




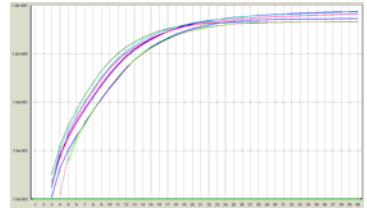
Introduction to Real-Time PCR

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Field Applications Scientist







What is Real-Time PCR?

Technology to sensitively detect the real-time PCR amplification of nucleic acid targets.



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How is Real-Time PCR similar to traditional PCR?


- Similar reagents (dNTPs, PCR buffer, *Taq* polymerase, etc.) are used

→



TGCAAACAGATTAGACATAGATAGACAGATTAGATAGACTTAGATGTTTGGCA
ACGTTTGCTAATCTGTATCTATCTGTCTAATCTATCTGAATCTACAACCGT

←

T G A T
A C G T
G G A C

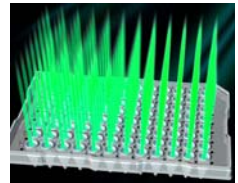




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How does Real-Time PCR work?

- Some form of **fluorescence** is added to the PCR mix



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How is Real-Time PCR similar to traditional PCR?

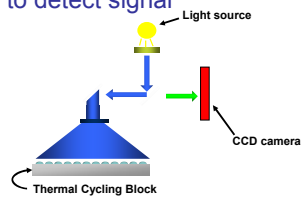
- Reactions are cycled in a temperature block:
 - » Denaturing of template
 - » Annealing of primers and probe
 - » Extension of primers to make new amplicons

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How does Real-Time PCR work?

- Real-Time instrument has a **thermal block**, a **light source** to excite fluorescence, as well as a **CCD camera** to detect signal



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How does real-time PCR work?

- As amplification proceeds, fluorescence will increase with product.

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How does Real-Time PCR work?

- Finally, data are presented graphically for easy analysis

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It all Starts with Good Sample Prep!

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Sample Preparation

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Ambion : The RNA Company

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RNA Isolation Products

Which RNA isolation kit is right for you?

12

THE RNA COMPANY
An Applied Biosystems Business

Ambion RNA Isolation Products

Tissue Disruption

- MELT™ **

Small RNA Isolation

- mirVana™ miRNA Isolation Kit
- PARIS™
- mirVana PARIS™ Kit

Bead-Based Isolation

- MagMAX™-96 Kits
- MagMAX™ Viral Kits **
- MagMAX™ Total Nucleic Acid Isolation Kit **

Total RNA Isolation ** RNA/DNA Kits

- RiboPure™ Kits
- RNAqueous® Family
- Tri Reagent™ **
- LeukoLOCK™
- RecoverAll™ Total Nucleic Acid Isolation from FFPE Tissues **

Complete Solution

- TaqMan® Gene Expression Cells-to-CT™
- TaqMan® miRNA Cells-to-CT™
- TaqMan® PreAmp Cells-to-CT™
- TaqMan® Fast Cells-to-CT™

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TaqMan® Gene Expression Cells-to-Ct™ Kit

- Go from cells to RNA in 7 minutes.
- No clean-up, no centrifugation, no precipitation – easily adaptable for high throughput.
- No loss of RNA.
- Lysis buffer compatible with downstream RT.
- Complete kit:
 - Lysis reagent
 - Reverse transcription reagents
 - TaqMan® Gene Expression Master Mix

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Sample Preparation

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TURBO DNA-free™: gentle on RNA

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Sample Preparation

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High Capacity RNA-to-cDNA Master Mix

Single-tube first strand synthesis:

- Very high efficiency – excellent conversion rate.
- Broad dynamic range – reproducible results over a large concentration range.
- Convenient 5x formulation.
- Optional no-RT control formulation tube.
- Liquid master mix at -20° – eliminates freeze/thaw cycles.

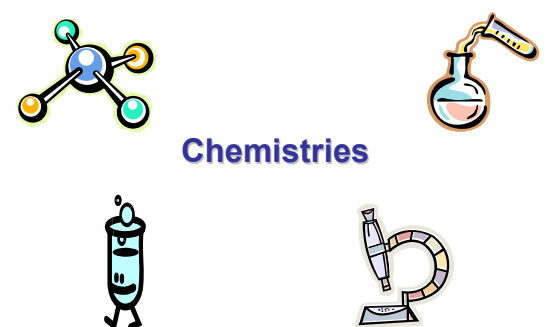
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Questions

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Chemistries

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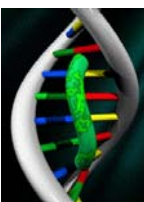
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Supported Fluorescent Chemistries

5'-Nuclease




SYBR® Green Dye



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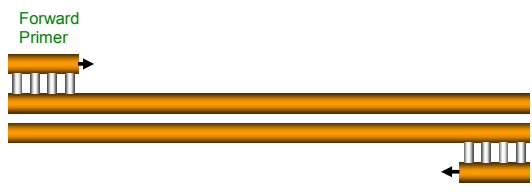
5'-Nuclease Chemistry (TaqMan® Assays)



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5'-nuclease assay uses two target-specific primers



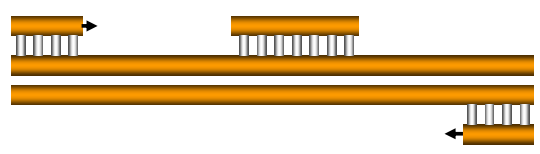
Forward Primer

Reverse Primer

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In addition, a third oligo, called a **probe**, sits in the middle



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The probe is labeled with two fluorescent dyes

Reporter dye Quencher dye

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Fluorescent Resonance Energy Transfer

- Theodor Förster (1946) described an energy transfer mechanism between two fluorescent molecules
- Fluorescent molecules within close proximity exhibit energy transfer from high to low

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Intact probe

- Quencher (low energy) and reporter (high energy) in close contact
- quencher “absorbs” signal

Light (excitation)

Energy

No fluorescent signal (from reporter)

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However, if probe can be split . . .

- . . . the reporter will be free to fluoresce

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However, if probe can be split . . .

- . . . the reporter will be free to fluoresce

Signal

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Denaturation

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Annealing

58-60°C 68-70°C

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Taq polymerase binds, then extends from upstream primer

Polymerase must be extending off of a 3' OH group

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What happens when Taq reaches the probe?

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Taq is special . . .

Exonuclease activity

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What happens when Taq reaches the probe?

Probe will get digested*

*Must be associated with a 5' hydrogen bond

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Taq starts to cleave probe, thereby releasing reporter . . .

5'-Nuclease activity digests probe

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Probe digested; Taq completes product

“Permanent” reporter signal generated in tube/well

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Real-Time amplification detection

Amplification Plot

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Recommended concentrations

- Probe: 200 – 250 nM (final concentration in reaction).
- Primers: 900 nM each.

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Tms of primers and probe

Probe's T_m should be several degrees higher than primers.

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7900HT Real-Time PCR System

- Dye choices

Reporter Molecules: FAM™, VIC®, JOE™, NED™, TET™

Quencher Molecules:
MGB (non-fluorescent), TAMRA™

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SYBR® Green I Reaction

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SYBR[®] Green Reaction (No Probe)

58-60°C

SYBR[®] Green I Dye

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SYBR[®] Green I dye

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SYBR[®] Green I dye

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SYBR[®] Green I dye

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SYBR[®] Green I dye

Denatured DNA:
No Signal

Double Stranded DNA:
→ Signal

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Real-Time monitoring of SYBR[®] Green I reactions


Amplification plot

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SYBR® Green I Dye

When SYBR® Green I Dye is added to a PCR reaction it binds to any double stranded DNA.



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SYBR® Green I Dye



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SYBR® Green I Dye



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SYBR® Green I Dye



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SYBR® Green I Dye



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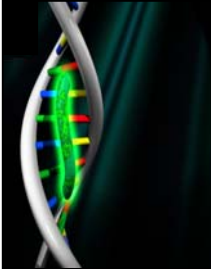
SYBR® Green I Dye



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Problem with SYBR® Green I Dye



Binds non-specifically to any double-stranded DNA

→ Signal from non-specific products

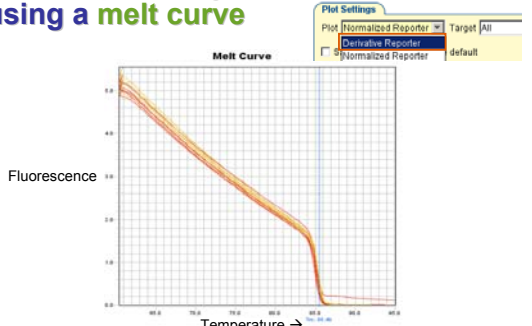
↓

Incorrect quantitative results

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Check specificity of reactions using a melt curve



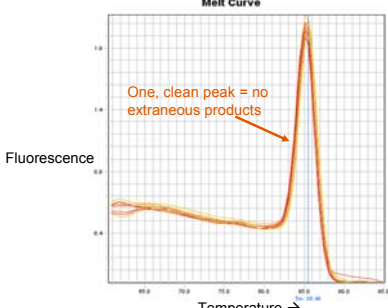
Fluorescence

Temperature →

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Melt curve: derivative view




Fluorescence

Temperature →

57

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Extra peaks in melt curve



Fluorescence

Temperature →

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What causes primer dimer?

- Primers have too much homology for each other

(Forward Primer) CGTTCGATACGCTAT

|||

(Reverse Primer) GCTACCTATGCGATA

- Primer : template ratio is too high

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Typical primer concentrations

		Forward primer		
		50nM	300nM	900nM
Reverse primer	50nM	SYBR®?		
	300nM			
	900nM			TaqMan®

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Run a primer matrix

Forward primer

	50nM	300nM	900nM
Reverse primer	50nM		
	300nM		
	900nM		

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Identify the primer combination with the most sensitivity . . .

- Lowest Ct
- Highest fluorescence signal
- Does **NOT** have to be equimolar

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Identify the primer combination with the most sensitivity . . .

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. . . that also shows minimal primer dimer

With this primer set, all primer combinations are clean.

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TaqMan®, or SYBR® Green? Hmm . . .

Which chemistry should you use?



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TaqMan®, or . . . SYBR® Green I Dye?


<ul style="list-style-type: none"> • Pros <ul style="list-style-type: none"> – More specific – No concern about dimers – Allows for multiplexing – Minimal optimization • Cons <ul style="list-style-type: none"> – Can be more expensive 	<ul style="list-style-type: none"> • Pros <ul style="list-style-type: none"> – Can be cheaper – Good for many genes, few samples • Cons <ul style="list-style-type: none"> – Less specific – Must run melt curves – No multiplexing – Optimization
--	--

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Questions?


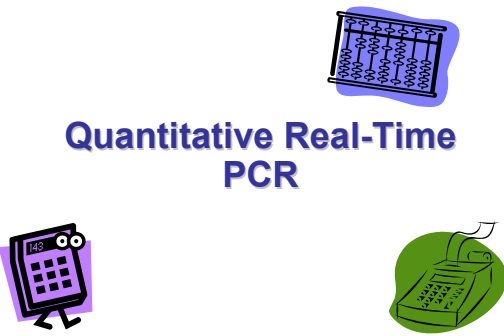
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Many possible applications


- Gene expression studies (e.g., mRNA)
- Copy Number Variation (transgenics)
- Gene expression studies (e.g., miRNA)
- siRNA knockdown validation
- Single Nucleotide Polymorphism (SNP) genotyping
- Viral detection
- Pathogen detection
- Human IDentification

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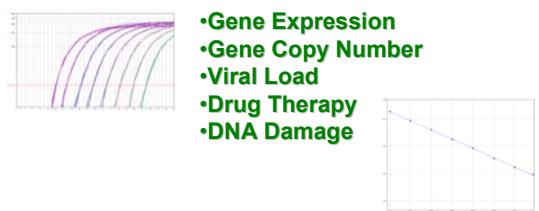
Quantitative Real-Time PCR

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Real-time quantitative PCR

Method to measure quantities of a nucleic acid target.




- Gene Expression
- Gene Copy Number
- Viral Load
- Drug Therapy
- DNA Damage

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PCR has three distinct phases




PCR product (log scale)

Early cycles

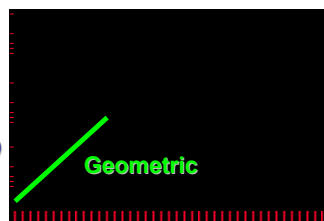
- Reagents in abundance
- PCR product doubles

Cycle #

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Geometric phase - Product doubles every cycle



PCR product (log scale)

Geometric

Cycle #

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PCR phases

PCR product (log scale)

Middle cycles

- Reagents running out
- Reaction slows down

Cycle #

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Linear phase - Reaction slows

PCR product (log scale)

Linear

Geometric

Cycle #

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PCR phases

PCR product (log scale)

Late cycles

- Important reagent(s) depleted
- Reaction stops

Cycle #

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Plateau phase - Reaction stops

PCR product (log scale)

Linear

Geometric

Plateau

Cycle #

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Traditional end-point PCR: plateau phase

PCR product (log scale)

Linear

Plateau

EtBr - Gel detection

Semi-quantitative, at best

Cycle #

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Real-Time PCR: Geometric phase

PCR product (log scale)

Linear

Plateau

EtBr - Gel detection

Precise and accurate quantitation

Cycle #

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What does Real-Time PCR do?

Provides easy access to high-quality geometric phase data.

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Real-Time Quantitative PCR: Absolute Quantification

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Use a standard curve

Do serial dilutions

A	1.00e+08	1.00e+08	1.00e+08	1.00e+07	1.00e+07	1.00e+07	1.00e+06	1.00e+06	1.00e+06	1.00e+05	1.00e+05	1.00e+05	1.00e+04	1.00e+04	1.00e+04	1.00e+03	1.00e+03	1.00e+03
B	Unknown #1	Unknown #1	Unknown #1	Unknown #1	Unknown #1	Unknown #1	Unknown #2	Unknown #2	Unknown #2	Unknown #2	Unknown #2	Unknown #2	Unknown #3	Unknown #3	Unknown #3	Unknown #3	Unknown #3	Unknown #3
C	Unknown #4	Unknown #4	Unknown #4	Unknown #4	Unknown #4	Unknown #4	Unknown #5	Unknown #5	Unknown #5	Unknown #5	Unknown #5	Unknown #5	Unknown #6	Unknown #6	Unknown #6	Unknown #6	Unknown #6	Unknown #6

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At end of run, interpolate unknown Cts to curve

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Two curve types

- Absolute standard curves:
 - Actual copy number of standard is known.
 - Bacterial / viral quantification
- Dilution (a.k.a. “relative standard”) curves
 - Only dilution factor of standard is known.
 - Gene expression

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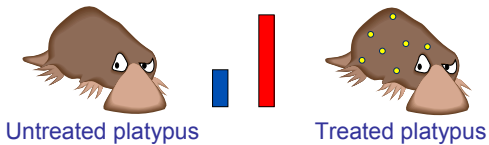
Real-Time Quantitative PCR: Relative Gene Expression

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Example experiment



Untreated platypus Treated platypus

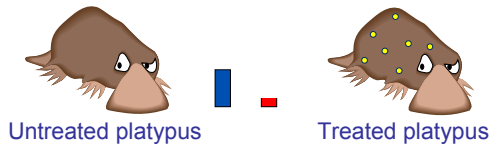
Gene of interest: **Plat1**

Big question: How is the expression of **Plat1** changing when I treat my platypi?

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Example experiment



Untreated platypus Treated platypus

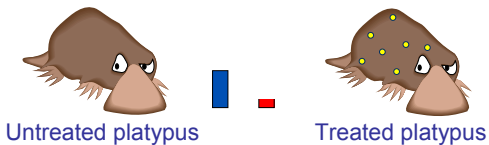
Gene of interest: **Plat1**

Big question: How is the expression of **Plat1** changing when I treat my platypi?

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Example experiment



Untreated platypus Treated platypus

Gene of interest: **Plat1**

Big question: How is the expression of **Plat1** changing when I treat my platypi?

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First, a few general recommendations

1) Use a sample prep method that yields **clean RNA of high integrity.**

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A few recommendations

- 1) Use a sample prep method that yields clean RNA of high integrity.
- 2) Be **consistent** in your **RNA isolation method** from sample to sample.
- 3) **DNase-treat** samples.
- 4) **Quantify unknown RNAs** prior to RT step.
- 5) Use a reverse transcription kit with a very **high-efficiency.**

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Three validations for a successful relative gene expression experiment



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Three separate validation experiments

1. What **control gene** should you use?
2. How much **RNA** should you use in your reverse transcription reactions?
3. What are the **PCR efficiencies** of your assays?

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Validation #1: What normalizer (control gene) should you use?



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For relative gene expression studies, we minimally look at two genes

Gene of interest (target)

Normalizing gene (control)

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What is a normalizer?

(a.k.a. “control gene,” “housekeeping gene,” “endogenous control”)

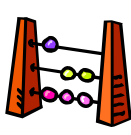
A gene that we show to be **expressed consistently** in all sample types, regardless of treatment, tissue origin, time point, etc.

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Function of a normalizer

To mathematically account for **sample-to-sample differences** in cDNA input amounts.



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Commonly used control genes

- 18s
- Beta-Actin
- GAPDH
- Cyclophilin
- HPRT
- GUS
- Etc.

Go to www.allgenes.com for a list of endogenous control genes / pre-developed Assays.

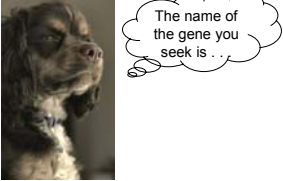
Important thing: finding a normalizer that's stable in your experimental system.

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Where to begin your search

Seek advice from the literature or from colleagues working in your system about what genes seem to remain stable.



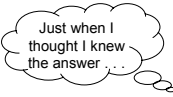
The name of the gene you seek is...

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Always validate your candidate normalizer gene

Don't simply trust what others say is a good choice as a normalizer. Prove that this gene is stable in your samples.



Just when I thought I knew the answer...

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How do you validate your normalizer?

- Isolate RNA from a representative group of samples and DNase-treat.
- Perform reverse transcription on each.
- RNase-treat; clean-up (get rid of free dNTPs).
- Quantify cDNAs.
- Do real-time with candidate normalizer using equal amounts of cDNA.
- Verify that Cts are consistent among samples.

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Two options for quantifying cDNA

Fluorometer (protocol: http://www.ambion.com/techlib/misc/cDNA_quant.html)



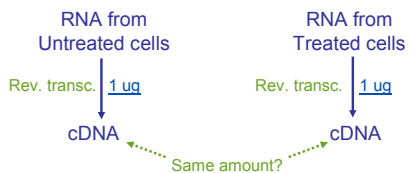
NanoDrop (1-2µl of undiluted sample)

Always check linear range of instrument!

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"Can I quantify RNA instead of cDNA for this validation?"



RNA from Untreated cells → Rev. transc. 1 µg → cDNA

RNA from Treated cells → Rev. transc. 1 µg → cDNA

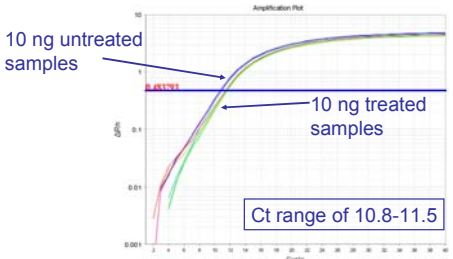
Same amount?

You will only produce the same amount of cDNA IF your two samples contain equal amounts of genomic DNA contamination, and IF they have the same RT efficiency.

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Untreated & treated samples amplified by control gene

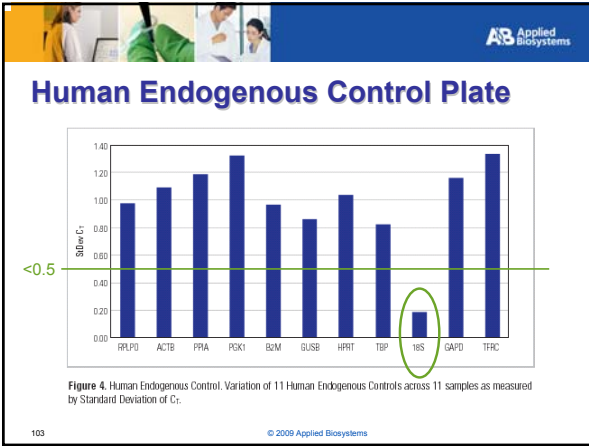


10 ng untreated samples

10 ng treated samples

Ct range of 10.8-11.5

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Questions?

Validation #2 : How much RNA should you use in your RT reactions?

What do we need to determine?

The **range of acceptable RNA concentrations** over which you observe linear reverse transcription efficiencies (*target-, sample set-, and RT kit-specific*).

Why do we care?

You want to make certain that we start with an **appropriate amount of RNA** for each gene.

Otherwise, your data could wind up being inaccurate.

How do we determine how much to use?

Run **RNA dilution curves** using all genes (normalizer and targets).

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How to set up RNA dilution curves

RNA (undil.)

This is a concentrated RNA sample, isolated and purified in a manner consistent with your other unknown RNAs. It can even be a mixture of unknowns.

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How to set up RNA dilution curves

RNA (undil.)

- 1:2 dilution
- 1:4
- 1:8
- 1:16

Do serial dilutions of the RNA. For higher concentration targets or large sample amounts, you may need a larger dilution factor (say, 1:5 or higher).

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How to set up RNA dilution curves

Individually convert each RNA into cDNA; use the same volume for each reverse transcription reaction.

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Finally . . .

Run in real-time with all genes, using **equal volumes** of each cDNA (in triplicate).

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Linear RNA dilution curves

(Note: each point run in triplicate)

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Not-so-linear dilution curves

Q: What's causing this effect?
A: Partial inhibition of RT step

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Effect of inhibitors on RT

Dirty sample → RNA (undil.) → RT → **less cDNA** (Partial inhibition)

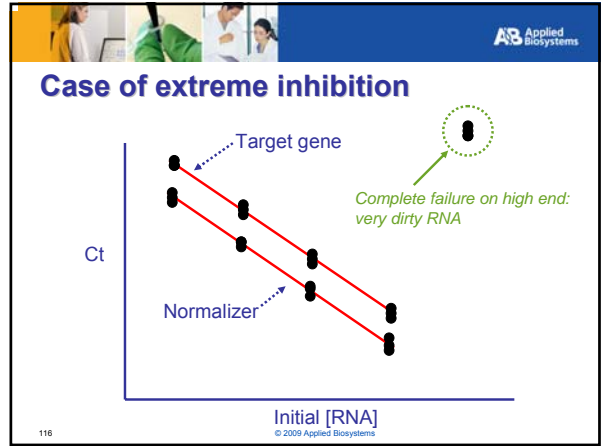
1:2 dilution → RT → cDNA

1:4 → RT → cDNA

1:8 → RT → cDNA

1:16 → RT → cDNA

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A small sampling of RT inhibitors

Inhibitors native to sample:

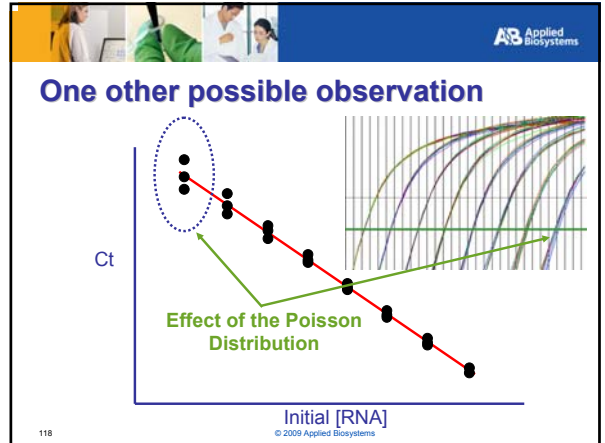
- Melanin
- Polysaccharides
- Hemoglobin
- Heparin
- Etc.

Inhibitors from RNA isolation step:

- EtOH
- Proteinase K
- Guanidinium
- Phenol

* Very dangerous: without consistent sample prep, contamination (and therefore inhibition) can vary dramatically from sample to sample.

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Poisson, molecularly speaking

30 uL / 9 molecules

How often do we end up with 3 molecules in each tube?

Answer: **Not too often.**

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Questions?

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Validation #3: What are the PCR efficiencies of my Assays?

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Two ways to do relative quantitative PCR

Comparative Ct ($\Delta\Delta Ct$) Method Relative Standard Curve Method

Sample-to-sample fold changes

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How do they differ?

Relative Standard Curve Method

- Run standard curves with each gene in each experiment
- More work, costlier, lower throughput

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How do they differ?

Comparative Ct ($\Delta\Delta Ct$) Method Relative Standard Curve Method

- No standard curves for each experiment
- Easier, cheaper, higher throughput

- Run standard curves with each gene in each experiment
- More work, costlier, lower throughput

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$\Delta\Delta Ct$ generally the method of choice

Comparative Ct ($\Delta\Delta Ct$) Method Relative Standard Curve Method

- No standard curves for each experiment
- Easier, cheaper, higher throughput

- Run standard curves with each gene in each experiment
- More work, costlier, lower throughput

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One big requirement of $\Delta\Delta Ct$

Your two genes (target and normalizer) must have approximately the *same amplification efficiencies!*

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Steps for doing $\Delta\Delta Ct$

Efficiencies are sometimes confirmed by **running the assays side-by-side** and confirming that they have parallel amplification curves.

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Target and control have equal efficiencies in geometric phase

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More mathematical approach . . .

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Run dilution curves and compare slopes

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Standard curves give us an idea of PCR efficiencies

- For example, a **slope value = -3.3** suggests the primers are amplifying with approximately 100% efficiency.
- A more negative number (say, -3.5) suggests a less than 100% efficient reaction.

Calculation: $E = 10^{(-1/\text{slope})} - 1$

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#1 mistake among my real-time customers

Generating inaccurate dilution curves (and thus inaccurate efficiency calculations).

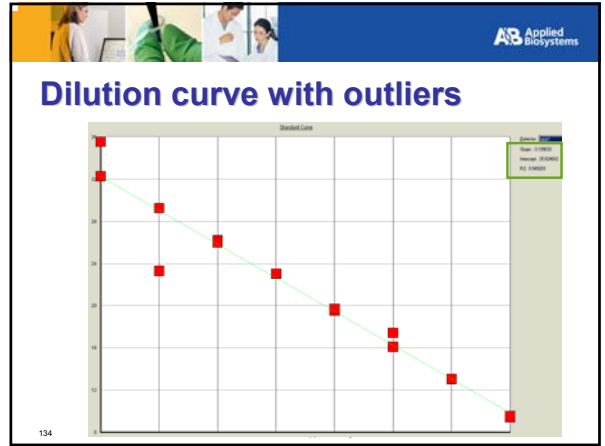
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Suggestions for accurate dilution curves

- Don't:
 - Make a three-point curve of two-fold dilutions.
- Do:
 - Make a minimum five-point curve of ten-fold dilutions (four logs).
 - Eliminate outlying replicates or, when necessary, entire dilution points.

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What's the efficiency?

Slope: -3.199033
 Intercept: 25.824602
 R2: 0.949283

Better than perfect . . .

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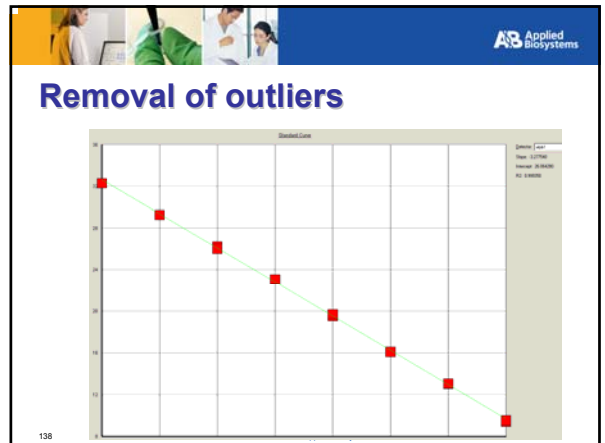
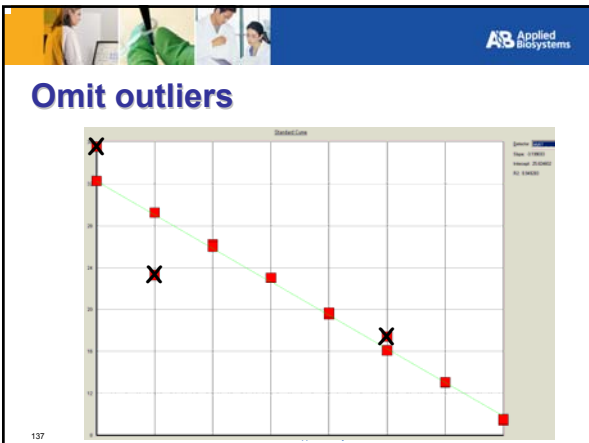
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Check correlation coefficient

Slope: -3.199033
 Intercept: 25.824602
 R2: 0.949283

Should be ≥ 0.99

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Correlation and slope now good

Slope: -3.277540
 Intercept: 26.064280
 R2: 0.999350

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Final suggestion for accurate dilution curves

- For low concentration targets, you may need to use **plasmid** to generate accurate curves.
 - Involves . . .
 - PCR-amplifying target
 - Cloning into a PCR-ready vector
 - Using this for dilution curve to check efficiency

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Back to validation . . .

Ct

Slope = -3.38

Slope = -3.32

Target

Normalizer

[Template]

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Slope values of control and target genes . . .

Should be within ~0.1

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Equal efficiencies allow us to choose the $\Delta\Delta C_t$ method

Comparative Ct ($\Delta\Delta C_t$) Method

Relative Standard Curve Method

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Steps for $\Delta\Delta C_T$

Perform **real-time** run using control gene and target gene on unknown samples (use at least triplicates per sample for each gene).

No-template controls (NTCs) – contamination check

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Example of $\Delta\Delta Ct$ math

Sample	X
Treated 1	24
Treated 2	20
Untreated	24

Avg. Ct values of replicates

X = Target

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Need to consider normalizer gene values

Sample	X	N
Treated 1	24	14
Treated 2	20	11
Untreated	24	13

Avg. Ct values of replicates

X = Target N = Normalizer

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Normalize data via subtraction

Sample	X	N	ΔCt
Treated 1	24	14	10
Treated 2	20	11	9
Untreated	24	13	11

X = Target N = Normalizer

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Why are we subtracting Ct values instead of dividing?

- Ct values are **exponents**, not linear values.
- Therefore, we should never literally divide Cts.
- In short, we divide Cts *through subtraction*.
(example: $2^{25} \div 2^{20} = 2^5$)

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Next, choose a **reference sample**

- This is a sample to which you will be comparing all other samples.
- Generally, this is the "untreated sample."
- Allows for easier sample-to-sample comparisons.

Instead of having . . .

Untreated:	.074 / .074
Treated 1:	.148 / .074
Treated 2:	.222 / .074

You will instead have . . .

Untreated:	1
Treated 1:	2-fold increase
Treated 2:	3-fold increase

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Pick a reference sample

Fold change in log form

Sample	X	N	ΔCt	$\Delta\Delta Ct$
Treated 1	24	14	10-11	-1
Treated 2	20	11	9-11	-2
Untreated	24	13	11-11	0

Still logs, so we must subtract

X = Target N = Normalizer

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Convert from log to linear

Sample	X	N	ΔCt	$\Delta\Delta Ct$	$2^{-\Delta\Delta Ct}$
Treated 1	24	14	10	-1	2
Treated 2	20	11	9	-2	4
Untreated	24	13	11	0	1

Ref. sample always has final value of 1

Relative quantification (fold change) values

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Best part about 7900 software? (RQ Manager 1.2)

Well	Sample No.	Target No.	Task	Ct	Ct Mean	ΔCt Mean	ΔCt SE	$\Delta\Delta Ct$	RQ
A1	Brain	185	UNKNOWN	10.915253	10.883143				
A2	Brain	OGDH	UNKNOWN	26.7171	26.800344	15.917	0.055	0	1
A3	Brain	EGR3	UNKNOWN	27.828683	27.899597	17.016	0.05	0	1
A4	Brain	OSGEP	UNKNOWN	29.244791	29.34477	18.462	0.053	0	1
A5	Brain	MAOB	UNKNOWN	25.75437	25.906	15.023	0.064	0	1
A6	Brain	SERPIND1	UNKNOWN	26.912061	26.92132	16.038	0.042	0	1
A7	Kidney	185	UNKNOWN	11.380488	11.50616				
A8	Kidney	OGDH	UNKNOWN	25.182674	25.221848	13.716	0.062	-2.202	4.6
A9	Kidney	EGR3	UNKNOWN	30.734765	30.922353	19.416	0.088	-2.4	0.188
A10	Kidney	OSGEP	UNKNOWN	29.940151	29.947079	17.441	0.057	-1.021	2.028
A11	Kidney	MAOB	UNKNOWN	25.134071	25.183148	13.677	0.06	-1.346	2.542
A12	Kidney	SERPIND1	UNKNOWN	25.847473	25.803164	14.297	0.058	-1.741	3.343

It does all the math for you!

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Questions?

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Where can I find technical help?

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Getting Started Guides

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Technical Support Hotline

1-800-762-4001

TAC (Instrument Support)

1-800-327-3002, option 4




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