**PROTOCOL** 

# Guidelines for comparing SYBR Green master mixes

Take the master mix challenge—compare your current master mix to Applied Biosystems™ PowerUp™ SYBR™ Green Master Mix using this simple protocol. In our own experiments, we found that PowerUp SYBR Green Master Mix outperformed other master mixes when comparing specificity, PCR efficiency, dynamic range, and precision over multiple targets.

This protocol is for the comparison of PowerUp SYBR Green Master Mix to one other master mix using  $20 \,\mu\text{L}$  reactions in triplicate. Adjust volumes as needed.

### **Reaction preparation**

1. Prepare 10-fold dilution series of template.

| Dilution         | Template                 | Nuclease-free water |
|------------------|--------------------------|---------------------|
| Undiluted        | 40 μL of 20 ng/μL DNA    | -                   |
| 10-1             | 4 μL of undiluted DNA    | 36 µL               |
| 10-2             | 4 μL of 10 <sup>-1</sup> | 36 µL               |
| 10-3             | 4 µL of 10 <sup>-2</sup> | 36 µL               |
| 10-4             | 4 μL of 10 <sup>-3</sup> | 36 µL               |
| 10 <sup>-5</sup> | 4 μL of 10 <sup>-4</sup> | 36 μL               |
| 10-6             | 4 μL of 10 <sup>-5</sup> | 36 µL               |

## **General guidelines**

- Use the manufacturer's recommended primer and template DNA concentrations
- Use the manufacturer's recommended thermal cycling parameters
- Run a standard curve to compare PCR efficiency, sensitivity, dynamic range, and precision
- Run reactions in triplicate to measure reproducibility
- Perform a melt curve to analyze specificity
- 2. Prepare enough master mix for 26 x 20  $\mu$ L reactions for each qPCR master mix to be tested, according to the volumes in the table below. Mix thoroughly.

| Component             | PowerUp SYBR Green Master Mix | Master mix for comparison     |
|-----------------------|-------------------------------|-------------------------------|
| qPCR master mix, 2X   | 260 μL                        | 260 μL                        |
| Forward primer, 10 µM | 26 μL*                        | Manufacturer's recommendation |
| Reverse primer, 10 µM | 26 μL*                        | Manufacturer's recommendation |
| Nuclease-free water   | 78 μL (final volume 390 μL)   | Adjust to 390 μL              |

<sup>\*</sup> Volumes shown are for 500 nM primer. The recommended primer concentration for PowerUp SYBR Green Master Mix is 300-800 nM.



- 3. Pipet 15 µL of the PowerUp SYBR Green mix prepared in step 2 to each well of a 96-well optical plate according to the plate map below.
- 4. Pipet 5 μL of the indicated dilution from step 1 into each well of the plate according to the plate map below. For notemplate control (NTC) reactions, use 5 μL of nuclease-free water.

|   | 1 | 2 | 3 | 4 | 5         | 6         | 7         | 8 | 9 | 10 | 11 | 12 |
|---|---|---|---|---|-----------|-----------|-----------|---|---|----|----|----|
| Α |   |   |   |   | Undiluted | Undiluted | Undiluted |   |   |    |    |    |
| В |   |   |   |   | 10-1      | 10-1      | 10-1      |   |   |    |    |    |
| С |   |   |   |   | 10-2      | 10-2      | 10-2      |   |   |    |    |    |
| D |   |   |   |   | 10-3      | 10-3      | 10-3      |   |   |    |    |    |
| Е |   |   |   |   | 10-4      | 10-4      | 10-4      |   |   |    |    |    |
| F |   |   |   |   | 10-5      | 10-5      | 10-5      |   |   |    |    |    |
| G |   |   |   |   | 10-6      | 10-6      | 10-6      |   |   |    |    |    |
| Н |   |   |   |   | NTC       | NTC       | NTC       |   |   |    |    |    |

- 5. Repeat steps 3–4 for the other master mix to be compared, using a new plate. Reactions can be loaded on the same plate if the thermal protocols are identical.
- 6. Mix the components thoroughly. Seal the plates, and briefly centrifuge to remove any bubbles.

#### **Real-time PCR**

- 1. Place the plate in the instrument.
- 2. Set the thermal cycling conditions.
  - For PowerUp SYBR Green Master Mix, use one of the following conditions:
  - Standard cycling (for most instruments and primer T<sub>m</sub> ≥60°C)

| Step                  | Temperature | Time   | Cycles |
|-----------------------|-------------|--------|--------|
| UDG activation        | 50°C        | 2 min  | Hold   |
| Polymerase activation | 95°C        | 2 min  | Hold   |
| Denaturation          | 95°C        | 15 sec | 40     |
| Annealing/extension   | 60°C*       | 1 min  | 40     |

 $<sup>^{*}</sup>$  For primers with  $T_{m}$  <60°C, please refer to the PowerUp SYBR Green Master Mix instruction manual.

Fast cycling (for Applied Biosystems<sup>™</sup> ViiA<sup>™</sup> 7, QuantStudio<sup>™</sup>, 7500 Fast, StepOne<sup>™</sup>, and StepOnePlus<sup>™</sup> instruments and primer T<sub>m</sub> ≥60°C)

| Step                  | Temperature | Time                     | Cycles |  |
|-----------------------|-------------|--------------------------|--------|--|
| UDG activation        | 50°C        | 2 min                    | Hold   |  |
| Polymerase activation | 95°C        | 2 min                    | Hold   |  |
| Denaturation          | 95°C        | 1* or 3 <sup>†</sup> sec | 40     |  |
| Annealing/extension   | 60°C‡       | 30 sec                   | 40     |  |

<sup>\*</sup> For ViiA 7 or QuantStudio instruments.

<sup>&</sup>lt;sup>†</sup> For 7500 Fast, StepOne, or StepOnePlus instruments.

 $<sup>^{\</sup>ddagger}$  For primers with  $T_m$  <60°C, please refer to the PowerUp SYBR Green Master Mix instruction manual.

• Include conditions for melt curve analysis after the PCR stage. On Applied Biosystems™ instruments, use the default continuous melt curve setting, which on most newer instruments are:

| Stage            | Step                  | Ramp rate  | Temperature | Time   |
|------------------|-----------------------|------------|-------------|--------|
|                  | Step 1                | 1.6°C/sec  | 95°C        | 15 sec |
| Melt curve stage | Step 2                | 1.6°C/sec  | 60°C        | 1 min  |
|                  | Step 3 (dissociation) | 0.15°C/sec | 95°C        | 15 sec |

• For Applied Biosystems instruments, use the following settings:

Experiment type: Standard curve

Reagent: SYBR Green reagents

Reporter: SYBR Quencher: None Passive reference dye: ROX™

Ramp speed: Standard or Fast (choose the corresponding thermal cycler profiles in step 2 above)

Melt curve ramp increment: Continuous

See the instrument instruction manual for more information or if using a different instrument.

3. Run the plate. Repeat the run setup for the other master mix being tested using the manufacturer's recommended thermal cycling profile.

#### **Data analysis**

In most qPCR systems, the data can be analyzed by the qPCR system software.

Slope and amplification efficiency: The amplification efficiency is calculated using the slope of the regression line of the standard curve. A slope of -3.323 indicates optimal 100% PCR amplification efficiency. Reactions with efficiencies of 100%  $\pm10\%$  over a broad dynamic range are needed to reliably use the  $\Delta\Delta C_{\rm t}$  method for gene expression analysis.

**Caution:** Don't be fooled by lower C<sub>t</sub> values when comparing master mixes. The only way to compare the sensitivity and performance of two master mixes is by performing a dilution series and examining the amplification efficiency, linearity, and precision across the dilution range.

 $R^2$  value (correlation coefficient): The  $R^2$  value is a measure of the closeness of fit between the regression line and the individual  $C_t$  data of the standard curve reactions. A value of 1.00 indicates a perfect fit between the regression line and the data. An  $R^2$  value >0.99 is desirable.

**Standard deviation (precision):** Calculate the standard deviation of the  $C_t$  values for each dilution. To be able to quantify a 2-fold dilution with  $\geq$ 95% confidence, the standard deviation of a dilution should be  $\leq$ 0.250.

**Melt curve (specificity):** View the melt curve using a derivative reporter plot (a plot of derivative reporter (–Rn) vs. temperature). A single peak indicates specific amplification, whereas multiple peaks or shoulders indicate nonspecific amplification or primer-dimer formation.

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