samples	44 Samples	72 Samples	94 Samples	144 Samples
Single cell RNA-Seq 10K cells, 50K reads/cell, 500 M reads/sample	PE100	1 Sample	2 Samples	2 Samples	3 Samples	4 Samples
Oncology Panel 10 Gb/sample (5000×, 1 Mb panel)	PE100/PE150	14 Samples	28 Samples	44 Samples	58 Samples	88 Samples
Microbial WGS 1 Gb/sample		132 Samples	264 Samples	432 Samples	564 Samples	864 Samples
Transcriptomics 6 Gb/sample	PE150	22 Samples	44 Samples	72 Samples	94 Samples	144 Samples
WES 100× average sequencing depth, 15 Gb/sample		8 Samples	16 Samples	28 Samples	36 Samples	56 Samples
WGS 30× average sequencing depth, 100 Gb/sample		1 Sample	2 Samples	4 Samples	5 Samples	8 Samples
WGBS 30× average sequencing depth, 120 Gb/sample		1 Sample	2 Samples	3 Samples	4 Samples	6 Samples
Oncology Targeted Methylation Panel 5 Gb (2000×, 0.5 Mb panel)		26 Samples	52 Samples	86 Samples	112 Samples	172 Samples
Forensic Identification 1 M reads/sample	SE400	/	/	1440 Samples	/	2880 Samples
16S 0.1 M reads/sample	PE300 (300M reads)	900 Samples	1800 Samples	/	/	/

* Sample numbers are calculated considering PE pooling variation and applications. For reference only.

Application Cases

Pathogen detection

Case 1: Pathogen detection - COVID-19

Sample: 6 serial dilutions of extracted RNA from isolated culture were subjected to ATOplex Sequencing and RT-qPCR.

Sequencing Platform: DNBSEQ-G400*

Results:

Table 1 Summary of ATOplex Sequencing

ID	Raw reads	SARS-CoV-2 mean depth	100X SARS-CoV-2 coverage	CT value of RT-qPCR	SARS-CoV-2%#
Dilution 10 ⁻¹	9,455,876	61102.3	99.8%	24.3	99.95%
Dilution 10 ⁻²	10,232,235	59012.7	99.8%	27.1	99.43%
Dilution 10 ⁻³	9,122,357	31140.3	99.8%	30.6	94.82%
Dilution 10 ⁻⁴	5,965,846	2951.4	99.8%	33.5	63.13%
Dilution 10 ⁻⁵	4,536,254	1036.6	95.3%	36.9	15.36%
Dilution 10 ⁻⁶	17,563,253	206.9	75.4%	NO CT	1.87%
Negative control	5,245,547	0.3	0.0%	NO CT	0.00%

#SARS-CoV-2 detection; SARS-CoV-2% < 0.05%, negative; SARS-CoV-2% > 0.1%, positive; SARS-CoV-2% = 0.05-0.1%, gray zone.

Conclusion:

ATOplex Sequencing can detect SARS-CoV-2 with 10 gradient dilutions (about 10-100 copies per ml) and assemble nearly full-length genome with 10 gradient dilutions (about 100-1000 copies per ml).

WGS

Case 2: Human WGS

Sample: 1025 DNA samples of Han Chinese in the Central Plains

Library: MGIEasy PCR-Free DNA Library Preparation Set

Sequencing Strategy: DNBSEQ-G400* FCL PE150

Results:

Table 2-1 Sequencing data quality

		Min	Median	Mean	Max	High quality	PASS
Total Reads		601727956	726056164	726494436	952285662	/	/
Mean Reads Length		150	150	150	150	/	/
Reads*	R1	100%	100%	100%	100%	=100%	=100%
	R2	100%	100%	100%	100%	=100%	=100%
Q30	R1	87.21%	90.43%	90.34%	92.91%	≥85%	≥80%
	R2	84.22%	89.79%	89.56%	92.00 %	≥85%	≥80%

*passed filter

Table 2-2 Key indicators of sequencing data analysis

	Min	Median	Mean	Max	High quality	PASS
Properly Paired	96.38%	98.27%	98.26%	98.88%	≥95%	≥90%
Raw Depth (GRCh38)	29.23	35.27	35.29	46.25	≥30	≥10
Mapping Rate	97.81%	99.99%	99.99%	100.00%	≥99%	≥95%
Duplication	0.25%	0.88%	0.99%	3.22%	/	/
Mean Insert Size	262.38	329.40	332.64	382.18	/	/
Insert Size SD	51.23	71.40	71.75	82.80	/	/

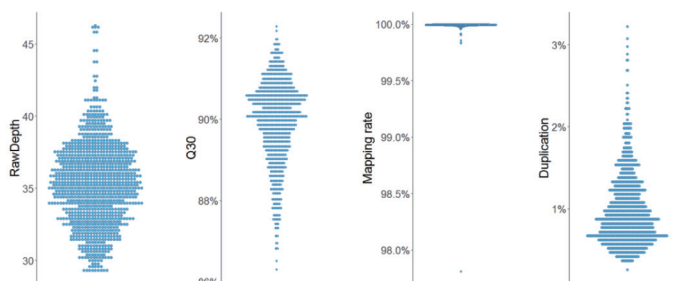


Figure 5. Excellent overall sequencing quality

Conclusions:

- 1) The raw depth of more than 98% of the samples is above 30X, with a lowest raw depth of 29.226X;
 - 2) The Q30 ratios of the bases in all samples are over 85%;
 - 3) Except for one sample (97%), the mapping rates of all other samples are greater than 99.5%;
 - 4) More than 95% of the samples have a duplication rate of less than 2%, with the highest rate also less than 4%;
- The DNBSEQ-G400* platform can produce high-quality WGS sequencing data with high Q30 and mapping rate, and low duplication rate, which can generate accurate and reliable whole-genome sequencing data.

Single-cell sequencing

Case3: DNBelab C4 RNA sequencing

DNBelab C Series Single-cell Omics Package is comprised of DNBelab C4 Pocket Single-Cell Lab, DNBelab C Series Single-cell Library Preparation Set, DNBSEQ™ sequencing platform and Single-cell Analysis Suite, all as part of a portable, instant, and one-stop single-cell research workflow.

Sample: Human 293T cell line: Murine 3T3 cell line =1:1

Library Preparation: DNBelab C Series Single-Cell Library Preparation Set

Sequencing Strategy: DNBSEQ-G400* FCL PE100

Data Results:

Table 3-1 Cell data results

Estimated Number of Cells	2,544
Estimated Number of Human Cells	1,309
Estimated Number of Mouse Cells	1,155
Fraction Reads in Cells	79.70%
Fraction Reads in Human Cells	80%
Fraction Reads in Mouse Cells	79.30%
Mean Reads per Cell	40,882
Mean Reads per Human Cell	41,485
Mean Reads per Mouse Cell	39,518
Median UMI Counts per Human Cell	28,915
Median UMI Counts per Mouse Cell	26,411
Median Genes per Human Cell	6,168
Median Genes per Mouse Cell	5,395

Table 3-2 Sequencing data results

Number of Reads	172,491,759
Reads Pass QC	148,377,085
Reads with Valid Barcodes	148,377,085
Filtered Reads with Failed Barcodes	23,040,453
Filtered Reads with Low Quality	1,074,221
Filtered Reads with Unknown Sample Barcodes	0
Q30 Bases in Cell Barcode	89.30%
Q30 Bases in Sample Barcode	0.00%
Q30 Bases in UMI	86.50%
Q30 Bases in RNA Read	79.80%

Table 3-3 Mapping results

Reads Mapped Confidently to Genome	95.20%
Reads Mapped Confidently to Gene	95.10%
Reads Mapped Confidently to Exonic Regions	66.30%
Reads Mapped Confidently to Intronic Regions	2.80%
Reads Mapped Antisense to Gene	5.70%

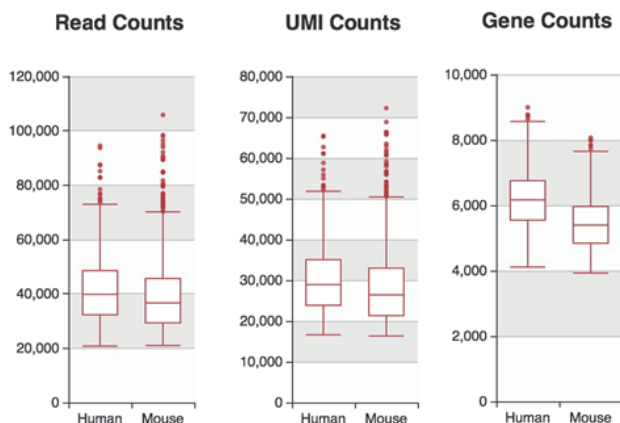


Figure 6. Data distribution

Conclusion:

The data output and quality performance of MGI DNBelab C4 single-cell library preparation products on the DNBSEQ-G400* platform meet expectations.

Appendix

© Hardware Parameters

	Model*	Intended Market
Model*	DNBSEQ-G400*	IVD
	DNBSEQ-G400RS*	RUO
Dimensions	1086 mm(L)×756 mm(W)×710 mm(H)	
Net Weight	200 kg	
Power	Type	100-240 V, 50/60 Hz
	Rated Power	1200 VA
Operating Environment Requirements**	Temperature	19°C-25°C
	Relative Humidity	20% RH-80% RH, non-condensing
	Atmospheric Pressure	70 kPa-106 kPa
	Waterproof Rating	IPX0
Control Computer Configurations***	CPU	Intel Xeon E5 10Core * 2 2.2GHz
	Internal Storage	256 GB RAM
	HDD	16 TB
	SSD	480 GB
	Operating System	Windows 10 Enterprise

* Only for model classification

** For indoor use only; The Flow Cells can be stored and transported at room temperature. No liquid medium is needed

*** Supporting the configurations and system updates of the computer

© Ordering Information

RUO*

Cat.No.	Product Name (Model)		User Manual
900-000170-00	FCL	Genetic Sequencer (DNBSEQ-G400RS*)	H-020-000094-00 NBSEQ-G400RS Genetic Sequencer User Manual_English_RUO_WH
1000016941		DNBSEQ-G400RS* High-throughput Sequencing Set (FCL SE50)	SOP-013-B01-082 DNBSEQ-G400RS High-throughput (Rapid) Sequencing Set User Manual
1000016943		DNBSEQ-G400RS* High-throughput Sequencing Set (FCL SE100)	
1000016946		DNBSEQ-G400RS* High-throughput Sequencing Set (FCL SE400)	
1000016950		DNBSEQ-G400RS* High-throughput Sequencing Set (FCL PE100)	
1000016952		DNBSEQ-G400RS* High-throughput Sequencing Set (FCL PE150)	
940-000151-00		DNBSEQ-G400RS* High-throughput Sequencing Set (FCL PE200)	
1000016998		DNBSEQ-G400RS* High-throughput Sequencing Set (Small RNA FCL SE50)	
1000016978		DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (FCS SE100)	
1000016980		DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (FCS PE100)	
1000016982	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (FCS PE150)	SOP-013-B01-050 High-throughput Sequencing Set (App-A) User Manual	
940-000152-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (FCS PE300)		
1000016993	DNBSEQ-G400RS* High-Throughput Sequencing Set (App-A FCL SE50)		
1000016994	DNBSEQ-G400RS* High-Throughput Sequencing Set (App-A FCL PE100)		
1000016995	DNBSEQ-G400RS* High-Throughput Sequencing Set (App-A FCL PE150)	H-T-042 DNBSEQ-G400RS High-throughput Rapid Sequencing Set (G400 SM Integration) User Manual	
940-000228-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (G400* SM App-A DB FCS PE150)		
940-000229-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (G400* SM App-A DB FCS PE100)		
940-000230-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (G400* SM App-A FCS SE100)		
940-000231-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (G400* SM DB FCS PE150)		
940-000232-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (G400* SM DB FCS PE100)		
940-000233-00	DNBSEQ-G400RS* High-throughput Rapid Sequencing Set (G400* SM DB FCS SE100)		
940-000622-00	Sequencer Cleaning Cartridge	Sequencer Cleaning Cartridge (DNBSEQ-G400*)	There is no manual for consumables, and the instructions for using the cleaning cartridge refer to the manual of the sequencing set

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

*All Products labeled solely for research use only which means it should not be used for clinical diagnosis.

IVD

Cat.No.	Product Name	Model	User Manual	
900-000168-00	Genetic Sequencer	DNBSEQ-G400*	H-020-000093-00 DNBSEQ-G400 Genetic Sequencer User Manual_English_IVD_WH	
1000022478	FCL	Universal Sequencing Reaction Kit	SOP-013-B01-130 Universal Sequencing Reaction Kit Instructions for Use (G400 SM FCL CE)	
1000022479		Universal Sequencing Reaction Kit		
1000022480		Universal Sequencing Reaction Kit		
1000022481		Universal Sequencing Reaction Kit		
1000022482		Universal Sequencing Reaction Kit		
1000022483	FCS	Universal Sequencing Reaction Kit	SOP-013-B01-128 Universal Sequencing Reaction Kit User Manual (G400 SM FCS CE)	
1000022484		Universal Sequencing Reaction Kit		
1000022485		Universal Sequencing Reaction Kit		
1000022549	FCS	Universal Sequencing Reaction Kit	SOP-013-B01-126 Universal Sequencing Reaction Kit User Manual	
1000022550		Universal Sequencing Reaction Kit		
1000022551		Universal Sequencing Reaction Kit		
1000017812	FCL	Universal Sequencing Reaction Kit	SOP-013-B01-134 Universal Sequencing Reaction Kit User Manual	
1000017813		Universal Sequencing Reaction Kit		
1000017814		Universal Sequencing Reaction Kit		
1000017815		Universal Sequencing Reaction Kit		
1000017816		Universal Sequencing Reaction Kit		
940-000204-00	FCS Integration	Universal Sequencing Reaction Kit	H-T-040 Universal Sequencing Reaction Kit Instructions for Use (G400 SM Integration)	
940-000205-00		Universal Sequencing Reaction Kit		
940-000206-00		Universal Sequencing Reaction Kit		
940-000207-00		Universal Sequencing Reaction Kit		
940-000208-00		Universal Sequencing Reaction Kit		
940-000209-00		Universal Sequencing Reaction Kit		
940-000622-00	Sequencer Cleaning Cartridge	Sequencer Cleaning Cartridge	DNBSEQ-G400*	There is no manual for consumables, and the instructions for using the cleaning cartridge refer to the manual of the sequencing set

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

© 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.

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