

Enabling Better Outcomes

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CÁC GIẢI PHÁP RIVN PHÂN PHỐI



Giải trình tự gen thế hệ thứ 2



Sinh tổng hợp DNA/RNA & hóa chất cho giải trình tự



Giải trình tự tế bào đơn



Kit giải trình tự tế bào đơn



Phân loại tế bào



Kháng thể & protein



ELISA kỹ thuật số



Đo cường độ biểu hiện gen



Xét nghiệm khối u ung thư từ mẫu máu



Hóa chất và vật tư tiêu hao

MGI INTRODUCTION



Ra đời vào năm 2016 – công ty con của tập đoàn BGI





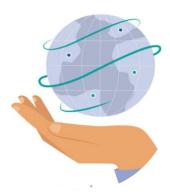
Shenzhen, China





1578 nhân viên, 34% R&D





50 nước và vùng lãnh thổ



> 1500 khách hàng

Make a great instrument and make it smart





HOME

TECHNOLOGY

PRODUCTS V

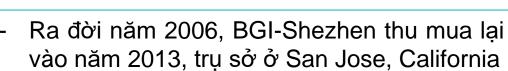
RESOURCES

DEMO DATA

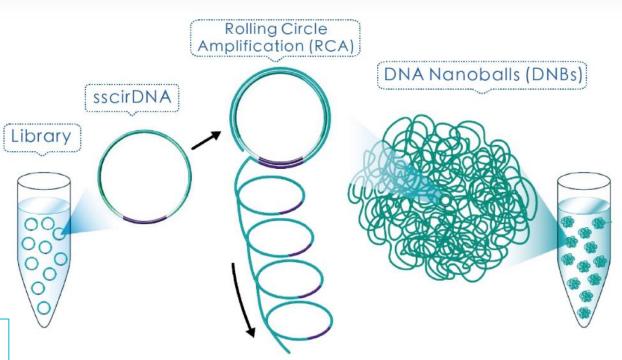
NEWS

ABOUT US V

What makes our DNBSEQ sequencing platforms more accurate and affordable? DNSBEQ technology is the key innovation....



- Tháng 6 năm 2018, Complete Genomics trở thành công ty sản suất thiết bị của MGI



MGI – GIẢI PHÁP TOÀN DIỆN TỪ ĐẦU ĐẾN CUỐI





MGI ZLIMS



HỆ THỐNG CHUẨN BỊ MẪU TỰ ĐỘNG

MGI SP-100 (16 samples) MGI SP-960 (96 samples)

HỆ THỐNG GIẢI TRÌNH TỰ

DNBSEQ-G99 (48G)
DNBSEQ-G50 (150Gb)
DNBSEQ-G400 (1440Gb)
DNBSEQ-T7 (6Tb)

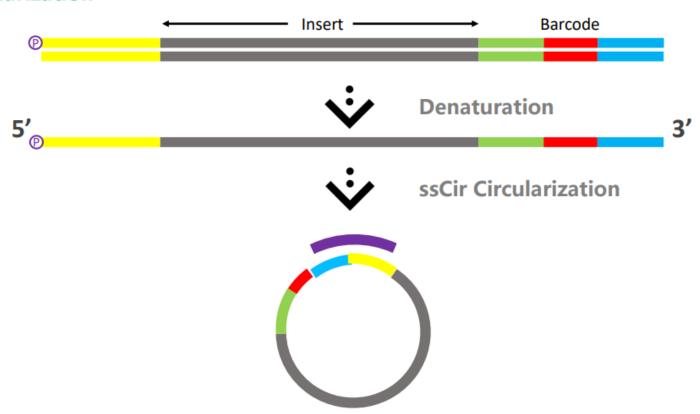
PHÂN TÍCH DỮ LIỆU





DNBSEQ™ technology principle — Circularization

Circularization









Signal is Enhanced by Making DNB









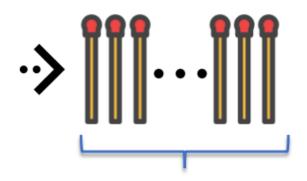




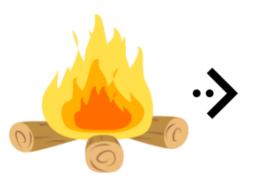


Low Intensity







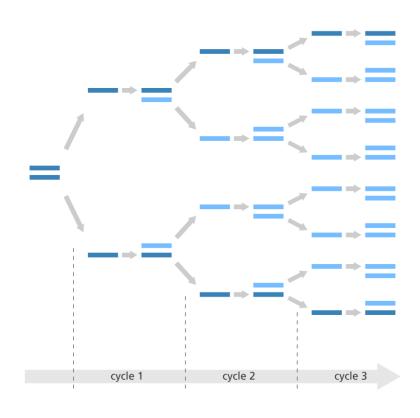




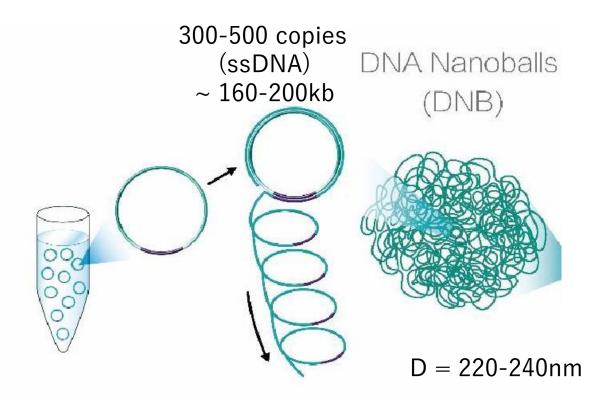
High Intensity

300~500 copies





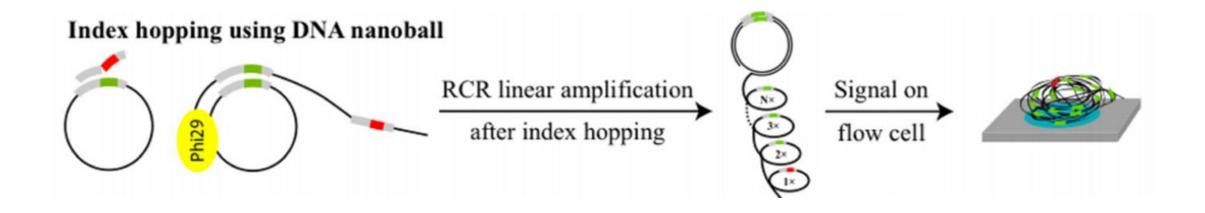
PCR



Phil29 DNA polymerase

Rolling Circle Replication (RCR)

Reduced Index Hoping

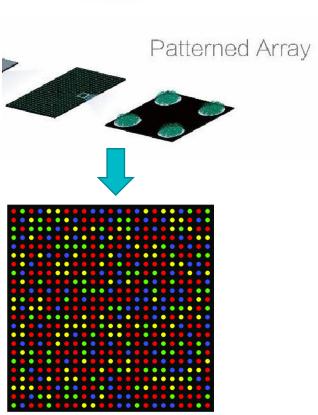


INDEX HOPING: Barcode mis-assignment



MGI

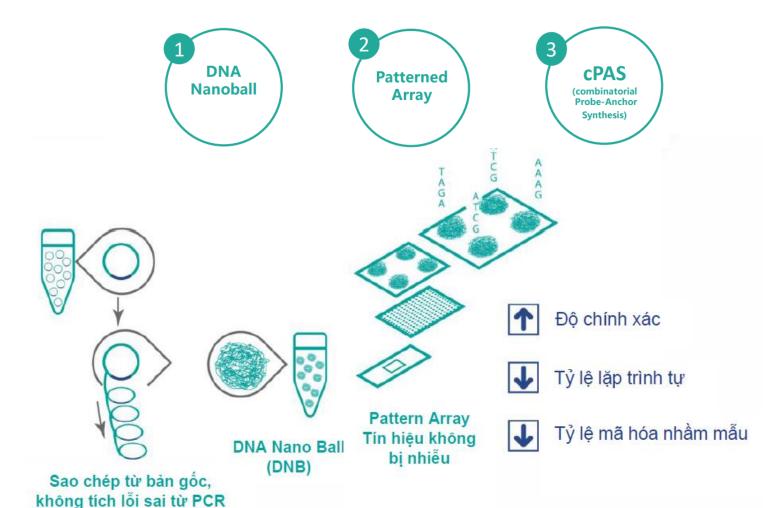




Patterned flowcell



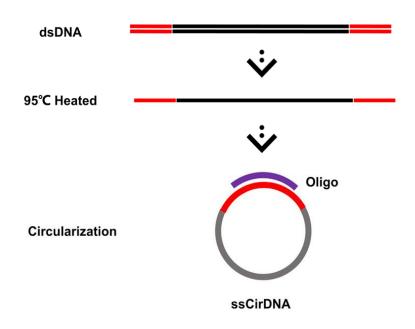
CÔNG NGHỆ DNBSEQ™

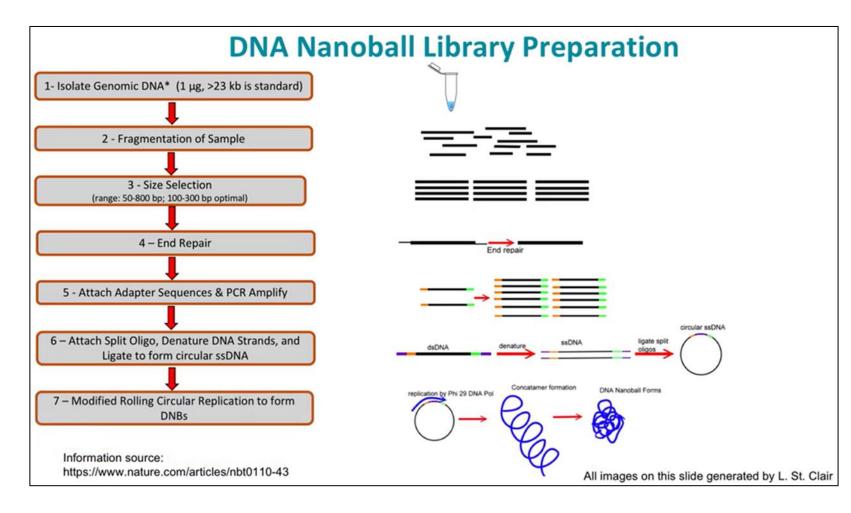


- Độ chính xác cao 99.4%, độ nhạy cao 98.8%
- Tiết kiệm chi phí đầu tư và vận hành
- Nền tảng mở có thể sử dụng kit chuẩn bị thư viện của bên thứ 3



Library preparation



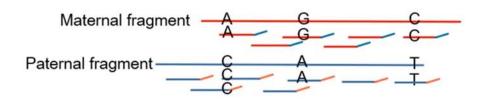




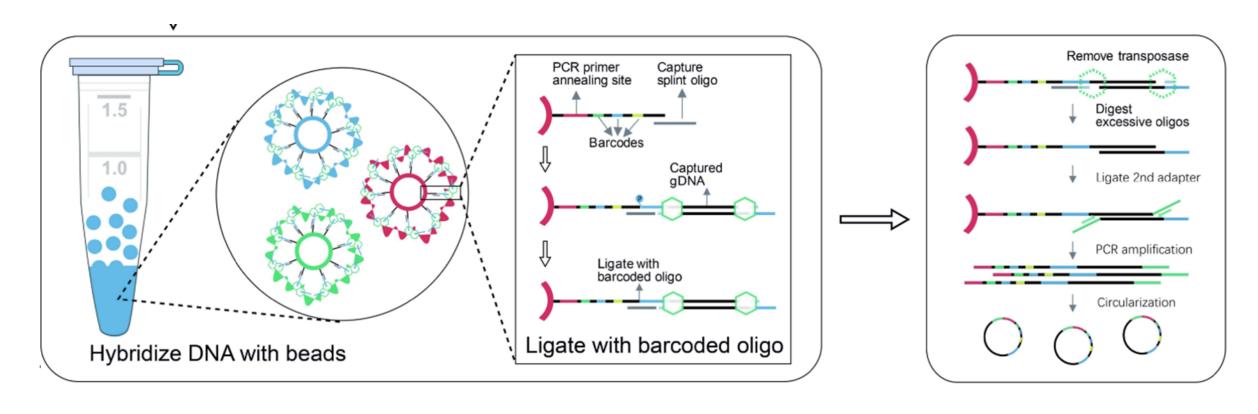


stLFR (Single tube Long Fragment Read) - MGI

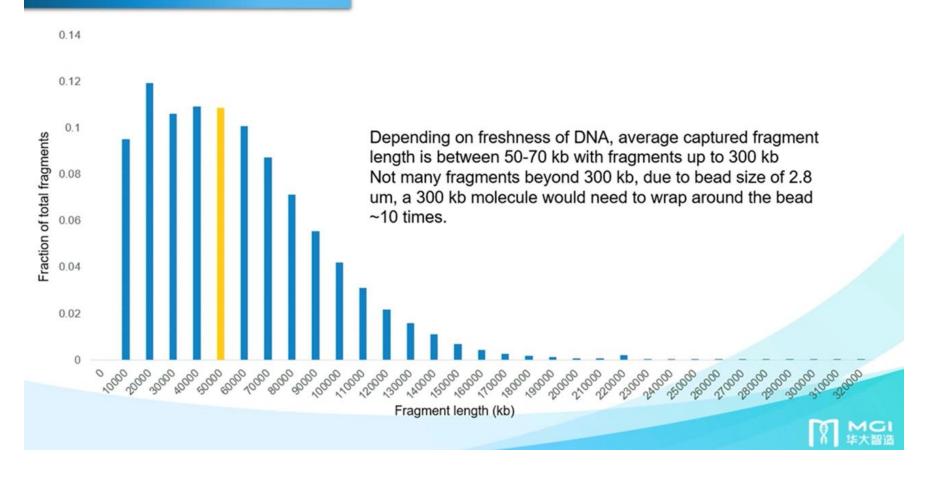
Co-barcoding DNA



- Linked short fragments construct long fragment. (addition of the same barcode to all sub-fragments of the original long DNA molecule)
- Low cost, low error rate
- Genome phasing (halotype, diploid)
- De novo assembling.
- Hight quality structural and variation detection.



Captured Fragment Length





Các hệ máy của MGI





Designed for Speed, Flexibility, and Simplicity

Streamlines your sequencing workflow for quicker results



- Rapid: PE150 ≤12h
- Flexible: Independent operation of dual flow cells
- Easy: Novel cartridge design, simply press-to-load

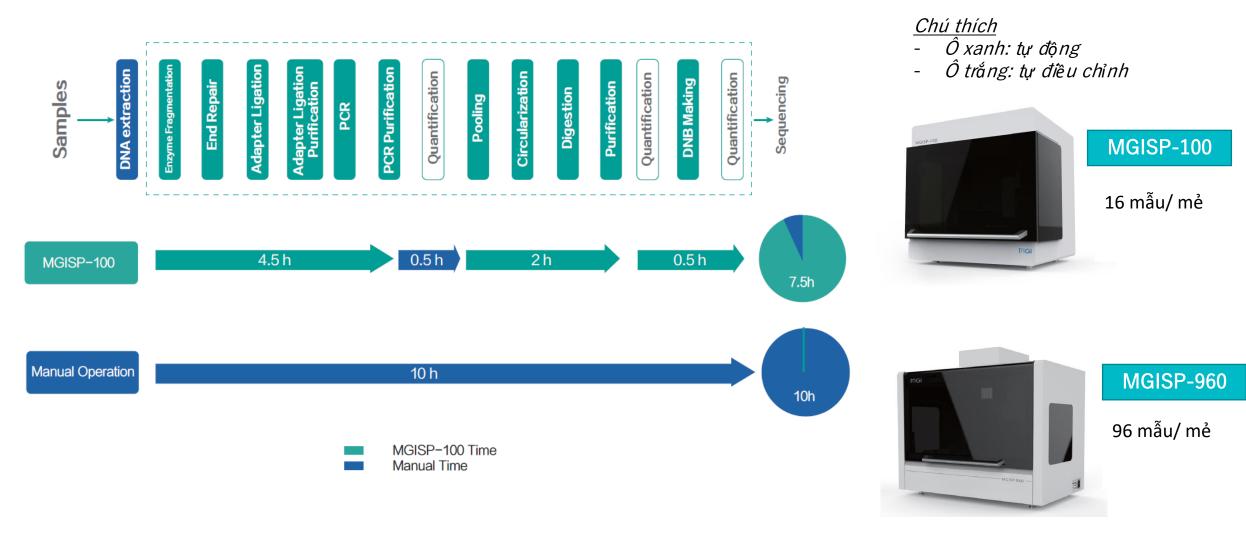


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PE150

THIẾT BỊ CHUẨN BỊ MẪU TỰ ĐỘNG

Quy trình tách chiết và chuẩn bị thư viện tự động







✓ NGHIÊN CỬU LÂM SÀNG

- Ung thư
- NIPT & PGS
- Bệnh truyền nhiễm (Covid 19, lao kháng thuốc....)
- Bệnh hiếm
- Định danh vi sinh vật gây bệnh

✓ PHÁP Y

- Xác định và truy vết tội phạm
- Danh tính hài cốt
- Xác định mối quan hệ cha con, họ hàng

MGHIÊN CỬU CƠ BẢN

- WGS, WES, RNA-seq, transcriptomics
- Xác định đột biến di truyền (SNV, CNV, indel...)
- Giải trình tự tế bào đơn

NÔNG NGHIỆP & THỰC PHẨM

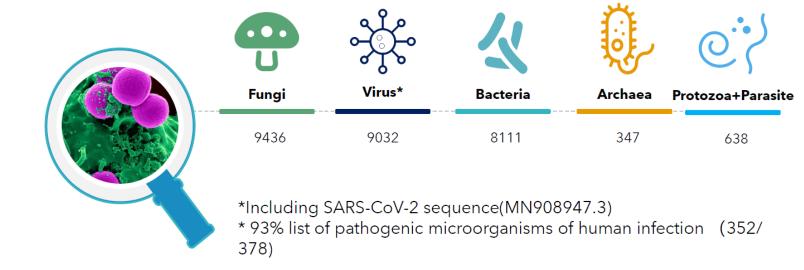
- Chọn giống vật nuôi cây trồng
- Định danh vi sinh vật trong thực phẩm,
 độc tố, gen kháng thuốc (metagenomics)

Metagenomics – PFI software



Reference Database

> Available more than 27,500 species



14 loài vật chủ





PFI result and report



Part1: Data QC statistics

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raitz. Ji	ix catet	ioi ies oi	JUC	ו כסוי	ucnu	IIICation	statistics
		,					

Sample	NT265-H1_DNA
Reads_Length	150.0
Raw_Reads	22,488,694
Raw_Base	3,373,304,100
Host_Reads	680
Host_Rate	0.00%
Clean_Reads	21,187,990
Clean_Base	3,178,198,500
Clean_Base_Rate	94.22%
Raw_Base_Q30	82.05%
Clean_Base_Q30	83.77%
GC_of_Raw_Base	35.44%
GC_of_Clean_Base	35.39%





	Asymmetica subplatement	21	1.000
ž.	Companidan Jonida		6704
	Description substicutes	4	5281
4	Cooreyani Gerupanan	5	0.99
5	Solorono agrado	ž.	9792
ž.	Salado mirrori		Settle
7	fereiti tereti	1	bes
	Landermanagemberens		1000
	Spiriture regions		5866
13	Perrodier risor	1	569
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column Barbings clock disclosured in pipe at the species licentification neo tex.	Journal ere the restation alternational, 2nd orderen Latin name include alternation (furnises or obscaled made of the gas plant.) It is a series of the control of the c	me of species, field schares blanches of SEC / The SEC is warrant of Second Sec	for of steadfed work of the made cooperate is the Brakers Abstrace of the 1.02
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ive abundance), 2nd column: Latin name of species, 3rd columber of classified reads of the species * 100 / The total

Subspecies	Reads
ScientificName	Numbe
ive abundance), 2	naeaf subspecies, 3rd d reads of the subspecies * 100

tification result		
Epochio Scientific Name	Seeds Seeder	Antativo Abundance
Spironena erinaceleuropoel	96	6.606
Schlatzona japoniture	9	0.006
Macrostomum Ignaco	7	0.995
Angiorisms senioum	1	0.000
Angiotrongolus cartonerius	1	2088
Councidadiós remanai	1	0066
Fenerativa glycher	1	0.056
àce ins	1	0.064
Nessor enertainer	1	0.056
Strangularidas papriliciais	1	0.058
wc Rankings (based on the relative abundance), 2nd calumns Latin name of the columni Salative abundance (humber of stacoffed reads of the species * the species (retrieval). CElocion result	species, 3rd column: Num 100 / The total number o	ber of classified read fireads classified in ti
- Parasi	te	Relative Abundance)
uc Rankings (based on the relative abundance). 2nd calumic Latin name of secies, 4th column: Dalative abundance (Number of classified reads of the su- cle at the species level).	subspecies, 3nd columns to despecies * 100 / The total	iumber of classified i i number of reads cla

- > Host rate: represent the microbial content in sequencing data.
- > Clean Base Q30: represent the sequencing quality

Metagenomics – PFI software

PFI result and report



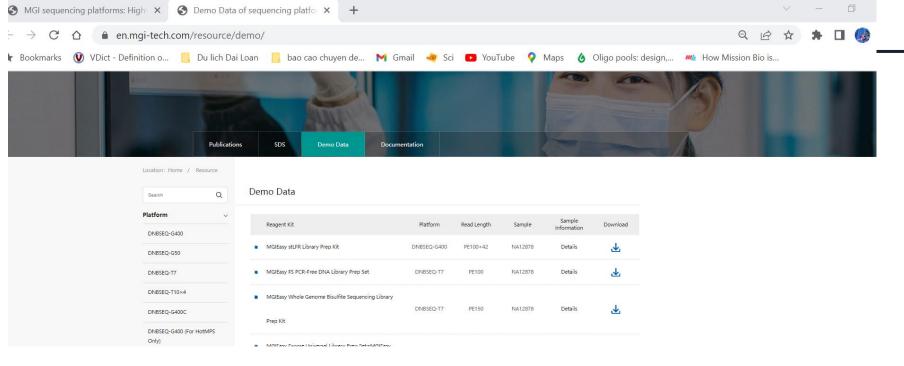
Part2: Bacteria identification statistics

No.	Species_Scientific Name	Reads_ Number	Relative_ Abundance (%)
1	Escherichia coli	636	17.55
2	Staphylococcus epidermidis	85	2.345
3	Variovorax paradoxus	75	2.07
4	Enterococcus faecalis	53	1.462
5	Pseudomonas yamanorum	33	0.911
6	Pseudomonas putida	27	0.745
7	Pseudomonas sp NS1(2017)	23	0.635
8	Pseudomonas fluorescens	22	0.607
9	Elizabethkingia meningoseptica	17	0.469
10	Pseudomonas azotoformans	17	0.469

^{*}interpersonal infectious pathogens will be high-light in red

Part3: Drug resistance genes annotation

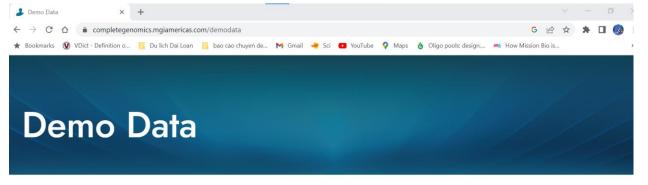
Group	Gene	Class	Mechanism	Туре	Coverage(%)	Depth
0235	MEG_4223 RequiresSNPConfirmation	Oxazolidinone	Oxazolidinone-resistant 235 rRNA mutation	Drugs	100.00	2.44e+04
QACG	MEG_5846	Drug and blocide resistance	Drug and biocide SMR efflux pumps	Multi- compound	100.00	1.54e+04
ANT4- PRIME	MEG_983	Aminoglycosides	Aminoglycoside O- nucleotidyltransferases	Drugs	100.00	1.42e+04
MLS23S	MEG_3977 RequiresSNPConfirmation	MLS	Macrolide-resistant 23S rRNA mutation	Drugs	100.00	1.17e+04
TETL	MEG_7095	Tetracyclines	Tetracycline resistance MFS efflux pumps	Drugs	100.00	1.17e+04
TETL	MEG_7097	Tetracyclines	Tetracycline resistance MFS efflux pumps	Drugs	100.00	1.06e+0
TETL	MEG_7101	Tetracyclines	Tetracycline resistance MFS efflux pumps	Drugs	100.00	9268.77
ANT4- PRIME	MEG_978	Aminoglycosides	Aminoglycoside O- nucleotidyltransferases	Drugs	100.00	9029.67
MLS23S	MEG_3992 RequiresSNPConfirmation	MLS	Macrolide-resistant 23S rRNA mutation	Drugs	93,32	7855.18
TETL	MEG_7096	Tetracyclines	Tetracycline resistance MFS efflux pumps	Drugs	100.00	7733.49





https://en.mgi-tech.com/resource/demo/

https://completegenomics.mgiamericas.com/demodata



	0	Reagent Kit	Platform	Read Length	Application	Organism	Sample Info	Download
Search	Q	MGIEasy RNA directional library prep set	DNBSEQ-G400	PE150	IncRNA	Homo sapiens	UHRR	1 4.25 GB
Sequencing Platform	~	MGIEasy RNA directional library prep set	DNBSEQ-G400	PE150	IncRNA	Homo sapiens	UHRR	4.50 GB
DNBSEQ-G400		MGIEasy small RNA library	DNRSEQ-G400	SE50	smPNA	Homo saniens	нвр	1 670 72 MP
T10x4		prep kit	DNBSEQ-G400	SE50	smRNA	Homo sapiens	HBR	₾ 639.72 MB

Phân tích kết quả demo DNBSEQ-G99



Tab1. Summary Information

Tab2. Biochemistry Information

Category	Value
SoftwareVersion	1.6.4.457
TemplateVersion	0.8.0
Reference	NULL
CycleNumber	310
ChipProductivity(%)	87.37
ImageArea	65
TotalReads(M)	133.22
Q30(%)	94.62
SplitRate(%)	99.11
Runon1(%)	0.11
Runon2(%)	0.12
Lag1(%)	0.12
Lag2(%)	0.18
ESR(%)	87.37
RecoverValue(AVG)	2.03

labz. Biodicinisa y information					
Category	Value				
ISW Version	1.1.1.264				
Machine ID	R1100700220101				
Sequence Type	PE150+10				
Recipe Version	0.6				
Sequence start time	2023-04-14 10:58:14.832				
Workflow type	Sequence				
BBS	NO				
Sequencing Cartridge ID	530-000948-00-W0023030202401				
Flow Cell ID	FT100016024				
DNB ID	20230414-testmgi				
Flow Cell Pos	Α				
Barcode Type	1-128				
Read1 Cycles	151				
Read2 Cycles	151				
Barcode	10				

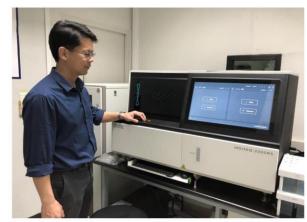
Fig10. Quality Proportion Distribution **[**10-20) **[**30-40] **[20-30]** 90 70 Percentage(%) 20 10 0 50 300 100 150 200 250



Xin cảm ơn Quý vị đã lắng nghe!



Global Reference Sites:



BIOTEC, Thailand



SAMRC, South Africa



Monash Unviersity, Australia

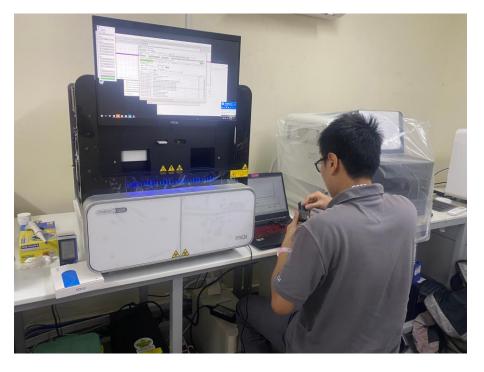


Karolinska Institute, Sweden





Hà Nội, 4/2023

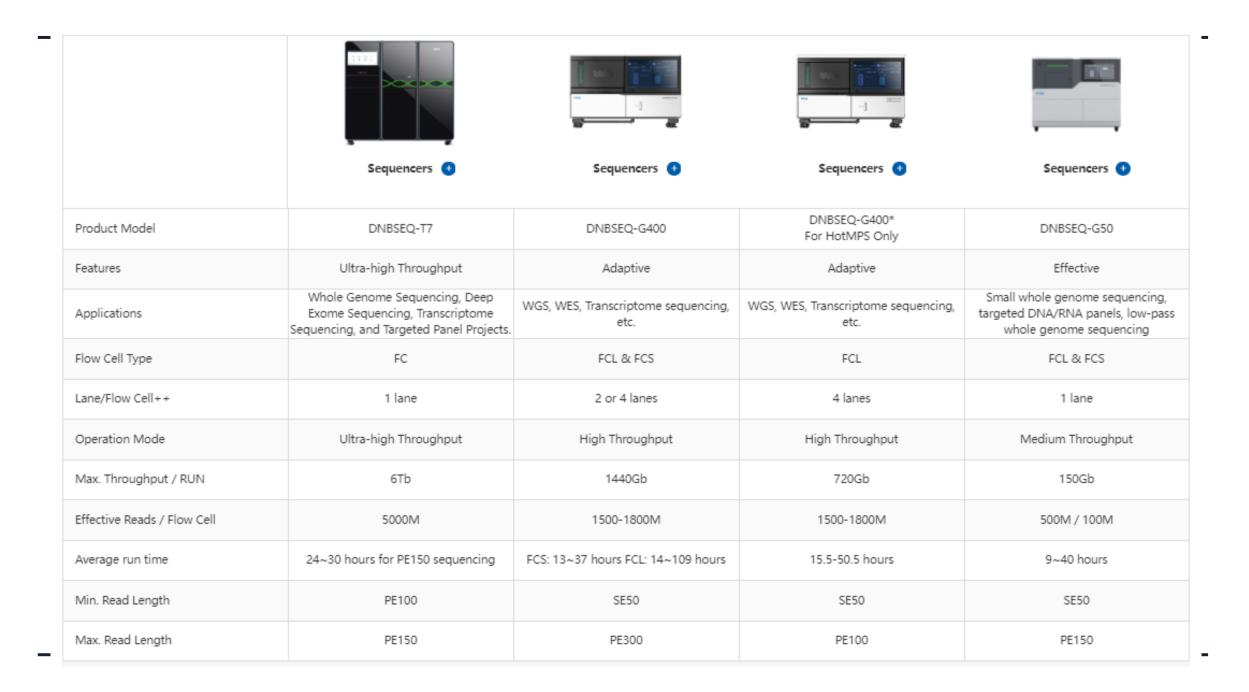


Sài Gòn, 4/2023

Bảng so sánh các hệ thống giải trình tự gene của MGI và Illumina

	MGISEQ-2000 (DNBSEQ-G400)	MGISEQ-200 (DNBSEQ-G50)	Illumina-NextSeq 550	Illumina- Miseq
	1 or 2 FC	1 FC		
Flow-cell/ run	FCS (2 lanes) / FCL (4 lanes)	FCL/FCS (1 lane)	1 FC (4 lanes)	1 FC (1 lane)
Max throughput	1440 Gb	150 Gb	120 Gb	15 Gb
Time run	13-98h	9-40h	9-30h	5-55h
Effective read	550M/2000M	500M/100M	400M	25M
Max read length	2 x 300bp	2 x 150bp	2 x 150bp	2 x 300bp
Quality score (Q30)	>90% PE150 *	>80% PE150	>75% PE150	>80% PE150
Compatible library	MGI, Illumina	MGI, Illumina	Illumina only	Illumina only
Customized Barcode input	Yes	Yes	No	No
Index hopping	0.0001%-0.0004%	0.0001%-0.0004%	0.1-2%	0.1-2%
Flowcell type	Pattern	Pattern	Random	Random

^(*) Sử dụng chế độ giải trình tự Cool MPS



	MGI	ILLUMINA	ILLUMINA
NIPT	MGISEQ-200	NEXTSEQ 550 – Veri Seq NIPT V2	NEXTSEQ 550 Veri Seq NIPT V1
Read lenght	50 bp (SE50)	2*36 bp (PE36)	36 bp (SE36)
Sequencing output	500M	400M	300-400M
Sequencing time	~ 9h	~ 14h	~ 7- 8h
Samples throughput	57 samples	48 samples	16 samples
Turnaround time	1 day	1 day	2 days



What are Q20 (Q30 / Q40) bases?

Eurofins Genomics is using a quality base calling software which examines the peaks around each base call to assign a quality score (Q) to each base call. Quality scores (Q) range from 4 to about 60, with higher values corresponding to higher quality. The quality scores are logarithmically linked to error probabilities, as shown in the following table:

Quality Score	Probability of a wrong base call	Accuracy of a base call
Q 10	1 in 10	90 %
Q 20	1 in 100	99 %
Q 30	1 in 1.000	99.9 %
Q 40	1 in 10.000	99.99 %
Q 50	1 in 100.000	99.999 %