# SYBR Green Fast qPCR Mix (2X)

ORIGENE EMPOWER YOUR RESEARCH

Catalog: NP100055

Size: 5 ml Components:

SYBR Green Fast qPCR Mix (2X)

50X ROX Reference Dye I

50X ROX Reference Dye II

#### Introduction

Real-time Quantitative PCR (qPCR) is a powerful technique in detecting initial DNA input in a PCR reaction by fluorescence signal accumulation. OriGene's SYBR Green Fast qPCR Mix (2X) is a fluorescence reagent for qPCR reactions using the SYBR® Green I. This product provides real-time data on DNA amplification during PCR by performing quantitative fluorescence signal detection on SYBR® /FAM channels. This product uses the antibody-based hot-start Tag enzyme for amplification, which greatly improves the specificity of the product while ensuring the amplification effect. At the same time, by optimizing the qPCR Mix Buffer system, the product is suitable for multiple species, providing a powerful tool for multidisciplinary experimental needs.

This product is a 2X pre-mix enzyme and contains all the components required for qPCR except primers and templates, providing great convenience for experimental manipulation.

## **Products Components**

Component	5 mL
SYBR Green Fast qPCR Mix (2X)*	1 mL X 5
50X ROX Reference Dye I	220 µL
50X ROX Reference Dye II	220 µL

<sup>\*</sup>Including OriGene's HotStart Taq DNA polymerase, Mg<sup>2+</sup>, dNTPs, SYBR® Green I...

## **Compatible Instruments**

Rox types	ypes qPCR Machines		
No ROX	Bio-Rad iCycler serious, Roche Light Cycler		
	serious Qiagen/Corbett serious and others		
ROX	ABI 7000/7300/7700/7900, ABI		
Reference	StepOne/StepOnePlus, Eppendorf and		
Dye I	others		
ROX	ABI 7500, ABI ViiATM7, ABI QuantaStudio		
Reference	serious, Stratagene serious, Corbett Rotor		
	Gene 3000 and others		

Note: The ROX Reference Dye is different for different instruments.

# **Products Storage**

-  $20^{\circ}$ C for long term storage and  $4^{\circ}$ C for a short period and **light protection** is demanded.

# **Materials Required**

- 1. EP tubes, PCR tubes and other related materials.
- 2. qPCR specific primers and templates.
- 3. qPCR plates and seal membrane.

## **Usage Notes**

- 1. Before using the SYBR Green Fast qPCR Mix (2X), please make sure that the mix is thawed completely and then placed it on ice for use.
- 2. Mix other qPCR components with Mix thoroughly and gently by pipetting or vortexing. After usage, place the Mix back to -20 °C for long time storage or 4 °C for short period usage.
- 3. The 2X SYBR Green Fast qPCR Mix (2X) contains *Taq* polymerase: All operations should be performed on ice.
- 4. This product is equipped with a specially designed ROX reference dye. ROX reference dye is added according to the qPCR instrument model.
- 5. To avoid contamination, pipette tips with filters is suggested.
- 6. To guarantee better qPCR results, DNA template in good quality is suggested.

### **Protocol:**

#### **Before Use:**

- Specificity of primers should be checked and a final concentration of 0.2 μM is suitable for most of primers.
- (2) The length of amplification products is usually range from 70 bp to 200 bp.
- (3) Dilute the template in gradient.
- (4) Add 1 pg-50 ng DNA as PCR templates and a "No Template Control sample" is suggested.
- (5) To ensure the confidence of experiment, at least 2 repeats of each samples is suggested.

#### **Experiment:**

1. Prepare the following reaction systems on ice

Components	Volume
SYBR Green Fast qPCR Mix (2X)	10 µL
Forward Primer (10 µM)	0.4 µL
Reverse Primer (10 µM)	0.4 µL
ROX	0.4 µL
gDNA or cDNA (<50 ng)	2 μL
RNase free ddH <sub>2</sub> O	to 20 μL

(1) Dissolve the SYBR Green Fast qPCR Mix (2X)

- at room temperature then placed it on ice for further usage. Before using, agitate the Mix thoroughly and centrifuge to collect all solution.
- (2) Calculate the amount of mix need, generally a 10% extra amount is suggested.
- (3) Dispense solution in sterile PCR or EP tubes in case of any contamination.
- (4) Add all components listed in above table, agitate the tubes gently to mix thoroughly (avoid bubbles) and centrifuge it.
- (5) Dispense the reaction solution into qPCR plates and seal the plates with optical membrane.
- (6) 2500 rpm centrifuge the qPCR plates to collect all solution.

#### 2. Program qPCR reaction as follows:

Stage 1	Denaturation	Reps:1	95℃	3min
Stage 2	Cylces	Reps:40-45	95℃	5s
			60°C	30-34s
Stage 3	Melt Curve	Reps:1	default	

\*Confirm there is a signal collection step after each extending step.

The extending time is varied according to different machines: 30s for StepOne Plus, 31s for 7300 and 34s for 7500.

#### Data Analysis:

- Draw a standard curve according to Ct values of endogenous gene. The value of R<sup>2</sup> should be more than 0.98 and the slope of curve should be in the range of -3 to -3.5 which means the PCR amplification efficiency is in the range of 90% to 120%.
- The standard deviation (STD) of Ct values should be less than 0.2 and the variation of Ct value for different experiment should be less than 0.5 (the threshold value of different experiments should be same when comparing Ct values).
- 3. The single melt curve indicate the no non-specific amplification products or primer dimmers, and the Tm value in melt curve is usually in the range of 80 to  $95\,^{\circ}\text{C}$ .

#### Troubleshooting

- 1) Melt Curve Show Multiple Peaks
  - a. **Primer Design:** Design the primer following basic primer design protocols.
  - b. **Primer Concentration Too High:** lower down the concentration of primers

#### 2) Unusual Amplification Curves

- a. Amplification Curve Not Smooth: Too low amplification signal, increase the template input and make sure the qPCR Mix is stored properly.
- Inconsistent Amplification Curve: Bubbles causes abnormal qPCR results, centrifuge the plate prior to running it.
- c. Abnormal Amplification Curves: the default baseline value of machine is set to be from 3 to 15, the baseline setting can be changed according actual amplification conditions. Besides, the degradation of template may affect the curve.

#### 3) No Amplification Curves after Reaction

- a. Not Enough PCR Cycles: the PCR cycle number is usually set to be 40. It should be noted a higher cycle number may increase the background signal.
- b. **Primer Degradation:** Use electrophoresis to confirm the Integrity of primers.
- c. Confirm the Signal Collection Step: the signal collection step are usually set to be after the annealing-extending step for two-step qPCR and after extending step for Three-step qCPR.
- d. **Template Input Too Low:** Increase template concentration or add extra repetition.

#### 4) Ct Value Too Late

- a. Template Degradation: Use freshly prepared template (Use electrophoresis to confirm Integrity of template)
- b. **Not Enough Initial Denaturation Time:**The SYBR Green Fast qPCR Mix (2X) uses
  Hot-Start *Taq* polymerase: the pre-denaturation time should be at least 3min.

- c. **Low Amplification Efficiency:** Optimize reaction condition or change primer.
- d. **Template Input Too Low:** Increase template concentration or add extra repeat
- e. **Template Degradation:** Use freshly prepared template (Use electrophoresis to confirm Integrity of template)
- f. Too Long PCR Products: The length of amplification products is usually in the range of 70 bp-200 bp.
- g. **PCR Inhabitation Reagent:** use new template or dilute the template.
- h. **Too Short Pre-denaturation Time** The SYBR Green Fast qPCR Mix (2X) contains Hot-Start *Taq* polymerase, the predenaturation time should be at least 3min.

#### 5) NTC Shows Amplification

- a. Contamination: Use sterile water to conduct experiment and the all operation is suggested to be done in clean room to avoid aerosol contamination.
- b. **Non-Specific PCR Products:** analyze with melt curve.

#### 6) Inconsistent Results

- c. Inconsistent Sample Added: Use proper pipetting techniques
- d. **Inconsistent Temperature in qPCR Machine:** ensure periodic machine calibration.
- e. **Template Concentration Too Low:** the lower template input, the poorer qPCR result is. Increase the template concentration.
- f. Inconsistent Threshold Set: when comparing the qPCR results in different plates, make sure the threshold value of each experiments is same.