

**Identification Kit for B.1.617 Lineage (L452R and E484Q) of SARS-CoV-2
(Fluorescence RT-PCR)
For Research Use Only. Not for use in diagnostic procedures.**

Instructions for Use*

***Note: Instructions for use are being provided to assist laboratory researchers conducting research related to B.1.617 lineage (L452R and E484Q) of SARS-CoV-2. This kit is for research use only, and these instructions should not be used to obtain clinical diagnostic results.**

【Product name】

Identification Kit for B.1.617 Lineage (L452R and E484Q) of SARS-CoV-2 (Fluorescence RT-PCR)

【Package size】

50 tests/kit

【Intended use】

The kit is a qualitative in vitro nucleic acid amplification assay to identify B.1.617 lineage (L452R and E484Q) of SARS-CoV-2 from throat swab, nasopharyngeal swab, sputum and Bronchoalveolar Lavage Fluid (BALF) specimen confirmed positive SARS-CoV-2 by RT-PCR for research purposes.

Multiple SARS-CoV-2 variants are circulating globally. Among them, the B.1.617 mutant strain that appeared in India in February 2021 has a higher transmission rate than other strains after research, of which L452R and E484Q are the main mutation sites.

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【Principles of the procedures】

The mutation detection is based on allele refractory mutation system (ARMS)-based quantitative PCR (qPCR). For L452R, and E484Q of SARS-CoV-2, sequence-specific primers and fluorescent probes were designed tailored for variant strain, respectively. ARMS primers can specifically identify variant strain using different fluorescent bands, enabling to differentiate mutant strains (L452R and E484Q) from wild strain through 1 test for each specimen in a single run.

In addition, internal reference is included in the kit to monitor the whole reactions to avoid false negative detection results.

【Key contents】

Contents (50 tests/kit)	Specification	Quantity	Description
Reaction Mix	1 mL/vial	1 vial	Reagent with primers and probe for amplification of ORF1ab, internal reference, L452R and E484Q
Enzyme Mix	120 µL/vial	1 vial	Taq DNA Polymerase, reverse transcriptase, UDG
Positive Control	750 µL/vial	1 vial	Mix solution of recombinant pseudo-viruses with target genes of L452R, E484Q, ORF1ab and internal reference
Blank Control	750 µL/vial	1 vial	DNase/RNase free H ₂ O

Notes: Components contained within a kit are intended to be used together. The reagents with different lot numbers cannot be mixed.

Materials required but not provided.

Table 1 Materials required but not provided.

Item	Validated products
Reagent	QIAamp Viral RNA Mini Kit (Cat. No. 52904 for 50 preps, 52906 for 250 preps) by QIAGEN
	TIANamp Virus RNA extraction Kit (Cat. No. YDP315-R) by TIANGEN
	MGIEasy Nucleic Acid Extraction Kit (Cat. No.1000020471 for 96 preps, 10000020261 for 1728 preps) by Wuhan MGI Tech Co., Ltd
	Solution for sputum decontamination
Extraction equipment (Optional)	DNA Sequencing Library Preparation System (MGISP-100RS) by Wuhan MGI Tech Co., Ltd
	High-throughput Automated Sample Preparation System (MGISP-960RS) by Wuhan MGI Tech Co., Ltd
Consumables	RNase/DNase-free tips for pipettes
	Disposable gloves
	RNase/DNase-free microcentrifuge tube, 8-tube strips for real-time PCR

【Storage and shelf-life】

The kit should be stored at temperature lower than -18 °C in dark. It is stable with shelf-life for 9 months from date of production in the claimed storage condition. Unpacked kit should avoid repeated thaw-freeze cycle (within 6 times). The kit can be transported at temperatures lower than -18 °C in dark conditions and is stable for 7 days.

The manufacture date and expiration date are provided on the product labels.

【Applicable instruments】

SLAN-96P PCR system; Applied Biosystems™ QuantStudio®5 Real-Time PCR Systems; Roche Light Cycler® 480 Real time PCR System; Fluorescent Quantitative PCR Detection system FQD-96A; Real-Time Quantitative Thermal Cycler MA-6000.

【Specimen】

Sample collection

- Collect fresh specimen of the following sample types. The operation of specimen collection should avoid possible contamination in collection, storage, and transportation. The specimen should be presumed contagious and be operated according to related regulations.
- **Throat swabs:** Carefully take out the swab from package and quickly rotate it around two sides of fauces, throat, and tonsil a few times applying pressure to collect as much secretions as possible. Avoid touching tongue. Break the swab stick and put the head into sampling solution in specimen tubes. Screw the tube cap tightly to ensure no leakage.
- **Nasopharyngeal swab:** Collected by professionals (HCP) using special micro cotton swabs. Simply put, when taking a nasopharyngeal swab sample, first insert the swab into the nostril, then move it forward gently into the nasopharynx, which is the area where the pharynx covers the roof of the mouth, and then rotate the swab for a period of time to collect secretions. Then carefully take out the swab and put it in a sterile virus transport medium, save the sample for subsequent analysis.
- **Sputum:** Collect sputum in the early morning after washing mouth. Take a deep breath. Hold the air for a few seconds. Breathe out slowly. Take another deep breath. Cough hard until sputum comes up in mouth. Spit the sputum into the sample bottle. Do this until there is enough sputum to cover the bottom of the bottle. Gas aspiration method can be used to collect sputum for those without sputum. Screw the tube cap tightly to ensure no leakage and seal the tube with film. The sputum should be delivered for testing immediately.
- **BALF:** Collect fresh qualified BALF without any pretreatment in a dry, sterile, DNase/RNase-free cryotube, and the amount to be submitted for inspection is not less than 3 mL.

Storage

- The specimen should be kept in proper condition, at temperature lower than -18 °C for no longer than 1 week and at temperature lower -70 °C for no longer than 6 months.

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- Frozen specimen should be thawed thoroughly while avoiding repeated thaw-freeze cycle.

Transportation

- The specimen should be shipped in low temperature condition using dry ice or ice bags.

【Laboratory procedures】 (Please read the procedures carefully before your operation)

Sample processing

- The fresh swab specimen should be collected to ensure the qualified RNA in terms of quality and quantity for the assay. RNA should be extracted using Nucleic Acid extracting Kit in line with the manufacturer’s instructions. Equivalent volumes of positive control and blank control should be processed simultaneously. The assay was assessed using the recommended RNA extraction kits by TIANGEN (YDP315-R), QIAGEN (50 Preps: 52904, 250 Preps: 52906) and MGIEasy Nucleic Acid Extraction Kit (96 Preps: 1000020471, 1728 Preps: 1000020261) by Wuhan MGI Tech Co., Ltd. 140 µL specimen is used by extraction kits from TIANGEN and QIAGEN. 200 µL specimen is needed by kit from MGI to extract nucleic acid manually and more than 160 µL specimen is needed for kit from MGI to extract nucleic acid automatically using High-throughput Automated Sample Preparation System (MGISP-960RS, Cat. No. 900-000154-00) or DNA Sequencing Library Preparation System (MGISP-100RS, Cat. No. 900-000206-00).
- Sputum should be mixed with equivalent volume of decontamination solution and shaken for about 30 minutes at ambient temperature followed by nucleic acid extraction.
- The extracted RNA should be tested immediately or stored at temperature lower than -70 °C for test later, and the storage time does not exceed 7 days.

Reagent preparation

- Take out all the kit contents and thaw them thoroughly at ambient temperature. Vortex and centrifuge briefly. The Enzyme Mix should be kept on ice continuously.
- Estimate the number of reactions (N) in the test, which includes the Blank Control (1 tube), Positive Control (1 tube), and specimens prepared, respectively.
- Prepare 8-tube strips for PCR based on the estimated N of reactions. PCR-Mix for testing ORF1ab, internal reference, L452R and E484Q should be prepared as shown in Table 2 below. Pipette 20 µL of PCR-Mix per tube into the 8-tube strips. Cap them tightly and transfer them to the sample processing area. The remaining Nucleic Acid Reaction Mix and Enzyme Mix should be stored at temperature lower than -18 °C immediately.

Table 2 PCR mix preparation for ORF1ab, internal reference, L452R and E484Q.

	Reaction Mix (µL)	Enzyme Mix (µL)
PCR-Mix	18×N	2×N

Add sample

- Add 10 µL extracted RNA of specimens, Blank Control, and Positive Control respectively into the 8-tube strips prefilled with PCR-Mix. Cap them tightly and centrifuge them at 2000 rpm for 10 seconds.
- Please refer to Table 3 below for an example of PCR tube layout in PCR plate.

Table 3 Example of PCR tube in PCR plate

	1	2	3	4	5	6	7	8	9	10	11	12
	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix	PCR-Mix
A	BC	Sample7										
B	PC	Sample8										
C	Sample1											
D	Sample2											
E	Sample3											
F	Sample4											
G	Sample5											

H	Sample6										
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Note: BC-Blank Control; PC-Positive Control

Real-time PCR

- Set the fluorescent channels: Please refer to the manufacturer’s instructions of thermocycler for detailed information on channel setting.

PCR-Mix:

- FAM channel (Reporter: FAM, Quencher: None) for ORF 1ab;
- VIC/HEX channel (Reporter: VIC/HEX, Quencher: None) for E484Q mutant strain;
- ROX channel (Reporter: ROX, Quencher: None) for L452R mutant strain;
- CY5 channel (Reporter: CY5, Quencher: None) for internal reference;

Reference Dye: None

Sample Volume: 30 µL

- Configure PCR protocol

Table 4 Configure PCR protocol

Step	Cycles	Temperature	Duration	Fluorescent signal collection
1	1 cycle	50 °C	10 min	No
2	1 cycle	95 °C	1 min	No
3	45 cycles	95 °C	5 sec	No
		58 °C	15 sec	Yes

Data analysis

- SLAN-96P real time PCR system

The starting and ending points of baseline should be set as 6 and 12 respectively.

The threshold of each fluorescent channel should be set separately. When setting the threshold for a channel, change the configuration of baseline optimization in basic parameter from automatic to manual. Then, manually set the threshold just above the maximum level of blank control curve (random noise curve) at all channels.

- Applied Biosystems™ QuantStudio®5 Real time PCR system

Baseline is set as default.

Threshold: In most cases, the auto threshold line function yields satisfying results. In some cases, it can be adjusted manually. When setting threshold, click [Show Plot Setting], select the target gene to view and the “Show: Threshold” as . Adjust the threshold through dragging it by mouse or inputting values directly, then, click [Analyze].

- Roche Light Cycler® 480 Real time PCR system

Baseline is set as default.

Threshold: In most cases, the auto threshold line function yields satisfying results. In some cases, it can be adjusted through slightly improving the standard curve error value by manually moving the threshold line up or down, fitting the line to the exponential portion of the amplification curve, higher than while horizontally paralleling the amplification curve of Blank control. Click [Analysis] to get results and [Report] to present them.

- Fluorescent Quantitative PCR Detection system FQD-96A

Baseline is set as default.

Threshold: In most cases, the auto threshold line function yields satisfying results. In some cases, it can be adjusted manually. When setting threshold, click [Analysis settings], select the target gene to view and the “Automatic threshold” as . Adjust the threshold by inputting values directly, then, click [Save and analyze].

- Real-Time Quantitative Thermal Cycler MA-6000

Baseline is set as default.

Threshold: In most cases, the auto threshold line function yields satisfying results. In some cases, it can be adjusted manually. When setting threshold, click [Analysis], select the target gene to view and the “Automatic threshold” as . Adjust the threshold by inputting values directly, then, hit the Enter key on the keyboard.

【Quality control】

- Blank Control:
Ct values at FAM, VIC/HEX and ROX channels are 0 or no data available. Ct value at CY5 channel is 0, no data available or higher than 38.
- Positive Control:
Ct values at FAM, CY5, ROX and VIC/HEX channels are all in S-shape with Ct values not higher than 35.
- Above requirements should be met in a single test. Otherwise, the test is invalid and may be retested in line with the package insert.

【Threshold and reference range】

- Reference range of the kit was determined based on the Receiver Operating Characteristic curve and percentile method. Cut-off values for positive L452R, and E484Q are Ct values not higher than 41. The identification of mutant strain of L452R and E484Q should be determined by Ct values in combination with Δ Ct.
- Δ Ct calculated using formula: Ct value of mutant strain- Ct value of ORF1ab.

Table 5 Δ Ct calculation method

Δ Ct	Allele	Fluorescent signal	Δ Ct value
/	ORF1ab	FAM(PCR-MIX)	/
Δ Ct1	E484Q	VIC(PCR-MIX)	$Ct_{E484Q} - Ct_{ORF1ab}$
Δ Ct2	L452R	ROX(PCR-MIX)	$Ct_{L452R} - Ct_{ORF1ab}$

Table 6 Reference range for different mutation.

Allele	Δ Ct value	Result
E484Q	Δ Ct1 \leq 6	E484Q (mutant strain)
	Δ Ct1 $>$ 6	Non-E484Q mutant
L452R	Δ Ct2 \leq 6	L452R (mutant strain)
	Δ Ct2 $>$ 6	Non-L452R mutant

- Cut-off value for internal reference was determined as 38, not higher than 38 as positive.

【Testing result interpretation】

- When Ct value of mutation strain is not higher than 41, Δ Ct should be calculated as Table 5 above (45 should be used in calculating Δ Ct when Ct value of ORF1ab is 0 or no Ct). Testing results should be interpreted as Table 6 above.
- When Ct value of mutation strain is higher than 41 and Ct value of ORF1ab gene is not higher than 41, the specimen is not a mutant strain of target gene.
- When Ct value of the mutation strain and ORF1ab gene are both higher than 41, the specimen was in low concentration of SARS-CoV-2 if Ct value of internal reference at CY5 not higher than 38. The sample with Ct

value of internal reference higher than 38 at CY5 should be re-extracted and retested.

Example for Result interpretation

Sample	Target (FAM/VIC/ROX)			Internal Reference (CY5)	Interpretation
	Mutant strain	ORF1ab	Δ Ct		
Sample 1	Sigmoidal amplification curve and Ct value is ≤ 41	Any	≤ 6	Any	Mutant strain
Sample 2	Sigmoidal amplification curve and Ct value is ≤ 41	Any	> 6	Any	Non mutant strain of target gene
Sample 3	0, no Ct or Ct value is > 41	Sigmoidal amplification curve and Ct value is ≤ 41	/	Any	Non mutant strain of target gene
Sample 4	0, no Ct or Ct value is > 41	0, no Ct or Ct value is > 41	/	Sigmoidal amplification curve and Ct value is ≤ 38	Low concentration of virus RNA.
Sample 5	0, no Ct or Ct value is > 41	0, no Ct or Ct value is > 41	/	0, no Ct or Ct value is > 38	Invalid test. Reextracted and retest.

【Limitation of the assay】

- This kit is intended for research use only for research involving the development of L452R and E484Q mutation detection of SARS-CoV-2 from positive SARS-CoV-2 throat swab, nasopharyngeal swab, sputum and BALF specimen. These instructions should not be used to obtain clinical diagnostic results.
- Incorrect results can be caused by improper operations in sample collection, transportation or processing, very low concentration of target virus in the specimens, mutations within the virus genome not covered by the kit's primers and/or probes, and uncontrolled external interference factors, such as PCR inhibitor. If necessary, other methods are recommended for further identification.

【Performance characteristics】

- The package is intact and the liquid contents are clear, transparent and with no sediments in it. All contents are in correct quantity as listed in the package insert.
- Positive Control is positive at FAM, CY5, ROX and VIC/HEX channel in testing while Blank Control is negative at all channels with Ct of internal reference at CY5 higher than 38 or no value.

【Warning and precautions】

- For Research Use Only. Not for use in diagnostic procedures. Please contact BGI Sales in the event of damage to the protective packaging.
- The kit should be stored and transported in claimed conditions. Thaw all kit components thoroughly and centrifuge them briefly before starting an assay. Avoid repeated thaw-freeze cycle.
- All contents in the package are prepared dedicatedly and validated for the intended research purpose. Replacing any of them will affect the performance of the kit. Components contained within a kit are intended to be used together. Do not mix components from different kit lots.
- Separate laboratory areas are recommended to perform predefined procedures of the assay.
 - a) 1st Area: Preparation Area—Prepare testing reagent.
 - b) 2nd Area: Sample processing Area—Process the specimen and controls.
 - c) 3rd Area: Amplification Area—Conduct PCR.

- All materials used in one area should always be remained in the area and should not be moved or used in other areas. After the assay procedures, the workbench and lab supplies should be cleaned and disinfected timely.
- To prevent the contamination from exogenous RNA, sample addition should follow the sequence of negative control, specimen RNA, and positive control. Filtered tips should be prepared and used separately in preparing reagent and sample addition.
- 8-tube strips for real time PCR should be capped tightly and transferred to specimen processing area immediately after addition of nucleic acid reaction mix. Pipette the samples exactly into the reaction mix in PCR tubes and avoid sticking the samples on the inside wall of the tube. Mineral oil should be added immediately, and the tubes should be capped tightly immediately after the addition.
- After the amplification is done, remove PCR tubes from the thermal cycler and discard them in a sealable plastic bag for autoclave and decontamination.
- The workbench and lab supplies should be cleaned and disinfected regularly using 75% ethanol or UV light.
- All pipette tips and centrifuge tubes in the assay should be DNase/RNase-free. The used centrifuge tubes and pipette tips should be discarded in waste bin with Clorox (84) disinfectant and disposed with other laboratory wastes after decontamination.
- Operator should receive professional training before operating.

【Disclaimer】

- These kits are distributed for research use only, not for clinical diagnostic purposes.

【References】

[1] Gu, Hongjing, Qi Chen, Guan Yang, Lei He, Hang Fan, Yong-Qiang Deng, Yanxiao Wang, et al. 2020. Adaptation of SARS-CoV-2 in BALB/c Mice for Testing Vaccine Efficacy. *Science* 369 (6511): 1603–7.

【Contact details】



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