SARS-CoV-2 Extended ELITE MGB® Kit (Cod.: RTS172ING) SARS-CoV-2 Extended – Elite Positive Control (Cod.: CTR172ING) QUICK GUIDE TO USE THE ASSAY in association with REAL TIME OPEN PLATFORMS





This document is available only in English.
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A. Intended use

The «SARS-CoV-2 Extended ELITe MGB® Kit» product is part of a qualitative multiplex nucleic acids reverse transcription and amplification and melting curve analysis assay, for the detection and discrimination of the mutations L452R, L452Q, E484K, E484Q, E484A, Q498R and N501Y of the S gene of Severe Acute Respiratory Syndrome Coronavirus 2 (SARS-CoV-2) in clinical samples from subjects infected by the

The assay is able to detect the mutations associated with the following variants: the Alpha variant (UK), lineage B.1.1.7, the Beta variant (South Africa), lineage B.1.351, the Gamma variant (Brazil), lineage P1, the Delta variant (India), lineage B.1.617.2, the Kappa variant (India), lineage B.1.617.1, the Epsilon variant (USA), lineage B.1.427/9, the Eta variant (Multiple countries), lineage B.1.525, the lota variant (USA), lineage B.1.526, the Lambda variant (Perù), lineage C.37 and the Mu variant (Colombia), lineage B.1.621 and the Omicron variant (Multiple countries), lineage B.1.529.

The product is used as a reflex test to identify the possible presence of the L452R and L452Q, N501Y and Q498R + N501Y, E484K, E484Q and E484A mutations of the SARS-Cov-2 S gene, in samples already diagnosed as positive for SARS-CoV-2.

The test is intended for Research Use Only. Before use, the laboratory should validate the whole process.

B. Matrices

C. Tube type collection

Respiratory Swabs

| Copan Ref. | Description |
|--------------|-------------|
| 360C or 305C | UTM kit |

D. SARS-CoV-2 Extended ELITe MGB® KIT (RTS172ING) content

| CoV-2 Extended PCR Mix (Neutral cap) | RT EnzymeMix (Black cap) | Maximum Shelf-life: 12 Months |
|--|--|---|
| W X 2 | RT X 2 | Storage temp.: below - 20 °C |
| 2 tubes of 1200 μL 96 reactions per kit 6 freeze-thaw cycles | 2 tubes of 20 μL 96 reactions per kit 6 freeze-thaw cycles | Prepare the complete reaction mixture in a 2 mL tube (Sarstedt Ref. 72694005, not provided) |

E. SARS-CoV-2 Extended - ELITe Positive Control (CTR172ING) content

| CoV-2 Ext Wild Type Positive Control (Black cap) | CoV-2 Ext Mutant Positive Control (Red cap) | Maximum Shelf-life: 24 Months |
|--|--|-------------------------------|
| PC X 2 | PC X 2 | Storage temp.: below - 20 °C |
| 2 tubes of 160 μL 4 sessions / tube 4 freeze-thaw cycles | 2 tubes of 160 μL 4 sessions / tube 4 freeze-thaw cycles | |

F. Complete reaction mixture Preparation

- 1. Thaw the CoV-2 Extended PCR Mix and RT EnzymeMix tubes and SARS-CoV-2 Extended ELITe Positive Control.
- 2. Mix gently and spin-down,
- 3. Reconstitute the complete reaction mixture in a 2 mL Sarstedt tube (Ref. 72694005) as shown below:

| Reagent | 1 Test | Samples N | Total reactions |
|------------------------|--------|-----------|-----------------|
| CoV-2 Extended PCR Mix | 20 μL | 1 to 5 | N + 1 |
| RT EnzymeMix | 0.3 μL | 6 to 12 | N + 2 |
| | | 13 to 24 | N + 3 |
| | | 25 to 48 | N + 4 |

- 4. Mix gently and spin-down.
- 5. Pipet 20 μL of complete reaction mixture in all microplate wells or Strip Tubes in use,
- Add 10 μL of extracted RNA in sample wells, 10 μL of molecular grade water in Negative Control well and 10 μL of each Positive Control in control wells. Note: Each one has to be mixed by pipetting 3 times into the reaction mixture,

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- 7. Seal the microplate with the amplification sealing sheet,
- 8. Transfer the microplate in the thermocycler and start.

G. Result Interpretation

| Sample | results: | | | | | | |
|---|-------------|--|---|---|-----------------------|-------------------------------------|--------------------------------------|
| Result of sample run | | | | | Inte | rpretation | |
| SARS-CoV-2 452L wild type | | | Th | The RNA of SARS-CoV-2 452L wild type was detected in the sample | | | |
| SARS-CoV-2 mutation L452R detected | | | T | he RNA of SAI | RS-CoV-2 452F | R mutant was detected in the sample | |
| SARS-CoV-2 mutation L452Q detected | | | TI | he RNA of SAF | RS-CoV-2 4520 | mutant was detected in the sample | |
| S | ARS-CoV-2 | 484E wild t | ype | Th | e RNA of SAR | S-CoV-2 484E | wild type was detected in the sample |
| SARS-0 | CoV-2 mutat | tion E484K | detected | T | he RNA of SAI | RS-CoV-2 484k | mutant was detected in the sample |
| SARS-0 | CoV-2 mutat | ion E484Q | detected | TI | he RNA of SAF | RS-CoV-2 4840 | mutant was detected in the sample |
| SARS-CoV-2 mutation E484A detected | | | T | he RNA of SAI | RS-CoV-2 484 <i>A</i> | mutant was detected in the sample | |
| SARS-CoV-2 501N wild type | | | The RNA of SARS-CoV-2 501N wild type was detected in the sample | | | | |
| SARS-CoV-2 mutation N501Y detected | | The RNA of SARS-CoV-2 501Y mutant was detected in the sample | | | | | |
| SARS-CoV-2 presumptive Q498R+N501Y detected | | The RNA of SARS-CoV-2 presumptive 498R+501Y was detected in the sample | | | | | |
| SAI | RS-CoV-2 45 | 2 NOT amp | lified | | The RNA of | SARS-CoV-2 45 | 52 was not detected in the sample |
| SAI | RS-CoV-2 48 | 4 NOT amp | lified | The RNA of SARS-CoV-2 484 was not detected in the sample | | | |
| SAI | RS-CoV-2 50 | 1 NOT amp | lified | The RNA of SARS-CoV-2 501 was not detected in the sample | | | |
| | Invalid | | | | Not va | lid result cause | ed by Internal Control failure |
| Sample Ct and Tm ranges: | | | | | | | |
| Ct 452 | Ct 484 | Ct 501 | Tm 452 | Tm 484 | Tm 501 | Ct RNase P | Result |
| Ct < 45 | | | 59.6 - 63.6 | | | +/- | SARS-CoV-2 452L wild type |
| Ct < 45 | | | 52.8 - 55.2 | | | +/- | SARS-CoV-2 mutation L452R detected |
| Ct < 45 | | | 55.3 - 57.7 | | | +/- | SARS-CoV-2 mutation L452Q detected |
| | | | | | | | |

+/-

+/-

+/-

+/-

Ct < 35

Ct > 35

SARS-CoV-2 484E wild type

SARS-CoV-2 mutation E484K detected

SARS-CoV-2 mutation E484Q detected

SARS-CoV-2 mutation E484A detected

SARS-CoV-2 501N wild type

SARS-CoV-2 mutation N501Y detected SARS-CoV-2 presumptive Q498R+N501Y

detected

SARS-CoV-2 NOT amplified

Invalid

64.4 - 68.1

58.5 - 61.3

55.7 - 58.4

62.0 - 64.3

| Positive Control | Ct and Tm | limits: |
|------------------|-----------|---------|

Ct < 45

Ct < 45

Ct > 45

Ct > 45

Ct < 45 Ct < 45

Ct < 45

Ct < 45

Ct > 45

Ct > 45

Ct > 45

Ct > 45

| Positive Control Ct and I'm lin | iits. | | | | | |
|--------------------------------------|----------|---------|-------------|--------------------|-------------|---------------------------|
| Controls | Target | Ct | 452 Tm | 484 Tm | 501 Tm | Result |
| CoV 2 Feb Mild Tono | L452 wt | Ct < 31 | | - 63.6 64.4 - 68.1 | 54.7 - 58.4 | Positive Control Valid |
| CoV-2 Ext Wild Type Positive Control | E484 wt | Ct < 31 | 59.6 - 63.6 | | | |
| Positive Control | N501 wt | Ct < 31 | | | | |
| CoV-2 Ext Mutant | 452R mut | Ct < 33 | | 58.5 – 61.3 | 59.6 - 65.6 | Positive Control Valid |
| Positive Control | 484K mut | Ct < 32 | 52.8 - 55.2 | | | |
| Positive Control | 501Y mut | Ct < 30 | | | | valiu |
| Negative Control | - | Ct > 45 | - | - | - | Negative Control Valid |

54.7 - 58.4

59.6 - 65.6

52.9 - 54.6

Note: The Ct and Tm Limits were defined on Bio-Rad CFX96 Dx instrument. The Ct and Tm Limits for ABI 7500 Fast Dx / 7500 / QuantStudio5 Dx shall be verified by users.

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H. Samples

- Sample inactivation is not required (ref. WHO guideline). The sample can be pretreated with a denaturant solution or by a heat
 incubation under a Biosafety cabinet of class II (BSC2). In case of this procedure, dispense 200 μL of sample into the tubes and no
 more than 200 μL of denaturant buffer. Note: This procedure is an off-label protocol and needs to be validated before use (ref WHO
 guidelines).
- 2. Handle and dispose of all biological samples as if they were able to transmit infectious agents even if the sample is inactivated.
- 3. Eluates obtained with extraction in association with SARS-CoV-2 ELITe MGB® Kit (Ref. RTS170ING) or SARS-CoV-2 PLUS ELITE MGB Kit (Ref. RTS180ING) can be used.
- 4. High-medium viral titre for SARS- CoV-2 allows to obtain better results.

I. References

- ECDC Reference: "Assessing SARS-CoV-2 circulation, variants of concern, non-pharmaceutical interventions and vaccine rollout in the EU/EEA, 15th update" June 2021.
- WHO Reference: "Laboratory testing for coronavirus disease (COVID-19) in suspected human cases, 2 March 2020".

J. Semi-automated extractions compatibility

ELITechGroup ELITe GALAXY

ELITE GALAXY is a closed instrument, but an open protocol is ready for use with SARS-CoV-2 Extended ELITe MGB® Kit. Please refer to your local ELITechGroup support to ask the required protocol to be upload into the instrument.

Sample preparation

| ELITe GALAXY – Extraction kit (Ref. INT02 | 1EX) | Mas |
|---|--------|------|
| Sample volume processed: | 300 μL | Mas |
| Sample dead volume (2mL tubes): | 100 μL | Elua |
| Sample dead volume (13x75 tubes) | 300 μL | Cont |
| Sample dead volume (16x100 tubes) | 600 μL | |
| Total elution volume: | 100 | |

 PCR setup

 Master Mix volume:
 20 μL

 Master Mix Dead volume:
 45 μL

 Eluate volume:
 10 μL

 Controls dead volume:
 30 μL

Qiagen QIAsymphony

QIAGEN QIAsymphony is a closed instrument that allows the usage of open protocols. Please refer to your local Qiagen support to ask an offer to provide you the required protocol.

Sample preparation

QlAsymphony - DSP Virus/Pathogen Midi kit Sample volume processed: 400 μ L Total elution volume: 85 μ L

PCR setup

| Master Mix volume: | 20 μL |
|-------------------------|-------|
| Master Mix Dead volume: | 60 μL |
| Eluate volume: | 10 μL |
| Controls dead volume: | 30 μL |

Abbott m2000sp

Abbott m2000sp is a closed instrument that allows the usage of open protocols. Please refer to your local Abbott support to ask an offer to provide you the required protocol. It can be needed enabling the fluorescence channels.

Sample preparation

Abbott m2000sp - mSample Preparation Systems DNA (CE) or mSample Preparation Systems RNA

Sample volume processed: $400~\mu L - 600~\mu L$ Total elution volume: $100~\mu L$

Note: m2000sp requires to extract the positive and negative controls. Substitute the controls with water and at the end remove them from the elution plate.

PCR setup

| Master Mix volume: | 20 μL |
|-------------------------|----------------------|
| Master Mix Dead volume: | 100 μL |
| Eluate volume: | 10 μL |
| Controls: | 10 μL - Manual input |

Note: Positive and negative controls are manually dispensed in the PCR plate after the automatic dispensation of the Master Mix and the patient samples eluates.

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Siemens Versant kPCR

Siemens Versant kPCR allows the usage of open protocols. Please refer to your local Siemens support to ask an offer to provide you the required protocol.

Sample preparation

Versant kPCR - Sample Preparation 1.0 Reagents KitMaster Mix volume:20 μLSample volume processed:400 μLMaster Mix Dead volume:45 μLTotal elution volume:100 μLEluate volume:10 μLControls dead volume:30 μL

MGISP-960

MGI Tech MGISP-960 is an automatic system for DNA /RNA extraction and PCR – setup. The **Biorad CFX-96** or **Thermo Fisher 7500 Fast DX / 7500** are used in association with this system. Please refer to your local ELITechGroup support to ask the required protocol.

Sample preparation

MGIEasy Magnetic Beads Virus DNA/RNA Extraction kit (EuroClone code 909-1000021043)

Sample volume processed: 180 µL
Dispense manually the sample in the "processing plate"
Total elution volume: 30 -50 µL

PCR setup

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PCR setup

| Master Mix Volume: | 20 μι |
|--|---|
| lf 1 plate is working: Dispense 240 μL of Master N | 1ix for each well in the first column (A) |
| If 2 plates are working: Dispense 480 µL of Maste | r Mix for each well in the first column (A) |
| Flusta valuma: | 10 |

Eluate volume: 10 μL Controls volume: 10 μL

GenePure PRO-Bioer

GenePure Pro-Bioer is an automatic system for DNA /RNA extraction. The ELITe InGenius® is used in association with this system. Please refer to your local ELITechGoup support to ask the required protocol.

Sample preparation

MagaBio Plus Virus DNA/RNA purification Kit

(code 909-BSC71S1E)

Sample volume processed: $300~\mu L$ Proteinase K (PK): $10~\mu L$ Dispense manually firstly the sample and then PK in the deep-well Total elution volume: $70~\mu L$

PCR setup

| Master Mix volume: | 20 μL |
|--------------------|-------|
| Eluate volume: | 10 μL |
| Controls volume: | 10 μL |

K. Real Time PCR thermal cycler compatibility

Reaction Volume

30 μL

Bio-Rad CFX96 Dx

Verify before use.

Amplified sequence and Channels setting

| Target | Gene | Channels | Threshold |
|----------|-------------------|----------|-----------|
| Target 1 | S gene, codon 452 | Cy5 | Auto |
| Target 2 | S gene, codon 484 | FAM | Auto |
| Target 3 | S gene, codon 501 | ROX | Auto |
| IC | Rnase P gene | VIC | Auto |

Baseline threshold settings

Setting Value Baseline Auto

Thermal Profile

| | Description | Temperature | Time |
|-----------------------------|----------------------------|-------------|-------------------|
| Hold | Reverse Transcription | 45 °C | 20:00 |
| Hold 2 | Pre-Denaturation | 95 °C | 02:00 |
| Cycling 44 cycles | Denaturation | 95 °C | 00:10 |
| | Annealing (+Plate Read) | 56 °C | 00:20 (+00:10) |
| | Extension | 72 °C | 00:20 |
| Dissociation Stage | Description | Temperature | Time |
| | | 95°C | 00:15 |
| | | 45 °C | 01:00 |
| | | 45 °C | 00:01 |
| | | 80 °C* | |

^{*}increment 0.5 °C

ABI 7500 Fast Dx / 7500 / QS-5 Dx

These settings could be theoretically compatible also with other similar instruments like the Quant Studio version 6/7 and 7500. Verify before use.

Amplified sequence and Channels setting

7500 Fast Dx / 7500

| Target | Gene | Channels | Threshold* | Quencher |
|----------|-------------------------|----------|------------|----------|
| Target 1 | S gene, codon 452 | Cy5 | 10000 | none |
| Target 2 | S gene, codon 484 | FAM | 10000 | none |
| Target 3 | S gene, codon 501 | ROX | 5000 | none |
| IC | Rnase P gene | VIC | 50000 | none |

^{*}TBD for 7500 instrument

Interpretation settings

| Setting | Value | Value |
|-----------|---------------|---------|
| Passive | 7500FDX | QS-5 Dx |
| Reference | none | none |
| Baseline* | Manual (6-15) | AUTO |

^{*}TBD for the other instruments

Thermal Profile

| | Description | Temperature | Time |
|----------------------|------------------------|-------------|-------|
| Hold | Reverse Transcription | 45 °C | 20:00 |
| Hold 2 | Pre-Denaturation | 95 °C | 02:00 |
| | Denaturation | 95 °C | 00:10 |
| Cycling 45 cycles | Annealing (Plate Read) | 56 °C | 00:30 |
| | Extension | 72 °C | 00:20 |
| | Description | Temperature | Time |
| Dissociation | | 95°C | 00:15 |
| Stage | | 45 °C | 01:00 |
| | | 80 °C | 00:15 |
| | | 60 °C^ | 00:15 |

For 7500 Fast Dx and QS5 Dx set the Run Mode as Fast 7500 ^For QS-5 DX the step at 60° C has not be set

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Note: For QS-5 DX flag on all Melt Curve Filter in Optical filter settings to activate dissociation stage.