

Công nghệ DNBSEQ – thiết bị giải trình tự MGI

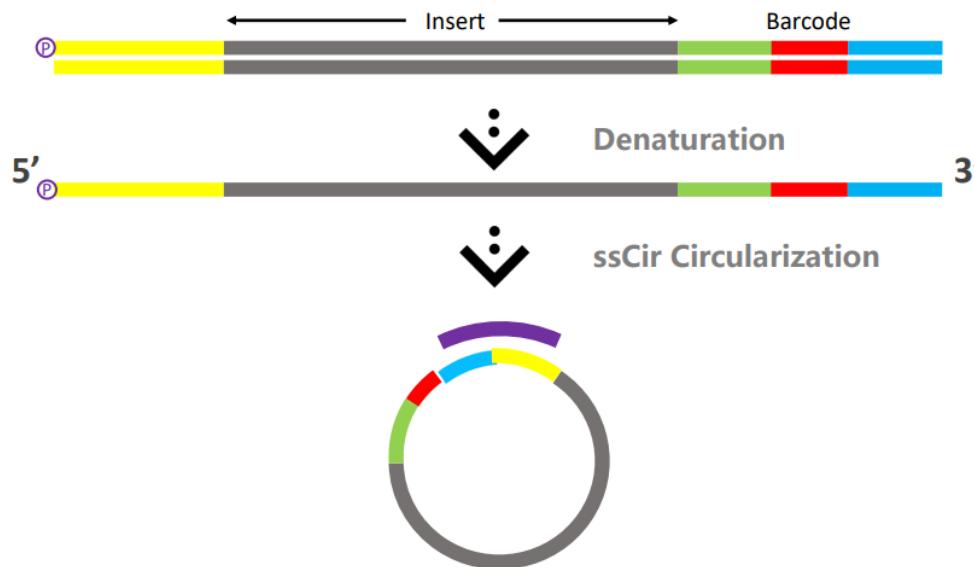
Ứng dụng trong phân tích hệ gen vi khuẩn và megenome vi khuẩn



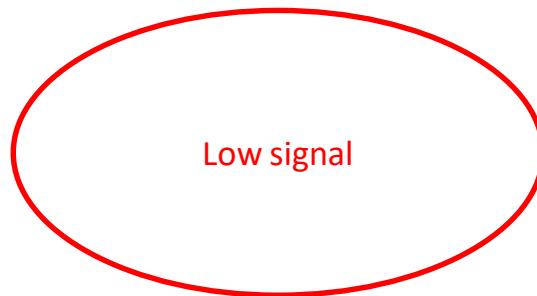
DNBSEQ: DNA NANOBALL SEQUENCING (giải trình tự quả cầu DNA có kích thước nano)

III DNBSEQ™ technology principle — Circularization

Circularization

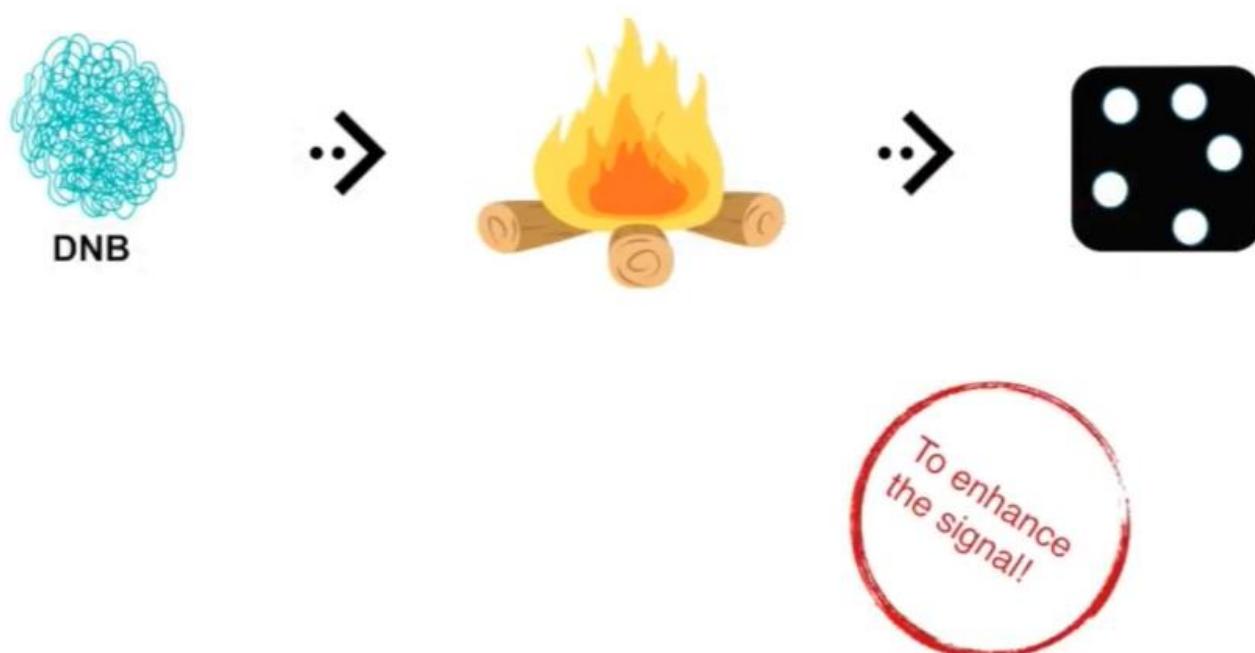


Tại sao chúng ta cần DNA nanoball



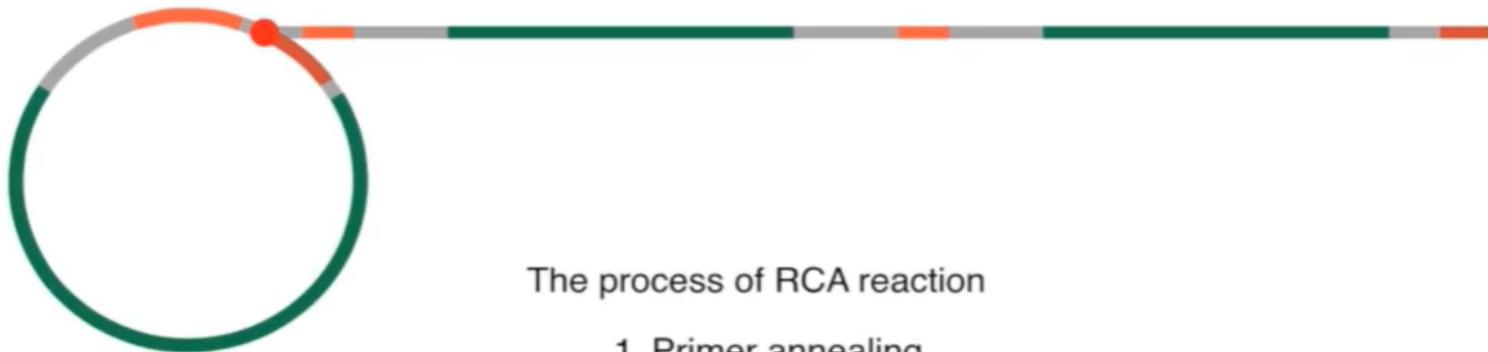
Low signal

Tại sao chúng ta cần DNA nanoball



Phản ứng tạo DNA Nanoball

RCA: Rolling Circle Amplification



The process of RCA reaction

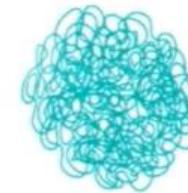
1. Primer annealing
2. Extension
3. Displacement of DNA strand
4. Continue extension

Phản ứng tạo DNA Nanoball

RCA: Rolling Circle Amplification



.....



- Based on the original template
- Linear amplification
- Low amplification bias
- No error accumulation

★ More accurate data
> 99.9% SNP Precision/Sensitivity
> 99% Indel Precision/Sensitivity

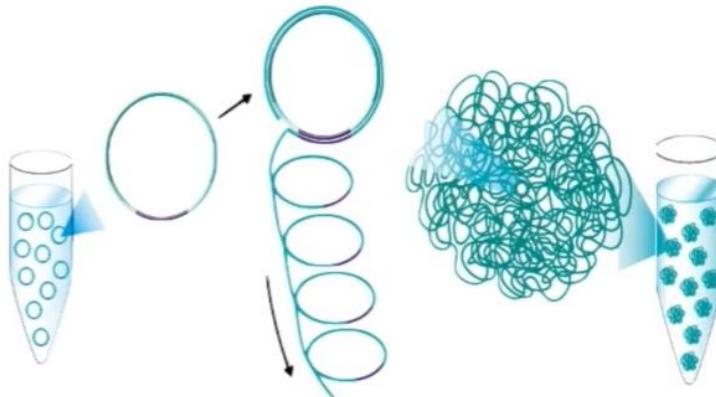
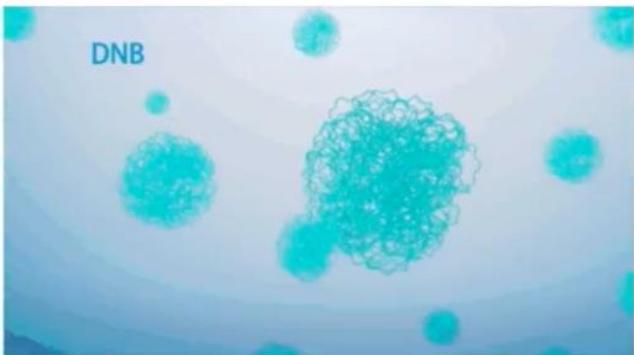
Phản ứng tạo DNA Nanoball



RCA: Rolling Circle Amplification

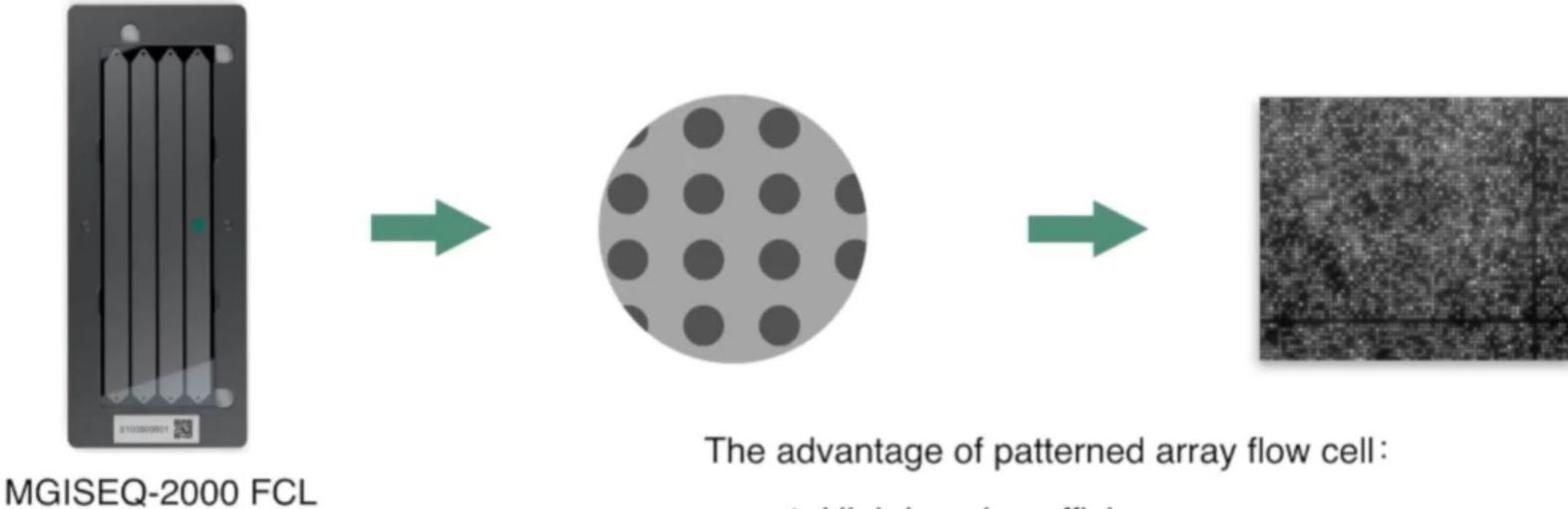
From ssCirDNA to DNBs

From 1 copy to 300-500 copies



Patterned array flow cell and DNA loading

Patterned array flow cell



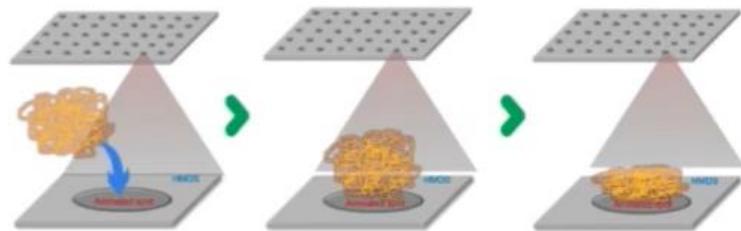
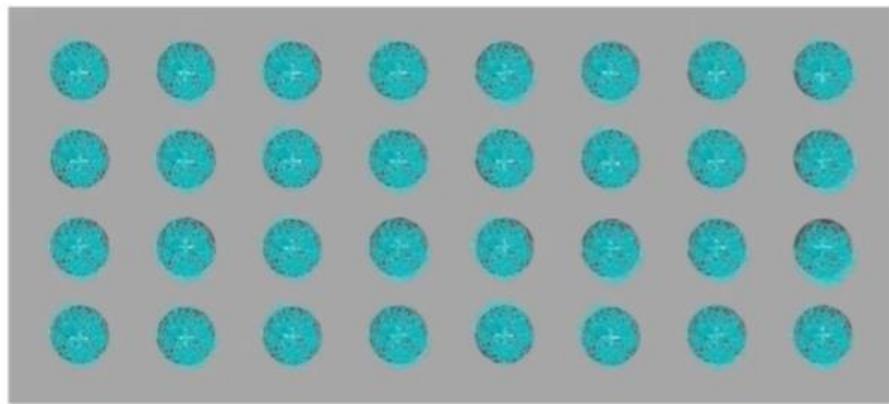
MGISEQ-2000 FCL

The advantage of patterned array flow cell:

1. High imaging efficiency
2. High density
3. High sequencing accuracy

Patterned array flow cell and DNA loading

DNB loading



The principle of DNB loading:

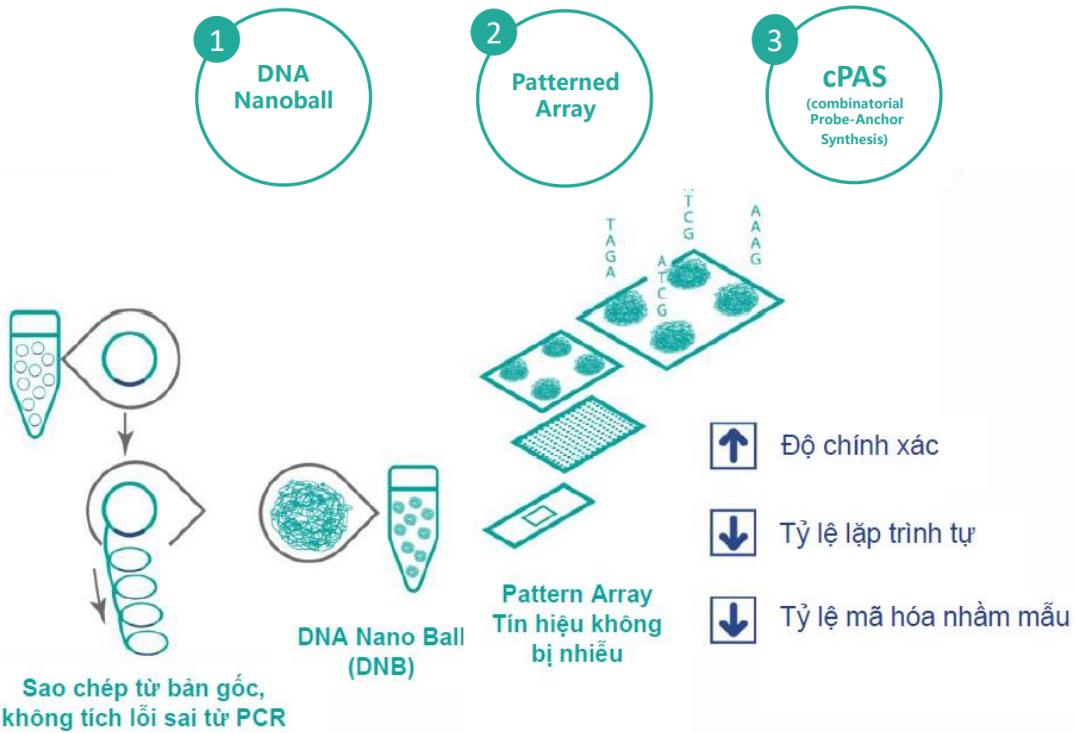
1. Sedimentate by gravity
2. Attracted to bind the spot

3. Combined with spot point under van der Waals force
4. Protein embedding

CÔNG NGHỆ DNBSEQ™ TECHNOLOGY

everlife
Research Instruments

华大智造
MG



- Độ chính xác cao 99.4%, độ nhạy cao 98.8%
- Tiết kiệm chi phí đầu tư và vận hành
- Nền tảng mở có thể sử dụng kit chuẩn bị thư viện của bên thứ 3

Complete DNBSEQ Product Portfolio



**E Series: Low-Throughput
Accessible for versatile
applications**

E25



G99



G50



G400



T7



T20×2



Targeted Gene Sequencing,
Gene expression,
Small WGS
(microbe, virus)

Targeted Gene Sequencing,
WES, Methylation sequencing,
Transcriptome Sequencing,
Low-pass WGS,
small WGS
(microbe, virus)

Low-pass WGS,
Metagenomics,
Targeted Gene Sequencing,
Small WGS
(microbe, virus),
Transcriptome sequencing

Large WGS, Single-cell sequencing, large panel sequencing, Transcriptome sequencing, Methylation sequencing, WES, 16s sequencing, Stereo-seq, Small RNA-seq, Low-pass WGS

Large WGS, Deep WES, Transcriptome sequencing, Large panel sequencing, Single-cell sequencing, Stereo-seq

T20×2 : 42,000-72,000Gb

T7* : 1,160-7,000Gb

G400: 55-1,440 Gb

G50: 10-150 Gb

G99: 8-48 Gb

E25 :
2.5-7.5 Gb

DNBSEQ – Q40

Sample name	Total Reads (M)	Q30(%)	Q40(%)	Split Rate(%)	ESR(%)	Mapping Rate(%)	Avg Error Rate (%)
G99-SM	119.18	94.82	/	98.36	78.76	99.05	0.27
G99-SM 2.0	135.08	97.26	93.36	98.35	89.27	99.21	0.14
G400-SM	506.83	95.2	/	98.95	84.21	99.83	0.16
G400-SM 2.0	532.12	97.98	94.77	98.98	88.38	99.88	0.09
T7-SM	6610.39	96.84	/	99.2	83.68	99.36	0.15
T7-SM 2.0	6972.46	97.09	92.5	99.2	82.73	99.85	0.14

Genetic Sequencer DNBSEQ-E25



DNBSEQ-E25 is a portable and easy-to-use sequencer designed to run sequencing and get the report on the go. The E25 has incorporated new features, including the **microfluidic based flow cell**, **integrated CMOS detection module**, **self-luminous dye**, and **computing module**, which make sequencing on the go feasible.



Ready to Use in 10 Minutes!

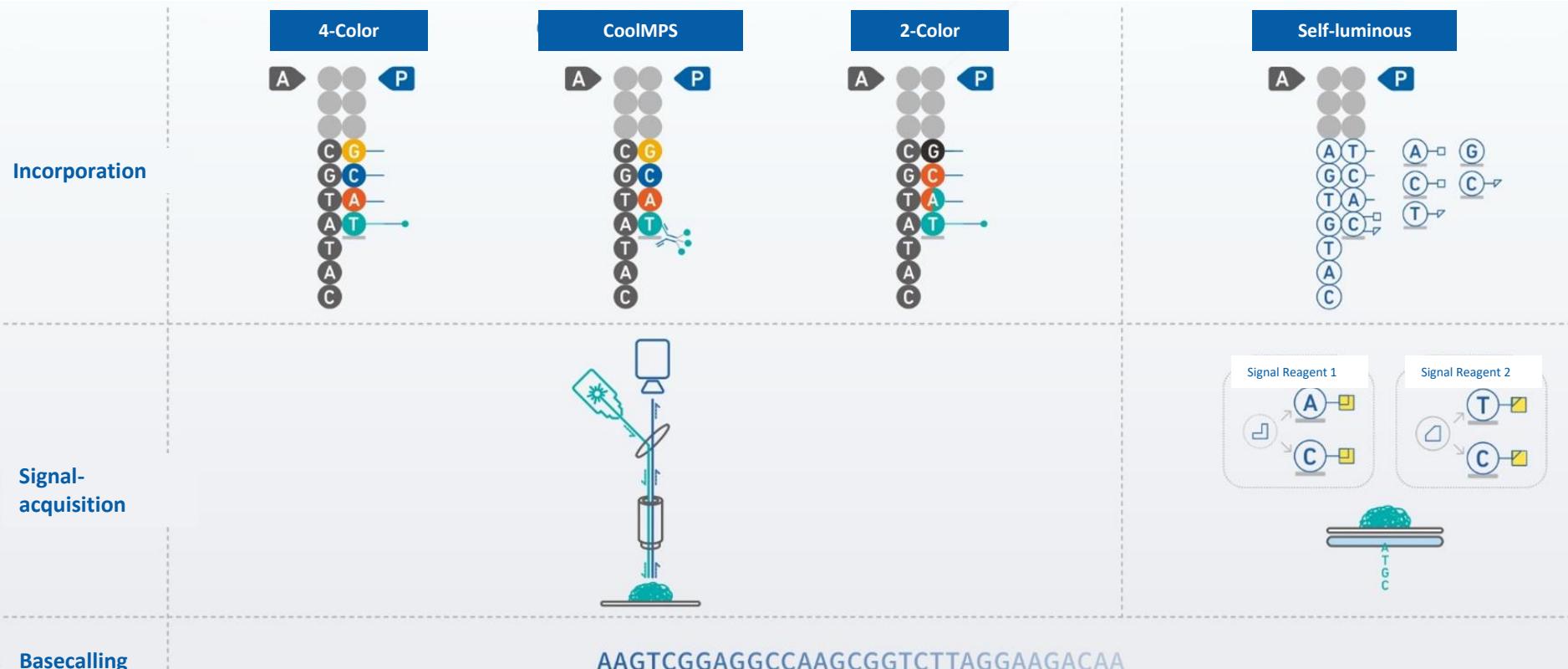
Easy-to-use cartridge
No setup required



Sample to Report in One System

Built-in bioinformatics enables full workflow from sample to report

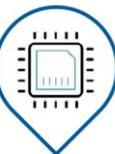
E-series: Unique self luminescence based techniques



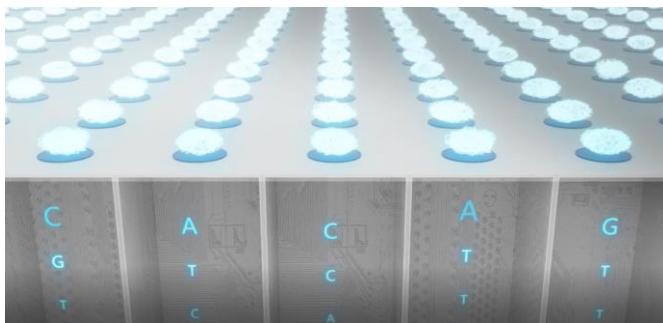
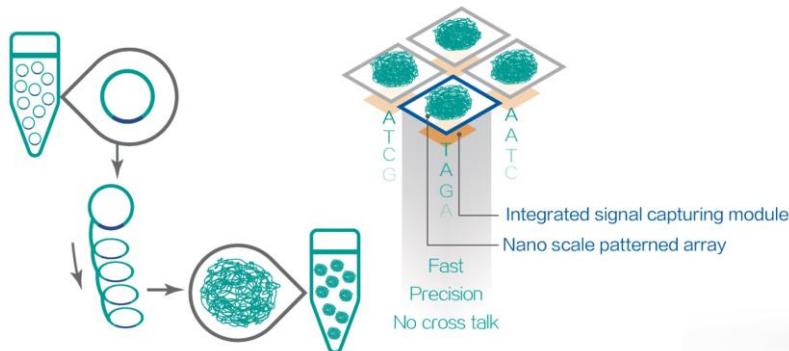
Integrated Reagent Cartridge and Flowcell



DNBSEQ™
core technology



Integrated flow cell
Extreme innovation



Self-luminescence based chemistry

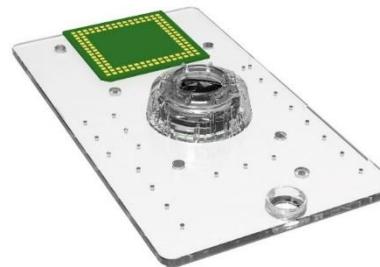
No excitation source required for sequencing, instrument
weighs less than 50 lbs, easy installation and portable

Microfluidics based flow cell

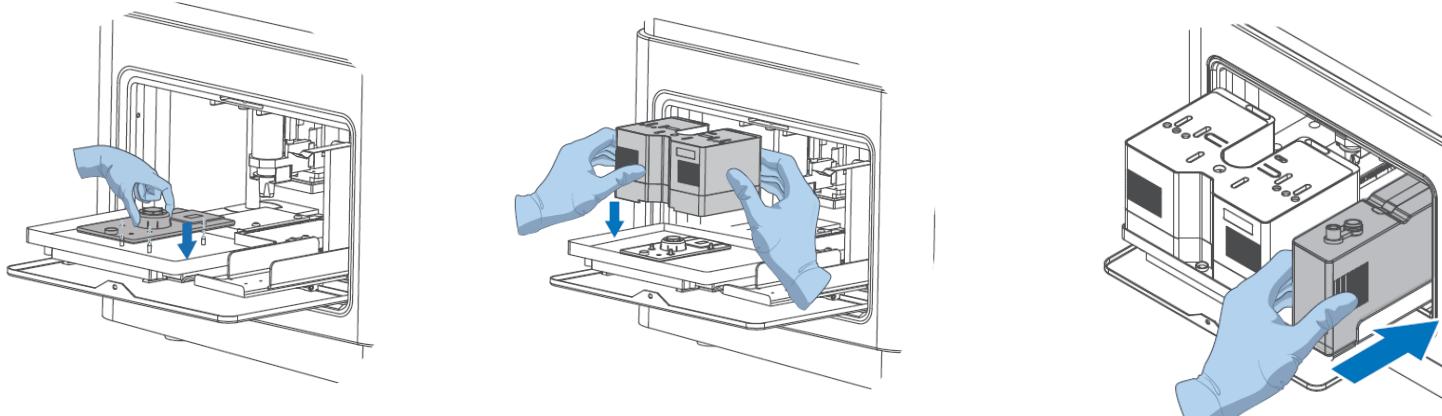
Reagents enter flowcell directly from reagent cartridge, no
instrument wash required between runs

Integrated CMOS module

Base signal can be captured directly without complicated optics



DNBSEQ-E25 : Portable Sequencer with Versatile Capability



DNBSEQ-E25 : Portable Sequencer with Versatile Capability

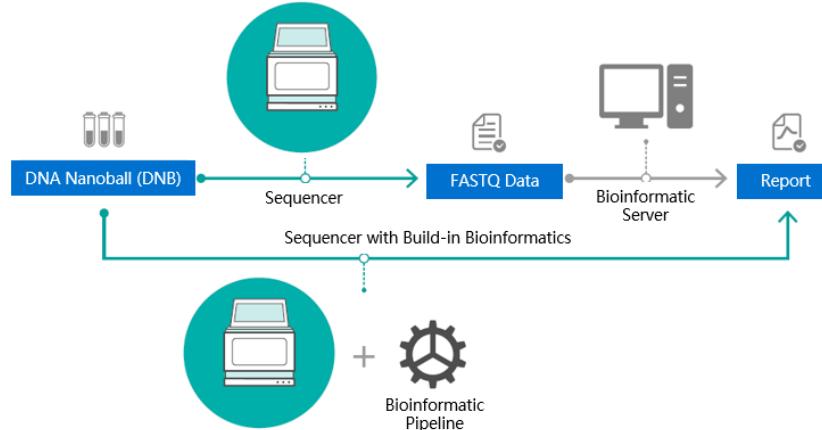


Supports MGI and App-C libraries and requires no primer substitutions

Reads	Read Length	Data Output	Run Time*	Q30
25M	SE100	2.5Gb	~5 hr	>90%
25M	PE150	7.5Gb	~20 hr	>80%

* The run time includes DNB loading and FASTQ generation time. Barcode sequencing time is excluded.

DNBSEQ-E25: Onboard Bioinformatics



With advanced model, bioinformatic pipeline can be installed into the computing module of sequencer, enabling one-stop DNB to Report process

Standard Model (DNBSEQ-E25)



Standard Computing Module

The standard model generates FASTQ data from sequencing in one system.

Advanced Model (DNBSEQ-E25A)



Enhanced Computing Module



Analysis Software

The advanced model includes an enhanced computing module that can run data analysis like WGS. Analysis software is an add-on.

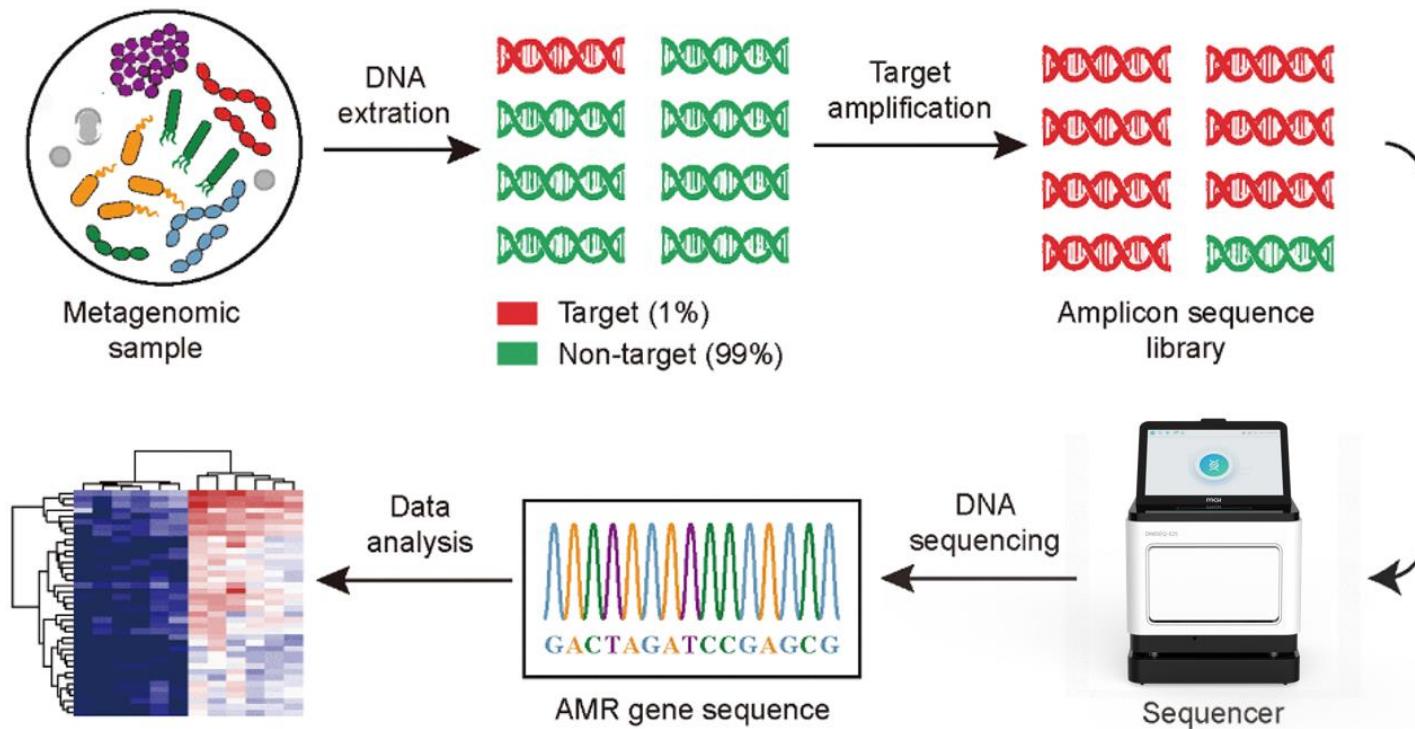
Application Overview



Application Overview of DNBSEQ-E25

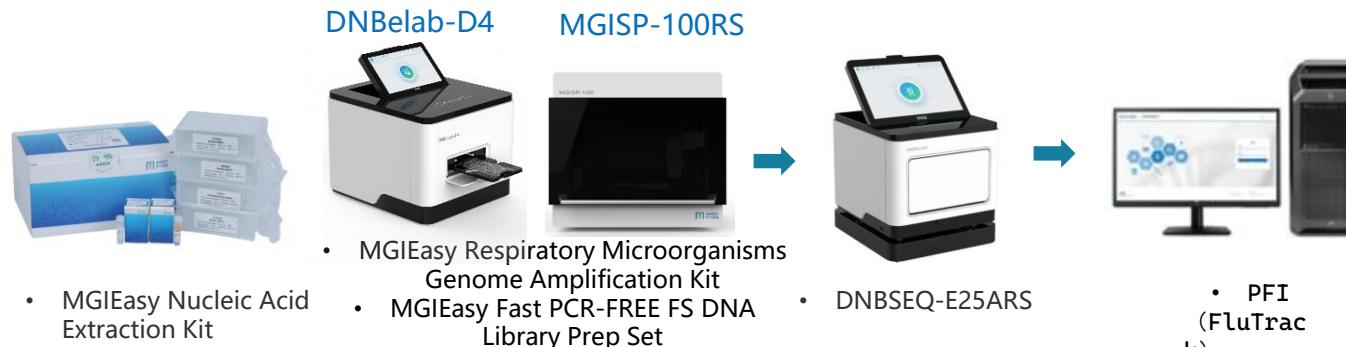
	Targeted Sequencing	Metagenomics Sequencing	Whole Genome (DNA/RNA)
Pathogenic Microorganisms	ATOPlex-based: COVID Influenza HIV Tuberculosis	Unknown Pathogen Surveillance	Cultivated Bacteria
Clinical Diagnostics	Infectious Diseases Identification Drug Resistance Small Cancer Panels Gastrointestinal Microbiota 16S	Infectious Diseases Identification	NIPT
Education & Forensics	DNA Trait for Genomics Education STR Sequencing		
Emerging New Field	Environmental DNA (eDNA) Food Ingredient Study Fisheries and Aquaculture Study		Plasmid Sequencing Synthetic Strand Verification DNA Storage

Targeted Panel for in-depth Pathogenic Study



Respiratory Microbial Sequencing

Respiratory microbial solution from RNA to report



Workflow

Sample Process	Library Preparation	Sequence	Analysis
0.5h	10h	15h	1h
Nucleic acid Extraction	RT-PCR PCR-free library DNB	Sequence	Data Analysis

*The above are the times of single sample.

Respiratory Microbial Sequencing

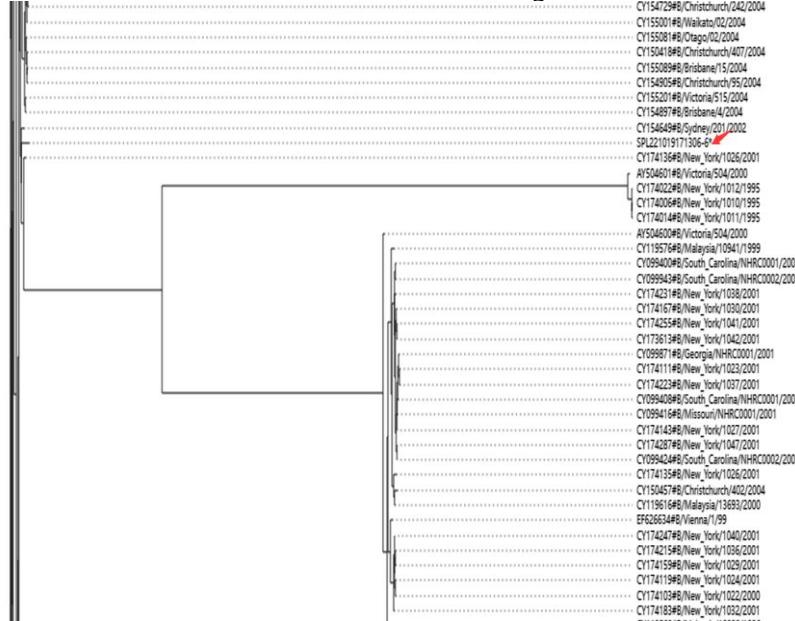
- Taking one of the samples as an example, the analysis results were displayed, and the identification results were shown in the following table:

Sample Name	Identification result	Virus relative ratio Pct value	Virus sequence number	Virus sequence ratio	Strain type (InfluenzaB)
SPL221019171306-6	Positive	99.79%	4,956,321	87.78%	Yamagata

- The genome assembly results were shown in the table below:

Sample name	Gene name	Fragment name	Start position (Query)	End position (Query)	Start position (Ref)	End position (Ref)	Alignment length	Fragm ent length	Assem bly completeness
SPL221019171306-6	PB1	B-seg1	1	2,347	13	2,359	2,347	2,369	99.07%
SPL221019171306-6	PB2	B-seg2	1	2,380	1	2,380	2,380	2,396	99.33%
SPL221019171306-6	PA	B-seg3	1	2,305	1	2,305	2,305	2,305	100.00%
SPL221019171306-6	HA	B-seg4	1	1,849	1	1,849	1,849	1,882	98.25%
SPL221019171306-6	NP	B-seg5	1	1,844	1	1,844	1,844	1,844	100.00%
SPL221019171306-6	NA	B-seg6	1	1,542	1	1,542	1,542	1,557	99.04%
SPL221019171306-6	M	B-seg7	1	1,190	1	1,190	1,190	1,190	100.00%
SPL221019171306-6	NS	B-seg8	1	1,057	41	1,097	1,057	1,097	96.35%

- The traceability analysis of this example sample was carried out, and the results were shown in the figure below:



Summary:

MGI's influenza sequencing solution based on the DNBSEQ-E25ARS platform has a wide subtype coverage, a high degree of automation, and excellent data quality. It can provide tool support for **the identification, typing, genome assembly, and traceability** of influenza viruses.

HIV Sequencing

HIV-1 solution provides full process from sample to analysis report to support drug resistance surveillance

DNBelab-D4



- MGIEasy Nucleic Acid Extraction Kit

MGISP-100RS



- ATOPlex RNA Multiplex PCR based Library Prep Set



- DNBSEQ-E25ARS

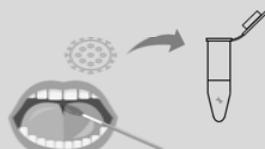


- PFI

Workflow

Sample Process

0.5h



Nucleic acid Extraction

Library Preparation

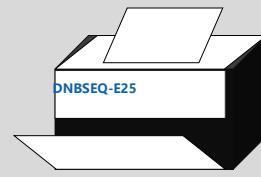
7.5h



RT-PCR PCR-free library DNB

Sequence

5h



Sequencing

Analysis

0.2h

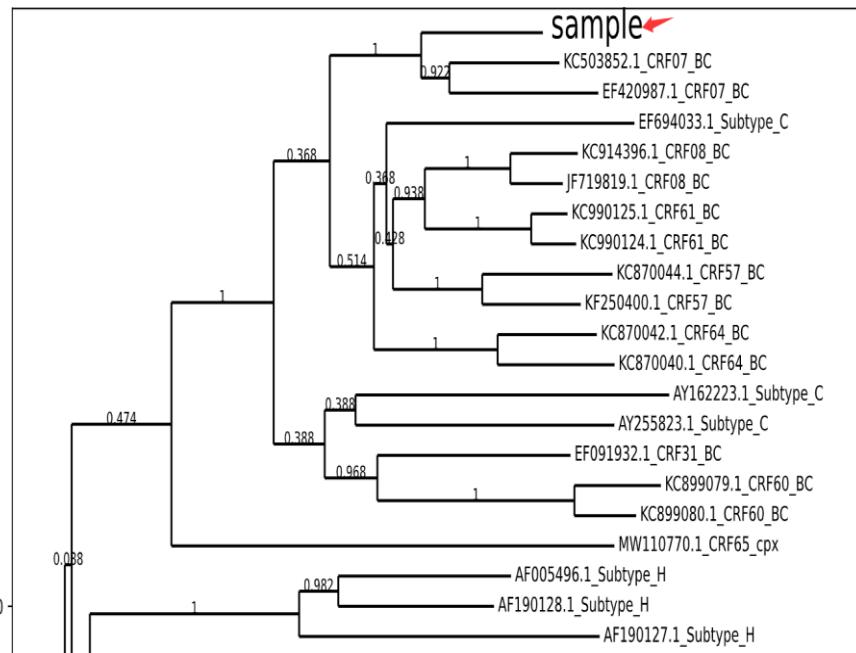


Data Analysis

*The above are the times of single sample.

HIV Sequencing

- Through evolutionary traceability analysis, it was found that the closest source subtype of this sample was CRF07_BC.



Summary:

MGI's HIV sequencing solution based on the **DNBSEQ-E25ARS platform** has a high degree of automation, excellent data quality, and powerful software functions, which can provide powerful tool support for AIDS **drug resistance monitoring** and evolution research.

- Analysis of drug-resistant loci revealed that the following susceptibility and low-level drug-resistant loci existed in the RT gene of this sample.

Drug Type	Drug name	Drug abbreviation	Gene	Mutant		Drug resistance scoring	Degree of resistance
NRTI	lamivudine					-	susceptibility
	emtricitabine	FTC	RT	T215A(1.08)		0	susceptibility
	abacavir	ABC	RT	T215A(1.08)		5	susceptibility
	didanosine	DDI	RT	T215A(1.08)		10	potential low-level resistance
	tenofovir disoproxil	TDF	RT	T215A(1.08)		5	susceptibility
	stavudine	D4T	RT	T215A(1.08)		20	low-level resistance

- The HIV drug resistance prediction software could also perform statistics and report on the mutation sites of the virus, some of the results are shown in the figure below:

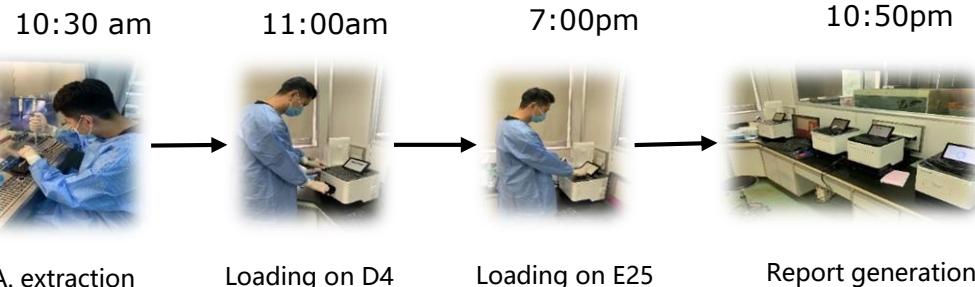
Gene	Drug resistance classification	Whether monitoring site	Wild type	Amino acid position	Mutant type	Wild type base	Genomic position	Mutant base	Mutation frequency (%)	Sequencing depth
PR	Other	no	V	3	I	G	2260	A	99.850000	672
PR	Other	no	T	12	P	A	2287	C	99.440000	2143
PR	Other	no	T	12	K	C	2288	A	5.220000	2202
PR	Other	no	I	13	V	A	2290	G	1.090000	2302

Covid-19 Sequencing

Government users (CDC)



12-hour ADE COVID solution enables DNBSEQ No.1 in China CDCs



Sample ID	Raw reads	Clean reads	1X Coverage	100X Coverage	Average depth	Total mutation	Clade ID
A	4149226	4146293	99.90%	99.83%	12337.44	19	20B
B	4164290	4160743	100%	99.30%	6844.32	18	20B
C	2064499	2062182	100%	99.64%	4422.87	0	19A
D	3073192	3067303	100%	99.72%	6571.62	0	19A
E	1916909	1912655	99.90%	99.26%	4159.81	0	19A



Targeted Microbial Sequencing (tNGS)



AccuGen Rapid Pathogen Identification: 328 pathogens + 150 drug resistant genes

E25 Sequencing: SE50(Achieved by SE100)



- Total nucleic acid
- Specimen:
 - Whole blood, swab eluate, sputum, BAL, urine, CSF, bone marrow, etc

- 1280 amplicons
- Nucleic acid $\geq 1\text{ng}/\mu\text{l}$
- Hands-on time: 2 hours

- SE50 (recommended)
- SE100, PE100, PE150
- 0.5 - 1M reads / sample
- 16-32 samples / run

- Qualitative and quantitative analysis
- Quality control of raw sequencing data, sequence alignment, and annotation analysis

1.5 h

6 h

2.5 h

0.5 h

Rapid Identification of Pathogenic Microorganisms and Drug Resistance Genes



- **Samples:** ZymoBIOMICS™ Microbial Community DNA Standard D6306 + SARS-CoV-2 QC standard + RSV virus as positive control. 4 libraries was prepared in 4 consecutive days
- **Sequencing strategy:** DNBSEQ-E25 RS, SE50

QC result:	Total reads	Q30	Split Rate
	27.75 M	97.85	95.55%

Type	Name	Relative Abundance					
		Sample 1	Sample 23	Sample	Sample 4	Average	SD
G-	<i>Escherichia coli</i>	12.36%	13.44%	14.73%	12.89%	13.36%	1.02%
G-	<i>Pseudomonas aeruginosa</i>	0.45%	0.50%	0.34%	0.35%	0.41%	0.08%
	<i>Salmonella enterica</i> subsp. <i>enterica</i> serovar						
G-	<i>Typhi</i>	11.22%	14.41%	12.79%	12.91%	12.83%	1.30%
G+	<i>Enterococcus faecalis</i>	12.50%	13.27%	10.76%	10.56%	11.77%	1.33%
G+	<i>Staphylococcus aureus</i>	1.43%	1.56%	0.76%	0.88%	1.16%	0.40%
G+	<i>Listeria monocytogenes</i>	0.94%	0.86%	0.58%	0.60%	0.75%	0.18%
F	<i>Cryptococcus neoformans</i>	0.90%	0.78%	0.55%	0.62%	0.71%	0.16%
F	<i>Saccharomyces cerevisiae</i>	0.17%	0.12%	0.10%	0.10%	0.12%	0.03%
V	<i>Respiratory syncytial virus</i>	58.92%	54.00%	58.66%	60.35%	57.98%	2.76%
V	Severe acute respiratory syndrome coronavirus 2	1.11%	1.05%	0.72%	0.74%	0.91%	0.20%

Results: The results of the 4 samples are consistent, indicating good repeatability of the method.

Clinical samples

- **Samples:** Bronchoalveolar lavage fluid
- **Sequencing strategy:** DNBSEQ-E25, SE50

QC result:

Total reads	Q30	Run time	Split Rate
24.66 M	93.65%	3.2 h	95.86%

QC Information

Item	QC Parameter	Detection Results	QC Standard
Identification of pathogenic microorganisms	Positive control (PC)	Qualified	Qualified
	Negative control (NC)	Qualified	Qualified
	Detection rate of internal reference	100%	100%
Overall evaluation of sequencing QC		Qualified	

Note:

1. Negative control (NC): Monitor the contamination of the whole detection process;
2. Positive control (PC): Artificial sequence is selected as PC, and the detection of PC can reflect whether the test process is qualified;
3. Internal reference: Select an artificial sequence different from PC and add it to each sample. The detection of internal reference can reflect whether the test process of each sample is qualified;
4. Overall evaluation of sequencing QC: Comprehensively evaluate the quality of sequencing in combination with sequencing parameters.

12s MiFish Sequencing

One-stop product solution from nucleic acid extraction to analysis report, saving your effort

DNA Extraction



MGIEasy Stool
Microbiome DNA
Extraction Kit

- ✓ Water sample is also available

Library Prep



- ATOPlexMiFish Panel
- ATOPlex DNA Dual BC Library Prep Set

Sequencing



DNBSEQ-E25RS



DNBSEQ-E25RS
High-Throughput
Sequencing Set(FCL
PE150)

Analysis&Report



PFI



Metabarcoding
Species Identification
Software (MetaSIS)

2h

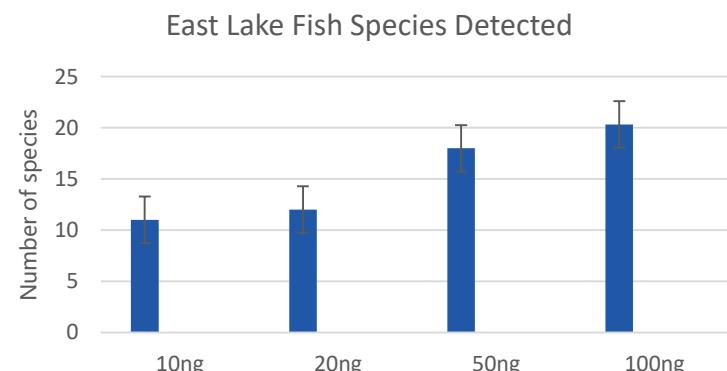
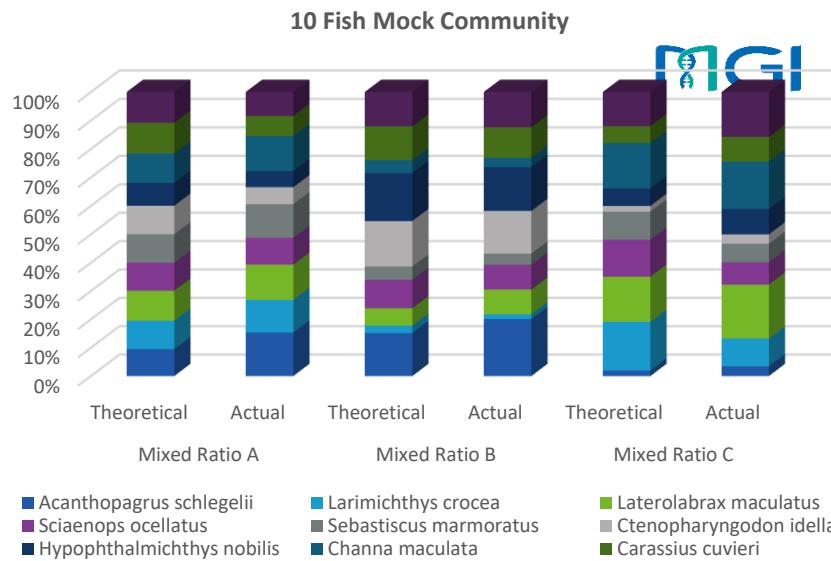
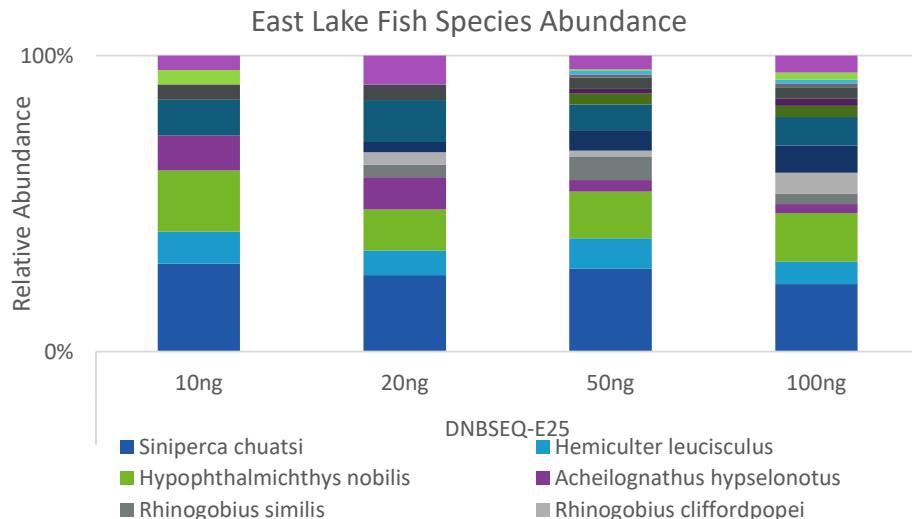
6h

21h

30min

12s MiFish Sequencing

- **Samples:** Microorganisms in water (with unique 12s MiFish primers)
- **Library prep:** ATOPlex DNA Dual Barcode Library Preparation Sequencing Set
- **Sequencing strategy:** PE150+10+10
- **Duration:** ~20h (includes barcode)



Result: Fish mock community species and abundance can be accurately determined and numerous fish species which inhabit a water body, even low-abundance fish which are not easily detected by traditional visual or catch survey methods can be detected.

On-Site Soil 16S Sequencing

Background: Researchers from Bioverse equipped their Desert Mobile Station with DNBSEQ-E25 and deployed this mobile station to northwestern China, where a ten-year long effort have been devoted to transforming desert into cultivated farm land.

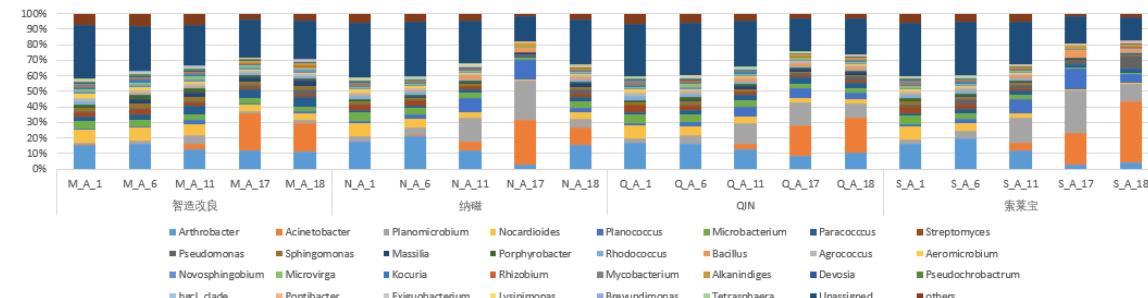
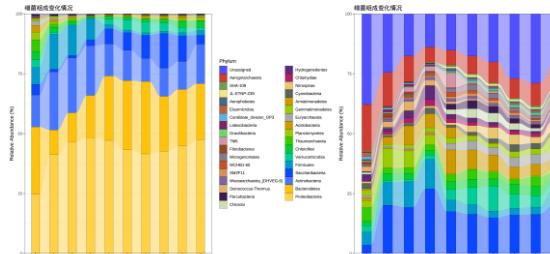
Samples: Targeted soil-based bacteria (with unique 16S primer pool)

Library Prep: MGIEasy Universal DNA Library Prep Set

Operation environment: High temperature condition and drastic day and night temperature change

Sequencing strategy: PE150+10

Duration: ~21h (includes barcode)



Result: DNBSEQ-E25RS can provide qualitative and quantitative analysis of the composition of soil microorganisms.

Metagenomics sequencing

mNGS solution from samples to bio-analysis to support pathogen monitoring



MGISP-NE32

DNBelab-D4

MGISP-100

Nucleic acid extraction
(manual or automated)

Library construction (manual,
automated)

DNBSEQ-E25 sequencing

Data analysis

Transcriptome

- MGIEasy RNA Library Prep Kit
- MGIEasy rRNA Depletion Kit

- DNBSEQ-E25RS High-throughput Sequencing Set

- Rapid Identification (FCL SE100)
- Assembly Analysis (FCL PE150)

➤ Platform of Microorganisms Fast Identification Software(Installed into DNBSEQ-E25ARS directly to achieve rapid identification)

➤ Uploading sequencing data via Zlims to the Microbial Rapid Identification Platform for assembly and other analysis

Macrogenome

- MGIEasy Blood Genomic DNA Extraction Kit
- MGIEasy Microbiome DNA Extraction Kit/Nucleic Acid Extraction Kit

- MGIEasy FS DNA Library Prep Set
- MGIEasy FS PCR-Free DNA Library Prep Set
- DNBelab-D4 FAST FCR-Free FS DNA Library Prep Set

Metagenomics sequencing

GI

- **Sample Type:** 99%NA12878+1% Zymobiomics Microbial community standards
- **Library prep:** MGIEasy Fast PCR-FREE FS DNA Library Prep Set
- **Read Length:** SE100+10
- **Duration:** ~5.5h
- **Bioinformatics:** Build-in PFI (Pathogen Fast Identification) pipeline

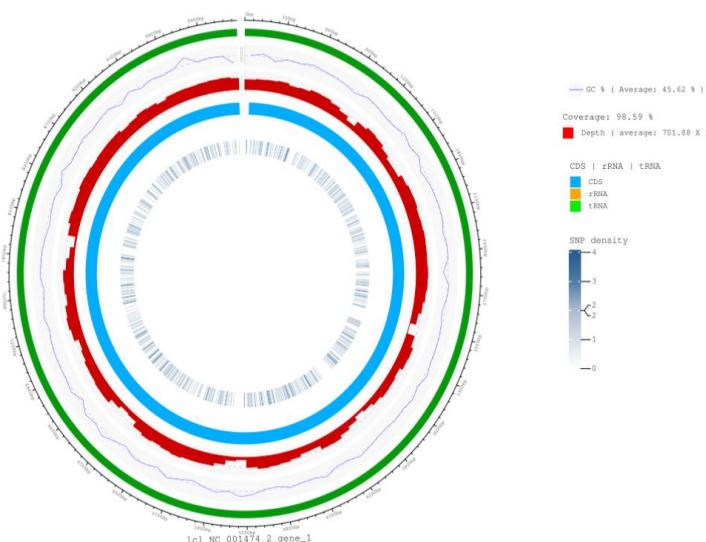


	No.	Species Scientific Name	Standard Abundance%	Test Abundance%
Bacteria	1	Salmonella enterica	12	15.01
	2	Limosilactobacillus fermentum	12	13.71
	3	Bacillus subtilis	12	11.52
	4	Enterococcus faecalis	12	11.75
	5	Listeria monocytogenes	12	12.53
	6	Staphylococcus aureus	12	12.32
	7	Pseudomonas aeruginosa	12	12.15
	8	Escherichia coli	12	7.93
Fungi	1	Cryptococcus neoformans	2	1.49
	2	Saccharomyces cerevisiae	2	1.26

Results: 8 bacterial and 2 fungal sequences were correctly detected in the standard, and the test abundance matched the theoretical abundance

Unknown Pathogenic Species

- ❑ **Sample Type :** Blood Serum from fever patient
- ❑ **Library prep :** MGIeasy RNA Library Prep Set
- ❑ **Read Length :** PE150+10
- ❑ **Duration :** ~19 hours (Includes barcode)
- ❑ **Bioinformatics :** Build-in PFI(Pathogen Fast Identification) pipeline, report can be seen on sequencer screen, MGAP



Results:

- ✓ RNA library construction of nucleic acids was extracted from serum samples, then the library was subjected to PE150 sequencing and a total of about 100,000 Dengue virus sequences were obtained in PFI.
- ✓ The approximately 100,000 Dengue virus sequences were further assembled and analyzed to obtain a consistent sequence of the virus with a coverage of more than 98.5% and an average coverage depth of >700x

◆ 2.2.2. Viruses

The table below shows the top 10 Viruses in the identification result, includes the reads number and relative abundance on species level and subspecies level.

⌚ Identification result

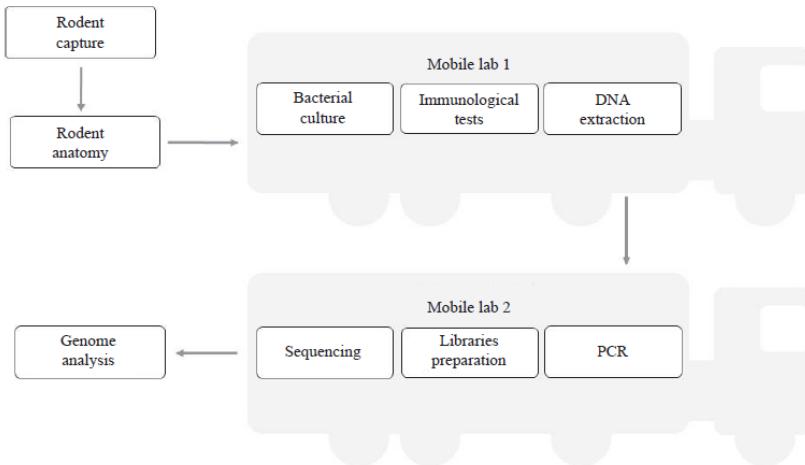
No.	Species ScientificName	Reads Number	Relative Abundance(%)
1	Dengue virus	99,538	10.017
2	Proteus virus Isfahan	1,442	0.145
3	Powassan virus	323	0.033

Chromosome	Data(%)	Avg Depth	Median	Coverage%
1cl_NC_001474_2_gene_1	100.00	701.88	566.0	98.59

Mobile Pathogen Identification Network

- ❑ **User Type:** Chinese Center for Disease Control and Prevention (CDC)
- ❑ **Sample Type:** Rodent
- ❑ **Library prep:** MGIEasy RNA Library Prep Set
- ❑ **Sequencing strategy:** SE100+10
- ❑ **Duration:** ~5.5h
- ❑ **Analysis Method:** PFI

The CLOSS(Co-Localization of sampling and sequencing) Model of the CDC Mobile Pathogen Identification Network Program:



Results:

- ✓ Species were precisely identified as *Meriones unguiculatus* (gerbil) and *Spermophilus dauricus* (citellus)
- ✓ No high-risk pathogens, such as *Y. pestis*, were found, but the pathogens such as *Bartonella grahamii* could be detected.

Machine ID	R31110100230020
Flow cell ID	A1221118095
Reagent ID	QSZ23083001
DNB ID	mouserNA0911
Start Sequence Time	2023/09/11 09:07:28
CycleNumber	100
ActivePixelsNum(M)	38.23
TotalReads(M)	28.79
LoadingRate%	91.23
ESR%	82.53
Q30%	96.89

CDC mobile exercise, highway within Inner Mongolia,
~80km/h



Culture-based Bacteria Identification

- **User Type:** A provincial Center for Disease Control and Prevention
- **Sample Type:** Nucleic acids extracted from cultured bacteria
- **Library prep:** DNBelab-D4RS FS DNA Library Prep Kit
- **Sequencing strategy:** SE100
- **Duration:** ~5h
- **Analysis Method:** PFI

Sample	Total Reads	Unclassified Reads Number	Unclassified Rate	Classified Reads Number	Classified Rate	Viruses	Bacteria	Archaea	Fungi	Protozoa	Metazoa Parasite	Human
A1201021647_DNA	22,981,594	1,866,362	8.12%	21,115,232	91.88%	30	21,111,133	19	205	52	65	3,728

◆ 2.2.1. Bacteria

The table below shows the top 10 Bacteria in the identification result, includes the reads number and relative abundance on species level and subspecies level.

⌚ Identification result

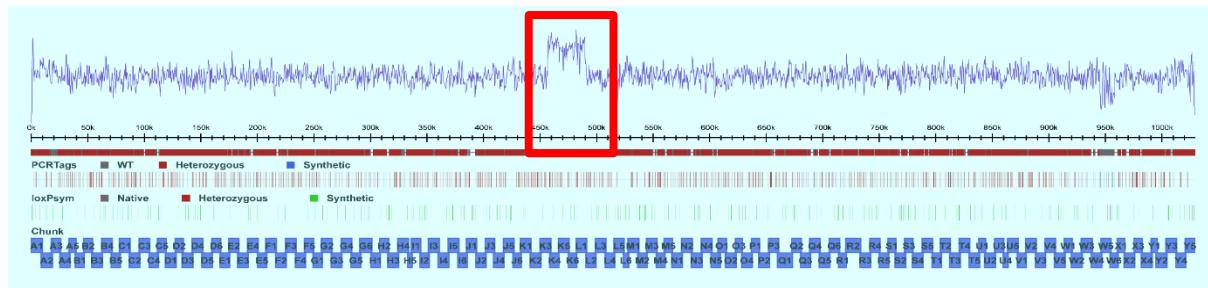
No.	Species ScientificName	Reads Number	Relative Abundance(%)
1	Vibrio cholerae	14,511,174	99.546
2	Vibrio mimicus	14,506	0.100
3	Vibrio metoecus	12,801	0.088
4	Vibrio parahaemolyticus	3,544	0.024
5	Staphylococcus hominis	2,930	0.020
6	Vibrio campbellii	2,488	0.017
7	Vibrio sp 2521-89	2,225	0.015
8	Vibrio vulnificus	1,925	0.013
9	Vibrio anguillarum	1,872	0.013
10	Enterovibrio norvegicus	1,606	0.011

Results:

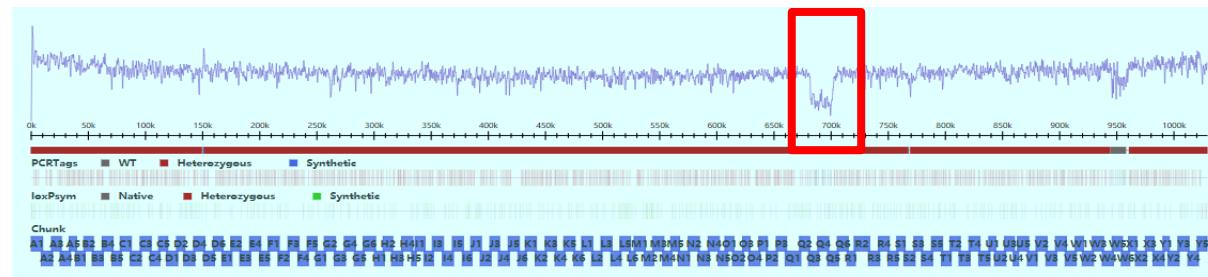
- ✓ The DNBSEQ-E25 produced a total of ~25M reads in a run, of which ~23M could be used for subsequent analysis and Q30 ≥95%.
- ✓ Classification analysis of the number of identified specific reads yielded, more than 99% of the reads as Vibrio cholerae, which is consistent with the expected results observed by customers using other assays after culture.

Small Whole Genome Sequencing

- **Sample type:** gDNA of *Saccharomyces cerevisiae* strain
- **Sequencing strategy :** SE100+10
- **Duration:** ~5.5h (includes barcode)



Repeats on chromosome : 456311-489810



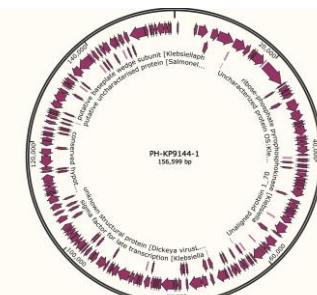
Target deletion location : 681673-
701557, normal deletion on chromosome

Small Whole Genome Sequencing

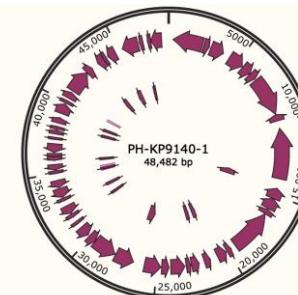
- **Sample type:** bacteriophage
- **Sequencing strategy:** SE100
- **Duration:** ~5.5h (includes barcode)

Sample	Clean_Reads	Clean_Bases	Q20_bases	Q20_Rate	Q30_bases	Q30_Rate
B3(pk-kp9144)	1.246414M	124.592529M	119.853172M	96.20%	102.510474M	82.28%
C3(ph-kp9140)	1.482452M	148.177924M	142.962061M	96.48%	122.691321M	82.80%
D3(3912-2)	881.099000K	88.070359M	84.379095M	95.80%	72.371917M	82.18%

Reference genomes

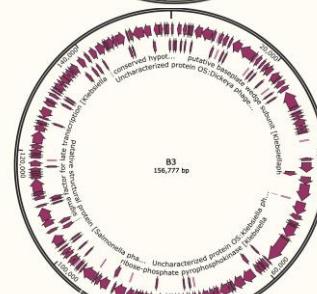


PH-KP9144-1
156,599bp

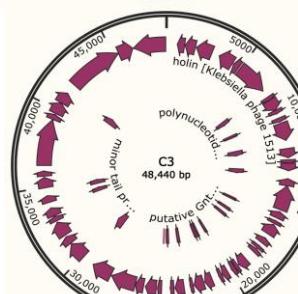


PH-KP9140-1
48,482bp

Samples



B3
156,777bp

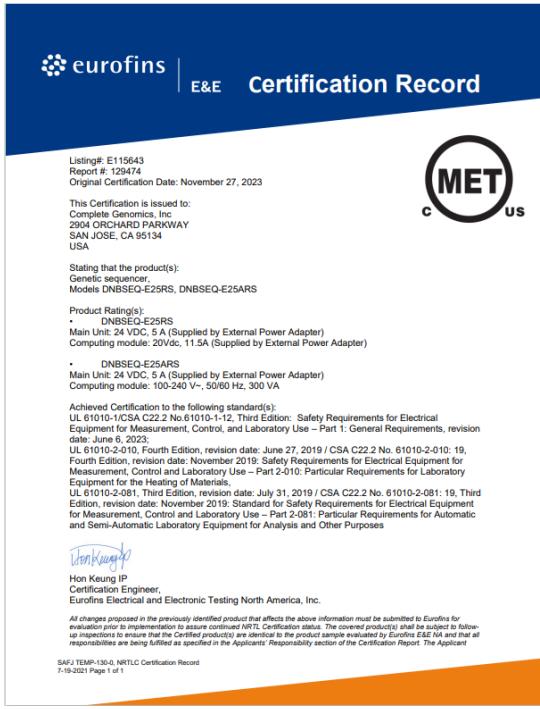


C3
48,440bp

Results: DNBSEQ-E25RS detects results with high similarity to the reference genomes

DNBSEQ-E25 Global Qualification

CE-IVDR expected 2024 Q1



ЕВРАЗИЙСКИЙ ЭКОНОМИЧЕСКИЙ СОЮЗ
ДЕКЛАРАЦИЯ О СООТВЕТСТВИИ



Заявитель Общество с ограниченной ответственностью "НОРД СЕРВИС"

Место нахождения и адрес места осуществления деятельности: Россия, Москва, 117545, проспект Вернадского, дом 131, корпус 5, комната 21, основной государственный регистрационный номер: 1117746930332, номер телефона: +74959025098, адрес электронной почты: msoor@nord-service@gmail.com

и/или Генеральный директор Гуреева Александра Борисовича
заявляет, что Оборудование лабораторное: геномный секвениатор, модель: DNBSEQ-E25RS, DNBSEQ-E25ARS, изготовлено: Qingdao MGI Tech Co., Ltd. Место нахождения и адрес места осуществления деятельности по изготовлению продукции: Китай, Building 4, No.2, Hengyunshan Road, Qingdao Area, Pilot Free Trade Zone, Shandong, China, Код ТН ВЭД ЕАЭС 9027500000. Серийный выпуск

соответствует требованиям

Технического регламента Таможенного союза "О безопасности низковольтного оборудования" (ТР ТС 004/2011), Технического регламента Таможенного союза "Электромагнитная совместимость технических средств" (ТР ТС 020/2011).

Декларации о соответствии приведены на основании

Протоколов испытаний № 221031085GZU-002, 221031085GZU-003 от 14.12.2022 года, 221031087GZU-001 от 30.12.2022 года, выданных испытательной лабораторией "Intertek Testing Services Shenzhen Ltd. Guangzhou Branch".

Схема лекарирования Документ

Дополнительная информация

ГОСТ ИСЕ 61010-1-2014 Безопасность метрологических контрольно-измерительных приборов и лабораторного оборудования. Часть 1. Общие требования ГОСТ ИСЕ 61010-2-010-2013 Безопасность электрических контрольно-измерительных приборов и лабораторного оборудования. Часть 2-010. Частные требования к лабораторному оборудованию для измерения материалов; ГОСТ Р МЭК 61326-1-2014 Оборудование электрическое для измерения, управления и лабораторного применения. Требования электромагнитной совместимости. Часть 1. Общие требования, (разделы 6 и 7). Условия хранения продукции в соответствии с требованиями ГОСТ 15150-69. Срок хранения (случай, годности) указан в прилагаемой к продукции эксплуатационной документации. Договор на выполнение функций иностранного изготовителя № 0203/23-01 от 03.02.2023.

Декларация о соответствии действительна с даты регистрации по 19.02.2028 включительно



М. П.

Гуреев Александр Борисович
(Ф.И.О. заявителя)

Регистрационный номер декларации о соответствии: ЕАЭС N RU Д-СН.РA01.В.94746/23

Дата регистрации декларации о соответствии: 26.02.2023



Order Information

Product Number	Product Name
Instrument (RUO)	
900-000537-00	DNBSEQ-E25RS(CE-RUO)
900-000538-00	DNBSEQ-E25ARS(CE-RUO)
Reagent Set (RUO)	
For library with MGI adapter: OneStep Make DNB (single/dual barcode) + Flow cell + Reagent cartridge	
940-000573-00	DNBSEQ-E25RS High-throughput Sequencing Set (FCL SE100)
940-000567-00	DNBSEQ-E25RS High-throughput Sequencing Set (FCL PE150)
For TruSeq/NexTera library: Conversion + OneStep Make DNB + Flow cell + Reagent cartridge	
940-000569-00	DNBSEQ-E25RS High-throughput Sequencing Set (App-C FCL SE100)
940-000574-00	DNBSEQ-E25RS High-throughput Sequencing Set (App-C FCL PE150)



Thank you!

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