Comprehensive And Professional qPCR Solution

Cited in about 8,000+ papers

Rapid reverse transcription

Hifair™ AdvanceFast 1st Strand cDNA Synthesis SuperMix for qPCR (gDNA digester plus) (11155ES)

Features

Quick and Easy
Reverse transcription completed in 5 minutes , total time 7 min

Reliable
High cDNA yield from degraded or inhibitor-containing RNA.

Efficient Synthesis
Higher cDNA yield, lower Ct.

Improved DNA Digestion
Removes more residual DNA

Sensitivity
Detects RNA down to 10 pg.

Stability
Room temperature storage (7 days) and 30 freeze-thaw cycles.

Performance

Rapid reverse transcription within 7 min

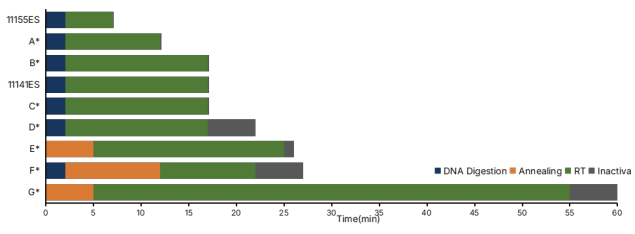

Figure 1. Workflow Comparison: 11155ES completes RT in 5 min (total 7+ min), faster than common reagents (17+ min). Ideal for high-throughput labs, especially water bath users.

High Sensitivity

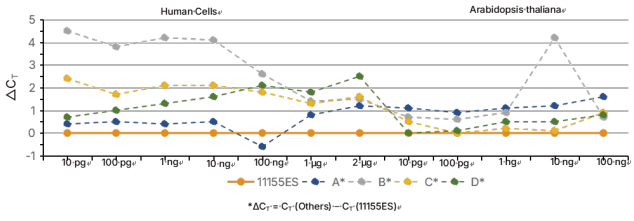

Figure 2. Higher Sensitivity Across a Range of RNA Inputs 293T cell RNA and Arabidopsis RNA were serially diluted, and cDNA synthesis was performed using different reverse transcription reagents according to their respective protocols. Subsequent dye-based qPCR analysis showed that the new product 11155ES outperforms other reagents, as indicated by the Delta CT values (ΔCT = CT (other RT products) – CT (11155ES)).

Create the most beautiful fluorescence quantitative curve

Universal qPCR --Hieffff UNICON™ Universal Blue qPCR Master Mix (11184ES)

Features

01 Universal
ROX dye premixed, Suitable for all qPCR instruments

02 Traceable blue dye

03 Support 46 min fast procedures

04 High Sensitivity
LOD ⩽ 0.2 copy /μL

Performance

A High precision: Detecting a two-fold difference in gene expression

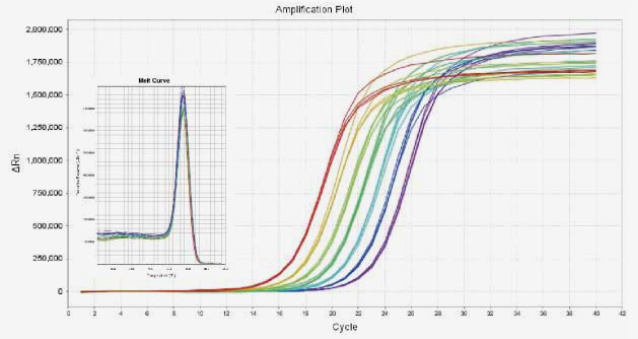

Figure 3. Hieff UNICON™ Universal Blue Master Mix has high accuracy and amplification efficiency. It can easily detect two-fold difference of GAPDH gene abundance using a series of diluted plasmid as template.

B Good system stability

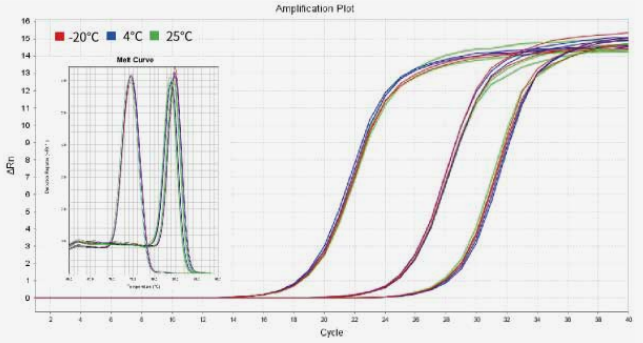

Figure 4. Hieff UNICON™ Universal Blue Master Mix has good stability. The reagent was placed at -20°C, 4°C, and 25°C for 7 days, and different types of genes were amplified using human cDNA as a template. The results showed that the reagent had good stability.

Highly sensitive colorimetric tracer fluorescence quantitative premix

Hieff UNICON™ ColorGPS qPCR SYBR Green Master Mix (No ROX/Low Rox/High Rox, 11188/89/90ES)

Pipetting Tracking

Reduces Risk of Missed or Incorrect Additions

Stability

Room temperature storage (24 hrs) and 20 freeze-thaw cycles without performance loss.

Performance

A Excellent Amplification

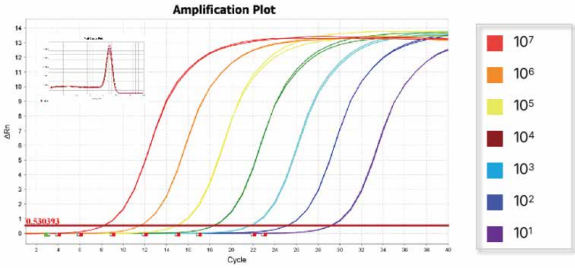

Figure 5. Reliable Results Across a Wide Dynamic Range

Using a 2 µL plasmid gradient (10^1-10^7) as the template, the target gene was amplified. Hieff UNICON™ ColorGPS Master Mix effectively detects templates across 7 orders of magnitude, delivering a strong linear relationship over a broad dynamic range.

B high precision

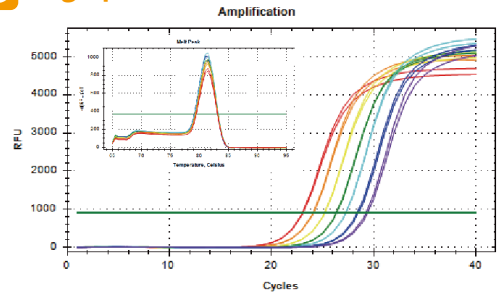

Figure 6. Accurately Detects 2-Fold Template Concentration Differences

Using 2µL of 2-fold serially diluted plasmid as the template, the target gene was amplified. Hieff UNICON™ ColorGPS Master Mix precisely distinguishes 2-fold concentration differences in template amounts.

C Pipetting Tracking: Reduces Risk of Missed or Incorrect Additions

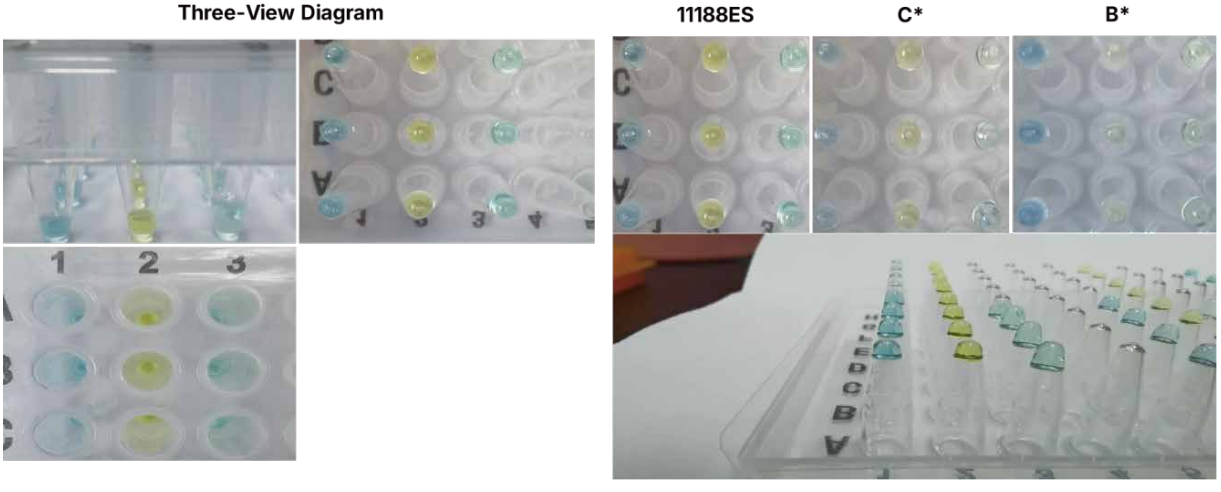

Figure 7. Pipetting Three-View Diagram.Color differences provide clear visual indicators. (blue-no template, green-the system has added the template)

Promotion

Applications	Name	Cat. No.	Size
Rapid reverse transcription	Hifair™ AdvanceFast 1st Strand cDNA Synthesis SuperMix for qPCR (gDNA digester plus)	11155ES60	100 T
Blue qPCR Mix (Dye method)	Hieff UNICON™ Universal Blue qPCR Master Mix	11184ES03 11184ES08	1 mL 5 × 1 mL
Blue qPCR Mix + Yellow Template Diluent(Dye method)	Hieff UNICON™ ColorGPS qPCR Master Mix (No Rox) Hieff UNICON™ ColorGPS qPCR Master Mix (Low Rox) Hieff UNICON™ ColorGPS qPCR Master Mix (High Rox)	11188ES03/11188ES08/ 11189ES03/11189ES08/ 11190ES03/11190ES08	1 mL 5×1 mL
RNA extraction	MolPure Cell/Tissue Total RNA Kit	19221ES50	50 T

Publication

01 Medina-Puche L,Tan H, Dogra V, et al. Cell. 2020;182(5):1109-1124. **(IF=66.850)**

02 Li Y, Wang D, Ping X, et al. Cell. 2022;185(6): 949-966. **(IF=66.850)**

03 SekiT, Yang Y, Sun X, et al. Nature. 2022;608(7922):421-428. **(IF=69.504)**

04 Chen P, Wang W, Liu R, et al. Nature. 2022;606(7914):550-556. **(IF=69.504)**

05 Dong W, Zhu Y, Chang H, et al. Nature. 2021; 589(7843):586-590. **(IF=69.504)**

06 Lu XY, Shi XJ, HuA, et al. Nature. 2020; 588(7838):479-484.**(IF=69.504)**

07 BiX, Wang K, Yang L, et al. Cell. 2021;184(5): 1377-1391.**(IF=66.850)**

08 Liu S, Hua Y, Wang J, et al. Cell. 2021;184(5): 1314-1329.e10. **(IF=66.850)**

09 Liu CX, LiX, Nan F, et al. Cell. 2019;177(4): 865-880. **(IF=66.850)**

10 Han X, Wang R, Zhou Y, et al. Cell. 2018; 172(5):1091-1107. **(IF=66.850)**

11 ChaiQ, Yu S, Zhong Y, et al. Science. 2022;378(6616). **(IF=66.850)**

12 Yu Q, Liu S, Yu L, et al. Nat Biotechnol. 2021;39(12):1581-1588. **(IF=46.297)**

13 Wang Z, Lu Z, Lin S, et al. Immunity. 2022;55(6): 1067-1081. **(IF=43.474)**

14 Bi Q, Wang C, Cheng G, et al. Immunity. 2022;55(8): 1466-1482. **(IF=43.474)**

15 Xiao J, Li W, Zheng X, et al. Immunity. 2020;52(1):109-122. **(IF=43.474)**

16 Gong Q, Wang YJ, He LF, et al. Nature. 2023, 622: 139–148 (2023) **(IF=69.504)**

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