Date: July 31, 2023

BD Integrated Diagnostic Solutions/
Kathy Barnecut
Staff Regulatory Affairs Specialist
Becton, Dickinson & Company
7 Loveton Circle
Sparks, Maryland 21152

Re: K230956
Trade/Device Name: BD Respiratory Viral Panel (BD RVP) for BD MAX System; BD Respiratory Viral Panel-SCV2 (BD RVP-SCV2) for BD MAX System
Regulation Number: 21 CFR 866.3981
Regulation Name: Device To Detect And Identify Nucleic Acid Targets In Respiratory Specimens From Microbial Agents That Cause The SARS-Cov-2 Respiratory Infection And Other Microbial Agents When In A Multi-Target Test
Regulatory Class: Class II
Product Code: QOF, QQX
Dated: April 4, 2023
Received: April 4, 2023

Dear Kathy Barnecut:

We have reviewed your Section 510(k) premarket notification of intent to market the device referenced above and have determined the device is substantially equivalent (for the indications for use stated in the enclosure) to legally marketed predicate devices marketed in interstate commerce prior to May 28, 1976, the enactment date of the Medical Device Amendments, or to devices that have been reclassified in accordance with the provisions of the Federal Food, Drug, and Cosmetic Act (Act) that do not require approval of a premarket approval application (PMA). You may, therefore, market the device, subject to the general controls provisions of the Act. Although this letter refers to your product as a device, please be aware that some cleared products may instead be combination products. The 510(k) Premarket Notification Database located at https://www.accessdata.fda.gov/scripts/cdrh/cfdocs/cfpmn/pmn.cfm identifies combination product submissions. The general controls provisions of the Act include requirements for annual registration, listing of devices, good manufacturing practice, labeling, and prohibitions against misbranding and adulteration. Please note: CDRH does not evaluate information related to contract liability warranties. We remind you, however, that device labeling must be truthful and not misleading.

If your device is classified (see above) into either class II (Special Controls) or class III (PMA), it may be subject to additional controls. Existing major regulations affecting your device can be found in the Code of Federal Regulations, Title 21, Parts 800 to 898. In addition, FDA may publish further announcements concerning your device in the Federal Register.

Please be advised that FDA's issuance of a substantial equivalence determination does not mean that FDA has made a determination that your device complies with other requirements of the Act or any Federal statutes and regulations administered by other Federal agencies. You must comply with all the Act's requirements, including, but not limited to: registration and listing (21 CFR Part 807); labeling (21 CFR Part 801 and Part 809); medical device reporting (reporting of medical device-related adverse events) (21 CFR 803) for devices or postmarketing safety reporting (21 CFR 4, Subpart B) for combination products (see https://www.fda.gov/combination-products/guidance-regulatory-information/postmarketing-safety-reporting-combination-products); good manufacturing practice requirements as set forth in the quality systems (QS) regulation (21 CFR Part 820) for devices or current good manufacturing practices (21 CFR 4, Subpart A) for combination products; and, if applicable, the electronic product radiation control provisions (Sections 531-542 of the Act); 21 CFR 1000-1050.

Also, please note the regulation entitled, "Misbranding by reference to premarket notification" (21 CFR Part 807.97). For questions regarding the reporting of adverse events under the MDR regulation (21 CFR Part 803), please go to https://www.fda.gov/medical-devices/medical-device-safety/medical-device-reporting-mdr-how-report-medical-device-problems.

For comprehensive regulatory information about medical devices and radiation-emitting products, including information about labeling regulations, please see Device Advice (https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-assistance) and CDRH Learn (https://www.fda.gov/training-and-continuing-education/cdrh-learn). Additionally, you may contact the Division of Industry and Consumer Education (DICE) to ask a question about a specific regulatory topic. See the DICE website (https://www.fda.gov/medical-devices/device-advice-comprehensive-regulatory-assistance/contact-us-division-industry-and-consumer-education-dice) for more information or contact DICE by email (DICE@fda.hhs.gov) or phone (1-800-638-2041 or 301-796-7100).

Sincerely,

Joseph Briggs -S

Joseph Briggs, Ph.D.
Deputy Branch Chief
Viral Respiratory and HPV Branch
Division of Microbiology Devices
OHT7: Office of In Vitro Diagnostics
Office of Product Evaluation and Quality
Center for Devices and Radiological Health

Enclosure

DEPARTMENT OF HEALTH AND HUMAN SERVICES
Food and Drug Administration

Indications for Use

Form Approved: OMB No. 0910-0120
Expiration Date: 06/30/2023
See PRA Statement below.

510(k) Number *(if known)*
K230956

Device Name
BD Respiratory Viral Panel for BD MAX™ System;
BD Respiratory Viral Panel-SCV2 for BD MAX™ System

Indications for Use *(Describe)*

BD Respiratory Viral Panel for BD MAX™ System:

BD Respiratory Viral Panel for BD MAX™ System is an automated multiplexed real-time reverse transcriptase polymerase chain reaction (RT- PCR) test intended for the simultaneous, qualitative detection and differentiation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), influenza A, influenza B, and/or respiratory syncytial virus (RSV) nucleic acid in nasopharyngeal swab (NPS) and anterior nasal swab (ANS) specimens from individuals with signs and symptoms of respiratory tract infection. Clinical signs and symptoms of respiratory tract infection due to SARS-CoV-2, influenza, and RSV can be similar.

BD Respiratory Viral Panel for BD MAX™ System is intended for use as an aid in the differential diagnosis of SARS-CoV-2, influenza A, influenza B, and/or RSV infection if used in conjunction with other clinical and epidemiological information, and laboratory findings. SARS-CoV- 2, influenza A, influenza B, and RSV viral nucleic acid are generally detectable in NPS and ANS specimens during the acute phase of infection.

Positive results do not rule out co-infection with other organisms. The agent(s) detected by the BD Respiratory Viral Panel for BD MAX™ System may not be the definitive cause of disease.

Negative results do not preclude SARS-CoV-2, influenza A, influenza B, and/or RSV infection.

The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.

BD Respiratory Viral Panel-SCV2 for BD MAX™ System:

BD Respiratory Viral Panel-SCV2 for BD MAX™ System is an automated multiplexed real-time reverse transcriptase polymerase chain reaction (RT-PCR) test intended for the simultaneous, qualitative detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral nucleic acid in nasopharyngeal swab (NPS) and anterior nasal swab (ANS) specimens from individuals with signs and symptoms of respiratory tract infection. SARS-CoV-2 viral RNA is generally detectable in NPS and ANS specimens during the acute phase of infection.

The BD Respiratory Viral Panel-SCV2 for BD MAX™ System is intended for use as an aid in the diagnosis of SARS-CoV-2 infection if used in conjunction with other clinical and epidemiological information, and laboratory findings.

Positive results do not rule out co-infection with other organisms. The agent detected by the BD Respiratory Viral Panel-SCV2 for BD MAX™ System may not be the definitive cause of disease.

Negative results do not preclude SARS-CoV-2 infection.

The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.

Type of Use *(Select one or both, as applicable)*

☒ Prescription Use (Part 21 CFR 801 Subpart D) ☐ Over-The-Counter Use (21 CFR 801 Subpart C)

CONTINUE ON A SEPARATE PAGE IF NEEDED.

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510(k) Summary

BD Respiratory Viral Panel for BD MAX™ System & BD Respiratory Viral Panel-SCV2 for BD MAX™ System

Summary Preparation Date:

06/30/2022

Submitted by:

Becton, Dickinson and Company
7 Loveton Circle
Sparks, MD 21152

Contact:

Kathy Barnecut, RAC
Staff Regulatory Affairs Specialist
Tel: 858-210-2284
Email: kathy.barnecut@bd.com

Device Trade Names:

BD Respiratory Viral Panel for BD MAX™ System (445373)
BD Respiratory Viral Panel-SCV2 for BD MAX™ System (445361)

Common Names:

Device to detect and identify nucleic acid targets in respiratory specimens from microbial agents that cause the SARS-CoV-2 respiratory infection and other microbial agents when in a multi-target test.

Regulatory Information

Regulation section:

866.3981 – Device to detect and identify nucleic acid targets in respiratory specimens from microbial agents that cause the SARS-CoV-2 respiratory infection and other microbial agents when in a multi-target test

Classification:

Class II

Panel:

Microbiology

Product Code(s):

QOF – Multi-Target Respiratory Specimen Nucleic Acid Test Including SARS-CoV-2 And Other Microbial Agents

QQX – Respiratory Specimen Nucleic Acid SARS-CoV-2 Test

Predicate Device

BioFire Respiratory Panel 2.1 (RP2.1) (DEN200031)

Device Establishment

Becton, Dickinson and Company
7 Loveton Circle
Sparks, MD 21152
Registration Number: 1119779

Performance Standards

Class II Special Controls as per 21 CFR 866.3981

Class II Special Controls Guidance Document: Testing for Detection and Differentiation of Influenza A Virus Subtypes Using Multiplex Nucleic Acid Assays, October 9, 2009.

Intended Use

BD Respiratory Viral Panel for BD MAX™ System:

BD Respiratory Viral Panel for BD MAX™ System is an automated multiplexed real-time reverse transcriptase polymerase chain reaction (RT- PCR) test intended for the simultaneous, qualitative detection and differentiation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), influenza A, influenza B, and/or respiratory syncytial virus (RSV) nucleic acid in nasopharyngeal swab (NPS) and anterior nasal swab (ANS) specimens from individuals with signs and symptoms of respiratory tract infection. Clinical signs and symptoms of respiratory tract infection due to SARS-CoV-2, influenza, and RSV can be similar.

BD Respiratory Viral Panel for BD MAX™ System is intended for use as an aid in the differential diagnosis of SARS-CoV-2, influenza A, influenza B, and/or RSV infection if used in conjunction with other clinical and epidemiological information, and laboratory findings. SARS-CoV- 2, influenza A, influenza B, and RSV viral nucleic acid are generally detectable in NPS and ANS specimens during the acute phase of infection.

Positive results do not rule out co-infection with other organisms. The agent(s) detected by the BD Respiratory Viral Panel for BD MAX™ System may not be the definitive cause of disease.

Negative results do not preclude SARS-CoV-2, influenza A, influenza B, and/or RSV infection.

The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.

BD Respiratory Viral Panel-SCV2 for BD MAX™ System:

BD Respiratory Viral Panel-SCV2 for BD MAX™ System is an automated multiplexed real-time reverse transcriptase polymerase chain reaction (RT-PCR) test intended for the simultaneous, qualitative detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral nucleic acid in nasopharyngeal swab (NPS) and anterior nasal swab (ANS) specimens from individuals with signs and symptoms of respiratory tract infection. SARS-CoV-2 viral RNA is generally detectable in NPS and ANS specimens during the acute phase of infection.

The BD Respiratory Viral Panel-SCV2 for BD MAX™ System is intended for use as an aid in the diagnosis of SARS-CoV-2 infection if used in conjunction with other clinical and epidemiological information, and laboratory findings.

Positive results do not rule out co-infection with other organisms. The agent detected by the BD Respiratory Viral Panel-SCV2 for BD MAX™ System may not be the definitive cause of disease.

Negative results do not preclude SARS-CoV-2 infection.

The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.

Special Conditions for Use Statement:

For Prescription Use Only
For in vitro diagnostic use only

Special Instrument Requirements:

BD Respiratory Viral Panel for BD MAX™ System and BD Respiratory Viral Panel-SCV2 for BD MAX™ System are performed on the BD MAX™ System.

Device Description

The BD Respiratory Viral Panel (BD RVP) and BD Respiratory Viral Panel-SCV2 (BD RVP-SCV2) along with the BD MAXTM System are comprised of an instrument with associated hardware and accessories, disposable microfluidic cartridges, master mixes, unitized reagent strips, and extraction reagents. The instrument automates sample preparation including target lysis, Total Nucleic Acid (TNA) extraction and concentration, reagent rehydration, target nucleic acid

amplification and detection using real-time PCR. The assay includes a Sample Processing Control (SPC) that is present in the Extraction Tube. The SPC monitors RNA extraction steps, thermal cycling steps, reagent integrity and the presence of inhibitory substances. The BD MAX™ System software automatically interprets test results. For the BD Respiratory Viral Panel for BD MAX™ System and BD Respiratory Viral Panel-SCV2 for BD MAX™ System, a test result may be called as POS, NEG or UNR (Unresolved) based on the amplification status of the targets and of the Sample Processing Control. IND (Indeterminate) or INC (Incomplete) results are due to BD MAX™ System failure.

Test Principle

The BD Respiratory Viral Panel for BD MAX™ System and BD Respiratory Viral Panel-SCV2 for BD MAX™ System assays are designed for use with a nasopharyngeal or anterior nasal swabs collected in BD Universal Viral Transport System (UVT) or Copan Universal Transport Media System (UTM). Once collected, the UVT/UTM patient sample is vortexed and 750ul is transferred to the BD Molecular RVP Sample Buffer Tube (SBT) provided with the BD Respiratory Viral Panel for BD MAX™ System. placed in the BD MAX™ System. For all sample types the SBTs are vortexed and then loaded into the BD MAX system along with the Unitized Reagent Strips, Master Mix, Extraction Tubes, and PCR Cartridges. No further operator intervention is necessary.

The BD RVP Unitized Reagent Strip contains a combination of lytic and extraction reagents designed to perform cell lysis and TNA extraction. Nucleic acids released from the target organisms are captured on magnetic affinity beads. The beads, together with the bound nucleic acids, are washed and the nucleic acids are eluted by a combination of heat and pH variation. Eluted TNA is added to neutralization buffer, mixed, and transferred to BD Respiratory Viral Panel master mix for rehydration. After reconstitution, the BD MAX™ System dispenses a fixed volume of RT-PCR-ready solution containing extracted nucleic acids into the PCR Cartridge. Microvalves on the cartridge are sealed by the system prior to initiating PCR in order to contain the amplification mixture and thus prevent evaporation and contamination.

The amplified cDNA targets are detected using hydrolysis (TaqMan®) probes, labeled at one end with a fluorescent reporter dye (fluorophore), and at the other end, with a quencher moiety. Probes labeled with different fluorophores are used to detect the target analytes in different optical channels of the BD MAX™ System. When the probes are in their native state, the fluorescence of the fluorophore is quenched due to its proximity to the quencher. However, in the presence of target cDNA, the probes hybridize to their complementary sequences and are hydrolyzed by the 5'–3' exonuclease activity of the DNA polymerase as it synthesizes the nascent strand along the cDNA template. As a result, the fluorophores are separated from the quencher molecules and fluorescence is emitted. The amount of fluorescence detected in the optical channels is directly proportional to the quantity of the corresponding probe that is hydrolyzed. The BD MAX™ System monitors these signals at each cycle of the PCR and interprets the data at the end of the reaction to provide qualitative test results for each analyte.

Substantial Equivalence[1]

Indication for Use Comparison:

The BD Respiratory Viral Panel for BD MAX™ System and BD Respiratory Viral Panel-SCV2 for BD MAX™ System have a similar intended use as their predicate device, except for fewer targeted analytes in the BD Respiratory Viral Panel for BD MAX™ System as opposed to the BioFire Respiratory Panel 2.1 (RP2.1), DEN200031. All BD Respiratory Viral Panel for BD MAX™ System analytes are included in the BioFire Respiratory Panel 2.1 (RP2.1). The BD Respiratory Viral Panel-SCV2 for BD MAX™ System has the same analyte target as the BioFire COVID-19 Test 2, K211079/K221460.

Technological Comparison:

The BD MAX™ Assays have similar principle of operation as their predicate, the BioFire Respiratory Panel 2.1 (RP2.1), DEN200031, and BioFire COVID-19 Test 2, K211079/K221460. All assay reagent kits contain the materials required to complete tests and includes the hydration solution, sample buffer, and sample handling components such as transfer pipettes. All assays, subject devices and predicates, are used to test patient samples in a closed system that stores all the necessary reagents for sample preparation reverse transcription, polymerase chain reaction (PCR), and detection in order to isolate, amplify, and detect nucleic acid from multiple pathogens. Minor differences can be observed in the detection chemistry where the BD Respiratory Viral Panel for BD MAX™ System and the BD Respiratory Viral Panel-SCV2 for BD MAX™ System utilize paired reporter and quencher fluorescence labeled probes (TaqMan Technology) as opposed to the BioFire Respiratory Panel 2.1 (RP2.1) and BioFire COVID-19 Test 2 which utilize a two Step Nested multiplex PCR where sequences from the first RT-PCR/PCR are amplified using fluorescence double stranded binding dye. The minor differences between the subject and predicate devices do not raise any new questions of safety or effectiveness.

Table 1 provides the similarities and differences between the BD Respiratory Viral Panel for BD MAX™ System and BD Respiratory Viral Panel-SCV2 for BD MAX™ System, respectively, in comparison to their predicate devices.

[1] The term "substantial equivalence" as used in this 510(k) notification is limited to the definition of substantial equivalence as found in the Federal Food, Drug and Cosmetic Act, as amended and as applied under 21 CFR 807, Subpart E under which a device can be marketed without pre-market approval or reclassification. A determination of substantial equivalency under this notification is not intended to have any bearing whatsoever on the resolution of patent infringement suits or any other patent matters. No statements related to, or in support of substantial equivalence herein shall be construed as an admission against interest under the US Patent Laws or their application by the courts.

Table 1. BD Respiratory Viral Panel for BD MAX™ System Substantial Equivalence Comparison

Device and Predicate Device	Subject Device (K230956)		DEN200031 (Predicate Device)
Device Trade Name	BD Respiratory Viral Panel for BD MAX™ System	BD Respiratory Viral Panel-SCV2 for BD MAX™ System	BioFire Respiratory Panel 2.1 (RP2.1)
Regulation Number	21 CFR 866.3981	21 CFR 866.3981	Same
Regulation Name	Multi-Target Respiratory Specimen Nucleic Acid Test Including Sars-Cov-2 And Other Microbial Agents	Multi-Target Respiratory Specimen Nucleic Acid Test Including Sars-Cov-2 And Other Microbial Agents	Same
Product Code	QOF	QQX	QOF

Device and Predicate Device	Subject Device (K230956)		DEN200031 (Predicate Device)
Intended Use	BD Respiratory Viral Panel for BD MAX™ System is an automated multiplexed real-time reverse transcriptase polymerase chain reaction (RT- PCR) test intended for the simultaneous, qualitative detection and differentiation of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2), influenza A, influenza B, and/or respiratory syncytial virus (RSV) nucleic acid in nasopharyngeal swab (NPS) and anterior nasal swab (ANS) specimens from individuals with signs and symptoms of respiratory tract infection. Clinical signs and symptoms of respiratory tract infection due to SARS-CoV-2, influenza, and RSV can be similar. BD Respiratory Viral Panel for BD MAX™ System is intended for use as an aid in the differential diagnosis of SARS-CoV-2, influenza A, influenza B, and/or RSV infection if used in conjunction with other clinical and epidemiological information, and laboratory findings. SARS-CoV- 2, influenza A, influenza B, and RSV viral nucleic acid are generally detectable in NPS and ANS specimens during the acute phase of infection. Positive results do not rule out co-infection with other organisms. The agent(s) detected	BD Respiratory Viral Panel-SCV2 for BD MAX™ System is an automated multiplexed real-time reverse transcriptase polymerase chain reaction (RT-PCR) test intended for the simultaneous, qualitative detection of severe acute respiratory syndrome coronavirus 2 (SARS-CoV-2) viral nucleic acid in nasopharyngeal swab (NPS) and anterior nasal swab (ANS) specimens from individuals with signs and symptoms of respiratory tract infection. SARS-CoV-2 viral RNA is generally detectable in NPS and ANS specimens during the acute phase of infection. The BD Respiratory Viral Panel-SCV2 for BD MAX™ System is intended for use as an aid in the diagnosis of SARS-CoV-2 infection if used in conjunction with other clinical and epidemiological information, and laboratory findings. Positive results do not rule out co-infection with other organisms. The agent detected by the BD Respiratory Viral Panel-SCV2 for BD MAX™ System may not be the definitive cause of disease. Negative results do not preclude SARS-CoV-2 infection.	The BIOFIRE Respiratory Panel 2.1 (RP2.1) is a PCR based multiplexed nucleic acid test intended for use with the BIOFIRE FilmArray 2.0 or BIOFIRE FilmArray Torch systems for the simultaneous qualitative detection and identification of multiple respiratory viral and bacterial nucleic acids in nasopharyngeal swabs (NPS) obtained from individuals suspected of respiratory tract infections, including COVID-19. The following organism types and subtypes are identified using the BIOFIRE RP2.1: • Adenovirus • Coronavirus 229E • Coronavirus HKU1 • Coronavirus NL63 • Coronavirus OC43 • Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV-2) • Human Metapneumovirus • Human Rhinovirus/Enterovirus • Influenza A, including subtypes H1, H1-2009, and H3 • Influenza B • Parainfluenza Virus 1 • Parainfluenza Virus 2 • Parainfluenza Virus 3 • Parainfluenza Virus 4 • Respiratory Syncytial Virus • Bordetella parapertussis (IS1001)

Device and Predicate Device	Subject Device (K230956)		DEN200031 (Predicate Device)
	by the BD Respiratory Viral Panel for BD MAX™ System may not be the definitive cause of disease. Negative results do not preclude SARS-CoV-2, influenza A, influenza B, and/or RSV infection. The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.	The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions.	• Bordetella pertussis (ptxP) • Chlamydia pneumoniae, and • Mycoplasma pneumoniae Nucleic acids from the respiratory viral and bacterial organisms identified by this test are generally detectable in NPS specimens during the acute phase of infection. The detection and identification of specific viral and bacterial nucleic acids from individuals exhibiting signs and/or symptoms of respiratory infection is indicative of the presence of the identified microorganism and aids in the diagnosis of respiratory infection if used in conjunction with other clinical and epidemiological information. The results of this test should not be used as the sole basis for diagnosis, treatment, or other patient management decisions. Negative results in the setting of a respiratory illness may be due to infection with pathogens that are not detected by this test, or lower respiratory tract infection that may not be detected by an NPS specimen. Positive results do not rule out coinfection with other organisms. The agent(s) detected by the BIOFIRE RP2.1 may not be the definite cause of disease. Additional laboratory testing (e.g., bacterial and viral culture, immunofluorescence, and radiography) may be necessary when evaluating a

Device and Predicate Device	Subject Device (K230956)		DEN200031 (Predicate Device)
			patient with possible respiratory tract infection.
Condition for use	For prescription use For in vitro diagnostic use only.		Same
Sample Types	Nasopharyngeal swab specimen Nasal swab specimen		Nasopharyngeal swab specimen
Patient Population	Individuals suspected of COVID-19 by their healthcare provider		Individuals suspected of respiratory tract infections, including COVID-19

Device and Predicate Device	Subject Device (K230956)		DEN200031 (Predicate Device)
Analyte Targets	The following organism types are identified using the BD Respiratory Viral Panel for BD MAX™ System: • Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV-2), • Influenza A, • Influenza B, and • Respiratory Syncytial Virus	SARS-CoV-2	The following organism types and subtypes are identified using the BioFire RP2.1: • Adenovirus, • Coronavirus 229E, • Coronavirus HKU1, • Coronavirus NL63, • Coronavirus OC43, • Severe Acute Respiratory Syndrome Coronavirus (SARS-CoV-2), • Human Metapneumovirus, • Human Rhinovirus/Enterovirus, • Influenza A, including subtypes H1, H1-2009, and H3, • Influenza B, • Parainfluenza Virus 1, • Parainfluenza Virus 2, • Parainfluenza Virus 3, • Parainfluenza Virus 4, • Respiratory Syncytial Virus, • Bordetella parapertussis (IS1001), • Bordetella pertussis (ptxP), • Chlamydia pneumoniae, and • • Mycoplasma pneumoniae
Sample Preparation Procedure	Automated by BD MAX™ System		Automated by BioFire FilmArray 2.0 or BioFire FilmArray Torch systems
Amplification Technology	Real-Time PCR		Nested multiplex RT-PCR
Analyte	RNA		RNA/DNA

Device and Predicate Device	Subject Device (K230956)	DEN200031 (Predicate Device)
Detection Chemistry	Paired reporter and quencher fluorescence labeled probes (TaqMan Technology) using fluorescence resonance energy transfer	Two Step Nested multiplex PCR: - Reverse transcription, followed by a multiplexed first stage PCR reaction (PCR1). Multiple simultaneous second stage PCR reactions (PCR2) to amplify sequences within the PCR1 products using fluorescence double stranded binding dye. Endpoint melting curve data to detect target specific amplicons
Control used	1. The RNA Internal Control (RNase P) 2. External Positive and negative controls	Two process controls: 1. RNA Process Control (IC) 2. PCR2 Control (A positive result indicates that PCR2 was successful)
Result Analysis	Based on PCR cycle threshold analysis	Endpoint melting curve data to detect target-specific amplicons
Test Interpretation	Automated test interpretation and report generation. User cannot access raw data.	Same
Time to Result	About 2 hours	About 45 min

Analytical Performance Evaluation

BD Respiratory Viral Panel for BD MAX™ System and BD Respiratory Viral Panel-SCV2 for BD MAX™ System performance testing provided as part of this submission was conducted in accordance with the Respiratory Viral Panel Multiplex Nucleic Acid Assay - Class II Special Control Guidance for Industry and FDA Staff [October 9, 2009] and Class II Special Controls as per 21 CFR 866.3981. Additional consideration was also taken in regarding of COVID-19 and the Policy for Evaluating Impact of Viral Mutations on COVID-19 Tests (Revised) [January 12, 2023] in terms of evaluating the impact of identified variants on the BD MAX-SARS-CoV-2 primers and probes.

BD Respiratory Viral Panel for BD MAX™ System:

Precision

Within-laboratory precision was evaluated for the BD Respiratory Viral Panel at one site with one (1) reagent lot. Testing was performed over twelve (12) days, with two (2) operators performing two (2) runs per day for a total of forty-eight (48) runs. Test samples were contrived in simulated nasopharyngeal matrix and included SARS-CoV-2, Influenza A, Influenza B, and RSV panel members. Each panel member was tested in three (3) replicates. The following target concentrations were used for each target organism contained in each panel member:

- Moderate positive (MP): 3x LoD
- Low Positive (LP): 2x LoD
- True Negative (TN): No target

Precision study results are described in Table 2.

Table 2. Overall Precision Study Results Using One Lot of the BD Respiratory Viral Panel (Percent Agreement with Expected Results)

Sample Concentration	SARS-CoV-2 (N), 95% CI	Flu A (N), 95% CI	Flu B (N), 95% CI	RSV (N), 95% CI
Moderate Positive (3x LoD)	100% (144/144) 97.4-100	100% (144/144) 97.4-100	100% (144/144) 97.4-100	100% (144/144) 97.4-100
Low Positive (2x LoD)	100% (144/144) 97.4-100	97.2% (140/144) 93.1-98.9	99.3% (143/144) 96.2-99.9	99.3% (143/144) 96.2-99.9
True Negative[a]	100% (288/288) 98.7-100	100% (288/288) 98.7-100	100% (288/288) 98.7-100	100% (288/288) 98.7-100

[a] For the True Negative category, the reported agreement indicates percent of negative results.

Reproducibility

For the Site-to-Site reproducibility study, three (3) sites (two external and one internal) were provided the same panels as described for the Precision study above. Each site performed testing on five (5) distinct days (consecutive or not), wherein each day, one (1) panel was tested by two (2) technologists. Each panel member was tested in three (3) replicates.

The site-to-site reproducibility is presented below in Table 3 by target analyte. Ct, internal criterion used to determine a final assay result, was selected as an additional means of assessing assay reproducibility. Overall mean Ct values with variance components (SD and %CV) are shown in Table 4.

Table 3. Site-to-Site Reproducibility Study Results using One (1) Lot of the BD Respiratory Viral Panel (Percent Agreement with Expected Results)

Sample Concentration	SARS-CoV-2 (N), 95% CI	Flu A (N), 95% CI	Flu B (N), 95% CI	RSV (N), 95% CI
Moderate Positive (3x LoD)	100% (90/90) 95.9-100	97.8% (88/90) 92.3-99.4	100% (90/90) 95.9-100	100% (90/90) 95.9-100
Low Positive (2x LoD)	100% (90/90) 95.9-100	96.7% (87/90) 90.7-98.9	100% (90/90) 95.9-100	100% (90/90) 95.9-100
True Negative[a]	100% (180/180) 97.9-100	100% (180/180) 97.9-100	100% (180/180) 97.9-100	100% (180/180) 97.9-100

[a] For the True Negative category, the reported agreement indicates percent of negative results.

Table 4. Site-to-Site Reproducibility Across Sites, Days, Runs, and Replicates (Ct Values)

Target	Level	N	Mean Ct	Within Run		Between Run		Between Day		Between Site		Total	
				SD	CV (%)	SD	CV (%)	SD	CV (%)	SD	CV (%)	SD	CV (%)
CoV-2	LP	90	33.3	0.74	2.2	0.00	0.0	0.00	0.0	0.54	1.6	0.92	2.8
CoV-2	MP	90	33.0	0.45	1.4	0.08	0.2	0.00	0.0	0.74	2.2	0.87	2.6
Flu A	LP	87	34.9	1.31	3.8	0.36	1.0	0.00	0.0	0.51	1.5	1.45	4.2
Flu A	MP	88	33.5	1.03	3.1	0.37	1.1	0.00	0.0	0.20	0.6	1.11	3.3
Flu B	LP	90	33.6	1.25	3.7	0.00	0.0	0.29	0.9	0.20	0.6	1.29	3.9
Flu B	MP	90	33.0	0.67	2.0	0.00	0.0	0.20	0.6	0.15	0.5	0.72	2.2
RSV	LP	90	32.4	1.32	4.1	0.00	0.0	0.00	0.0	0.00	0.0	1.32	4.1
RSV	MP	90	31.9	0.92	2.9	0.00	0.0	0.00	0.0	0.13	0.4	0.92	2.9

For the Lot-to-Lot reproducibility study, one (1) internal site was provided the same panels as described for the Precision study above. Three (3) reagent lots were tested across five (5) distinct days (consecutive or not) using one (1) BD MAX™, wherein each day, two (2) panels were tested by two (2) technologists. Each panel member was tested in three (3) replicates.

The lot-to-lot reproducibility is presented below in Table 5 by target analyte. Ct, internal criterion used to determine a final assay result, was selected as an additional means of assessing assay reproducibility. Overall mean Ct values with variance components (SD and %CV) are shown in Table 6.

Table 5. Lot-to-Lot Reproducibility Study Results using Three (3) Lots of the BD Respiratory Viral Panel (Percent Agreement with Expected Results)

Sample Concentration	SARS-CoV-2 (N), 95% CI	Flu A (N), 95% CI	Flu B (N), 95% CI	RSV (N), 95% CI
Moderate Positive (3x LoD)	99.4% (179/180) 96.9-99.9	100% (180/180) 97.9-100	98.9% (178/180) 96.0-99.7	100% (180/180) 97.9-100
Low Positive (2x LoD)	100% (180/180) 97.9-100	97.8% (176/180) 94.4-99.1	100% (180/180) 97.9-100	100% (180/180) 97.9-100
True Negative[a]	100% (360/360) 98.9-100	100% (360/360) 98.9-100	100% (360/360) 98.9-100	100% (360/360) 98.9-100

[a] For the True Negative category, the reported agreement indicates percent of negative results.

Table 6. Lot-to-Lot Reproducibility across Operators, Days, Runs, and Replicates (Ct Values)

Target	Level	N	Mean Ct	Lot		Day		Operator		Run		Within Run (Repeatability)		Total	
				SD	CV(%)	SD	CV(%)	SD	CV(%)	SD	CV(%)	SD	CV(%)	SD	CV(%)
CoV-2	MP	179	33.7	0.26	0.8	0.06	0.2	0.10	0.3	0.00	0.0	0.61	1.8	0.67	2.0
CoV-2	LP	180	33.9	0.24	0.7	0.18	0.5	0.12	0.3	0.00	0.0	0.64	1.9	0.72	2.1
Flu A	MP	180	33.2	0.26	0.8	0.00	0.0	0.00	0.0	0.00	0.0	1.05	3.2	1.08	3.3
Flu A	LP	176	34.3	0.44	1.3	0.44	1.3	0.00	0.0	0.23	0.7	1.40	4.1	1.55	4.5
Flu B	MP	178	33.3	0.30	0.9	0.36	1.1	0.00	0.0	0.16	0.5	1.30	3.9	1.39	4.2
Flu B	LP	180	34.1	0.00	0.0	0.17	0.5	0.00	0.0	0.22	0.6	1.20	3.5	1.23	3.6
RSV	MP	180	31.9	0.58	1.8	0.00	0.0	0.00	0.0	0.00	0.0	1.12	3.5	1.26	4.0
RSV	LP	180	32.7	0.60	1.8	0.00	0.0	0.00	0.0	0.05	0.1	0.87	2.7	1.06	3.2

Linearity

Not applicable. This is a qualitative assay.

Limit of Detection (LoD)

The analytical sensitivity of the BD Respiratory Viral Panel for BD MAX™ System was assessed in both nasopharyngeal and nasal clinical matrix across seven respiratory viruses. LoD studies determine the lowest detectable concentration of virus at which approximately 95% of all (true positive) replicates test positive. Analysis of SARS-CoV-2 was completed with a Probit statistical methodology. Analysis of three strains of influenza A (H1N1/Brisbane,

H1N1(pdm09)/Guangdong-Maonan, and H3N2/Kansas), influenza B (Colorado and Phuket/3073/13), RSV A and RSV B was completed with a limiting dilution with 3-fold serial dilutions between each level. A minimum of five determination levels and one negative level across three (3) reagent lots were tested. Confirmation of the estimated LoD was performed with one reagent lot in replicates of 20 prepared in nasopharyngeal and nasal matrix and are reported in Table 7. To confirm that the co-spiking of analytes does not impact analytical sensitivity, the LoD was also confirmed with one strain per analyte.

Table 7. BD Respiratory Viral Panel for BD MAX™ System Limit of Detection

Strain	LoD Concentration (in UVT)	
	Nasopharyngeal	Nasal
SARS-CoV-2 (USA-WA1/2020)	700 copies/mL	700 copies/mL
Influenza A/H1N1/Brisbane/59/07	5.6E-03 $TCID_{50}$/mL	5.6E-03 $TCID_{50}$/mL
Influenza A/H1N1/Guangdong-Maonan/ SWL 1536/19	2.49E-01 $TCID_{50}$/mL	2.49E-01 $TCID_{50}$/mL
Influenza A/H3N2/Kansas/14/17	2.8E-01 $TCID_{50}$/mL	2.8E-01 $TCID_{50}$/mL
Influenza B/Colorado/6/17	6.8E-03 $TCID_{50}$/mL	6.8E-03 $TCID_{50}$/mL
Influenza B/Phuket/3073/13	2.9E-02 $TCID_{50}$/mL	9.6E-03 $TCID_{50}$/mL
RSV A 2006 Isolate	3.1E-02 $TCID_{50}$/mL	3.1E-02 $TCID_{50}$/mL
RSV B CH93(18)-18	1.7E-02 $TCID_{50}$/mL	5.6E-03 $TCID_{50}$/mL

Inclusivity

An *in silico* alignment of the BD Respiratory Viral Panel primers and probes demonstrated that the performance of the BD Respiratory Viral Panel reagents for the BD MAX™ system is not directly impacted by the presence of mutations in known SARS-CoV-2 viral variants. As of June 10, 2022, BD continues to monitor all lineages and sublineages for the following WHO labeled Variants of Concern, Alpha, Beta, Gamma, Delta, and Mu. In all cases greater than 99% of the sequenced isolates are a perfect match to all primers and probes in either the N1 or N2 set. Given similar performance from both the N1 and N2 channel, either will back up the other in the event of performance degradation through genetic drift. Additionally, BD continues to monitor all lineages of the WHO Omicron label, including sublineages within BA.1, BA.2, BA.2.12.1, BA.3, BA.4, and BA.5. All Omicron genomes contain a mutation that affects the N1 probe 3 bases from the 5' end. (Mutation C28311T). Each Omicron sub-lineage has a percentage of sequences that are a perfect match to either the N1 or N2 primer-set as follows: BA.1 at 99.47%, BA.2 at 98.95%, BA.2.12.1 at 99.63%, BA.3 at 100%, BA.4 at 96.87% and BA.5 at 99.55%.

An *in-silico* comparison of the influenza A primer set was performed using all available high quality Influenza A M1 (matrix protein) gene sequences submitted to the NCBI GenBank database as of January 02, 2022 (n=44,468). Multiple alignment of the matrix gene showed that 90.3% of sequences are a perfect match to the primer/probe set while an additional 9.5% of sequences have a single base mismatch in the 5' end of a single primer. Multiple mismatches to the primers and probe occurred in only 0.2% of sequences.

An *in-silico* comparison of the influenza B primer sets was performed using all available high quality Influenza B M1 gene and HA gene sequences submitted to the NCBI GenBank database

as of January 02, 2022. A total of 11,683 matrix and 18,559 HA sequences were used in this analysis. Multiple alignment of the M1 gene showed that 97.1% of sequences are a perfect match to the primer/probe set and 76.7% of HA sequences are a perfect match.

An *in-silico* comparison of the RSV primer sets was performed using all available high quality RSV M gene and N gene sequences submitted to the NCBI GenBank database as of January 02, 2022 (N=3,443). Alignments against the M and N gene showed that the primer/probe sets are a perfect match to 83.0% of sequences in the database, 92.3% of the sequences were a perfect match to the M primer/probe set, and 90.1% were a perfect match to the N primer/probe set region. In total, 99.4% are a perfect match to either the M gene or the N gene primer sets.

BD Respiratory Viral Panel for BD MAX™ System was evaluated against multiple strains of SARS-CoV-2, influenza A H1N1 and H3N2, influenza B including both the Yamagata and Victoria lineages, and RSV including both A and B. A total of 11 SARS-CoV-2, 30 influenza A, 10 influenza B, and 5 RSV strains were evaluated at levels near the analytical LoD. Three replicates were tested for each strain. Refer to Table 8 for the BD Respiratory Viral Panel for BD MAX™ System analytical reactivity/inclusivity.

Table 8. Analytical Reactivity/Inclusivity for the BD Respiratory Viral Panel for the BD MAX™ System

Virus	Strain	Source	Concentration Detected	Relative LoD	Positive Results/ Total
SARS-CoV-2	Hong Kong/VM200001061/2020	ZeptoMetrix® 0810590CFHI	2100 copies/mL	3x LoD	3/3
	Italy-INMI1	ZeptoMetrix® 0810589CFHI	2100 copies/mL	3x LoD	3/3
	Alpha, (B.1.1.7) USA/ CA_CDC_5574/2020	ZeptoMetrix® 0810612CFHI	2100 copies/mL	3x LoD	3/3
	Alpha, (B.1.1.7) England/204820464/2020	ZeptoMetrix® 0810614CFHI	2100 copies/mL	3x LoD	3/3
	eta, (B.1.351) South Africa/ KRISP-K005325/2020	ZeptoMetrix® 0810613CFHI	2100 copies/mL	3x LoD	3/3
	Kappa, (B.1.617.1) USA/ CA-Stanford-15_S02/2021	ZeptoMetrix® 0810623CFHI	2100 copies/mL	3x LoD	3/3
	amma, (P1) Japan/ TY7-503/2021	ZeptoMetrix® 0810616CFHI	2100 copies/mL	3x LoD	3/3
	lta, (B.1.617.2) USA/ PHC658/2021	ZeptoMetrix® 0810624CFHI	2100 copies/mL	3x LoD	3/3
	Iota, (B.1.526_2021) NY-Wadsworth-21025952-01/2021	ZeptoMetrix® 0810619CFHI	2100 copies/mL	3x LoD	3/3
	Zeta, (P2_2021) NY-Wadsworth-21006055-01/2021	ZeptoMetrix® 0810618CFHI	2100 copies/mL	3x LoD	3/3
	Omicron (BA.1) USA/ GA-EHC-2811C/2021	ATCC® VR-3347HK	2100 copies/mL	3x LoD	3/3

Assay Measuring Range

Not applicable. This is a qualitative assay.

Interfering Substances

Twenty-three (23) biological and chemical substances that may be present in nasopharyngeal or anterior nasal swab specimens were evaluated for potential interference with the BD Respiratory Viral Panel for BD MAX™ System in the absence and presence of assay analytes (SARS-CoV-2, influenza A, influenza B, and RSV). Whole blood (human) was found to interfere at levels above 0.2% volume/volume for SARS-CoV-2. Results demonstrated no reportable interference from any other substance at the concentrations tested (refer to Table 9).

Table 9. Endogenous and Commercial Exogenous Substances Tested with BD Respiratory Viral Panel for the BD MAX™ System

Substance	Active Ingredient	Concentration Tested	Positive Testing (Positive/Total)				Negative Testing (Negative/ Total)	Result
			SARS- CoV-2	Influenza A	Influenza B	RSV		
Oral anesthetic and analgesic	Benzocaine	0.8 mg/mL	3/3	3/3	3/3	3/3	3/3	NI
	Menthol							
Biologicals	Purified Mucin	60 µg/mL	3/3	3/3	3/3	3/3	3/3	NI
	Whole Blood (human)	2% v/v	1/3	3/3	3/3	3/3	3/3	I
		0.2% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Leukocytes	2% v/v	3/3	3/3	3/3	3/3	3/3	NI
FluMist Quadrivalent Vaccine	Live, attenuated Flu A and Flu B strains	6.67% v/v	3/3	3/3	3/3	3/3	0/3	I
		6.67E-04% v/v	3/3	3/3	3/3	3/3	0/3	I
		6.67E-08% v/v	3/3	3/3	3/3	3/3	2/3	I
		6.67E-12% v/v	3/3	3/3	3/3	3/3	3/3	NI
Nasal Sprays/ Drops	Zinc	1 mg/mL	3/3	3/3	3/3	3/3	3/3	NI
	Phenylephrine	5% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Oxymetazoline	5% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Sodium Chloride with preservatives	5% v/v	3/3	3/3	3/3	3/3	3/3	NI
Corticosteroids	Beclomethasone	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Dexamethasone	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Flunisolide	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Triamcinolone	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Budesonide	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Mometasone	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Fluticasone	17% v/v	3/3	3/3	3/3	3/3	3/3	NI
Nasal Gel	Luffa opperculata	5% v/v	3/3	3/3	3/3	3/3	3/3	NI
	Sulfur							
Homeopathic Allergy Relief	Galphimia glauca							
	Histaminum hydrocloricum							
Antiviral Drug	Zanamivir	3.3 mg/mL	3/3	3/3	3/3	3/3	3/3	NI
Antibiotic	Mupirocin	10 mg/mL	3/3	3/3	3/3	3/3	3/3	NI
Antibacterial	Tobramycin	4 µg/mL	3/3	3/3	3/3	3/3	3/3	NI

Mixed Infection/Competitive Interference

To assess potential competitive interference between SARS-CoV-2, influenza A, influenza B, and RSV samples were tested in replicates of twenty (20) where low (approximately 2x their respective LoD) concentration of three analytes were mixed with high (approximately 1.00E+06 genome copies/mL in UVT) concentration of the other analyte. None of the analytes present at a very high concentration interfered with the detection of low levels of the other three analytes, refer to Table 10.

Table 10. Mixed Infection Results for the BD Respiratory Viral Panel for the BD MAX™ System

Condition	High Virus (1.00E+06 copies/mL)	Low Virus (~2x LoD)	Positive / Total			
			SARS-CoV-2	Flu A	Flu B	RSV
1	SARS-CoV-2	Flu A / Flu B / RSV	20/20	20/20	20/20	20/20
2	Flu A	SARS-CoV-2 / Flu B / RSV	20/20	20/20	20/20	20/20
3	Flu B	SARS-CoV-2 / Flu A / RSV	20/20	19/20	20/20	20/20
4	RSV	SARS-CoV-2 / Flu A / Flu B	19/20	19/20	19/20	20/20

Cross-Reactivity

An *in silico* analysis was performed to evaluate the potential for all primers and probes contained within the BD Respiratory Viral Panel for BD MAX™ System master mix to amplify and detect unintended organisms. Each primer was 'BLAST' against the full nt database and alignments were kept if there were no more than three (3) base pair mismatches across the length of the primer, the 3' end of the primer matched the subject sequence, and no gaps were introduced to "force" an alignment. The plus/minus orientation between the primer (query) and the subject (database sequence) was determined, and all two-primer combinations (including each primer with itself) were identified where one primer matched the plus strand and the other matched the minus, representing potential amplicons. Amplicons were kept if the minus strand primer was downstream of the plus strand primer and the resulting amplicons were less than or equal to 3,000 base pairs long.

SARS-CoV-2: All identified hits are either SARS-CoV-2 or a closely related coronavirus from non-human species. No relevant cross-reactivity was discovered.

Influenza A: No relevant cross-reactivity was discovered.

Influenza B: No relevant cross-reactivity was discovered.

Respiratory syncytial virus: No relevant cross-reactivity was discovered.

Additionally, fifty-two (52) organisms and one (1) nasopharyngeal pool were evaluated for cross-reactivity with the BD Respiratory Viral Panel for BD MAX™ System. The bacterial

cells, yeasts, and viruses were tested in the BD Molecular RVP Sample Buffer Tube. All organisms tested produced negative results when tested at the concentration listed in Table 11.

Table 11. BD Respiratory Viral Panel for the BD MAX™ System Cross-Reactivity Results

Organism	Source	Concentration Tested	Negative Results Obtained (Negative Result/Total)
Adenovirus - Type 1	ZeptoMetrix® 0810050CF	1.00E+05 $TCID_{50}$/mL	3/3
Adenovirus - Type 4	ZeptoMetrix® 0810070CF	1.00E+05 $TCID_{50}$/mL	3/3
Adenovirus - Type 7	ZeptoMetrix® 0810021CF	1.00E+05 $TCID_{50}$/mL	3/3
Aspergillus flavus	ZeptoMetrix® 0801598	1.00E+06 CFU/mL	3/3
Aspergillus fumigatus	ZeptoMetrix® 0801716	1.00E+06 CFU/mL	3/3
Aspergillus terreus	ZeptoMetrix® 0801827	1.00E+06 CFU/mL	3/3
Aspergillus niger	ZeptoMetrix® 0801601	1.00E+06 CFU/mL	3/3
Bordetella pertussis	ZeptoMetrix® 0801459	1.00E+06 CFU/mL	3/3
Bordetella parapertussis	ZeptoMetrix® 08001461	1.00E+06 CFU/mL	3/3
Candida albicans	ATCC® 18804	1.00E+06 CFU/mL	3/3
Chlamydophila pneumoniae	ATCC® 53592	1.00E+06 IFU/mL	3/3
Corynebacterium diphtheriae	ZeptoMetrix® 0801882	1.00E+06 CFU/mL	3/3
Cytomegalovirus	ZeptoMetrix® 0810003CF	1.00E+05 copies/mL	3/3
Enterovirus B (Echovirus 6)	ZeptoMetrix® 0810076CF	1.00E+05 units/mL	3/3
Enterovirus C (Coxsackievirus A16)	ZeptoMetrix® 0810107CF	1.00E+05 $TCID_{50}$/mL	3/3
Enterovirus D68	ZeptoMetrix® 0810237CF	1.00E+05 $TCID_{50}$/mL	3/3
Epstein Barr virus	ZeptoMetrix® 0810008CF	1.00E+05 copies/mL	3/3
Escherichia coli	ATCC® 35401	1.00E+06 CFU/mL	3/3
Fusobacterium necrophorum	ATCC® 25286	1.00E+06 CFU/mL	3/3
Haemophilus influenzae	ZeptoMetrix® 0801679	1.00E+06 CFU/mL	3/3
Herpes simplex virus Type 1	ZeptoMetrix® 0810005CF	1.00E+05 $TCID_{50}$/mL	3/3
Herpes simplex virus Type 2	ZeptoMetrix® 0810006CF	1.00E+05 $TCID_{50}$/mL	3/3
Human coronavirus 229E	ATCC® VR-740	1.00E+05 $TCID_{50}$/mL	3/3
Human coronavirus HKU1a	ATCC® VR-3262SD	1.00E+05 GC/mL	3/3
Human coronavirus NL63	ZeptoMetrix® 0810228CF	1.00E+07 copies/mL	3/3
Human coronavirus OC43	ZeptoMetrix® 0810024CF	1.00E+05 $TCID_{50}$/mL	3/3
Human Metapneumovirus	ZeptoMetrix® 0810161CF	1.00E+05 $TCID_{50}$/mL	3/3
Lactobacillus acidophilus	ATCC® 4356	1.00E+06 CFU/mL	3/3
Legionella pneumophila	ATCC® 33152	1.00E+06 CFU/mL	3/3
Measles	ZeptoMetrix® 0810025CF	1.00E+05 $TCID_{50}$/mL	3/3
MERS-coronavirus	ZeptoMetrix® 0810228CFHI	1.00E+07 copies/mL	3/3
Moraxella catarrhalis	ZeptoMetrix® 0801509	1.00E+06 CFU/mL	3/3
Mumps	ZeptoMetrix® 0810079CF	1.00E+05 $TCID_{50}$/mL	3/3

Mycobacterium tuberculosis[a]	ATCC® 25177DQ	1.00E+06 copies/mL	3/3
Mycoplasma genitalium	ATCC® 33530	1.00E+06 cells/mL	3/3
Mycoplasma pneumoniae	ATCC® 15531-TTR	1.00E+06 CFU/mL	3/3
Neisseria meningitidis	ATCC® 13077	1.00E+06 CFU/mL	3/3
Neisseria gonorrhoeae	ATCC® 19424	1.00E+06 CFU/mL	3/3
Parainfluenza virus 1	ZeptoMetrix® 0810014CF	1.00E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 2	ZeptoMetrix® 0810504CF	2.12E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 3	ZeptoMetrix® 0810016CF	1.00E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 4	ZeptoMetrix® 0810060BCF	1.00E+05 $TCID_{50}$/mL	3/3
Pneumocystis jirovecii	ATCC® PRA-159	1.00E+06 cells/mL	3/3
Expressed and pooled human nasopharyngeal swab matrix	Internal	N/A	3/3
Pseudomonas aeruginosa	ATCC® 10145	1.00E+06 CFU/mL	3/3
Rhinovirus	ZeptoMetrix® 0810284CF	1.00E+05 $TCID_{50}$/mL	3/3
SARS-Coronavirus[a]	ATCC® VR-3280SD	1.00E+05 GE/mL	3/3
Staphylococcus aureus	ATCC® 43300	1.00E+06 CFU/mL	3/3
Staphylococcus epidermidis	ATCC® 12228	1.00E+06 CFU/mL	3/3
Streptococcus pneumoniae	ZeptoMetrix® 0804222	1.00E+06 CFU/mL	3/3
Streptococcus pyogenes	ATCC® 49399	1.00E+06 CFU/mL	3/3
Streptococcus salivarius	ZeptoMetrix® 0801896	1.00E+06 CFU/mL	3/3
Varicella-zoster virus	ZeptoMetrix® 0810167CF	1.00E+07 copies/mL	3/3

[a] Genomic DNA or RNA tested

Microbial Interference

Fifty-two (52) organisms and one (1) nasopharyngeal pool were evaluated for potential interference with the BD Respiratory Viral Panel for BD MAX™ System. Organisms were tested at high concentration ($\geq 10^6$ CFU/mL, cells/mL, genome equivalents/mL, $\geq 10^5$ IFU/mL or $TCID_{50}$/mL, or highest concentration available) in the presence of assay analytes (SARS-CoV-2, influenza A, influenza B, and RSV) co-spiked at 3x LoD. Refer to Table 12.

Table 12. Microbial Interference Testing Results for the BD Respiratory Viral Panel for the BD MAX™ System

Organism	Source	Concentration Tested	Positive Results Obtained (Positive Results / Total)			
			SARS-CoV-2	Flu A	Flu B	RSV
Adenovirus - Type 1	ZeptoMetrix® 0810050CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Adenovirus - Type 4	ZeptoMetrix® 0810070CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Adenovirus -	ZeptoMetrix®	1.00E+05	3/3	3/3	3/3	3/3

Organism	Source	Concentration Tested	Positive Results Obtained (Positive Results / Total)			
			SARS-CoV-2	Flu A	Flu B	RSV
Type 7	0810021CF	$TCID_{50}$/mL				
Aspergillus flavus	ZeptoMetrix® 0801598	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Aspergillus fumigatus	ZeptoMetrix® 0801716	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Aspergillus terreus	ZeptoMetrix® 0801827	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Aspergillus niger	ZeptoMetrix® 0801601	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Bordetella pertussis	ZeptoMetrix® 0801459	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Bordetella parapertussis	ZeptoMetrix® 08001461	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Candida albicans	ATCC® 18804	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Chlamydophila pneumoniae	ATCC® 53592	1.00E+06 IFU/mL	3/3	3/3	3/3	3/3
Corynebacterium diphtheriae	ZeptoMetrix® 0801882	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Cytomegalovirus	ZeptoMetrix® 0810003CF	1.00E+05 copies/mL	3/3	3/3	3/3	3/3
Enterovirus B (Echovirus 6)	ZeptoMetrix® 0810076CF	1.00E+05 units/mL	3/3	3/3	3/3	3/3
Enterovirus C (Coxsackievirus A16)	ZeptoMetrix® 0810107CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Enterovirus D68	ZeptoMetrix® 0810237CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Epstein Barr virus	ZeptoMetrix® 0810008CF	1.00E+05 copies/mL	3/3	3/3	3/3	3/3
Escherichia coli	ATCC® 35401	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Fusobacterium necrophorum	ATCC® 25286	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Haemophilus influenzae	ZeptoMetrix® 0801679	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Herpes simplex virus Type 1	ZeptoMetrix® 0810005CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Herpes simplex virus Type 2	ZeptoMetrix® 0810006CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Human coronavirus 229E	ATCC® VR-740	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Human coronavirus HKU1[a]	ATCC® VR-3262SD	1.00E+05 GC/mL	3/3	3/3	3/3	3/3

Organism	Source	Concentration Tested	Positive Results Obtained (Positive Results / Total)			
			SARS-CoV-2	Flu A	Flu B	RSV
Human coronavirus NL63	ZeptoMetrix® 0810228CF	1.00E+07 copies/mL	3/3	3/3	3/3	3/3
Human coronavirus OC43	ZeptoMetrix® 0810024CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Human Metapneumovirus	ZeptoMetrix® 0810161CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Lactobacillus acidophilus	ATCC® 4356	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Legionella pneumophila	ATCC® 33152	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Measles	ZeptoMetrix® 0810025CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
MERS-coronavirus	ZeptoMetrix® 0810575CFHI	1.00E+07 copies/mL	3/3	3/3	3/3	3/3
Moraxella catarrhalis	ZeptoMetrix® 0801509	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Mumps	ZeptoMetrix® 0810079CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Mycobacterium tuberculosis[a]	ATCC® 25177DQ	1.00E+06 copies/mL	3/3	3/3	3/3	3/3
Mycoplasma genitalium	ATCC® 33530	1.00E+06 cells/mL	3/3	3/3	3/3	3/3
Mycoplasma pneumoniae	ATCC® 15531-TTR	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Neisseria meningitidis	ATCC® 13077	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Neisseria gonorrhoeae	ATCC® 19424	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Parainfluenza virus 1	ZeptoMetrix® 0810014CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Parainfluenza virus 2	ZeptoMetrix® 0810504CF	2.12E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Parainfluenza virus 3	ZeptoMetrix® 0810016CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Parainfluenza virus 4	ZeptoMetrix® 0810060BCF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
Pneumocystis jirovecii	ATCC® PRA-159	1.00E+06 cells/mL	3/3	3/3	3/3	3/3
Expressed and pooled human nasopharyngeal swab matrix	Internal	N/A	3/3	3/3	3/3	3/3
Pseudomonas aeruginosa	ATCC® 10145	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3

Organism	Source	Concentration Tested	Positive Results Obtained (Positive Results / Total)			
			SARS-CoV-2	Flu A	Flu B	RSV
Rhinovirus	ZeptoMetrix® 0810284CF	1.00E+05 $TCID_{50}$/mL	3/3	3/3	3/3	3/3
SARS-Coronavirus[a]	ATCC® VR-3280SD	1.00E+05 GE/mL	3/3	3/3	3/3	3/3
Staphylococcus aureus	ATCC® 43300	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Staphylococcus epidermidis	ATCC® 12228	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Streptococcus pneumoniae	ZeptoMetrix® 0804222	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Streptococcus pyogenes	ATCC® 49399	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Streptococcus salivarius	ZeptoMetrix® 0801896	1.00E+06 CFU/mL	3/3	3/3	3/3	3/3
Varicella-zoster virus	ZeptoMetrix® 0810167CF	1.00E+07 copies/mL	3/3	3/3	3/3	3/3

[a] Genomic DNA or RNA tested

Sample Stability

BD Respiratory Viral Panel for BD MAX™ System stability for SARS-CoV-2, influenza A, influenza B and RSV in nasopharyngeal matrix and in anterior nasal swab matrix expressed in UVT/UTM (neat) as well both post transfer of UVT/UTM matrix into sample buffer tubes (nested) was evaluated. Specimens were constructed using clinical nasopharyngeal or anterior nasal matrix spiked at 3X LoD. Refer to Table 13 for the BD Respiratory Viral Panel Assay for BD MAX™ System Specimen Stability.

Table 13. BD Respiratory Viral Panel Assay for BD MAX™ System Specimen Stability

Specimen Stability	Temperature	Duration
In UVT/UTM	25 ± 2 °C	12 hours
	2–8 °C	72 hours
In BD Molecular RVP Sample Buffer Tube	25 ± 2 °C	24 hours
	2–8 °C	120 hours

Assay Cut-off

The assay cut-off for the BD Respiratory Viral Panel for BD MAX™ was established based on PCR based metrics taken together by the BD MAX software algorithm to make the qualitative decision whether a curve is to be considered positive or negative. These metrics (e.g., Ct, RFU endpoints, signal-to-noise ratios) are initially set by default parameters defined by the instrument. As the product undergoes product development, the data is supplemented, and the algorithm is adjusted ("trained") using viral cultures spiked into clinical background matrices at levels surrounding the limit of detection and expected clinical range. In conclusion, testing of clinical specimens were used to confirm adequate separation between the value observed in positive specimens in each target detection channel and the assay cutoff.

Matrix Equivalency

Matrix Equivalency between nasopharyngeal swab, nasal swab, and simulated nasopharyngeal matrix was evaluated using heat inactivated SARS-CoV-2 (USA-WA/2020 strain), influenza A (H1N1/Brisbane), influenza B (Phuket/3073/13) and RSV A culture fluids spiked into negative nasopharyngeal, nasal and simulated matrix to prepare contrived low positive (approximately 2x LoD) and moderate positive (approximately 5x LoD) samples for each sample type. A total of thirty (30) low positive, fifteen (15) moderate positive, and fifteen (15) negative samples were tested.

Simulated nasopharyngeal matrix was demonstrated to be equivalent to nasopharyngeal and nasal in UVT matrix

Fresh vs Frozen

A study was performed with the BD Respiratory Viral Panel for BD MAX™ System using fresh and frozen nasopharyngeal swabs in UVT which showed that there were no adverse effects from freezing and thawing of specimens. The data generated are considered acceptable to support testing of archived, frozen specimens in the Clinical Study to evaluate the performance of the BD Respiratory Viral Panel for BD MAX™ System.

Carryover / Cross-Contamination

A study was conducted to investigate within-run carryover and between-run carryover while processing samples with high viral load of SARS-CoV-2 in the BD Respiratory Viral Panel for BD MAX™ System. High positive samples contained heat inactivated SARS-CoV-2 spiked into pooled nasal swab matrix at a concentration of ≥1.94E+07 copies/mL. The negative samples

consisted of simulated nasopharyngeal matrix without any target analyte. Twelve (12) replicates of the high positive panel member and 12 replicates of the negative panel member were tested in nine (9) runs by alternating negative and positive samples, using three BD MAX™ Systems. A total of 108 positive and 108 negative samples were tested. Of the 108 negative samples tested, one (1) false positive result was obtained (0.93%, 95% CI: 0.16–5.06%).

Expected Values

In the BD Respiratory Viral Panel for BD MAX™ System clinical study, reportable results from specimens compliant at the specimen and PCR levels were obtained from 8 geographically diverse sites. Nasopharyngeal specimens totaled 1,562 for all assay targets. Nasal specimens totaled 1,566 for all assay targets. The number and percentage of positive cases per target, as determined by BD Respiratory Viral Panel for BD MAX™ System, are presented in Table 14.

Table 14. BD Respiratory Viral Panel for BD MAX™ System Positivity Rate Per Target and Specimen Type

Analyte	Nasopharyngeal	Nasal
SARS-CoV-2	34.6% (541/1562)	32.2% (504/1566)
Flu A	4.2% (66/1562)	4.2% (66/1566)
Flu B	0.1% (1/1562)	0.0% (0/1566)
RSV	0.8% (12/1562)	0.8% (12/1566)

External Control Validation

Assay run controls are not provided as part of the BD Respiratory Viral Panel for BD MAX™ System. BD recommends the use of Microbiologics controls. Studies have been performed to verify the use of Microbiologics Helix Elite™ Molecular Standards with the BD Respiratory Viral Panel for BD MAX™ System. The combination of Microbiologics SARS-CoV-2 Positive Control, Influenza A/B and Respiratory Syncytial Virus (RSV) Positive Control will be used as the external positive control. Microbiologics Negative Cellularity Control (NCC) will be used as the external negative control.

Usability Study

A usability study has been performed to determine whether a representative sample of untrained professionals could correctly prepare samples for the BD MAX Respiratory Viral Panel for BD MAX™ System. The participants were presented with a representative mock sample, and all other materials required to process the mock sample. They were asked to go through simulating the assay preparation and perform every step as realistically as possible. The use scenario being studied in this evaluation was the expected use scenario that an intended user would go through when preparing samples for molecular assays in a clinical environment. The study demonstrated usability with the target user population for safe and effective use of the product.

BD Respiratory Viral Panel-SCV2 for BD MAX™ System:

Precision

Within-laboratory precision was evaluated for the BD Respiratory Viral Panel-SCV2 at one (1) site with one (1) reagent lot. Testing was performed over 12 days, with two operators performing 2 runs per day for a total of 48 runs. Test samples were contrived in simulated nasopharyngeal matrix and included SARS-CoV-2 panel members. Each panel member was tested in three replicates. The following target concentrations were used for each target organism contained in each panel member:

- Moderate positive (MP): 3x LoD
- Low Positive (LP): 2x LoD
- True Negative (TN): No target

Precision study results are described in Table 15.

Table 15. Overall Precision Study Results Using One Lot of the BD Respiratory Viral Panel (Percent Agreement with Expected Results)

Sample Concentration	SARS-CoV-2 (N), 95% CI
Moderate Positive (3x LoD)	100% (144/144), 97.4-100
Low Positive (2x LoD)	100% (144/144), 97.4-100
True Negative[a]	100% (288/288), 98.7-100

[a] For the True Negative category, the reported agreement indicates percent of negative results.

Reproducibility

For the Site-to-Site reproducibility study, three (3) sites (two external and one internal) were provided the same panels as described for the Precision study above. Each site performed testing on five (5) distinct days (consecutive or not), wherein each day, one (1) panel was tested by two (2) technologists. Each panel member was tested in three (3) replicates.

The qualitative and quantitative reproducibility is presented below in Table 16 by target analyte. Ct, internal criterion used to determine a final assay result, was selected as an additional means of assessing assay reproducibility. Overall mean Ct values with variance components (SD and %CV) are shown in Table 17.

Table 16. Site-to-Site Reproducibility Study Results using One (1) Lot of the BD Respiratory Viral Panel (Percent Agreement with Expected Results)

Sample Concentration	SARS-CoV-2 (N), 95% CI
Moderate Positive (3x LoD)	100% (90/90), 95.9-100
Low Positive (2x LoD)	100% (90/90), 95.9-100
True Negative[a]	100% (180/180), 97.9-100

[a] For the True Negative category, the reported agreement indicates percent of negative results.

Table 17. Site-to-Site Quantitative Reproducibility Across Sites, Days, Runs, and Replicates

Target	Level	N	Mean Ct	Within Run		Between Run		Between Day		Between Site		Total	
				SD	CV (%)	SD	CV (%)	SD	CV (%)	SD	CV (%)	SD	CV (%)
CoV-2	LP	90	33.3	0.74	2.2	0.00	0.0	0.00	0.0	0.54	1.6	0.92	2.8
CoV-2	MP	90	33.0	0.45	1.4	0.08	0.2	0.00	0.0	0.74	2.2	0.87	2.6

For the Lot-to-Lot reproducibility study, one (1) internal site was provided the same panels as described for the Precision study above. Three (3) reagent lots were tested across five (5) distinct days (consecutive or not) on one (1) BD MAX™, wherein each day, two (2) panels were tested by two (2) technologists. Each panel member was tested in three replicates.

The qualitative and quantitative reproducibility is presented below in Table 18 by target analyte. Ct, internal criterion used to determine a final assay result, was selected as an additional means of assessing assay reproducibility. Overall mean Ct values with variance components (SD and %CV) are shown in Table 19.

Table 18. Lot-to-Lot Reproducibility Study Results using Three (3) Lots of the BD Respiratory Viral Panel (Percent Agreement with Expected Results)

Sample Concentration	SARS-CoV-2 (N), 95% CI
Moderate Positive (3x LoD)	99.4% (179/180), 96.9-99.9
Low Positive (2x LoD)	100% (180/180), 97.9-100
True Negative[a]	100% (360/360), 98.9-100

[a] For the True Negative category, the reported agreement indicates percent of negative results.

Table 19. Lot-to-Lot Quantitative Reproducibility Across Operators, Days, Runs, and Replicates

Target	Level	N	Mean Ct	Lot		Day		Operator		Run		Within Run (Repeatability)		Total	
				SD	CV(%)	SD	CV(%)	SD	CV(%)	SD	CV(%)	SD	CV(%)	SD	CV(%)
CoV-2	MP	179	33.7	0.26	0.8	0.06	0.2	0.10	0.3	0.00	0.0	0.61	1.8	0.67	2.0
CoV-2	LP	180	33.9	0.24	0.7	0.18	0.5	0.12	0.3	0.00	0.0	0.64	1.9	0.72	2.1

Linearity

Not applicable. This is a qualitative assay.

Limit of Detection (LoD)

The analytical sensitivity of the BD Respiratory Panel-SCV2 for BD MAX™ System was assessed in both nasopharyngeal and nasal clinical matrices. LoD studies determine the lowest detectable concentration of virus at which approximately 95% of all (true positive) replicates test positive. Analysis of SARS-CoV-2 was completed with a Probit statistical methodology across three (3) reagent lots. Confirmation of the estimated LoD was performed with one reagent lot in replicates of 20 prepared in nasopharyngeal and nasal matrix are reported in Table 20.

Table 20. BD Respiratory Viral Panel-SCV2 for BD MAX™ System Limit of Detection

Strain	LoD Concentration (in UVT)	
	Nasopharyngeal	Nasal
SARS-CoV-2 (USA-WA1/2020)	700 copies/mL	700 copies/mL

Inclusivity

An *in silico* alignment of the BD Respiratory Viral Panel – SCV2 primers and probes demonstrated that the performance of the BD Respiratory Viral Panel – SCV2 reagents for the BD MAX™ system is not directly impacted by the presence of mutations in known SARS-CoV-2 viral variants. As of June 10, 2022, BD continues to monitor all lineages and sublineages for the following WHO labeled Variants of Concern, Alpha, Beta, Gamma, Delta, and Mu. In all cases greater than 99% of the sequenced isolates are a perfect match to all primers and probes in either the N1 or N2 set. Given similar performance from both the N1 and N2 channel, either will back up the other in the event of performance degradation through genetic drift. Additionally, BD continues to monitor all lineages of the WHO Omicron label, including sublineages within BA.1, BA.2, BA.2.12.1, BA.3, BA.4, and BA.5. All Omicron genomes contain a mutation that affects the N1 probe 3 bases from the 5' end. (Mutation C28311T). Each Omicron sublineage has a percentage of sequences that are a perfect match to either the N1 or N2 primer-set as follows: BA.1 at 99.47%, BA.2 at 98.95%, BA.2.12.1 at 99.63%, BA.3 at 100%, BA.4 at 96.87% and BA.5 at 99.55%.

BD Respiratory Viral Panel-SCV2 for BD MAX™ System was evaluated against multiple strains of SARS-CoV-2. A total of 11 SARS-CoV-2 strains were evaluated at levels near the analytical LoD. Three replicates were tested for each strain, refer to Table 21.

Table 21. Analytical Reactivity/Inclusivity for the BD Respiratory Viral Panel-SCV2 for the BD MAX™ System

Virus	Strain	Source	Concentration Detected	Relative LoD	Positive Results/Total
SARS-CoV-2	Hong Kong / VM200001061/2020	ZeptoMetrix 0810590CFHI	2100 copies/mL	3x LoD	3/3
	Italy-INMI1	ZeptoMetrix 0810589CFHI	2100 copies/mL	3x LoD	3/3
	Alpha, (B.1.1.7) USA / CA_CDC_5574/2020	ZeptoMetrix 0810612CFHI	2100 copies/mL	3x LoD	3/3
	Alpha, (B.1.1.7) England/204820464/2020	ZeptoMetrix 0810614CFHI	2100 copies/mL	3x LoD	3/3
	Beta, (B.1.351) South Africa / KRISP-K005325/2020	ZeptoMetrix 0810613CFHI	2100 copies/mL	3x LoD	3/3
	Kappa, (B.1.617.1) USA / CA-Stanford-15_ S02/2021	ZeptoMetrix 0810623CFHI	2100 copies/mL	3x LoD	3/3
	Gamma, (P1) Japan / TY7-503/2021	ZeptoMetrix 0810616CFHI	2100 copies/mL	3x LoD	3/3
	Delta, (B.1.617.2) USA / PHC658/2021	ZeptoMetrix 0810624CFHI	2100 copies/mL	3x LoD	3/3
	Iota, (B.1.526_2021) NY-Wadsworth-21025952-01/2021	ZeptoMetrix 0810619CFHI	2100 copies/mL	3x LoD	3/3
	Zeta, (P2_2021) NY-Wadsworth-21006055-01/2021	ZeptoMetrix 0810618CFHI	2100 copies/mL	3x LoD	3/3
	Omicron (BA.1) USA/GA-EHC- 2811C/2021	ATCC VR-3347HK	2100 copies/mL	3x LoD	3/3

Assay Measuring Range

Not applicable. This is a qualitative assay.

Interfering Substances

Twenty-four (24) biological and chemical substances that may be present in nasopharyngeal or anterior nasal swab specimens were evaluated for potential interference with the BD Respiratory Viral Panel-SCV2 for BD MAX™ System using simulated nasopharyngeal matrix. Whole blood (human) was found to interfere at levels above 0.2% volume/volume. Results demonstrated no reportable interference from any other substance tested at the reported clinically relevant concentrations (refer to Table 22).

Table 22. Endogenous and Commercial Exogenous Substances Tested with BD Respiratory Viral Panel-SCV2 for the BD MAX™ System

Substance	Active Ingredient	Concentration Tested	SARS-CoV-2 Positive Testing (Positive/Total)	Negative Testing (Negative/Total)	Result
Oral anesthetic and analgesic	Benzocaine	0.8 mg/mL	3/3	3/3	NI
	Menthol				
Biologicals	Purified Mucin	60 µg/mL	3/3	3/3	NI
	Whole Blood (human)	2% v/v	1/3	3/3	I
		0.2% v/v	3/3	3/3	NI
	Leukocytes	2% v/v	3/3	3/3	NI
FluMist Quadrivalent Vaccine	Live, attenuated Flu A and Flu B strains	6.67% v/v	3/3	3/3	NI
Nasal Sprays/Drops	Zinc	1 mg/mL	3/3	3/3	NI
	Phenylephrine	5% v/v	3/3	3/3	NI
	Oxymetazoline	5% v/v	3/3	3/3	NI
	Sodium Chloride with preservatives	5% v/v	3/3	3/3	NI
Corticosteroids	Beclomethasone	17% v/v	3/3	3/3	NI
	Dexamethasone	17% v/v	3/3	3/3	NI
	Flunisolide	17% v/v	3/3	3/3	NI
	Triamcinolone	17% v/v	3/3	3/3	NI
	Budesonide	17% v/v	3/3	3/3	NI
	Mometasone	17% v/v	3/3	3/3	NI
	Fluticasone	17% v/v	3/3	3/3	NI
Nasal Gel	Luffa operculata	5% v/v	3/3	3/3	NI
	Sulfur				
Homeopathic Allergy Relief	Galphimia glauca				
	Histaminum hydrocloricum				
Antiviral Drug	Zanamivir	3.3 mg/mL	3/3	3/3	NI
Antibiotic	Mupirocin	10 mg/mL	3/3	3/3	NI
Antibacterial	Tobramycin	4 µg/mL	3/3	3/3	NI

Cross-Reactivity

An *in silico* analysis was performed to evaluate the potential for all primers and probes contained within the BD Respiratory Viral Panel-SCV2 for BD MAX™ System master mix to amplify and detect unintended organisms. Each primer was 'BLAST' against the full nt database and alignments were kept if there were no more than three (3) base pair mismatches across the length of the primer, the 3' end of the primer matched the subject sequence, and no gaps were introduced to "force" an alignment. The plus/minus orientation between the primer (query) and the subject (database sequence) was determined, and all two-primer combinations (including each primer with itself) were identified where one primer matched the plus strand and the other matched the minus, representing potential amplicons. Amplicons were kept if

the minus strand primer was downstream of the plus strand primer and the resulting amplicons were less than or equal to 3,000 base pairs long.

SARS-CoV-2: All identified hits are either SARS-CoV-2 or a closely related coronavirus from non-human species. No relevant cross-reactivity was discovered.

Additionally, fifty-two (52) organisms and one (1) nasopharyngeal pool were evaluated for cross-reactivity with the BD Respiratory Viral Panel-SCV2 for BD MAX™ System. The bacterial cells, yeasts, and viruses were tested in the BD Molecular RVP Sample Buffer Tube. All organisms tested produced negative results when tested at the concentration listed in Table 23.

Table 23. BD Respiratory Viral Panel-SCV2 for the BD MAX™ System Cross-Reactivity Results

Organism	Source	Concentration Tested	Negative Results Obtained (Negative Result/Total)
Adenovirus - Type 1	ZeptoMetrix® 0810050CF	1.00E+05 $TCID_{50}$/mL	3/3
Adenovirus - Type 4	ZeptoMetrix® 0810070CF	1.00E+05 $TCID_{50}$/mL	3/3
Adenovirus - Type 7	ZeptoMetrix® 0810021CF	1.00E+05 $TCID_{50}$/mL	3/3
Aspergillus flavus	ZeptoMetrix® 0801598	1.00E+06 CFU/mL	3/3
Aspergillus fumigatus	ZeptoMetrix® 0801716	1.00E+06 CFU/mL	3/3
Aspergillus terreus	ZeptoMetrix® 0801827	1.00E+06 CFU/mL	3/3
Aspergillus niger	ZeptoMetrix® 0801601	1.00E+06 CFU/mL	3/3
Bordetella pertussis	ZeptoMetrix® 0801459	1.00E+06 CFU/mL	3/3
Bordetella parapertussis	ZeptoMetrix® 0801461	1.00E+06 CFU/mL	3/3
Candida albicans	ATCC® 18804	1.00E+06 CFU/mL	3/3
Chlamydophila pneumoniae	ATCC® 53592	1.00E+06 IFU/mL	3/3
Corynebacterium diphtheriae	ZeptoMetrix® 0801882	1.00E+06 CFU/mL	3/3
Cytomegalovirus	ZeptoMetrix® 0810003CF	1.00E+05 copies/mL	3/3
Enterovirus B (Echovirus 6)	ZeptoMetrix® 0810076CF	1.00E+05 units/mL	3/3
Enterovirus C (Coxsackievirus A16)	ZeptoMetrix® 0810107CF	1.00E+05 $TCID_{50}$/mL	3/3
Enterovirus D68	ZeptoMetrix® 0810237CF	1.00E+05 $TCID_{50}$/mL	3/3
Epstein Barr virus	ZeptoMetrix® 0810008CF	1.00E+05 copies/mL	3/3
Escherichia coli	ATCC® 35401	1.00E+06 CFU/mL	3/3
Fusobacterium necrophorum	ATCC® 25286	1.00E+06 CFU/mL	3/3
Haemophilus influenzae	ZeptoMetrix® 0801679	1.00E+06 CFU/mL	3/3
Herpes simplex virus Type 1	ZeptoMetrix® 0810005CF	1.00E+05 TCID50/mL	3/3
Herpes simplex virus Type 2	ZeptoMetrix® 0810006CF	1.00E+05 TCID50/mL	3/3
Human coronavirus 229E	ATCC® VR-740	1.00E+05 TCID50/mL	3/3
Human coronavirus HKU1[a]	ATCC® VR-3262SD	1.00E+05 GC/mL	3/3
Human coronavirus NL63	ZeptoMetrix® 0810228CF	1.00E+07 copies/mL	3/3
Human coronavirus OC43	ZeptoMetrix® 0810024CF	1.00E+05 $TCID_{50}$/mL	3/3
Human Metapneumovirus	ZeptoMetrix® 0810161CF	1.00E+05 $TCID_{50}$/mL	3/3
Influenza A	ZeptoMetrix® 0810244CF	1.00E+06 copies/mL	3/3
Influenza B	ZeptoMetrix® 0810515CF	1.00E+06 copies/mL	3/3

Organism	Source	Concentration Tested	Negative Results Obtained (Negative Result/Total)
Lactobacillus acidophilus	ATCC® 4356	1.00E+06 CFU/mL	3/3
Legionella pneumophila	ATCC® 33152	1.00E+06 CFU/mL	3/3
Measles	ZeptoMetrix® 0810025CF	1.00E+05 $TCID_{50}$/mL	3/3
MERS-coronavirus	ZeptoMetrix® 0810228CFHI	1.00E+07 copies/mL	3/3
Moraxella catarrhalis	ZeptoMetrix® 0801509	1.00E+06 CFU/mL	3/3
Mumps	ZeptoMetrix® 0810079CF	1.00E+05 $TCID_{50}$/mL	3/3
Mycobacterium tuberculosis[a]	ATCC® 25177DQ	1.00E+06 copies/mL	3/3
Mycoplasma genitalium	ATCC® 33530	1.00E+06 cells/mL	3/3
Mycoplasma pneumoniae	ATCC® 15531-TTR	1.00E+06 CFU/mL	3/3
Neisseria meningitidis	ATCC® 13077	1.00E+06 CFU/mL	3/3
Neisseria gonorrhoeae	ATCC® 19424	1.00E+06 CFU/mL	3/3
Parainfluenza virus 1	ZeptoMetrix® 0810014CF	1.00E+05 TCID50/mL	3/3
Parainfluenza virus 2	ZeptoMetrix® 0810504CF	2.12E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 3	ZeptoMetrix® 0810016CF	1.00E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 4	ZeptoMetrix® 0810060BCF	1.00E+05 $TCID_{50}$/mL	3/3
Pneumocystis jirovecii	ATCC® PRA-159	1.00E+06 cells/mL	3/3
Expressed and pooled human nasopharyngeal swab matrix	Internal	n/a	3/3
Pseudomonas aeruginosa	ATCC® 10145	1.00E+06 CFU/mL	3/3
Respiratory syncytial virus	ZeptoMetrix® 0810040CFA	1.00E+06 copies/mL	3/3
Rhinovirus	ZeptoMetrix® 0810284CF	1.00E+05 TCID50/mL	3/3
SARS-Coronavirus[a]	ATCC® VR-3280SD	1.00E+05 GE /mL	3/3
Staphylococcus aureus	ATCC® 43300	1.00E+06 CFU/mL	3/3
Staphylococcus epidermis	ATCC® 12228	1.00E+06 CFU/mL	3/3
Streptococcus pneumoniae	ZeptoMetrix® 0804222	1.00E+06 CFU/mL	3/3
Streptococcus pyogenes	ATCC® 49399	1.00E+06 CFU/mL	3/3
Streptococcus salivarius	ZeptoMetrix® 0801896	1.00E+06 CFU/mL	3/3
Varicella-zoster virus	ZeptoMetrix® 0810167CF	1.00E+07 copies/mL	3/3

[a] Genomic DNA or RNA tested.

Microbial Interference

Fifty-two (52) organisms and one (1) nasopharyngeal pool were evaluated for potential interference with the BD Respiratory Viral Panel-SCV2 for BD MAX™ System. Organisms were tested at high concentration ($\geq 10^6$ CFU/mL, cells/mL, genome equivalents/mL, $\geq 10^5$ IFU/mL or $TCID_{50}$/mL, or highest concentration available) in the presence of SARS-CoV-2 spiked at 3x LoD, refer to Table 24.

Table 24. Microbial Interference Testing Results for the BD Respiratory Viral Panel-SCV2 for the BD MAX™ System

Organism	Source	Concentration Tested	Positive / Total
			SARS-CoV-2
Adenovirus - Type 1	ZeptoMetrix® 0810050CF	1.00E+05 $TCID_{50}$/mL	3/3
Adenovirus - Type 4	ZeptoMetrix® 0810070CF	1.00E+05 $TCID_{50}$/mL	3/3
Adenovirus - Type 7	ZeptoMetrix® 0810021CF	1.00E+05 $TCID_{50}$/mL	3/3
Aspergillus flavus	ZeptoMetrix® 0801598	1.00E+06 CFU/mL	3/3
Aspergillus fumigatus	ZeptoMetrix® 0801716	1.00E+06 CFU/mL	3/3
Aspergillus terreus	ZeptoMetrix® 0801827	1.00E+06 CFU/mL	3/3
Aspergillus niger	ZeptoMetrix® 0801601	1.00E+06 CFU/mL	3/3
Bordetella pertussis	ZeptoMetrix® 0801459	1.00E+06 CFU/mL	3/3
Bordetella parapertussis	ZeptoMetrix® 0801461	1.00E+06 CFU/mL	3/3
Candida albicans	ATCC® 18804	1.00E+06 CFU/mL	3/3
Chlamydophila pneumoniae	ATCC® 53592	1.00E+06 IFU/mL	3/3
Corynebacterium diphtheriae	ZeptoMetrix® 0801882	1.00E+06 CFU/mL	3/3
Cytomegalovirus	ZeptoMetrix® 0810003CF	1.00E+05 copies/mL	3/3
Enterovirus B (Echovirus 6)	ZeptoMetrix® 0810076CF	1.00E+05 units/mL	3/3
Enterovirus C (Coxsackievirus A16)	ZeptoMetrix® 0810107CF	1.00E+05 $TCID_{50}$/mL	3/3
Enterovirus D68	ZeptoMetrix® 0810237CF	1.00E+05 $TCID_{50}$/mL	3/3
Epstein Barr virus	ZeptoMetrix® 0810008CF	1.00E+05 copies/mL	3/3
Escherichia coli	ATCC® 35401	1.00E+06 CFU/mL	3/3
Fusobacterium necrophorum	ATCC® 25286	1.00E+06 CFU/mL	3/3
Haemophilus influenzae	ZeptoMetrix® 0801679	1.00E+06 CFU/mL	3/3
Herpes simplex virus Type 1	ZeptoMetrix® 0810005CF	1.00E+05 $TCID_{50}$/mL	3/3
Herpes simplex virus Type 2	ZeptoMetrix® 0810006CF	1.00E+05 $TCID_{50}$/mL	3/3
Human coronavirus 229E	ATCC® VR-740	1.00E+05 $TCID_{50}$/mL	3/3
Human coronavirus HKU1[a]	ATCC® VR-3262SD	1.00E+05 GC/mL	3/3
Human coronavirus NL63	ZeptoMetrix® 0810228CF	1.00E+07 copies/mL	3/3
Human coronavirus OC43	ZeptoMetrix® 0810024CF	1.00E+05 $TCID_{50}$/mL	3/3
Human Metapneumovirus	ZeptoMetrix® 0810161CF	1.00E+05 $TCID_{50}$/mL	3/3
Influenza A	ZeptoMetrix® 0810244CF	1.00E+06 copies/mL	20/20
Influenza B	ZeptoMetrix® 0810515CF	1.00E+06 copies/mL	20/20
Lactobacillus acidophilus	ATCC® 4356	1.00E+06 CFU/mL	3/3
Legionella pneumophila	ATCC® 33152	1.00E+06 CFU/mL	3/3
Measles	ZeptoMetrix® 0810025CF	1.00E+05 $TCID_{50}$/mL	3/3
MERS-coronavirus	ZeptoMetrix® 0810228CFHI	1.00E+07 copies/mL	3/3
Moraxella catarrhalis	ZeptoMetrix® 0801509	1.00E+06 CFU/mL	3/3
Mumps	ZeptoMetrix® 0810079CF	1.00E+05 $TCID_{50}$/mL	3/3
Mycobacterium tuberculosis[a]	ATCC® 25177DQ	1.00E+06 copies/mL	3/3
Mycoplasma genitalium	ATCC® 33530	1.00E+06 cells/mL	3/3
Mycoplasma pneumoniae	ATCC® 15531-TTR	1.00E+06 CFU/mL	3/3
Neisseria meningitidis	ATCC® 13077	1.00E+06 CFU/mL	3/3
Neisseria gonorrhoeae	ATCC® 19424	1.00E+06 CFU/mL	3/3

Organism	Source	Concentration Tested	Positive / Total
			SARS-CoV-2
Parainfluenza virus 1	ZeptoMetrix® 0810014CF	1.00E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 2	ZeptoMetrix® 0810504CF	2.12E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 3	ZeptoMetrix® 0810016CF	1.00E+05 $TCID_{50}$/mL	3/3
Parainfluenza virus 4	ZeptoMetrix® 0810060BCF	1.00E+05 $TCID_{50}$/mL	3/3
Pneumocystis jirovecii	ATCC® PRA-159	1.00E+06 cells/mL	3/3
Pooled human expressed nasopharyngeal swab matrix	Internal	n/a	3/3
Pseudomonas aeruginosa	ATCC® 10145	1.00E+06 CFU/mL	3/3
Respiratory syncytial virus	ZeptoMetrix® 0810040CFA	1.00E+06 copies/mL	20/20
Rhinovirus	ZeptoMetrix® 0810284CF	1.00E+05 $TCID_{50}$/mL	3/3
SARS-Coronavirus[a]	ATCC® VR-3280SD	1.00E+05 GE /mL	3/3
Staphylococcus aureus	ATCC® 43300	1.00E+06 CFU/mL	3/3
Staphylococcus epidermis	ATCC® 12228	1.00E+06 CFU/mL	3/3
Streptococcus pneumoniae	ZeptoMetrix® 0804222	1.00E+06 CFU/mL	3/3
Streptococcus pyogenes	ATCC® 49399	1.00E+06 CFU/mL	3/3
Streptococcus salivarius	ZeptoMetrix® 0801896	1.00E+06 CFU/mL	3/3
Varicella-zoster virus	ZeptoMetrix® 0810167CF	1.00E+07 copies/mL	3/3

[a] Genomic DNA or RNA tested

Sample Stability

BD Respiratory Viral Panel-SCV2 for BD MAX™ System stability for SARS-CoV-2 in nasopharyngeal matrix and in anterior nasal swab matrix expressed in UVT/UTM (neat) as well both post transfer of UVT/UTM matrix into sample buffer tubes (nested) was evaluated. Specimens were constructed using clinical nasopharyngeal or anterior nasal matrix spiked at 3X LoD. Refer to Table 25 for the BD Respiratory Viral Panel-SCV2 Assay for BD MAX™ System Specimen Stability.

Table 25. BD Respiratory Viral Panel-SCV2 Assay for BD MAX™ System Specimen Stability

Specimen Stability	Temperature	Duration
In UVT/UTM	25 ± 2 °C	48 hours
	2–8 °C	72 hours
In BD Molecular RVP Sample Buffer Tube	25 ± 2 °C	48 hours
	2–8 °C	120 hours

Assay Cut-Off

The assay cut-off for the BD Respiratory Viral Panel-SCV2 for BD MAX™ was established based on PCR based metrics taken together by the BD MAX software algorithm to make the qualitative decision whether a curve is to be considered positive or negative. These metrics (e.g., Ct, RFU endpoints, signal-to-noise ratios) are initially set by default parameters defined by the instrument. As the product undergoes product development, the data is supplemented, and the algorithm is adjusted ("trained") using viral cultures spiked into clinical background matrices at levels

surrounding the limit of detection and expected clinical range. In conclusion, testing of clinical specimens were used to confirm adequate separation between the value observed in positive specimens in each target detection channel and the assay cutoff.

Matrix Equivalency

Equivalence between nasopharyngeal swab, nasal swab, and simulated nasopharyngeal matrix was evaluated using heat inactivated SARS-CoV-2 (USA-WA/2020 strain) spiked into negative nasopharyngeal, nasal and simulated matrix to prepare contrived low positive (approximately 2x LoD) and moderate positive (approximately 5x LoD) samples for each sample type. A total of thirty (30) low positive, fifteen (15) moderate positive, and fifteen (15) negative samples were tested.

Fresh vs Frozen

A study was performed with the BD Respiratory Viral Panel-SCV2 for BD MAX™ System using fresh and frozen nasopharyngeal swabs which showed that there were no adverse effects from freezing and thawing of specimens. The data generated are considered acceptable to support testing of archived, frozen specimens in the Clinical Study to evaluate the performance of the BD Respiratory Viral Panel-SCV2 for BD MAX™ System.

Carryover / Cross-Contamination

A study was conducted to investigate within-run carryover and between-run carryover while processing samples with high viral load of SARS-CoV-2 in the BD Respiratory Viral Panel – SCV2. High positive samples contained heat inactivated SARS-CoV-2 spiked into pooled nasal swab matrix at a concentration of ≥1.94E+07 copies/mL. The negative samples consisted of simulated nasopharyngeal matrix without any target analyte. Twelve (12) replicates of the high positive panel member and 12 replicates of the negative panel member were tested in nine (9) runs by alternating negative and positive samples, using three BD MAX™ Systems or a total of 108 positive and 108 negative samples tested. Of the 108 negative samples tested, one (1) false positive result was obtained (0.93%, 95% CI: 0.16–5.06%).

Expected Values

In the BD Respiratory Viral Panel-SCV2 for BD MAX™ System clinical study, reportable results from specimens compliant at the specimen and PCR levels were obtained from 8 geographically diverse sites. Nasopharyngeal and nasal specimens totaled 1,562 and 1,566 respectively. The number and percentage of positive cases per target, as determined by BD Respiratory Viral Panel-SCV2 for BD MAX™ System, are presented in Table 26.

Table 26. BD Respiratory Viral Panel-SCV2 for BD MAX™ System Positivity Rate per Specimen Type

Analyte	Nasopharyngeal	Nasal
SARS-CoV-2	34.6% (541/1562)	32.2% (504/1566)

External Control Validation

Assay run controls are not provided as part of the BD Respiratory Viral Panel-SCV2 for BD MAX™ System. BD recommends the use of Microbiologics controls. Studies have been performed to verify the use of Microbiologics Helix Elite™ Molecular Standards with the BD Respiratory Viral Panel-SCV2 for BD MAX™ System. The combination of Microbiologics SARS-CoV-2 Positive Control as positive external control. Microbiologics Negative Cellularity Control (NCC) will be used as the external negative control.

Usability Study

A usability study has been performed to determine whether a representative sample of untrained professionals could correctly prepare samples for the BD MAX Respiratory Viral Panel for BD MAX™ System. The participants were presented with a representative mock sample, and all other materials required to process the mock sample. They were asked to go through simulating the assay preparation and perform every step as realistically as possible. The use scenario being studied in this evaluation was the expected use scenario that an intended user would go through when preparing samples for molecular assays in a clinical environment. The study demonstrated usability with the target user population for safe and effective use of the product.

Clinical Performance Evaluation

BD Respiratory Viral Panel for BD MAX™ System Clinical Summary:

The performance of the BD Respiratory Viral Panel for BD MAX™ System was evaluated in comparison to a composite method of two out of three highly sensitive molecular assays (NAATs) that are FDA authorized under EUA for SARS-CoV-2. Any specimen that tested positive by two EUA assays was considered positive for SARS-CoV-2, whereas any specimen that tested negative by two EUA assays was considered negative. For influenza A, influenza B, and RSV, the performance of the BD Respiratory Viral Panel for BD MAX™ System was evaluated in comparison to an FDA-cleared high sensitivity RT-PCR assay.

Prospective Clinical Evaluation

Clinical performance characteristics of the BD Respiratory Viral Panel for BD MAX™ System were established during a multi-center study where subjects were prospectively enrolled at six geographically distinct U.S. study sites and two geographically distinct sites in Europe from January up to August 2022. Four sites performed BD Respiratory Viral Panel for BD MAX™ System testing and/or reference method testing. For consented adult or pediatric subjects presenting with symptoms of respiratory viral infection, one nasopharyngeal swab and/or one nasal swab were collected and placed in validated transport medium. From a total of 2,005 subjects enrolled, 1562 nasopharyngeal swabs and 1566 nasal swabs were included in the performance calculations. Between January and beginning of April 2022, specimens were prospectively collected from all comers meeting the study eligibility criteria and immediately frozen for later testing as prospective archived/frozen (Category II) specimens. Between mid-April up to August 2022, specimens were prospectively collected from all comers meeting the eligibility criteria and

tested fresh as prospective fresh (Category I). For nasopharyngeal specimens, the numbers of compliant specimens with reportable comparator and BD Respiratory Viral Panel for BD MAX™ System were 1,545 for SARS-CoV-2 and 1,562 for Flu A, Flu B, and RSV. For nasal specimens, the numbers of compliant specimens with reportable comparator and BD Respiratory Viral Panel for BD MAX™ System were 1,561 for SARS-CoV-2 and 1,564 for Flu A, Flu B, and RSV. Table 27 provides a summary of demographic and vaccination information for the 1562 nasopharyngeal swabs and 1566 nasal swabs included in the performance calculations.

Table 2. Demographic and Vaccination Summary for Prospective BD Respiratory Viral Panel for BD MAX™ System Clinical Evaluation

Demographics and Vaccination	**Characteristics**	**NP (N=1562)**	**NS (N=1566)**
Gender	Female	61.7% (963/1562)	61.6% (964/1566)
	Male	38.3% (599/1562)	38.4% (602/1566)
Age Group	0 - 5 years	1.3% (20/1562)	1.3% (20/1566)
	6 - 21 years	10.2% (159/1562)	10.2% (160/1566)
	22 - 59 years	57.5% (898/1562)	57.4% (899/1566)
	> 59 years	31.0% (485/1562)	31.1% (487/1566)
Patient Population	Outpatient	95.9% (1498/1562)	95.8% (1500/1566)
	Hospitalized	3.1% (48/1562)	3.1% (49/1566)
	Emergency	1.0% (15/1562)	1.0% (16/1566)
	Unknown	0.1% (1/1562)	0.1% (1/1566)
Immuno-compromised	Yes	3.3% (51/1562)	3.3% (51/1566)
	No	95.0% (1484/1562)	95.0% (1488/1566)
	Unknown	1.7% (27/1562)	1.7% (27/1566)
Received Flu Vaccine	No	72.5% (1132/1562)	72.6% (1137/1566)
	Yes	27.5% (430/1562)	27.4% (429/1566)
Received COVID-19 Vaccine	No	25.3% (395/1562)	25.5% (399/1566)
	Yes	74.7% (1167/1562)	74.5% (1167/1566)
Number of COVID-19 Vaccine Doses	1	4.9% (77/1562)	5.0% (78/1566)
	2	35.3% (552/1562)	35.2% (551/1566)
	3	31.6% (494/1562)	31.5% (494/1566)
	4	2.8% (44/1562)	2.8% (44/1566)

The BD Respiratory Viral Panel for BD MAX™ System prospective nasopharyngeal swab specimens testing performance data against comparator methods are provided in Table 28 by analyte.

Table 28. BD Respiratory Viral Panel for BD MAX™ System Clinical Performance Summary in Prospectively Collected Nasopharyngeal Swab Specimens

Analyte	Sample Type	Positive Percent Agreement		Negative Percent Agreement	
		% (TP/(TP+FN))	95% CI	% (TN/(TN + FP))	95% CI
SARS-CoV-2[a]	Fresh	99.5% (370/372)	(98.1%, 99.9%)	98.8% (641/649)	(97.6%, 99.4%)
	Frozen	97.4% (147/151)	(93.4%, 99.0%)	96.0% (358/373)	(93.5%, 97.5%)
	Overall	98.9% (517/523)	(97.5%, 99.5%)	97.7% (999/1022)	(96.6%, 98.5%)
Flu A[b]	Fresh	96.7% (58/60)	(88.6%, 99.1%)	99.3% (955/962)	(98.5%, 99.6%)
	Frozen	100.0% (1/1)	(20.7%, 100.0%)	100.0% (539/539)	(99.3%, 100.0%)
	Overall	96.7% (59/61)	(88.8%, 99.1%)	99.5% (1494/1501)	(99.0%, 99.8%)
Flu B[c]	Fresh	No data for PPA rate calculation		99.9% (1021/1022)	(99.4%, 100.0%)
	Frozen	No data for PPA rate calculation		100.0% (540/540)	(99.3%, 100.0%)
	Overall	No data for PPA rate calculation		99.9% (1561/1562)	(99.6%, 100.0%)
RSV	Fresh	100.0% (11/11)	(74.1%, 100.0%)	100.0% (1011/1011)	(99.6%, 100.0%)
	Frozen	100.0% (1/1)	(20.7%, 100.0%)	100.0% (539/539)	(99.3%, 100.0%)
	Overall	100.0% (12/12)	(75.8%, 100.0%)	100.0% (1550/1550)	(99.8%, 100.0%)

[a] SARS-CoV-2 was detected in 3/6 FN specimens with all three composite comparator methods. SARS-CoV-2 was detected in 15/23 FP specimens with one of the three composite comparator methods.
[b]Flu A was detected in both FN specimens when tested with an independent molecular method. Flu A was detected in 3/7 FP specimens when tested with an independent molecular method. Flu A was Equivocal in 1/7 FP specimens when tested with an independent method.
[c]Flu B was not detected in the single FP specimen when tested with an independent molecular method.

The BD Respiratory Viral Panel for BD MAX™ System prospective anterior nasal swab specimens testing performance data against comparator methods are provided in Table 29 by analyte.

Table 29. BD Respiratory Viral Panel for BD MAX™ System Clinical Performance Summary in Prospectively Collected Anterior Nasal Swab Specimens

		Positive Percent Agreement		Negative Percent Agreement	
Analyte	Sample Type	% (TP/(TP+FN))	95% CI	% (TN/(TN + FP))	95% CI
SARS-CoV-2[a]	Fresh	98.8% (340/344)	(97.0%, 99.5%)	98.2% (665/677)	(96.9%, 99.0%)
	Frozen	97.2% (138/142)	(93.0%, 98.9%)	96.7% (385/398)	(94.5%, 98.1%)
	Overall	98.4% (478/486)	(96.8%, 99.2%)	97.7% (1050/1075)	(96.6%, 98.4%)
Flu A[b]	Fresh	96.8% (61/63)	(89.1%, 99.1%)	99.6% (958/962)	(98.9%, 99.8%)
	Frozen	100.0% (1/1)	(20.7%, 100.0%)	100.0% (538/538)	(99.3%, 100.0%)
	Overall	96.9% (62/64)	(89.3%, 99.1%)	99.7% (1496/1500)	(99.3%, 99.9%)
Flu B	Fresh	No data for PPA rate calculation		100.0% (1025/1025)	(99.6%, 100.0%)
	Frozen	No data for PPA rate calculation		100.0% (539/539)	(99.3%, 100.0%)
	Overall	No data for PPA rate calculation		100.0% (1564/1564)	(99.8%, 100.0%)
RSV[c]	Fresh	100.0% (11/11)	(74.1%, 100.0%)	99.9% (1013/1014)	(99.4%, 100.0%)
	Frozen	0.0% (0/1)	(0.0%, 79.3%)	100.0% (538/538)	(99.3%, 100.0%)
	Overall	91.7% (11/12)	(64.6%, 98.5%)	99.9% (1551/1552)	(99.6%, 100.0%)

[a] SARS-CoV-2 was detected in 2/8 FN specimens with all three composite comparator methods. SARS-CoV-2 was detected in 17/25 FP specimens with one of the three composite comparator methods.

[b]Flu A was not detected in both FN specimens when tested with an independent molecular method. Flu A was detected in 1/4 FP specimens when tested with an independent molecular method.
[c]RSV was detected in the single FN specimen when tested with an independent molecular method. RSV was detected in the single FP specimen when tested with an independent molecular method.

Retrospective Clinical Evaluation

Clinical performance characteristics of the BD Respiratory Viral Panel for BD MAX™ System were determined from a total of 240 frozen retrospective nasopharyngeal swabs in UVT/UTM obtained from two (2) external sources with historical positive or negative results for either influenza B or RSV. The specimens were collected as part of routine patient care between December 2019 and January 2022. All the specimens were tested in a blinded and randomized fashion with the BD Respiratory Viral Panel for BD MAX™ System at three different testing sites and reference method (RM) at one testing site. The RM for influenza B, and RSV was an FDA-cleared high sensitivity RT-PCR assay. Table 30 provides a summary of demographic information for the 240 retrospective nasopharyngeal samples.

Table 30. Demographic Summary for Retrospective BD Respiratory Viral Panel for BD MAX™ System Clinical Evaluation: Nasopharyngeal Swab Samples

Demographics	Characteristics	Total (N=240)
Gender	Female	37.5% (90/240)
	Male	37.5% (90/240)
	Unknown	25.0% (60/240)
Age Group	0 - 5 years	26.7% (64/240)
	6 - 21 years	20.8% (50/240)
	22 - 59 years	32.5% (78/240)
	> 59 years	20.0% (48/240)

Table 31 describes the performance characteristics of the BD Respiratory Viral Panel for BD MAX™ System that were observed during the clinical evaluation.

Table 31. BD Respiratory Viral Panel for BD MAX™ System Clinical Performance Summary in Retrospective Nasopharyngeal Swab Specimens

	Positive Percent Agreement		Negative Percent Agreement	
Analyte	% (TP/(TP+FN))	95% CI	% (TN/(TN + FP))	95% CI
Flu B[a]	100.0% (58/58)	(93.8%, 100.0%)	98.9% (180/182)	(96.1%, 99.7%)
RSV[b]	98.4% (62/63)	(91.5%, 99.7%)	100.0% (177/177)	(97.9%, 100.0%)

[a] Influenza B was detected in 1/2 FP when tested with an independent molecular method.
[b]RSV was detected in the single FN when tested with an independent molecular method.

Clinical performance characteristics of the BD Respiratory Viral Panel for BD MAX™ System were determined from a total of 187 frozen retrospective nasal swabs in UVT/UTM obtained from six (6) external sources with historical positive or negative results for either influenza B or RSV. Specimens were collected between February 2021 and February 2023. All the specimens were tested in a blinded and randomized fashion with the BD Respiratory Viral Panel for BD MAX™ System at four different testing sites and reference method (RM) at one testing site. The RM for

influenza B, and RSV was an FDA-cleared high sensitivity RT-PCR assay. Table 32 provides a summary of demographic information for the 187 retrospective nasal samples.

Table 32: Demographic Summary for Retrospective BD Respiratory Viral Panel for BD MAX™ System Clinical Evaluation: Nasal Swab Samples

Demographics	Characteristics	Total (N=187)
Gender	Female	50.8% (95/187)
	Male	49.2% (92/187)
Age Group	0 - 5 years	8.6% (16/187)
	6 - 21 years	16.0% (30/187)
	22 - 59 years	62.0% (116/187)
	> 59 years	13.4% (25/187)

One (1) specimen generated an Unresolved (UNR) assay result for both Flu B and RSV and was excluded from the performance analysis. Table 33 describes the performance characteristics of the BD Respiratory Viral Panel for BD MAX™ System that were observed during the clinical evaluation.

Table 33: BD Respiratory Viral Panel for BD MAX™ System Clinical Performance Summary in Retrospective Nasal Swab Specimens

Analyte	Positive Percent Agreement		Negative Percent Agreement	
	% (TP/(TP+FN))	95% CI	% (TN/(TN + FP))	95% CI
Flu B[a]	100.0% (12/12)	(75.8%, 100.0%)	98.9% (172/174)	(95.9%, 99.7%)
RSV[b]	100.0% (15/15)	(79.6%, 100.0%)	99.4% (170/171)	(96.8%, 99.9%)

[a] Influenza B was detected in 2/2 FP when tested with an independent molecular method.

[b] Five of 20 RSV positive archived samples by the source laboratory were not confirmed by the comparator method. RSV was not detected in the single FN when tested with an independent molecular method.

Non-Reportable Rate

Of all the specimens initially evaluated with the BD Respiratory Viral Panel for BD MAX™ System Clinical, the initial total rates of non-reportable results were 0.9% and 1.1% for

nasopharyngeal and nasal specimens, respectively. Following a valid repeat, 0.1% remained non-reportable for both specimen types. Results are shown in Table 34.

Table 34. Non-Reportable Rates

Sample Type	Unresolved (UNR) Rate		Indeterminate (IND) Rate		Incomplete (INC) Rate		Total Non-Reportable Rate (UNR+IND+INC)	
	Initial (95% CI)	Valid Repeat (95% CI)	Initial (95% CI)	Valid Repeat (95% CI)	Initial (95% CI)	Valid Repeat (95% CI)	Initial (95% CI)	Valid Repeat (95% CI)
Nasopharyngeal	0.1% (1/1563) (0.0%, 0.4%)	0.1% (1/1563) (0.0%, 0.4%)	0.0% (0/1563) (0.0%, 0.2%)	0.0% (0/1563) (0.0%, 0.2%)	0.8% (13/1563) (0.5%, 1.4%)	0.0% (0/1563) (0.0%, 0.2%)	0.9% (14/1563) (0.5%, 1.5%)	0.1% (1/1563) (0.0%, 0.4%)
Nasal	0.1% (2/1568) (0.0%, 0.5%)	0.1% (2/1568) (0.0%, 0.5%)	0.1% (2/1568) (0.0%, 0.5%)	0.0% (0/1568) (0.0%, 0.2%)	0.8% (13/1568) (0.5%, 1.4%)	0.0% (0/1568) (0.0%, 0.2%)	1.1% (17/1568) (0.7%, 1.7%)	0.1% (2/1568) (0.0%, 0.5%)

Conclusion

The analytical and clinical information in this premarket notification is complete and supports a substantial equivalence decision for the BD Respiratory Viral Panel or BD MAX™ System and the BD Respiratory Viral Panel-SVC2 for BD MAX™ System.