




**BIO-RAD**

## Bio-Rad Real-Time PCR Detection System

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Version 1.0




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## Outline

- Part I: What is the real-time PCR?
  - Real-time PCR introduction
- Part II: Bio-Rad Real-Time PCR Detection System

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## 主要應用領域

- 基因表現
  - 藥物作用
  - 腫瘤指標
  - 基因調控
  - 基因治療
  - 微陣列基因晶片確認
  - 基因改造食品 (GMO)
- 病原菌偵測
  - 多重病原菌同時偵測 (Up to 5-Target)
  - 適合大量檢體篩選 (High throughput)
  - 定性, 定量 同時完成
  - 藥物治療成效的監控
- SNP 分型
  - 唯一可用 Taqman, Molecular Beacon 以及 FRET 三種方法的品牌

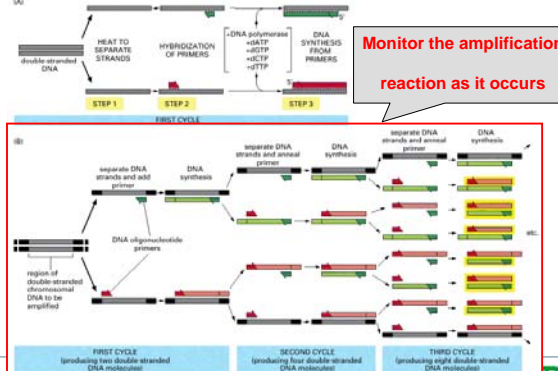
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## What is qPCR(Real Time PCR)?

Monitor the amplification reaction as it occurs

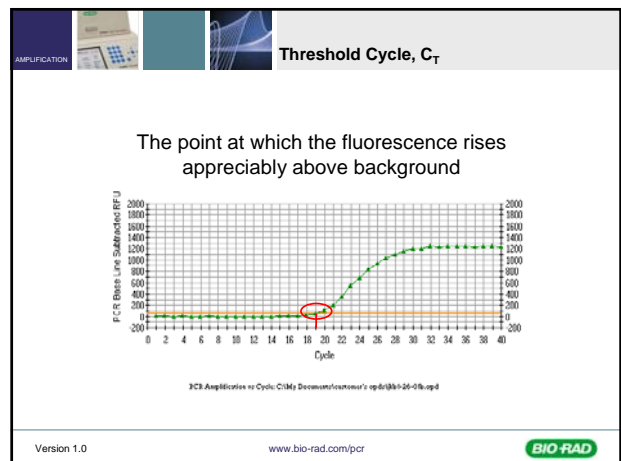
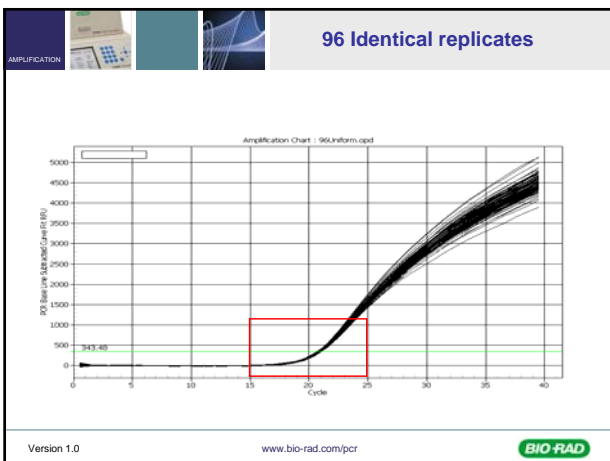
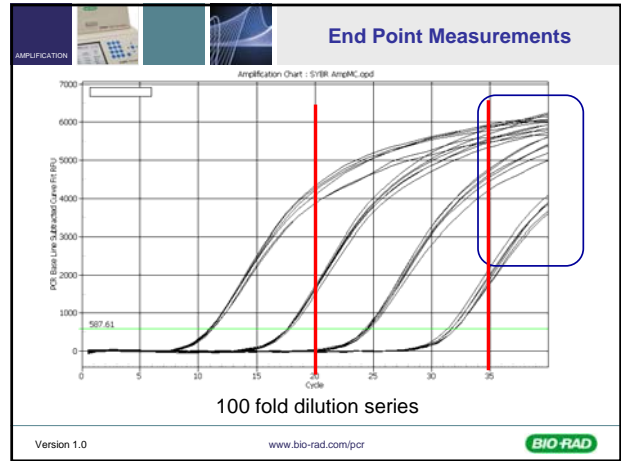
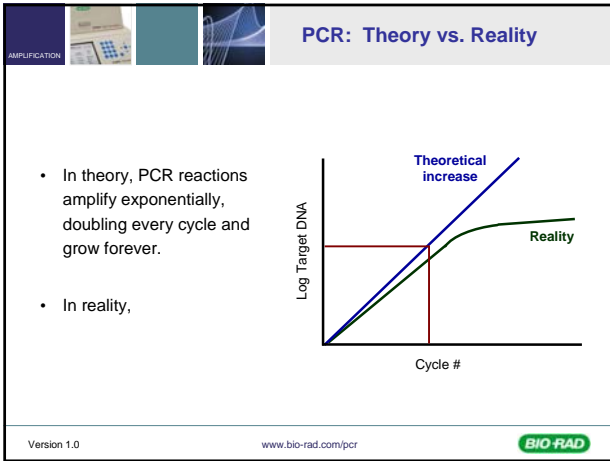


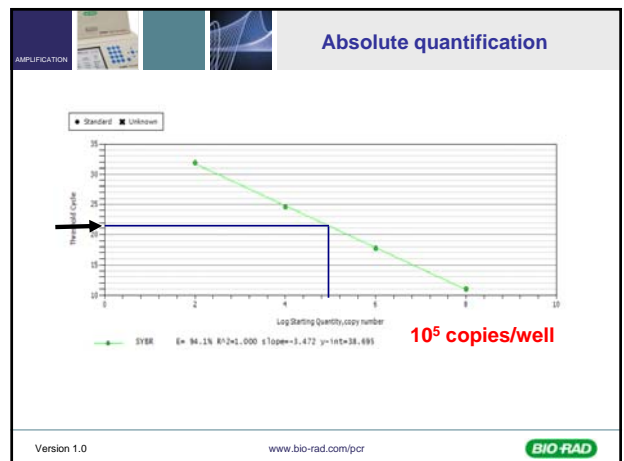
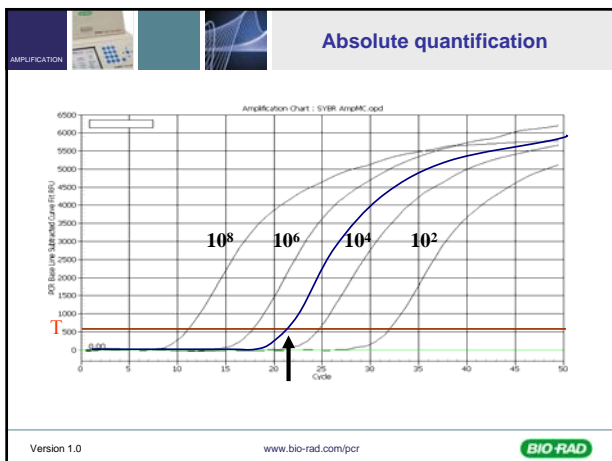
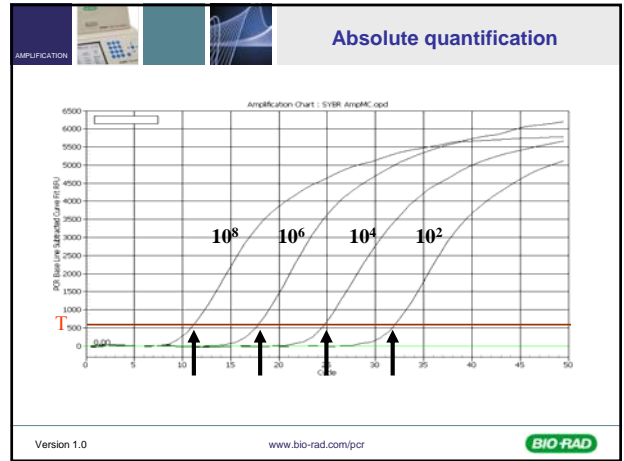
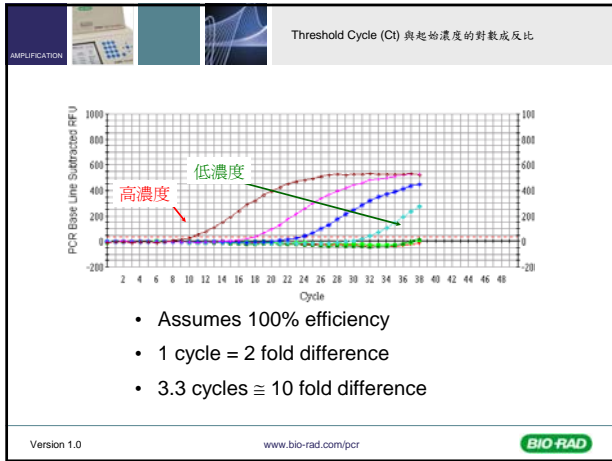
The diagram illustrates the qPCR process in three cycles:

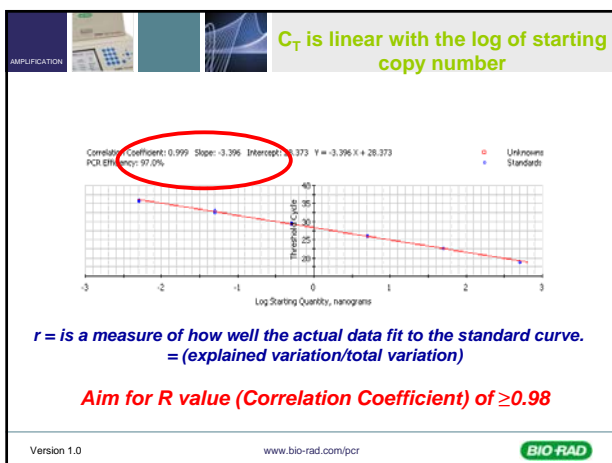
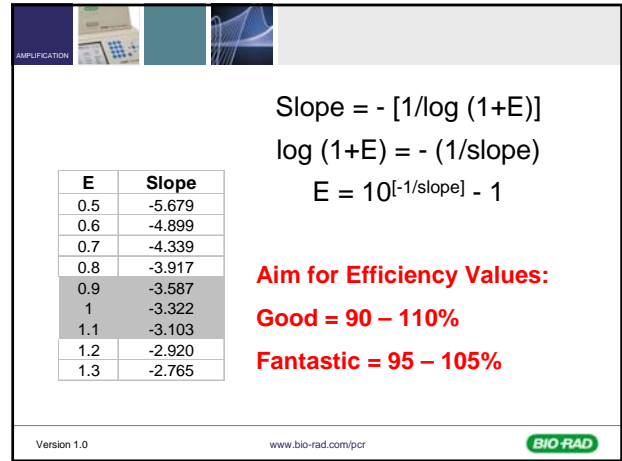
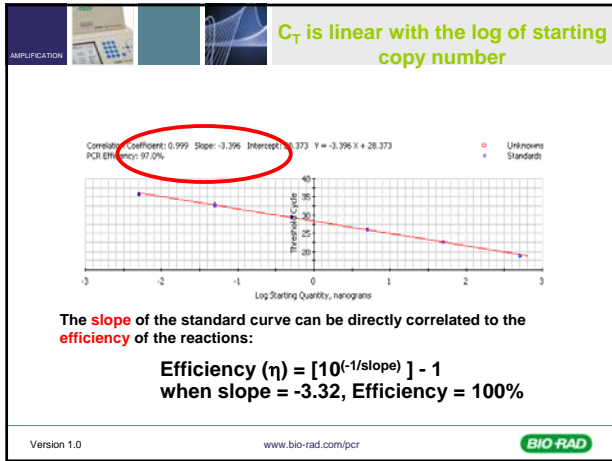
- STEP 1: HEAT TO SEPARATE STRANDS** - A double-stranded DNA molecule is heated to separate into two single strands.
- STEP 2: HYBRIDIZATION OF PRIMERS** - DNA polymerase, dNTPs (dATP, dCTP, dGTP, dTTP), and DNA synthesis from primers bind to the single strands.
- STEP 3: DNA SYNTHESIS FROM PRIMERS** - DNA synthesis from primers occurs, creating two new double-stranded DNA molecules.

The diagram shows that in the first cycle, two double-stranded DNA molecules are produced. In the second cycle, four double-stranded DNA molecules are produced. In the third cycle, eight double-stranded DNA molecules are produced. A red box highlights the first three cycles, and a red arrow points to the text "Monitor the amplification reaction as it occurs".

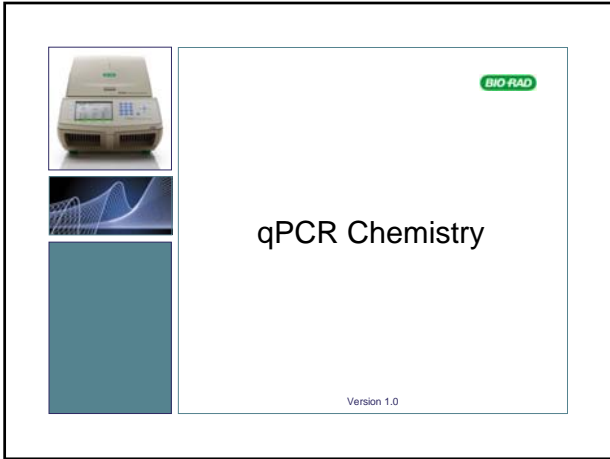
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- AMPLIFICATION
- Points to Remember**
- Threshold Cycle values ( $C_T$ ) have a direct relationship to the amount of starting template
  - 100% efficiency -  $2^n = \text{fold dilution}$
  - Efficiency of reactions between 90-110%
  - R value should be  $\geq 0.98$
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**qPCR Chemistry**

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**Real-Time PCR**

- These fluorescent molecules can be used
  - Non-specific DNA binding dyes
    - SYBR® Green
    - EvaGreen™
  - Specific Hybridization Probes/Primers
    - TaqMan™
    - molecular beacons
    - dual-oligo FRET pairs
    - Scorpions™/Amplifluor™/LUX™

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**DNA binding dyes**

**Add Master Mix & Sample**

**Denaturation**

**Annealing**

**Reaction Tube**

dNTPs  
Thermal Stable DNA Polymerase  
DNA binding dyes

Primers

Taq

BD

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**DNA binding dyes**

**Extension**

**Extension Continued Apply Excitation Wavelength**

**Repeat**

Taq

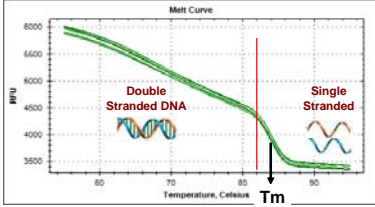
BD

λ

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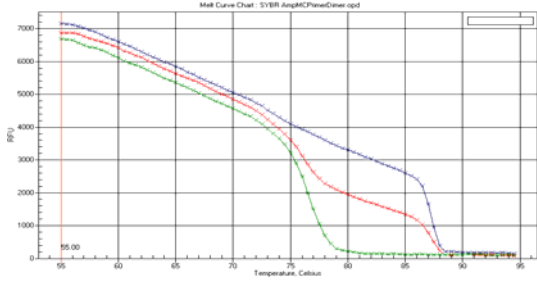
**Melt Curve Analysis**

- After real-time PCR amplification, a melt curve is performed where we monitor fluorescence as temperature increases.
- Melting temperature ( $T_m$ )
  - DNA is half double and half single-stranded
  - Depends on nucleotide content (GC-AT ratio) and length



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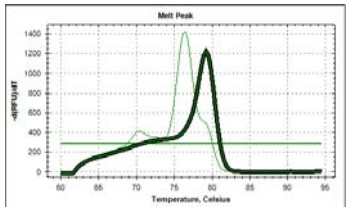
**Melt Curve Analysis**



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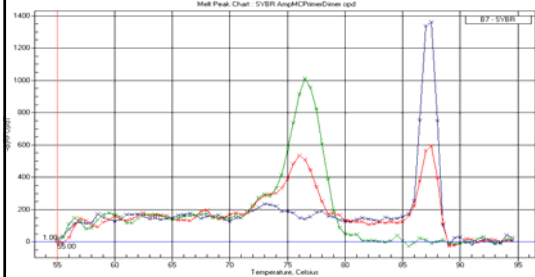
**Melt Curve Analysis**

- Distinguish products based on their  $T_m$ s
  - Plot negative rate of change of fluorescence vs. temp ( $-dI/dT$ ) for easy discrimination of products based on their  $T_m$ s




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**Melt Curve Analysis**



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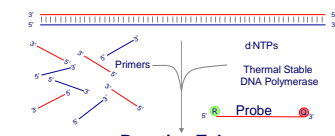
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## TaqMan – the “Hydrolysis” probes

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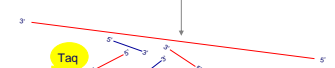
**Cleavage-based assay:  
TaqMan**

**Add Master Mix & Sample**

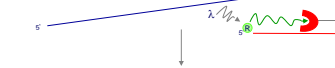


**Reaction Tube**

**Denaturation**



**Annealing**

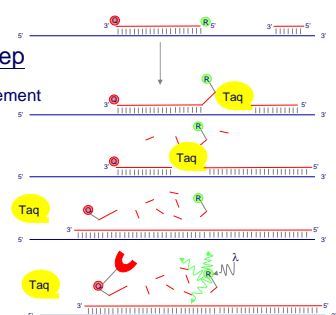


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**Cleavage-based assay:  
TaqMan**

**Extension Step**

1. Strand Displacement
2. Cleavage
3. Polymerization Complete
4. Detection



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**Which Method To Use?**

- Each method has advantages and disadvantages.
- One method may be more appropriate for an application over another
  - microarray, SNP, limited sample....
- Bio-Rad Real-Time Instrumentation is equipped to handle all chemistries.

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## Biorad Real-time PCR Instruments

Price

Mini-Opticon

CFX Connect

CFX96/384

Features & Flexibility

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## Tips for buying a real-time PCR

- Instrument performance
- Multiplexing capability
- Ease of use
- Flexibility of the consumables
- Customer support
- Warranty & ongoing service contract

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## Instrument performance

### Fast run times

### Well-to-well variability

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## Next Generation Thermal Cycling

- CFX96 builds on the precise thermal control of the C1000
  - Maintain uniformity even while ramping
  - 10 second settling - the time it takes all wells to reach temperature - is unsurpassed in the market

Max ramp rate	5°C/sec
Average ramp rate	3.3°C/sec
Temp Accuracy	± 0.2°C
Temp Uniformity	± 0.4°C in 10 sec
Temp Range	0-100°C

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### Max vs Average Ramp Rate

- Max ramp rate is achieved only at the steepest section of the curve, it is not maintained during the ramping period
- It takes time to ramp up to the max rate and then time to slow down to the next temperature

Higher Max ramp rate

Higher Ave ramp rate

Temperature (°C)

Time (s)

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### Max vs Average Ramp Rate

- A cycler ramping with a higher average ramp rate reaches target temperature faster than a cycler ramping with a higher Max ramp rate

Temperature (°C)

Time (s)

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### FAST PCR with SYBR Green

- Serial dilution of target from  $10^8$  to  $10^3$  copies
- Target detected using SYBR Green
- Amplification run time: 24 minutes

Protocol  
 95°C for 20 sec,  
 93°C for 3 sec,  
 60°C for 8 sec + Plate Read  
 GOTO 2, 29 X more times

Amplification

Fluorescence

Cycles

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AMPLIFICATION

### Next Generation Fast Block Design

- The honeycomb architecture promotes uniform heating and cooling of all wells of the block, even during ramping

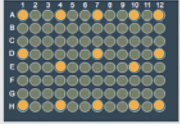
Mass-reduced sample block\*

\* Bio-Rad Patent Pending

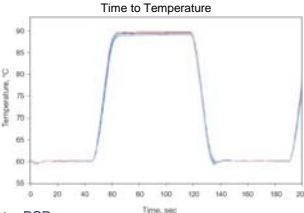
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### Unparalleled Temperature Uniformity

- Wells heat and cool at the same average rate to ensure block uniformity and to achieve a 10 second settling time
- The minimal overshoot ramping up and undershoot ramping down prevents non-specific amplification due to improper primer binding



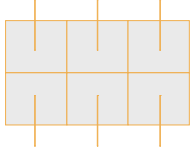
● Probe location



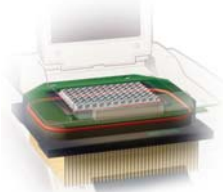
Uniform ramping + shorter settling times = Faster PCR

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### Thermal Reaction Module



6 Thermo Electrics (TEs) - Independent zones of thermal control, each with its own temperature sensor, provides uniform and reliable control of temperature across the block




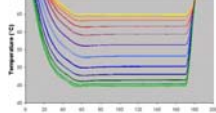
Bio-Rad patented O-ring hermetic seal forms an airtight barrier around the TE and extends the life of the heating and cooling elements

\*Patented by Bio-Rad

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### Thermal Cycler Gradient

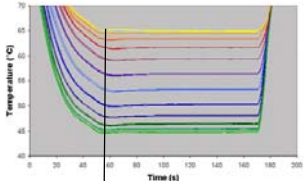
- Annealing temperature is critical for reaction specificity and efficiency
- Save valuable time optimizing annealing in a single experiment
  - Program up to a 24 C gradient
  - Back-to-front (back row is hotter)
  - 30-100 C range
  - "Dynamic Ramping" - Wells hit temperature set point together, and then maintain the same dwell time to eliminate time as a reaction variable

Color traces of temperature measurements from different columns on C1000 with 96Fast

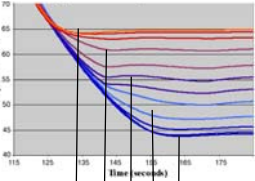
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### Dynamic vs. Steady Slope



ALL LANES reach target temp. at the same time

End user specifies the temperature **and** the ramp rate varies



Lane: 1 4 6 8 12  
Each lane reaches target temp. at a different time, ~30 second difference

End user specifies temperatures but has to use software to figure out ideal temp and hold time

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### Amplicon Secondary Structures

<http://mfold.rna.albany.edu/?q=DINAMelt/Quickfold>

- Bad location for primers
- Good location for primers

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### Effect of primer location

Primer A:  $\eta = 66.3\%$   
Primer B:  $\eta = 95.8\%$

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### Tips for buying a real-time PCR

- Instrument performance
- **Multiplexing capability**
- Ease of use
- Flexibility of the consumables
- Customer support
- Warranty
- Ongoing service contract

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### Next Generation Optical Technology

- CFX connect uses a scanning shuttle
  - 3 filtered LEDs for excitation
  - 3 filtered photodiodes for detection
- Save samples and reagent costs by multiplexing up to 2 targets
- Maximal excitation of dyes with a fixed optical path for all wells and no cross talk for better multiplexing
  - One LED fires at a time to independently illuminate and then detect fluorescence in a channel

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### Discrete Excitation and Detection

- Color separation yields pure dye signal in each channel

Non-color separated

Color separated

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### Filter Sets

Channel	Excitation (nm)	Detection (nm)	Calibrated Fluorophores
1	450-490	515-530	FAM™, SYBR Green I™
2	515-535	560-580	VIC®, HEX™, TET™, Cal Gold 540™
3	450-490	560-580	Accommodates FRET Chemistry

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### Excellent Uniformity at 10 $\mu$ l

FAM

Ave Ct = 19.29  $\pm$  0.10  
Max-Min = 0.58

All Channels

Ave Ct = 19.81  $\pm$  0.10  
Max-Min = 0.53

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### 2-Target Multiplexing

Fam

Hex

Standard Curves

Reaction efficiencies range from 97-99%

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### Start a run in just 3 steps

**Protocol setup**      **Channel setup**      **Run**

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### Add Repeats

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### Plate view and setup in anytime

	1	2	3	4	5	6	7	8	9	10	11	12	Well Group	Fluor-A	Target	Control	Sample
A	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	A00	Cy5			Blank
B	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	A09	Cy5			Blank
C	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	A10	Cy5			Blank
D	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	A11	Cy5			Blank
E	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	A12	Cy5			Blank
F	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	B00	Cy5			Blank
G	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	B02	Cy5			Blank
H	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	LINK	B03	Cy5			Blank

Step 1 of 4      95.0 °C for 00:02:10      Sample: 95.0 °C  
 Repeat 1 of 1      Remaining 01:05:10      Lid 105 °C

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Click right to export what you want

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Data Analysis

Absolute Quantization      Relative Quantization

Allelic Discrimination      End Point Analysis

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Relative Quantization

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Gene Expression Normalization - Comparative  $C_T$

- Relative Quantity ( $\Delta CT$ )
  - Not normalized
  - Normalization accomplished via equal loading of samples
  - Post analysis normalization
- Normalized Expression ( $\Delta\Delta CT$ )
  - Accounts for loading differences
  - Usually normalize to reference gene
  - Relative quantity of GOI is normalized by the relative quantity of the reference genes

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### Normalized Expression

- $\Delta\Delta CT$ 
  - Assume 100% efficiency
  - Only one Ref Gene
- Pfaffl Modification
  - Accounts for efficiency differences
  - Only one Ref Gene
- Vandesompele Method
  - Accounts for efficiency differences
  - Allows multiple reference genes for normalization

Simple  
↓  
Complex

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### Relative Quantification - $\Delta Ct$

	<b>GOI</b>
Tissue #1:	22
Tissue #2:	24
<hr/>	
Delta Ct:	$24 - 22 = 2$

**Fold induction =  $2^2 = 4$**

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### Comparative Ct Method (2- $\Delta\Delta Ct$ )

	<b>Reference</b>	GOI
Tissue #1:	21	22
Tissue #2:	20	24
<hr/>		
1 <sup>st</sup> Delta	Delta Ct #1:	$22 - 21 = 1$
	Delta Ct #2:	$24 - 20 = 4$
<hr/>		
2 <sup>nd</sup> Delta	Delta Ct:	$4 - 1 = 3$

**Fold induction =  $2^3 = 8$**

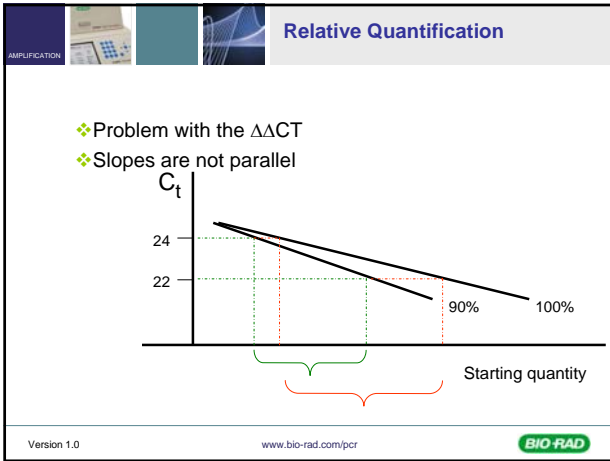
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### Relative Quantification

❖ Problem with the  $\Delta\Delta CT$

The graph illustrates the problem with the  $\Delta\Delta CT$  method. It shows a linear relationship between Ct values and the logarithm of starting quantity. A line with a 90% efficiency slope starts at Ct=24 and goes down to Ct=22. A bracket below the x-axis indicates the 'Starting quantity'.

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### Relative Quantification

$$\text{Fold induction} = \frac{\text{Efficiency}_{\text{target}}^{\text{deltaCt}_{\text{target}} (\text{control-sample})}}{\text{Efficiency}_{\text{reference}}^{\text{deltaCt}_{\text{reference}} (\text{control-sample})}}$$

(Pfaffl, 2001; Nucleic Acid Research)  $\text{Efficiency} = 10^{-1/\text{slope}}$

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### Relative Quantification – Pfaffl Modification

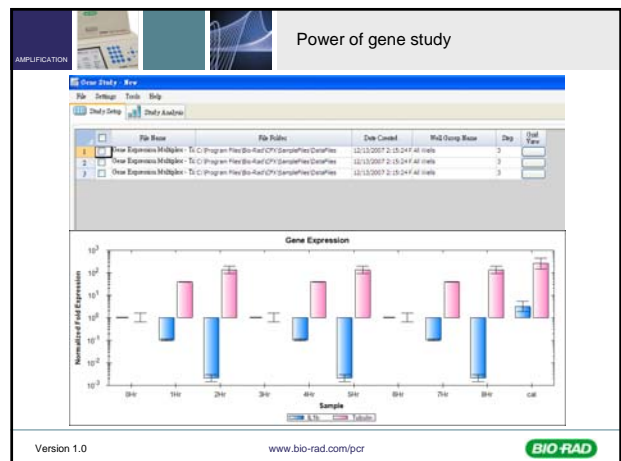
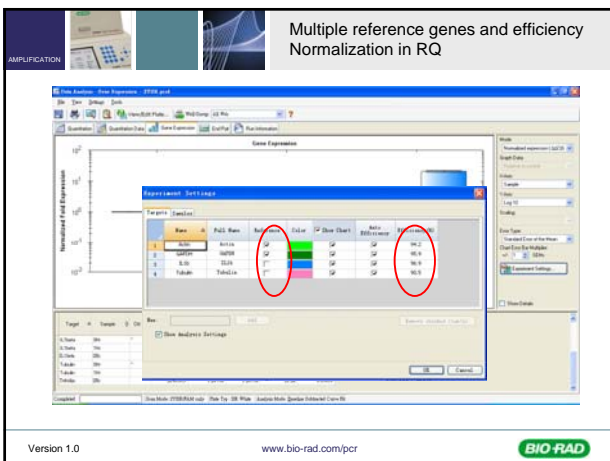
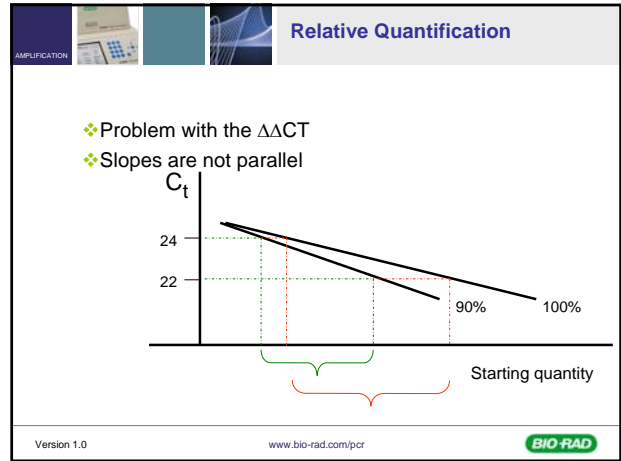
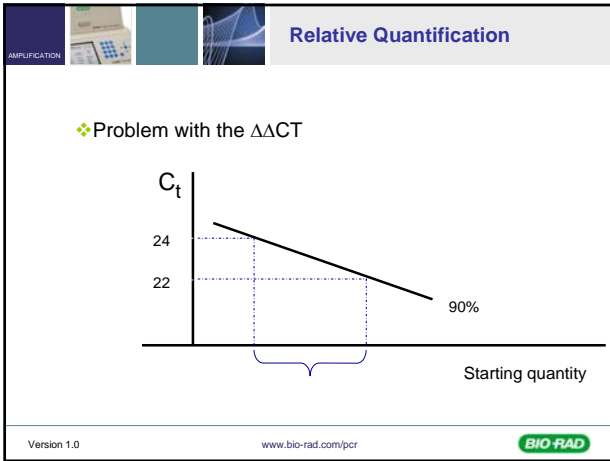
	Primer set #1 Reference	Primer set #2 GOI
Tissue #1:	21	22
Tissue #2:	20	24
(From Standard curve) Efficiency:	90% = 1.9	100% = 2
Delta Ct:	20-21 = -1	24-22 = 2

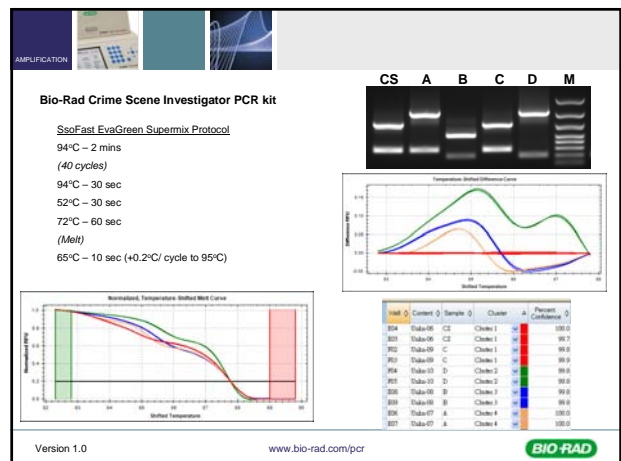
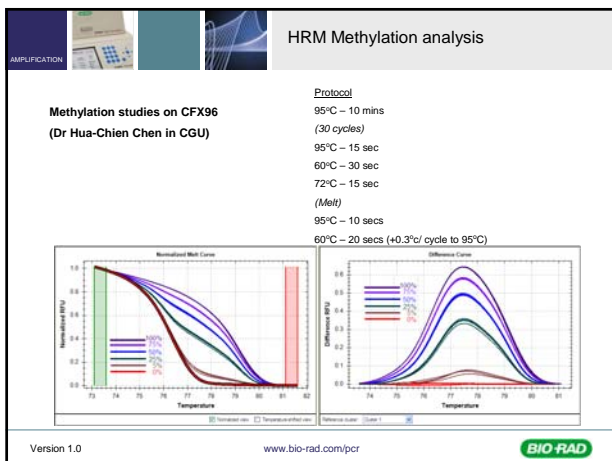
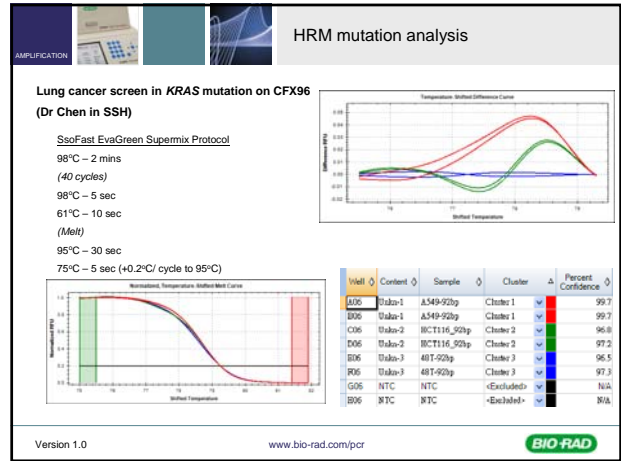
$$\text{Fold induction} = \frac{2_{\text{target}}^{\text{deltaCt}_{\text{target}} (24-22 = 2)}}{1.9_{\text{reference}}^{\text{deltaCt}_{\text{reference}} (20-21 = -1)}} = \frac{4}{0.53} = 7.5$$

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- ### Methods Comparison
- $\Delta Ct$  method: ( no reference gene )  
– Fold induction : 4
  - $\Delta\Delta Ct$  method: ( reference gene )  
– Fold induction : 8
  - Pfaffl modification: ( reference gene and efficiency )  
– Fold induction : 7.5
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**High-Resolution Melting in HLA-A**

**A. Pedigree**

**B. Normalized Melting Curve for Matching**

The figure shows an example of matching 11 siblings (CEPH family UT1331) using the HLA-A locus. The siblings separate into four matched groups. ([Zhou et al 2004](#))

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**Low maintenances**

Hassle free performance, LEDs do not degrade, so no need to change the light source or recalibrate

Auto- self test while turn on and thermal validation service as requested

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**Tips for buying a real-time PCR**

- Instrument performance
- Multiplexing capability
- Ease of use
- **Flexibility of the consumables**
- Customer support
- Warranty & ongoing service contract

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**Open system**


CFX96 fit all kinds of reagents and plastics (low-profile)

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AMPLIFICATION

Tips for buying a real-time PCR


- Instrument performance
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- **Warranty & ongoing service contract**

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AMPLIFICATION

Services of instruments

- **Customer supports**  
Bio-Rad Taiwan: Specialist X 2, Engineer X 4  
Genmall Biotech: Specialist X 6, Engineer X4
- **Warranty & ongoing service contract**  
By contract

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AMPLIFICATION

A new beginning

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,<sup>1\*</sup> Vladimir Benes,<sup>2</sup> Jeremy A. Garson,<sup>3,4</sup> Jan Hellemans,<sup>5</sup> Jim Hugggett,<sup>6</sup>  
Mikael Kubista,<sup>7,8</sup> Reinhold Mueller,<sup>9</sup> Tania Nolan,<sup>10</sup> Michael W. Pfaffl,<sup>11</sup> Gregory L. Shipley,<sup>12</sup>  
Jo Vandesompele,<sup>9</sup> and Carl T. Wittwer<sup>3,14</sup>

**57 Essential information**  
**(E) must be submitted with the manuscript**

**28 Desirable information**  
**(D) should be submitted if available**

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AMPLIFICATION

What is MIQE? It's a Checklist

Table 1. MIQE Checklist for authors, reviewers, and editors<sup>a</sup>

Category	Item to check	Author	Reviewer	Editor
Experimental Design	1. Study design	Y	Y	Y
	2. Sample size	Y	Y	Y
	3. Replicate samples	Y	Y	Y
	4. Replicate assays	Y	Y	Y
	5. Replicate runs	Y	Y	Y
	6. Randomization	Y	Y	Y
	7. Blinding	Y	Y	Y
	8. Control for contamination	Y	Y	Y
	9. Control for cross-talk	Y	Y	Y
	10. Control for carry-over	Y	Y	Y
Sample Information	11. Sample type	Y	Y	Y
	12. Sample source	Y	Y	Y
	13. Sample collection	Y	Y	Y
	14. Sample storage	Y	Y	Y
	15. Sample handling	Y	Y	Y
	16. Sample quality	Y	Y	Y
	17. Sample quantity	Y	Y	Y
	18. Sample purity	Y	Y	Y
	19. Sample integrity	Y	Y	Y
	20. Sample stability	Y	Y	Y
Nucleic Acid Extraction	21. Extraction method	Y	Y	Y
	22. Extraction kit	Y	Y	Y
	23. Extraction protocol	Y	Y	Y
	24. Extraction efficiency	Y	Y	Y
	25. Extraction purity	Y	Y	Y
	26. Extraction yield	Y	Y	Y
	27. Extraction quality	Y	Y	Y
	28. Extraction integrity	Y	Y	Y
	29. Extraction stability	Y	Y	Y
	30. Extraction reproducibility	Y	Y	Y
Reverse Transcription	31. RT method	Y	Y	Y
	32. RT kit	Y	Y	Y
	33. RT protocol	Y	Y	Y
	34. RT efficiency	Y	Y	Y
	35. RT purity	Y	Y	Y
	36. RT yield	Y	Y	Y
	37. RT quality	Y	Y	Y
	38. RT integrity	Y	Y	Y
	39. RT stability	Y	Y	Y
	40. RT reproducibility	Y	Y	Y
qPCR Target Information	41. Target name	Y	Y	Y
	42. Target accession number	Y	Y	Y
	43. Target length	Y	Y	Y
	44. Target GC content	Y	Y	Y
	45. Target complexity	Y	Y	Y
	46. Target specificity	Y	Y	Y
	47. Target sensitivity	Y	Y	Y
	48. Target stability	Y	Y	Y
	49. Target reproducibility	Y	Y	Y
	50. Target validation	Y	Y	Y
qPCR Oligonucleotides	51. Oligo name	Y	Y	Y
	52. Oligo sequence	Y	Y	Y
	53. Oligo length	Y	Y	Y
	54. Oligo GC content	Y	Y	Y
	55. Oligo complexity	Y	Y	Y
	56. Oligo specificity	Y	Y	Y
	57. Oligo sensitivity	Y	Y	Y
	58. Oligo stability	Y	Y	Y
	59. Oligo reproducibility	Y	Y	Y
	60. Oligo validation	Y	Y	Y
qPCR Protocol	61. Assay name	Y	Y	Y
	62. Assay type	Y	Y	Y
	63. Assay kit	Y	Y	Y
	64. Assay protocol	Y	Y	Y
	65. Assay efficiency	Y	Y	Y
	66. Assay purity	Y	Y	Y
	67. Assay yield	Y	Y	Y
	68. Assay quality	Y	Y	Y
	69. Assay integrity	Y	Y	Y
	70. Assay stability	Y	Y	Y
qPCR Validation	71. Validation method	Y	Y	Y
	72. Validation kit	Y	Y	Y
	73. Validation protocol	Y	Y	Y
	74. Validation efficiency	Y	Y	Y
	75. Validation purity	Y	Y	Y
	76. Validation yield	Y	Y	Y
	77. Validation quality	Y	Y	Y
	78. Validation integrity	Y	Y	Y
	79. Validation stability	Y	Y	Y
	80. Validation reproducibility	Y	Y	Y
Data Analysis	81. Analysis method	Y	Y	Y
	82. Analysis kit	Y	Y	Y
	83. Analysis protocol	Y	Y	Y
	84. Analysis efficiency	Y	Y	Y
	85. Analysis purity	Y	Y	Y
	86. Analysis yield	Y	Y	Y
	87. Analysis quality	Y	Y	Y
	88. Analysis integrity	Y	Y	Y
	89. Analysis stability	Y	Y	Y
	90. Analysis reproducibility	Y	Y	Y

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### Data Analysis

Item to check	Importance
Data analysis	
qPCR analysis program (source, version)	E
Method of $C_t$ determination	E
Outlier identification and disposition	E
Results for NTCs	E
Justification of number and choice of reference genes	E
Description of normalization method	E
Number and concordance of biological replicates	D
Number and stage (reverse transcription or qPCR) of technical replicates	E
Repeatability (Intraassay variation)	E
Reproducibility (Interassay variation, CV)	D
Power analysis	D
Statistical methods for results significance	E
Software (source, version)	E
$C_t$ or raw data submission with RDML	D

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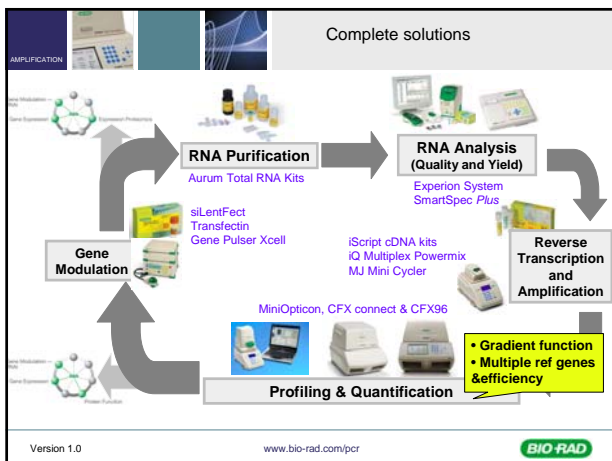
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### qPCR Validation

Item to check	Importance
qPCR validation	
Evidence of optimization (from gradients)	D
Specificity (gel, sequence, melt, or digest)	E
For SYBR Green I, $C_t$ of the NTC	E
Calibration curves with slope and y intercept	E
PCR efficiency calculated from slope	E
CIs for PCR efficiency or SE	D
$r^2$ of calibration curve	E
Linear dynamic range	E
$C_t$ variation at LOD	E
CIs throughout range	D
Evidence for LOD	E
If multiplex, efficiency and LOD of each assay	E

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- ### Mechanical Technology
- CFX384 and CFX96 use the same mechanical technology
  - We have performed over 1 million scans on a CFX96
    - 4 runs a day with 40 cycles, 250 working days = 25 years!
    - Shuttle positional shift less than 5 microsteps (~60 microns)
    - Difference is less than the thickness of a piece of paper!
- 
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