



# STUDY OBJECTIVES

#### **Using CDC and FDA Protocols and Guidance:**

- 1) Assess the feasibility of detecting nCoV2 genomic material with Empirical Bioscience QuantiTASE PLUS One-Step RT-qPCR reaction mix with EUA approved Primer/Probe materials
- 2) Determine Limit of Detection (LoD) for QuantiTASE PLUS for detection of nCoV2 genomic material
- 3) Compare performance of QuantiTASE PLUS with that of competitor products for the detection of nCoV2 genomic material in clinical samples.

#### MATERIALS AND METHODS

#### **Primer, Probe & Control Sets**

• 2019 nCoV CDC EUA kit: qPCR assay primers & probes Integrated DNA Technologies

#### **SARS-CoV-2 Synthetic RNA Template**

 Quantitative Synthetic Severe acute respiratory syndrome-related coronavirus (SARSCoV-2) RNA: ORF, E, N

#### **SARS-CoV-2 Genomic RNA Template**

Genomic RNA from SARS-Related Coronavirus 2, Isolate USA-WA1/2020

#### **RNA Extraction**

- · Omega Biotek Total RNA Extraction Kit
- Thermofisher MagMax RNA Extraction Kit

#### One Step RT-qPCR Kit

• Empirical Bioscience QuantiTASE One Step RT-PCR Kit

## **EQUIPMENT USED**

- Thermofisher Kingfisher Flex Nucleic Acid Extraction System
- Omega Biotek Total RNA Extraction Kit
- BioRad Touch CFX 96 Realtime PCR system
- ABI QuantStudio 3, QuantStudio 5 and QuantStudio 7 Real-time PCR systems

# LIMIT OF DETECTION (LoD)

The LoD study established the lowest concentration of SARS-CoV-2 (genome equivalent copies(cp)/ reaction) that can be detected by the N1 and N2 assays at least 95% of the time using the Empirical Bioscience QuantiTASE One-Step reagents.

For each assay (N1 and N2), a preliminary LoD was established by testing serial 10-fold dilutions of SARS-CoV-2 RNA. Following the 10-fold dilution series, 20 replicates containing various genome equivalent copy number of the SARS-CoV-2 synthetic RNA were performed to establish an LoD. The lowest concentration in total cp/reaction at which 19/20 replicates resulted in a Ct of less than 40 was established as the LoD for each assay.



## **REACTION SET UP**

| Reagent                        | Final Concentration                                  |
|--------------------------------|--|
| Nuclease Free Water            | N/A (Fill to 15µL)                                   |
| InhibiTAQ Plus MasterMix       | 1X   |
| RTScript Reverse Transcriptase | 5U/μL  |
| Primer/Probe Mix               | 500nM Primers, 125nM Probe                           |
| RNA Template                   | Added to specified genome equivalent copies/reaction |

Data from the serial dilution LoD studies was used as a template for starting concentrations of genomic RNA to be added to RT-qPCR reactions for obtaining an LoD on SARS-CoV2 genomic RNA.

Reagent MasterMix was assembled as before and per CDC guidelines and distributed into each well.

### THERMAL CYCLING PARAMETERS

| Stage           | Time   | Number of Steps                |
|-----------------|--------|--------------------------------|
| 1. 25°C         | 2 min  | 1 rep                          |
| 2. 50°C         | 15 min | 1 rep                          |
| 3. 95°C         | 2 min  | 1 rep                          |
| 4. Step 1, 95°C | 3 sec  |                                |
| 4. Step 2, 55°C | 30 sec | 45 reps for stage 4, steps 1/2 |

Thermal cycling parameters were run according to CDC guidelines. Reactions were amplified and analyzed with BioRad CFX96 Touch Real-Time PCR detection system (96 well) Thermofisher QuantStudio 3 (96 well), QuantStudio 5 (384 well) and QuantStudio 7 (384 well) Real-Time PCR detection systems.

## LOD FOR ALL SYSTEMS EVALUATED

| Assay | LoD (genome equivalent copies/reaction)       | Mean Ct (± std. dev.)<br>of positive replicates |  |
|-------|---|---|--|
| N1    | 5 copies/reaction –<br>100% positive (20/20)  | 37.05 ± 0.68                                    |  |
| N2    | 10 copies/reaction –<br>100% positive (20/20) | 37.01 ± 0.50                                    |  |



## PERFORMANCE DATA

# QuantiTASE PLUS & TaqPATH

|     |                                    |           | =X/20 | Average | Std. Dev |
|-----|------------------------------------|-----------|-------|---------|----------|
|     | Empirical                          | 20 copies | 20/20 | 34.58   | 0.308    |
|     | Empirical QuantiTASE  ThermoFisher | 10 copies | 20/20 | 36.28   | 0.554    |
| NI4 |                                    | 5 copies  | 20/20 | 37.05   | 0.682    |
| N1  |                                    | 20 copies | 20/20 | 34.04   | 0.338    |
|     |                                    | 10 copies | 20/20 | 35.21   | 0.443    |
|     | TaqPATH                            | 5 copies  | 19/20 | 37.59   | 1.005    |

LoD samples were prepared by spiking known copies of Genomic RNA into the RT-PCR reaction mix at the time of analysis. Thermal cycling parameters were run according to CDC guidelines. Reactions were amplified and analyzed with BioRad CFX96 Touch Real-Time PCR detection system (96 well) using the CDC recommended cycling conditions.

|         |                                    |           | =X/20 | Average | Std. Dev |
|---------|------------------------------------|-----------|-------|---------|----------|
| Empirio | Empirical                          | 20 copies | 20/20 | 35.91   | 0.328    |
| NIO     | N2 QuantiTASE ThermoFisher TaqPATH | 10 copies | 20/20 | 37.01   | 0.502    |
| INZ     |                                    | 20 copies | 20/20 | 37.08   | 0.854    |
|         |                                    | 10 copies | 20/20 | 37.94   | 0.491    |

|   |               |               | =X/20 | Average | Std. Dev |
|---|---------------|---------------|-------|---------|----------|
| RPP  Empirical QuantiTASE  ThermoFisher TaqPATH | 50,000 copies | 20/20         | 27.50 | 0.095   |          |
|   |               | 50,000 copies | 20/20 | 26.54   | 0.121    |

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## PERFORMANCE COMPARISON

## **Contrived Clinical Samples**

| Targets                     | N1  |  |   | N2  |  |   |
|-----------------------------|---|--|---|---|--|---|
| Master<br>Mix               | Empirical<br>QuantiTASE<br>Plus 1-Step<br>RT-qPCR<br>System | Thermo<br>Fisher<br>TaqPath<br>1-Step RT-qPCR<br>MasterMix, CG | Promega<br>GoTaq<br>Probe 1-Step<br>RT-qPCR<br>System | Empirical<br>QuantiTASE<br>Plus 1-Step<br>RT-qPCR<br>System | Thermo<br>Fisher<br>TaqPath<br>1-Step RT-qPCR<br>MasterMix, CG | Promega<br>GoTaq<br>Probe 1-Step<br>RT-qPCR<br>System |
| Positives/<br>Total         | 12/12   | 12/12  | 12/12   | 12/12   | 12/12  | 12/12   |
| Mean Ct.                    | 34.78   | 33.12  | 33.97   | 35.89   | 35.38  | 35.87   |
| Standard<br>Deviation<br>Ct | 0.31  | 0.24   | 0.20  | 0.27  | 0.25   | 0.16  |

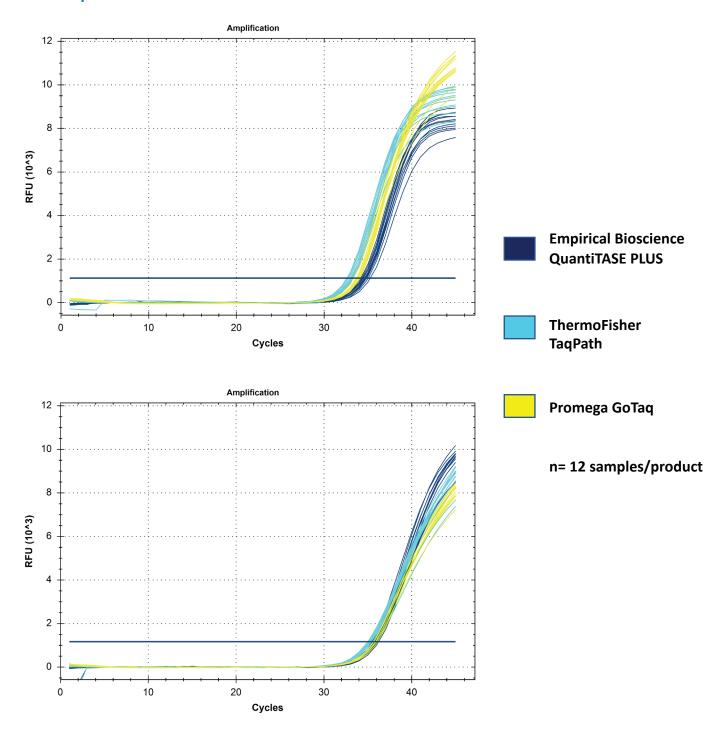
The QuantiTASE PLUS One-Step Universal RT-qPCR Kit SARS-CoV-2 was determined to be compatible with RNA extraction workflow at concentrations at or near LoD. Pooled negative OP swabs were spiked with genomic RNA. Input volume for extraction was  $250\mu$ L and elution volume was  $80\mu$ L. A  $5-\mu$ L aliquot of the eluate was added to the PCR reaction.

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## PERFORMANCE COMPARISON

# **Competitor Products**



Detection on N1 and N2 Genes of nCoV2: 50 copies of Genomic RNA added in a 20uL reaction. Reaction set up and RT-qPCR protocol were in accordance with CDC guidance.

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