Compare your current probe-based mix with TaqMan Fast Advanced Master Mix

Assess performance in your research workflow using a simple side-by-side serial dilution experiment for gene expression analysis

What to evaluate

Efficiency
Calculated from the standard curve slope

Linearity
R^2 value across the dilution series

Precision
Replicate C_t consistency at each dilution

Sensitivity
Lowest input with reproducible detection

General guidelines

- Consider testing multiple assays across a range of expression levels
- Use the manufacturer's recommended assay, template, and cycling conditions
- Keep plate format, reaction volume, and analysis settings consistent where possible
- Include a no-template control for each assay
- For duplex evaluation, confirm singleplex performance first
- Run reactions in triplicate to measure precision

Step 1: prepare a dilution series

Prepare a 10-fold dilution series from a single complementary DNA (cDNA) sample source. For comparison, the same dilution point can be used for all assays. This example provides enough volume to run one dilution point in triplicate for each real-time PCR (qPCR) assay mix, for up to four assay mixes (see diagram on page 2).

Dilution	Template	Nuclease-free water
Undiluted	100 µL cDNA template	-
10^{-1}	10 µL of undiluted	90 µL
10^{-2}	10 µL of 10^{-1}	90 µL
10^{-3}	10 µL of 10^{-2}	90 µL
10^{-4}	10 µL of 10^{-3}	90 µL
10^{-5}	10 µL of 10^{-4}	90 µL

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Step 2: set up the reactions

The reaction setup below uses a 20X Applied Biosystems™ TaqMan™ Assay (primer and probe) format in a 96-well plate with a 20 µL reaction volume. For other primer/probe assay formats, follow the manufacturer's recommended setup.

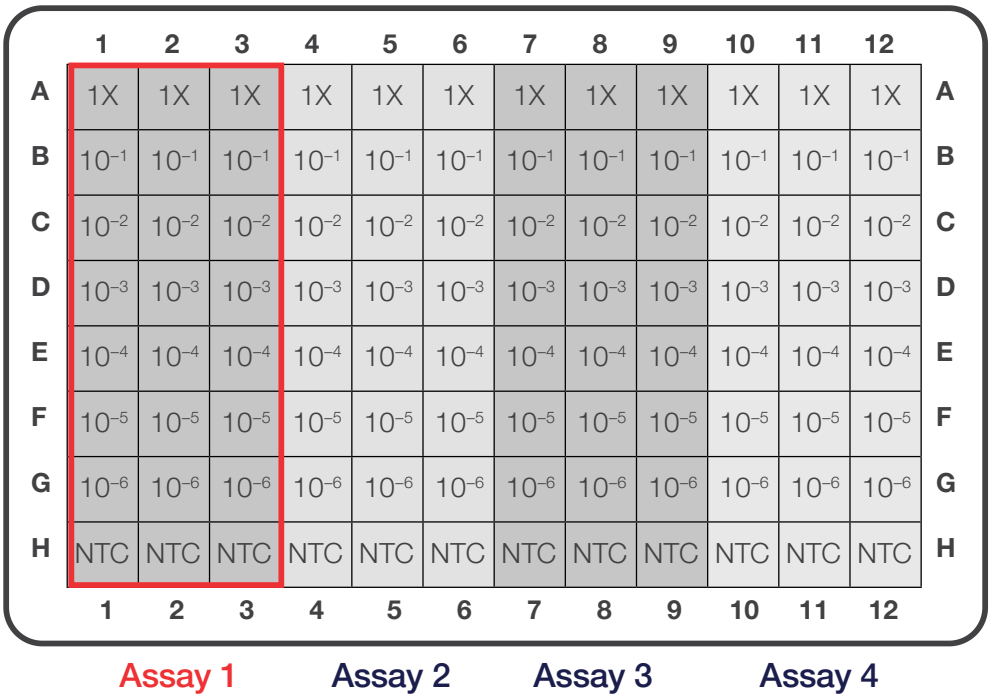
1. For the first assay, use the table below to prepare enough Applied Biosystems™ TaqMan™ Fast Advanced Master Mix reaction mix for 26 reactions (20 µL each). Mix thoroughly.

Component	Volume for 26 reactions
TaqMan Fast Advanced Master Mix (2X)	260 µL
Assay 1 (20X)	26 µL
Nuclease-free water	130 µL
Total volume	**416 µL**

Note: for 10 µL reactions in a 384-well plate, reduce all volumes by half.

2. Pipette 15 µL of the reaction mix containing TaqMan Fast Advanced Master Mix into the appropriate wells of a 96-well optical plate, according the plate map below.

3. Add 5 µL of each template dilution from step 1 into the appropriate wells, according to the plate map below. For no-template control (NTC) reactions, use 5 µL of nuclease-free water.



4. Repeat steps 1–3 for any additional qPCR mixes, up to four assays per plate.

5. Seal the plate, then briefly centrifuge.

6. Start your qPCR run.

7. If comparing performance to another master mix, repeat steps 1–6 using the other master mix and a new plate.

Step 3: run qPCR

Run each plate according to the cycling conditions provided in the reagent user documentation.

Fast cycling conditions for TaqMan Fast Advanced Master Mix

Step	Temperature	Time	Cycles
Optional UNG incubation	50°C	2 min	Hold
Polymerase activation	95°C	20 sec	Hold
Denaturation	95°C	1 sec	40x
Anneal/extend	60°C	20 sec	

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Will these cycling conditions work with my qPCR instrument?

The TaqMan Fast Advanced Master Mix user guide provides these cycling conditions as a starting point for most instruments, including Bio-Rad™ CFX Opus 96 and Roche™ LightCycler™ PRO systems.

Cycling conditions can vary by assay and instrument, so refer to the appropriate user documentation as needed.

Will the Applied Biosystems™ ROX™ dye in TaqMan Fast Advanced Master Mix affect the accuracy of my results?

TaqMan Fast Advanced Master Mix contains ROX dye as a passive reference. Some systems, such as Bio-Rad and Roche qPCR systems, do not use ROX dye for passive reference normalization.

If you are used to using a master mix without ROX dye, you may notice differences in C_t value or baseline signal. Evaluate efficiency, precision, linearity, and analytical sensitivity rather than relying on C_t value alone.

Refer to your instrument and analysis software documentation for dye compatibility and normalization settings.

Step 4: analyze the results

Review the standard curve in your analysis software to identify the slope of the standard curve, efficiency, R^2, and replicate C_t values. Refer to your software documentation for analysis instructions.

Efficiency

Review the efficiency value calculated by your analysis software from the slope of the standard curve. Values between 90–110% are generally acceptable.

Precision

Review the standard deviation (SD) of technical replicate C_t values at each dilution. Lower SD values indicate better replicate agreement, and SD ≤0.250 is generally acceptable.

Linearity

Review the R^2 value for the standard curve across the dilution series. Values closer to 1.0 indicate better linearity, and R^2 >0.99 is generally acceptable.

Analytical sensitivity

Review the dilution series to identify the lowest dilution with reproducible amplification across replicates.

Don't be misled by lower C_t values alone. Review the full dilution series and use the evaluation scorecard on the next page to compare results.

Evaluation scorecard

Use the scorecard below to compare performance for each assay across both qPCR mixes. When reviewing the dilution series, note that the usable dynamic range is defined by the portion of the dilution series where both amplification efficiency and linearity remain acceptable.

Tip: use the “Notes” column to capture observations from the dilution series, including the range where efficiency and linearity remain acceptable, replicate variability, or any setup or analysis issues.

Assay		Efficiency (%)	Linearity (R^2)	Precision (SD)	Analytical sensitivity	Notes
1	Current mix					
	TaqMan Fast Advanced Master Mix					
2	Current mix					
	TaqMan Fast Advanced Master Mix					
3	Current mix					
	TaqMan Fast Advanced Master Mix					
4	Current mix					
	TaqMan Fast Advanced Master Mix					

Finished your evaluation? Choose your next step

Complete the evaluation survey

Tell us how the master mix performed and request specialist follow-up for quote support (optional).

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TaqMan Fast Advanced Master Mix

Cat. Nos.: 4444556, 4444557, 4444558, 4444963, 4444964, 4444965

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