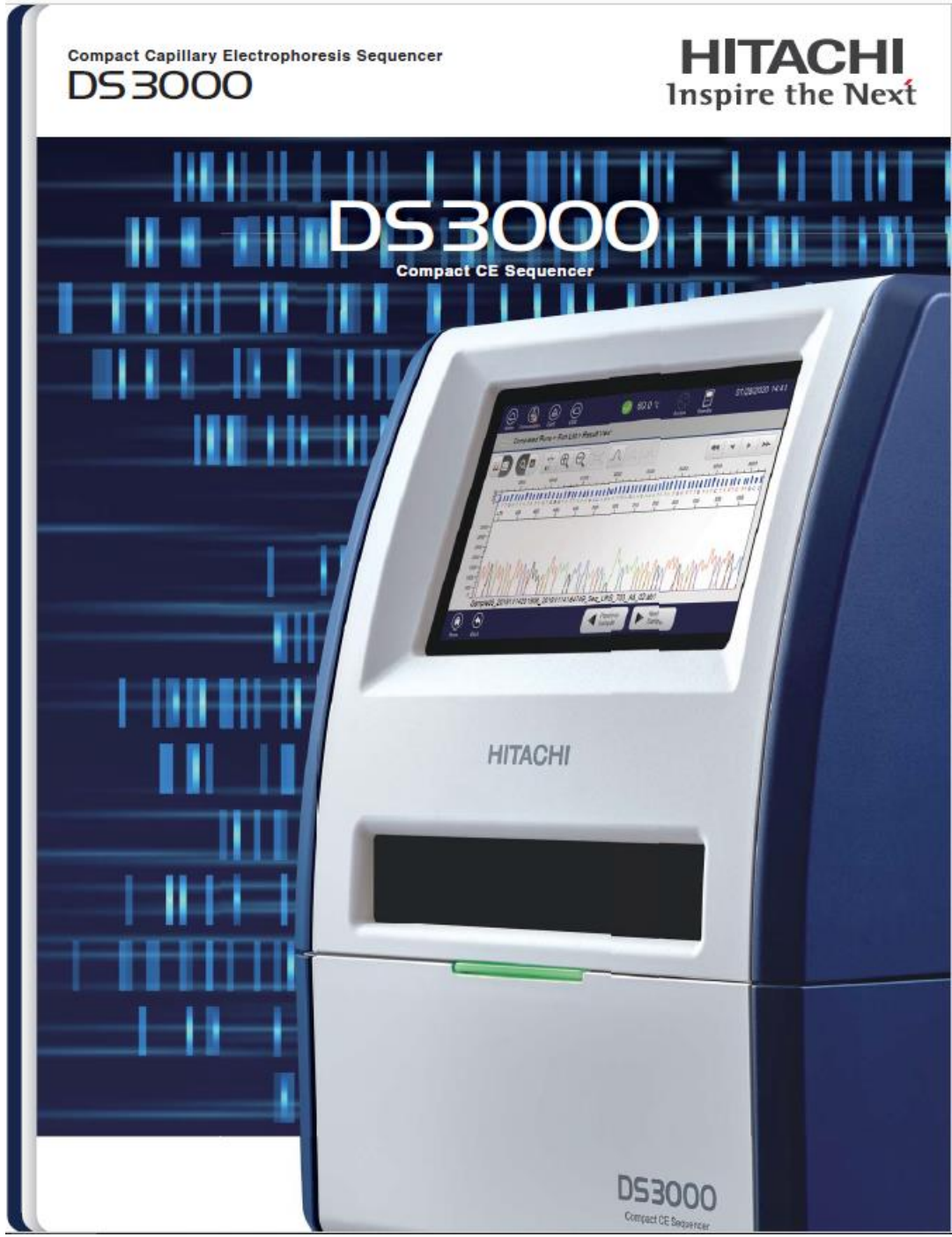
HITACHI
Inspire the Next

Spot color : PANTONE Cool Gray 11C + PANTONE 186C

DS3000
毛細管電泳DNA定序儀

產品專員 陳政廷 博士
冷泉港生物科技



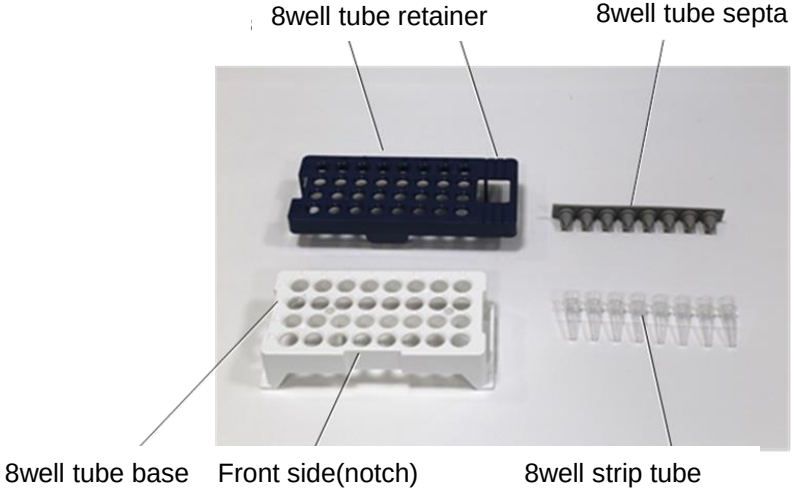
毛細管電泳定序儀介紹

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Compact CE Sequencer DS3000

HITACHI
Inspire the Next





- ✓ Dimension: 400 (W) x 600 (D) x 600 (H) mm, 40 kg
- ✓ Application: Sequencing (定序分析), Fragment analysis (片段分析)
- ✓ Number of capillaries(length) : 4根毛細管(36 cm)，一次可跑四個樣品
- ✓ Sample Tray: 32 well plate (4 x 8 well Strip Tube)
- ✓ Simultaneous detection: 6 colors

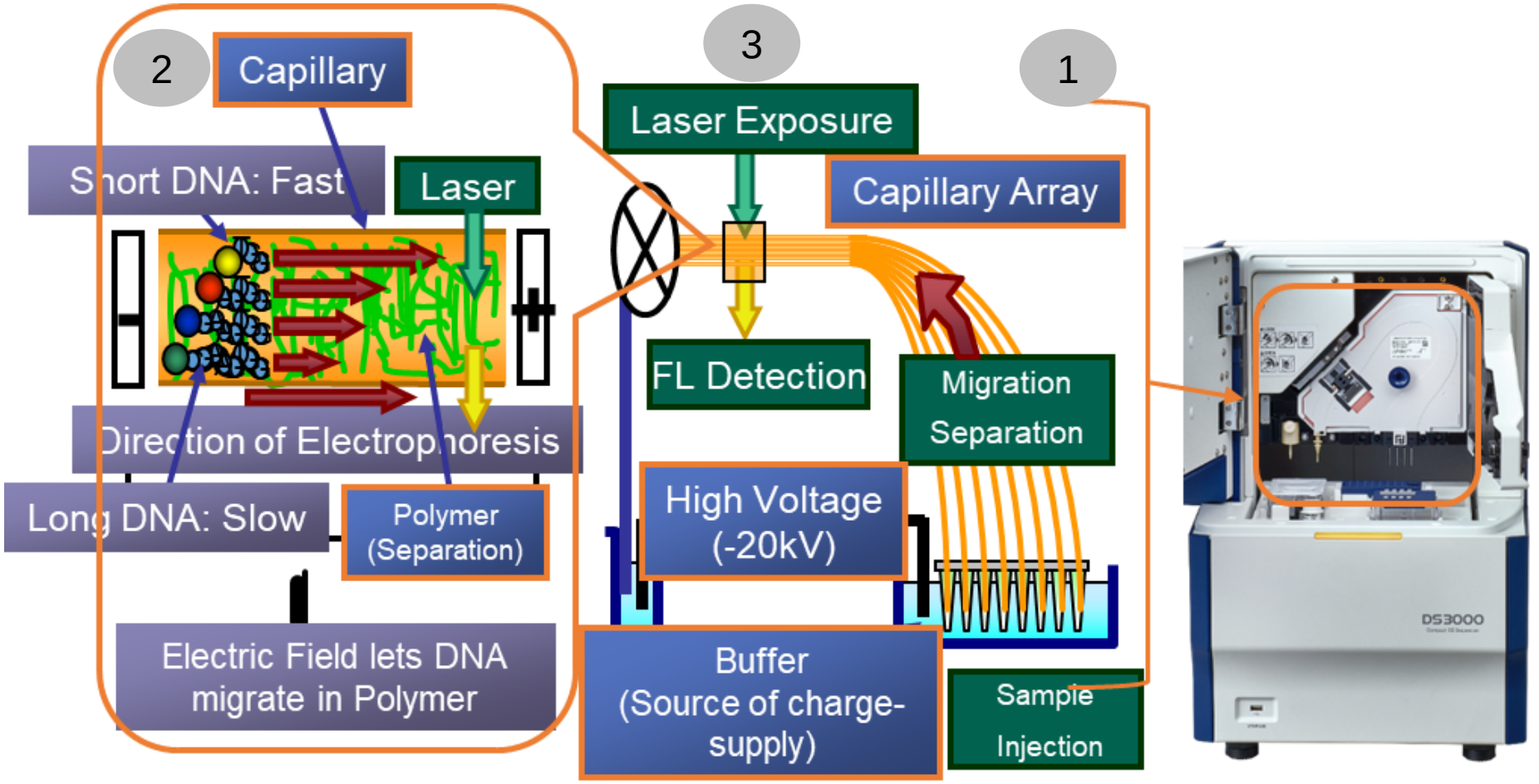
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毛細管電泳定序儀原理

1. DNA 帶負電在注有膠體的毛細管內進行電泳

2. DNA分子在膠體內的電泳速率取決於分子長度，越短越快、越長越慢。

3. 螢光物標定的DNA分子經由激發放出的螢光訊號可被儀器偵測

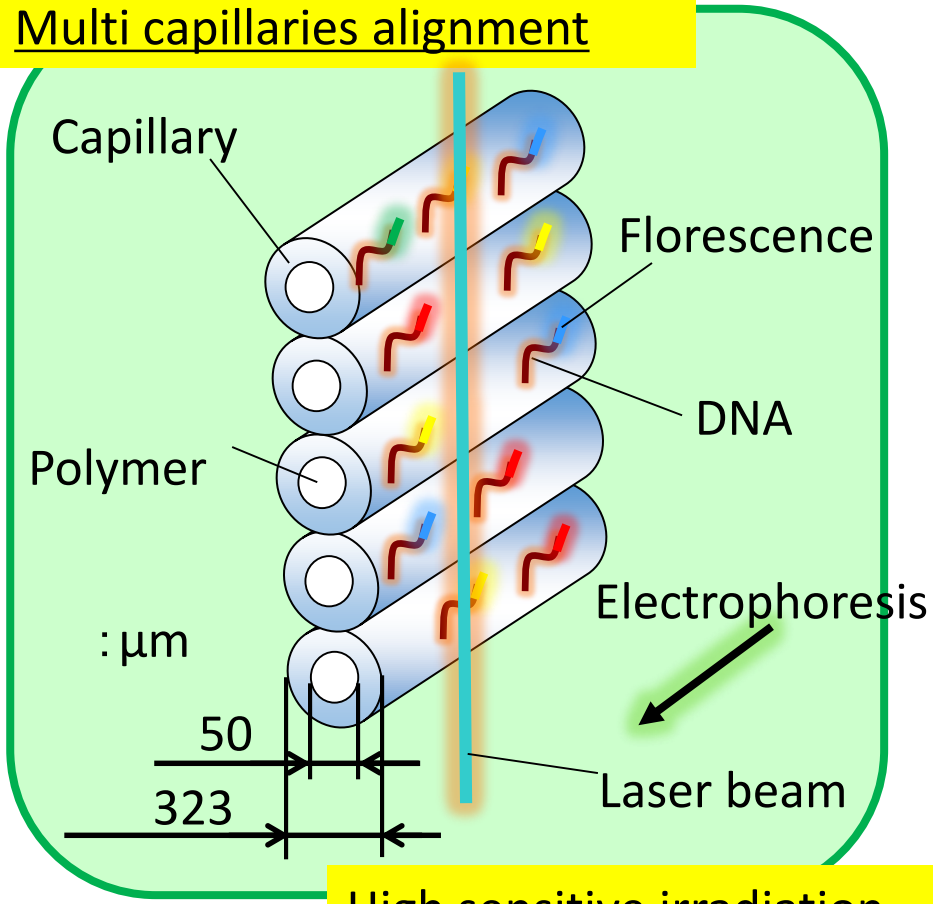


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Hitachi core technology（Multi focus）

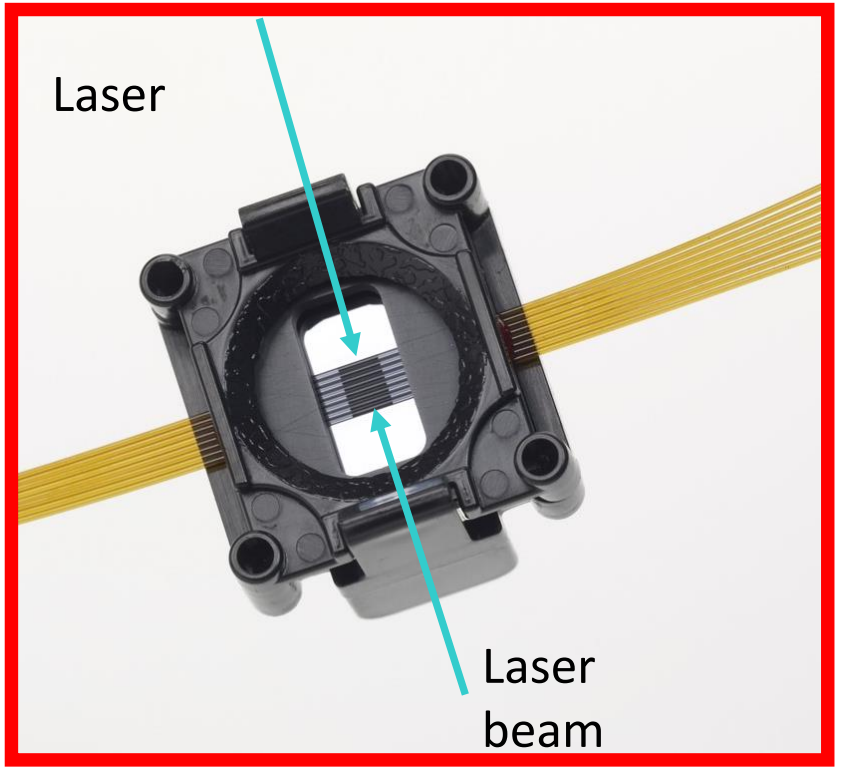
High sensitive multiflorous beam technology for high throughput and low cost analysis

Multi capillaries alignment



High sensitive irradiation

Irradiation unit



Capillary array

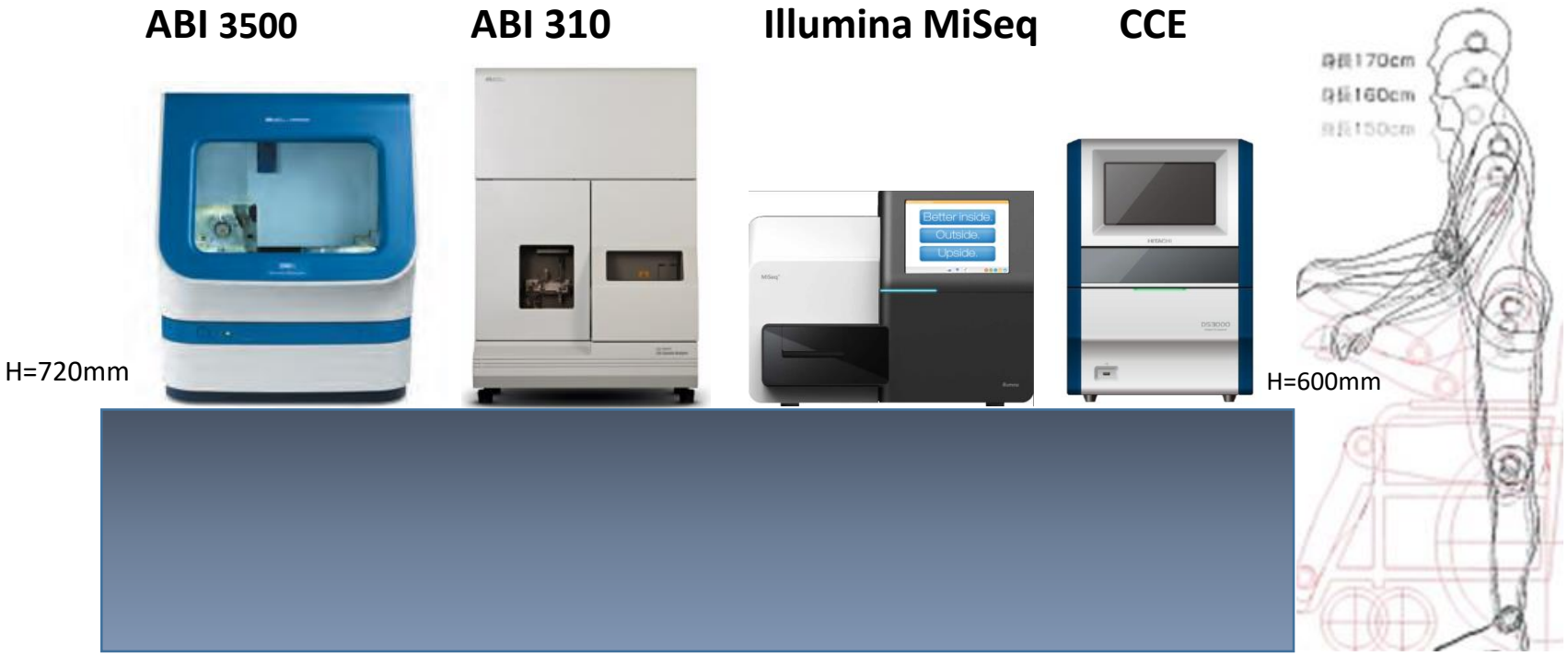
不佔太多空間的緊湊設計 Small footprint

■比傳統定序儀體積更小:

The compact design of size is W 400 mm x D 600 mm x H 600 mm, and the weigh is approx. 40 kg.（About ½ as the ratio with the conventional one.)

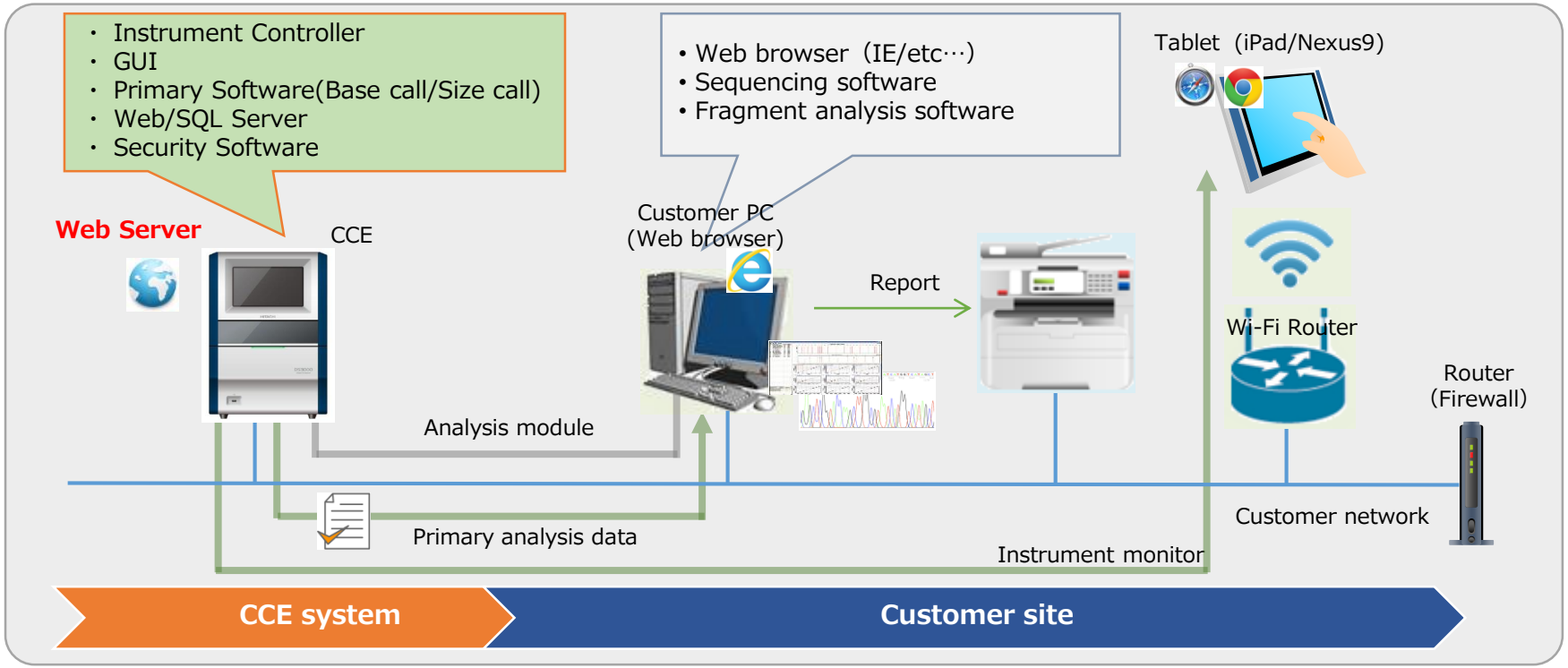
■觸碰面板不需額外PC:

CCE with touch panel computer (No additional PC space) will offer network access, which allow transfer via LAN connection to a host computer.



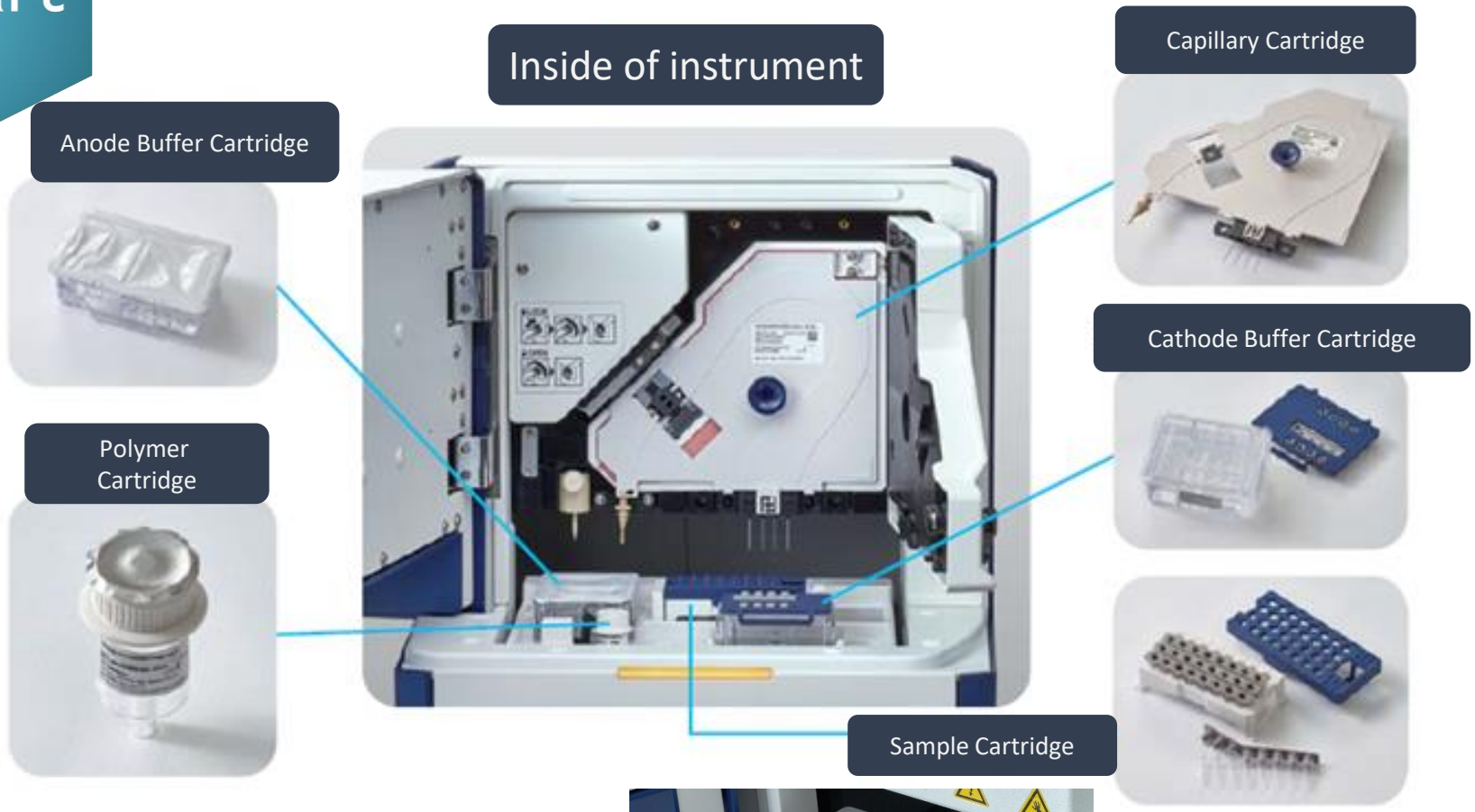
Web Application Software

Customers can utilize CCE at remote site via internal network (wired).



Cartridge-type consumable brings easy installations

Smart







Reagent guaranteed number of injections

Reagent	Max. number of injections	Mas number of samples
Capillary Cartridge	200 injections	800 samples
Anode Buffer Cathode Buffer	80 injections	320samples
Polymer 7 Polymer 4	16 injections	64 samples

Smart

Cartridge-type consumable brings easy installations

HITACHI
Inspire the Next





新式無pump設計，無須花時間清理pump，使用上更便利迅速

Reduced maintenance frequency

● No need to clean a pump
By developing a syringe-type polymer cartridge having a high-durability movable seal, and making the liquid transport system pump-less, eliminates pump maintenance.

● No need to remove bubbles
By adopting an unique polymer injection system, it is not necessary to remove bubbles at the time of polymer filling, reducing excess polymer consumption.

● Less frequent light source replacement
Pulse signal control means LD is only on during detection. The shortened illumination time increases the useful lifespan, especially when compared to complicated and expensive light sources such as Argon gas lasers.

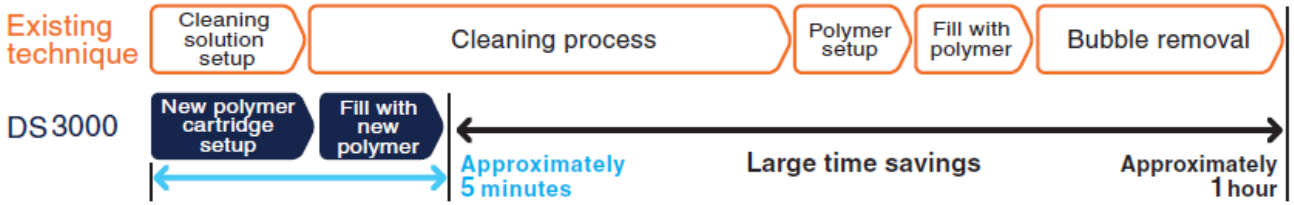
See the next page

較低的雷射光源更換頻率

整體操作時間更縮短、作業流程更省時便利

Workflow when changing the type of polymer

*Comparison to products from other companies



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Smart Less frequent light source replacement

✓ **Less frequent light source replacement**

Analog pulse signal control brings the long lifetime of light source.

Pulse signal control means LD is only on during detection. The shortened illumination time increases the useful lifespan, especially when compared to complicated and expensive light sources such as Argon gas lasers.

	DS3000 light source	Conventional light source
Light source	LD light source →Less frequent light source replacement (About 6-7 years) ★	Argon gas laser →High frequent light source replacement (About 2-3 years)
Light source lifetime	>10,000 hours ★	6,500 hours
Signal control method	Pulse signal oscillation ★	Continuous oscillation

雷射二極體光源比傳統argon laser價位更低，且在偵測訊號時才會啟動，提高使用壽命

Usability

DS3000 works with 3rd party secondary software

- ✓ Standard ab1(sequence)/fsa(fragment) file format is supported.

Sequencing analysis

Company	Software	application
Gene Codes Corporation TCA GENE AGT CODES	SEQUENCHER®	Trimming sequencing data, assemble, comparison of sequence
SOFTGENETICS® Software PowerTools for Genetic Analysis	MUTATION Surveyor® DNA Variant Analysis Software	In-Del analysis, mutation quantitative analysis, Bisulfite sequence analysis

Fragment analysis

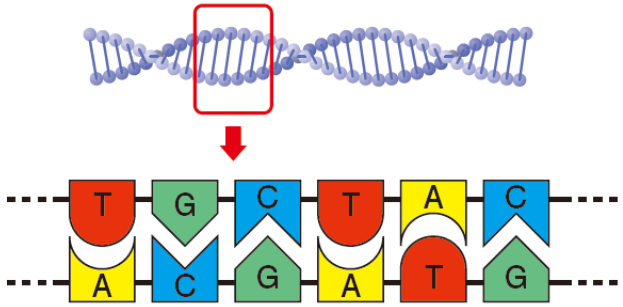
Company	Software	Application
SOFTGENETICS® Software PowerTools for Genetic Analysis	GeneMarker® The Biologist Friendly Software	MSI, MLPA, Trisomy/Aneuploidy, FragileX, Cystic Fibrosis, Fragment analysis auto-judgement and reporting
	ChimeRMarker Automated Chimerism Analysis Software	Specialize Chimerism analysis

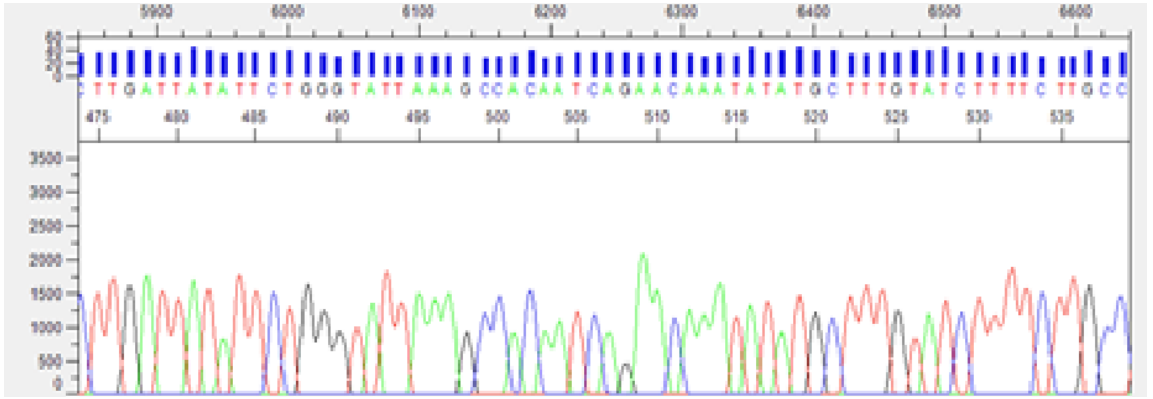
毛細管電泳定序儀應用

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■ Sequencing analysis (基因定序)

Method of the base sequence of ＤＮＡ





■ Fragment Analysis (片段分析)

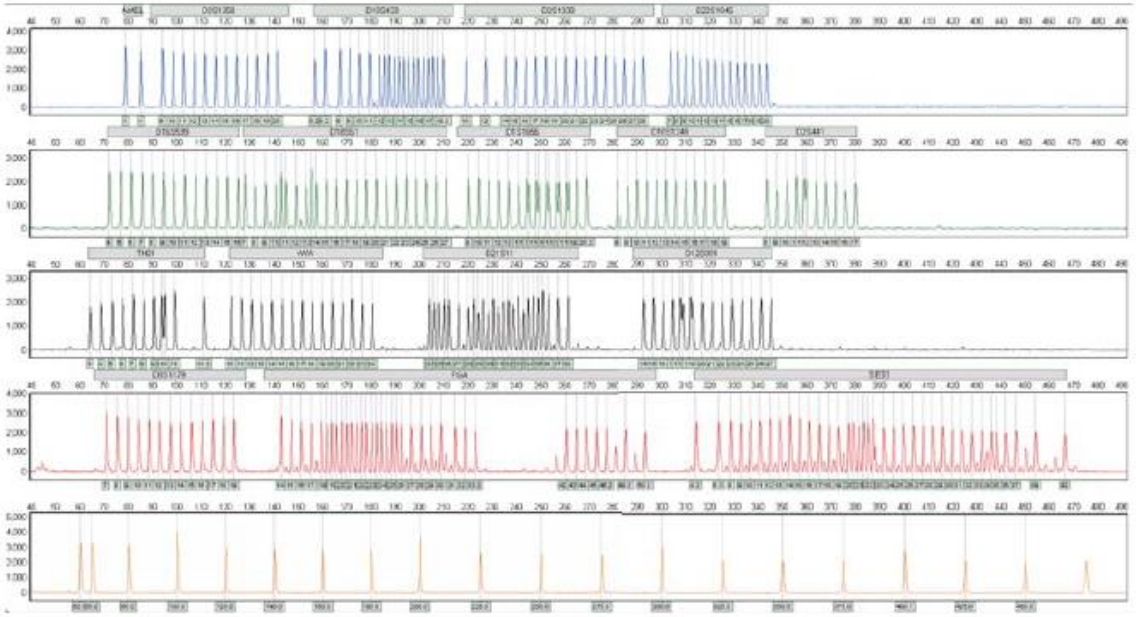
Method of analyzing the length of DNA fragments and obtaining the information based on fragments' appearance pattern

FragmentA CACACACACACACA

FragmentB CACACACACA ⟷ 4 bp shorter than fragmentA

FragmentC CACACACA ⟷ 6 bp shorter than fragmentA

The difference of length of fragments shows the different mobility shift



Basic idea of Sanger sequencing

Cell replication

The process of DNA synthesis and replication in a cell involves DNA helicase, DNA polymerase, DNA template, and deoxynucleotides. DNA replication starts when DNA helicase unravels the double-helix structure to expose single-stranded DNA and form a replication fork. RNA primase introduces a primer that binds to the single-stranded DNA. DNA polymerase then binds to the replication fork and starts DNA synthesis by sequentially adding nucleotides to the 3′-hydroxyl end of the RNA primer bound to the DNA template (Figure 1). The result is the creation of an "extension product."

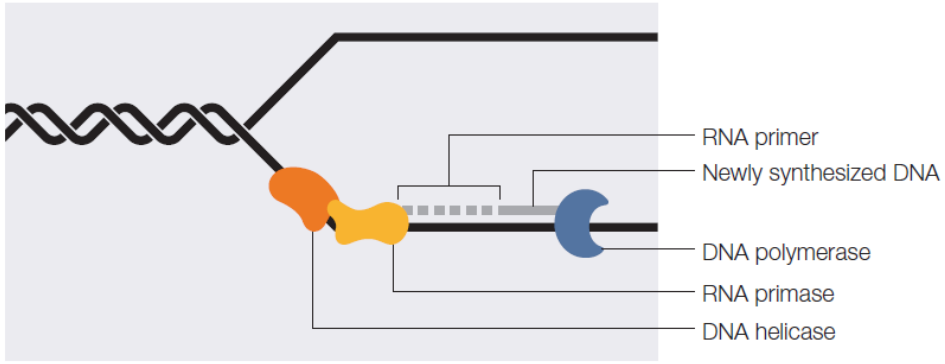
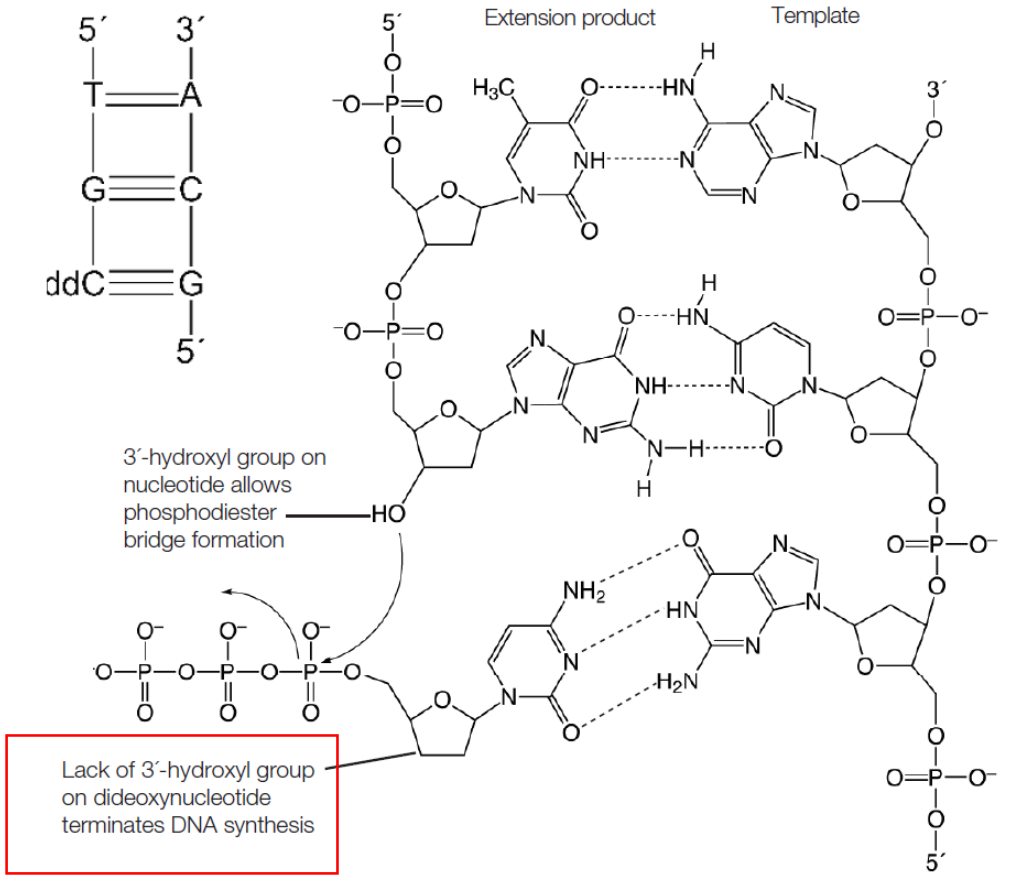


Figure 1. DNA replication fork.

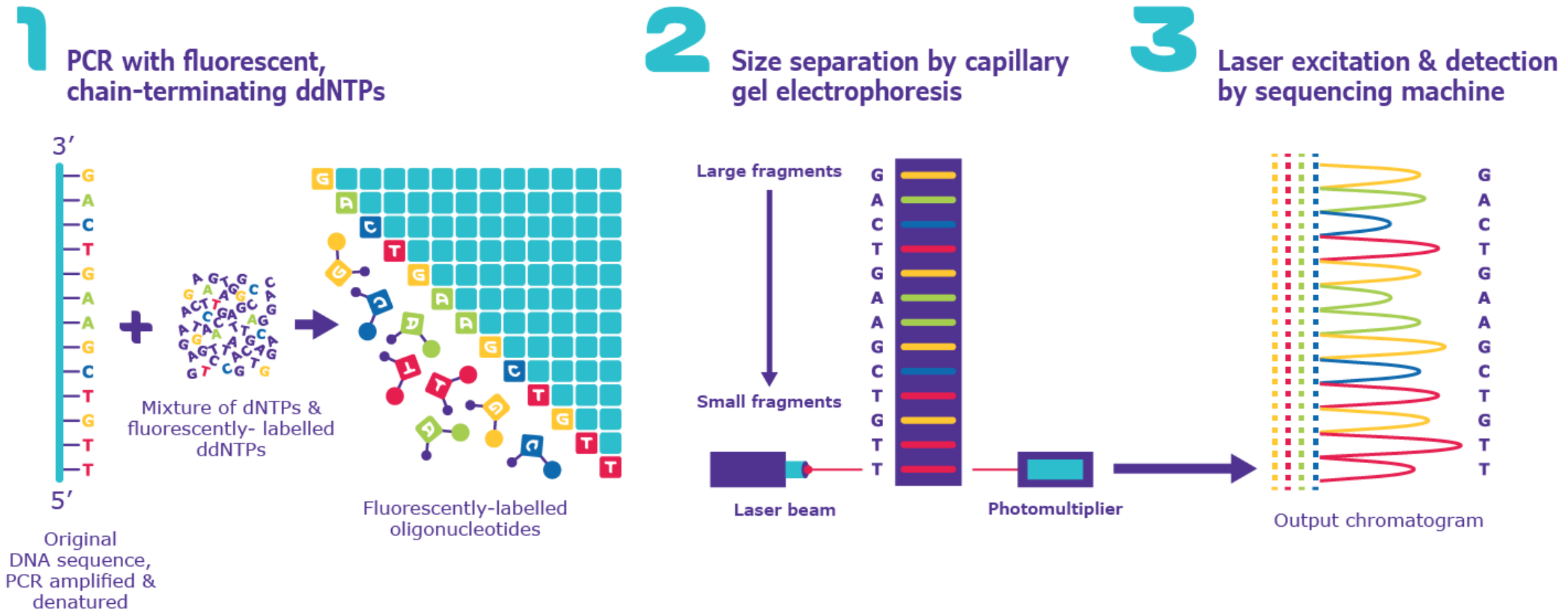
The extension product grows in the 5′ to 3′ direction by forming a phosphodiester bridge between the 3′-hydroxyl group at the growing end of the primer and the 5′-phosphate group of the incoming deoxynucleotide [1] (Figure 2).

當聚合酶接到dNTP可形成phosphodiester bond， 聚合反應可以繼續。



ddNTP與dNTP的差異只在3’端少一個氧原子，在進行PCR反應時，ddNTP會隨機的被加入正在合成的DNA片段中，一旦ddNTP被加入，因3’端少一個氧原子，無法與下一個核苷酸的5’-磷酸結合，使DNA合成中止

Basic idea of Sanger sequencing



Mutation analysis

A method to improve the resolution at the beginning of the reads.

A polymer for sequencing, in general, is not adequate to separate short nucleotides (~40 bp). Thus the basecalling quality at the beginning of the reads. A 5’ tailed primer improves the resolution and the basecalling quality.



定序分析可運用之領域

Validate recombinant DNA (重組DNA序列確認)

Plasmid cloning and its validation are one of the most routinely repeated work in any laboratory of molecular biology. Sanger sequencing is the gold standard for that.

Mutation analysis (突變點分析)

Single base substitution can dysregulate the function of the oncogenes. Now a number of mutations are used for companion diagnostics. Unique methodologies to improve the data reliability are also introduced.

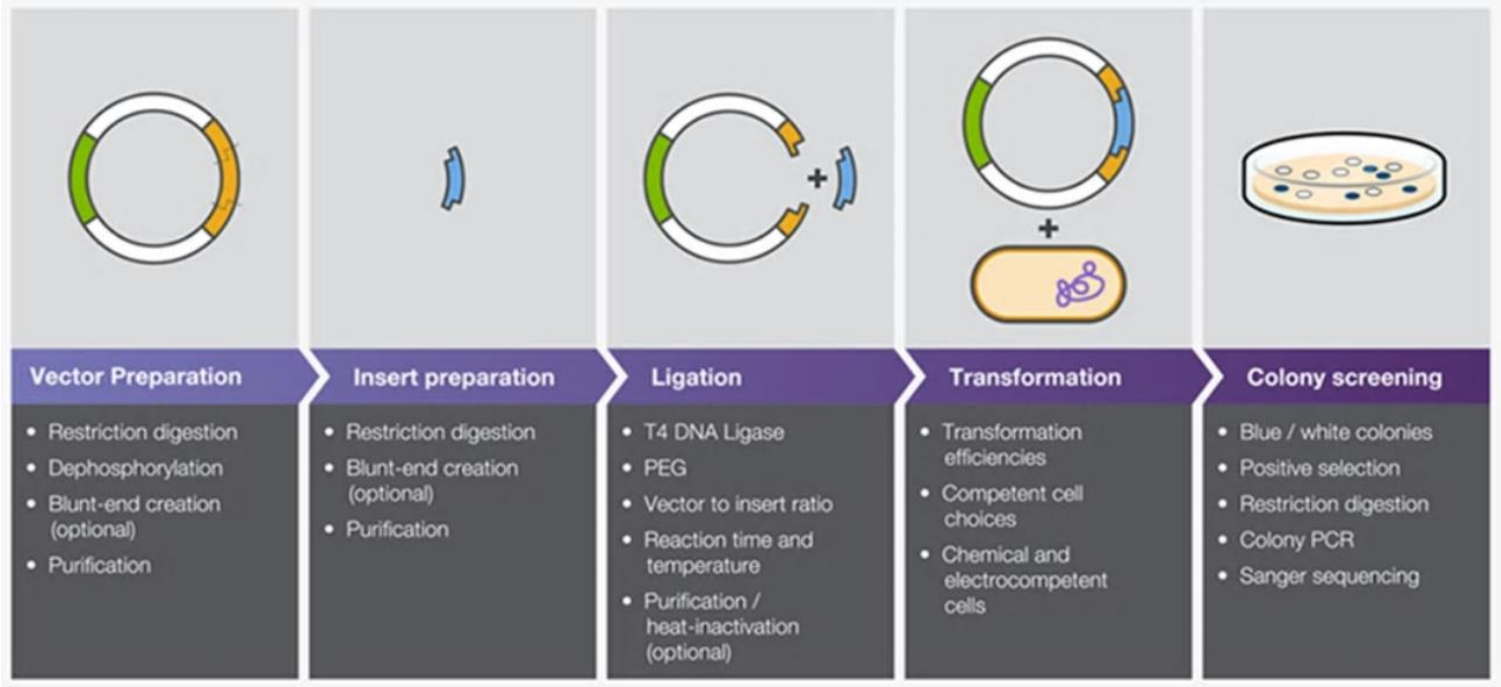
Quantifying the genome editing (確認基因編輯成功與否)

The success of CTRISPR-Cas9 system

Validate recombinant DNA (重組DNA序列確認)

For this routinely repeated work, researcher needs cheap, quick and simple method. Thus Sanger sequencing is the gold standard for this work.

DS3000 can provide **longer sequencing reads quickly**



DS3000		
run module	run time (approx.)	read length Blast CRL
Fast-seq	**30 min**	**ca. 650 bp**
Std-seq	1 hr	**ca. 830 bp**

SeqStudio		
run module	run time (approx.)	read length QV30CRL
ShortSeq	30 min	350 bp
MediumSeq	45 min	500 bp
LongSeq	<2 hrs	800 bp (QV20)

https://www.thermofisher.com/jp/ja/home/life-science/cloning/cloning-learning-center/invitrogen-school-of-molecular-biology/molecular-cloning/cloning/traditional-cloning-basics.html

Mutation analysis（突變點分析)

In cancer genetics, genetic mutation can be categorized into 2 types.

Germline mutation (生殖細胞突變)

A gene change in a body's reproductive cell (egg or sperm) that becomes incorporated into the DNA of every cell in the body of the offspring. Germline mutations are passed on from parents to offspring.

-> Mutation exist every cell in the body of the offspring.

Somatic mutation (體細胞突變)

An alteration in DNA that occurs after conception. Somatic mutations can occur in any of the cells of the body except the germ cells and therefore are not passed on to children.

-> Mutation exist only a part of the cell.

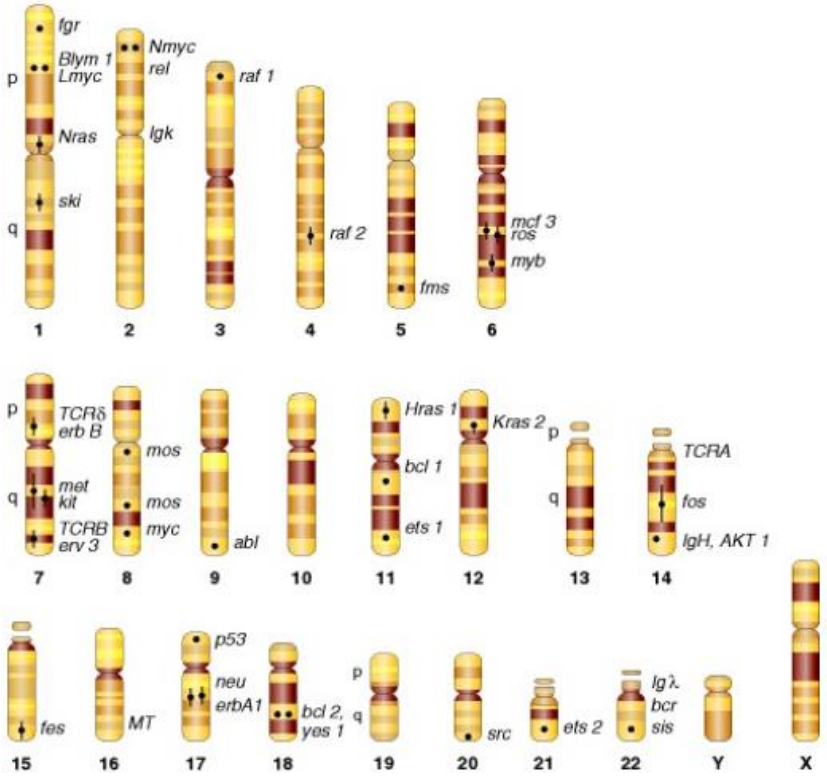
Mutation analysis (突變點分析)

Cancer is the second leading cause of death in most of the developed countries which accounting ~22 % of all deaths.

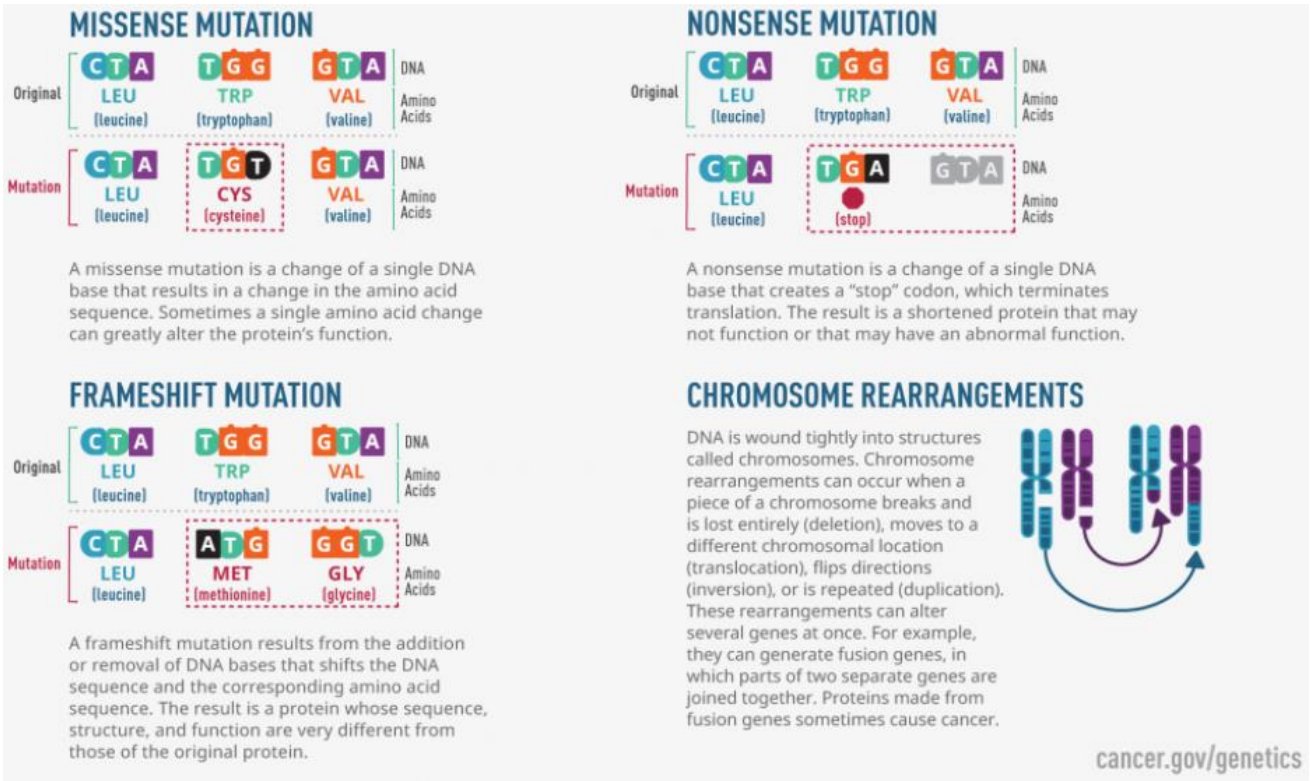
It is now getting clear that cancer is a genetic disease. Genetic mutation dysregulates special classes of gene, these are, proto-oncogene and tumor suppressor and introduce the tumorigenesis.

https://www.snpedia.com/index.php/Cancer
https://www.cancer.gov/about-cancer/causes-prevention/genetics
https://www.ncbi.nlm.nih.gov/books/NBK21809/

Identified proto-oncogene



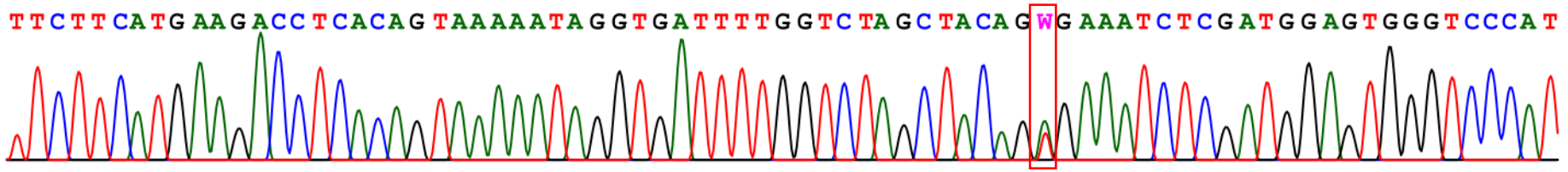
representative type of the genetic mutation



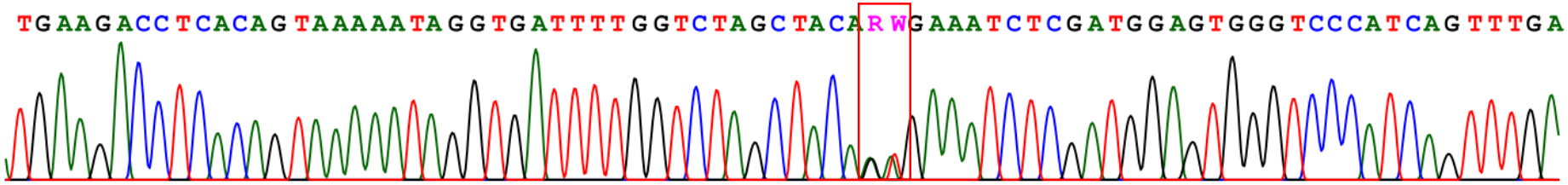
Mutation analysis (data obtained by DS3000)

Representative peak pattern of the somatic mutation (mixed base)

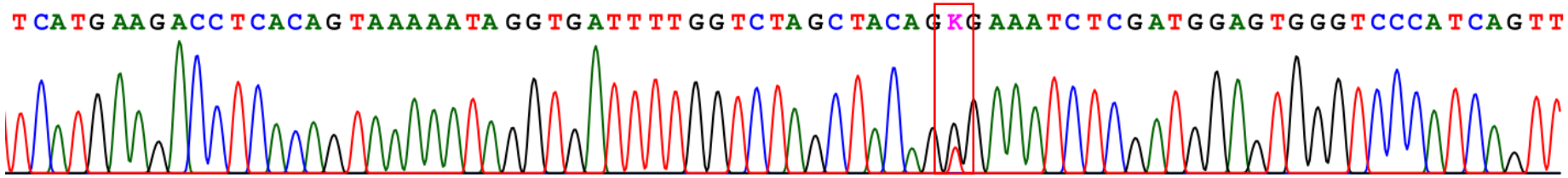
BRAF V600E (T/A 50 %)



BRAF V600K (GT/AA 50 %)



BRAF V600G (T/G 50 %)



BRAF: Member of growth signal transduction protein kinases. More than 30 mutations of the BRAF gene associated with human cancer.

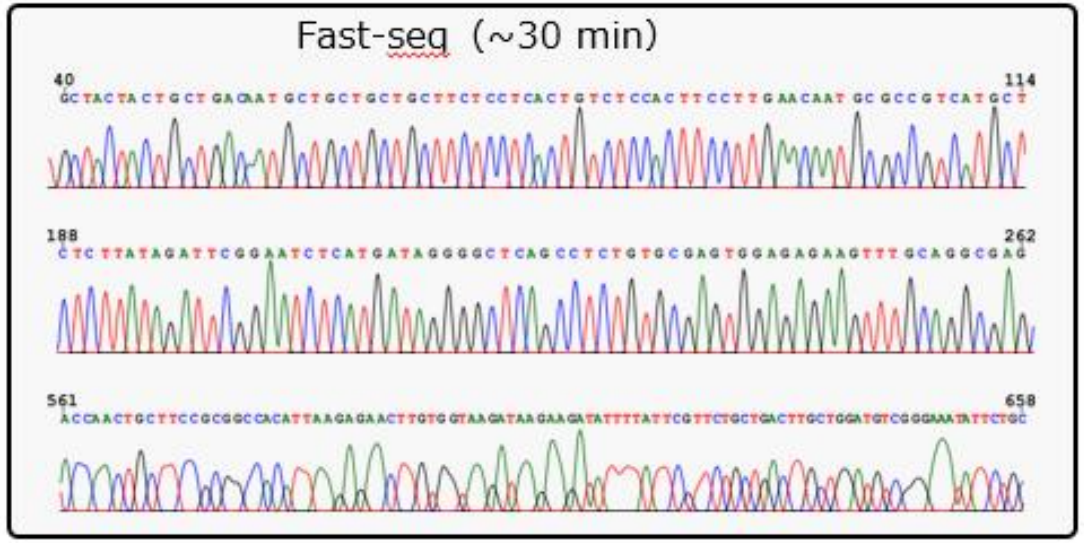
The frequency of the mutation varies on the cancer. Extreme example is the melanoma which frequency over 80 %.

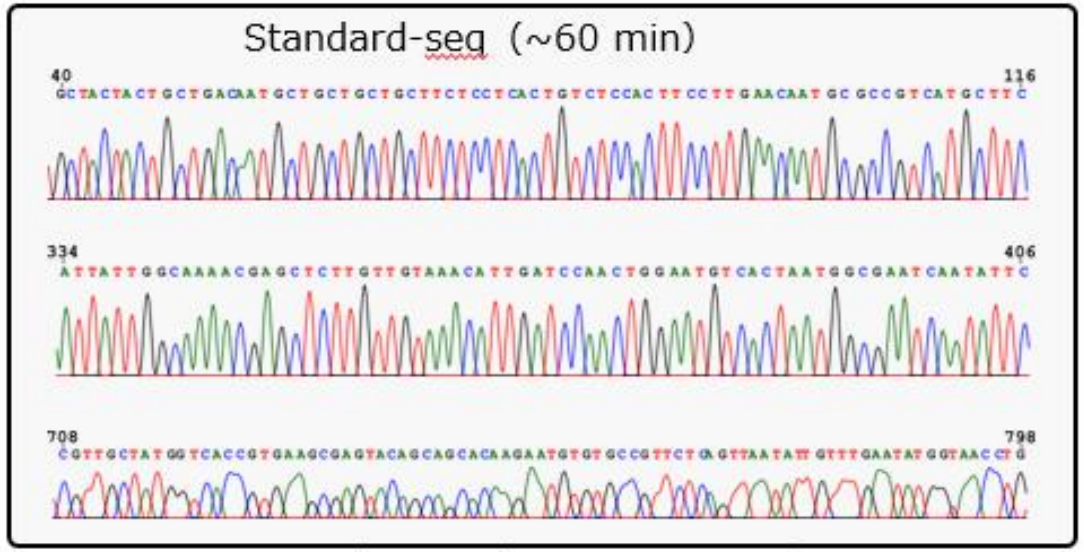
Representative data

DS3000 has two type of sequencing module.

Fast sequencing: run time = ~30 min, read length with quality > ~600 bp

Standard sequencing: run time = ~60 min, read length with quality > ~700 bp



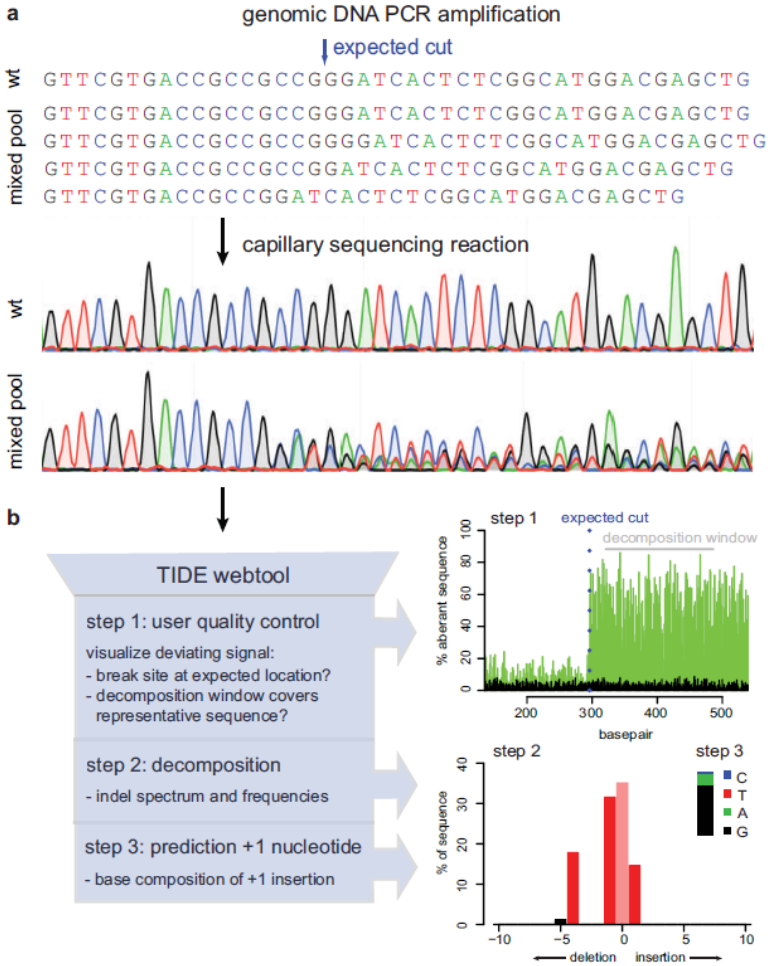


confidential

Quantifying genome editing

Targeted mutagenesis are considered to be one of the most challenging yet efficient tools for wide range of the research area including basic research, clinical examination and agriculture.

The efficacy and the mutation spectrum of genome editing methods can vary substantially depending on the target sequence. **Therefore, a simple and quick assay to accurately characterize and quantify the mutations is heeded.**



Several methods compatible with CE were suggested (TiDE, ICE, EditR). ICE can analyze multiple samples at once and thus preferred by the user who need a throughput.

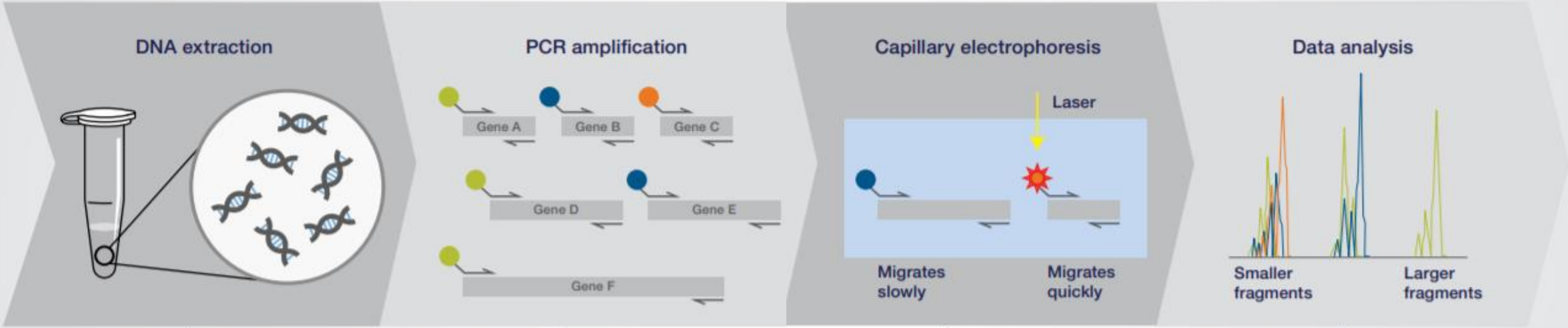
Caution: This method is not validated on DS3000 yet.

Nucleic Acids Research, 2014 1
doi: 10.1093/nar/gku936

Basic idea of Fragment analysis

Comprehensive solutions for your fragment analysis workflow

We offer a wide range of products and services to simplify each step of the fragment analysis workflow.



Choose from a range of genomic DNA extraction kits for sensitive, scalable purification (page 8).

Choose from Applied Biosystems™ 5′ fluorescently labeled primers and primer pairs (page 9).

The Applied Biosystems™ SeqStudio™ Genetic Analyzer is optimized for fragment analysis (page 10).

We offer a portfolio of Applied Biosystems™ software solutions for viewing and interpreting your fragment analysis results (page 13).

片段分析可運用之領域

DNAID/HID (human identification) (身份鑑定)

It provides crucial information in many cases of the crime scene, kinship analysis and natural disaster. Number of the cases of HID with CE is rapidly increasing in the world **(>300,000 cases / year** in National Police Agency in Japan). It also applied to livestock industry and agriculture.

STRs
are enriched in regulatory regions, manifest instability and variable length effects, and can impact multiple aspects of gene expression, splicing, and translation. Further, more than 30 Mendelian disorders are linked to STR expansions, including fragile X syndrome, amyotrophic lateral sclerosis (ALS), frontotemporal dementia (FTD), myotonic dystrophy, and Huntington's disease

MSI微衛星不穩定分析 可評估免疫療法用藥可行性

Analysis of oncogenic mutation and epi-mutation

MSI (microsatellite instability) test is covered by national insurance in Japan.
Copy number variation, DNA methylation analysis (MLPA) and SNPs (SNaPshot) are all available on CE.

DNAID/HID (human identification) (身份鑑定)

HID (human identification)/ STR (short tandem repeat)

There are various repeating sequences scattered in human genome DNA. STR, stands for short tandem repeat, is a tract of repetitive DNA in which certain repeating unit (generally 1-6 bps) are repeated ranging from 4 to over 40 times. Those surely inherit from parents. Thus unrelated person has different number of repeating unit. Commercially available kit can analyze 21 different STRs at once. Assuming each STR composed of 1 to 20 units, probability that the unrelated 2 person has same STR profile becomes 1 in 20^21 in theory. Regarding the biases of the number of the repeat, actually the probability shall be one in 4,700 trillion.

Case of TH01 loci

Sample A (9 times repeat) STR 短片段重複序列分析 可用於身份鑑定

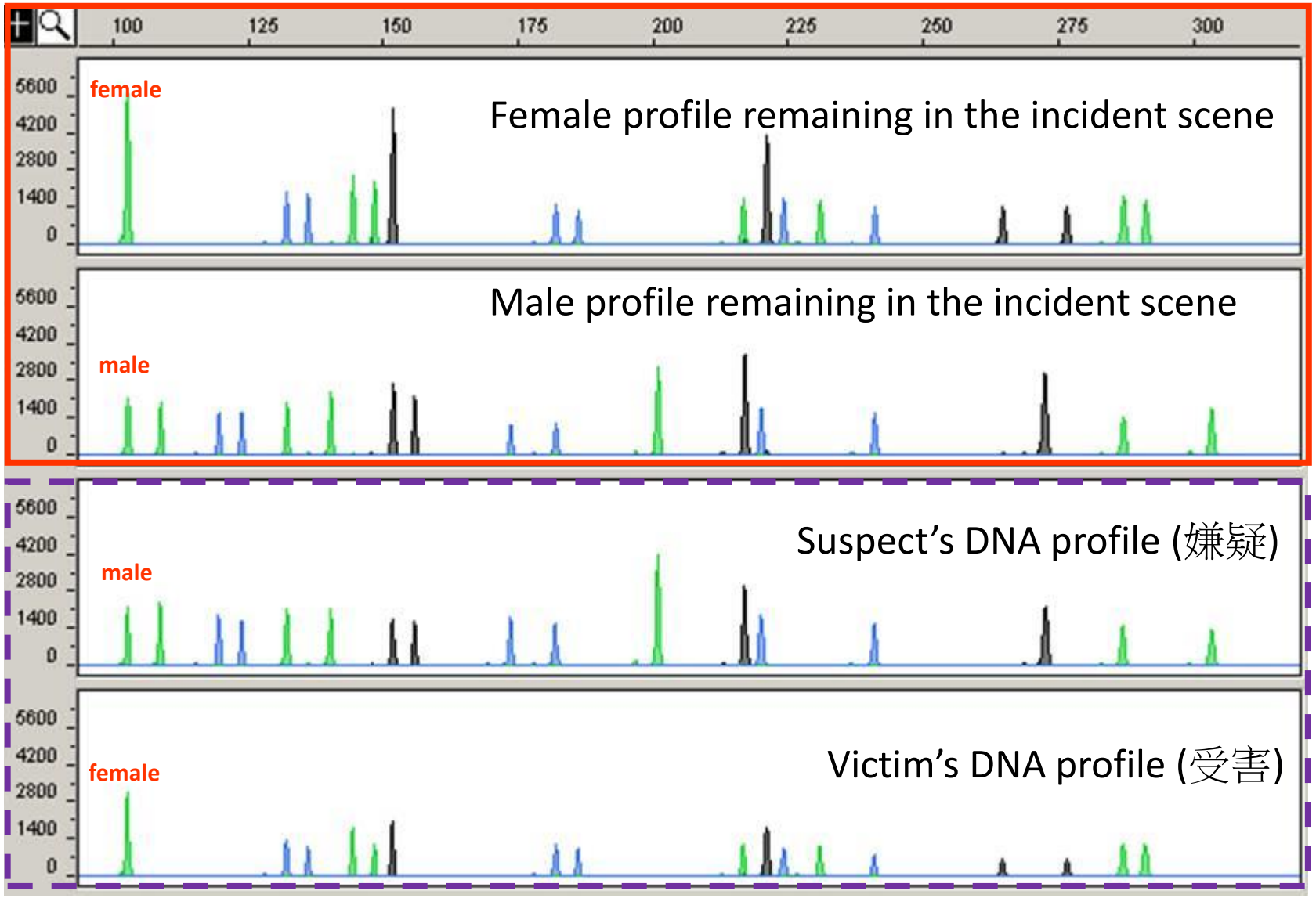


Sample B (8 times repeat)



STEP1: Amplification with a primer added with a fluorescent dye.
STEP2: Electrophoresis the amplified product and analyze the sequence length of the amplified product.

DNA sample collection from the incident site and analysis result



Results of analysis of victim and suspect's DNA profile

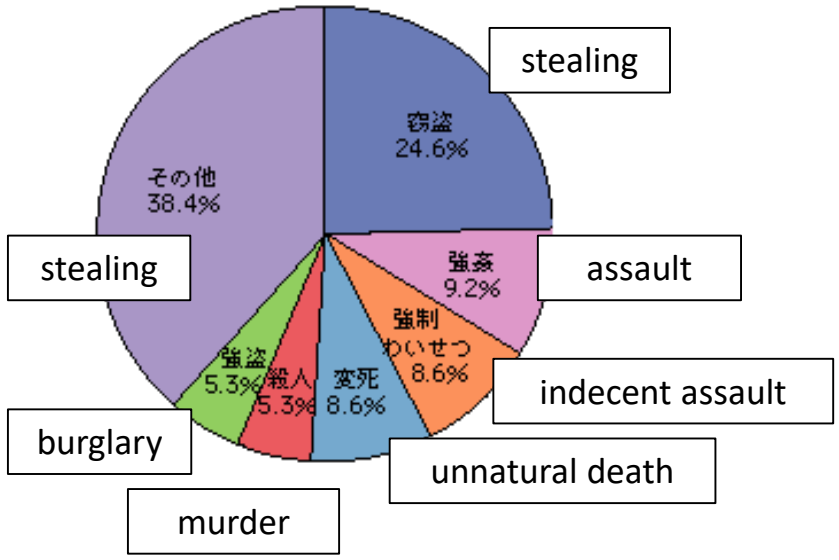
身份鑑定可用於刑事案件、親緣鑑定、重大災難事件死者身份鑑定。

Market size (日本市場)

Analysis example by Japanese police

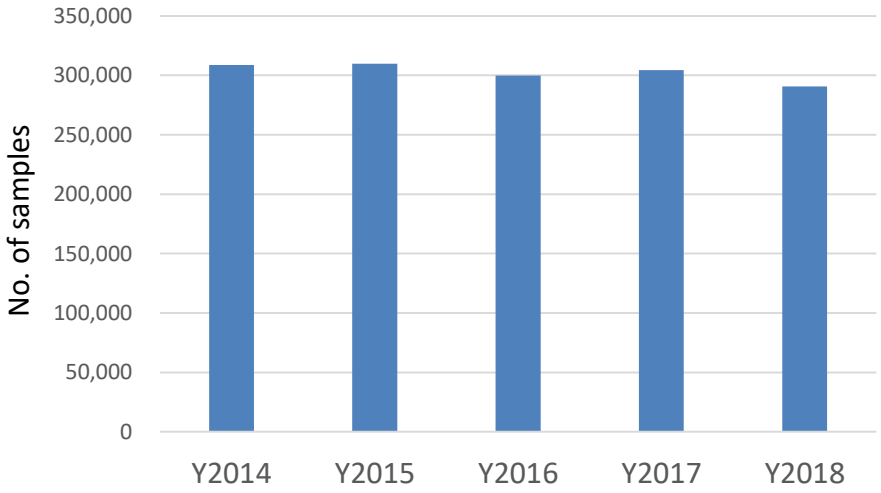
STR analysis utilized for various crimes, and its demand already close to 300,000 cases in Japan. In this market, consumers request **cheap, quick, simple and reliable** method. Therefore it is very natural that CE keeps mainstream even after emerging NGS.

Usage status of crime types in 2007



http://www.npa.go.jp/hakusyo/h20/honbun/html/kd320000.html

No. of samples analyzed on HID



https://www.npa.go.jp/hakusyo/r01/honbun/index.html

MSI (microsatellite instability)

Microsatellite instability is a phenomenon in which microsatellite repeat sequences exhibit a number of repetitions that is different from non-tumor (normal) tissue in tumor tissue, due to a decrease in the function of repairing mistakes in the nucleotide sequence generated during DNA replication. Microsatellite instability is observed in sporadic colorectal cancer other than Lynch syndrome in about 10-20%, but in patients with Lynch syndrome (HNPCC), it is frequently 80-90%.

Determine the result of microsatellite instability genetic test

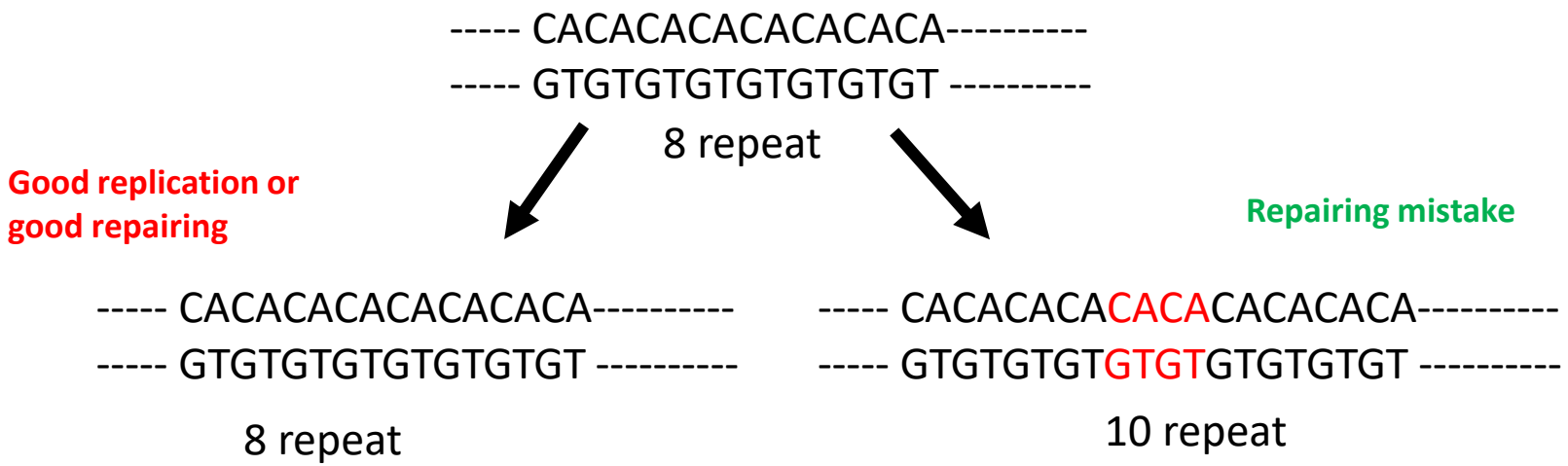
When using markers of 5 types (Bethesda panel)

MSI-H ･････When showing MSI in more than two markers

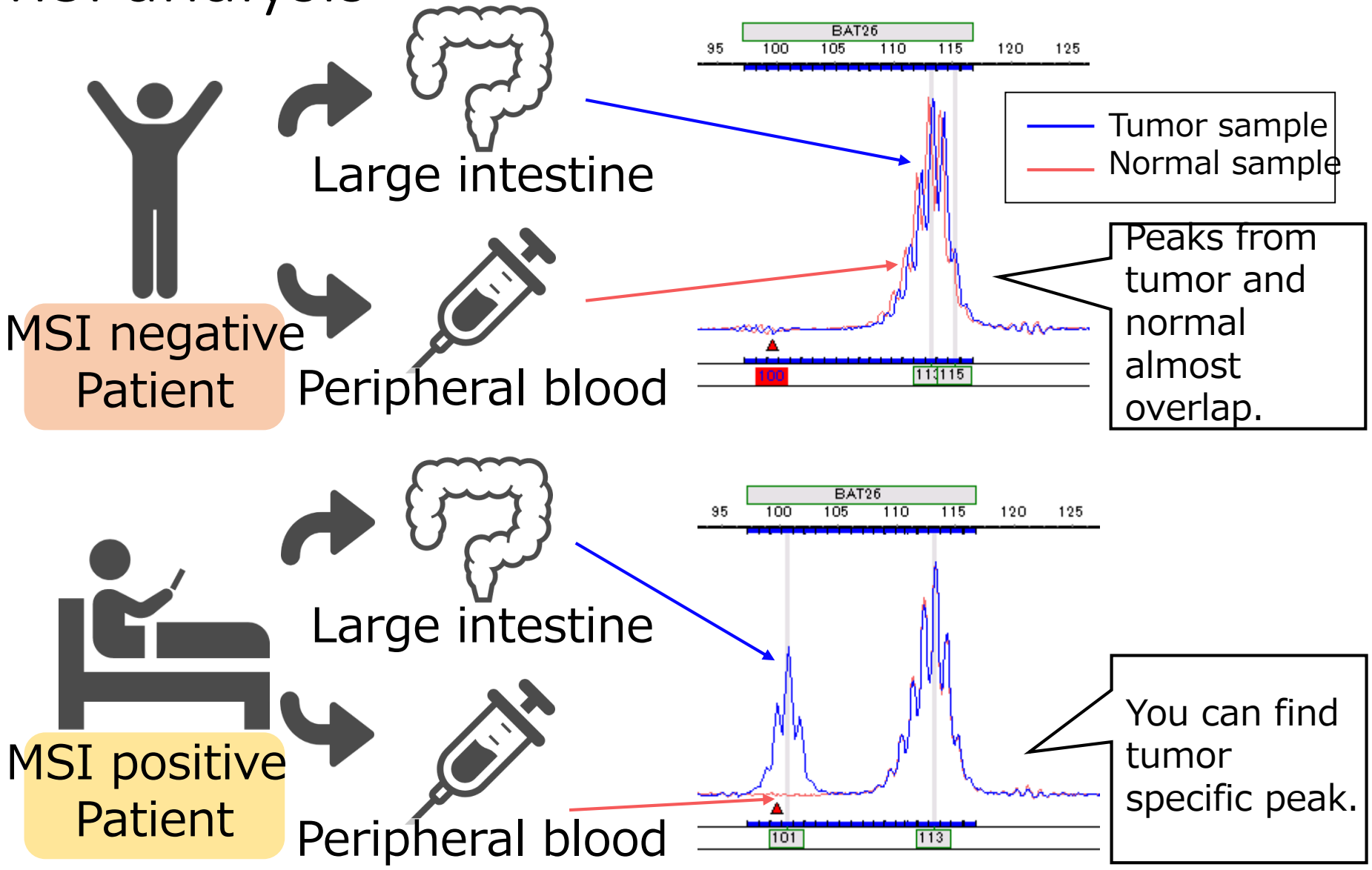
MSI-L ･････When showing MSI in one marker

MSS(stable)･･ When the MSI is not confirmed

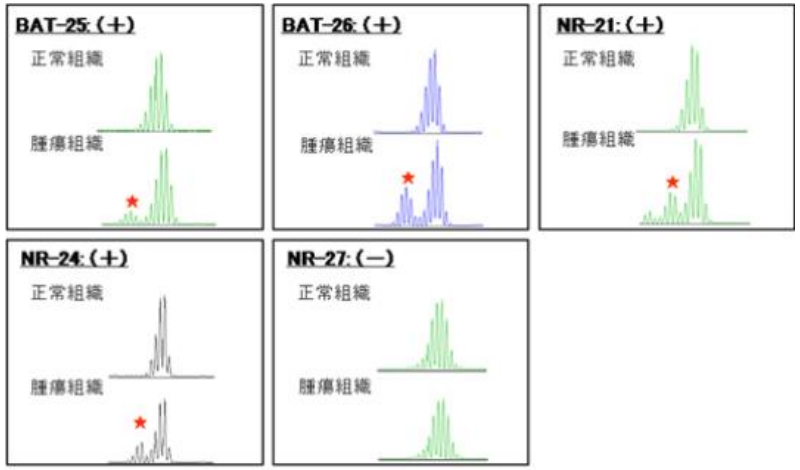
When MSI testing is carried out using more markers, it is judged as "MSI-H" when MSI is recognized at 30-40% or more of all markers, and "MSI-L" when it is less than 30-40%.



Process image of GeneMarker MSI analysis



Analysis of oncogenic mutation and epi-mutation



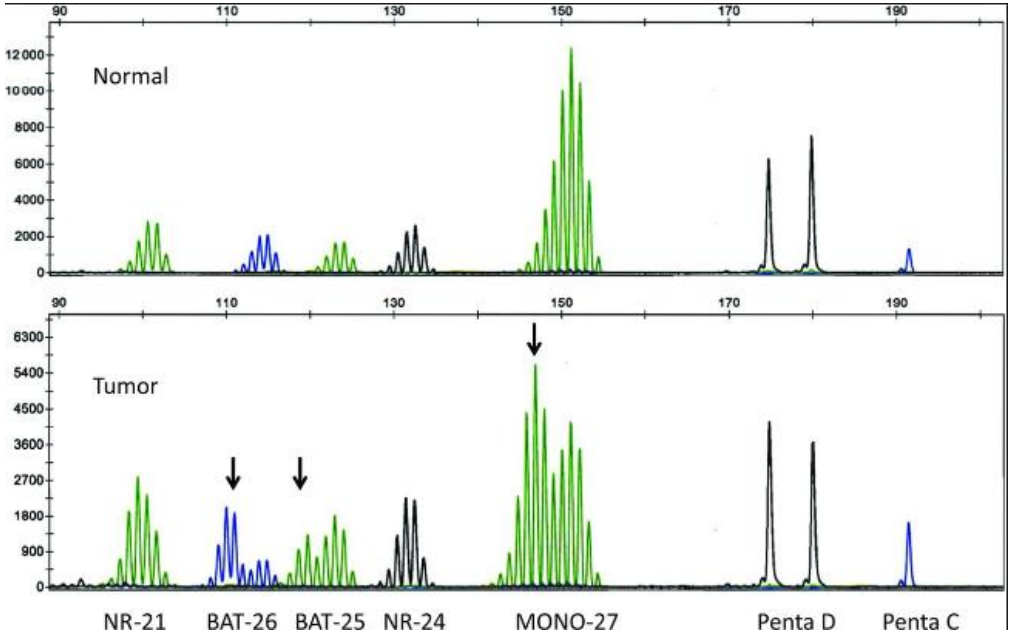
総合判定基準

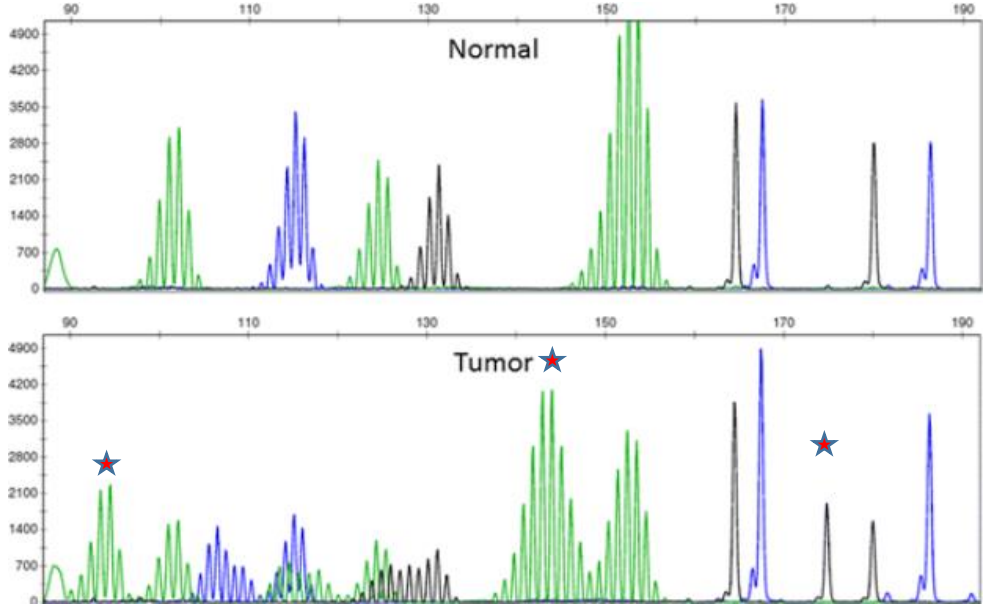
MSS(MS Stable)	：0マーカー
MSI-L(MSI-Low)	：1マーカー
MSI-H(MSI-High)	：2マーカー以上

MSI微衛星不穩定分析 可評估免疫療法用藥可行性

MSI test is covered by national insurance to judge the safe and effectiveness of Pembrolizumab and Nivolumab in Japan.

Analysis result of MSI sample





MLPA (Copy number variation)

Duplication of genes which resulted in the loss of genome integrity is a hallmark of cancer or tumorigenesis. Thus the study on copy number variation (CNV) is one of the major topic of cancer research. **MLPA**, which stands for Multiple Ligation-dependent Probe Amplification, is a simple, multiplex PCR technique that uses **a single primer pair to amplify up to 60 probes**.

The resulting products are subjected on CE. Peak heights comparison makes it possible to depict the gene duplications.

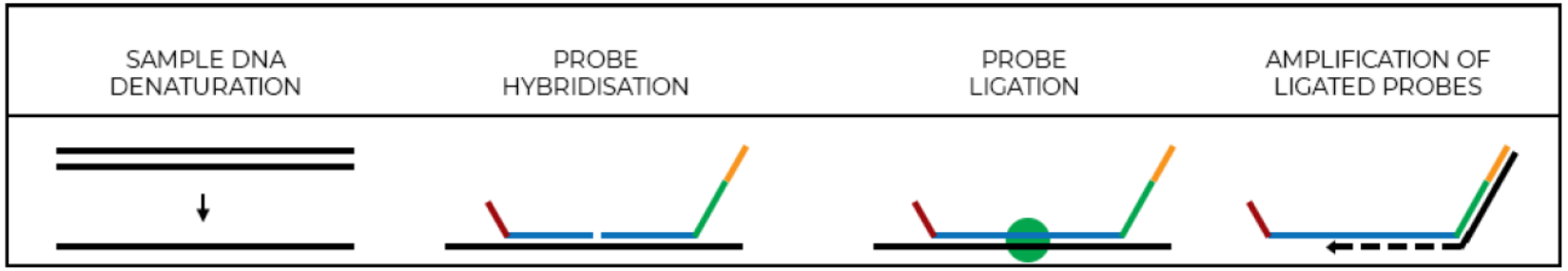
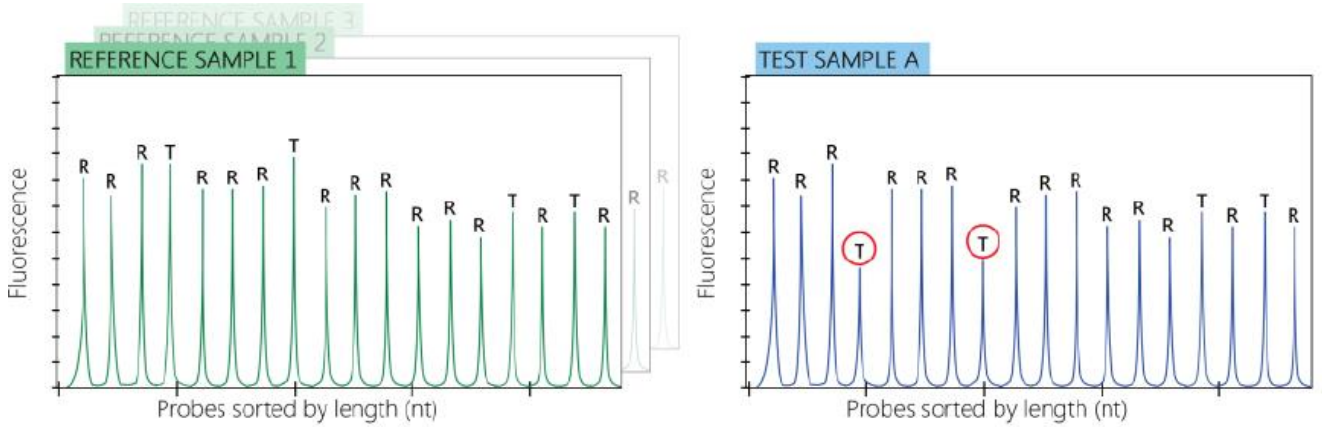


Figure 1. MLPA reaction.



https://www.mrcholland.com/technology/mlpa

MS-MLPA (DNA methylation) (基因沉默化)

DNA methylation regulates gene expression in a dynamic and reversible manner. Therefore DNA repair deficiency is occasionally found due to the aberrant methylation (referred to as epi-mutation) on DNA repair gene promoter. Cancer epigenomics is one of the most growing area in academia.

By utilizing methylation sensitive restriction enzyme, MS-MLPA enables researchers **to detect presence or absence of DNA methylation in multiple loci at once.**

HhaI cut only an unmethylated GCGC sequence.

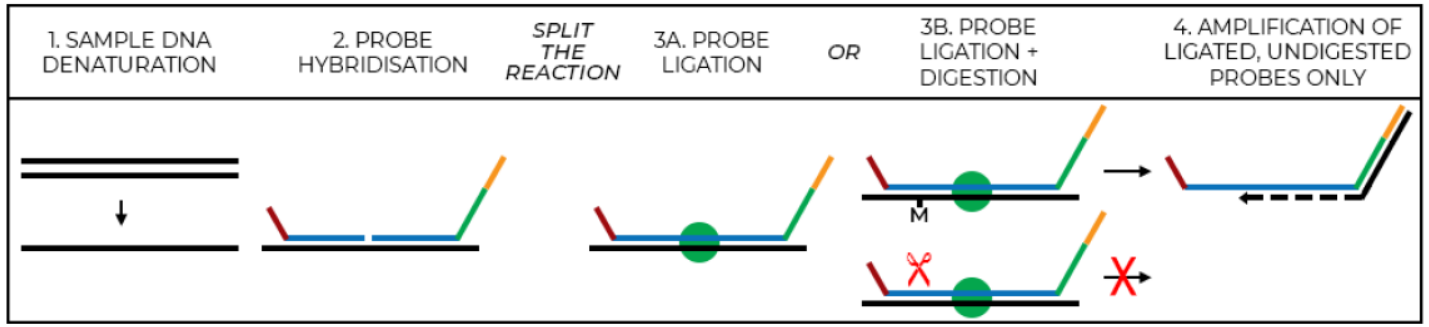
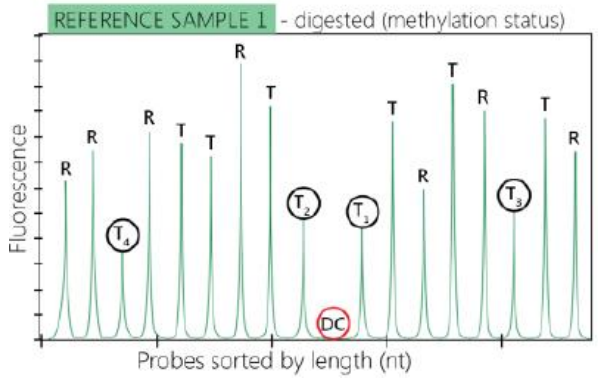
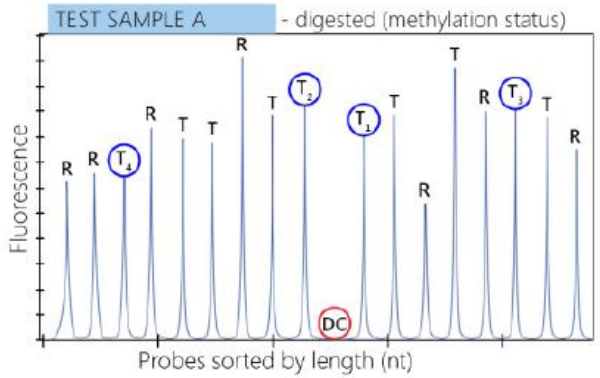
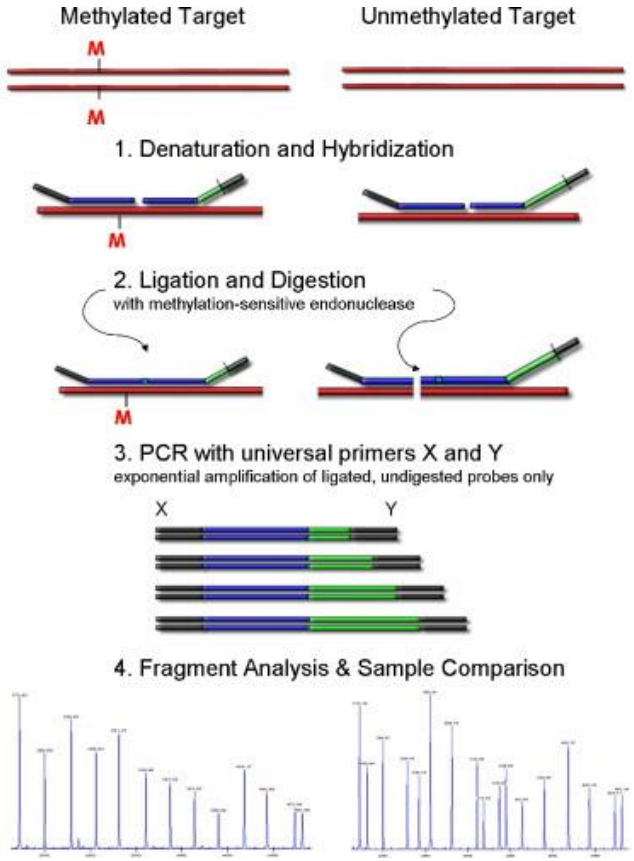


Figure 1. MS-MLPA reaction.



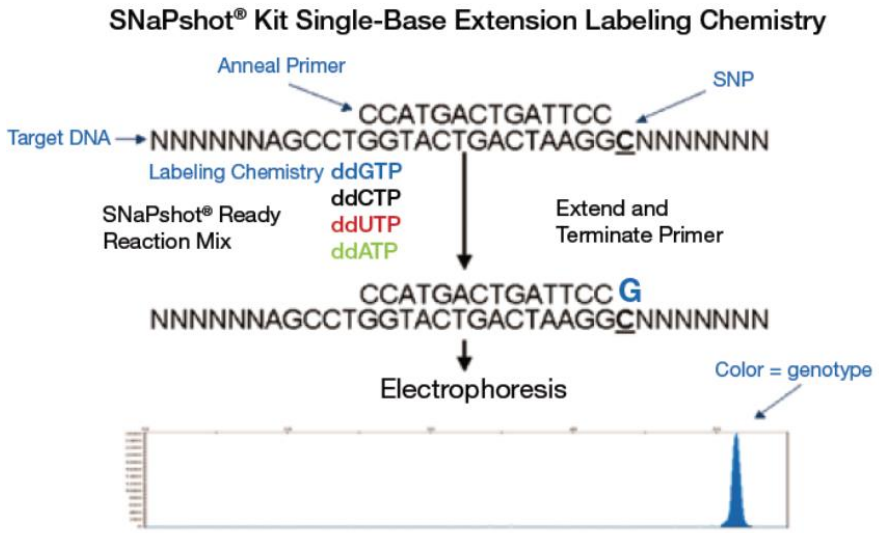


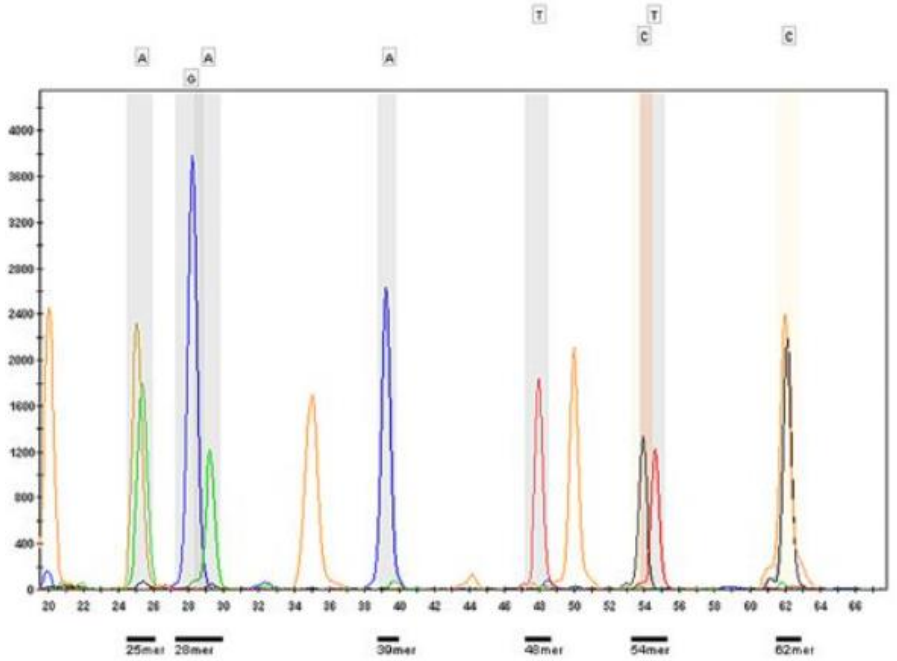


https://www.mrcholland.com/technology/mlpa

SNaPshot (SNP Genotyping by Fragment Analysis)

The stable substitution of the single base, so called the single-nucleotide polymorphysm (SNP), occasionally alter the function of the expression of genes in a cancer. SNaPshot which is developed by Thermo Fisher Scientific is a method to analyze up to **10 SNPs by single electrophoresis on CE.** SNapshot is available only for known SNPs





https://www.thermofisher.com/jp/ja/home/life-science/sequencing/dna-sequencing/snp-genotyping-variant-detection-sequencing/snp-genotyping-fragment-analysis.html

QF-PCR example

DEVYSER
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Principles of QF-PCR

Published: June 7, 2017

QF PCR analysis includes amplification, detection and analysis of chromosome-specific DNA sequences known as genetic markers or small tandem repeats (STRs).

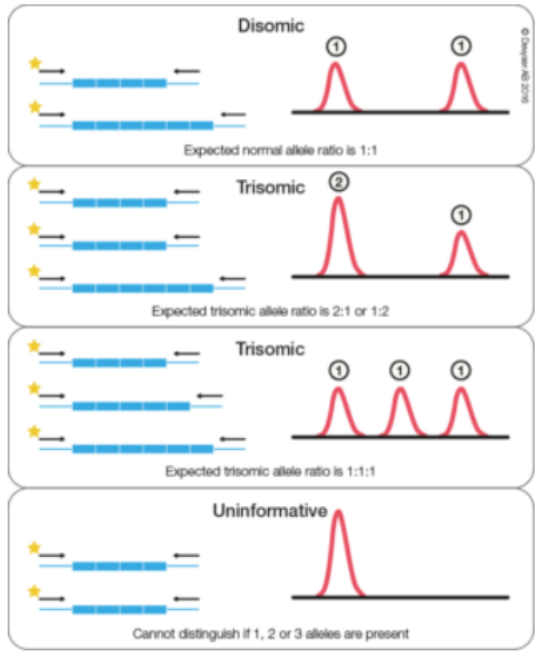
Fluorescently labeled marker specific primers are used for PCR amplification of individual markers and the copy number of each marker is indicative of the copy number of the chromosome. The resulting PCR products may be analyzed and quantified using an automated genetic analyzer.

The genetic markers/STRs may vary in length between individual chromosomes and subjects, depending on the number of repeated STRs. The relative copy number of each allele is determined by calculating the ratio of the peak areas or peak heights detected for each marker.

A normal diploid sample has the contribution of two of each of the investigated chromosomes. Two alleles of a chromosome specific marker are detected as two peaks in a 1:1 ratio when the marker is heterozygous and as one peak when the marker is homozygous (have alleles of same length). The detection of an additional allele as three peaks in a 1:1:1 ratio or as two peaks in a 2:1/1:2 ratio indicates the presence of an additional marker copy possibly corresponding to an additional chromosome, as in the case of trisomy. Subjects who are homozygous or monosomic for a specific marker will display only one peak.

for a specific marker will display only one peak.

The inability of STR marker analysis to distinguish subjects who are homozygous or monosomic is a major shortcoming when testing for sex chromosome abnormalities. When STRs specific for chromosome X are used, some samples from normal XX females may show homozygous QF PCR patterns, indistinguishable from those produced by samples with a single X, as in Turner syndrome. Incorporating additional X-chromosome STR markers into the analysis will reduce but not eliminate the likelihood of homozygosity. To facilitate the detection of monosomy X the Devyser QF PCR kits include X-chromosome counting markers for relative quantification of chromosome X to an autosomal chromosome.



QF-PCR example

Devyser Compact: one single mix, 26 genetic markers

Devyser Compact enables rapid prenatal aneuploidy detection of chromosomes 13, 18, 21 and XY in a single PCR mix.

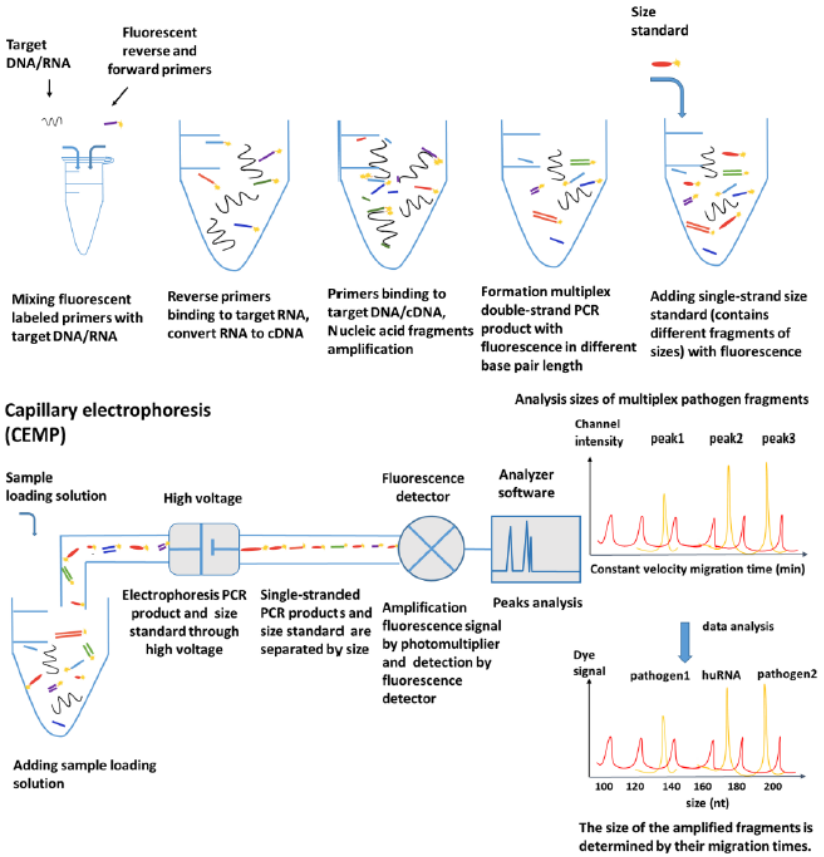
In addition to detecting Down, Edwards, Patau and Klinefelter syndromes, the Devyser Compact kit includes our patented technology for reliable diagnosis of Turner syndrome, using two dedicated X-chromosome counting markers. The CE-IVD certified Devyser Compact kit relies on quantitative, multiplex PCR amplification of 26 highly informative genetic markers in a single mix for rapid prenatal diagnosis of the most common autosomal and sex chromosome aneuploidies.

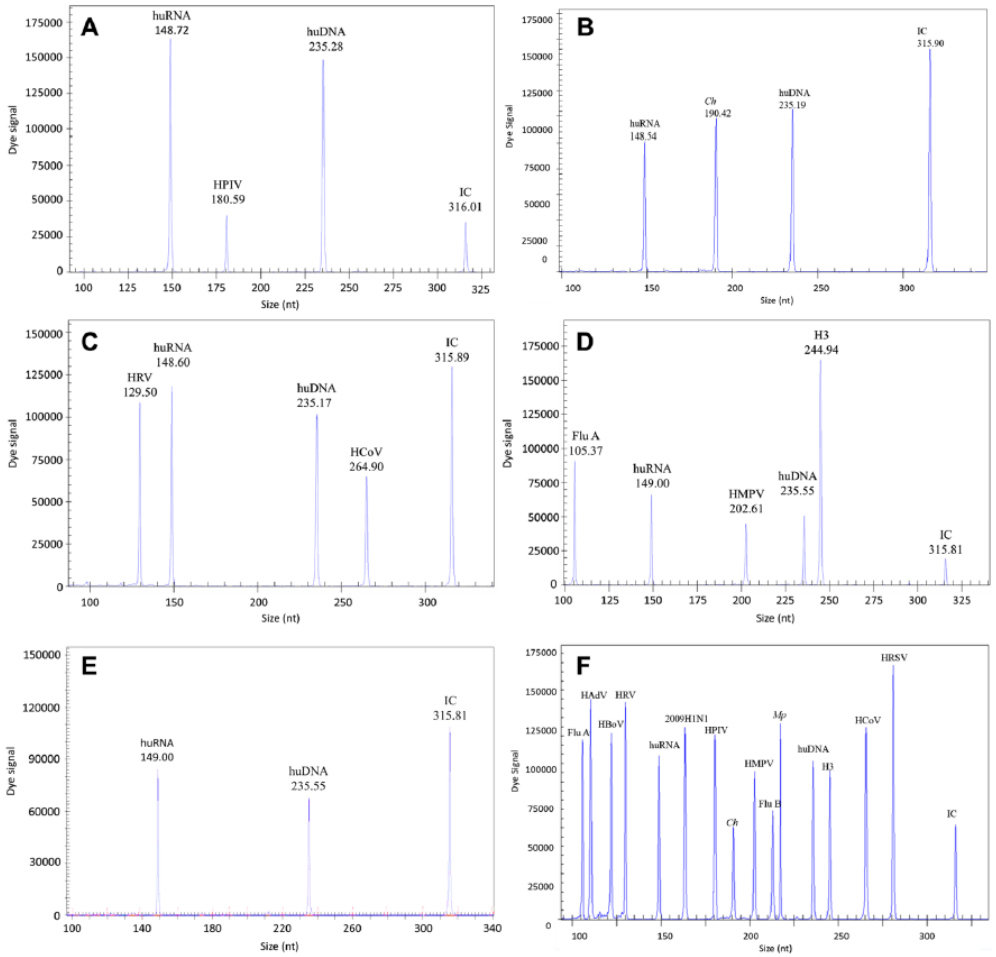
- Efficient and sensitive detection of chromosomal aneuploidies and maternal cell contamination (MCC) in DNA samples prior to microarray analysis
- No sample mix-up. One single tube per sample during PCR and detection reduces the risk of sample mix-up.
- Quick and easy implementation. All reagents needed to perform QF-PCR are provided in a single kit.

Pathogen detection(病原體檢測)

As exhibited by COVID-19 pandemic, cost and run time are critical factors for public health. Here is an example to detect multiple (up to 13) pathogens by utilizing a capillary sequencer. The authors used GEXP but the same methodology should be applicable on DS3000.

Please note that DS3000 is currently for RUO.





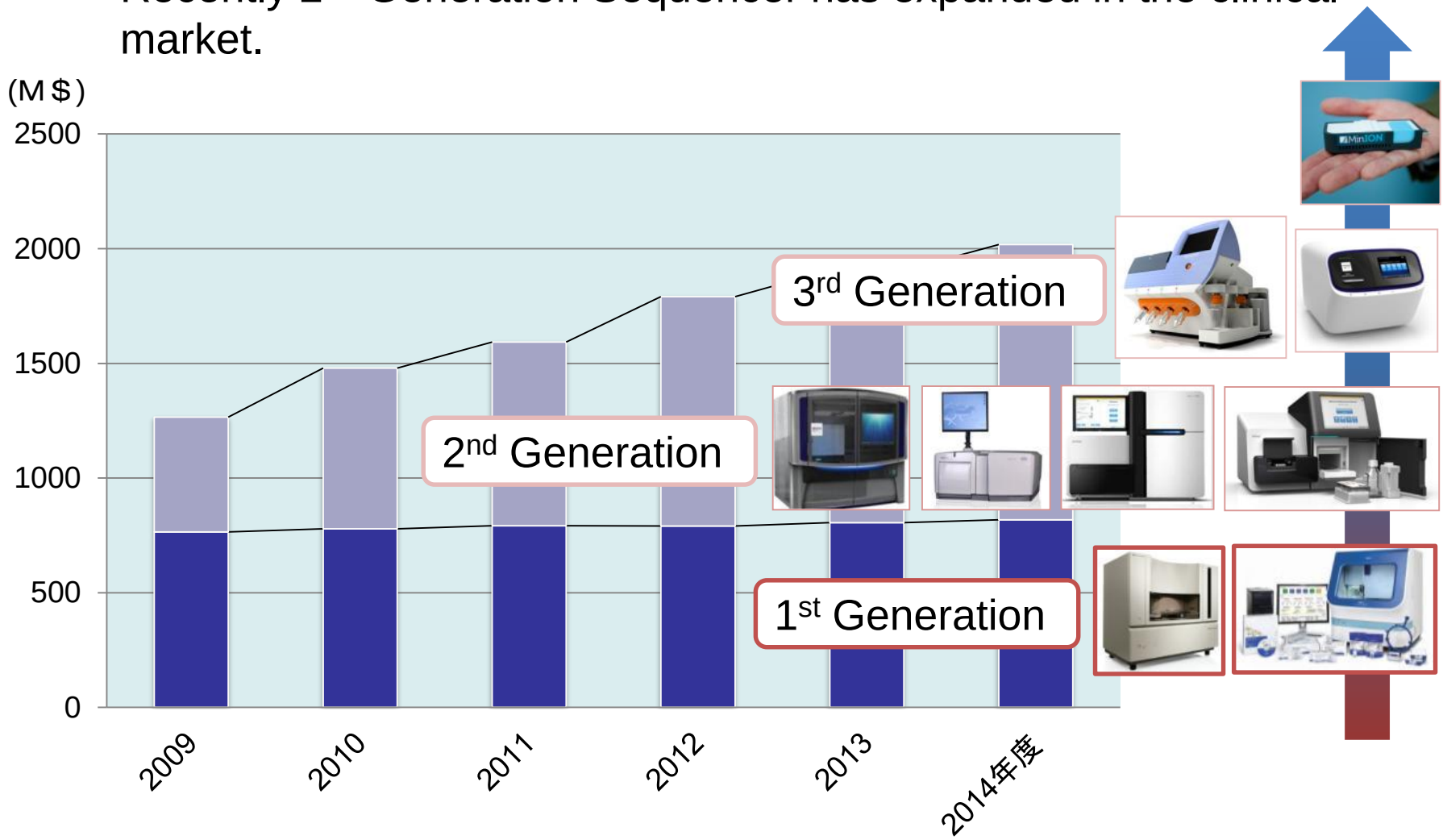
SLAS Technology
2019, Vol. 24(1) 105–116
© 2018 Society for Laboratory Automation and Screening
DOI: 10.1177/2472630318787452
journals.sagepub.com/home/jla
SAGE

比較廠牌和NGS

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NGS 與Sanger 比較

Market of DNA Sequencer – 1st Generation to 3rd Generation.
Recently 2nd Generation Sequencer has expanded in the clinical market.



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NGS 與 Sanger 比較

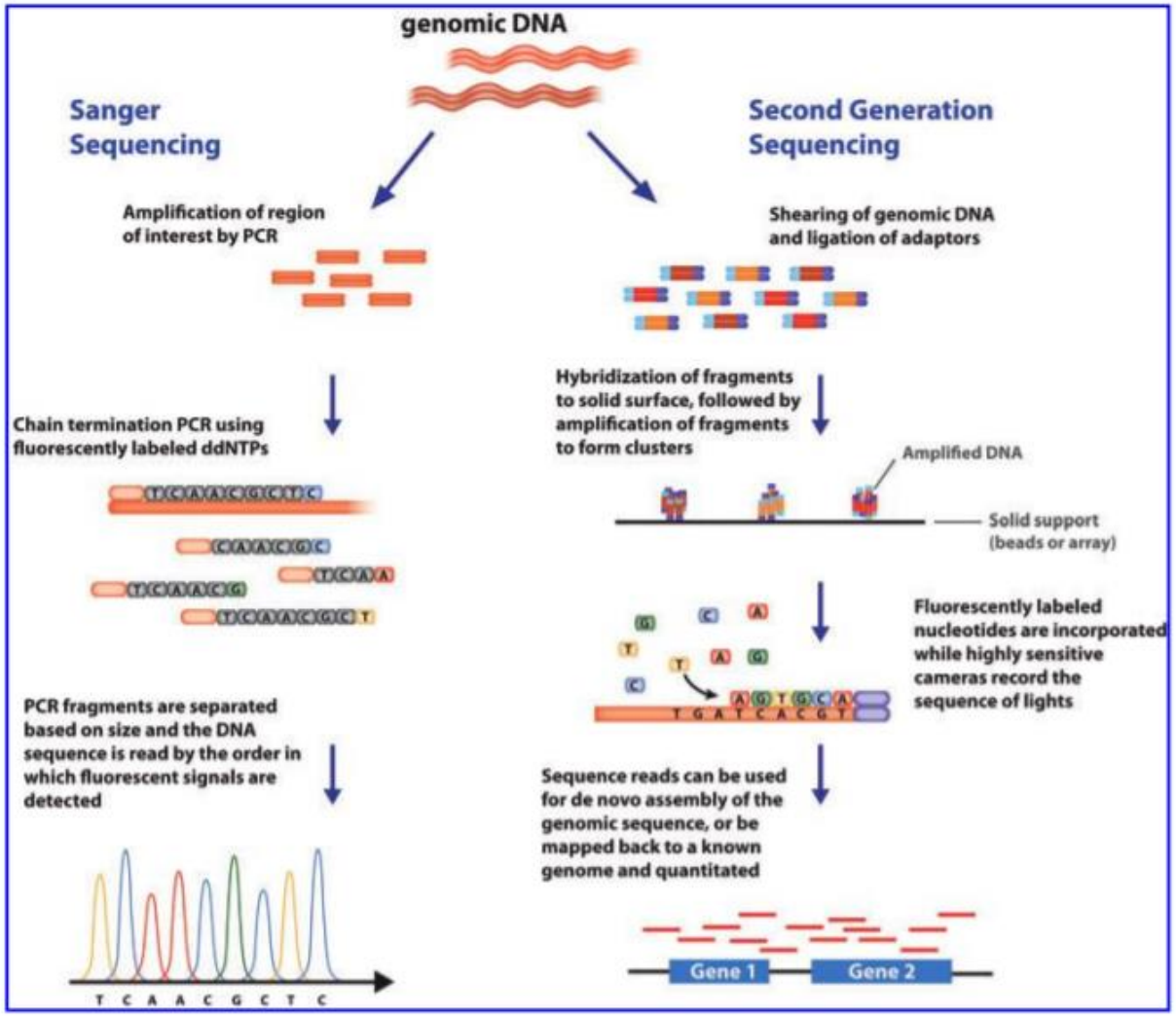
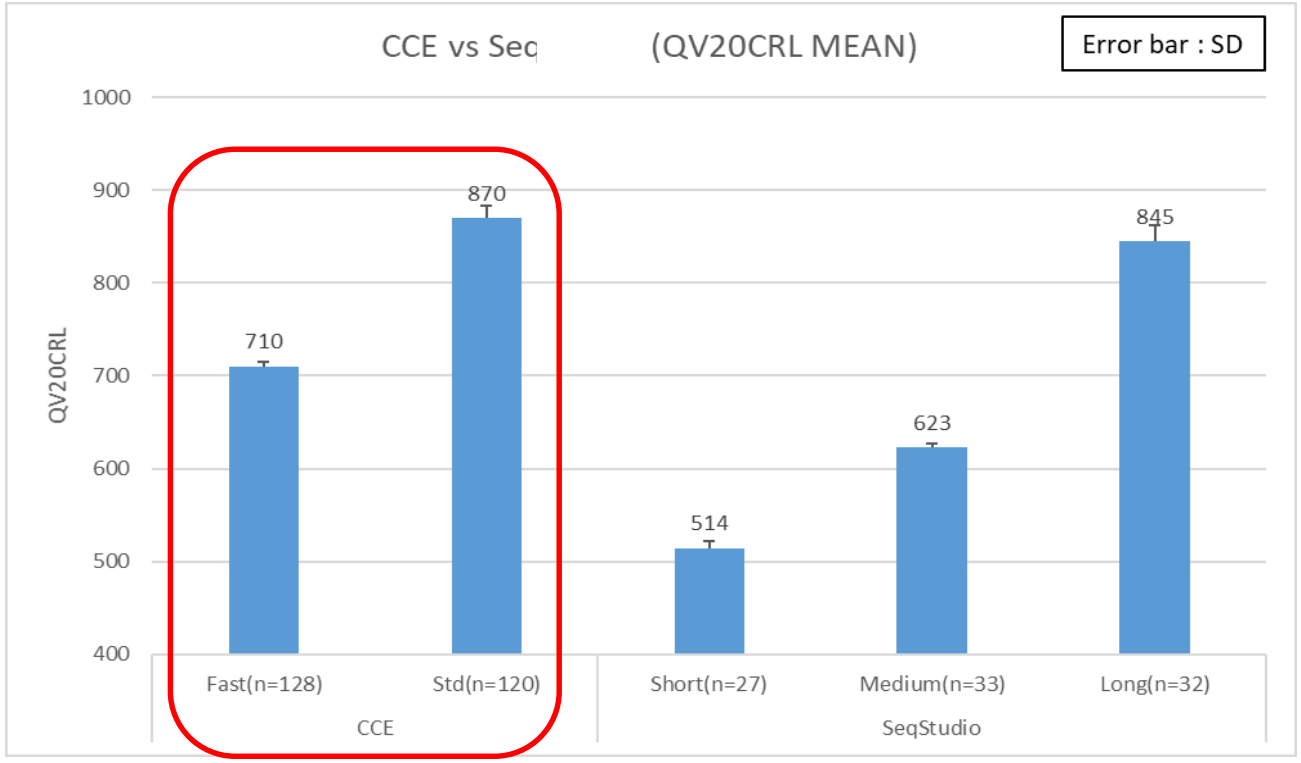


Figure 1. Comparison between Sanger sequencing and next-generation sequencing (NGS) technologies. Sanger sequencing is limited to determining the order of one fragment of DNA per reaction, up to a maximum length of ~700 bases. NGS platforms can sequence millions of DNA fragments in parallel in one reaction, yielding enormous amounts of data. To see this illustration in color, the reader is referred to the web version of this article at www.liebertpub.com/wound

DS3000 與 他牌比較



30min 60min 30min 45min <2hrs

DS3000		
run module	run time (approx.)	read length Blast CRL
Fast-seq	**30 min**	**ca. 650 bp**
Std-seq	1 hr	**ca. 830 bp**

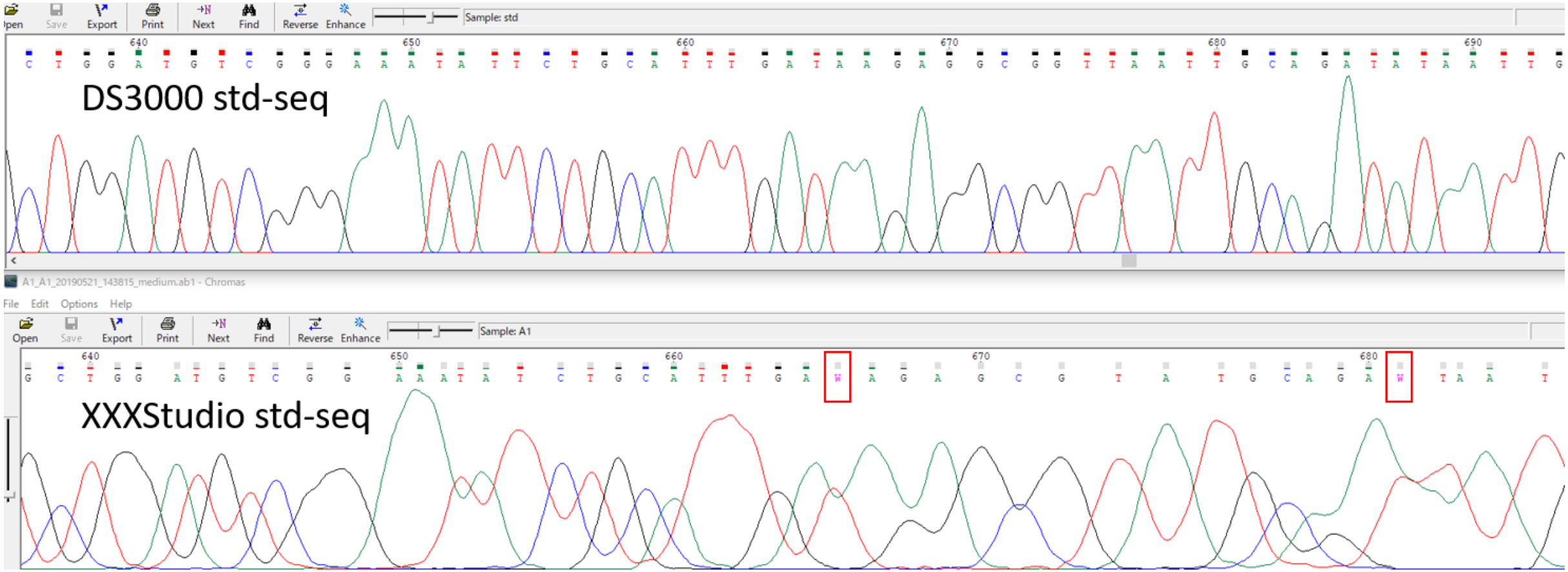
SeqStudio		
run module	run time (approx.)	read length QV30CRL
ShortSeq	30 min	350 bp
MediumSeq	45 min	500 bp
LongSeq	<2 hrs	800 bp (QV20)

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Comparison with XXX

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DS3000 exhibited superior resolution than XXX

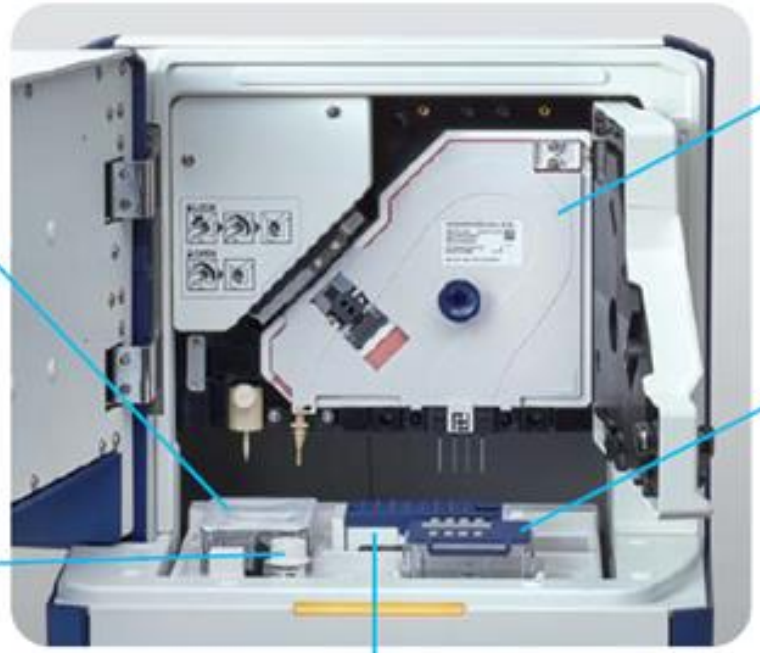


Erroneously called mixed base

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Comparison with XXX

Inside of instrument



Anode Buffer Cartridge



Polymer Cartridge



Capillary Cartridge



Cathode Buffer Cartridge





Sample Cartridge









每個反應約1.5倍價格

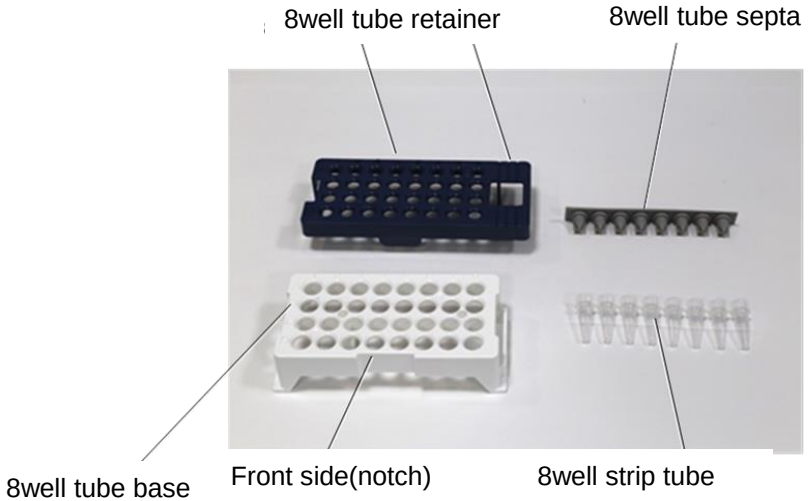
Compact CE Sequencer(DS3000) features

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- ✓ Dimension:400(W)x600(D)x600(H)mm



- ✓ Application: Sequencing(定序分析), Fragment analysis(片段分析)
- ✓ Number of capillaries(length) : 4根毛細管（36㎝）
- ✓ Sample Tray: 32 well plate (8 well Strip Tube)
- ✓ Simultaneous detection: 6 colors
- ✓ Consumable: Capillary Cartridge, Polymer Cartridge, Buffer Cartridge,Septa



Remark: The product is for research use only.

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Simple

Intuitive and Easy to use Touch Panel GUI screen

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Touch panel GUI(Main screen)

RUN menu

MAINTENANCE menu



REVIEW menu

PROTOCOL menu



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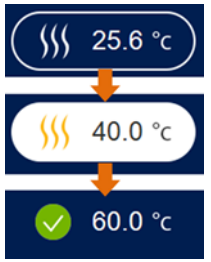
Touch panel GUI(Main screen)



Oven heater switch

RUN menu

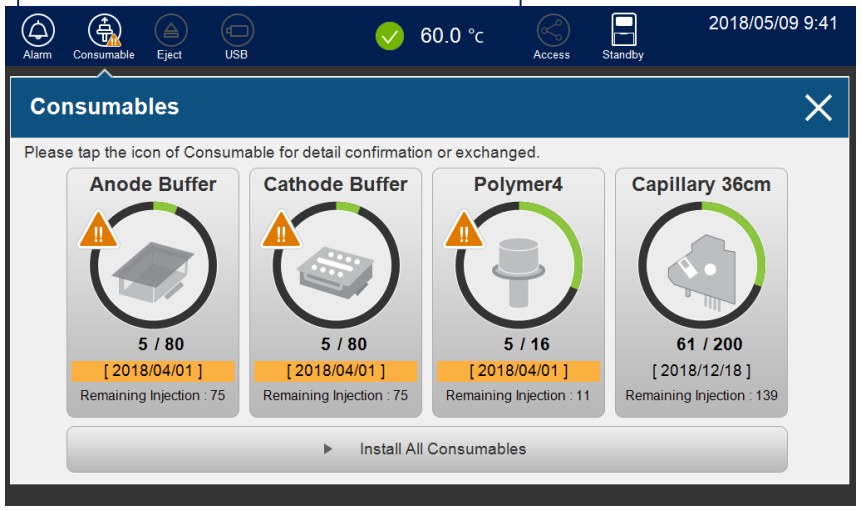
REVIEW menu

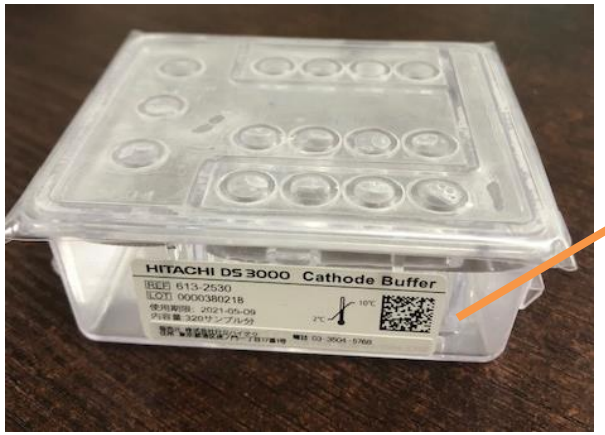


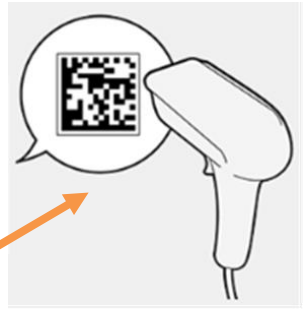
MAINTENANCE menu

PROTOCOL menu

Consumable Dashboard







2D Barcode

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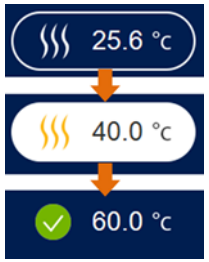
Touch panel GUI(Main screen)



RUN menu

MAINTENANCE menu

Oven heater switch



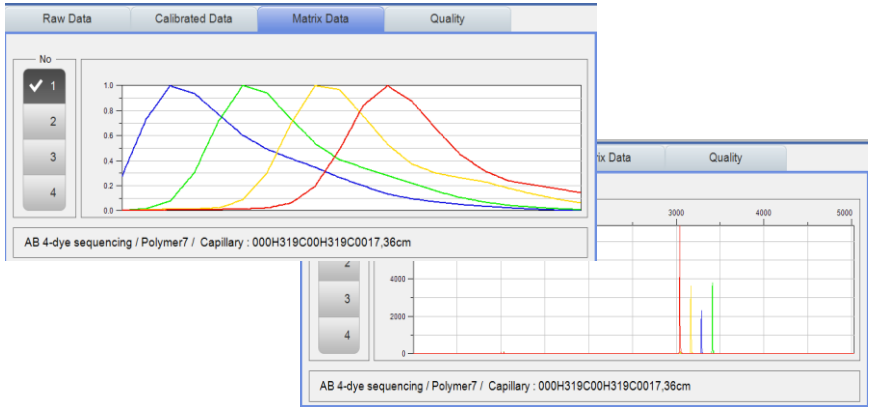
REVIEW menu

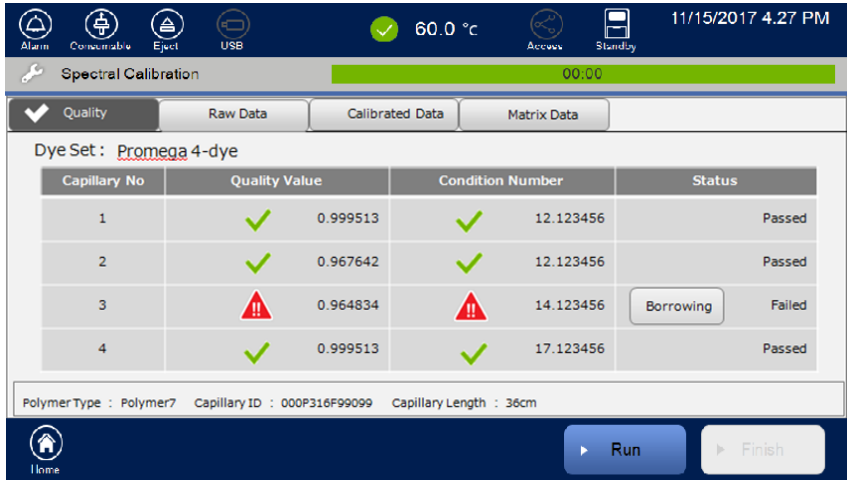
PROTOCOL menu

Calibration screen



Spectral Calibration





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Capillary array : 800 samples or 200 injections

- Polymer4:16 injections*4=64 samples
- Polymer7:16 injections*4=64 samples
- Anode Buffer Cartridge:80 injections
- Cathode Buffer Cartridge:80 injections

Simple

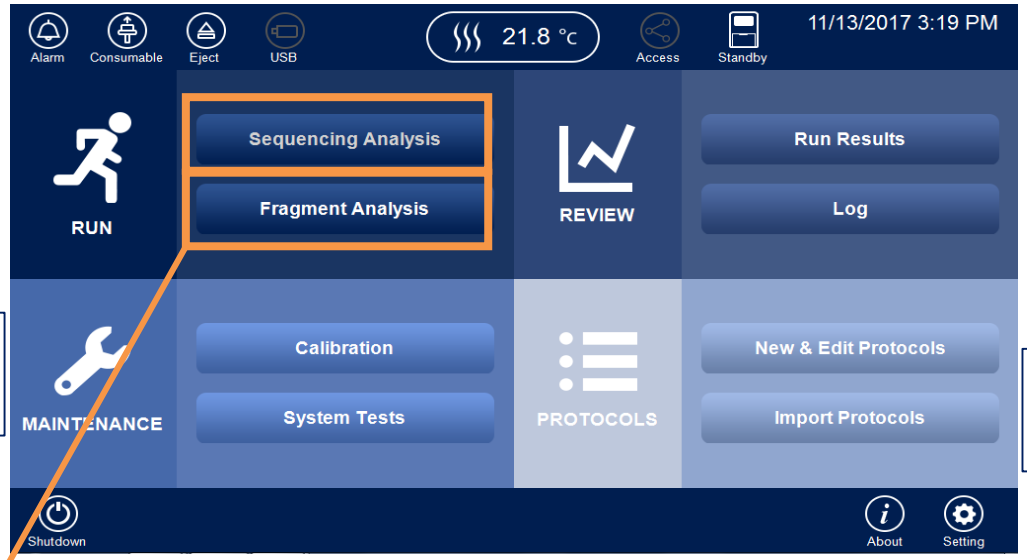
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Touch panel GUI(Main screen)

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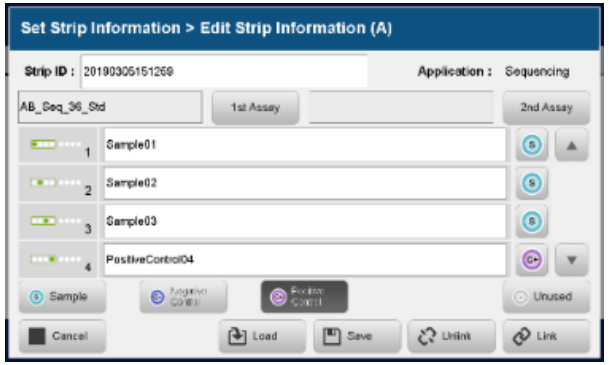
MAINTENANCE menu



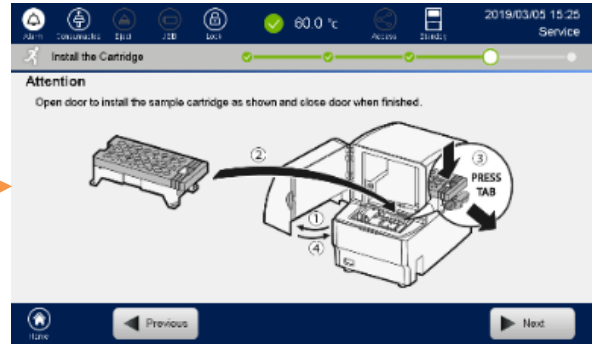
REVIEW menu

PROTOCOL menu

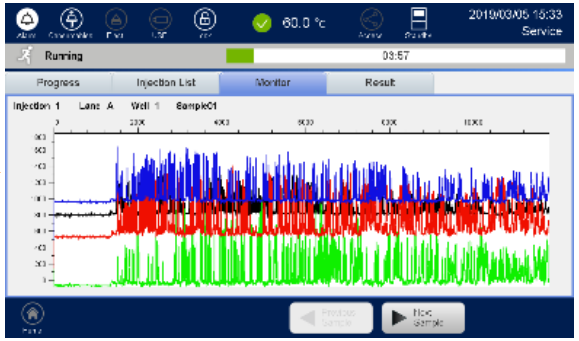




(Strip information at each well, Input Assay information)



(Sample cartridge setting)



(Real-time data during injection)

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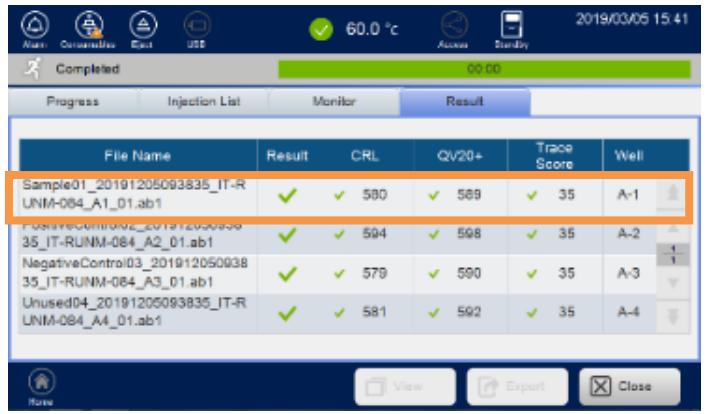
RUN menu

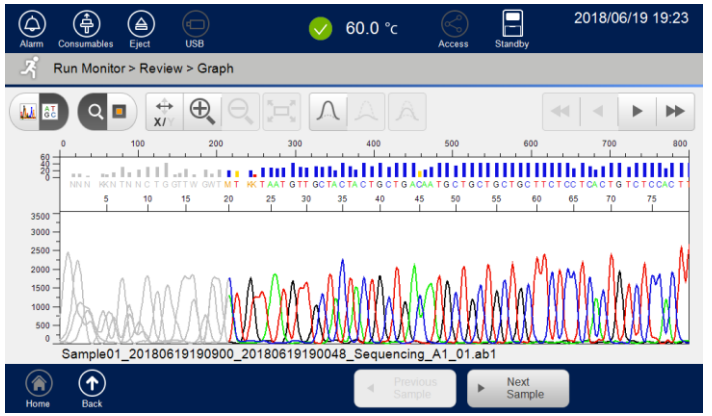
MAINTENANCE menu

REVIEW menu

PROTOCOL menu



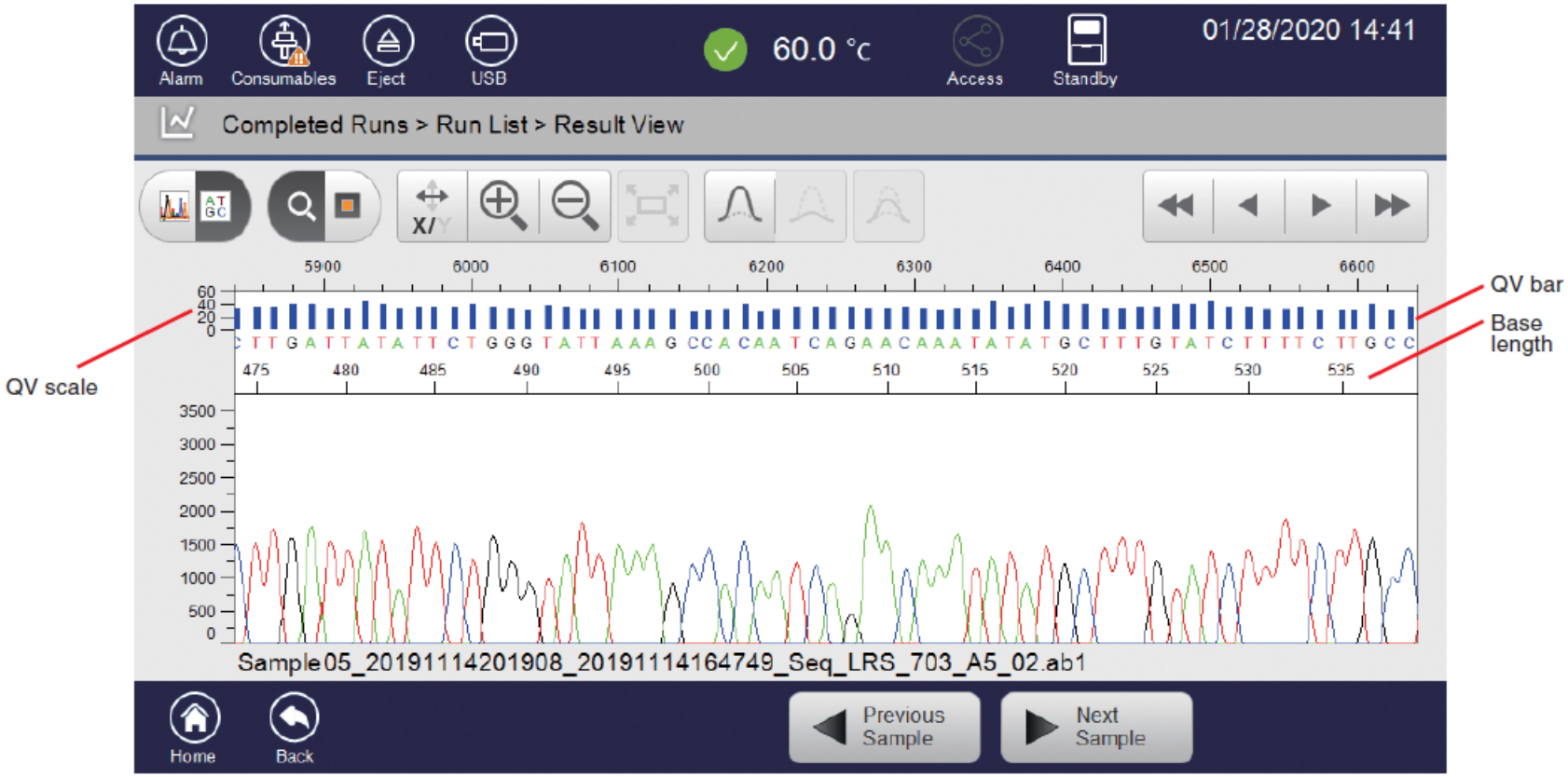




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可於面板上直接看到結果

Contiguous Read Length



GUI screen electropherogram data (Standard Sequencing example)

Sequencing was performed using the BigDye® Terminator v3.1 Sequencing Standard Kit in Standard Sequencing mode. The electropherogram data display demonstrates high resolution and accurate QV values were maintained at 500 bp. Contiguous Read Length of 600 bp or higher in Fast Sequencing mode, or at 700 bp or higher in Standard Sequencing are typical and reproducible.

Benchmark of CCE Sequencer

Detail Specification

Item	Spec.
Sample	4 sample/injection, 8wellx4 tube
Capillary	4ch 36cm
Consumable	Polymer cartridge（Polymer4,Polymer7） Anode Buffer（x3 Buffer） Cathode Buffer（x1Buffer）
Resolution（Fragment）/Time	>400base/<44min@Polymer4 >475base/<32min@Polymer7
Size, Weight	W400mm x D600mm x H600mm、<45kg
Start up	<15min
Light source	505nm±2nm 20mW LD
Detection range	520-690nm 6dye
Consumable handling	Easy of replacement < a few minutes
Instrument control	Touch panel PC
Accessory	Handy barcode reader, power cable

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Thank you very much for your interest in DS3000.

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