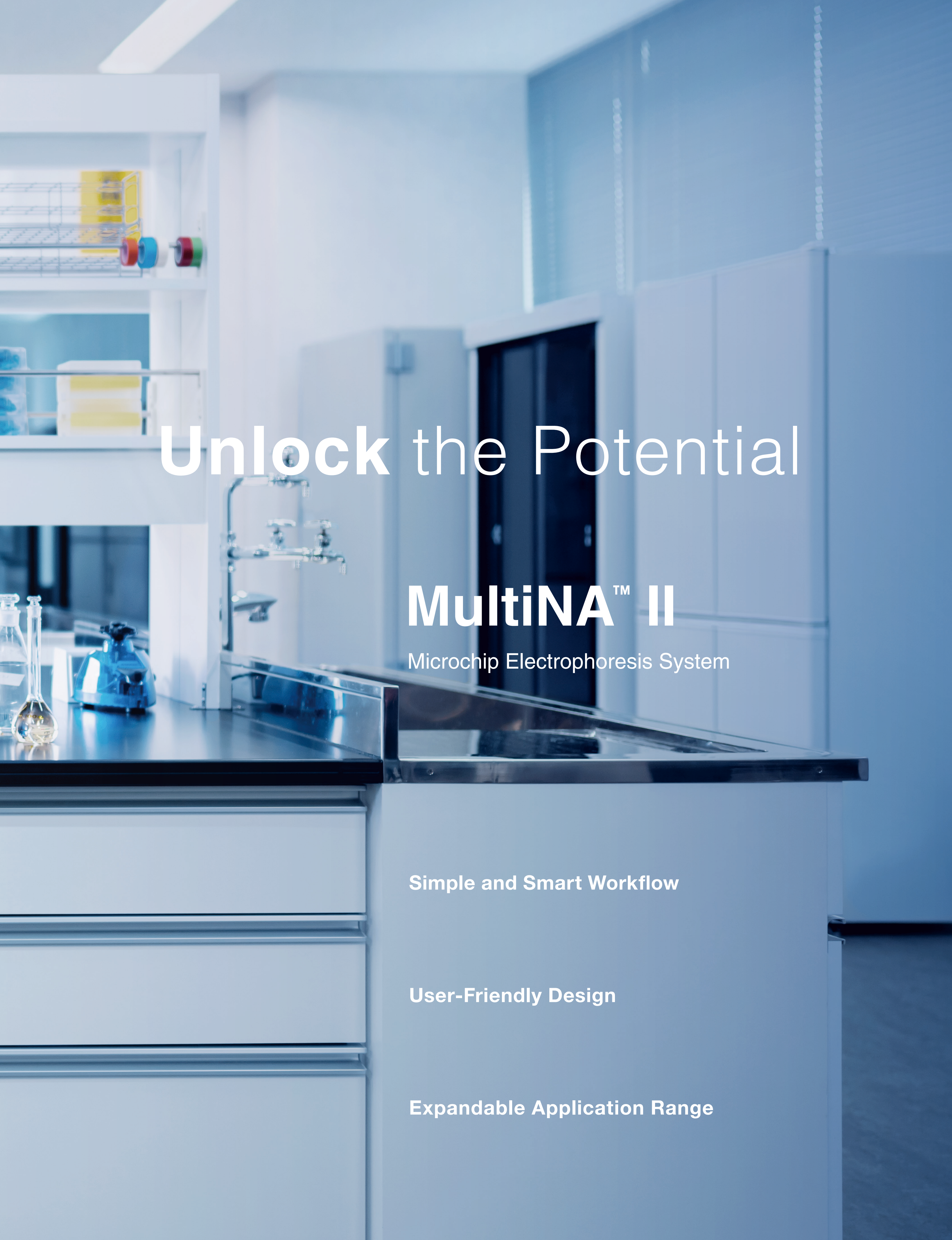
C297-E157

SHIMADZU
Excellence in Science

Microchip Electrophoresis System

MultiNA II MCE-301


SHIMADZU
MultiNA II
MICROCHIP ELECTROPHORESIS SYSTEM



Unlock the Potential

MultiNA™ II

Microchip Electrophoresis System

Simple and Smart Workflow

User-Friendly Design

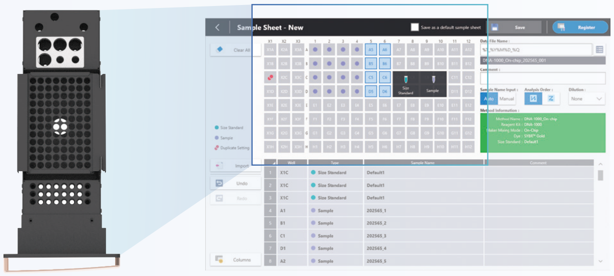
Expandable Application Range

Simple and Smart Workflow

Designed with the user in mind, MultiNA II enables efficient, reliable analysis using simple operations. The intuitive software provides clear-cut procedures for automatic analysis, significantly increasing laboratory productivity.

STEP 1 **Reliability**

Register analysis schedule

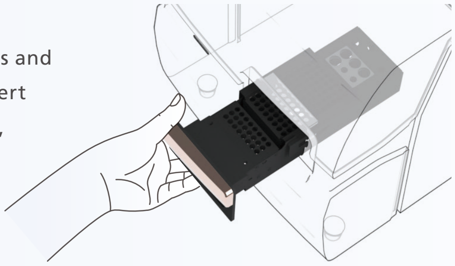


Because sample racks can be removed from the instrument for handling, samples can be registered while making sure they are handled properly. The software allows the analysis sequence to be selected using intuitive operations. It even allows schedules to be saved, imported, and exported.

STEP 2 **Operating Efficiency**

Place samples and reagents

Simply place the samples and reagents in the tray, insert the tray into the system, and start the analysis.



STEP 3 **Operating Efficiency**

Click the start button

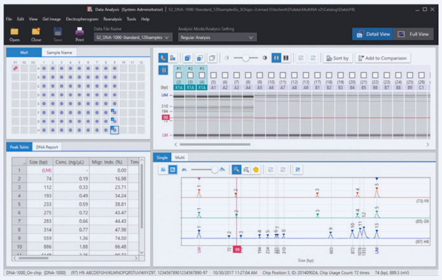
Dispense > Electrophorese > Separate > Detect > Rinse

Automatic Analysis

All steps from dispensing samples to rinsing the microchip are performed automatically by the system. Data is displayed successively, starting with the sample currently being analyzed, so results can be checked immediately.

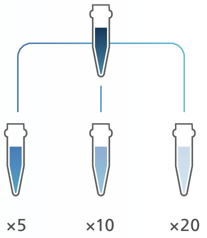
Convenience

Checking Analysis Results



Intuitive data analysis software enables instant confirmation of target information of interest.

Novel Functionality Achieves a New Workflow



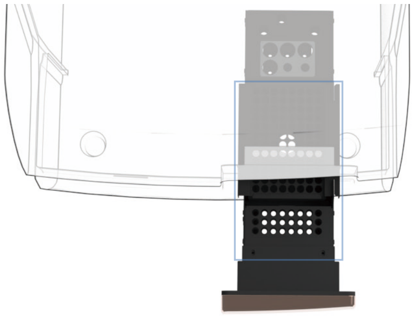
Automated Sample Dilution

Samples can be diluted with purified water to ensure the concentration is within the quantitatable concentration range. The system can automatically dilute samples to the specified concentration level (5, 10, or 20-fold dilution)*1.

*1 Dilution functionality is supported for up to 48 samples. Tubes for dispensing diluted samples are required separately.

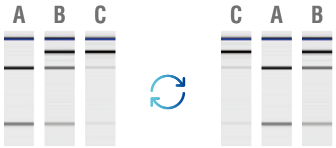
Adding Samples During Analysis

The system can be paused during an analysis to allow adding up to 120 samples. This is particularly useful when analyzing samples from multiple users because there is no need for the analyst to prepare all the samples at the same time or wait until the current analysis is finished.



Changing the Order of Gel Images

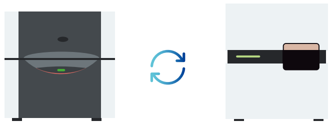
Gel images can be rearranged into any order, regardless of the actual sample analysis order.



Comparison/Analysis of Past Data

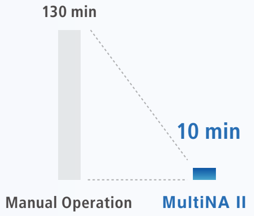
Past data can be displayed next to current data for comparison. Even data acquired using a previous model (MCE-202 MultiNA) can be loaded and analyzed*2.

*2 Data analysis is not supported for some reagent kits.



Operating Efficiency

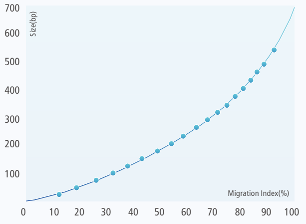
Automatic Analysis Significantly Shortens Analysis Time



Analysis can be started after 10 minutes of preparation. Fully automatic analysis significantly shortens operating time. In addition, the system enables overnight analysis, which provides time for focusing on research or business processes.

Reliability

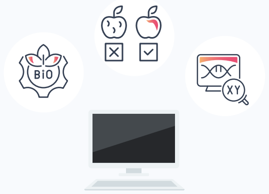
Calibration Curves Used for Automatic Prediction



Predicted sizes and concentrations are calculated automatically to provide numerically objective results. Each analysis is corrected using an internal standard reagent to provide reliable data.

Convenience

Convenience of Using Data



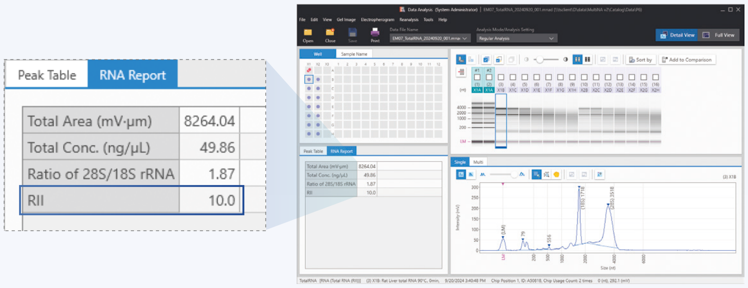
Dedicated data analysis software is equipped with a variety of functionality to support data processing based on specific applications.

Enhanced Analysis Functions

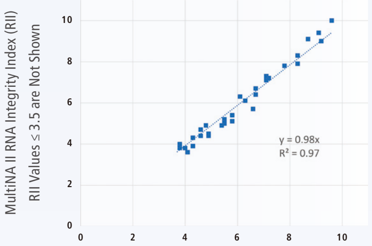
RNA

RNA Integrity Index (RII)

Extracted RNA continues to decompose as time elapses. MultiNA systems can calculate RII values as an independent method of evaluation. The correlation to integrity index values calculated by non-Shimadzu systems has a 0.95 or higher coefficient of determination value.



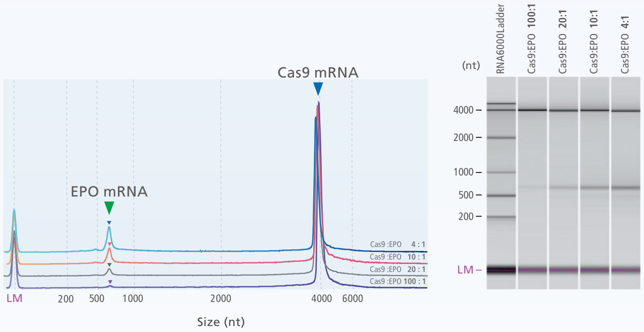
Total Area (mV·µm)	8264.04
Total Conc. (ng/µL)	49.86
Ratio of 28S/18S rRNA	1.87
RII	10.0



Comparison to Non-Shimadzu RNA Integrity Index Values
(Results from Shimadzu Independent Evaluation of Eukaryotes)

mRNA Analysis: Used for Purity Analysis

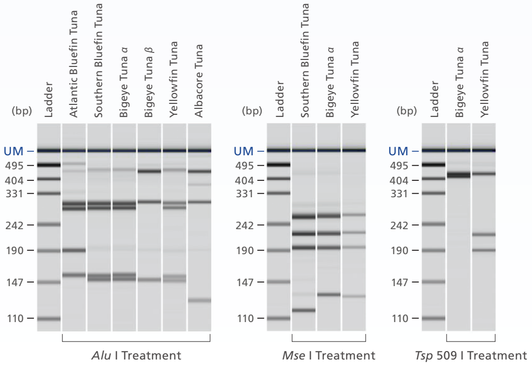
Cas9 mRNA (4522 nt) and EPO mRNA (859 nt) mixtures prepared to 4:1, 10:1, 20:1, and 100:1 concentration ratios were analyzed using the MultiNA. The EPO mRNA was clearly detectable for all ratios.



DNA

DNA Fingerprinting Analysis

For analysis with a positive control, the presence/absence of each DNA fragment in samples can be determined automatically. After analysis, results can be collectively listed or shown grouped with other samples of the same type.



Tuna PCR-RFLP Patterns

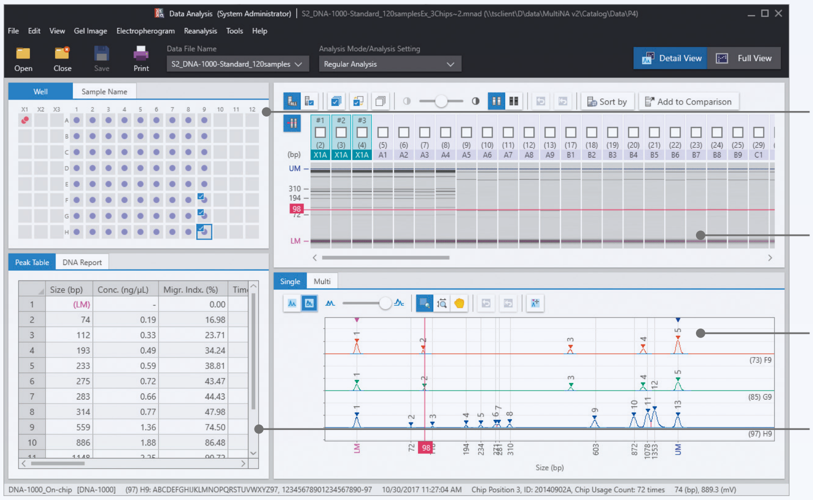
	Alu I Treatment							*Mse* I Treatment				*Tsp* 509 I Treatment	
Species	Atlantic Bluefin Tuna	Southern Bluefin Tuna	Bigeye Tuna α	Bigeye Tuna β	Yellowfin Tuna	Albacore Tuna	Species	Southern Bluefin Tuna	Bigeye Tuna α	Yellowfin Tuna	Species	Bigeye Tuna α	Yellowfin Tuna
298 bp	+	+	+	+	+	+	268 bp	+	+	+	429 bp	+	+
284 bp	+	+	+	–	+	–	220 bp	+	+	+	413 bp	+	–
190 bp	+	–	–	–	–	–	194 bp	+	+	+	218 bp	–	+
155 bp	+	+	+	–	+	–	133 bp	–	+	+	190 bp	–	+
148 bp	–	+	+	+	+	–	118 bp	+	–	–			

Tuna Discrimination Patterns

User- Friendly Design

Intuitive Software

In addition to rearranging gel images, it is easy to display size prediction values as size guides (red lines) within gel images or electropherograms.



Data Analysis (System Administrator) | S2_DNA-1000-Standard_120samplesEx_3Chips~2.mnad (\\tsclient\D\data\MultiNA v2\Catalog\Data\P4)

Data File Name: S2_DNA-1000-Standard_120samples

Analysis Mode/Analysis Setting: Regular Analysis

Peak Table

	Size (bp)	Conc. (ng/µL)	Migr. Indx. (%)
1	(LM)	-	0.00
2	74	0.19	16.98
3	112	0.33	23.71
4	193	0.49	34.24
5	233	0.59	38.81
6	275	0.72	43.47
7	283	0.66	44.43
8	314	0.77	47.98
9	559	1.36	74.50
10	886	1.88	86.48

DNA-1000_On-chip [DNA-1000] (97) H9: ABCDEFGHIJKLMNOPQRSTUVWXYZ97, 12345678901234567890-97 10/30/2017 11:27:04 AM Chip Position 3, ID: 20140902A, Chip Usage Count: 72 times 74 (bp), 889.3 (mV)

Sample Wells

Indicates the arrangement of samples within the rack

Gel Image

Savable as image data (JPG, BMP, or TIF)

Electropherograms

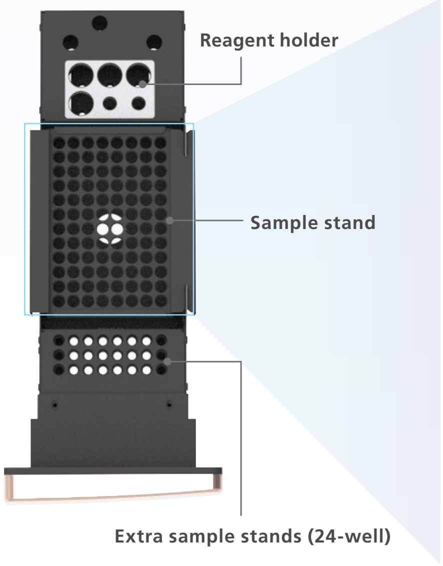
Savable as image data (JPG, BMP, or TIF)

Peak Table

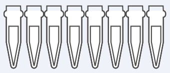
Size prediction values, concentrations, and other data can be output as a CSV file. Concentrations are calculated in terms of both ng/µL and nmol/L.

Removable Sample Rack

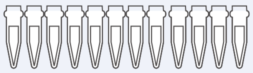
This removable rack holds up to 96 plates. Up to 2 types of reagent kits can be loaded in a mixed arrangement.

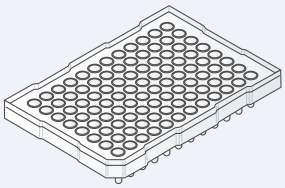


Set of 8 attached tubes



Set of 12 attached tubes





96-well plate

In addition to holding sets of 8 or 12 attached tubes, most commercially available 96-well plates can be installed as well. Samples can even be analyzed with the aluminum evaporation barrier film left attached.

Expandable Application Range

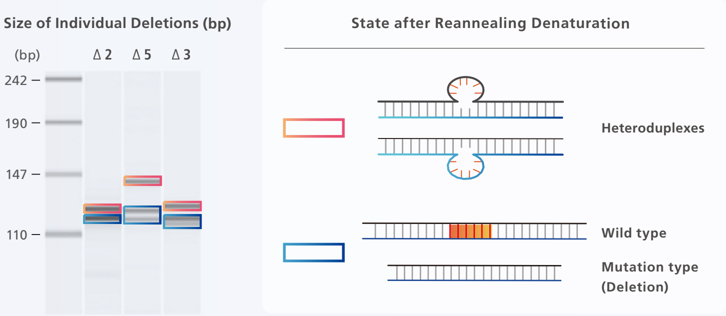
Genome Editing

Functionality for grouping analysis and molar concentration ratio analysis enables powerful support for screening genome-edited samples.

Detection of Deletion Mutations Induced by Genome Editing Tools

The availability of genome editing tools has enabled genetic modification of biological organisms. Consequently, research activity involving genome editing has expanded rapidly. Heteroduplex mobility assaying is a quick, easy, and inexpensive method for evaluating the introduction of mutations. Since electrophoresis of heteroduplex DNA tends to involve slower mobility, it can be used to determine the presence/absence of mutations and the genotype.

Sample
▼ PCR analysis
PCR products
▼ Thermal denaturation and annealing
Heteroduplexes
▼ Electrophoresis
Detect mutations



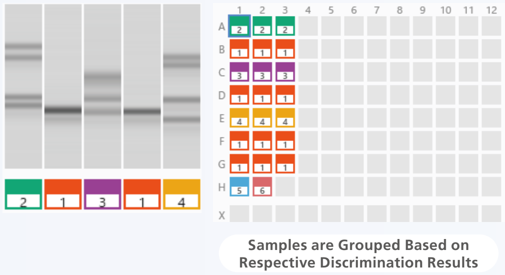
Detection of Deletion Mutations (Hetero) after the F1 Generation

Grouping Analysis

ANALYTICAL INTELLIGENCE

Correlation coefficient values are calculated from heteroduplex mobility assay results for each sample and then samples with the same mutation type are grouped. Consequently, discrimination between homo and hetero types and between mutation types, which had been accomplished visually, can now be detected automatically and displayed as a single list.

Discriminating between Band Patterns Based on Correlation Values



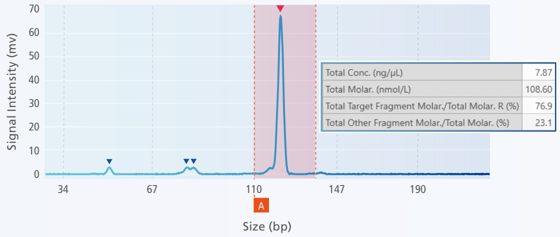
	1	2	3	4	5	6	7	8	9	10	11	12
A	2	2	2									
B	1	1	1									
C	3	3	3									
D	1	1	1									
E	4	4	4									
F	1	1	1									
G	1	1	1									
H	5	6										
X												

Samples are Grouped Based on Respective Discrimination Results

Molar Concentration Ratio Analysis

By specifying the target size range, the molar concentration ratio of peaks (bands) within that size range can be calculated. The mutation activity of the designed genome editing tool can be quantitatively evaluated by analyzing HMA, Cel-I assay, PCR-RFLP, and other data.

Example of Analyzing the Molar Concentration Ratio of PCR-RFLP Samples



Total Conc. (ng/μL)	7.87
Total Molar. (nmol/L)	108.60
Total Target Fragment Molar./Total Molar. R (%)	76.9
Total Other Fragment Molar./Total Molar. (%)	23.1

ANALYTICAL INTELLIGENCE

- Automated support functions utilizing digital technologies, such as M2M, IoT, and Artificial Intelligence (AI), that enable higher productivity and maximum reliability.
- Allows a system to monitor and diagnose itself, handle any issues during data acquisition without user input, and automatically behave as if it were operated by an expert.
- Supports the acquisition of high quality, reproducible data regardless of an operator's skill level for both routine and demanding applications.

NGS

With the high-sensitivity kit, smear analysis functionality, and RNA integrity index calculation, MultiNA II can easily evaluate the quality of NGS samples.

NGS Library Quality Control

In order to obtain good results from next-generation sequencers (NGS), the distribution and concentration of sizes in the NGS library must be properly understood. The smear analysis functionality can be used to calculate the average size and concentration values. Used in combination with a high-sensitivity kit, library data can be evaluated for concentrations down to 5 pg/μL.

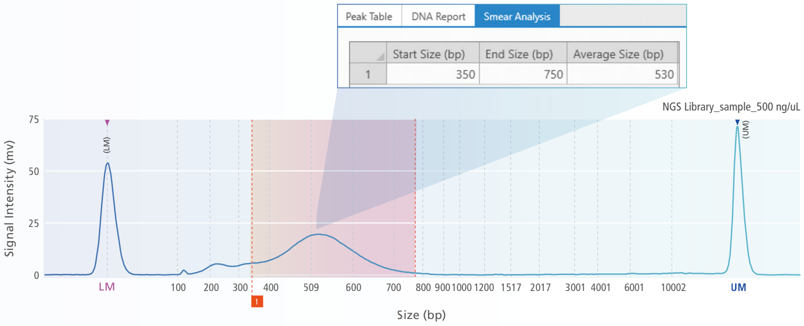
Sample

▼ Pretreatment with preparation kit

NGS library

▼ Electrophoresis

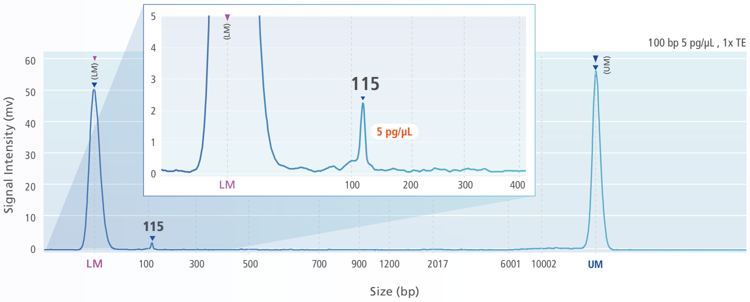
Smear analysis



	Start Size (bp)	End Size (bp)	Average Size (bp)
1	350	750	530

High-Sensitivity Kit

Used in combination with a high-sensitivity kit, library data can be evaluated for low concentrations.



Genotyping

DNA fingerprinting functionality makes it easy to identify genotypes.

Determining the Type of Meat Products

If it is difficult to identify the type of meat based on its appearance and texture, then it can be helpful to determine the type genetically. For example, depending on the freshness and processing status of meat, it may be difficult to identify the type of meat, but by using PCR analysis in combination with restriction enzyme treatment, the type of meat can be determined with high accuracy.

Sample

▼ DNA extraction

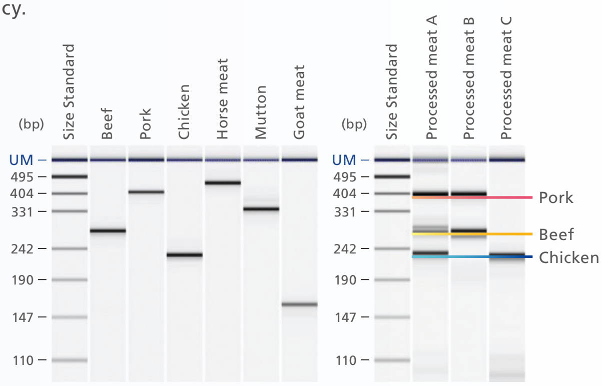
Purified DNA

▼ PCR analysis

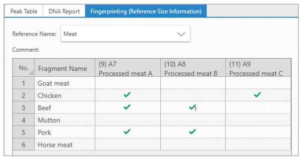
PCR products

▼ Electrophoresis

Determine variety



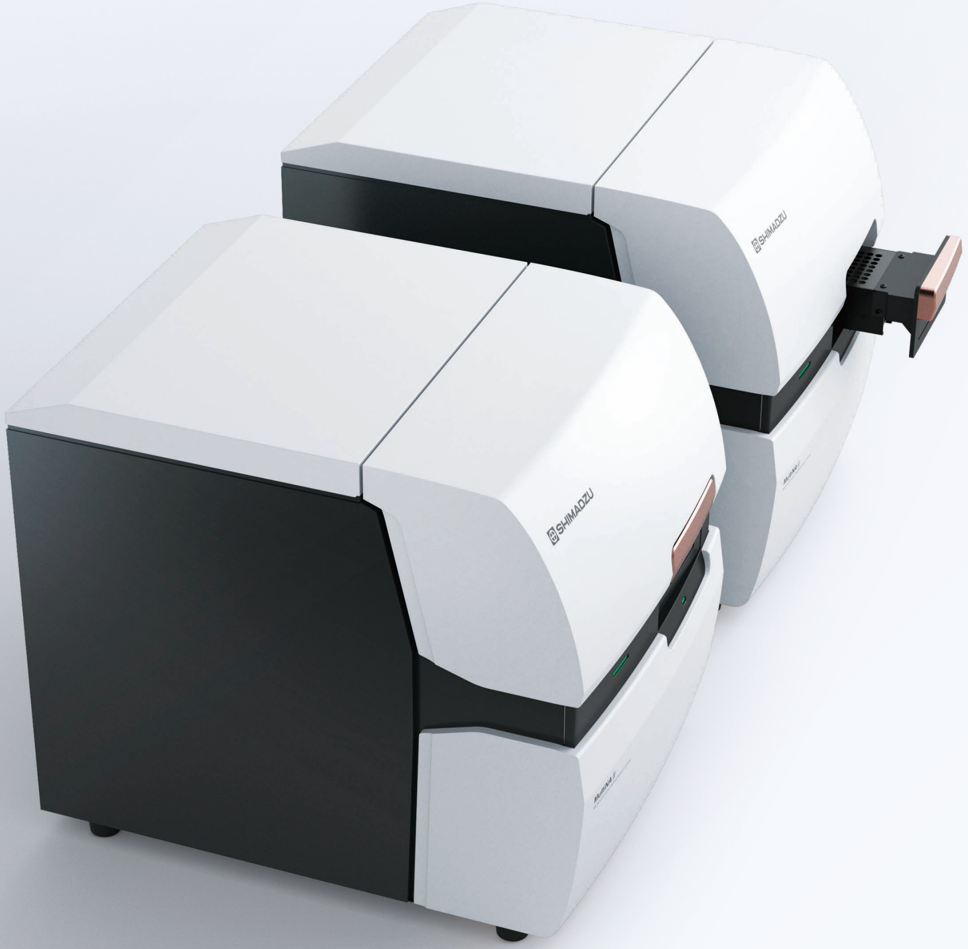
Gel Image of PCR Products from Meat Samples



Reference Name: Meat

Comment:

No.	Fragment Name	(9) A7 Processed meat A	(10) A8 Processed meat B	(11) A9 Processed meat C
1	Goat meat			
2	Chicken	✓		✓
3	Beef	✓	✓!	
4	Mutton			
5	Pork	✓	✓	
6	Horse meat			

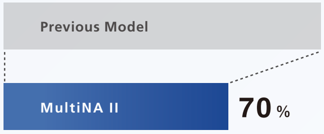


ECO Functions, Energy Savings

MultiNA II models achieve 30 % lower power consumption than previous models. In addition, the size is 27 % shorter than previous models, making it suitable even for confined laboratory spaces. Finally, it consumes over 40 % less purified water for rinsing, which helps reduce the volume of liquid waste and its environmental impact.

Energy Savings Achieved

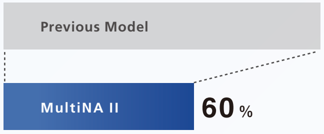
Comparison of Power Consumption by MultiNA II and Previous Model



Power consumption was reduced to 70 % of the previous model. That not only reduces running costs during analysis, but also contributes to achieving a carbon-free society by reducing CO_2 emissions.

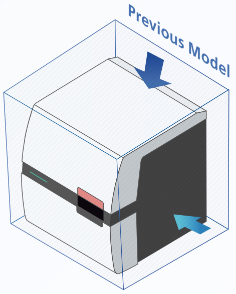
Water Savings

Purified Water Consumption by MultiNA II Compared to Previous Model



The purified water consumption for rinsing was reduced to less than 60 % of the previous model, which helps reduce the volume of liquid waste and its environmental impact.

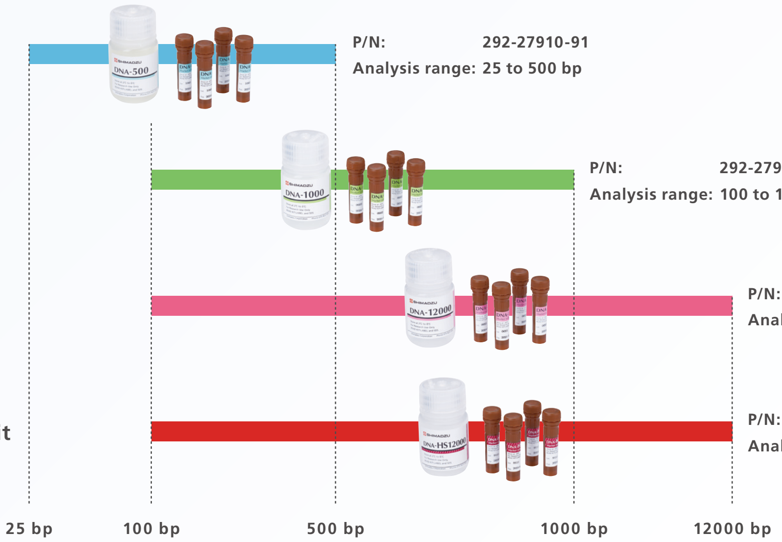
Requires Less Space



The MultiNA II has a 15 % smaller footprint and is 27 % shorter than the previous model (with the front door open). That makes it easier to install and requires less laboratory space.

Consumables

Reagent Kits for a Wide Range of Applications



DNA-500 Kit
P/N: 292-27910-91
Analysis range: 25 to 500 bp

DNA-1000 Kit
P/N: 292-27911-91
Analysis range: 100 to 1000 bp

DNA-12000 Kit
P/N: 292-36600-91
Analysis range: 100 to 12000 bp

DNA-HS12000 Kit
P/N: 292-36800-91
Analysis range: 100 to 12000 bp

RNA Kit
P/N: 292-27913-91
Analysis range: 200 to 6000 nt

Microchip

P/N: 292-36010-41
292-36010-58

Can be used for all reagent kits.
Can be used repeatedly due to rinsing by the system.

Microchip Cleaning Kit

P/N: 292-35925-91

Cleaning microchips with this kit can remove adsorbed components and improve (or restore) microchip separation performance.

Key Product Specifications

Resolution	5 bp (25 to 100 bp), 5 % (100 to 500 bp), 10 % (500 to 1000 bp), or 20 % (1000 to 12000 bp)
Sizing Accuracy	DNA-500 kit: ±5 bp (25 to 100 bp) or ±5 % (100 to 500 bp) DNA-1000 kit: ±15 % (100 to 1000 bp) DNA-12000 kit: ±15 % (100 to 12000 bp) DNA-HS12000 kit: ±15 % (100 to 12000 bp)
Supported Sample Quantities	2 to 50 µL for DNA analysis or 3 to 25 µL for RNA analysis
External Dimensions	W375 × D520 × H452 mm
Weight	39 kg
Power Supply	100 to 240 V at 300 VA max.

The above specification values are based on verification tests conducted using typical samples and analysis conditions, as specified by Shimadzu. The indicated specifications might not be achieved in some cases, depending on the actual samples and analysis conditions used.

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Shimadzu Corporation
www.shimadzu.com/an/