

cobas[®] Respiratory flex

Qualitative nucleic acid test for use on the cobas[®] 5800/6800/8800 systems

For in vitro diagnostic use

| cobas [®] Respiratory flex | P/N: 09623701190 |
|---|---------------------|
| For use on the cobas [®] 5800 system | |
| cobas [®] Respiratory flex Control Kit | P/N: 09623728190 |
| cobas [®] Buffer Negative Control Kit | P/N: 09051953190 |
| For use on the cobas [®] 6800/8800 systems | |
| cobas [®] Respiratory flex Control Kit | P/N: 09623728190 |
| cobas [®] Buffer Negative Control Kit | P/N: 09051953190 or |
| | P/N: 07002238190 |

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Intended use

cobas[°] Respiratory flex for use on the **cobas**[°] 5800/6800/8800 systems (**cobas**[°] Respiratory flex) is an automated, multiplex, nucleic acid test that utilizes real-time polymerase chain reaction (PCR) technology for simultaneous in vitro qualitative detection and differentiation of adenovirus (species B, C and E), common human coronaviruses (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, respiratory syncytial virus (RSV), and SARS-CoV-2 in nasopharyngeal swab specimens obtained from individuals with signs and symptoms of respiratory tract infections in conjunction with clinical and epidemiological risk factors.

The detection and identification of specific viral nucleic acids from individuals presenting with signs and symptoms of a respiratory infection aids in the diagnosis of respiratory infection if used in conjunction with other clinical and epidemiological information. Negative results do not preclude a respiratory infection and should not be used as the sole basis for treatment or other patient management decisions. Conversely, positive results do not rule out coinfection with other organisms, and the agent detected may not be the definite cause of disease.

Due to the genetic similarity between human rhinovirus and enterovirus, the **cobas**^{*} Respiratory flex test cannot reliably differentiate them.

Summary and explanation of the test

Background

Acute respiratory tract infections are significant causes of worldwide morbidity and mortality.¹⁻⁵ Acute upper respiratory tract infections (URTI), while less severe than lower respiratory tract infections (LRTI), are more common and a leading cause of physician visits and absenteeism.⁶ URTIs most frequently manifest as the "Common Cold," a self-limiting infection characterized by common symptoms such as a runny nose, nasal congestion, sneezing, cough, tiredness, sore throat, or fever. Common Colds are rarely bacterial and most are caused by viruses such as rhinovirus, metapneumovirus, coronavirus, parainfluenza, adenovirus, RSV, and influenza.⁶⁷

In higher-risk populations, such as infants, young children, elderly, or those with compromised immunity, transplants or chronic disease, URTIs can more often progress to serious LRTIs, such as pneumonia, bronchitis or bronchiolitis.^{8,9} However, the infectious signs and symptoms of URTIs are insufficient, especially in the early infectious phase, to definitively diagnose the causative pathogen or clinically distinguish them from LRTIs that can be caused by an even wider range of pathogens that includes viruses, bacteria and fungi.¹⁰ With nucleic acid amplification test (NAAT) technology, viral URTIs can be reliably detected using nasopharyngeal swab specimens in the outpatient setting, where a majority of the patients are presenting and where viral respiratory infections are more common.^{11,12} The detection of LRTIs often requires more invasive sampling (such as tracheal aspirates, induced sputum or bronchoalveolar lavage) that is typically performed in the inpatient or interventional setting. The value of more easily diagnosing the most common viral causes of URTIs is that it enables a more informed assessment, including the need for empiric antibiotic therapy, infection control measures, additional testing or hospitalization.¹³

Influenza, RSV, and severe acute respiratory syndrome coronavirus-2 (SARS-CoV-2) cause URTIs and frequently progress to LRTIs, which deserve particular attention due to their higher (relative to other URTIs) worldwide incidence, morbidity, and mortality.^{1,3,14} Effective diagnosis and differentiation of influenza, SARS-CoV-2, and RSV infection from other respiratory pathogens in select patients provides valuable diagnostic information. The global seasonality and clinical presentations of influenza and RSV overlap, with peaks of infectious activity occurring in the respective winter months for temperate climates in the Northern and Southern hemispheres.¹⁵ Reliable and accurate detection of influenza and RSV infections can help to target the use of antivirals and implementation of infection control measures, avoid inappropriate antibiotic use, reduce ancillary testing and hospitalizations, and identify local outbreaks of disease sooner.

COVID-19 cases first appeared in late 2019, as an outbreak of this novel coronavirus spread worldwide, prompting the World Health Organization (WHO) to declare a public health emergency of international concern in early 2020.^{16,17} Globally, as of January 2023, there have been more than 750 million confirmed cases of COVID-19 including 6.8 million deaths reported to WHO, although actual case numbers are estimated to be higher.¹⁸ The implicated pathogen, SARS-CoV-2, is an enveloped ribonucleic acid virus of zoonotic origin.¹⁹ Coronaviruses (CoVs) are a large family of viruses that are common in many different animal species, including some that are common in humans (e.g., 229E, NL63, OC43, and HKU1).^{19,20}

Influenza virus is globally estimated to cause over one billion infections and 500,000 deaths each year, with the highest burdens in infants, young children, the elderly, and those with underlying medical conditions, such as chronic lung disease.²¹ Influenza types A and B can cause human epidemics, however in the case of most human pandemics, novel strain emergence and a greater overall disease burden is attributed to type A.^{2,22} RSV is a leading cause of LRTIs and hospitalizations in infants and children, with most children having an RSV infection by two years of age.^{4,23} In children five years of age or younger, there are over three million hospitalizations and over 100,000 globally estimated deaths from lower respiratory RSV infections each year.⁴ More recently, due in part to diagnostic improvements, RSV has also been associated with a substantial disease and health economic burden in older adults as well.¹⁴

Explanation of the test

cobas[°] Respiratory flex is a qualitative nucleic acid test for the use on the **cobas**[°] 5800 system, **cobas**[°] 6800 system or **cobas**[°] 8800 system for the detection and differentiation of adenovirus (species B, C and E), common human coronaviruses (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, RSV, and SARS-CoV-2 RNA in nasopharyngeal swab samples collected in Copan Universal Transport Medium System (UTM-RT[®]) or BD[™] Universal Viral Transport System (UVT) or equivalent. The RNA IC, used to monitor the entire sample preparation and PCR amplification process, is introduced into each specimen during sample processing. In addition, the test utilizes external controls (a low titer positive control and a negative control).

Principles of the procedure

cobas[°] Respiratory flex is based on fully automated sample preparation (nucleic acid extraction and purification) followed by PCR amplification and detection. The **cobas**[°] 5800 system is designed as one integrated instrument. The **cobas**[°] 6800/8800 systems consist of the sample supply module, the transfer module, the processing module, and the analytic module. Automated data management is performed by the **cobas**[°] 5800 system or **cobas**[°] 6800/8800 systems software(s), which assigns results for all tests.

Results can be reviewed directly on the system screen, and printed as a report.

Nucleic acid from patient samples and added Internal Control RNA (RNA IC) molecules are simultaneously extracted.

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Nucleic acid is released by addition of proteinase and lysis reagent to the sample. The released nucleic acid binds to the silica surface of the added magnetic glass particles. Unbound substances and impurities, such as denatured protein, cellular debris and potential PCR inhibitors, are removed with subsequent wash steps and purified nucleic acid is eluted from the magnetic glass particles with elution buffer at elevated temperature. External controls (positive and negative) are processed in the same way.

Selective amplification of target nucleic acid from the sample is achieved by the use of target-specific forward and reverse primers detecting conserved viral genome regions as shown in Table 1.

| Targeted organism | Target gene (symbol) | |
|-----------------------------|---|--|
| Influenza A | Matrix protein 1 (M1) | |
| Influenza B | Non-structural protein NS-1/2 (NS1/NEP) | |
| Respiratory Syncytial Virus | Matrix protein (M) | |
| SARS-CoV-2 | ORF1 ab polyprotein (ORF1ab) and ORF 1a polyprotein (ORF1a) | |
| Adenovirus B/E | Terminal protein precursor (E2B) | |
| Adenovirus C | Capsid protein precursor (L3) | |
| Human Metapneumovirus | Matrix protein (M) | |
| Enterovirus/Rhinovirus | 5' untranslated region (5'UTR) | |
| Coronavirus OC43 | Replicase polyprotein 1 a/b (ORF1ab) | |
| Coronavirus HKU1 | Replicase polyprotein 1 a/b (ORF1ab) | |
| Coronavirus 229E | Replicase polyprotein 1 a/b (ORF1ab) | |
| Coronavirus NL63 | Replicase polyprotein 1 a/b (ORF1ab) | |
| Human Parainfluenza Virus 1 | L polymerase protein (L) | |
| Human Parainfluenza Virus 2 | Large protein (L) | |
| Human Parainfluenza Virus 3 | Nucleocapsid protein (N) | |
| Human Parainfluenza Virus 4 | Large protein (L) | |

 Table 1
 cobas[®] Respiratory flex target regions

Selective amplification of RNA IC is achieved by the use of non-competitive, sequence specific forward and reverse primers, which have no homology with the viral-target specific genomes. Amplified target is detected by the cleavage of fluorescently labeled oligonucleotide probes. Roche's temperature assisted generation of signal (TAGS) technology, short TAGS technology, is introduced to differentiate up to three targets per fluorescence channel, enabling the detection of 12 targets, and the Internal Control, per well. A thermostable DNA polymerase enzyme is used for amplification.

The **cobas**^{*} Respiratory flex master mix contains detection probes which are specific for adenovirus (species B, C and E), common human coronaviruses (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, RSV, and SARS-CoV-2, and the RNA Internal Control nucleic acid. Multiplicity of target detection is enabled with temperature-dependent quenching of cleaved fluorescent target-specific probes. This is achieved by separating signals from probes into introduced thermal channels, where fluorescence is acquired at two additional fixed temperatures for each amplification cycle.

During the PCR amplification step, hybridization of the probes to the specific single-stranded DNA template results in cleavage of the probe by the 5' to 3' exonuclease activity of the DNA polymerase, resulting in separation of the reporter and quencher dyes, and the generation of a fluorescent signal. Conventional probes release fluorescence signal immediately upon separation of reporter from quencher. TAGS probes rely on temperature dependent fluorescence activation, requiring both nuclease cleavage during the extension phase, as well as an increase in reaction temperature, to activate the otherwise dormant fluorophore. For this reason, during each PCR cycle the test captures fluorescence in five available fluorescence channels in combination with three thermal channels (detection of fluorescence at three defined temperatures T1, T2 and T3), which enables simultaneous detection and differentiation of the amplified adenovirus (species B, C and E), common human coronaviruses (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, RSV, and SARS-CoV-2 viral targets and the RNA IC.

The master mix includes deoxyuridine triphosphate (dUTP), instead of deoxythymidine triphosphate (dTTP), which is incorporated into the newly synthesized DNA (amplicon). Any contaminating amplicons from previous PCR runs are destroyed by the AmpErase enzyme [uracil-N-glycosylase], which is included in the PCR mix, when heated in the first thermal cycling step. However, newly formed amplicons are not destroyed since the AmpErase enzyme is inactivated once exposed to temperatures above 55°C.

Reagents and materials

The materials provided for the **cobas**^{*} Respiratory flex kit can be found in Table 2. Materials required, but not provided, can be found in Table 3 through Table 5 and Table 10 through Table 13.

cobas[®] Respiratory flex reagents and controls

All unopened reagents and controls shall be stored as recommended in Table 2 to Table 6.

Table 2cobas[®] Respiratory flex

(RESP FLEX)

Store at 2-8°C 192 test cassette (P/N 09623701190)

| | | Quantity per kit 192 tests |
|---|---|-------------------------------|
| Proteinase Solution (PASE) | Tris buffer, < 0.05% EDTA, calcium chloride, calcium acetate, 8% proteinase, glycerol | 22.3 mL |
| | EUH210: Safety data sheet available on request. EUH208: Contains Subtilisin from Bacillus subtilis. May produce an allergic reaction. | |
| RNA Internal ControlTris buffer, < 0.05% EDTA, < 0.001% non-target related armored RNA construct containing primer and probe specific sequence regions (non-infectious RNA in MS2 bacteriophage), < 0.1% sodium azide2 | | 21.2 mL |
| Elution Buffer (EB) | | |
| Master Mix Reagent 1Manganese acetate, potassium hydroxide, < 0.1% sodium azide | | 7.5 mL |
| Respiratory flex Master Mix Reagent 2 (RESP FLEX MMX-R2) | Tricine buffer, potassium acetate, < 18% dimethyl sulfoxide, glycerol, < 0.1% Tween 20, EDTA, < 0.12% dATP, dCTP, dGTP, dUTPs, < 0.01% upstream and downstream primers, < 0.01% Internal Control forward and reverse primers, < 0.01% fluorescent-labeled oligonucleotide probes and the RNA Internal Control, < 0.01% oligonucleotide aptamer, < 0.1% Z05D DNA polymerase, < 0.10% AmpErase (uracil- N-glycosylase) enzyme (microbial), < 0.1% sodium azide | 9.7 mL |

Table 3 cobas[®] Respiratory flex Control Kit

(RESP FLEX CTL)

Store at 2–8°C

(P/N 09623728190)

| Kit components | Reagent ingredients | Quantity per kit |
|--|--|-------------------------|
| Respiratory flex Positive Control (RESP FLEX CTL) | Tris buffer, < 0.05% Sodium azide, < 0.005% EDTA, 0.003% Poly rA, < 0.01% Non-infectious plasmid DNA (microbial) containing adenovirus sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing coronavirus (229E) sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human metapneumovirus sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing rhinovirus sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing influenza A sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing influenza B sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 1 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 2 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 3 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) containing human parainfluenza virus 4 sequence, < 0.01% Non-infectious plasmid DNA (microbial) c | 6.4 mL (16 x 0.4 mL) |

 Table 4
 cobas[®] Buffer Negative Control Kit

(BUF (-) C)

Store at 2-8°C

For use on the **cobas**[®] 5800 system, and the **cobas**[®] 6800/8800 systems with software version 2.0 or higher (P/N 09051953190) For use on the **cobas**[®] 6800/8800 systems with software version 1.4 (P/N 07002238190 or P/N 09051953190)

| Kit components | Reagent ingredients | Quantity per kit |
|--|--|----------------------|
| cobas [®] Buffer Negative Control (BUF (-) C) | Tris buffer, < 0.1% sodium azide, EDTA, 0.002% Poly rA RNA (synthetic) | 16 mL (16 x 1 mL) |

cobas[®] omni reagents for sample preparation

Table 5 cobas[®] omni reagents for sample preparation

| Reagents | Reagent ingredients | Quantity per kit | Safety symbol and warning* |
|--|---|---------------------|---|
| cobas [®] omni MGP Reagent (MGP) Store at 2–8°C (P/N 06997546190) | Magnetic glass particles, Tris buffer, 0.1% methyl-4 hydroxybenzoate, < 0.1% sodium azide | 480 tests | Not applicable |
| cobas [®] omni Specimen Diluent (SPEC DIL) Store at 2–8°C (P/N 06997511190) | Tris buffer, 0.1% methyl-4 hydroxybenzoate, < 0.1% sodium azide | 4 x 875 mL | Not applicable |
| cobas [®] omni Lysis Reagent (LYS) Store at 2–8°C (P/N 06997538190) | 43% (w/w) guanidine thiocyanate**, 5% (w/v) polydocanol**, 2% (w/v) dithiothreitol**, dihydro sodium citrate | 4 x 875 mL | DANGER H302: Harmful if swallowed H314: Causes severe skin burns and eye damage. H412: Harmful to aquatic life with long lasting effects. EUH032: Contact with acids liberates very toxic gas. EUH071: Corrosive to the respiratory tract. P273: Avoid release to the environment. P280: Wear protective gloves/ protective clothing/ eye protection/ face protection/ hearing protection. P301 + P330 + P331: IF SWALLOWED: Rinse mouth. Do NOT induce vomiting. P303 + P361 + P353: IF ON SKIN (or hair): Take off immediately all contaminated clothing. Rinse skin with water. P304 + P340 + P310: IF INHALED: Remove person to fresh air and keep comfortable for breathing. Immediately call a POISON CENTER/ doctor. P305 + P351 + P338 + P310: IF IN EYES: Rinse cautiously with water for several minutes. Remove contact lenses, if present and easy to do. Continue rinsing. Immediately call a POISON CENTER/ doctor. P303-84-0 Guanidinium thiocyanate 9002-92-0 Polidocanol 3483-12-3 (R*,R*)-1,4-dimercaptobutane-2,3-diol |
| cobas [®] omni Wash Reagent (WASH) Store at 15–30°C (P/N 06997503190) | Sodium citrate dihydrate, 0.1% methyl-4 hydroxybenzoate | 4.2 L | Not applicable |

* Product safety labeling primarily follows EU GHS guidance.

**Hazardous substance

Reagent storage requirements

Reagents shall be stored and will be handled as specified in Table 6 through Table 9.

When reagents are not loaded on the **cobas**^{*} 5800 or **cobas**^{*} 6800/8800 systems, store them at the corresponding temperature specified in Table 6.

| Reagent | Storage temperature |
|---|---------------------|
| cobas [®] Respiratory flex | 2–8°C |
| cobas [®] Respiratory flex Control Kit | 2–8°C |
| cobas [®] Buffer Negative Control Kit | 2–8°C |
| cobas [®] omni Lysis Reagent | 2-8°C |
| cobas [®] omni MGP Reagent | 2–8°C |
| cobas [®] omni Specimen Diluent | 2-8°C |
| cobas [®] omni Wash Reagent | 15–30°C |

 Table 6
 Reagent storage (when reagent is not on the system)

Reagent handling requirements for $cobas^{\ensuremath{\ensuremath{^{ extsf{m}}}}}$ 5800 system and $cobas^{\ensuremath{^{ extsf{m}}}}$ 6800/8800 systems

Reagents loaded onto the **cobas**[•] 5800 system or **cobas**[•] 6800/8800 systems are stored at appropriate temperatures and their expiration is monitored and enforced by the system. The system allows reagents to be used only if all of the reagent handling conditions shown in Table 7, Table 8 and Table 9 are met. The system automatically prevents use of expired reagents. Remaining open-kit stability and number of kit uses information for assay specific reagents is accessible through the system user interface.

Table 7Reagent expiry conditions monitored and enforced by the $cobas^{(8)}$ 5800 system

| Reagent | Open-kit stability | Number of kit uses | On-board stability |
|---|---------------------------|--------------------|----------------------|
| cobas [®] Respiratory flex | 180 days from first usage | 80 | 36 days from loading |
| cobas [®] Respiratory flex Control Kit | single vial use | 16 | 36 days from loading |
| cobas [®] Buffer Negative Control Kit | single vial use | 16 | 36 days from loading |

| Table 8 Reagent expiry conditions monitored and enforced by the cobas [®] 6800/8800 system |
|---|
|---|

| Reagent | Open-kit stability | NIIMNOF OF KIT LICOC | On-board stability (outside on board refrigerator) |
|---|---------------------------|----------------------|---|
| cobas [®] Respiratory flex | 180 days from first usage | 40 | 40 hours |
| cobas [®] Respiratory flex Control Kit | single vial use | 16 | 10 hours |
| cobas® Buffer Negative Control Kit | single vial use | 16 | 10 hours |

Table 9 shows the open-kit stability of the **cobas**[®] **omni** reagents. Prior to each run, the system verifies the open-kit stability and ensures sufficient fill volume. Therefore, these reagents have no number of kit uses or on-board stability assigned.

 Table 9
 cobas[®] omni reagent expiry condition enforced by the cobas[®] 5800/6800/8800 systems

| Reagent | Open-kit stability | | |
|--|--------------------------|--|--|
| cobas [®] omni MGP Reagent | 30 days from first usage | | |
| cobas [®] omni Lysis Reagent | 30 days from loading | | |
| cobas [®] omni Specimen Diluent | 30 days from loading | | |
| cobas [®] omni Wash Reagent | 30 days from loading | | |

Additional materials required for cobas[®] 5800/6800/8800 system

Table 10 Material for use on the $cobas^{(\!8\!)} 5800/6800/8800$ systems

| Material | P/N | |
|--|-------------|--|
| cobas [®] omni Lysis Reagent | 06997538190 | |
| cobas [®] omni MGP Reagent | 06997546190 | |
| cobas [®] omni Specimen Diluent | 06997511190 | |
| cobas [®] omni Wash Reagent | 06997503190 | |

Table 11 Consumables for use on the cobas® 5800 system*

| Material |
|--|
| cobas [®] omni Processing Plate 24 |
| cobas [®] omni Amplification Plate 24 |
| cobas [®] omni Liquid Waste Plate 24 |
| Tip CORE TIPS with Filter, 1 mL |
| Tip CORE TIPS with Filter, 300 μL |
| cobas [®] omni Liquid Waste Container |
| Solid Waste Bag or Solid Waste Bag With Insert |
| cobas [®] omni Secondary Tubes 13x75 (optional) |
| MPA RACK 13 or 16 MM |
| RD5 RACK – RD Standard rack |
| 16-position tube carrier |
| 5-position rack carrier |

*For Part Numbers please refer to the **cobas**^{*} 5800 system User Assistance.

Table 12 Consumables for use on cobas® 6800/8800 systems*

| Material |
|---|
| cobas [®] omni Processing Plate |
| cobas [®] omni Amplification Plate |
| cobas [®] omni Pipette Tips |
| cobas [®] omni Liquid Waste Container |
| Solid Waste Bag and Solid Waste Container or Solid Waste Bag With Insert and Kit Drawer |
| cobas [®] omni Secondary Tubes 13x75 (optional) |
| MPA RACK 13 or 16 MM |
| RD5 RACK – RD Standard rack |

*For Part Numbers please refer to the **cobas**^{*} 6800/8800 systems User Assistance.

Additional materials required for pre-analytic workflow

 Table 13
 Other materials required for pre-analytic workflow

| Material | P/N | | |
|--|-------------|--|--|
| cobas® Microbial Inactivation Solution | 08185476001 | | |

Instrumentation and software required

The **cobas**^{*} 5800 software, **cobas**^{*} 6800/8800 systems software and **cobas**^{*} Respiratory flex analysis package (ASAP) for the **cobas**^{*} 5800/6800/8800 systems shall be installed on the instrument.

For the **cobas**^{*} 5800 and **cobas**^{*} 6800/8800 systems with software 2.0 or higher, the Data Manager software and PC (or server) will be provided with the system.

For the cobas' 6800/8800 systems with software 1.4, the Instrument Gateway (IG) server will be provided with the system.

Table 14 Instrumentation

| Equipment | P/N | |
|--|-----------------------------|--|
| cobas [®] 5800 system | 08707464001 | |
| cobas [®] 6800 system | 05524245001 and 09575154001 | |
| cobas [®] 8800 system | 05412722001 and 09575146001 | |
| Sample Supply Module for cobas [®] 6800/8800 systems | 06301037001 and 09936882001 | |

Refer to the cobas[°] 5800 system or cobas[°] 6800/8800 systems - User Assistance for additional information.

Precautions and handling requirements

Warnings and precautions

As with any test procedure, good laboratory practice is essential to the proper performance of this assay. Due to the high sensitivity of this test, care should be taken to keep reagents and amplification mixtures free of contamination.

- For in vitro diagnostic use.
- All patient samples should be handled as if infectious, using good laboratory procedures as outlined in Biosafety Microbiological and Biomedical Laboratories and in the CLSI Document M29-A4, and in accordance with local regulations or standards.^{24,25} Only personnel proficient in handling infectious materials and the use of **cobas**^{*} Respiratory flex and the **cobas**^{*} 5800/6800/8800 systems should perform this procedure.
- All human-sourced materials should be considered potentially infectious and should be handled with universal precautions. If spillage occurs, immediately disinfect following appropriate site procedures.
- If spillage of samples in MIS (which contains guanidine thiocyanate) occurs, do not allow it to come in contact with sodium or potassium hypochlorite containing disinfectants. This mixture can produce a highly toxic gas.
- If spillage of samples in MIS occurs, FIRST clean with a suitable laboratory detergent and water, and then with 70% ethanol.
- MIS is light-sensitive and shipped in light-protective bottles. MIS must be stored upright.
- The use of sterile disposable pipettes and nuclease-free pipette tips is recommended. Use only supplied or specified required consumables to ensure optimal test performance.
- Safety Data Sheets (SDS) are available on request from your local Roche representative.
- Closely follow procedures and guidelines provided to ensure that the test is performed correctly. Any deviation from the procedures and guidelines may affect optimal test performance.
- False positive results may occur if carryover of samples is not adequately controlled during sample handling and processing.
- Inform your local competent authority and manufacturer about any serious incidents which may occur when using this assay.

Reagent handling

- Handle all reagents, controls, and samples according to good laboratory practice in order to prevent carryover of samples or controls.
- Before use, visually inspect each reagent cassette, diluent, lysis reagent, and wash reagent to ensure that there are no signs of leakage. If there is any evidence of leakage, do not use that material for testing.
- **cobas omni** Lysis Reagent and MIS contain guanidine thiocyanate, a potentially hazardous chemical. Avoid contact of reagents with the skin, eyes, or mucous membranes. If contact does occur, immediately wash with generous amounts of water, otherwise, burns can occur.
- **cobas** Respiratory flex test kit, **cobas** Respiratory flex Control Kit, **cobas** Buffer Negative Control Kit, **cobas omni** MGP Reagent, and **cobas omni** Specimen Diluent contain sodium azide as a preservative. Avoid contact of reagents with the skin, eyes, or mucous membranes. If contact does occur, immediately wash with generous amounts of water, otherwise, burns can occur. If these reagents are spilled, dilute with water before wiping dry.
- Do not allow **cobas**[•] **omni** Lysis Reagent or MIS, which contain guanidine thiocyanate, to contact sodium or potassium hypochlorite solution. This mixture can produce a highly toxic gas.
- Dispose of all materials that have come in contact with samples and reagents in accordance with country, state, and local regulations.

Good laboratory practice

- Do not pipette by mouth.
- Do not eat, drink, or smoke in designated work areas.
- Wear laboratory gloves, laboratory coats, and eye protection when handling samples and reagents. Gloves must be changed between handling samples and **cobas**^{*} Respiratory flex kits, **cobas**^{*} Respiratory flex Control Kit, **cobas**^{*} Buffer Negative Control Kit and **cobas**^{*} **omni** reagents to prevent contamination. Avoid contaminating gloves when handling samples and controls.
- Wash hands thoroughly after handling samples and kit reagents, and after removing the gloves.
- Thoroughly clean and disinfect all laboratory work surfaces with a freshly prepared solution of 0.5% sodium or potassium hypochlorite in distilled or deionized water. Follow by wiping the surface with 70% ethanol.
- If spills occur on the **cobas**[•] 5800 or **cobas**[•] 6800/8800 instrument, follow the instructions in the **cobas**[•] 5800 or **cobas**[•] 6800/8800 systems User Assistance to properly clean and decontaminate the surface of instrument(s).

Sample collection, transport, and storage

Note: Handle all samples and controls as if they are capable of transmitting infectious agents.

Store all samples at specified temperatures.

Sample stability is affected by elevated temperatures.

Always use caution when transferring specimens from a primary collection tube to a secondary tube.

Use pipettes with aerosol-barrier or positive-displacement tips to handle specimens.

Always use a new pipette tip for each specimen.

Ensure samples are equilibrated to room temperature prior to transfer into a **cobas® omni** Secondary Tube.

Sample collection

- Collect nasopharyngeal specimens according to standard collection technique using flocked or polyester-tipped swabs and immediately place in 3 mL of UTM-RT^{*} or UVT or equivalent.
- Refer to the Instructions For Use of the Collection Devices for hazard information.

Transport and storage

- Transportation of collected specimens must comply with all applicable regulations for the transport of etiologic agents.
- Samples collected in UTM-RT[®] or UVT or equivalent:
- After collection, specimens can be stored for up to 12 hours at 2-25°C followed by up to 3 days at 2-8°C and at ≤ -18°C for up to 30 days.
- Specimens are stable for up to three freeze/thaw cycles when frozen at \leq -18°C.

Instructions for use

Procedural notes

- Do not use **cobas** Respiratory flex , **cobas** Respiratory flex Control Kit, **cobas** Buffer Negative Control Kit, or **cobas omni** reagents after their expiry dates.
- Do not reuse consumables. They are for one-time use only.
- **cobas**^{*} Respiratory flex can be run with a sample volume of 1.2 mL (0.4 mL of sample and 0.8 mL of MIS) of which 850 µl is processed. The sample type "Diluted in **cobas**^{*} MIS" has to be selected to run **cobas**^{*} Respiratory flex.

Processing of nasopharyngeal specimens

Prior to running **cobas**[°] Respiratory flex on the **cobas**[°] 5800/6800/8800 systems, specimens have to be processed using a secondary tube with a maximum dead volume of 350µl. The **cobas**[°] **omni** Secondary Tube is the preferred option. Additional secondary tubes for testing **cobas**[°] Respiratory flex are available. Contact your local Roche representative for detailed testing instructions and an order of secondary tubes compatible with the instruments.

Note: Always use caution when transferring specimens from a primary collection tube to a secondary tube. Use pipettes with aerosol-barrier or positive-displacement tips to handle specimens.

Always use a new pipette tip for each specimen.

Ensure samples are equilibrated to room temperature prior to transfer into a **cobas omni** Secondary Tube.

Follow the steps below to transfer and dilute patient sample from a primary collection tube into a **cobas' omni** Secondary Tube:

- Confirm that the nasopharyngeal sample tube is properly labeled and contains a minimum of 0.4 mL of specimen. If stored frozen, thaw and equilibrate the sample to ambient temperature.
- Invert the MIS bottles two to four times before use.
- Transfer 0.8 mL of MIS into the prepared barcoded secondary tube. Prepared secondary tubes containing 0.8 mL of MIS can be stored closed for up to 7 days at 2-8°C.
- Unscrew the primary sample tube cap.
- Lift the cap and any attached swab to allow a pipette to be inserted into the sample tube.
- Transfer 0.4 mL into the prepared barcoded secondary tube containing MIS. No further mixing is required.
- Transfer the secondary tube to a rack.
- Close the primary sample tube cap.

Note: Nasopharyngeal specimens diluted in MIS may be stored for up to 8 hours at 37°C or 20 hours at 25°C.

Running cobas[®] Respiratory flex on cobas[®] 5800/6800/8800 systems

- The operation of the instruments is described in detail in the **cobas**^{*} 5800 system or **cobas**^{*} 6800/8800 systems User Assistance.
- Ensure that the specimen barcode labels on sample tubes are visible through the openings on the side of the sample racks. Refer to the **cobas**[°] 5800 system or **cobas**[°] 6800/8800 systems User Assistance for proper barcode specifications and additional information on loading sample tubes.
- Refer to the **cobas**^{*} 5800 system or **cobas**^{*} 6800/8800 systems User Assistance for proper maintenance of instruments.
- Figure 1 and Figure 2 summarize the test procedure on **cobas**^{*} 5800 system or **cobas**^{*} 6800/8800 systems, respectively.
- Running **cobas**^{*} Respiratory flex on **cobas**^{*} 5800 system and **cobas**^{*} 6800/8800 systems with software version 2.0 or higher enables flexible ordering options:
 - Configuring target groups: Each specimen can be tested for any combinations of viral targets (adenovirus, pan-coronavirus (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, RSV, and SARS-CoV-2.
 - Additional target calculation (digital reflex): Based on the initial test results additional targets out of the multiplex test panel can be ordered in the predefined time period. The additional ordered targets will then be calculated based on the already measured raw data. The sample does not need to be processed again to get the additional test results.
- When running **cobas**^{*} Respiratory flex on **cobas**^{*} 6800/8800 systems with software version 1.4:
 - Each specimen can be tested with one of the four available Assay Specific Analysis Packages (ASAPs) enabling full panel testing, predefined subgroups or an automated digital reflex option.
 - The automated digital reflex ASAP first calculates and displays a pre-defined set of targets (e.g. FluA, FluB, RSV, SARS-CoV-2).
 - If a sample is negative for these targets, the test will then automatically calculate and display the results of the remaining targets in the panel (automated digital reflex).
 - If a sample is positive or invalid for one of the initial targets, the additional targets will not be calculated.
 Each sample is handled independently of the other samples. That means that some samples will only have results for the most common targets while other samples will display results for a larger number of targets.

Figure 1 cobas[®] Respiratory flex test procedure on cobas[®] 5800 system

| 1 | Log onto the system |
|---|---|
| 2 | Loading samples onto the system Load sample racks onto the system The system prepares automatically Order tests |
| 3 | Refill reagents and consumables as prompted by the system Load test specific reagent cassette(s) Load control mini racks Load processing tips Load elution tips Load processing plates Load liquid waste plates Load amplification plates Load MGP cassette Refill specimen diluent Refill vash reagent |
| 4 | Start the run by choosing the Start processing button on the user interface, all subsequent runs will start automatically if not manually postponed |
| 5 | Review and export results |
| 6 | Remove and cap any sample tubes meeting the minimum volume requirements if needed for future use Clean up the instrument • Unload empty control cassettes • Empty amplification plate drawer • Empty liquid waste • Empty solid waste |

Figure 2 cobas[®] Respiratory flex test procedure on the cobas[®] 6800/8800 systems

| 1 | Log onto the system Press Start to prepare the system Order tests |
|---|--|
| 2 | Refill reagents and consumables as prompted by the system Load test specific reagent cassette Load control cassettes Load pipette tips Load processing plates Load MGP reagent Load amplification plates Refill specimen diluent Refill lysis reagent Refill wash reagent |
| 3 | Loading samples onto the system Load sample racks and clotted tip racks onto the sample supply module Confirm samples have been accepted into the transfer module |
| 4 | Start the run by choosing the Start manually button on the user interface or have it start automatically after 120 minutes or if the batch is full |
| 5 | Review and export results |
| 6 | Remove and cap any sample tubes meeting the minimum volume requirements if needed for future use Clean up the instrument • Unload empty control cassettes • Empty amplification plate drawer • Empty liquid waste • Empty solid waste |

Results

The **cobas**^{*} 5800 system and **cobas**^{*} 6800/8800 systems automatically detects adenovirus (species B, C and E), common human coronaviruses (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, RSV, and SARS-CoV-2 for each individually processed sample and control, displaying individual target results for samples as well as validity for controls.

Quality control and validity of results on the cobas[®] 5800 system and cobas[®] 6800/8800 systems with software version 2.0 or higher

- One **cobas**^{*} Buffer Negative Control [(-) Ctrl] and one **cobas**^{*} Respiratory flex Positive Control [RESP-FLEX (+) C] are processed at least every 72 hours or with every new kit lot. Positive and/or negative controls can be scheduled more frequently based on laboratory procedures and/or local regulations.
- In the software and/or report, check for flags and their associated results to ensure the result validity corresponding test results (refer to the x800 Data Manager User Assistance for a 'List of flag codes').

Validation of results is performed automatically by the instrument software based on control results.

NOTE: The **cobas**^{*} 5800 system and the **cobas**^{*} 6800/8800 systems with software version 2.0 or higher will be delivered with the standard setting of running a set of controls (positive and negative) with every run, but can be configured to a less frequent scheduling up to every 72 hours based on laboratory procedures and/or local regulations. Please contact your Roche service engineer and/or Roche customer technical support for more information.

Interpretation of results on the cobas[®] 5800 system and cobas[®] 6800/8800 systems with software version 2.0 or higher

The results of the samples are shown in the "Results" app of the software.

For a valid control batch, check each individual sample for flags in the software and/or report. The result interpretation should be as follows:

- Samples associated with a valid control batch are shown as 'Valid' in the "Control result" column if all Control Target Results reported valid. Samples associated with a failed control batch are shown as 'Invalid' in the "Control result" column if Control Results are reported invalid.
- If the associated controls of a sample result are invalid, a specific flag will be added to the sample result as follows:
 - $\circ~$ Q05D: Result validation failure because of an invalid positive control.
 - $\circ~$ Q06D: Result validation failure because of an invalid negative control.
- The values in "Result" column and in the detail view for individual sample target result should be interpreted as shown in Table 15.

If one or more sample targets are marked with 'Invalid' the software shows a flag in the "Flag" column. More information on why the sample target(s) is reported invalid including flag information is shown in the detail view.

Invalid results for one or more target combinations are possible and are reported out specifically for each target. If any individual target result is invalid, the presence or absence of that individual target cannot be determined.

 Table 15 Example of cobas[®] Respiratory flex results display on cobas[®] 5800 system and cobas[®] 6800/8800 systems with software version 2.0 or higher

| Sample ID | Test | Control Result | Flags* | Status | Result | Creation date/time |
|-----------|-----------|-------------------|----------|----------|-----------------------------|---------------------|
| Sample_01 | RESP-FLEX | Valid | | Released | Negative (12) | 7/7/2021 8:27:39 AM |
| Sample_C1 | RESP-FLEX | Valid | P | Released | Invalid (12) | 7/7/2021 8:27:39 AM |
| Sample_B1 | RESP-FLEX | Valid | | Released | Positive (1), Negative (11) | 7/7/2021 8:27:39 AM |
| Sample_B2 | RESP-FLEX | Valid | | Released | Negative (12) | 7/7/2021 8:27:39 AM |
| Sample_D1 | RESP-FLEX | Valid | | Released | Positive (2), Negative (10) | 7/7/2021 8:27:39 AM |
| Sample_A6 | RESP-FLEX | Valid | | Released | Negative (12) | 7/7/2021 8:27:39 AM |
| Sample_A2 | RESP-FLEX | Invalid | | Released | Invalid (12) | 7/7/2021 8:27:39 AM |

*The result overview shows a flag symbol in case of invalid results. Detailed flag descriptions are available in the result details.

Quality control and validity of results on the cobas[®] 6800/8800 systems with software version 1.4

- One **cobas**^{*} Buffer Negative Control [(-) Ctrl] and one **cobas**^{*} Respiratory flex Positive Control [RESP-FLEX (+) C] are processed with each batch.
- In the software and/or report, check for flags and their associated results to ensure the batch validity.
- The batch is valid if no flags appear for any controls. If the batch is invalid, repeat testing of the entire batch.
- All flags are described in the **cobas**[°] 6800/8800 systems User Assistance.

Validation of results is performed automatically by the instrument software based on control results.

Interpretation of results on the cobas® 6800/8800 systems with software version 1.4

For a valid batch, check each individual sample for flags in the software and/or report. The result interpretation should be as follows:

- A valid batch may include both valid and invalid sample results.
- Invalid results for one or more target combinations are possible and are reported out specifically for each target. If any individual target result is invalid, the presence or absence of that individual target cannot be determined.
- Other initial valid target results can be interpreted as described in the table. Results and their corresponding interpretation are shown in Table 15.

Results display examples for **cobas**^{*} Respiratory flex are shown in Table 16.

Table 16 Example of cobas[®] Respiratory flex results display on cobas[®] 6800/8800 systems with software version 1.4

| Sample ID | Test name* | Positive | Negative | Invalid | Valid | Status | Creation date/time |
|-----------|------------|----------|----------|---------|-------|--------------|------------------------|
| Sample_01 | RESP-FLEX | 0 | 12 | 0 | NA | Released | 7/7/2021 8:27:39 AM |
| Sample_C1 | RESP-FLEX | 0 | 0 | 12 | NA | Not Released | 7/7/2021 8:27:39 AM |
| Sample_B1 | RESP-FLEX | 1 | 11 | 0 | NA | Released | 7/7/2021 8:27:39 AM |
| Sample_B2 | RESP-FLEX | 4 | 8 | 0 | NA | Released | 7/7/2021 8:27:39 AM |
| Sample_D1 | RESP-FLEX | 0 | 12 | 0 | NA | Released | 7/7/2021 8:27:39 AM |
| Sample_A6 | RESP-FLEX | 0 | 12 | 0 | NA | Released | 7/7/2021 8:27:39 AM |
| Sample_A2 | RESP-FLEX | 0 | 0 | 12 | NA | Released | 7/7/2021 8:27:39 AM |

* Test name might differ depending on the chosen ASAP for **cobas**^{*} Respiratory flex

Interpretation of results for cobas® 5800/6800/8800 systems

The result interpretation should be as follows:

- A valid batch may include both valid and invalid sample results.
- Invalid results for one or more target combinations are possible and are reported out specifically for each channel.
- Results of this test should only be interpreted in conjunction with information available from clinical evaluation of the patient and patient history.

Results display examples for **cobas**[°] Respiratory flex are shown in Table 15 and Table 16.

Results and their corresponding interpretation for detecting adenovirus (species B, C, and E), common human coronaviruses (229E, HKU1, NL63, OC43), human metapneumovirus, human rhinovirus/enterovirus, influenza A virus, influenza B virus, parainfluenza viruses 1, 2, 3, and 4, RSV, and SARS-CoV-2 are shown below (Table 17).

Table 17 Target results for individual target result interpretation

| Target result* | Interpretation | | | | |
|---|--|--|--|--|--|
| Negative | No target signal detected for the corresponding viral target and IC signal detected. | | | | |
| Positive Target signal detected for the corresponding viral target and IC signal may or may not be detected. | | | | | |

*Shown for each of the 12 viral targets (influenza A virus (FluA), influenza B virus (FluB), respiratory syncytial virus (RSV), SARS-CoV-2 (SCoV2), adenovirus (AdV), human metapneumovirus (MPV), human rhinovirus/enterovirus (EVRV), common human coronavirus (CoV) and parainfluenza viruses 1 (hPIV1), 2 (hPIV2), 3 (hPIV3), and 4 (hPIV4) individually.

If any individual target result is invalid, the presence or absence of that individual target cannot be determined. Other initial valid target results can be interpreted as described in Table 17.

Procedural limitations

- **cobas**[°] Respiratory flex has been evaluated only for use in combination with the **cobas**[°] Respiratory flex Control Kit, **cobas**[°] Buffer Negative Control Kit, **cobas**[°] **omni** MGP Reagent, **cobas**[°] **omni** Lysis Reagent, **cobas**[°] **omni** Specimen Diluent, and **cobas**[°] **omni** Wash Reagent for use on the **cobas**[°] 5800/6800/8800 systems.
- Patient management decisions should not be made solely on the **cobas**^{*} Respiratory flex test results, but rather with the consideration of clinical observations, patient history, recent exposures, epidemiological information and other diagnostic information.
- Reliable results depend on proper sample collection, storage and handling procedures. Individuals should not eat, drink, smoke, vape, or use snuff tobacco products 30 minutes prior to sample collection.
- FluMist[®] Quadrivalent, a live quadrivalent intranasal vaccine may result in positive results for influenza A and influenza B. Recent administration of FluMist[®] within 6 weeks prior to collection was not evaluated to assess the potential impact of interference with other targets on the clinical performance of the assay.
- This test is intended to be used with nasopharyngeal swab samples collected in a UTM-RT[®] or UVT or equivalent. Testing of other sample types with **cobas**^{*} Respiratory flex may result in inaccurate results.
- Detection of respiratory viruses may be affected by sample collection methods, patient factors (e.g. presence of symptoms), and/or stage of infection.
- As with any molecular test, mutations within the target regions of **cobas**^{*} Respiratory flex could affect primer and/or probe binding, resulting in failure to detect the presence of virus.
- False negative or invalid results may occur due to interference. The Internal Control is included in **cobas**^{*} Respiratory flex to help identify the specimens containing substances that may interfere with nucleic acid isolation and PCR amplification.
- The addition of AmpErase enzyme into the **cobas**^{*} Respiratory flex Master Mix reagent enables selective amplification of target RNA and DNA; however, good laboratory practices and careful adherence to the procedures specified in this Instructions For Use document are necessary to avoid contamination of reagents.

Non-clinical performance evaluation

Key performance characteristics

Analytical sensitivity (Limit of Detection)

The limit of detection (LoD) of **cobas**[°] Respiratory flex was determined by analysis of serial co-formulated dilutions for human common coronavirus, RSV, influenza A, influenza B, SARS-CoV-2, adenovirus, rhinovirus, human metapneumovirus and human parainfluenza viruses 1, 2, 3 & 4 diluted in negative simulated clinical matrix stabilized in UTM[™]. Panels of at least five concentration levels plus a blank were tested over three lots of **cobas**[°] Respiratory flex reagents, multiple runs, days, operators, and instruments. The results as well as the materials used are shown in Table 18.

| Target | Strain / Isolate | LoD by Hit Rate ≥ 95% | 95% LoD PROBIT | 95% Confidence Interval | Concentration Unit | |
|---------------------------|---|--------------------------|-------------------|----------------------------|-----------------------|--|
| Influenza A (H1N1) | Brisbane/02/2018 | 1.00E+02 | 8.39E+01 | 6.59E+01 - 1.19E+02 | cp/mL | |
| Influenza A (H3N2) | A/Darwin/6/2021 | 5.00E+01 | 5.36E+01 | 4.06E+01 - 8.09E+01 | cp/mL | |
| Influenza B (Victoria) | B/Austria/1359417/2021 | 2.50E+02 | 2.28E+02 | 1.82E+02 - 3.16E+02 | cp/mL | |
| Influenza B (Yamagata) | Phuket/3073/13 | 8.00E+02 | 6.84E+02 | 5.57E+02 - 9.12E+02 | cp/mL | |
| RSV A | Respiratory Syncytial Virus A2 | 4.00E+03 | 3.28E+03 | 2.60E+03 - 4.58E+03 | cp/mL | |
| SARS-CoV-2 | 1st WHO International Standard NIBSC code 20/146 | 8.00E+01 | 7.07E+01 | 5.45E+01 - 1.04E+02 | IU/mL | |
| Adenovirus B | Type 3 Isolate 1921/08 | 5.00E+02 | 5.00E+02 | 4.30E+02 - 6.21E+02 | cp/mL | |
| Adenovirus C | 1st WHO International Standard NIBSC code 16/324 | 1.20E+02 | 7.77E+01 | 5.92E+01 - 1.14E+02 | IU/mL | |
| human Metapneumovirus | | | 1.96E+03 | 1.61E+03 - 2.55E+03 | cp/mL | |
| Rhinovirus B | Rhinovirus B B42 Zeptometrix 0810286CF | | 9.07E+02 | 7.29E+02 - 1.21E+03 | cp/mL | |
| Coronavirus 229E | ronavirus 229E 229E Zeptometrix 0810229CF | | 3.64E+02 | 2.83E+02 - 5.23E+02 | cp/mL | |
| Coronavirus NL63 | NL63 Zeptometrix 0810228CF- CL | 1.80E+02 | 1.77E+02 | 1.34E+02 - 2.72E+02 | cp/mL | |
| Coronavirus OC43 | OC43 Zeptometrix 0810024CF | 1.60E+03 | 8.53E+02 | 6.50E+02 - 1.27E+03 | cp/mL | |
| Coronavirus HKU1 | aRNA | 2.40E+02 | 1.84E+02 | 1.44E+02 - 2.58E+02 | cp/mL | |
| human Parainfluenza 1 | Type 1 Zeptometrix 0810014CF-CL | 3.00E+03 | 2.11E+03 | 1.82E+03 - 2.61E+03 | cp/mL | |
| human Parainfluenza 2 | Type 2 Zeptometrix 0810015CF-CL | 7.00E+02 | 6.85E+02 | 5.13E+02 - 1.06E+03 | cp/mL | |
| human Parainfluenza 3 | Type 3, Zeptometrix 0810016CF-CL | 3.80E+03 | 2.56E+03 | 2.15E+03 - 3.26E+03 | cp/mL | |
| human Parainfluenza 4 | Type 4a Zeptometrix 0810060CF-CL | 4.80E+04 | 3.05E+04 | 2.49E+04 - 4.02E+04 | cp/mL | |

Table 18 Limit of Detection by hit rate \geq 95% and 95% Probit, including confidence intervals

Precision - within laboratory

Precision of **cobas**^{*} Respiratory flex was determined by analysis of panels consisting of different cell culture strains in negative simulated clinical matrix stabilized in UTM^{**}. Two dilution levels were tested in 216 replicates for each level across three lots of **cobas**^{*} Respiratory flex reagents using six instruments and five operators over twelve testing days. Each sample was carried through the entire **cobas**^{*} Respiratory flex procedure on fully automated **cobas**^{*} 5800/6800/8800 systems. Therefore, the precision reported here represents all aspects of the test procedure. The results are shown in Table 19 and Table 20. The results of this study revealed that **cobas**^{*} Respiratory flex for use on the **cobas**^{*} 5800/6800/8800 systems consistently detects the presence of all targets by achieving \geq 95% hit rates around LoD (~1x LoD) and \geq 99% hit rates above LoD (~3x LoD).

| Target | Level | Positive Results | Total Results | Positivity % | Two-sided 95% CI Lower Bound | Two-sided 95% CI Upper Bound |
|--------------------------|---------|---------------------|------------------|--------------|---------------------------------|---------------------------------|
| Influenza A (H3N2) | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Influenza A (H3N2) | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Influenza B (Victoria) | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Influenza B (Victoria) | ~1x LoD | 215 | 216 | 99.54 | 97.45 | 99.99 |
| RSV A | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| RSV A | ~1x LoD | 214 | 216 | 99.07 | 96.70 | 99.89 |
| SARS-CoV-2 | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| SARS-CoV-2 | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Adenovirus B | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Adenovirus B | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Metapneumovirus | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Metapneumovirus | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Rhinovirus B | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Rhinovirus B | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Coronavirus 229E | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| Coronavirus 229E | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 1 | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 1 | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 2 | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 2 | ~1x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 3 | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 3 | ~1x LoD | 215 | 216 | 99.54 | 97.45 | 99.99 |
| human Parainfluenza 4 | ~3x LoD | 216 | 216 | 100 | 98.31 | 100 |
| human Parainfluenza 4 | ~1x LoD | 214 | 216 | 99.07 | 96.70 | 99.89 |
| N/A | Blank | 0 | 216 | 0 | 0.00 | 3.36 |

Table 19 Precision – Summary of hit rates and confidence intervals

09964517001-02EN

| Target | Level | Hit rate | Mean Ct | to | ment- D- Iment | Lot-t | o-Lot | Day-t | o-Day | Run-t | o-Run | Withi | n Run | То | otal |
|---------------------------|---------|----------|------------|------|----------------------|-------|-------------|-------|-------------|-------|-------------|-------|-------------|------|-------------|
| | | | | SD | CV % | SD | CV % | SD | CV % | SD | CV % | SD | CV % | SD | CV % |
| Influenza A (H3N2) | ~3x LoD | 100.00% | 37.33 | 0.08 | 0.22 | 0.08 | 0.21 | 0.00 | 0.00 | 0.07 | 0.20 | 0.48 | 1.28 | 0.50 | 1.33 |
| Influenza A (H3N2) | ~1x LoD | 100.00% | 39.06 | 0.13 | 0.34 | 0.14 | 0.35 | 0.23 | 0.59 | 0.00 | 0.00 | 1.02 | 2.60 | 1.06 | 2.71 |
| Influenza B (Victoria) | ∼3x LoD | 100.00% | 34.61 | 0.04 | 0.11 | 0.09 | 0.26 | 0.00 | 0.00 | 0.00 | 0.00 | 0.22 | 0.64 | 0.24 | 0.69 |
| Influenza B (Victoria) | ~1x LoD | 99.54% | 35.34 | 0.04 | 0.12 | 0.08 | 0.23 | 0.00 | 0.00 | 0.00 | 0.00 | 0.24 | 0.69 | 0.26 | 0.73 |
| RSV A | ~3x LoD | 100.00% | 33.20 | 0.06 | 0.18 | 0.08 | 0.25 | 0.04 | 0.11 | 0.00 | 0.00 | 0.19 | 0.58 | 0.22 | 0.66 |
| RSV A | ∼1x LoD | 99.07% | 33.62 | 0.04 | 0.11 | 0.05 | 0.16 | 0.02 | 0.06 | 0.02 | 0.06 | 0.24 | 0.70 | 0.25 | 0.73 |
| SARS-CoV-2 | ~3x LoD | 100.00% | 35.62 | 0.03 | 0.09 | 0.00 | 0.00 | 0.03 | 0.09 | 0.00 | 0.00 | 0.32 | 0.89 | 0.32 | 0.90 |
| SARS-CoV-2 | ∼1x LoD | 100.00% | 36.48 | 0.00 | 0.00 | 0.00 | 0.00 | 0.03 | 0.09 | 0.00 | 0.00 | 0.41 | 1.13 | 0.42 | 1.14 |
| Adenovirus B | ~3x LoD | 100.00% | 30.50 | 0.18 | 0.58 | 0.00 | 0.00 | 0.06 | 0.19 | 0.00 | 0.00 | 0.69 | 2.28 | 0.72 | 2.36 |
| Adenovirus B | ∼1x LoD | 100.00% | 31.22 | 0.07 | 0.21 | 0.06 | 0.18 | 0.02 | 0.07 | 0.00 | 0.00 | 0.16 | 0.52 | 0.19 | 0.59 |
| human Metapneumovirus | ~3x LoD | 100.00% | 34.18 | 0.08 | 0.24 | 0.02 | 0.06 | 0.05 | 0.15 | 0.00 | 0.00 | 0.24 | 0.70 | 0.26 | 0.76 |
| human Metapneumovirus | ~1x LoD | 100.00% | 35.15 | 0.08 | 0.23 | 0.02 | 0.07 | 0.04 | 0.11 | 0.00 | 0.00 | 0.30 | 0.86 | 0.32 | 0.90 |
| Rhinovirus B | ~3x LoD | 100.00% | 33.68 | 0.08 | 0.24 | 0.25 | 0.73 | 0.02 | 0.07 | 0.00 | 0.00 | 0.27 | 0.79 | 0.37 | 1.10 |
| Rhinovirus B | ∼1x LoD | 100.00% | 34.74 | 0.03 | 0.10 | 0.20 | 0.56 | 0.07 | 0.19 | 0.00 | 0.00 | 0.30 | 0.87 | 0.37 | 1.06 |
| Coronavirus 229E | ∼3x LoD | 100.00% | 33.11 | 0.12 | 0.36 | 0.05 | 0.15 | 0.00 | 0.00 | 0.00 | 0.00 | 0.45 | 1.36 | 0.47 | 1.41 |
| Coronavirus 229E | ∼1x LoD | 100.00% | 33.63 | 0.08 | 0.23 | 0.03 | 0.08 | 0.00 | 0.00 | 0.03 | 0.09 | 0.32 | 0.95 | 0.33 | 0.98 |
| human Parainfluenza 1 | ~3x LoD | 100.00% | 33.62 | 0.08 | 0.23 | 0.00 | 0.00 | 0.08 | 0.24 | 0.02 | 0.05 | 0.22 | 0.66 | 0.25 | 0.74 |
| human Parainfluenza 1 | ∼1x LoD | 100.00% | 34.46 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.00 | 0.34 | 0.99 | 0.34 | 0.99 |
| human Parainfluenza 2 | ~3x LoD | 100.00% | 34.83 | 0.14 | 0.41 | 0.07 | 0.21 | 0.10 | 0.28 | 0.05 | 0.13 | 0.59 | 1.70 | 0.62 | 1.79 |
| human Parainfluenza 2 | ~1x LoD | 100.00% | 36.45 | 0.11 | 0.30 | 0.06 | 0.17 | 0.15 | 0.41 | 0.00 | 0.00 | 0.80 | 2.21 | 0.83 | 2.27 |
| human Parainfluenza 3 | ~3x LoD | 100.00% | 34.82 | 0.06 | 0.17 | 0.04 | 0.12 | 0.04 | 0.11 | 0.00 | 0.00 | 0.21 | 0.59 | 0.22 | 0.64 |
| human Parainfluenza 3 | ~1x LoD | 99.54% | 35.72 | 0.09 | 0.25 | 0.02 | 0.06 | 0.04 | 0.11 | 0.00 | 0.00 | 0.26 | 0.72 | 0.27 | 0.77 |
| human Parainfluenza 4 | ~3x LoD | 100.00% | 35.00 | 0.09 | 0.26 | 0.00 | 0.00 | 0.01 | 0.02 | 0.04 | 0.12 | 0.26 | 0.75 | 0.28 | 0.80 |
| human Parainfluenza 4 | ~1x LoD | 99.07% | 35.65 | 0.07 | 0.20 | 0.02 | 0.05 | 0.04 | 0.12 | 0.00 | 0.00 | 0.31 | 0.88 | 0.33 | 0.91 |

Table 20 Precision - standard deviations and coefficients of variation of Ct values

Inclusivity

The inclusivity for the detection of different strains of influenza A, influenza B, RSV, SARS-CoV-2, adenovirus, human metapneumovirus, enterovirus, rhinovirus, human common coronavirus and human parainfluenza viruses 1, 2, 3 & 4 was assessed by testing relevant strains of each viral target. Each strain was tested with 3 replicates near LoD starting at ~3x LoD. The concentration which showed a 100% hit rate is shown in Table 21 through Table 30.

| Virus type | Strain | Vendor ID | 100% hit rate at |
|------------------|--|----------------------------|------------------|
| Influenza A H1N1 | New Caledonia/20/99 | 0810036CF | ~3x LoD |
| Influenza A H1N1 | Brisbane/59/07 | 0810244CF | ~3x LoD |
| Influenza A H1N1 | California/07/09 | 0810165CF | ~3x LoD |
| Influenza A H1N1 | NY/03/09 | 0810249CF | ~3x LoD |
| Influenza A H1N1 | A/Victoria/2570/2019 | SD-VIC219A-7 | ~3x LoD |
| Influenza A H1N1 | A/Wisconsin/588/2019 | SD-WA519A-8 | ~3x LoD |
| Influenza A H1N1 | A/Victoria/4897/2022 | SD-VIC9722B | ~3x LoD |
| Influenza A H1N1 | A/Wisconsin/67/2022 | SD-WI6722MS1B | ~6x LoD |
| Influenza A H1N1 | England/73/22 | GISAID ID EPI_ISL_15803829 | ~3x LoD |
| Influenza A H1N1 | England/55/22 | GISAID ID EPI_ISL_14387941 | ~3x LoD |
| Influenza A H3N2 | A/Port Chalmers/1/73 | VR-810 | ~3x LoD |
| Influenza A H3N2 | Texas/50/12 | 0810238CF | ~3x LoD |
| Influenza A H3N2 | A/Victoria/3/75 | VR-822 | ~3x LoD |
| Influenza A H3N2 | Wisconsin/67/05 | 0810252CF | ~3x LoD |
| Influenza A H3N2 | A/Darwin/9/2021 | SD-DRW921-6 | ~3x LoD |
| Influenza A H3N2 | Hong Kong/4801/14 | 0810526CF | ~3x LoD |
| Influenza A H3N2 | Hong Kong/8/68 | 0810250CF | ~3x LoD |
| Influenza A H3N2 | A/Perth/16/09 | 0810251CF | ~3x LoD |
| Influenza A H3N2 | Kansas/14/17 | 0810586CF | ~3x LoD |
| Influenza A H3N2 | Switzerland/9715293/13 | 0810511CF | ~3x LoD |
| Influenza A H5N1 | A/mallard/Wisconsin/2576/2009 | NR-31131 | ~3x LoD |
| Influenza A H5N2 | A/ruddy turnstone/New Jersey/828212/2001 | NR-44298 | ~3x LoD |
| Influenza A H5N3 | A/duck/Singapore/645/1997 | NR-3558 | ~3x LoD |
| Influenza A H7N2 | A/northern pintail/Illinois/10OS3959/2010 | NR-35979 | ~3x LoD |
| Influenza A H7N8 | A/mallard/Ohio/11OS2033/2011 | NR-36008 | ~3x LoD |
| Influenza A H7N9 | A/northern shoveler/Mississippi/110S145/2011 | NR-36001 | ~3x LoD |
| Influenza A H9N7 | A/shorebird/Delaware Bay/31/1996 | NR-45171 | ~3x LoD |

 Table 21
 Influenza A Inclusivity strains

 Table 22
 Influenza B Inclusivity strains

| Virus type | Strain | Vendor ID | 100% hit rate at |
|------------------------|------------------------|-----------|------------------|
| Influenza B – Victoria | Colorado/6/17 | 0810573CF | ~3x LoD |
| Influenza B – Victoria | B/Hong Kong/5/72 | VR-823 | ~3x LoD |
| Influenza B - Victoria | Brisbane/60/08 | 0810254CF | ~3x LoD |
| Influenza B - Victoria | Florida/02/06 | 0810037CF | ~3x LoD |
| Influenza B – Yamagata | B/Massachusetts/2/2012 | VR-1813 | ~3x LoD |
| Influenza B – Yamagata | B/Wisconsin/1/2010 | VR-1883 | ~3x LoD |
| Influenza B – Yamagata | B/Florida/4/2006 | VR-1804 | ~3x LoD |
| Influenza B – Yamagata | Texas/6/11 | 0810242CF | ~3x LoD |
| Influenza B – Yamagata | Florida/07/04 | 0810256CF | ~3x LoD |
| Influenza B – Unknown | B/Taiwan/2/62 | VR-295 | ~3x LoD |
| Influenza B – Unknown | B/Allen/45 | VR-102 | ~3x LoD |
| Influenza B – Unknown | B/Lee/40 | VR-101 | ~3x LoD |

Table 23 Respiratory Syncytial Virus Inclusivity strains

| Virus type | Strain | Vendor ID | 100% hit rate at |
|-------------|---------------|---------------|------------------|
| RSV Type A | 2006 Isolate | 0810040ACF-CL | ~3x LoD |
| RSV Type A | 02/2015 | 0810475CF | ~3x LoD |
| RSV Type A2 | A2 | VR-1540 | ~3x LoD |
| RSV Type B | CH93(18)-18 | 0810040CF-CL | ~3x LoD |
| RSV Type B | 9320 | VPL-030 | ~3x LoD |
| RSV Type B | B WV/14617/85 | VR-1400 | ~3x LoD |
| RSV Type B | 18537 | VR-1580 | ~3x LoD |

Table 24 SARS-CoV-2 Inclusivity strains

| Virus type | Strain | Vendor ID | 100% hit rate at |
|------------------------------|---------------------------------|----------------|------------------|
| SARS-CoV-2 Lineage B.1.1.7 | England/204820464/2020 | 0810614CFHI-CL | ~3x LoD |
| SARS-CoV-2 Lineage B.1.351 | South Africa/KRISP-K005325/2020 | 0810613CFHI-CL | ~3x LoD |
| SARS-CoV-2 Lineage P.1 | Japan/TY7-503/2021 | 0810616CFHI-CL | ~3x LoD |
| SARS-CoV-2 B.1.617.2 | USA/PHC658/2021 | 0810624CFHI-CL | ~3x LoD |
| SARS-CoV-2 Lineage B.1.1.529 | USA/MD-HP20874/2021 | 0810642CFHI-CL | ~3x LoD |
| SARS-CoV-2 | USA-WA1/2020 | 0810587CFHI | ~3x LoD |

 Table 25
 Adenovirus Inclusivity strains

| Virus type | Subtype | Vendor ID | 100% hit rate at |
|------------------------|---------|-----------|------------------|
| Human Mastadenovirus B | Туре 03 | 0810062CF | ~3x LoD |
| Human Mastadenovirus B | Туре 7А | 0810021CF | ~3x LoD |
| Human Mastadenovirus B | Type 11 | 0810112CF | ~3x LoD |
| Human Mastadenovirus B | Type 14 | 0810108CF | ~3x LoD |
| Human Mastadenovirus B | Type 16 | VR-17 | ~12x LoD |
| Human Mastadenovirus B | Type 21 | 0810116CF | ~6x LoD |
| Human Mastadenovirus B | Туре 34 | VR-716 | ~3x LoD |
| Human Mastadenovirus B | Туре 35 | VR-718 | ~3x LoD |
| Human Mastadenovirus C | Туре 1 | VR-1 | ~3x LoD |
| Human Mastadenovirus C | Туре 2 | VR-846 | ~3x LoD |
| Human Mastadenovirus C | Туре 5 | 0810020CF | ~3x LoD |
| Human Mastadenovirus C | Туре 6 | VR-6 | ~3x LoD |
| Human Mastadenovirus E | Туре 4 | 0810070CF | ~3x LoD |
| Human Mastadenovirus E | Type 4 | 0810326CF | ~3x LoD |

 Table 26
 Human Metapneumovirus Inclusivity strains

| Virus type | Type/Strain | Vendor ID | 100% hit rate at |
|--------------------------|-----------------------------|--------------|------------------|
| Human Metapneumovirus A1 | Type 9 – Strain: IA3-2002 | 0810160CF | ~3x LoD |
| Human Metapneumovirus A1 | Type 16 – Strain:IA10-2003 | 0810161CF-CL | ~3x LoD |
| Human Metapneumovirus A2 | Type 27 – Strain: IA27-2004 | 0810164CF | ~3x LoD |
| Human Metapneumovirus B1 | Type 5 – Strain: Peru3-2003 | 0810158CF-CL | ~6x LoD |
| Human Metapneumovirus B2 | Type 8 – Strain: Peru6-2003 | 0810159CF | ~3x LoD |
| Human Metapneumovirus B2 | Type 18 – Strain: IA18-2003 | 0810162CF | ~3x LoD |

Table 27 Enterovirus Inclusivity strains

| Virus type | Subtype | Vendor ID | 100% hit rate at |
|---------------|----------|-----------|------------------|
| Enterovirus A | Type A10 | VR-168 | ~3x LoD |
| Enterovirus A | Type 71 | VR-1775 | ~3x LoD |
| Enterovirus B | Type A9 | 0810017CF | ~3x LoD |
| Enterovirus B | Type B3 | 0810074CF | ~3x LoD |
| Enterovirus B | Type B4 | 0810075CF | ~3x LoD |
| Enterovirus B | Type 6 | 0810076CF | ~3x LoD |
| Enterovirus B | Type 9 | 0810077CF | ~3x LoD |
| Enterovirus B | Type 11 | 0810023CF | ~3x LoD |
| Enterovirus C | Type A21 | VR-850 | ~3x LoD |
| Enterovirus C | Type A24 | VR-1662 | ~3x LoD |
| Enterovirus D | Type 68 | VR-1823 | ~3x LoD |

 Table 28
 Rhinovirus Inclusivity strains

| Virus type | Subtype | Vendor ID | 100% hit rate at |
|--------------------|----------|------------|------------------|
| Human Rhinovirus A | Type 1A | 0810012CFN | ~3x LoD |
| Human Rhinovirus A | Type 2 | VR-482 | ~3x LoD |
| Human Rhinovirus A | Type 7 | VR-1601 | ~35x LoD* |
| Human Rhinovirus A | Type 16 | VR-283 | ~3x LoD |
| Human Rhinovirus A | Type 34 | VR-1365 | ~3x LoD |
| Human Rhinovirus A | Type 57 | VR-1600 | ~3x LoD |
| Human Rhinovirus A | Type 77 | VR-1187 | ~3x LoD |
| Human Rhinovirus A | Type 85 | VR-1195 | ~3x LoD |
| Human Rhinovirus B | Type 3 | VR-483 | ~3x LoD |
| Human Rhinovirus B | Type 14 | VR-284 | ~3x LoD |
| Human Rhinovirus B | Type 17 | VR-1663 | ~3x LoD |
| Human Rhinovirus B | Type: 27 | VR-502 | ~3x LoD |
| Human Rhinovirus B | Type 83 | VR-1193 | ~3x LoD |

*Human Rhinovirus Type 7 (ATCC VR-1601) is a strain that was in vitro derived from NIAID reagent V-127-001-021 (VR-117) by passage at ATCC and is not a clinical isolate with clinical significance. Based on in silico analysis that is representing a broader genetic variability of this subtype, type 7 strains of rhinovirus should be detected by **cobas**^{*} Respiratory flex.

 Table 29
 Common Coronavirus Inclusivity strains

| Virus type | Strain | Vendor ID | 100% hit rate at |
|-------------|--------|-----------|------------------|
| Coronavirus | 229E | 0810229CF | ~3x LoD |
| Coronavirus | 229E | VR-740 | ~3x LoD |
| Coronavirus | NL63 | NR-470 | ~3x LoD |
| Coronavirus | OC43 | VR-1558 | ~3x LoD |

Table 30 Human Parainfluenzavirus Inclusivity strains

| Virus type | Strain | Vendor ID | 100% hit rate at |
|-----------------------------|----------|------------|------------------|
| Human Parainfluenzavirus 1 | N/A | 0810014CF | ~3x LoD |
| Human Parainfluenzavirus 1 | C35 | VR-94 | ~3x LoD |
| Human Parainfluenzavirus 2 | N/A | 0810015CF | ~3x LoD |
| Human Parainfluenzavirus 2 | Greer | VR-92 | ~3x LoD |
| Human Parainfluenzavirus 3 | N/A | 0810016CF | ~3x LoD |
| Human Parainfluenzavirus 4A | N/A | 0810060CF | ~3x LoD |
| Human Parainfluenzavirus 4B | CH 19503 | VR-1377 | ~3x LoD |
| Human Parainfluenzavirus 4B | N/A | 0810060BCF | ~3x LoD |

Matrix equivalency

Equivalency between nasopharyngeal swabs and simulated clinical matrix stabilized in UTM-RT^{*} was evaluated. Pooled negative individual clinical specimens (nasopharyngeal) and simulated clinical matrix stabilized in UTM^{**} were spiked with three co-formulated panels containing human common coronavirus, RSV, influenza A & SARS-CoV-2 (panel 1), influenza B, adenovirus, rhinovirus & human parainfluenza virus 3 (panel 2) and human metapneumovirus, human parainfluenza viruses 1, 2 & 4 (panel 3) at a concentration level of ~2x LoD. Forty-two replicates per concentration were tested for each sample type. All replicates tested with the 2x LoD panel were positive for the respective viral target for both matrices with 100% hit rate.

Analytical specificity (cross-reactivity and microbial interference)

The analytical specificity of **cobas**[°] Respiratory flex was evaluated by testing a panel of microorganisms including those commonly found in the respiratory tract plus pooled human nasal wash.

The organisms listed in Table 31 were spiked at 1.00E+06 units/mL for bacteria and fungi and at 1.00E+05 units/mL for viruses unless otherwise noted. Testing was performed with each potential interfering organism in the absence and the presence of human common coronavirus, RSV, influenza A, influenza B, SARS-CoV-2, adenovirus, rhinovirus, human metapneumovirus and human parainfluenza viruses 1, 2, 3 & 4 target spiked at ~3x LoD.

Negative results were obtained with **cobas**^{\circ} Respiratory flex for all microorganism samples without viral target and positive results were obtained for all microorganism samples with viral target spiked at \sim 3x LoD.

 Table 31
 Microorganisms tested for analytical specificity/cross reactivity

| Microorganism | Concentration | | |
|--|-----------------------|--|--|
| Aspergillus flavus | 1.00E+06 CFU/mL | | |
| Bordetella parapertussis | 1.00E+06 CFU/mL | | |
| Bordetella pertussis | 1.00E+06 CFU/mL | | |
| Candida albicans | 1.00E+06 CFU/mL | | |
| Chlamydia pneumoniae | 1.00E+06 IFU/mL | | |
| Corynebacterium diphtheriae | 1.00E+06 CFU/mL | | |
| Cytomegalovirus | 1.00E+05 TCID50/mL | | |
| Epstein Barr virus | 1.00E+05 cp/mL | | |
| Escherichia coli | 1.00E+06 CFU/vial | | |
| Fusobacterium necrophorum | 1.00E+06 CFU/mL | | |
| Haemophilus influenzae | 1.00E+06 CFU/mL | | |
| Lactobacillus acidophilus | 1.00E+06 CFU/vial | | |
| Legionella pneumophila | 1.00E+06 CFU/mL | | |
| Measles virus | 1.00E+05 TCID50/mL | | |
| MERS-coronavirus | 1.00E+05 cp/mL | | |
| Moracella catarrhalis | 1.00E+06 CFU/mL | | |
| Mumps virus 1.00E+05 TCID50/mL | | | |
| Mycobacterium bovis | 1.00E+06 CFU/mL | | |
| Mycoplasma genitalium | 1.00E+06 CFU/vial | | |
| Mycoplasma pneumoniae | 1.00E+06 CCU/mL | | |
| Neisseria elongata | 1.00E+06 CFU/mL | | |
| Neisseria meningitidis | 1.00E+06 CFU/mL | | |
| Pneumocystis jirovecii | 5.00E+03 organisms/mL | | |
| Pseudomonas aeruginosa | 1.00E+06 CFU/mL | | |
| SARS-coronavirus (SARS-CoV-1) | 1.00E+05 cp/mL | | |
| Staphylococcus aureus 1.00E+06 CFU/mL | | | |
| Staphylococcus epidermidis 1.00E+06 CFU/mL | | | |
| Streptococcus pneumoniae 1.00E+06 CFU/mL | | | |
| | | | |
| Streptococcus pyogenes | 1.00E+06 CFU/mL | | |

Analytical specificity - interfering substances

Elevated levels of mucin (0.3 - 0.5% w/v) and whole blood (1.5 - 3.0% v/v) in simulated clinical matrix stabilized in UTM-RT^{*} were tested in the absence and in the presence of human common coronavirus, RSV, influenza A, influenza B, SARS-CoV-2, adenovirus, rhinovirus, human metapneumovirus and human parainfluenza viruses 1, 2, 3 & 4 target spiked at ~3x LoD. The tested endogenous interferences were shown not to interfere with the test performance of **cobas**^{*} Respiratory flex.

Additionally, negative clinical nasopharyngeal swab specimens collected in Remel media (M4RT, M5 and M6) as well as Greiner tubes (VACUETTE^{*} 3 mL Virus Stabilization Tube) were tested as equivalent collection media. The alternative collection media were tested unspiked and spiked at ~3x LoD. None of the alternative collection media showed interference with the test performance of **cobas**^{*} Respiratory flex.

In addition, drug compounds listed in Table 32 were tested in the presence and absence of all viral targets.

All potentially interfering substances, with the exception of FluMist[®] and Snuff Tobacco, have been shown to not interfere with the test performance. Negative results were obtained with **cobas**^{*} Respiratory flex for all samples without viral target and positive results were obtained for all samples with viral target.

As expected, FluMist[®] Quadrivalent, a live quadrivalent vaccine for administration by intranasal spray, consisting of two influenza A and two influenza B vaccine virus strains generated positive results for influenza A and influenza B and negative results for all other targets when solely testing FluMist[®].

Furthermore, Snuff Tobacco was identified as a potential interferent of **cobas**^{*} Respiratory flex as invalid results were generated when testing Snuff Tobacco at 0.1% (w/v) without viral target and negative/invalid results were observed when testing samples with viral targets.

| Generic drug name | Active Ingredient | Concentration | |
|-------------------------------------|---|--|--|
| AXOTIDE Diskus Multidose 250 mcg | Fluticasone propionate | 0.167 mg/mL | |
| BACTROBAN Nasal Ointment | Mupirocin | 0.20 mg/mL | |
| BUDESONID Sandoz Nasal Spray 64 mcg | Budesonide | 0.039 mg/mL | |
| CEPACOL Extra Strength Sore Throat | Benzocaine | 5 mg/mL | |
| Chloraseptic max | Phenol | 0.47 mg/mL | |
| FLUMIST [®] Quadrivalent | live attenuated influenza A and B viruses | 50000000 FFU/mL | |
| Heel Lufteel Nasal Spray | Luffa operculata Thryallis glauca Histaminum Sulphur | 2.99 mg/mL 2.99 mg/mL 1.5 mg/mL 1.5 mg/mL | |
| NASIVIN Pur Spray 0.05% | Oxymetazoline | 0.011 mg/mL | |
| OBRACIN Inj Solution 40 mg/mL | Tobramycin 0.018 mg/mL | | |
| RELENZA Disk 5 mg | Zanamivir | 0.0015 mg/mL | |
| TAMIFLU Kaps 75 mg | MIFLU Kaps 75 mg Oseltamivir | | |
| Snuff Tobacco | Nicotine | 0.1% w/v | |
| Vaseline | Petroleum Jelly 1% w/v | | |
| VICKS VapoRub | Eucalyptus Oil and Menthol 1% w/v | | |
| XYLOCAIN Spray 10% | Lidocain 2.68 mg/mL | | |

Table 32 Drug compounds tested for interference with cobas[®] Respiratory flex

Co-infection (competitive interference)

To assess potential competitive interference between the viral targets, a total of 30 panels composed of various combinations of the **cobas**^{*} Respiratory flex targets were tested. This includes combinations of all medically relevant respiratory tract co-infections as listed in Table 33. Twelve replicates were tested with one or two viral targets at ~3x LoD which were mixed with a target at high concentration (1.0E+06 units/mL). None of the targets present at very high concentration interfered with the detection of other viral targets at low concentration levels.

| Combination Target 1 (high) ≥ 1.00E+06 unit/mL | | Target 2 (low) ~3x LoD | Target 3 (low) ~3x LoD | |
|---|--------------------------|---------------------------|---------------------------|--|
| 1 | Influenza A | Adenovirus | SARS-CoV-2 | |
| 2 | Influenza B | Adenovirus | SARS-CoV-2 | |
| 3 | RSV | Adenovirus | SARS-CoV-2 | |
| 4 | Common human coronavirus | Influenza A | SARS-CoV-2 | |
| 5 | Adenovirus | Influenza A | SARS-CoV-2 | |
| 6 | EV/RV | RSV | SARS-CoV-2 | |
| 7 | hMPV | RSV | SARS-CoV-2 | |
| 8 | SARS-CoV-2 | EV/RV | Flu A | |
| 9 | Influenza B | EV/RV | Flu A | |
| 10 | RSV | EV/RV | Flu A | |
| 11 | hPIV-1 | Influenza B | Flu A | |
| 12 | hPIV-2 | Influenza B | Flu A | |
| 13 | hPIV-3 | SARS-CoV-2 | Flu A | |
| 14 | hPIV-4 | SARS-CoV-2 | Flu A | |
| 15 | Influenza A | Common human coronavirus | Flu B | |
| 16 | SARS-CoV-2 | Common human coronavirus | Flu B | |
| 17 | RSV | Common human coronavirus | Flu B | |
| 18 | CoV | RSV | Flu B | |
| 19 | Adenovirus | RSV | Flu B | |
| 20 | EV/RV | Influenza A Flu B | | |
| 21 | hMPV | Influenza A | Flu B | |
| 22 | Influenza A | EV/RV | RSV | |
| 23 | Influenza B | CoV | RSV | |
| 24 | SARS-CoV-2 | Adenovirus | RSV | |
| 25 | hPIV-1 | hPIV-1 SARS-CoV-2 | | |
| 26 | hPIV-2 | SARS-CoV-2 | RSV | |
| 27 | hPIV-3 | Influenza B RSV | | |
| 28 | hPIV-4 | Influenza B RSV | | |
| 29 | Adenovirus | EV/RV | - | |
| 30 | EV/RV | Adenovirus | - | |

Table 33 Combinations tested for potential competitive inhibition

Whole system failure

The whole system failure rate for **cobas**^{*} Respiratory flex was determined by testing 100 replicates of negative simulated clinical matrix spiked with viral target. These samples were tested at a concentration of ~3x LoD. The results of this study determined that all replicates were valid and positive for the corresponding viral targets, resulting in a whole system failure rate of 0% (upper one-sided 95% confidence interval 2.95%).

Cross contamination

The cross-contamination rate for **cobas**[°] Respiratory flex was determined by testing 480 replicates of negative simulated clinical matrix and 430 replicates of a high titer SARS-CoV-2 panel at approximately 6.50E+08 particles/mL. In total, five runs were performed on **cobas**[°] 6800/8800 systems and 25 runs were performed on **cobas**[°] 5800 system with positive and negative samples in a checkerboard configuration. All 480 replicates of the negative sample were negative, resulting in a cross-contamination rate of 0% (upper one-sided 95% confidence interval 0.62%).

Clinical performance evaluation

The clinical performance of **cobas**^{*} Respiratory flex on the **cobas**^{*} 5800/6800/8800 systems was evaluated versus FDA 510(k) cleared and CE-marked comparators in nasopharyngeal swab (NPS) specimens from symptomatic patients. The sample set consisted of a combination of prospective specimens that were frozen prior to testing on **cobas**^{*} Respiratory flex (prospective samples) and retrospective archived clinical specimens that were collected in UTM-RT^{*} or UVT.

A total of 1439 NPS specimens were included in the study (884 prospective and 555 archived) of which 1360 could be tested (824 prospective and 536 archived), and eventually 1306 (792 prospective and 514 archived) were evaluable. **cobas**^{*} Respiratory flex demonstrated good clinical performance, the respective overall Positive Percent Agreement (PPA) and Negative Percent Agreement (NPA) point estimates between **cobas**^{*} Respiratory flex and the respective comparators for the different target pathogens are summarized in Table 34.

| Target Virus | Sample Category | PPA (a/a+b) | PPA 95% CI | NPA (c/c+d) | NPA 95% CI | OPA (a + d/N) | OPA 95% CI |
|--------------------------|--------------------|--------------------|--------------------|----------------------|--------------------|----------------------|--------------------|
| Influenza A | Prospective | 100.0% (8/8) | (67.6%, 100.0%) | 99.5% (779/783) | (98.7%, 99.8%) | 99.5% (787/791) | (98.7%, 99.8%) |
| Influenza A | Archived | 100.0% (44/44) | (92.0%, 100.0%) | 98.2% (331/337) | (96.2%, 99.2%) | 98.4% (375/381) | (96.6%, 99.3%) |
| Influenza A | Overall | 100.0% (52/52) | (93.1%, 100.0%) | 99.1% (1110/1120) | (98.4%, 99.5%) | 99.1% (1162/1172) | (98.4%, 99.5%) |
| Influenza B | Prospective | 100.0% (1/1) | (20.7%, 100.0%) | 100.0% (791/791) | (99.5%, 100.0%) | 100.0% (792/792) | (99.5%, 100.0% |
| Influenza B | Archived | 100.0% (8/8) | (67.6%, 100.0%) | 99.4% (361/363) | (98.0%, 99.8%) | 99.5% (369/371) | (98.1%, 99.9%) |
| Influenza B | Overall | 100.0% (9/9) | (70.1%, 100.0%) | 99.8% (1152/1154) | (99.4%, 100.0%) | 99.8% (1161/1163) | (99.4%, 100.0%) |
| RSV | Prospective | 33.3% (1/3) | (6.1%, 79.2%) | 100.0% (789/789) | (99.5%, 100.0%) | 99.7% (790/792) | (99.1%, 99.9%) |
| RSV | Archived | 100.0% (47/47) | (92.4%, 100.0%) | 99.4% (333/335) | (97.8%, 99.8%) | 99.5% (380/382) | (98.1%, 99.9%) |
| RSV | Overall | 96.0% (48/50) | (86.5%, 98.9%) | 99.8% (1122/1124) | (99.4%, 100.0%) | 99.7% (1170/1174) | (99.1%, 99.9%) |
| SARS-CoV-2 | Prospective | 97.4% (76/78) | (91.1%, 99.3%) | 98.2% (701/714) | (96.9%, 98.9%) | 98.1% (777/792) | (96.9%, 98.8%) |
| SARS-CoV-2 | Archived | 100.0% (47/47) | (92.4%, 100.0%) | 0/0 | Not Calculable | 100.0% (47/47) | (92.4%, 100.0% |
| SARS-CoV-2 | Overall | 98.4% (123/125) | (94.4%, 99.6%) | 98.2% (701/714) | (96.9%, 98.9%) | 98.2% (824/839) | (97.1%, 98.9%) |
| Adenovirus | Prospective | 100.0% (2/2) | (34.2%, 100.0%) | 99.6% (785/788) | (98.9%, 99.9%) | 99.6% (787/790) | (98.9%, 99.9%) |
| Adenovirus | Archived | 100.0% (37/37) | (90.6%, 100.0%) | 95.6% (328/343) | (92.9%, 97.3%) | 96.1% (365/380) | (93.6%, 97.6%) |
| Adenovirus | Overall | 100.0% (39/39) | (91.0%, 100.0%) | 98.4% (1113/1131) | (97.5%, 99.0%) | 98.5% (1152/1170) | (97.6%, 99.0%) |
| Human Metapneumovirus | Prospective | 90.9% (10/11) | (62.3%, 98.4%) | 99.9% (780/781) | (99.3%, 100.0%) | 99.7% (790/792) | (99.1%, 99.9%) |
| Human Metapneumovirus | Archived | 97.7% (42/43) | (87.9%, 99.6%) | 99.7% (334/335) | (98.3%, 99.9%) | 99.5% (376/378) | (98.1%, 99.9%) |

Table 34 Summary of agreement analysis between cobas® Respiratory flex and comparators

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cobas[®] Respiratory flex

| Target Virus | Sample Category | PPA (a/a+b) | PPA 95% CI | NPA (c/c+d) | NPA 95% CI | OPA (a + d/N) | OPA 95% CI |
|---|--------------------|-------------------|--------------------|----------------------|--------------------|----------------------|-------------------|
| Human Metapneumovirus | Overall | 96.3% (52/54) | (87.5%, 99.0%) | 99.8% (1114/1116) | (99.3%, 100.0%) | 99.7% (1166/1170) | (99.1%, 99.9%) |
| Enterovirus and Rhinovirus | Prospective | 77.0% (47/61) | (65.1%, 85.8%) | 99.2% (725/731) | (98.2%, 99.6%) | 97.5% (772/792) | (96.1%, 98.4%) |
| Enterovirus and Rhinovirus | Archived | 96.9% (31/32) | (84.3%, 99.4%) | 96.8% (332/343) | (94.3%, 98.2%) | 96.8% (363/375) | (94.5%, 98.2%) |
| Enterovirus and Rhinovirus | Overall | 83.9% (78/93) | (75.1%, 90.0%) | 98.4% (1057/1074) | (97.5%, 99.0%) | 97.3% (1135/1167) | (96.2%, 98.1%) |
| Common Human Coronaviruses (229E, HKU1, NL63, OC43) | Prospective | 90.0% (18/20) | (69.9%, 97.2%) | 99.9% (771/772) | (99.3%, 100.0%) | 99.6% (789/792) | (98.9%, 99.9%) |
| Common Human Coronaviruses (229E, HKU1, NL63, OC43) | Archived | 98.4% (63/64) | (91.7%, 99.7%) | 91.0% (283/311) | (87.3%, 93.7%) | 92.3% (346/375) | (89.1%, 94.6%) |
| Common Human Coronaviruses (229E, HKU1, NL63, OC43) | Overall | 96.4% (81/84) | (90.0%, 98.8%) | 97.3% (1054/1083) | (96.2%, 98.1%) | 97.3% (1135/1167) | (96.2%, 98.1%) |
| Parainfluenza virus 1 | Prospective | 0/0 | Not Calculable | 100.0% (792/792) | (99.5%, 100.0%) | 100.0% (792/792) | (99.5%, 100.0%) |
| Parainfluenza virus 1 | Archived | 100.0% (40/40) | (91.2%, 100.0%) | 97.6% (327/335) | (95.4%, 98.8%) | 97.9% (367/375) | (95.8%, 98.9%) |
| Parainfluenza virus 1 | Overall | 100.0% (40/40) | (91.2%, 100.0%) | 99.3% (1119/1127) | (98.6%, 99.6%) | 99.3% (1159/1167) | (98.7%, 99.7%) |
| Parainfluenza virus 2 | Prospective | 100.0% (2/2) | (34.2%, 100.0%) | 100.0% (790/790) | (99.5%, 100.0%) | 100.0% (792/792) | (99.5%, 100.0%) |
| Parainfluenza virus 2 | Archived | 100.0% (44/44) | (92.0%, 100.0%) | 98.5% (330/335) | (96.6%, 99.4%) | 98.7% (374/379) | (96.9%, 99.4%) |
| Parainfluenza virus 2 | Overall | 100.0% (46/46) | (92.3%, 100.0%) | 99.6% (1120/1125) | (99.0%, 99.8%) | 99.6% (1166/1171) | (99.0%, 99.8%) |
| Parainfluenza virus 3 | Prospective | 100.0% (5/5) | (56.6%, 100.0%) | 100.0% (787/787) | (99.5%, 100.0%) | 100.0% (792/792) | (99.5%, 100.0%) |
| Parainfluenza virus 3 | Archived | 95.3% (41/43) | (84.5%, 98.7%) | 99.7% (336/337) | (98.3%, 99.9%) | 99.2% (377/380) | (97.7%, 99.7%) |
| Parainfluenza virus 3 | Overall | 95.8% (46/48) | (86.0%, 98.8%) | 99.9% (1123/1124) | (99.5%, 100.0%) | 99.7% (1169/1172) | (99.3%, 99.9%) |
| Parainfluenza virus 4 | Prospective | 100.0% (1/1) | (20.7%, 100.0%) | 100.0% (791/791) | (99.5%, 100.0%) | 100.0% (792/792) | (99.5%, 100.0%) |
| Parainfluenza virus 4 | Archived | 97.3% (36/37) | (86.2%, 99.5%) | 98.3% (337/343) | (96.2%, 99.2%) | 98.2% (373/380) | (96.2%, 99.1%) |
| Parainfluenza virus 4 | Overall | 97.4% (37/38) | (86.5%, 99.5%) | 99.5% (1128/1134) | (98.9%, 99.8%) | 99.4% (1165/1172) | (98.8%, 99.7%) |

Note: a = number of samples where both **cobas**[®] Respiratory flex and the comparator tests are positive; b = number of samples where **cobas**[®] Respiratory flex is negative and the comparator is positive; c = number of sample where **cobas**[®] Respiratory flex is positive and the comparator is negative; d = number of samples where both **cobas**[®] Respiratory flex and the comparator are negative; N = Total number of paired samples. PPA: Positive Percent Agreement. NPA: Negative Percent Agreement. OPA: Overall Percent Agreement.

RSV: respiratory syncytial virus, SARS-CoV-2: severe acute respiratory syndrome coronavirus 2

A total of 140 results showed discrepancy between the **cobas**^{*} Respiratory flex test and the respective comparator): of these, 113 results were positive by **cobas**^{*} Respiratory flex and negative by the comparator, while 27 results were negative by **cobas**^{*} Respiratory flex and positive with the comparator. Analysis of discrepant results of the 113 **cobas**^{*} Respiratory flex positive specimens after additional testing of the specimens by an alternative 510(k) cleared and CE-marked assay and/or DNA sequencing of the amplicons confirmed the presence of the target organisms in 104 specimens. In the remaining 9 samples discrepant results on **cobas**^{*} Respiratory flex were presumably low titer samples (Ct >30) (at or around the LoD of the candidate and comparator assays), where differences between analytical LoDs between methods can commonly lead to discrepancies.

Of the 27 **cobas**[•] Respiratory flex negative specimens, discrepant analysis was not possible for 1 sample due to limited sample volume. Discordant analysis testing was performed on the remaining 26 **cobas**[•] Respiratory flex negative specimens by an alternative 510(k) cleared and CE-marked NAAT. Discordant testing confirmed the initial **cobas**[•] Respiratory flex result in 16 samples and confirmed the results of the comparator test in 10 specimens.

Table 35 presents instances of multiple virus detection by **cobas**^{*} Respiratory flex. The most frequently identified combination, found in nine samples, was a combination of Adenovirus and Rhinovirus/Enterovirus. Out of these, six were also detected by a comparator test.

| Analyte 1 | Analyte 2 | Total Multiple Detections | Number of Specimen with False Positive Detections | False Positive Analyte(s) | |
|-----------------------------|-----------------------------|---------------------------------|--|--|--|
| Adenovirus | Rhinovirus/Enterovirus | 9 | 3 | Rhinovirus/Enterovirus (1), Adenovirus (2) | |
| Respiratory Syncytial Virus | Rhinovirus/Enterovirus | 8 | 3 | Rhinovirus/Enterovirus (2), Respiratory Syncytial Virus (1) | |
| Adenovirus | Respiratory Syncytial Virus | 6 | 5 | Adenovirus (5) | |
| Human Parainfluenza 1 | Rhinovirus/Enterovirus | 6 | 3 | Rhinovirus/Enterovirus (1), Human Parainfluenza 1 (2) | |
| Coronavirus | Influenza A | 5 | 3 | Influenza A (1), Coronavirus (2) | |
| Coronavirus | Respiratory Syncytial Virus | 5 | 4 | Coronavirus (4), Respiratory Syncytial Virus (1) | |
| Coronavirus | Rhinovirus/Enterovirus | 5 | 4 | Coronavirus (4), Rhinovirus/Enterovirus (1) | |
| Adenovirus | Coronavirus | 4 | 2 | Adenovirus (2) | |
| Adenovirus | Human Metapneumovirus | 3 | 1 | Adenovirus (1) | |
| Coronavirus | Human Metapneumovirus | 3 | 1 | Coronavirus (1) | |
| Coronavirus | Human Parainfluenza 3 | 3 | 2 Coronavirus (2) | | |
| Coronavirus | SARS-CoV-2 | 3 | 1 | Coronavirus (1) | |
| Human Parainfluenza 1 | Influenza A | 3 | 2 | Human Parainfluenza 1 (2) | |

Table 35 Multiple virus detection (≥ 3 instances) by **cobas**[®] Respiratory flex

Note: False positive is when a sample is detected by **cobas**[®] Respiratory flex but not detected by the comparator.

Additional information

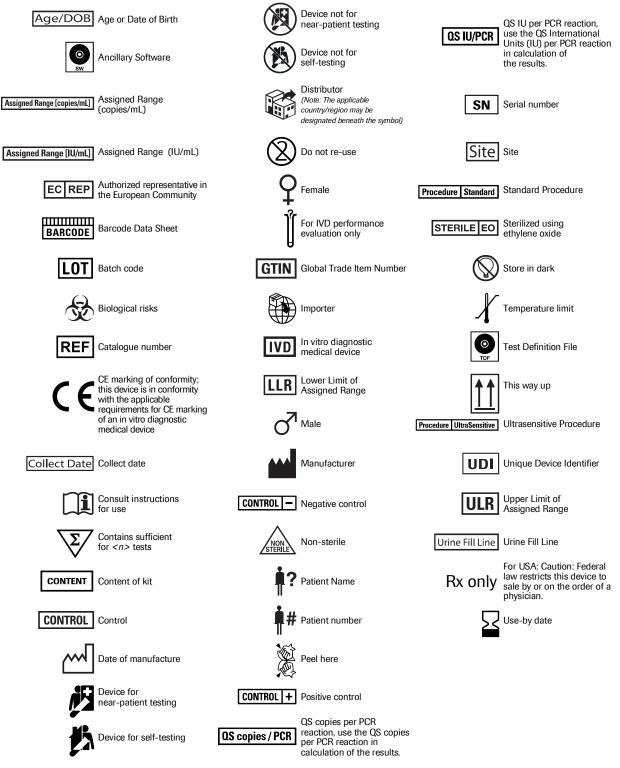
Key test features

| | Nasopharyngeal swab samples collected in the Copan UTM-RT [®] System or the BD [™] UVT System or equivalent diluted in cobas[®] MIS |
|---------------------------|---|
| Amount of sample required | 1.2 mL (0.4 mL patient sample diluted in 0.8 mL cobas ® MIS) |
| Sample processing volume | 0.85 mL |

Symbols

The following symbols are used in labeling for Roche PCR diagnostic products.

Table 36 Symbols used in labeling for Roche PCR diagnostics products



Technical support

For technical support (assistance) please reach out to your local affiliate: https://www.roche.com/about/business/roche_worldwide.htm

Manufacturer and importer

Table 37 Manufacturer and importer



Roche Molecular Systems, Inc. 1080 US Highway 202 South Branchburg, NJ 08876, USA www.roche.com

Made in USA



Roche Diagnostics GmbH Sandhofer Strasse 116 68305 Mannheim, Germany

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Document revision

| Document Revision Information | | | |
|-------------------------------|---|--|--|
| Doc. Rev. 1.0 08/2024 | First publishing. | | |
| Doc. Rev. 2.0 02/2025 | Updated IFU for x800 claim extension. Removed Rx Only from front page. Updated the harmonized symbol page. Adaptation of Table 18 : Probit and confidence Interval for Rhinovirus B and Human Parainfluenza 2. | | |
| | Adaptation of Table 28 : Hit rate for Human Rhinovirus Type 16. Corrected typos throughout the IFU. Added system software version 2.0 information for cobas [®] 6800/8800 systems. | | |
| | P/Ns of consumables removed, detailed information on consumables are referenced in the cobas [®] 5800 and cobas [®] 6800/8800 systems User Assistance. Please contact your local Roche Representative if you have any questions. | | |

The summary of safety and performance report can be found using the following link: https://ec.europa.eu/tools/eudamed