



正茂生物科技股份有限公司

Genmall Biotechnology Co., Ltd.

BIO-RAD

CFX Opus



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Genmall

qPCR Operation Training

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Outline



01

Principle of PCR

02

Principle of qPCR

03

Precautions of qPCR

04

Operation of qPCR

PCR

DNA

Principles

Elements

Procedure

What is Polymerase Chain Reaction ?

A common laboratory technique which is used to

“amplify” - copy - small segments of DNA (In Vitro) via

DNA polymerase and a pair of specific primers .

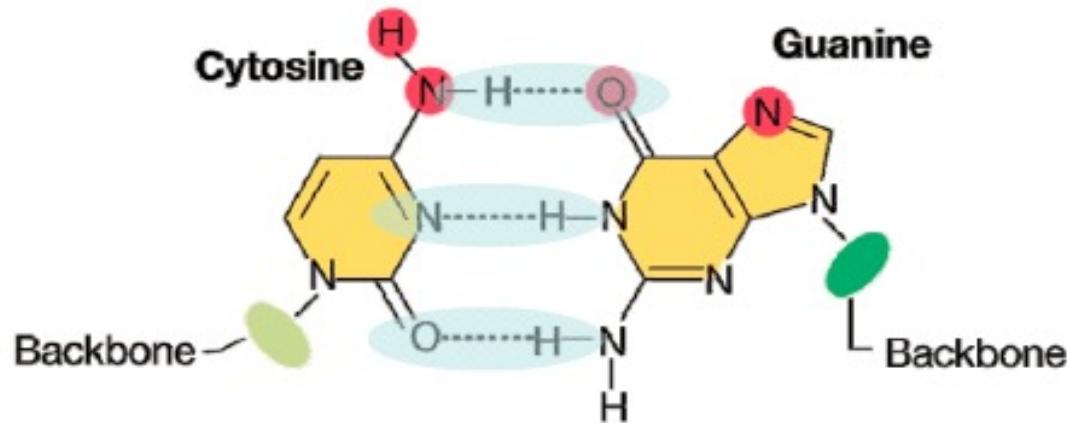
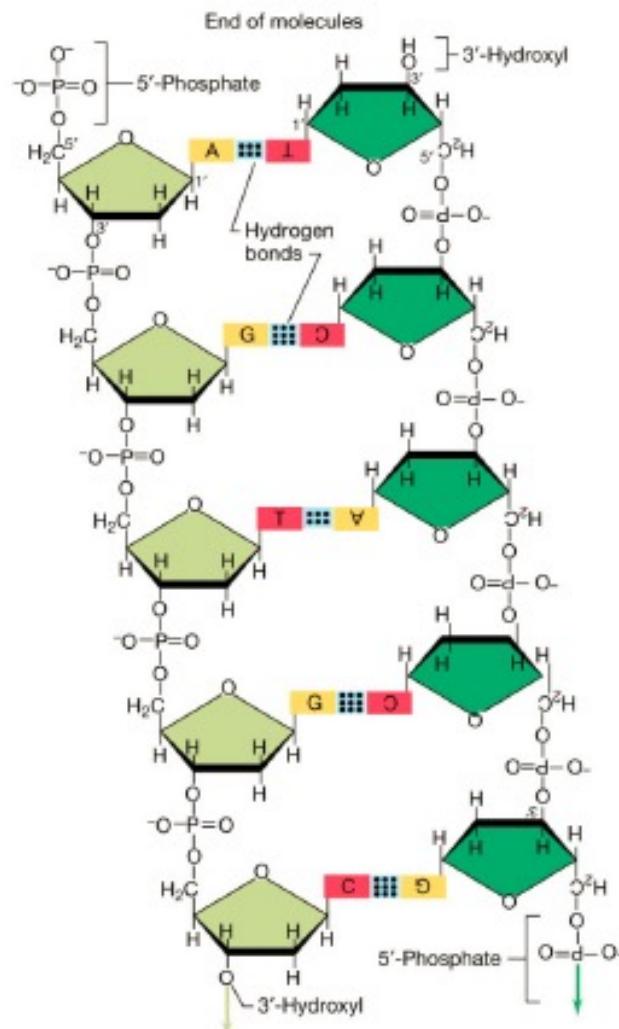
PCR

DNA

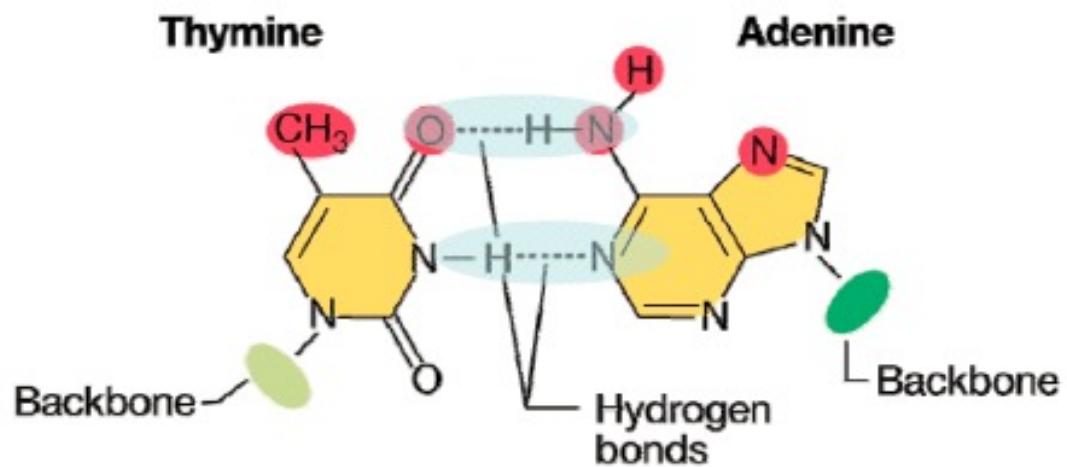
Principles

Elements

Procedure



GC pair > AT pair



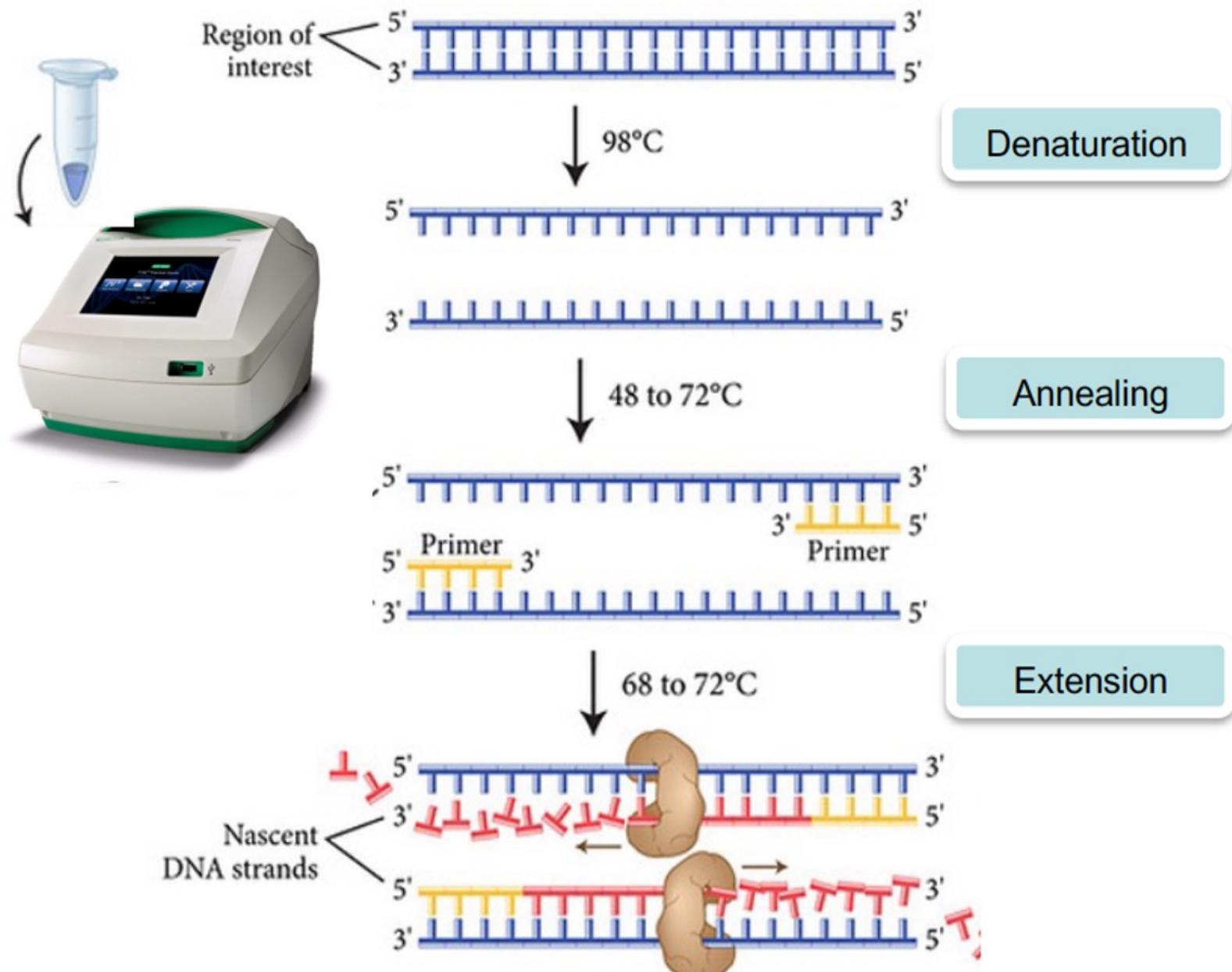
PCR

DNA

Principles

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Procedure



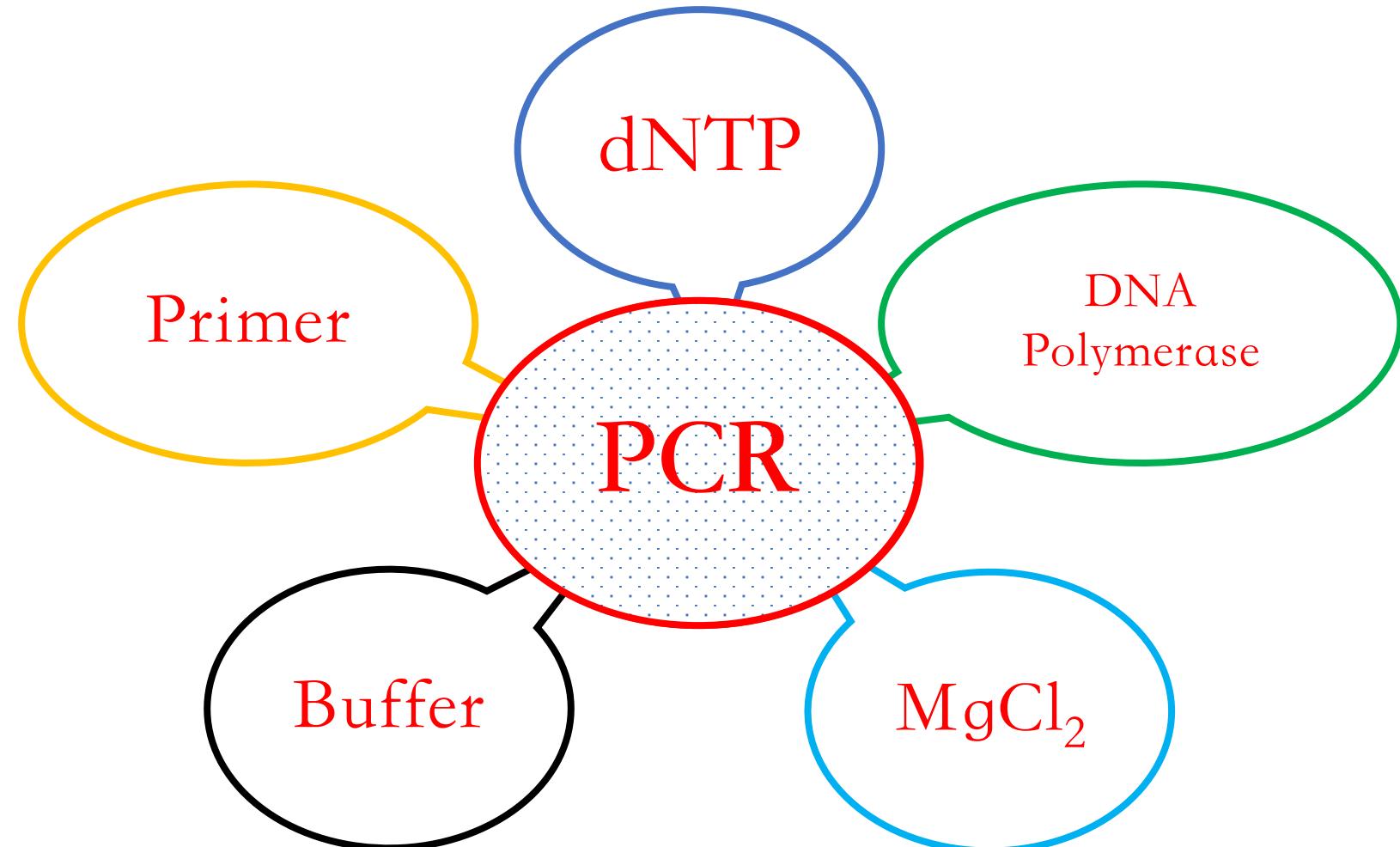
PCR

DNA

Principles

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PCR

DNA

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Procedure

✓ **DNA template** : A segment of DNA which can be used as a model for duplication.

✓ **Primer** : Two primers (**forward& reverse primer**) are used in each PCR reaction, and they are designed so that they flank the target region (**region that should be copied**).

✓ **DNA polymerase** : Synthesizes - builds - two new strands of DNA, using the original strands as templates.

PCR

DNA

Principles

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Procedure

✓ **Deoxynucleotide triphosphate (dNTP)** : There are four types of dNTP 「dATP、dGTP、dCTP、dTTP」 in PCR is to expand the growing DNA strand with the help of DNA polymerase. °

✓ **Magnesium chloride (MgCl₂)** : Magnesium ion (Mg^{2+}) functions as a **cofactor** for activity of DNA polymerases by enabling incorporation of dNTPs during polymerization.

✓ **Buffer** : Provides a suitable chemical environment for activity of DNA polymerase. The buffer pH is usually between 8.0 and 9.5 (KCl) and is often stabilized by Tris-HCl, which promotes primer annealing.

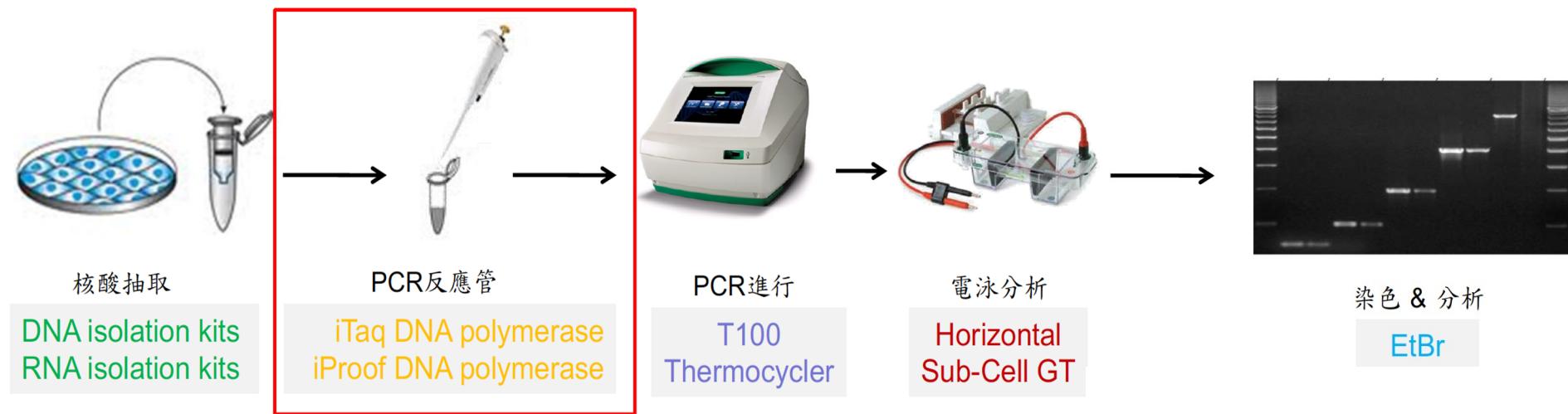
PCR

DNA

Principles

Elements

Procedure





2022 

— q P C R —

• • • •

qPCR

Comparison

Principle

C_T value

DNA binding dye

Hydrolysis probe

1. **Real-Time PCR** : divide into two parts : 「Real-time」 and 「PCR」
2. Real-Time PCR : It is also known as 「quantitative PCR」
3. Abbreviation : 「**Real Time RT-PCR**」 or 「**qPCR**」
4. Method : Add 「fluorescent DNA binding dye」 or 「probe」 for detection during DNA amplification (PCR)
5. Advantage : **qPCR** is sensitive, specific detection (via **fluorescence**) and quantification of nucleic acid targets during PCR cycle (so-called **Real time**).

qPCR

Comparison

Principle

 C_T value

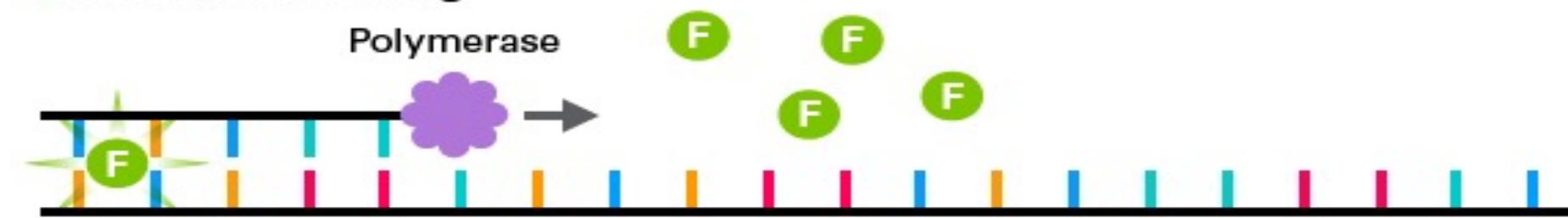
DNA binding dye

Hydrolysis probe

1 Heat denaturation



2 Primer annealing



3 Extension



PCR V.S. qPCR

qPCR

Comparison

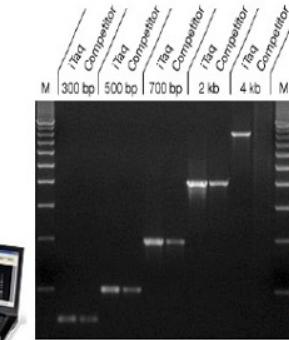
Principle

C_T value

DNA binding dye

Hydrolysis probe

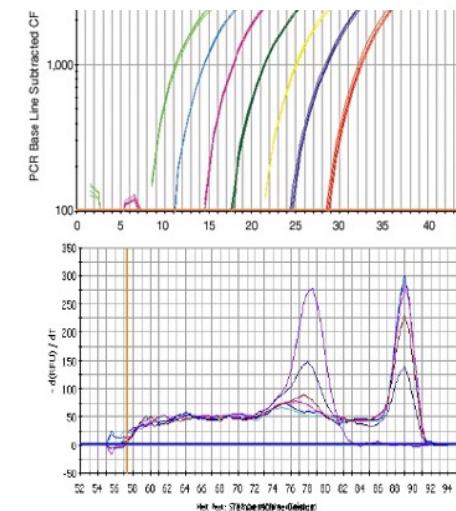
+Taq
+dNTP
+MgCl₂
+H₂O
+Buffer
+Template
+Primer
(On ice)



- End point
- Fuzzy data
- Labor intensive

3hrs (1.5 hrs labor)

+2x Master Mix
+H₂O
+Template
+Primer
(Room Temp)



- Online monitoring
- More sensitive
- Automated

<1 hrs (20 min labor)

qPCR

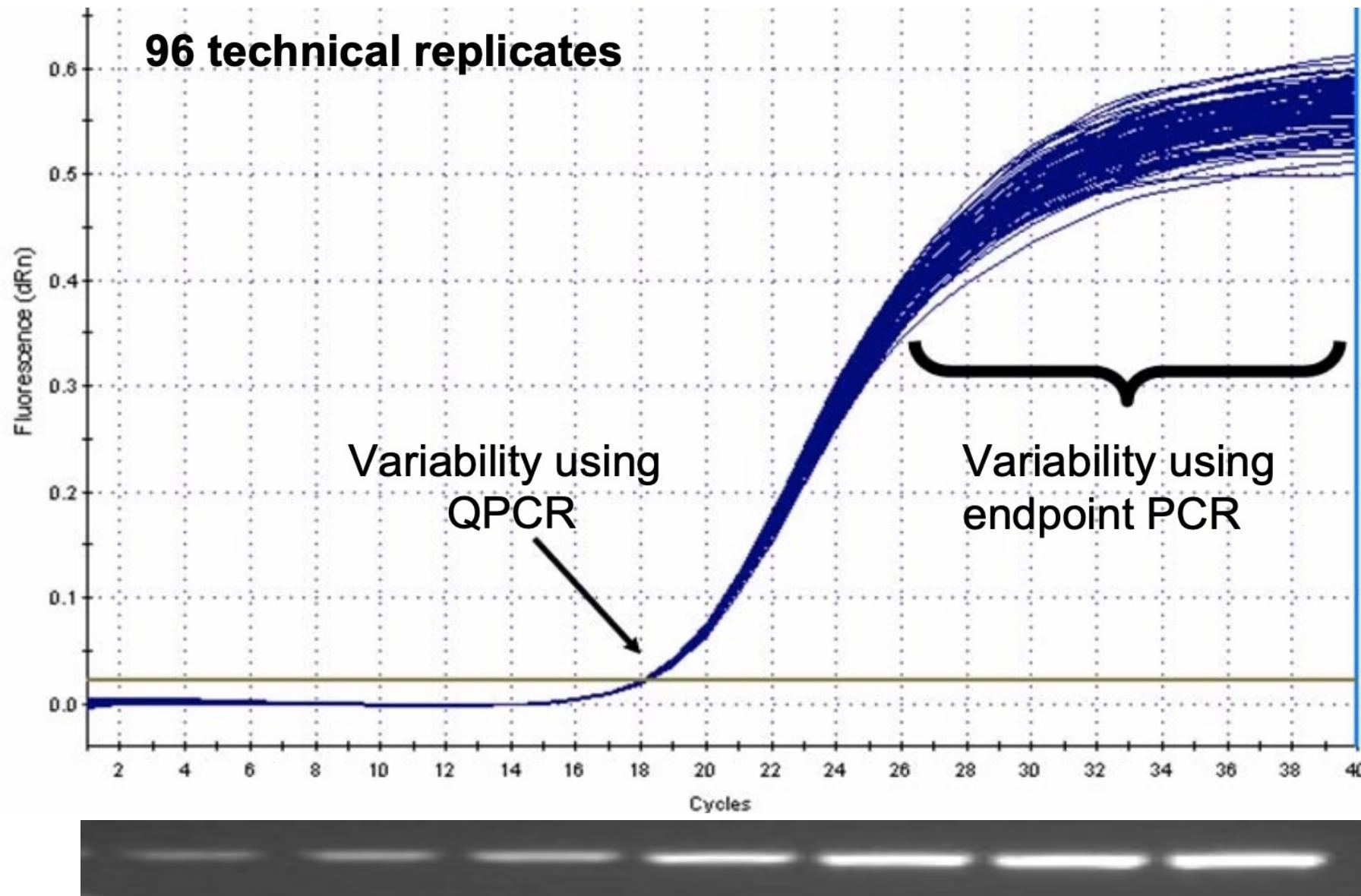
Comparison

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qPCR

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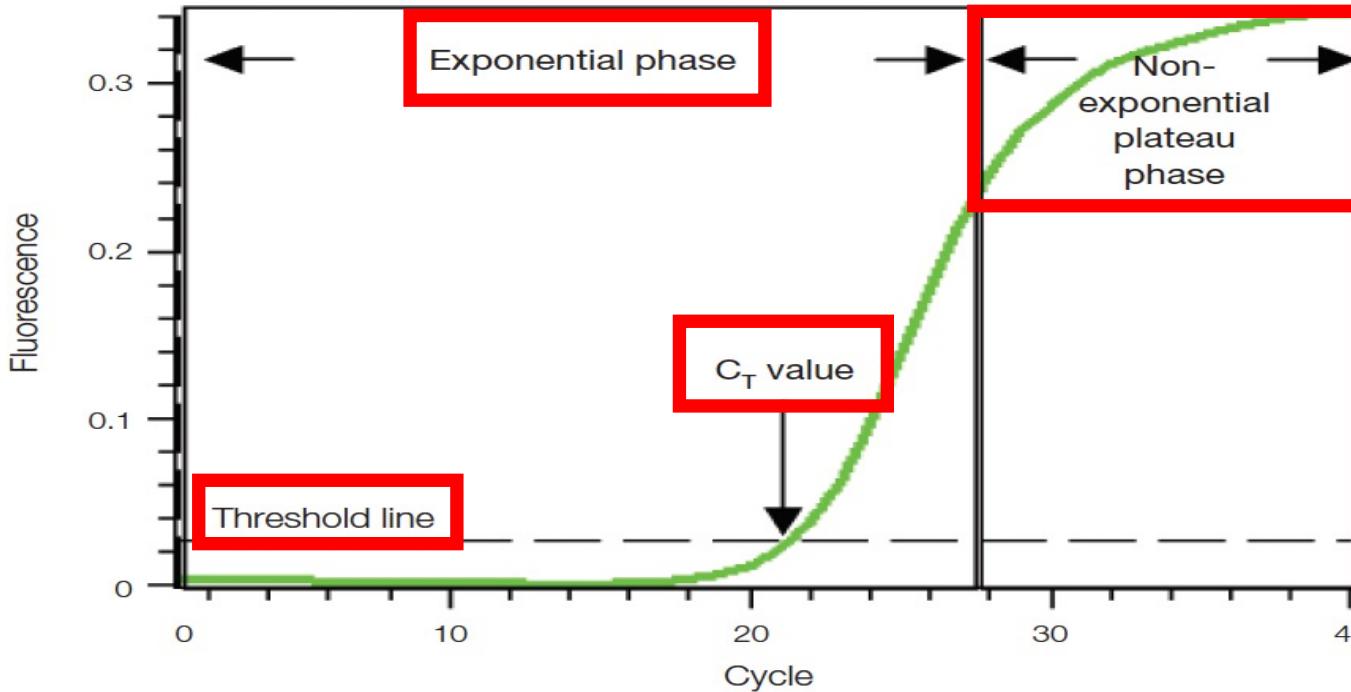


Fig. 1.1. Amplification plot. Baseline-subtracted fluorescence is shown.

- ✓ **Threshold line** (background or baseline) : At the start of the run, when the amount of PCR product is low, this produces very little fluorescence.
- ✓ **Exponential phase** : Once the amount of PCR product is amplified enough, it will enter the exponential phase. This is when the amount of PCR product doubles for every PCR cycle. 「 C_T 」 can be used and be defined as quantitative marker during this phase.
- ✓ **Non-exponential Plateau phase** : Once all of the reagents, such as nucleotides, have been used up in the PCR reaction, the amplification will slow and ultimately plateau. This is the region where no more PCR products cannot be produced.

qPCR

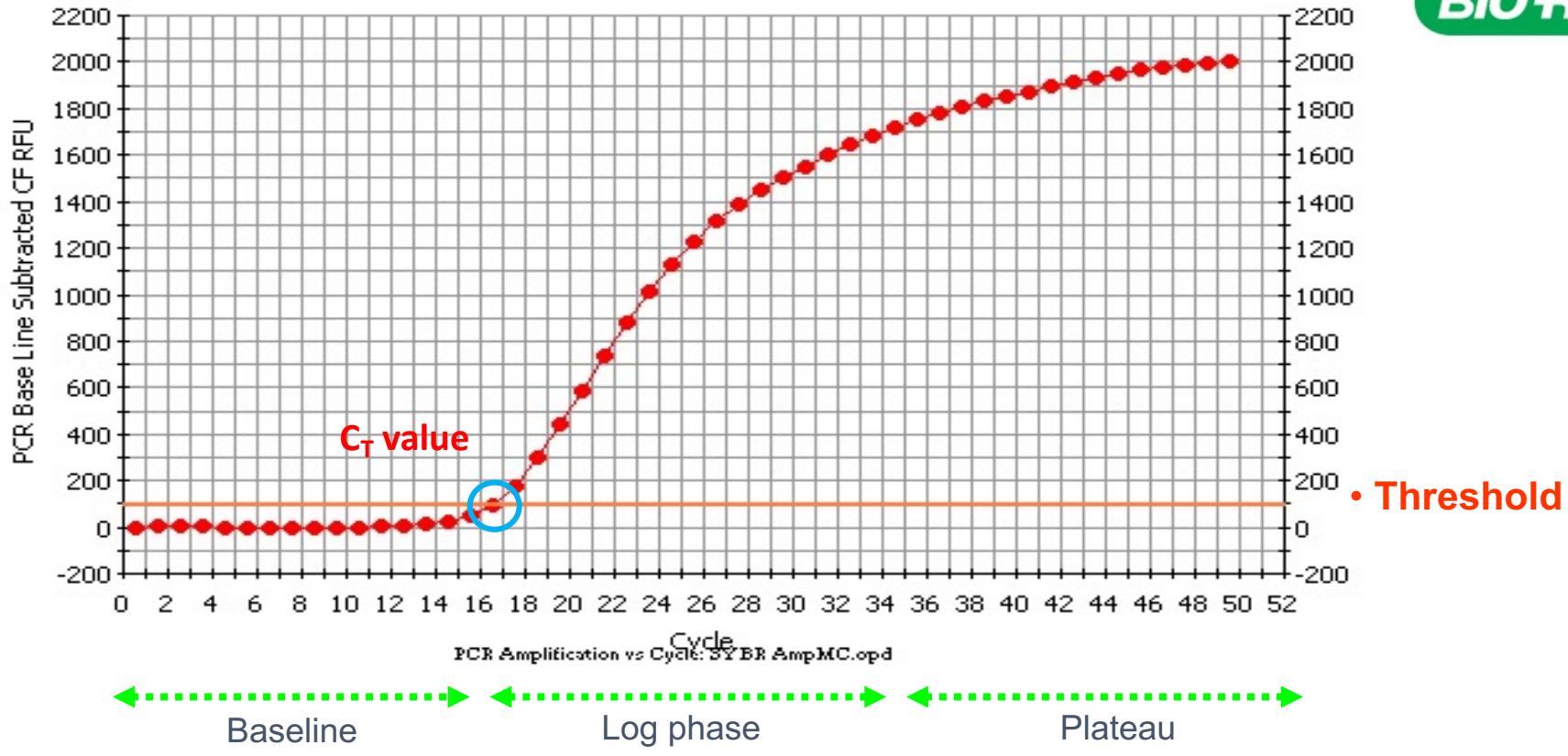
Comparison

Principle

C_T value

DNA binding dye

Hydrolysis probe



- ✓ **Threshold** : Basic reaction line of **background** which is derived from fluorescent reagents.
- ✓ **C_T (cycle threshold) / Cq (cycle quantification)** is defined as the number of cycles required for the fluorescent signal to **cross the threshold** (i.e. **exceeds background level**).

qPCR

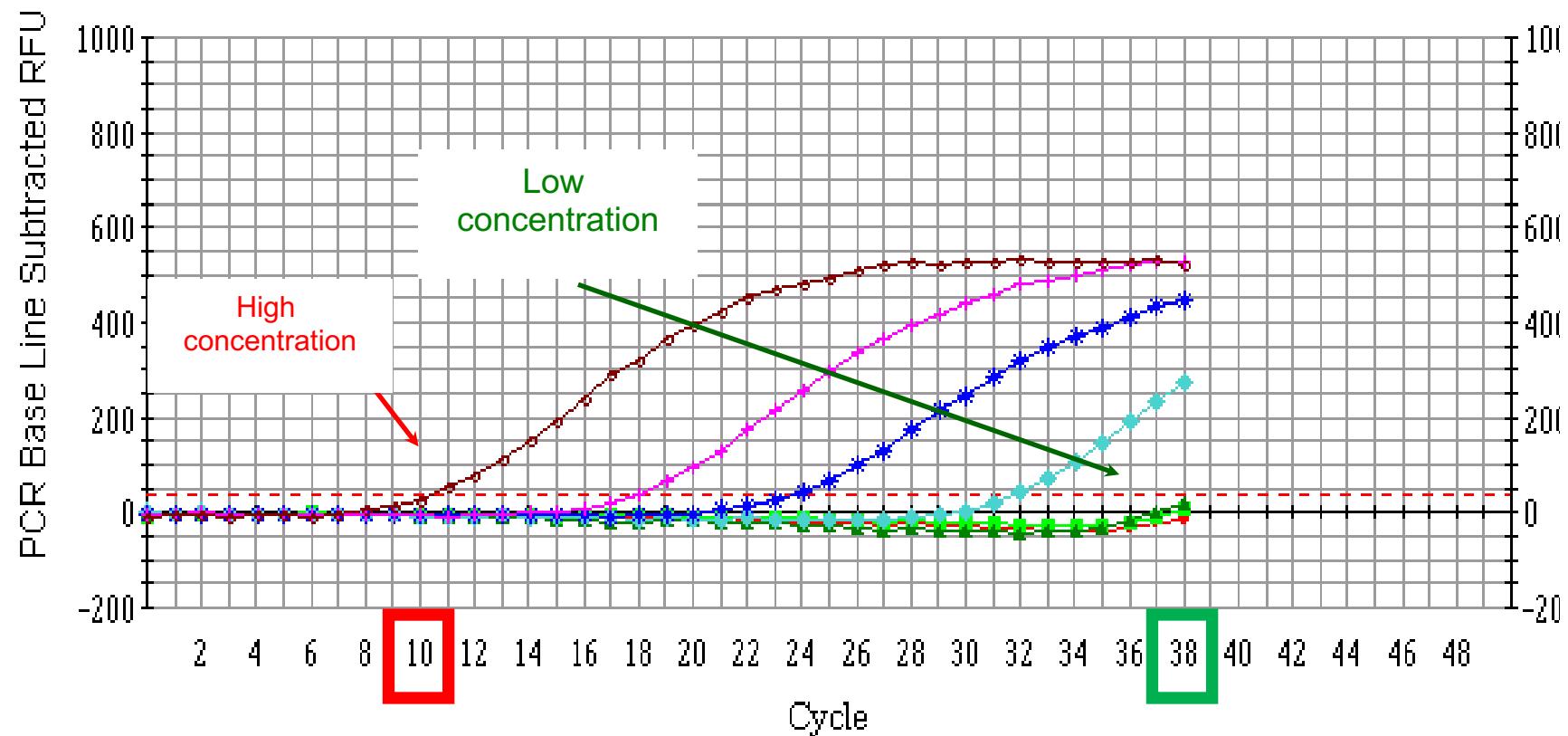
Comparison

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C_T value

DNA binding dye

Hydrolysis probe



C_T value are **inversely** proportional to the **amount** of target nucleic acid

qPCR

Comparison

Principle

C_T value

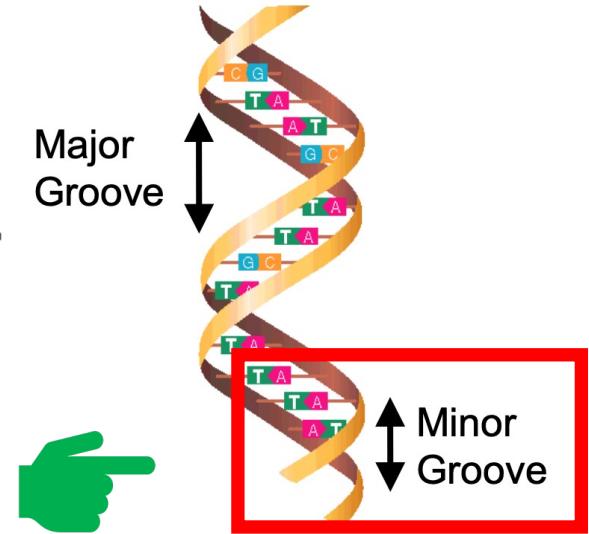
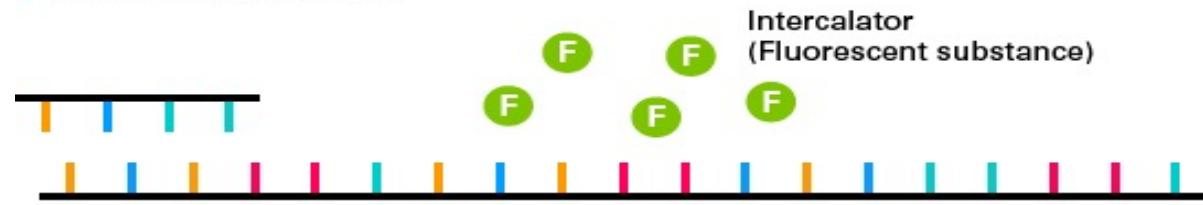
DNA binding dye

Hydrolysis probe

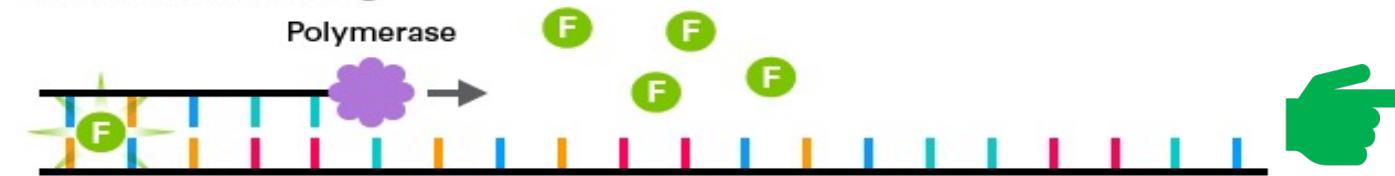
DNA binding dye – SYBR Green I

BIO-RAD

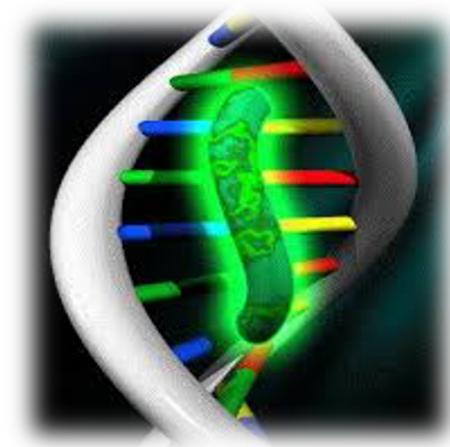
1 Heat denaturation



2 Primer annealing



3 Extension



SYBR Green I is a **dsDNA** binding dye, which can be used to quantify amplicon amount during the course of the PCR by tracking overall fluorescence emission.

DNA binding dye – SYBR Green I

BIO-RAD

qPCR

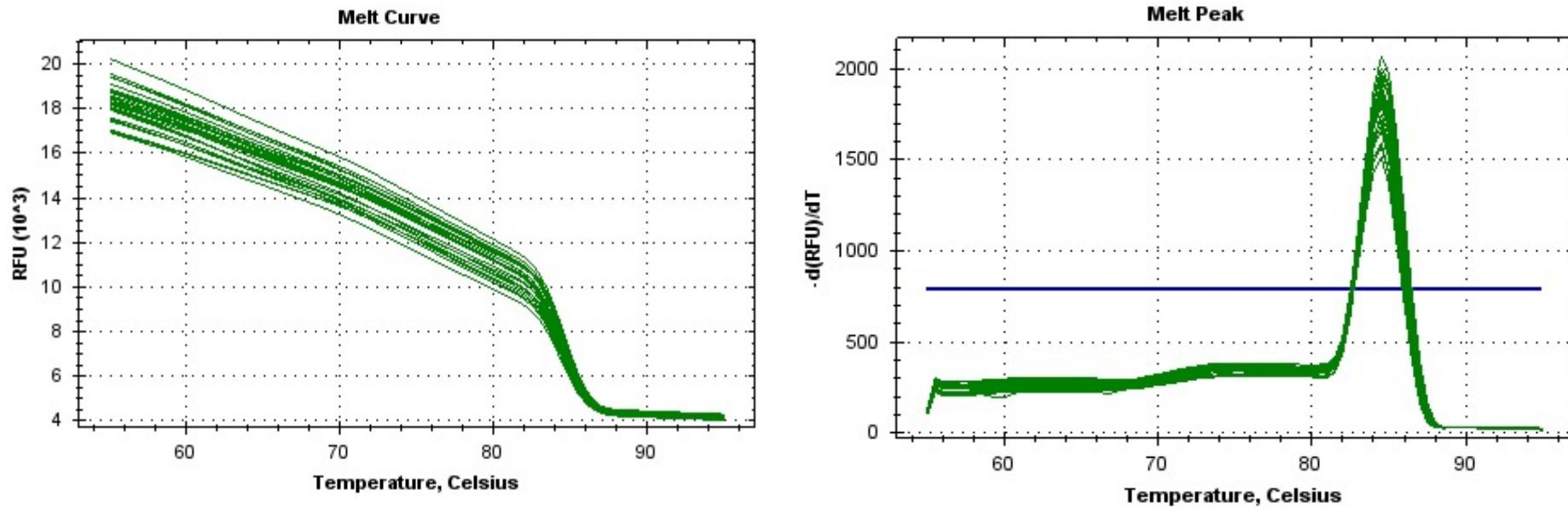
Comparison

Principle

C_T value

DNA binding dye

Hydrolysis probe



How to confirm the 「specificity」 of PCR products when performing SYBR Green qPCR experiments?

1. Method: Use the characteristics of DNA **Tm value** to ensure.
2. Analytical method :
 - ① **Melt Curve** (The upper left)
 - ② **Melt Peak** (The upper right)

qPCR

Comparison

Principle

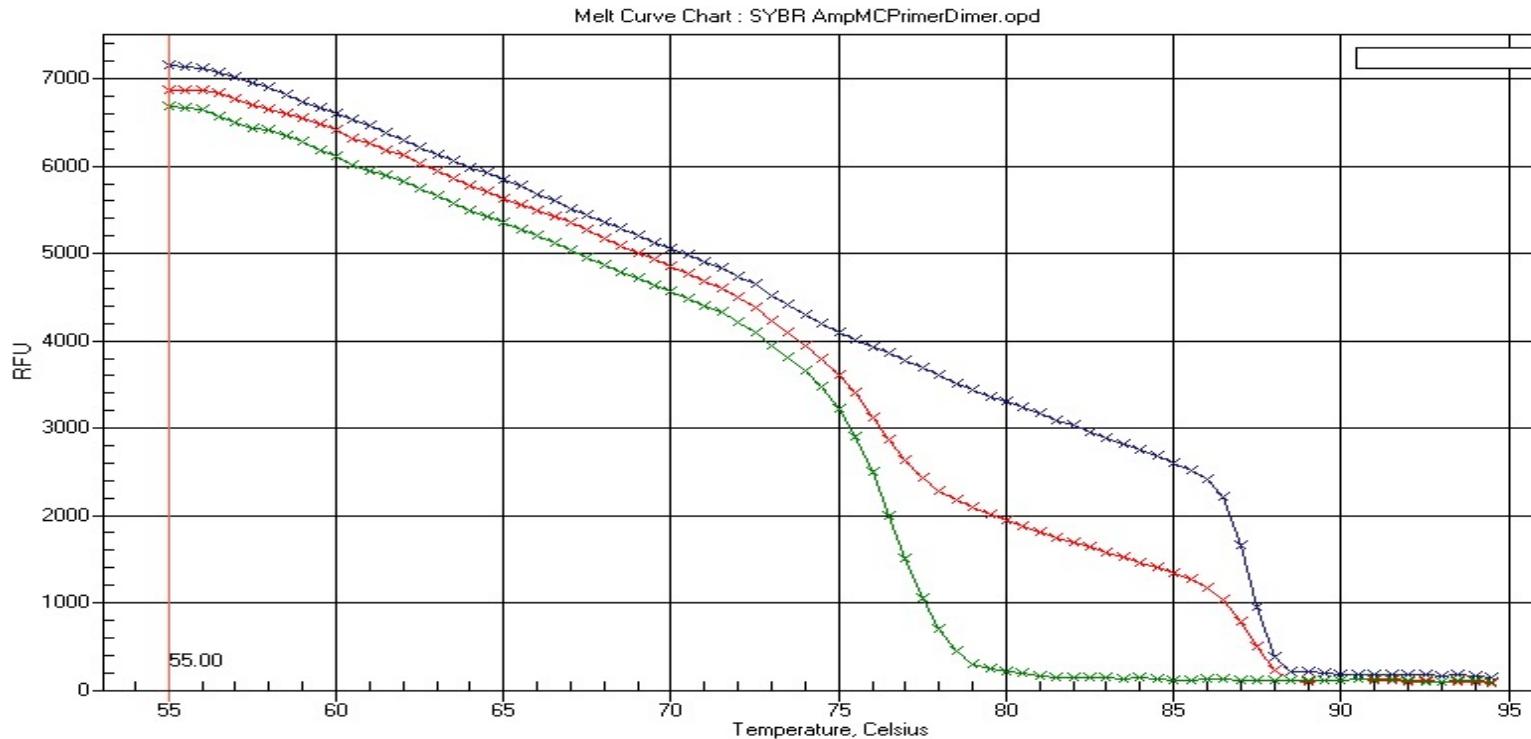
C_T value

DNA binding dye

Hydrolysis probe

Melting Curve - Tm value

BIO-RAD



➤ Melting temperature (Tm)

- ① The temperature at which **one half of the DNA duplex** will dissociate to become **single stranded** and indicates the duplex stability. °
- ② Depends on nucleotide content (**GC ratio**) and **length**

qPCR

Comparison

Principle

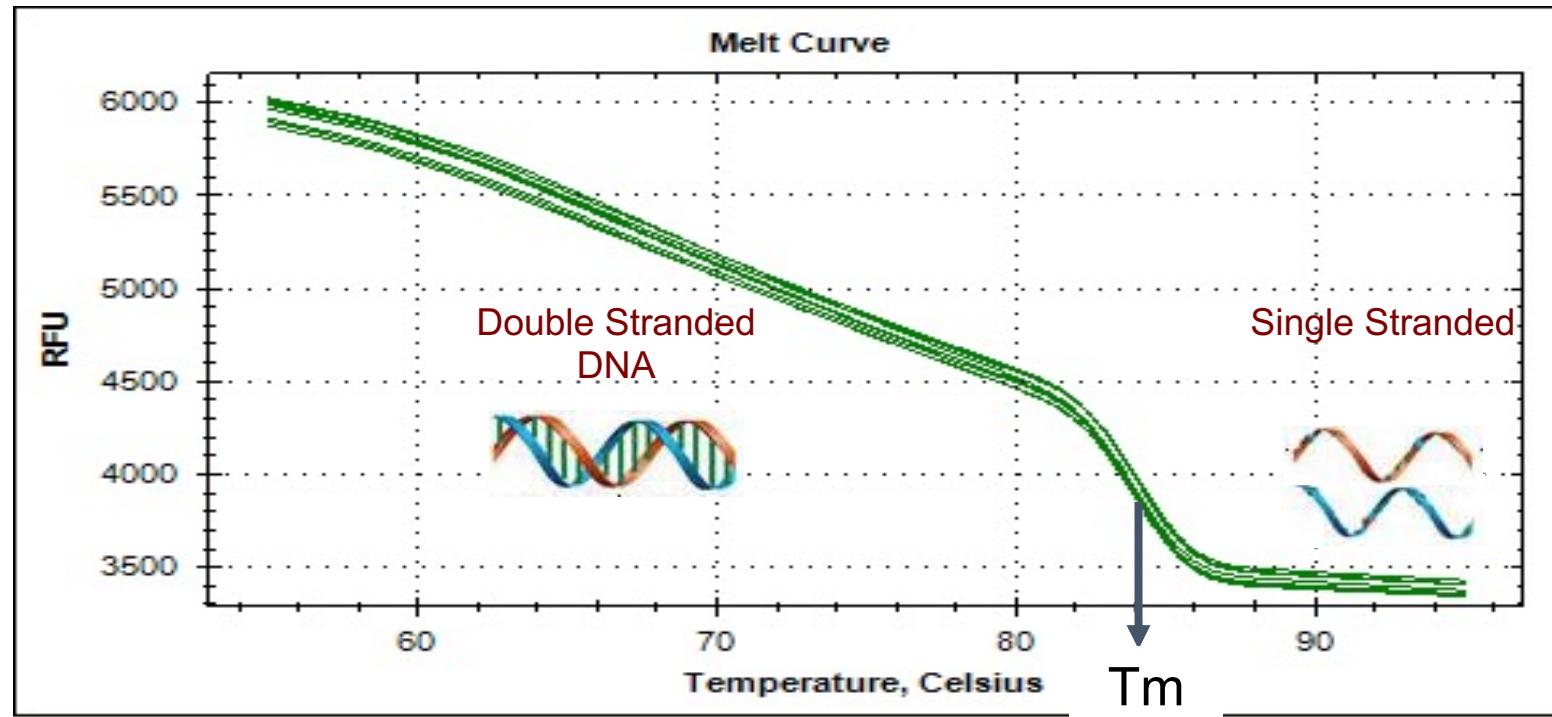
C_T value

DNA binding dye

Hydrolysis probe

Melting Curve - Tm value

BIO-RAD



➤ Melting temperature (Tm)

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qPCR

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Principle

C_T value

DNA binding dye

Hydrolysis probe

Melting Peak – T_m value

BIO-RAD

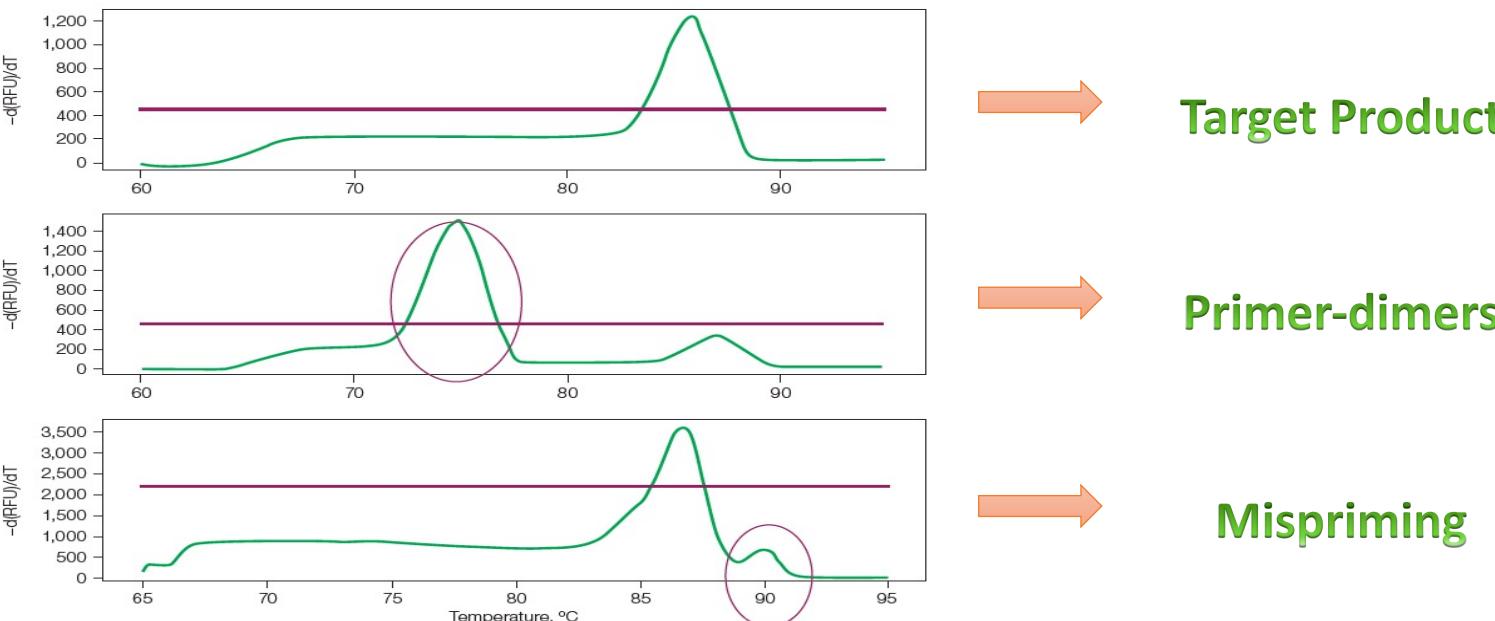


Fig. 6. Melt curve profiles. A, a single well-defined peak indicates a single specific product. B, two or more peaks indicate poor specificity. A typical primer-dimer (in red) is due to excess final primer concentrations. Primer-dimers typically amplify in the mid-70°C range. C, two or more peaks indicate poor specificity. A typical mispriming (in red) is shown.

➤ Melting temperature (T_m)

- ① The temperature at which **one half of the DNA duplex** will dissociate to become **single stranded** and indicates the duplex stability. °
- ② Depends on nucleotide content (**GC ratio**) and **length**

qPCR

Comparison

Principle

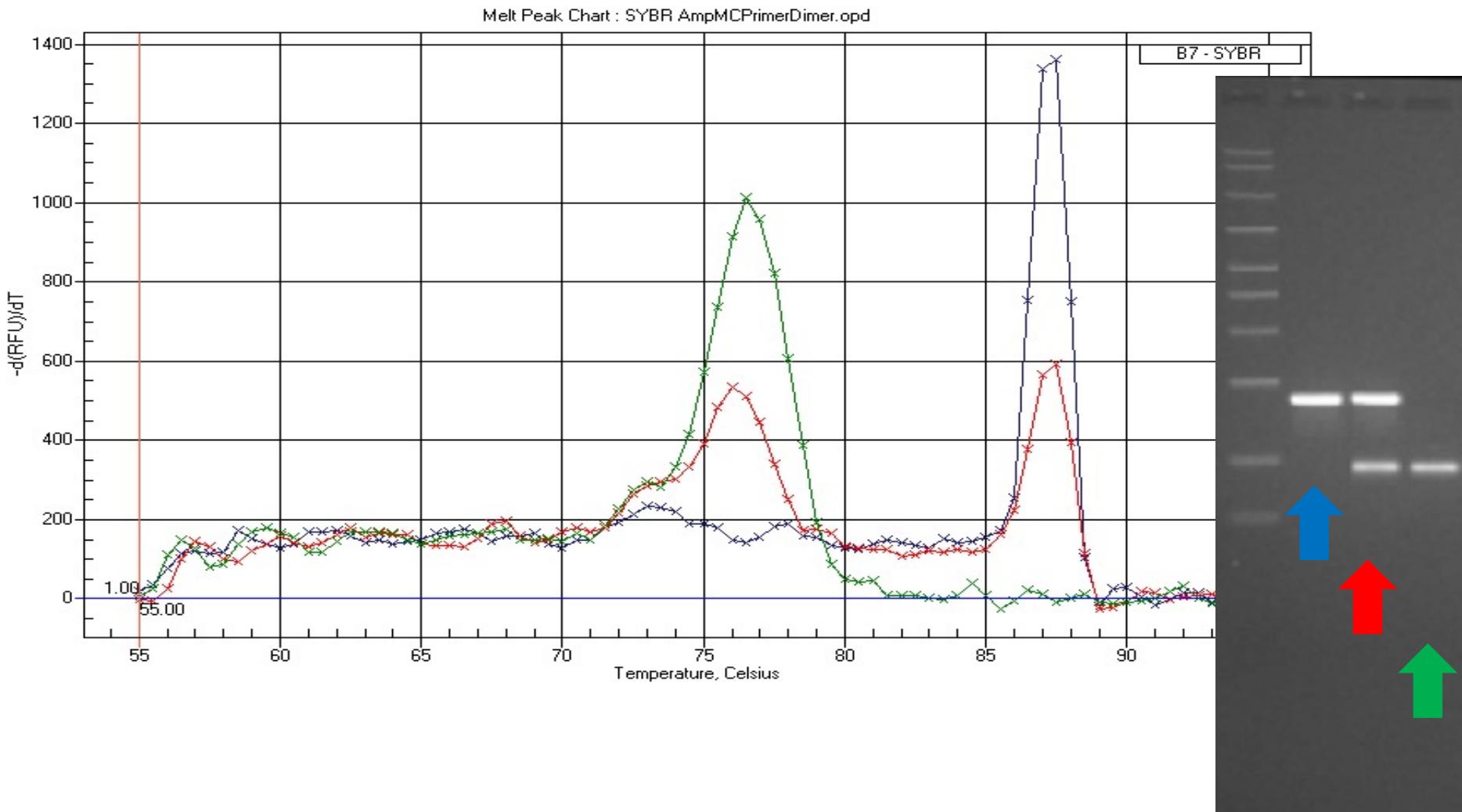
C_T value

DNA binding dye

Hydrolysis probe

Melting Peak – Tm value

BIO-RAD



qPCR

Comparison

Principle

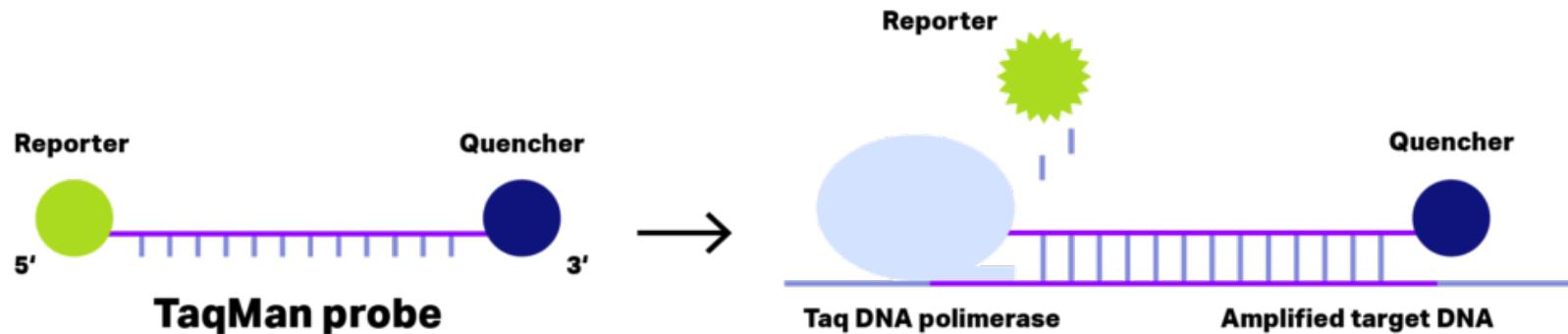
C_T value

DNA binding dye

Hydrolysis probe

Hydrolysis probe – TaqMan probe

BIO-RAD



- ① **Structure** : Labeled with a fluorescent **reporter at the 5' end** and a **quencher at the 3' end**.
- ② **Enzyme** : The dsDNA-specific **$5' \rightarrow 3'$ exonuclease** activity of *Taq*
- ③ **Principle** : The **reporter** is separated from the **quencher**, resulting in a fluorescence signal that is proportional to **the amount of amplified product** in the sample.
- ④ **Advantages** : **High specificity** and the ability to perform **multiplex** reactions.

qPCR

Comparison

Principle

C_T value

DNA binding dye

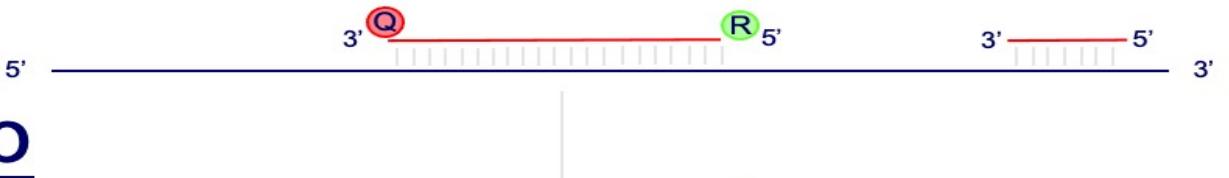
Hydrolysis probe

Hydrolysis probe – TaqMan probe

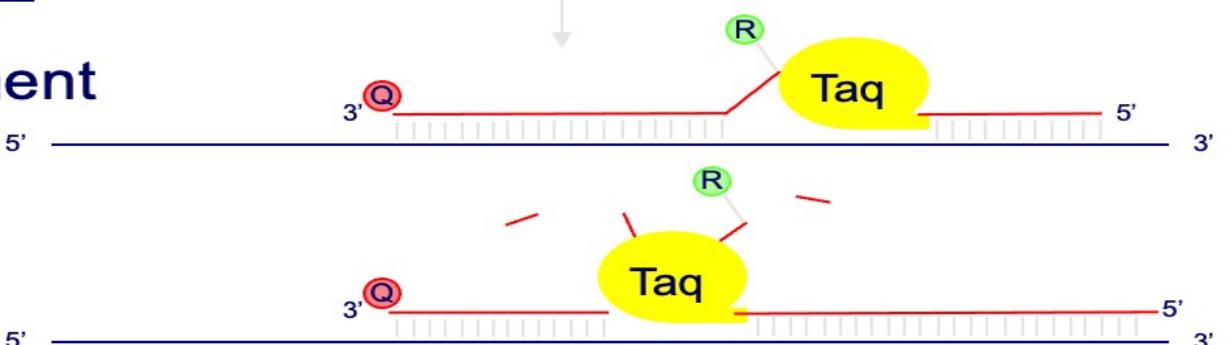
BIO-RAD

Extension Step

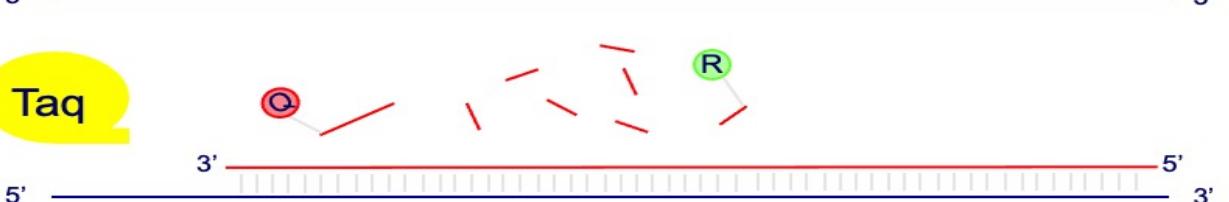
1. Strand Displacement



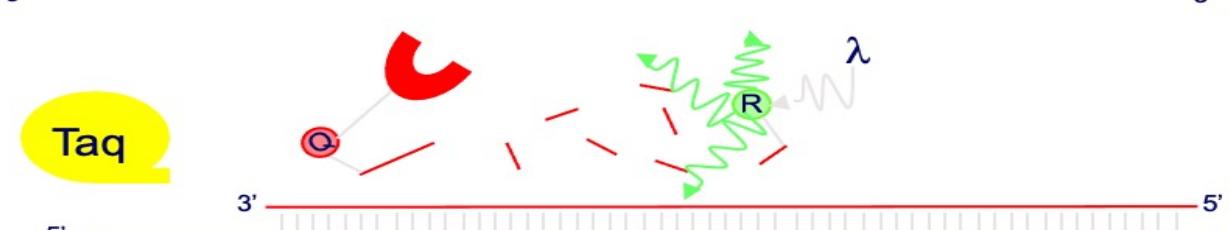
2. Cleavage



3. Polymerization Complete



4. Detection



qPCR

Comparison

Principle

C_T value

DNA binding dye

Hydrolysis probe

Binding dye v.s. Probe

BIO-RAD

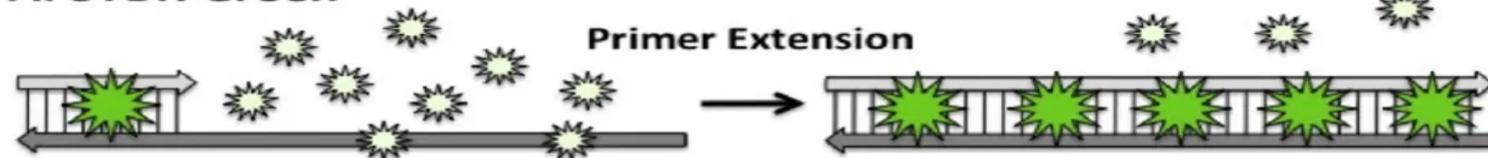
➤ SYBR Green I Dye

- ① Singleplex
- ② Non-specific
- ③ Binding site : **dsDNA**
- ④ Sensitivity : Middle (10 - 100 copies)
- ⑤ Notice : Avoid Primer-dimer formation
- ⑥ Cost: **Inexpensive**

➤ TaqMan Probe

- ① Multiplex
- ② **Highly Specific**
- ③ Binding site : **probe-specific region**
- ④ Sensitivity : High (1-10 copies)
- ⑤ Notice : **Specific fluorescent probe** is necessary. (Must be less than 30 bp)
- ⑥ Cost: **Expensive**

A. SYBR Green



B. TaqMan Probe





2022 

— Application —



Essential

Absolute Qu.

Relative Qu.

Application

MIQE

Notice

Standard Curve

- Linear standard curve : Coefficient of Correlation, $R^2 > 0.980$
- PCR Efficiency : $> 90 - 110\%$
- Equation :
 - ① Amplification efficiency, $E = 10^{-1/\text{slope}}$
 - ② % Efficiency = $(E - 1) \times 100\%$
- When $E < 90\%$: Might be interfered by **PCR inhibitors** in your sample or solution.
- When $E > 110\%$: Might be influenced by **pipetting error** or **primer-dimer**.

Essential

Absolute Qu.

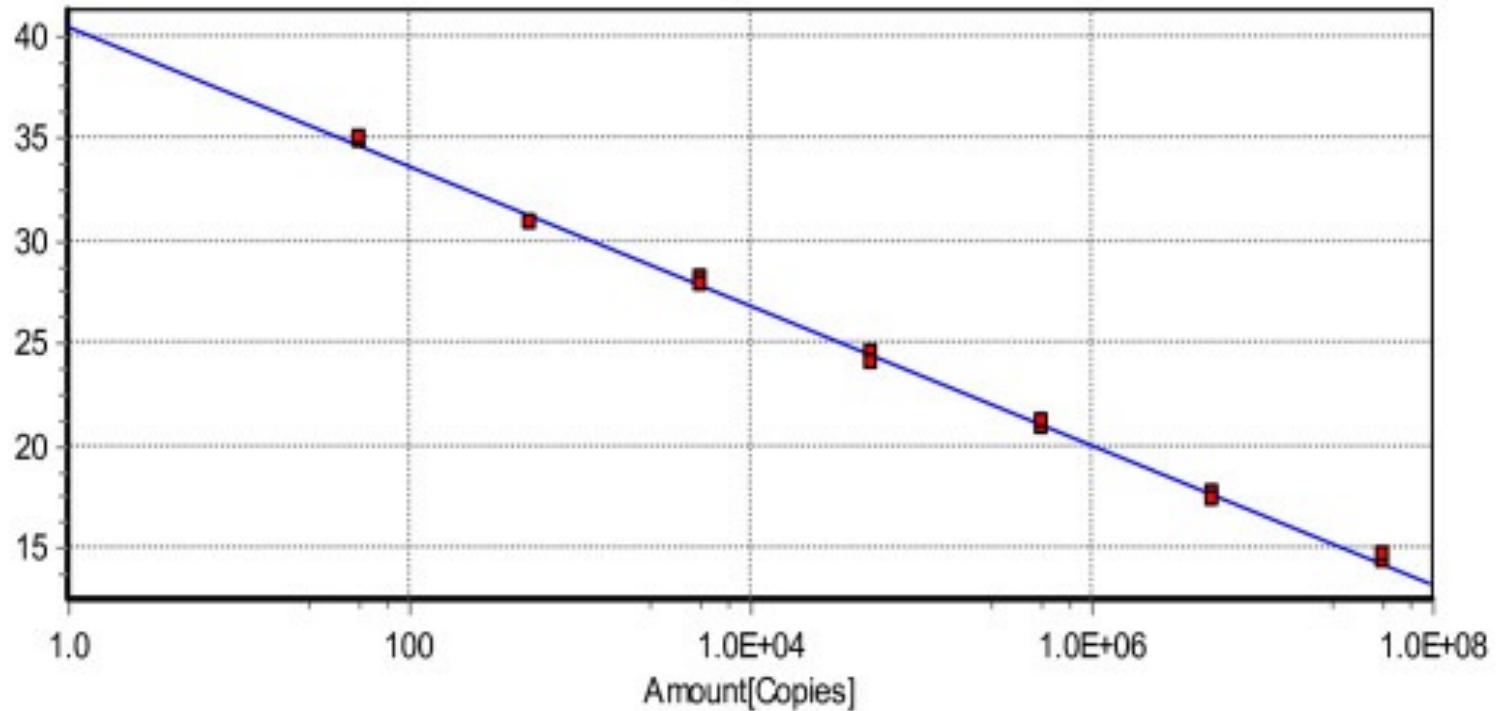
Relative Qu.

Application

MIQE

Notice

Standard Curve



Slope: -3.395

Y-Intercept: 40.47

Efficiency: 0.97

R^2: 0.998

Essential

Absolute Qu.

Relative Qu.

Application

MIQE

Notice

✓ 「Absolute quantification」 is performed by constructing a **standard curve** for each gene of the genes of interest (GOI) .

✓ Plotting the **quantification cycle (Cq) values** against **log[quantity]** of a dilution series of known GOI amount. (Interpolation)

✓ According to the different standard products, it is usually expressed in the form of common units as follows:

- ① Concentration unit : ng/ml 、 μ g/ml
- ② Measurement unit : ng 、 pg 、 copy number

✓ Note for absolute quantification : The slope of the standard curve and the correlation coefficient (R^2)

- ① Slope : 「 $3.0 \sim -3.6$ 」 , (Correspond to PCR efficiency from $90\% \sim 110\%$)
- ② Correlation coefficient : 「 $R^2 > 0.980$ 」

Essential

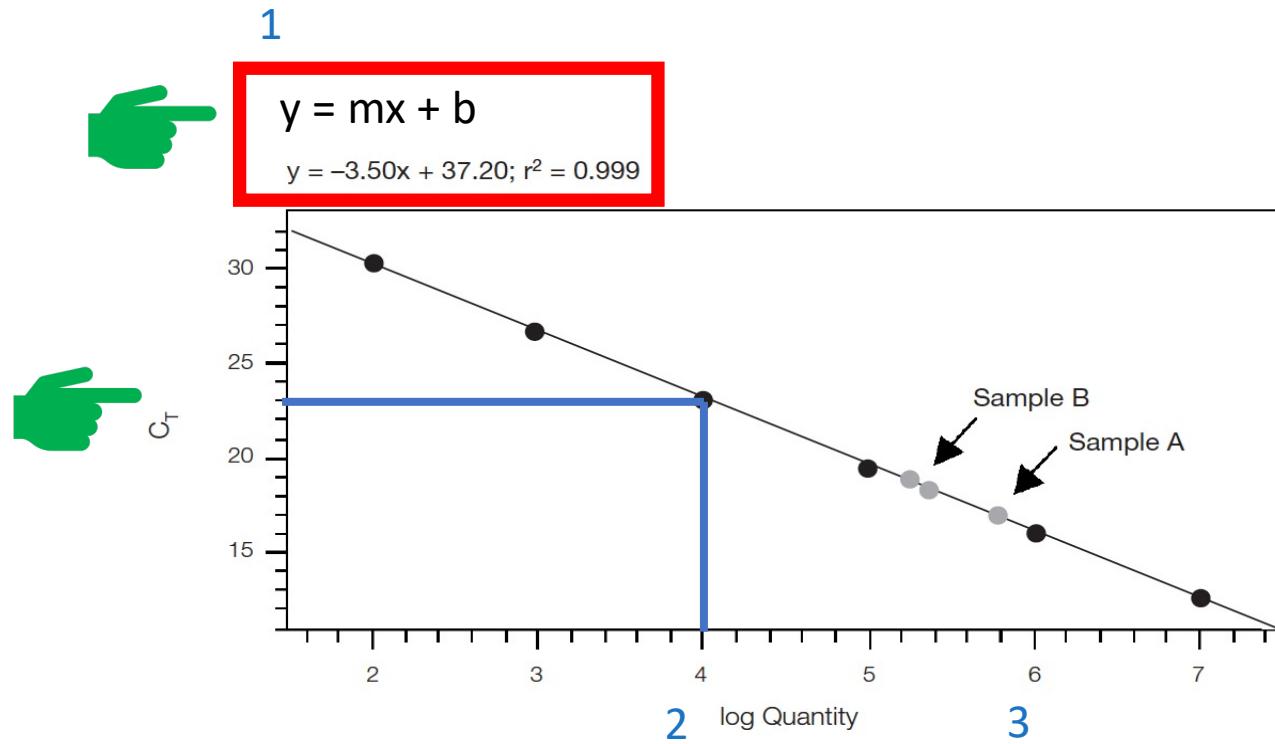
Absolute Qu.

Relative Qu.

Application

MIQE

Notice



2 3

Sample	Replicate	C_T	Copies
A	1	18.61	204,577
A	2	18.41	234,115
A	3	18.87	172,300
Average		$203,664 \pm 30,917$	
B	1	17.06	569,789
B	2	17.07	563,823
B	3	17.00	591,173
Average		$574,928 \pm 14,381$	



➤ $\Delta\Delta C_T$ (Livak)

Essential

Absolute Qu.

Relative Qu.

Application

MIQE

Notice

	Reference	Target
Tissue #1 (Control):	21	22
Tissue #2 (Test) :	20	24
<hr/>		
ΔC_T #1:		$22-21 = 1$
1 st Delta		
ΔC_T #2:		$24-20 = 4$
<hr/>		
2 nd Delta	$\Delta\Delta C_T$:	$1-4 = -3$
<hr/>		
	Fold induction =	$2^{-\Delta\Delta Ct} = 2^{-(-3)} = 8$

Essential Absolute Qu. Relative Qu.

Application

MIQE

Notice

Gene Expression

- ① Drug reaction
- ② Tumor marker
- ③ Gene regulation (siRNA/miRNA)
- ④ Gene therapy
- ⑤ Microarray
- ⑥ GMO detection

Pathogen detection

- ① Multiplex detection
- ② Multiple specimen detection
- ③ Synchronous analysis : Qualitative / Quantitative
- ④ Drug Safety and Effectiveness Monitoring

SNP Genotyping Analysis

- ① Evaluate the identified position of SNP
- ② Use for drug design
- ③ Genetic disease detection

Essential
Absolute Qu.
Relative Qu.

Application

MIQE

Notice

Clinical Chemistry 55:4
611–622 (2009)



Special Report

The MIQE Guidelines:
**Minimum Information for Publication of Quantitative
 Real-Time PCR Experiments**

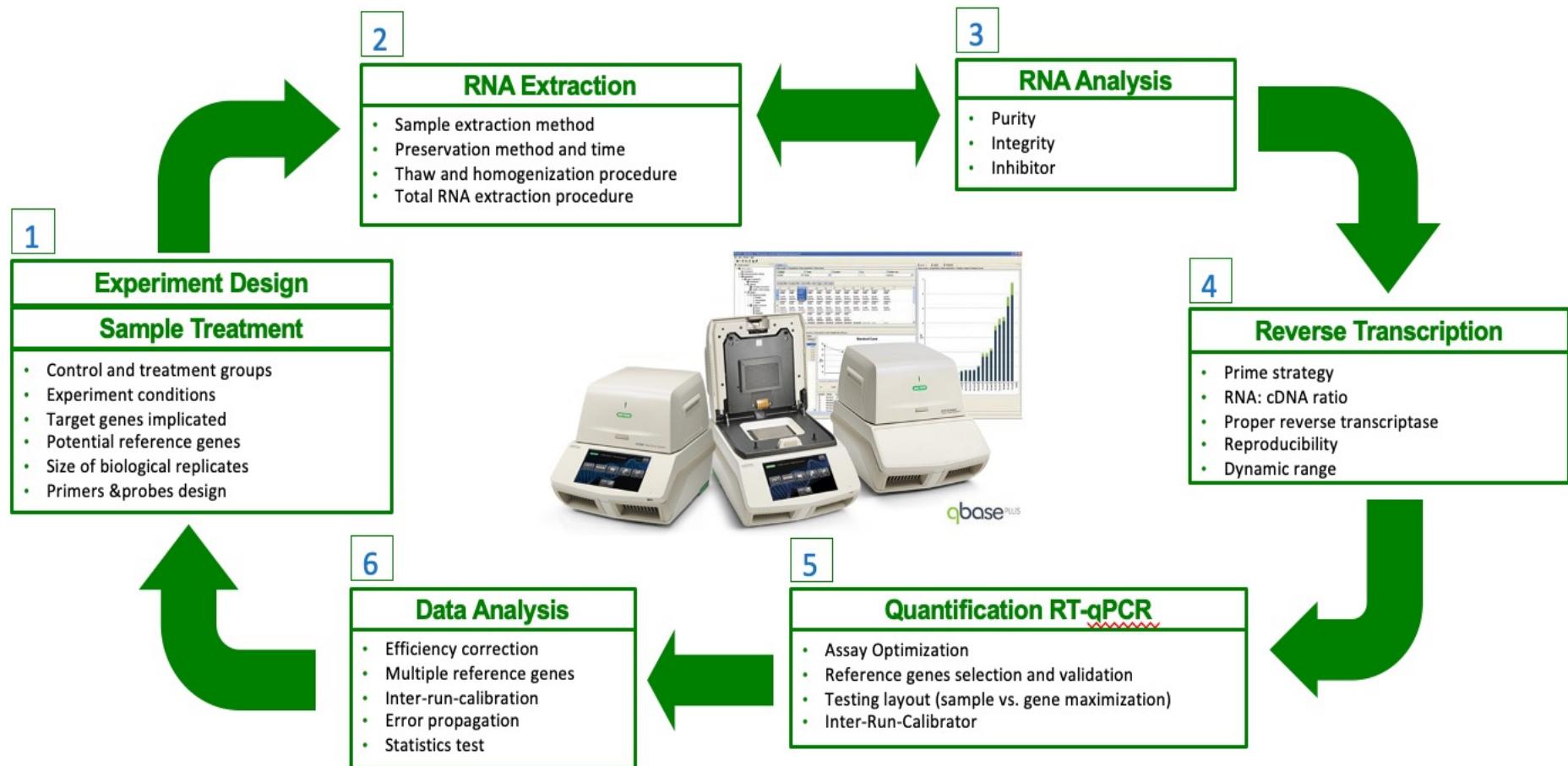
Stephen A. Bustin,^{1*} Vladimir Benes,² Jeremy A. Garson,^{3,4} Jan Hellemans,⁵ Jim Huggett,⁶
 Mikael Kubista,^{7,8} Reinhold Mueller,⁹ Tania Nolan,¹⁰ Michael W. Pfaffl,¹¹ Gregory L. Shipley,¹²
 Jo Vandesompele,⁵ and Carl T. Wittwer^{13,14}



Essential Absolute Qu. Relative Qu. Application

MIQE

Notice





MIQE guideline

1

檢核項目	重要性	說明
EXPERIMENTAL DESIGN		
Definition of experimental and control groups	E	
Number within each group	E	
Assay carried out by core lab or investigator's lab?	D	
Acknowledgement of authors' contributions	D	

1

SAMPLE		
Description	E	
Volume/mass of sample processed	D	
Microdissection or macrodissection	E	
Processing procedure	E	
If frozen - how and how quickly?	E	
If fixed - with what, how quickly?	E	
Sample storage conditions and duration (especially for FFPE samples)	E	

2 3

NUCLEIC ACID EXTRACTION		
Procedure and/or instrumentation	E	提供萃取的方法或儀器
Name of kit and details of any modifications	E	提供 Kit 的名稱/型號/批號/廠牌
Source of additional reagents used	D	是否有額外添加的試劑，有則註明型號廠牌
Details of DNase or RNase treatment	E	敘述對 DNase (for RNA 實驗) or RNase (for DNA 實驗) 的處理
Contamination assessment (DNA or RNA)	E	以尚未進行反轉錄的 RNA 樣本進行 qPCR，確認是否有產物
Nucleic acid quantification	E	核酸定量:使用的儀器廠牌/方法, OD260/OD280 比值，
Instrument and method	E	
Purity (A260/A280)	D	
Yield	D	計算濃度和總量
RNA integrity method/instrument	E	確認 RNA 品質:
RIN/RQI or Cq of 3' and 5' transcripts	E	求 RIN/RQI 值 ¹ ，跑膠確認 RNA 是否降解以及測試
Electrophoresis traces	D	
Inhibition testing (Cq dilutions, spike or other)	E	樣品內是否有抑制物質(效應) ²

4

REVERSE TRANSCRIPTION		
Complete reaction conditions	E	敘述反轉錄反應條件
Amount of RNA and reaction volume	E	RNA 量與反應體積
Priming oligonucleotide (if using GSP) and concentration	E	Primer 種類(廠牌)和濃度
Reverse transcriptase and concentration	E	反轉錄酵素(廠牌)和濃度
Temperature and time	E	溫度/時間/cycle 數
Manufacturer of reagents and catalogue numbers	D	試劑廠牌和型號
Cqs with and without RT	D	RT 試劑測試
Storage conditions of cDNA	D	記錄保存條件



MIQE guideline

5

qPCR TARGET INFORMATION

If multiplex, efficiency and LOD of each assay.	E	於同一試管做多基因定量才需要確定該項目
Sequence accession number	E	
Location of amplicon	D	
Amplicon length	E	
<i>In silico</i> specificity screen (BLAST, etc)	E	
Pseudogenes, retropseudogenes or other homologs?	D	
Sequence alignment	D	
Secondary structure analysis of amplicon	D	
Location of each primer by exon or intron (if applicable)	E	
What splice variants are targeted?	E	

5

qPCR OLIGONUCLEOTIDES

Primer sequences	E
RTPrimerDB Identification Number	D
Probe sequences	D ³
Location and identity of any modifications	E
Manufacturer of oligonucleotides	D
Purification method	D

Primer 或 Probe 合成的序列、廠商、純化方法等

5

qPCR PROTOCOL

Complete reaction conditions	E	敘述定量 PCR 實驗反應條件
Reaction volume and amount of cDNA/DNA	E	cDNA 量與反應體積
Primer, (probe), Mg ⁺⁺ and dNTP concentrations	E	
Polymerase identity and concentration	E	
Buffer/kit identity and manufacturer	E	
Exact chemical constitution of the buffer	D	
Additives (SYBR Green I, DMSO, etc.)	E	
Manufacturer of plates/tubes and catalog number	D	分析盤(管)廠牌和型號
Complete thermocycling parameters	E	反應條件(溫度/時間/cycles)
Reaction setup (manual/robotic)	D	反應設定
Manufacturer of qPCR instrument	E	儀器廠牌機型

Primer、鎂離子濃度、聚合酶濃度、緩衝液組成、其他添加物等

6

qPCR VALIDATION

Evidence of optimisation (from gradients)	D	是否有測試 annealing 溫度梯度
Specificity (gel, sequence, melt, or digest)	E	確認反應專一性
For SYBR Green I, C _q of the NTC	E	是否 NTC 控制組有產物
Standard curves with slope and y-intercept	E	
PCR efficiency calculated from slope	E	建立標準曲線 ⁴ ：由斜率推算 PCR 效率、計算信賴區間與標準差以及 r ²
Confidence interval for PCR efficiency or standard error	D	
r ² of standard curve	E	
Linear dynamic range	E	
C _q variation at lower limit	E	
Confidence intervals throughout range	D	
Evidence for limit of detection	E	
If multiplex, efficiency and LOD of each assay.	E	於同一試管做多基因定量計算效率和偵測極限

DATA ANALYSIS

qPCR analysis program (source, version)	E	分析程式/工具(版本)、分析方法 (threshold 或 regression) 以及敘述樣本盤排列方式等
C _q method determination	E	
Outlier identification and disposition	E	
Results of NTCs	E	NTC 控制組是否有產物
Justification of number and choice of reference genes	E	Reference gene 的數目和選擇
Description of normalisation method	E	敘述標準化方法
Number and concordance of biological replicates	D	生物樣本數
Number and stage (RT or qPCR) of technical replicates	E	單一生物樣本在儀器偵測的 n 值
Repeatability (intra-assay variation)	E	
Reproducibility (inter-assay variation, %CV)	D	計算重複性、再現性、使用何種統計方法、統計軟體(版本)
Power analysis	D	
Statistical methods for result significance	E	
Software (source, version)	E	
C _q or raw data submission using RDML	D	以 RDML 格式提供原始數據

Essential
Absolute Qu.
Relative Qu.
Application

MIQE

Notice

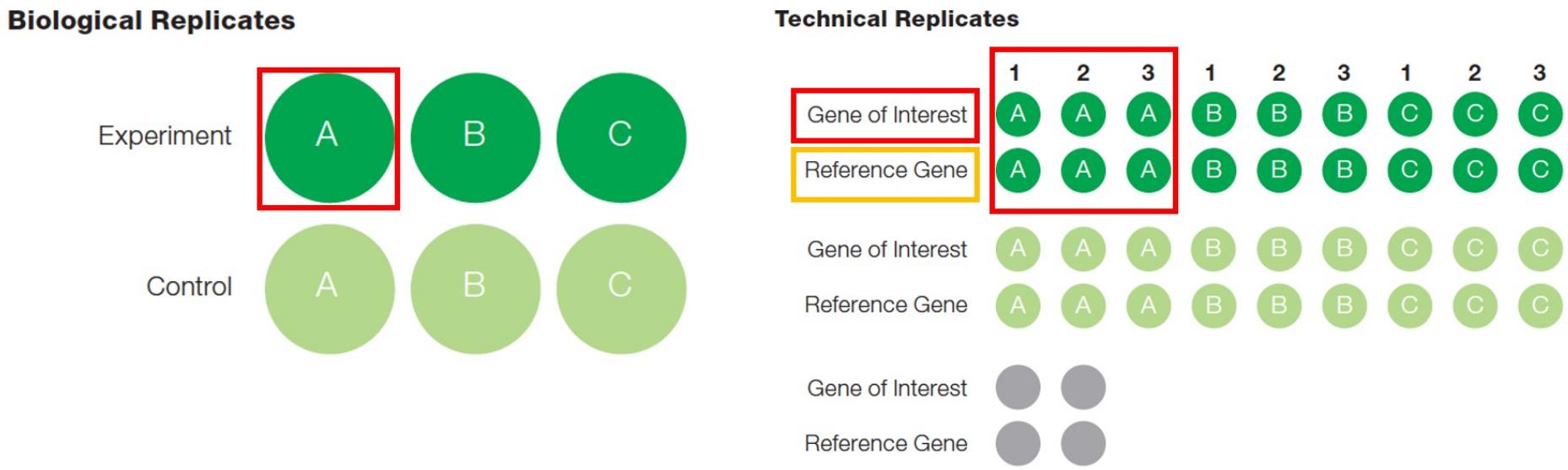


Fig. 6. Experimental replicates. All experiments should be designed with a combination of biological and technical replicates. This illustrates a simple experiment with triplicate biological samples from control (light green) and treatment/experimental (dark green) conditions. For each biological sample, three technical replicates are recommended for the gene of interest as well as for the reference gene(s). This results in a total of at least 36 samples plus the duplicate NTC (grey) for a total of >40 wells.

Essential

Absolute Qu.

Relative Qu.

Application

MIQE

Notice

Common 「PCR inhibitor」



★Red : From 「sample」

★Green : From 「reagent / solution」

Sample	Assay	Sample	Assay
Bile salts	Cholic acid	Cell lysates	MEM+FBS
	Deoxycholic acid		PBS
Polysaccharides	Polygalacturonic acid		Trypsin
Lipids	Cholesterol hydrochloride	Sample preparation	NaAc
Algae	Alginic acid		NaCl
Clay	Montmorillonite		EtOH
Blood	Heparin		Isopropanol
	Hematin		TRIzol
	EDTA		InstaGene Matrix
	Serum	Miscellaneous	Green tea
Soil	Humic acid		Chocolate
Textile	Indigo		Dust
Wine	Tannic acid		SDS
Plants	Cellulose		DMSO
	Pectin (for fiber control)		DTT
Hair, tissues	Melanin	Body fluids	Spermidine
Bones, teeth	CaCl ₂		Urea

Essential

Absolute Qu.

Relative Qu.

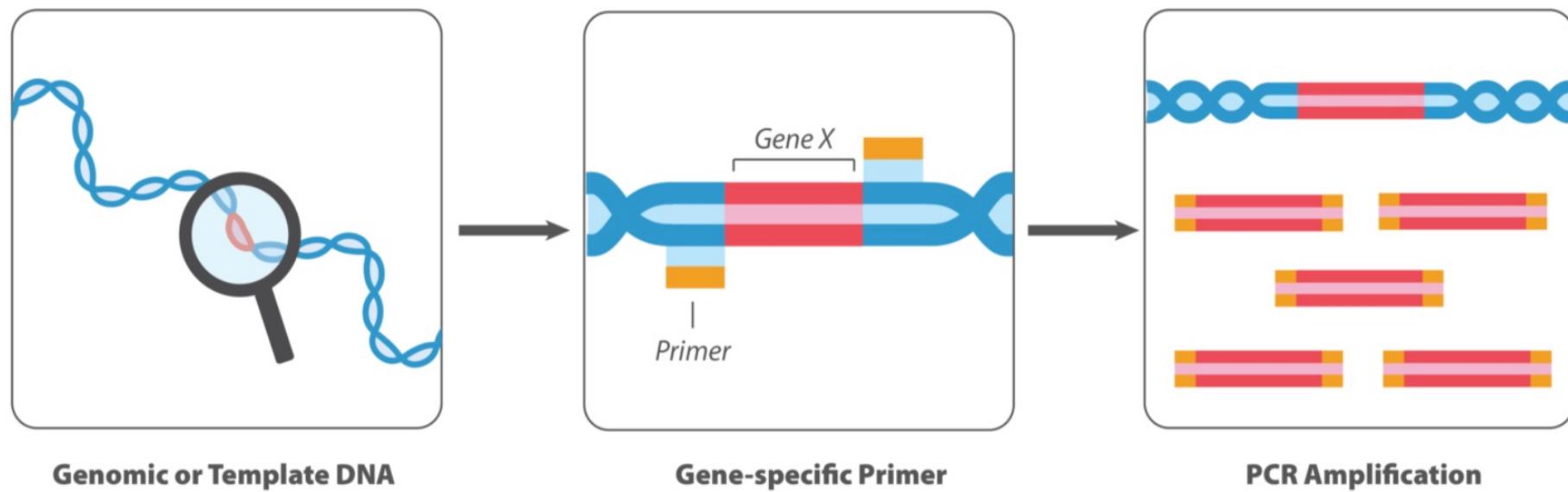
Application

MIQE

Notice

Amplicon

1. Recommended length : **75 - 200bp**
2. Regional structure : Should be **free of strong secondary structures**.
3. Repeats : Prevent **quadruple repeats of G or C** appear in designed region.
4. CG % : 40 - 60%



Essential

Absolute Qu.

Relative Qu.

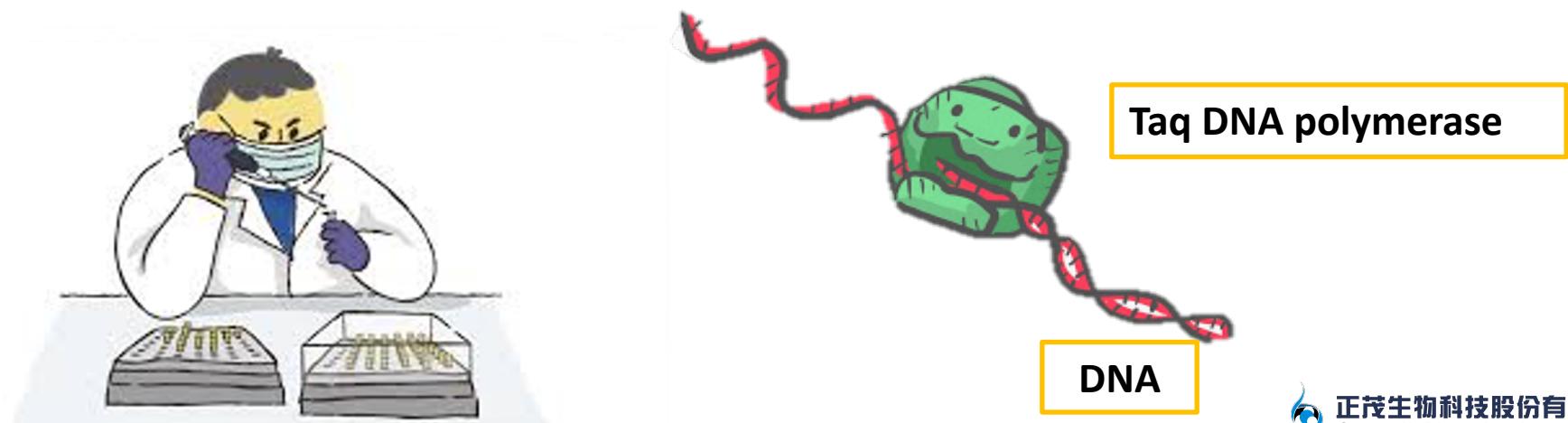
Application

MIQE

Notice

Primer design

1. Recommended length : **18 - 25bp**
2. Regional structure : Should be **free of strong secondary structures** and **self-complementarity** 「Primer-dimer」
3. Repeats : Prevent **triple repeats of G or C** appear in designed region.
4. CG % : **40 - 60%**
5. Tm value : **50 - 65°C** , Formula : $T_m = 4^{\circ}\text{C} (G + C) + 2^{\circ}\text{C} (A + T)$



(q)PCR - 產線支援

Essential

Absolute Qu.

Relative Qu.

Application

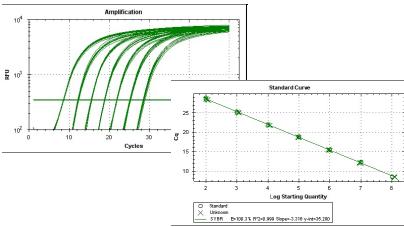
MIQE

Notice

PCR



CFX Manager Software



(q)PCR Reagents



Real-Time PCR (qPCR)



Automation options



(q)PCR consumables





2022 

— Operation —



System Overview - Front View

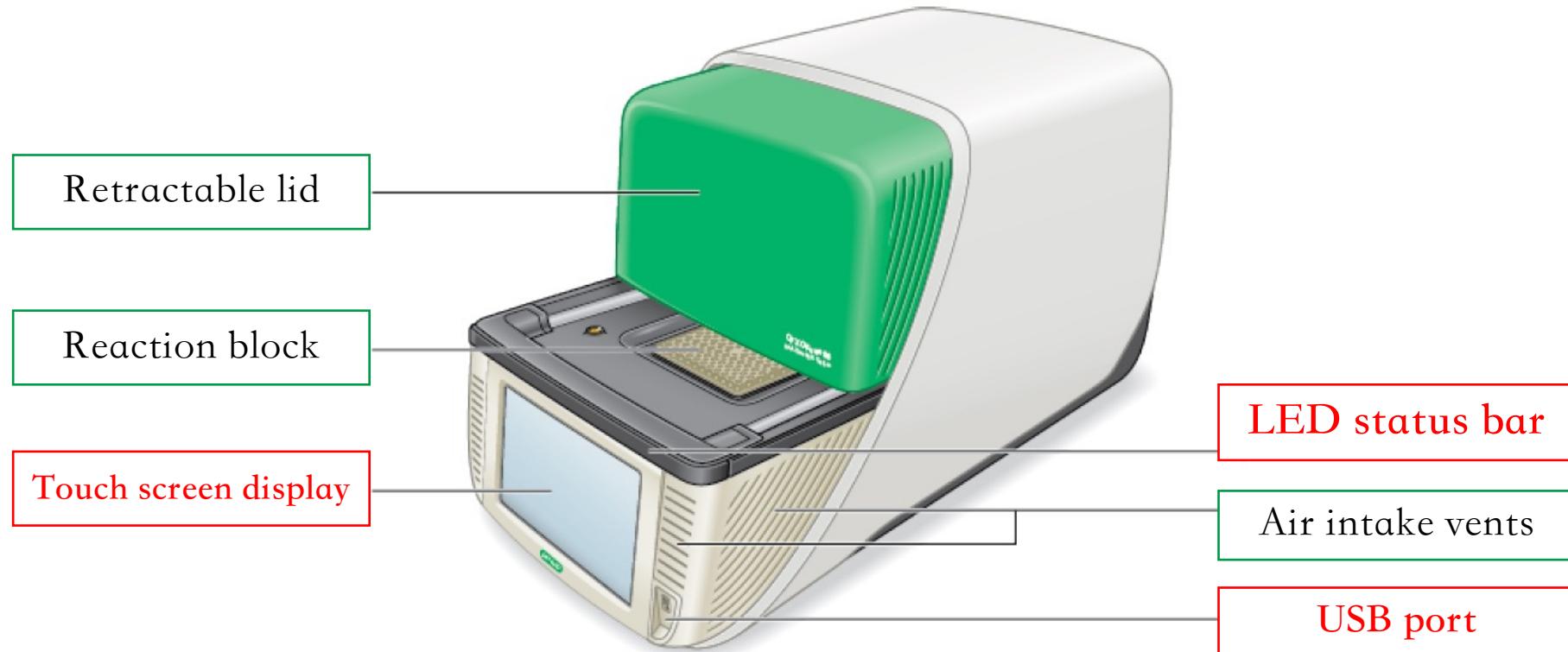
Appearance

Device Boot

Consumables

Software

Optics



System Overview - Back View

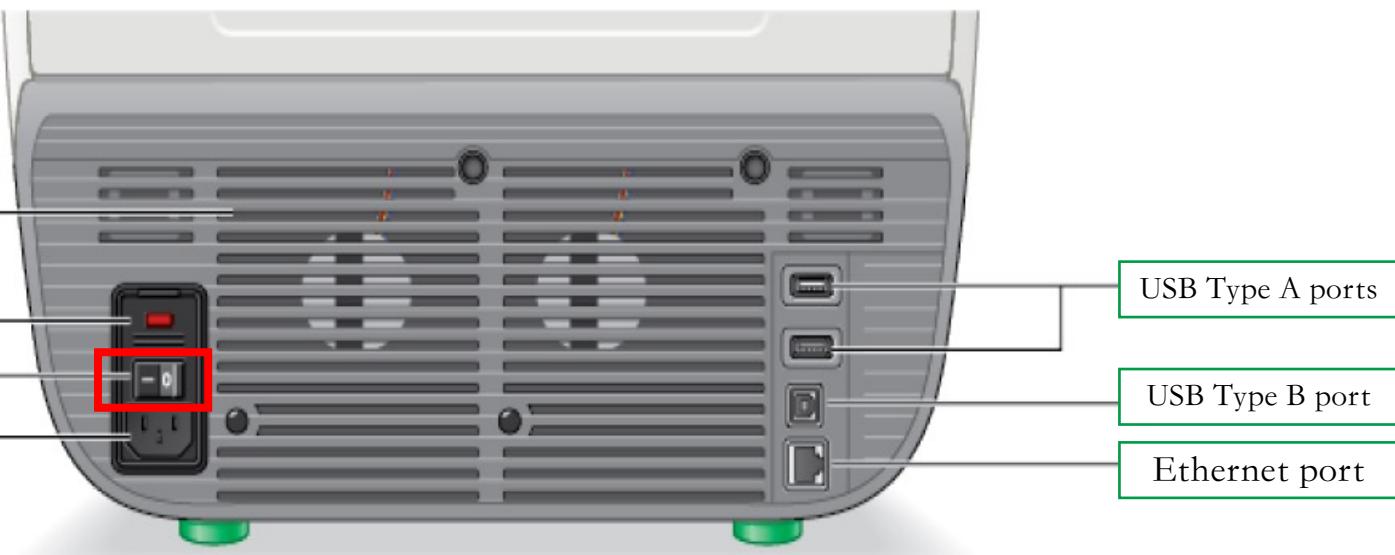
Appearance

Device Boot

Consumables

Software

Optics



Touch Screen Overview - Open lid

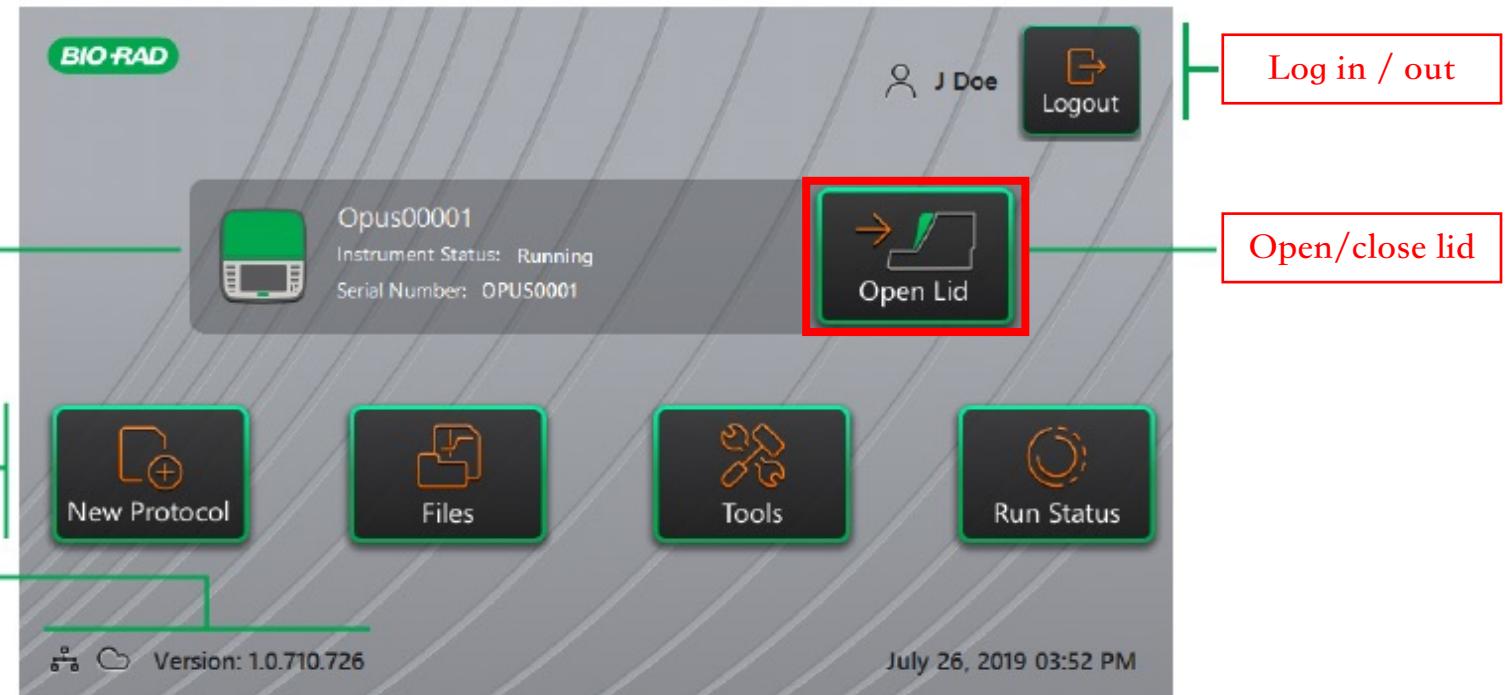
Appearance

Device Boot

Consumables

Software

Optics



Creating a Protocol

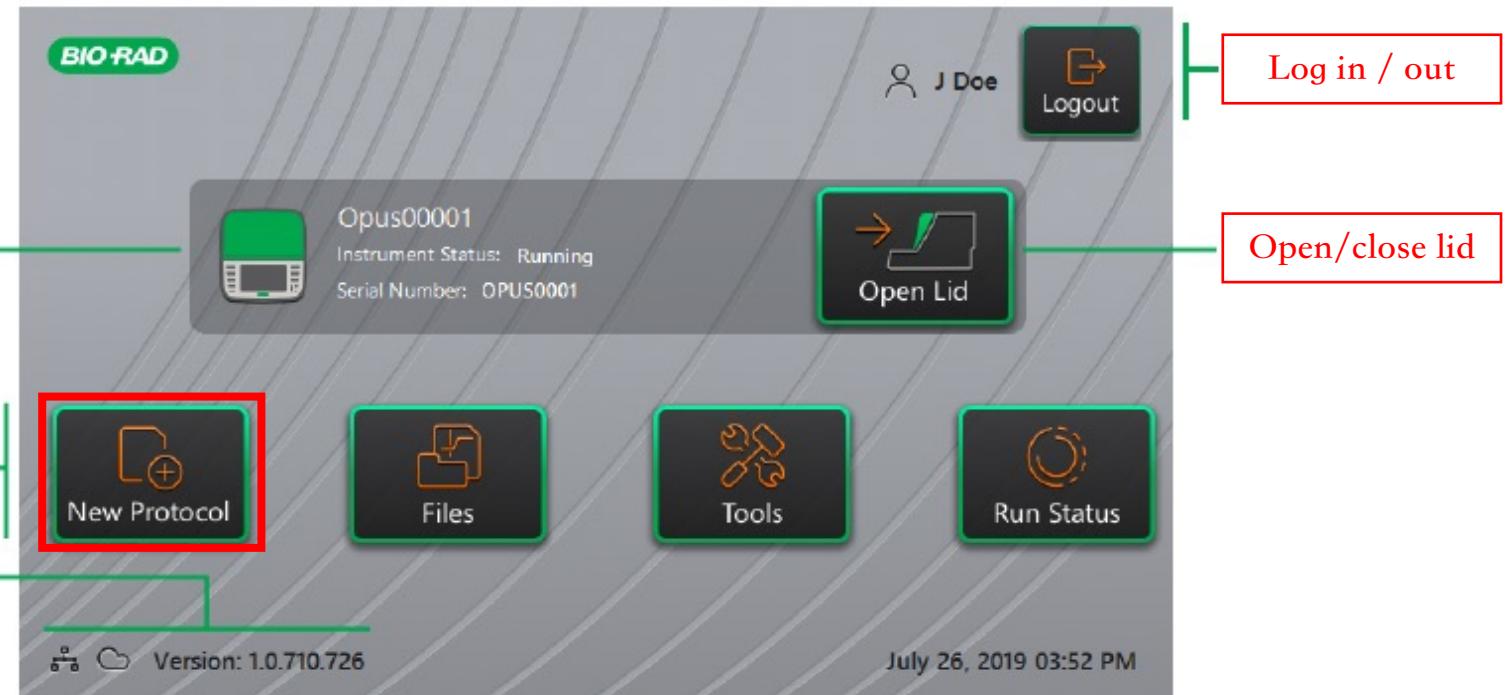
Appearance

Device Boot

Consumables

Software

Optics



Modifying the Settings in a Protocol Step

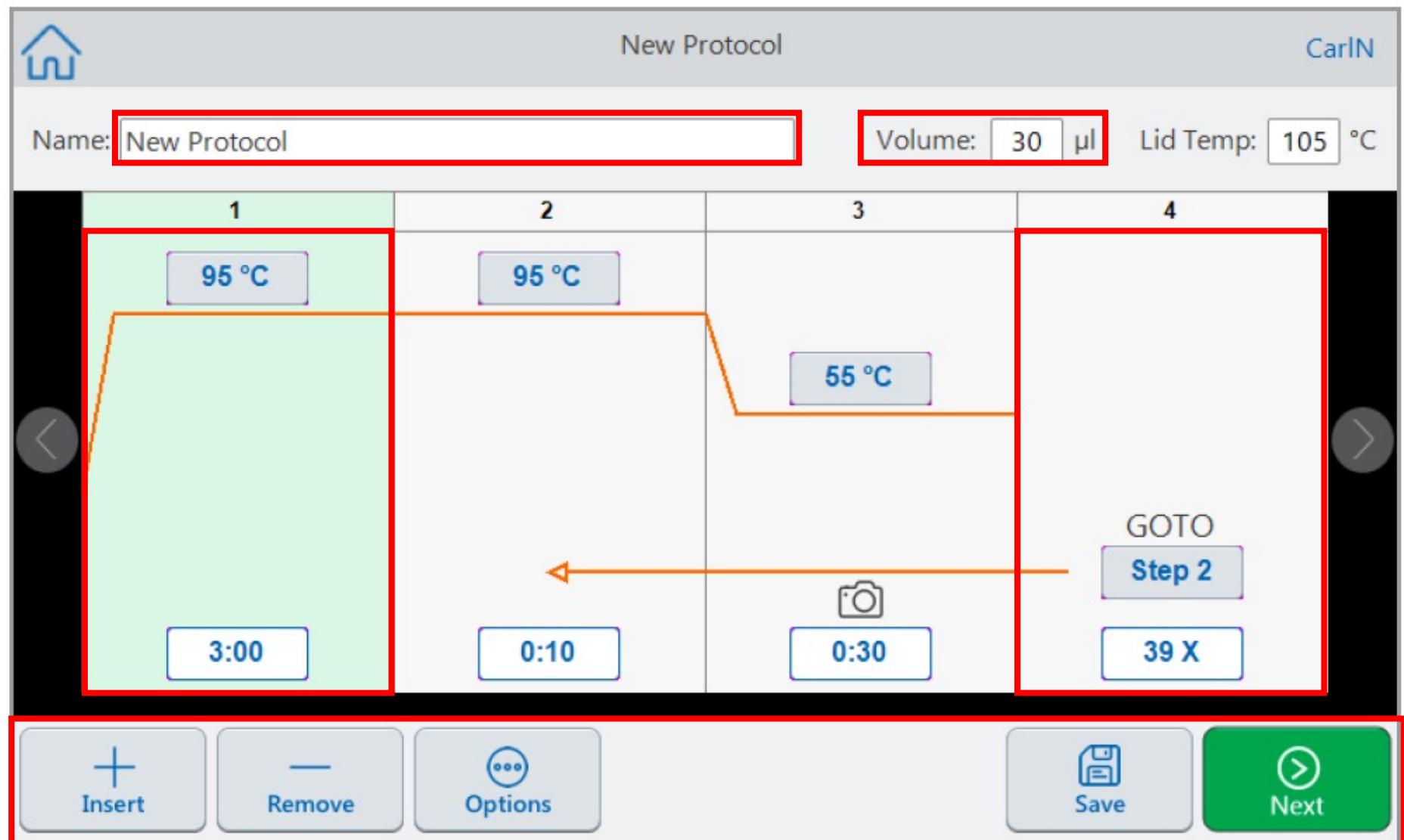
Appearance

Device Boot

Consumables

Software

Optics



Modifying the Settings in a Protocol Step

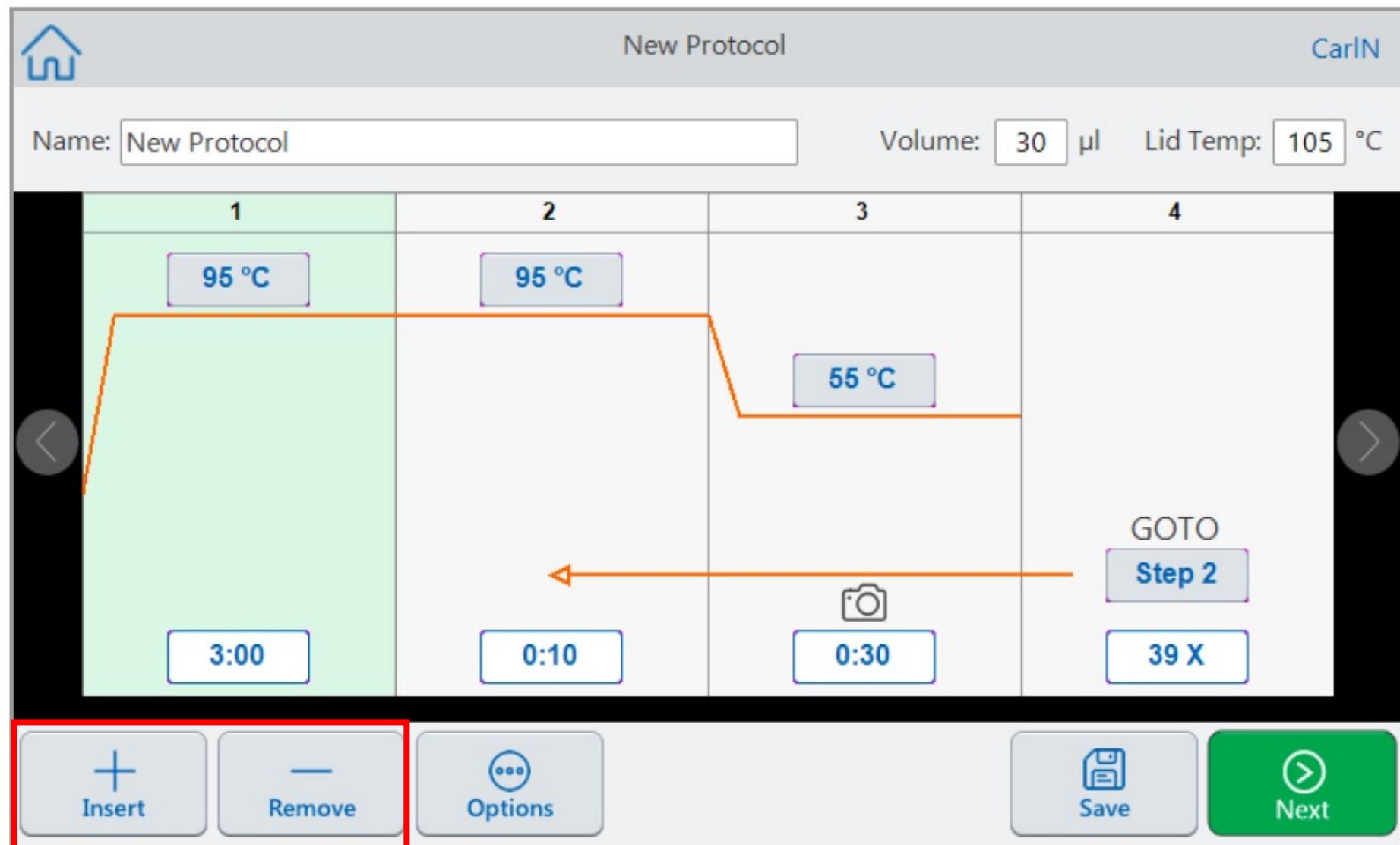
Appearance

Device Boot

Consumables

Software

Optics



Modifying the Settings in a Protocol Step

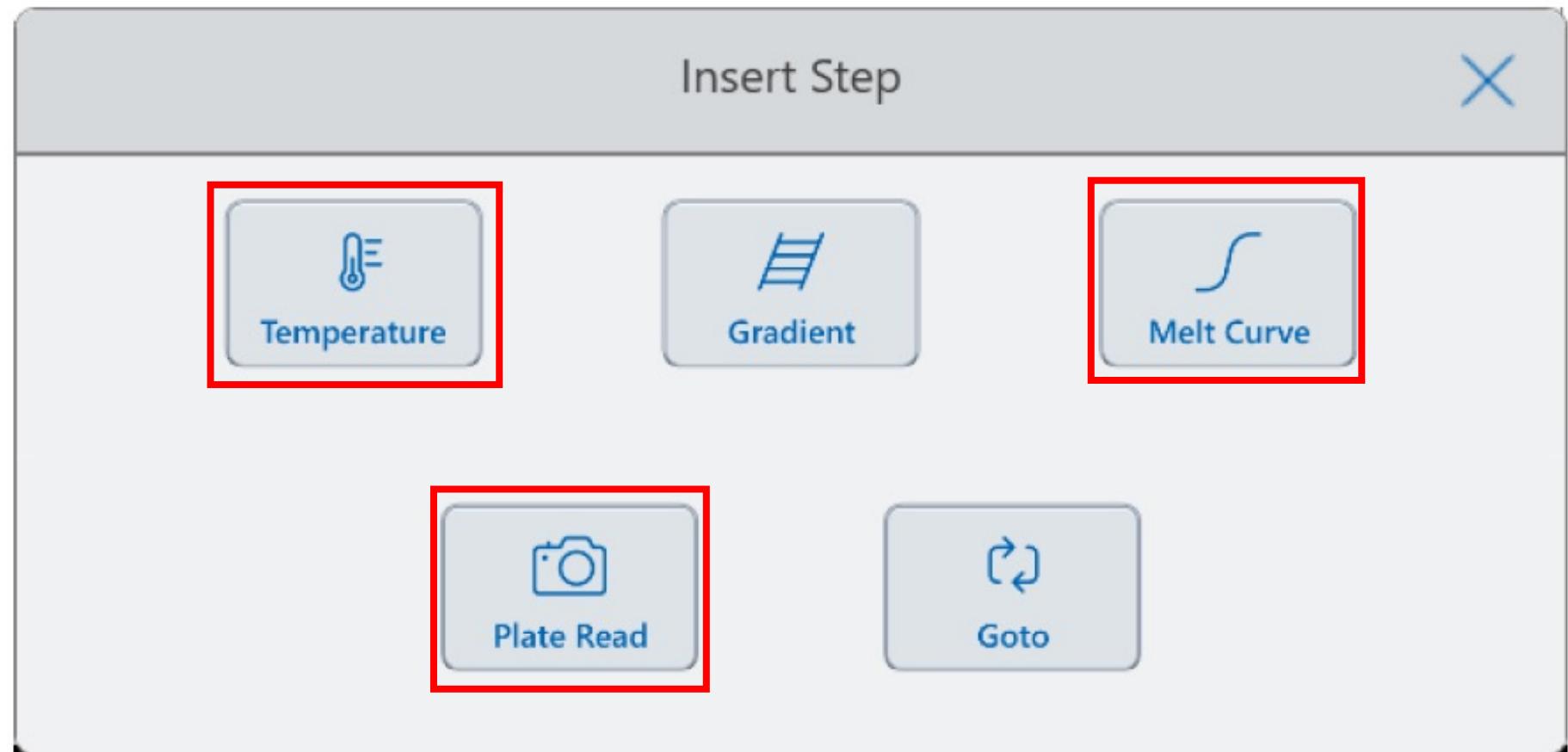
Appearance

Device Boot

Consumables

Software

Optics



Changing Target Gradient and Ramp Rate

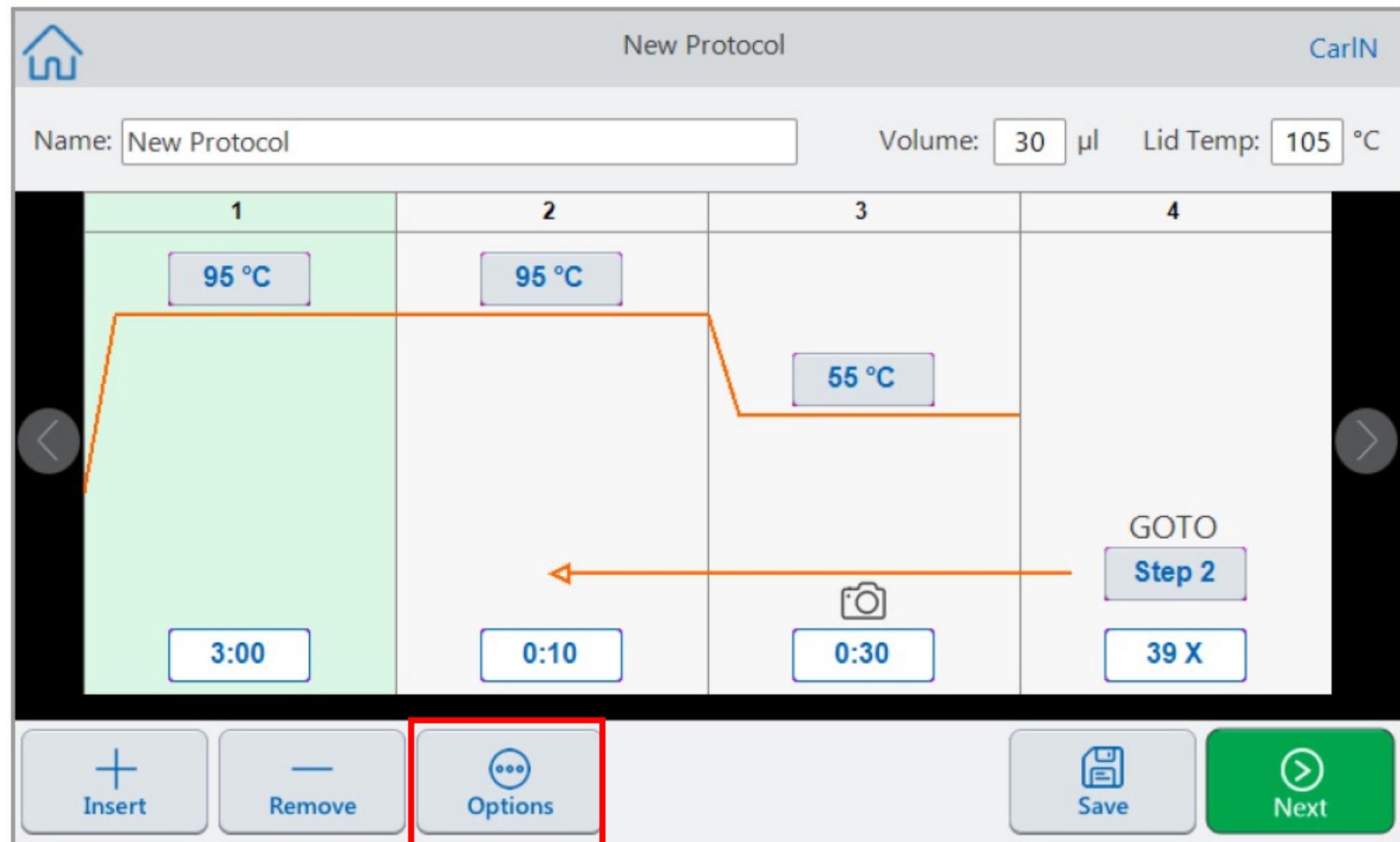
Appearance

Device Boot

Consumables

Software

Optics



Changing Target Gradient and Ramp Rate

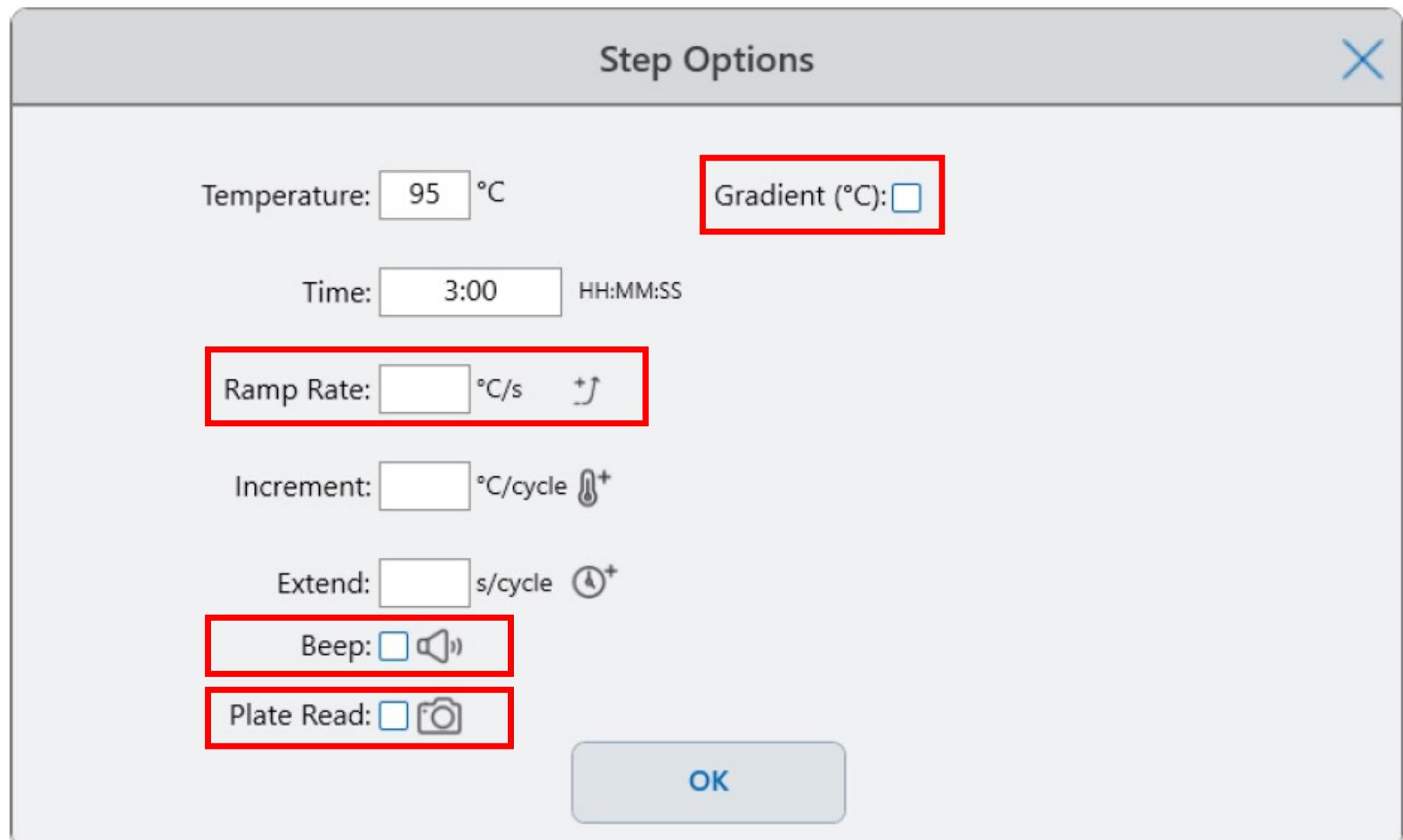
Appearance

Device Boot

Consumables

Software

Optics



Adding or Removing a Temperature Gradient

Appearance

Device Boot

Consumables

Software

Optics

Step Options X

Temperature: Gradient (°C):

Time: HH:MM:SS

Ramp Rate: °C/s 

Increment: °C/cycle 

Extend: s/cycle 

Beep: 

Plate Read: 

A	100
B	99.8
C	99.2
D	98.2
E	97.1
F	96.2
G	95.5
H	95

Saving a Protocol

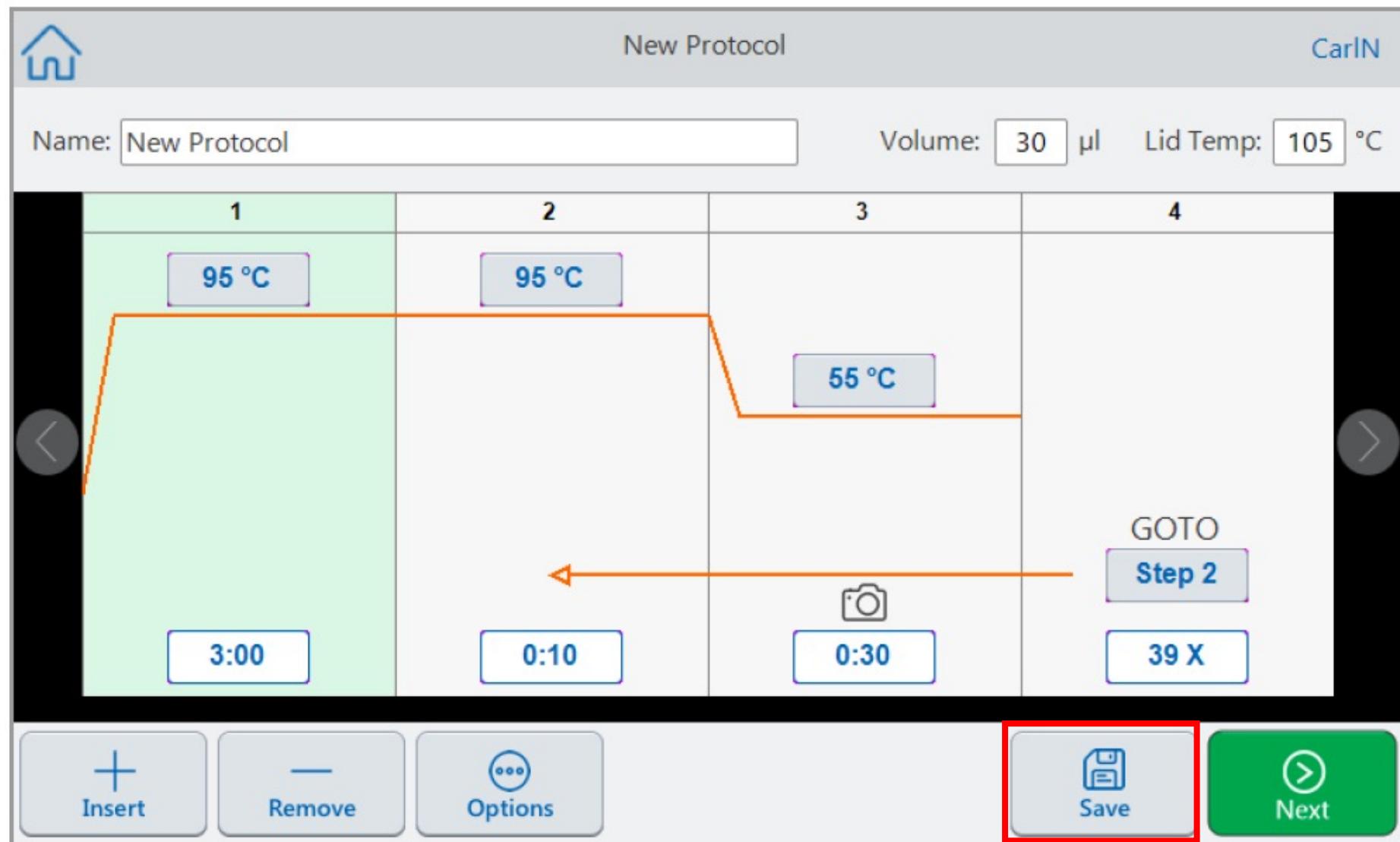
Appearance

Device Boot

Consumables

Software

Optics



Saving a Protocol

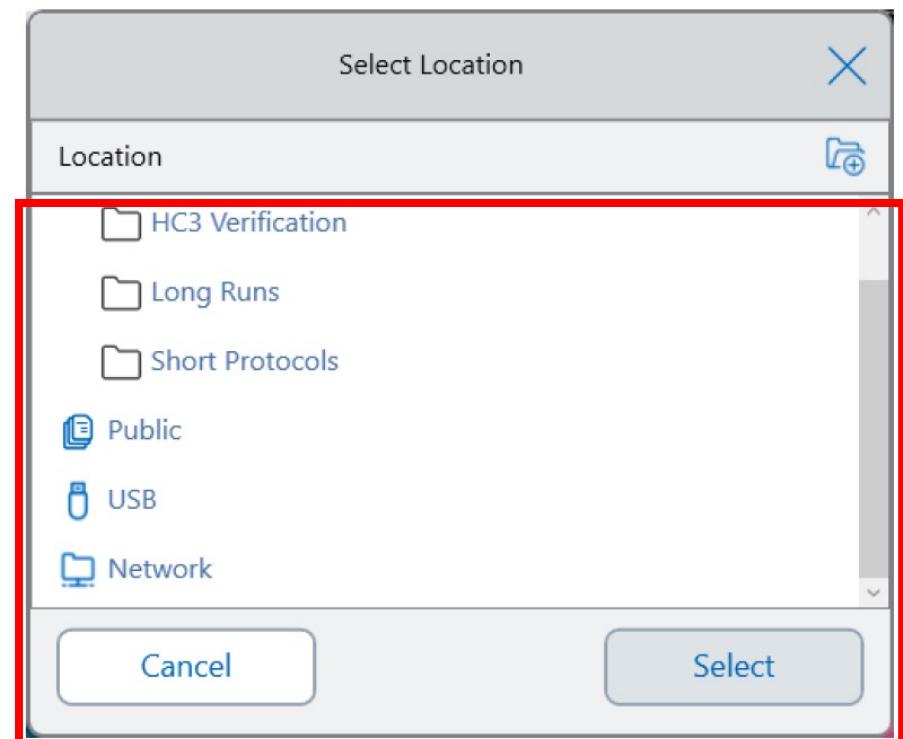
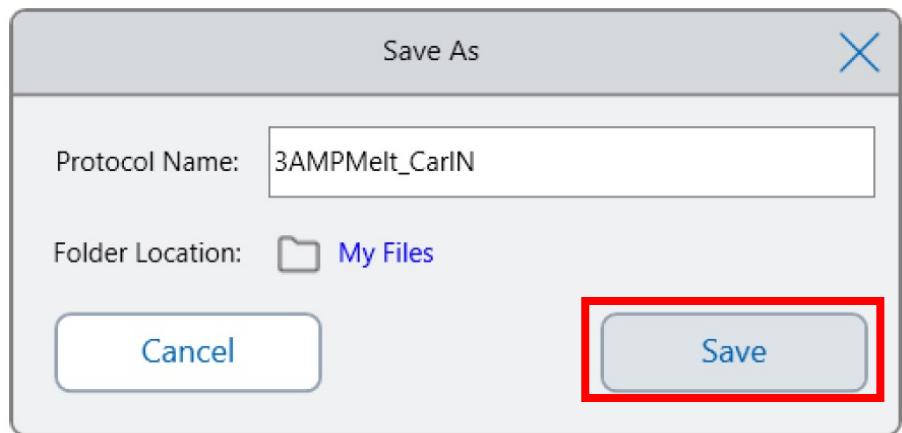
Appearance

Device Boot

Consumables

Software

Optics



Run Setup

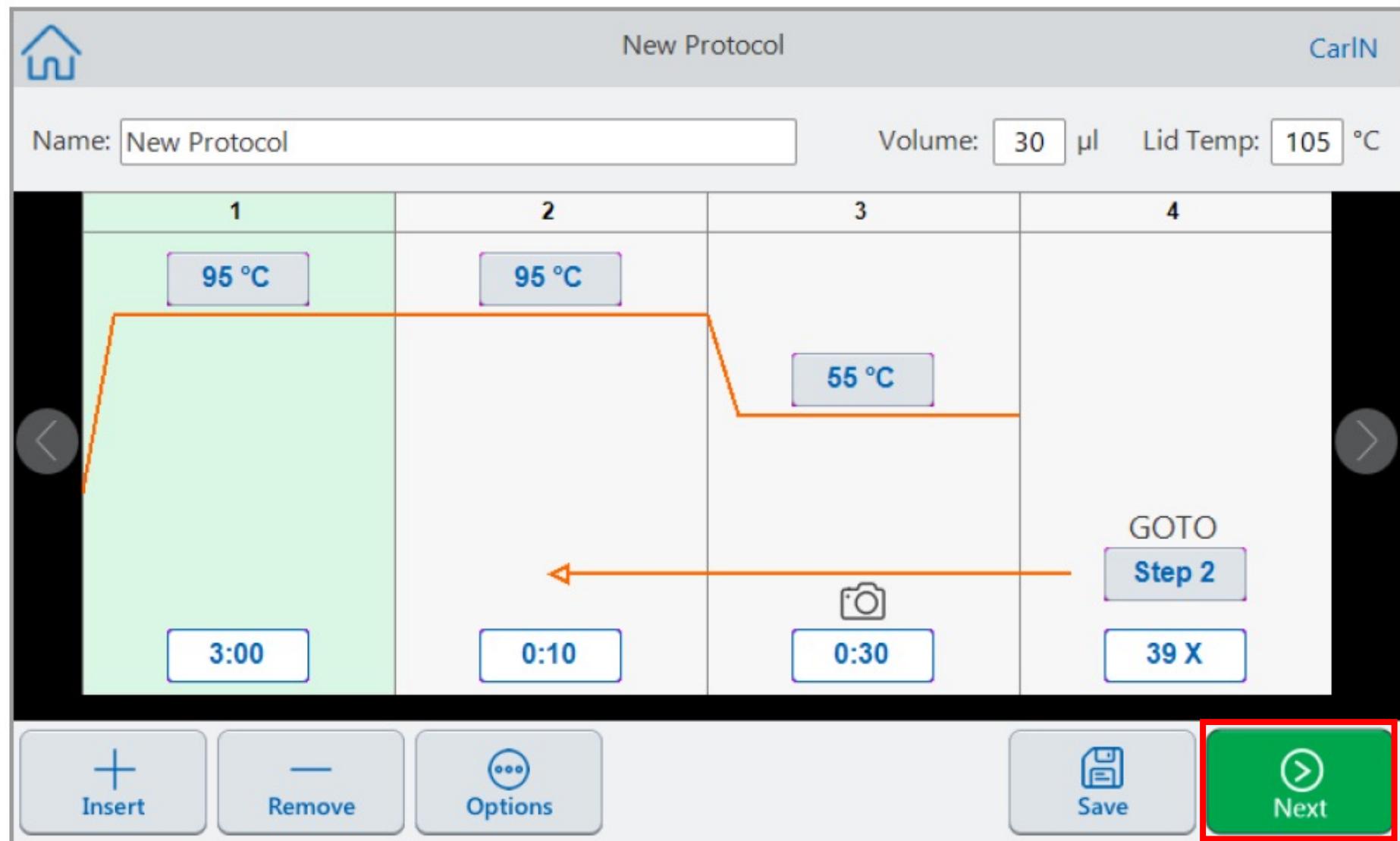
Appearance

Device Boot

Consumables

Software

Optics



Run Setup - Start Run

Appearance

Device Boot

Consumables

Software

Optics

Back Run Setup CARLN

Name: 3AMPMelt_CarLN Volume: 30 μ l Lid Temp: 105 $^{\circ}$ C

Scan Mode: SYBR/FAM All Channels FRET

Plate ID:

Run File Name: 3AMPMelt_CarLN_20191117_131432_OPUS0001_CARLN

Save Location: CARLN\...\CarLN

Notification: cnavar@celltech.com

Open Lid Run

Touch Screen Overview - Proceeding

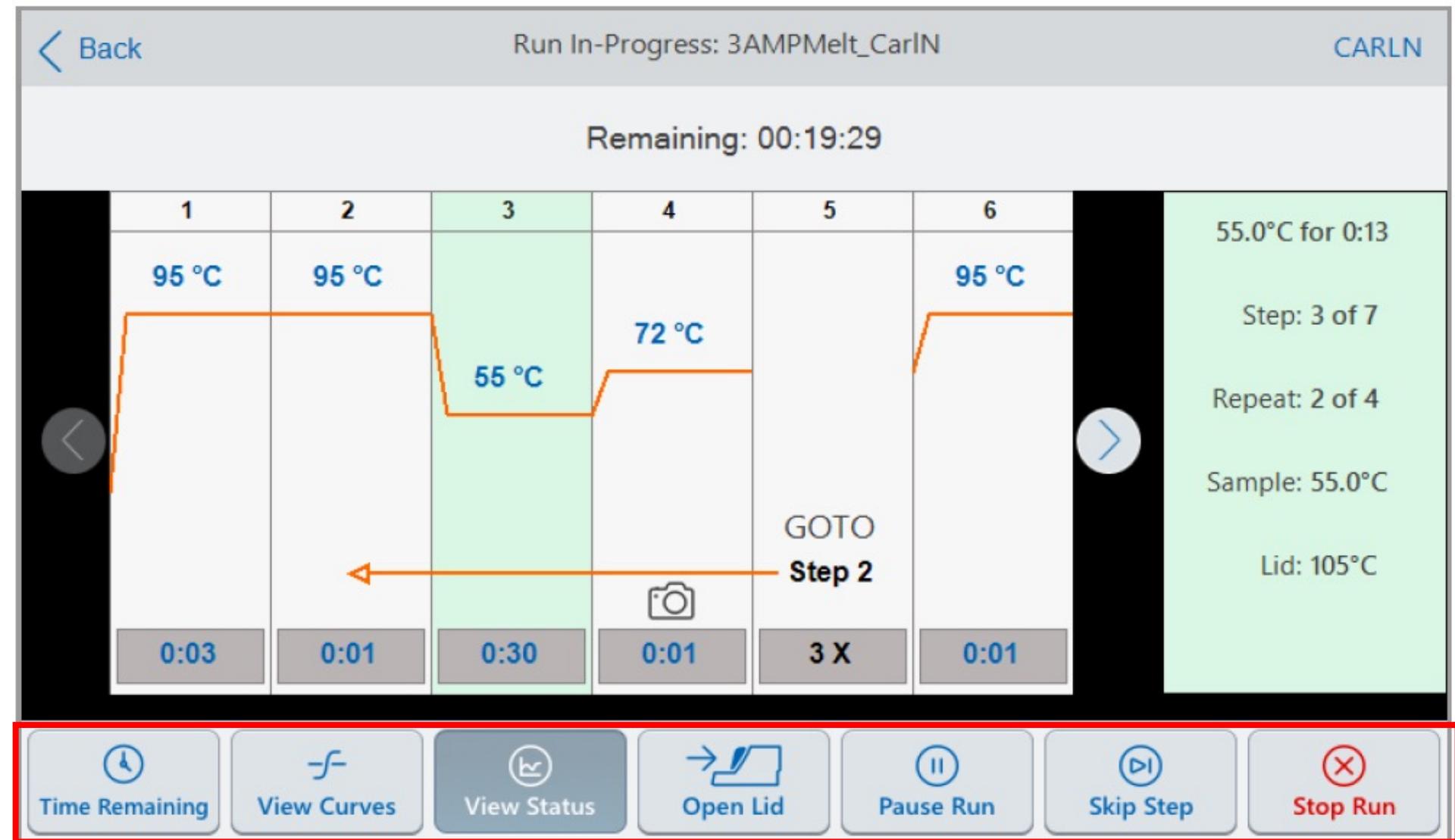
Appearance

Device Boot

Consumables

Software

Optics



Touch Screen Overview - File

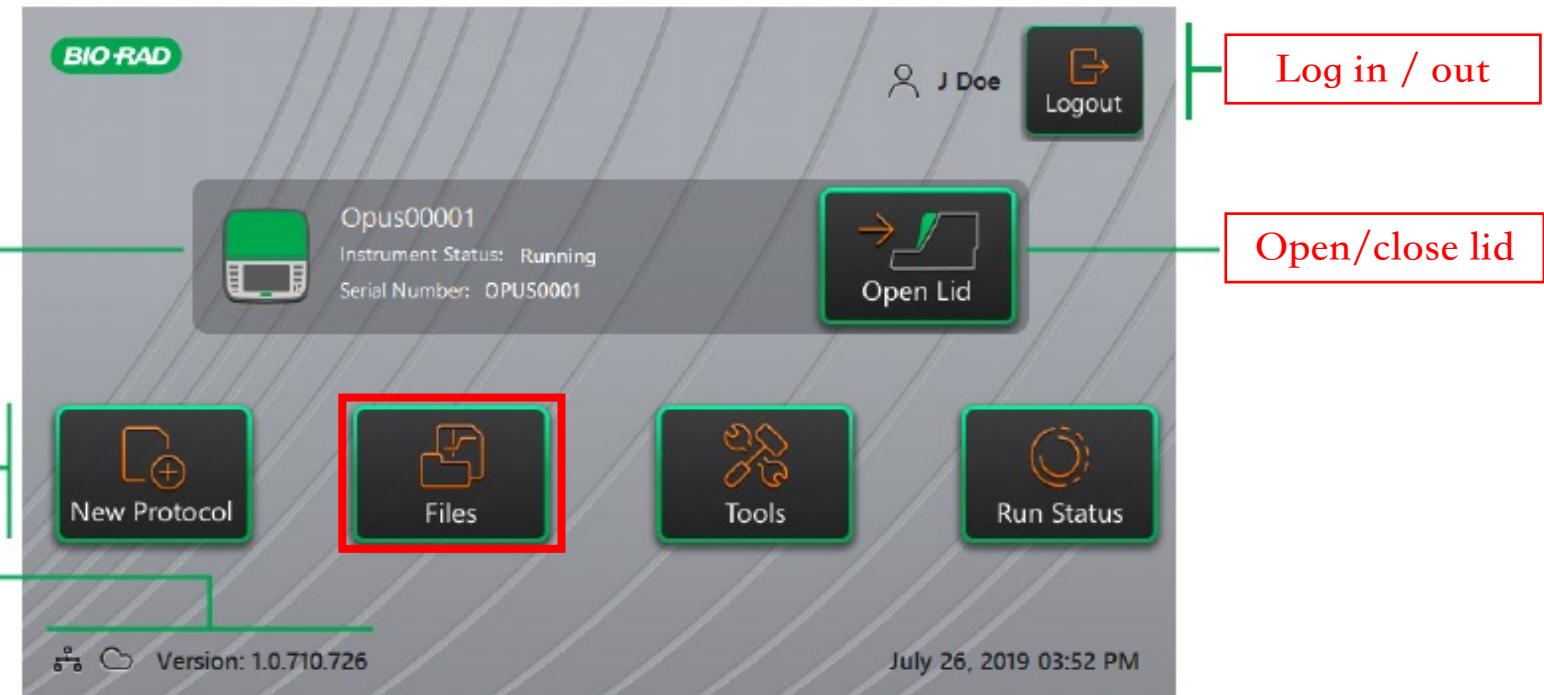
Appearance

Device Boot

Consumables

Software

Optics



The File Browser Screen

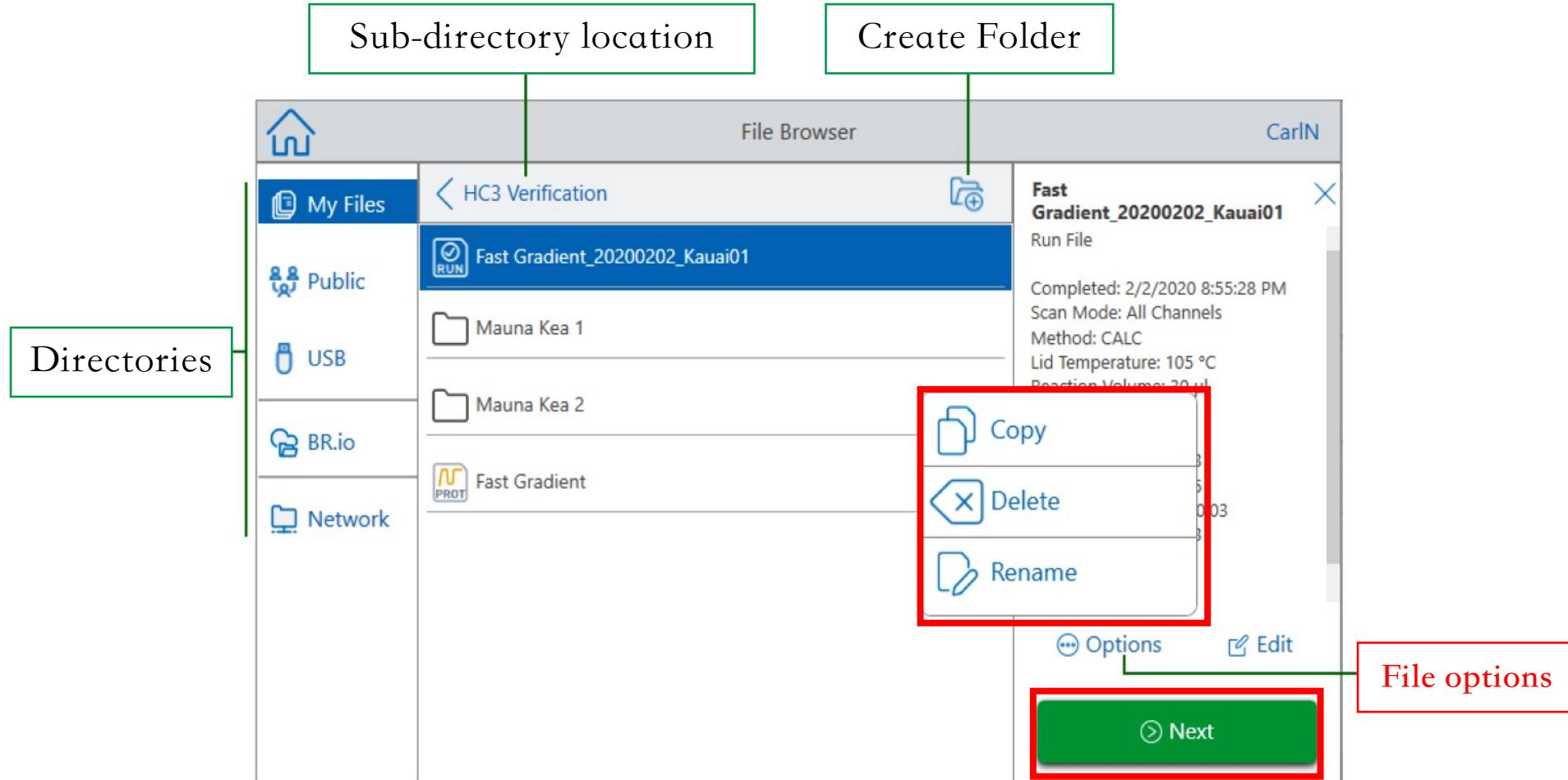
Appearance

Device Boot

Consumables

Software

Optics



Extracting and Editing a Protocol from a Run

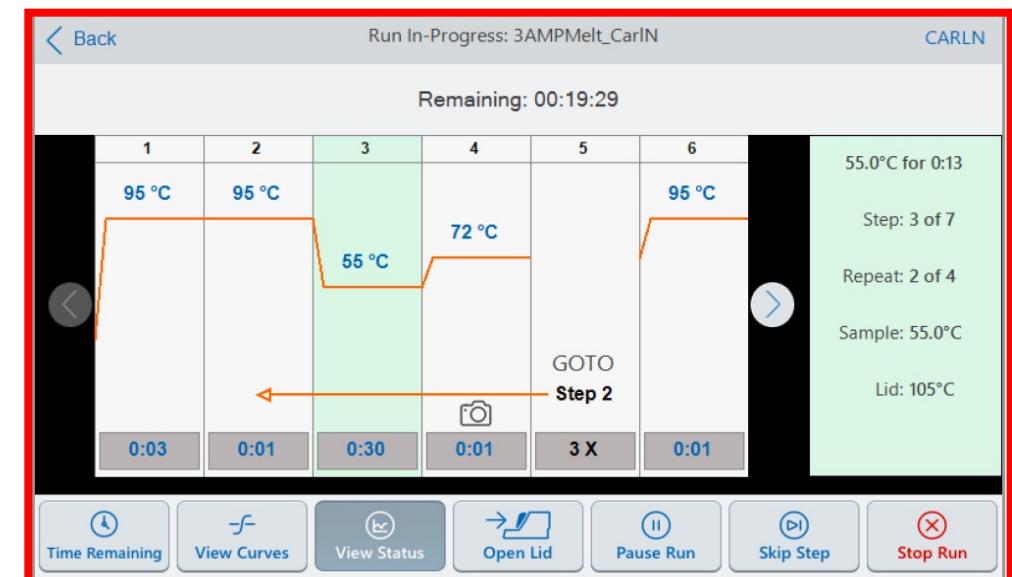
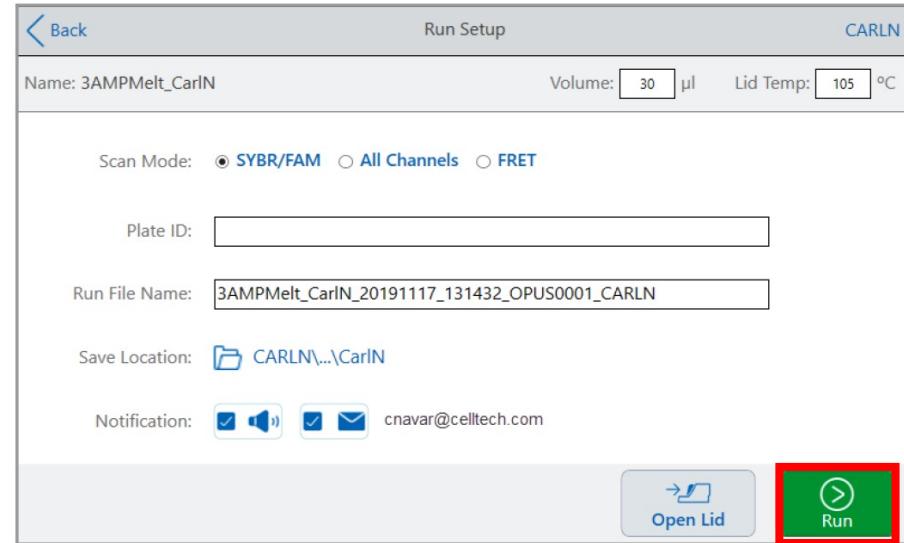
Appearance

Device Boot

Consumables

Software

Optics



Consumables - Specification

Appearance

Device Boot

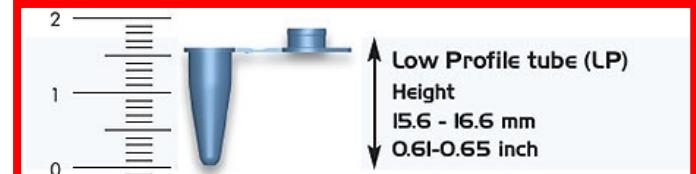
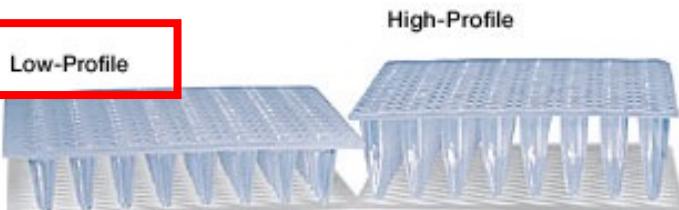
Consumables

Software

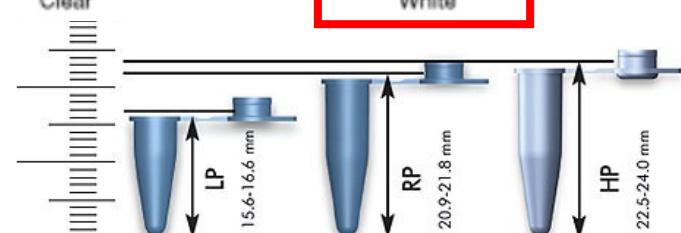
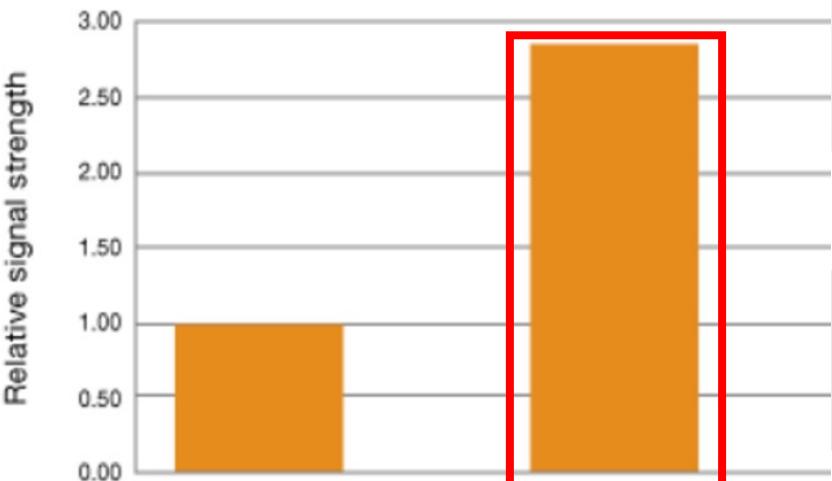
Optics



Low – Profile Only !!



Well Color Effect on Signal Strength



Notice for usage

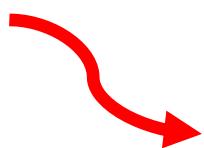
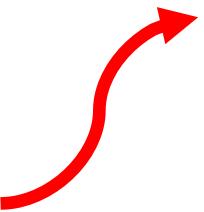
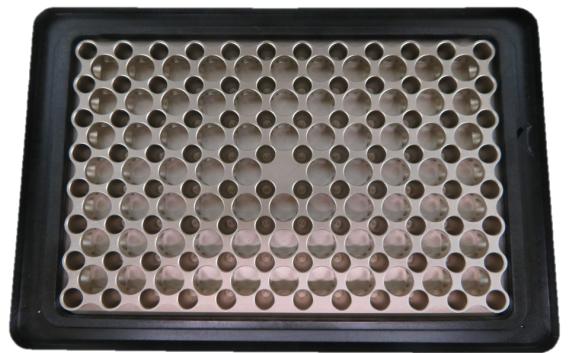
Appearance

Device Boot

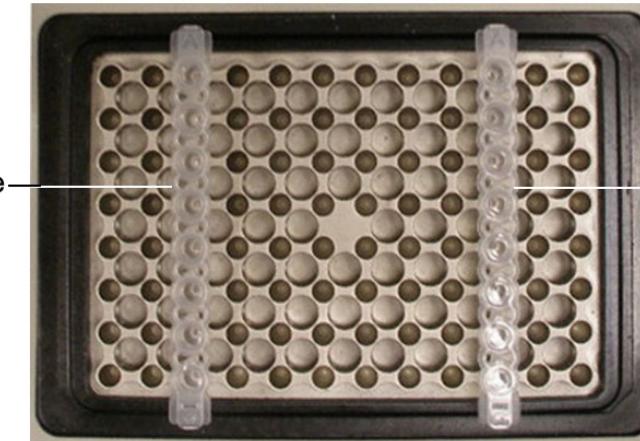
Consumables

Software

Optics



Filled tube
strip



Tube strip for
balance

Connection with Opus 96 - Overview

Appearance



BIO RAD CFX Maestro

Device Boot

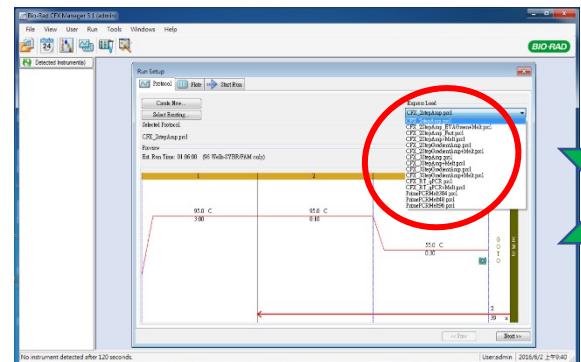


Consumables

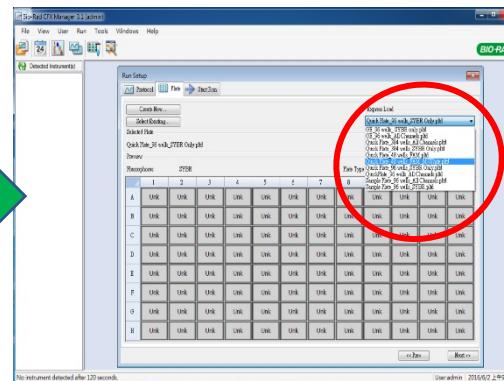
Software

Optics

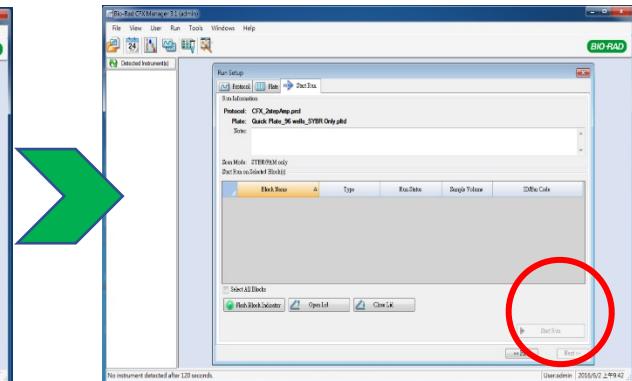
Protocol



Plate



Start Run



Start Run !

Operation setting - Overview

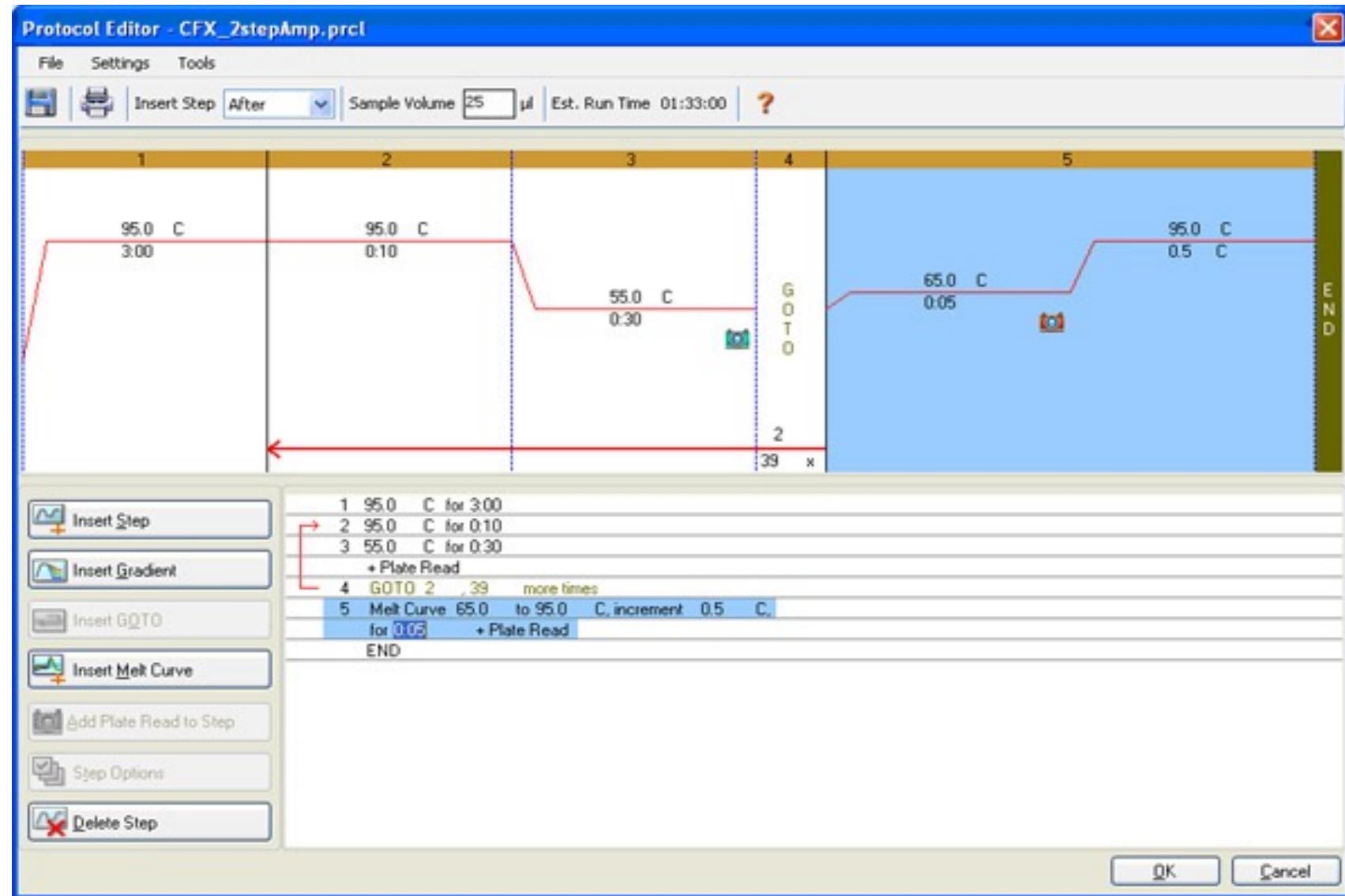
Appearance

Device Boot

Consumables

Software

Optics

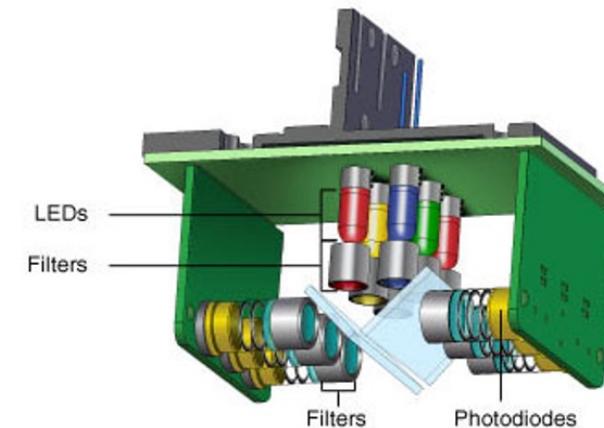


Optical design for detection

Appearance



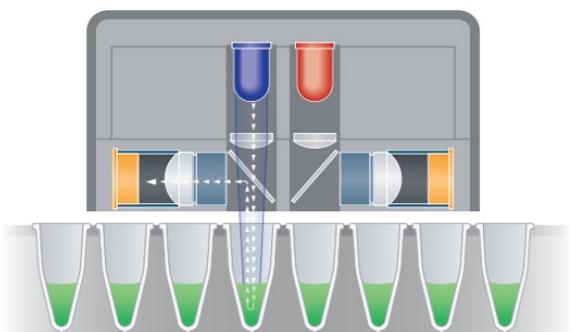
Device Boot



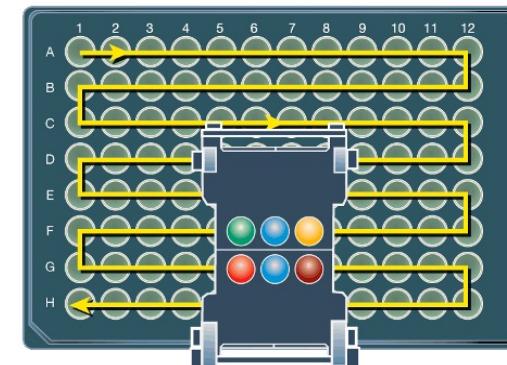
Consumables



Software



Optics



Optical design for detection

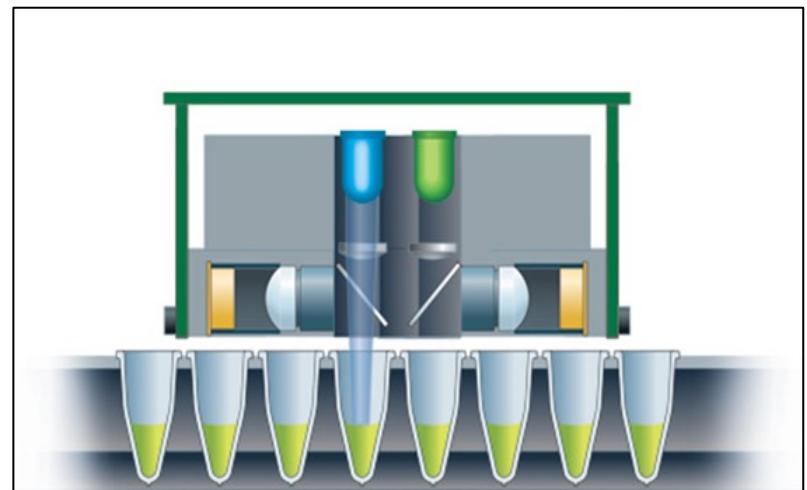
Appearance

Device Boot

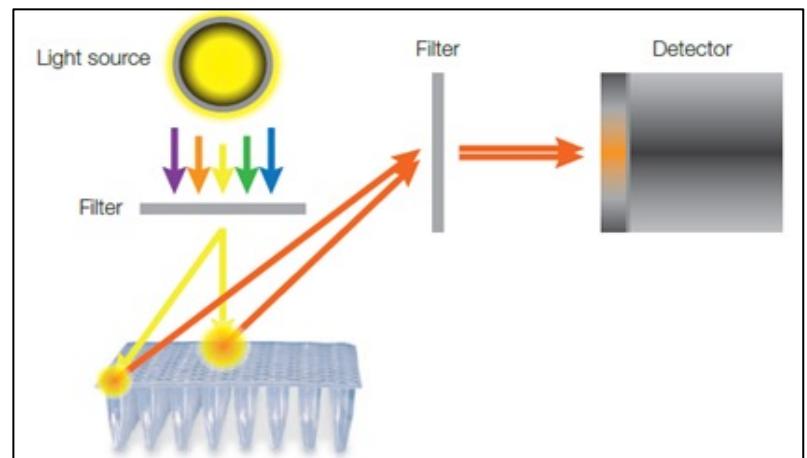
Consumables

Software

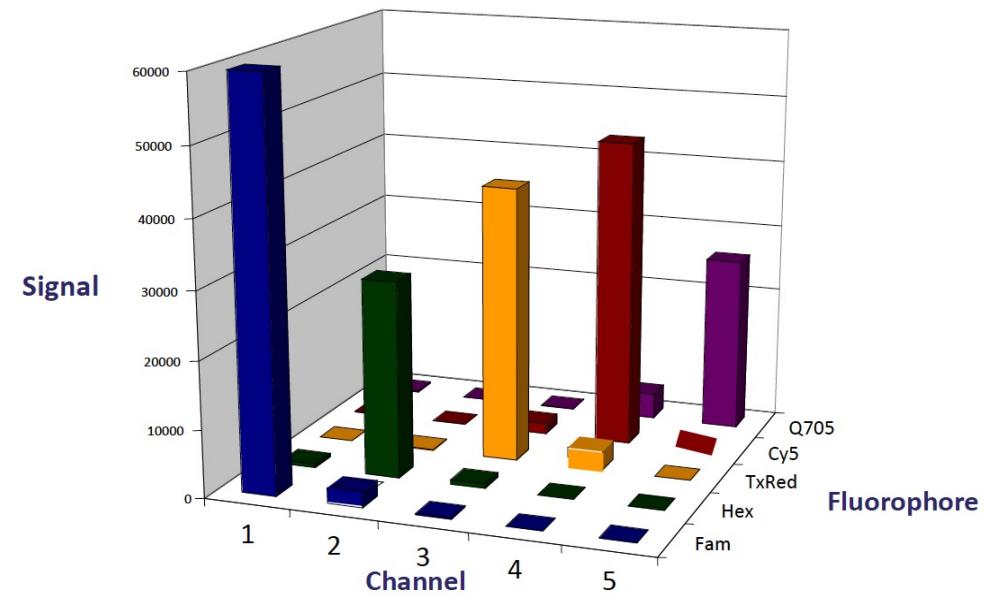
Optics



BIO-RAD



Competitor



Vertical light path : 「Rox dye」 calibration is **unnecessary**

Fluorescence : 「high **strength / specificity**」

Light source : **LEDs** with long lifespan, allowing you to use them right away

Optical application - Dye / Wave band

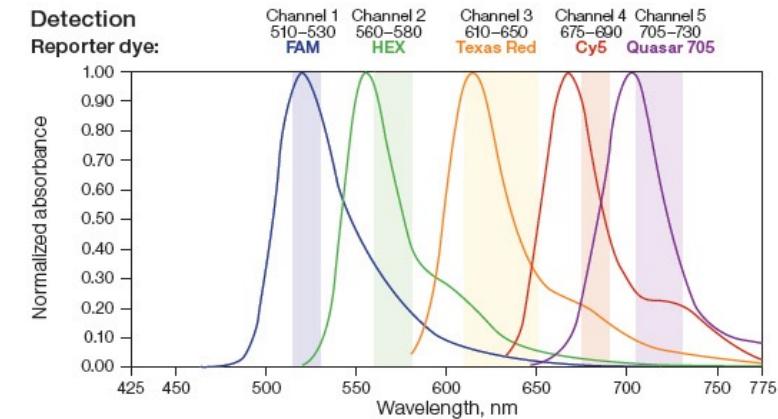
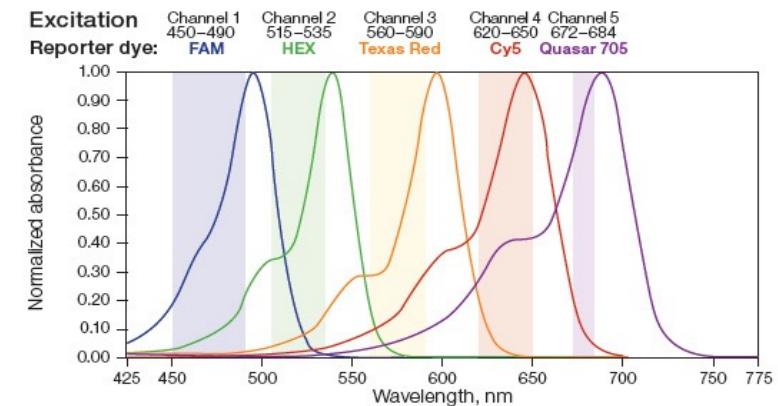
Appearance

Device Boot

Consumables

Software

Optics



Channel	Excitation (nm)	Detection (nm)	Calibrated Fluorophores
1	450-490	515-530	FAM™, SYBR Green I™, EvaGreen™
2	515-535	560-580	VIC®, HEX™, TET™, Cal Gold 540™
3	560-590	610-650	ROX™, Texas Red®, Cal Red 610™
4	620-650	675-690	Cy5, Quasar 670™
5	672-684	705-730	Quasar 705™
6	450-490	560-580	Accommodates FRET Chemistry



2022 

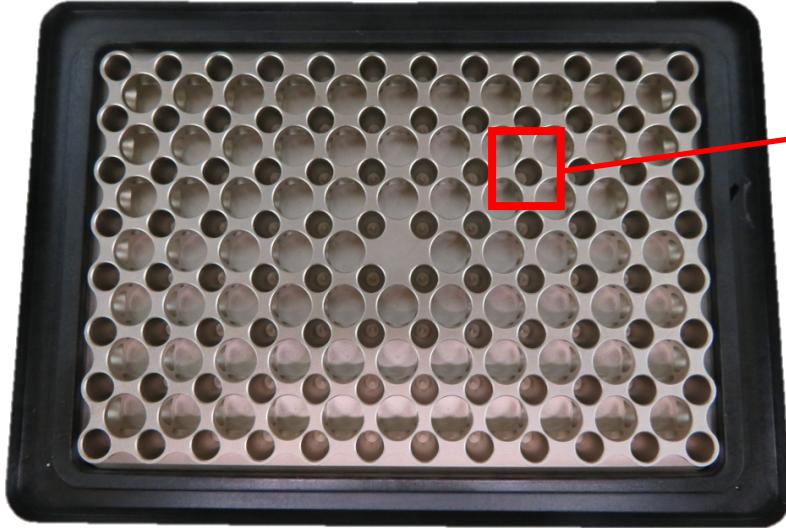
—Supplement—

• • • •

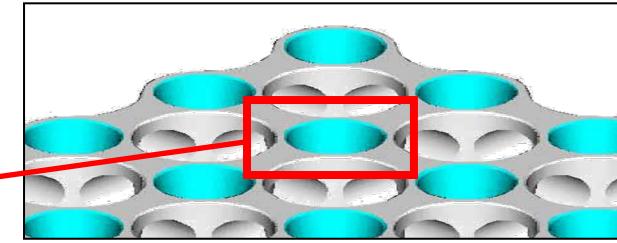
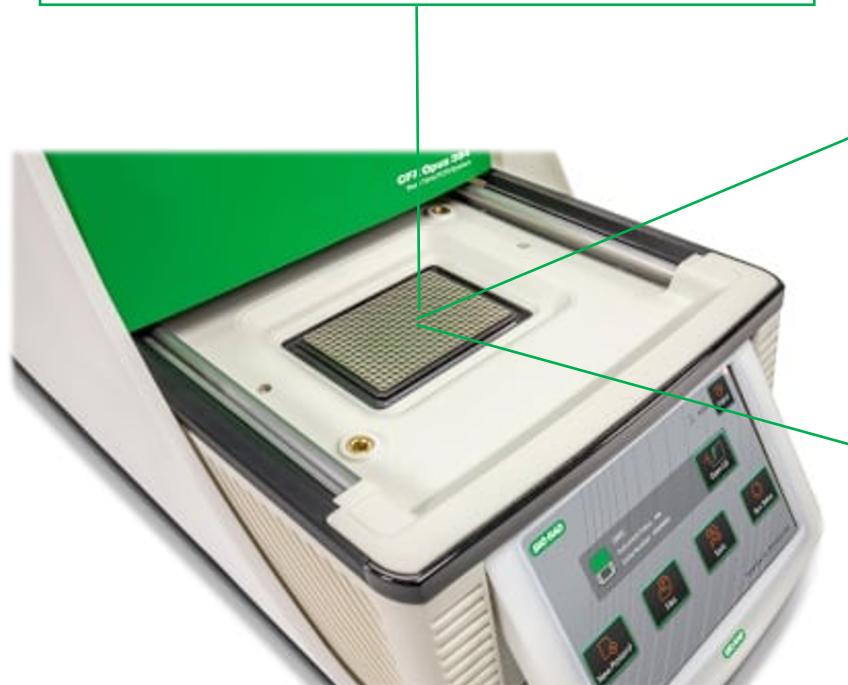
Blocks

Gradient

Application



Mass-reduced sample block

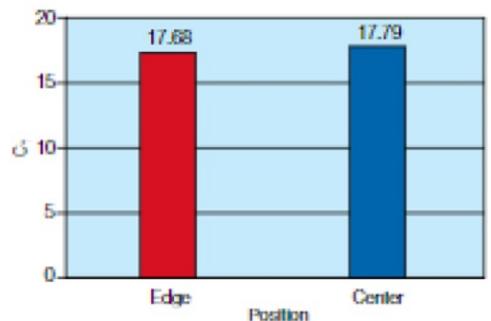
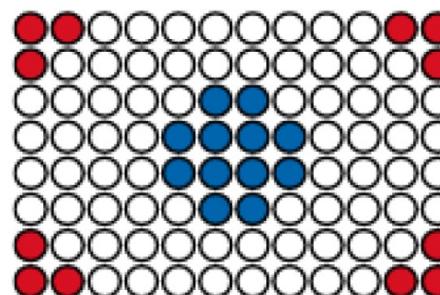


Uniform / Rapid heating

Max ramp rate	5°C / sec
Temp Accuracy	± 0.2°C
Temp Uniformity	± 0.3°C

Accurate temperature control

Uniformity ↑

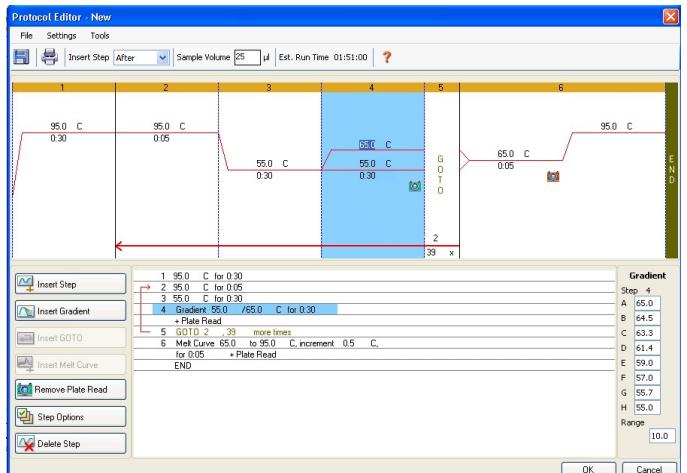


Supreme 「 uniformity 」 in any position

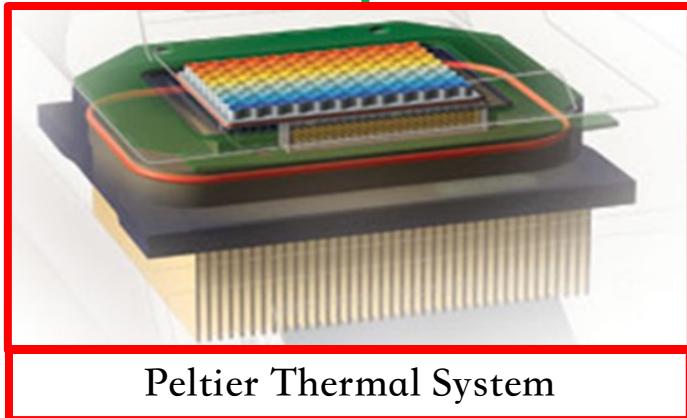
Blocks

Gradient

Application



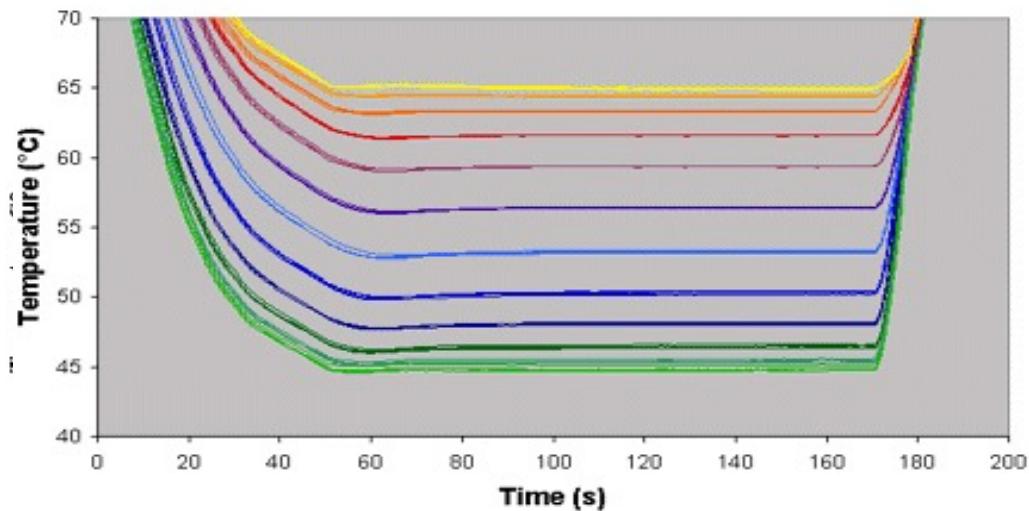
Graphical interface : friendly operation and setting



Peltier Thermal System

	1	2	3	4	5	6	7	8	9	10	11	12
A	70.0	Unk										
B	69.5	Unk										
C	68.4	Unk										
D	66.4	Unk										
E	64.0	Unk										
F	62.0	Unk										
G	60.7	Unk										
H	60.0	Unk										

Gradient temperature setting : 『1 - 24°C』



11

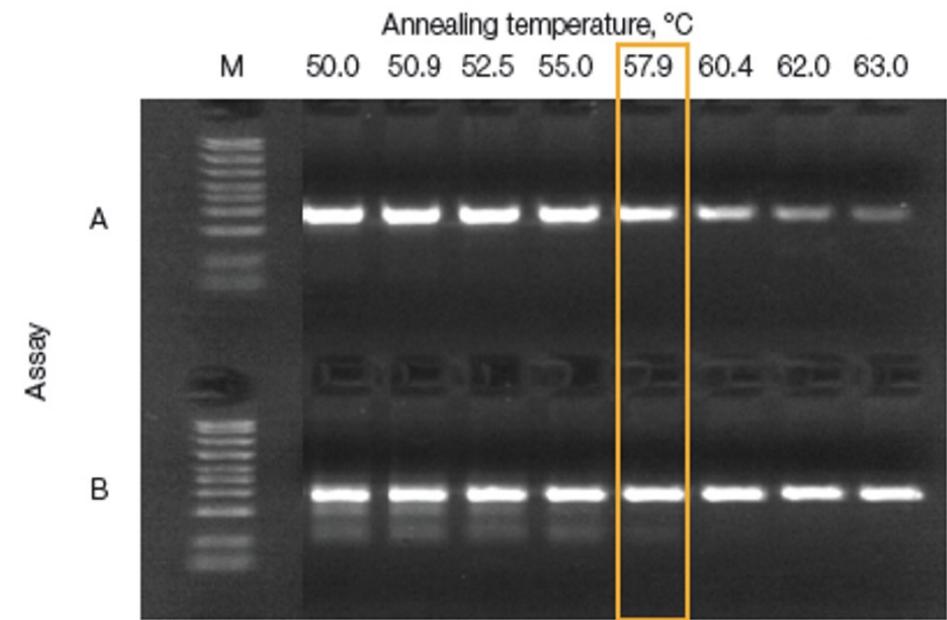
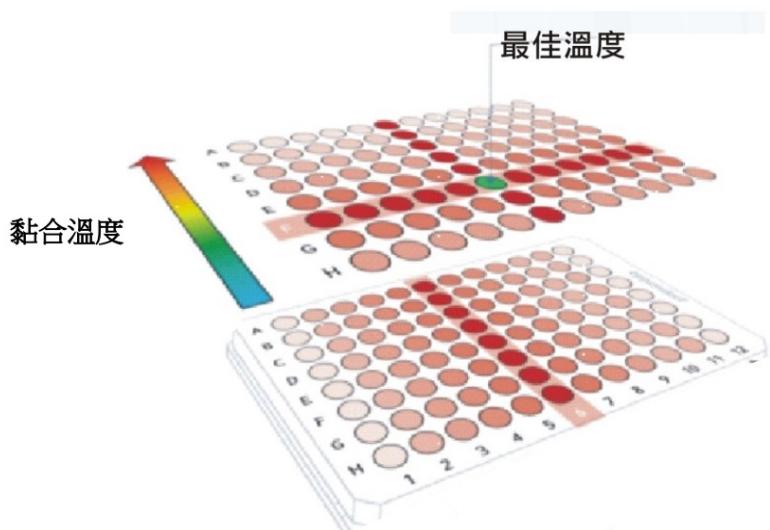
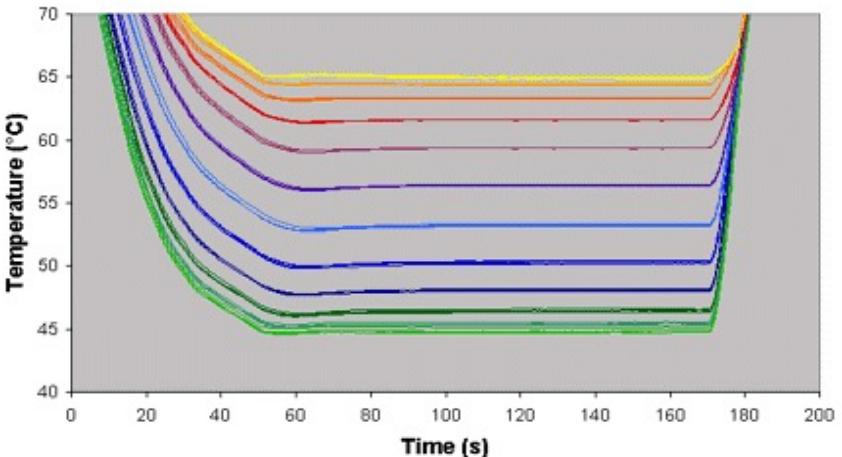
Same starting point / Reaction is accurate

30s

Blocks

Gradient

Application



Optimization of an assay results in better yields and specificity. Results show that assays A and B can be run at an **annealing temperature** of **57.9°C** on the same plate. Higher temperatures result in a reduced yield in assay A while lower temperatures result in nonspecific products in assay B. M, markers.



Thank You!

