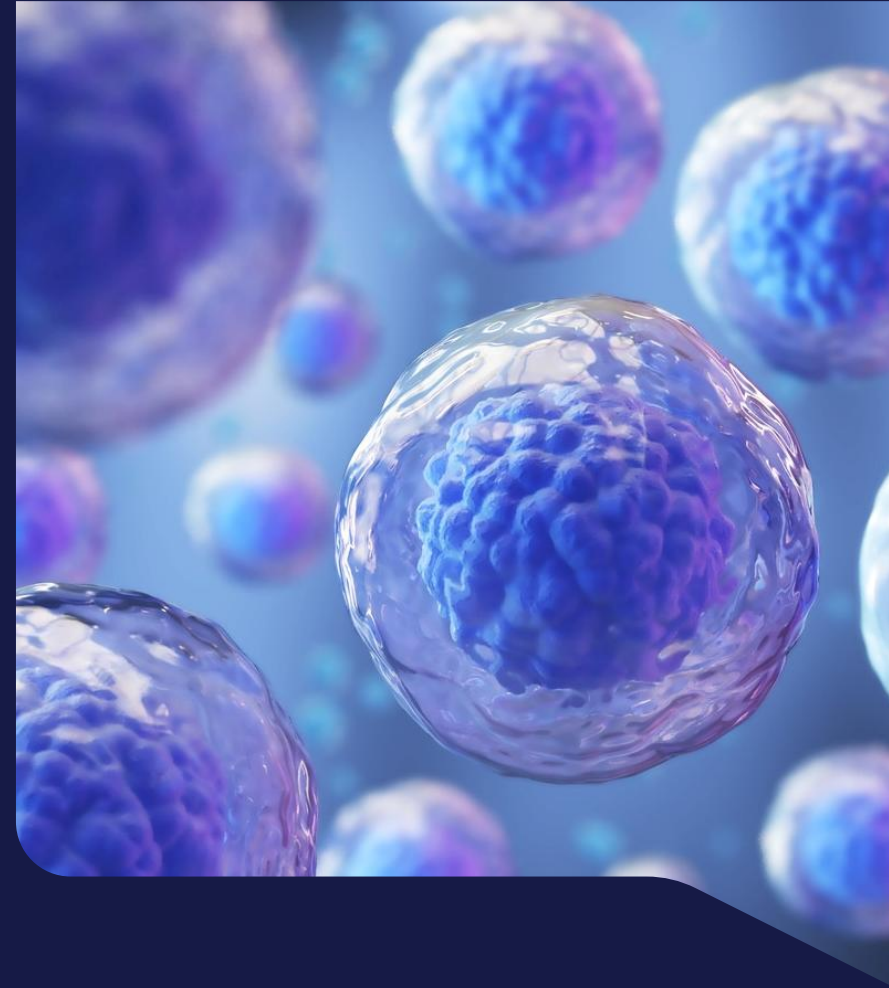


# Designing Robust Cell-Based Potency Assays: Strategic Frameworks and Emerging Biological Readouts



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**Catalent**  
Pharma Services™

# Agenda

## 01 Introduction & Considerations

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## 02 Readouts

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## 03 Strategy

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## 04 Roadmap Visualization

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## 05 Examples: Dose Response Curves

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## 06 mRNA Transcription Assay

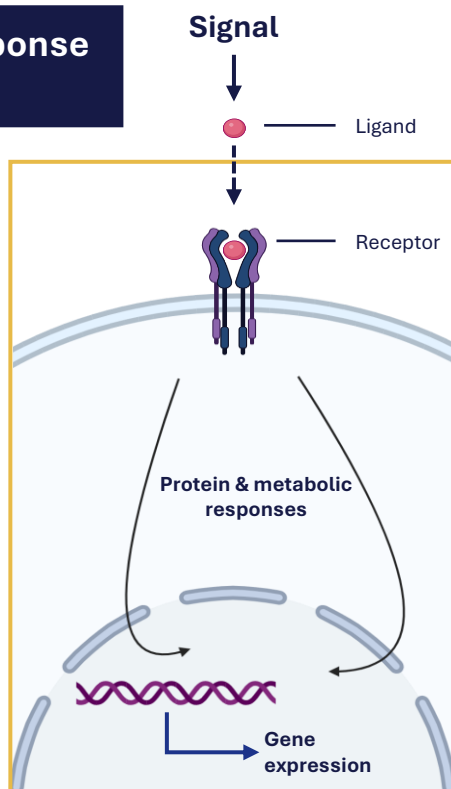
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## 07 Q&A



# Increased Regulatory Expectation for Robust Cell-Based Potency Assays in Biologics & CGT

## Harnessing Cell Response for Use in Bioassay



### Cellular responses

- Morphological Change
- Metabolic Change
- Proliferation, Survival

**ICH Q6B** -> validated cell-based potency assays

For commercial release & stability of large molecules for licensing in multiple countries

Must reflect the **MoA** of large molecules

Be **stability indicating** -> key for ensuring **Safety, Efficacy, Purity, Identity** and **Potency** of medicinal products

May be also utilized for **manufacture comparability assessments, extended characterization** and **formulation development**

ATMPs like CGT require a customized **“matrix”** panel of cell-based potency assays

For manufacturing, purification and release decisions

# Cell-Based Potency Method Development

## Aspects to Consider

### Cell Stimulation

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- Direct analyte interaction
- Ligand interaction
- Serum/growth factor starvation
- Co-culture required
- ECM interaction necessary
- Others, such a biomechanical, hypoxia, etc.



### Biological Response

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- The biological response should reflect the mechanism of action & be measurable
- Understand procedure to control for biological response drifts
- Start assay trending early to include relevant variables



### Curve Shapes

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- Most biological responses can be analyzed with 4-PF curves, but straight-line analysis is also an option
- Ensure curve represents optimized method before validation



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# Bioassay Readouts: Where Biology Meets Chemistry

Each of these assays use luminescent, colorimetric or fluorescent readouts to detect & quantify specific biochemical or cellular processes

## Cytotoxicity 01

- CytoTox-Glo™ assay measures a distinct protease activity associated with cytotoxicity
- alamarBlue™

## Enzymatic 02

- Caspase-Glo® assay measures caspase-3/7, enzymes that play a role in apoptosis

## Reporter 03

- cAMP-Glo™ assay measures cAMP, a second messenger important in many biological processes, by converting it to a luminescent signal

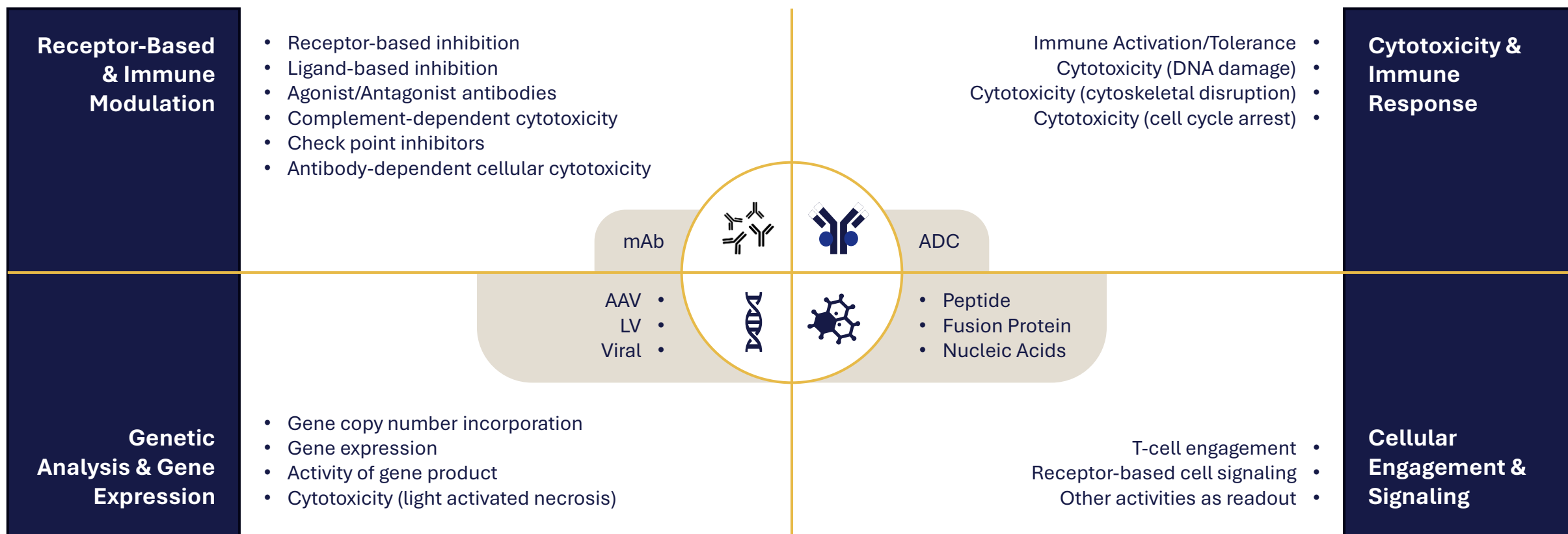
## Metabolic 04

- CellTiter-Glo® assay measures ATP as an indicator of metabolically active cells
- alamarBlue™

## Nucleic Acid 05

- Quantitative PCR (qPCR) and droplet digital PCR (ddPCR) which are used to quantify DNA or RNA from cells

# Bioassay Selection Framework for Different Biotherapeutic Formats



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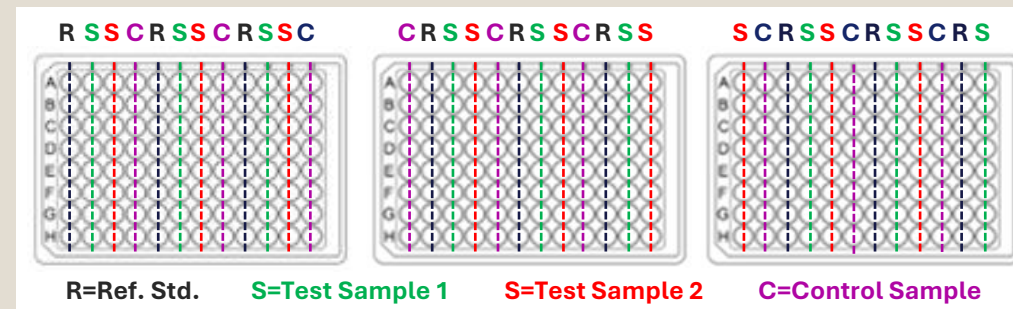


## Part 1 Cell Culturing Optimization

- Utilization of well characterized cells
- Evaluate continuous culture conversion to “thaw & use”
- Monitor critical parameters:
  - Reagents, cell viability, passage number, culture conditions & population doubling
- GMP banks produced based on mock banks:
  - Master & working banks recommended
  - Generated & tested under protocol (QA & client approved)
  - Tested for mycoplasma, bioburden & functionality

## Part 2 Assay

- Plate layout/uniformity (temperature/evaporation)
- Convert continuous culture to “thaw and use”
- Randomize distribution of replicates across plate
- Maximize throughput (horizontal vs vertical)
- Inclusion and trending assay control sample



### Pre-Validation Activities

- Performed under an agreed plan
- Involve multiple analysts/plate readers

### Phase Specific Method Validation

- Under protocol with criteria per pre-validation
- Minimum of two analysts
- Based on client needs and minimum requirements of Catalent SOPs

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# Roadmap to Validated Cell-Based Assay

## Aspects to Consider

### Sample & Reagent Management

- Sample handling
- Critical reagents
- Drug Substance/ Drug Product scope

01

### Assay Performance

- Incubation times
- Number of plates
- Assay parameters
- System suitability
- Robustness

02

### Process Control & Validation

- Locking steps
- Locking parameters
- Assay acceptance criteria
- Specifications
- Critical steps

03

### Data Integrity & Trending

- Data trending
- True ACS lot
- Specificity

04

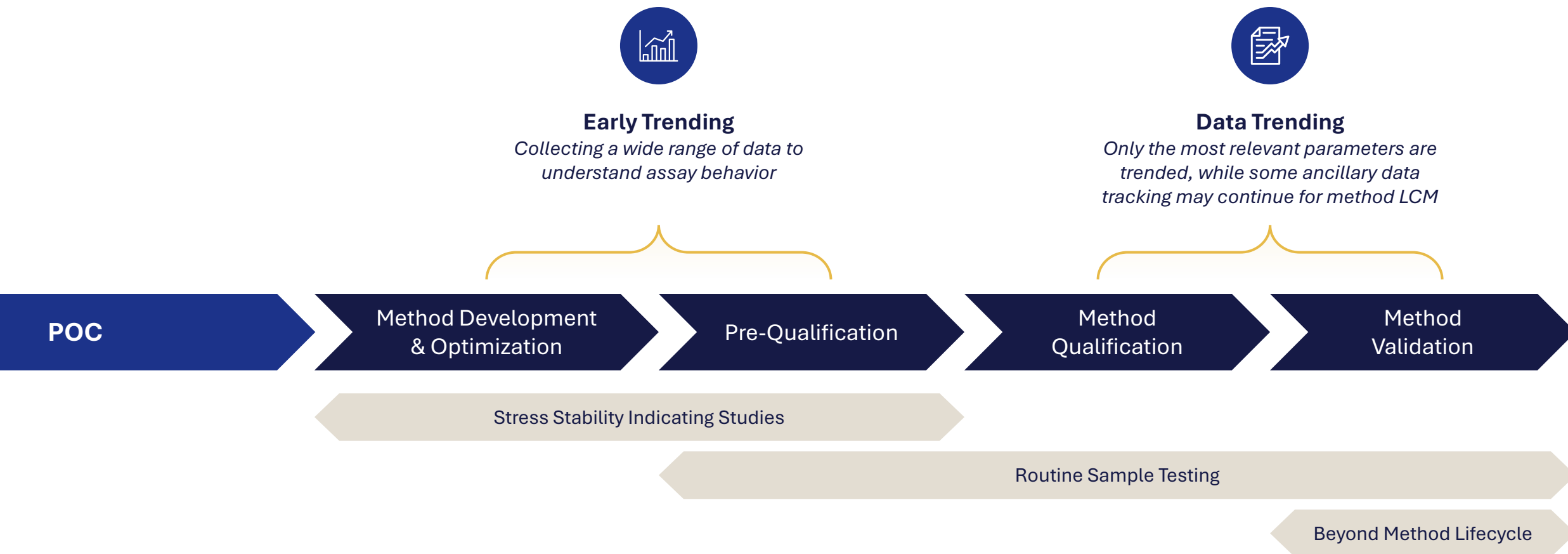
### Operator Considerations

- Training

05

# Roadmap to Validated Cell-Based Assay

From Initial POC Through Full Method Validation & Lifecycle Management (LCM)



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**05 Examples: Dose Response Curves**

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06 mRNA Transcription Assay

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07 Q&A



# Optimal Bioassay Dose Response Curves

Example

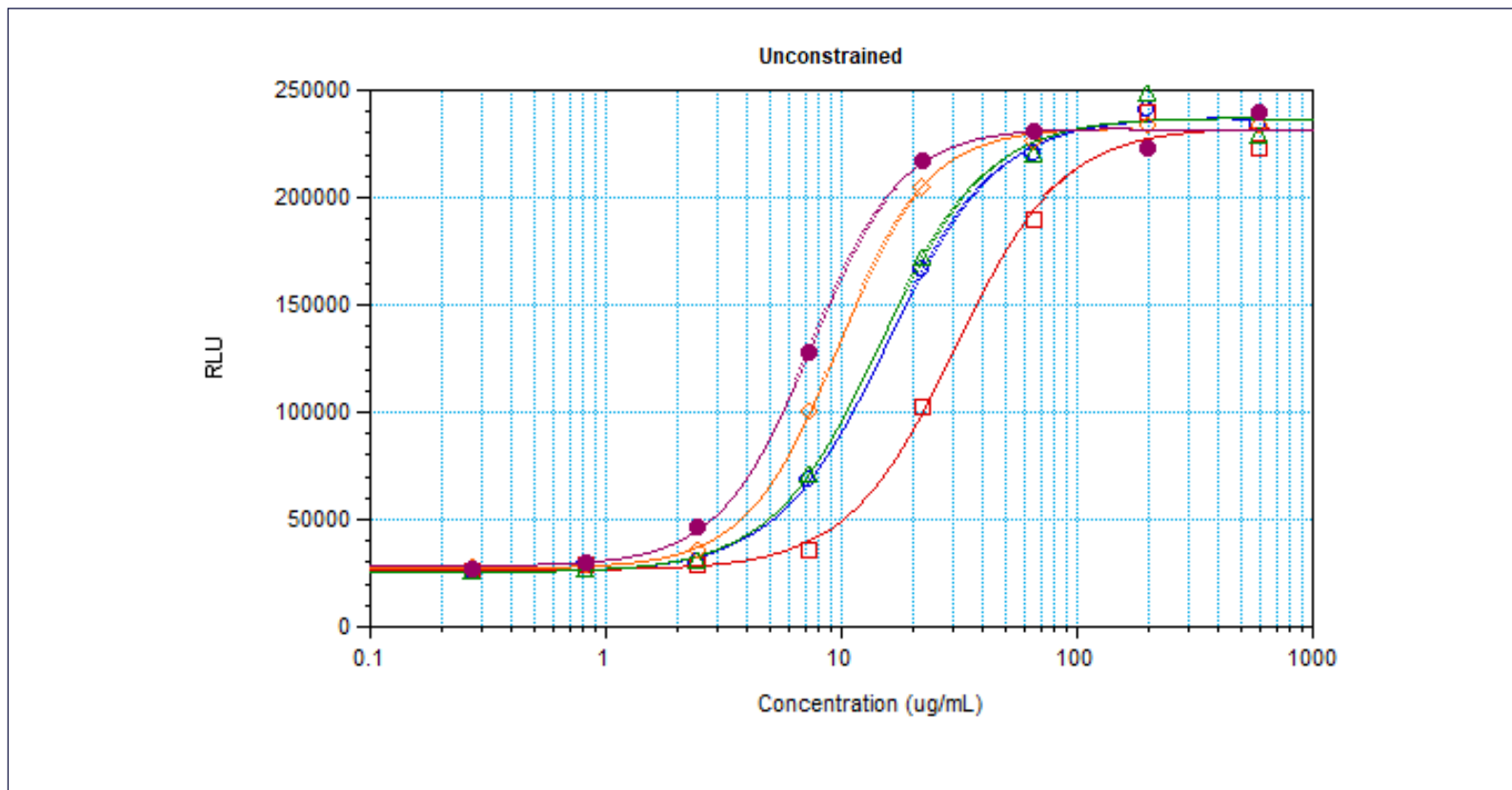


Drug dilution series generate biological responses



Accuracy/Precision across range of method

Example of well-balanced curves, with defined upper & lower asymptotes, more than one point at the linear range, good parallelism & responses across the assay range

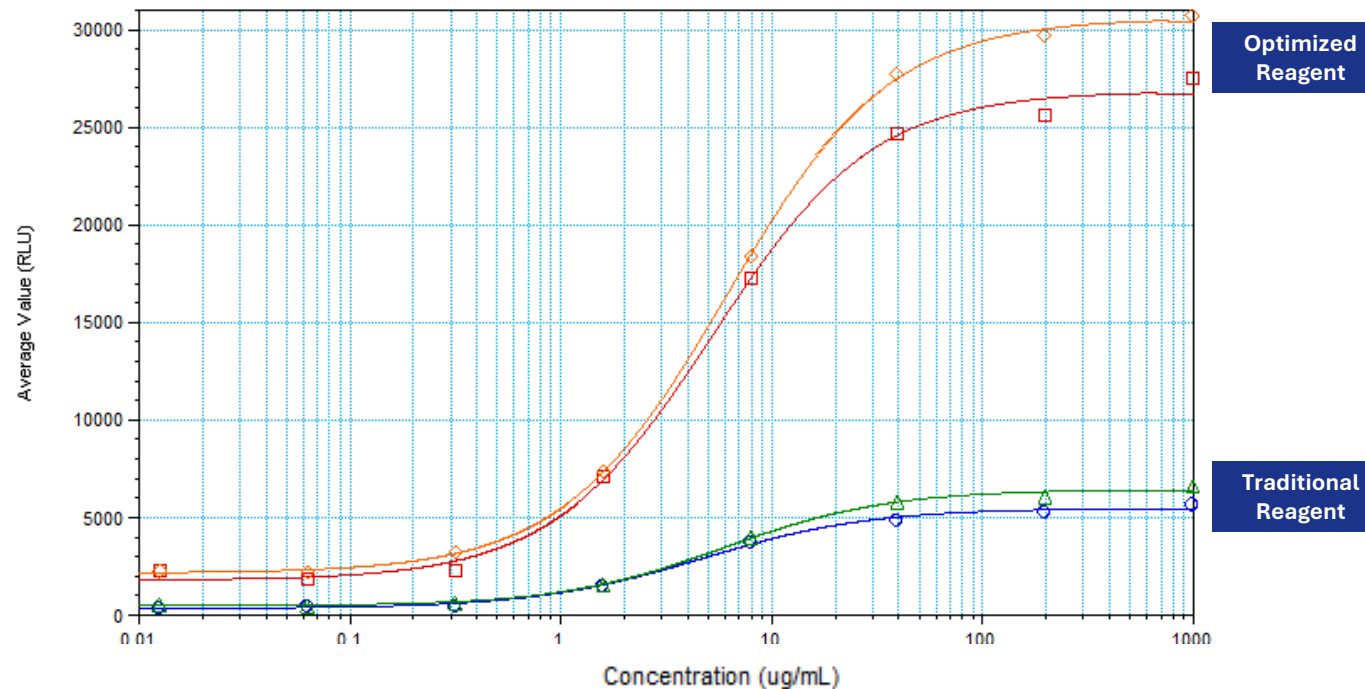


○ Ref. Std.    □ 50%    △ 100%    ◇ 150%    ● 200%

## Optimization of System Parameters

- Detection reagent choice: traditional versus optimized reagent

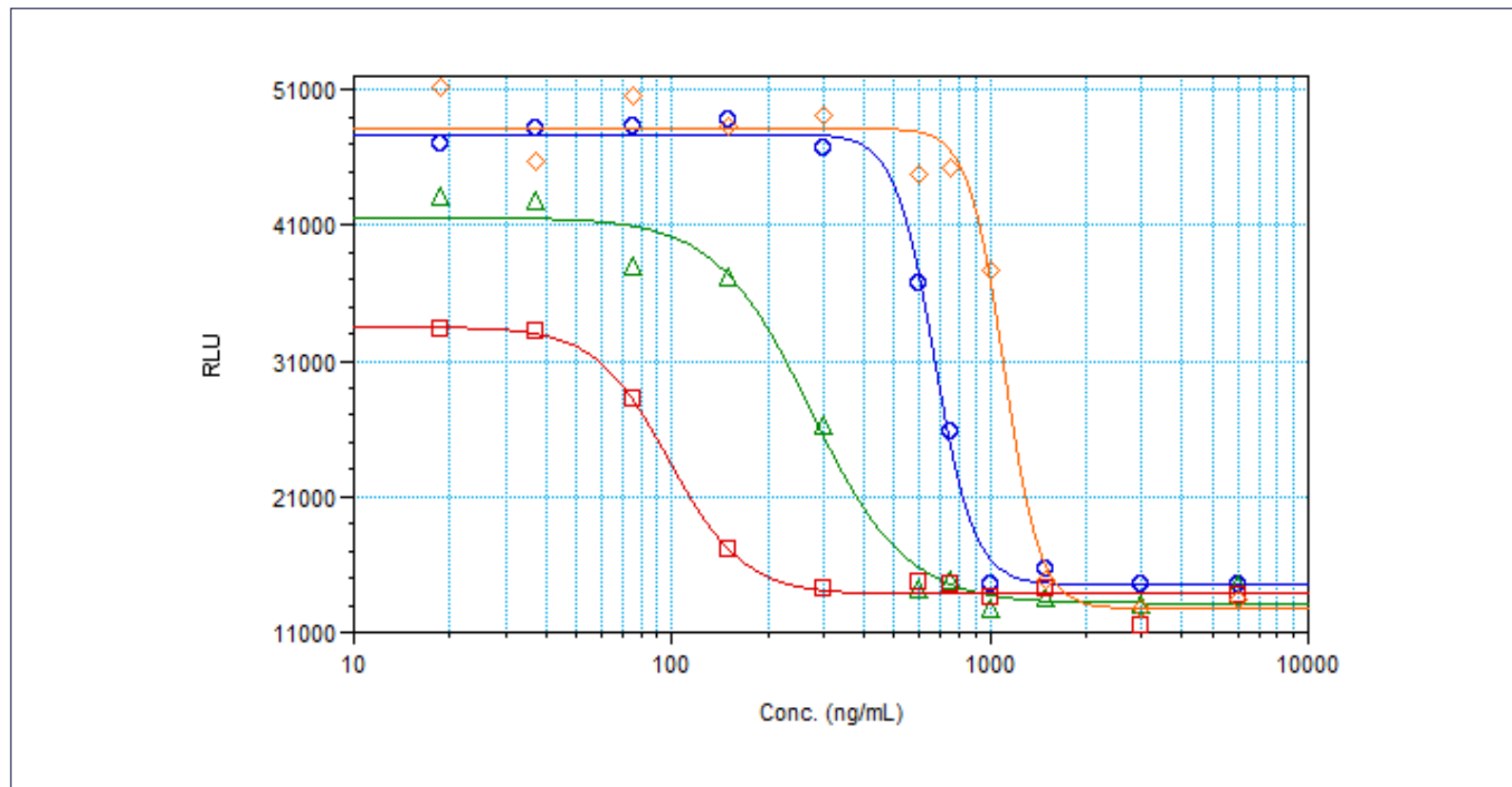
Trade-off between light intensity and duration of the signal using an optimized reagent



## Optimization of System Parameters

- mAb binds to ligand and neutralizes activity (apoptosis in this example)
- Choice of ligand concentration critical for optimal dose response

Ligand-induced cell stimulation must be evaluated for activity and not just rely on vendor's label claim concentrations

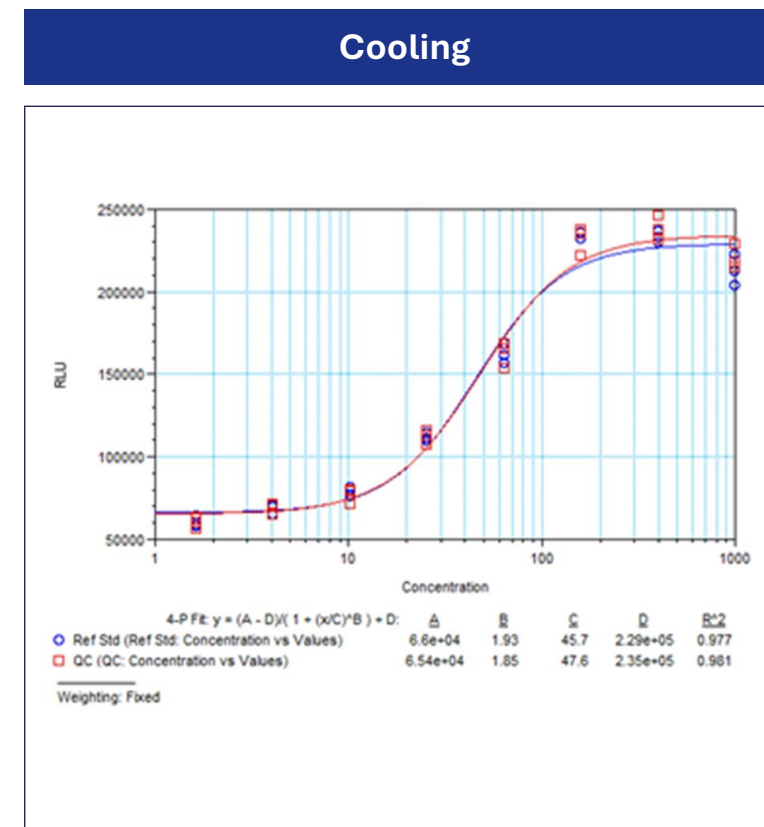
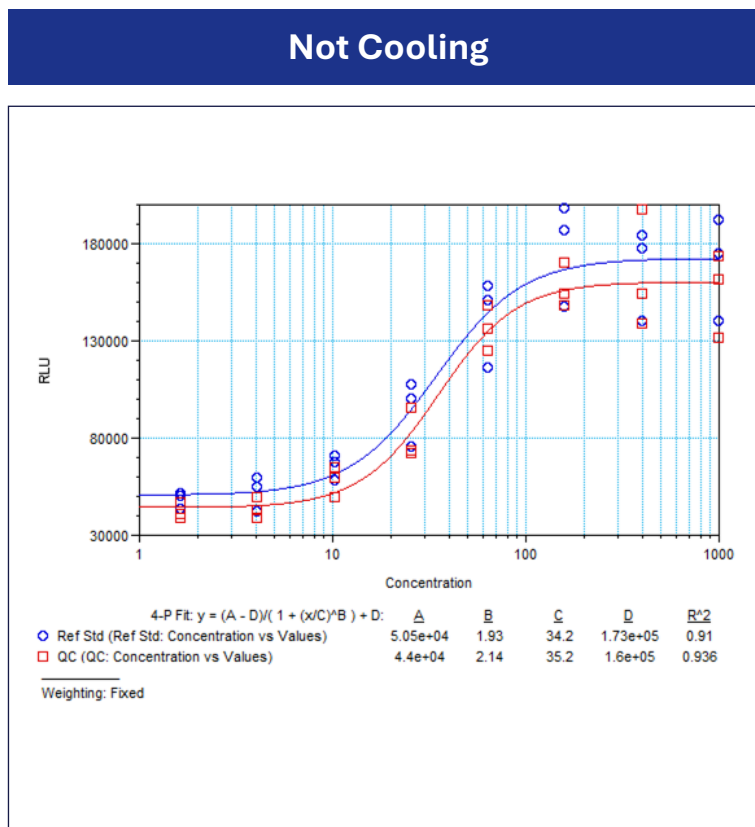


□ 100 ng/mL    △ 250 ng/mL    ○ 500 ng/mL    ◇ 1000 ng/mL

## Optimization of incubation with Luciferase substrate

- Identical dilutions used on 2 plates, one not cooled prior to substrate addition and the other cooled to RT for 15 min.
- Cooling may increase ambient O<sub>2</sub> solubility which is required during end point of reaction (Luciferase substrate requires ATP, oxygen and metallic cation).

Understanding factors potentially interfering with full reaction is important to avoid variability

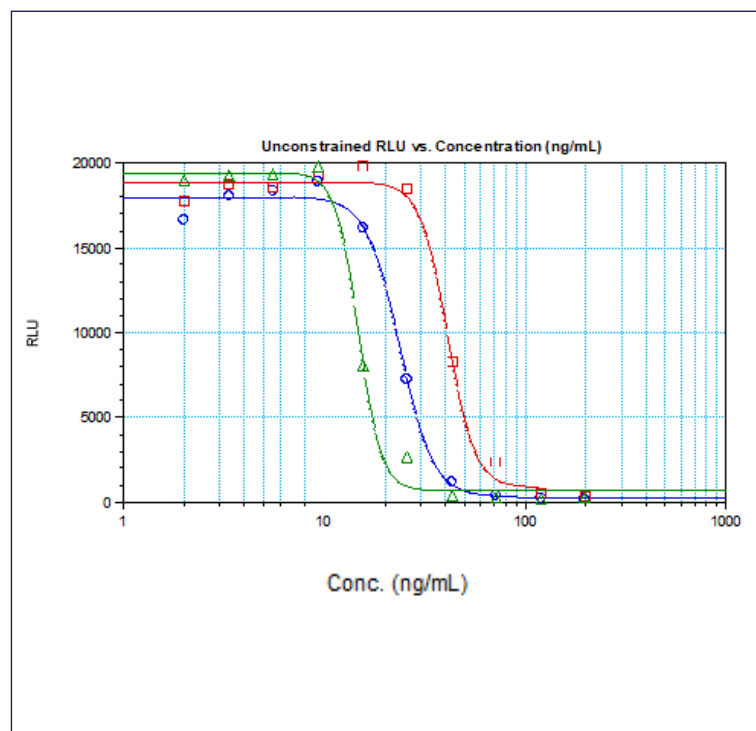


## Optimization of System Parameters

- Length of assay incubation dictated by drug MOA
- Comparison of curve shape across 3-day versus 4-day incubation

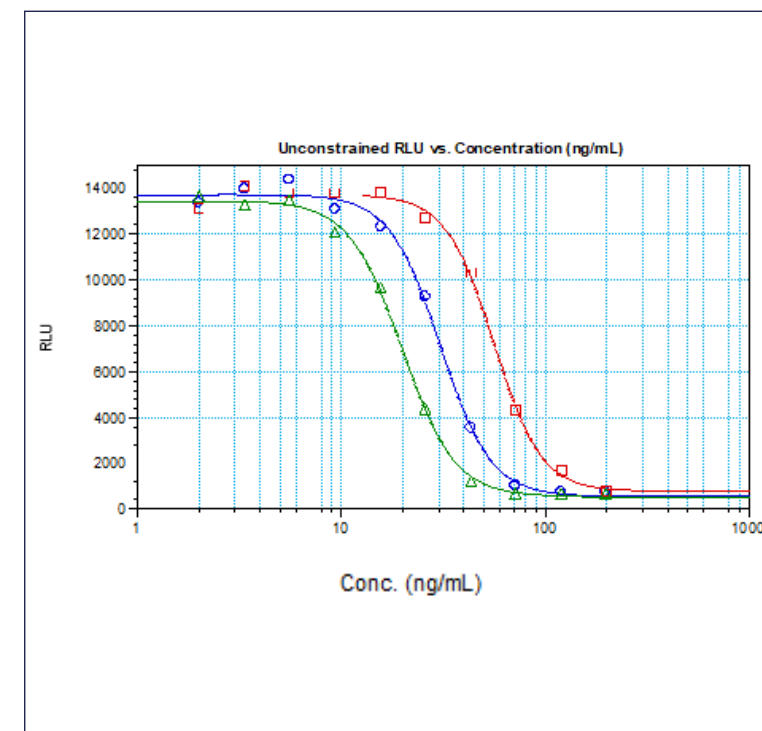
Extra day of incubation provides lesser steep curves, more points within hillslopes, preventing “cobra shapes”, improved parallelism & goodness of fit

### 3 Day



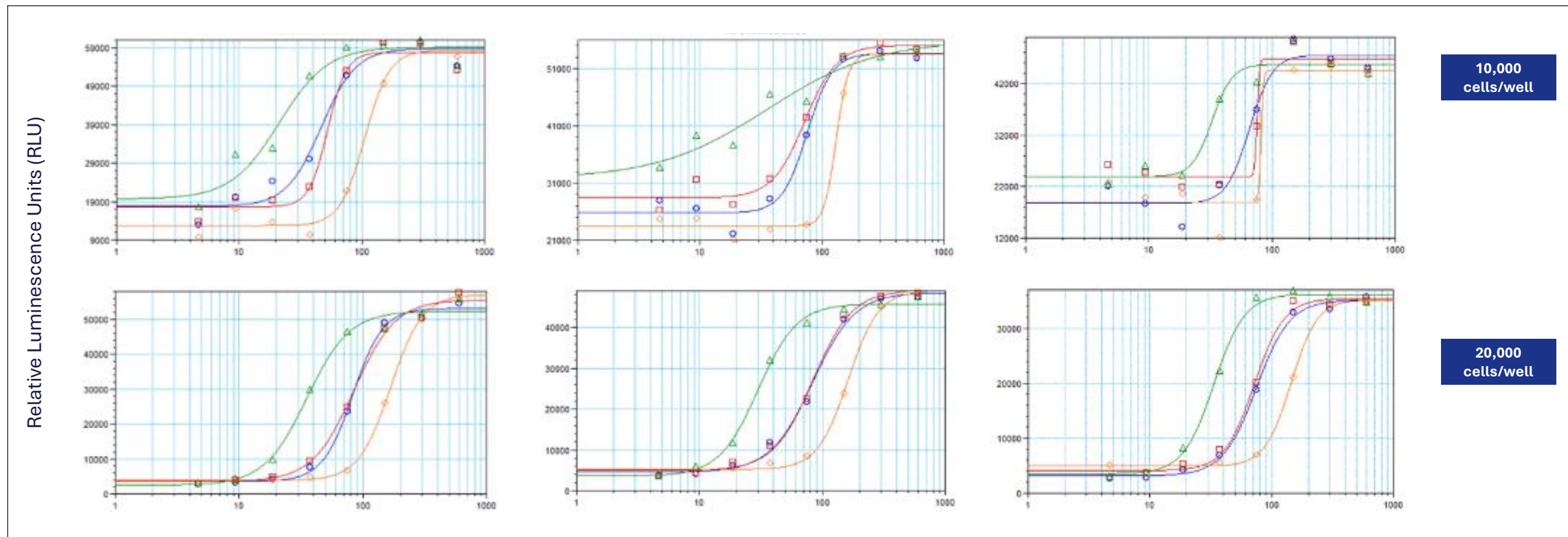
□ 50% ○ 100% △ 150%

### 4 Day



# Cell Density Comparison vs Curve Shapes

Example



10,000 cells/well

20,000 cells/well

○ Ref. Standard    □ ACS (100%)    △ TS1 (200% RS)    ◇ TS2 (50% RS)

Simple adjustment of cell density from 10,000 cells/well to 20,000 cells/well makes a difference in the response curves in terms of parallelisms & goodness of fit

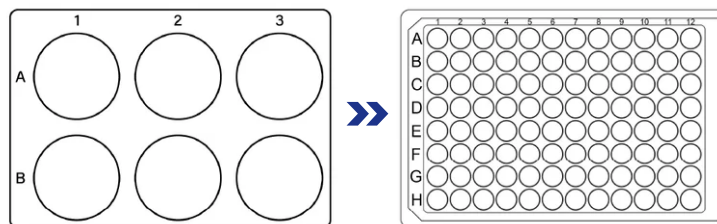
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## Challenge



Initial prototype: 6-well plate required RNA extraction before cDNA synthesis

## Limitations:

- Low throughput – Not suitable for GMP assays
- 96-well format still had RNA yield issues
- RNA extraction variability impacted assay robustness

## Solution



### ✓ Optimized direct lysis approach:

Cell lysis (~7 min)

Reverse transcription (~5 min)

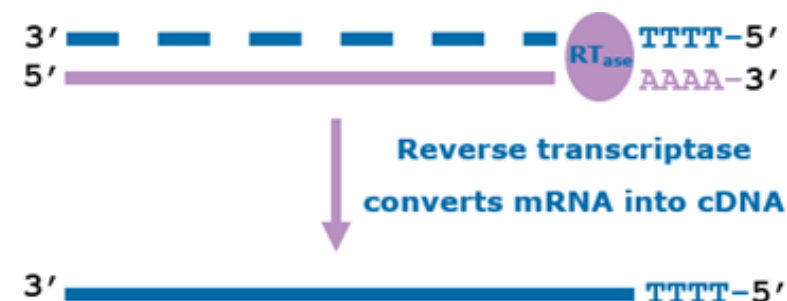
Fast real-time PCR (~35 min)

✓ No RNA extraction → Less variability

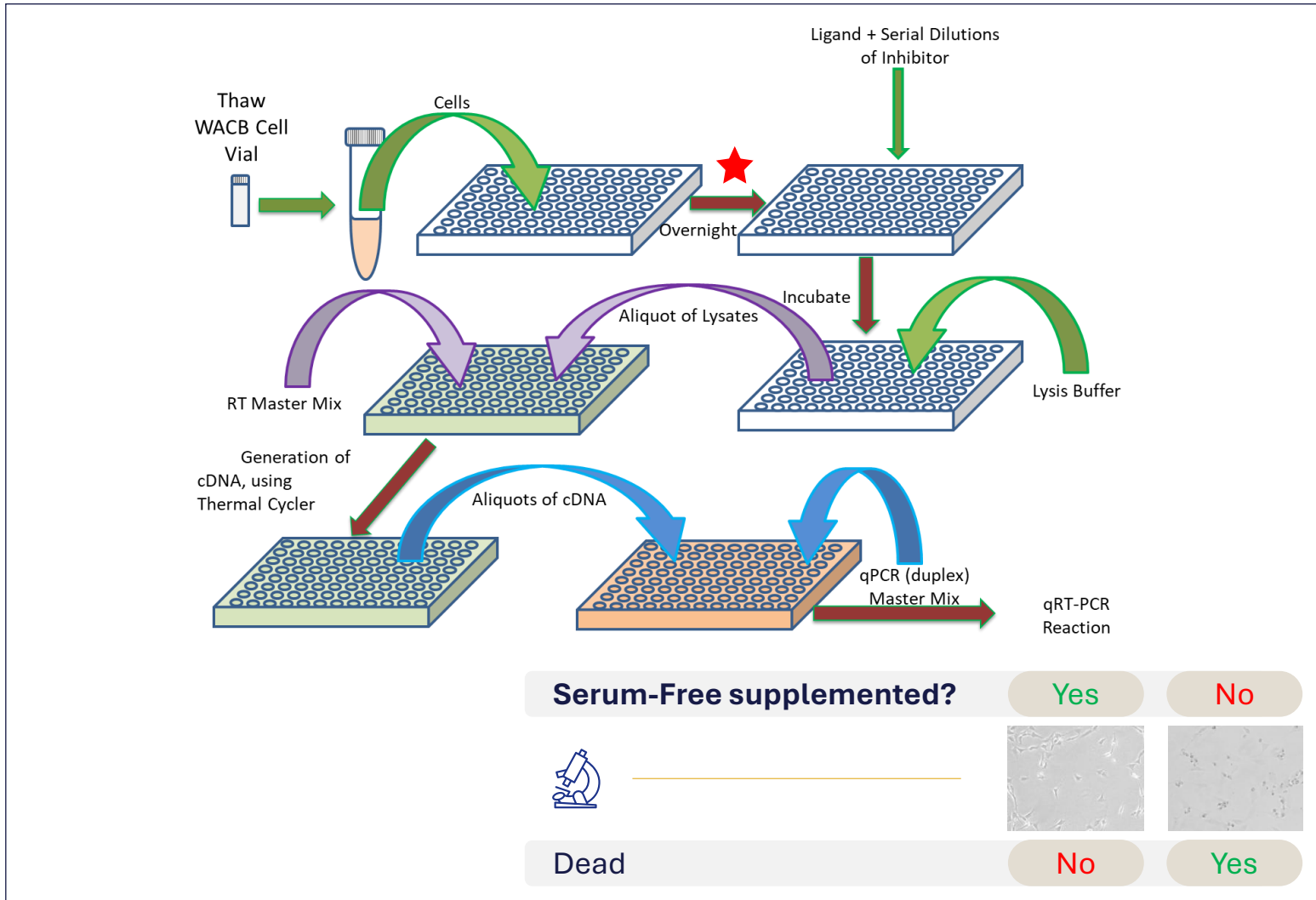
✓ Higher throughput & direct qPCR from lysates

✓ TaqMan multiplexing:

- Allows FAM (reference) vs VIC (target) for well-to-well normalization.



# Assay Schematical Overview



★ Critical step identified – cells are thawed directly on serum-free medium to allow maximization of response to ligand.

Cells previously treated with plasmid, ligand, or transgene are subjected to direct lysis



Cell lysate is subjected to reverse transcription to generate cDNA of transcript



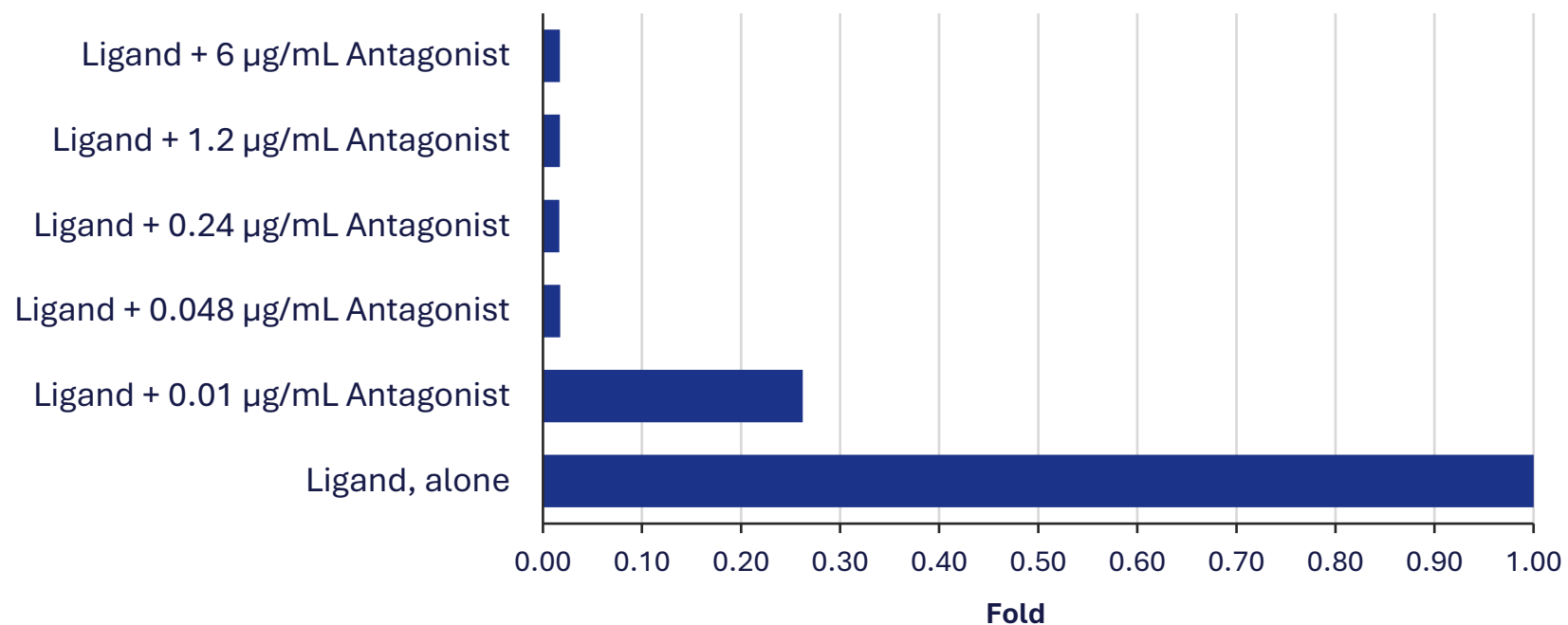
The cDNA is then placed into a qPCR duplex qPCR reaction to assess cycle threshold (C<sub>T</sub>) of the target & reference transcripts



Ligand and antagonist concentration titrated to find optimal induction concentration



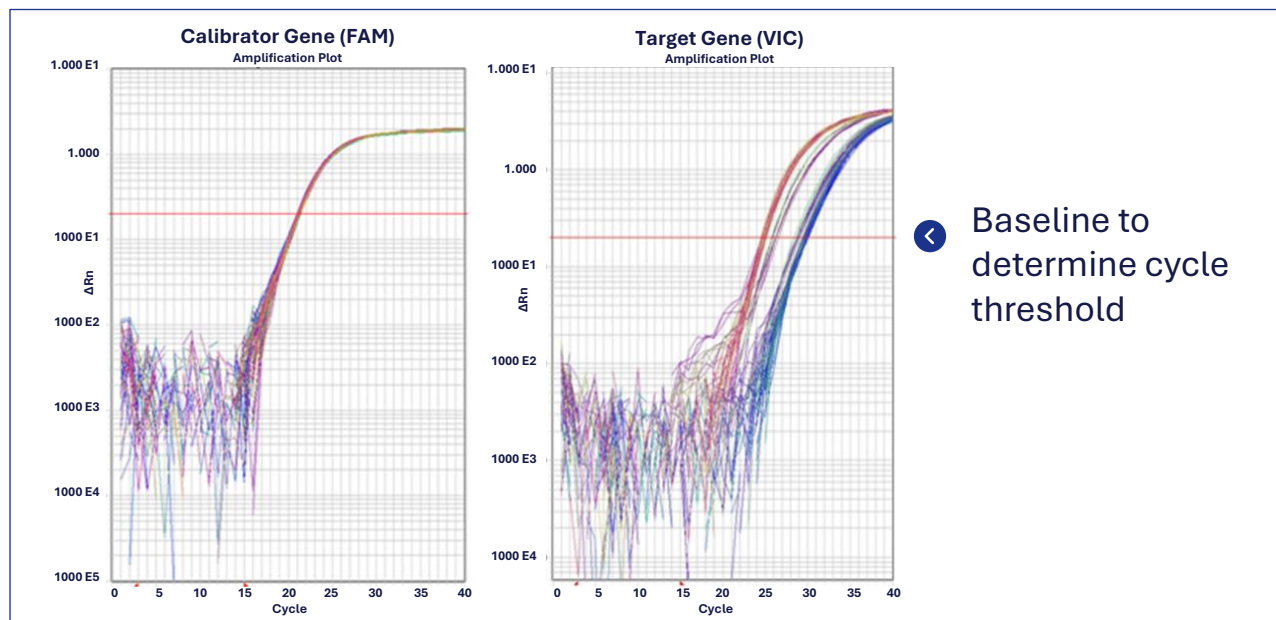
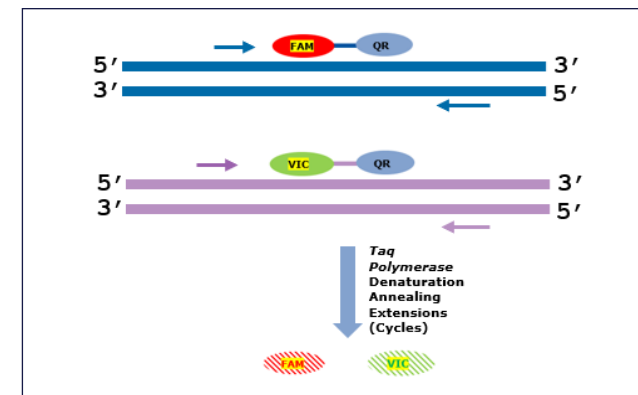
Fold-increase evaluated using  $\Delta\Delta C_T$  Analysis



Initial PoC with a limited number of data points. Ligand is tested at a fixed concentration & antagonist tested at titrated concentration to find optimal antagonistic working concentration

## Principle

- qPCR measures  $C_t$  for target (VIC) & reference (FAM) genes
- $\Delta C_t = \text{Target } C_t - \text{Reference } C_t$   
→ Plotted against ligand/vector dilution
- $\Delta C_t$  normalizes well-to-well variability for consistency



← Baseline to determine cycle threshold

## Raw Data

- Housekeeping gene (FAM) = Internal control (no treatment effect)
- Earlier  $C_t$  crossing → Higher mRNA expression
- Differential detection (FAM vs VIC) allows normalize well-to-well

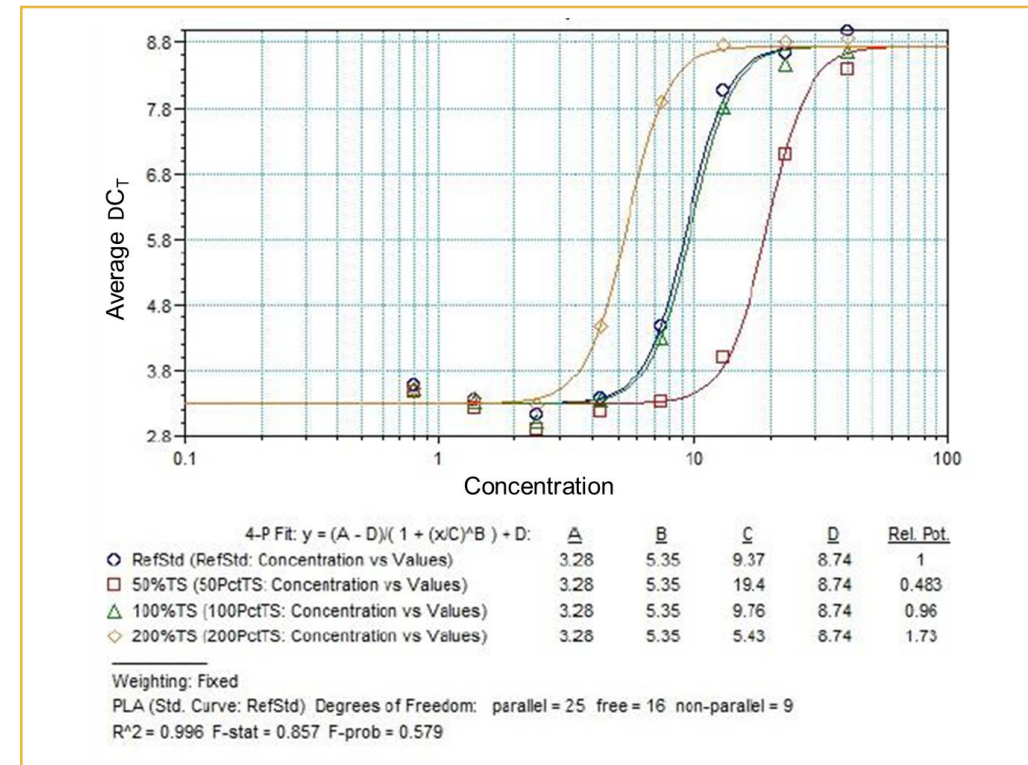
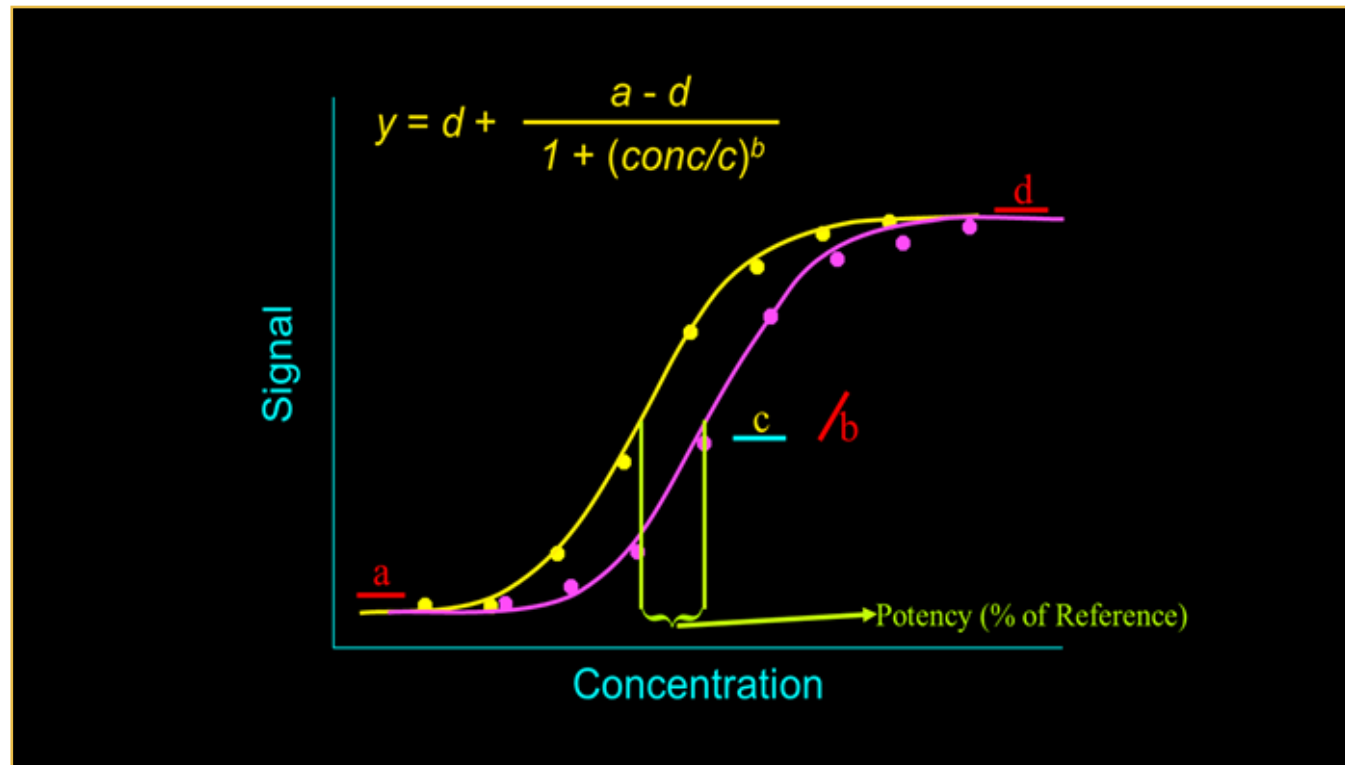


- ✓ Range of 5 concentrations/test samples tested (dilutional samples):
  - 50%, 70%, 100%, 140% and 200%

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- ✓ On each plate, all samples (in 8-point serial dilution), run as pseudo-replicates:
  - Reference standard
  - 3 independent preparations of the same test sample
  - Assay control sample

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- ✓ 3 plates run for each test sample (dilutional sample)
- ✓ 3 plates for 100% sample run by one analyst (for repeatability/intra-assay precision)
- ✓ 3 additional plates for 100% sample run by alternative analyst & combined with first three 100% sample plates (for intermediate/inter-assay precision)

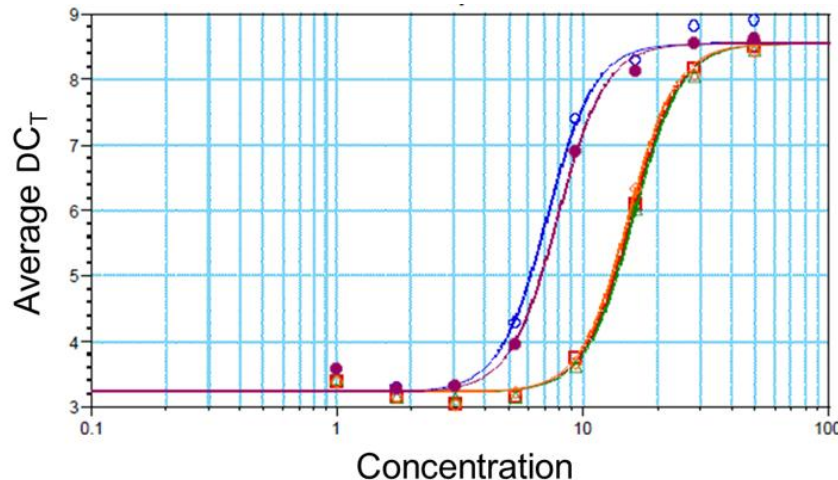
# Four Parameter Fit Analysis



ΔCT is plotted against sample concentration.  
 Plots shown are 200% and 50% of reference standard and control

# Qualification Results: Accuracy

## 50% Accuracy Level Test



4-P Fit:  $y = (A - D) / (1 + (x/C)^B) + D$

	A	B	C	D	Rel. Pot.
○ RefStd (RefStd: Concentration vs Values)	3.22	4.46	7.15	8.56	1
■ 50%TS1 (50PctTS1: Concentration vs Values)	3.22	4.46	15.8	8.56	0.453
△ 50%TS2 (50PctTS2: Concentration vs Values)	3.22	4.46	16.1	8.56	0.445
◇ 50%TS3 (50PctTS3: Concentration vs Values)	3.22	4.46	15.3	8.56	0.467
● ACS (ACS: Concentration vs Values)	3.22	4.46	7.9	8.56	0.905

Weighting: Fixed  
 PLA (Std. Curve: RefStd) Degrees of Freedom: parallel = 32 free = 20 non-parallel = 12  
 R<sup>2</sup> = 0.997 F-stat = 0.826 F-prob = 0.624

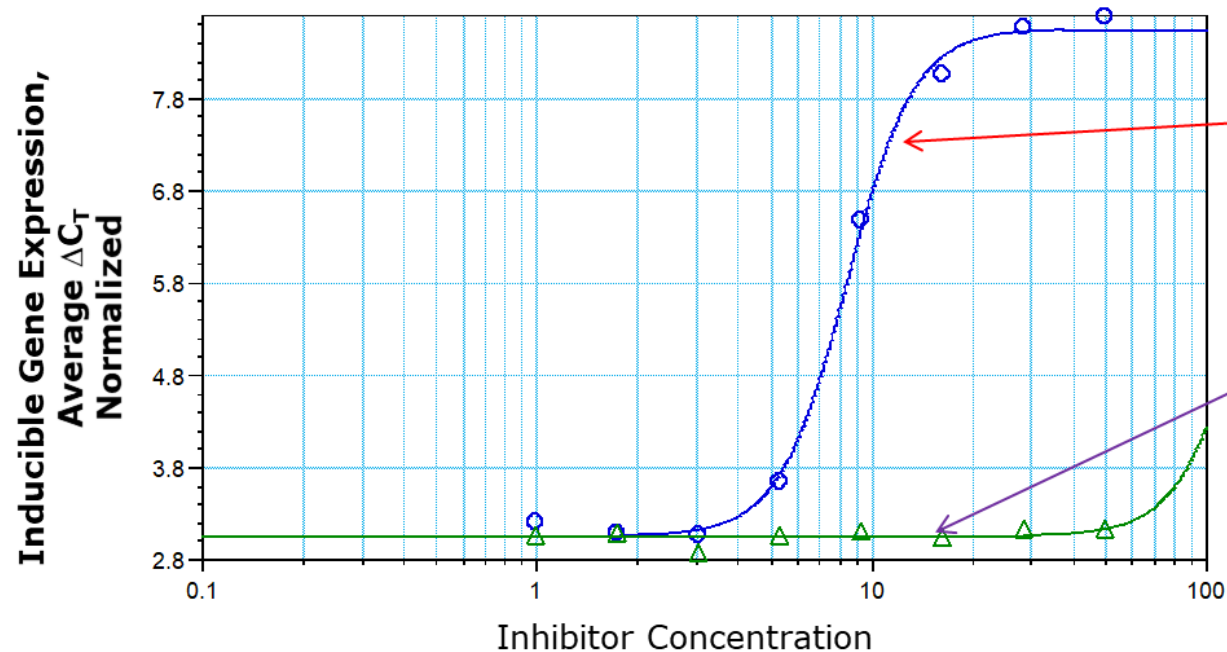
Expected Potency (% Relative Potency)	Observed Potency (% Relative Potency)	Accuracy (% of expected)
50	46.7	93%
70	66.0	94%
100	100.2	100%
140	142.0	101%
200	175.1	88%

# Qualification Results: Precision

	Reportable Potency Values (Mean of 3 independent values from same plate)	Averaged Values across the three plates	Intra-Assay (Repeatability) Precision	Inter-Assay (Intermediate) Precision
Analyst # 1	104.3	100.2	3.3%	4.4%
	100.1			
	96.3			
Analyst #2	103.4	103.2		
	109.3			
	96.9			

Repeatable results with high precision

# Qualification Results: Specificity



4-P Fit:  $y = (A - D)/(1 + (x/C)^B) + D$ :

	<u>A</u>	<u>B</u>	<u>C</u>	<u>D</u>	<u>Rel. Pot.</u>
● RS (RS: Concentration vs Values)	3.05	4.3	8.42	8.55	1
▲ TS (TS - Rep 2: Concentration vs Values)	3.05	4.3	135	8.55	0.0624

# These Assays Are Most Powerful When Integrated Into Broader Bioanalytical Workflows



Fits into overall assay panel for products



Powerful when used in conjunction with orthogonal assays

e.g., flow cytometry, mass spectrometry



Can evaluate performance of genes that impact metabolites

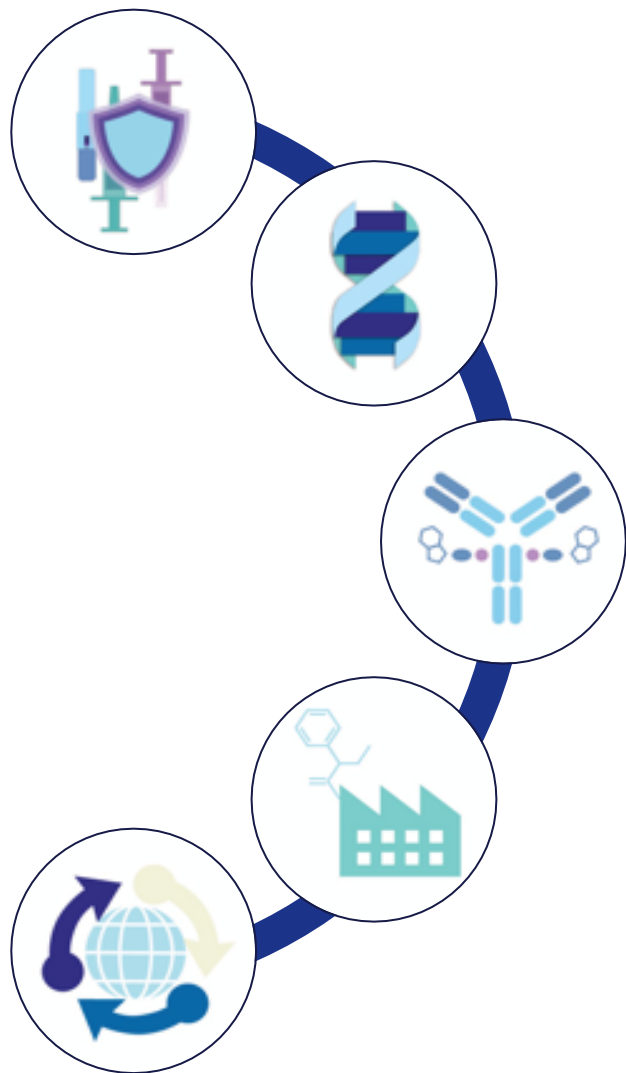
e.g., carbohydrates, proteoglycans, lipids



Can be used when gene products are difficult to quantify and coupled with sequencing could be used to verify gene expression editing



# Conclusion



↘  
Assess response  
at mRNA  
transcription

↘  
No variability  
due to RNA  
extraction &  
purification

↘  
Well-by-well  
normalization  
results in better  
precision

↘  
Assay has been  
successfully  
qualified

↘  
Assay is accurate  
and precise  
and suitable for  
cGMP use

↘  
Additional tool for  
gene therapy with  
potential to  
conversion to  
ddPCR/dPCR

# Thank you

Any questions?



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Account Director

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Tomorrow, 4/29 @ 12:00 PM  
Salons D-G

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# Comparison With Other Bioassay Readout Types

	<b>mRNA Transcriptional Assay by qPCR</b>	<b>Reporter Gene Assays</b>
<b>Advantages</b>	<p>Evaluates the mRNA expression of endogenous or exogenously introduced genes</p> <hr/> <p>Because amplification is involved, it is more sensitive to differences in response</p> <hr/> <p>Allows for analysis of transfected, transduced or edited gene activity</p>	<p>Evaluates response to ligand directly (reporter)</p> <hr/> <p>Options for off-the-shelf cell lines available</p> <hr/> <p>Evaluates functionally by product</p>
<b>Limitations</b>	<p>Analysis requires further transformation of raw data</p>	<p>Requires genetic engineering of cell line of interest</p>

# Context for CGT Assays

	ddPCR	mRNA Transcriptional Assay by qPCR	Flow Cytometry
Advantages	<p>Assess absolute gene copy number</p> <p>No standard curve required</p>	<p>Assess inserted or transferred gene construct functionality</p> <p>Verification of cell transcriptional activity</p>	<p>Evaluates translational activity</p> <p>Determines population of cells expressing transgene</p>
Limitations	<p>Low dynamic range</p> <p>Unable to indicate if gene construct is inserted functionally</p>	<p>Requires normalization using a housekeeping gene</p> <p>Multi-step assay</p>	<p>No amplification detectability limitations</p> <p>Could be difficult to standardize</p>