Altium

MGI

MET CB CE EAC

Portable and Easy-to-use

DNBSEQ E25

Genetic Sequencer

Easy Installation

Easy-to-use cartridge
No environmental requirement

Simple Sequencing

Ready-to-use in 10 minutes
Built-in bioinformatics

Portable and Easy-to-use
Genetic Sequencer

DNBSEQ-E25 is a small-sized and light-weighted genetic sequencer that can achieve high-speed and highly flexible sequencing. It also adopts microfluidics based flow cell, integrated CMOS module, and self-luminescence based chemistry, these features lower the operation threshold of a genetic sequencer.

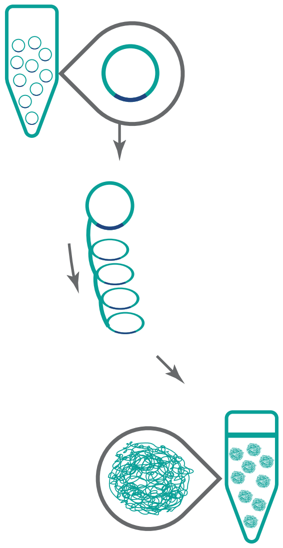
DNBSEQ™ Core Technology

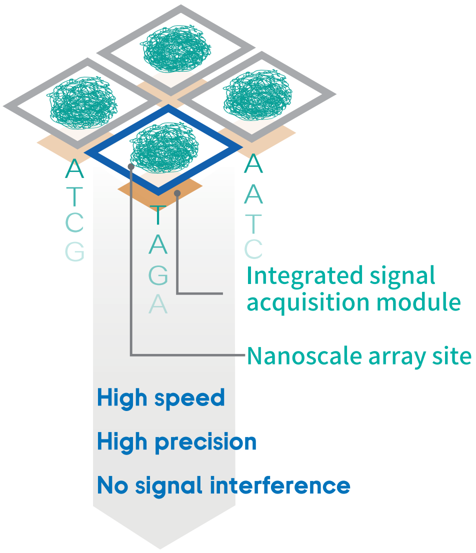
- ↑ Increased accuracy
- ↓ Decreased duplicates
- ↓ Reduced index hopping

\+

Integrated Sequencing Flow Cell

- ☑ Microfluidics based flow cell
- ☑ Integrated CMOS module
- ☑ Self-luminescence based chemistry





High speed

High precision

No signal interference

Performance Parameter

Read Lengths	Effective Reads[*]	Data Output	Run Time	Q30[**]
SE100	25M	2.5GB	~5h	>90%
PE150	25M	7.5GB	~20h	>80%
APP-C SE100[***]	20M	2.0 Gb	~5h	>90%
App-C PE150[***]	20M	6.0 Gb	~20h	>80%

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[*] The effective reads value is obtained according to the operation of a specific standard library, and the actual application library will fluctuate according to the sample type and library construction method

[**] The percentage of bases above Q30 and the running time are averaged over the entire run for a particular standard library. The practical application performance is affected by sample type, library quality, insert length and other factors.

[***] The App-C Sequencing Set includes the invertase module, eliminating the need to purchase additional conversion reagents.

[†] The existing kit supports SE50 and PE100 reads, and the instrument does not have SE50 and PE100 sequencing modes.

Standard model (DNBSEQ-E25)
Stable data output

Sequencer Main Unit + Standard Computing Module

Standard Computing Module

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

Extended model (DNBSEQ-E25A)
More room for adaptation and expansion

Sequencer Main Unit + Enhanced Computing Module + Plus

Extended Computing Module

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

Applications

Case 1 Detection of Unknown Pathogenic Microorganisms

Overview

Sample Types: Alveolar lavage, sputum, blood, cerebrospinal fluid, pharyngeal swabs, vaginal swabs
Library Prep.: TPSeq（Universal Panel and Gynecologic Panel）
Read Length: SE50

Results

- Total output of 28M, Q30>97%, showing outstanding performance and excellent sequencing quality
- Obtain accurate pathogen detection results within 12h, providing a better choice for pathogenic microorganism detection applications

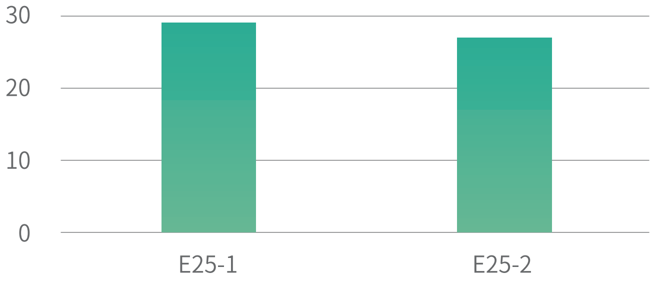

Fig. 2-1 Total reads results

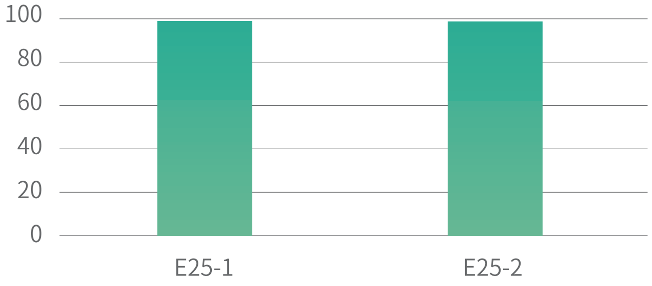

Fig. 2-2 Q30 results

Table 2-1 Analysis results

Sample: 001SY	
Pathogen	DNBSEQ-E25
Haemophilus influenzae	6208
Covid-19	1687
Prevotella intermedia	411
EB virus	260
Streptococcus anginosus	16
Pseudomonas aeruginosa	8

Sample: 002SY	
Pathogen	DNBSEQ-E25
Covid-19 OC43	10591
Streptococcus mitis	1919
HSV-1	2196
EB virus	2563
Cryptococcus neoformans	1714
C. psittaci	35
Canidia Albicans	24

Case 2 Rapid Identification of Pathogenic Microorganisms

Overview

Sample Types: ZymoBIOMICS™ Microbial Community DNA Standard and Bronchial-alveolar lavage fluid
Library Prep.: Pathogen Multiplex-PCR Library Prep Kit
Read Length: SE50

Results

- Total output of 28M, Q30>97%, showing excellent sequencing quality and exceeding the amount of data required for analysis
- Complete the entire sequencing process within 3h, allowing accurate identification of pathogenic microorganisms with high repeatability and accuracy

Table 3-1 Basic sequencing metrics generated by DNBSEQ-E25 with libraries constructed from HGT tNGS solution.

Sample	Total Reads (M)	Q30(%)	Split Rate(%)
Standard (DNA+RNA)	27.75	97.85	95.55
Bronchial-alveolar lavage fluid	24.66	93.65	95.86

Table 3-2 Abundance of microorganisms detected in each repeated sample

Type	Name	Sample 1	Sample 2	Sample 3	Sample 4	Average	SD
G-	Escherichia coli	12.36%	13.44%	14.73%	12.89%	13.36%	1.02%
G-	Pseudomonas aeruginosa	0.45%	0.50%	0.34%	0.35%	0.41%	0.08%
G-	Salmonella enterica subsp. enterica serovar Typhi	11.22%	14.41%	12.79%	12.91%	12.83%	1.30%
G+	Enterococcus faecalis	12.50%	13.27%	10.76%	10.56%	11.77%	1.33%
G+	Staphylococcus aureus	1.43%	1.56%	0.76%	0.88%	1.16%	0.40%
G+	Listeria monocytogenes	0.94%	0.86%	0.58%	0.60%	0.75%	0.18%
F	Cryptococcus neoformans	0.90%	0.78%	0.55%	0.62%	0.71%	0.16%
F	Saccharomyces cerevisiae	0.17%	0.12%	0.10%	0.10%	0.12%	0.03%
V	Respiratory syncytial virus	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%

Table 3-3 Relative abundance of the pathogens detected

Sample	Type	Name	Relative Abundance
tNGS-5-d	G-	Prevotella melaninogenica	71.57%
	G-	Neisseria subflava	10.40%
	G-	Veillonella parvula	0.81%
	G-	Capnocytophaga granulosa	0.39%
	G-	Veillonella dispar	10.68%
	G-	Campylobacter concisus	0.57%
	G-	Neisseria flavescens	0.47%
	G-	Capnocytophaga gingivalis	0.13%
	G+	Streptococcus sanguinis	2.34%
	G+	Cutibacterium acnes	1.40%
	G+	Schaalia odontolytica	0.21%
	G+	Streptococcus gordonii	0.21%
	G+	Staphylococcus capitis	0.18%
	MC	Chlamydia psittaci	0.65%

Applications

Case 3 Microbial Identification and Assembly

Overview

Sample Types: HIV-1, MTB Standards and real samples
Library Prep.: ATOPlex Series Library Preparation Sets
Read Length: PE150

Results

- Q30>90% and excellent of the sequencing data quality
- DNBSEQ-E25 can provide support for genome assembly, typing, traceability and drug resistance analysis of HIV-1 and MTB pathogens

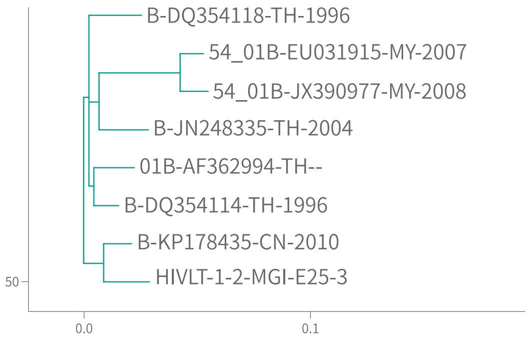

Fig. 3-1 Results of HIV-1 traceability

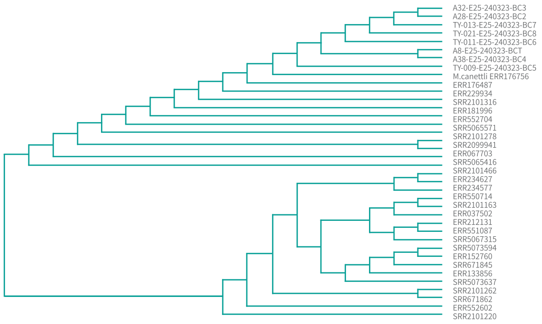

Fig. 3-2 Results of MTB traceability

Table 3-1 Analysis of HIV-1 drug-resistance

Drug Type	Drug Name	Drug Abbreviation	Gene	Mutation	Resistance Score	Resistance Degree
NRTI	Epivir	3TC	RT	M41L(10.08),K219N(96.66)	0	Susceptible
	Emtricitabine	FTC	RT	M41L(10.08),K219N(96.66)	0	Susceptible
	Abacavir	ABC	RT	M41L(10.08),K219N(96.66)	10	Potential low-level resistance
	Di-deoxyinosine	DDI	RT	M41L(10.08),K219N(96.66)	15	Low-level resistance
	Tenofovir	TDF	RT	M41L(10.08),K219N(96.66)	10	Potential low-level resistance
	Stavudine	D4T	RT	M41L(10.08),K219N(96.66)	25	Low-level resistance
	Aziclothymidine	AZT	RT	M41L(10.08),K219N(96.66)	25	Low-level resistance
NNRTI	Doravirine	DOR	RT	K103N(27.14),Y181C(99.56),H221Y(3.16)	25	Low-level resistance
	Efavirenz	EFV	RT	K103N(27.14),Y181C(99.56),H221Y(3.16)	100	High-level resistance
	Etravirine	ETR	RT	K103N(27.14),Y181C(99.56),H221Y(3.16)	40	Intermediate resistance
	Nevirapine	NVP	RT	K103N(27.14),Y181C(99.56),H221Y(3.16)	135	High-level resistance
	Rilpivirine	RPV	RT	K103N(27.14),Y181C(99.56),H221Y(3.16)	60	High-level resistance

Table 3-2 Results of MTB abundance, typing, and mutation detection

Sample ID	Types of TB Infection	TB Abundance	Drug-resistance Associated Mutation	Clade	SIT
A28	MTB	MTB(97.11)	0	Beijing	8.1%+0.1%
A32	MTB	MTB(96.40)	1	Beijing	14.7%+0.2%
A38	MTB	MTB(96.32)	0	Beijing	9.3%±0.4%
A8	MTB	MTB(96.32)	1	Beijing	16.5%0.2%
TY-009	MTB	MTB(95.86)	2	Beijing	16.0%0.6%
TY-011	Mixed	MTB(91.86); NTM(1.68)	0	Beijing	10.5%0.2%
TY-013	MTB	MTB(96.58)	0	Beijing	8.4%+0.3%
TY-021	MTB	MTB(96.49)	0	Beijing	16.4%0.1%

Case 4 Breast/Ovarian Cancer Genetic Testing (BRCA1/2 detection)

Overview

Sample Types: HD793 and HD795 DNA Standards
Library Prep.: BRCA1/2 Library Preparation Kit
Read Length: PE150

Results

- Total output of 25M, Q30>96%, the bases can be accurately identified and the sample data volume meets the requirements for analysis
- Both germline and somatic mutations can be accurately detected, and the detection frequency is close to the theoretical frequency

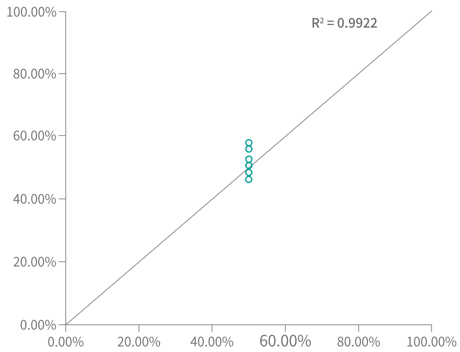

Fig. 4-1 Correlation analysis of variation detection in HD793

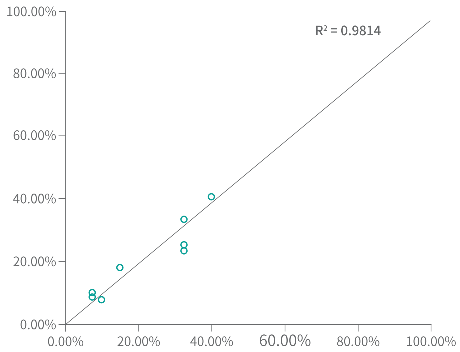

Fig. 4-2 Correlation analysis of variation detection in HD795

Table 4-1 Sequencing results

Sequencer	Sample	Q30 (%)	Mapping Rate (%)	Target Rate (%)
DNBSEQ-E25	HD793	96.73%	99.70%	96.10%
	HD795	96.69%	99.63%	96.10%

Table 4-2 HGT Horizon BRCA germline I DNA reference standard (HD793 – Sample 96)

Gene	GRCh37 coordinates	Coding	Protein	Expected VAF	DNBSEQ-E25 VAF
BRCA1	17:41246245	c.1303G>T	p.Asp435Tyr	50.00%	50.57%
BRCA1	17:41244000	c.3548A>G	p.Lys1183Arg	50.00%	46.35%
BRCA1	17:41245090	c.2458A>G	p.Lys820Glu	50.00%	48.49%
BRCA1	17:41244936	c.2612C>T	p.Pro871Leu	100.00%	99.84%
BRCA1	17:41234451	c.4327C>T	p.Arg1443Ter	0.00%	0.00%
BRCA1	17:41223094	c.4837A>G	p.Ser1613Gly	50.00%	58.05%
BRCA2	13:32912750	c.4258G>T	p.Asp1420Tyr	0.00%	0.00%
BRCA2	13:32937355	c.8021dup	p.Ile2675AspfsTer6	0.00%	0.00%
BRCA2	13:32913559	c.5073del	p.Lys1691AsnfsTer15	0.00%	0.00%
BRCA2	13:32913837	c.5351del	p.Asn1784ThrfsTer7	50.00%	52.78%
BRCA2	13:32906480	c.865A>C	p.Asn289His	50.00%	56.04%
BRCA2	13:32911463	c.2971A>G	p.Asn991Asp	50.00%	50.93%
BRCA2	13:32929387	c.7397T>C	p.Val2466Ala	100.00%	99.80%

Table 4-3 HGT Horizon BRCA somatic multiplex I DNA reference standard (HD795 – Sample81)

Gene	GRCh37 coordinates	Coding	Protein	Expected VAF	DNBSEQ-E25 VAF
BRCA1	17:41246245	c.1303G>T	p.Asp435Tyr	7.50%	8.95%
BRCA1	17:41244000	c.3548A>G	p.Lys1183Arg	7.50%	7.70%
BRCA1	17:41245090	c.2458A>G	p.Lys820Glu	7.50%	7.96%
BRCA1	17:41244936	c.2612C>T	p.Pro871Leu	15.00%	18.03%
BRCA1	17:41234451	c.4327C>T	p.Arg1443Ter	32.50%	25.28%
BRCA1	17:41223094	c.4837A>G	p.Ser1613Gly	7.50%	10.02%
BRCA2	13:32912750	c.4258G>T	p.Asp1420Tyr	32.50%	23.58%
BRCA2	13:32937355	c.8021dup	p.Ile2675AspfsTer6	10.00%	7.93%
BRCA2	13:32913559	c.5073del	p.Lys1691AsnfsTer15	32.50%	33.54%
BRCA2	13:32913837	c.5351del	p.Asn1784ThrfsTer7	40.00%	40.75%
BRCA2	13:32906480	c.865A>C	p.Asn289His	7.50%	8.43%
BRCA2	13:32911463	c.2971A>G	p.Asn991Asp	7.50%	8.21%
BRCA2	13:32929387	c.7397T>C	p.Val2466Ala	100.00%	99.80%

Applications

Case 5 16s rRNA Sequencing

Overview

Sample Types: ZymoBIOMICS™ Microbial Community DNA Standard
Library Prep.: 16S Amplicon Panel, MGIEasy Universal Library Preparation Kit (App-A)
Read Length: PE150

Results

- Total output of 27M, Q30>85%, the bases can be accurately identified and the sample data volume meets the requirements for analysis
- The 16S Amplicon Panel is compatible with the DNBSEQ-E25 platform, providing stable bacterial detection results regardless of different starting amounts and data volumes

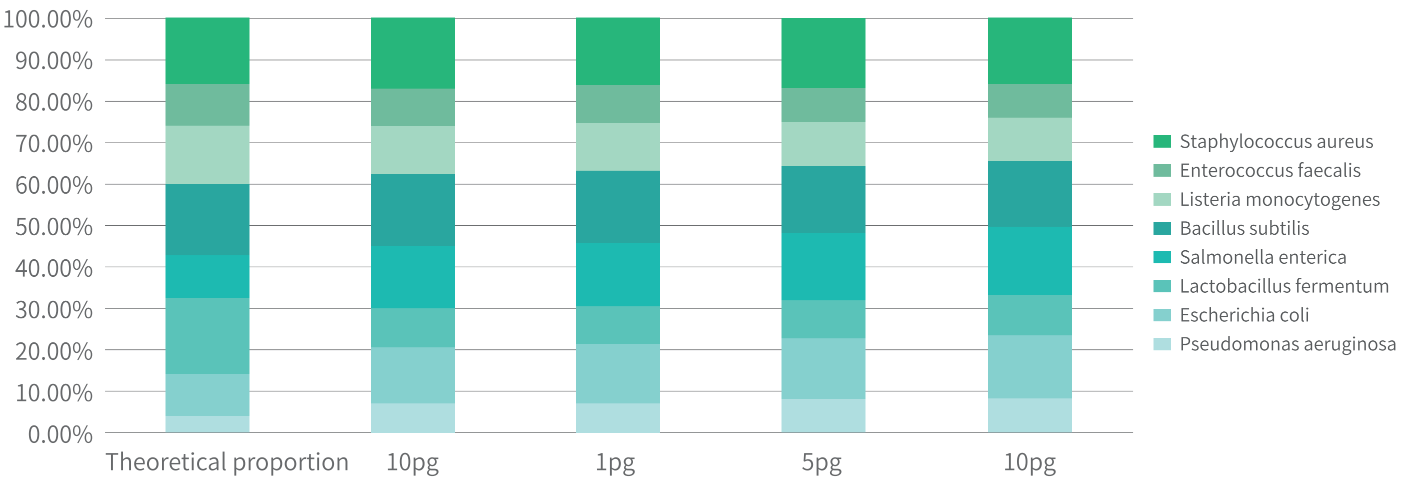

Fig. 5-1 Analysis results

Table 5-1 Sequencing results

Sequencer	Total Reads (M)	Q30 (%)	SplitRate (%)	Time (h)
DNBSEQ-E25	27.88	87.5	92.13	21

Table 5-2 Analysis results

Species Composition	Avg. GC (%)	Theoretical Proportion	10 pg Input (3 repeats)	1 pg Input (3 repeats)	5 pg Input (3 repeats)	2 pg Input (3 repeats)
Pseudomonas aeruginosa	66.2	4.2%	6.9%+0.2%	7.1%±0.2%	8.1%+0.1%	8.4%±0.1%
Escherichia coli	56.8	10.1%	13.9%±0.4%	14.4%+0.1%	14.7%+0.2%	14.9%±0.3%
Lactobacillus fermentum	52.8	18.4%	9.3%+0.2%	9.2%+0.2%	9.3%±0.4%	10.1%±0.1%
Salmonella enterica	52.2	10.4%	15.0%+0.3%	15.3%0.5%	16.5%0.2%	16.5%±0.3%
Bacillus subtilis	43.8	17.4%	17.7%±0.3%	17.5%0.6%	16.0%0.6%	16.1%±0.4%
Listeria monocytogenes	38	14.1%	11.6%0.1%	11.5%0.1%	10.5%0.2%	10.4%±0.1%
Enterococcus faecalis	37.5	9.9%	9.3%10.3%	9.3%+0.2%	8.4%+0.3%	8.3%±0.4%
Staphylococcus aureus	32.7	15.5%	16.3%0.3%	15.7%0.4%	16.4%0.1%	15.3%±0.5%

Case 6 HLA Sequencing

Overview

Sample Types: gDNA Standards
Library Prep.: HLAtyping Panel
Read Length: PE150

Results

- Q30 >85%, the bases can be accurately identified and the sample data volume meets the requirements for analysis
- DNBSEQ-E25 can get accurate and reliable HLA typing results, with the first two positions of typing being completely consistent

Table 6-1 HLA Typing Results

Class I UCLA DNA Reference (standard)		HLA-A		HLA-B		HLA-C	
C1-202	Expected	01:03	69:01	51:01	73:01	15:05	16:02
	Reported	A*01:03:01:02	A*69:01:01:01	B*51:01:01:10	B*73:01:01:01	C*15:05:01:01	C*16:02:01:01
C1-214	Expected	02:06	11:01	15:12	35:03	03:04	04:01
	Reported	A*02:06:01:01	A*11:01:01:01	B*15:12:01	B*35:03:01:03	C*03:04:01:22	C*04:01:01:14
C1-114	Expected	03:02	68:02	15:17	49:01	05:01	05:01
	Reported	A*03:02:01:01	A*68:02:01:01	B*15:17:01:01	B*49:01:01:01	C*05:01:01:02	C*05:01:01:02

Table 6-2 HLA Typing Results

Class II UCLA DNA Reference (standard)		DRB1		DRB3/4/5		DQA1	
C2-211	Expected	07:01:01	16:02:01	4*01:03:01:02N	5*01:01:01	01:02:02	02:01:01
	Reported	DRB1*07:01:01:02	DRB1*16:02:01:03	DRB4*01:03:01:02N	DRB5*01:01:01:01	DQA1*01:02:02:05	DQA1*02:01:01:01
C2-218	Expected	03:01:01	04:02:01	3*02:02:01	4*01:03:01	03:01:01	05:01:01
	Reported	DRB1*03:01:01:02	DRB1*04:02:01	DRB3*02:02:01:02	DRB4*01:03:01:03	DQA1*03:01:01:01	DQA1*05:01:01:02
C2-115	Expected	01:03	13:01:01	3*02:02:01	/	01:01:01	01:03:01
	Reported	DRB1*01:03:01:01	DRB1*13:01:01:01	DRB3*02:02:01:02	/	DQA1*01:01:01:01	DQA1*01:03:01:02

Table 6-3 HLA Typing Results

Class II UCLA DNA Reference (standard)		DQB1		DPA1		DPB1	
C2-211	Expected	03:03:02	05:02:01	01:03:01	02:01:01	04:01:01	10:01:01
	Reported	DQB1*03:03:02:01	DQB1*05:02:01:01	DPA1*01:03:01:04	DPA1*02:01:01:01	DPB1*04:01:01:06	DPB1*10:01:01:01
C2-218	Expected	02:01:01	03:02:01	01:03:01	03:01	02:01:02	18:01
	Reported	DQB1*02:01:01:01	DQB1*03:02:01:01	DPA1*01:03:01:71	DPA1*03:01:02:02	DPB1*02:01:02:10	DPB1*18:01:01:01
C2-115	Expected	05:01:01	06:03:01	01:03:01	/	02:01:02	04:01:01
	Reported	DQB1*05:01:01:03	DQB1*06:03:01:01	DPA1*01:03:01:01	DPA1*01:03:01:02	DPB1*02:01:02:78	DPB1*04:01:01:04

Case 7 Small Whole Genome Sequencing

Overview

Sample Types: gDNA of Saccharomyces cerevisiae strain
Library Prep.: MGIEasy Universal DNA Library Preparation Set
Read Length: SE100

Results

- Even coverage of sequencing data for accurate identification of tandem repeats, mutations, heterozygosity, and other conditions
- Allow samples to be sequenced immediately without the need to batch and send them out, reducing the sequencing validation time

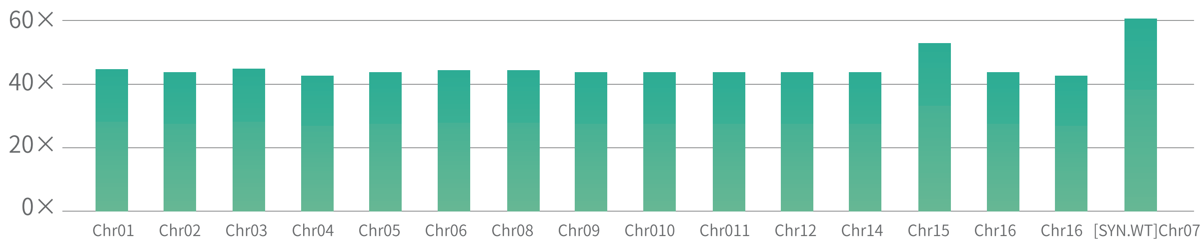

Fig. 7-1 Analysis results

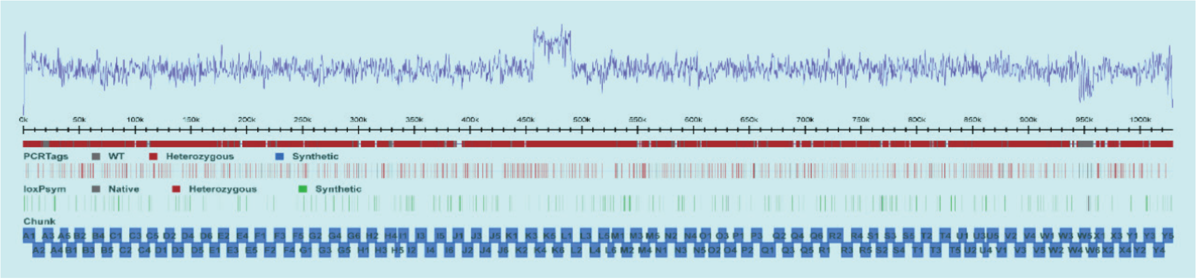

Fig. 7-2 Tandem repeats on chromosome at (456311-489810) target location

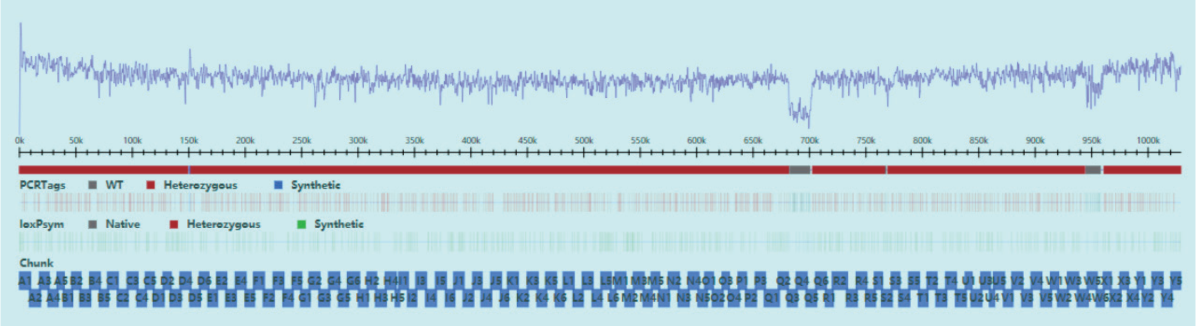

Fig. 7-3 Normal deletion on chromosome at (681673-701557) target deletion location

Hardware Parameter

Sequencer Main Unit

Models	DNBSEQ-E25、DNBSEQ-E25A*	
Dimensions	348 mm (L) × 312 mm (W) × 257 mm (H)	
Net Weight	~15kg	
Power	Rated Voltage and Power	24V DC, 5A
Touch Screen	LCD Touch Screen	
	Touch Screen Size	12.1 inch
	Touch Screen Resolution	1280 × 800
Maximum Sound Pressure	65 dBA	
Shell Protection Grade	IPX0	
Operating Environment Requirements	Temperature	15 ° C ~ 30 ° C
	Relative Humidty	20% RH ~ 80% RH
	Atmospheric Pressure	70 kPa~106 kPa
Shipping/Storage Environment	Temperature	-20 ° C ~ 50 ° C
	Relative Humidty	15% RH ~85% RH

*Both models have the same host configuration

Computing Module

Models	Standard (DNBSEQ-E25)	Enhanced (DNBSEQ-E25A)
CPU	i7-10700 (8 Core)	D-2183IT (16 Core)
Internal Storage	64G	128G
SSD	256GB SSD + 2T HDD	256GB SSD + 8T HDD
Power	20V DC, 11.5A	100-240V~50-60 Hz, 300VA
Net Weight	3.4kg	5.5kg
Dimensions	348 mm (L) × 312 mm (W) × 40 mm (H)	

Portable and Easy-to-use

DNBSEQ E25

Genetic Sequencer

Ordering Information

Cat. No	Product Name	Intended Market
900-000537-00	DNBSEQ-E25RS(CE-RUO)	RUO
900-000538-00	DNBSEQ-E25ARS(CE-RUO)	RUO
900-000715-00	DNBSEQ-E25RS(EAC)	RUO
900-000716-00	DNBSEQ-E25ARS(EAC)	RUO
940-000573-00	DNBSEQ-E25RS High-throughput Sequencing Set (FCL SE100)	RUO
940-000567-00	DNBSEQ-E25RS High-throughput Sequencing Set (FCL PE150)	RUO
940-000569-00	DNBSEQ-E25RS High-throughput Sequencing Set (App-C FCL SE100)	RUO
940-000574-00	DNBSEQ-E25RS High-throughput Sequencing Set (App-C FCL PE150)	RUO
900-000850-00	DNBSEQ-E25	IVD
900-000566-00	DNBSEQ-E25A	IVD
940-000601-00	Universal Sequencing Reaction Kit (E25 SM FCL SE100)	IVD
940-000604-00	Universal Sequencing Reaction Kit (E25 SM FCL PE150)	IVD

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Version: July 2024 I MGPA0522202-01

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*StandardMPS sequencing reagents are available in modified form in Germany, UK, Sweden, and Switzerland.

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