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Ver202501

Instructions for Plasmid Residual DNA Detection Kit (qPCR Fluorescent Probe Method)

(Cat.No. HG-ZL003)

CONTENTS

1. Product Instruction

To enhance viral safety, the essential component sequences required for virus preparation are split across different plasmids. A viral packaging system of three or four plasmids is used to prepare virus. However, these plasmids, as exogenous DNA, may remain as residuals in the final product. The "Technical Guidelines for Pharmaceutical Research and Evaluation of In Vivo Gene Therapy Products", issued by the CDE in May 2022, explicitly emphasize the potential risks of exogenous DNA being packaged into viral particles when selecting packaging plasmids for vectors such as AAV, which are prone to incorporating non-vector DNA.

The independently developed Plasmid Residual DNA Detection Kit from Hillgene can quantitatively detect residual plasmid DNA (e.g., from lentiviruses, adenoviruses, etc.) in samples. This is achieved through an analysis of common DNA sequences found in plasmids widely used in the market, such as replicons originating from ColE1/pMB1/pBR322/pUC. The kit employs the TaqMan fluorescent probe principle, offering high specificity, sensitivity, and reliable performance. It is suitable for detecting plasmid DNA residuals in biological product intermediates, semi-finished, and finished products. The kit is designed to work with Hillgene sample pretreatment kit (catalog number: HG-CL100) for preprocessing.

The kit includes plasmid quantitative reference standards (with traceability completed).

Detection Range: 4×10^{1} copies/μL to 4×10^{6} copies/μL

Formula:

$$\text{Plasmid copy number (copies/μL)}=6.02\times10^{14}\times C\div(B\times660)$$

C= Plasmid Concentration (ng/μL)

B= Plasmid Base Pair Number

2. Product Applications

The Plasmid Residual DNA Detection Kit enables the rapid and specific detection of plasmid DNA residuals derived from host cells in biological products.

3. Product Specifications

Product Name	Cat. No.	Specifications
Plasmid residual DNA detection kit (qPCR fluorescent probe method)	HG-ZL003	100 Reactions/Box

4. Product Contents

Contents	Specifications	Storage Conditions
Plasmid DNA Reference Standard (4×10^{7}copies/μL)	50μL×1	-20°C
Plasmid Primer&Probe MIX	550μL×1	
2x qPCR Reaction Buffer	1.2mL×1	
DNA Diluent	1.5mL×3	

Contents	Specifications	Storage Conditions
ROX High	50μL×1	-20°C
ROX Low	50μL×1	

Compatible Instruments (including but not limited to)

- ABI PRISM 7500
- FQD-96A(Bioer)
- CFX96(Bio-Rad)
- Roche Light Cycler 480

5. Storage Conditions and Expiration Date

Store the kit components under the specified storage conditions. Refer to the expiration date on the outer packaging for the shelf life.

6. Definition and Abbreviation

- No Template Control (NTC): Refers to a control that contains no template (positive or negative). In this kits, the NTC typically consists of enzyme-free water or diluent.
- Negative Control Sample (NCS): A sample treated under the same conditions as testing samples, such as a known uninfected sample, which undergoes extraction and amplification to yield a negative result. The NCS ensures consistency with the testing sample processing steps and has a clearly expected negative result.
- Extraction Recovery Control (ERC): A control prepared by mixing a sample and standard in a specific ratio, followed by extraction and amplification as per testing sample procedures. The final amplification results of the standard are used to monitor the accuracy of the entire detection process.

7. Requirement of Equipments, Instruments & Consumables

- 1.5mL or 2mL sterile low-adsorption centrifuge tubes
- 96-well qPCR plates or 8-strip PCR tubes compatible with the PCR instrument
- Sterile barrier pipette tips (1000μL, 200μL, 10μL, etc.)
- Anhydrous ethanol (analytical grade)
- 1×PBS buffer
- Isopropanol (analytical grade)
- Fluorescent quantitative PCR instrument
- Centrifuge
- Shaker
- Pipettes (e.g., 1000μL, 200μL, 10μL, etc.)
- Magnetic particle concentrator
- Water bath/metal bath

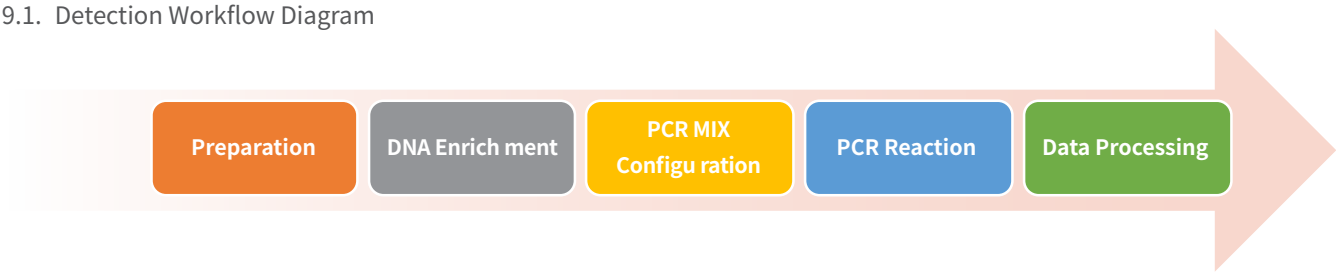
- Vortex mixer
- Magnetic Particle Concentrator

8. Precautions

- This kit has been validated for stability (e.g., freeze-thaw cycles) and does not require aliquoting.
- The preparation of negative samples and positive samples (reference materials and testing samples) must be conducted in separate areas. Personnel must wear appropriate protective gear, including masks, gloves, and cleanroom clothing.
- Replace pipette tips promptly between each step of sample addition to avoid cross-contamination and minimize the time tubes are left open.
- The kit must be used within its validity period.
- All components of the kit are recommended to be thawed in a low-temperature environment before use.
- Strict adherence to the instructions and exclusive use of the reagents supplied with this kit are necessary to ensure optimal detection performance.
- To ensure accurate results, sample pretreatment and purification should be completed on the same day as the subsequent qPCR detection.
- The final test results are closely related to the validity of the reagents, the operator's techniques, and the experimental environment.
- The Hillgene is responsible only for the quality of the kit itself and not for sample consumption caused by its use. Users should consider the amount of sample required and reserve enough before proceeding.
- This kit is for research use only and is not intended for clinical diagnostics.

9. Experimental Procedure

9.1. Detection Workflow Diagram



9.2. Preparations

It is recommended to use Hillgene's Host Cell Residual DNA (Magnetic Bead Method) Sample Pretreatment Kit (Catalog Number: HG-CL100) for sample pretreatment.

9.2.1.Prepare fresh 80% ethanol in a clean reagent bottle using anhydrous ethanol and sterile ultrapure water for each experiment.

9.2.2.Take out yeast tRNA and glycogen, and thaw them on an ice box. Thaw proteinase K at room temperature.

9.2.3.Preparation of binding solution for individual samples: Mix 9μL glycogen + 0.2μL yeast tRNA (do not add yeast tRNA if extracting yeast DNA). Note: The minimum pipetting volume should be no less than 3μL.

9.2.4.Preparation of washing solution: Before use, add 30mL of anhydrous ethanol to the washing solution, mix thoroughly, and label it. After each use, tightly close the bottle cap to maintain the ethanol content.

9.2.5.Turn on the metal bath and set the temperature to 65°C.

9.3. Reference Standard Preparation

Remove the plasmid quantitative standard from storage, thaw completely, and mix by gently flicking the tube several times. Spin the tube briefly at 6000 rpm for 3 seconds using a centrifuge. Repeat this three times. Prepare six clean 1.5mL centrifuge tubes labeled as ST1, ST2, ST3, ST4, ST5, and ST6. Dilution of the reference standard should be done by pipette mixing 20 times at a consistent speed without bubbles.

Tube Name	Dilution Voulume	Concentration(copies/μL)
ST1	10μL Reference Standard + 90μL DNA Diluent	4×10^6
ST2	10μL ST1 + 90μL DNA Diluent	4×10^5
ST3	10μL ST2 + 90μL DNA Diluent	4×10^4
ST4	10μL ST3 + 90μL DNA Diluent	4×10^3
ST5	10μL ST4 + 90μL DNA Diluent	4×10^2
ST6	10μL ST5 + 90μL DNA Diluent	4×10^1

9.4. Testing Sample Preparation

9.4.1.Testing Samples: Take 100μL of lentiviral formulation or other intermediate process samples as testing samples.

9.4.2.Extraction Recovery Control (ERC) Samples: Take 90μL of lentiviral formulation or other intermediate process samples and add 10μL of ST3 (as an example) to prepare ERC sample. (Note: It is recommended that the total amount of the standard in the ERC sample work system be 1–10 times that of the testing sample for optimal detection results.)

9.4.3.Negative Control Sample: Take 100μL of 1xPBS as the negative control sample (NCS) for extraction and amplification.

9.4.4.No Template Control (NTC): Take 100μL of DNA diluent as the no template control.

9.5. Extraction Steps

9.5.1.Transfer 100μL of each sample to a 1.5mL centrifuge tube for further extraction.

9.5.2.Add 25μL lysis buffer and 10μL proteinase K to each 100μL sample, vortex for 30 seconds, centrifuge briefly, and incubate at 65° C for 15 minutes.

9.5.3.After incubation, centrifuge the tubes briefly and sequentially add 9.2μL binding solution, 50μL lysis buffer, 150μL isopropanol, and 20μL magnetic beads (ensure beads are fully mixed before use). Vortex for 5 minutes and centrifuge briefly for 10 seconds.

9.5.4.Place the centrifuge tube on a magnetic particle concentrator and gently rotate it left and right until the beads aggregate on the side of the tube near the magnet. Keep the tube fixed on the magnetic particle concentrator, and use a pipette to carefully remove the supernatant without disturbing the beads.

9.5.5.Add 500μL washing solution (ensure ethanol is added before use), vortex for 30 seconds to disperse the beads, and ensure no beads stick to the tube wall. Centrifuge briefly for 10 seconds, place the tube back on the magnetic particle concentrator, and allow the beads to aggregate near the magnet. Let tube stand for 1 minute, then remove the supernatant

with a pipette.

9.5.6.Add 500μL freshly prepared 80% ethanol, vortex for 30 seconds to disperse the beads, and ensure no beads stick to the tube wall. Centrifuge briefly for 10 seconds, place the tube back on the magnetic particle concentrator, rotate gently, and allow the beads to aggregate near the magnet. Let it stand for 1 minute, then carefully remove the supernatant with a pipette.

9.5.7.To ensure residual ethanol is removed, centrifuge the tube briefly for 10 seconds, then place it on the magnetic particle concentrator and use a 10μL pipette to remove any remaining ethanol.

9.5.8.Open the tube cap and dry at room temperature (18–25 ° C) for 3–5 minutes (adjust drying time as needed based on visual observation to avoid over-drying). Note: Over-dried beads or residual ethanol can affect DNA recovery. Alternatively, blow-dry for 2 minutes if needed.

9.5.9.Remove the tube from the magnetic particle concentrator, add 100μL elution buffer to each tube, vortex for 1 minute, and incubate at 70° C for 7 minutes, vortexing every 2–3 minutes.

9.5.10.After incubation, centrifuge the tube at 12,000 g for 1 minute. Place the tube on the magnetic particle concentrator and wait for the beads to separate. Use a pipette to carefully transfer 90μL of the supernatant to a new 1.5mL centrifuge tube.

9.6. PCR-Fluorescent Probe Detection

9.6.1.Remove the plasmid DNA quantitative standard, plasmid Primer & Probe MIX, and 2x qPCR Reaction Buffer from the freezer and thaw on ice. Also, remove the DNA diluent and thaw at room temperature.

9.6.2.Preparation of qPCR Reaction Solution qPCR

Calculate the required number of reaction wells. Based on the number of reaction wells, calculate the total volume of qPCR MIX required. The number of wells should be calculated as follows :

Reaction wells = (6 Reference standards+ NCS + NTC + ERC + Testing Samples)×3.

Calculate the total amount of qPCR Mix required using this formula:

qPCR Mix = (number of reaction wells

+ 2 or 3) × 15 μL (2 or 3 accounts for operational losses).

Prepare the qPCR Mix as shown in the table below:

Contents	Reaction Volume(μL)
2x qPCR Reaction Buffer	10
Plasmid Primer&Probe Mix	4.6
ROX	0.4
Total Volume	15

Note: For instruments that do not require the addition of ROX, sterile, enzyme-free water can be used as a substitute. Please refer to the table below to find the appropriate ROX selection for your instrument. If your instrument model is not listed, please consult us or the manufacturer.

Instruments	ROX Reference Dye
ABI 5700, 7000, 7300, 7700, 7900HT Fast, StepOne, StepOne Plus	ROX High
ABI 7500, 7500 Fast, ViiA7, QuantStudio 3 and 5, QuantStudio 6,7,12k Flex. Stratagene MX3000P, MX3005P, MX4000P	ROX Low
Bio-Rad CFX96, CFX384, iCycler iQ, iQ 5, MyiQ, MiniOpticon, Opticon, Opticon 2, Chromo4.Roche Applied Science LightCycler 480, LightCycler 2.0; Lightcycler 96.Eppendorf Mastercycler ep realplex, realplex 2 s. Qiagen Corbett Rotor-Gene Q, Rotor-Gene 3000, Rotor-Gene 6000.	No ROX
Thermo Scientific PikoReal Cycler. Cepheid SmartCycler.Illumina Eco qPCR	

9.6.3.Preparation of qPCR Reaction Mixture:

Distribute 5μL of ST1, ST2, ST3, ST4, ST5, ST6, NTC, NCS, ERC, and the testing sample purified solution into each well of an 8-strip PCR tube containing 15μL of qPCR MIX. The total volume in each well should be 20μL.

Reference Standard	Reference Standard	Testing Samples
15μL qPCR Mix + 5μL ST1/2/3/4/5/6	15μL qPCR Mix + 5μL NTC/NCS/ERC Sample	15μL qPCR Mix + 5μL Testing Sample

Perform triplicates for each sample as parallel control. Centrifuge the strips at 6000 rpm for 10 seconds in a benchtop centrifuge to remove any air bubbles in the PCR tubes.

9.6.4.Example Layout of Reaction Wells:

/	1	2	3	4	5	6	7	8	9	10	11	12
A	ST1	ST1	ST1							S1	S1	S1
B	ST2	ST2	ST2							S2	S2	S2
C	ST3	ST3	ST3							S3	S3	S3
D	ST4	ST4	ST4									
E	ST5	ST5	ST5									
F	ST6	ST6	ST6							ERC-S1	ERC-S1	ERC-S1
G					NTC	NTC	NTC			ERC-S2	ERC-S2	ERC-S2
H					NCS	NCS	NCS			ERC-S3	ERC-S3	ERC-S3

Note: ST represents standard samples, NTC represents no-template control, NCS represents negative control sample, ERC represents extraction recovery control, S represents testing samples.

9.7. qPCR Reaction Program and Parameter Settings.

Example using the BIO-RAD CFX96 qPCR instrument:

9.7.1.Create a two-step PCR program with the following settings

Stage1	Initial Denaturation	Reps:1	95°C	3 Minutes
Stage2	Cycle Reaction	Reps:40	95°C	15 Seconds
			60°C	60 Seconds

Note: For the reaction volume is 20μL and set fluorescence collection of instrument at 60°C for 60 seconds. Other instrument models may require consultation with us or the manufacturer for specific settings.

9.7.2.Setting up the Reaction Plate: In the experiment setup, select Fluorophores and choose FAM for fluorescence. In the reaction plate layout, select the sample wells, choose Unknown under Sample Type, check FAM for fluorescence, and name the Target as ZL-DNA. Input the number of repeats for each sample and sample names. (Note: If the instrument requires the setup of a quencher and reference fluorescence, use "None" for the quencher and "ROX" for reference fluorescence.)

9.7.3.Setting up the Standard Curve Wells: For the standard curve wells, select Standard under Sample Type, check FAM for fluorescence, and name the Target as ZL-DNA. Input the repeat count for each dilution gradient and sample name. Set the concentrations of ST1, ST2, ST3, ST4, ST5, and ST6 to 4.00E+06, 4.00E+05, 4.00E+04, 4.00E+03, 4.00E+02, and 4.00E+01 (copies/μL), respectively.

9.7.4.Click Start Run on the Run screen to begin the PCR assay.

10. qPCR Result and Analysis qPCR

Example using the BIO-RAD CFX96 qPCR instrument:

10.1. Data Processing:

10.1.1.After the reaction is completed, the instrument will automatically set the baseline and threshold. You may adjust the threshold based on experience to improve linearity, amplification efficiency, and reduce deviations in triplicates.

10.1.2.Click on the Quantitation window to read the slope, intercept, amplification efficiency, and R^2 of the standard curve.

10.1.3.In the Quantitation Data window, the SQ Mean column will display the values for NTC and the testing samples, in units of copies/μL.

10.1.4.Click on Tools > Report or the Report button on the toolbar in the Data Analysis window to generate a report. In the options list, check Title, Run Settings, and Quantitation Data. Check Notes to input any comments. Adjust the font format if needed, or use a saved template. Click Update Report to preview and verify the report. Save the report as a PDF by clicking File > Save.

10.1.5.Recovery rate calculation formula:

$$\text{Recovery Rate} = \frac{(\text{ERC Concentration} \times V3) - (\text{Testing Sample Concetration} \times V2)}{\text{ERC Theoretical Concentration} \times V1} \times 100\%$$

V1=ERC Volume

V2= Testing Sample Volume

V3= Total Volume =V1+V2

10.2. System Suitability

10.2.1.The coefficient of variation (CV) between triplicates should be ⩽ 5%, excluding wells with Ct values above 35.

10.2.2.R^2 ⩾ 0.990, amplification efficiency should be 85%–110%.

10.2.3.NTC should show no Ct value or have Ct values that are at least 2 Ct values higher than the lowest concentration of the reference standard curve.

10.2.4.The average Ct value of the NCS should be higher than the lowest concentration of the standard curve.

10.2.5.The recovery rate of ERC should fall between 50% and 150%.。

11. Example diagram (Bio-Rad platform as an example)

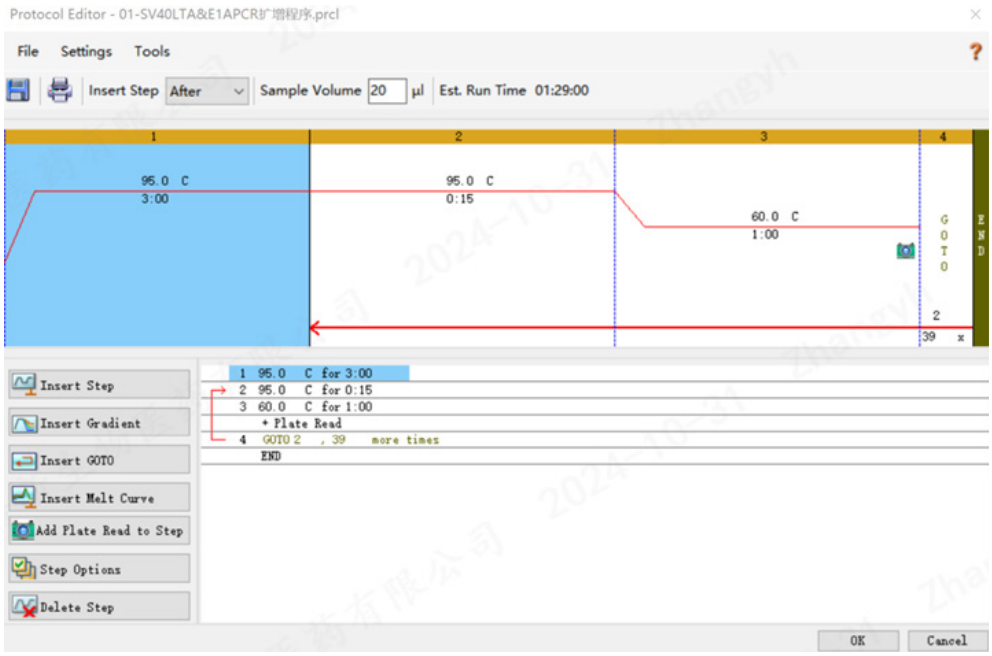


Figure 1. Example of PCR Amplification Procedure

1	2	3	4	5	6	7	8	9	10	11	12
Std-1 4.00E+06	Std-1 4.00E+06	Std-1 4.00E+06							Unk-1 S1	Unk-1 S1	Unk-1 S1
Std-2 4.00E+05	Std-2 4.00E+05	Std-2 4.00E+05							Unk-2 S2	Unk-2 S2	Unk-2 S2
Std-3 4.00E+04	Std-3 4.00E+04	Std-3 4.00E+04							Unk-3 S3	Unk-3 S3	Unk-3 S3
Std-4 4.00E+03	Std-4 4.00E+03	Std-4 4.00E+03									
Std-5 4.00E+02	Std-5 4.00E+02	Std-5 4.00E+02									
Std-6 4.00E+01	Std-6 4.00E+01	Std-6 4.00E+01							Unk-4 ERC-S1	Unk-4 ERC-S1	Unk-4 ERC-S1
				NTC-1 NTC	NTC-1 NTC	NTC-1 NTC			Unk-5 ERC-S2	Unk-5 ERC-S2	Unk-5 ERC-S2
				NTC-2 NCS	NTC-2 NCS	NTC-2 NCS			Unk-6 ERC-S3	Unk-6 ERC-S3	Unk-6 ERC-S3

Figure 2. Example of PCR Amplification Plate Layout

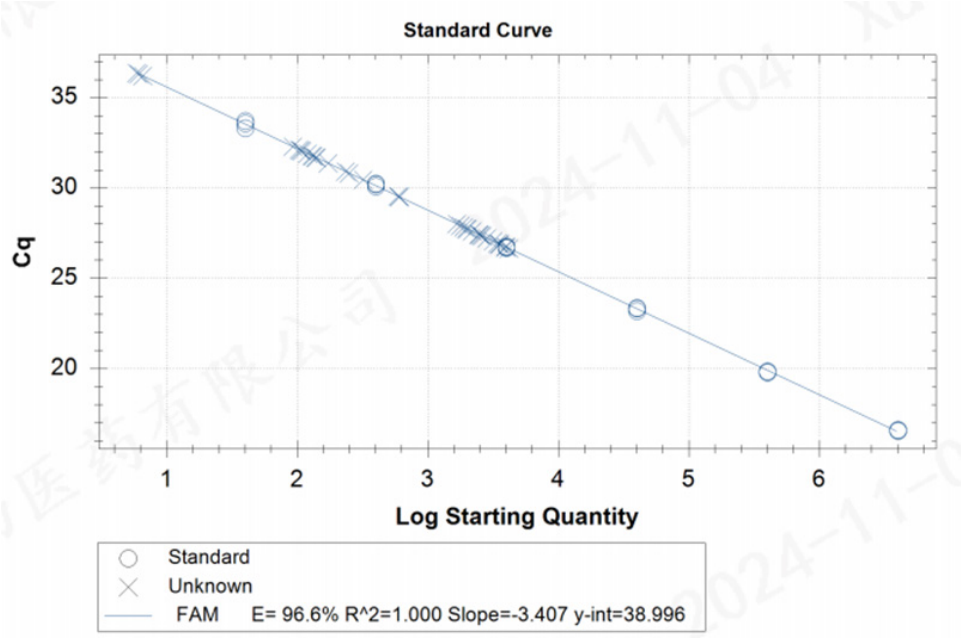


Figure 3. Example of Standard Curve

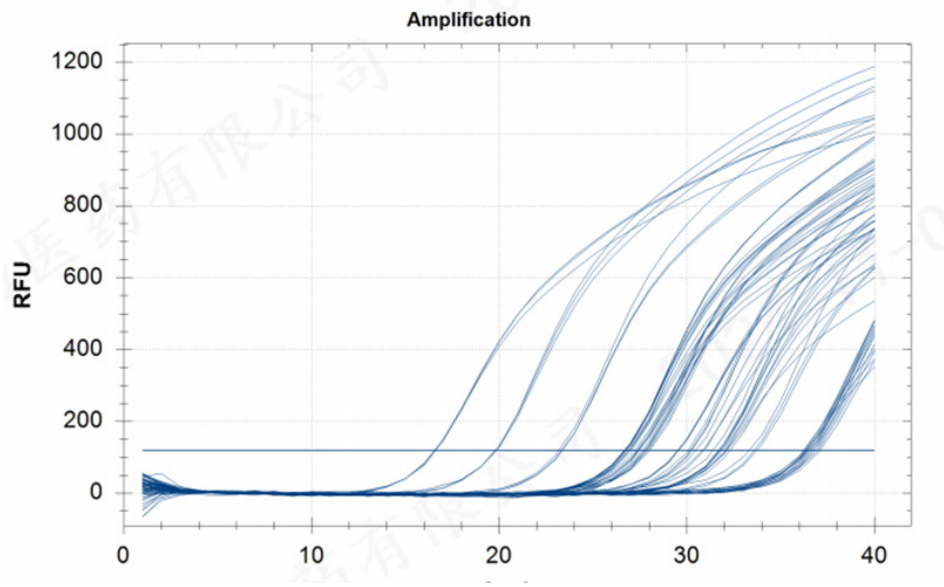


Figure 4: Example of Amplification Curve

12. Troubleshooting

No.	Problem Description	Possible causes	Countermeasures
1	No CT Value	The PCR program settings are wrong, and the steps for detecting the fluorescence signal are wrong.	Check whether the fluorescence selection and collection position in the program settings are correct.
		Primer or probe degradation	PAGE electrophoresis can be used to detect whether primers and probes are degraded.
		The template may be degraded or the amount of sample loaded may be insufficient.	If template degradation occurs, consider the introduction of impurities during sample preparation and repeated freeze-thaw cycles.
2	The value is not within the standard range	Calculation error occurred when preparing the reaction system	Recompound calculation results
3	Bad Standard Curve	Dilution, mixing or addition error of DNA reference standard makes the reference standard curve non-gradient	Check that the pipetting equipment is accurate; that the liquid does not stick to the wall during pipetting; that the liquid should be thoroughly mixed before each transfer (check whether the ROX line is abnormal); that the dilution multiple should be reasonable; and that the liquid is transferred according to the specified volume during pipetting.
		Reference standard degraded	Reference standard should be frozen and thawed repeatedly within a specified number of times
		Inhibitors present in template	Check the ROX line to see if it is abnormal and dilute the template again.
4	Abnormal CT Value	Degradation of various PCR reaction components or insufficient sample volume	Check whether the ROX line is abnormal, run a gel to verify whether the reaction components are degraded, reduce the dilution and repeat the experiment
		Inhibitors present in template	Check the ROX line to see if it is abnormal and dilute the template again.
5	Negative control Amplification signal	Reaction system components (e.g., DNA Diluent) are contaminated	During the experiment, the new Mix was replaced and the experiment was repeated; the reaction system was prepared in the clean bench
		Cross-contamination between samples; contamination caused by aerosols in the operating environment	Differentiate the laboratories to reduce aerosol contamination; use gun tips with filters; it is recommended to clean the environment accordingly during different processes, or to process and add samples in different environments.
		There is fluorescent dye residue on the instrument or PCR tube wall	Clean the instrument, perform background test and calibration; replace the tubing and avoid fluorescent dye contamination when using the tubing
6	Abnormal Amplification curve	The template concentration is too high, the template is degraded, or the system is not mixed and fully dissolved; the fluorescent dye is degraded;	Check the ROX line to see if it is abnormal and dilute the template again.

No.	Problem Description	Possible causes	Countermeasures
6	Abnormal Amplification curve	The consumables are not airtight enough, causing the liquid to evaporate, and the sample is not well gathered at the bottom of the tube; there are bubbles	Confirm whether it is sealed before loading, carefully check whether there are bubbles in the reaction tube, and check whether the liquid volume is abnormal when taking it out after the program ends.
		Improper instrument settings	The baseline is set improperly, and the endpoint value of the baseline is greater than the Ct value, such as the amplification curve is broken or slipping. The baseline endpoint should be reduced (Ct value - 4) and the data should be reanalyzed.
7	Low amplification efficiency	Fluorescent dye degradation	Check the ROX line to see if it is abnormal and dilute the template again.
		There are PCR inhibitors in the reaction system	Inhibitors are introduced when the template is added. The template should be appropriately diluted before adding it to the reaction system to reduce the influence of inhibitors.
		Dilution, mixing or addition error of DNA reference standard makes the reference standard curve non-gradient	Check that the pipetting equipment is accurate; that the liquid does not stick to the wall during pipetting; that the liquid should be thoroughly mixed before each transfer (check whether the ROX line is abnormal); that the dilution multiple should be reasonable; and that the liquid is transferred according to the specified volume during pipetting.
8	High amplification efficiency	Abnormal amplification occurs, the template concentration in the reaction system is too high	remove the wells with the highest template concentration and re-analyze the standard curve; re-dilute the sample
9	Amplification curve is not smooth	Reagents not mixed	Check the ROX line to see if it is abnormal and mix the reagents again
		Inhibitors present in template.	Re-dilute Samples
		There is some interference between the fluorescence signals	Check whether the machine model matches the applicable model and whether the fluorescent signal of the reagent kit is compatible with the corresponding model
10	Large differences in CT values	Inconsistent threshold line settings; instrument inconsistency	Unify the threshold line and the corresponding instrument parameters; because the target and component system selection of nucleic acid detection products on the market are not unified, the CT value of the standard curve of the kit will be different. If there is a national standard product, the national standard product can be used as an internal control product to compare the accuracy of the value.

13. Contact Information

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14. Notice for BuyerNotice to Buyer

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Please also comply with any applicable license requirements as described on the product webpage at https://www.hillgene.com.

For more product, intellectual property, and usage restriction information, visit https://www.hillgene.com.

Attachment 1: Safety Precautions

General Instructions

Improper use of this product may result in personal injury or damage to instruments or equipment. Ensure that all personnel using this product have received laboratory safety training and are familiar with the safety information in this document.

(1) Read and understand the user manual and safety information provided by the manufacturer before using instruments or equipment.

(2) Before handling chemicals, review the applicable Safety Data Sheets (SDS) and use appropriate personal protective equipment (gloves, protective clothing, goggles, etc.).

Biological Hazards

(1) Biological samples, such as tissues, body fluids, infectious pathogens, and blood from humans or animals, may pose risks of transmitting infectious diseases. Perform all work in facilities equipped with appropriate safety equipment, such as biosafety cabinets.

(2) Individuals working with potentially biohazardous materials must be trained per local regulations and institutional requirements.

Hazardous Waste

Waste generated by instruments may be hazardous. Follow the safety guidelines provided under "Biological Hazards."

Attachment 2: Related products (For more products, please consult Hillgene https://www.hillgene.com)

Category	Product Name	Cat. No.
Viral Detection	Human Residual DNA Detection Kit (qPCR)	HG-HD001
	Human Residual DNA Fragment Analysis Detection Kit (qPCR)	HG-HF001
	E.coli Residual DNA Detection Kit (qPCR)	HG-ED001
	Plasmid Residual DNA Detection Kit (qPCR)	HG-ZL001
	E1A&SV40LTA Residual DNA Detection Kit (Multiplex qPCR)	HG-EA001
	Nuclease ELISA Detection Kit	HG-BE001
	BSA ELISA Detection Kit	HG-BS001
	Trypsin ELISA Detection Kit	HG-TR001
	PG13 Residual DNA Detection Kit (qPCR)	HG-PG001
	Host Cell Residual DNA Sample Preprocessing Kit (Magnetic Bead Method)	HG-CL100
Viral Packaging	Blood/Tissue/Cell Genomic DNA Extraction Kit	HG-NA100
	293T HCP ELISA Detection Kit	HG-HCP001
	Lentiviral Packaging	HG-HIV-CUL-001

CELL THERAPY
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Welcome to order

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